GeneRank	symbol	chr	gene	regionStart	regionEnd	cell	validated	Primer.R1.sequence	Primer.S1.sequence	Primer.S2.sequence
1	NRAS	1	ENSG00000009307	115081615	115081707	HEK	yes	AATGGCAACCTGCAAGACTT	GAACAGCGCACACAACTTG	GTAAGTCAGATAAAACACTTCTTG
1	PKM2	15	ENSG00000067225	70282417	70282583	B	yes	TCAAGAAGCCCCGCCCC	CTGCCTCACGGGCAATCAG	TCAGCCTCACGAGCTATCAG
1	PKM2	15	ENSG00000067225	70282417	70282583	HEK	yes	TCAAGAAGCCCCGCCCC	CTGCCTCACGGGCAATCAG	TCAGCCTCACGAGCTATCAG
1	TXNDC5	6	ENSG00000188428	7986371	7986500	HEK	yes	CGGTGGCAGCAAGAAGAG	TCGAAGACCACGTTTTTCTTC	AGTCATTAGCTGCTTGCATTC
70	EIF3S6IP	22	ENSG00000100129	36612718	36612798	HEK	yes	GAGTTGACAGGCTGATGGC	GATCCACAAATTTGAGGAGCTT	GTTGACTTCTACATTGATAAGCTT
75	SFPQ	1	ENSG00000116560	35425391	35425439	B	no	AAATGCAGAAACGTAAAGAAATG	GCATGTCTCTTTCCCGTGG	CTCCTGAACCATAGGGATTGG
79	GNB2L1	5	ENSG00000204628	180597215	180597325	HEK	yes	AGGATGGCCAGGCCATGT	TGATCTTTCCCTCTAAATCCCA	AGCCAGCAAACAGAGTCCA
86	C17orf84	17	ENSG00000133030	17024646	17024708	HEK	yes	CGCGTGCTCAACTTGGAT	GGCCCATGCAGGAGAGT	AGAAACATCAGGTCCAAGAGT
105	TCF3	19	ENSG00000071564	1566284	1566519	B	yes	CCGCCAGCGAGATCAAG	AGCACCTCGTCCGTACTGCTG	CCTCGTCCTCGTCTGGGCTG
106	NONO	X	ENSG00000147140	70421559	70421672	HEK	yes	GTTGCCCATTTGCAGGTATTG	GGAAGAAATACTTCTCAAGGGT	CTGCAATCGAAGTTGAGGGT
108	MKI67	10	ENSG00000148773	129803182	129804261	B	yes	ATGTAATAACTATTATTGATCGTTCC	GAATCTTGAGCTTTCTCATCAG	GGTATTCCCTCACTCTCATCAG
109	ILF2	1	ENSG00000143621	151901805	151901895	HEK	no	GACAGCCTTTGGCCCTAAAC	TGTATAGCAGACCATGTCCTG	AGATATTTCAGAAGCAAGATCTG
115	APP	21	ENSG00000142192	26291546	26291602	HEK	yes	TCTCCCGCTGGTACTTTGA	TTGAGTAAACTTTGGGACATGG	GGCTGCTGTTGTAGGAATGG
129	CCT3	1	ENSG00000163468	154546973	154547104	HEK	yes	GCCCATGCCTTGACAGAAAA	GGGTGTGCTTGGCCCG	AGCAGAACTGCCGTCCG
153	STAG2	X	ENSG00000101972	123052385	123052495	HEK	yes	TGTTCTTTGATGGTGGCAAATC	AATCTTCAGCATGCCATTCG	TCAAACACCTCTTGATTATAATCG
164	DIS3	13	ENSG00000083520	72243220	72243284	HEK	no	GCTCTACATTGTCGAGAACTC	TGGAACCATGTCAATCCTCTT	AATACATGAAAATGCCAGCCTT
209	SMARCA4	19	ENSG00000127616	11005443	11005541	B	yes	CGGCTTCCGCTTGGGG	GGAGCCACCTCTAAAGGAG	GAGGAGCAGGATGAGGAG
212	LDHA	11	ENSG00000134333	18380963	18381136	B	yes	CCTTTGAGTTTGATCACCTCATA	AACATGGAGATTCCAGTGTGC	GCTTATTGTTTCAAATCCAGTGC
235	WHSC1	4	ENSG00000109685	1913864	1914090	HEK	yes	CACACAGCTGGCACACATAC	AACAAATTTTAAGACCAAGGTC	CCTTAACTGAGAATGAGGTC
263	WHSC1	4	ENSG00000109685	1913864	1914090	B	yes	CACACAGCTGGCACACATAC	AACAAATTTTAAGACCAAGGTC	CCTTAACTGAGAATGAGGTC
