

Supplementary Table 1. List of genes (including 2kb 5' and 3' to the gene) with a greater amount (measured in base pairs) of HTE DHS than all five background cell types DHS combined.

Gene Name	Gene RefSeq	Gene Chrom	Gene Strand	Start Minus 2kbp	Stop Plus 2kbp	TE DHS coverage(bp)	Background DHS coverage(bp)	Expression Value
KRT5	NM_000424	chr12	-	52906357	52916244	2264	306	15.76723
KRT6A	NM_005554	chr12	-	52878956	52889182	816	156	15.748045
TMSL3	NM_183049	chr4	-	91757640	91762270	176	0	15.7353
KRT17	NM_000422	chr17	-	39773690	39782883	3011	2547	15.61449
KRT6C	NM_173086	chr12	-	52860298	52869570	365	0	15.37582
EDF1	NM_153200	chr9	-	139755231	139762739	1854	1698	15.2039775
ANXA8L2	NM_001630	chr10	+	47744918	47765041	474	273	15.16625
H2AFZ	NM_002106	chr4	-	100867242	100873513	3459	3376	15.116015
GJB2	NM_004004	chr13	-	20759602	20769115	2787	2738	15.024885
FGFBP1	NM_005130	chr4	-	15935191	15941972	878	492	15.02352
PTHLH	NM_198966	chr12	-	28109015	28124895	3201	2654	14.96137833
SPRR1A	NM_005987	chr1	+	152954555	152960291	336	0	14.586635
PRKAR1A	NM_212472	chr17	+	66506541	66530911	2093	2057	14.521455
SPRR1B	NM_003125	chr1	+	153001677	153007377	1104	398	14.50909
SLC25A1	NM_005984	chr22	-	19161092	19168302	4127	3759	14.37009
GABARAPL1	NM_031412	chr12	+	10363487	10377725	2980	2932	14.36447
KLK5	NM_012427	chr19	-	51444557	51458345	667	514	14.36122
SERPINB3	NM_006919	chr18	-	61320429	61331198	419	349	14.35049
NUPR1	NM_012385	chr16	-	28546660	28552496	891	792	14.322175
CEACAM6	NM_002483	chr19	+	42257396	42278114	1285	724	14.291405
MARCKS	NM_002356	chr6	+	114176525	114186653	5430	5111	14.242325

KRT6B	NM_005555	chr12	-	52838433	52847911	351	0	14.240575
S100A9	NM_002965	chr1	+	153328328	153335504	1044	678	14.167335
MRPS15	NM_031280	chr1	-	36919360	36932041	2067	2054	14.14857
AKR1C1	NM_001353	chr10	+	5003452	5022159	1028	775	14.114515
FAM60A	NM_021238	chr12	-	31431518	31481122	3115	3083	14.08635
SCEL	NM_144777	chr13	+	78107807	78221399	1532	1002	14.0761
NARS	NM_004539	chr18	-	55265892	55291178	1156	1133	14.042685
PRDX4	NM_006406	chrX	+	23683643	23706515	1121	1027	14.03884
TINF2	NM_012461	chr14	-	24706849	24713881	1594	1446	14.035445
UGT1A1	NM_000463	chr2	+	234666917	234683946	868	161	13.983455
RPL36	NM_033643	chr19	+	5688270	5693679	4098	3868	13.9024975
PDPN	NM_198389	chr1	+	13908250	13946453	4083	2626	13.89192
SSH3	NM_017857	chr11	+	67068917	67082079	4898	3960	13.8244075
TRIP10	NM_004240	chr19	+	6737705	6753530	7349	6898	13.82371
CALML3	NM_005185	chr10	+	5564922	5570226	1408	719	13.81053
PIP4K2C	NM_024779	chr12	+	57982940	57999212	2999	2957	13.782845
GPX4	NM_002085	chr19	+	1101934	1108788	6073	6071	13.73975667
KCTD11	NM_001002914	chr17	+	7253206	7260263	4565	4373	13.73162
ZFP36	NM_003407	chr19	+	39895485	39902046	4849	3811	13.72992
CIRBP	NM_001280	chr19	+	1267265	1275172	3804	2943	13.71607
HMGB3	NM_005342	chrX	+	150149761	150161249	3059	2748	13.66429
NCDN	NM_014284	chr1	+	36021391	36034381	4298	3582	13.6359
COQ5	NM_032314	chr12	-	120939080	120968965	1360	1325	13.634705
PRSS8	NM_002773	chr16	-	31140752	31149152	4595	3851	13.618025

PRNP	NM_183079	chr20	+	4664795	4684235	1933	1746	13.60486
PAICS	NM_006452	chr4	+	57299913	57329535	1952	1902	13.484505
NAE1	NM_003905	chr16	-	66834779	66866880	1498	1120	13.466805
C1QBP	NM_001212	chr17	-	5334097	5344472	1382	1330	13.45343
BTG1	NM_001731	chr12	-	92532052	92541674	2694	2692	13.41024
NUS1	NM_138459	chr6	+	117994615	118033887	1660	1282	13.40878
PPP4R1	NM_005134	chr18	-	9544790	9616601	3151	3023	13.39344
PREP	NM_002726	chr6	-	105723440	105853000	3862	3733	13.33848
YTHDC1	NM_133370	chr4	-	69174103	69217825	1095	1079	13.32953
ESRP1	NM_017697	chr8	+	95651362	95721695	5131	4095	13.3271975
DYNLT1	NM_006519	chr6	-	159055505	159067805	2167	2149	13.3114
C6orf72	NM_138785	chr6	+	149885526	149914068	2403	2004	13.25113
EIF2S1	NM_004094	chr14	+	67825032	67855234	2069	1797	13.249685
NANOS1	NM_199461	chr10	+	120787226	120795855	2385	2362	13.24876
TSPAN13	NM_014399	chr7	+	16791349	16826162	1888	1588	13.198795
RAB38	NM_022337	chr11	-	87844413	87910636	1001	917	13.197265
SOX4	NM_003107	chr6	+	21591970	21600850	4534	4367	13.17126
ACTR10	NM_018477	chr14	+	58664831	58704354	1466	1465	13.116875
TMPRSS11E	NM_014058	chr4	+	69311165	69365323	540	531	13.11672
UFM1	NM_016617	chr13	+	38921940	38939144	1200	1142	13.11457
DSC3	NM_024423	chr18	-	28568050	28624782	3107	1343	13.09876
CCNG2	NM_004354	chr4	+	78076355	78093214	2306	2153	13.09432
ARF5	NM_001662	chr7	+	127226515	127233753	2026	1995	13.09363
ZNF703	NM_025069	chr8	+	37551299	37558397	5567	4645	13.08573

CSNK2A1	NM_177560	chr20	-	461336	526483	2599	2519	13.072325
BNC1	NM_001717	chr15	-	83922653	83955469	3866	3765	13.064775
FEM1A	NM_018708	chr19	+	4789726	4797572	1723	1398	13.06051
PRRG4	NM_024081	chr11	+	32849487	32878106	2523	2434	13.05982
UMPS	NM_000373	chr3	+	124447211	124470120	1996	1773	13.036375
CAPNS2	NM_032330	chr16	+	55598582	55603593	332	0	13.03131
SERPINB7	NM_003784	chr18	+	61440610	61474605	880	627	13.010615
ATF5	NM_012068	chr19	+	50429957	50439194	2514	2422	13.00015
PDCD5	NM_004708	chr19	+	33070102	33080330	1574	1445	12.993845
HN1L	NM_144570	chr16	+	1726276	1754074	3320	2799	12.971635
RDX	NM_002906	chr11	-	110098164	110169438	3177	2598	12.963145
NKX2-1	NM_003317	chr14	-	36983602	36990904	6783	5668	12.95704
SERPINB4	NM_002974	chr18	-	61302491	61313503	626	422	12.94
FZD6	NM_003506	chr8	+	104309057	104347095	1798	1467	12.926045
KCNK6	NM_004823	chr19	+	38808482	38821650	2415	2088	12.916985
KLF5	NM_001730	chr13	+	73631140	73653677	3558	2801	12.886225
ATP6V1D	NM_015994	chr14	-	67802587	67828592	1951	1755	12.84845
SLC6A8	NM_005629	chrX	+	152951750	152964049	5099	4528	12.837425
GJA1	NM_000165	chr6	+	121754743	121772874	1133	855	12.821655
PTTG1	NM_004219	chr5	+	159846863	159857747	1102	766	12.80344
PAAF1	NM_025155	chr11	+	73586031	73640780	2345	2330	12.788555
TMPRSS11D	NM_004262	chr4	-	68684592	68751717	725	560	12.787165
PLEC	NM_201384	chr8	-	144987319	145015759	21187	20904	12.777195
CEACAM3	NM_001815	chr19	+	42298532	42317592	1213	831	12.69175

KLK11	NM_144947	chr19	-	51523485	51532886	2850	2346	12.673705
IL18	NM_001562	chr11	-	112011974	112036841	1408	1327	12.64669
CXCL14	NM_004887	chr5	-	134904369	134916970	1862	1343	12.63403
GNB2	NM_005273	chr7	+	100269361	100278793	6781	6754	12.63339
TMEM11	NM_003876	chr17	-	21099261	21119909	4156	4100	12.631775
HIATL1	NM_032558	chr9	+	97134831	97225203	3150	2808	12.61111
RUSC1	NM_014328	chr1	+	155292216	155302910	3165	3154	12.59723
ADRM1	NM_175573	chr20	+	60876025	60885919	8090	7388	12.5791175
SLC25A4	NM_001151	chr4	+	186062415	186073539	1810	1592	12.55696
SSFA2	NM_006751	chr2	+	182754470	182797465	1610	1510	12.520845
APOBEC3C	NM_014508	chr22	+	39408263	39416826	1807	1500	12.497715
CD46	NM_172361	chr1	+	207923381	207970862	1947	1886	12.49447
GJB3	NM_024009	chr1	+	35244788	35253966	5123	4559	12.491675
DSG3	NM_001944	chr18	+	29025730	29060666	813	415	12.48767
ENTPD3	NM_001248	chr3	+	40426671	40472111	1895	1016	12.46067
DDT	NM_001355	chr22	-	24311552	24324020	2775	2420	12.448625
NOP56	NM_006392	chr20	+	2631252	2641040	1952	1724	12.39722
CXCL1	NM_001511	chr4	+	74733107	74738956	1774	1685	12.388935
MFSD1	NM_022736	chr3	+	158517713	158549509	1494	1170	12.3856
TSTA3	NM_003313	chr8	-	144692786	144701733	3460	3324	12.36481
UCHL3	NM_006002	chr13	+	76121925	76182069	1929	1681	12.35968
CST3	NM_000099	chr20	-	23612292	23620575	2195	1482	12.34836
DSC2	NM_024422	chr18	-	28643940	28684389	2653	1907	12.3417
PRMT2	NM_206962	chr21	+	48053525	48086864	4344	3842	12.323005

