Table S2: Differential AS events

Type	Gene Symbol	ExonID ID	chr	Strand	ExonStart_Blast	ExonEnd	upstreamExonStart	upstreamExonEnd	downstreamExonStart	downstreamExonEnd	InclusionCount_GSM89.cc	SkippingCount_GSM89.cc	InclusionCount_PC.IR	SkippingCount_PC.IR	InclusionFormLength	SkippingFormLength	Pvalue	FDR	InclusionLevel GSM89.cc	InclusionLevel PC.IR	InclusionDifference (GSM89.cc - PC.IR)
SE	SCN1A	ENSG00000144285	chr2	+	166051	166162	165910	166000	166300	166400	189,112.5	0	189,112.5	0	111	101	0	0	0.999	0.999	0.126
SE	SCN9A	ENSG00000169432	chr9	-	124889721	124889784	124889053	124889153	124890774	124891195	966,811.625	441,491.294	224,161.209	175,181.691	109	83	0	0	0.825	0.642	0.183
SE	KIF9-AS1	ENSG00000182853	chr10	+	118812655	118812814	118808207	118808328	118809128	118809228	82,531.38	128,125.146	49,149.889	19,158.149	157	86	0	0	0.627	0.363	0.264
SE	ANKH11	ENSG00000125593	chr10	-	61983686	61991251	61922562	61922623	61926098	61926228	367,931.295	804,721.755	844,795.871	411,056.691	107	83	0	0	0.696	0.662	0.035
SE	CBCP2	ENSG00000213923	chr1	-	17656040	17656099	17655917	17655984	17656722	17656782	28,277.125	24,462.29	217,281.278	232,294.225	59	83	0	0	0.564	0.824	-0.261
SE	PHKB2	ENSG00000117523	chr1	-	17656040	17656199	17655917	17655984	17656722	17656782	140613.251	1691,0165.1650	1021,0581.1163	862,898.908	83	86	0	0	0.57	0.293	0.277
SE	MAP2K7	ENSG00000076984	chr19	+	7997840	7997940	7997840	7997940	7997940	7998040	287,280.249	24,842.37	287,280.249	24,842.37	82	86	0	0	0.921	0.081	0.841
SE	SBF1	ENSG00000186754	chr10	+	27046463	27046670	27038526	27038712	27047990	27048167	362,314.355	156,171.182	207,277.268	107,241.232	160	86	0	0	0.655	0.497	0.158
SE	SEF2	ENSG00000188675	chr10	-	30079608	30079657	30077637	30077698	30080780	30080880	308,227.248	161,290.291	521,041.164	36,91.64	79	73	0	0	0.793	0.413	0.379
SE	SEF2	ENSG00000188675	chr10	-	30079608	30079651	30077627	30077698	30080780	30080795	318,928.526	161,290.291	1102,1181.1123	36,51.92	18	69	0	0	0.674	0.472	0.202
SE	SEF2	ENSG00000188675	chr10	-	30078667	30079651	30077627	30077698	30080780	30080795	277,291.292	161,290.291	589,636.170	36,51.92	118	69	0	0	0.807	0.614	0.193
SE	SH2	ENSG00000176810	chr15	+	63620295	63620327	63619347	63619453	63621017	63621138	2,5.5	222,176.199	18,58.58	11,5.9	44	78	0	0	0.015	0.039	-0.024
SE	SPAG9	ENSG00000133225	chr17	+	49053233	49053327	49052918	49052987	49054597	49054697	342,146.247	1380,1380.1401	962,1266.1457	973,1281.1461	94	95	0	0	0.352	0.337	0.015
SE	ARHGAP17	ENSG00000141750	chr16	-	24992683	24992918	24946790	24946960	24991607	24991668	422,276.157	43,14.18	142,109.118	96,938.93	305	86	0	0	0.734	0.718	0.016
SE	KLLN	ENSG00000182580	chr19	-	40052453	40052502	40050902	40050969	40052453	40052502	274,282.249	142,115.337	195,575.575	86,35.38	49	86	0	0	0.677	0.672	0.005
SE	SOS1GEF	ENSG00000179230	chr2	-	121438692	121438615	121437234	121437348	121441108	121441225	300,191.218	303,112.96	230,440.692	27,26.21	105	86	0	0	0.447	0.439	0.008
SE	CCDC147	ENSG00000213341	chr9	+	131438605	131438660	131437234	131437348	131441108	131441225	1,0.5	222,176.199	2,0.5	11,5.9	55	86	0	0	0.001	0.002	-0.001
SE	SIRT2	ENSG00000136201	chr19	-	6995721	6995720	6995658	6995653	6997768	6997824	124,125.192	264,505.168	97,97.92	82,82	8	0	0	0	0.056	0.035	0.02
SE	ISPD	ENSG00000182240	chr7	+	97401422	97401516	97396163	97396237	97401225	97401294	1,0.5	1464,1464.1512	2,0.5	317,317.328	260	86	0	0	0.001	0.004	-0.003
SE	ZKHA772	ENSG00000182628	chr17	+	34842778	34842892	34842478	34842629	34848656	34848741	137,265.286	143,195.116	621,585.577	35,35.42	49	80	0	0	0.809	0.762	0.047
SE	ARFIP1	ENSG00000125760	chr11	-	61671160	61671260	61670812	61670911	61672513	61672613	11,2	75,72.91	299,299.267	179,179.214	212	86	0	0	0.802	0.768	0.034
SE	LTGAE	ENSG00000164489	chr2	-	172364499	172364529	172362702	172362828	172365868	172371185	2232,2235.2167	724,721.668	2661,3193.2780	61,45.42	202	86	0	0	0.57	0.582	-0.012
SE	LRRC18	ENSG00000164392	chr3	+	185743122	185743189	185740399	185740488	185743998	185744089	8,7.13	99,83.7	35,54.57	21,52.87	68	86	0	0	0.196	0.341	-0.147
SE	CRH1BP	ENSG00000196233	chr8	+	95874160	95874230	95873849	95873900	95874998	95875071	412,351.380	94,67.81	302,395.279	8,8.6	85	45	0	0	0.766	0.801	-0.035
SE	ZGPAT	ENSG00000167369	chr1	-	32087158	32087169	32085718	32085830	32088549	32088650	142,146.247	7,8.6	194,194.249	7,8.6	89	87	0	0	0.77	0.762	0.008
SE	ADCY2	ENSG00000121281	chr5	-	48148862	48149791	48148837	48148919	48149969	48149969	353,188.151	7,8.6	255,332.272	76,117.111	162	87	0	0	0.68	0.727	-0.047
SE	FOXG1	ENSG00000176165	chr14	+	29267653	29267753	29267653	29267753	29267753	29267853	1,0.5	1,0.5	211,653.272	211,653.272	260	86	0	0	0.001	0.246	-0.245
SE	FOCAD	ENSG00000073921	chr11	+	65691512	65691536	65687565	65687725	65692571	65692721	45,26.39	256,227.249	161,140.145	12,18.13	17	53	0	0	0.354	0.263	0.09
SE	ETAA1	ENSG00000166796	chr2	+	79128368	79128424	79126189	79126349	79129649	79129763	664,620.949	1,0.5	164,163.121	2,2.4	247	86	0	0	0.807	0.991	-0.183
SE	ETAA1	ENSG00000127961	chr2	+	79128368	79128424	79124986	79125168	79129649	79129763	130,519.765	70,85.107	244,266.275	111,159.135	247	86	0	0	0.725	0.687	0.037
SE	GLUL2	ENSG00000135821	chr1	+	182891432	182891478	182888145	182888245	182888475	182888575	1,0.5	1491,1501.1546	8,5.6	267,267.278	47	27	0	0	0.991	0.882	0.107
SE	PDYN2	ENSG00000189163	chr17	-	79862079	79862133	79864035	79864179	79864329	79864474	20,18.11	134,100.109	79,107.88	54,70.69	47	38	0	0	0.108	0.127	-0.019
SE	ARFIP1	ENSG00000125761	chr11	-	61667550	61667592	61667012	61667111	61667916	61667966	1391,996.993	241,212.172	2091,2875.2872	179,179.214	242	86	0	0	0.615	0.685	-0.069
SE	GDF2	ENSG00000106261	chr14	-	53967002	53967122	53966026	53966037	53967956	53967956	1574,1588.1539	794,972.626	1818,1923.624	118,153.623	260	64	0	0	0.328	0.363	-0.035
SE	MYH7B7	ENSG00000251641	chr6	-	75254251	75254355	75253525	75253625	75254251	75254355	31,48.41	238,203.1	245,247.242	115,119.135	105	86	0	0	0.156	0.252	-0.096
SE	PDE6F4	ENSG00000197561	chr7	-	545067	545136	537931	538211	540752	540876	22,29.19	416,412.455	102,125.107	70,64.73	124	86	0	0	0.034	0.057	-0.022
SE	ZNF479	ENSG00000196378	chr6	-	76586243	76586325	76585455	76585553	76587215	76587316	106,75.15	175,155.14	54,75.12	14,41.14	84	86	0	0	0.419	0.245	0.174
SE	CXDC7	ENSG00000182473	chr17	+	74087223	74087316	74086439	74086478	74090694	74090692	288,236.250	2,0.5	522,159.112	84,132.95	148	52	0	0	0.57	0.582	-0.012
SE	ELNB	ENSG00000178687	chr4	-	185127563	185127623	185126575	185126675	185128597	185128697	1,0.5	1691,1691.1681	1802,1802.1744	1284,1284.1258	60	86	0	0	0.001	0.001	0
SE	ELNB	ENSG00000178687	chr4	-	185127563	185127656	185126575	185126675	185128597	185128697	1455,1493.1490	1802,1802.1744	4865,5265.5375	22,35.35	130	86	0	0	0.168	0.332	-0.167
SE	CDH23	ENSG00000179591	chr10	+	73287138	73287169	73287138	73287169	73287169	73287269	1491,1500.1497	1491,1491.1480	2014,2021.2021	1,0.5	31	101	0	0	0.995	0.993	0.002
SE	CNM12208	ENSG00000214008	chr5	+	133065172	133065215	133065125	133065189	133065349	133065447	548,447.393	68,85.86	854,825.822	23,23.15	213	86	0	0	0.765	0.663	0.102
SE	SETD1B	ENSG00000099381	chr12	-	122420558	122420600	122419975	122420088	122421347	122421447	185,174.197	78,55.71	1,0.5	1,0.5	136	86	0	0	0.61	0.581	0.029
