Rational Design and Application of DNA Origami Tessellation

by

Yue Tang

A Dissertation Presented in Partial Fulfillment
of the Requirements for the Degree
Doctor of Philosophy

Approved April 2023 by the
Graduate Supervisory Committee:

Hao Yan, Chair
Jia Guo
Nicholas Stephanopoulos

ARIZONA STATE UNIVERSITY

May 2023

ABSTRACT

Molecular tessellation research aims to elucidate the underlying principles that govern intricate patterns in nature and to leverage these principles to create precise and ordered structures across multiple scales, thereby facilitating the emergence of novel functionalities. DNA origami technology enables the fabrication of nearly arbitrary DNA architectures with nanoscale precision, which can serve as excellent building blocks for the construction of tessellation patterns. However, the size and complexity of DNA origami tessellation systems are currently limited by several unexplored factors relevant to the accuracy of essential design parameters, the applicability of design strategies, and the compatibility between different tiles. Here, a general design and assembly method are described for creating DNA origami tiles that grow into tessellation patterns with micrometer-scale order and nanometer-scale precision. A critical design parameter, interhelical distance (***D***), was identified, which determined the conformation of monomer tiles and the outcome of tessellation. Finely tuned ***D*** facilitated the accurate geometric design of monomer tiles with minimized curvature and improved tessellation capability. To demonstrate the generality of the design method, 9 tile geometries and 15 unique tile designs were generated. The designed tiles were assembled into single-crystalline lattices ranging from tens to hundreds of square micrometers with micrometer-scale, nearly defect-free areas readily visualized by atomic force microscopy. Two strategies were applied to further increase the complexity of DNA origami tessellation, including reducing the symmetry of monomer tiles and co-assembling tiles of various geometries. The designed 6 complex tilings that includes 5 Archimedean tilings and a 12-fold quasicrystal tiling yielded various tiling patterns that great in size and quality, indicating

the robustness of the optimized tessellation system. The described design and assembly approach can also be employed to create square DNA origami units for algorithmic self-assembly. As the square units assembled and expanded, they executed the binary function XOR, which generated the Sierpinski triangular pattern according to the predetermined instructions. This study will promote DNA-templated, programmable molecular and material patterning and open up new opportunities for applications in metamaterial engineering, nanoelectronics, and nanolithography.

ACKNOWLEDGMENTS

First and foremost, I would like to express my deepest gratitude to my research advisor, Dr. Hao Yan, for his unwavering support, encouragement, and invaluable guidance throughout the course of my Ph.D. journey. His insightful feedback, attention to detail, and dedication to excellence have inspired me to become a better researcher and academic. I am truly fortunate to have had the opportunity to learn from such a distinguished mentor.

I would also like to extend my heartfelt thanks to my dissertation committee members: Dr. Nicholas Stephanopoulos, and Dr. Jia Guo, for their insightful suggestions, and patience in reviewing my work in the past few years. Their expertise helped me to improve contents of this dissertation and shaped my research in this complex field of study.

I would like to acknowledge the contributions to my colleague Dr. Shuoxing Jiang who guided me to the new research area and gave me valuable insights and advice. I am grateful to my collaborators, especially those from the Center for Molecular Design and Biomimetics: Dr. Xiaodong Qi, Dr. Fei Zhang, Dr. Petr Šulc, Dr. Xu Zhou, Hao Liu, Liangxiao Chen and Lu Yu, for their stimulating discussions and suggestions on my research and career. I thank Leeza Abraham, Dr. Swarup Dey, Dr. Minghui Liu, Dr. Michael Matthies, Dr. Erik Poppleton, Dr. Raghu Pradeep, Abhay Prasad, Deeksha Satyabola, Dr. Guangbao Yao, Dr. Yang Xu, and Rong Zheng for their advice and supports through years that made my time both enjoyable and academically fulfilling.

My sincere appreciation goes to my friends and peers, who have been my pillars of strength during challenging times, providing me with the necessary motivation whenever

needed. I am particularly grateful for the friendship and support of Dr. Zhaoqing Yan and Jin Li who have shared this journey with me from the beginning.

Last but certainly not least, I owe my deepest gratitude to my family. To my parents, for instilling in me the values of perseverance, and humility, and for their unwavering belief on me. And finally, to my wife and daughter, for their love and support throughout this journey. This achievement would not have been possible without you all.

TABLE OF CONTENTS

Page

LIST OF FIGURES

Figure Page

Figure Page

Figure Page

CHAPTER 1

INTRODUCTION: STRUCTURAL DNA NANOTECHNOLOGY

1.1 Introduction of self-assembly

Self-assembly refers to the autonomous formation of organized structures from constituent components without human intervention[1-3]. This process typically transitions a system from a disorganized state to an ordered state and can manifest at various scales, ranging from molecular to planetary levels, with a multitude of interaction types[4]. Self-assembly is pervasive in nature and living systems, as evidenced by the DNA's double helix structure, protein aggregation and folding, and the organization of cells and living organisms, all of which are consequences of molecular self-assembly. During self-assembly, structural units spontaneously organize or aggregate into stable structures exhibiting specific geometric patterns, primarily driven by non-covalent bond interactions[1]. These organized structures often possess properties and functions that individual molecules or rudimentary molecular aggregates lack. Consequently, it is crucial to investigate the assembly of weak interactions within and between molecular aggregates at various levels, forming stable and ordered higher-level structures through synergistic effects[5]. Elucidating the relationship between molecular structure and higher-level molecular aggregate structure, as well as the interdependence of aggregate structure on its properties is essential. This understanding will enable the uncovering of the fundamental principles governing the multi-level construction of substances.

The bottom-up approach is a crucial aspect of nanotechnology, allowing the creation of new structures, materials, and functions at the nanoscale by utilizing single atoms or molecules[6]. Self-assembly technology, an essential method within the bottom-up

approach, has enabled scientists to obtain various self-assembled structures while continuously uncovering their principles and rules[1]. Traditional processing techniques (top-down approach) are often inadequate or even unfeasible when attempting to build devices using atoms or nanoscale functional aggregates as building blocks (bottom-up approach). By leveraging the weak interactions between these building blocks to facilitate automatic assembly, it becomes possible to develop new structures or materials with specific functions that cater to diverse needs[7]. This highlights the methodological significance and unique functionality of self-assembly, enabling the production of materials unattainable through conventional chemical synthesis or processing techniques[8]. Nevertheless, self-assembled structures are influenced by various factors, including solvent, assembly environment, and temperature, all of which significantly impact the final assembled product[9]. Due to the complexity of the assembly process, the principles governing self-assembly continue to be investigated and explored.

1.2 Structure of DNA

Nucleic acids, which store and transmit genetic information, encompass both deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). DNA (Figure 1.1), as the primary genetic material, contains nearly all the genetic information of organisms. In 1953, advances in X-ray crystal diffraction technology enabled researchers to obtain accurate images reflecting DNA's structural characteristics. Based on this information, James Watson and Francis Crick, working at the Cavendish Laboratory at the University of Cambridge, inferred the double-helix structure of the DNA molecule[10]. Over the following three decades, advancements in DNA sequencing and synthesis technologies, coupled with ongoing progress in microscopic techniques, led to the realization that DNA

could serve as more than just a carrier of genetic information; it could also be an effective building material for nanoarchitecture. The potential for DNA as a tool for constructing nanostructures stems from its numerous advantageous properties, such as small scale, stable and flexible structure, sequencing, and ease of manipulation[11]. While RNA, peptide nucleic acid (PNA), and even proteins are frequently utilized in nanotechnology, DNA offers unique properties that set it apart from other biological macromolecules.

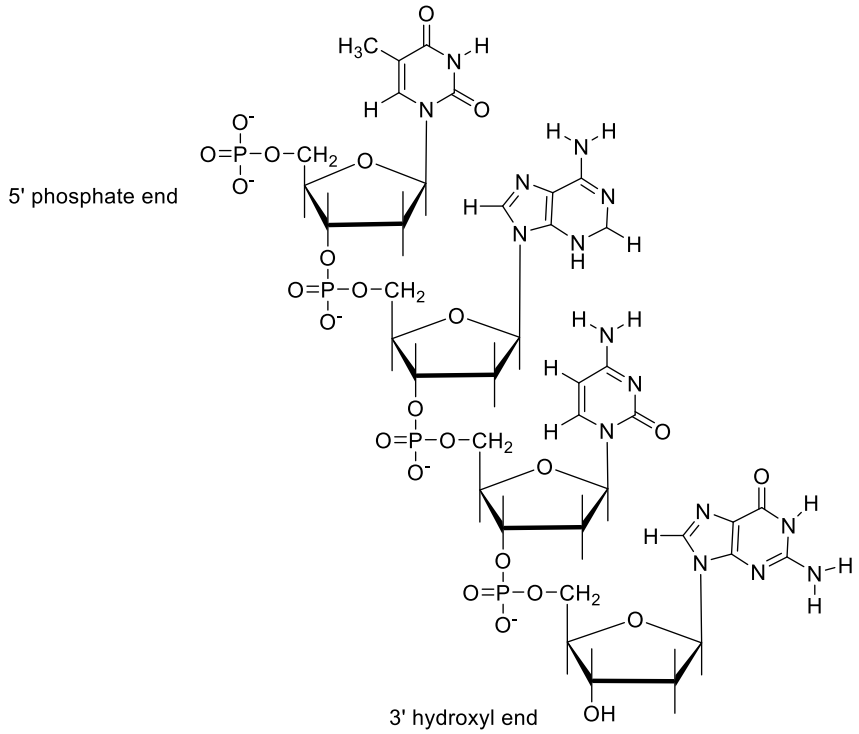

Figure 1.1. The primary structure of DNA.

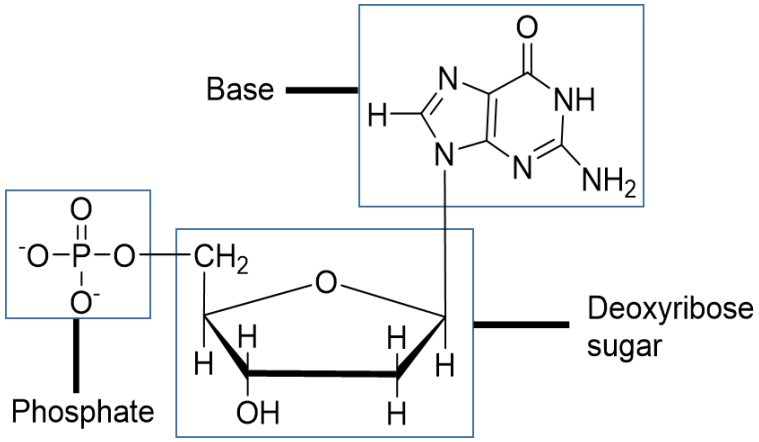

Figure 1.2. The structure of nucleotide.

DNA, an abbreviation for deoxyribonucleic acid, is a polymer consisting of multiple deoxyribonucleotides. Each nucleotide is composed of three components (Figure 1.2): a deoxyribose sugar (pentose sugar), a phosphate group, and a nitrogenous base[12].

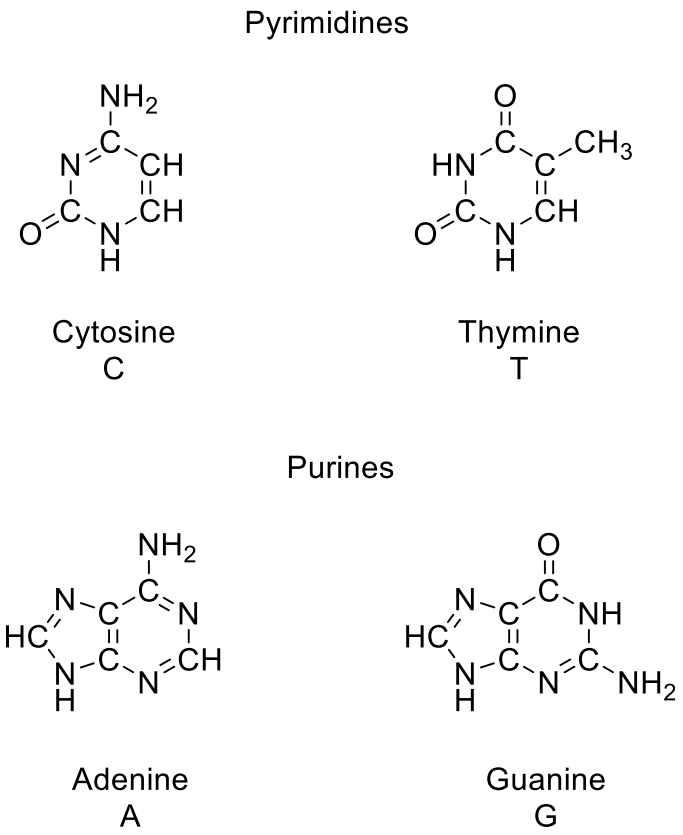

Figure 1.3. The structure of nitrogenous bases.

The bases are classified into two categories (Figure 1.3): the purine class, which includes adenine (A) and guanine (G), and the pyrimidine class, comprising cytosine (C) and thymine (T). Nucleotides are linked by phosphodiester bonds, formed through the covalent bonding of the 5'-phosphate group of one nucleotide with the 3'-hydroxyl group of another nucleotide. This bond exhibits directionality. Two single-stranded DNA molecules can combine in a reverse orientation to form a double-stranded structure via hydrogen bonds between base pairs. The base pairing principle dictates that one strand's A (or T) pairs with the other strand's T (or A), connected by two hydrogen bonds, while one strand's C (or G) pairs with the other strand's G (or C), held together by three hydrogen bonds.

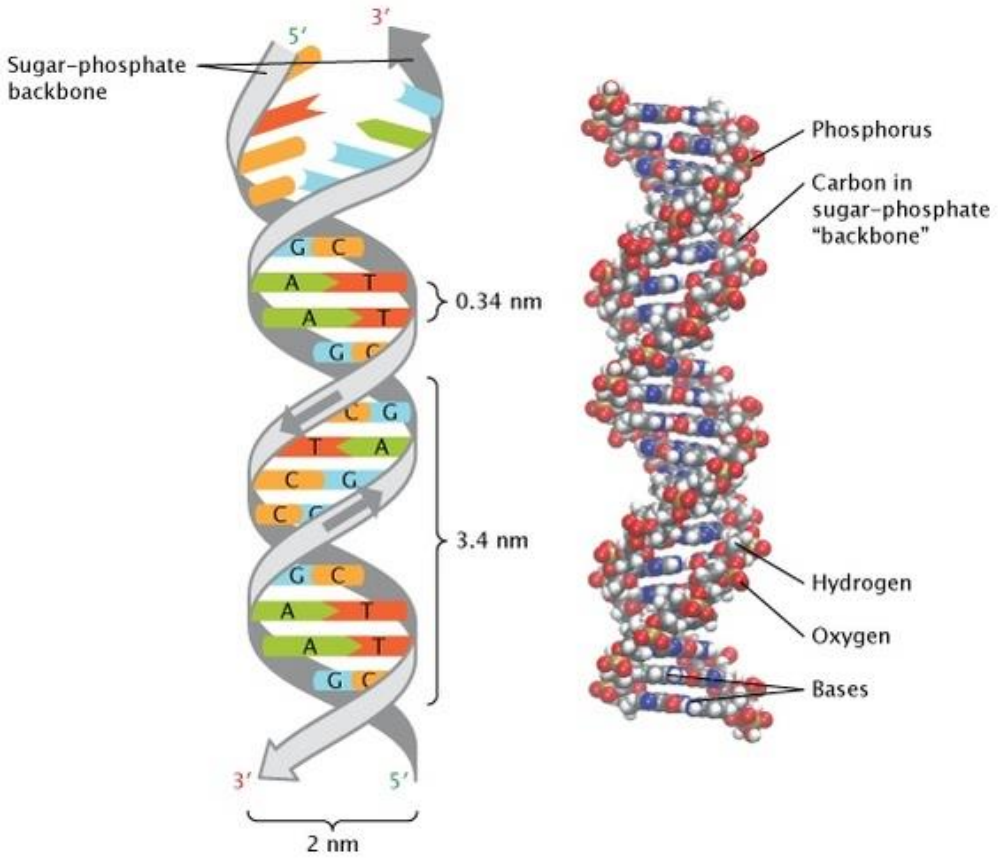

Figure 1.4. The double-helical structure of B-DNA[13].

1.3 DNA as a building material

DNA serves as an exceptional structural building material for constructing nanostructures, primarily due to its nanometer-scale structural geometry[14]. In most instances, two complementary DNA single strands combine, twisting to form a right-handed double helix structure known as B-DNA (Figure 1.4). The hydrophilic phosphate and sugar groups form the backbone, while the hydrophobic nitrogen-containing bases pair up with the base planes perpendicular to the helical axis. The helix features a major groove and a minor groove due to the base pairs' specific angle when forming hydrogen bonds. The B-DNA helix has a diameter of 2 nm, encompasses 10 base pairs per helical repeat, and has a helix pitch of 3.4 nm[12].

Secondly, the Watson-Crick base pairing principle allows for the predictable and programmable hybridization of DNA strands. Utilizing accumulated thermodynamic data, researchers can estimate the thermodynamic properties of a given DNA sequence and predict the hybridization energy of adenine-thymine (A-T) and cytosine-guanine (C-G) base pairs. Despite having only four types of bases, their permutations are virtually limitless. The DNA base sequence provides a means to store and encode vast amounts of information. With a DNA molecule N bases long, there are 4^N possible sequences capable of encoding 4^N distinct types of information[15]. Furthermore, the nanoscale size of DNA allows for high-density storage and encoding of information.

Thirdly, DNA structures exhibit a combination of rigidity and flexibility. Double-stranded DNA and single-stranded DNA possess distinct mechanical properties: double-stranded DNA is a rigid molecule, while single-stranded DNA is very flexible coiled-stranded. The elastic properties of DNA are also sequence-dependent; for instance, polythymine (poly T) is significantly softer than polyadenine (poly A)[16]. In fact, alternating between single and double strands and fully utilizing the staggered complementarity and partial complementarity of single strands are crucial design strategies in DNA nanotechnology[17]. Many self-assembled DNA structures can be regarded as a fusion of rigid structural components and flexible functional elements[18]. This characteristic enables the creation of various stable nanostructures and intricate nanodevices from DNA. Furthermore, advancements in organic chemistry and biology facilitate the synthesis, modification, and replication of any DNA sequence[14]. DNA is a biocompatible material that can be combined with other biological materials to construct

multi-component nanostructures, making it an exceptional building material for nanostructure construction[19].

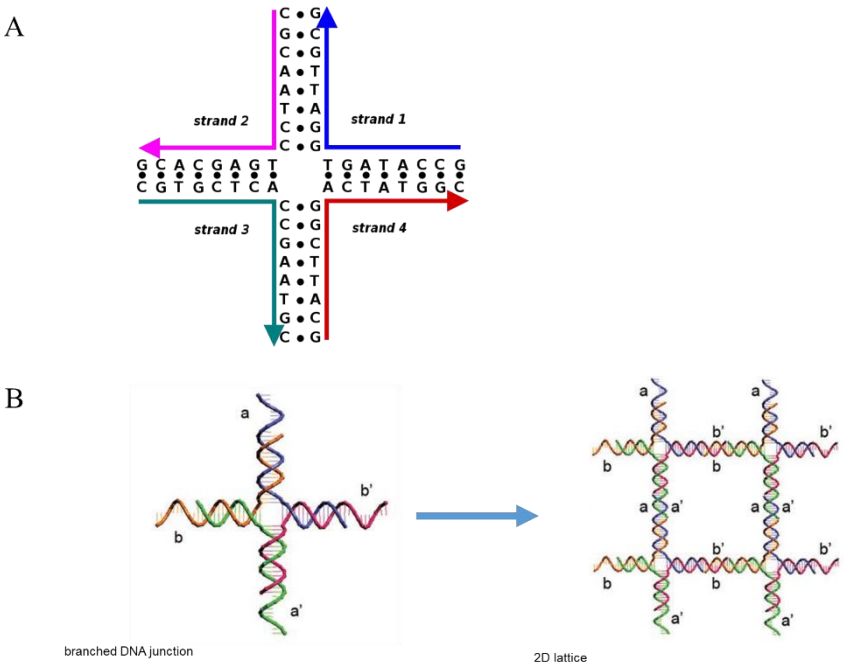

Figure 1.5. Foundation structures of structural DNA nanotechnology. (A) Structure of Holliday Junction[20]. (B) DNA junction structures in Seeman's original proposal[14].

1.4 Intro of DNA nanotechnology and tile self-assembly

The phenomenon of life serves as an inspiration for DNA self-assembly. In 1964, molecular biologist Robin Holliday discovered a unique DNA structural state[21] (Figure 1.5A). This state involves a cross structure formed by partial strand exchange between the double-stranded DNA of two homologous chromosomes, called the Holliday intermediate (Holliday junction). Natural Holliday intermediates can slide up and down along a pair of homologous DNA strands with the assistance of specific proteins, driven by ATP. This property holds significant implications for the preservation of genetic information and the recombination and variation of genes. In 1982, New York University chemist Nadrian C. Seeman suggested that DNA molecules could serve not only as genetic material but also as ideal nanoscale building blocks for constructing two-dimensional or three-dimensional structures[22] (Figure 1.5B). Geometric objects and periodic 2D or 3D lattices can be created using branched DNA junctions with complementary sticky-end cohesions. The fundamental building unit of the 2D DNA structure, known as a "DNA tile," is a four-arm-junction complex composed of four single-stranded DNA. Furthermore, the sequences of the four cohesive ends of each tile are specially designed, with 1 and 1' being complementary and 2 and 2' being complementary. A periodic two-dimensional DNA lattice can be constructed through complementary pairing between cohesive ends in different tiles. After over 30 years of exploration and hard work, Professor Seeman and his colleagues have constructed a variety of intricate DNA nanostructures, giving rise to a new field: structural DNA nanotechnology.

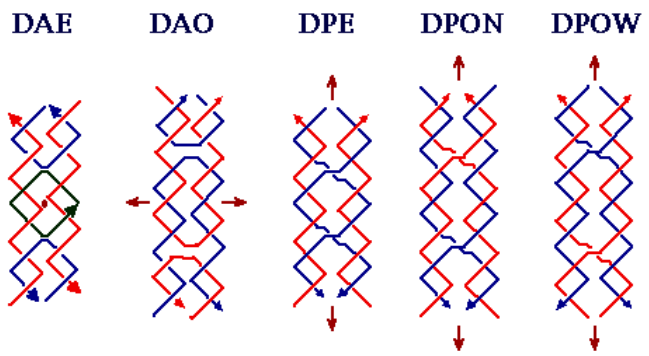

Figure 1.6. Schematic of the five different structural arrangements of double-crossover structures[23].

Although the "four-arm junction" may appear to exhibit four-way symmetry, it has been proven to possess only two-way symmetry. Building on this, the Seeman group developed double crossover (DX) tiles[23] (Figure 1.6), where each tile contains two intersections created by two double helices positioned side by side, comprising a total of 4 to 5 single strands. Seeman and Fu designed five DXs: DAE, DAO, DPE, DPON, and DPOW. In these abbreviations, D represents double crossover; A signifies the four chains forming the crossover point, with two consecutive chains in an antiparallel direction. Conversely, P indicates two consecutive chains at the crossover in the same direction, which is parallel. The letter O or E denotes whether an odd or even number of half helical turns are present in the double-crossover molecules, while W or N refers to a major (wide-groove) or minor (narrow-groove) separation between the crossovers. As DX tiles contain two relatively stable crossover structural units, their stiffness is twice that of general linear DNA double strands[24], enabling DX tiles to construct larger arrays. Li

initially used sticky ends to dock DX one-dimensionally and modified it with a hairpin loop[25]. Electrophoresis results revealed that all products were linear without cyclization. Winfree altered the crossover distances between DNA double helices, causing the two sticky ends of two tiles in the same direction to be translated and displaced[26]. This modification transformed the self-assembled structure from one-dimensional to two-dimensional.

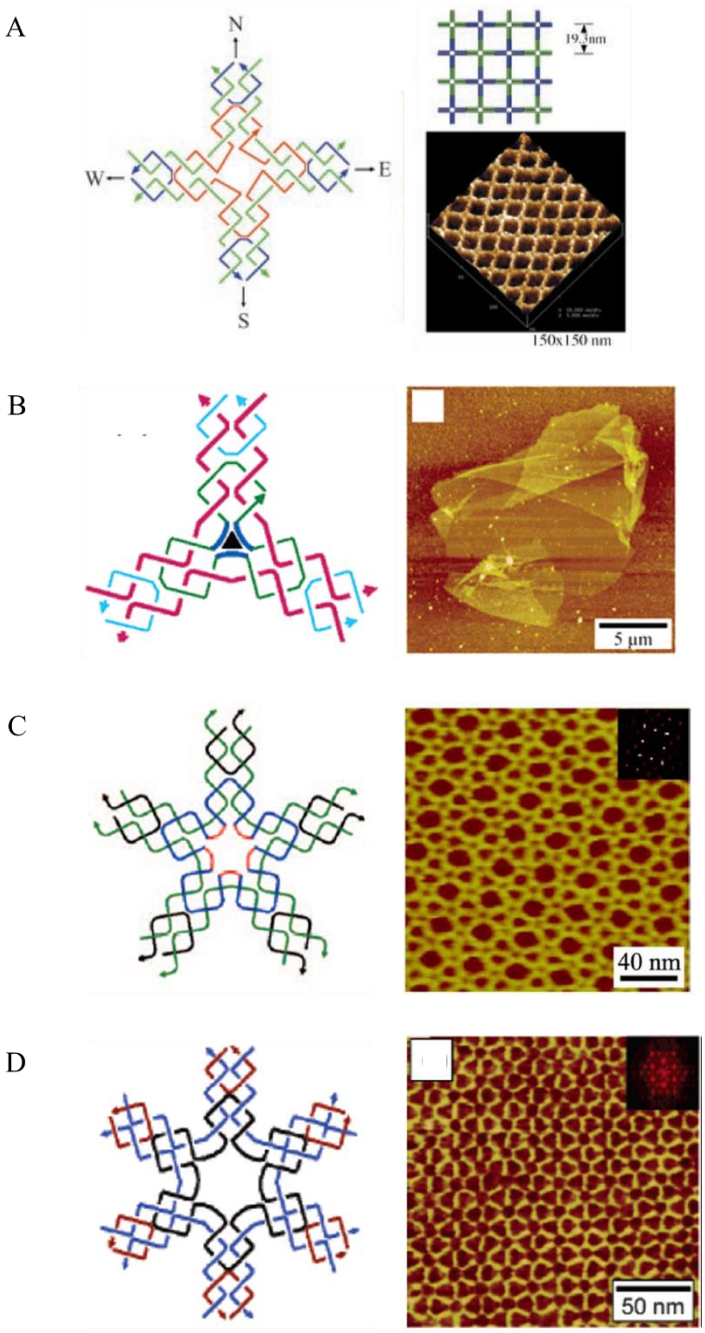

Figure 1.7. Multiarm DNA structural motifs. (A) 4 by 4 DNA tile[27]. (B) 3 by 4 DNA tile[28]. (C) 5 by 4 DNA tile[16]. (D) 6 by 4 DNA tile[29].

While DX tiles possess a stable structure, they only extend sticky ends in two directions for connection. In contrast, the four-armed junction DNA complex extends in four directions but is less stable. In 2003, Yan Hao integrated the features of these two

tiles and developed the 4 by 4 tile[27] (cross tile) (Figure 1.7A), which resembles a four-arm junction with an additional proprietary DNA strand on each arm. In this design, a central DNA strand binds with all four proprietary DNA strands from the four arms, totaling nine strands for the entire tile. Each arm contains a crossover, enhancing the overall structural stability. When sticky ends are extended from each end, a square lattice can form. This tile offers four codable orientations and more potential sticky ends. Chengde Mao designed each arm of the cross tile to have an identical sequence, resulting in complete symmetry. The 4-arm tile was expanded into 3/5/6-arm tiles[16, 28, 29] (Figure 1.7B-D), yielding a symmetrical tile series called N-point star DNA tiles, where N represents the number of tile arms. Each tile contains 2N+1 DNA strands according to this design. Due to the symmetry, only three types of DNA strands are needed to form each tile. The 3/4/6-point star DNA tiles were employed to assemble micron-scale arrays and construct symmetrical three-dimensional DNA structures with 3/5-pointed star DNA tiles.

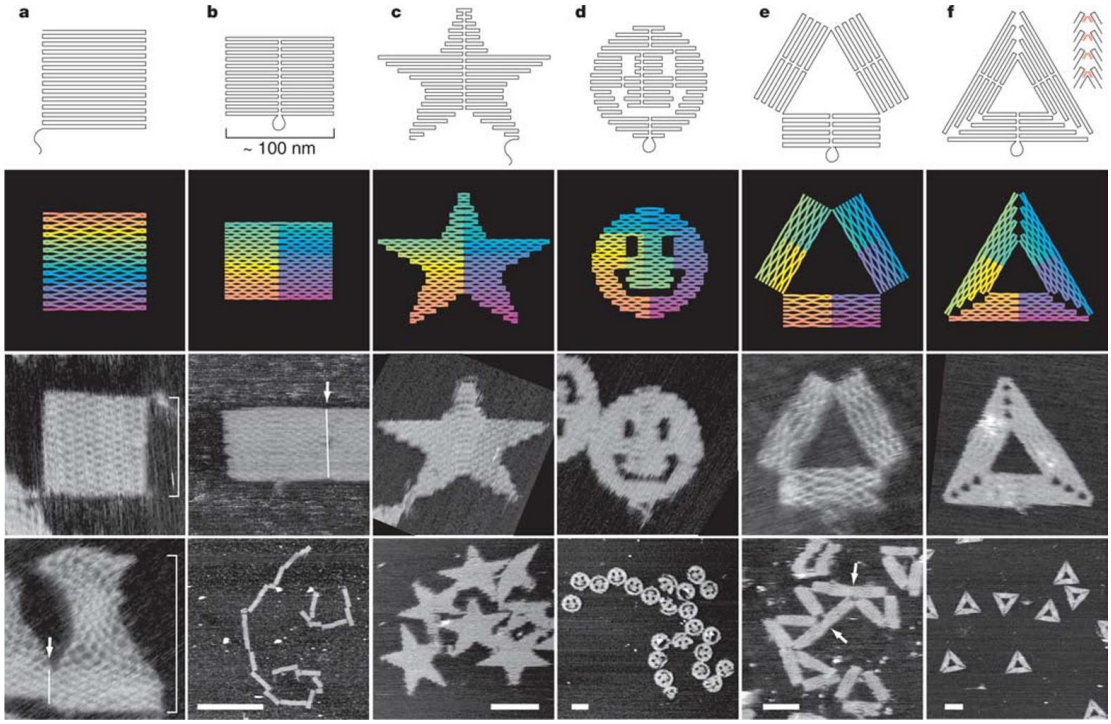

Figure 1.8. DNA origami structure and assembly.[30]

1.5 DNA origami

In 2006, Paul Rothemund introduced DNA origami[30] (Figure 1.8), marking a new era in DNA nanotechnology. Prior to this, DNA self-assembly was solely based on DNA tiles. DNA origami involves binding and folding a long DNA single strand into a specific shape, similar to folding a piece of paper. The long single-stranded DNA used is the M13mp18 phage, which is 7249 bases long and currently the most commercially available DNA single strand of this length, with no obvious sequence repeats in its domains. This long single-stranded DNA is also known as scaffold strands. Scaffold strands interact with short chains, called staple strands (or helper strands), which are divided into several segments complementary to specific parts of the long chain. When scaffold and helper strands are placed in solution and refolded, each helper strand acts like a staple, bringing together parts of the scaffold strands and guiding the spatial

configuration changes of the entire scaffold strand. By designing the binding position of each staple strand, the final scaffold strand can be folded into a specific shape. Rothemund's DNA origami design produced a solid figure rather than just a frame. Almost all bases in the scaffold strands are complemented by the staple strands, contributing to the stability and predictability of the product. To further ensure structural stability, crossover units fill the structure. The distance between adjacent crossovers is an integer multiple of the half-pitch, minimizing torsional force within the structure[30].

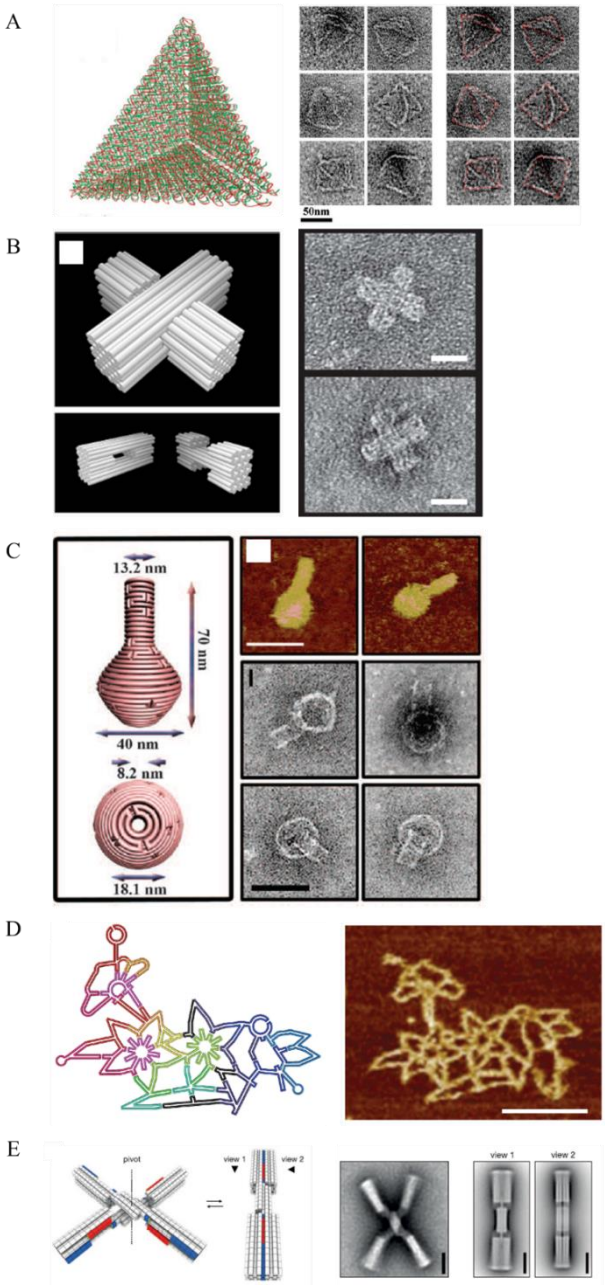

Figure 1.9. DNA origami nanostructures. (A) 3D caged DNA origami[31]. (B) 3D solid DNA origami[32]. (C) Curved DNA origami[33]. (D) Wireframe DNA origami[34]. (E) Dynamically reconfigurable DNA origami[35].

Utilizing DNA origami design, Rothemund successfully created a variety of structures, including polygons, seamed patterns, angled patterns, perforated patterns, and segmented patterns[30]. These DNA origami structures are approximately 100 nm in length

and width, with high product yields and unit sizes easily reaching 5 MDa. The experimental process for DNA origami is remarkably simple and convenient, in contrast to DNA tile assembly, which requires precise concentration ratios of each DNA strand and long-term annealing. The most significant advantage of DNA origami is the substantial increase in complexity and size of the assembled product. In recent years, numerous design strategies have been developed, resulting in a wide array of DNA origami structures and patterns (Figure 1.9), pushing the complexity of DNA origami to unprecedented levels. Following the proposal of these 2D DNA origami designs, researchers have also successfully developed 3D caged DNA origami[31], 3D solid DNA origami[32], curved DNA origami[33], wireframe DNA origami[34], and dynamically reconfigurable DNA origami[35].

1.6 Applications of DNA origami

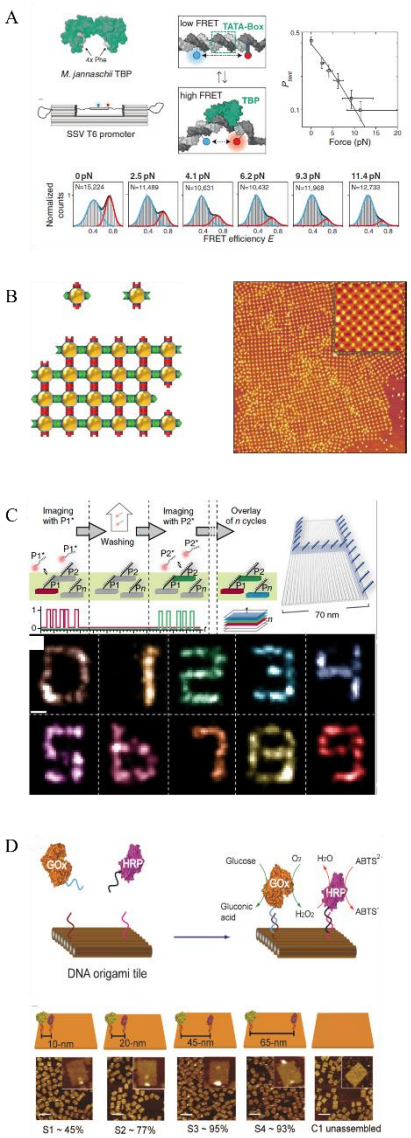

Figure 1.10. DNA origami for nanofabrication. DNA origami manufacture with (A) biomolecules[36], (B) nanoparticle synthesis[37], (C) nanolithography[38], and (D) artificial enzyme[39].

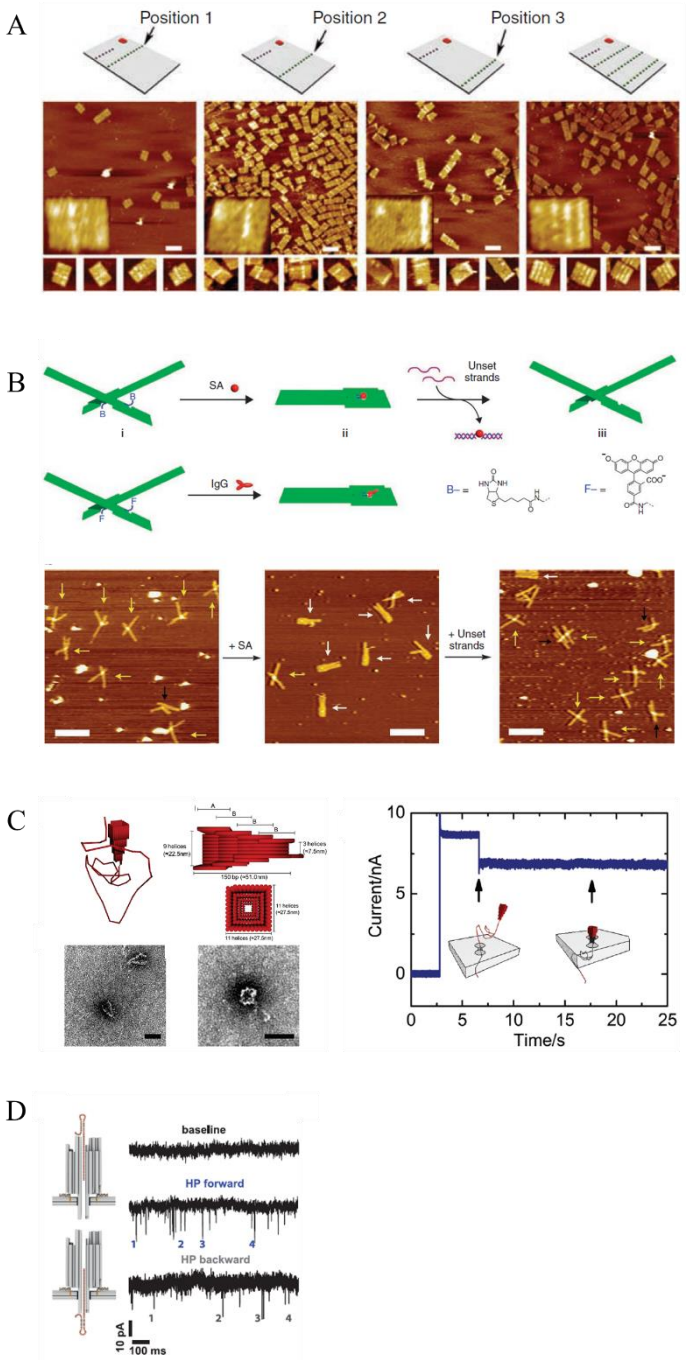

Figure 1.11. DNA origami for biosensing. DNA origami detection of (A) mRNA sequences[40] and (B) protein[41]. (C and D) DNA origami nanopore[42, 43].

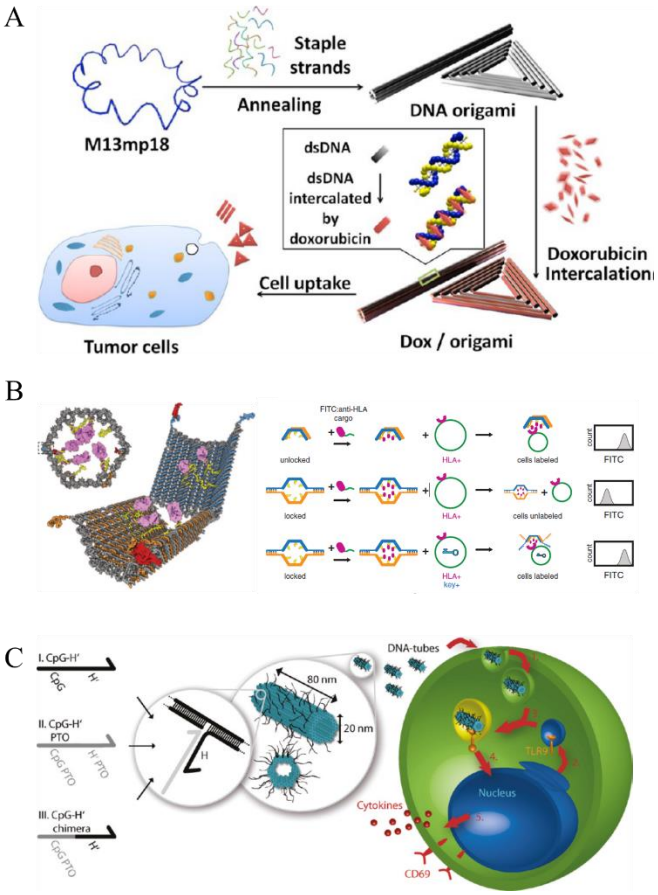

Figure 1.12. DNA origami for drug delivery. DNA origami carries (A) small molecules[44], (B) proteins[45], and (C) nucleic acids for therapy[46].

DNA origami's biological and structural features enable a wide range of applications[47], including but not limited to nanofabrication, biosensing, drug delivery, tessellation[48], and algorithmic operation[49]. DNA origami has been extensively used to create nanoscale constructs, serving as a template for biomolecule assembly[36] (Figure 1.10A), nanoparticle synthesis[37] (Figure 1.10B), nanolithography[38] (Figure 1.10C), and artificial enzyme production[39] (Figure 1.10D). In the realm of DNA origami biosensing, the addressability of DNA origami allows for precise placement of sensing elements[40, 41] (Figure 1.11A, B). In DNA origami nanopore technology, an analyte enters a thin membrane containing a single pore under an applied potential. This process enables

analyte sensing as the ion flow through the nanopore is altered[42, 43] (Figure 1.11C, D). DNA origami's biocompatibility, addressability, pattern and size complexity, and surface chemistry make it suitable for use as a delivery vehicle(Figure 1.12), carrying small molecules[44], proteins[45], and nucleic acids[46] for therapeutic purposes.

1.7 DNA origami tessellation

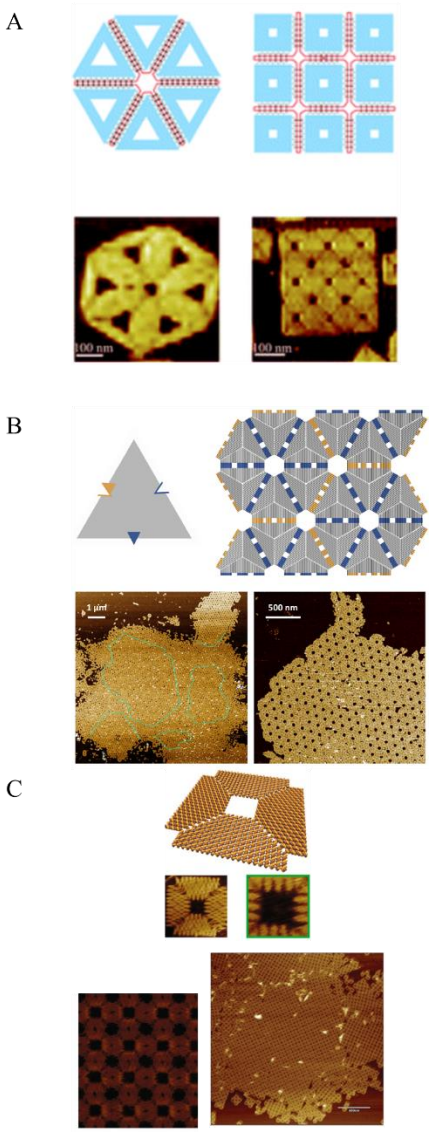

Figure 1.13. 2D DNA origami tessellation state of the art. DNA Origami tilings of (A) regular polygons by frames[50], (B) equilateral triangles[51] and (C) squares[52].

In DNA origami tessellation, there are two primary strategies for orienting DNA units. The first strategy involves organizing monomer origami within frames. As illustrated in Zhao's work[50] (Figure 1.13A), a DNA origami-based frame was designed to bind DNA origami units of different geometries, resulting in a limited-size array. The second strategy entails assembling individual origami into arrays using complementary sticky ends (Figure 1.13B, C). By employing this method, three regular polygons have been achieved using triangular[51], square[37, 52-54], and hexagonal wireframe DNA origami units[55]. The maximum lattice size attained is approximately 20 μm^2. DNA molecules are nanoscale in size and exhibit high operability. More importantly, their signal recognition and transmission capabilities are exceptional. The Watson-Crick base pairing principle ensures that the four types of DNA bases can form only two pairs: A-T and G-C. This characteristic makes DNA origami a suitable tool for algorithmic operations[56].

1.8 Challenges and Opportunities

The aim of molecular tessellation research is to understand the fundamental principles that govern intricate patterns in nature, from atomic to macroscopic scales, and leverage them to create precise and ordered structures across scales, enabling the emergence of novel functionalities. However, the lack of inherent modularity and customizable specificity in most molecular building blocks has limited the diversity and efficiency of tessellation dictated solely by their intrinsic self-organizing properties, necessitating the development of a versatile scaffolding material that simultaneously endows the target molecule with long-range order and local precision. DNA origami nanostructures are believed to be ideal building blocks for creating molecular scaffolds[57-59]. The characteristic programmability and addressability of DNA origami nanostructures

have enabled the rational design of nearly arbitrary DNA architectures and the precise arrangement of functional moieties on the tailored DNA templates[47, 60, 61]. However, limited by the length of the scaffold strand, the size of a DNA origami nanostructure is typically under 100 nm.

Significant efforts have been made in the past decade to scale up DNA origami into molecular patterns through hierarchical assembly[62-65]. However, the size and complexity that can be achieved by current DNA origami tessellation systems have been limited. For example, the area of single-crystalline lattices assembled from DNA origami tiles can hardly reach 20 mm^2 due to the excessive formation of nuclei and defects. Additionally, only the tilings of three regular polygons have been accomplished by DNA origami tessellation[51, 52, 55]. Direct co-assembly of size-compatible DNA origami tiles of distinct geometries into molecular patterns has been elusive.

To address these limitations, people need to understand what the general principles for the design of 2D DNA origami of arbitrary shapes for 2D tessellations are. Base on it to minimize the curvature, to control the angle and to tune the bond strength in the DNA origami self-assembly.

1.9 References

1. Whitesides, G. M.; Grzybowski, B., Self-assembly at all scales. *Science* **2002,** *295* (5564), 2418-2421.

2. Philp, D.; Stoddart, J. F., Self-assembly in natural and unnatural systems. *Angewandte Chemie International Edition in English* **1996,** *35* (11), 1154-1196.

3. Ball, P., The self-made tapestry: pattern formation in nature. **1999**.

4. Marth, J. D., A unified vision of the building blocks of life. *Nature cell biology* **2008,** *10* (9), 1015-1015.

5. Zhang, S., Fabrication of novel biomaterials through molecular self-assembly. *Nature biotechnology* **2003,** *21* (10), 1171-1178.

6. Li, J.; Ye, Q.; Cassell, A.; Ng, H. T.; Stevens, R.; Han, J.; Meyyappan, M., Bottom-up approach for carbon nanotube interconnects. *Applied Physics Letters* **2003,** *82* (15), 2491-2493.

7. Thiruvengadathan, R.; Korampally, V.; Ghosh, A.; Chanda, N.; Gangopadhyay, K.; Gangopadhyay, S., Nanomaterial processing using self-assembly-bottom-up chemical and biological approaches. *Reports on Progress in Physics* **2013,** *76* (6), 066501.

8. Whitesides, G. M.; Boncheva, M., Beyond molecules: Self-assembly of mesoscopic and macroscopic components. *Proceedings of the National Academy of Sciences* **2002,** *99* (8), 4769-4774.

9. Okesola, B. O.; Smith, D. K., Applying low-molecular weight supramolecular gelators in an environmental setting–self-assembled gels as smart materials for pollutant removal. *Chemical Society Reviews* **2016,** *45* (15), 4226-4251.

10. Watson, J. D.; Crick, F. H., Molecular structure of nucleic acids: a structure for deoxyribose nucleic acid. *Nature* **1953,** *171* (4356), 737-738.

11. Lund, K.; Williams, B.; Ke, Y.; Liu, Y.; Yan, H., DNA nanotechnology: a rapidly evolving field. *Current Nanoscience* **2006,** *2* (2), 113-122.

12. Ghosh, A.; Bansal, M., A glossary of DNA structures from A to Z. *Acta Crystallographica Section D: Biological Crystallography* **2003,** *59* (4), 620-626.

13. Pray, L., Discovery of DNA structure and function: Watson and Crick. *Nature Education* **2008,** *1* (1), 100.

14. Lin, C.; Liu, Y.; Rinker, S.; Yan, H., DNA tile based self-assembly: building

complex nanoarchitectures. *ChemPhysChem* **2006,** *7* (8), 1641-1647.

15. Smith, A., Nucleic acids to amino acids: DNA specifies protein. *Nature Education* **2008,** *1* (1), 126.

16. Zhang, C.; Su, M.; He, Y.; Zhao, X.; Fang, P. A.; Ribbe, A. E.; Jiang, W.; Mao, C., Conformational flexibility facilitates self-assembly of complex DNA nanostructures. *Proc Natl Acad Sci U S A* **2008,** *105* (31), 10665-9.

17. Seeman, N. C., An overview of structural DNA nanotechnology. *Mol Biotechnol* **2007,** *37* (3), 246-57.

18. Seeman, N. C., Nanomaterials based on DNA. *Annu Rev Biochem* **2010,** *79*, 65-87.

19. Bujold, K. E.; Lacroix, A.; Sleiman, H. F., DNA nanostructures at the interface with biology. *Chem* **2018,** *4* (3), 495-521.

20. Mao, C., The emergence of complexity: lessons from DNA. *PLoS Biol* **2004,** *2* (12), e431.

21. Holliday, R., A mechanism for gene conversion in fungi. *Genetics Research* **1964,** *5* (2), 282-304.

22. Seeman, N. C., Nucleic acid junctions and lattices. *J Theor Biol* **1982,** *99* (2), 237-47.

23. Fu, T. J.; Seeman, N. C., DNA double-crossover molecules. *Biochemistry* **1993,** *32* (13), 3211-20.

24. Sa-Ardyen, P.; Vologodskii, A. V.; Seeman, N. C., The flexibility of DNA double crossover molecules. *Biophys J* **2003,** *84* (6), 3829-37.

25. Li, X.; Yang, X.; Qi, J.; Seeman, N. C., Antiparallel DNA double crossover molecules as components for nanoconstruction. *Journal of the American Chemical Society* **1996,** *118* (26), 6131-6140.

26. Winfree, E.; Liu, F.; Wenzler, L. A.; Seeman, N. C., Design and self-assembly of two-dimensional DNA crystals. *Nature* **1998,** *394* (6693), 539-44.

27. Yan, H.; Park, S. H.; Finkelstein, G.; Reif, J. H.; LaBean, T. H., DNA-templated self-assembly of protein arrays and highly conductive nanowires. *Science* **2003,** *301* (5641), 1882-4.

28. He, Y.; Chen, Y.; Liu, H.; Ribbe, A. E.; Mao, C., Self-assembly of hexagonal DNA two-dimensional (2D) arrays. *J Am Chem Soc* **2005,** *127* (35), 12202-3.

29. He, Y.; Tian, Y.; Ribbe, A. E.; Mao, C., Highly connected two-dimensional crystals of DNA six-point-stars. *J Am Chem Soc* **2006,** *128* (50), 15978-9.

30. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

31. Ke, Y.; Sharma, J.; Liu, M.; Jahn, K.; Liu, Y.; Yan, H., Scaffolded DNA origami of a DNA tetrahedron molecular container. *Nano Lett* **2009,** *9* (6), 2445-7.

32. Douglas, S. M.; Dietz, H.; Liedl, T.; Högberg, B.; Graf, F.; Shih, W. M., Self-assembly of DNA into nanoscale three-dimensional shapes. *Nature* **2009,** *459* (7245), 414-418.

33. Han, D.; Pal, S.; Nangreave, J.; Deng, Z.; Liu, Y.; Yan, H., DNA origami with complex curvatures in three-dimensional space. *Science* **2011,** *332* (6027), 342-6.

34. Zhang, F.; Jiang, S.; Wu, S.; Li, Y.; Mao, C.; Liu, Y.; Yan, H., Complex wireframe DNA origami nanostructures with multi-arm junction vertices. *Nat Nanotechnol* **2015,** *10* (9), 779-84.

35. Gerling, T.; Wagenbauer, K. F.; Neuner, A. M.; Dietz, H., Dynamic DNA devices and assemblies formed by shape-complementary, non–base pairing 3D components. *Science* **2015,** *347* (6229), 1446-1452.

36. Nickels, P. C.; Wünsch, B.; Holzmeister, P.; Bae, W.; Kneer, L. M.; Grohmann, D.; Tinnefeld, P.; Liedl, T., Molecular force spectroscopy with a DNA origami–based nanoscopic force clamp. *Science* **2016,** *354* (6310), 305-307.

37. Liu, W.; Halverson, J.; Tian, Y.; Tkachenko, A. V.; Gang, O., Self-organized architectures from assorted DNA-framed nanoparticles. *Nature chemistry* **2016,** *8* (9), 867-873.

38. Jungmann, R.; Avendano, M. S.; Woehrstein, J. B.; Dai, M.; Shih, W. M.; Yin, P., Multiplexed 3D cellular super-resolution imaging with DNA-PAINT and Exchange-PAINT. *Nat Methods* **2014,** *11* (3), 313-8.

39. Fu, J.; Liu, M.; Liu, Y.; Woodbury, N. W.; Yan, H., Interenzyme substrate diffusion for an enzyme cascade organized on spatially addressable DNA nanostructures. *J Am Chem Soc* **2012,** *134* (12), 5516-9.

40. Ke, Y.; Lindsay, S.; Chang, Y.; Liu, Y.; Yan, H., Self-assembled water-soluble nucleic acid probe tiles for label-free RNA hybridization assays. *Science* **2008,** *319* (5860), 180-3.

41. Kuzuya, A.; Sakai, Y.; Yamazaki, T.; Xu, Y.; Komiyama, M., Nanomechanical DNA origami'single-molecule beacons' directly imaged by atomic force microscopy. *Nature communications* **2011,** *2* (1), 449.

42. Bell, N. A.; Engst, C. R.; Ablay, M.; Divitini, G.; Ducati, C.; Liedl, T.; Keyser, U. F., DNA origami nanopores. *Nano letters* **2012,** *12* (1), 512-517.

43. Langecker, M.; Arnaut, V.; Martin, T. G.; List, J.; Renner, S.; Mayer, M.; Dietz, H.; Simmel, F. C., Synthetic lipid membrane channels formed by designed DNA nanostructures. *Science* **2012,** *338* (6109), 932-6.

44. Jiang, Q.; Song, C.; Nangreave, J.; Liu, X.; Lin, L.; Qiu, D.; Wang, Z. G.; Zou, G.; Liang, X.; Yan, H.; Ding, B., DNA origami as a carrier for circumvention of drug resistance. *J Am Chem Soc* **2012,** *134* (32), 13396-403.

45. Douglas, S. M.; Bachelet, I.; Church, G. M., A logic-gated nanorobot for targeted transport of molecular payloads. *Science* **2012,** *335* (6070), 831-834.

46. Schuller, V. J.; Heidegger, S.; Sandholzer, N.; Nickels, P. C.; Suhartha, N. A.; Endres, S.; Bourquin, C.; Liedl, T., Cellular immunostimulation by CpG-sequence-coated DNA origami structures. *ACS Nano* **2011,** *5* (12), 9696-702.

47. Wang, P.; Meyer, T. A.; Pan, V.; Dutta, P. K.; Ke, Y., The beauty and utility of DNA origami. *Chem* **2017,** *2* (3), 359-382.

48. Tikhomirov, G.; Petersen, P.; Qian, L., Fractal assembly of micrometre-scale DNA origami arrays with arbitrary patterns. *Nature* **2017,** *552* (7683), 67-71.

49. Fan, S.; Cheng, J.; Liu, Y.; Wang, D.; Luo, T.; Dai, B.; Zhang, C.; Cui, D.; Ke, Y.; Song, J., Proximity-Induced Pattern Operations in Reconfigurable DNA Origami Domino Array. *Journal of the American Chemical Society* **2020,** *142* (34), 14566-14573.

50. Zhao, Z.; Liu, Y.; Yan, H., Organizing DNA origami tiles into larger structures using preformed scaffold frames. *Nano Lett* **2011,** *11* (7), 2997-3002.

51. Tikhomirov, G.; Petersen, P.; Qian, L., Triangular DNA Origami Tilings. *J Am Chem Soc* **2018**.

52. Aghebat Rafat, A.; Sagredo, S.; Thalhammer, M.; Simmel, F. C., Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities. *Nature chemistry* **2020,** *12* (9), 852-859.

53. Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C., Crystalline two-dimensional DNA-origami arrays. *Angew Chem Int Ed Engl* **2011,** *50* (1), 264-7.

54. Tikhomirov, G.; Petersen, P.; Qian, L., Programmable disorder in random DNA tilings. *Nat Nanotechnol* **2017,** *12* (3), 251-259.

55. Wang, P.; Gaitanaros, S.; Lee, S.; Bathe, M.; Shih, W. M.; Ke, Y., Programming Self-Assembly of DNA Origami Honeycomb Two-Dimensional Lattices and Plasmonic Metamaterials. *J Am Chem Soc* **2016,** *138* (24), 7733-40.

56. Andersen, E. S.; Dong, M.; Nielsen, M. M.; Jahn, K.; Lind-Thomsen, A.; Mamdouh, W.; Gothelf, K. V.; Besenbacher, F.; Kjems, J., DNA origami design of dolphin-shaped structures with flexible tails. *ACS Nano* **2008,** *2* (6), 1213-8.

57. Pinheiro, A. V.; Han, D.; Shih, W. M.; Yan, H., Challenges and opportunities for structural DNA nanotechnology. *Nat Nanotechnol* **2011,** *6* (12), 763-72.

58. Zhang, F.; Nangreave, J.; Liu, Y.; Yan, H., Structural DNA nanotechnology: state of the art and future perspective. *J Am Chem Soc* **2014,** *136* (32), 11198-211.

59. Seeman, N. C.; Sleiman, H. F., DNA nanotechnology. *Nature Reviews Materials* **2017,** *3* (1), 1-23.

60. Hong, F.; Zhang, F.; Liu, Y.; Yan, H., DNA Origami: Scaffolds for Creating Higher Order Structures. *Chem Rev* **2017,** *117* (20), 12584-12640.

61. Dey, S.; Fan, C.; Gothelf, K. V.; Li, J.; Lin, C.; Liu, L.; Liu, N.; Nijenhuis, M. A.; Saccà, B.; Simmel, F. C., DNA origami. *Nature Reviews Methods Primers* **2021,** *1* (1), 13.

62. Aghebat Rafat, A.; Pirzer, T.; Scheible, M. B.; Kostina, A.; Simmel, F. C., Surface-Assisted Large-Scale Ordering of DNA Origami Tiles. *Angewandte Chemie International Edition* **2014,** *53* (29), 7665-7668.

63. Woo, S.; Rothemund, P. W., Self-assembly of two-dimensional DNA origami lattices using cation-controlled surface diffusion. *Nat Commun* **2014,** *5*, 4889.

64. Suzuki, Y.; Endo, M.; Sugiyama, H., Lipid-bilayer-assisted two-dimensional self-assembly of DNA origami nanostructures. *Nature communications* **2015,** *6* (1), 8052.

65. Suzuki, Y.; Sugiyama, H.; Endo, M., Complexing DNA origami frameworks through sequential self-assembly based on directed docking. *Angewandte Chemie International Edition* **2018,** *57* (24), 7061-7065.

CHAPTER 2

DNA ORIGAMI TWO-DIMENSIONAL TESSELLATION

Adapted with permission from Yue Tang, Hao Liu, Qi Wang, Xiaodong Qi, Lu Yu, Petr Šulc, Fei Zhang, Hao Yan, Shuoxing Jiang. **DNA Origami Tessellations** (manuscript under review).

2.1 Abstract

Molecular tessellation research aims to elucidate the underlying principles that govern intricate patterns in nature and to leverage these principles to create precise and ordered structures across multiple scales, thereby facilitating the emergence of novel functionalities. DNA origami technology enables the fabrication of nearly arbitrary DNA architectures with nanoscale precision, which can serve as excellent building blocks for the construction of tessellation patterns. However, the size and complexity of DNA origami tessellation systems are currently limited by several unexplored factors relevant to the accuracy of essential design parameters, the applicability of design strategies. Here, a general design and assembly method were described for creating DNA origami tiles that grow into tessellation patterns with micrometer-scale order and nanometer-scale precision. A critical design parameter, interhelical distance (***D***), was identified, which determined the conformation of monomer tiles and the outcome of tessellation. Finely tuned ***D*** facilitated the accurate geometric design of monomer tiles with minimized curvature and improved tessellation capability. The generality of the design method was demonstrated by 9 tile geometries, 15 unique tile designs. The designed tiles were assembled into single-crystalline lattices ranging from tens to hundreds of square micrometers with micrometer-scale, nearly defect-free areas readily visualized by atomic

force microscopy. This study will promote DNA-templated, programmable molecular and material patterning and open up new opportunities for applications in metamaterial engineering, nanoelectronics, and nanolithography.

2.2 Introduction

Tessellation is a mathematical concept that involves the arrangement of geometric shapes to completely cover a plane without gaps or overlaps[1]. It appears in various natural and artificial structural forms, spanning scales from the atomic to the macroscopic. The study of tessellation not only helps elucidate the fundamental principles underlying the intricate patterns observed in these systems, but also enlightens the development of functional materials with desired properties. In particular, the tessellation of nanoscale building blocks, including colloidal nanoparticles[2, 3], organic compounds[4-6], and biomolecules[7-9] via bottom-up self-assembly provides a versatile means of engineering two-dimensional materials whose properties can be tailored by altering the long-range order or the local arrangement of constituent units, which has been the common focus of nanomaterials, supramolecular chemistry, and molecular science. Exotic properties can emerge from the ordered arrangements of functional modules that interact with and modulate electromagnetic waves[10, 11], electric[12] or magnetic fields[13, 14], and cells[9, 15], holding promise for applications in photonic crystals, plasmonic metamaterials, electronics, and bioactive materials. However, the lack of inherent modularity and customizable specificity in the majority of nanoobjects has limited the diversity and efficiency of tessellation dictated solely by their intrinsic self-organizing properties, necessitating the development of a versatile scaffolding material that simultaneously endows the target nanoobject with long-range order and local

precision. Programmable DNA self-assembly is advantageous in the fabrication of molecular scaffolds, as it features rational geometric design, nanoscale precision, and user-defined specificity encoded by Watson-Crick base pairing[16-18]. More importantly, the order and precision prescribed in the DNA scaffolds can be transferred to molecules or materials lacking self-organizing capability[19-22], significantly broadening the scope of material manufacturing.

Among various design strategies, the DNA origami technique[23], which involves folding a long single-stranded DNA (scaffold) by hundreds of short synthetic oligonucleotides (staples) into designed shapes, is exceptionally versatile in manufacturing delicate nanostructures. The characteristic programmability and addressability of DNA origami nanostructures have enabled the rational design of nearly arbitrary DNA architectures and the precise arrangement of functional moieties on the tailored DNA templates[24-26]. However, limited by the length of the scaffold strand, the size of a DNA origami nanostructure is typically under 100 nm. Great efforts have been made in the past decade to scale up DNA origami into molecular patterns via hierarchical assembly, either in solution[19, 27-31] or on a supported surface[32-35]. Several nontrivial design guidelines were identified, including curvature correction by matching rules[27, 29, 31], the preference of collective weak bonds[19, 29, 30], and the balance of structural flexibility and rigidity. These works also demonstrated the profound potential of DNA molecular patterns in metamaterial engineering[19] and single-molecule biophysical assays[31].

Further increasing the size and complexity of the molecular patterns assembled from DNA origami tiles has been challenging. In order to balance out the intrinsic curvature of monomer tiles, the majority of current DNA origami tessellation systems rely on

curvature-correcting matching rules that periodically alter the orientation of tiles via rotation[27, 29-31]. In contrast, those without curvature correction tend to form nanotubes or defect-prone polycrystalline lattices. Secondly, the area of single-crystalline lattices assembled from DNA origami tiles can hardly reach 20 μm^2 due to the excessive formation of nuclei and defects. Moreover, only the tilings of three regular polygons - equilateral triangles[30], squares[27-29, 31] and regular hexagons[19] - have been accomplished by DNA origami tessellation. It is as-yet unknown how to apply current tiling methods to low-symmetry tiles.

To address these limitations, here, we present a general approach for creating DNA origami tiles that self-assemble into tessellation patterns with increased size and complexity (Figure 2.1a). We ascribed the limited tessellation capability of DNA origami tiles to the curvature induced by suboptimal design parameters and identified interhelical distance (***D***) as a critical parameter determining the conformation of DNA origami tiles. A statistical analysis of the tile multimerization products revealed the optimal ***D*** range of 2.70 ± 0.05 nm. Finely tuned ***D*** facilitated accurate geometric design of DNA origami tiles, enabling the assembly of 15 tile designs of 9 different geometries into 9 unique tessellation patterns covering Platonic and Laves tilings. Crystalline lattices were obtained for all designs with micrometer-scale, nearly defect-free areas readily visualized by atomic force microscopy (AFM). Remarkably, without implementing any curvature correction mechanism, two regular polygonal designs produced single-crystalline lattices over 120 μm^2. As demonstrated by 6 Laves tiling patterns, the system stayed robust as tile symmetry reduced or as unique tile species increased, further increasing the complexity that could be achieved by DNA origami tessellation. This study exploited

finely tuned design parameters to generalize and optimize the construction of DNA origami tessellation patterns that could serve as a larger template for metamaterial engineering, nanolithography, and nanoelectronics.

2.3 Design workflow

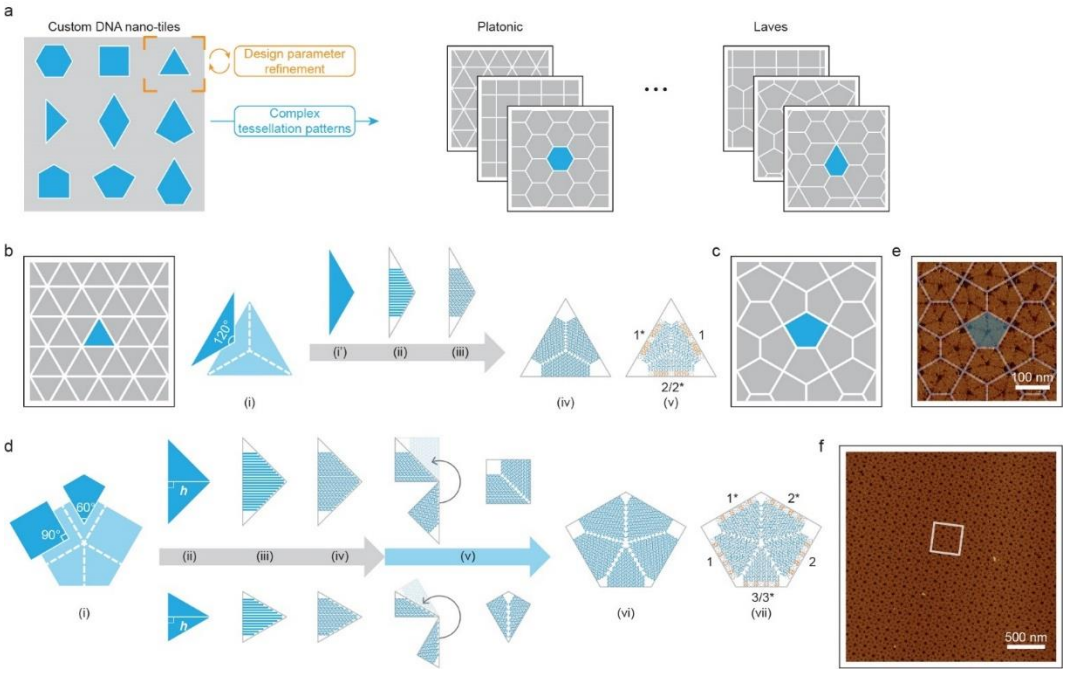

Figure 2.1. **Overview and the design workflow for DNA origami tessellation patterns.** (a) Overview of this study. Design parameters were refined based on equilateral triangular tiles and then generalized to tiles of other geometries. The enriched tile toolbox enabled various tessellation patterns, including Platonic and Laves tilings. (b) The design workflow for equilateral triangular tiling (left) involves five steps (i-v). (i) The monomer tile is split into three isosceles triangular subunits, each with a 120° vertex angle. This simplifies the design of the complete tile to the design of its subunit (i'). (ii) The subunit is depicted by evenly spaced, parallel line segments. (iii) The line segments are then converted into DNA double-helical domains. (iv) Three copies of the subunit are fitted together to create the prototypic tile. (v) The design is finalized by generating the scaffold strand (gray), core (blue), and edge (orange) staple strands, assigning sequences, and defining matching rules. (c) The Cairo pentagonal tiling is a pattern composed of tiles without rotational symmetry. (d) The design workflow for Cairo pentagonal tile involves a different splitting strategy and an additional reconfiguration step. (i) The monomer tile is split into two types of quadrilateral subunits, one is square and the other is kite-shaped. (ii) Both types of subunits can be derived from isosceles triangular subunits and sequentially converted into line segments (iii) and DNA double helices (iv) following a similar procedure used in the design of the equilateral triangular tile. (v) The isosceles triangular subunits in the form of DNA double helices are reconfigured to obtain the

desired quadrilateral subunits by rotating one-half of the subunit around its apex. (vi) Two copies of the square subunits and three copies of the kite-shaped subunits can be fitted together into the complete Cairo pentagonal tile. (vii) The design is finalized by generating the scaffold strand (gray), core (blue), and edge (orange) staple strands, assigning sequences, and defining matching rules. (e) A DNA origami tessellation pattern corresponding to the one in (c) is visualized by atomic force microscopy (AFM). The sample pattern is superimposed on the AFM image. Scale bar: 100 nm. (f) A zoomed-out AFM image showing the micrometer-scale order of the DNA origami tessellation pattern. The area corresponding to (e) is marked by a white box. Scale bar: 500 nm.

The workflow for designing regular tiling patterns involves five steps (Figure 2.1b, a more detailed workflow is provided in Figure 2.2). For example, in the case of equilateral triangular tiling, the repeating unit, an equilateral triangular tile, can be split into three identical isosceles triangular subunits sharing the centroid of the triangle (Figure 2.1b, i). The subunit can be represented by an even number of evenly-spaced, parallel line segments perpendicularly aligned at the base of the isosceles triangle (Figure 2.1b, ii). Since each line segment is a simplified model of a DNA duplex, their lengths are defined in an arithmetic progression manner in order to approximate the contour of the subunit and further rounded to integral numbers of base pairs. Next, line segments are converted to double-helical domains based on the structural features of B-DNA (Figure 2.1b, iii). Each nucleotide is abstracted into a point in Euclidean space with (x, y, z)-coordinates calculated. Three copies of the subunit are fitted together to create the prototypic tile (Figure 2.1b, iv), where the coordinates are used to calculate the lengths of single-stranded linkers for nucleotides to be connected in the subsequent steps. The tile design is finalized in Tiamat[36], a graphical user interface program for designing DNA nanostructures and sequences (Figure 2.1b, v). In this step, isolated double-helical domains are integrated into an intact DNA origami tile by adding single-stranded linkers,

crossover linkages, and nick points based on established DNA origami design principles. Matching rules are encoded by adding single-stranded overhangs (termed sticky ends) to selected staple strands on the edges of the tile. Edge staple strands that are not selected for presenting sticky ends are deleted, leaving the scaffold unpaired. This workflow generally applies to the design of regular polygonal tiles. One can customize the vertex angle, the number and lengths of constituent DNA double helices in the isosceles triangular subunit to obtain a range of regular polygonal tiles suitable for finite assemblies and tilings.

Generalizing the workflow to tile designs that lack rotational symmetry requires a different splitting strategy and an additional reconfiguration step. Taking Cairo pentagonal tiling (Figure 2.1c), a pattern that has not been achieved through DNA origami tessellation, as an example, we present a workflow for the modular design of DNA origami tiles with reduced symmetry (Figure 2.1d and Figure 2.5). Instead of splitting the geometry of interest into isosceles triangular subunits, an alternative strategy is taken to split the Cairo pentagon into two types of quadrilateral subunits (Figure 2.1d, i): one square and the other kite-shaped. Each subunit is derived from an isosceles triangular subunit, similar to those of regular polygons (Figure 2.1d, ii). The isosceles triangular subunits are sequentially converted into line segments (Figure 2.1d, iii) and DNA double-helical domains (Figure 2.1d, iv) following a similar procedure for designing regular polygonal tiles. Next, the subunits in the form of double helices are reconfigured from isosceles triangular into quadrilateral by rotating half of the helices about the apex of the original isosceles triangle (Figure 2.1d, v). The complete tile can be assembled from two copies of the square subunits and three copies of the kite-shaped

subunits (Figure 2.1d, vi) and finalized using Tiamat (Figure 2.1d, vii). To verify the tiling efficiency of the designed tile, the chemically synthesized staples and bacteriophage-derived scaffold are mixed in a buffer containing magnesium ions and subjected to a one-pot annealing process. As visualized by AFM, the designed DNA origami tessellation pattern exhibits nanometer-scale precision (Figure 2.1e) and micrometer-scale order (Figure 2.1f). The design method does not rely on the rotational symmetry of regular polygons and therefore is theoretically applicable to arbitrary convex polygonal tiles for tessellation.

2.4 Detailed design workflow

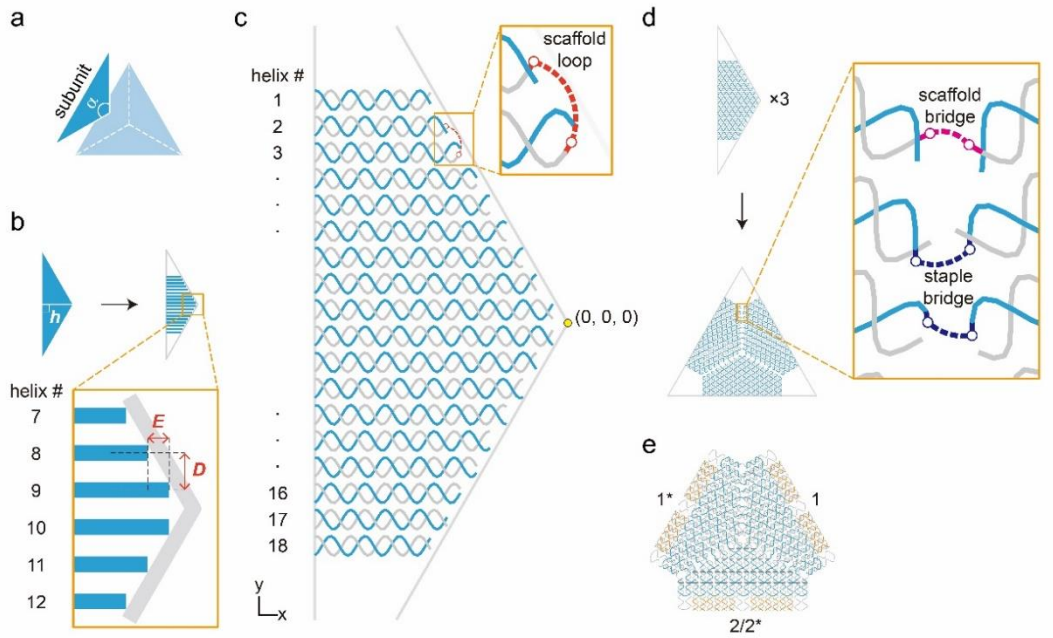

Figure 2.2. **Design workflow of p3120 equilateral triangular DNA origami tile.** (a) The tile of interest consists of three copies of a repeating subunit equivalent to an isosceles triangle with a 120° vertex angle (α). (b) Based on its dimension and geometry, the subunit is converted to an even number of regularly-spaced line segments perpendicularly aligned at the edge opposite to α. Each line segment is a simplified representation of a DNA double helix. Inset: Two parameters, interhelical distance (***D***) and helical extension (***E***), are defined to describe the distance between neighboring DNA helices and their difference in length, respectively. (c) Line segments are converted to double-stranded DNA in the Euclidean space based on the structural features of B-form DNA. The (0, 0, 0) point is assigned to the vertex of the subunit. Each nucleotide is abstracted into a point with (x, y, z)-coordinates calculated. The strands for creating the scaffold are gray-colored, while their complementary strands for creating staples are blue-colored. The distances between the two terminal nucleotides of the gray strands in the $(2j)^{th}$ and $(2j+1)^{th}$ duplexes (j = 1, 2, 3,…, 8) are calculated based on their (x, y, z)-coordinates to obtain the minimal lengths of single-stranded linkages (termed scaffold loops) connecting them. Inset: Illustration of an example scaffold loop connecting the terminal nucleotides (marked by red circles) of the gray strands in the second and third duplexes. (d) Three copies of the subunit are reoriented to constitute an equilateral triangle. Inset: Neighboring subunits are bridged by two types of single-stranded linkages. The scaffold bridge connects the two terminal nucleotides (marked by magenta circles) of the gray strands in the 1^{st} and the 18^{th} duplexes of two neighboring subunits, which allows the scaffold strand to travel from one subunit to another. The staple bridge connects the terminal nucleotides (marked by navy circles) of the blue strands in the 2^{nd} through the 17^{th} helices of two neighboring subunits. (e) With all design parameters calculated, the tile design is created using Tiamat[36], a design software tool for DNA

nanostructures, and finalized by generating the scaffold strand (gray), core (blue) and edge (orange) staple strands, assigning sequences to scaffold and staples, and defining the matching rule.

We take p3120 equilateral triangular tile as a representative example to introduce the detailed design workflow of regular polygonal tiles and the definition of design parameters. Though a similar workflow was reported previously, changes are made to improve the general applicability and tessellation outcome. Considering the 3-fold rotational symmetry, the design of a complete equilateral triangular tile can be simplified to the design of its repeating subunit, an isosceles triangle with a 120° vertex angle (α = 120°, Figure 2.2a). The subunit is first converted to an even number of regularly-spaced line segments perpendicularly aligned at the base of the isosceles triangle (Figure 2.2b). Each line segment is a simplified representation of a DNA double helix. In this case, there are 18 of them in the subunit (***H*** = 18). The compactness of DNA double helices is described by the interhelical distance (***D*** = 2.70 nm), which is the distance between the central axes of neighboring helices. The difference in length between neighboring double helices is described by the helical extension (***E***), ideally, which is associated with ***D*** through the tangent function.

$$tan\frac{\alpha}{2} = \frac{\boldsymbol{D}}{\boldsymbol{E}}$$

E can be further decomposed to the rise per base pair along the helical axis (***r***) multiplied by the average number of additional base pairs per helix ($\boldsymbol{n}_{\mathrm{bp}}$). Assuming **r** is 0.34 nm for B-form DNA, $\boldsymbol{n}_{\mathrm{bp}}$ can be calculated from ***D***.

$$\boldsymbol{n}_{bp} = \frac{\boldsymbol{E}}{\boldsymbol{r}} = \frac{\boldsymbol{D}}{\boldsymbol{r} \cdot tan\frac{\alpha}{2}} \approx 4.585\ bp$$

We number the line segments from 1 to 18 and assign 36 bp to the shortest one. The number of base pairs in the j^{th} helix can be calculated as follows and further rounded to an integral number.

If j is from 1 to 9,

$$Number\ of\ base\ pairs = 36 + (j-1)\boldsymbol{n}_{bp}$$

If j is from 10 to 18,

$$Number\ of\ base\ pairs = 36 + (\boldsymbol{H}-j)\boldsymbol{n}_{bp}$$

For this design, the number of base pairs in the 1^{st} through the 9^{th} double helices are 36, 41, 45, 50, 54, 59, 64, 68, and 73, respectively. The number of base pairs in the 10^{th} through the 18^{th} double helices are in reverse order (i.e., 73, 68, …, 41, 36). One can also assign the number of base pairs in the longest double helix and calculate the lengths of the rest similarly. The height ($\boldsymbol{h}$) of the subunit can be calculated from the longest double helix (73 bp). A small gap is added to prevent DNA helices from being crowded at the center of the tile.

$$\boldsymbol{h} = (73-1) \times 0.34 + gap$$

$$gap = \frac{\boldsymbol{D}}{tan\frac{\alpha}{2}}$$

Next, the (0, 0, 0) point is assigned to the vertex of the subunit, and the line segments are converted to DNA double helices in the Euclidean space based on the structural features of B-form DNA (Figure 2.2c) using parameters including $\boldsymbol{r}$ (0.34 nm/bp), the diameter of DNA double helix (2 nm), and the double-helical twist density (10.44 bp/turn). A 15° correction is introduced to unify the phases of neighboring helices. Each nucleotide is abstracted into a point with (x, y, z)-coordinates calculated. There are

two types of nucleotides, one for creating the scaffold strand and the other for creating the staples.

For the former, the (x, y, z)-coordinates of the i^{th} nucleotide in the j^{th} helix are as follows.

$$x = -\boldsymbol{h} + 0.34(i-1)$$

If j is odd,

$$y = \frac{\boldsymbol{D}-2}{2} + \left(\frac{\boldsymbol{H}}{2} - j\right)\boldsymbol{D} + (1 - \cos\left(\frac{360°(i-1)}{10.44} + 15°\right)$$

$$z = -\sin\left(\frac{360°(i-1)}{10.44} + 15°\right)$$

If j is even,

$$y = -\frac{\boldsymbol{D}-2}{2} + \left(\frac{\boldsymbol{H}}{2} - j + 1\right)\boldsymbol{D} - (1 - \cos\left(\frac{360°(i-1)}{10.44} - 15°\right)$$

$$z = \sin\left(\frac{360°(i-1)}{10.44} - 15°\right)$$

For the staple strand, the (x, y, z)-coordinates of the i^{th} nucleotide in the j^{th} helix are as follows.

$$x = -\boldsymbol{h} + 0.34(i-1)$$

If j is odd,

$$y = \frac{\boldsymbol{D}-2}{2} + \left(\frac{\boldsymbol{H}}{2} - j\right)\boldsymbol{D} + (1 - \cos\left(\frac{360°(i-1)}{10.44} + 150° + 15°\right)$$

$$z = -\sin\left(\frac{360°(i-1)}{10.44} + 150° + 15°\right)$$

If j is even,

$$y = -\frac{\boldsymbol{D}-2}{2} + \left(\frac{\boldsymbol{H}}{2} - j + 1\right)\boldsymbol{D} - \left(1 - \cos\left(\frac{360°(i-1)}{10.44} - 150° - 15°\right)\right.$$

$$z = \sin\left(\frac{360°(i-1)}{10.44} - 150° - 15°\right)$$

Three copies of the subunit are made, and a rotation matrix is used to rotate nucleotides in the xy-plane to assemble an equilateral triangle (Figure 2.2d).

$$\begin{bmatrix}\cos\theta & -\sin\theta \\ \sin\theta & \cos\theta\end{bmatrix}\begin{bmatrix}x \\ y\end{bmatrix} = \begin{bmatrix}x\cos\theta - y\sin\theta \\ x\sin\theta + y\cos\theta\end{bmatrix}$$

Single-stranded linkages are needed to integrate isolated DNA double helices into a complex structure. The distance between any two nucleotides to be connected can be calculated from their (x, y, z)-coordinates. For example, to connect a nucleotide at (x_1, y_1, z_1) to another nucleotide at (x_2, y_2, z_2), the linker length can be calculated as follows.

$$linker\ length = \frac{\sqrt{(x_1-x_2)^2 + (y_1-y_2)^2 + (z_1-z_2)^2}}{0.4} - 1$$

As illustrated in Figure 2.2c, the $(2j)^{th}$ helix is connected to the $(2j+1)^{th}$ helix (j = 1, 2, 3,…, 8) via a scaffold loop, which allows the scaffold strand to route back when reaching the boundary of the subunit. For this design, the lengths of scaffold loops are 7, 7, 7, 7, 6, 8, 9, and 9 nt, respectively.

As illustrated in Figure 2.2d, the 1^{st} helix of a subunit is connected to the $\boldsymbol{H}^{th}$ helix of its neighbor via a scaffold bridge, allowing the scaffold strand to travel from one subunit to another. The length of the scaffold bridge is 4 nt in this design. Moreover, the $(j+1)^{th}$ helix of a subunit is connected to the $(\boldsymbol{H}\text{-}j)^{th}$ helix of its neighbor (j = 1, 2, 3,…, 8) via a staple bridge. The lengths of staple bridges from the vertex to the center of the tile are 5, 5, 4, 2, 1, 0, 2, and 2 nt, respectively.

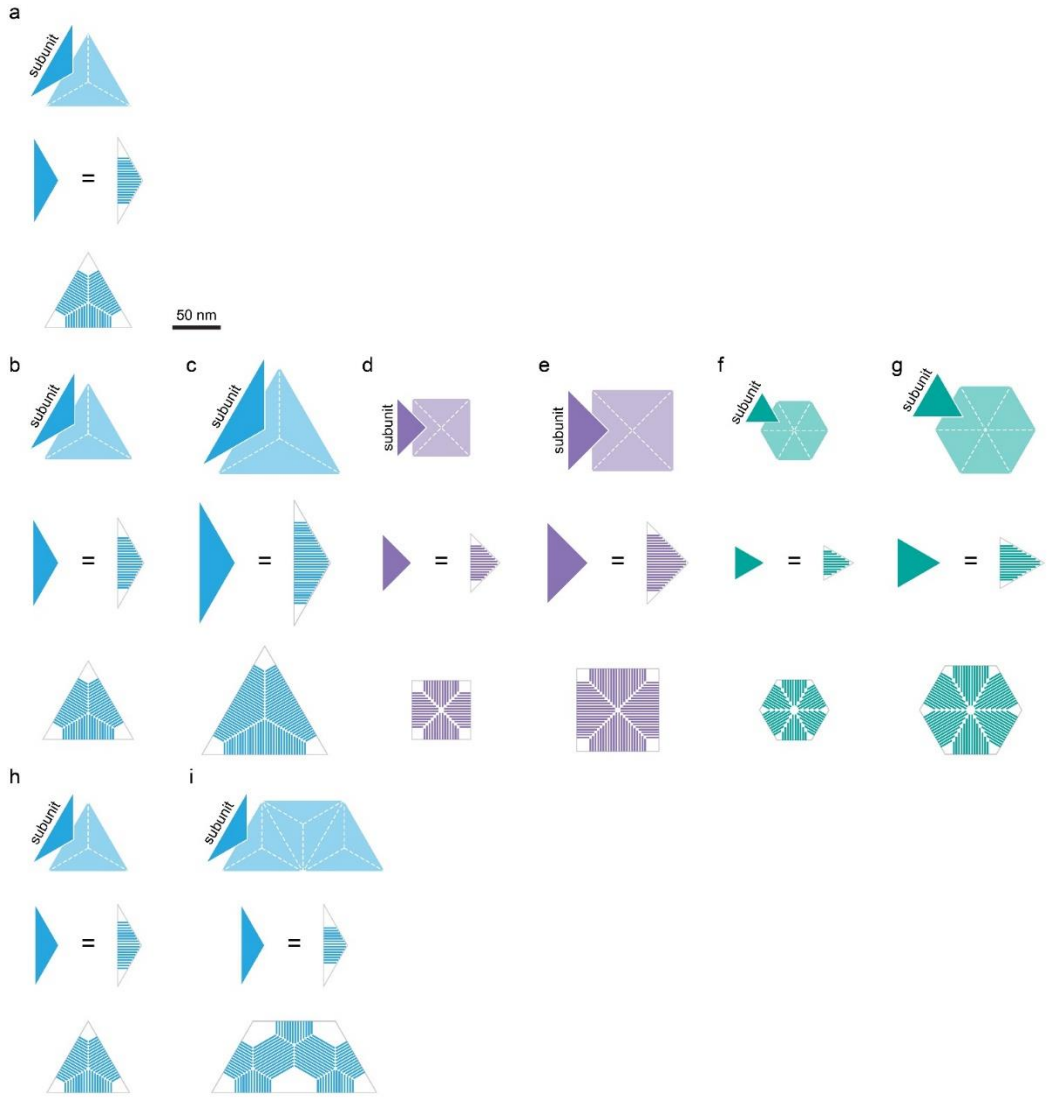

Figure 2.3. **Schematic illustrations of the isosceles triangular subunits of tiles for regular tilings.** (a) p3120 equilateral triangular tile, (b) p3548 equilateral triangular tile, (c) M13mp18 equilateral triangular tile, (d) p3548 square tile, (e) M13mp18 square tile, (f) p3548 regular hexagonal tile, (g) M13mp18 regular hexagonal tile, (h) p2820 equilateral triangular tile, and (i) M13mp18 half hexagonal tile. From top to bottom: schematic of the subunit composing a tile, a simplified illustration of DNA double helices composing the subunit (each line segment is a simplified representation of a DNA double helix), and a simplified illustration of the tile composed of double helices. Tile designs are colored differently based on their geometries. All tiles and subunits are drawn to scale. Scale bar: 50 nm.

With all design parameters calculated, the tile is created using Tiamat[36], a graphical user interface program for the design of DNA nanostructures and sequences, and finalized by generating the scaffold and staples, assigning sequences, and defining the matching rule (Figure 2.2e). The design workflow applies to equilateral triangular (α = 120°), square (α = 90°), and regular hexagonal (α = 60°) tiles. One can change the values of α, ***H***, and the length of the shortest /longest double helix to access a wide variety of DNA origami tile designs for regular tilings (Figure 2.3).

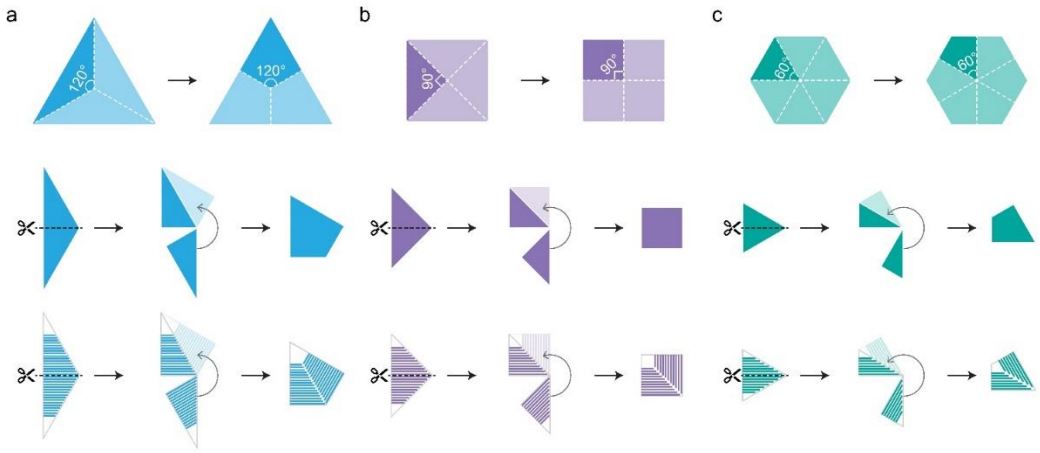

Figure 2.4. **Schematic illustrations of regular polygonal tiles composed of quadrilateral subunits.** (a) equilateral triangular, (b) square, and (c) regular hexagonal tiles. All tiles and subunits are drawn to scale. Scale bar: 50 nm.

Typically, tiles for regular tilings, including equilateral triangular, square, and regular hexagonal tiles (Figure 2.4), are decomposed into isosceles triangular subunits to simplify the design workflow. However, the isosceles triangular subunits for different tile geometries are not compatible with each other, making it difficult to generalize the design workflow to low-symmetry tiles. To address this limitation, we introduce an additional step in which the isosceles triangular subunits are transformed into quadrilateral ones by rotating half of the subunit about the apex of the isosceles triangle. The resultant

quadrilateral subunit occupies one corner of a regular polygon, whose internal angle pointing to the center of the tile is the same as the vertex angle of its isosceles triangular counterpart. More importantly, quadrilateral subunits for different tile geometries can be combined for the design of low-symmetry tiles.

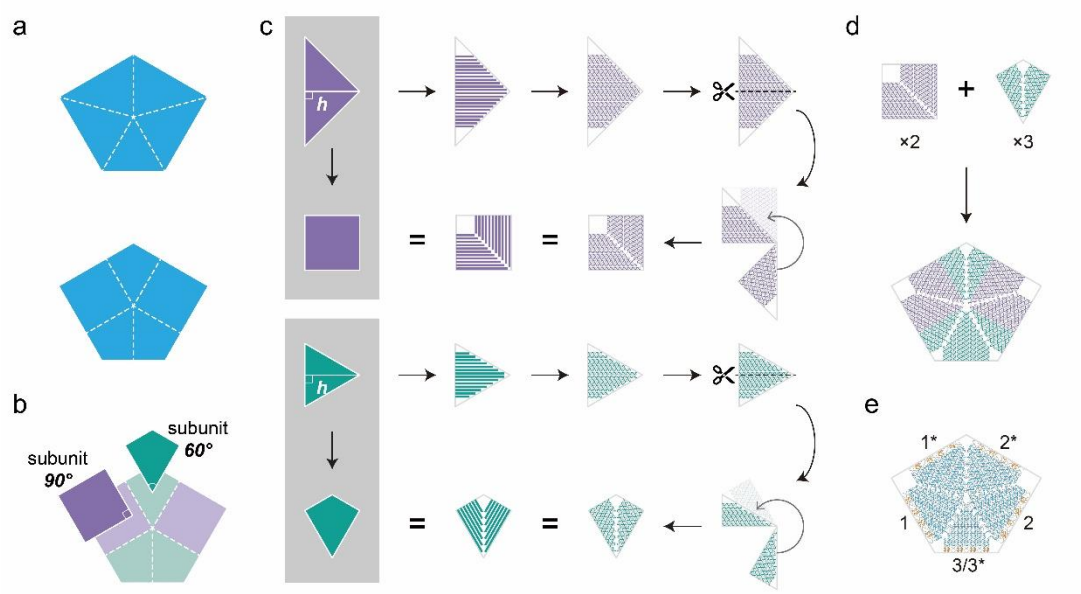

Figure 2.5. **Design workflow of M13mp18 Cairo pentagonal DNA origami tile.** (a) There are two ways to split the Cairo pentagon into subunits, at the vertices or at the edges. The former leads to five triangular subunits, while the latter leads to five quadrilateral subunits. Typically, the central point shared by all subunits is the center of the Cairo pentagon's incircle. Therefore, the second splitting strategy involves fewer unique subunits and is preferred for the design of low-symmetry tiles, including the Cairo pentagon and others. (b) The design of the Cairo pentagonal tile can be simplified to the design of two unique subunits, one is square (purple) and the other is kite-shaped (green), which are named ***90°*** or ***60°*** based on the degree of their vertex angle (i.e., the internal angle pointing to the center of the tile). (c) Both subunits are derived from isosceles triangular subunits analogous to those composing regular polygonal tiles. The isosceles triangular subunits are sequentially converted to line segments and DNA double helices following the procedure for designing regular polygonal tiles. Differently, the subunits in the form of double helices are split evenly into two halves. By rotating one-half of the subunit around the shared vertex using a rotation matrix, the desired square and kite-shaped subunits can be generated. In this step, design parameters, including the number and lengths of DNA double helices and the lengths of various single-stranded loops, are calculated separately for both subunits. (d) Two copies of the ***90°*** subunits and three copies of the ***60°*** subunits can assemble into the complete Cairo pentagonal tile. (e) With all design parameters calculated, the tile design is created using Tiamat and finalized by

generating the scaffold strand (gray), core (blue) and edge (orange) staple strands, assigning sequences to scaffold and staples, and defining the matching rule.

We take M13mp18 Cairo pentagonal tile as a representative example to introduce the design workflow of low-symmetry tiles for Laves tilings. Similar to the design of regular polygonal tiles, we start with the splitting of the Cairo pentagon into subunits (Figure 2.5a). Due to the lack of rotational symmetry, the strategy typically used for regular polygons gets complicated for low-symmetry tiles, as more unique triangular subunits are involved in the design. An alternative strategy is taken in which the geometry of interest is split into quadrilateral subunits by drawing perpendiculars from the center of the Cairo pentagon's incircle to each side. The Cairo pentagon is thus split into two types of quadrilateral subunits (Figure 2.5b), one is square and the other is kite-shaped. We name each subunit based on the degree of its internal angle pointing to the center of the tile (***90°*** for the square subunit and ***60°*** for the kite-shaped one). Despite the different geometries, both subunits are derived from isosceles triangular subunits composing regular polygonal tiles. The ***90°*** and ***60°*** subunits can be traced back to the subunit for a square tile ($\alpha = 90°$) and a regular hexagonal tile ($\alpha = 60°$), respectively (Figure 2.5c). Similar to the procedure for designing regular polygonal tiles, both isosceles triangular subunits are sequentially converted to line segments and DNA double helices. With the number of double helices in the subunit (***H***) and the length of the shortest/longest helix assigned, the length of each helix can be calculated and further converted to the (x, y, z)-coordinates of nucleotides, from which the lengths of scaffold loops can be calculated. Next, the subunits in the form of double helices are transformed from isosceles triangular into quadrilateral by rotating half of the helices about the apex of the original isosceles

triangle (Figure 2.5c). The resultant subunits have DNA double helices arranged in pairs, where the lengths of scaffold and staple bridges can be calculated. Although two subunits are designed and transformed separately, the following requirements must be met to ensure their compatibility, so that two copies of the ***90°*** subunits and three copies of the ***60°*** subunits can assemble into the complete Cairo pentagonal tile (Figure 2.5d).

1. Basic design parameters, including ***D***, ***r***, the diameter of DNA double helix, and the double-helical twist density, are shared by both subunits.

2. The same ***h*** is shared by both subunits.

3. The sum of ***H***s for both subunits must be a multiple of 4.

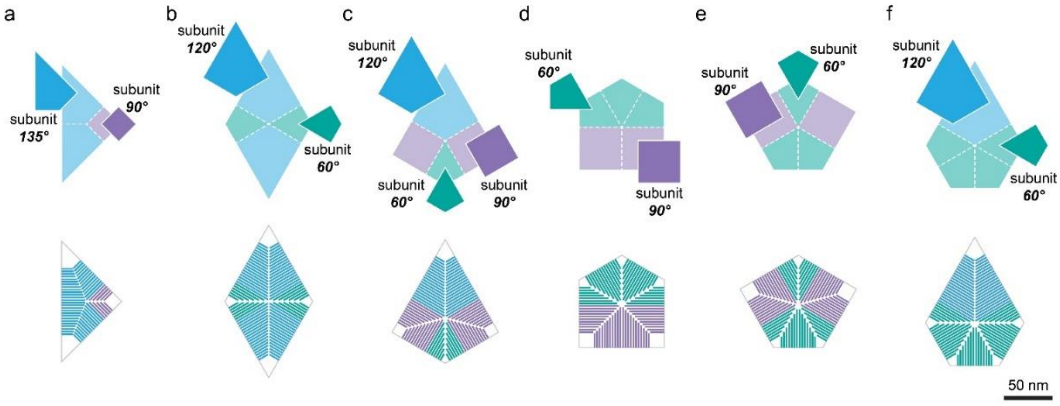

Figure 2.6. **Schematic illustrations of the subunits composing low-symmetry tiles.** Including (a) p3548 isosceles right triangular tile, (b) M13mp18 rhombic tile, (c) M13mp18 kite tile, (d) M13mp18 prismatic pentagonal tile, (e) M13mp18 Cairo pentagonal tile, and (f) p8064 floret pentagonal tile. Each low-symmetry tile is decomposed into subunits that are named based on the internal angle pointing to the center of the tile and colored differently based on their counterparts in regular polygonal tiles. All tiles and subunits are drawn to scale. Scale bar: 50 nm.

Finally, with all design parameters calculated for both subunits, the Cairo pentagonal tile is created using Tiamat and finalized by generating the scaffold and staples, assigning sequences, and defining the matching rule (Figure 2.5e). By applying the same design

workflow, other five low-symmetry tiles include p3548 isosceles right triangular tile, M13mp18 rhombic tile, M13mp18 kite tile, M13mp18 prismatic pentagonal tile and p8064 floret pentagonal tile are also designed for Laves tilings (Figure 2.6).

2.5 Interhelical distance as a critical design parameter

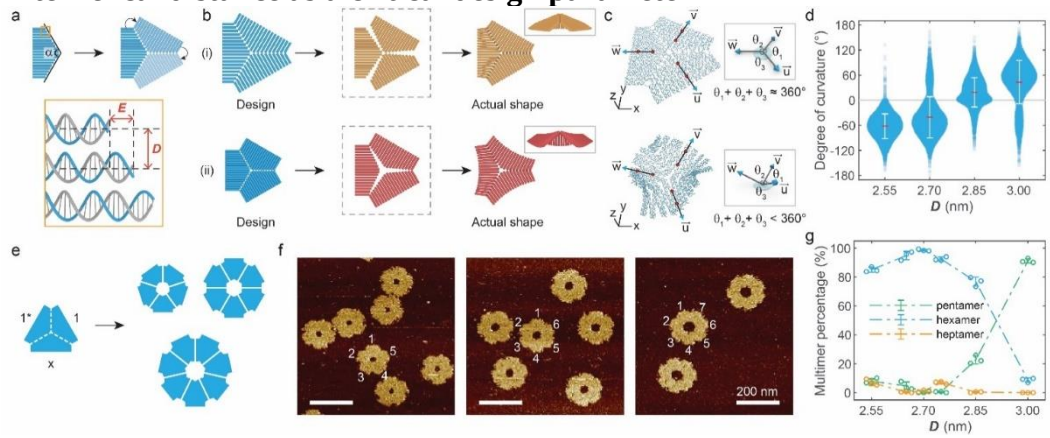

Figure 2.7. **Refining design parameters to minimize tile curvature.** (a) Given its 3-fold rotational symmetry, equilateral triangular tiles are usually designed by rotating a repeating subunit corresponding to one-third of the complete tile about the C_3 axis. Ideally, the vertex angle (α) of the repeating subunit is accurately 120° to ensure the flatness of the tile. Inset: Two design parameters, the interhelical distance (***D***) and helix extension (***E***), determine the shape and dimension of the repeating subunit and further the conformation of the tile. (b) There are two undesired situations when ***D*** is overestimated (i) or underestimated (ii) in the design process. In the actual tile, however, helices tend to adjust their spacing, from which tension can be generated (dashed box), resulting in a curved tile. Inset: Side view of the curved tile. (c) Tile conformations were studied by the oxDNA model. To quantitatively compare the curvature of different tile designs, three vectors, $\vec{u}$, $\vec{v}$, and $\vec{w}$, are defined. Each represents the helical direction of a repeating subunit. Inset: The sum of angles between each pair of vectors ($\theta_1 + \theta_2 + \theta_3$) can be exploited to quantify the curvature of a tile. (d) Curvature analysis of four equilateral triangular tiles designed based on ***D*** ranging from 2.55 to 3.00 nm with 0.15 nm intervals. The degree of curvature is defined as the deviation of ($\theta_1 + \theta_2 + \theta_3$) from 360° with plus or minus indicating the direction of curvature. The mean (red) and standard deviation (white) were also calculated for each design. (e) A mixture of multimeric complexes composed of 5-7 monomer tiles can be assembled from equilateral triangular tiles encoded with two edges complementary to each other (marked by 1 and 1*) and an inert third edge (marked by an "x"). The proportion of multimeric complexes can be exploited to deduce the curvature of tiles. (f) Representative AFM images of different multimeric complexes. From left to right: pentamers, hexamers, and heptamers. Scale bar: 200 nm. (g) A statistical analysis of multimer distribution as a function of ***D***. When ***D*** is in the range of 2.70 ± 0.05 nm, the percentage of hexamer can be as high as 99%.

Taking equilateral triangular tile, one of the simplest geometries that can tile the plane, as a model, we look into design parameters that may induce curvature and seek the possibilities to minimize curvature by design. Tiles of this geometry are generally designed by rotating a repeating subunit resembling an isosceles triangle with a 120° vertex angle (α) about the C_3 axis (Figure 2.7a). Two associated design parameters, interhelical distance (***D***) and helical extension (***E***), determine the shape and dimension of the repeating subunit. ***D*** is defined as the average distance between the central axes of neighboring helices, which describes the compactness of the structure. ***E*** is defined as the common difference in length between neighboring helices, which equals the rise per base pair (***r***) multiplied by the number of additional base pairs per helix ($\boldsymbol{n}_{bp}$). ***D*** and ***E*** are along two orthogonal axes and strictly follow the tangent function. Assuming **r** is 0.34 nm for B-form DNA, for a given α, $\boldsymbol{n}_{bp}$ can be calculated from ***D***.

$$tan\frac{\alpha}{2} = \frac{\boldsymbol{D}}{\boldsymbol{E}}$$

$$\boldsymbol{n}_{bp} = \frac{\boldsymbol{E}}{\boldsymbol{r}} = \frac{\boldsymbol{D}}{\boldsymbol{r} \cdot tan\frac{\alpha}{2}}$$

There are two undesired situations when ***D*** is overestimated or underestimated (Figure 2.7b). In the former case, DNA helices are loosely arranged in the design, while the actual tile tends to contract in size under experimental conditions, inducing tension at its corners. Conversely, in the latter case, DNA helices are tightly arranged in the designed structure. The actual tile tends to expand, inducing tension at its center. The monomer tiles are curved in both cases, and the tiling process will deviate from the 2D plane. Therefore, it can be inferred that finding the optimal ***D*** to minimize tension-

induced curvature is a promising strategy to enhance the geometric design of DNA origami tiles for tessellation.

Towards this goal, we designed four equilateral triangular tiles with ***D*** ranging from 2.55 to 3.00 nm with 0.15 nm intervals and investigated ***D***-dependent tile conformations using a coarse-grained model, oxDNA[37-39]. To quantitatively compare the curvature of different tile designs, we defined three vectors, namely $\vec{u}$, $\vec{v}$, $\vec{w}$, to describe the helical directions of each composing subunit (Figure 2.7c). The curvature could be estimated by the sum of the angles between each pair of vectors (i.e., $\theta_1 + \theta_2 + \theta_3$). For a flat tile, the sum is approximately 360°. The more curved a tile is, the more the sum deviates from 360°. Therefore, the degree of curvature was defined as the deviation of the sum from 360° (i.e., $360° - \theta_1 - \theta_2 - \theta_3$), while the direction of curvature (i.e., upwards or downwards) was determined by $(\vec{u} \times \vec{v}) \cdot \vec{w}$. The vector-based curvature analysis was applied to all configurations sampled throughout the simulation trajectory (Figure 2.7d). Due to the single-layer construct, all designed tiles exhibited a high degree of flexibility and conformational dynamics (Supplementary Figure S2.3). The 2.55 nm, 2.70 nm, and 3.00 nm designs had a dominant curvature direction taken by more than 80% of configurations, while the 2.85 nm design could more easily access opposite curvature directions. As ***D*** increased from 2.55 to 3.00 nm, the curvature of tile decreased at first and subsequently increased. We treat the simulation results mainly as a qualitative reference to evidence the influence of ***D*** on tile curvature. The model currently does not capture sequence-dependent effects on the duplex curvature or of multivalent ions, and due to its coarse-grained nature, it does not capture the conformations of Holliday junctions[40]. These factors may impact the prediction of tile curvature.

To experimentally determine the optimal ***D***, we encoded the equilateral triangular tiles with two edges complementary to each other and left the third edge inert (Figure 2.7e). Ideally, equilateral triangular tiles guided by this matching rule assemble exclusively into hexamers. However, if the tile is curved, the multimerization process is accompanied by the accumulation of curvature, which perturbs the correct vertex arrangement of tiles and results in multimeric complexes other than hexamers. Thus, the distribution of multimerization products can be exploited to deduce the optimal ***D***. The cooling ramp was controlled slow enough (-0.1 °C/30 min) to keep the multimerization process close to thermodynamic equilibrium. As expected, multimeric complexes composed of 5, 6, or 7 monomer tiles were assembled, which could be unambiguously distinguished by AFM (Figure 2.7f). As ***D*** increased from 2.55 to 3.00 nm, statistical analysis of multimer distribution revealed a clear trend for each species (Figure 2.2g and Supplementary Figure S2.4). The percentage of hexamer peaked at 2.70 nm (~99%) and dropped to ~9% at 3.00 nm, along with the marked increase of pentamer from <10% to ~91% (Supplementary Table S2.11 and S2.12). For all designs tested, heptamer stayed below 7%. To further narrow down the range of ***D***, two additional designs (***D*** = 2.65 and 2.75 nm, respectively) were included. Both produced >90% hexamers but did not outcompete the 2.70 nm design (Supplementary Figure S2.5). Therefore, the optimal ***D*** was in the range of 2.70 ± 0.05 nm under the experimental conditions, which was used for subsequent tile designs. Despite the slight difference in cation concentrations, our result agrees with the ***D*** measured by small-angle X-ray scattering (SAXS). Finally, by changing the third edge from inert to self-complementary, the 2.70 nm tile design yielded micrometer-scale single-crystalline lattices (Supplementary Figure S2.6), which

confirmed the effectiveness of ***D*** optimization. Notably, ***D*** can be varied under different cationic conditions and origami design principles[41]. The statistical analysis strategy employed here correlates the subtle change in ***D*** with the distribution of multimerization products, presenting a general and straightforward alternative that works under various buffer conditions. Refined design parameters will facilitate the rational design of DNA-based dynamic systems such as localized DNA computing[42], nanorobotics[43], and molecular binding assays[31], whose performance relies on the precise placement of functional components on the DNA origami scaffold.

2.6 Regular tilings

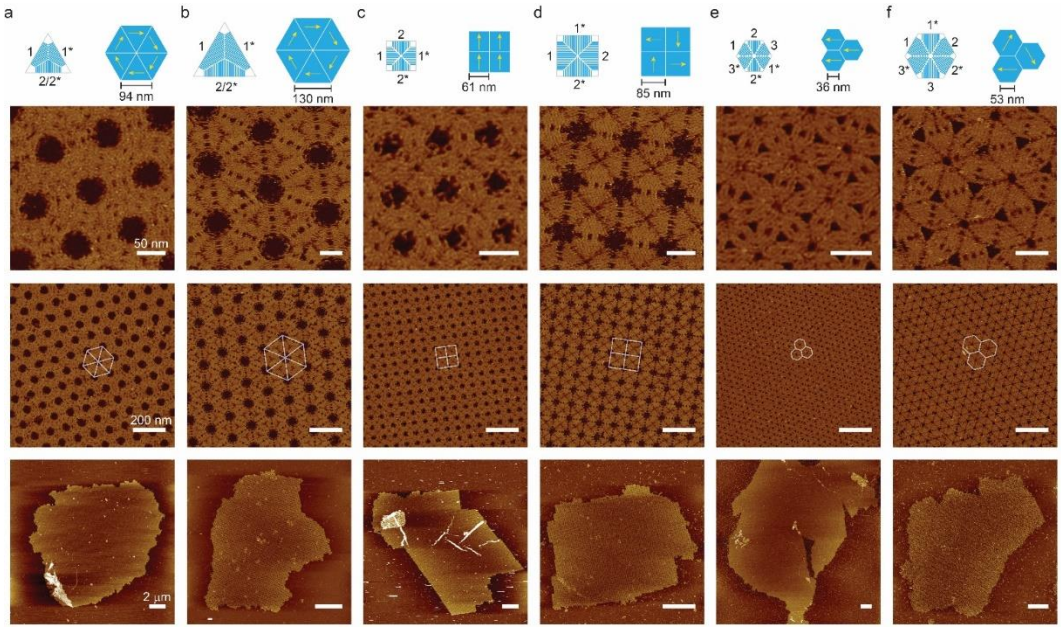

Figure 2.8. **Regular tilings.** Two groups of regular tessellation patterns were assembled from tiles based on a short scaffold strand, p3548 (a, c, e), and a long scaffold strand, M13mp18 (b, d, f), respectively. Each group included three tile geometries: equilateral triangle, square, and regular hexagon. From top to bottom in each column: schematic illustrations of the monomer tile (left) and tile arrangement within the lattice (right). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. The monomer size is estimated from the number and lengths of constituent double-helices using the geometry attributes of standard B-form DNA. The relative orientations of tiles within a lattice are marked by yellow arrows. A zoomed-in AFM image showing the detailed tile arrangement and inter-tile connections. Scale bar: 50 nm. A 1 μm-by-1 μm AFM image

showing a nearly defect-free area on the lattice. Scale bar: 200 nm. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice. Scale bar: 2 μm.

The optimized ***D*** was first applied to designing regular tessellation (also known as Platonic tiling) patterns. Two groups of tiles, each including three geometries: equilateral triangle (Figure 2.8a and 2.8b), square (Figure 2.8c and 2.8d), and regular hexagon (Figure 2.8e and 2.8f), were constructed based on p3548 (a customized scaffold comprised of 3,548 nt) and M13mp18 (a 7,249-nt scaffold widely used for building DNA origami nanostructures), respectively. As visualized by AFM, all six designs produced micrometer-scale single-crystalline lattices, suggesting that ***D*** is generally applicable to DNA origami tiles of different sizes and rotational symmetries. The best lattice could grow up to ~350 μm^2 with the largest dimension exceeding 20 μm (Figure 2.8e), which contained ~10^5 monomer tiles. Moreover, nearly defect-free areas were readily located for all designs in the high-magnification AFM images, in which ordered repeats of cavities and the connections between tiles were clearly visible. Finely-tuned ***D*** improved the geometric design of monomer tiles and reduced the dependence of tessellation on curvature correction. Remarkably, two designs, the square and regular hexagonal tiles based on the p3548 scaffold, produced high-quality single-crystalline lattices without implementing curvature-correcting mechanism (Figure 2.8c and 2.8e). The resultant lattices are composed of monomer tiles taking the same orientation, opening up new opportunities for applications requiring the exact patterning of functional molecules on the DNA template with sequence-level consistency.

In terms of size and quality, the tessellation patterns based on the p3548 scaffold were superior to those based on the M13mp18 scaffold, which could be attributed to two factors. Firstly, the p3548 tiles comprise a shorter scaffold and fewer staple strands. Simpler structure makes them less prone to common defects in DNA origami assembly, such as nicked scaffold, missing staples, or staple misincorporation. Secondly, more unpaired regions are exposed on the M13mp18 tiles, which can mediate the stochastic attachment of free tiles (or groups of tiles) onto a growing lattice, resulting in surface defects (analogous to adatom in crystallography). Additional loop interactions also promote excessive spontaneous nucleation and the rapid consumption of free tiles, hindering lattice growth. Therefore, it can be inferred that to further scale up DNA origami tessellation systems to the macroscopic scale, improved monomer integrity, defect inhibition, and nucleation control are promising routes to take.

2.7 Isohedral tilings with lower symmetry

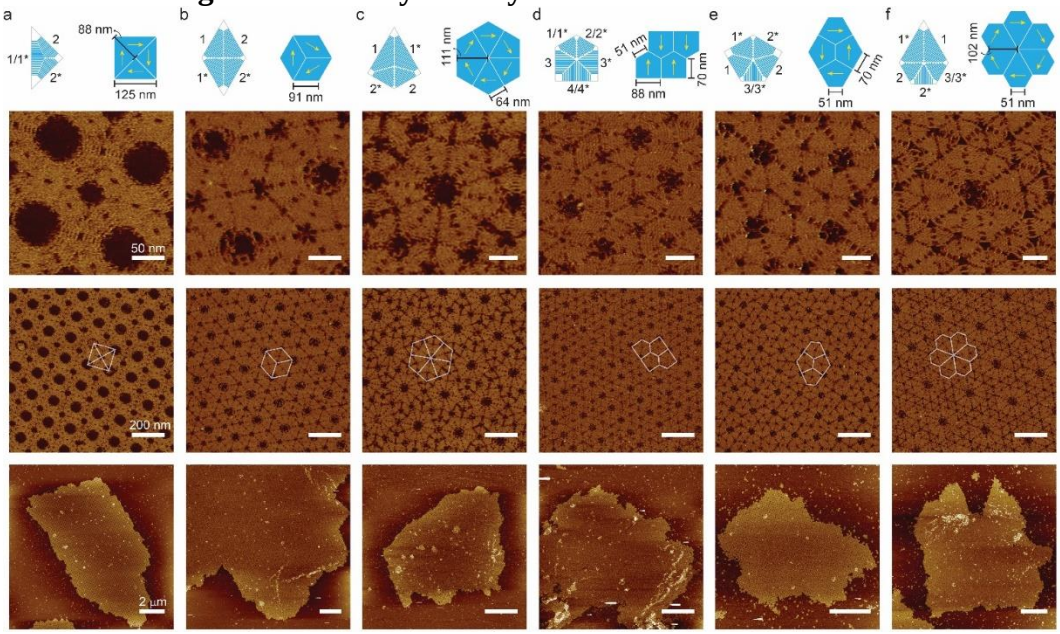

Figure 2.9. **Tessellation patterns assembled from low-symmetry tiles.** Tiles of six different geometries, including isosceles right triangle (a), rhombus (b), kite (c), prismatic pentagon (d), Cairo pentagon (e), and floret pentagon (f), were designed and assembled

into tessellation patterns. From top to bottom in each column: schematic illustrations of the monomer tile (left) and tile arrangement within the lattice (right). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. The monomer size is estimated from the number and lengths of constituent double-helices using the geometry attributes of standard B-form DNA. The relative orientations of tiles within a lattice are marked by yellow arrows. A zoomed-in AFM image showing the detailed tile arrangement and inter-tile connections. Scale bar: 50 nm. A 1 μm-by-1 μm AFM image showing a nearly defect-free area on the lattice. Scale bar: 200 nm. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice. Scale bar: 2 μm.

Current DNA origami tessellation systems mostly focus on three regular tilings. To demonstrate the versatility of our system, we designed six tessellation patterns composed of low-symmetry tiles, which are the duals of semiregular tilings (categorized as Laves tilings[1]). The tile geometries included isosceles right triangle (Figure 2.9a), rhombus (Figure 2.9b), kite (Figure 2.9c), prismatic pentagon (Figure 2.9d), Cairo pentagon (Figure 2.9e), and floret pentagon (Figure 2.9f). With the exception of the rhombic tile, the rest five tiles lack rotational symmetry and involve a combination of different interior angles and side lengths. Following the thermodynamic guidelines derived from regular tilings, bond connections were assigned to monomer tiles based on the included angle between each pair of complementary edges and the corresponding vertex arrangement (Supplementary Table S2.21-S2.26). The aim was to synchronize the pairing temperature of each edge during thermal annealing by taking into account its geometric context within the tiling pattern. For instance, complementary edges forming a 60° angle (e.g., 1 and 1* of the kite tile) were assigned with ΔG_{edge} equivalent to that of the equilateral triangular tile.

Robust tessellation was facilitated by accurate geometric design and rational bond assignment. Despite the reduced symmetry of monomer tiles, all six designs yielded crystalline lattices that were comparable in size to regular tilings. Among them, the rhombille tiling produced the largest single-crystalline lattice consisted of over 2×10^4 rhombic tiles and measured 150 μm^2 (Figure 2.9b). The detailed connections between tiles were consistent with the intended design as visualized in imaging areas free of defects.

The prismatic pentagonal tiling (Figure 2.9d) was the only one that did not produce a large single-crystalline lattice. It appeared more susceptible to excessive spontaneous nucleation, where fragments growing from separate nuclei fused into polycrystalline lattices. Similarly to regular tilings, the primary type of defect observed was undesired tile attachment onto the lattice. In addition, a second type of defect (resembling an interstitial defect in crystallography) was identified in the isosceles right triangular tiling (Supplementary Figure S2.13), which was caused by tiles that were inserted into the cavities of the lattice (~58 nm in diameter).

2.8 Discussion

In summary, we generalize the design of DNA origami tiles for tessellation by finely tuning a critical design parameter (***D***), which enables crystalline lattices with great diversity and complexity. 12 out of 13 unique tile designs yield single-crystalline lattices, confirming the effectiveness of ***D*** optimization. Notably, the improved geometric design reduces the dependence of DNA origami tiling on rotation-based curvature correction, as evidenced by several high-quality lattices with all composing monomer tiles taking the

same orientation. Tessellation remains robust as tile symmetry reduces, suggesting the general applicability of $\boldsymbol{D}$ to a wide variety of geometries.

2.9 Material and Methods

See APPENDIX A.

2.10 References

1. Grünbaum, B.; Shephard, G. C., *Tilings and patterns*. Courier Dover Publications: 1987.

2. Talapin, D. V.; Shevchenko, E. V.; Bodnarchuk, M. I.; Ye, X.; Chen, J.; Murray, C. B., Quasicrystalline order in self-assembled binary nanoparticle superlattices. *Nature* **2009,** *461* (7266), 964-967.

3. Nagaoka, Y.; Zhu, H.; Eggert, D.; Chen, O., Single-component quasicrystalline nanocrystal superlattices through flexible polygon tiling rule. *Science* **2018,** *362* (6421), 1396-1400.

4. Wasio, N. A.; Quardokus, R. C.; Forrest, R. P.; Lent, C. S.; Corcelli, S. A.; Christie, J. A.; Henderson, K. W.; Kandel, S. A., Self-assembly of hydrogen-bonded two-dimensional quasicrystals. *Nature* **2014,** *507* (7490), 86-89.

5. Urgel, J. I.; Ecija, D.; Lyu, G.; Zhang, R.; Palma, C.-A.; Auwaerter, W.; Lin, N.; Barth, J. V., Quasicrystallinity expressed in two-dimensional coordination networks. *Nature Chemistry* **2016,** *8* (7), 657-662.

6. Zhang, Y.-Q.; Paszkiewicz, M.; Du, P.; Zhang, L.; Lin, T.; Chen, Z.; Klyatskaya, S.; Ruben, M.; Seitsonen, A. P.; Barth, J. V., Complex supramolecular interfacial tessellation through convergent multi-step reaction of a dissymmetric simple organic precursor. *Nature chemistry* **2018,** *10* (3), 296-304.

7. Gonen, S.; DiMaio, F.; Gonen, T.; Baker, D., Design of ordered two-dimensional arrays mediated by noncovalent protein-protein interfaces. *Science* **2015,** *348* (6241), 1365-1368.

8. Tanrikulu, I. C.; Forticaux, A.; Jin, S.; Raines, R. T., Peptide tessellation yields micrometre-scale collagen triple helices. *Nature chemistry* **2016,** *8* (11), 1008-1014.

9. Ben-Sasson, A. J.; Watson, J. L.; Sheffler, W.; Johnson, M. C.; Bittleston, A.; Somasundaram, L.; Decarreau, J.; Jiao, F.; Chen, J.; Mela, I., Design of biologically active binary protein 2D materials. *Nature* **2021,** *589* (7842), 468-473.

10. Shi, Q.; Gómez, D. E.; Dong, D.; Sikdar, D.; Fu, R.; Liu, Y.; Zhao, Y.; Smilgies, D. M.; Cheng, W., 2D freestanding Janus gold nanocrystal superlattices. *Advanced Materials* **2019,** *31* (28), 1900989.

11. Lee, Y. H.; Shi, W.; Lee, H. K.; Jiang, R.; Phang, I. Y.; Cui, Y.; Isa, L.; Yang, Y.; Wang, J.; Li, S., Nanoscale surface chemistry directs the tunable assembly of silver octahedra into three two-dimensional plasmonic superlattices. *Nature communications* **2015,** *6* (1), 6990.

12. Whitham, K.; Yang, J.; Savitzky, B. H.; Kourkoutis, L. F.; Wise, F.; Hanrath, T., Charge transport and localization in atomically coherent quantum dot solids. *Nature materials* **2016,** *15* (5), 557-563.

13. Chen, H.; Voigt, L.; Kubus, M.; Mihrin, D.; Mossin, S.; Larsen, R. W.; Kegnaes, S.; Piligkos, S.; Pedersen, K. S., Magnetic Archimedean Tessellations in Metal-Organic Frameworks. *J Am Chem Soc* **2021,** *143* (35), 14041-14045.

14. Wu, L.; Jubert, P. O.; Berman, D.; Imaino, W.; Nelson, A.; Zhu, H.; Zhang, S.; Sun, S., Monolayer assembly of ferrimagnetic Co(x)Fe(3-x)O4 nanocubes for magnetic recording. *Nano Lett* **2014,** *14* (6), 3395-9.

15. Kim, T.; Hong, J.; Kim, J.; Cho, J.; Kim, Y., Two-Dimensional Peptide Assembly via Arene-Perfluoroarene Interactions for Proliferation and Differentiation of Myoblasts. *J Am Chem Soc* **2023,** *145* (3), 1793-1802.

16. Pinheiro, A. V.; Han, D.; Shih, W. M.; Yan, H., Challenges and opportunities for structural DNA nanotechnology. *Nat Nanotechnol* **2011,** *6* (12), 763-72.

17. Zhang, F.; Nangreave, J.; Liu, Y.; Yan, H., Structural DNA nanotechnology: state of the art and future perspective. *J Am Chem Soc* **2014,** *136* (32), 11198-211.

18. Seeman, N. C.; Sleiman, H. F., DNA nanotechnology. *Nature Reviews Materials* **2017,** *3* (1), 1-23.

19. Wang, P.; Gaitanaros, S.; Lee, S.; Bathe, M.; Shih, W. M.; Ke, Y., Programming Self-Assembly of DNA Origami Honeycomb Two-Dimensional Lattices and Plasmonic Metamaterials. *J Am Chem Soc* **2016,** *138* (24), 7733-40.

20. Liu, X.; Zhang, F.; Jing, X.; Pan, M.; Liu, P.; Li, W.; Zhu, B.; Li, J.; Chen, H.; Wang, L.; Lin, J.; Liu, Y.; Zhao, D.; Yan, H.; Fan, C., Complex silica composite nanomaterials templated with DNA origami. *Nature* **2018,** *559* (7715), 593-598.

21. Sun, W.; Shen, J.; Zhao, Z.; Arellano, N.; Rettner, C.; Tang, J.; Cao, T.; Zhou, Z.; Ta, T.; Streit, J. K., Precise pitch-scaling of carbon nanotube arrays within three-dimensional DNA nanotrenches. *Science* **2020,** *368* (6493), 874-877.

22. Shen, J.; Sun, W.; Liu, D.; Schaus, T.; Yin, P., Three-dimensional nanolithography guided by DNA modular epitaxy. *Nature Materials* **2021,** *20* (5), 683-690.

23. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

24. Wang, P.; Meyer, T. A.; Pan, V.; Dutta, P. K.; Ke, Y., The beauty and utility of

DNA origami. *Chem* **2017,** *2* (3), 359-382.

25. Hong, F.; Zhang, F.; Liu, Y.; Yan, H., DNA Origami: Scaffolds for Creating Higher Order Structures. *Chem Rev* **2017,** *117* (20), 12584-12640.

26. Dey, S.; Fan, C.; Gothelf, K. V.; Li, J.; Lin, C.; Liu, L.; Liu, N.; Nijenhuis, M. A.; Saccà, B.; Simmel, F. C., DNA origami. *Nature Reviews Methods Primers* **2021,** *1* (1), 13.

27. Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C., Crystalline two-dimensional DNA-origami arrays. *Angew Chem Int Ed Engl* **2011,** *50* (1), 264-7.

28. Liu, W.; Halverson, J.; Tian, Y.; Tkachenko, A. V.; Gang, O., Self-organized architectures from assorted DNA-framed nanoparticles. *Nature chemistry* **2016,** *8* (9), 867-873.

29. Tikhomirov, G.; Petersen, P.; Qian, L., Programmable disorder in random DNA tilings. *Nat Nanotechnol* **2017,** *12* (3), 251-259.

30. Tikhomirov, G.; Petersen, P.; Qian, L., Triangular DNA Origami Tilings. *J Am Chem Soc* **2018**.

31. Aghebat Rafat, A.; Sagredo, S.; Thalhammer, M.; Simmel, F. C., Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities. *Nature chemistry* **2020,** *12* (9), 852-859.

32. Aghebat Rafat, A.; Pirzer, T.; Scheible, M. B.; Kostina, A.; Simmel, F. C., Surface-assisted large-scale ordering of DNA origami tiles. *Angew Chem Int Ed Engl* **2014,** *53* (29), 7665-8.

33. Woo, S.; Rothemund, P. W., Self-assembly of two-dimensional DNA origami lattices using cation-controlled surface diffusion. *Nat Commun* **2014,** *5*, 4889.

34. Suzuki, Y.; Endo, M.; Sugiyama, H., Lipid-bilayer-assisted two-dimensional self-assembly of DNA origami nanostructures. *Nature communications* **2015,** *6* (1), 8052.

35. Suzuki, Y.; Sugiyama, H.; Endo, M., Complexing DNA origami frameworks through sequential self-assembly based on directed docking. *Angewandte Chemie International Edition* **2018,** *57* (24), 7061-7065.

36. Williams, S.; Lund, K.; Lin, C.; Wonka, P.; Lindsay, S.; Yan, H. In *Tiamat: a three-dimensional editing tool for complex DNA structures*, DNA Computing: 14th International Meeting on DNA Computing, DNA 14, Prague, Czech Republic, June 2-9, 2008. Revised Selected Papers 14, Springer: 2009; pp 90-101.

37. Ouldridge, T. E.; Louis, A. A.; Doye, J. P., Structural, mechanical, and thermodynamic properties of a coarse-grained DNA model. *The Journal of chemical physics* **2011,** *134* (8), 02B627.

38. Snodin, B. E.; Randisi, F.; Mosayebi, M.; Šulc, P.; Schreck, J. S.; Romano, F.; Ouldridge, T. E.; Tsukanov, R.; Nir, E.; Louis, A. A., Introducing improved structural properties and salt dependence into a coarse-grained model of DNA. *The Journal of chemical physics* **2015,** *142* (23), 06B613_1.

39. Poppleton, E.; Romero, R.; Mallya, A.; Rovigatti, L.; Šulc, P., OxDNA. org: a public webserver for coarse-grained simulations of DNA and RNA nanostructures. *Nucleic acids research* **2021,** *49* (W1), W491-W498.

40. Snodin, B. E.; Schreck, J. S.; Romano, F.; Louis, A. A.; Doye, J. P., Coarse-grained modelling of the structural properties of DNA origami. *Nucleic acids research* **2019,** *47* (3), 1585-1597.

41. Fischer, S.; Hartl, C.; Frank, K.; Radler, J. O.; Liedl, T.; Nickel, B., Shape and Interhelical Spacing of DNA Origami Nanostructures Studied by Small-Angle X-ray Scattering. *Nano Lett* **2016,** *16* (7), 4282-7.

42. Chatterjee, G.; Dalchau, N.; Muscat, R. A.; Phillips, A.; Seelig, G., A spatially localized architecture for fast and modular DNA computing. *Nature Nanotechnology* **2017,** *12*, 920.

43. Chao, J.; Wang, J.; Wang, F.; Ouyang, X.; Kopperger, E.; Liu, H.; Li, Q.; Shi, J.; Wang, L.; Hu, J.; Wang, L.; Huang, W.; Simmel, F. C.; Fan, C., Solving mazes with single-molecule DNA navigators. *Nat Mater* **2019,** *18* (3), 273-279.

CHAPTER 3

DNA ORIGAMI COMPLEX TILING

Adapted with permission from Yue Tang, Hao Liu, Qi Wang, Xiaodong Qi, Lu Yu, Petr Šulc, Fei Zhang, Hao Yan, Shuoxing Jiang. **DNA Origami Tessellations** (manuscript under review).

3.1 Abstract

The DNA origami technology enables the rational design of nearly arbitrary DNA architectures with nanometer precision at the sub-100 nm scale. Yet, the scaled-up self-assembly of DNA origami into higher-order molecular patterns has faced challenges in size and complexity. Here, a general design and assembly method of DNA origami tiles were described for tessellation by finely tuned tile-tile interaction to self-assemble into tessellation patterns with increased size and complexity. 6 tile designs of DNA origami complex tilings confirming the effectiveness. These DNA origami complex tilings include five Archimedean tilings and a 12-fold quasicrystal tiling. The various tiling patterns that rivaled Platonic tilings in size and quality, indicating the robustness of the optimized tessellation system. This work addresses the limitations in the size and complexity of DNA origami tessellation and paves the way for user-defined, programmable patterning of molecules or materials across scales where new properties may arise. It opens up new opportunities for applications in metamaterial engineering, nanoelectronics, and nanolithography.

3.2 Introduction

Tessellation is the arrangement of repeating geometric shapes to cover a plane with no gaps or overlaps[1]. The tessellation of nanoscale building blocks including colloidal nanoparticles[2, 3], organic compounds[4-6], and biomolecules[7-9] via bottom-up self-assembly provides a versatile means of engineering two-dimensional materials whose properties can be tailored by altering the long-range order or the local arrangement of constituent units, which has been the common focus of nanomaterials, supramolecular chemistry, and molecular science. Two-dimensional complex tilings exemplify the variety and intricacy of designs and formations achievable through the arrangement of elementary geometric figures[10, 11]. These patterns hold significant relevance across disciplines such as mathematics, the arts, and architecture. In the realm of two-dimensional complex tilings, there are examples such as Archimedean tilings[12, 13], quasicrystals[14-16], Girih tilings[17], and Wang tilings[18, 19]. Archimedean tilings represent periodic tessellations formed by aligning regular polygons edge-to-edge around a vertex, yielding intriguing properties within the emergent patterns[1]. In contrast, quasicrystals are characterized by their ordered yet non-periodic structures[14]. These quasicrystalline patterns possess the ability to occupy all available space continuously while exhibiting an absence of translational symmetry. However, the lack of modularity and customizable specificity in the majority of nanoobjects has limited the diversity and efficiency of tessellation dictated solely by their inherent self-organizing properties, necessitating the development of a versatile scaffolding material that simultaneously endows the target nanoobject with long-range order and local precision. Programmable DNA self-assembly offers significant benefits in the creation of molecular scaffolds, as it incorporates rational geometric design,

nanoscale accuracy, and user-defined specificity through Watson-Crick base pairing[20-22]. Crucially, the order and precision embedded in the DNA scaffolds can be transferred to molecules or materials that lack self-organizing capabilities[23-26], substantially expanding the range of material fabrication possibilities.