PKP2	NM_004572	chr12	-	32941678	33051781	2941	2156	12.287155
PLBD1	NM_024829	chr12	-	14654595	14722792	2626	1302	12.27064
TMEM30B	NM_001017970	chr14	-	61742087	61750531	1906	1428	12.264215
NCCRP1	NM_001001414	chr19	+	39685602	39694523	2746	2559	12.2582
SERINC1	NM_020755	chr6	-	122762491	122794953	835	807	12.256545
TFCP2L1	NM_014553	chr2	-	121972162	122044779	4473	4160	12.22148
IDH3B	NM_174856	chr20	-	2637039	2646844	1183	1063	12.21752
SERPINB13	NM_012397	chr18	+	61252532	61268434	438	206	12.21259
MSMB	NM_138634	chr10	+	51547551	51564593	1362	1228	12.1906675
SMAD1	NM_005900	chr4	+	146400949	146482326	3596	3315	12.188885
C20orf4	NM_015511	chr20	+	34822445	34846854	1497	1144	12.140885
LMO4	NM_006769	chr1	+	87792149	87816608	5498	5470	12.138215
ZNF562	NM_017656	chr19	-	9757336	9787777	1276	1132	12.133065
DNM1L	NM_012063	chr12	+	32830135	32900585	1762	1484	12.11321667
C12orf54	NM_152319	chr12	+	48874284	48892298	1185	370	12.10712
DNASE2	NM_001375	chr19	-	12984023	12994336	2011	1908	12.104695
SAAL1	NM_138421	chr11	-	18099888	18129639	972	811	12.060585
FBNP1L	NM_017737	chr1	+	93911686	94022219	3834	2948	12.056625
TCEAL3	NM_032926	chrX	+	102860832	102866856	1355	1073	12.0566075
VSNL1	NM_003385	chr2	+	17719805	17839707	5240	4408	12.043515
CLCA4	NM_012128	chr1	+	87010757	87048433	796	0	12.036785
AGR2	NM_006408	chr7	-	16830262	16846739	1011	770	12.02685
TUSC1	NM_001004125	chr9	-	25674385	25680857	1626	1538	12.025205
INTS12	NM_020395	chr4	-	106601783	106631882	1274	1247	12.01615

DNAJB14	NM_001031723	chr4	-	100818708	100869880	1471	1242	11.9846925
PPIC	NM_000943	chr5	-	122357076	122374426	2166	2124	11.984645
UPK1B	NM_006952	chr3	+	118890423	118926001	2239	1970	11.978865
SESN3	NM_144665	chr11	-	94904131	94966247	1675	1274	11.97292
PIGG	NM_017733	chr4	+	490987	535321	3501	2552	11.9697
USO1	NM_003715	chr4	+	76647827	76737367	2079	1907	11.96663
STEAP1	NM_012449	chr7	+	89781687	89796142	1454	1208	11.906755
ZBED2	NM_024508	chr3	-	111309745	111316167	917	451	11.90485
WDR41	NM_018268	chr5	-	76726067	76790333	1193	1161	11.90359
MFSD2A	NM_032793	chr1	+	40418782	40437629	4321	3399	11.90122
DIABLO	NM_138929	chr12	-	122690207	122714069	2009	1810	11.88122667
ABCC10	NM_033450	chr6	+	43397487	43420164	2090	1711	11.870745
YEATS4	NM_006530	chr12	+	69751530	69786577	1329	1220	11.80925
PDCD2	NM_144781	chr6	-	170888833	170895749	1315	1217	11.79592
IVNS1ABP	NM_006469	chr1	-	185263520	185288462	2366	2181	11.79067
RNPC3	NM_017619	chr1	+	104066576	104099860	1288	1234	11.771865
NUDT16L1	NM_032349	chr16	+	4741692	4747861	5197	5125	11.76317
PAPD4	NM_173797	chr5	+	78906241	78984472	1054	993	11.759015
SMNDC1	NM_005871	chr10	-	112050796	112066708	1346	1309	11.74236
CLTB	NM_007097	chr5	-	175817454	175845541	5076	4458	11.73723
CDS1	NM_001263	chr4	+	85502055	85574494	3421	1627	11.728725
PUF60	NM_078480	chr8	-	144896545	144913538	11762	11581	11.7271625
BRMS1	NM_015399	chr11	-	66102802	66114583	4553	4206	11.722805
C16orf42	NM_001001410	chr16	-	1397239	1403874	2226	1945	11.711785

GPR109A	NM_177551	chr12	-	123183838	123189905	1157	996	11.703265
GJB5	NM_005268	chr1	+	35218719	35226113	2322	1884	11.68649
ARFGEF1	NM_006421	chr8	-	68107895	68257913	3290	3249	11.686335
ACP2	NM_001610	chr11	-	47258851	47272458	1647	1518	11.682445
GALE	NM_001127621	chr1	-	24120087	24128061	3696	3350	11.678335
TMPRSS4	NM_019894	chr11	+	117945725	117992557	3226	2294	11.6690425
CROT	NM_021151	chr7	+	86972949	87031113	1126	1082	11.664475
HMG20B	NM_006339	chr19	+	3570941	3581082	4941	4537	11.663005
TMEM68	NM_152417	chr8	-	56649318	56687886	1345	1202	11.60894
REPIN1	NM_014374	chr7	+	150066256	150073134	3212	2978	11.60765
RABEP1	NM_004703	chr17	+	5183556	5291133	2635	2465	11.60277
TFPI2	NM_006528	chr7	-	93513743	93522066	1121	1086	11.590905
GPR109B	NM_006018	chr12	-	123197301	123203440	1007	993	11.590215
RAB32	NM_006834	chr6	+	146862826	146878087	2285	2097	11.582055
CGGBP1	NM_003663	chr3	-	88099098	88110147	1661	1605	11.569585
BAP1	NM_004656	chr3	-	52433023	52446010	3894	3599	11.55741
TAB2	NM_015093	chr6	+	149637434	149734748	2425	2390	11.505655
NMU	NM_006681	chr4	-	56459396	56504466	1925	1485	11.497885
YIPF5	NM_030799	chr5	-	143535727	143552279	830	748	11.4961125
A2ML1	NM_144670	chr12	+	8973148	9031378	1192	1019	11.48883
GATAD1	NM_021167	chr7	+	92074763	92090743	1882	1665	11.47406
DVL2	NM_004422	chr17	-	7126659	7139864	2159	1789	11.471365
C14orf101	NM_017799	chr14	+	57044509	57118233	1352	1156	11.44763
PPAPDC2	NM_203453	chr9	+	4660296	4667259	2480	2190	11.445525

AK3	NM_016282	chr9	-	4709156	4743228	2249	1762	11.434975
HES2	NM_019089	chr1	-	6473292	6481980	5462	4937	11.42107
MYST1	NM_182958	chr16	+	31126983	31144715	5055	4605	11.418885
SLC35A5	NM_017945	chr3	+	112278893	112305004	1718	1649	11.39886
LGALS9C	NM_001040078	chr17	+	18378097	18400260	2113	1860	11.391385
STUB1	NM_005861	chr16	+	728113	734769	4986	4567	11.39031
MRPL23	NM_021134	chr11	+	1966500	1979840	6429	6422	11.372725
ATRN	NM_139322	chr20	+	3449663	3598551	2646	2443	11.372185
MMP10	NM_002425	chr11	-	102639231	102653360	691	436	11.37004
PLEKHJ1	NM_018049	chr19	-	2231153	2238329	4951	4921	11.3586
ENOPH1	NM_021204	chr4	+	83349724	83384245	3397	3227	11.35489
MLLT10	NM_004641	chr10	+	21821099	22034560	4035	3948	11.35025
ZNF498	NM_145115	chr7	+	99212569	99232031	2271	1541	11.344585
PPBP	NM_002704	chr4	-	74850154	74855908	163	0	11.335625
CPEB2	NM_182646	chr4	+	15002296	15073778	4187	4130	11.307885
PIGO	NM_152850	chr9	-	35086686	35098580	1024	988	11.2829875
ARL4C	NM_005737	chr2	-	235399684	235407694	3770	3179	11.280385
ARHGAP8	NM_181335	chr22	+	45146436	45260665	6472	5105	11.27462
FANCL	NM_018062	chr2	-	58384376	58470516	869	868	11.26252
NAPG	NM_003826	chr18	+	10523871	10554767	1382	1323	11.24886
SNX7	NM_152238	chr1	+	99125234	99228057	2528	2337	11.247565
NR4A2	NM_006186	chr2	-	157178942	157191288	2922	2852	11.23115
RNF146	NM_030963	chr6	+	127586018	127611505	1674	1525	11.22947
CSTA	NM_005213	chr3	+	122042009	122062816	594	0	11.220925

MINA	NM_153182	chr3	-	97658659	97693296	1420	1316	11.2177725
ARNTL2	NM_020183	chr12	+	27483986	27575467	4813	3994	11.21116
WDR43	NM_015131	chr2	+	29115531	29173081	2376	1767	11.20869
KLK13	NM_015596	chr19	-	51557461	51570368	572	537	11.204115
RRM2B	NM_015713	chr8	-	103214727	103253347	1844	1694	11.203575
GAS2L1	NM_152237	chr22	+	29700995	29710775	8465	8346	11.18762333
DALRD3	NM_018114	chr3	-	49050433	49060468	4721	4588	11.140315
PLS1	NM_002670	chr3	+	142340264	142434506	940	706	11.12484
PSG9	NM_002784	chr19	-	43755433	43775683	580	345	11.11606
SIX2	NM_016932	chr2	-	45230322	45238543	6909	6402	11.10281
C10orf57	NM_025125	chr10	+	81836424	81854308	1713	1245	11.099945
LDOC1L	NM_032287	chr22	-	44886448	44896006	1669	1616	11.08344
C20orf11	NM_017896	chr20	+	61567439	61581828	2218	2049	11.078215
MORC2	NM_014941	chr22	-	31320598	31366188	2924	2326	11.076065
SLC15A2	NM_021082	chr3	+	121611169	121665035	1090	259	11.0742
CCDC111	NM_152683	chr4	+	185568765	185618113	2535	2282	11.06678
FAM160B2	NM_022749	chr8	+	21944712	21963892	6591	5660	11.06086
MRPL27	NM_016504	chr17	-	48443226	48452563	979	972	11.00685833
SPINK5	NM_006846	chr5	+	147441533	147518926	248	107	10.97009
ZNF414	NM_032370	chr19	-	8574214	8581049	3352	3161	10.95982
MOBK12C	NM_201403	chr1	-	47071385	47084564	3018	3015	10.953505
GJB6	NM_006783	chr13	-	20794099	20807373	2008	1530	10.946035
IRX2	NM_033267	chr5	-	2744277	2753770	6808	5987	10.9399
LNX2	NM_153371	chr13	-	28118048	28196721	4105	3986	10.93573

