

Table. S1 Regions enriched for Oct-4 in human cancer cells

chr	start	end	length	summit	tags	fold_enrichment	annotation	gene	+/-	distance to TSS
chr21	46394394	46394633	240	131	57	5.81	FTCD	NM_206965	-	-13512
chr19	8397507	8397697	191	50	9	29.55	36952	NM_001005415	+	-13511
chr12	102861529	102861824	296	177	41	9.03	HSP90B1	NM_003299	+	-13506
chr6	49520242	49520459	218	129	19	10.37	MUT	NM_000255	-	-13502
chr8	17971585	17971706	122	62	6	35.46	ASAH1	NM_177924	-	-13485
chrX	46835947	46836199	253	160	32	9.05	RGN	NM_004683	+	-13481
chr3	9932311	9932989	679	627	33	12.43	IL17RE	NM_144640	+	-13478
chr10	96701255	96701899	645	463	78	5.04	CYP2C9	NM_000771	+	-13470
chr11	76184346	76185389	1044	55	49	5.35	TSKU	NM_015516	+	-13457
chr3	52817148	52817303	156	92	48	7.32	ITIH3	NM_002217	+	-13450
chr12	119438751	119438911	161	52	11	21.21	COQ5	NM_032314	-	-13446
chr1	25550672	25550841	170	61	8	17.42	TMEM50A	NM_014313	+	-13444
chr14	38584112	38584315	204	75	7	17.75	SEC23A	NM_006364	-	-13442
chr6	112528547	112528796	250	140	14	27.89	LOC619208	NM_001033564	+	-13430
chr10	112260781	112261043	263	144	13	8.98	DUSP5	NM_004419	+	-13429
chr3	95087857	95088067	211	59	11	47.28	PROS1	NM_000313	-	-13421
chr3	9947062	9947194	133	60	8	13.63	IL17RC	NM_153460	+	-13413
chr2	86293182	86293487	306	62	17	15.68	MRPL35	NM_016622	+	-13397
chr17	45540990	45541090	101	51	9	14.97	PDK2	NM_002611	+	-13396
chr20	42476564	42476723	160	96	9	14.06	HNF4A	NM_178850	+	-13386
chr1	40206580	40206772	193	81	24	6.59	MFSD2	NM_032793	+	-13376
chr3	52798685	52800020	1336	1227	392	7.8	ITIH1	NM_002215	+	-13373

chr17	1625059	1625364	306	107	57	5.04	SERPINF1	NM_002615	+	-13356
chr19	55184740	55184877	138	78	10	18.18	VRK3	NM_001025778	-	-13342
chr3	187784328	187784497	170	116	12	9.96	DNAJB11	NM_016306	+	-13337
chr21	45712566	45713170	605	358	109	5.99	COL18A1	NM_030582	+	-13319
chr17	38318914	38319658	745	550	104	5.05	G6PC	NM_000151	+	-13318
chr19	50122826	50123069	244	185	38	6.19	APOC1	NM_001645	+	-13309
chr19	54853285	54853397	113	57	8	19.52	SR-A1	NM_021228	+	-13309
chr11	34430069	34430356	288	221	41	8.43	CAT	NM_001752	+	-13303
chr8	86576587	86576790	204	145	24	8.21	CA2	NM_000067	+	-13293
chr19	46202073	46202328	256	102	21	16.24	CYP2B6	NM_000767	+	-13285
chr6	122819311	122819469	159	108	9	16.64	SERINC1	NM_020755	-	-13278
chr11	18385222	18385959	738	435	127	7.52	LDHA	NM_005566	+	-13273
chr10	51254940	51255626	687	393	46	7.74	NCOA4	NM_005437	+	-13254
chr11	2368167	2368373	207	111	46	7.79	CD81	NM_004356	+	-13251
chr2	237671902	237672069	168	62	6	14.64	COPS8	NM_006710	+	-13247
chr6	109807458	109807659	202	87	11	18.82	CD164	NM_006016	-	-13244
chr12	45051162	45051472	311	148	22	11.84	SLC38A2	NM_018976	-	-13234
chr13	40942733	40942931	199	139	7	19.52	RGC32	NM_014059	+	-13220
chr3	32981103	32981289	187	53	6	23.64	CCR4	NM_005508	+	-13220
chr16	86434175	86434346	172	46	7	12.73	SLC7A5	NM_003486	-	-13216
chr5	10343646	10343920	275	202	42	7.65	CMBL	NM_138809	-	-13213
chr21	29363554	29363732	179	119	6	22.88	CCT8	NM_006585	-	-13212
chr3	150687993	150688320	328	227	31	8.29	TM4SF4	NM_004617	+	-13197
chr1	159448743	159448920	178	94	27	11.73	NDUFS2	NM_004550	+	-13192
chr20	29578948	29579083	136	60	9	15.93	HM13	NM_178582	+	-13182
chr7	100068768	100069148	381	96	57	6.59	TFR2	NM_003227	-	-13173

