

Todas as Seqs

Anexo 1

	AgilentProbelD	Sequence	TargetID	GeneSymbol
1	A_33_P3323188 728743	TATTTCTACAGGTTGCTGACTCCTGCGGGAGCTGACTGAGTGGAATAAATGTTCTCTCAA	ref NR_027237	entg LOC728743
2	A_24_P336276,A_24_P588897 28232	GAACTCAAGTCTACGCTTTGGGAGTTCTTTTCTCCTCCTTCGTTTGTGGGCTTCATC	ref NM_001145044	entg SLCO3A1
3	A_23_P21990 9963	GAAGACACTCCAGAAAAATACAGAAACTGCATCTGTGTGCACCAAGGTCTGAAAAAATGACT	ref NM_152685	entg SLC23A1
4	A_33_P3284463 427	TGTCCACTTCATTTTGTATAATCACAGTTGTGTTCTCTGACACTCAATAAACAGTCACTGG	ref NM_177924	entg ASAH1
5	A_33_P3349912 401258	GTTTGTATGCTGTGCACATCTTACCATCATCACAAATTGAATATACAACATGTGCCAGGC	ref NM_001257357	entg RAB44
6	A_23_P157283 79161	CCCTCAACTACCTCCAAAAACCGTTGAATATATCTTTTGCTGTCTGCATCTCTTTGAGTAG	ref NM_024315	entg TMEM243
7	A_23_P152136 64785	CCAGATTGTGCAGATGCAAACTTAGGCTGTCTTGATGCAAACTTAGAACCCACAGAAATGC	ref NM_001126129	entg GINS3
8	A_23_P62901 7832	TTTTAGAAGCAGCCTCATGGTCTCATGCTTAATCTTGCTCTCTCTCTCTTTATGATG	ref NM_006763	entg BTG2
9	A_23_P156284 1627	TTGGGAAAATATCACTTTGTATTCTCTGTCCAGGGCTTCAGATATTTTGCACGAATTTTA	ref NM_080881	entg DBN1
10	A_23_P202939 334	CGTCACAGGAGTCTTTGTAATGCTTGACAGTTGATGTCGATGCTCACTGCTTCTGCTTT	ref NM_001642	entg APLP2
11	A_23_P357717 8115	TTTCCCCCTTTATAGATGGTGCACGCACCTGGGTGTACAAAGTTGTATGTGGCATGAAT	ref NM_021966	entg TCL1A
12	A_33_P3461039 728705	CAAGATTGTAGCCACTCCTGGGAGATTTTGCATTTTACGGTTATTAAAAAGCCATAACTC	gb AK055712	entg LOC728705

13	A_33_P3421728 1608	ATCCCTTATTTCTATCTTATTCTGATTCTGGCCATGCTACAAACATGTTCTCACCTGCC	ref NM_001346	entg DGKG
14	A_23_P104798 3606	TTGAATGACCAAGTTCTCTTCATTGACCAAGGAAATCGGCCCTCTATTTGAAGATATGACT	ref NM_001562	entg IL18
15	A_24_P350245,A_33_P3259775 80005	TCAAGATGTGGAGCTCTCCTTGCAGATCGGTGACACAGTTCACATCCTGGAGATGTACGA	ref NM_024940	entg DOCK5
16	A_24_P109644	ACTCTGTTGCATTGCTAIGGCCGGGACAAGGTCAIGTTCTCTTTGAGGCCAGCGCCGCT	gb AF229166	entg LOC220077
17	A_23_P53736 23014	TTCATGGGGCTCCAGGAAGCCTGTATCACCTGTGTAAGTTGGTATTTGGGCACCTTTATAT	ref NM_033624	entg FBXO21
18	A_23_P105862,A_33_P3223495,A_33_...	ATATGTAAAGGGCCATTCTTAAGTTCTCTCCTTAAACTTAATGCTGTCAAGTGTAGATG	ref NM_023037	entg FRY
19	A_23_P331748 945	GGGACCAAAGGCTGATCTTGGAGATTTAACTCCCCACAGGCAATGGGTTTATAGACATT	ref NM_001772	entg CD33
20	A_23_P4294 7775	GAAACCTTATAAGTGTAGTGACTGTGGGAAAACCTTCAAACAGAGCTCAAACCTCGGTCA	ref NM_014519	entg ZNF232
21	A_23_P214330 1992	TGCCGACCATCCATTCTTTTCTTTATTTCGGCATAATTCTCAGGTAGCATCCTATTCTT	ref NM_030666	entg SERPINB1
22	A_33_P3231297 8804	CTGAAAACTGCAAAAGTGAACTTAACTGAGATCCAGCAACAGGTTCTGTTTAAAGAAAAAT	ref NM_003851	entg CREG1
23	A_24_P20630 51176	GCCCCAAAAGTGCATCCTAACGTTTGTCAATCCAGTTTGAGTTAATGTGTGAGCATTTT	ref NM_016269	entg LEF1
24	A_23_P5601 1796	ATCCTTACTCCTGCATTGTTCTTTGCCAGAGACCTATTTAAAAAATTTTAAAAATTCTCATT	ref NM_001381	entg DOK1
25	A_24_P203056 605	TCGCCAAGAACCCTGGTTAGAGGCATAAAGACCTTTTTTACCCTTACCTAAATTTTTTCCC	ref NM_020993	entg BCL7A
26	A_33_P3290403,A_23_P50081 3613	CAGATCACCTTGTGGAAGATTTAAATTATTCTGAGTTGCGAGAGAGGTTTCTTTCACACA	ref NM_014214	entg IMP2
27	A_33_P3415560,A_23_P416813 284406	GTAAGAAGGCCCTTAGGGCAACATTCACACCTTACTCATCTGAAAAATTCATAATGTAA	ref NM_133466	entg ZFP82

28	A_23_P169470 1025	TTCTTCAACAGGAGAAATTTACTGTGTTTCTTTTGGTTCCATTGTTGGAGACATTCTCTG	ref NM_001261	entg CDK9
28	A_33_P3225690 9658	GTGACCCAGTCCTGTTTCTCTGTGTTTTAGTTATTAAGAAATTTCTGTACCCAAAAGTG	ref NM_014643	entg ZNF516
30	A_23_P168951 22882	CCCGCTCTGTAGCATGATCAGTACTATTGTGACATTAAACAAACAATAAGAATCTT	ref NM_014943	entg ZHX2
31	A_24_P29595,A_23_P82047 134957	AAC TGCGGCCATGTTATCAAGTGCAGAGTCAATTTCTAAACATGCTCATGAGATTATGTT	ref NM_001127715	entg STXBPS
32	A_23_P131435,A_24_P396702 9936	ATATCAGCATTTGGTGATTGCTAGCACGGTAATTTTGACAGTTTTGGGAGCAATCATTTGG	ref NM_001198759	entg LY75-CD302
33	A_33_P3410409,A_23_P416608,A_24_...	ATAAATACCTTTGATCTAAGGGTTCAGCCTTTCAATGTGACACAAGGAAAGTATTTCTACA	ref NM_001122606	entg LAMP2
34	A_33_P3251985,A_23_P166677 64747	ATGATACTGGATTCTCGGGGGTATTTGTTTTGGAAAGTGTTCTTCATTGCCTGTGTTTCT	ref NM_022736	entg MFSD1
35	A_24_P945283 1741	ACTCCTTCATCTCTAACAGAGGAAGAACTGTATTATCAAACTTATGGTCTACCCCATGAA	ref NM_021120	entg DLG3
36	A_23_P113034 83938	GTCAGCTTGGAAAAGGATGAGGAAGACTACAAGAGATACAGATGCTTTGTTCTGTACAAG	ref NM_032024	entg C10orf11
37	A_24_P213788 641518	AGATTAATGCAGAAACAAGGTCGTTAGTCTCATTTGTTTATCCAGTTACTAGCTGCATAGAT	ref NR_029373	entg LEF1-AS1
38	A_33_P3329356	CGGCTTCAGGAGTACAAGTTTCCCCATCAAAAGGTTTGGAAATAAATTACACTAAAAAATTG	ref AA769836	
39	A_33_P3238690,A_23_P350187,A_33_...	ACTTCAACCTTTTTGTTCTAAAAAATTCAGGGATATTTTCAGCTCATGCTCTCCCTATGCCA	ref NM_001127208	entg TET2
40	A_33_P3241521,A_32_P197561,A_24_...	ACATGGTCTCAGCCGTGAACAGAGAAGAGTGCTTTGCGACCAGTCGTCAGACCCCGACCT	ref NM_001290360	entg EBF1
41	A_23_P62188 55906	GGGAGGGGGGATATTTTCTTCTTAAGTAGTTTTACATTGCCACAGTGTGTATGTGTTC	ref NM_001178032	entg ZC4H2

42	A_23_P408271 51170	CACCTAGTTTTCTGAAAACTGATTTACCAGGTTTAGGTTGATGTCATCTAATAGTGCCAG	ref NM_016245	entg HSD17B11
43	A_23_P133293,A_24_P212481 79772	AGCAACCCAGTAAGTACAGTTATCAAAAAATACTAGGAAACTATATCCATAICGCTTTTGG	ref NM_024717	entg MCTP1
44	A_24_P325046,A_23_P124855 84186	TGCACCTACTCTGTAACTAACTGCGATTATAAAATGAAACAATCTCTTCTAATTGGC	ens ENST00000322831	entg ZCCHC7
45	A_23_P145408,A_33_P3272580 2519	GCCATGGACAGCCACTTAACTGGATTCTTTGGAGCAAAATGGCATTATGGTAGAACTGC	ref NM_032020	entg FUCA2
46	A_33_P3257165,A_32_P88120 29799	AAATGACAAAAGTCCAAAACTTTCCAAAGCGTATCTGCCGAACTGTCACCGAACGTACAGCT	ref NM_013313	entg YPEL1
47	A_23_P23279 92241	TTAGTCTCTTCTATTGGGTAGCTCTTGCTTTAATATTCTGTTGGTGAGTGTAAGGGAT	ref NM_052862	entg RCSD1
48	A_23_P165061 166	GTGCTGTATAIAGTCAGCTTATCTCGTGTCAATCGTCTGATCTCTACAGAGAGAAAGTG	ref NM_198969	entg AES
49	A_23_P214681,A_24_P252130 5467	TCTACAATGCCTACCTGAAAAAATTCAACATGACCAAAAAAGAGGCCCGCAGCATCCTCA	ref NM_177435	entg PPARD
50	A_23_P62659,A_24_P276628 5538	TAGCATGTCAGTTTGGAGAAATGATGAGCTACGCCCTTGATGAAAGAACCCGTGTGGTGCT	ref NM_000310	entg PPT1
51	A_23_P106973,A_33_P33368188 10801	AGGCTCTGTTCTCAATGGCCTTTTGCTACGTGCTCTCCCGAGAAAATTTGCTTTTTGTAT	ref NM_006640	entg SEPT9
52	A_23_P157495 5533	TGTCAACACATTTGTGAAGTCTTGTGCTATAAAGGGGAACTTCCCCCTAATAAAAGGGCCT	ref NM_001243974	entg PPP3CC
53	A_23_P127663 79056	TGGGCACACAAAAAGGATTTAGGGTATTTAAAAAATCTATGTCTCTCCCATCTCACTGACT	ref NM_024081	entg PRRG4
54	A_24_P365365 6929	TGGATGATTGGGACTTTAAACGACCCTCTTTCAAGTGGAATTCAGAGACCTGTCCTGTAT	ref NM_003200	entg TCF3
55	A_33_P3351290,A_23_P84596 51237	GTGCTTCTGCTCAAACGGCTCTCTTGCCACTTTATTTTCCCGAGAGACTGCTCCTAT	ens ENST00000509591	entg MZB1
56	A_23_P83175 401494	CATCCTTTTTGTGGTGATCACCAGTCAAGAGGAAAGTCCAAAGAGAAATATGTGGTGTGTGT	ref NM_001010915	entg PTPLAD2

57	A_23_P346969 5291	AAGAAAGCACTCAAACAGTTTAAAGCAAAAATTTGATGAGGCGCTCAGGGAAAGCTGGACTA	ref NM_006219	entg PIK3CB
58	A_33_P3321050,A_23_P111240,A_24_...	GGTAATGGCTCTGTATCTGAAAAAACACCACCTCTGGAGGAACAGGCAGAGATAAGAAA	ref NM_001100165	entg PHACTR2
59	A_24_P915196 203197	ATGTGGCCATGGTGTAGGCAGTGTCAATGTCTTCGAGTGAGAGTGAAGGTGTTAACTCATT	ref NM_153045	entg C9orf91
60	A_32_P105083 348751	TCCTCAAGTTTCAGTGTCTCAATATATATTTCCGATCAAGACTACAAGAGATCAGTCATTAC	ref NR_034096	entg FTCDNL1

Anexo 2

	Sequence	TargetID	GeneSymbol	PrpbeChromosome	Location
6	CAGGGAAAGGCATCTGGTCTGTCTGGAAAGCAAACATTATGTGGCCTCTGGTAGTTTTT	ref NM_002015	entg FOXO1	hs chr13:41130768-41130709	
6	ATTTAATGCATGATAGACACATATGAGGGGAATAGTCTAGATGGCTCCTCTCAGTACTT	ref NM_001287427	entg CCND3	hs chr6:41903252-41903193	
6	TCCTCAAGTTTCAGTGTCTCAATATATTTCCGATCAAGACTACAAGAGATCAGTCATTAC	ref NR_034096	entg FTCDNL1	hs chr2:200710883-200710824	
3	TCTAAACATAAAGAAAGCTCTTCTGTCCGGTTACTTTATGCAGATTGCTCGGGATGTTGA	ref NM_018180	entg DHX32	hs chr10:127527612-127526940	
6	CATTGGTGTGCAGATGAGTTGTAAAGCCAACTGAAAGAGTTCCTTCAAGAAAGTTCCTC	ref NM_001287219	entg RPS6KC1	hs chr1:213446224-213446283	
5	CTCAGTGAGAACGGTTGTCCCTGGATGCCGTGTGGGTTTGGTTCGGTGCTTCTCCACT	ref NM_032206	entg NLRC5	hs chr16:57077428-57077487	
7	CCAGATTGTGCAGATGCAAACTTAGGCTGTCTTGATGCAAACTTAGAACACACAGAAATGC	ref NM_001126129	entg GINS3	hs chr16:58439799-58439858	
6	CCCTCAACTACCTCCAAAACCGTTGAATATATTCTTTGCTGTGCTGCATCTCTTTGAGTAG	ref NM_024315	entg TMEM243	hs chr7:86827335-	

6	TTTTAGAAAGCAGCCTCATGGTCTCATGCTTAATCTTGCTCTCTCTCTCTTATGATG	ref NM_006763	entg BTG2	86827276
9				hs chr1:203278454-203278513
6	GCAATATCTGTTACTAGAGAACAATCCCATGTGTTTAAACTCTTCACTTCTTAGATGCAT	ref NM_001193460	entg MSRB3	hs chr12:65860358-65860417
6	GGGCCCCAAGGAACCAATTTATCACCCCATGACTGACGGAGTCTGAGAAAAAGCGAGAAGAA			
7	G	ref NM_002342	entg L1BR	hs chr12:6500070-6500129
6				hs chr19:10754558-10754617
8	TGGACATGCATTAAAGGGTCTATTAGCTTTCTCCGCTCTGTCTCAACAGCTGAGATGGG	ref NM_020428	entg SLC44A2	hs chr11:130014421-130014480
1	CGTCACAGGAGTCTTTGTAATGCTTGACAGTTGATGTCGATGCTCACTGCTTCTGCTTT	ref NM_001642	entg APLP2	hs chrY:21152726-21152667
0				hs chr15:90226612-90226553
6	CTACATGGGAACAAACAGATCGAACAGTTTTGAAGCTACTGTGTGTGAATGAACACTC	ref NM_013230	entg CD24	hs chr11:112020870-112020811
9	GTTAGGGTGTITTTAGGCTTGGAAGTAGTACCTACTTTAAAAGATGGCCTCTTGGTGGGA	ref NM_003847	entg PEX11A	hs chr8:25101212-25101271
7				hs chr19:51742998-51743057
0	TTGAATGACCAAGTCTCTTCATTGACCAAGGAAATCGGCCTCTATTTGAAGATATGACT	ref NM_001562	entg IL18	hs chr1:159752201-159752260
1	TCAAGATGTGGAGCTCTCCTTGCAGATCGGTGACACAGTTCACATCCTGGAGATGTACGA	ref NM_024940	entg DOCK5	hs chr18:11999126-11999185
5				hs chr1:93312831-93312772
1	GGGACCAAGGCTGATTCTTGGAGATTTAACTCCCCACAGGCAATGGGTTTATAGACATT	ref NM_001772	entg CD33	hs chr3:183547249-
9				
7	AAGTGGACTAAAGTATTAAACCCTCTAGCTCCCATTTGGCTGAAGACACTGAAGTAGCCCCA	ref NM_017823	entg DUSP23	
1				
2	CAGATCACCTTGTGGAAGATTTAATTATTTCTGAGTTGCGAGAGAGGTTTCCTTCACACA	ref NM_014214	entg IMPA2	
6	TGGAACCAAGAAAAAGAAATAGTGCTATTTGATAAGCCAACTAGAGGAACTACTGTACAA	ref NM_001252273	entg FAM69A	
7	A	ref NM_018622	entg PARL	
2	CCCCAGTCCGTGCTTTTAGAATGTGAATGATGATAAAGTTGTGAAATAAAGGTTTCTA			

3						183547190
1					entg LOC72874 3	hs chr7:150109494- 150109553
		TATTTCTACAGGTTGCTGACTCCTGCGGAGCTGACTGAGTGGAATAAATGTTCTCTCAA	ref NR_027237			
3						hs chr8:123986299- 123986358
0		CCCGCCTCTGTTAGCATGATCAGTACTATTGTGACATTAAACAACAATAAGATCTT	ref NM_014943		entg ZHX2	
7						hs chr17:41844207- 41844148
4		ATTAGAGCGCCAAATGTTTCTCTCAATCTTAAAGCAGTATACCTTTCCACAGGCTCG	ref NM_004090		entg DUSP3	
3					entg LY75- CD302	hs chr2:160628550- 160628491
2		ATATCAGCATTGGTGATTGCTAGCACGGTAATTTTGACAGTTTTGGGAGCAATCATTTGG	ref NM_001198759			
3						hs chrX:119575645- 119575586
3		ATAAATACCTTTGATCTAAGGGTTCAGCCCTTTCAATGTGACACAAGGAAAGTATTCTACA	ref NM_001122606		entg LAMP2	
3		GTCAGCTTGGAAAAGGATGAGGAAGACTACAAGAGATACAGATGCTTTGTTCTGTACAA				hs chr10:77807021- 77818442
6		G	ref NM_032024		entg C10orf11	
7		TAAGGACTCCAAGATGTACAAGGACCGCATCGAGGCCATCCTGCTGCAGATGGAGGAGG				hs chr9:139264280- 139264221
5		T	ref NM_052814		entg CARD9	
3						hs chrX:69725254- 69725313
5		ACTCCTTCATCTTAACAGAGGAAGAACTGTATTATCAAACCTTATGGTCTACCCATGAA	ref NM_021120		entg DLG3	
3						hs chr4:109097321- 109097380
7		AGATTAAATGCAGAACAAAGGTCGTTAGTCTCATTTGTTATCCAGTTACTAGCTGCATAGAT	ref NR_029373		entg LEF1-AS1	
7						hs chr16:69342827- 69342886
6		CTTGAGTAGCACATCAACATACAGCATTGTACATTACAATGAAAAATGTGTAACCTTAAGGG	ref NM_006750		entg SNTB2	
7						hs chr1:23832992- 23832933
7		CTTTATGAGCACCATGTAAGCCTCCTTGTATTGAGATAATTGGCATTAAACATTAAACT	ref NM_004091		entg E2F2	
2						hs chr4:108968805- 108968746
3		GCCCCAAACTGTATCCTCAACGTTTGTCAATCCAGTTTGAGTTAATGTGCTGAGCATTTT	ref NM_016269		entg LEF1	
7						hs chr5:138855656- 138855597
8		GTGCTTCAACCTGTGAAATGGGATCATAATCACTGCCTTACCTCCCTCACGGTTGTTGT	ref NM_198282		entg TMEM173	
7		GTCACCTGTTGAAGAGGATGACACCATCATGGAAGAATTGGTAGATAATCATATGCGCAAAA	ref NM_018946		entg NANS	hs chr9:100845266-

9	A				100845325
3					hs chr4:109177933-109177992
8		CGGCTTCAGGAGTACAAGTTTCCCCATCAAGGTTTGGAATAAATTACACTAAAAAATTG	ref AA769836	n/a	
4					hs chr5:158135091-158135032
0		ACATGGTCTCAGCCGTGAACAGAGAAGAGTGCTTTGCGACCAGTCGTCAGACCCCGACACCT	ref NM_001290360	entg EBF1	
4					hs chrX:64136455-64136396
1		GGGAGGGGGATATTTTCTTCCTTAAGTAGTTTACATTGCCACAGTGTGTAIGTTC	ref NM_001178032	entg ZC4H2	
4					hs chr4:88258426-88258367
2		CACCTAGTTTTCTGAAAACTGATTTACCAGGTTTAGGTTGATGTCACTAATAGTGCCAG	ref NM_016245	entg HSD17B11	
8					hs chr4:55606511-55606570
0		AAAGTGGTTGTAGTTATAGATGTCTAGGTACTTCAGGGGCACCTTCATTGAGAGTTTTGT	ref NM_000222	entg KIT	
4			ens ENST0000032283		hs chr9:37186845-37186904
4		TGCACCTACTCTGTAACTAACTGCGATTTATAAAATGAAACAATCTCTTAATTTGGC	1	entg ZCCHC7	
8					hs chr2:70187305-70187246
1		TCTGTCAATTGCTTTGAAGCCCATTTGTGCCTTATGCCAATAATTCAATTGCTGCAAAACAC	ref NM_152792	entg ASPRV1	
4					hs chr1:167674981-167675040
7		TTAGTCTCTTCTTATTGGGTAGCTCTTGCTTTAATAATTCTGTTTGGTGAGTGTAAAGGGAT	ref NM_052862	entg RCSD1	
8					hs chr8:121550176-121550117
2		TTGCCCTGTGCTTGATGCATGCAITTTCAAGCAAGTAATAAAGCAGCCTCATTTAATTCT	ref NM_021021	entg SNTB1	
4					hs chr6:35391843-35391902
9		TCTACAATGCCTACCTGAAAAAAGTTCACATGACCAAAAAAGAGGCCCGCAGCATCCTCA	ref NM_177435	entg PPARD	
5					hs chr17:75496557-75496616
1		AGGCTCTGTTCCCTCAATGGCCTTTTGCTACGTGCCTCCCGAGAAATTTGCTCTTTTGTAT	ref NM_006640	entg SEPT9	
8					hs chr13:74260392-74260333
3		AATGGTGTCTCAGACATATTCTGTTGGTGCAATTGCTTTTCTGTATTCAACTTTCCTATGA	ref NM_007249	entg KLF12	
5					hs chr8:22398566-22398625
2		TGTCAACACATTTGTGAAGTCTTTGTGCTATAAAGGGGAAGTTCCTTAATAAAAGGGCCT	ref NM_001243974	entg PPP3CC	
8		CAGTTTCAGCCGTTGAACACATAGGAATGTCTGTGGGTGACTCTACTGTGCTTTATCTTT	ref NM_182760	entg SUMF1	hs chr3:4403152-4403094

89	A_19_P00320362	GCACTGTGACTATAGGATCATGGATCAGAGGCTGCTTCCTCTTTGG TTCTGGGCATCAGC	ref NR_034143	entg CASC14	hs chr6:22136652- 22136593
90	A_33_P3226995 924	AAACTGTGCTCGTGGCGGATAAGAAATTCGGGGCATGTGTGGTG TACGAGGACATGTCG	ref NM_006137	entg CD7	hs chr17:80273301- 80273242
91	A_23_P58647,A_33_P340341 8 1495	TGCTTTTTAGGCTACAGTGTCTCGATGCCATAATCAGAACACACTT TTTTCCCTCTTC	ref NM_0012903 07	entg CTNNA1	hs chr5:138270387- 138270446
92	A_19_P00317462	CTATCTATCTGAATCCTAAACCAGCTCAGAAGATTTTAAAGTCATAT GACCTTGATTGTT	ens ENST000005 63287	entg LOC1019 29333	hs chr15:74770507- 74770448
93	A_23_P209055 933	GCCTCAGGCACAAGAAATGTGGACTATGTGATCCTCAAAACATTGA CACTGGATGGGCTG	ref NM_001771	entg CD22	hs chr19:35837555- 35837614
94	A_33_P3234277,A_23_P3091 3 3113	CTGAGGGTGTGCTGAGAGCCTCTTCCTGCCCCAGAACAGATTACAG CTCCACAAAGTTCC	ref NM_0012425 24	entg HLA- DPA1	hs chr6:33036945- 33036886
89	A_19_P00317141	GGAATCGGAGGTGCCTGGGTCACTCACAGAGCCAAACAAATACA ATTAGCTATTGCAAA	ref NR_034143	entg CASC14	hs chr6:22136557- 22136498
95	A_23_P303260,A_33_P33737 07 8417	GTCTGATGTTTACGGGGGAGAGTGTAGTTACTAAAAATGTTTAAACA TAATTTGGAAGAAG	ref NM_003569	entg STX7	hs chr6:132781224- 132781165
96	A_32_P356316,A_33_P32789 68 3111	TGGAAAGGTGTTTCTCTCACTCTGTCTTAAGGCTTGATAAAGTCAT TAAATTGTGTTT	ref NM_002119	entg HLA-DOA	hs chr6:32972029- 32971970
97	A_23_P7697 6643	GCTGATAAAATACTGGGAAGCATTCCTACCTGAAGCCAAAGCCATT GCCTAGCAATAAGA	ref NM_0012781 99	entg SNX2	hs chr5:122163341- 122165351
98	A_19_P00806169	TTATAAATTATGCCATCCTCCCTAGAAATGAGAATGCACAGCAAGCG GCAGACAATCACCC	gb EU250753		hs chr6:22147443- 22147384
99	A_23_P103775,A_33_P34060 30 84230	AAACTCTGAAGATTGGAAAAAACAGCCTAICTGTACTTTACCCGAA AATTGGAAATTTGC	ref NM_032270	entg LRR8C	hs chr1:90180324- 90180383
11	A_23_P357717 8115	TTTCCCCCTTATAGATGGTCACGCACCTGGGTGTTACAAAAGTTGT ATGTGGCATGAAT	ref NM_021966	entg TCL1A	hs chr14:96176337- 96176290
69	A_33_P3369844 100133941	CTACATGGGAACAAACAGATCGAACAGTTTTTGAAGCTACTGTGTGT GTGAATGAACACTC	ref NM_013230	entg CD24	hs chrY:21152726- 21152667