Among the numerous design approaches, the DNA origami technique[27] stands out for its versatility in creating intricate nanostructures. This method involves folding a long single-stranded DNA (scaffold) using hundreds of short synthetic oligonucleotides (staples) to form pre-determined shapes. The inherent programmability and addressability of DNA origami nanostructures facilitate the rational design of nearly any DNA architecture and the precise organization of functional elements on custom DNA templates[28-30]. However, expanding the size and complexity of molecular patterns assembled from DNA origami tiles remains challenging. To date, DNA origami tessellation has only successfully achieved the tiling of three regular polygons: equilateral triangles[31], squares[32-35], and regular hexagons[23]. In addition, the complexity of patterns created by a single tile geometry is limited. So far, there is only one example of tile co-assembly by docking a second tile species into the cavities of a preassembled lattice[36]. Direct co-assembly of size-compatible DNA origami tiles of distinct geometries into molecular patterns has been elusive.

To address these limitations, here, we applied the general approach from our previous work for creating DNA origami tiles with the optimal interhelical distance (***D***) range of 2.70 ± 0.05 nm and finely tuned tile-tile interaction to self-assemble into tessellation patterns with increased size and complexity. In this study, seven DNA origami tile designs self-assembled into six distinct 2D complex tessellation patterns,

encompassing five Archimedean tilings and one 12-fold quasicrystal tiling (Figure 3.1a). The tile design is finalized in Tiamat, a graphical user interface program for designing DNA nanostructures and sequences (Figure 3.1b). Atomic force microscopy (AFM) enabled the visualization of micrometer-scale crystalline lattices with minimal defects (Figure 3.1c and Figure 3.1d). The demonstrated complex tiling patterns remained robust as tile symmetry decreased or as the number of unique tile species increased, further expanding the potential complexity attainable through DNA origami tessellation. This research harnessed finely tuned tile-tile interaction to generalize and optimize the creation of DNA origami tessellation patterns, potentially serving as a larger template for metamaterial engineering, nanolithography, and nanoelectronics.

3.3 Design workflow

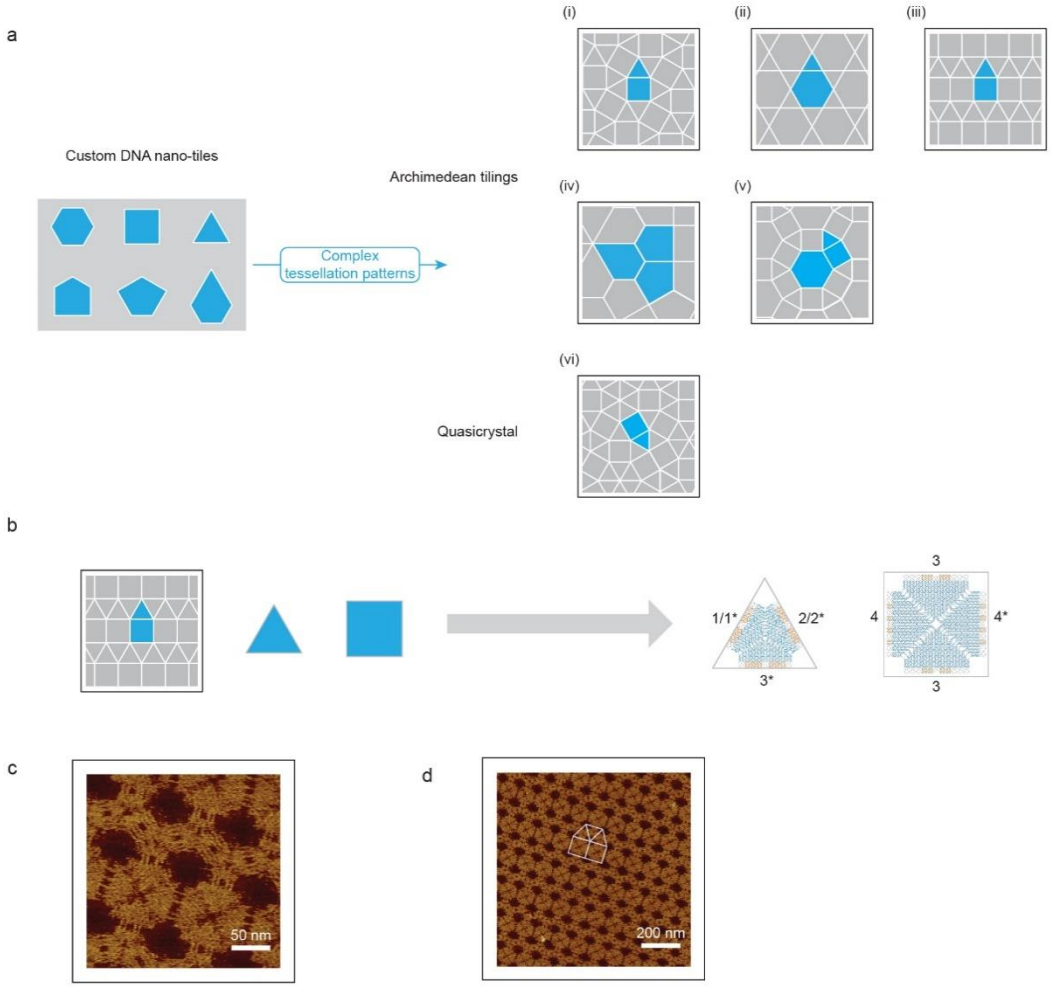

Figure 3.1. **Overview of DNA origami complex tessellation patterns.** (a) Overview of the tillings. DNA origami tile designs with six geometries self-assembled into six complex tessellation patterns, includes five Archimedean tilings and one 12-fold quasicrystal tiling. (b) The designed Elongated triangular tiling ($3^3.4^2$) involves triangular and square DNA origami units to co-assemble into tessellation patterns. The designs are finalized on Tiamat[37] by generating the scaffold strand (gray), core (blue), and edge (orange) staple strands, assigning sequences, and defining matching rules. (c) A DNA origami tessellation pattern corresponding to the one in (b) is visualized by atomic force microscopy (AFM). The sample pattern is superimposed on the AFM image. Scale bar: 50 nm. (d) A zoomed-out AFM image showing large scale of the DNA origami tessellation pattern. Scale bar: 200 nm.

3.4 Thermodynamic Analysis of Tile Interactions

Tile-tile interaction is a critical factor determining the outcome of tessellation. Intuitively, insufficient or excess tile-tile interaction may result in incomplete consumption or nonspecific aggregations of tiles, respectively. Two types of bonds, 2-nt sticky end hybridization and blunt end stacking, were used to 'glue' tiles together, whose binding free energies could be estimated from the DNA nearest-neighbor parameters for hybridization[38] and stacking[39] (Supplementary Table S3.9), respectively, and further summed up to obtain the total binding free energy for each pair of complementary edges (ΔG_{edge}, Supplementary Table S3.10-S3.17). We analyzed the strength and uniformity of bond interaction for regular tilings and found two empirical rules. Firstly, a higher ΔG_{edge} is needed for tiles with a lower coordination number to assemble into lattices. It is because, in the growth stage, tiles with a higher coordination number can simultaneously form bonds with more tiles on the growth frontier of a lattice[40], reducing the minimal requirement for the ΔG_{edge} contributed by each edge. Secondly, a balanced ΔG_{edge} facilitates unbiased lattice growth via single-tile incorporation. The difference in ΔG_{edge} between two pairs of complementary edges was less than 8 % for equilateral triangular and square tiles. For regular hexagonal tiles involving three pairs of complementary edges, the difference was no more than 7% for the two thermodynamically dominant pairs. Understanding the role of ΔG_{edge} could effectively reduce the trial and error before identifying the optimal bond design.

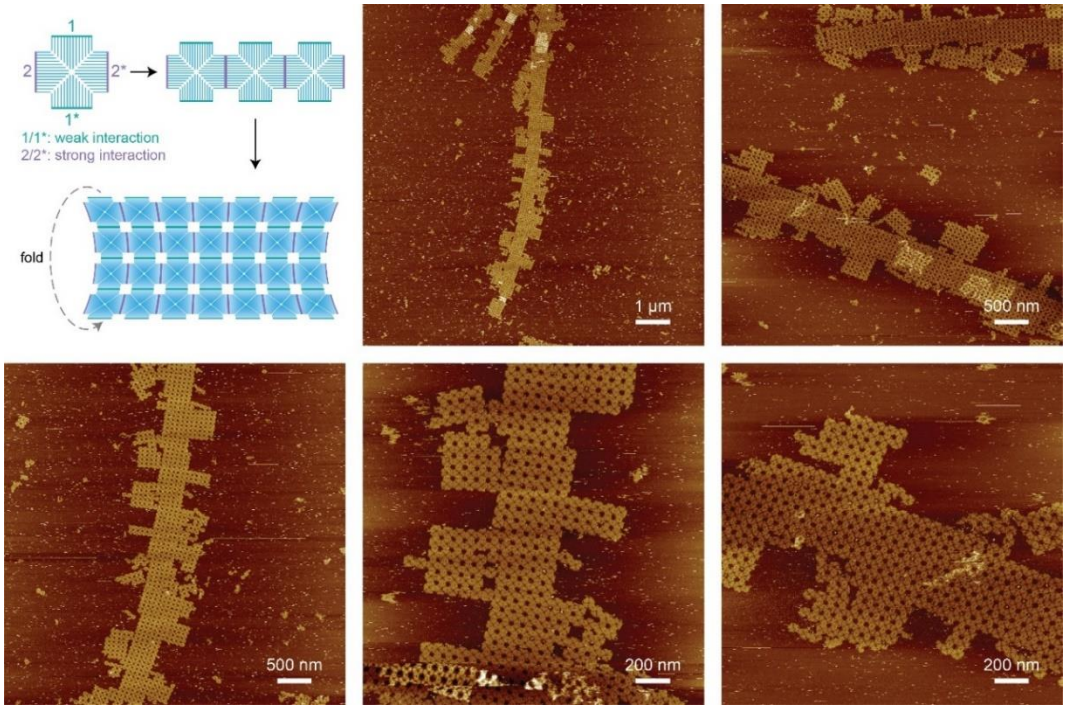

Figure 3.2. **Design and AFM characterization of nanotubes assembled from p3548 square DNA origami tiles with imbalanced tile-tile interactions.** The monomer tile is encoded with two opposite edges complementary to each other. In contrast to the same tile encoded with balanced interaction, which produces high-quality single-crystalline lattices, tiles with imbalanced bond interactions assemble exclusively into nanotubes, suggesting the role of thermodynamics in determining the outcome of tessellation.

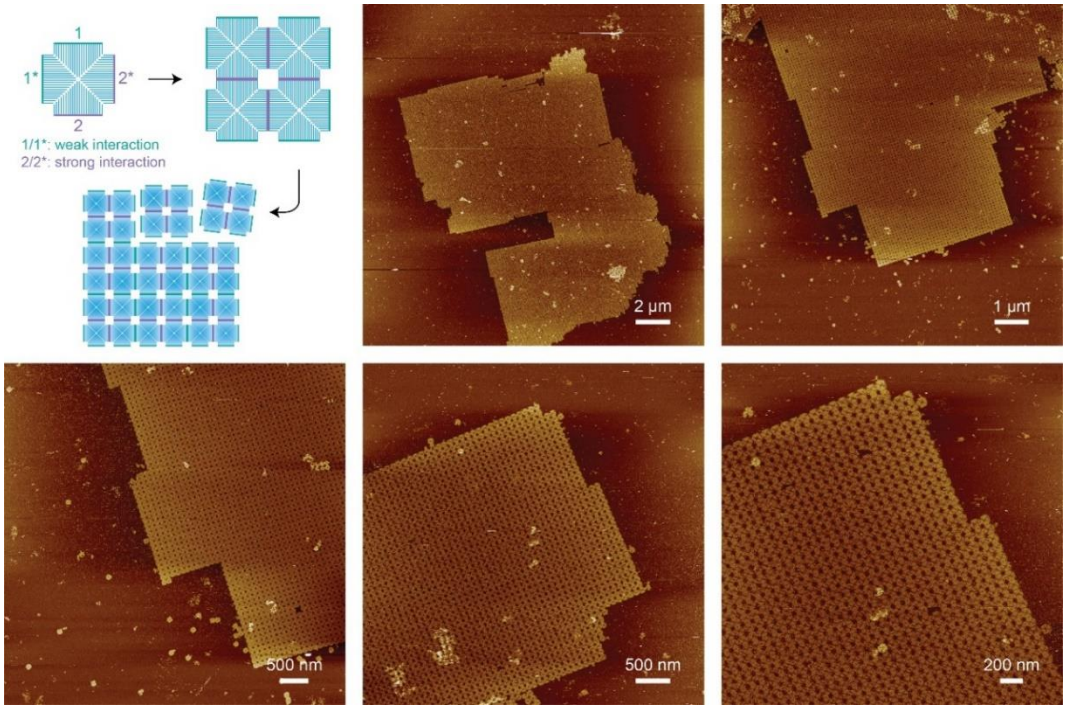

Figure 3.3. **Design and AFM characterization of 2D lattices assembled from M13mp18 square DNA origami tiles with imbalanced tile-tile interactions.** The monomer tile is encoded with two pairs of neighboring edges complementary to each other. Intriguingly, the tiling was not hindered by imbalanced tile-tile interactions. Single-crystalline lattices with neat edges were obtained, which can be attributed to the hierarchical pathway of lattice growth via the formation and incorporation of 2-by-2 tetramers, as evidenced by the notches and stairs on the edges of the lattice.

To elucidate the impacts of imbalanced ΔG_{edge} on tessellation, we designed two derivative square tiles. Imbalanced ΔG_{edge} was detrimental to square tiling without curvature correction, resulting in highly anisotropic lattice growth and nanotube formation (Figure 3.2). In contrast, the square tiling with rotation-based curvature correction exhibited better resistance to imbalanced ΔG_{edge}, resulting in the formation of single-crystalline lattices (Figure 3.3). Intriguingly, the resultant lattices had neat edges, in contrast to the jagged contour of its counterpart with balanced ΔG_{edge}, which could be attributed to the hierarchical pathway of lattice growth via the formation and assembly of 2-by-2 tetramers. The tetrameric intermediate presented identical bonds on all four edges,

which prevented the imbalanced ΔG_{edge} in monomer tiles from propagating throughout the lattice and allowed for balanced lattice growth. Taken together, our results suggest that matching rule and thermodynamic pathway are two critical factors determining the outcome of tessellation, in addition to geometric design.

3.5 Complex tilings

Theoretically, tiles with different geometries can co-assemble into tessellation patterns more complex than those assembled from one tile type, but realizing this concept using DNA origami tiles has remained challenging for several reasons. Co-assembly involves multiple tile species with mutually compatible size, geometry, and bond interaction, which are not readily attainable. Besides, as tile species increase, the tessellation process will be guided by more complex matching rules and become more prone to assembly defects. Moreover, tiles with drastically different sizes and coordination numbers can have distinct self-assembly behaviors, which need to be synchronized in one-pot annealing. Our tile designs featured precisely-defined geometry and unified bond connectivity while exhibiting improved size and quality in tilings constructed from a single tile type, which motivated us to explore the possibility of creating semiregular tessellation (also known as Archimedean tiling) patterns via the co-assembly of size-compatible, regular polygonal tiles.

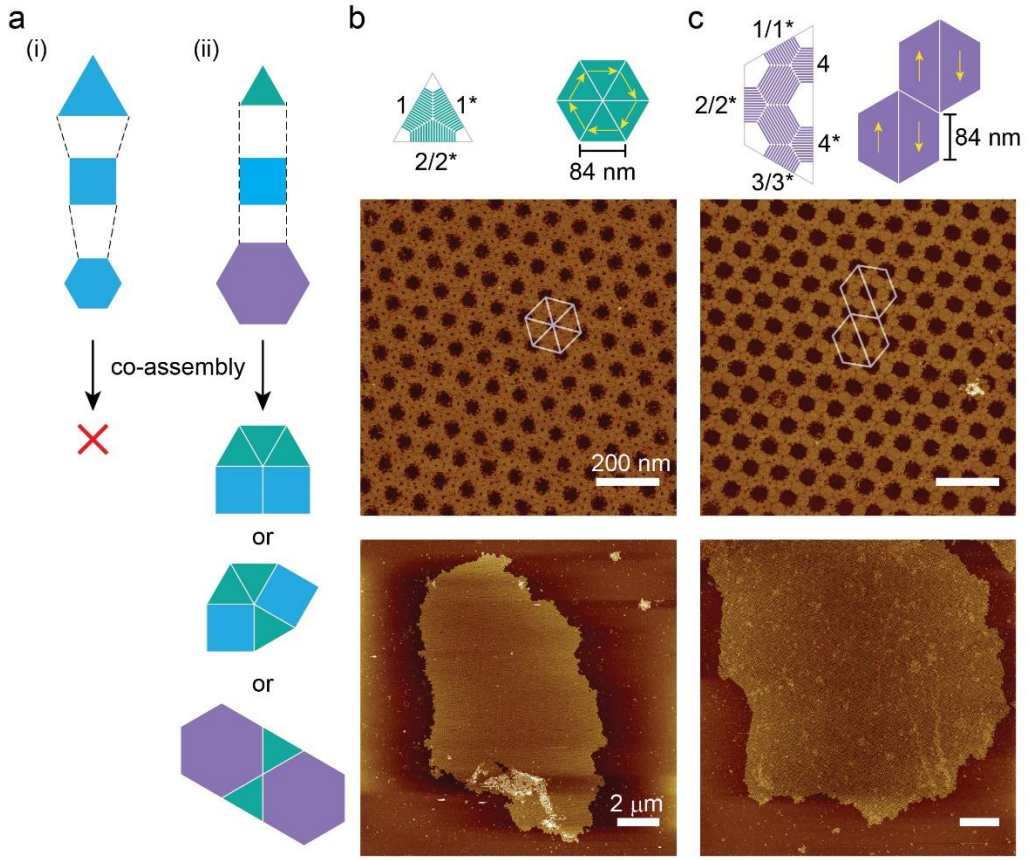

Figure 3.4. **Regular tilings assembled from equilateral triangular and regular hexagonal tiles.** (a) Tiling a plane with incompatible geometries is unattainable (i), while regular polygonal tiles with compatible sizes can co-assemble into semiregular tessellation patterns (ii). (b-c) Regular tilings assembled from equilateral triangular (b) and regular hexagonal tiles (c) with sizes that are compatible with the square tile based on the M13mp18 scaffold. (b and c) From top to bottom in each column: schematic illustrations of the monomer tile(s) (left) and tile arrangement within the lattice (right). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. The monomer size is estimated from the number and lengths of constituent double-helices using the geometry attributes of standard B-form DNA. The relative orientations of tiles within a lattice are marked by yellow arrows. Tiles that can take more than one possible orientation are marked by multiple yellow arrows. A zoomed-in AFM image showing the detailed tile arrangement and inter-tile connections. A 1 μm-by-1 μm AFM image showing a nearly defect-free area on the lattice. Scale bar: 200 nm. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice. Scale bar: 2 μm.

Tile size compatibility is one of the essential prerequisites for semiregular tiling (Figure 3.4a) since the propagation of patterns can be readily disrupted by the mismatches between monomer tiles with discrepant sizes. In our designs, tile size can be adjusted by extending or shortening helices collectively by the same number of base pairs. For example, by adding one base pair per helix, the side lengths of square tiles and equilateral triangular tiles are expected to increase by 0.68 nm ($2\boldsymbol{r}$) and 1.18 nm ($2\sqrt{3}\boldsymbol{r}$), respectively. We adopted the square tile based on the M13mp18 scaffold (calculated side length: 84.9 nm) and customized the equilateral triangular and regular hexagonal tiles accordingly.

The size-compatible equilateral triangular tile with a calculated side length of 84.4 nm was designed based on a miniaturized scaffold composed of 2,820 nt (p2820). Double-helices in this tile were held together by a combination of double-crossover and single-crossover linkages to adapt to the short scaffold strand, different from prevailing origami designs commonly based on the double-crossover linkages. As a result, the design that produced single-crystalline lattices (Figure 3.4b), consistent with the fact that helices are more widely spaced when held together by fewer crossover linkages[41].

For a size-compatible regular hexagonal tile, the scaffold strand was estimated to be approximately 20,000 nt. Considering the reduced amplification yield for long scaffold strands and the high synthesis cost of staple strands, we took an alternative route to build this tile (calculated side length: 84.4 nm) by dimerizing two isosceles-trapezoid-shaped DNA origami components based on the M13mp18 scaffold (Figure 3.4c), leaving a hole (~47 nm in diameter) at the center of the dimer. Likewise, single-crystalline lattices were obtained in the 2.75 nm ***D*** design containing single-crossover linkages. The characteristic

arrangements of bonds enabled the hexagonal tile and both components to be distinguished in AFM images. Interstitial defects were also observed in the lattice, which resulted from the lack of continuity in the tile's surface area and malformed tiles embedded in the cavities. Nonetheless, the tessellation proceeded with reasonable fidelity, suggesting the robustness of this system.

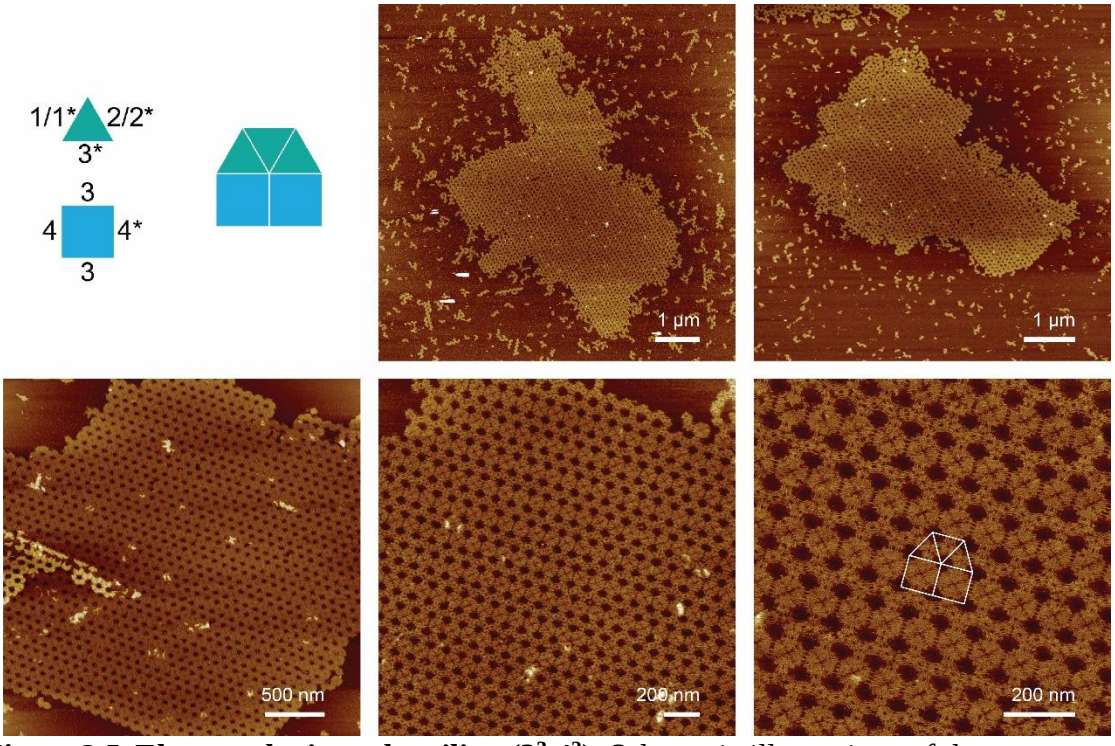

Figure 3.5. **Elongated triangular tiling ($3^3.4^2$).** Schematic illustrations of the monomer tile(s) (left) and tile arrangement within the lattice (right). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. A 1 µm-by-1 µm AFM image showing a nearly defect-free area on the lattice. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice.

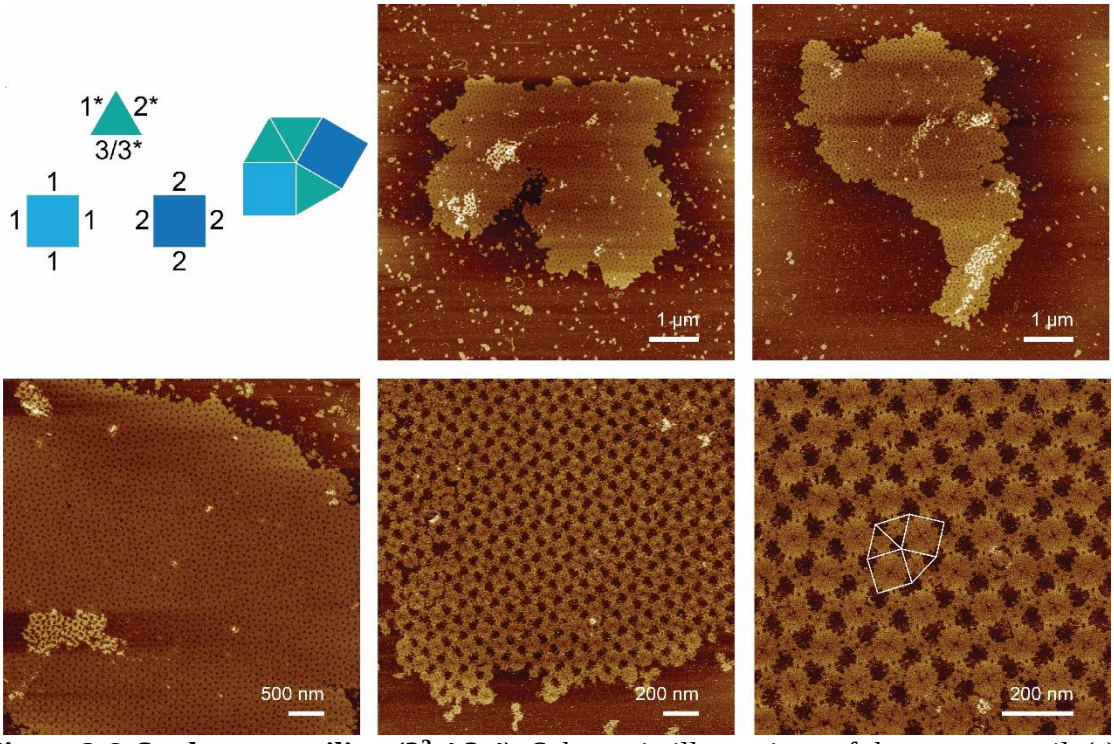

Figure 3.6. **Snub square tiling (3^2.4.3.4).** Schematic illustrations of the monomer tile(s) (left) and tile arrangement within the lattice (right). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. A 1 µm-by-1 µm AFM image showing a nearly defect-free area on the lattice. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice.

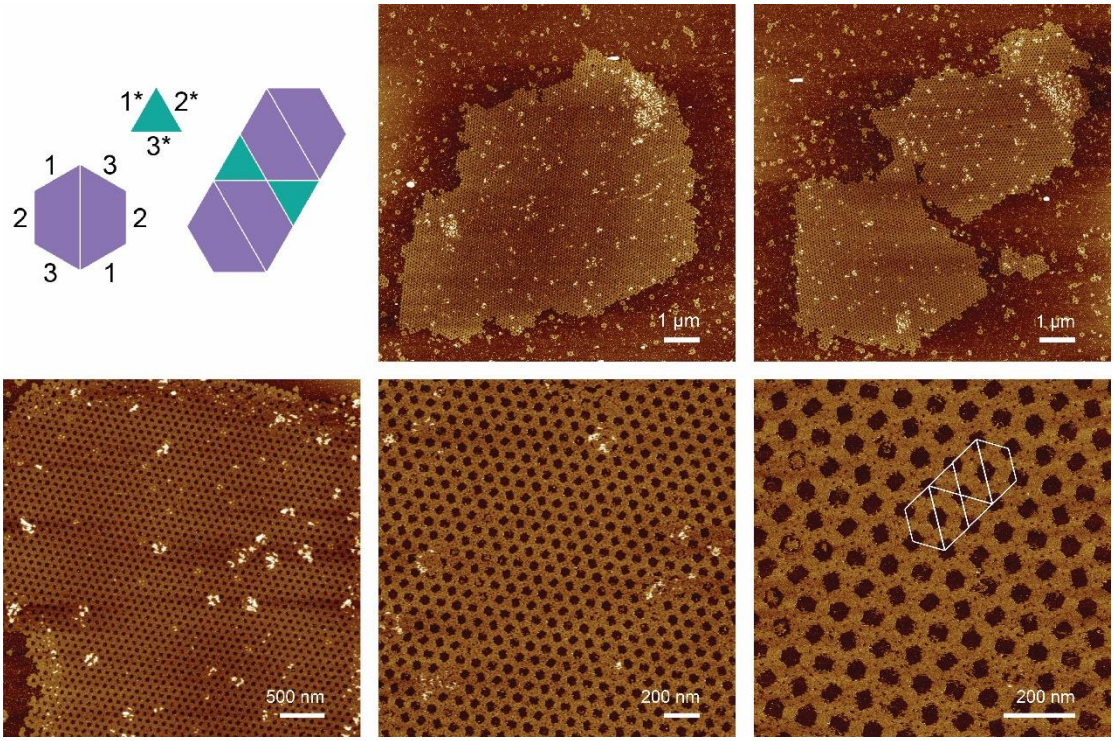

Figure 3.7. **Trihexagonal tiling (3.6.3.6).** Schematic illustrations of the monomer tile(s) (left) and tile arrangement within the lattice (right). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. A 1 μm-by-1 μm AFM image showing a nearly defect-free area on the lattice. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice.

Confirmed the tessellation capability of three compatible regular polygonal tiles, we encoded them with more complex matching rules to build three semiregular tilings of different rotational symmetries: the elongated triangular tiling ($3^3.4^2$, Figure 3.5), the snub square tiling ($3^2.4.3.4$, Figure 3.6), and the trihexagonal tiling (3.6.3.6, Figure 3.7). The numeric symbols are termed Cundy & Rollett's notations[42], which describe the vertex configuration of tilings (i.e., the number and types of regular polygons around each vertex). Semiregular tilings were prepared in two steps, in which monomer tiles were separately annealed and subsequently mixed for co-assembly. Single-crystalline lattices were obtained for all three designs with micrometer-scale, nearly defect-free areas

visualized by AFM, but the ($3^3.4^2$) tiling was inferior to the other two in size. In the ($3^3.4^2$) tiling, triangular and square tiles with a molar ratio of 2:1 were patterned into alternating rows. This arrangement allowed the 0.5 nm difference in their side lengths to accumulate during assembly, hindering lattice growth. To compensate for the size discrepancy, the triangular tiles were slightly stretched along the rows they assembled, which deformed the lattice (Figure 3.5). In the ($3^2.4.3.4$) and (3.6.3.6) tilings, square or hexagonal tiles were spaced by triangular tiles, preventing the discrepancy in tile size from accumulating along a specific growth direction. The resultant lattices had size and quality rivaling isohedral tilings. The ($3^2.4.3.4$) tiling involves a triangular tile and two differentially coded square tiles with a molar ratio of 4:1:1. Dimers of triangular tiles were arranged in a chiral way but of opposite handedness around each type of square tile, making the resultant lattice achiral. The (3.6.3.6) tiling demonstrated similar characteristics, including symmetry, defects, and patterns of cavities, to the hexagonal tiling in Figure 3.4c. These two designs could be distinguished by the shapes of cavities on the lattice. In the former, the hexagonal and rectangular cavities were located at the center and vertices of the hexagonal tiles, respectively, while in the latter, only hexagonal cavities existed.

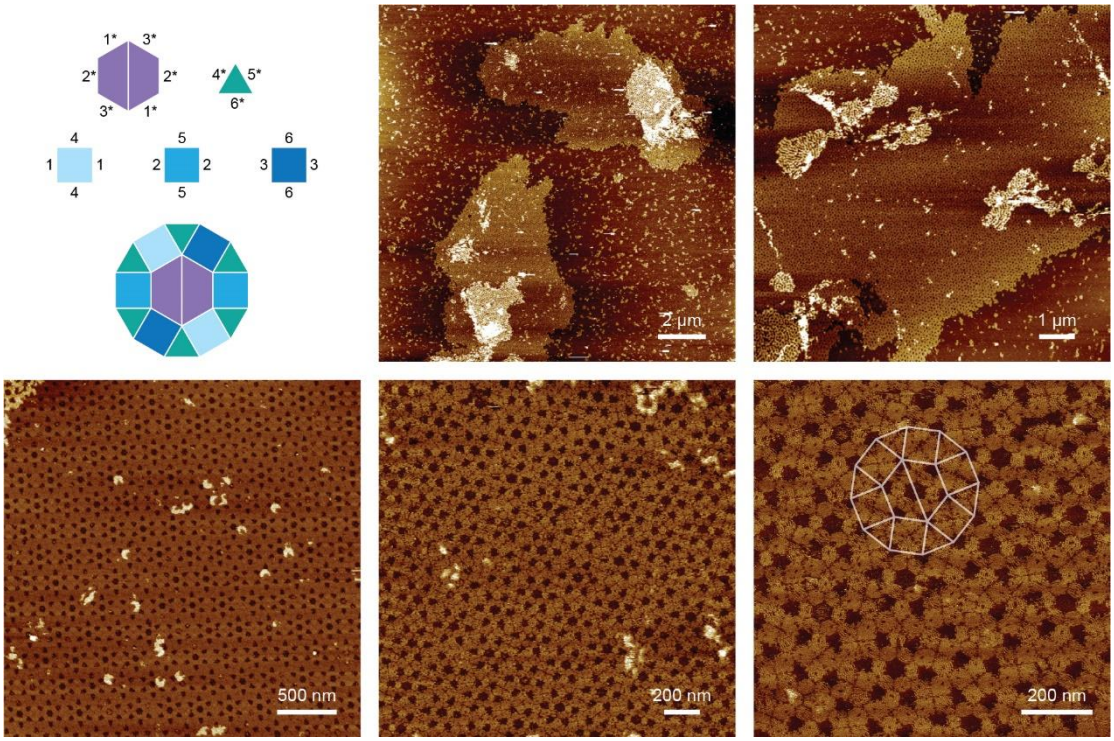

Figure 3.8. **Rhombitrihexagonal (3.4.6.4) tiling.** Schematic illustrations of the monomer tile(s) (top) and tile arrangement within the lattice (bottom). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. A 1 µm-by-1 µm AFM image showing a nearly defect-free area on the lattice. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice.

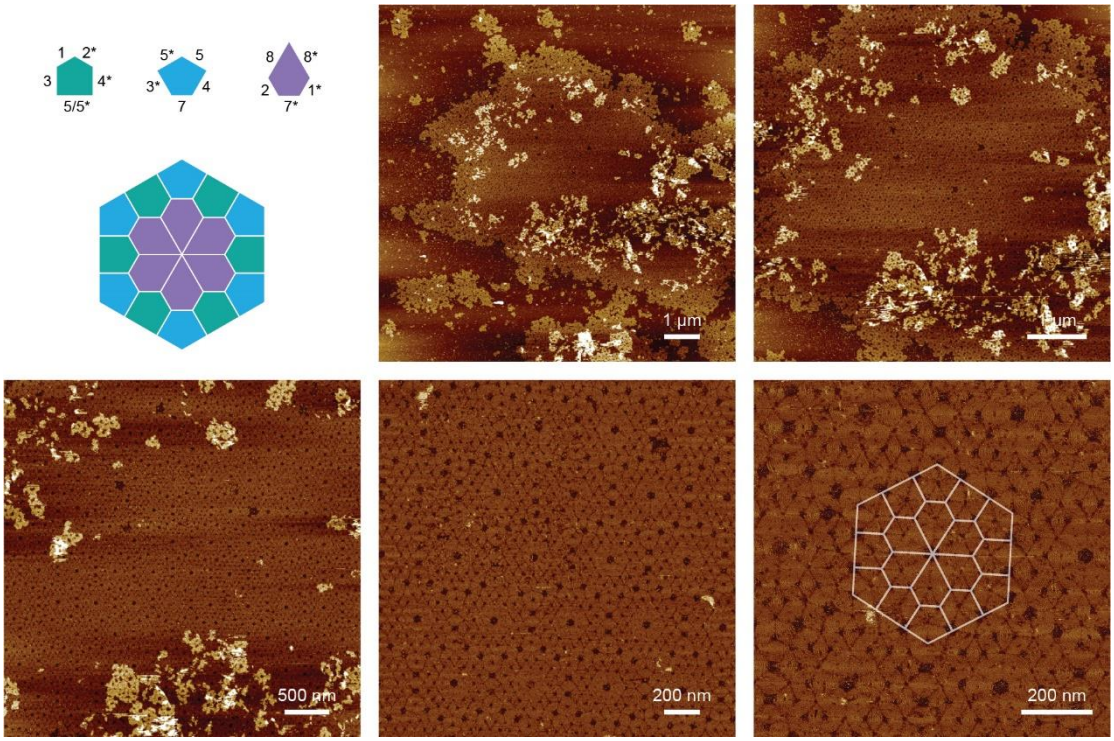

Figure 3.9. **3-isohedral pentagonal DNA origami tiling.** Schematic illustrations of the monomer tile(s) (top) and tile arrangement within the lattice (bottom). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. A 1 µm-by-1 µm AFM image showing a nearly defect-free area on the lattice. A schematic illustrating the arrangement of tiles within the lattice is superimposed on the AFM image for better visualization. A zoomed-out AFM image showing the size and overall quality of the crystalline lattice.

Next, to explore the complexity limit of DNA origami tessellation, we attempted to co-assemble three different geometries into a semiregular rhombitrihexagonal tiling (3.4.6.4, Figure 3.8) and a complex 3-isohedral pentagonal tiling (Figure 3.9). As more unique tile species (up to 5) were involved, the specificity imparted by the short sticky ends became inadequate to define their matching rules strictly, resulting in increased adatom and interstitial defects. Despite this, polycrystalline lattices with micrometer-scale, nearly defect-free areas were observed for both designs, demonstrating the highest level of complexity that this system could achieve.

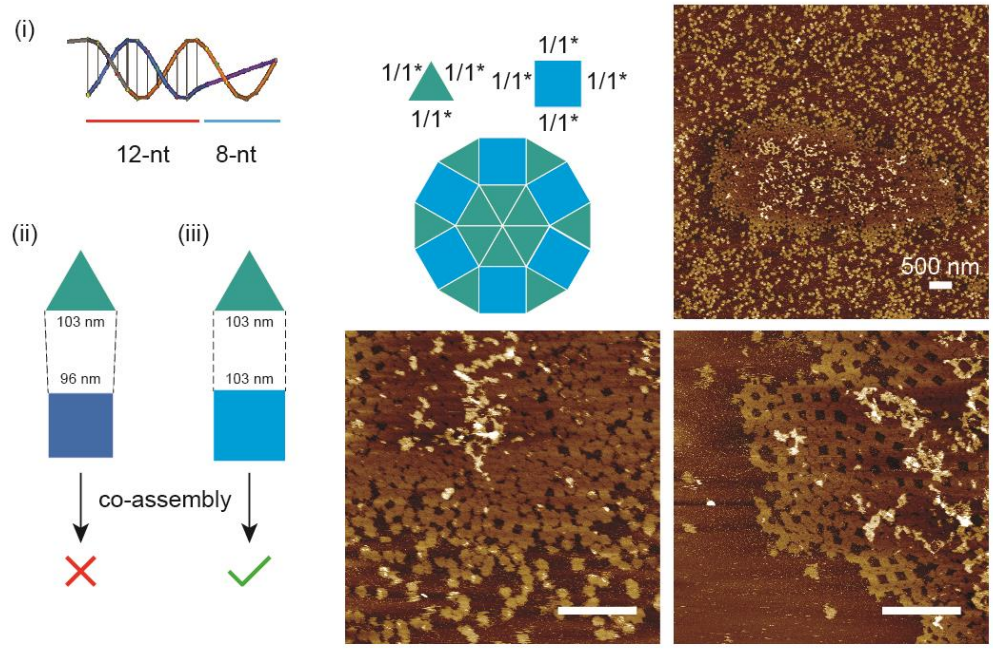

Figure 3.10. **12-fold quasicrystal tiling.** Tile-tile interaction is provided by DNA-DNA kissing loop which has a 12-nt double helix domain and an 8-nt single helix binding domain. Tiling a plane with incompatible geometries is unattainable (ii), while regular polygonal tiles with compatible sizes can co-assemble into semiregular tessellation patterns (iii). Schematic illustrations of the monomer tile(s) (top) and tile arrangement within the lattice (bottom). Matching rules are denoted by Arabic numerals and asterisks, where n and n* refer to two complementary edges, and n/n* refers to a self-complementary edge. AFM images scale bar: 500 nm.

Finally, we encoded the equilateral triangular tiles and square tile with a matching rule which is differ to other tilings in this work to build 12-fold quasicrystal tiling (Figure 3.10). Since the sequence of a DNA origami nanostructure can hardly be freely defined because it is primarily determined by the scaffold sequence used. The 2-nt sticky ends is not competent to self-assembly the tiles. Here, we applied DNA-DNA kissing loop[43-45] to provide tile-tile interactions to co-assemble the 12-fold quasicrystal tiling (Figure 3.10(i)). This kissing loop extension has a double strand domain with 12-nt and a single strand domain with 8-nt. One single strand closed stem-loop would hybridize and wrap around to its sequence complementary single strand loop and generate a helical structure.

The side lengths of the p2820 based equilateral triangular tiles and M13mp18 based square tile will add up to 103 nm and 96 nm, respectively (Figure 3.10(ii)). To compatibility with the size of equilateral triangular tile, a square tile with a calculated side length of 103 nm was designed based on the scaffold composed of 8064 nt (Figure 3.10(iii)).

The 12-fold quasicrystal tiling did not produce a large single-crystalline lattice so far. Its tile-tile interaction appeared to be not fine-tuned, where high aggregations on polycrystalline lattices and many fragments on backgrounds.

3.6 Discussion

In summary, we generalize the design of DNA origami tiles for tessellation by finely tuned tile-tile interaction to self-assemble into tessellation patterns with increased size and complexity. 6 tile designs of DNA origami complex tilings confirming the effectiveness. We demonstrate the co-assembly of two or more unique tile species into semiregular tiling patterns, enabling DNA origami tilings beyond isohedral. Overall, our work addresses the limitations in the size and complexity of DNA origami tessellation and paves the way for user-defined, programmable patterning of molecules or materials across scales where new properties may arise.

3.7 Material and Methods

See APPENDIX B.

3.8 Referance

1. Grünbaum, B.; Shephard, G. C., *Tilings and patterns*. Courier Dover Publications: 1987.

2. Talapin, D. V.; Shevchenko, E. V.; Bodnarchuk, M. I.; Ye, X.; Chen, J.; Murray, C. B., Quasicrystalline order in self-assembled binary nanoparticle superlattices. *Nature* **2009,** *461* (7266), 964-967.

3. Nagaoka, Y.; Zhu, H.; Eggert, D.; Chen, O., Single-component quasicrystalline nanocrystal superlattices through flexible polygon tiling rule. *Science* **2018,** *362* (6421), 1396-1400.

4. Wasio, N. A.; Quardokus, R. C.; Forrest, R. P.; Lent, C. S.; Corcelli, S. A.; Christie, J. A.; Henderson, K. W.; Kandel, S. A., Self-assembly of hydrogen-bonded two-dimensional quasicrystals. *Nature* **2014,** *507* (7490), 86-89.

5. Urgel, J. I.; Ecija, D.; Lyu, G.; Zhang, R.; Palma, C.-A.; Auwaerter, W.; Lin, N.; Barth, J. V., Quasicrystallinity expressed in two-dimensional coordination networks. *Nature Chemistry* **2016,** *8* (7), 657-662.

6. Zhang, Y.-Q.; Paszkiewicz, M.; Du, P.; Zhang, L.; Lin, T.; Chen, Z.; Klyatskaya, S.; Ruben, M.; Seitsonen, A. P.; Barth, J. V., Complex supramolecular interfacial tessellation through convergent multi-step reaction of a dissymmetric simple organic precursor. *Nature chemistry* **2018,** *10* (3), 296-304.

7. Gonen, S.; DiMaio, F.; Gonen, T.; Baker, D., Design of ordered two-dimensional arrays mediated by noncovalent protein-protein interfaces. *Science* **2015,** *348* (6241), 1365-1368.

8. Tanrikulu, I. C.; Forticaux, A.; Jin, S.; Raines, R. T., Peptide tessellation yields micrometre-scale collagen triple helices. *Nature chemistry* **2016,** *8* (11), 1008-1014.

9. Ben-Sasson, A. J.; Watson, J. L.; Sheffler, W.; Johnson, M. C.; Bittleston, A.; Somasundaram, L.; Decarreau, J.; Jiao, F.; Chen, J.; Mela, I., Design of biologically active binary protein 2D materials. *Nature* **2021,** *589* (7842), 468-473.

10. Robinson, R. M., Undecidability and nonperiodicity for tilings of the plane. *Inventiones mathematicae* **1971,** *12*, 177-209.

11. Mozes, S., Tilings, substitution systems and dynamical systems generated by them. *Journal d'Analyse Mathématique* **1989,** *53* (1), 139-186.

12. Grunbaum, B.; Shephard, G. C., Tilings by Regular Polygons. *Mathematics Magazine* **1977,** *50* (5), 227-247.

13. Zhang, F.; Liu, Y.; Yan, H., Complex Archimedean tiling self-assembled from DNA nanostructures. *J Am Chem Soc* **2013,** *135* (20), 7458-61.

14. Levine, D.; Steinhardt, P. J., Quasicrystals: a new class of ordered structures. *Physical review letters* **1984,** *53* (26), 2477.

15. Senechal, M., *Quasicrystals and geometry*. CUP Archive: 1996.

16. Liu, L.; Li, Z.; Li, Y.; Mao, C., Rational Design and Self-Assembly of Two-Dimensional, Dodecagonal DNA Quasicrystals. *J Am Chem Soc* **2019,** *141* (10), 4248-4251.

17. Lu, P. J.; Steinhardt, P. J., Decagonal and quasi-crystalline tilings in medieval Islamic architecture. *science* **2007,** *315* (5815), 1106-1110.

18. Cohen, M. F.; Shade, J.; Hiller, S.; Deussen, O., Wang tiles for image and texture generation. *ACM Transactions on Graphics (TOG)* **2003,** *22* (3), 287-294.

19. Winfree, E., *Algorithmic self-assembly of DNA*. California Institute of Technology: 1998.

20. Pinheiro, A. V.; Han, D.; Shih, W. M.; Yan, H., Challenges and opportunities for structural DNA nanotechnology. *Nat Nanotechnol* **2011,** *6* (12), 763-72.

21. Zhang, F.; Nangreave, J.; Liu, Y.; Yan, H., Structural DNA nanotechnology: state of the art and future perspective. *J Am Chem Soc* **2014,** *136* (32), 11198-211.

22. Seeman, N. C.; Sleiman, H. F., DNA nanotechnology. *Nature Reviews Materials* **2017,** *3* (1), 1-23.

23. Wang, P.; Gaitanaros, S.; Lee, S.; Bathe, M.; Shih, W. M.; Ke, Y., Programming Self-Assembly of DNA Origami Honeycomb Two-Dimensional Lattices and Plasmonic Metamaterials. *J Am Chem Soc* **2016,** *138* (24), 7733-40.

24. Liu, X.; Zhang, F.; Jing, X.; Pan, M.; Liu, P.; Li, W.; Zhu, B.; Li, J.; Chen, H.; Wang, L.; Lin, J.; Liu, Y.; Zhao, D.; Yan, H.; Fan, C., Complex silica composite nanomaterials templated with DNA origami. *Nature* **2018,** *559* (7715), 593-598.

25. Sun, W.; Shen, J.; Zhao, Z.; Arellano, N.; Rettner, C.; Tang, J.; Cao, T.; Zhou, Z.; Ta, T.; Streit, J. K., Precise pitch-scaling of carbon nanotube arrays within three-dimensional DNA nanotrenches. *Science* **2020,** *368* (6493), 874-877.

26. Shen, J.; Sun, W.; Liu, D.; Schaus, T.; Yin, P., Three-dimensional nanolithography guided by DNA modular epitaxy. *Nature Materials* **2021,** *20* (5), 683-690.

27. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

28. Wang, P.; Meyer, T. A.; Pan, V.; Dutta, P. K.; Ke, Y., The beauty and utility of DNA origami. *Chem* **2017,** *2* (3), 359-382.

29. Hong, F.; Zhang, F.; Liu, Y.; Yan, H., DNA Origami: Scaffolds for Creating Higher Order Structures. *Chem Rev* **2017,** *117* (20), 12584-12640.

30. Dey, S.; Fan, C.; Gothelf, K. V.; Li, J.; Lin, C.; Liu, L.; Liu, N.; Nijenhuis, M. A.; Saccà, B.; Simmel, F. C., DNA origami. *Nature Reviews Methods Primers* **2021,** *1* (1), 13.

31. Tikhomirov, G.; Petersen, P.; Qian, L., Triangular DNA Origami Tilings. *J Am Chem Soc* **2018**.

32. Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C., Crystalline two-dimensional DNA-origami arrays. *Angew Chem Int Ed Engl* **2011,** *50* (1), 264-7.

33. Liu, W.; Halverson, J.; Tian, Y.; Tkachenko, A. V.; Gang, O., Self-organized architectures from assorted DNA-framed nanoparticles. *Nature chemistry* **2016,** *8* (9), 867-873.

34. Tikhomirov, G.; Petersen, P.; Qian, L., Programmable disorder in random DNA tilings. *Nat Nanotechnol* **2017,** *12* (3), 251-259.

35. Aghebat Rafat, A.; Sagredo, S.; Thalhammer, M.; Simmel, F. C., Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities. *Nature chemistry* **2020,** *12* (9), 852-859.

36. Suzuki, Y.; Sugiyama, H.; Endo, M., Complexing DNA origami frameworks through sequential self - assembly based on directed docking. *Angewandte Chemie International Edition* **2018,** *57* (24), 7061-7065.

37. Williams, S.; Lund, K.; Lin, C.; Wonka, P.; Lindsay, S.; Yan, H. In *Tiamat: a three-dimensional editing tool for complex DNA structures*, DNA Computing: 14th International Meeting on DNA Computing, DNA 14, Prague, Czech Republic, June 2-9, 2008. Revised Selected Papers 14, Springer: 2009; pp 90-101.

38. SantaLucia Jr, J.; Hicks, D., The thermodynamics of DNA structural motifs. *Annu. Rev. Biophys. Biomol. Struct.* **2004,** *33*, 415-440.

39. Kilchherr, F.; Wachauf, C.; Pelz, B.; Rief, M.; Zacharias, M.; Dietz, H., Single-molecule dissection of stacking forces in DNA. *Science* **2016,** *353* (6304), aaf5508.

40. Minev, D.; Wintersinger, C. M.; Ershova, A.; Shih, W. M., Robust nucleation control via crisscross polymerization of highly coordinated DNA slats. *Nature communications* **2021,** *12* (1), 1741.

41. Fischer, S.; Hartl, C.; Frank, K.; Radler, J. O.; Liedl, T.; Nickel, B., Shape and Interhelical Spacing of DNA Origami Nanostructures Studied by Small-Angle X-ray Scattering. *Nano Lett* **2016,** *16* (7), 4282-7.

42. Coxeter, H., Mathematical Models. By HM Cundy and AP Rollett. Pp. 286. 25s. 1961.(Oxford University Press). *The Mathematical Gazette* **1962,** *46* (358), 331-331.

43. Tomizawa, J.-i., Control of cole 1 plasmid replication: the process of binding of RNA I to the primer transcript. *Cell* **1984,** *38* (3), 861-870.

44. Barbault, F.; Huynh-Dinh, T.; Paoletti, J.; Lancelot, G., A new peculiar DNA structure: NMR solution structure of a DNA kissing complex. *Journal of Biomolecular Structure and Dynamics* **2002,** *19* (4), 649-658.

45. Barth, A.; Kobbe, D.; Focke, M., DNA–DNA kissing complexes as a new tool for the assembly of DNA nanostructures. *Nucleic Acids Research* **2016,** *44* (4), 1502-1513.

CHAPTER 4

ALGORITHMIC SELF-ASSEMBLY OF DNA ORIGAMI

4.1 Abstract

Conventional integrated circuit technology in electronic computers is nearing the limits of its capabilities. In light of this, the development of DNA computers has attracted significant interest. DNA computers utilize base pairings of four types of nucleotides and are built on the principle of complementary base pairing. Current methods for reading DNA computer signals are expensive and challenging to automate. In this study, a series of square DNA origami units were introduced that algorithmically self-assemble into a Sierpiński triangular pattern while performing the XOR function. All four edges of the square origami are identical in 2D space, and the unique geometry of the DNA origami capitalizes on the geometric differences of various bond arrangements. The '1-bit' and '0-bit' information is transmitted through distinct pathways, and the output information can be read not only by atomic force microscopy (AFM) but also by non-invasive methods such as stochastic optical reconstruction microscopy (STORM) and DNA-PAINT. This work has the potential for further development and broader applications, including the design of nanoscale combinatorial circuits, devices, and networks.

4.2 Introduction

The birth of the electronic computer marked a milestone in human history. However, the increasing demand for higher integration levels poses significant challenges to conventional integrated circuit technology, which is approaching the limits of what current techniques can achieve[1-4]. Recognizing this, the development of DNA computers has garnered widespread attention[5-8]. DNA is composed of four types of nucleotides bases and stores biological genetic information through their unique arrangements[9-12]. DNA computers are built upon these distinctive base pairings. In fact, DNA molecules can be viewed as strings composed of four different symbols of four bases which can be encoded based on the principle of complementary base pairing[13-15]. While DNA molecules have successfully realized various complex biochemical circuits[16-20], the output of DNA computer signals has always been a challenge. Currently, the characterization of single DNA computer molecules mainly relies on expensive and difficult-to-automate techniques such as atomic force microscopy (AFM) and single-molecule fluorescence spectroscopy.

DNA origami technique, which involves folding a long single-stranded DNA (scaffold) by hundreds of short DNA strands (staples) into designed shapes[21], is exceptionally versatile in manufacturing delicate nanostructures with different shapes and sizes[22-26]. Here, we present a series of square DNA origami units to algorithmic self-assemble into Sierpiński triangular pattern while operation XOR function[27-31]. In this work, SQ origami is geometrically more similar to Wang Tile[32, 33], all four edges are identical in 2D space. The output Information can be read not only by AFM, but also by non-invasive method like STORM, DNA-PAINT, etc[34, 35]. The unique geometry of the

DNA origami makes use of the geometric difference of different bond arrangements. '1-bit' and '0-bit' are propagated through distinct path. Also, 5'- and 3'- bond in this origami units are intrinsically orthogonal to each other. DNA origami will not bind once flipped.

4.3 Design with p3548 square DNA origami

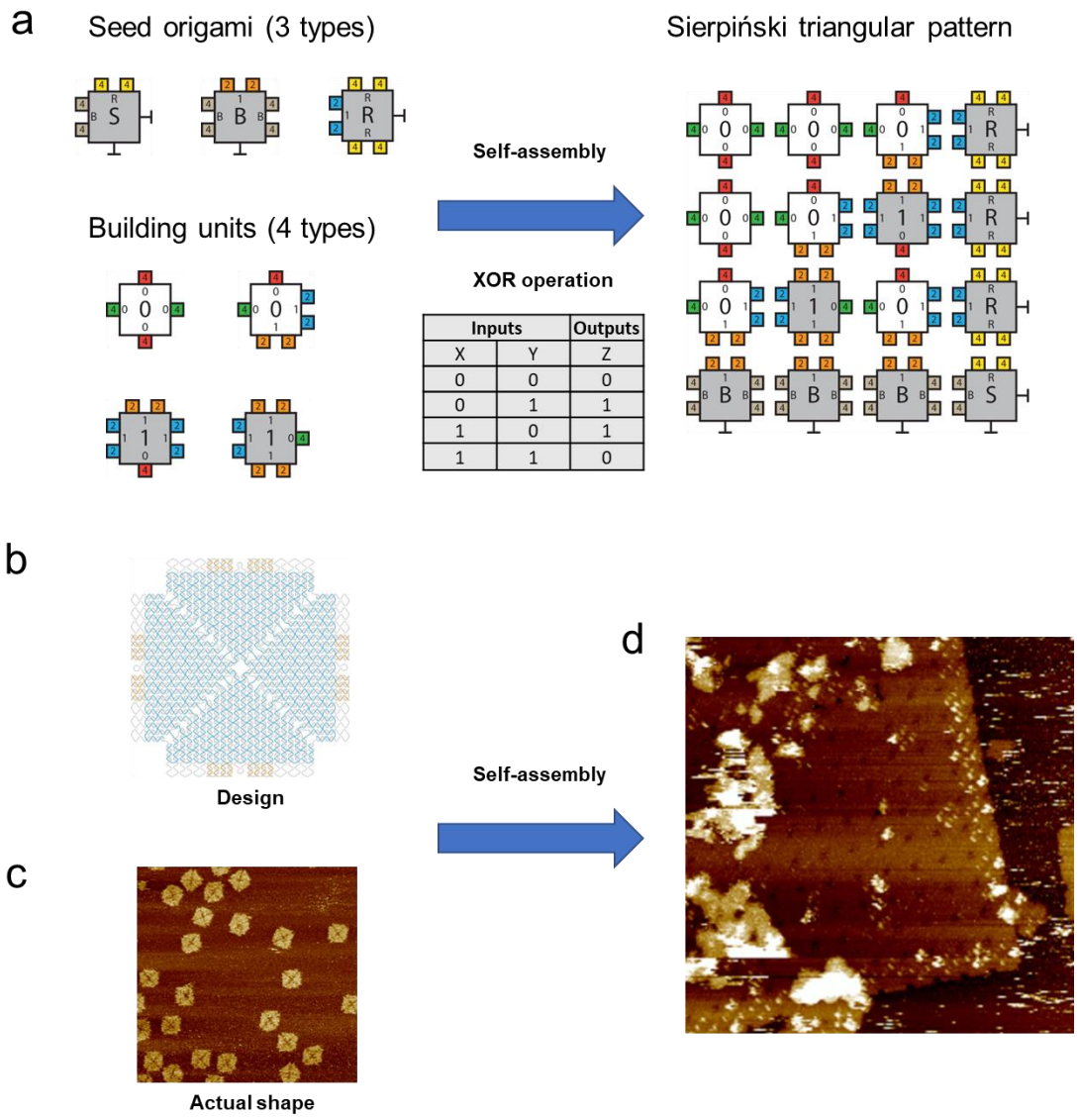

Figure 4.1. **Workflow of algorithmic self-Assembly of DNA origami into Sierpiński triangular pattern.** (a) Overview of the design of Sierpiński triangular pattern from square units. This Sierpiński triangular pattern is composed through the XOR logical operation by 3 types of seed units and 4 types of building units. (b) The design of operation units, which is a M13mp18 square DNA origami with different sticky end

arrangements. The designs are finalized on Tiamat[36] by generating the scaffold strand (gray), core (blue), and edge (orange) staple strands, assigning sequences, and defining matching rules. (c) A DNA origami operation unit corresponding to the one in (b) is visualized by atomic force microscopy (AFM). (d) An AFM image showing Sierpiński triangular pattern which assembled by origami units.

The process of algorithmically self-assembling DNA origami into a Sierpiński triangular pattern consists of four stages (Figure 4.1). This pattern is composed of two series of units: seed origami and building units (Figure 4.1a). Seed origami includes type S, type B, and type R units. Type S units act as nucleation sites for the pattern and initially assemble with type B and type R units. The type B/type R units then bind with other type B/type R units, forming a right-angle frame. Subsequently, the four types of building units - type 00, type 11, type 01, and type 10 units - programmably assemble from the bottom to the top and from left to right directions, starting with the type B/ type R units on the right-angle frame. These building units also serve as algorithm units for the XOR operation.

In the building units, the sticky end arrangements on their bottom and right sides represent '1-bit' or '0-bit' input, while the sticky end arrangements on their top and left sides represent '1-bit' or '0-bit' output. As the seed origami and building units self-assemble into a 2D lattice, they exhibit the Sierpiński triangular pattern, as programmed by the XOR operation. The square unit design is finalized in Tiamat (Figure 4.1b) using the M13mp18 (a 7,249-nt scaffold widely used for building DNA origami nanostructures) and visualized through atomic force microscopy (AFM) (Figure 4.1c). The self-assembled 2D lattice of seed origami and building units, displaying the Sierpiński triangular pattern, is also characterized (Figure 4.1d).

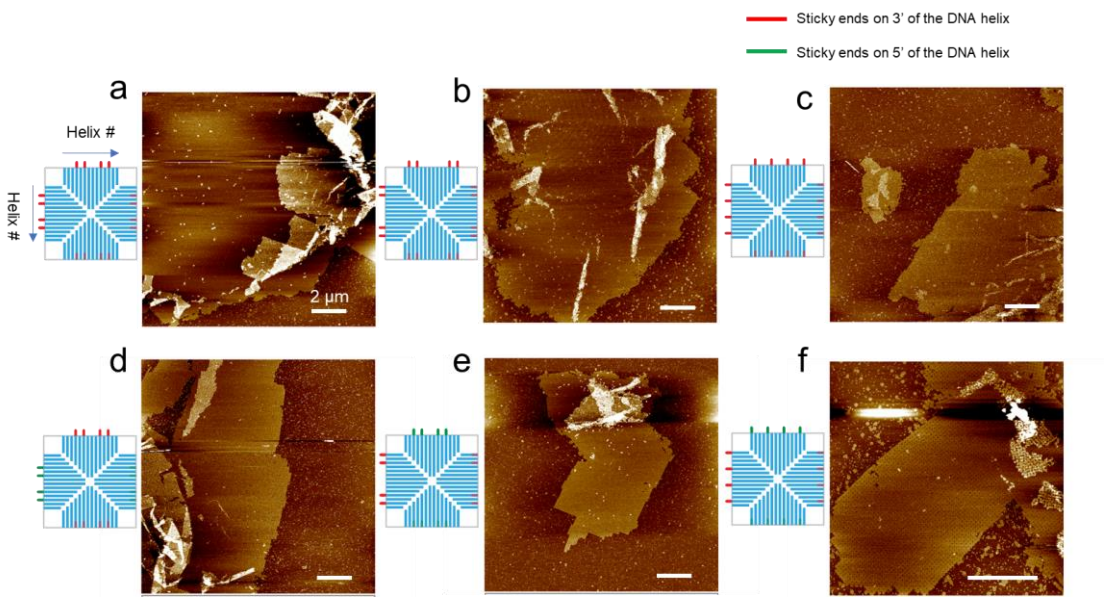

Figure 4.2. **2D lattices assembled from p3548 square DNA origami with different sticky end arrangements.** (a) The p3548 square DNA origami units with the sticky end arrangement give at 4th, 6th, 10th, and 12th helix on the top; accept at 4th, 6th, 10th, and 12th helix on the bottom; give at 3rd, 5th, 9th, and 11th helix on the left; and accept at 3rd, 5th, 9th and, 11th helix on the right. (b) The p3548 square DNA origami units with the sticky end arrangement give at 2nd, 4th, 12th, and 14th helix on the top; accept at 2nd, 4th, 12th, and 14th helix on the bottom; give at 1st, 3rd, 11th, and 13th helix on the left; and accept at 1st, 3rd, 11th, and 13th helix on the right. (c) The p3548 square DNA origami units with the sticky end arrangement give at 2nd, 6th, 10th, and 14th helix on the top; accept at 2nd, 6th, 10th, and 14th helix on the bottom; give at 1st, 5th, 9th, and 13th helix on the left; and accept at 1st, 5th, 9th, and 13th helix on the right. (d) The p3548 square DNA origami units with the sticky end arrangement give at 4th, 6th, 10th, and 12th helix on the top; accept at 4th, 6th, 10th, and 12th helix on the bottom; give at 4th, 6th, 10th, and 12th helix on the left; and accept at 4th, 6th, 10th, and 12th helix on the right. (e) The p3548 square DNA origami units with the sticky end arrangement give at 3rd, 5th, 9th, and 11th helix on the top; accept at 3rd, 5th, 9th, and 11th helix on the bottom; give at 1st, 3rd, 11th, and 13th helix on the left; and accept at 1st, 3rd, 11th, and 13th helix on the right. (f) The p3548 square DNA origami unit with the sticky end arrangement gives at 1st, 5th, 9th, and 13th helix on the top; accept at 1st, 5th, 9th, and 13th helix on the bottom; give at 1st, 5th, 9th, and 13th helix on the left; and accept at 1st, 5th, 9th, and 13th helix on the right. Scale bar: 2 μm.

Initially, the square units were designed based on p3548 (a customized scaffold consisting of 3,548 nt). In order to create the Sierpiński triangular pattern, the square units possess varying sticky end arrangements on their distinct unit sides. This necessitates the selection of square DNA origami capable of forming a 2D lattice with diverse sticky end configurations. As visualized by atomic force microscopy (AFM), all six square designs yielded micrometer-scale lattices (Figure 4.2). Despite having different sticky end arrangements, as seen in Figure 4.2d-f, the square units were still able to grow

up to dimensions exceeding 10 μm, exhibiting nearly defect-free areas.

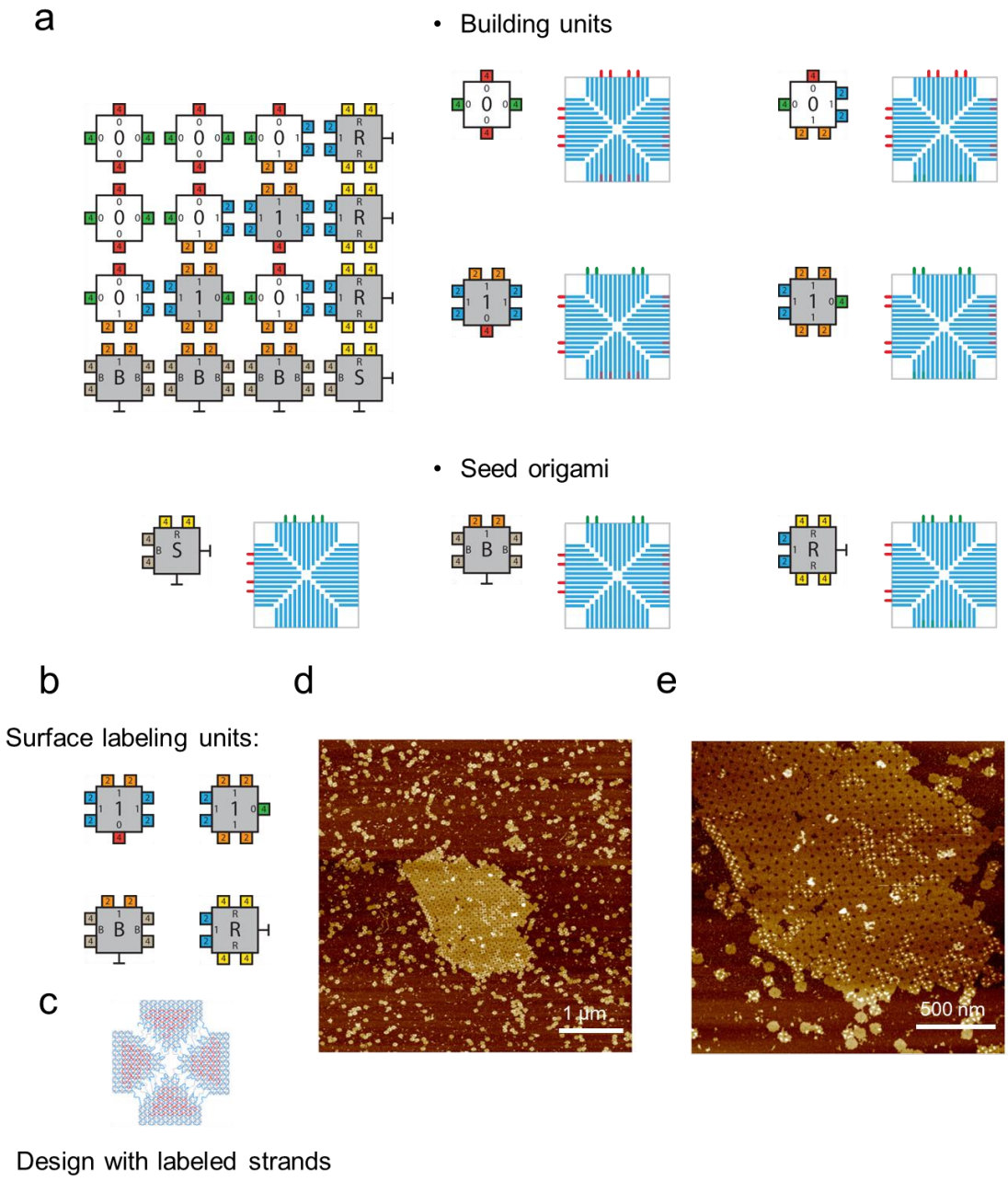

Figure 4.3. **Sierpiński triangular pattern assembled from p3548 square DNA origami units.** (a) The sticky end arrangements of the 4 types of building units and 3 types of seed origami. The edges of the bottom side and the right side of type S seed origami, the bottom side of type B seed origami, and the right side of type R seed origami have hairpin blocking strands. (b) 4 types of units are selected for surface label: type 01 building unit, type 10 building unit, type B seed origami, and type R seed origami. (c) The design of surface labeled units. Core staple strands (red) with 20-nt of ploy A extension. (d) A zoomed-out AFM image showing the Sierpiński triangular pattern. Scale

bar: 1 μm. (e) A zoomed-in AFM image showing the Sierpiński triangular pattern. Scale bar: 500 nm.

The building units and seed origami, created using the p3548 square DNA origami, were assigned distinct sticky end configurations to facilitate algorithmic assembly (Figure 4.2a). In order to enable pattern information to be read via AFM, two types of building units and two types of seed origami were chosen for surface labeling (Figure 4.2b). To label the square DNA origami, ten core staple strands in each triangular subunit were extended with 20-nt of poly A (Figure 4.2c). During the lattice annealing process, the addition of complementary poly T resulted in modified aggregation visible in the captured AFM images. However, the zoom-out and zoom-in AFM images (Figure 4.2d, e) of the 2D lattice with the Sierpiński triangular pattern did not meet expectations, as the lattice size failed to grow substantially.

To assess whether surface modifications on the square units could affect lattice size and pattern, four square DNA origami designs with varying numbers and sites of surface labeling strands were prepared (Figure S4.2). The different patterns of captured arrays, ranging from large arrays to tube-like structures, suggest that surface labeling strands can alter the curvature of the origami units and limit the growth of the 2D lattice. Moreover, the seed origami pattern did not display a consistent line pattern, indicating that the seed origami failed to function as a nucleation site and guide lattice formation. The surface-labeled unit patterns also did not align well with the Sierpiński triangle pattern. Even through the different building units had assigned different sticky end arrangements, the specificity imparted by the number of helixes became inadequate to define their matching

rules strictly, resulting in increased defects. To mitigate this issue, a larger square design with a greater number of helices on each side is recommended.

4.4 Design with M13mp18 square DNA origami

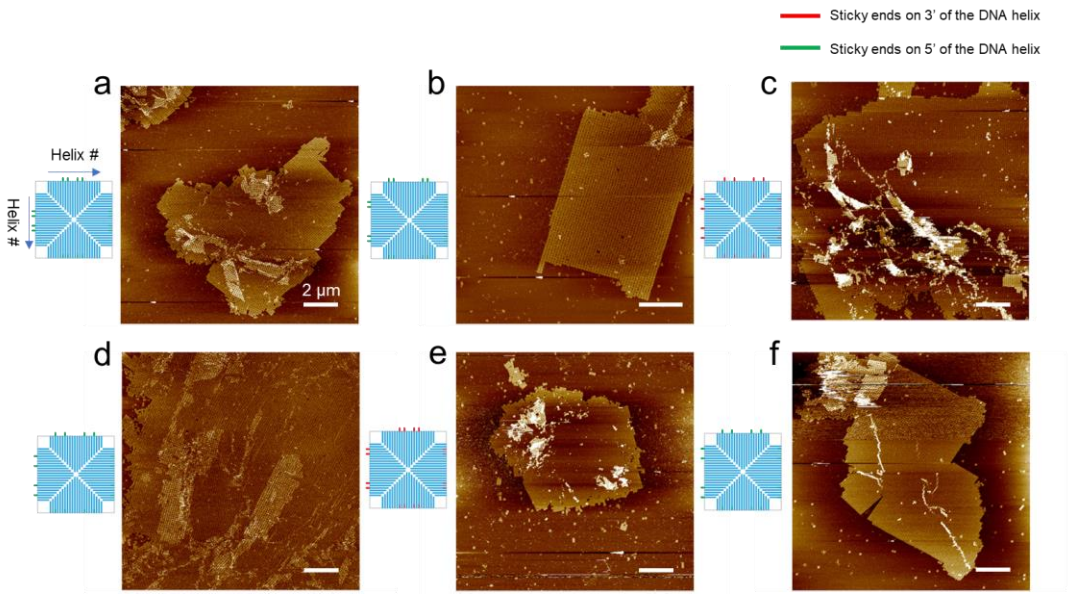

Figure 4.4. **2D lattices assembled from M13mp18 square DNA origami with different sticky end arrangements.** (a) The M13mp18 square DNA origami units with the sticky end arrangement give at 7th, 9th, 13th, and 15th helix on the top; accept at 7th, 9th, 13th, and 15th helix on the bottom; give at 8th, 10th, 14th, and 16th helix on the left; and accept at 8th, 10th, 14th, and 16th helix on the right. (b) The M13mp18 square DNA origami units with the sticky end arrangement give at 3rd, 5th, 17th, and 19th helix on the top; accept at 3rd, 5th, 17th, and 19th helix on the bottom; give at 4th, 6th, 18th, and 20th helix on the left; and accept at 4th, 6th, 18th, and 20th helix on the right. (c) The M13mp18 square DNA origami units with the sticky end arrangement give at 4th, 8th, 16th, and 20th helix on the top; accept at 4th, 8th, 16th, and 20th helix on the bottom; give at 3rd, 7th, 15th, and 19th helix on the left; and accept at 3rd, 7th, 15th, and 19th helix on the right. (d) The M13mp18 square DNA origami units with the sticky end arrangement give at 3rd, 7th, 15th, and 19th helix on the top; accept at 3rd, 7th, 15th, and 19th helix on the bottom; give at 4th, 8th, 16th, and 20th helix on the left; and accept at 4th, 8th, 16th, and 20th helix on the right. (e) The M13mp18 square DNA origami units with the sticky end arrangement give at 8th, 10th, 14th, and 16th helix on the top; accept at 8th, 10th, 14th, and 16th helix on the bottom; give at 3rd, 5th, 17th, and 19th helix on the left; and accept at 3rd, 5th, 17th, and 19th helix on the right. (f) The M13mp18 square DNA origami unit with the sticky end arrangement gives at 3rd, 7th, 15th and, 19th helix on the top; accept at 3rd, 7th, 15th, and 19th helix on the bottom; give at 2nd, 6th, 14th, and 18th helix on the left; and accept at 2nd, 6th, 14th, and 18th helix on the right. Scale bar: 2 μm.

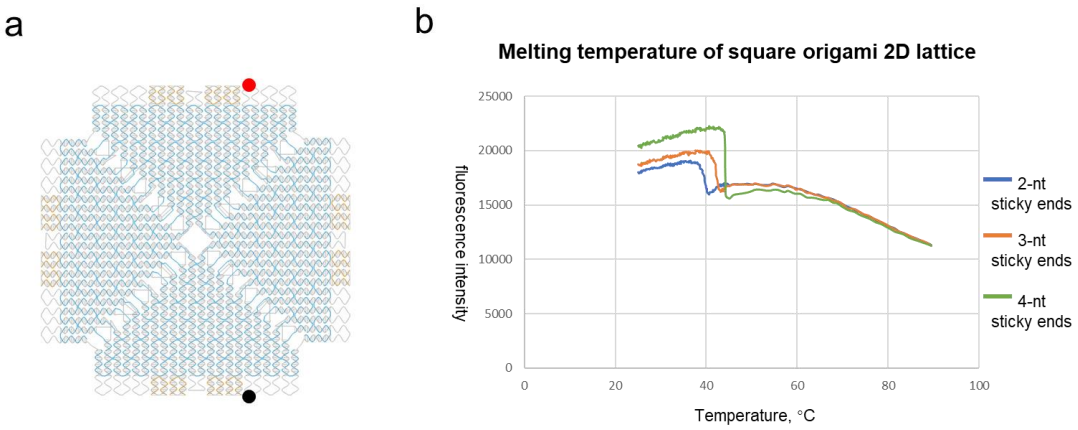

Figure 4.5. **Melting temperature measurements of square DNA origami.** (a) The design of DNA origami unit for fluorescence experiments to test its melting temperature. A FAM fluorophore (red) is attached to the 3’ end of one edge staple strand on the top side and a TAMRA quencher (black) is also attached at the 5’ end of edge staple strand on the bottom side, which allow the fluorophore and quencher could be placed face to face once the lattice was formed. (b) The results of melting temperature of the square units from 2D lattice to monomers. The melting points of the units with 2-nt, 3-nt and 4-nt sticky ends were 41.0 °C, 44.3 °C, and 45.2 °C.

Subsequently, the square units were designed using the M13mp18 scaffold. The adaptability of this square DNA origami to form a 2D lattice with varying sticky end configurations was verified (Figure 4.4). In order to decrease the number of nucleation sites in the M13mp18 square units, seed origami with different sticky end lengths were evaluated. The seed origami was intended to assemble first at a higher temperature than the building units during the lattice annealing process. This approach would guide the assembly of building units, thereby significantly improving their addressability.

To determine the melting point of the 2D lattice of square origami, a FAM fluorophore (red) was attached to the 3' end of one edge staple strand on the top side of the square origami (Figure 4.5a), and a TAMRA quencher (black) was also attached to the 5' end of the edge staple strand on the bottom side, allowing the fluorophore and quencher to be positioned face-to-face once the lattice was formed. In the fluorescence

experiments (Figure 4.5b), the melting points of the units with 2-nt, 3-nt, and 4-nt sticky ends were found to be 41.0°C, 44.3°C, and 45.2°C, respectively. Additionally, the M13mp18 square DNA origami monomers could be effectively formed at 50°C (Figure S4.3), which allowed the preparation of lattices assembled from two or more tile species (Sierpiński triangular pattern) at 50°C for the initial step.

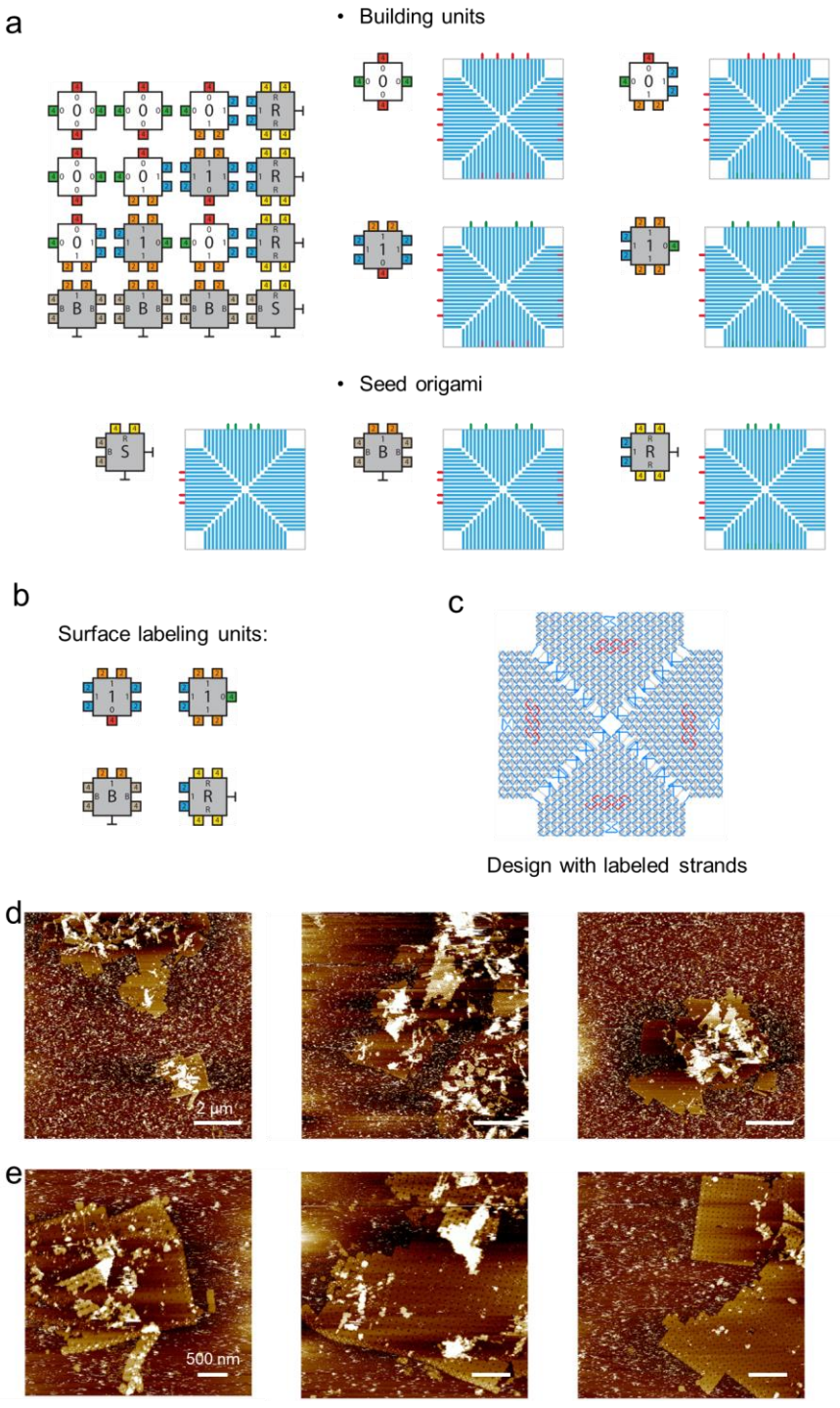

Figure 4.6. **Design and AFM characterization of 2D lattices assembled from M13mp18 square DNA origami.** (a) The sticky end arrangements of the 4 types of building units and 3 types of seed origami. The edges of the bottom side and the right side of type S seed origami, the bottom side of type B seed origami, and the right side of type R seed origami have hairpin blocking strands. (b) 4 types of units are selected for surface label: type 01 building unit, type 10 building unit, type B seed origami, and type

R seed origami. (c) The design of surface labeled units. Core staple strands (red) with 20-nt of ploy A and biotin extension. (d) A zoomed-out AFM image showing the Sierpiński triangular pattern. Scale bar: 2 μm. (e) A zoomed-in AFM image showing the Sierpiński triangular pattern. Scale bar: 500 nm.

The M13mp18 square DNA origami-based building units and seed origami were assigned various sticky end configurations for conducting the algorithmic assembly (Figure 4.6a). In order to enable the pattern information to be read using AFM, two types of building units and two types of seed origami were chosen for surface labeling (Figure 4.6b). To label the square DNA origami, three core staple strands in each triangular subunit were biotin-labeled to bind with streptavidin (Figure 4.6c). Zoomed-out and zoomed-in AFM images (Figure 4.6d, e) of the 2D lattice with the Sierpiński triangular pattern were captured. In this design, the arrays could achieve sizes on the micrometer scale. The zoomed-in images showed a linear-like label at the edge of the array. The surface label pattern suggested that the assembly was guided by a single type of either type B seed origami or type R seed origami, rather than an origami frame assembled by all three types of seed origami. Further optimization of the annealing program and tile design could prove beneficial for this process.

4.5 Discussion

In conclusion, we have developed a series of square DNA origami units that algorithmically self-assemble into a Sierpiński triangular pattern while executing the XOR function. Our design employs M13mp18 square DNA origami to form a 2D lattice with six distinct sticky end arrangements. By introducing seed origami with longer sticky ends (3-nt), we facilitate initial assembly at higher temperatures, which guides the building units during the lattice annealing process. Following the surface labeling of

DNA units with biotin, the Sierpiński triangular pattern was captured, demonstrating that the assembly is directed by the seed origami. This research holds promise for future advancements and wider applications, such as designing nanoscale combinatorial circuits, devices, and networks.

4.6 Material and Methods

See APPENDIX B.

4.7 Referance

1. Lloyd, S., Ultimate physical limits to computation. *Nature* **2000,** *406* (6799), 1047-1054.

2. Markov, I. L., Limits on fundamental limits to computation. *Nature* **2014,** *512* (7513), 147-154.

3. Peercy, P. S., The drive to miniaturization. *Nature* **2000,** *406* (6799), 1023-1026.

4. Kitano, H., Computational systems biology. *Nature* **2002,** *420* (6912), 206-210.

5. Adleman, L. M., Molecular computation of solutions to combinatorial problems. *science* **1994,** *266* (5187), 1021-1024.

6. Benenson, Y.; Paz-Elizur, T.; Adar, R.; Keinan, E.; Livneh, Z.; Shapiro, E., Programmable and autonomous computing machine made of biomolecules. *Nature* **2001,** *414* (6862), 430-434.

7. Ma, Q.; Zhang, C.; Zhang, M.; Han, D.; Tan, W., DNA Computing: Principle, Construction, and Applications in Intelligent Diagnostics. *Small Structures* **2021,** *2* (11), 2100051.

8. Liu, Q.; Wang, L.; Frutos, A. G.; Condon, A. E.; Corn, R. M.; Smith, L. M., DNA computing on surfaces. *Nature* **2000,** *403* (6766), 175-179.

9. Lund, K.; Williams, B.; Ke, Y.; Liu, Y.; Yan, H., DNA nanotechnology: a rapidly evolving field. *Current Nanoscience* **2006,** *2* (2), 113-122.

10. Ghosh, A.; Bansal, M., A glossary of DNA structures from A to Z. *Acta Crystallographica Section D: Biological Crystallography* **2003,** *59* (4), 620-626.

11. Pray, L., Discovery of DNA structure and function: Watson and Crick. *Nature Education* **2008,** *1* (1), 100.

12. Lin, C.; Liu, Y.; Rinker, S.; Yan, H., DNA tile based self-assembly: building complex nanoarchitectures. *ChemPhysChem* **2006,** *7* (8), 1641-1647.

13. Gibbons, A.; Amos, M.; Hodgson, D., DNA computing. *Current opinion in biotechnology* **1997,** *8* (1), 103-106.

14. Ezziane, Z., DNA computing: applications and challenges. *Nanotechnology* **2005,** *17* (2), R27.

15. Paun, G.; Rozenberg, G.; Salomaa, A., *DNA computing: new computing paradigms*.

Springer Science & Business Media: 2005.

16. Qian, L.; Winfree, E., Scaling up digital circuit computation with DNA strand displacement cascades. *Science* **2011,** *332* (6034), 1196-201.

17. Qian, L.; Winfree, E.; Bruck, J., Neural network computation with DNA strand displacement cascades. *Nature* **2011,** *475* (7356), 368-72.

18. Woods, D.; Doty, D.; Myhrvold, C.; Hui, J.; Zhou, F.; Yin, P.; Winfree, E., Diverse and robust molecular algorithms using reprogrammable DNA self-assembly. *Nature* **2019,** *567* (7748), 366-372.

19. Tikhomirov, G.; Petersen, P.; Qian, L., Fractal assembly of micrometre-scale DNA origami arrays with arbitrary patterns. *Nature* **2017,** *552* (7683), 67-71.

20. Genot, A.; Baccouche, A.; Sieskind, R.; Aubert-Kato, N.; Bredèche, N.; Bartolo, J.; Taly, V.; Fujii, T.; Rondelez, Y., High-resolution mapping of bifurcations in nonlinear biochemical circuits. *Nature chemistry* **2016,** *8* (8), 760-767.

21. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

22. Ke, Y.; Sharma, J.; Liu, M.; Jahn, K.; Liu, Y.; Yan, H., Scaffolded DNA origami of a DNA tetrahedron molecular container. *Nano Lett* **2009,** *9* (6), 2445-7.

23. Douglas, S. M.; Dietz, H.; Liedl, T.; Högberg, B.; Graf, F.; Shih, W. M., Self-assembly of DNA into nanoscale three-dimensional shapes. *Nature* **2009,** *459* (7245), 414-418.

24. Han, D.; Pal, S.; Nangreave, J.; Deng, Z.; Liu, Y.; Yan, H., DNA origami with complex curvatures in three-dimensional space. *Science* **2011,** *332* (6027), 342-6.

25. Zhang, F.; Jiang, S.; Wu, S.; Li, Y.; Mao, C.; Liu, Y.; Yan, H., Complex wireframe DNA origami nanostructures with multi-arm junction vertices. *Nat Nanotechnol* **2015,** *10* (9), 779-84.

26. Gerling, T.; Wagenbauer, K. F.; Neuner, A. M.; Dietz, H., Dynamic DNA devices and assemblies formed by shape-complementary, non–base pairing 3D components. *Science* **2015,** *347* (6229), 1446-1452.

27. Rothemund, P. W.; Papadakis, N.; Winfree, E., Algorithmic self-assembly of DNA Sierpinski triangles. *PLoS Biol* **2004,** *2* (12), e424.

28. Fujibayashi, K.; Hariadi, R.; Park, S. H.; Winfree, E.; Murata, S., Toward reliable algorithmic self-assembly of DNA tiles: A fixed-width cellular automaton pattern. *Nano*

Letters **2008,** *8* (7), 1791-1797.

29. Winfree, E., Algorithmic Self-Assembly of DNA: Theoretical Motivations and 2D Assembly Experiments. *J Biomol Struct Dyn* **2000,** *17 Suppl 1*, 263-70.

30. Winfree, E., *Algorithmic self-assembly of DNA*. California Institute of Technology: 1998.

31. Mao, C.; LaBean, T. H.; Relf, J. H.; Seeman, N. C., Logical computation using algorithmic self-assembly of DNA triple-crossover molecules. *Nature* **2000,** *407* (6803), 493-6.

32. Wang, H., Proving theorems by pattern recognition—II. *Bell system technical journal* **1961,** *40* (1), 1-41.

33. Cohen, M. F.; Shade, J.; Hiller, S.; Deussen, O., Wang tiles for image and texture generation. *ACM Transactions on Graphics (TOG)* **2003,** *22* (3), 287-294.

34. Jungmann, R.; Steinhauer, C.; Scheible, M.; Kuzyk, A.; Tinnefeld, P.; Simmel, F. C., Single-molecule kinetics and super-resolution microscopy by fluorescence imaging of transient binding on DNA origami. *Nano letters* **2010,** *10* (11), 4756-4761.

35. Jungmann, R.; Avendano, M. S.; Woehrstein, J. B.; Dai, M.; Shih, W. M.; Yin, P., Multiplexed 3D cellular super-resolution imaging with DNA-PAINT and Exchange-PAINT. *Nat Methods* **2014,** *11* (3), 313-8.

36. Williams, S.; Lund, K.; Lin, C.; Wonka, P.; Lindsay, S.; Yan, H. In *Tiamat: a three-dimensional editing tool for complex DNA structures*, DNA Computing: 14th International Meeting on DNA Computing, DNA 14, Prague, Czech Republic, June 2-9, 2008. Revised Selected Papers 14, Springer: 2009; pp 90-101.

CHAPTER 5

SUMMARY AND OUTLOOK

5.1 Main

Molecular tessellation research aims to elucidate the underlying principles that govern intricate patterns in nature and to leverage these principles to create precise and ordered structures across multiple scales, thereby facilitating the emergence of novel functionalities. DNA origami technology enables the fabrication of nearly arbitrary DNA architectures with nanoscale precision, which can serve as excellent building blocks for the construction of tessellation patterns. Here, we describe a general design and assembly method for creating DNA origami tiles that grow into tessellation patterns with micrometer-scale order and nanometer-scale precision. A critical design parameter, interhelical distance (***D***), was identified, which determined the conformation of monomer tiles and the outcome of tessellation. Finely tuned ***D*** facilitated the accurate geometric design of monomer tiles with minimized curvature and improved tessellation capability. To demonstrate the generality of the design method, 9 tile geometries and 15 unique tile designs were generated. The designed tiles were assembled into single-crystalline lattices ranging from tens to hundreds of square micrometers with micrometer-scale, nearly defect-free areas readily visualized by atomic force microscopy. We took two strategies to further increase the complexity of DNA origami tessellation, including reducing the symmetry of monomer tiles and co-assembling tiles of various geometries. The designed 6 complex tilings that includes 5 Archimedean tilings and a 12-fold quasicrystal tiling yielded various tiling patterns that great in size and quality, indicating the robustness of the optimized tessellation system. The described design and assembly approach can also

be employed to create square DNA origami units for algorithmic self-assembly. As the square units assembled and expanded, they executed the binary function XOR, which generated the Sierpinski triangular pattern according to the predetermined instructions.

We draw two clues from this study that are useful for future research. Firstly, design parameters with angstrom-level or better precision are in demand for designing higher-order self-assemblies of DNA, but resources for high-precision design parameters are limited. Among techniques commonly used for DNA nanostructure characterization, cryogenic electron microscopy (cryo-EM) provides the route for high-resolution structural determination in solution. Due to excessive conformational heterogeneity, the accurate structural validation of single-layer DNA origami nanostructures with cryo-EM has been challenging[1]. Assembling DNA origami tiles into 2D lattices is expected to effectively reduce the conformational dynamics of monomer tiles and facilitate the visualization of structural features in high resolution, which can, in turn, guide further design refinement. Our system sets the structural foundation for establishing this feedback loop. Secondly, sequence design is nontrivial in determining the global conformation and the self-assembly thermodynamics of DNA origami tiles. Owing to the cooperativity imparted by the scaffold strand, monomer DNA origami nanostructures can be folded in a nearly quantitative manner without being severely influenced by different sequence assignments[2]. However, the ample design space of scaffold sequence assignment has been largely overlooked. Unlike tiles composed of short oligonucleotides, whose sequences can be arbitrarily defined to achieve a perfectly symmetric sequence design, the sequence of a DNA origami nanostructure can hardly be freely defined because it is primarily determined by the scaffold sequence used. DNA origami tiles are

intrinsically asymmetric at the sequence level, regardless of their geometries. This study provides multiple examples that are useful for elucidating the role of sequence with further thermodynamic analysis.

In addition to the continuous refinement of design parameters and rational sequence design, to further advance DNA origami tessellation systems, defect suppression, nucleation control, sustained growth, and shape recognition are viable strategies to take. Two types of point defects, adatom and interstitial, are commonly observed in the DNA origami tessellation systems. Both originate from the undesired interactions between monomer tiles and lattices mediated by unpaired loop regions, which can be minimized by optimizing the routing path of the scaffold strand. Secondly, tilings reported here begin with spontaneous nucleation and terminate primarily due to the exhaustion of free tiles. Inhibiting excessive spontaneous nucleation by introducing pre-formed seeds and sustaining lattice growth by replenishing free tiles may serve the purpose of further scaling up. Besides, the finite combinatorial possibilities of short sticky ends can only endow the tiling with limited specificity, especially when the tiling involves multiple unique tile species. Integrating shape complementarity as an additional proofreading mechanism can facilitate correct tile recognition and compensate for the deficiencies in specificity. Optimizations in these aspects are expected to further improve the size and quality of DNA origami tessellation patterns and hold promise for extending the remarkable advantages of DNA origami to the macroscopic scale.

More broadly, the design method has the potential to be compiled or incorporated into automatic design software tools to make it available to non-experts[3]. It can also be generalized to more rigid, multi-layer DNA tile constructs that overcome the intrinsic

flexibility of single-layer DNA origami and better support long-range patterning of bulky cargos, such as nanoparticles and carbon nanotubes, for applications in nanoplasmonics and nanoelectronics. Other potential applications include interfacing with large guests such as cells and bacteria, hosting long-range light-harvesting and energy transfer molecular systems, and integrating with conventional lithographic materials and techniques. Overall, our work addresses the limitations in the size and complexity of DNA origami tessellation and paves the way for user-defined, programmable patterning of molecules or materials across scales where new properties may arise.

5.2 References

1. Kube, M.; Kohler, F.; Feigl, E.; Nagel-Yüksel, B.; Willner, E. M.; Funke, J. J.; Gerling, T.; Stömmer, P.; Honemann, M. N.; Martin, T. G., Revealing the structures of megadalton-scale DNA complexes with nucleotide resolution. *Nature communications* **2020,** *11* (1), 6229.

2. Sobczak, J. P.; Martin, T. G.; Gerling, T.; Dietz, H., Rapid folding of DNA into nanoscale shapes at constant temperature. *Science* **2012,** *338* (6113), 1458-61.

3. Huang, C.-M.; Kucinic, A.; Johnson, J. A.; Su, H.-J.; Castro, C. E., Integrated computer-aided engineering and design for DNA assemblies. *Nature Materials* **2021,** *20* (9), 1264-1271.

REFERENCES

Chapter 1 References

1. Whitesides, G. M.; Grzybowski, B., Self-assembly at all scales. *Science* **2002,** *295* (5564), 2418-2421.

2. Philp, D.; Stoddart, J. F., Self-assembly in natural and unnatural systems. *Angewandte Chemie International Edition in English* **1996,** *35* (11), 1154-1196.

3. Ball, P., The self-made tapestry: pattern formation in nature. **1999**.

4. Marth, J. D., A unified vision of the building blocks of life. *Nature cell biology* **2008,** *10* (9), 1015-1015.

5. Zhang, S., Fabrication of novel biomaterials through molecular self-assembly. *Nature biotechnology* **2003,** *21* (10), 1171-1178.

6. Li, J.; Ye, Q.; Cassell, A.; Ng, H. T.; Stevens, R.; Han, J.; Meyyappan, M., Bottom-up approach for carbon nanotube interconnects. *Applied Physics Letters* **2003,** *82* (15), 2491-2493.

7. Thiruvengadathan, R.; Korampally, V.; Ghosh, A.; Chanda, N.; Gangopadhyay, K.; Gangopadhyay, S., Nanomaterial processing using self-assembly-bottom-up chemical and biological approaches. *Reports on Progress in Physics* **2013,** *76* (6), 066501.

8. Whitesides, G. M.; Boncheva, M., Beyond molecules: Self-assembly of mesoscopic and macroscopic components. *Proceedings of the National Academy of Sciences* **2002,** *99* (8), 4769-4774.

9. Okesola, B. O.; Smith, D. K., Applying low-molecular weight supramolecular gelators in an environmental setting–self-assembled gels as smart materials for pollutant removal. *Chemical Society Reviews* **2016,** *45* (15), 4226-4251.

10. Watson, J. D.; Crick, F. H., Molecular structure of nucleic acids: a structure for deoxyribose nucleic acid. *Nature* **1953,** *171* (4356), 737-738.

11. Lund, K.; Williams, B.; Ke, Y.; Liu, Y.; Yan, H., DNA nanotechnology: a rapidly evolving field. *Current Nanoscience* **2006,** *2* (2), 113-122.

12. Ghosh, A.; Bansal, M., A glossary of DNA structures from A to Z. *Acta Crystallographica Section D: Biological Crystallography* **2003,** *59* (4), 620-626.

13. Pray, L., Discovery of DNA structure and function: Watson and Crick. *Nature Education* **2008,** *1* (1), 100.

14. Lin, C.; Liu, Y.; Rinker, S.; Yan, H., DNA tile based self-assembly: building complex nanoarchitectures. *ChemPhysChem* **2006,** *7* (8), 1641-1647.

15. Smith, A., Nucleic acids to amino acids: DNA specifies protein. *Nature Education* **2008,** *1* (1), 126.

16. Zhang, C.; Su, M.; He, Y.; Zhao, X.; Fang, P. A.; Ribbe, A. E.; Jiang, W.; Mao, C., Conformational flexibility facilitates self-assembly of complex DNA nanostructures. *Proc Natl Acad Sci U S A* **2008,** *105* (31), 10665-9.

17. Seeman, N. C., An overview of structural DNA nanotechnology. *Mol Biotechnol* **2007,** *37* (3), 246-57.

18. Seeman, N. C., Nanomaterials based on DNA. *Annu Rev Biochem* **2010,** *79*, 65-87.

19. Bujold, K. E.; Lacroix, A.; Sleiman, H. F., DNA nanostructures at the interface with biology. *Chem* **2018,** *4* (3), 495-521.

20. Mao, C., The emergence of complexity: lessons from DNA. *PLoS Biol* **2004,** *2* (12), e431.

21. Holliday, R., A mechanism for gene conversion in fungi. *Genetics Research* **1964,** *5* (2), 282-304.

22. Seeman, N. C., Nucleic acid junctions and lattices. *J Theor Biol* **1982,** *99* (2), 237-47.

23. Fu, T. J.; Seeman, N. C., DNA double-crossover molecules. *Biochemistry* **1993,** *32* (13), 3211-20.

24. Sa-Ardyen, P.; Vologodskii, A. V.; Seeman, N. C., The flexibility of DNA double crossover molecules. *Biophys J* **2003,** *84* (6), 3829-37.

25. Li, X.; Yang, X.; Qi, J.; Seeman, N. C., Antiparallel DNA double crossover molecules as components for nanoconstruction. *Journal of the American Chemical Society* **1996,** *118* (26), 6131-6140.

26. Winfree, E.; Liu, F.; Wenzler, L. A.; Seeman, N. C., Design and self-assembly of two-dimensional DNA crystals. *Nature* **1998,** *394* (6693), 539-44.

27. Yan, H.; Park, S. H.; Finkelstein, G.; Reif, J. H.; LaBean, T. H., DNA-templated self-assembly of protein arrays and highly conductive nanowires. *Science* **2003,** *301* (5641), 1882-4.

28. He, Y.; Chen, Y.; Liu, H.; Ribbe, A. E.; Mao, C., Self-assembly of hexagonal DNA two-dimensional (2D) arrays. *J Am Chem Soc* **2005,** *127* (35), 12202-3.

29. He, Y.; Tian, Y.; Ribbe, A. E.; Mao, C., Highly connected two-dimensional crystals of DNA six-point-stars. *J Am Chem Soc* **2006,** *128* (50), 15978-9.

30. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

31. Ke, Y.; Sharma, J.; Liu, M.; Jahn, K.; Liu, Y.; Yan, H., Scaffolded DNA origami of a DNA tetrahedron molecular container. *Nano Lett* **2009,** *9* (6), 2445-7.

32. Douglas, S. M.; Dietz, H.; Liedl, T.; Högberg, B.; Graf, F.; Shih, W. M., Self-assembly of DNA into nanoscale three-dimensional shapes. *Nature* **2009,** *459* (7245), 414-418.

33. Han, D.; Pal, S.; Nangreave, J.; Deng, Z.; Liu, Y.; Yan, H., DNA origami with complex curvatures in three-dimensional space. *Science* **2011,** *332* (6027), 342-6.

34. Zhang, F.; Jiang, S.; Wu, S.; Li, Y.; Mao, C.; Liu, Y.; Yan, H., Complex wireframe DNA origami nanostructures with multi-arm junction vertices. *Nat Nanotechnol* **2015,** *10* (9), 779-84.

35. Gerling, T.; Wagenbauer, K. F.; Neuner, A. M.; Dietz, H., Dynamic DNA devices and assemblies formed by shape-complementary, non–base pairing 3D components. *Science* **2015,** *347* (6229), 1446-1452.

36. Nickels, P. C.; Wünsch, B.; Holzmeister, P.; Bae, W.; Kneer, L. M.; Grohmann, D.; Tinnefeld, P.; Liedl, T., Molecular force spectroscopy with a DNA origami–based nanoscopic force clamp. *Science* **2016,** *354* (6310), 305-307.

37. Liu, W.; Halverson, J.; Tian, Y.; Tkachenko, A. V.; Gang, O., Self-organized architectures from assorted DNA-framed nanoparticles. *Nature chemistry* **2016,** *8* (9), 867-873.

38. Jungmann, R.; Avendano, M. S.; Woehrstein, J. B.; Dai, M.; Shih, W. M.; Yin, P., Multiplexed 3D cellular super-resolution imaging with DNA-PAINT and Exchange-PAINT. *Nat Methods* **2014,** *11* (3), 313-8.

39. Fu, J.; Liu, M.; Liu, Y.; Woodbury, N. W.; Yan, H., Interenzyme substrate diffusion for an enzyme cascade organized on spatially addressable DNA nanostructures. *J Am Chem Soc* **2012,** *134* (12), 5516-9.

40. Ke, Y.; Lindsay, S.; Chang, Y.; Liu, Y.; Yan, H., Self-assembled water-soluble nucleic acid probe tiles for label-free RNA hybridization assays. *Science* **2008,** *319* (5860),

180-3.

41. Kuzuya, A.; Sakai, Y.; Yamazaki, T.; Xu, Y.; Komiyama, M., Nanomechanical DNA origami'single-molecule beacons' directly imaged by atomic force microscopy. *Nature communications* **2011,** *2* (1), 449.

42. Bell, N. A.; Engst, C. R.; Ablay, M.; Divitini, G.; Ducati, C.; Liedl, T.; Keyser, U. F., DNA origami nanopores. *Nano letters* **2012,** *12* (1), 512-517.

43. Langecker, M.; Arnaut, V.; Martin, T. G.; List, J.; Renner, S.; Mayer, M.; Dietz, H.; Simmel, F. C., Synthetic lipid membrane channels formed by designed DNA nanostructures. *Science* **2012,** *338* (6109), 932-6.

44. Jiang, Q.; Song, C.; Nangreave, J.; Liu, X.; Lin, L.; Qiu, D.; Wang, Z. G.; Zou, G.; Liang, X.; Yan, H.; Ding, B., DNA origami as a carrier for circumvention of drug resistance. *J Am Chem Soc* **2012,** *134* (32), 13396-403.

45. Douglas, S. M.; Bachelet, I.; Church, G. M., A logic-gated nanorobot for targeted transport of molecular payloads. *Science* **2012,** *335* (6070), 831-834.

46. Schuller, V. J.; Heidegger, S.; Sandholzer, N.; Nickels, P. C.; Suhartha, N. A.; Endres, S.; Bourquin, C.; Liedl, T., Cellular immunostimulation by CpG-sequence-coated DNA origami structures. *ACS Nano* **2011,** *5* (12), 9696-702.

47. Wang, P.; Meyer, T. A.; Pan, V.; Dutta, P. K.; Ke, Y., The beauty and utility of DNA origami. *Chem* **2017,** *2* (3), 359-382.

48. Tikhomirov, G.; Petersen, P.; Qian, L., Fractal assembly of micrometre-scale DNA origami arrays with arbitrary patterns. *Nature* **2017,** *552* (7683), 67-71.

49. Fan, S.; Cheng, J.; Liu, Y.; Wang, D.; Luo, T.; Dai, B.; Zhang, C.; Cui, D.; Ke, Y.; Song, J., Proximity-Induced Pattern Operations in Reconfigurable DNA Origami Domino Array. *Journal of the American Chemical Society* **2020,** *142* (34), 14566-14573.

50. Zhao, Z.; Liu, Y.; Yan, H., Organizing DNA origami tiles into larger structures using preformed scaffold frames. *Nano Lett* **2011,** *11* (7), 2997-3002.

51. Tikhomirov, G.; Petersen, P.; Qian, L., Triangular DNA Origami Tilings. *J Am Chem Soc* **2018**.

52. Aghebat Rafat, A.; Sagredo, S.; Thalhammer, M.; Simmel, F. C., Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities. *Nature chemistry* **2020,** *12* (9), 852-859.

53. Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C., Crystalline two-dimensional DNA-

origami arrays. *Angew Chem Int Ed Engl* **2011,** *50* (1), 264-7.

54. Tikhomirov, G.; Petersen, P.; Qian, L., Programmable disorder in random DNA tilings. *Nat Nanotechnol* **2017,** *12* (3), 251-259.

55. Wang, P.; Gaitanaros, S.; Lee, S.; Bathe, M.; Shih, W. M.; Ke, Y., Programming Self-Assembly of DNA Origami Honeycomb Two-Dimensional Lattices and Plasmonic Metamaterials. *J Am Chem Soc* **2016,** *138* (24), 7733-40.

56. Andersen, E. S.; Dong, M.; Nielsen, M. M.; Jahn, K.; Lind-Thomsen, A.; Mamdouh, W.; Gothelf, K. V.; Besenbacher, F.; Kjems, J., DNA origami design of dolphin-shaped structures with flexible tails. *ACS Nano* **2008,** *2* (6), 1213-8.

57. Pinheiro, A. V.; Han, D.; Shih, W. M.; Yan, H., Challenges and opportunities for structural DNA nanotechnology. *Nat Nanotechnol* **2011,** *6* (12), 763-72.

58. Zhang, F.; Nangreave, J.; Liu, Y.; Yan, H., Structural DNA nanotechnology: state of the art and future perspective. *J Am Chem Soc* **2014,** *136* (32), 11198-211.

59. Seeman, N. C.; Sleiman, H. F., DNA nanotechnology. *Nature Reviews Materials* **2017,** *3* (1), 1-23.

60. Hong, F.; Zhang, F.; Liu, Y.; Yan, H., DNA Origami: Scaffolds for Creating Higher Order Structures. *Chem Rev* **2017,** *117* (20), 12584-12640.

61. Dey, S.; Fan, C.; Gothelf, K. V.; Li, J.; Lin, C.; Liu, L.; Liu, N.; Nijenhuis, M. A.; Saccà, B.; Simmel, F. C., DNA origami. *Nature Reviews Methods Primers* **2021,** *1* (1), 13.

62. Aghebat Rafat, A.; Pirzer, T.; Scheible, M. B.; Kostina, A.; Simmel, F. C., Surface-Assisted Large-Scale Ordering of DNA Origami Tiles. *Angewandte Chemie International Edition* **2014,** *53* (29), 7665-7668.

63. Woo, S.; Rothemund, P. W., Self-assembly of two-dimensional DNA origami lattices using cation-controlled surface diffusion. *Nat Commun* **2014,** *5*, 4889.

64. Suzuki, Y.; Endo, M.; Sugiyama, H., Lipid-bilayer-assisted two-dimensional self-assembly of DNA origami nanostructures. *Nature communications* **2015,** *6* (1), 8052.

65. Suzuki, Y.; Sugiyama, H.; Endo, M., Complexing DNA origami frameworks through sequential self-assembly based on directed docking. *Angewandte Chemie International Edition* **2018,** *57* (24), 7061-7065.

Chapter 2 References

1. Grünbaum, B.; Shephard, G. C., *Tilings and patterns*. Courier Dover Publications: 1987.

2. Talapin, D. V.; Shevchenko, E. V.; Bodnarchuk, M. I.; Ye, X.; Chen, J.; Murray, C. B., Quasicrystalline order in self-assembled binary nanoparticle superlattices. *Nature* **2009,** *461* (7266), 964-967.

3. Nagaoka, Y.; Zhu, H.; Eggert, D.; Chen, O., Single-component quasicrystalline nanocrystal superlattices through flexible polygon tiling rule. *Science* **2018,** *362* (6421), 1396-1400.

4. Wasio, N. A.; Quardokus, R. C.; Forrest, R. P.; Lent, C. S.; Corcelli, S. A.; Christie, J. A.; Henderson, K. W.; Kandel, S. A., Self-assembly of hydrogen-bonded two-dimensional quasicrystals. *Nature* **2014,** *507* (7490), 86-89.

5. Urgel, J. I.; Ecija, D.; Lyu, G.; Zhang, R.; Palma, C.-A.; Auwaerter, W.; Lin, N.; Barth, J. V., Quasicrystallinity expressed in two-dimensional coordination networks. *Nature Chemistry* **2016,** *8* (7), 657-662.

6. Zhang, Y.-Q.; Paszkiewicz, M.; Du, P.; Zhang, L.; Lin, T.; Chen, Z.; Klyatskaya, S.; Ruben, M.; Seitsonen, A. P.; Barth, J. V., Complex supramolecular interfacial tessellation through convergent multi-step reaction of a dissymmetric simple organic precursor. *Nature chemistry* **2018,** *10* (3), 296-304.

7. Gonen, S.; DiMaio, F.; Gonen, T.; Baker, D., Design of ordered two-dimensional arrays mediated by noncovalent protein-protein interfaces. *Science* **2015,** *348* (6241), 1365-1368.

8. Tanrikulu, I. C.; Forticaux, A.; Jin, S.; Raines, R. T., Peptide tessellation yields micrometre-scale collagen triple helices. *Nature chemistry* **2016,** *8* (11), 1008-1014.

9. Ben-Sasson, A. J.; Watson, J. L.; Sheffler, W.; Johnson, M. C.; Bittleston, A.; Somasundaram, L.; Decarreau, J.; Jiao, F.; Chen, J.; Mela, I., Design of biologically active binary protein 2D materials. *Nature* **2021,** *589* (7842), 468-473.

10. Shi, Q.; Gómez, D. E.; Dong, D.; Sikdar, D.; Fu, R.; Liu, Y.; Zhao, Y.; Smilgies, D. M.; Cheng, W., 2D freestanding Janus gold nanocrystal superlattices. *Advanced Materials* **2019,** *31* (28), 1900989.

11. Lee, Y. H.; Shi, W.; Lee, H. K.; Jiang, R.; Phang, I. Y.; Cui, Y.; Isa, L.; Yang, Y.; Wang, J.; Li, S., Nanoscale surface chemistry directs the tunable assembly of silver octahedra into three two-dimensional plasmonic superlattices. *Nature communications* **2015,** *6* (1), 6990.

12. Whitham, K.; Yang, J.; Savitzky, B. H.; Kourkoutis, L. F.; Wise, F.; Hanrath, T.,

Charge transport and localization in atomically coherent quantum dot solids. *Nature materials* **2016,** *15* (5), 557-563.

13. Chen, H.; Voigt, L.; Kubus, M.; Mihrin, D.; Mossin, S.; Larsen, R. W.; Kegnaes, S.; Piligkos, S.; Pedersen, K. S., Magnetic Archimedean Tessellations in Metal-Organic Frameworks. *J Am Chem Soc* **2021,** *143* (35), 14041-14045.

14. Wu, L.; Jubert, P. O.; Berman, D.; Imaino, W.; Nelson, A.; Zhu, H.; Zhang, S.; Sun, S., Monolayer assembly of ferrimagnetic Co(x)Fe(3-x)O4 nanocubes for magnetic recording. *Nano Lett* **2014,** *14* (6), 3395-9.

15. Kim, T.; Hong, J.; Kim, J.; Cho, J.; Kim, Y., Two-Dimensional Peptide Assembly via Arene-Perfluoroarene Interactions for Proliferation and Differentiation of Myoblasts. *J Am Chem Soc* **2023,** *145* (3), 1793-1802.

16. Pinheiro, A. V.; Han, D.; Shih, W. M.; Yan, H., Challenges and opportunities for structural DNA nanotechnology. *Nat Nanotechnol* **2011,** *6* (12), 763-72.

17. Zhang, F.; Nangreave, J.; Liu, Y.; Yan, H., Structural DNA nanotechnology: state of the art and future perspective. *J Am Chem Soc* **2014,** *136* (32), 11198-211.

18. Seeman, N. C.; Sleiman, H. F., DNA nanotechnology. *Nature Reviews Materials* **2017,** *3* (1), 1-23.

19. Wang, P.; Gaitanaros, S.; Lee, S.; Bathe, M.; Shih, W. M.; Ke, Y., Programming Self-Assembly of DNA Origami Honeycomb Two-Dimensional Lattices and Plasmonic Metamaterials. *J Am Chem Soc* **2016,** *138* (24), 7733-40.

20. Liu, X.; Zhang, F.; Jing, X.; Pan, M.; Liu, P.; Li, W.; Zhu, B.; Li, J.; Chen, H.; Wang, L.; Lin, J.; Liu, Y.; Zhao, D.; Yan, H.; Fan, C., Complex silica composite nanomaterials templated with DNA origami. *Nature* **2018,** *559* (7715), 593-598.

21. Sun, W.; Shen, J.; Zhao, Z.; Arellano, N.; Rettner, C.; Tang, J.; Cao, T.; Zhou, Z.; Ta, T.; Streit, J. K., Precise pitch-scaling of carbon nanotube arrays within three-dimensional DNA nanotrenches. *Science* **2020,** *368* (6493), 874-877.

22. Shen, J.; Sun, W.; Liu, D.; Schaus, T.; Yin, P., Three-dimensional nanolithography guided by DNA modular epitaxy. *Nature Materials* **2021,** *20* (5), 683-690.

23. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

24. Wang, P.; Meyer, T. A.; Pan, V.; Dutta, P. K.; Ke, Y., The beauty and utility of DNA origami. *Chem* **2017,** *2* (3), 359-382.

25. Hong, F.; Zhang, F.; Liu, Y.; Yan, H., DNA Origami: Scaffolds for Creating Higher Order Structures. *Chem Rev* **2017,** *117* (20), 12584-12640.

26. Dey, S.; Fan, C.; Gothelf, K. V.; Li, J.; Lin, C.; Liu, L.; Liu, N.; Nijenhuis, M. A.; Saccà, B.; Simmel, F. C., DNA origami. *Nature Reviews Methods Primers* **2021,** *1* (1), 13.

27. Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C., Crystalline two-dimensional DNA-origami arrays. *Angew Chem Int Ed Engl* **2011,** *50* (1), 264-7.

28. Liu, W.; Halverson, J.; Tian, Y.; Tkachenko, A. V.; Gang, O., Self-organized architectures from assorted DNA-framed nanoparticles. *Nature chemistry* **2016,** *8* (9), 867-873.

29. Tikhomirov, G.; Petersen, P.; Qian, L., Programmable disorder in random DNA tilings. *Nat Nanotechnol* **2017,** *12* (3), 251-259.

30. Tikhomirov, G.; Petersen, P.; Qian, L., Triangular DNA Origami Tilings. *J Am Chem Soc* **2018**.

31. Aghebat Rafat, A.; Sagredo, S.; Thalhammer, M.; Simmel, F. C., Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities. *Nature chemistry* **2020,** *12* (9), 852-859.

32. Aghebat Rafat, A.; Pirzer, T.; Scheible, M. B.; Kostina, A.; Simmel, F. C., Surface-assisted large-scale ordering of DNA origami tiles. *Angew Chem Int Ed Engl* **2014,** *53* (29), 7665-8.

33. Woo, S.; Rothemund, P. W., Self-assembly of two-dimensional DNA origami lattices using cation-controlled surface diffusion. *Nat Commun* **2014,** *5*, 4889.

34. Suzuki, Y.; Endo, M.; Sugiyama, H., Lipid-bilayer-assisted two-dimensional self-assembly of DNA origami nanostructures. *Nature communications* **2015,** *6* (1), 8052.

35. Suzuki, Y.; Sugiyama, H.; Endo, M., Complexing DNA origami frameworks through sequential self-assembly based on directed docking. *Angewandte Chemie International Edition* **2018,** *57* (24), 7061-7065.

36. Williams, S.; Lund, K.; Lin, C.; Wonka, P.; Lindsay, S.; Yan, H. In *Tiamat: a three-dimensional editing tool for complex DNA structures*, DNA Computing: 14th International Meeting on DNA Computing, DNA 14, Prague, Czech Republic, June 2-9, 2008. Revised Selected Papers 14, Springer: 2009; pp 90-101.

37. Ouldridge, T. E.; Louis, A. A.; Doye, J. P., Structural, mechanical, and thermodynamic properties of a coarse-grained DNA model. *The Journal of chemical*

physics **2011,** *134* (8), 02B627.

38. Snodin, B. E.; Randisi, F.; Mosayebi, M.; Šulc, P.; Schreck, J. S.; Romano, F.; Ouldridge, T. E.; Tsukanov, R.; Nir, E.; Louis, A. A., Introducing improved structural properties and salt dependence into a coarse-grained model of DNA. *The Journal of chemical physics* **2015,** *142* (23), 06B613_1.

39. Poppleton, E.; Romero, R.; Mallya, A.; Rovigatti, L.; Šulc, P., OxDNA. org: a public webserver for coarse-grained simulations of DNA and RNA nanostructures. *Nucleic acids research* **2021,** *49* (W1), W491-W498.

40. Snodin, B. E.; Schreck, J. S.; Romano, F.; Louis, A. A.; Doye, J. P., Coarse-grained modelling of the structural properties of DNA origami. *Nucleic acids research* **2019,** *47* (3), 1585-1597.

41. Fischer, S.; Hartl, C.; Frank, K.; Radler, J. O.; Liedl, T.; Nickel, B., Shape and Interhelical Spacing of DNA Origami Nanostructures Studied by Small-Angle X-ray Scattering. *Nano Lett* **2016,** *16* (7), 4282-7.

42. Chatterjee, G.; Dalchau, N.; Muscat, R. A.; Phillips, A.; Seelig, G., A spatially localized architecture for fast and modular DNA computing. *Nature Nanotechnology* **2017,** *12*, 920.

43. Chao, J.; Wang, J.; Wang, F.; Ouyang, X.; Kopperger, E.; Liu, H.; Li, Q.; Shi, J.; Wang, L.; Hu, J.; Wang, L.; Huang, W.; Simmel, F. C.; Fan, C., Solving mazes with single-molecule DNA navigators. *Nat Mater* **2019,** *18* (3), 273-279.

Chapter 3 References

1. Grünbaum, B.; Shephard, G. C., *Tilings and patterns*. Courier Dover Publications: 1987.

2. Talapin, D. V.; Shevchenko, E. V.; Bodnarchuk, M. I.; Ye, X.; Chen, J.; Murray, C. B., Quasicrystalline order in self-assembled binary nanoparticle superlattices. *Nature* **2009,** *461* (7266), 964-967.

3. Nagaoka, Y.; Zhu, H.; Eggert, D.; Chen, O., Single-component quasicrystalline nanocrystal superlattices through flexible polygon tiling rule. *Science* **2018,** *362* (6421), 1396-1400.

4. Wasio, N. A.; Quardokus, R. C.; Forrest, R. P.; Lent, C. S.; Corcelli, S. A.; Christie, J. A.; Henderson, K. W.; Kandel, S. A., Self-assembly of hydrogen-bonded two-dimensional quasicrystals. *Nature* **2014,** *507* (7490), 86-89.

5. Urgel, J. I.; Ecija, D.; Lyu, G.; Zhang, R.; Palma, C.-A.; Auwaerter, W.; Lin, N.; Barth, J. V., Quasicrystallinity expressed in two-dimensional coordination networks. *Nature Chemistry* **2016,** *8* (7), 657-662.

6. Zhang, Y.-Q.; Paszkiewicz, M.; Du, P.; Zhang, L.; Lin, T.; Chen, Z.; Klyatskaya, S.; Ruben, M.; Seitsonen, A. P.; Barth, J. V., Complex supramolecular interfacial tessellation through convergent multi-step reaction of a dissymmetric simple organic precursor. *Nature chemistry* **2018,** *10* (3), 296-304.

7. Gonen, S.; DiMaio, F.; Gonen, T.; Baker, D., Design of ordered two-dimensional arrays mediated by noncovalent protein-protein interfaces. *Science* **2015,** *348* (6241), 1365-1368.

8. Tanrikulu, I. C.; Forticaux, A.; Jin, S.; Raines, R. T., Peptide tessellation yields micrometre-scale collagen triple helices. *Nature chemistry* **2016,** *8* (11), 1008-1014.

9. Ben-Sasson, A. J.; Watson, J. L.; Sheffler, W.; Johnson, M. C.; Bittleston, A.; Somasundaram, L.; Decarreau, J.; Jiao, F.; Chen, J.; Mela, I., Design of biologically active binary protein 2D materials. *Nature* **2021,** *589* (7842), 468-473.

10. Robinson, R. M., Undecidability and nonperiodicity for tilings of the plane. *Inventiones mathematicae* **1971,** *12*, 177-209.

11. Mozes, S., Tilings, substitution systems and dynamical systems generated by them. *Journal d'Analyse Mathématique* **1989,** *53* (1), 139-186.

12. Grunbaum, B.; Shephard, G. C., Tilings by Regular Polygons. *Mathematics Magazine* **1977,** *50* (5), 227-247.

13. Zhang, F.; Liu, Y.; Yan, H., Complex Archimedean tiling self-assembled from DNA nanostructures. *J Am Chem Soc* **2013,** *135* (20), 7458-61.

14. Levine, D.; Steinhardt, P. J., Quasicrystals: a new class of ordered structures. *Physical review letters* **1984,** *53* (26), 2477.

15. Senechal, M., *Quasicrystals and geometry*. CUP Archive: 1996.

16. Liu, L.; Li, Z.; Li, Y.; Mao, C., Rational Design and Self-Assembly of Two-Dimensional, Dodecagonal DNA Quasicrystals. *J Am Chem Soc* **2019,** *141* (10), 4248-4251.

17. Lu, P. J.; Steinhardt, P. J., Decagonal and quasi-crystalline tilings in medieval Islamic architecture. *science* **2007,** *315* (5815), 1106-1110.

18. Cohen, M. F.; Shade, J.; Hiller, S.; Deussen, O., Wang tiles for image and texture generation. *ACM Transactions on Graphics (TOG)* **2003,** *22* (3), 287-294.

19. Winfree, E., *Algorithmic self-assembly of DNA*. California Institute of Technology: 1998.

20. Pinheiro, A. V.; Han, D.; Shih, W. M.; Yan, H., Challenges and opportunities for structural DNA nanotechnology. *Nat Nanotechnol* **2011,** *6* (12), 763-72.

21. Zhang, F.; Nangreave, J.; Liu, Y.; Yan, H., Structural DNA nanotechnology: state of the art and future perspective. *J Am Chem Soc* **2014,** *136* (32), 11198-211.

22. Seeman, N. C.; Sleiman, H. F., DNA nanotechnology. *Nature Reviews Materials* **2017,** *3* (1), 1-23.

23. Wang, P.; Gaitanaros, S.; Lee, S.; Bathe, M.; Shih, W. M.; Ke, Y., Programming Self-Assembly of DNA Origami Honeycomb Two-Dimensional Lattices and Plasmonic Metamaterials. *J Am Chem Soc* **2016,** *138* (24), 7733-40.

24. Liu, X.; Zhang, F.; Jing, X.; Pan, M.; Liu, P.; Li, W.; Zhu, B.; Li, J.; Chen, H.; Wang, L.; Lin, J.; Liu, Y.; Zhao, D.; Yan, H.; Fan, C., Complex silica composite nanomaterials templated with DNA origami. *Nature* **2018,** *559* (7715), 593-598.

25. Sun, W.; Shen, J.; Zhao, Z.; Arellano, N.; Rettner, C.; Tang, J.; Cao, T.; Zhou, Z.; Ta, T.; Streit, J. K., Precise pitch-scaling of carbon nanotube arrays within three-dimensional DNA nanotrenches. *Science* **2020,** *368* (6493), 874-877.

26. Shen, J.; Sun, W.; Liu, D.; Schaus, T.; Yin, P., Three-dimensional nanolithography guided by DNA modular epitaxy. *Nature Materials* **2021,** *20* (5), 683-690.

27. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

28. Wang, P.; Meyer, T. A.; Pan, V.; Dutta, P. K.; Ke, Y., The beauty and utility of DNA origami. *Chem* **2017,** *2* (3), 359-382.

29. Hong, F.; Zhang, F.; Liu, Y.; Yan, H., DNA Origami: Scaffolds for Creating Higher Order Structures. *Chem Rev* **2017,** *117* (20), 12584-12640.

30. Dey, S.; Fan, C.; Gothelf, K. V.; Li, J.; Lin, C.; Liu, L.; Liu, N.; Nijenhuis, M. A.; Saccà, B.; Simmel, F. C., DNA origami. *Nature Reviews Methods Primers* **2021,** *1* (1), 13.

31. Tikhomirov, G.; Petersen, P.; Qian, L., Triangular DNA Origami Tilings. *J Am Chem Soc* **2018**.

32. Liu, W.; Zhong, H.; Wang, R.; Seeman, N. C., Crystalline two-dimensional DNA-origami arrays. *Angew Chem Int Ed Engl* **2011,** *50* (1), 264-7.

33. Liu, W.; Halverson, J.; Tian, Y.; Tkachenko, A. V.; Gang, O., Self-organized architectures from assorted DNA-framed nanoparticles. *Nature chemistry* **2016,** *8* (9), 867-873.

34. Tikhomirov, G.; Petersen, P.; Qian, L., Programmable disorder in random DNA tilings. *Nat Nanotechnol* **2017,** *12* (3), 251-259.

35. Aghebat Rafat, A.; Sagredo, S.; Thalhammer, M.; Simmel, F. C., Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities. *Nature chemistry* **2020,** *12* (9), 852-859.

36. Suzuki, Y.; Sugiyama, H.; Endo, M., Complexing DNA origami frameworks through sequential self - assembly based on directed docking. *Angewandte Chemie International Edition* **2018,** *57* (24), 7061-7065.

37. Williams, S.; Lund, K.; Lin, C.; Wonka, P.; Lindsay, S.; Yan, H. In *Tiamat: a three-dimensional editing tool for complex DNA structures*, DNA Computing: 14th International Meeting on DNA Computing, DNA 14, Prague, Czech Republic, June 2-9, 2008. Revised Selected Papers 14, Springer: 2009; pp 90-101.

38. SantaLucia Jr, J.; Hicks, D., The thermodynamics of DNA structural motifs. *Annu. Rev. Biophys. Biomol. Struct.* **2004,** *33*, 415-440.

39. Kilchherr, F.; Wachauf, C.; Pelz, B.; Rief, M.; Zacharias, M.; Dietz, H., Single-molecule dissection of stacking forces in DNA. *Science* **2016,** *353* (6304), aaf5508.

40. Minev, D.; Wintersinger, C. M.; Ershova, A.; Shih, W. M., Robust nucleation control via crisscross polymerization of highly coordinated DNA slats. *Nature communications* **2021,** *12* (1), 1741.

41. Fischer, S.; Hartl, C.; Frank, K.; Radler, J. O.; Liedl, T.; Nickel, B., Shape and Interhelical Spacing of DNA Origami Nanostructures Studied by Small-Angle X-ray Scattering. *Nano Lett* **2016,** *16* (7), 4282-7.

42. Coxeter, H., Mathematical Models. By HM Cundy and AP Rollett. Pp. 286. 25s. 1961.(Oxford University Press). *The Mathematical Gazette* **1962,** *46* (358), 331-331.

43. Tomizawa, J.-i., Control of cole 1 plasmid replication: the process of binding of RNA I to the primer transcript. *Cell* **1984,** *38* (3), 861-870.

44. Barbault, F.; Huynh-Dinh, T.; Paoletti, J.; Lancelot, G., A new peculiar DNA structure: NMR solution structure of a DNA kissing complex. *Journal of Biomolecular Structure and Dynamics* **2002,** *19* (4), 649-658.

45. Barth, A.; Kobbe, D.; Focke, M., DNA–DNA kissing complexes as a new tool for the assembly of DNA nanostructures. *Nucleic Acids Research* **2016,** *44* (4), 1502-1513.

Chapter 4 References

1. Lloyd, S., Ultimate physical limits to computation. *Nature* **2000,** *406* (6799), 1047-1054.

2. Markov, I. L., Limits on fundamental limits to computation. *Nature* **2014,** *512* (7513), 147-154.

3. Peercy, P. S., The drive to miniaturization. *Nature* **2000,** *406* (6799), 1023-1026.

4. Kitano, H., Computational systems biology. *Nature* **2002,** *420* (6912), 206-210.

5. Adleman, L. M., Molecular computation of solutions to combinatorial problems. *science* **1994,** *266* (5187), 1021-1024.

6. Benenson, Y.; Paz-Elizur, T.; Adar, R.; Keinan, E.; Livneh, Z.; Shapiro, E., Programmable and autonomous computing machine made of biomolecules. *Nature* **2001,** *414* (6862), 430-434.

7. Ma, Q.; Zhang, C.; Zhang, M.; Han, D.; Tan, W., DNA Computing: Principle, Construction, and Applications in Intelligent Diagnostics. *Small Structures* **2021,** *2* (11), 2100051.

8. Liu, Q.; Wang, L.; Frutos, A. G.; Condon, A. E.; Corn, R. M.; Smith, L. M., DNA computing on surfaces. *Nature* **2000,** *403* (6766), 175-179.

9. Lund, K.; Williams, B.; Ke, Y.; Liu, Y.; Yan, H., DNA nanotechnology: a rapidly evolving field. *Current Nanoscience* **2006,** *2* (2), 113-122.

10. Ghosh, A.; Bansal, M., A glossary of DNA structures from A to Z. *Acta Crystallographica Section D: Biological Crystallography* **2003,** *59* (4), 620-626.

11. Pray, L., Discovery of DNA structure and function: Watson and Crick. *Nature Education* **2008,** *1* (1), 100.

12. Lin, C.; Liu, Y.; Rinker, S.; Yan, H., DNA tile based self-assembly: building complex nanoarchitectures. *ChemPhysChem* **2006,** *7* (8), 1641-1647.

13. Gibbons, A.; Amos, M.; Hodgson, D., DNA computing. *Current opinion in biotechnology* **1997,** *8* (1), 103-106.

14. Ezziane, Z., DNA computing: applications and challenges. *Nanotechnology* **2005,** *17* (2), R27.

15. Paun, G.; Rozenberg, G.; Salomaa, A., *DNA computing: new computing paradigms*. Springer Science & Business Media: 2005.

16. Qian, L.; Winfree, E., Scaling up digital circuit computation with DNA strand displacement cascades. *Science* **2011,** *332* (6034), 1196-201.

17. Qian, L.; Winfree, E.; Bruck, J., Neural network computation with DNA strand displacement cascades. *Nature* **2011,** *475* (7356), 368-72.

18. Woods, D.; Doty, D.; Myhrvold, C.; Hui, J.; Zhou, F.; Yin, P.; Winfree, E., Diverse and robust molecular algorithms using reprogrammable DNA self-assembly. *Nature* **2019,** *567* (7748), 366-372.

19. Tikhomirov, G.; Petersen, P.; Qian, L., Fractal assembly of micrometre-scale DNA origami arrays with arbitrary patterns. *Nature* **2017,** *552* (7683), 67-71.

20. Genot, A.; Baccouche, A.; Sieskind, R.; Aubert-Kato, N.; Bredèche, N.; Bartolo, J.; Taly, V.; Fujii, T.; Rondelez, Y., High-resolution mapping of bifurcations in nonlinear biochemical circuits. *Nature chemistry* **2016,** *8* (8), 760-767.

21. Rothemund, P. W., Folding DNA to create nanoscale shapes and patterns. *Nature* **2006,** *440* (7082), 297-302.

22. Ke, Y.; Sharma, J.; Liu, M.; Jahn, K.; Liu, Y.; Yan, H., Scaffolded DNA origami of a DNA tetrahedron molecular container. *Nano Lett* **2009,** *9* (6), 2445-7.

23. Douglas, S. M.; Dietz, H.; Liedl, T.; Högberg, B.; Graf, F.; Shih, W. M., Self-assembly of DNA into nanoscale three-dimensional shapes. *Nature* **2009,** *459* (7245), 414-418.

24. Han, D.; Pal, S.; Nangreave, J.; Deng, Z.; Liu, Y.; Yan, H., DNA origami with complex curvatures in three-dimensional space. *Science* **2011,** *332* (6027), 342-6.

25. Zhang, F.; Jiang, S.; Wu, S.; Li, Y.; Mao, C.; Liu, Y.; Yan, H., Complex wireframe DNA origami nanostructures with multi-arm junction vertices. *Nat Nanotechnol* **2015,** *10* (9), 779-84.