chr1	226002287	226002475	189	77	8	13.84	C1orf142	NM_053052	+	-13156
chr10	104407297	104407507	211	60	17	6.03	TRIM8	NM_030912	+	-13152
chr3	52816705	52817004	300	199	76	6.18	ITIH3	NM_002217	+	-13151
chr4	71916875	71917105	231	94	11	27.06	GRSF1	NM_002092	-	-13148
chr22	34119508	34120232	725	377	63	9.86	HMOX1	NM_002133	+	-13146
chr16	16164361	16164620	260	102	20	19.03	ABCC6	NM_001171	-	-13129
chr9	134908934	134909061	128	60	8	34.16	GTF3C5	NM_012087	+	-13128
chr5	1867435	1867626	192	84	24	5.27	NDUFS6	NM_004553	+	-13118
chr12	15939596	15939729	134	83	6	26.14	STRAP	NM_007178	+	-13117
chr7	65191230	65191384	155	71	19	7.38	ASL	NM_001024943	+	-13116
chr1	23592941	23593255	315	61	28	9.22	TCEA3	NM_003196	-	-13114
chr10	33249170	33249351	182	122	15	7.11	ITGB1	NM_033666	-	-13107
chr17	6958100	6958471	372	145	56	8.85	ASGR2	NM_080914	-	-13107
chr9	13109538	13109684	147	62	11	17.22	MPDZ	NM_003829	-	-13107
chr13	46256373	46256499	127	43	7	18.69	ESD	NM_001984	-	-13107
chr1	218347040	218347183	144	53	8	14.76	IARS2	NM_018060	+	-13106
chr6	30816254	30816596	343	54	24	7.53	FLOT1	NM_005803	-	-13105
chr9	138437414	138438037	624	513	55	6.09	PMPCA	NM_015160	+	-13101
chr6	52656717	52656940	224	155	10	16.89	TMEM14A	NM_014051	+	-13098
chr12	119660984	119661142	159	61	15	10.15	ACADS	NM_000017	+	-13094
chr6	56443857	56444087	231	110	9	11.81	DST	NM_015548	-	-13092
chr3	9946726	9946869	144	85	7	15.25	IL17RC	NM_153460	+	-13088
chr1	46554843	46555050	208	155	13	12.18	UQCRH	NM_006004	+	-13084
chr2	86293019	86293172	154	93	6	10.46	MRPL35	NM_016622	+	-13082
chr9	36217235	36217495	261	195	14	8.92	GNE	NM_005476	-	-13055
chr20	61067420	61067552	133	59	11	17.43	C20orf59	NM_022082	+	-13049

