

**Table S1. Primers for sgRNA synthesis**

No.	Name	Sequence (5'-3')
1	tyr-sg1	CAGTGCTTTGGCAACTTCAT <b>GGG</b>
2	tyr-sg2	CCGTTCATCCACCCCGGTGA <b>AGG</b>
3	il2rg-sg1	CCCACAGACGCTAAAACACTAC <b>AGG</b>
4	rag1-sg1	CTCAAGCCACAAGGAGTCGA <b>AGG</b>
5	rag1-sg2	ATGTCTCCTTCGACTCCTTG <b>TGG</b>
6	tyr-sg1-top-oligo	CCGGCAGTGCTTTGGCAACTTCAT
7	tyr-sg1-bottom-oligo	AAACATGAAGTTGCCAAAGCACTG
8	tyr-sg2-top-oligo	CCGGCCGTTTCATCCACCCCGGTGA
9	tyr-sg2-bottom-oligo	AAACTCACCGGGGTGGATGAACGG
10	il2rg-sg1-top-oligo	CCGGCCCACAGACGCTAAAACACTAC
11	il2rg-sg1-bottom-oligo	AAACGTAGTTTTAGCGTCTGTGGG
12	rag1-sg1-top-oligo	CCGGCTCAAGCCACAAGGAGTCGA
13	rag1-sg1-bottom-oligo	AAACTCGACTCCTTGTGGCTTGAG
14	rag1-sg2-top-oligo	CCGGATGTCTCCTTCGACTCCTTG
15	rag1-sg2-bottom-oligo	AAACCAAGGAGTCGAAGGAGACAT
16	T7-tyr-sg1-F	TTAATACGACTCACTATAGCAGTGCTTTGGCAACTTCAT
17	T7-tyr-sg2-F	TTAATACGACTCACTATAGCCGTTTCATCCACCCCGGTGA
18	T7-il2rg-sg1-F	TTAATACGACTCACTATAGCCCACAGACGCTAAAACACTAC
19	T7-rag1-sg1-F	TTAATACGACTCACTATAGCTCAAGCCACAAGGAGTCGA
20	T7-rag1-sg2-F	TTAATACGACTCACTATAGATGTCTCCTTCGACTCCTTG
21	sgRNA-R	AAAAGCACCGACTCGGTGCC

Note: 1-5: sgRNAs targeting the *TYR*, *IL2RG* and *RAG1* genes. Roughening marker for the PAM locus; 6-15: Oligos for the generation of sgRNA expression plasmids; 16-21: Primers for generating DNA templates of sgRNAs by PCR amplification of sgRNA plasmids.

**Table S2. The primers for the target gene loci**

Target gene locus	Primer	Sequence (5'-3')
TYR-exon1	TYR-TA-clone-Forward	GTACTGCCTGCTCTGGACTTT
	TYR-TA-clone-Reverse	GGATGCTGGGCTGAGTAGATT
IL2RG-exon3	IL2RG-TA-clone-Forward	TGATAAAGTCCAGGAGTGTGGC
	IL2RG-TA-clone-Reverse	ATCACTCAGGGTGC GAAGG
RAG1-exon2	RAG1-TA-clone-Forward	TTGTGAACACATCCTGGCCG
	RAG1-TA-clone-Reverse	GATGGCCAAGCAAACAGCAG