SE	CLSTN1	ENSG00000171663	chr1	-	9797551	9797622	9796342	9796430	9801511	9801616	931,701.756	353,356.333	128,247.317	788,864.802	102	86	0	0	0.689	0.617	0.072
SE	ANXA13	ENSG00000114956	chr4	-	65433406	65433477	65432918	65432989	65433918	65433989	1,0.5	2,2.4	2,2.5	2,2.5	69	83	0	0	0.854	0.854	0.000
SE	TBEBR1	ENSG00000196896	chr6	-	42231057	42231306	42227076	42227461	42233343	42233592	365,303.149	215,167.163	385,443.667	61,77.64	321	86	0	0	0.913	0.827	0.085
SE	CSMD3	ENSG00000183117	chr8	+	113883192	113883253	113882545	113882645	113884760	113884860	96,74.81	798,665.76	1,0.5	236,198.94	128	86	0	0	0.012	0.551	-0.539
SE	MGLL	ENSG00000074416	chr3	-	127616445	127616714	127609918	127609989	127608033	127608153	7,6.2	1139,1118.1282	89,102.125	336,435.354	139	83	0	0	0.061	0.203	-0.141
SE	DNM3AS	ENSG00000224078	chr1	+	171551447	171551542	171549167	171549268	171551838	171551938	927,977.243	93,79.18	530,541.576	7,6.2	100	78	0	0	0.879	0.907	-0.028
SE	GMA2157	ENSG00000225649	chr10	-	24815625	24815649	24825702	24825822	24833609	24833697	74,74.80	240,226.187	99,115.96	7,16.37	142	86	0	0	0.517	0.542	-0.026
SE	ZNF512	ENSG00000183779	chr6	+	43763084	43763153	43762333	43762433	43763684	43763784	1,0.5	142,142.1	2,0.5	139,139.1	70	86	0	0	0.667	0.811	-0.144
SE	ARFIP2	ENSG00000181634	chr4	-	152760084	152760202	152756757	152756882	152759729	152759829	48,54.89	239,237.220	262,291.251	120,130.136	172	86	0	0	0.812	0.727	0.085
SE	GRM7	ENSG00000168959	chr3	-	146946622	146946763	146945662	146945762	147000291	147000391	1,0.5	1,0.5	1,0.5	1,0.5	142	86	0	0	0.001	0.001	0
SE	GRM7	ENSG00000168959	chr3	-	146946622	146946763	146945662	146945762	147000291	147000391	1,0.5	1,0.5	1,0.5	1,0.5	69	86	0	0	0.001	0.001	0
SE	GRM7	ENSG00000168959	chr3	-	146946622	146946763	146945662	146945762	147000291	147000391	1,0.5	1,0.5	1,0.5	1,0.5	69	86	0	0	0.001	0.001	0
SE	MYO1A	ENSG00000180539	chr9	+	70423189	70423253	70418023	70418169	70423739	70423848	8,6.2	1,0.5	2,0.5	2,0.5	65	86	0	0	0.762	0.591	0.171
SE	MYO1A	ENSG00000180539	chr9	+	70423189	70423253	70418023	70418169	70423739	70423848	1,0.5	1,0.5	2,0.5	2,0.5	65	86	0	0	0.762	0.591	0.171
SE	EPG5	ENSG00000182606	chr1	+	79799852	79799892	79795762	79795822	79802023	79802122	4001,4004.4000	1949,2129.1987	2949,2129.2882	1962,1962.1935	41	86	0	0	0.679	0.675	0.003
SE	EPG5	ENSG00000182606	chr1	+	79799852	79799892	79795762	79795822	79802023	79799981	148,162.186	4371,3181.4151	429,399.808	2321,2118.1972	41	86	0	0	0.092	0.541	-0.449
SE	SHD2	ENSG00000136235	chr10	+	95122751	95122811	95120718	95120851	95125896	95125996	1288,1319.1326	135,175.147	543,543.602	413,419.446	58	86	0	0	0.923	0.824	0.099
SE	TMPO	ENSG00000120802	chr12	-	98938728	98938859	98931252	98931350	98940135	98940225	1057,725.891	56,72.86	1874,1792.1787	11,6.8	173	92	0	0	0.817	0.821	-0.003
SE	SDHAF2	ENSG00000119955	chr11	-	61025617	61025683	61024969	61025069	61026485	61026585	221,248.232	219,64.58	1,0.5	1,0.5	67	86	0	0	0.98	0.543	0.437
SE	TYK2	ENSG00000105397	chr9	-	6964503	6964592	6964279	6964357	6966450	6966550	1608,1727.1692	19,83.57	1015,1196.1157	49,83.57	105	86	0	0	0.815	0.629	0.185
SE	CIC	ENSG00000213928	chr19	-	42389519	42389553	42388204	42388353	42390553	42390653	1483,514.525	164,216.207	965,965.1000	6,3.4	189	86	0	0	0.914	0.513	0.401
SE	SSU88	ENSG00000189187	chr11	+	60682	60693	60673	60678	60704	60764	1110,988.1017	101,217.205	917,1116.891	21,25.12	223	86	0	0	0.717	0.672	0.045
SE	UXT	ENSG00000177757	chr6	+	44284214	44284257	44284012	44284085	44287583	44287648	1625,758	1,0.5	2,0.5	2,0.5	44	86	0	0	0.651	0.679	-0.028
SE	ANKRD17143	ENSG00000177143	chr5	+	162942521	162942577	162941503	162941593	162947648	162947748	350,264.272	143,112.92	539,572.588	51,38.55	62	86	0	0	0.645	0.693	-0.047
SE	USP2	ENSG00000180704	chr9	+	76756089	76756209	76754867	76754963	76756775	76756895	19,14.14	431,395.435	262,287.287	34,44.44	28	86	0	0	0.88	0.818	0.062
SE	WNK1	ENSG00000060237	chr12	-	988758	988937	987985	987527	989865	989965	444,408.379	161,135.131	126,147.136	261,264.253	111	86	0	0	0.218	0.298	-0.08
SE	WNK1	ENSG00000060237	chr12	-	988758	988937	987985	987527	989865	989965	1,0.5	1,0.5	1,0.5	1,0.5	69	86	0	0	0.001	0.001	0
SE	ADAM33	ENSG00000149451	chr20	+	15501479	15501491	15501228	15501330	15503723	15503885	245,185.222	156,138.163	186,167.154	108,107.102	63	86	0	0	0.586	0.572	0.014
SE	ADAM33	ENSG00000149451	chr20	+	15501479	15501491	15501228	15501330	15503723	15503885	1,0.5	1,0.5	188,188.188	106,107.96	268	63	0	0	0.993	0.977	0.015
SE	LAS1L	ENSG00000164389	chr4	+	64754349	64754415	64752349	64752438	64754349	64754434	1376,936.928	1,1.5	1568,1584.1511	136,175.128	175	43	0	0	0.993	0.987	0.006
SE	LAS1L	ENSG00000164389	chr4	+	64754349	64754415	64752349	64752438	64754349	64754434	1,0.5	1,0.5	1,0.5	1,0.5	69	43	0	0	0.714	0.714	0
SE	BAAP2	ENSG00000175866	chr17	+	79084713	79084759	79082076	79082169	79085169	79085269	79,51.15	49,26.32	87,115.77	27,34.21	39	29	0	0	0.192	0.392	-0.2
SE	SPRY2	ENSG00000164056	chr14	+	44055518	44055549	44054918	44054985	44055811	44055900	1,0.5	1,0.5	1,0.5	1,0.5	205	86	0	0	0.001	0.001	0
SE	CCDC32	ENSG00000152492	chr8	-	145092850	145092978	145087707	145087825	145097947	145098063	138,136.155	1556,1393.1570	1624,1721.1776	521,656.678	107	86	0	0	0.612	0.614	-0.002
SE	ELF2	ENSG00000136699	chr13	+	26781060	26781164	26780664	26780765	26782665	26782765	1,0.5	1,0.5	1,0.5	1,0.5	105	86	0	0	0.667	0.667	0
SE	KIAA0922	ENSG00000196155	chr4	+	178861364	178861442	178858775	178858851	178863553	178863659	50,65.48	148,131.143	173,256.264	36,37.26	104	69	0	0	0.135	0.214	-0.08
SE	DTNB	ENSG00000138101	chr8	+	101148863	101148922	101145237	101145337	101149144	101149244	80,74.118	144,116.118	28,19.127	28,19.127	177	86	0	0	0.371	0.157	0.214
SE	EIF2B4	ENSG00000115715	chr8	+	17771248	17771349	17763922	17763977	17772138	17772239	168,175.125	163,176.152	248,252.226	23,24.31	177	86	0	0	0.575	0.328	0.245
SE	PTPRF	ENSG00000142949	chr1	+	43667747	43667849	43664599	43664685	43668095	43668195	1,0.5	1,0.5	1,0.5	1,0.5	102	86	0	0	0.667	0.667	0
SE	SYT10	ENSG00000164524	chr19	+	19226474	19226561	19226107	19226199	19229793	19229794	167,154.529	155,93.98	121,86.90	88,88.108	148	74	0	0	0.717	0.563	0.154
SE	SYT10	ENSG00000164524	chr19	+	19226474	19226561	19226107	19226199	19229793	19229794	1,0.5	86,83.8	1,0.5	127,61.155	136	52	0	0	0.667	0.614	0.053
SE	SYT10	ENSG00000164524	chr19	+	19226747	19226561	19226107	19226199	19227260	19227355	279,248.259	86,83.85	143,125.166	127,61.155	152	52	0	0	0.597	0.717	-0.12
SE	SYT10	ENSG00000164524	chr19	+	19226747	19226561	19226107	19226199	19227260	19227355	1,0.5	1,0.5	1,0.5	1,0.5	136	52	0	0	0.667	0.667	0
SE	SPIA2	ENSG00000120883	chr16	+	2403570	2403585	2403547	2403628	2403619	2403624	412,413.377	105,113.107	827,995.822	28,37.26	185	74	0	0	0.615	0.596	0.019
SE	CNM4	ENSG00000188641	chr9	+	139466604	139466667	139465750	139465842	139467149	139467249	42,27.24	872,768.841	607,663.655	197,214.553	72	86	0	0	0.593	0.835	-0.242
SE	SPAR2	ENSG00000131678	chr18	-	12659753	12659927	12654344	12654482	12663349	12663490	33,39.27	423,435.433	381,348.348	87,89.89	246	86	0	0	0.027	0.018	0.01
