Table SI. Summary of B cell receptor sequences and clones.

Group	Sample	Number of total sequences	Number of total clones	[a]Number of clonal families	% of sequences belonging to clonal families	[b]Top 2 clones by frequency
Tumor_mDX400	G2M107	1,639,450	3,673	143 (3.9%)	98.0	IGHV1-11_IGHJ2_TGTGGAAGGGGGGAACTATTTGACTACTGG_GRGELFDY (85.2%)
						IGHV10-3_IGHJ4_TGTGTGAGAGTCGATGGTTACTACCCATATTACTATGCTATGGACTACTGG_VRVDGYYPYYYAMDY (1.6%)
Tumor_mDX400	G2M116	2,774,225	7,274	411 (5.7%)	97.6	IGHV14-4_IGHJ3_TGTACTACTAACTGGCGCTGG_TTNWR (35.3%)
						IGHV2-9-1_IGHJ4_TGTGCCACCCCCTTTACTACGGTAGTAGATTACTATGCTATGGACTACTGG_ATPFTTVVDYYAMDY (4.6%)
Tumor_mDX400	G2M119	2,358,362	2,342	153 (6.5%)	99.0	IGHV1-55_IGHJ4_TGTGCAAGAATTTATTACTACGGTAGTAGCTATGCTATGGACTACTGG_ARIYYYGSSYAMDY (15.6%)
						IGHV1-11_IGHJ2_TGTGGAAGGGGGGAACTTTTTGACTACTGG_GRGELFDY (14.9%)

Tumor_mDX400	G2M120	2,363,556	2,979	172 (5.8%)	98.2	IGHV1-64_IGHJ3_TGTGCAAGATCGGTCTACCTTCACTTTTTTGCTTACTGG_ARSVYLHFFAY (45.3%)
						IGHV1-64_IGHJ4_TGTGCAAAGATTTGCTCACTACGGTATTACTATGCTATGGACTACTGG_AKICSLRYYYAMDY (17.8%)
Tumor_mDX400	G2M124	2,595,359	7,066	408 (5.8%)	96.9	IGHV7-3_IGHJ2_TGTGTAAGATATAAGTACTACTTTGACTACTGG_VRYKYYFDY (14.1%)
						IGHV1-11_IGHJ2_TGTGGAAGGGGGGAGTATTTTGACTACTGG_GRGEYFDY (7.4%)
Tumor_mDX400	G2M132	2,282,879	1,640	109 (6.7%)	99.2	IGHV14-4_IGHJ4_TGTACTAGGAGTGACTCAGAGTTACCTATGGACTACTGG_TRSDSELPMDY (56.3%)
						IGHV1-85_IGHJ4_TGTGCAAGAGGGAGAGATGATGGTTACTACTATGCTATGGACTACTGG_ARGRDDGYYYAMDY (15.1%)
Tumor_mDX400	G2M138	2,431,283	6,259	391 (6.3%)	97.4	IGHV1-11_IGHJ2_TGTGGAAGGGGGGAGTACTTTGACTACTGG_GRGEYFDY (18.7%)

						IGHV1-64_IGHJ2_TGTGCAAGAGGTGGTGATGGTTACCCGTACTACTTTGACTACTGG_ARGGDGYPYYFDY (13.3%)
Tumor_mIgG1	G1M106	1,629,828	1,928	163 (8.5%)	99.4	IGHV1-55_IGHJ1_TGTGCAAGAGGCTATTACTACGGTAGTAGGTACTTCGATGTCTGG_ARGYYYGSRYFDV (28.4%)
						IGHV3-6_IGHJ4_TGTGCAAGAGATGGTTCTTATGCTATGGACTACTGG_ARDGSYAMDY (15.4%)
Tumor_mIgG1	G1M110	1,898,334	4,101	239 (5.8%)	97.9	IGHV2-9_IGHJ3_TGTGTCAAACGGGACTACGGAACTACCTACTGGTTTGCTTACTGG_VKRDYGTTYWFAY (30.5%)
						IGHV1-62-2_IGHJ2_TGTGCAAGAGGAAGTAACTACTTTGACTACTGG_ARGSNYFDY (11.5%)
Tumor_mIgG1	G1M114	1,871,064	3,776	173 (4.6%)	98.3	IGHV8-12_IGHJ3_TGTGCTCGAAGGGGGTACTATGATTACGACTGGTTTGCTTACTGG_ARRGYYDYDWFAY (32.7%)
						IGHV1-55_IGHJ1_TGTGCAAGACGGGACTACGGTAGTAGCTACTGGTACTTCGATGTCTGG_ARRDYGSSYWYFDV (6.9%)