chr2	213870245	213870404	160	58	6	17.22	SPAG16	NM_001025436	+	-13044
chr19	46608406	46608585	180	91	13	11.86	BCKDHA	NM_000709	+	-13042
chr22	49057174	49057300	127	68	10	8.9	MAPK11	NM_002751	-	-13031
chr12	7187045	7187252	208	59	10	14.64	CLSTN3	NM_014718	+	-13019
chr20	47999181	47999338	158	68	11	29.28	ZNF313	NM_018683	+	-13018
chr17	76829443	76829690	248	197	24	5.71	C17orf56	NM_144679	-	-13017
chr7	27544448	27544601	154	72	11	20.29	HIBADH	NM_152740	-	-13014
chr1	65671343	65671912	570	161	35	5.84	LEPR	NM_001003680	+	-13007
chr10	81841281	81841411	131	61	6	17.43	C10orf57	NM_025125	+	-13006
chr20	1383622	1383807	186	126	6	17.75	NSFL1C	NM_182483	-	-12995
chr16	30693635	30694103	469	180	27	7.85	RNF40	NM_014771	+	-12973
chr7	72658161	72658421	261	176	16	6.69	MLXIPL	NM_032951	-	-12962
chr19	38390004	38390284	281	150	18	8.23	LRP3	NM_002333	+	-12955
chr16	48670073	48670335	263	122	8	19.25	HEATR3	NM_182922	+	-12954
chr1	57105781	57106002	222	130	18	10.56	C8A	NM_000562	+	-12936
chr3	122878414	122878571	158	48	6	19.52	GOLGB1	NM_004487	-	-12932
chr11	20354672	20354843	172	88	10	34.16	HTATIP2	NM_006410	+	-12920
chr1	89303423	89303510	88	45	6	21.96	GBP1	NM_002053	-	-12917
chr10	104406762	104407265	504	276	30	8.3	TRIM8	NM_030912	+	-12910
chr6	43148942	43149067	126	60	15	7.99	KLC4	NM_201522	+	-12908
chr19	40994870	40995633	764	77	78	6.71	PRODH2	NM_021232	-	-12902
chr2	267241	267789	549	422	31	7.75	ACP1	NM_004300	+	-12894
chr9	138455513	138455770	258	61	18	7.81	INPP5E	NM_019892	-	-12878
chr15	88141694	88142004	311	156	36	8.28	ANPEP	NM_001150	-	-12875
chr2	27175779	27176496	718	360	167	5.84	KHK	NM_000221	+	-12873
chr19	10026841	10027028	188	117	14	15.14	LOC388503	NM_001013640	+	-12870

chr22	30682328	30683347	1020	61	66	5.69	YWHAH	NM_003405	+	-12869
chr3	150385746	150386081	336	108	42	5.25	CP	NM_000096	-	-12858
chr4	40133218	40133350	133	97	9	13.63	FLJ20273	NM_019027	-	-12853
chr19	4621171	4621416	246	134	18	12.01	C19orf10	NM_019107	-	-12851
chr16	65565172	65565480	309	165	17	7.92	FLJ21736	NM_024922	+	-12842
chr12	119660708	119660881	174	84	29	8.01	ACADS	NM_000017	+	-12833
chr16	2754928	2755484	557	234	39	5.32	SRRM2	NM_016333	+	-12830
chr18	54970731	54970933	203	92	12	11.89	SEC11C	NM_033280	+	-12829
chr19	54108540	54108669	130	56	13	6.98	NUCB1	NM_006184	+	-12817
chr7	95063378	95063565	188	127	8	13.76	PDK4	NM_002612	-	-12817
chr13	28184793	28185032	240	60	13	7.03	LOC283537	NM_181785	-	-12813
chr1	38207916	38208053	138	54	7	35.46	SF3A3	NM_006802	-	-12813
chr10	73258539	73258864	326	254	37	7.56	PSAP	NM_002778	-	-12803
chr6	26485797	26486162	366	218	17	8.04	BTN3A2	NM_007047	+	-12786
chr1	199731932	199732064	133	61	9	15.58	CSRP1	NM_004078	-	-12782
chr9	127015470	127015657	188	51	10	13.76	RABEPK	NM_005833	+	-12780
chr7	100068468	100068750	283	156	29	7.78	TFR2	NM_003227	-	-12775
chr1	165789223	165789648	426	58	19	12.47	CREG1	NM_003851	-	-12772
chr1	27746367	27746540	174	124	6	23.43	AHDC1	NM_001029882	-	-12770
chr10	135202979	135203614	636	332	113	5.52	CYP2E1	NM_000773	+	-12758
chr5	150402278	150402447	170	110	13	12.44	TNIP1	NM_006058	-	-12747
chr3	50230094	50230453	360	162	37	7.03	SLC38A3	NM_006841	+	-12745
chr12	121567752	121567960	209	155	9	20.5	FLJ11021	NM_198261	-	-12733
chr21	39112197	39112446	250	191	25	20.74	ETS2	NM_005239	+	-12728
chr3	113193041	113193315	275	140	10	23.12	ABHD10	NM_018394	+	-12727
chr19	39560491	39560633	143	87	11	11.98	GPI	NM_000175	+	-12725