10	0	A_23_P27332 6925	AGAGGCATCGAATCATGCGACAGATGTAAAGGGTCCAAGTTGCCACATTGCTTCATT	ref NM_001083962	entg TCF4	hs chr18:52895486-52895237
10	1	A_23_P250347 814	AGGTGCAAGCCTTAGAGAAAGTTAAAGGTGCAGATATAAATGCTGAAGAGCCCCCAAAA	ref NM_001744	entg CAMK4	hs chr5:110819929-110819988
10	2	A_33_P3250133,A_23_P72059 54621	TGGAAGCTACATCGAAGATGAGCTCTTCATTGAGCTTTGATTGACCTGTACCCCTGGT	ref NM_019086	entg VSI10	hs chr12:118503705-118503646
10	3	A_33_P3308914 10518	TCCTCACTGGTGTGCTGTCCACAGATTTGTGAACCTCCTGGTAGTAAACACTTTTGCATC	ref NM_006383	entg CIB2	hs chr15:78397052-78396993
10	4	A_23_P161156 220929	GTGCTTTATGGTGGTCTTAGTCACAAAGATCAAAACACAGGATTGGTGTGAGTGAACGG	ref NM_001143769	entg ZNF438	hs chr10:31133829-31133770
10	5	A_24_P17870 10866	TTGTGCTTGGTTGTTTCAGGGCCATTTTCAGGTTTGGGTGTTTTCTGGGGATGTTAACATGG	ref NR_040662	entg HCP5	hs chr6:31432645-31432704
10	6	A_23_P91697 9215	AAGATTCACGTATCCATCTGGAGACCTACAGGAAGAAAGTGATTGGTTCCTCTGGTTCT	ref NM_004737	entg LARGE	hs chr22:33669391-33669332
10	7	A_23_P14302 79686	TTGACGTTTTCCTCCCTTCTTTGTGCAAGTTGGAAGTAGCAGTTTCTAAAGATGG	ref NR_026779	entg LINC00341	hs chr14:95873748-95873689
10	8	A_23_P212568 50852	ATTTGGCTCCTATTGAAGATGGCTTCTAAGAAAAACAAGATGCACAGAGGACACAGAAGGA	ref NM_016388	entg TRAT1	hs chr3:108572748-108572807
10	9	A_24_P64344,A_33_P3363637 29760	TAAGCGAGTATATAATATTCCTGTGCGATTATTTGAAGCAACAAAAAATATGCTCTGGG	ref NM_013314	entg BLNK	hs chr10:97956745-97956686
11	0	A_24_P838448 401237	TTCACCTGTCTAAATTTTCCAGAGCCCCCTCATATAAGGAACTGTATTATTGGTATAATCATC	ref NR_015410	entg CASC15	hs chr6:22194466-22194525
11	1	A_32_P351968 3109	GGACTATGCTGTAAACCAAAATTATTGTCCAAGGCTATATTTCTGGGATGAATATAATCTGA	ref NM_002118	entg HLA-DMB	hs chr6:32902563-32902504
11	2	A_23_P121702 132299	AGACTCTCAGCCTTCAGCTTCCTAAATTCGTGTCTGTGACTTTCGAAGTTTTTAAACC	ref NM_001014446	entg OCIAD2	hs chr4:48887525-48887466
11	3	A_33_P3355014 161145	CTCTGTCTCTCTTTTCACATTTGTGACACATAAAATATACTGGTGTGTGTCTCCAGGA	ref NM_182526	entg TMEM229B	hs chr14:67937042-67936983

11	4	A_32_P232559 439949	GCTTGGAGGAAACCCAGTTTGCACCTATTTGATGAGGAATTTGGCCAC CAAACCACTGATAC	ref NR_036502	entg PRKCQ- AS1	hs chr10:6626088- 6626147
11	5	A_33_P3314594,A_23_P4146 54 326624	TTTAGCCCTCCTGGGTTAAGAGCCAGATAAAGGAGAAATCCCTTTCC TAGGTTTGGAAATGT	ref NM_175738	entg RAB37	hs chr17:72742734- 72742793
89		A_19_P00317357	CACGATTGAGCAGCACTGTGACTATAGGATCATGGATCAGAGGCT GCTTCCTCTTTGGTT	ref NR_034143	entg CASC14	hs chr6:22136664- 22136605
11	6	A_23_P6293,A_33_P3385909 53347	TTTCAGAGGGCGTCTTAGTCTCACCCCAATGTGATTTGTAGAAAGCAC GAGACGCACCTTTTA	ref NM_018961	entg UBASH3A	hs chr21:43867379- 43867438
11	7	A_23_P343935 54583	GAGGGTTGAACCTCAATAAACCTTCAGATTCGGTCGGTAAAGACGTC TTCTAGAGCCTTTG	ref NM_022051	entg EGLN1	hs chr1:231502208- 231502149
11	8	A_23_P62920 22920	TGTGTGGGTTGGGTTAATTTTGGATCTTTGCCTAATAATGCATGTTG ATGTTATTGTGGG	ref NM_0012045 17	entg KIFAP3	hs chr1:169890773- 169890714
40		A_33_P3241521,A_32_P1975 61,A_24_...	ACATGGTCTCAGCCGTGAAACAGAAAGAGTGCTTTCGCACCAGTCGT CAGACCCCAGACCT	ref NM_0012903 60	entg EBF1	hs chr5:158135091- 158135032
11	9	A_23_P342934 7090	GAGGGGGGAAAGTGATAAACCTACAGGGTTGTGAGTCTGAAAA GAGGATCCCCCTCACC	ref NM_005078	entg TLE3	hs chr15:70341255- 70341196
12	0	A_23_P106675 5336	GAGTCAGCAACAGCAAGTTTACTCATAGAAGCTGGGGTATGTGT GTAAGGGTATTGTGT	ref NM_002661	entg PLCG2	hs chr16:81991575- 81991634
12	1	A_23_P327370,A_23_P22854 54858	CCTGGGGGTTTTGTGTCGTGACACTTTGTCTCAAGGAGATTCCACA TAGGGGATTGAATT	ref NM_017712	entg PGPEP1	hs chr19:18480282- 18480341
12	2	A_23_P201628 3915	ACCTTAATTACACTCCCCGCAACACAGCCATTATTTATTGTCTAGCTC CAGTTATCTGTA	ref NM_002293	entg LAMC1	hs chr1:183114406- 183114465
12	3	A_33_P3233135 55614	CTTACTTTCAATTCTCAAGATGAGGCTCTTTGGCTAATCTCACATTT GACAAGACTCTAA	ref NM_0011998 66	entg KIF16B	hs chr20:16347850- 16347791
44		A_24_P325046,A_23_P12485 5 84186	TGCACCTACTCTGTAAACCCTAACTGCGATTATATAAAATGAAACAACTCT CTTCTAATTGGC	ens ENST000003 22831	entg ZCCHC7	hs chr9:37186845- 37186904
12	4	A_33_P3368159,A_23_P1431 73 84174	AGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACCTCAACTG GAAAGAGCTGGACA	ref NM_032214	entg SLA2	hs chr20:35242768- 35242709

12	5	A_33_P3344618,A_33_P3398 634 7942	CCGGAAGAGCAGCTGCCCTCCGACCCCTCACTTTGTGCCTTTAGTA AACACTGTGCTTTG	ref NM_007162	entg TFEB	hs chr6:41651777- 41651718
89		A_19_P00322653	CTGGGCATCAGCCTCATGTCCACTCAAAGTAAAGTGGCCCCTCTGAT TGGAATCGGAGGTG	ref NR_034143	entg CASC14	hs chr6:22136604- 22136545
12	6	A_24_P289383 55636	TGTAAATTGCTGCCAACTGTAGTAATGATGCTTTTAATAAAAGTGA CCCATGATATGCAG	ref NM_017780	entg CHD7	hs chr8:61779398- 61779457
12	7	A_23_P11995,A_33_P337719 9 5052	TCAGGATTATGGGGTCTTAAAGGCTGATGAAGGGCACTCTCGTTTCAGG GGCCTTTTATCAT	ref NM_002574	entg PRDX1	hs chr1:45980589- 45980295
12	8	A_33_P3336397	CCATGCACATGTCAGAGATTGTTGTAATGTTTCTTCTTGCAATGAT CTCATCACATTTT	ref NR_104614	entg LOC1005 06688	hs chr5:987403- 987344
12	9	A_33_P3259557,A_24_P9370 3 440104	GCTACAATGGGAGGGAGGAGAACATGGGAGCATGTGAATAAAA TGGCATTAAATACTGA	ref NR_036476	entg TMEM19 8B	hs chr12:56229970- 56230029
13	0	A_23_P113572 930	TACATGCCAGTGACACTTCCAGTCCCTTTGTATTCCTTAAATAAAC TCAATGAGCTCTT	ref NM_0011780 98	entg CD19	hs chr16:28950600- 28950659
13	1	A_23_P30495 3156	GCCTCTTAGTGATTGTCTGCATTGTTATTGTGGAAGATTACCTT TTCTGTTGTACGT	ref NM_000859	entg HMGCR	hs chr5:74657651- 74657710
13	2	A_33_P3407344,A_24_P865 3 87119	CAAGCTGTGAAGAGTACCCCTTCACATGAAGGAGTAGGATTCCTTTT AATCCTATAGCTTT	ref NM_0010424 75	entg CEP85L	hs chr6:118786298- 118786239
13	3	A_33_P3286873,A_23_P3467 6 919	TAGAGGAGACCTCACATTTGACCTTGGAAAAGTTGGAGGAAGGGCT GGAGGAGGGCTCCAG	ens ENST000004 83825	entg CD247	hs chr1:167404630- 167404571
13	4	A_19_P00812235	AGAAATTTCTCTTTCAGGCTGGGGATGAGAGCCCAACGCTTTCATTT CAGAACATCTCAG	ens AF205211	n/a	hs chr12:122031423 -122031364
13	5	A_32_P91042 100129034	GTGGGGCCCAATGAAGCCAAATCTCTTTTGATACATATGCAGTCCTGT AAGAAATGCATTCA	ref NR_027406	entg LOC1001 29034	hs chr9:127120692- 127120751
13	6	A_33_P3419998,A_24_P7568 0,A_23_P...	GCCTATTGGCTGAACATTATGCTACTTTCAGATATTAAAAATGGTGTT CCTTTGAATCGTG	ref NM_0010399 60	entg SLC4A8	hs chr12:51902921- 51902980
13	7	A_32_P130788,A_33_P32664 29 148418	TAATTTGTTTCTGAAGAAAATTTGCCGAGAGTTACAGGTCAAAAAGC CTTGTTACTAGTAC	ref NM_0010109 71	entg SAMMD13	hs chr1:84816209- 84816268

13	8	A_23_P22096 5747	GCAAAGAAATCCAGGAAACCCCAAGAGGCTGAGAAATCTTTTGTCTA CCATAGAAATTATTA	ref NM_0011996 49	entg PTK2	hs chr8:141669169- 141669110
13	9	A_19_P00330475	TGACAGGTTGTGATACCTCCTTATGCAATAACCAACCCTACCTGCTTT GCTACTAGAAATT	tc THC2698203		hs chr15:074782262 -074782203
14	0	A_33_P3253144,A_32_P1210 85,A_33_...	ATAGTGTGCAGACTCACAGATAATAAAGCTCAGAGCAGCTCCCCGG CAGGGGCACTCACGG	ref NM_024872	entg DOK3	hs chr5:176930812- 176930753
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	AgilentProbelID	Sequence	TargetID	GeneSymbol
141	A_23_P50137 51320	ATTGAAACCTAATCTCTAGCTGCCGCTTGAGATATGAACGAATGTTACCAAGCATGT	ref NM_016626	entg MEX3C
142	A_33_P3400389 26010	CCGTATGGTTGTGTCATCCTCTCTTAATCATTTTACTAATCTAATAATCAGCTCTAGC	ref NM_001282735	entg SPATS2L
143	A_19_P00328985	CCTGCTTCCCAGCTTTGTACTAAGAATAATTGGTTACCTTGCTTATGGAAAAACGAGGATG	ref NR_026966.1	entg LOC100130
144	A_19_P00321766	ACTTCCACTCAAAATTGCTTTCTCTCACAGTCTGACTGCGAGAGTTGTGAAAAATTGGGAT	ens ENST00000606336	entg CASC15
145	A_24_P360269,A_33_P3254121,A_33_... A_24_P111054,A_33_P3317797,A_23_...	AAGCCAGGATGAGGAAGTACAGACAAATTGGTCAGATAGAACTGTGCCCTCAGCAAGCAAGA CCATGTGTCCCCTCTATGTGGAATGTTAACGATATCCCACTGTTTCTGGTGTCCTTCT	ref NM_003730 ens ENST00000377414	entg RNASET2 entg SLC2A5
146	A_33_P3285868 114757	GCAACCGCCGTCCTCTTTCTAGTTTCTGATGTTGTAAACAGACCCAGCTGTGTCAT	ref NM_134268	entg CYGB
147	A_23_P31721 1875	AGTTCACTGATTCTGAAGTGTTCTTCCCTAATACTTTTCTTACTTCACAAAACCTTCAACC	ref NM_001951	entg E2F5
148	A_23_P92967 4338	AAGCATATCTACCCATGGCGGAAAAATGAAGTCAGAAAGATTTGTAGTGACATTAGGCAGA	ref NM_004531	entg MOCS2

150	A_23_P311670,A_33_P3240063 256369	GATCTGATTAAGGAGTTCATGTTGGACAAAATGGAGACTGTAAGACTGATCGCACTGCTC	ref NR_024184	entg LINC00521
151	A_23_P160559 1893	GATGAACAGGTCAACTGCTTCAACATCAATTATCTGAGGAACGTGGCTCTAGTGTCTGGA	ref NM_001202858	entg ECM1
152	A_23_P355471,A_33_P3307886,A_23_...	TGGTGGCCAGCGTGTGTGGCTGCCCTTCTGGTCTTCATTGCCCAGACAGTGTGCGAA	ref NM_201636	entg TBXA2R
110	A_19_P00320525	TTTCTGGATATACCTCTTAATTGCAAGCAGGAGAGTCTTCAGAGTTTTCTGTGGTGGTG	ens ENST00000606336	entg CASC15
153	A_23_P402319 202309	TTCAGCAGAATCATCTTAAACCTGCCAAACTTATCCTTCCTTCACAGCTTTGCTTTTCT	ref NM_152687	entg GAPT
154	A_23_P128215 8835	CCAAGTTGCTCTGAATTGCTAACCATGGACATAAACAGTTGTCTCCCTTCTACTGTGT	ref NM_001270470	entg SOCS2
155	A_23_P255328,A_33_P3342126 56978	CCTGTGCTCTGAGCCATACTTCCCTATATGACAGCATAGCTTTCATAGCTCTCAAGTCTA	ref NM_020226	entg PRDM8
156	A_24_P329353 80228	TTGAGGAGGCTGAGTTATTTGAGGGCTGTGCAAAAGTACGCTAGGCTCAAATTCCTTTT	ref NM_001271818	entg ORAI2
157	A_24_P48403 7525	CTGGTACTAAAAAATTGGTGTGTTTTTCTGTTTACGTAACTGCTTAGTATTGACACTC	ref NM_005433	entg YES1
158	A_23_P311640 3268	TAGTTAGCTGTTGGTGCATGTTTGGATACCAGTGTTTTATATTATACATAGAGAGGAT	ref NM_006076	entg AGFG2
159	A_33_P3216292 55357	CACTGCCTCTATAGGGTAACCTGGAACATTCTCTAGGTTATATCAATATAAAACAATGTA	ref NM_001267571	entg TBC1D2
160	A_32_P219279 114794	GGGCTCTGAACCTGTGAACCCCTTGCTGTGTACGAAACTTTCCTCTGAGGGCCTTG	ref NM_052906	entg ELFN2
161	A_33_P3288924	TCTCTGGGTTCCCTGTCTATTCTCGGCCCTTCTGCAGCTTCTGAGCATGACAGGCAGGGAT	gb AK098478	
162	A_23_P130169 9755	TCTTGTGTTCCCTGCAGGCCAGTCCTGTCTCCTTTCCTGTTCTGCCCACTCTGGGGA	ref NM_014726	entg TBKBP1
110	A_19_P00321754	CTAGGATTCTCATGCTTAACATGCATCTTACTGGTCTCTTTATGAAGAGCTTTCCTCTTG	ref NR_015410.1	entg CASC15

163	A_19_P00330122	CATGGTTGCGTCAGTGA	CTATCTATCAAGAA	TAACTATGTGATATGTGCCACAAAGT	ens ENST00000605917	entg CASC15
164	A_24_P418408 375061	CTGCATTACTAACTGCCCAGTGATTCGGTGAAAGCTTTTTACTGAAAAAGTTAACATTTC	ref NM_198552	entg FAM89A		
165	A_19_P00321750	ATCTCAAGCCATTCTGGAGAAAGCACCAAAAGCCACTTTTGCTTATACTGGGAGAATAGTTT	ens ENST00000606197	entg CASC15		
165	A_24_P838448 401237	TTCACTGTCTAATTTCCAGAGCCCCCTCATATAAGGAACTGTATTATTGGTATAATCATC	ref NR_015410	entg CASC15		
166	A_19_P00803685	ATATTTTCCTATTCAGACCTCAGGGCTATTTTGGGACCTACAAATAAAATGGGATCCCAG	ref NM_001164440	entg ANKRD333B		
167	A_32_P209208,A_23_P380379 84698	GACATGGATGTATTCGTTTCTGATCATGAGAAAGAGGGCTCTTGTCATACATAICGTTCCAT	ref NM_032606	entg CAPS2		
168	A_19_P00316921	GCAGTTACACCAACATCAATCAAGGAAACCCACAGGCTGAGCTCACACGGTTGAAGCAG	ens ENST00000444265	entg CASC15		
169	A_23_P31765 5569	AAATTCTCATTAATACTGTGTTTGATGGCCTCTGCTGTGTTTTAACATCGTGCTTCTTAT	ref NM_181839	entg PKIA		
170	A_23_P139704 1848	GCTTGTGTTGTCGCAAAGGGGATAATCTGGGAAAGACACCAAAATCATGGGCTCACTTTAA	ref NM_001946	entg DUSP6		
171	A_33_P3366336 388228	CTTTGGCCCTGAGAAAGTTTTTAAATGTGTATTACTTCTCTAAACATGACGATTGCTA	ref NM_001024401	entg SBK1		
172	A_24_P376760,A_33_P3334404,A_33_...	AGGCTCTGAATCCAGTTTTACCTACATAAGATTGAGGAAATTTCTTGACTACTTAAGAAG	ref NM_001215	entg CA6		
173	A_33_P3313864	CGATGTGGTAATGTCGCTGTTAAACGCACTTCTCATTTGTTAGAAATAAAAAATGACTCAA	ref NM_017653.3	entg DYM		
174	A_19_P00317324	AATATCATCGAGTCCTAGGGAAAGCCTGCTGTTTTTGAAAGTGGACAAAAAGAGGGGATT	gb AK097998			
175	A_33_P3364268,A_23_P120227,A_33_...	AGAGTGAGCCGCAATTGTTCTGAAAAATGTCAAACGAGGCTTCTGTTTGCACCTGCAGAT	ref NM_030915	entg LBH		
176	A_23_P169873 7221	GTGGAGTGGACGTTTGCTCGCTCCAAGCTGTATCTGTCTACTTCCGAGAGGGCCTGACA	ref NR_002720	entg TRPC2		

177	A_23_P50357_A_33_P3378915 23370	GCTAATTATTTTACAATGATTACAACATTTCTCTCACTGCGGATATTTCTGACCCGCTT	ref NM_001130955	entg ARHGEF18
110				
	A_19_P00321748	GAGGAATGTGTGTTTCTAGTGTGTCAGCAATAAACTTCTTGGAATTTGTTTCTCATC	ens ENST00000606197	entg CASC15
178				
	A_23_P60180 25	AGGCCCTAGCTTTACGCTCATCACCTAAACTTGACTTTATTTTCTGATAGAAATGGTT	ref NM_007313	entg ABL1
179				
	A_33_P3221253 4026	GTGACTGATCTAGTTTCTCAGCTGTATGCAAAAGTAATCTTTCAAAGACTAGGTTAAGAT	ref NM_005578	entg LPP
180				
	A_32_P135517 100506105	TGCTGGCCCCCAATGTTTGCATCATATAAACCCATTGCCTAATTTTACAGTTGAGAAAATAA	gb AK123826	
181				
	A_23_P207445 5608	ACAGCATCAATAGAAAAGTCATCTTTGAGATAATTTAACCCCTGCCTCTCAGAGGGTTTTCT	ref NM_002758	entg MAP2K6
182				
	A_23_P383986 51363	ATTGAAGTTCTTTTGTCTCAAAAAGTTGTGACCGTGTAAATTGTACTCCCTTAGTCC	ref NM_001270764	entg CHST15
183				
	A_33_P3276053,A_33_P3234015 8994	AAGATAACTCAGGCAGGGTGGACATCACTGGATGGACAAGACTGGTGGGGCTGAGCTTGG	gb BU428864	entg LUMD1
184				
	A_23_P259098 80345	AGACAAAGGAATTCCTTGGGGGAGATAAATGACAGACTGAACAAAGATACTCTCAGCATCC	ref NM_025231	entg ZSCAN16
185				
	A_24_P107859 161742	TACTGTTTATATATTTGAATGCTGCTACAACAGATGATCTTCATCCCTGAAGTTTTTCAGC	ref NM_152594	entg SPRED1
186				
	A_23_P124642 10125	ATTAACAGCAGGGTCACTTCTCATTTTCTTTGCTGACTTACCCTTTTACTGACCGTTGTG	ref NM_005739	entg RASGRP1
187				
	A_32_P46214 285195	TTTTTTCCTTTCCAAACAGAAATCTCTGGGGGCACAAGTTTTACACTCAAGCTAAGTATAAC	ref NM_173653	entg SLC9A9
188				
	A_32_P68746 55234	GAGGACTTTGTGCTCTACTGTTTCAGTACAGCCACTGGCAAACCTGGAAAGAACTTTGACA	ref NM_018225	entg SMU1
189				
	A_24_P419120 23299	GAATAAGCATTCTTATTCCTAGTTGTAGGGACTCCTATTTTACCTTCCGTTACAGTGT	ref NM_015250	entg BICD2
190	A_24_P278747 894	ATCGGGCCATTGGATTTTTTCCATTATGTTTCATCACCCCTTATATCATGTACCTCAGATCT	ref NM_001759	entg CCND2

191	A_19_P00316010	TTTTCCGTCAAAGTGCTTGCTATGGCTTTCATAGCTGGGACAAGTAACATTAAGTATTCA	ens ENST00000588041	n/a
192	A_24_P149124,A_33_P3391290 9315	GTGGCATTATATGATAGAGTTGCAGTTGTGTACTGCTGAAATGCAGGGCTTTTGTAAACAGTG	ref NM_001142483	entg NREP
193	A_23_P210176,A_33_P3231447 3655	ATTCTGTAAACACAGGTTATAACAGTGTTTAAAGTCTCAGTTCTTGCTTGGGGAACCTTG	ref NM_000210	entg ITGA6
110	A_19_P00318323	GATGACAGAAACAGAGAGTAAGTCAGAGCTGGCTGCCTGACAGATAAAAAAGGAAATGACC	ref NR_015410	entg CASC15
194	A_23_P107513 79959	ATGCTTCGATCTCCTTTCTGTGAAGAAATAATCTGTTGCCGTGGAGACCAAGTGC GACT	ref NM_024899	entg CEP76
195	A_23_P160406,A_33_P3293346,A_33_...	TTGTAGGACTGCAGTTCTGAATTTTGGGTTAAAGGTTTTGGCTGCTGTAAGAAATGTGAAT	ref NM_016121	entg KCTD3

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	AgilentProbeID	Sequence	TargetID	GeneSymbol	ProbeChromosomeLocation
19	A_23_P147397 79659	ATATTCTCGGATGAGTGCATCTCTTTGCCTGTTTACACAAAGTGCTG AAAGGGATCGTGT	ref NM_001080463	entg DYNC2H1	hs chr11:103349837-103349896
19	A_23_P26570 146456	GTGGTCGACAGCCAGAGCCCTTGTTATTATTCTTCTGGGATCCTGC AACTGTAATTTCTT	ref NM_144676	entg TMED6	hs chr16:69377424-69377365
19	A_23_P74112,A_33_P326861 2,A_24_P...	GGTGAAAGCAACATGTATCCCTTAGACTACTAACGGTATATGTTG TTCTTATGTATTG	ref NM_170743	entg IFNLR1	hs chr1:24480826-24480767
19	A_23_P424712 84865	AGAACTGGAAGCTTGGAGGAAAGCATACTGGAGAATAAGCTACAA AGAGCCTGGGCTTAA	ref NM_032779	entg CCDC142	hs chr2:74701583-74701524
20	A_24_P835500 162073	TTCGTTTTCTCTTGAGGTTGGAGTAAATTTGCACCTTTGAATCATGT GGGTCATTTGGGG	ref NM_001034841	entg ITPR1L2	hs chr16:19132844-19132903
20	A_23_P83498 10642	TCTTAGCAAAACAATAGATAAAATTAGGTAGTGGCAGCTCCACTTGC	ref NM_006546	entg IGF2BP1	hs chr17:47132379-

