Table S1. List of 307 selected genes for targeted sequencing

ABCA7
ACTB
ACTG1
ADAP1
ADCK2
AICDA
AK3
ANKRD11
AP3D1
APOBEC3C
APOBEC3F
ARHGAP30
ARID1A
ARID1B
ARID5A
ARID5B
ATM
ATR
B2M
B3GNT7
BBC3
BCL10
CARD11
CCND3
CD58
CD79B
CDC42BPB
CDKN2A
CDKN2B
CELSR2
CEP164
CHRNA7
CHRNG
CIITA
CILP2
CK1a
CLIP3
COX19
CPEB2
CREB3
CREBBP
CRHBP
CRIPAK
CS
EP300
EPPK1
ETS1
ETV6
EZH2
FAM186A
FAM189B
FAM219B
FAM47C
FAR2
FAS
FBN3
FBXW7
FCRL1
FLG2
FLNC
FLOT2
FOXO1
FOXP3
FUT6
FZD10
GABBR1
HS1BP3
ID3
IDH1
IDH2
IGH VDJ
IGLL5
IGSF3
INSL4
IRAK1
IRF4
IRX3
ITPKB
ITPR3
JAK2
JAK3
KDM5A
KIT
KLF2
KLHL14
KMT2D
KPNB1
LAMC3
MFSD12
MIR17HG
MLL2
MLL3
MPDZ
MPEG1
MRC2
MSL2
MST1L
MUC17
MUC4
MYBPC3
MYC
MYD88 (L265P site)
MYLK2
MYO15A
MYO18A
MYOM2
NBEAL2
NBPF12
NEFL
NES
PAX5
PCDH17
PCGF2
PCNA
PDGFRB
PIK3CA
PIM1
PLCγ2
PLD2
PLEC
PLK1
POGZ
POU2F2
POU4F3
PRDM1
PRG4
PRKCB
PRKCD
PTEN
PTPN1
PTPN23
PTPRD
SCRIB
SEMA6D
SETD1B
SETD5
SETDB1
SGK1
SHMT1
SIPA1L3
SLC1A1
SMC1A
SOBP
SOCS1
SOGA2
SPATA31C1
SPEN
SPTBN1
SRCIN1
SRGAP3
STAT3
STAT6
SYK
TBL1XR1
TRAF2
TRAF5
TRIB3
TRIM56
TSHZ3
TSR1
TTN
TUBA3C
UBE3B
UGT1A1
UGT1A8
USP27X
WBSCR28
WNK2
WNT10B
XPO1 (E571K site)
ZAP70
ZFAT
ZFP36L1
ZIC2
ZNF235
ZNF343

(immune-related genes)
ADORA2A
BTLA
CD274
CD276
CD28
CD47
CD70
CD80
CD86
CTLA4
FGL1
HAVCR2
ICOS
ICOSLG
IDO1
LAG3
LGALS9
NT5E
PDCD1
PDCD1LG2
SIRPA

BCL11A	CSMD1	GAGE2B	LILRA1	NEU4	RCL1	TCF3	ZNF385A	TIGIT
BCL2	CXCR4	GAREM	LILRA2	NF1	REC8	TCHH	ZNF585A	TNFRSF14
BCL6	DCHS1	GLIS3	LILRA5	NFKB1	RELN	TET2	ZNF585B	TNFRSF18
BIRC3	DDX3X	GNA13	LILRA6	NFKB2	REM1	THEG	ZNF608	TNFRSF4
BIRC6	DGKZ	GNAS	LRP1	NHSL1	RFTN1	TLN2	ZNF646	TNFRSF9
BRAF	DHX40	GRIA1	LRP1B	NOD1	RNF10	TMEM184A	ZNF672	TNFSF14
BRCA2	DMXL1	GRIN2D	LYN	NOTCH1	RNF216	TMEM63A	ZNF783	TNFSF18
BTG1	DNAI1	HIST1H1C	MAP1A	NOTCH2	ROBO1	TMSB4X	ZNF785	TNFSF4
BTG2	DNMT3A	HIST1H1D	MCL1	NOVA2	ROBO2	TNFAIP3	ZNF814	TNFSF9
BTK	DTX1	HIST1H1E	MDM2	NR2F1	RREB1	TNXB		VSIR
BTNL8	DUSP2	HIST1H2AM	MDM4	NUMBL	RRM2	TP53		
CACNA1I	EBF1	HOXA3	MEF2B	OR10A2	RSBN1	TP63		
CALR	ECE2	HRAS	MFHAS1	OSBPL3	SBSN	TP73		

Table S2. Validated somatic mutations in the targeted sequencing cohort by Sanger sequencing

Gene Name	Chromosome start position	Chromosome end position	Refence nucleotide	Observation nucleotide	Forwoard primer	Reverse primer
NT5E	86160041	86160041	C	T	CCTAGCTGCTCGCCCCTACTCG	CAGCCCGGCTCCTCTCTCAGTC
	86199242	86199242	T	C	GAACACAGCAGCAGGTGAAAAG	TGTGTGTCCTTCAGGCTAGGTT
ADORA2A	24836830	24836830	C	T	CATGCTAGGTTGGAACAACTGC	AGGCGTAGATGAAGGGATTCAC
	24837293	24837293	A	G	CTGAGGCAGCAAGAACCTTTC	GGTCTCCTGGCACTCTCTCTCT
CD274	5457327	5457327	T	G	AGACCTGGCTGCACTAATTGTC	CATGGCTCTGTGTTGTTTGTCTC
	5462955	5462955	C	T	GAACCAGCCTGCATTGATACTC	ATGCTAGGTGCTAGGGGACAGT
	5457398	5457398	C	T	AGACCTGGCTGCACTAATTGTC	CATGGCTCTGTGTTGTTTGTCTC
PDCD1LG2	5557707	5557707	T	C	GCACTTAGAATAGGGCCTGGTG	GCTCTGAGTGGGTTTAGCATGA
	5557629	5557629	C	G	GTGGATGAGCTGATAGGTGCAG	CAGTGCATTGGGTTACCATGAA