Tumor_mIgG1	G1M121	3,111,405	3,663	215 (5.9%)	98.8	IGHV1-53_IGHJ4_TGTGCAAGATTCTACTATAGTAACTATCCTTACTATGCTATGGACTACTGG_ARFYYSNYPYYAMDY (13.1%)
						IGHV1-55_IGHJ1_TGTGCAAGACGTTACTACGGTAGTAGCTACTGGTACTTCGATGTCTGG_ARRYYGSSYWYFDV (11.8%)
Tumor_mIgG1	G1M122	2,462,173	2,272	260 (11.4%)	99.2	IGHV1-72_IGHJ2_TGTGCACCAGGGGGTAGTACCTTTGACTACTGG_APGGSTFDY (31.6%)
						IGHV1-64_IGHJ3_TGTGCAAGCCAAGACTTTTACTATGGTTACGACGCGGCCTGGTTTGCTTACTGG_ASQDFYYGYDAAWFAY (9.9%)
Tumor_mIgG1	G1M126	1,882,294	4,217	245 (5.8%)	97.9	IGHV1-54_IGHJ4_TGTGCAAGAGGGGACTATGATTACTCCTACTATGCTATGGACTACTGG_ARGDYDYSYYAMDY (17.2%)
						IGHV5-17_IGHJ2_TGTGCAAGGCGGGGATGGTTCCTTGACTACTGG_ARRGWFLDY (6.4%)

Tumor_mIgG1	G1M130	2,062,861	2,779	319 (11.5%)	98.5	IGHV1-74_IGHJ2_TGTGCAAACCCATCCCTTGACTACTGG_ANPSLDY (45.0%)
						IGHV1-55_IGHJ1_TGTGCAAGGAGGGACTACGGTAGTAGCTACTGGTACTTCGATGTCTGG_ARRDYGSSYWYFDV (5.8%)
Tumor_mIgG1	G1M131	2,561,059	3,330	283 (8.5%)	98.2	IGHV1-54_IGHJ4_TGTGCAAGAGAGGGTTACCCTTATGCTATGGACTACTGG_AREGYPYAMDY (13.4%)
						IGHV1-55_IGHJ1_TGTGCAAGAAAGTACTACGGTAGTAGCTACTGGTACTTCGATGTCTGG_ARKYYGSSYWYFDV (10.2%)
Spleen_mDX400	G2M107	2,746,428	77,959	1420 (1.8%)	87.7	IGHV1-64_IGHJ1_TGTGCAAGAAACCGGGACTGGTACTTCGATGTCTGG_ARNRDWYFDV (15.6%)
						IGHV1-26_IGHJ3_TGTGCAAGGTATTACTACGGTAGTAGCTCGTTTGCTTACTGG_ARYYYGSSSFAY (8.7%)
Spleen_mDX400	G2M108	2,811,644	96,826	1302 (1.3%)	89.0	IGHV1-26_IGHJ3_TGTGCAAGACACTACTATGATTCCTCGTTTGCTTACTGG_ARHYYDSSFAY (14.2%)