1		TTAGGTTAGGGGG			47132438
20		TAGTTGGTCCCTATGTTGGAAGTAAAAAGTGAAGCACCTTTATTTTG			hs chr15:93586835-
2	A_23_P372308 56963	GTTGTGTTTGCTCA	ref NM_020211	entg RGMA	93586776
20	A_33_P3343493,A_23_P9330	TGTTCCACCAAGATTGGTGGTCCACACGGTCTTCACAAAGAAGGA			hs chr6:29574946-
3	2 2550	AGAAAAAGAAAGGAGT	ref NM_001470	entg GABBR1	29574887
20	A_33_P3327479,A_24_P3514	GGAGAGAGATTGGGTGCAATTGGCTCTTCTTTGAATAAAAAAGCT			hs chr3:44956813-
4	20 51304	CTTTGCTCACCCCTC	ref NM_016598	entg ZDHC3	44956754
20	A_33_P3272563,A_23_P1386	CCTCAGGTGACAGTTACACTGCTCCTTTAAAGAGTCATTTACATAA			hs chr10:15147956-
5	93 9397	TTTGTATCAAAAT	ref NM_004808	entg NMT2	15147897
20		AGACTCTTTGGAGAAAAGACGTGTGATTTCTCCAGACTTTAAAG	ref NM_0010318		hs chr18:61647137-
6	A_24_P147461 5271	AATACTGTCAGAAG	48	entg SERPINB8	61648978
20	A_23_P217384,A_24_P93730	AAACGTGTTGCTCTCTTCACAGTATTATGTGTAAAGTCATTGTTTAA	ref NM_0012720		hs chrX:15844638-
7	6,A_33_P...	AGCACGAATGTTT	71	entg AP1S2	15844579
20		AGAGCCAGAGAAAGTCCCTCTCTGTGTCAGAAACAACCTTTGTAACA	ref NM_0011780		hs chr12:025070755
8	A_33_P3317761	TTTATTAACTGAC	91.1	entg BCAT1	-025070696
20		TGCTTTTGCATAGTTCCACTCTCTCAGATACATGTATCTAATGAAA			hs chr6:159460015-
9	A_23_P339588 117289	CTGAATAAATCCG	ref NM_138810	entg TAGAP	159459956
21		GAAAAGGAGCCTGGTGGGAGACCACCTGCACCCCAAAACAAATCCT	ref NM_0011228		hs chr5:150058791-
0	A_32_P88415 91977	TTCTTCTCTGAGAA	53	entg MYOZ3	150058850
21		CATCCACAAAAGAAAGACCAAGCTTTGTCCAAAAGAGGAAGAGATGG			hs chrX:14038346-
1	A_24_P156576 54960	AGACTGAGTCAGATG	ref NM_017856	entg GEMIN8	14038287
21	A_23_P77103,A_33_P341348	CAGCACTTCCAGTTTAGAACGCAATGTTTCTAGAGACATATTGGCT			hs chr15:45366186-
2	3 6652	GTTTGTTTTGATGA	ref NM_003104	entg SORD	45366245
21		CTCCAGATCGTTCTCGAACTTTCCCCACTACTCCATAATAAAAATGT	ens ENST000005	entg LOC1005	hs chr19:56821760-
3	A_19_P00320907	ATACTTGTGTGAAA	87247	06374	56821819
21		CAGTTACTTTGGAGCTGCTAGACTGGTTTCTGTGTGGTAAATTGC			hs chr22:26125179-
4	A_33_P3220919 157	CTATATAAAATCTG	ref NM_005160	entg ADRBK2	26125238
21	A_23_P85004 1730	TGGAAACTACATGAACCTCAGGCTCAAGAAATGCCAGTCTTTGGGA	ref NM_007309	entg DIAPH2	hs chrX:96369895-

5		TTTAAGATCAACTT			96369954
21		TTTGAGTTTACAGGAGTGAGAACTCTCTTGCATGGTGAGATGG	ref NR_022011	entg PWARSN	hs chr15:25228582-25228641
6	A_33_P3418668 347746	GGAACATTTAATTC			
21	A_24_P270496,A_33_P33476	TCCAGAGCTAATCAGAAGCATAATATCTCCTGGATATCATGAAGCA	ref NM_006491	entg NOVA1	hs chr14:26941540-26939652
7	97 4857	AGATATAAGAGAGAAG	ref NM_001099678	entg LRRCS8	hs chr3:120044380-120044323
21		CAGGTGCTACTAGACTTTTACCTAACATTAGTCTTTCTCAATAGTTG			
8	A_32_P190049 116064	TTGTAAAGGATAG			
21		GCTGACTTTGGCTTTCACATTTTGTCTTCCAGAGCTAACTGATAAG	ref NM_152280	entg SVT11	hs chr1:155854303-155854362
9	A_24_P248240 23208	AGTGGAGGAGGAA	ref NM_001017440	entg CALN1	hs chr7:71275474-71275415
22		GACATGCAAAAGGATAACTCTGGAAGAGTTGAAGCACATTCTCTATC			
0	A_24_P380567 83698	ATGCCTTCCGAGAC			
22		GCACAGTATGCAGGTAGGCCTAATGGGGGAAGATGGTAATATAAA	ref NM_198066	entg GNPNAT1	hs chr14:53242094-53242035
1	A_23_P429184 64841	AGCAAGAAAGTATTTT	ref NM_001184902	entg CARD8	hs chr19:48711576-48711517
22		CAGCGCAATGAATGCTCAAGTTGGGGTGGCGTTAGAAATTCATA			
2	A_24_P14260 22900	AAAGCTTTTATATGC			
22	A_23_P215566,A_33_P33168	AATGGCTTCGGACAAAATATCTCTGAGTTCTGTGTATTTTCAGTCAA	ref NM_001621	entg AHR	hs chr7:17384999-17385058
3	00 196	AACTTTAAACCTG			
22	A_23_P52806,A_33_P324094	TTGTGGGGTGCATGGAGGAATTGGGACCTGGTTATGTTGTTATTCT	ref NM_012104	entg BACE1	hs chr11:117156561-117156502
4	1,A_33_P...	CGGACTGTGAATTT			
22		TCCCTGGTAATCTGTAGAACCTTCTCCTAGGAAATGGTGAAGTCTA	ref NM_005652	entg TERF2	hs chr16:69390200-69390141
5	A_23_P417200 7014	TTAGGAGCCACTTG			
22	A_33_P3415923,A_23_P3792	ATGTGGGGGCCCACTTTTGTACATGTACCACCTCCCTTTCCTCTT	ref NM_175736	entg FMNL3	hs chr12:50038814-50038755
6	00 91010	ACTGTACATAAAC	ref NM_001135154	entg SLC39A14	hs chr8:22272367-22273292
22	A_24_P383356,A_23_P59950 23516	CTTTTTCACAGAGAAGATCTTGAAGATTCTTCTTAAGCAGAAAAAT			
7		GAGCATCATCATGG			
22		AGCAACACTTTATCCATTTTATTCTGAGAATGTGCAGGAGGGGTTAG	ref NM_025159	entg CXorf21	hs chrX:30577524-30577465
8	A_23_P62227 80231	TGAAGGGGAATTAA	ref NM_138959	entg VANG1	hs chr1:116233919-
22	A_24_P199655 81839	ATTCATCATACTCTCTGAAGAGTTTCATAGACCCCAATCTCACAAAT			

9		TTGTCCTTCGCTT	
23		TGAACAGATTTTGAAGGCCGAGTACGAGTTTGACTCTCCTTACTGG	
0	A_23_P121215 8536	GACGACATCTCTGA	ref NM_003656 entg CAMK1 116233978
23	A_23_P10442,A_33_P330853	GCACATTCATCTTAAATCTTATAGTATTTATCCACCCAAACCCCGAGA	hs chr18:21742185-21742126
1	4 114876	CTGAGATACTGCT	ref NM_080597 entg OSBPL1A 21742126
23		CTGGCTACACTGCTTTTAGAATGCTCTTTCTCATGAAGCAAGGAAA	hs chr10:70454164-70454223
2	A_19_P00806490	TAAATTTGTTTTGAA	ref NM_030625 entg IEI1 70454223
23		TGTGTCAACAGATGGATCACTGGAATGTGGGATTCTGAAACAGA	hs chr3:99897343-99897402
3	A_23_P132874 84319	AATGAAACTGTCCTT	ref NM_032359 entg CMSS1 99897402
23		TGCTCATCCATCTATGTTTTTGGTAACTCAGTTTGGAATTTTCAGT	hs chr12:117153885-117153826
4	A_23_P13797 79794	GTCTGTCTTCCCT	ref NM_024738 entg C12orf49 117153826
23	A_23_P311895,A_33_P33921	TAAATACGTTGCCTCAATATAAGGTTTGGGCTATTCTGTGTTTCTA	hs chr6:45866699-45866640
5	77,A_23_...	TAGAAGCAACTG	ref NM_001114086 entg CLIC5 45866640
23	A_32_P143048,A_23_P25197	TGGATGATGACAAGAACGTTAGCAAGGGTGTCTAAAGTCCTATAGA	hs chr1:52803579-52805830
6	4 9372	TGGGAAGTCCATGGA	ref NM_004799 entg ZFYVE9 52805830
23		TATATCCAACCTTATGTACCTTGCAAACTTGCTGCTGGAATTTGACTGT	hs chr2:148782621-148782680
7	A_32_P2103	ATGTGCAAAACAG	ref NM_0183284 entg MBD5 148782680
23		TTTGGTTGTTGACAATGAAGCACCATTATGTGACTCTTCATATAACC	hs chr19:31765938-31765879
8	A_23_P361014 57616	CTTTTTTCTACGG	ref NM_020856 entg TSHZ3 31765879
23		AGTCCTAGACTGAAGTCAGTAGGAATTCAGTATTGTGTCTAAATT	hs chr18:19236897-19236838
9	A_23_P305759 171586	CTGTGGATGATGTT	ref NM_138340 entg ABHD3 19236838
24		ATTGACTACGTGCTTTACAAGGCAGTTTCTGGGTTTACATCTCCTG	hs chr6:109764264-109764508
0	A_23_P82162 6610	TAAGAGTTTTGAA	ref NM_003080 entg SMPD2 109764508
24		GCTCATCTGTACATACTGTTTCTCTATGACATTACTGTATTTAAGAAA	hs chr1:165877122-165877181
1	A_23_P487 7371	ACACCATGGAGAT	ref NM_012474 entg UCK2 165877181
24	A_33_P3324786,A_23_P1431	ATTTGAAGTTTCTATCTGGGCTCATTTCCAGCTGTTTCAGGGTTCGGA	hs chr20:61477326-61477267
2	47 10732	TTCTCTGAAGGCTT	ens ENST00000217162 entg TCFL5 61477267
24	A_23_P390148,A_32_P22199	ATAAATTTCTGTGCCAAATGCATGGTTTTTCCACTTAGCATTCAAAAAT	ref NM_014636 entg RALGPS1 hs chr9:129985021-

3	1 9649	GTTGCATAGAGAG				129985080
18		TACTGTTTATATATTTGAATGCTGCTACAACAGATGATCTTCATCCC				hs chr15:38645760-
5	A_24_P107859 161742	TGAAGTTTTTCAGC		ref NM_152594	entg SPRED1	38645819
24	A_33_P3344292,A_24_P3835	ATTGCAAGTTTTCTGCGCGGGGAAGATCTGTTGCTGGTGGCGGT		ens ENST000005		hs chr14:55033854-
4	23,A_33_...	TCTTAAGCACGGCG		54335	entg SAMD4A	55033913
24	A_24_P344416,A_33_P32668	AAATTGGATGCATAAAGTAATATTTACAGATGTGGGGAGATGTAA				hs chr18:28571094-
5	98 1825	TAAAACAAATATTAAC		ref NM_024423	entg DSC3	28571035
24	A_33_P3265514,A_33_P3247	CCAAACCTGCCACATGTTTCATATATCTAAATCTATCCTAAATGTTCC				hs chr21:10906861-
6	392 7179	TTGAAGTATTTA		ref NM_199261	entg TPTE	10906802
24	A_33_P3319161,A_23_P6051	GTGATCAACAAGCAGACGCGCAAAACAAGCAAAATCTGGCTATCTTCTC				hs chr9:71679899-
7	7 2395	CATCCAGGTATGTA		ref NM_181425	entg FXN	71679958
24	A_23_P412476,A_33_P33794	CACCTTTCAGTGGTGGCCTCTGGAGAACCAAGTGTCTGTTCTCTGAC				hs chr2:11725943-
8	06,A_23_...	AACCTGCTGAAAAAT		ref NM_148903	entg GREB1	11726002
24	A_24_P388570,A_33_P33141	GTGCATGAGTTTTATGCTGAAGCCGGGTGATTTGTTGTACTTTCCCA				hs chr3:97677915-
9	46 84864	GAGGAACCATTCAT		ref NM_032778	entg MINA	97673301
25		CCTCTGGTTCAAACCTTCGCGTGGCAATTTTCACATTATTTAAAAAAG		ref NM_0010804		hs chr19:48988597-
0	A_33_P3266928 114783	ACAAAAACAACCTT		34	entg LMTK3	48988538
25		ATACTTTTAGAAGACTATTTCTCTAGGGGTGACCCCTATGCACAGAG				hs chr2:124608248-
1	A_19_P00809233	GCCCTGAAGCAGAT		gb L19367	n/a	124608189
25	A_23_P307392,A_33_P34231	GGATCGAGCAGCCTTCTTCTTTGGGACCCCTCGATATCCCATGGAA			entg LOC1027	hs chr14:73075947-
2	85,A_33_...	TGCTCGCACGTTCT		ref XR_432995	25171	73075888
25		GTTTTTCATTCACATCTCCAAAGGTCCTCTACCTTAGAAGAAAGAAAG			entg LOC1001	hs chr8:61878759-
3	A_33_P3366175 100130298	AAAGAGGGAAAGAG		ref NR_034003	30298	61878700
25	A_33_P3233099,A_24_P3026	TTTGTCTCCAGTTTAGTTTCTCCAGAACACAGGAGGAAAAAGTGAA				hs chr2:131674555-
4	85,A_23_...	CCGACCATCAAGTG		ref NM_015320	entg ARHGEF4	131674614
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255	A_32_P42925,A_24_P75230 103910	TGATGTAATTATCCAGACCTTTCTGCCACTTAGCACTTGTAATAATCAGACTGGAAATGG	ref NM_001144944	entg MYL12B
256	A_23_P56759 51315	GATATCCGTGTTCATACCACCTTTTCTTATGTGAATAGGTTCTTTAACTTTAACAAAAGGC	ref NM_016618	entg KRCC1
257	A_24_P376391 23129	CGAGGCTGTAGCTGGGCTACTTGATCTTGCTGAAAGTGTCTTCTAAAGATAGCACCACCTTT	ref NM_015103	entg PLXND1
258	A_33_P3375002 144481	ATGTTCTAGATGCACAGATTGGGGGCTTGATTGACAACCTGACACCTCACTCTAAATCC	ref NR_038263	entg SOCS2-AS1
259	A_23_P140738 9780	GTCATCGGCAAGTTCGTGCGCGGATTCTTCAGCGAGATCTCGCACTCCATTATGTTTCGAG	ref NM_001142864	entg PIEZO1
260	A_23_P46378 55650	AAGTGAAGATTGTGCGTATTCCAAGTCTAAAATACACCTGGATCTGTCTAGTCAATCAACA	ref NM_001202554	entg PIGV
261	A_33_P3234864,A_33_P3234859,A_33...	TTAAAGGAGAAAGAAATATCTGTCTGCTGAATGCTGTCGACCAAGGCCCGAGTTTCTTGGCT	ref NM_007124	entg UTRN
262	A_23_P28582	GCCTCTCAGTGCATTTGGAACTTGCTTATGCATTGGAATAAATTGAGTCAGCTGCTCGTT	ens ENST00000608013	n/a
263	A_33_P3235856 6096	GCCTGTGTCCTGGAGGCCTATACCTCTGTTATTTTCTGATACAAAAATAAAACTTAAAAAA	ref NM_006914	entg RORB
264	A_24_P396753,A_33_P3325978 28951	GGACCATCCTTGTTTCTACAGATTTTAGCGTCTCGAATTCAGCATATGGTGCTAAGGA	ref NM_021643	entg TRIB2
265	A_23_P167920 28514	ATGGGTGAACTGAATTACGCCCTAAGAAGCATGCACTGCCTGAGTGATATATTGTGGATTCT	ref NM_005618	entg DLL1
266	A_23_P114057 54910	CCTAGGAGGAGGGCTCCTAACAGTGTAACCTTATTGTGTCCCGCGTATTATTGTGTTGA	ref NM_017789	entg SEMA4C
267	A_23_P368779 163071	TTCAATTAATTTTCTGACTGTACCTAACATGTGAGGAGGACATATTGGAAGGGAGCTCAAG	ref NM_153608	entg ZNF114
268	A_33_P3417305	TTCCGATACTGCCTTTCCTACAAGGAGCTCAAGCACAAAGCGGCTATGCAGGTACCACTGA	agp A_33_P3417305	n/a

269	A_33_P3338928 1601	GATCAGCCACAACTGTTTTGTACATACTTAATTTCTCATGCACTTTTCTGTATGCAAA	ref NM_001343	entg DAB2
154	A_23_P128215 8835	CCAAGTTGCTTGAAATTGCTAACCAATGGACATAAACAGTTGTCTCCCTTCTACTGIGT	ref NM_001270470	entg SOCS2
270	A_23_P207940	AGGAGAGATTACTTTTGTAATTGTACTGCCATTCCTACTGTATTTTATACITTTTGGCAGC	gb AK091525	n/a
271	A_33_P3255664,A_23_P62953,A_24_P...	AGTCTGGGCCAGTAAAGCCACCAGGCCATTTTCCTGCTTCGGACAIGCTTTCTCAGCTGC	ens ENST00000474046	entg PBX1
272	A_23_P147711 4881	TGGAGTGGTGGGACTGAAGATGCCCCGTTACTGTCTCTTTGGGGATACAGTCAACACACAGC	ref NM_000906	entg NPR1
273	A_33_P3332066,A_24_P86868,A_33_P...	TGAGAAAGAGGAAGCAATATGTGAAATCTCTCTCCAGGGTGTGAAAAGTAAAGGCTTTTT	ref NM_212554	entg METTL10
274	A_33_P3294053 51239	GGAGTAGATTTGGTGTGGCTAAAAGTGTTTAAGACTGGACAGATGATCATATTTCTAAATT	ref NM_016466	entg ANKRD39
275	A_23_P350754 10819	CGTGTGTGACACCTTCACCAATAACATAGTCATGATTTCCTTGCTGCCATATTTGGTT	ref NR_045002	entg OR7E14P
276	A_33_P3402086,A_33_P3402091 10461	TGGCCAAAGAGGGCTCTGCTGATCTGCTGTGCTGTGCCAAAGGAAAAAATCTCTGGTGTAGATA	ref NM_006343.2	entg MERTK
277	A_32_P1445,A_23_P309701 5771	TGGGTCTTATCTCAGACCCCAGATCAAACTGAGATTCTCATACATGGCTATAACAGAAGGA	ref NM_080423	entg PTPN2
278	A_23_P60210 6013	CATCTTGTCTAAATTTACACACATAGTCTTGATGACATTTCACTGATGCTTCTGTCAAGGTC	ref NM_006911	entg RLN1
279	A_33_P3222341,A_23_P84189 26207	GCGGGTGACTTTTGTGCATTCGTTTTAAATTTTGGAAAATCTCTTTTTCTCCCTCGC	ref NM_012417	entg PITPNC1
280	A_23_P126757 65123	CTTGTTTGTCTGAAGGGACGTTTTATAGTCACTATCCACATGCCAGTGTGAAATGGGC	ref NM_023015	entg INTS3
281	A_33_P3340342,A_23_P88865 123920	AGACTGTTTCAAAGAAGAGCTCATAGACTGACTGGTCCAGAAGACAGAGGGGTACAACAGT	ref NM_144601	entg CMTM3
258	A_19_P00807670	CAAGAGAAGCAGGCTCTCCCTTCTGAAATGATGATGATAATGACCATACAGGTCAACT	ref NR_038263	entg SOCS2-AS1

282	A_33_P3259135 27065	GTGGACTTTATTGACTGTGAATTCATTTACATGTAACTTCTGACATTTTCACTCTGTGCAA	ref NM_001287763	entg NSG1
283	A_33_P3223338,A_23_P250413 64098	ACATGTGACCACAGACTGAATGGCTTAAACCACAGAAACCTACTGTCTTACAGTGCTGCA	ens ENST000000453888	entg PARVG
284	A_23_P98910 4033	AGGTTCTCAGAAATGACCGTAAGATAGCTTACATTTCTCTCTTTTGCCCTTTATCTCCTCCAA	ref NM_006152	entg LRMP
285	A_32_P34444 80206	TCCAGATGTAAACCCCAAACTTGACACAAAAAGAACACAGATTGTTTACCTGTTGTGG	ref NM_001281740	entg FHOD3
286	A_19_P00322333	AACTTTTCGATTTTCTCTGTACAATCTTCACTGGTCTCTCTGTGAGAGGAGGGGAC	ens ENST000000578280	entg LOC101059
287	A_24_P33982 284021	GTGGTGATAATCCTAATTCTGGCTTTTGGGTACTGCCAAATACAAAACAGAAAAGCT	ref NM_001291317	entg MILR1
288	A_33_P3323722 10123	CATCATCCTTCTCTTTGTTTCCATAGCCTTTTATAATGCATATATGATGCTGTGAACAG	ref NM_001282431	entg ARL4C
289	A_24_P365807 1947	GGTGGCAGTCGGAAGGGTTTTGTTTTGTTTCTGTGTCATTTGTGTAAATACTAGTCT	ref NM_004429	entg EFNB1
290	A_32_P62863 29970	AGTTCCTTTTATAGATGTGCTATTAAACATTCTGTGGATTGAGAGGGTTCCTTGAAAGTTT	ref NM_001197113	entg IQCJ-SCHIP
291	A_19_P00323196	CACTGGAAGCTGGGCAAGAGCTGGGATGGATGAGACCAAGCGCAATACTTTACTTATTA	gb AK129632	entg C5orf56
292	A_23_P209731,A_23_P209735 80210	TCAGGGCTAAAGGAAGCGGGAATTGACTTTCTTAAGCTTTGTTTGATTACAGTGTGAAGA	ref NM_025139	entg ARMC9
293	A_19_P00802794	ACACACAGCACCCCTCAAGACTCCCTGTGATCCTGGGATGCACTCAACGAAGAGTGTGTGG	ref NR_038263	entg SOCS2-AS1
294	A_33_P3379811 196415	CTGTGTAGCATTTCTCTCTGGTTAAGAACAATGCAGATAATCCAAATAAACAGATTTTGACT	ref NM_001101339	entg C12orf77
294	A_23_P28834,A_33_P3289371 116154	CTATCAGAAGAAAACTGTTGTTGGCTTTCAACCTTGTTTACAGTTCTGCAGTGTAAATG	ref NM_080672	entg PHACTR3

295	A_23_P169934 353116	AGATGCACCCCTGAAAACTGACCCCTCAAACAGACTGTCTGATTTGAGGATGGACATTGAA	ref NM_178314	entg RILPL1
296	A_33_P3327108 51701	GCACACTTTCTGGTCACTTTGTACAAATGTAGATTGAAGTACAGTGGTGAAAAACATTAAA	ref NM_016231	entg NLK
297	A_23_P382775 27113	AGTCTGGGAGTGGGGAGGGATGGCCCGAGCCTGTAAAGATACTGTATATGCGCTGCTGTAGA	ref NM_014417	entg BBC3
298	A_23_P215024,A_33_P3244473 55227	TTTTTCTGAATAAGTCTCTCATAAATGAGTGCAGTGTGACACTGTGCCTACTCTGATGGT	ref NM_018214	entg LRRC1
299	A_33_P3323914	ATAGGGAAGCCCATGCCGGAGCTGAAAAACCTGCAACAACAAAAAGCATCTAAATACTGC	agp A_33_P3323914	n/a
300	A_24_P941866,A_33_P3388983 441108	TTTCTTTTCTTTAGAGAGCCTTTTGTCTTTTGTCCATTATATACTATAATTTGGGTTA	gb AK096941	entg C5orf56
301	A_24_P914625,A_33_P3254335 389206	TGCAAAAGGAAACAACAACAACTTCTGCCTTTTGTAGGGTTTTCACTGACTCTCTACAAAAATT	ref NM_001159547	entg BEND4
302	A_24_P12136 170591	TGCAGGACCTGGATGCCAATAAGGACAACGAAGTGGATTTTAATGAATTCGTGGTCATGG	ref NM_130772	entg S100Z
303	A_24_P169092 84441	GACCCAATCAGCTAAGCACACACAGATTTTGCCTAAATTTGAATCAGTCAGGGAACAGGGTTGA	ref NM_032427	entg MAMIL2
190	A_24_P278747 894	ATCGGGCCATTGGATTTTTCATTATGTTTCATCACCCCTTATATCATGTACCTCAGATCT	ref NM_001759	entg CCND2
304	A_23_P338325 2004	GTA CTGCTTTCTTCAAACCTCTCAGAAATCCTGATGACGTCTGGCCACAATAAGGACTCA	ref NM_005230	entg ELK3
305	A_33_P3391517,A_33_P3212172 79856	ATGTGGATCCCTATGTTTGCAACCCCTCCCCAGGTGAGGAGGTGCCTAGATATGGGGCTA	ens ENST00000560945	entg SNX22
306	A_23_P212042,A_23_P386320 4241	CGACACCAACATCTTCACCGTGTATGGACTGCTGGACAAGGCCAGGACCTGTTTGGAGA	ref NM_005929	entg MFI2
307	A_33_P3217983 51703	CTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTA	ref NM_203380	entg ACSL5
308	A_33_P3352827,A_23_P62647 6504	TTATCTAGGAGATCGCTACAAGTTTTTATCTGGAGAAATCTCACCCCTGGGGATACGGGAAAG	ref NM_003037	entg SLAMF1

