Novel *GPR34* and *CCR6* mutation and distinct genetic profiles in MALT lymphomas of different sites

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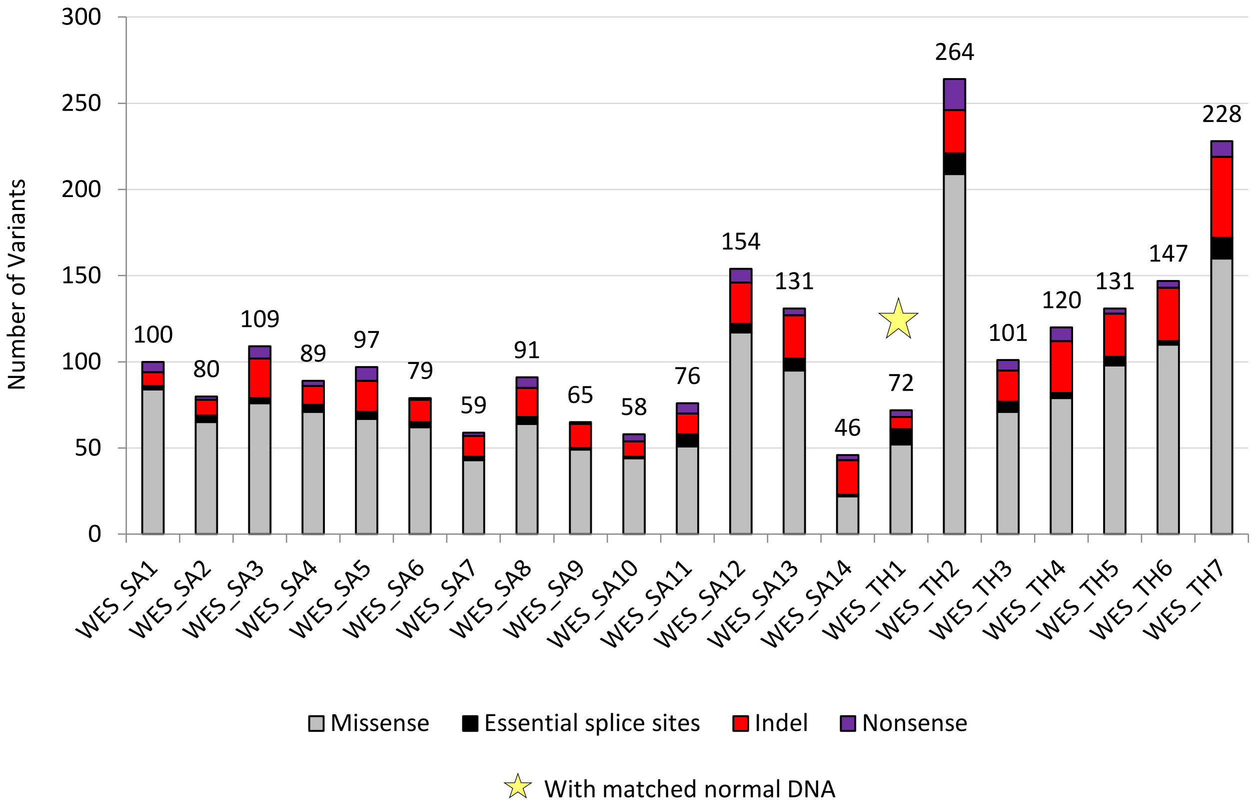


Figure S1. Number of variants detected by WES in 21 cases of salivary gland and thyroid MALT lymphoma.

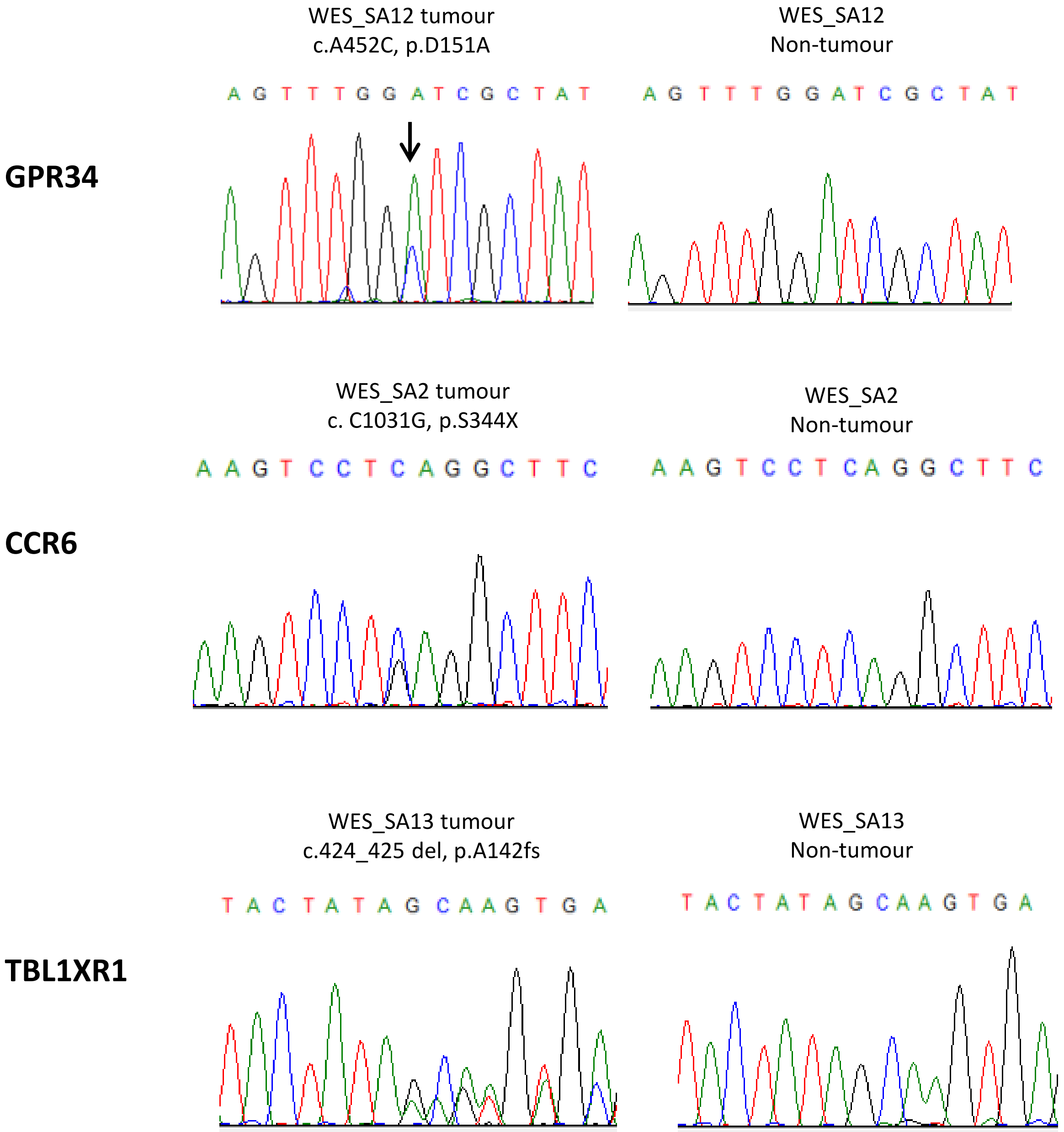
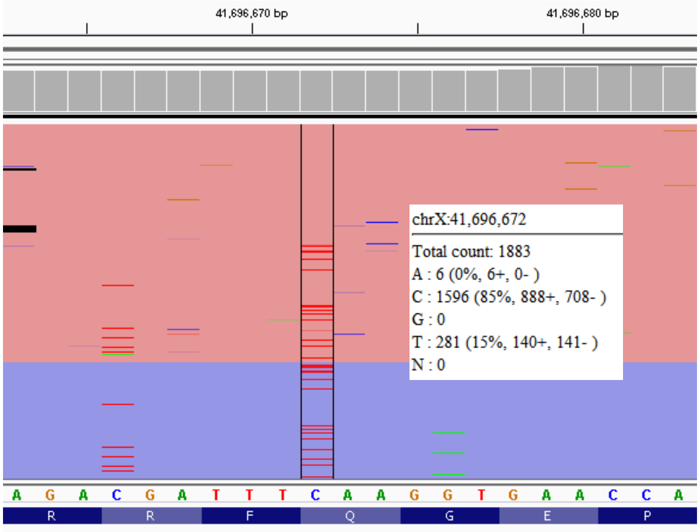


Figure S2. Validation of variants identified by WES in MALT lymphoma by Sanger sequencing.

GPR34

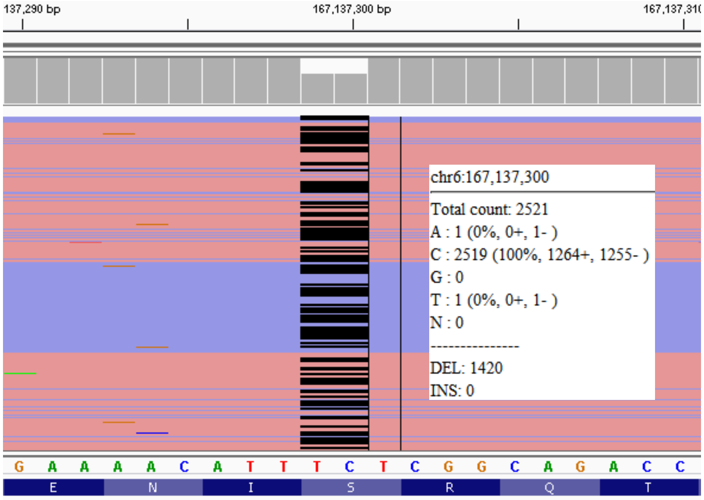
SA_060
Nonsense
c.1039C>T, p.Q347X



```
chrX:41,696,672
Total count: 1883
A : 6 (0%, 6+, 0- )
C : 1596 (85%, 888+, 708- )
G : 0
T : 281 (15%, 140+, 141- )
N : 0
```

CCR6

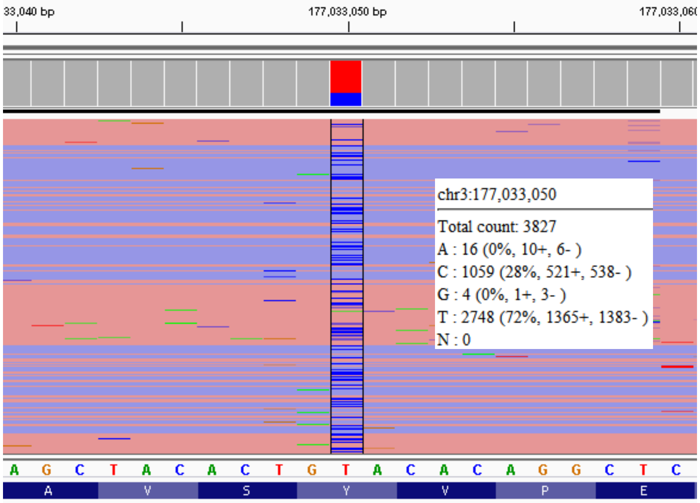
GA_018
Frameshift
c.1069_1070del, p.S357fs



```
chr6:167,137,300
Total count: 2521
A : 1 (0%, 0+, 1- )
C : 2519 (100%, 1264+, 1255- )
G : 0
T : 1 (0%, 0+, 1- )
N : 0
---------------
DEL: 1420
INS: 0
```

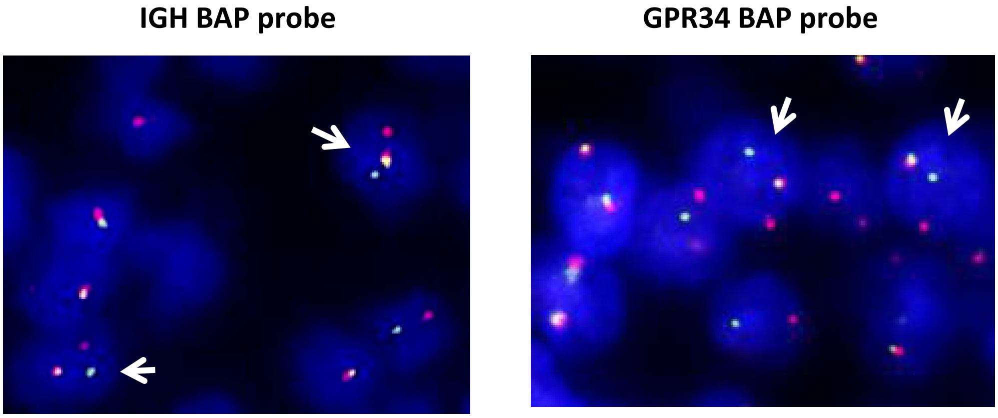
TBL1XR1

SA_062
Missense
c. 1337A>G p.Y446C



```
chr3:177,033,050
Total count: 3827
A : 16 (0%, 10+, 6- )
C : 1059 (28%, 521+, 538- )
G : 4 (0%, 1+, 3- )
T : 2748 (72%, 1365+, 1383- )
N : 0
```

Figure S3. Example of mutations detected by Fluidigm PCR and Illumina MiSeq sequencing.

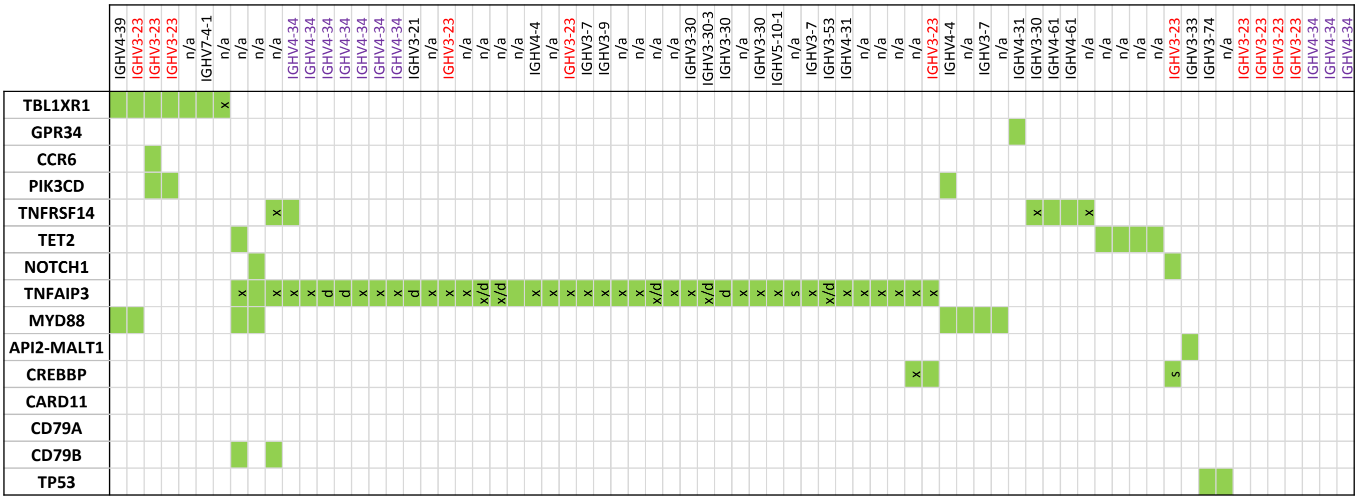


IGH BAP probe

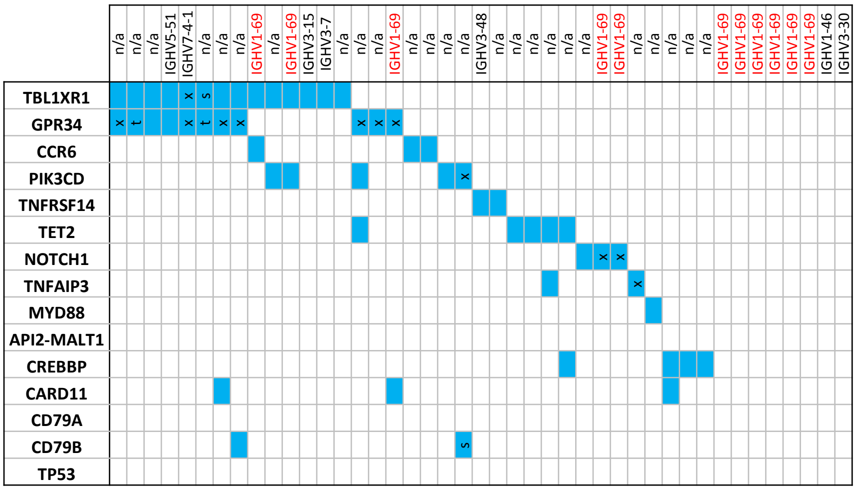
GPR34 BAP probe

Figure S4. Example of interphase FISH for detection of t(X;14)(p11;q32)/IGH-GPR34. Nuclei showing split signals are indicated by an arrow

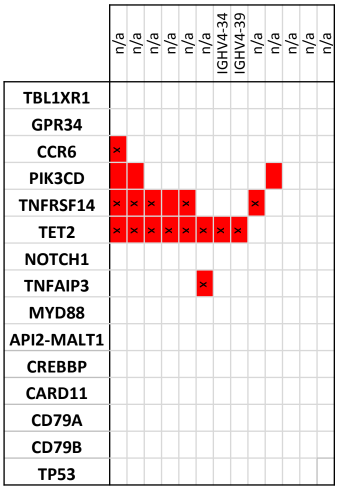
Ocular Adnexa *



Salivary Gland *



Thyroid



Stomach

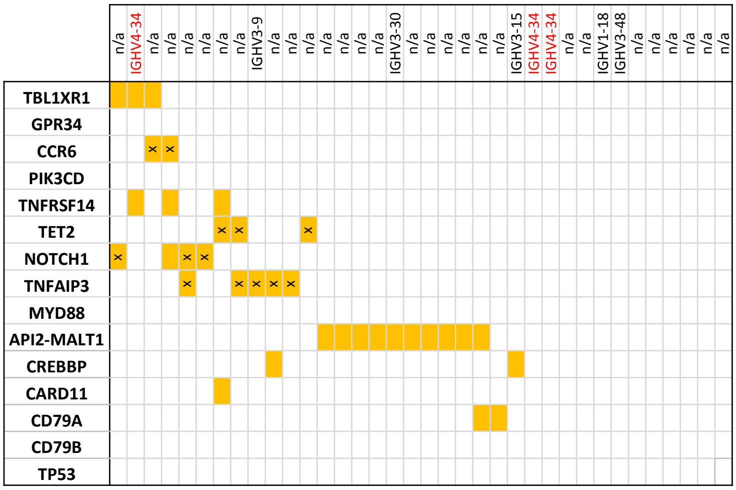


Figure S5. Heatmaps showing distribution of mutations in MALT lymphomas of the ocular adnexa (n=115), salivary gland (n=58), stomach (n=36) and thyroid (n=13). *Samples lacking the described changes are not included. x denotes nonsense or frameshift mutations, d indicates deletion, t indicates translocation.