Table S3. Validated gene fusions in PD-L1/L2 loci by Sanger sequencing

Sample ID	Gene fusion	Forwoard primer	Reverse primer
DL242	CD274-SP140	CAAATGTTGTTTGGGTCATGCT	GTAGGGCTGGGTCATTGCTTAG
DL267	CD274-PDCD1LG2	ACTTCTCCATGCTGTTCCCATT	GCCTCAGTCAACTTGGAGACAA

Table S4. List of primary antibodies used in immunohistochemistry

Method	Antigen	Clone	Species	Dilution	Company	Catalog no.
immunohistochemistry	PD-L1	E1L3N	Rabbit	1:200	Cell Signaling Tech	#13684
	PD-L2	D7U8C	Rabbit	1:100	Cell Signaling Tech	#82723
	CD73	D7F9A	Rabbit	1:100	Cell Signaling Tech	#13160
	A2aR	polyclonal	Rabbit	1:350	Abcam	ab3461
multiplexed immunofluorescence	PD-1	D7D5W	Rabbit	1/(200×5)	Cell Signaling Tech	#84651
	A2aR	polyclonal	Rabbit	1/(700×5)	Abcam	ab3461
	CD8	polyclonal	Rabbit	1/(200×5)	Abcam	ab4055

Table S5. Summary of the whole-exome sequencing data of the 42 paired cases of diffuse large B-cell lymphoma

Patient ID	Sample type	Average sequencing depth on target	Coverage of target region	Fraction of target covered with at least 20×	Fraction of target covered with at least 50×
DL004T	tumor tissue	91.91	99.92%	97.23%	75.14%
DL006T	tumor tissue	105.23	99.92%	96.90%	75.30%
DL008T	tumor tissue	79.87	97.61%	94.58%	69.80%
DL012T	tumor tissue	82.37	99.68%	96.78%	71.80%
DL014T	tumor tissue	98.28	99.94%	96.98%	73.18%
DL015T	tumor tissue	81.98	99.67%	96.54%	69.30%
DL016T	tumor tissue	94.11	99.93%	96.16%	67.66%
DL017T	tumor tissue	102.23	99.69%	97.96%	80.55%
DL023T	tumor tissue	82.56	99.68%	96.76%	68.90%
DL024T	tumor tissue	80.06	99.69%	96.14%	66.51%
DL026T	tumor tissue	99.6	99.94%	96.26%	69.52%
DL027T	tumor tissue	86.61	99.93%	96.89%	69.49%
DL028T	tumor tissue	92.82	99.93%	96.65%	69.58%
DL029T	tumor tissue	87.83	99.70%	95.19%	63.85%
DL030T	tumor tissue	85.99	99.69%	96.28%	67.93%
DL031T	tumor tissue	90.73	99.68%	96.57%	72.73%
DL037T	tumor tissue	89.52	99.93%	96.78%	72.82%
DL040T	tumor tissue	94.37	99.92%	96.86%	72.21%
DL041T	tumor tissue	80.24	99.69%	96.23%	67.67%
DL042T	tumor tissue	86.5	99.90%	96.23%	70.47%
DL043T	tumor tissue	94.19	99.92%	97.07%	75.06%
DL044T	tumor tissue	81.59	99.92%	95.67%	66.81%
DL045T	tumor tissue	91.45	99.67%	96.72%	74.12%
DL046T	tumor tissue	84.14	99.66%	96.14%	69.79%
DL047T	tumor tissue	86.63	99.91%	96.02%	69.97%
DL048T	tumor tissue	93.39	99.93%	97.09%	75.07%
DL049T	tumor tissue	88.5	99.91%	96.51%	70.08%
DL050T	tumor tissue	100.77	99.92%	97.44%	75.80%
DL052T	tumor tissue	95.26	99.67%	96.50%	72.80%
DL054T	tumor tissue	99.74	99.91%	96.95%	75.98%
DL055T	tumor tissue	95.35	99.67%	96.67%	74.48%
DL056T	tumor tissue	102.36	99.71%	97.64%	80.08%
DL057T	tumor tissue	100.45	99.70%	97.11%	77.33%
DL058T	tumor tissue	82.59	99.68%	95.98%	67.72%
DL059T	tumor tissue	90.65	99.92%	96.79%	70.79%
DL060T	tumor tissue	90.57	99.91%	96.61%	73.27%

