BOR-Papers in Press. Published as DOI: 10.1095/biolreprod.113.110403

Supplemental Table S1. List of genes (including 2kb 5' and 3' to the gene) with a greater amount (measured in base pairs) of HEE DHS than all five background cell types DHS combined.

Gene Name	Gene RefSeq	Gene Chrom	Gene Strand	Start Minus 2kbp	Stop Plus 2kbp	Epid34 DHS coverage(bp)	Background DHS coverage(bp)	Expression Value
SPP1	NM_001040060	chr4	+	88894800	88906564	1295	684	15.31562
MMP7	NM_002423	chr11	-	102389237	102403479	760	579	15.10625333
EFEMP1	NM_004105	chr2	-	56091100	56152357	2038	2036	14.78808667
PABPC3	NM_030979	chr13	+	25668274	25674705	524	244	14.67791
PON2	NM_001018161	chr7	-	95032172	95066385	1421	1284	14.43800333
NBPF9	NM_001037675	chr1	+	144612957	144830811	1178	1106	14.43445
HNRNPC	NM_031314	chr14	-	21675294	21739639	1391	1085	14.39878667
CFI	NM_000204	chr4	-	110659846	110725336	577	303	14.39341333
APEH	NM_001640	chr3	+	49709433	49722935	2555	2521	14.37357
SLC34A2	NM_006424	chr4	+	25655433	25682369	3887	2622	14.28186333
SDCBP	NM_005625	chr8	+	59463726	59497420	2020	1788	14.26345333
CNDP2	NM_018235	chr18	+	72161498	72192690	4000	3578	14.15377667
LUM	NM_002345	chr12	-	91495230	91507543	675	0	14.14639
CLDND1	NM_019895	chr3	-	98232315	98243911	1306	1266	14.01781667
MGST3	NM_004528	chr1	+	165598448	165626856	2376	2300	14.01042333
CXCL5	NM_002994	chr4	-	74859357	74866417	752	650	14.00936667
PSMB1	NM_002793	chr6	-	170842202	170864418	1652	1429	14.00592
SERPINA1	NM_001127707	chr14	-	94841082	94859030	2477	2242	13.96405
DHX9	NM_001357	chr1	+	182806437	182859118	1849	1740	13.95021
PCSK5	NM_006200	chr9	+	78503558	78810347	8493	5287	13.94123667
SLPI	NM_003064	chr20	-	43878877	43885207	896	542	13.93328333

IDH1	NM_005896	chr2	-	209098951	209121807	1993	1831	13.93305333
MGST1	NM_145792	chr12	+	16498074	16519345	1735	1363	13.92062667
RBMX	NM_002139	chrX	-	135953604	135964940	1022	936	13.89907667
PAM	NM_138822	chr5	+	102199525	102368809	2190	1417	13.89734667
FXR1	NM_005087	chr3	+	180628232	180702540	2083	1390	13.86024667
MECOM	NM_005241	chr3	-	168799285	168866094	3374	2761	13.84218667
TFPI2	NM_006528	chr7	-	93513743	93522066	1357	1086	13.84152
COX7C	NM_001867	chr5	+	85911782	85918584	1027	949	13.82769
RRAGA	NM_006570	chr9	+	19047370	19053022	1298	1222	13.78594667
NUS1	NM_138459	chr6	+	117994615	118033887	1250	1250	13.77609667
ESD	NM_001984	chr13	-	47343389	47373368	1562	1192	13.69275667
PTPRM	NM_002845	chr18	+	7565312	8408860	18643	18642	13.65163667
CCNG1	NM_199246	chr5	+	162862575	162874023	1348	1149	13.63533667
PAPSS1	NM_005443	chr4	-	108532820	108643420	3243	3236	13.62608333
STRAP	NM_007178	chr12	+	16033286	16058411	1119	1088	13.59099333
ITGB8	NM_002214	chr7	+	20368723	20457383	4414	3247	13.58012
BUB3	NM_004725	chr10	+	124911758	124926887	1634	1503	13.56413667
ATIC	NM_004044	chr2	+	216174677	216216497	1418	1088	13.55137
DSG2	NM_001943	chr18	+	29076025	29130815	3267	2854	13.53777333
FAN1	NM_014967	chr15	+	31194074	31237311	2485	1766	13.53539333
IL8	NM_000584	chr4	+	74604273	74611434	360	348	13.52494333
SC4MOL	NM_006745	chr4	+	166246816	166266226	1513	1427	13.50223667
PLRG1	NM_002669	chr4	-	155455660	155473524	1177	903	13.44799
CTSC	NM_148170	chr11	-	88051979	88072942	1773	1707	13.41631667

LMBRD1	NM_018368	chr6	-	70383639	70509050	2140	1779	13.40866667
PPP2CB	NM_001009552	chr8	-	30641124	30672353	2080	1991	13.39413667
GSS	NM_000178	chr20	-	33514234	33545602	2593	2411	13.38384
DCDC2	NM_016356	chr6	-	24169981	24360281	6436	4101	13.32556333
ARL2BP	NM_012106	chr16	+	57277036	57289546	1851	1773	13.3255
UGT1A1	NM_000463	chr2	+	234666917	234683946	166	156	13.31664667
PSMA4	NM_002789	chr15	+	78830745	78843564	1069	966	13.31300333
GALNT14	NM_024572	chr2	-	31131331	31363572	11055	10217	13.29403
STARD3NL	NM_032016	chr7	+	38215931	38272271	3845	2466	13.28636667
RBP1	NM_002899	chr3	-	139234274	139260672	3553	2789	13.26728667
CA2	NM_000067	chr8	+	86374129	86395722	1706	1438	13.23236
SNURF	NM_022804	chr15	+	25198068	25215977	1386	1285	13.23075
TOM1L1	NM_005486	chr17	+	52976050	53041329	2983	2824	13.23029333
MPZL2	NM_144765	chr11	-	118125626	118137252	1279	581	13.22402
CXCL1	NM_001511	chr4	+	74733107	74738956	2082	1836	13.21966333
LYPD1	NM_144586	chr2	-	133400335	133430482	3353	2802	13.21647
YTHDC1	NM_133370	chr4	-	69174103	69217825	1339	1084	13.18628333
SCEL	NM_144777	chr13	+	78107807	78221399	1602	1002	13.17517
MMADHC	NM_015702	chr2	-	150424145	150446331	921	917	13.17244667
SRP54	NM_003136	chr14	+	35450102	35500774	1126	1119	13.16236333
TPR	NM_003292	chr1	-	186278784	186346458	1915	1652	13.15271333
CDH2	NM_001792	chr18	-	25528928	25759446	8356	5038	13.15203667
PICALM	NM_007166	chr11	-	85666483	85782109	2475	2389	13.14395333
API5	NM_006595	chr11	+	43331503	43368081	1898	1324	13.13356667

GPR39	NM_001508	chr2	+	133172145	133406170	8279	5673	13.12276333
NDUFA12	NM_018838	chr12	-	95363108	95399512	2403	1716	13.11502
SUCLA2	NM_003850	chr13	-	48514789	48577463	1410	1275	13.09896667
ADAMTS1	NM_006988	chr21	-	28206604	28219729	5127	4382	13.03184333
GOLM1	NM_177937	chr9	-	88639056	88717117	4157	4065	13.02910333
JKAMP	NM_016475	chr14	+	59949159	59974082	1929	1472	13.02374
TSC22D1	NM_183422	chr13	-	45005653	45152702	6388	6221	13.01578667
PARL	NM_018622	chr3	-	183545171	183604694	1651	1624	13.00689
PDZK1IP1	NM_005764	chr1	-	47647259	47657772	3787	3371	13.00285333
SLC6A8	NM_005629	chrX	+	152951750	152964049	5518	4902	12.99914667
PLOD2	NM_182943	chr3	-	145785226	145881283	3006	2848	12.93156667
C5orf13	NM_004772	chr5	-	111062998	111094946	2778	2772	12.93023333
LIMCH1	NM_014988	chr4	+	41360802	41704062	12495	7867	12.92734333
GTF2H2	NM_001515	chr5	-	70328949	70365498	434	206	12.91038333
HSPB8	NM_014365	chr12	+	119614593	119634552	4341	3220	12.91033333
SERINC1	NM_020755	chr6	-	122762491	122794953	823	752	12.90449333
F8A1	NM_012151	chrX	+	154112633	154118337	1070	0	12.90137
PDE4D	NM_006203	chr5	-	58262864	58884325	13146	9354	12.89957667
PSMD10	NM_170750	chrX	-	107325435	107336849	1450	1444	12.89826333
HSPH1	NM_006644	chr13	-	31708761	31738118	1885	1774	12.88920333
NBPF11	NM_183372	chr1	-	146030540	146084634	735	357	12.88478667
RGPD5	NM_032260	chr2	+	110548333	110592597	486	476	12.87046
COPS2	NM_004236	chr15	-	49415469	49449855	1525	1249	12.86908333
STAG3L1	NM_018991	chr7	+	74986445	74998991	733	267	12.84695667

BTBD10	NM_032320	chr11	-	13407554	13486839	2550	2478	12.81099
HGD	NM_000187	chr3	-	120345013	120403419	1416	1335	12.79418
NEO1	NM_002499	chr15	+	73342823	73599548	6214	6153	12.78349333
KIAA0196	NM_014846	chr8	-	126034501	126106062	1948	1931	12.77622
FAM48A	NM_017569	chr13	-	37581449	37635851	1189	1135	12.77184
SNRPB2	NM_198220	chr20	+	16708607	16724418	976	941	12.76326
SESTD1	NM_178123	chr2	-	179964417	180131351	3509	3175	12.75868333
ITFG1	NM_030790	chr16	-	47187296	47497016	3230	2747	12.75200667
MPHOSPH8	NM_017520	chr13	+	20205786	20249600	1428	1375	12.69814
STAG3L2	NM_001025202	chr7	-	74297281	74308732	1076	0	12.67779
SLC7A2	NM_003046	chr8	+	17394284	17430078	499	0	12.67655
STAG3L3	NM_001013739	chr7	-	72467025	72478456	1080	188	12.67651333
HIF1AN	NM_017902	chr10	+	102293639	102315682	1118	930	12.6684
METTL5	NM_014168	chr2	-	170666266	170683354	1406	1406	12.65131667
ARMCX3	NM_177948	chrX	+	100876349	100884832	1206	703	12.64878667
HMGN3	NM_138730	chr6	-	79908960	79946456	1471	1358	12.63577333
INTS10	NM_018142	chr8	+	19672916	19711587	2145	2124	12.63421
DNM1L	NM_012063	chr12	+	32830135	32900585	1371	1291	12.62181667
10-Sep	NM_178584	chr2	-	110298374	110373784	4021	3990	12.61254333
GLIPR1	NM_006851	chr12	+	75872511	75897717	1451	1163	12.58948333
RDH10	NM_172037	chr8	+	74205263	74239517	4320	4279	12.58934667
PIGK	NM_005482	chr1	-	77552665	77687133	1274	1256	12.56511
THY1	NM_006288	chr11	-	119286653	119296247	3267	2931	12.54076667
CCNG2	NM_004354	chr4	+	78076355	78093214	2343	2120	12.53879667

TMED7	NM_181836	chr5	-	114946903	114963877	1182	1177	12.53711333
SGPP2	NM_152386	chr2	+	223287320	223425618	5418	5073	12.51367333
ERH	NM_004450	chr14	-	69844838	69867022	1311	1210	12.49809333
PDPN	NM_198389	chr1	+	13908250	13946453	3117	2626	12.48838667
ATF5	NM_012068	chr19	+	50429957	50439194	2446	2422	12.48236667
BLMH	NM_000386	chr17	-	28573221	28621075	2036	1989	12.47401333
KCNJ15	NM_170737	chr21	+	39642427	39675747	2049	1776	12.45815333
WDR11	NM_018117	chr10	+	122608685	122671039	840	808	12.45783
FZD6	NM_003506	chr8	+	104309057	104347095	1441	1435	12.45606333
PLAA	NM_001031689	chr9	-	26901366	26949469	1275	1051	12.44619
KDM5A	NM_001042603	chr12	-	387221	500621	1754	1610	12.43652
UFM1	NM_016617	chr13	+	38921940	38939144	1762	1402	12.42937
GNG11	NM_004126	chr7	+	93549014	93557827	854	610	12.41454667
PTPRD	NM_130393	chr9	-	8312244	8735947	4615	1336	12.39274667
ADH5	NM_000671	chr4	-	99990128	100011932	1454	1313	12.38376333
CASP6	NM_032992	chr4	-	110607783	110626630	1638	1514	12.37953667
MOCS2	NM_176806	chr5	-	52391893	52407599	1848	1091	12.35737
FAM86C	NM_152563	chr11	+	71496555	71514281	1978	1943	12.35055667
SSFA2	NM_006751	chr2	+	182754470	182797465	1703	1568	12.34941333
CDH6	NM_004932	chr5	+	31191794	31327238	3902	2515	12.34425333
LRIG3	NM_153377	chr12	-	59263935	59316263	2912	2856	12.34270333
MRPS30	NM_016640	chr5	+	44807025	44817619	1497	1495	12.34230667
DHX36	NM_020865	chr3	-	153991455	154044287	1077	894	12.34009333
HEATR1	NM_018072	chr1	-	236710303	236769842	1196	1041	12.33025

PTPRK	NM_002844	chr6	-	128287922	128843820	6739	5612	12.32358333
GFM2	NM_170691	chr5	-	74015029	74065043	1653	1470	12.32118333
IER3IP1	NM_016097	chr18	-	44679411	44704746	2061	1617	12.31664667
FHOD3	NM_025135	chr18	+	33875700	34362019	26209	25267	12.31550667
GJA1	NM_000165	chr6	+	121754743	121772874	1927	855	12.31350667
TMEM47	NM_031442	chrX	-	34643179	34677406	2005	1919	12.30862667
RND3	NM_005168	chr2	-	151322708	151346181	3394	2042	12.30081333
SHISA2	NM_001007538	chr13	-	26616733	26627199	3174	3144	12.29960667
SLC35F2	NM_017515	chr11	-	107659715	107731915	3562	3315	12.28929333
KIAA0020	NM_014878	chr9	-	2802153	2846131	2686	2081	12.27362
ST8SIA2	NM_006011	chr15	+	92935138	93013959	5941	4460	12.25886
NUPL1	NM_014089	chr13	+	25873664	25918562	1156	1021	12.24987667
TCEAL3	NM_032926	chrX	+	102860832	102866856	1429	1073	12.24000333
ABCD3	NM_002858	chr1	+	94881931	94986220	2131	1999	12.23961667
COMMD6	NM_203497	chr13	-	76097348	76113992	1001	980	12.22949333
DIRAS3	NM_004675	chr1	-	68509643	68518461	1385	1092	12.21181667
GNPNAT1	NM_198066	chr14	-	53239909	53260387	1292	1254	12.20877333
CDK13	NM_031267	chr7	+	39987957	40138734	4203	4043	12.20332
UGT2B15	NM_001076	chr4	-	69510313	69538375	172	0	12.19812333
WDR12	NM_018256	chr2	-	203743321	203778950	1954	1910	12.19458667
PKN2	NM_006256	chr1	+	89147920	89303939	3366	3207	12.18711667
RUSC2	NM_014806	chr9	+	35488005	35563896	7134	5894	12.18598333
RAP1GDS1	NM_021159	chr4	+	99180525	99367013	3881	3718	12.18469667
UBE3A	NM_130839	chr15	-	25580394	25686129	2433	2338	12.16936

RAB32	NM_006834	chr6	+	146862826	146878087	2373	2182	12.16122
ZNF277	NM_021994	chr7	+	111844641	111985990	3256	2876	12.13605
MCTP2	NM_018349	chr15	+	94839428	95029182	2201	2036	12.13400333
PDCD5	NM_004708	chr19	+	33070102	33080330	1546	1426	12.11428
TMX4	NM_021156	chr20	-	7959714	8002394	2530	1880	12.10581667
DERA	NM_015954	chr12	+	16062184	16192316	4324	2777	12.10322667
CFTR	NM_000492	chr7	+	117118015	117310719	1758	1462	12.08874
LRRC16A	NM_017640	chr6	+	25277654	25622759	9263	8903	12.07948333
TBC1D3C	NM_001001418	chr17	-	34744117	34810092	146	0	12.07351333
ZNF83	NM_018300	chr19	-	53113616	53143645	1605	1422	12.07035
COL4A4	NM_000092	chr2	-	227865425	228031276	4801	4312	12.06538667
GCNT3	NM_004751	chr15	+	59901980	59914211	1413	1174	12.06383667
HOOK1	NM_015888	chr1	+	60278531	60344051	1881	1686	12.05523333
F8A2	NM_001007523	chrX	+	154112648	154117766	1070	0	12.05106
KLHDC2	NM_014315	chr14	+	50232785	50251857	2159	2039	12.04757
ZWINT	NM_032997	chr10	-	58115197	58123035	744	658	12.04629333
STK32B	NM_018401	chr4	+	5051525	5504726	11797	10906	12.04489
THOC2	NM_001081550	chrX	-	122732410	122868905	2805	2374	12.01738
GUCY1B3	NM_000857	chr4	+	156678124	156730784	2674	2044	12.01625
HBP1	NM_012257	chr7	+	106807458	106844975	2953	2806	12.01144667
NEFL	NM_006158	chr8	-	24806467	24816132	1856	679	12.00451667
SLC35B3	NM_015948	chr6	-	8411299	8437795	1554	1032	11.99172333
TAB2	NM_015093	chr6	+	149637434	149734748	2429	2241	11.98417333
NCALD	NM_032041	chr8	-	102696768	102805440	3734	3466	11.98361667

