

Table S1 List of genes included in the designed panel

Gene									
<i>ACTB</i>	<i>AHR</i>	<i>AKT1</i>	<i>AKT2</i>	<i>AKT3</i>	<i>ARID1A</i>	<i>ARNT</i>	<i>ATM</i>	<i>ATP2C2</i>	<i>B2M</i>
<i>BCL10</i>	<i>BCL2</i>	<i>BCL6</i>	<i>BCR</i>	<i>BIRC3</i>	<i>BRAF</i>	<i>BRCA2</i>	<i>BTG1</i>	<i>BTK</i>	<i>CARD11</i>
<i>CCND2</i>	<i>CCND3</i>	<i>CD44</i>	<i>CD58</i>	<i>CD70</i>	<i>CD79A</i>	<i>CD79B</i>	<i>CDKN2A</i>	<i>CDKN2B</i>	<i>CIITA</i>
<i>COL4A2</i>	<i>CREBBP</i>	<i>DDX3X</i>	<i>DNMT3A</i>	<i>EP300</i>	<i>ETV6</i>	<i>EZH2</i>	<i>FANCA</i>	<i>FAS</i>	<i>FBXW7</i>
<i>FOXO1</i>	<i>GNAI3</i>	<i>GNAI2</i>	<i>HDAC1</i>	<i>HDAC4</i>	<i>HDAC7</i>	<i>HIST1H1C</i>	<i>HIST1H1E</i>	<i>HMGB1</i>	<i>ID3</i>
<i>IDH1</i>	<i>IDH2</i>	<i>IKBKB</i>	<i>IRF4</i>	<i>IRF8</i>	<i>JAK1</i>	<i>JAK2</i>	<i>JAK3</i>	<i>KDM2B</i>	<i>KIT</i>
<i>KLHL6</i>	<i>KMT2C</i>	<i>KMT2D</i>	<i>KRAS</i>	<i>MALT1</i>	<i>MAP3K14</i>	<i>MAP3K7</i>	<i>MEF2B</i>	<i>MEF2C</i>	<i>MPL</i>
<i>MTOR</i>	<i>MYC</i>	<i>MYD88</i>	<i>NFKBIA</i>	<i>NOTCH1</i>	<i>NOTCH2</i>	<i>NRAS</i>	<i>P4HA2</i>	<i>PAX5</i>	<i>PDGFRA</i>
<i>PIK3CA</i>	<i>PIK3CD</i>	<i>PIK3CG</i>	<i>PIK3R1</i>	<i>PIK3R2</i>	<i>PIM1</i>	<i>POU2F2</i>	<i>PRDM1</i>	<i>PRKCB</i>	<i>PTEN</i>
<i>PTPN1</i>	<i>RHOA</i>	<i>RHOH</i>	<i>S1PR2</i>	<i>SETD2</i>	<i>SGK1</i>	<i>SOCS1</i>	<i>SPEN</i>	<i>SPIB</i>	<i>STAT3</i>
<i>STAT5A</i>	<i>STAT5B</i>	<i>STAT6</i>	<i>TBC1D10C</i>	<i>TBL1XR1</i>	<i>TCF3</i>	<i>TET2</i>	<i>TMEM30A</i>	<i>TNFAIP3</i>	<i>TNFRSF11A</i>
<i>TNFRSF14</i>	<i>TP53</i>	<i>TRAF2</i>	<i>TRAF3</i>	<i>TRAF5</i>	<i>UNC5C</i>				

Table S2 Mutation frequencies comparison between our and Western studies on DLBCL

Gene	Our study	Morin et al.*(1)	Pasqualucci et al.*(2)	Lohr et al.*(3)	Zhang et al.*(4)	Mottok et al.(5)	Schiff et al.(6)	Arcaini et al.(7)	Asmar et al.(8)	Quivoron et al.(9)	Trinh et al.(10)
<i>KMT2D</i>	30%	32%	23%	29%	—	—	—	—	—	—	—
<i>PIM1</i>	26%	17%	14%	31%	12%	—	—	—	—	—	—
<i>SOCS1</i>	24%	—	—	6%	3%	27%	16%	—	—	—	—
<i>MYD88</i>	21%	13%	8%	12%	15%	—	—	—	—	—	—
<i>BTG1</i>	20%	14%	—	16%	10%	—	—	—	—	—	—
<i>HIST1H1E</i>	18%	—	—	14%	7%	—	—	—	—	—	—
<i>CD79B</i>	18%	8%	12%	16%	8%	—	—	—	—	—	—
<i>SPEN</i>	17%	—	—	6%	—	—	—	1%	—	—	—
<i>KMT2C</i>	16%	—	—	4%	18%	—	—	—	—	—	—
<i>CREBBP</i>	13%	15%	18%	16%	4%	—	—	—	—	—	—
<i>SGK1</i>	13%	20%	—	10%	5%	—	—	—	—	—	—
<i>CIITA</i>	13%	5%	—	10%	—	—	—	—	—	—	—
<i>TBL1XR1</i>	11%	—	—	6%	—	—	—	—	—	—	—
<i>TET2</i>	11%	6%	—	0%	—	—	—	—	12%	6%	—
<i>CD70</i>	11%	7%	—	10%	—	—	—	—	—	—	—
<i>ARID1A</i>	10%	—	—	4%	5%	—	—	—	—	—	—
<i>FOXO1</i>	10%	5%	—	0%	—	—	—	—	—	—	9%
<i>KLHL6</i>	10%	10%	—	8%	—	—	—	—	—	—	—
<i>TNFRSF14</i>	10%	8%	—	22%	—	—	—	—	—	—	—
<i>CARD11</i>	10%	10%	10%	20%	11%	—	—	—	—	—	—
<i>B2M</i>	10%	8%	13%	10%	4%	—	—	—	—	—	—
<i>ATP2C2</i>	9%	—	—	2%	—	—	—	—	—	—	—
<i>HIST1H1C</i>	9%	9%	—	14%	8%	—	—	—	—	—	—
<i>IRF4</i>	9%	9%	—	2%	—	—	—	—	—	—	—
<i>NOTCH2</i>	9%	—	—	4%	7%	—	—	9%	—	—	—
<i>FAS</i>	9%	4%	—	0%	—	—	—	—	—	—	—
<i>TP53</i>	9%	12%	17%	24%	5%	—	—	—	—	—	—
<i>MEF2B</i>	8%	15%	8%	18%	3%	—	—	—	—	—	—
<i>NOTCH1</i>	8%	—	2%	8%	—	—	—	2%	—	—	—
<i>POU2F2</i>	8%	—	—	8%	5%	—	—	—	—	—	—
<i>FANCA</i>	7%	—	—	2%	—	—	—	—	—	—	—
<i>GNA13</i>	7%	15%	—	20%	7%	—	—	—	—	—	—
<i>STAT3</i>	7%	9%	—	10%	—	—	—	—	—	—	—
<i>STAT6</i>	7%	5%	—	4%	—	—	—	—	—	—	—
<i>BCL6</i>	7%	8%	—	8%	3%	—	—	—	—	—	—
<i>PRDM1</i>	7%	—	12%	0%	1%	—	—	—	—	—	—
<i>TNFAIP3</i>	7%	3%	15%	2%	10%	—	—	—	—	—	—
<i>ACTB</i>	7%	—	—	10%	—	—	—	—	—	—	—
<i>PTEN</i>	7%	—	—	2%	—	—	—	—	—	—	—
<i>ETV6</i>	6%	—	—	6%	—	—	—	—	—	—	—
<i>BCL2</i>	6%	28%	9%	22%	4%	—	—	—	—	—	—
<i>BCR</i>	6%	—	—	10%	—	—	—	—	—	—	—
<i>CD58</i>	6%	5%	6%	10%	—	—	—	—	—	—	—
<i>KDM2B</i>	6%	—	7%	2%	—	—	—	—	—	—	—
<i>DDX3X</i>	6%	—	—	0%	—	—	—	—	—	—	—
<i>IRF8</i>	6%	12%	—	6%	5%	—	—	—	—	—	—
<i>BCL10</i>	5%	4%	—	2%	—	—	—	—	—	—	—
<i>EP300</i>	5%	4%	5%	6%	—	—	—	—	—	—	—
<i>PRKCB</i>	5%	—	—	4%	—	—	—	—	—	—	—
<i>BIRC3</i>	4%	—	—	0%	—	—	—	—	—	—	—
<i>BRCA2</i>	4%	1%	—	4%	5%	—	—	—	—	—	—
<i>EZH2</i>	4%	22%	6%	14%	1%	—	—	—	—	—	—
<i>FBXW7</i>	4%	—	—	4%	5%	—	—	—	—	—	—
<i>JAK2</i>	4%	—	—	0%	—	—	—	—	—	—	—
<i>MTOR</i>	4%	—	—	0%	3%	—	—	—	—	—	—
<i>MYC</i>	4%	—	6%	8%	1%	—	—	—	—	—	—
<i>NFKBIA</i>	4%	—	—	8%	—	—	—	—	—	—	—
<i>PAX5</i>	4%	—	—	2%	—	—	—	—	—	—	—

PIK3CG	4%	—	—	2%	—	—	—	—	—	—	—
S1PR2	4%	2%	—	6%	—	—	—	—	—	—	—
BRAF	4%	—	—	4%	—	—	—	—	—	—	—
CDKN2A	4%	—	—	0%	—	—	—	—	—	—	—
TCF3	4%	—	—	2%	—	—	—	—	—	—	—
COL4A2	4%	6%	—	0%	—	—	—	—	—	—	—
BTB	3%	—	—	4%	—	—	—	—	—	—	—
HDAC4	3%	—	—	0%	—	—	—	—	—	—	—
HDAC7	3%	7%	—	2%	—	—	—	—	—	—	—
P4HA2	3%	—	—	0%	—	—	—	—	—	—	—
SETD2	3%	—	—	4%	5%	—	—	—	—	—	—
AKT3	3%	—	—	0%	—	—	—	—	—	—	—
ARNT	2%	—	—	0%	—	—	—	—	—	—	—
ATM	2%	—	—	0%	—	—	—	—	—	—	—
CCND3	2%	6%	6%	6%	—	—	—	—	—	—	—
CD79A	2%	—	—	0%	—	—	—	—	—	—	—
DNMT3A	2%	—	—	2%	—	—	—	—	—	—	—
GNAI2	2%	—	—	4%	—	—	—	—	—	—	—
HDAC1	2%	—	—	0%	—	—	—	—	—	—	—
JAK3	2%	—	—	0%	—	—	—	—	—	—	—
MALT1	2%	3%	—	0%	—	—	—	—	—	—	—
PDGFRA	2%	—	—	0%	4%	—	—	—	—	—	—
PIK3CA	2%	—	—	2%	—	—	—	—	—	—	—
PIK3R1	2%	—	—	2%	4%	—	—	—	—	—	—
PIK3R2	2%	—	—	2%	—	—	—	—	—	—	—
SPIB	2%	3%	—	0%	—	—	—	—	—	—	—
TMEM30A	2%	4%	6%	4%	5%	—	—	—	—	—	—
TRAF5	2%	—	—	0%	—	—	—	—	—	—	—
UNC5C	2%	—	—	10%	—	—	—	—	—	—	—
AKT2	1%	—	—	0%	—	—	—	—	—	—	—
CD44	1%	—	—	0%	—	—	—	—	—	—	—
HMGB1	1%	—	2%	0%	—	—	—	—	—	—	—
IDH2	1%	—	—	0%	—	—	—	—	—	—	—
IKBKB	1%	—	—	0%	—	—	—	—	—	—	—
JAK1	1%	—	—	0%	—	—	—	—	—	—	—
KIT	1%	—	—	0%	1%	—	—	—	—	—	—
MAP3K14	1%	—	—	0%	—	—	—	—	—	—	—
MEF2C	1%	—	—	4%	—	—	—	—	—	—	—
MPL	1%	—	—	0%	5%	—	—	—	—	—	—
NRAS	1%	—	—	0%	—	—	—	—	—	—	—
PIK3CD	1%	2%	—	2%	4%	—	—	—	—	—	—
PTPN1	1%	—	—	0%	—	—	—	—	—	—	—
RHOH	1%	—	—	0%	—	—	—	—	—	—	—
STAT5A	1%	—	—	0%	—	—	—	—	—	—	—
TBC1D10C	1%	—	—	0%	—	—	—	—	—	—	—
TNFRSF11	1%	—	—	0%	—	—	—	—	—	—	—
TRAF2	1%	—	—	0%	—	—	—	—	—	—	—
AHR	0%	—	—	0%	4%	—	—	—	—	—	—
AKT1	0%	—	—	0%	—	—	—	—	—	—	—
CCND2	0%	—	—	0%	—	—	—	—	—	—	—
CDKN2B	0%	—	—	0%	—	—	—	—	—	—	—
ID3	0%	—	—	0%	—	—	—	—	—	—	—
IDH1	0%	—	—	0%	5%	—	—	—	—	—	—
KRAS	0%	—	—	4%	—	—	—	—	—	—	—
MAP3K7	0%	—	—	0%	—	—	—	—	—	—	—
RHOA	0%	—	—	0%	4%	—	—	—	—	—	—
STAT5B	0%	—	—	2%	—	—	—	—	—	—	—
TRAF3	0%	—	1%	0%	—	—	—	—	—	—	—

Note: * They were next generation sequencing studies. Cell line data were excluded, and only DLBCL samples were considered for mutation frequencies.