SE	ARHGEF12	ENSG00000196914	chr11	+	118657036	118657094	118655705	118657038	118657038	118657138	679,546.581	44,51.7	31,31.1	286,281.279	57	86	0	0	0.957	0.761	0.196
SE	SMARCA2	ENSG00000080503	chr9	+	128627016	128627052	128625937	128626070	128630736	128630848	303,327.265	792,696.782	487,591.454	270,301.274	58	86	0	0	0.377	0.411	-0.034
SE	BLK	ENSG00000136213	chr8	+	101570653	101570686	101570563	101570667	101577927	101577967	39,20.57	364,326.777	343,326.818	192,138.144	172	86	0	0	0.915	0.714	0.201
SE	SHTN1A	ENSG00000197535	chr5	+	52635313	52635394	52632392	52632501	52638557	52638658	432,416.451	153,188.186	69,78.75	14,18.64	168	86	0	0	0.264	0.296	-0.032
SE	MSRA4T1	ENSG00000164366	chr8	+	43651572	43651643	43648896	43649000	43652000	43652100	1,0.5	1,0.5	1,0.5	1,0.5	72	86	0	0	0.667	0.667	0
SE	MAK21	ENSG00000125629	chr6	+	39966581	39966702	39965669	39965691	39969272	39969302	232,221.285	1211,1199.1182	527,582.638	505,539.505	183	86	0	0	0.076	0.081	-0.005
SE	MFSD9	ENSG00000168899	chr8	+	101685216	101685326	101682655	101682755	101687355	101687455	1,0.5	255,224.232	36,44.32	435,434.441	112	86	0	0	0.013	0.511	-0.498
SE	GPR56	ENSG00000153136	chr16	-	57675498	57675620	57662918	57662714	57684564	57684263	417,621.348	180,135.120	332,414.263	3,10.10	104	86	0	0	0.507	0.581	-0.07
SE	RSU1P67	ENSG00000183943	chr2	+	130600504	130600556	130600504	130600556	130601853	130601953	2,2.5	19,21.9	1,0.5	1,0.5	53	86	0	0	0.941	0.556	0.385
SE	SUN2	ENSG00000164828	chr7	-	889156	889240	882977	883157	891610	891719	93,101.83	15,16.38	335,70.338	0,1.5	154	86	0	0	0.512	0.063	0.449
SE	ANXA6CF2	ENSG00000188486	chr5	+	150318512	150318553	150316973	150317073	150320453	150320553	866,375.320	127,138.96	1,0.5	21,38.5	77	86	0	0	0.579	0.267	0.312
SE	CDH8	ENSG00000261026	chr11	+	95221257	95221334	95219667	95219793	95226398	95226465	4,2.3	317,32	166,198.200	1,0.5	159	86	0	0	0.114	0.011	0.103
SE	CDH8	ENSG00000261026	chr11	+	95221257	95221334	95219667	95219793	95226398	95226465	7,4.5	8,5.5	1,0.5	1,0.5	159	86	0	0	0.667	0.667	0
SE	CDH8	ENSG00000261026	chr11	+	95221257	95221334	95221381	95221612	95226398	95226465	4,2.3	2387,1993.2083	167,198.198	236,244.222	159	56	0	0	0.01	0.152	-0.141
SE	CDH8	ENSG00000261026	chr11	+	95221257	95221334	95221381	95221612	95226398	95226465	23,20.17	2387,1993.2083	167,198.198	236,244.222	159	56	0	0	0.127	0.125	0.002
SE	CDH8	ENSG00000261026	chr11	+	95221257	95221334	95221381	95221612	95226398	95226465	1,0.5	2387,1993.2083	1,0.5	236,244.222	159	56	0	0	0.667	0.667	0
SE	CDH8	ENSG00000261026	chr11	+	95229651	95229753	95221381	95221612	95226398	95226465	23,20.17	78,69.89	980,1114.968	56,58.34	174	86	0	0	0.127	0.125	0.002
SE	CDH8	ENSG00000261026	chr11	+	95229651	95229753	95221381	95221612	95226398	95226465	1,0.5	78,69.89	1,0.5	1,0.5	174	86	0	0	0.667	0.667	0
SE	CDH8	ENSG00000261026	chr11	+	95229651	95229753	95226658	95226787	95226398	95226465	0,0.5	13,2.5	136,136.136	0,0.8	144	56	0	0	0.0	0.183	-0.183
SE	CDH8	ENSG00000261026	chr11	+	95229651	95229753	95227187	95227318	95226398	95226465	0,0.5	41,21.17	47,50.68	2,2.4	144	56	0	0	0.0	0.457	-0.457
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95221381	95221612	95226398	95226465	266,282.259	2387,1993.2083	2782,3052.2872	236,244.222	246	56	0	0	0.921	0.828	0.093
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95221381	95221612	95226398	95226465	128,119.132	83,75.87	1396,1427.1412	56,58.34	246	56	0	0	0.606	0.961	-0.355
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95221381	95221612	95226398	95226465	0,0.5	83,75.87	1,0.5	1,0.5	246	56	0	0	0.0	0.667	-0.667
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95226658	95226787	95226398	95226465	0,0.5	13,2.5	136,136.136	0,0.8	144	56	0	0	0.0	0.183	-0.183
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95227187	95227318	95226398	95226465	0,0.5	41,21.17	47,50.68	2,2.4	144	56	0	0	0.0	0.457	-0.457
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95227187	95227318	95226398	95226465	266,282.259	2387,1993.2083	2782,3052.2872	236,244.222	246	56	0	0	0.921	0.828	0.093
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95227187	95227318	95226398	95226465	128,119.132	83,75.87	1396,1427.1412	56,58.34	246	56	0	0	0.606	0.961	-0.355
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95227187	95227318	95226398	95226465	0,0.5	83,75.87	1,0.5	1,0.5	246	56	0	0	0.0	0.667	-0.667
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95226658	95226787	95226398	95226465	0,0.5	13,2.5	136,136.136	0,0.8	144	56	0	0	0.0	0.183	-0.183
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95227187	95227318	95226398	95226465	0,0.5	41,21.17	47,50.68	2,2.4	144	56	0	0	0.0	0.457	-0.457
SE	CDH8	ENSG00000261026	chr11	+	95232782	95232966	95227187	95227318	95226398	95226465	266,282.259	2387,1993.2083	2782,3052.2872	236,244.222	246	56

52	585087	CNG000000007676	2015	1	1101810158	1101811176	1191792040	1191808625	1191816043	1185_1132_1073	111,90,88	1071,1025,1016	62,31,18	160	86	1.28-09	4.47E-07	0.66E,0.801E-007	0.95E,0.96E,0.879	-0.113
52	607824	CNG000000007674	2015	1	1160865	1160845	1160786	1160762	1160312	1160154	1842,1311,1168	22,20,18	992,972,955	74,73,67	167	86	1.53E-09	5.28E-07	0.65E,0.851E-007	0.81T,0.82T,0.82	-0.117
52	607825	CNG000000007675	2015	1	1160863	1160844	1160785	1160761	1160311	1160153	1842,1311,1168	22,20,18	992,972,955	74,73,67	167	86	1.53E-09	5.28E-07	0.65E,0.851E-007	0.81T,0.82T,0.82	-0.117
52	61047	CNG000000016838	2007	1	985933	985670	982977	982157	981037	980128	576,182,115	51,36,8	395,421,318	0,1,1	183	86	1.76E-09	6.16E-07	0.84E,0.87E,0.84	1.02E,0.95E,0.884	-0.103
52	61048	CNG000000016842	2007	1	1000842	1000841	1000379	1000378	1000377	1000376	194,193,192	19,18,17	194,193,192	19,18,17	183	86	1.76E-09	6.16E-07	0.84E,0.87E,0.84	1.02E,0.95E,0.884	-0.103
52	620812	CNG000000018183	2015	1	1699867	1699837	1699819	1699802	1699793	1699792	5,4,2	248,236,227	192,182,165	31,21,30	1100	86	2.05E-09	7.16E-07	0.8E,0.91E,0.86	0.88E,0.91E,0.87	-0.113
52	620813	CNG000000018184	2015	1	1699866	1699836	1699818	1699801	1699792	1699791	5,4,2	248,236,227	192,182,165	31,21,30	1100	86	2.05E-09	7.16E-07	0.8E,0.91E,0.86	0.88E,0.91E,0.87	-0.113
52	696018	CNG000000018453	2015	1	1828258	1828257	1828256	1828255	1828254	1828253	1,0,0	1,0,0	1,0,0	0,0,0	1	86	2.29E-09	8.00E-07	0.79E,0.79E,0.79	0.79E,0.79E,0.79	-0.000
52	696148	CNG000000018451	2015	1	1861619	1861618	1861617	1861616	1861615	1861614	76,43,40	80,41,38	85,108,102	32,21,17	78	86	2.29E-09	8.13E-07	0.56E,0.621E-007	0.74E,0.85E,0.80	-0.281
52	697927	CNG000000018452	2015	1	1864833	1864832	1862878	1862877	1862876	1862875	1468,467,18	80,36,35	80,36,35	32,1,31	32	86	2.29E-09	8.13E-07	0.61E,0.621E-007	0.89E,0.89E,0.879	-0.251
52	55158	CNG000000018187	2015	1	40893	41037	40872	40826	41822	41821	261,231,207	28,26,18	201,211,207	0,1,1	210	86	4.58E-09	1.50E-06	0.77E,0.781E,0.80	1.02E,0.96E,0.887	-0.213
52	58918	CNG000000018188	2015	1	45065	45064	45063	45062	45061	45060	204,203,28	34,27,21	129,125,121	76,51,47	160	86	5.62E-09	1.95E-06	0.66E,0.751E-007	0.84E,0.84E,0.84	-0.000
52	58199	CNG000000018187	2015	1	40968	41037	40872	40826	41822	41821	272,261,226	28,26,18	212,281,217	0,1,1	222	86	6.57E-09	2.22E-06	0.76E,0.75E,0.82	1.02E,0.97E,0.888	-0.199