Supplementary Table S1: Cases of MALT lymphoma investigated by whole exome sequencing.

Sample	Site	DNA origin	QC	Diagnosis	Sex	Age	Notable Features
WES_SA1	Salivary gland	FFPE	600	MALT	Male	71	t(14;18)(q32;q21) *IGH-MALT1*
WES_SA2	Salivary gland	FFPE	600	MALT	Female	67	
WES_SA3	Salivary gland	FFPE	400	MALT	Female	68	
WES_SA4	Salivary gland	FFPE	400	MALT	Female	49	
WES_SA5	Salivary gland	FFPE	400	MALT	Male	68	
WES_SA6	Salivary gland	FFPE	600	MALT	Female	74	
WES_SA7	Salivary gland	FFPE	400	MALT	Female	71	
WES_SA8	Salivary gland	FFPE	400	MALT	Female	64	
WES_SA9	Salivary gland	FFPE	400	MALT	Female	44	t(14;18)(q32;q21) *IGH-MALT1*
WES_SA10	Salivary gland	FFPE	300	MALT	Male	NK	
WES_SA11	Salivary gland	FFPE	300	MALT	Female	NK	
WES_SA12	Salivary gland	FFPE	400	MALT	Male	32	
WES_SA13	Salivary gland	FFPE	600	MALT	Female	35	
WES_SA14	Salivary gland	HMW	-	MALT	NK	NK	
WES_TH1	Thyroid	FFPE	300	MALT + DLBCL	Female	NK	Matched Germline DNA
WES_TH2	Thyroid	FFPE	300	MALT + DLBCL	Female	72	
WES_TH3	Thyroid	FFPE	400	MALT	Female	65	
WES_TH4	Thyroid	FFPE	600	MALT	Female	69	
WES_TH5	Thyroid	FFPE	600	MALT	Female	45	
WES_TH6	Thyroid	FFPE	600	MALT	Female	50	
WES_TH7	Thyroid	HMW	-	MALT	NK	NK	

NK = Not Known

Supplementary Table S2: Primers and conditions used for multiplex PCR with Fluidigm Access Array

Gene	Exon	Primer name	Genomic sequence amplified (hg38)	Forward primer	Reverse primer	Amplicon size (bp)
CCR6	Exon 3	CCR6_E2-3_1	chr6:167136069+167136258	GTGAGCTGAAGGGGCTGA	CGCTGAAATTCATTGATTCCT	190
		CCR6_E2-3_2	chr6:167136175+167136376	TTTGGGTTCACTSTGGCTACT	ACAAATAGCCTGGAGAACTGC	202
		CCR6_E2-3_3	chr6:167136310+167136475	ACTCAGTTGATTCTGAGATGTTACTGT	TCTGTCATAGACCTGGCCTTC	166
		CCR6_E2-3_4	chr6:167136410+167136611	CCTCCTGGGGAATATTCTGG	GATGGCATAGATGCCTTTTAGC	202
		CCR6_E2-3_5	chr6:167136501+167136691	GCAGACATCCTCTTTGTTCTTACTC	AATGACTTAGTCRCYTGTACAATG	191
		CCR6_E2-3_6	chr6:167136626+167136839	GATGCTGCTCCTGACTTGC	AGTCTGGTACTTGGGTTCACAG	214
		CCR6_E2-3_7	chr6:167136765+167136961	TCCAGCTCAACTTTTGTCTTCA	GCTTGCACCAAGGTTTTGAC	197
		CCR6_E2-3_8	chr6:167136889+167137093	TCTTTGGTTTCTTTATCCCTTTG	CAGGATCGGTTCATTTTACCC	205
		CCR6_E2-3_9	chr6:167137020+167137205	CTGGCTTGTCAGATTCCTCATA	GTTTCTGAACTTCTGCCCAAT	186
		CCR6_E2-3_10	chr6:167137140+167137343	CTGGCTTTCCTGCACTGCT	GGACGACRCATTGTCGTTAT	204
		CCR6_E2-3_11	chr6:167137212+167137396	CTGAAGATCYTGAAGGACCTGT	GAGTATGTTTCACAYRTGCCTTAG	185
FGFR3	Exon 7	R_FGFR3_E7H	chr4:1801810+1801988	CCCTGAGCRTCATCTGC	ACCTTGCTRCCRTTCACCT	179
	Exon 9	R_FGFR3_E9H	chr4:1804318+1804531	ATGTCTTTGCAGCCGAGGA	CTTTCTGTTACCTGTCGMTTGAG	214
	Exon 14	FGFR3_E14H	chr4:1806041+1806224	CCTTCCCCAGTGCATCC	AGGCGTCYTACTGGCATGA	184
FOXO1	Exon 2	FOXO1_E2_1	chr13:40560761-40560925	TGTAGAATAGGAAGTTTTGCAAGC	CACCCTCTGGATTGAGCATC	165
		FOXO1_E2_2	chr13:40560656-40560831	CAGCAAGTTCATTCGTGTGC	ACTGGAGAGATGCTTTCTTCTTG	176
		FOXO1_E2_3	chr13:40560540-40560730	CTGCATCCATGGACAACAAC	AGTTCGAGGRCGAAATGTACT	191
		FOXO1_E2_4	chr13:40560435-40560616	TTTCCAAATGGCCTGCAA	GGCAGATGGRGGGTACA	182
		FOXO1_E2_5	chr13:40560297-40560499	TTATGACYGAACAGGATGATCT	CATGGTRCCAGGTGAGG	203
		FOXO1_E2_6	chr13:40560185-40560390	TCCCGAAAACATGGAAAATC	GGGGCAAAGGGCTCAT	206
		FOXO1_E2_7	chr13:40560063-40560246	TTCACCCAGCCCAAACTAC	AATGTCATTATGGGGAGGAGAGT	184
		FOXO1_E2_8	chr13:40559927-40560127	ATAACTGTGCGCCTGGACTC	GGGAGCTGRGATTCATCATT	201
		FOXO1_E2_9	chr13:40559847-40560004	TCATGATGGGCCCTAATTC	GTGGGGCATGGTGCTTAC	158
		FOXO1_E2_10	chr13:40559715-40559924	ACCCACCSTGGACATGC	AAGGCCCATTCTGCCATAG	210
		FOXO1_E2_11	chr13:40559617-40559826	GACCCAAGTGAAGACACCTGTA	CCATCCATGAGGTCATTCC	210
		FOXO1_E2_12	chr13:40559516-40559692	GTGACTTGGATGGCATGTTC	CTAACCCTCAGCCTGACACC	177
		R_FOXO1_E2_13	chr13:40559384-40559579	AACCAAAGCTTCCCACACAG	AAAGATCCCTCTCTGCAAGG	196
		GPR34_E3_1	chrX:41695524+41695673	AAATGACTCAATGTTTGGCATTC	TGACTGAAGTTGTCGTCATTGTT	150
		GPR34_E3_2	chrX:41695601+41695784	AGCACTTTCACTTTTTGATCTCC	TTTCATCCATGGGACAGGTA	184

GPR34	Exon 3	GPR34_E3_3	chrX:41695712+41695901	ACCAATCATAGCGACCAACC	GAATGGAATTTCTTTTACGGTGA	190
		R_GPR34_E3_4	chrX:41695825+41696020	TTTCATCRTGGGACTGGTTG	AACCTTGCACAGAATCACACCT	196
		GPR34_E3_5	chrX:41695950+41696130	GCCTCCCTTTCCGAATAATG	ATTGCCTTCCGTTGCTGTAT	181
		GPR34_E3_6	chrX:41696055+41696239	GCATTATTTTGCTTGGATTCAT	TGTGGAATTATGCCCTCCTT	185
		GPR34_E3_7	chrX:41696175+41696374	TTGCTCTTGGTGGATTCCTAA	CCTCAATAGATTCYTCCCAATCTT	200
		GPR34_E3_8	chrX:41696280+41696485	AAGCCATTTTTAACTTCATTCTTGT	GGCATGATAGGGAASAAAACATA	206
		GPR34_E3_9	chrX:41696386+41696550	GAGGTCAAAATTTCCTAATTCTGGT	TGAACAATTTSTTTCCAGTAGCAA	165
		GPR34_E3_10	chrX:41696489+41696639	CGATTCATCTACATTTCTTCACAGC	TGCGAATGTTACTGGACATCA	151
		GPR34_E3_11	chrX:41696555+41696746	ACCAATGAGATCATGCTGGTT	TGCCACAGATGTATCATGCAG	192
		GPR34_E3_12	chrX:41696648+41696829	TGCCAACTTCTTTTTAGACGATT	TTCAAAGAATTAAGAGGCTGCAT	182
IKBKB	Exon 7	IKBKB_Ex7	chr8:42306316+42306502	TCAGCTTTCTCCTTCCTTTTG	AGGACAGGAGCCCCACAA	187
NOTCH1	Exon 34	R2_NOTCH1_E34_1	chr9:136497450-136497634	TCTGGTGATGGAACCTTGG	GCAGGCGGTCCATATGAT	185
		NOTCH1_E34_2	chr9:136497289-136497503	TGCTGCTGGACCACTTTG	CTTGAGGCTGCCCAGGTA	215
		NOTCH1_E34_3	chr9:136497192-136497406	GCTGCTGGACGAGTACAACC	ACTTCTTCCTCCGTGCCTTG	215
		NOTCH1_E34_4	chr9:136497111-136497281	TGCAGGGCAAGAAGGTC	GGTAGCCATGGGGTGACTC	171
		NOTCH1_E34_5	chr9:136496972-136497175	CTGCCTSCTGGACAGCTC	GCCATCTCGGGCTTGG	204
		NOTCH1_E34_6	chr9:136496837-136497044	ACCACCTGCCTGGGATG	GACCCRCCCACAGTGAA	208
		NOTCH1_E34_7	chr9:136496716-136496930	CACCTCGTCTCTCCCACCT	GGAGGGGGCCTGTGTG	215
		NOTCH1_E34_8	chr9:136496632-136496786	TGGTGCCGAACCAATACAAC	GGGCAGGCCCTGGTAG	155
		NOTCH1_E34_9	chr9:136496521-136496713	GCAGCATGGCATGGTAGG	TTGCTGCTGYTGGATGTTT	193
		NOTCH1_E34_10	chr9:136496418-136496610	CCTCACCTGGTGCAGACC	CCTGGCTYRGCTCTCC	193
		NOTCH1_E34_11	chr9:136496309-136496496	CCACAGCYRCACCTTG	GTCACGGGTGGGACCAG	188
		NOTCH1_E34_12	chr9:136496206-136496389	CCTGGCGGTGCACACTAT	GGTGAGGAAGGGGTGCTC	184
		NOTCH1_E34_13	chr9:136496103-136496276	ACAGCTACTCCTCGCCTGTG	GGGACTGCATGCTGGTG	174
		NOTCH1_E34_14	chr9:136496002-136496185	CCAGTGGTCCAGCTCGT	CATCCACAGAGCGCACA	184
	UTR	NOTCH1_E34_3UTR	chr9:136495628-136495810	TGAGAGCCAGGGTTTTCCTA	CTGGACGCCCCAGGAG	183
	Exon 3	PIK3CD_E3	chr1:9710407+9710621	CATTTCTTCATTTTTAGGACAACTG	TCTGAGGACCGGATGGAG	215
	Exons 4-5	PIK3CD_E4-5_1	chr1:9715492+9715688	CCCAGTGGCTGCCTTG	GCAGGAAGGGCTGCAC	197
		PIK3CD_E4-5_2	chr1:9715625+9715838	ACAGCGGAGCAGCAAGAG	GGGAGGGCTGSGTCAG	214
		PIK3CD_E4-5_3	chr1:9715725+9715908	TGAAGAAGCTCATCAAYTCACAGA	ACATCTTGGCGCGAAAGTC	184
		PIK3CD_E4-5_4	chr1:9715847+9716033	AGGCCTCCACGAGTTTGACT	GAGCCGCAGGGTACCAG	187
		PIK3CD_E4-5_5	chr1:9715959+9716148	GCCTGGCTGCAGTACAGTTT	GGAGTTTCACAGAGGAAGTGCT	190
	Exon 6	PIK3CD_E6_1	chr1:9716333+9716509	TGAACTCCCCAGACCCTACC	TCTTCCGCAGGGCACA	177

PIK3CD	Exon 6	PIK3CD_E6_2	chr1:9716442+9716653	GAGCTTCACCTTCCAGGTGTC	GAGCCCAGAGTGCAGAGG	212
	Exon 7	PIK3CD_E7_1	chr1:9716895+9717099	ATCCTGGTGTCCAGGGAGT	AGGAATGGGAGGTGGTTTG	205
		PIK3CD_E7_2	chr1:9717007+9717185	GTCCATTCCTCCTCCATCCT	GGCCAGTAGCACATGGAGTT	179
	Exon 8	PIK3CD_E8	chr1:9717485+9717694	AGACAAGCTGCACTTTGAGC	CTCCAGGATACAGCCACCTT	210
	Exon 9	PIK3CD_E9_1	-	GCCTCTGCCTCCTCACC	GTACAGCGCAAAGCAGAGAC	205
		PIK3CD_E9_2	chr1:9718786+9718972	GAAGCAGCRGCTGGAGT	AGGGGCTGTACTGGCTCTC	187
	Exon 10	PIK3CD_E10	chr1:9719884+9720067	CTGAGTGGCTGTCCTCACCT	TCTGGGACCCTCACACTCC	184
	Exon 11	PIK3CD_E11	chr1:9720074+9720279	GGTCACCCCTCTACAACTTCA	CAGCCCCTCAGCCTCAC	206
	Exon 13	PIK3CD_E13_1	chr1:9720705+9720895	TGGAACCAGAGCCCTCAC	CATGCTTGTTCCACTTGGTG	191
		PIK3CD_E13_2	chr1:9720799+9720971	GAGAAGGACCTGGTGTGGAA	GTGGGTAGCCAGAGGCTGT	173
	Exon 14	PIK3CD_E14_1	chr1:9721062+9721221	CCCTTACCCTGACCACCTC	AAGGAGCSTACGTGGCAAT	160
		PIK3CD_E14_2	chr1:9721125+9721321	AGATGCTCTACCTKCTGTGCT	CCAGAGCCCACGTCCT	197
	Exon 15	PIK3CD_E15_1	chr1:9721386+9721576	AGCTCCCTCCTGTCCTGAGT	GAAAAGGAAGTGGCCGATCT	191
		PIK3CD_E15_2	chr1:9721475+9721652	CTGGTGCAGGTGCTCAAGTA	AGTGGCCTTCCAGGGAGA	178
	Exons 16-18	PIK3CD_E16-18_1	chr1:9721734+9721944	AGGCTCAGCCCTCCCTTC	CAGGTCCCAGCCTCGAC	211
		PIK3CD_E16-18_2	chr1:9721848+9722055	GCTGATGAAGCAGGTGAGG	CTTGGTCTGGGGCTTGG	208
		PIK3CD_E16-18_3	chr1:9721977+9722189	GGAAGCACTGAGCAAACTGA	GGTGGGAGGAACCCTTGT	213
		PIK3CD_E16-18_4	chr1:9722134+9722318	ACCCTGCTGGCTGAAGTCT	CTGCCTGCCTCCTCGTT	185
		PIK3CD_E16-18_5	chr1:9722249+9722447	AGCAGTGCACCTTCATGG	CCAGGATTCTGTCTTCTCCAC	199
	Exon 19	PIK3CD_E19	chr1:9722456+9722644	GGCTTGGGTGTAGCTGGA	ACAGACACCAAGGGACGATG	189
	Exon 20	PIK3CD_E20_1	chr1:9723062+9723263	CAAGTGGCCTCAGGGACA	CAGGGCATCCTTGTTGAAG	202
		PIK3CD_E20_2	chr1:9723182+9723343	ACTCCGTTCAGACACCATCG	TCCACACCTCTTGGAAAGGA	162
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		PIK3CD_E21_2	chr1:9723983+9724173	GAGCCATTGAGGAGTTCACC	GCTGTGTGCTAGGCAGAGG	191
	Exon 22	PIK3CD_E22_1	chr1:9724209+9724397	TGTCTCCCCTGGATTCTCTC	GTCTTCCCCTGCTGAATCAC	189
		PIK3CD_E22_2	chr1:9724281+9724489	CCACATTGATTTTGGCCACT	GGGAACCTCTGCCCTGTT	209
	Exon 23	PIK3CD_E23_1	chr1:9724763+9724931	GGAGTTCCCAGAGCCTCACT	GATACTGGATGTCTTTGGAGCA	169
		PIK3CD_E23_2	chr1:9724823+9725032	AGGGCCTACACCATCCTG	TGGGGCCTACTGCATTC	210
	Exon 24	PIK3CD_E24_1	chr1:9726847+9727053	GACGCATCCCAGAGCAAG	GGAGCCACTACTGCCTGTTG	207
		PIK3CD_E24_2	chr1:9726915+9727104	CTGGCACTGGGGAAAACAG	TGCTTGGTCCCCACGAC	190
	Exon 3	TBL1XR1_E3	chr3:177064819-177065024	AGGGTTATATCCTGTGTTGTGACC	AAGTTCAACGGTTTGGACTGA	206
	Exon 4	TBL1XR1_E4_1	chr3:177053812-177054014	TGGGATTTGAAAAGATGATGG	TTTCTGGATGATAGAAATCAATGC	203
		TBL1XR1_E4_2	chr3:177053694-177053886	GAAAGCCATATCAGTCAGTCCA	TGAATAAGCAAGCAAGACAGC	193