263	CTPS	1	ENSG00000171793	41247053	41247149	HEK	no	CAGCCTTTCTGGAGGTAATGT	GGAAATTGTGGAGTTAGAAGATC	CCGCCACCGATTTGAGATC
275	LRPPRC	2	ENSG00000138095	44057798	44057919	HEK	no	AGGTGGCCTAGGTGGTAGT	TCACATCATACACAGCACCTA	ATCAATCTCTGGTATGTCACCTA
304	KPNB1	17	ENSG00000108424	43082751	43082809	HEK	yes	AGCCACCTCTGCTGATATTG	CCGTGGAGAACCTGCCC	GACCGTGTCTCCCGCCC
306	FXR1	3	ENSG00000114416	182175795	182175886	HEK	yes	GAGTGTTTTCTTCTTTTAAGGTATTA	CTAAAAACAAGAAAGAAATGGCA	GTTAATGAAAATGGGCTAGGCA
309	CCT6A	7	ENSG00000146731	56093549	56093708	HEK	no	CCCAAGCAGTCAGGACTTAG	GATTTGTTGTTATTAATCAAAAGGGA	TCATTAGAGTATGAGAAAACGGA
312	MPI	15	ENSG00000178802	72969921	72970048	HEK	yes	GAAGGGCAGGTTGCCATTAA	GACAAGCCTTATGCAGAGTTG	CCGCGAGTTGTGGATGG
358	SMARCA4	19	ENSG00000127616	11002406	11002569	HEK	no	TCCACGTTGAGCTTGTACTT	ACTGGAATCCTCACCAGGAC	AATACCTCAGGCTTGATGGAC
360	PSAP	10	ENSG00000197746	73255600	73255656	HEK	yes	GGATAATGGGGACGTTTGCC	TGGCTGATATAGTTCTTGCATAT	CACAGATCTCCTTGGGTTGTAT
378	NASP	1	ENSG00000132780	45845580	45846596	HEK	yes	CCAGCATATCCCAGGCAAG	CAGATGAAAGAGGGTGAAGAAA	GTAGAAAATAATGATAACATAGATGAAA
381	MATR3	5	ENSG00000015479	138641915	138641996	HEK	yes	ACGCCAAGAAAAAGGATCAATA	TGCATGTGCAGTTTTCAGATG	GCAGATGCAACTGCAGATG
394	PRPF8	17	ENSG00000174231	1530973	1531098	HEK	no	ATCAGCTCCTGACAGACTTG	TTCATTCCAGTCTTCATCCTGT	AACATTGGGAGTATGGTACTGT
429	MDC1	6	ENSG00000137337	30783322	30784113	HEK	yes	AGATCTGGACCTACAAGCTAC	ATGGTTCATCTAGGGTACCTG	TGCAATTCAGGAGGCCTG
439	HDAC1	1	ENSG00000116478	32570278	32570430	HEK	no	CTGAGGGGTTGGGGAAGAA	ACCCAGAGGAGAAGAAAGAAG	GACAAGCGCATCTCGAAAG
467	NP_006653.1	16	ENSG00000080603	30652716	30652830	HEK	yes	TCATCTTCTGCCCGACACA	ACAGCCTATTTCAAACAGCAG	GGGATGTCCACATATATAGCAG
503	GANAB	11	ENSG00000089597	62158358	62158423	HEK	yes	CATGGCTGAGGGACCCTAC	ATTAACCTTATCCGAGAAAGAG	GGTCTTTTGATCCTTGCGAG
511	SF3B2	11	ENSG00000087365	65592195	65592380	HEK	no	CGGGAGAGGTGGTTCTTGT	GCTGCCAAACAGAAGCAA	ATTTATGACATGTCCACGCAA
516	KHSRP	19	ENSG00000088247	6366256	6366312	B	no	CTGGGAAGAGTATTACAAAAAGAT	GGTGGCCACTTGCGCTT	GGCCAGGAAGCCCCCTT
525	KIAA0515	9	ENSG00000130723	133339662	133341743	HEK	yes	CCTCCTTCTCTGCCTTTTTAC	CGCCTTTGAAAGTGAAAAGATC	ATGGACATGCGTGTCAGATC
564	NUP210	3	ENSG00000132182	13404803	13404953	HEK	no	CTGGACTCCGAAGGGAACA	CCAAGAAAGTGAGGATTCGC	GCAGGGCGTACATTCGC
577	EIF2A	3	ENSG00000144895	151752833	151752902	HEK	yes	TTCAAGGCAAACTGCCTTCA	AGCACAGTGTTTCCAAGGGA	GCCGCTCTTGACAGGGA