52	599512	CNG000000018189	2015	1	1312810	1312809	1312808	1312807	1312806	1312805	1126,968	178,173,166	108,108,105	157,146,136	312	86	8.37E-09	2.82E-06	0.66E,0.81E,0.731	0.86E,0.126E,0.108	-0.315
52	599513	CNG000000018190	2015	1	1312811	1312809	1312808	1312807	1312806	1312805	1126,968	178,173,166	108,108,105	157,146,136	312	86	8.37E-09	2.82E-06	0.66E,0.81E,0.731	0.86E,0.126E,0.108	-0.315
52	61047	CNG000000016842	2007	1	1000842	1000841	1000379	1000378	1000377	1000376	194,193,192	19,18,17	194,193,192	19,18,17	183	86	1.76E-09	6.16E-07	0.84E,0.87E,0.84	1.02E,0.95E,0.884	-0.103
52	61048	CNG000000016838	2007	1	985933	985670	982977	982157	981037	980128	576,182,115	51,36,8	395,421,318	0,1,1

S1	CNPR	CNG000000007369	chr22	+	13349505	13349620	13349802	13349820	13349749	13349738	285,251,299	46,46,38	205,249,215	16,11,9	201	55	0.000169421	0.026316816	0.026316816	0.574,0.606,0.58	0.574,0.615,0.602	-0.217
S2	ARFGEF1	CNG000000015339	chr12	+	43919349	43919349	43919349	43919349	43919349	43919349	312,276,292	2,2,2	181,199,178	21,9,11	50	26	0.000169421	0.027579689	0.068,0.03,0.065	0.838,0.912,0.87	0.838,0.912,0.87	-0.112
S3	ZC3H7A	CNG000000016130	chr9	+	116483691	116483691	116483691	116483691	116483691	116483691	41,41,41	1,1,1	38,38,38	28,28,28	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S4	SLC25A39	CNG000000016130	chr9	+	116483691	116483691	116483691	116483691	116483691	116483691	31,31,31	47,52,51	48,55,51	34	60	0.000169421	0.029451605	0.164,0.529,0.432	0.677,0.793,0.738	0.677,0.793,0.738	-0.267
S5	DNTT	CNG000000019265	chr10	+	94239889	94239889	94239889	94239889	94239889	94239889	41,41,41	249,239,246	41,41,41	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S6	SMG1P4	CNG000000019265	chr10	+	94239889	94239889	94239889	94239889	94239889	94239889	41,41,41	72,63,65	186,211,197	72,63,65	231	86	0.000169421	0.031939223	0.812,0.937,0.864	0.752,0.783,0.811	0.752,0.783,0.811	0.121
S7	ZNF492	CNG000000021645	chr11	+	118620977	118620977	118620977	118620977	118620977	118620977	31,31,31	37,37,37	31,31,31	37,37,37	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S8	ZFP1	CNG000000022187	chr12	+	124810147	124810147	124810147	124810147	124810147	124810147	31,31,31	248,239,246	31,31,31	248,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S9	SCORE	CNG000000024698	chr19	+	12495958	12495958	12495958	12495958	12495958	12495958	41,41,41	249,239,246	41,41,41	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S10	ACTN4	CNG000000025147	chr19	+	39232933	39232933	39232933	39232933	39232933	39232933	31,31,31	83,90,91	126,130,129	108	86	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S11	CNN2	CNG000000026767	chr11	+	65223649	65223649	65223649	65223649	65223649	65223649	31,31,31	249,239,246	31,31,31	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S12	CNN2BB	CNG000000026767	chr11	+	65223649	65223649	65223649	65223649	65223649	65223649	31,31,31	249,239,246	31,31,31	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S13	DENND5A	CNG000000027354	chr11	+	86648	86648	86648	86648	86648	86648	289,281,275	27,40,28	216,241,215	25,41,27	152	56	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S14	ZNF185	CNG000000047394	chr5	+	152160951	152160951	152160951	152160951	152160951	152160951	152160,767	152,204,227	181,191,148	51,87,85	85,123,93	103	63	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	-0.000
S15	CPE1	CNG000000048219	chr4	+	144638659	144638659	144638659	144638659	144638659	144638659	31,31,31	7,8,4	31,31,31	6,6,1	78	62	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S16	SLC26A1	CNG000000076890	chr16	+	75219351	75219351	75219351	75219351	75219351	75219351	710,642,672	2041,2041,2021	216,257,243	2414,2351,2318	115	85	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S17	TMEM179B27	CNG000000079147	chr17	+	75060877	75060877	75060877	75060877	75060877	75060877	31,31,31	249,239,246	31,31,31	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
S18	HHIP1	CNG000000092218	chr14	+	100118582	100118582	100118582	100118582	100118582	100118582	261,237,195	1,0,2	84,65,48	0,0,1	719	86	0.000169421	0.034832711	0.983,1.0,0.921	1.0,1.0,0.891	1.0,1.0,0.891	0.091
S19	GRAMD1B	CNG000000094304	chr11	+	124846499	124846499	124846499	124846499	124846499	124846499	31,31,31	47,37,32	614,542,549	52,45,43	168	73	0.000169421	0.034832711	0.983,0.921,0.903	0.846,0.891,0.875	0.846,0.891,0.875	0.091
S20	DTX2	CNG000000097203	chr7	+	76090626	76090626	76090626	76090626	76090626	76090626	22,16,5	65,41,37	71,72,65	79,81,80	192	86	0.000169421	0.037540555	0.125,0.119,0.079	0.287,0.285,0.266	0.287,0.285,0.266	-0.166
S21	FSTL1 [SIGDIT]	CNG000000098832	chr3	+	123973447	123973447	123973447	123973447	123973447	123973447	31,31,31	2,4,5	2,2,1	6,1,1	52	28	0.000169421	0.037540555	0.125,0.119,0.079	0.991,0.984,0.977	0.991,0.984,0.977	-0.166
S22	LSM7	CNG000000100423	chr8	+	10567906	10568030	10568030	10568030	10568030	10568030	193,257,227	689,612,612	821,870,857	18,42,39	108	86	0.000169421	0.038035554	0.728,0.752,0.76	0.862,0.893,0.863	0.862,0.893,0.863	-0.116
S23	ANKRD22	CNG000000100423	chr8	+	10568022	10568022	10568022	10568022	10568022	10568022	193,257,227	234,260,240	241,267,252	35,33,33	225	86	0.000169421	0.038035554	0.728,0.752,0.76	0.867,0.777,0.71	0.867,0.777,0.71	0.156
S24	SCN9A1	CNG000000101613	chr10	+	76716181	76716181	76716181	76716181	76716181	76716181	187,188	188,187,139	57,110,121	105,121,93	143	70	0.000169421	0.038342057	0.110,0.152,0.144	0.237,0.305,0.242	0.237,0.305,0.242	-0.122
S25	ATAD1A	CNG000000101613	chr10	+	76716181	76716181	76716181	76716181	76716181	76716181	187,188	1629,1627,1587	81,81,81	1791,1787,1662	1,1,1	27	0.000169421	0.038342057	0.110,0.152,0.144	0.564,0.893,0.917	0.564,0.893,0.917	-0.353
S26	SFC1XX	CNG000000104193	chr12	+	42655256	42655256	42655256	42655256	42655256	42655256	179,150,150	474,427,417	324,309,356	365,363,312	268	86	0.000169421	0.038342057	0.110,0.152,0.144	0.912,0.908,0.897	0.912,0.908,0.897	-0.090
S27	ADGRD1B-C	CNG000000107227	chr16	+	51227727	51227727	51227727	51227727	51227727	51227727	71,71,71	71,84,57	26,35,35	19,27,14	84	86	0.000169421	0.038342057	0.110,0.152,0.144	0.752,0.752,0.748	0.752,0.752,0.748	-0.153
S28	TMM194	CNG000000215505	chr12	+	15554565	15554565	15554565	15554565	15554565	15554565	535,519,499	15,9,10	1431,1025,1492	65,37,38	328	86	0.000169421	0.038342057	0.771,0.832,0.822	0.934,0.937,0.901	0.934,0.937,0.901	-0.116
S29	ARHGAP8	CNG000000219158	chr22	+	43247782	43247782	43247782	43247782	43247782	43247782	1145,1145,1145	1145,1145,1145	846,848,847	1145,1145,1145	1	1	0.000169421	0.038342057	0.217,0.375,0.302	0.848,0.912,0.849	0.848,0.912,0.849	-0.216
S30	DDX5L	CNG000000219158	chr22	+	43247782	43247782	43247782	43247782	43247782	43247782	117,101,116	11,8,9	117,101,116	31,38,32	177	86	0.000169421	0.038342057	0.217,0.375,0.302	0.182,0.228,0.201	0.182,0.228,0.201	-0.216
S31	PPP 2R5C-2	CNG000000224679	chr7	+	148367810	148367810	148367810	148367810	148367810	148367810	54,58,62	54,58,62	179,179,179	31,31,31	179	86	0.000169421	0.038342057	0.217,0.375,0.302	0.364,0.347,0.337	0.364,0.347,0.337	-0.241

Type	Gene Symbol	Ensemb ID	chr	Strand	1stExonStart_0base	1stExonEnd	2nd0ExonStart_0base	2ndExonEnd	upstreamExonStart	upstreamExonEnd	downstreamExonStart	downstreamExonEnd	inclusionCount_G0409.cc	SkippingCount_G0409.cc	inclusionCount_PC-30	SkippingCount_PC-30	InclusionFormLength	SkippingFormLength	Pvalue	FDR	inclusionLevel-G0409.cc	inclusionLevel-PC-30	inclusionDifference (G0409.cc - PC-30)