ZNF589	NM_016089	chr3	+	48280594	48314480	2880	2395	10.92373
YEATS2	NM_018023	chr3	+	183413604	183532414	3500	3339	10.894635
CECR5	NM_033070	chr22	-	17616408	17642170	2179	1925	10.89274
C19orf24	NM_017914	chr19	+	1273518	1281244	4908	3777	10.888385
VGLL1	NM_016267	chrX	+	135612309	135640967	271	0	10.86132
ZNF398	NM_170686	chr7	+	148842558	148882119	2467	2099	10.856575
CRCT1	NM_019060	chr1	+	152484976	152490482	1613	1057	10.83777
FAM35A	NM_019054	chr10	+	88852951	88953223	2292	2198	10.833905
ENSA	NM_207168	chr1	-	150597520	150604099	1123	1021	10.83251167
KCNJ5	NM_000890	chr11	+	128759311	128789952	6138	5891	10.83195
SNAPC2	NM_003083	chr19	+	7983192	7990137	3767	3335	10.79973
ENDOG	NM_004435	chr9	+	131578777	131586956	3057	3050	10.799005
C9orf85	NM_182505	chr9	+	74524421	74590372	2543	2484	10.798225
LCE3E	NM_178435	chr1	-	152536128	152541249	639	394	10.77159
FBXW5	NM_018998	chr9	-	139832885	139841174	4413	3740	10.74843333
DLK2	NM_206539	chr6	-	43416088	43425787	3562	2399	10.734435
THSD1	NM_199263	chr13	-	52949301	52982630	1185	1065	10.72583
EID2	NM_153232	chr19	-	40027445	40032839	1342	1263	10.71709
ZNF426	NM_024106	chr19	-	9636679	9651304	1392	933	10.71308
KRT24	NM_019016	chr17	-	38852241	38862003	812	0	10.709845
ANKRD9	NM_152326	chr14	-	102971196	102978129	6060	5671	10.70912
SPATA5L1	NM_024063	chr15	+	45692517	45715617	1946	1893	10.687095
RNF39	NM_170769	chr6	-	30036041	30045627	2732	2715	10.686155
FOXE1	NM_004473	chr9	+	100613535	100620998	3882	3579	10.67052

C3orf78	NM_001124767	chr3	+	52568619	52576587	2128	2043	10.660745
IRS2	NM_003749	chr13	-	110404182	110440915	7527	6111	10.65387
FOXD1	NM_004472	chr5	-	72740083	72746353	2357	2253	10.64131
JMJD8	NM_001005920	chr16	-	729665	736440	4911	4202	10.636545
PROS1	NM_000313	chr3	-	93589879	93694935	1914	1642	10.591775
C12orf41	NM_017822	chr12	-	49044993	49078036	1239	1207	10.58853
JOSD2	NM_138334	chr19	-	51007257	51016346	3671	3516	10.56813
APOBEC3B	NM_004900	chr22	+	39376403	39390784	3639	3451	10.560305
QPCT	NM_012413	chr2	+	37569751	37602466	2547	2502	10.55911
CNDP2	NM_018235	chr18	+	72161498	72192690	3758	3291	10.54087
C11orf93	NM_001136105	chr11	+	111167974	111181354	2078	1835	10.535725
SLC25A17	NM_006358	chr22	-	41163637	41217393	1213	1099	10.52902
NR2C1	NM_003297	chr12	-	95412056	95469405	1286	1241	10.511385
OSTM1	NM_014028	chr6	-	108360611	108397942	2225	2022	10.5068
LRRN1	NM_020873	chr3	+	3839119	3891388	2417	1313	10.49871
LCE1E	NM_178353	chr1	+	152756751	152762902	448	220	10.4987
DCLRE1A	NM_014881	chr10	-	115592482	115615860	1831	1676	10.487165
PRPF39	NM_017922	chr14	+	45551300	45586805	1526	1310	10.480015
PKIB	NM_181795	chr6	+	122929375	123049519	2592	1480	10.452605
CHMP4C	NM_152284	chr8	+	82642686	82673749	1498	1171	10.414445
GJD3	NM_152219	chr17	-	38514903	38522946	4149	3681	10.40955
RAB27B	NM_004163	chr18	+	52493838	52559212	1612	1382	10.400955
C9orf69	NM_152833	chr9	-	139004425	139012732	3906	2958	10.397455
NDUFA4L2	NM_020142	chr12	-	57626684	57636476	5769	5356	10.373

SERAC1	NM_032861	chr6	-	158528534	158591313	2444	2237	10.348165
LCE1C	NM_178351	chr1	-	152775309	152781108	489	0	10.34552
ABCC5	NM_005688	chr3	-	183635722	183737728	3681	3479	10.341125
PCSK5	NM_006200	chr9	+	78503558	78810347	5967	5287	10.31702
SPRY1	NM_199327	chr4	+	124315954	124326908	3195	2764	10.3036125
CTXN1	NM_206833	chr19	-	7987379	7993052	3689	2382	10.29321
C1orf59	NM_144584	chr1	-	109188908	109206149	1495	1426	10.280945
DMRT2	NM_181872	chr9	+	1048618	1059555	3407	2960	10.27857
HLA-G	NM_002127	chr6	+	29792754	29800900	322	199	10.273635
THAP1	NM_199003	chr8	-	42689815	42700475	1584	1512	10.271085
HPS6	NM_024747	chr10	+	103823145	103829794	2105	1772	10.268285
FAM83B	NM_001010872	chr6	+	54709567	54808820	3801	2982	10.261605
POGLUT1	NM_152305	chr3	+	119185783	119215555	1363	1191	10.257365
FAM84A	NM_145175	chr2	+	14770808	14782169	3726	2975	10.249965
SLC12A2	NM_001046	chr5	+	127417481	127527381	3015	2938	10.243415
ZNF135	NM_007134	chr19	+	58568605	58583111	1329	1172	10.2424
DENND2C	NM_198459	chr1	-	115125194	115214733	2848	1763	10.231145
VPS36	NM_016075	chr13	-	52984735	53026764	2605	2468	10.23045
SOX2	NM_003106	chr3	+	181427720	181434224	4426	2263	10.22905
SMARCAD1	NM_020159	chr4	+	95127014	95214444	1085	933	10.212175
ABCA12	NM_173076	chr2	-	215794264	216005152	2682	2524	10.18816
TBRG4	NM_199122	chr7	-	45137697	45153318	1816	1685	10.181765
SDR16C5	NM_138969	chr8	-	57210568	57235242	1845	1247	10.178005
IRX5	NM_005853	chr16	+	54963109	54970396	6373	5424	10.16918

AGAP9	NM_001190810	chr10	+	48213722	48239509	243	0	10.160345
TRIM68	NM_018073	chr11	-	4617900	4631438	1418	1081	10.154115
BARX2	NM_003658	chr11	+	129243879	129324175	4196	2205	10.142245
GINS3	NM_022770	chr16	+	58424296	58442049	1387	1348	10.09046
MSL2	NM_018133	chr3	-	135865758	135916689	3190	2919	10.089925
PTPRZ1	NM_002851	chr7	+	121511157	121704091	3047	2018	10.08715
C1orf190	NM_001013615	chr1	+	46667004	46688929	2836	2665	10.085325
LY6G6C	NM_025261	chr6	-	31684423	31691511	1402	643	10.068535
PLEKHN1	NM_032129	chr1	+	899875	912485	5408	5150	10.063765
KLF16	NM_031918	chr19	-	1850396	1865565	12282	12221	10.05217
LZTS2	NM_032429	chr10	+	102754963	102769588	7213	6707	10.024915
RNPEPL1	NM_018226	chr2	+	241506102	241520144	4901	4705	10.01952
CYP4X1	NM_178033	chr1	+	47487238	47518424	1194	937	10.003795
SOCS4	NM_199421	chr14	+	55491842	55518207	1271	1180	9.995595
TMEM80	NM_174940	chr11	+	693614	706130	4547	4353	9.98517
BMPR1B	NM_001203	chr4	+	95677126	96081602	5372	3368	9.983985
SLC16A9	NM_194298	chr10	-	61408520	61471650	2921	1968	9.98083
SAP30	NM_003864	chr4	+	174290091	174300684	2645	2608	9.965805
CKAP2	NM_018204	chr13	+	53027493	53052764	1658	1637	9.9657
UCK1	NM_031432	chr9	-	134397181	134408663	4157	3791	9.960145
CCDC3	NM_031455	chr10	-	12936623	13045705	3395	2456	9.942935
FAM110C	NM_001077710	chr2	-	36812	48589	3309	3037	9.94275
KRT31	NM_002277	chr17	-	39547975	39555845	992	240	9.941685
RFX7	NM_022841	chr15	-	56380729	56537484	2442	2313	9.94161

TYSND1	NM_173555	chr10	-	71895731	71908497	2902	2795	9.92802
ZNF654	NM_018293	chr3	+	88186260	88195815	235	220	9.923455
DACT2	NM_214462	chr6	-	168705582	168722403	2479	2356	9.91734
PRR21	NM_001080835	chr2	-	240979228	240984400	474	0	9.89413
SPSB3	NM_080861	chr16	-	1824711	1834582	7105	4184	9.87558
NUP62CL	NM_017681	chrX	-	106364655	106451671	1868	1589	9.87353
USP43	NM_153210	chr17	+	9546948	9635004	5730	5597	9.86906
SOX21	NM_007084	chr13	-	95359877	95366390	4749	4367	9.847125
DEPDC7	NM_139160	chr11	+	33035726	33057129	1166	1053	9.845615
SIPA1L2	NM_020808	chr1	-	232531710	232653244	1978	1568	9.838925
TREM2	NM_018965	chr6	-	41124244	41132923	271	176	9.83238
KLHL17	NM_198317	chr1	+	893965	903100	6692	6585	9.82833
NDUFB3	NM_002491	chr2	+	201934460	201952474	1198	1072	9.827385
CARD17	NM_001007232	chr11	-	104961194	104974159	138	0	9.817725
CEP57L1	NM_173830	chr6	+	109448505	109487116	350	329	9.81236
ASF1A	NM_014034	chr6	+	119213239	119232336	2296	2279	9.808815
CAPS	NM_080590	chr19	+	5912191	5918223	2189	2067	9.79182
SLC7A4	NM_004173	chr22	-	21381005	21388848	1326	1199	9.78683
MSGN1	NM_001105569	chr2	+	17995784	18000368	536	346	9.77404
BCL11B	NM_138576	chr14	-	99633623	99739823	17582	16688	9.765045
NEDD1	NM_152905	chr12	+	97298999	97349470	1675	1561	9.75054
TPSB2	NM_024164	chr16	-	1276334	1282186	2958	2748	9.714775
SIRPB2	NM_001134836	chr20	-	1453234	1474234	1821	1081	9.707925
SPCS3	NM_021928	chr4	+	177239088	177255397	1603	1317	9.688255