145	A_24_P360269,A_33_P3254121,A_33_...	AAGCCAGGATGAGGAAGTACAGACAATTGGTCAGATAGAACTGTGCCTCACTAAGCAAGA	ref NM_003730	entg RNASET2
309	A_24_P317907,A_33_P3313314,A_33_...	TCCTGGTCTTTAGATGCAAAACCATTAATAACACTATCTTATCTCATAGTTTTTTCAGGGG	ref NM_001290294	entg SORBS1
Anexo 7				
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310	A_23_P55020 146722	GGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATAGAGAGGTTATTCTTGCTGAT	ref NM_001289086	entg CD300LF
311	A_23_P110167 4258	AATATCTGGACCTCAATATTGCCAAGAAACTGAGGGCGGCAATTCTAACTTTTCTCTTCC	ref NM_002413	entg MGST2
312	A_23_P374389 170394	ACTCAGCTTGGTCTCCCGCAGGCTTCAGAAAAACCCAAATTGCACGTGTGGGATTCTTCCC	ref NM_138499	entg PWWP2B
313	A_32_P452655 654346	TGACCAGAGTGTCTCTTCAGGGGACTGGCTCCTTTCCCAGTGTCCCTTAAAAATAAAGAAA	ref NM_001040078	entg LGALS9C
314	A_33_P3220015	TTCAATCCTTACCATCAAGTCCGTAGAGAAAGAAAGACATGGCCGTTTACTACTGTGCTGC	ens ENST00000390341	ens T cell receptor Symbol;Acc:1228
315	A_24_P250535,A_24_P942517 56255	GTGTTTGTTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTG	ref NM_021156	entg TMX4
59	A_24_P915196 203197	ATGTGGCCATGGTGTAGGCAGTGCAATGTCTTCGAGTGAGAGTGAAGGTGGTAACTCATT	ref NM_153045	entg C9orf91
316	A_19_P00807336	TAATGATATCAATGATGTCAAAACAGCTGAAACCTGGCTACTTTAGAAGCTACTGTGGACTG	ref NM_021129	entg PPA1
317	A_33_P3276713,A_33_P3276718 3082	TTATCGAGGTCTCATGGATCATACAGAAATCAGGCAAGATTTGTCAGCGCTGGGATCATCA	ref NM_001010931	entg HGF

331	A_32_P104063 643911	TCAGTTGTCACGCAGAAAGGTTAAGCTGTATTTGATTGCCAGTTTTACTGAAAATGCT	ref NR_110453	entg CRNDE
332	A_23_P36658 4257	TTTTTTGTGGATATGGAGTTACTCTTTCCATGGCTTACAGGTTGCTGAAAAAGTAAATTG	ref NM_001260512	entg MGST1
333	A_33_P3410589 131583	IAGCACTGTTCTGTTCTGTTTGCACGCCAGTGGGAGAGAAATAAAGAGGAAAAATTAAAC	ref NM_153690	entg FAM43A
334	A_23_P259594 9465	GAAGATAAGCTCCAGGTCTTATCGTATCCCTTGCCATCTGAACTTGTTGCACTGCTTCT	ref NM_016377	entg AKAP7
335	A_24_P98555,A_32_P138004 404636	TAAATGATGGAGAGTTATATTGCAGTTCTCACAAAGGGGATATGCCAGAGTGAAGAAAA	ref NM_207009	entg FAM45A
336	A_23_P387031,A_33_P3341722 91522	CAAGTCTCCACCCAGAACTCTGGCCAAAAATGGCTCTCTAGTGGGCTGTGCAGGCAAA	ref NM_173465	entg COL23A1
337	A_23_P155939 152687	AAGAAATGTGGCAAAGCTTTCATATGGTCCGCAAGCCTGAATGAACATAAAGAAATATTCATA	ref NM_001286054	entg ZNF595
338	A_23_P18017 1359	GCCAAGTATATCTCAAGCATACTTCTTAAAGAACTGCCCTCTGTTTGGAAATAAGCCAAT	ref NM_001870	entg CPA3
339	A_19_P00325965	CACCCTATCAACGTCGTATCACAAACCCCATTTCTTAATAATAGTTTCTTCACATTAGAAA	agp A_19_P00325965	n/a
340	A_33_P3292854 811	GGGTCCAGATTGGCTCACACTGAGAAATGTAAGAACTACAAACAAAAATTTCTATTAAATT	ref NM_004343	entg CALR
341	A_23_P79978 57419	TTGATTCTGTGCACATTTTGCACCTGGTTTATGGCGATTGTTTCTTGACGGATAGTGT	ref NM_020689	entg SLC24A3
342	A_23_P391506,A_33_P3280875 10625	ATGGATAAAATATTGGTTGGGATGACTTGGTGTCTAATGTGTAGTGTACACACCTAACTT	ref NM_006469	entg IVNS1ABP
343	A_23_P47857,A_32_P52816 51768	TATCTGTTCTTTGCATAAATATTATGGTGCCCTTATTGATATATGGTAAGGGGTACTAGG	ref NM_016551	entg TM7SF3
344	A_24_P47182 7414	ATGGGGTTCAAGAGAGTAATGGTTTCATATTTCTTATCACCACAGTAAGTTCCTACTAG	ref NM_014000	entg VCL

345	A_23_P13364 4925	GATGAGCTTCAGAAACAAAAGAAGAGCTACAACGTCAGCATGATCAACTGGAGGCTCAG	ref NM_005013	entg NUCB2
346	A_33_P3296940,A_24_P223124 64778	GTTAATCCAGGTGAGACTTTCACAATAAGAGCAGAGGATGGAACACTTCAGTGCATTCAA	ref NM_022763	entg FNDC3B
316	A_23_P161338,A_33_P3271241 5464	TTCCATCACCGAGAAAAACTAATGAGATTCTCTGGAAATACAAAGCTGATATTGCTACATCG	ref NM_021129	entg PPA1
347	A_23_P11685 5321	GAAATGGCAGCAGTTTCTGATGTCTGAGGCAGTTTGCAATCCCATGACAACTGGATTAAAA	ref NM_024420	entg PLA2G4A
348	A_23_P64129,A_24_P307580 10553	AAAGTCAGCATGTTTTAACTTTGTGTTTTACTATCCTCAGGCATCCATTCCAATCAAGA	ref NM_001098522	entg HTATIP2
232	A_19_P00806490	CTGGCTACACTGCTTTAGAAATGCTCTTTCTCATGAAGCAAGGAAAAATAAATTTGTTTGAA	ref NM_030625	entg TET1
349	A_19_P00318331	CCGTGTCTCAATGTCTGCACCAATAAAAGAACACAGAAAGTCAGAGTTTCCATAAAATAA	gb CA313052	
350	A_24_P810697,A_33_P3239587,A_24_...	CTGCACACCTTAGATAAAAAAGAACATTTTAAAAAGCAGAGTTCACCTTTCACTCCAGTCTCC	ref NM_001008529	entg MXRA7
351	A_23_P250800 10402	ATGTCACGAAAGTTCACCTAGCTGGTTTTAAATACAACTTTTCTGACCTCAAGAGTCCTTT	ref NM_006100	entg ST3GAL6
331	A_19_P00322533	GACTCATTGTGAGTGCTAGTTCTCTGTAGGATGCCACTGGAAATGTTGAAATGAAAAAAT	ref NR_110453	entg CRNDE
329	A_19_P00328996	TTGTTATTAGTGCTGTGAAAAAGACCCTGAGCTATACCAGCCCTTGGTTCTCCAGCCT	ens ENST00000419300	entg LINC00963
352	A_19_P00319027	GAAAAAGCTCTTCTCTATGCCCAGTATTGCTACCTGATAGGTGAAAAAAGGTATCACAG	ens ENST00000484091	entg RFX8
353	A_23_P166797 64108	CAAGCAGGATCAAGTTTGTAGAATAAACACTGGTTTCTTAGCCATCCTCTGAAAAACAGTA	ref NM_022147	entg RTP4
345	A_19_P00807637	GTGTAAGCTTGTGACTAAAAATAGTTCTGGATGGAAGACCATTCAGTATCTTCTGAAAAAA	ref NM_005013	entg NUCB2

354	A_24_P340066 2000	GCGTGTTCCAGCAGTTGGCAATTAAGTGCCTTTTCTAATAAAATCAGTTTATTATGAC	ref NM_001127197	entg ELF4
355	A_19_P00317128	ATGCAAGGGGGAAGATAGAAGAACAATAATTCACCCTAATGTAGTGTCTTTAGACCGTG	ens ENST00000444184	entg LINC00963
356	A_23_P217319 2258	TTGCAATGGAAGAAAGTTGGGTTCCTTGGCATAGAGTTGCATGATATGTAAGAATTTTGTCGA	ref NM_004114	entg FGF13
357	A_33_P3400273 6402	CTGAAAAGGTTACCCCTGTAACATGCAATTTTGCATTTGAATAAAGCCTGCTTTTAAAGTGT	ref NM_000655	entg SELL
331	A_19_P00318645	ATTAAAAATCCTCAGTTGTCACGCAGAAGAAGGTTAAGCTGTATTTGATTGCCAGTTTTAC	ref NR_110453	entg CRNDE
358	A_23_P214603 10211	ATGGGGGCAGCCAAAGTGA CTGGGAAGTACTGGACATTTCTAACTCGCTGCCAGAGAGT	ref NM_005803	entg FLOT1
359	A_19_P00320723	ATATGAAGAGTGAGAACTGTCTACATCTAAGCTCTTTTGAGAACAATACCAGCTGAGCG	ref NR_040059	entg SRP14-AS1
360	A_23_P331479 170954	AGTTATTAAATCTGTTTCTCTAGTGGTTCACAATTGAACTGAAATTGAGATGGTGTCGG	ref NM_133471	entg PPP1R18
361	A_23_P114414,A_33_P3219572 79836	CACCTTCCCCACTGCCGTCGGGGGAGTCTTCTTGTAATATATCTAATTGCAATAACAT	ref NM_001031855	entg LONRF3
Anexo 8				

	Sequence	TargetID	GeneSymbol	ProbeChromosomeLocation
362	CAAGACCTGCTTATATTTTGCTTTATAGATGTAGCATGTTGTTATTGCCTCATG	ref NM_144599	entg NIPA1	hs chr15:23043421-23043362
363	GGCTCATGGTGACTATGGATTAAAGGAATGACTATCACATGAATCTGGGCCAAATTCCTAGA	ref NM_033411	entg RWDD2A	hs chr6:83905856-83905915

364	AATTTGTCCTTTAAAGCAATTCACCTGACTTTGTGGATAACAATTCACCTGACTTTGTGGAT	gb AK127152	entg IQCD	hs chr12:113640158-113640099
365	TATTTGTTTGCAACACACTAGTTAATTTAAACCTGTGACTAGTTATCTCTACCGAAGGTG	ref NM_001281834	entg GCSAML	hs chr1:247739043-247739102
366	TTTTGCCTAATGTCCCTGCCTCTAGGTTTCATGAATGAATTAAGGTTTCATGAACGCTGCG	ref NM_015015	entg KDM4B	hs chr19:5153547-5153606
367	GGAACCGATGGCCATTAAACATGAACTGAACGGTTAAAGCACAGTCTATGGAACGCTA	ref NM_015833	entg ADARB1	hs chr21:46646134-46646193
368	CAGTATTCAGGTATTGGCAGTATGCAAAATGAGCAATTGAGTGACTCCTTTCCATATGAA	ref NM_002908	entg REL	hs chr2:61149596-61149655
16	ACTCTGTTCATTGCTATGGCCGGGACAAGGTCATGTTCTCTTTGAGGCCAGCGCCGCT	gb AF229166	entg LOC220077	hs chr11:71961724-71961665
369	TCCTAGAAAACCCATTGTGTCTCTGGATCTCTAGCACATTACTAAAAGAGCCTCTGCTTT	ref NM_001143819	entg TPCN1	hs chr12:113736326-113736385
370	ACTGCCCCATCTGTAAATGAGGGACTTACATTAAATTCCTACAGCTCCTTTCAGCTTGA	ens ENST00000564611	entg DHRS11	hs chr17:34953383-34953442
371	GAGTACATTTCAAAAAATGACAACCTAACCCCATCTATGAACACATTGGATATGCCACCCTA	ref NM_001293070	entg CHN2	hs chr7:29440292-29440351
372	TGGAGGACGCCATGCTGGACACCTACGACCTGGTATATGAGCAGGCGATGAAAAGGTACGT	ref NM_139022	entg TSPAN32	hs chr11:2334885-2334944
373	GCAAAAGGTTTTCAAGTCCTAGTCCATCATGACCACATAGCTGGAATACACTTATTTCACTT	gb TCONS_00019580		hs chr11:13000853-13000794
374	TACAACTATGTGACTTAGTGCAACAACACATTTGTGAAATAACCTACTCCTATATACTGAC	ref NM_153634	entg CPNE8	hs chr12:39046654-39046595
372	TATCTGCTTTCCAAAAACATGGAGCTAAGATCCAGCACTGAGAAGATGGGCAATTCCTAG	gb TCONS_00019580		hs chr11:13000682-13000623
375	TGGTAGTAAACACAGAGGGCCAGTAACGGGTCGTAATGACTTATTGTGGATAACAAAGA	ref NM_001198625	entg RUNX1T1	hs chr8:92972310-92972251
24	ATCCTTACTCCTGCAATTGTTCTTTGCCAGAGACCTATTTAAAAATTTTAAAAATTCTCATT	ref NM_001381	entg DOK1	hs chr2:74784597-74784656

376	GACAAACACACCTTTTATACCAATCAGTATCCTCTGTTCAITTAATAAACTGGCTATCCATT	ref NM_144994	entg ANKRD23	hs chr2:97503711-97503652
377	AAGTCCTAGGTTCCCATATTTAAGACCAGTCTTTGTCTAGTTGGGATCTTTATGTCACATA	ref NM_003264	entg TLR2	hs chr4:154626406-154626465
166	ATATTTTCCTATTTCAGACCTCAGGGGCTATTTTGGGACCTACAAATAAATGGGATTCCCCAG	ref NM_001164440	entg ANKRD33B	hs chr5:10657671-10657730
378	GTTTAGTGCTCAGTTTCAAAATGCATAGAAATGTTTGCCCTGCAAAACAATGATATACAACAT	gb BC041859	entg LOC780529	hs chr13:79173671-79173730
379	GACCTGACCCCTACTCCCTGCCCTAGATAGTTTATTATTATTATTTTGGGGTCTCTT	ref NM_033158	entg HYAL2	hs chr3:50355325-50355266
380	GTACTTAAGATGCCCTTGTTCAATTTATTTGTCCTGTGCAATAAATACACCTTGATTTGAGT	ref NR_026932	entg PDCD4-AS1	hs chr10:112629567-112629508
381	TAGTCGGGGGTGGCTGCCAGGGGGCAAGGAGAAAGCACCCGACAATCTTTGATTACTGAA	ref NM_000683	entg ADRA2C	hs chr4:3770121-3770180
113	CTCTGTCTCTTCCTTTTCACATTTGTGCACATAAAATATACTGGTGTGTTGTTCAGGA	ref NM_182526	entg TMEM229B	hs chr14:67937042-67936983
382	TTCTCTCTGACACCACTGGGCCCTGCAATGATGAACATGGTGGGCAGTGTGGGTATACC	ref NM_014964	entg EPN2	hs chr17:19237459-19237518
383	CCTCTGTTCTGTGTAATTTCTGTAATGGAAATCTTTACAAATTCCTCCAAAACGGTATTTAGAC	ref NM_033390	entg ZC3H12C	hs chr11:110042213-110042272
384	GTTGGCTTTATTGGAAAAAATATGGAGGCTTGAAAAATGCCACCCAGTCAGAAGAAGAGA	ref NM_020744	entg MTA3	hs chr2:42935109-42935168
385	TGGAATCGGGTGCAGCTGAATAGGCACCCCAAAAGTCCGTGACTAAATTCGTTTGTCTTT	ref NM_030796	entg VOPP1	hs chr7:55538749-55538690
386	GAAGGCTTTATTGTATCAGAGCAGTGCTAAAAATTTCTAGGACAGAAACAACACCAGTACTG	ref NM_032812	entg PLXDC2	hs chr10:20568719-20568778
387	GCTGTGAAATGTATCAACCCCTCATCTAATTTTTGTAGTACAAAATGACATCCTGATTCCT	ref NM_001080481	entg USP45	hs chr6:99880709-99880650
388	GGCACACACCTGTCTGTAAACCTGTTTTGTGCTCTGAAAGCAAAATAGTCTCTGAGCAAAAAA	ref NM_001031680	entg RUNX3	hs chr1:25227597-

389	GAAACCAACCTGTTACTGTACTGTGTGTTGTAATAATCATGCCCCTTTATATCCTGTATATTGG	ref NM_001136265	entg IFFO2	25227538
390	TGGGCCTCATTTAAGGGATTCTGATGAGCCGATGGCCCTGGAGGCAGCCCATTAAGCA	ref NM_015492	entg C15orf39	hs chr1:19230868-19230809
391	GAAAAACAGCTAATACATGCTAGGCTTGATATCTAGGCGATGGTTGGTAGGTGAGCAA	gb BC028196	entg IBC1D1	hs chr15:75504433-75504492
392	CCAGCTGCCCTATTGATTAAAGCTTTCCTGTTGAATGACAAAGTATGTGTTTGTAAATT	ref NM_000956	entg PTGER2	hs chr4:37954280-37954339
393	AGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCCTTAACTCCCTAAATTA	ref NM_153837	entg GPR114	hs chr14:52794430-52794489
394	AATGAGCCCATGAGCACAAAGTCAGAAAAAGGAAAAATGTACTTTTCATCAGAAGCAGTAAAG	ref NM_153605	entg CRYBG3	hs chr16:57610060-57610119
395	ATTCTACAAATATTCGACATCTCCATATACTCACTCCTTTCCCCCTGAGTGGAGAGA	ref NR_038904	entg LINC00958	hs chr3:97562046-97562105
231	GCACATTCACTTAAATCTTATAGTATTTATCCACCCAAACCCAGACTGAGATACTGCT	ref NM_080597	entg OSBPL1A	hs chr11:13001700-13001641
396	ATATTTCTTAAAAACCAACCATTGAAACGTAATGGTAACCACTGGCCCTGTCTCCACCT	ref DB056119	n/a	hs chr18:21742185-21742126
397	TCCAGGCTTTATATTCTGCTGAGAAAGCCAAAGCTGGAAGATGAGCATCTCGTTTCTTCT	ref NM_001113207	entg TSTD1	hs chr11:012983510-012983451
398	CTGCTAAGGTAGTGAATAAATCAGTAATGCAATATTGTGGTCCAAACTACTCTTTGCAC	ref NM_015187	entg SEL1L3	hs chr1:161007823-161007764
399	ACCAAAACAGGGAGCTGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACCTTAGA	ref NM_006813	entg PNRC1	hs chr4:25749158-25749099
400	GGAAACACTACATTTGCTCACAGATGATTTCTTCTGAATGCTCCCGAACTACTGACTTTGA	ref NM_001037341	entg PDE4B	hs chr6:89793857-89793916
352	GAAAAAGCTCTTTCTTCTATGCCCAGTATTGCTACCTGATAGGTGAAAAAAGGTATCACAG	ens ENST00000484091	entg RFX8	hs chr1:66839789-66839848
				hs chr2:102067115-

414	A_24_P335620 8140	TTTCAGTCGTTGTGCTTTTTTGTGTTGTGCTAACGCTTACTAAATTTAAAGATGCTGTCG	ref NM_003486	entg SLC7A5
415	A_23_P112311 22954	AGACATCATATCCCGTAACATTATGTCTCAGTCTGATCGTCTTTACCAGTATGAAAGTC	ref NM_012210	entg TRIM32
416	A_23_P101950 4190	TTAAAGATTACGTGCTTCTTTGGTACAGGTTTIGGAATGACAGTTTATCGTCATGCTGTTA	ref NM_005917	entg MDH1
417	A_23_P170581	AATCAACATGGAAAAGCACGACCCACATGGTTTCAATAGAACTTGCCTCTGAACCTGACT	ref XR_172185	entg LOC64255
418	A_24_P941557,A_33_P3248439,A_23_...	CAGCCAATATGCAACAGGATAATTGAATGTTCAATTAATGCTTCCAAGTAAAAAGCCATTTG	ref NM_001011703	entg MVB12B
419	A_33_P3366998,A_23_P822206,A_23_P...	CATTTATATTTTACTAATGGTTATGATGACTTTAATAACTTTCAAAGGATTATGGGGATT	ens ENST00000368287	entg ECHDC1
420	A_33_P3386935,A_32_P149298,A_33_...	CCAGAAGTGAACATTTCTCTGAATTTGATGCTTATTATGCCCATGCATGTTGTTATACTT	ref NM_032506	entg KIAA1841
421	A_23_P120153 284996	AGATGACTTTAGGATTGCAATTTTCCCTTTATTGCCTCATTTCTTGTGACGCCTTGTTG	ref NM_173647	entg RNF149
422	A_32_P517749,A_23_P417331 6197	GTATCCATGAATAATCCTGGAACAATATTGCTTGTTATTCCTGTCATAGAACAGGTTTGT	ref NM_004586	entg RPS6KA3
200	A_24_P835500 162073	TTCGTTTTCTCTGCAGGTTGGAGTAAATTTGCACCTTTGAATCATGTGGGTCATTTGGGG	ref NM_001034841	entg ITPR1P12
423	A_23_P112634 201895	GGGGTTGCTGGGATTGTGTGAAAGAAAAATTAGAACCACGCTGTATTACATTTACCTTG	ref NM_174921	entg SMIM14
424	A_33_P3369920,A_33_P3269650,A_33_...	ATCATCAACACAAATATTCTCTTTCACAAAAGGGACCTCAAGTAACCTTAGGCTGGAGGGC	gb AK124574	entg LOC10012
425	A_19_P00812892	GAACTGTGCTCCCAGGGCAATCCAGCTTCTGCTCTCTTTTACTACTACTTCATGTAATGA	ens ENST00000566733	
426	A_23_P114282,A_24_P808100 28985	GGGCTGTGGCATATGAAGACATATAAATGAGCCTCAGAAGGAATGCACCTTGGGCTAAATA	ref NM_014060	entg MCTS1
367	A_23_P211207,A_33_P33399061 104	GGAACCGATGGGCCATTAAACATGAACCTGAACGGTTAAAGCAGCACAGTCTATGGAACGCTA	ref NM_015833	entg ADARB1

427	A_33_P3281795 11343	TTTAGAGCTAAAGGAATCAGGTACACTACAGCTAATCTTAATAAATCCGATGTTTCGGG	ref NM_007283	entg MGLL
428	A_33_P3878772 3717	GGCCAGCATTATAAGCAGGTGTATACITTTAGCTTGATGCCATGTACTGTAATAATTT	ref NM_004972	entg JAK2
429				
430	A_24_P942068 26115	AGGTTTTCTATGACTCAGATGTAAAGGACTTTCTCTGTACAGTATATTATCCAATGCGATG	ref NM_025185	entg TANC2
	A_33_P32226955,A_24_P928052,A_24_...	CACATCATTAGAACCCAGGCCATTAAAGCTCATTGAAACTGAGTTTCTTTTCCTATAAAAT	tc THC2768644	
431				
	A_23_P88201 55012	CTTACGAGAACAGAGAGGCTCTTGTTGCAAAATGACAGTGAAAACTCTGCAGACCTTGATG	ref NM_017917	entg PPP2R3C
432	A_23_P368996 115399	CAAACCAACATTTCCAGCTCTCAGGTGTACAGAAATGCGGTTTACTTTGTAGGCCACGTT	ref NM_198075	entg LRRC56
433				
	A_33_P3636590 8801	CTGCTAAGACATTTCAAGCAAAATAGCTATTACACACTACTGCAGATTTTACAGGTTTCTAA	ref NM_003848	entg SUCLG2
434				
	A_33_P3273599,A_32_P118372 27152	TTCATGTGGCTTATTGGAAAGAAATCTGACAAAGTTGTGCTAATTGGCTGCTGCTGAAG	ref NM_015693	entg INTU
435				
	A_23_P11201 2857	AGTAGGAGTGAAAGCACTTCAGAAATTTAAACCAGGATACTCCCTGCATGATACATCTGTG	ref NM_001097579	entg GPR34
436				
	A_23_P51508 11266	AGCTTGGGAAGAAACTTGCAGATGATATGTGCTGCCTTTGCTTCTTATCATTCATGGCAG	ref NM_007240	entg DUSP12
437				
	A_32_P176550,A_33_P3217689 133746	AGAACCATCTTTCAATGCACTGAAAAAGTCATCTGAAAAAATAGCTTCTCCATATCAGCT	ref NM_152405	entg JMY
438				
	A_23_P259272 55884	AACGTTACATGACTCGTTGAGAAAAGTTGAGGAAATTCCTCTACCACCTTTGTGCTTGAA	ref NM_018639	entg WSB2
439				
	A_23_P69810 84803	GTAACAAAGAGCTTAGTTTCCCTTGTTGAATGCTGTAGATCTGTACCTAGTACCCCTCC	ref NM_032717	entg AGPAT9
440				
	A_19_P00801759	AGGACATTAGATTGTGAGTGTAGACCATCGTCAGTAGCCCTTTGAGGAACAGAGTCAGTTG	gb AK094279	
441	A_24_P405298,A_24_P396720 5500	GTATTAGGTTAGGTCACAAAGGTTTATCTGAGGTGATTAAATAAACTTCTGATTGGAG	ref NM_002709	entg PPP1CB