SE	CARM1	CNG00000007369	chr19	+	16506359	16506541	16506359	16506972	16506412	16506545	4659,4615,4628	28,21,29	2,0,0	0,0,0	0	0	0	0	1.0,0.996,0.999	0.822,0.735,0.836	0.822,0.735,0.836	0.197
SE	CYNE	CNG00000008968	chr6	+	151783182	151783182	151783182	151783182	151783182	151783182	348,330,348	93,70,91	0,0,0	0,0,0	1169	86	0	0	1.0,0.992,0.999	0.874,0.914,0.907	0.874,0.914,0.907	0.033
SE	FLCN	CNG00000009292	chr17	+	2149838527	2149838664	2149836327	2149836429	2149838412	2149838527	1125,1132,1001	84,486,545	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.81,0.794,0.828	0.122,0.113,0.119	-0.694
SE	ZNF292	CNG00000009292	chr17	+	39675051	39675051	39675051	39675051	39674917	39675051	2,2,2	1,1,1	1,1,1	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	ERBB2	CNG00000009292	chr17	+	39674968	39675051	39674968	39675051	39674917	39675051	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	ERBB2	CNG00000009292	chr17	+	39687914	39687914	39687914	39687914	39687914	39687914	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	TOR1AIP1	CNG00000010368	chr1	+	150351138	150351138	150351138	150351138	150351138	150351138	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	TMC4	CNG00000012638	chr9	+	114000000	114000000	114000000	114000000	113999900	114000000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	SYCE1	CNG00000013544	chr1	+	154600000	154600000	154600000	154600000	154599900	154600000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	SYCE1L	CNG00000013544	chr1	+	154600000	154600000	154600000	154600000	154599900	154600000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	ZNF658	CNG00000014138	chr2	+	73000000	73000000	73000000	73000000	72999900	73000000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872	0.010
SE	ZNF185	CNG00000015339	chr12	+	43919349	43919349	43919349	43919349	43919349	43919349	312,276,292	2,2,2	181,199,178	21,9,11	50	26	0.000169421	0.027579689	0.068,0.03,0.065	0.838,0.912,0.87	0.838,0.912,0.87	-0.112
SE	ZC3H7A	CNG00000016130	chr9	+	116483691	116483691	116483691	116483691	116483691	116483691	41,41,41	1,1,1	38,38,38	28,28,28	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	SLC25A39	CNG00000016130	chr9	+	116483691	116483691	116483691	116483691	116483691	116483691	31,31,31	47,52,51	48,55,51	34	60	0.000169421	0.029451605	0.164,0.529,0.432	0.677,0.793,0.738	0.677,0.793,0.738	-0.267
SE	DNTT	CNG00000019265	chr10	+	94239889	94239889	94239889	94239889	94239889	94239889	41,41,41	249,239,246	41,41,41	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	SMG1P4	CNG00000019265	chr10	+	94239889	94239889	94239889	94239889	94239889	94239889	41,41,41	72,63,65	186,211,197	72,63,65	231	86	0.000169421	0.031939223	0.812,0.937,0.864	0.752,0.783,0.811	0.752,0.783,0.811	0.121
SE	ZNF492	CNG00000021645	chr11	+	118620977	118620977	118620977	118620977	118620977	118620977	31,31,31	37,37,37	31,31,31	37,37,37	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	ZFP1	CNG00000022187	chr12	+	124810147	124810147	124810147	124810147	124810147	124810147	31,31,31	248,239,246	31,31,31	248,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	SCORE	CNG00000024698	chr19	+	12495958	12495958	12495958	12495958	12495958	12495958	41,41,41	249,239,246	41,41,41	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	ACTN4	CNG00000025147	chr19	+	39232933	39232933	39232933	39232933	39232933	39232933	31,31,31	83,90,91	126,130,129	108	86	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	CNN2	CNG00000026767	chr11	+	65223649	65223649	65223649	65223649	65223649	65223649	31,31,31	249,239,246	31,31,31	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	CNN2BB	CNG00000026767	chr11	+	65223649	65223649	65223649	65223649	65223649	65223649	31,31,31	249,239,246	31,31,31	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	DENND5A	CNG00000027354	chr11	+	86648	86648	86648	86648	86648	86648	289,281,275	27,40,28	216,241,215	25,41,27	152	56	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	ZNF185	CNG00000047394	chr5	+	152160951	152160951	152160951	152160951	152160951	152160951	152160,767	152,204,227	181,191,148	51,87,85	85,123,93	103	63	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	-0.000
SE	CPE1	CNG00000048219	chr4	+	144638659	144638659	144638659	144638659	144638659	144638659	31,31,31	7,8,4	31,31,31	6,6,1	78	62	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	SLC26A1	CNG00000076890	chr16	+	75219351	75219351	75219351	75219351	75219351	75219351	710,642,672	2041,2041,2021	216,257,243	2414,2351,2318	115	85	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	TMEM179B27	CNG00000079147	chr17	+	75060877	75060877	75060877	75060877	75060877	75060877	31,31,31	249,239,246	31,31,31	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962	-0.000
SE	HHIP1	CNG00000092218	chr14	+	100118582	100118582	100118582	100118582	100118582	100118582	261,237,195	1,0,2	84,65,48	0,0,1	719	86	0.000169421	0.034832711	0.983,1.0,0.921	1.0,1.0,0.891	1.0,1.0,0.891	0.091
SE	GRAMD1B	CNG00000094304	chr11	+	124846499	124846499	124846499	124846499	124846499	124846499	31,31,31	47,37,32	614,542,549	52,45,43	168	73	0.000169421	0.034832711	0.983,0.921,0.903	0.846,0.891,0.875	0.846,0.891,0.875	0.091
SE	DTX2	CNG00000097203	chr7	+	76090626	76090626	76090626	76090626	76090626	76090626	22,16,5	65,41,37	71,72,65	79,81,80	192	86	0.000169421	0.037540555	0.125,0.119,0.079	0.287,0.285,0.266	0.287,0.285,0.266	-0.166
SE	FSTL1 [SIGDIT]	CNG00000098832	chr3	+	123973447	123973447	123973447	123973447	123973447	123973447	31,31,31	2,4,5	2,2,1	6,1,1	52	28	0.000169421	0.037540555	0.125,0.119,0.079	0.991,0.984,0.977	0.991,0.984,0.977	-0.166
SE	LSM7	CNG00000100423	chr8	+	10567906	10568030	10568030	10568030	10568030	10568030	193,257,227	689,612,612	821,870,857	18,42,39	108	86	0.000169421	0.038035554	0.728,0.752,0.76	0.862,0.893,0.863	0.862,0.893,0.863	-0.116
SE	ANKRD22	CNG00000100423	chr8	+	10568022	10568022	10568022	10568022	10568022	10568022	193,257,227	234,260,240	241,267,252	35,33,33	225	86	0.000169421	0.038035554	0.728,0.752,0.76	0.867,0.777,0.71	0.867,0.777,0.71	0.156
SE	SCN9A1	CNG00000101613	chr10	+	76716181	76716181	76716181	76716181	76716181	76716181	187,188	188,187,139	57,110,121	105,121,93	143	70	0.000169421	0.038342057	0.110,0.152,0.144	0.237,0.305,0.242	0.237,0.305,0.242	-0.122
SE	ATAD1A	CNG00000101613	chr10	+	76716181	76716181	76716181	76716181	76716181	76716181	187,188	1629,1627,1587	81,81,81	1791,1787,1662	1,1,1	27	0.000169421	0.038342057	0.110,0.152,0.144	0.564,0.893,0.917	0.564,0.893,0.917	-0.353
SE	SFC1XX	CNG00000104193	chr12	+	42655256	42655256	42655256	42655256	42655256	42655256	179,150,150	474,427,417	324,309,356	365,363,312	268	86	0.000169421	0.038342057	0.110,0.152,0.144	0.912,0.908,0.897	0.912,0.908,0.897	-0.090
SE	ADGRD1B-C	CNG00000107227	chr16	+	51227727	51227727	51227727	51227727	51227727	51227727	71,71,71	71,84,57	26,35,35	19,27,14	84	86	0.000169421	0.038342057	0.110,0.152,0.144	0.752,0.752,0.748	0.752,0.752,0.748	-0.153
SE	TMM194	CNG00000215505	chr12	+	15554565	15554565	15554565	15554565	15554565	15554565	535,519,499	15,9,10	1431,1025,1492	65,37,38	328	86	0.000169421	0.038342057	0.771,0.832,0.822	0.934,0.937,0.901	0.934,0.937,0.901	-0.116