TBL1XR1	Exon 5	TBL1XR1_E5_1	chr3:177051672-177051857	TGAATTCAGAAAGTTCCTAAAAATG	CGGCATCTATCAGGGACAG	186
		TBL1XR1_E5_2	chr3:177051528-177051735	CAAATCCAGGATGGTACCTTGT	CCTCCCCATTTGCTGTGTT	208
		TBL1XR1_E5_3	chr3:177051381-177051584	CTGCAGCCAGCCAACAA	CAACAAACCCCTGTGATATGAG	204
	Exon 6	TBL1XR1_E6_1	chr3:177050500-177050680	AAGAAATCACCCATCCACCA	CAGGGTTCCAGGCACAGATA	181
		TBL1XR1_E6_2	chr3:177050374-177050574	TTGAAATCCCTCCTAATAAAGCTG	TGGCCACAACTAAGCAACAA	201
	Exon 7	TBL1XR1_E7_1	chr3:177050031-177050210	TGTAAATATGTTGCCTTGTTCTGA	GGAACATCTTGCCCTCCTTC	180
		TBL1XR1_E7_2	chr3:177049920-177050099	GAACAGCACCAGTGGCTCTA	AACCCTGCCGTGAGTATGAG	180
	Exons 8-9	TBL1XR1_E8&9_1	chr3:177047488-177047698	GGCACTCACAAGTAGGCAAA	TCTTTAGTCCATATTCTGGCAAAC	211
		TBL1XR1_E8&9_2	chr3:177047362-177047551	AGAGTGAAGGTACACTTCTAGCAAC	GGCCTTTAYGCTGCCCTA	190
		TBL1XR1_E8&9_3	chr3:177047273-177047474	ATTTTCCTTYTTACTTTGTTGTTGA	CCTTTACAGAACTTAATGAGCTTTTAC	202
	Exon 10	TBL1XR1_E10	chr3:177046080-177046294	CCACTCTGACATTTCATATTGCTG	GAAAAACAGAAYCAAGCTCCA	215
	Exon 11	TBL1XR1_E11_1	chr3:177038301-177038507	TGGTTCAAAGCTAAAACTCTTGG	AAGGTTTCTTACCGTATGTCCTTG	207
		TBL1XR1_E11_2	chr3:177038259-177038431	CAGCATTGGATGTTGATTGG	TGAAACATTACTTGTTAATCATGACC	173
	Exon 12	TBL1XR1_E12	chr3:177038035-177038238	TGTTTAATATTCAAGTAGCTACCCAGT	AATGGCCAGAGCAACCATAC	204
	Exon 13	TBL1XR1_E13_1	chr3:177034204-177034379	AAATATACTCATTGWRTGGAAAAATAATTG	AACATAAGGTTGGCATTTGGA	176
		TBL1XR1_E13_2	chr3:177034102-177034315	TGAAACAAGACAATTGTGTCCA	TCCACTTCATGAAATCTTCCCTA	214
	Exon 14	TBL1XR1_E14_1	chr3:177033015-177033223	TTGGCTGAATATGGGAGGTT	CCAGATACCTGCCATCAGGA	209
		TBL1XR1_E14_2	chr3:177032881-177033093	GGGATATGCATCCATACCTTG	AATGACAACCAAATGGTGAGG	213
	Exon 15	TBL1XR1_E15	chr3:177026339-177026553	TGTAATATTTTTATTTCAGCATTTGGA	CACACCCTCTTTGGAAACACT	215
	Exon 16	TBL1XR1_E16	chr3:177025456-177025660	TTCCATGATTATTATGCTTTACCAA	TGTACACATTCATAGTCGGTCCA	205
		TET2_E3_1	chr4:105233906+105234076	AGAGGGCAGCCTTGTGG	TGAGCTCTCTCAGGCAGTGG	171
		TET2_E3_2	chr4:105233987+105234186	TCCATTCCTGATACCATCACC	TTTCTTGTGTAAAGTCAGGACTCA	200
		TET2_E3_3	chr4:105234095+105234296	CACCAAGTGGCACTCTTTCA	AGCCTTTTGKTCTTGTTTCAA	202
		TET2_E3_4	chr4:105234215+105234419	TGGAGGAATAAAACGCACAG	TGCATTTTCTTGGGCTACAG	205
		TET2_E3_5	chr4:105234324+105234506	AGCCAAGAAAGAAATCCAGGT	TTTCCCCTCCTGCTCATTC	183
		TET2_E3_6	chr4:105234455+105234664	CAGTGGGCMTGAAAATCC	GCAATGGAAACACAATCTGG	210
		TET2_E3_7	chr4:105234595+105234803	TGGAACACACACATGGTGAA	CTTTGGAGGCAGCTCAGAGT	209
		TET2_E3_8	chr4:105234707+105234913	GGCTACTAATGAGTTGTCCTGTGA	TGTTGTAGTTGTTCTGGTTTCTGA	207
		TET2_E3_9	chr4:105234823+105235028	AGGCCTGTGATGCTGATGAT	AGCTTGCAAATTGCTGCTG	206
		TET2_E3_10	chr4:105234928+105235136	TTGAGATATGCCCATCTCCTG	TGGTGTGGTASTGGCAGAAA	209
		TET2_E3_11	chr4:105235075+105235283	GTGCTTACTTCAAGCAAAGCTCA	CCTTAAAAGTGTTGTGTTACTTTGG	209
		TET2_E3_12	chr4:105235213+105235397	GCACTCTGAATGGTRGAGTTT	CACACAATTAYTCTGAGGCCTTT	185
		TET2_E3_13	chr4:105235300+105235497	GTAAACCTGAGGCACCACCT	AAATTGGTGGGTTATGCTTGA	198

TET2	Exon 3	TET2_E3_14	chr4:105235429+105235643	TGACTGTTCCATTGTGTTCTGAG	CAATTCAATCCATCCTGGTTTC	215
		TET2_E3_15	chr4:105235573+105235782	GAGACAAGGAGCAAACACGA	CCCCAGGCATGTTGGA	210
		TET2_E3_16	chr4:105235715+105235899	GTATCAACCCAATCTCTCCAATCA	ACTGGAGATGTTGGTCCACTGT	185
		TET2_E3_17	chr4:105235843+105236045	ACCAAGTTGAAATGAATCAAGG	CTGTTTCAACACTGGGGACA	203
		TET2_E3_18	chr4:105235956+105236163	CATGTGCAGTCACTGTGTGG	TTTGAGGGAGATGTGAACTCTG	208
		TET2_E3_19	chr4:105236086+105236286	ACTCACACCTTTTGCAACATAAGC	CCACTTTAGTCTGGCCAAAGAAT	201
		TET2_E3_20	chr4:105236234+105236423	AAGCAACRATGATCAGCAAAGA	TGCACTTGATTTCATGGTCTG	190
		TET2_E3_21	chr4:105236339+105236521	TCATAATGTCYAAATGGGACTG	TGGGTCTTGTTTCCTGCAA	183
		TET2_E3_22	chr4:105236437+105236607	TTTCTTGTTCAAACAATWCACACCT	TCTGCTCCTGTTCTTGAAAGC	171
		TET2_E3_23	chr4:105236552+105236755	TAATGTGATCCCAAAGCAAGAT	GTGTGACTTCCTCCCTGGTC	204
		R_TET2_E3_24	chr4:105236687+105236883	TCAGCAAAGGTACTTGATACATAACC	TTGGCCTGTRCATCTGACTA	197
		TET2_E3_25	chr4:105236789+105236990	TGCTGCTCTAAGGTGGCATC	ACAGCTTGMAGGYGGATTCT	202
		TET2_E3_26	chr4:105236931+105237106	CCACCAGAAAACAAAACATGG	TTTACTTGCTTCTGTGATTTGAGA	176
		R_TET2_E3_27	chr4:105237039+105237206	AAGCAGTTTCACGYCAAGT	TGAAGAAGTTGTTKGCTGCTCT	168
		TET2_E3_28	chr4:105237152+105237365	TGCTGCAGAACTTGATAGCC	TTTCTGGSACTTACCTACACATCT	214
		TET2_E3_29	chr4:105237301+105237463	TGGATACACCTGTCAAGAYTCAATA	CAAATTGCTGCCAGACTCAA	163
	Exon 4	TET2_E4_1	chr4:105241237+105241426	TTAGAGCCCTTAATGTGTAGTTGG	TCTTCCATGATTTCTCTAATAGCTG	190
		TET2_E4_2	chr4:105241369+105241518	TTTATACCCATCTAGGAGCAGGTC	GTTTACTGCTTTGTGTGTGAAGG	150
	Exon 5	R_TET2_E5	chr4:105242763+105242973	CAAATATTTTGATTGCCTCTTGA	AAATGCCCAAGATTTAAGACCA	211
	Exon 6	TET2_E6_1	chr4:105243542+105243738	GTTTGGGATGGAATGGTGAT	ATTTCCTCAGCGTCTCGGTA	197
		TET2_E6_2	chr4:105243655+105243865	TGATTCTCATCCTGGTGTGG	GCACGCTGAACTCTCTTCCT	211
	Exon 7	TET2_E7_1	chr4:105259558+105259759	TCAGCTGCACAGCCTATATAATG	TCATCCCCAAGCAGCTTAAA	202
		TET2_E7_2	chr4:105259701+105259902	AATGGATGTAAGTTTGCCAGAAG	AGTGTGTATCTACAGTTTGGGAAAA	202
	Exon 8	TET2_E8_1	chr4:105261655+105261846	TGTTTGGGATTCAAAATGTAAGG	GATTATTATAYGCATCAGGTGCAAG	192
		TET2_E8_2	chr4:105261776+105261980	TCATTTGCAAAACCTGTCCA	CAGTGGTTTCAACARTTAAGAGGA	205
	Exon 9	TET2_E9	chr4:105269576+105269778	TACTTTCGCATTCACACACACTT	CAGCTGCTAAGCTGTCCTCA	203
	Exon 10	TET2_E10_1	chr4:105272510+105272689	CACGTTTTCTTTGGGACCTG	CTCCTGAGCTTCCACACTCC	180
		R_TET2_E10_2	chr4:105272585+105272774	GACAATCGAGAATTTGGAGGA	GGCAAGTCTTGACTGGCTCT	190
		TET2_E10_3	chr4:105272710+105272913	CATTCAGGTACTGAGTTCTTTTCG	AACTGTTTAGCCTGGCTTGC	204
		TET2_E10_4	chr4:105272823+105273005	CCCTGGAGAACAGCTCAAAT	AAGTTGATGGGRGCAAAAC	183
		TET2_E11_1	chr4:105274998+105275209	TCATCAACATCAAAGATACCTGTTT	TGGTGGATCCAGAAGCAGA	212
		TET2_E11_2	chr4:105275131+105275324	CAGCAGAGACCCCAGCAG	GCAGCTTGAGATGAGGTGGA	194
		TET2_E11_3	chr4:105275241+105275445	TCCTTATCCAAACTCTTCACACA	ATATGGGGAGCAGTTGTCCA	205

	Exon 11	TET2_E11_4	chr4:105275373+105275562	TTTGAATCAGAATACCCAATATCC	TCCAAACCTTGGCTGGTAA	190
		TET2_E11_5	chr4:105275498+105275709	GCCAAGACCCTCTGTCTAAGC	GAAGTGGCCATCCATCTCAT	212
		TET2_E11_6	chr4:105275622+105275819	TGGTTTCAGCAGTTGTACCATTA	GGAGCTGCAYTGTAGTTATGGAT	198
		TET2_E11_7	chr4:105275741+105275947	TGAGCAATCCAAACATGGAC	GGACACAAGCAGTTCTATCATGG	207
		TET2_E11_8	chr4:105275870+105276052	ATGACATGCTTTCCCACACA	ACCAGACCTCATCGTTGTCC	183
		TET2_E11_9	chr4:105275974+105276149	GCTAATGGTCAGGAAAAGCAG	AGCTCACGCTTTGCACACT	176
		TET2_E11_10	chr4:105276068+105276260	GCTTTCTGGATCCTGACATTG	CAAAGAGCCAAGCCATGTT	193
		TET2_E11_11	chr4:105276177+105276388	CAATAGGAATCACCCCACCA	AAGTTTCATGTGGCTCAGCA	212
		TET2_E11_12	chr4:105276317+105276485	GCCCAGACTATGTGCCTCA	GTGAAGGCATATGGAGATGTAGTT	169
		R_TET2_E11_13	chr4:105276419+105276617	CTCTTGCCGAAAGGACCAT	ACTGTGACCTTTCCCCACTG	199
TNFRSF14	Exon 1	R_TNFRSF14_E1	chr1:2556631+2556813	CTGGGTTCCCGAGCTG	CATGGGGAAGAGATCTGTGG	183
	Exon 2	TNFRSF14_E2	chr1:2557696+2557910	ATCTCCCAATGCCTGTCCT	GGGTGTCTGGGGCAGAA	215
	Exon 3	TNFRSF14_E3_1	chr1:2558246+2558458	GTCTCCCTGCTTGGGCTCT	CATTTGGCACTGCAGACACT	213
		TNFRSF14_E3_2	chr1:2558377+2558565	GGGCACAGTGTGTGAACC	CCTTCCTGGGGCACTGT	189
	Exon 4	TNFRSF14 _E4_1	chr1:2559726+2559911	CCCTGGCAGCAGTCCTT	GTCCTGGACRATGCAGAAGT	186
		TNFRSF14 _E4_2	chr1:2559844+2560023	GGAACTGCTCCAGGACAGAG	GGACCAGGGTGGAAATGG	180
	Exon 5	TNFRSF14_E5	chr1:2560542+2560756	CTCACAGACAAGCAGTCCCTA	CTCCCCAGGGCACAGA	215
	Exon 6	TNFRSF14_E6_1	chr1:2561609+2561788	TGAGGCTGAGTGAACACTGG	TGATTAGGCCAACTGTGGAG	180
		TNFRSF14_E6_2	chr1:2561721+2561880	CTGGGTATGGTGGTTTCTCTC	GGTGACAGAGCTCCAAGAGG	160
	Exon 8	TNFRSF14_E8_1	chr1:2563060+2563254	CAAACTGAAAGCAGTAAAATGAACC	CCCGTGAATGAGGGTATTGT	195
		TNFRSF14_E8_2	chr1:2563165+2563341	AGAAGGTGAGGCCACAGTCA	AGGTGGACAGCCTCTTTCAG	177
CD79B	Exon 2	CD79B_ex2_1	chr17:63931281-63931479	CAGGACATAGTCGCACACAACT	AGTAGCTCCGGGAACATAGAGG	200
	Exon 3	CD79B_ex3_1	chr17:63930024-63930219	CTAGGGTGGGGCGGACAG	CATGGAAGAGTCCCAGAACGAAT	196
		CD79B_ex3_2	chr17:63930111-63930300	CTCCGAGGTGTTGTTGCACTTCT	CAGCGCCTCCGGCAAT	190
		CD79B_ex3_3	chr17:63930239-63930431	GCTGCTGGGGATTCTCGTC	AGGAAGATGCCAAGCGGAATG	193
	Exon 4	CD79B_ex4_1	chr17:63929673-63929858	CACAACGAGAGCTGGGGAGA	GGAACACGCTGAAGGATGGT	186
		CD79B_ex4_2	chr17:63929772-63929943	TGTCCAGCAGCAGGAAGATAG	AGGCCTAAAAGGTGGACTGTG	172
	Exon 5	CD79B_ex5_1	chr17:63929362-63929539	CCCAACCACACCAGCAGATAGT	GGCCCAGCAGGGGATG	178
	Exon 6	CD79B_ex6_1	chr17:63929167-63929351	CTCCGAAGCAGTCACTGAGG	GGCCTGAGTTCCACTTAATGTC	186
CD79A	Exon 2	CD79A_ex2_1	chr19:41878940-41879106	AATGTGTCACCATCCCCAG	AGGTGACGTTGGCGTTGTT	167
		CD79A_ex2_2	chr19:41879015-41879213	GCACAAGGTCCCAGCATCAT	CCCATGGCTCTTGTTCACATTCT	199
		CD79A_ex2_3	chr19:41879135-41879330	GTGGCCCCCTGAGTTCTTG	AGCGGGACAGTGGGAGTAGG	196
	Exon 3	CD79A_ex3_1	chr19:41879480-41879679	GAGGCTAGGGAGGGCAAGAG	TGACTCAGAGGTCCGAGGG	200