USP38	NM_032557	chr4	+	144104068	144145142	1171	1000	11.95469333
UBQLN2	NM_013444	chrX	+	56588024	56595444	2122	1923	11.92732667
CCL2	NM_002982	chr17	+	32580294	32586221	1235	776	11.92628
UGT2B4	NM_021139	chr4	-	70343881	70363627	485	0	11.92305
H2AFJ	NM_177925	chr12	+	14925268	14932937	1854	1096	11.92128333
C12orf11	NM_018164	chr12	-	27056110	27093255	1331	1326	11.91927
ARMC10	NM_031905	chr7	+	102713326	102742206	1898	1831	11.91748667
GPR126	NM_198569	chr6	+	142621054	142769404	4782	3532	11.914
SMG1	NM_015092	chr16	-	18814173	18939727	1232	993	11.90554667
CXCL6	NM_002993	chr4	+	74700271	74706478	801	160	11.89899333
NUP37	NM_024057	chr12	-	102465971	102514362	784	746	11.8971
SIPA1L2	NM_020808	chr1	-	232531710	232653244	4517	1428	11.85162667
RASSF6	NM_201431	chr4	-	74436860	74488341	2821	2698	11.84747333
LDOC1	NM_012317	chrX	-	140267929	140273311	1604	1291	11.83592667
CDK1	NM_033379	chr10	+	62536210	62556611	1063	1052	11.82769667
EPB41L4A	NM_022140	chr5	-	111496313	111757011	8611	7377	11.82413667
SLC35A5	NM_017945	chr3	+	112278893	112305004	1769	1649	11.81831667
KCNK1	NM_002245	chr1	+	233747748	233810259	5572	5559	11.81811333
PRRG1	NM_001173490	chrX	+	37206581	37318549	2946	2725	11.81093333
PRPF38A	NM_032864	chr1	+	52868217	52885993	1565	1513	11.80767667
PSD3	NM_206909	chr8	-	18382811	18668406	6110	5001	11.80005333
TXNDC9	NM_005783	chr2	-	99933485	99954861	1934	1630	11.78905
SC5DL	NM_006918	chr11	+	121161386	121186120	1817	1745	11.77519
NBN	NM_002485	chr8	-	90943562	90998900	1872	1003	11.77346333

TRHDE	NM_013381	chr12	+	72664527	73061423	4814	3706	11.76718667
HPS3	NM_032383	chr3	+	148845369	148893306	2169	1769	11.76647333
FZD1	NM_003505	chr7	+	90891781	90900133	3983	3197	11.75897667
FLRT3	NM_198391	chr20	-	14302637	14320314	750	750	11.75687667
PCM1	NM_006197	chr8	+	17778364	17889458	2026	1868	11.75633
HSPA2	NM_021979	chr14	+	65005184	65011955	1924	1510	11.75348667
EDIL3	NM_005711	chr5	-	83236124	83682612	2614	2391	11.744
PTHLH	NM_198966	chr12	-	28109015	28124895	3261	2654	11.73952333
MACC1	NM_182762	chr7	-	20172277	20259014	1892	1702	11.73704
ZSWIM6	NM_020928	chr5	+	60626098	60844000	6799	6216	11.72610667
CCNC	NM_005190	chr6	-	99988261	100018691	1042	942	11.72589
SPOCK1	NM_004598	chr5	-	136308985	136837019	21169	20811	11.72166
EXOC1	NM_178237	chr4	+	56717814	56773245	1498	1471	11.70089333
ETFDH	NM_004453	chr4	+	159591275	159631842	2067	2060	11.69390667
FABP5	NM_001444	chr8	+	82190783	82199009	1556	1468	11.6792
MINA	NM_153182	chr3	-	97658659	97693296	1963	1316	11.67571
GIGYF2	NM_015575	chr2	+	233560013	233727290	4456	3976	11.67361667
NUDT16	NM_152395	chr3	+	131098607	131109675	2029	1773	11.66349
DCAF13	NM_015420	chr8	+	104424940	104457681	1285	1095	11.65314
CGGBP1	NM_003663	chr3	-	88099098	88110147	1739	1601	11.65173667
ARL1	NM_001177	chr12	-	101784913	101803573	1490	1371	11.64319
NEDD1	NM_152905	chr12	+	97298999	97349470	1738	1685	11.63934667
C14orf101	NM_017799	chr14	+	57044509	57118233	1619	1167	11.63282667
DEPDC1	NM_017779	chr1	-	68937833	68964800	1040	979	11.63236667

RAB11FIP2	NM_014904	chr10	-	119762425	119808115	2706	1688	11.60315333
MRPL48	NM_016055	chr11	+	73496915	73577657	1578	1319	11.59085667
KIAA2026	NM_001017969	chr9	-	5917006	6010004	2662	2437	11.56352
PPARGC1A	NM_013261	chr4	-	23791642	23893701	3362	1964	11.55832667
MFSD1	NM_022736	chr3	+	158517713	158549509	1711	1275	11.55478333
COL12A1	NM_080645	chr6	-	75792040	75917624	5384	5060	11.54634
CDC73	NM_024529	chr1	+	193089086	193225943	1577	1513	11.54109667
KIAA1468	NM_020854	chr18	+	59852522	59976356	2434	1654	11.54071667
GAR1	NM_032993	chr4	+	110734664	110747894	1185	954	11.53560667
NUP50	NM_153645	chr22	+	45558550	45585891	2355	2301	11.53367333
AK3	NM_016282	chr9	-	4709156	4743228	1685	1677	11.52997333
CASP4	NM_033306	chr11	-	104811592	104829423	275	242	11.52310667
GFRA1	NM_145793	chr10	-	117814440	118033820	11824	6845	11.51789333
DIMT1L	NM_014473	chr5	-	61682349	61701729	1098	1049	11.51108
ZC4H2	NM_018684	chrX	-	64134248	64198414	2281	2128	11.50773333
PAPD4	NM_173797	chr5	+	78906241	78984472	1501	1123	11.49856667
USP14	NM_005151	chr18	+	156481	215740	1549	1510	11.49659
DDX18	NM_006773	chr2	+	118570253	118591954	1048	1032	11.49288667
NRG1	NM_013964	chr8	+	32403726	32624559	6195	5591	11.48789333
C8orf84	NM_153225	chr8	-	73974776	74007508	1421	1302	11.48747667
PPAPDC1A	NM_001030059	chr10	+	122214464	122351368	9356	6171	11.48468667
GDA	NM_004293	chr9	+	74762291	74869141	2678	1265	11.48084
ARHGEF35	NM_001003702	chr7	-	143881174	143894792	337	0	11.47266333
VWA5A	NM_198315	chr11	+	123984109	123997544	1653	1653	11.45647333

ARFIP1	NM_014447	chr4	+	153699110	153835064	2917	2336	11.45
GRB14	NM_004490	chr2	-	165347321	165480361	3511	3450	11.44441667
PYROXD1	NM_024854	chr12	+	21588536	21626183	1047	785	11.43846
PPIL3	NM_130906	chr2	-	201733677	201755850	1217	1182	11.43693
DCAF12L2	NM_001013628	chrX	-	125295480	125302081	1964	930	11.42758
AKTIP	NM_022476	chr16	-	53523190	53539171	2267	2083	11.41648
ERGIC2	NM_016570	chr12	-	29491577	29536144	1130	1092	11.40830333
SOSTDC1	NM_015464	chr7	-	16499104	16507475	820	634	11.40014667
AGPAT9	NM_032717	chr4	+	84455651	84529027	3818	3295	11.39611667
C14orf149	NM_144581	chr14	-	59937404	59953074	2205	1414	11.38765333
LRRN1	NM_020873	chr3	+	3839119	3891388	2991	1313	11.38233667
ARHGAP11B	NM_001039841	chr15	+	30916877	30933014	1713	1666	11.38069667
FGA	NM_021871	chr4	-	155504427	155513898	378	337	11.37541667
KIAA1804	NM_032435	chr1	+	233461512	233522895	3862	2053	11.36302667
GCOM1	NM_152451	chr15	+	57882100	57979563	5061	4438	11.35022333
HAVCR1	NM_012206	chr5	-	156454529	156487488	2292	629	11.3488
MED6	NM_005466	chr14	-	71048955	71069385	1087	920	11.34776667
UPRT	NM_145052	chrX	+	74491892	74526733	1257	1188	11.34657333
MUDENG	NM_018229	chr14	+	57733604	57758798	1455	1324	11.34435333
KIAA0776	NM_015323	chr6	+	96967700	97005152	1054	1037	11.34316
C9orf116	NM_144654	chr9	-	138385024	138393762	2829	2635	11.32939
PARP8	NM_024615	chr5	+	49960770	50144357	3774	2931	11.31364333
KCNIP1	NM_014592	chr5	+	169929046	170165637	13192	12215	11.30984
SDAD1	NM_018115	chr4	-	76869066	76914114	1735	1484	11.30594333

ARHGAP24	NM_031305	chr4	+	86849424	86925824	2253	1218	11.28959667
MAPKSP1	NM_021970	chr4	-	100797493	100817704	1038	897	11.28451
KLHL14	NM_020805	chr18	-	30250632	30354975	5413	4823	11.27212667
ZNF133	NM_003434	chr20	+	18267119	18299641	1908	1835	11.26831
FGFBP1	NM_005130	chr4	-	15935191	15941972	533	0	11.26569
CHIC2	NM_012110	chr4	-	54873956	54932789	1186	1174	11.25949333
SIRPG	NM_080816	chr20	-	1607796	1640426	1290	1077	11.25712667
CCNJ	NM_019084	chr10	+	97801157	97822626	1781	1657	11.25058667
ZBED2	NM_024508	chr3	-	111309745	111316167	1528	235	11.2449
MITF	NM_198178	chr3	+	69983749	70019489	549	424	11.23726333
MCM8	NM_182802	chr20	+	5929296	5977832	2479	1719	11.23698
KLHL9	NM_018847	chr9	-	21329016	21337430	1027	725	11.23282
ELTD1	NM_022159	chr1	-	79353447	79474496	1191	697	11.21805667
PARG	NM_003631	chr10	-	51024323	51373332	3003	1812	11.21621
GPX8	NM_001008397	chr5	+	54453982	54465130	1051	851	11.20760667
ATP8A2	NM_016529	chr13	+	25944207	26597421	16920	13213	11.20549
NPY1R	NM_000909	chr4	-	164243115	164255749	2065	1623	11.20303333
GAS1	NM_002048	chr9	-	89557275	89564105	3303	2944	11.20059
CD200	NM_005944	chr3	+	112049914	112083659	999	296	11.19922333
CCDC59	NM_014167	chr12	-	82744081	82754200	1248	966	11.19162667
UNC80	NM_182587	chr2	+	210634715	210866025	2941	2240	11.19043333
WFDC2	NM_006103	chr20	+	44096392	44112173	1725	1260	11.18562667
GTF2E1	NM_005513	chr3	+	120459556	120503917	1788	1752	11.17516
RNF128	NM_194463	chrX	+	105967892	106042247	2900	2147	11.17390333

ZNF93	NM_031218	chr19	+	20009720	20048383	1779	1619	11.17142333
PRR15	NM_175887	chr7	+	29601425	29608912	4046	3084	11.16858667
INTS12	NM_020395	chr4	-	106601783	106631882	1154	1092	11.16671333
CLDN10	NM_182848	chr13	+	96083851	96234011	6990	6641	11.16190333
COMMD2	NM_016094	chr3	-	149454255	149472287	943	760	11.15752
GPR110	NM_153840	chr6	-	46965811	47012083	1140	479	11.15692
RASL11B	NM_023940	chr4	+	53726493	53735003	1949	1790	11.13235333
TSPYL5	NM_033512	chr8	-	98283712	98292177	1225	986	11.13214667
DYNC2LI1	NM_016008	chr2	+	43999176	44039150	1316	1305	11.13041667
STC1	NM_003155	chr8	-	23697432	23714321	2413	2047	11.12587667
HMGXB4	NM_001003681	chr22	+	35651443	35693801	1631	1479	11.11993667
CAND1	NM_018448	chr12	+	67661059	67710389	2052	2005	11.11858
TMEM106B	NM_018374	chr7	+	12248846	12278891	1315	1064	11.10702
CXCL3	NM_002090	chr4	-	74900310	74906491	1256	1220	11.10666667
PLS1	NM_002670	chr3	+	142340264	142434506	1908	1285	11.09314
VMA21	NM_001017980	chrX	+	150563655	150579837	2218	1847	11.08045667
CDK20	NM_178432	chr9	-	90579357	90591696	1247	974	11.07255
DZIP1	NM_198968	chr13	-	96228454	96298958	3803	3681	11.06840333
PDE3A	NM_000921	chr12	+	20520195	20835882	5271	4810	11.06361333
BHMT2	NM_017614	chr5	+	78363545	78387898	2075	1355	11.05905333
LRRC40	NM_017768	chr1	-	70608483	70673362	1095	984	11.04136
ZNF350	NM_021632	chr19	-	52465591	52492080	798	574	11.03117667
KRT5	NM_000424	chr12	-	52906357	52916244	1136	0	11.02139667
GPC4	NM_001448	chrX	-	132433062	132551206	6100	5906	11.01728667

TERF1	NM_017489	chr8	+	73919095	73961988	1601	1325	11.0138
DDX60	NM_017631	chr4	-	169135440	169241959	1193	1134	11.01327
EXTL2	NM_001439	chr1	-	101335939	101362419	2242	2143	11.01309333
SUPT7L	NM_014860	chr2	-	27871677	27888450	1263	1247	11.00405
DCAF12L1	NM_178470	chrX	-	125681364	125688843	2893	827	10.99159
ZNF268	NM_152943	chr12	+	133755993	133785698	914	907	10.98835333
KLHL8	NM_020803	chr4	-	88080212	88143675	1631	1411	10.98746
RASEF	NM_152573	chr9	-	85595315	85680044	3885	2604	10.97708667
PLXDC2	NM_032812	chr10	+	20103370	20571116	10517	4226	10.97394333
ZXDA	NM_007156	chrX	-	57929862	57939068	1918	1629	10.97101667
HRCT1	NM_001039792	chr9	+	35904187	35909139	3170	2900	10.96631667
CACYBP	NM_014412	chr1	+	174966890	174983164	1784	1719	10.96576333
CCNT2	NM_058241	chr2	+	135674391	135716585	1905	1786	10.96075
LSM6	NM_007080	chr4	+	147094833	147113214	990	959	10.94801
SOS2	NM_006939	chr14	-	50581844	50700100	3098	2936	10.94541667
UGT2B7	NM_001074	chr4	+	69960191	69980706	470	0	10.94426667
RNPC3	NM_017619	chr1	+	104066576	104099860	1250	1239	10.94241333
SLC4A4	NM_003759	chr4	+	72202768	72439805	3356	2956	10.93077667
NCAM1	NM_181351	chr11	+	112829993	113151159	7799	7162	10.92723
EPS8	NM_004447	chr12	-	15771073	15944511	5673	5074	10.92216333
GNG5	NM_005274	chr1	-	84962004	84974263	1523	1395	10.91883333
ZZZ3	NM_015534	chr1	-	78028188	78150344	2358	2172	10.91756333
PLBD1	NM_024829	chr12	-	14654595	14722792	2384	1378	10.91702
LPHN3	NM_015236	chr4	+	62360837	62940169	3691	1264	10.91411333

LPHN2	NM_012302	chr1	+	82264080	82460108	4543	3570	10.91384
B3GNT5	NM_032047	chr3	+	182969030	182993180	3226	3087	10.91195333
CCDC14	NM_022757	chr3	-	123630272	123682256	1137	878	10.90704333
HERC6	NM_017912	chr4	+	89297889	89366250	2085	2023	10.90218333
CHD1	NM_001270	chr5	-	98188906	98264239	1125	1086	10.90196
GINS1	NM_021067	chr20	+	25386321	25431192	1439	1436	10.89673667
PIGN	NM_176787	chr18	-	59709456	59856290	2735	2430	10.89447667
SELK	NM_021237	chr3	-	53917224	53927990	1376	1257	10.88521333
TSPAN6	NM_003270	chrX	-	99881793	99893795	1261	1188	10.87950667
BARD1	NM_000465	chr2	-	215591273	215676429	2442	2423	10.87420667
C12orf35	NM_018169	chr12	+	32110351	32148044	2374	2342	10.85548
ANXA8	NM_001040084	chr10	+	48253223	48273369	348	0	10.81976667
FGF9	NM_002010	chr13	+	22243213	22280641	7568	7340	10.81442667
SNCA	NM_007308	chr4	-	90643248	90760128	3901	3413	10.81252667
GRIP1	NM_021150	chr12	-	66739209	67074926	4125	3865	10.80986
ZNF763	NM_001012753	chr19	+	12073867	12093199	1620	1574	10.79593667
FAM122B	NM_145284	chrX	-	133901594	133932386	1947	1534	10.79281333
TMEM133	NM_032021	chr11	+	100860809	100866667	172	0	10.78722333
SSTR1	NM_001049	chr14	+	38675202	38684269	3396	3307	10.78271667
DNER	NM_139072	chr2	-	230220343	230581287	10578	7023	10.78213667
C18orf55	NM_014177	chr18	+	71813744	71828205	1458	1325	10.76974667
SLC3A1	NM_000341	chr2	+	44500595	44549963	1420	878	10.75729333
CLEC4E	NM_014358	chr12	-	8683899	8695559	625	0	10.72959333
PROM1	NM_006017	chr4	-	15967847	16079742	2697	1748	10.71245667