SE	ARHGAP8	CNG00000219158	chr22	+	43247782	43247782	43247782	43247782	43247782	43247782	1145,1145,1145	1145,1145,1145	846,848,847	1145,1145,1145	1	1	0.000169421	0.038342057	0.217,0.375,0.302	0.848,0.912,0.849	0.848,0.912,0.849	-0.216
SE	DDX5L	CNG00000219158	chr22	+	43247782	43247782	43247782	43247782	43247782	43247782	117,101,116	11,8,9	117,101,116	31,38,32	177	86	0.000169421	0.038342057	0.217,0.375,0.302	0.182,0.228,0.201	0.182,0.228,0.201	-0.216
SE	PPP 2R5C-2	CNG00000224679	chr7	+	148367810	148367810	148367810	148367810	148367810	148367810	54,58,62	54,58,62	179,179,179	31,31,31	179	86	0.000169421	0.038342057	0.217,0.375,0.302	0.364,0.347,0.337	0.364,0.347,0.337	-0.241

Type	Gene Symbol	Ensemb ID	chr	Strand	riExonStart_0base	riExonEnd	upstreamExonStart	upstreamExonEnd	downstreamExonStart	downstreamExonEnd	inclusionCount_G0409.cc	SkippingCount_G0409.cc	inclusionCount_PC-30	SkippingCount_PC-30	InclusionFormLength	SkippingFormLength	Pvalue	FDR	inclusionLevel-G0409.cc	inclusionLevel-PC-30	inclusionDifference (G0409.cc - PC-30)
SE	CARM1	CNG00000007369	chr19	+	16506359	16506541	16506359	16506972	16506412	16506545	4659,4615,4628	28,21,29	2,0,0	0,0,0	0	0	0	0	1.0,0.996,0.999	0.822,0.735,0.836	0.822,0.735,0.836
SE	CYNE	CNG00000008968	chr6	+	151783182	151783182	151783182	151783182	151783182	151783182	348,330,348	93,70,91	0,0,0	0,0,0	1169	86	0	0	1.0,0.992,0.999	0.874,0.914,0.907	0.874,0.914,0.907
SE	FLCN	CNG00000009292	chr17	+	2149838527	2149838664	2149836327	2149836429	2149838412	2149838527	1125,1132,1001	84,486,545	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.81,0.794,0.828	0.122,0.113,0.119
SE	ZNF292	CNG00000009292	chr17	+	39675051	39675051	39675051	39675051	39674917	39675051	2,2,2	1,1,1	1,1,1	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	ERBB2	CNG00000009292	chr17	+	39674968	39675051	39674968	39675051	39674917	39675051	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	ERBB2	CNG00000009292	chr17	+	39687914	39687914	39687914	39687914	39687914	39687914	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	TOR1AIP1	CNG00000010368	chr1	+	150351138	150351138	150351138	150351138	150351138	150351138	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	TMC4	CNG00000012638	chr9	+	114000000	114000000	114000000	114000000	113999900	114000000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	SYCE1	CNG00000013544	chr1	+	154600000	154600000	154600000	154600000	154599900	154600000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	SYCE1L	CNG00000013544	chr1	+	154600000	154600000	154600000	154600000	154599900	154600000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	ZNF658	CNG00000014138	chr2	+	73000000	73000000	73000000	73000000	72999900	73000000	1,1,1	0,0,0	0,0,0	0,0,0	1,1,1	86	0	0	0.122,0.113,0.119	0.872,0.862,0.872	0.872,0.862,0.872
SE	ZNF185	CNG00000015339	chr12	+	43919349	43919349	43919349	43919349	43919349	43919349	312,276,292	2,2,2	181,199,178	21,9,11	50	26	0.000169421	0.027579689	0.068,0.03,0.065	0.838,0.912,0.87	0.838,0.912,0.87
SE	ZC3H7A	CNG00000016130	chr9	+	116483691	116483691	116483691	116483691	116483691	116483691	41,41,41	1,1,1	38,38,38	28,28,28	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962
SE	SLC25A39	CNG00000016130	chr9	+	116483691	116483691	116483691	116483691	116483691	116483691	31,31,31	47,52,51	48,55,51	34	60	0.000169421	0.029451605	0.164,0.529,0.432	0.677,0.793,0.738	0.677,0.793,0.738
SE	DNTT	CNG00000019265	chr10	+	94239889	94239889	94239889	94239889	94239889	94239889	41,41,41	249,239,246	41,41,41	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962
SE	SMG1P4	CNG00000019265	chr10	+	94239889	94239889	94239889	94239889	94239889	94239889	41,41,41	72,63,65	186,211,197	72,63,65	231	86	0.000169421	0.031939223	0.812,0.937,0.864	0.752,0.783,0.811	0.752,0.783,0.811
SE	ZNF492	CNG00000021645	chr11	+	118620977	118620977	118620977	118620977	118620977	118620977	31,31,31	37,37,37	31,31,31	37,37,37	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962
SE	ZFP1	CNG00000022187	chr12	+	124810147	124810147	124810147	124810147	124810147	124810147	31,31,31	248,239,246	31,31,31	248,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962
SE	SCORE	CNG00000024698	chr19	+	12495958	12495958	12495958	12495958	12495958	12495958	41,41,41	249,239,246	41,41,41	249,239,246	3	3	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962
SE	ACTN4	CNG00000025147	chr19	+	39232933	39232933	39232933	39232933	39232933	39232933	31,31,31	83,90,91	126,130,129	108	86	0.000169421	0.029896861	0.092,0.092,0.092	0.962,0.962,0.962	0.962,0.962,0.962
SE	CNN2	CNG00000026767	chr11	+	65223649	65223649	65223649	65223649	65223649	65223649

61	C9orf89	ENSG00000061233	chr9	+	95873869	95874671	95873869	95874669	95874671	468,604,454	96,47,21	145,170,162	8,8,6	1547	65	0.150-05	0.0064	0.226,0.275,0.335	0.432,0.472,0.531	-0.252
62	GUCY1	ENSG00000007292	chr10	+	277200	278801	277200	278802	278801	480,606,462	418,35	182,202,228	22,20,21	1565	63	0.120-05	0.0064	0.721,0.771,0.832	0.119,0.166,0.219	0.296
63	ZNF365	ENSG00000129993	chr10	-	62756828	62788994	62756828	62788994	62788994	96,96,96	96,96,96	96,96,96	2,0,0,0	173	86	0.140-05	0.0064	0.163,0.214,0.271	0.417,0.459,0.519	0.169
64	PMS1	ENSG00000183765	chr10	+	78328819	78328734	78328819	78329572	78328734	456,458,581	68,79,82	312,360,320	27,30,19	671	86	0.430-05	0.0064	0.262,0.312,0.365	0.491,0.532,0.587	-0.169
65	ZEB1	ENSG00000085567	chr10	-	31865483	31865483	31865483	31865483	31865483	96,96,96	96,96,96	96,96,96	0,0,0,0	1000	86	0.000-05	0.0064	0.118,0.167,0.224	0.367,0.412,0.472	0.167
66	KCNQ1	ENSG00000053900	chr11	-	132297519	132298629	132295519	132297519	132298519	36,64,19	22,22,22	5,7,1	24,58,17	649	53	0.230-05	0.0067	0.238,0.293,0.338	0.637,0.691,0.686	0.142
67	ARHGEF17	ENSG00000141613	chr11	+	61811000	61811000	61811000	61811000	61811000	96,96,96	96,96,96	96,96,96	2,0,0,0	1000	86	0.000-05	0.0069	0.147,0.196,0.252	0.398,0.441,0.502	0.147
68	ORC6L1	ENSG00000138798	chr11	-	125197607	125198076	125197607	125197728	125197728	8,27,2	5,15,1	10,17,1	1,1,1,1	559	86	0.000-05	0.0070	0.182,0.230,0.13	0.767,0.810,0.797	0.177
69	SERTAD2B	ENSG00000149503	chr17	+	12814760	12817727	12814760	12817135	12817727	303,400,248	200,215,223	236,280,284	436,427,424	277	86	0.000-05	0.0086	0.262,0.302,0.347	0.142,0.168,0.17	0.119
70	TRA2A	ENSG00000136450	chr7	+	22942335	22942351	22942335	22942338	22942351	96,96,96	79,90,96	79,90,84	97,90,95	352	86	0.000-05	0.0101	0.408,0.452,0.498	0.257,0.291,0.372	0.192
71	SKIV2L	ENSG00000213293	chr6	+	31832480	31832480	31832480	31832480	31832480	302,603,592	27,28,17	383,372,1008	9,9,5,4	526	86	0.000-05	0.0103	0.825,0.775,0.851	0.547,0.591,0.865	-0.131
72	CDS2	ENSG00000152651	chr16	+	70542308	70542351	70542308	70542352	70542351	539,624,251	379,304,251	177,349,199	39,14,45	865	52	0.000-05	0.0111	0.12,0.166,0.07	0.604,0.651,0.653	0.076
73	ACAN1	ENSG00000080271	chr5	-	88167316	88168191	88167316	88168093	88168191	96,96,96	65,29,29	1214,1193,1212	131,121,119	1041	49	0.000-05	0.0127	0.614,0.647,0.685	0.41,0.44,0.47	0.18