	Exon 4	CD79A_ex4_1	chr19:41880599-41880779	CATCCAGGAGGGTCTGAAAGATA	CTAACACAACTGCCCCTACCC	181
		CD79A_ex4_1_new2	chr19:41880619-41880781	ATATTCACCTCCCCCTGCTC	CCCTAACACAACTGCCCCTA	180
	Exon 5	CD79A_ex5_1	chr19:41880840-41881038	ATGTTCGCTGCCTCATTTCCAT	CTGAGACACTGGAGCTGGGTG	199
MYD88	Exon 1	MYD88_ex1_1	chr3:38138414-38138585	CCTACTAGCACCATCACCAGACC	CTGCCCTACAATCTGGAGCC	172
		MYD88_ex1_2	chr3:38138487-38138675	CTTCTTACGCCCCCCACATC	CGGTCGGGTCGCATTGTC	189
		MYD88_ex1_3	chr3:38138593-38138775	CTTCTCGGAAAGCGAAAGCCG	GAGAGCAGCCAGGGGAAGG	183
		MYD88_ex1_4	chr3:38138699-38138888	CCATGGCTGCAGGAGGTCC	TGCCGGATCTCCAAGTACTCAAA	190
		MYD88_ex1_5	chr3:38138793-38138959	CCGCCTGTCTCTGTTCTTGA	CTACAGAGGCGCCAGGG	167
		MYD88_ex1_6	chr3:38138874-38139084	CTTGGAGATCCGGCAACTG	CGGAAAGTCAGCCTCCTCAC	211
	Exon 2	MYD88_ex2_1	chr3:38139793-38139992	CTGGATCCTGACTGTGGGTAAAG	GGTCATCAAGTGTGGTGATGC	200
		MYD88_ex2_2	chr3:38139858-38140051	CCACAGAGGAGGATTGCCA	ACACCACAATGTCCTATTCCACC	194
	Exon 3	MYD88_ex3_1	chr3:38140314-38140506	AGGGGACTCTTGGCTGGA	AGACACACACAACTTCAGTCGAT	193
		MYD88_ex3_2	chr3:38140412-38140610	CCTTCATCTGCTATTGCCCCAG	CTTCATGCATCCACGCACC	199
	Exon 4	MYD88_ex4_1	chr3:38140696-38140895	TCCCAGGGGATATGCTGAACTAAG	CACCTACACATTCCCTCATTCTCT	200
	Exon 5	MYD88_ex5_1	chr3:38141069-38141260	GACTGGGCTTGTCCCACCA	GGCGAGTCCAGAACCAAGATTT	192
		MYD88_ex5_2	chr3:38141151-38141325	GATCCCCATCAAGTACAAGGCA	CAGACAGATACACACACACCCAGG	175
PRDM1	Exon 1	PRDM1_ex9_1	chr6:106086471-106086659	GAGGTGCGCGTCTGTGC	GGAAAAGAAAATAAAGTTTTCAGATCAATT	189
	Exon 2	PRDM1_ex10_1	chr6:106088128-106088304	GTCATAGCCTCTCAGAAGGAGCCA	CACAGAGTCATATCCGCATCCTC	177
		PRDM1_ex10_2	chr6:106088230-106088429	GAGGTTTCAGGGATTGGCAG	ACTTGAAAAGCAGATTCCTTGGT	200
		PRDM1_ex10_3	chr6:106088329-106088508	GTGTACATACATTGTGAACGACCAC	CAAGTAGGGAGATTTGGCACC	180
	Exon 3	PRDM1_ex11_1	chr6:106095553-106095724	TGAAAAGATTGGTTAACATTTTATAGTCAAAG	TATTTCCTGTTGGCGTTCTTAGG	172
		PRDM1_ex11_2	chr6:106095605-106095800	TCCTGTTTAGGTTATTGGAGTGATGAG	ACCCAGCTCTTTTAGCTCCATTT	196
	Exon 4	PRDM1_ex5_3	chr6:106099414-106099604	TGTCAGAACGGGATGAACATCTAC	CAGAACCGACATTACTGGCATTTT	191
		PRDM1_ex5r_1	chr6:106099277-106099462	TGCCTGTCTTCTCTTTTGGAC	CAGGGATGGGCTTAATGGT	186
		PRDM1_ex5r_2	chr6:106099350-106099532	GAAAAGCAACTGGATGCGCTATG	TCTCCGGGATAAGGGTAGTGAAG	183
	Exon 5	PRDM1_ex6_1	chr6:106104763-106104962	TGGCAGTTTTGCTTCAGTTCTC	GGTAGAGGTCCTTTCCTTTGGAG	200
		PRDM1_ex6_10	chr6:106105572-106105755	CCTCAGATGGAGCCCGGA	TTGGGCTGCACCACATGTT	184
		PRDM1_ex6_11	chr6:106105686-106105881	CCTGTAGCCCCACAAGCG	TTGATCTTGCCGTTCTGCTTC	196
		PRDM1_ex6_9	chr6:106105475-106105662	CTCTTCCCGAGGCTGTGC	GCCCCGGTAAAGGAGAAGG	188
		PRDM1_ex6r_1	chr6:106104889-106105057	CCCAAAGAGAGAGTACAGCGTG	GTAAACGACCCGAGGGTAGAAG	169
		PRDM1_ex6r_3	chr6:106105035-106105232	CCTTCTACCCTCGGGTCGTTTAC	TCCCAGGGCTGCTGTGAG	198
		PRDM1_ex6r_4	chr6:106105144-106105342	CATTCCATCCTCCACCACTCC	GGGTGCGTAGCCAGGGTA	199
		PRDM1_ex6r_5	chr6:106105271-106105468	CGGGACTCCTACGCTTACTTG	GTTGTTGATGCCATTCATGCT	198

		PRDM1_ex6r_6	chr6:106105375-106105567	GTACAACGCTCACTACCCCAAGT	CGAGCTCGGGAGAGAAGTGG	193
		PRDM1_ex6s_2	chr6:106105819-106106013	AAGAAACATGACCGGCTACAAGAC	GATACCCCATGGAAAGCAAGCTA	195
		PRDM1_ex6t_2	chr6:106104945-106105142	AAGGAAAGGACCTCTACCGTTCTA	GGGAGCGAGTGATGTACGTG	198
	Exon 6	PRDM1_ex7_2	chr6:106106333-106106532	GCTTGAGAGCAGAGCTAACACAT	GGTCAGAAGGTCTACCCAGAAA	200
	Exon 7	PRDM1_ex8b_1	chr6:106106838-106107027	CTCCCGTTGGCAACTCTTAATC	GTGCACAAACTGGGTGAACTTG	190
		PRDM1_ex8b_2	chr6:106106928-106107124	TAGCAGCACCAGCAATCTCAAG	GGTGAACCTTGAGGCTACAGAGA	197
		PRDM1_ex8b_3	chr6:106107028-106107227	CTGAAACTGCACAAGCGTCTG	TCAGCATTGTCACTGATGTCAAAC	200
		PRDM1_ex8b_4	chr6:106107159-106107306	GCTGCCCTTGGAAGATCTG	CTCTTTTCTGACCACGGCCA	170
		PRDM1_ex8b_5	chr6:106107232-106107417	CTCGAGGACGTGGAGGATG	AGGCAACTTCATGAGGGGTAGAT	186
		PRDM1_ex8b_6	chr6:106107359-106107541	TCCTCTCCTCAGGGTGCAG	ACCCTGACTCACCAAGTCATAACT	183
TNFAIP3	Exon 2	TNFAIP3_ex2_2	chr6:137871260-137871449	TTTGAGCAATATGCGGAAAGC	CTGGATGTTTCTGTCGATGAGG	190
		TNFAIP3_ex2_2r_1	chr6:137871141-137871343	CAGGCAGCTATAGAGGAGTCGT	TGATGAATGATCCCATTAGTAGGT	203
		TNFAIP3_ex2r_1	chr6:137871354-137871538	ATGCACCGATACACACTGGA	ACAGAACAAGTCTTACCGTTCGTT	185
		TNFAIP3_ex2r_2	chr6:137871426-137871623	GCCCTCATCGACAGAAACATC	TGATTTGAGTTTGGGCTTGTCCTA	198
	Exon 3	TNFAIP3_ex3_1	chr6:137874772-137874962	TCTGAAAACCTTTGCTGGGTC	AAGTTGCGTGTGTCTGTTTCCT	191
		TNFAIP3_ex3_2	chr6:137874881-137875080	ACATGTGGGGCGTTCAGG	CCACCATGGAGCTCTGTTAGTAGA	200
	Exon 4	TNFAIP3_ex4_1	chr6:137875638-137875814	CAGGGAGTACAGGATACATTCAAGC	TTCTGAGGATGTTGCAAAGGAC	177
		TNFAIP3_ex4_2	chr6:137875676-137875860	CGCTCCCCTTAGAACTGGAATGA	GATCCGTGATCTGCAGGCAT	185
	Exon 5	TNFAIP3_ex5_1	chr6:137875918-137876114	AGTTCAGGTAACAGAGTTCAATGGA	GCCGAGAACAATGGGGTATC	197
		TNFAIP3_ex5_2	chr6:137876024-137876219	TTCCAATTTCGCCCCTTTG	ACCCTGATGTTTCAGTGTCTAGTT	196
	Exon 6	TNFAIP3_ex6_1	chr6:137877020-137877213	CCTATGGCCTTGTTTAGTAGAATACTG	GGACGGGGATTTCTATCACC	194
		TNFAIP3_ex6_2	chr6:137877101-137877290	CAGAGACCGGGGAAGATTTG	TGACACAGGAGAGAGCTGAACA	190
	Exon 7	TNFAIP3_ex7_1	chr6:137878378-137878570	TCTTGTGTGTGATTTTGTGTATTCTC	AGGTTCCATGGGATTCTGG	193
		TNFAIP3_ex7r_1	chr6:137878434-137878632	TGGATGAAGCTAACTTACCAAAAGA	ATGAAGAAGGGGCAGTTGG	199
		TNFAIP3_ex7r_2	chr6:137878551-137878746	CCCAGAATCCCATGGAACCT	GCCATGCCAGGGAGCC	196
		TNFAIP3_ex7r_3	chr6:137878666-137878865	CTCAGAGAGGCGGCAAAAG	TGGTCTCACTGAACAGAAAAGG	200
		TNFAIP3_ex7r_4	chr6:137878756-137878939	CTCTCGGGGAGAAGCCTATG	GCAACGTTCACAAAATCCGT	184
		TNFAIP3_ex7r_5	chr6:137878866-137879064	CTGCCATGAAGTGCAGGAG	AAGCAAGTACTGCAGATCCCA	199
		TNFAIP3_ex7r_6	chr6:137878962-137879149	CCAGCCACGCCCCAGAC	CGAGGGATCTGACTTGGAACG	188
		TNFAIP3_ex7r_7	chr6:137879071-137879259	GACTACAGCAGAGGCCTCCTCC	CTCGTCCCCGTCCTGTCC	189
		TNFAIP3_ex7r_8	chr6:137879178-137879353	CTTGCCACAGAGCTGGAAAC	ACGTTTGTTTTCTCTGTACTCGATG	176
		TNFAIP3_ex7r_9	chr6:137879278-137879470	CTGCGTGTATTTTGGGACTCC	CACGGTAGGTCCTGACAGTTCT	193
	Exon 8	TNFAIP3_ex8_1	chr6:137880005-137880196	TGTCAGCATCTCTGTATCGGTG	AACACTTCTGGCAGTATCCTTCA	192

	Exon 8	TNFAIP3_ex8_2	chr6:137880109-137880307	TCCAGGTTCCAGAACACCATTC	CAGCAAAAAGCATCGAACACACG	199
	Exon 9	TNFAIP3_ex9_1	chr6:137880964-137881164	TGTGCTCTCCCTAAGAAATGTGAG	TGGGATGCTGACACTCCAT	201
		TNFAIP3_ex9_2	chr6:137881066-137881263	CCACACAAAGCACCTCAAGG	CATTGCCAAAATGATCACAGG	198
		TNFAIP3_ex9r_1	chr6:137881140-137881328	CTCTGCATGGAGTGTCAGCAT	TGTTTCCGGTTAGCCATACATCT	189
		TNFAIP3_ex9r_2	chr6:137881244-137881429	CTGTGATCATTTTGGCAATGC	ACCCTTAAGCCCACTGTTGC	186
CARD11	Exon 5	CARD11_ex5_1	chr7:2944146-2944313	TTGAGCCCTGGTGACATTTG	GTCAAGGTGAAGGACGACAACTA	168
		CARD11_ex5_2	chr7:2944214-2944409	CGAGTTGGAGGTCTCGGCT	AAGAAGCAGATGACGCTGACG	196
		CARD11_ex5_4r_2	chr7:2944458-2944630	GTCCTTGGCCTTCATCTGCT	GAGTGAGTGAATGAATGGCACC	173
		CARD11_ex5r_1	chr7:2944314-2944512	CAGCTCGTCATTGTAGCTGTCC	GCACTTCCTGATGAACGAGGTC	199
	Exon 6	CARD11_ex6_1	chr7:2939667-2939831	ACCCTGGCAGGTTCATCGT	CCAAGAAGGAGCAGGTTCTGG	165
		CARD11_ex6_2	chr7:2939789-2939984	ATTTCATTCTCCCGCTCCAG	TTCTGAGTGTTTCTTGCCACC	196
	Exon 7	CARD11_ex7_1	chr7:2938597-2938795	GTCCTGCTGACACACACCACT	ATCCTGGACATCTTGGAACACG	187
		CARD11_ex7r_1	chr7:2938669-2938853	CCACTCCCACCTTGTCTCG	AAACCTCCTCCCTCCCACC	185
	Exon 8	CARD11_ex8_1	chr7:2937809-2937991	GTTGCACTGGACAAAACACTCTG	CCTGGGAAAGGACTGTGAAATG	183
		CARD11_ex8_2	chr7:2937916-2938104	CTCCCGCTCCACCTCCTC	GCAGAGAACAGCTTTCAGTCCTGA	189
	Exon 9	CARD11_ex9_1	chr7:2936990-2937178	AGGGCCCACCTGGCTTC	GGACAAGTACAGGAAGCAGATCC	189
		CARD11_ex9_2	chr7:2937076-2937258	CTTGCTCTCCAGGTTGACGATG	CTTCGTCCCGCTTCTCCC	183
TP53	Exon 2	TP53_E00001596491_1	chr17:7676440-7676622	TTTCGCTTCCCACAGGTCTC	CAGCCAGACTGCCTTCCG	182
	Exon 4	TP53_E00001612188_1	chr17:7675942-7676103	ATACGGCCAGGCATTGAAGT	CCTCCTGGCCCCTGTC	161
		TP53_E00001612188_2	chr17:7676041-7676202	GGAAACCGTAGCTGCCCTG	AAGACCCAGGTCCAGATGAA	161
		TP53_E00002359670	chr17:7676161-7676308	CAGCCTCTGGCATTCTGG	CCTGGTCCTCTGACTGCTCT	147
	Exon 5	TP53_E00001255919_5	chr17:7675043-7675207	AGCTGCTCACCATCGCTA	CCAACTGGCCAAGACCT	164
		TP53_E00001255919_6	chr17:7675107-7675276	TGTGCTGTGACTGCTTGTAG	TGCCCTGACTTTCAACTCTGT	169
	Exon 6	TP53_E00001255919_1	chr17:7674753-7674956	GGAGGTCAAATAAGCAGCAGG	AGCATCTTATCCGAGTGGAAGG	183
		TP53_E00001255919_3	chr17:7674911-7675088	TCCAAATACTCCACACGCAAA	GCTGCCCCCACCATGAG	177
	Exon 7	TP53_E00001665758_1	chr17:7674114-7674313	GGGGTCAGAGGCAAGCAG	CTTGGGCCTGTGTTATCTCC	199
	Exon 8	TP53_E00001789298_3	chr17:7673685-7673869	TGTCCTGCTTGCTTACCTCG	GCCTCTTGCTTCTCTTTTCCT	184
	Exon 9	TP53_E00001789298_1	chr17:7673468-7673665	AGAAAACGGCATTTTGAGTGT	AAGGGTGCAGTTATGCCTCA	197
		TP53_E00001789298_2	chr17:7673590-7673757	CTGGTGTTGTTGGGCAGT	ATCTCCGCAAGAAAGGGGAG	167
	Exon 10	TP53_00001404886_13	chr17:7673266-7673416	TCTGTATCAGGCAAAGTCATAGAA	GCCTCAAAGACAATGGCTCC	150
		TP53_E00001728015_1	chr17:7670541-7670736	GGAATCCTATGGCTTTCCAACC	CCCCCTCCTCTGTTGCTG	195
	Exon 11	TP53_E00001757276_1	chr17:7669532-7669712	GACCCAAAACCCAAAATGGC	TCCCTGCTTCTGTCTCCTAC	180
	Exon 1	B2M_ex1	chr15:44711454-44711661	CGGGCCTTGTCCTGATT	GCAGAGCGGGAGAGGAAG	208

B2M	Exon 2	B2M_ex2_1	chr15:44715326-44715512	AATGTAAACACTTGGTGCCTGATA	ATGGATGAAACCCAGACACA	187
		B2M_ex2_2	chr15:44715423-44715629	GTACTCCAAAGATTCAGGTTTACTCA	GGGTGAATTCAGTGTAGTACAAGAGA	207
		B2M_ex2_3	chr15:44715456-44715664	CAGCAGAGAATGGAAAGTCAAAT	GTTCACACGGCAGGCATAC	209
		B2M_ex2_4	chr15:44715577-44715752	GTCTTTCAGCAAGGACTGGTCT	TGACTACTCATACACYACTTMCAGCAG	176
CD58	Exon 2	CD58_ex2_1	chr1:116544473-116544655	TGCCACCAAAGTCATGTTGT	TTTCCAGTTCTGCAACTTTATCC	183
		CD58_ex2_2	chr1:116544381-116544580	AAATATATGGTGTTGTGTATGGGAAT	TGATGATGTTAAGTTGRAGARAGTGAGG	200
		CD58_ex2_3	chr1:116544293-116544468	TGASTTCAGAGCTTTCTCATCYTT	AACTTATGGAATACTCACCAAGCAC	176
		CD58_ex2_4	chr1:116544186-116544367	ATGAARTGGAATCGCCAAAT	AAACCCTGACAACAGGTAACATC	182
	Exon 3	CD58_ex3_1	chr1:116536169-116536354	TGCTCAAGGAGTTTGTCTGC	ATTGGACTTCAATGCTTCCA	186
		CD58_ex3_2	chr1:116536054-116536217	TCTCCCACACTAACTTGTGCAT	TCATTTTCCATCTTAAAATATATACTGGT	164
		CD58_ex3_3	chr1:116535955-116536133	CTTATAATGTACTCATGGGATTGTCC	ATTTACTCACCGCTGCTTGG	169
		CD58_ex3_4	chr1:116535892-116536042	AAATACAGTGTACTCTTAGCAATCCAT	AATTGTGAACCTTGTGTTAGTCACC	151
CREBBP	Exon 2	CREBBP_ex2_1	chr16:3850899-3851081	CATAGAAACGTGGCAGTTGG	TGGAAGCAGCATCTGGAAC	183
		CREBBP_ex2_2	chr16:3850771-3850980	GATCTTCCTGATGAGCTGATACC	GTTCGGCTGCCCTTGAG	210
		CREBBP_ex2_4	chr16:3850563-3850731	CCTCTGAGCCAGGGAGATT	TCATGCAGATACCAWGTCCA	169
		CREBBP_ex2_5	chr16:3850482-3850635	CAAGCACAAAAGCAAGTGG	GCCCTTGTGAAGCCTGATTA	154
		CREBBP_ex2_6	chr16:3850364-3850541	ACCCAGGCCTCCTCAATAGT	GTTAGGGTCTCAGCCAGCA	178
		CREBBP_ex2_7	chr16:3850232-3850441	AGGAAGGGGAGCTGGAATG	CGCATTACTCGGAGGGAAA	210
	Exon 5	CREBBP_ex5_1	chr16:3791991-3792245	CAGCCTGTTTGTAAGTTGAGGA	TCGCTTGTCACTGGCATTT	200
		CREBBP_ex5_2	chr16:3791870-3792062	TCTCATTGGAAGAACTGCACA	CTGCACTCCATGGCTCATAA	193
	Exon 6	CREBBP_ex6_1	chr16:3782813-3782995	AAATCATTCGTGGGCYTCTC	GCATGGAGCTGGGGTCTAT	183
		CREBBP_ex6_2	chr16:3782693-3782887	TTGGTTCTGTTGGCACAGG	TGAGAGTCCTCATCTGCTGGT	195
		CREBBP_ex6_3	chr16:3782618-3782806	CCTATGCTGCTCTCGGACTC	CCATCACTCCATTCCCTTTG	189
	Exon 8	CREBBP_ex8	chr16:3780701-3780906	GGATGAAGTGTCTTTATTTCCTCCT	ACATCTATGAAACTGCAAAACTGTTAC	206
	Exon 12	CREBBP_ex12_1	chr16:3774592-3774758	GCAAGTTGTAATTCTGTTTTCCTG	TCATCTGGACAGAGTGGTTCA	167
		CREBBP_ex12_2	chr16:3774521-3774673	ATGTCCTTGGGGAACGTC	CATGTGAGAGGGAGGGCTA	153
	Exon 16	CREBBP_ex16_1	chr16:3767820-3768012	GGTTTTAACAAACCTGTTTTAGGC	TTCATCCACTTCCATTGGTTC	193
		CREBBP_ex16_2	chr16:3767734-3767904	GGAGGAGGATTTGCAAGGA	TGCGAAGGAGATGTTGACTG	171
		CREBBP_ex16_3	chr16:3767680-3767867	GAAACAGACATAGCAGAGCAGAAA	AAGCAGCATGCTTTAATAAGGTAA	188
	Exon 17	CREBBP_ex17_1	chr16:3758853-3759001	AGTGTCTTTTCTTGATGTTTTCTCTG	CTGGAATTCCGAGGAGCTG	149
		CREBBP_ex17_2	chr16:3758782-3758944	CCTCATGCCAACCCTAGAAG	CAAGAGATAAAACAATGGACACTCA	163
	Exon 18	CREBBP_ex18_1	chr16:3757941-3758115	GCCAGATGAGACTGGCATTT	GAGCCAGACGTCGTCCAC	175
		CREBBP_ex18_2	chr16:3757820-3758006	ATCAAGCGGAAGCTGGAC	AGCAATATCCAAGGGACTGC	187