26. Gerling, T.; Wagenbauer, K. F.; Neuner, A. M.; Dietz, H., Dynamic DNA devices and assemblies formed by shape-complementary, non–base pairing 3D components.

Science **2015,** *347* (6229), 1446-1452.

27. Rothemund, P. W.; Papadakis, N.; Winfree, E., Algorithmic self-assembly of DNA Sierpinski triangles. *PLoS Biol* **2004,** *2* (12), e424.

28. Fujibayashi, K.; Hariadi, R.; Park, S. H.; Winfree, E.; Murata, S., Toward reliable algorithmic self-assembly of DNA tiles: A fixed-width cellular automaton pattern. *Nano Letters* **2008,** *8* (7), 1791-1797.

29. Winfree, E., Algorithmic Self-Assembly of DNA: Theoretical Motivations and 2D Assembly Experiments. *J Biomol Struct Dyn* **2000,** *17 Suppl 1*, 263-70.

30. Winfree, E., *Algorithmic self-assembly of DNA*. California Institute of Technology: 1998.

31. Mao, C.; LaBean, T. H.; Relf, J. H.; Seeman, N. C., Logical computation using algorithmic self-assembly of DNA triple-crossover molecules. *Nature* **2000,** *407* (6803), 493-6.

32. Wang, H., Proving theorems by pattern recognition—II. *Bell system technical journal* **1961,** *40* (1), 1-41.

33. Cohen, M. F.; Shade, J.; Hiller, S.; Deussen, O., Wang tiles for image and texture generation. *ACM Transactions on Graphics (TOG)* **2003,** *22* (3), 287-294.

34. Jungmann, R.; Steinhauer, C.; Scheible, M.; Kuzyk, A.; Tinnefeld, P.; Simmel, F. C., Single-molecule kinetics and super-resolution microscopy by fluorescence imaging of transient binding on DNA origami. *Nano letters* **2010,** *10* (11), 4756-4761.

35. Jungmann, R.; Avendano, M. S.; Woehrstein, J. B.; Dai, M.; Shih, W. M.; Yin, P., Multiplexed 3D cellular super-resolution imaging with DNA-PAINT and Exchange-PAINT. *Nat Methods* **2014,** *11* (3), 313-8.

36. Williams, S.; Lund, K.; Lin, C.; Wonka, P.; Lindsay, S.; Yan, H. In *Tiamat: a three-dimensional editing tool for complex DNA structures*, DNA Computing: 14th International Meeting on DNA Computing, DNA 14, Prague, Czech Republic, June 2-9, 2008. Revised Selected Papers 14, Springer: 2009; pp 90-101.

Chapter 5 References

Gerling, T.; Stömmer, P.; Honemann, M. N.; Martin, T. G., Revealing the structures of megadalton-scale DNA complexes with nucleotide resolution. *Nature communications* **2020,** *11* (1), 6229.

2. Sobczak, J. P.; Martin, T. G.; Gerling, T.; Dietz, H., Rapid folding of DNA into nanoscale shapes at constant temperature. *Science* **2012,** *338* (6113), 1458-61.

3. Huang, C.-M.; Kucinic, A.; Johnson, J. A.; Su, H.-J.; Castro, C. E., Integrated computer-aided engineering and design for DNA assemblies. *Nature Materials* **2021,** *20* (9), 1264-1271.

APPENDIX A

SUPPLEMENTAL INFORMATION FOR CHAPTER 2

S2.1 Materials and Methods

S2.1.1 Synthesis of customized DNA scaffold strands

Three customized DNA scaffold strands (p2820, p3120, and p3548) were synthesized and utilized in this study. The phagemid vector with 2820 base pairs (bp) was synthesized by deleting a DNA fragment of 141 bp from pBlueScript II SK(+) vector using Q5 site-directed mutagenesis kit (New England Biolabs). For p3120 and p3548, customized DNA fragments were synthesized and inserted into pBlueScript II SK(+) vector by Bio Basic Inc. (biobasic.com) to form phagemid vectors with 3210 bp and 3548 bp, respectively. To synthesize DNA scaffold strands, the phagemid vector (2820 bp, 3120 bp, or 3548 bp) was co-transformed into *E. coli* DH5α competent cells with a helper plasmid pSB4423, a kind gift from Dr. Stanley Brown (Niels Bohr Institute, Denmark). The DNA scaffold strands were amplified and purified as described previously[1]. The mass concentration of each strand was measured by NanoDrop™ 2000 spectrophotometer (Thermo Scientific) and converted to molar concentration using the average molecular weight of a DNA nucleotide (330 g/mol). Sequences of these scaffold strands are summarized in Section S2.7.1.

S2.1.2 Sample preparation

The M13mp18 single-stranded DNA was purchased from Bayou Biolabs (P-107, 1 μg/μL). The p8064 single-stranded DNA was purchased from tilibit nanosystems (M1-51, 100 nM). Both DNA strands were used as received without further purification. Sequences of both scaffold strands are summarized in Section S2.7.1.

Staple strands were categorized based on their positions and functions within the DNA origami tiles: core staples fold the scaffold strand into the designed geometry; edge

staples present sticky ends and base stackings that "glue" monomer DNA origami tiles together into higher-order assemblies. All staple strands were purchased from Integrated DNA Technologies (idtdna.com) at 100 μM in RNase-free water and were used as received without further purification. Sequences of staple strands are summarized in Section S2.7.2.

The multimeric complexes assembled from p3120 equilateral triangular tiles were prepared by mixing the p3120 scaffold strand (5 nM) and corresponding staple strands (50 nM/each) in 1× TAE/Mg^{2+} buffer (Tris base 40 mM, acetic acid 20 mM, $EDTA{\cdot}Na_2{\cdot}12H_2O$ 2 mM, $(CH_3COO)_2Mg{\cdot}4H_2O$ 12.5 mM) and annealing the mixture from 80 °C to 20 °C in ~101 h. The annealing procedure was controlled using DNA Engine Tetrad® 2 Thermal Cycler (Bio-Rad). The samples were heated up to 80 °C, held at 80 °C for 10 min, cooled from 80 °C to 40 °C at -1 °C/min, held at 40 °C for 10 min, cooled from 40 °C to 20 °C at -0.1 °C/30 min, and held at 15 °C until use.

The lattices assembled from a single tile species were prepared by mixing the scaffold strand (25 nM), core staple strands (250 nM/each), and edge staple strands (375 nM/ea) in 1× TAE/Mg^{2+} buffer. The samples were annealed following the same procedure used for multimeric complexes.

The lattices assembled from two or more tile species were prepared in two steps. Firstly, different tile species were prepared in separate tubes by mixing the scaffold strand (25 nM), core staple strands (250 nM/each), and edge staple strands (375 nM/ea) in 1× TAE/Mg^{2+} buffer. The mixtures were heated up to 80 °C, held at 80 °C for 10 min, cooled from 80 °C to 40 °C at -1 °C/min, and held at 40 °C until Step 2. In Step 2, different tile

species were mixed in one tube preheated to 40 °C, held at 40 °C for 30 min, annealed from 40 °C to 20 °C at -0.1 °C/30 min, and held at 15 °C until use.

S2.1.3 AFM imaging

For multimeric complexes imaging, the samples were diluted to 3 nM using 1× TAE/Mg^{2+} buffer. 5 μL of the diluted sample was deposited onto a freshly cleaved mica surface (Ted Pella) and incubated for 5 min. Then, 60 μL 1× TAE/Mg^{2+} buffer was added onto the mica surface and removed by compressed air. This step was repeated twice to minimize the imaging background from excess staples. Subsequently, the mica surface was covered by 60 μL 1× TAE/Mg^{2+} buffer, and 10 μL $NiCl_2$ solution (100 mM) was added to assist adsorption. The samples were imaged in "ScanAsyst in Fluid" mode with a ScanAsyst-liquid+ tip on the MultiMode 8 AFM (Bruker).

For the imaging of lattices, the samples were diluted to 5 nM (scaffold concentration) using 1× TAE/Mg^{2+} buffer. 10 μL of the diluted sample was deposited onto a freshly cleaved mica surface and incubated for 5 min. The rest steps were the same as the imaging of multimeric complexes.

S2.2 Designs of DNA Origami Tile

S2.2.1 Design parameters of DNA origami tiles

S2.2.1.1 Design parameters of p3120 equilateral triangular DNA origami tiles for oxDNA simulation and AFM-based statistical analysis

Table S2.1. Design parameters of six p3120 equilateral triangular DNA origami tiles based on different ***D*** values.

Design name	**[TR]_p3120**					
Rise per base pair, ***r*** (nm)	0.34					
Interhelical distance, ***D*** (nm)	2.55	2.65	2.70	2.75	2.85	3.00
Number of helices per subunit	18					
Minimum helix length (bp)	38	37	36	36	35	34
Maximum helix length (bp)	73	73	73	73	74	75
Lengths of helices (bp)	38/42/47/51/55/60/64/68/73	37/41/46/50/55/59/64/68/73	36/41/45/50/54/59/64/68/73	36/41/45/50/55/59/64/69/73	35/40/45/50/54/59/64/69/74	34/39/44/49/54/59/65/70/75
Lengths of scaffold	6/7/6/7/6/8/9/7	6/6/7/7/6/7/8/8	7/7/7/7/6/8/9/9	7/6/7/7/6/8/8/9	6/7/7/7/7/8/9/9	7/7/7/7/9/8/8/9

loops (nt)						
Length of the scaffold bridge (nt)	1	1	4	3	5	6
Lengths of staple bridges (nt)	6/5/5/4/3/1/2/2	6/5/5/4/1/0/2/2	5/5/4/2/1/0/2/2	5/5/4/4/1/0/0/2	5/5/4/2/2/1/0/0	4/3/3/2/2/3/3/2

S2.2.1.2 Design parameters of DNA origami tiles for regular tilings

Table S2.2. Design parameters of p3120 equilateral triangular DNA origami tile (***D*** = 2.70 nm) for regular tiling.

Design name	**[TR]_p3120**
Rise per base pair, ***r*** (nm)	0.34
Interhelical distance, ***D*** (nm)	2.70
Number of helices per subunit	18
Minimum helix length (bp)	36
Maximum helix length (bp)	73
Lengths of helices (bp)	36/41/45/50/54/59/64/68/73
Lengths of scaffold loops (nt)	7/7/7/7/6/8/9/9
Length of the scaffold bridge (nt)	4
Lengths of staple bridges (nt)	5/5/4/2/1/0/2/2

Table S2.3. Design parameters of three regular polygonal DNA origami tiles based on the p3548 scaffold.

Design name	**[TR]_p3548**	**[SQ]_p3548**	**[HE]_p3548**
Rise per base pair, ***r*** (nm)	0.34	0.332	0.332
Interhelical distance, ***D*** (nm)	2.69	2.65	2.65
Number of helices per subunit	20	14	10
Minimum helix length (bp)	35	34	27
Maximum helix length (bp)	76	82	81
Lengths of helices (bp)	35/40/44/49/53/ 58/62/67/72/76	34/42/50/58/ 66/74/82	27/41/54/68/81
Lengths of scaffold loops (nt)	7/7/6/8/8/6/6/7/9	10/10/12/12/10/10	14/11/11/15
Length of the scaffold bridge (nt)	5	11	1
Lengths of staple bridges (nt)	4/3/2/0/0/4/4/4/5	8/8/3/6/9/8	8/2/4/9

Table S2.4. Design parameters of three regular polygonal DNA origami tiles based on the M13mp18 scaffold.

Design name	**[TR]_M13**	**[SQ]_M13**	**[HE]_M13**
Rise per base pair, ***r*** (nm)	0.332	0.34	0.332
Interhelical distance, ***D*** (nm)	2.60	2.69	2.65
Number of helices per subunit	32	22	14
Minimum helix length (bp)	38	39	40
Maximum helix length (bp)	106	118	123
Lengths of helices (bp)	38/43/47/52/56/61/65/70/74/ 79/83/88/92/97/101/106	39/47/55/63/71/79/ 86/94/102/110/118	40/54/68/81/ 95/109/123
Lengths of scaffold loops (nt)	7/8/8/7/7/7/7/11/ 6/5/6/9/10/10/8	9/11/8/10/8/ 8/9/8/10/8	12/13/12/11/14/13
Length of the scaffold bridge (nt)	2	3	6
Lengths of staple bridges (nt)	5/6/6/6/6/4/3/1/ 1/5/5/7/6/7/6	2/4/7/6/0/ 4/7/7/1/5	9/8/5/1/4/8

S2.2.1.3 Design parameters of low-symmetry tiles for Laves tilings

Table S2.5. Design parameters of p3548 isosceles right triangular DNA origami tile.

Design name	**[irTR]_p3548**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.70	
Composing subunit	Subunit ***135°***	Subunit ***90°***
Number of helices per subunit	26	10
Minimum helix length (bp)	35	37
Maximum helix length (bp)	74	69
Lengths of helices (bp)	35/38/41/44/48/51/54/ 58/61/64/67/71/74	37/45/53/61/69
Lengths of scaffold loops (nt)	6/6/8/5/7/7/9/ 9/4/10/6/6	12/7/8/10
Length of the scaffold bridge (nt)	4	1
Lengths of staple bridges (nt)	0/4/4/2/4/1/ 0/4/3/5/4/0	6/1/6/7

Table S2.6. Design parameters of M13mp18 rhombic DNA origami tile.

Design name	**[RH]_M13**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***120°***	Subunit ***60°***
Number of helices per subunit	36	12
Minimum helix length (bp)	34	34
Maximum helix length (bp)	112	103
Lengths of helices (bp)	34/39/43/48/53/57/62/66/71/75/ 80/85/89/94/98/103/107/112	34/48/62/76/89/103
Lengths of scaffold loops (nt)	7/7/8/8/7/7/7/7/9/ 9/9/7/6/6/6/7/8	12/12/9/12/12
Length of the scaffold bridge (nt)	6	9
Lengths of staple bridges (nt)	3/1/1/0/4/4/6/5/6/ 5/5/6/5/6/5/4/3	1/4/8/9/7

Table S2.7. Design parameters of M13mp18 kite DNA origami tile.

Design name	**[KT]_M13**		
Rise per base pair, ***r*** (nm)	0.34		
Interhelical distance, ***D*** (nm)	2.69		
Composing subunit	Subunit ***120°***	Subunit ***90°***	Subunit ***60°***
Number of helices per subunit	38	22	14
Minimum helix length (bp)	33	33	24
Maximum helix length (bp)	115	112	106
Lengths of helices (bp)	33/37/42/46/51/56/60/ 65/69/74/78/83/88/92/ 97/101/106/110/115	33/41/49/57/65/72/ 80/88/96/104/112	24/37/51/65/ 79/92/106
Lengths of scaffold loops (nt)	7/8/6/6/7/6/6/7/7/ 7/8/8/8/8/6/4/6/7	9/10/8/10/10/ 9/9/8/9/9	12/13/13/14/12/12
Length of the scaffold bridge (nt)	5	7	7
Lengths of staple bridges (nt)	2/2/5/5/5/6/5/6/5/ 6/6/5/5/4/2/1/2/2	7/7/3/3/7/8/4/3/7/7	2/6/8/9/6/2

Table S2.8. Design parameters of M13mp18 prismatic pentagonal DNA origami tile.

Design name	**[PT-prism]_M13**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***90°***	Subunit ***60°***
Number of helices per subunit	22	14
Minimum helix length (bp)	44	35
Maximum helix length (bp)	123	117
Lengths of helices (bp)	44/52/60/68/76/83/ 91/99/107/115/123	35/48/62/76/ 90/103/117
Lengths of scaffold loops (nt)	10/9/9/9/10/ 10/9/9/8/9	12/12/13/15/12/12
Length of the scaffold bridge (nt)	7	6
Lengths of staple bridges (nt)	7/7/2/4/7/ 7/3/4/7/7	1/5/8/9/7/3

Table S2.9. Design parameters of M13mp18 Cairo pentagonal DNA origami tile.

Design name	**[PT-Cairo]_M13**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***90°***	Subunit ***60°***
Number of helices per subunit	22	14
Minimum helix length (bp)	42	35
Maximum helix length (bp)	122	116
Lengths of helices (bp)	42/50/58/66/74/82/ 90/98/106/114/122	35/49/62/76/ 89/103/116
Lengths of scaffold loops (nt)	7/12/8/12/8/ 8/12/8/12/7	12/13/14/14/13/12
Length of the scaffold bridge (nt)	9	7
Lengths of staple bridges (nt)	6/9/8/3/7/ 8/7/1/7/8	2/6/9/9/6/2

Table S2.10. Design parameters of p8064 floret pentagonal DNA origami tile.

Design name	**[PT-floret]_p8064**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***120°***	Subunit ***60°***
Number of helices per subunit	42	14
Minimum helix length (bp)	35	35
Maximum helix length (bp)	126	117
Lengths of helices (bp)	35/39/44/48/53/57/62/67/71/76/80/85/ 89/94/99/103/108/112/117/121/126	35/48/62/76/ 90/103/117
Lengths of scaffold loops (nt)	6/7/8/6/6/7/7/6/6/7/ 7/8/8/8/7/5/4/6/7/8	12/12/13/ 15/12/12
Length of the scaffold bridge (nt)	5	6
Lengths of staple bridges (nt)	4/3/1/0/4/4/4/6/5/6/ 5/6/6/5/6/5/4/3/1/1	1/5/8/9/7/3

S2.2.2 Tiamat designs of DNA origami tiles

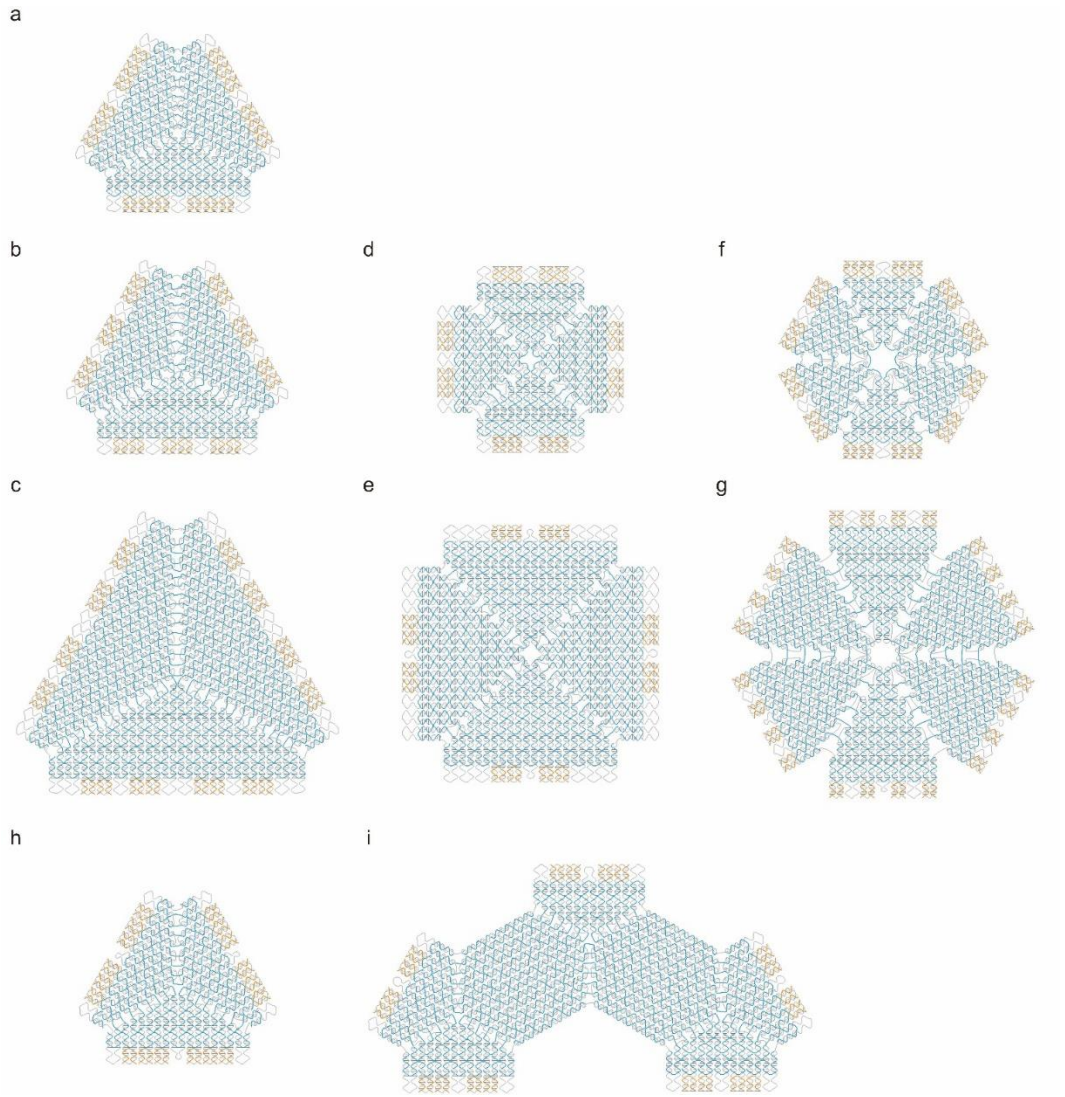

Figure S2.1. Tiamat designs of DNA origami tiles for regular tilings. (a) p3120 equilateral triangular tile, (b) p3548 equilateral triangular tile, (c) M13mp18 equilateral triangular tile, (d) p3548 square tile, (e) M13mp18 square tile, (f) p3548 regular hexagonal tile, (g) M13mp18 regular hexagonal tile, (h) p2820 equilateral triangular tile, and (i) M13mp18 half hexagonal tile. The scaffold strand (gray) is folded by core staple strands (blue) into the target shape, which can be further linked together by edge staple strands (orange) into 2D lattices.

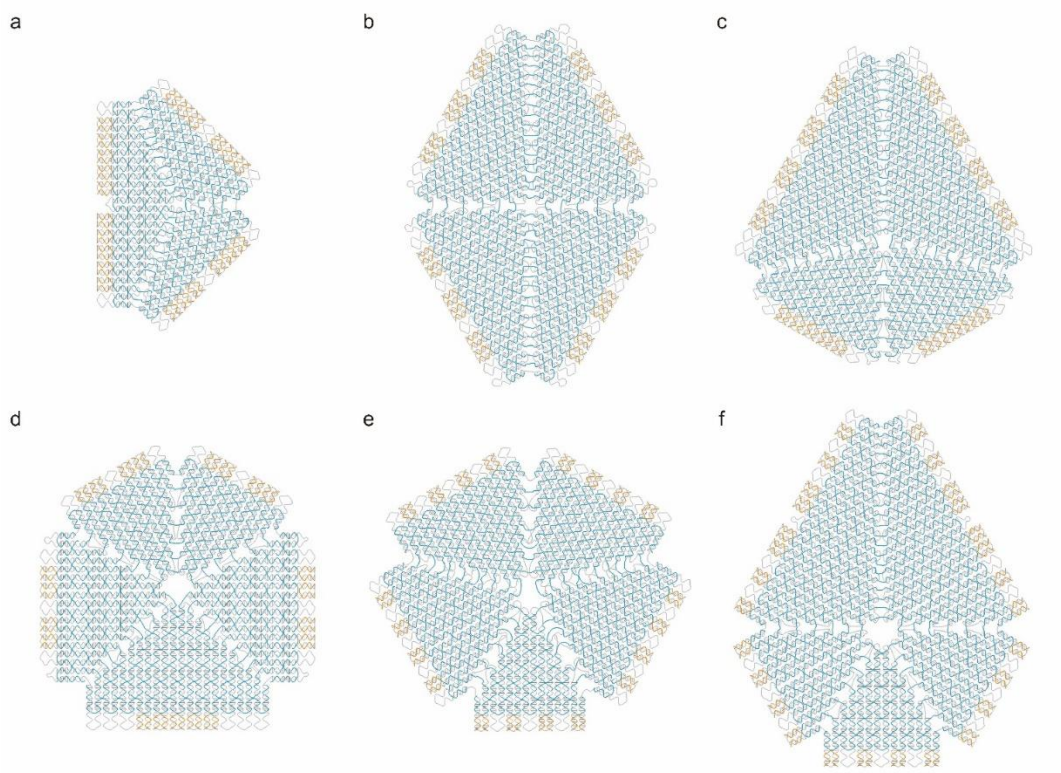

Figure S2.2. Tiamat designs of low-symmetry tiles for Laves tilings. (a) p3548 isosceles right triangular tile, (b) M13mp18 rhombic tile, (c) M13mp18 kite tile, (d) M13mp18 prismatic pentagonal tile, (e) M13mp18 Cairo pentagonal tile, and (f) p8064 floret pentagonal tile. The scaffold strand (gray) is folded by core staple strands (blue) into the target shape, which can be further linked together by edge staple strands (orange) into 2D lattices.

S2.3 Curvature Analysis via oxDNA Simulation

S2.3.1 Simulation procedure

We used an extended version of the oxDNA model[2-4], oxDNA2, to study the curvature of equilateral triangular DNA origami tiles designed based on ***D*** values ranging from 2.55 nm to 3.00 nm with 0.15 nm intervals. In this model, each DNA nucleotide is presented as a rigid body subject to multiple interactions such as hydrogen bonding, (coaxial) stacking, and electrostatic repulsion. The interactions are parameterized to reproduce the basic structure, thermodynamic, and mechanical properties of single-stranded and double-stranded DNA.

Designs of DNA origami tiles were prepared using Tiamat and converted into the oxDNA format using TacoxDNA[5], a webserver-based suite for converting the blueprints generated with common DNA design software tools into the inputs for molecular dynamics simulations. The simulations were conducted under a condition equivalent to 1 M salt concentration (monovalent ion, modeled with Debye-Hückel potential) at 25 °C (set with an Andersen-like thermostat). For each tile design, the individual simulation step was set to ~0.015 ps, and the simulation was run for ~75 μs. It is important to note that the timescales used in the coarse-grained model do not directly correspond to experimental timescales and may underestimate the actual experimental time that the simulation would correspond to. We saved a configuration every 5×10^5 steps during the simulation with a total number of 10^4 configurations captured throughout the simulation trajectory for each tile design for curvature analysis.

S2.3.2 Curvature analysis

To quantitatively compare the curvature of equilateral triangular DNA origami tiles designed based on different ***D*** values, we defined three vectors, namely $\vec{u}$, $\vec{v}$, and $\vec{w}$, to represent the helical direction of each isosceles triangular subunit composing the tile. Specifically, in each subunit, there are two double-crossover linkages between the two central double-helices. The (x, y, z)-coordinates of the four staple nucleotides at each double-crossover linkage were averaged to obtain the initial and the terminal points of the three vectors. Each vector started from the double-crossover linkage near the center of the tile and pointed outwards along the helical direction to the second crossover linkage. The sum of the angles between each pair of vectors ($\theta_1 + \theta_2 + \theta_3$) was calculated to estimate the tile's curvature. For example, the sum is approximately 360° for a flat tile. The more curved a tile is, the more the sum deviates from 360°. Therefore, we defined the degree of curvature as the deviation of the sum from 360° (i.e., $360° - \theta_1 - \theta_2 - \theta_3$). The direction of curvature (i.e., upwards or downwards) was determined by the plus or minus of $(\vec{u} \times \vec{v}) \cdot \vec{w}$. This approach was applied to every configuration sampled throughout the simulation trajectory to determine the degree and direction of its curvature. The vector-based curvature analysis mainly serves as a rough estimation owing to the non-uniform distribution of curvature throughout the tile. Nonetheless, a clear trend was revealed for the four tile designs we examined. As the value of ***D*** increases from 2.55 to 3.00 nm, the degree of curvature initially decreases before subsequently increasing, while the preferential direction of curvature shifts from downwards to upwards (Supplementary Figure S2.3). These observations suggest that ***D*** plays a vital role in determining the conformation of DNA origami tiles.

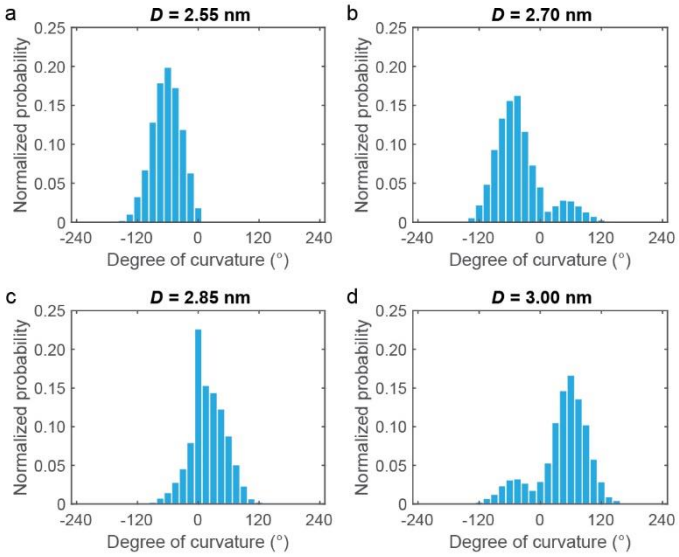

Figure S2.3. Histograms illustrating the distributions of curvature for four tile designs based on ***D*** values ranging from 2.55 to 3.00 nm with 0.15 nm intervals.

S2.4 Statistical Analysis of DNA Origami Tile Multimerization

S2.4.1 AFM characterization of multimers assembled from equilateral triangular DNA origami tiles

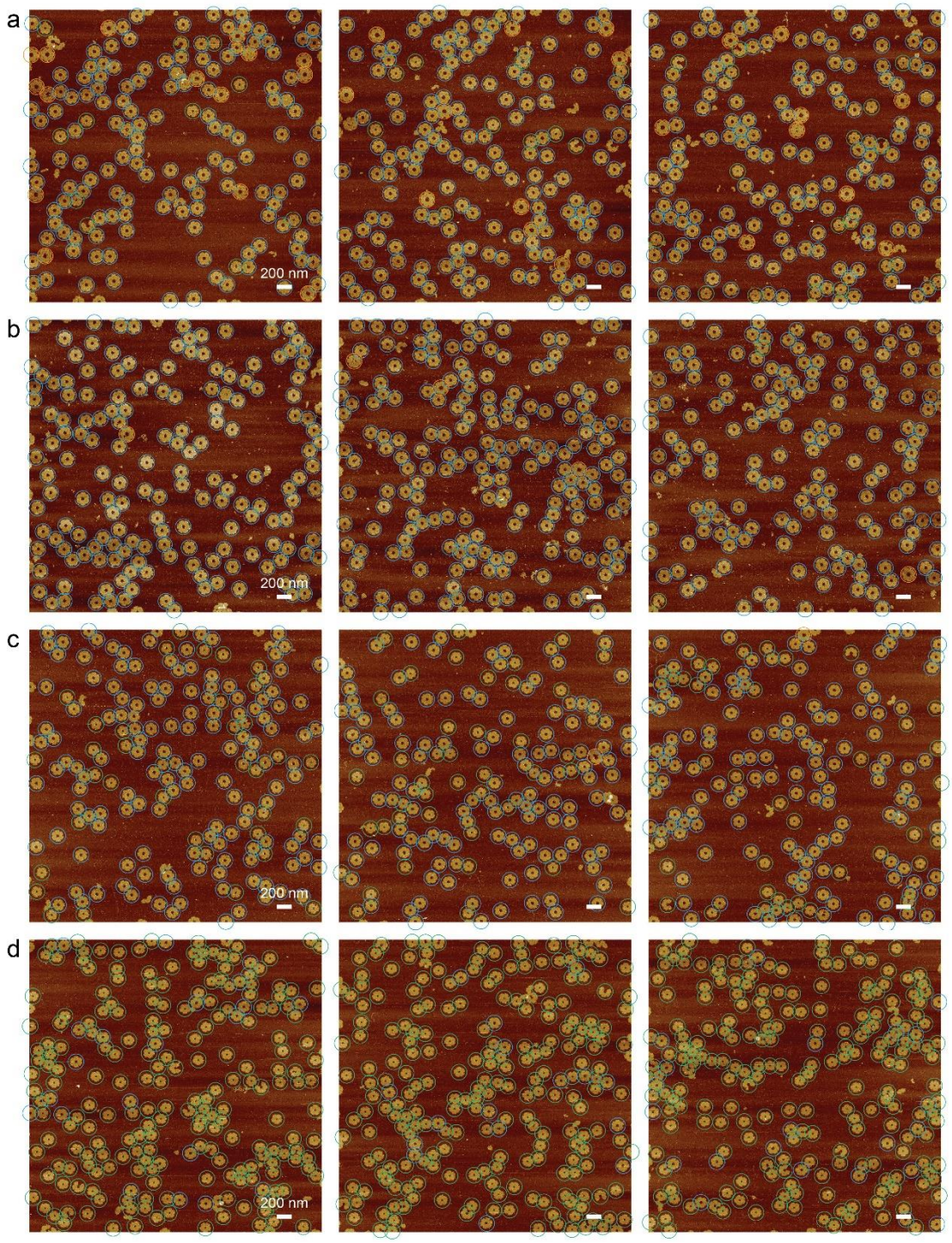

Figure S2.4. AFM characterization and analysis of multimeric complexes assembled from p3120 equilateral triangular DNA origami tiles. Four monomer tiles were designed based on different ***D*** values, including 2.55 nm (a), 2.70 nm (b), 2.85 nm (c), and 3.00 nm (d). Three non-overlapping AFM images (from left to right: #1, #2, #3) were analyzed for each design with pentamers, hexamers, and heptamers marked by green, blue, and orange circles, respectively. Scale bars: 200 nm.

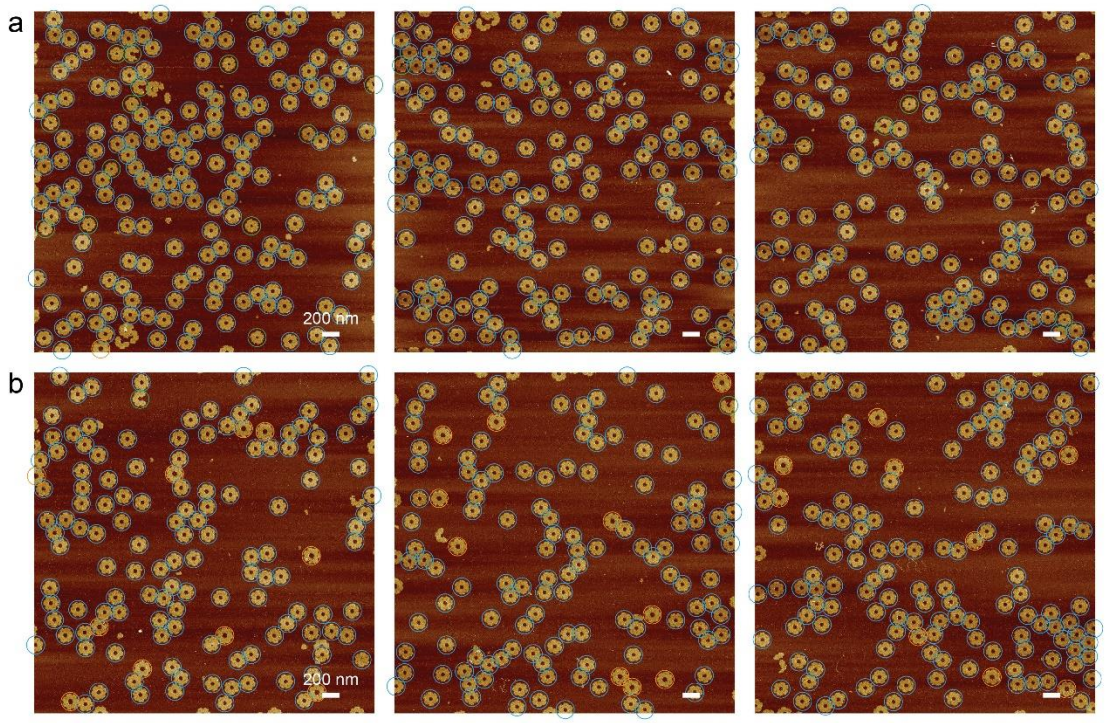

Figure S2.5. AFM characterization and analysis of multimers assembled from two additional tiles designed based on 2.65 nm (a) and 2.75 nm (b) ***D***, respectively. Three non-overlapping AFM images (from left to right: #1, #2, #3) were analyzed for each design with pentamers, hexamers, and heptamers marked by green, blue, and orange circles, respectively. Scale bars: 200 nm.

S2.4.2 Statistical analysis of multimers assembled from equilateral triangular tiles

Table S2.11. Summary of the statistical analysis of multimers assembled from p3120 equilateral triangular tiles based on different ***D*** values.

D (nm)	AFM image	Total number of multimers	Count and percentage of pentamers	Count and percentage of hexamers	Count and percentage of heptamers
2.55	#1	160	11 (6.88%)	134 (83.75%)	15 (9.38%)
	#2	163	11 (6.75%)	142 (87.12%)	10 (6.13%)
	#3	168	17 (10.12%)	142 (84.52%)	9 (5.36%)
2.65	#1	180	14 (7.78%)	165 (91.67%)	1 (0.56%)
	#2	164	6 (3.66%)	157 (95.73%)	1 (0.61%)
	#3	147	4 (2.72%)	143 (97.28%)	0 (0.00%)
2.70	#1	166	0 (0.00%)	165 (99.40%)	1 (0.60%)
	#2	185	0 (0.00%)	182 (98.38%)	3 (1.62%)
	#3	156	2 (1.28%)	153 (98.08%)	1 (0.64%)
2.75	#1	137	1 (0.73%)	126 (91.97%)	10 (7.30%)
	#2	131	1 (0.76%)	120 (91.60%)	10 (7.63%)
	#3	152	0 (0.00%)	143 (94.08%)	9 (5.92%)
2.85	#1	177	36 (20.34%)	141 (79.66%)	0 (0.00%)
	#2	162	42 (25.93%)	119 (73.46%)	1 (0.62%)
	#3	172	38 (22.09%)	133 (77.33%)	1 (0.58%)
3.00	#1	226	205 (90.71%)	21 (9.29%)	0 (0.00%)
	#2	228	212 (92.98%)	16 (7.02%)	0 (0.00%)
	#3	223	201 (90.13%)	22 (9.87%)	0 (0.00%)

Table S2.12. Mean percentage and standard deviation of multimers assembled from p3120 equilateral triangular tiles based on different ***D*** values.

D (nm)	Pentamer	Hexamer	Heptamer
2.55	7.91% ± 1.91%	85.13% ± 1.76%	6.96% ± 2.13%
2.65	4.72% ± 2.69%	94.89% ± 2.90%	0.39% ± 0.34%
2.70	0.43% ± 0.74%	98.62% ± 0.69%	0.96% ± 0.58%
2.75	0.50% ± 0.43%	92.55% ± 1.34%	6.95% ± 0.91%
2.85	22.79% ± 2.86%	76.81% ± 3.13%	0.40% ± 0.35%
3.00	91.27% ± 1.51%	8.73% ± 1.51%	0.00% ± 0.00%

S2.4.3 2D lattices assembled from p3120 equilateral triangular tiles (*D* = 2.70 nm)

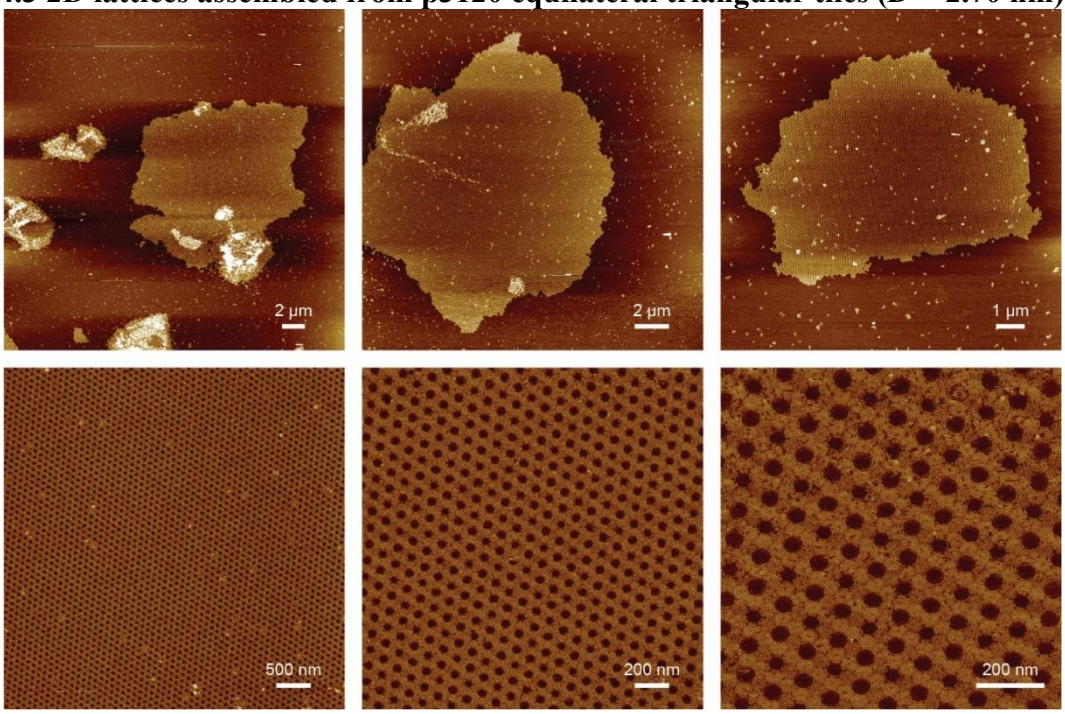

Figure S2.6. AFM images of 2D lattices assembled from p3120 equilateral triangular DNA origami tiles (***D*** = 2.70 nm).

S2.5 Additional AFM Images

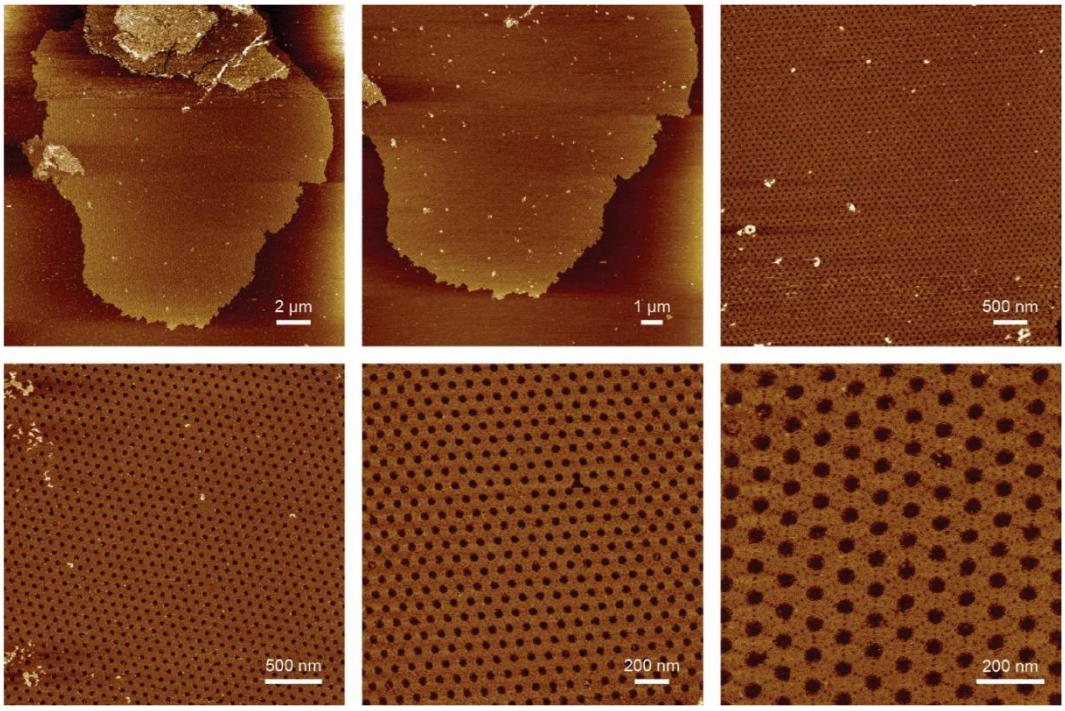

Figure S2.7. Additional AFM images of 2D lattices assembled from p3548 equilateral triangular DNA origami tiles.

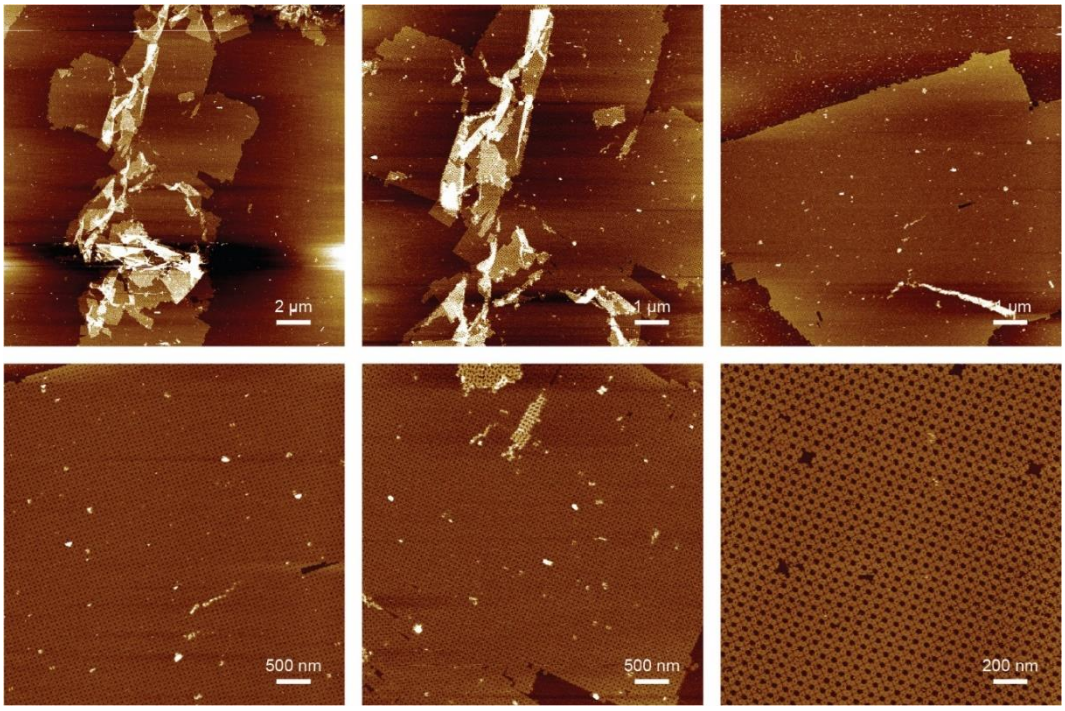

Figure S2.8. Additional AFM images of 2D lattices assembled from p3548 square DNA origami tiles.

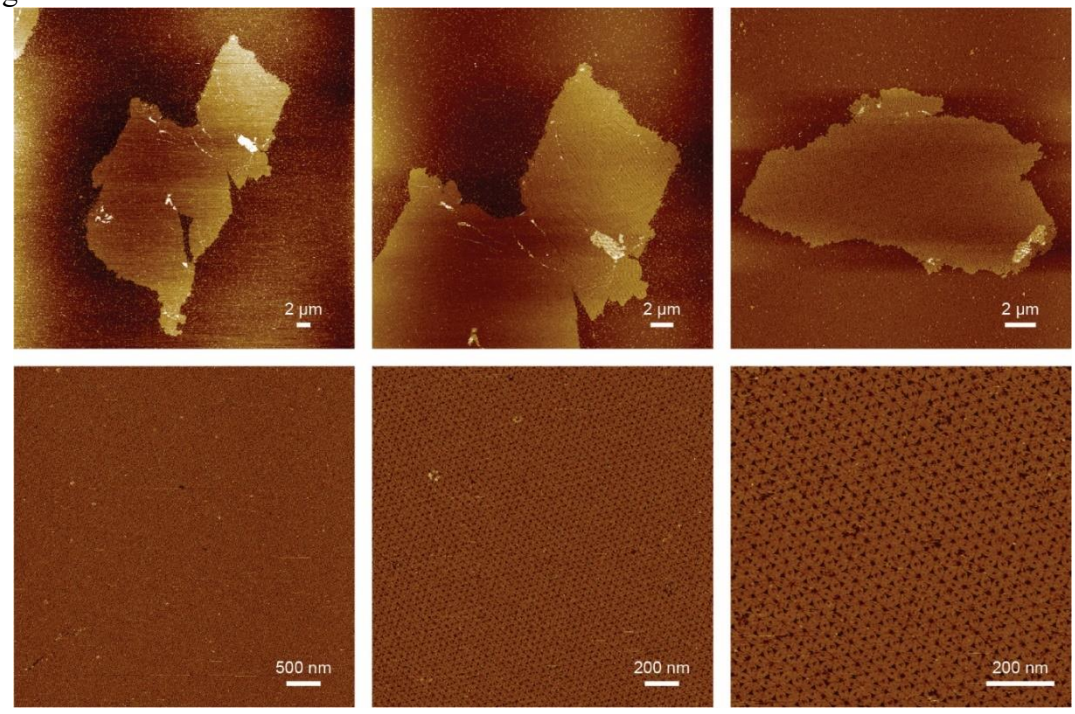

Figure S2.9. Additional AFM images of 2D lattices assembled from p3548 regular hexagonal DNA origami tiles.

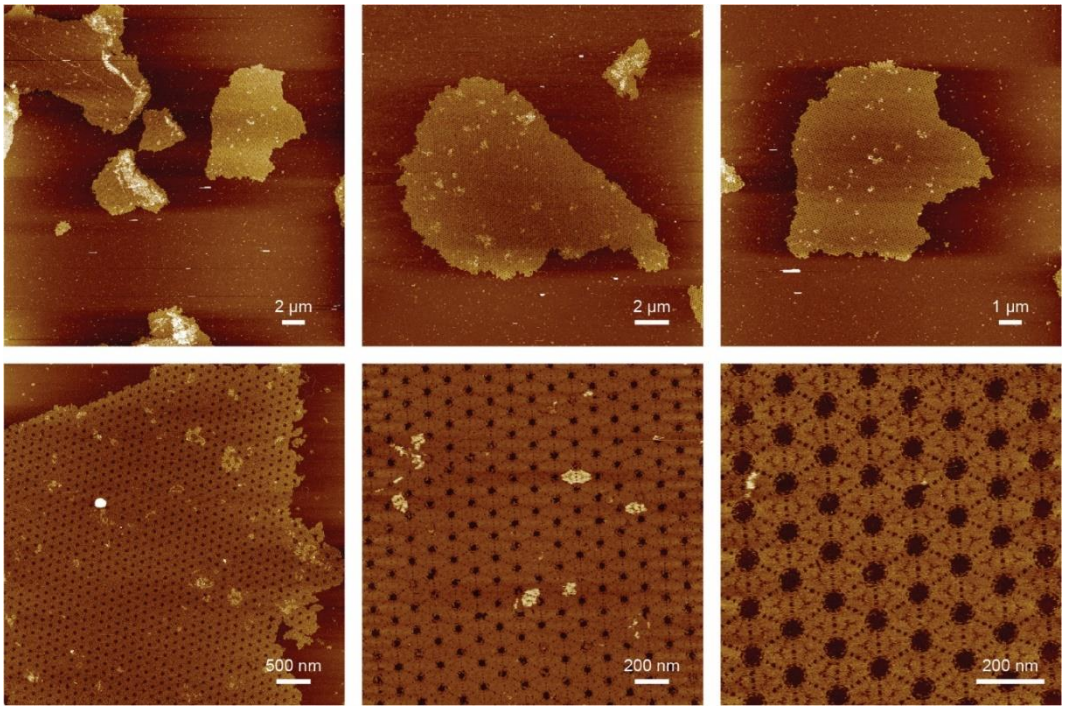

Figure S2.10. Additional AFM images of 2D lattices assembled from M13mp18 equilateral triangular DNA origami tiles.

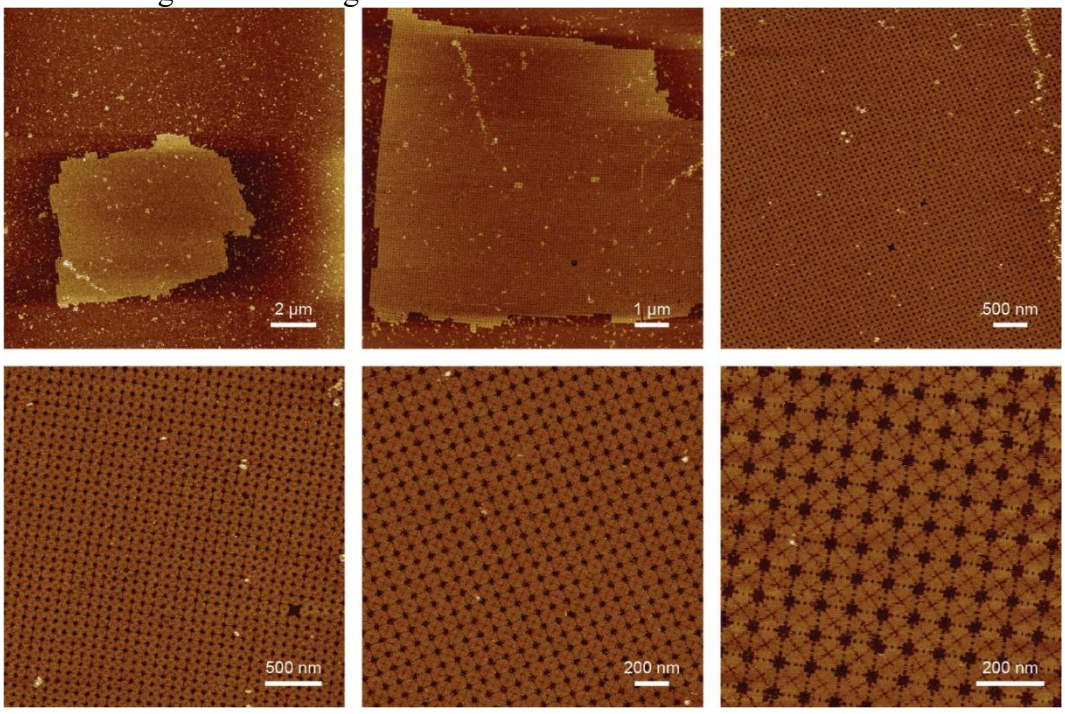

Figure S2.11. Additional AFM images of 2D lattices assembled from M13mp18 square DNA origami tiles.

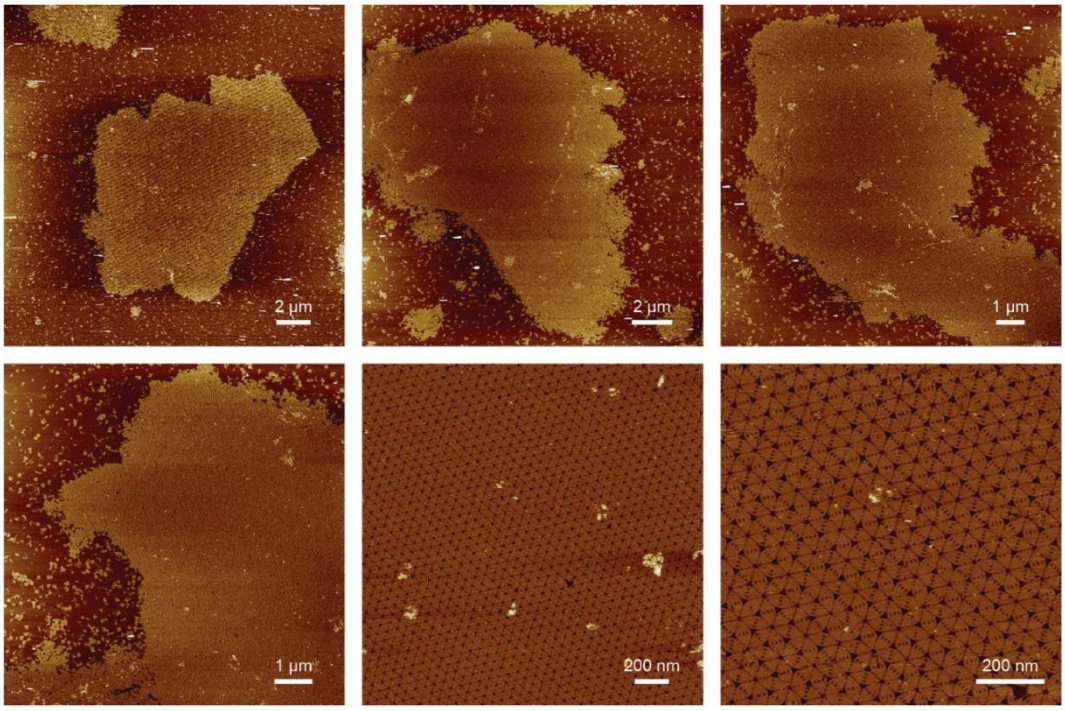

Figure S2.12. Additional AFM images of 2D lattices assembled from M13mp18 regular hexagonal DNA origami tiles.

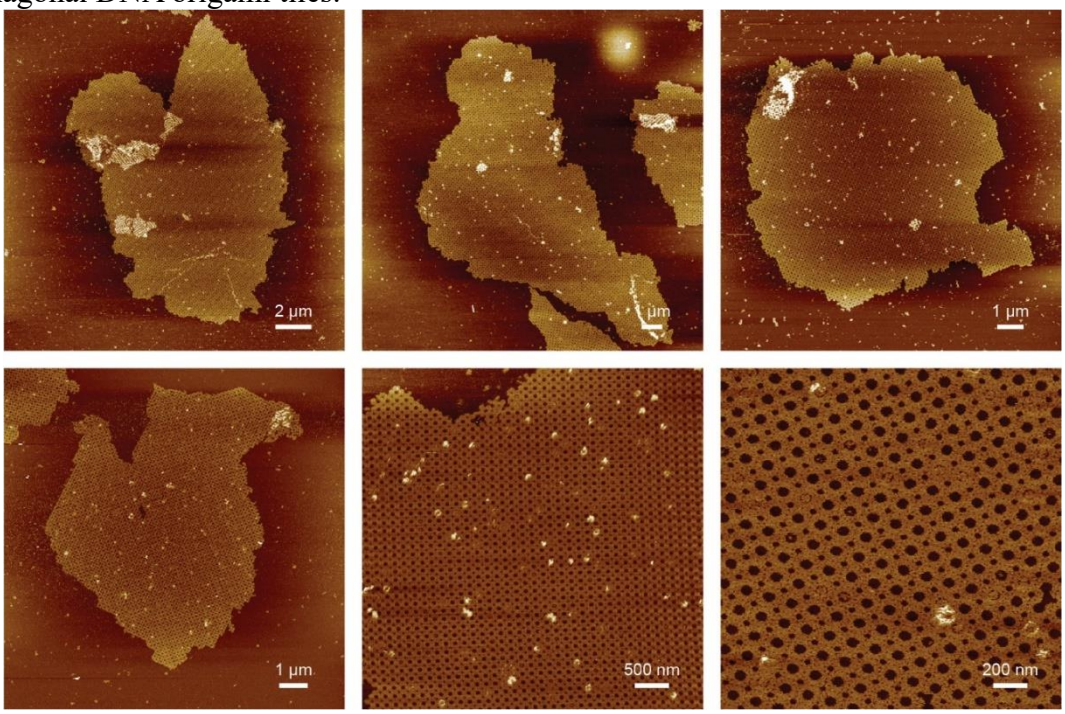

Figure S2.13. Additional AFM images of 2D lattices assembled from p3548 isosceles right triangular DNA origami tiles.

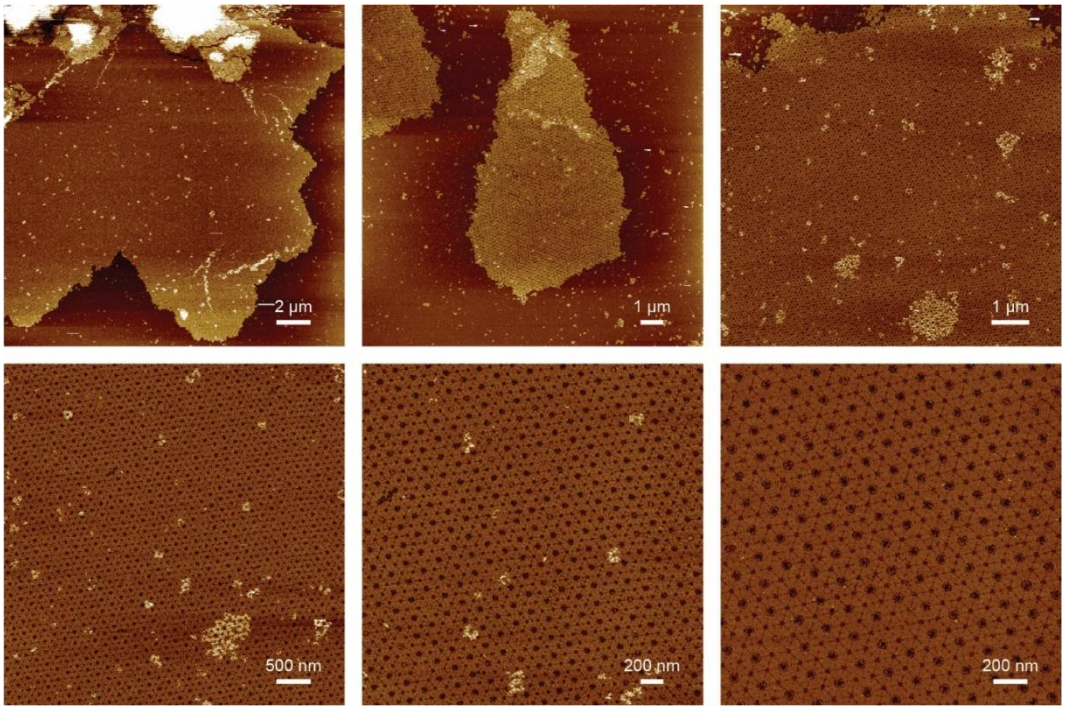

Figure S2.14. Additional AFM images of 2D lattices assembled from M13mp18 rhombic DNA origami tiles.

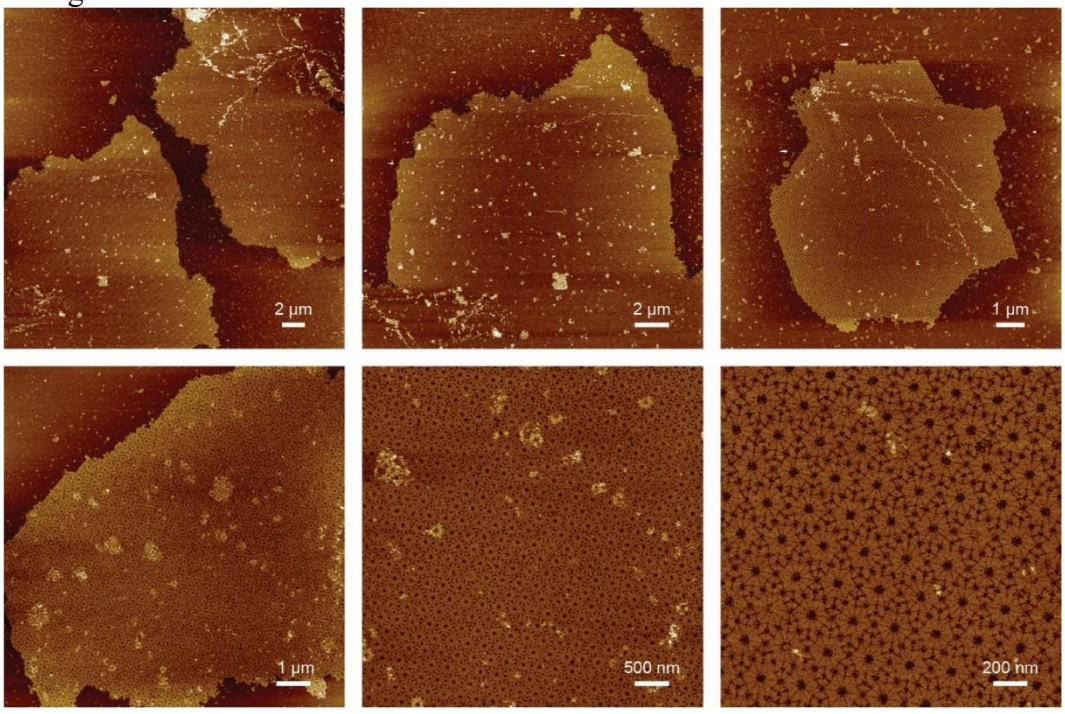

Figure S2.15. Additional AFM images of 2D lattices assembled from M13mp18 kite DNA origami tiles.

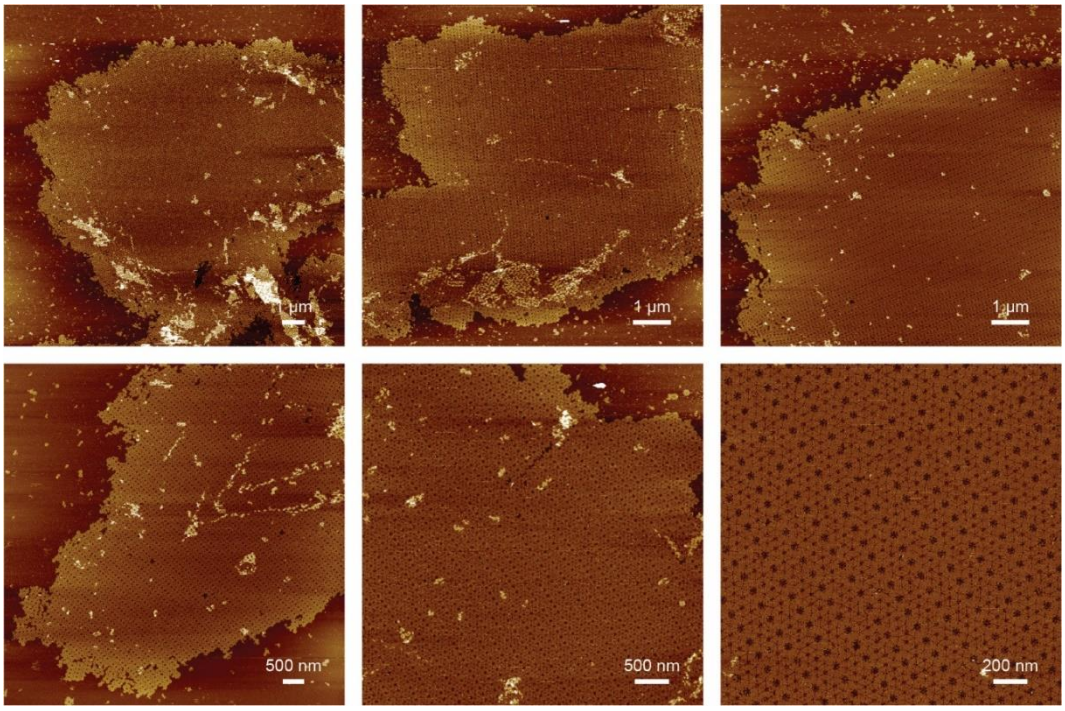

Figure S2.16. Additional AFM images of 2D lattices assembled from M13mp18 prismatic pentagonal DNA origami tiles.

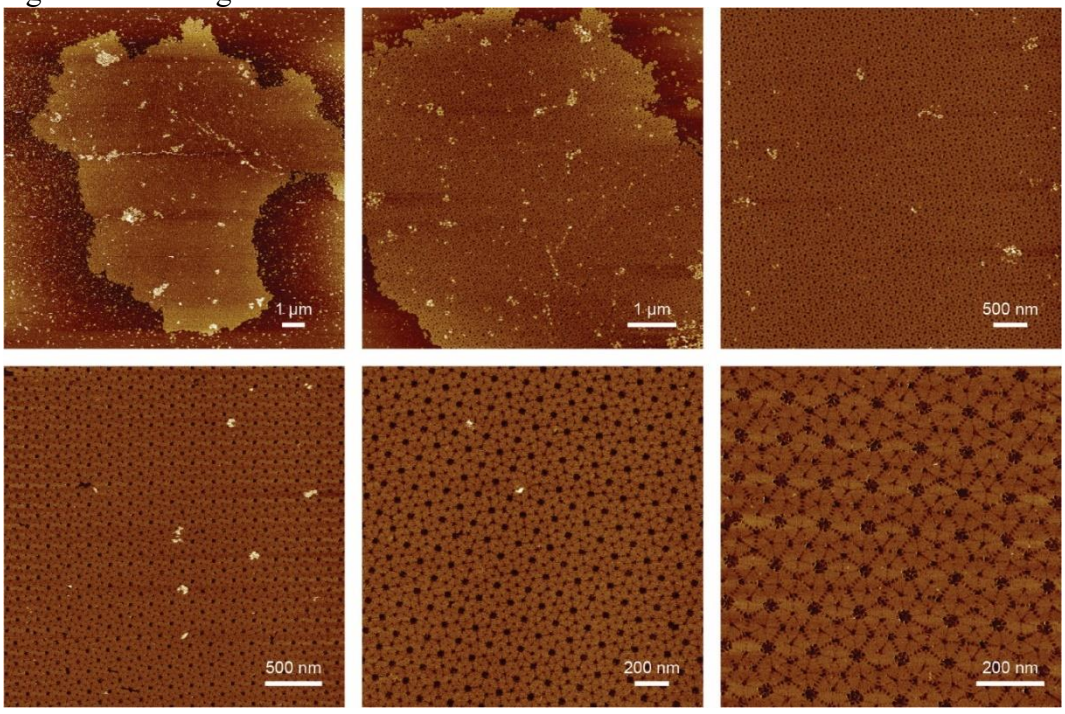

Figure S2.17. Additional AFM images of 2D lattices assembled from M13mp18 Cairo pentagonal DNA origami tiles.

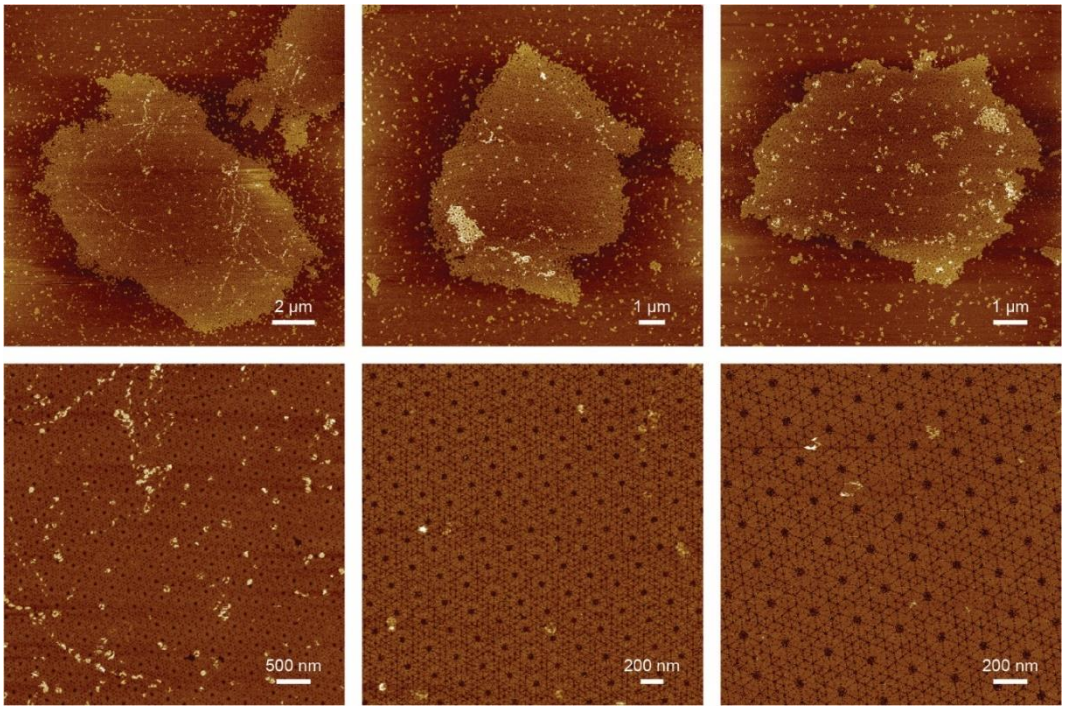

Figure S2.18. Additional AFM images of 2D lattices assembled from p8064 floret pentagonal DNA origami tiles.

S2.6 Thermodynamic Analysis of Tile Interactions

S2.6.1 Nearest-neighbor parameters for the thermodynamic analysis

We exploited the nearest neighbor model[6] to analyze the thermodynamic free energy of tile-tile interaction. 2-nt sticky end hybridization and blunt end stacking are the two types of interactions holding tiles together. Typically, each edge staple strand presents one 2-nt sticky end and one blunt end, whose binding free energy (ΔG_{bond}) can be calculated from the nearest-neighbor parameters for DNA hybridization and stacking adapted from the literature[6,7] (Table S2.15) and further summed up to obtain the total binding free energy for each pair of complementary edges (ΔG_{edge}).

Specifically, the sequence of a 2-nt sticky end can be read from the Tiamat design from 5' to 3' as "NNN/N" or "N/NNN" (N = A, T, C, or G), where the first and fourth "N"s are the coaxial stacking bases flanking the 2-nt sticky end and the slash represents

the two nucleotides lacking backbone linkage. Therefore, “NNN/N” corresponds to a 2-nt sticky end presented at the 3’-end of an edge staple, while “NNN/N” corresponds to a 2-nt sticky end at the 5’-end. The thermodynamic free energy of either case can be calculated by adding up the nearest-neighbor free energy of each pair of neighboring dinucleotides (ΔG_{NN}). Similarly, the sequence of a blunt end can be read from 5’- to 3’-end as “N/N”, whose free energy (ΔG_{stack}) can be found in the literature[9]. Further, ΔG_{bond} can be calculated by adding the contributions from these two portions.

Depending on the matching rule, a tile’s edge can either be complementary to another edge or self-complementary. The complementarity in the former case is denoted by “n & n*” (n = 1, 2, 3, …), whose ΔG_{edge} is the sum of each involved ΔG_{bond}. Self-complementary edge is denoted by “n/n*”, where half of the edge staple strands possess ΔG_{bond} identical to the other half. Therefore, its ΔG_{edge} is the sum of each unique ΔG_{bond} multiplied by 2.

Table S2.13. Nearest-neighbor parameters adapted from the literature[7].

Nearest-neighbor sequence (from 5' to 3')	Nearest-neighbor free energy (ΔG_{NN}) converted to 20 mM $MgCl_2$ (kcal/mol)	Stacking free energy (ΔG_{stack}) in 20 mM $MgCl_2$ (kcal/mol)
AA	-1.80	-1.36
AC	-2.32	-2.03
AG	-2.09	-1.60
AT	-1.64	-2.35
CA	-2.33	-0.81
CC	-2.63	-1.64
CG	-3.23	-2.06
CT	-2.09	-1.60
GA	-2.16	-1.39
GC	-3.21	-3.42
GG	-2.63	-1.64
GT	-2.32	-2.03
TA	-1.37	-1.01
TC	-2.16	-1.39
TG	-2.33	-0.81
TT	-1.80	-1.36

S2.6.2 Thermodynamic analysis of DNA origami tiles

S2.6.2.1 Thermodynamic analysis of DNA origami tiles for regular tilings

Table S2.14. Thermodynamic analysis of complementary edges in p3120 equilateral triangular tile (***D*** = 2.70 nm).

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GAT/A	C/A	-5.89	-49.35
	#2	TAG/T	G/C	-9.20	
	#3	ACG/G	C/A	-8.99	
	#4	GAT/C	A/A	-7.32	
	#5	CAA/G	G/T	-8.25	
	#6	CCC/T	A/T	-9.70	
2/2*	#7	TTG/C	C/C	-8.98	-45.62 (-22.81×2)
	#8	CAA/T	T/T	-7.13	
	#9	AGA/T	C/A	-6.70	

Table S2.15. Thermodynamic analysis of complementary edges in p3548 equilateral triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GAA/A	G/C	-9.18	-55.90
	#2	GGA/T	G/C	-9.85	
	#3	ACC/G	A/T	-10.53	
	#4	AGC/G	G/T	-10.56	
	#5	TAC/T	C/G	-7.84	
	#6	CAG/A	T/T	-7.94	
2/2*	#7	GGA/A	G/A	-7.98	-55.48 (-27.74×2)
	#8	ACC/C	A/T	-9.93	
	#9	GGG/C	T/T	-9.83	

Table S2.16. Thermodynamic analysis of complementary edges in p3548 square tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	TTT/T	G/G	-7.04	-34.98
	#2	GGG/A	A/T	-9.77	
	#3	CCT/G	G/G	-8.69	
	#4	GCC/C	T/A	-9.48	
2 & 2*	#5	CCC/A	T/G	-8.40	-33.92
	#6	CTG/T	G/G	-8.38	
	#7	CGA/G	T/C	-8.87	
	#8	CTC/C	T/C	-8.27	

Table S2.17. Thermodynamic analysis of complementary edges in p3548 regular hexagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GCA/C	C/C	-9.50	-36.70
	#2	CGA/A	G/C	-10.61	
	#3	TAC/G	T/C	-8.31	
	#4	CAA/A	A/T	-8.28	
2 & 2*	#5	GGA/A	A/A	-7.95	-34.26
	#6	CAC/G	T/G	-8.69	
	#7	TAG/C	G/C	-10.09	
	#8	ATC/T	G/G	-7.53	
3 & 3*	#9	TAA/C	G/G	-7.13	-28.53
	#10	ATA/A	T/G	-5.62	
	#11	TTG/T	C/C	-8.09	
	#12	TTC/T	C/C	-7.69	

Table S2.18. Thermodynamic analysis of complementary edges in M13mp18 equilateral triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GTT/G	T/C	-7.84	-63.53
	#2	ATC/C	T/C	-7.82	
	#3	AAC/A	A/A	-7.81	
	#4	ATA/C	G/T	-7.36	
	#5	GAG/C	T/T	-8.82	
	#6	CCT/T	A/C	-8.55	
	#7	GAA/G	A/A	-7.41	
	#8	TAC/C	C/T	-7.92	
2/2*	#9	TTG/A	C/A	-7.10	-59.56 (-29.78×2)
	#10	CCA/G	G/A	-8.44	
	#11	ATT/T	T/C	-6.63	
	#12	CTT/A	A/T	-7.61	

Table S2.19. Thermodynamic analysis of complementary edges in M13mp18 square tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CGT/A	A/C	-8.95	-33.04
	#2	AAA/C	T/C	-7.31	
	#3	ACA/A	G/G	-8.09	
	#4	CAC/G	C/A	-8.69	
2 & 2*	#5	GCG/C	T/G	-10.46	-35.67
	#6	ACA/C	T/C	-8.36	
	#7	ATA/C	C/C	-6.97	
	#8	CCG/C	C/A	-9.88	

Table S2.20. Thermodynamic analysis of complementary edges in M13mp18 regular hexagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	TTA/A	T/T	-6.33	-30.73
	#2	TAT/T	A/G	-6.41	
	#3	GAC/G	C/C	-9.35	
	#4	GCT/G	T/A	-8.64	
2 & 2*	#5	TCA/A	T/T	-7.65	-32.62
	#6	ATA/C	A/G	-6.93	
	#7	ATT/C	A/G	-7.20	
	#8	TCC/C	G/C	-10.84	
3 & 3*	#9	CCT/A	T/A	-7.10	-32.45
	#10	AAG/T	C/C	-7.85	
	#11	GAC/C	A/C	-9.14	
	#12	TTG/G	A/G	-8.36	

S2.6.2.2 Thermodynamic analysis of DNA origami tiles for Laves tilings

Table S2.21. Thermodynamic analysis of complementary edges in p3548 isosceles right triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1/1*	#1	AGG/G	G/T	-10.13	-87.50 (-43.75×2)
	#2	CAA/C	A/A	-7.81	
	#3	GGA/G	A/G	-7.70	
	#4	TGA/C	C/T	-9.17	
	#5	CTG/C	C/G	-8.94	
2 & 2*	#6	GGG/G	C/T	-9.49	-54.48
	#7	GGC/C	G/C	-11.89	
	#8	CCA/T	C/T	-8.20	
	#9	CTG/A	C/G	-8.64	
	#10	CTT/C	G/C	-9.47	
	#11	TAC/T	T/A	-6.79	

Table S2.22. Thermodynamic analysis of complementary edges in M13mp18 rhombic tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CCA/T	A/A	-7.96	-45.54
	#2	ATA/C	A/A	-6.69	
	#3	GGT/T	C/G	-8.81	
	#4	CTC/A	T/A	-7.59	
	#5	TTG/A	C/G	-8.35	
	#6	GTA/T	C/A	-6.14	
2 & 2*	#7	TCG/A	G/T	-9.58	-51.07
	#8	CTA/A	G/G	-6.90	
	#9	CGA/T	G/A	-8.42	
	#10	CTC/G	A/T	-9.83	
	#11	CCC/A	A/A	-8.95	
	#12	CTC/A	T/G	-7.39	

Table S2.23. Thermodynamic analysis of complementary edges in M13mp18 kite tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	TAA/T	G/A	-6.20	-65.49
	#2	CCA/A	C/C	-8.40	
	#3	AAG/A	A/C	-8.08	
	#4	CGC/A	T/A	-9.78	
	#5	GAA/A	A/A	-7.12	
	#6	CAA/G	A/A	-7.58	
	#7	CCG/C	C/C	-10.71	
	#8	TGT/A	C/T	-7.62	
2 & 2*	#9	*N/A*	T/A & G/G	-2.65	-21.85
	#10	*N/A*	G/A & G/C	-4.81	
	#11	CTT/T	A/A	-7.05	
	#12	*N/A*	T/T & C/T	-2.96	
	#13	*N/A*	G/T & A/T	-4.38	

Table S2.24. Thermodynamic analysis of complementary edges in M13mp18 prismatic pentagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1/1*	#1	TGG/A	A/C	-9.15	-29.94 (-14.97×2)
	#2	ATT/A	T/A	-5.82	
2/2*	#3	CTA/A	T/A	-6.27	-32.20 (-16.10×2)
	#4	GGC/C	T/T	-9.83	
3 & 3*	#5	ATA/A	T/T	-6.17	-26.88
	#6	TAA/A	T/A	-5.98	
	#7	TCA/T	G/G	-7.77	
	#8	GAT/T	A/A	-6.96	
4/4*	#9	AGC/A	A/A	-8.99	-57.80 (-28.90×2)
	#10	CGC/C	A/T	-11.42	
	#11	C/GGG	*N/A*	-8.49	

Table S2.25. Thermodynamic analysis of complementary edges in M13mp18 Cairo pentagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	AAA/C	G/G	-7.56	-32.33
	#2	CTT/T	T/A	-6.70	
	#3	CCG/G	T/G	-9.30	
	#4	ACA/G	G/T	-8.77	
2 & 2*	#5	TTA/A	G/A	-6.36	-29.19
	#6	GCC/A	A/G	-9.77	
	#7	TAT/A	T/T	-5.74	
	#8	TAA/A	A/T	-7.32	
3/3*	#9	G/TAC	G/G	-7.65	-35.76 (-17.88×2)
	#10	T/GAC	G/C	-10.23	

Table S2.26. Thermodynamic analysis of complementary edges in p8064 floret pentagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CGT/T	A/C	-9.38	-66.78
	#2	CAA/G	A/C	-8.25	
	#3	ATT/A	T/G	-5.62	
	#4	GAC/C	C/A	-7.92	
	#5	AGC/G	A/C	-10.56	
	#6	GTA/T	G/T	-7.36	
	#7	TGC/A	C/T	-9.47	
	#8	TCT/G	C/C	-8.22	
2 & 2*	#9	ACG/G	T/A	-9.19	-32.19
	#10	CAT/C	A/A	-7.49	
	#11	AGG/T	C/A	-7.85	
	#12	GAT/T	C/G	-7.66	
3/3*	#13	GTA/G	T/A	-6.79	-31.86 (-15.93×2)
	#14	GGT/C	G/T	-9.14	

S2.7 DNA Sequences

S2.7.1 Sequences of scaffold strands

S2.7.1.1 Sequence of the customized p3120 scaffold

CGATACGCTGAGGTATCGATGGCCCTGATTCAGAGCTCGCTACGTGTTTTAGCT
GCCATTGATTGCTAACCCTTAGGCAAAATATTGAAGCATGTAGTCCTCCCTATC
CGAGCTGGACAGAGTGGTAATCTCCCATTGCATCCAAGCTTATCGATACCGTCG
ACCTCGAGGGGGGGCCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACGC
GCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTA
CCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCG
AAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGA
ATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGC
GCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTC
TTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGG
GGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAA
ACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTT
TCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAAC
TGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTG
CCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCG
AATTTTAACAAAATATTAACGCTTACAATTTAGGTGGCACTTTTCGGGGAAATG
TGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTC
ATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATG
AGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTC
CTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAG
TTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCT
TGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTC
TGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTC
GCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAA
AAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAAC
CATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGA
AGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATC
GTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCAC
GATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTAC
TTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTT
GCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAA
ATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAG
ATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACT
ATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCA
TTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTT
CATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCA
AAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAG
ATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAA
ACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTAC

CAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACT
GTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACC
GCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGA
TAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGC
AGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAAC
GACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACG
CTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAA
CAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAG
TCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTC
AGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTC
CTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATT
CTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCC
GAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAA
TACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAC
GACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGA
GTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTA
TGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGAC
CATGATTACGCCAAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGG
AGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCA
GGAATTCGAACGGTCTCAGTCATGGATCA

S2.7.1.2 Sequence of the customized p3548 scaffold

GTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAA
TACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATA
ATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCC
CTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAA
AGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTG
GATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCC
AATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGAC
GCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGT
TGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAG
AATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTC
TGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGG
GGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATAC
CAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCG
CAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGA
CTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGG
CTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGT
ATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTAC
ACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGA
TAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATA
TACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGAT
CCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTG
AGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTC
TGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTT
TGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAG
CAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACC
ACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTAC
CAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGA
CGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCA
CACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCG
TGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTAT
CCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGG
GGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAG
CGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAG
CAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTT
CTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGA
GCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCG
AGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCC
GATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTG
AGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTA
CACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTT
CACACAGGAAACAGCTATGACCATGATTACGCCAAGCGCGCAATTAACCCTCA
CTAAAGGGAACAAAAGCTGGAGCTCCACCGCGGTGGCGGCCGCTCTAGAACT
AGTGGATCCCCCGGGCTGCAGGAATTCTGACGGTCTCACTGTTCGGTCATTGT

GACACGTCGAGAAGTCCTGCCACTGTACGAGAGTTTTTTCCGCAGTACAGCTT
CCTTTTACGGGCCTTCTCCCTCTTTTTTCGGATAGAAGGTATCTTGATACACATG
GGTCGTTCGATGTGCATCAGACTTCAAGGTGACGTCGAATTGCACCACTCTTC
CGACTACACGCACGCTTTTTTCCTAACGTGTACAAGGTTTTACCATGCCAGGGT
TGCTTTTTTCCTATCCTGGTTGGAGCGGACTGCGTTTCGTGCTGGCCGAATAAT
TGCTGCGCTGAGGCTAGGCGTTGGCTTATCTTGCCCCGATGGATAACTTCTTTT
TTCCAACTATCCACCCGATTTTGAGCTCTCTGCGTATCTTTTTTCCCTGGCAGAT
TTGTCGTTGATTTTGTCCGTAGTCCGCTGATGCCAGTATCAGATGCCGGCGAGT
CACGTTAAGCCAGGGATCTCGATTGGTGACTTTTTTCCTGTCAATCGCTCAATT
TTCACGCCACCAGTCTTGTTTTTTCTGAGCTGGTTCTACGTGGGTACGAACGTA
CAGACAGATGAGCTCACCATTGCACCAAAGCTTATCGATACCGTCGACCTCGA
GGGGGGGCCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCA
CTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACT
TAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGG
CCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGAC
GCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCG
TGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTT
CCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTC
CCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGAT
TAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCT
TTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAAC
AACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATT
TCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTT
AACAAAATATTAACGCTTACAATTTAG

S2.7.1.3 Sequence of the M13mp18 scaffold

TGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGA
CTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTGAT
TTATAAGGGATTTTGCCGATTTCGGAACCACCATCAAACAGGATTTTCGCCTGC
TGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGT
GAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTG
GCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCA
GCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAAT
TAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCC
GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACA
GCTATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCG
ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTG
GGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCG
CCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTG
CGCAGCCTGAATGGCGAATGGCGCTTTGCCTGGTTTCCGGCACCAGAAGCGGT
GCCGGAAAGCTGGCTGGAGTGCGATCTTCCTGAGGCCGATACTGTCGTCGTCC
CCTCAAACTGGCAGATGCACGGTTACGATGCGCCCATCTACACCAACGTGACC
TATCCCATTACGGTCAATCCGCCGTTTGTTCCCACGGAGAATCCGACGGGTTGT
TACTCGCTCACATTTAATGTTGATGAAAGCTGGCTACAGGAAGGCCAGACGCG
AATTATTTTTGATGGCGTTCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT
TTAATGCGAATTTTAACAAAATATTAACGTTTACAATTTAAATATTTGCTTATACA
ATCTTCCTGTTTTTGGGGCTTTTCTGATTATCAACCGGGGTACATATGATTGACA
TGCTAGTTTTACGATTACCGTTCATCGATTCTCTTGTTTGCTCCAGACTCTCAGG
CAATGACCTGATAGCCTTTGTAGATCTCTCAAAAATAGCTACCCTCTCCGGCAT
TAATTTATCAGCTAGAACGGTTGAATATCATATTGATGGTGATTTGACTGTCTCC
GGCCTTTCTCACCCTTTTGAATCTTTACCTACACATTACTCAGGCATTGCATTTA
AAATATATGAGGGTTCTAAAAATTTTTATCCTTGCGTTGAAATAAAGGCTTCTCC
CGCAAAAGTATTACAGGGTCATAATGTTTTTGGTACAACCGATTTAGCTTTATG
CTCTGAGGCTTTATTGCTTAATTTTGCTAATTCTTTGCCTTGCCTGTATGATTTAT
TGGATGTTAATGCTACTACTATTAGTAGAATTGATGCCACCTTTTCAGCTCGCGC
CCCAAATGAAAATATAGCTAAACAGGTTATTGACCATTTGCGAAATGTATCTAA
TGGTCAAACTAAATCTACTCGTTCGCAGAATTGGGAATCAACTGTTATATGGAA
TGAAACTTCCAGACACCGTACTTTAGTTGCATATTTAAAACATGTTGAGCTACA
GCATTATATTCAGCAATTAAGCTCTAAGCCATCCGCAAAAATGACCTCTTATCA
AAAGGAGCAATTAAAGGTACTCTCTAATCCTGACCTGTTGGAGTTTGCTTCCG
GTCTGGTTCGCTTTGAAGCTCGAATTAAAACGCGATATTTGAAGTCTTTCGGGC
TTCCTCTTAATCTTTTTGATGCAATCCGCTTTGCTTCTGACTATAATAGTCAGGG
TAAAGACCTGATTTTTGATTTATGGTCATTCTCGTTTTCTGAACTGTTTAAAGCA
TTTGAGGGGGATTCAATGAATATTTATGACGATTCCGCAGTATTGGACGCTATCC
AGTCTAAACATTTTACTATTACCCCCTCTGGCAAAACTTCTTTTGCAAAAGCCT
CTCGCTATTTTGGTTTTTATCGTCGTCTGGTAAACGAGGGTTATGATAGTGTTGC
TCTTACTATGCCTCGTAATTCCTTTTGGCGTTATGTATCTGCATTAGTTGAATGTG
GTATTCCTAAATCTCAACTGATGAATCTTTCTACCTGTAATAATGTTGTTCCGTT
AGTTCGTTTTATTAACGTAGATTTTTCTTCCCAACGTCCTGACTGGTATAATGAG

CCAGTTCTTAAAATCGCATAAGGTAATTCACAATGATTAAAGTTGAAATTAAAC
CATCTCAAGCCCAATTTACTACTCGTTCTGGTGTTTCTCGTCAGGGCAAGCCTT
ATTCACTGAATGAGCAGCTTTGTTACGTTGATTTGGGTAATGAATATCCGGTTC
TTGTCAAGATTACTCTTGATGAAGGTCAGCCAGCCTATGCGCCTGGTCTGTACA
CCGTTCATCTGTCCTCTTTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTGACC
GTCTGCGCCTCGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTCGACAC
AATTTATCAGGCGATGATACAAATCTCCGTTGTACTTTGTTTCGCGCTTGGTATA
ATCGCTGGGGGTCAAAGATGAGTGTTTTAGTGTATTCTTTTGCCTCTTTCGTTTT
AGGTTGGTGCCTTCGTAGTGGCATTACGTATTTTACCCGTTTAATGGAAACTTC
CTCATGAAAAAGTCTTTAGTCCTCAAAGCCTCTGTAGCCGTTGCTACCCTCGTT
CCGATGCTGTCTTTCGCTGCTGAGGGTGACGATCCCGCAAAAGCGGCCTTTAA
CTCCCTGCAAGCCTCAGCGACCGAATATATCGGTTATGCGTGGGCGATGGTTGT
TGTCATTGTCGGCGCAACTATCGGTATCAAGCTGTTTAAGAAATTCACCTCGAA
AGCAAGCTGATAAACCGATACAATTAAAGGCTCCTTTTGGAGCCTTTTTTTTGG
AGATTTTCAACGTGAAAAAATTATTATTCGCAATTCCTTTAGTTGTTCCTTTCTA
TTCTCACTCCGCTGAAACTGTTGAAAGTTGTTTAGCAAAATCCCATACAGAAA
ATTCATTTACTAACGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACT
ATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAA
ACTCAGTGTTACGGTACATGGGTTCCTATTGGGCTTGCTATCCCTGAAAATGAG
GGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTGGCG
GTACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCTATACTTATATCAA
CCCTCTCGACGGCACTTATCCGCCTGGTACTGAGCAAAACCCCGCTAATCCTA
ATCCTTCTCTTGAGGAGTCTCAGCCTCTTAATACTTTCATGTTTCAGAATAATAG
GTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCACTGTTACTCAAG
GCACTGACCCCGTTAAAACTTATTACCAGTACACTCCTGTATCATCAAAAGCCA
TGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTGGCT
TTAATGAGGATTTATTTGTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCTC
AACCTCCTGTCAATGCTGGCGGCGGCTCTGGTGGTGGTTCTGGTGGCGGCTCT
GAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAG
GCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCA
AACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAGTC
TGACGCTAAAGGCAAACTTGATTCTGTCGCTACTGATTACGGTGCTGCTATCGA
TGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTGCTACTGGTGA
TTTTGCTGGCTCTAATTCCCAAATGGCTCAAGTCGGTGACGGTGATAATTCACC
TTTAATGAATAATTTCCGTCAATATTTACCTTCCCTCCCTCAATCGGTTGAATGT
CGCCCTTTTGTCTTTGGCGCTGGTAAACCATATGAATTTTCTATTGATTGTGACA
AAATAAACTTATTCCGTGGTGTCTTTGCGTTTCTTTTATATGTTGCCACCTTTAT
GTATGTATTTTCTACGTTTGCTAACATACTGCGTAATAAGGAGTCTTAATCATGC
CAGTTCTTTTGGGTATTCCGTTATTATTGCGTTTCCTCGGTTTCCTTCTGGTAAC
TTTGTTCGGCTATCTGCTTACTTTTCTTAAAAAGGGCTTCGGTAAGATAGCTATT
GCTATTTCATTGTTTCTTGCTCTTATTATTGGGCTTAACTCAATTCTTGTGGGTTA
TCTCTCTGATATTAGCGCTCAATTACCCTCTGACTTTGTTCAGGGTGTTCAGTTA
ATTCTCCCGTCTAATGCGCTTCCCTGTTTTTATGTTATTCTCTCTGTAAAGGCTG
CTATTTTCATTTTTGACGTTAAACAAAAAATCGTTTCTTATTTGGATTGGGATAA
ATAATATGGCTGTTTATTTTGTAACTGGCAAATTAGGCTCTGGAAAGACGCTCG

TTAGCGTTGGTAAGATTCAGGATAAAATTGTAGCTGGGTGCAAAATAGCAACT
AATCTTGATTTAAGGCTTCAAAACCTCCCGCAAGTCGGGAGGTTCGCTAAAAC
GCCTCGCGTTCTTAGAATACCGGATAAGCCTTCTATATCTGATTTGCTTGCTATT
GGGCGCGGTAATGATTCCTACGATGAAAATAAAAACGGCTTGCTTGTTCTCGAT
GAGTGCGGTACTTGGTTTAATACCCGTTCTTGGAATGATAAGGAAAGACAGCC
GATTATTGATTGGTTTCTACATGCTCGTAAATTAGGATGGGATATTATTTTCTTG
TTCAGGACTTATCTATTGTTGATAAACAGGCGCGTTCTGCATTAGCTGAACATG
TTGTTTATTGTCGTCGTCTGGACAGAATTACTTTACCTTTTGTCGGTACTTTATAT
TCTCTTATTACTGGCTCGAAAATGCCTCTGCCTAAATTACATGTTGGCGTTGTTA
AATATGGCGATTCTCAATTAAGCCCTACTGTTGAGCGTTGGCTTTATACTGGTAA
GAATTTGTATAACGCATATGATACTAAACAGGCTTTTTCTAGTAATTATGATTCC
GGTGTTTATTCTTATTTAACGCCTTATTTATCACACGGTCGGTATTTCAAACCATT
AAATTTAGGTCAGAAGATGAAATTAACTAAAATATATTTGAAAAAGTTTTCTCG
CGTTCTTTGTCTTGCGATTGGATTTGCATCAGCATTTACATATAGTTATATAACCC
AACCTAAGCCGGAGGTTAAAAAGGTAGTCTCTCAGACCTATGATTTTGATAAAT
TCACTATTGACTCTTCTCAGCGTCTTAATCTAAGCTATCGCTATGTTTTCAAGGA
TTCTAAGGGAAAATTAATTAATAGCGACGATTTACAGAAGCAAGGTTATTCACT
CACATATATTGATTTATGTACTGTTTCCATTAAAAAAGGTAATTCAAATGAAATT
GTTAAATGTAATTAATTTTGTTTTCTTGATGTTTGTTTCATCATCTTCTTTTGCTC
AGGTAATTGAAATGAATAATTCGCCTCTGCGCGATTTTGTAACTTGGTATTCAA
AGCAATCAGGCGAATCCGTTATTGTTTCTCCCGATGTAAAAGGTACTGTTACTG
TATATTCATCTGACGTTAAACCTGAAAATCTACGCAATTTCTTTATTTCTGTTTTA
CGTGCAAATAATTTTGATATGGTAGGTTCTAACCCTTCCATTATTCAGAAGTATA
ATCCAAACAATCAGGATTATATTGATGAATTGCCATCATCTGATAATCAGGAATA
TGATGATAATTCCGCTCCTTCTGGTGGTTTCTTTGTTCCGCAAAATGATAATGTT
ACTCAAACTTTTAAAATTAATAACGTTCGGGCAAAGGATTTAATACGAGTTGTC
GAATTGTTTGTAAAGTCTAATACTTCTAAATCCTCAAATGTATTATCTATTGACG
GCTCTAATCTATTAGTTGTTAGTGCTCCTAAAGATATTTTAGATAACCTTCCTCA
ATTCCTTTCAACTGTTGATTTGCCAACTGACCAGATATTGATTGAGGGTTTGAT
ATTTGAGGTTCAGCAAGGTGATGCTTTAGATTTTTCATTTGCTGCTGGCTCTCA
GCGTGGCACTGTTGCAGGCGGTGTTAATACTGACCGCCTCACCTCTGTTTTATC
TTCTGCTGGTGGTTCGTTCGGTATTTTTAATGGCGATGTTTTAGGGCTATCAGTT
CGCGCATTAAAGACTAATAGCCATTCAAAAATATTGTCTGTGCCACGTATTCTTA
CGCTTTCAGGTCAGAAGGGTTCTATCTCTGTTGGCCAGAATGTCCCTTTTATTA
CTGGTCGTGTGACTGGTGAATCTGCCAATGTAAATAATCCATTTCAGACGATTG
AGCGTCAAAATGTAGGTATTTCCATGAGCGTTTTTCCTGTTGCAATGGCTGGCG
GTAATATTGTTCTGGATATTACCAGCAAGGCCGATAGTTTGAGTTCTTCTACTCA
GGCAAGTGATGTTATTACTAATCAAAGAAGTATTGCTACAACGGTTAATTTGCG
TGATGGACAGACTCTTTTACTCGGTGGCCTCACTGATTATAAAAACACTTCTCA
GGATTCTGGCGTACCGTTCCTGTCTAAAATCCCTTTAATCGGCCTCCTGTTTAG
CTCCCGCTCTGATTCTAACGAGGAAAGCACGTTATACGTGCTCGTCAAAGCAA
CCATAGTACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTAC
GCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTT
TCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATC

GGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAA
AAACTTGATTTGGGTGATGGTTCACGTAGTGGGCCATCGCCC

S2.7.1.4 Sequence of the p8064 scaffold

TGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGA
CTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTGAT
TTATAAGGGATTTTGCCGATTTCGGAACCACCATCAAACAGGATTTTCGCCTGC
TGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGT
GAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTG
GCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCA
GCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAAT
TAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCC
GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACA
GCTATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCAACTGTGA
GGAGGCTCACGGACGCGAAGAACAGGCACGCGTGCTGGCAGAAACCCCCGG
TATGACCGTGAAAACGGCCCGCCGCATTCTGGCCGCAGCACCACAGAGTGCA
CAGGCGCGCAGTGACACTGCGCTGGATCGTCTGATGCAGGGGGCACCGGCAC
CGCTGGCTGCAGGTAACCCGGCATCTGATGCCGTTAACGATTTGCTGAACACA
CCAGTGTAAGGGATGTTTATGACGAGCAAAGAAACCTTTACCCATTACCAGCC
GCAGGGCAACAGTGACCCGGCTCATACCGCAACCGCGCCCGGCGGATTGAGT
GCGAAAGCGCCTGCAATGACCCCGCTGATGCTGGACACCTCCAGCCGTAAGC
TGGTTGCGTGGGATGGCACCACCGACGGTGCTGCCGTTGGCATTCTTGCGGTT
GCTGCTGACCAGACCAGCACCACGCTGACGTTCTACAAGTCCGGCACGTTCC
GTTATGAGGATGTGCTCTGGCCGGAGGCTGCCAGCGACGAGACGAAAAAACG
GACCGCGTTTGCCGGAACGGCAATCAGCATCGTTTAACTTTACCCTTCATCACT
AAAGGCCGCCTGTGCGGCTTTTTTTACGGGATTTTTTTATGTCGATGTACACAA
CCGCCCAACTGCTGGCGGCAAATGAGCAGAAATTTAAGTTTGATCCGCTGTTT
CTGCGTCTCTTTTTCCGTGAGAGCTATCCCTTCACCACGGAGAAAGTCTATCTC
TCACAAATTCCGGGACTGGTAAACATGGCGCTGTACGTTTCGCCGATTGTTTCC
GGTGAGGTTATCCGTTCCCGTGGCGGCTCCACCTCTGAAAGCTTGGCACTGGC
CGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATC
GCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGC
ACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTTGC
CTGGTTTCCGGCACCAGAAGCGGTGCCGGAAAGCTGGCTGGAGTGCGATCTT
CCTGAGGCCGATACTGTCGTCGTCCCCTCAAACTGGCAGATGCACGGTTACGA
TGCGCCCATCTACACCAACGTGACCTATCCCATTACGGTCAATCCGCCGTTTGT
TCCCACGGAGAATCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAA
GCTGGCTACAGGAAGGCCAGACGCGAATTATTTTTGATGGCGTTCCTATTGGTT
AAAAAATGAGCTGATTTAACAAAAATTTAATGCGAATTTTAACAAAATATTAAC
GTTTACAATTTAAATATTTGCTTATACAATCTTCCTGTTTTTGGGGCTTTTCTGAT
TATCAACCGGGGTACATATGATTGACATGCTAGTTTTACGATTACCGTTCATCGA
TTCTCTTGTTTGCTCCAGACTCTCAGGCAATGACCTGATAGCCTTTGTAGATCT
CTCAAAAATAGCTACCCTCTCCGGCATTAATTTATCAGCTAGAACGGTTGAATA
TCATATTGATGGTGATTTGACTGTCTCCGGCCTTTCTCACCCTTTTGAATCTTTA
CCTACACATTACTCAGGCATTGCATTTAAAATATATGAGGGTTCTAAAAATTTTT
ATCCTTGCGTTGAAATAAAGGCTTCTCCCGCAAAAGTATTACAGGGTCATAATG
TTTTTGGTACAACCGATTTAGCTTTATGCTCTGAGGCTTTATTGCTTAATTTTGC

TAATTCTTTGCCTTGCCTGTATGATTTATTGGATGTTAATGCTACTACTATTAGTA
GAATTGATGCCACCTTTTCAGCTCGCGCCCCAAATGAAAATATAGCTAAACAG
GTTATTGACCATTTGCGAAATGTATCTAATGGTCAAACTAAATCTACTCGTTCGC
AGAATTGGGAATCAACTGTTATATGGAATGAAACTTCCAGACACCGTACTTTAG
TTGCATATTTAAAACATGTTGAGCTACAGCATTATATTCAGCAATTAAGCTCTAA
GCCATCCGCAAAAATGACCTCTTATCAAAAGGAGCAATTAAAGGTACTCTCTA
ATCCTGACCTGTTGGAGTTTGCTTCCGGTCTGGTTCGCTTTGAAGCTCGAATTA
AAACGCGATATTTGAAGTCTTTCGGGCTTCCTCTTAATCTTTTTGATGCAATCCG
CTTTGCTTCTGACTATAATAGTCAGGGTAAAGACCTGATTTTTGATTTATGGTCA
TTCTCGTTTTCTGAACTGTTTAAAGCATTTGAGGGGGATTCAATGAATATTTATG
ACGATTCCGCAGTATTGGACGCTATCCAGTCTAAACATTTTACTATTACCCCCTC
TGGCAAAACTTCTTTTGCAAAAGCCTCTCGCTATTTTGGTTTTTATCGTCGTCT
GGTAAACGAGGGTTATGATAGTGTTGCTCTTACTATGCCTCGTAATTCCTTTTGG
CGTTATGTATCTGCATTAGTTGAATGTGGTATTCCTAAATCTCAACTGATGAATC
TTTCTACCTGTAATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATTTTTCT
TCCCAACGTCCTGACTGGTATAATGAGCCAGTTCTTAAAATCGCATAAGGTAAT
TCACAATGATTAAAGTTGAAATTAAACCATCTCAAGCCCAATTTACTACTCGTT
CTGGTGTTTCTCGTCAGGGCAAGCCTTATTCACTGAATGAGCAGCTTTGTTACG
TTGATTTGGGTAATGAATATCCGGTTCTTGTCAAGATTACTCTTGATGAAGGTC
AGCCAGCCTATGCGCCTGGTCTGTACACCGTTCATCTGTCCTCTTTCAAAGTTG
GTCAGTTCGGTTCCCTTATGATTGACCGTCTGCGCCTCGTTCCGGCTAAGTAAC
ATGGAGCAGGTCGCGGATTTCGACACAATTTATCAGGCGATGATACAAATCTCC
GTTGTACTTTGTTTCGCGCTTGGTATAATCGCTGGGGGTCAAAGATGAGTGTTT
TAGTGTATTCTTTTGCCTCTTTCGTTTTAGGTTGGTGCCTTCGTAGTGGCATTAC
GTATTTTACCCGTTTAATGGAAACTTCCTCATGAAAAAGTCTTTAGTCCTCAAA
GCCTCTGTAGCCGTTGCTACCCTCGTTCCGATGCTGTCTTTCGCTGCTGAGGGT
GACGATCCCGCAAAAGCGGCCTTTAACTCCCTGCAAGCCTCAGCGACCGAATA
TATCGGTTATGCGTGGGCGATGGTTGTTGTCATTGTCGGCGCAACTATCGGTAT
CAAGCTGTTTAAGAAATTCACCTCGAAAGCAAGCTGATAAACCGATACAATTA
AAGGCTCCTTTTGGAGCCTTTTTTTTGGAGATTTTCAACGTGAAAAAATTATTA
TTCGCAATTCCTTTAGTTGTTCCTTTCTATTCTCACTCCGCTGAAACTGTTGAAA
GTTGTTTAGCAAAATCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACG
ACAAAACTTTAGATCGTTACGCTAACTATGAGGGCTGTCTGTGGAATGCTACA
GGCGTTGTAGTTTGTACTGGTGACGAAACTCAGTGTTACGGTACATGGGTTCC
TATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTT
CTGAGGGTGGCGGTTCTGAGGGTGGCGGTACTAAACCTCCTGAGTACGGTGAT
ACACCTATTCCGGGCTATACTTATATCAACCCTCTCGACGGCACTTATCCGCCTG
GTACTGAGCAAAACCCCGCTAATCCTAATCCTTCTCTTGAGGAGTCTCAGCCTC
TTAATACTTTCATGTTTCAGAATAATAGGTTCCGAAATAGGCAGGGGGCATTAA
CTGTTTATACGGGCACTGTTACTCAAGGCACTGACCCCGTTAAAACTTATTACC
AGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAAT
TCAGAGACTGCGCTTTCCATTCTGGCTTTAATGAGGATTTATTTGTTTGTGAATA
TCAAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTGGCGGCGGCT
CTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGG
TTCTGAGGGTGGCGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCC

GGTGATTTTGATTATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGA
AAATGCCGATGAAAACGCGCTACAGTCTGACGCTAAAGGCAAACTTGATTCTG
TCGCTACTGATTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCC
TTGCTAATGGTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAATGG
CTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTT
ACCTTCCCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCGCTGGTAA
ACCATATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTT
GCGTTTCTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTGCTAACAT
ACTGCGTAATAAGGAGTCTTAATCATGCCAGTTCTTTTGGGTATTCCGTTATTAT
TGCGTTTCCTCGGTTTCCTTCTGGTAACTTTGTTCGGCTATCTGCTTACTTTTCT
TAAAAAGGGCTTCGGTAAGATAGCTATTGCTATTTCATTGTTTCTTGCTCTTATT
ATTGGGCTTAACTCAATTCTTGTGGGTTATCTCTCTGATATTAGCGCTCAATTAC
CCTCTGACTTTGTTCAGGGTGTTCAGTTAATTCTCCCGTCTAATGCGCTTCCCT
GTTTTTATGTTATTCTCTCTGTAAAGGCTGCTATTTTCATTTTTGACGTTAAACA
AAAAATCGTTTCTTATTTGGATTGGGATAAATAATATGGCTGTTTATTTTGTAAC
TGGCAAATTAGGCTCTGGAAAGACGCTCGTTAGCGTTGGTAAGATTCAGGATA
AAATTGTAGCTGGGTGCAAAATAGCAACTAATCTTGATTTAAGGCTTCAAAAC
CTCCCGCAAGTCGGGAGGTTCGCTAAAACGCCTCGCGTTCTTAGAATACCGGA
TAAGCCTTCTATATCTGATTTGCTTGCTATTGGGCGCGGTAATGATTCCTACGAT
GAAAATAAAAACGGCTTGCTTGTTCTCGATGAGTGCGGTACTTGGTTTAATACC
CGTTCTTGGAATGATAAGGAAAGACAGCCGATTATTGATTGGTTTCTACATGCT
CGTAAATTAGGATGGGATATTATTTTCTTGTTCAGGACTTATCTATTGTTGATAA
ACAGGCGCGTTCTGCATTAGCTGAACATGTTGTTTATTGTCGTCGTCTGGACAG
AATTACTTTACCTTTTGTCGGTACTTTATATTCTCTTATTACTGGCTCGAAAATGC
CTCTGCCTAAATTACATGTTGGCGTTGTTAAATATGGCGATTCTCAATTAAGCCC
TACTGTTGAGCGTTGGCTTTATACTGGTAAGAATTTGTATAACGCATATGATACT
AAACAGGCTTTTTCTAGTAATTATGATTCCGGTGTTTATTCTTATTTAACGCCTT
ATTTATCACACGGTCGGTATTTCAAACCATTAAATTTAGGTCAGAAGATGAAAT
TAACTAAAATATATTTGAAAAAGTTTTCTCGCGTTCTTTGTCTTGCGATTGGATT
TGCATCAGCATTTACATATAGTTATATAACCCAACCTAAGCCGGAGGTTAAAAA
GGTAGTCTCTCAGACCTATGATTTTGATAAATTCACTATTGACTCTTCTCAGCGT
CTTAATCTAAGCTATCGCTATGTTTTCAAGGATTCTAAGGGAAAATTAATTAATA
GCGACGATTTACAGAAGCAAGGTTATTCACTCACATATATTGATTTATGTACTGT
TTCCATTAAAAAAGGTAATTCAAATGAAATTGTTAAATGTAATTAATTTTGTTTT
CTTGATGTTTGTTTCATCATCTTCTTTTGCTCAGGTAATTGAAATGAATAATTCG
CCTCTGCGCGATTTTGTAACTTGGTATTCAAAGCAATCAGGCGAATCCGTTATT
GTTTCTCCCGATGTAAAAGGTACTGTTACTGTATATTCATCTGACGTTAAACCTG
AAAATCTACGCAATTTCTTTATTTCTGTTTTACGTGCAAATAATTTTGATATGGTA
GGTTCTAACCCTTCCATTATTCAGAAGTATAATCCAAACAATCAGGATTATATTG
ATGAATTGCCATCATCTGATAATCAGGAATATGATGATAATTCCGCTCCTTCTGG
TGGTTTCTTTGTTCCGCAAAATGATAATGTTACTCAAACTTTTAAAATTAATAAC
GTTCGGGCAAAGGATTTAATACGAGTTGTCGAATTGTTTGTAAAGTCTAATACT
TCTAAATCCTCAAATGTATTATCTATTGACGGCTCTAATCTATTAGTTGTTAGTGC
TCCTAAAGATATTTTAGATAACCTTCCTCAATTCCTTTCAACTGTTGATTTGCCA
ACTGACCAGATATTGATTGAGGGTTTGATATTTGAGGTTCAGCAAGGTGATGCT

TTAGATTTTTCATTTGCTGCTGGCTCTCAGCGTGGCACTGTTGCAGGCGGTGTT
AATACTGACCGCCTCACCTCTGTTTTATCTTCTGCTGGTGGTTCGTTCGGTATTT
TTAATGGCGATGTTTTAGGGCTATCAGTTCGCGCATTAAAGACTAATAGCCATTC
AAAAATATTGTCTGTGCCACGTATTCTTACGCTTTCAGGTCAGAAGGGTTCTAT
CTCTGTTGGCCAGAATGTCCCTTTTATTACTGGTCGTGTGACTGGTGAATCTGC
CAATGTAAATAATCCATTTCAGACGATTGAGCGTCAAAATGTAGGTATTTCCAT
GAGCGTTTTTCCTGTTGCAATGGCTGGCGGTAATATTGTTCTGGATATTACCAG
CAAGGCCGATAGTTTGAGTTCTTCTACTCAGGCAAGTGATGTTATTACTAATCA
AAGAAGTATTGCTACAACGGTTAATTTGCGTGATGGACAGACTCTTTTACTCGG
TGGCCTCACTGATTATAAAAACACTTCTCAGGATTCTGGCGTACCGTTCCTGTC
TAAAATCCCTTTAATCGGCCTCCTGTTTAGCTCCCGCTCTGATTCTAACGAGGA
AAGCACGTTATACGTGCTCGTCAAAGCAACCATAGTACGCGCCCTGTAGCGGC
GCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGC
CAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTT
CGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATT
TAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTTGGGTGATGGTTCAC
GTAGTGGGCCATCGCCC

S2.7.2 Sequences of staple strands

S2.7.2.1 Staple strand sequences of p3120 equilateral triangular tiles for multimerization

Table S2.27. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.55 nm).

Name	Sequence
[TR]_p3120_255_core_1	TCAGGGTTATTTAGAAAAATAAAGCGTTAA
[TR]_p3120_255_core_2	CAAAAACAGGAAGGCAAAATGCACACGGAAATGTTGAAGCATTTA
[TR]_p3120_255_core_3	TTGAATACTCATACTTTTTTTGTTCGATGTAAGATC
[TR]_p3120_255_core_4	TTACCGCTGTTGTTTTTTTTTCAATATTA
[TR]_p3120_255_core_5	AAATCGGCTGCCACCTAAATTGTAACAAATAG
[TR]_p3120_255_core_6	GGGTTCCGCGCATTTTTTACGGGATAATA
[TR]_p3120_255_core_7	TCCCTTATATTTGCACTGCATAATTCTCTTGCCTTTTCCGAAAAGAAAA
[TR]_p3120_255_core_8	TATTTTGCTCATTTTTTAACCACAGTTTGG
[TR]_p3120_255_core_9	GGGCGATGGGGTTGAGTGTTGTTCATAGGCCG
[TR]_p3120_255_core_10	AACAAGAAAAGGGCGAAAAACCCCCTAAAG
[TR]_p3120_255_core_11	CCGAGATAGCCCACTACGTGAACCGGGTCGAG
[TR]_p3120_255_core_12	CACTCATGGTAAGAATAGA
[TR]_p3120_255_core_13	AAAGCGAAAAGCACTAAATCGGAAGTCTATCA
[TR]_p3120_255_core_14	TTTGATCACTTCTTCATCGTCGTTTGTTAAGTTT
[TR]_p3120_255_core_15	GTGCCGTAAGGAGCGGGCGCTAGGACGCTGCGCGTAACCATTCGCTAT
[TR]_p3120_255_core_16	GGAGCCCACGTGGCGAGAAAGGTAATGCGC
[TR]_p3120_255_core_17	CGGGCCTCCCACACCCGCCGCGCTAAGGGAAG
[TR]_p3120_255_core_18	AGAAGGTAATTCGGTCGCGCTGGCAATTATCCAC

[TR]_p3120_255_core_19	CGCTACAACTGTTGGGAAGGGCGGTAACGC
[TR]_p3120_255_core_20	TCGACGGTACGACTCACTATAGGGCAAGGCGATTAAGTTGGATCGGTG
[TR]_p3120_255_core_21	TACGCCAGCTATTAATGAA
[TR]_p3120_255_core_22	TGTCGTGCCTTTGGGGGATGTGCTGCGAATTGGTTTTAACATACGAACC
[TR]_p3120_255_core_23	CAGGGTTGTGAGCGCGCGTAATATCGATAA
[TR]_p3120_255_core_24	GCTTGGAGATAGGGAGGACTACATGGCAGC
[TR]_p3120_255_core_25	TCCGCTCACAATTTTTTCCCCCCTCGAGG
[TR]_p3120_255_core_26	TGTTGGCCGCCACCGTTTTTTGTTAGCAATCAATGC
[TR]_p3120_255_core_27	TTCAATATTTTGTTTTTAGCTCCAGCTTT
[TR]_p3120_255_core_28	TAAAACACCATCGATACCTCAGCGTATCG
[TR]_p3120_255_core_29	TGCACCCTTTCACCAGCGTTTCTGGGTGA
[TR]_p3120_255_core_30	AACTTTAGCGAAAACTCTCAAGCCCACTCG
[TR]_p3120_255_core_31	GATGCTTTCTGAGAATAGTGTACATAGCAG
[TR]_p3120_255_core_32	CCGCGCCATGCGGCGACCGAGTTGCTCTTACTGTCATGCCGAAGTAAG
[TR]_p3120_255_core_33	CCCCCATCTCCGATCGTTGTCAATCCGTAA
[TR]_p3120_255_core_34	AACTTTATCATCGTGGTGTCACGCTTCAGCTCCGGTTCCCAGTGTTAT
[TR]_p3120_255_core_35	TTGGCCGCAACGATCAAGGCGAGTTTGCCATT
[TR]_p3120_255_core_36	GTTGCCGGTTTGCGCAACGTTGTACATGAT
[TR]_p3120_255_core_37	GCTACAGGCCGCCTCCATCCAGTCGCTCCAGA
[TR]_p3120_255_core_38	GGCTTACGACCCACGCTCACCGTATTAATT
[TR]_p3120_255_core_39	TCCCCGTCCAATAAACCAGCCAGCGGTCCTGC
[TR]_p3120_255_core_40	AAGTCGGAATTGGCGACGCTCAAGTCTTGCGCAG
[TR]_p3120_255_c	TTTATCAGGTGTAGATAACTACGATATCTCAG

ore_41	
[TR]_p3120_255_core_42	TATATATAATCAGTGAGGCACCTACGGGAG
[TR]_p3120_255_core_43	TGGCGCTTTTTTGCCTGAC
[TR]_p3120_255_core_44	TTCGTTCATTTTTCACGCTGTAGGTTCTTGAGTTTTTAATTAAAACTAT
[TR]_p3120_255_core_45	CGATCTGTATGAAGTTTTAAATCAAAAAGGAT
[TR]_p3120_255_core_46	GACGCTCGTCATGAGATTATCAATCTAAAG
[TR]_p3120_255_core_47	CTTCACCTAGATTTTTTTAAGACACGACT
[TR]_p3120_255_core_48	CCGGCAAACAAACCACCGCTGGTTACGCGCAGAAAAACGGGGTCT
[TR]_p3120_255_core_49	TCTAAAGGATCTCAATTTTTTGCTACACTAGACTTG
[TR]_p3120_255_core_50	AAGTGGTGGCCTTTTTTCCTTTGATCTTT
[TR]_p3120_255_core_51	ATTTGGTAAAAAGAGTTGGTAGCTCTTGA
[TR]_p3120_255_core_52	AGCCACTCGGTGCTACAGAGTTAGGACAGT
[TR]_p3120_255_core_53	GCTCCAACCGACCGCTGCGCCTCTGGCAGC
[TR]_p3120_255_core_54	TATCGCCATATCCGGTAACTATCGATCTCAGTTCGGTGTACCGCCTTT
[TR]_p3120_255_core_55	GAAGCTCTTACCGGATACCTGTGGTCGTTC
[TR]_p3120_255_core_56	TAACGCAGGCATCACAAAAATCGAAACCCGACAGGACTATGGGAAGCG
[TR]_p3120_255_core_57	CTCCCTTCAAAGATACCAGGCGTTTCCGCCCC
[TR]_p3120_255_core_58	AGCAAAACGTTTTTCCATAGGCTCCCCCTG
[TR]_p3120_255_core_59	CCTGACGAGAAAGAACATGTGAGCCTGCGGCG
[TR]_p3120_255_core_60	ATTGGGCCGCTCGGTCGTTCGGAAAAGGCC
[TR]_p3120_255_core_61	TCGGCCAACAGCTCACTCAAAGGCTCAGGGGA
[TR]_p3120_255_core_62	AGCGGTATCGCGCGGGGAGAGGCGCGCTTTCC
[TR]_p3120_255_core_63	CTGGGGTGTTGCGCTCACTGCCGTTTGCGT

[TR]_p3120_255_core_64	AGTCGGGAAGCCGGAAGCATAAAGAATTGTTA
[TR]_p3120_255_core_65	TGAGGGTCTGTTTCCTGTGTGATGTAAAGC
[TR]_p3120_255_core_66	GATCCATGACTGAGACCGTTCGCACTAGTTCTAGAGCCCCTTTAG

Table S2.28. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.55 nm).

Name	**Sequence**
[TR]_p3120_255_edge_1	AAACGTTCTTCGGGAAAGTGCTCATCATTG
[TR]_p3120_255_edge_2	CTCAACCAAGTCATTTCTGTGACTGGTGAG
[TR]_p3120_255_edge_3	TAGCTCCTTCGGTCGTTGTGCAAAAAAGCG
[TR]_p3120_255_edge_4	TTCGCCAGTTAATAGGAAGCTAGAGTAAGT
[TR]_p3120_255_edge_5	CAATGATACCGCGACATCTGGCCCCAGTGC
[TR]_p3120_255_edge_6	AGTTACCAATGCTTGAGTAAACTTGGTCTG
[TR]_p3120_255_edge_7	GTTAAGGGATTTTGAGTGGAACGAAAACTC
[TR]_p3120_255_edge_8	TTGCAAGCAGCAGATAGCGGTGGTTTTTTT
[TR]_p3120_255_edge_9	GTAATCATGGTCATAGTAATTGCGCGCTTGGCGA
[TR]_p3120_255_edge_10	AACTCACATTAATTGCGCCTAATGAGTGAGCTTA
[TR]_p3120_255_edge_11	GCTCACTGACTCGCTGGCTCTTCCGCTTCCTCGT
[TR]_p3120_255_edge_12	AAGGCCGCGTTGCTGGGGCCAGGAACCGTAAAAG
[TR]_p3120_255_edge_13	GTTCCGACCCTGCCGCCCTCGTGCGCTCTCCTTG
[TR]_p3120_255_edge_14	GAACCCCCCGTTCAGCGCTGGGCTGTGTGCACAC
[TR]_p3120_255_edge_15	GAGCGAGGTATGTAGGGGTAACAGGATTAGCAAC
[TR]_p3120_255_edge_16	AGCCAGTTACCTTCGGATCTGCGCTCTGCTGAGT
[TR]_p3120_255_edge_17	GTGTCGTAGACAC GATACATATTTGAATGTATTGTCTCATGAGCG GTGTCGTAGACAC
[TR]_p3120_255_edge_18	GTGTCGTAGACACATTTTTGTTAAATCAGTTAAAATTCGCGTTAAGTGTCGTAGACAC
[TR]_p3120_255_edge_19	GTGTCGTAGACACCGTGGACTCCAACGTCGTCCACTATTAAAGAAGTGTCGTAGACAC
[TR]_p3120_255_edge_20	GTGTCGTAGACACCGGGGAAAGCCGGCGACCGATTTAGAGCTTGAGTGTCGTAGACAC
[TR]_p3120_255_edge_21	GTGTCGTAGACACCCATTCAGGCTGCGCAGGGCGCGTCCCATTCGGTGTCGTAGACAC

[TR]_p3120_255_edge_22	GTGTCGTAGACACTGTAAAACGACGGCCATTCCCAGTCACGACGTGTGTCGTAGACAC
[TR]_p3120_255_edge_23	GTGTCGTAGACACCACTCTGTCCAGCTCGTGCAATGGGAGATTACGTGTCGTAGACAC

Table S2.29. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.65 nm).

Name	**Sequence**
[TR]_p3120_265_core_1	TCAGGGTTATTTAGAAAAATAATAAGCGTT
[TR]_p3120_265_core_2	GGTGAGCAAAAACAGGAAGGCACGGAAATGTTGAATAGCATTTA
[TR]_p3120_265_core_3	TTGAACTCATACTCTTTTTTTGTTGAGATCAAAA
[TR]_p3120_265_core_4	CTCTCAAGGATTTTTTTTCAATATTA
[TR]_p3120_265_core_5	CGAAATCGAGTGCCACCTAAATTGACAAATAG
[TR]_p3120_265_core_6	GGGTTCCGCGCTTTTTCCCGGCGTCAA
[TR]_p3120_265_core_7	AATCCCTTTGTTATGGCAGCAGACCGAGTTTTTCCCCGAAAGCAA
[TR]_p3120_265_core_8	AATATTTAGCTCATTTTTTAACTCCAGTTT
[TR]_p3120_265_core_9	CAGGGCGATAGGGTTGAGTGTTGTCAATAGGC
[TR]_p3120_265_core_10	GGAACAATCAAAGGGCGAAAAAAACCCTAA
[TR]_p3120_265_core_11	GACCGAGATGGCCCACTACGTGAATGGGGTCG
[TR]_p3120_265_core_12	AGTGTTATCAAAAGAATA
[TR]_p3120_265_core_13	AGAAAGCGTAAAGCACTAAATCGGCCGTCTAT
[TR]_p3120_265_core_14	TTTTCCATCTTTGGTATGTCACGCTCTTTCAAGT
[TR]_p3120_265_core_15	AGGTGCCGAAAGGAGCGGGCGCTATCACGCTGCGCGTAACTCTTCGCT
[TR]_p3120_265_core_16	AGGGAGCGAACGTGGCGAGAAACTTAATGC
[TR]_p3120_265_core_17	TGCGGGCCCACCACACCCGCCGCGGGAAGGGA
[TR]_p3120_265_core_18	ATCAAATACTTAGCGGGGGCGCTGGCTTCACAGA

[TR]_p3120_265_core_19	GCCGCTACAACTGTTGGGAAGGGTTGGGTA
[TR]_p3120_265_core_20	TCGAGGTCTAATACGACTCACTATGCTGCAAGGCGATTAAGCGATCGG
[TR]_p3120_265_core_21	ATTACGCCAAATGAATCG
[TR]_p3120_265_core_22	CGTGCCAGTAAAGGGGGATGTAGGGCGAATTTTATACGAGCCTGT
[TR]_p3120_265_core_23	ACGCCAGGCCAGTGAGCGCGCGGACGGTAT
[TR]_p3120_265_core_24	CGATAAGAGCTCGGATAGGGAGGCAATCAA
[TR]_p3120_265_core_25	TCACAATTCCATTTTTCGGGCCCCCCC
[TR]_p3120_265_core_26	CCTTACCGCGGTGGTTTTTTCTAAGGGTTAGACT
[TR]_p3120_265_core_27	ACATGCTTCAATTTTTAGCTTTTGTTC
[TR]_p3120_265_core_28	TGGCAGCCATCGATACCTCAGCGTATCG
[TR]_p3120_265_core_29	GATCCGGCAAACAAACCACCGCAGATTACGCGCAGATTTCTACG
[TR]_p3120_265_core_30	ATCTAAAAAAGGATTTTTTTGGCTACACTATCTT
[TR]_p3120_265_core_31	GAAGTGGTGGCTTTTTAAGATCCTTTG
[TR]_p3120_265_core_32	TGTAACCTTTACTTTCACCAGCGTTTCT
[TR]_p3120_265_core_33	GCCACATACGTTCTTCGGGGCGCAGTTCGA
[TR]_p3120_265_core_34	CCATCCGACCAAGTCATTCTGAAATACCGC
[TR]_p3120_265_core_35	TACGGGATGAATAGTGTATGCGGCCTGCATAATTCTCTTACGTTGTCA
[TR]_p3120_265_core_36	TACATGACTTCGGTCCTCCGATCTGTCATG
[TR]_p3120_265_core_37	GGTCCTGCGCTACAGGCATCGTGGTGGCTTCATTCAGCTCTTGGCCGC
[TR]_p3120_265_core_38	GAAGTAAGCGGTTCCCAACGATCACAACGTTG
[TR]_p3120_265_core_39	TATTAATAGTTAATAGTTTGCGAGGCGAGT
[TR]_p3120_265_core_40	TTGCCATTAACTTTATCCGCCTCCGCTCACCG
[TR]_p3120_265_c	TACGGGATACCGCGAGACCCACATCCAGTC

ore_41	
[TR]_p3120_265_core_42	TGCCTGACTTTATCAGCAATAAACGCAGAAGT
[TR]_p3120_265_core_43	GAGCCAGCCTTGAAACTCAAGTCAGATTAGGGCC
[TR]_p3120_265_core_44	GCTCCAGATCCCCGTCGTGTAGATGAGGCACC
[TR]_p3120_265_core_45	ATCTAAACAATGCTTAATCAGTAACTACGA
[TR]_p3120_265_core_46	CGCTTTCTCATCCATAGT
[TR]_p3120_265_core_47	CTGTCTATTACGCTGTAGGTACTTGAGTCTTTTTCCTTTTACGAT
[TR]_p3120_265_core_48	TATCTCAGAATTAAAAATGAAGTTTTATCAAA
[TR]_p3120_265_core_49	GGGTCTGATTTTGGTCATGAGATTAAATCA
[TR]_p3120_265_core_50	AAGGATCTTCATTTTTTAAGACACGAC
[TR]_p3120_265_core_51	GATCCATGACTGAGACCGTTCTCTAGAGCGGCCGCCTAGTGAGG
[TR]_p3120_265_core_52	GTATTTGGGAAAAAGAGTTGGTAGCTCT
[TR]_p3120_265_core_53	CAGCCACGCGGTGCTACAGAGTGAAGGACA
[TR]_p3120_265_core_54	CTCCAAGCGACCGCTGCGCCTTACTGGCAG
[TR]_p3120_265_core_55	TTATCGCCATCCGGTAACTATCGTTCTCAGTTCGGTGTAGCCTTTCTC
[TR]_p3120_265_core_56	GCTCCCTCCGGATACCTGTCCGGTCGTTCG
[TR]_p3120_265_core_57	CGCAGGAATCACAAAAATCGACGCCCGACAGGACTATAAAAAGCGTGG
[TR]_p3120_265_core_58	CCTTCGGGGATACCAGGCGTTTCCGCCCCCCT
[TR]_p3120_265_core_59	AAAAGGCTTTTCCATAGGCTCCCCCTGGAA
[TR]_p3120_265_core_60	GACGAGCAAGAACATGTGAGCAAACGGCGAGC
[TR]_p3120_265_core_61	GGGCGCTTCGGTCGTTCGGCTGAGGCCAGC
[TR]_p3120_265_core_62	GCCAACGCCTCACTCAAAGGCGGTGGGGATAA
[TR]_p3120_265_core_63	GGTATCAGGCGGGGAGAGGCGGTTTTTCCAGT

[TR]_p3120_265_core_64	GGGTGCCGCGCTCACTGCCCGCTGCGTATT
[TR]_p3120_265_core_65	CGGGAAACCGGAAGCATAAAGTGTTTATCCGC
[TR]_p3120_265_core_66	GTTAATTTCCTGTGTGAAATTGAAAGCCTG

Table S2.30. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.65 nm).

Name	**Sequence**
[TR]_p3120_265_edge_1	CTCATCATTGGAAAAGCAGAACTTTAAAAG
[TR]_p3120_265_edge_2	CTGGTGAGTACTCATAAGATGCTTTTCTGT
[TR]_p3120_265_edge_3	AAAGCGGTTAGCTCTCCCCCATGTTGTGCA
[TR]_p3120_265_edge_4	GTAAGTAGTTCGCCTGTTGCCGGGAAGCTA
[TR]_p3120_265_edge_5	CAGTGCTGCAATGAGGGCTTACCATCTGGC
[TR]_p3120_265_edge_6	GGTCTGACAGTTACGTATATATGAGTAAAC
[TR]_p3120_265_edge_7	ACTCACGTTAAGGGACGCTCAGTGGAACGA
[TR]_p3120_265_edge_8	TTGTTTGCAAGCAGCTGGTAGCGGTGGTTT
[TR]_p3120_265_edge_9	CATGGTCATAGCTGTTGCGCGCTTGGCGTAATTG
[TR]_p3120_265_edge_10	TCACATTAATTGCGTTTAATGAGTGAGCTAACGA
[TR]_p3120_265_edge_11	CACTGACTCGCTGCGCCTTCCGCTTCCTCGCTAA
[TR]_p3120_265_edge_12	GCCGCGTTGCTGGCGTCAGGAACCGTAAAAAGGA
[TR]_p3120_265_edge_13	CCGACCCTGCCGCTTACGTGCGCTCTCCTGTTCC
[TR]_p3120_265_edge_14	AACCCCCCGTTCAGCCCTGGGCTGTGTGCACGTT
[TR]_p3120_265_edge_15	AGAGCGAGGTATGTAGTGGTAACAGGATTAGCAA
[TR]_p3120_265_edge_16	GAAGCCAGTTACCTTCGTATCTGCGCTCTGCTTT
[TR]_p3120_265_edge_17	GTGTCGTAGACACGATACATATTTGAATGTATTGTCTCATGAGCGGTGTCGTAGACAC
[TR]_p3120_265_edge_18	GTGTCGTAGACACAAATTTTTGTTAAATCTGTTAAAATTCGCGTTGTGTCGTAGACAC
[TR]_p3120_265_edge_19	GTGTCGTAGACACAACGTGGACTCCAACGGAGTCCACTATTAAAGGTGTCGTAGACAC
[TR]_p3120_265_edge_20	GTGTCGTAGACACGACGGGGAAAGCCGGCCCCCGATTTAGAGCTTGTGTCGTAGACAC
[TR]_p3120_265_edge_21	GTGTCGTAGACACCGCCATTCAGGCTGCGCAGGGCGCGTCCCATTGTGTCGTAGACAC

[TR]_p3120_265_edge_22	GTGTCGTAGACACACGTTGTAAAACGACGGGTTTTCCCAGTCACGGTGTCGTAGACAC
[TR]_p3120_265_edge_23	GTGTCGTAGACACGATTACCACTCTGTCCCTTGGATGCAATGGGAGTGTCGTAGACAC

Table S2.31. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.70 nm).