74	ROBO2	ENSG00000185156	chr3	-	77458603	77458603	77458603	77458603	77458603	96,96,96	49,62,85	64,63,63,62	76,75,97	183	52	0.000-05	0.0134	0.148,0.194,0.236	0.681,0.747,0.726	0.345
75	CDC13A	ENSG00000091129	chr1	-	1615561	1616091	1615561	1615785	1616088	96,96,96	41,19,27	93,65,54	5,5,5	277	86	0.000-05	0.0134	0.177,0.862,0.116	1.0,0.608,1.0	-0.728
76	SNCB	ENSG00000070327	chr5	+	176053198	176053762	176053198	176053737	176053762	0,2,2	0,0,10	7,8,6	0,1,1	269	86	0.000-05	0.0143	0.0,0.099,0.08	1.0,0.556,0.889	-0.45
77	SMARCD2	ENSG00000092201	chr17	+	15093710	15093710	15093710	15093768	15093710	326,287,218	49,49,46	122,181,161	43,41,31	1041	86	0.000-05	0.0148	0.353,0.330,0.381	0.134,0.153,0.19	0.148
78	TMEM120A	ENSG00000188477	chr7	+	75627600	75627600	75627600	75627684	75627600	96,87,85	102,108,125	112,108,116	97,89,70	585	86	0.000-05	0.0148	0.314,0.341,0.373	0.312,0.325,0.39	-0.154
79	SLC25	ENSG00000017858	chr15	+	85756055	85757594	85756055	85756329	85757297	455,758	711,550,547	31,48,55	278,487,542	96,197,108	86	0.000-05	0.0173	0.514,0.550,0.577	0.350,0.392,0.317	0.196
80	CherPsb	ENSG00000166206	chr1	+	26358040	26357992	26358040	26358040	26357992	26357752	1681,1849,1581	27,34,11	393,585,563	13,28,1	1579	86	0.000-05	0.0200	0.752,0.756,0.816	0.586,0.595,0.647	0.209
81	ZNF496	ENSG00000008438	chr19	+	18991000	18991386	18991000	18991256	18991386	18991385	87,98,98	18,47,47	36,11,97	20,21,19	263	75	0.000-05	0.0286	0.1,0.1,0.273	0.151,0.171,0.199	-0.214
82	MYO1E	ENSG00000137724	chr15	+	170757026	170758665	170757026	170758665	170758665	454,256,224	20,15,7	70,62,47	12,17,3	910	86	0.000-05	0.0297	0.671,0.617,0.702	0.053,0.013,0.077	0.283
83	FICD1	ENSG00000101511	chr22	+	38469779	38470458	38469779	38469830	38470311	38470458	144,141,129	75,52,45	90,110,109	115,124,106	512	66	0.000-05	0.0299	0.141,0.189,0.137	0.261,0.07,0.081	0.105
84	BIRC2	ENSG00000113211	chr11	+	62566010	62567958	62566010	62566047	62567958	62567958	2214,1791,1573	160,98,103	1132,1118,1118	1132,1151,1149	1817	85	0.000-05	0.0326	0.21,0.232,0.2	0.113,0.117,0.113	0.105
85	AHR0CR	ENSG00000197670	chr10	+	105007347	105007962	105007347	105007458	105007914	105007962	211,150,192	72,67,58	178,206,216	162,203,145	683	66	0.000-05	0.0375	0.169,0.163,0.232	0.09,0.085,0.119	0.105
86	DUPTA	ENSG00000197592	chr12	+	27883850	27883148	27883850	27883968	27883148	27883148	367,351,360	32,19,15	203,215,161	87,32,38	649	86	0.000-05	0.0377	0.677,0.752,0.761	0.364,0.446,0.536	0.249
87	DKKBP-PLA2G6B	ENSG00000165895	chr14	+	32128672	32129138	32128672	32128729	32128938	32129138	87,98,76	67,69,83	27,50,40	93,81,77	285	70	0.000-05	0.0384	0.232,0.263,0.188	0.067,0.132,0.113	0.116
88	SCAT2	ENSG00000100897	chr14	+	24584350	24584958	24584350	24584625	24584753	24584958	751,710,770	4,15,6	661,742,527	16,21,15	140	4	0.000-05	0.0388	0.814,0.714,0.787	0.403,0.509,0.542	0.283
89	CCNK	ENSG00000090861	chr6	+	99967102	99968712	99967102	99967208	99968543	99968712	141,119,74	7,4,2	28,42,44	12,5,5	1407	86	0.0010	0.0465	0.552,0.645,0.643	0.125,0.12,0	-0.272
90	MAGI2GT	ENSG00000103166	chr9	+	68841680	68842440	68841680	68842123	68842433	68842440	2318,2147,2088	1326,1228,1179	255,214,227	203,208,145	262	86	0.0011	0.0492	0.349,0.363,0.332	0.247,0.222,0.237	0.113

Type	Gene Symbol	Ensembl ID	chr	Strand	longEsonStart_0Base	longEsonEnd	shortEsonStart	shortEsonEnd	flankingEsonStart	flankingEsonEnd	InclusionCount_GSM89:U	SkippingCount_GSM89:U	InclusionCount_PC:W	SkippingCount_PC:W	InclusionFormLength	SkippingFormLength	Pirahue	FOX	Inclusionlevel-GSM89:U	Inclusionlevel-PC:W	InclusionDifference (GSM89:U - PC:W)
Sas	FFLAB	ENSG00000231756	chr7	+	99954372	99954561	99954372	99954561	99955982	99955989	96,47,32	0,2,1	99,66,29	71,70,54	134	86	0	0	1.62,0.982,0.964	0.802,0.777,0.109	0.858
Sas	ADAM33	ENSG00000149527	chr1	-	153016379	153016559	153016379	153016559	153016730	153016845	208,167,116	162,108,146	71,86,78	978,1098,981	193	65	0	0	0.592,0.342,0.211	0.024,0.036,0.026	0.26
Sas	SMARCB1	ENSG00000099956	chr22	-	24118065	24118065	24118065	24118236	24118236	24118875	360,749,793	272,242,275	151,625,560	718,714,706	106	86	0	0	0.72,0.712,0.7	0.416,0.466,0.431	0.288
Sas	FAM110B	ENSG00000186868	chr8	-	132015498	132015700	132015498	132015595	132015746	132015768	138,139,155	129,156,132	22,18,26	136,146,116	177	86	0	0	0.164,0.287,0.362	0.092,0.057,0.098	0.249
Sas	SMARCC2	ENSG00000139613	chr12	-	56158836	56158915	56158836	56158915	56157528	56157549	1681,1511,1319	127,138,94	1655,1981,1775	21,18,21	408	77	0	0	0.684,0.681,0.647	0.932,0.866,0.931	-0.237
Sas	CTNND1	ENSG00000198561	chr11	+	57529368	57529395	57529368	57529528	57564608	57566427	119,92,117	621,576,625	121,196,156	9,7,9	152	86	0	0	0.095,0.083,0.096	0.884,0.942,0.907	-0.82
Sas	CTNND1	ENSG00000198561	chr11	+	57529368	57529395	57529368	57529528	57568836	57569135	84,92,89	368,98,109	131,207,161	19,18,29	152	86	0	0	0.904,0.773,0.726	0.796,0.867,0.791	0.116
Sas	PNGII	ENSG00000224624	chr6	-	99851704	99852678	99852678	99852678	99856016	99856086	544,474,468	32,42,22	299,316,351	105,79,103	846	86	1.27E-14	5.84E-12	0.633,0.519,0.633	0.224,0.288,0.257	0.35
Sas	SRSF6/C22	ENSG00000075856	chr7	-	75326055	75327759	75326055	75326076	75513368	75513505	112,61,14	7,2	39,58,55	36,31,28	795	83	9.13E-14	3.58E-11	0.852,0.912,0.146	0.061,0.061,0.092	0.827
Sas	PIL9B	ENSG00000121756	chr7	+	99954372	99954506	99954372	99954561	99955982	99955989	46,38,26	155,116,112	117,135,113	53,117,74	120	76	3.09E-12	1.14E-09	0.158,0.174,0.128	0.583,0.805,0.892	-0.34
Sas	SRPP40	ENSG00000206511	chr2	-	99172015	99172275	99172015	99172156	99175025	99175058	200,159,146	16,18,11	385,435,357	1,3,1	129	26	7.21E-12	2.62E-08	0.752,0.727,0.662	0.007,0.068,0.007	-0.304
Sas	SLC9B1	ENSG00000086758	chr5	-	53570024	53570024	53570846	53570924	53569503	53569503	786,812,670	366,345,285	1276,1358,1312	242,233,229	114	76	4.64E-11	1.43E-08	0.588,0.611,0.61	0.779,0.792,0.793	-0.185
Sas	C21orf2	ENSG00000160226	chr21	+	45750705	45750799	45750705	45750799	45756073	45756103	69,50,56	69,50,56	235,235,164	92,126,71	612	86	3.09E-08	8.76E-07	0.118,0.098,0.189	0.301,0.257,0.301	-0.179
Sas	CDPD2	ENSG00000141030	chr17	-	17176025	17176322	17174322	17174322	17179108	17179159	73,52,50	2,0,0	27,36,30	36,12,9	210	86	1.70E-08	4.67E-06	0.637,1.0,1.0	0.469,0.551,0.577	0.467
Sas	FUBP	ENSG00000136688	chr17	-	58127583	58127656	58127583	58127623	58130376	58130879	413,640,580	42,50,25	2007,2570,2247	302,297,380	93	52	5.51E-08	1.36E-05	0.876,0.863,0.939	0.718,0.728,0.743	0.15
Sas	DMP2	ENSG00000126576	chr15	+	55660885	55660885	55660885	55660885	55667963	55667965	656,392,649	200,162,144	497,490,467	457,289,367	98	36	1.46E-07	3.38E-05	0.656,0.472,0.534	0.285,0.356,0.399	0.198
Sas	BRD42	ENSG00000137592	chr8	+	7181356	7181537	7181356	7181537	7182157	7182172	8,3,2	37,31,8	28,17,7	77,63,31	122	86	1.95E-07	4.22E-05	0.055,0.052,0.057	0.269,0.268,0.587	-0.588
Sas	PARP2	ENSG00000129484	chr14	+	20801890	20801890	20801890	20801890	20801952	20801953	389,396,286	235,218,197	246,240,277	373,260,355	96	64	3.58E-07	7.34E-05	0.526,0.473,0.492	0.395,0.308,0.342	0.179
Sas	ERGIC1	ENSG00000085978	chr2	+	234181611	234181611	234181611	234181698	234181611	234181611	271,266,239	113,119,101	102,171,114	152,175,114	791	80	1.17E-06	0.0002	0.195,0.179,0.193	0.064,0.07,0.086	0.116