						IGHV1-69_IGHJ2_TGTGCAAGAGACTACGGTAGTAGCCCTGACTACTGG_ARDYGSSPDY (9.0%)
Spleen_mDX400	G2M116	2,588,153	70,632	1023 (1.5%)	91.3	IGHV1-72_IGHJ2_TGTGCAAGAGGGGGTAGTACCTCGTGGTACTTTGACTACTGG_ARGGSTSWYFDY (16.8%)
						IGHV1-53_IGHJ3_TGTGCAAGAGTGAGGGACTATGGTTACGCCTGGTTTGCTTACTGG_ARVRDYGYAWFAY (8.3%)
Spleen_mDX400	G2M119	3,336,660	77,127	1584 (2.1%)	90.7	IGHV1-76_IGHJ2_TGTGCAAGAAGGGGGAATGGATACTACTTTGACTACTGG_ARRGNGYYFDY (14.0%)
						IGHV1-64_IGHJ2_TGTACAAGATCCCATAACTGGTTCTTTGACTACTGG_TRSHNWFFDY (14.0%)
Spleen_mDX400	G2M120	2,919,719	148,332	2167 (1.5%)	84.0	IGHV1-26_IGHJ3_TGTGCAAGAAACTACTACGGTAGTAGCGTCTTTGCTTACTGG_ARNYYGSSVFAY (8.5%)
						IGHV1-64_IGHJ2_TGTGCAAGATTGAACTACGGTAGTAGCTACTTTGACTACTGG_ARLNYGSSYFDY (6.3%)

Spleen_mDX400	G2M124	2,437,873	148,512	1441 (1.0%)	83.2	IGHV1-55_IGHJ1_TGTGCAAGACGTTACTACGGTAGTAGCTACTGGTACTTCGATGTCTGG_ARRYYGSSYWYFDV (16.7%)
						IGHV1-26_IGHJ2_TGTGCAAGCTATTACTACGGTAGTAGCCTCTACTGG_ASYYYGSSLY (7.2%)
Spleen_mDX400	G2M129	2,380,322	113,621	2260 (2.0%)	81.6	IGHV14-4_IGHJ3_TGTTCTACACACTACAGGTGG_STHYR (9.7%)
						IGHV1-26_IGHJ2_TGTGCAAGATTGAACTACGGTAGTAGCCACTTTGACTACTGG_ARLNYGSSHFDY (6.4%)
Spleen_mDX400	G2M132	2,408,097	175,972	2159 (1.2%)	76.9	IGHV1-26_IGHJ2_TGTGCAAGATTGAACTACGGTAGTAGCTACTTTGACTACTGG_ARLNYGSSYFDY (27.3%)
						IGHV1-69_IGHJ2_TGTACAAGAGGGCCACTTCCGAGGTTTGACTACTGG_TRGPLPRFDY (3.7%)
Spleen_mDX400	G2M138	2,505,608	141,319	1640 (1.2%)	82.8	IGHV1-26_IGHJ2_TGTGCCACCTATTACTACGGTAGTAGCCTCTACTGG_ATYYYGSSLY (14.3%)

						IGHV1-76_IGHJ2_TGTGCAAGAAGAGGGAATGGCTACTACTTTGACTACTGG_ARRGNGYYFDY (8.8%)
Spleen_mIgG1	G1M102	2,678,001	98,983	1557 (1.6%)	86.1	IGHV1-26_IGHJ3_TGTGCAAGATATTACTACGGTAGTAGCCATTTTGCTTACTGG_ARYYYGSSHFAY (10.7%)
						IGHV1-80_IGHJ2_TGTGCAAGGGGGCGGTTCTGG_ARGRF (8.5%)
Spleen_mIgG1	G1M106	2,538,363	43,351	1628 (3.8%)	89.1	IGHV1-26_IGHJ2_TGTGCAAGACTAAACTACGGTAGTAGCGACTTTGACTACTGG_ARLNYGSSDFDY (13.6%)
						IGHV5-4_IGHJ4_TGTGCACCGAACTGGGACGGGGATTACTATGCTATGGACTACTGG_APNWDGDYYAMDY (6.2%)
Spleen_mIgG1	G1M114	2,227,652	115,481	1474 (1.3%)	83.8	IGHV1-26_IGHJ1_TGTGCAAGTTATTACTACGGTAGTAGCCTCGTCTGG_ASYYYGSSLV (11.8%)
						IGHV1-55_IGHJ1_TGTGCAAGAAGGTACTACGGTAGTAGCTACTGGTACTTCGATGTCTGG_ARRYYGSSYWYFDV (7.4%)