DL061T	tumor tissue	99.39	99.93%	97.77%	78.15%
DL063T	tumor tissue	88.87	99.93%	94.81%	63.97%
DL064T	tumor tissue	123.07	99.94%	98.35%	83.54%
DL065T	tumor tissue	93.71	99.92%	96.71%	72.51%
DL066T	tumor tissue	97.45	99.92%	97.26%	75.95%
DL067T	tumor tissue	99.13	99.93%	97.70%	78.35%
DL004W	blood	95.46	99.93%	97.43%	73.31%
DL006W	blood	83.71	99.93%	94.99%	62.28%
DL008W	blood	94.34	99.93%	97.58%	73.81%
DL012W	blood	92.42	99.68%	97.22%	72.85%
DL014W	blood	88.68	99.93%	97.10%	71.02%
DL015W	blood	123.2	99.69%	98.67%	86.44%
DL016W	blood	77.7	99.92%	95.82%	63.92%
DL017W	blood	104.43	99.69%	98.09%	80.08%
DL023W	blood	113.18	99.69%	98.37%	83.81%
DL024W	blood	94.2	99.69%	97.66%	76.44%
DL026W	blood	99.88	99.94%	97.77%	75.74%
DL027W	blood	89.5	99.93%	96.81%	68.75%
DL028W	blood	87.78	99.94%	97.26%	71.61%
DL029W	blood	105.6	99.71%	97.77%	76.08%
DL030W	blood	73.86	99.68%	94.59%	59.33%
DL031W	blood	95.64	99.69%	97.46%	73.77%
DL037W	blood	116.74	99.94%	98.67%	88.02%
DL040W	blood	90.78	99.93%	96.39%	68.20%
DL041W	blood	84.89	99.71%	95.41%	64.15%
DL042W	blood	96.64	99.93%	96.62%	69.89%
DL043W	blood	110.61	99.93%	97.90%	78.23%
DL044W	blood	98.6	99.95%	96.88%	71.58%
DL045W	blood	97.72	99.69%	97.02%	73.09%
DL046W	blood	92.56	99.68%	97.09%	74.48%
DL047W	blood	117.63	99.94%	98.25%	81.05%
DL048W	blood	86.69	99.94%	96.17%	66.40%
DL049W	blood	97.66	99.93%	97.26%	74.03%
DL050W	blood	109.35	99.92%	98.15%	81.40%
DL052W	blood	84.55	99.67%	96.26%	68.48%
DL054W	blood	113.6	99.93%	98.06%	79.89%
DL055W	blood	84.09	99.69%	95.57%	65.03%
DL056W	blood	102.52	99.71%	97.38%	75.38%
DL057W	blood	98.74	99.71%	96.90%	71.71%
DL058W	blood	86.37	99.68%	96.84%	72.27%

DL059W	blood	73.33	99.90%	95.05%	60.48%
DL060W	blood	93.02	99.93%	94.85%	63.92%
DL061W	blood	95.25	99.93%	95.64%	66.52%
DL063W	blood	64.15	99.91%	92.90%	52.68%
DL064W	blood	94.3	99.94%	96.22%	68.03%
DL065W	blood	85.06	99.92%	95.04%	63.17%
DL066W	blood	101.66	99.93%	97.58%	76.47%
DL067W	blood	85.79	99.93%	95.59%	65.01%

Table S6. Summary in mutations of immune-related genes identified by whole-exome sequencing in 42 patients with diffuse large B-cell lymphoma

Gene ID	Gene name	Protein	Alias	Number of mutations	Patient ID	Mutation type
3122	HLA-DRA	Ligand		4	DL012, DL015, DL023, DL067	missense
29126	CD274	Ligand	PD-L1, B7H1	0		
80380	PDCD1LG2	Ligand	PD-L2, CD273	0		
5133	PDCD1	Receptor	PD-1, CD279	1	DL043	missense
3902	LAG3	Receptor		1	DL043	frameshift
2267	FGL1	Ligand		0		
5817	PVR	Ligand	CD155, HVED, PVS	1	DL061	missense
79037	PVRIG	Receptor	CD112R	1	DL040	missense
201633	TIGIT	Receptor		0		
5819	NECTIN2	Ligand	CD112, HVEB, PVRL2	0		
10225	CD96	Receptor		0		
10666	CD226	Receptor		1	DL041	missense
8744	TNFSF9	Ligand	CD137L, 4-1BBL	1	DL050	missense
3604	TNFRSF9	Receptor	CD137, 4-1BB	0		
8995	TNFSF18	Ligand	GITRL	0		
8784	TNFRSF18	Receptor	GITR	0		
51744	CD244	Receptor	2B4	0		
23308	ICOSLG	Ligand	ICOSL, B7H2	3	DL023, DL044, DL058	missense
29851	ICOS	Receptor	CD278	0		
7292	TNFSF4	Ligand	OX40L, CD134L, CD252	0		
7293	TNFRSF4	Receptor	OX40, CD134	1	DL063	frameshift
970	CD70	Ligand	TNFSF7	4	DL024, DL027, DL048, DL067	missense, nonsense, frameshift
939	CD27	Receptor	TNFRSF7	1	DL046	missense
84868	HAVCR2	Ligand	Tim-3	3	DL026, DL048, DL060	CDS-indel
3965	LGALS9	Receptor	GALECTINE-9	1	DL004	missense
953	ENTPD1	Ligand	CD39	0		
3620	IDO1	Ligand		0		
4907	NT5E	Ligand	CD73	1	DL029	missense
135	ADORA2A	Receptor	A2aR	3	DL008, DL054, DL061	missense

8764	TNFRSF14	Receptor	CD270, HVEM, HVEA, LIGHTR	4	DL006, DL012, DL030, DL065	missense, frameshift
8740	TNFSF14	Ligand	CD258, HVEML, LIGHT	0		
80381	CD276	Receptor	B7-H3	8	DL012, DL015, DL023, DL026, DL027, DL042, DL047, DL061	missense
941	CD80	Ligand	B7-1	0		
942	CD86	Ligand	B7-2	0		
940	CD28	Receptor		0		
1493	CTLA4	Receptor	CD152	0		
958	CD40	Receptor	TNFRSF5	0		
959	CD40LG	Ligand	CD40L, CD154, TNFSF5	0		
961	CD47	Ligand		0		
140885	SIRPA	Receptor		0		
64115	VSIR	Receptor	VISTA, B7H5	0		