EXOSC5	NM_020158	chr19	-	41890274	41905257	1497	1213	9.652285
SPRR3	NM_005416	chr1	+	152972221	152978333	431	0	9.651565
CCNA1	NM_003914	chr13	+	37004407	37019020	1424	1292	9.648305
TP53AIP1	NM_022112	chr11	-	128803268	128815295	3641	1912	9.63656
CCDC138	NM_144978	chr2	+	109401217	109494848	1503	1213	9.62468
TREM1	NM_018643	chr6	-	41241710	41256458	756	737	9.612575
CHAC1	NM_024111	chr15	+	41243634	41250718	2914	2669	9.60963
TTBK2	NM_173500	chr15	-	43034540	43215008	2890	2793	9.59962
SMPD1	NM_001007593	chr11	+	6409642	6418229	1351	1275	9.584655
MED30	NM_080651	chr8	+	118530963	118554502	1005	906	9.579155
SMOC2	NM_022138	chr6	+	168839829	169070675	12648	11698	9.56561
NXT2	NM_018698	chrX	+	108777008	108789914	1499	1289	9.550125
C12orf29	NM_001009894	chr12	+	88427266	88445938	959	901	9.548995
SERTAD3	NM_203344	chr19	-	40944746	40952283	2633	2448	9.545135
CHL1	NM_006614	chr3	+	236648	453098	3559	2383	9.53591
KRTAP10-2	NM_198693	chr21	-	45968316	45973389	2276	1191	9.51689
WDR54	NM_032118	chr2	+	74646883	74654883	2739	1924	9.51029
C3orf63	NM_015224	chr3	-	56652158	56700075	266	253	9.49665
ZNF626	NM_145297	chr19	-	20825507	20846403	814	756	9.49131
ZMYM5	NM_001142684	chr13	-	20395622	20439777	3627	3487	9.490745
FBN2	NM_001999	chr5	-	127591599	127875736	3880	3066	9.449785
BBOX1	NM_003986	chr11	+	27060507	27151355	1143	1143	9.43296
RNF222	NM_001146684	chr17	-	8292021	8303145	1608	1367	9.428305
TMPRSS11F	NM_207407	chr4	-	68916914	68997588	1027	0	9.422205

SUSD4	NM_017982	chr1	-	223392159	223539545	5820	5685	9.419095
ACVR2A	NM_001616	chr2	+	148600568	148690394	2410	2233	9.401385
DRD2	NM_016574	chr11	-	113278315	113348002	4930	3928	9.39099
ZC3H8	NM_032494	chr2	-	112971437	113014665	1376	905	9.381055
ZNF606	NM_025027	chr19	-	58486439	58516715	1549	1431	9.36385
HTR7	NM_019860	chr10	-	92498574	92619672	4865	4210	9.355475
MPST	NM_021126	chr22	+	37413700	37427864	4202	4089	9.35158
SERF1A	NM_022968	chr5	+	69319070	69330526	939	799	9.34901
CCDC113	NM_014157	chr16	+	58281838	58319735	2495	1614	9.343995
STOX2	NM_020225	chr4	+	184824507	184940876	4655	4406	9.341645
MUC16	NM_024690	chr19	-	8957518	9094019	637	297	9.341315
C4orf19	NM_018302	chr4	+	37583853	37597133	243	138	9.335395
CCDC66	NM_001141947	chr3	+	56589182	56657849	1079	1019	9.330405
C20orf46	NM_018354	chr20	-	1159213	1167118	2644	2576	9.326765
UBL4B	NM_203412	chr1	+	110653060	110658570	464	259	9.324015
ADAM28	NM_021777	chr8	+	24149578	24195613	427	341	9.3238925
NLGN4X	NM_181332	chrX	-	5806081	6148707	5145	4359	9.301035
CAPN6	NM_014289	chrX	-	110486325	110515775	680	591	9.281865
ZFP42	NM_174900	chr4	+	188914923	188928200	840	756	9.27113
SATB1	NM_002971	chr3	-	18387132	18468830	1614	1607	9.26758
CYP2J2	NM_000775	chr1	-	60356978	60394424	710	590	9.265115
ZFP28	NM_020828	chr19	+	57048315	57070171	1693	1591	9.259765
NEK3	NM_001146099	chr13	-	52704777	52735997	1177	1150	9.25709
SREK1IP1	NM_173829	chr5	-	64011976	64066497	1003	989	9.245685

LPCAT2	NM_017839	chr16	+	55540911	55622583	1944	1264	9.245245
PSG5	NM_002781	chr19	-	43669893	43692689	691	591	9.241305
ZNF211	NM_198855	chr19	+	58142533	58156148	1003	946	9.23055
IL1RL1	NM_016232	chr2	+	102925960	102970498	1194	892	9.2186825
TSSC4	NM_005706	chr11	+	2421521	2427107	2398	1940	9.20646
MBOAT2	NM_138799	chr2	-	8994699	9145877	3881	3433	9.199095
DAPL1	NM_001017920	chr2	+	159649827	159674497	917	792	9.17009
PHPT1	NM_014172	chr9	+	139741254	139747491	4976	4320	9.167215
DYRK1B	NM_006484	chr19	-	40313988	40326842	4723	4507	9.16566
MAPK8	NM_139049	chr10	+	49607685	49645184	682	211	9.142105
BAZ2B	NM_013450	chr2	-	160173488	160475060	3414	3319	9.12264
PROL1	NM_021225	chr4	+	71261597	71277915	100	0	9.11901
RPUSD1	NM_058192	chr16	-	832972	840384	6226	5488	9.098555
ZNF22	NM_006963	chr10	+	45494271	45502778	1949	1762	9.09407
PELI1	NM_020651	chr2	-	64317784	64373606	1851	1786	9.087135
RNMTL1	NM_018146	chr17	+	683511	697742	4204	2915	9.08262
TTC36	NM_001080441	chr11	+	118396208	118403741	2340	2214	9.072245
HRASLS	NM_020386	chr3	+	192956916	192990645	1053	860	9.05415
NAP1L2	NM_021963	chrX	-	72430152	72436685	584	579	9.04906
LIG4	NM_206937	chr13	-	108857790	108869883	1454	1424	9.04767
CD274	NM_014143	chr9	+	5448501	5472568	1327	1239	9.04725
OSBPL6	NM_145739	chr2	+	179182969	179262876	655	357	9.04609
FAM183A	NM_001101376	chr1	+	43611592	43624068	1038	600	9.03901
ZNF551	NM_138347	chr19	+	58191355	58203170	1016	1002	9.032465

C2orf85	NM_173821	chr2	+	242809884	242817483	4552	4420	9.02815
RAD52	NM_134424	chr12	-	1019253	1060864	2222	1911	9.02462
KPRP	NM_001025231	chr1	+	152728504	152736530	1023	135	9.02005
ATOH1	NM_005172	chr4	+	94748076	94753143	1599	928	9.01169
CYP4B1	NM_001099772	chr1	+	47262668	47287022	507	82	8.98142
ZNF662	NM_207404	chr3	+	42945400	42962826	1080	913	8.97512
NKX6-1	NM_006168	chr4	-	85412434	85421388	4015	3898	8.97485
C22orf26	NM_018280	chr22	-	46444337	46452025	3994	3962	8.9692
ODF2L	NM_020729	chr1	-	86813775	86864026	1344	1227	8.956075
PATZ1	NM_032052	chr22	-	31719788	31744250	6391	6329	8.955265
FOXA2	NM_153675	chr20	-	22559640	22568102	4765	4675	8.95196
MRPS34	NM_023936	chr16	-	1819894	1825141	5188	4799	8.95044
EYA1	NM_172060	chr8	-	72107666	72270980	2118	1240	8.94867
CGB8	NM_033183	chr19	-	49548893	49554369	538	501	8.94105
MRGPRX3	NM_054031	chr11	+	18140500	18162028	396	0	8.940185
FAIM	NM_018147	chr3	+	138325917	138354214	1969	1810	8.936795
DGCR14	NM_022719	chr22	-	19115790	19134191	2900	2276	8.926185
FLG	NM_002016	chr1	-	152272649	152299680	186	0	8.923855
FUT4	NM_002033	chr11	+	94275015	94285065	2681	2075	8.9159
LY6K	NM_017527	chr8	+	143779527	143787585	2145	2056	8.91484
IRX3	NM_024336	chr16	-	54315210	54322379	5892	5590	8.904885
GLRB	NM_001166061	chr4	+	157995275	158095243	1727	1481	8.904145
CGB5	NM_033043	chr19	+	49545100	49550569	341	323	8.901765
ISL1	NM_002202	chr5	+	50676956	50692564	3648	2215	8.86956

A2M	NM_000014	chr12	-	9218302	9270559	252	0	8.855895
CCDC34	NM_080654	chr11	-	27368417	27386796	1058	935	8.855225
PRKCQ	NM_006257	chr10	-	6467103	6624239	3179	3037	8.85415
NOL12	NM_024313	chr22	+	38080342	38091486	2187	1534	8.840565
FAM150A	NM_207413	chr8	-	53444595	53480022	2102	1798	8.81972
LENG9	NM_198988	chr19	-	54970977	54976895	4398	4141	8.81879
LILRA4	NM_012276	chr19	-	54842690	54852422	182	161	8.815315
CCDC8	NM_032040	chr19	-	46911584	46918920	1446	1043	8.798635
APLNR	NM_005161	chr11	-	56999050	57006928	225	0	8.777
ZNF524	NM_153219	chr19	+	56109728	56116505	3375	3252	8.768765
FLRT2	NM_013231	chr14	+	85994486	86096271	5407	4832	8.764455
C20orf141	NM_080739	chr20	+	2793655	2798477	1283	1086	8.76127
POF1B	NM_024921	chrX	-	84530393	84636749	506	165	8.753825
ZNF789	NM_213603	chr7	+	99068513	99087218	1483	1432	8.74977
ACN9	NM_020186	chr7	+	96743903	96813076	1835	1438	8.727795
SLC2A12	NM_145176	chr6	-	134306717	134375790	1823	1686	8.72735
CBLN3	NM_001039771	chr14	-	24893738	24900732	3926	3829	8.7207
ZNF470	NM_001001668	chr19	+	57076888	57096263	1119	1112	8.71214
KLK9	NM_012315	chr19	-	51503767	51514891	2337	2192	8.706975
ASPDH	NM_001114598	chr19	-	51012855	51019143	5288	5229	8.6999
SLC6A15	NM_182767	chr12	-	85251265	85308607	1559	1457	8.691775
CYP4V2	NM_207352	chr4	+	187110672	187136618	2773	2638	8.68791
TCEAL2	NM_080390	chrX	+	101378658	101384685	1515	1457	8.682865
CHST9	NM_031422	chr18	-	24493593	24767290	3623	2887	8.67163