Spleen_mIgG1	G1M115	2,716,358	170,783	1993 (1.2%)	79.3	IGHV1-55_IGHJ1_TGTGCAAGAAGATATTACTACGGTAGTAGCTGGTACTTCGATGTCTGG_ARRYYYGSSWYFDV (6.5%)
						IGHV1-76_IGHJ1_TGTGCAAGAAGCCCTTCGTACTTCGATGTCTGG_ARSPSYFDV (4.9%)
Spleen_mIgG1	G1M121	2,667,397	122,675	1412 (1.2%)	85.3	IGHV1-26_IGHJ2_TGTGCACCTTACTACGGTAGTAGCTCCTTCTACTGG_APYYGSSSFY (53.7%)
						IGHV1-53_IGHJ3_TGTGCAAGTGGTAACTTTGCTTACTGG_ASGNFAY (2.4%)
Spleen_mIgG1	G1M122	2,610,317	163,022	1771 (1.1%)	81.6	IGHV1-18_IGHJ3_TGTGCAAGAAAGGAAGATGATTACGACGACCGGGCCTGGTTTGCTTACTGG_ARKEDDYDDRAWFAY (7.9%)
						IGHV1-26_IGHJ4_TGTGCAAGTTATTACTACGGTAGTAGCCTCTACTGG_ASYYYGSSLY (5.1%)
Spleen_mIgG1	G1M126	2,646,464	184,519	2054 (1.1%)	82.0	IGHV1-26_IGHJ2_TGTGCAAGACTTAACTACGGTAGTAGCTACTTTGACTACTGG_ARLNYGSSYFDY (18.1%)

						IGHV1-26_IGHJ2_TGTGCAACCTATTACTACGGTAGTAGCCTTTACTGG_ATYYYGSSLY (5.8%)
Spleen_mIgG1	G1M130	2,691,326	173,211	1979 (1.1%)	80.6	IGHV1-26_IGHJ3_TGTGCAAGATGGGCCTACGGTAGTAGCTACTTTGCTTACTGG_ARWAYGSSYFAY (4.9%)
						IGHV1-26_IGHJ3_TGTGCCACTTATTACTACGGTAGTTCCCTTTACTGG_ATYYYGSSLY (4.6%)
Spleen_mIgG1	G1M131	2,708,328	143,518	1721 (1.2%)	85.3	IGHV1-26_IGHJ2_TGTGCAAGATTGAACTACGGTAGTAGCCACTTTGACTACTGG_ARLNYGSSHFDY (16.7%)
						IGHV1-61_IGHJ2_TGTGCAAGATCGGGGCCCTATAGTAACTACGGCTACTTTGACTACTGG_ARSGPYSNYGYFDY (5.8%)
DLN_mDX400	G2M107	2,130,722	133,511	2009 (1.5%)	79.2	IGHV1-72_IGHJ4_TGTGCAAGGGAATTTATTACTACGGTACCTCTGGCTATGGACTACTGG_AREFITTVPLAMDY (15.9%)
						IGHV5-4_IGHJ4_TGTGCAAGTAACTACGTGAGGGCTATGGACTACTGG_ASNYVRAMDY (9.9%)