Name	**Sequence**
[TR]_p3120_270_core_1	CGCCACATAGCAGAACTTTAGGGGCGAAAACTCTCATGTAACC
[TR]_p3120_270_core_2	TTCGAAGGATCTTATTTTTACTCAACCAAATGC
[TR]_p3120_270_core_3	CACTCGTCACCAGCGTTTCTGGACACGGAA
[TR]_p3120_270_core_4	TTTTCTGTGATTTTTTGAGATCCAG
[TR]_p3120_270_core_5	TCATGAGCAAAGGGAATAAGGGCGGTGAGCAA
[TR]_p3120_270_core_6	AAACAGGAAGGTTTTCAGAAGTAAGT
[TR]_p3120_270_core_7	ATGTTGAAAGCATTTATCAGGGCATTTCCC
[TR]_p3120_270_core_8	ACATATTTTGTGTCACGCTCGGTCCTCCTTCCGCAAAGGAT
[TR]_p3120_270_core_9	TAAATCAGATAGGGGTTCCGCGCATTATTGTC
[TR]_p3120_270_core_10	CGAAAAGTAAAATTCGCGTTAATTGAGTGT
[TR]_p3120_270_core_11	ATAAACAACTCATTTTTTAACCAACTTATAAA
[TR]_p3120_270_core_12	TTGCTACAGTTTAGAAAA
[TR]_p3120_270_core_13	AAACCGTCATAGACCGAGATAGGGATTTTTGT
[TR]_p3120_270_core_14	ATCCTAGGCTTCCGGAGCAATAAACCTTGGCAAA
[TR]_p3120_270_core_15	TGTTCCAGGACTCCAACGTCAAGCACTAAA
[TR]_p3120_270_core_16	TCAAAAGATATCAGGGCGATGGCCAATCAAGTTTTTTGGGGGGAAGAA
[TR]_p3120_270_core_17	GAAAGGAAGTCGAGGTGCCGTAAAAGGGCGAA
[TR]_p3120_270_core_18	GTGCCCAGTTTACCCTCACTACGTGATTCCTGTC

[TR]_p3120_270_core_19	TCGGAACGGGAAAGCCGGCGAAGCTGCGCG
[TR]_p3120_270_core_20	CTCTTCGCCATTCAGGCTGCGCAACAAGTGTAGCGGTCACCGTGGCGA
[TR]_p3120_270_core_21	AGCGAAAGGCTGTGTGAA
[TR]_p3120_270_core_22	TAACCACGCGCGTCCCATTCGCTATTACGC
[TR]_p3120_270_core_23	GGTCATAGTCTAGGGCGCTGGCTGTTGGTTCCTGCAGTCAT
[TR]_p3120_270_core_24	CAGCTGGTGGGTAACGCCAGGGAGTGAGCG
[TR]_p3120_270_core_25	ACTGAGACCGTTTTTTCGGTGCGGGC
[TR]_p3120_270_core_26	CAATTGCTTCAATATTTTTAACGACGGCCTTTT
[TR]_p3120_270_core_27	CCCAGTCACGTTTTTTAAGGGTTAG
[TR]_p3120_270_core_28	CGCGTAACGGGCCCCCCCTCGAGGTCG
[TR]_p3120_270_core_29	CAGCCACTGGTAACAGGATTGTTCTTGAAGTGGTGTTTGGTAT
[TR]_p3120_270_core_30	AGTAGCCTAACTACTTTTTTTCAGCCCGAGGGC
[TR]_p3120_270_core_31	CTGCGCTTGGTAGCTCTTGATCCAGATTAC
[TR]_p3120_270_core_32	TGTGTGCACGTTTTTCTAGAAGGAC
[TR]_p3120_270_core_33	GGAACGAATTTTGTTTGCAAGCAGCGGCAAAC
[TR]_p3120_270_core_34	AAACCACCGCTTTTTTCTCCCTTCGG
[TR]_p3120_270_core_35	GCGCAGATTCTACGGGGTCTGAAGATCCTT
[TR]_p3120_270_core_36	CACGTTAATCGCTCAAGTCAGGATACCTTTGTGGTTTAACT
[TR]_p3120_270_core_37	TTACCAATAAAAGGATCTTCACCTCGCTCAGT
[TR]_p3120_270_core_38	TTAAATTTATGAGTAAACTTGGCGTGTAGA
[TR]_p3120_270_core_39	GATTATCAGCTTAATCAGTGAGGCTTTCGTTC
[TR]_p3120_270_core_40	AGCATCACATGGTCATGA
[TR]_p3120_270_co	CGCTCACCTTGCCTGACTCCCCGTTCTGACAG

re_41	
[TR]_p3120_270_core_42	TCTAACCTATTGGTTATCAAAGGCGGTTGATCTG
[TR]_p3120_270_core_43	TAACTACCTGCAATGATACCGCATCCGCCT
[TR]_p3120_270_core_44	ATCCATAGGGCTCCAGATTTATCAAGGGCCGAGCGCAGAATGTTGCCA
[TR]_p3120_270_core_45	CGCAACGTGTGGTCCTGCAACTTTGAGACCCA
[TR]_p3120_270_core_46	CCATCCAGTAGTTCGCCAGTTACATTCAGC
[TR]_p3120_270_core_47	TGGCCGCAGCGGTTAGCTCCTTCGTCGTTTGGTATGGCTTATAGTTTG
[TR]_p3120_270_core_48	TCCGGTTATGTTGTGCAAAAAAGTGTTATC
[TR]_p3120_270_core_49	ACTCATGCATGCCATCCGTAAGGTCATTCT
[TR]_p3120_270_core_50	GAGAATACGGCGTCAATACGGGATAAT
[TR]_p3120_270_core_51	TATCGATAAGCTTGGATGCAATAGGGAGGACTACACAATGGCA
[TR]_p3120_270_core_52	GCTAAAAACCTCAGCGTATCGTGTTCTAGA
[TR]_p3120_270_core_53	TGGCGTAACCCGGGGGATCCACTAGATCCATG
[TR]_p3120_270_core_54	GCGGCCGTTAGTGAGGGTTAATACAACATA
[TR]_p3120_270_core_55	TGCGTTGCCCGCTCACAATTCCACTGCGCGCT
[TR]_p3120_270_core_56	CGAGCCGTGAGTGAGCTAACTCGAGAGGCG
[TR]_p3120_270_core_57	ATTGTTATGCTCACTGCCCGCTTTCAGCTGCA
[TR]_p3120_270_core_58	CTGCGGCGTCGGCCAACGCGCGGGACATTAAT
[TR]_p3120_270_core_59	GTTTGCGACTCGCTGCGCTCGGCATGTGAG
[TR]_p3120_270_core_60	TTAATGAAAGCGGTATCAGCTCACTCCACAGAATCAGGGGCCCTGACG
[TR]_p3120_270_core_61	CTCCGCCCATAACGCAGGAAAGAATCGTTCGG
[TR]_p3120_270_core_62	CAAAAGGCGTTGCTGGCGTTTTCAGGACTA
[TR]_p3120_270_core_63	GAAGCGTGACCCTGCCGCTTACCGAGGTGGCGAAACCCGATCCATAGG

[TR]_p3120_270_core_64	TAAAGATCGCTCTCCTGTTCCGGCGCTTTC
[TR]_p3120_270_core_65	TCATAGCCGTTCGCTCCAAGCTCCGCTGCG
[TR]_p3120_270_core_66	CCTTATCGACACGACTTATCGCCACTG

Table S2.32. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.70 nm).

Name	**Sequence**
[TR]_p3120_270_edge_1	AATCAGGGCCATCGATCACGTAGCGAGCTCTGAT
[TR]_p3120_270_edge_2	CCAGCTTTTGTTCCCTCCACCGCGGTGGAGCTAG
[TR]_p3120_270_edge_3	AGCCTGGGGTGCCTAAGAAGCATAAAGTGTAACG
[TR]_p3120_270_edge_4	GCTTCCTCGCTCACTGTATTGGGCGCTCTTCCCC
[TR]_p3120_270_edge_5	AACCGTAAAAAGGCCGCCAGCAAAAGGCCAGGAT
[TR]_p3120_270_edge_6	TGGAAGCTCCCTCGTGACCAGGCGTTTCCCCCAA
[TR]_p3120_270_edge_7	TCAGTTCGGTGTAGGTTCACGCTGTAGGTATCCC
[TR]_p3120_270_edge_8	GAGTCCAACCCGGTAACGGTAACTATCGTCTTTA
[TR]_p3120_270_edge_9	AATTCTCTTACTGTGTTATGGCAGCACTGC
[TR]_p3120_270_edge_10	TTACATGATCCCCCCCCAACGATCAAGGCG
[TR]_p3120_270_edge_11	GGAAGCTAGAGTAAGTCTATTAATTGTTGC
[TR]_p3120_270_edge_12	ATCTGGCCCCAGTGGATACGGGAGGGCTTA
[TR]_p3120_270_edge_13	CAATCTAAAGTATAAAAAATGAAGTTTTAA
[TR]_p3120_270_edge_14	GATCCTTTGATCTTAAAAAAGGATCTCAAG
[TR]_p3120_270_edge_15	TTCGGAAAAAGAGTCTGCTGAAGCCAGTTA
[TR]_p3120_270_edge_16	GGCGGTGCTACAGAAGCAGAGCGAGGTATG
[TR]_p3120_270_edge_17	GTGTCGTAGACACCAGCATCTTTTACTTTGCACCCAA CTGATCTTGTGTCGTAGACAC

[TR]_p3120_270_edge_18	GTGTCGTAGACACTTTTTCAATATTATTGATACTCATAC TCTTCCGTGTCGTAGACAC
[TR]_p3120_270_edge_19	GTGTCGTAGACACAGCGTTAATATTTTGTTGCCACCTA AATTGTAGTGTCGTAGACAC
[TR]_p3120_270_edge_20	GTGTCGTAGACACCACTATTAAAGAACGTGTTTGGAA CAAGAGTCGTGTCGTAGACAC
[TR]_p3120_270_edge_21	GTGTCGTAGACACGATTTAGAGCTTGACGCCTAAAGG GAGCCCCCGTGTCGTAGACAC
[TR]_p3120_270_edge_22	GTGTCGTAGACACAATGCGCCGCTACAGGCACACCCG CCGCGCTTGTGTCGTAGACAC
[TR]_p3120_270_edge_23	GTGTCGTAGACACTGCAAGGCGATTAAGTCGAAAGGG GGATGTGCGTGTCGTAGACAC

Table S2.33. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.75 nm).

Name	**Sequence**
[TR]_p3120_275_core_1	GCAACTGTTGGGAAGGGCGAAGCTGGCGAAAGGGGGCCAGGGT
[TR]_p3120_275_core_2	TAACGATGTGCTGCTTTTTCACGCTGCGCAGGG
[TR]_p3120_275_core_3	TTTCCCAGCGCGTAATACGACTCGATAAGC
[TR]_p3120_275_core_4	CGCTGGCAAGTTTTTTTAAGTTGGG
[TR]_p3120_275_core_5	ATTTTGCCTCGAGGTCGACGGTATCACTATAG
[TR]_p3120_275_core_6	GGCGAATTGGGTTTTAGCCCCCGATT
[TR]_p3120_275_core_7	TTGGATGTAGGGAGGACTACATGCCATCGA
[TR]_p3120_275_core_8	GGTTAGCATACTCCAACGTCATCGGAACCTTTTGCCCCCCCTAAG
[TR]_p3120_275_core_9	CTAGTTCTCGAGCTCTGAATCAGGGCTTCAAT
[TR]_p3120_275_core_10	TACCTCAATTCCTGCAGCCCGGAATCATGG
[TR]_p3120_275_core_11	ACACGTAGAGAGCGGCCGCCACCGCCTTTAGT

[TR]_p3120_275_core_12	ACTATTAAAGCAGCTAAA
[TR]_p3120_275_core_13	AAGCATAAATTGCGCGCTTGGCGTGGGATCCA
[TR]_p3120_275_core_14	GTTCCGGTGGCGTTAAATTTTGTTAATTGCTTTT
[TR]_p3120_275_core_15	TCATAGCATTCCACACAACATACCAGTCGG
[TR]_p3120_275_core_16	GAGGGTTAAGTGTAAAGCCTGGGGACATTAATTGCGTTGCCTCTTCCG
[TR]_p3120_275_core_17	ATTGGGCGGCTCACTGCCCGCTTTCGAGCCGG
[TR]_p3120_275_core_18	GATCAAAAAATAACTCTGCCTAATGATTCAAGAA
[TR]_p3120_275_core_19	GAAACCTGCGCGGGGAGAGGCGGAGCGGTA
[TR]_p3120_275_core_20	GTAAAAAGGGAAAGAACATGTGAGGTCGTTCGGCTGCGGCGTTTGCGT
[TR]_p3120_275_core_21	CTTCCTCGCTATTTGGTA
[TR]_p3120_275_core_22	TCAGCTCTCAGGGGATAACGCAGCCGCGTT
[TR]_p3120_275_core_23	ACACTAGATTCGCTGCGCTCGCAAAAGGCTTTTAGACACGAGGCT
[TR]_p3120_275_core_24	GCTGGCGTCACAAAAATCGACGATAAAGAT
[TR]_p3120_275_core_25	TTGAGTCCAACTTTTGGCCAGGAACC
[TR]_p3120_275_core_26	TCGCTAGGTATCTCTTTTTCGACAGGACTCTCA
[TR]_p3120_275_core_27	AGTCAGAGGTTTTTTTGTAGGTCGT
[TR]_p3120_275_core_28	ACCAGGCTCTCCTGTTCCGACCCTGCC
[TR]_p3120_275_core_29	CTCCTTCGGTCCTCCGATCGCTCATGGTTATGGCACCGTAAGA
[TR]_p3120_275_core_30	CCATGCACTGCATATTTTTGGTATGGCTTTCGT
[TR]_p3120_275_core_31	GGTGTCACGCTTTTTTACTGTCATG
[TR]_p3120_275_core_32	TGCTTTTTGAGAATAGTGTATGCACATAGC
[TR]_p3120_275_core_33	ATCCAGTTTCAGTGCTGCAATTCCGCCTCTTTTCGTCAATATGAG
[TR]_p3120_275_c	AGAACTTGGGCGAAAACTCTCATTTTACTT

ore_34	
[TR]_p3120_275_core_35	GGCTTACCAACCCACTCG
[TR]_p3120_275_core_36	TGCACCCAGAAATGTTGAATACTCTTGAAGCA
[TR]_p3120_275_core_37	TCACCAGATGCCGCAAAAAAGGGCGGATAC
[TR]_p3120_275_core_38	TTTATCAGAATTGTAAGCGTTAATATTTTTGTTAAATCAGAAGAGTCC
[TR]_p3120_275_core_39	ATATTTGCCGCGCACATTTCCCTAGGCCGA
[TR]_p3120_275_core_40	TTTGGAACCTCATTTTTTAACCAACGAAAAGT
[TR]_p3120_275_core_41	GCCACCTAGGTTATTGTCTCATGAGAATAAGG
[TR]_p3120_275_core_42	AATCGGCGATAGGGTTGAGTGTCTATCAGG
[TR]_p3120_275_core_43	GCGATGGTTTTGGGGTCGAGGTGACGGGGA
[TR]_p3120_275_core_44	TAGAGCTTGCCGTAAAGCACTAAAAAGGGCGAAAAACCGTTGTTCCAG
[TR]_p3120_275_core_45	CACACCCGTCCCATTCGCCATTCAGGC
[TR]_p3120_275_core_46	AAGCCGGAAAGGAGCGGGCGCTGTAACCAC
[TR]_p3120_275_core_47	GCGACACGACTGATCTTCAGCATCAGGATCTT
[TR]_p3120_275_core_48	ATTAATACTCTGAGTACAATCTAAAGTTTTCAAT
[TR]_p3120_275_core_49	ACCGCTGTCGGGATAATACCGCGCCGGCGACC
[TR]_p3120_275_core_50	GAGTTGCTCTTTTTTCTATTAATTGT
[TR]_p3120_275_core_51	TACCGGATACCTGTCCGCCTTCATAGCTCACGCTGTCCAAGCT
[TR]_p3120_275_core_52	GGGCTGTCGCCTTATCCGGTAAGCAGCCAC
[TR]_p3120_275_core_53	TGGTAACTACAGAGTTCTTGAACCTTCGGA
[TR]_p3120_275_core_54	TCTGCGCTAGCAGATTACGCGCAGCTTTGATC
[TR]_p3120_275_core_55	AAAAGAGGCTGGTAGCGGTGGTTGGAACGA
[TR]_p3120_275_core_56	TTTTCTACAAATGAAGTTTTAAATAACTTGGTCTGACAGTTACGGGAG

[TR]_p3120_275_core_57	AAACTCAAAGGATCTTCACCTAGTGAGGCA
[TR]_p3120_275_core_58	AACTACGATACCAATGCTTAATCAGATCCTTT
[TR]_p3120_275_core_59	TAAATTAAGGGGTCTGACGCTCAGTTTTTTGT
[TR]_p3120_275_core_60	CCTATCTGCCTGACTCCCCGTCCGCTCACC
[TR]_p3120_275_core_61	GGCTCCAGGCCGAGCGCAGAAGAGCTAGAG
[TR]_p3120_275_core_62	TGCCGGGATGGTCCTGCAACTTTAGATACCGCGAGACCCAGTGTAGAT
[TR]_p3120_275_core_63	TCCGGTTATGTTGTGCAAAAAAGCGGT
[TR]_p3120_275_core_64	TAAGTAGCCATTGCTACAGGCACATTCAGC
[TR]_p3120_275_core_65	TTGCAAGCCTGCTGAAGCCAGTTAGTGGTGGC
[TR]_p3120_275_core_66	CTAACTACCTTATCGCCACTGGCACTATCGTC

Table S2.34. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.75 nm).

Name	**Sequence**
[TR]_p3120_275_edge_1	AAGGGAAGAAAGCGCGAACGTGGCGAGAAA
[TR]_p3120_275_edge_2	ACCCTAATCAAGTTCCCACTACGTGAACCA
[TR]_p3120_275_edge_3	AAAGAATAGACCGAAAAATCCCTTATAAAT
[TR]_p3120_275_edge_4	AACAAATAGGGGTTAATGTATTTAGAAAAA
[TR]_p3120_275_edge_5	AACAGGAAGGCAAACGTTTCTGGGTGAGCA
[TR]_p3120_275_edge_6	GAAAACGTTCTTCGTAAAAGTGCTCATCAT
[TR]_p3120_275_edge_7	CAACCAAGTCATTCCTGTGACTGGTGAGTA
[TR]_p3120_275_edge_8	CCGCAGTGTTATCATTGTCAGAAGTAAGTT
[TR]_p3120_275_edge_9	TTCAGCCCGACCGCTGGTGCACGAACCCCCCGGG
[TR]_p3120_275_edge_10	GGTATGTAGGCGGTGCAGGATTAGCAGAGCGATC

[TR]_p3120_275_edge_11	CGGCAAACAAACCACCTTGGTAGCTCTTGATCCA
[TR]_p3120_275_edge_12	TCATGAGATTATCAAACGTTAAGGGATTTTGGTA
[TR]_p3120_275_edge_13	TCGTTCATCCATAGTTCAGCGATCTGTCTATTAA
[TR]_p3120_275_edge_14	ACCAGCCAGCCGGAAGGATTTATCAGCAATAATG
[TR]_p3120_275_edge_15	TTGCGCAACGTTGTTGTTCGCCAGTTAATAGTCT
[TR]_p3120_275_edge_16	AGTTACATGATCCCCCCCCCAACGATCAAGGCGGG
[TR]_p3120_275_edge_17	GTGTCGTAGACACACGACGGCCAGTGAGCGTCACGAC GTTGTAAAGTGTCGTAGACAC
[TR]_p3120_275_edge_18	GTGTCGTAGACACCTCTGTCCAGCTCGGACAATGGGA GATTACCAGTGTCGTAGACAC
[TR]_p3120_275_edge_19	GTGTCGTAGACACGACTGAGACCGTTCGAGCGTATCG TGATCCATGTGTCGTAGACAC
[TR]_p3120_275_edge_20	GTGTCGTAGACACTTGTTATCCGCTCACATGTTTCCTG TGTGAAAGTGTCGTAGACAC
[TR]_p3120_275_edge_21	GTGTCGTAGACACTAATGAATCGGCCAACGTCGTGCC AGCTGCATGTGTCGTAGACAC
[TR]_p3120_275_edge_22	GTGTCGTAGACACACGGTTATCCACAGAAACTCAAAG GCGGTAATGTGTCGTAGACAC
[TR]_p3120_275_edge_23	GTGTCGTAGACACGCCCCCCTGACGAGCATTTTTCCAT AGGCTCCGTGTCGTAGACAC

Table S2.35. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.85 nm).

Name	**Sequence**
[TR]_p3120_285_core_1	ATCAGGGGTATTTAGAAAAATAGTAAGCGT
[TR]_p3120_285_core_2	CAAAAACAGGAAGGCAAAACGGAAATGTTGAATAAAGCATTT
[TR]_p3120_285_core_3	ATTGCTCATACTCTTTTTATCCAGTTCTCAA
[TR]_p3120_285_co	GGATCTTACCTTTTTTTTCAATATT

re_4	
[TR]_p3120_285_core_5	CCGAAATCAAGTGCCACCTAAATTAACAAATA
[TR]_p3120_285_core_6	GGGGTTCCGCGTTTTTCAATACGGGA
[TR]_p3120_285_core_7	AAATCCCTTTCAGCACTGCATATTGCTCTTTCCCCGAAGGCA
[TR]_p3120_285_core_8	TAATATTCAGCTCATTTTTTAATTCCAGTT
[TR]_p3120_285_core_9	TCAGGGCGATAGGGTTGAGTGTTGCCAATAGG
[TR]_p3120_285_core_10	TGGAACAGTCAAAGGGCGAAAAACCCTAAA
[TR]_p3120_285_core_11	AGACCGAGATGGCCCACTACGTGAGGGGTCGA
[TR]_p3120_285_core_12	ATCACTCATTCAAAAGAAT
[TR]_p3120_285_core_13	GAAAGCGAAAAGCACTAAATCGGAACCGTCTA
[TR]_p3120_285_core_14	TTTTACCATCTGGCTTCACGCTCGTCGTCAAGTT
[TR]_p3120_285_core_15	GGTGCCGTAAGGAGCGGGCGCTAGGCTGCGCGTAACCACCCGCTATTA
[TR]_p3120_285_core_16	GGGAGCCAACGTGGCGAGAAAGATGCGCCG
[TR]_p3120_285_core_17	GGCCTCTTACACCCGCCGCGCTTAGAAGGGAA
[TR]_p3120_285_core_18	ATCAGTAATAGGTCACGGCGCTGGCAACCACAGA
[TR]_p3120_285_core_19	CTACAGGTGTTGGGAAGGGCGAGTAACGCC
[TR]_p3120_285_core_20	GTCGACGGCGACTCACTATAGGGCAAGGCGATTAAGTTGGTCGGTGCG
[TR]_p3120_285_core_21	CGCCAGCTGTTTAATGAAT
[TR]_p3120_285_core_22	GTCGTGCCTTGGGATGTGCTGCGAATTGGTTCATACGAACCT
[TR]_p3120_285_core_23	AGGGTTTTGAGCGCGCGTAATATATCGATA
[TR]_p3120_285_core_24	AGCTTGGGGATAGGGAGGACTATCAATGGC
[TR]_p3120_285_core_25	GCTCACAATTCTTTTCCCCCCTCGAG
[TR]_p3120_285_core_26	TCCCACCGCGGTGTTTTTGGTTAGCAACATG

[TR]_p3120_285_core_27	CTTCAATATTTTTTTCAGCTTTTGT
[TR]_p3120_285_core_28	AGCTAAATCGATACCTCAGCGTATCG
[TR]_p3120_285_core_29	ACGGGAGACCGCGAGACCCACGCAGTCTAT
[TR]_p3120_285_core_30	GGCAAACAAACCACCGCTGATTACGCGCAGAAAATTCTACGG
[TR]_p3120_285_core_31	TCTTAAAGGATCTTTTTTACACTAGAAGAAG
[TR]_p3120_285_core_32	TGGTGGCCTATTTTTGATCCTTTGA
[TR]_p3120_285_core_33	GGTCTGATTTTGGTCATGAGATTAAATCAA
[TR]_p3120_285_core_34	ATCTCAGCATTAAAAATGAAGTTTTATCAAAA
[TR]_p3120_285_core_35	AGGATCTTCACTTTTACACGACTTAT
[TR]_p3120_285_core_36	TGTCTATTTTTGTAGGTATCTCAGTCCAATTCTTTTAAGATC
[TR]_p3120_285_core_37	TCTAAAGAATGCTTAATCAGTGACTACGAT
[TR]_p3120_285_core_38	CTCCAGATCCCCGTCGTGTAGATAAGGCACCT
[TR]_p3120_285_core_39	TTTCTCATATTCCATAGTT
[TR]_p3120_285_core_40	GCCTGACTTTATCAGCAATAAACCGAAGTGGT
[TR]_p3120_285_core_41	CCATTGCTTTTATCCGCCTCCATCCTCACCGG
[TR]_p3120_285_core_42	TAATTGTTAATAGTTTGCGCAAGTTACATG
[TR]_p3120_285_core_43	CCTGCAACACAGGCATCGTGGTGTCATTCAGCTCCGGTTCGCAGTGTT
[TR]_p3120_285_core_44	ATCCCCCTCCTCCGATCGTTGTGCCATCCG
[TR]_p3120_285_core_45	TAAGATGCATTCTGAGAATAGTCGCCACAT
[TR]_p3120_285_core_46	TAATACCGGTATGCGGCGACCGAGATTCTCTTACTGTCATCAGAAGTA
[TR]_p3120_285_core_47	CCACTCGCTTTCACCAGCGTTTCTGG
[TR]_p3120_285_core_48	AGCAGAATCGGGGCGAAAACTCGATGTAAC
[TR]_p3120_285_co	AGTTGGCCCCAACGATCAAGGCGACGTTGTTG

re_49	
[TR]_p3120_285_core_50	CGCAAGCCAGAACCCGTCAAGTCAGAGGGCCGAG
[TR]_p3120_285_core_51	TTGGGCGGCTCGGTCGTTCGGCAGGCCAGC
[TR]_p3120_285_core_52	CATGACTGAGACCGTTCGATCTAGAGCGGCCGCCTTTAGTGA
[TR]_p3120_285_core_53	GGGTTAATTTCCTGTGTGAAATGTAAAGCC
[TR]_p3120_285_core_54	GTCGGGAAGCCGGAAGCATAAAGTTGTTATCC
[TR]_p3120_285_core_55	TGGGGTGTTGCGCTCACTGCCCTTTGCGTA
[TR]_p3120_285_core_56	GCGGTATCGCGCGGGGAGAGGCGGGCTTTCCA
[TR]_p3120_285_core_57	CGGCCAACAGCTCACTCAAAGGCGGGGGATAA
[TR]_p3120_285_core_58	GACGAGCAAGAACATGTGAGCAAATGCGGCGA
[TR]_p3120_285_core_59	AAAAGGCTTTTCCATAGGCTCCTGGAAGCT
[TR]_p3120_285_core_60	CGCAGGAATCACAAAAATCGACGCACAGGACTATAAAGATCGTGGCGC
[TR]_p3120_285_core_61	CCCTCGTGATACCTGTCCGCCTTTCGCTCC
[TR]_p3120_285_core_62	AAGCTGGCGCTGCGCCTTATCCGCAGCAGC
[TR]_p3120_285_core_63	CGCCACTGGGTAACTATCGTCTTGAGTTCGGTGTAGGTCGTTCTCCCT
[TR]_p3120_285_core_64	TTTGGTAAAAAGAGTTGGTAGCTCTT
[TR]_p3120_285_core_65	CACTGGTTGCTACAGAGTTCTTGGACAGTA
[TR]_p3120_285_core_66	TCGGGAAGACCAGGCGTTTCCCCCGCCCCCCT

Table S2.36. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.85 nm).

Name	**Sequence**
[TR]_p3120_285_edge_1	TTGGAAAACGTTCTCTTTAAAAGTGCTCAT
[TR]_p3120_285_edge_2	GTACTCAACCAAGTCTTTTCTGTGACTGGT

[TR]_p3120_285_edge_3	GTTAGCTCCTTCGGATGTTGTGCAAAAAAG
[TR]_p3120_285_edge_4	AGTAGTTCGCCAGTTGCCGGGAAGCTAGAG
[TR]_p3120_285_edge_5	AGTGCTGCAATGATGGCTTACCATCTGGCC
[TR]_p3120_285_edge_6	GTCTGACAGTTACCTATATATGAGTAAACT
[TR]_p3120_285_edge_7	CTCACGTTAAGGGACGCTCAGTGGAACGAA
[TR]_p3120_285_edge_8	TTTGCAAGCAGCAGGTAGCGGTGGTTTTTT
[TR]_p3120_285_edge_9	ATCATGGTCATAGCTGTTGCGCGCTTGGCGTACA
[TR]_p3120_285_edge_10	ACTCACATTAATTGCGCCTAATGAGTGAGCTAGA
[TR]_p3120_285_edge_11	CTCACTGACTCGCTGCCTCTTCCGCTTCCTCGCG
[TR]_p3120_285_edge_12	GCCGCGTTGCTGGCGTCAGGAACCGTAAAAAGTA
[TR]_p3120_285_edge_13	ACCCTGCCGCTTACCGGCGCTCTCCTGTTCCGCC
[TR]_p3120_285_edge_14	CCCCGTTCAGCCCGACGCTGTGTGCACGAACCTG
[TR]_p3120_285_edge_15	CGAGGTATGTAGGCGGAACAGGATTAGCAGAGAA
[TR]_p3120_285_edge_16	GCCAGTTACCTTCGGATCTGCGCTCTGCTGAATG
[TR]_p3120_285_edge_17	GTGTCGTAGACACGGATACATATTTGAATTTATTGTCTC ATGAGCGTGTCGTAGACAC
[TR]_p3120_285_edge_18	GTGTCGTAGACACTAAATTTTTGTTAAATTTGTTAAAAT TCGCGTGTGTCGTAGACAC
[TR]_p3120_285_edge_19	GTGTCGTAGACACGAACGTGGACTCCAACAGAGTCCA CTATTAAAGTGTCGTAGACAC
[TR]_p3120_285_edge_20	GTGTCGTAGACACACGGGGAAAGCCGGCGCCCGATTT AGAGCTTGGTGTCGTAGACAC
[TR]_p3120_285_edge_21	GTGTCGTAGACACATTCAGGCTGCGCAACGCGCGTCC CATTCGCCGTGTCGTAGACAC
[TR]_p3120_285_edge_22	GTGTCGTAGACACGTAAAACGACGGCCAGTCCCAGTC

	ACGACGTTGTGTCGTAGACAC
[TR]_p3120_285_edge_23	GTGTCGTAGACACCCACTCTGTCCAGCTCATGCAATGG GAGATTAGTGTCGTAGACAC

Table S2.37. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 3.00 nm).

Name	**Sequence**
[TR]_p3120_300_core_1	TATCAGGTGTATTTAGAAAAATTTGTAAGC
[TR]_p3120_300_core_2	AAAAACAGGAAGGCAAAACGGAAATGTTGAATAGAAGCATT
[TR]_p3120_300_core_3	TATTCTCATACTTTTTAGTTCGATGATC
[TR]_p3120_300_core_4	TTACCGCTGTTTTTTCAATAT
[TR]_p3120_300_core_5	GGCCGAAAAAAAGTGCCACCTAAAAAACAAAT
[TR]_p3120_300_core_6	AGGGGTTCCGTTTCGGGATAATA
[TR]_p3120_300_core_7	CAAAATCCTTGCATAATTCTCTTGCCCGGTTTTCCCCGTCGG
[TR]_p3120_300_core_8	GTTAATAATCAGCTCATTTTTTGTTCCAGT
[TR]_p3120_300_core_9	ATCAGGGCGATAGGGTTGAGTGTTAACCAATA
[TR]_p3120_300_core_10	TTGGAACCGTCAAAGGGCGAAACCCTAAAG
[TR]_p3120_300_core_11	TAGACCGAGATGGCCCACTACGTGGGGTCGAG
[TR]_p3120_300_core_12	CATGGTTATGTTTATCAAAAGAA
[TR]_p3120_300_core_13	AAAGCGAAAAGCACTAAATCGGAAAACCGTCT
[TR]_p3120_300_core_14	TTTGAACCATCTTTTCATTCACGCTCGTCGTTTTTTCAAGTTT
[TR]_p3120_300_core_15	GTGCCGTAAGGAGCGGGCGCTAGGGCGTAACCACCACACCTTACGCCA
[TR]_p3120_300_core_16	GGAGCCCACGTGGCGAGAAAGGCCGCTACA
[TR]_p3120_300_core_17	CTTCGCTACGCCGCGCTTAATGCGAAGGGAAG
[TR]_p3120_300_core_18	TCAGGGTAATATTTACGCTGCGCGCTGGCAAGTTTCCACAGAA

[TR]_p3120_300_core_19	GGGCGCGGGAAGGGCGATCGGTCCAGGGTT
[TR]_p3120_300_core_20	ACGGTATCACTATAGGGCGAATTGATTAAGTTGGGTAACGGCGGGCCT
[TR]_p3120_300_core_21	GCTGGCGAAATTTCATTAATGAA
[TR]_p3120_300_core_22	CTGTCGTGTTTGCTGCAAGGCGGGTACCGTTAACATACAAAC
[TR]_p3120_300_core_23	TTCCCAGCGCGTAATACGACTCGATAAGCT
[TR]_p3120_300_core_24	TGGATGCAGGGAGGACTACATGAATGGCAG
[TR]_p3120_300_core_25	CGCTCACAATTTTCTCGAGGTCG
[TR]_p3120_300_core_26	TTCCACCGCGGTTTTTTAGCAATCCTTC
[TR]_p3120_300_core_27	AATATTTTGTTTCAGCTTTTG
[TR]_p3120_300_core_28	CTAAAACCGATACCTCAGCGTATCG
[TR]_p3120_300_core_29	GGTCTGATTTTGGTCATGAGATTTAAATCA
[TR]_p3120_300_core_30	CAAACAAACCACCGCTGGTTACGCGCAGAAAAATTCTACGG
[TR]_p3120_300_core_31	TCTTAAGGATCTTTTTCTAGAAGGTGGT
[TR]_p3120_300_core_32	GGCCTAACTTTTATCCTTTGA
[TR]_p3120_300_core_33	TATCTCAGAATTAAAAATGAAGTTTATCAAAA
[TR]_p3120_300_core_34	AGGATCTTCATTTACTTATCGCC
[TR]_p3120_300_core_35	CTGTCTATTTTATCTCAGTTCGACCCGGTTTCCTTTTACGAT
[TR]_p3120_300_core_36	ATCTAAACAATGCTTAATCAGTACTACGAT
[TR]_p3120_300_core_37	CTCCAGATCCCCGTCGTGTAGATAGAGGCACC
[TR]_p3120_300_core_38	ACGGGAGACCGCGAGACCCACGGTCTATTA
[TR]_p3120_300_core_39	GCCTGACTTTATCAGCAATAAACCAGTGGTCC
[TR]_p3120_300_core_40	CATAGCTCACTTTATCCATAGTT
[TR]_p3120_300_c	ATTGCTACTATCCGCCTCCATCCACTCACCGG

ore_41	
[TR]_p3120_300_core_42	CAGAAGCCAGCTTTCGACAGGCAAGTCAGAGGTTTGCCGAGCG
[TR]_p3120_300_core_43	TGCAACTTAGGCATCGTGGTGTCAGCTCCGGTTCCCAACGTTATCACT
[TR]_p3120_300_core_44	ATTGTTGATAGTTTGCGCAACGTGATCCCC
[TR]_p3120_300_core_45	CCGCAGTGATCAAGGCGAGTTACATTGTTGCC
[TR]_p3120_300_core_46	CATGTTGGATCGTTGTCAGAAGGTAAGATG
[TR]_p3120_300_core_47	CCGCGCCAGCGACCGAGTTGCTCTTACTGTCATGCCATCCTAAGTTGG
[TR]_p3120_300_core_48	CTTTTCTAGAATAGTGTATGCGCATAGCAG
[TR]_p3120_300_core_49	AACTTTAGCGAAAACTCTCAAGGTAACCCA
[TR]_p3120_300_core_50	CTCGTGCTTTCACCAGCGTTTCTGG
[TR]_p3120_300_core_51	AGGGTTAGTTTCCTGTGTGAAAGTGTAAAG
[TR]_p3120_300_core_52	ATGACTGAGACCGTTCGATCTAGAGCGGCCGCCCTTTAGTG
[TR]_p3120_300_core_53	CAGTCGGGGAGCCGGAAGCATAAATTGTTATC
[TR]_p3120_300_core_54	CCTGGGGCGTTGCGCTCACTGCGTTTGCGT
[TR]_p3120_300_core_55	AGCGGTATCGCGCGGGGAGAGGCGCCGCTTTC
[TR]_p3120_300_core_56	ATTGGGCCGCTCGGTCGTTCGGGGCCAGCA
[TR]_p3120_300_core_57	TCGGCCAACAGCTCACTCAAAGGCGGGATAAC
[TR]_p3120_300_core_58	ACGAGCATGAACATGTGAGCAAAACTGCGGCG
[TR]_p3120_300_core_59	GCAGGAAACACAAAAATCGACGCTACTATAAAGATACCAGCGCTTTCT
[TR]_p3120_300_core_60	AAAGGCCTTTCCATAGGCTCCGGCTCCCTC
[TR]_p3120_300_core_61	AAGCGTGGGCGTTTCCCCCTGGAACCCCCCTG
[TR]_p3120_300_core_62	GTGCGCTCTGTCCGCCTTTCTCCCAAGCTG
[TR]_p3120_300_core_63	ACTGGCAGTATCGTCTTGAGTCCAGTGTAGGTCGTTCGCTCCTTCGGG

[TR]_p3120_300_core_64	GGCTGTGGCCTTATCCGGTAACCAGCCACT
[TR]_p3120_300_core_65	GGTAACAACAGAGTTCTTGAAGACAGTATT
[TR]_p3120_300_core_66	TGGTATCAAGAGTTGGTAGCTCTTG

Table S2.38. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 3.00 nm).

Name	**Sequence**
[TR]_p3120_300_edge_1	AAACGTTCTTCGGGAAAGTGCTCATCATTG
[TR]_p3120_300_edge_2	ACCAAGTCATTCTGGTGACTGGTGAGTACT
[TR]_p3120_300_edge_3	TCCTTCGGTCCTCCTGCAAAAAAGCGGTTA
[TR]_p3120_300_edge_4	TAGTTCGCCAGTTACCGGGAAGCTAGAGTA
[TR]_p3120_300_edge_5	AGTGCTGCAATGATGGCTTACCATCTGGCC
[TR]_p3120_300_edge_6	GGTCTGACAGTTACGTATATATGAGTAAAC
[TR]_p3120_300_edge_7	CTCACGTTAAGGGACGCTCAGTGGAACGAA
[TR]_p3120_300_edge_8	TTGCAAGCAGCAGATAGCGGTGGTTTTTTT
[TR]_p3120_300_edge_9	AATCATGGTCATAGCTATTGCGCGCTTGGCGTGA
[TR]_p3120_300_edge_10	TAACTCACATTAATTGTGCCTAATGAGTGAGCCA
[TR]_p3120_300_edge_11	GCTCACTGACTCGCTGGCTCTTCCGCTTCCTCGC
[TR]_p3120_300_edge_12	CCGCGTTGCTGGCGTTAGGAACCGTAAAAAGGAG
[TR]_p3120_300_edge_13	GCCGCTTACCGGATACCTCCTGTTCCGACCCTCC
[TR]_p3120_300_edge_14	TCAGCCCGACCGCTGCTGCACGAACCCCCCGTTT
[TR]_p3120_300_edge_15	GTATGTAGGCGGTGCTGGATTAGCAGAGCGAGAA
[TR]_p3120_300_edge_16	CAGTTACCTTCGGAAATGCGCTCTGCTGAAGCGT
[TR]_p3120_300_edge_17	GTGTCGTAGACACCGGATACATATTTGAAGTTATTG TCTCATGAGGTGTCGTAGACAC
[TR]_p3120_300_edge_18	GTGTCGTAGACACGTTAAATTTTTGTTAATTTTGTTA AAATTCGCGTGTCGTAGACAC
[TR]_p3120_300_edge_19	GTGTCGTAGACACAGAACGTGGACTCCAAAAGAGT CCACTATTAAGTGTCGTAGACAC

[TR]_p3120_300_edge_20	GTGTCGTAGACACCGGGGAAAGCCGGCGACCGATT TAGAGCTTGAGTGTCGTAGACAC
[TR]_p3120_300_edge_21	GTGTCGTAGACACGGCTGCGCAACTGTTGTCCCATT CGCCATTCAGTGTCGTAGACAC
[TR]_p3120_300_edge_22	GTGTCGTAGACACCGACGGCCAGTGAGCGTCACGA CGTTGTAAAAGTGTCGTAGACAC
[TR]_p3120_300_edge_23	GTGTCGTAGACACTCTGTCCAGCTCGGATAATGGGA GATTACCACGTGTCGTAGACAC

S2.7.2.2 Staple strand sequences of tiles for regular tilings

Table S2.39. Core staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.70 nm).

Name	Sequence
[TR]_p3120_core_1	CGCCACATAGCAGAACTTTAGGGGCGAAAACTCTCATGTAACC
[TR]_p3120_core_2	TTCGAAGGATCTTATTTTTACTCAACCAAATGC
[TR]_p3120_core_3	CACTCGTCACCAGCGTTTCTGGACACGGAA
[TR]_p3120_core_4	TTTTCTGTGATTTTTTGAGATCCAG
[TR]_p3120_core_5	TCATGAGCAAAGGGAATAAGGGCGGTGAGCAA
[TR]_p3120_core_6	AAACAGGAAGGTTTTCAGAAGTAAGT
[TR]_p3120_core_7	ATGTTGAAAGCATTTATCAGGGCATTTCCC
[TR]_p3120_core_8	ACATATTTTGTGTCACGCTCGGTCCTCCTTCCGCAAAGGAT
[TR]_p3120_core_9	TAAATCAGATAGGGGTTCCGCGCATTATTGTC
[TR]_p3120_core_10	CGAAAAGTAAAATTCGCGTTAATTGAGTGT
[TR]_p3120_core_11	ATAAACAACTCATTTTTTAACCAACTTATAAA
[TR]_p3120_core_12	TTGCTACAGTTTAGAAAA
[TR]_p3120_core_13	AAACCGTCATAGACCGAGATAGGGATTTTTGT
[TR]_p3120_core_14	ATCCTAGGCTTCCGGAGCAATAAACCTTGGCAAA
[TR]_p3120_core_15	TGTTCCAGGACTCCAACGTCAAGCACTAAA
[TR]_p3120_core_16	TCAAAAGATATCAGGGCGATGGCCAATCAAGTTTTTTGGGGGGAAGAA
[TR]_p3120_core_17	GAAAGGAAGTCGAGGTGCCGTAAAAGGGCGAA
[TR]_p3120_core_18	GTGCCCAGTTTACCCTCACTACGTGATTCCTGTC
[TR]_p3120_core_19	TCGGAACGGGAAAGCCGGCGAAGCTGCGCG
[TR]_p3120_core_20	CTCTTCGCCATTCAGGCTGCGCAACAAGTGTAGCGGTCACCGTGGCGA
[TR]_p3120_core	AGCGAAAGGCTGTGTGAA

_21	
[TR]_p3120_core_22	TAACCACGCGCGTCCCATTCGCTATTACGC
[TR]_p3120_core_23	GGTCATAGTCTAGGGCGCTGGCTGTTGGTTCCTGCAGTCAT
[TR]_p3120_core_24	CAGCTGGTGGGTAACGCCAGGGAGTGAGCG
[TR]_p3120_core_25	ACTGAGACCGTTTTTTCGGTGCGGGC
[TR]_p3120_core_26	CAATTGCTTCAATATTTTTAACGACGGCCTTTT
[TR]_p3120_core_27	CCCAGTCACGTTTTTTAAGGGTTAG
[TR]_p3120_core_28	CGCGTAACGGGCCCCCCCTCGAGGTCG
[TR]_p3120_core_29	CAGCCACTGGTAACAGGATTGTTCTTGAAGTGGTGTTTGGTAT
[TR]_p3120_core_30	AGTAGCCTAACTACTTTTTTTCAGCCCGAGGGC
[TR]_p3120_core_31	CTGCGCTTGGTAGCTCTTGATCCAGATTAC
[TR]_p3120_core_32	TGTGTGCACGTTTTTCTAGAAGGAC
[TR]_p3120_core_33	GGAACGAATTTTGTTTGCAAGCAGCGGCAAAC
[TR]_p3120_core_34	AAACCACCGCTTTTTTCTCCCTTCGG
[TR]_p3120_core_35	GCGCAGATTCTACGGGGTCTGAAGATCCTT
[TR]_p3120_core_36	CACGTTAATCGCTCAAGTCAGGATACCTTTGTGGTTTAACT
[TR]_p3120_core_37	TTACCAATAAAAGGATCTTCACCTCGCTCAGT
[TR]_p3120_core_38	TTAAATTTATGAGTAAACTTGGCGTGTAGA
[TR]_p3120_core_39	GATTATCAGCTTAATCAGTGAGGCTTTCGTTC
[TR]_p3120_core_40	AGCATCACATGGTCATGA
[TR]_p3120_core_41	CGCTCACCTTGCCTGACTCCCCGTTCTGACAG
[TR]_p3120_core_42	TCTAACCTATTGGTTATCAAAGGCGGTTGATCTG
[TR]_p3120_core_43	TAACTACCTGCAATGATACCGCATCCGCCT

[TR]_p3120_core_44	ATCCATAGGGCTCCAGATTTATCAAGGGCCGAGCGCAGAATGTTGCCA
[TR]_p3120_core_45	CGCAACGTGTGGTCCTGCAACTTTGAGACCCA
[TR]_p3120_core_46	CCATCCAGTAGTTCGCCAGTTACATTCAGC
[TR]_p3120_core_47	TGGCCGCAGCGGTTAGCTCCTTCGTCGTTTGGTATGGCTTATAGTTTG
[TR]_p3120_core_48	TCCGGTTATGTTGTGCAAAAAAGTGTTATC
[TR]_p3120_core_49	ACTCATGCATGCCATCCGTAAGGTCATTCT
[TR]_p3120_core_50	GAGAATACGGCGTCAATACGGGATAAT
[TR]_p3120_core_51	TATCGATAAGCTTGGATGCAATAGGGAGGACTACACAATGGCA
[TR]_p3120_core_52	GCTAAAAACCTCAGCGTATCGTGTTCTAGA
[TR]_p3120_core_53	TGGCGTAACCCGGGGGATCCACTAGATCCATG
[TR]_p3120_core_54	GCGGCCGTTAGTGAGGGTTAATACAACATA
[TR]_p3120_core_55	TGCGTTGCCCGCTCACAATTCCACTGCGCGCT
[TR]_p3120_core_56	CGAGCCGTGAGTGAGCTAACTCGAGAGGCG
[TR]_p3120_core_57	ATTGTTATGCTCACTGCCCGCTTTCAGCTGCA
[TR]_p3120_core_58	CTGCGGCGTCGGCCAACGCGCGGGACATTAAT
[TR]_p3120_core_59	GTTTGCGACTCGCTGCGCTCGGCATGTGAG
[TR]_p3120_core_60	TTAATGAAAGCGGTATCAGCTCACTCCACAGAATCAGGGGCCCTGACG
[TR]_p3120_core_61	CTCCGCCCATAACGCAGGAAAGAATCGTTCGG
[TR]_p3120_core_62	CAAAAGGCGTTGCTGGCGTTTTCAGGACTA
[TR]_p3120_core_63	GAAGCGTGACCCTGCCGCTTACCGAGGTGGCGAAACCCGATCCATAGG
[TR]_p3120_core_64	TAAAGATCGCTCTCCTGTTCCGGCGCTTTC
[TR]_p3120_core_65	TCATAGCCGTTCGCTCCAAGCTCCGCTGCG
[TR]_p3120_core	CCTTATCGACACGACTTATCGCCACTG

_66	

Table S2.40. Edge staples of p3120 equilateral triangular DNA origami tile (***D*** = 2.70 nm).

Name	**Sequence**
[TR]_p3120_edge_1	AATCAGGGCCATCGATCACGTAGCGAGCTCTGAT
[TR]_p3120_edge_2	CCAGCTTTTGTTCCCTCCACCGCGGTGGAGCTAG
[TR]_p3120_edge_3	AGCCTGGGGTGCCTAAGAAGCATAAAGTGTAACG
[TR]_p3120_edge_4	TTCCTCGCTCACTGTATTGGGCGCTCTT
[TR]_p3120_edge_5	AACCGTAAAAAGGCCGCCAGCAAAAGGCCAGGAT
[TR]_p3120_edge_6	TGGAAGCTCCCTCGTGACCAGGCGTTTCCCCCAA
[TR]_p3120_edge_7	TCAGTTCGGTGTAGGTTCACGCTGTAGGTATCCC
[TR]_p3120_edge_8	GTCCAACCCGGTAACGGTAACTATCGTC
[TR]_p3120_edge_9	AATTCTCTTACTGTGTTATGGCAGCACTGC
[TR]_p3120_edge_10	TTACATGATCCCCCCCCAACGATCAAGGCG
[TR]_p3120_edge_11	GGAAGCTAGAGTAAGTCTATTAATTGTTGC
[TR]_p3120_edge_12	ATCTGGCCCCAGTGGATACGGGAGGGCT
[TR]_p3120_edge_13	CAATCTAAAGTATAAAAAATGAAGTTTTAA
[TR]_p3120_edge_14	GATCCTTTGATCTTAAAAAAGGATCTCAAG
[TR]_p3120_edge_15	TTCGGAAAAAGAGTCTGCTGAAGCCAGTTA
[TR]_p3120_edge_16	GGCGGTGCTACAGAAGCAGAGCGAGGTA
[TR]_p3120_edge_17	CAAGGCGATTAAGTCGAAAGGGGGATGTGC
[TR]_p3120_edge_18	TGCGCCGCTACAGGCACACCCGCCGCGCTT
[TR]_p3120_edge_19	TTTAGAGCTTGACGCCTAAAGGGAGCCCCC
[TR]_p3120_edge_20	CTATTAAAGAACGTGTTTGGAACAAGAG
[TR]_p3120_edge_21	AGCGTTAATATTTTGTTGCCACCTAAATTGTAGA
[TR]_p3120_edge_22	TTTTTCAATATTATTGATACTCATACTCTTCCAA
[TR]_p3120_edge_23	CAGCATCTTTTACTTTGCACCCAACTGATCTTTG

Table S2.41. Core staples of p3548 equilateral triangular DNA origami tile.

Name	**Sequence**
[TR]_p3548_core_1	AAGCAGCAGATTACGCGCATTTTCTACGGGGTCTAGGGATTT
[TR]_p3548_core_2	GTTAGACGCTCAGTTTTCAGTTACCTGGTA
[TR]_p3548_core_3	TCTGCGCTCTTTAAAACTCAC
[TR]_p3548_core_4	TGGTCATTTTTAAATTAAAAATAGTTACCA
[TR]_p3548_core_5	AAATCAATCTTTGCAGAGCGAG
[TR]_p3548_core_6	GACTCCCCGTAAACTTGGTCTGACGAAGTTTT

[TR]_p3548_core_7	ATGCTTAATTTCGTTCATCCATGCTGCAAT
[TR]_p3548_core_8	TGTAGATTGTGCACGAACTGGTAAATATGAGTCG
[TR]_p3548_core_9	GGGCCGAGACCATCTGGCCCCAGTAGTTGCCT
[TR]_p3548_core_10	GCTCCAAGCTTTTTGATACGGGAG
[TR]_p3548_core_11	GGCTTCGCAGAAGTGGTCCTGAGTCTATT
[TR]_p3548_core_12	GATACCGAGCAATAAACCAGCCAGTAGTTC
[TR]_p3548_core_13	ATCCCAACTTTTGCGCTGGAAGCTCTTTTCCTCC
[TR]_p3548_core_14	CGTTTGGTCCGGGAAGCTAGAGTAAGCCGGAA
[TR]_p3548_core_15	GCCAGTTAGGCATCGTGGTGTCTCGGTCCT
[TR]_p3548_core_16	AATTGTTGATGGCTTCATTCAGCTCCCCATGT
[TR]_p3548_core_17	TAATTCTCAAAGCGGTTAGCTCCTACGCTCGT
[TR]_p3548_core_18	GATCCCGGTTCCCAACGTTTTTAGGCCAGGA
[TR]_p3548_core_19	TCACATTAAGTTGGGTATTTTTGAGTTACAT
[TR]_p3548_core_20	TGTGCAAATTACTGTCATGCCATCACTGGTGAGTACTCAAAGTGC
[TR]_p3548_core_21	CCGATCGCTCATGGTTATGGCAATAGTGTA
[TR]_p3548_core_22	CCGCCGTATTTTTGTGCGTAAGATGTTTTACCCG
[TR]_p3548_core_23	ACTTTAAACCAAGTCATTCTGAGAGCACTGCA
[TR]_p3548_core_24	TGCGGCGATAATACCGCGCCACCTTACCGC
[TR]_p3548_core_25	AAGGCAAACTTTTACTTTCACCAGGAAAACTCTCAAGGATATAGCAGA
[TR]_p3548_core_26	TCATCATTGGTTTTAACCCTAAAG
[TR]_p3548_core_27	AGCACTATTCTTCGGGGCCGTTTCAACGTGGTAA
[TR]_p3548_core_28	TGTTGAGACTGATCTTCAGCATATGCCGCA
[TR]_p3548_cor	AAAAAGGATACTCTTCCTTTTTGTCTCATG

e_29	
[TR]_p3548_core_30	AGAGTCCACTTTCAAAAACAGG
[TR]_p3548_core_31	CGAATCAGCTCATTTTTAGGGTTATTCAAT
[TR]_p3548_core_32	ATTATTGAATTTCCAATAGGC
[TR]_p3548_core_33	AGCGGATATAGGGGTTCCGCGCACAT
[TR]_p3548_core_34	CTTCTATCCGAAAAAAGAGGAAAAAACTCTCGTATGACCGAA
[TR]_p3548_core_35	ACAACAGTGGCAGTTTTCGTGTAGTCTACA
[TR]_p3548_core_36	CGTTAGGAATTTCGACGTGTC
[TR]_p3548_core_37	AGAGTTGGGTAGCGGTGGTTTTTTTG
[TR]_p3548_core_38	ACAGAGTAGAAGGACAGTATTTTCGGAAAA
[TR]_p3548_core_39	CCTTATCGACACGACTTATCGCGCGGTGCT
[TR]_p3548_core_40	GTATGTAGCACTGGCAGCAGCCACCCCCCGTTCAGCCCGATCAGTTCG
[TR]_p3548_core_41	CCTTTCTCACGCTGTAGGTATCCCGCTGCG
[TR]_p3548_core_42	CCGCGTTGACCAGGCGTTTCCCCCTCTCCTGTTCCGACCCCGTTC
[TR]_p3548_core_43	GTGTAGGTTGCCGCTTACCGGATAACAGGACT
[TR]_p3548_core_44	CCCCCTGAGGTGGCGAAACCCGCCTGTCCG
[TR]_p3548_core_45	ATAAAGATCTGGCGTTTTTCCATACCACAGAA
[TR]_p3548_core_46	TCGTTCGCGGTAATACGGTTATGGCTCCGC
[TR]_p3548_core_47	CGCTTCCTTAACGCAGGAAAGAACTAAAAAGG
[TR]_p3548_core_48	ACCGATGTGAGCAAAAGTTTTTTTTCCCAG
[TR]_p3548_core_49	TCAGGGGACGCTCACTGACTCGCTAGCTGCAT
[TR]_p3548_core_50	CATTAATGAAACCTGTCGTGCCGCGCTCGG
[TR]_p3548_core_51	CTGGGCGGCCAACGCGCGGGGCGCTCTTC

[TR]_p3548_core_52	TGGGAGAGTTTTACGTTGTACGTTCTTTTCGTAT
[TR]_p3548_core_53	TAATGAATGTGCCTAATGAGTGAGCAATTCCA
[TR]_p3548_core_54	GCTTGGCATTGTTATCCGCTCACTAACTCA
[TR]_p3548_core_55	TCAGCGGACTTTTTAGTGTAAAGC
[TR]_p3548_core_56	GCCGGAAAAAATCAACGACCTAGCTTTGTTACGA
[TR]_p3548_core_57	CACAACATCCCTTTAGTGAGGGTTCCGCCACC
[TR]_p3548_core_58	CAGTGAGCTAGTTCTAGAGCGGAATTGCGC
[TR]_p3548_core_59	GCGGTGGAGCTTAGCAATTATT
[TR]_p3548_core_60	CGAAAAGTGCCACCTAAATTAAATTTTTGTTAAAATCGGCAA
[TR]_p3548_core_61	GGTGCAAAACGACCCATGTGTATCAA
[TR]_p3548_core_62	CAGTCCGCATGGTAAAACCTTGGGAAGAGT
[TR]_p3548_core_63	CGCAGAGAAGTTATCCATCGGGACGAAACG
[TR]_p3548_core_64	CGGCCAGCGCAAGATAAGCCAACGCAAATCTGCCAGGGAACGCCGGCA
[TR]_p3548_core_65	TGAGCGATGGCTTAACGTGACTAAAAGATA
[TR]_p3548_core_66	AAAACGACGGTGAGCTCATCTGTCAGAACCAGCTCAGAAATGGCA
[TR]_p3548_core_67	TCTGATACAAACAAGACTGGTGGCTAAGCTTT
[TR]_p3548_core_68	CTCACTAGGTCGACGGTATCGAGTGAAAAT
[TR]_p3548_core_69	GGTGCAATGGCCAGTGAGCGCGCGCAGCTGGC
[TR]_p3548_core_70	AGGCTGCTCTTCGCTATTACGCTAATACGA
[TR]_p3548_core_71	CGCCGCTAGATGTGCTGCAAGGCGGACGTTGT
[TR]_p3548_core_72	GAAAGGGGCAGGGCGCGTCCCATTAGGGCGCT
[TR]_p3548_core_73	AAGCCGGAAAGGAGCGGGCGCTCGCCATTC
[TR]_p3548_cor	GGAGCTAGCGGTCACGCTGCGGCTTAATG

e_74	
[TR]_p3548_core_75	GGCAAGTGCCCCGATTTAGAGCTTTTGGGGTC
[TR]_p3548_core_76	ACCGTCTCCCTAATCAAGTTTTGACGGGGA
[TR]_p3548_core_77	GAGGTGCCGACTCCAACGTCAAAGTTGGAACA
[TR]_p3548_core_78	AATCCCTGAGTGTTGTTCCAGTGGCGAAAA

Table S2.42. Edge staples of p3548 equilateral triangular DNA origami tile.

Name	**Sequence**
[TR]_p3548_edge_1	ATCTTCACCTAGATCCGAGATTATCAAAAAGGGA
[TR]_p3548_edge_2	TCTCAGCGATCTGTCTATCAGTGAGGCACCTACC
[TR]_p3548_edge_3	TTGTTGCCATTGCTACAATAGTTTGCGCAACGGG
[TR]_p3548_edge_4	CCGCAGTGTTATCATTGTCAGAAGTAAGTT
[TR]_p3548_edge_5	CACTCGTGCACCCAATCCAGTTCGATGTAA
[TR]_p3548_edge_6	AATGTTGAATACTCGAATAAGGGCGACACG
[TR]_p3548_edge_7	TAACTACGGCTACACTTCTTGAAGTGGTGGCCAG
[TR]_p3548_edge_8	GAGTCCAACCCGGTAACGGTAACTATCGTCTTAC
[TR]_p3548_edge_9	TCGACGCTCAAGTCAGACGAGCATCACAAAAAGC
[TR]_p3548_edge_10	TCAGCTCACTCAAAGGGCTGCGGCGAGCGGTACC
[TR]_p3548_edge_11	CTGTTTCCTGTGTGAAGTAATCATGGTCATAGGA
[TR]_p3548_edge_12	CAGCCCGGGGGATCCAACCGTCAGAATTCCTGAA
[TR]_p3548_edge_13	ACCGAGATAGGGTTTATAAATCAAAAGAAT
[TR]_p3548_edge_14	TACGTGAACCATCAATCAGGGCGATGGCCC
[TR]_p3548_edge_15	GATCGGTGCGGGCCGCAACTGTTGGGAAGG
[TR]_p3548_edge_16	GGGCCCCCCCTCGATAGGGCGAATTGGGTA
[TR]_p3548_edge_17	TAGTTGGAAAAAAGAGCTCAAAATCGGGTG
[TR]_p3548_edge_18	AAAAGCAACCCTGGCTCCAACCAGGATAGG

Table S2.43. Core staples of p3548 square DNA origami tile.

Name	**Sequence**
[SQ]_p3548_core_1	CTAAATTGTAAGCGTTAAAAATCAGCTCATTTTAAAAGAAT
[SQ]_p3548_core_2	TATAAATCTTAACCAATAGTTTTTTTTATTGTCTCATGTCAATATT
[SQ]_p3548_core_3	ATTGAAGCATTTTTTTTTTGCAAAATCCCT
[SQ]_p3548_core_4	GACTCCAACGTCAAAGGGCTTTTCTGGGTGAGC
[SQ]_p3548_core_5	AAGTGCTCCTTCAGCATCTTTTACTTTTTTTTTCTATCAGGGCG
[SQ]_p3548_core	AGACCGAAGAGTCCACTATTAACCTAATCA

_6	
[SQ]_p3548_core_7	TAGAGCTTCTACGTGAACCATCACAGAACGTG
[SQ]_p3548_core_8	GGAGCGGGGAACGTGGCGATTTTTTTTTCCACATAGCAGTTGCCCGG
[SQ]_p3548_core_9	ATGGCCCAGACGGGGAAAGCCGGCCGCTAGGG
[SQ]_p3548_core_10	AGTTTTTAACCCTAAAGGGAGCTGCGCGTA
[SQ]_p3548_core_11	GCGCAACTAGTGTAGCGGTCACGCCCCCGATT
[SQ]_p3548_core_12	CGTCAATACGGTTTTTTTTAGAAAGCGAAA
[SQ]_p3548_core_13	CCTCTTCGCTATTTTTTTTAGGACTTCTCG
[SQ]_p3548_core_14	CGCTGGCAGTTGGGAAGGGCGATCATGTGCTG
[SQ]_p3548_core_15	ACCACCAGCGTCCCATTCGCCACAGGGTTT
[SQ]_p3548_core_16	CGAATTGGTTAAGTTGGGTAACGCTTCAGGCT
[SQ]_p3548_core_17	ACGTGTCAGGAAAAAACTCTTTTTTTTTGCGAAAGGGGGGGTGCGGG
[SQ]_p3548_core_18	CAAGGCGAGTACCGGGCCCCCCCTCGATTTTTTGTGTAGTCGGA
[SQ]_p3548_core_19	ACCTTGTACACGTTAGGAATTTATCGATAAGC
[SQ]_p3548_core_20	TCCCAGTGCGTAATACGACTCACTCATCTG
[SQ]_p3548_core_21	TTTGGTGCAATGGTGAGCTATAGGG
[SQ]_p3548_core_22	GAGCGATTGACTTTTTTTTGCCTAGCCTCA
[SQ]_p3548_core_23	TCTGTACACAAGACTGGTGGCGGATCCCTG
[SQ]_p3548_core_24	GCGCAGCAATCGGGGCAAGTTTTTTTTTCACCAATCGATGAAAATT
[SQ]_p3548_core_25	GCTTAACGGACTACGGACAAAATCA
[SQ]_p3548_core_26	CGTAAAAAGGCCGCGTTGCGAGCATCACAAAAATAAAGATA
[SQ]_p3548_core_27	CAGGACTATCGACGCTCAATTTTTTTTTCAAAGGCGGTTTCGGCTG
[SQ]_p3548_core_28	CGGCGAGCGGTTTTTTTTTGCGAAACCCGA

[SQ]_p3548_core_29	GATACCTGTCCGCCTTTCTTTTTTAATGAATCG
[SQ]_p3548_core_30	ATTCCACACAGTCGGGAAACCTGTCGTTTTTTTAGCGTGGCGCT
[SQ]_p3548_core_31	CCAGGCGTGTTCCGACCCTGCCTCTCAGTT
[SQ]_p3548_core_32	TGCGCCTTGCTCACGCTGTAGGTAGCTTACCG
[SQ]_p3548_core_33	CACTGGCACTTGAGTCCAATTTTTTTTTAAATTGTTATCCGTAATCA
[SQ]_p3548_core_34	TTCTCATAATCCGGTAACTATCGTGCAGCCAC
[SQ]_p3548_core_35	CGGTGTAAACCCCCCGTTCAGCGTATGTAG
[SQ]_p3548_core_36	GGTATCTGGGATTAGCAGAGCGAGCCGACCGC
[SQ]_p3548_core_37	TGGTCATAGCTTTTTTTTTCGACTTATCGC
[SQ]_p3548_core_38	CGGAAAAAGAGTTTTTTTTAGTTGGCCGCA
[SQ]_p3548_core_39	TGGTAACACGCTCTGCTGAAGCCACAAACCAC
[SQ]_p3548_core_40	GCGGTGCGCTACACTAGAAGGATTGCAAGC
[SQ]_p3548_core_41	GACGCTCAGCGGTGGTTTTTTTGTCAGTATTT
[SQ]_p3548_core_42	GTGTTATCTCCTCCGATCGTTTTTTTTTGATCCGGCAAAGTTACCTT
[SQ]_p3548_core_43	CGCTGGTAGTGGAACGAAAACTCACGTTTTTTTTGCCATTGCTA
[SQ]_p3548_core_44	TCGCCAGTTAATAGTTTGCTTTTGGTCATGAGA
[SQ]_p3548_core_45	AGCAGATCTTTGATCTTTTCTATCACCTAG
[SQ]_p3548_core_46	TTATCAAAAAGGATCTCGGGGTCT
[SQ]_p3548_core_47	TGACAGTTACCTTTTTTTTCCGGAAGGGCC
[SQ]_p3548_core_48	ATCCTTTAGTATATATGAGTAACTATCTCA
[SQ]_p3548_core_49	GAGCGCAGTATCAGCAATATTTTTTTTCAGTGAGGCACACTTGGTC
[SQ]_p3548_core_50	GCGATCTCCCGTCGTGTAGATAACT
[SQ]_p3548_core	GCCAGGGAAAAAAGATACAAAAAGAAGTTATCCATTATT

_51	CG
[SQ]_p3548_core_52	GCCAGCAAAAAGCAACCCTGGCTTGAAGTC
[SQ]_p3548_core_53	GCCCGTAAGCAATTCGACGTCACCATGGTAAA
[SQ]_p3548_core_54	AGAGTGGTAAGGAAGCTGTACTGCCAATGACC
[SQ]_p3548_core_55	TGATGCACTATCCGAAAAAAGATGCAGCCC
[SQ]_p3548_core_56	AGTGAGGGAGACCGTCAGAATTCCGGGAGAAG
[SQ]_p3548_core_57	GAACAGTGTTAATTGCGCGCTTGGCGCTCACA
[SQ]_p3548_core_58	GGGGGATGAGCTCCAGCTTTTGAGCATAAA
[SQ]_p3548_core_59	CCGCTTTCCAACATACGAGCCGGATTCCCTTT
[SQ]_p3548_core_60	GTGTAAAATTAATTGCGTTGCGAGGCGGTT
[SQ]_p3548_core_61	GCCAACGCGCGGGGAGCTCACTGC
[SQ]_p3548_core_62	TGCGTATCGCTGCGCTCGGTCGAATACGGT
[SQ]_p3548_core_63	TATCCACGAGCAAAAGGCCAGCAAA
[SQ]_p3548_core_64	GGGCTTACCATCTGGCCCCACCGGCTCCAGATTAAGTGGTC
[SQ]_p3548_core_65	CTGCAACGCCGGGAAGCTAGAGCGTTTGGT
[SQ]_p3548_core_66	CAAAAAAGGTGGTGTCACGCTCGTTAAGTAGT
[SQ]_p3548_core_67	CAGGCATCCGGTTAGCTCCTTCGGACTCATGG
[SQ]_p3548_core_68	ATGGCTTGTTACATGATCCCCCTTACTGTC
[SQ]_p3548_core_69	GTGTATGCGCACTGCATAATTCTCATGTTGTG
[SQ]_p3548_core_70	TTATGGCAGGCGACCGAGTTGCTCAACTTTAA
[SQ]_p3548_core_71	ATGCCATTCAACCAAGTCATTCCTTCGGGG
[SQ]_p3548_core_72	CAACTGATATCATTGGAAAACGTTTGAGAATA
[SQ]_p3548_core_73	CGAAAACTCGATGTAACCCACTAATGCCGC

[SQ]_p3548_core_74	AAAAACAGGAAGGCAACGTGCACC
[SQ]_p3548_core_75	AAAAAAGCATACTCTTCCTTTTAGCGGATA
[SQ]_p3548_core_76	CATATTTTCCGCGCACATTTCCCCG

Table S2.44. Edge staples of p3548 square DNA origami tile.

Name	**Sequence**
[SQ]_p3548_edge_1	GGAAATGTTGAATACTGGAATAAGGGCGACACCC
[SQ]_p3548_edge_2	GCTGTTGAGATCCAGTTCTCAAGGATCTTACCTG
[SQ]_p3548_edge_3	CCAACGATCAAGGCGACATTCAGCTCCGGTTCGA
[SQ]_p3548_edge_4	CAGTCTATTAATTGTTTTTATCCGCCTCCATCTC
[SQ]_p3548_edge_5	AACCAGGATAGGAACGAAACGCAGTCCGCT
[SQ]_p3548_edge_6	TATCAAGATACCTTCATCGAACGACCCATG
[SQ]_p3548_edge_7	GTGAGCTAACTCACGCCTGGGGTGCCTAAT
[SQ]_p3548_edge_8	CTCGCTCACTGACTTGGGCGCTCTTCCGCT
[SQ]_p3548_edge_9	GTTCCAGTTTGGAACAGATAGGGTTGAGTGTTTT
[SQ]_p3548_edge_10	TAAAGCACTAAATCGGTGGGGTCGAGGTGCCGGG
[SQ]_p3548_edge_11	GACGGCCAGTGAGCGCCACGACGTTGTAAAACCT
[SQ]_p3548_edge_12	AACCAGCTCAGAAAAAGTTCGTACCCACGTAGCC
[SQ]_p3548_edge_13	TTAAATCAATCTAATAAATTAAAAATGAAG
[SQ]_p3548_edge_14	ATCTCAAGAAGATCTACGCGCAGAAAAAAA
[SQ]_p3548_edge_15	GGGCTGTGTGCACGGGTCGTTCGCTCCAAG
[SQ]_p3548_edge_16	CTCGTGCGCTCTCCTTTCCCCCTGGAAGCT

Table S2.45. Core staples of p3548 regular hexagonal DNA origami tile.

Name	**Sequence**
[HE]_p3548_core_1	GTAAACTTGGTCCTATCTCAGCGATCAACTACGA
[HE]_p3548_core_2	GTGTAGATTGTCTATTTCTTTTTTTTAAAAAGGATCGAAAACTC
[HE]_p3548_core_3	TACGGGATACCGCGAGACCCACAATTGTTG
[HE]_p3548_core_4	TACAGGCACTCCATCCAGTCTATTGCTCACCGGCTCCAGATCCCCGTC
[HE]_p3548_core_5	TTTGCAAGGGATTTTTTGCCTGACTTTATCAG
[HE]_p3548_core_6	CAATAAACCTGCAACTTTATCCGCTCGTGGTGTCACGCTCCAACGATC
[HE]_p3548_core_7	TGGTCCAGCCTTTTGGTGGGATCC

[HE]_p3548_core_8	CCGGGAATTGCGCAACGTTGTTGTTGTGCA
[HE]_p3548_core_9	GGCAAACAAACCATTTTTTTTTCCGAGCGCAGAAG
[HE]_p3548_core_10	TCACTCATTTACATGATCCCCCATGCCATTGC
[HE]_p3548_core_11	GGAAGTCACCTTTTGTTCCGTCGT
[HE]_p3548_core_12	TTGGTATGGCTTCTTTTTTTTTGTGAGCAAAAACA
[HE]_p3548_core_13	AAAAAGCGAAGTAAGTTGGCCGTCATGCCATCCGTAAAAGTCATTCTG
[HE]_p3548_core_14	AAGGCGAGGGTTATGTTTGCTCATTCAGCATC
[HE]_p3548_core_15	AACGTTCTCGCCACATAGTTTTTTTTTCTCTTACTGCAGTGTTA
[HE]_p3548_core_16	ATACCTGTCCGCATAGCTCACGCTGTGCACGAAC
[HE]_p3548_core_17	GGCTGTGTAGGTATCTCATTTTTTTTAAGATACCAGCGCTCAAG
[HE]_p3548_core_18	CCCCCGTATCGTCTTGAGTCCATGGCCTAA
[HE]_p3548_core_19	TCGGAAAAAGAGTTCTTGAAGTGGACCCGGTAAGACACGACCAAGCTG
[HE]_p3548_core_20	AGCAAAAGGGCGAAATTGTTCGCTCTTATCGC
[HE]_p3548_core_21	CACTGGCAATGTAGGCGGTGCTACAGAGTTGGTAGCTCTTTTTTTTTG
[HE]_p3548_core_22	GAGGTGCAGCTTTTTGAGCAATCA
[HE]_p3548_core_23	CTACGGCCGCTCTGCTGAAGCCGAAAAAAA
[HE]_p3548_core_24	GGGGATAACGCAGTTTTTTTTTGGATTAGCAGAGC
[HE]_p3548_core_25	ACGTTAAGCAGCAGATTACGCGCAAGTTACCT
[HE]_p3548_core_26	GGATCTCGACGCTCAGTGGAACTTCACCTAGATCCTTAAGTATATATG
[HE]_p3548_core_27	ACTCCAACGTCCCCACTACGTGAACCATCGGAAC
[HE]_p3548_core_28	AGCACTAAATCACCCTAATTTTTTTTAAGAATAGACCCAATAGG
[HE]_p3548_core_29	CCTAAAGCCGGCGAACGTGGCGGCCGCTAC
[HE]_p3548_cor	GCCTCTTCCCGCCGCGCTTAATGCAGAAAGGAAGGGAAG

e_30	ATGCCGTAA
[HE]_p3548_core_31	TCCCCGAAGGCAAAATTGTCGAGGAAGCGAAA
[HE]_p3548_core_32	GGAGCGGGCGCGTAACCACCACACGCTATTACGCCAGCTGGGGTAACG
[HE]_p3548_core_33	CGCTGCGCTATTTTTTCCGATGTA
[HE]_p3548_core_34	AGGGCGCGTTGGGAAGGGCGATTGTAAAAC
[HE]_p3548_core_35	TTTAGAAAAATAATTTTTTTTTAGTGTAGCGGTCA
[HE]_p3548_core_36	TCGAGGTCTTCCCAGTCACGACGTCGGTGCGG
[HE]_p3548_core_37	ATTCGAGCCATTTTAAGTTGCGAA
[HE]_p3548_core_38	AGGGGGATGTGCTTTTTTTTTTCAGCGCAGCAATT
[HE]_p3548_core_39	GACGGCCCGAATTGGGTACCGGGCTCATCTGTCTGTAAACAAGACTGG
[HE]_p3548_core_40	CCAGGGTTGACGGTATTGGCATCACCATCGGG
[HE]_p3548_core_41	CGGACAAACGTGACTCGCTTTTTTTTGCAATGGTGAGCCCCCCC
[HE]_p3548_core_42	GAATAGTGTATTACGGGATAATACCGTCGGGGCG
[HE]_p3548_core_43	AAAACTCGATGTAACCCACTCGCACGGAAA
[HE]_p3548_core_44	TCTCATGAAAGGGAATAAGGGCGATGCACCCAACTGATCTCATTGGAA
[HE]_p3548_core_45	TTTTACTTGCAAAATGCCGCAAAAGCGGATACATATTTGACGCACATT
[HE]_p3548_core_46	TGTTGAATGAAGCATTTATCAGGTAAGCGT
[HE]_p3548_core_47	CCGAAATCAAGTGCCACCTAAATTGGTTATTG
[HE]_p3548_core_48	TAATATTCAGCTCATTTTTTAACGAGATAGGGTTGAGTAAAGAACGTG
[HE]_p3548_core_49	CCTTTAGTGAGTAGCTGTTTCCTGTGCATAAAGT
[HE]_p3548_core_50	GCCGGAAGTGAAATTGTTTTTTTTTTTTCCTGCAGCCGACGTGT
[HE]_p3548_core_51	GTAAAGCTAATTGCGTTGCGCTGCTTCCTC
[HE]_p3548_core_52	AGGCGGTATATTGGGCGCTCTTCCCACTGCCCGCTTTCCAACATACGA

[HE]_p3548_core_53	ATACCTTCCCGAACATTCCACACAGTCGGGAA
[HE]_p3548_core_54	ACCTGTCGGGAGAGGCGGTTTGCGATACGGTTATCCACAGAAAAGGCC
[HE]_p3548_core_55	CGCGGTGCCATTTTCATGTCCTTG
[HE]_p3548_core_56	GCTCACTGCGAGCGGTATCAGCAGGCCGCG
[HE]_p3548_core_57	AAGTCTGATGCACTTTTTTTTTGAATCGGCCAACG
[HE]_p3548_core_58	TCAGAGGTGCCAGGAACCGTAAAATCACTCAA
[HE]_p3548_core_59	TTGCTGGCATCACAAAAATCGAGCGTTTCCCCCTGGAGCCGCTTACCG
[HE]_p3548_core_60	GGCGTGAAAATAGATCCCTGGCTTAAATCAACGA
[HE]_p3548_core_61	CAAATCTATCGGGTGGATAGTTATAGGAAA
[HE]_p3548_core_62	GAAGAGTGGTCCGCTCCAACCAGGGGAAAAAAGAAGTTATGCGGACTA
[HE]_p3548_core_63	GCAAGATAGCCAGCACGAAACGCAGTGCAATTCGACGTCAGTATCAAG
[HE]_p3548_core_64	AAAGCAAGGAAAAAAGCGTGCGGAGAAGGC
[HE]_p3548_core_65	CACAATGATATCCGAAAAAAGAGGTGTAGTCG
[HE]_p3548_core_66	CCGTAAAAGTGGCAGGACTTCTCCGGGGGATCCACTACAGCTTTTGTT

Table S2.46. Edge staples of p3548 regular hexagonal DNA origami tile.

Name	**Sequence**
[HE]_p3548_edge_1	AAGCGTGGCGCTTTCTCCTTTCTCCCTTCGGGGA
[HE]_p3548_edge_2	GCCTTATCCGGTAACTTCAGCCCGACCGCTGCAC
[HE]_p3548_edge_3	CTTTTCTACGGGGTCTAAGAAGATCCTTTGATAG
[HE]_p3548_edge_4	GTTTTAAATCAATCTATTAAATTAAAAATGAATC
[HE]_p3548_edge_5	ACCAGCTCAGAAAACGTTCGTACCCACGTA
[HE]_p3548_edge_6	GACTCACTATAGGGAGTGAGCGCGCGTAAT
[HE]_p3548_edge_7	CTTGACGGGGAAAGGGAGCCCCCGATTTAG
[HE]_p3548_edge_8	TATCAGGGCGATGGAAAGGGCGAAAAACCG
[HE]_p3548_edge_9	CTTAATCAGTGAGGCACTGACAGTTACCAATGCA
[HE]_p3548_edge_10	CCCAGTGCTGCAATGAGGGCTTACCATCTGGCGA
[HE]_p3548_edge_11	CCTCCGATCGTTGTCAGGTTAGCTCCTTCGGTAC
[HE]_p3548_edge_12	TGGTGAGTACTCAACCGATGCTTTTCTGTGACAA

[HE]_p3548_edge_13	CCGCGGTGGAGCTCGTTCTAGAGCGGCCGC
[HE]_p3548_edge_14	AAAAACTCTCGTACAGGAAGCTGTACTGCG
[HE]_p3548_edge_15	GCAGAGAGCTCAAAGCCAGGGAAAAAAGAT
[HE]_p3548_edge_16	AAAGTCACCAATCGTGAGCGATTGACAGGA
[HE]_p3548_edge_17	GGCGTAATCATGGTCAGGTTAATTGCGCGCTTAA
[HE]_p3548_edge_18	GTGAGCTAACTCACATCTGGGGTGCCTAATGATA
[HE]_p3548_edge_19	CCGCCCCCCTGACGAGCGTTTTTCCATAGGCTTG
[HE]_p3548_edge_20	CTCCTGTTCCGACCCTAGCTCCCTCGTGCGCTTC
[HE]_p3548_edge_21	CAAGAGTCCACTATTGTTGTTCCAGTTTGG
[HE]_p3548_edge_22	AATTTTTGTTAAATTTGTTAAAATTCGCGT
[HE]_p3548_edge_23	TTGAGATCCAGTTCTCAAGGATCTTACCGC
[HE]_p3548_edge_24	TTGCCCGGCGTCAAGCGGCGACCGAGTTGC

Table S2.47. Core staples of M13mp18 equilateral triangular DNA origami tile.

Name	**Sequence**
[TR]_M13_core_1	GGGCGATGGCCCACTACGTGAAGAGGTGCCGTAAAGCGAGCTTGA
[TR]_M13_core_2	GATTTAACTAAATCGGAATTTTTGAGTGTTGTTCCAAAAGA
[TR]_M13_core_3	CGGGGAAAAAGCGAAAGGAGCGGCCGCGCT
[TR]_M13_core_4	ATAGCCCGAGTTTTTTGGGAGCCCCC
[TR]_M13_core_5	TCGTTAGACGTAACCACCACACCCGGCGCTA
[TR]_M13_core_6	GGGCGCTGGCAAGTTTTTTTCAAGCGGTCCACGCTGGTTTGTTGCCCTT
[TR]_M13_core_7	TAATGCGCGAGCACGTATAACGCGCCAGAA
[TR]_M13_core_8	CGGCCGGCCCTGAGTTTTTTCACGCTGCGATCAG
[TR]_M13_core_9	ATTAACCGTTAGACAGGAACGGTATGCTTTCC
[TR]_M13_core_10	AGCGGGAGCTTTTTTTTAATGAAT
[TR]_M13_core_11	TCCTGAGAAAAGAGTCTGTCCAGGTAATAT
[TR]_M13_core_12	AAGGGATTTTGTAGCAATACTTCTTGAGTAGA
[TR]_M13_core_13	TTCCACACAGTCGGGAAACCTGTCGTTTTTAGGCCGATTA
[TR]_M13_core_14	TGACGCTCAACTATCGGCCTTGCTTCACGCAA
[TR]_M13_core_15	TTTCCTGTCATCACTTGCCTTGATTATTTGTTATCCGCTG
[TR]_M13_core_16	CCAGAACCGCTCATGGAAATACTTCTGACC
[TR]_M13_core_17	AGAACTCAAATCGTCTGAAATGGAAAGGGACA
[TR]_M13_core_18	GAACTGATAACAGAGATAGAACCCCTACATTT
[TR]_M13_core_19	AGTAATAATTATTTACATTGGCAGTTGCAAGGCGATTAAGTCGCCAGCT
[TR]_M13_core_20	TGAAAGCATGGCTATTAGTCTTCAGCAGCA
[TR]_M13_core_21	TTCTGGCCAGCCCTAAAACATCGCAACACCGC
[TR]_M13_cor	GGCGAAAGGGGGTTTTTAGTCACACGACC

e_22	
[TR]_M13_core_23	GTCAGTTGGTGCCACGCTGAGAGCTAATGCGC
[TR]_M13_core_24	GAGGAAGGAGGCGGTCAGTATTCATTAAAA
[TR]_M13_core_25	ATACCGAACGAACCACCTTTTTGGGGACGACGACAGTATCGGCCTCATGGGCGCA
[TR]_M13_core_26	AATGAAAATCAAACCCTCAATCCAATTCGA
[TR]_M13_core_27	CTGCAACAGCAAATCAACAGTTGATTTGAGGA
[TR]_M13_core_28	AATAGGAACGTGCATCTGCCAGTTTTTTTGATAAAACAGAGGTGTTATCTA
[TR]_M13_core_29	TTTTGCGGTATTAGACTTTACAAAAATATCTG
[TR]_M13_core_30	GGAATTATCAATAGATAATACAAAGGAATT
[TR]_M13_core_31	AAATATCTTTATTTTTTATTTTTTAACC
[TR]_M13_core_32	CAACTCGTAAAAGTTTGAGTAACGTAAAAC
[TR]_M13_core_33	TTTAGAAGAACAAAGAAACCACCAGGTTAGAA
[TR]_M13_core_34	TAGAGCCGTCATCATATTCCTGATTTGTTTGGATTATACTGCTTTGAA
[TR]_M13_core_35	AAATTTTTGTTAAATTTTTTTTTAACAACTAATAGAT
[TR]_M13_core_36	CTTTTACAATCAAAATTATTTGCACATTATCA
[TR]_M13_core_37	CCTGATTTCTGAATAATGGAAGGAAGGAGC
[TR]_M13_core_38	CCTGATATCAGATGATGTTTTTTGAGATCT
[TR]_M13_core_39	AGAAATAAGATGAATATACAGTAAATTAAT
[TR]_M13_core_40	CCTACCATTCGGGAGAAACAATAAAAGAAGAT
[TR]_M13_core_41	GAGTAGGTAATAAGTTTTTTTTTATATAAT
[TR]_M13_core_42	GTGAGTGAAAACATCAAGAAAACAAACAGTAC
[TR]_M13_core_43	GCTATTACAATTACCTGAGCAACGGATTCG
[TR]_M13_core_44	TACCAAGTTACAAAATTTTTTTCACCCTCAGAGCCGC

[TR]_M13_core_45	TACATTTAAACAGTACATAAATTATCAAAA
[TR]_M13_core_46	GATGAAACATAACCTTGCTTCTGTATTAAGAC
[TR]_M13_core_47	ATTCATTTATTAATTTTCCCTTTTTTTTTGCACCGTAATCAGTCTCAGAAC
[TR]_M13_core_48	CGCCACCCTCATTTTTTAGAGGCGAATT
[TR]_M13_core_49	AAATGCTGGAGTCAATAGTGAATTCAATATAT
[TR]_M13_core_50	TCACCAATGAAACCATCTTTTTCCTTGAAAACATAGCGATAGCTTAGAAATCGTC
[TR]_M13_core_51	TCATAGGGGTTGGGTTATATAATGAAATAC
[TR]_M13_core_52	GCTGAGAAATGCAAATCCAATCGCTAATTTCA
[TR]_M13_core_53	AGCCTGTTCCTAAATTTAATGGTTCTATATGT
[TR]_M13_core_54	AACCGATTGGTTTACCAGCGCCAATTCAAATATATTTTAGTAAGACAAA
[TR]_M13_core_55	GAACGCGAGAAATTTTTAGGGCGACATTC
[TR]_M13_core_56	CGACCGTCCGGAATCATAATTACATATTTA
[TR]_M13_core_57	TCTTCTGATAGTATCATATGCGTTACGCTCAA
[TR]_M13_core_58	ACCGACAACTTAATTGAGAATCGCCTAGAAAA
[TR]_M13_core_59	AAATTCTTGGCATGATTAATACCCAATTTAAAGCCAATAC
[TR]_M13_core_60	ACAACGCCCAGTAATAAGAGAAACGCGCCT
[TR]_M13_core_61	CAGTAGGGAAGGTAAAGTAATTCTGTTTTTCCCAATAATA
[TR]_M13_core_62	TGTAGAAAGTTCAGCTAATGCAGATATAAAGT
[TR]_M13_core_63	GTTTATCTATCCCATCCTAATTCGGGTATT
[TR]_M13_core_64	AACATCCAATCAATTTTTTTACAGAGAGAAACCC
[TR]_M13_core_65	ACAAGAATTTTTTTTACAATAAAC
[TR]_M13_core_66	AAAAATGAAAATAGTTTTTTCTTTCCTTATCATTCCAAGAATACGAGCA
[TR]_M13_cor	AAACCAATTTATTTTCATCGTATATAGAAG

e_67	
[TR]_M13_core_68	AATTTGCAACGCTAACGATTTTTAAGCAAATCAGAGGAATC
[TR]_M13_core_69	ATTACCGCGCTTTTTTTCCAGAGCCT
[TR]_M13_core_70	GCTTATCCGAACCTCCCGACTTGCGGGAG
[TR]_M13_core_71	TTTGAAGCCTTAAATCAAGATTTATCCTGAATCTTACCCAGTTAC
[TR]_M13_core_72	AAAATAAAAACGATTTTTTGTTGAAGCGCA
[TR]_M13_core_73	AGAGAGATATAACATAAAAACAGGTAACGTC
[TR]_M13_core_74	TTAGACGGAGGGTAATTGAGCGATAGCTAT
[TR]_M13_core_75	CGAGGAAAAAACAATGAAATAGCACTAATATC
[TR]_M13_core_76	CTTACCGGAACAAAGTTACCAGAGAAAATA
[TR]_M13_core_77	AGAGCAAGCGCAATAATAACGGAAGACTCCTT
[TR]_M13_core_78	TCACAATCGTATGTTAGCAAACGTAAGGAAAC
[TR]_M13_core_79	CATACATCACCACGGAATAAGTTTCATTAA
[TR]_M13_core_80	ATTACGCAAATAGAAAATTCATATGAGGGAGG
[TR]_M13_core_81	TAGCACCAATATTGACGGAAATTATTATTTTG
[TR]_M13_core_82	AGGTGAAATTAGAGCCAGCAAACATCGGCA
[TR]_M13_core_83	GAAGGTAATTACCATTAGCAAGGCTTTGCCTT
[TR]_M13_core_84	AGAGCCACGACTGTAGCGCGTTTTATCACCAG
[TR]_M13_core_85	CGCCACCAGCGACAGAATCAAGCGGAAACG
[TR]_M13_core_86	TTTTCGGTCATAATCAAAATCAAGACGATT
[TR]_M13_core_87	TAGCGTCACACCGGAACCGCCTCCCCGCCAGC
[TR]_M13_core_88	AATTTACCGAGGTTGAGGCAGGTCCCGGAACC
[TR]_M13_core_89	TTTTGATCCACCACCAGAGCCGCTCAGAGC

[TR]_M13_core_90	GGCCTTGCAGAATGGAAAGCGCAAAGTATT
[TR]_M13_core_91	ATTGACAGGTTCCAGTAAGCGTCAGCCTATTT
[TR]_M13_core_92	CACCAGAAGATACAGGAGTGTACTACAGTGCCCGTATAAAGAATAGGT
[TR]_M13_core_93	GATAAGTGATTATTCTGAAACATGAGTCTCTG
[TR]_M13_core_94	TAGCCCGCAGTTAATGCCCCCTTACATGGC
[TR]_M13_core_95	AAGAGGCGGGGTTTTGCTCAGTTCAGGGAT
[TR]_M13_core_96	CGGAACCTCCGTCGAGAGGGTTGAAACCGCCA
[TR]_M13_core_97	ACAAACCGGAGAGGGTATTTTTTGTGCCTT
[TR]_M13_core_98	CGCCTGTAGCCACCACCCTCATTTACCAGGCG
[TR]_M13_core_99	TTAGCGTAACCGCCACCCTCAGTATAAGTA
[TR]_M13_core_100	GTATCACCGTACTCATTTTTTTACATTATGACCCTGT
[TR]_M13_core_101	AGCAAGCTTCGTCACCAGTACAAACAGTTT
[TR]_M13_core_102	CCCTCAGAGCATTCCACAGACAGCTTTTCTGT
[TR]_M13_core_103	ACCCTCAGAACGATCTAAAGTTTTTTTTTACCATTAGATACATATAAAGCT
[TR]_M13_core_104	AAATCGGTTGTTTTTTTTTAGTACCGCC
[TR]_M13_core_105	AAAATCTCTTGCTAAACAACTTTCAACTACAA
[TR]_M13_core_106	CTGCGAACGAGTAGATTTTTTTGTCTTTCCAGACGTTAGTAAATGAACCTCATAG
[TR]_M13_core_107	CAGCGGACGAATAATAATTTTTTTGCGCCG
[TR]_M13_core_108	ATGGGATTCAAAAAAAAGGCTCCAGGTGAATT
[TR]_M13_core_109	GTTAAAGGAGCTTGATACCGATAGTCACGTTG
[TR]_M13_core_110	GCTCCTTTCTCCAACAGGTCAGGATATCAGCTTGCTTTCGAAAAGGAGC
[TR]_M13_core_111	CTTTAATTGTATTTTTTGTACCTTTAATT
[TR]_M13_cor	ACAATGATCGGTCGCTGAGGCTTGAGGACT

e_112	
[TR]_M13_core_113	TCTTAAACCCGCTTTTGCGGGATCCGGAACGA
[TR]_M13_core_114	CACCAACCACGGCTACAGAGGCTTTGCAGGGA
[TR]_M13_core_115	CCCTCAGTTCAAAAATCAGAGAATGATTTACAGCATGTCA
[TR]_M13_core_116	AAAGACTAATACGTAATGCCACTACCAAGC
[TR]_M13_core_117	GGGTAGCATAAAACGAAAGAGGCAAATTTTTTTTGCAAAA
[TR]_M13_core_118	CTGCTCCATGACCCCCAGCGATTATACGAAGG
[TR]_M13_core_119	GCGAAACTAAATTGTGTCGAAAGGGAACCG
[TR]_M13_core_120	ATCTTTGTTACTTATTTTTTTTAGGAATAAAAAA
[TR]_M13_core_121	CCAAAATAGTTTTTTAAAACACTC
[TR]_M13_core_122	AGAAAGATTCATCATTTTTTGGCGCAGACGGTCAATCATAATCCGCGAC
[TR]_M13_core_123	AACTGACAGACCAGGCGCATAGACCGGATA
[TR]_M13_core_124	ATTATATTACCTTATGCGTTTTTATCTTGACAAGAGCTGGC
[TR]_M13_core_125	TGACCTTCATTTTTTTGAACTGGCTC
[TR]_M13_core_126	TTCATTACAGTGAATAAGGCTTGCCCTGA
[TR]_M13_core_127	AGAAACACCAGAACGAGTAGTATTTAATCATTGTGAACCAGTCAG
[TR]_M13_core_128	GACGTTGACGGAACAACATTATCAGATACA
[TR]_M13_core_129	ACGACGATCCACATTCAACTAATGTACAGGT
[TR]_M13_core_130	TAACGCCCTATCATAACCCTCGGTAAAATG
[TR]_M13_core_131	ATGCTTTAGCCAGAGGGGGTAATATTTACCAG
[TR]_M13_core_132	TTTAGACAATATTCATTGAATCAGCGGATT
[TR]_M13_core_133	GAAGTTTTAACAGTTCAGAAAACGGTCTTTAC
[TR]_M13_core_134	AAAGCGAATTATAGTCAGAAGCAACCCCTCAA

[TR]_M13_core_135	GCATCAATATCGCGTTTTAATTGCTTAATT
[TR]_M13_core_136	CCTGACTACCAGACCGGAAGCAAATGATAAGA
[TR]_M13_core_137	GTTTCATTTTGCGGATGGCTTAGACGAGCTTC
[TR]_M13_core_138	GCTGAATCAACTAAAGTACGGTCGAGCTGA
[TR]_M13_core_139	GGTCATTTCCATATAACAGTTGATTAACCTGT
[TR]_M13_core_140	GCAAAGAAATTTTCATTTGGGGCGGTCTGGAA
[TR]_M13_core_141	TCAGAGCTTCGCAAATGGTCAATCCCAATT
[TR]_M13_core_142	AAAGGTGATCCAATAAATCATACCTCATAT
[TR]_M13_core_143	TTAGCTATTTAGCAAAATTAAGCATATTTCAA
[TR]_M13_core_144	GACAGTCATAAAAATTTTTAGAACCAGGCAAG
[TR]_M13_core_145	CCGTTCTTGCGGGAGAAGCCTTATAAAGCC
[TR]_M13_core_146	ATTTTAATCAAAAGGGTGAGAAAACTAGCA
[TR]_M13_core_147	CGCAAGGAAATCACCATCAATATGCAAACAAG
[TR]_M13_core_148	AATACTTTAGCTGATAAATTAATGGGCTATCAGGTCATTGTTCGCATT
[TR]_M13_core_149	GCAAATATTGAACGGTAATCGTAAAGGCCGGA
[TR]_M13_core_150	GTTAAAACCTGAGAGTCTGGAGATATTCAA
[TR]_M13_core_151	TGTCAATCCAAAAACAGGAAGATCAACATT
[TR]_M13_core_152	AGAATCGATTAAATTGTAAACGTTTTCGCGTC
[TR]_M13_core_153	TGGGATAGCTGTAGCCAGCTTTCATTGTATAA
[TR]_M13_core_154	TCGTAACCGCCATCAAAAATAAAATATTTT
[TR]_M13_core_155	AAATGTGAACAAACGGCGGATTCGCTTCTG
[TR]_M13_core_156	TGGCCTTCGTCACGTTGGTGTAGAGGAAGATC
[TR]_M13_cor	TCGGTGCGGCCAGCTTTCCGGCACGACCGTAA

e_157	
[TR]_M13_core_158	GTGCCGGTGCGCAACTGTTGGGTTGTAAAA
[TR]_M13_core_159	GCACTCCAGGCCTCTTCGCTATTATGGGTAAC
[TR]_M13_core_160	CTCGAATTTTTCCCAGTCACGACGAAGGGCGA
[TR]_M13_core_161	CGACGGCCTAGAGGATCCCCGGGCATAAAG
[TR]_M13_core_162	GCCAGGGTCGTAATCATGGTCATAGCTCACAA
[TR]_M13_core_163	CGCTTTCCAACATACGAGCCGGAAGTACCGAG
[TR]_M13_core_164	TGTAAAGTTAATTGCGTTGCGCCGGTTTGC
[TR]_M13_core_165	CACCGCCTAACGCGCGGGGAGAGGTCACTGCC
[TR]_M13_core_166	GTATTGGACGGGCAACAGCTGACCCCAGCA
[TR]_M13_core_167	GGCGAAAAATCCCTTATAAATCAGTTTGGA
[TR]_M13_core_168	ACAAGAGCAAAGGGCGAAAAACCGTCTAT

Table S2.48. Edge staples of M13mp18 equilateral triangular DNA origami tile.

Name	**Sequence**
[TR]_M13_edge_1	ACTATGGTTGCTTTGACCGCTACAGGGCGCGTTG
[TR]_M13_edge_2	AGTGAGGCCACCGAGTAAGTGTTTTTATAATCCA
[TR]_M13_edge_3	CAGACAATATTTTTGAGTAAGAATACGTGGCATT
[TR]_M13_edge_4	TTGCTGAACCTCAAATAATCTAAAGCATCACCTT
[TR]_M13_edge_5	ACCTTTTTTAATGGAACAATTTCATTTGAA
[TR]_M13_edge_6	TAACCTCCGGCTTATCTGAGAGACTACCTT
[TR]_M13_edge_7	GAGGCATTTTCGAGCAACATGTAATTTAGG
[TR]_M13_edge_8	AACAAGAAAAATAAAACAATAGATAAGTCC
[TR]_M13_edge_9	GTTCCGAAATCGGCAAATCCTGTTTGATGGTGTC
[TR]_M13_edge_10	CCTGAACAAAGTCAGGAGAATTAACTGAAC
[TR]_M13_edge_11	GTAAGCAGATAGCCAAGCCCTTTTTAAGAA
[TR]_M13_edge_12	AGTGAGCTAACTCACACCTGGGGTGCCTAATGAA
[TR]_M13_edge_13	TGAGCCATTTGGGATTATCACCGTCACCGA
[TR]_M13_edge_14	CATTCGCCATTCAGGCAAACCAGGCAAAGCGCCT
[TR]_M13_edge_15	TCGGATTCTCCGTGGGAGCGAGTAACAACCCGAG
[TR]_M13_edge_16	ATCCTCATTAAAGCATATTCACAAACAAAT
[TR]_M13_edge_17	ATGTGTAGGTAAAGATATGCAATGCCTGAGTAAA

[TR]_M13_edge_18	CCGTAACACTGAGTCCAATAGGAACCCATG
[TR]_M13_edge_19	AACTAAAGGAATTGGTGAGAATAGAAAGGA
[TR]_M13_edge_20	ACATGTTTTAAATATGATAATGCTGTAGCTCAAC
[TR]_M13_edge_21	CATTAAACGGGTAATTTTCATGAGGAAGTT
[TR]_M13_edge_22	CTGCGGAATCGTCATATGGATAGCGTCCAATATC
[TR]_M13_edge_23	CATAGTAAGAGCAACAAAAAGGAATTACGAGGTT
[TR]_M13_edge_24	GATGAACGGTGTACCAACTTTGAAAGAGGA

Table S2.49. Core staples of M13mp18 square DNA origami tile.

Name	**Sequence**
[SQ]_M13_core_1	GCTGAGGCTTGCAGGGAGTTAAACGAAAGACAGCATCGCATGAGGA
[SQ]_M13_core_2	AGGCAAAAGGACTAAAGACTTTTTGAACGA
[SQ]_M13_core_3	GGGTAGCAACTTTCGAGGTGAA
[SQ]_M13_core_4	AGTTTCCAAGGCACCAACCTAAGATTTGTA
[SQ]_M13_core_5	TGAGAAGTTTATCATTTTGGCTTTGAGAATAC
[SQ]_M13_core_6	GCGCAGACAACAAAGTACAACGGAAACGAAAG
[SQ]_M13_core_7	ACTAAAACACTTTTTTTTCAGCGGAG
[SQ]_M13_core_8	TCATCGCCCATGTTACTTAGCCGTAATCTT
[SQ]_M13_core_9	AAGCGCGAGGTCAATCATAAGGGACAGGCGCA
[SQ]_M13_core_10	GATTTTGCTAAACAACTTTTTTCCCCAGCGATTATACC
[SQ]_M13_core_11	GCTTGCCCCTGACCTTCATCAAGAGGAACGAG
[SQ]_M13_core_12	GTAAATTGAACGGTGTACAGACACCGAA
[SQ]_M13_core_13	CTGACCAACTTACCGTAACA
[SQ]_M13_core_14	GACAAGAAAGCTGCTCATTCAGAAATCTAC
[SQ]_M13_core_15	TAGGCTGGTGACGAGAAACACCAGGCTCATTA
[SQ]_M13_core_16	TCAGTACCAATAGGTTTTGGACAGATGGGCTT
[SQ]_M13_core	TAGGAATAAGGACGTTGGGAAGAATGAATAAG

_17	
[SQ]_M13_core_18	TAACGCCCGATTTTAAGAACTGAACGAGTA
[SQ]_M13_core_19	GAGATGGTTTTTTTTTTGGGGTTTTGC
[SQ]_M13_core_20	GTTAATAAGAAAGATTCATCAGTTTAGACT
[SQ]_M13_core_21	TACCAGTCCCACATTCAACTAATGGAAGTTTT
[SQ]_M13_core_22	ACCTTATGAAAAGGAATTACGAGGAAAACCAA
[SQ]_M13_core_23	CCTCAAGAGAAGGATTTTTTTTTTTAATCATTGTGAATT
[SQ]_M13_core_24	TGCTTTAAGGGTAATAGTAAAATGTTGAGATT
[SQ]_M13_core_25	ATAAATCGAGGCTTTTGCAAAACAGATACA
[SQ]_M13_core_26	AGATTACCCTGACTATTATAGTTTACCAGACGACGATACATAGT
[SQ]_M13_core_27	AAGAGCAACATGAATGGAAAG
[SQ]_M13_core_28	GGATAGCATATTCATTGAATCCGAAGCAAA
[SQ]_M13_core_29	GCCAGAGGACAGTTCAGAAAACGATTTTAATT
[SQ]_M13_core_30	AATAGCGAAAAAATCAGGTCTTTAAGAGGAAGCCCGAAAGGCTCAACA
[SQ]_M13_core_31	ACCTTTTTTTTTTAGCCCCCTATCCTCATTTTTTACCCTCGT
[SQ]_M13_core_32	CGGATGGCAAAGCGAACCAGACCGCCCTCAAA
[SQ]_M13_core_33	TGCTGTAACTTCAAATATCGCGGAATGACC
[SQ]_M13_core_34	CAGAAGCATTTTTCTGTCGTGATAAATCATTTTTCAAGAAAA
[SQ]_M13_core_35	CTCCAACCTTTTGATAAGAGGTTTTGACCA
[SQ]_M13_core_36	CGAGCTTCTTAGAGCTTAATTGCTTGATTCCC
[SQ]_M13_core_37	GCTTTCCAGTTTGCATCAAAA
[SQ]_M13_core_38	TGAAAAGGGAACGAGTAGATTTAGCATTTTTG
[SQ]_M13_core_39	GCAAAGAATAGTAGTAGCATTATTCCATATAACAGTGAATATAA

[SQ]_M13_core_40	TGTTTTAAATATGCAATTTTTTTAAGCTTGCATGCCTGC
[SQ]_M13_core_41	TTAGATAATATTTTCATTTGGGCATAAAGC
[SQ]_M13_core_42	AATTCTGCTGGCATCAATTCTACTAATTAGCAAAATTAAGGGATAAAA
[SQ]_M13_core_43	AGTTTCAACATCCATTTTCGCTTCTGGACGTT
[SQ]_M13_core_44	GTAAAACGACTTTTTTTGGTGTCTGGA
[SQ]_M13_core_45	CAACGCAACAATAAAGCCTCAGAGGCGCGAGC
[SQ]_M13_core_46	TAAATCGTTTTGCGGGAGAAGCTCAAAAGG
[SQ]_M13_core_47	CAGCCAGCTTTACAGGCAAG
[SQ]_M13_core_48	ATCTACAGCTGATAAATTAATGATGTGTAGGTAAAGATCTTTATTT
[SQ]_M13_core_49	ATTTTTAGAACCCTCATTTTTTCCCGTCGGATTCTCCG
[SQ]_M13_core_50	GTGAGAAATATTCAACCGTTCTAAAGGCTA
[SQ]_M13_core_51	TGAGTACCGGAGAGTTTTGTTAAAATTCAACA
[SQ]_M13_core_52	TTAAATGTGATTTTTTTATGCAATGCC
[SQ]_M13_core_53	TCAGGTCCGATGAACGGTAATCGTAAAACT
[SQ]_M13_core_54	TTGTAAACGTTTTTTTTGAGAG
[SQ]_M13_core_55	TCCAGAGCCTAATTTGCCAGTTACAAATAAGAAACGATACATAAAA
[SQ]_M13_core_56	GAGCGCTACTTTACAGAGAGAATATTTTTG
[SQ]_M13_core_57	TTTAACGTCATTAGGTTTTGAA
[SQ]_M13_core_58	ACAGGGACTGAACAAAGTCAGACAATAGCT
[SQ]_M13_core_59	TTTTATCCTCCCGATTTTATAGCAGCATATCA
[SQ]_M13_core_60	ACCGAGGAAGAAACAATGAAATAGGGGTAATT
[SQ]_M13_core_61	GAGAGATAACTTTTTTTAGCAAGCCGT
[SQ]_M13_core	ATCTTACCCGAACAAAGTTACCTGGCAACA

_62	
[SQ]_M13_core_63	TAAGAGCAAACGCAATAATAACGGGTTAGCAA
[SQ]_M13_core_64	ACCAAGTACCGCACTCTTTTTTGAGTTAAGCCCAATAA
[SQ]_M13_core_65	ATATGGTTAATACATACATAAAGGAGAAGGAA
[SQ]_M13_core_66	GACATTCCTTATTACGCAGTATAATACC
[SQ]_M13_core_67	CAAAAGAACTTGCAGAACGC
[SQ]_M13_core_68	TATAAAATTGTCACAATCAATAGCAAAATC
[SQ]_M13_core_69	ACGTAGAATACCAGCGCCAAAGACCACCGACT
[SQ]_M13_core_70	TACCAGCAACATGTTTTTTAAGACTCAACCGA
[SQ]_M13_core_71	CACCGTAATTGGGAATTAGAGCCAGAAAATTC
[SQ]_M13_core_72	CCTTTAGGTGAATTATCACCGTAAAAGGGC
[SQ]_M13_core_73	TTGAGGGAGGTTTTTTTTACAAATTCT
[SQ]_M13_core_74	ACCAGTAACCAATGAAACCATCACCCTCAG
[SQ]_M13_core_75	TGAGCCATTCAGTAGCGACAGAATCCACCACC
[SQ]_M13_core_76	CATTAAAGCGTCAGACTGTAGCGCCTTTTCAT
[SQ]_M13_core_77	AGCCTGTTTAGTATCATTTTTTTATTGACGGAAATTATT
[SQ]_M13_core_78	GAGCCGCCCTCCCTCAGAGCCGCCGATAGCAG
[SQ]_M13_core_79	CAGGTCATCACCGGAACCAGAGCAAGTTTG
[SQ]_M13_core_80	CGCAGTATTCACAAACAAATAATATTAGCGTTTGCCATGTTTTC
[SQ]_M13_core_81	ATCGGCATTTTGCTTAGGTTG
[SQ]_M13_core_82	AACCGCCAGCCGCCACCAGAACAATAAGTT
[SQ]_M13_core_83	GGAACCGCGCCAGCATTGACAGGACATGGCTT
[SQ]_M13_core_84	AATCAAAAGACGATTGGCCTTGATCTCTGAATTTACCGTTCTGAGACT

[SQ]_M13_core_85	TCGGAACCACAGGAGTGTACTGGTCACCACCA
[SQ]_M13_core_86	TAAGAGGCCAGTAAGCGTCATAGGTTGAGG
[SQ]_M13_core_87	TTAACGGACAGTTAATGCCCCCAATAGGTG
[SQ]_M13_core_88	TTGATGATTATTATTCTGAAACATCCGTCGAG
[SQ]_M13_core_89	CCCTCAGATATAAGTATAGCCCGGTGCCTATT
[SQ]_M13_core_90	CTGAGTTCAGGGATAGCAAGCCCAGGCGGATAAGTGGAAAGTAT
[SQ]_M13_core_91	TATCACCAACCGCCACCCTCAGCATTCCAC
[SQ]_M13_core_92	AGGGTTGAGCCACCACCCTCATTTTTCGTCACCAGTACAACTGTATGG
[SQ]_M13_core_93	TGAATTTTACTACAACGCCTGTAGAACCGCCA
[SQ]_M13_core_94	AGACAGCTCGTCTTTCCAGACGAAGGAATT
[SQ]_M13_core_95	TTTCTTGCCTTTAATTGTATCGTAGAAAGGAACAACTATTAGTAAA
[SQ]_M13_core_96	GCGAATAAAGGCTCCAAAAGGAAAACAGCT
[SQ]_M13_core_97	TGATACCCCCACGCATAACCGATATATTCG
[SQ]_M13_core_98	AAGAATACGTGGCACAGACAATAACTGATAGCCCTAAAAGGTGAGG
[SQ]_M13_core_99	TAAAGCATGCAGAAGATAAAACAGACATCG
[SQ]_M13_core_100	CCATTAAAAATTTTTACATTGG
[SQ]_M13_core_101	CGGTCAGGAGCCAGCAGCAAATAAGGAATT
[SQ]_M13_core_102	TCAAACCGTCTGAATTTTAACCACCACACCTT
[SQ]_M13_core_103	GATAATACGCAAATCAACAGTTGAGAAAAATC
[SQ]_M13_core_104	GCTGAACCTCTTTTTTTGTAGAAGAAC
[SQ]_M13_core_105	GAGGAAGCTAATAGATTAGAGCCATTATCA
[SQ]_M13_core_106	GTCAGTTGATTTGAGGATTTAGAACCGAACGT
[SQ]_M13_core	GATTAGTAATAACATCTTTTTTCCTCAATCAATATCTG

_107	
[SQ]_M13_core_108	TGATGGCATTAAAAGTTTGAGTAACGTCAATA
[SQ]_M13_core_109	TTGGATTTATTAAATCCTTTGCGTATTA
[SQ]_M13_core_110	GACTTTACAACAGGAGGCCG
[SQ]_M13_core_111	TTTTGCGTCATCATATTCCTGATCAGATGA
[SQ]_M13_core_112	TATTAATTATTCATCAATATAATCTAAAGAAA
[SQ]_M13_core_113	AAAGGACAGAGCGGTTTTACAACTCGATACTT
[SQ]_M13_core_114	AATACCAAATTTTCAGGTTTAACGTTATCAGA
[SQ]_M13_core_115	TTATTCACACGTAAAACAGAAACTGATTGT
[SQ]_M13_core_116	CTGAATAATGTTTTTTTACGTGGCGAG
[SQ]_M13_core_117	ATATACAAACGGATTCGCCTGAAATAACCT
[SQ]_M13_core_118	TTGCGTAGGTTACAAAATCGCGCAGGAAACAG
[SQ]_M13_core_119	ATTATTTGTTTCAATTACCTGAGCTAACAATT
[SQ]_M13_core_120	AGAGCTTGACGGGGAATTTTTTTAACCTACCATATCAAA
[SQ]_M13_core_121	AGCGATAGTCAATATATGTGAGTGTTGCTTTG
[SQ]_M13_core_122	TCAATAGATTACCTTTTTTAATGAGGCGAA
[SQ]_M13_core_123	GGTTATATAGGTCTGAGAGACTCAAAATTAATTACATTAAAAGA
[SQ]_M13_core_124	AGATGATGAATGCCCGAGATA
[SQ]_M13_core_125	TGCTTCTTCCCTTAGAATCCTTCAAATATA
[SQ]_M13_core_126	TACATAAACTTAGATTAAGACGCTATCGCAAG
[SQ]_M13_core_127	TCATTTGATGAATTTATCAAAATCATAACTATATGTAAATCTAGAAAA
[SQ]_M13_core_128	TAAGGCGTCGCGAGAAAACTTTTTGAAAACAT
[SQ]_M13_core_129	ATAATTAGCTGATGCAAATCCAGAGAAGAG

[SQ]_M13_core_130	TTTTAGTTGAAATACCGACCGTTTAACAAC
[SQ]_M13_core_131	ACAAAGAATAAATAAGAATAAACACAACAGTA
[SQ]_M13_core_132	CAAAAGGTTTGAGAATCGCCATATGTGATAAA
[SQ]_M13_core_133	GCCTGTGACGACGACAATAAATATAAAGCCAACGCTCCGGAATC
[SQ]_M13_core_134	GCCAACAAATAAGAGAATATAAAATAATAT
[SQ]_M13_core_135	GGGCTTAAAAAGTAATTCTGTCCATTATCAACAATAGATAGGTATTAA
[SQ]_M13_core_136	CAAGAACGAGTCCTGAACAAGAAAAGTACCGA
[SQ]_M13_core_137	CCCATCCTCGGCTGTCTTTCCTATTACCGC
[SQ]_M13_core_138	GCCTTAGAGGCGTTTTAGCGAATTTCATCGTAGGAATCTATCATTC
[SQ]_M13_core_139	GCCCAATGTATTCTAAGAACGCAATCAAGA
[SQ]_M13_core_140	TTAGTTGATCTTACCAACGCTAACGAGCGT
[SQ]_M13_core_141	ATGTCAATCATATGTACCCCGGTTTGTATAAGCAAATATTAAATCA
[SQ]_M13_core_142	AGCTTTCATCGCATTAAATTTTTGTTTAAA
[SQ]_M13_core_143	GCTCATTTCGCGTCTGGCCTTCTAATGGGA
[SQ]_M13_core_144	GACAGTATAACGGCGGATTGACCGCTGTAGCC
[SQ]_M13_core_145	TAGGTCAATCTGCCAGTTTGAGTGTTGGGA
[SQ]_M13_core_146	TGGGAACACGGCCTCAGGAAGATCCAAAGCGC
[SQ]_M13_core_147	GGCGATTAATTCAGGCTGCGCAACGGGACGAC
[SQ]_M13_core_148	CAGTCACGTGCCGGAAACCAGGGCACTC
[SQ]_M13_core_149	AGGGCGAGGCGAAAGGGGGATGAGCTGTTT
[SQ]_M13_core_150	CATTCGCCAGTTGGGTAACGCCAGGGTACCGA
[SQ]_M13_core_151	TAAAGCCTTCGTAATCATGGTCATTGCTGCAA
[SQ]_M13_core	TCACATTTCTAGAGGATCCCCGGGTTTTCC

_152	
[SQ]_M13_core_153	CCTGTGTATACGAGCCGGAAGCCAGTGAGA
[SQ]_M13_core_154	GCTCGAATGGGGTGCCTAATGAGTGTATTGGG
[SQ]_M13_core_155	AGGTCGACAATTGCGTTGCGCTCAATCGGCCA
[SQ]_M13_core_156	GGTCCACGTGGTTTTTCTTTTCACATAAAGTG
[SQ]_M13_core_157	TCCTGTTGGAGAGGCGGTTTGCGAGCTAAC
[SQ]_M13_core_158	GGGTTGATCGGCAAAATCCCTTCCAGCTGCATTAATGACTGCCC
[SQ]_M13_core_159	CGGGCAAGCCCTGAGAGAGTTGCGAAAAAC
[SQ]_M13_core_160	CGCCAGGGCTGGTTTGCCCCAGCATATTAAAG
[SQ]_M13_core_161	ACGCGCGGTGATGGTGGTTCCGAAAGTGTTGTTCCAGTTTCCCGATTT
[SQ]_M13_core_162	GGTGCCGTCTCCAACGTCAAAGGGCAGCAAGC
[SQ]_M13_core_163	GGGAGCCGGAACAAGAGTCCACGGCGAAAA
[SQ]_M13_core_164	CGTCTATCAAATCAAGTTTTTTCGGTCACG
[SQ]_M13_core_165	AACGTGGAAAAGCACTAAATCGGAAGGAGCGG
[SQ]_M13_core_166	CTTTGACGGCGCTGGCAAGTGTAGGGGGTCGA
[SQ]_M13_core_167	ATTAAATTTCCTCGTTAGAATAGGGAAGAAAGCGAAACCCTAAA
[SQ]_M13_core_168	CTGCGCGCTACAGGGCGCGTACCTGAGAAG
[SQ]_M13_core_169	GCGCTAGGAGCACGTATAACGTGCGGGATTTTAGACAGGAACTTCTTT
[SQ]_M13_core_170	GTAGCAATACGGTACGCCAGAATCTATGGTTG
[SQ]_M13_core_171	TGTTTTTGTCCATCACGCAAATAATATCCA
[SQ]_M13_core_172	CAGATTCATTTTGACGCTCAATTATCGGCCTTGCTGGTTAACCGTT
[SQ]_M13_core_173	GAACAATTCATGGAAATACCTACACCAGTC
[SQ]_M13_core_174	ACACGACATAGAACCCTTCTGACCTGAAAG

Table S2.50. Edge staples of M13mp18 square DNA origami tile.

Name	Sequence
[SQ]_M13_edge_1	GCATTTTCGAGCCAGTTGTAATTTAGGCAGAGCG
[SQ]_M13_edge_2	CCTAAATTTAATGGTTTAATTTCATCTTCTGACA
[SQ]_M13_edge_3	CATCGGGAGAAACAATGTAACAGTACCTTTTATA
[SQ]_M13_edge_4	AGAAGGAGCGGAATTAGAACAAAGAAACCACCCG
[SQ]_M13_edge_5	CTATTACGCCAGCTTCGGTGCGGGCCTCTT
[SQ]_M13_edge_6	CAATTCCACACAACGAAATTGTTATCCGCT
[SQ]_M13_edge_7	CGTGAACCATCACCCAGGGCGATGGCCCAC
[SQ]_M13_edge_8	CGCTTAATGCGCCGTAACCACCACACCCGC
[SQ]_M13_edge_9	CCAAATCAACGTAACAACCGGATATTCATTACGT
[SQ]_M13_edge_10	CAACATTATTACAGGTAAACGAACTAACGGAAAA
[SQ]_M13_edge_11	GTACCTTTAATTGCTCAGGTCAGGATTAGAGACA
[SQ]_M13_edge_12	AATAACCTGTTTAGCTCATTTCGCAAATGGTCAC
[SQ]_M13_edge_13	ACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ]_M13_edge_14	CAGTGCCCGTATAAGGTCAGTGCCTTGAGT
[SQ]_M13_edge_15	AGGCCGGAAACGTCGCACCATTACCATTAG
[SQ]_M13_edge_16	GGAATAAGTTTATTGAAACGCAAAGACACC

Table S2.51. Core staples of M13mp18 regular hexagonal DNA origami tile.

Name	Sequence
[HE]_M13_core_1	GGGCGATGGCCCACTACGTGAACCGCCGTAAAGCACTAAGGAAGAAA
[HE]_M13_core_2	ACCCGCCGGTGGCGAGAAAGGAAGATCGGAAC
[HE]_M13_core_3	CCTAAAGGGAGCCCCTTTTTTTTTAATAGCCCGAGATAG
[HE]_M13_core_4	GCGAAAGGTCACGCTGCGCGTAATTTTAGA
[HE]_M13_core_5	CGGCGAACCGCTTAATGCGCCGCTAGCGGGAG
[HE]_M13_core_6	CGGCAAAATCCCTTTTTTTTTTGACGGGGAAAGC
[HE]_M13_core_7	GAGTCTGTGAGGCCGATTAAAGGGACCACCAC
[HE]_M13_core_8	GCAATACCCTCGTTAGAATCAGACAGGG
[HE]_M13_core_9	CGCGTACTATGGTTTTTGTGGTTTTTCTTTTCACCATCGGCCA
[HE]_M13_core_10	CAGGAACATCAGTGAGGCCACCGCTCAATC
[HE]_M13_core	CTAAACAGCCATCACGCAAATTAAAAAAACGC

_11	
[HE]_M13_core_12	TGCTTTTTCTTTGATTAGTAATGAACAATA
[HE]_M13_core_13	ATCCGCTCGGGAGAGGCGGTTTGCGTCACGTATAACG
[HE]_M13_core_14	TAATAAAAATACCTACATTTTGACGAGTAAAA
[HE]_M13_core_15	GAACCCTAGCCATTGCAACAGGCCGTTGTA
[HE]_M13_core_16	CGCGAAAGAATACGTGGCACATTGCTGGTAATATCCAAACAT
[HE]_M13_core_17	CACTTGCCTGTTTTGCTGTTTCCT
[HE]_M13_core_18	GTCTGAAAGATTCACCAGTCACGAGGTGAG
[HE]_M13_core_19	TCATGGAAGGGACATTCTGGCCAATACCGAAC
[HE]_M13_core_20	TTACCGCCTCTGACCTGAAAGCGTACTGATAG
[HE]_M13_core_21	CTCGAATTCGTAATTTTTTTTCAAACTATCGGCC
[HE]_M13_core_22	CTAAAGCAAGCAGAAGATAAAACAACGACCAG
[HE]_M13_core_23	AAACCCTCATCGCCATTAAAAACAGAGATA
[HE]_M13_core_24	GACAATATTTTTGTTTTTTTTTGAGAGACTACCT
[HE]_M13_core_25	GCGGTCAAGAGCCAGCAGCAAACAACTAAT
[HE]_M13_core_26	GAACCACCTCACCTTGCTGAACCTAAGGTTATCTAAAATACTCGTATT
[HE]_M13_core_27	CCCTAAAACAATCAATATCTGGTCATACATCAAGAAA
[HE]_M13_core_28	GAATTTATCATTTTGTCTTTAATG
[HE]_M13_core_29	AACATTATACAAACAATTCGACAATCTTTAGGAGCACTAATGAAAAAT
[HE]_M13_core_30	TGAGCAAAAGAATTTTTAGTTGAAAGGAATTGAGGCAAATATC
[HE]_M13_core_31	AGATTAGGAAGTATTAGACTTTCATTTTGC
[HE]_M13_core_32	AAATCCTTTGCCCTTTTTTTTGATTTTCAGGTTT
[HE]_M13_core_33	GGAACAATATTCCTGATTATCAGATGATGGC

[HE]_M13_core_34	GTAAAACAGAAATAATTTTTTTTTTTTAAAAGTTTGAGT
[HE]_M13_core_35	TCAATATAATCCTGATTGTTTGGATACCATATCAAAATTAGTACCTT
[HE]_M13_core_36	CGCAGAGGATGAATATACAGTAACATTTGCAC
[HE]_M13_core_37	TTACATCTTGAATACCAAGTTACAGTACAT
[HE]_M13_core_38	AACGTCAGCGAATTATTCATTTCAAATTTCAT
[HE]_M13_core_39	CTTAGAATCCTTTTTTAATGGAAACAAAATCG
[HE]_M13_core_40	GATTAAGTTAATTACATTTAACATTACC
[HE]_M13_core_41	AAATCAATCGTCGCTATTAATTAGAAAACT
[HE]_M13_core_42	TTGAATTACCTTGAAAACATAGCGGATGCAAA
[HE]_M13_core_43	ACAAAAACGCTGAGAAGAGTCAAGGTTGGG
[HE]_M13_core_44	TTTGAAATCAAGACAAAGAACGCGAATTTTCC
[HE]_M13_core_45	TTAAATACTATATGTAAATGCTATAGCTTA
[HE]_M13_core_46	CTTACTCATAATTACTAGAAATTTTAACCTCCGGCTTATAGT
[HE]_M13_core_47	TTTTCAAATCTTCTGACCTAAACATGTAAT
[HE]_M13_core_48	TCCAATCGACCGACCGTGTGATAATAATTGAG
[HE]_M13_core_49	TTATATAAAGAATAAACACCGGAACAGTATAA
[HE]_M13_core_50	AATTCTGTTATTTAACAACGCCAATTTAATGG
[HE]_M13_core_51	GTTCAGCCTCAACAGTAGGGCTATAAGGCG
[HE]_M13_core_52	AAGCCTGTTTAGTTTTTTTTTCAGTATGTTAGCA
[HE]_M13_core_53	TTAGGCAAAAGTACCGACAAAATAGAAACC
[HE]_M13_core_54	AATCGCCACCAGACGACGACAATAAAAATAATATCCCATCAACAAGCA
[HE]_M13_core_55	AGCCAACGTAATGCAGAACGCGCCTTGTAATTGAGCG
[HE]_M13_core	ATGATTAAGATTTTTATACAAATT

_56	
[HE]_M13_core_57	ATAGCAAGTACCGCACTCATCGAGCTAATTTACGAGCATGGGTAAAGT
[HE]_M13_core_58	TGAACACCCTGATTTTTGATAAGTCCTGAACAAGAAACAACAT
[HE]_M13_core_59	AATCAATGGGTATTAAACCAAGCAAATCAG
[HE]_M13_core_60	AGCCGTTTTTATTTTTTTTTTTACAAAATAAACA
[HE]_M13_core_61	ATATAGATTTTAGCGAACCTCCCGACTTGCG
[HE]_M13_core_62	CGTCTTTCCAGAGCCTTTTTTTTTTCATTACCGCGCCCA
[HE]_M13_core_63	TTTGAAGCCTTAAATCAAGATTAGTGAATCTTACCAACGATAAGAAA
[HE]_M13_core_64	CAGGGAAGATTTATCCCAATCCAACTAACGAG
[HE]_M13_core_65	CGATTTTTTACAGAGAGAATAAAAGAAACA
[HE]_M13_core_66	GCCATATTCGCATTAGACGGGAGAACAAGAAT
[HE]_M13_core_67	AAAGTTACGCCCAATAATAAGAGCCATAAAAA
[HE]_M13_core_68	TAATAACTCAGAGAGATAACCCATTAAC
[HE]_M13_core_69	ATGAAATGAAAAGTAAGCAGATAATCAATA
[HE]_M13_core_70	TGAGTTAACAGAAGGAAACCGAGGAAAGACAC
[HE]_M13_core_71	CTAATAGGAATACCCAAAAGAAACATAAAG
[HE]_M13_core_72	CCGATTGAAAGTTTATTTTGTCACAGCCGAAC
[HE]_M13_core_73	AAATTATATATAAAAGAAACGCAAACGCAA
[HE]_M13_core_74	CAGTAATCACCGTCACCGACTAACGTAGAAAATACATCTGGC
[HE]_M13_core_75	GAAAATTAAAGACAAAAGGGCGTCAGTAGC
[HE]_M13_core_76	CACGGAATGGGAGGGAAGGTAAATCACCAATG
[HE]_M13_core_77	GTGGCAACTCATTAAAGGTGAATTGCACCATT
[HE]_M13_core_78	TAGCCCCCGATAGCAGCACCGTAAACATTCAA

[HE]_M13_core_79	TAATCAACAAGGCCGGAAACGTATTGACGG
[HE]_M13_core_80	TGAGCCATTTGGGTTTTTTTTGAGAATAGAAAGG
[HE]_M13_core_81	GACAGAAGTTTTCATCGGCATTCCTCAGAG
[HE]_M13_core_82	AAACCATCTTATTAGCGTTTGCCAACCCTCAGAACCGCCACTTGATAT
[HE]_M13_core_83	ACCATTAGAATCACCGGAACCAGAGTCACCACCCTCA
[HE]_M13_core_84	CTTTCAACAGTTTTGCAAAATCAC
[HE]_M13_core_85	GCAGTCTCAGGTCAGACGATTGGCCCCTCAGAGCCACCACTTCGGTCA
[HE]_M13_core_86	CCCTCAGAACCGTTTTTGCCTCCCTCAGAGCCGCCTCTTTTCA
[HE]_M13_core_87	CCGCCACACAGGAGGTTGAGGCTGAATTTA
[HE]_M13_core_88	TCACAAACAAATATTTTTTTTGAGAAGGATTAGG
[HE]_M13_core_89	CCGTTCCGGAGTGTACTGGTAATAAGTTTTA
[HE]_M13_core_90	AAGTATTAAGAGGCTTTTTTTTTTGCCAGAATGGAAAGC
[HE]_M13_core_91	TCAGTGCCTTGAGTAACAGTGCCCGAACCTATTATTCTGAGGCGGAT
[HE]_M13_core_92	GGTTTAGTGGTTTTGCTCAGTACCAAACATGA
[HE]_M13_core_93	AAGTGCCTAGGTGTATCACCGTGTCACCAG
[HE]_M13_core_94	ATTAGCGGACCGCCACCCTCAGAAATAGGAAC
[HE]_M13_core_95	GTTTTGTCCGTAACACTGAGTTTCACTCAGGA
[HE]_M13_core_96	ATTTTCTGGGATAGCAAGCCCACCGCCA
[HE]_M13_core_97	TACAAACCATAGTTAGCGTAACTGTATCGG
[HE]_M13_core_98	CCATGTACGTCTTTCCAGACGTTACCAAAAAA
[HE]_M13_core_99	TTTTCAGTATGGGATTTTGCTAGCGAATAA
[HE]_M13_core_100	AGTTGCGCAAAAGGAGCCTTTAATGATCTAAA
[HE]_M13_core	ACGCATATCACGTTGAAAATCTGTAAATGA

_101	
[HE]_M13_core_102	AGCAGGCTGAGGCTTGCAGGGAACAACTAAAGGAATTAACAA
[HE]_M13_core_103	TTTATCATTCTTAAACAGCTTGTCATGAGG
[HE]_M13_core_104	AAGGCTCCCGACAATGACAACAACGGCTACAG
[HE]_M13_core_105	TAATTTTTACCGATATATTCGGTCCGAAAGAC
[HE]_M13_core_106	GAGGCAAAAGGACTAAAGACTTTTATACCGAT
[HE]_M13_core_107	TGACCCCAACGAGGGTAGCAACCATCGCCC
[HE]_M13_core_108	AGTTAAAGGCCGCTTTTTTTTTATTATAGTCAGA
[HE]_M13_core_109	AAGTTTCGAAGGCACCAACCTAGCTCCATG
[HE]_M13_core_110	AGGCTTTGAGAATACACTAAAACACGCCTGATAAATTGTGAGATGAAC
[HE]_M13_core_111	AGCATCGGCAGCGATTATACCAAGCTCATAACCCTCG
[HE]_M13_core_112	AAAATCAGGTTTTTCGTCACCCTC
[HE]_M13_core_113	GAGTAATCAACTTTGAAAGAGGACTCGAAATCCGCGACCTAAACGAAA
[HE]_M13_core_114	CGAGGCATAGTATTTTTAACGGAGATTTGTATCATCTCATCTT
[HE]_M13_core_115	TTACTTAGGAACCGAACTGACCTTGACAAG
[HE]_M13_core_116	GGTGTACAGACCATTTTTTTTCAGGACGTTGGGA
[HE]_M13_core_117	AACCGGACTCATTCAGTGAATAAGGCTTGCC
[HE]_M13_core_118	TTTTAAGAACTGGCTTTTTTTTTTGCTGACCTTCATCAA
[HE]_M13_core_119	AGAAACACCAGAACGAGTAGTAAATCATTGTGAATTACCAACTAACG
[HE]_M13_core_120	AATGCAGACTACGTTAATAAAACGTTATGCGA
[HE]_M13_core_121	GAACAACATTTAGGAATACCACTTTGCCAG
[HE]_M13_core_122	AGAAAAATTACATAACGCCAAAAGCCAAAATA
[HE]_M13_core_123	TTCATTGACTTTTGCAAAAGAAGTATTCAACT

[HE]_M13_core_124	TTCAGAAAGACGACGATAAAAAGAATTA
[HE]_M13_core_125	AGGGGGTATACTGCGGAATCGTCGAACCAG
[HE]_M13_core_126	GCGAGAGGATCCCCCTCAAATGCTTCAAATAT
[HE]_M13_core_127	TTTACCAACGAGAATGACCATATCAAAAAG
[HE]_M13_core_128	TCCTTTTGAATTCGAGCTTCAAAGCATAAATA
[HE]_M13_core_129	CTTAGAGGAAGCCCGAAAGACTTTAAACAG
[HE]_M13_core_130	GAAGTAATGCTGTAGCTCAACAGCAAAGCGGATTGCAAATCA
[HE]_M13_core_131	ACCGGAAGATTAGAGAGTACCTTACATTTC
[HE]_M13_core_132	CGCGTTTTATAAGAGGTCATTTTTTGCGAACG
[HE]_M13_core_133	ATTAAGAGCTTAATTGCTGAATATTTCATTCC
[HE]_M13_core_134	TCAATTCTTAGTTTGACCATTAGATTAATTGC
[HE]_M13_core_135	CAATAAAGTTGATTCCCAATTCGCGGATGG
[HE]_M13_core_136	ATGTTTTAAATATTTTTTTTTACCAGGCAAAGCG
[HE]_M13_core_137	GCAAATGGGGCGCGAGCTGAAATTATGACC
[HE]_M13_core_138	AGTAGATTACTAATAGTAGTAGCAAGCATAAAGCTAAATCTTAAATGC
[HE]_M13_core_139	ATATAACATCATACAGGCAAGGCAATGTAGCCAGCTTT
[HE]_M13_core_140	GGCACCGCTTTTTTACGGTGTCTG
[HE]_M13_core_141	AAAGGCCGAGAACCCTCATATATTGGTTGTACCAAAAACAAGGTGGCA
[HE]_M13_core_142	AAAATAATTCGCTTTTTTAAGCAATAAAGCCTCAGTTAACATC
[HE]_M13_core_143	CTGTAATAGGATAAAAATTTTTGAGACAGT
[HE]_M13_core_144	AATGCCTGAGTAATTTTTTTTGTTGATAATCAGA
[HE]_M13_core_145	CAAATCATAAATTAATGCCGGAGAGGGTAGC
[HE]_M13_core	ACTAGCATGTCAATCTTTTTTTTTATTCAAAAGGGTGAG

_146	
[HE]_M13_core_147	TGAGAGATCTACAAAGGCTATCAGAATCGATGAACGGTATATAAGCA
[HE]_M13_core_148	CTCATTTTAAAAACAGGAAGATTGATCGTAAA
[HE]_M13_core_149	AATATTTGCATTAAATTTTTGTAAACGGCG
[HE]_M13_core_150	AAAGCCCCTTAACCAATAGGAACGGAGTAACA
[HE]_M13_core_151	CAGTTTGAGATTCTCCGTGGGAACTAAATCAG
[HE]_M13_core_152	AGGAAGAACATTAAATGTGAGCCCATCA
[HE]_M13_core_153	GATTGACGCGCATCGTAACCGTGGGGGATG
[HE]_M13_core_154	ACCCGTCGGGGGACGACGACAGTAGGGCCTCT
[HE]_M13_core_155	CATCATCGCACTCCAGCCAGCCTGCGCAA
[HE]_M13_core_156	GTTGTAAAACGCCAGCTGGCGAAAGCATCTGC
[HE]_M13_core_157	TGCCTGCAAGGGCGATCGGTGCTCGGCCTC
[HE]_M13_core_158	GTGTGATCCCCGGGTACCGAGCCATTCGCCATTCAGGTTTCC
[HE]_M13_core_159	TGCTGCAGCCAGGGTTTTCCCAGGGTGCCT
[HE]_M13_core_160	TCGCTATTACGACGGCCAGTGCCAATACGAGC
[HE]_M13_core_161	CTGTTGGGAGGTCGACTCTAGAGGAAATTGTT
[HE]_M13_core_162	CTGTCGTGTAAAGTGTAAAGCCTGGTCACGAC
[HE]_M13_core_163	ACGCGCGACAATTCCACACAACAGCTTGCA
[HE]_M13_core_164	AATGAGTTGCCCGCTTTCCAGTCGCCTGGC
[HE]_M13_core_165	CGGAAGCACCAGCTGCATTAATGAAGTGAGACGGGCAACATCCGAAAT
[HE]_M13_core_166	GGTTGAGTCCTGTTTGATGGTGGTGCTGATTGCCCTTCACCGGGAAAC
[HE]_M13_core_167	CCTGAGACCAGCAGGCGAAAATGTTGTTCC
[HE]_M13_core_168	AGTTTGGCAACGTCAAAGGGCGAAAAACCGT

Table S2.52. Edge staples of M13mp18 regular hexagonal DNA origami tile.