ZNF433	NM_001080411	chr19	-	12123530	12148526	1153	1036	8.671205
CHRM4	NM_000741	chr11	-	46404638	46410108	3468	3421	8.666975
MCART2	NM_001034172	chr18	-	29337657	29342844	114	0	8.653635
EFCAB7	NM_032437	chr1	+	63987011	64040365	949	885	8.646905
MXD4	NM_006454	chr4	-	2247158	2265740	5864	5505	8.644575
FOLH1	NM_004476	chr11	-	49166185	49232223	688	672	8.6199675
LRIT1	NM_015613	chr10	-	85989274	86003218	438	319	8.597085
NUDT10	NM_153183	chrX	+	51073081	51082378	2215	2137	8.596395
HRH2	NM_022304	chr5	+	175106462	175113559	303	200	8.577695
EME2	NM_001010865	chr16	+	1821227	1828240	6646	4157	8.54587
KIAA1328	NM_020776	chr18	+	34407078	34807289	2432	2212	8.54407
GSTT2	NM_000854	chr22	+	24320312	24328107	1997	1457	8.54297
KIAA1919	NM_153369	chr6	+	111578480	111592262	1438	1410	8.540285
GATM	NM_001482	chr15	-	45651320	45672981	1152	1008	8.536585
IFNK	NM_020124	chr9	+	27522310	27528497	434	205	8.532695
PLAC8L1	NM_001029869	chr5	-	145461874	145485947	602	335	8.53041
TWIST1	NM_000474	chr7	-	19153089	19159296	3277	2790	8.528955
OSCP1	NM_206837	chr1	-	36891899	36918087	2076	1851	8.5205325
TEX101	NM_031451	chr19	+	43890761	43924768	753	0	8.504125
FOXD2	NM_004474	chr1	+	47899687	47908364	5401	5237	8.500285
ACBD5	NM_145698	chr10	-	27482141	27531809	1910	1801	8.4988
RTP1	NM_153708	chr3	+	186913272	186921254	987	590	8.496085
C6	NM_001115131	chr5	-	41140334	41263541	409	280	8.48318
GLIPR1L1	NM_152779	chr12	+	75726461	75766170	704	647	8.48229

SCXB	NM_001080514	chr8	+	145488601	145494132	4847	4677	8.472695
SULT1E1	NM_005420	chr4	-	70704928	70727871	586	157	8.46898
HYI	NM_031207	chr1	-	43914822	43921661	2583	2386	8.46687
MYL5	NM_002477	chr4	+	669709	677818	7649	6966	8.43995
RIBC2	NM_015653	chr22	+	45807572	45830296	2183	1967	8.433865
ALX1	NM_006982	chr12	+	85672034	85697562	1723	1554	8.426795
S100A12	NM_005621	chr1	-	153344182	153350076	694	584	8.409455
ZNF177	NM_003451	chr19	+	9471694	9495294	142	0	8.4056
PCDH7	NM_032457	chr4	+	30720035	31150424	5730	5581	8.401675
DUS3L	NM_020175	chr19	-	5783151	5793250	3773	3287	8.394535
ZMYND17	NM_001024593	chr10	-	75181335	75195320	240	0	8.38612
TRIM45	NM_025188	chr1	-	117651675	117666412	1380	1247	8.38089
OSBPL7	NM_145798	chr17	-	45882731	45901148	3686	3660	8.3795475
ATP13A4	NM_032279	chr3	-	193117864	193274697	1331	409	8.3504
RNF175	NM_173662	chr4	-	154629310	154683388	2292	1897	8.343875
C13orf31	NM_153218	chr13	+	44451967	44470069	1490	1277	8.341395
ATHL1	NM_025092	chr11	+	287136	297689	6557	6233	8.33568
C3orf30	NM_152539	chr3	+	118862995	118872303	645	433	8.332445
KRT75	NM_004693	chr12	-	52815852	52830111	1276	714	8.32483
ESCO2	NM_001017420	chr8	+	27630056	27664425	1138	1086	8.306545
HMGB2	NM_002129	chr4	-	174250525	174257596	2131	2022	8.28392
FOXD4L1	NM_012184	chr2	+	114254659	114260728	559	227	8.281415
FZD10	NM_007197	chr12	+	130645030	130652286	2694	2534	8.260565
HPGD	NM_001145816	chr4	-	175409326	175445793	1502	1069	8.25736

NHLH2	NM_005599	chr1	-	116376997	116385748	2068	1708	8.251295
CXCL3	NM_002090	chr4	-	74900310	74906491	1284	939	8.24825
GJA5	NM_181703	chr1	-	147226330	147234715	774	472	8.24526
IL1RAP	NM_134470	chr3	+	190229838	190350074	4586	4352	8.244805
EDIL3	NM_005711	chr5	-	83236124	83682612	2702	2574	8.241255
TDRKH	NM_006862	chr1	-	151742039	151765011	2190	1990	8.23386
MGAM	NM_004668	chr7	+	141693677	141808548	1107	408	8.230015
RECQL4	NM_004260	chr8	-	145734665	145745211	5787	5721	8.209135
OR10S1	NM_001004474	chr11	-	123845401	123850399	371	0	8.2011
CRYBB2	NM_000496	chr22	+	25613610	25629837	1890	1325	8.192905
C9orf123	NM_033428	chr9	-	7794489	7801800	1078	1034	8.179175
KRTAP12-3	NM_198697	chr21	+	46075847	46080259	217	188	8.179055
SLAMF7	NM_021181	chr1	+	160707075	160726602	721	176	8.172315
C4orf48	NM_001168243	chr4	+	2041718	2047698	5080	4719	8.168295
FOXI2	NM_207426	chr10	+	129533536	129541451	2163	1824	8.16379
ZNF428	NM_182498	chr19	-	44109374	44126015	2091	1946	8.139205
MEP1A	NM_005588	chr6	+	46759092	46809520	1138	113	8.12878
TRMU	NM_018006	chr22	+	46729296	46755238	7746	6262	8.126024
GLI4	NM_138465	chr8	+	144347605	144361102	8081	7960	8.124615
C18orf62	NM_001037331	chr18	-	73119825	73141590	758	748	8.113605
NPPB	NM_002521	chr1	-	11915519	11920993	1092	782	8.111615
USP51	NM_201286	chrX	-	55509047	55517632	2015	1896	8.1052
SYDE2	NM_032184	chr1	-	85621354	85668729	2001	1993	8.085775
SLITRK6	NM_032229	chr13	-	86364920	86375484	314	273	8.08181

CNTN1	NM_175038	chr12	+	41084356	41466095	2645	1560	8.073015
IZUMO4	NM_001039846	chr19	+	2094866	2101584	4089	3416	8.061198333
WFDC6	NM_080827	chr20	-	44160834	44170135	324	0	8.061145
C16orf68	NM_024109	chr16	+	8713525	8742080	2434	2282	8.04464
ZNF571	NM_016536	chr19	-	38053153	38087674	1529	1517	8.03249
LILRA3	NM_006865	chr19	-	54797853	54806266	154	147	8.01969
ZFP57	NM_001109809	chr6	-	29638167	29646932	1401	521	8.006545
ABP1	NM_001091	chr7	+	150547571	150560380	683	683	8.001735
C5orf38	NM_178569	chr5	+	2750260	2757512	6130	6100	7.99812
ZNF429	NM_001001415	chr19	+	21686435	21723080	1137	1029	7.975385
FOXD4	NM_207305	chr9	-	114232	120418	646	380	7.966735
KRTAP19-1	NM_181607	chr21	-	31850362	31854637	85	0	7.949915
FZD8	NM_031866	chr10	-	35925175	35932363	4392	4117	7.94913
COX6A2	NM_005205	chr16	-	31437053	31441722	1225	1112	7.936395
ZNF430	NM_025189	chr19	+	21201424	21244853	1276	1156	7.934905
CDH9	NM_016279	chr5	-	26878707	27040690	160	0	7.92571
PAGE4	NM_007003	chrX	+	49591904	49600571	37	0	7.92158
ARID2	NM_152641	chr12	+	46121618	46303820	2958	2924	7.89893
WDR72	NM_182758	chr15	-	53803936	54053860	1235	905	7.898405
CLEC18B	NM_001011880	chr16	-	74440527	74457369	544	520	7.893225
CXorf57	NM_018015	chrX	+	105853158	105924674	855	855	7.88238
KRT33A	NM_004138	chr17	-	39500369	39509057	622	130	7.876315
C6orf138	NM_207499	chr6	-	47865343	48038426	755	69	7.875975
C8orf30A	NM_016458	chr8	+	145435878	145442829	3602	3011	7.86598

ENPP5	NM_021572	chr6	-	46125760	46140718	595	514	7.850805
TOX3	NM_001146188	chr16	-	52469916	52583715	2240	1830	7.84675
SLC5A1	NM_000343	chr22	+	32437017	32511012	2194	1944	7.84092
KEL	NM_000420	chr7	-	142636199	142661504	1874	1183	7.836565
FOLH1B	NM_153696	chr11	+	89390463	89433887	238	53	7.821425
LCE3D	NM_032563	chr1	-	152549858	152554981	520	437	7.81877
TRPC1	NM_003304	chr3	+	142441264	142528730	1719	1696	7.78144
C11orf65	NM_152587	chr11	-	108251725	108340259	1359	1178	7.77869
OR52M1	NM_001004137	chr11	+	4564419	4569375	245	135	7.77045
ACTR8	NM_022899	chr3	-	53899092	53918230	1411	1318	7.770265
PENK	NM_006211	chr8	-	57351511	57360594	1875	983	7.766385
CDK5R2	NM_003936	chr2	+	219822396	219828878	4898	4832	7.76284
IER5L	NM_203434	chr9	-	131935829	131942541	5318	5236	7.74995
EIF2C4	NM_017629	chr1	+	36271826	36323189	1823	1775	7.74161
FEZF2	NM_018008	chr3	-	62353345	62361191	3804	3486	7.73766
CYP2A13	NM_000766	chr19	+	41592366	41604100	372	325	7.73482
EFCAB1	NM_024593	chr8	-	49633951	49649871	638	564	7.707335
ST6GAL2	NM_032528	chr2	-	107416054	107505564	2334	2050	7.694645
CSAG1	NM_153478	chrX	+	151901226	151911519	187	117	7.69193
FAM117B	NM_173511	chr2	+	203497899	203636481	3475	2829	7.6758
SLC29A4	NM_153247	chr7	+	5320559	5345705	6681	6481	7.650645
GUCY1A2	NM_000855	chr11	-	106555908	106891172	3719	2969	7.64223
DEFB4A	NM_004942	chr8	+	7750197	7756238	247	189	7.63967
BMP2	NM_001200	chr20	+	6746743	6762911	3388	3149	7.632695