		CREBBP_ex18_3	chr16:3757702-3757888	TTTGCAGTAAGCTTGCAGAGG	TGCACATATGCACTCCCAGT	187
	Exon 20	CREBBP_ex20	chr16:3751676-3751836	TTCACCCAAGTATGGCCTTC	TTTAAGGTCACCCTCCCTCA	161
	Exon 23	CREBBP_ex23	chr16:3744817-3744991	CAGTCTYATCATACCRCTATTATTTTGC	CCAAAGAACAATGGGGACAA	175
	Exon 24	CREBBP_ex24_1	chr16:3740416-3740575	TCACCTRCTCCTTCTGGACT	CTTGACCTCCACCYTCTTGT	160
		CREBBP_ex24_2	chr16:3740318-3740489	GCCAGAATCACCCTGAAGC	CAAGAGCTTTGCAGAGAGCA	172
	Exon 26	CREBBP_ex26	chr16:3738531-3738702	CTGAGTTAAACATGTGCCTCCTT	AGTTCCAAATAATTTAATCCAAACTCA	172
	Exon 27	CREBBP_ex27_1	chr16:3736654-3736835	TGTGTGCGTGGGTCCTG	TAGTCATGGATGATCCGCTCT	182
		CREBBP_ex27_2	chr16:3736598-3736757	CATTGCCACCCACCTGAT	ATCCTCCCCTCAGTTGTGAC	160
	Exon 28	CREBBP_ex28_1	chr16:3736116-3736316	ATGGGACTCTGCCACACC	CTAACACATTGGGCCAGAAAT	201
		CREBBP_ex28_2	chr16:3736008-3736190	AAGCAACTGAAGACAGGCTCA	GCAATGGAGCTCAGAGAAGG	183
	Exon 29	CREBBP_ex29_1	chr16:3731810-3731973	ACTTGCCTGGTCTCACAGC	TGGGACAGGTCATTGGACA	164
		CREBBP_ex29_2	chr16:3731679-3731883	AAGAACAAAAGCAGCATCAGC	CCACCACAGACCTGCACAC	205
	Exon 30	CREBBP_ex30_1	chr16:3731376-3731577	AGCCACCTGCCTATTCTGC	CCATCCATGAGGTCACAGC	202
		CREBBP_ex30_2	chr16:3731276-3731477	GCAGGTCTTCTTCGTGATCC	GTGCAGCTCCACCAGCAT	202
		CREBBP_ex30_3	chr16:3731183-3731360	CACCCTMGCCAGAGACAA	AGGGCCTACCTCYCACAC	178
		CREBBP_ex30_4	chr16:3731076-3731243	CAACGAGTGCAAGCACCA	GAGTCAGTGCAGCCACCAT	168
EP300	Exon 2	EP300_ex2_1	chr22:41117106-41117290	TGCTTATTGAGAACAATATAGAGCAGT	TGTCTGAAGCTGATTAATATCACCAC	185
		EP300_ex2_2	chr22:41117209-41117389	GGAGCACGACTTACCAGATGA	GCCACCAACTCCCATATTGA	181
		EP300_ex2_3	chr22:41117321-41117520	AAACATAAACAGCTGTCAGAATTGC	GGTCCACTAGTGCCCATCC	200
		EP300_ex2_4	chr22:41117428-41117580	TCCTGGATTAGGTTTGATAAATAGC	ATGGCAGGCTGATTTACTGG	153
		EP300_ex2_5	chr22:41117482-41117659	CTTGACTTCTCCCAACATGG	ATTAGGCATTATCCCTTGTCCA	178
		EP300_ex2_6	chr22:41117585-41117768	ATGAACACAGGGATGAATGC	CCTGCTGAAGAGGCTCAGTC	184
		EP300_ex2_7	chr22:41117698-41117889	ACAGAATATGCAGTACCCAAACC	ACCCTCCATCCATCATGACA	192
	Exon 5	EP300_ex5_1	chr22:41129807-41129999	CTTATTAAGTGGTCAACAAGTTAGCTATT	TTGATTTCTCTTATCACCAGCATT	193
		EP300_ex5_2	chr22:41129926-41130115	ACTGGAAGAATTGTACAAGACATGA	TTCAACATAGTACAACACCACAGG	190
	Exon 6	EP300_ex6_1	chr22:41131292-41131488	CGTAACAATAATTTTGTGGGGTTT	GGGATCAATCTGACTAACAGTGC	197
		EP300_ex6_2	chr22:41131411-41131581	GGACTTGGAAATCCTAGCTCTCT	CTGCTGGTTCTTTGCTTGC	171
		EP300_ex6_3	chr22:41131508-41131683	ATGCAGCTCTTGGACTACCC	TCATTTACTRACACAACCAATACCA	176
	Exon 9	EP300_ex9_1	chr22:41140093-41140242	ATTAAATGCTGACATGATATTACAGTGG	TTCATACATGTCCCCTTCAACTT	150
		EP300_ex9_2	chr22:41140173-41140364	TGCTTTAAAAGACAGACGGATG	GTGTCCYCCGTCTGAAGC	192
	Exon 14	EP300_ex14_1	chr22:41149656-41149849	CTTTGTTTAATCAGTTTGTGTCCTAAA	GGAAGCTGGGGACAGTGAAT	194
		EP300_ex14_2	chr22:41149761-41149940	GCACAAATGTCTAGTTCTTCCTG	CTGCTGAGCCCCTATGCTT	180
		EP300_ex14_3	chr22:41149855-41150030	CAGCTCTTCATCAGAATTCACC	CCTTGGAGGGGGATGTAGAG	176

		EP300_ex14_4	chr22:41149961-41150131	AGCCCCTGTTCCTACACCTC	TGTGSGCRAGGCTGCTG	171
		EP300_ex14_5	chr22:41150077-41150274	CTTCACTTCCTGCTGCACCT	ATGGAAATGGCCCAGAAGTA	198
	Exon 27	EP300_ex27_1	chr22:41170331-41170516	ACTTGTGGTTTAAAATGTAGCCTTC	CATTCCTGCAGTCGCTTG	186
		EP300_ex27_2	chr22:41170406-41170614	TTACACAACAGGGCATATTTGG	TCCAGATCTAYTGTCAGCACCT	209
	Exon 28	EP300_ex28_1	chr22:41172436-41172633	TCTGTATAATCAATGKTTTAAAAGAACATA	TCGTTTTCTCTCTTCTTCCTCCT	198
		EP300_ex28_2	chr22:41172563-41172760	GTGATTTCTGGCCCAATGTT	CCTGAAAGCTTTAAAACCCAAT	198
	Exon 29	EP300_ex29_1	chr22:41173497-41173701	GCTAGTAAAATAAGTTACAGGCATAAGATT	CCCTACTCAGGCTGCTCTTATT	205
		EP300_ex29_2	chr22:41173630-41173839	AGGGAGACAGCAAAAATGCTAA	ATGCCTGGCCAGAAATCTT	210
	Exon 30	EP300_ex30_1	chr22:41176143-41176325	CCAGGAGGCAGAGGTTGTAGT	GGATGAGAGGATCAGGATCAA	183
		EP300_ex30_2	chr22:41176241-41176419	TTTCAGGTCTTCTTTGTGATCC	GTGGACCACTGGGCTCTTC	179
		EP300_ex30_3	chr22:41176327-41176521	CTGCGATCTGATGGATGGT	ACAGTACAGTGCCAGCGTGT	195
		EP300_ex30_4	chr22:41176442-41176622	CACACGCAGAGCCAGGAC	GCATCCCACAGGCCTCTAT	181
EZH2	Exon 12	EZH2_ex12	chr7:148816603-148816799	TGTGACTGTGCCTCTTGTCAG	CCAACAACAGCCCTTAGGAA	197
	Exon 16	EZH2_ex16_1	chr7:148811614-148811815	CAGTGATAGCTTTTGTTTTCATTCTG	CAGTGCCTTACCTCTCCACAG	202
		EZH2_ex16_2	chr7:148811527-148811717	CTATTGCTGGCACCATCTGA	TCCAATCAAACCCACAGACTT	191
	Exon 18	EZH2_ex18	chr7:148809249-148809422	TCACTGGGCTGTGCTTACTTT	TTCAAGTCCATCATCACAGGA	174
KDM2B	Exon 4	KDM2B_ex4_1	chr12:121574541-121574697	GGGAAAGGATCTCTCTTGGAA	ACTTACCCACTAGGAGTTTGACG	157
		KDM2B_ex4_2	chr12:121574465-121574608	CTCCTCTTTCCCCAGGATG	GTCTAAATGGGCAGGTGGTG	144
	Exon 9	KDM2B_ex9_1	chr12:121521020-121521216	CTCTTCTCCACTCCCTGCAC	GCATGGGCACGTTAAAGC	197
		KDM2B_ex9_2	chr12:121520905-121521110	CCCACCCCAGGTTGGAT	TATGACCTGTCCCACACACC	206
	Exon 14	KDM2B_ex14	chr12:121445247-121445437	GTTCTCCCTGGCTCCTCAG	CACCACCTGTCCCCACTG	191
	Exon 23	KDM2B_ex23_1	chr12:121430319-121430507	TGGCCTTCACACCTCACAT	ACTTGCCCAAACTGGACACT	189
		KDM2B_ex23_2	chr12:121430262-121430435	CTTCAAACGCTGTGGAAACA	CCCGTATTTACATACTTATCCTTGG	174
MEF2B	Exon 3	MEF2B_ex3_1	chr19:19149332-19149528	GCATGTTCGAGGAAGGGTTA	GCGCTGTTGAAGATGATGAG	197
		MEF2B_ex3_2	chr19:19149207-19149411	AAGTTCGGGCTGATGAAGAA	GGAGGAGGACCTGGGGTA	205
	Exon 4	MEF2B_ex4	chr19:19147679-19147869	GGGTAAGGGTCTACCCTGTTGT	GGGCCAGGGAGTCACTT	191
	Exon 5	MEF2B_ex5	chr19:19146993-19147204	CCATCCCTTCTCTACCCACA	AGCCCCTCAGGACCTCAC	212
	Exon 6	MEF2B_ex6	chr19:19146709-19146916	GGCCTGCCTGTCCTCTCT	TCATCAGCCCTGCCACAC	208
	Exon 7	MEF2B_ex7	chr19:19146478-19146690	GGGTGTGGGCCTCAGTTT	GTGGGAGGGTGTGGAACC	213
	Exon 5	MLL2_ex5_1	chr12:49054026-49054202	TGCCTGAACTGTTTGTCTGG	TTTTCATGGATAGGAAGGAACC	177
		MLL2_ex5_2	chr12:49053923-49054091	CTGGATGTCCACGGCTTTAC	CCAAGGCACATTTGGTCTCT	169
	Exon 6	MLL2_ex6_1	chr12:49053551-49053736	ATTCTGTGCCCATGGAGTG	CAGGCCCCGTGATAGTGAT	186
		MLL2_ex6_2	chr12:49053426-49053632	GCTGTGCAGTGTGTGAGG	CCCTAACCTGTGTTGTGCCTA	207

MLL2	Exon 7	MLL2_ex7_1	chr12:49053216-49053412	CAGTCGGAGAAGGCCTGTTA	CCAAGAGTGAGCAGGCAGTT	197
		MLL2_ex7_2	chr12:49053156-49053324	CAGGAAACCTGGGAATGACT	GCTGTAGCAGACACAGTTAGGG	169
	Exon 13	MLL2_ex13_1	chr12:49048678-49048845	CCCAACACCAAAGAGGAAAG	TCTGTGTTGGAGAAGAGAACCA	168
		MLL2_ex13_2	chr12:49048600-49048776	CCATCAGGTTGCTGACATTG	CCTCTCACCAAACACACACATAC	177
	Exon 14	MLL2_ex14	chr12:49047947-49048148	TTGTAGCGTCATAGTAGACTGGATCT	CTTGGGCCCTGAACTCAC	202
	Exon 17	MLL2_ex17	chr12:49046000-49046196	TCCTCCAGTCTCTGTTCTCCA	GGTCCTGTCCCAAAGCAAG	197
	Exon 20	MLL2_ex20	chr12:49044385-49044560	TTCTGATTTGCCTCCATCTCTT	CCCATCCCAGGACCTCAC	176
	Exon 21	MLL2_ex21	chr12:49044135-49044339	AGCGGCTTCTCATCCACA	CCCTGGGTCTCTCTAGCATT	205
	Exon 23	MLL2_ex23_1	chr12:49043650-49043827	CCTGCAGGGCATGAAGAA	GGAGTTCCTTCCTTTCTGAGC	178
		MLL2_ex23_2	chr12:49043574-49043783	GGAAGCCTTCTTTGGGAAG	CCAGCTCCTAAGCCAGAAGA	210
	Exon 25	MLL2_ex25	chr12:49043017-49043228	CCATCCTGGCCTTGACC	CCTCCTCCTTCTCCCATAGAA	212
	Exon 26	MLL2_ex26	chr12:49042717-49042928	TCACCTGAACTTCCCAGTCTT	TCAGACCACTCCCACCTGTA	212
	Exon 32	MLL2_ex32_1	chr12:49039463-49039664	TGATTGGAGTAGRATGGGCTTAT	CGACTCAGCTGCTCAAAGG	202
		MLL2_ex32_2	chr12:49039380-49039540	AGCAGCTGCAGGAGCAGT	AAGGTGGAGCAACCTTCAATA	161
	Exon 33	MLL2_ex33	chr12:49039203-49039395	AAGGTTGCTCCACCTTCATC	GAACCTCCTGGAGCCTCAC	193
	Exon 35	MLL2_ex35	chr12:49034770-49034955	CTTGGTTCTCCCCTCTCCA	GGGAAAGAAAAGGGCCAAC	186
	Exon 36	MLL2_ex36	chr12:49034558-49034753	GGCTCCCCTCCCTACTTGT	TCCTACTCCCACCTGACCAC	196
	Exon 42	MLL2_ex42_2	chr12:49030225-49030432	TGAGTAACCCGCCGACAC	GGTTTGGACTCCAGCTACCA	208
	Exon 44	MLL2_ex44_1	chr12:49029127-49029280	AGTCTGCAGGGCTGTAGCAA	GGCCTGAGCCCAGATGAG	154
		MLL2_ex44_2	chr12:49028984-49029193	CCAGCTTCATCCCCTGAG	AACACTTGGCCGCCTCTC	210
	Exon 46	MLL2_ex46	chr12:49027990-49028199	AGCTCACCTCAGACACTTGG	GCTTCCCTGCCACACTCA	210
	Exon 48	MLL2_ex48_10	chr12:49026190-49026399	ACAGCTGCTGCCTCACCA	GAGGCGTCAGTGAAGACCAG	210
		MLL2_ex48_11	chr12:49026137-49026301	ACAATCRTCGCTGCTGCTAT	ACTTTTCCCATTCCATATTATCCA	165
		MLL2_ex48_2	chr12:49027009-49027213	CTTCCCCCTTGGCACCT	CGCACTCCTTTCCATTTCTT	205
		MLL2_ex48_3	chr12:49026922-49027120	CTCTGCCACTGGCCTCAT	TGCTCCATAAACTCTGCCACT	199
		MLL2_ex48_4	chr12:49026792-49026990	GCTGCTGACCATCCAGAAG	CACCCACAGGTCCAGGTC	199
		MLL2_ex48_5	chr12:49026683-49026866	TTCTGTCATGAGGAGGGTGA	ACAGGGAGCACTTGGTTAGC	184
		MLL2_ex48_6	chr12:49026572-49026772	GGTCCACGGAGGTGTATGAG	GCATGGTCTTGTCCTTGAAGA	201
		MLL2_ex48_7	chr12:49026483-49026667	CCACCAGCAGCTGCAATC	CTCGTCCCGCTCAATGTAGA	185
		MLL2_ex48_8	chr12:49026360-49026569	TGTCCAATGCATAAGATCAAGG	GGCACTATGAAAGTCAGCCATC	210
		MLL2_ex48_9	chr12:49026304-49026464	ATCATTCAGCGGGGAGAAC	GTGCGGAGGCTCCAATAG	161
	Exon 51	MLL2_ex51_1	chr12:49022759-49022920	GGTCTGAGGGAGAGCTGTCTT	CGCCGGTACTGAGATGACTT	162
		MLL2_ex51_2	chr12:49022653-49022843	AGGCATATCAGAGCACCTTCA	CTCGATAACCATTGTGTGCTTT	191