Name	**Sequence**
[HE]_M13_edge_1	TTTTTGGGGTCGAGGTATCACCCAAATCAAGTTA
[HE]_M13_edge_2	GAGAAGTGTTTTTATAGGTACGCCAGAATCCTAT
[HE]_M13_edge_3	CAACAGTGCCACGCTGGTATTAACACCGCCTGAC
[HE]_M13_edge_4	AGCGGAATTATCATCAAGAAACCACCAGAAGGCT
[HE]_M13_edge_5	AAGAACGTGGACTCAACAAGAGTCCACTAT
[HE]_M13_edge_6	TGCGTTGCGCTCACGAGCTAACTCACATTA
[HE]_M13_edge_7	GTTGGTGTAGATGGCGTAATGGGATAGGTC
[HE]_M13_edge_8	GGAGCAAACAAGAGGTCATTGCCTGAGAGT
[HE]_M13_edge_9	TTAATTTCAACTTTAATTGGGCTTGAGATGGTCA
[HE]_M13_edge_10	GACTGGATAGCGTCCAAATAGTAAAATGTTTATA
[HE]_M13_edge_11	GCTATATTTTCATTTGGTCAATAACCTGTTTATT
[HE]_M13_edge_12	CAACCGTTCTAGCTGACCATCAATATGATATTCC
[HE]_M13_edge_13	ACGTAACAAAGCTGTATTCATTACCCAAAT
[HE]_M13_edge_14	CGTAATGCCACTACCATTAAACGGGTAAAA
[HE]_M13_edge_15	CCACAGACAGCCCTTACAACGCCTGTAGCA
[HE]_M13_edge_16	CCCTGCCTATTTCGGTATAAACAGTTAATG
[HE]_M13_edge_17	AGCTACAATTTTATCCTTGCTATTTTGCACCCCT
[HE]_M13_edge_18	CCGAAGCCCTTTTTAAAGCAATAGCTATCTTAAG
[HE]_M13_edge_19	CGTCAGACTGTAGCGCTCAAGTTTGCCTTTAGAC
[HE]_M13_edge_20	GGCTTTTGATGATACAAGTAAGCGTCATACATTG
[HE]_M13_edge_21	AAGAACGCGAGGCGAGGCTTATCCGGTATT
[HE]_M13_edge_22	TAATAAGAGAATATGAGGCATTTTCGAGCC
[HE]_M13_edge_23	CTTGCTTCTGTAAATATATGTGAGTGAATA
[HE]_M13_edge_24	GAAGGGTTAGAACCTTATACTTCTGAATAA

S2.7.2.3 Staple strand sequences of low-symmetry tiles for Laves tilings

Table S2.53. Core staples of p3548 isosceles right triangular DNA origami tile.

Name	Sequence
[irTR]_p3548_core_1	ATGAGTAAACTTGGTCTGATCTCAGCGATCTGTCTGACTCCC
[irTR]_p3548_core_2	TGCCTATTTCGCATGAGAGTTAAGGGATTTTTCATAGT
[irTR]_p3548_core_3	CGTCGTGTGGCCCCAGTGCTGCTTTATCAG
[irTR]_p3548_core_4	CTCCAGAAATGATACCGCGATTTTGCAGAAAAAAAGGTGTTTGC
[irTR]_p3548_core_5	AAGCAGCAGATTCGCTCACCGG
[irTR]_p3548_core_6	CAATAAAGTCCTGCAACTTTATCGCCAGTT
[irTR]_p3548_core_7	TATGGCTTGCTAGAGTAAGTAGTTCCGCCTCC
[irTR]_p3548_core_8	ATCCAGTCTATTTTTTTGCTGAAGCCAG
[irTR]_p3548_core_9	CAGCTCCACTGGCAGCAGATTTGGTTCCGGGAACATT
[irTR]_p3548_core_10	AATAGTTGTGGTGTCACGCTCGCATGTTGT
[irTR]_p3548_core_11	TTATCACTGAGTTACATGATCCCCTCGTTTGG
[irTR]_p3548_core_12	GTGTAGGAAGACACGACTTATTTTTCCAACGATCAAGGCCATGGTT
[irTR]_p3548_core_13	GCAAAAATCAGAAGTAAGTTGGTGTGACTG
[irTR]_p3548_core_14	GCGTCAATCCGTAAGATGCTTTTCCCGCAGTG
[irTR]_p3548_core_15	ATGGCAGCACTTTTCTCAGTTCG
[irTR]_p3548_core_16	TCATAGCTCACGTTTTTTTCTCTTACTGT
[irTR]_p3548_core_17	CATGCCATACGGGATAATACCGCGCATCATTGGAAAACGTCTTTCACC
[irTR]_p3548_core_18	GTGAGTAGGCGACCGAGTTGCTTCTCAAGG
[irTR]_p3548_core_19	ATCTTTTATCTTCGGGGCGAAAACCTTGCCCG
[irTR]_p3548_core_20	TGCTCCACATAGTTTTCCCGACAGTCAAGTCAGAGTTAAAAG

[irTR]_p3548_core_21	ATCTTACCGTGCACCCAACTGATAAGGGCG
[irTR]_p3548_core_22	AAAAGGCTTTTCCATAGGCTCCAGCTCCCT
[irTR]_p3548_core_23	GAAGCGTGGGCGTTTCCCCCTGGAGCCCCCCT
[irTR]_p3548_core_24	GACGAGCAGCCAGCAAAAGGCCAGAGCTCACT
[irTR]_p3548_core_25	AGCAAAAGTCACAAAAATCGACGCGACTATAAAGATACCAGCGCTTTC
[irTR]_p3548_core_26	CGTGCGCCCTGTCCGCCTTTCTGGGCTGTG
[irTR]_p3548_core_27	AACCCGGTTCGTTCGCTCCAAGCTCCCTTCGG
[irTR]_p3548_core_28	TGCACGACCGGTAACTATCGTCTAGCAGAG
[irTR]_p3548_core_29	TTACCTTCACACTAGAAGGACAGTCCACTGGTAACAGGATTTGAGTCC
[irTR]_p3548_core_30	CGAGGTAGGCCTAACTACGGCTGGAAAAAG
[irTR]_p3548_core_31	AGTTGGTTAGCGGTGGTTTTTTATCTCAAG
[irTR]_p3548_core_32	AAGATCCGGAACGAAAACTCACTTATCAAA
[irTR]_p3548_core_33	AAGGATCTTTTAAATCAATCTAAAGT
[irTR]_p3548_core_34	TATTTTGTTAAAATTCGCGTTAATAGGCCGAAATCGTTGTTCCA
[irTR]_p3548_core_35	CTATCAGGGAGATAGGGTTGAGTGGCAA
[irTR]_p3548_core_36	AATCCCTTATTTTTTTATTTGAATGTATTTTATCAGGG
[irTR]_p3548_core_37	AAATTCATGATTAGACCGCGA
[irTR]_p3548_core_38	GTTTGGAAACGTCAAAGGGCGAAAAGCACT
[irTR]_p3548_core_39	CGAGAAAGGGGGTCGAGGTGCCGTAAAACCGT
[irTR]_p3548_core_40	TGGCCCACTATTTTTTCAGGAAGGCA
[irTR]_p3548_core_41	AGCGTTTCTGGGTGTTTTTTTCATCACCCTAATCA
[irTR]_p3548_core_42	AGTTTTTTGAAGGGAAGAAAGCGATGTAGCGGTCACGCTGTGCGGGCC

[irTR]_p3548_core_43	AAATCGGACGGGGAAAGCCGGCCCGCCGCG
[irTR]_p3548_core_44	TTATTGTCGCCGCAAAAAAGGGAATCTTCAGC
[irTR]_p3548_core_45	ACACGGATATTATTGAAGCATTAGAAAAAT
[irTR]_p3548_core_46	AAACAAACCACCTAAATTGTAAGCGTTA
[irTR]_p3548_core_47	GGTAAAACCTTGTACACGTGGTGCAATTCGACGTGAACGACC
[irTR]_p3548_core_48	CATCCACCTTGCCTCAGCATAAGCCAACTTTTGATGCA
[irTR]_p3548_core_49	CATGTGTGAAGGCCCGTAAAAGAGGACTTC
[irTR]_p3548_core_50	CAGTGGCGAAGCTGTACTGCTTTTCCAGGGAAAAAAGGGACAAA
[irTR]_p3548_core_51	ATCAACGACATTAACTCTCGTA
[irTR]_p3548_core_52	TCGACGTTTCCTGCAGCCCGGGTTCCCTTT
[irTR]_p3548_core_53	TATCCGCTGGAGCTCCAGCTTTTGGGATCCAC
[irTR]_p3548_core_54	TAGTTCTAGAGCTTTTGATTGACAGGAA
[irTR]_p3548_core_55	ATTCCACCCCCCCCTCGATGGCGTGTCCGCGGTCACA
[irTR]_p3548_core_56	AGTGAGGAGCTGTTTCCTGTGTTGGGGTGC
[irTR]_p3548_core_57	ACCTGTCGCATAAAGTGTAAAGCCGAAATTGT
[irTR]_p3548_core_58	GATGTGCGGCGAATTGGGTACTTTTATACGAGCCGGAAGTGCCAGC
[irTR]_p3548_core_59	CTAATGAACTGCCCGCTTTCCATCTTCCGC
[irTR]_p3548_core_60	CAAAGGCGTTTGCGTATTGGGCGCGTCGGGAA
[irTR]_p3548_core_61	TGCATTAATGTTTGCGAAAGGGG
[irTR]_p3548_core_62	TCTTCGCTATTATTTTTCAACGCGCGGGG
[irTR]_p3548_core_63	AGAGGCGGGTAATACGGTTATCCAAACATGTG
[irTR]_p3548_core_64	TTCCTCGGCGGCGAGCGGTATCGAACCGTA

[irTR]_p3548_core_65	AAAGCAGAATCATTTTCTGGCAAGAAGGAGCGGGCACGCAGG
[irTR]_p3548_core_66	GCGATCGGCGCGTAACCACCACACGAACGTGG
[irTR]_p3548_core_67	CTTAATGAGGCTGCGCAACTGTTGGGTAAC
[irTR]_p3548_core_68	CACTATAGTGCAAGGCGATTAAGTTGGGAAGG
[irTR]_p3548_core_69	GCCAGGGCAGTGAGCGCGCGTAAAGCTTTG
[irTR]_p3548_core_70	AAAAGTCAGAAAAAACAAGACTGGGGTCGACGGTATCGATATACGACT
[irTR]_p3548_core_71	GTGCAATCGTAGAACCAGCTCACCAATCGA
[irTR]_p3548_core_72	GATCCCTGCATCAGCGGACTACATACGCAG
[irTR]_p3548_core_73	AGAGCTCATCCATCGGGGCAAGGCAGCAAT
[irTR]_p3548_core_74	TATTCGGTAGGAAAAAAGCAACCCTG

Table S2.54. Edge staples of p3548 isosceles right triangular DNA origami tile.

Name	**Sequence**
[irTR]_p3548_edge_1	GTGTAGTCGGAAGAGTTAGGAAAAAAGCGTGCTA
[irTR]_p3548_edge_2	TCCGAAAAAAGAGGGAATCAAGATACCTTCTAGG
[irTR]_p3548_edge_3	AGTGAGACCGTCAGAAGTCACAATGACCGAACAA
[irTR]_p3548_edge_4	GCGTAATCATGGTCATGTTAATTGCGCGCTTGGA
[irTR]_p3548_edge_5	TAATTGCGTTGCGCTCGTGAGCTAACTCACATGA
[irTR]_p3548_edge_6	GCTCGGTCGTTCGGCTCTCACTGACTCGCTGCTG
[irTR]_p3548_edge_7	CCGCTTACCGGATATCTCCTGTTCCGACCC
[irTR]_p3548_edge_8	CCGCTGCGCCTTATACCCCCCGTTCAGCCC
[irTR]_p3548_edge_9	GTTCTTGAAGTGGTTGTAGGCGGTGCTACA
[irTR]_p3548_edge_10	CAAACCACCGCTGGAGCTCTTGATCCGGCA
[irTR]_p3548_edge_11	GTCTGACGCTCAGTTTTGATCTTTTCTACG
[irTR]_p3548_edge_12	AATTAAAAATGAAGTTCACCTAGATCCTTT
[irTR]_p3548_edge_13	TCCGCTCCAACCAGGACCAGCACGAAACGCAGAT
[irTR]_p3548_edge_14	TTGGAAAAAAGAAGTTAAAATCGGGTGGATAGGG
[irTR]_p3548_edge_15	CCGGCATCTGATACTGGGCTTAACGTGACTCGGC
[irTR]_p3548_edge_16	TGTACGTTCGTACCCAGGTGAGCTCATCTGTCCA
[irTR]_p3548_edge_17	GTTGTAAAACGACGGCTTTTCCCAGTCACGACGG
[irTR]_p3548_edge_18	GTCCCATTCGCCATTCCGCCGCTACAGGGCGCTG
[irTR]_p3548_edge_19	CCCGATTTAGAGCTTGAACCCTAAAGGGAGCCTT
[irTR]_p3548_edge_20	AAAGAACGTGGACTCCACAAGAGTCCACTATTAC

[irTR]_p3548_edge_21	AGCTCATTTTTTAACCAAATTTTTGTTAAATCAT
[irTR]_p3548_edge_22	CAGTGAGGCACCTACAGTTACCAATGCTTA

Table S2.55. Core staples of M13mp18 rhombic DNA origami tile.

Name	**Sequence**
[RH]_M13_core_1	AACCCATGTACCGTAACAACAACGC
[RH]_M13_core_2	CTGTAGCATAACGATCTAAAGTTTTCTGTA
[RH]_M13_core_3	AGTACCGTTCATAGTTAGCGTTCCACAGTTTAGAACCGCGGTTT
[RH]_M13_core_4	TGGGATTTACAACTAAAGGAATTCAAAAAA
[RH]_M13_core_5	ACAGCTTGAAAAGGAGCCTTTAATGTGAGAATAGAAAGGATGCTAAA
[RH]_M13_core_6	CAACTTTCAATCTCAGTACCA
[RH]_M13_core_7	CGTATAGCGGAGCGGATGTATCGGTTTTTTAGTGCC
[RH]_M13_core_8	AAGGCTCCATACCGATAGTTGCGACCGATA
[RH]_M13_core_9	GAGGGTAGCGCTGAGGCTTGCAGGTTTCTTAA
[RH]_M13_core_10	AAAGCGGGGTCAGTGCCTTGTTTTTGCTTTCGAGGTGAAGAGTT
[RH]_M13_core_11	TATTCGGTCAACGGCTACAGAGGTTTCCAT
[RH]_M13_core_12	AAAGGCCGCTTTTGTTTTTTAATAAATCCTCATT
[RH]_M13_core_13	TACCAAGCTAAAATACGTAATGCCATCGGAAC
[RH]_M13_core_14	AAGACAGCACTACGAAGGCACCAACTCATCTTTGACCCCCAGCCGGAA
[RH]_M13_core_15	TTGGCCTTGATATTCATTTTTTCACCCTCAGCAGCGA
[RH]_M13_core_16	TAAACGGGGCGAAACAAAGTACAGTCGAAA
[RH]_M13_core_17	CTAAAACACCTAAAACGAAATTTTTTCGGAACCGCCTCATCACCGG
[RH]_M13_core_18	CTGGCTGACTGCTCCATGTTACTTAGCGATTA
[RH]_M13_core_19	AACCAGAGCTTTTTAAGAATACA
[RH]_M13_core_20	TCCGCGACCCTTCATCAAGAGTAATCAACG
[RH]_M13_core_21	CGAGGCGCCGGTGTACAGACCAGGTAAGGCTT
[RH]_M13_core	CCAGAACAAGAGGACAGATGAAAGACGGTC

_22	
[RH]_M13_core_23	AATCATAAGGGAACTTTTTAAACGTCACCAATG
[RH]_M13_core_24	TTATACCACTGCTCATTCAGTGAACGCATAGG
[RH]_M13_core_25	ATTCATTACCATTAGCATTTTTTACCAACTTTGAGAGTAG
[RH]_M13_core_26	TAACAAAGGTCAGGACGTTGGGAGAACAAC
[RH]_M13_core_27	GCCCTGACTATGCGATTTTAAGAACAGTTGAG
[RH]_M13_core_28	TTCAACTCATTGTGAATTACCTGAGAAACA
[RH]_M13_core_29	TAAATTGGGCTTTTTTCAATAGAAA
[RH]_M13_core_30	AGGCTTTTAGGTAGAAAGATTCATCTGGCTCA
[RH]_M13_core_31	ACTTTAATAATGCAGATACATAACGCAACACT
[RH]_M13_core_32	AATAAGTTTATTTTTTTTGGTTTAATTTCA
[RH]_M13_core_33	ATTATTACGCAAAAGAAGTTTTGGATAGCG
[RH]_M13_core_34	ATTTAGGAGACGATAAAAACCAAAATATTCAT
[RH]_M13_core_35	GCTTTAACCTCGTTTACCAGACATACCACA
[RH]_M13_core_36	AAGAGCCAAAAGGTTTTTGCCCTTTTTTAGC
[RH]_M13_core_37	AAAGACTTTGCGGAATCGTCATAAATAGCGAG
[RH]_M13_core_38	ATCATAACACAGTTCAGAAAACGAACTATTAT
[RH]_M13_core_39	AATAGCTATTTTTAGGCATAGT
[RH]_M13_core_40	TCCAATACCAAATATCGCGTTTTCAAACTC
[RH]_M13_core_41	TGAATCCCTCAAAAAGATTAAGAGCTTTAATT
[RH]_M13_core_42	GAGGTCATTGCAAAGCGGATTGCACCTCAAAT
[RH]_M13_core_43	TATTTACCCCAAAAATTTTTTTTTTACCCTGGAATGA
[RH]_M13_core_44	CCATAAATCAAATTTCAAATAAGAAAC

[RH]_M13_core_45	TCAGCTAATGCAGAACGCCCTGAACAAGAAAAATATCATTC
[RH]_M13_core_46	ATCGTAGGATCGGCTGTCTTTCCTTAATATC
[RH]_M13_core_47	CCATCCTAATTTTTTCGAGCC
[RH]_M13_core_48	CAAGAACACAAGCAAGCCGTTTGGTTTTGA
[RH]_M13_core_49	CAATAAATCATTACCGCGCCCAGGCGTTT
[RH]_M13_core_50	ACATGTAATTTTTTAGAAACCAAT
[RH]_M13_core_51	AACGCTAACTCCCGACTTGCGGGATTATTTTC
[RH]_M13_core_52	AACGCGAATAGCAAGCAAATTTTTTTTAAACACCGGAATCATACCG
[RH]_M13_core_53	AGCCTTAACAATTTTATCCTGACGCATTAG
[RH]_M13_core_54	TAGCGAACCGAGCGTCTTTCCAGATTTACAGA
[RH]_M13_core_55	TAGCAGCCGCCTAATTTGCCAGTTATTCTAAG
[RH]_M13_core_56	ACTACCTTTAAATAAGGCGTTTTTTTTTGGCTTATCCGGTACAAAAT
[RH]_M13_core_57	AGATAACCCATAAAAACAGGGAAGATCTTACC
[RH]_M13_core_58	AAACAGCCTTGTTTAACGTCAAAAGCAAGAAA
[RH]_M13_core_59	GATTTTATATTATTTTTTTTTTAATCATAGGGAGAAG
[RH]_M13_core_60	TAAATCGTATGCAAATCCAATCGTATATTT
[RH]_M13_core_61	AAATGCTGCGCTATTAATTAATTTCATTTGAA
[RH]_M13_core_62	AGTATCATTTCATCTTCTGACCTACTATATGT
[RH]_M13_core_63	AATCCTTGAGGTTGGGTTATATAAAATTTAAT
[RH]_M13_core_64	ACCGTGTGATTTAACCTCCGGCTTAAAACATA
[RH]_M13_core_65	AAACATCACTTAGATTAAGACGCTTCTGAGAG
[RH]_M13_core_66	TAGTTAATATGCGTTATACAAATGGGCTTA
[RH]_M13_core	GGTTTGAAATAATTACTAGAAAAACGCCA

_67	
[RH]_M13_core_68	AGTAATATCGCCATATTTAACAAGCCTGTTT
[RH]_M13_core_69	ATTGAGAAAGAGAATATAAAGTATCCAGACGACGACAATAA
[RH]_M13_core_70	ACGGGAGGTAATTGAGCGCTAACGGAATAC
[RH]_M13_core_71	GAGAATAACACAAGAATTGAGTTAACCAGAAG
[RH]_M13_core_72	ACAAAGTTAGCCCAATAATAAGAATGAAAA
[RH]_M13_core_73	CATACATAGGAAACGCAATAATAATATCAGAG
[RH]_M13_core_74	CAATGAAAAAGAAAAGTAAGCAGACACCACGG
[RH]_M13_core_75	CCAAAAGTATGTTAGCAAACGTGGGAGGGA
[RH]_M13_core_76	GAAACCGAAAGGTGGCAACATATACAAAGACA
[RH]_M13_core_77	ACCAGCGCAAAGAAACGCAAAGATAGCCGA
[RH]_M13_core_78	TTTGGGAAACATTCAACCGATTGAAGAAAATA
[RH]_M13_core_79	AGGTAAAATCACCGTCACCGACCAAGTTTG
[RH]_M13_core_80	AAAGGGCGTTAGAGCCAGCAAAATGATAGCAG
[RH]_M13_core_81	AAACCATCCACCAGTAGCACCATATGGTTT
[RH]_M13_core_82	GTTTGCCATCAGTAGCGACAGAATTTGAGCCA
[RH]_M13_core_83	CCTTTAGTCGGTCATAGCCCCCTCAGAGCC
[RH]_M13_core_84	CACCGTAATCTTTTCATAATCAAACCTCAGAGCCGCCACCTCAGACGA
[RH]_M13_core_85	GAGGCAGGCTCAGAACCGCCACCCTTATTAGC
[RH]_M13_core_86	ACCACCCGCCGCCAGCATTGACGTCTCTGA
[RH]_M13_core_87	GTTTTAACCAGAATGGAAAGCGCAAGGAGGTT
[RH]_M13_core_88	ATTTACCATACAGGAGTGTACTCCTGCCTA
[RH]_M13_core_89	GGCGGATAGAGAAGGATTAGGATTAAACAGTTAATGCCCGGTAATAA

[RH]_M13_core_90	TTTCGGAGGCTGAGACTCCTCAAAGTGCCG
[RH]_M13_core_91	TCGAGAGTCACCGTACTCAGGACACCCTCA
[RH]_M13_core_92	GAACCGCTTCAGGGATAGCAAGCCC
[RH]_M13_core_93	GAGCTAAACAGGAGGCCGGTACGCC
[RH]_M13_core_94	AGAATCCTCACCGAGTAAAAGAGATACTTC
[RH]_M13_core_95	CCGCGCTTAATCAGTGAGGCGAGAAGTGTTTCGCTACAGACCCG
[RH]_M13_core_96	TTTGATTATGCTGGTAATATCCAAAAACGC
[RH]_M13_core_97	CCAGTCACATACCTACATTTTGACCTCAAACTATCGGCCTGTAATAA
[RH]_M13_core_98	CATCACTTGCTGAAAGGAAGG
[RH]_M13_core_99	CATCGCGAACGAAGAAGCTCAATCGTTTTTGTGAAC
[RH]_M13_core_100	TCATGGAAACGACCAGTAATAAATCTGACC
[RH]_M13_core_101	CGCCATTATAAGAATACGTGGCACCAGATTCA
[RH]_M13_core_102	AAGAAATCAGGGCGATGGCCTTTTGATTATTTACATTGGAGACA
[RH]_M13_core_103	TGAAAGCGAAAATACCGAACGAAGTCAGTA
[RH]_M13_core_104	ATATTTTTGAATGGTTTTTTCCCTTATAAATCAA
[RH]_M13_core_105	TCTGGTCAGCCTGCAACAGTGCCATAAAACAT
[RH]_M13_core_106	GATAGCCCCGCTGAGAGCCAGCAGCAAATATCAAACCCTCGAGCCGTC
[RH]_M13_core_107	GTGGTTCCGAAATCGGTTTTTCTTTAATGCGCGAACT
[RH]_M13_core_108	TTAACACCGTTGGCAAATCAACAATCTTTA
[RH]_M13_core_109	CTGAACCTCAAATGAAAAATTTTTTTCGCCAGGGTGGTGGAGAGGC
[RH]_M13_core_110	AATTTTAAAACAACTAATAGATTAAATCAATA
[RH]_M13_core_111	GGTTTGCGTTTTTTATCACCTTG
[RH]_M13_core	GGAGCACTAAGTTTGAGTAACATGGAGCGG

_112	
[RH]_M13_core_113	AATAGATATAAATCCTTTGCCCGACAGATGAT
[RH]_M13_core_114	AATCCTGTTCGACAACTCGTATATACATTT
[RH]_M13_core_115	GAGGATTTAGAAGTTTTTTCACAACATACGAGC
[RH]_M13_core_116	AAATTGCGTCATATTCCTGATTATACGTTATT
[RH]_M13_core_117	CAAGGCTATCCGCTCACTTTTTTTTTACAAACAAATTGTT
[RH]_M13_core_118	AATTATCATAGATTTTCAGGTTTTTACATC
[RH]_M13_core_119	GGCAATTCTTTGCACGTAAAACAGTGATTGCT
[RH]_M13_core_120	AAAATCGACCATATCAAAATTAATCAATAT
[RH]_M13_core_121	TGGATTATACTTTTTGGATGTGCTG
[RH]_M13_core_122	TTACCTTTCAATAACGGATTCGCCAAATAAAG
[RH]_M13_core_123	TAGAACCTCGCAGAGGCGAATTATGATGAAAC
[RH]_M13_core_124	TTACGCCAGCTGTTTTTTTAATGGAAGGGT
[RH]_M13_core_125	GGGAGAAATTTAATGGAAACAGTGCTTCTG
[RH]_M13_core_126	TTGAATACTTACATTTAACAATTTTCCCTTAG
[RH]_M13_core_127	GCGATAGAGAAAACAAAATTAACAAGTTAC
[RH]_M13_core_128	AGATTCATTTCAATTTTTGTGTAGATGCGTA
[RH]_M13_core_129	ATGGGATAGTTTTAGCAAAAGA
[RH]_M13_core_130	AGTCAATAGTGATTTTGTATAAGCAAA
[RH]_M13_core_131	TAAATCATACAGGCAAGGAAAGCCTCAGAGCATTTTATTTC
[RH]_M13_core_132	TAGGTAAATTTTGCGGGAGAAGCCAAAGCTA
[RH]_M13_core_133	AATCGGTTGTTAACCTGTTTA
[RH]_M13_core_134	AACGCAAAAATGCAATGCCTGATTTGAGAG

[RH]_M13_core_135	AATACGATTCAAAAGGGTGAGCTGATAAA
[RH]_M13_core_136	ATACATTTCGTTTTATGACCCTGT
[RH]_M13_core_137	GTAATCGTGGAGAGGGTAGCTATTGTAATGTG
[RH]_M13_core_138	TTCTAGAAAGGCCGGAGACTTTTTTTTTTGCTGAATATAATGATAA
[RH]_M13_core_139	ATCTACAGCAAACAAGAGAATCTAACCAAT
[RH]_M13_core_140	TTAATGCCAAAACTAGCATGTCAAGCATTAAA
[RH]_M13_core_141	TAAAATTCTCATATGTACCCCGGATTCAACCG
[RH]_M13_core_142	AGTCAGAATTTGCGGATGGTTTTTTTTTATCAATATGATTTGATAAT
[RH]_M13_core_143	ATGTGAGCAAATCAGCTCATTTTTGATGAACG
[RH]_M13_core_144	CAGAAAAGAATTGTAAACGTTAATCAAACGGC
[RH]_M13_core_145	TATGCAACCAGGATTAGAGAGTACGAAGCCCG
[RH]_M13_core_146	CAACAGGTTAAAGTACGGTGTCTAATTCTG
[RH]_M13_core_147	GCTCCTTTTGCTGTAGCTCAACATATTAG
[RH]_M13_core_148	GCTATATTAGATTTAGTTTGACCGTTTTAAA
[RH]_M13_core_149	CGAACGAGTTTCATTTGGGGCGCACTAATAGTAGTAGCATT
[RH]_M13_core_150	AGGAACGTAGCCAGCTTTCATCTCGCACTC
[RH]_M13_core_151	TTTTTGTTGAGTAACAACCCGTCGAGGGGACG
[RH]_M13_core_152	CCAGTTTGGATTCTCCGTGGGAAATTTTGT
[RH]_M13_core_153	GGCTGCGCATCGGCCTCAGGAAGAAACATTAA
[RH]_M13_core_154	GGATTGACGGCGCATCGTAACCGTCTTCGCTA
[RH]_M13_core_155	CAGCCAGGGCAAAGCGCCATTCACGACGGC
[RH]_M13_core_156	ACGACAGTAACTGTTGGGAAGGGCCGCCAGGG
[RH]_M13_core	TTGGGTAAGATCGGTGCGGGCCTGCATCTG

_157	
[RH]_M13_core_158	TCGTAATCGTCACGACGTTGTAAAGCCATTCA
[RH]_M13_core_159	CAGTGCCATCCCCGGGTACCGAAGCTAACT
[RH]_M13_core_160	TTTTCCCAATGGTCATAGCTGTTTTAAAGTGT
[RH]_M13_core_161	CGGAAGCACCTGTGTGAAATTGTGATTAAG
[RH]_M13_core_162	ATTAATGAGGGTGCCTAATGAGTGGCTCGAAT
[RH]_M13_core_163	CACATTAGGGAAACCTGTCGTGGATTGCCC
[RH]_M13_core_164	AAAGCCTGATCGGCCAACGCGCGGTTTTCTTTTCACCAGTGTTTGATG
[RH]_M13_core_165	AAAATCCTGAGACGGGCAACAGCTCCAGCTGC
[RH]_M13_core_166	TTCACCGACGCTGGTTTGCCCCTGAGTGTT
[RH]_M13_core_167	AACCGTCTTAGCCCGAGATAGGGTAGCAGGCG
[RH]_M13_core_168	GTTCCAGGACTCCAACGTCAAATTGGGGTC
[RH]_M13_core_169	GAAGAAATTGACGGGGAAAGCCGACCCAAATCAAGTTTTGGGCGAAA
[RH]_M13_core_170	GAGGTGCCCCCCGATTTAGAGCGCGAAAGG
[RH]_M13_core_171	AGCGGGCGCGCGTAACCACCACGGCGCGTA
[RH]_M13_core_172	CTATGGTCTTTCCTCGTTAGAATCA

Table S2.56. Edge staples of M13mp18 rhombic DNA origami tile.

Name	**Sequence**
[RH]_M13_edge_1	TTTTGCACCCAGCTAATCAAGATTAGTTGC
[RH]_M13_edge_2	AACAAAGTCAGAGGAATTAACTGAACACCC
[RH]_M13_edge_3	ATTAAAGGTGAATTTATTGACGGAAATTAT
[RH]_M13_edge_4	TTTCATCGGCATTTCGTCAGACTGTAGCGC
[RH]_M13_edge_5	CATGGCTTTTGATGGTTCCAGTAAGCGTCA
[RH]_M13_edge_6	TGAAAGTATTAAGAACCTATTATTCTGAAA
[RH]_M13_edge_7	AGAAAACTTTTTCAAACAAGACAAAGAACGCGTA
[RH]_M13_edge_8	GTGAGTGAATAACCTTACATAAATCAATATATTG
[RH]_M13_edge_9	AAAGAAACCACCAGAATATCATTTTGCGGAACTC

[RH]_M13_edge_10	GAAGGTTATCTAAAATGTTGAAAGGAATTGAGGT
[RH]_M13_edge_11	ACAGAGATAGAACCCTAGGGACATTCTGGCCATA
[RH]_M13_edge_12	AGCCATTGCAACAGGAGAACAATATTACCGCCCA
[RH]_M13_edge_13	ACGTTGAAAATCTCGCGAATAATAATTTTT
[RH]_M13_edge_14	ATCGCCCACGCATACCGACAATGACAACAA
[RH]_M13_edge_15	GCCTGATAAATTGTACGGAGATTTGTATCA
[RH]_M13_edge_16	TATTCATTACCCAAATCTTGACAAGAACCG
[RH]_M13_edge_17	AAATGTTTAGACTGCCAGAGGGGGTAATAG
[RH]_M13_edge_18	AACCAGACCGGAAGAATTCGAGCTTCAAAG
[RH]_M13_edge_19	GGAACCCTAAAGGGAGCGTAAAGCACTAAATCTC
[RH]_M13_edge_20	ACTATTAAAGAACGTGTTTGGAACAAGAGTCCCC
[RH]_M13_edge_21	TGCCCGCTTTCCAGTCATTGCGTTGCGCTCACTC
[RH]_M13_edge_22	AGGTCGACTCTAGAGGAAGCTTGCATGCCTGCGA
[RH]_M13_edge_23	GCGTCTGGCCTTCCTGCCATCAAAAATAATTCTA
[RH]_M13_edge_24	TGCCTGAGAGTCTGGAAAGGCTATCAGGTCATCG

Table S2.57. Core staples of M13mp18 kite DNA origami tile.

Name	**Sequence**
[KT]_M13_core_1	AAAGACTTTTTCATGAGGGTAAAATACGTAATAAAGAATA
[KT]_M13_core_2	AGGCAGCCACTACGATTTTTTTGCTTTTGCGGGCTGA
[KT]_M13_core_3	CACTAAAAGCGCGAAACAAAGTGGAACGAG
[KT]_M13_core_4	GGCTTGCAGGGAGTTTTTTTCCTAAAACGAAAG
[KT]_M13_core_5	TGTACAGATCCATGTTACTTAGCCACAACGGAGATTTGTA
[KT]_M13_core_6	TCATCGCCTGTTTCGAGGTGAAT
[KT]_M13_core_7	GCGCAGATTTGAAAGAGGACAGGCTGCTCA
[KT]_M13_core_8	CGACCTGCCCAGGCGCATAGGCTGCGGATATT
[KT]_M13_core_9	CGGTTTATCATTTTCGAAATCCG
[KT]_M13_core_10	TGGTTTAAAAATCAACGTAACAAAATGAACGG
[KT]_M13_core_11	AAGAACGCTGACCTTTTTTTTTCTAAACAACAATGAA
[KT]_M13_core_12	TTCAGTGCGAGTAGTAAATTGGTATTACAG
[KT]_M13_core_13	CATTACCCTTTCAACTTTAATCATTACGTTAA
[KT]_M13_core_14	TTTTCTGTATGTTTTTTTTGTAATCTTGAC
[KT]_M13_core_15	CCAAAAGGACTAACGGAACAACATGCTTGAGA
[KT]_M13_core_16	CACTATCTTGGGAAGAAAAATCTGTGAATTACCTTAT
[KT]_M13_core_17	GCGATTTTAATTTTATTTTCAGGG
[KT]_M13_core_18	GTAGAAATCAACTAATGCAGATGGAATCGT
[KT]_M13_core_19	TAAAACGAAATTACGAGGCATAGTAAATGTTT
[KT]_M13_core_20	TCAGGACGATAACCCTCGTTTACCAAAAGAAG
[KT]_M13_core_21	CCTCAGAGCCTTTATTATACCAG

[KT]_M13_core_22	AAATCAAATAGCGTCCAATACTGCACATAACG
[KT]_M13_core_23	ATAGTCAGAGGGGGTAATAGTAAAGAGCAA
[KT]_M13_core_24	TTTGCAGACGACGATTTTTTTTTGAAACATGACCCTG
[KT]_M13_core_25	CATAAATGTTCAGAAAACGAGACCAACAGG
[KT]_M13_core_26	AGACTGGAAATCAGGTCTTTACCCAGCTTCAA
[KT]_M13_core_27	TTTTGCCAGAAGCAAAGCGGATTG
[KT]_M13_core_28	CCTATTTCGGAACTTTTTTTATAGCGAGAGGCT
[KT]_M13_core_29	AATTTACGATACAGGAGTGTACCAGGCGGA
[KT]_M13_core_30	AGGTTTAGGGGTTTTGCTCAGTACTGGTAATA
[KT]_M13_core_31	AGTTTTAACCAGAATGGAAAGCGCAGAGCCGC
[KT]_M13_core_32	CATTAAAGCGGGGTCAGTGCCTTGAGGATTAG
[KT]_M13_core_33	TCAAGAGAAGTAACAGTGCCCGTATATTCACAAACAAAAGCCACCA
[KT]_M13_core_34	TGGCCTTGATAAACAGTTAATGCCAAGTATTAAGAGGCTGACCGCCAC
[KT]_M13_core_35	TAAGTGCATAGGTGTATCACCGACCAGTAC
[KT]_M13_core_36	GATTAGCGTACCGCCACCCTCAGAGGAACCCA
[KT]_M13_core_37	ATAGCAAGCCCAATAACCGCCACCCTCAGAAGACTCC
[KT]_M13_core_38	AATAGAAACTAAAGTTTTGTCGTCAACACTGAGTTTCGTCTACTCAGG
[KT]_M13_core_39	AAACTACAGTTAGCGTAACGATGGAACAAC
[KT]_M13_core_40	TGTACCGTTTTCCAGACGTTAGTATTTCAACAGTTTCAGCAATTGTAT
[KT]_M13_core_41	ACAACATGTTCAGCTAAAGTCCTGAACAAGAAGAGCATGT
[KT]_M13_core_42	TTACAAATAATTATTTTCTGTAATTTAGGTTTCCTAAT
[KT]_M13_core_43	AGAAACCCAAGAACGGGTATTATTTCATCG

[KT]_M13_core_44	AAGAACGCAGCAAGCCGTTTTTATAACCA
[KT]_M13_core_45	AGTACCGCACTTTTTACAAATTCTT
[KT]_M13_core_46	TAGGAATATAGAAGGCTTATCCCTTAAATC
[KT]_M13_core_47	CGTTTTTTTTACCTAAATTTATGTTTTTAACAGAGG
[KT]_M13_core_48	GCGTCTTTCGGGAGGTTTTGAAGCGGTATTCT
[KT]_M13_core_49	AAGATTACTGAATCTTACCAACAAACGATT
[KT]_M13_core_50	AACCTCGTTAATTTCATCTTTTTTTACCTCCCGACTTGCCAGAG
[KT]_M13_core_51	AAGCGCATTCCCAATCCAAATAAGGCTAACGA
[KT]_M13_core_52	CCTAATTTGCCATTTTTGACTACCTTTTT
[KT]_M13_core_53	TTTTGTTGAGAGAATAACATAATTGAGTTA
[KT]_M13_core_54	CCATATTATTTATAGACGGGAGAATTAAAGCGCTAA
[KT]_M13_core_55	AATCATAGGTTTTTTTAAATAAACAG
[KT]_M13_core_56	AAGAAAAGAGATAACCCACAAGAAAAACAGGG
[KT]_M13_core_57	AATTGCTGAACACCCTTTTTTAAATCAATATACTTTT
[KT]_M13_core_58	AGCCCAAGCTATCTTACCGAAGCAGTATGT
[KT]_M13_core_59	TATCAGAGTAAGCAGATAGCCGAAAAGAACTG
[KT]_M13_core_60	TTAATGGAAATTTTTTGTCAGAGGGT
[KT]_M13_core_61	CGGAATAAAAGACTCCTTATTACGCCCTTTTT
[KT]_M13_core_62	AAATTCATAACGGAATACCCAACAAAGTTACC
[KT]_M13_core_63	AGAAGGAAACTTTTTTACGGATTCGC
[KT]_M13_core_64	TAGCAAAATAAAAGAAACGCAAAGGTGAAT
[KT]_M13_core_65	GCATGATTGTTTATTTTGTCACAAGAAGGTAA

[KT]_M13_core_66	CAATACATCGGGAGTTTTTAACGCAATAATATG
[KT]_M13_core_67	TTACCATTGGAAATTATTCATTAAAGACACCA
[KT]_M13_core_68	GAAACCAACCGATTGAGGGAGGTCAATAGA
[KT]_M13_core_69	GTTTACCAGCTTTTTCAGATGATGG
[KT]_M13_core_70	TATCACCCAGCAAAATCACCAGTTTGCCAT
[KT]_M13_core_71	ATATTGACAGCAAGGCCGGAAACGCGGCATTT
[KT]_M13_core_72	CGACATTCATCGATAGCAGCACCGTCCTTTAGC
[KT]_M13_core_73	CATCATATTCTTTTGACAAAAGGG
[KT]_M13_core_74	CACCCTCAAGCCCCCTTATTAGCGTAGCACCA
[KT]_M13_core_75	CCCTCAGGTAGCGCGTTTTCATTCACCAAT
[KT]_M13_core_76	TTTGAATCAGTTTAGGAGCAAGGTTATCTAAATGAATCAAG
[KT]_M13_core_77	TAAAGGACTCCAAAAAAAAGGCTACCGATAGTTGCGCCCGATAT
[KT]_M13_core_78	TTCTTAAACAGCTTGATCCAAAAGGAGCCTTTGGAGTGAG
[KT]_M13_core_79	ATTCGGTCGATCGTCACCCTCAGACGGCTACAGAGGCTTT
[KT]_M13_core_80	CTTTTCAGGAACCGCCTCCCTCAGTCTCTG
[KT]_M13_core_81	TCGGTCATGAACCGCCACCCTCAGTAAATCCT
[KT]_M13_core_82	GTCAGACTAGCCGCCACCAGAACCCAGACGAT
[KT]_M13_core_83	AGGCAGGTACCACCAGAGCCGCCGTTTCGCCATTAAAAATACTAATGCGC
[KT]_M13_core_84	GAACTGATAGCCCTTTGACAGGAGGTTG
[KT]_M13_core_85	ACCAGTCAACAGAGATAGAACCCAGTGCCA
[KT]_M13_core_86	ACCCTCAATTAACACCGCCTGCAACTTCTGAC
[KT]_M13_core_87	CTGAAAGCTGGATTATTTACATTGTTTGATTA

[KT]_M13_core_88	GTCTGAAAGTAAGAATACGTGGCAGGTGAGGC
[KT]_M13_core_89	CAACAGTAGAAGATAAAACAGACAGACAAT
[KT]_M13_core_90	ATTTTTGTACCTACATTTTGACGAAGAACT
[KT]_M13_core_91	CATGGAAAAATGGCTATTAGTCTTCGAACGAA
[KT]_M13_core_92	CGCTGAGCCTTGCTGAACCTCATTTACAAA
[KT]_M13_core_93	GGTCAGTATCAATATCTGGTCAGTATAATACA
[KT]_M13_core_94	CCACCAGCTGAAAGGAATTGAGGACTAACAACTAATAGATCGGAATTAT
[KT]_M13_core_95	CATTATCATTTAGAAGTATTAGACAATATCAA
[KT]_M13_core_96	GAAGGAGTAGAGCCGTCAATAGTGGCAAAT
[KT]_M13_core_97	CAATTCGATTAATTTTAAAAGTAGGGTTAG
[KT]_M13_core_98	TTTGAGGATTTTGCGGAACAAAGATGATTGTT
[KT]_M13_core_99	GGTTTAACACTTCTGAATAATGGATTGAGTAA
[KT]_M13_core_100	CTGATTGCTTGTAACAGTACCTTTTTCATCAATATAATCCAACCACCA
[KT]_M13_core_101	AACCTACTAAAGAAATTGCGTAAATTATTC
[KT]_M13_core_102	TGGATTATGTCAGATGAATATACATGAATACC
[KT]_M13_core_103	ATTTAACAAAATCGCGCAGAGGCGGATTTTCA
[KT]_M13_core_104	ATTTCAAATCAAGAAAACAAAACGCTATTA
[KT]_M13_core_105	AAGTTACAATTTCATTTGAATTACTGTGAGTGAATAACCTTGAATTTATCAA
[KT]_M13_core_106	ATTAATTCTTAGATTAAGACGCATATAACT
[KT]_M13_core_107	GTCAATAGTGCTTCTGTAAATCGTTTAATTAC
[KT]_M13_core_108	ATATTTTACGGCTTAGGTTGGGTTTGAGAAGA
[KT]_M13_core_109	ATATGTAAACGCGAGAAAACTTCGACCGTG

[KT]_M13_core_110	ACCAGAGCCTGTTTAGTATCATAATGGTTTGAAATACTTTCAAAT
[KT]_M13_core_111	TGATAAAATAATTACTAGAAAATATAAAGCCAACGCTTTAACAA
[KT]_M13_core_112	CGCCAACAGAGCCAGTAATAAGATCTGTCCAGACGACGAC
[KT]_M13_core_113	AACATCCAGGCAAAGAATTAGCAGGTTGTAC
[KT]_M13_core_114	AATCAAATTATTTTTGGGAATG
[KT]_M13_core_115	CAAAAACCCTTTATTTCAACGCGTCAAATC
[KT]_M13_core_116	CGGAGACAAAGGATAAAAATTTTTAGCATAAAGCTA
[KT]_M13_core_117	CTGGTTTATTTTTTTCAGAGAA
[KT]_M13_core_118	CCCTCATATATTTTTTTTTTTCTAAAGTACGGTGT
[KT]_M13_core_119	ACCATCAAATGCCGGAGAGGGTTTGTATAA
[KT]_M13_core_120	CAGGAAGAAGCTATTTTTGAGAGAAGAAAGGC
[KT]_M13_core_121	TAGGTAAAGATTCAAAAGGGTGTCTACAAA
[KT]_M13_core_122	CTCAACATGTTTTTTTTTTGAGTAATGTG
[KT]_M13_core_123	GGCTATCATGATAATCAGAAAAGCTTTTTAAC
[KT]_M13_core_124	ACCCCGGTGGTCATTGCCTGAGAGTCT
[KT]_M13_core_125	GGAGCAAACATTTTTTAAAGACTTCA
[KT]_M13_core_126	GCAAATATTCGCATTAAATTTTGTTGGTGT
[KT]_M13_core_127	TAGGTCACTGTTAAATCAGCTCATCCCAAAAA
[KT]_M13_core_128	TGGGAACAACGCCATCAAAAATACATATGT
[KT]_M13_core_129	AAACTAGCATGTCAATATTCGCGT
[KT]_M13_core_130	CATCAAAAAGATTTACGGTAATCGTA
[KT]_M13_core_131	AGAGCTTAAGACCGGAAGCAAACTATGACCAT

[KT]_M13_core_132	AATATCGCGTTTTAATTCGTGACTATT
[KT]_M13_core_133	TCAGGATGAGGTCATTTTTGCGAACAGTTG
[KT]_M13_core_134	AGCGAACCATTGCTGAATATAATGCTGTAG
[KT]_M13_core_135	GTCAATAACCTGAAGTTTCATTCCATATGATGGCTT
[KT]_M13_core_136	ATTCCCATAGATACATTTCGCAGCGCGAGCTGAAAAGAATAGTAG
[KT]_M13_core_137	CCCTGAGAGAGTTGCAGGAAAATCCTGTTTGAAAAGAATA
[KT]_M13_core_138	AATCATGGTGGTTCCTTTTTTTGGCGCCAGGGGCGCG
[KT]_M13_core_139	GCCCGAGGAGTCCACTATTAAACCCAAATC
[KT]_M13_core_140	GGGAGAGGCGGTTTTTTTTTAAAATCCCTTATA
[KT]_M13_core_141	TTAGAGCTACTACGTGAACCATCAGAACGTGGACTCCAAC
[KT]_M13_core_142	GTCAAAGGGCTTTAGCTAACTCA
[KT]_M13_core_143	AAGTTTTGAACCCTAAAGGGAGCGGTCACG
[KT]_M13_core_144	GATGGCCCTGACGGGGAAAGCCGGAGGAGCGG
[KT]_M13_core_145	CTGGGGTGCCTTTCTATCAGGGC
[KT]_M13_core_146	CTTTGACGGCGCTGGCAAGTGTAGCCCCCGAT
[KT]_M13_core_147	AGCGAACGAACGTGGTTTTTTTCGACTCTAGGTGCCA
[KT]_M13_core_148	CTGCGCGCTACAGGGCGCGTACAGTGAGGC
[KT]_M13_core_149	GCGCTAGGAGCACGTATAACGTGCACGCCAGA
[KT]_M13_core_150	AGCTTGCATGCTTTTTTTTGAAGGGAAGAA
[KT]_M13_core_151	GTAATAACAAGTGTTTTTATAATCTATGGTTG
[KT]_M13_core_152	CAAACTATTAGACAGGAACGGTTTTCCTCGTTAGAAT
[KT]_M13_core_153	CAGAGCGGGATTTTTCGCCATTCA

[KT]_M13_core_154	CACCGAGTTGTAGCAATACTTCGCAGATTC
[KT]_M13_core_155	ATCCTGAGATCACTTGCCTGAGTAGCTCAATC
[KT]_M13_core_156	AAGGGATTTCGGCCTTGCTGGTAAAAAACGCT
[KT]_M13_core_157	AAACCAGGCATTTAGGCCGATTA
[KT]_M13_core_158	CAGGATATCCAGAACTTTTTTTATGTGAGCGACCTGT
[KT]_M13_core_159	AGCCAGCTTTCATTTTTTTTCCAGCCATTGCAA
[KT]_M13_core_160	CAATAGGAAACGGCGGATTGACCGGCACTCCA
[KT]_M13_core_161	CTGGCCTTGTAACAACCCGTCGGAGGTGCCGG
[KT]_M13_core_162	AGATGGGGGACGACGACAGTATTTACGCCA
[KT]_M13_core_163	CTTCGCTACGGCCTCAGGAAGATCTAATGGGA
[KT]_M13_core_164	GGCTGCGCAACTGTTTCCGGCACCGCTTCTTTCTCCG
[KT]_M13_core_165	GCCAGCTTGGGAAGGGCGATCGGTTGTAAAAC
[KT]_M13_core_166	GCTGGCGGGTAACGCCAGGGTTTCATGGTC
[KT]_M13_core_167	ATTCGTAATTCCCAGTCACGACGTGCGGGCCT
[KT]_M13_core_168	GACGGCCAAGGATCCCCGGGTACCTGTAAAGC
[KT]_M13_core_169	ATAGCTGTCCACACAACATACGCTCACTGCCCGCTTTAATGAAT
[KT]_M13_core_170	CATTAATTGCGTTGCGAGCCGGAAGCATAAAGGAGCTCGA
[KT]_M13_core_171	CGGCCAACTGGTTTTTCTTTTCAAGCTGATTGCCCTTCAC

Table S2.58. Edge staples of M13mp18 kite DNA origami tile.

Name	**Sequence**
[KT]_M13_edge_1	AACCGAACTGACCAACCGGTCAATCATAAGGG
[KT]_M13_edge_2	ACGAGAAACACCAGAAAATAAGGCTTGCCCTG
[KT]_M13_edge_3	TAGGAATACCACATGATTCATCAGTTGAGA
[KT]_M13_edge_4	TCAAATGCTTTAAACAATTCATTGAATCCCCC

[KT]_M13_edge_5	TTGCTCCTTTTGATAATAGAGAGTACCTTTAA
[KT]_M13_edge_6	GTTATCCGCTCACAATTTTCCTGTGTGAAATT
[KT]_M13_edge_7	CAAGGCGATTAAGTTGAAAGGGGGATGTGCTG
[KT]_M13_edge_8	ATCTGCCAGTTTGAGGCGCATCGTAACCGTGCTT
[KT]_M13_edge_9	TAATATTTTGTTAAAATTTAAATTGTAAACGT
[KT]_M13_edge_10	TTCTAGCTGATAAATTATATGATATTCAACCG
[KT]_M13_edge_11	AGCAAGCAAATCAGATCATTACCGCGCCCAATAA
[KT]_M13_edge_12	CAGCTACAATTTTATCGTTGCTATTTTGCACCCA
[KT]_M13_edge_13	CAATGAAATAGCAATATAATAAGAGCAAGAAAAG
[KT]_M13_edge_14	ATAAAGGTGGCAACATCGTAGAAAATACATACGC
[KT]_M13_edge_15	AACCAGAGCCACCACCTAATCAAAATCACCGGAA
[KT]_M13_edge_16	ATACATGGCTTTTGATCGTTCCAGTAAGCGTCAA
[KT]_M13_edge_17	CACAGACAGCCCTCATAACGCCTGTAGCATTCCG
[KT]_M13_edge_18	TTTTCACGTTGAAAATATTGCGAATAATAATTGT
[KT]_M13_edge_19	TAAACACCGGAATCTAAGGCGTTAAATAAG
[KT]_M13_edge_20	ATCGCAAGACAAAGAATGCTGATGCAAATC
[KT]_M13_edge_21	ATGATGAAACAAACTTACCTGAGCAAAAGA
[KT]_M13_edge_22	ACGTAAAACAGAAACATATCAAAATTATTT
[KT]_M13_edge_23	AATCTAAAGCATCAAGCCAGCAGCAAATGA
[KT]_M13_edge_24	GGGACATTCTGGCCACACGACCAGTAATAA
[KT]_M13_edge_25	CGCTTAATGCGCCGTAACCACCACACCCGC
[KT]_M13_edge_26	AAAGCACTAAATCGTTGGGGTCGAGGTGCC

Table S2.59. Core staples of M13mp18 prismatic pentagonal DNA origami tile.

Name	**Sequence**
[PT-prism]_M13_core_1	ACTGAACACCCTGAACAAAGTCAGAGGGCAAGAA TTGAGTTAATAAGAAAA
[PT-prism]_M13_core_2	ACCCAAAATTACCGAAGCCCTTTTGCCCAATA
[PT-prism]_M13_core_3	ATAAGAGCAAGAATTTTTTTGATTTTTTGTTTA
[PT-prism]_M13_core_4	GTAAGCAAGGAAACGCAATAATATATAAAA
[PT-prism]_M13_core_5	TATTTTGCTATCCCAATCCAATTTTTTTAGCAATAGC T ATCGAACTGGC
[PT-prism]_M13_core_6	TTACCAGCACATAAAGGTGGCAACAACGGAAT
[PT-prism]_M13_core_7	ATGATTAAAACGTAGAAAATACATGCCAAAGACAA A AGGGGGTGAATT
[PT-prism]_M13_core_8	TTAGCAGACTCTTCAAGAGGAGG
[PT-prism]_M13_core_9	GAAACGCAATCAATAGAAAATTTTGGGAAT
[PT-prism]_M13_core_10	TTTTGAAGTTTTCAGTATG
[PT-	AAACCATCCACCGACTTGAGCCATCATATGGT

prism]_M13_core_11	
[PT-prism]_M13_core_12	GACAGAAAAATTATTCATTAAACGACATTC
[PT-prism]_M13_core_13	AACCGATTGAGGTTTTTTTAGTACCGCACTCATCGAGAAGTCTTTCC
[PT-prism]_M13_core_14	TAGAGCCCAAGGCCGGAAACGTCAGAGCCA
[PT-prism]_M13_core_15	ATCACCGTGATAGCAGCACCGTAATGCCATCT
[PT-prism]_M13_core_16	GACGGTCAAGTTTGCCTTTAGCATTTTCG
[PT-prism]_M13_core_17	TAAAGTAATCCAAGAACGGGTTTTTTTTTAAATATT
[PT-prism]_M13_core_18	CTCAGAGCTCAAAATCACCGGAACCACCAATG
[PT-prism]_M13_core_19	CGCCGCCCCCCTTATTAGCGTTTCAGTAGC
[PT-prism]_M13_core_20	ATCGGCGTCATTTTACCGCCAGT
[PT-prism]_M13_core_21	CCACCGGCCGCCACCCTCAGAGACAGGAGT
[PT-prism]_M13_core_22	TTTCATAACGCCACCAGAACCACCTCCAGTAA
[PT-prism]_M13_core_23	GTCATAGCAGCATTGACAGGAGGTGAATGGAA
[PT-prism]_M13_core_24	AATAAGAGTTTTGCGTTTTC
[PT-prism]_M13_core_25	ATGCCCCCCATGGCTTTTGATGATCCACCACC
[PT-prism]_M13_core_26	TGAAACACTCTGAATTTACCGTACCAGAGC
[PT-prism]_M13_core_27	GGCGGATACTGAGACTCCTCAAGAATCCTCATTAAA GCCATGAGGCAG
[PT-prism]_M13_core_28	GTCAGACGATTGGTTTTTTTTTAATGGTTTGAA
[PT-prism]_M13_core_29	GTACTGGAACAGTGCCCGTATATTTAGTAC
[PT-prism]_M13_core_30	GCGTCATATGCCTATTTCGGAACCCCCGGAAT
[PT-prism]_M13_core_31	AGCGCAGTTGAAAGTATTAAGAGGAGTGCCGT
[PT-prism]_M13_core_32	TCATCTTCTTTTTTTCACAAACAAATAAGAAGGATTA GGATTTTTTTTGAAGCAAA

[PT-prism]_M13_core_33	CAAAATCGCTTAGGTTGGGTTAGTTTAGTA
[PT-prism]_M13_core_34	AGAATCGCTTACTAGAAAAAGCCTTATAACTA
[PT-prism]_M13_core_35	TATGTAAAGAGAAGAGTCAATAGTACATTTAA
[PT-prism]_M13_core_36	AAGACGCTTGCTGATGCAAATCCAAACACCGG
[PT-prism]_M13_core_37	ATTTAGGCGTTAAATAAGAATAATCGCAAG
[PT-prism]_M13_core_38	ACAAAGAAAAACATAGCGATAGTAATGGAA
[PT-prism]_M13_core_39	AATCCTTGACGCGAGAAAACTTTTCGTGTGAT
[PT-prism]_M13_core_40	ATACCGACTCAAATATATTTTAGTCGCTATTAAT
[PT-prism]_M13_core_41	ACTTGCACCCTTCTGACCTGAAAGTTTAAATCGTTAATT
[PT-prism]_M13_core_42	TCATATGCGCTCAACAGTAGGGCGCGCCTG
[PT-prism]_M13_core_43	AATCATAACATATTTAACAACGCCGACAATAA
[PT-prism]_M13_core_44	AAATAAGGCAGAGGCATTTTCGAGACAAAAGG
[PT-prism]_M13_core_45	GTAGAAACTTCAGCTAATGCAGAACTTAATTG
[PT-prism]_M13_core_46	TTATCATTTCTGTCCAGACGACAACATGTA
[PT-prism]_M13_core_47	TTTATCAATCCCATCCTAATTTTCATTACC
[PT-prism]_M13_core_48	ACAACATGCAATCAATAATCGGCTCAAGCAAG
[PT-prism]_M13_core_49	TTTTAGCGATTTTCATCGTAGGAAACGAGCAT
[PT-prism]_M13_core_50	GCGCCCACGGTATTCTAAGAACATCCTGAA
[PT-prism]_M13_core_51	CCGTTTTTAACCTCCCGACTTGCGTTAGTTGC
[PT-prism]_M13_core_52	ACGTCAAAAAACAGCCATATTATTACCCAGCTACAAT TTTGCGAGGCG
[PT-prism]_M13_core_53	TCTTACCTGCCAGTTACAAAATAATGAAAA
[PT-prism]_M13_core_54	TAGCAGCATAAAAACAGGGAAGCGCATTAGACGGG

[PT-prism]_M13_core_55	ACGGTAATCGTAAAACTAGAGAAAAGCCCCAAAACATTAAAT
[PT-prism]_M13_core_56	CCTTCCTGATTTTGTTAAAATTCGACAGGAA
[PT-prism]_M13_core_57	GATTGTATAATTAGCTATTTTTGAGAGATGATATTC
[PT-prism]_M13_core_58	TTTTGTTCATCAAAAATAATTCGTGTAGAT
[PT-prism]_M13_core_59	TTAATTAGCCAGCTTTCATCAGCGGATTG
[PT-prism]_M13_core_60	ATATTTTATAGCTGATAAATTAATTTTTATTGTAAACG
[PT-prism]_M13_core_61	GATCGCACGGGATAGGTCACGTTGGCGTCTGG
[PT-prism]_M13_core_62	TCTGGTGCCGTGGGAACAAACGACATT
[PT-prism]_M13_core_63	AAATGTGATTTTTTTTAAAAATTTTTAGAATACTTTT
[PT-prism]_M13_core_64	GGGCGCAGACGACAGTATCGGCTTGGGTAA
[PT-prism]_M13_core_65	ACCGTAATTCCAGCCAGCTTTCCGGCGAAAGG
[PT-prism]_M13_core_66	ATTCTCCGGAAACCAGGCAAAGGTGCGGG
[PT-prism]_M13_core_67	AGCTGAAAAAGCCTTTATTTTTTTTTTTTCCGTCGG
[PT-prism]_M13_core_68	CAGGTCGACTGCAAGGCGATTAAGCTCAGGAA
[PT-prism]_M13_core_69	GCTCGAACTATTACGCCAGCTGGCACCGCT
[PT-prism]_M13_core_70	CGATCGCGCCATTCTTTTTTTTTTTCATTTATACAT
[PT-prism]_M13_core_71	CGCCAGGCCAGTGCCAAGCTTGAATTGCGT
[PT-prism]_M13_core_72	GGGATGTGCTCTAGAGGATCCCCGTGGGGTGC
[PT-prism]_M13_core_73	CCTCTTCGTTCGTAATCATGGTCACATACGAG
[PT-prism]_M13_core_74	CTCCAGTCAATATTTCGCAACTGTTGGGAAGGGGTTTCC
[PT-prism]_M13_core_75	AATGCTGTACGGTGTCTGGAAGTCATACAG
[PT-prism]_M13_core_76	TACCAAAAATTAACATCCAATAAATTTCATTC
[PT-	CATATAACGCTTAGAGCTTAATTGAGAAGCAA

prism]_M13_core_77	
[PT-prism]_M13_core_78	TGCGGATGAGTTGATTCCCAATTCTACTAATA
[PT-prism]_M13_core_79	GCGGGAGAGGTGGCATCAATTCTGCGAACG
[PT-prism]_M13_core_80	AGTAGATTCCTTTTGATAAGAGGAGGAAGC
[PT-prism]_M13_core_81	TTAATTGCTTAGTTTGACCATTAGGGGGCGCG
[PT-prism]_M13_core_82	TTCGCAAATGACAGGTCAGGATTAGATTTAATTC
[PT-prism]_M13_core_83	GCAAGGCAGAGCATAAAGCTAAAATGTGTA
[PT-prism]_M13_core_84	GTAGTAGCACATTATGACCCTGTAACCCTCAT
[PT-prism]_M13_core_85	AACCGTTCAATGCAATGCCTGAGTATCGGTTG
[PT-prism]_M13_core_86	GGTAAAGAAATCACCATCAATATCTACAAA
[PT-prism]_M13_core_87	GGCTATCCTGGAGCAAACAAGAGAAT
[PT-prism]_M13_core_88	GGGATAGCCACCGTACTCAGGAGGAACAGTTA
[PT-prism]_M13_core_89	CGCCACCCAGAGCCACCACCCTATGAATTT
[PT-prism]_M13_core_90	AGGTGTATAAGCCCAATAGGAACCTAAAGTTT
[PT-prism]_M13_core_91	AGCGAAAGATGCCACTACGAATTTTTTTCTTTGAAAG AGGATAACAAAG
[PT-prism]_M13_core_92	CGGCTACGGAAGTTTCCATTAAAATACACT
[PT-prism]_M13_core_93	CATAAGGGAACCGTTTTTTTCTAAAACGAAAGA
[PT-prism]_M13_core_94	AAAACACCGAAACAAAGTACAACGGAGATTTGTAT
[PT-prism]_M13_core_95	TGATAAATTGTGTCGAAATCCGCGACCTGGAACGAGGC GCAGAAGACCAGG
[PT-prism]_M13_core_96	AATCAACGCAGATGAACGGTGTACCGGTCAAT
[PT-prism]_M13_core_97	CGCATAGAAGAACCGGATATTCGATGGTTT
[PT-prism]_M13_core_98	GTCAGGACAGTAAATTGGGCTTGAATTACCCA

[PT-prism]_M13_core_99	CTGCTCATAAACACCAGAACGAGTGTTGGGAAGAAAA ATCTTGAGATT
[PT-prism]_M13_core_100	TGCCAGAGATAGCGTCCAATACTGACTTCAAATATCGC GTGAGTACCT
[PT-prism]_M13_core_101	TAGGAATAAAAAACCAAAATAGCGTATTCATT
[PT-prism]_M13_core_102	GAATCCCCGCATCAAAAAGATTAAGTCATTTT
[PT-prism]_M13_core_103	AAACGAGCTGACTATTATAGTCCTGAATAT
[PT-prism]_M13_core_104	AGCGGATTCTCAAATGCTTTAAACTTTACCAG
[PT-prism]_M13_core_105	TAACGCCCTATCATAACCCTCGAGTTCAGA
[PT-prism]_M13_core_106	CCGAAAGCGGAATCGTCATAAAAGAGGCTT
[PT-prism]_M13_core_107	GAGCTTCAAAGCGTTTTTTTTTGCTCAGTACCA
[PT-prism]_M13_core_108	ACGACGATCCACATTCAACTAATGTTATACCA
[PT-prism]_M13_core_109	AATTTCATTAAGAACTGGCTCACAGATACA
[PT-prism]_M13_core_110	TTGCAAAAGAAAGATTCATCAGTACGTTAA
[PT-prism]_M13_core_111	TAAAACGAACTATTTTTTTAAAGGAGCCTTTAATTGTA TTTTTTTCA
[PT-prism]_M13_core_112	TGTCGTCTGAATTGCGAATAATAACGGTTTAT
[PT-prism]_M13_core_113	AACTAAAGTTCCAGACGTTAGTAACATTTTCA
[PT-prism]_M13_core_114	GTAACACTTGATATAAGTATAGTATTATTC
[PT-prism]_M13_core_115	CGAGAGGGTGAGTTTCGTCACCAGACAGACAG
[PT-prism]_M13_core_116	CAACGCGCTGAGCTAACTCACATTCATGCCTG
[PT-prism]_M13_core_117	GCGCCAGATAAAGTGTAAAGCCGGTACCGA
[PT-prism]_M13_core_118	CTGAGTTGTAGCAATTTTTTTTCCACACAATAGCT
[PT-prism]_M13_core_119	GGAACAATCAAAGGGCGAAAAACCGT

[PT-prism]_M13_core_120	GGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCCGT GGCGA
[PT-prism]_M13_core_121	CTGCGCGTGGGGAAAGCCGGCGAAACTAAAT
[PT-prism]_M13_core_122	CGGAACCCTATATAGGGTTGAGTGTTGTCGAAATCG
[PT-prism]_M13_core_123	CTTCACCGCCTTATAAATCAAAATTTTTGATTTAGAGC
[PT-prism]_M13_core_124	TTGACAACCACCACACCCGCCTATAACGT
[PT-prism]_M13_core_125	GAAAGGACGCTGGCAAGTGTAGGGAGCTAA
[PT-prism]_M13_core_126	TTATAATCCGTTAGAATCAGAGCGCGGTCACG
[PT-prism]_M13_core_127	CGAGCACGGCGCTTAATGCGCTTTTTTTTGACGGGCAA CAGCCGTATTGG
[PT-prism]_M13_core_128	AAGGGACATCGGCCTTGCTGGTAAAAGAGTCTGTCCA GCTTTGA
[PT-prism]_M13_core_129	CCGGAAGCGGTGGTTTTTCTTTTTTTTTTCGTACTATGG TTTCACGCAA
[PT-prism]_M13_core_130	ATTAACCGTAGAAGAACTCAAACTATTCTGGCCAACA GAGTATTTTTG
[PT-prism]_M13_core_131	AAAACGCGTCTGAAATGGATTAAATACCGA
[PT-prism]_M13_core_132	ACAGGAGCGCCAGAATCCTGAGCAACAGGA
[PT-prism]_M13_core_133	GGCAGATTTTACCGCCAGCCATTGAAGTGTTT
[PT-prism]_M13_core_134	GAACAATACACCAGTCACACGACCCGAACTGA
[PT-prism]_M13_core_135	GCTTTCCTAGTGAGGCCACCGAGTAATATCCA
[PT-prism]_M13_core_136	TGTGTGAAATTGTTTAGTAATAACATC
[PT-prism]_M13_core_137	CTAATGAGGGGGAGAGGCGGTTTGTGATTGCC
[PT-prism]_M13_core_138	TGCGCTCGCCAGCTGCATTAATTTGCAGCA
[PT-prism]_M13_core_139	GCAAAATCCCTGGCCCTGAGAGAGGAATCGGC

[PT-prism]_M13_core_140	AGCGGTCGTTTGATGGTGGTTCTCCAGTTT
[PT-prism]_M13_core_141	GTGCCACGAAACATCGCCATTAAATTTACATT
[PT-prism]_M13_core_142	ATCTAAATTAGTCTTTAATGCGAGTAATAA
[PT-prism]_M13_core_143	AATTTGAGTGAATATTTTTTTCACAGACAAATAGA
[PT-prism]_M13_core_144	TTAAATCGAGTAACATTATCATTTTG
[PT-prism]_M13_core_145	AAAGAAACCACCAGAAGGATGATTATCAGATGA TGAACCTAC
[PT-prism]_M13_core_146	CGTCAGATAATAATGGAAGGGTTAGGCAATT
[PT-prism]_M13_core_147	CATCAATATATTTTACAAACAATTCGACGCCGTCAA
[PT-prism]_M13_core_148	TGGTCAGTACATTTGAGGATTTATTTTTTGGATTATA C
[PT-prism]_M13_core_149	TTCTGGAATATACAGTAACAGCCAAGTTA
[PT-prism]_M13_core_150	CATATCAATTGCGTAGATTTTCTCATTTCA
[PT-prism]_M13_core_151	CAATTTCACGCAGAGGCGAATTATAGGTTTAA
[PT-prism]_M13_core_152	TTTGAATATACCTTTTACATCTTTTTTTTATCAAACC CT CAAAATGAAAA
[PT-prism]_M13_core_153	AGCGATAGTAATGGAAACAGTACTGATTGC
[PT-prism]_M13_core_154	AATGGCTAGCATCACCTTGCTTTTTTTTTAACGGAT TC GCCATAAATCA
[PT-prism]_M13_core_155	ATTACCTAAAACAAAATTAATTGAATTTAT
[PT-prism]_M13_core_156	CAAAATCGTTTGAATTACCTTTTTCTTAGATT
[PT-prism]_M13_core_157	TAGCCCTACTGAGAGCCAGCAGCATCAATATC
[PT-prism]_M13_core_158	ACGAACCCAGTATTAACACCGCGAAAGGAA
[PT-prism]_M13_core_159	TAGATAATTGGCAAATCAACAGTTCTGCAACA
[PT-prism]_M13_core_160	TTGAGGAAACTAATAGATTAGAAACTCGTA
[PT-	TCGTCATAAAGGCCGCTTTTTTTTTGCCCTGAC

prism]_M13_core_161	GAGTCAGTT
[PT-prism]_M13_core_162	TATTCCTACAAACTACAACTTTTATGTTTAGACT GGGGGGTT
[PT-prism]_M13_core_163	TTACCGCCAGTAATAAGAGTTTTGCGTTTTCATC GGCGTCAT
[PT-prism]_M13_core_164	TCAAGAGGAGGTTTTGAAGTTTTCAGTATGTTA GCAGACTCT

Table S2.60. Edge staples of M13mp18 prismatic pentagonal DNA origami tile.

Name	**Sequence**
[PT-prism]_M13_edge_1	TGAAACAAACATCAAGGAGCAAAAGAAGATGATA
[PT-prism]_M13_edge_2	ACCTTTTTAACCTCCGATAGGTCTGAGAGACTAA
[PT-prism]_M13_edge_3	GAACAAGAAAAATAATACAATAGATAAGTCCTCA
[PT-prism]_M13_edge_4	ATATAGAAGGCTTATCATAGCAAGCAAATCAGAT
[PT-prism]_M13_edge_5	AGCAATAAAGCCTCAAAGAATTAGCAAAAT
[PT-prism]_M13_edge_6	ATATGCAACTAAAGTAGCTCAACATGTTTT
[PT-prism]_M13_edge_7	TAGTAAGAGCAACAAAAAGGAATTACGAGG
[PT-prism]_M13_edge_8	TACCTTATGCGATTACTTTAATCATTGTGA
[PT-prism]_M13_edge_9	CGCCACCCTCAGAAAACCGCCTCCCTCAGA
[PT-prism]_M13_edge_10	ACCATTACCATTAGAGCAAAATCACCAGTA
[PT-prism]_M13_edge_11	GGGGTCAGTGCCTTGAGTTAATAAGTTTTAAC
[PT-prism]_M13_edge_12	TCAGAACCGCCACCCTCTCAGAACCGCCACCCGC
[PT-prism]_M13_edge_13	ACTTTCAACAGTTTCAGGGATTTTGCTAAACAGC
[PT-prism]_M13_edge_14	AGACAGGAACGGTAGCCGATTAAAGGGATT
[PT-prism]_M13_edge_15	AGCGGGCGCTAGGGAGGGAAGAAAGCGAAA
[PT-prism]_M13_edge_16	ACAGAGGTGAGGCGGTACCAGCAGAAGATAAATT
[PT-prism]_M13_edge_17	CTTTAGGAGCACTAACAGGTTATCTAAAATATGG
[PT-prism]_M13_edge_18	CAGTTTGAGGGGACTCGTAACCGTGCATCT
[PT-prism]_M13_edge_19	ACCAATAGGAACGCAAATCAGCTCATTTTT
[PT-prism]_M13_edge_20	TCGGGAAACCTGTCGTACTGCCCGCTTTCCAGGC
[PT-prism]_M13_edge_21	AGCAGGCGAAAATCCTCACGCTGGTTTGCCCCTA

Table S2.61. Core staples of M13mp18 Cairo pentagonal DNA origami tile.

Name	**Sequence**
[PT-Cairo]_M13_core_1	AAACAAATAAATCCTCATTTACCGTTCCAGTAAGGCCTTGA
[PT-Cairo]_M13_core_2	ATGAAAGTTTTTAACGGGGTCAGTCGTCATAC
[PT-Cairo]_M13_core_3	ATGGCTTTTGTTCCCTCAGAGCCGCCACCACTCAGAGC
[PT-Cairo]_M13_core_4	GTAACAGTTTCGGAACCTATTATCCCGGAA
[PT-Cairo]_M13_core_5	TTTTCGGTTCAGAACCGCCACCCTTTTTTTGTACTGGTAATAA GATTAAGAG
[PT-Cairo]_M13_core_6	CGCCACCCGTTGATATAAGTATAGTCTGAAAC
[PT-Cairo]_M13_core_7	GCTGAGACAAGTGCCGTCGAGAGGTCAGAGCC
[PT-Cairo]_M13_core_8	AGGCGGATTCCTCAAGAGAAGTTTTTTTTTTGTAGCGCGTT TTTCAGTAGC
[PT-Cairo]_M13_core_9	TAGGTGTACTCAGAACCGCCACCCCAGACG
[PT-Cairo]_M13_core_10	CCTCATAGCATTTTCAGGGATAGCTCAGTACC
[PT-Cairo]_M13_core_11	TATTGACGCAAGTTTGCCTTTTTTTTTGGGGTTTTGCAAGCCCAA
[PT-Cairo]_M13_core_12	GAATAGAAAAGTTTTGTCGTCTTTCTCAGAAC
[PT-Cairo]_M13_core_13	ACCACCCTTTAGCGTAACGATCTAAGGAACAA
[PT-Cairo]_M13_core_14	TAGGAACGCCTGTAGCATTCCATTTTCACGT
[PT-Cairo]_M13_core_15	ACTACAACCCATGTACCTTTTTTAGGGAGGGAAGCGCCAAAG ACAAAAACAAAGTT
[PT-Cairo]_M13_core_16	TTAGTAAATTTCAACAGTTTCAGCGCCCAC
[PT-Cairo]_M13_core_17	GCTTGATAATTGCGAATAATAATTCAGACAGC
[PT-Cairo]_M13_core_18	CAGCTTGCTCTCCAAAAAAAAGGCCAGTACAA
[PT-Cairo]_M13_core_19	CGGAATTTAGCCGAGGGCGATTCGTCACTCCAAAAGGAGCTT TTTTTTAAGCCT
[PT-	GTATGTTAAACATATAAAAGAAATTGGGAA

Cairo]_M13_core_20	
[PT-Cairo]_M13_core_21	AAACCATCCACCGACTTGAGCCATCGCAAAGA
[PT-Cairo]_M13_core_22	CACCACGGTGATTAAGACTCCTTATGAGTTAA
[PT-Cairo]_M13_core_23	AAGAAACACCCAAAAGAACTGGCAAATAAGTTTATTTTG TGGTGAATT
[PT-Cairo]_M13_core_24	GACAGAATGAAATTATTCATTAAACACAATCAATAGAAA ACAATAATA
[PT-Cairo]_M13_core_25	CGAAGCCGAAACCGAGGAAACGTTCATATGGTTTACCA GGTAAA
[PT-Cairo]_M13_core_26	TTAGAGCCCAAGGCCGGAAACGTGCGTTTG
[PT-Cairo]_M13_core_27	ATCACCGTGATAGCAGCACCGTAACATCGGCA
[PT-Cairo]_M13_core_28	CGCCACCCCATAGCCCCCTTATTACACCAATG
[PT-Cairo]_M13_core_29	CCATCTTTACCGGAACCGCCTCCGAACCAC
[PT-Cairo]_M13_core_30	CACCAGAGGTCAGACGATTGGCCTTGA
[PT-Cairo]_M13_core_31	AATACCACATTCAACTAATGCAGATAAGAGCAACACTAT CAAAAAGAAG
[PT-Cairo]_M13_core_32	TCATAAATAGCGAGAGGCTTTTGCTAACCCTC
[PT-Cairo]_M13_core_33	GTTTACCAGACTTTTTTTTATACCAGTCAGGACGTTTGAATTAC
[PT-Cairo]_M13_core_34	TTTTGCCTAGCGTCCAATACTGTACCCTGA
[PT-Cairo]_M13_core_35	CAGTGAATATTTTAAGAACTTTTTTTTTAAAACCAAAA TATTCATTG
[PT-Cairo]_M13_core_36	CAAATATCTCAAAAATCAGGTCTTCGGAATCG
[PT-Cairo]_M13_core_37	AATCCCCCTCATTTTTTTTAGCTGCTCATT
[PT-Cairo]_M13_core_38	CTATTATTTAAGAGGAAGCCCGTTGCGGAT
[PT-Cairo]_M13_core_39	ACCATAAAGCGTTTTAATTCGAGCCTTTAATT
[PT-	CGGATATTCATTACCCAAATTTAGTTCAGAAAACGAG

Cairo]_M13_core_40	AATG
[PT-Cairo]_M13_core_41	AGTACGGTTGATAAGAGGTCATTTAAAGACTT
[PT-Cairo]_M13_core_42	CAGTTGATCAGGATTAGAGAGTACTTCAAAGC
[PT-Cairo]_M13_core_43	GAACCAGACCGTTTTTTTTACTTAGCCGG
[PT-Cairo]_M13_core_44	GGCTTAGACATGTTTTAAATATTGGCATCA
[PT-Cairo]_M13_core_45	GCTCCTTTGTCTGGAAGTTTCATTTATATTTT
[PT-Cairo]_M13_core_46	CCATTAAATCCGCGACCTGTTTTTTTTCTCCAACAGGTT CCCAATTC
[PT-Cairo]_M13_core_47	AAAATTAAGCGCGAGCTGAAAAGGGCAACTAA
[PT-Cairo]_M13_core_48	CTAAATCGCAATAACCTGTTTAGCCCATATAA
[PT-Cairo]_M13_core_49	TGCGAACGAGTTTTTTTTGAGGAAGTTT
[PT-Cairo]_M13_core_50	ATTCTACTACAGGCAAGGCAAAAGGGTGAG
[PT-Cairo]_M13_core_51	CATTTGGGGCAATAAAGCCTCAGAATGCCTGA
[PT-Cairo]_M13_core_52	CATTTCGCAAATGGTGTTGTACCAAAAACAATTTTTAG
[PT-Cairo]_M13_core_53	CTTTGAGGACTATGACCATTAGATA
[PT-Cairo]_M13_core_54	ATGCCGGATAGGTAAAGATTCAAAGAATTAGC
[PT-Cairo]_M13_core_55	TACAAAGGATATATTTTAAATGCAGCATAAAG
[PT-Cairo]_M13_core_56	CTGGAGCACAACGCAAGGATAAAATTATGACC
[PT-Cairo]_M13_core_57	CTGTAATACTTTTTTTTTTGTATCGGTTTAT
[PT-Cairo]_M13_core_58	AAAGGCCCAACCGTTCTAGCTGTTGTATAA
[PT-Cairo]_M13_core_59	GTAATGTGGAGGGTAGCTATTTTTTGATAATC
[PT-Cairo]_M13_core_60	AACCCTCCTATCAGGTCATTGCAAACTAG
[PT-Cairo]_M13_core_61	TTATTTAACAAGTTTGAGACGAAAAACCGTCTTTTTTT TTGAGTCAATAGTG

[PT-Cairo]_M13_core_62	TCACCCTCCAATGACAACAACCATCGGAGTGA
[PT-Cairo]_M13_core_63	CTAAAGGACCGATAGTTGCGCCGAAGCAGCGA
[PT-Cairo]_M13_core_64	TGAAAATTTCGAGGTGAATTTCAACGGCTACAGAGG
[PT-Cairo]_M13_core_65	GCATAACCTAAAGGCCGCTTTTGGAGGCAA
[PT-Cairo]_M13_core_66	ATACGTAAATCGGAACGAGGGTAGCTTAAACA
[PT-Cairo]_M13_core_67	AACGGAGACCAACCTAAAACGAAACGGGATCG
[PT-Cairo]_M13_core_68	AAGACAGCTGCCACTACGAAGGCATTTGTATC
[PT-Cairo]_M13_core_69	AAGAATACATACCAAGCGCGAAACCAACTT
[PT-Cairo]_M13_core_70	AACGAGGCATAAATTGTGTCGAAACGGGTAAA
[PT-Cairo]_M13_core_71	TAATCTTGAAGGGAACCGAACTGACAAAGTAC
[PT-Cairo]_M13_core_72	ATCGCCTGGCAGACGGTCAATCATACAAGAAC
[PT-Cairo]_M13_core_73	TGAAAGAGGGCTGGCTGACCTTCAGAAACA
[PT-Cairo]_M13_core_74	CTTATGCGAAGGCTTGCCCTGACGATCAAGAG
[PT-Cairo]_M13_core_75	CCAGAACGCAACTTTAATCATTGGGGAAGA
[PT-Cairo]_M13_core_76	AAAATCTATTACAGGTAGAAAGATTCATCAGTTG
[PT-Cairo]_M13_core_77	CTTATCCGGTATTCTAAGACGGGAGGTTTTGAAGACG CTAA
[PT-Cairo]_M13_core_78	TCCAAATAATCCTGAATCTTACCACCTTAAAT
[PT-Cairo]_M13_core_79	CAAGATTAGTTTTACCGCACTCATCGAGAAGGCTGTC T
[PT-Cairo]_M13_core_80	CGAGCGTCAACAGCCATATTATTACACCCT
[PT-Cairo]_M13_core_81	CCTGTTTACATTCCAAGAACGGGTTTTTTCCCAGCTA CAATTTTAGAAACGA
[PT-Cairo]_M13_core_82	GCCCAATACGGGAGAATTAACTGATATCCCAA
[PT-Cairo]_M13_core_83	TTTTTTGTAGGGAAGCGCATTAGAATAAGAGC
[PT-	ATAAAAACTTAACGTCAAAAATTTTTTTTTGTTCAGC

Cairo]_M13_core_84	TAATGCGTAAAGTA
[PT-Cairo]_M13_core_85	GAACAAAGATAACCCACAAGAATTTACGCA
[PT-Cairo]_M13_core_86	ACGGAATAATGAAATAGCAATAGCAGAATAAC
[PT-Cairo]_M13_core_87	CATATGCGCAGACGACGATTTTTTTTTCTTTACAGAGTATCTTAC
[PT-Cairo]_M13_core_88	ACCAGAAGCTTTTTAAGTTTTTTAAAGCCTGTAAATAAGA
[PT-Cairo]_M13_core_89	AATCCAAAAATATATTTTAGTTAATTGAGA
[PT-Cairo]_M13_core_90	GAGAATATCTCAACAGTAGGGCTTAATTTCAT
[PT-Cairo]_M13_core_91	CTTCTGACTAACTATATGTAAATGATAACCTT
[PT-Cairo]_M13_core_92	GGGTTATACTAAATTTAATGGTTTCAGTATAA
[PT-Cairo]_M13_core_93	ATTCTGTCTTATACAAATTCTTACGAAATACC
[PT-Cairo]_M13_core_94	GACCGTGTCCTTTTTAACCTCCGGTTAATTTT
[PT-Cairo]_M13_core_95	GAGACTAGATAAATAAGGCGTTTTAGTAT
[PT-Cairo]_M13_core_96	ATAAACACAATTTATCAAAATCATGCGATAGC
[PT-Cairo]_M13_core_97	ATCGCCAAGGCATTTTCGAGCCCCTGAACA
[PT-Cairo]_M13_core_98	AGCCAACGAAAGTACCGACAAAAGAGAACGCG
[PT-Cairo]_M13_core_99	TTCCTTATTCAACAATAGATAAGTAGTAATAA
[PT-Cairo]_M13_core_100	AGAAAAAAACCAATCAATAATCCAAGCAAG
[PT-Cairo]_M13_core_101	CCGTTTTATAGCAAGCAAATCAGATA
[PT-Cairo]_M13_core_102	TGCGCAACTGTTGGGAAGGAGCTGGCGAAAGGGGAACGACG
[PT-Cairo]_M13_core_103	TTCGTAATAGTCACGACGTTGTAAGATGTGCT
[PT-Cairo]_M13_core_104	GCAAGGCGATTTGTATCGGCCTCAGGAAGACGCATCGT
[PT-Cairo]_M13_core_105	GCCAGTGCGATCCCCGGGTACCGAGTGAGC
[PT-Cairo]_M13_core_106	GTGAGCGAATCTGCCAGTTTGAGTTTTTTCGCCAGGGTTTTCCCCATGGTCA

[PT-Cairo]_M13_core_107	CTGCATTACCTGGGGTGCCTAATGAGCTCGAA
[PT-Cairo]_M13_core_108	TAGCTGTTAGCATAAAGTGTAAAGATGAATCG
[PT-Cairo]_M13_core_109	GAGCCGGATCCTGTGTGAAATTTTTTTTTTCAGCTT TCATCAAACGCCATC
[PT-Cairo]_M13_core_110	TAACTCACAGTCGGGAAACCTGTCGAAAAT
[PT-Cairo]_M13_core_111	GAGTTGCAGCGGGGAGAGGCGGTTCAACATAC
[PT-Cairo]_M13_core_112	CATGTCAATTCGCGTCTGTTTTTTTTTCAATTCCA CATGCGTATT
[PT-Cairo]_M13_core_113	AGGGTTGAGGTTTGCCCCAGCAGGCGTGCCAG
[PT-Cairo]_M13_core_114	GCCAACGCGCAAGCGGTCCACGCTGTGTTGTT
[PT-Cairo]_M13_core_115	GGGCGCCCCCTTCACCGCCTGGTTAAAGAAC
[PT-Cairo]_M13_core_116	GCTGATTGAGGGTGGTTTTTTTTGTAATCGTACTGAG AGT
[PT-Cairo]_M13_core_117	CCTGTTTGAAATCAAAAGAATAGGAGCCCC
[PT-Cairo]_M13_core_118	GGTCGAGGGAACAAGAGTCCACTACCCTGAGA
[PT-Cairo]_M13_core_119	CGTGAACCTCCAACGTCAAAGGGCGGGCAACA
[PT-Cairo]_M13_core_120	CAGCTCATCCCAAAAACAGGAAGAATAAATTA
[PT-Cairo]_M13_core_121	AAAAATAATCATATGTACCCCGGTGAGAGATC
[PT-Cairo]_M13_core_122	GCAAATATTCGCATTAAATTTTTTCTCCGT
[PT-Cairo]_M13_core_123	AGAAAAGCTTTTTAACCAATAGGACATTAAAT
[PT-Cairo]_M13_core_124	AACCGTGCGTAACAACCCGTCGGATGTTAAAT
[PT-Cairo]_M13_core_125	GGGAACAGTTGGTGTAGATGGGTCGCACTC
[PT-Cairo]_M13_core_126	CAGCCAGGGCAAAGCGCCATTCGCCA
[PT-Cairo]_M13_core_127	GCCTGCAACAGTGCCACGCTGAGAGCTGCTGAACC TCAAATTTGAGGAA
[PT-Cairo]_M13_core_128	ACATTTGACAACAGTTGAAAGGAAATCAAACC
[PT-	CTCAATCAATATTTTTTTTTAATGCGCGAACTGATA

Cairo]_M13_core_129	TGGCACAG
[PT-Cairo]_M13_core_130	GGTTATCGATTAGAGCCGTCAATAAAAGTT
[PT-Cairo]_M13_core_131	GATTCACCTTTGAATGGCTTTTTTTTTTAGTTGGC AAATGGATTTAG
[PT-Cairo]_M13_core_132	TTCCTGATCGAACGTTATTAATTTTAGATAAT
[PT-Cairo]_M13_core_133	AAGTATTAGACTTTTTTTTTTACATTGGCA
[PT-Cairo]_M13_core_134	TGAGTAAGAAGGAGCGGAATTAAAACAGAA
[PT-Cairo]_M13_core_135	CCTTTGCCTATCAGATGATGGCAAAGAACCTA
[PT-Cairo]_M13_core_136	TTTTGACGCTCAATCGTCTTTTTCGACAACTCGTATTA AAT
[PT-Cairo]_M13_core_137	TACATCGGAAATTATTTGCACGTATCATCATA
[PT-Cairo]_M13_core_138	ATTGCTTTGAATAATGGAAGGGTTTTCATCAA
[PT-Cairo]_M13_core_139	TATAATCCTGATTTTTTTTAGCAATACTT
[PT-Cairo]_M13_core_140	ATAAAGAGAATATACAGTAACAACAATTTC
[PT-Cairo]_M13_core_141	CCATATCAGAGAAACAATAACGGAAAACATCA
[PT-Cairo]_M13_core_142	TACTATGGTCACGCAAATTTTTTTTTTATTATACTT CTGAATACCAA
[PT-Cairo]_M13_core_143	GCTTCTGTAAATTAATTACATTTAGTACCTTT
[PT-Cairo]_M13_core_144	CCCTTAGAAAGAAGATGATGAAACTTCGCCTG
[PT-Cairo]_M13_core_145	GTTACAAAATTTTTTTTTACAGGGCGCG
[PT-Cairo]_M13_core_146	ATTTGAAAATATATGTGAGTGACTGATGCA
[PT-Cairo]_M13_core_147	AGAAAACAAAATCGTCGCTATTAACTTAGGTT
[PT-Cairo]_M13_core_148	CAATTACCTGAGCAAATCCTTGAAAACATAAGGTCTG A
[PT-Cairo]_M13_core_149	CACCCGCCGCGCTAATTATTCATTT
[PT-Cairo]_M13_core_150	TTAGATTAAGACTTTTTTTGATGGCCCACTA
[PT-Cairo]_M13_core_151	GGAGCGGGATCGGAACCCTAAAGGCCCGAGAT

[PT-Cairo]_M13_core_152	CCAGTTTGTGCCGTAAAGCACTAACGCTAGGG
[PT-Cairo]_M13_core_153	GTGGACATCACCCAAATCAAGTGCGCGTAACCACCA
[PT-Cairo]_M13_core_154	CGATTTAGGAAAGGAAGGGAAGAGGGAGCT
[PT-Cairo]_M13_core_155	ACGAGCACAGTGTAGCGGTCACGCTTTTTTGG
[PT-Cairo]_M13_core_156	TTTATAATTCGTTAGAATCAGAGCAAGCGAAA
[PT-Cairo]_M13_core_157	CGCTGGCAGTATAACGTGCTTTCCCAGTGAGG
[PT-Cairo]_M13_core_158	AAACAGGAACGCCAGAATCCTGATCAAACT
[PT-Cairo]_M13_core_159	CTTTGATTTAAAAGAGTCTGTCCATTGCTTTG
[PT-Cairo]_M13_core_160	CATGGAAAGCCTGAGTAGAAGAACGAAGTGTT
[PT-Cairo]_M13_core_161	CCACCGAGAGTAATAACATCACTTTACCTACA
[PT-Cairo]_M13_core_162	ATCGGCCTGCCATTGCAACAGGAATAAAAG
[PT-Cairo]_M13_core_163	ACAATATTAGTCACACGACCAGTAAAAACGCT
[PT-Cairo]_M13_core_164	GGACATTCAAGCGTAAGAATACGGCCCTAA
[PT-Cairo]_M13_core_165	AACATCGCGATAAAACAGAGGTGAGGCGGTCAGT

Table S2.62. Edge staples of M13mp18 Cairo pentagonal DNA origami tile.

Name	**Sequence**
[PT-Cairo]_M13_edge_1	AATGCCCCCTGCCTATGCCCGTATAAACAGTTTA
[PT-Cairo]_M13_edge_2	GATTTTGCTAAACAACTGAATTTTCTGTATGGCC
[PT-Cairo]_M13_edge_3	TACGCTAATATCAGAGAGTCAGAGGGTAATTGAG
[PT-Cairo]_M13_edge_4	GCACCATTACCATTAGAGCAAAATCACCAG
[PT-Cairo]_M13_edge_5	GACGAACCTCCCGACTTGACGCGAGGCGTTTTAG
[PT-Cairo]_M13_edge_6	CAGGAGGTTGAGGCAGCCGCCGCCAGCATT
[PT-Cairo]_M13_edge_7	ATGTTTAGACTGGAAGAGGGGGTAATAGTA
[PT-Cairo]_M13_edge_8	TGAGATGGTTTAATTTAGTAGTAAATTGGGCTAA
[PT-Cairo]_M13_edge_9	AATGCTGTAGCTCAAGCTTAATTGCTGAAT
[PT-Cairo]_M13_edge_10	TTGACCCCCAGCGATTACTAAAACACTCATCTAT
[PT-Cairo]_M13_edge_11	ATCAATATGATATTGGAGACAGTCAAATCA
[PT-Cairo]_M13_edge_12	CGAGAAAACTTTTTCTCGCAAGACAAAGAACCG

[PT-Cairo]_M13_edge_13	TTTACGAGCATGTAGATAATATCCCATCCTAACA
[PT-Cairo]_M13_edge_14	GGTCGACTCTAGAGCAAGCTTGCATGCCTG
[PT-Cairo]_M13_edge_15	GCAAAATCCCTTATATGGTGGTTCCGAAAT
[PT-Cairo]_M13_edge_16	ATGGGATAGGTCACAACGGCGGATTGACCG
[PT-Cairo]_M13_edge_17	GCACTAACAACTAATATAAAATATCTTTAGGAAA
[PT-Cairo]_M13_edge_18	AGGTTTAACGTCAGATAATTGCGTAGATTTTCTT
[PT-Cairo]_M13_edge_19	TAGACAGGAACGGTGGCCGATTAAAGGGAT
[PT-Cairo]_M13_edge_20	CCCTTCTGACCTGATGGCCAACAGAGATAG

Table S2.63. Core staples of p8064 floret pentagonal DNA origami tile.

Name	**Sequence**
[PT-floret]_p8064_core_1	ATCATTACCGCGCCCAATATATTCTAAGAACGCGCGGGAGGT
[PT-floret]_p8064_core_2	ACTTGAGGCGTTTTTTTTATCATTCCAATA
[PT-floret]_p8064_core_3	TTTGAAGCAGCTACAATTTTATGCCAGTTA
[PT-floret]_p8064_core_4	ATCGGCTGTTTACCTCCCG
[PT-floret]_p8064_core_5	AAAAATGATTCCAGAGCCTAATTTCCTGAATC
[PT-floret]_p8064_core_6	TTACCAACGTGCCTGTTTA
[PT-floret]_p8064_core_7	CAAAATAGAAACGATTTTTTGTAGACGGGA
[PT-floret]_p8064_core_8	AGGCATAATGCGCGTCTAAATAGCAGCTTTTAATTT
[PT-floret]_p8064_core_9	CCCACAAGAACAGGGAAGCGCATTTTAACGTC
[PT-floret]_p8064_core_10	GAATTAAGAGCGCTAATATCAGCTTTTTAA
[PT-floret]_p8064_core_11	TCATAATTTATTTAACAACGCCATTTTAGAGAATAACATAAAAATTGAGT
[PT-floret]_p8064_core_12	GGAATACCCTATCTTACCGAAGCCAGAGATAA
[PT-floret]_p8064_core_13	TAAGCCCAAATGAAATAGCAATAGCAAAAGAACTGGCATGTAGAAAAT
[PT-floret]_p8064_core_1	AAACATAATTTTTAAAGTTAAATATTTTTTCAAG

4	
[PT-floret]_p8064_core_15	GAAAAGTAACCGAGGAAACGCAAAAAGAAA
[PT-floret]_p8064_core_16	CAGCGCCAAAAGGTGGCAACATATATAATAAC
[PT-floret]_p8064_core_17	AAACGATTAAGACTCCTTTTTTTATAACTATATGTACCTCC
[PT-floret]_p8064_core_18	CGCAAAGAATAGAAAATTCATAGGGAATTA
[PT-floret]_p8064_core_19	ACATACATAAGACAAAAGGGCGACTGAATTAT
[PT-floret]_p8064_core_20	GGCTTAGGTTGGTTTTTTCAGTATGTTAGC
[PT-floret]_p8064_core_21	ACCATCGACCGACTTGAGCCATTTTGGTTTAC
[PT-floret]_p8064_core_22	CAGAATCATTATTCATTAAAGGATTCAACC
[PT-floret]_p8064_core_23	GATTGAGGGAGGGATTTTTAGTGAATAACCTTG
[PT-floret]_p8064_core_24	GAGCCAGAGGCCGGAAACGTCAAAATCACC
[PT-floret]_p8064_core_25	CACCGTCATAGCAGCACCGTAATCCCTTATTA
[PT-floret]_p8064_core_26	TTCGCCATAAATCAATTTTTTTTATTGACGGAAAAGTT
[PT-floret]_p8064_core_27	ACCGCCACCATCTTTTCATAATCACCAATGAA
[PT-floret]_p8064_core_28	CGCCACCTTTCGGTCATAGCCCAGTAGCGA
[PT-floret]_p8064_core_2	TGCCTTTAGCGTTTTTTACAATAACGGA

9	
[PT-floret]_p8064_core_30	GGAACCACCCTCAGAGCCGCCAAGCGCAGT
[PT-floret]_p8064_core_31	GCGTTTGCCCTCAGAGCCACCACCACAAATAA
[PT-floret]_p8064_core_32	ATCGGCATAGAACCACCACCAGAGCAGGTCAG
[PT-floret]_p8064_core_33	GTACCTTTTACATTTTTTGTAGCGCGTTTTC
[PT-floret]_p8064_core_34	TAATAAGTTAAAGCCAGAATGGAACCCTCAGA
[PT-floret]_p8064_core_35	AACAGTGCCTTGATATTCACAACTCAGAGC
[PT-floret]_p8064_core_36	TGAGGCCGCCGCCATTTTTTTCATATTCCACCAG
[PT-floret]_p8064_core_37	CTCTGAATTGATGATACAGGAGGGATAAGT
[PT-floret]_p8064_core_38	ATCCTCATTTTAACGGGGTCAGTGTAGGATTA
[PT-floret]_p8064_core_39	ACGATTGGCCCGTATAAACAGTTATTAAGAGG
[PT-floret]_p8064_core_40	AAGGAGCGGTTTTTACAGGAGGT
[PT-floret]_p8064_core_41	TAGTACCGTTGCTCAGTACCAGGCTGTACTGG
[PT-floret]_p8064_core_42	GAACCGCCCTCAAGAGAAGGATCCTTGAGT
[PT-floret]_p8064_core_43	TTTCAGGGCTGAAACATGAAAGTAATGCCCCC
[PT-floret]_p8064_core_4	TGCCTATTTCTTTTGTTGAAAGGA

4	
[PT-floret]_p8064_core_45	GCCGTCGTGTATCACCGTACTCAGTTTTGT
[PT-floret]_p8064_core_46	GCGGGGTTCCACCCTCAGAACCGCAGACAGCC
[PT-floret]_p8064_core_47	CTGAGACTCACCCTCAGAGCCACCAGTACAAA
[PT-floret]_p8064_core_48	AATATGTTGGCATTTTATTATTATAGCAAGCCCTACAGAC
[PT-floret]_p8064_core_49	GTTTCAGCTAGCGTAACGATCTAAAGGAGGTT
[PT-floret]_p8064_core_50	TAAAGGACCTGTAGCATTCCACCACCCTCA
[PT-floret]_p8064_core_51	TTGAAAATACTGAGTTTCGTCACCACCCTCAT
[PT-floret]_p8064_core_52	CGTCTTTATTTTGCTAAACAACTGCGCCGA
[PT-floret]_p8064_core_53	CTCATAGTGGAGTGAGAATAGAAAGTGAATTT
[PT-floret]_p8064_core_54	CTACAACGATTGCGAATAATAATTAATTGTAT
[PT-floret]_p8064_core_55	CCGTAACCTCCAAATTTAGTAAGA
[PT-floret]_p8064_core_56	GAAATTGTTTAGTAATACTGAAAGCGTAAGAATTACCCATGTA
[PT-floret]_p8064_core_57	AAAACGCGTCTGAAATGGATTAGCAGAAGA
[PT-floret]_p8064_core_58	CAGCAAATACCGAACGAACCACCATTTACATT
[PT-floret]_p8064_core_5	GGCAGATTTTACCGCCAGCCATTGAAGTGTTT

9	
[PT-floret]_p8064_core_60	GAACAATACACCAGTCACACGACCCATCGCCA
[PT-floret]_p8064_core_61	TGAACCTCTGATAGCCCTAAAAAGTAATAA
[PT-floret]_p8064_core_62	AAGGGACATCGGCCTTGCTGGTAAAAGAGT
[PT-floret]_p8064_core_63	CTCAAACTATTCTGGCCAACAGAGGTCTTTAA
[PT-floret]_p8064_core_64	GGCTATTAATAGAACCCTTCTGACACATCACT
[PT-floret]_p8064_core_65	TAAAACAAACAGTGCCACGCTGACATTTGA
[PT-floret]_p8064_core_66	TTAAAAATGAAAAATCTAAAGCATCAACTAAT
[PT-floret]_p8064_core_67	TGCGCGAACAAATATCAAACCCTCAGGTTATC
[PT-floret]_p8064_core_68	ATTGAGGAAATCAATATCTGGTCATTTTGAAT
[PT-floret]_p8064_core_69	CGTTATTAGCCGTCAATAGATAATAGAGCCAG
[PT-floret]_p8064_core_70	TCATTTTCTTTAGGAGCACTAACACCTTGC
[PT-floret]_p8064_core_71	GGATTTATCGTATTAAATCCTTATGGAAGG
[PT-floret]_p8064_core_72	AGATTAGAATTTTAAAAGTTTGAGAATCCTGA
[PT-floret]_p8064_core_73	TAAAATATGCGGAACAAAGAAACCTGATTATCAGATGATGCAGTAACA
[PT-floret]_p8064_core_7	AATTGCGTATTATACTTCTGAATATGCCCGAA

4	
[PT-floret]_p8064_core_75	GAATATAGCAATTCATCAATATTAACATTA
[PT-floret]_p8064_core_76	GTTAGAATGCACGTAAAACAGATTCATTTC
[PT-floret]_p8064_core_77	TTGTTTGGAGATTTTCAGGTTTAAACCAAGTT
[PT-floret]_p8064_core_78	ACAATTTCGCGCAGAGGCGAATTAAATAAAGA
[PT-floret]_p8064_core_79	CTTCTGTATTAATGGAAACAGTACTGATTGCTTTGAATCGTCAGAT
[PT-floret]_p8064_core_80	AATTACCGAAAACAAAATTAATTCCTTGAA
[PT-floret]_p8064_core_81	ACAAAATCATTTGAATTACCTTTTAATCGTCG
[PT-floret]_p8064_core_82	AGGTCTGATAATTTTCCCTTAGAATACATTTA
[PT-floret]_p8064_core_83	AACATAGAATAGTGAATTTATCAACGCGAG
[PT-floret]_p8064_core_84	CTATTAATGAGACTACCTTTTTAAAATGCTGA
[PT-floret]_p8064_core_85	TACCGACCCAATCGCAAGACAAAGAAAATCAT
[PT-floret]_p8064_core_86	AAAACTTGACCTAAATTTAATGTTAGTATC
[PT-floret]_p8064_core_87	TGCAAATCGTGTGATAAATAAGGCCACCGGAA
[PT-floret]_p8064_core_88	AATCGCCAACTAGAAAAAGCCTGTGTTTGAAA
[PT-floret]_p8064_core_8	ATATGCGCTCAACAGTAGGGCTAGTAATAA

9	
[PT-floret]_p8064_core_90	TCAACAATAAACAACATGTTCAGCGAGGCATTTTCGAGCCTAATTGAG
[PT-floret]_p8064_core_91	GAGAATACCAGACGACGACAATAGATAAGT
[PT-floret]_p8064_core_92	CCTGAACCATGTAGAAACCAATCAAGAACG
[PT-floret]_p8064_core_93	GGTATTAGCCGTTTTTATTTTCATCG
[PT-floret]_p8064_core_94	CTTCACCGCCTTATAAATCAAAATTTTTGATTTAGAGC
[PT-floret]_p8064_core_95	TAATGCGCTTTTTTTTGACGGGCAACAGCCGTATTGG
[PT-floret]_p8064_core_96	TGCCTGAGTTGTAGCAATTTTTTTTCCACACAATAGCTGTT
[PT-floret]_p8064_core_97	CGTTTTCTGCCTGTTCTTCGCGAATTGCGT
[PT-floret]_p8064_core_98	CAACGCGCTGAGCTAACTCACATTTCCGTGAG
[PT-floret]_p8064_core_99	CCTCCTCATGCTGCGGCCAGAATGAAGGTTTC
[PT-floret]_p8064_core_100	CTCTGTGGCAGTTGAGGATCCCCGTGGGGTGC
[PT-floret]_p8064_core_101	GCGCCAGATAAAGTGTAAAGCCGGTACCGA
[PT-floret]_p8064_core_102	CCGGAAGCGGTGGTTTTTCTTTTTTTTTTCGTACTA
[PT-floret]_p8064_core_103	GCTCGAACAGTGTCACTGCGCGCACTGGTG
[PT-floret]_p8064_core_1	TAACGGCAATCAGACGATCCAGCGTTCGTAATCATGGTCACATACGAG

04	
[PT-floret]_p8064_core_105	TCCTGTGTTGCCGGTGCCCCCTGCTCAGATGCCTTTTTT TGAAGATCGCCTGCCAGT
[PT-floret]_p8064_core_106	CTAATGAGGGGGAGAGGCGGTTTGTGATTGCC
[PT-floret]_p8064_core_107	TGCGCTCGCCAGCTGCATTAATTTGCAGCA
[PT-floret]_p8064_core_108	GCAAAATCCCTGGCCCTGAGAGAGGAATCGGC
[PT-floret]_p8064_core_109	AGCGGTCGTTTGATGGTGGTTCTCCAGTTT
[PT-floret]_p8064_core_110	ATCGGAACCCTATATAGGGTTGAGTGTTGTCGAAATCG
[PT-floret]_p8064_core_111	GGAACAATCAAAGGGCGAAAAACCGT
[PT-floret]_p8064_core_112	TGGTTTCACGCAAATTAACCGTAGAAGAA
[PT-floret]_p8064_core_113	CTGTCCAGCTTTGACGAGCACGGCGCT
[PT-floret]_p8064_core_114	TTGACAACCACCACACCCGCCTATAACGT
[PT-floret]_p8064_core_115	CTGCGCGTGGGGAAAGCCGGCGAAACTAA
[PT-floret]_p8064_core_116	GGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCCGTGGCGA
[PT-floret]_p8064_core_117	GAAAGGACGCTGGCAAGTGTAGGGAGCTAA
[PT-floret]_p8064_core_118	TTATAATCCGTTAGAATCAGAGCGCGGTCACG
[PT-floret]_p8064_core_1	GCTTTCCTAGTGAGGCCACCGAGTAATATCCA

19	
[PT-floret]_p8064_core_120	ACAGGAGCGCCAGAATCCTGAGCAACAGGA
[PT-floret]_p8064_core_121	TTCAGAGGTTTCTCCGTGGTGAATTTTTTTTCGTCTCG
[PT-floret]_p8064_core_122	GTGGTGCCTTTTTTTTAACGACGGCCAGTTTGGGTAA
[PT-floret]_p8064_core_123	ATCAACACTCCGTGGGAACAAATCAGGCTG
[PT-floret]_p8064_core_124	GGGATGTGAAGCGCCATTCGCCATCGGCGGAT
[PT-floret]_p8064_core_125	TGACCGTACTGGCCTTCCTGTAGCCCCGGTTG
[PT-floret]_p8064_core_126	ATTCGCGTATGGGATAGGTCACGTTGCCGGAA
[PT-floret]_p8064_core_127	CGCCAGGCGGCACCGCTTCTGGTGGTGTAG
[PT-floret]_p8064_core_128	CAGCTTTCGTTTTCCCAGTCTTTTTTTTTCAGCTTACG GCTCAAATCGT
[PT-floret]_p8064_core_129	ATGGGCGCAATAGGAACGCCATGGAAGATT
[PT-floret]_p8064_core_130	TAAATTGTCAGCTCATTTTTTAACCATCGTAACCGTGC ATACTCCAGC
[PT-floret]_p8064_core_131	CCTGACTTTTTTCGCATACGACGATTTCCAGCGG
[PT-floret]_p8064_core_132	TTGAGGGGTAAATTTTTGTTAAATAAACGTTAATTTTT T TAAAGCGGATAAAATCAG
[PT-floret]_p8064_core_133	ACCAGGCACTGCAAGGCGATTAAGGCCAAGCT
[PT-floret]_p8064_core_1	CGCAACTCTATTACGCCAGCTGACGGATAA

34	
[PT-floret]_p8064_core_135	AGATAGACTGGAGCCGCCACGGGAGCGAAAGG
[PT-floret]_p8064_core_136	CCTCACCTTACCAGTCCCGGAAGAAACAGC
[PT-floret]_p8064_core_137	CGTTCCGGCAAATACGGAAAAAGAGACGCATTTGTGAG
[PT-floret]_p8064_core_138	GGATCAATGGGCGGTTGTGTACATCG
[PT-floret]_p8064_core_139	TGTTCAGGGAGGTGTCCAGCATCGTCG
[PT-floret]_p8064_core_140	TCGCTATGCCAACGGCAGCACCAGCGGGG
[PT-floret]_p8064_core_141	CCGCAAGAGGCAGCCTCCGGCCAGATTGC
[PT-floret]_p8064_core_142	AAAAATCCCGTAAAAAAAGAGTTAAACGATGCTGAGCACATC
[PT-floret]_p8064_core_143	CTCATAAGGTGCTGGTCTGGTCATCCGCCG
[PT-floret]_p8064_core_144	TTTGCTCGGGCGCTTTCGCACTCAAGCAGCAA
[PT-floret]_p8064_core_145	TCATTGCATCATAAACATCCCTTACCTGTGCA
[PT-floret]_p8064_core_146	GGCGCGGGGCTGGTAATGGGTACGGCGGGC
[PT-floret]_p8064_core_147	GTACGGTGACCTGTTTAGCTATATTTTTCGCAAGGATA
[PT-floret]_p8064_core_148	TCTAGCTGTTTTTTTTTGTTTTAAATATGTTAGAGCT
[PT-floret]_p8064_core_1	GTAATAGGCGGAATCGTCATAAAAAGCGAA

49	
[PT-floret]_p8064_core_150	TAAGAGGTTTTTAATTCGAGCTTCATATTCAT
[PT-floret]_p8064_core_151	TGAATCCCGCAAAAGAAGTTTTGCAGGTAGAA
[PT-floret]_p8064_core_152	AGGCTTTTCCTCAAATGCTTTAAAGACTTCAA
[PT-floret]_p8064_core_153	TAATTGCAGAGGAAGCCCGAAACAGTTCAG
[PT-floret]_p8064_core_154	AAAGATTATGAATATAATGCTTTTTTTTTCGGAGAGGGTAGCAAATATT
[PT-floret]_p8064_core_155	AAAACGAACGATAAAAACCAAAATACCACA
[PT-floret]_p8064_core_156	TACATAACCCTCGTTTACCAGACGGAATGACCATAAATCATGCATCAA
[PT-floret]_p8064_core_157	GTCTTTACGCAACACTATCATAACGCCAAAAGGTTTTTTTGGAGCCTTTTTTTCACG
[PT-floret]_p8064_core_158	ATATCGCGCATTTTTGCGGATGGCCAACTAAA
[PT-floret]_p8064_core_159	CCAGACCGTACCTTTAATTGCTCATATAAC
[PT-floret]_p8064_core_160	GGTCAATATCTGGAAGTTTCATTCCCTTTTGA
[PT-floret]_p8064_core_161	AGTTGATACCATTAGATACATTGGCATCAA
[PT-floret]_p8064_core_162	TTGCGGGAGAAGTGCGCGAGCTGAAAAGGTTCGCAAAT
[PT-floret]_p8064_core_163	TTCTACTACAGGCAAGGCAAAGAATT
[PT-floret]_p8064_core_1	GTATAAGCTATTTTTGAGAGATACCGT

64	
[PT-floret]_p8064_core_165	AAAATATCAATATGATATTCACTACAAAG
[PT-floret]_p8064_core_166	AAATCACCTTTTAGAACCCTCATATACTT
[PT-floret]_p8064_core_167	ATTAAGCAATAAAGCCTCAATTATGACCCTGTAATATTTTAA
[PT-floret]_p8064_core_168	ATGCAATGGTGAGAAAGGCCGGCTGGAGCA
[PT-floret]_p8064_core_169	ATAATCAGGTCATTGCCTGAGAGTAGACAGTC
[PT-floret]_p8064_core_170	GCTATCAGAAAAGCCCCAAAAACACAAAAATA
[PT-floret]_p8064_core_171	AACAAGAGTCAATCATATGTACCAGCTTTC
[PT-floret]_p8064_core_172	AGGACTAACTAAAACACTCATCTTTTTTGGCTGGCTGA
[PT-floret]_p8064_core_173	TGGGCTTGTTTTTTTTGCAACGGCTACAGTCACCCTC
[PT-floret]_p8064_core_174	TTAAAGGCGCTTGATACCGATAGTTTTCAACA
[PT-floret]_p8064_core_175	AGCAGCGCAGCTTGCTTTCGAGGGAACAAC
[PT-floret]_p8064_core_176	CGGTTTATAAAGACAGCATCTTTTTTTTTTTCAACTTTAATAATGCAGA
[PT-floret]_p8064_core_177	CTTAAACACGCTTTTGCGGGATCGAGGCTTTG
[PT-floret]_p8064_core_178	CAATGACCGGTCGCTGAGGCTTAAGTTTCC
[PT-floret]_p8064_core_1	AGAATACAAGACTTTTTCATGAGGGCAGGGAG

79	
[PT-floret]_p8064_core_180	ATTAAACCAACCTAAAACGAAAAACAAAGT
[PT-floret]_p8064_core_181	AACGGTGTACAGTGATTATACCAAGCGCGAGAGGCAAA
[PT-floret]_p8064_core_182	ACAACGGAAATCCGCGACCTGCTCCA
[PT-floret]_p8064_core_183	TTCAACTCATTGTGAATTACCTTAAAT
[PT-floret]_p8064_core_184	CCTTCACACCAGAACGAGTAGTATGCGAT
[PT-floret]_p8064_core_185	GACGAGAAATCAAGAGTAATCTTGAGATG
[PT-floret]_p8064_core_186	TTAGCCGGAACGAGGCGCAACTTTGAAAGAGGACACAAGAAC
[PT-floret]_p8064_core_187	CGGATATATTCAGTGAATAAGGGTCAGGAC
[PT-floret]_p8064_core_188	AGATTCATCTGGCTCATTATACCACTTGCCCT
[PT-floret]_p8064_core_189	TTTAAGAACAGTTGAGATTTAGGAATAGCGAG
[PT-floret]_p8064_core_190	GTTGGGAGAACAACATTATTACCAGAGGGG

Table S2.64. Edge staples of p8064 floret pentagonal DNA origami tile.

Name	**Sequence**
[PT-floret]_p8064_edge_1	TGCTATTTTGCACCCCTTAAATCAAGATTA
[PT-floret]_p8064_edge_2	GTCAGAGGGTAATTCTGAACACCCTGAACA
[PT-floret]_p8064_edge_3	ATTTTGTCACAATCACACCACGGAATAAGT
[PT-floret]_p8064_edge_4	CATTACCATTAGCACAAAATCACCAGTAGC
[PT-floret]_p8064_edge_5	GTCATACATGGCTTTTTACCGTTCCAGTAA
[PT-floret]_p8064_edge_6	TAGCCCGGAATAGGAGAGGGTTGATATAAG

[PT-floret]_p8064_edge_7	ATAACCGATATATTAACAACCATCGCCCAC
[PT-floret]_p8064_edge_8	GATAAATTGTGTCGAGATTTGTATCATCGC
[PT-floret]_p8064_edge_9	CATCCTAATTTACGAGAAGAAAAATAATATCCGT
[PT-floret]_p8064_edge_10	CAGTATAAAGCCAACGTTATACAAATTCTTACAA
[PT-floret]_p8064_edge_11	GACGCTGAGAAGAGTCCGATAGCTTAGATTAATT
[PT-floret]_p8064_edge_12	ATGAAACAAACATCAATGAGCAAAAGAAGATGAC
[PT-floret]_p8064_edge_13	CAAACAATTCGACAACGAAGTATTAGACTTTAGC
[PT-floret]_p8064_edge_14	TATTAACACCGCCTGCGAGGTGAGGCGGTCAGTA
[PT-floret]_p8064_edge_15	TTAGACAGGAACGGTAGCCGATTAAAGGGATTGC
[PT-floret]_p8064_edge_16	CAAGTTTTTTGGGGTCGAACCATCACCCAAATCT
[PT-floret]_p8064_edge_17	GTTGTACCAAAAACGAGCATAAAGCTAAAT
[PT-floret]_p8064_edge_18	CGTAAAACTAGCATGAATCGATGAACGGTA
[PT-floret]_p8064_edge_19	TGCGGGCCTCTTCGGTTGGGAAGGGCGATC
[PT-floret]_p8064_edge_20	TTGCCGCCAGCAGTACTTAAATTTCTGCTC
[PT-floret]_p8064_edge_21	ACATCCAATAAATCATAATAGTAGTAGCATTACG
[PT-floret]_p8064_edge_22	AGGTCAGGATTAGAGAGGAAGCAAACTCCAACAT
[PT-floret]_p8064_edge_23	ATAAAACGAACTAACGAGAAAAATCTACGTTAGG
[PT-floret]_p8064_edge_24	GGAACCGAACTGACCAGACGGTCAATCATAAGAT
[PT-floret]_p8064_edge_25	GTGATGAAGGGTAACCGCACAGGCGGCCTT
[PT-floret]_p8064_edge_26	AACGTGGACTCCAACGGAGTCCACTATTAAAGTA
[PT-floret]_p8064_edge_27	CACTGTTGCCCTGCTTGCGGTATGAGCCGG
[PT-floret]_p8064_edge_28	TCGGGAAACCTGTCGTACTGCCCGCTTTCCAGGT

2.8 References

1 Qi, X. *et al.* Programming molecular topologies from single-stranded nucleic acids. *Nat. Commun.* **9**, 4579, (2018).

2 Snodin, B. E. *et al.* Introducing improved structural properties and salt dependence into a coarse-grained model of DNA. *J. Chem. Phys.* **142**, 234901, (2015).

3 Ouldridge, T. E., Louis, A. A. & Doye, J. P. Structural, mechanical, and thermodynamic properties of a coarse-grained DNA model. *J. Chem. Phys.* **134**, 085101, (2011).

4 Sulc, P. *et al.* Sequence-dependent thermodynamics of a coarse-grained DNA model. *J. Chem. Phys.* **137**, 135101, (2012).

5 Suma, A. *et al.* TacoxDNA: A user-friendly web server for simulations of complex DNA structures, from single strands to origami. *J. Comput. Chem.* **40**, 2586-2595, (2019).

6 SantaLucia, J., Jr. & Hicks, D. The thermodynamics of DNA structural motifs. *Annu. Rev. Biophys. Biomol. Struct.* **33**, 415-440, (2004).

7 Kilchherr, F. *et al.* Single-molecule dissection of stacking forces in DNA. *Science* **353**, (2016).

APPENDIX B

SUPPLEMENTAL INFORMATION FOR CHAPTER 3

S3.1 Materials and Methods

S3.1.1 Synthesis of customized DNA scaffold strands

Three customized DNA scaffold strands (p2820 and p3548) were synthesized and utilized in this study. The phagemid vector with 2820 base pairs (bp) was synthesized by deleting a DNA fragment of 141 bp from pBlueScript II SK(+) vector using Q5 site-directed mutagenesis kit (New England Biolabs). For p3120 and p3548, customized DNA fragments were synthesized and inserted into pBlueScript II SK(+) vector by Bio Basic Inc. (biobasic.com) to form phagemid vectors with 3210 bp and 3548 bp, respectively. To synthesize DNA scaffold strands, the phagemid vector (2820 bp, or 3548 bp) was co-transformed into *E. coli* DH5α competent cells with a helper plasmid pSB4423, a kind gift from Dr. Stanley Brown (Niels Bohr Institute, Denmark). The DNA scaffold strands were amplified and purified as described previously[1]. The mass concentration of each strand was measured by NanoDrop™ 2000 spectrophotometer (Thermo Scientific) and converted to molar concentration using the average molecular weight of a DNA nucleotide (330 g/mol). Sequences of these scaffold strands are summarized in Section S3.5.1.

S3.1.2 Sample preparation

The M13mp18 single-stranded DNA was purchased from Bayou Biolabs (P-107, 1 μg/μL). The p8064 single-stranded DNA was purchased from tilibit nanosystems (M1-51, 100 nM). Both DNA strands were used as received without further purification. Sequences of both scaffold strands are summarized in Section S3.5.1.

Staple strands were categorized based on their positions and functions within the DNA origami tiles: core staples fold the scaffold strand into the designed geometry; edge

staples present sticky ends and base stackings that "glue" monomer DNA origami tiles together into higher-order assemblies. All staple strands were purchased from Integrated DNA Technologies (idtdna.com) at 100 μM in RNase-free water and were used as received without further purification. Sequences of staple strands are summarized in Section S3.5.2.

The multimeric complexes assembled from p3120 equilateral triangular tiles were prepared by mixing the p3120 scaffold strand (5 nM) and corresponding staple strands (50 nM/each) in 1× TAE/Mg^{2+} buffer (Tris base 40 mM, acetic acid 20 mM, EDTA·Na_2·$12H_2O$ 2 mM, $(CH_3COO)_2Mg·4H_2O$ 12.5 mM) and annealing the mixture from 80 °C to 20 °C in ~101 h. The annealing procedure was controlled using DNA Engine Tetrad® 2 Thermal Cycler (Bio-Rad). The samples were heated up to 80 °C, held at 80 °C for 10 min, cooled from 80 °C to 40 °C at -1 °C/min, held at 40 °C for 10 min, cooled from 40 °C to 20 °C at -0.1 °C/30 min, and held at 15 °C until use.

The lattices assembled from a single tile species were prepared by mixing the scaffold strand (25 nM), core staple strands (250 nM/each), and edge staple strands (375 nM/ea) in 1× TAE/Mg^{2+} buffer. The samples were annealed following the same procedure used for multimeric complexes.

The lattices assembled from two or more tile species were prepared in two steps. Firstly, different tile species were prepared in separate tubes by mixing the scaffold strand (25 nM), core staple strands (250 nM/each), and edge staple strands (375 nM/ea) in 1× TAE/Mg^{2+} buffer. The mixtures were heated up to 80 °C, held at 80 °C for 10 min, cooled from 80 °C to 40 °C at -1 °C/min, and held at 40 °C until Step 2. In Step 2,

different tile species were mixed in one tube preheated to 40 °C, held at 40 °C for 30 min, annealed from 40 °C to 20 °C at -0.1 °C/30 min, and held at 15 °C until use.

S3.1.3 AFM imaging

For multimeric complexes imaging, the samples were diluted to 3 nM using 1× TAE/Mg^{2+} buffer. 5 μL of the diluted sample was deposited onto a freshly cleaved mica surface (Ted Pella) and incubated for 5 min. Then, 60 μL 1× TAE/Mg^{2+} buffer was added onto the mica surface and removed by compressed air. This step was repeated twice to minimize the imaging background from excess staples. Subsequently, the mica surface was covered by 60 μL 1× TAE/Mg^{2+} buffer, and 10 μL $NiCl_2$ solution (100 mM) was added to assist adsorption. The samples were imaged in "ScanAsyst in Fluid" mode with a ScanAsyst-liquid+ tip on the MultiMode 8 AFM (Bruker).

For the imaging of lattices, the samples were diluted to 5 nM (scaffold concentration) using 1× TAE/Mg^{2+} buffer. 10 μL of the diluted sample was deposited onto a freshly cleaved mica surface and incubated for 5 min. The rest steps were the same as the imaging of multimeric complexes.

S3.2 Designs of DNA Origami Tiles

S3.2.1 Design parameters of DNA origami tiles

Table S3.1. Design parameters of p2820 equilateral triangular DNA origami tile.

Design name	**[TR]_p2820**
Rise per base pair, ***r*** (nm)	0.34
Interhelical distance, ***D*** (nm)	2.75
Number of helices per subunit	18
Minimum helix length (bp)	31
Maximum helix length (bp)	68
Lengths of helices (bp)	31/36/40/45/50/54/59/64/68
Lengths of scaffold loops (nt)	6/8/7/7/8/7/6/4
Length of the scaffold bridge (nt)	5
Lengths of staple bridges (nt)	3/5/5/5/5/4/4/5

Table S3.2. Design parameters of M13mp18 scaffold square DNA origami tile.

Design name	**[SQ]_M13**
Rise per base pair, ***r*** (nm)	0.34
Interhelical distance, ***D*** (nm)	2.69
Number of helices per subunit	22
Minimum helix length (bp)	39
Maximum helix length (bp)	118
Lengths of helices (bp)	39/47/55/63/71/79/ 86/94/102/110/118
Lengths of scaffold loops (nt)	9/11/8/10/8/ 8/9/8/10/8
Length of the scaffold bridge (nt)	3
Lengths of staple bridges (nt)	2/4/7/6/0/ 4/7/7/1/5

Table S3.3. Design parameters of M13mp18 half hexagonal DNA origami tile.

Design name	**[hHE]_M13**
Rise per base pair, ***r*** (nm)	0.34
Interhelical distance, ***D*** (nm)	2.75
Number of helices per subunit	14
Minimum helix length (bp)	40
Maximum helix length (bp)	68
Lengths of helices (bp)	40/45/50/54/59/64/68
Lengths of scaffold loops (nt)	8/7/7/8/7/6
Length of the scaffold bridge (nt)	5
Lengths of staple bridges (nt)	5/5/5/4/4/5

Table S3.4. Design parameters of p8064 scaffold square DNA origami tile.

Design name	**[SQ]_p8064**
Rise per base pair, ***r*** (nm)	0.34
Interhelical distance, ***D*** (nm)	2.69
Number of helices per subunit	18
Minimum helix length (bp)	76
Maximum helix length (bp)	139
Lengths of helices (bp)	76/84/92/100/108/116/ 123/131/139
Lengths of scaffold loops (nt)	11/8/10/8/8/ 9/8/10
Length of the scaffold bridge (nt)	6
Lengths of staple bridges (nt)	7/6/0/5/6/ 7/1/5

Table S3.5. Design parameters of M13mp18 prismatic pentagonal DNA origami tile.

Design name	**[PT-prism]_M13**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***90°***	Subunit ***60°***
Number of helices per subunit	22	14
Minimum helix length (bp)	44	35
Maximum helix length (bp)	123	117
Lengths of helices (bp)	44/52/60/68/76/83/ 91/99/107/115/123	35/48/62/76/ 90/103/117
Lengths of scaffold loops (nt)	10/9/9/9/10/ 10/9/9/8/9	12/12/13/15/12/12
Length of the scaffold bridge (nt)	7	6
Lengths of staple bridges (nt)	7/7/2/4/7/ 7/3/4/7/7	1/5/8/9/7/3

Table S3.6. Design parameters of M13mp18 Cairo pentagonal DNA origami tile.

Design name	**[PT-Cairo]_M13**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***90°***	Subunit ***60°***
Number of helices per subunit	22	14
Minimum helix length (bp)	42	35
Maximum helix length (bp)	122	116
Lengths of helices (bp)	42/50/58/66/74/82/ 90/98/106/114/122	35/49/62/76/ 89/103/116
Lengths of scaffold loops (nt)	7/12/8/12/8/ 8/12/8/12/7	12/13/14/14/13/12
Length of the scaffold bridge (nt)	9	7
Lengths of staple bridges (nt)	6/9/8/3/7/ 8/7/1/7/8	2/6/9/9/6/2

Table S3.7. Design parameters of p8064 floret pentagonal DNA origami tile.

Design name	**[PT-floret]_p8064**	
Rise per base pair, ***r*** (nm)	0.34	
Interhelical distance, ***D*** (nm)	2.69	
Composing subunit	Subunit ***120°***	Subunit ***60°***
Number of helices per subunit	42	14
Minimum helix length (bp)	35	35
Maximum helix length (bp)	126	117
Lengths of helices (bp)	35/39/44/48/53/57/62/67/71/76/80/85/ 89/94/99/103/108/112/117/121/126	35/48/62/76/ 90/103/117
Lengths of scaffold loops (nt)	6/7/8/6/6/7/7/6/6/7/ 7/8/8/8/7/5/4/6/7/8	12/12/13/ 15/12/12
Length of the scaffold bridge (nt)	5	6
Lengths of staple bridges (nt)	4/3/1/0/4/4/4/6/5/6/ 5/6/6/5/6/5/4/3/1/1	1/5/8/9/7/3

S3.2.2 Tiamat designs of DNA origami tiles

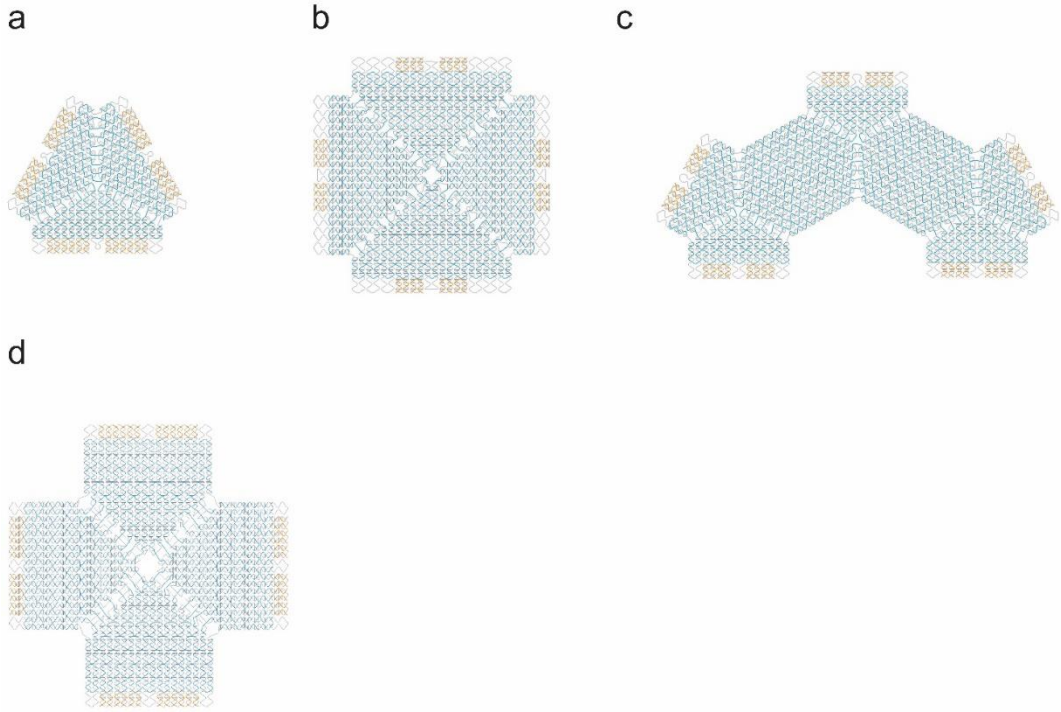

Figure S3.1. Tiamat[2] designs of DNA origami tiles for regular tilings. (a) p2820 equilateral triangular tile, (b) M13mp18 square tile, (c) M13mp18 half hexagonal tile. The scaffold strand (gray) is folded by core staple strands (blue) into the target shape.