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Table S3 List of mutations identified in *DDX3X* by targeted sequencing

Sample	Gene	RefSeq	Chromosome	Position	Reference allele	Alteration allele	Mutation type	cDNA change	AA Change	Alteration frequency	Read-depth
10	<i>DDX3X</i>	NM_001356	chrX	41204450	A	C	Missense	c.A1043C	p.E348A	0.096926714	846
24	<i>DDX3X</i>	NM_001356	chrX	41204703	G	A	Missense	c.G1217A	p.G406E	0.215231788	906
26	<i>DDX3X</i>	NM_001356	chrX	41203332	T	C	Missense	c.T815C	p.L272S	0.812658228	395
84	<i>DDX3X</i>	NM_001356	chrX	41204476	T	G	Missense	c.T1069G	p.F357V	0.32032032	999
87	<i>DDX3X</i>	NM_001356	chrX	41205629	G	A	Missense	c.G1463A	p.R488H	0.859832636	478
63	<i>DDX3X</i>	NM_001356	chrX	41202606	T	C	Splice site	c.679+2T>C	NA	0.113367174	591

Abbreviations: AA, amino acid; NA, not available.

Table S4 Mutations identified in pathway genes by targeted sequencing

Sample	Gene	RefSeq	Chromosome	Position	Reference allele	Alteration allele	Mutation type	cDNA change	AA change	Alteration frequency	Read depth
1	<i>CD79A</i>	NM_001783	chr19	42384801	A	C	Missense	c.A563C	p.Y188S	0.61827957	186
27	<i>CD79A</i>	NM_001783	chr19	42384800	T	G	Missense	c.T562G	p.Y188D	0.22429907	214
1	<i>CD79B</i>	NM_001039933	chr17	62006606	C	G	Missense	c.G673C	p.E225Q	0.45898004	451
1	<i>CD79B</i>	NM_001039933	chr17	62006666	T	A	Missense	c.A613T	p.T205S	0.43841336	479
1	<i>CD79B</i>	NM_001039933	chr17	62006804	T	C	Missense	c.A584G	p.H195R	0.50455927	329
16	<i>CD79B</i>	NM_001039933	chr17	62007135	C	G	Missense	c.G547C	p.D183H	0.08402204	726
18	<i>CD79B</i>	NM_001039933	chr17	62006799	A	C	Missense	c.T589G	p.Y197D	0.37265918	534
							Frameshift				
23	<i>CD79B</i>	NM_001039933	chr17	62006796	CGTAG	C	deletion	c.588_591del	p.T196fs	0.11578947	475
25	<i>CD79B</i>	NM_001039933	chr17	62006799	A	G	Missense	c.T589C	p.Y197H	0.40480591	541
33	<i>CD79B</i>	NM_001039933	chr17	62006799	A	T	Missense	c.T589A	p.Y197N	0.25128205	390
37	<i>CD79B</i>	NM_001039933	chr17	62006798	T	C	Missense	c.A590G	p.Y197C	0.48341232	211
37	<i>CD79B</i>	NM_001039933	chr17	62006807	T	C	Missense	c.A581G	p.D194G	0.47524752	202
39	<i>CD79B</i>	NM_001039933	chr17	62006836	C	T	Splice site	553-1G>A	NA	0.22682927	410
53	<i>CD79B</i>	NM_001039933	chr17	62006798	T	G	Missense	c.A590C	p.Y197S	0.16302187	503
53	<i>CD79B</i>	NM_001039933	chr17	62006817	T	C	Missense	c.A571G	p.M191V	0.15686275	459
54	<i>CD79B</i>	NM_001039933	chr17	62006799	A	G	Missense	c.T589C	p.Y197H	0.85530547	311
61	<i>CD79B</i>	NM_001039933	chr17	62006798	T	A	Missense	c.A590T	p.Y197F	0.44803695	433
63	<i>CD79B</i>	NM_001039933	chr17	62006616	C	G	Missense	c.G663C	p.W221C	0.19575856	613
74	<i>CD79B</i>	NM_001039933	chr17	62008737	C	G	Missense	c.G79C	p.V27L	0.34496124	774
88	<i>CD79B</i>	NM_001039933	chr17	62006836	C	A	Splice site	c.553-1G>T	NA	0.29787234	329
92	<i>CD79B</i>	NM_001039933	chr17	62006680	A	C	Missense	c.T599G	p.L200R	0.25086306	869
92	<i>CD79B</i>	NM_001039933	chr17	62008737	C	T	Missense	c.G79A	p.V27I	0.35180055	722
92	<i>CD79B</i>	NM_001039933	chr17	62008750	T	G	Splice site	c.68-2A>C	NA	0.34104938	648
93	<i>CD79B</i>	NM_001039933	chr17	62006680	A	C	Missense	c.T599G	p.L200R	0.48508946	503
96	<i>CD79B</i>	NM_001039933	chr17	62006798	T	C	Missense	c.A590G	p.Y197C	0.69432314	458
23	<i>BTk</i>	NM_001287344	chrX	100630250	C	T	Missense	c.G125A	p.S42N	0.24092409	303
					GTACGTA						
					TCACCCC						
					TTGAGGG						
					TCCCCTGA						
					AGAAGTG						
					GATGCTT						
30	<i>BTk</i>	NM_001287344	chrX	100613402	AGTCA	T	Frameshift	c.1077_1099del	p.G359fs	0.14692982	456
83	<i>BTk</i>	NM_001287344	chrX	100630254	C	T	Missense	c.G121A	p.E41K	0.34414414	555
17	<i>CARD11</i>	NM_032415	chr7	2983886	T	G	Missense	c.A644C	p.K215T	0.55855856	999
20	<i>CARD11</i>	NM_032415	chr7	2977603	A	C	Missense	c.T1081G	p.Y361D	0.42988506	870
24	<i>CARD11</i>	NM_032415	chr7	2972204	G	C	Missense	c.C1535G	p.S512C	0.556	1000
60	<i>CARD11</i>	NM_032415	chr7	2983885	C	G	Missense	c.G645C	p.K215N	0.197	1000
65	<i>CARD11</i>	NM_032415	chr7	2977584	G	A	Missense	c.C1100T	p.T367M	0.38386648	719
77	<i>CARD11</i>	NM_032415	chr7	2962890	C	T	Missense	c.G2018A	p.G673D	0.40439276	774
79	<i>CARD11</i>	NM_032415	chr7	2979381	A	C	Splice site	c.864+2T>G	NA	0.39899833	599
82	<i>CARD11</i>	NM_032415	chr7	2962792	G	A	Missense	c.C2116T	p.L706F	0.48028674	558
83	<i>CARD11</i>	NM_032415	chr7	2979435	C	T	Missense	c.G812A	p.R271Q	0.23923924	999
83	<i>CARD11</i>	NM_032415	chr7	2979495	A	G	Missense	c.T752C	p.L251P	0.24224224	999
83	<i>CARD11</i>	NM_032415	chr7	2985468	A	T	Missense	c.T343A	p.F115I	0.24481328	964
94	<i>CARD11</i>	NM_032415	chr7	2968244	G	A	Missense	c.C1742T	p.A581V	0.48050314	795
63	<i>MALT1</i>	NM_006785	chr18	56409112	A	G	Missense	c.A1619G	p.H540R	0.08643815	671
82	<i>MALT1</i>	NM_006785	chr18	56338904	C	T	Missense	c.C29T	p.A10V	0.58974359	39
82	<i>MALT1</i>	NM_006785	chr18	56363613	T	C	Missense	c.T392C	p.V131A	0.17156863	204
82	<i>MALT1</i>	NM_006785	chr18	56414849	T	A	Nonsense	c.T2250A	p.Y750X	0.426	1000
82	<i>MALT1</i>	NM_006785	chr18	56363596	A	T	Splice site	c.377-2A>T	NA	0.1512605	119
							Frameshift				
24	<i>BCL10</i>	NM_003921	chr1	85733572	AG	A	deletion	c.439delC	p.L147X	0.22808989	890
50	<i>BCL10</i>	NM_003921	chr1	85736463	T	C	Missense	c.A184G	p.R62G	0.27755511	998
							Frameshift				
52	<i>BCL10</i>	NM_003921	chr1	85733392	AG	A	deletion	c.619delC	p.L207fs	0.27653061	980
55	<i>BCL10</i>	NM_003921	chr1	85733594	C	A	Nonsense	c.G418T	p.E140X	0.46740859	629
65	<i>BCL10</i>	NM_003921	chr1	85733329	C	T	Missense	c.G683A	p.R228H	0.38812785	876
8	<i>PRKCB</i>	NM_002738	chr16	24183630	G	A	Missense	c.G1279A	p.D427N	0.40574506	557
27	<i>PRKCB</i>	NM_002738	chr16	24135291	A	G	Missense	c.A1054G	p.S352G	0.204	1000
27	<i>PRKCB</i>	NM_002738	chr16	24196802	G	A	Missense	c.G1636A	p.E546K	0.16090584	839
60	<i>PRKCB</i>	NM_002738	chr16	24231406	C	T	Missense	c.C1988T	p.T663I	0.28248588	885
68	<i>PRKCB</i>	NM_002738	chr16	23847659	G	C	Missense	c.G163C	p.D55H	0.13043478	736
75	<i>PRKCB</i>	NM_002738	chr16	24226023	T	G	Missense	c.T1908G	p.H636Q	0.31530612	980
1	<i>TCF3</i>	NM_001136139	chr19	1646419	G	A	Missense	c.C80T	p.P27L	0.98538012	342
7	<i>TCF3</i>	NM_001136139	chr19	1622210	T	C	Missense	c.A665G	p.H222R	0.48691099	191

