SUPPLEMENTARY TABLE S1. PRIMER INFORMATION OF THE 41 VARIANTS VALIDATED BY SANGER SEQUENCING

Chr	*Position*	*Reference allele*	*Alternate allele*	*Gene*	*Forward primer*	*Reverse primer*
1	17316456	C	T	*ATP13A2*	GAGGCTAACCCAGAGTTCCA	CCGTGAGGAAGGAGACAGAG
1	160340766	C	A	*NHLH1*	AGAGACTGAGTCGGGCTTCA	CTGAGTTCAGACGTCCAGCA
2	219267800	C	T	*CTDSP1*	GACCTCGTGAGGTAGGACTGG	CTACTGGGTCTGCGTACTGGG
3	50684626	G	T	*MAPKAPK3*	GTAGTGCCACAGACCCCACT	CACCACACTGAATGGCGTAG
3	129390026	A	C	*TMCC1*	TTCTTTTGCAGCTGGAGGAT	TCGAACGGTTGGAAGTAAGC
4	74270076	T	A	*ALB*	GAGAAAACAGTTCCAGATGGTAAA	CTTACGTGCATCTCGACGAA
5	79368179	A	G	*THBS4*	TGGCCCAGGCAGAAGTGAC	TCGACAGCCTGGGAGATAGT
5	133295603	T	C	*C5orf15*	CTTTTGGTGGCAGGCTGTATGATG	ACAGAGGAGTAGGCGAGGGATGAG
5	136997689	T	C	*KLHL3*	AACCCGTTTAGAGCACATGG	GCCGTCATACACATCCACTG
5	176520192	A	G	*FGFR4*	ATGTTGGGAGCTGGGAGGGACTGA	CGGGGCCGCTGGAGGAGA
6	46655960	T	ins.	*TDRD6*	GCGGCGCCGAGTGAGGTAAAT	CTAGCACGCAGCCCAGCACTTC
7	141321533	AT	del.	*AGK*	TTTGTGCATGAGTGCATGTG	TTTCATTATAACCTCATTTGAACTGC
7	150938678	C	T	*SMARCD3*	CCCTGGGCTCCTTCCTTTCTCT	GGGCCTGAACTAGAATCCTGGTC
9	140352197	G	T	*NSMF*	ACGCGGCAGGCAGGCTCACTCAG	CTGGGCACATCCGGGGCACTCC
10	29782280	T	G	*SVIL*	AGATTAAGTAAGGGCCTGGGAAGC	CGCCGCCGTGATGGAGT
10	94267395	CAT	C	*IDE*	TGCCCCAACACCCTTTCT	ACGATGCCTTTCCCCTTAGT
10	120832522	T	C	*EIF3A*	CTTGGCAAAGGAGGGGTTAT	GTTATGGTGGCGCTGAATCT
11	74459941	C	T	*RNF169*	CGTACTGCCCCGCCCTCCACTCTT	CAACGGCGGCGACAACACCAACA
11	129744416	G	A	*NFRKB*	AGAGCGGATTCACCAAGCACAAG	GACTGGGGTGGGTGGCATACTG
12	7171685	A	C	*C1S*	TGAAATGTGATCCCTTGACG	GAAGTTGGAAGGGTGGACAA
12	95486473	T	C	*FGD6*	CTTGGATCGAAGGCTCCCAT	TGGTTTATGAGGGGAAATATGCT
14	24710238	AC	A-	*TINF2*	CTGGGGCAAAACATGTAAGG	GATGGTCCCTGAGGAAGATG
14	55836494	G	A	*ATG14*	CAGTGAATTTTGTGGCGAAA	GCTCGTTAACGGTGTCCAGT
14	94088825	T	A	*UNC79*	GGCCCCTCCGGTAAAAATG	CTGCCTGGGAACAATCTGAATCTT
16	31434433	A	C	*ITGAD*	CTCCCAAAGTGCTGGGATTA	CACACGGTATCGATGCTCAG
16	31434434	G	A	*ITGAD*	CTCCCAAAGTGCTGGGATTA	CACACGGTATCGATGCTCAG
16	65005565	T	C	*CDH11*	TATTTATGGGCCACCTTTCTCTT	TTATTATTTCCGGTTTCTTCTTCA
16	67916998	C	G	*EDC4*	TACAGCGCATCGTTAAGGGTGAGG	CAAGGTGGGCTAGGTGGGAAGAAA
16	70161297	G	C	*PDPR*	GATGGCAGACTACTCAAACAAACT	GGCCCAAGCTCCTCCCAACAAG
16	70304179	G	A	*AARS*	GGCAGCTTGAGTCTCTGCTT	AGCCTGGAAAACTCCACAGA
17	78318734	AT	A-	*RNF213*	CAAGAAGGCTCTGTCGAAGG	TGGTCAGAGGTGTGGAGTGA
18	61006104	C	T	*KDSR*	ACAATTTGTTTGGCCACCTG	TGATTTAGAATCCAGATGGACCTT
19	35175846	C	T	*ZNF302*	TTGGAATATACAGAATGCGACA	CCGTGATAAACACTGCTTCTCTT
19	46376146	G	C	*FOXA3*	CCTATTTCACTGGCCTGGAG	CAAGAGCTTCGTGGTGTGAG
19	57932175	G	T	*ZNF17*	GGCCTTTTTATTGCTGTGAA	AAAGGATTTCCCACAAATGC
20	5155891	T	G	*CDS2*	AGCTCAGGGCCCTCATCTCAG	ACCCCCGTCAATTCCCACAA
20	23358093	C	T	*NAPB*	AACACAGACTTGGCGAGCTT	CATGGGGTAATTCCTGTTCC
20	31466614	G	C	*EFCAB8*	TGAAGGCTGAGACCATTTTGC	CAAAGGACATCAGGCAGCAG
20	50407707	G	T	*SALL4*	GAGAGAGACCCTTCGTGTGC	GGTGGCCTTGTCAATGTTCT
22	21351254	A	G	*LZTR1*	TGTTTGCGGCCCCCTACTACTACG	CAGGCACGGCGATTCTTCACAA
9	132845876	T	C	*GPR107*	TGGGTACATGGTGGTGAATG	ATTTCTCTCCCATGGCCTTT