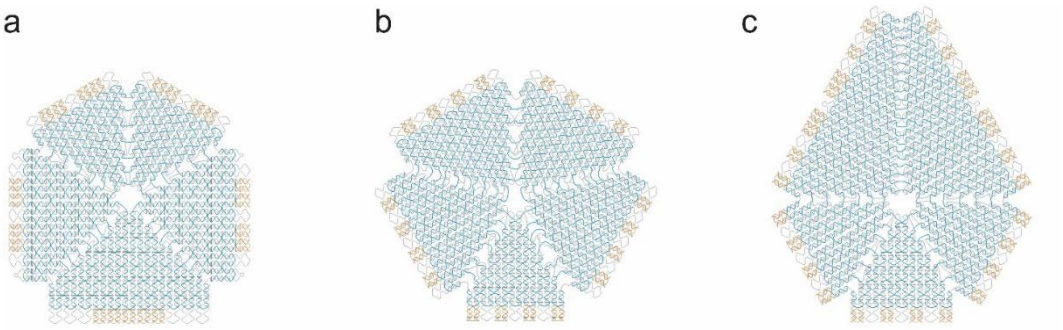

Figure S3.2. Tiamat designs of low-symmetry tiles for Laves tilings. (a) M13mp18 prismatic pentagonal tile, (b) M13mp18 Cairo pentagonal tile, and (c) p8064 floret pentagonal tile. The scaffold strand (gray) is folded by core staple strands (blue) into the target shape.

S3.3 Additional AFM Images

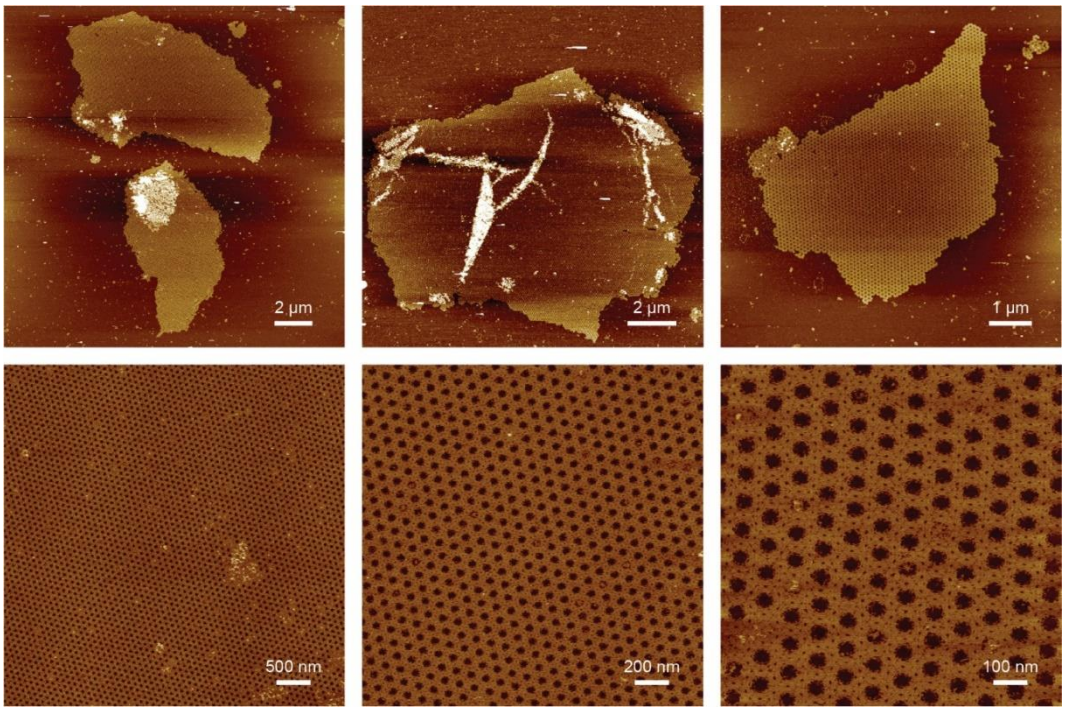

Figure S3.3. Additional AFM images of 2D lattices assembled from p2820 equilateral triangular DNA origami tiles.

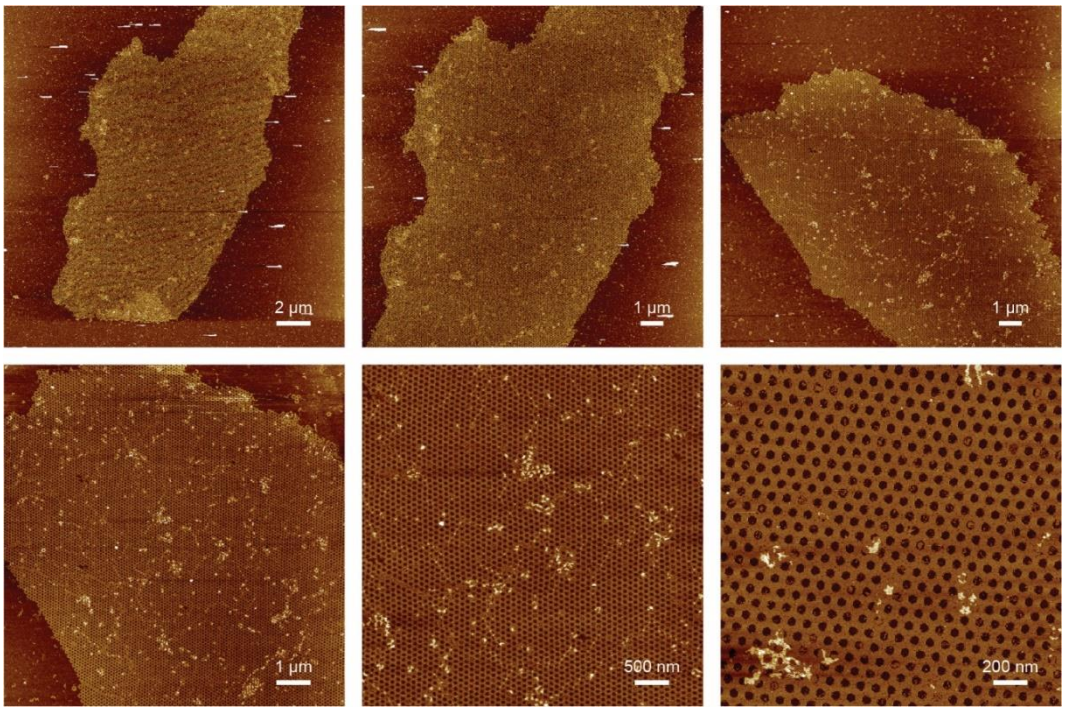

Figure S3.4. Additional AFM images of 2D lattices assembled from M13mp18 half hexagonal DNA origami tiles.

S3.4 Thermodynamic Analysis of Tile Interactions

S3.4.1 Nearest-neighbor parameters for the thermodynamic analysis

We exploited the nearest neighbor model[3] to analyze the thermodynamic free energy of tile-tile interaction. 2-nt sticky end hybridization and blunt end stacking are the two types of interactions holding tiles together. Typically, each edge staple strand presents one 2-nt sticky end and one blunt end, whose binding free energy (ΔG_{bond}) can be calculated from the nearest-neighbor parameters for DNA hybridization and stacking adapted from the literature[3,4] (Table S3.8) and further summed up to obtain the total binding free energy for each pair of complementary edges (ΔG_{edge}).

Specifically, the sequence of a 2-nt sticky end can be read from the Tiamat design from 5' to 3' as "NNN/N" or "N/NNN" (N = A, T, C, or G), where the first and fourth "N"s are the coaxial stacking bases flanking the 2-nt sticky end and the slash represents the two nucleotides lacking backbone linkage. Therefore, "NNN/N" corresponds to a 2-nt sticky end presented at the 3'-end of an edge staple, while "NNN/N" corresponds to a 2-nt sticky end at the 5'-end. The thermodynamic free energy of either case can be calculated by adding up the nearest-neighbor free energy of each pair of neighboring dinucleotides (ΔG_{NN}). Similarly, the sequence of a blunt end can be read from 5'- to 3'-end as "N/N", whose free energy (ΔG_{stack}) can be found in the literature[9]. Further, ΔG_{bond} can be calculated by adding the contributions from these two portions.

Depending on the matching rule, a tile's edge can either be complementary to another edge or self-complementary. The complementarity in the former case is denoted by "n & n*" (n = 1, 2, 3, …), whose ΔG_{edge} is the sum of each involved ΔG_{bond}. Self-complementary edge is denoted by "n/n*", where half of the edge staple strands possess

ΔG_{bond} identical to the other half. Therefore, its ΔG_{edge} is the sum of each unique ΔG_{bond} multiplied by 2.

Table S3.8. Nearest-neighbor parameters adapted from the literature[4].

Nearest-neighbor sequence (from 5' to 3')	Nearest-neighbor free energy (ΔG_{NN}) converted to 20 mM $MgCl_2$ (kcal/mol)	Stacking free energy (ΔG_{stack}) in 20 mM $MgCl_2$ (kcal/mol)
AA	-1.80	-1.36
AC	-2.32	-2.03
AG	-2.09	-1.60
AT	-1.64	-2.35
CA	-2.33	-0.81
CC	-2.63	-1.64
CG	-3.23	-2.06
CT	-2.09	-1.60
GA	-2.16	-1.39
GC	-3.21	-3.42
GG	-2.63	-1.64
GT	-2.32	-2.03
TA	-1.37	-1.01
TC	-2.16	-1.39
TG	-2.33	-0.81
TT	-1.80	-1.36

S3.4.2 Thermodynamic analysis of DNA origami tiles

S3.4.2.1 Thermodynamic analysis of DNA origami tiles for regular tilings

Table S3.9. Thermodynamic analysis of complementary edges in p3120 equilateral triangular tile (***D*** = 2.70 nm).

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GAT/A	C/A	-5.89	-49.35
	#2	TAG/T	G/C	-9.20	
	#3	ACG/G	C/A	-8.99	
	#4	GAT/C	A/A	-7.32	
	#5	CAA/G	G/T	-8.25	
	#6	CCC/T	A/T	-9.70	
2/2*	#7	TTG/C	C/C	-8.98	-45.62 (-22.81×2)
	#8	CAA/T	T/T	-7.13	
	#9	AGA/T	C/A	-6.70	

Table S3.10. Thermodynamic analysis of complementary edges in p3548 equilateral triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GAA/A	G/C	-9.18	-55.90
	#2	GGA/T	G/C	-9.85	
	#3	ACC/G	A/T	-10.53	
	#4	AGC/G	G/T	-10.56	
	#5	TAC/T	C/G	-7.84	
	#6	CAG/A	T/T	-7.94	
2/2*	#7	GGA/A	G/A	-7.98	-55.48 (-27.74×2)
	#8	ACC/C	A/T	-9.93	
	#9	GGG/C	T/T	-9.83	

Table S3.11. Thermodynamic analysis of complementary edges in p3548 square tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	TTT/T	G/G	-7.04	-34.98
	#2	GGG/A	A/T	-9.77	
	#3	CCT/G	G/G	-8.69	
	#4	GCC/C	T/A	-9.48	
2 & 2*	#5	CCC/A	T/G	-8.40	-33.92
	#6	CTG/T	G/G	-8.38	
	#7	CGA/G	T/C	-8.87	
	#8	CTC/C	T/C	-8.27	

Table S3.12. Thermodynamic analysis of complementary edges in p3548 regular hexagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GCA/C	C/C	-9.50	-36.70
	#2	CGA/A	G/C	-10.61	
	#3	TAC/G	T/C	-8.31	
	#4	CAA/A	A/T	-8.28	
2 & 2*	#5	GGA/A	A/A	-7.95	-34.26
	#6	CAC/G	T/G	-8.69	
	#7	TAG/C	G/C	-10.09	
	#8	ATC/T	G/G	-7.53	
3 & 3*	#9	TAA/C	G/G	-7.13	-28.53
	#10	ATA/A	T/G	-5.62	
	#11	TTG/T	C/C	-8.09	
	#12	TTC/T	C/C	-7.69	

Table S3.13. Thermodynamic analysis of complementary edges in M13mp18 equilateral triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	GTT/G	T/C	-7.84	-63.53
	#2	ATC/C	T/C	-7.82	
	#3	AAC/A	A/A	-7.81	
	#4	ATA/C	G/T	-7.36	
	#5	GAG/C	T/T	-8.82	
	#6	CCT/T	A/C	-8.55	
	#7	GAA/G	A/A	-7.41	
	#8	TAC/C	C/T	-7.92	
2/2*	#9	TTG/A	C/A	-7.10	-59.56 (-29.78×2)
	#10	CCA/G	G/A	-8.44	
	#11	ATT/T	T/C	-6.63	
	#12	CTT/A	A/T	-7.61	

Table S3.14. Thermodynamic analysis of complementary edges in M13mp18 square tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CGT/A	A/C	-8.95	-33.04
	#2	AAA/C	T/C	-7.31	
	#3	ACA/A	G/G	-8.09	
	#4	CAC/G	C/A	-8.69	
2 & 2*	#5	GCG/C	T/G	-10.46	-35.67
	#6	ACA/C	T/C	-8.36	
	#7	ATA/C	C/C	-6.97	
	#8	CCG/C	C/A	-9.88	

Table S3.15. Thermodynamic analysis of complementary edges in M13mp18 regular hexagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	TTA/A	T/T	-6.33	-30.73
	#2	TAT/T	A/G	-6.41	
	#3	GAC/G	C/C	-9.35	
	#4	GCT/G	T/A	-8.64	
2 & 2*	#5	TCA/A	T/T	-7.65	-32.62
	#6	ATA/C	A/G	-6.93	
	#7	ATT/C	A/G	-7.20	
	#8	TCC/C	G/C	-10.84	
3 & 3*	#9	CCT/A	T/A	-7.10	-32.45
	#10	AAG/T	C/C	-7.85	
	#11	GAC/C	A/C	-9.14	
	#12	TTG/G	A/G	-8.36	

Table S3.16. Thermodynamic analysis of complementary edges in p2820 equilateral triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	ATA/A	T/T	-6.17	-44.36
	#2	ATG/A	G/G	-7.77	
	#3	TCT/T	C/A	-6.86	
	#4	AAG/A	C/G	-8.11	
	#5	TTC/T	G/C	-9.47	
	#6	TTA/A	T/A	-5.98	
2/2*	#7	C/TGT	G/A	-8.13	-50.66 (-25.33×2)
	#8	G/GAG	C/T	-8.48	
	#9	T/GGA	A/G	-8.72	

Table S3.17. Thermodynamic analysis of complementary edges in M13mp18 half hexagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1/1*	#1	TAT/A	A/T	-6.73	-33.38 (-16.69×2)
	#2	GCG/A	A/A	-9.96	
2/2*	#3	CCC/G	A/C	-10.52	-37.60 (-18.80×2)
	#4	CGT/A	A/A	-8.28	
3/3*	#5	TCA/G	A/G	-8.18	-31.56 (-15.78×2)
	#6	AAC/T	G/A	-7.60	
4 & 4*	#7	A/TAA	A/G	-6.41	-26.53
	#8	A/ATA	A/A	-6.17	
	#9	A/CTA	C/A	-6.59	
	#10	T/TTC	C/T	-7.36	

S3.4.2.2 Thermodynamic analysis of DNA origami tiles for Laves tilings

Table S3.18. Thermodynamic analysis of complementary edges in p3548 isosceles right triangular tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1/1*	#1	AGG/G	G/T	-10.13	-87.50 (-43.75×2)
	#2	CAA/C	A/A	-7.81	
	#3	GGA/G	A/G	-7.70	
	#4	TGA/C	C/T	-9.17	
	#5	CTG/C	C/G	-8.94	
2 & 2*	#6	GGG/G	C/T	-9.49	-54.48
	#7	GGC/C	G/C	-11.89	
	#8	CCA/T	C/T	-8.20	
	#9	CTG/A	C/G	-8.64	
	#10	CTT/C	G/C	-9.47	
	#11	TAC/T	T/A	-6.79	

Table S3.19. Thermodynamic analysis of complementary edges in M13mp18 rhombic tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CCA/T	A/A	-7.96	-45.54
	#2	ATA/C	A/A	-6.69	
	#3	GGT/T	C/G	-8.81	
	#4	CTC/A	T/A	-7.59	
	#5	TTG/A	C/G	-8.35	
	#6	GTA/T	C/A	-6.14	
2 & 2*	#7	TCG/A	G/T	-9.58	-51.07
	#8	CTA/A	G/G	-6.90	
	#9	CGA/T	G/A	-8.42	
	#10	CTC/G	A/T	-9.83	
	#11	CCC/A	A/A	-8.95	
	#12	CTC/A	T/G	-7.39	

Table S3.20. Thermodynamic analysis of complementary edges in M13mp18 kite tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	TAA/T	G/A	-6.20	-65.49
	#2	CCA/A	C/C	-8.40	
	#3	AAG/A	A/C	-8.08	
	#4	CGC/A	T/A	-9.78	
	#5	GAA/A	A/A	-7.12	
	#6	CAA/G	A/A	-7.58	
	#7	CCG/C	C/C	-10.71	
	#8	TGT/A	C/T	-7.62	
2 & 2*	#9	*N/A*	T/A & G/G	-2.65	-21.85
	#10	*N/A*	G/A & G/C	-4.81	
	#11	CTT/T	A/A	-7.05	
	#12	*N/A*	T/T & C/T	-2.96	
	#13	*N/A*	G/T & A/T	-4.38	

Table S3.21. Thermodynamic analysis of complementary edges in M13mp18 prismatic pentagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1/1*	#1	TGG/A	A/C	-9.15	-29.94 (-14.97×2)
	#2	ATT/A	T/A	-5.82	
2/2*	#3	CTA/A	T/A	-6.27	-32.20 (-16.10×2)
	#4	GGC/C	T/T	-9.83	
3 & 3*	#5	ATA/A	T/T	-6.17	-26.88
	#6	TAA/A	T/A	-5.98	
	#7	TCA/T	G/G	-7.77	
	#8	GAT/T	A/A	-6.96	
4/4*	#9	AGC/A	A/A	-8.99	-57.80 (-28.90×2)
	#10	CGC/C	A/T	-11.42	
	#11	C/GGG	*N/A*	-8.49	

Table S3.22. Thermodynamic analysis of complementary edges in M13mp18 Cairo pentagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	AAA/C	G/G	-7.56	-32.33
	#2	CTT/T	T/A	-6.70	
	#3	CCG/G	T/G	-9.30	
	#4	ACA/G	G/T	-8.77	
2 & 2*	#5	TTA/A	G/A	-6.36	-29.19
	#6	GCC/A	A/G	-9.77	
	#7	TAT/A	T/T	-5.74	
	#8	TAA/A	A/T	-7.32	
3/3*	#9	G/TAC	G/G	-7.65	-35.76 (-17.88×2)
	#10	T/GAC	G/C	-10.23	

Table S3.23. Thermodynamic analysis of complementary edges in p8064 floret pentagonal tile.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CGT/T	A/C	-9.38	-66.78
	#2	CAA/G	A/C	-8.25	
	#3	ATT/A	T/G	-5.62	
	#4	GAC/C	C/A	-7.92	
	#5	AGC/G	A/C	-10.56	
	#6	GTA/T	G/T	-7.36	
	#7	TGC/A	C/T	-9.47	
	#8	TCT/G	C/C	-8.22	
2 & 2*	#9	ACG/G	T/A	-9.19	-32.19
	#10	CAT/C	A/A	-7.49	
	#11	AGG/T	C/A	-7.85	
	#12	GAT/T	C/G	-7.66	
3/3*	#13	GTA/G	T/A	-6.79	-31.86 (-15.93×2)
	#14	GGT/C	G/T	-9.14	

S3.4.3 Square tiles with imbalanced bond interactions

Table S3.24. Thermodynamic analysis of p3548 square tile with imbalanced bond interaction.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	CCC/A	T/G	-8.40	-27.34
	#2	CGG/C	C/T	-10.67	
	#3	CTC/C	T/C	-8.27	
2 & 2*	#4	G/CTA	G/C	-10.09	-33.01
	#5	A/AGG	C/C	-8.16	
	#6	A/AAT	G/G	-6.88	
	#7	A/AGG	T/T	-7.88	

Table S3.25. Thermodynamic analysis of M13mp18 square tile with imbalanced bond interaction.

Complementarity	Bond	Sequence of 2-nt sticky end	Sequence of blunt end	ΔG_{bond} (kcal/mol)	ΔG_{edge} (kcal/mol)
1 & 1*	#1	ACC/A	C/G	-9.34	-31.92
	#2	TCA/A	A/A	-7.65	
	#3	GGT/A	A/C	-8.35	
	#4	CAA/T	C/A	-6.58	
2 & 2*	#5	TGC/A	G/C	-11.29	-37.37
	#6	TCC/T	A/C	-8.91	
	#7	CCA/T	A/T	-8.95	
	#8	CAG/A	C/C	-8.22	

S3.5 DNA Sequences

S3.5.1 Sequences of scaffold strands

S3.5.1.1 Sequence of the customized p2820 scaffold

GTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAA
ATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCA
ATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTT
ATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTG
GTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCG
AACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACG
TTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCC
GTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAA
TGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATG
ACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGG
CCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTT
GCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTG
AATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGG
CAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGG
CAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGC
GCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAG
CGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCC
GTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAA
TAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCA
GACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTT
AAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTA
ACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGA
TCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAA
ACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTT
TTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCT
AGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACA
TACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTC
GTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGG
TCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT
ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC
CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGG
AGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCT
GTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGG
GGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTG
GCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCT
GTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCC
GAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAA
TACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAC
GACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGA

GTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGT
ATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
ACCATGATTACGCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACGCGCG
CTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCC
AACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAA
GAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAAT
GGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCG
CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCT
TCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGG
GGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAA
CTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTT
TCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAA
CTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATT
TTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAA
CGCGAATTTTAACAAAATATTAACGCTTACAATTTAG

S3.5.1.2 Sequence of the M13mp18 scaffold

TGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGG
ACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTG
ATTTATAAGGGATTTTGCCGATTTCGGAACCACCATCAAACAGGATTTTCGCC
TGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGC
GGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACC
CTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAAT
GCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACG
CAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATG
CTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGG
AAACAGCTATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCT
AGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGT
CGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATC
CCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC
CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTTGCCTGGTTTCCGGCA
CCAGAAGCGGTGCCGGAAAGCTGGCTGGAGTGCGATCTTCCTGAGGCCGATA
CTGTCGTCGTCCCCTCAAACTGGCAGATGCACGGTTACGATGCGCCCATCTAC
ACCAACGTGACCTATCCCATTACGGTCAATCCGCCGTTTGTTCCCACGGAGAA
TCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAAGCTGGCTACAGG
AAGGCCAGACGCGAATTATTTTTGATGGCGTTCCTATTGGTTAAAAAATGAG
CTGATTTAACAAAAATTTAATGCGAATTTTAACAAAATATTAACGTTTACAAT
TTAAATATTTGCTTATACAATCTTCCTGTTTTTGGGGCTTTTCTGATTATCAAC
CGGGGTACATATGATTGACATGCTAGTTTTACGATTACCGTTCATCGATTCTC
TTGTTTGCTCCAGACTCTCAGGCAATGACCTGATAGCCTTTGTAGATCTCTCA
AAAATAGCTACCCTCTCCGGCATTAATTTATCAGCTAGAACGGTTGAATATCA
TATTGATGGTGATTTGACTGTCTCCGGCCTTTCTCACCCTTTTGAATCTTTACC
TACACATTACTCAGGCATTGCATTTAAAATATATGAGGGTTCTAAAAATTTTT
ATCCTTGCGTTGAAATAAAGGCTTCTCCCGCAAAAGTATTACAGGGTCATAAT
GTTTTTGGTACAACCGATTTAGCTTTATGCTCTGAGGCTTTATTGCTTAATTTT
GCTAATTCTTTGCCTTGCCTGTATGATTTATTGGATGTTAATGCTACTACTATT
AGTAGAATTGATGCCACCTTTTCAGCTCGCGCCCCAAATGAAAATATAGCTA
AACAGGTTATTGACCATTTGCGAAATGTATCTAATGGTCAAACTAAATCTACT
CGTTCGCAGAATTGGGAATCAACTGTTATATGGAATGAAACTTCCAGACACC
GTACTTTAGTTGCATATTTAAAACATGTTGAGCTACAGCATTATATTCAGCAA
TTAAGCTCTAAGCCATCCGCAAAAATGACCTCTTATCAAAAGGAGCAATTAA
AGGTACTCTCTAATCCTGACCTGTTGGAGTTTGCTTCCGGTCTGGTTCGCTTTG
AAGCTCGAATTAAAACGCGATATTTGAAGTCTTTCGGGCTTCCTCTTAATCTT
TTTGATGCAATCCGCTTTGCTTCTGACTATAATAGTCAGGGTAAAGACCTGAT
TTTTGATTTATGGTCATTCTCGTTTTCTGAACTGTTTAAAGCATTTGAGGGGGA
TTCAATGAATATTTATGACGATTCCGCAGTATTGGACGCTATCCAGTCTAAAC
ATTTTACTATTACCCCCTCTGGCAAAACTTCTTTTGCAAAAGCCTCTCGCTATT
TTGGTTTTTATCGTCGTCTGGTAAACGAGGGTTATGATAGTGTTGCTCTTACT
ATGCCTCGTAATTCCTTTTGGCGTTATGTATCTGCATTAGTTGAATGTGGTATT
CCTAAATCTCAACTGATGAATCTTTCTACCTGTAATAATGTTGTTCCGTTAGTT

CGTTTTATTAACGTAGATTTTTCTTCCCAACGTCCTGACTGGTATAATGAGCC
AGTTCTTAAAATCGCATAAGGTAATTCACAATGATTAAAGTTGAAATTAAAC
CATCTCAAGCCCAATTTACTACTCGTTCTGGTGTTTCTCGTCAGGGCAAGCCT
TATTCACTGAATGAGCAGCTTTGTTACGTTGATTTGGGTAATGAATATCCGGT
TCTTGTCAAGATTACTCTTGATGAAGGTCAGCCAGCCTATGCGCCTGGTCTGT
ACACCGTTCATCTGTCCTCTTTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTG
ACCGTCTGCGCCTCGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTCG
ACACAATTTATCAGGCGATGATACAAATCTCCGTTGTACTTTGTTTCGCGCTT
GGTATAATCGCTGGGGGTCAAAGATGAGTGTTTTAGTGTATTCTTTTGCCTCT
TTCGTTTTAGGTTGGTGCCTTCGTAGTGGCATTACGTATTTTACCCGTTTAATG
GAAACTTCCTCATGAAAAAGTCTTTAGTCCTCAAAGCCTCTGTAGCCGTTGCT
ACCCTCGTTCCGATGCTGTCTTTCGCTGCTGAGGGTGACGATCCCGCAAAAGC
GGCCTTTAACTCCCTGCAAGCCTCAGCGACCGAATATATCGGTTATGCGTGGG
CGATGGTTGTTGTCATTGTCGGCGCAACTATCGGTATCAAGCTGTTTAAGAAA
TTCACCTCGAAAGCAAGCTGATAAACCGATACAATTAAAGGCTCCTTTTGGA
GCCTTTTTTTTGGAGATTTTCAACGTGAAAAAATTATTATTCGCAATTCCTTTA
GTTGTTCCTTTCTATTCTCACTCCGCTGAAACTGTTGAAAGTTGTTTAGCAAA
ATCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACGACAAAACTTTA
GATCGTTACGCTAACTATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGT
TTGTACTGGTGACGAAACTCAGTGTTACGGTACATGGGTTCCTATTGGGCTTG
CTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGG
CGGTTCTGAGGGTGGCGGTACTAAACCTCCTGAGTACGGTGATACACCTATTC
CGGGCTATACTTATATCAACCCTCTCGACGGCACTTATCCGCCTGGTACTGAG
CAAAACCCCGCTAATCCTAATCCTTCTCTTGAGGAGTCTCAGCCTCTTAATAC
TTTCATGTTTCAGAATAATAGGTTCCGAAATAGGCAGGGGGCATTAACTGTTT
ATACGGGCACTGTTACTCAAGGCACTGACCCCGTTAAAACTTATTACCAGTAC
ACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCA
GAGACTGCGCTTTCCATTCTGGCTTTAATGAGGATTTATTTGTTTGTGAATATC
AAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTGGCGGCGGCTCT
GGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGGTT
CTGAGGGTGGCGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGG
TGATTTTGATTATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGAA
AATGCCGATGAAAACGCGCTACAGTCTGACGCTAAAGGCAAACTTGATTCTG
TCGCTACTGATTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGC
CTTGCTAATGGTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAAT
GGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAAT
ATTTACCTTCCCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCGCTG
GTAAACCATATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGT
GTCTTTGCGTTTCTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTG
CTAACATACTGCGTAATAAGGAGTCTTAATCATGCCAGTTCTTTTGGGTATTC
CGTTATTATTGCGTTTCCTCGGTTTCCTTCTGGTAACTTTGTTCGGCTATCTGC
TTACTTTTCTTAAAAAGGGCTTCGGTAAGATAGCTATTGCTATTTCATTGTTTC
TTGCTCTTATTATTGGGCTTAACTCAATTCTTGTGGGTTATCTCTCTGATATTA
GCGCTCAATTACCCTCTGACTTTGTTCAGGGTGTTCAGTTAATTCTCCCGTCTA
ATGCGCTTCCCTGTTTTTATGTTATTCTCTCTGTAAAGGCTGCTATTTTCATTTT

TGACGTTAAACAAAAAATCGTTTCTTATTTGGATTGGGATAAATAATATGGCT
GTTTATTTTGTAACTGGCAAATTAGGCTCTGGAAAGACGCTCGTTAGCGTTGG
TAAGATTCAGGATAAAATTGTAGCTGGGTGCAAAATAGCAACTAATCTTGAT
TTAAGGCTTCAAAACCTCCCGCAAGTCGGGAGGTTCGCTAAAACGCCTCGCG
TTCTTAGAATACCGGATAAGCCTTCTATATCTGATTTGCTTGCTATTGGGCGC
GGTAATGATTCCTACGATGAAAATAAAAACGGCTTGCTTGTTCTCGATGAGT
GCGGTACTTGGTTTAATACCCGTTCTTGGAATGATAAGGAAAGACAGCCGAT
TATTGATTGGTTTCTACATGCTCGTAAATTAGGATGGGATATTATTTTTCTTGT
TCAGGACTTATCTATTGTTGATAAACAGGCGCGTTCTGCATTAGCTGAACATG
TTGTTTATTGTCGTCGTCTGGACAGAATTACTTTACCTTTTGTCGGTACTTTAT
ATTCTCTTATTACTGGCTCGAAAATGCCTCTGCCTAAATTACATGTTGGCGTT
GTTAAATATGGCGATTCTCAATTAAGCCCTACTGTTGAGCGTTGGCTTTATAC
TGGTAAGAATTTGTATAACGCATATGATACTAAACAGGCTTTTTCTAGTAATT
ATGATTCCGGTGTTTATTCTTATTTAACGCCTTATTTATCACACGGTCGGTATT
TCAAACCATTAAATTTAGGTCAGAAGATGAAATTAACTAAAATATATTTGAA
AAAGTTTTCTCGCGTTCTTTGTCTTGCGATTGGATTTGCATCAGCATTTACATA
TAGTTATATAACCCAACCTAAGCCGGAGGTTAAAAAGGTAGTCTCTCAGACC
TATGATTTTGATAAATTCACTATTGACTCTTCTCAGCGTCTTAATCTAAGCTAT
CGCTATGTTTTCAAGGATTCTAAGGGAAAATTAATTAATAGCGACGATTTACA
GAAGCAAGGTTATTCACTCACATATATTGATTTATGTACTGTTTCCATTAAAA
AAGGTAATTCAAATGAAATTGTTAAATGTAATTAATTTTGTTTTCTTGATGTTT
GTTTCATCATCTTCTTTTGCTCAGGTAATTGAAATGAATAATTCGCCTCTGCGC
GATTTTGTAACTTGGTATTCAAAGCAATCAGGCGAATCCGTTATTGTTTCTCC
CGATGTAAAAGGTACTGTTACTGTATATTCATCTGACGTTAAACCTGAAAATC
TACGCAATTTCTTTATTTCTGTTTTACGTGCAAATAATTTTGATATGGTAGGTT
CTAACCCTTCCATTATTCAGAAGTATAATCCAAACAATCAGGATTATATTGAT
GAATTGCCATCATCTGATAATCAGGAATATGATGATAATTCCGCTCCTTCTGG
TGGTTTCTTTGTTCCGCAAAATGATAATGTTACTCAAACTTTTAAAATTAATA
ACGTTCGGGCAAAGGATTTAATACGAGTTGTCGAATTGTTTGTAAAGTCTAAT
ACTTCTAAATCCTCAAATGTATTATCTATTGACGGCTCTAATCTATTAGTTGTT
AGTGCTCCTAAAGATATTTTAGATAACCTTCCTCAATTCCTTTCAACTGTTGAT
TTGCCAACTGACCAGATATTGATTGAGGGTTTGATATTTGAGGTTCAGCAAGG
TGATGCTTTAGATTTTTCATTTGCTGCTGGCTCTCAGCGTGGCACTGTTGCAG
GCGGTGTTAATACTGACCGCCTCACCTCTGTTTTATCTTCTGCTGGTGGTTCGT
TCGGTATTTTTAATGGCGATGTTTTAGGGCTATCAGTTCGCGCATTAAAGACT
AATAGCCATTCAAAAATATTGTCTGTGCCACGTATTCTTACGCTTTCAGGTCA
GAAGGGTTCTATCTCTGTTGGCCAGAATGTCCCTTTTATTACTGGTCGTGTGA
CTGGTGAATCTGCCAATGTAAATAATCCATTTCAGACGATTGAGCGTCAAAA
TGTAGGTATTTCCATGAGCGTTTTTCCTGTTGCAATGGCTGGCGGTAATATTG
TTCTGGATATTACCAGCAAGGCCGATAGTTTGAGTTCTTCTACTCAGGCAAGT
GATGTTATTACTAATCAAAGAAGTATTGCTACAACGGTTAATTTGCGTGATGG
ACAGACTCTTTTACTCGGTGGCCTCACTGATTATAAAAACACTTCTCAGGATT
CTGGCGTACCGTTCCTGTCTAAAATCCCTTTAATCGGCCTCCTGTTTAGCTCCC
GCTCTGATTCTAACGAGGAAAGCACGTTATACGTGCTCGTCAAAGCAACCAT
AGTACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCG

CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCT
TCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGG
GGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAA
CTTGATTTGGGTGATGGTTCACGTAGTGGGCCATCGCCC

S3.5.1.3 Sequence of the p8064 scaffold

TGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA
GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCT
TTTGATTTATAAGGGATTTTGCCGATTTCGGAACCACCATCAAACAGGATTTT
CGCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCC
AGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAAC
CACCCTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCAT
TAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCA
ACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTT
ATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACAC
AGGAAACAGCTATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCC
TCAACTGTGAGGAGGCTCACGGACGCGAAGAACAGGCACGCGTGCTGGCAG
AAACCCCCGGTATGACCGTGAAAACGGCCCGCCGCATTCTGGCCGCAGCACC
ACAGAGTGCACAGGCGCGCAGTGACACTGCGCTGGATCGTCTGATGCAGGGG
GCACCGGCACCGCTGGCTGCAGGTAACCCGGCATCTGATGCCGTTAACGATT
TGCTGAACACACCAGTGTAAGGGATGTTTATGACGAGCAAAGAAACCTTTAC
CCATTACCAGCCGCAGGGCAACAGTGACCCGGCTCATACCGCAACCGCGCCC
GGCGGATTGAGTGCGAAAGCGCCTGCAATGACCCCGCTGATGCTGGACACCT
CCAGCCGTAAGCTGGTTGCGTGGGATGGCACCACCGACGGTGCTGCCGTTGG
CATTCTTGCGGTTGCTGCTGACCAGACCAGCACCACGCTGACGTTCTACAAGT
CCGGCACGTTCCGTTATGAGGATGTGCTCTGGCCGGAGGCTGCCAGCGACGA
GACGAAAAAACGGACCGCGTTTGCCGGAACGGCAATCAGCATCGTTTAACTT
TACCCTTCATCACTAAAGGCCGCCTGTGCGGCTTTTTTTACGGGATTTTTTTAT
GTCGATGTACACAACCGCCCAACTGCTGGCGGCAAATGAGCAGAAATTTAAG
TTTGATCCGCTGTTTCTGCGTCTCTTTTTCCGTGAGAGCTATCCCTTCACCACG
GAGAAAGTCTATCTCTCACAAATTCCGGGACTGGTAAACATGGCGCTGTACG
TTTCGCCGATTGTTTCCGGTGAGGTTATCCGTTCCCGTGGCGGCTCCACCTCT
GAAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTG
GCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGT
AATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGA
ATGGCGAATGGCGCTTTGCCTGGTTTCCGGCACCAGAAGCGGTGCCGGAAAG
CTGGCTGGAGTGCGATCTTCCTGAGGCCGATACTGTCGTCGTCCCCTCAAACT
GGCAGATGCACGGTTACGATGCGCCCATCTACACCAACGTGACCTATCCCAT
TACGGTCAATCCGCCGTTTGTTCCCACGGAGAATCCGACGGGTTGTTACTCGC
TCACATTTAATGTTGATGAAAGCTGGCTACAGGAAGGCCAGACGCGAATTAT
TTTTGATGGCGTTCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAA
TGCGAATTTTAACAAAATATTAACGTTTACAATTTAAATATTTGCTTATACAA
TCTTCCTGTTTTTTGGGGCTTTTCTGATTATCAACCGGGGTACATATGATTGACA
TGCTAGTTTTACGATTACCGTTCATCGATTCTCTTGTTTGCTCCAGACTCTCAG
GCAATGACCTGATAGCCTTTGTAGATCTCTCAAAAATAGCTACCCTCTCCGGC
ATTAATTTATCAGCTAGAACGGTTGAATATCATATTGATGGTGATTTGACTGT
CTCCGGCCTTTCTCACCCTTTTGAATCTTTACCTACACATTACTCAGGCATTGC
ATTTAAAATATATGAGGGTTCTAAAAATTTTTATCCTTGCGTTGAAATAAAGG
CTTCTCCCGCAAAAGTATTACAGGGTCATAATGTTTTTGGTACAACCGATTTA

GCTTTATGCTCTGAGGCTTTATTGCTTAATTTTGCTAATTCTTTGCCTTGCCTG
TATGATTTATTGGATGTTAATGCTACTACTATTAGTAGAATTGATGCCACCTT
TTCAGCTCGCGCCCCAAATGAAAATATAGCTAAACAGGTTATTGACCATTTGC
GAAATGTATCTAATGGTCAAACTAAATCTACTCGTTCGCAGAATTGGGAATC
AACTGTTATATGGAATGAAACTTCCAGACACCGTACTTTAGTTGCATATTTAA
AACATGTTGAGCTACAGCATTATATTCAGCAATTAAGCTCTAAGCCATCCGCA
AAAATGACCTCTTATCAAAAGGAGCAATTAAAGGTACTCTCTAATCCTGACC
TGTTGGAGTTTGCTTCCGGTCTGGTTCGCTTTGAAGCTCGAATTAAAACGCGA
TATTTGAAGTCTTTCGGGCTTCCTCTTAATCTTTTTGATGCAATCCGCTTTGCT
TCTGACTATAATAGTCAGGGTAAAGACCTGATTTTTGATTTATGGTCATTCTC
GTTTTCTGAACTGTTTAAAGCATTTGAGGGGGATTCAATGAATATTTATGACG
ATTCCGCAGTATTGGACGCTATCCAGTCTAAACATTTTACTATTACCCCCTCT
GGCAAAACTTCTTTTGCAAAAGCCTCTCGCTATTTTGGTTTTTATCGTCGTCTG
GTAAACGAGGGTTATGATAGTGTTGCTCTTACTATGCCTCGTAATTCCTTTTG
GCGTTATGTATCTGCATTAGTTGAATGTGGTATTCCTAAATCTCAACTGATGA
ATCTTTCTACCTGTAATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATT
TTTCTTCCCAACGTCCTGACTGGTATAATGAGCCAGTTCTTAAAATCGCATAA
GGTAATTCACAATGATTAAAGTTGAAATTAAACCATCTCAAGCCCAATTTACT
ACTCGTTCTGGTGTTTCTCGTCAGGGCAAGCCTTATTCACTGAATGAGCAGCT
TTGTTACGTTGATTTGGGTAATGAATATCCGGTTCTTGTCAAGATTACTCTTG
ATGAAGGTCAGCCAGCCTATGCGCCTGGTCTGTACACCGTTCATCTGTCCTCT
TTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTGACCGTCTGCGCCTCGTTCC
GGCTAAGTAACATGGAGCAGGTCGCGGATTTCGACACAATTTATCAGGCGAT
GATACAAATCTCCGTTGTACTTTGTTTCGCGCTTGGTATAATCGCTGGGGGTC
AAAGATGAGTGTTTTAGTGTATTCTTTTGCCTCTTTCGTTTTAGGTTGGTGCCT
TCGTAGTGGCATTACGTATTTTACCCGTTTAATGGAAACTTCCTCATGAAAAA
GTCTTTAGTCCTCAAAGCCTCTGTAGCCGTTGCTACCCTCGTTCCGATGCTGTC
TTTCGCTGCTGAGGGTGACGATCCCGCAAAAGCGGCCTTTAACTCCCTGCAA
GCCTCAGCGACCGAATATATCGGTTATGCGTGGGCGATGGTTGTTGTCATTGT
CGGCGCAACTATCGGTATCAAGCTGTTTAAGAAATTCACCTCGAAAGCAAGC
TGATAAACCGATACAATTAAAGGCTCCTTTTGGAGCCTTTTTTTTGGAGATTT
TCAACGTGAAAAAATTATTATTCGCAATTCCTTTAGTTGTTCCTTTCTATTCTC
ACTCCGCTGAAACTGTTGAAAGTTGTTTAGCAAAATCCCATACAGAAAATTC
ATTTACTAACGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACTAT
GAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAAA
CTCAGTGTTACGGTACATGGGTTCCTATTGGGCTTGCTATCCCTGAAAATGAG
GGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTGGCG
GTACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCTATACTTATATC
AACCCTCTCGACGGCACTTATCCGCCTGGTACTGAGCAAAACCCCGCTAATCC
TAATCCTTCTCTTGAGGAGTCTCAGCCTCTTAATACTTTCATGTTTCAGAATAA
TAGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCACTGTTACT
CAAGGCACTGACCCCGTTAAAACTTATTACCAGTACACTCCTGTATCATCAAA
AGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATT
CTGGCTTTAATGAGGATTTATTTGTTTGTGAATATCAAGGCCAATCGTCTGAC
CTGCCTCAACCTCCTGTCAATGCTGGCGGCGGCTCTGGTGGTGGTTCTGGTGG

CGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCT
GAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAA
AGATGGCAAACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACG
CGCTACAGTCTGACGCTAAAGGCAAACTTGATTCTGTCGCTACTGATTACGGT
GCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGG
TGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAATGGCTCAAGTCGGTGACG
GTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCTCCCTC
AATCGGTTGAATGTCGCCCTTTTGTCTTTGGCGCTGGTAAACCATATGAATTT
TCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTTGCGTTTCTTTTA
TATGTTGCCACCTTTATGTATGTATTTTCTACGTTTGCTAACATACTGCGTAAT
AAGGAGTCTTAATCATGCCAGTTCTTTTGGGTATTCCGTTATTATTGCGTTTCC
TCGGTTTCCTTCTGGTAACTTTGTTCGGCTATCTGCTTACTTTTCTTAAAAAGG
GCTTCGGTAAGATAGCTATTGCTATTTCATTGTTTCTTGCTCTTATTATTGGGC
TTAACTCAATTCTTGTGGGTTATCTCTCTGATATTAGCGCTCAATTACCCTCTG
ACTTTGTTCAGGGTGTTCAGTTAATTCTCCCGTCTAATGCGCTTCCCTGTTTTT
ATGTTATTCTCTCTGTAAAGGCTGCTATTTTCATTTTTGACGTTAAACAAAAA
ATCGTTTCTTATTTGGATTGGGATAAATAATATGGCTGTTTATTTTGTAACTGG
CAAATTAGGCTCTGGAAAGACGCTCGTTAGCGTTGGTAAGATTCAGGATAAA
ATTGTAGCTGGGTGCAAAATAGCAACTAATCTTGATTTAAGGCTTCAAAACCT
CCCGCAAGTCGGGAGGTTCGCTAAAACGCCTCGCGTTCTTAGAATACCGGAT
AAGCCTTCTATATCTGATTTGCTTGCTATTGGGCGCGGTAATGATTCCTACGA
TGAAAATAAAAACGGCTTGCTTGTTCTCGATGAGTGCGGTACTTGGTTTAATA
CCCGTTCTTGGAATGATAAGGAAAGACAGCCGATTATTGATTGGTTTCTACAT
GCTCGTAAATTAGGATGGGATATTATTTTTCTTGTTCAGGACTTATCTATTGTT
GATAAACAGGCGCGTTCTGCATTAGCTGAACATGTTGTTTATTGTCGTCGTCT
GGACAGAATTACTTTACCTTTTGTCGGTACTTTATATTCTCTTATTACTGGCTC
GAAAATGCCTCTGCCTAAATTACATGTTGGCGTTGTTAAATATGGCGATTCTC
AATTAAGCCCTACTGTTGAGCGTTGGCTTTATACTGGTAAGAATTTGTATAAC
GCATATGATACTAAACAGGCTTTTTCTAGTAATTATGATTCCGGTGTTTATTCT
TATTTAACGCCTTATTTATCACACGGTCGGTATTTCAAACCATTAAATTTAGG
TCAGAAGATGAAATTAACTAAAATATATTTGAAAAAGTTTTCTCGCGTTCTTT
GTCTTGCGATTGGATTTGCATCAGCATTTACATATAGTTATATAACCCAACCT
AAGCCGGAGGTTAAAAAGGTAGTCTCTCAGACCTATGATTTTGATAAATTCA
CTATTGACTCTTCTCAGCGTCTTAATCTAAGCTATCGCTATGTTTTCAAGGATT
CTAAGGGAAAATTAATTAATAGCGACGATTTACAGAAGCAAGGTTATTCACT
CACATATATTGATTTATGTACTGTTTCCATTAAAAAAGGTAATTCAAATGAAA
TTGTTAAATGTAATTAATTTTGTTTTCTTGATGTTTGTTTCATCATCTTCTTTTG
CTCAGGTAATTGAAATGAATAATTCGCCTCTGCGCGATTTTGTAACTTGGTAT
TCAAAGCAATCAGGCGAATCCGTTATTGTTTCTCCCGATGTAAAAGGTACTGT
TACTGTATATTCATCTGACGTTAAACCTGAAAATCTACGCAATTTCTTTATTTC
TGTTTTACGTGCAAATAATTTTGATATGGTAGGTTCTAACCCTTCCATTATTCA
GAAGTATAATCCAAACAATCAGGATTATATTGATGAATTGCCATCATCTGAT
AATCAGGAATATGATGATAATTCCGCTCCTTCTGGTGGTTTCTTTGTTCCGCA
AAATGATAATGTTACTCAAACTTTTAAAATTAATAACGTTCGGGCAAAGGAT
TTAATACGAGTTGTCGAATTGTTTGTAAAGTCTAATACTTCTAAATCCTCAAA

TGTATTATCTATTGACGGCTCTAATCTATTAGTTGTTAGTGCTCCTAAAGATAT
TTTAGATAACCTTCCTCAATTCCTTTCAACTGTTGATTTGCCAACTGACCAGAT
ATTGATTGAGGGTTTGATATTTGAGGTTCAGCAAGGTGATGCTTTAGATTTTT
CATTTGCTGCTGGCTCTCAGCGTGGCACTGTTGCAGGCGGTGTTAATACTGAC
CGCCTCACCTCTGTTTTATCTTCTGCTGGTGGTTCGTTCGGTATTTTTAATGGC
GATGTTTTAGGGCTATCAGTTCGCGCATTAAAGACTAATAGCCATTCAAAAAT
ATTGTCTGTGCCACGTATTCTTACGCTTTCAGGTCAGAAGGGTTCTATCTCTGT
TGGCCAGAATGTCCCTTTTATTACTGGTCGTGTGACTGGTGAATCTGCCAATG
TAAATAATCCATTTCAGACGATTGAGCGTCAAAATGTAGGTATTTCCATGAGC
GTTTTTCCTGTTGCAATGGCTGGCGGTAATATTGTTCTGGATATTACCAGCAA
GGCCGATAGTTTGAGTTCTTCTACTCAGGCAAGTGATGTTATTACTAATCAAA
GAAGTATTGCTACAACGGTTAATTTGCGTGATGGACAGACTCTTTTACTCGGT
GGCCTCACTGATTATAAAAACACTTCTCAGGATTCTGGCGTACCGTTCCTGTC
TAAAATCCCTTTAATCGGCCTCCTGTTTAGCTCCCGCTCTGATTCTAACGAGG
AAAGCACGTTATACGTGCTCGTCAAAGCAACCATAGTACGCGCCCTGTAGCG
GCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACT
TGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCAC
GTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCC
GATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTTGGGTGATGGT
TCACGTAGTGGGCCATCGCCC

S3.5.2 Sequences of staple strands

S3.5.2.1 Staple strand sequences of tiles for regular tilings

Table S3.26. Core staples of M13mp18 square DNA origami tile.

Name	Sequence
[SQ]_M13_core_1	GCTGAGGCTTGCAGGGAGTTAAACGAAAGACAGCATCGCATGAGGA
[SQ]_M13_core_2	AGGCAAAAGGACTAAAGACTTTTTGAACGA
[SQ]_M13_core_3	GGGTAGCAACTTTCGAGGTGAA
[SQ]_M13_core_4	AGTTTCCAAGGCACCAACCTAAGATTTGTA
[SQ]_M13_core_5	TGAGAAGTTTATCATTTTGGCTTTGAGAATAC
[SQ]_M13_core_6	GCGCAGACAACAAAGTACAACGGAAACGAAAG
[SQ]_M13_core_7	ACTAAAACACTTTTTTTTTCAGCGGAG
[SQ]_M13_core_8	TCATCGCCCATGTTACTTAGCCGTAATCTT
[SQ]_M13_core_9	AAGCGCGAGGTCAATCATAAGGGACAGGCGCA
[SQ]_M13_core_10	GATTTTGCTAAACAACTTTTTTCCCCAGCGATTATACC
[SQ]_M13_core_11	GCTTGCCCCTGACCTTCATCAAGAGGAACGAG
[SQ]_M13_core_12	GTAAATTGAACGGTGTACAGACACCGAA
[SQ]_M13_core_13	CTGACCAACTTACCGTAACA
[SQ]_M13_core_14	GACAAGAAAGCTGCTCATTCAGAAATCTAC
[SQ]_M13_core_15	TAGGCTGGTGACGAGAAACACCAGGCTCATTA
[SQ]_M13_core_16	TCAGTACCAATAGGTTTTGGACAGATGGGCTT
[SQ]_M13_core_17	TAGGAATAAGGACGTTGGGAAGAATGAATAAG
[SQ]_M13_core_18	TAACGCCCGATTTTAAGAACTGAACGAGTA
[SQ]_M13_core_19	GAGATGGTTTTTTTTTTGGGGTTTTGC
[SQ]_M13_core	GTTAATAAGAAAGATTCATCAGTTTAGACT

_20	
[SQ]_M13_core_21	TACCAGTCCCACATTCAACTAATGGAAGTTTT
[SQ]_M13_core_22	ACCTTATGAAAAGGAATTACGAGGAAAACCAA
[SQ]_M13_core_23	CCTCAAGAGAAGGATTTTTTTTTTTAATCATTGTGAATT
[SQ]_M13_core_24	TGCTTTAAGGGTAATAGTAAAATGTTGAGATT
[SQ]_M13_core_25	ATAAATCGAGGCTTTTGCAAAACAGATACA
[SQ]_M13_core_26	AGATTACCCTGACTATTATAGTTTACCAGACGACGATACATAGT
[SQ]_M13_core_27	AAGAGCAACATGAATGGAAAG
[SQ]_M13_core_28	GGATAGCATATTCATTGAATCCGAAGCAAA
[SQ]_M13_core_29	GCCAGAGGACAGTTCAGAAAACGATTTTAATT
[SQ]_M13_core_30	AATAGCGAAAAAATCAGGTCTTTAAGAGGAAGCCCGAAAGGCTCAACA
[SQ]_M13_core_31	ACCTTTTTTTTTTAGCCCCCTATCCTCATTTTTTACCCTCGT
[SQ]_M13_core_32	CGGATGGCAAAGCGAACCAGACCGCCCTCAAA
[SQ]_M13_core_33	TGCTGTAACTTCAAATATCGCGGAATGACC
[SQ]_M13_core_34	CAGAAGCATTTTTCTGTCGTGATAAATCATTTTTCAAGAAAA
[SQ]_M13_core_35	CTCCAACCTTTTGATAAGAGGTTTTGACCA
[SQ]_M13_core_36	CGAGCTTCTTAGAGCTTAATTGCTTGATTCCC
[SQ]_M13_core_37	GCTTTCCAGTTTGCATCAAAA
[SQ]_M13_core_38	TGAAAAGGGAACGAGTAGATTTAGCATTTTTG
[SQ]_M13_core_39	GCAAAGAATAGTAGTAGCATTATTCCATATAACAGTGAATATAA
[SQ]_M13_core_40	TGTTTTAAATATGCAATTTTTTTAAGCTTGCATGCCTGC
[SQ]_M13_core_41	TTAGATAATATTTTCATTTGGGCATAAAGC
[SQ]_M13_core_42	AATTCTGCTGGCATCAATTCTACTAATTAGCAAAATTAAGGGATAAAA

[SQ]_M13_core_43	AGTTTCAACATCCATTTTCGCTTCTGGACGTT
[SQ]_M13_core_44	GTAAAACGACTTTTTTTGGTGTCTGGA
[SQ]_M13_core_45	CAACGCAACAATAAAGCCTCAGAGGCGCGAGC
[SQ]_M13_core_46	TAAATCGTTTTGCGGGAGAAGCTCAAAAGG
[SQ]_M13_core_47	CAGCCAGCTTTACAGGCAAG
[SQ]_M13_core_48	ATCTACAGCTGATAAATTAATGATGTGTAGGTAAAGATCTTTATTT
[SQ]_M13_core_49	ATTTTTAGAACCCTCATTTTTTCCCGTCGGATTCTCCG
[SQ]_M13_core_50	GTGAGAAATATTCAACCGTTCTAAAGGCTA
[SQ]_M13_core_51	TGAGTACCGGAGAGTTTTGTTAAAATTCAACA
[SQ]_M13_core_52	TTAAATGTGATTTTTTTATGCAATGCC
[SQ]_M13_core_53	TCAGGTCCGATGAACGGTAATCGTAAAACT
[SQ]_M13_core_54	TTGTAAACGTTTTTTTTGAGAG
[SQ]_M13_core_55	TCCAGAGCCTAATTTGCCAGTTACAAATAAGAAACGATACATAAAA
[SQ]_M13_core_56	GAGCGCTACTTTACAGAGAGAATATTTTTG
[SQ]_M13_core_57	TTTAACGTCATTAGGTTTTGAA
[SQ]_M13_core_58	ACAGGGACTGAACAAAGTCAGACAATAGCT
[SQ]_M13_core_59	TTTTATCCTCCCGATTTTATAGCAGCATATCA
[SQ]_M13_core_60	ACCGAGGAAGAAACAATGAAATAGGGGTAATT
[SQ]_M13_core_61	GAGAGATAACTTTTTTTAGCAAGCCGT
[SQ]_M13_core_62	ATCTTACCCGAACAAAGTTACCTGGCAACA
[SQ]_M13_core_63	TAAGAGCAAACGCAATAATAACGGGTTAGCAA
[SQ]_M13_core_64	ACCAAGTACCGCACTCTTTTTTGAGTTAAGCCCAATAA
[SQ]_M13_core	ATATGGTTAATACATACATAAAGGAGAAGGAA

_65	
[SQ]_M13_core_66	GACATTCCTTATTACGCAGTATAATACC
[SQ]_M13_core_67	CAAAAGAACTTGCAGAACGC
[SQ]_M13_core_68	TATAAAATTGTCACAATCAATAGCAAAATC
[SQ]_M13_core_69	ACGTAGAATACCAGCGCCAAAGACCACCGACT
[SQ]_M13_core_70	TACCAGCAACATGTTTTTTAAGACTCAACCGA
[SQ]_M13_core_71	CACCGTAATTGGGAATTAGAGCCAGAAAATTC
[SQ]_M13_core_72	CCTTTAGGTGAATTATCACCGTAAAAGGGC
[SQ]_M13_core_73	TTGAGGGAGGTTTTTTTTACAAATTCT
[SQ]_M13_core_74	ACCAGTAACCAATGAAACCATCACCCTCAG
[SQ]_M13_core_75	TGAGCCATTCAGTAGCGACAGAATCCACCACC
[SQ]_M13_core_76	CATTAAAGCGTCAGACTGTAGCGCCTTTTCAT
[SQ]_M13_core_77	AGCCTGTTTAGTATCATTTTTTTATTGACGGAAATTATT
[SQ]_M13_core_78	GAGCCGCCCTCCCTCAGAGCCGCCGATAGCAG
[SQ]_M13_core_79	CAGGTCATCACCGGAACCAGAGCAAGTTTG
[SQ]_M13_core_80	CGCAGTATTCACAAACAAATAATATTAGCGTTTGCCATGTTTTC
[SQ]_M13_core_81	ATCGGCATTTTGCTTAGGTTG
[SQ]_M13_core_82	AACCGCCAGCCGCCACCAGAACAATAAGTT
[SQ]_M13_core_83	GGAACCGCGCCAGCATTGACAGGACATGGCTT
[SQ]_M13_core_84	AATCAAAAGACGATTGGCCTTGATCTCTGAATTTACCGTTCTGAGACT
[SQ]_M13_core_85	TCGGAACCACAGGAGTGTACTGGTCACCACCA
[SQ]_M13_core_86	TAAGAGGCCAGTAAGCGTCATAGGTTGAGG
[SQ]_M13_core_87	TTAACGGACAGTTAATGCCCCCAATAGGTG

[SQ]_M13_core_88	TTGATGATTATTATTCTGAAACATCCGTCGAG
[SQ]_M13_core_89	CCCTCAGATATAAGTATAGCCCGGTGCCTATT
[SQ]_M13_core_90	CTGAGTTCAGGGATAGCAAGCCCAGGCGGATAAGTGGAAAGTAT
[SQ]_M13_core_91	TATCACCAACCGCCACCCTCAGCATTCCAC
[SQ]_M13_core_92	AGGGTTGAGCCACCACCCTCATTTTTCGTCACCAGTACAACTGTATGG
[SQ]_M13_core_93	TGAATTTTACTACAACGCCTGTAGAACCGCCA
[SQ]_M13_core_94	AGACAGCTCGTCTTTCCAGACGAAGGAATT
[SQ]_M13_core_95	TTTCTTGCCTTTAATTGTATCGTAGAAAGGAACAACTATTAGTAAA
[SQ]_M13_core_96	GCGAATAAAGGCTCCAAAAGGAAAACAGCT
[SQ]_M13_core_97	TGATACCCCCACGCATAACCGATATATTCG
[SQ]_M13_core_98	AAGAATACGTGGCACAGACAATAACTGATAGCCCTAAAAGGTGAGG
[SQ]_M13_core_99	TAAAGCATGCAGAAGATAAAACAGACATCG
[SQ]_M13_core_100	CCATTAAAAATTTTTACATTGG
[SQ]_M13_core_101	CGGTCAGGAGCCAGCAGCAAATAAGGAATT
[SQ]_M13_core_102	TCAAACCGTCTGAATTTTAACCACCACACCTT
[SQ]_M13_core_103	GATAATACGCAAATCAACAGTTGAGAAAAATC
[SQ]_M13_core_104	GCTGAACCTCTTTTTTTGTAGAAGAAC
[SQ]_M13_core_105	GAGGAAGCTAATAGATTAGAGCCATTATCA
[SQ]_M13_core_106	GTCAGTTGATTTGAGGATTTAGAACCGAACGT
[SQ]_M13_core_107	GATTAGTAATAACATCTTTTTTCCTCAATCAATATCTG
[SQ]_M13_core_108	TGATGGCATTAAAAGTTTGAGTAACGTCAATA
[SQ]_M13_core_109	TTGGATTTATTAAATCCTTTGCGTATTA
[SQ]_M13_core	GACTTTACAACAGGAGGCCG

_110	
[SQ]_M13_core_111	TTTTGCGTCATCATATTCCTGATCAGATGA
[SQ]_M13_core_112	TATTAATTATTCATCAATATAATCTAAAGAAA
[SQ]_M13_core_113	AAAGGACAGAGCGGTTTTACAACTCGATACTT
[SQ]_M13_core_114	AATACCAAATTTTCAGGTTTAACGTTATCAGA
[SQ]_M13_core_115	TTATTCACACGTAAAACAGAAACTGATTGT
[SQ]_M13_core_116	CTGAATAATGTTTTTTTACGTGGCGAG
[SQ]_M13_core_117	ATATACAAACGGATTCGCCTGAAATAACCT
[SQ]_M13_core_118	TTGCGTAGGTTACAAAATCGCGCAGGAAACAG
[SQ]_M13_core_119	ATTATTTGTTTCAATTACCTGAGCTAACAATT
[SQ]_M13_core_120	AGAGCTTGACGGGGAATTTTTTTAACCTACCATATCAAA
[SQ]_M13_core_121	AGCGATAGTCAATATATGTGAGTGTTGCTTTG
[SQ]_M13_core_122	TCAATAGATTACCTTTTTTAATGAGGCGAA
[SQ]_M13_core_123	GGTTATATAGGTCTGAGAGACTCAAAATTAATTACATTAAAAGA
[SQ]_M13_core_124	AGATGATGAATGCCCGAGATA
[SQ]_M13_core_125	TGCTTCTTCCCTTAGAATCCTTCAAATATA
[SQ]_M13_core_126	TACATAAACTTAGATTAAGACGCTATCGCAAG
[SQ]_M13_core_127	TCATTTGATGAATTTATCAAAATCATAACTATATGTAAATCTAGAAAA
[SQ]_M13_core_128	TAAGGCGTCGCGAGAAAACTTTTTGAAAACAT
[SQ]_M13_core_129	ATAATTAGCTGATGCAAATCCAGAGAAGAG
[SQ]_M13_core_130	TTTTAGTTGAAATACCGACCGTTTAACAAC
[SQ]_M13_core_131	ACAAAGAATAAATAAGAATAAACACAACAGTA
[SQ]_M13_core_132	CAAAAGGTTTGAGAATCGCCATATGTGATAAA

[SQ]_M13_core_133	GCCTGTGACGACGACAATAAATATAAAGCCAACGCTCCGGAATC
[SQ]_M13_core_134	GCCAACAAATAAGAGAATATAAAATAATAT
[SQ]_M13_core_135	GGGCTTAAAAAGTAATTCTGTCCATTATCAACAATAGATAGGTATTAA
[SQ]_M13_core_136	CAAGAACGAGTCCTGAACAAGAAAAGTACCGA
[SQ]_M13_core_137	CCCATCCTCGGCTGTCTTTCCTATTACCGC
[SQ]_M13_core_138	GCCTTAGAGGCGTTTTAGCGAATTTCATCGTAGGAATCTATCATTC
[SQ]_M13_core_139	GCCCAATGTATTCTAAGAACGCAATCAAGA
[SQ]_M13_core_140	TTAGTTGATCTTACCAACGCTAACGAGCGT
[SQ]_M13_core_141	ATGTCAATCATATGTACCCCGGTTTGTATAAGCAAATATTAAATCA
[SQ]_M13_core_142	AGCTTTCATCGCATTAAATTTTTGTTTAAA
[SQ]_M13_core_143	GCTCATTTCGCGTCTGGCCTTCTAATGGGA
[SQ]_M13_core_144	GACAGTATAACGGCGGATTGACCGCTGTAGCC
[SQ]_M13_core_145	TAGGTCAATCTGCCAGTTTGAGTGTTGGGA
[SQ]_M13_core_146	TGGGAACACGGCCTCAGGAAGATCCAAAGCGC
[SQ]_M13_core_147	GGCGATTAATTCAGGCTGCGCAACGGGACGAC
[SQ]_M13_core_148	CAGTCACGTGCCGGAAACCAGGGCACTC
[SQ]_M13_core_149	AGGGCGAGGCGAAAGGGGGATGAGCTGTTT
[SQ]_M13_core_150	CATTCGCCAGTTGGGTAACGCCAGGGTACCGA
[SQ]_M13_core_151	TAAAGCCTTCGTAATCATGGTCATTGCTGCAA
[SQ]_M13_core_152	TCACATTTCTAGAGGATCCCCGGGTTTTCC
[SQ]_M13_core_153	CCTGTGTATACGAGCCGGAAGCCAGTGAGA
[SQ]_M13_core_154	GCTCGAATGGGGTGCCTAATGAGTGTATTGGG
[SQ]_M13_core	AGGTCGACAATTGCGTTGCGCTCAATCGGCCA

_155	
[SQ]_M13_core_156	GGTCCACGTGGTTTTTCTTTTCACATAAAGTG
[SQ]_M13_core_157	TCCTGTTGGAGAGGCGGTTTGCGAGCTAAC
[SQ]_M13_core_158	GGGTTGATCGGCAAAATCCCTTCCAGCTGCATTAATGACTGCCC
[SQ]_M13_core_159	CGGGCAAGCCCTGAGAGAGTTGCGAAAAAC
[SQ]_M13_core_160	CGCCAGGGCTGGTTTGCCCCAGCATATTAAAG
[SQ]_M13_core_161	ACGCGCGGTGATGGTGGTTCCGAAAGTGTTGTTCCAGTTTCCCGATTT
[SQ]_M13_core_162	GGTGCCGTCTCCAACGTCAAAGGGCAGCAAGC
[SQ]_M13_core_163	GGGAGCCGGAACAAGAGTCCACGGCGAAAA
[SQ]_M13_core_164	CGTCTATCAAATCAAGTTTTTTCGGTCACG
[SQ]_M13_core_165	AACGTGGAAAAGCACTAAATCGGAAGGAGCGG
[SQ]_M13_core_166	CTTTGACGGCGCTGGCAAGTGTAGGGGGTCGA
[SQ]_M13_core_167	ATTAAATTTCCTCGTTAGAATAGGGAAGAAAGCGAAACCCTAAA
[SQ]_M13_core_168	CTGCGCGCTACAGGGCGCGTACCTGAGAAG
[SQ]_M13_core_169	GCGCTAGGAGCACGTATAACGTGCGGGATTTTAGACAGGAACTTCTTT
[SQ]_M13_core_170	GTAGCAATACGGTACGCCAGAATCTATGGTTG
[SQ]_M13_core_171	TGTTTTTGTCCATCACGCAAATAATATCCA
[SQ]_M13_core_172	CAGATTCATTTTGACGCTCAATTATCGGCCTTGCTGGTTAACCGTT
[SQ]_M13_core_173	GAACAATTCATGGAAATACCTACACCAGTC
[SQ]_M13_core_174	ACACGACATAGAACCCTTCTGACCTGAAAG

Table S3.27. Edge staples of M13mp18 square DNA origami tile.

Name	**Sequence**
[SQ]_M13_edge_1	GCATTTTCGAGCCAGTTGTAATTTAGGCAGAGCG

[SQ]_M13_edge_2	CCTAAATTTAATGGTTTAATTTCATCTTCTGACA
[SQ]_M13_edge_3	CATCGGGAGAAACAATGTAACAGTACCTTTTATA
[SQ]_M13_edge_4	AGAAGGAGCGGAATTAGAACAAAGAAACCACCCG
[SQ]_M13_edge_5	CTATTACGCCAGCTTCGGTGCGGGCCTCTT
[SQ]_M13_edge_6	CAATTCCACACAACGAAATTGTTATCCGCT
[SQ]_M13_edge_7	CGTGAACCATCACCCAGGGCGATGGCCCAC
[SQ]_M13_edge_8	CGCTTAATGCGCCGTAACCACCACACCCGC
[SQ]_M13_edge_9	CCAAATCAACGTAACAACCGGATATTCATTACGT
[SQ]_M13_edge_10	CAACATTATTACAGGTAAACGAACTAACGGAAAA
[SQ]_M13_edge_11	GTACCTTTAATTGCTCAGGTCAGGATTAGAGACA
[SQ]_M13_edge_12	AATAACCTGTTTAGCTCATTTCGCAAATGGTCAC
[SQ]_M13_edge_13	ACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ]_M13_edge_14	CAGTGCCCGTATAAGGTCAGTGCCTTGAGT
[SQ]_M13_edge_15	AGGCCGGAAACGTCGCACCATTACCATTAG
[SQ]_M13_edge_16	GGAATAAGTTTATTGAAACGCAAAGACACC

Table S3.28. Core staples of p2820 equilateral triangular DNA origami tile.

Name	**Sequence**
[TR]_p2820_core_1	GAGGCACATAGTTGCCTGACTCTGATACCG
[TR]_p2820_core_2	TAGAGTAGGGCCGAGCGCAGAAGGCCCCAGTGCTGCAACCCGTC
[TR]_p2820_core_3	GGTAACTATCGTTTTTGGCTTACCATCT
[TR]_p2820_core_4	GTGGTTTGTTGCCGGGAAGCTGGTGTCACGCTCGTGATCA
[TR]_p2820_core_5	ATTAACCTGCAACTTTATTTTGCGCTTTCTCATGCCTT
[TR]_p2820_core_6	TCTCCCTTCGGTTTTTCCATCCAGTCT
[TR]_p2820_core_7	CGAGACCAACCAGCCAGCCGGAAAGTAGTT
[TR]_p2820_core_8	CGCCAGTTTGCCATTGCTACAGCCCCCATG
[TR]_p2820_core_9	AAAAAAAAGAACGTGGATTTTCCGGTTCCCAACCGTTT
[TR]_p2820_core_10	GGTATGGCTTCTTTTTGTCAAAGGGCG
[TR]_p2820_core_11	CTGTCATTGGCCGCAGTGTTATAGGCGAGTTACATGATGCATCG
[TR]_p2820_core_12	CACTCATGGTTATTTTCAGCTCATTTTT
[TR]_p2820_core_13	TTGTGCAGTTGTCAGAAGTAAGTGCCATCC

[TR]_p2820_core_14	TCTCTTACGGCGACCGAGTTTTTTTGTATTTAGAAAAAATTCGCG
[TR]_p2820_core_15	TTAAATTTTTTTTTTACTGCATAAT
[TR]_p2820_core_16	GTAAGATTCATTCTGAGAATAGCGGGATAA
[TR]_p2820_core_17	TAAACAATGAGCGGATACATTTTTTGCCCGGCGTCAATATGTATG
[TR]_p2820_core_18	AAATAATAATTTTCAAGGGGGCGAAATTTTTCACGG
[TR]_p2820_core_19	TACCGCGTGGAAAACGTTCTTCGATCTTAC
[TR]_p2820_core_20	TAACTACGATTTTTTCCAACCCGGT
[TR]_p2820_core_21	AAGACACCTTGAAGTGGTGGTTTTTTCTGACAGTTACCGTGTAGA
[TR]_p2820_core_22	AATGCTAAGTATATATGAGTTTTTTTACGGCTACACTAGAGAGTT
[TR]_p2820_core_23	GAGAAAGGGTTTCAAACGCTCTTGATTTTTTGTCAT
[TR]_p2820_core_24	TCAAGAAGATCCTTTACGAAAACTCACGTTTTATCAAA
[TR]_p2820_core_25	AAGGATCTTTTAAATCAATCTATAATCAGT
[TR]_p2820_core_26	CGCTGTTCCAACTGATCTTCAG
[TR]_p2820_core_27	TTCCGCGAAGCGTTAATATTTTATCGGCAA
[TR]_p2820_core_28	ATGGCCTTGGAACAAGAGTCCATAACCAATAGGCCGAAGTTAAA
[TR]_p2820_core_29	CTATTCCGTCTATCAGGGCGCTAAATCGGAACCCTCCGGC
[TR]_p2820_core_30	AATCCCTGAGTGTTGTTCCAGTCACTACGT
[TR]_p2820_core_31	GAACCATGGGTCGAGGTGCCGTGAAGGGAA
[TR]_p2820_core_32	AAACCCAAAAATCGACGTTTTTGACGGGGAAAGAAAGG
[TR]_p2820_core_33	GAGCCCCCGATTTTTTCAGAGGTGGCG
[TR]_p2820_core_34	TCGCCACGTAACCACCACACCCGAACGTGGCGAGAAAGAAAGCA
[TR]_p2820_core_35	GCCGCGCTTAATTTTTGGATAACGCAGG
[TR]_p2820_core	GAAAGCGAGCGGTCACGCTGCGTTCAGGCT

_36	
[TR]_p2820_core_37	GTCCCATAGGGGGATGTGCTTTTTTTGGGCGCTCTTCCAATACGG
[TR]_p2820_core_38	TTATCCACAGTTTTTTACAGGGCGC
[TR]_p2820_core_39	GCGCAACGCTATTACGCCAGCTAACGCCAG
[TR]_p2820_core_40	GCTTCCCGGGGAGAGGCGGTTTTTTCGATTAAGTTGGGTGGCGAA
[TR]_p2820_core_41	GCTCACATTTTTCGAATACTCACTATTTTTTGTTGC
[TR]_p2820_core_42	GGTTTTCAGCGCGCGTAATACGTGGGTACC
[TR]_p2820_core_43	TTTACTTTCACCAGCTGCCGCAAAAAAGGGGTTGAATA
[TR]_p2820_core_44	CTCATACCAGGGTTATTGTCTCAATAGGGG
[TR]_p2820_core_45	GGCGTAATTATCCGCTCACAAT
[TR]_p2820_core_46	TGACTCGATCAGCTCACTCAAAAAAGGCCA
[TR]_p2820_core_47	GATACCCCGCCCCCCTGACGAGAAAGAACATGTGAGCAGGCGGT
[TR]_p2820_core_48	CATCACGACAGGACTATAAAACCGGATACCTGTCCAGCTC
[TR]_p2820_core_49	GCAAAAGGTTTTTCCATAGGCTAGGCGTTT
[TR]_p2820_core_50	CCCCCTGCCTGTTCCGACCCTGAGTTCGGT
[TR]_p2820_core_51	GACTTACCGCTGCGCCTTATCCACGCTGTAGGTATCTCCCGCTT
[TR]_p2820_core_52	GTAGGTCCCCCGTTCAGCCCGATCGCCACT
[TR]_p2820_core_53	GGCAGCATGTAGGCGGTGCTACAAGGACAG
[TR]_p2820_core_54	TATTTGGGAAAAAGAGTTGGTAAAACCACC
[TR]_p2820_core_55	ACAACATACGAGCCGTGAGTGAGCTAACTCACTGCCCG
[TR]_p2820_core_56	CTTTCCAGAATCGGCCAACGCGTCGCTCAC
[TR]_p2820_core_57	GCTGGTAACGCGCAGAAAAAAA

Table S3.29. Edge staples of p2820 equilateral triangular DNA origami tile.

Name	Sequence
[TR]_p2820_edge_1	AAAACGACGGCCAGTGCCAGTCACGACGTTGTTA
[TR]_p2820_edge_2	CGGTGCGGGCCTCTTCTGTTGGGAAGGGCGATTC
[TR]_p2820_edge_3	GGGCGCTGGCAAGTGTAAAGGAGCGGGCGCTAAG
[TR]_p2820_edge_4	AGACCGAGATAGGGTTTATAAATCAAAAGAATCT
[TR]_p2820_edge_5	GTGCCACCTAAATTGTCACATTTCCCCGAAAATG
[TR]_p2820_edge_6	TTATTGAAGCATTTATTCTTCCTTTTTCAATATA
[TR]_p2820_edge_7	AATTAAAAATGAAGTTCACCTAGATCCTTT
[TR]_p2820_edge_8	TATTTCGTTCATCCCTATCTCAGCGATCTG
[TR]_p2820_edge_9	ATTTATCAGCAATACACGCTCACCGGCTCC
[TR]_p2820_edge_10	TCGGTCCTCCGATCAAAAAGCGGTTAGCTC
[TR]_p2820_edge_11	AGTACTCAACCAAGGCTTTTCTGTGACTGG
[TR]_p2820_edge_12	AAAGTGCTCATCATCCACATAGCAGAACTT
[TR]_p2820_edge_13	TGTGCCAGCTGCATTAATGTCGGGAAACCTGTCG
[TR]_p2820_edge_14	GAGGCTGCGGCGAGCGGTCTGCGCTCGGTCGTTC
[TR]_p2820_edge_15	GGAGGCCGCGTTGCTGGCGCCAGGAACCGTAAAA
[TR]_p2820_edge_16	AAGCCAGTTACCTTCGTATCTGCGCTCTGC
[TR]_p2820_edge_17	TTAGCAGAGCGAGGTAGCCACTGGTAACAG
[TR]_p2820_edge_18	GCTGTGTGCACGAACCGTTCGCTCCAAGCT

Table S3.30. Core staples of M13mp18 half hexagonal DNA origami tile.

Name	Sequence
[hHE]_M13_core_1	AAAACATCGCCATTAAAAATACCGGAGGCGGTCAGTATTATGAAAAA
[hHE]_M13_core_2	TTTTTATGCAAGCAAATCAGATATAGAAGGC
[hHE]_M13_core_3	TACGAGCCCTTATCATTCCAAGGCAAGCCG
[hHE]_M13_core_4	TCCTGAGATTAGTTGCTATTTTTTTCTCATCGAGAACAAAACGGG
[hHE]_M13_core_5	CGGTATTCTAAGAACGCGAGGCGTGAAGCCTTAAATCAAATCTTACC
[hHE]_M13_core_6	AACGTAGATCCTTATTACGCAGTAAAACAGGG
[hHE]_M13_core_7	AAGCGCATAGAGAGAATAACATAATGTTAGCA
[hHE]_M13_core_8	TAAGAATTAGTCTTTAATGCGCGAACTGATA
[hHE]_M13_core_9	ATGGCTATACGTGGCACAGACAATAAACCGTC
[hHE]_M13_core_10	TATCAGGGAACGTCAAAGGGCGAAATTTTTGA

[hHE]_M13_core_11	CTGAAATACGACCAGTAATAAATGAAAGCG
[hHE]_M13_core_12	CAGCAAAACACCGCCTGCAATTTTTGAACCCTTCTGACCAGGGAC
[hHE]_M13_core_13	TACATTTATTCTGGCCAACATTTTTCGCTGAGAGCCAGGGCAAAT
[hHE]_M13_core_14	CCAGTCACGGATTATTTACATTGGCCCCCGAT
[hHE]_M13_core_15	TTAGAGCTGGAACCCTAAAGGGAGCAGATTCA
[hHE]_M13_core_16	TGCCTGAAATATCCAGAACAATTCAATCGT
[hHE]_M13_core_17	TGACGCATTACCGCCAGCCATTTCTTTGATTAGTAATATCAGTG
[hHE]_M13_core_18	CAACAGTTGATTTTTTGGAAATACC
[hHE]_M13_core_19	GCAACAGGAAAATTTTTGAGGAAGGTTA
[hHE]_M13_core_20	TTGCTGGTGTAGAAGAACTCAAACCACACCCG
[hHE]_M13_core_21	CCGCGCTTCGCTGCGCGTAACCACTATCGGCC
[hHE]_M13_core_22	AAGAGCAGAAGTGTTTTTATAAACATCACT
[hHE]_M13_core_23	AAAGTCCCACAAGAATTGAGAGGCCACCGAGTAAAATACT
[hHE]_M13_core_24	TTATTACAACTCGTATTTTTTACCGTTGTAGCAAGAGT
[hHE]_M13_core_25	CTGTCCATCACTTTTTTTGCCCGAACG
[hHE]_M13_core_26	AATCCTGAAGAAACAATGAAATAGCAATAGCT
[hHE]_M13_core_27	ATCTTACCTTTTAGACAGGAACGGTACGCCAG
[hHE]_M13_core_28	CCTTTACTAGACGGGAGAATTACCAATAAT
[hHE]_M13_core_29	TTAAGCACTGAACACCCTGAACTAACGTCAAAAATGAACATATT
[hHE]_M13_core_30	GATAACAGAGGGTAATTTTTTCATTTTCGAGCCGCCAA
[hHE]_M13_core_31	CATGTAATTTATTTTTAATATCAGAGA
[hHE]_M13_core_32	AACGCTATACAAAATAAACAGCAATAGCAG
[hHE]_M13_core	ATCAACAATAGATTTTCGATTTTTTGTT

_33	
[hHE]_M13_core_34	CCAATCCAAATTTTTTGAACAAGAA
[hHE]_M13_core_35	AAATAATTATTAAACCAAGTTTTTTAGCTACAATTTTAATTTATC
[hHE]_M13_core_36	TTGCCAGTACGAGCGTCTTTCCAGCAAAGACA
[hHE]_M13_core_37	AAAGGGCGTATGGTTTACCAGCGCAGCCTAAT
[hHE]_M13_core_38	GAGGTTTTTTTAGCGAACCTCCCGATTTGGGA
[hHE]_M13_core_39	ATTAGAGCGTCACCGACTTGAGCCACTTGCGG
[hHE]_M13_core_40	AAGGTAACATGTTCAGCTAATGTCCTAATT
[hHE]_M13_core_41	ATCCCACAGAACGCGCCTGTTTTAAGAGAATATAAAGTAGAATC
[hHE]_M13_core_42	AATTCTTAGTAGGGCTTAATTGACCGACAA
[hHE]_M13_core_43	TTAAAAGCCTGTTTAGTATCGCCATATTTAACAACAGTAA
[hHE]_M13_core_44	ATTTTAGTTGAAATACCGACCGGTTATACA
[hHE]_M13_core_45	ATATGCTGTGATAAATAAGGCGACGCGAGAAAACTTTTCTATAT
[hHE]_M13_core_46	GAAAATAAGAATAAACATTTTTATACTTCTGAACAATA
[hHE]_M13_core_47	TAATCCTGATTTTTTTCATAATTACTA
[hHE]_M13_core_48	TCATAGGGGTTGGGTTATATAATCAAATAT
[hHE]_M13_core_49	CAGTAACAGTACTTTTGCAAGACAAAGA
[hHE]_M13_core_50	CTGATGCAAATTTTTATCGGGAGAA
[hHE]_M13_core_51	ACAATAAGCAAAAGAAGATGTTTTTGAAGAGTCAATAGGTAAATG
[hHE]_M13_core_52	AGTGAATAACCTTGCTTCTGTAAACTTGAAAACATAGCGTATCAAAA
[hHE]_M13_core_53	TGAATTATAGCTTAGATTAATTTTTCAAACATCAAGAAAACCTGA
[hHE]_M13_core_54	AATTACATGGAAACAGTACATAAATCAATAT
[hHE]_M13_core_55	TGCTTTGTTATTCATTTCAATTACAAAATT

[hHE]_M13_core_56	AAATTATAGATTTTCAGGTTTACGCCTGAT
[hHE]_M13_core_57	CGGATTACGTCAGATGAATATAGAAGGGTTAGAACCTATATCAG
[hHE]_M13_core_58	TTTGCGGCATCATATTCCTGATCCATATCA
[hHE]_M13_core_59	ATTCGAATTTTAAAAGTTTGATGATGGCAATTCATTAATG
[hHE]_M13_core_60	ACAACTAGAGGATTTAGAAGTAATTATCAT
[hHE]_M13_core_61	AGTAACTTAGACTTTACAAACATCTAAAATATCTTTAGTCAGTT
[hHE]_M13_core_62	TCTAAAGTCAATCAATATCTGGGAGCACTA
[hHE]_M13_core_63	TTAGCAAGGCCGGAAACGTCACCAAGCGACAGAATCAAGTTTCGGTC
[hHE]_M13_core_64	AAATCCCTGAGTGTTGTTCCAGTTTGGAACA
[hHE]_M13_core_65	ATCTGCCATAGATGGGCGCATCGTTAGCCCGAGATAGGGTTTATA AATCAAAAGAAAACCGTGC
[hHE]_M13_core_66	TGCCCTTGGTCCACGCTGGTTTAATCGGCA
[hHE]_M13_core_67	GGTGCCTGAACCATCACCCATTTTTGATGGTGGTTCCGAGCCCCA
[hHE]_M13_core_68	CCACTATTAAAGAACGTGGACTCCCGATGGCCCACTACGGTAAAGCA
[hHE]_M13_core_69	TATCACCCAGCAAAATCACCAGTAGCACCAT
[hHE]_M13_core_70	AAATTCAACATTCAACCGATTGAGGTGAAT
[hHE]_M13_core_71	CGGCATTTTGCCTTTAGCGTTTTTTAAATTATTCATTAAAGGGAG
[hHE]_M13_core_72	TATTTTGGGAAGGTAAATATTTTTTAGCGCGTTTTCATCCACCGG
[hHE]_M13_core_73	TTAAGACAAATACATACATAAATCAATAGA
[hHE]_M13_core_74	TCACAAGGTGGCAACATATAAAGAATACCCAAAAGAACAAAAGT
[hHE]_M13_core_75	AACCGCCTCCTTTTTGGAATAAGTT
[hHE]_M13_core_76	AGAAACGCAAAGTTTTCCGCCACCCTCA
[hHE]_M13_core_77	AAAGGGAGAAGCCCTTTTTAAGTGGCATGA

[hHE]_M13_core_78	GCTTTCAGAGCGGGAGCTAAAAGCAGATAGCCGAATAACG
[hHE]_M13_core_79	TCATTTGGCCTTGATATTTTTGAAACGCAATAACAAAG
[hHE]_M13_core_80	TTACCAGAAGGTTTTTCAAATAAATCC
[hHE]_M13_core_81	GCGGTCAAATGCGCCGCTACAGGGCCGATT
[hHE]_M13_core_82	ACAGGAGGCGCGTACTATGGTTGGCGCTAGGGCGCTGGGCGAAC
[hHE]_M13_core_83	AGAATGACGAGCACGTATTTTTAACTCACATTAGCCTG
[hHE]_M13_core_84	GGGTGCCTAATTTTTTCTTTCCTCGTT
[hHE]_M13_core_85	CTAAATCTGACGGGGAAAGCCGCAAGTGTA
[hHE]_M13_core_86	GGGCGCCAGGGTTTTTGCGAAAGGAGCG
[hHE]_M13_core_87	GAAAGGAAGGTTTTTCTTTTCACCA
[hHE]_M13_core_88	GTGAGACGCAGGCGAAAATCTTTTTTTTTTGGGGTCGAGTGGCGA
[hHE]_M13_core_89	ATTCGCCAGTGCCGGAAACCAGGCGAGAGTTGCAGCAAGC CACCGCCTGGCCCTGAAAAGCGCC
[hHE]_M13_core_90	GTCGGGACCAACGCGCGGGGAGCAGCTGAT
[hHE]_M13_core_91	GGGCAAAGGCGGTTTGCGTATTGTTGCGCTCACTGCCCGCCGGA
[hHE]_M13_core_92	TTTCCCAGGATTAAGTTGGGTAACTGCATTAATGAATCGGAACCTGTCGTGCCAGCGCCAGGGT
[hHE]_M13_core_93	ATCGTCACCACACAACATACGAGCTTTCCA
[hHE]_M13_core_94	CATCGTGCAGGGAGTTAAAGAGCATAAAGTGTAAAATTGC
[hHE]_M13_core_95	GGAACGAGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCCTCAGCAGCGAAAGACAGCATC
[hHE]_M13_core_96	ATCAGCTTACCGATAGTTGCGCTTTGCGGG
[hHE]_M13_core_97	GCCGCTCGACAATGACAACAACAGGAGCCTTTAATTGTTAATTT
[hHE]_M13_core_98	AGGCTCCCACGCATAACTTTTAGTGCCCGTATAAACGG
[hHE]_M13_core_99	GGTCAGTGCCTTTTTTTTCGGTCGCTG

[hHE]_M13_core_100	CAGCTTGATGCTTTCGAGGTGAATACACTAAA
[hHE]_M13_core_101	ACACTCATAAAGAGGCAAAAGAATTTCTTAAA
[hHE]_M13_core_102	AACAGTTAGGAATTGCGAATAAATCGGTTT
[hHE]_M13_core_103	GTTTTGCTCAGTTTTTAAAGGCTCCAAA
[hHE]_M13_core_104	TTGAAAATCTTTTTTGGATAAGTGC
[hHE]_M13_core_105	CGTCGAGCGCCACCCTCAGATTTTTTGTATGGGATTTTTTTCACG
[hHE]_M13_core_106	ACAACTAATCAGCGGAGTGAGAATTAGCCGGA
[hHE]_M13_core_107	ACGAGGCGCCTGCTCCATGTTACTAGAAAGGA
[hHE]_M13_core_108	TACAACGCCTGTAGCATTCCACAGTTTTGTCGTCTTTCCCAACTTTC
[hHE]_M13_core_109	GCTAAAAGACGTTAGTAAATTTTTTACCCTCAGAGCCACCAGAAC
[hHE]_M13_core_110	ATCTAAAGACAGCCCTCATAGTTATGACCTTC
[hHE]_M13_core_111	ATCAAGAGAGGCGCATAGGCTGGCGCGTAACG
[hHE]_M13_core_112	TTTTCAGTAACACTGAGTTTCGTCACCAGTA
[hHE]_M13_core_113	TATAGCCTAGTACCGCCACCCTCACCCTCA
[hHE]_M13_core_114	ACCTATTACTCCTCAAGAGAAGGATATAAG
[hHE]_M13_core_115	AGGGTTGATTAGGATTAGCGGGTTAATGCCCCCTGCCTAGTGTA
[hHE]_M13_core_116	ATTTACCTTTTGATGATACAGGATTTCGGA
[hHE]_M13_core_117	ACGATAAAGCCAGAATGGAACTGGTAATAAGTTTTAACAG
[hHE]_M13_core_118	CCCTCAGCCAGCATTGACAGGAGTCTCTGA
[hHE]_M13_core_119	AGCGCAGGTTGAGGCAGGTCAGGAACCGCCACCCTCAGGAGCCA
[hHE]_M13_core_120	ATAGCCCAAATCACCGGAACCAAGCCACCA
[hHE]_M13_core_121	CCCAAATCAACGTAACAAAGCTGCAACACCAGAACGAGTTTGTGAAT
[hHE]_M13_core	CATCAACTCTCCGTGGGAACAAACGGCGGAT

_122	
[hHE]_M13_core_123	TGTTAAATTTTTAACCAATAGGCCAGCTTT
[hHE]_M13_core_124	AGCTTTGACAGTATCGGCCTTTTTTTGGCCTTCCTGTAGAACGCC
[hHE]_M13_core_125	GTAATGGGATAGGTCACGTTGGTGGTTTGAGGGGACGACCCGGCACC
[hHE]_M13_core_126	ACAGACCTAATCTTGACAAGAACCGGATATT
[hHE]_M13_core_127	TCCGCGACAGACGGTCAATCATAACGGTGT
[hHE]_M13_core_128	TAATCAAGTAAATTGGGCTTTTTTTAAAGAGGACAGATGAAGGGA
[hHE]_M13_core_129	GCCTGATACCGAACTGACCATTTTTTTAATTTCAACTTCTACGTT
[hHE]_M13_core_130	TAAAACGCTTTGACCCCCAGCGTGTCGAAA
[hHE]_M13_core_131	AAATTGATTATACCAAGCGCGAAATGCCACTACGAAGGAGAGGC
[hHE]_M13_core_132	AATAAAACGATTTTTTTGTATCATC
[hHE]_M13_core_133	AACAAAGTACAATTTTGAACAACATTAT
[hHE]_M13_core_134	TAGCTGTGGTAGCAACGGCTACCACCAACC
[hHE]_M13_core_135	AGCTTTACCGAGCTCGAATTTTTGAGGACTAAAGATACGT
[hHE]_M13_core_136	GATAACACTATCATAACTTTTAAACGGGTAAAACTTTT
[hHE]_M13_core_137	TCATGAGGAAGTTTTTTACCAGACGAC
[hHE]_M13_core_138	GCAAGGCTCACGACGTTGTAAACATGGTCA
[hHE]_M13_core_139	CGTAATACGACGGCCAGTGCCACAGCTGGCGAAAGGGGTGTTGG
[hHE]_M13_core_140	CCGGGGCATGCCTGCAGTTTTTATCAGGTCATTTATTT
[hHE]_M13_core_141	TTGAGAGATCTTTTTTCTAGAGGATCC
[hHE]_M13_core_142	GCTTCTGTTCAGGCTGCGCAACGATGTGCT
[hHE]_M13_core_143	AAACAGGAAGATTTTTTCGCTATTACGC
[hHE]_M13_core_144	GATCGGTGCGTTTTTGCAAATATTT

[hHE]_M13_core_145	AAATTGTATCAAAAATAATTTTTTTTCGCACTCCAGCCGAAGGGC
[hHE]_M13_core_146	CGATGAAGTACCCCGGTTGATATAATATTT
[hHE]_M13_core_147	AAACGTATCAGAAAAGCCCCAAAGAGTCTGGAGCAAACATTAAT
[hHE]_M13_core_148	GCCGGAGCGTTCTAGCTGATAAAAGAGAAT
[hHE]_M13_core_149	AGAACGTAGGTAAAGATTCAGCCGGAGAGGGTAGCGCCTG
[hHE]_M13_core_150	CAAAAACCCTTTATTTCAACGCTGAGAAAG
[hHE]_M13_core_151	AAAGGGAAGGATAAAAATTTTTAGCATAAAGCTAAATCGGCAAG
[hHE]_M13_core_152	AATGTCCTCATATATTTTTTTCAAATGCTTTAACATAA
[hHE]_M13_core_153	ATATTCATTGATTTTTAATGCCTGAGT
[hHE]_M13_core_154	AGGTGGCCCAATAAATCATACAGGTTGTAC
[hHE]_M13_core_155	GAAGCCCGAAAGTTTTATAAAGCCTCAG
[hHE]_M13_core_156	ATTAGCAAAATTTTTATATCGCGTT
[hHE]_M13_core_157	TTAATTCTGATAAGAGGTCATTTTTTATTTTCATTTGGGCAAAGA
[hHE]_M13_core_158	TCCATATAACAGTTGATTCCCAATGATACATTTCGCAAAAGCTGAAA
[hHE]_M13_core_159	GGCGCGTGGTCAATAACCTGTTTTTCGGATGGCTTAGAGTCCTTT
[hHE]_M13_core_160	CTGAATAAACTAAAGTACGGTGTCTGGAAGT
[hHE]_M13_core_161	ACCAGACAGTACCTTTAATTGCCTTAATTG
[hHE]_M13_core_162	TCAAAAAGCAAAGCGGATTGCACAAAGCGA
[hHE]_M13_core_163	GAGCTTTCAAAAAGATTAAGAGTCAGAAAACGAGAATGCGTCCA
[hHE]_M13_core_164	AGAAGTTGTTTAGACTGGATAGACCATAAA
[hHE]_M13_core_165	AGCAAAAACCAAAATAGCGAATACTGCGGAATCGTACAGT
[hHE]_M13_core_166	GAGATTTAACGCCAAAAGGAATTTTGCAAA
[hHE]_M13_core	GAGGCTTACGAGGCATAGTAAGTACAGGTAGAAAGATTA

_167	AAAAT
[hHE]_M13_core_168	TACCTTACAGGACGTTGGGAAGCATCAGTT

Table S3.31. Edge staples of M13mp18 half hexagonal DNA origami tile.

Name	**Sequence**
[hHE]_M13_edge_1	TTTAACCTCCGGCTTATCTGAGAGACTACCTTAT
[hHE]_M13_edge_2	ACCTAAATTTAATGGTTTAATTTCATCTTCTGCG
[hHE]_M13_edge_3	AATCGGCTGTCTTTATGTAGAAACCAATCA
[hHE]_M13_edge_4	ACGACAATAAACAAAGTAATTCTGTCCAGA
[hHE]_M13_edge_5	CATCTTTTCATAATCACCTTATTAGCGTTTGCCC
[hHE]_M13_edge_6	ACCACCAGAGCCGCCGAGCCGCCACCAGAACCGT
[hHE]_M13_edge_7	GTACTCAGGAGGTTCGGAATAGGTGTATCA
[hHE]_M13_edge_8	ATTAAGAGGCTGAGATTCTGAAACATGAAA
[hHE]_M13_edge_9	GGCTCATTATACCAGTTGCGATTTTAAGAACTCA
[hHE]_M13_edge_10	ACTAATGCAGATACATAGGAATACCACATTCAAC
[hHE]_M13_edge_11	GGTCAGGATTAGAGCGGAAGCAAACTCCAA
[hHE]_M13_edge_12	TATTATAGTCAGAATCAGGTCTTTACCCTG
[hHE]_M13_edge_13	TAATCGCGCAGAGGCGAAAATACCAAGTTACAAA
[hHE]_M13_edge_14	ATAATAAAGAAATTGCGTTTGCACGTAAAACAGA
[hHE]_M13_edge_15	CTAATAGATAATACATTTATAGATTAGAGCCGTC
[hHE]_M13_edge_16	TTCTCAAATATCAAACCCCATCACCTTGCTGAAC
[hHE]_M13_edge_17	GTAGTAGCATTAACATATCAATTCTACTAA
[hHE]_M13_edge_18	ACTTTTGCGGGAGAAGATTATGACCCTGTA
[hHE]_M13_edge_19	AGCATGTCAATCATATCGGTAATCGTAAAA
[hHE]_M13_edge_20	TGTTAAATCAGCTCATATTCGCATTAAATT

Table S3.32. Core staples of p8064 square DNA origami tile.

[SQ]_p8064_core_1	AGAACGCGGCAAGCCGTTTTTATT
[SQ]_p8064_core_2	AAACCAAGTACCGCACTCATCGAGAACAA AGGCGTTTTAGCGAACCTACAATT
[SQ]_p8064_core_3	TAAGAAACAATCTTACCAACGCTAGTATTCTA
[SQ]_p8064_core_4	GAAAATACTATTTTGCACCCAGCTCCCGACTTGCGGG
[SQ]_p8064_core_5	AGGTTTTTTTTTTCCAGAC
[SQ]_p8064_core_6	TTCATCGTAGGAATCTAGAAGGCTTATCCGACGAGCG T
[SQ]_p8064_core_7	TTATCCTGGATTTTTTGTTTAACGAAGTCAGA
[SQ]_p8064_core_8	TTAGTTGGCAGCCTTTACAGAGAAGACGGGAG
[SQ]_p8064_core_9	CTAGAAACGACAAAAGGTAAATTTTTTATCAAGA
[SQ]_p8064_core_1	TTACCGAAGAGCGCTAATATCAGAAATCCAAA

0	
[SQ]_p8064_core_11	ATAGCCGTGAACACCCTGAACATCAAAAAT
[SQ]_p8064_core_12	CGCATTGAATAACCGGAAAGGCGTTA
[SQ]_p8064_core_13	CTTTCCACATATTATTTATCCCGAGATAAC
[SQ]_p8064_core_14	GGGTAATTGCCCTTTTTAAGAAAAATACATAC
[SQ]_p8064_core_15	AATTAACAACAAAGTTACCAGAATTATTACGC
[SQ]_p8064_core_16	AATAAGTTTTTCAGGGAAG
[SQ]_p8064_core_17	CAAAGACAGGCAACATATAAAAGATAGCTATC
[SQ]_p8064_core_18	GGGAGGGTAGCAAACGTAGAAAGTAAGCAG
[SQ]_p8064_core_19	TCATTAAAGCATGATTAAGACTCCGGAAACCGAGGAAACG
[SQ]_p8064_core_20	CAATAATTTTTTAGAGTC
[SQ]_p8064_core_21	CCACAAGACAATGAAATAGCAAAACGCAAA
[SQ]_p8064_core_22	ATAAAGGTAAAGGGCGACATTCAACCATCGAT
[SQ]_p8064_core_23	AGTATGTAAGGTAAATATTGACGATTAGCAAG
[SQ]_p8064_core_24	AGAACTGGGTGAATTATCACCGAGCCAGCA
[SQ]_p8064_core_25	GTTACAAAGCTTAGATTAAGTTTTTTTCCCAAA
[SQ]_p8064_core_26	TTAGCGTTCGTAATCAGTAGCGACACCAGCGC
[SQ]_p8064_core_27	ACCGGAAACGTCACCAATGAAACCGATTGA
[SQ]_p8064_core_28	CCCTCAGACAGTAGCACCATTACCGAAATTAT
[SQ]_p8064_core_29	AATTAGTCACCGTGCTTTGACAATA
[SQ]_p8064_core_30	GACACCAAAATTCATATGGTTTAGAATCAA
[SQ]_p8064_core_31	AGCAGCACTGCCATCTTTTCATAAAGACGATT
[SQ]_p8064_core_3	GCCGGAACCAGAGCCACCACCGGCGCCAGCAT

2	
[SQ]_p8064_core_33	AAATCACGCCGCCACCCTCAGAGAGCCGCC
[SQ]_p8064_core_34	ACGGATTCTTTTTCATTTGGG
[SQ]_p8064_core_35	TTTTGATGTATTCACAAACAAATACCCCCTTA
[SQ]_p8064_core_36	TTTTAACAGGTTGAGGCAGGTCTCAAAATC
[SQ]_p8064_core_37	GCCCGTATCCACCACCAGAGCCGCAACCGCCT
[SQ]_p8064_core_38	TTTTGCAAAAACTCCCTCAACCGCC
[SQ]_p8064_core_39	ACCCTCAGTTTTTCGAGAGGC
[SQ]_p8064_core_40	GTTTGCCCATTTTCGGTCATAGAATCCTCA
[SQ]_p8064_core_41	GGCCTTGAATACAGGAGTGTACTGCAAGAGAA
[SQ]_p8064_core_42	TGACAGGGGGGTCAGTGCCTTGAAACATGAAA
[SQ]_p8064_core_43	ACCAGAAAAACAGTTAATGCTTTTTTTCAACTT
[SQ]_p8064_core_44	ACTCAGGAATTAGCGGGGTTTTGCTACATGGC
[SQ]_p8064_core_45	CCGCCACGAGGCTGAGACTCCTGTAATAAG
[SQ]_p8064_core_46	GAACCTATTATTCTGAGTAACAGT
[SQ]_p8064_core_47	TTAAAGCTTCCAGTAAGCGTCATCAGTACC
[SQ]_p8064_core_48	GGATTAGGGGTTTAGTACCGCCACAACACTGA
[SQ]_p8064_core_49	GTATTAACCTCAGAACCGCCACCATAGCAAGC
[SQ]_p8064_core_50	TGAGATTTTTTTATTTCG
[SQ]_p8064_core_51	CGTTAGTAACCAGTACAAACTACAATCACCGT
[SQ]_p8064_core_52	GCTAAACGAACCCATGTACCGTCCTCAGAA
[SQ]_p8064_core_53	CGGTCACTTAGCTCAGGGCTCAGAGC
[SQ]_p8064_core_5	CACCACTTTTTGGCGCAGA

4	
[SQ]_p8064_core_55	AGGCGGAGCCCGGAATAGGTGTACGCCTGT
[SQ]_p8064_core_56	GTTTCGTCAATGAATTTTCTGTATAAGGAATT
[SQ]_p8064_core_57	CCAATAGAACTTTCAACAGTTTTTTTTCATTAAA
[SQ]_p8064_core_58	AATTTCTTTAATTTTTTCACGTTGTTTCCAGA
[SQ]_p8064_core_59	AGAAAGGAACAACTAGGGATTTT
[SQ]_p8064_core_60	AGCATTCTAAAGTTTTGTCGTCAAAATCTC
[SQ]_p8064_core_61	GCGAATAAAAACAGCTTGATACCGATAGTTGCGCCGA
[SQ]_p8064_core_62	TTTCATTTTTTTTGAGAAT
[SQ]_p8064_core_63	CAAAAAATTTATCAGCTTGCTTTCGAGGTG
[SQ]_p8064_core_64	GGTAGCAATATTCGGTCGCTGAGG
[SQ]_p8064_core_65	CAACAACCATCGCCCACGCATAACCGAT ACGGCTACAGAGGCTTTTACGAAGG
[SQ]_p8064_core_66	GATTTGTATAAAACGAAAGAGGCAGGAACGAG
[SQ]_p8064_core_67	AATCCGCAATACGTAATGCCACGAGGACTAAAGACTT
[SQ]_p8064_core_68	CTTGCAGGGAGTTAAGCGAAAGACAGCATCAAAGAA TA
[SQ]_p8064_core_69	CACCAACCTCATCGCCTGATAAATAAGAGGAC
[SQ]_p8064_core_70	CGGGTAAGACCTGCTCCATGTTAATCATAAGG
[SQ]_p8064_core_71	AACAAAGCGGTGTACAGACCAGGCACAACGGA
[SQ]_p8064_core_72	CCCTGACACTGACCAACTTTGATGTGTCGA
[SQ]_p8064_core_73	CACTAAAAGCGCGAAACAAAGTGCATAGGC
[SQ]_p8064_core_74	AGATGAACTGCTCATTCAGTGAATAGGACGTT
[SQ]_p8064_core_75	GAACCGAGAGAAACACCAGAACGCGATTTTAA
[SQ]_p8064_core_7	AACTAATGAAATCTACGTTAATAAATCAACGT

6	
[SQ]_p8064_core_77	TACGAGGCTCATTATACCAGTCAAGGCTTG
[SQ]_p8064_core_78	ACCCTCGTTGTGAATTACCTTATGAGTAGTAAATTGGGCT
[SQ]_p8064_core_79	TGGCTGAATATTCATTACCCAAAACGAACT
[SQ]_p8064_core_80	GGGAAGAACAGATACATAACGCCACGGAATCG
[SQ]_p8064_core_81	GAACTGGCATAGTAAGAGCAACAAAATGTTTA
[SQ]_p8064_core_82	TAATCATTTACCAGACGACGATAAAAGAAG
[SQ]_p8064_core_83	TATAGTCAATTCATTGAATCCCCCCCACATTC
[SQ]_p8064_core_84	AGATTAATAGCGTCCAATACTGAAAGGAAT
[SQ]_p8064_core_85	ATCGCGTTAGAGGGGGTAATAGTACTATCATA
[SQ]_p8064_core_86	AACGGAATGAGATTTAGGAATATCAAATGC
[SQ]_p8064_core_87	TCATAAATGAAGCAAAGCGGATTGGGCTTAGA
[SQ]_p8064_core_88	GACTGGAGAGGAAGCCCGAAAGACTCCTTTTG
[SQ]_p8064_core_89	TTTTGCCTTAATTCGAGCTTCAACAGGTCA
[SQ]_p8064_core_90	TCCCAATTGCTGAATATAATGCTGCTGACTAT
[SQ]_p8064_core_91	ACCATTAGTCATTTTTGCGGATCATCAAAA
[SQ]_p8064_core_92	ACCTGTTTAGAGTACCTTTAATTGCTTCAAAT
[SQ]_p8064_core_93	CAGCTTCGGTGGTACTCCAAAGCGA
[SQ]_p8064_core_94	ACCAGACCTTTTTCACGCAAC
[SQ]_p8064_core_95	TTTAAACAATCAGGTCTTTACCTAGCTCAA
[SQ]_p8064_core_96	GCTTAATTCTGCGAACGAGTAGATTAAATCAT
[SQ]_p8064_core_97	ATAAGAGGATACATTTCGCAAATTTCTACTAA
[SQ]_p8064_core_9	GGATTAGAGCTATATTTTCATTTTTTTTGGGCG

8	
[SQ]_p8064_core_99	TTTTGCGGGGCAAAGAATTAGCAACAGTTGAT
[SQ]_p8064_core_100	GATAAAAAGCATTAACATCCAATTAGTTTG
[SQ]_p8064_core_101	GAAAAGGTGGCATCAAGGTCAATA
[SQ]_p8064_core_102	CATGTTTTTTCATTCCATATAAAATTAAGC
[SQ]_p8064_core_103	ACAGGCAAGAGAAGCCTTTATTTCGCCGGAGA
[SQ]_p8064_core_104	TAGTAGTATTTTTAGAACCCTCAGTGTAGGTA
[SQ]_p8064_core_105	ATTTGCTTTTTTCGAGCT
[SQ]_p8064_core_106	CAGGTCATTCACCATCAATATGATTGTAATAC
[SQ]_p8064_core_107	GAGAATCAAAAGGGTGAGAAAGAACGCAAG
[SQ]_p8064_core_108	ACGACGTAACGCAGTAATTATATTTT
[SQ]_p8064_core_109	AAATGCTTTTTTCCCAGTC
[SQ]_p8064_core_110	AATAAAGAAAACATTATGACCCATTCAACC
[SQ]_p8064_core_111	CAGTCAAATGCCTGAGAGTCTGGAGGTTGATA
[SQ]_p8064_core_112	AAGATTCGATGAACGGTAATCTTTTTTCAGTATC
[SQ]_p8064_core_113	AATCAGCTAGCCCCAAAAACAGGAAAGGCTAT
[SQ]_p8064_core_114	AATCATATGTACCCCGCAAACAA
[SQ]_p8064_core_115	GTTCTAGTTTGAGAGATCTACAAGATTGTA
[SQ]_p8064_core_116	ATCAGAAACATTTTTTAACCAATAGGAACGCCATCAA
[SQ]_p8064_core_117	GTTTGATTTTTTTCATGTC
[SQ]_p8064_core_118	TAAGCAAAAATTCGCATTAAATTTTTGTTA
[SQ]_p8064_core_119	GTTGGTGTTCATCAACATTAAATG
[SQ]_p8064_core_1	TTCGCGTCTGGCCTTCCTGTAGCCAGC

20	TTAGATGGGCGCATCGTAAGCCAGCT
[SQ]_p8064_core_121	TCGCTATTCCGCTTCTGGTGCCGGTAGGTCAC
[SQ]_p8064_core_122	TGCTGCAGGAAGATCGCACTCCACCGTGCATCTGCCA
[SQ]_p8064_core_123	TGAGCGAGTAACAACTTGACCGTAATGGGAAAACCAGG
[SQ]_p8064_core_124	TTCCGGCAACGCCAGCTGGCGAAAGAGGTGGA
[SQ]_p8064_core_125	GGCCTCAAGGCGATTAAGTTGGGTTGTAAAAC
[SQ]_p8064_core_126	TCCGTGGTGGGAACGGATAACCTCGGGCCTCT
[SQ]_p8064_core_127	GAGACGCAGTGCCAAGCTTTCAGGGGGATG
[SQ]_p8064_core_128	CAAAGCGAAGGGCGATCGGTGCACCGGAAA
[SQ]_p8064_core_129	GCCGCCACGAAGGGATAGCTCTCATAGTGATG
[SQ]_p8064_core_130	GACGGCCAGAAACAGCGGATCAAATCCCGTAA
[SQ]_p8064_core_131	ATAACGGAAGTTAAACGATGCTGAAGACTTTC
[SQ]_p8064_core_132	GCGTGGTCGCACAGGCGGCCTTCGGAAAAA
[SQ]_p8064_core_133	AAGAATGCACATCGACATAAAAAAACTTAAATTTCTGCTC
[SQ]_p8064_core_134	CAATCGGGAATTTGTGAGAGATTTGCCGTT
[SQ]_p8064_core_135	AAGGGTAAACGTGCCGGACTTGTAGCGCGGTT
[SQ]_p8064_core_136	AAAAAGCGCTGGTCTGGTCAGCAATTGCAGGC
[SQ]_p8064_core_137	GTTGTGTCAACGGCAGCACCGTACGGCTGG
[SQ]_p8064_core_138	AATCGTTAAGCCGGGTCACTGTTGACATCCTC
[SQ]_p8064_core_139	GCAGCCACACTCAATCCGCCGGGAACGTCA
[SQ]_p8064_core_140	GACGATCCCAGCATCAGCGGGGTCGCAACCGC
[SQ]_p8064_core_141	CCGGCAAGCCTCCGGCCAGAGCCCCTGCGG
[SQ]_p8064_core_1	GCGGTATGACGGCATCAGATGCCGTCTTCGCG

42	
[SQ]_p8064_core_143	GCTTTCGGCGGTGCCGGTGCCCCACCGGGGGT
[SQ]_p8064_core_144	AGGTGTCAGCGCAGTGTCACTGCCAGAATG
[SQ]_p8064_core_145	TCACAATTCCTCCTCACAGTTGAGGTTCAGCA
[SQ]_p8064_core_146	ATAAAGTAGCACGCGTGCCTGTGGTTACCT
[SQ]_p8064_core_147	TGAGCTAACCGTTTTCACGGTCATCTGCATCA
[SQ]_p8064_core_148	TTGAGTGAACGTTCTGCGGCGCGCC
[SQ]_p8064_core_149	TGTGCACTTTTTTTTAAAAGT
[SQ]_p8064_core_150	CTGGTAACCCTTACACTGGTGTGATCCCCG
[SQ]_p8064_core_151	TCCGTGAGCCACACAACATACGAGGGCCAACG
[SQ]_p8064_core_152	TTCTGCCGTAAAGCCTGGGGTGCAAACCTGTC
[SQ]_p8064_core_153	CGGCGGGCTCACATTAATTGTTTTTTTACGCTG
[SQ]_p8064_core_154	CTGAGAGAGAGGCGGTTTGCGTATTTATCCGC
[SQ]_p8064_core_155	TTTGCCCCTGCATTAATGAATCCCGGAAGC
[SQ]_p8064_core_156	CCGCTTTCCAGTCGGGCTAATGAG
[SQ]_p8064_core_157	GGTACCGTCCTGTGTGAAATTGTGGGCGCC
[SQ]_p8064_core_158	CGCGGGGAGTTGCAGCAAGCGGTCATAGGGTT
[SQ]_p8064_core_159	GTGCCAGCAGCAGGCGAAAATCCAATCCCTTA
[SQ]_p8064_core_160	CGCCTGTTTTTTCACTGC
[SQ]_p8064_core_161	CTACGTGATTCCAGTTTGGAACAAGCCTGGCC
[SQ]_p8064_core_162	GGGGTCGAAAGAATAGCCCGAGCACGCTGG
[SQ]_p8064_core_163	TCACACTTTACACGGCAATGTTTGAT
[SQ]_p8064_core_1	GGTGGTTTTTTTTCACCAG

64	
[SQ]_p8064_core_165	AGGGTGGTGATTGCCCTTCACCGAGTCCAC
[SQ]_p8064_core_166	GAGTGTTGACCATCACCCAAATCATTTAGAGC
[SQ]_p8064_core_167	TAAATCAAGGTGCCGTAAAGCTTTTTTTCACGCA
[SQ]_p8064_core_168	CGCGTAACGAAAGCCGGCGAACGTATGGCCCA
[SQ]_p8064_core_169	AAAGGGAGCCCCCGAAGTTTTTT
[SQ]_p8064_core_170	TATTAAACCGTCTATCAGGGCGGGCGAGAA
[SQ]_p8064_core_171	TTGACGGGCACCACACCCGCCGCGCTTAATGCGCCGC
[SQ]_p8064_core_172	GTAAAATTTTTTTAACCCT
[SQ]_p8064_core_173	AGGAAGGTGGCAAGTGTAGCGGTCACGCTG
[SQ]_p8064_core_174	AATCCTGAGTATAACGTGCTTTCC
[SQ]_p8064_core_175	GCGCGTACTATGGTTGCTTTGACGA GCACGAAGTGTTTTTATAATTCTTTGAT
[SQ]_p8064_core_176	AAAAACGCACATCACTTGCCTGAGTACGCCAG
[SQ]_p8064_core_177	GCTCAATCGTTGTAGCAATACTCAGTGAGGCCACCGA
[SQ]_p8064_core_178	TCGTTAGAATCAGAGTTTAGACAGGAACGGTAGAAGAA
[SQ]_p8064_core_179	TAGTAATATCATGGAAATACCTACAGAGATAG
[SQ]_p8064_core_180	AATTAACCGTCTGAAATGGATTAGACCAGTAA
[SQ]_p8064_core_181	ATCGCCATTGACCTGAAAGCGTAAGCAACAGG
[SQ]_p8064_core_182	CAGAAGAGACATTCTGGCCAACATTTTGAC
[SQ]_p8064_core_183	CTCAAACTTACCGCCAGCCATTGAATACGT
[SQ]_p8064_core_184	AACCCTTCTAAAAATACCGAACGACAAACCCT
[SQ]_p8064_core_185	TAAAAGGTAAAACAGAGGTGAGGCTAAAGCAT
[SQ]_p8064_core_1	AGAGCCGTATCTGGTCAGTTGGCACCTAAAAC

86	
[SQ]_p8064_core_187	TAGAAGTCTGAACCTCAAATATACCACCAG
[SQ]_p8064_core_188	AACTCGTAGCAGCAAATGAAAAATCGGTCAGTATTAACAC
[SQ]_p8064_core_189	GGCACAGGCGCGAACTGATAGCAATCAACA
[SQ]_p8064_core_190	CAATCAATCAATAGATAATACATTGATTATCA
[SQ]_p8064_core_191	CACCTTGATTAGACTTTACAAACCCAGAAGGA
[SQ]_p8064_core_192	AGAGCCATTAAATCCTTTGCCCAACATTAT

Table S3.33. Core staples of M13mp18 prismatic pentagonal DNA origami tile.

Name	**Sequence**
[PT-prism]_M13_core_1	ACTGAACACCCTGAACAAAGTCAGAGGGCAA GAATTGAGTTAATAAGAAAA
[PT-prism]_M13_core_2	ACCCAAAATTACCGAAGCCCTTTTGCCCAATA
[PT-prism]_M13_core_3	ATAAGAGCAAGAATTTTTTTGATTTTTTGTTTA
[PT-prism]_M13_core_4	GTAAGCAAGGAAACGCAATAATATATAAAA
[PT-prism]_M13_core_5	TATTTTGCTATCCCAATCCAATTTTTTTAGCAA TAGCTATCGAACTGGC
[PT-prism]_M13_core_6	TTACCAGCACATAAAGGTGGCAACAACGGAAT
[PT-prism]_M13_core_7	ATGATTAAAACGTAGAAAATACATGCCAAAG ACAAAAGGGGGTGAATT
[PT-prism]_M13_core_8	TTAGCAGACTCTTCAAGAGGAGG
[PT-prism]_M13_core_9	GAAACGCAATCAATAGAAAATTTTGGGAAT
[PT-prism]_M13_core_10	TTTTGAAGTTTTCAGTATG
[PT-prism]_M13_core_11	AAACCATCCACCGACTTGAGCCATCATATGGT
[PT-prism]_M13_core_12	GACAGAAAAATTATTCATTAAACGACATTC
[PT-prism]_M13_core_13	AACCGATTGAGGTTTTTTTAGTACCGCACTC ATCGAGAAGTCTTTCC
[PT-prism]_M13_core_14	TAGAGCCCAAGGCCGGAAACGTCAGAGCCA
[PT-prism]_M13_core_15	ATCACCGTGATAGCAGCACCGTAATGCCATCT
[PT-prism]_M13_core_16	GACGGTCAAGTTTGCCTTTAGCATTTTCG
[PT-prism]_M13_core_17	TAAAGTAATCCAAGAACGGGTTTTTTTTTAAATATT
[PT-prism]_M13_core_18	CTCAGAGCTCAAAATCACCGGAACCACCAATG
[PT-prism]_M13_core_19	CGCCGCCCCCCTTATTAGCGTTTCAGTAGC
[PT-prism]_M13_core_20	ATCGGCGTCATTTTACCGCCAGT
[PT-prism]_M13_core_21	CCACCGGCCGCCACCCTCAGAGACAGGAGT
[PT-	TTTCATAACGCCACCAGAACCACCTCCAGTAA

prism]_M13_core_22	
[PT-prism]_M13_core_23	GTCATAGCAGCATTGACAGGAGGTGAATGGAA
[PT-prism]_M13_core_24	AATAAGAGTTTTGCGTTTTC
[PT-prism]_M13_core_25	ATGCCCCCCATGGCTTTTGATGATCCACCACC
[PT-prism]_M13_core_26	TGAAACACTCTGAATTTACCGTACCAGAGC
[PT-prism]_M13_core_27	GGCGGATACTGAGACTCCTCAAGAATCCTCATT AAAGCCATGAGGCAG
[PT-prism]_M13_core_28	GTCAGACGATTGGTTTTTTTTTAATGGTTTGAA
[PT-prism]_M13_core_29	GTACTGGAACAGTGCCCGTATATTTAGTAC
[PT-prism]_M13_core_30	GCGTCATATGCCTATTTCGGAACCCCCGGAAT
[PT-prism]_M13_core_31	AGCGCAGTTGAAAGTATTAAGAGGAGTGCCGT
[PT-prism]_M13_core_32	TCATCTTCTTTTTTTCACAAACAAATAAGAAGGA TTAGGATTTTTTTTGAAGCAAA
[PT-prism]_M13_core_33	CAAAATCGCTTAGGTTGGGTTAGTTTAGTA
[PT-prism]_M13_core_34	AGAATCGCTTACTAGAAAAAGCCTTATAACTA
[PT-prism]_M13_core_35	TATGTAAAGAGAAGAGTCAATAGTACATTTAA
[PT-prism]_M13_core_36	AAGACGCTTGCTGATGCAAATCCAAACACCGG
[PT-prism]_M13_core_37	ATTTAGGCGTTAAATAAGAATAATCGCAAG
[PT-prism]_M13_core_38	ACAAAGAAAAACATAGCGATAGTAATGGAA
[PT-prism]_M13_core_39	AATCCTTGACGCGAGAAAACTTTTCGTGTGAT
[PT-prism]_M13_core_40	ATACCGACTCAAATATATTTTAGTCGCTATTAAT
[PT-prism]_M13_core_41	ACTTGCACCCTTCTGACCTGAAAGTTTAAATCGTTAA TT
[PT-prism]_M13_core_42	TCATATGCGCTCAACAGTAGGGCGCGCCTG
[PT-prism]_M13_core_43	AATCATAACATATTTAACAACGCCGACAATAA
[PT-prism]_M13_core_44	AAATAAGGCAGAGGCATTTTCGAGACAAAAGG

[PT-prism]_M13_core_45	GTAGAAACTTCAGCTAATGCAGAACTTAATTG
[PT-prism]_M13_core_46	TTATCATTTCTGTCCAGACGACAACATGTA
[PT-prism]_M13_core_47	TTTATCAATCCCATCCTAATTTTCATTACC
[PT-prism]_M13_core_48	ACAACATGCAATCAATAATCGGCTCAAGCAAG
[PT-prism]_M13_core_49	TTTTAGCGATTTTCATCGTAGGAAACGAGCAT
[PT-prism]_M13_core_50	GCGCCCACGGTATTCTAAGAACATCCTGAA
[PT-prism]_M13_core_51	CCGTTTTTAACCTCCCGACTTGCGTTAGTTGC
[PT-prism]_M13_core_52	ACGTCAAAAAACAGCCATATTATTACCCA GCTACAATTTTGCGAGGCG
[PT-prism]_M13_core_53	TCTTACCTGCCAGTTACAAAATAATGAAAA
[PT-prism]_M13_core_54	TAGCAGCATAAAAACAGGGAAGCGCATTAGACGGG
[PT-prism]_M13_core_55	ACGGTAATCGTAAAACTAGAGAAAAGCCCCAAAAC ATTAAAT
[PT-prism]_M13_core_56	CCTTCCTGATTTTGTTAAAATTCGACAGGAA
[PT-prism]_M13_core_57	GATTGTATAATTAGCTATTTTTGAGAGATGATATTC
[PT-prism]_M13_core_58	TTTTGTTCATCAAAAATAATTCGTGTAGAT
[PT-prism]_M13_core_59	TTAATTAGCCAGCTTTCATCAGCGGATTG
[PT-prism]_M13_core_60	ATATTTTATAGCTGATAAATTAATTTTTATTGTAAACG
[PT-prism]_M13_core_61	GATCGCACGGGATAGGTCACGTTGGCGTCTGG
[PT-prism]_M13_core_62	TCTGGTGCCGTGGGAACAAACGACATT
[PT-prism]_M13_core_63	AAATGTGATTTTTTTTAAAAATTTTTAGAATACTTTT
[PT-prism]_M13_core_64	GGGCGCAGACGACAGTATCGGCTTGGGTAA
[PT-prism]_M13_core_65	ACCGTAATTCCAGCCAGCTTTCCGGCGAAAGG
[PT-prism]_M13_core_66	ATTCTCCGGAAACCAGGCAAAGGTGCGGG
[PT-	AGCTGAAAAAGCCTTTATTTTTTTTTTTTCCGTCGG

prism]_M13_core_67	
[PT-prism]_M13_core_68	CAGGTCGACTGCAAGGCGATTAAGCTCAGGAA
[PT-prism]_M13_core_69	GCTCGAACTATTACGCCAGCTGGCACCGCT
[PT-prism]_M13_core_70	CGATCGCGCCATTCTTTTTTTTTTTCATTTATACAT
[PT-prism]_M13_core_71	CGCCAGGCCAGTGCCAAGCTTGAATTGCGT
[PT-prism]_M13_core_72	GGGATGTGCTCTAGAGGATCCCCGTGGGGTGC
[PT-prism]_M13_core_73	CCTCTTCGTTCGTAATCATGGTCACATACGAG
[PT-prism]_M13_core_74	CTCCAGTCAATATTTCGCAACTGTTGGGAAGGGGTTTCC
[PT-prism]_M13_core_75	AATGCTGTACGGTGTCTGGAAGTCATACAG
[PT-prism]_M13_core_76	TACCAAAAATTAACATCCAATAAATTTCATTC
[PT-prism]_M13_core_77	CATATAACGCTTAGAGCTTAATTGAGAAGCAA
[PT-prism]_M13_core_78	TGCGGATGAGTTGATTCCCAATTCTACTAATA
[PT-prism]_M13_core_79	GCGGGAGAGGTGGCATCAATTCTGCGAACG
[PT-prism]_M13_core_80	AGTAGATTCCTTTTGATAAGAGGAGGAAGC
[PT-prism]_M13_core_81	TTAATTGCTTAGTTTGACCATTAGGGGGCGCG
[PT-prism]_M13_core_82	TTCGCAAATGACAGGTCAGGATTAGATTTAATTC
[PT-prism]_M13_core_83	GCAAGGCAGAGCATAAAGCTAAAATGTGTA
[PT-prism]_M13_core_84	GTAGTAGCACATTATGACCCTGTAACCCTCAT
[PT-prism]_M13_core_85	AACCGTTCAATGCAATGCCTGAGTATCGGTTG
[PT-prism]_M13_core_86	GGTAAAGAAATCACCATCAATATCTACAAA
[PT-prism]_M13_core_87	GGCTATCCTGGAGCAAACAAGAGAAT
[PT-prism]_M13_core_88	GGGATAGCCACCGTACTCAGGAGGAACAGTTA
[PT-prism]_M13_core_89	CGCCACCCAGAGCCACCACCCTATGAATTT

[PT-prism]_M13_core_90	AGGTGTATAAGCCCAATAGGAACCTAAAGTTT
[PT-prism]_M13_core_91	AGCGAAAGATGCCACTACGAATTTTTTTCTT TGAAAGAGGATAACAAAG
[PT-prism]_M13_core_92	CGGCTACGGAAGTTTCCATTAAAATACACT
[PT-prism]_M13_core_93	CATAAGGGAACCGTTTTTTTCTAAAACGAAAGA
[PT-prism]_M13_core_94	AAAACACCGAAACAAAGTACAACGGAGATTTGTAT
[PT-prism]_M13_core_95	TGATAAATTGTGTCGAAATCCGCGACCTGGA ACGAGGCGCAGAAGACCAGG
[PT-prism]_M13_core_96	AATCAACGCAGATGAACGGTGTACCGGTCAAT
[PT-prism]_M13_core_97	CGCATAGAAGAACCGGATATTCGATGGTTT
[PT-prism]_M13_core_98	GTCAGGACAGTAAATTGGGCTTGAATTACCCA
[PT-prism]_M13_core_99	CTGCTCATAAACACCAGAACGAGTGTTGG GAAGAAAAATCTTGAGATT
[PT-prism]_M13_core_100	TGCCAGAGATAGCGTCCAATACTGACTTC AAATATCGCGTGAGTACCT
[PT-prism]_M13_core_101	TAGGAATAAAAAACCAAAATAGCGTATTCATT
[PT-prism]_M13_core_102	GAATCCCCGCATCAAAAAGATTAAGTCATTTT
[PT-prism]_M13_core_103	AAACGAGCTGACTATTATAGTCCTGAATAT
[PT-prism]_M13_core_104	AGCGGATTCTCAAATGCTTTAAACTTTACCAG
[PT-prism]_M13_core_105	TAACGCCCTATCATAACCCTCGAGTTCAGA
[PT-prism]_M13_core_106	CCGAAAGCGGAATCGTCATAAAAGAGGCTT
[PT-prism]_M13_core_107	GAGCTTCAAAGCGTTTTTTTTTGCTCAGTACCA
[PT-prism]_M13_core_108	ACGACGATCCACATTCAACTAATGTTATACCA
[PT-prism]_M13_core_109	AATTTCATTAAGAACTGGCTCACAGATACA
[PT-prism]_M13_core_110	TTGCAAAAGAAAGATTCATCAGTACGTTAA
[PT-prism]_M13_core_111	TAAAACGAACTATTTTTTTAAAGGAGCC TTTAATTGTATTTTTTTCA
[PT-	TGTCGTCTGAATTGCGAATAATAACGGTTTAT

prism]_M13_core_112	
[PT-prism]_M13_core_113	AACTAAAGTTCCAGACGTTAGTAACATTTTCA
[PT-prism]_M13_core_114	GTAACACTTGATATAAGTATAGTATTATTC
[PT-prism]_M13_core_115	CGAGAGGGTGAGTTTCGTCACCAGACAGACAG
[PT-prism]_M13_core_116	CAACGCGCTGAGCTAACTCACATTCATGCCTG
[PT-prism]_M13_core_117	GCGCCAGATAAAGTGTAAAGCCGGTACCGA
[PT-prism]_M13_core_118	CTGAGTTGTAGCAATTTTTTTTCCACACAATAGCT
[PT-prism]_M13_core_119	GGAACAATCAAAGGGCGAAAAACCGT
[PT-prism]_M13_core_120	GGGCGATGGCCCACTACGTGAGGTGCCG TAAAGCCGTGGCGA
[PT-prism]_M13_core_121	CTGCGCGTGGGGAAAGCCGGCGAAACTAAAT
[PT-prism]_M13_core_122	CGGAACCCTATATAGGGTTGAGTGTTGTCGAAATCG
[PT-prism]_M13_core_123	CTTCACCGCCTTATAAATCAAAATTTTTGATTTAGAG C
[PT-prism]_M13_core_124	TTGACAACCACCACACCCGCCTATAACGT
[PT-prism]_M13_core_125	GAAAGGACGCTGGCAAGTGTAGGGAGCTAA
[PT-prism]_M13_core_126	TTATAATCCGTTAGAATCAGAGCGCGGTCACG
[PT-prism]_M13_core_127	CGAGCACGGCGCTTAATGCGCTTTTTTTTG ACGGGCAACAGCCGTATTGG
[PT-prism]_M13_core_128	AAGGGACATCGGCCTTGCTGGTAAAAGA GTCTGTCCAGCTTTGA
[PT-prism]_M13_core_129	CCGGAAGCGGTGGTTTTTCTTTTTTTTTTC GTACTATGGTTTCACGCAA
[PT-prism]_M13_core_130	ATTAACCGTAGAAGAACTCAAACTATTCTG GCCAACAGAGTATTTTTG
[PT-prism]_M13_core_131	AAAACGCGTCTGAAATGGATTAAATACCGA
[PT-prism]_M13_core_132	ACAGGAGCGCCAGAATCCTGAGCAACAGGA
[PT-prism]_M13_core_133	GGCAGATTTTACCGCCAGCCATTGAAGTGTTT
[PT-prism]_M13_core_134	GAACAATACACCAGTCACACGACCCGAACTGA

[PT-prism]_M13_core_135	GCTTTCCTAGTGAGGCCACCGAGTAATATCCA
[PT-prism]_M13_core_136	TGTGTGAAATTGTTTAGTAATAACATC
[PT-prism]_M13_core_137	CTAATGAGGGGGAGAGGCGGTTTGTGATTGCC
[PT-prism]_M13_core_138	TGCGCTCGCCAGCTGCATTAATTTGCAGCA
[PT-prism]_M13_core_139	GCAAAATCCCTGGCCCTGAGAGAGGAATCGGC
[PT-prism]_M13_core_140	AGCGGTCGTTTGATGGTGGTTCTCCAGTTT
[PT-prism]_M13_core_141	GTGCCACGAAACATCGCCATTAAATTTACATT
[PT-prism]_M13_core_142	ATCTAAATTAGTCTTTAATGCGAGTAATAA
[PT-prism]_M13_core_143	AATTTGAGTGAATATTTTTTTCACAGACAAATAGA
[PT-prism]_M13_core_144	TTAAATCGAGTAACATTATCATTTTG
[PT-prism]_M13_core_145	AAAGAAACCACCAGAAGGATGATTATCA GATGATGAACCTAC
[PT-prism]_M13_core_146	CGTCAGATAATAATGGAAGGGTTAGGCAATT
[PT-prism]_M13_core_147	CATCAATATATTTTACAAACAATTCGACGCCGTCAA
[PT-prism]_M13_core_148	TGGTCAGTACATTTGAGGATTTATTTTTTGGATTATAC
[PT-prism]_M13_core_149	TTCTGGAATATACAGTAACAGCCAAGTTA
[PT-prism]_M13_core_150	CATATCAATTGCGTAGATTTTCTCATTTCA
[PT-prism]_M13_core_151	CAATTTCACGCAGAGGCGAATTATAGGTTTAA
[PT-prism]_M13_core_152	TTTGAATATACCTTTTACATCTTTTTTTTA TCAAACCCTCAAAATGAAAA
[PT-prism]_M13_core_153	AGCGATAGTAATGGAAACAGTACTGATTGC
[PT-prism]_M13_core_154	AATGGCTAGCATCACCTTGCTTTTTTT TTAACGGATTCGCCATAAATCA
[PT-prism]_M13_core_155	ATTACCTAAAACAAAATTAATTGAATTTAT
[PT-prism]_M13_core_156	CAAAATCGTTTGAATTACCTTTTTCTTAGATT
[PT-	TAGCCCTACTGAGAGCCAGCAGCATCAATATC

prism]_M13_core_157	
[PT-prism]_M13_core_158	ACGAACCCAGTATTAACACCGCGAAAGGAA
[PT-prism]_M13_core_159	TAGATAATTGGCAAATCAACAGTTCTGCAACA
[PT-prism]_M13_core_160	TTGAGGAAACTAATAGATTAGAAACTCGTA
[PT-prism]_M13_core_161	TCGTCATAAAGGCCGCTTTTTTTTTGCCCTGACGAGTCAGTT
[PT-prism]_M13_core_162	TATTCCTACAAACTACAACTTTTATGTTTAGACTGGGGGGTT
[PT-prism]_M13_core_163	TTACCGCCAGTAATAAGAGTTTTGCGTTTTCATCGGCGTCAT
[PT-prism]_M13_core_164	TCAAGAGGAGGTTTTGAAGTTTTCAGTATGTTAGCAGACTCT

Table S3.34. Core staples of M13mp18 Cairo pentagonal DNA origami tile.