		<u>GTAAATAATGTGCAACTTAGATCAGTGCCTCGTCTCT</u>
11	mm4 intergenic _GRXCR1 YIPF 7_8_35561499	<u>ACCTGGACCTGGAGTCTCTCTTTTCAGTGAGCAGCATTACAGTTCATGATGACAAGAAAGAAAGCATTAGACCC</u> CTTATTTCTGAATAATTTGAGTCCAAAATACTAGATAGTTCCTTCTCTCTGCTGTTATTTCTCAGAATCAG CCAACCTTACTTTTTGAACACTTTAATGATAGAACAAATAAATAGGCAACTACCCACTCGGAGCAAGAGGTTCT TTCAATCTCCAGGCCTGTAGAGATAAGTGCATTTCTCAGTCAATTTACCCCTCTGTGCTGCATCTGCAGCCTCA GGACACCATGGTCTCTTCACTGGGGTGGGTGGACAGGAGCCTCTGCACCACTCTGTTTAAAGCTCAAAGTTAT CGTCTTATAGGGGTTGTGGTTTATCACCAGAACCAAAACAAAGAGAAATTTGCTTTCAAATCTCCAAAAGTTGTGCC TGAGCAACACTCCTGTGCTGGAGATTACAAAGCCTTTTATAAAGACAGCTTTTGGCTTATCCCTCTGACCC TTCTGTCCACAATACTAGCATTTTACTGCCAACTCCATCTCTTCCATCCCGCCTTTCCAAGAA
12	mm4 intergenic _7SK CXCL11 8_75897346	<u>TTCTTGGAAAGGCGGGATGGAGAAGGATGGAAGTGGCAGTAAAATGCTAGTATTTGTGGACAAGAGGGTTCAGA</u> AGGGATAAGCCAAAAGCTGTCTTTATAAAGGCTTTGTAATCTCCAGGCACAAGGAGTGTGCTCAGGCACA ACTTTGGAGATTTGAAAGACAATCTCTTTGTTGGGTTCTGGTGATAAAACCACAACCCTATAAGACGATAACT TGAGCTTTAAACAGAAGTGGTGCAGAGGCTCTGTCCACCCACCCAGTGAAGGAACCATGGTGTCTGAGGC TGCAGATGGCAGCAAGAAGGGGTAATGACTGAGGAAATGCATTTACTCTACAGGCCTGAGATGGAAGAAC CTCTGTCTCCGAGGTGGTAAAGTGCCTATTTATTGTTCTATCATTAAAGTGTCAAAAAGTAAGGTTGGCTGAT TCTGAGAAAATAACAGCAAGGAAGAGAAAGCACTATCTAGAGTATTTTGGACTAAAATGTAAGTAAAGGG GTCTAATGCTTTCTTTCTGTATCATTTGAAGCTGAATGCTGCTCACTGAAAAGAGAGACTCCAGGTCCAGGT
13	mm3 intergenic _ENSSSCG000 00015055 REX O2_9_46805059	<u>CACCTTGTCTGAGCCTTGGTTCCTTGCCTCCAGAGAGCTGACTCCCTTCACTGGGGTGGATGAGCAGGAGAG</u> ACAGAGACCTGGCCCTCCCGAAACAGATGGAAGTGAAGCTGACAAGGTAGGTGCCATTTGAGGTCGCTCACTTCC CCGAGGCGCTGCCTGCAGGGCTGGGGAGGACATCTGGCCCTCAGGAAATCCCGCCATATGGCTTCTGCATCC CAAGTGGTCCCTCACCTCCAGCAGGACATCCGGCTGATCCCCCTGCAGTATGTGTCTAGGGCTGAGGATGGT GTGCTGTGTGTGGCGCTGGTGGTGGAGGTCACGTGGGTGAAGGGTCTGGGTGGCAACAGGTTCTGTGAT CCTTTTATCTTAGCTGTCTCTGTGGTGAATCTGCCGGATCCAGTGGTGTATATGGAGTAAGACCATTGGA AGGATTTCTGTGATGATAAAGTAGGCACCTCTTAGTCACTAACTTAATGTGACATATGTACACACTGA GCCGGTCTCTTT
14	mm4 exon EN _SSSCG0000002 6203_9_470674 92	<u>ACTACTGGAGAGTGGGCACTGTCCAGATGAACGTATAGATCTTTTCTAAAATGGCTTCTATAGAGTCCAAA</u> GTTGATATACTCATGCTGTTGGCTAAATCAAAGGATCAACATTTGGCTAAATCATTACTGATTTGCTCAGGTA GTCTCCAGAAGTAATTACTTACCTTTCAAAGAGGCTCTTTCTTTCTTTGCTAAAATAAGACGCTTTCTGTGTTGG AATCCATGTGGGTTAAGTGCAGCACAGGGTATGCTGAGGCTCAGGCAGTAGAAGGCTCCCTGGTCTCTGGTA TCCAGGTACTCACACAGTTAACTCTTGAATTTAAACCAGAGACAAATACTGTTGACTGGGAGCTTACCACCTG GCAAAGTGGCTGTGAAGATCACCTTGTGAGCCTTGGTTCTTGGCCCTCCAGAGACTGACACCGTCACTG GGCTGGATGAGCAGGAGAGACAGAGACACCTGGCCCTCCCGAACAGAGTGAAGCTGACAAGGTAGGTGCCAT
15	mm4 intergenic _MYC FAM84B 4_12886286	<u>CTCCTAGCCCAATGAATCTGCTTGAATCCATCACCTGGGTGGATTACAGTGTATGCACCAGCCCTCTCATGTCT</u> CCCCATTGCTACTTTCAGACTTTTTGCTCCTCTCTACCATGCTGCCTTCTCTTGGAGGCCTAGGCCATCTTT CAACTGTTCTATTGTCCCTTTCCCACTCCCTGGAGACGTGGGTCTGGCTCAGGGTCTCTCTTACCTCACTT TTCCATCATACGACTGACTGCAGTGGCCATAAGAAACAATGCATTCAGCCTCCCTGCTTCTTCACTTCTGACCT TTCACCTCCCTGTGGTCTTCACTCCGCTCCAGCCCACTCCAAGTTCATACTCTGATGTCAGACCAAAAT GCTCCATCTCAGCAGCTTCACTTCACTTCTCTGCTGTATGCTGGCTTCTCAAAGTCTGGCCCTTCTATGTTT CCCTCTATTTTCTCTTGGCCCTCAGTGTCTCCCACTTCACTGTTGCTGTGACTCAGCTAGGTCCTCCCTGCTTGA TTATCGGAAGCCTTGACTTCTCAGCTCTGCCACAACCATTAGCAAGGCCCAATCTTGTCA