442	A_33_P3408221 729799	ACAGCATGGTGGAATTGCCTCTGATCTGCAAAAGGAGAGGCGTGCAGGGCTCGCATGTGA	ref NR_026952	entg SEC14L1P
443	A_32_P206401 169714	AACCCTTCAAACTAAACTTTAGCCCTTTTGGCTGGTGAATGCTCTTTAGCTGGGGTGAC	ref NM_181701	entg QSOX2
444	A_23_P1533286 10780	TCAGCTGGCGATCAAAATCTGTAAAGTCATCACAAAAATCATGCTGCTGTAACAATTTATG	ref NM_006630	entg ZNF234
445	A_32_P159334,A_23_P25215 5965	TATTTATGTTTAAAAACACAGAAATAAAATAACTTAAGATTTTTATCCAAGTGGTCAGTGTT	ref NM_002907	entg RECQL
446	A_23_P349083 115548	GTGAAAATGGTTAAACTTCTGCACCTTCTTAGTTACCAACAGCTTTCATACCAAGTATTGGG	ref NM_138782	entg FCHO2
447	A_33_P3322450,A_23_P128174 117177	CCATCATTAATCTTGAAGAAATGTGTGCTTGTTAAATTTTTGTATGGAAGCCAGGAGT	ens ENST00000378815	entg RAB3IP
388	A_33_P3221748,A_23_P51231 864	GGCACACACCTGTCTGTAACTGTTTTGTGCTCTGAAAGCAAATAGTCTGAGCAAAAAA	ref NM_001031680	entg RUNX3
448	A_23_P321511,A_24_P555473 115123	TCGGACCAATCAGAGGGTGATTCTCTCTCATTCCAAAGTCTGTCAATGTACCTTCTAACCA	ref NM_178450	entg MARCH3
449	A_23_P44974 28998	ATGGAGTAAAAACAACTGCTACAGTTCAGCACCTGTTTTATGTGCCGGAATCACTGTGGGA	ref NM_014078	entg MRPL13
450	A_23_P169257 944	TTCAGGAAGAAAAGCGCCTCTCTACCATACAGTATTTTCATCCCTCCAAACACTTGGGCAAA	ref NM_001244	entg TNFSF8
451	A_33_P3349496	TTCTAGCATTGTTAGGGAGATTAAATGTGATCATGCATTCAAGGGCTTAGCACGGGGCCA	ref XR_429106	entg CEP83
452	A_23_P122174 7518	AAACCAAACTGATCTCTCTGGGTGGCTTCAGCTGCTGAAGTAAAGATGATTCATTAT	ref NM_022550	entg XRCC4
453	A_23_P58862,A_23_P398172 57579	AGCACCATCTTTGAGGGTACGCAGATTTTCTGAGGCATTCCTTTGTTTGAGCATCCAA	ref NM_001105531	entg FAM135A
454	A_23_P102391 30061	CTCATGTTATCATCATTAGTAGTCTGTGTTGTAGAACATGAGGGTGTAAAGCCTTCAGCT	ref NM_014585	entg SLC40A1

455	A_19_P00317706	CAGATGTGTGCTGCTTTTGTGTGATTTTGCCATTCTTCAACAAAGTTAAAGAGCCTCAA	ens ENST00000467541	entg KANK1
456	A_23_P25003 6249	TGTATTTTCCCCTCAAGATTATCAACTGTGTGTCGACAGTGAATATTCAATCTGTGTACC	ref NM_001247997	entg CLIP1
457	A_23_P25566 1880	CTGAAACGGCAAGTCAGTGTATCGATTTCTAGTGCTGTGAAGTCAGCCCTGAAGAAAAAT	ref NM_004951	entg GPR183
458	A_19_P00322495	TTCATCAAAGGGGCTATGAGCTAGACCTGCAGATTAAACACGCAGATGTGGCCTTAAAAAA	ref NM_001195131	entg TSTD3
459	A_33_P3341676 4205	CAAGCTGGACTTTGTTGCCATCCTTGAGATGAACCTTTTAAGAAAAATAAGTTAATCTCA	ref NM_001171894	entg MEF2A
460	A_23_P2573 84216	ATGAGAGCAGCACATCCACCATTACAAATATTCGTATATCTTTCTGCAAAATATGGCTCT	ref NM_032256	entg TMEM111
461	A_32_P66222,A_33_P3401902,A_32_P...	CTGTGACAAAGAAAAATAGAACACCTTTTGATACAGGCTGTCCATTGCCAGGAAGAGGCTTG	ref NM_001012421	entg ANKRD20
462	A_33_P3259865 400798	TTTAATATATGGGCAAATGTACATGGTAGGCTAGACTGGAGCACTTGCTACACTGCCTT	ref NR_033186	entg C1orf220
463	A_33_P3212490 23405	CATGCTGCAGAAATTTGCAGTCTGCACCTTATGGATCACAATTACCTTTAGTTGTTTTT	ref NM_001195573	entg DICER1
464	A_23_P76538 54997	GCTCGTCTGCGCACCTTGTGTCTTGAGGGTATGGTATGTGGGACTTCGGCTGTTTTATC	ref NM_017899	entg TESC
465	A_24_P173746,A_33_P3291998 55103	AAAGGCTACCGAAAGAAAAACATTTCAAATCAACATCCAATAAGAACGTATCTGTGATAGG	ref NM_152663	entg RALGPS2
466	A_33_P3663705,A_32_P149546 9696	TTAAGAGCATGTGTGCGGAAATTCCTCAGAGTGCTCAGAGTCCCTGTATTTTTTATACCTT	ref NM_014675	entg CROCC
467	A_33_P3244931 1622	AAATAACCAGTTAAACCAGCTACTCAAGGCTGCTCACCATACGGCTCTAACAGATTAGGG	ref NM_001079863	entg DBI
468	A_23_P46604,A_24_P45367 57185	TGGAGATCATTCTGTTCTGCTGCTCTACTTACAAGGAGAAGAACGCCAACAAACA	ref NM_020448	entg NIPAL3

469

A_23_P382705 160335	AAAGTAGTGTTCCTATGGCATTAGTGTGTTTGTGAGAAAGGTAAATGTAGTGAGAAAGGT	ref NM_152588	entg TMTC2
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Anexo 10

	Agilent Probe ID	Sequence	TargetID	GeneSymbol
470	A_23_P58396 56034	CATGGATAATTTTTATGTACAGAAAGTATGTCTCTTAACCAAGTTCACATTATTGTACTCTGGC	ref NM_016205	entg PDGFC
471	A_23_P58132 399	AAAGCTTGGTGTTTTCTCTGGGTACACCCCAAGCAGCGTCTCTTTTGGATACAGTTATT	ref NM_001278359	entg RHOH
472	A_33_P3276784	TCCATGTGCTTCAGCGCCTTCTCGGCTTCATCTGGATTCTCAAACTCTACGTACGCATAG	ens ENST00000454671	
473	A_33_P3799936,A_33_P3215575 55160	ATAAAGTCTGTACATAATTGGAGCTCTGGGAGATGCTGGAAATAAAAGACAAAGAGTTACATC	ref NM_018125	entg ARHGEF10
474	A_33_P3630129 440918	GGCTCTTTCCCTATGCATTAAATAGAAAAATCCTATGGGATTACATTCATGTTTGCTTTC	gb AK128708	entg FLJ46875
475	A_32_P230547 85440	GTGACCCAAAGCTCTTCAGACATCATAATAAACTGCGACTCTGCTTTAAAGATTTTACTA	ref NM_001271999	entg DOCK7
476	A_23_P19226 29940	GCAGTCTTCTCATAGATAGCTGTATTTTATTATGTTGTACTCTTCTTGTTCCCAATCA	ref NM_013352	entg DSE
477	A_23_P50907 3685	AAAGAGTGATTAAGTGAGGTTATTTACCCCTAAATGGTCCATTCTGCATTGTATTTTCAGG	ref NM_002210	entg ITGAV
478	A_33_P3293381,A_24_P295590 83937	ATGCAAGCCGAACATGTCTCGCCATCTCTTGTTCTATCTTTAAAAATTCACACGAATTTAG	ens ENST00000428466	entg RASSF4
479	A_32_P76853 653075	CTATTCTTCAACCACCTTGGTTACTCTGACATAGGAATTTACTTCTTTTCTTTTGAATGG	ref NM_001282484	entg GOLGA8R
480	A_33_P3423445 100129543	CACAACTTTCTAAGATTGAACCAAGTAAGAACCAAGAGTCTTAACCAGAGCAAAAAATGTAT	ref XM_006722596	entg ZNF730

481	A_33_P3370284 29924	TGAATCCTTGGTGATGATTTTGGCAACTTTGGGAATAAATGGCAATTCCACGGGCTTGG	ref NM_001130071	entg EPN1
482	A_33_P3317553 100288615	GGGCTGAAAGAAGCTGTGTCCTATTCAAGATATCACAGTGAAATATTTTAATTAGACAG	ref NR_036650	entg WHAMMM
269	A_33_P3338928 1601	GATCAGCCACACAACACTGTTTGTACATACTTATTTTCTCATGCACCTTTTCTGTATGCAAA	ref NM_001343	entg DAB2
483	A_23_P417282 3480	AAATCAAACCAAGAGCGGGATGGAATGGATGCACCGCAAAATAATGCATTTTCTGAGTTT	ref NM_000875	entg IGF1R
484	A_23_P208009 90701	TTCAAGTATGCTCTTTGGCTGTAAATGGGTGCATATGTGTACTAAACGTAATCCTAA	ref NM_033280	entg SEC11C
485	A_32_P167471 79789	CTGGTCTATTGAGCAGATTGAATGTTTCTTATTGTGCAGGGCTTAATTGACTATGCTG	ref NM_024734	entg CLMN
479	A_32_P2392,A_23_P37623 23015	TTCTTTTTTAATTCATAATTGTAGGTCAATTAGCGTGCAATCGAGTTTGCCCTTACGTG	ref NM_001282484	entg GOLGA8R
486	A_33_P3399935,A_33_P3347452,A_33...	TGCAAGTGCTCAAACACCCGTGGTGGTGCAACAGAGAGTACCTGTCCCCAAACCAGCTCA	ref NM_021135	entg RPS6KA2
487	A_33_P3378659,A_33_P3225625 445347	AAACACCTCTGCATATTACATGTACCTCCTCTCTCTCAAGAGTGTGGTCTATTTTGC	ref NM_001003799	entg TARP
332	A_23_P36658 4257	TTTTTTGTTGGATATGGAGTTACTCTTTCCATGGCTTACAGTTGCTGAAAAGTAAATTG	ref NM_001260512	entg MGST1
488	A_33_P3289406 91450	CCAAGATGAAGTCATGCTGTGCTTTGGAAATGGTAGATGCTCATTTATGTAAATCATAAAT	ref NR_026998	entg LOC91450
311	A_23_P110167 4258	AATATCTGGACCTCAATATTGCCAAGAAACTGAGGCGGCAATTTCTAATTTTCTCTTCC	ref NM_002413	entg MGST2
489	A_23_P59547,A_33_P3393836 51251	TATCCTTACTCTCGAAGTGTTCCTTTGTATAACTGAAGTATTTTCAGATATGGTGAATG	ref NM_001166118	entg NT5C3A
490	A_24_P331655 653319	TAGTTTTCCCATCTGTAAAACTCAGAAACGCAGTTGGAAAGTCCTTATTTCATTTAGTAAG	ref NM_001040715	entg KIAA0895

491	A_23_P141715 25941	AATGTTCCATGAAACCTCTCAAGTACACAATTGTAIGTTCTTTGTATCCCTTACCACAAA	ref NM_015476	entg TPGS2
492	A_23_P88069 10186	TTCCAGTCATTGGATCGTGTCTTTCTTTGTCCATTATTGTAAGTGTGCTGTACCAATTTA	ref NM_005780	entg LHFP
493	A_33_P3407945 55266	CTTTTCATGGAAAGAGCTCTAIGTAACAGCATAATAAAAGTGCCTACCTAGCAGCATAAA	ref NM_018279	entg TMEM119
494	A_23_P423457 256987	TTTTGGTTCTTTAAACTTCTGCTGTTGGGGCCATGTGCTCAGGAGCTTCTTCATTCCA	ref NM_001174071	entg SERINC5
495	A_24_P12435 135112	ACGTTTCACCTCAAGTTCCTCTACTGAGGACTCTTGACTAACAGCATACTGGCAGTTTCAC	ref NM_001199620	entg NCOA7
496	A_24_P173754,A_23_P113161 81563	AAAGCCAAACAAGAAATTCCTCAGAATGCTGGATGAAAAAATTGAAAAAGGGTCGGGATTACT	ref NM_030806	entg C1orf21
497	A_23_P19115 23708	AAATTGGTCCAGAGAAAGGACTAAGCAATTTTCTTGATGCCTCTGCAAGATACTGTGAGG	ref NM_018094	entg GSPT2
498	A_23_P153026 2548	CTGGGAACTCAGGAAAAATTCACAGGACTTGGGAGATTCTAAATCTTAAGTGCAATTATTT	ref NM_000152	entg GAA
499	A_23_P417942 54874	CTGTTCTTTTCAAGCTACTGTTGTGTTTCTTCTAAAGCAGGATTTGCTTCCGTAGGAGGCA	ref NM_001024948	entg FNBPL1
500	A_33_P3296479,A_33_P3508822 351	AAGAAAGTGACAATGTGGATTCTGCTGATGCGGAGGAGGATGACTCGGATGCTGGTGGG	ref NM_001204303	entg APP
501	A_33_P3295056 5790	AATGACCTTGAGCGACAGGAGGATGAGCAGGACACAGACTATGACCACGTCGCGGATGGT	ref NM_005608	entg PTPRCAP
502	A_23_P99661 55701	AACAATAGGAGGGGTGTGACAGGGGAACCGTAGACTTTATATATGTAAATTACTGTTATTAT	ref NM_001278529	entg ARHGEF4
503	A_33_P3219095 728606	TCCAGCCTATGTCTAACTTTCTAGCAGATAATGGCAATAAAAAATGTTTGGGTCCAACATT	ref NR_024259	entg PCAT18
504	A_33_P3415633,A_23_P329890 219902	TCTCCCCACGCCCTAAGTGGTTTGTGAAGGCTGGGGGAGTAGCGATGTATGCTGTGTTCT	ref NM_001198670	entg TMEM136

505	A_23_P305550,A_33_P3375368 2859	TATGGCTGGAGTTCCCATGCCTGCCAATCTCTGTGCACTGCGAGTCAGCTCCGATACTT	ref NM_001195382	entg GPR35
506	A_33_P3333960 100188949	GCTGCCTGTTTTGTTTAACCCGTGAGCTAAGAAATAGTTTTTACCTATTTTAAGTAGTTG	ref NR_024464	entg LINC0042
507	A_24_P148717 1230	CTTTTCAAGTTGGGTGATAIGTTGGTAGATTCTAATGGCTTTATTGCAGCGATTAATAAC	ref NM_001295	entg CCR1
508	A_33_P3251209	ACAAAAACATGATCCTTCAICAGTACTGGGAAGTCTGGAACAGCTAAGCCTGGAGTGAAG	agp A_33_P3251209	n/a
509	A_33_P3414389 10603	ACGCCAAGCTCTTCAGTGAAGACACGATGTTATTAAAAAGCCTGTTTTAGGGACTGC AAAA	ref NM_020979	entg SH2B2
510	A_23_P78053 81558	GACTCTATTTTCTCCCAAGACACTATTTTTGCAGCTGTTTGAAGTTTGTAATATTTCCG	ref NM_030802	entg FAM117A
511	A_33_P3281940 6120	ATCAATCTATTAAAGAAATGTTTGCTCAGAAGCTGCTCAGAAACGTTCTCTTGATCGGTGA	ref NM_001278283	entg RPE
512	A_33_P3262814 221035	GGCTGAGATAAATTTGCCAATGCAAAATACAGTTGTGCTTAATCTCTGCACATTGGAAATTA	ref NM_001001330	entg REEP3
513	A_23_P169838,A_23_P147070,A_33_P...	TTTCACTCTCTTAGAATTGGAACTATGCAGTTAAGGCAGATAAAATGTACAGATGTTTC	ref NM_001130965	entg SUN1
514	A_23_P206733,A_33_P3241269,A_33_...	ACCTGAAGAGCTTCAAGCTGAAAGGAATTTCCACACTGTCCCTACATGGTCGGAAATTAA	ref NM_001266	entg CES1
302	A_24_P12136 170591	TGCAGGACCTGGATGCCAATAAGGACAACGAAGTGGAATTTTAATGAATTCGTGGTCATGG	ref NM_130772	entg S100Z
515	A_24_P85181 64145	ATGCCTTGTTGTATTACCCTGTCTAATACACTAAGGATACTTACTCATTTGACTTGCA	ref NM_022340	entg ZFYVE20
516	A_33_P3294961,A_23_P259621 7462	TAAAAACATTTAAAAATTAGCCAGGCATGGTGGTGGATGCCCTAGAGTCCCCTGACTTGG	ens ENST00000398475	entg LAT2
517	A_23_P114839 2275	AGGGCAGCAGTTACCTCCCGGGATGAAGATCCCTACTGTGTGGCCTGTTTGGAGAACT	ref NM_004468	entg FHL3
518	A_32_P84009 146223	GCCCTCAATTTTCCCCCTTTCATTTGAAGGACCAGTTTTTTCATGGTACTTGCTTGATCT	ref NM_181521	entg CMTM4

519	A_24_P271696 653219	GGTGATCTGCAAGAGCTGCATCAGTCAGTCAAAACACCGGGGATAAAATCTGGATTTGGGTTCCGG	ref NM_001097594	entg XAGE1B
520	A_23_P159027,A_33_P3219398 25925	GAAGCTTTGAGTGTTCAAGGTTTCCTTAATGATTTACGCAGCCAAATCTTGAATCAG	ref NM_015461	entg ZNF521
464	A_23_P76538 54997	GCTCGICGCGCACCTTGIGICTTGTAGGGTATGGAIGGACCTTCGCTGTTTTATC	ref NM_017899	entg TESC
521	A_23_P116512 79899	ATGACTGTTAGCCAGTTTACAACTTTTTACCATCGATGTACACATTTGATATTTGTGCAG	ref NM_001160167	entg PRR5L
522	A_23_P50368,A_33_P3387561 126014	GGGACCTGGAGAACTTTTCTGTCTTACAAGAGGATTGTAAAATGGACCAATCAGCACTCT	ref NM_206818	entg OSCAR
523	A_19_P00806320	ATTCCACTTGATCAACTTAATTCCTTTTCTTTATCTCTCCGTCACCTCCCTTTTCTC	ref NM_152862	entg ARPC2
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	agilentProbelID	Sequence	TargetID	GeneSymbol
524	A_32_P45009 3417	GTTCTGGTGCATAGATGTCCCATTTTGTGAGGTAGAGCTGTGCATTAAACTTGCACATG	ref NM_001282387	entg IDH1
525	A_19_P00810361	TGATTCCAAGAAACAAGTATTGCTTCCAGTATGAAGTGTGAGCGATTCACAATCTTCAAC	gb TCONS_l2_00022932	
526	A_33_P3251093 206358	GATCCTGTTTGGGGTTTGACATGGATCGTATGTTAAGCTTTTCTTTTCAATAAATGA	ref NM_078483	entg SLC36A1
527	A_33_P3358342 6478	CATATGCTTGCTATTTAAAGCTGTGTGTTGGTTTTTGTTTTTCTGCCACATTCAGTGT	ref NM_005067	entg SIAH2
528	A_33_P3241753,A_23_P76557 55967	GTAATTACTCTTTTACTGTTTACCATTCACTATAATTCACAATTAAAATTGTGTGACTAA	ref NM_018838	entg NDUFA12

529	A_32_P108156 114614	TTAACAGTGTATGATGCCTGTTACTAGCATTCACATGGAACAAATTGCTGCCGTGGGAGG	ref NR_001458	entg MIR155HG
530	A_33_P3215123,A_32_P85813 5910	TTTTCTAGATGTCGTATCCAACTTCGCAGTCATGAGAACAAAAGTGTGCCCAGCAGGC	ref NM_001100426	entg RAP1GDS
531	A_33_P3270776,A_23_P10542 94031	GGCCACCATCAAAGACATCGACAAGAGTCGGACATTGCCACCATCAAGATCCATCCCAA	ref NM_053044	entg HTRA3
532	A_19_P00317432	GCTAGTCAGCTGCAGCTGCATCTTCACGAACTCGGTGGGGAACGGGATGCAGATTTTTT	ref NR_110687	entg LOC10192
321	A_23_P423331,A_33_P3277784 84628	AACTATTTTTGTTGTATTCACTGTCCCTGCAAGGGGGACGGGGGAGCACTGGTCA	ref NM_032536	entg NTNG2
536	A_23_P143559 8218	CATGTCACCTCCAGCAGCACAGGGGACGCAATGGGAGGCAGGGACACCTGGACAATATTTA	ref NM_007098	entg CLTCL1
534	A_23_P128532 121053	TTGAAAAACATTGATGGGCCTCATAGTAAAGTTATACAAATGGATGTGGCTTGTGTGAGA	ref NM_152318	entg C12orf45
535	A_19_P00320719	CAAGAGCAGCAAATGTGGTTTCATCAAGTGGGAAGAAAGCAGCAATTTAAAAATAACTTTT	ref NM_002393	entg MDM4
536	A_33_P3227788 53354	CTGAGCACCGTCTTTAATTTCCATATCTTCAAGTCTTGAAGAAGTTGATGTTAATTGAAG	ref NM_148977	entg PANK1
483	A_23_P417282 3480	AAATCAAAACCAGAAAGGCGGGATGGAATGGATGCACCGCAAATAATGCATTTTCTGAGTTT	ref NM_000875	entg IGF1R
537	A_24_P244100 54788	AAGGAAGTTCGGTAAGGAAATGTCAAATCTGGTTTTTAAACAAGGTCCAACCCCTGCAATG	ref NM_001002762	entg DNAJB12
538	A_33_P3253528,A_24_P273865 9477	TTTGATGTGCTTATGGTGAAGCTCAAGGGCTTTTCCAGAGTGCTAAGGCCAGCAAGATT	ref NM_004275	entg MED20
539	A_33_P3279241,A_23_P169978 57507	AAACAACCACTGAATCTAAAGCACTGGATTTTGCTCCAGCAGCATGCTAACCAATACCGCA	ref NM_020747	entg ZNF608
540	A_33_P3327847 8879	CTGGGTAGGCAAAGTCAGATTTTGTGAGAACCTTTTCTGATTTGAAGTTTAAATTACCT	ref NM_003901	entg SGPL1

541	A_23_P345118 5292	GCCTGCTGGTTTATCTGAGTGAAATACTGTACAGGGGAATAAAAGAGATCTTATTTTT	ref NM_001243186	entg PIM1
542	A_33_P3391005,A_24_P108311,A_24_...	AAATTTCCAGTACATATGCGGTCAAAGACATCTTTAAACCCCAATGACCTTGGCCCCCTT	ref NM_001144967	entg NEDD4L
543	A_23_P210690 57761	ACACTGGGGTCCACAATCCAGGTCCATACTACTAGGTTTTGGATACCATGAGTATGTAT	ref NM_0211158	entg TRIB3
544	A_23_P349676 150726	GTAAGATGCCCTTTGCTGAATGTACCTGAGTGTATGTAATTTAAAAAGGACTCACATGGGCA	ref NM_001080410	entg FBXO41
545	A_23_P89812 55748	AGACTCTGTCTCTACAAAAAGTTTAAGAAATGAGCCAGACATGGTGTATGCCTGTAG	ref NM_018235	entg CNDP2
546	A_24_P44780,A_33_P3408949 125336	CTCAAGAGGAAGAGGAAGTACTTCAAGGTATTCGAGGTTACCAAGACGACAGAGAGCTTT	ref NM_001145472	entg LOXHD1
333	A_33_P3410589 131583	TAGCACTGTTCTGTTCTGTTGCACGCCAGTGGGAGAGAGATAAAGAGGAAAAATTTAAC	ref NM_153690	entg FAM43A
547	A_19_P00319323	CATCATCTTGACAGTACTTTCCTGGATGAGTGTTCAGGAAACATGAAAAAGTTTTTAAACA	ens ENST00000497307	entg PLD1
548	A_19_P00328361	ACATAGTAAATTGTCCCCAAAGGCCAGCACCTCAGACACCTTCCTTTCACTTTGTAAAG	ref KF773846	n/a
549	A_33_P3413053 4682	CATATATAAAGGGCATTCTCTACAAATGTGCCGTTTTAAGAATAAAACCCCTCAAATCT	ref NM_002484	entg NUBP1
550	A_24_P4816 23710	GGATTGGCTTTGATAGAGGAATGGGGATGATGTAAAGTTTACAGTATTCCTGGGGTTTAAT	ref NM_031412	entg GABARAP
551	A_23_P79545 8802	TCCTTTTAATGGAACAGATTTTATTGACTGCCCTCGAAATCTTTTGAACGATTCGCCAC	ref NM_003849	entg SUCLG1
552	A_19_P00812504	GAACAGTGGTGTTTGCACAAATGCTACTCTTTGTTTTAACCTAGTCATGTGTAAAAAGTG	tc THC2743589	
553	A_23_P27947 84306	AGCATGCTCAAGAGTGCTAATTTAGGTCCTTCTGTGGAAATTTGGAACAAATTC TAGTTTAC	ref NM_032346	entg PDCD2L
554	A_33_P3210760	TGTTTAGCTCCCTGTTCTCCGCAGCCCCGAAAGAAATGGCATGCAGCCTCTTCTGCTCCTC	gb AI205683	