51	<i>TCF3</i>	NM_001136139	chr19	1612366	A	T	Missense	c.T1653A	p.N551K	0.20143027	839
74	<i>TCF3</i>	NM_003200	chr19	1615283	C	G	Splice site	c.1822+1G>C	NA	0.66580311	386
3	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.77741935	930
4	<i>MYD88</i>	NM_002468	chr3	38182292	G	A	Missense	c.G728A	p.S243N	0.1516035	686
18	<i>MYD88</i>	NM_002468	chr3	38182032	C	G	Missense	c.C656G	p.S219C	0.65265265	999
44	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.58758759	999
53	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.124	1000
54	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.4184953	638
58	<i>MYD88</i>	NM_002468	chr3	38182292	G	A	Missense	c.G728A	p.S243N	0.45422535	852
59	<i>MYD88</i>	NM_001172567	chr3	38182073	C	T	Missense	c.C697T	p.P233S	0.51439299	799
61	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.39033457	807
67	<i>MYD88</i>	NM_002468	chr3	38181430	A	G	Missense	c.A443G	p.D148G	0.24742268	679
71	<i>MYD88</i>	NM_002468	chr3	38182292	G	A	Missense	c.G728A	p.S243N	0.22238806	670
73	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.6242485	998
75	<i>MYD88</i>	NM_002468	chr3	38182259	T	C	Missense	c.T695C	p.M232T	0.828	1000
77	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.36499466	937
78	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.10079576	754
80	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.33333333	990
85	<i>MYD88</i>	NM_002468	chr3	38182292	G	A	Missense	c.G728A	p.S243N	0.382	1000
86	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.76203576	727
89	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.47484909	497
92	<i>MYD88</i>	NM_002468	chr3	38182641	T	C	Missense	c.794T>C	p.L265P	0.31034483	870
13	<i>TNFAIP3</i>	NM_006290	chr6	138201292	C	G	Missense	c.C1991G	p.T664S	0.51680672	952
18	<i>TNFAIP3</i>	NM_006290	chr6	138199898	G	T	Missense	c.G1316T	p.R439L	0.76744186	473
19	<i>TNFAIP3</i>	NM_006290	chr6	138192661	T	A	Splice site	c.295+2T>A	NA	0.32890365	903
42	<i>TNFAIP3</i>	NM_006290	chr6	138198327	T	G	Nonsense Frameshift	c.T920G	p.L307X	0.1521511	953
50	<i>TNFAIP3</i>	NM_006290	chr6	138192500	TAC	T	deletion Frameshift	c.137_138del	p.Y46fs	0.34455959	772
63	<i>TNFAIP3</i>	NM_006290	chr6	138199944	TG	T	deletion	c.1363delG	p.G455fs	0.46687211	649
72	<i>TNFAIP3</i>	NM_006290	chr6	138196937	G	A	Missense	c.G599A	p.C200Y	0.45682731	996
63	<i>TRAF2</i>	NM_021138	chr9	139794078	A	C	Missense	c.A221C	p.H74P	0.28211009	872
63	<i>TRAF2</i>	NM_021138	chr9	139794896	G	A	Missense Frameshift	c.G290A	p.R97H	0.27731092	476
2	<i>TRAF5</i>	NM_004619	chr1	211527763	CAG	C	deletion	c.231_232del	p.T77fs	0.45183888	571
15	<i>TRAF5</i>	NM_004619	chr1	211534057	A	G	Missense	c.A557G	p.N186S	0.572	1000
32	<i>IKBKB</i>	NM_001556	chr8	42179896	G	A	Missense	c.G1870A	p.E624K	0.26394558	735
27	<i>TNFRSF11A</i>	NM_003839	chr18	60021678	C	T	Missense	c.C338T	p.A113V	0.22285714	350
26	<i>BIRC3</i>	NM_001165	chr11	102207742	T	C	Missense	c.T1724C	p.L575P	0.35930736	924
55	<i>BIRC3</i>	NM_001165	chr11	102207510	T	A	Nonsense Frameshift	c.T1599A	p.Y533X	0.28526316	950
60	<i>BIRC3</i>	NM_001165	chr11	102195756	ATTAC	A	deletion	c.517_520del	p.L173fs	0.24855491	865
80	<i>BIRC3</i>	NM_001165	chr11	102206864	A	G	Missense	c.A1492G	p.T498A	0.527	1000
26	<i>MAP3K14</i>	NM_003954	chr17	43344938	G	A	Missense Frameshift	c.C2161T	p.P721S	0.46892655	531
5	<i>NFKBIA</i>	NM_020529	chr14	35871687	T TTGACCA	TG	insertion Frameshift	c.818dupC	p.T273fs	0.34229576	967
5	<i>NFKBIA</i>	NM_020529	chr14	35873711	TC	T	deletion	c.132_139del	p.Q44fs	0.07588358	962
38	<i>NFKBIA</i>	NM_020529	chr14	35873643	G	C	Missense	c.C208G	p.L70V	0.37325905	359
57	<i>NFKBIA</i>	NM_020529	chr14	35873643	G	C	Missense Frameshift	c.C208G	p.L70V	0.08351648	455
63	<i>NFKBIA</i>	NM_020529	chr14	35873801	CG GAGGGG GCCTGTG	C	deletion Frameshift	c.49delC	p.R17fs	0.23762376	707
5	<i>NOTCH1</i>	NM_017617	chr9	139391169	TGCTC	G	deletion	c.7005_7021del	p.L2335fs	0.29573935	399
15	<i>NOTCH1</i>	NM_017617	chr9	139402576	C	T	Missense	c.G3341A	p.R1114H	0.54366812	458
21	<i>NOTCH1</i>	NM_017617	chr9	139402523	G	A	Missense	c.C3394T	p.R1132C	0.53564547	519
29	<i>NOTCH1</i>	NM_017617	chr9	139413048	C	T	Missense	c.G1094A	p.R365H	0.45707657	431
44	<i>NOTCH1</i>	NM_017617	chr9	139403458	C	T	Missense Frameshift	c.G3035A	p.G1012D	0.48780488	246
63	<i>NOTCH1</i>	NM_017617	chr9	139390734	G	GA	insertion	c.7456dupT	p.S2486fs	0.20465116	645
74	<i>NOTCH1</i>	NM_017617	chr9	139391593	C	T	Missense	c.G6598A	p.V2200M	0.51290685	891
79	<i>NOTCH1</i>	NM_017617	chr9	139400212	G	A	Missense	c.C4136T	p.T1379M	0.40174672	458
1	<i>NOTCH2</i>	NM_024408	chr1	120458147	G	A	Nonsense	c.C7198T	p.R2400X	0.4637931	580
9	<i>NOTCH2</i>	NM_024408	chr1	120458161	G	C	Nonsense	c.C7184G	p.S2395X	0.38345865	798
57	<i>NOTCH2</i>	NM_024408	chr1	120539664	C	G	Missense	c.G707C	p.C236S	0.27444052	849
62	<i>NOTCH2</i>	NM_024408	chr1	120548153	G	A	Missense Frameshift	c.C214T	p.R72C	0.128	1000
71	<i>NOTCH2</i>	NM_024408	chr1	120458435	TG	T	deletion	c.6909delC	p.P2303fs	0.14652015	546
83	<i>NOTCH2</i>	NM_024408	chr1	120612014	C	A	Missense	c.G7T	p.A3S	0.15212982	986
86	<i>NOTCH2</i>	NM_024408	chr1	120480033	T	A	Missense	c.A3394T	p.T1132S	0.36363636	495
92	<i>NOTCH2</i>	NM_024408	chr1	120612014	C	A	Missense	c.G7T	p.A3S	0.11875694	901

96	NOTCH2	NM_024408	chr1	120612014	C	A	Missense	c.G7T	p.A3S	0.20666667	750
1	SPEN	NM_015001	chr1	16255496	C	T	Nonsense	c.C2761T	p.Q921X	0.93665158	884
4	SPEN	NM_015001	chr1	16254644	C	T	Nonsense	c.C1909T	p.R637X	0.1601467	818
10	SPEN	NM_015001	chr1	16202717	G	A	Missense	c.G425A	p.R142H	0.08138101	811
12	SPEN	NM_015001	chr1	16174588	G	A	Nonsense	c.G26A	p.W9X	0.71590909	352
16	SPEN	NM_015001	chr1	16259744	C	T	Nonsense	c.C7009T	p.R2337X	0.07880133	901
23	SPEN	NM_015001	chr1	16199421	C	T	Missense	c.C194T	p.S65L	0.50578339	951
27	SPEN	NM_015001	chr1	16258427	C	T	Nonsense	c.C5692T	p.R1898X	0.197	1000
29	SPEN	NM_015001	chr1	16259097	C	T	Missense	c.C6362T	p.P2121L	0.4959893	748
							Frameshift	c.3982_3985d			
32	SPEN	NM_015001	chr1	16256716	ACTAT	A	deletion	el	p.L1328fs	0.23360656	976
							Frameshift	c.1459_1462d			
48	SPEN	NM_015001	chr1	16245483	TGCTA	T	deletion	el	p.A487fs	0.37737738	999
48	SPEN	NM_015001	chr1	16255877	G	T	Nonsense	c.G3142T	p.E1048X	0.40781563	998
71	SPEN	NM_015001	chr1	16254929	C	T	Nonsense	c.C2194T	p.R732X	0.17313746	953
75	SPEN	NM_015001	chr1	16174611	G	T	Missense	c.G49T	p.V17L	0.64	525
75	SPEN	NM_015001	chr1	16256456	C	T	Nonsense	c.C3721T	p.R1241X	0.586	1000
84	SPEN	NM_015001	chr1	16255449	A	T	Missense	c.A2714T	p.N905I	0.52252252	999
87	SPEN	NM_015001	chr1	16245427	G	T	Missense	c.G1402T	p.D468Y	0.07738095	840
91	SPEN	NM_015001	chr1	16259097	C	T	Missense	c.C6362T	p.P2121L	0.44839068	901
96	SPEN	NM_015001	chr1	16259097	C	T	Missense	c.C6362T	p.P2121L	0.60275862	725
20	FBXW7	NM_033632	chr4	153247367	G	A	Nonsense	c.C1435T	p.R479X	0.6856492	439
37	FBXW7	NM_033632	chr4	153251907	G	A	Nonsense	c.C1099T	p.R367X	0.14842301	539
40	FBXW7	NM_033632	chr4	153245410	A	G	Missense	c.T1781C	p.L594P	0.094	1000
40	FBXW7	NM_033632	chr4	153247366	C	T	Missense	c.G1436A	p.R479Q	0.09268795	971
93	FBXW7	NM_033632	chr4	153249384	C	T	Missense	c.G1394A	p.R465H	0.27027027	999
21	PIK3CA	NM_006218	chr3	178943785	C	T	Missense	c.C2452T	p.R818C	0.33120341	939
35	PIK3CA	NM_006218	chr3	178928079	G	A	Missense	c.G1357A	p.E453K	0.23933403	961
68	PIK3CD	NM_005026	chr1	9780849	A	C	Missense	c.A1571C	p.Y524S	0.13	500
34	PIK3CG	NM_002649	chr7	106508037	G	A	Missense	c.G31A	p.V11M	0.49044586	157
49	PIK3CG	NM_002649	chr7	106509408	C	A	Missense	c.C1402A	p.L468M	0.657082	939
63	PIK3CG	NM_002649	chr7	106515234	G	A	Missense	c.G2377A	p.A793T	0.09834254	905
96	PIK3CG	NM_002649	chr7	106523575	C	G	Missense	c.C2727G	p.H909Q	0.488	1000
63	PIK3R1	NM_181523	chr5	67593274	A	T	Nonsense	c.A2020T	p.K674X	0.23207776	823
83	PIK3R1	NM_181523	chr5	67591125	T	C	Missense	c.T1718C	p.L573P	0.23823824	999
63	PIK3R2	NM_005027	chr19	18278059	T	C	Missense	c.T1679C	p.M560T	0.26204819	664
77	PIK3R2	NM_005027	chr19	18273072	G	A	Missense	c.G962A	p.S321N	0.50337079	445
63	AKT2	NM_001626	chr19	40748466	G	A	Missense	c.C416T	p.A139V	0.26742301	617
36	AKT3	NM_005465	chr1	243736225	TA	T	Splice site	c.819+2T>-	NA	0.25	192
54	AKT3	NM_005465	chr1	243736225	TA	T	Splice site	c.819+2T>-	NA	0.27513228	378
77	AKT3	NM_005465	chr1	243800989	A	G	Missense	c.T485C	p.V162A	0.3618202	901
1	PTEN	NM_000314	chr10	89624240	T	C	Missense	c.T14C	p.I5T	0.41795231	713
26	PTEN	NM_000314	chr10	89624275	C	T	Nonsense	c.C49T	p.Q17X	0.40723982	884
26	PTEN	NM_000314	chr10	89624287	T	C	Missense	c.T61C	p.F21L	0.41230068	878
26	PTEN	NM_000314	chr10	89685283	A	T	Nonsense	c.A178T	p.K60X	0.357022	591
42	PTEN	NM_000314	chr10	89653867	G	A	Splice site	c.164+1G>A	NA	0.15899582	717
55	PTEN	NM_000314	chr10	89624306	G	A	Splice site	c.79+1G>A	NA	0.42416452	778
							Frameshift				
75	PTEN	NM_000314	chr10	89653861	AGTAAG	A	deletion	c.160_164del	p.V54fs	0.33495935	615
84	PTEN	NM_000314	chr10	89692851	T	G	Missense	c.T335G	p.L112R	0.31162325	998
84	PTEN	NM_000314	chr10	89692910	G	A	Missense	c.G394A	p.G132S	0.32532533	999
95	PTEN	NM_000314	chr10	89624287	T	A	Missense	c.T61A	p.F21I	0.24102564	975
11	MTOR	NM_004958	chr1	11190767	C	T	Missense	c.G5432A	p.R1811H	0.5	562
58	MTOR	NM_004958	chr1	11181402	C	A	Missense	c.G6834T	p.L2278F	0.46998723	783
63	MTOR	NM_004958	chr1	11182038	G	A	Missense	c.C6808T	p.R2270W	0.34080717	446
78	MTOR	NM_004958	chr1	11298609	T	C	Missense	c.A1852G	p.I618V	0.48996656	598
4	SGK1	NM_001143676	chr6	134495706	C	G	Missense	c.G380C	p.R127T	0.1828125	640
4	SGK1	NM_001143676	chr6	134495648	C	T	Splice site	c.437+1G>A	NA	0.18738404	539
5	SGK1	NM_005627	chr6	134495942	T	G	Missense	c.A4C	p.T2P	0.30745342	966
7	SGK1	NM_001143676	chr6	134494207	G	C	Missense	c.C788G	p.T263S	0.07674944	886
14	SGK1	NM_001143676	chr6	134496787	G	A	Nonsense	c.C13T	p.Q5X	0.42207792	154
30	SGK1	NM_001143676	chr6	134493891	C	T	Missense	c.G856A	p.E286K	0.08757396	845
30	SGK1	NM_001143676	chr6	134494418	C	G	Missense	c.G696C	p.K232N	0.12363239	914
30	SGK1	NM_001143676	chr6	134495170	C	G	Missense	c.G486C	p.E162D	0.247851	698
30	SGK1	NM_001143676	chr6	134495650	G	A	Missense	c.C436T	p.H146Y	0.11972789	735
30	SGK1	NM_001143676	chr6	134495714	C	G	Missense	c.G372C	p.K124N	0.12903226	868
30	SGK1	NM_001143676	chr6	134495724	G	C	Missense	c.C362G	p.A121G	0.2627907	860
30	SGK1	NM_005627	chr6	134495884	A	T	Missense	c.T62A	p.V21E	0.15106117	801
30	SGK1	NM_001143676	chr6	134495648	C	G	Splice site	c.437+1G>C	NA	0.26849315	730
42	SGK1	NM_001143676	chr6	134495159	G	A	Missense	c.C497T	p.A166V	0.13195343	773
46	SGK1	NM_001143676	chr6	134493361	G	T	Missense	c.C1041A	p.S347R	0.40186916	642
46	SGK1	NM_001143676	chr6	134493449	A	T	Nonsense	c.T953A	p.L318X	0.30932203	472