chr3	187852731	187853561	831	507	88	7.21	FETUB	NM_014375	+	-12719
chr19	19329339	19329497	159	104	6	18.3	KIAA0892	NM_015329	+	-12715
chr6	2957732	2957943	212	110	12	12.42	NQO2	NM_000904	+	-12714
chr17	2551965	2552130	166	111	11	8.78	KIAA0664	NM_015229	-	-12701
chr15	48799594	48799730	137	82	7	23.64	SPPL2A	NM_032802	-	-12700
chr12	51850121	51850410	290	60	15	16.98	CSAD	NM_015989	-	-12696
chr3	129266414	129266587	174	54	8	15.29	SEC61A1	NM_013336	+	-12686
chr17	7447800	7447956	157	106	6	23.64	FXR2	NM_004860	-	-12685
chr8	27417020	27417235	216	76	22	10.54	EPHX2	NM_001979	+	-12674
chr6	33056618	33057087	470	57	41	5.9	BRD2	NM_005104	+	-12673
chr2	150146884	150147066	183	89	12	10.72	C2orf25	NM_015702	-	-12669
chr10	12163520	12163643	124	68	6	29.55	DHTKD1	NM_018706	+	-12667
chr21	46354773	46355118	346	119	14	8.13	COL6A2	NM_058175	+	-12658
chrX	119466837	119467040	204	95	17	6.72	LAMP2	NM_013995	-	-12648
chr1	1323457	1323594	138	62	12	20.2	CCNL2	NM_001039577	-	-12640
chr19	3486277	3486591	315	205	19	25.62	FZR1	NM_016263	+	-12638
chr1	143614194	143614579	386	194	19	6.78	PDE4DIP	NM_001002811	-	-12632
chr12	119660442	119660678	237	79	35	6.94	ACADS	NM_000017	+	-12630
chr6	133056817	133057049	233	125	21	18.76	VNN1	NM_004666	-	-12625
chr6	30815895	30816110	216	160	13	8.43	FLOT1	NM_005803	-	-12619
chr16	11692643	11693055	413	61	21	20.5	TXNDC11	NM_015914	-	-12612
chr22	29135399	29135543	145	55	13	21.96	SEC14L2	NM_012429	+	-12611
chr12	7186710	7186843	134	77	8	13.73	CLSTN3	NM_014718	+	-12610
chr4	100458851	100459159	309	160	57	6.87	ADH1B	NM_000668	-	-12608
chr9	138454854	138455498	645	81	59	8.37	INPP5E	NM_019892	-	-12606
chr9	122992680	122992832	153	51	13	26.88	RAB14	NM_016322	-	-12596

chr1	119725225	119725507	283	121	36	5.52	HAO2	NM_001005783	+	-12583
chr22	23293941	23294185	245	85	22	8.61	SNRPD3	NM_004175	+	-12568
chr2	219959596	219959727	132	85	6	14.64	DNPEP	NM_012100	-	-12567
chr20	42475749	42475896	148	49	8	15.17	HNF4A	NM_178850	+	-12559
chr17	19504948	19505205	258	186	19	10.39	ALDH3A2	NM_001031806	+	-12550
chr14	63937250	63937392	143	61	9	14.66	MTHFD1	NM_005956	+	-12547
chr6	36582053	36582190	138	62	6	17.43	STK38	NM_007271	-	-12541
chr15	48799355	48799568	214	154	10	18.8	SPPL2A	NM_032802	-	-12538
chr16	70612484	70612678	195	135	10	19.52	DHODH	NM_001025193	+	-12535
chr22	28526976	28527127	152	62	6	23.64	ASCC2	NM_032204	-	-12525
chr16	46848029	46848232	204	104	11	14.64	LONP2	NM_031490	+	-12521
chr4	3496409	3496608	200	90	12	20.5	LRPAP1	NM_002337	-	-12516
chr9	112058512	112058643	132	61	22	6.44	TXN	NM_003329	-	-12513
chr6	30659539	30659659	121	61	7	17.08	ABCF1	NM_001025091	+	-12511
chr17	77406596	77406833	238	75	45	7.26	P4HB	NM_000918	-	-12508
chr7	99095985	99096259	275	110	31	8.05	CYP3A5	NM_000777	-	-12506
chr1	24013243	24013459	217	82	23	9.53	HMGCL	NM_000191	-	-12505
chr7	94839388	94839617	230	154	47	6.73	PON3	NM_000940	-	-12496
chr12	9123937	9124055	119	60	15	10.46	A2M	NM_000014	-	-12485
chr16	67709792	67710144	353	228	20	7.88	HAS3	NM_138612	+	-12484
chr12	102860415	102860798	384	234	39	6.49	HSP90B1	NM_003299	+	-12480
chr17	43492576	43493219	644	302	76	5.23	NFE2L1	NM_003204	+	-12475
chr12	122647001	122647495	495	163	38	6.76	TMED2	NM_006815	+	-12467
chr19	19499795	19500058	264	167	58	5.8	NDUFA13	NM_015965	+	-12463
chr3	47442507	47442644	138	90	6	19.52	SCAP	NM_012235	-	-12457
chr11	107509732	107509917	186	105	35	5.69	ACAT1	NM_000019	+	-12450