WDR36	NM_139281	chr5	+	110425868	110468201	1191	872	10.69591667
KIAA1217	NM_019590	chr10	+	24495718	24838773	17122	14401	10.69547333
CCDC58	NM_001017928	chr3	-	122076434	122104075	2105	1940	10.69397333
PKIA	NM_181839	chr8	+	79426334	79517486	1755	1566	10.69295
WDR72	NM_182758	chr15	-	53803936	54053860	4033	911	10.69282
ZNF254	NM_203282	chr19	+	24267974	24314655	925	898	10.69099333
SLC29A4	NM_153247	chr7	+	5320559	5345705	6511	6310	10.68930667
CTTNBP2	NM_033427	chr7	-	117348704	117515562	6944	6038	10.68846333
INPP4B	NM_003866	chr4	-	142947180	143769605	10150	6166	10.6837
RAP2C	NM_021183	chrX	-	131335051	131354190	2653	2208	10.67525667
NHLRC3	NM_001017370	chr13	+	39610453	39626247	1142	1124	10.67385
ALG13	NM_018466	chrX	+	110922344	110935624	1178	1167	10.67025333
ANXA8L2	NM_001630	chr10	+	47744918	47765041	916	0	10.66552333
C10orf57	NM_025125	chr10	+	81836424	81854308	1485	1245	10.6564
TSPAN12	NM_012338	chr7	-	120425372	120500178	3765	2606	10.65367
DAB2	NM_001343	chr5	-	39369778	39427336	2606	2502	10.65216
MYSM1	NM_001085487	chr1	-	59123588	59167748	987	868	10.64717
LPAR1	NM_057159	chr9	-	113634052	113802366	5697	4916	10.64475
NDUFAF2	NM_174889	chr5	+	60238954	60450865	2997	2716	10.63148667
PLK4	NM_014264	chr4	+	128800014	128822378	1247	1201	10.62907
YARS2	NM_001040436	chr12	-	32897475	32910875	1669	1458	10.62639667
ACMSD	NM_138326	chr2	+	135594184	135661603	1793	1026	10.61939333
ACSM3	NM_202000	chr16	+	20773310	20799639	1316	1206	10.60905667
VPS4B	NM_004869	chr18	-	61054423	61091753	1504	1503	10.60867667

TNFAIP6	NM_007115	chr2	+	152212103	152238561	1927	1706	10.59460333
DYNC2H1	NM_001377	chr11	+	102978158	103352592	2548	1823	10.59105
DPH5	NM_015958	chr1	-	101453178	101493363	1815	1534	10.57792667
MTIF3	NM_152912	chr13	-	28007774	28026740	2502	1565	10.57507667
PRKD1	NM_002742	chr14	-	30043685	30398900	5314	5275	10.56626
CCNA1	NM_003914	chr13	+	37004407	37019020	1870	1292	10.56602333
CXorf26	NM_016500	chrX	+	75390769	75400034	1122	1063	10.56522333
FPR1	NM_002029	chr19	-	52247024	52257151	550	418	10.56351333
C13orf34	NM_024808	chr13	+	73300040	73332329	1390	1248	10.55311667
KIAA0586	NM_014749	chr14	+	58892708	59017550	2097	1671	10.55271
NKRF	NM_017544	chrX	-	118720298	118741847	1833	1746	10.54615
CWC25	NM_017748	chr17	-	36955444	36983590	2788	2575	10.54525667
TFCP2L1	NM_014553	chr2	-	121972162	122044779	5200	4781	10.54521
EREG	NM_001432	chr4	+	75228858	75256478	2462	1797	10.54132333
ADNP2	NM_014913	chr18	+	77864913	77900229	1731	1655	10.53821333
ZNF385D	NM_024697	chr3	-	21460488	21794817	5206	4951	10.53065333
KCTD14	NM_023930	chr11	-	77724759	77736321	1856	1237	10.53002
FAM84A	NM_145175	chr2	+	14770808	14782169	4054	3168	10.51916333
ZBTB33	NM_006777	chrX	+	119382605	119394252	1570	1560	10.50362333
CHL1	NM_006614	chr3	+	236648	453098	5752	2268	10.50297667
ENTPD3	NM_001248	chr3	+	40426671	40472111	1958	1465	10.49581333
TOX3	NM_001146188	chr16	-	52469916	52583715	2466	1830	10.49441333
MMP1	NM_002421	chr11	-	102658639	102670967	676	646	10.48739
ZC3HC1	NM_016478	chr7	-	129656124	129693234	1236	1151	10.48241333

SLCO4C1	NM_180991	chr5	-	101567690	101634254	1509	1136	10.47595333
F3	NM_001993	chr1	-	94992730	95009414	1820	1626	10.47441333
AASDH	NM_181806	chr4	-	57202455	57255639	1356	1221	10.4638
ZNF658	NM_033160	chr9	-	40769400	40794113	469	0	10.46268667
RIMS2	NM_014677	chr8	+	104829414	105267452	4700	2105	10.45099
PNO1	NM_020143	chr2	+	68383003	68405095	1526	1359	10.44387333
KITLG	NM_003994	chr12	-	88884568	88976251	2986	2463	10.43207
BMPR1B	NM_001203	chr4	+	95677126	96081602	7136	3752	10.42898667
PCP4	NM_006198	chr21	+	41237345	41303323	1757	753	10.42871667
ZNF33B	NM_006955	chr10	-	43082553	43135993	1708	1112	10.42694667
RRM2B	NM_015713	chr8	-	103214727	103253347	1714	1620	10.42678
DDIT4L	NM_145244	chr4	-	101105025	101113656	1397	1200	10.41877667
USP43	NM_153210	chr17	+	9546948	9635004	5359	3811	10.41370333
AADAT	NM_182662	chr4	-	170979371	171013373	1832	1356	10.41118667
FAM110C	NM_001077710	chr2	-	36812	48589	3205	1707	10.41079667
RAB38	NM_022337	chr11	-	87844413	87910636	1420	1006	10.41032333
RNF20	NM_019592	chr9	+	104294131	104327627	1110	993	10.40348667
PPM1L	NM_139245	chr3	+	160471994	160790818	6477	5728	10.39806667
LAMA1	NM_005559	chr18	-	6939884	7119814	5873	5283	10.39628
ST6GAL2	NM_032528	chr2	-	107416054	107505564	3062	2050	10.38855667
STARD4	NM_139164	chr5	-	110832020	110850158	1145	1132	10.38598667
P4HA3	NM_182904	chr11	-	73975700	74024700	2557	2236	10.38052667
NCAPG	NM_022346	chr4	+	17810523	17848488	1387	1242	10.37890667
NR1H4	NM_005123	chr12	+	100865677	100959644	3176	2367	10.36888667

KRT6A	NM_005554	chr12	-	52878956	52889182	483	147	10.36125333
OSGIN2	NM_004337	chr8	+	90912094	90942096	1504	1427	10.36025667
SEMA6A	NM_020796	chr5	-	115777249	115912552	9021	6099	10.35802667
GPR27	NM_018971	chr3	+	71801199	71806329	1357	1351	10.35734333
SPCS3	NM_021928	chr4	+	177239088	177255397	1425	1344	10.35608667
IMPA1	NM_005536	chr8	-	82567149	82600590	851	850	10.35451333
C3orf52	NM_024616	chr3	+	111803180	111839045	4099	3946	10.35398667
ZNF22	NM_006963	chr10	+	45494271	45502778	1769	1762	10.35192667
SERF1A	NM_022968	chr5	+	69319070	69330526	810	808	10.34925333
LCORL	NM_153686	chr4	-	17842837	18025484	3140	2648	10.34846
CYTL1	NM_018659	chr4	-	5014312	5023198	518	516	10.34475
GCA	NM_012198	chr2	+	163198581	163221149	1087	835	10.31845333
USPL1	NM_005800	chr13	+	31189828	31235687	1814	1787	10.31685667
DYNC1LI1	NM_016141	chr3	-	32565461	32614367	1678	1495	10.31415
DMRTA1	NM_022160	chr9	+	22444838	22454473	1501	1402	10.30007
C12orf39	NM_030572	chr12	+	21677254	21686211	1618	849	10.29660333
ZNF626	NM_145297	chr19	-	20825507	20846403	1221	872	10.28107667
FAM83B	NM_001010872	chr6	+	54709567	54808820	3720	534	10.27930667
CPVL	NM_031311	chr7	-	29033245	29188154	4857	4381	10.26449
TRIM68	NM_018073	chr11	-	4617900	4631438	1243	1154	10.26056667
NPFFR2	NM_053036	chr4	+	72902847	73015919	1594	335	10.25931
C18orf21	NM_031446	chr18	+	33550586	33561242	961	952	10.25070333
NEK3	NM_001146099	chr13	-	52704777	52735997	1059	1058	10.22516333
HIST2H2BF	NM_001161334	chr1	-	149752243	149785929	1304	782	10.22199

ZCCHC4	NM_024936	chr4	+	25312394	25374006	2140	2043	10.21909333
KRT16	NM_005557	chr17	-	39764029	39771080	448	295	10.19135
ARMCX5	NM_022838	chrX	+	101852424	101861086	1438	1290	10.15255667
KAAG1	NM_181337	chr6	+	24355129	24360513	2036	1045	10.15134667
CASD1	NM_022900	chr7	+	94137168	94188329	2058	1977	10.14869333
KIAA1598	NM_018330	chr10	-	118642304	118767089	4765	4718	10.14706667
CHN1	NM_001822	chr2	-	175662040	175872171	6576	6574	10.14616667
MNS1	NM_018365	chr15	-	56718927	56759336	1082	970	10.13362333
POLR3F	NM_006466	chr20	+	18446031	18467287	1327	1301	10.13094333
RASSF10	NM_001080521	chr11	+	13028968	13035654	3508	2858	10.12547333
UQCRFS1	NM_006003	chr19	-	29696165	29706137	1518	1512	10.11635
NAAA	NM_014435	chr4	-	76832807	76864167	2221	1984	10.11349667
SERBP1	NM_015640	chr1	-	67871491	67898124	1814	1730	10.10971667
FGFR2	NM_022970	chr10	-	123235842	123359973	8707	7962	10.10248333
SEMA6D	NM_153619	chr15	+	48008684	48068421	5284	4224	10.09892333
C10orf118	NM_018017	chr10	-	115879972	115936365	2459	1898	10.09796333
GJB4	NM_153212	chr1	+	35223340	35231326	2887	1154	10.09441667
CHMP2B	NM_014043	chr3	+	87274411	87306699	1266	1119	10.0943
PRRG4	NM_024081	chr11	+	32849487	32878106	2762	1670	10.08126333
SIKE1	NM_025073	chr1	-	115310103	115325309	753	749	10.08103667
ASTE1	NM_014065	chr3	-	130730719	130747647	869	856	10.07039667
DSC2	NM_024422	chr18	-	28643940	28684389	2133	1928	10.06863
SPAG16	NM_024532	chr2	+	214147114	215277226	6477	6345	10.06637
MANEA	NM_024641	chr6	+	96023411	96059327	1190	809	10.06598667

MOSPD2	NM_152581	chrX	+	14889525	14941460	2964	2511	10.06209
NEFM	NM_005382	chr8	+	24769272	24778607	2843	2043	10.05453667
CNTNAP3	NM_033655	chr9	-	39070762	39290301	774	87	10.04796
TRIM23	NM_033228	chr5	-	64883505	64922188	1540	1230	10.03952667
WDFY3	NM_014991	chr4	-	85588691	85889545	6631	6026	10.03767667
UPK1B	NM_006952	chr3	+	118890423	118926001	3135	1088	10.02635667
ACP6	NM_016361	chr1	-	147117166	147144635	2007	1673	10.02444333
CLSTN2	NM_022131	chr3	+	139652025	140288920	11268	6966	10.01848
COL4A3	NM_000091	chr2	+	228027279	228181509	4380	2850	10.01318
FREM2	NM_207361	chr13	+	39259171	39463268	4159	549	10.00802333
C9orf82	NM_024828	chr9	-	26838681	26894827	1477	999	9.997986667
GREB1L	NM_001142966	chr18	+	18820201	19104792	8152	7056	9.993523333
BRWD3	NM_153252	chrX	-	79922985	80067234	2940	2344	9.992926667
ZNF264	NM_003417	chr19	+	57700866	57736215	1434	1388	9.98878
TPP2	NM_003291	chr13	+	103247284	103333524	2657	2233	9.98024
SLN	NM_003063	chr11	-	107576099	107584788	931	98	9.97346
ZNF304	NM_020657	chr19	+	57860643	57873266	1066	930	9.95129
CTH	NM_153742	chr1	+	70874899	70907535	1650	1385	9.95114
ODF2L	NM_020729	chr1	-	86813775	86864026	1180	1150	9.949363333
CYP8B1	NM_004391	chr3	-	42911682	42919634	1870	885	9.941673333
UBXN2B	NM_001077619	chr8	+	59321821	59366061	1239	1173	9.931196667
SAMD5	NM_001030060	chr6	+	147827826	147893158	4405	3393	9.927116667
YTHDC2	NM_022828	chr5	+	112847389	112932985	1872	1853	9.92682
SAP30	NM_003864	chr4	+	174290091	174300684	2714	2638	9.924806667

PKP2	NM_004572	chr12	-	32941678	33051781	3480	2153	9.912643333
GPR87	NM_023915	chr3	-	151009874	151036637	1567	914	9.912133333
ZBTB7C	NM_001039360	chr18	-	45551744	45569495	2584	1335	9.90545
PDE10A	NM_006661	chr6	-	165738776	166077585	7151	5849	9.902183333
FKTN	NM_006731	chr9	+	108318409	108405400	985	954	9.89978
C18orf62	NM_001037331	chr18	-	73119825	73141590	2087	748	9.889626667
JPH2	NM_175913	chr20	-	42803455	42818219	2096	1431	9.88269
HLA-G	NM_002127	chr6	+	29792754	29800900	745	301	9.8814
ZNF85	NM_003429	chr19	+	21104057	21135504	887	840	9.878053333
EPHA4	NM_004438	chr2	-	222280745	222439011	8318	7431	9.873156667
TUBE1	NM_016262	chr6	-	112389858	112410752	995	951	9.865663333
DBT	NM_001918	chr1	-	100650476	100717410	2599	1671	9.863536667
GPRIN3	NM_198281	chr4	-	90163427	90231162	3486	2075	9.863
BMP2	NM_001200	chr20	+	6746743	6762911	3426	3134	9.834646667
CTSO	NM_001334	chr4	-	156843268	156877049	1678	1511	9.824616667
C3orf63	NM_015224	chr3	-	56652158	56700075	933	253	9.82459
POLQ	NM_199420	chr3	-	121148271	121266854	3303	3149	9.816253333
ZNF607	NM_032689	chr19	-	38185262	38212692	1214	1049	9.814623333
SNAP25	NM_130811	chr20	+	10197475	10290066	3834	3629	9.814253333
FBXL3	NM_012158	chr13	-	77577387	77603332	1667	1653	9.81201
PAQR3	NM_001040202	chr4	-	79837092	79862583	980	804	9.799776667
HHIP	NM_022475	chr4	+	145565171	145661882	4852	1646	9.794453333
ERCC8	NM_000082	chr5	-	60167657	60242906	1801	1585	9.789046667
WDR43	NM_015131	chr2	+	29115531	29173081	1997	1779	9.78363

FAM72D	NM_207418	chr1	-	143894450	143915144	841	690	9.772186667
FAM72A	NM_001123168	chr1	+	206136909	206157075	1401	590	9.772186667
GPAM	NM_020918	chr10	-	113907620	113945526	1388	1229	9.77077
TFB1M	NM_016020	chr6	-	155576788	155637627	2135	1739	9.76946
NETO1	NM_153181	chr18	-	70412785	70534935	1825	383	9.76435
NLGN1	NM_014932	chr3	+	173114242	174003117	9336	5503	9.761963333
S1PR1	NM_001400	chr1	+	101700303	101709077	3107	2288	9.761376667
BTC	NM_001729	chr4	-	75669446	75721883	1756	1450	9.753986667
RDH14	NM_020905	chr2	-	18733987	18743960	1352	1204	9.74985
ZNF280D	NM_017661	chr15	-	56920372	57027788	1140	1016	9.74948
LRRC6	NM_012472	chr8	-	133582445	133689814	1747	1412	9.741466667
CEP78	NM_032171	chr9	+	80848989	80883984	1827	1731	9.737906667
C3orf14	NM_020685	chr3	+	62303394	62321321	1180	1078	9.734993333
CYP2R1	NM_024514	chr11	-	14897554	14915752	1805	1753	9.722873333
SLC12A2	NM_001046	chr5	+	127417481	127527381	2670	2565	9.72207
C12orf26	NM_032230	chr12	+	82750274	82875017	2527	1243	9.711266667
DNAJC19	NM_145261	chr3	-	180699496	180709563	938	899	9.711133333
SLC8A1	NM_021097	chr2	-	40337284	40659445	4725	4186	9.69346
LSM5	NM_012322	chr7	-	32522943	32532024	904	696	9.685223333
PRKCQ	NM_006257	chr10	-	6467103	6624239	7446	5202	9.6798
SLITRK4	NM_173078	chrX	-	142708593	142725020	3409	1255	9.67953
HSPA13	NM_006948	chr21	-	15741435	15757510	1224	1121	9.661396667
TUSC1	NM_001004125	chr9	-	25674385	25680857	1648	1538	9.654203333
DBC1	NM_014618	chr9	-	121926906	122133740	5446	1986	9.648323333