FBXO8	NM_012180	chr4	-	175155808	175207403	1582	1521	7.62431
GABRG3	NM_033223	chr15	+	27214427	27780374	5668	3955	7.616405
PTPRD	NM_130393	chr9	-	8312244	8735947	2766	1336	7.6164
PRMT8	NM_019854	chr12	+	3598423	3705139	4292	3934	7.60614
LEP	NM_000230	chr7	+	127879329	127899683	985	937	7.57826
STX19	NM_001001850	chr3	-	93731213	93749455	384	0	7.56018
NKX2-4	NM_033176	chr20	-	21374003	21380048	1849	1629	7.554645
GALNT12	NM_024642	chr9	+	101567979	101614360	4229	4146	7.549235
CCK	NM_001174138	chr3	-	42297316	42307440	1846	1818	7.54731
LASS3	NM_178842	chr15	-	100938598	101086926	1570	845	7.539645
POU3F4	NM_000307	chrX	+	82761267	82766776	957	740	7.527765
UCP1	NM_021833	chr4	-	141479048	141491960	1089	995	7.51818
CXCR2	NM_001557	chr2	+	218988734	219003977	339	126	7.495795
PTF1A	NM_178161	chr10	+	23479458	23485182	3413	2842	7.48868
CLDN8	NM_199328	chr21	-	31584322	31590470	219	0	7.48612
RAB19	NM_001008749	chr7	+	140101841	140128051	629	560	7.45721
ZFP2	NM_030613	chr5	+	178320914	178362211	1276	1004	7.45263
CCDC11	NM_145020	chr18	-	47751561	47794866	2070	1684	7.445045
PHKA1	NM_002637	chrX	-	71796662	71936030	4192	4038	7.441685
RBP2	NM_004164	chr3	-	139169724	139197353	484	331	7.43861
MESPI1	NM_018670	chr15	-	90291096	90296541	2142	1994	7.425455
HSPB9	NM_033194	chr17	+	40272754	40277372	2176	1520	7.41326
LRFN2	NM_020737	chr6	-	40357371	40557127	7420	5947	7.38609
RNF2	NM_007212	chr1	+	185012549	185073741	1904	1718	7.38139

SNX18	NM_052870	chr5	+	53811591	53818835	1913	1880	7.380715
ANKK1	NM_178510	chr11	+	113256511	113273141	1302	829	7.37709
C5orf43	NM_001048249	chr5	-	60451534	60460303	1272	1226	7.36838
SH2D1A	NM_002351	chrX	+	123478130	123509011	340	0	7.364625
CHML	NM_001821	chr1	-	241790165	241801233	441	428	7.353325
CYSLTR1	NM_006639	chrX	-	77526128	77585088	902	336	7.35327
OR10A3	NM_001003745	chr11	-	7958121	7963068	116	0	7.34732
KRT37	NM_003770	chr17	-	39574807	39582823	899	358	7.340675
GYS2	NM_021957	chr12	-	21687121	21759782	432	177	7.33584
MBD2	NM_015832	chr18	-	51727045	51753159	1865	1809	7.3192375
PGLYRP1	NM_005091	chr19	-	46520410	46528557	1205	936	7.318175
MFSD6L	NM_152599	chr17	-	8698426	8704668	763	133	7.317695
ERP27	NM_152321	chr12	-	15064974	15093464	586	349	7.290685
STK32A	NM_145001	chr5	+	146612577	146730393	1801	1130	7.28586
ZNF319	NM_020807	chr16	-	58026571	58035763	5069	3770	7.280485
KLF14	NM_138693	chr7	-	130415394	130420889	1675	1660	7.28012
H2BFM	NM_001164416	chrX	+	103292514	103299022	119	0	7.2742
ZIK1	NM_001010879	chr19	+	58093626	58105759	818	791	7.2735
CLDN25	NM_001101389	chr11	+	113648516	113653208	915	489	7.26823
LYZL4	NM_144634	chr3	-	42436573	42454066	177	0	7.261845
RIN1	NM_004292	chr11	-	66097540	66106001	3621	3462	7.25799
TDRD6	NM_001168359	chr6	+	46653610	46674057	267	222	7.252165
ZC3HAV1L	NM_080660	chr7	-	138708450	138722776	2380	2216	7.251905
C2orf61	NM_173649	chr2	-	47353585	47384518	399	360	7.23381

ZNF347	NM_032584	chr19	-	53639955	53664323	1133	976	7.233375
PSG3	NM_021016	chr19	-	43223792	43246669	216	0	7.230035
IL1F10	NM_173161	chr2	+	113823545	113835428	1019	214	7.2233475
S100G	NM_004057	chrX	+	16666279	16674792	100	0	7.22068
OAZ3	NM_016178	chr1	+	151737129	151745807	622	0	7.216245
ATP13A5	NM_198505	chr3	-	192990829	193098515	861	531	7.21511
GDA	NM_004293	chr9	+	74762291	74869141	1666	1631	7.19519
SST	NM_001048	chr3	-	187384692	187390202	292	272	7.180285
TIGD5	NM_032862	chr8	+	144678072	144684486	5348	5022	7.17221
DDIT4L	NM_145244	chr4	-	101105025	101113656	1342	1200	7.164355
PARP15	NM_152615	chr3	+	122332523	122357537	495	349	7.15906
KCNS2	NM_020697	chr8	+	99437248	99445024	2207	1918	7.151235
MCM9	NM_153255	chr6	-	119229760	119258304	1303	1205	7.131725
ARHGDIG	NM_001176	chr16	+	328604	335004	6025	5984	7.1145
SOX14	NM_004189	chr3	+	137481577	137486397	1213	853	7.104185
UGT2B15	NM_001076	chr4	-	69510313	69538375	51	0	7.08356
PPP4R4	NM_058237	chr14	+	94638647	94748073	3540	3307	7.0661775
SDR9C7	NM_148897	chr12	-	57314936	57330190	329	227	7.060185
ZNF80	NM_007136	chr3	-	113951478	113958426	47	0	7.05912
LRRC66	NM_001024611	chr4	-	52857864	52885787	245	0	7.04454
C12orf39	NM_030572	chr12	+	21677254	21686211	1005	849	7.034685
RASGEF1B	NM_152545	chr4	-	82346217	82395062	3609	1691	7.01997
BHLHE41	NM_030762	chr12	-	26270957	26280004	4559	4531	7.00431
DUSP21	NM_022076	chrX	+	44701247	44706135	617	573	6.99094

RDH16	NM_003708	chr12	-	57343214	57353419	641	569	6.970065
IBSP	NM_004967	chr4	+	88718700	88735602	83	0	6.967165
SPOCK3	NM_016950	chr4	-	167652534	168157742	2719	1832	6.936455
MAGEL2	NM_019066	chr15	-	23886694	23894994	2348	1363	6.918345
IL1F5	NM_173170	chr2	+	113814213	113824321	444	0	6.91387
CXCL9	NM_002416	chr4	-	76920621	76930642	381	222	6.912545
COL21A1	NM_030820	chr6	-	55919386	56114379	2189	1666	6.88939
SNTG2	NM_018968	chr2	+	944552	1373385	7920	7428	6.87619
DSCAM	NM_001389	chr21	-	41382341	42221040	6839	2801	6.86484
IL1F9	NM_019618	chr2	+	113733604	113745228	71	0	6.861105
DMRT3	NM_021240	chr9	+	974962	993733	3006	2762	6.85526
UGT2B17	NM_001077	chr4	-	69400901	69436246	159	0	6.844095
ACTL7A	NM_006687	chr9	+	111622601	111628036	487	381	6.838355
SLN	NM_003063	chr11	-	107576099	107584788	142	98	6.8363
ACTBL2	NM_001017992	chr5	-	56773841	56780637	120	95	6.83282
AMPD1	NM_001172626	chr1	-	115213718	115240240	472	265	6.828385
SOSTDC1	NM_015464	chr7	-	16499104	16507475	213	0	6.827585
CCDC67	NM_181645	chr11	+	93061881	93173637	1038	457	6.81278
SPRR4	NM_173080	chr1	+	152941126	152947070	312	0	6.808745
MT1B	NM_005947	chr16	+	56683809	56689117	648	522	6.803505
HHLA2	NM_007072	chr3	+	108019330	108099127	562	535	6.7911
RBMXL3	NM_001145346	chrX	+	114421961	114429432	231	0	6.786725
SCN2B	NM_004588	chr11	-	118031517	118049338	3724	3360	6.78128
NOS1	NM_000620	chr12	-	117646775	117801608	6898	5956	6.761075

FREM2	NM_207361	chr13	+	39259171	39463268	1145	546	6.75432
RBFOX1	NM_145893	chr16	+	7380749	7765341	1811	1027	6.7518775
KRT1	NM_006121	chr12	-	53066518	53076192	478	212	6.74943
AMIGO3	NM_198722	chr3	-	49752265	49759239	2041	1760	6.749085
CNGA4	NM_001037329	chr11	+	6258328	6267708	190	0	6.74636
KIR2DL4	NM_002255	chr19	+	55313065	55327973	132	0	6.72467
KBTBD8	NM_032505	chr3	+	67046725	67063633	1436	1299	6.69751
C2orf71	NM_001029883	chr2	-	29282556	29299128	2793	1670	6.682395
KRT32	NM_002278	chr17	-	39613763	39625639	778	747	6.667765
CALCB	NM_000728	chr11	+	15093144	15102178	1214	1058	6.654455
TSSK2	NM_053006	chr22	+	19116319	19122137	1496	163	6.63054
DNASE2B	NM_058248	chr1	+	84872032	84882692	269	194	6.624435
TAS2R14	NM_023922	chr12	-	11088851	11093807	239	222	6.62417
H1FNT	NM_181788	chr12	+	48720761	48726063	490	0	6.609765
XAGE3	NM_133179	chrX	-	52889556	52899120	62	0	6.59945
C1QTNF7	NM_031911	chr4	+	15427627	15449792	377	121	6.59393
HS6ST3	NM_153456	chr13	+	96741091	97493813	3635	3563	6.59356
C1orf49	NM_032126	chr1	+	178480210	178493790	657	628	6.59318
DSEL	NM_032160	chr18	-	65171817	65185968	1691	1543	6.58966
IFT57	NM_018010	chr3	-	107877657	107943418	823	815	6.588315
OR1N2	NM_001004457	chr9	+	125313447	125318442	76	0	6.563205
IGSF11	NM_152538	chr3	-	118617477	118866899	2331	2237	6.56115
PIWIL1	NM_004764	chr12	+	130820431	130858878	2323	1504	6.560385
EFCAB6	NM_198856	chr22	-	43922622	44210218	6326	4595	6.55535