chr22	35249148	35249287	140	89	10	18.45	EIF3S7	NM_003753	-	-12444
chr17	18184061	18184362	302	173	41	6.63	SHMT1	NM_004169	-	-12443
chr5	134114329	134114543	215	108	8	29.28	CAMLG	NM_001745	+	-12439
chr6	99967127	99967356	230	172	10	18.77	C6orf111	NM_032870	-	-12433
chr11	66129279	66129684	406	324	26	9.25	CCS	NM_005125	+	-12419
chr1	65083790	65083909	120	61	7	30.14	JAK1	NM_002227	-	-12415
chr3	147282201	147282331	131	74	6	24.4	PLOD2	NM_000935	-	-12414
chr12	50925449	50925633	185	67	10	16.25	KRT7	NM_005556	+	-12413
chr17	24406210	24406455	246	72	35	6.12	PIPOX	NM_016518	+	-12412
chr2	190145800	190145973	174	59	8	25.84	SLC40A1	NM_014585	-	-12411
chr18	45576079	45576270	192	133	24	8.9	ACAA2	NM_006111	-	-12398
chr1	184543863	184544988	1126	935	169	7.07	PRG4	NM_005807	+	-12388
chr4	159825204	159825333	130	74	7	14.64	ETFDH	NM_004453	+	-12388
chr7	154730627	154732847	2221	1693	548	5.55	INSIG1	NM_198337	+	-12372
chr7	137423864	137424086	223	165	23	5.6	AKR1D1	NM_005989	+	-12351
chr21	43358562	43358721	160	58	19	14.64	CBS	NM_000071	-	-12350
chr6	52776518	52776693	176	58	24	9.45	GSTA1	NM_145740	-	-12346
chr6	160474958	160475189	232	116	45	5.34	SLC22A1	NM_153187	+	-12337
chr11	34429089	34429368	280	80	37	11.79	CAT	NM_001752	+	-12315
chr10	88812376	88812515	140	69	19	6.56	GLUD1	NM_005271	-	-12293
chr9	138738990	138739137	148	88	8	15.17	FAM69B	NM_152421	+	-12287
chr20	7823757	7823912	156	84	32	5.48	HAO1	NM_017545	-	-12282
chr3	58165466	58165668	203	143	21	15.85	DNASE1L3	NM_004944	-	-12275
chr21	44556462	44556624	163	78	15	13.13	PFKL	NM_002626	+	-12267
chr10	82033568	82033818	251	138	36	6.12	MAT1A	NM_000429	-	-12262
chr6	31001864	31002222	359	62	16	7.88	VARSL	NM_020442	+	-12262

chr5	114989204	114989356	153	87	6	13.73	TMED7	NM_181836	-	-12255
chr20	60143585	60143838	254	197	13	8.68	LSM14B	NM_144703	+	-12251
chr5	16516680	16516876	197	136	8	11.54	ZNF622	NM_033414	-	-12248
chr16	2754052	2754887	836	186	45	8.23	SRRM2	NM_016333	+	-12233
chr1	154497681	154497870	190	115	8	13.91	SMG5	NM_015327	-	-12230
chr3	129833427	129833729	303	126	31	14.2	RPN1	NM_002950	-	-12227
chr12	9123427	9123772	346	147	56	6.13	A2M	NM_000014	-	-12202
chr15	37672383	37672766	384	193	24	7.5	THBS1	NM_003246	+	-12195
chr6	33056318	33056602	285	81	33	6.07	BRD2	NM_005104	+	-12188
chr6	31708392	31708755	364	138	18	11.99	BAT2	NM_004638	+	-12180
chr22	19470267	19470557	291	134	84	6.72	SERPIND1	NM_000185	+	-12175
chr17	38316340	38318508	2169	650	600	5.34	G6PC	NM_000151	+	-12168
chr12	119660000	119660211	212	104	30	5.28	ACADS	NM_000017	+	-12163
chr11	58479230	58479456	227	80	28	7.89	GLYATL1	NM_080661	+	-12159
chr12	49740025	49740481	457	316	28	29.28	LETMD1	NM_015416	+	-12131
chr5	162877146	162877289	144	59	9	17.67	MAT2B	NM_013283	+	-12127
chr21	44389082	44390049	968	431	180	5.06	C21orf33	NM_004649	+	-12126
chr7	100322591	100322793	203	144	14	13.01	ARS2	NM_015908	+	-12123
chr1	54144366	54144562	197	142	13	17.37	DIO1	NM_001039716	+	-12114
chr1	154557181	154557479	299	165	9	17.43	CCT3	NM_001008800	-	-12104
chr1	210859265	210860693	1429	1052	182	5.54	ATF3	NM_004024	+	-12077
chr16	55534440	55535323	884	427	121	6.23	HERPUD1	NM_001010989	+	-12075
chr7	65189768	65190342	575	426	30	17.34	ASL	NM_001024943	+	-12074
chr17	77273331	77273486	156	95	6	14.64	HGS	NM_004712	+	-12062
chr2	43904890	43905172	283	166	16	13.81	ABCG5	NM_022436	-	-12057
chr1	1153697	1154201	505	213	31	7.39	SDF4	NM_016176	-	-12050