GUCY1A3	NM_001130687	chr4	+	156585860	156645386	2692	1972	9.64561
SLC25A40	NM_018843	chr7	-	87461812	87507693	1555	1492	9.62554
CCDC18	NM_206886	chr1	+	93643918	93746269	3127	2529	9.6163
MRPL13	NM_014078	chr8	-	121406081	121459648	1527	1033	9.611476667
ZNF680	NM_178558	chr7	-	63978253	64025506	1423	1279	9.607923333
IRAK1BP1	NM_001010844	chr6	+	79575187	79610321	1190	1104	9.606626667
KCNH1	NM_172362	chr1	-	210849655	211309458	8642	7423	9.598546667
CNTNAP2	NM_014141	chr7	+	145811451	148120089	10914	9209	9.573486667
CD1D	NM_001766	chr1	+	158147735	158158217	1353	1207	9.56964
FGFR1OP2	NM_015633	chr12	+	27089303	27121582	1331	1326	9.567953333
PTPLAD2	NM_001010915	chr9	-	21004363	21033636	1418	1313	9.567366667
RASSF9	NM_005447	chr12	-	86196329	86232319	2172	958	9.567136667
CLDN16	NM_006580	chr3	+	190103659	190131933	794	702	9.557223333
CPEB2	NM_182646	chr4	+	15002296	15073778	4308	4146	9.55647
GULP1	NM_016315	chr2	+	189155388	189462653	6138	3812	9.5562
SYT13	NM_020826	chr11	-	45259851	45309885	4826	3573	9.554943333
IFI44	NM_006417	chr1	+	79113475	79131764	375	349	9.55327
LOXL4	NM_032211	chr10	-	100005441	100030008	4948	4905	9.534183333
CCDC66	NM_001141947	chr3	+	56589182	56657849	999	988	9.52786
B3GALT5	NM_033173	chr21	+	41027252	41036816	1158	828	9.52639
ADAM28	NM_021777	chr8	+	24149578	24195613	629	339	9.522073333
SEPSECS	NM_016955	chr4	-	25119625	25164205	1622	1565	9.51889
DNAH5	NM_001369	chr5	-	13688435	13946590	5945	927	9.517973333
ZNF492	NM_020855	chr19	+	22815124	22852473	1196	628	9.511596667

ARHGEF26	NM_015595	chr3	+	153837147	153977617	3628	3437	9.510793333
PELI1	NM_020651	chr2	-	64317784	64373606	2090	1641	9.488613333
SESN3	NM_144665	chr11	-	94904131	94966247	2127	1438	9.48257
PPP1R9A	NM_017650	chr7	+	94534947	94927728	6428	3234	9.47995
FAM59A	NM_022751	chr18	-	29845475	30052448	6080	5611	9.47817
FGF2	NM_002006	chr4	+	123745861	123821391	4083	3991	9.47691
NPY5R	NM_006174	chr4	+	164263089	164275087	1552	381	9.476416667
FIGN	NM_018086	chr2	-	164462116	164594514	3128	3082	9.471493333
ANKRD18A	NM_147195	chr9	-	38569359	38622361	2713	2578	9.471276667
ALS2CR8	NM_024744	chr2	+	203775115	203853061	2945	2559	9.467766667
SPOPL	NM_001001664	chr2	+	139257348	139332806	2350	1976	9.446453333
BAZ2B	NM_013450	chr2	-	160173488	160475060	4435	3380	9.433616667
XKR4	NM_052898	chr8	+	56013015	56440711	10509	5627	9.431743333
CEACAM3	NM_001815	chr19	+	42298532	42317592	869	831	9.43057
ARSJ	NM_024590	chr4	-	114819438	114902879	3309	2092	9.427806667
CDS1	NM_001263	chr4	+	85502055	85574494	2460	1885	9.424953333
ZNF285	NM_152354	chr19	-	44887806	44907778	851	805	9.423296667
KIN	NM_012311	chr10	-	7795365	7831945	1900	1854	9.422823333
MGAM	NM_004668	chr7	+	141693677	141808548	3189	408	9.41074
RAD52	NM_134424	chr12	-	1019253	1060864	2120	2069	9.410536667
ZNF334	NM_199441	chr20	-	45127705	45144195	724	586	9.40254
HPGD	NM_001145816	chr4	-	175409326	175445793	1338	559	9.401013333
SPATA18	NM_145263	chr4	+	52915591	52965459	2675	2167	9.399676667
CHST9	NM_031422	chr18	-	24493593	24767290	6020	2792	9.395873333

SEMA3C	NM_006379	chr7	-	80369852	80550668	3358	2811	9.392226667
AKAP7	NM_138633	chr6	+	131569502	131606674	1279	685	9.392016667
ZNF470	NM_001001668	chr19	+	57076888	57096263	1264	1112	9.378056667
NAA16	NM_024561	chr13	+	41883339	41953167	1843	1826	9.37306
STAC	NM_003149	chr3	+	36420095	36591497	6430	5214	9.36826
IFIT1	NM_001548	chr10	+	91150320	91165745	1349	1038	9.366623333
SLC16A12	NM_213606	chr10	-	91188049	91297314	4598	3707	9.345923333
C6orf138	NM_207499	chr6	-	47865343	48038426	1367	69	9.338243333
FAM153A	NM_173663	chr5	-	177148363	177209506	390	100	9.337343333
DMBT1	NM_017579	chr10	+	124318179	124405253	4059	3335	9.336523333
PCOTH	NM_001135816	chr13	+	24461590	24468243	1958	1512	9.33524
HNF4G	NM_004133	chr8	+	76450201	76481062	259	0	9.327913333
CGB5	NM_033043	chr19	+	49545100	49550569	352	305	9.32702
CDKL2	NM_003948	chr4	-	76499702	76557722	1321	982	9.30918
SCAND3	NM_052923	chr6	-	28537405	28557113	1528	1094	9.304783333
COBLL1	NM_014900	chr2	-	165539256	165699929	4844	4203	9.30446
ANKRD50	NM_020337	chr4	-	125583202	125635888	2230	2137	9.290986667
IL1F10	NM_173161	chr2	+	113823545	113835428	593	214	9.28121
TXNDC16	NM_020784	chr14	-	52895306	53021302	3403	3015	9.269836667
KPNA1	NM_002264	chr3	-	122138746	122235787	2639	2590	9.269683333
ARL6	NM_177976	chr3	+	97481593	97519374	1192	850	9.267786667
MACROD2	NM_080676	chr20	+	13974144	16035842	24253	20328	9.259123333
C9orf102	NM_001010895	chr9	+	98635898	98733123	1700	1602	9.246706667
KLHL20	NM_014458	chr1	+	173682078	173757841	1523	1050	9.239623333

BOR-Papers in Press. Published as DOI: 10.1095/biolreprod.113.110403

APBA1	NM_001163	chr9	-	72040447	72289276	8705	8262	9.233093333
UGT8	NM_003360	chr4	+	115541521	115600203	351	317	9.232343333
COL22A1	NM_152888	chr8	-	139598476	139928237	7554	6156	9.22053
ANO5	NM_213599	chr11	+	22212720	22306914	2070	1977	9.2195
ZFP42	NM_174900	chr4	+	188914923	188928200	1244	274	9.20709
TRAM1L1	NM_152402	chr4	-	118002708	118008737	664	523	9.207043333
C2orf67	NM_152519	chr2	-	210883433	211038052	2369	2135	9.19704
DMGDH	NM_013391	chr5	-	78291427	78367450	3352	2892	9.192483333
TM4SF18	NM_138786	chr3	-	149034283	149053549	326	0	9.183423333
TRPM3	NM_206948	chr9	-	73396776	73485975	1464	297	9.176156667
PAPPA2	NM_021936	chr1	+	176430305	176662342	4512	3049	9.174263333
KLF8	NM_007250	chrX	+	56256820	56316323	2525	1733	9.168266667
ENPP2	NM_006209	chr8	-	120567317	120653107	3187	2873	9.15386
PTER	NM_030664	chr10	+	16476965	16557737	1689	1582	9.149416667
ZNF433	NM_001080411	chr19	-	12123530	12148526	1298	1036	9.12931
ZNF681	NM_138286	chr19	-	23919995	23943694	1064	853	9.12869
UGT3A2	NM_174914	chr5	-	36033117	36069024	320	232	9.12766
CKAP2L	NM_152515	chr2	-	113493442	113524255	1894	1630	9.122036667
C13orf31	NM_153218	chr13	+	44451967	44470069	1438	1277	9.10155
FAM134B	NM_019000	chr5	-	16471145	16511032	1890	1566	9.101546667
ORC1	NM_004153	chr1	-	52836499	52872144	1565	1513	9.101516667
ZNF257	NM_033468	chr19	+	22233264	22275904	795	701	9.086206667
ZNF667	NM_022103	chr19	-	56948691	56990771	1902	1605	9.08085
LRRC31	NM_024727	chr3	-	169555027	169589661	2054	1734	9.064913333

STEAP2	NM_152999	chr7	+	89838998	89868993	1088	993	9.059893333
CPS1	NM_001875	chr2	+	211419324	211545832	816	780	9.045333333
LRFN5	NM_152447	chr14	+	42074762	42375753	3981	1155	9.02487
HIC2	NM_015094	chr22	+	21769691	21807751	2803	1985	9.014283333
SLC5A9	NM_001135181	chr1	+	48686355	48716317	2845	2303	9.009916667
AQP11	NM_173039	chr11	+	77298678	77323402	1922	1777	9.009746667
MAGEE1	NM_020932	chrX	+	75646044	75653747	1155	1134	8.993353333
ZNF782	NM_001001662	chr9	-	99577271	99618390	868	729	8.987566667
SLC17A3	NM_006632	chr6	-	25843326	25876472	430	233	8.986316667
EYA4	NM_172105	chr6	+	133560493	133855259	3488	2626	8.98359
EDAR	NM_022336	chr2	-	109508925	109607829	8168	7720	8.982746667
FEM1C	NM_020177	chr5	-	114854606	114882592	1392	1305	8.97989
RFX7	NM_022841	chr15	-	56380729	56537484	2551	2304	8.977626667
PDE1A	NM_005019	chr2	-	183005181	183389254	3073	2845	8.97616
C12orf29	NM_001009894	chr12	+	88427266	88445938	985	918	8.96963
TAGLN3	NM_013259	chr3	+	111715584	111734736	1930	1849	8.958713333
SST	NM_001048	chr3	-	187384692	187390202	811	243	8.951036667
FZD7	NM_003507	chr2	+	202897308	202905161	3629	3412	8.946353333
DCLK1	NM_004734	chr13	-	36340788	36707515	11242	8996	8.923333333
FBN2	NM_001999	chr5	-	127591599	127875736	5487	1971	8.916773333
ADAMTS3	NM_014243	chr4	-	73144685	73436517	7388	6608	8.91665
HRASLS	NM_020386	chr3	+	192956916	192990645	1278	1125	8.909063333
NRK	NM_198465	chrX	+	105064534	105204603	2943	2192	8.90548
C21orf91	NM_017447	chr21	-	19159282	19193704	1985	1869	8.903146667

ZNF75D	NM_007131	chrX	-	134417721	134431966	577	532	8.896763333
ZNF682	NM_033196	chr19	-	20113225	20152278	968	874	8.887793333
GALNT4	NM_003774	chr12	-	89911188	89920536	2069	2064	8.886403333
ZNF154	NM_001085384	chr19	-	58209808	58222580	906	888	8.884146667
KCTD4	NM_198404	chr13	-	45764986	45777176	377	0	8.877496667
IL33	NM_033439	chr9	+	6239676	6259983	668	345	8.86943
SLC25A32	NM_030780	chr8	-	104408864	104429469	1559	1095	8.868
ZNF649	NM_023074	chr19	-	52390486	52410306	1920	1860	8.861746667
MYO5B	NM_001080467	chr18	-	47347154	47723452	16837	14487	8.857126667
BARX2	NM_003658	chr11	+	129243879	129324175	2757	2493	8.85065
C9orf123	NM_033428	chr9	-	7794489	7801800	1363	1277	8.842363333
C6orf141	NM_001145652	chr6	+	49516111	49521809	1873	1137	8.83881
ZNF454	NM_182594	chr5	+	178366192	178395219	1417	1268	8.838596667
EIF5A2	NM_020390	chr3	-	170604202	170628427	2151	1923	8.835623333
OPN1LW	NM_020061	chrX	+	153407723	153426508	675	0	8.825923333
GPR173	NM_018969	chrX	+	53076504	53111797	5599	5393	8.820716667
C1QTNF9B	NM_001007537	chr13	-	24463426	24473126	1233	1059	8.79536
CLEC18A	NM_182619	chr16	+	69982808	69999890	1287	667	8.794433333
MRPS14	NM_022100	chr1	-	174981126	174994562	1036	984	8.786956667
SYNJ2BP	NM_018373	chr14	-	70831211	70885808	976	919	8.778643333
TP53AIP1	NM_022112	chr11	-	128803268	128815295	2348	1912	8.77534
ZFP2	NM_030613	chr5	+	178320914	178362211	982	977	8.757306667
FABP3	NM_004102	chr1	-	31836098	31847924	2631	1968	8.74651
ACVR2A	NM_001616	chr2	+	148600568	148690394	2702	2233	8.730503333

HMGB2	NM_002129	chr4	-	174250525	174257596	2240	2098	8.727066667
DPY19L2	NM_173812	chr12	-	63950691	64064355	1122	0	8.71714
FAM71F1	NM_032599	chr7	+	128353441	128373798	1069	670	8.71705
ESRRG	NM_206595	chr1	-	216674586	217264977	12539	3334	8.70754
CLEC18B	NM_001011880	chr16	-	74440527	74457369	1246	520	8.704683333
MZT1	NM_001071775	chr13	-	73280493	73303939	1583	1505	8.704066667
C10orf119	NM_024834	chr10	-	121586970	121634395	2023	1852	8.70262
HLF	NM_002126	chr17	+	53340319	53404427	4769	4512	8.69911
SMARCAD1	NM_020159	chr4	+	95127014	95214444	1018	1012	8.6949
BCL2L15	NM_001010922	chr1	-	114417434	114432170	851	303	8.68299
RSPO3	NM_032784	chr6	+	127438046	127520185	3413	3377	8.68064
OVGP1	NM_002557	chr1	-	111954935	111972400	1480	1457	8.659673333
CCDC144B	NM_182568	chr17	-	18484720	18530846	497	418	8.655593333
ABCB1	NM_000927	chr7	-	87130946	87344565	4604	4117	8.652056667
CHRM3	NM_000740	chr1	+	239790371	240074718	2649	1528	8.649906667
ZNF418	NM_133460	chr19	-	58431250	58448741	822	459	8.646946667
C11orf58	NM_014267	chr11	+	16758146	16781902	1273	1259	8.64625
FBXL4	NM_012160	chr6	-	99319599	99397850	2245	2064	8.642893333
ZNF25	NM_145011	chr10	-	38236793	38267454	1103	1099	8.642203333
ANXA10	NM_007193	chr4	+	169011705	169110894	2548	1138	8.641663333
EFNA5	NM_001962	chr5	-	106710588	107008597	10694	10218	8.62335
KCNK2	NM_014217	chr1	+	215254558	215412437	3723	1853	8.620786667
BEST4	NM_153274	chr1	-	45247255	45255427	2172	2086	8.61789
CYP2J2	NM_000775	chr1	-	60356978	60394424	1481	589	8.61358

FGF12	NM_021032	chr3	-	191857682	192128839	3896	2863	8.598336667
OR52M1	NM_001004137	chr11	+	4564419	4569375	469	135	8.596756667
NECAB1	NM_022351	chr8	+	91801919	91973631	2047	901	8.59323
FAM153B	NM_001079529	chr5	+	175509907	175545458	443	0	8.591026667
ZNF235	NM_004234	chr19	-	44788499	44811179	1148	1123	8.575633333
ORMDL1	NM_016467	chr2	-	190632991	190651098	1333	1327	8.566566667
CLEC18C	NM_173619	chr16	+	70205926	70222799	1287	540	8.56377
ZNF718	NM_001039127	chr4	+	51275	158491	3545	3331	8.56277
SPATA12	NM_181727	chr3	+	57092467	57111461	1552	1234	8.557803333
LIPT2	NM_001144869	chr11	-	74200921	74206756	1598	1453	8.556363333
SYNJ1	NM_203446	chr21	-	33999067	34102352	3718	3324	8.554113333
FERD3L	NM_152898	chr7	-	19182403	19187045	259	143	8.553913333
KLHDC7A	NM_152375	chr1	+	18805422	18814481	2277	2061	8.55252
TRIM61	NM_001012414	chr4	-	165873596	165900819	2164	1481	8.548256667
NOX4	NM_016931	chr11	-	89055520	89226654	3223	1047	8.545666667
SLC18A1	NM_003053	chr8	-	20000364	20042718	1745	856	8.5433
ZNF662	NM_207404	chr3	+	42945400	42962826	1111	913	8.53554
TCEAL5	NM_001012979	chrX	-	102526616	102533798	272	0	8.530966667
ACSM2B	NM_182617	chr16	-	20546081	20589696	749	451	8.52046
ACCN1	NM_183377	chr17	-	31338104	31622007	15873	12014	8.51793
ITGA1	NM_181501	chr5	+	52082134	52251486	4983	4804	8.517926667
ZNF790	NM_206894	chr19	-	37306329	37331285	1370	1278	8.514793333
ODZ2	NM_001122679	chr5	+	166709841	167693163	20587	19343	8.502196667
PSKH2	NM_033126	chr8	-	87058689	87083852	311	0	8.497056667