FGF9	NM_002010	chr13	+	22243213	22280641	7442	7340	6.54429
TSSK1B	NM_032028	chr5	-	112766249	112772729	388	59	6.529985
UNC45B	NM_173167	chr17	+	33472834	33518365	3793	3227	6.522525
PPP3R2	NM_147180	chr9	-	104351895	104359284	625	43	6.52028
DUXA	NM_001012729	chr19	-	57661092	57680857	115	0	6.510855
HTR1B	NM_000863	chr6	-	78169946	78175121	1020	391	6.499335
KCTD4	NM_198404	chr13	-	45764986	45777176	272	0	6.497035
REN	NM_000537	chr1	-	204121942	204137466	2025	1794	6.47526
MAGEE2	NM_138703	chrX	-	75000821	75007080	190	38	6.45914
SCGN	NM_006998	chr6	+	25650427	25704009	1368	1178	6.45038
OPRM1	NM_001145287	chr6	+	154405640	154442595	796	0	6.4375425
ZNF257	NM_033468	chr19	+	22233264	22275904	395	392	6.435435
ZAR1	NM_175619	chr4	+	48490307	48498423	2309	2027	6.43152
NECAB1	NM_022351	chr8	+	91801919	91973631	614	503	6.43013
CALCRL	NM_005795	chr2	-	188205847	188315022	778	723	6.41602
APLF	NM_173545	chr2	+	68692689	68809295	1579	1218	6.401225
ARSF	NM_004042	chrX	+	2982851	3032748	559	465	6.400815
SLITRK5	NM_015567	chr13	+	88322868	88333871	3011	2835	6.39942
IQCF1	NM_152397	chr3	-	51926890	51939387	549	0	6.38671
GRXCR1	NM_001080476	chr4	+	42893281	43034674	389	206	6.37243
OR7A10	NM_001005190	chr19	-	14949758	14954690	140	0	6.36118
IRAK1BP1	NM_001010844	chr6	+	79575187	79610321	1150	1104	6.357615
IL21	NM_021803	chr4	-	123531781	123544212	189	0	6.33611
LANCL3	NM_198511	chrX	+	37428820	37538751	3507	3363	6.334715

C2orf51	NM_152670	chr2	+	88822167	88831104	194	186	6.334415
LOC154872	NM_001024603	chr7	-	124415344	124432865	553	514	6.327125
ANKRD7	NM_019644	chr7	+	117862710	117884785	227	0	6.32234
CWH43	NM_025087	chr4	+	48986263	49066096	1020	581	6.313845
SORCS3	NM_014978	chr10	+	106398857	107026994	4582	3992	6.30426
C10orf96	NM_198515	chr10	+	118081938	118141542	275	0	6.304025
CHRNA9	NM_017581	chr4	+	40335467	40358974	1357	1302	6.2979
GPLD1	NM_177483	chr6	-	24471324	24491800	447	444	6.29129
CSMD1	NM_033225	chr8	-	2790873	4854329	6919	4156	6.28079
DEFB125	NM_153325	chr20	+	66349	79297	321	0	6.260385
AADAC	NM_001086	chr3	+	151529859	151548277	473	336	6.247835
ADAMTS20	NM_025003	chr12	-	43746010	43947725	965	869	6.244205
PCDHAC2	NM_031883	chr5	+	140344350	140351007	835	583	6.244135
CYP39A1	NM_016593	chr6	-	46515443	46622524	1770	1367	6.24118
CST8	NM_005492	chr20	+	23469764	23478656	136	0	6.21506
CRISPLD1	NM_031461	chr8	+	75894706	75948794	1280	757	6.207585
APOL5	NM_030642	chr22	+	36111917	36127530	706	125	6.1961
EGR3	NM_004430	chr8	-	22543172	22552816	5765	5608	6.168005
LRIT3	NM_198506	chr4	+	110770484	110795472	232	0	6.16
SLC22A14	NM_004803	chr3	+	38345443	38361860	321	96	6.127885
RASSF10	NM_001080521	chr11	+	13028968	13035654	3171	3141	6.118145
DYNLRB2	NM_130897	chr16	+	80572852	80586542	1180	953	6.110545
DPY19L2	NM_173812	chr12	-	63950691	64064355	162	0	6.107365
OR13F1	NM_001004485	chr9	+	107264542	107269504	413	0	6.101825

LYG2	NM_175735	chr2	-	99856709	99873571	339	0	6.099285
ABHD13	NM_032859	chr13	+	108868761	108888604	1243	1168	6.09743
C17orf77	NM_152460	chr17	+	72579055	72592349	160	118	6.07561
PCDHGA9	NM_032089	chr5	+	140780518	140787007	675	663	6.049475
ZP4	NM_021186	chr1	-	238039162	238056223	1046	241	6.037375
PAGE2	NM_207339	chrX	+	55113495	55121261	138	129	6.03717
C16orf82	NM_001145545	chr16	+	27076217	27082488	143	70	6.01739
GAB4	NM_001037814	chr22	-	17440825	17491113	112	0	6.0145225
RSAD2	NM_080657	chr2	+	7015794	7040364	528	476	6.004325
OR56A5	NM_001146033	chr11	-	5986781	5991725	322	0	6.00399
SERPINB12	NM_080474	chr18	+	61221391	61236245	93	0	5.97628
GPR111	NM_153839	chr6	+	47622324	47667534	1997	1297	5.9745
ZNF345	NM_003419	chr19	+	37339265	37372471	1765	1527	5.969525
CLDN17	NM_012131	chr21	-	31536239	31540972	473	0	5.954885
SMC1B	NM_148674	chr22	-	45737943	45811501	1969	1364	5.932555
RBM11	NM_144770	chr21	+	15586464	15602694	637	369	5.92598
KCNH8	NM_144633	chr3	+	19188015	19579136	2483	2330	5.92406
DSC1	NM_024421	chr18	-	28707212	28744820	842	0	5.92287
SEMG2	NM_003008	chr20	+	43848008	43855100	158	0	5.9145
SCGB2A1	NM_002407	chr11	+	61974138	61983412	243	125	5.913205
DYDC1	NM_138812	chr10	-	82093860	82118501	2132	325	5.902485
TRPM3	NM_206948	chr9	-	73396776	73485975	527	297	5.893175
STK31	NM_032944	chr7	+	23747995	23874128	1334	1231	5.88677
IGFL2	NM_001135113	chr19	+	46649498	46666562	90	0	5.883935

OR9A4	NM_001001656	chr7	+	141616674	141621621	257	0	5.88003
MOS	NM_005372	chr8	-	57023499	57028542	830	685	5.87645
PLA2G3	NM_015715	chr22	-	31528791	31538470	1131	1129	5.84243
ALB	NM_000477	chr4	+	74267970	74289130	85	34	5.837035
NPFRR2	NM_053036	chr4	+	72902847	73015919	374	335	5.82842
ARSH	NM_001011719	chrX	+	2922652	2953427	615	177	5.821465
KRT71	NM_033448	chr12	-	52935691	52948932	1294	886	5.817405
ZNF582	NM_144690	chr19	-	56892646	56906890	1356	902	5.78686
SERPINA9	NM_175739	chr14	-	94927056	94944671	742	685	5.778815
UGT2B7	NM_001074	chr4	+	69960191	69980706	455	0	5.777145
HEPFL1	NM_001098672	chr11	+	93752376	93849375	972	300	5.771325
CRYGD	NM_006891	chr2	-	208984329	208991314	258	118	5.75637
TET2	NM_017628	chr4	+	106065941	106165929	3522	3425	5.753995
HRG	NM_000412	chr3	+	186381796	186398024	307	161	5.74779
MAEL	NM_032858	chr1	+	166956517	166993448	144	0	5.741415
MUM1L1	NM_152423	chrX	+	105410296	105454950	555	0	5.728975
PIK3C2G	NM_004570	chr12	+	18412472	18803353	2459	2147	5.719945
ZPLD1	NM_175056	chr3	+	102151857	102200686	356	314	5.713835
AGBL1	NM_152336	chr15	+	86683240	87574284	5958	2841	5.703565
ELAVL2	NM_004432	chr9	-	23688101	23828064	2672	1916	5.700865
C10orf140	NM_207371	chr10	-	21800407	21816612	4461	4278	5.693865
NOX4	NM_016931	chr11	-	89055520	89226654	1411	1047	5.69181
LRAT	NM_004744	chr4	+	155663161	155676271	1262	701	5.67938
TFAP2B	NM_003221	chr6	+	50784437	50817327	2883	1597	5.67887

BTG4	NM_017589	chr11	-	111336254	111385065	1579	1250	5.665735
HS3ST2	NM_006043	chr16	+	22823858	22929660	2561	2279	5.66503
SCN9A	NM_002977	chr2	-	167049695	167234498	2222	1821	5.659625
CST5	NM_001900	chr20	-	23854570	23862381	832	677	5.657185
OR2C3	NM_198074	chr1	-	247691432	247699142	664	68	5.6545
CDH12	NM_004061	chr5	-	21748971	22855732	3118	2776	5.65222
CST11	NM_130794	chr20	-	23429039	23435483	205	73	5.651845
ASCL4	NM_203436	chr12	+	108166160	108172422	698	350	5.648305
KCNC2	NM_153748	chr12	-	75431894	75605512	1271	836	5.637091667
OR1D5	NM_014566	chr17	-	2963961	2968902	183	0	5.616735
PON3	NM_000940	chr7	-	94987182	95027688	1087	1087	5.61358
AVPR1B	NM_000707	chr1	+	206222281	206233483	1693	1594	5.603695
TMEM207	NM_207316	chr3	-	190144442	190169666	386	223	5.591435
FAM184A	NM_024581	chr6	-	119278994	119401813	1738	1611	5.58763
BTBD8	NM_183242	chr1	+	92543860	92615402	1246	1110	5.57481
PTH	NM_000315	chr11	-	13511599	13519568	140	0	5.573965
RFX6	NM_173560	chr6	+	117196374	117255327	1204	1053	5.551085
C4orf39	NM_153027	chr4	+	165876098	165882274	1131	821	5.541275
RNF17	NM_031277	chr13	+	25336299	25456059	698	234	5.53185
LMO3	NM_018640	chr12	-	16699305	16761432	1067	936	5.522015
PHYHIPL	NM_032439	chr10	+	60934346	61009535	2075	2027	5.503185
CD3D	NM_001040651	chr11	-	118207787	118215460	452	379	5.502795
KRT27	NM_181537	chr17	-	38931058	38940787	336	267	5.489855
SLC7A3	NM_032803	chrX	-	70143428	70152976	593	120	5.488075