DLN_mDX400	G2M108	2,540,522	241,372	955 (0.4%)	84.1	IGHV1-69_IGHJ2_TGTGCAAGATGGAGATACTTTGACTACTGG_ARWRYFDY (17.7%)
						IGHV1-64_IGHJ2_TGTGCAAGTATGAACTGGTACTTTGACTACTGG_ASMNWYFDY (6.2%)
DLN_mDX400	G2M116	2,433,730	178,394	758 (0.4%)	87.1	IGHV1-7_IGHJ2_TGTGCAAGATCCTATGATTACGACTACTGG_ARSYDYDY (8.2%)
						IGHV1-64_IGHJ2_TGTGCAAGAGAGAGGAACTGGTACTACTTTGACTACTGG_ARERNWYYFDY (6.4%)
DLN_mDX400	G2M118	2,091,316	225,246	903 (0.4%)	82.1	IGHV1-59_IGHJ3_TGTGCAAGAGGCTACGGTAGTGGCTACCGGTTTGCTTACTGG_ARGYGSGYRFAY (9.7%)
						IGHV1-80_IGHJ2_TGTGCAAGAGATGGTTACTACTTTGACTACTGG_ARDGYYFDY (3.0%)
DLN_mDX400	G2M119	2,167,218	100,070	1839 (1.8%)	84.1	IGHV5-6_IGHJ2_TGTGCAAGACATAAAGACTACGGTAGTAGCTTCTTTGACTACTGG_ARHKDYGSSFFDY (5.4%)

						IGHV1-7_IGHJ2_TGTGCAAGAAATGGTAACTACGTTGACTACTTTGACTACTGG_ARNGNYVDYFDY (4.2%)
DLN_mDX400	G2M120	2,073,558	83,660	971 (1.2%)	88.3	IGHV2-3_IGHJ2_TGTGCCAAATTCGATGATTACGAGGACTACTGG_AKFDDYEDY (30.0%)
						IGHV1-69_IGHJ1_TGTGCAAGGGCGGGACTGGGCCGCTACTTCGATGTCTGG_ARAGLGRYFDV (16.2%)
DLN_mDX400	G2M124	2,405,313	97,723	256 (0.3%)	93.1	IGHV1-72_IGHJ2_TGTGCAAGAGGGGGAGGTCACTTTGACTACTGG_ARGGGHFDY (33.3%)
						IGHV14-3_IGHJ2_TGTGCTAGATGGGGCCCCTACTACTTTGACTACTGG_ARWGPYYFDY (20.5%)
DLN_mDX400	G2M129	2,339,561	194,135	1244 (0.6%)	83.8	IGHV14-4_IGHJ2_TGTACTACGGTAGTAAACTACTGG_TTVVNY (7.1%)
						IGHV1-72_IGHJ1_TGTGCAAGAGATTACTACGGTCGTAGCTACTGGTACTTCGATGTCTGG_ARDYYGRSYWYFDV (6.2%)

DLN_mDX400	G2M132	2,565,975	178,363	680 (0.4%)	87.9	IGHV6-3_IGHJ3_TGCACAGAGATATGGTCGTTTGCTTACTGG_TEIWSFAY (9.8%)
						IGHV1-55_IGHJ1_TGTGCAAGATATGGTAACTACGACTGGTACTTCGATGTCTGG_ARYGNYDWYFDV (7.4%)
DLN_mDX400	G2M138	2,407,216	231,240	814 (0.4%)	83.9	IGHV1-74_IGHJ2_TGTGCAGATGGTTACTTTGACTACTGG_ADGYFDY (13.6%)
						IGHV1-53_IGHJ1_TGTGCAAGAACAGGGAATTACTACGGTAGTAGGTACTGGTACTTCGATGTCTGG_ARTGNYYGSRYWYFDV (8.8%)
DLN_mIgG1	G1M102	2,540,247	129,901	1678 (1.3%)	84.9	IGHV1-26_IGHJ2_TGTGCAAGATTGAATGATGGTTACTCCCTCTTTGACTACTGG_ARLNDGYSLFDY (17.7%)
						IGHV1-55_IGHJ1_TGTGCAAGAGAGGCATTACTAGGGTATTACTGGTACTTCGATGTCTGG_AREALLGYYWYFDV (6.0%)
DLN_mIgG1	G1M106	1,936,816	46,369	412 (0.9%)	94.0	IGHV1-53_IGHJ2_TGTGCAAGATGGGGGATCTATGATGGTTTCCCTTTTGACTACTGG_ARWGIYDGFPFDY (38.1%)