TMEM168	NM_022484	chr7	-	112403785	112432479	1784	1684	8.48736
SLIT2	NM_004787	chr4	+	20253233	20622789	9307	7416	8.468766667
USP51	NM_201286	chrX	-	55509047	55517632	1900	1896	8.464683333
PTN	NM_002825	chr7	-	136910090	137030547	1669	646	8.46368
COL11A1	NM_080630	chr1	-	103340021	103576053	2830	1790	8.46094
GABRP	NM_014211	chr5	+	170208721	170243051	1744	1360	8.447533333
C8orf48	NM_001007090	chr8	+	13422350	13427798	675	512	8.43731
IL1RAP	NM_134470	chr3	+	190229838	190350074	4043	4025	8.428566667
LYG1	NM_174898	chr2	-	99898699	99919640	328	0	8.423503333
RIMBP3B	NM_001128635	chr22	+	21736038	21745456	1655	272	8.421826667
DTWD1	NM_020234	chr15	+	49911224	49939334	1238	1200	8.4137
SPATA17	NM_138796	chr1	+	217802693	218042485	2722	1649	8.41058
C2orf15	NM_144706	chr2	+	99756183	99769929	1301	1275	8.400713333
SOX11	NM_003108	chr2	+	5830797	5843518	5212	4965	8.390413333
ILDR2	NM_199351	chr1	-	166885994	166946562	4446	4056	8.384896667
NGF	NM_002506	chr1	-	115826535	115882858	4157	3612	8.38479
ANKRD34B	NM_001004441	chr5	-	79850572	79868305	2560	1832	8.366906667
CSTF2T	NM_015235	chr10	-	53453244	53461356	1167	907	8.364336667
USP15	NM_006313	chr12	+	62652185	62801899	1841	1641	8.359253333
ANKRD20A3	NM_001012419	chr9	-	43087970	43135545	541	437	8.34319
SPC25	NM_020675	chr2	-	169725399	169748945	928	706	8.326946667
PF4	NM_002619	chr4	-	74844794	74849716	712	427	8.318713333
ARL14	NM_025047	chr3	+	160392946	160398236	470	463	8.318076667
SERPINB3	NM_006919	chr18	-	61320429	61331198	502	0	8.31625

PRLHR	NM_004248	chr10	-	120350914	120357161	2171	1733	8.31088
ZNF330	NM_014487	chr4	+	142140047	142157851	1424	1127	8.305356667
PCDHAC2	NM_031883	chr5	+	140344350	140351007	692	583	8.303953333
IL20RB	NM_144717	chr3	+	136674705	136731921	2674	2644	8.303576667
SPIN3	NM_001010862	chrX	-	57015262	57023989	1282	1183	8.30324
KIAA1524	NM_020890	chr3	-	108266716	108310492	1226	1092	8.302336667
LRRC52	NM_001005214	chr1	+	165511476	165535186	402	167	8.283746667
SLC35F3	NM_173508	chr1	+	234038677	234462263	14980	14337	8.28287
FBXL17	NM_001163315	chr5	-	107192732	107719800	7056	6966	8.279616667
OPN1MW	NM_000513	chrX	+	153446083	153464353	81	0	8.275933333
ZNF577	NM_032679	chr19	-	52372549	52393230	851	786	8.267206667
SLITRK3	NM_014926	chr3	-	164902506	164916470	1595	354	8.265353333
RG9MTD2	NM_152292	chr4	-	100465862	100486826	1462	1199	8.264903333
DNAJC12	NM_201262	chr10	-	69568964	69599938	1148	741	8.25743
ZNF202	NM_003455	chr11	-	123592995	123614364	1935	1900	8.24553
PELO	NM_015946	chr5	+	52081772	52100453	2488	2293	8.231923333
TIMD4	NM_138379	chr5	-	156344291	156392267	920	767	8.223426667
PCDH10	NM_032961	chr4	+	134068468	134114733	5076	1344	8.214736667
C1orf161	NM_152367	chr1	+	116652374	116679862	2037	1955	8.202723333
C14orf105	NM_018168	chr14	-	57934593	57962577	1368	1251	8.197293333
VTCN1	NM_024626	chr1	-	117684207	117755550	2626	1817	8.17842
CSMD3	NM_198124	chr8	-	113233157	114391383	1233	761	8.168913333
FAM92A1	NM_145269	chr8	+	94710771	94742672	1909	1643	8.157553333
C11orf45	NM_145013	chr11	-	128767458	128777593	3615	2155	8.154063333

FAT4	NM_024582	chr4	+	126235565	126416088	4223	3479	8.149796667
PDGFD	NM_033135	chr11	-	103775912	104037028	4912	3954	8.146963333
UGT2A3	NM_024743	chr4	-	69792175	69819510	362	0	8.132733333
CDKN2B	NM_078487	chr9	-	22000900	22011313	1749	1669	8.12908
HACE1	NM_020771	chr6	-	105173966	105309795	2595	2272	8.098266667
EPHA6	NM_173655	chr3	+	97156488	97369422	869	305	8.09539
ZNF177	NM_003451	chr19	+	9471694	9495294	429	297	8.094753333
ZNF708	NM_021269	chr19	-	21471961	21514213	839	783	8.090926667
FAM117B	NM_173511	chr2	+	203497899	203636481	2778	2645	8.077053333
HERC5	NM_016323	chr4	+	89376266	89429315	1336	1219	8.069643333
ACTBL2	NM_001017992	chr5	-	56773841	56780637	758	0	8.069193333
KSR2	NM_173598	chr12	-	117888815	118408029	18727	16295	8.062223333
ZNF585A	NM_199126	chr19	-	37638999	37665334	792	781	8.058466667
C5orf49	NM_001089584	chr5	-	7829509	7853265	2213	1822	8.03249
PTX3	NM_002852	chr3	+	157152578	157163418	2139	1516	8.03157
PPFIA2	NM_003625	chr12	-	81651354	82155110	3932	2456	8.020926667
C6orf170	NM_152730	chr6	-	121398625	121657645	1535	1451	8.017136667
DSEL	NM_032160	chr18	-	65171817	65185968	1672	1541	8.011056667
TRPC1	NM_003304	chr3	+	142441264	142528730	1754	1543	8.003906667
PTGS2	NM_000963	chr1	-	186638942	186651560	987	986	7.990313333
FANCF	NM_022725	chr11	-	22642077	22649388	1465	1385	7.98393
C1orf114	NM_021179	chr1	-	169362112	169398671	522	321	7.982126667
MFSD6L	NM_152599	chr17	-	8698426	8704668	426	133	7.97743
PMAIP1	NM_021127	chr18	+	57565190	57573539	2682	2492	7.970483333

H2AFB1	NM_001017990	chrX	+	154111315	154115834	1070	0	7.969603333
ANKRD20A1	NM_032250	chr9	+	67924759	67971841	444	0	7.968853333
APOOL	NM_198450	chrX	+	84256896	84350325	1658	1501	7.95892
OSBPL6	NM_145739	chr2	+	179182969	179262876	696	357	7.958546667
SYCP3	NM_153694	chr12	-	102120424	102135251	160	0	7.954966667
XAGE3	NM_133179	chrX	-	52889556	52899120	25	0	7.947006667
IFI27	NM_005532	chr14	+	94575077	94585034	767	702	7.93915
ZNF347	NM_032584	chr19	-	53639955	53664323	1436	987	7.936873333
H2AFB2	NM_001017991	chrX	+	154608434	154612784	1030	259	7.906906667
EXOC8	NM_175876	chr1	-	231466480	231475579	2109	2099	7.90503
SLC22A2	NM_003058	chr6	-	160635792	160681964	1382	881	7.901396667
ACSM5	NM_017888	chr16	+	20418854	20454282	1605	1604	7.879156667
ENPP5	NM_021572	chr6	-	46125760	46140718	909	514	7.866266667
ZNF596	NM_173539	chr8	+	180198	199340	1402	1391	7.8637
KRT222	NM_152349	chr17	-	38809870	38823417	325	0	7.859013333
PNMA6A	NM_032882	chrX	+	152238837	152244646	1208	603	7.853063333
OR10H5	NM_001004466	chr19	+	15902857	15907807	226	0	7.851786667
ATP6V0A4	NM_130841	chr7	-	138389037	138460783	2565	2519	7.850596667
PRSS1	NM_002769	chr7	+	142455317	142462928	646	457	7.841913333
ANKRD20A2	NM_001012421	chr9	+	42366301	42413411	352	0	7.841846667
ZNF141	NM_003441	chr4	+	329594	369692	2838	2536	7.837766667
LRRC19	NM_022901	chr9	-	26991133	27007692	501	0	7.836026667
CXCL14	NM_004887	chr5	-	134904369	134916970	1654	1200	7.81933
ATF7IP2	NM_024997	chr16	+	10520723	10579496	663	366	7.8186

BANK1	NM_017935	chr4	+	102709762	102997970	3078	2657	7.818543333
THSD7A	NM_015204	chr7	-	11408060	11873825	4112	3164	7.811536667
SLC17A4	NM_005495	chr6	+	25752925	25783404	492	230	7.806203333
LRRIQ1	NM_032165	chr12	+	85428097	85520637	1146	956	7.796276667
MTNR1B	NM_005959	chr11	+	92700787	92717949	1702	764	7.790416667
JPH1	NM_020647	chr8	-	75144937	75235563	4794	4620	7.787883333
ZNF793	NM_001013659	chr19	+	37995839	38036240	1417	1188	7.771293333
C6orf165	NM_001031743	chr6	+	88115688	88176192	1803	1791	7.766326667
NMBR	NM_002511	chr6	-	142394743	142411937	490	414	7.763123333
ZNF599	NM_001007248	chr19	-	35246977	35266135	994	991	7.744113333
C2orf80	NM_001099334	chr2	-	209028069	209056774	771	759	7.743733333
CACNA2D3	NM_018398	chr3	+	54154691	55110585	24344	20023	7.73848
OR2S2	NM_019897	chr9	-	35955103	35960152	457	198	7.72102
MEFV	NM_000243	chr16	-	3290026	3308628	1033	410	7.72083
CLDN20	NM_001001346	chr6	+	155583145	155599683	642	445	7.716463333
GBA3	NM_020973	chr4	+	22692546	22823193	1297	413	7.70968
INSC	NM_001042536	chr11	+	15134482	15270755	6134	6117	7.69776
TMEM232	NM_001039763	chr5	-	109753196	110064451	1093	888	7.696036667
ZNF385B	NM_152520	chr2	-	180304709	180728233	6890	6565	7.69056
SATB1	NM_002971	chr3	-	18387132	18468830	1900	1579	7.68808
NRXN3	NM_138970	chr14	+	79743652	80332761	7121	1607	7.682996667
MYO3A	NM_017433	chr10	+	26221000	26503466	2045	1056	7.678856667
DEFB4A	NM_004942	chr8	+	7750197	7756238	731	189	7.676706667
ZNF10	NM_015394	chr12	+	133705212	133738050	1232	1223	7.666333333

KRT71	NM_033448	chr12	-	52935691	52948932	1065	948	7.64365
C10orf68	NM_024688	chr10	+	32854649	33173793	1810	1501	7.643406667
LINGO2	NM_152570	chr9	-	27946526	28721304	1898	747	7.6351
CNTF	NM_000614	chr11	+	58388144	58395206	596	42	7.628703333
C5orf43	NM_001048249	chr5	-	60451534	60460303	1312	1193	7.626503333
PKHD1	NM_170724	chr6	-	51583645	51954424	5922	2886	7.61982
C6orf225	NM_001033564	chr6	+	112406672	112425994	995	951	7.61896
FOLH1	NM_004476	chr11	-	49166185	49232223	1562	672	7.617233333
SCGB1D4	NM_206998	chr11	-	62061752	62068537	468	427	7.605303333
WISP3	NM_198239	chr6	+	112373369	112392888	285	0	7.600693333
ANAPC10	NM_014885	chr4	-	145914311	146021369	2423	2046	7.577823333
HIST2H3D	NM_001123375	chr1	-	149782778	149787237	282	0	7.567716667
DPPA4	NM_018189	chr3	-	109042986	109058420	376	113	7.561973333
ITIH2	NM_002216	chr10	+	7743234	7793484	446	0	7.56015
INHBA	NM_002192	chr7	-	41726599	41744707	3281	2412	7.552276667
C11orf93	NM_001136105	chr11	+	111167974	111181354	1985	1835	7.542083333
CCDC54	NM_032600	chr3	+	107094186	107099482	474	36	7.536353333
TLL1	NM_012464	chr4	+	166792408	167026994	4500	3042	7.53516
TMEM174	NM_153217	chr5	+	72467021	72472971	333	0	7.524673333
CALCRL	NM_005795	chr2	-	188205847	188315022	968	723	7.520716667
CERKL	NM_201548	chr2	-	182399399	182523835	1915	1523	7.518376667
ZFP57	NM_001109809	chr6	-	29638167	29646932	685	372	7.511043333
CNTN5	NM_175566	chr11	+	98889869	100229474	4146	649	7.507283333
KCNJ5	NM_000890	chr11	+	128759311	128789952	7241	5698	7.506706667

BOR-Papers in Press. Published as DOI: 10.1095/biolreprod.113.110403

FAM151B	NM_205548	chr5	+	79781798	79840207	1353	1253	7.50341
CYP39A1	NM_016593	chr6	-	46515443	46622524	1725	1351	7.496613333
GUCY1A2	NM_000855	chr11	-	106555908	106891172	5284	2988	7.48635
FAM189A2	NM_004816	chr9	+	71942239	72009371	2185	960	7.471203333
KRT23	NM_015515	chr17	-	39076950	39095837	1262	916	7.471093333
RNF175	NM_173662	chr4	-	154629310	154683388	2843	1937	7.468826667
SLC14A2	NM_007163	chr18	+	43192764	43265061	5264	5136	7.462763333
GPR137C	NM_001099652	chr14	+	53017864	53106432	2856	2505	7.4423
C11orf87	NM_207645	chr11	+	109290844	109301894	1900	1296	7.441846667
PANX3	NM_052959	chr11	+	124479451	124492252	181	130	7.429723333
KRT76	NM_015848	chr12	-	53159937	53173130	474	168	7.4267
POLR3B	NM_018082	chr12	+	106749434	106905977	3394	2828	7.423713333
NCF1	NM_000265	chr7	+	74186307	74205660	1229	603	7.423583333
RASGEF1B	NM_152545	chr4	-	82346217	82395062	2384	2027	7.42119
DEFB125	NM_153325	chr20	+	66349	79297	347	0	7.41848
DPPA2	NM_138815	chr3	-	109010633	109037365	351	287	7.417943333
ARHGEF38	NM_017700	chr4	+	106471775	106554838	2759	1039	7.414583333
CRISPLD1	NM_031461	chr8	+	75894706	75948794	2138	757	7.406186667
ZNF845	NM_138374	chr19	+	53835000	53860123	1331	1331	7.393286667
EPHA7	NM_004440	chr6	-	93947738	94131301	3576	2591	7.388303333
HEATR7B2	NM_173489	chr5	-	40996120	41073445	64	0	7.384906667
DAPL1	NM_001017920	chr2	+	159649827	159674497	1981	578	7.38351
SLC45A2	NM_016180	chr5	-	33942719	33986781	891	872	7.379783333
ITGA4	NM_000885	chr2	+	182319617	182404469	1541	1380	7.376936667

CNTN1	NM_175038	chr12	+	41084356	41466095	3286	1536	7.37438
C9orf66	NM_152569	chr9	-	211106	217894	1406	1165	7.371676667
DNAH7	NM_018897	chr2	-	196600425	196935537	3325	3268	7.36405
C10orf67	NM_153714	chr10	-	23603518	23635773	1964	1316	7.36169
KRT31	NM_002277	chr17	-	39547975	39555845	315	240	7.35927
MPP7	NM_173496	chr10	-	28337921	28573068	3397	3346	7.356656667
ADAMTS16	NM_139056	chr5	+	5138441	5322413	6089	3611	7.352233333
OR51G2	NM_001005238	chr11	-	4933947	4938894	480	152	7.350033333
MURC	NM_001018116	chr9	+	103338334	103352174	790	671	7.347213333
PCDH20	NM_022843	chr13	-	61981817	61991656	2043	709	7.33975
EDNRB	NM_003991	chr13	-	78467614	78494967	1800	1529	7.334076667
PPP2R2B	NM_181678	chr5	-	145967066	146463034	3583	3015	7.325846667
ADAM22	NM_021723	chr7	+	87561700	87828450	3600	2004	7.31599
PRSS55	NM_198464	chr8	+	10381054	10398334	791	401	7.29941
IFNA1	NM_024013	chr9	+	21438438	21443316	54	0	7.2863
CALCA	NM_001741	chr11	-	14988046	14995833	2478	805	7.268536667
FBXO8	NM_012180	chr4	-	175155808	175207403	1927	1614	7.260073333
CTNND2	NM_001332	chr5	-	10969950	11906111	11854	4333	7.250223333
ARMC4	NM_018076	chr10	-	28099095	28289978	2887	2031	7.24758
RNF2	NM_007212	chr1	+	185012549	185073741	2511	1790	7.24682
ST8SIA4	NM_175052	chr5	-	100219013	100240971	2576	704	7.2343
RYR3	NM_001036	chr15	+	33601175	34160304	14301	7334	7.233426667
MAB21L2	NM_006439	chr4	+	151501075	151507846	298	244	7.223663333
CRH	NM_000756	chr8	-	67086610	67092847	1125	1090	7.222423333