46	SGK1	NM_001143676	chr6	134495147	G	A	Missense	c.C509T	p.P170L	0.36347197	553
46	SGK1	NM_001143676	chr6	134495211	C	T	Missense	c.G445A	p.V149I	0.39926063	541
46	SGK1	NM_001143676	chr6	134495650	G	A	Missense	c.C436T	p.H146Y	0.5631068	206
46	SGK1	NM_001143676	chr6	134495652	T	A	Missense	c.A434T	p.K145I	0.56038647	207
46	SGK1	NM_001143676	chr6	134495653	T	A	Nonsense	c.A433T	p.K145X	0.56038647	207
46	SGK1	NM_001143676	chr6	134495655	C	T	Missense	c.G431A	p.C144Y	0.56730769	208
46	SGK1	NM_001143676	chr6	134495659	C	T	Missense	c.G427A	p.A143T	0.57603687	217
46	SGK1	NM_001143676	chr6	134495706	C	G	Missense	c.G380C	p.R127T	0.4470339	472
46	SGK1	NM_001143678	chr6	134496758	C	G	Missense	c.G42C	p.E14D	0.38888889	126
46	SGK1	NM_001143676	chr6	134495648	C	G	Splice site	c.437+1G>C	NA	0.5631068	206
46	SGK1	NM_001143676	chr6	134495725	C	G	Splice site	c.362-1G>C	NA	0.42802303	521
48	SGK1	NM_001143676	chr6	134495183	G	A	Missense	c.C473T	p.P158L	0.4352518	834
59	SGK1	NM_001143676	chr6	134495150	G	C	Missense	c.C506G	p.S169C	0.51554828	611
59	SGK1	NM_001143676	chr6	134495664	G	C	Missense	c.C422G	p.S141C	0.16185897	624
67	SGK1	NM_001143676	chr6	134495650	G	A	Missense	c.C436T	p.H146Y	0.29137931	580
79	SGK1	NM_001143676	chr6	134495724	G	C	Missense	c.C362G	p.A121G	0.37003058	981
92	SGK1	NM_001143676	chr6	134492047	T	C	Missense	c.A1330G	p.I444V	0.70841889	487
63	JAK1	NM_002227	chr1	65323452	C	T	Missense	c.G1345A	p.A449T	0.25434116	979
40	JAK2	NM_004972	chr9	5078333	G	C	Missense	c.G2020C	p.V674L	0.563	1000
61	JAK2	NM_004972	chr9	5090802	G	A	Missense	c.G2950A	p.V984M	0.45730994	855
65	JAK2	NM_004972	chr9	5064964	C	G	Missense	c.C1138G	p.H380D	0.452	1000
78	JAK2	NM_004972	chr9	5126714	A	G	Missense	c.A3322G	p.N1108D	0.47731092	595
1	JAK3	NM_000215	chr19	17954665	C	A	Missense	c.G229T	p.D77Y	0.68205805	758
17	JAK3	NM_000215	chr19	17953136	C	T	Missense	c.G850A	p.G284R	0.46634615	208
								Nonframeshift	c.1847_1849d		
4	STAT3	NM_139276	chr17	40475060	CCTT	C	deletion	el	p.616_617c	0.14666667	600
12	STAT3	NM_139276	chr17	40475070	T	G	Missense	c.A1840C	p.S614R	0.11818182	660
								Nonframeshift	c.1847_1849d		
30	STAT3	NM_139276	chr17	40475060	CCTT	C	deletion	el	p.616_617c	0.20887246	541
55	STAT3	NM_139276	chr17	40485708	C	A	Missense	c.G1032T	p.Q344H	0.33183857	669
55	STAT3	NM_139276	chr17	40486035	G	T	Missense	c.C830A	p.T277N	0.32832833	999
								Frameshift			
63	STAT3	NM_139276	chr17	40468878	C	CG	insertion	c.2185dupC	p.R729fs	0.20754717	848
63	STAT3	NM_139276	chr17	40481583	A	T	Missense	c.T1222A	p.F408I	0.16985951	783
68	STAT3	NM_139276	chr17	40474420	C	A	Missense	c.G1981T	p.D661Y	0.115	1000
83	STAT3	NM_139276	chr17	40481465	T	A	Missense	c.A1244T	p.E415V	0.29445074	883
83	STAT3	NM_139276	chr17	40481466	C	A	Nonsense	c.G1243T	p.E415X	0.29218573	883
63	STAT5A	NM_003152	chr17	40461415	A	G	Missense	c.A2135G	p.D712G	0.23324397	746
63	STAT5A	NM_003152	chr17	40461476	G	T	Missense	c.G2196T	p.Q732H	0.07651007	745
12	STAT6	NM_003153	chr12	57490463	C	A	Missense	c.G2436T	p.E812D	0.49746193	591
24	STAT6	NM_003153	chr12	57496661	T	C	Missense	c.A1256G	p.D419G	0.22945205	876
49	STAT6	NM_003153	chr12	57498330	C	G	Missense	c.G1129C	p.E377Q	0.42914172	501
50	STAT6	NM_003153	chr12	57496661	T	G	Missense	c.A1256C	p.D419A	0.45205479	803
50	STAT6	NM_003153	chr12	57496668	T	A	Missense	c.A1249T	p.N417Y	0.45646438	758
60	STAT6	NM_003153	chr12	57496661	T	C	Missense	c.A1256G	p.D419G	0.41255144	972
79	STAT6	NM_003153	chr12	57496661	T	G	Missense	c.A1256C	p.D419A	0.35907723	997
95	STAT6	NM_003153	chr12	57496661	T	G	Missense	c.A1256C	p.D419A	0.63681592	804
4	SOCS1	NM_003745	chr16	11349154	T	C	Missense	c.A182G	p.H61R	0.18819188	271
4	SOCS1	NM_003745	chr16	11349329	C	T	Missense	c.G7A	p.A3T	0.1732852	277
5	SOCS1	NM_003745	chr16	11348988	G	C	Missense	c.C348G	p.S116R	0.314367	703
8	SOCS1	NM_003745	chr16	11348988	G	C	Missense	c.C348G	p.S116R	0.48717949	429
								CCGGGGGG			
								CCGGGGGC			
								CGGGACC			
								GCGGGGC			
								ACGGCCG			
								CGGGCGC			
								Nonframeshift			
15	SOCS1	NM_003745	chr16	11349184	G	C	deletion	c.110_151del	p.37_51del	0.2027972	286
21	SOCS1	NM_003745	chr16	11348807	G	C	Missense	c.C529G	p.L177V	0.40206186	582
21	SOCS1	NM_003745	chr16	11349146	A	C	Missense	c.T190G	p.Y64D	0.375	344
24	SOCS1	NM_003745	chr16	11349287	C	T	Missense	c.G49A	p.A17T	0.26255708	438
30	SOCS1	NM_003745	chr16	11348762	C	T	Missense	c.G574A	p.A192T	0.12837838	444
30	SOCS1	NM_003745	chr16	11348807	G	C	Missense	c.C529G	p.L177V	0.47165533	441
30	SOCS1	NM_003745	chr16	11348853	C	A	Missense	c.G483T	p.M161I	0.12258065	465
30	SOCS1	NM_003745	chr16	11348866	G	C	Missense	c.C470G	p.A157G	0.15065502	458
30	SOCS1	NM_003745	chr16	11348880	C	G	Missense	c.G456C	p.E152D	0.13943355	459
30	SOCS1	NM_003745	chr16	11348888	G	C	Missense	c.C448G	p.L150V	0.49689441	483
30	SOCS1	NM_003745	chr16	11348908	C	G	Missense	c.G428C	p.S143T	0.09381238	501
30	SOCS1	NM_003745	chr16	11348988	G	C	Missense	c.C348G	p.S116R	0.53320683	527
30	SOCS1	NM_003745	chr16	11349199	G	A	Missense	c.C137T	p.P46L	0.36075949	158
30	SOCS1	NM_003745	chr16	11349287	C	G	Missense	c.G49C	p.A17P	0.43283582	201
30	SOCS1	NM_003745	chr16	11349301	G	A	Missense	c.C35T	p.A12V	0.43349754	203