						IGHV1-74_IGHJ2_TGTGCAAGAGGAGGATATGATTACCCTCTTGACTACTGG_ARGGYDYPLDY (12.8%)
DLN_mIgG1	G1M110	2,730,046	90,182	966 (1.1%)	91.8	IGHV1-4_IGHJ1_TGTGCAAGATCAACCCATTACTACGGTAGCCCTTGGGACTTCGATGTCTGG_ARSTHYYGSPWDFDV (12.5%)
						IGHV1-72_IGHJ2_TGTGCAAGAGTGGAATATGGTAACTACCTTGACTACTGG_ARVEYGNYLDY (8.2%)
DLN_mIgG1	G1M115	3,226,606	267,466	1687 (0.6%)	84.7	IGHV1-22_IGHJ2_TGTGCAAGAGAGGGTATCTACTATGGTAACTTAAGACTTTACTACTTTGACTACTGG_AREGIYYGNLRLYYFDY (9.3%)
						IGHV1-7_IGHJ4_TGTGGAAGATCTTTTTTCTCTGATGGTTACCACTATGCTTTGGACTACTGG_GRSFFSDGYHYALDY (8.2%)
DLN_mIgG1	G1M121	2,934,943	69,813	2237 (3.2%)	69.4	IGHV1-64_IGHJ1_TGTGCAAGAGACTTACTGGGACGGTACTTCGATGTCTGG_ARDLLGRYFDV (11.1%)

						IGHV2-3_IGHJ2_TGTGCCAAACCCGGGGGTAGTAGCTACTTTGACTACTGG_AKPGGSSYFDY (5.4%)
DLN_mIgG1	G1M122	2,611,820	114,845	2840 (2.5%)	70.9	IGHV1-4_IGHJ2_TGTGCAAGATCGAGCTACGGCTACTTTGACTACTGG_ARSSYGYFDY (15.8%)
						IGHV5-6_IGHJ4_TGTGCAAGATTGATCGACTACGGTAGTTATGCTATGGACTACTGG_ARLIDYGSYAMDY (15.3%)
DLN_mIgG1	G1M126	3,030,532	392,682	4037 (1.0%)	71.3	IGHV1-4_IGHJ4_TGTGCAAGAGGAGTTAGTAACTACATTTTACATCATTATGCTATGGACTACTGG_ARGVSNYILHHYAMDY (9.2%)
						IGHV1-72_IGHJ4_TGTGCAAGATGGGATGTTAATTATTATGTTATGGACTACTGG_ARWDVNYYVMDY (7.0%)
DLN_mIgG1	G1M130	2,775,212	272,345	5092 (1.9%)	66.3	IGHV14-3_IGHJ3_TGTGCTAGAGATGATAACTACGTCTGGTTTGCTTACTGG_ARDDNYVWFAY (5.2%)
						IGHV1-54_IGHJ1_TGTGCAAGAGCCTGGCATTACTACGGTAGTA

						GAGACTACTGGTACTTCGATGTCTGG_ARAWHYYGSRDYWYFDV (4.9%)
DLN_mIgG1	G1M131	2,000,105	87,881	349 (0.4%)	92.6	IGHV1-61_IGHJ4_TGTGCAAGAGATTACTACGGTAGTATAGGGTATGCTATGGACTACTGG_ARDYYGSIGYAMDY (20.7%)
						IGHV1-76_IGHJ4_TGTGCAAGAGACGACGGCTACTATGCTATGGACTACTGG_ARDDGYYAMDY (20.3%)

[a] A clonal family has at least two different sequences with each sequence having no less than 3 copies; [b] Each clone was represented by its most abundant sequence (V_J_junction nucleotide sequence_ complementarity determining region 3 amino acid sequence) with the proportion of sequences belonging to the clone enclosed in parentheses. DLN, tumor draining lymph node; IGHV, immunoglobulin heavy chain variable gene; mDX400, murine anti-PD-1; mIgG1, murine immunoglobulin G1.