16	mm4 intergenic _Gap POR_GL8 94019.2_2673	<u>TCTCAGTGACCTCTCTGGGGCCCTACCCACCATTCCTTTGCTGAGCTCAGCCTTTATGTCACCTCTTATTTG</u> ACGCTTAGGTAAGATCACTGCTGTCTGAGTACTTTGATCCACGAGACATGCCCGCTCACCGTCTGGGTGAA CTGGGTCTGTACAAAGGTTTGGAGGACAGTAAAGAACATGAACCTTATGTGCACCTTCTCTGAACCCAGTTGTG CTGACTCTGTAGGTCACCTGGGGTGGTTTCAACGCAAAACAAGGGTGGCGGTTCTGACACCGAGGAAAATGG ACCAACCAATTTGTTGGCTTCTCTCGGAGGTGGGGTTTAAAGGTGGGACACGACTTCCAGGCCTTGAAGATGTG GGTTTTGGAAGAAGGCACTGTGGTTCAGTTAAAGGGTGTCAACCTGTGGATTAAGAACCACTGACCTGGCAT TACCTGGACATCGTGACCCAGTCCCTATGCAATAGGATTTGCCAATCTAAAAGGTCACCTACCACGACC
17	mm3 intergenic _ZNF251 C8orf 33_4_75151	<u>GGGACATGGGAGGAAAAGGCCAGGCTAGAGGGGAGTGGGTGCCAGGTGGAGCCATGGGGTGGGGTCTTTCT</u> GGGTCTGAGCTGGGAATGGACGAGCAGGTGGTGTGAGTGTGACCCAGGAAAGCTGCCTGGTGCACAAAGTCTGAA CCCCTTACAGGGAAAAGGCCCTCTGGGTGAGCCCAAAACAGGATTTGAAGACAAATGCCAGCAAAAGGAAGGAT TTGTAACCAAAACCCAGTGAAGGGAAAGGATGCACTGCCCTAAGAGGAGGGCTCTGAGAGCTGGTCCCTCAT GGGGCAGTGGAACTGCCGGGAGCGGGCCGTCACCTGGGTGGATGGAGGGTGCAGCCCCCTCGGTGGC CCACATCTGCGCTTCGGTGGTACTTGGCTTCTCCGGCCCTCGCTTCCAGCCTGCTGAGTGGGGTACAGAA GCACGGGCTGACTAGTATTTGCTCTAACGGGGCGCAAGGGGTCTTGGGAAATCTCCGGGAACG
18	mm4 intron HS _6ST2_X_12498 7558	<u>ATTGCACTTCCCTCCAGGTTTTCCATAGTGCAGCCATTAGAAGAGCCTGAACCTTGTCTTTATGAGGCCCT</u> CTCAAAGTGGGCTGTCAACGGGTTGATGGTTCGGTTTACAAGATTGAAGACTTGGGCTGTAAAGACTGTG CTCTTGAAAAGTCAATAGGAGGGCCCCGGGCCAAGCTTTTACACCTGATGCTGAAATCCCGGGGCAATTTAC CCCCGTGAACACACACATTCACCTCACCCACAAGTAATTTGCTTCCGCTGGGCTGGGAGTAGTTACCTATGCAA AATAACAACAGGAGGTAGCGGGATGCAAGCGGGGACGGGATGCTGGGGTGGTTTGTGATTTTTCAGCTCAAA AGAAGAAACAATTTCAAGAAACTGTTTCAAGGACTTTGCAATTTTGCAGAAATTTTCTCTTTTGGCATCTCTGAGA CCGAACGATCAATCTGTGACCGGTCTATACCCGGGACCTGTCAATACCTGACG
19	mm4 intergenic _KCNIP1 KCN MB1_16_57833 329	<u>AGAGCAATCAAGGCCGTCAATTGCTAATCAGTAACTACGCAAGGACAAACGGTGAAGGCTGGGTGGGAGC</u> GGGGAGCGGATGTGATGTTGGCGTATCTGCTGGGATGTTGGGGAGGTGGTCTCTGGGAGACTTACGGGGAGGA GACCCGGCAGGGGGAGAGGGGACAGTCCGATCTGCACTTACTTTGCTCTTGTCTCACTTCTCTGCTCTGCT TCCAGGAGCCGCTCCTCCACTCGGGAAAGGTGCACAGCCTGAGCCAGGTGCTGCGGGTCCATTCTCTCCCTC CGTTTCCGATGACAATTTCTGGTGAACCTCTCAAGCCACAACCACTCGAAACATCAGGTTGTTTCCATTTCC TTCTCTTTCTGTTACCGACTTCACTGGCAGTCTTGGCTCTTCTTCCGGCAGCAACTCACCCCTCGCTTCC TGCCTGGGCAAGCCCTGCTCTCTGCTCGGCTAAGCAACCCCTGTTCCAGCCTTCTCTCTGACTCCAGGAC CT
20	mm4 intergenic _SNORA51 U6 13_200586772	<u>TGAGACATCTTTCCTGCTGTGTTAGAAAATGATGATTTTGAATTTACTGCCCATTATGATTTATAAATATCCA</u> TTTAAAAATGAGTTACAGTTACTCCCGGGTTGGTTACTAGGGTATAGGATCACTGATATATATTTGTC TTGTTACCAAATAAGGACAAGGGTCAATTTTACTCACTCTTTTACCACTTAAATCAGGTTGATTAATAAATAA TCCATGAATAACTTGAATCACTATGAAATGAAATCTGCTCACTATGCTTGCATTAATTTGTTACATCACTGCTG TTTCACTGCTCTTTCTTAAACAACAATAAATACTCAGCCTTGAATTTCCATAGAAATAAGAACTAATCTTTTG ACCTAGAGCTATAACTACGGCAAAAGAGTAGAAAAATCACACCATGTTAAATAGATACATTAATTTTACCTCT AAAAAGACAAATACTGGATGCAATTAATAAATAAGAGTCAATGTTTAAATTTTCACTGCTCAAGAACTAAGTGT AATTTATTTCTCCCTCAATTTGTTGAAAAGTATTTTATTGCTGAGGCACTACTCAGGAAATCAGGA
21	mm4 intergenic _ENSSSCG000 00025926 ENSS SCG000000116 05_13_7792426	<u>GGTTTTGACGCTTCACTGTGGCCATAGAGGGTATTTTATATCTTATTTAACATGAGTGAGAGCTTGAACCTGT</u> GAGCCTGGGAGTCAATGGCCATAAAACAGGTGTTACCTGGGAACCATGTTCTGTCTGAGACTGACCCAGGGG TGAGGGGCGTCAACCTGATGGAGAGGACAGGACAGCCAGCCAGCTGAGCTCAAGGAGGTGCCAGGAGGCT CTTGCTAGACAGTGGCATTTGCTGAGTCTGAAATGCAATTTGACTAAGTTGATCTCACTCAAGTCAAGAAAAACA ATATTTTCACTATAACCTGGCCCTCTGATAACCACAGGGAACCTGACAGACACTTTGGAGACAGCTCTTCCC AGATCAATGTTTTCAAGAGAGAATAAAGTTAAAGAGCAAAAGTAAATGTTCTTCTGGGACGCGGTGTTCTGTC TCCCAGCTGGGATCTTACTTTTCTACAGACACTAAAATTACAGGCTGCAGAGAGGTAAGTCTATGACCT