555	A_23_P315571 23180	TTTATCATGTGTATATCGTCCAGAAAGTATTAAGGCTTTAGGTAGATGCAACTGGCGAAC	ref NM_015150	entg RFTN1
556	A_23_P112596 132	GATCAAGACCAGAAAGAAATTATTGATACCAATGGAGCTGGAGATGCAATTGTGGAGGT	ref NM_001123	entg ADK
557	A_24_P88554 8799	AATGATGCTATGTGTAGCACTTGCTGTGTAATACTCTGTACAAATGATTCTGTGTAATAAGCT	ref NM_003846	entg PEX11B
558	A_23_P117157 8803	GTGTTCTGTGTTATTGTTCTTTTCTTTTATAGTGTGTGGAGATTGTAATTGCCATCTAGG	ref NM_003850	entg SUCLA2
448	A_23_P321511,A_24_P555473 115123	TCGGACCAATCAGAGGGTGATTCTCTCTCATTCCAAAAGTCTGTCAATGTACCTTCTAAACCA	ref NM_178450	entg MARCH3
559	A_19_P00322310	TGGTAACCACTTGCCAGCTGCAACTTTGACGCATATTATCAGGATAGGTGAGATTGATGG	ref NR_038303	entg LINC01094
560	A_23_P204782,A_23_P105730,A_23_P...	ATGAGACAGGGTAATGAAAACTTGGGGAAGTGGTAAGTTTTTGCATGCTACAAGATTTT	ref NM_001205029	entg MDM1
393	A_23_P206293,A_33_P3245799 221188	AGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTCTTTAACTCCCTAAATTA	ref NM_153837	entg GPR114
122	A_23_P201628 3915	ACCTTAATTACACTCCCGCAACACAGCCATTATTTTATTGTCTAGCTCCAGTTATCTGTA	ref NM_002293	entg LAMC1
561	A_23_P140301 5684	TGAACTAGAACTCAGCTGGGTGGTGAAATTAAGTAAATGGAAGACATGAAATTGTTCCAAA	ref NM_002788	entg PSMA3
562	A_23_P321452 118987	GGCTACAAGCTCTAACACTTCTTATGATTCACACAGAGCAGGCATTGAAGATATAGAAA	ref NM_173791	entg PDZD8
563	A_33_P3329686 5413	ACTTCGTGAAGCTGCGCAACATGCTCATCCGCACGCATATGCACGACCTCAAGGACGTGA	ref NM_001009939	entg SEPT5
564	A_24_P283288 1432	AATGAAGACTGTGAGCTGAAGATTCTGGATTTTGGACTGGCTCGGCACACAGATGATGAA	ref NM_139013	entg MAPK14
565	A_24_P172481 10346	TGCCCTTTAAAAAGATTGAAGAAAGAGAAAACTTGTCAACTCATATCCACGTTATCTAGCAA	ref NM_006074	entg TRIM22

566	A_33_P3881262 1441	TCCATCCAGCCCCACCCAATGGCCTTTGTGCTTGTTCCCTATAACTTCAGTATTGTAAA	ref NM_156039	entg CSF3R
567	A_19_P00805705	ACTGTCTCAATGGAATTGAAACTTTGTGTCTCTGGCTAGAGGAGACTTCTGACACAG	ref NM_001109662	entg HECTD4
568	A_33_P3651911 286109	AAGTGAATGTATTGGCTTAGCCAAATCACTACAGAAGGTGGTTCCTAAATACCTTTTAGT	ens ENST000000560295	
569	A_33_P3325871	GTGGTAAGGCTCTGTGCGGCAGGCCGGGCTTCCGGGAGGACCTGGTCTGGATCGGTCACC	ref XR_244911	entg FLJ38668
568	A_19_P00317929	CTCTGGTACACTTCAGATTACTTACCTAATACATATTGAGGGCTTTTAACCCCTTAGTTTT	ens ENST000000560295	
547	A_19_P00320889	ATAGAAAAATCCTGTGCATTGGTGAGTTGGCCCTGACCACCATTCTTCTTAGCATGCTGAA	ens ENST000000497307	entg PLD1
570	A_33_P3415092,A_33_P3415087 1184	TTTTCACTTAGCACAGATTTGTAAATTATGCATGTAATAAAGCACAGCCTTATCCACCCTG	ref NM_001127899	entg CLCN5
571	A_23_P99253 8825	TTGAGGGAAAGCTACTTGTATCAAAACATCCGATAGTCACAAATTTGAAACCGTGCTTCAGA	ref NM_004664	entg LIN7A
572	A_33_P3298425,A_23_P380181 8543	AGCTCTCATCAATGGCCATTTGAATTCACCTTCAGAGCAATCCACTACTGCCAGACCAGAA	ref NM_006769	entg LMO4
360	A_23_P331479 170954	AGTTATTTAATTCGTGTTTCTCCTAGTGGTTCACAAATTGAACTGAATTGAGATGGTGTCGG	ref NM_133471	entg PPP1R18
361	A_23_P114414,A_33_P3219572 79836	CACCTTCCCCACTGCCGTCGGGGGAGTCTTCTTGTAATAATATCTAATTGCAATAACAT	ref NM_001031855	entg LONRF3
573	A_33_P3333820 54926	GCCCATCTGTCTACTAATAAAAAATGTGAAATAAAAAATACCTGTATTGCTACTTCCCCCATGAA	ref NM_017811	entg UBE2R2
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	AgilentProbeID	Sequence	TargetID	GeneSymbol

574	A_32_P96692,A_23_P422718 5429	CTGAGCCTGTAGCTAACGCATAAGCACAGTGATTCATAAAACATTTTATTCTGTACA	ref NM_006502	entg POLH
575	A_23_P213385 10409	TCAATGCCAATCCTCCAATCTCTCTCCAGATAATTTTGGGAGTGACAAACATTCCTC	ref NM_006317	entg BASP1
576	A_23_P59787 51631	TACTGTGCAAGGCACCAAGGACATAAAATACGTACTTGCAAAGATTCAGATGAGCTGTT	ref NM_001270643	entg LUC7L2
577	A_33_P3358342 6478	CATATGCTTGCTAATTTAAAGCTGTGTGTTGGTTTGTTTTCTGCCACATTCACTAGTTT	ref NM_005067	entg SIAH2
578	A_33_P3390656,A_23_P7562 23305	ATGTGTGAGAGGACCAAAATGTGTCAAAGGCTACTTGAAAGATCCAGACAGGACGAAAGGA	ref NM_001009185	entg ACSL6
579	A_33_P3375467,A_33_P3375466 2822	AACTGGTAGCTTTCTGTTTGGAAATTACTTCTCACATGGCGGCAGATGTCAGCTGGCATA	ref NM_001503	entg GPLD1
579	A_32_P86763,A_24_P923251 7052	CTCCACACCAGTGGCCTCGTGGTTATTAGCAAAGGCTGGTAATGTGAAGGCCCAAGAGCA	ref NM_004613	entg TGM2
579	A_32_P108156 114614	TTAACAGTGTATGATGCCTGTACTAGCATTCACATGGAACAAAATTGCTGCCGTGGGAGG	ref NR_001458	entg MIR155HG
580	A_23_P27810 84775	CAACCTTATGGAGTGAGCAGCCACCCTTTGGGCTCATCTGGACGACGTGCTTTGACACA	ref NM_032689	entg ZNF607
580	A_33_P3215123,A_32_P85813 5910	TTTTCTAGATGTCGTATCCAACTTCGCAGTCATGAGAACAAAAGTTGCCCCAGCAGGC	ref NM_001100426	entg RAP1GDS1
581	A_24_P44462,A_33_P3335966,A_23_P...	CCTTGAAAGCATTAATGGCTGCAGAGGATAAGTACTCGCAGAAAGGAGACAGATATGAGG	ref NM_000366	entg TPM1
582	A_32_P62997 55872	AGCTCTGGAAACAGATGCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCGTAAATAACT	ref NM_018492	entg PBK
583	A_24_P98914 5213	GGGCACCTCTAGTGCTACTGTAGATATCACTTACTCAGTTAGAAATTTTCTAAAAATAAA	ref NM_001166686	entg PFKM
584	A_32_P68533,A_32_P82189 84140	TTCTCCATCAGGGGCAAAATGTTTACTTGTAATTTTCTTCTACAGTTCGTGTTAAATTAC	ref NM_032180	entg FAM161A

138	A_23_P22096 5747	GCAAAGAATTCAGGAAACCAAGAGGCTGAGAAATCTTTGTCTACCATAGAAATTATTA	ref NM_001199649	entg PTK2
585	A_33_P3390853 550643	GGTGACATCCTGTTCTTGGTATAAAGCTTTATATTCCTATAAATCCATTAAAGGCCCAAT	ref NR_015367	entg LINC01420
586	A_32_P112881,A_23_P368896 29934	GTCAGAGGCCCAATTTCTGCTGTGTAATAATCCTGACTCGGGGCTTTTATTACGAAAA	ref NM_001256185	entg SNX12
587	A_23_P215070 95681	AGAGCTGTTCTAATCTGCGTTTGCATGTTAAGTGTTAAATCAAAACATTCCTTACGTGC	ref NM_018718	entg CEP41
588	A_33_P3234124 151176	ATCATGGGCTGGAGAGCAGCAGTGAGCTCTTCACCATCTCTGTGAATGGCGTCTGTAC	ref NM_001291832	entg FAM132B
589	A_32_P219148 497257	TCCCCGTCCACGTTACCGCATTCAGAGCTTGGGTACCTGGACACTGAACTCAGGTGAAT	gb BC030211	entg LOC729732
590	A_33_P3209491,A_33_P3738458,A_24_...	TTGAAACTCTCCTGTGCTGTGTTTGTGCGTGTGTGTGAGAGCACATCAGTGTGT	ref NM_022648	entg TNS1
591	A_33_P3229335 128312	AGTACACCAGCTCCAAAGTGAGGCGTTCCTCGGGCTCCTGAACCCAAAGGCTCTTTTCAGA	ref NM_175055	entg HIST3H2BB
592	A_23_P86021 8991	AAGCTGAGACTGTGGCAATGTGTGAGTCAATACATTTACTGACCACTGTTGCTTGTTG	ref NM_001258289	entg SELENBP1
538	A_33_P3253528,A_24_P273865 9477	TTTGATGTGCTTATGGTGAAGCTCAAGGGCTTTTCCAGAGTGCTAAGGCCAGCAAGATT	ref NM_004275	entg MED20
540	A_33_P3327847 8879	CTGGGTAGGCAAGTCAGATTTTGGAGAACCTTTTTCCTGAATTTGAAGTTTTAATTACCT	ref NM_003901	entg SGPL1
542	A_33_P3391005,A_24_P108311,A_24_...	AAATTTCCAGTACATATGCGGTCAAAGACATCTTTAAACCCCAATGACCTTGGCCCCCTT	ref NM_001144967	entg NEDD4L
593	A_23_P476,A_33_P3215953 9019	GCGCTAATTTCTGATGGGAGCACTCAAAAGGCATTACTTAGAGATTGAAATTTCAAACATA	ref NM_003953	entg MPZL1
594	A_23_P98310,A_24_P256552 1479	AGCATTTTATCACATTTTCTGAAAACAAATTGTTCTTGTTTGTCTATGTAGATCTCTGCC	ref NM_001326	entg CSTF3
595	A_33_P3252394,A_24_P120934 10912	GGCAATGCTTCGTTTTCTAAAGGATGCTGCTGTTGAAGCTTTTGAAATTTTACAATAAACTT	ref NM_006705	entg GADD45G

596	A_33_P3398897 5860	GGAGGCTTTTAATCTGATGTTCTCAGAAGGGGTGGATTAAATCCTGAAATAAATATT	ref NM_000320	entg QDPR
597	A_33_P3280779,A_23_P97853,A_33_P...	TTGATTGCTTACAAACGGAAGCGCCAAAACAAACTTGAAGTTGTCTGAAAAGCTTGCTCT	ref NM_001270374	entg TMEM254
598	A_23_P303210,A_23_P53467 121457	TTTAGGTTCCAACTGIGTTAGACATGAGTTTGCTAGATCCATGGTCTCTAGATGGTTTAC	ref NM_153687	entg KBIP
599	A_19_P00810862	CTCTGGCAGCATAATATTACCATACACCATATTACCTTATAATTGCCATTACAGTTCCTT	ref KJ423406	
600	A_24_P379165,A_33_P3249793 4303	GAAAGAGCTCCCTACGGACCAGGTATAGAGAAAAGGTCTATGCAGAAAATAGGTTAGAGTTT	ref NM_005938	entg FOXO4
601	A_23_P166196,A_33_P3265304 25980	TTCCTCTCTAGACAAGTACACAGGCCTGCCACCTGACATCAAACTGTTGTACTATGATCA	ref NM_015511	entg AAR2
602	A_33_P3249414 25893	CCCCCAATGCTGGTTGTATGTGGTTATCATTCATCTGTATTTGTTGAATGAATAAATG	ref NM_015431	entg TRIM58
603	A_23_P29225 25793	GTGCTGATCTCGAGTGTTATTTTCTGATTGTGGTTGAGAGTTGCACCTCCAGAAACCT	ref NM_012179	entg FBXO7
604	A_23_P38677 10650	CAAAGCCTTCCAGAAAGTTTCTGTGCTTATGAAAGCGTATGTGTGGCCTTTCTCTCCCT	ref NM_001142405	entg SLMO1
605	A_23_P380815 26128	TACTTGATAGATTCTTGTAAGAAAAAATGCTGGGTAATGTACCTGGTAACAAGCCTGTT	ref NM_015634	entg KIAA1279
529	A_19_P00812504	GAAACAGTGGTGTTCACAAAATGTCTACTTTTGTTTTAACTAGTCATGTGTAAAAAGTG	ref NR_001458.3	entg MIR155HG
606	A_24_P281975 79158	AGATCATGATCTCAACAATATTCTCCAAAATGGCATACATCTTTTGTACAAAGAACTTG	ref NM_024312	entg GNPTAB
555	A_23_P315571 23180	TTTATCATGTGTATATCGTCCAGAAAAGTATTAAGGCTTTAGGTAGATGCAACTGGCGAAC	ref NM_015150	entg RFTN1
607	A_33_P3278220,A_24_P386323 10244	GTGTGTGTGTACATGTGTATGTACTATCACCCCAAAATTAATTAATTAATGTTAACATCTC	ens ENST00000373544	entg RABEPK

608	A_23_P392384,A_33_P3260034,A_33_...	TCAACCATCTTCTTTCTGAAAGACCAAAATCTAATGTAAACCAGTAACGTGAGGACTGCCTAA	ref NM_001185095	entg AIF1L
609	A_23_P170857,A_23_P336554 3556	AATTAATGGTTTAAATATATGCTATAGGACGTTCCATGCCAGGTTAACAAAGAACTG	ref NM_001167928	entg IL1RAP
557	A_24_P88554 8799	AATGATGCTATGTAAGCACTTGCTGTAAATCCTGTACAAATGATTCGTGTAAATAGCT	ref NM_003846	entg PEX11B
610	A_24_P942112,A_23_P209987 84172	GATCATCTTGATATATACTTCTGCAATTATAAGATGTTTTTTGATGATGAGAGCTTTCCTA	gb AK001678	entg POLR1B
448	A_23_P321511,A_24_P555473 115123	TCGGACCAATCAGAGGGTGATTCTCTCATTCCAAAAGTCTGTCATGTACCTTCTAAACCA	ref NM_178450	entg MARCH3
611	A_23_P134167 57107	AGCTTAAGAGAACACTGTTCTGTTTGAAATGCTTCTGTCACTGAAATGGCTTAATTAG	ref NM_020381	entg PDSS2
612	A_33_P3233916 55553	GCTGGTGGAGAACAAAGGACTGTTCTTTAGGACTGAAACTTGATTTTGCTCATAGTAAGT	ref NM_017508	entg SOX6
613	A_33_P3381870,A_23_P219117 2039	GTGTGACCATGCTGGGGAGGGGACTCTGCTTGGAATTAAGAGTTGCATTGGGTCCT	ref NM_001978	entg DMTN
614	A_33_P3449397 56339	TCCATAGCCATGGCTCTGTAAAGCTAAACCTGAAGAGTGATATTTGTACAATAGCTTTCTT	ref NM_019852	entg METTL3
615	A_33_P3318292 6421	CATTTCCCATTTTCTGTTTTTAAAGACCAACAAATCTCAAGCCCTATAAATGGCTTGT	ref NM_005066	entg SFPO
616	A_23_P26895 51174	ATCGAAGAAGAGGACTTTTTAGACAGTTTCACGTCATTAGAGCAGGTTGTGCCAGTTAC	ref NM_016261	entg TUBD1
460	A_23_P2573 84216	ATGAGAGCAGCACATCCCACCATTTACAAATATTCGTATATCTTTCTGCAAAATATGGCTCT	ref NM_032256	entg TMEM117
617	A_23_P321935,A_23_P57474 23762	CAAGGCCCATACGTGCTGTCCGGCTCGTGGGATGAACAAATGGAGTGCTCCAAGGTCAT	ref NM_030758	entg OSBP2
618	A_33_P3360728 645	ACATGAGGAGCAAAGGAAGGGGCAATAAATGTTGAGCCAAGAGCTTCAAATTTACTCTAG	ref NM_000713	entg BLVRB

619	A_23_P161399,A_33_P3263902,A_33_...	AGTTAAGTTCAGCACTGTCTCATTTTAATGTAAAGATTGCTTCCATTTTCTACAGGC	ref NM_130439	entg MXI1
620	A_32_P385587 212	CAGGCCTACTCCTGTCTTCTGCTTTGTTGTGTGCCTCTAGCTGAATTGAGCCTAAAAATA	ref NM_000032	entg ALAS2
621	A_24_P926507,A_23_P55616,A_33_P3...	GAATAAACACAGAAATAGGGAAGTAAACCTACAAATAATTTAGGGAGAAGCTCACTTCTTCC	ref NM_001146037	entg SLC14A1
Anexo 13				
	AgilentProbelID	Sequence	TargetID	GeneSymbol
622	A_33_P3227472 113675	CTCCTGGACTGCTTCTTTGGCTCTCCGACAACCTCCGGCCAATAAACACATTCTGAAATTG	ref NM_138432	entg SDSL
623	A_24_P416370 3214	CAGCAGAAGCCTCTCTCTAGACTGAAAAATGAATGTGAAACTAGGAAATAAAATGTGCC	ref NM_024015	entg HOXB4
624	A_24_P260639 3007	CAGCCAAAGAACGCCCAAGAGGTGGCTGGCGCGCTACCCCGAAGAAAAAGCATCAAAAAAGA	ref NM_005320	entg HIST1H1
625	A_23_P301896,A_23_P201079,A_33_P...	TTGCATACCAGGTTTTACACTTGCACTCTCTAATAGAGATTAAAAACAACAAATTGCGCTC	ref NM_015866	entg PRDM2
626	A_23_P167599 54463	ACTGAAGACTTTGAACACTTGCTTTTGTGATTGCTTATGTCAATTAGTGCCTCATGACTG	ref NM_001034850	entg FAM134
627	A_23_P501538 3200	TAATTCTTTAAACGGTAACGATGCAATAAACCAGAGAAGATCCAGCTTTTGAACACAG	ref NM_153631	entg HOXA3
64	A_23_P104109 26750	CATTGGTGTGCAGATGAGTTGTAAAGCCCAACTGAAAGAGTTCCTTCAAGAAGTTCCTC	ref NM_001287219	entg RPS6KC1
628	A_23_P50946,A_33_P3233906 10267	ACCTCTGGAAGGGTCCCAGCCTAGACTGCTTACCCCATAGCCACATTGTGGATGAGTG	ref NM_005855	entg RAMP1

629	A_23_P343594 55230	TCCCACTTAATCCAACCCAGATTTCATTCAACTTAAAGGATTTAATTGGCATTGTGAG	ref NM_018218	entg USP40
630	A_33_P3377529 3201	TTCTTACTTGCAATTATTTAAGACACTGTTACAGAGATACTGTTGTCCCTTCTGGGGCA	ref NM_002141	entg HOXA4
631	A_33_P3312288	TTGACTCACCAACAGAGGGGAACACAATTTGGTCCATGGTAAAAATATTCCTTGGTATTAAT	gb TCONS_I2_00025732	
632	A_23_P43071 51001	CCAAGGCTGCTAACTGGAAGTCTGGAACCCGTGAAGGAAAAATATGAAGGTTTATCGTCTT	ref NM_015942	entg MTERFD
633	A_23_P70968 3204	GAAAAGCGTCTTTAAGAGACTCACTGCTGTTTTACTTACAAAAATGGGAAAAATAAAAGAAA	ref NM_006896	entg HOXA7
634	A_33_P3303414 4121	GGACCATCTTTATGACCTGCTTCTGTTTTCTCAATATCATACATTGGTGTATGTCAAAGA	ref NM_005907	entg MAN1A1
635	A_33_P3424864	GGAACTGCCAGAGCTTCTCTACGGCTTGAAAGCCCAAGCTAATCAGTAACCCGTGAGA	tc THC2551759	
636	A_33_P3225046,A_23_P23829 947	TC TTGGGCATCACTGGCTATTTCTTGATGAATCGCCGCAGCTGGAGCCCCACAGGAGAAA	ref NM_001025109	entg CD34
637	A_23_P309361 113802	CAGACTGCAGTGAGCCCTGAGAAAGATATGAGGGTTTAAAAACGGGTGCTTTCCTTTGATT	ref NM_144584	entg HENMT1
638	A_24_P330303 122786	TTGCAGATATTGGAATGTATGGAAGTATCTCAGTCTCTGCATAAGAGGATTAAAGTATGA	ref NM_001042481	entg FRMD6
639	A_23_P153897 2788	CCCTGCCTCGGAGAACCCCTTTAAGGACAAAGAACCTTGTTATTTTATAACTGTGTTCC	ref NM_052847	entg GNG7
640	A_33_P3236881 100532736	GTCACCATTTGGACAGTCTCCCTGATGGACCCTCAGTCTTCTCATGAATAAAATTCCTTCAA	ref NM_001204088	entg MINOS1 NBL1
328	A_19_P00804546	GACATTGAATGACTGTATGCTGCTTTTGATTTCCGTTAATATGGGCAACTGTCCAATTAA	ens ENST00000440570	
641	A_33_P3822503 1489	CACTGCCTCCCAGCAGATCTGTGGAGACAAAAACAAGCAACACCTTAAAAAGAGTTTTATTT	ref NM_001330	entg CTF1
350	A_24_P810697,A_33_P3239587,A_24_...	CTGCACACCTTAGATATAAAGAACATTTTAAAGCAGAGGTTACATTTTCACTCCAGTCTCC	ref NM_001008529	entg MXRA7

642	A_33_P3382924 6678	CCACATACCTAGATCTCCAGATGTCAATTTCCCTCTCTTATTTTAAGTTATGTTAAGATT	ref NM_003118	entg SPARC
486	A_33_P3399935,A_33_P3347452,A_33...	TGCAAGTGCTCAAAACACCCGTGGTGTCAACAGAGAGTACCTGTCCCAAAACCAAGCTCA	ref NM_021135	entg RPS6KA2
374	A_24_P56240 144402	TACAACTATGIGACTTAGTGACAAACACATTTIGGAAATAACCTACTCTATATACIGAC	ref NM_153634	entg CPNE8
643	A_23_P141549,A_32_P20367 6201	GTCAAACCTAGATGGCAGCCGGCTCATAAAGGTTCAATTTGGACAAAGCACAGCAGAACAAAT	ref NM_001011	entg RPS7
644	A_23_P422794 286053	CATTGTTGCGATGATTGAGTCCAGGCAAAAGCGGAAGAAAAAGGCCTATTGCCCCTCAAAT	ref NM_173685	entg NSMCE2
645	A_23_P416178,A_33_P3287825 64753	AGAAGAGGCCCTTCTGTGTCAAAGAACCCGGGGGAAGAATGCTAATAAGAACATGAACA	ref NM_022742	entg CCDC136
646	A_33_P3342628 57801	CCCGTTCTAGGGCCGTGGCCTTGCCGAGACTGTAGCAGAGAAAAACGTATTATTATTCC	ref NM_021170	entg HES4
647	A_32_P131143 100130717	AAGGACACCAACGGCAGCATCAGCAAGTCCGTGTGTCTCCCAATAAGTGGTGTCTCC	ref NR_024482	entg CECR5-A
648	A_33_P3299958	GTGTGTGAAGACTACTATGATGAGCTGTGCACAGCTCAATAAAATCTCAGTCAATTAATTT	ref CK824920	n/a
649	A_23_P255104 10184	CCAAAAGAGTTAAAGGCACGACTGGGATTTCTTCTGAGACTGTGGTGAAACTCCTTCCAA	ref NM_005779	entg LHFPL2
650	A_24_P266285,A_23_P19852 23288	CCACAGGCCCTTGGCACCTCTACCTGGGGATGACGTCAACTCCGATGATTCGACGATAAT	ref NM_152558	entg IQCE
651	A_19_P00317101	ATGTGCCGTGGCTAGGTTTTTCTCTCATATTTGTAGGCTTTCATGTGAAGCTCCCTTA	ref BC014370	n/a
652	A_32_P210642 51162	AAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCC	ref NM_016215	entg EGFL7
653	A_33_P3402329 84848	AAACAGTGGGCTGTACTCCAGTGTCTGGGACATTGAATGACTGTATGCTGCTTTTGATTTC	ref NR_024607	entg MIR503H
654	A_33_P3318530 441204	CAAAATCCCACCAACCAAGACAGACTAATGAATTGTGGTATATTATTGTAAGTCTCT	ref NR_015364	entg LOC4412

