

# The Immunosignature of Canine Lymphoma: Characterization and Diagnostic Application

## Supplemental Material

Table S1. Individual results of dogs predicted as healthy or B cell lymphoma in the iterative training and testing.<sup>1</sup>

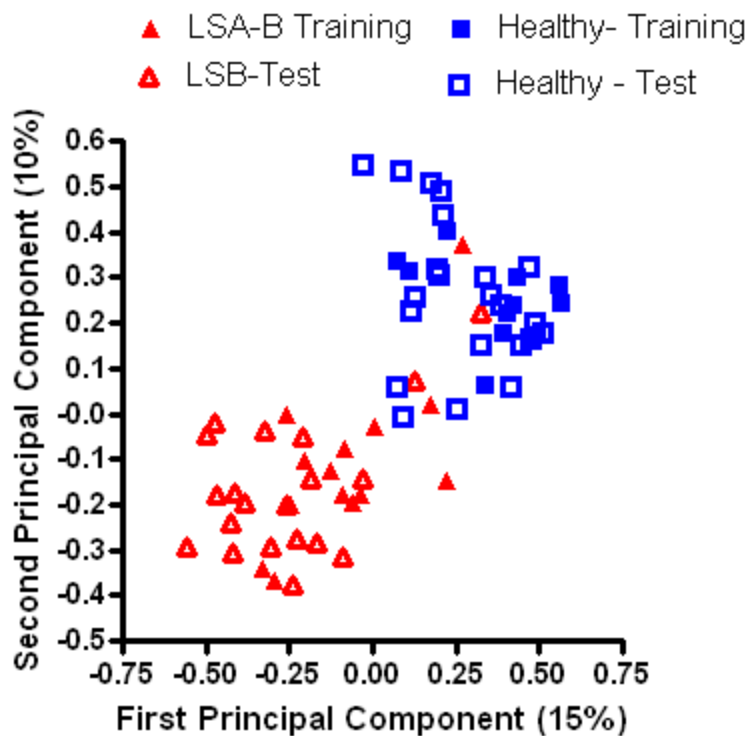
Individual	Healthy			Individual	B Cell Lymphoma		
	Correct <sup>2</sup>	Incorrect <sup>3</sup>	Accuracy <sup>4</sup>		Correct	Wrong	Accuracy
18	1511	120	92.64	1090	1362	194	87.53
31	1212	383	75.99	1093	1539	0	100.00
33	1593	1	99.94	1137	336	1201	21.86
35	471	1146	29.13	1144	1523	19	98.77
36	1526	151	91.00	1165	1532	14	99.09
4	31	1575	1.93	1167	1500	0	100.00
42	1575	0	100.00	13	1543	0	100.00
46	22	1591	1.36	231546	1586	0	100.00
49	1363	232	85.45	246620	1569	5	99.68
6	1484	95	93.98	247645	1193	310	79.37
201	1622	0	100.00	247659	1372	111	92.52
202	1590	27	98.33	247690	1470	1	99.93
203	1593	0	100.00	248661	1462	0	100.00
204	786	865	47.61	250947	1434	15	98.96
205	1587	1	99.94	251181	1575	0	100.00
206	1449	150	90.62	251332	1376	141	90.71
207	21	1602	1.29	251661	561	993	36.10
208	1613	1	99.94	252343	1280	220	85.33
209	1516	30	98.06	252353	1567	0	100.00
210	1605	2	99.88	252590	1336	244	84.56
211	1558	0	100.00	253357	1365	236	85.26
212	1424	207	87.31	253509	1431	172	89.27
213	1643	29	98.27	255800	1399	108	92.83
214	928	759	55.01	256744	1501	4	99.73
215	1676	0	100.00	256807	1050	490	68.18
216	1594	20	98.76	257195	1536	34	97.83
217	1682	22	98.71	258923	647	945	40.64
218	1502	174	89.62	260583	1058	514	67.30
219	1577	0	100.00	262527	1542	16	98.97
220	1652	0	100.00	262725	1596	0	100.00
221	1671	0	100.00	262948	1525	0	100.00
222	1626	0	100.00	263141	1518	30	98.06
223	1616	0	100.00	263293	1505	0	100.00
224	1644	0	100.00	263451	1536	0	100.00
225	1643	0	100.00	263814	1484	63	95.93
226	1593	13	99.19	671	1524	3	99.80
227	1605	0	100.00	819	1527	11	99.28
				822	1450	71	95.33
				863	1352	173	88.66

<sup>1</sup>Dogs were iteratively divided into two sets (15% training and 85%) for 10,000 iterations. The training set was used to select peptides and train an SVM for prediction of the test set.

<sup>2</sup>The number of times a dog was predicted correctly when in the training set

<sup>3</sup> The number of times a dog was predicted incorrectly when in the training set

<sup>4</sup> The individual accuracy for a given dog



**Figure S1. Classification of an independent test set into LSA patients and healthy dogs.**

The 340 peptides identified as informative between LSA and healthy dogs ( $p < 0.05$  with FDR and greater than 1.5 fold difference between classes) were used to train a support vector machine and predict a test set of dogs. The variance of all dogs in both the training set (solid symbols) and test set (open symbols) are presented in a principal component analysis. The first two principal components are presented as the x and y scalar values and each symbol represents the replicate average for a single dog. Peptides were selected on the training set using the KPL conjugate. The Jackson conjugate was used for both the training and test set in this assay.