577	EIF2A	3	ENSG00000144895	151783677	151783742	HEK	no	ATATTCTGTGTATACCAATGGGTTT	AAACAGCTAGAAAAAAATCAGTTG	AAAAATCAAGAACCTAAAGAAGTTG
642	PFKL	21	ENSG00000141959	44557949	44557993	HEK	no	GATGATGATGTTCAGTCGGGA	GCCGGCACTGCGGGTA	CACCACTGCCCAGAGGTA
647	RCC1	1	ENSG00000180198	28729622	28729714	HEK	yes	CCTCAGCCTGCACAACATC	CAGAAAACCCGACCAGTCT	AAGCAAGAAGGTGAAGGTCT
707	NCAPD2	12	ENSG00000010292	6508940	6509020	HEK	no	CAAAAAAGCACTGAAGATGGAC	GTTCCGCACATCCCGAAC	CTTTCCACACCATCATGAAAAC
848	DUS1L	17	ENSG00000169718	77609506	77609581	HEK	no	CGGGCCCTGGAGGAAGA	GAACACACATCTGTTGCCCTT	TTAAAAAGCAATCCGTGACCTT
984	WNK1	12	ENSG00000060237	859000	860426	B	yes	GTAGCCAGTACTTCTGTCGG	GGAGATGTTCTGTACCAGGGC	AGTATCAGCTGGAAAACAGGGC
1049	PSAT1	9	ENSG00000135069	80106690	80106759	HEK	yes	ACCAAGCTCCTGTCACCAC	TGTGCGGGAATTGCTAGC	TTGGCATTAGTGTTCTTGAGC
1057	WNK1	12	ENSG00000060237	859000	860426	HEK	yes	GTAGCCAGTACTTCTGTCGG	GGAGATGTTCTGTACCAGGGC	AGTATCAGCTGGAAAACAGGGC
1208	UPF1	19	ENSG00000005007	18819553	18819642	B	yes	GATGAAGCCGAGGAGGAAG	GGAAATACTTCTGGCAGCCA	ATACACGCCTGCAGCCA
1333	MARS	12	ENSG00000166986	56196295	56196387	HEK	no	CTTTTTCTTCTTGCCTTTAGGG	GGATGAAGTGACAAAACAAGGA	TTGGAGGGGGCCAGGGA
1516	GLTSCR2	19	ENSG00000105373	52950417	52950592	HEK	no	CTCGAGGCTCGATCATATTC	CTGGGGCGGCTCAAGTA	GCTGTGCACAGGCTGGTA
1543	TM9SF2	13	ENSG00000125304	98970291	98970384	HEK	no	AGGCATATTATCCACAATCCAG	AATTGAACCTTCACCATATAAGTTT	CTTCCTTATGAATACACAGCTTT
1565	CCT8	21	ENSG00000156261	29354733	29354852	HEK	no	CAGTATGCTATTAAGAAGTTTGC	AGCAGGGACTTCAGCCTC	TGGTTTTGCCATGATGATCTC
1664	TCOF1	5	ENSG00000070814	149731762	149731992	HEK	no	CCTCCTCTGGCTTCCCTG	GGGACACGAAGCCAGGTA	ATGAGACAGACGTGGAGGTA
2374	MBTPS1	16	ENSG00000140943	82684294	82684403	HEK	no	ATGGGATATACAGGTGCTAATGT	TGCCATGGCCCAACCCAT	AAACCAAGATGTGTAAGATACCAT
2429	IPO7	11	ENSG00000205339	9401129	9401263	HEK	yes	AGCAGTGGTAGGAGAAATGAA	TGAAGCCCCATATACAAGGC	TGTTGGTGTCCAGCAAGGC
2515	ALDH5A1	6	ENSG00000112294	24610730	24610813	B	no	GGCCCGCCTGTCCTTTG	AATAATCACAGCTGAAAGTGGA	AGGTCTCCGCCAAGGGA
2629	PRPF40A	2	ENSG00000196504	153228898	153229012	HEK	no	GGAGTTACAAAATATGGACAAAGAA	TTCATGTAATTCATCTAAAAATATCTG	GATCAAGTGCAGTTGATCCTG
3662	COPE	19	ENSG00000105669	18884793	18884855	HEK	no	GGTGAGAAGACAGCGAAATG	CTCTCTGGGCTTGATAGCTT	ACCACACCGAACTTCCTCTT
3826	ADRM1	20	ENSG00000130706	60312019	60312232	HEK	no	CAATGCTCCTCATCCTGGTC	GGGAACGTGGAAGACGAC	GGGCGCGAGGCAGGAC
3869	NRD1	1	ENSG00000078618	52075747	52075880	HEK	yes	GCTCTGAACAAGGGTGATGC	TAGGGTAGACATGGTACCCA	CTTATCAACAACTTCAGAACCA