0	CCTTGCC
22	mm4_intron_LE O1_1_13291197 4
23	mm4_intron_EN SSSCG0000002 3000_11_77173 365
24	mm4_intergenic _ENSSSCG000 00020902 ENSS SCG000000253 82_GL893949.2 _212771
25	mm4_intergenic _CH242-112D2. 1 U6_X_350395 02
26	mm4_intergenic _U6 ENSSSCG0 0000029792_16 _3113621
27	mm4_intron_U6 _17_68743603
28	mm4_intergenic _ENSSSCG000 00011811 TPRG 1_13_13560157 4
29	mm4_intergenic _ENSSSCG000 00025817 TTC1 4_13_12762113 4
30	mm4_intron_EN SSSCG0000001 5082_9_499990 94
31	mm4_intergenic _U6 ENSSSCG0 0000028308_1_ 45132160
32	mm3_intergenic _ENSSSCG000
	<u>AGTTCTGCCTGAGAGGAGGGGATCTGGATAGACATGGACCTGTAATTTAGCACCTGAGGGACTATGTAGAG AATATGCCTGTGTGGAGTTCTTAAAGCCCGAGATTTGCATATATACACTGTAGGAGGATATTTAGGCTCCTGCCTG ATAAAAGGAAGTGGAAAGACAAGGCTTTGTAGTGAAGGAGAAAGGAGTATGTCCTGTGCAGCTTTGGCC TTCGCTGGATCTGCCACTTCCCTCTCCACAGACACTCAAGTCAGATCTTTGAGAGCCAGGCTAAGCCTTTGTTT GCGTGGTTCCAGGATCTGGTTGAGAAGCCTTGGGAACATGTTGAAGTGATAGCTCTGGAAAAATCATTATTGTA GATATTAATACTCTGCACTTTTCTCTGTTGAAGATAATAATGGAACATGGATCTGTTGGAGGTGCAGATGATA TATCTTCAGGGAGTGATGGAGAAGATAAACCCACTACTCCAGGACAACCTGTTGAAGTAAATAGCAATGTG AGCTGGGGAGAGAACT</u>
	<u>TCTGTCCAGCAGCTGTCAAGGTTGAATTCAGTACGCAAGCTGGAGCTACCCATTGAGAGGAAATTAATAAAAT ACCTCCTCACTGCTTCTACCCTGATTTCTTGAAGCTGTTATCGTCTGTGAATGAAATCCTATGTAACCCCC AACCTACGCTAAACAACCTGGCAACGTAATTTCTCTAAATCCCTTCTGTAATTCCTGACATAATTTCTCTTCCA CCAGAATAACCCATAATGACAAGTACGTTAGTTAGACAGTTTTTTGGTATAGTATTTTCCATGAAATTTTATCA TTTTGGTATTAATACCGTTTCTCAGAGAATGGGAGTGTAGCTTCCAGAAGTTCACAAATTAATTTTAACTATGT TAAAAACAAGGCATTTGCTCTCAGGAGAATGGAATCAGGAATCCAGTAGGAAAAATGGTGGGATTATGGGTA TTATACATAATCACATAATAGTTGCCAAATGTTTTAGTGCCTTTAGTGTCTTTGAAAAGTATCTGTGTTTTCC CACCAGGCA</u>
	<u>TGCCTGGTGGGAAAAACAAGTACTTTTCAAAGACACTAAAATTCATAAAAACAAATTTGGCAAATATTATGTGA TTATGTATAAATACCCATAATCCACCAATTTCTACTGGAATTCCTGATTCCTGAGAGCAAAATGCC TTGTTTTTAAACATAGTTAAAAATAAATTTGTGAACCTTCTGGAAGCTAACACTCCCATCTCTGAGAAACGGTATTA ATACCAAAATGATAAAATTTTCATGGAAAAACTATAACCAAAAAAAGTCTAACTAACGTAAGTGTCAATGTTGG GTTATTTCTGGTGAAGGAAGAAATATGTCAGGAATACAGAAGGGATTAGGAAAAATACGTTGCCACTGTTT TAGCGTAGGTTGGGGGGTGTAGCATAGGATTTCAATTCAGCAGACGTAACAGTTACAGAAATCAGGGTAGA AGCAGTGAGGAGGTAATTTAGTAATTTCTCTCAATGGGTAGCTCCAGCTGGCTCAGTGAATTAACCTTGAC AGCTGCTGGACAGA</u>
	<u>AGGTTTCTTCTGCCAAAATTTAAATTAATAATGTTTTTATCCTTCTAAATCCATTTGTTTTGACTTGGCAAA ATGCCATAAAAAGAAAAATGCCTCTACCTGTAGCTTTAGTGTCTATGGTTTCACTAGCATTGGACTTTGAAACT AGTCACATCCAGAACATTTCTATCAAGAAAAAAGGTCAAAATCCGAGAGACAGAAATTTCACTTGCAGTCCAG ATTTTGAAGAAGACTCAATTTGCTGTTCATTAACACTGAGTCATTTTTTGTACTTGTACTACAGATACCTACA GCATTGCTCTGAAGTTGATTCTAGTTAATATGCGATATCATAAATTTTCAAATAAAGAGTAAAAAAATCTTT GAGACAACCTCAGGTGAAATCTACATGACAAGCAACTGTTAATCAAGAAGTGAAGGGACTAAAATGTTAGA CTCTAGAGGGACCAATTAAGTATTGGCAATTAATGTTGATATCTATAAATAAGTTAACAGAAAAATACCT AAAATCTCTATTATGGTATGGTATGATATTATGCGGCCAAGG</u>
	<u>CTACCCACCTGCTTTCCAGATCAGGAGCTACACCTAATTTGTCTCAATGTACCAAGTACTGACTTGCAAAATA AAACCCACCTCTGTTCAAGGCTCATGATTTCTAGGTGCTTCAAATAATTTTTTAATGGAATAAATATTTTTA AGTTGCTGCATAACATTTTTATCAAATAAAGATGAACCTTCAAATGATGGTCAAATTTTAAAAATGGCCACAT TTAGAAAGGTTTACGGTTCTTTTTTATTTCTTATCCCTAGAACATCCATGATTAATACATGCAAGTACTTGA CTGGAGATTTTCTATCTTATACAGTTTCTACAGACTCAACAACAAAAAGTTGCAACTTGGGACAGACTGCGCA AGAAATATTTCTCATTCTGAAAGAAGCAGTGTGCTGTTTCTAATTTTTCTTATCTGTTTCCAGACTTGTCTT ACAAAGTACACACAGATGTTAAATTAAGTGGCTGGGAGAAGGGAGAGGGAGAAAAATCTTACTCTTACATG CAGCTGACTGAGG</u>
	<u>GGGTAATGAGGAGGGCTCGACCGAAGCACGTTAACTTCCCGTGGCCTGAGCCGTTCTGTGGAAGATTGAAA GCGAAAGTCCACAATTAGCCATTAAAGCTTGGGACCGCGGGTCTGGAGATTTATTTTAAATGCGCAGAC AAGAATGGCACTGAAAGAGCCATGAGGTGCAGGAGAAAAATAAAAAGCAGCAAGGAAGACTCGGCTGACGGCT GCAAGAAGCCGTTGGAGACGCTTGAATCTTTTATTTATAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT GGACTTATCGGGGTTCCACAGCCGCTGCGCTGACCCCTCTCCCTCGGACACGCGCTGGGCTGTGGTCTGGGT CCCGGAGGACAGACGGGGCTGGCCTGGGGCTGGCCGATCTGGGCGAGCATTGGGANAGGGCTTTTGT CTAGCGACTTGGGAAGCCAGGGCTCTCTCGGTCGGTAGATAAAATCTCCTGGTGGTGGCCTGGGAGCCG CAGAGCCCGGGAGCTGTGACTGAAAAAGAAAAATTTCTGATCATGCCTTCTCTGTTGGGCTCAAAACAAAATG CT</u>
	<u>TGGGAGGAGGATAGAGTGGTGGGAGACAACCACAGCCGCTTGAACCTACAGGTGCAGAATATGCCAGAAAGTT TGAGAAAAGAAAGTCTAAATTCATCTGTTACACTGTTGATCTGGGAACTAGGGAGTTATCTTCTTGAATGA GCCATTAATAAATATGTCAGACTTCTATATGATATTTGATTATTAATAAATCTGAAGTAAACGTAATTTCACTCAG TCAAATGGAATAAAGAGACTTGAATCTTTTATTTATAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT CTCTGTGCTCTGACTGCTATCTGCTAGCCCTCTGAAGCTAACGGCCACCACAGCCAGGCTCGTGTGATGTTG ACAGTGCCACCAGAGGGACTAGAGGCACACTACAGTTTACAGCCGGGTTCTCCCTCTTCTTCTTCTTCTTCTT ATTGCTGTGGCTTCCACTTTTATAAAATCTTCTCTACTCCAAAAAGTGAGGAAGTTTCAACTAAATGTAGCT TCATCTTATCTTACTTATCCACAGAGCTAAACTTGAATGTGGTGGCTCATGATCTCC</u>
	<u>AAGAGGTAGGAGGGGCGATTACATGATATAAGCAACCCAACTTCCAGGTGGGAAGCCCCACAGACGAGAA AGCAACTGGTTTACAGAGACTAATCTACAGAGGTGAGAGTCTGAGCCCAATGTCAGGGCCCTATGCTGAGCA ACTGACATGGGGAATAGACCCTGGAGCACCTGATATTGAAGATCAGTGGGGTTATGTTTCAAGAGCTCCATGG GACTTTGGGAAATGGAGACCACATTTTAAAGATGCTCATAGACTTTGACGTGCACTGGTCCCAGGGCAATGC AAAGTCTCCTGGAATCTGGATCATATCTGGCTACATCTTGGAGATTCTCTGGGAAAAACAGGGGGTGAATG TGGCTTCTGACAGGAGAAGGGCATTGGAAGCAAACTCTCAGGAATACTCAGCAGCATTCTTCTTCTGAGGGT GCCATTAAGGAAATCTGGCCCCACCATCAG CACTGAGAAGC</u>
	<u>GCCTGGAAGAGACACCTGTCTCTGGGGTGGAGCTGTGTTGGTGGAGACAGAGCGGAGGCTGGGGAGCCAGGG AGCCTGGGCTTCTACCTCTCACCCCTCTGGGGTCTGGGTTTTTCCCATCCCTCCGGCATAGCCATGTCCCGGG TCTCCAAGGCAGTGTGGCACAAGCATGGCCAGGAGTGGTCTGTTGCAAGAGCTCTCAAGCTCAGGCTTCC ATGATGCCTGCTCTGGGAGTATCTTCTCATCTTGGAGTGAAGGGCTGGCTCCATGCACTTAAGCGACAGAGG TGTTTGTCTGTCTTCTTCTGTGTCCACCGACTTAAATTTCCAGGGCTTTCTGGAGCCAGGCAAGGAGAG ATCCAAATCGCTCATTCAGGAGGTGGGTGGACACATGGGAGGTTGGGGTGTCTATCCACCTGCTGACCTTGGAC TCCAAAGCCATCTGGGAGGACTTCTTGGCCCTGGGTCTCAGTTTACCCTGCTGTGGGAGCCAGCTCCACAG AAGGACAG</u>
	<u>TCTTCTCCCTGCTTCTCATCTTTGCTCTGCTCTCAGTGATAGTTCTGTTACCAATGGTTTCTCTTAGGCAGCA GTTCTGTGATAGTTGTTTCCAGCGACAACCCCTTAAACATCTAATGCAATATCTAACCCCTTAAAAATCTTATG TTTTGTTCTGGATCCCTTTGAAGGTGAAATACTACTGTGATCATCTCTGTAGGGCAGTTTATAACATTTATACAT TTCTTAAACATTTGTTGAACACTTAAATATTGAAACATTTGCAAGAACAGTAATGAACACTCCGGTTGGAATCTC TGTAATAGGAAGCATGCGGTAAGGTAAGGAGAGGCACTTACCCTGGAAGTTCTCTAGACAGTTGGGTTGAGTGT TCCCTAGTAGCATCAGGAAGTTGACCTGTACATCTTTAGAGGCTTTCACAGCTGGAAGAAGAGTACACTGCCC TCCACTCTTGTGCTTAGAGTAGGTTCTATGCCATGCTATGATGCCAGGATGCTCCACCTCAAAGGTGTTCCA GAGGAAAGCCATCTCTCTCTAGGTAGGTTCCAAACCCAGGT</u>
	<u>TGCTCCCTGGCTTTTCGATTTTTTCGCTCAAGCCAAAGGAGCAGAGGGCATCAAGTTGGGCATCCTTTCCAAGC GTGCTTGTGGAGAGGAACTCTGGCAGCAGAGCGTCTCCAGCTGCAACACGGACCTGGTCTGTGCCCCGCT</u>