		MLL2_ex51_3	chr12:49022550-49022753	GCACCGAATGGAAGAACAA	GCAGACTATGCACCACAATGG	204
RANK	Exon 2	RANK_E2	chr18:62348143-62348352	TGCCTGACCTCAGTGTTCTTT	CGCGTCTATCCAATTTCTTTT	210
	Exon 3	RANK_E3	chr18:62349782-62349956	GGTTGCATTTTTCTCCCTCA	ACTGACAGGACGGGCTCAC	175
	Exon 4	RANK_E4	chr18:62354360-62354560	TGGCCACTGACCTGTCTCTT	GACAGACGCAMACATCCAAC	201
	Exon 5	RANK_E5	chr18:62358204-62358373	TTTGTTTGTTCTGTCTGGGTTG	CCATCTCTTCTGACTCCTTTGTT	170
	Exon 6	RANK_E6	chr18:62359911-62360091	CAAGCWTATAAAACCAAAGCACTG	CTGGGGCACATCTATCAACC	181
	Exon 7	RANK_E7	chr18:62361611-62361820	GATTTGTTTTTCAAYTGCGTAAA	TTGCAAAAACCACCATAGACA	210
	Exon 8	RANK_E8	chr18:62366674-62366833	CTTGAAGTCCTTATCCTTGCTTT	TGTGACTAGGATGGCTCTACCA	160
	Exon 9	RANK_E9_P1	chr18:62368671-62368870	TGCCTCTGCCTTCTGAATGT	TAGGGACCACCTCCTACACA	200
		RANK_E9_P2	chr18:62368768-62368949	GTGTCTTACTGCTGACTCTGGA	GGGCATCTGTCTGAAGCTGT	182
		RANK_E9_P3	chr18:62368881-62369084	GAAGATGSCAGGATGCTCTC	GCACTGGCTTAAACTGTCATTC	204
		RANK_E9_P4	chr18:62369001-62369168	TTCCTCACTGAGCCTGGAAG	GGACATGGGAGTCCAATCA	168
		RANK_E9_P5	chr18:62369095-62369283	CACAGAGCMCAGTGGGTTCA	CCTCCCCAGGAGGGTTC	189
		RANK_E9_P6	chr18:62369226-62369421	AGCCCCAGCCCCAACT	GGAGCCTCCCATCAGC	196
		RANK_E9_P7	chr18:62369346-62369547	GGCCTTCCCCCTGAAGA	CCCAAACCCTGTACCAAGAA	202
	Exon 10	RANK_E10_P1	chr18:62384671-62384851	CCCCGGAACCTTCCTCT	CTGCGAGGTCTGGCTGA	186
		RANK_E10_P2	chr18:62384761-62384912	TGGAAACAGTAACBCCACGTTC	GCGCCAGGGTCTCCTC	152
		RANK_E10_P4	chr18:62384919-62385074	ACTCCTTCGCSGGGAAC	CCCTGGCTCCGAGCTT	156
TRAF3	Exon 2	TRAF3_E2_P1	chr14:102870109-102870312	CTTTTGCTTTCCCAAAGCTG	TCCTTGTTCAGGGACAAAAAC	204
		TRAF3_E2_P2	chr14:102870206-102870408	AGTCSAGTAAAAAGATGGACTCTC	CCCACACTCGGTCTGCTT	203
		TRAF3_E2_P3	chr14:102870340-102870527	GTGGAGGACAAGTACAAGTGTGA	TTTTTAGAGAAACGAATGAAGGA	188
	Exon 3	TRAF3_E3	chr14:102871869-102872030	CAAGAAAGGGACTTCCACTCTAA	TGTGAAAAGTATTACCCAGCTGAA	162
	Exon 4	TRAF3_E4_P1	chr14:102875548-102875702	TTTGCCTTGTCCAAAGTAGC	CTGCACAACCTCTGCTTTC	155
		TRAF3_E4_P2	chr14:102875632-102875817	GGATAATTGCTGCAAGAGAGAAA	TGCCACATCCTACTGACCAC	186
	Exon 5	TRAF3_E5_P1	chr14:102876261-102876460	CATTTCTTTAGGGTTTCATTGC	CCTTCTCCACGTGGTCTCG	200
		TRAF3_E5_P2	chr14:102876367-102876549	AAAAATGATTGCCATTTTGAAG	CCTGYGGAATGGGAGGAC	183
	Exon 6	TRAF3_E6	chr14:102886131-102886321	GGGACTGAAGGAAGACAGGTT	CACGCARCCCTGAGGA	191
	Exon 7	TRAF3_E7	chr14:102889529-102889728	TGCCACAACTCACGTCTCTT	GGAGTCCAGAGCTTGCATGT	156
	Exon 8	TRAF3_E8	chr14:102891297-102891448	TGAATGCCTCACATGTTTGC	TCCCATAGCAGCAGGAAAG	152
	Exon 9	TRAF3_E9_P1	chr14:102897162-102897365	GCTAACAGAAGGCCTATATTGTGAA	CATTTCCTTTTGTCTCTCAATTTC	204
		TRAF3_E9_P2	chr14:102897264-102897447	TCCTTGTTGCAGAATGAAAGTG	CAAGCTCCTCCACCCTTTG	184
	Exon 10	TRAF3_E10_P1	chr14:102903228-102903429	TGCTTTTTAACACCTTTGGTTTG	CTGTGTTCCGAGCCACTTG	202
		TRAF3_E10_P2	chr14:102903333-102903524	GCAGACAGCATGAAGAGCAG	TGTACCTAACATAGCCCTCATCC	192

	Exon 11	TRAF3_E11_P1	chr14:102905182-102905364	TCATTCACCAAACCCTCCTC	CTTCCGCCGCTTGTAGTC	183
		TRAF3_E11_P2	chr14:102905278-102905483	GACATGGACCTGCGCTTC	GTCCCCTTCCCCATCC	206
		TRAF3_E11_P3	chr14:102905402-102905584	GCCAGCCTTTCTACACTGGT	ACCCCTGATCCATCAGCAT	183
		TRAF3_E11_P4	chr14:102905502-102905702	TGTCATCATGCGTGGAGAAT	ACAGTTTGGGCCACAAAGAC	201
		TRAF3_E11_P5	chr14:102905634-102905827	CAGCTTCAAGAAGCCCACTG	CAGAGGAGTTGCCTTCTGCT	194

The CS1 tag (ACACTGACGACATGGTTCTACA) was added to the 5' of the forward primer and the CS2 tag (TACGGTAGCAGAGACTTGGTCT) was added to the 5' of the reverse primer and used for barcoding.

Fluidigm PCR conditions

95°C 15 sec, 80°C 30 sec, 60°C 30 sec, 72°C 1 min, 8 cycles of 95°C 15 sec, 60°C 30 sec, 72°C 1 min, and 5 cycles of 95°C 15 sec, 80°C 30 sec, 60°C 30 sec, 72°C 1 min

Supplementary Table S3: Immunoglobulin heavy chain rearrangements in MALT lymphomas

Sample	IGHV	Homology	IGHJ	IGHD
M_CU_001	IGHV1-18	96.02%	IGHJ2	IGHD2-8
M_GA_012	IGHV1-18	82.70%	IGHJ3	IGHD2-21
M_GB_001	IGHV1-2	98.10%	-	-
M_SA_001	IGHV1-46	97.83%	-	-
WES_SA14	IGHV1-69	96.84%	IGHJ4	IGHD5-24
M_SA_002	IGHV1-69	88.44%	IGHJ4	IGHD5-24
M_SA_006	IGHV1-69	88.24%	IGHJ4	IGHD4-11
M_SA_010	IGHV1-69	99.44%	IGHJ4	IGHD5-24
M_SA_018	IGHV1-69	96.08%	IGHJ2	-
M_SA_021	IGHV1-69	96.65%	IGHJ4	IGHD3-10
M_SA_045	IGHV1-69	96.55%	-	-
M_SA_046	IGHV1-69	91.33%	IGHJ4	IGHD3-22
WES_SA3	IGHV1-69	95.92%	IGHJ4	IGHD3-10
WES_SA5	IGHV1-69	95.45%	-	-
WES_SA6	IGHV1-69	91.02%	IGHJ4	IGHD4-11
M_TO_001	IGHV1-69	90.81%	IGHJ4	IGHD2-21
M_OA_009	IGHV2-26	87.13%	IGHJ6	IGHD4-23
M_OA_094	IGHV2-5	95.05%	IGHJ5	IGHD3-9
M_OA_056	IGHV2-70	100%	IGHJ4	IGHD5-24
M_OA_006	IGHV3-11	92.35%	-	-
M_OA_085	IGHV3-11	90.31%	IGHJ3	IGHD1-1
M_GA_009	IGHV3-15	98.43%	IGHJ4	IGHD6-6
M_SA_007	IGHV3-15	96.07%	IGHJ4	IGHD3-3
M_LU_002	IGHV3-21	98.37%	IGHJ6	IGHD1-26
M_OA_016	IGHV3-21	98.91%	IGHJ6	IGHD3-3
M_OA_007	IGHV3-23	91.30%	IGHJ5	IGHD4-11
M_OA_020	IGHV3-23	93.29%	IGHJ4	IGHD1-14
M_OA_027	IGHV3-23	93.41%	IGHJ4	IGHD1-14
M_OA_043	IGHV3-23	94.35%	IGHJ4	IGHD3-16
M_OA_045	IGHV3-23	89.18%	IGHJ4	IGHD3-10
M_OA_048	IGHV3-23	92.81%	IGHJ6	IGHD6-6
M_OA_054	IGHV3-23	92.21%	IGHJ4	IGHD1-14
M_OA_061	IGHV3-23	92.31%	IGHJ4	IGHD1-14
M_OA_066	IGHV3-23	91.53%	IGHJ4	IGHD2-15
M_OA_081	IGHV3-23	93.41%	IGHJ4	IGHD3-10
M_OA_082	IGHV3-23	93.91%	IGHJ4	IGHD3-16
M_OA_083	IGHV3-30	91.50%	IGHJ4	IGHD2-15
M_OA_093	IGHV3-30	92.83%	IGHJ4	IGHD5-18
M_SA_035	IGHV3-30	82.51%	-	-
M_GA_025	IGHV3-30	96.47%	-	-
M_OA_049	IGHV3-30	87.50%	IGHJ6	IGHD5-18
M_OA_078	IGHV3-30	86.81%	-	-
M_OA_079	IGHV3-30-3	94.78%	IGHJ4	IGHD3-10
M_LU_025	IGHV3-33	94.90%	IGHJ4	IGHD2-15
M_OA_050	IGHV3-33	87.10%	IGHJ3	IGHD5-24
M_OA_069	IGHV3-33	90.53%	-	-
M_OA_004	IGHV3-43	93.98%	IGHJ5	IGHD2-21

M_GA_027	IGHV3-48	94.74%	-	-
M_OA_026	IGHV3-48	93.94%	-	-
M_OA_055	IGHV3-48	94.02%	IGHJ4	IGHD3-3
M_OA_098	IGHV3-48	97.58%	IGHJ6	IGHD4-17
M_SA_050	IGHV3-48	94.08%	-	-
M_OA_099	IGHV3-53	94.72%	IGHJ5	IGHD4-23
M_CU_005	IGHV3-7	89.01%	-	-
M_OA_015	IGHV3-7	89.16%	IGHJ5	IGHD1-14
M_OA_051	IGHV3-7	83.51%	-	-
M_OA_058	IGHV3-7	92.16%	-	-
M_OA_059	IGHV3-7	94.04%	IGHJ6	IGHD6-19
M_OA_097	IGHV3-7	94.42%	IGHJ6	IGHD6-13
M_SA_012	IGHV3-7	97.02%	IGHJ3	IGHD3-22
M_SA_038	IGHV3-7	96.15%	IGHJ3	IGHD3-22
M_OA_030	IGHV3-73	96.06%	-	-
M_LU_003	IGHV3-74	93.98%	IGHJ6	IGHD5-18
M_LU_029	IGHV3-74	93.26%	-	-
M_OA_041	IGHV3-74	95.97%	IGHJ4	IGHD3-3
M_OA_057	IGHV3-74	94.76%	IGHJ4	IGHD1-14
M_OA_102	IGHV3-74	91.94%	IGHJ3	IGHD6-13
M_GA_019	IGHV3-9	94.89%	IGHJ5	IGHD4-11
M_OA_053	IGHV3-9	93.90%	-	-
M_OA_003	IGHV4-31	94.95%	IGHJ5	IGHD2-15
M_OA_100	IGHV4-31	93.23%	IGHJ6	IGHD2-21
M_GA_010	IGHV4-34	95.10%	IGHJ4	IGHD6-13
M_GA_011	IGHV4-34	77.55%	IGHJ6	IGHD3-22
M_GA_017	IGHV4-34	95.03%	IGHJ4	IGHD5-18
M_OA_017	IGHV4-34	100%	-	-
M_OA_019	IGHV4-34	94.74%	IGHJ5	IGHD2-15
M_OA_029	IGHV4-34	83.33%	IGHJ4	IGHD4-17
M_OA_044	IGHV4-34	93.20%	IGHJ3	-
M_OA_047	IGHV4-34	91.27%	IGHJ4	IGHD3-22
M_OA_052	IGHV4-34	94.69%	IGHJ6	IGHD3-9
M_OA_062	IGHV4-34	88.66%	-	-
M_OA_070	IGHV4-34	98.91%	-	-
M_OA_086	IGHV4-34	96.45%	IGHJ5	IGHD6-6
M_OA_088	IGHV4-34	96.67%	IGHJ6	IGHD3-3
WES_TH1	IGHV4-34	83.82%	IGHJ6	IGHD5-12
M_LU_004	IGHV4-38-2	91.67%	IGHJ1	IGHD6-13
WES_TH5	IGHV4-39	88.89%	-	-
M_OA_025	IGHV4-39	91.11%	-	-
M_SI_008	IGHV4-39	97.22%	-	-
M_OA_010	IGHV4-4	89.46%	IGHJ5	IGHD1-20
M_OA_040	IGHV4-4	87.22%	-	-
M_OA_091	IGHV4-4	86.11%	-	-
M_OA_012	IGHV4-59	84.52%	IGHJ3	IGHD3-3
M_OA_068	IGHV4-61	94.08%	IGHJ4	IGHD3-10
M_OA_076	IGHV4-61	93.10%	IGHJ3	IGHD1-26
M_OA_090	IGHV5-10-1	96.50%	IGHJ4	IGHD3-3
M_OA_095	IGHV5-10-1	95.16%	IGHJ5	IGHD3-16

M_OA_024	IGHV6-1	94.98%	IGHJ5	IGHD6-19
WES_SA13	IGHV7-4-1	97.27%	-	-
M_OA_071	IGHV7-4-1	93.24%	-	-
M_OA_075	IGHV7-4-1	90.30%	-	-

Supplementary Table S4: Performance data of whole exome sequencing.

Sample	Total Reads (PE)	Total Bases (Gb)	Unmapped reads(%)	Mapped (Gb)	Mapped Reads (%)	Unique mapped (Gb)	Unique mapped Reads (%)	Coverage >10 reads (%)	Coverage >30 reads (%)
WES_SA1_Tumour	47294129	7.09	9.85	6.37	89.78	5.73	90.01	87.93	72.89
WES_SA2_Tumour	62714816	9.41	9.61	8.47	90.01	7.41	87.48	89.44	77.98
WES_SA3_Tumour	79725004	11.96	10.14	10.69	89.41	9.17	85.79	90.41	80.89
WES_SA4_Tumour	67265526	10.09	10.14	9.00	89.19	7.70	85.55	89.08	78.06
WES_SA5_Tumour	70018173	10.50	10.47	9.33	88.88	8.21	87.96	89.06	78.24
WES_SA6_Tumour	65828315	9.87	9.27	8.92	90.32	7.77	87.17	87.89	75.45
WES_SA7_Tumour	20098097	3.01	3.21	2.89	95.87	2.53	87.54	87.59	66.36
WES_SA8_Tumour	29339146	4.40	2.31	4.27	97.08	3.77	88.16	91.88	77.96
WES_SA9_Tumour	27527009	4.13	3.13	3.96	95.97	3.46	87.26	91.32	77.01
WES_SA10_Tumour	14736256	2.21	6.87	1.93	87.47	1.71	88.27	74.66	31.62
WES_SA11_Tumour	17685306	2.65	4.30	2.46	92.78	2.18	88.42	86.44	58.61
WES_SA12_Tumour	32079599	4.81	2.77	4.64	96.47	4.13	89.00	92.81	80.69
WES_SA13_Tumour	34163373	5.12	2.58	4.96	96.78	4.37	88.08	93.05	81.4
WES_TH1_Tumour	54496948	8.17	11.12	7.20	88.12	4.66	64.76	85.67	68.88
WES_TH1_Normal	62988730	9.45	9.92	8.46	89.57	6.89	81.36	89.02	77.38
WES_TH2_Tumour	56827985	8.52	14.91	6.63	77.81	4.19	63.11	83.43	63.00
WES_TH3_Tumour	24526288	3.68	4.07	3.50	95.18	3.07	87.63	90.03	73.04
WES_TH4_Tumour	37822356	5.67	2.91	5.47	96.42	4.94	90.22	93.63	82.89
WES_TH5_Tumour	34810481	5.22	2.87	5.04	96.48	4.49	89.09	93.23	81.98
WES_TH6_Tumour	33647078	5.05	2.92	4.87	96.43	4.37	89.77	93.28	81.31

* Parameters for WES_SA14 and WES_TH7 are unavailable due to the closure of the sequencing centre

Supplementary Table S5: A shortlist of potential pathogenic variants identified by WES, which were confirmed as somatic changes.