655	A_33_P3309859	ATACCAATAGCATGAACTGCTTTCTTCTGAACTGAAGGCAAGCCCATATGGTTGCCACT	ref CB305856	n/a
656	A_23_P316511 3213	ACATTTTAAAAACAGACAAGATGGCTAGGCCATCACCAACCAACGGACTTACCTTACAT	ref NM_002146	entg HOXB3
657	A_23_P107283,A_33_P3271273 3212	ATTAAACTCTAGGGGACTTTCTTAAAAATAACTAGAGGGACCTATTTTCTCTTTTTTA	ref NM_002145	entg HOXB2
658	A_23_P93772 3202	ACCCGCAGAAGGAGGATTGAAATAGCACATGCTCTTTGCCTCTCCGAGAGACAAATTAAA	ref NM_019102	entg HOXA5
500	A_33_P3296479,A_33_P3508822 351	AAGAAAAGTGACAATGTGGATTCTGCTGATGCGGAGGAGGATGACTCGGATGCTGGTGGG	ref NM_001204303	entg APP
659	A_33_P3415698 126259	CATTTCTGTAATGATGGAICTCGCTCCCACTTTCCCCAAGAACCCTAAATAAAGGCTTG	ref NM_144615	entg TMIGD2
660	A_23_P16058 162979	TCCTGTGTGCAAGAAGACCCTCAGCTCCTTCAGCAACCTCAAAGTGACATGCGCTCACA	ref NM_145288	entg ZNF296
661	A_33_P3368495	GCTCGTGTGACTTTGTGACCTTTTATGTTTTCTATGGGCAATAAAGGCCAAGAGAGCTC	gb AK057067	
662	A_33_P3404641 150381	CTGCTACCATCTTAATAACTTTTCTGGCAATACACGACGATGATTGTTTATGTTAATCTC	ref NR_027034	entg PRR34-A
663	A_33_P3780123 440952	CGTTTGTGGGAGGAATCTGGAAACTGTATTATAATAGACACCCCTTTTATCTGATATTAT	gb AK057627	entg EIF1B-AS
664	A_23_P24616 54414	ACAGATCTCTTTGTATTCTCTCAAGCCCCAACCATTCTGTTCTTCAATCTAAATAGT	ref NM_001199922	entg SIAE
665	A_33_P3332860,A_24_P936122 8675	GAGAGATTCGCCAGATTGTACAGTCCATTTCTGACCTGAATGAAATATTCAGGGACTTAG	ref NM_001001433	entg STX16
666	A_23_P66682 3216	ATTAATTTTCTATGTGTGTGTGTAGTCTTGCTTAGCTCTGGACGTGAAATACTTCG	ref NM_018952	entg HOXB6
461	A_32_P66222,A_33_P3401902,A_32_P...	CTGTGACAAAGAAAAATAGAACACCTTTTGATACAGGCTGTCCATTGCCAGGAAGAGGCTTG	ref NM_001012421	entg ANKRD2
667	A_33_P3377130,A_23_P134125 4217	AATCATAACATCAAGCCGCACTGGATGTTTGCTTAGACAGTATCATTCGGAAGGCGGTA	ref NM_005923	entg MAP3K5

668	A_23_P500998,A_33_P3416231 3205	AAACAGTTGCATAGAGTATAGCTCTGTAGTGGAAATATGCTTCTGTATAACTAGGCTGTT	ref NM_152739	entg HOXA9
669	A_33_P3348887,A_23_P71821 5090	GCCACACTTTCCCTGAGCTACATGCCTTGATAAGTGCAATTCAGAGCAATAGGAGGAAAA	ref NM_006195	entg PBX3
670	A_33_P3311663	ACGAATAAAACCCAAAGCGTTCCAGCAGCCATTTTGAAITTAAGTTTCCACCCGACAAAGC	ref XR_245014	entg MEIS1-A
671	A_24_P130363 753	AAAGATTTCACCTGTCACGTATCTGCCTCTTTACCTGAGCAATGGTGAGTTCTTAGA	ref NM_001003674	entg LDLRAD4
672	A_23_P40989 8975	TGAGATGGAGAAATAATGCCAATGCAAACATTATTTCTGAGGCCAAGCCGAAAGGACCTAG	ref NM_003940	entg USP13
673	A_24_P319736,A_33_P3342942 4211	AGGAGGCATGGAAACCAAAAGGCCGTGTTTAGAAGCCTAATTGTCACATCAAGCATCA	ref NM_002398	entg MEIS1
674	A_33_P3465247,A_33_P3382217 11127	GGGGAACAGTTCATACTATAGAGAGTTACAGTTTAGATGTATGTGTAAATCGATTAGCTA	ref NM_007054	entg KIF3A
Anexo 14				
	AgilentProbelID	Sequence	TargetID	GeneSymbol
675	A_33_P3259973,A_32_P204795 10012...	TGTGGTTTCAACCCTACTTCTGCATCTTAAAGACACTGTATGGTTTCAGCAGTAGTGCCC	ref NR_036522	entg ZNF667-AS1
676	A_23_P83835 84197	TGGTCCGATTCCATTGTTTGATATTACAAAGCATGCAAGAGCCAGACTCCCTCAGAAA	ref NM_032237	entg POMK
677	A_23_P31399 5445	CATTGACCCAGAAATGTA TGGA TGTA TGTAATTTTATTCAGTAAGGAACGGCCCTT	ref NM_000305	entg PON2
626	A_23_P167599 54463	ACTGAAGACTTTGAACACTTGCTTTTGTGATTGCTTATGTCATTAGTGCCTCATGACTG	ref NM_001034850	entg FAM134B

678	A_24_P142743 1265	TGTGTTTCTATGCCCGCAAGTTTCAGGAAGTATTCACAAAAGAAAAATACATTTTTTCC	ref NM_004368	entg CNN2
679	A_23_P346006 9236	TATGGTCGCACTAATGGAAGACAAAATGGCAAATCTTGAAATAGAAATTGGGGCAATTACCT	ref NM_004748	entg CCPG1
680	A_19_P00806287	TTTTCAAATAATGTATCCCTTGCTCTTCATCTTTGGTGAGTATGTGTCTATTTCTCTCA	ref MIR100HG	entg MIR100HG
258	A_33_P3375002 144481	ATGTTCTAGATGCACAGATTTGGGGGCTTGATTGACAACCTGACACCTCACTCTAAATCC	ref NR_038263	entg SOCS2-AS1
681	A_33_P3372099,A_23_P302672 115265	CCTGTTATGCTTACAAAATGGTGATGGCTTATGGAAGGCTGTTAAATTAATATTCCTGTT	ref NM_145244	entg DDIT4L
682	A_23_P161076,A_33_P3278013,A_33_...	GAGTTTCTTATGTGCCCTGGTGGACACTTGGCCACCACCTCTGTGAGTAAAAAGTGAAATAA	ref NM_001767	entg CD2
683	A_23_P146946 1474	TCAGTCTCTAAAGCACAACTGTGTGCAGATGTGATAAGTCCCCGAGGGCGAAGGCCATTG	ref NM_001323	entg CST6
684	A_33_P3294533,A_23_P420281 5579	AATTCTAGTCTTCCAGGATTCACGGTGCACATGCTGGCATTCAACATGTGGAAAGCTTGT	ref NM_002738	entg PRKCB
685	A_24_P392060,A_33_P3282384 375484	TATATTGCCTGTTAATTGACTGTAAATGAATAGGGGGTAGAAAACAAAAGGATCAAGTGTG	ref NM_198567	entg SIMC1
686	A_33_P3379506,A_23_P311020 129531	GGAGTCACGGAGTGCTGTTGGAAAGTTCAATACTCTTCTTCAATACATGACCGAGAAAATTA	ref NM_138798	entg MITD1
687	A_33_P3327265 9840	CAGACCAGAACTGCGTCGGTCTTTAAGCCAGCAGCCACAGGACACTTTTGACTTGGAGGA	ref NM_001136030	entg TESPA1
688	A_24_P322741 3588	CTTCTGTTTTTCTCCTTCCATTGTCTGGATGAGAAATGAITGTTTTTGACAAAGCTAAGTGTC	ref NM_000628	entg IL10RB
154	A_23_P128215 8835	CCAAGTTGTCCTTGAATTGTCTAACCATGGACATAAACAGTTGTCTCCCTTCTACTGTGT	ref NM_001270470	entg SOCS2
689	A_23_P211850 57406	TGGGCCCTCTTTTCTATTCAATGTGCTACTAAGAACCCTTGGATGTAACATACTAGTTAG	ref NM_020676	entg ABHD6
690	A_24_P185709,A_23_P154806,A_33_P...	TTTCCATCTGAGGGTACAGGAAGTACCAGGACCTGTTTCAGTTTTTGAATCCTGCAAGCA	ref NM_001258329	entg EPB41L1

691	A_33_P3265935	GATTGTTCTGAAAAGATAATGCCAACTCGGAACCTAGGAAACCATCCAGTGGGTTTCTGCA	agp A_33_P3265935	entg LOC38815
692	A_24_P50368 414899	TCAGAGACCTTCTCTATTTAACCGAGGATACAAAGTTACATTGTTATGCAATTCCTCTGCTGA	ref NM_001001786	entg BLID
693	A_23_P380614,A_33_P3375314 10079	IGTGAIGACACACATAATGAICTTTTCGTTCTGAGCGACTCTACTTTCATTGTTTGCCA	ref NM_006045	entg AIP9A
694	A_24_P265832 56670	TTCTCACTTTTATCAGCATAGATCGATACTTGATAATTAAGTATCCTTTCCGAGAACACC	ref NM_033050	entg SUCNR1
695	A_19_P00315493	ATATATTCTTCAGTGTGATTAGGTGAGTCAGGAATTTTCTCTGGAGACTGCCTAAAT	ref NR_027046	entg LOC14547
696	A_19_P00805523	TCGAGCACTTGTTTTGTAGTACCTCCTGTGGCCATCTCCACAGTGTATATTGAAAG	ref NR_039989	entg MIR4458H
697	A_32_P40463 119369	GGGAAAAGTTCATCTCTATTTTGGTCCACAAGGATCAAGTGCTTATGAACCAAGACCAAA	ref NR_002779	entg NUDT9P1
698	A_32_P123629,A_23_P308305,A_23_P...	TGCCGTGACTTATCCAACCTGTGAACTGATTGTGATCTGCTTGTTGTTGTTGGTGT	ref NM_001292030	entg TTC39C
699	A_23_P205519 63874	ATGGTTCCAGCTCAATCCACCCCTGACCCATCTGTGAGCTTTTCCAGGGAGCCGTTT	ref NM_022060	entg ABHD4
258	A_19_P00807670	CAAAGAGAAGCAGGCTCTCCCCTTCTGAAATGATGAGTGATAATGACCATACAGGTCAACT	ref NR_038263	entg SOCS2-AS1
700	A_33_P3236703 441459	CATAAGAATTCTACTTCAAACCCACAGACTTCAAATAAAGTCAAGAACTCCTTGACTGA	ref NM_001244752	entg ANKRD18B
701	A_23_P252062,A_33_P3350726 5468	CCAAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCTGCGAAAGCCTTTTGGTGACTTTAT	ref NM_138711	entg PPARG
702	A_19_P00805452	TGAAAACACAATTACAGTACAGTGTCCGCAATGCTGGTCTTTGATTCAACGCATAAATTG	gb TCONS_j2_00020391	n/a
703	A_23_P420431 150165	CAGAGGTGGGCCATAGAATCCTACACTACAGCTTTCAGTTTTTTAGAAAAATGTGATAAT	ref NM_175878	entg XKR3
704	A_19_P00801007	GTTTCCTTGTTCTTTTTTCTCCACGAGATACTGGTTTACTTTAGTTAAATGTAAAT	tc THC2668456	

705	A_23_P90895,A_33_P3345663,A_24_P...	ACTTTCATACCTACACAGAAACAGAGGATTCAAATTTTCTGTGATTCTGCCATTGACA	ref NM_001193475	entg PPP1R21
706	A_23_P101374,A_33_P3348782 29785	AGTCACCCCTTTTAAAGCACCCCTGATTCTACCAAATGCAAACACATCTGGGTCTGCGATT	ref NM_030622	entg CYP2S1
707	A_24_P4054 7205	GAGACTGTGAGAAATTGTGCTCTGGATCGAAGTTTTCACATTGGCTGTACAAAGTICGAG	ref NM_0033302	entg TRIP6
258	A_19_P00802794	ACACACAGCACCCCTCAAGACTCCCTGTGATCCTGGGATGCACTCAACGAAGAGTGTGTGG	ref NR_038263	entg SOCS2-AS1
708	A_19_P00804277	TAGTGATGAAATGAAGTCCACTAACTTCTCTCTGCTTACTTCCACCCTCAATAACATATT	gb AI300542	n/a
709	A_23_P71503 78998	AGTGACTGTCAGCAAGCATGTGTGACTGAAATGGTATCCAGTTCTTACGTATTGTTTGG	ref NR_026785	entg RHPN1-AS
710	A_33_P3268868	GCTGAATGAGTTAGTGAGAACTGGGTCTTCATATCTTTTTTAAAAATTGGCTGCTTTT	tc THC2674845	n/a
711	A_33_P3279109 7627	AGATTGTGGTAGATACTTCCCTGGCCTTAGAGAAAGAGAGTTGCTTTTGCCCTCTTTGGA	ens ENST00000575234	entg ZNF75A
712	A_19_P00812782	GGCAGTGAATGAAAAATGGTTCCATTGCTTAAAGCTTCCTAATTCATAGGCATATTCTT	tc THC2652826	n/a
713	A_24_P120115,A_23_P209394,A_23_P...	GAAATTCTTGCACTCAGTATGCATGGTATATCCAGATTCTTGGCCAAATTTGCCTGTAT	ref NM_001127183	entg CFLAR
714	A_23_P401700,A_24_P232365 54518	GTGATGGGAAACTTCTCACTGATGTGCTCAAGTACAGGCATAACCAATTAACCCAGTAGAG	ref NM_019043	entg APBB1IP
715	A_24_P125283 10014	CCCACTCCTTGCTTGTCTCCCTGGATATGGATTTCAGTTAAGTATTTTGTAAACCCGTTA	ref NM_001015053	entg HDAC5
716	A_23_P51410,A_32_P103291 64754	TCAGGCAACTCGTAATGACATTTTCAACATTTTCATGAGAGAGAAATACAGGATGCCTCTC	ref NM_001167740	entg SMYD3
717	A_33_P3244249,A_32_P305888 79628	CTTAATTGTGCTGACAAAAATGATGTAAACAGCACAAATGGAGCATCTTTGTTTGTGATTG	ens ENST00000513604	entg SH3TC2

718	A_33_P3293362,A_33_P3247205 64757	AGTTAAAGCAACCAACTTCAGGGCCCAATATTGTAAATTCAGGATGCGATGCTCTATGCAGA	ref NM_022746	entg MARC1
719	A_23_P421116 9374	TTGGGGAATATCTGTGGCCTATGAGGCCCATCTCAGGTTTGGGGATCCCCCAGTCCCTAT	ref NM_005155	entg PPT2
720	A_23_P34827 57657	GAGAAGGACCGGTTTACCTTTAGAGTTTGTGTTTCTCTGAGTTTGCTGTT	ref NM_020897	entg HCN3
721	A_23_P39799,A_24_P88763 84695	GAGTGACTTTACCAACAATGCAATGAAATGTAAGTGCAAATATGATGGACATAGAAATCTG	ref NM_032603	entg LOXL3
722	A_24_P943566,A_32_P52018,A_33_P3...	TGGCTGACTAGTTTAATAGGTTTATCCCACTGAAATTTGCATTTGTACAAAATGTCACCTG	ens ENST00000379350	entg PHACTR1
723	A_33_P3527721 284219	TGTTTGCAATTACGCTAGGTCATTCCATTGTCCTTAAAAAATGAGAACCTTTCTGATTG	gb AK094436	entg LOC284219
724	A_33_P3305093 100125288	TGTGGCAGATGTGGAGTGTCCTGGACCCCACTTCAGGAAGGTTAAACCCAGCTTCACCCT	ref NM_001103167	entg ZGLP1
725	A_19_P00805982	GTGTTTGAACCTACTCTAACCAACTGTCAAAAAGCTGTGTTAAGTGATTCTCTGACAAAG	ens ENST00000434459	entg AKR1C1
726	A_23_P7099 175	TGCCAAAAAGTGATTTCAAGAATCCAGAAGCATTTTCCAGAAATCTTTGGGGCTGTTATA	ref NM_000027	entg AGA
727	A_23_P121480,A_33_P3370575 4345	CTGCTTACTGCTTTGCTAATAGCTGGCCTTGCTAGAATCCTTGGTTTCACTGCTGTTCTT	ref NM_001004196	entg CD200
728	A_19_P00807628	CAGTGAGACTTTTTCCGAAGAATCCCTTTTAAAAATGACCTCAAGCTGACCTTCCTGATGC	ref NR_033896	entg FLJ46906
729	A_23_P143885 50650	TTAATTAGAATCAGCTAGCCAGATTAGTAACCTCTTTGTCCAGCCTTGATTTACAGTGCA	ref NM_001128616	entg ARHGEF3
Anexo 15				
	AgilentProbelD	Sequence	TargetID	GeneSymbol
730	A_23_P141863,A_24_P324640 27300	AGCTATCAGTGCAGCGTGTATTAAAGCAGCGGTTGTGACTCATTTGAACATCAGAGGACATA	ref NM_014480	entg ZNF544

529	A_32_P108156 114614	TTAACAGTGTATGATGCCTGTTACTAGCATTACATGGAAACAATTGCTGCCGTGGGAGG	ref NR_001458	entg MIR155HG
731	A_24_P218587 9440	AAAGTGCCTAAAGTGTGCCCATTAATATGAGGATAGATTAGGCTCATAGCCCTTTTGGT	ref NM_004268	entg MED17
732	A_24_P272313,A_33_P3326578 343990	ATCCTGGAIGGAACITGCCAGAAAAGAAICTCAAAGCTTGGAGTGACATGCCCCAGATTAT	ref NM_207362	entg KIAA1211L
733	A_24_P860797 400961	AGTTAAATGGACTGTCAGTCAGTGAAGGTCATGATTCTGAAGATATTTTGAGCAAAAGTA	ref NM_020459	entg PAIP28
734	A_33_P3360665,A_23_P792221 90	ATAGTGTCGAAGAAGGAAGATTTGACGTTGTTCATTGTCCAGCTGGGACCTAATGCTGG	ref NM_001105	entg ACVR1
258	A_33_P3375002 144481	ATGTTCTAGATGCACAGATTTGGGGGCTTGATTGACAAACCTGACACCTCACTCTAAATCC	ref NR_038263	entg SOCS2-AS1
681	A_33_P3372099,A_23_P302672 115265	CCTGTTATGCTTACAAAATGGTGATGGCTTATGGAAGGCTGTTAAATTAATATTCCTGTT	ref NM_145244	entg DDIT4L
735	A_24_P113686 54680	AACTTACCCTTGTGAGACAAGTTTTCTACTTGAGAAACTCCTAGTACAATGTCTTATACT	ref NM_017953	entg ZNHIT6
736	A_23_P32577,A_33_P3316786 1602	AATATTAAATGCTAGTTGTTCTATATTATAACCACATTTGGGCTCTATGCAAGCCCTTGG	ref NM_080759	entg DACH1
737	A_33_P3336617,A_33_P3336622 224	AAACGGTTCAACAAAGAAAAAACTCGGTCTCCTGTTGCTCACTTTCCTGGGTATTGTAGCC	ref NM_000382	entg ALDH3A2
738	A_23_P21548 79658	GATCAGGAGGGGAATGTCAGGATTCGCAAAATGGACTTTTCATTTGTCCAGTATTGGGAC	ref NM_024605	entg ARHGAP10
739	A_24_P942354 5306	GGTTGGTTCCTAGTGCTACTTGTTTACAAAATACACTTTGTAGAAATTGATTAGATTACC	ref NM_006224	entg PITPNA
740	A_33_P3414912,A_33_P3414907,A_33...	ACCTGGGAAAAAAGACAAACCAGATGTTGGAGGCTTTTGAACAAAAAGGACTTCTCTTTAG	ref NM_001200056	entg NPL
741	A_33_P3252524,A_24_P62505 23127	CTCAATGTTTGGCTTTTATTATGGCCACTCGAGTCAGGATGCTCTATTTATAAAGATA	ref NM_015101	entg COLGALT2

742	A_23_P161909 932	TAATATCCAGTCATTAAAGGAGTTGTCACTCTTCATCAGAGTCACCGGACCTATGCAATTA	ref NM_006138	entg MS4A3
743	A_24_P217365 23243	GTGAAATGGTGAATAGCAAATGACCTCCITTAACAAAGACACTCATCTCAAAACAATGCC	ref NM_001195098	entg ANKRD28
689	A_23_P211850 57406	TGGGCCTCTTTTCTATTTCAAATGTGCTACTAAGAAACCCTTGGATGTAACATACTAGTTAG	ref NM_020676	entg ABHD6
744	A_33_P3234197 80263	CCCTGCCAAGGCTTCACCTGTATATATTTTGTGTCTTCTGAAACTCTTGATTTCITA	ref NM_025188	entg TRIM45
745	A_23_P94319 9920	ATAGTGCAGAGCCTCGTATGTTTGTGCTCATGCCGAGATGAAATAAATCACGCAGAAA	ref NM_014867	entg KBTBD11
746	A_23_P406448,A_24_P126139 51209	AAGATAGGGAGCCCTTTAAAAATGTGCCCCAAATTGATCAGTCAGTAGTGTAAGAAATAAC	ref NM_016370	entg RAB9B
209	A_23_P339588 117289	TGCTTTTGTATAGTTCCTCTCTCAGATACATGTAICTAATGAAACTGAATAAATCCG	ref NM_138810	entg TAGAP
747	A_24_P95029 8887	TGCTTTGATTCAGCTTTGATGTTTCAAGAAGTGTCCCCCTCTGTGAGTTAATGTTTCCT	ref NM_006024	entg TAX1BP1
748	A_33_P3337267,A_33_P3337272 441478	AGGAGCTGCAGTCGCTGCTGCAGAACAATGACCAACTGGGAGTTCAACGTGAACCTCGTTCG	ref NM_001004354	entg NRARP
749	A_23_P208182 89790	GGCGGATTATGCAGAAAGTCAAGTTCCAATGAGGGTCTCTTAGGGCTTTAGGACTGGGACTT	ref NM_033130	entg SIGLEC10
750	A_19_P00324182	ATGGCAGTAAGTTAAGGGAAATATGGGGTGCTGGACCTGTGATACACATGACTGCTTTAGT	agp A_19_P00324182	ENTPD-AS-1
751	A_23_P319423 8645	CTGTGAAAATGTTTTAATGAACCAATGTTGTTGCTGGTGTCTGGCATCGCGCACACTGTA	ref NM_003740	entg KCNK5
752	A_23_P129903 147166	ACATTCTCCAGCTGCTCTCTTTTGCTCCATAIGGTGCTGTTCTCTATGTGTTTGCAGTAA	ref NM_001037330	entg TRIM16L
697	A_32_P40463 119369	GGGAAAAAGTTCAATCTCTATTTTGGTCCACAAGGATCAAGTGCTTATGAACCAGACCAAA	ref NR_002779	entg NUDT9P1
440	A_19_P00801759	AGGACATTAGATTTGTCAGTGAGACCATCGTCAGTAGCCTTTTGAGGAACAGAGTCAGTTG	gb AK094279	

753	A_33_P3269109,A_23_P69573,A_33_P_...	GAGATGGGACAACTCTGTGAAAAAATCTTCAAGGGTAAGGAAAAACATAATACTATCTTGA	ens ENST00000512983	entg GUCY1A3
754	A_23_P170467 9960	TTAGTTTTGTCAATGGTAGTGACTTACTGAACATGGGCACCAACTAATTTTGTGTTGTT	ref NM_006537	entg USP3
755	A_23_P259141,A_33_P3357609 81030	ATGTTTTGAGTCCCAACAAAATTCATAATCAAAACAATAATCCCAACTGGGTGCAGTGGCTCA	ref NM_030776	entg ZBP1
756	A_24_P186379 282969	AGCCCTGGCAAAGATAGAGAGGTTTGAGTTTTATGAACGGGCTAAGAAAGGCTTTTGTCTGT	ref NM_001098483	entg FUOM
701	A_23_P252062,A_33_P3350726 5468	CCAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCCTGCGAAAGCCTTTTGGTGACTTTAT	ref NM_138711	entg PPARG
757	A_33_P3367692,A_23_P114740,A_33_...	GGCTACAAGATTGAAGGAGATGAAGAAATGCATTGTCAGACGATGTTTTTGGAGTAAA	ref NM_001014975	entg CFH
386	A_23_P161424 84898	GAAGGCTTTATTGTATCAGAGCAGTGCTAAAAATTTCTAGGACAGAACAACACCAGTACTG	ref NM_032812	entg PLXDC2
758	A_19_P00331901	CCTGCAGCCTCCAGAAGTGTTATCTTAGACCCCATCATTTGCAACAAAGAAAATCTCTCAGT	tc THC2528616	
759	A_19_P00803587	CCAAATGGCCCCCTTGAGTATTTTTATTGACTTGTACACACATTTTGTCTTTGATGTCT	ens ENST00000324344	entg DCUN1D3
760	A_33_P3410459 950	GTTCACTTCATGCGGTTCTTGACATGTTTATTCTACCCCTTAATGCAATGAAATGTTTCA	ref NM_001204255	entg SCARB2
706	A_23_P101374,A_33_P3348782 29785	AGTCACCCCTTTTAAAGCACCCCTGATTCTACCAAATGCAAAACACATCTGGGTCTGCGATT	ref NM_030622	entg CYP2S1
448	A_23_P321511,A_24_P555473 115123	TCGGACCAATCAGAGGGTGATTCTCCTCATTCCAAAGTCTGTCAATGTACCTTCTAACCA	ref NM_178450	entg MARCH3
761	A_32_P104000 123879	GGTTTCAGTTAGAGGGTCCTCTGTATTTTTCCATTTAAAAAGTATGTCCTCATAAAAAC	ref NM_173475	entg DCUN1D3
762	A_33_P3414851,A_23_P201002 55182	TCCACCAGCAATGGTGAAAGCAGCAAGCAGGAGGCCATGCAGAAGACCTGCAAGAAACAGC	ref NM_018150	entg RNF220