CDH18	NM_004934	chr5	-	19471153	19990354	1307	617	5.482075
POM121L2	NM_033482	chr6	-	27274840	27282012	1113	1007	5.480885
SYCP2	NM_014258	chr20	-	58436616	58509210	820	776	5.469715
KCNMB2	NM_181361	chr3	+	178252222	178564218	2549	2212	5.449785
IL3	NM_000588	chr5	+	131394345	131400897	1434	1149	5.4478
SRD5A2	NM_000348	chr2	-	31747654	31808041	1567	659	5.44109
RGPD4	NM_182588	chr2	+	108441386	108511001	102	0	5.435795
TMPRSS11A	NM_182606	chr4	-	68774017	68831233	540	408	5.43044
ABRA	NM_139166	chr8	-	107769709	107784473	685	681	5.42522
MPPED2	NM_001584	chr11	-	30429616	30604041	486	403	5.406955
KHDRBS2	NM_152688	chr6	-	62387863	62998101	870	837	5.40383
C2orf40	NM_032411	chr2	+	106680111	106696610	63	0	5.403615
TEDDM1	NM_172000	chr1	-	182365250	182371752	714	406	5.401435
KRTAP4-11	NM_033059	chr17	-	39271432	39276607	176	0	5.39603
GPR101	NM_054021	chrX	-	136110305	136115834	1357	1038	5.385405
ZNF486	NM_052852	chr19	+	20276081	20310985	1509	1227	5.384355
DAOA	NM_172370	chr13	+	106116362	106145384	265	0	5.37897
LINGO2	NM_152570	chr9	-	27946526	28721304	1643	1261	5.36444
AQP4	NM_004028	chr18	-	24430006	24444576	652	480	5.35759
NMUR2	NM_020167	chr5	-	151769100	151786841	245	159	5.35315
LPHN3	NM_015236	chr4	+	62360837	62940169	1666	1264	5.347195
HIST1H2BJ	NM_021058	chr6	-	27098093	27102576	1116	1078	5.340975
KLRC1	NM_213658	chr12	-	10596636	10609216	258	0	5.336833333
TMPRSS12	NM_182559	chr12	+	51234699	51283664	933	568	5.33561

RP1	NM_006269	chr8	+	55526625	55545395	915	706	5.325195
GPR12	NM_005288	chr13	-	27327337	27336923	1634	1578	5.306065
NAT2	NM_000015	chr8	+	18246753	18260724	394	122	5.289635
OR7A5	NM_017506	chr19	-	14935137	14941277	95	0	5.282815
ADAM7	NM_003817	chr8	+	24296507	24368276	497	449	5.278945
GUCA1C	NM_005459	chr3	-	108624640	108674678	688	457	5.27306
GABRA5	NM_001165037	chr15	+	27110271	27196358	4279	3410	5.265305
KLRC3	NM_007333	chr12	-	10566181	10575195	423	192	5.26202
TTC29	NM_031956	chr4	-	147626177	147869035	808	533	5.2574
CA3	NM_005181	chr8	+	86349054	86363268	72	0	5.254765
LCE1B	NM_178349	chr1	+	152782445	152787586	367	0	5.246285
NPHP3	NM_153240	chr3	-	132397452	132443277	1742	1728	5.22285
MC2R	NM_000529	chr18	-	13880041	13917536	1455	1239	5.203155
KLB	NM_175737	chr4	+	39406471	39455154	1202	1182	5.179405
EPHA3	NM_182644	chr3	+	89154672	89451496	2418	1609	5.1720975
SPINK6	NM_205841	chr5	+	147580355	147596701	301	0	5.16761
NT5C1B	NM_033253	chr2	-	18742135	18772839	448	244	5.138775
XK	NM_021083	chrX	+	37543131	37593384	1598	1298	5.124365
C7	NM_000587	chr5	+	40907597	40985043	263	0	5.12205
LPL	NM_000237	chr8	+	19794580	19826771	1106	1016	5.120795
SLC26A7	NM_134266	chr8	+	92259514	92408947	1450	1178	5.117265
TEX15	NM_031271	chr8	-	30687058	30708534	110	0	5.111785
DYDC2	NM_032372	chr10	+	82114556	82129830	1664	325	5.103495
EPHA7	NM_004440	chr6	-	93947738	94131301	3320	2591	5.10189

C10orf113	NM_001177483	chr10	-	21412690	21437489	273	0	5.08054
BAI3	NM_001704	chr6	+	69343630	70101404	2907	2621	5.075795
HIST1H2AG	NM_021064	chr6	+	27098815	27103315	1116	1078	5.07573
RPE65	NM_000329	chr1	-	68892505	68917643	435	337	5.0523
TLL1	NM_012464	chr4	+	166792408	167026994	4508	3824	5.040215
KRTAP2-4	NM_033184	chr17	-	39219366	39224132	500	285	5.036965
WIF1	NM_007191	chr12	-	65442402	65517347	452	324	5.033465
KLRK1	NM_007360	chr12	-	10522950	10544641	217	45	5.032745
ADAMTS19	NM_133638	chr5	+	128794101	129076377	2950	2490	5.032245
OR2H1	NM_030883	chr6	+	29424228	29434100	207	0	5.0322
KCNV1	NM_014379	chr8	-	110977231	110988960	924	318	5.02032
ART3	NM_001179	chr4	+	76993861	77035956	1215	879	5.018255
SPAM1	NM_153189	chr7	+	123563284	123602101	315	0	5.0166325
PRSS54	NM_001080492	chr16	-	58311899	58330952	1265	117	5.008025
FGL1	NM_201553	chr8	-	17719898	17754914	466	336	4.9983375
SCN3A	NM_006922	chr2	-	165942028	166062578	227	0	4.997805
SLC5A7	NM_021815	chr2	+	108600993	108632444	186	0	4.990015
CALCR	NM_001742	chr7	-	93051797	93206043	1435	1197	4.984715
ST8SIA4	NM_175052	chr5	-	100219013	100240971	762	674	4.9830375
POTEC	NM_001137671	chr18	-	14509735	14545600	44	0	4.98231
CENPC1	NM_001812	chr4	-	68335987	68413257	1022	890	4.969985
LHX8	NM_001001933	chr1	+	75592117	75629219	692	578	4.96153
CA1	NM_001738	chr8	-	86238456	86292343	412	238	4.93995
SLC17A6	NM_020346	chr11	+	22357665	22403047	292	161	4.922945

MAGEA4	NM_002362	chrX	+	151082707	151095643	605	378	4.91411
SOST	NM_025237	chr17	-	41829097	41838157	3186	2541	4.906105
PLCZ1	NM_033123	chr12	-	18834114	18892919	1018	906	4.90241
DEFB110	NM_001037728	chr6	-	49974849	49991695	97	0	4.90197
GPR149	NM_001038705	chr3	-	154053459	154149505	344	185	4.88907
HHIP	NM_022475	chr4	+	145565171	145661882	2111	1102	4.88151
SYNPR	NM_144642	chr3	+	63426751	63604598	628	451	4.851435
POU3F2	NM_005604	chr6	+	99280578	99288667	3929	3923	4.818575
LRRC3B	NM_052953	chr3	+	26662298	26754266	1648	1162	4.808025
AMIGO2	NM_181847	chr12	-	47467488	47475735	2531	2438	4.80576
CLGN	NM_004362	chr4	-	141307605	141350816	1470	1437	4.803665
SMCP	NM_030663	chr1	+	152848796	152859524	1130	777	4.803345
GZMB	NM_004131	chr14	-	25098159	25105433	487	0	4.77329
C14orf39	NM_174978	chr14	-	60900672	60954765	816	0	4.770665
CLEC5A	NM_013252	chr7	-	141625155	141648784	339	0	4.764725
SLC10A2	NM_000452	chr13	-	103694346	103721197	449	140	4.76383
SCN2A	NM_021007	chr2	+	166148339	166250821	924	692	4.74905
HRNR	NM_001009931	chr1	-	152182556	152198670	575	0	4.739165
ICOS	NM_012092	chr2	+	204799469	204828299	541	85	4.73868
CXorf22	NM_152632	chrX	+	35935849	36010270	653	0	4.700705
MAGEC2	NM_016249	chrX	-	141288126	141295077	261	182	4.67852
PGR	NM_000926	chr11	-	100898353	101002545	2457	1971	4.63997
OXGR1	NM_080818	chr13	-	97635971	97648605	760	441	4.63972
DIRAS2	NM_017594	chr9	-	93370112	93407109	561	421	4.553535

HMGCLL1	NM_019036	chr6	-	55297169	55446013	680	642	4.50821
SYT10	NM_198992	chr12	-	33526346	33594755	1199	1069	4.455865
UNC13C	NM_001080534	chr15	+	54303099	54922807	1064	781	4.35839
FGF20	NM_019851	chr8	-	16848332	16861675	1245	1111	4.305195
C1orf68	NM_001024679	chr1	+	152689996	152694906	389	0	
TSTD1	NM_001113207	chr1	-	161005420	161010775	1126	937	
LOC642587	NM_001104548	chr1	+	209600166	209607893	1964	475	
RGPD2	NM_001078170	chr2	-	88054716	88127287	320	42	
RGPD6	NM_001123363	chr2	-	111269377	111338310	462	376	
PSAPL1	NM_001085382	chr4	-	7430019	7438701	3141	2332	
SERF1B	NM_022978	chr5	+	69319076	69340935	939	799	
FAM169A	NM_015566	chr5	-	74071397	74164616	2409	2369	
FAM153C	NM_001079527	chr5	+	177433687	177476657	306	0	
ZNF879	NM_001136116	chr5	+	178448774	178463389	828	806	
C6orf58	NM_001010905	chr6	+	127896317	127914961	364	194	
LOC389493	NM_001145712	chr7	-	56180372	56186091	625	259	
ZNF727	NM_001159522	chr7	+	63503819	63540928	438	383	
WEE2	NM_001105558	chr7	+	141406151	141433072	334	0	
LOC100127983	NM_001190972	chr8	-	91968704	91999486	1194	1157	
LRRC69	NM_001129890	chr8	+	92112845	92233465	857	789	
SCXA	NM_001008271	chr8	+	145488601	145494132	4847	4677	
ANKRD20A4	NM_001098805	chr9	+	69379979	69427110	131	67	
KRTAP5-5	NM_001001480	chr11	+	1649031	1654160	731	698	

LOC283299	NM_001190788	chr11	-	7870296	7929503	1999	1959
KLRF2	NM_001190765	chr12	+	10032086	10050433	229	0
SLC15A5	NM_001170798	chr12	-	16339417	16432620	502	64
C12orf71	NM_001080406	chr12	-	27231988	27237456	856	626
SFTA3	NM_001101341	chr14	-	36940492	36984991	5891	4350
CT62	NM_001102658	chr15	-	71400581	71409840	2780	2221
GOLGA6C	NM_001164404	chr15	+	75548897	75567797	412	381
LGALS9B	NM_001042685	chr17	-	20351174	20372849	2786	2017
LOC730755	NM_001165252	chr17	-	39213491	39218345	1206	1040
KRTAP4-7	NM_033061	chr17	+	39238457	39243397	723	516
KRTAP4-8	NM_031960	chr17	-	39251232	39256376	529	68
KRTAP4-9	NM_001146041	chr17	+	39259639	39264741	471	431
LOC643008	NM_001162995	chr17	+	73627512	73639487	4925	4230
FLJ22184	NM_001190467	chr19	-	7931603	7941327	5793	5734
ZNF878	NM_001080404	chr19	-	12152618	12169128	1173	1029
SRRM5	NM_001145641	chr19	+	44114251	44120651	151	65
F8A3	NM_001007524	chrX	-	154685144	154690262	207	71
H2AFB3	NM_080720	chrX	-	154687078	154691597	207	71