BMP5	NM_021073	chr6	-	55618236	55742376	1548	1183	7.22171
RAG1	NM_000448	chr11	+	36587561	36603311	558	0	7.217613333
FOLH1B	NM_153696	chr11	+	89390463	89433887	451	53	7.199763333
S100A8	NM_002964	chr1	-	153360506	153365550	290	0	7.190516667
SFTPA2	NM_001098668	chr10	-	81313606	81322164	925	741	7.167826667
GYS2	NM_021957	chr12	-	21687121	21759782	745	345	7.161156667
C9orf71	NM_153237	chr9	-	71149496	71157784	396	218	7.15929
CCKAR	NM_000730	chr4	-	26481016	26494043	504	232	7.14076
RPA3	NM_002947	chr7	-	7674573	7760239	3454	2997	7.131253333
FAM71B	NM_130899	chr5	-	156587342	156595280	510	291	7.130626667
TPTE	NM_199261	chr21	-	10904741	10992921	1233	683	7.121176667
ACADL	NM_001608	chr2	-	211050714	211092216	2043	1195	7.08747
LRRC4C	NM_020929	chr11	-	40133751	40317665	2600	935	7.07297
KRT79	NM_175834	chr12	-	53213229	53230078	1706	1299	7.065403333
SULT1E1	NM_005420	chr4	-	70704928	70727871	890	157	7.054636667
GRIK2	NM_175768	chr6	+	101844859	102519959	2941	1443	7.053396667
DUSP27	NM_001080426	chr1	+	167062085	167100403	1317	1300	7.0378
KCNQ3	NM_004519	chr8	-	133139254	133495005	7311	7274	7.03728
NOVA1	NM_006491	chr14	-	26937322	27068961	2106	1649	7.03382
CYP4A22	NM_001010969	chr1	+	47601105	47616527	356	316	7.02836
FRA10AC1	NM_145246	chr10	-	95425638	95464330	1624	1306	7.02298
C11orf30	NM_020193	chr11	+	76154067	76264590	2405	2216	7.021296667
ASTN1	NM_207108	chr1	-	176835952	177136025	4024	4006	7.01059
SYT14	NM_153262	chr1	+	210109536	210339634	3114	2865	7.006193333

MAEL	NM_032858	chr1	+	166956517	166993448	307	0	7.005006667
CRYGD	NM_006891	chr2	-	208984329	208991314	632	118	7.004726667
GSC	NM_173849	chr14	-	95232558	95238500	2352	2075	7.001316667
FAM81B	NM_152548	chr5	+	94725046	94788145	2518	854	6.998743333
RTKN2	NM_145307	chr10	-	63950951	64030467	2759	2483	6.998536667
DDX43	NM_018665	chr6	+	74102283	74129290	704	678	6.976933333
SULT1C4	NM_006588	chr2	+	108992419	109006271	971	905	6.966126667
C15orf32	NM_153040	chr15	+	93012905	93046348	473	0	6.962356667
SNRPE	NM_003094	chr1	+	203828738	203842281	1626	1358	6.94875
ZNF471	NM_020813	chr19	+	57017210	57042270	1442	1220	6.947133333
SIRPB2	NM_001134836	chr20	-	1453234	1474234	1214	590	6.947126667
IGSF5	NM_001080444	chr21	+	41115332	41176024	1332	519	6.938006667
KRT37	NM_003770	chr17	-	39574807	39582823	525	358	6.92469
GABRB1	NM_000812	chr4	+	47031293	47430448	2921	2225	6.91558
GC	NM_000583	chr4	-	72605409	72651889	729	0	6.903153333
FMO1	NM_002021	chr1	+	171215661	171257114	1605	1535	6.894933333
LHFPL3	NM_199000	chr7	+	103967102	104551004	6743	6275	6.89033
CSMD1	NM_033225	chr8	-	2790873	4854329	7388	6744	6.88385
SORCS3	NM_014978	chr10	+	106398857	107026994	16991	3912	6.881363333
CH25H	NM_003956	chr10	-	90963692	90969072	1505	1257	6.872543333
LYZL4	NM_144634	chr3	-	42436573	42454066	116	0	6.859406667
C11orf65	NM_152587	chr11	-	108251725	108340259	2376	1458	6.857273333
DEPDC4	NM_152317	chr12	-	100644040	100662858	1918	1789	6.853966667
IQUB	NM_178827	chr7	-	123090234	123176719	3472	2639	6.846893333

ELAVL2	NM_004432	chr9	-	23688101	23828064	2134	1916	6.84502
MDGA2	NM_182830	chr14	-	47306826	47814439	999	677	6.837626667
ATOH1	NM_005172	chr4	+	94748076	94753143	1666	928	6.83708
CNTNAP5	NM_130773	chr2	+	124780862	125674864	5117	2968	6.826883333
TRIM40	NM_138700	chr6	+	30102508	30118513	377	255	6.824136667
MAGEE2	NM_138703	chrX	-	75000821	75007080	219	38	6.819833333
FCGR1B	NM_001017986	chr1	-	120924906	120937945	915	870	6.81264
IFT57	NM_018010	chr3	-	107877657	107943418	1220	889	6.803266667
IL7	NM_000880	chr8	-	79643003	79719759	1881	1513	6.80252
LRRC66	NM_001024611	chr4	-	52857864	52885787	350	0	6.800823333
SLFN13	NM_144682	chr17	-	33760113	33777857	2365	2269	6.798883333
C8orf85	NM_001025357	chr8	+	117948462	117958240	630	603	6.792843333
SLC16A9	NM_194298	chr10	-	61408520	61471650	2326	1993	6.782086667
FAM171B	NM_177454	chr2	+	187556787	187630513	1583	1535	6.78081
CNTN6	NM_014461	chr3	+	1132627	1447279	2919	422	6.766636667
RFPL1	NM_021026	chr22	+	29832570	29840445	637	65	6.766036667
CYP4B1	NM_001099772	chr1	+	47262668	47287022	2170	0	6.764783333
IL20RA	NM_014432	chr6	-	137319106	137368299	3108	2328	6.757263333
CRNN	NM_016190	chr1	-	152379717	152388751	515	0	6.757066667
ZNF233	NM_181756	chr19	+	44762074	44781469	949	515	6.737293333
TAS2R38	NM_176817	chr7	-	141670429	141675574	89	0	6.735506667
GJB5	NM_005268	chr1	+	35218719	35226113	1666	1081	6.72231
ZNF43	NM_003423	chr19	-	21985750	22020971	864	862	6.722083333
AOAH	NM_001637	chr7	-	36550547	36766155	5342	2339	6.718476667

DEFB130	NM_001037804	chr8	-	12166469	12177826	57	0	6.702316667
NRAP	NM_198060	chr10	-	115346581	115425806	2055	1240	6.69577
ACRV1	NM_020115	chr11	-	125540227	125552943	102	0	6.691946667
TNP1	NM_003284	chr2	-	217722180	217726783	38	0	6.688626667
TRIM9	NM_052978	chr14	-	51460783	51564423	4057	3721	6.688133333
OR10T2	NM_001004475	chr1	-	158366310	158371257	379	0	6.679003333
GSTA5	NM_153699	chr6	-	52694539	52712894	859	509	6.678786667
LYG2	NM_175735	chr2	-	99856709	99873571	911	0	6.665983333
POU6F2	NM_007252	chr7	+	39015607	39506391	7587	4581	6.663856667
SIAH3	NM_198849	chr13	-	46352414	46427847	5438	2676	6.6544
PCDH7	NM_032457	chr4	+	30720035	31150424	5687	3281	6.637556667
C6	NM_001115131	chr5	-	41140334	41263541	974	0	6.61537
FCRL2	NM_030764	chr1	-	157713521	157748923	157	110	6.612503333
LRAT	NM_004744	chr4	+	155663161	155676271	2942	736	6.60896
SLC5A1	NM_000343	chr22	+	32437017	32511012	2413	1838	6.606013333
SMR3A	NM_012390	chr4	+	71224491	71234824	103	0	6.601716667
ANKK1	NM_178510	chr11	+	113256511	113273141	1594	792	6.58015
F8	NM_019863	chrX	-	154062062	154116578	1327	984	6.574773333
KCNH7	NM_173162	chr2	-	163277755	163697241	2105	1602	6.572356667
HTR1B	NM_000863	chr6	-	78169946	78175121	1867	391	6.56779
FLJ37543	NM_173667	chr5	+	60931634	61004363	1677	1399	6.561573333
APLF	NM_173545	chr2	+	68692689	68809295	2681	2098	6.54479
IQCF6	NM_001143833	chr3	-	51810575	51815010	292	86	6.52413
IGSF10	NM_178822	chr3	-	151151776	151178498	1951	1573	6.50781

CCNH	NM_001239	chr5	-	86688080	86710837	1740	1397	6.505603333
WDR16	NM_145054	chr17	+	9477942	9548777	3363	2873	6.50507
MEP1A	NM_005588	chr6	+	46759092	46809520	842	113	6.500013333
ANKRD31	NM_001164443	chr5	-	74362120	74534704	2348	1345	6.486586667
HIST1H2AG	NM_021064	chr6	+	27098815	27103315	1267	1185	6.47545
PARK2	NM_013988	chr6	-	161766588	163150835	32226	19292	6.468696667
NTRK2	NM_006180	chr9	+	87281464	87640506	10903	9481	6.46621
TSPAN8	NM_004616	chr12	-	71516875	71553780	475	425	6.460593333
RGS22	NM_015668	chr8	-	100971274	101120345	2041	1435	6.443663333
ANXA13	NM_004306	chr8	-	124691032	124751648	2530	2490	6.443443333
PAQR9	NM_198504	chr3	-	142678072	142684179	1546	1422	6.41949
TIMP4	NM_003256	chr3	-	12192566	12202648	1447	1119	6.41577
ZC3H6	NM_198581	chr2	+	113031176	113099641	1430	1329	6.413413333
ZMAT4	NM_024645	chr8	-	40386109	40757344	5639	4244	6.409296667
KBTBD3	NM_198439	chr11	-	105919823	105950466	1143	1079	6.402593333
FLRT2	NM_013231	chr14	+	85994486	86096271	5000	4633	6.393956667
TAS2R14	NM_023922	chr12	-	11088851	11093807	317	222	6.39324
FGF14	NM_175929	chr13	-	102371203	103056125	13223	7157	6.374593333
FAM123A	NM_199138	chr13	-	25740670	25747858	1723	1222	6.368123333
MTHFD2L	NM_001144978	chr4	+	75021827	75170815	3557	3349	6.346456667
SPEF2	NM_144722	chr5	+	35615987	35673677	1387	1323	6.33451
CDH18	NM_004934	chr5	-	19471153	19990354	2392	617	6.319633333
OPRM1	NM_001145287	chr6	+	154405640	154442595	724	0	6.31322
OR6Q1	NM_001005186	chr11	+	57796423	57801379	488	0	6.305476667

CBLN2	NM_182511	chr18	-	70201913	70213724	3113	2990	6.304436667
CLASP2	NM_015097	chr3	-	33535737	33761849	3262	3223	6.30385
RPRM	NM_019845	chr2	-	154331850	154337323	2323	1619	6.299873333
NPBWR1	NM_005285	chr8	+	53850466	53855455	2853	2455	6.27375
FRMPD2	NM_001018071	chr10	-	49362600	49484942	4601	4031	6.27272
DEFB131	NM_001040448	chr4	+	9444258	9454241	196	0	6.270706667
DSG3	NM_001944	chr18	+	29025730	29060666	231	0	6.266193333
TRPM6	NM_017662	chr9	-	77335409	77505011	3593	3050	6.26415
ZNF474	NM_207317	chr5	+	121463213	121491267	1393	1353	6.260826667
SCGB3A2	NM_054023	chr5	+	147256272	147263757	283	0	6.260793333
TCP11	NM_018679	chr6	-	35083847	35111188	1525	1161	6.249923333
SLITRK5	NM_015567	chr13	+	88322868	88333871	4569	1926	6.24441
HTR1A	NM_000524	chr5	-	63254276	63259547	621	374	6.231
KCNK18	NM_181840	chr10	+	118954998	118971811	881	160	6.211976667
CST11	NM_130794	chr20	-	23429039	23435483	118	73	6.17327
C5orf46	NM_206966	chr5	-	147270269	147288102	194	0	6.1605
KCTD16	NM_020768	chr5	+	143548435	143858945	3988	3080	6.147406667
SH3GL2	NM_003026	chr9	+	17576951	17799123	2479	1254	6.14092
TINAG	NM_014464	chr6	+	54171201	54256951	981	432	6.137623333
FCRL3	NM_052939	chr1	-	157645976	157672648	404	237	6.13325
EML5	NM_183387	chr14	-	89079172	89261097	3547	3004	6.116703333
KCNJ1	NM_153767	chr11	-	128705913	128739269	5093	2930	6.116663333
IQCF1	NM_152397	chr3	-	51926890	51939387	382	0	6.116106667
ERP27	NM_152321	chr12	-	15064974	15093464	510	349	6.11078

ADAMTS18	NM_199355	chr16	-	77314023	77471012	2990	2961	6.1088
ADAM7	NM_003817	chr8	+	24296507	24368276	1005	352	6.09283
CA3	NM_005181	chr8	+	86349054	86363268	1227	109	6.083006667
CCDC11	NM_145020	chr18	-	47751561	47794866	1937	1335	6.082136667
OR13J1	NM_001004487	chr9	-	35867458	35872399	403	0	6.07976
EAF2	NM_018456	chr3	+	121552032	121607374	1627	1604	6.0765
CALCB	NM_000728	chr11	+	15093144	15102178	2395	807	6.07011
C4orf26	NM_178497	chr4	+	76479256	76491928	1140	1006	6.069723333
FABP7	NM_001446	chr6	+	123098644	123107219	313	0	6.068493333
SH3GL3	NM_003027	chr15	+	84114089	84289494	5301	4916	6.059283333
TTR	NM_000371	chr18	+	29169728	29180987	980	436	6.054853333
EFCAB1	NM_024593	chr8	-	49633951	49649871	985	564	6.05365
RUNDC3B	NM_138290	chr7	+	87255727	87463614	2006	1867	6.047316667
FGL1	NM_201553	chr8	-	17719898	17754914	430	336	6.042663333
FAM110B	NM_147189	chr8	+	58905111	59064278	8567	7678	6.00724
SEMA3D	NM_152754	chr7	-	84622870	84753248	828	559	6.00686
C13orf35	NM_207440	chr13	+	113299356	113340812	2355	2052	6.006486667
DSG4	NM_177986	chr18	+	28954738	28995881	809	227	6.00094
LRRTM1	NM_178839	chr2	-	80527001	80533488	1752	1292	5.985626667
EPHA5	NM_182472	chr4	-	66183279	66537654	2947	1868	5.973083333
MCM9	NM_153255	chr6	-	119229760	119258304	1402	1228	5.967956667
LOC643037	NM_001190462	chr11	+	94243693	94267290	1633	1241	5.966033333
MC4R	NM_005912	chr18	-	58036562	58042002	571	411	5.964736667
TTC29	NM_031956	chr4	-	147626177	147869035	1314	656	5.954533333

NPY	NM_000905	chr7	+	24321805	24333485	1710	889	5.95069
C4orf39	NM_153027	chr4	+	165876098	165882274	1288	821	5.94499
AFP	NM_001134	chr4	+	74299931	74323493	1292	1143	5.92978
SPINK13	NM_001040129	chr5	+	147646421	147667774	1023	278	5.929196667
NR3C2	NM_001166104	chr4	-	148997913	149365673	5912	4975	5.9225
SLC2A13	NM_052885	chr12	-	40146821	40501662	5499	5304	5.91522
PI15	NM_015886	chr8	+	75734770	75769265	672	431	5.90475
DENND2C	NM_198459	chr1	-	115125194	115214733	1620	1526	5.900953333
ZNF98	NM_001098626	chr19	-	22571897	22607149	661	606	5.891453333
C4orf6	NM_005750	chr4	+	5524881	5531528	572	201	5.890843333
GRXCR1	NM_001080476	chr4	+	42893281	43034674	1571	206	5.888733333
SCGB2A1	NM_002407	chr11	+	61974138	61983412	738	267	5.88642
HAO2	NM_016527	chr1	+	119909400	119938752	785	733	5.885893333
SLC10A2	NM_000452	chr13	-	103694346	103721197	893	140	5.8844
ADAMTS20	NM_025003	chr12	-	43746010	43947725	1183	708	5.879003333
SERPINB4	NM_002974	chr18	-	61302491	61313503	494	139	5.86783
KLKB1	NM_000892	chr4	+	187146670	187181626	500	394	5.862446667
CYP4X1	NM_178033	chr1	+	47487238	47518424	1271	937	5.860453333
CLDN25	NM_001101389	chr11	+	113648516	113653208	521	436	5.85886
GRM7	NM_181874	chr3	+	6900800	7785219	8196	3990	5.857726667
C3orf77	NM_001145030	chr3	+	44281376	44375591	859	809	5.847366667
XIRP2	NM_152381	chr2	+	167757973	168118262	1925	1008	5.84554
C14orf177	NM_182560	chr14	+	99175948	99186104	174	0	5.842276667
GUCA1C	NM_005459	chr3	-	108624640	108674678	1984	457	5.8121

SCGB1D2	NM_006551	chr11	+	62007722	62014281	767	730	5.8119
TDRD9	NM_153046	chr14	+	104392815	104521005	2790	2530	5.801546667
C17orf77	NM_152460	chr17	+	72579055	72592349	196	118	5.79319
C3orf30	NM_152539	chr3	+	118862995	118872303	500	433	5.78657
IMPG1	NM_001563	chr6	-	76629060	76784336	1315	846	5.782016667
SGCZ	NM_139167	chr8	-	13945371	15097793	1884	1511	5.78151
GPR116	NM_015234	chr6	-	46818240	46924676	2607	2014	5.771003333
SFTPA1	NM_005411	chr10	+	81368693	81377200	1563	1532	5.75822
VWC2L	NM_001080500	chr2	+	215274459	215442654	2078	999	5.753863333
PIK3C2G	NM_004570	chr12	+	18412472	18803353	2697	2219	5.739816667
RGN	NM_152869	chrX	+	46935773	46954713	2188	2155	5.71291
SLC27A6	NM_014031	chr5	+	128299208	128371336	906	766	5.70586
SPICE1	NM_144718	chr3	-	113159563	113236035	2101	1790	5.701663333
ATP13A5	NM_198505	chr3	-	192990829	193098515	1693	531	5.69588
UCP1	NM_021833	chr4	-	141479048	141491960	1657	995	5.690673333
CCDC129	NM_194300	chr7	+	31554976	31695304	329	328	5.687226667
DYNLRB2	NM_130897	chr16	+	80572852	80586542	998	860	5.68312
NPSR1	NM_207173	chr7	+	34695895	34919945	4676	4448	5.683096667
CCL1	NM_002981	chr17	-	32685397	32692253	837	630	5.670763333
PKD2L2	NM_014386	chr5	+	137223123	137278157	631	554	5.666293333
GRIN2B	NM_000834	chr12	-	13712408	14135023	11586	2911	5.652796667
RBP2	NM_004164	chr3	-	139169724	139197353	1290	221	5.649246667
DCLK3	NM_033403	chr3	-	36751911	36783353	725	724	5.626766667
FGF13	NM_033642	chrX	-	137711732	137823516	1957	1650	5.621776667