Sample	Position	Ref	Alt	Type	Gene	Exon	Transcript	Protein	cDNA change	Amino Acids change	AAF
WES_TH1	4:105235860	-	A	frameshift insertion	TET2	exon3	NM_001127208	NP_001120680	c.1919_1920insA	p.Q640fs	0.11
WES_TH7	4:105236227	-	C	frameshift insertion	TET2	exon3	NM_001127208	NP_001120680	c.2286_2287insC	p.H762fs	0.19
WES_TH3	4:105237285	C	-	frameshift deletion	TET2	exon3	NM_001127208	NP_001120680	c.3343delC	p.P1115fs	0.23
WES_SA4	4:105243760	G	C	nonsynonymous SNV	TET2	exon6	NM_001127208	NP_001120680	c.3785G>C	p.R1262P	0.41
WES_TH7	4:105261790	T	C	nonsynonymous SNV	TET2	exon8	NM_001127208	NP_001120680	c.3986T>C	p.L1329P	0.18
WES_TH3	4:105275764	A	-	frameshift deletion	TET2	exon11	NM_001127208	NP_001120680	c.5254delA	p.K1752fs	0.27
WES_SA12	3:177038113	G	C	nonsynonymous SNV	TBL1XR1	exon12	NM_024665	NP_078941	c.1107C>G	p.D369E	0.33
WES_SA8	3:177050011	A	G	nonsynonymous SNV	TBL1XR1	exon7	NM_024665	NP_078941	c.688T>C	p.S230P	0.17
WES_SA13	3:177051506	GC	-	frameshift deletion	TBL1XR1	exon5	NM_024665	NP_078941	c.424_425del	p.A142fs	0.29
WES_SA12	X:41696085	A	C	nonsynonymous SNV	GPR34	exon3	NM_001097579	NP_001091048	c.452A>C	p.D151A	0.44
WES_SA13	X:41696672	C	T	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1039C>T	p.Q347X	0.14
WES_SA8	X:41696693	G	T	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1060G>T	p.E354X	0.18
WES_TH3	1:9723235	C	T	nonsynonymous SNV	PIK3CD	exon20	NM_005026	NP_005017	c.2537C>T	p.A846V	0.22
WES_SA5	1:9726972	G	A	nonsynonymous SNV	PIK3CD	exon24	NM_005026	NP_005017	c.3061G>A	p.E1021K	0.24
WES_TH3	6:167137238	T	A	stopgain	CCR6	exon3	NM_004367	NP_004358	c.1008T>A	p.C336X	0.24
WES_SA2	6:167137261	C	G	stopgain	CCR6	exon3	NM_004367	NP_004358	c.1031C>G	p.S344X	0.24
WES_TH7	1:2556700	G	A	stopgain	TNFRSF14	exon1	NM_003820	NP_003811	c.36G>A	p.W12X	0.25
WES_TH3	1:2558376	-	G	frameshift insertion	TNFRSF14	exon3	NM_003820	NP_003811	c.213_214insG	p.T71fs	0.15
WES_SA3	9:136496197	AG	-	frameshift deletion	NOTCH1	exon34	NM_017617	NP_060087	c.7541_7542del	p.P2514fs	0.53
WES_TH1	8:42306376	A	G	nonsynonymous SNV	IKBKB	exon7	NM_001556	NP_001547	c.511A>G	p.K171E	0.26
WES_SA12	4:1801838	G	A	nonsynonymous SNV	FGFR3	exon7	NM_000142	NP_000133	c.743G>A	p.R248H	0.18
WES_TH7	13:40560724	G	A	nonsynonymous SNV	FOXO1	exon2	NM_002015	NP_002006	c.767C>T	p.S256F	0.21

Supplementary Table S6: Variants detected in novel genes by Fluidigm Access Array and Illumina MiSeq sequencing

Sample	Position	Type	Gene	Exon	Transcript	Protein	cDNA change	Amino acid change	AAF	Somatic Status	PolyPhen2	COSMIC
M_OA_061	6:167136707	nonsynonymous SNV	CCR6	exon3	NM_004367	NP_004358	c.477A>C	p.R159S	0.44	Unknown	0.11 / benign	-
M_SA_045	6:167137235	stopgain	CCR6	exon3	NM_004367	NP_004358	c.1005G>A	p.W335X	0.16	Previously Reported	-	COSM3860401
WES_TH3	6:167137238	stopgain	CCR6	exon3	NM_004367	NP_004358	c.1008T>A	p.C336X	0.24	Somatic	-	-
M_SA_059	6:167137252	frameshift insertion	CCR6	exon3	NM_004367	NP_004358	c.1023_1024insC	p.Y341fs	0.11	Somatic	-	-
WES_SA2	6:167137261	stopgain	CCR6	exon3	NM_004367	NP_004358	c.1031C>G	p.S344X	0.24	Somatic	-	-
M_GA_044	6:167137285	nonsynonymous SNV	CCR6	exon3	NM_004367	NP_004358	c.1055A>G	p.Y352C	0.30	Unknown	0.81 / possibly damaging	-
M_GA_018	6:167137299	frameshift deletion	CCR6	exon3	NM_004367	NP_004358	c.1069_1070del	p.S357fs	0.32	Somatic	-	-
WES_SA12	4:1801838	nonsynonymous SNV	FGFR3	exon7	NM_000142	NP_000133	c.743G>A	p.R248H	0.18	Somatic	1 / probably damaging	COSM1757310
M_OA_082	4:1801863	nonsynonymous SNV	FGFR3	exon7	NM_000142	NP_000133	c.768G>T	p.Q256H	0.48	Unknown	0.99 / probably damaging	-
M_SA_030	4:1804395	nonsynonymous SNV	FGFR3	exon9	NM_000142	NP_000133	c.1141G>A	p.V381M	0.11	Unknown	0.89 / possibly damaging	-
M_SA_015	4:1804435	nonsynonymous SNV	FGFR3	exon9	NM_000142	NP_000133	c.1181C>T	p.T394M	0.30	Somatic	0.22 / benign	-
M_GA_018	13:40560529	nonsynonymous SNV	FOXO1	exon2	NM_002015	NP_002006	c.962C>T	p.A321V	0.19	Somatic	1 / probably damaging	-
WES_TH7	13:40560724	nonsynonymous SNV	FOXO1	exon2	NM_002015	NP_002006	c.767C>T	p.S256F	0.21	Somatic	1 / probably damaging	-
M_OA_003	X:41695884	nonsynonymous SNV	GPR34	exon3	NM_001097579	NP_001091048	c.251G>A	p.R84H	0.18	Previously Reported	0.94 / possibly damaging	COSM275353
WES_SA12	X:41696085	nonsynonymous SNV	GPR34	exon3	NM_001097579	NP_001091048	c.452A>C	p.D151A	0.44	Somatic	1 / probably damaging	-
M_SA_063	X:41696612	nonsynonymous SNV	GPR34	exon3	NM_001097579	NP_001091048	c.979T>A	p.Y327N	0.43	Somatic	1 / probably damaging	-
M_SA_054	X:41696651	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1018C>T	p.Q340X	0.27	Unknown	-	-
M_SA_008	X:41696666	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1033C>T	p.R345X	0.18	Somatic	-	-
M_SA_013	X:41696672	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1039C>T	p.Q347X	0.21	Previously Reported	-	-
M_SA_060	X:41696672	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1039C>T	p.Q347X	0.14	Previously Reported	-	-
WES_SA13	X:41696672	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1039C>T	p.Q347X	0.14	Somatic	-	-
M_SA_021	X:41696681	frameshift insertion	GPR34	exon3	NM_001097579	NP_001091048	c.1047_1048dupC	p.E349fs	0.07	Unknown	-	-
WES_SA8	X:41696693	stopgain	GPR34	exon3	NM_001097579	NP_001091048	c.1060G>T	p.E354X	0.18	Somatic	-	-
WES_TH1	8:42306376	nonsynonymous SNV	IKBKB	exon7	NM_001556	NP_001547	c.511A>G	p.K171E	0.26	Somatic	1 / probably damaging	COSM4944023
M_GA_040	9:136496197	frameshift deletion	NOTCH1	exon34	NM_017617	NP_060087	c.7541_7542del	p.P2514fs	0.31	Previously Reported	-	COSM12774
M_GA_045	9:136496197	frameshift deletion	NOTCH1	exon34	NM_017617	NP_060087	c.7541_7542del	p.P2514fs	0.42	Previously Reported	-	COSM12774
WES_SA11	9:136496197	frameshift deletion	NOTCH1	exon34	NM_017617	NP_060087	c.7541_7542del	p.P2514fs	0.29	Somatic	-	COSM12774
WES_SA3	9:136496197	frameshift deletion	NOTCH1	exon34	NM_017617	NP_060087	c.7541_7542del	p.P2514fs	0.53	Somatic	-	COSM12774
M_OA_007	9:136496489	nonsynonymous SNV	NOTCH1	exon34	NM_017617	NP_060087	c.7250C>G	p.P2417R	0.34	Unknown	0.67 / possibly damaging	-
M_GA_034	9:136496908	frameshift deletion	NOTCH1	exon34	NM_017617	NP_060087	c.6831delT	p.P2277fs	0.16	Unknown	-	-
M_GA_018	9:136497204	nonsynonymous SNV	NOTCH1	exon34	NM_017617	NP_060087	c.6535C>T	p.R2179W	0.13	Somatic	0.99 / probably damaging	-
M_SA_064	9:136497282	nonsynonymous SNV	NOTCH1	exon34	NM_017617	NP_060087	c.6457G>A	p.V2153M	0.12	Somatic	0.01 / benign	-

M_OA_110	9:136497388	nonsynonymous SNV	NOTCH1	exon34	NM_017617	NP_060087	c.6351C>A	p.N2117K	0.27	Unknown	0.65 / possibly damaging	-
M_SA_037	1:9716542	stopgain	PIK3CD	exon6	NM_005026	NP_005017	c.703C>T	p.Q235X	0.14	Unknown	-	-
M_SA_060	1:9716984	nonsynonymous SNV	PIK3CD	exon7	NM_005026	NP_005017	c.806G>A	p.G269E	0.20	Unknown	0.99 / probably damaging	-
M_TH_001	1:9717608	nonsynonymous SNV	PIK3CD	exon8	NM_005026	NP_005017	c.1002C>G	p.N334K	0.26	Unknown	1 / probably damaging	-
M_OA_048	1:9717612	nonsynonymous SNV	PIK3CD	exon8	NM_005026	NP_005017	c.1006G>A	p.D336N	0.38	Unknown	0.98 / probably damaging	-
M_OA_010	1:9720174	nonsynonymous SNV	PIK3CD	exon11	NM_005026	NP_005017	c.1402G>A	p.A468T	0.50	Unknown	0.97 / probably damaging	-
M_OA_061	1:9720228	nonsynonymous SNV	PIK3CD	exon11	NM_005026	NP_005017	c.1456C>T	p.P486S	0.11	Unknown	1 / probably damaging	-
WES_TH3	1:9723235	nonsynonymous SNV	PIK3CD	exon20	NM_005026	NP_005017	c.2537C>T	p.A846V	0.22	Somatic	0.99 / probably damaging	-
M_SA_031	1:9724349	nonsynonymous SNV	PIK3CD	exon22	NM_005026	NP_005017	c.2792C>T	p.P931L	0.16	Somatic	1 / probably damaging	-
M_SA_030	1:9726972	nonsynonymous SNV	PIK3CD	exon24	NM_005026	NP_005017	c.3061G>A	p.E1021K	0.14	Previously Reported	1 / probably damaging	COSM1581454
WES_SA5	1:9726972	nonsynonymous SNV	PIK3CD	exon24	NM_005026	NP_005017	c.3061G>A	p.E1021K	0.24	Somatic	1 / probably damaging	COSM1581454
WES_TH2	1:9727042	nonsynonymous SNV	PIK3CD	exon24	NM_005026	NP_005017	c.3131A>G	p.Q1044R	0.24	Unknown	0.99 / probably damaging	-
M_OA_071	3:177032999	nonsynonymous SNV	TBL1XR1	exon14	NM_024665	NP_078941	c.1388A>T	p.D463V	0.45	Previously Reported	0.96 / probably damaging	COSM5708568
M_SA_062	3:177033050	nonsynonymous SNV	TBL1XR1	exon14	NM_024665	NP_078941	c.1337A>G	p.Y446C	0.28	Somatic	0.94 / possibly damaging	COSM5045122
M_OA_025	3:177033050	nonsynonymous SNV	TBL1XR1	exon14	NM_024665	NP_078941	c.1337A>G	p.Y446C	0.30	Previously Reported	0.94 / possibly damaging	COSM5045122
M_SA_030	3:177033050	nonsynonymous SNV	TBL1XR1	exon14	NM_024665	NP_078941	c.1337A>G	p.Y446C	0.27	Previously Reported	0.94 / possibly damaging	COSM5045122
M_LU_027	3:177033051	nonsynonymous SNV	TBL1XR1	exon14	NM_024665	NP_078941	c.1336T>G	p.Y446D	0.44	Previously Reported	0.99 / probably damaging	COSM5045122
M_SA_012	3:177033121	nonframeshift deletion	TBL1XR1	exon14	NM_024665	NP_078941	c.1264_1266del	p.422_422del	0.17	Somatic	-	-
M_OA_046	3:177034271	nonsynonymous SNV	TBL1XR1	exon13	NM_024665	NP_078941	c.1177G>A	p.E393K	0.67	Unknown	0.99 / probably damaging	-
M_LU_027	3:177038113	nonsynonymous SNV	TBL1XR1	exon12	NM_024665	NP_078941	c.1107C>G	p.D369E	0.41	Previously Reported	0.99 / probably damaging	-
WES_SA12	3:177038113	nonsynonymous SNV	TBL1XR1	exon12	NM_024665	NP_078941	c.1107C>G	p.D369E	0.33	Somatic	0.99 / probably damaging	-
M_SA_008	3:177038113	nonsynonymous SNV	TBL1XR1	exon12	NM_024665	NP_078941	c.1107C>G	p.D369E	0.10	Previously Reported	0.99 / probably damaging	-
M_SA_063	3:177038169	nonsynonymous SNV	TBL1XR1	exon12	NM_024665	NP_078941	c.1051G>A	p.E351K	0.27	Somatic	1 / probably damaging	-
M_GA_044	3:177038316	nonsynonymous SNV	TBL1XR1	exon11	NM_024665	NP_078941	c.1044T>A	p.H348Q	0.17	Unknown	1 / probably damaging	-
M_SA_045	3:177038381	nonframeshift deletion	TBL1XR1	exon11	NM_024665	NP_078941	c.977_979del	p.326_327del	0.15	Unknown	-	-
WES_SA5	3:177038381	nonframeshift deletion	TBL1XR1	exon11	NM_024665	NP_078941	c.977_979del	p.326_327del	0.25	Unknown	-	-
M_SA_054	3:177038425	nonsynonymous SNV	TBL1XR1	exon11	NM_024665	NP_078941	c.935T>C	p.L312S	0.27	Unknown	0.99 / probably damaging	-
M_GA_040	3:177038435	splice site	TBL1XR1	exon11	NM_024665	NP_078941	c.926-1G>T	.	0.24	Previously Reported	-	-
M_SA_065	3:177038435	splice site	TBL1XR1	exon11	NM_024665	NP_078941	c.926-1G>T	.	0.20	Somatic	-	-
M_GA_017	3:177038435	splice site	TBL1XR1	exon11	NM_024665	NP_078941	c.926-1G>C	.	0.29	Somatic	-	COSM5650935
M_OA_043	3:177046134	nonsynonymous SNV	TBL1XR1	exon10	NM_024665	NP_078941	c.920A>G	p.H307R	0.21	Previously Reported	0.99 / probably damaging	COSM5708585
M_CU_008	3:177046138	nonsynonymous SNV	TBL1XR1	exon10	NM_024665	NP_078941	c.916T>G	p.F306L	0.12	Unknown	0.71 / possibly damaging	-
M_SA_033	3:177047501	nonframeshift deletion	TBL1XR1	exon8	NM_024665	NP_078941	c.749_751del	p.250_251del	0.12	Somatic	-	-
M_SA_063	3:177047513	nonsynonymous SNV	TBL1XR1	exon8	NM_024665	NP_078941	c.739G>A	p.G247R	0.21	Previously Reported	1 / probably damaging	COSM1235152
WES_SA8	3:177050011	nonsynonymous SNV	TBL1XR1	exon7	NM_024665	NP_078941	c.688T>C	p.S230P	0.17	Somatic	1 / probably damaging	-
WES_SA13	3:177050115	nonsynonymous SNV	TBL1XR1	exon7	NM_024665	NP_078941	c.584T>A	p.I195K	0.17	Unknown	1 / probably damaging	-