37	SOCS1	NM_003745	chr16	11349077	G	A	Missense	c.C259T	p.H87Y	0.18560606	264
38	SOCS1	NM_003745	chr16	11348962	C	G	Missense	c.G374C	p.S125T	0.24683544	474
38	SOCS1	NM_003745	chr16	11349047	G	C	Missense	c.C289G	p.P97A	0.21967213	305
38	SOCS1	NM_003745	chr16	11349103	C	T	Missense	c.G233A	p.G78E	0.16666667	180
38	SOCS1	NM_003745	chr16	11349112	T	C	Missense	c.A224G	p.D75G	0.16363636	165
38	SOCS1	NM_003745	chr16	11349139	C	G	Missense	c.G197C	p.R66P	0.23333333	150
38	SOCS1	NM_003745	chr16	11349199	G	A	Missense	c.C137T	p.P46L	0.17021277	141
38	SOCS1	NM_003745	chr16	11349332	C	G	Missense	c.G4C	p.V2L	0.20467836	171
39	SOCS1	NM_003745	chr16	11348807	G	C	Missense	c.C529G	p.L177V	0.237691	589
39	SOCS1	NM_003745	chr16	11349093	C	T	Nonsense	c.G243A	p.W81X	0.23737374	396
39	SOCS1	NM_003745	chr16	11349329	C	T	Missense	c.G7A	p.A3T	0.20168067	357
42	SOCS1	NM_003745	chr16	11348725	A	G	Missense	c.T611C	p.L204P	0.1023766	547
42	SOCS1	NM_003745	chr16	11348749	A	G	Missense	c.T587C	p.L196P	0.1130742	566
42	SOCS1	NM_003745	chr16	11348988	G	C	Missense	c.C348G	p.S116R	0.11741425	758
42	SOCS1	NM_003745	chr16	11349018	G	C	Missense	c.C318G	p.S106R	0.15542522	682
42	SOCS1	NM_003745	chr16	11349077	G	A	Missense	c.C259T	p.H87Y	0.08552632	456
42	SOCS1	NM_003745	chr16	11349265	T	G	Missense	c.A71C	p.E24A	0.078125	320
48	SOCS1	NM_003745	chr16	11348706	C	A	Missense	c.G630T	p.Q210H	0.39095315	619
48	SOCS1	NM_003745	chr16	11348831	G	A	Missense	c.C505T	p.R169C	0.3803056	589
48	SOCS1	NM_003745	chr16	11348971	C	T	Missense	c.G365A	p.G122E	0.34085779	886
48	SOCS1	NM_003745	chr16	11348972	C	A	Nonsense	c.G364T	p.G122X	0.34308211	889
48	SOCS1	NM_003745	chr16	11349093	C	G	Missense	c.G243C	p.W81C	0.37772926	458
48	SOCS1	NM_003745	chr16	11349206	C	T	Missense	c.G130A	p.A44T	0.43333333	330
48	SOCS1	NM_003745	chr16	11349263	G	C	Missense	c.C73G	p.P25A	0.31042654	422
CGCAGCGG							Frameshift				
50	SOCS1	NM_003745	chr16	11348836	GG	C	deletion	c.492_499del	p.A164fs	0.24582339	419
50	SOCS1	NM_003745	chr16	11348845	G	A	Missense	c.C491T	p.A164V	0.24475524	429
51	SOCS1	NM_003745	chr16	11349214	G	A	Missense	c.C122T	p.P41L	0.22352941	340
							Frameshift				
57	SOCS1	NM_003745	chr16	11349142	CG	C	deletion	c.193delC	p.R65fs	0.09950249	201
58	SOCS1	NM_003745	chr16	11349082	C	T	Missense	c.G254A	p.S85N	0.43316832	404
58	SOCS1	NM_003745	chr16	11349334	A	C	Missense	c.T2G	p.M1R	0.46153846	286
58	SOCS1	NM_003745	chr16	11349335	T	C	Missense	c.A1G	p.M1V	0.44210526	285
60	SOCS1	NM_003745	chr16	11349163	A	G	Missense	c.T173C	p.F58S	0.24199288	281
60	SOCS1	NM_003745	chr16	11349329	C	T	Missense	c.G7A	p.A3T	0.23076923	260
63	SOCS1	NM_003745	chr16	11348813	G	A	Nonsense	c.C523T	p.Q175X	0.26666667	510
63	SOCS1	NM_003745	chr16	11348908	C	G	Missense	c.G428C	p.S143T	0.08049536	646
63	SOCS1	NM_003745	chr16	11348933	A	C	Missense	c.T403G	p.F135V	0.21604938	648
63	SOCS1	NM_003745	chr16	11348963	T	G	Missense	c.A373C	p.S125R	0.20858896	652
63	SOCS1	NM_003745	chr16	11348971	C	G	Missense	c.G365C	p.G122A	0.20094192	637
63	SOCS1	NM_003745	chr16	11348972	C	T	Missense	c.G364A	p.G122R	0.48657188	633
63	SOCS1	NM_003745	chr16	11348984	T	G	Missense	c.A352C	p.K118Q	0.22291022	646
63	SOCS1	NM_003745	chr16	11348989	C	T	Missense	c.G347A	p.S116N	0.27848101	632
63	SOCS1	NM_003745	chr16	11349241	G	A	Missense	c.C95T	p.S32L	0.22256098	328
63	SOCS1	NM_003745	chr16	11349301	G	C	Missense	c.C35G	p.A12G	0.22772277	303
63	SOCS1	NM_003745	chr16	11349324	G	T	Missense	c.C12A	p.H4Q	0.20357143	280
63	SOCS1	NM_003745	chr16	11349386	C	G	Splice site	NA	NA	0.23312883	163
67	SOCS1	NM_003745	chr16	11348889	C	G	Missense	c.G447C	p.E149D	0.23802164	647
70	SOCS1	NM_003745	chr16	11349033	G	C	Missense	c.C303G	p.F101L	0.27056277	462
70	SOCS1	NM_003745	chr16	11349146	A	T	Missense	c.T190A	p.Y64N	0.26587302	252
70	SOCS1	NM_003745	chr16	11349236	C	A	Missense	c.G100T	p.A34S	0.27272727	297
70	SOCS1	NM_003745	chr16	11349290	C	T	Missense	c.G46A	p.A16T	0.30111524	269
70	SOCS1	NM_003745	chr16	11349320	G	A	Nonsense	c.C16T	p.Q6X	0.30241935	248
81	SOCS1	NM_003745	chr16	11348977	G	A	Missense	c.C359T	p.A120V	0.46757679	586
							Frameshift				
85	SOCS1	NM_003745	chr16	11349327	TGC	T	deletion	c.7_8del	p.A3fs	0.28928571	280
CGCTGGC							Frameshift				
95	SOCS1	NM_003745	chr16	11349010	G	C	deletion	c.319_325del	p.R107fs	0.37683284	682
95	SOCS1	NM_003745	chr16	11348713	G	A	Missense	c.C623T	p.P208L	0.32409012	577
95	SOCS1	NM_003745	chr16	11348791	A	T	Missense	c.T545A	p.I182N	0.3037037	540
95	SOCS1	NM_003745	chr16	11348808	C	G	Missense	c.G528C	p.E176D	0.52427184	515
95	SOCS1	NM_003745	chr16	11348900	A	T	Missense	c.T436A	p.C146S	0.33135215	673
95	SOCS1	NM_003745	chr16	11348911	T	C	Missense	c.A425G	p.E142G	0.15285714	700
95	SOCS1	NM_003745	chr16	11348927	G	C	Missense	c.C409G	p.L137V	0.19066148	771
95	SOCS1	NM_003745	chr16	11348962	C	G	Missense	c.G374C	p.S125T	0.18397997	799
95	SOCS1	NM_003745	chr16	11349093	C	A	Missense	c.G243T	p.W81C	0.53741497	294
95	SOCS1	NM_003745	chr16	11349097	T	A	Missense	c.A239T	p.Y80F	0.30388693	283
95	SOCS1	NM_003745	chr16	11349099	G	C	Missense	c.C237G	p.F79L	0.31521739	276
95	SOCS1	NM_003745	chr16	11349328	G	A	Missense	c.C8T	p.A3V	0.18421053	228
95	SOCS1	NM_003745	chr16	11349332	C	T	Missense	c.G4A	p.V2I	0.45045045	222
95	SOCS1	NM_003745	chr16	11349333	C	T	Missense	c.G3A	p.M1I	0.4529148	223
30	PTPN1	NM_002827	chr20	49177964	G	A	Missense	c.G128A	p.R43Q	0.2978236	873

