Supplementary Table 1

Group A	Group B	SNPs	Total A	Hit A	Total B	Hit B	Pvalue	Enrich-ment	95% Lower	95% Upper
ABC DLBCL	GCB DLBCL	Q584H	103	2	132	0	1.91E-01	Inf	-	-
ABC DLBCL	Non-ABC DLBCL	Q584H	103	2	458	0	3.34E-02	Inf	-	-
ABC DLBCL	GO exome all	Q584H	103	2	6220	12	2.11E-02	10.06	2.28	44.40
ABC DLBCL	1000 genomes	Q584H	103	2	1094	4	8.75E-02	5.31	0.98	28.65
ABC DLBCL	Healthy ctrl. (GO exomes+1000 Genomes)	Q584H	103	2	7314	16	2.53E-02	8.88	2.07	38.11
ABC DLBCL	GCB DLBCL	Q622L	103	6	132	1	4.55E-02	7.69	0.94	62.87
ABC DLBCL	Non-ABC DLBCL	Q622L	103	6	458	3	1.75E-03	8.89	2.19	36.18
ABC DLBCL	GO exome all	Q622L	103	6	6100	47	2.21E-04	7.56	3.31	17.29
ABC DLBCL	1000 genomes	Q622L	103	6	1094	5	1.14E-04	12.75	3.96	41.05
ABC DLBCL	Healthy ctrl. (GO exomes+1000 Genomes)	Q622L	103	6	7194	52	1.53E-04	8.06	3.54	18.34
ABC DLBCL	GCB DLBCL	Q584H + Q622L	103	8	132	1	1.15E-02	10.25	1.30	80.67
ABC DLBCL	Non-ABC DLBCL	Q584H + Q622L	103	8	458	3	1.03E-04	11.86	3.09	45.52
ABC DLBCL	GO exome all	Q584H + Q622L	103	8	6100	59	1.28E-05	8.03	3.94	16.37
ABC DLBCL	1000 genomes	Q584H + Q622L	103	8	1094	9	2.92E-05	9.44	3.72	23.95
ABC DLBCL	Healthy ctrl. (GO exomes+1000 Genomes)	Q584H + Q622L	103	8	7194	68	1.02E-05	8.22	4.05	16.65

Supplementary Table 1: Enrichment of two rare SNPs among ABC DLBCL tumors. Two sided p-values for differences in prevalence were calculated using a Fisher's exact test. Confidence levels for the enrichment values were calculated using a normal approximation to the log enrichment. Confidence intervals for prevalence estimates were calculated using the Clopper-Pearson method.