00022189 U6_9_103420505	<u>GCCCACCGCGCTGACAACCTCCACACCCACAAGAAACCGCCCGTGTGGCAGCAGTCATCGCACGGGCTTCTGTG CACAAAGCTTAAGGAGCCCTTAATAGAAAATAATGTGTCCAGAGCCAAAGCAGAGCTGGAGGTGGTGGCTG ATGACATGGGTCTTTCTGGGGTCTGCGAGGACTAGGTAGCCCTTCACTCTCGACATTTGGCCGAGTGTGTG CCTTGAAATCTGCCTCTCCAGAGACATAGACGCCACCCACAAACTCTCACTCACGACACCCACCTCGCCTCTG NNNNNNNNNNNNNNNNNNGCCGAAGTGTAGGTACTGGCCATGCTCT</u>
33 mm4_intron_CC DC88B_2_6994 077	<u>GATCCTGTACCACCACAGACCTCCAGACTTTGGGGTGGACCCCTTCTCAGGTGCTCTCTCCACCACCCCTTC CTGCTTGACCCCTTCCCTTGCCTTAACCCCTTGTGGCTTGTGCCCCGTCAGAGGAGGCGGTGGAGGAGCTA GAAGGCATCCTTAGGCTATTGCTGGGGCGTCCGTGACAGGTGAGCGGGGGGAGGGAAGGTTACGGTCTGCTTT GGCCGACAGAGTGGGACACTCCGGCTCAGCCTCGTCCCTTCTCCCGCAGTGTGACACCAGGAACTTTCATC CGACACATCCAGGCGCTCAGCCTCGACGTCCAGAGTGTAGCTGGCTGCCGCATCCAGGAGGTACACCTTTGACT GGCACATGCCATGACAGGACACCTGTCCCCACTTCGTTGGTGAAGTGTTCCTCGCCTCCAGGTGACCCA GCCCGCACGGGCATGGTGTGCACTGGCTGGCCTGACCTGGCAGCTGGCCGCCCGGAGCTGGAGATGT GTGCC</u>
34 mm4_intergenic_ENSSSCG000 00025823 ENSS SCG000000103 68_14_9535715 4	<u>AGGTGTAGCCCTTTGGTCTGATGTCTGCCCCGACCCCTTGTGGCTGAAGTTGGTATGGGGGCTTGTGCTG TAGGCTTCTGATGGGACTGGTGCCTGCCACTGGTAGGTGGAAGTATTCTATCACTGTAGTGTGGGTTTT GTCTCTGGGTGAGATTGGAGCTGGCTGGGTGCTGGGAGTACTTTAGGCAGCTGTTTGTGATGGTGGGGCT GTGATCCCAACAGATTATTGTTGACTGGGACTTCTTAGTCTGATGGTGGGGCCAGATTATCCAAAATGGC CACTGTAGAGGACACATGCTGATGATTATTTCAAGACCTTTGCCCTCAATGTCTTCCACAGCCAGTCA CCGTTTTCCAGGAGATTCTCAAGAAGTCAATCGGGTGTGACCCAGATACCTATGGAGTCTGTCTTGCCT CGGACCTAGCACACATGAAAGCTGTGTGCACCTTCAAG</u>
35 mm4_intron_NR 6A1_1_2990843 67	<u>AGGGCATTGGAATGGGTCTTAAAGGCGAGTAGGAGTTCTTAGTGAAGATTGGTGTTCAGGGTGGAAAGA ATAGACTCAGGGACAAAGAGGAGTGTGAGGCTTCTTGGAAACCAGAGGCTTCTTGTGGCTTGTAGAGGAA GATAATGGGCAAAAGGAGGGCCATGGTGGACCATAGTGTGGAAGACAAGCAACCAAGCTCTCCAGAACTCG GATATGGGGTGGAGGGGAGGAACTTGGGTCTCTCCAGAGAGTTCAGGAAATCCCAAGTTAAATAA GTTCTCTTCTGAAGGAGAACAGAGGTATCCTGAGCACCAGTCTAACATGTATCAATTCCTTGTCAAAGA TATCAGAGGAAGAGATCGAAAGGATTATGTCTGGCAGGAATTTAGGAAGAAGCAATCACTGGAGCAACCAT GGTGACAGCGACACAGTTCCTGGAAACAGGGCTCAGAGAGCAACACGCCCTCACTGGGTCCACACTGTCT CCAAGGTGAGTCAAG</u>
36 mm4_intergenic_SNORA70 5S_rRNA_11_5868 4299	<u>CCTGGCTTCCCTTCCATCAGCAATGTCTCCCTTATTACAACCTCATATATTTGCCAGACCTAAACCTCCCTCC CAGAGAAGACCATGAGTTTCAGCCAGGACTGACACATCCAGCATTTGATCCTTTAGTCTATTCCAGCCACA TGGAGTAGAGTGGAGCAAACTGGATAAGTATTAGTCTACAAGACTGTCTCATCCATTTAGTAGGAAAGAACCAG CAACTATTAATACTAGGTTCTGCTCACTATTGTCATGAATTCAGGGAGTAATATTTAGAAAATAGGTCATGGTAT CATATTTAGAAAATTGATCTTTCAACAAAAGTTAAAAATGCAACCCAGGCTCTGAACTACATGAAGGGGACGN NNNNNNNNNNNNNNNNNNTGGCCACTTTCCTCAAGAGTTCAGAAACACACATAAAAAATGTTAGTATATA TTCATTCAATCCTTTCAGTCTCTTACACCCAGTTGAGTAAGCAAGT</u>
37 mm4_intron_H OGA1_14_1184 69185	<u>CTTACCAGGAGTCCCTTACCAGCAGCAGGAGGAGTGTCTGGGACGATGTCGACCAAGAAACTCCCAAGGAGTC GTAAAAATCTCGGCCACGGAGGAGCCAGTGGCCGCGCTGGCTGCCTGTACCAAGGACATTGACGCCAAGG GATCAGCAGCTGGCCAACTCCATGTGTCAGCGGTGTCATGGCGTGCAGAACTCAGGCCACTGGAGTCCAAAGGA TACAACCAAGGAAGAGTGAAGCGCTCAGGAGGTGCAAGTAAAGCTGAAAGGCAATTTCTTCCACCGCGGG AAGCCACATAGCTGGCGCAACCAACGACACCTTCCATAGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNAAGCTGCCAACCCAGCCATTAGACCACCTAACCCAGGATGGACATGCCCTTCC CCAACCAAGGCTGGCACACACAGGCCGTGTTTCTCCGATGGGGCA</u>
38 mm4_intron_T MEM182_3_53 891758	<u>CATTCATGCTGCCTTCCACGGGAAGCCTCCCATCTACTAAGAAGGCATGGCTATGTTTTACACCACCTGCCTCC CAAATACCAAAATCCAAACAAACAGGGTACAGACCAGACACAAGAACAGCAACCGTACGCTCTGAAGT GGGGCAAAAGACTCACTGAGTAACTAGTCCACCCCTGAGAACAGGAACACTGGGGAAGTGGGGGATGTTGG TAGAGCTGAAGCCACAAGGAAGCAATGGTAGCTGATCCAGAGGAACCTGGCCGTCACAATCAGAGGTTGG GAATAGGACTCAGGCCACAGAGAGGGCAGAAAAAGCAGAGGAGGCTCTCTGCACAGAGAGAAGCAGAGGGGAC GGCAAGAAAGAAAAACCAAGTGAAGGGGAGCGAGAAATAGAGAACCAGACAGAAATGGGGATAAAGTTTCC CCGGAACTTAAATCCTCGGACCTGCTATTCCCGCCCTTGGTTACTTC</u>
39 mm4_intron_LG ALS8_14_5886 1814	<u>CCAATGTGGACAAAACCTTCCACAACATTAAGAAATTAATAAAAAAGGTAGCAGTCTGTCTTCATAAGGCTTA GTAAAACTATAGTAAAACTCAACACTCTCTTGTGTTAGAACTGATCACTAAGAAAAATAGCCACAATGCNNNNN NNNNNNTTACTCTGGAATGTGGTATCATGACCTGTCCACAGCGCAGCAGAGGCCACTGGGAGCCCTAAGTGC AGCTGCTGTCTAAAGTAGCACTACCCCTCAGTTCCTTCTCGGAAATGAAGCGCTGGCTATTTTTGTTTCA AGTCTGTAGCTGAAGGTGTAACCCCGAAATACCAGTTCATATTACAGGATATGACAGGATTTAATCTA TAAAAATTTTCTAATAACATTCAAATAAGGCATCTGTGTAGTAAGACCAGAACTGAAAGTACAACCTGACCA TCATTTCTCTGGCTTGTAGCCAAAGATTACACTTCAGTAACCCCTTGACAGGCAGC</u>
40 mm4_intergenic_NAMPT CCD C71L_9_116980 314	<u>TGGTTCGAGAAAAGCTCCAGAGAAAGCAGCTCTCTCAAGGGACTTCTGCAACTACACAGTCTTCTCATTT ACTTTGTGCAAAAAGACCAACTCTTCTACCAACAGCCCTCATGTGAAGGCTCTTTCTCAGAGCTTGCATA TGTCAATTAACCTTTCTATCCCAAGCAACTCTTCCAAAGGCTCGCTGGCAGCTGAGGCTCTATAGATGTCTACT GAGCCAGCATGTGGATGTGAAACAAGATGCCACATGCCACAAGGAGGTGAGGGCACCAAAATATTCACACTTC TCTGTTCTCAAGAAAAGTATAGGCTATGACCTATGCAATGAAACTATGGGAAAAGTCCAACTAGATTTTGAAG TGAGAACCAAGTTATTTATATGCTAAAGAAAGCAGGAGCCCTGGGGCTAGAGTCTCAGGGATGCTTCAACA CAAGAGGAGAAAAGCTGGAGATGGAGGGGGTCTGGACGGTGGAGAGGCACAGGGATGAGGGGAGCCAGCAG GAGGGTTAGAGGGCAGGAGAG</u>
41 mm3_intergenic_KIT U6_8_438 56928	<u>GTACCACCAAGCTCCTTCCCAAGAACTACATTCAGCACCCTCTATCCAGCCACCATCACTTTGAATTTGTCTG AGCATTGTGCTTTATCTCTATTGATTTGGTGCATCTGTTAGCAGCAGATGTCTTAGGATAATTGCTTCTCACTTT ATGCCATTTACGCTCAGGAAAAATTTCTAAGAACCACTATTGTGGATAGTGTGGGGTGTAGTTTTGAACATGC CAATAAAATGGTTATACCATTACAAAGGATTAGAGGAATCCACAAATTTCTCAGGCCAAGGATTATCCATAGG CTATGAAGTTCATCAATGACCCAGTGGGTAATAAAGAGAAAATTCGAGATCCCAAACTCAAGGAGACGA ATGAGACAGATGAGACCTTTATGGTGGACAGAGAAGCAGAGAAGCTTCTCCATTCATGACCTCAGAAAAC AAAGTTGTGTGACACAAGATTGAAGTACCAAGATCTGACTGCAGTTTCTGGGGCCCTAAAAAGGAGGTG GGAGCATGTTTTGGG</u>
42 mm4_intron_EN SSSCG0000000 8043_3_423558 45	<u>CGTGGCATCAGACAAAGCTGGAAGTGGCAGTGGGGCTGGGGCTGAAGTCACTGTGCCACCTGGCCCTCCGCC GCCCTGTGCAGGAGGGGGCGGGCTGTCTGGATGCTTTCAGGGGGCTGAATGATCCAGGGAGCACCTAGGGAGGG TACCTGGGTGGGAGGAGCAGCTGGCCAAGCTAGGACCTGAGGGTGTGGGGCTGGTGTGCCACAGCAGGGGG CTGGAGGGTGTGGCTGGGCGAGGAGGGGCTGTGTCAGGGACTGGGCTGCATCCCAAGCTCAGGACTCAGGGA ATCGCAGGAGACAGAAGGCACAGAGGAGTGTAGAGAAAACGGCCAAGGGCGCAGGAGGTACAGACTGGGGC CTGATTGCCAGCCACTGGGCTCTGGGTGAAGGCCAGGTCCTGTCTCCATGGGTTCAGACTCAGGATTTAGG ACAGCCAGGACTGGCTTCCAGTCTCTCCCTGTAGTGGGGCAAGGCTGGGCATGAGTTGGAGGGAGGGTTT GGGCAGGAAGACGTGGCCCTGCAGCTGGGCGCTGAGATCGGAGGATGGATGCTGCTCTTCCAGGACATT</u>
43 mm3_intergenic_SL13A4 ENS SSCG00000026	<u>CAGAAGGTTCCTCCGTCACCGCTCAGTGGAGCGCAGGAGTCTCCACAGAGACAGGCTCGGGTGTCTG TGCTCTGCTCCGCCCTCCCTCCTCAGCAGCTTGGTCTGGAGAGCTAAAGCTTCCCTCCCTCCCATATATC GTCTCTCAATCAGCTCTTCTGAAAACAGGACAGACAAAAGCTGTCTGGTTCCTCAGAGGCTGAGGCTCA ACAGCTGAAGAGTCTCACTGGGTTGATGTTATTCTAATTTGTAATCCCTTTAGAGACTGCAAGGAGAAATC</u>