Table S7. Summary of the targeted sequencing data of the 188 patients with diffuse large B-cell lymphoma

Patient ID	Average sequencing depth on target	Coverage of target region	Fraction of target covered with at least 50×	Fraction of target covered with at least 100×
DL004T	364.59	99.01%	94.71%	90.52%
DL005T	637.25	99.06%	96.65%	94.56%
DL006T	342.63	98.88%	94.76%	90.38%
DL008T	911.41	98.97%	96.76%	95.27%
DL011T	991.66	99.14%	97.36%	96.05%
DL012T	744.84	99.06%	96.69%	94.72%
DL013T	717.74	99.07%	96.80%	94.84%
DL014T	615.34	98.74%	95.67%	93.13%
DL015T	1255.31	98.66%	95.24%	93.48%
DL016T	171.24	99.36%	93.09%	77.47%
DL017T	1544.94	98.94%	96.96%	95.88%
DL019T	676.09	99.11%	96.81%	94.77%
DL020T	682.05	98.89%	95.95%	94.01%
DL023T	1090.76	98.54%	93.24%	90.77%
DL024T	1102.73	99.11%	97.50%	96.28%
DL026T	1223.89	99.07%	97.70%	96.66%
DL027T	857.6	98.89%	96.86%	95.47%
DL028T	815.65	99.00%	96.78%	94.96%
DL029T	994.44	99.06%	97.21%	95.76%
DL030T	592.41	98.65%	95.72%	93.38%
DL031T	1097.6	99.00%	97.15%	95.66%
DL037T	1072.01	98.97%	96.40%	94.56%
DL038T	1089.37	98.91%	96.54%	95.03%
DL039T	867.44	99.04%	95.52%	93.25%
DL040T	1112.03	99.08%	97.46%	96.39%
DL041T	1550.26	98.93%	97.24%	96.24%
DL042T	1026.57	98.95%	97.19%	96.04%
DL043T	1622.47	99.02%	97.63%	96.90%
DL044T	1121.91	98.85%	97.04%	96.17%
DL045T	1730.27	99.00%	97.58%	96.81%
DL046T	874.71	98.88%	96.77%	95.26%
DL047T	870.08	98.86%	96.62%	95.13%
DL048T	912.53	98.62%	94.74%	92.71%
DL049T	849.47	99.06%	96.72%	95.11%
DL050T	916.07	98.97%	97.01%	95.76%
DL052T	845.75	98.83%	95.65%	93.70%

DL053T	862.27	98.75%	95.68%	93.71%
DL054T	1007.16	99.05%	97.43%	96.24%
DL055T	867.73	98.78%	96.52%	95.05%
DL056T	977.04	99.05%	97.28%	96.10%
DL057T	891.63	98.88%	96.92%	95.60%
DL058T	751.7	98.94%	97.03%	95.70%
DL059T	811.54	98.88%	96.68%	95.22%
DL060T	1064.48	98.92%	96.95%	95.74%
DL061T	911.38	98.92%	96.18%	94.47%
DL063T	865.62	99.03%	97.07%	95.75%
DL064T	619.56	99.02%	96.25%	93.97%
DL065T	573.87	98.93%	96.05%	93.62%
DL066T	452.75	99.24%	96.79%	94.76%
DL067T	1007.74	99.11%	97.48%	96.39%
DL202	1048.63	99.02%	97.26%	96.24%
DL203	1096.82	99.35%	97.37%	95.99%
DL204	1105.67	99.31%	97.50%	96.26%
DL205	1326.03	99.23%	97.73%	96.78%
DL206	939.96	99.28%	97.19%	95.98%
DL207	1156.64	99.11%	97.44%	96.33%
DL208	774.25	99.00%	96.16%	94.17%
DL209	797.95	99.15%	96.62%	94.74%
DL210	726.04	99.00%	96.33%	94.48%
DL211	838.81	99.12%	96.81%	95.23%
DL212	819.84	98.95%	96.61%	95.04%
DL213	585.79	99.02%	95.88%	93.43%
DL214	1075.28	98.94%	97.12%	95.84%
DL215	952.42	99.24%	97.25%	96.03%
DL216	795.41	99.08%	96.67%	94.97%
DL217	930.17	98.93%	96.78%	95.46%
DL218	681.66	99.28%	96.42%	94.78%
DL219	1106.22	99.13%	97.41%	96.29%
DL220	684.1	99.28%	96.78%	95.16%
DL221	671.29	99.21%	96.70%	95.22%
DL222	991.89	99.13%	97.33%	96.10%
DL223	399.11	99.03%	96.92%	95.59%
DL224	892.9	99.20%	97.10%	95.84%
DL226	600.97	99.00%	96.31%	94.24%
DL227	858.05	98.94%	96.86%	95.69%
DL228	807.59	99.05%	96.98%	95.64%