Name	**Sequence**
[PT-Cairo]_M13_core_1	AAACAAATAAATCCTCATTTACCGTTCCAGTAAGGCCTTGA
[PT-Cairo]_M13_core_2	ATGAAAGTTTTTAACGGGGTCAGTCGTCATAC
[PT-Cairo]_M13_core_3	ATGGCTTTTGTTCCCTCAGAGCCGCCACCACTCAGAGC
[PT-Cairo]_M13_core_4	GTAACAGTTTCGGAACCTATTATCCCGGAA
[PT-Cairo]_M13_core_5	TTTTCGGTTCAGAACCGCCACCCTTTTTTTGTACTGGTAATAAGATTAAGAG
[PT-Cairo]_M13_core_6	CGCCACCCGTTGATATAAGTATAGTCTGAAAC
[PT-Cairo]_M13_core_7	GCTGAGACAAGTGCCGTCGAGAGGTCAGAGCC
[PT-Cairo]_M13_core_8	AGGCGGATTCCTCAAGAGAAGTTTTTTTTTTGTAGCGCGTTTTTCAGTAGC
[PT-Cairo]_M13_core_9	TAGGTGTACTCAGAACCGCCACCCCAGACG
[PT-Cairo]_M13_core_10	CCTCATAGCATTTTCAGGGATAGCTCAGTACC
[PT-Cairo]_M13_core_11	TATTGACGCAAGTTTGCCTTTTTTTTTGGGGTTTTGCAAGCCCAA
[PT-Cairo]_M13_core_12	GAATAGAAAAGTTTTGTCGTCTTTCTCAGAAC
[PT-Cairo]_M13_core_13	ACCACCCTTTAGCGTAACGATCTAAGGAACAA

[PT-Cairo]_M13_core_14	TAGGAACGCCTGTAGCATTCCATTTTCACGT
[PT-Cairo]_M13_core_15	ACTACAACCCATGTACCTTTTTTAGGGAGGGAAGCG CCAAAGACAAAAACAAAGTT
[PT-Cairo]_M13_core_16	TTAGTAAATTTCAACAGTTTCAGCGCCCAC
[PT-Cairo]_M13_core_17	GCTTGATAATTGCGAATAATAATTCAGACAGC
[PT-Cairo]_M13_core_18	CAGCTTGCTCTCCAAAAAAAAGGCCAGTACAA
[PT-Cairo]_M13_core_19	CGGAATTTAGCCGAGGGCGATTCGTCACTCCAAAAG G AGCTTTTTTTTAAGCCT
[PT-Cairo]_M13_core_20	GTATGTTAAACATATAAAAGAAATTGGGAA
[PT-Cairo]_M13_core_21	AAACCATCCACCGACTTGAGCCATCGCAAAGA
[PT-Cairo]_M13_core_22	CACCACGGTGATTAAGACTCCTTATGAGTTAA
[PT-Cairo]_M13_core_23	AAGAAACACCCAAAAGAACTGGCAAATAAGTTTATT T TGTGGTGAATT
[PT-Cairo]_M13_core_24	GACAGAATGAAATTATTCATTAAACACAATCAATAGA AAACAATAATA
[PT-Cairo]_M13_core_25	CGAAGCCGAAACCGAGGAAACGTTCATATGGTTTAC CA GGTAAA
[PT-Cairo]_M13_core_26	TTAGAGCCCAAGGCCGGAAACGTGCGTTTG
[PT-Cairo]_M13_core_27	ATCACCGTGATAGCAGCACCGTAACATCGGCA
[PT-Cairo]_M13_core_28	CGCCACCCCATAGCCCCCTTATTACACCAATG
[PT-Cairo]_M13_core_29	CCATCTTTACCGGAACCGCCTCCGAACCAC
[PT-Cairo]_M13_core_30	CACCAGAGGTCAGACGATTGGCCTTGA
[PT-Cairo]_M13_core_31	AATACCACATTCAACTAATGCAGATAAGAGCAACACT ATCAAAAAGAAG
[PT-Cairo]_M13_core_32	TCATAAATAGCGAGAGGCTTTTGCTAACCCTC
[PT-Cairo]_M13_core_33	GTTTACCAGACTTTTTTTTATACCAGTCAGGACGTT TGAATTAC
[PT-Cairo]_M13_core_34	TTTTGCCTAGCGTCCAATACTGTACCCTGA

[PT-Cairo]_M13_core_35	CAGTGAATATTTAAGAACTTTTTTTTAAAACCAAAATATTCATTG
[PT-Cairo]_M13_core_36	CAAATATCTCAAAAATCAGGTCTTCGGAATCG
[PT-Cairo]_M13_core_37	AATCCCCCTCATTTTTTTTAGCTGCTCATT
[PT-Cairo]_M13_core_38	CTATTATTTAAGAGGAAGCCCGTTGCGGAT
[PT-Cairo]_M13_core_39	ACCATAAAGCGTTTTAATTCGAGCCTTTAATT
[PT-Cairo]_M13_core_40	CGGATATTCATTACCCAAATTTAGTTCAGAAAACGAGAATG
[PT-Cairo]_M13_core_41	AGTACGGTTGATAAGAGGTCATTTAAAGACTT
[PT-Cairo]_M13_core_42	CAGTTGATCAGGATTAGAGAGTACTTCAAAGC
[PT-Cairo]_M13_core_43	GAACCAGACCGTTTTTTTTACTTAGCCGG
[PT-Cairo]_M13_core_44	GGCTTAGACATGTTTTAAATATTGGCATCA
[PT-Cairo]_M13_core_45	GCTCCTTTGTCTGGAAGTTTCATTTATATTTT
[PT-Cairo]_M13_core_46	CCATTAAATCCGCGACCTGTTTTTTTTCTCCAACAGGTTCCCAATTC
[PT-Cairo]_M13_core_47	AAAATTAAGCGCGAGCTGAAAAGGGCAACTAA
[PT-Cairo]_M13_core_48	CTAAATCGCAATAACCTGTTTAGCCCATATAA
[PT-Cairo]_M13_core_49	TGCGAACGAGTTTTTTTTGAGGAAGTTT
[PT-Cairo]_M13_core_50	ATTCTACTACAGGCAAGGCAAAAGGGTGAG
[PT-Cairo]_M13_core_51	CATTTGGGGCAATAAAGCCTCAGAATGCCTGA
[PT-Cairo]_M13_core_52	CATTTCGCAAATGGTGTTGTACCAAAAACAATTTTTAG
[PT-Cairo]_M13_core_53	CTTTGAGGACTATGACCATTAGATA
[PT-Cairo]_M13_core_54	ATGCCGGATAGGTAAAGATTCAAAGAATTAGC
[PT-Cairo]_M13_core_55	TACAAAGGATATATTTTAAATGCAGCATAAAG
[PT-Cairo]_M13_core_56	CTGGAGCACAACGCAAGGATAAAATTATGACC
[PT-	CTGTAATACTTTTTTTTTTGTATCGGTTTAT

Cairo]_M13_core_57	
[PT-Cairo]_M13_core_58	AAAGGCCCAACCGTTCTAGCTGTTGTATAA
[PT-Cairo]_M13_core_59	GTAATGTGGAGGGTAGCTATTTTTTGATAATC
[PT-Cairo]_M13_core_60	AACCCTCCTATCAGGTCATTGCAAACTAG
[PT-Cairo]_M13_core_61	TTATTTAACAAGTTTGAGACGAAAAACCGTCTTTTTTTTTGAGTCAATAGTG
[PT-Cairo]_M13_core_62	TCACCCTCCAATGACAACAACCATCGGAGTGA
[PT-Cairo]_M13_core_63	CTAAAGGACCGATAGTTGCGCCGAAGCAGCGA
[PT-Cairo]_M13_core_64	TGAAAATTTCGAGGTGAATTTCAACGGCTACAGAGG
[PT-Cairo]_M13_core_65	GCATAACCTAAAGGCCGCTTTTGGAGGCAA
[PT-Cairo]_M13_core_66	ATACGTAAATCGGAACGAGGGTAGCTTAAACA
[PT-Cairo]_M13_core_67	AACGGAGACCAACCTAAAACGAAACGGGATCG
[PT-Cairo]_M13_core_68	AAGACAGCTGCCACTACGAAGGCATTTGTATC
[PT-Cairo]_M13_core_69	AAGAATACATACCAAGCGCGAAACCAACTT
[PT-Cairo]_M13_core_70	AACGAGGCATAAATTGTGTCGAAACGGGTAAA
[PT-Cairo]_M13_core_71	TAATCTTGAAGGGAACCGAACTGACAAAGTAC
[PT-Cairo]_M13_core_72	ATCGCCTGGCAGACGGTCAATCATACAAGAAC
[PT-Cairo]_M13_core_73	TGAAAGAGGGCTGGCTGACCTTCAGAAACA
[PT-Cairo]_M13_core_74	CTTATGCGAAGGCTTGCCCTGACGATCAAGAG
[PT-Cairo]_M13_core_75	CCAGAACGCAACTTTAATCATTGGGGAAGA
[PT-Cairo]_M13_core_76	AAAATCTATTACAGGTAGAAAGATTCATCAGTTG
[PT-Cairo]_M13_core_77	CTTATCCGGTATTCTAAGACGGGAGGTTTTGAAGACGCTAA
[PT-Cairo]_M13_core_78	TCCAAATAATCCTGAATCTTACCACCTTAAAT
[PT-Cairo]_M13_core_79	CAAGATTAGTTTTACCGCACTCATCGAGAAGGCTGTCT

[PT-Cairo]_M13_core_80	CGAGCGTCAACAGCCATATTATTACACCCT
[PT-Cairo]_M13_core_81	CCTGTTTACATTCCAAGAACGGGTTTTTTCCCAGCT ACAATTTTAGAAACGA
[PT-Cairo]_M13_core_82	GCCCAATACGGGAGAATTAACTGATATCCCAA
[PT-Cairo]_M13_core_83	TTTTTTGTAGGGAAGCGCATTAGAATAAGAGC
[PT-Cairo]_M13_core_84	ATAAAAACTTAACGTCAAAAATTTTTTTTTGTTCA GCTAATGCGTAAAGTA
[PT-Cairo]_M13_core_85	GAACAAAGATAACCCACAAGAATTTACGCA
[PT-Cairo]_M13_core_86	ACGGAATAATGAAATAGCAATAGCAGAATAAC
[PT-Cairo]_M13_core_87	CATATGCGCAGACGACGATTTTTTTTTCTTTACAG AGTATCTTAC
[PT-Cairo]_M13_core_88	ACCAGAAGCTTTTTAAGTTTTTTAAAGCCTGTAAATA AGA
[PT-Cairo]_M13_core_89	AATCCAAAAATATATTTTAGTTAATTGAGA
[PT-Cairo]_M13_core_90	GAGAATATCTCAACAGTAGGGCTTAATTTCAT
[PT-Cairo]_M13_core_91	CTTCTGACTAACTATATGTAAATGATAACCTT
[PT-Cairo]_M13_core_92	GGGTTATACTAAATTTAATGGTTTCAGTATAA
[PT-Cairo]_M13_core_93	ATTCTGTCTTATACAAATTCTTACGAAATACC
[PT-Cairo]_M13_core_94	GACCGTGTCCTTTTTAACCTCCGGTTAATTTT
[PT-Cairo]_M13_core_95	GAGACTAGATAAATAAGGCGTTTTAGTAT
[PT-Cairo]_M13_core_96	ATAAACACAATTTATCAAAATCATGCGATAGC
[PT-Cairo]_M13_core_97	ATCGCCAAGGCATTTTCGAGCCCCTGAACA
[PT-Cairo]_M13_core_98	AGCCAACGAAAGTACCGACAAAAGAGAACGCG
[PT-Cairo]_M13_core_99	TTCCTTATTCAACAATAGATAAGTAGTAATAA
[PT-Cairo]_M13_core_100	AGAAAAAAACCAATCAATAATCCAAGCAAG
[PT-Cairo]_M13_core_101	CCGTTTTATAGCAAGCAAATCAGATA
[PT-	TGCGCAACTGTTGGGAAGGAGCTGGCGAAAGGG

Cairo]_M13_core_102	GAACGACG
[PT-Cairo]_M13_core_103	TTCGTAATAGTCACGACGTTGTAAGATGTGCT
[PT-Cairo]_M13_core_104	GCAAGGCGATTTGTATCGGCCTCAGGAAGACGCATCGT
[PT-Cairo]_M13_core_105	GCCAGTGCGATCCCCGGGTACCGAGTGAGC
[PT-Cairo]_M13_core_106	GTGAGCGAATCTGCCAGTTTGAGTTTTTTCGCCAGGGTTTTCCCCATGGTCA
[PT-Cairo]_M13_core_107	CTGCATTACCTGGGGTGCCTAATGAGCTCGAA
[PT-Cairo]_M13_core_108	TAGCTGTTAGCATAAAGTGTAAAGATGAATCG
[PT-Cairo]_M13_core_109	GAGCCGGATCCTGTGTGAAATTTTTTTTTTCAGCTTTCATCAAACGCCATC
[PT-Cairo]_M13_core_110	TAACTCACAGTCGGGAAACCTGTCGAAAAT
[PT-Cairo]_M13_core_111	GAGTTGCAGCGGGGAGAGGCGGTTCAACATAC
[PT-Cairo]_M13_core_112	CATGTCAATTCGCGTCTGTTTTTTTTTCAATTCCACATGCGTATT
[PT-Cairo]_M13_core_113	AGGGTTGAGGTTTGCCCCAGCAGGCGTGCCAG
[PT-Cairo]_M13_core_114	GCCAACGCGCAAGCGGTCCACGCTGTGTTGTT
[PT-Cairo]_M13_core_115	GGGCGCCCCCTTCACCGCCTGGTTAAAGAAC
[PT-Cairo]_M13_core_116	GCTGATTGAGGGTGGTTTTTTTTGTAATCGTACTGAGAGT
[PT-Cairo]_M13_core_117	CCTGTTTGAAATCAAAAGAATAGGAGCCCC
[PT-Cairo]_M13_core_118	GGTCGAGGGAACAAGAGTCCACTACCCTGAGA
[PT-Cairo]_M13_core_119	CGTGAACCTCCAACGTCAAAGGGCGGGCAACA
[PT-Cairo]_M13_core_120	CAGCTCATCCCAAAAACAGGAAGAATAAATTA
[PT-Cairo]_M13_core_121	AAAAATAATCATATGTACCCCGGTGAGAGATC
[PT-Cairo]_M13_core_122	GCAAATATTCGCATTAAATTTTTTCTCCGT
[PT-Cairo]_M13_core_123	AGAAAAGCTTTTTAACCAATAGGACATTAAAT
[PT-Cairo]_M13_core_124	AACCGTGCGTAACAACCCGTCGGATGTTAAAT

[PT-Cairo]_M13_core_125	GGGAACAGTTGGTGTAGATGGGTCGCACTC
[PT-Cairo]_M13_core_126	CAGCCAGGGCAAAGCGCCATTCGCCA
[PT-Cairo]_M13_core_127	GCCTGCAACAGTGCCACGCTGAGAGCTGCTG AACCTCAAATTTGAGGAA
[PT-Cairo]_M13_core_128	ACATTTGACAACAGTTGAAAGGAAATCAAACC
[PT-Cairo]_M13_core_129	CTCAATCAATATTTTTTTTTAATGCGCGAACT GATATGGCACAG
[PT-Cairo]_M13_core_130	GGTTATCGATTAGAGCCGTCAATAAAAGTT
[PT-Cairo]_M13_core_131	GATTCACCTTTGAATGGCTTTTTTTTTTAG TTGGCAAATGGATTTAG
[PT-Cairo]_M13_core_132	TTCCTGATCGAACGTTATTAATTTTAGATAAT
[PT-Cairo]_M13_core_133	AAGTATTAGACTTTTTTTTTTACATTGGCA
[PT-Cairo]_M13_core_134	TGAGTAAGAAGGAGCGGAATTAAAACAGAA
[PT-Cairo]_M13_core_135	CCTTTGCCTATCAGATGATGGCAAAGAACCTA
[PT-Cairo]_M13_core_136	TTTTGACGCTCAATCGTCTTTTTCGACAACTCGTATTA AAT
[PT-Cairo]_M13_core_137	TACATCGGAAATTATTTGCACGTATCATCATA
[PT-Cairo]_M13_core_138	ATTGCTTTGAATAATGGAAGGGTTTTCATCAA
[PT-Cairo]_M13_core_139	TATAATCCTGATTTTTTTTAGCAATACTT
[PT-Cairo]_M13_core_140	ATAAAGAGAATATACAGTAACAACAATTTC
[PT-Cairo]_M13_core_141	CCATATCAGAGAAACAATAACGGAAAACATCA
[PT-Cairo]_M13_core_142	TACTATGGTCACGCAAATTTTTTTTTTAT TATACTTCTGAATACCAA
[PT-Cairo]_M13_core_143	GCTTCTGTAAATTAATTACATTTAGTACCTTT
[PT-Cairo]_M13_core_144	CCCTTAGAAAGAAGATGATGAAACTTCGCCTG
[PT-Cairo]_M13_core_145	GTTACAAAATTTTTTTTTACAGGGCGCG
[PT-Cairo]_M13_core_146	ATTTGAAAATATATGTGAGTGACTGATGCA
[PT-	AGAAAACAAAATCGTCGCTATTAACTTAGGTT

Cairo]_M13_core_147	
[PT-Cairo]_M13_core_148	CAATTACCTGAGCAAATCCTTGAAAACATAAGGTCTGA
[PT-Cairo]_M13_core_149	CACCCGCCGCGCTAATTATTCATTT
[PT-Cairo]_M13_core_150	TTAGATTAAGACTTTTTTTGATGGCCCACTA
[PT-Cairo]_M13_core_151	GGAGCGGGATCGGAACCCTAAAGGCCCGAGAT
[PT-Cairo]_M13_core_152	CCAGTTTGTGCCGTAAAGCACTAACGCTAGGG
[PT-Cairo]_M13_core_153	GTGGACATCACCCAAATCAAGTGCGCGTAACCACCA
[PT-Cairo]_M13_core_154	CGATTTAGGAAAGGAAGGGAAGAGGGAGCT
[PT-Cairo]_M13_core_155	ACGAGCACAGTGTAGCGGTCACGCTTTTTTGG
[PT-Cairo]_M13_core_156	TTTATAATTCGTTAGAATCAGAGCAAGCGAAA
[PT-Cairo]_M13_core_157	CGCTGGCAGTATAACGTGCTTTCCCAGTGAGG
[PT-Cairo]_M13_core_158	AAACAGGAACGCCAGAATCCTGATCAAACT
[PT-Cairo]_M13_core_159	CTTTGATTTAAAAGAGTCTGTCCATTGCTTTG
[PT-Cairo]_M13_core_160	CATGGAAAGCCTGAGTAGAAGAACGAAGTGTT
[PT-Cairo]_M13_core_161	CCACCGAGAGTAATAACATCACTTTACCTACA
[PT-Cairo]_M13_core_162	ATCGGCCTGCCATTGCAACAGGAATAAAAG
[PT-Cairo]_M13_core_163	ACAATATTAGTCACACGACCAGTAAAAACGCT
[PT-Cairo]_M13_core_164	GGACATTCAAGCGTAAGAATACGGCCCTAA
[PT-Cairo]_M13_core_165	AACATCGCGATAAAACAGAGGTGAGGCGGTCAGT

Table S3.35. Core staples of p8064 floret pentagonal DNA origami tile.

Name	**Sequence**
[PT-floret]_p8064_core_1	ATCATTACCGCGCCCAATATATTCTAAGAACGCGCGGGAGGT
[PT-floret]_p8064_core_2	ACTTGAGGCGTTTTTTTTATCATTCCAATA

[PT-floret]_p8064_core_3	TTTGAAGCAGCTACAATTTTATGCCAGTTA
[PT-floret]_p8064_core_4	ATCGGCTGTTTACCTCCCG
[PT-floret]_p8064_core_5	AAAAATGATTCCAGAGCCTAATTTCCTGAATC
[PT-floret]_p8064_core_6	TTACCAACGTGCCTGTTTA
[PT-floret]_p8064_core_7	CAAAATAGAAACGATTTTTTGTAGACGGGA
[PT-floret]_p8064_core_8	AGGCATAATGCGCGTCTAAATAGCAGCTTTTAATTT
[PT-floret]_p8064_core_9	CCCACAAGAACAGGGAAGCGCATTTTAACGTC
[PT-floret]_p8064_core_10	GAATTAAGAGCGCTAATATCAGCTTTTTAA
[PT-floret]_p8064_core_11	TCATAATTTATTTAACAACGCCATTTTAGAGAATAACATAAAAATTGAGT
[PT-floret]_p8064_core_12	GGAATACCCTATCTTACCGAAGCCAGAGATAA
[PT-floret]_p8064_core_13	TAAGCCCAAATGAAATAGCAATAGCAAAAGAACTGGCATGTAGAAAAT
[PT-floret]_p8064_core_14	AAACATAATTTTTAAAGTTAAATATTTTTTCAAG
[PT-floret]_p8064_core_15	GAAAAGTAACCGAGGAAACGCAAAAAGAAA
[PT-floret]_p8064_core_16	CAGCGCCAAAAGGTGGCAACATATATAATAAC
[PT-floret]_p8064_core_17	AAACGATTAAGACTCCTTTTTTTATAACTATATGTACCTCC
[PT-floret]_p8064_core_18	CGCAAAGAATAGAAAATTCATAGGGAATTA
[PT-floret]_p8064_core_19	ACATACATAAGACAAAAGGGCGACTGAATTAT
[PT-	GGCTTAGGTTGGTTTTTTCAGTATGTTAGC

floret]_p8064_core_20	
[PT-floret]_p8064_core_21	ACCATCGACCGACTTGAGCCATTTTGGTTTAC
[PT-floret]_p8064_core_22	CAGAATCATTATTCATTAAAGGATTCAACC
[PT-floret]_p8064_core_23	GATTGAGGGAGGGATTTTTAGTGAATAACCTTG
[PT-floret]_p8064_core_24	GAGCCAGAGGCCGGAAACGTCAAAATCACC
[PT-floret]_p8064_core_25	CACCGTCATAGCAGCACCGTAATCCCTTATTA
[PT-floret]_p8064_core_26	TTCGCCATAAATCAATTTTTTTTATTGACGGAAAAGTT
[PT-floret]_p8064_core_27	ACCGCCACCATCTTTTCATAATCACCAATGAA
[PT-floret]_p8064_core_28	CGCCACCTTTCGGTCATAGCCCAGTAGCGA
[PT-floret]_p8064_core_29	TGCCTTTAGCGTTTTTTACAATAACGGA
[PT-floret]_p8064_core_30	GGAACCACCCTCAGAGCCGCCAAGCGCAGT
[PT-floret]_p8064_core_31	GCGTTTGCCCTCAGAGCCACCACCACAAATAA
[PT-floret]_p8064_core_32	ATCGGCATAGAACCACCACCAGAGCAGGTCAG
[PT-floret]_p8064_core_33	GTACCTTTTACATTTTTTGTAGCGCGTTTTC
[PT-floret]_p8064_core_34	TAATAAGTTAAAGCCAGAATGGAACCCTCAGA
[PT-	AACAGTGCCTTGATATTCACAACTCAGAGC

floret]_p8064_core_35	
[PT-floret]_p8064_core_36	TGAGGCCGCCGCCATTTTTTTCATATTCCACCAG
[PT-floret]_p8064_core_37	CTCTGAATTGATGATACAGGAGGGATAAGT
[PT-floret]_p8064_core_38	ATCCTCATTTTAACGGGGTCAGTGTAGGATTA
[PT-floret]_p8064_core_39	ACGATTGGCCCGTATAAACAGTTATTAAGAGG
[PT-floret]_p8064_core_40	AAGGAGCGGTTTTTACAGGAGGT
[PT-floret]_p8064_core_41	TAGTACCGTTGCTCAGTACCAGGCTGTACTGG
[PT-floret]_p8064_core_42	GAACCGCCCTCAAGAGAAGGATCCTTGAGT
[PT-floret]_p8064_core_43	TTTCAGGGCTGAAACATGAAAGTAATGCCCCC
[PT-floret]_p8064_core_44	TGCCTATTTCTTTTGTTGAAAGGA
[PT-floret]_p8064_core_45	GCCGTCGTGTATCACCGTACTCAGTTTTGT
[PT-floret]_p8064_core_46	GCGGGGTTCCACCCTCAGAACCGCAGACAGCC
[PT-floret]_p8064_core_47	CTGAGACTCACCCTCAGAGCCACCAGTACAAA
[PT-floret]_p8064_core_48	AATATGTTGGCATTTTATTATTATAGCAAGCCCTACAGAC
[PT-floret]_p8064_core_49	GTTTCAGCTAGCGTAACGATCTAAAGGAGGTT
[PT-	TAAAGGACCTGTAGCATTCCACCACCCTCA

floret]_p8064_core_50	
[PT-floret]_p8064_core_51	TTGAAAATACTGAGTTTCGTCACCACCCTCAT
[PT-floret]_p8064_core_52	CGTCTTTATTTTGCTAAACAACTGCGCCGA
[PT-floret]_p8064_core_53	CTCATAGTGGAGTGAGAATAGAAAGTGAATTT
[PT-floret]_p8064_core_54	CTACAACGATTGCGAATAATAATTAATTGTAT
[PT-floret]_p8064_core_55	CCGTAACCTCCAAATTTAGTAAGA
[PT-floret]_p8064_core_56	GAAATTGTTTAGTAATACTGAAAGCGTAAGAATTACCCATGTA
[PT-floret]_p8064_core_57	AAAACGCGTCTGAAATGGATTAGCAGAAGA
[PT-floret]_p8064_core_58	CAGCAAATACCGAACGAACCACCATTTACATT
[PT-floret]_p8064_core_59	GGCAGATTTTACCGCCAGCCATTGAAGTGTTT
[PT-floret]_p8064_core_60	GAACAATACACCAGTCACACGACCCATCGCCA
[PT-floret]_p8064_core_61	TGAACCTCTGATAGCCCTAAAAAGTAATAA
[PT-floret]_p8064_core_62	AAGGGACATCGGCCTTGCTGGTAAAAGAGT
[PT-floret]_p8064_core_63	CTCAAACTATTCTGGCCAACAGAGGTCTTTAA
[PT-floret]_p8064_core_64	GGCTATTAATAGAACCCTTCTGACACATCACT
[PT-	TAAAACAAACAGTGCCACGCTGACATTTGA

floret]_p8064_core_65	
[PT-floret]_p8064_core_66	TTAAAAATGAAAAATCTAAAGCATCAACTAAT
[PT-floret]_p8064_core_67	TGCGCGAACAAATATCAAACCCTCAGGTTATC
[PT-floret]_p8064_core_68	ATTGAGGAAATCAATATCTGGTCATTTTGAAT
[PT-floret]_p8064_core_69	CGTTATTAGCCGTCAATAGATAATAGAGCCAG
[PT-floret]_p8064_core_70	TCATTTTCTTTAGGAGCACTAACACCTTGC
[PT-floret]_p8064_core_71	GGATTTATCGTATTAAATCCTTATGGAAGG
[PT-floret]_p8064_core_72	AGATTAGAATTTTAAAAGTTTGAGAATCCTGA
[PT-floret]_p8064_core_73	TAAAATATGCGGAACAAAGAAACCTGATTATCAGATGATGCAGTAACA
[PT-floret]_p8064_core_74	AATTGCGTATTATACTTCTGAATATGCCCGAA
[PT-floret]_p8064_core_75	GAATATAGCAATTCATCAATATTAACATTA
[PT-floret]_p8064_core_76	GTTAGAATGCACGTAAAACAGATTCATTTC
[PT-floret]_p8064_core_77	TTGTTTGGAGATTTTCAGGTTTAAACCAAGTT
[PT-floret]_p8064_core_78	ACAATTTCGCGCAGAGGCGAATTAAATAAAGA
[PT-floret]_p8064_core_79	CTTCTGTATTAATGGAAACAGTACTGATTGCTTTGAATCGTCAGAT
[PT-	AATTACCGAAAACAAAATTAATTCCTTGAA

floret]_p8064_core_80	
[PT-floret]_p8064_core_81	ACAAAATCATTTGAATTACCTTTTAATCGTCG
[PT-floret]_p8064_core_82	AGGTCTGATAATTTTCCCTTAGAATACATTTA
[PT-floret]_p8064_core_83	AACATAGAATAGTGAATTTATCAACGCGAG
[PT-floret]_p8064_core_84	CTATTAATGAGACTACCTTTTTAAAATGCTGA
[PT-floret]_p8064_core_85	TACCGACCCAATCGCAAGACAAAGAAAATCAT
[PT-floret]_p8064_core_86	AAAACTTGACCTAAATTTAATGTTAGTATC
[PT-floret]_p8064_core_87	TGCAAATCGTGTGATAAATAAGGCCACCGGAA
[PT-floret]_p8064_core_88	AATCGCCAACTAGAAAAAGCCTGTGTTTGAAA
[PT-floret]_p8064_core_89	ATATGCGCTCAACAGTAGGGCTAGTAATAA
[PT-floret]_p8064_core_90	TCAACAATAAACAACATGTTCAGCGAGGCATTTTCGAGCCTAATTGAG
[PT-floret]_p8064_core_91	GAGAATACCAGACGACGACAATAGATAAGT
[PT-floret]_p8064_core_92	CCTGAACCATGTAGAAACCAATCAAGAACG
[PT-floret]_p8064_core_93	GGTATTAGCCGTTTTTATTTTCATCG
[PT-floret]_p8064_core_94	CTTCACCGCCTTATAAATCAAAATTTTTGATTTAGAGC
[PT-	TAATGCGCTTTTTTTTGACGGGCAACAGCCGTATTGG

floret]_p8064_core_95	
[PT-floret]_p8064_core_96	TGCCTGAGTTGTAGCAATTTTTTTTCCACACAATAGCTGTT
[PT-floret]_p8064_core_97	CGTTTTCTGCCTGTTCTTCGCGAATTGCGT
[PT-floret]_p8064_core_98	CAACGCGCTGAGCTAACTCACATTTCCGTGAG
[PT-floret]_p8064_core_99	CCTCCTCATGCTGCGGCCAGAATGAAGGTTTC
[PT-floret]_p8064_core_100	CTCTGTGGCAGTTGAGGATCCCCGTGGGGTGC
[PT-floret]_p8064_core_101	GCGCCAGATAAAGTGTAAAGCCGGTACCGA
[PT-floret]_p8064_core_102	CCGGAAGCGGTGGTTTTTCTTTTTTTTTTCGTACTA
[PT-floret]_p8064_core_103	GCTCGAACAGTGTCACTGCGCGCACTGGTG
[PT-floret]_p8064_core_104	TAACGGCAATCAGACGATCCAGCGTTCGTAATCATGGTCACATACGAG
[PT-floret]_p8064_core_105	TCCTGTGTTGCCGGTGCCCCCTGCTCAGATGCCTTTTTTTGAAGATCGCCTGCCAGT
[PT-floret]_p8064_core_106	CTAATGAGGGGGAGAGGCGGTTTGTGATTGCC
[PT-floret]_p8064_core_107	TGCGCTCGCCAGCTGCATTAATTTGCAGCA
[PT-floret]_p8064_core_108	GCAAAATCCCTGGCCCTGAGAGAGGAATCGGC
[PT-floret]_p8064_core_109	AGCGGTCGTTTGATGGTGGTTCTCCAGTTT
[PT-	ATCGGAACCCTATATAGGGTTGAGTGTTGTCGAAATCG

floret]_p8064_core_110	
[PT-floret]_p8064_core_111	GGAACAATCAAAGGGCGAAAAACCGT
[PT-floret]_p8064_core_112	TGGTTTCACGCAAATTAACCGTAGAAGAA
[PT-floret]_p8064_core_113	CTGTCCAGCTTTGACGAGCACGGCGCT
[PT-floret]_p8064_core_114	TTGACAACCACCACACCCGCCTATAACGT
[PT-floret]_p8064_core_115	CTGCGCGTGGGGAAAGCCGGCGAAACTAA
[PT-floret]_p8064_core_116	GGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCCGTGGCGA
[PT-floret]_p8064_core_117	GAAAGGACGCTGGCAAGTGTAGGGAGCTAA
[PT-floret]_p8064_core_118	TTATAATCCGTTAGAATCAGAGCGCGGTCACG
[PT-floret]_p8064_core_119	GCTTTCCTAGTGAGGCCACCGAGTAATATCCA
[PT-floret]_p8064_core_120	ACAGGAGCGCCAGAATCCTGAGCAACAGGA
[PT-floret]_p8064_core_121	TTCAGAGGTTTCTCCGTGGTGAATTTTTTTTCGTCTCG
[PT-floret]_p8064_core_122	GTGGTGCCTTTTTTTTAACGACGGCCAGTTTGGGTAA
[PT-floret]_p8064_core_123	ATCAACACTCCGTGGGAACAAATCAGGCTG
[PT-floret]_p8064_core_124	GGGATGTGAAGCGCCATTCGCCATCGGCGGAT
[PT-	TGACCGTACTGGCCTTCCTGTAGCCCCGGTTG

floret]_p8064_core_125	
[PT-floret]_p8064_core_126	ATTCGCGTATGGGATAGGTCACGTTGCCGGAA
[PT-floret]_p8064_core_127	CGCCAGGCGGCACCGCTTCTGGTGGTGTAG
[PT-floret]_p8064_core_128	CAGCTTTCGTTTTCCCAGTCTTTTTTTTTCAGCTTACGGCTCAAATCGT
[PT-floret]_p8064_core_129	ATGGGCGCAATAGGAACGCCATGGAAGATT
[PT-floret]_p8064_core_130	TAAATTGTCAGCTCATTTTTTAACCATCGTAACCGTGCATACTCCAGC
[PT-floret]_p8064_core_131	CCTGACTTTTTTCGCATACGACGATTTCCAGCGG
[PT-floret]_p8064_core_132	TTGAGGGGTAAATTTTTGTTAAATAAACGTTAATTTTTTTAAAGCGGATAAAATCAG
[PT-floret]_p8064_core_133	ACCAGGCACTGCAAGGCGATTAAGGCCAAGCT
[PT-floret]_p8064_core_134	CGCAACTCTATTACGCCAGCTGACGGATAA
[PT-floret]_p8064_core_135	AGATAGACTGGAGCCGCCACGGGAGCGAAAGG
[PT-floret]_p8064_core_136	CCTCACCTTACCAGTCCCGGAAGAAACAGC
[PT-floret]_p8064_core_137	CGTTCCGGCAAATACGGAAAAAGAGACGCATTTGTGAG
[PT-floret]_p8064_core_138	GGATCAATGGGCGGTTGTGTACATCG
[PT-floret]_p8064_core_139	TGTTCAGGGAGGTGTCCAGCATCGTCG
[PT-	TCGCTATGCCAACGGCAGCACCAGCGGGG

floret]_p8064_core_140	
[PT-floret]_p8064_core_141	CCGCAAGAGGCAGCCTCCGGCCAGATTGC
[PT-floret]_p8064_core_142	AAAAATCCCGTAAAAAAAGAGTTAAACGATGCTGAGCACATC
[PT-floret]_p8064_core_143	CTCATAAGGTGCTGGTCTGGTCATCCGCCG
[PT-floret]_p8064_core_144	TTTGCTCGGGCGCTTTCGCACTCAAGCAGCAA
[PT-floret]_p8064_core_145	TCATTGCATCATAAACATCCCTTACCTGTGCA
[PT-floret]_p8064_core_146	GGCGCGGGGCTGGTAATGGGTACGGCGGGC
[PT-floret]_p8064_core_147	GTACGGTGACCTGTTTAGCTATATTTTTCGCAAGGATA
[PT-floret]_p8064_core_148	TCTAGCTGTTTTTTTTTGTTTTAAATATGTTAGAGCT
[PT-floret]_p8064_core_149	GTAATAGGCGGAATCGTCATAAAAAGCGAA
[PT-floret]_p8064_core_150	TAAGAGGTTTTTAATTCGAGCTTCATATTCAT
[PT-floret]_p8064_core_151	TGAATCCCGCAAAAGAAGTTTTGCAGGTAGAA
[PT-floret]_p8064_core_152	AGGCTTTTCCTCAAATGCTTTAAAGACTTCAA
[PT-floret]_p8064_core_153	TAATTGCAGAGGAAGCCCGAAACAGTTCAG
[PT-floret]_p8064_core_154	AAAGATTATGAATATAATGCTTTTTTTTTCGGAGAGGGTAGCAAATATT
[PT-	AAAACGAACGATAAAAACCAAAATACCACA

floret]_p8064_core_155	
[PT-floret]_p8064_core_156	TACATAACCCTCGTTTACCAGACGGAATGACCATAAATCATGCATCAA
[PT-floret]_p8064_core_157	GTCTTTACGCAACACTATCATAACGCCAAAAGGTTTTTTTGGAGCCTTTTTTTCACG
[PT-floret]_p8064_core_158	ATATCGCGCATTTTTGCGGATGGCCAACTAAA
[PT-floret]_p8064_core_159	CCAGACCGTACCTTTAATTGCTCATATAAC
[PT-floret]_p8064_core_160	GGTCAATATCTGGAAGTTTCATTCCCTTTTGA
[PT-floret]_p8064_core_161	AGTTGATACCATTAGATACATTGGCATCAA
[PT-floret]_p8064_core_162	TTGCGGGAGAAGTGCGCGAGCTGAAAAGGTTCGCAAAT
[PT-floret]_p8064_core_163	TTCTACTACAGGCAAGGCAAAGAATT
[PT-floret]_p8064_core_164	GTATAAGCTATTTTTGAGAGATACCGT
[PT-floret]_p8064_core_165	AAAATATCAATATGATATTCACTACAAAG
[PT-floret]_p8064_core_166	AAATCACCTTTTAGAACCCTCATATACTT
[PT-floret]_p8064_core_167	ATTAAGCAATAAAGCCTCAATTATGACCCTGTAATATTTTAA
[PT-floret]_p8064_core_168	ATGCAATGGTGAGAAAGGCCGGCTGGAGCA
[PT-floret]_p8064_core_169	ATAATCAGGTCATTGCCTGAGAGTAGACAGTC
[PT-	GCTATCAGAAAAGCCCCAAAAACACAAAAATA

floret]_p8064_core_170	
[PT-floret]_p8064_core_171	AACAAGAGTCAATCATATGTACCAGCTTTC
[PT-floret]_p8064_core_172	AGGACTAACTAAAACACTCATCTTTTTTGGCTGGCTGA
[PT-floret]_p8064_core_173	TGGGCTTGTTTTTTTTGCAACGGCTACAGTCACCCTC
[PT-floret]_p8064_core_174	TTAAAGGCGCTTGATACCGATAGTTTTCAACA
[PT-floret]_p8064_core_175	AGCAGCGCAGCTTGCTTTCGAGGGAACAAC
[PT-floret]_p8064_core_176	CGGTTTATAAAGACAGCATCTTTTTTTTTTCAACTTTAATAATGCAGA
[PT-floret]_p8064_core_177	CTTAAACACGCTTTTGCGGGATCGAGGCTTTG
[PT-floret]_p8064_core_178	CAATGACCGGTCGCTGAGGCTTAAGTTTCC
[PT-floret]_p8064_core_179	AGAATACAAGACTTTTTCATGAGGGCAGGGAG
[PT-floret]_p8064_core_180	ATTAAACCAACCTAAAACGAAAAACAAAGT
[PT-floret]_p8064_core_181	AACGGTGTACAGTGATTATACCAAGCGCGAGAGGCAAA
[PT-floret]_p8064_core_182	ACAACGGAAATCCGCGACCTGCTCCA
[PT-floret]_p8064_core_183	TTCAACTCATTGTGAATTACCTTAAAT
[PT-floret]_p8064_core_184	CCTTCACACCAGAACGAGTAGTATGCGAT
[PT-	GACGAGAAATCAAGAGTAATCTTGAGATG

floret]_p8064_core_185	
[PT-floret]_p8064_core_186	TTAGCCGGAACGAGGCGCAACTTTGAAAGAGGACACAAGAAC
[PT-floret]_p8064_core_187	CGGATATATTCAGTGAATAAGGGTCAGGAC
[PT-floret]_p8064_core_188	AGATTCATCTGGCTCATTATACCACTTGCCCT
[PT-floret]_p8064_core_189	TTTAAGAACAGTTGAGATTTAGGAATAGCGAG
[PT-floret]_p8064_core_190	GTTGGGAGAACAACATTATTACCAGAGGGG

S5.2.2 Staple strand sequences of tiles for semiregular tilings

Table S3.36. Edge staples of elongated triangular ($3^3.4^2$) DNA origami tiling.

Name	Sequence
[SQ]_33344_edge_1	AAATCCGCGACCTGCTCTGATAAATTGTGTCGAG
[SQ]_33344_edge_2	CAACATTATTACAGGTAAACGAACTAACGGAACC
[SQ]_33344_edge_3	GTACCTTTAATTGCTCAGGTCAGGATTAGAGACA
[SQ]_33344_edge_4	TATGACCCTGTAATACGTTGTACCAAAAACATTT
[SQ]_33344_edge_5	AAACCAATCAATAATAATTTACGAGCATGT
[SQ]_33344_edge_6	TAAATTTAATGGTTTAATTTCATCTTCTGA
[SQ]_33344_edge_7	TCGGGAGAAACAATGTAACAGTACCTTTTA
[SQ]_33344_edge_8	AGGAGCACTAACAAGTTATCTAAAATATCT
[SQ]_33344_edge_9	TCGTACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ]_33344_edge_10	AAAACAGTGCCCGTATAAGGTCAGTGCCTTGAGT
[SQ]_33344_edge_11	GGCAAGGCCGGAAACGTCGCACCATTACCATTAG
[SQ]_33344_edge_12	GAACGGAATAAGTTTATTGAAACGCAAAGACACC
[SQ]_33344_edge_13	GACGCTATTACGCCAGCTTCGGTGCGGGCCTCTT
[SQ]_33344_edge_14	GGCACAATTCCACACAACGAAATTGTTATCCGCT
[SQ]_33344_edge_15	AATACGTGAACCATCACCCAGGGCGATGGCCCAC
[SQ]_33344_edge_16	TCCGCGCTTAATGCGCCGTAACCACCACACCCGC
[TR]_33344_edge_17	ATTGAAGCATTTATTCTTCCTTTTTCAATA
[TR]_33344_edge_18	GCCACCTAAATTGTCACATTTCCCCGAAAA
[TR]_33344_edge_19	ACCGAGATAGGGTTTATAAATCAAAAGAAT
[TR]_33344_edge_20	GGGCGCTGGCAAGTGTAAAGGAGCGGGCGCTAAG
[TR]_33344_edge_21	CGGTGCGGGCCTCTTCTGTTGGGAAGGGCGATGT
[TR]_33344_edge_22	AAAACGACGGCCAGTGCCAGTCACGACGTTGTTT
[TR]_33344_edge_23	TAAAAGTGCTCATCATCCACATAGCAGAACTTTA
[TR]_33344_edge_24	TGAGTACTCAACCAAGGCTTTTCTGTGACTGGTC
[TR]_33344_edge_25	CTTCGGTCCTCCGATCAAAAAGCGGTTAGCTCAG
[TR]_33344_edge_26	ATTTATCAGCAATACACGCTCACCGGCTCC
[TR]_33344_edge_27	TATTTCGTTCATCCCTATCTCAGCGATCTG
[TR]_33344_edge_28	AATTAAAAATGAAGTTCACCTAGATCCTTT
[TR]_33344_edge_29	GGCTGCGGCGAGCGGTCTGCGCTCGGTCGT
[TR]_33344_edge_30	AGGCCGCGTTGCTGGCGCCAGGAACCGTAA
[TR]_33344_edge_31	GCTGTGTGCACGAACCGTTCGCTCCAAGCT
[TR]_33344_edge_32	TTAGCAGAGCGAGGTAGCCACTGGTAACAG

Table S3.37. Edge staples of snub square ($3^2.4.3.4$) DNA origami tiling.

Name	Sequence
[SQ_1]_33434_edge_1	GAAGAAGGAGCGGAATTAGAACAAAGAAACCACC
[SQ_1]_33434_edge_2	GGCATCGGGAGAAACAATGTAACAGTACCTTTTA
[SQ_1]_33434_edge_3	AACCTAAATTTAATGGTTTAATTTCATCTTCTGA

[SQ_1]_33434_edge_4	TCGCATTTTCGAGCCAGTTGTAATTTAGGCAGAG
[SQ_1]_33434_edge_5	GAACGGAATAAGTTTATTGAAACGCAAAGACACC
[SQ_1]_33434_edge_6	GGCAAGGCCGGAAACGTCGCACCATTACCATTAG
[SQ_1]_33434_edge_7	AAAACAGTGCCCGTATAAGGTCAGTGCCTTGAGT
[SQ_1]_33434_edge_8	TCGTACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ_1]_33434_edge_9	GACCAAATCAACGTAACAACCGGATATTCATTAC
[SQ_1]_33434_edge_10	GGCAACATTATTACAGGTAAACGAACTAACGGAA
[SQ_1]_33434_edge_11	AAGTACCTTTAATTGCTCAGGTCAGGATTAGAGA
[SQ_1]_33434_edge_12	TCAATAACCTGTTTAGCTCATTTCGCAAATGGTC
[SQ_1]_33434_edge_13	GACGCTATTACGCCAGCTTCGGTGCGGGCCTCTT
[SQ_1]_33434_edge_14	GGCACAATTCCACACAACGAAATTGTTATCCGCT
[SQ_1]_33434_edge_15	AATACGTGAACCATCACCCAGGGCGATGGCCCAC
[SQ_1]_33434_edge_16	TCCGCGCTTAATGCGCCGTAACCACCACACCCGC
[SQ_2]_33434_edge_17	ATCCAAATCAACGTAACAACCGGATATTCATTAC
[SQ_2]_33434_edge_18	TACAACATTATTACAGGTAAACGAACTAACGGAA
[SQ_2]_33434_edge_19	ATGTACCTTTAATTGCTCAGGTCAGGATTAGAGA
[SQ_2]_33434_edge_20	AAAATAACCTGTTTAGCTCATTTCGCAAATGGTC
[SQ_2]_33434_edge_21	ATCGCTATTACGCCAGCTTCGGTGCGGGCCTCTT
[SQ_2]_33434_edge_22	TACACAATTCCACACAACGAAATTGTTATCCGCT
[SQ_2]_33434_edge_23	ATTACGTGAACCATCACCCAGGGCGATGGCCCAC
[SQ_2]_33434_edge_24	AACGCGCTTAATGCGCCGTAACCACCACACCCGC
[SQ_2]_33434_edge_25	ATAGAAGGAGCGGAATTAGAACAAAGAAACCACC
[SQ_2]_33434_edge_26	TACATCGGGAGAAACAATGTAACAGTACCTTTTA
[SQ_2]_33434_edge_27	ATCCTAAATTTAATGGTTTAATTTCATCTTCTGA
[SQ_2]_33434_edge_28	AAGCATTTTCGAGCCAGTTGTAATTTAGGCAGAG
[SQ_2]_33434_edge_29	ATACGGAATAAGTTTATTGAAACGCAAAGACACC
[SQ_2]_33434_edge_30	TACAAGGCCGGAAACGTCGCACCATTACCATTAG
[SQ_2]_33434_edge_31	ATAACAGTGCCCGTATAAGGTCAGTGCCTTGAGT
[SQ_2]_33434_edge_32	AAGTACCGCCACCCTCAGGTACTCAGGAGGTTTA
[TR]_33434_edge_33	TATTTCGTTCATCCCTATCTCAGCGATCTG
[TR]_33434_edge_34	ATTTATCAGCAATACACGCTCACCGGCTCC
[TR]_33434_edge_35	TGAGTACTCAACCAAGGCTTTTCTGTGACTGGTC
[TR]_33434_edge_36	CTTCGGTCCTCCGATCAAAAAGCGGTTAGCTCAG
[TR]_33434_edge_37	CGGTGCGGGCCTCTTCTGTTGGGAAGGGCG
[TR]_33434_edge_38	GGGCGCTGGCAAGTGTAAAGGAGCGGGCGC
[TR]_33434_edge_39	AGACCGAGATAGGGTTTATAAATCAAAAGA
[TR]_33434_edge_40	GTGCCACCTAAATTGTCACATTTCCCCGAA
[TR]_33434_edge_41	TTAGCAGAGCGAGGTAGCCACTGGTAACAG
[TR]_33434_edge_42	GCTGTGTGCACGAACCGTTCGCTCCAAGCT
[TR]_33434_edge_43	AGGCCGCGTTGCTGGCGCCAGGAACCGTAA
[TR]_33434_edge_44	GGCTGCGGCGAGCGGTCTGCGCTCGGTCGT

Table S3.38. Edge staples of trihexagonal $(3.6)^2$ DNA origami tiling.

Name	**Sequence**

[TR]_3636_edge_1	CTGCGGCGAGCGGTCTGCGCTCGGTCGTTC
[TR]_3636_edge_2	GCCGCGTTGCTGGCGCCAGGAACCGTAAAA
[TR]_3636_edge_3	TGTGTGCACGAACCGTTCGCTCCAAGCTGG
[TR]_3636_edge_4	AGCAGAGCGAGGTAGCCACTGGTAACAGGA
[TR]_3636_edge_5	GTGCGGGCCTCTTCTGTTGGGAAGGGCGAT
[TR]_3636_edge_6	GCGCTGGCAAGTGTAAAGGAGCGGGCGCTA
[TR]_3636_edge_7	ACCGAGATAGGGTTTATAAATCAAAAGAAT
[TR]_3636_edge_8	GCCACCTAAATTGTCACATTTCCCCGAAAA
[TR]_3636_edge_9	TATTTCGTTCATCCCTATCTCAGCGATCTG
[TR]_3636_edge_10	ATTTATCAGCAATACACGCTCACCGGCTCC
[TR]_3636_edge_11	TCGGTCCTCCGATCAAAAAGCGGTTAGCTC
[TR]_3636_edge_12	AGTACTCAACCAAGGCTTTTCTGTGACTGG
[TR]_3636_edge_13	TGACGCTCAGTGGAGATCTTTTCTACGG
[TR]_3636_edge_14	AATTAAAAATGAAGTTCACCTAGATCCT
[TR]_3636_edge_15	AAAGTGCTCATCATCCACATAGCAGAAC
[TR]_3636_edge_16	ACCCACTCGTGCACGAGATCCAGTTCGA
[TR]_3636_edge_17	GCAAGCAGCAGATTGCGGTGGTTTTTTT
[TR]_3636_edge_18	GCCAGTTACCTTCGTATCTGCGCTCTGC
[TR]_3636_edge_19	CCAGCTGCATTAATGTCGGGAAACCTGT
[TR]_3636_edge_20	CCTGGGGTGCCTAAGAAGCATAAAGTGT
[TR]_3636_edge_21	CCTGTGTGAAATTGTCATGGTCATAGCT
[TR]_3636_edge_22	AACGACGGCCAGTGCCAGTCACGACGTT
[TR]_3636_edge_23	ATTGAAGCATTTATTCTTCCTTTTTCAA
[TR]_3636_edge_24	ACAGGAAGGCAAAAGTTTCTGGGTGAGC
[HE]_3636_edge_25	TTTAACCTCCGGCTTATCTGAGAGACTACCTTTT
[HE]_3636_edge_26	ACCTAAATTTAATGGTTTAATTTCATCTTCTGGC
[HE]_3636_edge_27	CGACGACAATAAACAAAGTAATTCTGTCCAGAAG
[HE]_3636_edge_28	ATAATCGGCTGTCTTTATGTAGAAACCAATCAGG
[HE]_3636_edge_29	CATCTTTTCATAATCACCTTATTAGCGTTTGCCG
[HE]_3636_edge_30	ACCACCAGAGCCGCCGAGCCGCCACCAGAACCGG
[HE]_3636_edge_31	GTATTAAGAGGCTGAGATTCTGAAACATGAAAAG
[HE]_3636_edge_32	CCGTACTCAGGAGGTTCGGAATAGGTGTATCAGT
[HE]_3636_edge_33	GGCTCATTATACCAGTTGCGATTTTAAGAACTTG
[HE]_3636_edge_34	ACTAATGCAGATACATAGGAATACCACATTCACT
[HE]_3636_edge_35	ACTATTATAGTCAGAATCAGGTCTTTACCCTGAG
[HE]_3636_edge_36	CAGGTCAGGATTAGAGCGGAAGCAAACTCCAATC
[HE]_3636_edge_37	TAATCGCGCAGAGGCGAAAATACCAAGTTACAAA
[HE]_3636_edge_38	ATAATAAAGAAATTGCGTTTGCACGTAAAACAGA
[HE]_3636_edge_39	CTAATAGATAATACATTTATAGATTAGAGCCGTC
[HE]_3636_edge_40	TTCTCAAATATCAAACCCCATCACCTTGCTGAAC
[HE]_3636_edge_41	TGTTAAATCAGCTCATATTCGCATTAAATT
[HE]_3636_edge_42	AGCATGTCAATCATATCGGTAATCGTAAAA
[HE]_3636_edge_43	ACTTTTGCGGGAGAAGATTATGACCCTGTA

[HE]_3636_edge_44	GTAGTAGCATTAACATATCAATTCTACTAA
[HE]_3636_edge_45	ATTACCTTTTTTAATTTAACAATTTCAT
[HE]_3636_edge_46	AGGAGCGGAATTATAACAAAGAAACCAC
[HE]_3636_edge_47	GATAAAACAGAGGTAACGAACCACCAGC
[HE]_3636_edge_48	ACAACCCGTCGGATATTAAATGTGAGCG
[HE]_3636_edge_49	ATATGATATTCAACACAGTCAAATCACC
[HE]_3636_edge_50	TAGTTTGACCATTATCTGCGAACGAGTA
[HE]_3636_edge_51	TTTCCCTTAGAATCTCGTCGCTATTAAT
[HE]_3636_edge_52	TACCGCGCCCAATATTTCATCGTAGGAA
[HE]_3636_edge_53	GCACCGTAATCAGTATGAAACCATCGAT
[HE]_3636_edge_54	GAACCCATGTACCGGGATAGCAAGCCCA
[HE]_3636_edge_55	TTGCCCTGACGAGATCATTCAGTGAATA
[HE]_3636_edge_56	TGTTTTAAATATGCTAATGCTGTAGCTC

Table S3.39. Edge staples of rhombitrihexagonal (3.4.6.4) DNA origami tiling.

Name	**Sequence**
[HE]_3464_edge_1	TTTAGTTTGACCATTATCTGCGAACGAGTA
[HE]_3464_edge_2	GTAGTAGCATTAACATATCAATTCTACTAA
[HE]_3464_edge_3	ACTTTTGCGGGAGAAGATTATGACCCTGTA
[HE]_3464_edge_4	AGCATGTCAATCATATCGGTAATCGTAAAA
[HE]_3464_edge_5	TGTTAAATCAGCTCATATTCGCATTAAATT
[HE]_3464_edge_6	TAACAACCCGTCGGATATTAAATGTGAGCG
[HE]_3464_edge_7	GAGAATTACCTTTTTTAATTTAACAATTTCATTT
[HE]_3464_edge_8	TAATCGCGCAGAGGCGAAAATACCAAGTTACAAA
[HE]_3464_edge_9	ATAATAAAGAAATTGCGTTTGCACGTAAAACAGA
[HE]_3464_edge_10	CTAATAGATAATACATTTATAGATTAGAGCCGTC
[HE]_3464_edge_11	TTCTCAAATATCAAACCCCATCACCTTGCTGAAC
[HE]_3464_edge_12	AGAAGATAAAACAGAGGTAACGAACCACCAGCAG
[HE]_3464_edge_13	ATATGATATTCAACACAGTCAAATCACC
[HE]_3464_edge_14	AGGAGCGGAATTATAACAAAGAAACCAC
[HE]_3464_edge_15	TGTTTTAAATATGCTAATGCTGTAGCTCAA
[HE]_3464_edge_16	GGTCAGGATTAGAGCGGAAGCAAACTCCAA
[HE]_3464_edge_17	TATTATAGTCAGAATCAGGTCTTTACCCTG
[HE]_3464_edge_18	TAATGCAGATACATAGGAATACCACATTCA
[HE]_3464_edge_19	CTCATTATACCAGTTGCGATTTTAAGAACT
[HE]_3464_edge_20	TTGCCCTGACGAGATCATTCAGTGAATAAG
[HE]_3464_edge_21	GAACCCATGTACCGGGATAGCAAGCCCAAT
[HE]_3464_edge_22	GTACTCAGGAGGTTCGGAATAGGTGTATCA
[HE]_3464_edge_23	ATTAAGAGGCTGAGATTCTGAAACATGAAA
[HE]_3464_edge_24	CACCAGAGCCGCCGAGCCGCCACCAGAACC
[HE]_3464_edge_25	TCTTTTCATAATCACCTTATTAGCGTTTGC
[HE]_3464_edge_26	GCACCGTAATCAGTATGAAACCATCGATAG

[HE]_3464_edge_27	TACCGCGCCCAATATTTCATCGTAGGAATC
[HE]_3464_edge_28	AATCGGCTGTCTTTATGTAGAAACCAATCA
[HE]_3464_edge_29	ACGACAATAAACAAAGTAATTCTGTCCAGA
[HE]_3464_edge_30	CTAAATTTAATGGTTTAATTTCATCTTCTG
[HE]_3464_edge_31	TAACCTCCGGCTTATCTGAGAGACTACCTT
[HE]_3464_edge_32	TTTCCCTTAGAATCTCGTCGCTATTAATTA
[SQ_1]_3464_edge_33	GACAACAACCATCGGATAGTTGCGCCGA
[SQ_1]_3464_edge_34	AAATCTCCAAAAAAATAATTTTTTCACG
[SQ_1]_3464_edge_35	ATTAACTGAACACCAGCGCATTAGACGG
[SQ_1]_3464_edge_36	TATTTATCCCAATCCAAAATAAACAGCC
[SQ_1]_3464_edge_37	CAAAAACAGGAAGATGATAATCAGAAAA
[SQ_1]_3464_edge_38	CCATCAAAAATAATTTTTAACCAATAGG
[SQ_1]_3464_edge_39	AACAGGAAAAACGCATTACCGCCAGCCA
[SQ_1]_3464_edge_40	TCTGGCCAACAGAGCAGTAATAAAAGGG
[SQ_1]_3464_edge_41	GTCACCCTCAGCAGGGCCGCTTTTGCGG
[SQ_1]_3464_edge_42	GTAATGCCACTACGATTAAACGGGTAAA
[SQ_1]_3464_edge_43	TCACCATCAATATGAGGCCGGAGACAGT
[SQ_1]_3464_edge_44	GCAAACAAGAGAATATTGCCTGAGAGTC
[SQ_1]_3464_edge_45	CAATTTTATCCTGACTATTTTGCACCCA
[SQ_1]_3464_edge_46	AGAAGGCTTATCCGAGCAAGCAAATCAG
[SQ_1]_3464_edge_47	CAGTGCCACGCTGATATTAACACCGCCT
[SQ_1]_3464_edge_48	TCTTTAATGCGCGATTTTTGAATGGCTA
[SQ_1]_3464_edge_49	TATGACCCTGTAATACGTTGTACCAAAAACATGC
[SQ_1]_3464_edge_50	AATAACCTGTTTAGCTCATTTCGCAAATGGTCGG
[SQ_1]_3464_edge_51	GTACCTTTAATTGCTCAGGTCAGGATTAGAGAAC
[SQ_1]_3464_edge_52	CAACATTATTACAGGTAAACGAACTAACGGAAAC
[SQ_1]_3464_edge_53	CCAAATCAACGTAACAACCGGATATTCATTACCA
[SQ_1]_3464_edge_54	AAATCCGCGACCTGCTCTGATAAATTGTGTCGCA
[SQ_1]_3464_edge_55	AAAAGTAAGCAGATAGCGAAGCCCTTTTTAAGAA
[SQ_1]_3464_edge_56	ACGGAATAAGTTTATTGAAACGCAAAGACACCCG
[SQ_1]_3464_edge_57	CAAGGCCGGAAACGTCGCACCATTACCATTAGGG
[SQ_1]_3464_edge_58	AACAGTGCCCGTATAAGGTCAGTGCCTTGAGTAG
[SQ_1]_3464_edge_59	GTACCGCCACCCTCAGGTACTCAGGAGGTTTAGT
[SQ_1]_3464_edge_60	ACGATCTAAAGTTTTGCCTCATAGTTAGCGTATT
[SQ_1]_3464_edge_61	CCGAGTAAAAGAGTCTATAATCAGTGAGGCCATT
[SQ_1]_3464_edge_62	CGCGCTTAATGCGCCGTAACCACCACACCCGCGT
[SQ_1]_3464_edge_63	TACGTGAACCATCACCCAGGGCGATGGCCCACAG
[SQ_1]_3464_edge_64	CACAATTCCACACAACGAAATTGTTATCCGCTGG
[SQ_1]_3464_edge_65	CGCTATTACGCCAGCTTCGGTGCGGGCCTCTTCG
[SQ_1]_3464_edge_66	CGCATCGTAACCGTGCCGTTGGTGTAGATGGGAA
[SQ_1]_3464_edge_67	TTAGGAGCACTAACAAGTTATCTAAAATATCTCA
[SQ_1]_3464_edge_68	AGAAGGAGCGGAATTAGAACAAAGAAACCACCCA
[SQ_1]_3464_edge_69	CATCGGGAGAAACAATGTAACAGTACCTTTTAAC

[SQ_1]_3464_edge_70	CCTAAATTTAATGGTTTAATTTCATCTTCTGAAC
[SQ_1]_3464_edge_71	GCATTTTCGAGCCAGTTGTAATTTAGGCAGAGGG
[SQ_1]_3464_edge_72	AGAAACCAATCAATAATAATTTACGAGCATGTGC
[SQ_2]_3464_edge_73	GACAACAACCATCGGATAGTTGCGCCGA
[SQ_2]_3464_edge_74	AAATCTCCAAAAAAATAATTTTTTCACG
[SQ_2]_3464_edge_75	ATTAACTGAACACCAGCGCATTAGACGG
[SQ_2]_3464_edge_76	TATTTATCCCAATCCAAAATAAACAGCC
[SQ_2]_3464_edge_77	CAAAAACAGGAAGATGATAATCAGAAAA
[SQ_2]_3464_edge_78	CCATCAAAAATAATTTTTAACCAATAGG
[SQ_2]_3464_edge_79	AACAGGAAAAACGCATTACCGCCAGCCA
[SQ_2]_3464_edge_80	TCTGGCCAACAGAGCAGTAATAAAAGGG
[SQ_2]_3464_edge_81	GTCACCCTCAGCAGGGCCGCTTTTGCGG
[SQ_2]_3464_edge_82	GTAATGCCACTACGATTAAACGGGTAAA
[SQ_2]_3464_edge_83	TCACCATCAATATGAGGCCGGAGACAGT
[SQ_2]_3464_edge_84	GCAAACAAGAGAATATTGCCTGAGAGTC
[SQ_2]_3464_edge_85	CAATTTTATCCTGACTATTTTGCACCCA
[SQ_2]_3464_edge_86	AGAAGGCTTATCCGAGCAAGCAAATCAG
[SQ_2]_3464_edge_87	CAGTGCCACGCTGATATTAACACCGCCT
[SQ_2]_3464_edge_88	TCTTTAATGCGCGATTTTTGAATGGCTA
[SQ_2]_3464_edge_89	ACGATCTAAAGTTTTGCCTCATAGTTAGCGTACA
[SQ_2]_3464_edge_90	GTACCGCCACCCTCAGGTACTCAGGAGGTTTACA
[SQ_2]_3464_edge_91	AACAGTGCCCGTATAAGGTCAGTGCCTTGAGTAC
[SQ_2]_3464_edge_92	CAAGGCCGGAAACGTCGCACCATTACCATTAGGT
[SQ_2]_3464_edge_93	ACGGAATAAGTTTATTGAAACGCAAAGACACCCC
[SQ_2]_3464_edge_94	AAAAGTAAGCAGATAGCGAAGCCCTTTTTAAGAG
[SQ_2]_3464_edge_95	TATGACCCTGTAATACGTTGTACCAAAAACATTG
[SQ_2]_3464_edge_96	AATAACCTGTTTAGCTCATTTCGCAAATGGTCGG
[SQ_2]_3464_edge_97	GTACCTTTAATTGCTCAGGTCAGGATTAGAGAAG
[SQ_2]_3464_edge_98	CAACATTATTACAGGTAAACGAACTAACGGAAGC
[SQ_2]_3464_edge_99	CCAAATCAACGTAACAACCGGATATTCATTACTT
[SQ_2]_3464_edge_100	AAATCCGCGACCTGCTCTGATAAATTGTGTCGAA
[SQ_2]_3464_edge_101	CGCATCGTAACCGTGCCGTTGGTGTAGATGGGAG
[SQ_2]_3464_edge_102	CGCTATTACGCCAGCTTCGGTGCGGGCCTCTTCC
[SQ_2]_3464_edge_103	CACAATTCCACACAACGAAATTGTTATCCGCTGT
[SQ_2]_3464_edge_104	TACGTGAACCATCACCCAGGGCGATGGCCCACAC
[SQ_2]_3464_edge_105	CGCGCTTAATGCGCCGTAACCACCACACCCGCCA
[SQ_2]_3464_edge_106	CCGAGTAAAAGAGTCTATAATCAGTGAGGCCACA
[SQ_2]_3464_edge_107	TTAGGAGCACTAACAAGTTATCTAAAATATCTAA
[SQ_2]_3464_edge_108	AGAAGGAGCGGAATTAGAACAAAGAAACCACCTT
[SQ_2]_3464_edge_109	CATCGGGAGAAACAATGTAACAGTACCTTTTAGC
[SQ_2]_3464_edge_110	CCTAAATTTAATGGTTTAATTTCATCTTCTGAAG
[SQ_2]_3464_edge_111	GCATTTTCGAGCCAGTTGTAATTTAGGCAGAGGG
[SQ_2]_3464_edge_112	AGAAACCAATCAATAATAATTTACGAGCATGTTG

[SQ_3]_3464_edge_113	GACAACAACCATCGGATAGTTGCGCCGA
[SQ_3]_3464_edge_114	AAATCTCCAAAAAAATAATTTTTTCACG
[SQ_3]_3464_edge_115	ATTAACTGAACACCAGCGCATTAGACGG
[SQ_3]_3464_edge_116	TATTTATCCCAATCCAAAATAAACAGCC
[SQ_3]_3464_edge_117	CAAAAACAGGAAGATGATAATCAGAAAA
[SQ_3]_3464_edge_118	CCATCAAAAATAATTTTTAACCAATAGG
[SQ_3]_3464_edge_119	AACAGGAAAAACGCATTACCGCCAGCCA
[SQ_3]_3464_edge_120	TCTGGCCAACAGAGCAGTAATAAAAGGG
[SQ_3]_3464_edge_121	GTCACCCTCAGCAGGGCCGCTTTTGCGG
[SQ_3]_3464_edge_122	GTAATGCCACTACGATTAAACGGGTAAA
[SQ_3]_3464_edge_123	TCACCATCAATATGAGGCCGGAGACAGT
[SQ_3]_3464_edge_124	GCAAACAAGAGAATATTGCCTGAGAGTC
[SQ_3]_3464_edge_125	CAATTTTATCCTGACTATTTTGCACCCA
[SQ_3]_3464_edge_126	AGAAGGCTTATCCGAGCAAGCAAATCAG
[SQ_3]_3464_edge_127	CAGTGCCACGCTGATATTAACACCGCCT
[SQ_3]_3464_edge_128	TCTTTAATGCGCGATTTTTGAATGGCTA
[SQ_3]_3464_edge_129	AGAAACCAATCAATAATAATTTACGAGCATGTAT
[SQ_3]_3464_edge_130	GCATTTTCGAGCCAGTTGTAATTTAGGCAGAGTT
[SQ_3]_3464_edge_131	CCTAAATTTAATGGTTTAATTTCATCTTCTGAAC
[SQ_3]_3464_edge_132	CATCGGGAGAAACAATGTAACAGTACCTTTTACG
[SQ_3]_3464_edge_133	AGAAGGAGCGGAATTAGAACAAAGAAACCACCAT
[SQ_3]_3464_edge_134	TTAGGAGCACTAACAAGTTATCTAAAATATCTAT
[SQ_3]_3464_edge_135	CGCATCGTAACCGTGCCGTTGGTGTAGATGGGTA
[SQ_3]_3464_edge_136	CGCTATTACGCCAGCTTCGGTGCGGGCCTCTTTG
[SQ_3]_3464_edge_137	CACAATTCCACACAACGAAATTGTTATCCGCTCT
[SQ_3]_3464_edge_138	TACGTGAACCATCACCCAGGGCGATGGCCCACAG
[SQ_3]_3464_edge_139	CGCGCTTAATGCGCCGTAACCACCACACCCGCTC
[SQ_3]_3464_edge_140	CCGAGTAAAAGAGTCTATAATCAGTGAGGCCATA
[SQ_3]_3464_edge_141	TATGACCCTGTAATACGTTGTACCAAAAACATAT
[SQ_3]_3464_edge_142	AATAACCTGTTTAGCTCATTTCGCAAATGGTCTT
[SQ_3]_3464_edge_143	GTACCTTTAATTGCTCAGGTCAGGATTAGAGAAC
[SQ_3]_3464_edge_144	CAACATTATTACAGGTAAACGAACTAACGGAACG
[SQ_3]_3464_edge_145	CCAAATCAACGTAACAACCGGATATTCATTACAT
[SQ_3]_3464_edge_146	AAATCCGCGACCTGCTCTGATAAATTGTGTCGAT
[SQ_3]_3464_edge_147	ACGATCTAAAGTTTTGCCTCATAGTTAGCGTATA
[SQ_3]_3464_edge_148	GTACCGCCACCCTCAGGTACTCAGGAGGTTTATC
[SQ_3]_3464_edge_149	AACAGTGCCCGTATAAGGTCAGTGCCTTGAGTAG
[SQ_3]_3464_edge_150	CAAGGCCGGAAACGTCGCACCATTACCATTAGCT
[SQ_3]_3464_edge_151	ACGGAATAAGTTTATTGAAACGCAAAGACACCTG
[SQ_3]_3464_edge_152	AAAAGTAAGCAGATAGCGAAGCCCTTTTTAAGTA
[TR]_3464_edge_153	CCTGGGGTGCCTAAGAAGCATAAAGTGT
[TR]_3464_edge_154	GCAAGCAGCAGATTGCGGTGGTTTTTTT
[TR]_3464_edge_155	TGACGCTCAGTGGAGATCTTTTCTACGG

[TR]_3464_edge_156	ACCCACTCGTGCACGAGATCCAGTTCGA
[TR]_3464_edge_157	ACAGGAAGGCAAAAGTTTCTGGGTGAGC
[TR]_3464_edge_158	CCTGTGTGAAATTGTCATGGTCATAGCT
[TR]_3464_edge_159	AAAGTGCTCATCATCCACATAGCAGAACTT
[TR]_3464_edge_160	AGTACTCAACCAAGGCTTTTCTGTGACTGG
[TR]_3464_edge_161	TCGGTCCTCCGATCAAAAAGCGGTTAGCTC
[TR]_3464_edge_162	ATTTATCAGCAATACACGCTCACCGGCTCC
[TR]_3464_edge_163	TATTTCGTTCATCCCTATCTCAGCGATCTG
[TR]_3464_edge_164	AATTAAAAATGAAGTTCACCTAGATCCTTT
[TR]_3464_edge_165	GCCAGTTACCTTCGTATCTGCGCTCTGCTG
[TR]_3464_edge_166	AGCAGAGCGAGGTAGCCACTGGTAACAGGA
[TR]_3464_edge_167	TGTGTGCACGAACCGTTCGCTCCAAGCTGG
[TR]_3464_edge_168	GCCGCGTTGCTGGCGCCAGGAACCGTAAAA
[TR]_3464_edge_169	CTGCGGCGAGCGGTCTGCGCTCGGTCGTTC
[TR]_3464_edge_170	CCAGCTGCATTAATGTCGGGAAACCTGTCG
[TR]_3464_edge_171	AACGACGGCCAGTGCCAGTCACGACGTTGT
[TR]_3464_edge_172	GTGCGGGCCTCTTCTGTTGGGAAGGGCGAT
[TR]_3464_edge_173	GCGCTGGCAAGTGTAAAGGAGCGGGCGCTA
[TR]_3464_edge_174	ACCGAGATAGGGTTTATAAATCAAAAGAAT
[TR]_3464_edge_175	GCCACCTAAATTGTCACATTTCCCCGAAAA
[TR]_3464_edge_176	ATTGAAGCATTTATTCTTCCTTTTTCAATA

Table S3.40. Edge staples of 3-isohedral pentagonal DNA origami tiling.

Name	**Sequence**
[PT-floret]_3-isohedral_edge_1	CTTAGAAGGCTTATCCGGGCAAGCAAATCAGATA
[PT-floret]_3-isohedral_edge_2	CCGTTGCTATTTTGCACCCCTTAAATCAAGATTA
[PT-floret]_3-isohedral_edge_3	AAATCCCAATCCAAATAAAACAGCCATATTATTT
[PT-floret]_3-isohedral_edge_4	ACAAGTCAGAGGGTAATTCTGAACACCCTGAACA
[PT-floret]_3-isohedral_edge_5	TAAAAGTTACCAGAAGGAAAGCAGATAGCCGAAC
[PT-floret]_3-isohedral_edge_6	AATTATTTTGTCACAATCACACCACGGAATAAGT
[PT-floret]_3-isohedral_edge_7	TGACCATTACCATTAGCACAAAATCACCAGTAGC
[PT-floret]_3-isohedral_edge_8	TAGCGTCATACATGGCTTTTTACCGTTCCAGTAA
[PT-floret]_3-isohedral_edge_9	AGTATAGCCCGGAATAGGAGAGGGTTGATATAAG
[PT-floret]_3-isohedral_edge_10	ACGAATTTTCTGTATGGGCCAGACGTTAGTAAAT

[PT-floret]_3-isohedral_edge_11	TTGCATAACCGATATATTAACAACCATCGCCCAC
[PT-floret]_3-isohedral_edge_12	AAGCCACTACGAAGGCACGGGTAAAATACGTAAT
[PT-floret]_3-isohedral_edge_13	ATCTGATAAATTGTGTCGAGATTTGTATCATCGC
[PT-floret]_3-isohedral_edge_14	CATCGAGAACAAGCAAAACCAAGTACCGCA
[PT-floret]_3-isohedral_edge_15	CATCCTAATTTACGAGAAGAAAAATAATAT
[PT-floret]_3-isohedral_edge_16	GGTAAAGTAATTCTGTTAAAGTACCGACAA
[PT-floret]_3-isohedral_edge_17	CAGTATAAAGCCAACGTTATACAAATTCTT
[PT-floret]_3-isohedral_edge_18	GTTAATTTCATCTTCTTTTCAAATATATTT
[PT-floret]_3-isohedral_edge_19	GACGCTGAGAAGAGTCCGATAGCTTAGATT
[PT-floret]_3-isohedral_edge_20	ATGAAACAAACATCAATGAGCAAAAGAAGA
[PT-floret]_3-isohedral_edge_21	CAAACAATTCGACAACGAAGTATTAGACTT
[PT-floret]_3-isohedral_edge_22	TATTAACACCGCCTGCGAGGTGAGGCGGTC
[PT-floret]_3-isohedral_edge_23	ATTTTGACGCTCAATCTCATGGAAATACCT
[PT-floret]_3-isohedral_edge_24	TTAGACAGGAACGGTAGCCGATTAAAGGGA
[PT-floret]_3-isohedral_edge_25	GGAGCGGGCGCTAGGGAGGGAAGAAAGCGA
[PT-floret]_3-isohedral_edge_26	CAAGTTTTTTGGGGTCGAACCATCACCCAA
[PT-floret]_3-isohedral_edge_27	AACCGAACTGACCAGACGGTCAATCATA
[PT-floret]_3-isohedral_edge_28	CGTAACAAAGCTGCTCTCATTACCCAAATCAAAG
[PT-floret]_3-isohedral_edge_29	ATAAAACGAACTAACGAGAAAAATCTACGTTATC
[PT-floret]_3-isohedral_edge_30	AGGTCAGGATTAGAGAGGAAGCAAACTCCAACGC
[PT-floret]_3-isohedral_edge_31	GAGTAGATTTAGTTTGTCCCAATTCTGCGAACTA
[PT-floret]_3-isohedral_edge_32	ATCCAATAAATCATAATAGTAGTAGCAT
[PT-floret]_3-	GTTGTACCAAAAACGAGCATAAAGCTAA

isohedral_edge_33	
[PT-floret]_3-isohedral_edge_34	TAAAGATTCAAAAGGCCTGAGTAATGTGTA
[PT-floret]_3-isohedral_edge_35	CGTAAAACTAGCATGAATCGATGAACGGTA
[PT-floret]_3-isohedral_edge_36	TGCGGGCCTCTTCGGTTGGGAAGGGCGATC
[PT-floret]_3-isohedral_edge_37	GTACAGCGCCATGTGGAAACAATCGGCGAA
[PT-floret]_3-isohedral_edge_38	TTGCCGCCAGCAGTACTTAAATTTCTGC
[PT-floret]_3-isohedral_edge_39	GTGATGAAGGGTAACCGCACAGGCGGCC
[PT-floret]_3-isohedral_edge_40	TAGAACGTCAGCGTCGGAACGTGCCGGACT
[PT-floret]_3-isohedral_edge_41	CACTGTTGCCCTGCTTGCGGTATGAGCCGG
[PT-floret]_3-isohedral_edge_42	GGGAAACCTGTCGTACTGCCCGCTTTCCAG
[PT-floret]_3-isohedral_edge_43	CAGGCGAAAATCCTCACGCTGGTTTGCCCC
[PT-floret]_3-isohedral_edge_44	CGTGGACTCCAACGGAGTCCACTATTAA
[PT-Cairo]_3-isohedral_edge_45	AAATTACGAGGCATAGTACATAACGCCAAAAGGA
[PT-Cairo]_3-isohedral_edge_46	AGAAATGTTTAGACTGGAAGAGGGGGTAATAGTA
[PT-Cairo]_3-isohedral_edge_47	AGGATTGCATCAAAAAGAAGTCAGAAGCAAAGCG
[PT-Cairo]_3-isohedral_edge_48	ATATAATGCTGTAGCTCAAGCTTAATTGCTGAAT
[PT-Cairo]_3-isohedral_edge_49	AGAACATCCAATAAATCATAATAGTAGTAGCATT
[PT-Cairo]_3-isohedral_edge_50	ATCCATCAATATGATATTGGAGACAGTCAAATCA
[PT-Cairo]_3-isohedral_edge_51	GCTAATATTTTGTTAAAATTTAAATTGTAAACGT
[PT-Cairo]_3-isohedral_edge_52	TGTAATGGGATAGGTCACAACGGCGGATTGACCG
[PT-Cairo]_3-isohedral_edge_53	CCCTGGTGCCGGAAACCACTTTCCGGCACCGCTT
[PT-Cairo]_3-isohedral_edge_54	CGAACCACCAGCAGAACATTAAAAATACCG
[PT-Cairo]_3-isohedral_edge_55	AACCCTTCTGACCTGATGGCCAACAGAGAT

[PT-Cairo]_3-isohedral_edge_56	AACAATATTACCGCCATGCTGGTAATATCC
[PT-Cairo]_3-isohedral_edge_57	TTTAGACAGGAACGGTGGCCGATTAAAGGG
[PT-Cairo]_3-isohedral_edge_58	CCGGCGAACGTGGCGAAGCTTGACGGGGAA
[PT-Cairo]_3-isohedral_edge_59	CGGCAAAATCCCTTATATGGTGGTTCCGAA
[PT-Cairo]_3-isohedral_edge_60	TCACTGCCCGCTTTCCATTAATTGCGTTGC
[PT-Cairo]_3-isohedral_edge_61	CAGGTCGACTCTAGAGCAAGCTTGCATGCC
[PT-Cairo]_3-isohedral_edge_62	TCTTCGCTATTACGCCGCGATCGGTGCGGG
[PT-Cairo]_3-isohedral_edge_63	AGATGGTTTAATTTAGTAGTAAATTGGG
[PT-Cairo]_3-isohedral_edge_64	ACAGACCAGGCGCATAGACAGATGAACGGTGTAT
[PT-Cairo]_3-isohedral_edge_65	TTGACCCCCAGCGATTACTAAAACACTCATCTCA
[PT-Cairo]_3-isohedral_edge_66	GATTTTGCTAAACAACTGAATTTTCTGTATGGAA
[PT-Cairo]_3-isohedral_edge_67	GTTTAGTACCGCCACCTCACCGTACTCAGGAGTA
[PT-Cairo]_3-isohedral_edge_68	TGCCCCCTGCCTATGCCCGTATAAACAG
[PT-Cairo]_3-isohedral_edge_69	GGAGGTTGAGGCAGCCGCCGCCAGCATT
[PT-Cairo]_3-isohedral_edge_70	CGGAACCAGAGCCACCTCATAATCAAAATCACGG
[PT-Cairo]_3-isohedral_edge_71	GCACCATTACCATTAGAGCAAAATCACCAGTAAT
[PT-Cairo]_3-isohedral_edge_72	CGCTAATATCAGAGAGTCAGAGGGTAATTGAGGG
[PT-Cairo]_3-isohedral_edge_73	TGCCAGTTACAAAATATTTCCAGAGCCTAATTAC
[PT-Cairo]_3-isohedral_edge_74	AACCTCCCGACTTGACGCGAGGCGTTTT
[PT-Cairo]_3-isohedral_edge_75	TACGAGCATGTAGATAATATCCCATCCT
[PT-Cairo]_3-isohedral_edge_76	TGTAATTTAGGCAGTATTTAACAACGCCAA
[PT-Cairo]_3-isohedral_edge_77	GAGAAAACTTTTTCTCGCAAGACAAAGAAC
[PT-Cairo]_3-	GTTTAACGTCAGATAATTGCGTAGATTTTC

isohedral_edge_78	
[PT-Cairo]_3-isohedral_edge_79	CAAAGAAACCACCACATTATCATTTTGCGG
[PT-Cairo]_3-isohedral_edge_80	ACTAACAACTAATATAAAATATCTTTAG
[PT-prism]_3-isohedral_edge_81	ACAGAAATAAAGAAAAATTATTTGCACG
[PT-prism]_3-isohedral_edge_82	TGAAACAAACATCAAGGAGCAAAAGAAGATGACA
[PT-prism]_3-isohedral_edge_83	ACCTTTTTAACCTCCGATAGGTCTGAGAGACTGC
[PT-prism]_3-isohedral_edge_84	GAACAAGAAAAATAATACAATAGATAAGTCCTAG
[PT-prism]_3-isohedral_edge_85	ATATAGAAGGCTTATCATAGCAAGCAAATCAGAA
[PT-prism]_3-isohedral_edge_86	TCCAGAGCCTAATTAACGCTAACGAGCG
[PT-prism]_3-isohedral_edge_87	AATTTTAAAAGTTTCTTTGCCCGAACGT
[PT-prism]_3-isohedral_edge_88	CTTTAGGAGCACTAACAGGTTATCTAAAATATTG
[PT-prism]_3-isohedral_edge_89	ACAGAGGTGAGGCGGTACCAGCAGAAGATAAAGT
[PT-prism]_3-isohedral_edge_90	TTAGACAGGAACGGTAGCCGATTAAAGGGATTTC
[PT-prism]_3-isohedral_edge_91	GGAGCGGGCGCTAGGGAGGGAAGAAAGCGAAAAG
[PT-prism]_3-isohedral_edge_92	AGTTTTTTGGGGTCGAACCATCACCCAA
[PT-prism]_3-isohedral_edge_93	CGTGGACTCCAACGGAGTCCACTATTAA
[PT-prism]_3-isohedral_edge_94	CAGGCGAAAATCCTCACGCTGGTTTGCCCC
[PT-prism]_3-isohedral_edge_95	GGGAAACCTGTCGTACTGCCCGCTTTCCAG
[PT-prism]_3-isohedral_edge_96	CAGTTTGAGGGGACTCGTAACCGTGCATCT
[PT-prism]_3-isohedral_edge_97	ACCAATAGGAACGCAAATCAGCTCATTTTT
[PT-prism]_3-isohedral_edge_98	CCCGGTTGATAATCCATGTCAATCATAT
[PT-prism]_3-isohedral_edge_99	AGAGTAATCTTGACGCTGGCTGACCTTC
[PT-prism]_3-isohedral_edge_100	TACCTTATGCGATTACTTTAATCATTGTGA

[PT-prism]_3-isohedral_edge_101	TAGTAAGAGCAACAAAAAGGAATTACGAGG
[PT-prism]_3-isohedral_edge_102	ATATGCAACTAAAGTAGCTCAACATGTTTT
[PT-prism]_3-isohedral_edge_103	AGCAATAAAGCCTCAAAGAATTAGCAAAAT
[PT-prism]_3-isohedral_edge_104	GGCCGGAGACAGTCATTCAAAAGGGTGA
[PT-prism]_3-isohedral_edge_105	CATCAGAGAGATAACCCATAATTGAGCGCTAATA
[PT-prism]_3-isohedral_edge_106	CTTACCAGAAGGAAACCGGATAGCCGAACAAAGT
[PT-prism]_3-isohedral_edge_107	GAAAGTTTATTTTGTCACAAAGACACCACGGAAT
[PT-prism]_3-isohedral_edge_108	CAGCACCATTACCATTAGAGCAAAATCACCAGTA
[PT-prism]_3-isohedral_edge_109	CCGCCGCCACCCTCAGAAAACCGCCTCCCTCAGA
[PT-prism]_3-isohedral_edge_110	GGGGTCAGTGCCTTGAGTTAATAAGTTTTAAC
[PT-prism]_3-isohedral_edge_111	GCGATTATACCAAGCGTCATCTTTGACCCC
[PT-prism]_3-isohedral_edge_112	AAAGACTTTTTCATGAAGAGGCTTTGAGGA
[PT-prism]_3-isohedral_edge_113	CAATGACAACAACCATCCGATAGTTGCGCC
[PT-prism]_3-isohedral_edge_114	ACTTTCAACAGTTTCAGGGATTTTGCTAAA
[PT-prism]_3-isohedral_edge_115	TCAGAACCGCCACCCTCTCAGAACCGCCAC

Table S3.41. Edge staples of 12-fold quasicrystal DNA origami tiling.

[SQ]_p8064_edge_1	CAACCCTAAAGTAAAACGTGCCGAACTTTAG GGTTGGCGGGCGCTAGGGCGCGAAGAAA
[SQ]_p8064_edge_2	TCCGTTGCTCGGAAAAACTGTGCGCCGAGC AACGGAGTCAAAGGGCGAAAAAGAACGTG
[SQ]_p8064_edge_3	GCTACTTTCCCTAAAACCTTCCAGAGGGAA AGTAGCTGAGACGGGCAACAGCTTTTTCT
[SQ]_p8064_edge_4	GCTACGTCATGCAAAAGACCTGGCGCA TGACGTAGCCATGGTCATAGCTGTTAGCTCGA
[SQ]_p8064_edge_5	CCGTTTTTTCTATACCTCCATAAAAGC CAGGTCATGGAGGTATAG
[SQ]_p8064_edge_6	TACAGCGCCGGCCCGTTGCCGAAAAC TGGAAGGCGGCAACGGGCC

[SQ]_p8064_edge_7	CCATTCAGGAAGGCCTAAGCTAAAACG CACAGTAGCTTAGGCCTT
[SQ]_p8064_edge_8	ATTCTCCGTGTTAGTATTAAGAAAATCG GCACGCTTAATACTAAC
[SQ]_p8064_edge_9	GCGAAAGGAACGGGTTTTGCGAAAAAG CGAGGACGCAAAACCCGT
[SQ]_p8064_edge_10	GACTCCAACCCACCAATGCTAAAAAGA CGTGCTTAGCATTGGTGG
[SQ]_p8064_edge_11	TTTCACCAGGGTGGAGGCAATAAAAGT CGCAGAATTGCCTCCACC
[SQ]_p8064_edge_12	ATTCGTAATGCTACTTTGTACAAAACAC ACGTGGTACAAAGTAGC
[SQ]_p8064_edge_13	TGGATCACCCCCAAAACACGTGTGGGGG GTGATCCACGTCTCGTCGCTGGCAACGCGGT
[SQ]_p8064_edge_14	GAGGGCCTGACTAAAATCTGCGACAGTC AGGCCCTCATGTTTACCAGTCCCGCGAAACG
[SQ]_p8064_edge_15	AATCTCGAAATTAAAAAGCACGTCAATT TCGAGATTCTGCGCAACTGTTGGGCCATTCG
[SQ]_p8064_edge_16	TATTTAAGCATCAAAATCCTCGCTGATG CTTAAATAGGGAACAAACGGCGGACCGTCGG
[SQ]_p8064_edge_17	CTCGTCATAAACATTGGGTAAAGGTTTC
[SQ]_p8064_edge_18	TCAGATAATTACCGCGCCCAATAGTTAG TATTAAGAAAATCGGCACGCTTAATACTAAC
[SQ]_p8064_edge_19	AAACAGCGAGCCTAATTTGCCAGAAGG CCTAAGCTAAAACGCACAGTAGCTTAGGCCTT
[SQ]_p8064_edge_20	GCAAGAAAATTGAGTTAAGCCCAGGCC CGTTGCCGAAAACTGGAAGGCGGCAACGGGCC
[SQ]_p8064_edge_21	CAATAGACGGAATAAGTTTATTTCTATA CCTCCATAAAAGCCAGGTCATGGAGGTATAG
[SQ]_p8064_edge_22	GCTACGTCATGCAAAAGACCTGGCGCAT GACGTAGCGTCTCTGAA
[SQ]_p8064_edge_23	GCTACTTTCCCTAAAACCTTCCAGAGGG AAAGTAGCGGTTGATAT
[SQ]_p8064_edge_24	TCCGTTGCTCGGAAAAACTGTGCGCCGA GCAACGGAAGTTAGCGT
[SQ]_p8064_edge_25	CAACCCTAAAGTAAAACGTGCCGAACT TTAGGGTTGCCTTTAATT
[SQ]_p8064_edge_26	TATTTAAGCATCAAAATCCTCGCTGAT GCTTAAATAGCAAGCAAA
[SQ]_p8064_edge_27	AATCTCGAAATTAAAAAGCACGTCAA TTTCGAGATTTTACAAAAT
[SQ]_p8064_edge_28	GAGGGCCTGACTAAAATCTGCGACAG TCAGGCCCTCATAATAAGA
[SQ]_p8064_edge_29	TGGATCACCCCCAAAACACGTGTGGG GGGTGATCCATGTCACAAT

[SQ]_p8064_edge_30	TTTACCGCAGAATGGAAAGCGCAGCT ACTTTGTACAAAACACACGTGGTACAAAGTAGC
[SQ]_p8064_edge_31	AAGTATATAAGTGCCGTCGAGAGGGT GGAGGCAATAAAAGTCGCAGAATTGCCTCCACC
[SQ]_p8064_edge_32	AACGATCCACAGACAGCCCTCATCCA CCAATGCTAAAAAGACGTGCTTAGCATTGGTGG
[SQ]_p8064_edge_33	GTATCGGAAGGCTCCAAAAGGAGACG GGTTTTGCGAAAAAGCGAGGACGCAAAACCCGT
[SQ]_p8064_edge_34	CGCGTTTTCATCGGTTTAGCGTCAGACT
[SQ]_p8064_edge_35	AAGGGATCGGGAGCTAAACAGGAGTT AGTATTAAGAAAATCGGCACGCTTAATACTAAC
[SQ]_p8064_edge_36	AACAATATATCGGCCTTGCTGGTAAGG CCTAAGCTAAAACGCACAGTAGCTTAGGCCTT
[SQ]_p8064_edge_37	CTTTAATACAATATTTTTGAATGGGCC CGTTGCCGAAAACTGGAAGGCGGCAACGGGCC
[SQ]_p8064_edge_38	ATCTTTAGGAATTGAGGAAGGTTCTAT ACCTCCATAAAAGCCAGGTCATGGAGGTATAG
[SQ]_p8064_edge_39	GCTACGTCATGCAAAAGACCTGGCGCA TGACGTAGCTTTTTTAAT
[SQ]_p8064_edge_40	GCTACTTTCCCTAAAACCTTCCAGAGG GAAAGTAGCAAAGAACGC
[SQ]_p8064_edge_41	TCCGTTGCTCGGAAAAACTGTGCGCCG AGCAACGGAAATCGCCAT
[SQ]_p8064_edge_42	CAACCCTAAAGTAAAACGTGCCGAACT TTAGGGTTGTAATATCCC
[SQ]_p8064_edge_43	TATTTAAGCATCAAAATCCTCGCTGAT GCTTAAATAGGCCGATTA
[SQ]_p8064_edge_44	AATCTCGAAATTAAAAAGCACGTCAAT TTCGAGATTAATATCCAG
[SQ]_p8064_edge_45	GAGGGCCTGACTAAAATCTGCGACAGT CAGGCCCTCGCTATTAGT
[SQ]_p8064_edge_46	TGGATCACCCCCAAAACACGTGTGGGG GGTGATCCAATCTAAAAT
[SQ]_p8064_edge_47	GGAAACATTTCATTTGAATTACCGCTA CTTTGTACAAAACACACGTGGTACAAAGTAGC
[SQ]_p8064_edge_48	GAGAAAAAATCCAATCGCAAGACGGT GGAGGCAATAAAAGTCGCAGAATTGCCTCCACC
[SQ]_p8064_edge_49	ATTTAACGTAGGGCTTAATTGAGCCAC CAATGCTAAAAAGACGTGCTTAGCATTGGTGG
[SQ]_p8064_edge_50	ATCCTAATCCTGAACAAGAAAAAACGG GTTTTGCGAAAAAGCGAGGACGCAAAACCCGT
[SQ]_p8064_edge_51	GAAGGGTTAGAACCTTATACTTCTGAAT
[SQ]_p8064_edge_52	CAACCCTAAAGTAAAACGTGCCGAACTT TAGGGTTGCGTTAATAT
[SQ]_p8064_edge_53	TCCGTTGCTCGGAAAAACTGTGCGCCGA

	GCAACGGAGGAGAGGGT
[SQ]_p8064_edge_54	GCTACTTTCCCTAAAACCTTCCAGAGGG AAAGTAGCTAAATCGGT
[SQ]_p8064_edge_55	GCTACGTCATGCAAAAGACCTGGCGCAT GACGTAGCGTACGGTGT
[SQ]_p8064_edge_56	CATCAGTCAACATTATTACAGGTCTATAC CTCCATAAAAGCCAGGTCATGGAGGTATAG
[SQ]_p8064_edge_57	GAACCGGCCTTCATCAAGAGTAAGGCCC GTTGCCGAAAACTGGAAGGCGGCAACGGGCC
[SQ]_p8064_edge_58	TATACCAACACTCATCTTTGACCAAGGCC TAAGCTAAAACGCACAGTAGCTTAGGCCTT
[SQ]_p8064_edge_59	CTCAGCAAGGCCGCTTTTGCGGGGTTAGT ATTAAGAAAATCGGCACGCTTAATACTAAC
[SQ]_p8064_edge_60	TTTGTTAATATTTAAATTGTAAAACGGGT TTTGCGAAAAAGCGAGGACGCAAAACCCGT
[SQ]_p8064_edge_61	AGCTATTCTGATAAATTAATGCCCCACCA ATGCTAAAAAGACGTGCTTAGCATTGGTGG
[SQ]_p8064_edge_62	TGTACCACCTCAGAGCATAAAGCGGTGG AGGCAATAAAAGTCGCAGAATTGCCTCCACC
[SQ]_p8064_edge_63	CTGGAAGTAAATATGCAACTAAAGCTAC TTTGTACAAAACACACGTGGTACAAAGTAGC
[SQ]_p8064_edge_64	TGGATCACCCCCAAAACACGTGTGGGGG GTGATCCAAGAAAGATT
[SQ]_p8064_edge_65	GAGGGCCTGACTAAAATCTGCGACAGTC AGGCCCTCTCTTGACAA
[SQ]_p8064_edge_66	AATCTCGAAATTAAAAAGCACGTCAATT TCGAGATTCCCAGCGAT
[SQ]_p8064_edge_67	TATTTAAGCATCAAAATCCTCGCTGATG CTTAAATAATCGTCACC
[SQ]_p8064_edge_68	GACCATAAATCAAAAGTTCAGAAAACGA
[TR]_p2820_edge_69	TCTACGGGGGTTAGTATTAAGAAAATCGG CACGCTTAATACTAAC
[TR]_p2820_edge_70	AGATCCTTTAAGGCCTAAGCTAAAACGCA CAGTAGCTTAGGCCTT
[TR]_p2820_edge_71	AGCGATCTGGGCCCGTTGCCGAAAACTGG AAGGCGGCAACGGGCC
[TR]_p2820_edge_72	ACCGGCTCCCTATACCTCCATAAAAGCC AGGTCATGGAGGTATAG
[TR]_p2820_edge_73	GCTACGTCATGCAAAAGACCTGGCGCAT GACGTAGCCTTCGGTCCTCCGATCAAAAAGC
[TR]_p2820_edge_74	GCTACTTTCCCTAAAACCTTCCAGAGGG AAAGTAGCTGAGTACTCAACCAAGGCTTTTC
[TR]_p2820_edge_75	TCCGTTGCTCGGAAAAACTGTGCGCCG AGCAACGGATAAAAGTGCTCATCATCCACATA
[TR]_p2820_edge_76	CAACCCTAAAGTAAAACGTGCCGAACT

	TTAGGGTTGTAACCCACTCGTGCACGAGATCC
[TR]_p2820_edge_77	TATTTAAGCATCAAAATCCTCGCTGAT GCTTAAATATCTGACGCTCAGTGGAGATCTTT
[TR]_p2820_edge_78	AATCTCGAAATTAAAAAGCACGTCAAT TTCGAGATTTAAATTAAAAATGAAGTTCACCT
[TR]_p2820_edge_79	GAGGGCCTGACTAAAATCTGCGACAGT CAGGCCCTCTCTATTTCGTTCATCCCTATCTC
[TR]_p2820_edge_80	TGGATCACCCCCAAAACACGTGTGGGG GGTGATCCAAGATTTATCAGCAATACACGCTC
[TR]_p2820_edge_81	GGTTAGCTCGCTACTTTGTACAAAACA CACGTGGTACAAAGTAGC
[TR]_p2820_edge_82	TGTGACTGGGGTGGAGGCAATAAAAGT CGCAGAATTGCCTCCACC
[TR]_p2820_edge_83	GCAGAACTTCCACCAATGCTAAAAAG ACGTGCTTAGCATTGGTGG
[TR]_p2820_edge_84	AGTTCGATGACGGGTTTTGCGAAAAA GCGAGGACGCAAAACCCGT
[TR]_p2820_edge_85	AAAGTGTAAGTTAGTATTAAGAAAAT CGGCACGCTTAATACTAAC
[TR]_p2820_edge_86	AACCTGTCGAAGGCCTAAGCTAAAAC GCACAGTAGCTTAGGCCTT
[TR]_p2820_edge_87	CGGTCGTTCGGCCCGTTGCCGAAAAC TGGAAGGCGGCAACGGGCC
[TR]_p2820_edge_88	ACCGTAAAACTATACCTCCATAAAAG CCAGGTCATGGAGGTATAG
[TR]_p2820_edge_89	GCTACGTCATGCAAAAGACCTGGCGC ATGACGTAGCGCTGTGTGCACGAACCGTTCGCT
[TR]_p2820_edge_90	GCTACTTTCCCTAAAACCTTCCAGAG GGAAAGTAGCTTAGCAGAGCGAGGTAGCCACTG
[TR]_p2820_edge_91	TCCGTTGCTCGGAAAAACTGTGCGCCG AGCAACGGAAAGCCAGTTACCTTCGTATCTGC
[TR]_p2820_edge_92	CAACCCTAAAGTAAAACGTGCCGAAC TTTAGGGTTGTTGCAAGCAGCAGATTGCGGTGG
[TR]_p2820_edge_93	TATTTAAGCATCAAAATCCTCGCTGAT GCTTAAATAAGCCTGGGGTGCCTAAGAAGCAT
[TR]_p2820_edge_94	AATCTCGAAATTAAAAAGCACGTCAAT TTCGAGATTTGCCAGCTGCATTAATGTCGGGA
[TR]_p2820_edge_95	GAGGGCCTGACTAAAATCTGCGACAGT CAGGCCCTCGGCTGCGGCGAGCGGTCTGCGCT
[TR]_p2820_edge_96	TGGATCACCCCCAAAACACGTGTGGGG GGTGATCCAAGGCCGCGTTGCTGGCGCCAGGA
[TR]_p2820_edge_97	CCAAGCTGGGCTACTTTGTACAAAAC ACACGTGGTACAAAGTAGC
[TR]_p2820_edge_98	GTAACAGGAGGTGGAGGCAATAAAAG TCGCAGAATTGCCTCCACC

[TR]_p2820_edge_99	GCTCTGCTGCCACCAATGCTAAAAAGA CGTGCTTAGCATTGGTGG
[TR]_p2820_edge_100	TTTTTTTGTACGGGTTTTGCGAAAAAG CGAGGACGCAAAACCCGT
[TR]_p2820_edge_101	GGTGAGCAAGTTAGTATTAAGAAAAT CGGCACGCTTAATACTAAC
[TR]_p2820_edge_102	TTTTCAATAAAGGCCTAAGCTAAAAC GCACAGTAGCTTAGGCCTT
[TR]_p2820_edge_103	CCCCGAAAAGGCCCGTTGCCGAAAAC TGGAAGGCGGCAACGGGCC
[TR]_p2820_edge_104	CAAAAGAATCTATACCTCCATAAAAG CCAGGTCATGGAGGTATAG
[TR]_p2820_edge_105	GCTACGTCATGCAAAAGACCTGGCG CATGACGTAGCGGGCGCTGGCAAGTGTAAAGGAG
[TR]_p2820_edge_106	GCTACTTTCCCTAAAACCTTCCAGAG GGAAAGTAGCCGGTGCGGGCCTCTTCTGTTGGG
[TR]_p2820_edge_107	TCCGTTGCTCGGAAAAACTGTGCGCC GAGCAACGGAAAAACGACGGCCAGTGCCAGTCA
[TR]_p2820_edge_108	CAACCCTAAAGTAAAACGTGCCGAA CTTTAGGGTTGTTCCTGTGTGAAATTGTCATGGT
[TR]_p2820_edge_109	TATTTAAGCATCAAAATCCTCGCTGA TGCTTAAATAAAACAGGAAGGCAAAAGTTTCTG
[TR]_p2820_edge_110	AATCTCGAAATTAAAAAGCACGTCA ATTTCGAGATTTTATTGAAGCATTTATTCTTCCT
[TR]_p2820_edge_111	GAGGGCCTGACTAAAATCTGCGACA GTCAGGCCCTCGTGCCACCTAAATTGTCACATTT
[TR]_p2820_edge_112	TGGATCACCCCCAAAACACGTGTGG GGGGTGATCCAAGACCGAGATAGGGTTTATAAAT
[TR]_p2820_edge_113	CGGGCGCTAGCTACTTTGTACAAAA CACACGTGGTACAAAGTAGC
[TR]_p2820_edge_114	AAGGGCGATGGTGGAGGCAATAAA AGTCGCAGAATTGCCTCCACC
[TR]_p2820_edge_115	CGACGTTGTCCACCAATGCTAAAA AGACGTGCTTAGCATTGGTGG
[TR]_p2820_edge_116	CATAGCTGTACGGGTTTTGCGAAAAA GCGAGGACGCAAAACCCGT

3.6 References

1 Qi, X. *et al.* Programming molecular topologies from single-stranded nucleic acids. *Nat. Commun.* **9**, 4579, (2018).

2 Williams, S. *et al.* in *DNA Computing. DNA 2008. Lecture Notes in Computer Science* Vol. 5347 90-101 (Springer, Berlin, Heidelberg, 2009).

3 SantaLucia, J., Jr. & Hicks, D. The thermodynamics of DNA structural motifs. *Annu. Rev. Biophys. Biomol. Struct.* **33**, 415-440, (2004).

4 Kilchherr, F. *et al.* Single-molecule dissection of stacking forces in DNA. *Science* **353**, (2016).
399
399

APPENDIX C

SUPPLEMENTAL INFORMATION FOR CHAPTER 4

S4.1 Materials and Methods

S4.1.1 Synthesis of customized DNA scaffold strands

Three customized DNA scaffold strands (p3548) were synthesized and utilized in this study. The phagemid vector with 2820 base pairs (bp) was synthesized by deleting a DNA fragment of 141 bp from pBlueScript II SK(+) vector using Q5 site-directed mutagenesis kit (New England Biolabs). For p3548, customized DNA fragments were synthesized and inserted into pBlueScript II SK(+) vector by Bio Basic Inc. (biobasic.com) to form phagemid vectors with 3548 bp. To synthesize DNA scaffold strands, the phagemid vector (3548 bp) was co-transformed into *E. coli* DH5α competent cells with a helper plasmid pSB4423, a kind gift from Dr. Stanley Brown (Niels Bohr Institute, Denmark). The DNA scaffold strands were amplified and purified as described previously[1]. The mass concentration of each strand was measured by NanoDrop™ 2000 spectrophotometer (Thermo Scientific) and converted to molar concentration using the average molecular weight of a DNA nucleotide (330 g/mol). Sequences of these scaffold strands are summarized in Section S4.4.1.

S4.1.2 Sample preparation

The M13mp18 single-stranded DNA was purchased from Bayou Biolabs (P-107, 1 μg/μL). DNA strands were used as received without further purification. Sequences of scaffold strands are summarized in Section S4.4.1.

Staple strands were categorized based on their positions and functions within the DNA origami tiles: core staples fold the scaffold strand into the designed geometry; edge staples present sticky ends and base stackings that “glue” monomer DNA origami tiles together into higher-order assemblies. All staple strands were purchased from Integrated

DNA Technologies (idtdna.com) at 100 μM in RNase-free water and were used as received without further purification. Sequences of staple strands are summarized in Section S4.4.2.

The multimeric complexes assembled from p3548 equilateral triangular tiles were prepared by mixing the p3548 scaffold strand (5 nM) and corresponding staple strands (50 nM/each) in 1× TAE/Mg^{2+} buffer (Tris base 40 mM, acetic acid 20 mM, EDTA·Na_2·12H_2O 2 mM, $(CH_3COO)_2Mg$·4H_2O 12.5 mM) and annealing the mixture from 80 °C to 20 °C in ~101 h. The annealing procedure was controlled using DNA Engine Tetrad® 2 Thermal Cycler (Bio-Rad). The samples were heated up to 80 °C, held at 80 °C for 10 min, cooled from 80 °C to 40 °C at -1 °C/min, held at 40 °C for 10 min, cooled from 40 °C to 20 °C at -0.1 °C/30 min, and held at 15 °C until use.

The lattices assembled from a single tile species were prepared by mixing the scaffold strand (25 nM), core staple strands (250 nM/each), and edge staple strands (375 nM/ea) in 1× TAE/Mg^{2+} buffer. The samples were annealed following the same procedure used for multimeric complexes.

The lattices assembled from two or more tile species were prepared in two steps. Firstly, different tile species were prepared in separate tubes by mixing the scaffold strand (25 nM), core staple strands (250 nM/each), and edge staple strands (375 nM/ea) in 1× TAE/Mg^{2+} buffer. The mixtures were heated up to 80 °C, held at 80 °C for 10 min, cooled from 80 °C to 40 °C at -1 °C/min, and held at 40 °C until Step 2. In Step 2, different tile species were mixed in one tube preheated to 40 °C, held at 40 °C for 30 min, annealed from 40 °C to 20 °C at -0.1 °C/30 min, and held at 15 °C until use.

S4.1.3 Fluorescence experiments for melting temperature measurement.

For melting temperature measurement, on one side of the square DNA origami unit, A FAM fluorophore was attached to the 3' end of an edge staple strand and a TAMRA quencher was also attached at the 5' end of edge staple strand on the opposite side, which allow the fluorophore and quencher could be placed face to face once the lattice was formed. All fluorophore and quencher strands were purchased from Integrated DNA Technologies (idtdna.com) at 100 μM with HPLC purification.

The lattices assembled with FAM fluorophore and TAMRA quencher labeled were heated up to 90 °C, held at 90 °C for 30 min, cooled from 90 °C to 45 °C at -1 °C/min, held at 45 °C for 5 min, cooled from 45 °C to 25 °C at -1 °C/5 min, and held at 25 °C until use. The samples were evaluated in "MxPro" program, Quantitative PCR mode, on Mx3000P qPCR System (Stratagene).

S4.1.4 AFM imaging

For multimeric complexes imaging, the samples were diluted to 3 nM using 1× TAE/Mg^{2+} buffer. 5 μL of the diluted sample was deposited onto a freshly cleaved mica surface (Ted Pella) and incubated for 5 min. Then, 60 μL 1× TAE/Mg^{2+} buffer was added onto the mica surface and removed by compressed air. This step was repeated twice to minimize the imaging background from excess staples. Subsequently, the mica surface was covered by 60 μL 1× TAE/Mg^{2+} buffer, and 10 μL $NiCl_2$ solution (100 mM) was added to assist adsorption. The samples were imaged in "ScanAsyst in Fluid" mode with a ScanAsyst-liquid+ tip on the MultiMode 8 AFM (Bruker).

For the imaging of lattices, the samples were diluted to 5 nM (scaffold concentration) using 1× TAE/Mg^{2+} buffer. 10 μL of the diluted sample was deposited

onto a freshly cleaved mica surface and incubated for 5 min. The rest steps were the same as the imaging of multimeric complexes.

S4.2 Designs of DNA Origami Tile

S4.2.1 Design parameters of DNA origami tiles

Table S4.1. Design parameters of three regular polygonal DNA origami tiles based on the p3548 scaffold.

Design name	**[SQ]_p3548**
Rise per base pair, ***r*** (nm)	0.332
Interhelical distance, ***D*** (nm)	2.65
Number of helices per subunit	14
Minimum helix length (bp)	34
Maximum helix length (bp)	82
Lengths of helices (bp)	34/42/50/58/ 66/74/82
Lengths of scaffold loops (nt)	10/10/12/12/10/10
Length of the scaffold bridge (nt)	11
Lengths of staple bridges (nt)	8/8/3/6/9/8

Table S4.2. Design parameters of three regular polygonal DNA origami tiles based on the M13mp18 scaffold.

Design name	**[SQ]_M13**
Rise per base pair, ***r*** (nm)	0.34
Interhelical distance, ***D*** (nm)	2.69
Number of helices per subunit	22
Minimum helix length (bp)	39
Maximum helix length (bp)	118
Lengths of helices (bp)	39/47/55/63/71/79/ 86/94/102/110/118
Lengths of scaffold loops (nt)	9/11/8/10/8/ 8/9/8/10/8
Length of the scaffold bridge (nt)	3
Lengths of staple bridges (nt)	2/4/7/6/0/ 4/7/7/1/5

S4.2.2 Tiamat designs of DNA origami tiles

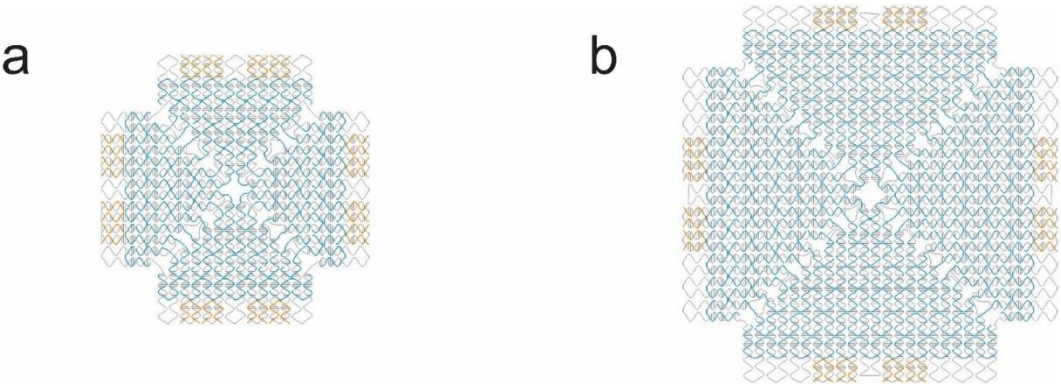

Figure S4.1. Tiamat[2] designs of DNA origami tiles for regular tilings. (a) p3548 square tile, and (b) M13mp18 square tile. The scaffold strand (gray) is folded by core staple strands (blue) into the target shape, which can be further linked together by edge staple strands (orange) into 2D lattices.

S4.3 Additional AFM Images

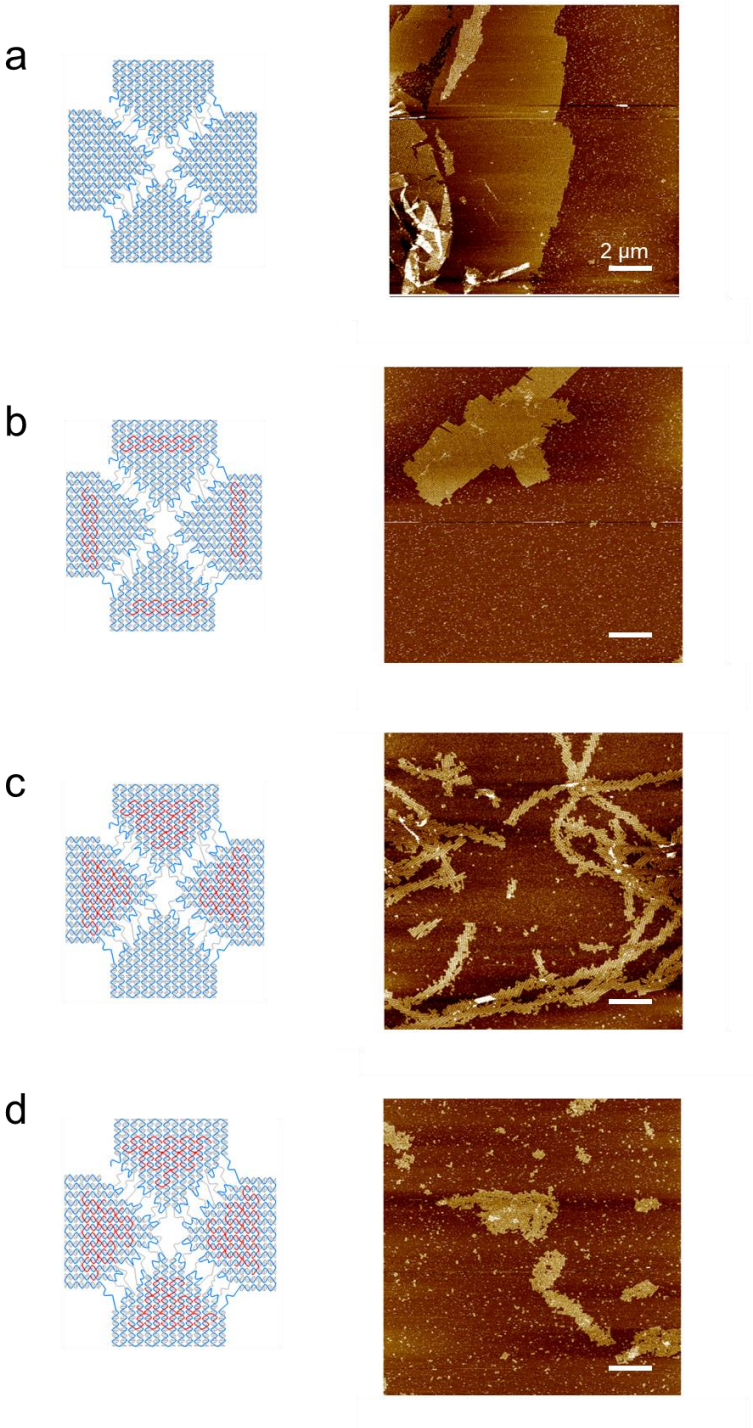

Figure S4.2. AFM images of 2D lattice assembled from M13mp18 square DNA origami, (a) without any poly A surface labeling strands, (b) with five poly A surface labeling strands in each subunit, (c) with ten poly A surface labeling strands in three of the four subunits, (d) with ten poly A surface labeling strands in each subunit.

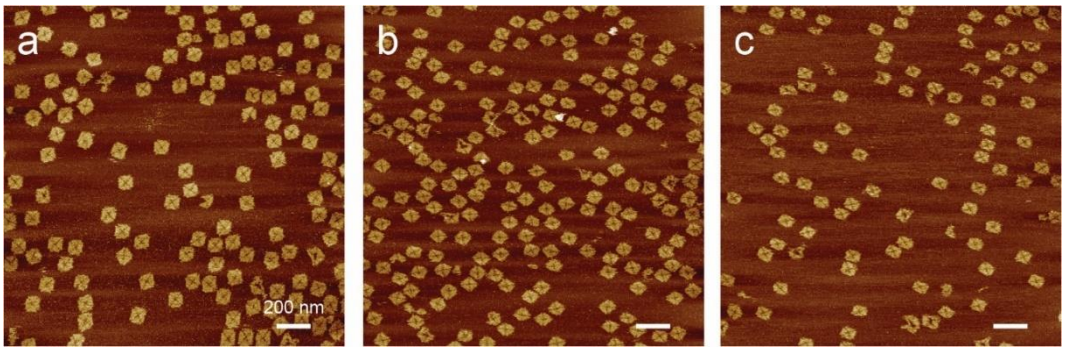

Figure S4.3. AFM images of M13mp18 square DNA origami monomers annealed end at (a) 40 °C, (b) 45 °C and (c) 50 °C.

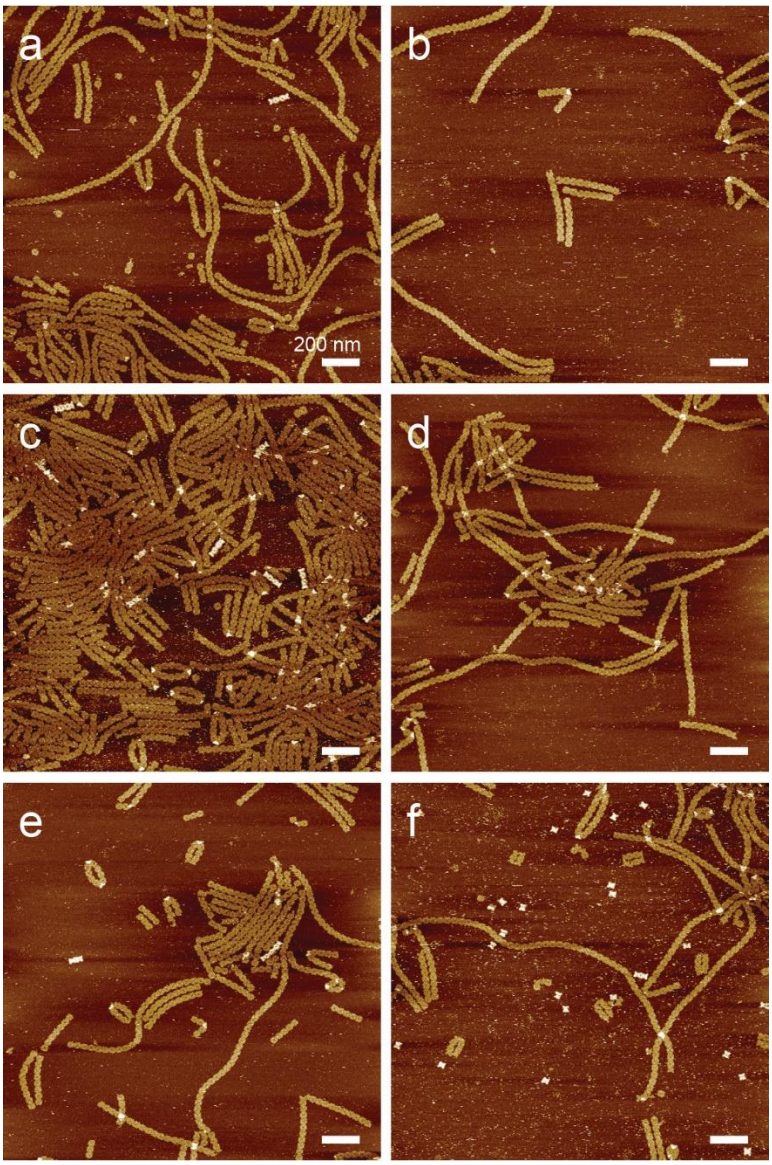

Figure S4.4. AFM images of 2D linear structure assembled from M13mp18 square DNA seed origami, type B (a, c, and e) and type R (b, d, and f). The tile-tile interaction of square DNA origami units is provided by 2-nt sticky end (a and b), 3-nt sticky end (c and d), and 4-nt sticky end (e and f).

S4.4 DNA Sequences

S4.4.1 Sequences of scaffold strands

S4.4.1.1 Sequence of the customized p3548 scaffold

GTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAA
ATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCA
ATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTT
ATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTG
GTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCG
AACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACG
TTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCC
GTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAA
TGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATG
ACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGG
CCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTT
GCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTG
AATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGG
CAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGG
CAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGC
GCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAG
CGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCC
GTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAA
TAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCA
GACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTT
AAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTA
ACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGA
TCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAA
ACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTT
TTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCT
AGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACA
TACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTC
GTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGG
TCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT
ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC
CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGG
AGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCT
GTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGG
GGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTG
GCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCT
GTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCC
GAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAA
TACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAC
GACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGA

GTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGT
ATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCT
GGAGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTG
CAGGAATTCTGACGGTCTCACTGTTCGGTCATTGTGACACGTCGAGAAGTCCT
GCCACTGTACGAGAGTTTTTTCCGCAGTACAGCTTCCTTTTACGGGCCTTCTC
CCTCTTTTTTCGGATAGAAGGTATCTTGATACACATGGGTCGTTCGATGTGCA
TCAGACTTCAAGGTGACGTCGAATTGCACCACTCTTCCGACTACACGCACGCT
TTTTTCCTAACGTGTACAAGGTTTTACCATGCCAGGGTTGCTTTTTTCCTATCC
TGGTTGGAGCGGACTGCGTTTCGTGCTGGCCGAATAATTGCTGCGCTGAGGCT
AGGCGTTGGCTTATCTTGCCCCGATGGATAACTTCTTTTTTCCAACTATCCACC
CGATTTTGAGCTCTCTGCGTATCTTTTTTCCCTGGCAGATTTGTCGTTGATTTT
GTCCGTAGTCCGCTGATGCCAGTATCAGATGCCGGCGAGTCACGTTAAGCCA
GGGATCTCGATTGGTGACTTTTTTCCTGTCAATCGCTCAATTTTCACGCCACC
AGTCTTGTTTTTTCTGAGCTGGTTCTACGTGGGTACGAACGTACAGACAGATG
AGCTCACCATTGCACCAAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCC
CGGTACCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTC
GTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCT
TGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACC
GATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCT
GTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGC
TACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCT
CGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAG
GGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGT
GATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGAC
GTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACAC
TCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGG
CCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAAC
AAAATATTAACGCTTACAATTTAG

S4.4.1.2 Sequence of the M13mp18 scaffold

TGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGG
ACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTG
ATTTATAAGGGATTTTGCCGATTTCGGAACCACCATCAAACAGGATTTTCGCC
TGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGC
GGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACC
CTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAAT
GCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACG
CAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATG
CTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGG
AAACAGCTATGACCATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCT
AGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGT
CGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATC
CCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC
CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTTGCCTGGTTTCCGGCA
CCAGAAGCGGTGCCGGAAAGCTGGCTGGAGTGCGATCTTCCTGAGGCCGATA
CTGTCGTCGTCCCCTCAAACTGGCAGATGCACGGTTACGATGCGCCCATCTAC
ACCAACGTGACCTATCCCATTACGGTCAATCCGCCGTTTGTTCCCACGGAGAA
TCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAAGCTGGCTACAGG
AAGGCCAGACGCGAATTATTTTTGATGGCGTTCCTATTGGTTAAAAAATGAG
CTGATTTAACAAAAATTTAATGCGAATTTTAACAAAATATTAACGTTTACAAT
TTAAATATTTGCTTATACAATCTTCCTGTTTTTGGGGCTTTTCTGATTATCAAC
CGGGGTACATATGATTGACATGCTAGTTTTACGATTACCGTTCATCGATTCTC
TTGTTTGCTCCAGACTCTCAGGCAATGACCTGATAGCCTTTGTAGATCTCTCA
AAAATAGCTACCCTCTCCGGCATTAATTTATCAGCTAGAACGGTTGAATATCA
TATTGATGGTGATTTGACTGTCTCCGGCCTTTCTCACCCTTTTGAATCTTTACC
TACACATTACTCAGGCATTGCATTTAAAATATATGAGGGTTCTAAAAATTTTT
ATCCTTGCGTTGAAATAAAGGCTTCTCCCGCAAAAGTATTACAGGGTCATAAT
GTTTTTGGTACAACCGATTTAGCTTTATGCTCTGAGGCTTTATTGCTTAATTTT
GCTAATTCTTTGCCTTGCCTGTATGATTTATTGGATGTTAATGCTACTACTATT
AGTAGAATTGATGCCACCTTTTCAGCTCGCGCCCCAAATGAAAATATAGCTA
AACAGGTTATTGACCATTTGCGAAATGTATCTAATGGTCAAACTAAATCTACT
CGTTCGCAGAATTGGGAATCAACTGTTATATGGAATGAAACTTCCAGACACC
GTACTTTAGTTGCATATTTAAAACATGTTGAGCTACAGCATTATATTCAGCAA
TTAAGCTCTAAGCCATCCGCAAAAATGACCTCTTATCAAAAGGAGCAATTAA
AGGTACTCTCTAATCCTGACCTGTTGGAGTTTGCTTCCGGTCTGGTTCGCTTTG
AAGCTCGAATTAAAACGCGATATTTGAAGTCTTTCGGGCTTCCTCTTAATCTT
TTTGATGCAATCCGCTTTGCTTCTGACTATAATAGTCAGGGTAAAGACCTGAT
TTTTGATTTATGGTCATTCTCGTTTTCTGAACTGTTTAAAGCATTTGAGGGGGA
TTCAATGAATATTTATGACGATTCCGCAGTATTGGACGCTATCCAGTCTAAAC
ATTTTACTATTACCCCCTCTGGCAAAACTTCTTTTGCAAAAGCCTCTCGCTATT
TTGGTTTTTATCGTCGTCTGGTAAACGAGGGTTATGATAGTGTTGCTCTTACT
ATGCCTCGTAATTCCTTTTGGCGTTATGTATCTGCATTAGTTGAATGTGGTATT
CCTAAATCTCAACTGATGAATCTTTCTACCTGTAATAATGTTGTTCCGTTAGTT

CGTTTTATTAACGTAGATTTTTCTTCCCAACGTCCTGACTGGTATAATGAGCC
AGTTCTTAAAATCGCATAAGGTAATTCACAATGATTAAAGTTGAAATTAAAC
CATCTCAAGCCCAATTTACTACTCGTTCTGGTGTTTCTCGTCAGGGCAAGCCT
TATTCACTGAATGAGCAGCTTTGTTACGTTGATTTGGGTAATGAATATCCGGT
TCTTGTCAAGATTACTCTTGATGAAGGTCAGCCAGCCTATGCGCCTGGTCTGT
ACACCGTTCATCTGTCCTCTTTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTG
ACCGTCTGCGCCTCGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTCG
ACACAATTTATCAGGCGATGATACAAATCTCCGTTGTACTTTGTTTCGCGCTT
GGTATAATCGCTGGGGGTCAAAGATGAGTGTTTTAGTGTATTCTTTTGCCTCT
TTCGTTTTAGGTTGGTGCCTTCGTAGTGGCATTACGTATTTTACCCGTTTAATG
GAAACTTCCTCATGAAAAAGTCTTTAGTCCTCAAAGCCTCTGTAGCCGTTGCT
ACCCTCGTTCCGATGCTGTCTTTCGCTGCTGAGGGTGACGATCCCGCAAAAGC
GGCCTTTAACTCCCTGCAAGCCTCAGCGACCGAATATATCGGTTATGCGTGGG
CGATGGTTGTTGTCATTGTCGGCGCAACTATCGGTATCAAGCTGTTTAAGAAA
TTCACCTCGAAAGCAAGCTGATAAACCGATACAATTAAAGGCTCCTTTTGGA
GCCTTTTTTTTGGAGATTTTCAACGTGAAAAAATTATTATTCGCAATTCCTTTA
GTTGTTCCTTTCTATTCTCACTCCGCTGAAACTGTTGAAAGTTGTTTAGCAAA
ATCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACGACAAAACTTTA
GATCGTTACGCTAACTATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGT
TTGTACTGGTGACGAAACTCAGTGTTACGGTACATGGGTTCCTATTGGGCTTG
CTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGG
CGGTTCTGAGGGTGGCGGTACTAAACCTCCTGAGTACGGTGATACACCTATTC
CGGGCTATACTTATATCAACCCTCTCGACGGCACTTATCCGCCTGGTACTGAG
CAAAACCCCGCTAATCCTAATCCTTCTCTTGAGGAGTCTCAGCCTCTTAATAC
TTTCATGTTTCAGAATAATAGGTTCCGAAATAGGCAGGGGGCATTAACTGTTT
ATACGGGCACTGTTACTCAAGGCACTGACCCCGTTAAAACTTATTACCAGTAC
ACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCA
GAGACTGCGCTTTCCATTCTGGCTTTAATGAGGATTTATTTGTTTGTGAATATC
AAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTGGCGGCGGCTCT
GGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGGTT
CTGAGGGTGGCGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGG
TGATTTTGATTATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGAA
AATGCCGATGAAAACGCGCTACAGTCTGACGCTAAAGGCAAACTTGATTCTG
TCGCTACTGATTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGC
CTTGCTAATGGTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAAT
GGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAAT
ATTTACCTTCCCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCGCTG
GTAAACCATATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGT
GTCTTTGCGTTTCTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTG
CTAACATACTGCGTAATAAGGAGTCTTAATCATGCCAGTTCTTTTGGGTATTC
CGTTATTATTGCGTTTCCTCGGTTTCCTTCTGGTAACTTTGTTCGGCTATCTGC
TTACTTTTCTTAAAAAGGGCTTCGGTAAGATAGCTATTGCTATTTCATTGTTTC
TTGCTCTTATTATTGGGCTTAACTCAATTCTTGTGGGTTATCTCTCTGATATTA
GCGCTCAATTACCCTCTGACTTTGTTCAGGGTGTTCAGTTAATTCTCCCGTCTA
ATGCGCTTCCCTGTTTTTATGTTATTCTCTCTGTAAAGGCTGCTATTTTCATTTT

TGACGTTAAACAAAAAATCGTTTCTTATTTGGATTGGGATAAATAATATGGCT
GTTTATTTTGTAACTGGCAAATTAGGCTCTGGAAAGACGCTCGTTAGCGTTGG
TAAGATTCAGGATAAAATTGTAGCTGGGTGCAAAATAGCAACTAATCTTGAT
TTAAGGCTTCAAAACCTCCCGCAAGTCGGGAGGTTCGCTAAAACGCCTCGCG
TTCTTAGAATACCGGATAAGCCTTCTATATCTGATTTGCTTGCTATTGGGCGC
GGTAATGATTCCTACGATGAAAATAAAAACGGCTTGCTTGTTCTCGATGAGT
GCGGTACTTGGTTTAATACCCGTTCTTGGAATGATAAGGAAAGACAGCCGAT
TATTGATTGGTTTCTACATGCTCGTAAATTAGGATGGGATATTATTTTTCTTGT
TCAGGACTTATCTATTGTTGATAAACAGGCGCGTTCTGCATTAGCTGAACATG
TTGTTTATTGTCGTCGTCTGGACAGAATTACTTTACCTTTTGTCGGTACTTTAT
ATTCTCTTATTACTGGCTCGAAAATGCCTCTGCCTAAATTACATGTTGGCGTT
GTTAAATATGGCGATTCTCAATTAAGCCCTACTGTTGAGCGTTGGCTTTATAC
TGGTAAGAATTTGTATAACGCATATGATACTAAACAGGCTTTTTCTAGTAATT
ATGATTCCGGTGTTTATTCTTATTTAACGCCTTATTTATCACACGGTCGGTATT
TCAAACCATTAAATTTAGGTCAGAAGATGAAATTAACTAAAATATATTTGAA
AAAGTTTTCTCGCGTTCTTTGTCTTGCGATTGGATTTGCATCAGCATTTACATA
TAGTTATATAACCCAACCTAAGCCGGAGGTTAAAAAGGTAGTCTCTCAGACC
TATGATTTTGATAAATTCACTATTGACTCTTCTCAGCGTCTTAATCTAAGCTAT
CGCTATGTTTTCAAGGATTCTAAGGGAAAATTAATTAATAGCGACGATTTACA
GAAGCAAGGTTATTCACTCACATATATTGATTTATGTACTGTTTCCATTAAAA
AAGGTAATTCAAATGAAATTGTTAAATGTAATTAATTTTGTTTTCTTGATGTTT
GTTTCATCATCTTCTTTTGCTCAGGTAATTGAAATGAATAATTCGCCTCTGCGC
GATTTTGTAACTTGGTATTCAAAGCAATCAGGCGAATCCGTTATTGTTTCTCC
CGATGTAAAAGGTACTGTTACTGTATATTCATCTGACGTTAAACCTGAAAATC
TACGCAATTTCTTTATTTCTGTTTTACGTGCAAATAATTTTGATATGGTAGGTT
CTAACCCTTCCATTATTCAGAAGTATAATCCAAACAATCAGGATTATATTGAT
GAATTGCCATCATCTGATAATCAGGAATATGATGATAATTCCGCTCCTTCTGG
TGGTTTCTTTGTTCCGCAAAATGATAATGTTACTCAAACTTTTAAAATTAATA
ACGTTCGGGCAAAGGATTTAATACGAGTTGTCGAATTGTTTGTAAAGTCTAAT
ACTTCTAAATCCTCAAATGTATTATCTATTGACGGCTCTAATCTATTAGTTGTT
AGTGCTCCTAAAGATATTTTAGATAACCTTCCTCAATTCCTTTCAACTGTTGAT
TTGCCAACTGACCAGATATTGATTGAGGGTTTGATATTTGAGGTTCAGCAAGG
TGATGCTTTAGATTTTTCATTTGCTGCTGGCTCTCAGCGTGGCACTGTTGCAG
GCGGTGTTAATACTGACCGCCTCACCTCTGTTTTATCTTCTGCTGGTGGTTCGT
TCGGTATTTTTAATGGCGATGTTTTAGGGCTATCAGTTCGCGCATTAAAGACT
AATAGCCATTCAAAAATATTGTCTGTGCCACGTATTCTTACGCTTTCAGGTCA
GAAGGGTTCTATCTCTGTTGGCCAGAATGTCCCTTTTATTACTGGTCGTGTGA
CTGGTGAATCTGCCAATGTAAATAATCCATTTCAGACGATTGAGCGTCAAAA
TGTAGGTATTTCCATGAGCGTTTTTCCTGTTGCAATGGCTGGCGGTAATATTG
TTCTGGATATTACCAGCAAGGCCGATAGTTTGAGTTCTTCTACTCAGGCAAGT
GATGTTATTACTAATCAAAGAAGTATTGCTACAACGGTTAATTTGCGTGATGG
ACAGACTCTTTTACTCGGTGGCCTCACTGATTATAAAAACACTTCTCAGGATT
CTGGCGTACCGTTCCTGTCTAAAATCCCTTTAATCGGCCTCCTGTTTAGCTCCC
GCTCTGATTCTAACGAGGAAAGCACGTTATACGTGCTCGTCAAAGCAACCAT
AGTACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCG

CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCT
TCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGG
GGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAA
CTTGATTTGGGTGATGGTTCACGTAGTGGGCCATCGCCC

S4.4.2 Sequences of staple strands

S4.4.2.1 Staple strand sequences of p3548 square tiles for multimerization

Table S4.3. Core staples of p3548 square DNA origami tile.