054_18_143677 87	CATCTGCCTTACCAGAGAGCAAACGAGTGACGCTCTCTTTGGGAGAAAGTCTCACCAGCACTTGAGCC TAACATCAGCTCCTTTCTCCTAAGGGTTCTGTCTGAGTTCTCCACACAAAGGCAGTTCTACGAAGGCCTCT CTGTGGCTATCAGCACTTATCATTACTTCAAGTCCCTTAAAGCATCTTTCTCAATAGTCTCTATGCTTGG ACCAAAATCTGTAAAGAAATAGTGTTCCTCAGGAAAGAGGCTGGCTG
44 mm4_intergenic _U6 ENSSSCG0 0000021497_10 _78541669	<u>AGCCATCTGGGATCCTCTGTTTCATTTTGATAGTTT</u> AGCTTCATAGATTCCTCTAGAAGACAGCTTGTCTGTCA CATTCTCCTGGAAGAGTCCATGGTCTTGAGAGCCGATTTCTTTACATATTGTAGCTGCAGCAAAGATTGAACAG GGCCCTCAAATCATGAACCTGTTGGCTTGGGAACATCTCTTAGGGCTGTGATCATGGAAAATTTGCCTCCTCACTA TTCCTACTGTGCAATTTTCTTCCATTCCTTGTGGAAAAATGTATATTCTAGCAACAATCATTCAAAAAGTAAT AGAAAATGCTGTTCAAATTTGCATTATATATAATTAATTCAAAATGACATGAGNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNTTCAATGCTAAATTAATAGATTAACCCCATTTCTAATTACCCTCCTGTGAAAATCA TTGAATCTACTGAATTTTGGCCAGAAATTTTAAAGTACCAATAAAAAGATTTAGTCTTCATCTGTCTAGCT AAGTATATTCCTTTCGTTAAAAATCTGAGAAACATGTCCTTCACATTT <u>CAGGCTCTCTCCTCCACT</u>
45 mm4_intergenic _GORAB MET TL11B_4_8817 5014	<u>CTTAGGCTTCTCCCGCTTGGAAATCCCGATTGCAATG</u> TACTAGTAAGACCTATCAATTTCTCATTTTAAGCAATATT TCAGAGATTTAAAAATGCGAGCGTTGTTAAAGTACATATAGTCAGGATGATTTAAAAAGAAACCCTATTTTAATT TTTCAGATTTCTTCTCAGTGTTCATTTTAAACACAGTTATTTGGCTTACATTTAAAAATCCCATGGGTGG CATTGGCTTTAGTGTGCAATATTTTAAAAACAGAAATAAAGGAGTAGGCTAAAAATAAAATACTTAAAGAAAC GATTTGTAATGAGTATTGAGACTTAAATAGGTGATTAGAAAGTGGGATGTTTGGAAATCTCTTTGTAACTTTTAA GCTTTTATACCTAAAAGGATTTTGAATATAGGTGTCCACAACACTTCATTTTAAATGTGGACTCATTTTCCC TAGCATTTAAAAGTTAAAATGTATCCAAAAGGATTGGAAGGAGACAGCTTCATCCAGTTTTTGAACCTAAACT NNNNNNNNNNNTTAAAGATTATCTAGCTCCGAAATAATAGATGGGG
46 mm4_intergenic _RNF19B ENSS SCG00000303 12_6_83284851	<u>GACCCTCAGTGCCTGAACTCTTCTCTTTAGGAAAGAGGATGGCTT</u> CACTGGGAAAAATACTCTGAAAAACCTTTT AAGCTGAAGGTGTGATCTTGAAGCTCCAGAGGCAGCTGCGATGGAGGCAACAAAGAAAGAGGATTTGGGATTTG AATTTGTTCTAAAATGCCACAAATGTTTAAAGTACCAAGGACTCAGAGAAATCTACCAGAAACTGGAGATTGA ATTTGGGAAATGGGCAGGAACCAAGGTAGGGGTGGAGTTGGGGTGGGACAGAAGGGAGGCAGGAAAGCC AGCCAGGGACACCCTACTCCCTACTCAACCCTAGGAATGGTAGGAGACATTTCTCCCTCCTCATGGGG GCTACATGAAGGCCGAATAGGCTTGAGCTTGACAGGTGGTAGGGGTGAGGGGGTACTGTGACCAGGAGACAGG AGAGGAAGCCACCCTCAACCCTAAGCTTCATGCAGTGGGG
47 mm4_exon_LST 1_7_27539143	<u>CGATGTGCCTCTTCTGGGTTCTCCCGCTTTCGCGCTCCCTCT</u> ACCCTTGGCCTGGAAAGTCCAGGGAGGG AGTTCCAGCACCTACGCCACCACCCTCCCTCTCCATGCCCGGGAGGCTAAGGCCAAGTGGAGTATCAT TTGTGATTGATCTAGTGGCAACGGCTGCAGACCAATGTCCTTCTTCTGGCCCTCAGAGGAGCTTGAAGCTT AAACACCATCTTACCCAATGACTCCCTACTTGCACCCAGAAATGGGCGCCAGGGTCACTGGCTCAGGTTTTGG TGGTGGCCAAAACCTAAGCTGGGGCTTGGAGTGGACGGAGCAGCCTGAGACACAGAAGGTGGTAAATAGTCTTTA CTGGGGGACCATAGGCAGCCCTGACTACCCGCTCGGGTTAGGGGAGGCGGCTGGGGGGCTCAGTGGGCTTG TCCTTGGCAATGACGGCGTAGTCCGACTGAGATCCTCTTGTCTCTTCCCTTCCCTTGGGGAGGGTGTCTCCG TACTGGCAGCCTCAGCAGGGTTCATAGTAGGGCTCC
48 mm4_intron_EN SSSCG0000002 1813_9_118320 042	<u>ATCAACACCACAGACCTGCCCTTCCAGATAGACTGGAATG</u> TATCTTCTGTCAACATCGTGGTCCCTAAAATC AGCCTGCATAGCCTCATTCTTACTTTTACAGAGTGTCAATTTCTGACGTTTCTTCCATGAGAGGGCTCAAAACGG TAATTTCTCTTTCTTAAAGGAAACAACCAATGGTGAGTGAAGTAAAAAACGTTGTCTTTTGGGAAGGATGC TCCTTGAGAGAACACACACTTAAGCAGAAGTAAATTTAATCTTGAAGATTTAGGGGATAGTGCCTGGGGT ATGTTCAAAGAATCTTTAAAAGTGCATTTCTCATGCAGTACATGTGATTTTGAAGGCAACCAACTGACATTT CTAATGTATGCTGAGCCTACAGGTAGACAACAATGCCACACCCTGTCAAATTTCTATGGTGCCTTCGAATCCT TGTGGCCTTGCATCTAAATGTCTGCATAGCAACGATTGGAGAGGCT
49 mm4_intron_EN SSSCG0000001 5700_15_20000 512	<u>CCCAAGCATGCATTGGCAA</u> GTTTGGATTTGTTGTTGTTGTTGTTGCACAAACCTCTTTTATTGCCGTAGGATCAAT GAGAAAAGGATCTTCTCTTAGTGATCTCAGAGAGGGAGACAATGAAGGAAGAAAGTGTACAGAACTGCGAGA ACGTGGTTGAGGAAGCATGGGTGAAGTGTGAGTTCTTGGAGATGAGTTGTGAGGAAGCACTGAGACAAGTCTA TAAAAGGGATTGTTTACTCGTTCAGGCAGTGGAAACACAGCAGTAGAGGTAATTCATGAGATCTGAAGGCAGCG CATGCCGAGTTCATGTTTACGCCCTGACCTCTTAAACCTCTGATCCAATCTTTGTAATGACTATGATTATGATCT CTGTCTTACCTCAGTGTGACAGTGGACGTTATGCCAGTTATATAATGTACAGAAGATGAATTATATAAAT ATTAGTAGTGTACCTTGGAAATCCTTGGAGTGAATTTGCTTTTTAAAAAATAATTAGTTTTCCACCCTACT
50 mm4_intron_EN SSSCG0000000 4369_1_815801 39	<u>TGAAGACTGGCACCTGAAGCC</u> AAATCCTACTTGCCTTGGAGCCTGGTATCCCTGGGAGAAACTCTTAAAGTA TCAGTAAATAATTGATCACTTAATCCTTCTTCTTCTTCTTGGCCCTCAGTGGGCCCTCCTCATTTTCTC CAGCCCGCACTGTTCCACTTATTAGTAAACAGTTAAATCTTTTGGCAAGTTGACACGCTCTGGAAGAGCTAA GTGGCAGCAAGGGGTGAGTGAGATTGTGAGCAACTTGGAGAAAATATCTGGCCACTCTGGACTCACCGGCCCTT GACCTCTCATTGTACAATAGCTTTTGGAGGAGAAAATCTTTTGGTAGGGGGGAAAAAATGTTTTCAATGTTTCC <b>TTGCTCTCTTTGGT</b> CATGAGATGGCTTATTCTTTTTTAAACGAGCCGGCTTATTAGCTGGGTTTCAAATA TTCTAAAACCTTACGCTGTTTGAAGTATGTTATAAATGGAGAAGAGGTTCTGTAAAAGTGTCTCTGTCC <u>GCATGACTCAGCGCTAAC</u>