DL229	1079.72	99.31%	97.67%	96.59%
DL230	680.9	99.08%	96.50%	94.64%
DL231	637.31	98.87%	96.38%	94.48%
DL232	917.86	98.99%	97.35%	96.24%
DL233	740.38	98.85%	96.35%	94.44%
DL234	655.73	98.95%	96.36%	94.55%
DL235	808.59	98.91%	96.69%	95.22%
DL237	670.12	98.98%	96.38%	94.14%
DL238	662.72	98.86%	96.35%	94.34%
DL239	967.25	98.93%	97.07%	95.94%
DL240	693.58	99.06%	96.73%	95.08%
DL241	747.81	99.12%	96.80%	95.21%
DL242	902.86	98.88%	95.56%	93.58%
DL243	619.76	98.95%	96.38%	94.59%
DL244	594.96	99.05%	96.70%	94.75%
DL245	546.04	98.76%	96.29%	93.64%
DL246	997.81	98.87%	96.80%	95.40%
DL247	1071.35	99.06%	97.24%	96.11%
DL248	469.78	98.80%	95.62%	93.19%
DL249	1027.21	99.14%	97.01%	95.91%
DL250	861.62	99.03%	97.40%	96.12%
DL251	1331.04	99.12%	97.38%	96.43%
DL252	764.45	98.86%	96.86%	95.56%
DL253	1056.14	99.00%	97.05%	95.86%
DL254	775.16	98.91%	96.63%	95.06%
DL255	691.15	99.14%	96.52%	94.91%
DL256	633.02	98.93%	96.67%	95.49%
DL257	540.89	98.77%	96.28%	94.67%
DL258	655.9	98.93%	96.87%	95.60%
DL259	772.98	98.97%	96.75%	95.40%
DL260	1201.09	99.14%	97.50%	96.49%
DL261	1246.59	99.11%	97.54%	96.61%
DL262	542.89	98.84%	96.19%	94.38%
DL263	1010.87	98.90%	97.11%	95.92%
DL264	989.05	98.89%	97.12%	95.84%
DL265	487.92	98.84%	96.24%	94.12%
DL266	815.52	99.06%	97.08%	95.73%
DL267	792.07	99.03%	96.78%	95.54%
DL268	717.74	99.07%	96.49%	94.73%
DL269	1088.04	99.06%	97.55%	96.52%

DL270	843.94	99.10%	96.80%	95.28%
DL271	830.11	99.18%	97.20%	95.67%
DL272	909.86	99.12%	97.06%	95.73%
DL273	736.76	99.07%	97.09%	95.79%
DL274	773.09	98.97%	96.65%	95.40%
DL275	793.68	99.09%	96.96%	95.41%
DL276	664.7	99.03%	96.67%	94.76%
DL278	190	98.85%	92.15%	81.34%
DL279	713.13	99.10%	96.83%	95.13%
DL280	1108.89	99.22%	97.69%	96.54%
DL281	1073.08	99.03%	97.44%	96.28%
DL282	1104.4	99.22%	97.28%	96.36%
DL283	1368.2	99.18%	97.64%	96.67%
DL284	1325.22	99.14%	97.11%	96.11%
DL285	1169.59	98.89%	96.95%	95.80%
DL287	864.95	99.06%	97.27%	96.04%
DL288	1227.02	98.87%	94.88%	92.77%
DL289	1215.97	98.90%	97.32%	96.36%
DL290	754.77	98.61%	92.96%	89.91%
DL291	799.01	98.97%	96.79%	95.30%
DL292	697.58	98.60%	92.71%	89.30%
DL293	584.68	98.19%	89.72%	85.35%
DL294	480.62	99.01%	89.56%	84.37%
DL295	782.46	98.87%	96.63%	95.10%
DL296	688.53	98.94%	90.40%	85.90%
DL297	860.24	98.96%	97.04%	96.05%
DL298	709.95	98.33%	90.63%	86.97%
DL299	521.79	99.01%	95.80%	92.65%
DL300	914.47	98.94%	96.77%	95.29%
DL301	482.74	98.87%	95.64%	92.53%
DL302	591.38	98.46%	92.49%	88.98%
DL303	637.65	98.69%	93.35%	90.20%
DL304	757.08	98.65%	93.63%	90.57%
DL305	496.24	98.71%	95.05%	91.78%
DL306	1323.33	98.96%	97.29%	96.25%
DL307	1227.49	98.90%	97.03%	95.88%
DL308	1134.11	99.00%	97.09%	96.02%
DL309	600.99	98.65%	93.30%	89.96%
DL310	627.06	98.77%	96.05%	94.00%
DL311	610.17	98.82%	96.01%	93.64%

DL312	744.64	98.83%	96.51%	94.93%
DL313	957.15	98.35%	92.41%	89.74%
DL314	867.47	98.85%	96.71%	95.32%
DL315	640.66	98.73%	95.77%	93.31%
DL316	870.1	98.75%	95.94%	94.11%
DL317	886.66	98.60%	93.51%	90.78%
DL318	910.54	98.98%	97.09%	95.93%
DL319	698.14	99.01%	96.48%	95.00%
DL320	1172.45	98.92%	96.75%	95.41%
DL321	573.3	98.93%	96.28%	93.97%
DL322	620.14	98.99%	96.37%	94.19%
DL323	651.26	98.95%	96.48%	94.38%
DL324	1258.33	98.91%	97.16%	96.09%
DL325	1287.57	99.08%	97.52%	96.54%
DL328	873.78	98.97%	96.99%	95.68%
DL329	1086.82	99.07%	96.94%	95.55%
DL330	926.27	98.91%	97.12%	95.83%
DL331	909.9	98.98%	97.05%	95.78%
DL332	935.91	98.79%	96.14%	94.27%
DL333	1070.7	98.77%	94.36%	92.20%
DL334	1058.69	98.95%	97.32%	96.24%
DL335	875.75	99.00%	97.06%	95.82%
DL336	884.67	98.92%	97.02%	95.71%
DL337	916.44	98.87%	96.79%	95.55%
DL338	795.01	98.94%	96.64%	95.11%
DL339	849.85	98.90%	96.85%	95.37%
DL341	936.21	98.97%	96.79%	95.39%
DL342	1054.39	98.88%	96.52%	95.03%
DL343	1222.28	98.94%	97.33%	96.37%
DL344	1044.35	98.96%	97.08%	95.92%
DL345	886.48	98.86%	96.91%	95.65%
DL346	855.53	99.05%	97.21%	95.93%