MEOX2	NM_005924	chr7	-	15648835	15728309	1550	570	5.617513333
CLCA4	NM_012128	chr1	+	87010757	87048433	459	0	5.616803333
C9orf170	NM_001001709	chr9	+	89761557	89776642	1267	1020	5.604433333
C8A	NM_000562	chr1	+	57318441	57385895	3211	2606	5.604096667
NKAIN3	NM_173688	chr8	+	63159499	63905629	2769	2572	5.59882
FGL2	NM_006682	chr7	-	76820686	76831151	599	572	5.597223333
DKK2	NM_014421	chr4	-	107840957	107959454	2107	1483	5.591583333
GABRG3	NM_033223	chr15	+	27214427	27780374	12209	10379	5.587266667
FAM5B	NM_021165	chr1	+	177138631	177253559	4941	4384	5.583483333
OTOL1	NM_001080440	chr3	+	161212594	161223731	434	0	5.571823333
TMEM213	NM_001085429	chr7	+	138480737	138492770	676	155	5.544383333
TDRD1	NM_198795	chr10	+	115937027	115994064	715	290	5.543323333
ZNF804A	NM_194250	chr2	+	185461091	185806215	2932	1724	5.525923333
C2orf40	NM_032411	chr2	+	106680111	106696610	598	0	5.505043333
FCGR1A	NM_000566	chr1	+	149752248	149766075	1022	782	5.504243333
PDZRN4	NM_013377	chr12	+	41829539	41970393	1206	955	5.499076667
SCGB1D1	NM_006552	chr11	+	61955708	61963010	398	390	5.492763333
CYP4Z1	NM_178134	chr1	+	47531158	47585993	1516	1307	5.489493333
CACNA1E	NM_000721	chr1	+	181450714	181772716	7620	6560	5.48375
SLC17A8	NM_139319	chr12	+	100748855	100817838	2017	1871	5.477936667
FUT9	NM_006581	chr6	+	96461843	96665489	1308	788	5.477286667
SNTG2	NM_018968	chr2	+	944552	1373385	11983	7224	5.470396667
GPR111	NM_153839	chr6	+	47622324	47667534	1860	848	5.467583333
SDR16C5	NM_138969	chr8	-	57210568	57235242	657	368	5.452346667

AKR1C4	NM_001818	chr10	+	5236796	5262913	173	0	5.436963333
NDUFA4	NM_002489	chr7	-	10970813	10981814	1609	1473	5.421543333
C10orf90	NM_001004298	chr10	-	128111572	128212011	4453	3183	5.420523333
PCDH17	NM_001040429	chr13	+	58203787	58305066	3787	2261	5.41307
DEFB1	NM_005218	chr8	-	6726095	6737530	602	216	5.412643333
C1QTNF7	NM_031911	chr4	+	15427627	15449792	248	121	5.410456667
HTR3D	NM_182537	chr3	+	183747330	183759158	803	353	5.40968
CYP2C9	NM_000771	chr10	+	96696413	96751149	515	199	5.40831
SULT1C3	NM_001008743	chr2	+	108861649	108883808	558	0	5.40672
TRHR	NM_003301	chr8	+	110097674	110133813	558	232	5.404086667
DMP1	NM_004407	chr4	+	88569452	88587513	804	235	5.39372
GKN1	NM_019617	chr2	+	69199703	69210113	93	0	5.38787
FBXO39	NM_153230	chr17	+	6677550	6692966	646	631	5.384236667
KLRK1	NM_007360	chr12	-	10522950	10544641	254	0	5.378533333
ZCCHC13	NM_203303	chrX	+	73522023	73526870	289	67	5.36611
TMEM195	NM_001004320	chr7	-	15237941	15603641	1549	1179	5.363106667
CRYGB	NM_005210	chr2	-	209005295	209012878	78	0	5.358286667
STEAP4	NM_024636	chr7	-	87903742	87938210	883	175	5.352076667
SLC26A7	NM_134266	chr8	+	92259514	92408947	2085	1318	5.34671
CTNNA3	NM_013266	chr10	-	67677723	69457950	6121	4164	5.345466667
GRIA4	NM_001112812	chr11	+	105479409	105786232	3721	2297	5.33697
MBL2	NM_000242	chr10	-	54523138	54533461	853	304	5.325776667
QRFPR	NM_198179	chr4	-	122247795	122304182	1854	380	5.325543333
TMEM196	NM_152774	chr7	-	19756936	19814405	1588	675	5.318046667

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CYTIP	NM_004288	chr2	-	158269129	158302605	319	263	5.31388
KCNA4	NM_002233	chr11	-	30029763	30040489	855	400	5.312906667
ABCB5	NM_178559	chr7	+	20684964	20798638	668	520	5.305126667
ADAM30	NM_021794	chr1	-	120434154	120441114	282	147	5.29937
TDRD6	NM_001168359	chr6	+	46653610	46674057	123	118	5.29416
FAM19A1	NM_213609	chr3	+	68051452	68596772	1917	167	5.2916
HRG	NM_000412	chr3	+	186381796	186398024	59	0	5.290763333
TEX28	NM_001586	chrX	-	153496930	153525439	899	420	5.284883333
ATP13A4	NM_032279	chr3	-	193117864	193274697	665	286	5.27979
SLC30A10	NM_018713	chr1	-	220085604	220103994	2036	2009	5.279216667
C5orf40	NM_001001343	chr5	-	156766605	156774730	838	621	5.278576667
THSD7B	NM_001080427	chr2	+	137746460	138437288	4551	1267	5.276903333
LRP1B	NM_018557	chr2	-	140986994	142891271	7814	4986	5.269043333
AGBL4	NM_032785	chr1	-	48996525	50491627	14834	10944	5.261573333
FAT3	NM_001008781	chr11	+	92083260	92631636	7519	4992	5.260423333
CXorf57	NM_018015	chrX	+	105853158	105924674	1411	855	5.256323333
VSTM1	NM_198481	chr19	-	54542078	54569208	303	0	5.252543333
CRB1	NM_201253	chr1	+	197235332	197449586	1997	1151	5.239483333
GSTA2	NM_000846	chr6	-	52612883	52630362	654	72	5.23877
C8orf79	NM_020844	chr8	+	12801181	12889285	3788	3237	5.237116667
GAP43	NM_002045	chr3	+	115340149	115442335	3331	3111	5.236653333
NOL4	NM_003787	chr18	-	31429062	31805516	3274	2921	5.20967
ZNF483	NM_133464	chr9	+	114285445	114308713	1258	1075	5.202453333
APOH	NM_000042	chr17	-	64206145	64227557	323	279	5.198523333

NCKAP5	NM_207481	chr2	-	133427370	134328032	15738	13980	5.19697
KLRC2	NM_002260	chr12	-	10581204	10590593	419	185	5.195896667
SLITRK6	NM_032229	chr13	-	86364920	86375484	265	116	5.186656667
DHRS9	NM_199204	chr2	+	169921543	169954678	2872	2050	5.183496667
FGF1	NM_033137	chr5	-	141969741	141995727	819	765	5.16702
DBF4	NM_006716	chr7	+	87503542	87540857	1615	1492	5.162363333
KLRC1	NM_213658	chr12	-	10596636	10609216	86	0	5.15463
SLC28A3	NM_022127	chr9	-	86891090	86985414	4066	2988	5.148996667
HHLA2	NM_007072	chr3	+	108019330	108099127	902	394	5.123023333
GSTA1	NM_145740	chr6	-	52654176	52670665	461	166	5.1198
RAG2	NM_000536	chr11	-	36611491	36621830	793	772	5.118173333
PROK2	NM_021935	chr3	-	71818804	71836358	848	629	5.115
SLC6A15	NM_182767	chr12	-	85251265	85308607	2395	1243	5.090433333
TMPRSS11E	NM_014058	chr4	+	69311165	69365323	661	531	5.089206667
MUM1L1	NM_152423	chrX	+	105410296	105454950	1369	0	5.078156667
LRRN3	NM_018334	chr7	+	110729060	110767510	581	450	5.072023333
MDH1B	NM_001039845	chr2	-	207600487	207632051	1116	1031	5.067656667
AGXT2	NM_031900	chr5	-	34996204	35050241	3734	1949	5.06276
ST6GALNAC3	NM_152996	chr1	+	76538387	77098670	6222	5288	5.060906667
PXDNL	NM_144651	chr8	-	52230135	52724006	6095	5631	5.055203333
S100A12	NM_005621	chr1	-	153344182	153350076	713	584	5.039206667
OR10J5	NM_001004469	chr1	-	159502866	159507798	130	0	5.03398
NRG3	NM_001165973	chr10	+	83635441	84748936	9500	4080	5.032486667
KRT24	NM_019016	chr17	-	38852241	38862003	780	0	5.02987

PLAC4	NM_182832	chr21	-	42545156	42559167	141	0	5.019246667
ZBBX	NM_024687	chr3	-	166956075	167100072	650	504	5.01632
FGF5	NM_033143	chr4	+	81185740	81214172	2669	2453	5.01561
MOS	NM_005372	chr8	-	57023499	57028542	949	685	5.013323333
STOML3	NM_145286	chr13	-	39538060	39566997	365	0	5.005576667
FAM183A	NM_001101376	chr1	+	43611592	43624068	698	600	4.980273333
C4orf31	NM_024574	chr4	-	121954780	121995674	1621	1280	4.979143333
RNF148	NM_198085	chr7	-	122339718	122345022	120	0	4.975346667
MPPED2	NM_001584	chr11	-	30429616	30604041	2062	403	4.97484
PLCB1	NM_182734	chr20	+	8111294	8867548	15852	15783	4.94767
KRT20	NM_019010	chr17	-	39030139	39043496	117	94	4.9472
GABRB2	NM_021911	chr5	-	160713434	160977131	2632	2323	4.943196667
AGTR1	NM_032049	chr3	+	148445965	148462791	670	161	4.943103333
C1orf173	NM_001002912	chr1	-	75031793	75141423	1250	886	4.919833333
GAD2	NM_001134366	chr10	+	26503234	26592049	2818	2755	4.919753333
DSC3	NM_024423	chr18	-	28568050	28624782	2588	1343	4.917396667
ZP4	NM_021186	chr1	-	238039162	238056223	733	0	4.89231
C8orf45	NM_173518	chr8	+	67780982	67836284	1718	1479	4.888073333
COL21A1	NM_030820	chr6	-	55919386	56114379	2339	1666	4.880486667
IFLTD1	NM_152590	chr12	-	25627014	25708179	1347	1045	4.876443333
PNLIPRP1	NM_006229	chr10	+	118348488	118370687	866	573	4.87596
OGN	NM_033014	chr9	-	95144247	95168938	257	233	4.864266667
C7orf71	NM_001145531	chr7	+	26675488	26688925	857	575	4.853873333
TEDDM1	NM_172000	chr1	-	182365250	182371752	1054	576	4.831476667

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PLA2G7	NM_005084	chr6	-	46670051	46705152	1872	1329	4.83087
IFNK	NM_020124	chr9	+	27522310	27528497	409	214	4.817246667
MAGEB4	NM_002367	chrX	+	30258055	30264309	98	0	4.811253333
EYA1	NM_172060	chr8	-	72107666	72270980	1362	1230	4.799046667
TAC1	NM_013998	chr7	+	97359269	97371785	1156	450	4.79203
RNF180	NM_178532	chr5	+	63459669	63515340	1721	1708	4.78512
KHDRBS2	NM_152688	chr6	-	62387863	62998101	897	837	4.784996667
FAM71D	NM_173526	chr14	+	67654108	67697268	1147	784	4.77706
GLP2R	NM_004246	chr17	+	9727379	9795023	4594	2887	4.775306667
TNNI3K	NM_015978	chr1	+	74699083	75012109	1193	1127	4.770146667
GRID2	NM_001510	chr4	+	93223548	94695650	4985	3289	4.752163333
CFHR4	NM_006684	chr1	+	196855210	196889764	513	217	4.7432
KCNJ3	NM_002239	chr2	+	155553091	155715015	1368	305	4.741693333
C4orf37	NM_174952	chr4	-	98478023	99066392	3755	1954	4.734733333
AQP4	NM_004028	chr18	-	24430006	24444576	792	480	4.734376667
C10orf113	NM_001177483	chr10	-	21412690	21437489	391	315	4.716356667
FIBIN	NM_203371	chr11	+	27013626	27020633	1373	1063	4.70228
PRSS54	NM_001080492	chr16	-	58311899	58330952	434	264	4.697146667
CD1B	NM_001764	chr1	-	158295738	158303322	224	158	4.689543333
CD96	NM_198196	chr3	+	111258924	111373207	3290	2799	4.677676667
DIRAS2	NM_017594	chr9	-	93370112	93407109	686	421	4.672206667
DYDC1	NM_138812	chr10	-	82093860	82118501	911	325	4.651786667
FBXO48	NM_001024680	chr2	-	68687503	68696391	2153	1208	4.642736667
CDH7	NM_033646	chr18	+	63415486	63550176	1368	62	4.635853333

DYDC2	NM_032372	chr10	+	82114556	82129830	911	325	4.634616667
KRTAP4-7	NM_033061	chr17	+	39238457	39243397	538	516	4.630396667
C9orf135	NM_001010940	chr9	+	72433729	72523149	2246	2154	4.622846667
COLEC10	NM_006438	chr8	+	120077422	120121203	1050	886	4.622066667
TSLP	NM_033035	chr5	+	110405388	110415723	2019	1965	4.61945
IL22RA2	NM_181310	chr6	-	137462955	137496786	1770	1676	4.61457
CYP2C18	NM_001128925	chr10	+	96441249	96497948	290	0	4.607646667
HMGCLL1	NM_019036	chr6	-	55297169	55446013	979	508	4.57281
HCRTR2	NM_001526	chr6	+	55037069	55149419	436	215	4.572323333
IL12B	NM_002187	chr5	-	158739789	158759482	2090	1774	4.571823333
AKR1D1	NM_005989	chr7	+	137759176	137805051	1009	499	4.567713333
MTTP	NM_000253	chr4	+	100483238	100547155	1552	1120	4.555853333
SLC30A8	NM_173851	chr8	+	118145335	118190954	234	159	4.553843333
LMO3	NM_018640	chr12	-	16699305	16761432	1717	936	4.546366667
CWH43	NM_025087	chr4	+	48986263	49066096	755	669	4.54235
C9orf84	NM_173521	chr9	-	114446899	114547780	1376	591	4.535396667
GPRC6A	NM_148963	chr6	-	117111246	117152199	230	169	4.529403333
C3orf57	NM_001040100	chr3	-	161060578	161091872	2206	1920	4.525413333
C13orf36	NM_203451	chr13	+	37246047	37273976	984	385	4.511733333
CNBD1	NM_173538	chr8	+	87876674	88396956	2108	522	4.511163333
C7	NM_000587	chr5	+	40907597	40985043	319	0	4.50509
KRT27	NM_181537	chr17	-	38931058	38940787	279	267	4.50308
SLC36A2	NM_181776	chr5	-	150692537	150729152	1412	1141	4.49875
FOXR2	NM_198451	chrX	+	55647831	55654622	407	0	4.497933333

KCNV1	NM_014379	chr8	-	110977231	110988960	2200	318	4.49178
CCDC67	NM_181645	chr11	+	93061881	93173637	1504	963	4.486743333
HCN1	NM_021072	chr5	-	45257350	45698221	2777	1127	4.481356667
OR4F6	NM_001005326	chr15	+	102343921	102348862	686	324	4.480283333
SLC7A3	NM_032803	chrX	-	70143428	70152976	674	120	4.45648
KCTD8	NM_198353	chr4	-	44173918	44452825	2094	1907	4.45383
ENAM	NM_031889	chr4	+	71492459	71514537	872	0	4.452706667
PNLIPRP3	NM_001011709	chr10	+	118185422	118239469	774	628	4.452286667
TMC1	NM_138691	chr9	+	75134715	75453268	7739	7670	4.4502
DKK4	NM_014420	chr8	-	42229584	42236675	316	0	4.435093333
SYCP2	NM_014258	chr20	-	58436616	58509210	919	848	4.42777
DEFB110	NM_001037728	chr6	-	49974849	49991695	236	0	4.42562
USH2A	NM_206933	chr1	-	215794234	216598739	7090	3961	4.424496667
FAM19A2	NM_178539	chr12	-	62100039	62588552	2145	1946	4.41884
KLRC3	NM_007333	chr12	-	10566181	10575195	378	192	4.40324
FBXO40	NM_016298	chr3	+	121310168	121351140	111	51	4.400556667
C13orf39	NM_001010977	chr13	-	103336095	103348855	54	0	4.39267
SLC35F4	NM_001080455	chr14	-	58028638	58065616	243	0	4.383096667
DCX	NM_178153	chrX	-	110535006	110657461	1659	803	4.37208
BMP3	NM_001201	chr4	+	81950117	81980686	1503	1374	4.36486
MUSK	NM_005592	chr9	+	113429049	113565279	1974	1958	4.36397
SPINK7	NM_032566	chr5	+	147689988	147697482	181	0	4.363883333
CDH12	NM_004061	chr5	-	21748971	22855732	3877	2931	4.360436667
ZCCHC5	NM_152694	chrX	-	77909564	77916826	828	716	4.35805