Note: Primers underlined, off-target sites in bold. Replace ambiguous bases with N. The potential off-target sites corresponding to tyr-sg1, tyr-sg2, il2rg-sg1, rag1-sg1, and rag1-sg2 were 1-10, 11-20, 21-30, 31-40, and 41-50, respectively.

**Table S4. *TYR* mutation of F<sub>0</sub> generation piglets**

Piglet ID	Sex	Genotypes	Indel
		<u>GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACTTCATGGG</u>	WT
a1	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACTTCATGGG	allele 1: WT
a2	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCA-----TCGACTC GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCA-----CCTTGGC	allele 1: $\Delta$ 352 allele 2: A→G, $\Delta$ 352
a3	Female	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTT-----TGGG --TCCC-----GGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAA-----GGG GTTCCCCTTCA-----CATGGG	allele 1: +1, $\Delta$ 11 allele 2: $\Delta$ 14 allele 3: $\Delta$ 70
a4	Female	GTTCCCCTTC--CGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAA-----A--GGG GTTCCCCTTCA-----CATGGG	allele 1: $\Delta$ 7 allele 2: $\Delta$ 70
b5	Female	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCTTTGGC-----GACTTTTGG AGGCACCCC-----TGGG	allele 1: $\Delta$ 67 allele 2: $\Delta$ 93
b6	Male	GTTCCCCTTCAGTTCATCTCCCGGGGTGGAT//CAGTGCTTTGGCAACTTCTCCATGGG GTTCCC-----CTTCATGGG	allele 1: +10, +3 allele 2: $\Delta$ 72
b7	Female	GTTCCATCCC-----CCGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAAC-----ATGGG GTTCCC-----GGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACT-----TGGG	allele 1: +2, $\Delta$ 7 allele 2: $\Delta$ 10
b8	Female	GTTCCCCT-----GGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAA-----CATGGG GTTCCCCT-----GGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACT-----GGG GTTCCCCTTCACCGGGGTGGATG-----CATGGG AGGGGTTCCT-----CATGGG	allele 1: $\Delta$ 8 allele 2: $\Delta$ 8 allele 3: $\Delta$ 58 allele 4: $\Delta$ 115
c9	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAAC-----ATGGG	allele 1: $\Delta$ 3
c10	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACTTCATGGG GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACT-----TGGG GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACT-----TGGG	allele 1: WT allele 2: $\Delta$ 3 allele 3: T→C, $\Delta$ 3
c11	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACTTCATGGG GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACTTCATGGG GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAAC-----ATGGG GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAAC-----ATGGG GTTCCC-----CTTCATGGG	allele 1: WT allele 2: +1 allele 3: $\Delta$ 3 allele 4: T→C, $\Delta$ 3 allele 5: $\Delta$ 72
c12	Female	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACT-----TGGG	allele 1: $\Delta$ 3
d13	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACTTCATGGG GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTTTGGCAACT-----ATGGG	allele 1: WT allele 2: $\Delta$ 2
d14	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTT-----TGGG CCCTGGGGAG-----TTGTAAGTTT	allele 1: $\Delta$ 11 allele 2: $\Delta$ 184
d15	Male	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTT-----TGGG	allele 1: $\Delta$ 11
d16	Female	GTTCCCCTTCACCGGGGTGGATGAACGGGAG//TGCCAGTGCTT-----TGGG	allele 1: $\Delta$ 11

Note: Underlines mark target sites. Red text indicates base insertion; yellow highlighting indicates base mutation; (-) indicates base deletion. (+) denotes the number of inserted bases; ( $\Delta$ ) denotes the number of deleted bases; (→) represents the mutant base.

**Table S5. *IL2RG* mutation of F<sub>0</sub> generation piglets**

Piglet ID	Sex	Genotypes	Indel
		<u>GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT</u>	WT
c9	Male	GAACCCAGGAGGCAGGACCCACAGACGCT-----GGGTAATTTGAAAT	allele 1: $\Delta$ 15
c10	Male	GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT	allele 1: WT allele 2: A→G
c11	Male	GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT	allele 1: WT
c12	Female	GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT GAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTTGAAAT	allele 1: WT allele 2: A→G allele 3: +1

Note: Underlines mark target sites. Red text indicates base insertion; yellow highlighting indicates base mutation; (-) indicates base deletion. (+) denotes the number of inserted bases; ( $\Delta$ ) denotes the number of deleted bases; (→) represents the mutant base.