Table S8. List of identified somatic nonsilent mutations involving CD73/A2aR and PD-1/PD-L1/L2 loci in 188 patients with diffuse large B-cell lymphoma

Gene Name	Patient ID*	Chromosome Position	Location	Base Change	Amino Acid Change	db SNP rs#ID	COSMIC	1000G	prediction by SIFT
NT5E	DL029T	chr6:86160041	Exon 1	C>T	Ala62Val	*	*	*	Deleterious
	DL204,DL212,DL294	chr6:86199242	Exon6	T>C	Met379Thr	rs2229524	COSM5001961	0.16	Tolerated
ADORA2A	DL242	chr22:24836830	Exon3E	C>T	Arg205*	rs1424402107	COSM6206953	*	*
	DL300	chr22:24837293	Exon3E	A>G	Asn359Ser	rs201152556	*	*	Deleterious
CD274	DL065T	chr9:5457327	Exon 3	T>G	Ile101Ser	*	*	*	*
	DL227	chr9:5462955	Exon 4	C>T	Gln173*	*	*	*	*
	DL288	chr9:5457398	Exon 3	C>T	Arg125*	rs897885359	*	*	Deleterious
PDCD1LG2	DL256	chr9: 5557629	Exon 5	C>G	Pro215Arg	rs561507956	*	*	Deleterious
	DL008T,DL011T,DL026T, DL266,DL303,DL311, DL315,DL330	chr9:5557707	Exon 5	T>C	Ile241Thr	rs7854413	COSM3982895	0.28	Deleterious

Table S9. Significantly enriched gene sets involved in negatively regulating the immune response in the high PD-L1/CD73 expression group versus the low PD-L1/CD73 expression group by gene set enrichment analysis in the internal cohort

Description (PD-L1)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	133	0.680	2.759	0.000	0.000	3783	tags=48%, list=14%, signal=42%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	362	0.520	2.362	0.000	0.000	3659	tags=36%, list=14%, signal=31%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	115	0.581	2.332	0.000	0.000	3432	tags=37%, list=13%, signal=33%
GOBP_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	49	0.669	2.306	0.000	0.000	2940	tags=49%, list=11%, signal=44%
GOBP_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	20	0.850	2.378	0.000	0.000	2940	tags=75%, list=11%, signal=67%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	268	0.563	2.466	0.000	0.000	3585	tags=37%, list=13%, signal=33%
GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	55	0.492	1.740	0.001	0.010	2371	tags=24%, list=9%, signal=22%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	183	0.391	1.646	0.000	0.001	3455	tags=26%, list=13%, signal=23%

Description (CD73)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	362	0.430	1.272	0.004	0.006	7462	tags=35%, list=28%, signal=26%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	268	0.463	1.359	0.001	0.001	7556	tags=37%, list=28%, signal=27%
GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	55	0.572	1.569	0.003	0.005	5249	tags=33%, list=20%, signal=26%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	183	0.565	1.654	0.000	0.000	5308	tags=37%, list=20%, signal=30%
GSE9650_EFFECTOR_VS_EXHAUSTED_CD8_TCELL_DN	182	0.556	1.628	0.000	0.000	6251	tags=41%, list=23%, signal=31%
GSE9650_EXHAUSTED_VS_MEMORY_CD8_TCELL_UP	183	0.507	1.484	0.000	0.000	5763	tags=34%, list=22%, signal=27%

Table S10. Significantly enriched gene sets involved in negatively regulating the immune response in the high PD-L1/CD73 expression group versus the low PD-L1/CD73 expression group by gene set enrichment analysis in the GSE117556 cohort

Description (PD-L1)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	142	0.576	2.305	0.000	0.000	3325	tags=39%, list=16%, signal=33%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	377	0.523	2.309	0.000	0.000	3921	tags=40%, list=19%, signal=33%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	121	0.555	2.168	0.000	0.000	3898	tags=40%, list=19%, signal=33%
GOBP_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	52	0.539	1.873	0.001	0.002	3898	tags=38%, list=19%, signal=31%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	325	0.527	2.297	0.000	0.000	2610	tags=28%, list=13%, signal=25%
GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	72	0.447	1.622	0.005	0.014	1923	tags=24%, list=9%, signal=22%
GOBP_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	22	0.616	1.787	0.004	0.013	3898	tags=55%, list=19%, signal=44%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	178	0.453	1.852	0.000	0.000	2518	tags=25%, list=12%, signal=22%
GSE9650_EXHAUSTED_VS_MEMORY_CD8_TCELL_UP	179	0.406	1.660	0.000	0.001	4084	tags=32%, list=20%, signal=26%

Description (CD73)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	377	0.362	1.620	0.000	0.000	4649	tags=34%, list=22%, signal=27%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	121	0.387	1.522	0.003	0.007	4034	tags=31%, list=19%, signal=25%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	325	0.361	1.595	0.000	0.000	3407	tags=23%, list=16%, signal=20%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	178	0.474	1.953	0.000	0.000	3358	tags=37%, list=16%, signal=31%
GSE9650_EFFECTOR_VS_EXHAUSTED_CD8_TCELL_DN	178	0.442	1.821	0.000	0.000	2769	tags=28%, list=13%, signal=24%
GSE9650_EXHAUSTED_VS_MEMORY_CD8_TCELL_UP	179	0.434	1.789	0.000	0.000	4861	tags=42%, list=23%, signal=33%