84	MPL	NM_005373	chr1	43812466	G	A	Missense	c.G1169A	p.R390H	0.32252836	617
81	NRAS	NM_002524	chr1	115256424	T	A	Missense	c.A287T	p.Y96F	0.49928469	699
42	BRAF	NM_004333	chr7	140434420	A	T	Missense	c.T2278A	p.Y760N	0.11447811	891
57	BRAF	NM_004333	chr7	140494242	G	A	Missense	c.C1006T	p.P336S	0.0907781	694
63	BRAF	NM_004333	chr7	140624476	C	A	Missense	c.G28T	p.G10C	0.12389381	113
70	BRAF	NM_004333	chr7	140550014	T	TA	Splice site Frameshift	c.139-2->T c.155_156ins	NA	0.22030238	463
1	GNA13	NM_006572	chr17	63052556	C	CAGGAT	insertion	ATCCT	p.L52fs	0.45733788	586
5	GNA13	NM_006572	chr17	63052631	C	G	Missense Frameshift	c.G81C c.997_1000de	p.Q27H	0.3693495	907
42	GNA13	NM_006572	chr17	63010508	CGTTT	C	deletion Frameshift	l	p.K333fs	0.115	1000
63	GNA13	NM_006572	chr17	63010815	GT	G	deletion	c.693delA	p.K231fs	0.276	1000
63	GNA13	NM_006572	chr17	63049800	C	T	Nonsense	c.G330A	p.W110X	0.24640884	905
68	GNA13	NM_006572	chr17	63052533	C	A	Missense Nonframeshift	c.G179T	p.G60V	0.13846154	715
70	GNA13	NM_006572	chr17	63010926	CTTG	C	deletion Frameshift	c.580_582del c.110_111ins AGATCGAC	p.194_194c	0.26846847	555
84	GNA13	NM_006572	chr17	63052601	G	GCATTG	insertion	AAATG	p.C37_L38	0.20864865	925
84	GNA13	NM_006572	chr17	63049718	C	A	Nonsense	c.G412T	p.E138X	0.28986961	997
27	S1PR2	NM_004230	chr19	10334663	T	A	Missense	c.A919T	p.R307W	0.48711944	427
63	S1PR2	NM_004230	chr19	10334663	T	A	Missense Frameshift	c.A919T	p.R307W	0.22580645	341
68	S1PR2	NM_004230	chr19	10334697	C	CA	insertion	c.884dupT	p.L295fs	0.12860892	381
90	S1PR2	NM_004230	chr19	10334663	T	A	Missense	c.A919T	p.R307W	0.47683924	367
7	ARID1A	NM_006015	chr1	27087377	A	G	Missense	c.A1951G	p.M651V	0.44647887	710
14	ARID1A	NM_006015	chr1	27101442	C	A	Missense	c.C4724A	p.P1575Q	0.21791768	413
27	ARID1A	NM_006015	chr1	27059218	A	C	Missense Frameshift	c.A1855C	p.T619P	0.4923913	920
35	ARID1A	NM_006015	chr1	27057892	T	TA	insertion	c.1601dupA	p.Y534_P5	0.32522124	452
48	ARID1A	NM_006015	chr1	27023819	C	T	Nonsense	c.C925T	p.Q309X	0.35769231	260
68	ARID1A	NM_006015	chr1	27106237	C	G	Missense	c.C5848G	p.R1950G	0.517	1000
82	ARID1A	NM_006015	chr1	27056209	C	T	Missense Frameshift	c.C1205T	p.S402L	0.45088161	794
84	ARID1A	NM_006015	chr1	27023476	CT	C	deletion	c.583delT	p.Y195fs	0.32357247	683
84	ARID1A	NM_006015	chr1	27023540	T	C	Missense	c.T646C	p.Y216H	0.28688525	732
86	ARID1A	NM_006015	chr1	27023567	C	T	Missense Nonframeshift	c.C673T	p.P225S	0.17391304	368
92	ARID1A	NM_006015	chr1	27023404	CCAA	C	deletion Frameshift	c.511_513del	p.171_171c	0.10970464	474
3	CREBBP	NM_004380	chr16	3830771	AT	A	deletion Frameshift	c.1784delA c.1063_1064d	p.H595fs	0.3408393	977
4	CREBBP	NM_004380	chr16	3843538	CTG	C	deletion	el	p.Q355fs	0.15615616	666
4	CREBBP	NM_004380	chr16	3832701	C	G	Missense	c.G1557C	p.R519S	0.14823009	452
7	CREBBP	NM_004380	chr16	3788617	C	T	Missense	c.G4337A	p.R1446H	0.12723449	951
19	CREBBP	NM_004380	chr16	3788646	A	T	Missense	c.T4308A	p.S1436R	0.69169169	999
32	CREBBP	NM_004380	chr16	3789636	C	T	Missense	c.G4223A	p.C1408Y	0.37672584	507
42	CREBBP	NM_004380	chr16	3832706	T	C	Missense	c.A1552G	p.M518V	0.11755486	638
52	CREBBP	NM_004380	chr16	3788657	A	T	Missense	c.T4297A	p.Y1433N	0.37981859	882
56	CREBBP	NM_004380	chr16	3823913	G	A	Nonsense Frameshift	c.C2302T	p.R768X	0.3875969	645
63	CREBBP	NM_004380	chr16	3900710	GA	G	deletion	c.385delT	p.S129fs	0.25	576
72	CREBBP	NM_004380	chr16	3819324	T	C	Missense	c.A2911G	p.R971G	0.44615385	845
83	CREBBP	NM_004380	chr16	3808015	A	G	Missense Frameshift	c.T3404C c.4404_4405d	p.L1135P	0.32817869	582
93	CREBBP	NM_004380	chr16	3786805	CCT	C	deletion	el	p.T1468fs	0.28318584	791
8	EP300	NM_001429	chr22	41569735	G	T	Missense	c.G4726T	p.V1576L	0.50642202	545
18	EP300	NM_001429	chr22	41566522	T	G	Missense Frameshift	c.T4399G c.44_45insGC	p.Y1467D	0.351	1000
50	EP300	NM_001429	chr22	41489052	G	GGCCT	insertion Frameshift	CT	p.R15fs	0.24946237	465
63	EP300	NM_001429	chr22	41566524	CA	C	deletion	c.4402delA	p.K1468fs	0.23734533	889
63	EP300	NM_001429	chr22	41513611	G	A	Missense	c.G515A	p.G172D	0.267	1000
78	EP300	NM_001429	chr22	41565529	G	A	Missense	c.G4195A	p.D1399N	0.08652482	705
31	DNMT3A	NM_175629	chr2	25463588	C	T	Nonsense	c.G2094A	p.W698X	0.36096718	579
57	DNMT3A	NM_175629	chr2	25468133	G	A	Nonsense	c.C1543T	p.Q515X	0.47520661	484
7	EZH2	NM_004456	chr7	148508728	A	T	Missense	c.T1936A	p.Y646N	0.09882353	850
19	EZH2	NM_004456	chr7	148508728	A	T	Missense	c.T1936A	p.Y646N	0.33229167	960
24	EZH2	NM_004456	chr7	148508728	A	T	Missense	c.T1936A	p.Y646N	0.20168067	952
24	EZH2	NM_004456	chr7	148508799	G	C	Missense	c.C1865G	p.A622G	0.21372328	889
87	EZH2	NM_004456	chr7	148508727	T	C	Missense	c.A1937G	p.Y646C	0.44618834	892

64	HDAC1	NM_004964	chr1	32797709	G	A	Missense	c.G1238A	p.R413Q	0.46816479	267
68	HDAC1	NM_004964	chr1	32790085	G	T	Missense	c.G286T	p.V96F	0.155	1000
6	HDAC4	NM_006037	chr2	240036859	C	T	Missense	c.G1666A	p.V556M	0.6975	400
49	HDAC4	NM_006037	chr2	240061448	T	C	Missense	c.A910G	p.N304D	0.26666667	645
49	HDAC4	NM_006037	chr2	240111758	G	A	Missense	c.C110T	p.A37V	0.09259259	162
75	HDAC4	NM_006037	chr2	240098241	C	T	Missense	c.G358A	p.A120T	0.64011799	339
21	HDAC7	NM_015401	chr12	48187256	G	A	Missense	c.C1574T	p.S525F	0.30952381	168
21	HDAC7	NM_015401	chr12	48190923	A	C	Missense	c.T580G	p.S194A	0.38422392	786
53	HDAC7	NM_015401	chr12	48189035	C	T	Missense	c.G1216A	p.A406T	0.43793103	290
80	HDAC7	NM_015401	chr12	48187256	G	A	Missense	c.C1574T	p.S525F	0.16571429	175
80	HDAC7	NM_015401	chr12	48190798	A	G	Splice site	c.703+2T>C	NA	0.15467075	653
1	HIST1H1C	NM_005319	chr6	26056380	G	C	Missense	c.C277G	p.L93V	0.48376623	616
19	HIST1H1C	NM_005319	chr6	26056356	C	T	Missense	c.G301A	p.A101T	0.71881838	914
30	HIST1H1C	NM_005319	chr6	26056498	C	G	Missense	c.G159C	p.E53D	0.14824798	742
38	HIST1H1C	NM_005319	chr6	26056289	G	T	Missense	c.C368A	p.A123E	0.09323583	547
67	HIST1H1C	NM_005319	chr6	26056475	G	A	Missense	c.C182T	p.A61V	0.20653319	949
85	HIST1H1C	NM_005319	chr6	26056530	G	C	Missense	c.C127G	p.L43V	0.3488665	794
86	HIST1H1C	NM_005319	chr6	26056205	G	A	Missense	c.C452T	p.A151V	0.17410229	919
86	HIST1H1C	NM_005319	chr6	26056266	G	A	Missense	c.C391T	p.P131S	0.17978848	851
86	HIST1H1C	NM_005319	chr6	26056305	G	A	Missense	c.C352T	p.P118S	0.17059484	891
86	HIST1H1C	NM_005319	chr6	26056464	C	G	Missense	c.G193C	p.A65P	0.132	1000
92	HIST1H1C	NM_005319	chr6	26056419	T	G	Missense	c.A238C	p.I80L	0.52071669	893
93	HIST1H1C	NM_005319	chr6	26056323	C	T	Missense	c.G334A	p.A112T	0.11440108	743
1	HIST1H1E	NM_005321	chr6	26156850	A	T	Missense	c.A232T	p.S78C	0.39230769	390
1	HIST1H1E	NM_005321	chr6	26156937	C	T	Missense	c.C319T	p.L107F	0.36200717	279
6	HIST1H1E	NM_005321	chr6	26157105	G	A	Missense	c.G487A	p.A163T	0.29526462	359
7	HIST1H1E	NM_005321	chr6	26156929	C	T	Missense	c.C311T	p.S104F	0.09176471	425
12	HIST1H1E	NM_005321	chr6	26156811	G	A	Missense	c.G193A	p.A65T	0.378125	640
30	HIST1H1E	NM_005321	chr6	26156766	G	T	Missense	c.G148T	p.A50S	0.22363636	550
30	HIST1H1E	NM_005321	chr6	26156925	G	C	Missense	c.G307C	p.G103R	0.30635838	346
30	HIST1H1E	NM_005321	chr6	26156937	C	G	Missense	c.C319G	p.L107V	0.3088685	327
30	HIST1H1E	NM_005321	chr6	26157109	C	G	Missense	c.C491G	p.A164G	0.40069686	287
30	HIST1H1E	NM_005321	chr6	26157163	A	G	Missense	c.A545G	p.K182R	0.32236842	304
38	HIST1H1E	NM_005321	chr6	26156937	C	T	Missense	c.C319T	p.L107F	0.13173653	334
38	HIST1H1E	NM_005321	chr6	26157090	G	T	Missense	c.G472T	p.A158S	0.18589744	312
38	HIST1H1E	NM_005321	chr6	26157117	G	C	Missense	c.G499C	p.A167P	0.18575851	323
39	HIST1H1E	NM_005321	chr6	26156876	C	A	Missense	c.C258A	p.S86R	0.19601838	653
44	HIST1H1E	NM_005321	chr6	26157184	C	T	Missense	c.C566T	p.A189V	0.37888199	483
62	HIST1H1E	NM_005321	chr6	26156985	G	C	Missense	c.G367C	p.A123P	0.55907781	347
68	HIST1H1E	NM_005321	chr6	26156874	A	C	Missense	c.A256C	p.S86R	0.08846761	633
68	HIST1H1E	NM_005321	chr6	26156985	G	T	Missense	c.G367T	p.A123S	0.10684932	365
70	HIST1H1E	NM_005321	chr6	26156971	C	T	Missense	c.C353T	p.P118L	0.5046729	321
72	HIST1H1E	NM_005321	chr6	26157252	A	G	Missense	c.A634G	p.K212E	0.37516513	757
80	HIST1H1E	NM_005321	chr6	26156745	C	T	Missense	c.C127T	p.L43F	0.088	1000
85	HIST1H1E	NM_005321	chr6	26156935	A	G	Missense	c.A317G	p.K106R	0.45146727	443
86	HIST1H1E	NM_005321	chr6	26156926	G	T	Missense	c.G308T	p.G103V	0.17434211	608
86	HIST1H1E	NM_005321	chr6	26157012	G	C	Missense	c.G394C	p.A132P	0.13849765	426
86	HIST1H1E	NM_005321	chr6	26157099	C	T	Missense	c.C481T	p.P161S	0.18623482	494
91	HIST1H1E	NM_005321	chr6	26157187	A	G	Missense	c.A569G	p.K190R	0.13305613	481
92	HIST1H1E	NM_005321	chr6	26156985	G	C	Missense	c.G367C	p.A123P	0.17717718	333
76	IDH2	NM_002168	chr15	90633719	C	T	Missense	c.G365A	p.R122H	0.52089136	359
3	KDM2B	NM_032590	chr12	121877834	G	A	Missense	c.C3655T	p.R1219C	0.24383562	365
3	KDM2B	NM_032590	chr12	121880596	T	C	Missense	c.A2648G	p.N883S	0.37837838	148
5	KDM2B	NM_032590	chr12	121878978	G	A	Missense	c.C3343T	p.P1115S	0.50888325	788
23	KDM2B	NM_032590	chr12	121891060	G	A	Missense	c.C1822T	p.R608W	0.11904762	672
46	KDM2B	NM_032590	chr12	121880183	G	A	Missense	c.C3061T	p.R1021C	0.45989305	187
73	KDM2B	NM_032590	chr12	121880545	G	A	Missense	c.C2699T	p.A900V	0.55018587	269
90	KDM2B	NM_032590	chr12	122013710	C	T	Missense	c.G326A	p.R109Q	0.44062947	699
2	KMT2C	NM_170606	chr7	151970840	C	T	Missense	c.G962A	p.S321N	0.08608609	999
								Nonframeshift	c.11362_1136		
3	KMT2C	NM_170606	chr7	151859297	GAGA	G	deletion	4del	p.3788_378	0.28059072	948
5	KMT2C	NM_170606	chr7	151860520	G	A	Missense	c.C10142T	p.P3381L	0.34	1000
5	KMT2C	NM_170606	chr7	151864263	G	C	Missense	c.C9718G	p.Q3240E	0.387	1000
16	KMT2C	NM_170606	chr7	151851136	G	A	Missense	c.C12235T	p.L4079F	0.47547548	999
25	KMT2C	NM_170606	chr7	151970840	C	T	Missense	c.G962A	p.S321N	0.083	1000
31	KMT2C	NM_170606	chr7	151875096	C	CT	Splice site	c.7443-1->A	NA	0.29787234	94
37	KMT2C	NM_170606	chr7	151962290	C	G	Missense	c.G1017C	p.K339N	0.1280683	937
42	KMT2C	NM_170606	chr7	152012286	T	C	Missense	c.A527G	p.N176S	0.53853854	999
								Frameshift			
48	KMT2C	NM_170606	chr7	151927050	AG	A	deletion	c.2933delC	p.S978fs	0.13069909	987
53	KMT2C	NM_170606	chr7	151945124	T	C	Missense	c.A2395G	p.N799D	0.08708709	999
58	KMT2C	NM_170606	chr7	151874971	G	A	Missense	c.C7567T	p.P2523S	0.49190939	618