**Table S6. *RAG1* mutation of F<sub>0</sub> generation piglets**

Piglet ID	Sex	Genotypes	Indel
		ATATAATCACCATATCTCAAGCCACAAGGAGTCGAAGGAGACATTGTGCATATTAAT	WT
d13	Male	ATATAATCACCATATCTCAAGCCACAAGGAGTTCGAAGGAGACATTGTGCATATTAAT ATATAATCACCATATCTCAAGCCACAAGGAGTTCGAAGGAGACATTGTGCATATTAAT	allele 1: +1 allele 2: T→A, +1
d14	Male	ATATAATCACCATATCTCAAGCCACAAGGAGTTCGAAGGAGACATTGTGCATATTAAT ATATAATCACCATATCTCAAGCCACAAGGAGTCGAAGGAGACATTGTGCATATTAAT	allele 1: +1 allele 2: +1
d15	Male	ATATAATCACCATATCTCAAGCCACAAGGAGTTCGAAGGAGACATTGTGCATATTAAT ATATAATCACCATATCTCAAGCCACAAGGAGTTCGAAGGAGACATTGTGCATATTAAT	allele 1: +1 allele 2: +2
d16	Female	ATATAATCACCATATCTCAAGCCAC-----AAGGAGACATTGTGCATATTAAT	allele 1: △9

Note: Underlines mark target sites. Red text indicates base insertion; yellow highlighting indicates base mutation; (-) indicates base deletion. (+) denotes the number of inserted bases; (△) denotes the number of deleted bases; (→) represents the mutant base.

**Table S7. *IL2RG* mutation of F<sub>1</sub> generation piglets**

Piglet ID	Sex	Genotypes	Indel
		GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	WT
1	Male	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT
2	Male	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT
3	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT GGAACCCAGGAGGCAGGACCCACAGACGCTAAAA-----CAGGATCTGGGTAATTGGAAAT	allele 1: WT allele 2: △3
4	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT GGAACCCAGGAGGCAGGACCCACAGACGCTAAAA-----CAGGATCTGGGTAATTGGAAAT	allele 1: WT allele 2: △3
5	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT allele 2: +1
6	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT
30	Male	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: +1
31	Male	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: +1
32	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT allele 2: +1
33	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT allele 1: A→G
34	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT
35	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT
36	Female	GGAACCCAGGAGGCAGGACCCACAGACGCTAAAACTACAGGATCTGGGTAATTGGAAAT	allele 1: WT

Note: Underlines mark target sites. Red text indicates base insertion; yellow highlighting indicates base mutation; (-) indicates base deletion. (+) denotes the number of inserted bases; (△) denotes the number of deleted bases; (→) represents the mutant base.



**Table S8. *TYR* mutation of F<sub>1</sub> generation piglets**

Piglet ID	Sex	Genotypes	Indel
		<u>GTTCCCCTTACCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCAACTTCATGGG</u>	WT
1	Male	GTTCCCCTTACCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCA-----TGGG GTTCCCCTTACCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCA-----TG <sup>A</sup> G	allele 1: $\Delta$ 6 allele 2: $\Delta$ 6, G→A
2	Male	GTTCCCCTTACCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCA-----TGGG	allele 1: $\Delta$ 6
3	Female	GTTCCCCTTACCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCA-----TGGG	allele 1: $\Delta$ 6
4	Female	GTTCCCCTTACCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCAAC-----ATGGG	allele 1: $\Delta$ 3
5	Female	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
6	Female	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
7	Female	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
8	Male	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCACTCC-----CCGGGTGGATGAACGGG/TGCCAGTGCTTTGGCAAC-----ATGGG	allele 1: +10, +3 allele 2: +2, $\Delta$ 7
9	Female	GTTCCC-----CTTCATGGG GTTCACTCC-----CCGGGTGGATGAACGGG/TGCCAGTGCTTTGGCAAC-----ATGGG	allele 1: $\Delta$ 72 allele 2: +2, $\Delta$ 7
10	Male	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG	allele 1: +10, +3
11	Female	GTTCCC-----CTTCATGGG GTTCACTCC-----CCGGGTGGATGAACGGG/TGCCAGTGCTTTGGCAAC-----ATGGG	allele 1: $\Delta$ 72 allele 2: +2, $\Delta$ 7
12	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCACTCC-----CCGGGTGGATGAACGGGAG/TGCCAGTGCTTTGGCAAC-----ATGGG	allele 1: +10, +3 allele 2: +2, $\Delta$ 7
13	Male	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCCCCTTACCGGGTGGATG-----CATGGG	allele 1: +10, +3 allele 2: $\Delta$ 58
14	Female	GTTCCC-----CTTCATGGG GTTCCCCTTCA-----AC <sup>T</sup> TCATGGG	allele 1: $\Delta$ 72 allele 2: T→C, $\Delta$ 66
15	Male	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG AGGGGTTCCT-----CATGGG	allele 1: +10, +3 allele 2: $\Delta$ 115
16	Female	GTTCCC-----CTTCATGGG GTTCCCCTTACCGGGTGGATG-----CATGGG	allele 1: $\Delta$ 72 allele 2: $\Delta$ 58
17	Female	GTTCCC-----CTTCATGGG AGGGGTTCCT-----CATGGG	allele 1: $\Delta$ 72 allele 2: $\Delta$ 115
18	Female	GTTCCC-----CTTCATGGG GTTCCCCTTACCGGGTGGATG-----CATGGG	allele 1: $\Delta$ 72 allele 2: $\Delta$ 58
19	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCCCCTTCA <u>ACC</u> GGGTGGATGAACGGGAG/TGCCAGTGCTT-----TGGG	allele 1: +10, +3 allele 2: +1, $\Delta$ 11
20	Female	GTTCCC-----CTTCATGGG GTTCCCCTTCA <u>ACC</u> GGGTGGATGAACGGGAG/TGCCAGTGCTT-----TGGG	allele 1: $\Delta$ 72 allele 2: +1, $\Delta$ 11
21	Male	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCCCCTTCA <u>ACC</u> GGGTGGATGAACGGGAG/TGCCAGTGCTT-----TGGG	allele 1: +10, +3 allele 2: +1, $\Delta$ 11
22	Male	GTTCCC-----CTTCATGGG GTTCCCCTTCA <u>ACC</u> GGGTGGATGAACGGGAG/TGCCAGTGCTT-----TGGG	allele 1: $\Delta$ 72 allele 2: +1, $\Delta$ 11
23	Female	GTTCCC-----CTTCATGGG CCCTGGGACC-----CCT-----GGGGT/TGCCAGTGCTTTGGCAA-----TGGG	allele 1: $\Delta$ 72 allele 2: $\Delta$ 18
24	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCCCCTTCA <u>ACC</u> GGGTGGATGAACGGGAG/TGCCAGTGCTT-----TGGG	allele 1: +10, +3 allele 2: +1, $\Delta$ 11
25	Male	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG	allele 1: +10, +3
26	Female	GTTCCC-----CTTCATGGG AGGCACCC-----TGGG	allele 1: $\Delta$ 72 allele 2: $\Delta$ 93
27	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG AGGCACCC-----TGGG	allele 1: +10, +3 allele 2: $\Delta$ 93
28	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG GTTCCCCTTCA <u>TCC</u> CCGGGTGGATGAACGG/TGCCAGTGCTT-----GG	allele 1: +10, +3 allele 2: +3, $\Delta$ 12
29	Female	GTTCCC-----CTTCATGGG AGGCACCC-----TGGG	allele 1: $\Delta$ 72 allele 2: $\Delta$ 93
30	Male	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
31	Male	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
32	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG	allele 1: +10, +3
33	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG	allele 1: +10, +3
34	Female	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
35	Female	GTTCCC-----CTTCATGGG	allele 1: $\Delta$ 72
36	Female	GTTCCCCTTCA <u>GTTCACTCC</u> CCGGGTGGAT/CAGTGCTTTGGCAACTTC <u>TCC</u> ATGGG	allele 1: +10, +3

Note: Underlines mark target sites. Red text indicates base insertion; yellow highlighting indicates base mutation; (-) indicates base deletion. (+) denotes the number of inserted bases; ( $\Delta$ ) denotes the number of deleted bases; (→) represents the mutant base.