Table S11. Significantly enriched gene sets involved in negatively regulating the immune response in the high PD-L1/CD73 expression group versus the low PD-L1/CD73 expression group by gene set enrichment analysis in the GSE31312 cohort

Description (PD-L1)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	137	0.661	2.680	0.000	0.000	1576	tags=37%, list=7%, signal=35%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	356	0.547	2.488	0.000	0.000	1712	tags=30%, list=8%, signal=28%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	119	0.581	2.302	0.000	0.000	1571	tags=31%, list=7%, signal=29%
GOBP_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	50	0.634	2.129	0.000	0.000	2660	tags=42%, list=12%, signal=37%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	260	0.551	2.422	0.000	0.000	2546	tags=32%, list=12%, signal=29%
GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	58	0.485	1.696	0.005	0.015	1370	tags=22%, list=6%, signal=21%
GOBP_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	21	0.767	2.113	0.000	0.000	1506	tags=43%, list=7%, signal=40%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	184	0.500	2.101	0.000	0.000	1662	tags=22%, list=8%, signal=21%
GSE9650_EFFECTOR_VS_EXHAUSTED_CD8_TCELL_DN	185	0.340	1.428	0.012	0.030	3301	tags=25%, list=15%, signal=22%
GSE9650_EXHAUSTED_VS_MEMORY_CD8_TCELL_UP	186	0.394	1.654	0.000	0.001	2979	tags=28%, list=14%, signal=24%

Description (CD73)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	137	0.330	1.547	0.003	0.011	5870	tags=38%, list=27%, signal=28%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	356	0.261	1.374	0.005	0.017	3709	tags=24%, list=17%, signal=20%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	119	0.352	1.618	0.001	0.006	3503	tags=27%, list=16%, signal=23%
GOBP_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	59	0.397	1.588	0.007	0.022	2798	tags=25%, list=13%, signal=22%
GOBP_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	50	0.461	1.765	0.001	0.006	5536	tags=48%, list=26%, signal=36%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	260	0.330	1.680	0.000	0.000	4931	tags=32%, list=23%, signal=25%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	184	0.312	1.527	0.003	0.013	2960	tags=28%, list=14%, signal=24%
GSE9650_EFFECTOR_VS_EXHAUSTED_CD8_TCELL_DN	185	0.323	1.584	0.001	0.004	3060	tags=26%, list=14%, signal=23%

Table S12. Significantly enriched gene sets involved in negatively regulating the immune response in the high PD-L1/CD73 expression group versus the low PD-L1/CD73 expression group by gene set enrichment analysis in the GSE147986 cohort

Description (PD-L1)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	133	0.435	2.127	0.000	0.000	3070	tags=37%, list=16%, signal=31%
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	113	0.392	1.864	0.000	0.000	2036	tags=28%, list=11%, signal=25%
GOBP_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	59	0.413	1.774	0.001	0.010	3377	tags=39%, list=17%, signal=32%
GOBP_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	49	0.520	2.162	0.000	0.000	2897	tags=43%, list=15%, signal=37%
GOBP_NEGATIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	20	0.690	2.283	0.000	0.001	2897	tags=55%, list=15%, signal=47%

Description (CD73)	Set Size	Enrichment Score	NES	p value	FDR q value	Rank	Leading edge
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	350	0.382	1.442	0.001	0.002	4620	tags=31%, list=24%, signal=24%
GOBP_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	257	0.400	1.489	0.001	0.003	4533	tags=34%, list=23%, signal=27%
GOBP_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	57	0.544	1.711	0.001	0.003	3528	tags=35%, list=18%, signal=29%
GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	174	0.483	1.746	0.000	0.000	3907	tags=40%, list=20%, signal=32%
GSE9650_EFFECTOR_VS_EXHAUSTED_CD8_TCELL_DN	173	0.507	1.833	0.000	0.000	4560	tags=46%, list=24%, signal=35%
GSE9650_EXHAUSTED_VS_MEMORY_CD8_TCELL_UP	174	0.466	1.685	0.000	0.000	3052	tags=30%, list=16%, signal=25%

Table S13. Numbers of different types of CD8$^+$ T cells per patient in the single-cell RNA sequencing cohort

Sample ID	total CD8$^+$ T cells	dysfunctional CD8$^+$ T cells (cluster 1)	percentage of dysfunctional CD8$^+$ T cells	No. of PD-1 and/or A2aR expression on CD8$^+$ T cells
DLBCL002	1111	237	21%	366
DLBCL007	284	173	61%	190
DLBCL008	460	356	77%	359
DLBCL111	2381	1139	48%	1160

adjusted

Sample ID	total CD8$^+$ T cells	dysfunctional CD8$^+$ T cells (cluster 1)	percentage of dysfunctional CD8$^+$ T cells	No. of PD-1 and/or A2aR expression on CD8$^+$ T cells
DLBCL002	2381	507	21%	784
DLBCL007	2381	1450	61%	1592
DLBCL008	2381	1842	77%	1858
DLBCL111	2381	1139	48%	1160

Table S14. Numbers of CD8$^+$ T cells with PD-1 and A2aR expression per mm^2 in the overall population