Sas	ARSH	ENSG00000164662	chr2	+	48711668	48711668	48711668	48711822	48714041	48714161	2137,1651,1952	125,70,110	2845,2615,2550	53,15,28	367	85	1.54E-06	0.0003	0.798,0.86,0.804	0.635,0.923,0.855	-0.114
Sas	SLC25A1	ENSG00000157765	chr22	+	21889910	21890274	21890910	21890274	21890910	21890910	585,554,621	0,0,0	805,857,719	41,21,21	232	86	1.69E-05	0.0025	1,0,1,0,1,0	0.675,0.913,0.846	0.1
Sas	MAPK12	ENSG00000188130	chr6	+	27268463	27268463	27268463	27269120	27268463	27268625	83,24,30	239,261,163	239,261,163	116,109,94	124	86	2.51E-05	0.0042	0.631,0.893,0.856	0.673,0.845,0.715	0.155
Sas	GAN	ENSG00000171288	chr19	+	38076569	38076689	38076569	38076689	38078353	38078931	169,114,119	81,92,34	267,215,228	83,91,76	213	63	6.18E-05	0.0066	0.237,0.218,0.229	0.802,0.823,0.896	-0.569
Sas	ZC3H13X	ENSG00000180675	chr11	+	20076432	20076432	20076432	20076623	20079032	20079076	418,416,589	258,206,214	205,205,207	238,239,240	138	47	5.03E-05	0.0077	0.356,0.409,0.482	0.442,0.467,0.224	0.144
Sas	RUVC	ENSG00000012983	chr10	+	76675582	76675582	76675582	76675739	76675739	76675580	341,735,575	140,92,139	816,1105,1126	347,295,321	380	83	0.0002	0.0104	0.585,0.685,0.597	0.446,0.496,0.438	0.2
Sas	BTAF1	ENSG00000085664	chr10	+	92718821	92718939	92718821	92718939	92719541	92719637	86,54,55	68,68,55	37,42,32	135,113,130	107	83	0.0002	0.0124	0.604,0.358,0.357	0.119,0.162,0.132	0.238
Sas	KATNA	ENSG00000166425	chr19	+	7673155	7673269	7673155	7673269	7673703	7673735	1331,960,1917	132,105,182	3716,4350,2114	31,49,18	351	49	0.0003	0.0175	0.617,0.642,0.543	0.703,0.727,0.766	-0.163
Sas	FAM149B1	ENSG00000161617	chr11	+	113722233	113722693	113722693	113722693	113721302	113721385	22,19,10	5,1,11	5,3,3	17,18,10	312	76	0.0003	0.0461	0.328,0.263,0.169	0.014,0.036,0.068	0.213

Type	Gene Symbol	Ensembl ID	chr	Strand	longEsonStart_0Base	longEsonEnd	shortEsonStart	shortEsonEnd	flankingEsonStart	flankingEsonEnd	InclusionCount_GSM89:U	SkippingCount_GSM89:U	InclusionCount_PC:W	SkippingCount_PC:W	InclusionFormLength	SkippingFormLength	Pirahue	FOX	Inclusionlevel-GSM89:U	Inclusionlevel-PC:W	InclusionDifference (GSM89:U - PC:W)
Sas	CERS6	ENSG00000157819	chr6	+	19056205	19056412	19056412	19056412	19057072	829,769,816	0,3,1	707,780,704	58,216,10	639	86	0	0	1.12,0.962,0.991	0.843,0.876,0.987	0.107
Sas	SRSF4	ENSG00000116216	chr6	+	79799958	79799961	79799961	79799961	79799961	79797062	43,35,28	637,1035,1014	536,585,682	1914,2118,1972	18	15	0	0	0.01,0.083,0.007	0.183,0.187,0.169	-0.173
Sas	FUS/RH56	ENSG00000089280	chr16	-	20420616	20420616	20420616	20420616	20420616	20420615	215,156,139	77,62,19	248,281,348	15,11,11	138	86	0	0	0.616,0.687,0.816	0.843,0.919,0.941	-0.407
Sas	PLCD4	ENSG00000131556	chr2	-	219898927	219898964	219898927	219898964	219894958	219897035	1035,1007,1072	768,663,701	534,539,585	14,15,12	572	86	0	0	0.611,0.659,0.692	0.952,0.941,0.979	-0.443
Sas	RPN2	ENSG00000035387	chr3	+	149682600	149682673	149682600	149682673	149686314	149686317	1664,1576,1603	710,545,654	1872,1718,1592	1818,1736,1661	390	86	0	0	0.666,0.691,0.652	0.315,0.317,0.32	0.342
Sas	CDPD2	ENSG00000141030	chr17	-	17171148	17171159	17171159	17171159	17174322	17174322	84,63,77	4,1,5	68,57,67	60,45,80	167	86	0	0	0.891,0.907,0.893	0.399,0.426,0.294	0.594
Sas	FAM122B	ENSG00000171346	chr9	+	139800396	139800413	139800396	139800413	139802397	139802397	2039,1936,3679	68,89,86	3000,2949,3670	24,23,25	1003	86	2.20E-05	0.379-12	0.752,0.827,0.826	0.913,0.917,0.896	-0.206
Sas	GMDT	ENSG00000136433	chr13	+	76490875	76490875	76490968	76490875	76490861	76490921	316,294,334	1061,1003,1081	241,235,276	231,214,272	160	86	7.23E-15	4.72E-12	0.168,0.113,0.146	0.193,0.287,0.351	-0.188
Sas	PSMP	ENSG00000197796	chr10	+	75585764	75585764	75585764	75585764	75585935	75585935	479,258,285	2084,2057,2081	77,68,64	2098,2016,1965	92	50	3.78E-14	1.16E-11	0.186,0.095,0.189	0.035,0.026,0.03	0.126
Sas	CDPD2	ENSG00000141030	chr17	-	17171148	17171159	17171159	17171159	17174322	17174322	153,119,127	464,387,375	76,70,77	1177,1459,1420	104	63	1.94E-13	1.01E-10	0.12,0.125,0.123	0.02,0.019,0.019	0.104
Sas	GFI1/1	ENSG00000161405	chr1	+	92236227	92237257	92236227	92237257	92240586	92240586	1073,814,1273	671,617,601	641,1118,1091	844,784,798	986	68	6.78E-13	1.51E-10	0.614,0.662,0.618	0.503,0.526,0.508	0.105
Sas	GPAA1	ENSG00000197858	chr8	+	145145922	145145922	145145922	145145922	145149315	145149315	5241,4667,4713	8,7,1	6412,4709,4149	35,40,52	628	86	8.35E-10	3.59E-07	0.989,0.988,0.992	0.895,0.876,0.901	0.099
Sas	DNM1L	ENSG00000087470	chr1	-	153101052	153101052	153101052	153101052	153100755	153100755	28,25,22	21,14,13	9,6,7	109,99,119	731	86	8.64E-09	1.45E-06	0.568,0.576,0.61	0.009,0.007,0.007	0.561
Sas	ACSL4	ENSG00000068366	chr5	+	108926364	108926495	108926364	108926495	108939372	108939425	147,158,142	30,41,27	64,56,74	44,52,50	325	86	3.62E-08	1.61E-05	0.659,0.552,0.658	0.172,0.152,0.175	0.248
Sas	GIP	ENSG00000151611	chr9	+	96408604	96408677	96408677	96408677	96408677	96408677	191,156,143	9,9,7	30,60,69	16,23,20	1351	86	7.68E-07	0.0003	0.842,0.724,0.67	0.243,0.242,0.17	0.499
Sas	ACSL4	ENSG00000068366	chr5	+	108926364	108926364	108926364	108926495	108939372	108939425	91,94,103	30,41,27	32,37,42	44,52,50	212	86	6.19E-07	0.0002	0.407,0.332,0.467	0.172,0.152,0.154	0.249
Sas	SNTB	ENSG00000184363	chr22	+	31452561	31452561	31452561	31452561	31455155	31455155	561,330,541	44,40,56	51,35,28	57,30,52	102	86	1.08E-06	0.0004	0.56,0.275,0.15	0.558,0.356,0.1	0.249
Sas	SPG20.2P	ENSG00000225993	chr6	-	90041592	90042744	90042649	90042744	90042649	90042649	91,53,61	21,42,24	14,19,18	53,11,12	588	62	1.72E-06	0.0011	0.198,0.113,0.03	0.015,0.033,0.021	0.118
Sas	AUPP	ENSG00000171607	chr2	+	74756429	74756429	74756429	74756429	74756756	74756756	1843,1566,1562	45,16,14	2584,2191,1813	87,87,90	249	86	7.41E-06	0.0019	0.973,0.963,0.97	0.877,0.882,0.89	0.087
Sas	LBX2OS	ENSG00000192932	chr8	+	103747641	103748601	103747641	103747793	103748748	103749105	1036,1030,983	263,179,165	959,1142,958	170,719,640	285	86	7.14E-06	0.0019	0.454,0.453,0.487	0.214,0.128,0.215	0.132
Sas	SNPH	ENSG00000183398	chr2	+	1276419	1277065	1276966	1277065	1277297	1277397	204,151,112	118,73,85	28,44,59	68,91,71	621	86	1.13E-05	0.0027	0.104,0.163,0.101	0.054,0.067,0.105	0.124
Sas	DDP2	ENSG00000136011	chr8	+	131222295	131222465	131222828	131222465	131221845	131221916	113,2,116	13,0,19	149,143,172	60,50,56	114	83	1.29E-05	0.0054	0.889,0.953,0.856	0.647,0.706,0.694	0.197
Sas	KCNQ3	ENSG00000184156	chr2	-	135778842	135779066	135779066	135779066	135798396	135798396	239,208,221	25,27,24	205,243,237	8,8,9	762	86	0.0001	0.0107	0.522,0.469,0.51	0.797,0.779,0.77	-0.261
Sas	CDF2	ENSG00000181671	chr1	+	110666787	110666812	110666681	110666812	110666968	110666968	6376,570,782	5,4,4	91,132,102	16,2,10	904	86	0.0001	0.0207	0.901,0.907,0.946	0.741,0.833,0.675	0.182
Sas	PPIB	ENSG00000166794	chr12	+	120662600	120662620	120662600	120662679	120669501	120669501	4589,3840,3950	5226,4649,4650	2953,3480,3338	1994,2395,2211	216	86	0.0001	0.0258	0.359,0.337,0.353	0.371,0.387,0.376	-0.018
Sas	GIPR2	ENSG00000064393	chr7	-	128290831	128290928	128290831	128290928	128305146	128305308	1845,1685,1720	386,407,362	1041,1212,1131	206,489,398	160	86	0.0001	0.0295	0.761,0.691,0.759	0.586,0.571,0.668	0.130