VSIG1	NM_182607	chrX	+	107286198	107324415	876	785	4.351753333
SLC9A4	NM_001011552	chr2	+	103087760	103152432	2245	1814	4.3495
CA10	NM_020178	chr17	-	49705672	50238133	4371	2187	4.345063333
RGS4	NM_005613	chr1	+	163036762	163048593	1154	928	4.344676667
B3GALT1	NM_020981	chr2	+	168673180	168729367	883	868	4.33914
SCN2A	NM_021007	chr2	+	166148339	166250821	732	692	4.337046667
MS4A2	NM_000139	chr11	+	59854135	59867941	371	0	4.295183333
WDR52	NM_018338	chr3	-	113079710	113162362	1127	939	4.29184
LIPF	NM_004190	chr10	+	90422092	90440573	250	0	4.290986667
UPP2	NM_173355	chr2	+	158956380	158994667	1483	0	4.277013333
KRTAP2-4	NM_033184	chr17	-	39219366	39224132	481	285	4.274023333
P2RY13	NM_176894	chr3	-	151042094	151049338	280	120	4.272776667
LRRC67	NM_001013626	chr8	-	67898365	67942787	1167	805	4.267313333
RALYL	NM_173848	chr8	+	85093584	85836079	2399	1574	4.26634
CALCR	NM_001742	chr7	-	93051797	93206043	2108	332	4.266076667
OLR1	NM_002543	chr12	-	10308897	10326791	251	132	4.25703
SNTN	NM_001080537	chr3	+	63636342	63652892	214	125	4.25419
NKAIN2	NM_153355	chr6	+	124123067	125148787	7478	3885	4.24992
KLHL1	NM_020866	chr13	-	70272723	70684626	2649	378	4.24349
STK32A	NM_145001	chr5	+	146612577	146730393	1731	932	4.240746667
CNKSR2	NM_014927	chrX	+	21390534	21674814	3509	3271	4.238903333
PI3	NM_002638	chr20	+	43801538	43807186	633	0	4.22789
SRD5A2	NM_000348	chr2	-	31747654	31808041	2179	647	4.226886667
CTNNA2	NM_004389	chr2	+	79738058	80877989	13677	12433	4.223716667

SPACA1	NM_030960	chr6	+	88755505	88778551	331	0	4.181406667
SERPINB7	NM_003784	chr18	+	61440610	61474605	502	466	4.18119
TRPC4	NM_016179	chr13	-	38208771	38445940	3706	3570	4.172936667
CPA3	NM_001870	chr3	+	148581041	148616873	549	441	4.17208
ADAMTS19	NM_133638	chr5	+	128794101	129076377	2516	2490	4.163113333
FSHR	NM_181446	chr2	-	49187294	49383667	792	443	4.158563333
FMR1NB	NM_152578	chrX	+	147060847	147110188	434	88	4.14892
TRPC7	NM_020389	chr5	-	135546997	135703165	4585	4140	4.138326667
SPATA16	NM_031955	chr3	-	172605145	172861059	2190	1859	4.1328
BRS3	NM_001727	chrX	+	135568123	135576599	394	256	4.126413333
C12orf50	NM_152589	chr12	-	88371814	88425177	256	235	4.123656667
ART4	NM_021071	chr12	-	14980243	14998414	1655	1609	4.123323333
PF4V1	NM_002620	chr4	+	74717011	74722199	559	404	4.122693333
AMTN	NM_212557	chr4	+	71382296	71400460	353	0	4.122496667
TMPRSS11F	NM_207407	chr4	-	68916914	68997588	827	536	4.110846667
UNC5D	NM_080872	chr8	+	35090973	35654182	9383	2413	4.10822
TACR3	NM_001059	chr4	-	104508623	104642974	1266	1170	4.095683333
ROBO2	NM_002942	chr3	+	77087292	77701115	4282	3187	4.07763
GRM1	NM_001114329	chr6	+	146346780	146760732	3331	2738	4.073343333
ADAM18	NM_014237	chr8	+	39440085	39589584	968	289	4.073276667
ANGPTL1	NM_004673	chr1	-	178816668	178842216	162	87	4.072236667
MRGPRX2	NM_054030	chr11	-	19074001	19084229	597	0	4.06963
LRRC3B	NM_052953	chr3	+	26662298	26754266	1634	1026	4.06671
PLCZ1	NM_033123	chr12	-	18834114	18892919	2058	1845	4.065086667

RERG	NM_032918	chr12	-	15258714	15376412	2148	1573	4.062493333
TEK	NM_000459	chr9	+	27107145	27232173	3151	2709	4.058883333
CHODL	NM_024944	chr21	+	19615148	19641688	1211	486	4.053703333
WNT16	NM_057168	chr7	+	120967088	120983159	1452	900	4.04489
SLC4A10	NM_022058	chr2	+	162478843	162843787	1840	807	4.041323333
GALNT3	NM_004482	chr2	-	166602311	166652804	2271	2013	4.032506667
IRS4	NM_003604	chrX	-	107973725	107981608	3307	3298	4.028343333
GREM2	NM_022469	chr1	-	240650871	240777463	4524	3539	4.019723333
KCNC2	NM_153748	chr12	-	75431894	75605512	2074	836	4.016113333
FSTL5	NM_020116	chr4	-	162303047	163087187	2307	1414	4.006843333
C1orf110	NM_178550	chr1	-	162822085	162840606	792	656	3.984393333
HSD17B13	NM_178135	chr4	-	88222939	88246057	406	0	3.97718
PTPRZ1	NM_002851	chr7	+	121511157	121704091	1974	1960	3.973356667
TMPRSS15	NM_002772	chr21	-	19639431	19777971	505	394	3.971153333
WIF1	NM_007191	chr12	-	65442402	65517347	452	324	3.949286667
ATP6V0D2	NM_152565	chr8	+	87109137	87168455	1297	1161	3.947896667
SPOCK3	NM_016950	chr4	-	167652534	168157742	2207	1605	3.942303333
CARTPT	NM_004291	chr5	+	71012988	71018876	755	306	3.93852
CXorf22	NM_152632	chrX	+	35935849	36010270	918	0	3.925833333
MCHR2	NM_032503	chr6	-	100365784	100444115	601	359	3.910576667
VIP	NM_194435	chr6	+	153069931	153082903	241	160	3.908176667
TMEM207	NM_207316	chr3	-	190144442	190169666	337	0	3.908143333
OPN5	NM_181744	chr6	+	47747773	47796117	1383	894	3.89396
GPC5	NM_004466	chr13	+	92048933	93521488	6313	4806	3.88813

SLC5A7	NM_021815	chr2	+	108600993	108632444	552	0	3.887013333
SCN3A	NM_006922	chr2	-	165942028	166062578	716	0	3.8859
PCDH9	NM_203487	chr13	-	66874964	67806469	8570	6449	3.884723333
HIST1H2BJ	NM_021058	chr6	-	27098093	27102576	1267	1185	3.884056667
FGF23	NM_020638	chr12	-	4475391	4490895	368	293	3.881563333
TBX22	NM_016954	chrX	+	79275740	79289269	483	112	3.878673333
SLC17A6	NM_020346	chr11	+	22357665	22403047	354	161	3.870706667
AVPR1A	NM_000706	chr12	-	63538214	63548591	1791	457	3.87042
GABRA2	NM_001114175	chr4	-	46249579	46393397	1537	494	3.8703
NRXN1	NM_138735	chr2	-	50143641	50576895	1089	1022	3.869076667
RIT2	NM_002930	chr18	-	40321190	40697658	1470	554	3.8598
ART3	NM_001179	chr4	+	76993861	77035956	927	879	3.85165
DACH1	NM_080760	chr13	-	72010096	72443331	3996	3397	3.827156667
CXCL13	NM_006419	chr4	+	78430905	78534989	2669	2597	3.819393333
LPPR4	NM_014839	chr1	+	99727846	99777139	944	692	3.805623333
SEMA3E	NM_012431	chr7	-	82991220	83280480	2320	1991	3.793366667
C18orf34	NM_198995	chr18	-	30515364	31022686	4235	2273	3.781016667
RPE65	NM_000329	chr1	-	68892505	68917643	789	332	3.769826667
PHYHIPL	NM_032439	chr10	+	60934346	61009535	2045	2027	3.752473333
UNC13C	NM_001080534	chr15	+	54303099	54922807	2028	676	3.746846667
SPINK6	NM_205841	chr5	+	147580355	147596701	76	0	3.74003
FAM55B	NM_182495	chr11	+	114547198	114579653	290	0	3.727333333
OXGR1	NM_080818	chr13	-	97635971	97648605	1136	441	3.722506667
GPR174	NM_032553	chrX	+	78424467	78429727	412	0	3.721056667

OLFM3	NM_058170	chr1	-	102266125	102464791	323	182	3.710246667
DEFB135	NM_001033017	chr8	+	11837828	11844100	755	679	3.707733333
STATH	NM_003154	chr4	+	70859646	70870174	234	0	3.705416667
BEX4	NM_001127688	chrX	+	102468018	102474096	1316	1269	3.701263333
FAM5C	NM_199051	chr1	-	190064795	190448760	2263	257	3.681236667
C9orf57	NM_001128618	chr9	-	74664295	74677522	171	0	3.663606667
GRIA2	NM_001083620	chr4	+	158139818	158289227	3248	2492	3.65406
F9	NM_000133	chrX	+	138610893	138647618	973	498	3.640973333
C6orf118	NM_144980	chr6	-	165691151	165725112	1050	954	3.631183333
YIPF7	NM_182592	chr4	-	44622352	44655659	317	310	3.623373333
SLITRK1	NM_052910	chr13	-	84449341	84458529	1030	0	3.610986667
IL2	NM_000586	chr4	-	123370624	123379651	338	0	3.608116667
GADL1	NM_207359	chr3	-	30765690	30938154	2604	1805	3.594323333
OR9Q1	NM_001005212	chr11	+	57789351	57951039	4892	3572	3.57575
GPM6A	NM_201592	chr4	-	176552086	176925649	2116	812	3.56894
ASZ1	NM_130768	chr7	-	117001274	117069578	454	306	3.568516667
CADM2	NM_153184	chr3	+	85773630	86125580	748	0	3.563513333
GNGT1	NM_021955	chr7	+	93533818	93542486	357	255	3.556886667
SPHKAP	NM_030623	chr2	-	228842668	229048362	1836	1035	3.532726667
ANKRD30B	NM_001145029	chr18	+	14746237	14854738	377	139	3.526506667
TMPRSS11A	NM_182606	chr4	-	68774017	68831233	757	173	3.521186667
ABCD2	NM_005164	chr12	-	39943020	40015844	1292	697	3.521083333
XCL1	NM_002995	chr1	+	168543854	168553316	1014	195	3.514163333
SLITRK2	NM_032539	chrX	+	144897345	144909361	2084	1900	3.501973333

NPY2R	NM_000910	chr4	+	156127779	156140229	1171	0	3.501163333
PCDH15	NM_033056	chr10	-	55578858	56563052	1479	1243	3.499886667
FGF20	NM_019851	chr8	-	16848332	16861675	1136	1111	3.466806667
MGAT4C	NM_013244	chr12	-	86371035	87234682	2344	2314	3.4463
FAM190A	NM_207491	chr4	+	91154180	91705155	3534	1266	3.442766667
GNAT3	NM_001102386	chr7	-	80085985	80143243	673	315	3.433026667
NDST4	NM_022569	chr4	-	115746925	116037033	621	0	3.43039
THEMIS	NM_001164687	chr6	-	128027337	128241777	656	602	3.404476667
ZSWIM2	NM_182521	chr2	-	187690205	187715898	821	803	3.396243333
DCDC2B	NM_001099434	chr1	+	32672693	32683798	792	737	
FAM72B	NM_001100910	chr1	+	120837003	120857682	1897	464	
TCHH	NM_007113	chr1	-	152076791	152088557	1764	1426	
RGPD6	NM_001123363	chr2	-	111269377	111338310	668	376	
RGPD8	NM_001164463	chr2	-	113123944	113193223	845	769	
LOC150786	NM_001077637	chr2	-	132116063	132123732	683	578	
UGT1A8	NM_019076	chr2	+	234524289	234683946	5734	5388	
UGT1A10	NM_019075	chr2	+	234543121	234683952	5734	5388	
UGT1A9	NM_021027	chr2	+	234578542	234683952	5585	4960	
UGT1A7	NM_019077	chr2	+	234588582	234683946	5585	4960	
UGT1A6	NM_205862	chr2	+	234598319	234683946	5585	4827	
ULK4	NM_017886	chr3	-	41286088	42005661	14581	13789	
FLJ25363	NM_001145553	chr3	+	109126835	109216015	418	143	
GEMC1	NM_001146686	chr3	-	190568524	190582466	928	616	
KIAA1109	NM_015312	chr4	+	123089756	123285915	746	706	

PABPC4L	NM_001114734	chr4	-	135115487	135124904	1586	1140	
FAM160A1	NM_001109977	chr4	+	152328396	152586785	7175	6903	
RAPGEF2	NM_014247	chr4	+	160186996	160283302	1881	1438	
DDX60L	NM_001012967	chr4	-	169275884	169403639	4074	3897	
DUX4L5	NM_001127389	chr4	+	190990091	190995704	199	0	
DUX4L3	NM_001164467	chr4	+	190990091	190995704	199	0	
FAM159B	NM_001164442	chr5	+	63984133	64016018	1581	1208	
GTF2H2C	NM_001098728	chr5	+	68854049	68890730	244	0	
SERF1B	NM_022978	chr5	+	69319076	69340935	810	808	
FAM169A	NM_015566	chr5	-	74071397	74164616	2436	2369	
C5orf52	NM_001145132	chr5	+	157096559	157109163	1332	1292	
ATP10B	NM_025153	chr5	-	159988125	160281220	4141	2908	
FAM153C	NM_001079527	chr5	+	177433687	177476657	649	0	
ZNF879	NM_001136116	chr5	+	178448774	178463389	859	806	
ZNF389	NM_001145129	chr6	+	28127549	28139377	951	622	
C6orf103	NM_024694	chr6	+	146918134	147138598	1778	1740	
LOC389493	NM_001145712	chr7	-	56180372	56186091	423	0	
ZNF736	NM_001170905	chr7	+	63771184	63812018	1138	800	
PCLO	NM_033026	chr7	-	82381319	82794198	2710	2094	
TMEM229A	NM_001136002	chr7	-	123668968	123675524	1319	1302	
FAM86B2	NM_001137610	chr8	-	12281122	12295853	1432	1381	
TOMM5	NM_001134485	chr9	-	37586410	37594637	766	731	
FOXD4L6	NM_001085476	chr9	-	69197478	69204205	131	0	
ANKRD20A4	NM_001098805	chr9	+	69379979	69427110	408	67	

ANXA8L1	NM_001098845	chr10	-	47155987	47176041	467	0	
C10orf131	NM_001130446	chr10	+	97665720	97700416	1759	1533	
SLC15A5	NM_001170798	chr12	-	16339417	16432620	408	64	
ZAR1L	NM_001136571	chr13	-	32875906	32888092	304	295	
C13orf38	NM_001144986	chr13	-	36803213	36873993	2058	1159	
FAM155A	NM_001080396	chr13	-	107818877	108521461	13071	9124	
C14orf38	NM_001164399	chr14	-	59969783	60045550	1472	1225	
C14orf184	NM_001080113	chr14	-	92036786	92043384	1244	1129	
FAM189A1	NM_015307	chr15	-	29410453	29864928	16805	15522	
CTXN2	NM_001145668	chr15	+	48481865	48497952	551	352	
SHISA9	NM_001145205	chr16	+	12993475	13007508	1565	1557	
FTO	NM_001080432	chr16	+	53735873	54150380	10400	9765	
CCDC144A	NM_014695	chr17	+	16591637	16680312	724	236	
TBC1D3H	NM_001123392	chr17	-	34743934	34759051	146	0	
LOC730755	NM_001165252	chr17	-	39213491	39218345	1142	1040	
KRTAP4-9	NM_001146041	chr17	+	39259639	39264741	493	431	
LOC642597	NM_001145194	chr18	-	5141670	5199256	577	569	
ZNF506	NM_001145404	chr19	-	19901518	19934561	795	785	
ZNF90	NM_007138	chr19	+	20186801	20233978	1390	1323	
ZNF726	NM_001190829	chr19	+	24095682	24108518	808	784	
ZNF814	NM_001144989	chr19	-	58378745	58402443	1048	684	
SPINT3	NM_006652	chr20	-	44139099	44146265	190	0	
RIMBP3	NM_015672	chr22	-	20453992	20463787	2107	0	
RIMBP3C	NM_001128633	chr22	-	21897956	21907751	2311	133	

CXorf49	NM_001145140	chrX	-	70932222	70940136	4033	3811	
FAM127B	NM_001134321	chrX	-	134182961	134188222	1577	1346	
LOC100287428	NM_001170944	chrX	+	152238817	152245403	1841	603	
OPN1MW2	NM_001048181	chrX	+	153446083	153463638	81	0	
F8A3	NM_001007524	chrX	-	154685144	154690262	899	0	
H2AFB3	NM_080720	chrX	-	154687078	154691597	899	0	