Sample ID	No. of CD8$^+$ T cells with PD-1 expression/mm^2	No. of CD8$^+$ T cells with A2aR expression/mm^2
4	19.9	22.7
8	0.0	0.0
9	33.2	5.3
11	0.1	0.0
12	11.4	0.2
14	57.3	26.0
15	8.1	0.0
17	9.2	2.2
18	9.3	5.4
20	1.0	2.9
21	0.6	2.2
22	23.5	8.4
24	1.6	0.0
25	25.0	5.3
26	133.5	143.4
30	8.0	0.0
31	41.7	9.4
32	20.8	0.2
34	8.3	0.0
37	112.0	0.0
38	6.9	0.0
40	128.7	2.0
43	0.2	0.0
45	197.3	19.4
46	32.4	3.6
49	68.5	0.1
50	41.6	82.8
51	0.2	0.0
55	44.9	0.0
56	5.3	11.6
57	7.4	0.0
59	0.0	0.0
60	7.1	0.0
61	8.4	0.0
62	7.2	0.0

65	32.7	0.0
68	54.6	59.7
69	8.2	22.2
70	7.1	33.4
71	19.1	17.7
73	11.0	0.0
74	9.3	0.1
76	0.0	0.0
79	7.1	0.0
80	9.2	11.2
81	153.7	40.0
82	0.0	25.6
83	2.5	0.0
85	82.4	74.4
88	0.1	0.0
89	0.0	0.0
91	38.7	60.0
92	3.6	243.2
93	0.0	0.0
95	0.0	0.0
96	11.4	15.3
97	3.5	0.2
98	196.1	22.7
99	42.8	14.1
100	50.8	105.7
203	0.6	10.9
204	32.0	20.9
205	76.2	0.5
207	26.8	0.0
210	107.2	113.9
213	132.6	10.6
214	8.7	4.5
216	7.1	35.6
226	3.4	0.2
229	0.2	0.4
231	0.2	31.0
232	1.4	0.7
234	0.0	6.4
237	4.9	1.7
238	0.1	3.0

239	46.7	194.5
240	8.3	18.2
241	107.6	0.0
242	33.3	28.3
243	10.8	23.3
244	16.2	3.4
245	2.8	5.9
246	3.2	0.0
248	19.8	26.9
249	0.3	0.0
250	227.4	45.8
252	23.1	87.1
253	1.1	10.1
254	19.5	0.0
255	17.0	13.9
256	10.1	10.0
257	1.2	1.4
258	2.4	0.0
259	41.4	72.2
261	5.5	12.8
262	51.0	48.7
263	3.6	0.0
264	50.5	17.0
265	101.8	123.3
266	77.0	38.8
268	234.3	74.8
269	8.1	10.8
270	3.5	36.7
271	3.6	10.1
272	5.9	32.8
273	7.1	4.6
274	11.6	2.3
277	8.7	0.1
279	22.5	44.4

Table S15. Association of dysfunctional CD8$^+$ T cells (PD-1$^+$CD8$^+$ T cells) and clinicopathological parameters

Parameters	**N (%)**	**PD-1$^-$CD8$^+$ T cells**	**PD-1$^+$CD8$^+$ T cells**	***p* value**
Sex				
Male	54 (49.5)	27 (50.0)	27 (49.1)	0.924
Female	55 (50.5)	27 (50.0)	28 (50.9)	
Age (years)				
≤60	70 (64.2)	42 (77.8)	28 (50.9)	0.003
>60	39 (35.8)	12 (22.2)	27 (49.1)	
B symptom				
Yes	19 (17.4)	6 (11.1)	13 (23.6)	0.085
No	90 (82.6)	48 (88.9)	42 (76.4)	
Clinical stage				
I-II	57 (52.3)	34 (63.0)	23 (41.8)	0.027
III-IV	52 (47.7)	20 (37.0)	32 (58.2)	
LDH				
Normal	57 (52.3)	33 (61.1)	24 (43.6)	0.068
High	52 (47.7)	21 (38.9)	31 (56.4)	
IPI Scores				
0-2	77 (70.6)	45 (83.3)	32 (58.2)	0.004
3-5	32 (29.4)	9 (16.7)	23 (41.8)	
Subtypes				
GCB	45 (41.3)	26 (48.1)	19 (34.5)	0.329
Non-GCB	56 (51.4)	25 (46.3)	31 (56.4)	
Unclassified	8 (7.3)	3 (5.6)	5 (9.1)	

Table S16. Association of dysfunctional CD8$^+$ T cells (A2aR$^+$CD8$^+$ T cells) and clinicopathological parameters

Parameters	***N* (%)**	**A2aR$^-$CD8$^+$ T cells**	**A2aR$^+$CD8$^+$ T cells**	***p* value**
Sex				
Male	54 (49.5)	13 (43.3)	41 (51.9)	0.424
Female	55 (50.5)	17 (56.7)	38 (48.1)	
Age (years)				
≤60	70 (64.2)	22 (73.3)	48 (60.8)	0.221
>60	39 (35.8)	8 (26.7)	31 (39.2)	
B symptom				
Yes	19 (17.4)	2 (6.7)	17 (21.5)	0.068
No	90 (82.6)	28 (93.3)	62 (78.5)	
Clinical stage				
I-II	57 (52.3)	23 (76.7)	34 (43.0)	0.002
III-IV	52 (47.7)	7 (23.3)	45 (57.0)	
LDH				
Normal	57 (52.3)	20 (66.7)	37 (46.8)	0.064
High	52 (47.7)	10 (33.3)	42 (53.2)	
IPI Scores				
0-2	77 (73.8)	26 (86.7)	51 (64.6)	0.024
3-5	32 (26.2)	4 (13.3)	28 (35.4)	
Subtypes				
GCB	45 (41.3)	11 (36.7)	34 (43.0)	0.793
Non-GCB	56 (51.4)	17 (56.7)	39 (49.4)	
Unclassified	8 (7.3)	2 (6.6)	6 (7.6)	