63	KMT2C	NM_170606	chr7	151845357	C	A	Missense	c.G13655T	p.S4552I	0.1718107	972	
78	KMT2C	NM_170606	chr7	152132717	C	T	Missense	c.G155A	p.R52K	0.66666667	393	
90	KMT2C	NM_170606	chr7	151935841	A	G	Missense	c.T2603C	p.I868T	0.401	1000	
91	KMT2C	NM_170606	chr7	152132801	G	A	Missense	c.C71T	p.A24V	0.47658402	363	
							Frameshift	c.15950_1595				
1	KMT2D	NM_003482	chr12	49418461	AAT	A	deletion	1del	p.Y5317fs	0.28915663	913	
							Frameshift					
3	KMT2D	NM_003482	chr12	49446461	TG	T	deletion	c.1143delC	p.P381fs	0.42785235	596	
4	KMT2D	NM_003482	chr12	49446347	C	T	Missense	c.G1258A	p.G420R	0.13	500	
7	KMT2D	NM_003482	chr12	49431178	G	A	Nonsense	c.C9961T	p.R3321X	0.10652921	582	
12	KMT2D	NM_003482	chr12	49425724	C	T	Missense	c.G12764A	p.G4255D	0.53038674	362	
18	KMT2D	NM_003482	chr12	49433506	C	A	Splice site	c.8046+1G>T	NA	0.35344828	464	
19	KMT2D	NM_003482	chr12	49447050	G	C	Nonsense	c.C894G	p.Y298X	0.336	1000	
							Frameshift					
21	KMT2D	NM_003482	chr12	49433594	AC	A	deletion	c.7958delG	p.G2653fs	0.33333333	708	
25	KMT2D	NM_003482	chr12	49446816	C	A	Nonsense	c.G994T	p.E332X	0.28533686	757	
30	KMT2D	NM_003482	chr12	49432209	T	C	Missense	c.A8930G	p.N2977S	0.42	900	
33	KMT2D	NM_003482	chr12	49425041	G	C	Missense	c.C13447G	p.L4483V	0.07541899	716	
37	KMT2D	NM_003482	chr12	49416114	C	T	Missense	c.G16361A	p.R5454Q	0.39480519	385	
39	KMT2D	NM_003482	chr12	49431649	G	A	Missense	c.C9490T	p.R3164W	0.51688693	681	
42	KMT2D	NM_003482	chr12	49416133	G	A	Nonsense	c.C16342T	p.R5448X	0.08938547	895	
47	KMT2D	NM_003482	chr12	49431181	C	T	Missense	c.G9958A	p.A3320T	0.6089613	491	
56	KMT2D	NM_003482	chr12	49425577	G	A	Missense	c.C12911T	p.P4304L	0.43333333	270	
56	KMT2D	NM_003482	chr12	49440507	G	A	Nonsense	c.C4303T	p.Q1435X	0.39393939	726	
60	KMT2D	NM_003482	chr12	49433394	G	A	Nonsense	c.C8053T	p.R2685X	0.42894057	387	
63	KMT2D	NM_003482	chr12	49445511	C	T	Missense	c.G1955A	p.R652H	0.2605042	714	
					GTTCCTCC							
					TAGGTGG							
65	KMT2D	NM_003482	chr12	49448317	GCAGGT	G	Frameshift	deletion	c.375_393del	p.T125fs	0.21984733	655
							Frameshift					
65	KMT2D	NM_003482	chr12	49448340	AGG	A	deletion	c.369_370del	p.G123fs	0.23776224	572	
							Frameshift					
65	KMT2D	NM_003482	chr12	49448348	AG	A	deletion	c.362delC	p.P121fs	0.25168919	592	
65	KMT2D	NM_003482	chr12	49421078	G	A	Nonsense	c.C14671T	p.Q4891X	0.43896104	385	
65	KMT2D	NM_003482	chr12	49448338	T	A	Missense	c.A373T	p.T125S	0.2369338	574	
70	KMT2D	NM_003482	chr12	49437166	T	C	Missense	c.A5513G	p.E1838G	0.35146444	717	
								c.14075+1G>				
73	KMT2D	NM_003482	chr12	49423183	C	A	Splice site	T	NA	0.49840256	626	
								c.14075+2T>				
81	KMT2D	NM_003482	chr12	49423182	A	T	Splice site	A	NA	0.40031397	637	
							Frameshift					
85	KMT2D	NM_003482	chr12	49434758	TC	T	deletion	c.6794delG	p.G2265fs	0.33030853	551	
86	KMT2D	NM_003482	chr12	49426466	G	A	Missense	c.C12022T	p.H4008Y	0.46478873	710	
87	KMT2D	NM_003482	chr12	49447416	G	A	Missense	c.C682T	p.R228C	0.45775536	793	
91	KMT2D	NM_003482	chr12	49425900	C	G	Missense	c.G12588C	p.Q4196H	0.50073421	681	
92	KMT2D	NM_003482	chr12	49431346	G	A	Nonsense	c.C9793T	p.Q3265X	0.27643312	785	
							Nonframeshift	c.16489_1649				
93	KMT2D	NM_003482	chr12	49415855	AGAT	A	deletion	1del	p.5497_549	0.26526527	999	
							Frameshift					
95	KMT2D	NM_003482	chr12	49447845	AG	A	deletion	c.588delC	p.P196fs	0.60444444	675	
95	KMT2D	NM_003482	chr12	49440143	A	C	Missense	c.T4483G	p.Y1495D	0.19247312	930	
95	KMT2D	NM_003482	chr12	49440186	A	T	Nonsense	c.T4440A	p.C1480X	0.18577075	759	
24	MEF2B	NM_001145785	chr19	19261528	A	T	Missense	c.T17A	p.I6N	0.25737898	847	
28	MEF2B	NM_001145785	chr19	19260064	C	T	Missense	c.G229A	p.E77K	0.52867384	558	
32	MEF2B	NM_001145785	chr19	19260165	A	C	Missense	c.T128G	p.I43R	0.26514132	743	
39	MEF2B	NM_001145785	chr19	19260124	A	T	Missense	c.T169A	p.Y57N	0.22506394	782	
43	MEF2B	NM_001145785	chr19	19256610	C	T	Missense	c.G1103A	p.R368Q	0.51546392	194	
							Frameshift					
63	MEF2B	NM_001145785	chr19	19257101	CG	C	deletion	c.861delC	p.P287fs	0.15976331	169	
							Frameshift					
76	MEF2B	NM_001145785	chr19	19260237	A	AC	insertion	c.55dupG	p.V19fs	0.12280702	570	
85	MEF2B	NM_001145785	chr19	19260222	C	T	Missense	c.G71A	p.R24Q	0.34266667	750	
37	MEF2C	NM_001193347	chr5	88018503	A	G	Missense	c.T1370C	p.I457T	0.59663866	476	
67	SETD2	NM_014159	chr3	47129680	G	A	Nonsense	c.C5200T	p.Q1734X	0.25584112	856	
84	SETD2	NM_014159	chr3	47098370	A	G	Missense	c.T6904C	p.C2302R	0.50554995	991	
95	SETD2	NM_014159	chr3	47162915	C	T	Missense	c.G3211A	p.V1071I	0.88387824	887	
					AAAAGCT							
12	TET2	NM_001127208	chr4	106157106	C	A	Frameshift	c.2008_2014d				
							deletion	el	p.K670fs	0.35198135	858	
							Frameshift					
12	TET2	NM_001127208	chr4	106157969	T	TA	insertion	c.2871dupA	p.L957fs	0.41271443	991	
21	TET2	NM_001127208	chr4	106157786	T	G	Missense	c.T2687G	p.L896R	0.347	1000	
29	TET2	NM_001127208	chr4	106156867	C	A	Missense	c.C1768A	p.L590I	0.49195171	994	