M_SA_007	3:177050136	nonsynonymous SNV	TBL1XR1	exon7	NM_024665	NP_078941	c.563C>T	p.S188F	0.21	Somatic	1 / probably damaging	COSM5414958
M_TO_001	3:177050479	nonsynonymous SNV	TBL1XR1	exon6	NM_024665	NP_078941	c.559G>T	p.G187W	0.18	Somatic	1 / probably damaging	-
M_OA_048	3:177050487	nonframeshift deletion	TBL1XR1	exon6	NM_024665	NP_078941	c.549_551del	p.183_184del	0.40	Unknown	-	-
M_OA_061	3:177050513	nonsynonymous SNV	TBL1XR1	exon6	NM_024665	NP_078941	c.525T>G	p.C175W	0.17	Unknown	1 / probably damaging	-
WES_SA13	3:177051506	frameshift deletion	TBL1XR1	exon5	NM_024665	NP_078941	c.424_425del	p.A142fs	0.29	Somatic	-	-
M_OA_077	3:177051507	stopgain	TBL1XR1	exon5	NM_024665	NP_078941	c.423_424insTA	A142_N143delin	0.57	Unknown	-	-
M_TH_009	4:105234759	stopgain	TET2	exon3	NM_001127208	NP_001120680	c.817C>T	p.Q273X	0.26	Somatic	-	COSM214588
M_OA_065	4:105234771	nonsynonymous SNV	TET2	exon3	NM_001127208	NP_001120680	c.829G>A	p.A277T	0.51	Previously Reported	0.47/ possibly damaging	COSM200502
M_SA_036	4:105235171	nonsynonymous SNV	TET2	exon3	NM_001127208	NP_001120680	c.1229C>T	p.P410L	0.18	Somatic	0.1 / benign	-
M_GA_003	4:105235551	stopgain	TET2	exon3	NM_001127208	NP_001120680	c.1609G>T	p.E537X	0.64	Somatic	-	-
M_OA_014	4:105235570	nonsynonymous SNV	TET2	exon3	NM_001127208	NP_001120680	c.1628G>T	p.G543D	0.51	Unknown	0 / benign	-
M_CU_001	4:105235684	nonsynonymous SNV	TET2	exon3	NM_001127208	NP_001120680	c.1742G>A	p.R581H	0.13	Unknown	0 / benign	-
WES_TH1	4:105235860	frameshift insertion	TET2	exon3	NM_001127208	NP_001120680	c.1919insA	p.Q640fs	0.11	Somatic	-	-
WES_TH7	4:105236227	frameshift insertion	TET2	exon3	NM_001127208	NP_001120680	c.2286insC	p.H762fs	0.19	Somatic	-	-
M_GA_001	4:105236455	frameshift insertion	TET2	exon3	NM_001127208	NP_001120680	c.2513_2514ins16	p.T838fs	0.24	Unknown	-	-
WES_SA10	4:105236703	nonsynonymous SNV	TET2	exon3	NM_001127208	NP_001120680	c.2761A>G	p.I921V	0.35	Unknown	0 / benign	-
M_OA_060	4:105237229	nonsynonymous SNV	TET2	exon3	NM_001127208	NP_001120680	c.3287C>G	p.T1096R	0.26	Unknown	0.99 / probably damaging	-
M_GA_037	4:105237254	frameshift deletion	TET2	exon3	NM_001127208	NP_001120680	c.3312_3313del	p.F1104fs	0.13	Unknown	-	-
WES_TH3	4:105237285	frameshift deletion	TET2	exon3	NM_001127208	NP_001120680	c.3343delC	p.P1115fs	0.23	Somatic	-	COSM1318622
M_TH_007	4:105237295	frameshift deletion	TET2	exon3	NM_001127208	NP_001120680	c.3353_3356del	p.N1118fs	0.58	Unknown	-	-
M_GA_001	4:105243756	nonsynonymous SNV	TET2	exon6	NM_001127208	NP_001120680	c.3781C>A	p.R1261S	0.28	Previously Reported	1 / probably damaging	COSM4170060
M_SA_060	4:105243759	nonsynonymous SNV	TET2	exon6	NM_001127208	NP_001120680	c.3784C>T	p.R1262W	0.35	Previously Reported	1 / probably damaging	COSM5564331
WES_SA4	4:105243760	nonsynonymous SNV	TET2	exon6	NM_001127208	NP_001120680	c.3785G>C	p.R1262P	0.41	Somatic	1 / probably damaging	COSM5879022
M_SA_051	4:105243774	nonsynonymous SNV	TET2	exon6	NM_001127208	NP_001120680	c.3799G>A	p.E1267K	0.28	Somatic	1 / probably damaging	-
M_TH_009	4:105259622	frameshift deletion	TET2	exon7	NM_001127208	NP_001120680	c.3807delA	p.R1269fs	0.19	Somatic	-	-
WES_TH5	4:105259626	frameshift insertion	TET2	exon7	NM_001127208	NP_001120680	c.3812dupG	p.C1271fs	0.13	Unknown	-	-
M_TH_007	4:105259635	stopgain	TET2	exon7	NM_001127208	NP_001120680	c.3820C>T	p.Q1274X	0.39	Previously Reported	-	COSM96488
WES_TH7	4:105261790	nonsynonymous SNV	TET2	exon8	NM_001127208	NP_001120680	c.3986T>C	p.L1329P	0.18	Somatic	1 / probably damaging	COSM4170038
M_OA_115	4:105269641	nonsynonymous SNV	TET2	exon9	NM_001127208	NP_001120680	c.4076G>C	p.R1359P	0.25	Unknown	1 / probably damaging	-
M_LU_015	4:105269674	nonsynonymous SNV	TET2	exon9	NM_001127208	NP_001120680	c.4109G>A	p.G1370E	0.15	Unknown	1 / probably damaging	COSM41852
M_TH_001	4:105269748	splice site	TET2	exon9	NM_001127208	NP_001120680	c.4182+1G>A	.	0.19	Unknown	-	-
M_TH_001	4:105272905	frameshift deletion	TET2	exon10	NM_001127208	NP_001120680	c.4524_4537del	p.A1508fs	0.12	Unknown	-	-
M_TH_002	4:105275569	stopgain	TET2	exon11	NM_001127208	NP_001120680	c.5059C>T	p.Q1687X	0.19	Somatic	-	COSM43421
WES_TH3	4:105275764	frameshift deletion	TET2	exon11	NM_001127208	NP_001120680	c.5254delA	p.K1752fs	0.27	Somatic	-	-
WES_TH1	4:105276065	frameshift deletion	TET2	exon11	NM_001127208	NP_001120680	c.5555delA	p.Q1852fs	0.32	Unknown	-	-
M_TH_002	4:105276128	nonsynonymous SNV	TET2	exon11	NM_001127208	NP_001120680	c.5618T>C	p.I1873T	0.19	Somatic	1 / probably damaging	COSM41741

M_OA_080	4:105276404	nonsynonymous SNV	TET2	exon11	NM_001127208	NP_001120680	c.5894T>C	p.L1965P	0.47	Unknown	0.99 / probably damaging	-
WES_TH3	1:2556666	nonsynonymous SNV	TNFRSF14	exon1	NM_003820	NP_003811	c.2T>C	p.M1T	0.20	Unknown	0.97 / probably damaging	-
WES_TH7	1:2556667	nonsynonymous SNV	TNFRSF14	exon1	NM_003820	NP_003811	c.3G>A	p.M1I	0.27	Previously Reported	0.92 / possibly damaging	COSM5947672
WES_TH7	1:2556700	stopgain	TNFRSF14	exon1	NM_003820	NP_003811	c.36G>A	p.W12X	0.25	Somatic	-	COSM5950233
M_TH_001	1:2556701	stopgain	TNFRSF14	exon1	NM_003820	NP_003811	c.37A>T	p.R13X	0.41	Unknown	-	-
M_OA_076	1:2557774	nonsynonymous SNV	TNFRSF14	exon2	NM_003820	NP_003811	c.118C>T	p.P40S	0.53	Unknown	0.98 / probably damaging	-
M_OA_033	1:2557797	stopgain	TNFRSF14	exon2	NM_003820	NP_003811	c.141C>G	p.Y47X	0.47	Unknown	-	-
M_OA_033	1:2558347	stopgain	TNFRSF14	exon3	NM_003820	NP_003811	c.183T>A	p.Y61X	0.41	Unknown	-	-
M_LU_027	1:2558359	nonframeshift deletion	TNFRSF14	exon3	NM_003820	NP_003811	c.195_212del	p.65_71del	0.61	Unknown	-	-
WES_TH3	1:2558376	frameshift insertion	TNFRSF14	exon3	NM_003820	NP_003811	c.213insG	p.T71fs	0.15	Somatic	-	-
M_GA_017	1:2558381	nonsynonymous SNV	TNFRSF14	exon3	NM_003820	NP_003811	c.217A>G	p.T73A	0.39	Somatic	0.99 / probably damaging	-
M_GA_018	1:2558382	nonsynonymous SNV	TNFRSF14	exon3	NM_003820	NP_003811	c.218C>T	p.T73I	0.12	Somatic	0.99 / probably damaging	-
M_TH_009	1:2559832	nonsynonymous SNV	TNFRSF14	exon4	NM_003820	NP_003811	c.314T>C	p.L105P	0.51	Unknown	1 / probably damaging	-
M_GA_037	1:2559921	nonsynonymous SNV	TNFRSF14	exon4	NM_003820	NP_003811	c.403T>C	p.C135R	0.25	Unknown	1 / probably damaging	-
M_OA_068	1:2559921	nonsynonymous SNV	TNFRSF14	exon4	NM_003820	NP_003811	c.403T>C	p.C135R	0.15	Unknown	1 / probably damaging	-
M_OA_052	1:2560629	nonsynonymous SNV	TNFRSF14	exon5	NM_003820	NP_003811	c.466G>A	p.E156K	0.52	Unknown	0.99 / probably damaging	-
M_OA_089	1:2560657	frameshift insertion	TNFRSF14	exon5	NM_003820	NP_003811	c.495insC	p.C165fs	0.46	Unknown	-	-
M_SA_050	1:2560681	nonsynonymous SNV	TNFRSF14	exon5	NM_003820	NP_003811	c.518A>G	p.N173S	0.12	Somatic	0.14 / benign	-
M_OA_049	1:2560707	stopgain	TNFRSF14	exon5	NM_003820	NP_003811	c.544C>T	p.Q182X	0.73	Unknown	-	-
M_TH_002	1:2560713	stopgain	TNFRSF14	exon5	NM_003820	NP_003811	c.550A>T	p.K184X	0.40	Somatic	-	-
M_TH_008	1:2561672	splice site	TNFRSF14	exon6	NM_003820	NP_003811	c.552-1G>A	.	0.30	Unknown	-	-
M_SA_058	1:2563149	nonsynonymous SNV	TNFRSF14	exon8	NM_003820	NP_003811	c.728G>A	p.R243Q	0.53	Germline	0.64 / possibly damaging	COSM28384

Supplementary Table S7: Variants detected in genes previously screened by Fluidigm Access Array and Illumina MiSeq sequencing

Sample	Position	Type	Gene	Exon	Transcript	Protein	cDNA change	Amino acid change	AAF	Somatic Status	PolyPhen2	COSMIC
M_SA_056	15:44711548	nonsynonymous SNV	B2M	exon1	NM_004048	NP_004039	c.2T>C	p.M1T	0.16	Previously reported	0.39 / benign	COSM144529
M_SA_054	7:2939888	nonframeshift deletion	CARD11	exon6	NM_032415	NP_115791	c.723_725del	p.241_242del	0.22	Unknown	-	-
M_GA_037	7:2944251	nonsynonymous SNV	CARD11	exon5	NM_032415	NP_115791	c.645G>T	p.K215N	0.14	Previously reported	0.99 / probably damaging	COSM85974
M_SA_057	7:2944447	nonframeshift deletion	CARD11	exon5	NM_032415	NP_115791	c.426_449del	p.142_150del	0.44	Unknown	-	-
M_SA_062	1:116536117	stopgain	CD58	exon3	NM_001779	NP_001770	c.476G>A	p.W159X	0.13	Previously reported	-	COSM894401
M_GA_031	19:41879011	nonsynonymous SNV	CD79A	exon2	NM_001783	NP_001774	c.101G>C	p.W34S	0.27	Unknown	0.68 / possibly damaging	-
M_GA_031	19:41879187	nonsynonymous SNV	CD79A	exon2	NM_001783	NP_001774	c.277A>G	p.I93V	0.24	Unknown	0.71 / possibly damaging	-
M_SA_055	16:3731371	nonsynonymous SNV	CREBBP	exon30	NM_004380	NP_004371	c.4993G>A	p.D1665N	0.12	Previously reported	1 / probably damaging	COSM6005471
M_LU_037	16:3731804	nonsynonymous SNV	CREBBP	exon29	NM_004380	NP_004371	c.4862T>C	p.L1621P	0.19	Unknown	0.99 / probably damaging	-
M_GA_035	16:3738605	nonsynonymous SNV	CREBBP	exon26	NM_004380	NP_004371	c.4348T>A	p.Y1450N	0.25	Unknown	1 / probably damaging	-
M_SA_057	16:3744933	nonsynonymous SNV	CREBBP	exon23	NM_004380	NP_004371	c.3943A>C	p.T1315P	0.13	Unknown	0.97 / probably damaging	-
M_SA_060	22:41173740	nonsynonymous SNV	EP300	exon29	NM_001429	NP_001420	c.4735G>A	p.D1579N	0.17	Unknown	1 / probably damaging	-
M_GA_042	22:41176505	nonsynonymous SNV	EP300	exon30	NM_001429	NP_001420	c.5038C>T	p.R1680C	0.15	Previously reported	1 / probably damaging	COSM96420
M_SA_055	12:49026794	nonsynonymous SNV	KMT2D	exon48	NM_003482	NP_003473	c.15172G>A	p.V5058M	0.16	Previously reported	1 / probably damaging	COSM4702413
M_SA_060	12:49034667	splice site	KMT2D	exon36	NM_003482	NP_003473	c.10356-1G>A	.	0.12	Unknown	-	-
M_SA_060	12:49046113	nonsynonymous SNV	KMT2D	exon17	NM_003482	NP_003473	c.4645G>A	p.E1549K	0.19	Unknown	0.98 / probably damaging	-
M_SA_062	19:19149297	nonsynonymous SNV	MEF2B	exon3	NM_001145785	NP_001139257	c.187G>A	p.D63N	0.23	Unknown	1 / probably damaging	-
M_OA_103	3:38140801	nonsynonymous SNV	MYD88	exon4	NM_002468	NP_002459.2	c.728G>A	p.S243N	0.48	Previously reported	1 / probably damaging	COSM85943
M_OA_110	3:38141150	nonsynonymous SNV	MYD88	exon5	NM_002468	NP_002459.2	c.794T>C	p.L265P	0.37	Previously reported	1 / probably damaging	COSM85940
M_SA_052	3:38141150	stoploss	MYD88	exon5	NM_002468	NP_002459.2	c.794T>C	p.L265P	0.34	Previously reported	1 / probably damaging	COSM85940
M_GA_033	6:106104827	stopgain	PRDM1	exon5	NM_001198	NP_001189	c.667C>T	p.Q223X	0.36	Unknown	-	-
M_GA_028	6:106105266	nonsynonymous SNV	PRDM1	exon5	NM_001198	NP_001189	c.1106A>G	p.E369G	0.13	Unknown	0.52 / possibly damaging	-
M_SA_061	6:137871402	stopgain	TNFAIP3	exon2	NM_006290	NP_006281	c.175C>T	p.Q59X	0.25	Unknown	-	-
M_OA_110	6:137871453	nonsynonymous SNV	TNFAIP3	exon2	NM_006290	NP_006281	c.226A>T	p.T76S	0.51	Unknown	0 / benign	-
M_OA_107	6:137871495	frameshift deletion	TNFAIP3	exon2	NM_006290	NP_006281	c.268_269del	p.R90fs	0.53	Unknown	-	-
M_LU_037	6:137871521	frameshift insertion	TNFAIP3	exon2	NM_006290	NP_006281	c.294_295insTTAG	p.N98fs	0.59	Unknown	-	-
M_OA_105	6:137874824	nonframeshift deletion	TNFAIP3	exon3	NM_006290	NP_006281	c.296_316del	p.99_106del	0.30	Unknown	-	-
M_GA_001	6:137874997	stopgain	TNFAIP3	exon3	NM_006290	NP_006281	c.448C>T	p.Q150X	0.18	Unknown	-	-
M_OA_114	6:137875997	frameshift insertion	TNFAIP3	exon5	NM_006290	NP_006281	c.637insA	p.D212fs	0.15	Unknown	-	-
M_GA_034	6:137877094	frameshift deletion	TNFAIP3	exon6	NM_006290	NP_006281	c.824delT	p.L275fs	0.16	Previously reported	-	-
M_OA_105	6:137877127	frameshift insertion	TNFAIP3	exon6	NM_006290	NP_006281	c.858insA	p.L286fs	0.23	Unknown	-	-
M_OA_109	6:137877127	frameshift insertion	TNFAIP3	exon6	NM_006290	NP_006281	c.858insA	p.L286fs	0.16	Unknown	-	-

M_GA_035	6:137878788	stopgain	TNFAIP3	exon7	NM_006290	NP_006281	c.1343G>A	p.W448X	0.50	Previously reported	-	COSM3734944
M_GA_046	6:137880200	nonsynonymous SNV	TNFAIP3	exon8	NM_006290	NP_006281	c.2036T>C	p.I679T	0.49	Unknown	0.99 / probably damaging	-
M_SA_051	6:137881243	nonsynonymous SNV	TNFAIP3	exon9	NM_006290	NP_006281	c.2297C>T	p.A766V	0.24	Unknown	0.99 / probably damaging	-
M_OA_106	18:62354444	nonsynonymous SNV	TNFRSF11A	exon4	NM_003839	NP_003830	c.337G>A	p.A113T	0.12	Unknown	0.86 / possibly damaging	-
M_SA_051	18:62360004	nonsynonymous SNV	TNFRSF11A	exon6	NM_003839	NP_003830	c.571G>A	p.D191N	0.12	Unknown	1 / probably damaging	-
M_SA_060	14:102871948	nonsynonymous SNV	TRAF3	exon4	NM_145725	NP_663777	c.277G>A	p.E93K	0.27	Unknown	0.55 / possibly damaging	-
M_GA_040	14:102875678	nonsynonymous SNV	TRAF3	exon5	NM_145725	NP_663777	c.352C>T	p.R118W	0.52	Previously reported	1 / probably damaging	COSM144683
M_SA_065	14:102886219	nonsynonymous SNV	TRAF3	exon7	NM_145725	NP_663777	c.601G>A	p.V201M	0.16	Unknown	0 / benign	-
M_SA_066	14:102903370	frameshift deletion	TRAF3	exon11	NM_145725	NP_663777	c.1076_1107del	p.N359fs	0.44	Unknown	-	-
M_SA_052	14:102903403	frameshift deletion	TRAF3	exon11	NM_145725	NP_663777	c.1109_1110del	p.S370fs	0.35	Unknown	-	-
M_SA_052	14:102903412	nonframeshift deletion	TRAF3	exon11	NM_145725	NP_663777	c.1118_1135del	p.373_379del	0.17	Unknown	-	-
M_GA_001	14:102905590	stopgain	TRAF3	exon12	NM_145725	NP_663777	c.1513C>T	p.R505X	0.20	Previously reported	-	COSM4049221
M_GA_038	14:102905674	nonsynonymous SNV	TRAF3	exon12	NM_145725	NP_663777	c.1597G>A	p.G533S	0.29	Unknown	1 / probably damaging	-

Supplementary Table S8: Correlation between genetic changes and site involvement in ocular adnexal MALT lymphomas.

Site	TNFAIP3	TBL1XR1	MYD88	TNFRSF14	CREBBP	TP53	IGHV3-23	IGHV4-34
Conjunctiva (n=19)	37%	**26%** ***P* =0.002**	0%	0%	11%	0%	**55%** ***P* =0.002**	18%
Orbit (n=40)	43%	0%	5%	**13%** ***P* =0.04**	0%	0%	4%	22%
Orbit+Conjunctiva (n=23)	35%	9%	**17%** ***P* =0.03**	0%	4%	9%	13%	7%
Lacrimal gland (n=16)	19%	0%	0%	6%	0%	0%	15%	15%

Significant findings are shown in bold