Name	Sequence
[SQ]_p3548_core_1	CTAAATTGTAAGCGTTAAAAATCAGCTCATTTTAAAAGAAT
[SQ]_p3548_core_2	TATAAATCTTAACCAATAGTTTTTTTTATTGTCTCATGTCAATATT
[SQ]_p3548_core_3	ATTGAAGCATTTTTTTTTTGCAAAATCCCT
[SQ]_p3548_core_4	GACTCCAACGTCAAAGGGCTTTTCTGGGTGAGC
[SQ]_p3548_core_5	AAGTGCTCCTTCAGCATCTTTTACTTTTTTTTTCTATCAGGGCG
[SQ]_p3548_core_6	AGACCGAAGAGTCCACTATTAACCTAATCA
[SQ]_p3548_core_7	TAGAGCTTCTACGTGAACCATCACAGAACGTG
[SQ]_p3548_core_8	GGAGCGGGGAACGTGGCGATTTTTTTTTCCACATAGCAGTTGCCCGG
[SQ]_p3548_core_9	ATGGCCCAGACGGGGAAAGCCGGCCGCTAGGG
[SQ]_p3548_core_10	AGTTTTTAACCCTAAAGGGAGCTGCGCGTA
[SQ]_p3548_core_11	GCGCAACTAGTGTAGCGGTCACGCCCCCGATT
[SQ]_p3548_core_12	CGTCAATACGGTTTTTTTTAGAAAGCGAAA
[SQ]_p3548_core_13	CCTCTTCGCTATTTTTTTTAGGACTTCTCG
[SQ]_p3548_core_14	CGCTGGCAGTTGGGAAGGGCGATCATGTGCTG
[SQ]_p3548_core_15	ACCACCAGCGTCCCATTCGCCACAGGGTTT
[SQ]_p3548_core_16	CGAATTGGTTAAGTTGGGTAACGCTTCAGGCT
[SQ]_p3548_core_17	ACGTGTCAGGAAAAAACTCTTTTTTTTTGCGAAAGGGGGGGTGCGGG
[SQ]_p3548_core_18	CAAGGCGAGTACCGGGCCCCCCCTCGATTTTTTGTGTAGTCGGA
[SQ]_p3548_core_19	ACCTTGTACACGTTAGGAATTTATCGATAAGC
[SQ]_p3548_core	TCCCAGTGCGTAATACGACTCACTCATCTG

_20	
[SQ]_p3548_core_21	TTTGGTGCAATGGTGAGCTATAGGG
[SQ]_p3548_core_22	GAGCGATTGACTTTTTTTTGCCTAGCCTCA
[SQ]_p3548_core_23	TCTGTACACAAGACTGGTGGCGGATCCCTG
[SQ]_p3548_core_24	GCGCAGCAATCGGGGCAAGTTTTTTTTTCACCAATCGATGAAAATT
[SQ]_p3548_core_25	GCTTAACGGACTACGGACAAAATCA
[SQ]_p3548_core_26	CGTAAAAAGGCCGCGTTGCGAGCATCACAAAAATAAAGATA
[SQ]_p3548_core_27	CAGGACTATCGACGCTCAATTTTTTTTTCAAAGGCGGTTTCGGCTG
[SQ]_p3548_core_28	CGGCGAGCGGTTTTTTTTTGCGAAACCCGA
[SQ]_p3548_core_29	GATACCTGTCCGCCTTTCTTTTTTAATGAATCG
[SQ]_p3548_core_30	ATTCCACACAGTCGGGAAACCTGTCGTTTTTTTAGCGTGGCGCT
[SQ]_p3548_core_31	CCAGGCGTGTTCCGACCCTGCCTCTCAGTT
[SQ]_p3548_core_32	TGCGCCTTGCTCACGCTGTAGGTAGCTTACCG
[SQ]_p3548_core_33	CACTGGCACTTGAGTCCAATTTTTTTTTAAATTGTTATCCGTAATCA
[SQ]_p3548_core_34	TTCTCATAATCCGGTAACTATCGTGCAGCCAC
[SQ]_p3548_core_35	CGGTGTAAACCCCCCGTTCAGCGTATGTAG
[SQ]_p3548_core_36	GGTATCTGGGATTAGCAGAGCGAGCCGACCGC
[SQ]_p3548_core_37	TGGTCATAGCTTTTTTTTTCGACTTATCGC
[SQ]_p3548_core_38	CGGAAAAAGAGTTTTTTTTAGTTGGCCGCA
[SQ]_p3548_core_39	TGGTAACACGCTCTGCTGAAGCCACAAACCAC
[SQ]_p3548_core_40	GCGGTGCGCTACACTAGAAGGATTGCAAGC
[SQ]_p3548_core_41	GACGCTCAGCGGTGGTTTTTTTGTCAGTATTT
[SQ]_p3548_core_42	GTGTTATCTCCTCCGATCGTTTTTTTTTGATCCGGCAAAGTTACCTT

[SQ]_p3548_core_43	CGCTGGTAGTGGAACGAAAACTCACGTTTTTTTTGCCATTGCTA
[SQ]_p3548_core_44	TCGCCAGTTAATAGTTTGCTTTTGGTCATGAGA
[SQ]_p3548_core_45	AGCAGATCTTTGATCTTTTCTATCACCTAG
[SQ]_p3548_core_46	TTATCAAAAAGGATCTCGGGGTCT
[SQ]_p3548_core_47	TGACAGTTACCTTTTTTTTCCGGAAGGGCC
[SQ]_p3548_core_48	ATCCTTTAGTATATATGAGTAACTATCTCA
[SQ]_p3548_core_49	GAGCGCAGTATCAGCAATATTTTTTTTCAGTGAGGCACACTTGGTC
[SQ]_p3548_core_50	GCGATCTCCCGTCGTGTAGATAACT
[SQ]_p3548_core_51	GCCAGGGAAAAAAGATACAAAAAGAAGTTATCCATTATTCG
[SQ]_p3548_core_52	GCCAGCAAAAAGCAACCCTGGCTTGAAGTC
[SQ]_p3548_core_53	GCCCGTAAGCAATTCGACGTCACCATGGTAAA
[SQ]_p3548_core_54	AGAGTGGTAAGGAAGCTGTACTGCCAATGACC
[SQ]_p3548_core_55	TGATGCACTATCCGAAAAAAGATGCAGCCC
[SQ]_p3548_core_56	AGTGAGGGAGACCGTCAGAATTCCGGGAGAAG
[SQ]_p3548_core_57	GAACAGTGTTAATTGCGCGCTTGGCGCTCACA
[SQ]_p3548_core_58	GGGGGATGAGCTCCAGCTTTTGAGCATAAA
[SQ]_p3548_core_59	CCGCTTTCCAACATACGAGCCGGATTCCCTTT
[SQ]_p3548_core_60	GTGTAAAATTAATTGCGTTGCGAGGCGGTT
[SQ]_p3548_core_61	GCCAACGCGCGGGGAGCTCACTGC
[SQ]_p3548_core_62	TGCGTATCGCTGCGCTCGGTCGAATACGGT
[SQ]_p3548_core_63	TATCCACGAGCAAAAGGCCAGCAAA
[SQ]_p3548_core_64	GGGCTTACCATCTGGCCCCACCGGCTCCAGATTAAGTGGTC
[SQ]_p3548_core	CTGCAACGCCGGGAAGCTAGAGCGTTTGGT

_65	
[SQ]_p3548_core_66	CAAAAAAGGTGGTGTCACGCTCGTTAAGTAGT
[SQ]_p3548_core_67	CAGGCATCCGGTTAGCTCCTTCGGACTCATGG
[SQ]_p3548_core_68	ATGGCTTGTTACATGATCCCCCTTACTGTC
[SQ]_p3548_core_69	GTGTATGCGCACTGCATAATTCTCATGTTGTG
[SQ]_p3548_core_70	TTATGGCAGGCGACCGAGTTGCTCAACTTTAA
[SQ]_p3548_core_71	ATGCCATTCAACCAAGTCATTCCTTCGGGG
[SQ]_p3548_core_72	CAACTGATATCATTGGAAAACGTTTGAGAATA
[SQ]_p3548_core_73	CGAAAACTCGATGTAACCCACTAATGCCGC
[SQ]_p3548_core_74	AAAAACAGGAAGGCAACGTGCACC
[SQ]_p3548_core_75	AAAAAAGCATACTCTTCCTTTTAGCGGATA
[SQ]_p3548_core_76	CATATTTTCCGCGCACATTTCCCCG

Table S4.4. Edge staples of p3548 square DNA origami seed origami type R.

[SQ]_p3548_seed_origami_type R_1	ATATAAACAAATAGGGGTGAATGTATTTAG AAAA
[SQ]_p3548_seed_origami_type R_2	CTGGAAATGTTGAATACTGGAATAAGGGCG ACAC
[SQ]_p3548_seed_origami_type R_3	TGGCTGTTGAGATCCAGTTCTCAAGGATCT TACC
[SQ]_p3548_seed_origami_type R_4	GCTGTGACTGGTGAGTACCCGTAAGATGCT TTTC
[SQ]_p3548_seed_origami_type R_5	ATCCAACGATCAAGGCGACATTCAGCTCCG GTTC
[SQ]_p3548_seed_origami_type R_6	CTCAGTCTATTAATTGTTTTTATCCGCCTCC ATC
[SQ]_p3548_seed_origami_type R_7	ACCCGCGAGACCCACGCTCAGTGCTGCAAT GATA
[SQ]_p3548_seed_origami_type R_8	CGGGTGGATAGTTGGAGCAGAGAGCTCAA A
[SQ]_p3548_seed_origami_type R_9	CCAACCAGGATAGGAACGAAACGCAGTCC G

[SQ]_p3548_seed_origami_type R_10	TGTATCAAGATACCTTCATCGAACGACCCA
[SQ]_p3548_seed_origami_type R_11	GGCCGCCACCGCGGTGCCACTAGTTCTAGA
[SQ]_p3548_seed_origami_type R_12	GAGTGAGCTAACTCACGCCTGGGGTGCCTA
[SQ]_p3548_seed_origami_type R_13	TCCTCGCTCACTGACTTGGGCGCTCTTCCG
[SQ]_p3548_seed_origami_type R_14	GCAGGAAAGAACATGTAGAATCAGGGGAT A
[SQ]_p3548_seed_origami_type R_15	GCGTTAAATTTTTGTTTATTTTGTTAAAATT CCA
[SQ]_p3548_seed_origami_type R_16	GTTCCAGTTTGGAACAGATAGGGTTGAGTG TTTT
[SQ]_p3548_seed_origami_type R_17	AACCAGCTCAGAAAAAGTTCGTACCCACGT AGCC
[SQ]_p3548_seed_origami_type R_18	TGATACTGGCATCAGCGTGACTCGCCGGCA TCGG
[SQ]_p3548_seed_origami_type R_19	GTGTCGTAGACACCATAGTTGCCTGACTCG TCTAT TTCGTTCATCGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type R_20	GTGTCGTAGACACTTTTAAATCAATCTAAT AAATT AAAAATGAAGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type R_21	GTGTCGTAGACACGGATCTCAAGAAGATCT ACGC GCAGAAAAAAAGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type R_22	GTGTCGTAGACACTGGTGGCCTAACTACGT ACAG AGTTCTTGAAGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type R_23	GTGTCGTAGACACCTGGGCTGTGTGCACGG GTCG TTCGCTCCAAGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type R_24	GTGTCGTAGACACCCCTCGTGCGCTCTCCTT TCCC CCTGGAAGCTGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type R_25	GTGTCGTAGACACGGCTCCGCCCCCCTGAC TGGC GTTTTTCCATAGTGTCGTAGACAC

Table S4.5. Edge staples of p3548 square DNA origami seed origami type B.

[SQ]_p3548_seed_origami_type B_1	GCGTTAAATTTTTGTTTATTTTGTTAAAATT CCA
[SQ]_p3548_seed_origami_type B_2	GTTCCAGTTTGGAACAGATAGGGTTGAGTG TTTT

[SQ]_p3548_seed_origami_type B_3	TAAAGCACTAAATCGGTGGGGTCGAGGTGC CGGG
[SQ]_p3548_seed_origami_type B_4	TGCGCCGCTACAGGGCCACCCGCCGCGCTT AATG
[SQ]_p3548_seed_origami_type B_5	GACGGCCAGTGAGCGCCACGACGTTGTAAA ACCT
[SQ]_p3548_seed_origami_type B_6	AACCAGCTCAGAAAAAGTTCGTACCCACGT AGCC
[SQ]_p3548_seed_origami_type B_7	TGATACTGGCATCAGCGTGACTCGCCGGCA TCGG
[SQ]_p3548_seed_origami_type B_8	TAGTTGCCTGACTCGTCTATTTCGTTCATC
[SQ]_p3548_seed_origami_type B_9	TTAAATCAATCTAATAAATTAAAAATGAAG
[SQ]_p3548_seed_origami_type B_10	ATCTCAAGAAGATCTACGCGCAGAAAAAA A
[SQ]_p3548_seed_origami_type B_11	GTGGCCTAACTACGTACAGAGTTCTTGAAG
[SQ]_p3548_seed_origami_type B_12	GGGCTGTGTGCACGGGTCGTTCGCTCCAAG
[SQ]_p3548_seed_origami_type B_13	CTCGTGCGCTCTCCTTTCCCCCTGGAAGCT
[SQ]_p3548_seed_origami_type B_14	CTCCGCCCCCCTGACTGGCGTTTTTCCATA
[SQ]_p3548_seed_origami_type B_15	ATATAAACAAATAGGGGTGAATGTATTTAG AAAA
[SQ]_p3548_seed_origami_type B_16	CTGGAAATGTTGAATACTGGAATAAGGGCG ACAC
[SQ]_p3548_seed_origami_type B_17	CTCAGTCTATTAATTGTTTTTATCCGCCTCC ATC
[SQ]_p3548_seed_origami_type B_18	ACCCGCGAGACCCACGCTCAGTGCTGCAAT GATA
[SQ]_p3548_seed_origami_type B_19	GTGTCGTAGACACCGGGTGGATAGTTGGAG CAGA GAGCTCAAAATGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type B_20	GTGTCGTAGACACCCAACCAGGATAGGAAC GAAA CGCAGTCCGCTGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type B_21	GTGTCGTAGACACTGTATCAAGATACCTTC ATCGA ACGACCCATGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type B_22	GTGTCGTAGACACGGCCGCCACCGCGGTGC CACT AGTTCTAGAGCGTGTCGTAGACAC

[SQ]_p3548_seed_origami_type B_23	GTGTCGTAGACACGAGTGAGCTAACTCACG CCTG GGGTGCCTAATGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type B_24	GTGTCGTAGACACTCCTCGCTCACTGACTT GGGC GCTCTTCCGCTGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type B_25	GTGTCGTAGACACGCAGGAAAGAACATGT AGAA TCAGGGGATAACGTGTCGTAGACAC

Table S4.6. Edge staples of p3548 square DNA origami seed origami type S.

[SQ]_p3548_seed_origami_type S_1	GCGTTAAATTTTTGTTTATTTTGTTAAAATT CCA
[SQ]_p3548_seed_origami_type S_2	GTTCCAGTTTGGAACAGATAGGGTTGAGTG TTTT
[SQ]_p3548_seed_origami_type S_3	TAAAGCACTAAATCGGTGGGGTCGAGGTGC CGGG
[SQ]_p3548_seed_origami_type S_4	TGCGCCGCTACAGGGCCACCCGCCGCGCTT AATG
[SQ]_p3548_seed_origami_type S_5	GACGGCCAGTGAGCGCCACGACGTTGTAAA ACCT
[SQ]_p3548_seed_origami_type S_6	AACCAGCTCAGAAAAAGTTCGTACCCACGT AGCC
[SQ]_p3548_seed_origami_type S_7	TGATACTGGCATCAGCGTGACTCGCCGGCA TCGG
[SQ]_p3548_seed_origami_type S_8	ATATAAACAAATAGGGGTGAATGTATTTAG AAAA
[SQ]_p3548_seed_origami_type S_9	CTGGAAATGTTGAATACTGGAATAAGGGCG ACAC
[SQ]_p3548_seed_origami_type S_10	TGGCTGTTGAGATCCAGTTCTCAAGGATCTT ACC
[SQ]_p3548_seed_origami_type S_11	GCTGTGACTGGTGAGTACCCGTAAGATGCT TTTC
[SQ]_p3548_seed_origami_type S_12	ATCCAACGATCAAGGCGACATTCAGCTCCG GTTC
[SQ]_p3548_seed_origami_type S_13	CTCAGTCTATTAATTGTTTTTATCCGCCTCC ATC
[SQ]_p3548_seed_origami_type S_14	ACCCGCGAGACCCACGCTCAGTGCTGCAAT GATA
[SQ]_p3548_seed_origami_type S_15	GTGTCGTAGACACCGGGTGGATAGTTGGAG CAGA GAGCTCAAAATGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_16	GTGTCGTAGACACCCAACCAGGATAGGAAC GAAA CGCAGTCCGCTGTGTCGTAGACAC

[SQ]_p3548_seed_origami_type S_17	GTGTCGTAGACACTGTATCAAGATACCTTC ATCGA ACGACCCATGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_18	GTGTCGTAGACACGGCCGCCACCGCGGTGC CACT AGTTCTAGAGCGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_19	GTGTCGTAGACACGAGTGAGCTAACTCACG CCTG GGGTGCCTAATGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_20	GTGTCGTAGACACTCCTCGCTCACTGACTTG GGC GCTCTTCCGCTGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_21	GTGTCGTAGACACGCAGGAAAGAACATGTA GAA TCAGGGGATAACGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_22	GTGTCGTAGACACCATAGTTGCCTGACTCG TCTA TTTCGTTCATCGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_23	GTGTCGTAGACACTTTTAAATCAATCTAAT AAAT TAAAAATGAAGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_24	GTGTCGTAGACACGGATCTCAAGAAGATCT ACG CGCAGAAAAAAAGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_25	GTGTCGTAGACACTGGTGGCCTAACTACGT ACA GAGTTCTTGAAGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_26	GTGTCGTAGACACCTGGGCTGTGTGCACGG GTC GTTCGCTCCAAGGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_27	GTGTCGTAGACACCCCTCGTGCGCTCTCCTT TC CCCCTGGAAGCTGTGTCGTAGACAC
[SQ]_p3548_seed_origami_type S_28	GTGTCGTAGACACGGCTCCGCCCCCCTGAC TGG CGTTTTTCCATAGTGTCGTAGACAC

Table S4.7. Edge staples of p3548 square DNA origami building units type 00.

[SQ]_p3548_building_units_type 00_1	GGAAATGTTGAATACTGGAATAAGGGCGA CACCC
[SQ]_p3548_building_units_type 00_2	GCTGTTGAGATCCAGTTCTCAAGGATCTTA CCTG
[SQ]_p3548_building_units_type 00_3	CCAACGATCAAGGCGACATTCAGCTCCGG TTCGA

[SQ]_p3548_building_units_type00_4	CAGTCTATTAATTGTTTTTATCCGCCTCCATCTC
[SQ]_p3548_building_units_type00_5	AACCAGGATAGGAACGAAACGCAGTCCGCT
[SQ]_p3548_building_units_type00_6	TATCAAGATACCTTCATCGAACGACCCATG
[SQ]_p3548_building_units_type00_7	GTGAGCTAACTCACGCCTGGGGTGCCTAAT
[SQ]_p3548_building_units_type00_8	CTCGCTCACTGACTTGGGCGCTCTTCCGCT
[SQ]_p3548_building_units_type00_9	GTTCCAGTTTGGAACAGATAGGGTTGAGTGTTTT
[SQ]_p3548_building_units_type00_10	TAAAGCACTAAATCGGTGGGGTCGAGGTGCCGGG
[SQ]_p3548_building_units_type00_11	GACGGCCAGTGAGCGCCACGACGTTGTAAAACCT
[SQ]_p3548_building_units_type00_12	AACCAGCTCAGAAAAAGTTCGTACCCACGTAGCC
[SQ]_p3548_building_units_type00_13	TTAAATCAATCTAATAAATTAAAAATGAAG
[SQ]_p3548_building_units_type00_14	ATCTCAAGAAGATCTACGCGCAGAAAAAAA
[SQ]_p3548_building_units_type00_15	GGGCTGTGTGCACGGGTCGTTCGCTCCAAG
[SQ]_p3548_building_units_type00_16	CTCGTGCGCTCTCCTTTCCCCCTGGAAGCT

Table S4.8. Edge staples of p3548 square DNA origami building units type 11.

[SQ]_p3548_building_units_type01_1	GGAAATGTTGAATACTGGAATAAGGGCGACACCC
[SQ]_p3548_building_units_type01_2	GCTGTTGAGATCCAGTTCTCAAGGATCTTACCTG
[SQ]_p3548_building_units_type01_3	CCAACGATCAAGGCGACATTCAGCTCCGGTTCGA
[SQ]_p3548_building_units_type01_4	CAGTCTATTAATTGTTTTTATCCGCCTCCATCTC
[SQ]_p3548_building_units_type01_5	GTTCCAGTTTGGAACAGATAGGGTTGAGTGTTTT
[SQ]_p3548_building_units_type01_6	TAAAGCACTAAATCGGTGGGGTCGAGGTGCCGGG
[SQ]_p3548_building_units_type01_7	GACGGCCAGTGAGCGCCACGACGTTGTAAAACCT
[SQ]_p3548_building_units_type01_8	AACCAGCTCAGAAAAAGTTCGTACCCACGTAGCC

[SQ]_p3548_building_units_type 01_9	TAGTTGCCTGACTCGTCTATTTCGTTCATC
[SQ]_p3548_building_units_type 01_10	TTAAATCAATCTAATAAATTAAAAATGAA G
[SQ]_p3548_building_units_type 01_11	CTCGTGCGCTCTCCTTTCCCCCTGGAAGCT
[SQ]_p3548_building_units_type 01_12	CTCCGCCCCCCTGACTGGCGTTTTTCCATA
[SQ]_p3548_building_units_type 01_13	CGGGTGGATAGTTGGAGCAGAGAGCTCAA A
[SQ]_p3548_building_units_type 01_14	CCAACCAGGATAGGAACGAAACGCAGTCC G
[SQ]_p3548_building_units_type 01_15	TCCTCGCTCACTGACTTGGGCGCTCTTCCG
[SQ]_p3548_building_units_type 01_16	GCAGGAAAGAACATGTAGAATCAGGGGAT A

Table S4.9. Edge staples of p3548 square DNA origami building units type 01.

[SQ]_p3548_building_units_type 10_1	AACCAGGATAGGAACGAAACGCAGTCCGC T
[SQ]_p3548_building_units_type 10_2	TATCAAGATACCTTCATCGAACGACCCAT G
[SQ]_p3548_building_units_type 10_3	GTGAGCTAACTCACGCCTGGGGTGCCTAA T
[SQ]_p3548_building_units_type 10_4	CTCGCTCACTGACTTGGGCGCTCTTCCGCT
[SQ]_p3548_building_units_type 10_5	GCGTTAAATTTTTGTTTATTTTGTTAAAATT CCA
[SQ]_p3548_building_units_type 10_6	GTTCCAGTTTGGAACAGATAGGGTTGAGT GTTTT
[SQ]_p3548_building_units_type 10_7	AACCAGCTCAGAAAAAGTTCGTACCCACG TAGCC
[SQ]_p3548_building_units_type 10_8	TGATACTGGCATCAGCGTGACTCGCCGGC ATCGG
[SQ]_p3548_building_units_type 10_9	TAGTTGCCTGACTCGTCTATTTCGTTCATC
[SQ]_p3548_building_units_type 10_10	TTAAATCAATCTAATAAATTAAAAATGAA G
[SQ]_p3548_building_units_type 10_11	CTCGTGCGCTCTCCTTTCCCCCTGGAAGCT
[SQ]_p3548_building_units_type 10_12	CTCCGCCCCCCTGACTGGCGTTTTTCCATA
[SQ]_p3548_building_units_type 10_13	ATATAAACAAATAGGGGTGAATGTATTTA GAAAA

[SQ]_p3548_building_units_type 10_14	CTGGAAATGTTGAATACTGGAATAAGGGC GACAC
[SQ]_p3548_building_units_type 10_15	CTCAGTCTATTAATTGTTTTTATCCGCCTCC ATC
[SQ]_p3548_building_units_type 10_16	ACCCGCGAGACCCACGCTCAGTGCTGCAA TGATA

Table S4.10. Edge staples of p3548 square DNA origami building units type 10.

[SQ]_p3548_building_units_type 11_1	GTTCCAGTTTGGAACAGATAGGGTTGAGT GTTTT
[SQ]_p3548_building_units_type 11_2	TAAAGCACTAAATCGGTGGGGTCGAGGTG CCGGG
[SQ]_p3548_building_units_type 11_3	GACGGCCAGTGAGCGCCACGACGTTGTAA AACCT
[SQ]_p3548_building_units_type 11_4	AACCAGCTCAGAAAAAGTTCGTACCCACG TAGCC
[SQ]_p3548_building_units_type 11_5	TAGTTGCCTGACTCGTCTATTTCGTTCATC
[SQ]_p3548_building_units_type 11_6	TTAAATCAATCTAATAAATTAAAAATGAA G
[SQ]_p3548_building_units_type 11_7	CTCGTGCGCTCTCCTTTCCCCCTGGAAGCT
[SQ]_p3548_building_units_type 11_8	CTCCGCCCCCCTGACTGGCGTTTTTCCATA
[SQ]_p3548_building_units_type 11_9	ATATAAACAAATAGGGGTGAATGTATTTA GAAAA
[SQ]_p3548_building_units_type 11_10	CTGGAAATGTTGAATACTGGAATAAGGGC GACAC
[SQ]_p3548_building_units_type 11_11	CTCAGTCTATTAATTGTTTTTATCCGCCTCC ATC
[SQ]_p3548_building_units_type 11_12	ACCCGCGAGACCCACGCTCAGTGCTGCAA TGATA
[SQ]_p3548_building_units_type 11_13	CGGGTGGATAGTTGGAGCAGAGAGCTCAA A
[SQ]_p3548_building_units_type 11_14	CCAACCAGGATAGGAACGAAACGCAGTCC G
[SQ]_p3548_building_units_type 11_15	TCCTCGCTCACTGACTTGGGCGCTCTTCCG
[SQ]_p3548_building_units_type 11_16	GCAGGAAAGAACATGTAGAATCAGGGGAT A

S4.4.2.1 Staple strand sequences of M13mp18 square tiles for multimerization

Table S4.11. Core staples of M13mp18 square DNA origami tile.

Name	Sequence
[SQ]_M13_core_1	GCTGAGGCTTGCAGGGAGTTAAACGAAAGACAGCATCGCATGAGGA
[SQ]_M13_core_2	AGGCAAAAGGACTAAAGACTTTTTGAACGA
[SQ]_M13_core_3	GGGTAGCAACTTTCGAGGTGAA
[SQ]_M13_core_4	AGTTTCCAAGGCACCAACCTAAGATTTGTA
[SQ]_M13_core_5	TGAGAAGTTTATCATTTTGGCTTTGAGAATAC
[SQ]_M13_core_6	GCGCAGACAACAAAGTACAACGGAAACGAAAG
[SQ]_M13_core_7	ACTAAAACACTTTTTTTTTCAGCGGAG
[SQ]_M13_core_8	TCATCGCCCATGTTACTTAGCCGTAATCTT
[SQ]_M13_core_9	AAGCGCGAGGTCAATCATAAGGGACAGGCGCA
[SQ]_M13_core_10	GATTTTGCTAAACAACTTTTTTCCCCAGCGATTATACC
[SQ]_M13_core_11	GCTTGCCCCTGACCTTCATCAAGAGGAACGAG
[SQ]_M13_core_12	GTAAATTGAACGGTGTACAGACACCGAA
[SQ]_M13_core_13	CTGACCAACTTACCGTAACA
[SQ]_M13_core_14	GACAAGAAAGCTGCTCATTCAGAAATCTAC
[SQ]_M13_core_15	TAGGCTGGTGACGAGAAACACCAGGCTCATTA
[SQ]_M13_core_16	TCAGTACCAATAGGTTTTGGACAGATGGGCTT
[SQ]_M13_core_17	TAGGAATAAGGACGTTGGGAAGAATGAATAAG
[SQ]_M13_core_18	TAACGCCCGATTTTAAGAACTGAACGAGTA
[SQ]_M13_core_19	GAGATGGTTTTTTTTTTGGGGTTTTGC
[SQ]_M13_core_20	GTTAATAAGAAAGATTCATCAGTTTAGACT
[SQ]_M13_core	TACCAGTCCCACATTCAACTAATGGAAGTTTT

_21	
[SQ]_M13_core_22	ACCTTATGAAAAGGAATTACGAGGAAAACCAA
[SQ]_M13_core_23	CCTCAAGAGAAGGATTTTTTTTTTTAATCATTGTGAATT
[SQ]_M13_core_24	TGCTTTAAGGGTAATAGTAAAATGTTGAGATT
[SQ]_M13_core_25	ATAAATCGAGGCTTTTGCAAAACAGATACA
[SQ]_M13_core_26	AGATTACCCTGACTATTATAGTTTACCAGACGACGATACATAGT
[SQ]_M13_core_27	AAGAGCAACATGAATGGAAAG
[SQ]_M13_core_28	GGATAGCATATTCATTGAATCCGAAGCAAA
[SQ]_M13_core_29	GCCAGAGGACAGTTCAGAAAACGATTTTAATT
[SQ]_M13_core_30	AATAGCGAAAAAATCAGGTCTTTAAGAGGAAGCCCGAAAGGCTCAACA
[SQ]_M13_core_31	ACCTTTTTTTTTTAGCCCCCTATCCTCATTTTTTACCCTCGT
[SQ]_M13_core_32	CGGATGGCAAAGCGAACCAGACCGCCCTCAAA
[SQ]_M13_core_33	TGCTGTAACTTCAAATATCGCGGAATGACC
[SQ]_M13_core_34	CAGAAGCATTTTTCTGTCGTGATAAATCATTTTTCAAGAAAA
[SQ]_M13_core_35	CTCCAACCTTTTGATAAGAGGTTTTGACCA
[SQ]_M13_core_36	CGAGCTTCTTAGAGCTTAATTGCTTGATTCCC
[SQ]_M13_core_37	GCTTTCCAGTTTGCATCAAAA
[SQ]_M13_core_38	TGAAAAGGGAACGAGTAGATTTAGCATTTTTG
[SQ]_M13_core_39	GCAAAGAATAGTAGTAGCATTATTCCATATAACAGTGAATATAA
[SQ]_M13_core_40	TGTTTTAAATATGCAATTTTTTTAAGCTTGCATGCCTGC
[SQ]_M13_core_41	TTAGATAATATTTTCATTTGGGCATAAAGC
[SQ]_M13_core_42	AATTCTGCTGGCATCAATTCTACTAATTAGCAAAATTAAGGGATAAAA
[SQ]_M13_core_43	AGTTTCAACATCCATTTTCGCTTCTGGACGTT

[SQ]_M13_core_44	GTAAAACGACTTTTTTTGGTGTCTGGA
[SQ]_M13_core_45	CAACGCAACAATAAAGCCTCAGAGGCGCGAGC
[SQ]_M13_core_46	TAAATCGTTTTGCGGGAGAAGCTCAAAAGG
[SQ]_M13_core_47	CAGCCAGCTTTACAGGCAAG
[SQ]_M13_core_48	ATCTACAGCTGATAAATTAATGATGTGTAGGTAAAGATCTTTATTT
[SQ]_M13_core_49	ATTTTTAGAACCCTCATTTTTTCCCGTCGGATTCTCCG
[SQ]_M13_core_50	GTGAGAAATATTCAACCGTTCTAAAGGCTA
[SQ]_M13_core_51	TGAGTACCGGAGAGTTTTGTTAAAATTCAACA
[SQ]_M13_core_52	TTAAATGTGATTTTTTTATGCAATGCC
[SQ]_M13_core_53	TCAGGTCCGATGAACGGTAATCGTAAAACT
[SQ]_M13_core_54	TTGTAAACGTTTTTTTTGAGAG
[SQ]_M13_core_55	TCCAGAGCCTAATTTGCCAGTTACAAATAAGAAACGATACATAAAA
[SQ]_M13_core_56	GAGCGCTACTTTACAGAGAGAATATTTTTG
[SQ]_M13_core_57	TTTAACGTCATTAGGTTTTGAA
[SQ]_M13_core_58	ACAGGGACTGAACAAAGTCAGACAATAGCT
[SQ]_M13_core_59	TTTTATCCTCCCGATTTTATAGCAGCATATCA
[SQ]_M13_core_60	ACCGAGGAAGAAACAATGAAATAGGGGTAATT
[SQ]_M13_core_61	GAGAGATAACTTTTTTTAGCAAGCCGT
[SQ]_M13_core_62	ATCTTACCCGAACAAAGTTACCTGGCAACA
[SQ]_M13_core_63	TAAGAGCAAACGCAATAATAACGGGTTAGCAA
[SQ]_M13_core_64	ACCAAGTACCGCACTCTTTTTTGAGTTAAGCCCAATAA
[SQ]_M13_core_65	ATATGGTTAATACATACATAAAGGAGAAGGAA
[SQ]_M13_core	GACATTCCTTATTACGCAGTATAATACC

_66	
[SQ]_M13_core_67	CAAAAGAACTTGCAGAACGC
[SQ]_M13_core_68	TATAAAATTGTCACAATCAATAGCAAAATC
[SQ]_M13_core_69	ACGTAGAATACCAGCGCCAAAGACCACCGACT
[SQ]_M13_core_70	TACCAGCAACATGTTTTTTAAGACTCAACCGA
[SQ]_M13_core_71	CACCGTAATTGGGAATTAGAGCCAGAAAATTC
[SQ]_M13_core_72	CCTTTAGGTGAATTATCACCGTAAAAGGGC
[SQ]_M13_core_73	TTGAGGGAGGTTTTTTTTACAAATTCT
[SQ]_M13_core_74	ACCAGTAACCAATGAAACCATCACCCTCAG
[SQ]_M13_core_75	TGAGCCATTCAGTAGCGACAGAATCCACCACC
[SQ]_M13_core_76	CATTAAAGCGTCAGACTGTAGCGCCTTTTCAT
[SQ]_M13_core_77	AGCCTGTTTAGTATCATTTTTTTATTGACGGAAATTATT
[SQ]_M13_core_78	GAGCCGCCCTCCCTCAGAGCCGCCGATAGCAG
[SQ]_M13_core_79	CAGGTCATCACCGGAACCAGAGCAAGTTTG
[SQ]_M13_core_80	CGCAGTATTCACAAACAAATAATATTAGCGTTTGCCATGTTTTC
[SQ]_M13_core_81	ATCGGCATTTTGCTTAGGTTG
[SQ]_M13_core_82	AACCGCCAGCCGCCACCAGAACAATAAGTT
[SQ]_M13_core_83	GGAACCGCGCCAGCATTGACAGGACATGGCTT
[SQ]_M13_core_84	AATCAAAAGACGATTGGCCTTGATCTCTGAATTTACCGTTCTGAGACT
[SQ]_M13_core_85	TCGGAACCACAGGAGTGTACTGGTCACCACCA
[SQ]_M13_core_86	TAAGAGGCCAGTAAGCGTCATAGGTTGAGG
[SQ]_M13_core_87	TTAACGGACAGTTAATGCCCCCAATAGGTG
[SQ]_M13_core_88	TTGATGATTATTATTCTGAAACATCCGTCGAG

[SQ]_M13_core_89	CCCTCAGATATAAGTATAGCCCGGTGCCTATT
[SQ]_M13_core_90	CTGAGTTCAGGGATAGCAAGCCCAGGCGGATAAGTGGAAAGTAT
[SQ]_M13_core_91	TATCACCAACCGCCACCCTCAGCATTCCAC
[SQ]_M13_core_92	AGGGTTGAGCCACCACCCTCATTTTTCGTCACCAGTACAACTGTATGG
[SQ]_M13_core_93	TGAATTTTACTACAACGCCTGTAGAACCGCCA
[SQ]_M13_core_94	AGACAGCTCGTCTTTCCAGACGAAGGAATT
[SQ]_M13_core_95	TTTCTTGCCTTTAATTGTATCGTAGAAAGGAACAACTATTAGTAAA
[SQ]_M13_core_96	GCGAATAAAGGCTCCAAAAGGAAAACAGCT
[SQ]_M13_core_97	TGATACCCCCACGCATAACCGATATATTCG
[SQ]_M13_core_98	AAGAATACGTGGCACAGACAATAACTGATAGCCCTAAAAGGTGAGG
[SQ]_M13_core_99	TAAAGCATGCAGAAGATAAAACAGACATCG
[SQ]_M13_core_100	CCATTAAAAATTTTTACATTGG
[SQ]_M13_core_101	CGGTCAGGAGCCAGCAGCAAATAAGGAATT
[SQ]_M13_core_102	TCAAACCGTCTGAATTTTAACCACCACACCTT
[SQ]_M13_core_103	GATAATACGCAAATCAACAGTTGAGAAAAATC
[SQ]_M13_core_104	GCTGAACCTCTTTTTTTGTAGAAGAAC
[SQ]_M13_core_105	GAGGAAGCTAATAGATTAGAGCCATTATCA
[SQ]_M13_core_106	GTCAGTTGATTTGAGGATTTAGAACCGAACGT
[SQ]_M13_core_107	GATTAGTAATAACATCTTTTTTCCTCAATCAATATCTG
[SQ]_M13_core_108	TGATGGCATTAAAAGTTTGAGTAACGTCAATA
[SQ]_M13_core_109	TTGGATTTATTAAATCCTTTGCGTATTA
[SQ]_M13_core_110	GACTTTACAACAGGAGGCCG
[SQ]_M13_core	TTTTGCGTCATCATATTCCTGATCAGATGA

_111	
[SQ]_M13_core_112	TATTAATTATTCATCAATATAATCTAAAGAAA
[SQ]_M13_core_113	AAAGGACAGAGCGGTTTTACAACTCGATACTT
[SQ]_M13_core_114	AATACCAAATTTTCAGGTTTAACGTTATCAGA
[SQ]_M13_core_115	TTATTCACACGTAAAACAGAAACTGATTGT
[SQ]_M13_core_116	CTGAATAATGTTTTTTTACGTGGCGAG
[SQ]_M13_core_117	ATATACAAACGGATTCGCCTGAAATAACCT
[SQ]_M13_core_118	TTGCGTAGGTTACAAAATCGCGCAGGAAACAG
[SQ]_M13_core_119	ATTATTTGTTTCAATTACCTGAGCTAACAATT
[SQ]_M13_core_120	AGAGCTTGACGGGGAATTTTTTTAACCTACCATATCAAA
[SQ]_M13_core_121	AGCGATAGTCAATATATGTGAGTGTTGCTTTG
[SQ]_M13_core_122	TCAATAGATTACCTTTTTTAATGAGGCGAA
[SQ]_M13_core_123	GGTTATATAGGTCTGAGAGACTCAAAATTAATTACATTAAAAGA
[SQ]_M13_core_124	AGATGATGAATGCCCGAGATA
[SQ]_M13_core_125	TGCTTCTTCCCTTAGAATCCTTCAAATATA
[SQ]_M13_core_126	TACATAAACTTAGATTAAGACGCTATCGCAAG
[SQ]_M13_core_127	TCATTTGATGAATTTATCAAAATCATAACTATATGTAAATCTAGAAAA
[SQ]_M13_core_128	TAAGGCGTCGCGAGAAAACTTTTTGAAAACAT
[SQ]_M13_core_129	ATAATTAGCTGATGCAAATCCAGAGAAGAG
[SQ]_M13_core_130	TTTTAGTTGAAATACCGACCGTTTAACAAC
[SQ]_M13_core_131	ACAAAGAATAAATAAGAATAAACACAACAGTA
[SQ]_M13_core_132	CAAAAGGTTTGAGAATCGCCATATGTGATAAA
[SQ]_M13_core_133	GCCTGTGACGACGACAATAAATATAAAGCCAACGCTCCGGAATC

[SQ]_M13_core_134	GCCAACAAATAAGAGAATATAAAATAATAT
[SQ]_M13_core_135	GGGCTTAAAAAGTAATTCTGTCCATTATCAACAATAGATAGGTATTAA
[SQ]_M13_core_136	CAAGAACGAGTCCTGAACAAGAAAAGTACCGA
[SQ]_M13_core_137	CCCATCCTCGGCTGTCTTTCCTATTACCGC
[SQ]_M13_core_138	GCCTTAGAGGCGTTTTAGCGAATTTCATCGTAGGAATCTATCATTC
[SQ]_M13_core_139	GCCCAATGTATTCTAAGAACGCAATCAAGA
[SQ]_M13_core_140	TTAGTTGATCTTACCAACGCTAACGAGCGT
[SQ]_M13_core_141	ATGTCAATCATATGTACCCCGGTTTGTATAAGCAAATATTAAATCA
[SQ]_M13_core_142	AGCTTTCATCGCATTAAATTTTTGTTTAAA
[SQ]_M13_core_143	GCTCATTTCGCGTCTGGCCTTCTAATGGGA
[SQ]_M13_core_144	GACAGTATAACGGCGGATTGACCGCTGTAGCC
[SQ]_M13_core_145	TAGGTCAATCTGCCAGTTTGAGTGTTGGGA
[SQ]_M13_core_146	TGGGAACACGGCCTCAGGAAGATCCAAAGCGC
[SQ]_M13_core_147	GGCGATTAATTCAGGCTGCGCAACGGGACGAC
[SQ]_M13_core_148	CAGTCACGTGCCGGAAACCAGGGCACTC
[SQ]_M13_core_149	AGGGCGAGGCGAAAGGGGGATGAGCTGTTT
[SQ]_M13_core_150	CATTCGCCAGTTGGGTAACGCCAGGGTACCGA
[SQ]_M13_core_151	TAAAGCCTTCGTAATCATGGTCATTGCTGCAA
[SQ]_M13_core_152	TCACATTTCTAGAGGATCCCCGGGTTTTCC
[SQ]_M13_core_153	CCTGTGTATACGAGCCGGAAGCCAGTGAGA
[SQ]_M13_core_154	GCTCGAATGGGGTGCCTAATGAGTGTATTGGG
[SQ]_M13_core_155	AGGTCGACAATTGCGTTGCGCTCAATCGGCCA
[SQ]_M13_core	GGTCCACGTGGTTTTTCTTTTCACATAAAGTG

_156	
[SQ]_M13_core_157	TCCTGTTGGAGAGGCGGTTTGCGAGCTAAC
[SQ]_M13_core_158	GGGTTGATCGGCAAAATCCCTTCCAGCTGCATTAATGACTGCCC
[SQ]_M13_core_159	CGGGCAAGCCCTGAGAGAGTTGCGAAAAAC
[SQ]_M13_core_160	CGCCAGGGCTGGTTTGCCCCAGCATATTAAAG
[SQ]_M13_core_161	ACGCGCGGTGATGGTGGTTCCGAAAGTGTTGTTCCAGTTTCCCGATTT
[SQ]_M13_core_162	GGTGCCGTCTCCAACGTCAAAGGGCAGCAAGC
[SQ]_M13_core_163	GGGAGCCGGAACAAGAGTCCACGGCGAAAA
[SQ]_M13_core_164	CGTCTATCAAATCAAGTTTTTTCGGTCACG
[SQ]_M13_core_165	AACGTGGAAAAGCACTAAATCGGAAGGAGCGG
[SQ]_M13_core_166	CTTTGACGGCGCTGGCAAGTGTAGGGGGTCGA
[SQ]_M13_core_167	ATTAAATTTCCTCGTTAGAATAGGGAAGAAAGCGAAACCCTAAA
[SQ]_M13_core_168	CTGCGCGCTACAGGGCGCGTACCTGAGAAG
[SQ]_M13_core_169	GCGCTAGGAGCACGTATAACGTGCGGGATTTTAGACAGGAACTTCTTT
[SQ]_M13_core_170	GTAGCAATACGGTACGCCAGAATCTATGGTTG
[SQ]_M13_core_171	TGTTTTTGTCCATCACGCAAATAATATCCA
[SQ]_M13_core_172	CAGATTCATTTTGACGCTCAATTATCGGCCTTGCTGGTTAACCGTT
[SQ]_M13_core_173	GAACAATTCATGGAAATACCTACACCAGTC
[SQ]_M13_core_174	ACACGACATAGAACCCTTCTGACCTGAAAG

Table S4.12. Edge staples of M13mp18 square DNA origami seed origami type R.

[SQ]_M13_seed_origami_type R_1	CTTGTACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ]_M13_seed_origami_type R_2	GCTAACAGTGCCCGTATAAGGTCAGTGCCTTGAGT
[SQ]_M13_seed_origami_type R_3	CACCAAGGCCGGAAACGTCGCACCATTACCATTAG

[SQ]_M13_seed_origami_type R_4	CGCACGGAATAAGTTTATTGAAACGCAAAG ACACC
[SQ]_M13_seed_origami_type R_5	CGCTATTACGCCAGCTTCGGTGCGGGCCT
[SQ]_M13_seed_origami_type R_6	CACAATTCCACACAACGAAATTGTTATCC
[SQ]_M13_seed_origami_type R_7	TACGTGAACCATCACCCAGGGCGATGGCC
[SQ]_M13_seed_origami_type R_8	CGCGCTTAATGCGCCGTAACCACCACACC
[SQ]_M13_seed_origami_type R_9	ACGTAATGCCACTACGATTAAACGGGTAAA ATAT
[SQ]_M13_seed_origami_type R_10	CCAAATCAACGTAACAACCGGATATTCATTA CGC
[SQ]_M13_seed_origami_type R_11	AATAACCTGTTTAGCTCATTTCGCAAATGGT CAG
[SQ]_M13_seed_origami_type R_12	AATCACCATCAATATGAGGCCGGAGACAGT CAAA
[SQ]_M13_seed_origami_type R_13	GTGTCGTAGACACTACAATTTTATCCTGACT ATTTT GCACCCAGCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_14	GTGTCGTAGACACATAGAAGGCTTATCCGAG CAAG CAAATCAGATGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_15	GTGTCGTAGACACAGAAACCAATCAATAAT AATTT ACGAGCATGTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_16	GTGTCGTAGACACGCATTTTCGAGCCAGTTG TAATT TAGGCAGAGGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_17	GTGTCGTAGACACCCTAAATTTAATGGTTTA ATTTC ATCTTCTGAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_18	GTGTCGTAGACACCATCGGGAGAAACAATG TAACA GTACCTTTTAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_19	GTGTCGTAGACACAGAAGGAGCGGAATTAG AACA AAGAAACCACCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_20	GTGTCGTAGACACTTAGGAGCACTAACAAGT TATC TAAAATATCTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type R_21	GTGTCGTAGACACAACAGTGCCACGCTGATA TTAA CACCGCCTGCGTGTCGTAGACAC

[SQ]_M13_seed_origami_type R_22	GTGTCGTAGACACAGTCTTTAATGCGCGATT TTTG AATGGCTATTGTGTCGTAGACAC

Table S4.13. Edge staples of M13mp18 square DNA origami seed origami type B.

[SQ]_M13_seed_origami_type B_1	CCAAATCAACGTAACAACCGGATATTCATTA CGCA
[SQ]_M13_seed_origami_type B_2	CAACATTATTACAGGTAAACGAACTAACGG AACCT
[SQ]_M13_seed_origami_type B_3	GTACCTTTAATTGCTCAGGTCAGGATTAGAG ACAT
[SQ]_M13_seed_origami_type B_4	AATAACCTGTTTAGCTCATTTCGCAAATGGT CAGA
[SQ]_M13_seed_origami_type B_5	TTTTCGAGCCAGTTGTAATTTAGGCAGAG
[SQ]_M13_seed_origami_type B_6	AAATTTAATGGTTTAATTTCATCTTCTGA
[SQ]_M13_seed_origami_type B_7	CGGGAGAAACAATGTAACAGTACCTTTTA
[SQ]_M13_seed_origami_type B_8	AGGAGCGGAATTAGAACAAAGAAACCACC
[SQ]_M13_seed_origami_type B_9	AAGAAAATCTCCAAAAAAATAATTTTTTCAC GTT
[SQ]_M13_seed_origami_type B_10	TTGTACCGCCACCCTCAGGTACTCAGGAGGT TTA
[SQ]_M13_seed_origami_type B_11	GCACGGAATAAGTTTATTGAAACGCAAAGA CACC
[SQ]_M13_seed_origami_type B_12	TTGAATTAACTGAACACCAGCGCATTAGACG GGA
[SQ]_M13_seed_origami_type B_13	GTGTCGTAGACACCCCAAAAACAGGAAGAT GATA ATCAGAAAAGCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_14	GTGTCGTAGACACCGCCATCAAAAATAATTT TTAA CCAATAGGAAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_15	GTGTCGTAGACACCGCATCGTAACCGTGCCG TTGG TGTAGATGGGGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_16	GTGTCGTAGACACCGCTATTACGCCAGCTTC GGTG CGGGCCTCTTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_17	GTGTCGTAGACACCACAATTCCACACAACG AAAT TGTTATCCGCTGTGTCGTAGACAC

[SQ]_M13_seed_origami_type B_18	GTGTCGTAGACACTACGTGAACCATCACCCA GGG CGATGGCCCACGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_19	GTGTCGTAGACACCGCGCTTAATGCGCCGTA ACC ACCACACCCGCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_20	GTGTCGTAGACACCCGAGTAAAAGAGTCTA TAAT CAGTGAGGCCAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_21	GTGTCGTAGACACGCAACAGGAAAAACGCA TTAC CGCCAGCCATTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type B_22	GTGTCGTAGACACATTCTGGCCAACAGAGC AGTA ATAAAAGGGACGTGTCGTAGACAC

Table S4.14. Edge staples of M13mp18 square DNA origami seed origami type S.

[SQ]_M13_seed_origami_type S_1	CTTGTACCGCCACCCTCAGGTACTCAGGAGG TTTA
[SQ]_M13_seed_origami_type S_2	GCTAACAGTGCCCGTATAAGGTCAGTGCCTT GAGT
[SQ]_M13_seed_origami_type S_3	CACCAAGGCCGGAAACGTCGCACCATTACC ATTAG
[SQ]_M13_seed_origami_type S_4	CGCACGGAATAAGTTTATTGAAACGCAAAG ACACC
[SQ]_M13_seed_origami_type S_5	CCAAATCAACGTAACAACCGGATATTCATTA CGCA
[SQ]_M13_seed_origami_type S_6	CAACATTATTACAGGTAAACGAACTAACGG AACCT
[SQ]_M13_seed_origami_type S_7	GTACCTTTAATTGCTCAGGTCAGGATTAGAG ACAT
[SQ]_M13_seed_origami_type S_8	AATAACCTGTTTAGCTCATTTCGCAAATGGT CAGA
[SQ]_M13_seed_origami_type S_9	GTGTCGTAGACACCCCAAAAACAGGAAGAT GATA ATCAGAAAAGCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_10	GTGTCGTAGACACCGCCATCAAAAATAATTT TTAA CCAATAGGAAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_11	GTGTCGTAGACACCGCATCGTAACCGTGCCG TTGG TGTAGATGGGGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_12	GTGTCGTAGACACCGCTATTACGCCAGCTTC GGTG CGGGCCTCTTGTGTCGTAGACAC

[SQ]_M13_seed_origami_type S_13	GTGTCGTAGACACCACAATTCCACACAACGA AATT GTTATCCGCTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_14	GTGTCGTAGACACTACGTGAACCATCACCCA GGGC GATGGCCCACGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_15	GTGTCGTAGACACCGCGCTTAATGCGCCGTA ACCA CCACACCCGCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_16	GTGTCGTAGACACCCGAGTAAAAGAGTCTAT AAT CAGTGAGGCCAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_17	GTGTCGTAGACACGCAACAGGAAAAACGCA TTAC CGCCAGCCATTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_18	GTGTCGTAGACACATTCTGGCCAACAGAGCA GTAA TAAAAGGGACGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_19	GTGTCGTAGACACTACAATTTTATCCTGACT ATTTT GCACCCAGCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_20	GTGTCGTAGACACATAGAAGGCTTATCCGAG CAA GCAAATCAGATGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_21	GTGTCGTAGACACAGAAACCAATCAATAAT AATT TACGAGCATGTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_22	GTGTCGTAGACACGCATTTTCGAGCCAGTTG TAAT TTAGGCAGAGGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_23	GTGTCGTAGACACCCTAAATTTAATGGTTTA ATT TCATCTTCTGAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_24	GTGTCGTAGACACCATCGGGAGAAACAATG TAA CAGTACCTTTTAGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_25	GTGTCGTAGACACAGAAGGAGCGGAATTAG AA CAAAGAAACCACCGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_26	GTGTCGTAGACACTTAGGAGCACTAACAAGT TA TCTAAAATATCTGTGTCGTAGACAC
[SQ]_M13_seed_origami_type S_27	GTGTCGTAGACACAACAGTGCCACGCTGATA TT AACACCGCCTGCGTGTCGTAGACAC

[SQ]_M13_seed_origami_type S_28	GTGTCGTAGACACAGTCTTTAATGCGCGATT TTT GAATGGCTATTGTGTCGTAGACAC

Table S4.15. Edge staples of M13mp18 square DNA origami building units type 00.

[SQ]_M13_building_units_type0 0_1	ACGATCTAAAGTTTTGCCTCATAGTTAGCG TACG
[SQ]_M13_building_units_type0 0_2	AACAGTGCCCGTATAAGGTCAGTGCCTTGA GTCA
[SQ]_M13_building_units_type0 0_3	CAAGGCCGGAAACGTCGCACCATTACCATT AGTA
[SQ]_M13_building_units_type0 0_4	AAAAGTAAGCAGATAGCGAAGCCCTTTTTA AGCC
[SQ]_M13_building_units_type0 0_5	CATCGTAACCGTGCCGTTGGTGTAGATGGG
[SQ]_M13_building_units_type0 0_6	CAATTCCACACAACGAAATTGTTATCCGCT
[SQ]_M13_building_units_type0 0_7	CGTGAACCATCACCCAGGGCGATGGCCCA C
[SQ]_M13_building_units_type0 0_8	GAGTAAAAGAGTCTATAATCAGTGAGGCC A
[SQ]_M13_building_units_type0 0_9	AAATCCGCGACCTGCTCTGATAAATTGTGT CGAG
[SQ]_M13_building_units_type0 0_10	CAACATTATTACAGGTAAACGAACTAACGG AACC
[SQ]_M13_building_units_type0 0_11	GTACCTTTAATTGCTCAGGTCAGGATTAGA GACA
[SQ]_M13_building_units_type0 0_12	TATGACCCTGTAATACGTTGTACCAAAAAC ATTT
[SQ]_M13_building_units_type0 0_13	AAACCAATCAATAATAATTTACGAGCATGT
[SQ]_M13_building_units_type0 0_14	TAAATTTAATGGTTTAATTTCATCTTCTGA
[SQ]_M13_building_units_type0 0_15	TCGGGAGAAACAATGTAACAGTACCTTTTA
[SQ]_M13_building_units_type0 0_16	AGGAGCACTAACAAGTTATCTAAAATATCT

Table S4.16. Edge staples of M13mp18 square DNA origami building units type 11.

[SQ]_M13_building_units_type0 1_1	ACGATCTAAAGTTTTGCCTCATAGTTAGCG TACG
[SQ]_M13_building_units_type0 1_2	AACAGTGCCCGTATAAGGTCAGTGCCTTGA GTCA
[SQ]_M13_building_units_type0 1_3	CAAGGCCGGAAACGTCGCACCATTACCATT AGTA

[SQ]_M13_building_units_type01_4	AAAAGTAAGCAGATAGCGAAGCCCTTTTTAAGCC
[SQ]_M13_building_units_type01_5	AAATCCGCGACCTGCTCTGATAAATTGTGTCGAG
[SQ]_M13_building_units_type01_6	CAACATTATTACAGGTAAACGAACTAACGGAACC
[SQ]_M13_building_units_type01_7	GTACCTTTAATTGCTCAGGTCAGGATTAGAGACA
[SQ]_M13_building_units_type01_8	TATGACCCTGTAATACGTTGTACCAAAAACATTT
[SQ]_M13_building_units_type01_9	AGAAGGCTTATCCGAGCAAGCAAATCAGAT
[SQ]_M13_building_units_type01_10	ATTTTCGAGCCAGTTGTAATTTAGGCAGAG
[SQ]_M13_building_units_type01_11	AAGGAGCGGAATTAGAACAAAGAAACCACC
[SQ]_M13_building_units_type01_12	CAGTGCCACGCTGATATTAACACCGCCTGC
[SQ]_M13_building_units_type01_13	CGCCATCAAAAATAATTTTTAACCAATAGG
[SQ]_M13_building_units_type01_14	CGCTATTACGCCAGCTTCGGTGCGGGCCTC
[SQ]_M13_building_units_type01_15	CGCGCTTAATGCGCCGTAACCACCACACCC
[SQ]_M13_building_units_type01_16	GCAACAGGAAAAACGCATTACCGCCAGCCA

Table S4.17. Edge staples of M13mp18 square DNA origami building units type 01.

[SQ]_M13_building_units_type10_1	CATCGTAACCGTGCCGTTGGTGTAGATGGG
[SQ]_M13_building_units_type10_2	CAATTCCACACAACGAAATTGTTATCCGCT
[SQ]_M13_building_units_type10_3	CGTGAACCATCACCCAGGGCGATGGCCCAC
[SQ]_M13_building_units_type10_4	GAGTAAAAGAGTCTATAATCAGTGAGGCCA
[SQ]_M13_building_units_type10_5	ACGTAATGCCACTACGATTAAACGGGTAAAATAT
[SQ]_M13_building_units_type10_6	CCAAATCAACGTAACAACCGGATATTCATTACGC
[SQ]_M13_building_units_type10_7	AATAACCTGTTTAGCTCATTTCGCAAATGGTCAG
[SQ]_M13_building_units_type10_8	AATCACCATCAATATGAGGCCGGAGACAGTCAAA

[SQ]_M13_building_units_type10_9	AGAAGGCTTATCCGAGCAAGCAAATCAGAT
[SQ]_M13_building_units_type10_10	ATTTTCGAGCCAGTTGTAATTTAGGCAGAG
[SQ]_M13_building_units_type10_11	AAGGAGCGGAATTAGAACAAAGAAACCACC
[SQ]_M13_building_units_type10_12	CAGTGCCACGCTGATATTAACACCGCCTGC
[SQ]_M13_building_units_type10_13	AAGAAAATCTCCAAAAAAATAATTTTTTCACGTT
[SQ]_M13_building_units_type10_14	TTGTACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ]_M13_building_units_type10_15	GCACGGAATAAGTTTATTGAAACGCAAAGACACC
[SQ]_M13_building_units_type10_16	TTGAATTAACTGAACACCAGCGCATTAGACGGGA

Table S4.18. Edge staples of M13mp18 square DNA origami building units type 10.

[SQ]_M13_building_units_type11_1	ACGTAATGCCACTACGATTAAACGGGTAAAATAT
[SQ]_M13_building_units_type11_2	CCAAATCAACGTAACAACCGGATATTCATTACGC
[SQ]_M13_building_units_type11_3	AATAACCTGTTTAGCTCATTTCGCAAATGGTCAG
[SQ]_M13_building_units_type11_4	AATCACCATCAATATGAGGCCGGAGACAGTCAAA
[SQ]_M13_building_units_type11_5	AAACCAATCAATAATAATTTACGAGCATGT
[SQ]_M13_building_units_type11_6	TAAATTTAATGGTTTAATTTCATCTTCTGA
[SQ]_M13_building_units_type11_7	TCGGGAGAAACAATGTAACAGTACCTTTTA
[SQ]_M13_building_units_type11_8	AGGAGCACTAACAAGTTATCTAAAATATCT
[SQ]_M13_building_units_type11_9	AAGAAAATCTCCAAAAAAATAATTTTTTCACGTT
[SQ]_M13_building_units_type11_10	TTGTACCGCCACCCTCAGGTACTCAGGAGGTTTA
[SQ]_M13_building_units_type11_11	GCACGGAATAAGTTTATTGAAACGCAAAGACACC
[SQ]_M13_building_units_type11_12	TTGAATTAACTGAACACCAGCGCATTAGACGGGA
[SQ]_M13_building_units_type11_13	CGCCATCAAAAATAATTTTTAACCAATAGG

[SQ]_M13_building_units_type11_14	CGCTATTACGCCAGCTTCGGTGCGGGCCTC
[SQ]_M13_building_units_type11_15	CGCGCTTAATGCGCCGTAACCACCACACCC
[SQ]_M13_building_units_type11_16	GCAACAGGAAAAACGCATTACCGCCAGCCA

4.5 References

1 Qi, X. *et al.* Programming molecular topologies from single-stranded nucleic acids. *Nat. Commun.* **9**, 4579, (2018).

2 Williams, S. *et al.* in *DNA Computing. DNA 2008. Lecture Notes in Computer Science* Vol. 5347 90-101 (Springer, Berlin, Heidelberg, 2009).

APPENDIX D

PERMISSIONS TO USE COPYRIGHTED MATERIALS

JOHN WILEY AND SONS LICENSE
TERMS AND CONDITIONS

Apr 12, 2023

This Agreement between Mr. Yue Tang ("You") and John Wiley and Sons ("John Wiley and Sons") consists of your license details and the terms and conditions provided by John Wiley and Sons and Copyright Clearance Center.

License Number	5526751188688
License date	Apr 12, 2023
Licensed Content Publisher	John Wiley and Sons
Licensed Content Publication	ChemPhysChem
Licensed Content Title	DNA Tile Based Self-Assembly: Building Complex Nanoarchitectures
Licensed Content Author	Hao Yan, Sherri Rinker, Yan Liu, et al
Licensed Content Date	Aug 3, 2006
Licensed Content Volume	7
Licensed Content Issue	8
Licensed Content Pages	7
Type of use	Dissertation/Thesis
Requestor type	University/Academic

Format	Electronic
Portion	Figure/table
Number of figures/tables	1
Will you be translating?	No
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 1, page 1642
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Publisher Tax ID	EU826007151
Total	0.00 USD

Terms and Conditions

TERMS AND CONDITIONS

This copyrighted material is owned by or exclusively licensed to John Wiley & Sons, Inc. or one of its group companies (each a"Wiley Company") or handled on behalf of a society with which a Wiley Company has exclusive publishing rights in relation to a particular work (collectively "WILEY"). By clicking "accept" in connection with completing this licensing transaction, you agree that the following terms and conditions apply to this transaction (along with

the billing and payment terms and conditions established by the Copyright Clearance Center Inc., ("CCC's Billing and Payment terms and conditions"), at the time that you opened your RightsLink account (these are available at any time at http://myaccount.copyright.com).

Terms and Conditions

- The materials you have requested permission to reproduce or reuse (the "Wiley Materials") are protected by copyright.

- You are hereby granted a personal, non-exclusive, non-sub licensable (on a stand-alone basis), non-transferable, worldwide, limited license to reproduce the Wiley Materials for the purpose specified in the licensing process. This license, **and any CONTENT (PDF or image file) purchased as part of your order,** is for a one-time use only and limited to any maximum distribution number specified in the license. The first instance of republication or reuse granted by this license must be completed within two years of the date of the grant of this license (although copies prepared before the end date may be distributed thereafter). The Wiley Materials shall not be used in any other manner or for any other purpose, beyond what is granted in the license. Permission is granted subject to an appropriate acknowledgement given to the author, title of the material/book/journal and the publisher. You shall also duplicate the copyright notice that appears in the Wiley publication in your use of the Wiley Material. Permission is also granted on the understanding that nowhere in the text is a previously published source acknowledged for all or part of this Wiley Material. Any third party content is expressly excluded from this permission.

- With respect to the Wiley Materials, all rights are reserved. Except as expressly granted by the terms of the license, no part of the Wiley Materials may be copied, modified, adapted (except for minor reformatting required by the new Publication), translated, reproduced, transferred or distributed, in any form or by any means, and no derivative works may be made based on the Wiley Materials without the prior permission of the respective copyright owner.**For STM Signatory Publishers clearing permission under the terms of the STM Permissions Guidelines only, the terms of the license are extended to include subsequent editions and for editions in other languages, provided such editions are for the work as a whole in situ and does not involve the separate exploitation of the permitted figures or extracts,** You may not alter, remove or suppress in any manner any copyright, trademark or other notices displayed by the Wiley Materials. You may not license, rent, sell, loan, lease, pledge, offer as security, transfer or assign the Wiley Materials on a stand-alone basis, or any of the rights granted to you hereunder to any other person.

- The Wiley Materials and all of the intellectual property rights therein shall at all times remain the exclusive property of John Wiley & Sons Inc,

the Wiley Companies, or their respective licensors, and your interest therein is only that of having possession of and the right to reproduce the Wiley Materials pursuant to Section 2 herein during the continuance of this Agreement. You agree that you own no right, title or interest in or to the Wiley Materials or any of the intellectual property rights therein. You shall have no rights hereunder other than the license as provided for above in Section 2. No right, license or interest to any trademark, trade name, service mark or other branding ("Marks") of WILEY or its licensors is granted hereunder, and you agree that you shall not assert any such right, license or interest with respect thereto

- NEITHER WILEY NOR ITS LICENSORS MAKES ANY WARRANTY OR REPRESENTATION OF ANY KIND TO YOU OR ANY THIRD PARTY, EXPRESS, IMPLIED OR STATUTORY, WITH RESPECT TO THE MATERIALS OR THE ACCURACY OF ANY INFORMATION CONTAINED IN THE MATERIALS, INCLUDING, WITHOUT LIMITATION, ANY IMPLIED WARRANTY OF MERCHANTABILITY, ACCURACY, SATISFACTORY QUALITY, FITNESS FOR A PARTICULAR PURPOSE, USABILITY, INTEGRATION OR NON-INFRINGEMENT AND ALL SUCH WARRANTIES ARE HEREBY EXCLUDED BY WILEY AND ITS LICENSORS AND WAIVED BY YOU.

- WILEY shall have the right to terminate this Agreement immediately upon breach of this Agreement by you.

- You shall indemnify, defend and hold harmless WILEY, its Licensors and their respective directors, officers, agents and employees, from and against any actual or threatened claims, demands, causes of action or proceedings arising from any breach of this Agreement by you.

- IN NO EVENT SHALL WILEY OR ITS LICENSORS BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR ENTITY FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, EXEMPLARY OR PUNITIVE DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, PROVISIONING, VIEWING OR USE OF THE MATERIALS REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION, DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION SHALL APPLY NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

- Should any provision of this Agreement be held by a court of competent jurisdiction to be illegal, invalid, or unenforceable, that provision shall be deemed amended to achieve as nearly as possible the same economic effect as the original provision, and the legality, validity and

enforceability of the remaining provisions of this Agreement shall not be affected or impaired thereby.

- The failure of either party to enforce any term or condition of this Agreement shall not constitute a waiver of either party's right to enforce each and every term and condition of this Agreement. No breach under this agreement shall be deemed waived or excused by either party unless such waiver or consent is in writing signed by the party granting such waiver or consent. The waiver by or consent of a party to a breach of any provision of this Agreement shall not operate or be construed as a waiver of or consent to any other or subsequent breach by such other party.

- This Agreement may not be assigned (including by operation of law or otherwise) by you without WILEY's prior written consent.

- Any fee required for this permission shall be non-refundable after thirty (30) days from receipt by the CCC.

- These terms and conditions together with CCC's Billing and Payment terms and conditions (which are incorporated herein) form the entire agreement between you and WILEY concerning this licensing transaction and (in the absence of fraud) supersedes all prior agreements and representations of the parties, oral or written. This Agreement may not be amended except in writing signed by both parties. This Agreement shall be binding upon and inure to the benefit of the parties' successors, legal representatives, and authorized assigns.

- In the event of any conflict between your obligations established by these terms and conditions and those established by CCC's Billing and Payment terms and conditions, these terms and conditions shall prevail.

- WILEY expressly reserves all rights not specifically granted in the combination of (i) the license details provided by you and accepted in the course of this licensing transaction, (ii) these terms and conditions and (iii) CCC's Billing and Payment terms and conditions.

- This Agreement will be void if the Type of Use, Format, Circulation, or Requestor Type was misrepresented during the licensing process.

- This Agreement shall be governed by and construed in accordance with the laws of the State of New York, USA, without regards to such state's conflict of law rules. Any legal action, suit or proceeding arising out of or relating to these Terms and Conditions or the breach thereof shall be instituted in a court of competent jurisdiction in New York County in the State of New York in the United States of America and each party hereby consents and submits to the personal jurisdiction of such court, waives any objection to venue in such court and consents to service of process by registered or certified mail, return receipt requested, at the last

known address of such party.

WILEY OPEN ACCESS TERMS AND CONDITIONS

Wiley Publishes Open Access Articles in fully Open Access Journals and in Subscription journals offering Online Open. Although most of the fully Open Access journals publish open access articles under the terms of the Creative Commons Attribution (CC BY) License only, the subscription journals and a few of the Open Access Journals offer a choice of Creative Commons Licenses. The license type is clearly identified on the article.

The Creative Commons Attribution License

The Creative Commons Attribution License (CC-BY) allows users to copy, distribute and transmit an article, adapt the article and make commercial use of the article. The CC-BY license permits commercial and non-

Creative Commons Attribution Non-Commercial License

The Creative Commons Attribution Non-Commercial (CC-BY-NC)License permits use, distribution and reproduction in any medium, provided the original work is properly cited and is not used for commercial purposes.(see below)

Creative Commons Attribution-Non-Commercial-NoDerivs License

The Creative Commons Attribution Non-Commercial-NoDerivs License (CC-BY-NC-ND) permits use, distribution and reproduction in any medium, provided the original work is properly cited, is not used for commercial purposes and no modifications or adaptations are made. (see below)

Use by commercial "for-profit" organizations

Use of Wiley Open Access articles for commercial, promotional, or marketing purposes requires further explicit permission from Wiley and will be subject to a fee.

Further details can be found on Wiley Online Library
http://olabout.wiley.com/WileyCDA/Section/id-410895.html

Other Terms and Conditions:

v1.10 Last updated September 2015

Questions? customercare@copyright.com.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE
LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530451157764
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	DNA-Templated Self-Assembly of Protein Arrays and Highly Conductive Nanowires
Licensed Content Author	Hao Yan, Sung Ha Park, Gleb Finkelstein, John H. Reif, et al.
Licensed Content Date	Sep 26, 2003
Licensed Content Volume	301
Licensed Content Issue	5641
Volume number	301
Issue number	5641
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 1
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS

Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.

The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."

All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.

This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

Self-Assembly of Hexagonal DNA Two-Dimensional (2D) Arrays

Author: Yu He, Yi Chen, Haipeng Liu, et al
Publication: Journal of the American Chemical Society
Publisher: American Chemical Society
Date: Sep 1, 2005

SPRINGER NATURE LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and Springer Nature ("Springer Nature") consists of your license details and the terms and conditions provided by Springer Nature and Copyright Clearance Center.

License Number	5530460117498
License date	Apr 15, 2023
Licensed Content Publisher	Springer Nature
Licensed Content Publication	Nature
Licensed Content Title	Folding DNA to create nanoscale shapes and patterns
Licensed Content Author	Paul W. K. Rothemund
Licensed Content Date	Mar 16, 2006
Type of Use	Thesis/Dissertation
Requestor type	non-commercial (non-profit)
Format	electronic
Portion	figures/tables/illustrations
Number of figures/tables/illustrations	1
High-res required	no
Will you be translating?	no
Circulation/distribution	1 - 29
Author of this Springer Nature content	no
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 2.
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

Springer Nature Customer Service Centre GmbH Terms and Conditions

The following terms and conditions ("Terms and Conditions") together with the terms specified in your [RightsLink] constitute the License ("License") between you as Licensee and Springer Nature Customer Service Centre GmbH as Licensor. By clicking 'accept' and completing the transaction for your use of the material ("Licensed Material"), you confirm your acceptance of and obligation to be bound by these Terms and Conditions.

1. Grant and Scope of License

1. 1. The Licensor grants you a personal, non-exclusive, non-transferable, non-sublicensable, revocable, world-wide License to reproduce, distribute, communicate to the public, make available, broadcast, electronically transmit or create derivative works using the Licensed Material for the purpose(s) specified in your RightsLink Licence Details only. Licenses are granted for the specific use requested in the order and for no other use, subject to these Terms and Conditions. You acknowledge and agree that the rights granted to you under this License do not include the right to modify, edit, translate, include in collective works, or create derivative works of the Licensed Material in whole or in

part unless expressly stated in your RightsLink Licence Details. You may use the Licensed Material only as permitted under this Agreement and will not reproduce, distribute, display, perform, or otherwise use or exploit any Licensed Material in any way, in whole or in part, except as expressly permitted by this License.

1. 2. You may only use the Licensed Content in the manner and to the extent permitted by these Terms and Conditions, by your RightsLink Licence Details and by any applicable laws.

1. 3. A separate license may be required for any additional use of the Licensed Material, e.g. where a license has been purchased for print use only, separate permission must be obtained for electronic re-use. Similarly, a License is only valid in the language selected and does not apply for editions in other languages unless additional translation rights have been granted separately in the License.

1. 4. Any content within the Licensed Material that is owned by third parties is expressly excluded from the License.

1. 5. Rights for additional reuses such as custom editions, computer/mobile applications, film or TV reuses and/or any other derivative rights requests require additional permission and may be subject to an additional fee. Please apply to journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

2. Reservation of Rights

Licensor reserves all rights not expressly granted to you under this License. You acknowledge and agree that nothing in this License limits or restricts Licensor's rights in or use of the Licensed Material in any way. Neither this License, nor any act, omission, or statement by Licensor or you, conveys any ownership right to you in any Licensed Material, or to any element or portion thereof. As between Licensor and you, Licensor owns and retains all right, title, and interest in and to the Licensed Material subject to the license granted in Section 1.1. Your permission to use the Licensed Material is expressly conditioned on you not impairing Licensor's or the applicable copyright owner's rights in the Licensed Material in any way.

3. Restrictions on use

3. 1. Minor editing privileges are allowed for adaptations for stylistic purposes or formatting purposes provided such alterations do not alter the original meaning or intention of the Licensed Material and the new figure(s) are still accurate and representative of the Licensed Material. Any other changes including but not limited to, cropping, adapting, and/or omitting material that affect the meaning, intention or moral rights of the author(s) are strictly prohibited.

3. 2. You must not use any Licensed Material as part of any design or trademark.

3. 3. Licensed Material may be used in Open Access Publications (OAP), but any such reuse must include a clear acknowledgment of this permission visible at the same time as the figures/tables/illustration or abstract and which must indicate that the Licensed Material is not part of the governing OA license but has been reproduced with permission. This may be indicated according to any standard referencing system but must include at a minimum 'Book/Journal title, Author, Journal Name (if applicable), Volume (if applicable), Publisher, Year, reproduced with permission from SNCSC'.

4. STM Permission Guidelines

4. 1. An alternative scope of license may apply to signatories of the STM Permissions Guidelines ("STM PG") as amended from time to time and made available at https://www.stm-assoc.org/intellectual-property/permissions/permissions-guidelines/.

4. 2. For content reuse requests that qualify for permission under the STM PG, and which may be updated from time to time, the STM PG supersede the terms and conditions contained in this License.

4. 3. If a License has been granted under the STM PG, but the STM PG no longer apply at the time of publication, further permission must be sought from the Rightsholder. Contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

5. Duration of License

5. 1. Unless otherwise indicated on your License, a License is valid from the date of purchase ("License Date") until the end of the relevant period in the below table:

Reuse in a medical communications project	Reuse up to distribution or time period indicated in License

Reuse in a dissertation/thesis	Lifetime of thesis
Reuse in a journal/magazine	Lifetime of journal/magazine
Reuse in a book/textbook	Lifetime of edition
Reuse on a website	1 year unless otherwise specified in the License
Reuse in a presentation/slide kit/poster	Lifetime of presentation/slide kit/poster. Note: publication whether electronic or in print of presentation/slide kit/poster may require further permission.
Reuse in conference proceedings	Lifetime of conference proceedings
Reuse in an annual report	Lifetime of annual report
Reuse in training/CME materials	Reuse up to distribution or time period indicated in License
Reuse in newsmedia	Lifetime of newsmedia
Reuse in coursepack/classroom materials	Reuse up to distribution and/or time period indicated in license

6. Acknowledgement

6. 1. The Licensor's permission must be acknowledged next to the Licensed Material in print. In electronic form, this acknowledgement must be visible at the same time as the figures/tables/illustrations or abstract and must be hyperlinked to the journal/book's homepage.

6. 2. Acknowledgement may be provided according to any standard referencing system and at a minimum should include "Author, Article/Book Title, Journal name/Book imprint, volume, page number, year, Springer Nature".

7. Reuse in a dissertation or thesis

7. 1. Where 'reuse in a dissertation/thesis' has been selected, the following terms apply: Print rights of the Version of Record are provided for; electronic rights for use only on institutional repository as defined by the Sherpa guideline (www.sherpa.ac.uk/romeo/) and only up to what is required by the awarding institution.

7. 2. For theses published under an ISBN or ISSN, separate permission is required. Please contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

7. 3. Authors must properly cite the published manuscript in their thesis according to current citation standards and include the following acknowledgement: *'Reproduced with permission from Springer Nature'.*

8. License Fee

You must pay the fee set forth in the License Agreement (the "License Fees"). All amounts payable by you under this License are exclusive of any sales, use, withholding, value added or similar taxes, government fees or levies or other assessments. Collection and/or remittance of such taxes to the relevant tax authority shall be the responsibility of the party who has the legal obligation to do so.

9. Warranty

9. 1. The Licensor warrants that it has, to the best of its knowledge, the rights to license reuse of the Licensed Material. **You are solely responsible for ensuring that the material you wish to license is original to the Licensor and does not carry the copyright of another entity or third party (as credited in the published version).** If the credit line on any part of the Licensed Material indicates that it was reprinted or adapted with permission from another source, then you should seek additional permission from that source to reuse the material.

9. 2. EXCEPT FOR THE EXPRESS WARRANTY STATED HEREIN AND TO THE EXTENT PERMITTED BY APPLICABLE LAW, LICENSOR PROVIDES THE LICENSED MATERIAL "AS IS" AND MAKES NO OTHER REPRESENTATION OR WARRANTY. LICENSOR EXPRESSLY DISCLAIMS ANY LIABILITY FOR ANY CLAIM ARISING FROM OR OUT OF THE CONTENT, INCLUDING BUT NOT LIMITED TO ANY ERRORS, INACCURACIES, OMISSIONS, OR DEFECTS CONTAINED THEREIN, AND ANY IMPLIED OR EXPRESS WARRANTY AS TO MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. IN NO EVENT SHALL LICENSOR BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, PUNITIVE, OR EXEMPLARY DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, VIEWING OR USE OF THE LICENSED MATERIAL REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION,

DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION APPLIES NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

10. Termination and Cancellation

10. 1. The License and all rights granted hereunder will continue until the end of the applicable period shown in Clause 5.1 above. Thereafter, this license will be terminated and all rights granted hereunder will cease.

10. 2. Licensor reserves the right to terminate the License in the event that payment is not received in full or if you breach the terms of this License.

11. General

11. 1. The License and the rights and obligations of the parties hereto shall be construed, interpreted and determined in accordance with the laws of the Federal Republic of Germany without reference to the stipulations of the CISG (United Nations Convention on Contracts for the International Sale of Goods) or to Germany´s choice-of-law principle.

11. 2. The parties acknowledge and agree that any controversies and disputes arising out of this License shall be decided exclusively by the courts of or having jurisdiction for Heidelberg, Germany, as far as legally permissible.

11. 3. This License is solely for Licensor's and Licensee's benefit. It is not for the benefit of any other person or entity.

Questions? For questions on Copyright Clearance Center accounts or website issues please contact springernaturesupport@copyright.com or +1-855-239-3415 (toll free in the US) or +1-978-646-2777. For questions on Springer Nature licensing please visit https://www.springernature.com/gp/partners/rights-permissions-third-party-distribution

Other Conditions:

Version 1.4 - Dec 2022

Questions? E-mail us at customercare@copyright.com.

SPRINGER NATURE LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and Springer Nature ("Springer Nature") consists of your license details and the terms and conditions provided by Springer Nature and Copyright Clearance Center.

License Number	5530460335893
License date	Apr 15, 2023
Licensed Content Publisher	Springer Nature
Licensed Content Publication	Nature
Licensed Content Title	Self-assembly of DNA into nanoscale three-dimensional shapes
Licensed Content Author	Shawn M. Douglas et al
Licensed Content Date	May 21, 2009
Type of Use	Thesis/Dissertation
Requestor type	non-commercial (non-profit)
Format	electronic
Portion	figures/tables/illustrations
Number of figures/tables/illustrations	1
High-res required	no
Will you be translating?	no
Circulation/distribution	1 - 29
Author of this Springer Nature content	no
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 2.
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

Springer Nature Customer Service Centre GmbH Terms and Conditions

The following terms and conditions ("Terms and Conditions") together with the terms specified in your [RightsLink] constitute the License ("License") between you as Licensee and Springer Nature Customer Service Centre GmbH as Licensor. By clicking 'accept' and completing the transaction for your use of the material ("Licensed Material"), you confirm your acceptance of and obligation to be bound by these Terms and Conditions.

1. Grant and Scope of License

1. 1. The Licensor grants you a personal, non-exclusive, non-transferable, non-sublicensable, revocable, world-wide License to reproduce, distribute, communicate to the public, make available, broadcast, electronically transmit or create derivative works using the Licensed Material for the purpose(s) specified in your RightsLink Licence Details only. Licenses are granted for the specific use requested in the order and for no other use, subject to these Terms and Conditions. You acknowledge and agree that the rights granted to you under this License do not include the right to modify, edit, translate, include in collective works, or create derivative works of the Licensed Material in whole or in

part unless expressly stated in your RightsLink Licence Details. You may use the Licensed Material only as permitted under this Agreement and will not reproduce, distribute, display, perform, or otherwise use or exploit any Licensed Material in any way, in whole or in part, except as expressly permitted by this License.

1. 2. You may only use the Licensed Content in the manner and to the extent permitted by these Terms and Conditions, by your RightsLink Licence Details and by any applicable laws.

1. 3. A separate license may be required for any additional use of the Licensed Material, e.g. where a license has been purchased for print use only, separate permission must be obtained for electronic re-use. Similarly, a License is only valid in the language selected and does not apply for editions in other languages unless additional translation rights have been granted separately in the License.

1. 4. Any content within the Licensed Material that is owned by third parties is expressly excluded from the License.

1. 5. Rights for additional reuses such as custom editions, computer/mobile applications, film or TV reuses and/or any other derivative rights requests require additional permission and may be subject to an additional fee. Please apply to journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

2. Reservation of Rights

Licensor reserves all rights not expressly granted to you under this License. You acknowledge and agree that nothing in this License limits or restricts Licensor's rights in or use of the Licensed Material in any way. Neither this License, nor any act, omission, or statement by Licensor or you, conveys any ownership right to you in any Licensed Material, or to any element or portion thereof. As between Licensor and you, Licensor owns and retains all right, title, and interest in and to the Licensed Material subject to the license granted in Section 1.1. Your permission to use the Licensed Material is expressly conditioned on you not impairing Licensor's or the applicable copyright owner's rights in the Licensed Material in any way.

3. Restrictions on use

3. 1. Minor editing privileges are allowed for adaptations for stylistic purposes or formatting purposes provided such alterations do not alter the original meaning or intention of the Licensed Material and the new figure(s) are still accurate and representative of the Licensed Material. Any other changes including but not limited to, cropping, adapting, and/or omitting material that affect the meaning, intention or moral rights of the author(s) are strictly prohibited.

3. 2. You must not use any Licensed Material as part of any design or trademark.

3. 3. Licensed Material may be used in Open Access Publications (OAP), but any such reuse must include a clear acknowledgment of this permission visible at the same time as the figures/tables/illustration or abstract and which must indicate that the Licensed Material is not part of the governing OA license but has been reproduced with permission. This may be indicated according to any standard referencing system but must include at a minimum 'Book/Journal title, Author, Journal Name (if applicable), Volume (if applicable), Publisher, Year, reproduced with permission from SNCSC'.

4. STM Permission Guidelines

4. 1. An alternative scope of license may apply to signatories of the STM Permissions Guidelines ("STM PG") as amended from time to time and made available at https://www.stm-assoc.org/intellectual-property/permissions/permissions-guidelines/.

4. 2. For content reuse requests that qualify for permission under the STM PG, and which may be updated from time to time, the STM PG supersede the terms and conditions contained in this License.

4. 3. If a License has been granted under the STM PG, but the STM PG no longer apply at the time of publication, further permission must be sought from the Rightsholder. Contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

5. Duration of License

5. 1. Unless otherwise indicated on your License, a License is valid from the date of purchase ("License Date") until the end of the relevant period in the below table:

Reuse in a medical communications project	Reuse up to distribution or time period indicated in License

Reuse in a dissertation/thesis	Lifetime of thesis
Reuse in a journal/magazine	Lifetime of journal/magazine
Reuse in a book/textbook	Lifetime of edition
Reuse on a website	1 year unless otherwise specified in the License
Reuse in a presentation/slide kit/poster	Lifetime of presentation/slide kit/poster. Note: publication whether electronic or in print of presentation/slide kit/poster may require further permission.
Reuse in conference proceedings	Lifetime of conference proceedings
Reuse in an annual report	Lifetime of annual report
Reuse in training/CME materials	Reuse up to distribution or time period indicated in License
Reuse in newsmedia	Lifetime of newsmedia
Reuse in coursepack/classroom materials	Reuse up to distribution and/or time period indicated in license

6. Acknowledgement

6. 1. The Licensor's permission must be acknowledged next to the Licensed Material in print. In electronic form, this acknowledgement must be visible at the same time as the figures/tables/illustrations or abstract and must be hyperlinked to the journal/book's homepage.

6. 2. Acknowledgement may be provided according to any standard referencing system and at a minimum should include "Author, Article/Book Title, Journal name/Book imprint, volume, page number, year, Springer Nature".

7. Reuse in a dissertation or thesis

7. 1. Where 'reuse in a dissertation/thesis' has been selected, the following terms apply: Print rights of the Version of Record are provided for; electronic rights for use only on institutional repository as defined by the Sherpa guideline (www.sherpa.ac.uk/romeo/) and only up to what is required by the awarding institution.

7. 2. For theses published under an ISBN or ISSN, separate permission is required. Please contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

7. 3. Authors must properly cite the published manuscript in their thesis according to current citation standards and include the following acknowledgement: *'Reproduced with permission from Springer Nature'.*

8. License Fee

You must pay the fee set forth in the License Agreement (the "License Fees"). All amounts payable by you under this License are exclusive of any sales, use, withholding, value added or similar taxes, government fees or levies or other assessments. Collection and/or remittance of such taxes to the relevant tax authority shall be the responsibility of the party who has the legal obligation to do so.

9. Warranty

9. 1. The Licensor warrants that it has, to the best of its knowledge, the rights to license reuse of the Licensed Material. **You are solely responsible for ensuring that the material you wish to license is original to the Licensor and does not carry the copyright of another entity or third party (as credited in the published version).** If the credit line on any part of the Licensed Material indicates that it was reprinted or adapted with permission from another source, then you should seek additional permission from that source to reuse the material.

9. 2. EXCEPT FOR THE EXPRESS WARRANTY STATED HEREIN AND TO THE EXTENT PERMITTED BY APPLICABLE LAW, LICENSOR PROVIDES THE LICENSED MATERIAL "AS IS" AND MAKES NO OTHER REPRESENTATION OR WARRANTY. LICENSOR EXPRESSLY DISCLAIMS ANY LIABILITY FOR ANY CLAIM ARISING FROM OR OUT OF THE CONTENT, INCLUDING BUT NOT LIMITED TO ANY ERRORS, INACCURACIES, OMISSIONS, OR DEFECTS CONTAINED THEREIN, AND ANY IMPLIED OR EXPRESS WARRANTY AS TO MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. IN NO EVENT SHALL LICENSOR BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, PUNITIVE, OR EXEMPLARY DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, VIEWING OR USE OF THE LICENSED MATERIAL REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION,

DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION APPLIES NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

10. Termination and Cancellation

10. 1. The License and all rights granted hereunder will continue until the end of the applicable period shown in Clause 5.1 above. Thereafter, this license will be terminated and all rights granted hereunder will cease.

10. 2. Licensor reserves the right to terminate the License in the event that payment is not received in full or if you breach the terms of this License.

11. General

11. 1. The License and the rights and obligations of the parties hereto shall be construed, interpreted and determined in accordance with the laws of the Federal Republic of Germany without reference to the stipulations of the CISG (United Nations Convention on Contracts for the International Sale of Goods) or to Germany´s choice-of-law principle.

11. 2. The parties acknowledge and agree that any controversies and disputes arising out of this License shall be decided exclusively by the courts of or having jurisdiction for Heidelberg, Germany, as far as legally permissible.

11. 3. This License is solely for Licensor's and Licensee's benefit. It is not for the benefit of any other person or entity.

Questions? For questions on Copyright Clearance Center accounts or website issues please contact springernaturesupport@copyright.com or +1-855-239-3415 (toll free in the US) or +1-978-646-2777. For questions on Springer Nature licensing please visit https://www.springernature.com/gp/partners/rights-permissions-third-party-distribution

Other Conditions:

Version 1.4 - Dec 2022

Questions? E-mail us at customercare@copyright.com.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE LICENSE TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530460845123
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	DNA Origami with Complex Curvatures in Three-Dimensional Space
Licensed Content Author	Dongran Han, Suchetan Pal, Jeanette Nangreave, Zhengtao Deng, et al.
Licensed Content Date	Apr 15, 2011
Licensed Content Volume	332
Licensed Content Issue	6027
Volume number	332
Issue number	6027
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 3.
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS

Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.

The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."

All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.

This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

SPRINGER NATURE LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and Springer Nature ("Springer Nature") consists of your license details and the terms and conditions provided by Springer Nature and Copyright Clearance Center.

License Number	5530460951647
License date	Apr 15, 2023
Licensed Content Publisher	Springer Nature
Licensed Content Publication	Nature Nanotechnology
Licensed Content Title	Complex wireframe DNA origami nanostructures with multi-arm junction vertices
Licensed Content Author	Fei Zhang et al
Licensed Content Date	Jul 20, 2015
Type of Use	Thesis/Dissertation
Requestor type	non-commercial (non-profit)
Format	electronic
Portion	figures/tables/illustrations
Number of figures/tables/illustrations	1
High-res required	no
Will you be translating?	no
Circulation/distribution	1 - 29
Author of this Springer Nature content	no
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 3
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

Springer Nature Customer Service Centre GmbH Terms and Conditions

The following terms and conditions ("Terms and Conditions") together with the terms specified in your [RightsLink] constitute the License ("License") between you as Licensee and Springer Nature Customer Service Centre GmbH as Licensor. By clicking 'accept' and completing the transaction for your use of the material ("Licensed Material"), you confirm your acceptance of and obligation to be bound by these Terms and Conditions.

1. Grant and Scope of License

1. 1. The Licensor grants you a personal, non-exclusive, non-transferable, non-sublicensable, revocable, world-wide License to reproduce, distribute, communicate to the public, make available, broadcast, electronically transmit or create derivative works using the Licensed Material for the purpose(s) specified in your RightsLink Licence Details only. Licenses are granted for the specific use requested in the order and for no other use, subject to these Terms and Conditions. You acknowledge and agree that the rights granted to you under this License do not include the right to modify, edit, translate, include in collective works, or create derivative works of the Licensed Material in whole or in

part unless expressly stated in your RightsLink Licence Details. You may use the Licensed Material only as permitted under this Agreement and will not reproduce, distribute, display, perform, or otherwise use or exploit any Licensed Material in any way, in whole or in part, except as expressly permitted by this License.

1. 2. You may only use the Licensed Content in the manner and to the extent permitted by these Terms and Conditions, by your RightsLink Licence Details and by any applicable laws.

1. 3. A separate license may be required for any additional use of the Licensed Material, e.g. where a license has been purchased for print use only, separate permission must be obtained for electronic re-use. Similarly, a License is only valid in the language selected and does not apply for editions in other languages unless additional translation rights have been granted separately in the License.

1. 4. Any content within the Licensed Material that is owned by third parties is expressly excluded from the License.

1. 5. Rights for additional reuses such as custom editions, computer/mobile applications, film or TV reuses and/or any other derivative rights requests require additional permission and may be subject to an additional fee. Please apply to journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

2. Reservation of Rights

Licensor reserves all rights not expressly granted to you under this License. You acknowledge and agree that nothing in this License limits or restricts Licensor's rights in or use of the Licensed Material in any way. Neither this License, nor any act, omission, or statement by Licensor or you, conveys any ownership right to you in any Licensed Material, or to any element or portion thereof. As between Licensor and you, Licensor owns and retains all right, title, and interest in and to the Licensed Material subject to the license granted in Section 1.1. Your permission to use the Licensed Material is expressly conditioned on you not impairing Licensor's or the applicable copyright owner's rights in the Licensed Material in any way.

3. Restrictions on use

3. 1. Minor editing privileges are allowed for adaptations for stylistic purposes or formatting purposes provided such alterations do not alter the original meaning or intention of the Licensed Material and the new figure(s) are still accurate and representative of the Licensed Material. Any other changes including but not limited to, cropping, adapting, and/or omitting material that affect the meaning, intention or moral rights of the author(s) are strictly prohibited.

3. 2. You must not use any Licensed Material as part of any design or trademark.

3. 3. Licensed Material may be used in Open Access Publications (OAP), but any such reuse must include a clear acknowledgment of this permission visible at the same time as the figures/tables/illustration or abstract and which must indicate that the Licensed Material is not part of the governing OA license but has been reproduced with permission. This may be indicated according to any standard referencing system but must include at a minimum 'Book/Journal title, Author, Journal Name (if applicable), Volume (if applicable), Publisher, Year, reproduced with permission from SNCSC'.

4. STM Permission Guidelines

4. 1. An alternative scope of license may apply to signatories of the STM Permissions Guidelines ("STM PG") as amended from time to time and made available at https://www.stm-assoc.org/intellectual-property/permissions/permissions-guidelines/.

4. 2. For content reuse requests that qualify for permission under the STM PG, and which may be updated from time to time, the STM PG supersede the terms and conditions contained in this License.

4. 3. If a License has been granted under the STM PG, but the STM PG no longer apply at the time of publication, further permission must be sought from the Rightsholder. Contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

5. Duration of License

5. 1. Unless otherwise indicated on your License, a License is valid from the date of purchase ("License Date") until the end of the relevant period in the below table:

Reuse in a medical communications project	Reuse up to distribution or time period indicated in License

Reuse in a dissertation/thesis	Lifetime of thesis
Reuse in a journal/magazine	Lifetime of journal/magazine
Reuse in a book/textbook	Lifetime of edition
Reuse on a website	1 year unless otherwise specified in the License
Reuse in a presentation/slide kit/poster	Lifetime of presentation/slide kit/poster. Note: publication whether electronic or in print of presentation/slide kit/poster may require further permission.
Reuse in conference proceedings	Lifetime of conference proceedings
Reuse in an annual report	Lifetime of annual report
Reuse in training/CME materials	Reuse up to distribution or time period indicated in License
Reuse in newsmedia	Lifetime of newsmedia
Reuse in coursepack/classroom materials	Reuse up to distribution and/or time period indicated in license

6. Acknowledgement

6. 1. The Licensor's permission must be acknowledged next to the Licensed Material in print. In electronic form, this acknowledgement must be visible at the same time as the figures/tables/illustrations or abstract and must be hyperlinked to the journal/book's homepage.

6. 2. Acknowledgement may be provided according to any standard referencing system and at a minimum should include "Author, Article/Book Title, Journal name/Book imprint, volume, page number, year, Springer Nature".

7. Reuse in a dissertation or thesis

7. 1. Where 'reuse in a dissertation/thesis' has been selected, the following terms apply: Print rights of the Version of Record are provided for; electronic rights for use only on institutional repository as defined by the Sherpa guideline (www.sherpa.ac.uk/romeo/) and only up to what is required by the awarding institution.

7. 2. For theses published under an ISBN or ISSN, separate permission is required. Please contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

7. 3. Authors must properly cite the published manuscript in their thesis according to current citation standards and include the following acknowledgement: *'Reproduced with permission from Springer Nature'.*

8. License Fee

You must pay the fee set forth in the License Agreement (the "License Fees"). All amounts payable by you under this License are exclusive of any sales, use, withholding, value added or similar taxes, government fees or levies or other assessments. Collection and/or remittance of such taxes to the relevant tax authority shall be the responsibility of the party who has the legal obligation to do so.

9. Warranty

9. 1. The Licensor warrants that it has, to the best of its knowledge, the rights to license reuse of the Licensed Material. **You are solely responsible for ensuring that the material you wish to license is original to the Licensor and does not carry the copyright of another entity or third party (as credited in the published version).** If the credit line on any part of the Licensed Material indicates that it was reprinted or adapted with permission from another source, then you should seek additional permission from that source to reuse the material.

9. 2. EXCEPT FOR THE EXPRESS WARRANTY STATED HEREIN AND TO THE EXTENT PERMITTED BY APPLICABLE LAW, LICENSOR PROVIDES THE LICENSED MATERIAL "AS IS" AND MAKES NO OTHER REPRESENTATION OR WARRANTY. LICENSOR EXPRESSLY DISCLAIMS ANY LIABILITY FOR ANY CLAIM ARISING FROM OR OUT OF THE CONTENT, INCLUDING BUT NOT LIMITED TO ANY ERRORS, INACCURACIES, OMISSIONS, OR DEFECTS CONTAINED THEREIN, AND ANY IMPLIED OR EXPRESS WARRANTY AS TO MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. IN NO EVENT SHALL LICENSOR BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, PUNITIVE, OR EXEMPLARY DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, VIEWING OR USE OF THE LICENSED MATERIAL REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION,

DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION APPLIES NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

10. Termination and Cancellation

10. 1. The License and all rights granted hereunder will continue until the end of the applicable period shown in Clause 5.1 above. Thereafter, this license will be terminated and all rights granted hereunder will cease.

10. 2. Licensor reserves the right to terminate the License in the event that payment is not received in full or if you breach the terms of this License.

11. General

11. 1. The License and the rights and obligations of the parties hereto shall be construed, interpreted and determined in accordance with the laws of the Federal Republic of Germany without reference to the stipulations of the CISG (United Nations Convention on Contracts for the International Sale of Goods) or to Germany´s choice-of-law principle.

11. 2. The parties acknowledge and agree that any controversies and disputes arising out of this License shall be decided exclusively by the courts of or having jurisdiction for Heidelberg, Germany, as far as legally permissible.

11. 3. This License is solely for Licensor's and Licensee's benefit. It is not for the benefit of any other person or entity.

Questions? For questions on Copyright Clearance Center accounts or website issues please contact springernaturesupport@copyright.com or +1-855-239-3415 (toll free in the US) or +1-978-646-2777. For questions on Springer Nature licensing please visit https://www.springernature.com/gp/partners/rights-permissions-third-party-distribution

Other Conditions:

Version 1.4 - Dec 2022

Questions? E-mail us at customercare@copyright.com.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE LICENSE TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530461036677
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	Dynamic DNA devices and assemblies formed by shape-complementary, non–base pairing 3D components
Licensed Content Author	Thomas Gerling, Klaus F. Wagenbauer, Andrea M. Neuner, Hendrik Dietz
Licensed Content Date	Mar 27, 2015
Licensed Content Volume	347
Licensed Content Issue	6229
Volume number	347
Issue number	6229
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 1
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS

Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.

The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."

All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.

This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE
LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530461417969
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	Molecular force spectroscopy with a DNA origami–based nanoscopic force clamp
Licensed Content Author	Philipp C. Nickels, Bettina Wünsch, Phil Holzmeister, Wooli Bae, et al.
Licensed Content Date	Oct 21, 2016
Licensed Content Volume	354
Licensed Content Issue	6310
Volume number	354
Issue number	6310
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 3
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS
Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.
The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."
All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.
This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

SPRINGER NATURE LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and Springer Nature ("Springer Nature") consists of your license details and the terms and conditions provided by Springer Nature and Copyright Clearance Center.

License Number	5530470154708
License date	Apr 15, 2023
Licensed Content Publisher	Springer Nature
Licensed Content Publication	Nature Chemistry
Licensed Content Title	Self-organized architectures from assorted DNA-framed nanoparticles
Licensed Content Author	Wenyan Liu et al
Licensed Content Date	Jun 13, 2016
Type of Use	Thesis/Dissertation
Requestor type	non-commercial (non-profit)
Format	electronic
Portion	figures/tables/illustrations
Number of figures/tables/illustrations	1
High-res required	no
Will you be translating?	no
Circulation/distribution	1 - 29
Author of this Springer Nature content	no
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 3
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

Springer Nature Customer Service Centre GmbH Terms and Conditions

The following terms and conditions ("Terms and Conditions") together with the terms specified in your [RightsLink] constitute the License ("License") between you as Licensee and Springer Nature Customer Service Centre GmbH as Licensor. By clicking 'accept' and completing the transaction for your use of the material ("Licensed Material"), you confirm your acceptance of and obligation to be bound by these Terms and Conditions.

1. Grant and Scope of License

1. 1. The Licensor grants you a personal, non-exclusive, non-transferable, non-sublicensable, revocable, world-wide License to reproduce, distribute, communicate to the public, make available, broadcast, electronically transmit or create derivative works using the Licensed Material for the purpose(s) specified in your RightsLink Licence Details only. Licenses are granted for the specific use requested in the order and for no other use, subject to these Terms and Conditions. You acknowledge and agree that the rights granted to you under this License do not include the right to modify, edit, translate, include in collective works, or create derivative works of the Licensed Material in whole or in

part unless expressly stated in your RightsLink Licence Details. You may use the Licensed Material only as permitted under this Agreement and will not reproduce, distribute, display, perform, or otherwise use or exploit any Licensed Material in any way, in whole or in part, except as expressly permitted by this License.

1. 2. You may only use the Licensed Content in the manner and to the extent permitted by these Terms and Conditions, by your RightsLink Licence Details and by any applicable laws.

1. 3. A separate license may be required for any additional use of the Licensed Material, e.g. where a license has been purchased for print use only, separate permission must be obtained for electronic re-use. Similarly, a License is only valid in the language selected and does not apply for editions in other languages unless additional translation rights have been granted separately in the License.

1. 4. Any content within the Licensed Material that is owned by third parties is expressly excluded from the License.

1. 5. Rights for additional reuses such as custom editions, computer/mobile applications, film or TV reuses and/or any other derivative rights requests require additional permission and may be subject to an additional fee. Please apply to journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

2. Reservation of Rights

Licensor reserves all rights not expressly granted to you under this License. You acknowledge and agree that nothing in this License limits or restricts Licensor's rights in or use of the Licensed Material in any way. Neither this License, nor any act, omission, or statement by Licensor or you, conveys any ownership right to you in any Licensed Material, or to any element or portion thereof. As between Licensor and you, Licensor owns and retains all right, title, and interest in and to the Licensed Material subject to the license granted in Section 1.1. Your permission to use the Licensed Material is expressly conditioned on you not impairing Licensor's or the applicable copyright owner's rights in the Licensed Material in any way.

3. Restrictions on use

3. 1. Minor editing privileges are allowed for adaptations for stylistic purposes or formatting purposes provided such alterations do not alter the original meaning or intention of the Licensed Material and the new figure(s) are still accurate and representative of the Licensed Material. Any other changes including but not limited to, cropping, adapting, and/or omitting material that affect the meaning, intention or moral rights of the author(s) are strictly prohibited.

3. 2. You must not use any Licensed Material as part of any design or trademark.

3. 3. Licensed Material may be used in Open Access Publications (OAP), but any such reuse must include a clear acknowledgment of this permission visible at the same time as the figures/tables/illustration or abstract and which must indicate that the Licensed Material is not part of the governing OA license but has been reproduced with permission. This may be indicated according to any standard referencing system but must include at a minimum 'Book/Journal title, Author, Journal Name (if applicable), Volume (if applicable), Publisher, Year, reproduced with permission from SNCSC'.

4. STM Permission Guidelines

4. 1. An alternative scope of license may apply to signatories of the STM Permissions Guidelines ("STM PG") as amended from time to time and made available at https://www.stm-assoc.org/intellectual-property/permissions/permissions-guidelines/.

4. 2. For content reuse requests that qualify for permission under the STM PG, and which may be updated from time to time, the STM PG supersede the terms and conditions contained in this License.

4. 3. If a License has been granted under the STM PG, but the STM PG no longer apply at the time of publication, further permission must be sought from the Rightsholder. Contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

5. Duration of License

5. 1. Unless otherwise indicated on your License, a License is valid from the date of purchase ("License Date") until the end of the relevant period in the below table:

Reuse in a medical communications project	Reuse up to distribution or time period indicated in License

Reuse in a dissertation/thesis	Lifetime of thesis
Reuse in a journal/magazine	Lifetime of journal/magazine
Reuse in a book/textbook	Lifetime of edition
Reuse on a website	1 year unless otherwise specified in the License
Reuse in a presentation/slide kit/poster	Lifetime of presentation/slide kit/poster. Note: publication whether electronic or in print of presentation/slide kit/poster may require further permission.
Reuse in conference proceedings	Lifetime of conference proceedings
Reuse in an annual report	Lifetime of annual report
Reuse in training/CME materials	Reuse up to distribution or time period indicated in License
Reuse in newsmedia	Lifetime of newsmedia
Reuse in coursepack/classroom materials	Reuse up to distribution and/or time period indicated in license

6. Acknowledgement

6. 1. The Licensor's permission must be acknowledged next to the Licensed Material in print. In electronic form, this acknowledgement must be visible at the same time as the figures/tables/illustrations or abstract and must be hyperlinked to the journal/book's homepage.

6. 2. Acknowledgement may be provided according to any standard referencing system and at a minimum should include "Author, Article/Book Title, Journal name/Book imprint, volume, page number, year, Springer Nature".

7. Reuse in a dissertation or thesis

7. 1. Where 'reuse in a dissertation/thesis' has been selected, the following terms apply: Print rights of the Version of Record are provided for; electronic rights for use only on institutional repository as defined by the Sherpa guideline (www.sherpa.ac.uk/romeo/) and only up to what is required by the awarding institution.

7. 2. For theses published under an ISBN or ISSN, separate permission is required. Please contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

7. 3. Authors must properly cite the published manuscript in their thesis according to current citation standards and include the following acknowledgement: *'Reproduced with permission from Springer Nature'.*

8. License Fee

You must pay the fee set forth in the License Agreement (the "License Fees"). All amounts payable by you under this License are exclusive of any sales, use, withholding, value added or similar taxes, government fees or levies or other assessments. Collection and/or remittance of such taxes to the relevant tax authority shall be the responsibility of the party who has the legal obligation to do so.

9. Warranty

9. 1. The Licensor warrants that it has, to the best of its knowledge, the rights to license reuse of the Licensed Material. **You are solely responsible for ensuring that the material you wish to license is original to the Licensor and does not carry the copyright of another entity or third party (as credited in the published version).** If the credit line on any part of the Licensed Material indicates that it was reprinted or adapted with permission from another source, then you should seek additional permission from that source to reuse the material.

9. 2. EXCEPT FOR THE EXPRESS WARRANTY STATED HEREIN AND TO THE EXTENT PERMITTED BY APPLICABLE LAW, LICENSOR PROVIDES THE LICENSED MATERIAL "AS IS" AND MAKES NO OTHER REPRESENTATION OR WARRANTY. LICENSOR EXPRESSLY DISCLAIMS ANY LIABILITY FOR ANY CLAIM ARISING FROM OR OUT OF THE CONTENT, INCLUDING BUT NOT LIMITED TO ANY ERRORS, INACCURACIES, OMISSIONS, OR DEFECTS CONTAINED THEREIN, AND ANY IMPLIED OR EXPRESS WARRANTY AS TO MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. IN NO EVENT SHALL LICENSOR BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, PUNITIVE, OR EXEMPLARY DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, VIEWING OR USE OF THE LICENSED MATERIAL REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION,

DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION APPLIES NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

10. Termination and Cancellation

10. 1. The License and all rights granted hereunder will continue until the end of the applicable period shown in Clause 5.1 above. Thereafter, this license will be terminated and all rights granted hereunder will cease.

10. 2. Licensor reserves the right to terminate the License in the event that payment is not received in full or if you breach the terms of this License.

11. General

11. 1. The License and the rights and obligations of the parties hereto shall be construed, interpreted and determined in accordance with the laws of the Federal Republic of Germany without reference to the stipulations of the CISG (United Nations Convention on Contracts for the International Sale of Goods) or to Germany´s choice-of-law principle.

11. 2. The parties acknowledge and agree that any controversies and disputes arising out of this License shall be decided exclusively by the courts of or having jurisdiction for Heidelberg, Germany, as far as legally permissible.

11. 3. This License is solely for Licensor's and Licensee's benefit. It is not for the benefit of any other person or entity.

Questions? For questions on Copyright Clearance Center accounts or website issues please contact springernaturesupport@copyright.com or +1-855-239-3415 (toll free in the US) or +1-978-646-2777. For questions on Springer Nature licensing please visit https://www.springernature.com/gp/partners/rights-permissions-third-party-distribution

Other Conditions:

Version 1.4 - Dec 2022

Questions? E-mail us at customercare@copyright.com.

SPRINGER NATURE LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and Springer Nature ("Springer Nature") consists of your license details and the terms and conditions provided by Springer Nature and Copyright Clearance Center.

License Number	5530470253487
License date	Apr 15, 2023
Licensed Content Publisher	Springer Nature
Licensed Content Publication	Nature Methods
Licensed Content Title	Multiplexed 3D cellular super-resolution imaging with DNA-PAINT and Exchange-PAINT
Licensed Content Author	Ralf Jungmann et al
Licensed Content Date	Feb 2, 2014
Type of Use	Thesis/Dissertation
Requestor type	non-commercial (non-profit)
Format	electronic
Portion	figures/tables/illustrations
Number of figures/tables/illustrations	1
High-res required	no
Will you be translating?	no
Circulation/distribution	1 - 29
Author of this Springer Nature content	no
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 3
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

Springer Nature Customer Service Centre GmbH Terms and Conditions

The following terms and conditions ("Terms and Conditions") together with the terms specified in your [RightsLink] constitute the License ("License") between you as Licensee and Springer Nature Customer Service Centre GmbH as Licensor. By clicking 'accept' and completing the transaction for your use of the material ("Licensed Material"), you confirm your acceptance of and obligation to be bound by these Terms and Conditions.

1. Grant and Scope of License

1. 1. The Licensor grants you a personal, non-exclusive, non-transferable, non-sublicensable, revocable, world-wide License to reproduce, distribute, communicate to the public, make available, broadcast, electronically transmit or create derivative works using the Licensed Material for the purpose(s) specified in your RightsLink Licence Details only. Licenses are granted for the specific use requested in the order and for no other use, subject to these Terms and Conditions. You acknowledge and agree that the rights granted to you under this License do not include the right to modify, edit, translate, include in collective works, or create derivative works of the Licensed Material in whole or in

part unless expressly stated in your RightsLink Licence Details. You may use the Licensed Material only as permitted under this Agreement and will not reproduce, distribute, display, perform, or otherwise use or exploit any Licensed Material in any way, in whole or in part, except as expressly permitted by this License.

1. 2. You may only use the Licensed Content in the manner and to the extent permitted by these Terms and Conditions, by your RightsLink Licence Details and by any applicable laws.

1. 3. A separate license may be required for any additional use of the Licensed Material, e.g. where a license has been purchased for print use only, separate permission must be obtained for electronic re-use. Similarly, a License is only valid in the language selected and does not apply for editions in other languages unless additional translation rights have been granted separately in the License.

1. 4. Any content within the Licensed Material that is owned by third parties is expressly excluded from the License.

1. 5. Rights for additional reuses such as custom editions, computer/mobile applications, film or TV reuses and/or any other derivative rights requests require additional permission and may be subject to an additional fee. Please apply to journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

2. Reservation of Rights

Licensor reserves all rights not expressly granted to you under this License. You acknowledge and agree that nothing in this License limits or restricts Licensor's rights in or use of the Licensed Material in any way. Neither this License, nor any act, omission, or statement by Licensor or you, conveys any ownership right to you in any Licensed Material, or to any element or portion thereof. As between Licensor and you, Licensor owns and retains all right, title, and interest in and to the Licensed Material subject to the license granted in Section 1.1. Your permission to use the Licensed Material is expressly conditioned on you not impairing Licensor's or the applicable copyright owner's rights in the Licensed Material in any way.

3. Restrictions on use

3. 1. Minor editing privileges are allowed for adaptations for stylistic purposes or formatting purposes provided such alterations do not alter the original meaning or intention of the Licensed Material and the new figure(s) are still accurate and representative of the Licensed Material. Any other changes including but not limited to, cropping, adapting, and/or omitting material that affect the meaning, intention or moral rights of the author(s) are strictly prohibited.

3. 2. You must not use any Licensed Material as part of any design or trademark.

3. 3. Licensed Material may be used in Open Access Publications (OAP), but any such reuse must include a clear acknowledgment of this permission visible at the same time as the figures/tables/illustration or abstract and which must indicate that the Licensed Material is not part of the governing OA license but has been reproduced with permission. This may be indicated according to any standard referencing system but must include at a minimum 'Book/Journal title, Author, Journal Name (if applicable), Volume (if applicable), Publisher, Year, reproduced with permission from SNCSC'.

4. STM Permission Guidelines

4. 1. An alternative scope of license may apply to signatories of the STM Permissions Guidelines ("STM PG") as amended from time to time and made available at https://www.stm-assoc.org/intellectual-property/permissions/permissions-guidelines/.

4. 2. For content reuse requests that qualify for permission under the STM PG, and which may be updated from time to time, the STM PG supersede the terms and conditions contained in this License.

4. 3. If a License has been granted under the STM PG, but the STM PG no longer apply at the time of publication, further permission must be sought from the Rightsholder. Contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

5. Duration of License

5. 1. Unless otherwise indicated on your License, a License is valid from the date of purchase ("License Date") until the end of the relevant period in the below table:

Reuse in a medical communications project	Reuse up to distribution or time period indicated in License

Reuse in a dissertation/thesis	Lifetime of thesis
Reuse in a journal/magazine	Lifetime of journal/magazine
Reuse in a book/textbook	Lifetime of edition
Reuse on a website	1 year unless otherwise specified in the License
Reuse in a presentation/slide kit/poster	Lifetime of presentation/slide kit/poster. Note: publication whether electronic or in print of presentation/slide kit/poster may require further permission.
Reuse in conference proceedings	Lifetime of conference proceedings
Reuse in an annual report	Lifetime of annual report
Reuse in training/CME materials	Reuse up to distribution or time period indicated in License
Reuse in newsmedia	Lifetime of newsmedia
Reuse in coursepack/classroom materials	Reuse up to distribution and/or time period indicated in license

6. Acknowledgement

6. 1. The Licensor's permission must be acknowledged next to the Licensed Material in print. In electronic form, this acknowledgement must be visible at the same time as the figures/tables/illustrations or abstract and must be hyperlinked to the journal/book's homepage.

6. 2. Acknowledgement may be provided according to any standard referencing system and at a minimum should include "Author, Article/Book Title, Journal name/Book imprint, volume, page number, year, Springer Nature".

7. Reuse in a dissertation or thesis

7. 1. Where 'reuse in a dissertation/thesis' has been selected, the following terms apply: Print rights of the Version of Record are provided for; electronic rights for use only on institutional repository as defined by the Sherpa guideline (www.sherpa.ac.uk/romeo/) and only up to what is required by the awarding institution.

7. 2. For theses published under an ISBN or ISSN, separate permission is required. Please contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

7. 3. Authors must properly cite the published manuscript in their thesis according to current citation standards and include the following acknowledgement: *'Reproduced with permission from Springer Nature'.*

8. License Fee

You must pay the fee set forth in the License Agreement (the "License Fees"). All amounts payable by you under this License are exclusive of any sales, use, withholding, value added or similar taxes, government fees or levies or other assessments. Collection and/or remittance of such taxes to the relevant tax authority shall be the responsibility of the party who has the legal obligation to do so.

9. Warranty

9. 1. The Licensor warrants that it has, to the best of its knowledge, the rights to license reuse of the Licensed Material. **You are solely responsible for ensuring that the material you wish to license is original to the Licensor and does not carry the copyright of another entity or third party (as credited in the published version).** If the credit line on any part of the Licensed Material indicates that it was reprinted or adapted with permission from another source, then you should seek additional permission from that source to reuse the material.

9. 2. EXCEPT FOR THE EXPRESS WARRANTY STATED HEREIN AND TO THE EXTENT PERMITTED BY APPLICABLE LAW, LICENSOR PROVIDES THE LICENSED MATERIAL "AS IS" AND MAKES NO OTHER REPRESENTATION OR WARRANTY. LICENSOR EXPRESSLY DISCLAIMS ANY LIABILITY FOR ANY CLAIM ARISING FROM OR OUT OF THE CONTENT, INCLUDING BUT NOT LIMITED TO ANY ERRORS, INACCURACIES, OMISSIONS, OR DEFECTS CONTAINED THEREIN, AND ANY IMPLIED OR EXPRESS WARRANTY AS TO MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. IN NO EVENT SHALL LICENSOR BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, PUNITIVE, OR EXEMPLARY DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, VIEWING OR USE OF THE LICENSED MATERIAL REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION,

DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION APPLIES NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

10. Termination and Cancellation

10. 1. The License and all rights granted hereunder will continue until the end of the applicable period shown in Clause 5.1 above. Thereafter, this license will be terminated and all rights granted hereunder will cease.

10. 2. Licensor reserves the right to terminate the License in the event that payment is not received in full or if you breach the terms of this License.

11. General

11. 1. The License and the rights and obligations of the parties hereto shall be construed, interpreted and determined in accordance with the laws of the Federal Republic of Germany without reference to the stipulations of the CISG (United Nations Convention on Contracts for the International Sale of Goods) or to Germany´s choice-of-law principle.

11. 2. The parties acknowledge and agree that any controversies and disputes arising out of this License shall be decided exclusively by the courts of or having jurisdiction for Heidelberg, Germany, as far as legally permissible.

11. 3. This License is solely for Licensor's and Licensee's benefit. It is not for the benefit of any other person or entity.

Questions? For questions on Copyright Clearance Center accounts or website issues please contact springernaturesupport@copyright.com or +1-855-239-3415 (toll free in the US) or +1-978-646-2777. For questions on Springer Nature licensing please visit https://www.springernature.com/gp/partners/rights-permissions-third-party-distribution

Other Conditions:

Version 1.4 - Dec 2022

Questions? E-mail us at customercare@copyright.com.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE
LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530470431520
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	Self-Assembled Water-Soluble Nucleic Acid Probe Tiles for Label-Free RNA Hybridization Assays
Licensed Content Author	Yonggang Ke, Stuart Lindsay, Yung Chang, Yan Liu, et al.
Licensed Content Date	Jan 11, 2008
Licensed Content Volume	319
Licensed Content Issue	5860
Volume number	319
Issue number	5860
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 2
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS

Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.

The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."

All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.

This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE
LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530470795504
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	Synthetic Lipid Membrane Channels Formed by Designed DNA Nanostructures
Licensed Content Author	Martin Langecker, Vera Arnaut, Thomas G. Martin, Jonathan List, et al.
Licensed Content Date	Nov 16, 2012
Licensed Content Volume	338
Licensed Content Issue	6109
Volume number	338
Issue number	6109
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 3
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS

Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.

The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."

All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.

This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

THE AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE
LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and The American Association for the Advancement of Science ("The American Association for the Advancement of Science") consists of your license details and the terms and conditions provided by The American Association for the Advancement of Science and Copyright Clearance Center.

License Number	5530470929503
License date	Apr 15, 2023
Licensed Content Publisher	The American Association for the Advancement of Science
Licensed Content Publication	Science
Licensed Content Title	A Logic-Gated Nanorobot for Targeted Transport of Molecular Payloads
Licensed Content Author	Shawn M. Douglas, Ido Bachelet, George M. Church
Licensed Content Date	Feb 17, 2012
Licensed Content Volume	335
Licensed Content Issue	6070
Volume number	335
Issue number	6070
Type of Use	Thesis / Dissertation
Requestor type	Scientist/individual at a research institution
Format	Electronic
Portion	Text Excerpt
Number of pages requested	1
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 1
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

American Association for the Advancement of Science TERMS AND CONDITIONS

Regarding your request, we are pleased to grant you non-exclusive, non-transferable permission, to republish the AAAS material identified above in your work identified above, subject to the terms and conditions herein. We must be contacted for permission for any uses other than those specifically identified in your request above.

The following credit line must be printed along with the AAAS material: "From [Full Reference Citation]. Reprinted with permission from AAAS."

All required credit lines and notices must be visible any time a user accesses any part of the AAAS material and must appear on any printed copies and authorized user might make.

This permission does not apply to figures / photos / artwork or any other content or materials included in your work that are credited to non-AAAS sources. If the requested material is sourced to or references non-AAAS sources, you must obtain authorization from that source as well before using that material. You agree to hold harmless and indemnify AAAS against any claims arising from your use of any content in your work that is credited to non-AAAS sources.

SPRINGER NATURE LICENSE
TERMS AND CONDITIONS

Apr 15, 2023

This Agreement between Mr. Yue Tang ("You") and Springer Nature ("Springer Nature") consists of your license details and the terms and conditions provided by Springer Nature and Copyright Clearance Center.

License Number	5530471204147
License date	Apr 15, 2023
Licensed Content Publisher	Springer Nature
Licensed Content Publication	Nature Chemistry
Licensed Content Title	Barcoded DNA origami structures for multiplexed optimization and enrichment of DNA-based protein-binding cavities
Licensed Content Author	Ali Aghebat Rafat et al
Licensed Content Date	Jul 13, 2020
Type of Use	Thesis/Dissertation
Requestor type	non-commercial (non-profit)
Format	electronic
Portion	figures/tables/illustrations
Number of figures/tables/illustrations	1
High-res required	no
Will you be translating?	no
Circulation/distribution	1 - 29
Author of this Springer Nature content	no
Title	Rational Design and Application of DNA Origami Tessellation
Institution name	Arizona State University
Expected presentation date	Apr 2023
Portions	Figure 1
Requestor Location	Mr. Yue Tang 1201 S MCCLINTOCK DR APT 234 TEMPE, AZ 85281 United States Attn: Mr. Yue Tang
Total	**0.00 USD**

Terms and Conditions

Springer Nature Customer Service Centre GmbH Terms and Conditions

The following terms and conditions ("Terms and Conditions") together with the terms specified in your [RightsLink] constitute the License ("License") between you as Licensee and Springer Nature Customer Service Centre GmbH as Licensor. By clicking 'accept' and completing the transaction for your use of the material ("Licensed Material"), you confirm your acceptance of and obligation to be bound by these Terms and Conditions.

1. Grant and Scope of License

1. 1. The Licensor grants you a personal, non-exclusive, non-transferable, non-sublicensable, revocable, world-wide License to reproduce, distribute, communicate to the public, make available, broadcast, electronically transmit or create derivative works using the Licensed Material for the purpose(s) specified in your RightsLink Licence Details only. Licenses are granted for the specific use requested in the order and for no other use, subject to these Terms and Conditions. You acknowledge and agree that the rights granted to you under this License do not include the right

to modify, edit, translate, include in collective works, or create derivative works of the Licensed Material in whole or in part unless expressly stated in your RightsLink Licence Details. You may use the Licensed Material only as permitted under this Agreement and will not reproduce, distribute, display, perform, or otherwise use or exploit any Licensed Material in any way, in whole or in part, except as expressly permitted by this License.

1. 2. You may only use the Licensed Content in the manner and to the extent permitted by these Terms and Conditions, by your RightsLink Licence Details and by any applicable laws.

1. 3. A separate license may be required for any additional use of the Licensed Material, e.g. where a license has been purchased for print use only, separate permission must be obtained for electronic re-use. Similarly, a License is only valid in the language selected and does not apply for editions in other languages unless additional translation rights have been granted separately in the License.

1. 4. Any content within the Licensed Material that is owned by third parties is expressly excluded from the License.

1. 5. Rights for additional reuses such as custom editions, computer/mobile applications, film or TV reuses and/or any other derivative rights requests require additional permission and may be subject to an additional fee. Please apply to journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

2. Reservation of Rights

Licensor reserves all rights not expressly granted to you under this License. You acknowledge and agree that nothing in this License limits or restricts Licensor's rights in or use of the Licensed Material in any way. Neither this License, nor any act, omission, or statement by Licensor or you, conveys any ownership right to you in any Licensed Material, or to any element or portion thereof. As between Licensor and you, Licensor owns and retains all right, title, and interest in and to the Licensed Material subject to the license granted in Section 1.1. Your permission to use the Licensed Material is expressly conditioned on you not impairing Licensor's or the applicable copyright owner's rights in the Licensed Material in any way.

3. Restrictions on use

3. 1. Minor editing privileges are allowed for adaptations for stylistic purposes or formatting purposes provided such alterations do not alter the original meaning or intention of the Licensed Material and the new figure(s) are still accurate and representative of the Licensed Material. Any other changes including but not limited to, cropping, adapting, and/or omitting material that affect the meaning, intention or moral rights of the author(s) are strictly prohibited.

3. 2. You must not use any Licensed Material as part of any design or trademark.

3. 3. Licensed Material may be used in Open Access Publications (OAP), but any such reuse must include a clear acknowledgment of this permission visible at the same time as the figures/tables/illustration or abstract and which must indicate that the Licensed Material is not part of the governing OA license but has been reproduced with permission. This may be indicated according to any standard referencing system but must include at a minimum 'Book/Journal title, Author, Journal Name (if applicable), Volume (if applicable), Publisher, Year, reproduced with permission from SNCSC'.

4. STM Permission Guidelines

4. 1. An alternative scope of license may apply to signatories of the STM Permissions Guidelines ("STM PG") as amended from time to time and made available at https://www.stm-assoc.org/intellectual-property/permissions/permissions-guidelines/.

4. 2. For content reuse requests that qualify for permission under the STM PG, and which may be updated from time to time, the STM PG supersede the terms and conditions contained in this License.

4. 3. If a License has been granted under the STM PG, but the STM PG no longer apply at the time of publication, further permission must be sought from the Rightsholder. Contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

5. Duration of License

5. 1. Unless otherwise indicated on your License, a License is valid from the date of purchase ("License Date") until the end of the relevant period in the below table:

Reuse in a medical communications project	Reuse up to distribution or time period indicated in License
Reuse in a dissertation/thesis	Lifetime of thesis
Reuse in a journal/magazine	Lifetime of journal/magazine
Reuse in a book/textbook	Lifetime of edition
Reuse on a website	1 year unless otherwise specified in the License
Reuse in a presentation/slide kit/poster	Lifetime of presentation/slide kit/poster. Note: publication whether electronic or in print of presentation/slide kit/poster may require further permission.
Reuse in conference proceedings	Lifetime of conference proceedings
Reuse in an annual report	Lifetime of annual report
Reuse in training/CME materials	Reuse up to distribution or time period indicated in License
Reuse in newsmedia	Lifetime of newsmedia
Reuse in coursepack/classroom materials	Reuse up to distribution and/or time period indicated in license

6. Acknowledgement

6. 1. The Licensor's permission must be acknowledged next to the Licensed Material in print. In electronic form, this acknowledgement must be visible at the same time as the figures/tables/illustrations or abstract and must be hyperlinked to the journal/book's homepage.

6. 2. Acknowledgement may be provided according to any standard referencing system and at a minimum should include "Author, Article/Book Title, Journal name/Book imprint, volume, page number, year, Springer Nature".

7. Reuse in a dissertation or thesis

7. 1. Where 'reuse in a dissertation/thesis' has been selected, the following terms apply: Print rights of the Version of Record are provided for; electronic rights for use only on institutional repository as defined by the Sherpa guideline (www.sherpa.ac.uk/romeo/) and only up to what is required by the awarding institution.

7. 2. For theses published under an ISBN or ISSN, separate permission is required. Please contact journalpermissions@springernature.com or bookpermissions@springernature.com for these rights.

7. 3. Authors must properly cite the published manuscript in their thesis according to current citation standards and include the following acknowledgement: *'Reproduced with permission from Springer Nature'.*

8. License Fee

You must pay the fee set forth in the License Agreement (the "License Fees"). All amounts payable by you under this License are exclusive of any sales, use, withholding, value added or similar taxes, government fees or levies or other assessments. Collection and/or remittance of such taxes to the relevant tax authority shall be the responsibility of the party who has the legal obligation to do so.

9. Warranty

9. 1. The Licensor warrants that it has, to the best of its knowledge, the rights to license reuse of the Licensed Material. **You are solely responsible for ensuring that the material you wish to license is original to the Licensor and does not carry the copyright of another entity or third party (as credited in the published version).** If the credit line on any part of the Licensed Material indicates that it was reprinted or adapted with permission from another source, then you should seek additional permission from that source to reuse the material.

9. 2. EXCEPT FOR THE EXPRESS WARRANTY STATED HEREIN AND TO THE EXTENT PERMITTED BY APPLICABLE LAW, LICENSOR PROVIDES THE LICENSED MATERIAL "AS IS" AND MAKES NO OTHER REPRESENTATION OR WARRANTY. LICENSOR EXPRESSLY DISCLAIMS ANY LIABILITY FOR ANY CLAIM ARISING FROM OR OUT OF THE CONTENT, INCLUDING BUT NOT LIMITED TO ANY ERRORS, INACCURACIES, OMISSIONS, OR DEFECTS CONTAINED THEREIN, AND ANY IMPLIED OR EXPRESS WARRANTY AS TO MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. IN NO EVENT SHALL LICENSOR BE LIABLE TO YOU OR ANY OTHER PARTY OR ANY OTHER PERSON OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, INDIRECT, PUNITIVE, OR EXEMPLARY DAMAGES, HOWEVER CAUSED, ARISING OUT OF OR IN CONNECTION WITH THE DOWNLOADING, VIEWING OR USE OF THE LICENSED

MATERIAL REGARDLESS OF THE FORM OF ACTION, WHETHER FOR BREACH OF CONTRACT, BREACH OF WARRANTY, TORT, NEGLIGENCE, INFRINGEMENT OR OTHERWISE (INCLUDING, WITHOUT LIMITATION, DAMAGES BASED ON LOSS OF PROFITS, DATA, FILES, USE, BUSINESS OPPORTUNITY OR CLAIMS OF THIRD PARTIES), AND WHETHER OR NOT THE PARTY HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES. THIS LIMITATION APPLIES NOTWITHSTANDING ANY FAILURE OF ESSENTIAL PURPOSE OF ANY LIMITED REMEDY PROVIDED HEREIN.

10. Termination and Cancellation

10. 1. The License and all rights granted hereunder will continue until the end of the applicable period shown in Clause 5.1 above. Thereafter, this license will be terminated and all rights granted hereunder will cease.

10. 2. Licensor reserves the right to terminate the License in the event that payment is not received in full or if you breach the terms of this License.

11. General

11. 1. The License and the rights and obligations of the parties hereto shall be construed, interpreted and determined in accordance with the laws of the Federal Republic of Germany without reference to the stipulations of the CISG (United Nations Convention on Contracts for the International Sale of Goods) or to Germany´s choice-of-law principle.

11. 2. The parties acknowledge and agree that any controversies and disputes arising out of this License shall be decided exclusively by the courts of or having jurisdiction for Heidelberg, Germany, as far as legally permissible.

11. 3. This License is solely for Licensor's and Licensee's benefit. It is not for the benefit of any other person or entity.

Questions? For questions on Copyright Clearance Center accounts or website issues please contact springernaturesupport@copyright.com or +1-855-239-3415 (toll free in the US) or +1-978-646-2777. For questions on Springer Nature licensing please visit https://www.springernature.com/gp/partners/rights-permissions-third-party-distribution

Other Conditions:

Version 1.4 - Dec 2022

Questions? E-mail us at customercare@copyright.com.

PNAS Permissions 8:37 AM (5 hours ago)

to me

Dear Dr. Tang,

Thank you for your message. Permission is granted for your use of the material as described in your request. Please include a complete citation for the original PNAS article when reusing the material, and include "Copyright (2008) National Academy of Sciences, U.S.A." as a copyright note. Because this material published between 1993 and 2008, a copyright note is needed. There is no charge for this material, either. Let us know if you have any questions.

Best regards,
Eric Cain for
Diane Sullenberger
PNAS Executive Editor

From: Yue Tang <ytang86@asu.edu>
Sent: Saturday, April 15, 2023 3:58 PM
To: PNAS Permissions <PNASPermissions@nas.edu>
Subject: Permission to use figures in the dissertation

Hello,

This is Yue Tang, a PhD student from Arizona State University. I am writing to request permission to reuse the figure in my dissertation.

Material information:
PNAS,
Conformational flexibility facilitates self-assembly of complex DNA nanostructures,
Chuan Zhang, Min Su, Yu He, Xin Zhao, Ping-an Fang, Alexander E. Ribbe, Wen Jiang, and Chengde Mao.
August 5, 2008. 105 (31) 10665-10669.
Figure 1 and Figure 4.

Personal information:
Yue Tang, PhD candidate, Arizona State University.
Email: ytang86@asu.edu,
Tel: 614-256-4800,
Mail: 1001 S McAlister Ave, Biodesign Institute A_A115, Tempe, AZ, 85287.

Information about the reused material:
Type: Dissertation;
Title: Rational Design and Application of DNA Origami Tessellation;
Author: Yue Tang
Number of copies: 1
Nonprofit use

Best,

Yue Tang

APPENDIX E

CO-AUTHER APPROVAL

I verified that the following co-authors have approved me to our publications in my dissertation.

Hao Yan (Arizona State University)

Shuoxing Jiang (Nanjing University)