454	A_23_P102391 30061	CTCATGTTATCATCATTAGTGATCTGTGTGTAGAACATGAGGGTGTAAGCCTTCAGCCT	ref NM_014585	entg SLC40A1
763	A_23_P8981 6770	TCATTAGTAGACATGTTCCCTATTGCTTTCATAGGCACCAGTCAGAAATAAGAATCATA	ref NM_000349	entg STAR
764	A_23_P94921,A_33_P3386835 6575	TTTTTTGATAGCGGGAGGAGGAAGTACGACTAAATGTTGGAGCCTGAAAACATATGGAAATG	ref NM_001257180	entg SLC20A2
765	A_32_P86739 399726	CTGACTTTTCCAGCTAAGTTTCCCTCAATAAAAAAGCCCGCTTCTGGGAAAGACAGAA	ref NM_001010911	entg CASC10
766	A_32_P46981 440498	CATTTTCAAGCTCTGACGGCAACATTAAACCTCAGAATGGAAGAAATGGGAAATCGCATTT	ref NM_001136180	entg HSBP1L1
767	A_23_P160787 5195	GTTCAITTTGTGTGATCATGTATAGACCTCAGAACGGAAGATAGGACTGTATATAATTGTA	ref NM_004565	entg PEX14
768	A_23_P211007,A_33_P3251430 8204	TGGACATGACGCTGTGGTTAAGCTTTGTGAAAGAAATGTGCTTTGATTCGAAGGGTCTT	ref NM_003489	entg NRIP1
769	A_24_P722216 55526	CTCTAGATTATATACCTTTTCTTACCATATACCTCAGTGTATCCTTCCTGTGTCAAGC	ref NM_018706	entg DHTKD1
770	A_33_P3343290,A_23_P306933 160760	TTGAAGATTGGCCTTCATTTTCTCGATGTTCTTCCATGATGGGATGGAGGTGTTCAAGTG	ref NM_139283	entg PPTC7
771	A_33_P3281567,A_23_P351467 8418	ACACGTGGTGAAGAAATGGTCTACTCTGGGATGAGTTGTATATAGGATTCCAAACACGGCT	ref NR_002174	entg CMAHP
132	A_33_P3407344,A_24_P865 387119	CAAGCTGTGAAGAGTACCCCTTCACATGAAGGAGTAGGATTCCTTTTAAATCCTATAGCTTT	ref NM_001042475	entg CEP85L
772	A_24_P65060 84206	GTGGGTTCCATGATACTTATTATAGAACACACAGTGGATCCTTTTTGAATGTTCTGTGGAAG	ref NM_032246	entg MEX3B
249	A_24_P388570,A_33_P3314146 84864	GTGCATGAGTTTATGCTGAAGCCGGGTGATTGTTGTACTTTCCAGAGGAACCATTCAT	ref NM_032778	entg MINA
773	A_33_P3342410 29904	GTGGCCTGCGTTACAGATTATTTTGGCATATGTACTAAGTCCATTTTCTCTTACAAA	ref NM_013302	entg EEF2K

774

A_23_P113382,A_33_P3252083 23426	TAACTAAGACGTATGCTATTCCTATGCAACAAATTATCAAAACAGGATATGTCTTGAC	ref NM_021150	entg GRIP1
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677

A_23_P31399 5445	CATTGACCCAGAAATGTATGGCATGTGTAGTTAATTTTATCCAGTAAGGAACGGCCCTT	ref NM_000305	entg PON2
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	AgilentProbelD	Sequence
1	A_33_P3323188 728743	TATTTCTACAGGTTGCTGACTCTCTGCGGAGCTGACTGAGTGAATAAATGTTCTCTCAA
60	A_23_P47004 55760	TCTAAACATAAGAAAGCTCTTCTGTCCGGTTACTTTATGCAGATTGCTCGGGATGTTGA
775	A_24_P141214 2040	GGGTGACATTTGTAACATTTCCCTCTTTGAGACTCTGAGTTCACCTAGAGAAAGTCTAAGCA
64	A_23_P104109 26750	CATTTGGTGTGCAGATGAGTTGTAAAGCCAACTGAAAGAGTTCCTTCAAGAAGTTCCTC
7	A_23_P152136 64785	CCAGATTGTGCAGATGCAAACTTAGGCTGTCTTGATGCAAACTTAGAACACAGAAATGC
6	A_23_P157283 79161	CCCTCAACTACTCCAAAAACCGTTGAATATATCTTTGCTGTCTGCATCTCTTTGAGTAG
8	A_23_P62901 7832	TTTTAGAAAGCAGCCTCATGGTCTCATGCTTAATCTTGCTCTCTCTCTCTTTATGATG
66	A_33_P3278313 253827	GCAATATCTGTTACTAGAGAACATTCCTCATGTGTTTAAACTCTTCACTCTTAGATGCAT
9	A_23_P156284 1627	TTGGGAAAATATCATTGTTATCTCTGTCCAGGGCTTCAGATATTTTGCACGAAATTTA
10	A_23_P202939 334	CGTCACAGGAGTCTTTGTAATGCTTGACAGTTGATGTCGATGCTCACTGCTTCTGCTTT
776	A_33_P3226985 8851	CTGACAAAGTCATGAAGCTCAGTTGGCTGTAATTAATCCCTTCCCTTATTTTAT
12	A_33_P3461039 728705	CAAGATTGTAGCCACTCTCTGGGAGATTTTGCATTTTACGGTTATTTAAAGCCATAACTC
777	A_33_P3215933,A_24_P270033 196264	CATGACTTCCCTTTCAATGAATTATGCTGTAATTGAATGAAGAAATTTCTTCTGAGC
11	A_23_P357717 8115	TTTCCCCCTTTATAGATGGTCACGCACCTGGGTGTACAAAGTTGTATGTGGCATGAAT
740	A_33_P3414912,A_33_P3414907,A_33...	ACCTGGGAAAAAAGACAAACCAGATGTTGGAGGCTTTTGAACAAAAGGACTTCTTTAG
70	A_23_P37560 8800	GTTAGGGTGTTTTTAGGCTTGGAACACTAGTACTACTTTAAAAGATGGCCTCTTGGTGGGA
14	A_23_P104798 3606	TTGAATGACCAAGTCTCTTTCATTGACCAAGGAAATCGGCCTCTATTTGAAGATATGACT

778	A_23_P152791 9120	GAGATATGTAGAAAGACTCTTTGGTTCACATTCGATATTAATAAGTAGCATGAACCTGG
779	A_24_P921321,A_33_P3309561 5795	TGAAATGCTTGTACTTATTGAGCTAAACAAGCTTTGGTACTGTGTGATTGCTTGGCC
780	A_23_P28334,A_33_P3221960 8807	CTAAGATTTCCAGTGGTCCGAGCAGAATCAGAAAATACAGCTACTTCTGCTTATGGCT
19	A_23_P331748 945	GGGACCAAAGGCTGATTCTTGGAGATTTAACTCCCAAGGCAATGGGTTTATAGACATT
781	A_33_P3385121 100129322	TGTGAGGTGATAGAAATGCTGATTGCTTGCCTTGATCATTTGGCGTCCACAAATGTATATATAA
23	A_24_P20630 51176	GCCCAAACTGTCATCCTAACGTTTTGTCAATTCAGTTTGAATTAATGTGCTGAGCATTTT
71	A_33_P3272698 54935	AAGTGGACTAAAGTATTAAACCCTCTAGTCCCATTTGGCTGAAGACACTGAAGTAGCCCA
782	A_23_P80594,A_24_P281988 23228	TTTGCTTTGCACCTACTAATGAGAAATAATTCCGGGATTTTAAAGCACAACTGGAATAGC
33	A_33_P3410409,A_23_P416608,A_24_...	ATAAATACCTTTGATCTAAGGGTTCAGCCTTTCAATGTGACACAAGGAAAGTATTCTACA
36	A_23_P113034 83938	GTCAGCTTGGAAAGGATGAGGAAGACTACAAGAGATACAGATGCTTTTGTCTGTACAAG
75	A_33_P3389573,A_23_P500433 64170	TAAGGACTCCAAGATGTACAAGGACCGCATCGAGGCCATCCTGCTGCAGATGGAGGAGGT
37	A_24_P213788 641518	AGATTAATGCAGAACAAAGTCTGTAGTCTCATTGTTTATCCAGTTACTAGTGCATAGAT
783	A_33_P3251876,A_24_P208567,A_33_...	TTCTTTACTTAATGCCTGCAAAAACAGTCAAGCCAGGTAGAGACGAACCGGAAGCTTTGC
784	A_23_P257578 10011	TGGTAGGAGTTAAAAGATTAAATTCAGAAAAGAGGAGTCTGTTTTCAGAGGAGGCAGCCA
78	A_23_P61371 340061	GTGCTTCAACCTGTGAAATGGGATCATAATCACTGCCTTACCTCCCTCACGGTTGTTGT
785	A_33_P3329356	CGGCTTCAGGAGTACAAGTTTCCCCATCAAAGGTTTGGAAATAATTACACTAAAAAATTG
786	A_23_P4161,A_24_P339416 22901	AAAGGCTCATCTTACTTGTAAACATGGACTGCTCAATCACTATTAAAAAGTCAGTTTAGG
40	A_33_P3241521,A_32_P197561,A_24_...	ACATGGTCTCAGCCGTGAAACAGAAAGAGTGCTTTTCGCACCAGTCGTCAGACCCAGACCT
787	A_33_P3242820,A_33_P3415247 115110	ACCATGCCTGTGTGTTATCTCCCATGAAAAGTCACCTAGGCCGAGCATGGTGCTCACG
788	A_33_P3252068,A_23_P359897 80853	TGCCATGGCAGTAACCATGAGGTAGGCAGTTGTATCGCTATGATAAACCCAGTGGAAATGT
41	A_23_P62188 55906	GGGAGGGGGATAATTTTCTTCTTAAGTAGTTTTACATTGCCACAGTGTGTATGTGTTT
42	A_23_P408271 51170	CACCTAGTTTTCTGAAAACTGATTTACCAGGTTTAGGTTGATGTCATCTAATAGTGCCAG
80	A_23_P110253,A_33_P3407034,A_33_...	AAAGTGGTTGTAGTTATAGATGCTAGGTACTTCAGGGGCACCTTCATTGAGAGTTTGT
44	A_24_P325046,A_23_P124855 84186	TGCACCTACTCTGTAACCTAACTGCGATTATAAAAATGAAAAACAATCTCTTCTAATTGGC
789	A_33_P3285580,A_33_P3591972 132158	CTGCACAGTGAATGTTTTGATAGGATTCATTACTTGTCTCCATAAATGTCAATTTTGGATC

47	A_23_P23279 92241	TTAGTCTCTTATTGGGTAGCTCTTGCTTTAATAATTCGTGTTTGGTGAGTGAAGGGAT
713	A_24_P120115,A_23_P209394,A_23_P...	GAAATTCITGCAITCAGTATGCAITGGTATATCCAGATTCITGGCCAAATTTGCGCTGTAT
34	A_33_P3251985,A_23_P166677 64747	ATGATACTGGATTCTCGGGGGTATTGTTTTTGGAAAGTGTCTTTCATTGCGCTGTGTTTCT
48	A_23_P165061 166	GTGCTGTATATAGTCAGCTTATCTCGTGTTCATCAATCGTCTGATCTCTACAGAGAGAAAGTG
49	A_23_P214681,A_24_P252130 5467	TCTACAAATGCCTACCTGAAAAACTTCAACATGACCAAAAGAAAGGCCCGCAGCATCCTCA
51	A_23_P106973,A_33_P33368188 10801	AGGCTCTGTTCCCTCAATGGCCTTTTGCTACGTGCTCCCGAGAAAATTTGCTTTTGTAT
52	A_23_P157495 5533	TGTCAACACATTTGTGAAGTCTTGTGCTATAAAGGGGAACTTCCCCTAATAAAAGGGCCT
790	A_24_P206736 7702	GGGCAATACAGTAAATTTTCAIGTTACTCTTTTATCAGATCACAACCTCCTAGAGTCTAC
84	A_23_P69242 285362	CAGTTCAGCCGTTGAACACATAGGAATGCTGTGGGGTGACTCTACTGTGCTTTATCTTT
85	A_33_P3839334 153546	TGCCATCCTGTATTAAACAATGTATGGACAGAGTGGAAACAACAGCAAAAGCAAAAAATAAA
791	A_23_P211212 80781	CGGTGGGGCTGGTTCTGTAAATGTGTGTGATGTGAAGCCAATTCAGACAGGCAAAATAAAA
792	A_24_P184555,A_33_P3380098,A_33_...	CTGTAAACTTCCAAAGCTGGCTTTTCCCATTTCAATTCCTGTGATTTATGCCAATAAAGTT
54	A_24_P365365 6929	TGGATGATTGGGACTTTAAACGACCCTCTTTCAGGTGGATTCAGAGACCTGTCTCTGTAT
88		
55	A_33_P3255544,A_23_P41734 55819	TAGTGAACATTGTACCTGTCTCTATGTGCAAACTTAATATATTGAAGGCCCTGGGAATTGT
45	A_33_P3351290,A_23_P84596 51237	GTGCTTCCTGCTCAAAACGGCTCTCTTGCCACTTTATTTTCCCCAGAGACTCTGCTCCTAT
793	A_23_P145408,A_33_P3272580 2519	GCCATGGACAGCCACTTAAGTGGATTTCTTTGGAGCAAAATGGCATTATGTTAGAACTGC
	A_33_P3219750,A_23_P253561 79183	TCTGCAACTATTAACTCTGGAGGCTATATCTATTTTGTGTTTTTGTGTTGGGGGGTGG
60	A_32_P105083 348751	TCCTCAAGTTTCAGTGTCTCAATATATTTTCCGATCAAGACTACAAGAGATCAGTCATTAC

216	A_33_P3418668 347745	TTTGAGTTTACAGGAGTGAGAAGTCCTCTCTTGATGGTGAGATGGGGAAACATTTAAATTC	NR_022011	Homo sapiens Prader Willi/Angelman region RNA, SNRPN neighbor 1 [NR_022011]
253	A_33_P3366175 100130298	GTTTTTCATTCACATCTCCAAAGGTCCTCTACCTTAGAAGAAAGAAAGAGGGAAGAG	NR_034003	Homo sapiens hCG1816373-like [LOC100130298], long non-coding RNA [NR_034003]
258	A_33_P3375002 144481	ATGTTCTAGATGCACAGATTGGGGGCTTGATTGACAACTGACACCTCACTCTAAATCC	NR_038263	Homo sapiens SOCS2 antisense RNA 1 (SOCS2-AS1), long non-coding RNA [NR_038263]
275	A_23_P350754 10819	CGTGTGTGACACCTTCACCAATAACATAGTCATGTATTTCTTGCTGCCATATTTGGTT	NR_045002	Homo sapiens olfactory receptor, family 7, subfamily E, member 1 coding RNA [NR_045002]
328	A_19_P00804546	GACATTGAATGACTGTATGCTGCTTTTGATTTCCGTTAATATGGGCAACTGTCCAATTAA	ENST00000440570	
331	A_19_P00322533, A_19_P00318645, A_23_P423331, A_33_P3277784 84628, A_32_P104063 643911	GACTCATTGTGAGTGCTAGTTCTCTGTAGGATGCCACTGGAAATGTTGAAATGAAAAAT	NR_110453	colorectal neoplasia differentially expressed (non-protein coding)
339	A_19_P00325965	CACCCTATCAACGCTGTATATCAACACCCCATCTTAATAATAGTTTCTTCACATTAGAAA		
359	A_19_P00320723	ATATGAAGAGTGAGAACTGTCTACATCTAAGTCTCTTTGAGAAACAATACCAGCTGAGCG	NR_040059	SRP14 antisense RNA1 (head to head)
329	A_19_P00317128, A_19_P00327354, A_19_P00328996	ATGCAAGGGGGGAAGATAGAAGAAACAAAATTTACCCCTAATGTAGTGTCTTTAGACCCGTG	ENST00000444184	long intergenic non-protein coding RNA 963
380	A_33_P3645465 282997	GTACTTAAGATGCCCTTGTTCAITTTATTTGTCCTGTGCAATAAATACACCTTGATTGAGT	NR_026932	Homo sapiens PDCD4 antisense RNA 1 (PDCD4-AS1), long non-coding RNA [NR_026932]
395	A_19_P00321872	ATTTCTACAAATATTTGACATCTCCATATACTACTCTCTTTCCCTGAGTGGAGAGA	NR_038904	Homo sapiens long intergenic non-protein coding RNA 958 (LINC00958) [NR_038904]
442	A_33_P3408221 729799	ACAGCATGGTGGAAATGCCTCTGATCTGCAAGGAGAGGCGTGAGGGCTCGCATGTGA	NR_026952	Homo sapiens SEC14-like 1 pseudogene 1 (SEC14L1P1), non-coding RNA [NR_026952]
488	A_33_P3289406 91450	CCAAGATGAAGTCATGCTGTGCTTTGGAAATGGTAGATGCTCATTTATGTAAAAATCATAAT	NR_026998	Homo sapiens uncharacterized LOC91450 (LOC91450), long non-coding RNA [NR_026998]
503	A_33_P3219095 728606	TCCAGCCTATGTCTAACTTCTAGCAGATAATGGCAATAAAAAATGTTGGTGCCAACTT	NR_024259	Homo sapiens prostate cancer associated transcript 18 (non-protein coding) [NR_024259]

506	A_33_P3333960 100188949	GCTGCCTGTTTTTTAAACCCGTGAGCTAAGAAATAGTTTACCTATTTAAGTAGTTG	NR_024464	ref Homo sapiens long intergenic non-protein coding RNA 426 (LOC101927151) [NR_024464]
525	A_19_P00810361	TGATTCAGAACAAGTATTTGCTTCAGTATGAAGTGTACGAGTTCAATCTTCAAC	TCONS_I2_00022932	Homo sapiens mRNA for B-cell neoplasia associated transcript, (B-cell neoplasia associated transcript) [MIR155HG]
529	A_32_P108156 114614, A_19_P00812504	TTAACAGTGATGATGCCTGTTACTAGCATTACATGGAACAAATTGCTGCCGTGGGAGG	NR_001458	Homo sapiens MIR155 host gene (non-protein coding) [MIR155HG] [NR_001458]
532	A_19_P00317432	GCTAGTCAGCTGCAGCTGCATCTTCACGAACTCGGTGGGGAACGGGATGCAGATTTTTT	NR_110687	Homo sapiens uncharacterized LOC101927151 (LOC101927151), non-coding RNA [NR_110687]
548	A_19_P00328361	ACATAGTGAAATTGTCCCAAGGCCAGCACCTCAGACACCTTCTTTCACTTTGTAAAG	n/a	Homo sapiens long intergenic non-protein coding RNA 673 (LINC01101) [LINC01101]
559	A_19_P00322310	TGGTAACCACTTGCCAGCTGCAACTTTGACGCATATTATCAGGATAGGTGAGATTGATGG	NR_038303	Homo sapiens long intergenic non-protein coding RNA 1094 (LINC01101) [NR_038303]
568	A_33_P3651911 286109, A_19_P00317929	AAGTGAATGTATTGGCTTAGCCAAATCACTACAGAAGGTGTTCTCTAAATACCTTTTAGT	ENST00000560295	ens cancer susceptibility candidate 7 (non-protein coding) [Source:HGNC Symbol;Acc:ENST00000560295]
529	A_32_P108156 114614, A_19_P00812504	TTAACAGTGATGATGCCTGTTACTAGCATTACATGGAACAAATTGCTGCCGTGGGAGG	NR_001458	Homo sapiens MIR155 host gene (non-protein coding) [MIR155HG] [NR_001458]
585	A_33_P3390853 550643	GGTGACATCCTGTTCTTGTGTATAACTTTATATTCCTATAAATCCATTAAAGGCCCCCAAT	NR_015367	Homo sapiens long intergenic non-protein coding RNA 1420 (LINC01101) [NR_015367]
654	A_33_P3312288	TTGACTCACCACAGAGGGGAACACAAATTTGGTCCATGGTAAATATTCCTTGGTATTAAAT	NR_015364.2	Homo sapiens uncharacterized LOC441204 (LOC441204), long non-coding RNA [NR_015364.2]
328	A_19_P00804546	GACATTGAATGACTGTATGCTGCTTTTGATTTCGTTAATATGGGCAACTGTCCAATTAA	ENST00000440570	MIR503 host gene (non-protein coding) [Source:HGNC Symbol;Acc:ENST00000440570]
647	A_32_P131143 100130717	AAGGACACCAACGGCAGCATCAGCAAGTCCGTGTTGTCTCCCAATAAGTGGTGTCTCC	NR_024482	Homo sapiens CECRS antisense RNA 1 (CECR5-AS1), transcript variant 1 [NR_024482]
653	A_33_P3402329 84848	AAACAGTGGGCTGTACTCCAGTGTGGGACATTGAATGACTGTATGCTGCTTTTGATTTC	NR_024607	Homo sapiens MIR503 host gene (non-protein coding) [MIR503HG] [NR_024607]
675	A_33_P3259973,A_32_P204795 10012...	TGTGGTTTCAACCCTACTTCTGCATCTTAAAGACACTGTATGGTTTCAGCAGTAGTGCCC	NR_036522	Homo sapiens ZNF667 antisense RNA 1 (head to head) [ZNF667-AS1] [NR_036522]
680	A_19_P00806287	TTTTCCAAAATAATGATATCCCTTGCTTCATCTTTGGTGAGTATGTGTTCTATTCTCTCA	MIR100HG	Homo sapiens mir-100-let-7a-2 cluster host gene (non-protein coding) [MIR100HG]
258	A_33_P3375002 144481	ATGTTCTAGATGCAGATTTGGGGCTTGATTGACAACCTGACACCTCACTCTAAATCC	NR_038263	Homo sapiens SOCS2 antisense RNA 1 (SOCS2-AS1), long non-coding RNA [NR_038263]
691	A_33_P3265935	GATTGTTCTGAAGATAATGCGCACTCGGAACCTAGGAAACCAATCCAGTGGGTTCTGCA	n/a	Homo sapiens golgin A2 pseudogene (LOC388152), non-coding RNA [LOC388152] [LOC388152]

695	A_19_P00315493	ATATATTCTTCAGTGTGATTAGGTGAGTGAGTCAGGAATTTTCTCTGGAGACTGCCTAAAT	NR_027046	Homo sapiens uncharacterized LOC145474 [LOC145474], long non-coding RNA [NR_027046]
696	A_19_P00805523	TCGAGCACTGGTTTTGTAGTACCTCCTGTGGCCATCTCCACAGTGTCATATTGAAAG	NR_039989	Homo sapiens MIR4458 host gene (non-protein coding) [MIR4458] [NR_039989]
258	A_19_P00807670	CAAGAGAAGCAGGCTCTCCCTTCTGAAATGATGAGTGATAATGACCATACAGGTCAACT	NR_038263	Homo sapiens SOCS2 antisense RNA 1 (SOCS2-AS1), long non-coding RNA [NR_038263]
258	A_19_P00802794	ACACACAGCACCTCAAGACTCCCTGTGATCCTCTGGGATGCACTCAACGAAGAGTGTGGG	NR_038263	Homo sapiens SOCS2 antisense RNA 1 (SOCS2-AS1), long non-coding RNA [NR_038263]
709	A_23_P71503 78998	AGTGACTGTCAGCAAGCATGTGACTGAAATGGTATCCAGTTCTTACGTATTGTTTTG	NR_026785	Homo sapiens RHPN1 antisense RNA 1 (head to head) [RHPN1-AS1] [NR_026785]
728	A_19_P00807628	CAGTGAGACTTTTCCGAAGAAATCCCTTTTAAATGACCTCAAGCTGACCTTCCTGATGC	NR_033896	Homo sapiens uncharacterized LOC441172 [FJ46906], long non-coding RNA [NR_033896]
529	A_32_P108156 114614	TTAACAGTGTATGATGCCTGTTACTAGCATTCACATGGAACAAATTGCTGCCGTGGGAGG	NR_001458	Homo sapiens MIR155 host gene (non-protein coding) [MIR155HG] [NR_001458]
258	A_33_P3375002 144481	ATGTTCTAGATGCACAGATTGGGGGCTTGATTGACAACTGACACCTCACTCTAAATCC	NR_038263	Homo sapiens SOCS2 antisense RNA 1 (SOCS2-AS1), long non-coding RNA [NR_038263]
765	A_32_P86739 399726	CTGACTTTCCAGCTAAGTTTCCCTCAATAAAAAAGCCCGCTTCTGGGAAAGACAGAA	NM_001010911	Homo sapiens cancer susceptibility candidate 10 (CASC10), mRNA [NM_001010911]
771	A_33_P3281567_A_23_P351467 8418	ACACGTGGTGAAGAAATGGTCTACTCTGGGATGAGTTGTATATAGGATTCCAAACACGGCT	NR_002174	Homo sapiens cytidine monophospho-N-acetylneuraminic acid hydrolase transcript variant 1, non-coding RNA [NR_002174]
750	A_19_P00324182	ATGGCAGTAAGTTAAGGGAATATGGGGTGCTGGACCTGTGATACACATGACTGCTTTAGT	NR_038444.1	Homo sapiens ENTPD1 antisense RNA 1 (ENTPD1-AS1), long non-coding RNA [NR_038444.1]
1	A_33_P3323188 728743	TATTCTACAGGTGCTGACTCTCGGGGAGCTGACTGAGTGGAAATAATGTTCTCTCAA	NR_027237	Homo sapiens zinc finger protein pseudogene [LOC728743], non-coding RNA [NR_027237]
37	A_24_P213788 641518	AGATTAATGCAGAACCAAGGTCGTAGTCTCATTGTTTATCCAGTTACTAGCTGCATAGAT	NR_029373	Homo sapiens LEF1 antisense RNA 1 (LEF1-AS1), transcript variant 1 [NR_029373]
787	A_33_P3242820_A_33_P3415247 115110	ACCATGCCTGTGTATTATCTCCCATGAAAGTACCTAGGCCGAGCATGGTGGCTCACG	NR_026927	Homo sapiens uncharacterized LOC115110 [LOC115110], long non-coding RNA [NR_026927]

Anexo 17