30	TET2	NM_001127208	chr4	106196316	A	G	Missense	c.A4649G	p.H1550R	0.34700315	634
31	TET2	NM_001127208	chr4	106156069	C	T	Nonsense	c.C970T	p.Q324X	0.28	1000
31	TET2	NM_001127208	chr4	106157980	G	T	Nonsense	c.G2881T	p.E961X	0.367	1000
					TTTGCAA						
					AATGGAG		Frameshift				
38	TET2	NM_001127208	chr4	106155363	GAATAA	T	deletion	c.265_283del	p.L89fs	0.15035461	705
47	TET2	NM_001127208	chr4	106196349	C	G	Missense	c.C4682G	p.S1561C	0.50180072	833
							Frameshift	c.1693_1697d			
57	TET2	NM_001127208	chr4	106156791	GATTGA	G	deletion	el	p.I565fs	0.162	1000
57	TET2	NM_001127208	chr4	106156768	C	T	Nonsense	c.C1669T	p.Q557X	0.352	1000
63	TET2	NM_001127208	chr4	106197255	C	T	Missense	c.C5588T	p.A1863V	0.079	1000
							Frameshift				
64	TET2	NM_001127208	chr4	106157997	GC	G	deletion	c.2899delC	p.Q967fs	0.452	1000
							Frameshift				
64	TET2	NM_001127208	chr4	106180783	T	TG	insertion	c.3812dupG	p.C1271fs	0.44430538	799
							Frameshift				
82	TET2	NM_001127208	chr4	106158268	GA	G	deletion	c.3170delA	:p.E1057fs,	0.26	1000
							Frameshift				
82	TET2	NM_001127208	chr4	106180783	T	TG	insertion	c.3812dupG	p.C1271fs	0.2337376	907
5	B2M	NM_004048	chr15	45003764	T	G	Nonsense	c.T20G	p.L7X	0.46819338	393
							Frameshift				
14	B2M	NM_004048	chr15	45003780	ACT	A	deletion	c.37_38del	p.L13fs	0.52141058	397
19	B2M	NM_004048	chr15	45007732	T	C	Missense	c.T179C	p.L60P	0.321	1000
19	B2M	NM_004048	chr15	45007753	A	T	Missense	c.A200T	p.E67V	0.329	1000
49	B2M	NM_004048	chr15	45003764	T	G	Nonsense	c.T20G	p.L7X	0.79545455	352
65	B2M	NM_004048	chr15	45003747	G	A	Missense	c.G3A	p.M1I	0.77118644	354
75	B2M	NM_004048	chr15	45003808	C	T	Nonsense	c.C64T	p.Q22X	0.82326622	447
80	B2M	NM_004048	chr15	45007620	G	A	Splice site	c.68-1G>A	NA	0.17467761	853
82	B2M	NM_004048	chr15	45003745	A	G	Missense	c.A1G	p.M1V	0.30107527	372
								c.67+4GTGA			
83	B2M	NM_004048	chr15	45003811	CGTGA	C	Splice site	>-	NA	0.40751445	346
95	B2M	NM_004048	chr15	45003764	T	G	Nonsense	c.T20G	p.L7X	0.78271605	405
24	CD58	NM_001779	chr1	117086940	A	T	Nonsense	c.T357A	p.Y119X	0.23212192	853
24	CD58	NM_001779	chr1	117113523	A	G	Splice site	c.70+2T>C	NA	0.16608997	289
							Frameshift				
31	CD58	NM_001779	chr1	117087110	CT	C	deletion	c.186delA	p.K62fs	0.107	1000
48	CD58	NM_001779	chr1	117113594	T	C	Missense	c.A1G	p.M1V	0.65644172	163
							Frameshift				
52	CD58	NM_001779	chr1	117087122	G	GT	insertion	c.174dupA	p.Q59fs	0.359	1000
83	CD58	NM_001779	chr1	117078761	G	A	Nonsense	c.C454T	p.R152X	0.48427673	636
92	CD58	NM_001779	chr1	117113592	C	T	Missense	c.G3A	p.M1I	0.31794872	195
4	CD70	NM_001252	chr19	6590114	C	T	Missense	c.G196A	p.G66R	0.14448669	526
							Nonframeshift				
8	CD70	NM_001252	chr19	6590118	GTGATTC	G	deletion	c.186_191del	p.62_64del	0.3121547	362
16	CD70	NM_001252	chr19	6586126	G	A	Nonsense	c.C487T	p.R163X	0.16018307	437
48	CD70	NM_001252	chr19	6590113	C	T	Splice site	c.196+1G>A	NA	0.77677419	775
63	CD70	NM_001252	chr19	6586119	T	G	Missense	c.A494C	p.D165A	0.55887522	569
63	CD70	NM_001252	chr19	6590147	A	T	Missense	c.T163A	p.W55R	0.09179416	719
67	CD70	NM_001252	chr19	6590114	C	T	Missense	c.G196A	p.G66R	0.28915663	415
68	CD70	NM_001252	chr19	6590114	C	T	Missense	c.G196A	p.G66R	0.27444254	583
					CGAAGCG		Frameshift				
71	CD70	NM_001252	chr19	6590890	CTGG	C	deletion	c.114_123del	p.I38fs	0.118	1000
							Frameshift	c.111_112ins			
71	CD70	NM_001252	chr19	6590902	T	TC	insertion	G	p.I38fs	0.116	1000
71	CD70	NM_001252	chr19	6590903	G	C	Missense	c.C111G	p.C37W	0.11711712	999
74	CD70	NM_001252	chr19	6590148	C	T	Splice site	c.163-1G>A	NA	0.71904762	840
75	CD70	NM_001252	chr19	6590913	A	C	Missense	c.T101G	p.L34R	0.86379115	881
83	CD70	NM_001252	chr19	6591012	A	G	Missense	c.T2C	p.M1T	0.68410853	516
9	CIITA	NM_001286402	chr16	11001303	A	G	Missense	c.A1957G	p.S653G	0.58188153	861
16	CIITA	NM_001286402	chr16	11000835	C	T	Missense	c.C1489T	p.L497F	0.53640777	824
							Frameshift				
24	CIITA	NM_001286402	chr16	10971232	G	GC	insertion	c.46dupC	p.E15fs	0.18193384	786
50	CIITA	NM_001286402	chr16	10971240	G	A	Splice site	c.52+1G>A	NA	0.29232996	691
61	CIITA	NM_001286402	chr16	10989149	G	C	Missense	c.G63C	p.Q21H	0.53813559	472
							Frameshift				
63	CIITA	NM_001286402	chr16	10992583	AT	A	deletion	c.353delT	p.I118fs	0.2457293	761
67	CIITA	NM_001286402	chr16	10995936	C	T	Missense	c.C526T	p.P176S	0.46511628	516
72	CIITA	NM_001286402	chr16	10971239	G	A	Missense	c.G52A	p.G18S	0.46746348	753
72	CIITA	NM_001286402	chr16	11012358	C	T	Missense	c.C3127T	p.L1043F	0.47674419	430
84	CIITA	NM_001286402	chr16	11001533	C	G	Missense	c.C2187G	p.I729M	0.47452229	942
93	CIITA	NM_001286402	chr16	11001533	C	G	Missense	c.C2187G	p.I729M	0.47982063	892

							Frameshift					
95	CIITA	NM_001286402	chr16	10995372	CT	C	deletion	c.442delT	p.F148fs	0.27720739	487	
95	CIITA	NM_001286402	chr16	11000499	A	T	Missense	c.A1153T	p.T385S	0.215	600	
96	CIITA	NM_001286402	chr16	11000547	G	A	Missense	c.G1201A	p.V401M	0.62441315	852	
7	TNFRSF14	NM_003820	chr1	2488123	G	A	Nonsense	c.G20A	p.W7X	0.12709832	417	
8	TNFRSF14	NM_003820	chr1	2489232	A	G	Missense	c.A137G	p.E46G	0.73255814	172	
							Frameshift					
19	TNFRSF14	NM_003820	chr1	2489189	G	GC	insertion	c.95dupC	p.A32fs	0.52538071	394	
24	TNFRSF14	NM_003820	chr1	2489886	C	T	Nonsense	c.C283T	p.Q95X	0.26760563	568	
52	TNFRSF14	NM_003820	chr1	2488138	G	A	Nonsense	c.G35A	p.W12X	0.55514706	272	
68	TNFRSF14	NM_003820	chr1	2489899	G	C	Missense	c.G296C	p.C99S	0.16078431	510	
68	TNFRSF14	NM_003820	chr1	2492068	G	A	Missense	c.G466A	p.E156K	0.38607595	316	
70	TNFRSF14	NM_003820	chr1	2488138	G	A	Nonsense	c.G35A	p.W12X	0.37898089	314	
82	TNFRSF14	NM_003820	chr1	2488165	T	A	Nonsense	c.T62A	p.L21X	0.54977376	442	
							Frameshift					
83	TNFRSF14	NM_003820	chr1	2492096	G	GC	insertion	c.495dupC	p.C165fs	0.60042283	473	
85	TNFRSF14	NM_003820	chr1	2493240	G	T	Missense	c.G680T	p.R227I	0.69811321	742	

Abbreviations: AA, amino acid; NA, not available.

Table S5 Potential therapeutic targets based on gene mutations in DLBCL

Gene	Therapeutic agent
<i>CD79A/CD79B</i>	BTK inhibitors (ibrutinib), SYK inhibitors (fostamatinib, entospletinib), PKC inhibitors (sotrastaurin)
<i>MYD88</i>	IRAK1/4 inhibitors
<i>EZH2</i>	EZH2 inhibitors (tazemetostat, GSK126)
<i>CARD11</i>	MALT1 inhibitors
<i>CREBBP/EP300</i>	HDAC inhibitors (panobinostat, vorinostat, mocetinostat, abexinostat)
<i>TNFAIP3</i>	Proteasome inhibitors (bortezomib, carfilzomib)
<i>JAK3</i>	JAK inhibitors
<i>SOCS1</i>	JAK inhibitors
<i>STAT6</i>	STAT inhibitors
<i>NOTCH1</i>	Notch inhibitors
<i>NOTCH2</i>	Notch inhibitors
<i>SPEN</i>	Notch inhibitors

Table S6 Univariate survival analysis for 41 genes in patients with DLBCL

Gene	All patients		R-CHOP group		All patients		R-CHOP group	
	<i>P</i> (PFS)	FDR	<i>P</i> (PFS)	FDR	<i>P</i> (OS)	FDR	<i>P</i> (OS)	FDR
<i>KMT2D</i>	0.014	0.177	0.032	0.395	0.028	0.261	0.046	0.288
<i>SOCS1</i>	0.113	0.662	0.271	0.803	0.063	0.441	0.141	0.588
<i>MYD88</i>	0.061	0.464	0.011	0.204	0.172	0.688	0.024	0.200
<i>MYD88 L265P</i>	0.007	0.133	0.000183	0.006771	0.088	0.481	0.009	0.113
<i>CD79B</i>	0.335	0.792	0.185	0.803	0.944	0.979	0.632	0.830
<i>PIM1</i>	0.883	0.963	0.679	0.837	0.803	0.979	0.527	0.830
<i>BTG1</i>	0.813	0.963	0.797	0.894	0.512	0.979	0.329	0.830
<i>SPEN</i>	0.679	0.963	0.471	0.803	0.775	0.979	0.500	0.830
<i>TBL1XR1</i>	0.438	0.876	0.178	0.803	0.919	0.979	0.370	0.830
<i>SGK1</i>	0.810	0.963	0.437	0.803	0.674	0.979	0.947	0.986
<i>HIST1H1E</i>	0.255	0.792	0.973	0.973	0.474	0.979	0.985	0.986
<i>CREBBP</i>	0.825	0.963	0.706	0.843	NA	NA	NA	NA
<i>TET2</i>	0.369	0.792	0.507	0.803	NA	NA	NA	NA
<i>KLHL6</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>TNFRSF14</i>	0.141	0.670	0.401	0.803	NA	NA	NA	NA
<i>B2M</i>	0.920	0.963	0.784	0.894	0.929	0.979	0.255	0.830
<i>FAS</i>	0.320	0.792	0.436	0.803	NA	NA	NA	NA
<i>TP53</i>	0.007	0.133	0.194	0.803	0.024	0.261	0.428	0.830
<i>KMT2C</i>	0.963	0.963	0.648	0.837	0.854	0.979	0.440	0.830
<i>CIITA</i>	0.354	0.792	0.453	0.803	0.448	0.979	0.594	0.830
<i>CARD11</i>	0.677	0.963	0.514	0.803	0.614	0.979	0.540	0.830
<i>IRF4</i>	0.632	0.963	0.670	0.837	0.103	0.481	0.126	0.588
<i>NOTCH2</i>	0.708	0.963	NA	NA	0.894	0.979	NA	NA
<i>POU2F2</i>	0.122	0.662	0.382	0.803	0.483	0.979	NA	NA
<i>HIST1H1C</i>	0.222	0.792	0.167	0.803	0.405	0.979	0.269	0.830
<i>MEF2B</i>	0.365	0.792	0.480	0.803	NA	NA	NA	NA
<i>NOTCH1</i>	0.661	0.963	0.325	0.803	0.860	0.979	0.664	0.830
<i>GNAI3</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>STAT3</i>	0.225	0.792	0.334	0.803	NA	NA	NA	NA
<i>STAT6</i>	0.817	0.963	0.556	0.803	0.523	0.979	NA	NA
<i>ETV6</i>	0.910	0.963	0.564	0.803	0.436	0.979	0.986	0.986
<i>CD70</i>	0.375	0.792	0.556	0.803	0.692	0.979	0.973	0.986
<i>BCL6</i>	0.946	0.963	0.417	0.803	NA	NA	NA	NA
<i>ACTB</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>CD58</i>	0.293	0.792	0.617	0.837	NA	NA	NA	NA
<i>ARID1A</i>	0.489	0.929	0.927	0.957	0.737	0.979	0.597	0.830
<i>FOXO1</i>	0.957	0.963	0.931	0.957	NA	NA	NA	NA
<i>PRDM1</i>	0.608	0.963	0.846	0.921	NA	NA	NA	NA
<i>PTEN</i>	0.811	0.963	0.432	0.803	0.995	0.995	0.660	0.830
<i>BCL2</i>	0.023	0.219	0.161	0.803	0.000306	0.008568	0.005	0.113
<i>DDX3X</i>	NA	NA	NA	NA	NA	NA	NA	NA
<i>EP300</i>	0.686	0.963	0.349	0.803	0.793	0.979	0.944	0.986

Abbreviation: R-CHOP, rituximab, cyclophosphamide, doxorubicin, vincristine, and prednisone; PFS, progression-free survival; OS, overall survival; FDR, false discovery rate; NA, not available.