chr1	153175692	153175867	176	90	9	14.64	PMVK	NM_006556	-	-12035
chr15	99682642	99682775	134	59	11	23.53	PCSK6	NM_138320	-	-12028
chr19	19499453	19499622	170	98	25	9.04	NDUFA13	NM_015965	+	-12027
chr1	244965903	244966020	118	60	11	9.5	SCCPDH	NM_016002	+	-12020
chr15	32175393	32175532	140	56	8	14.35	C15orf24	NM_020154	-	-12016
chrX	152425464	152425617	154	91	26	5.01	BGN	NM_001711	+	-12013
chr10	7881973	7882100	128	69	13	10.31	ATP5C1	NM_001001973	+	-12002
chr19	3485801	3485948	148	91	6	15.41	FZR1	NM_016263	+	-11995
chr5	115179710	115180311	602	176	55	5.76	CDO1	NM_001801	-	-11981
chr1	119724634	119724902	269	197	47	5.91	HAO2	NM_001005783	+	-11978
chrX	74201644	74201807	164	81	7	27.11	ABCB7	NM_004299	-	-11976
chr1	2324324	2325043	720	95	65	7.3	RER1	NM_007033	+	-11970
chr14	20237238	20238729	1492	1008	276	8.33	RNASE4	NM_194431	+	-11958
chr9	138454400	138454844	445	127	30	8.14	INPP5E	NM_019892	-	-11952
chr5	74028569	74028706	138	57	8	29.28	HEXB	NM_000521	+	-11940
chr1	65670522	65670844	323	252	17	12.61	LEPROT	NM_017526	+	-11938
chr19	17250659	17251162	504	187	30	5.37	HSPC142	NM_001033549	+	-11931
chr10	69726641	69726771	131	55	13	23.02	MAWBP	NM_001033083	-	-11928
chr6	43857670	43857843	174	115	15	14.51	VEGFA	NM_001025369	+	-11913
chr9	113376833	113376981	149	61	36	5.45	LTB4DH	NM_012212	-	-11908
chr17	5330113	5330244	132	77	6	21.53	DERL2	NM_016041	-	-11908
chr1	57179088	57179379	292	60	73	5.65	C8B	NM_000066	-	-11907
chr2	43980115	43980295	181	62	8	15.9	LRPPRC	NM_133259	-	-11904
chr12	55787183	55787360	178	61	6	15.69	STAT6	NM_003153	-	-11899
chr10	113911427	113911505	79	40	6	18.3	GPAM	NM_020918	-	-11894
chr12	68277202	68277367	166	60	11	10.94	CCT2	NM_006431	+	-11893

chr19	5549742	5549886	145	98	6	22.88	SAFB2	NM_014649	-	-11876
chr16	8906539	8906705	167	125	7	21.53	USP7	NM_003470	-	-11855
chr19	2199436	2199664	229	149	10	17.43	SF3A2	NM_007165	+	-11849
chr17	24405663	24405891	229	142	37	8.05	PIPOX	NM_016518	+	-11848
chr6	139148052	139148192	141	59	7	28.34	CCDC28A	NM_015439	+	-11843
chr20	48951903	48952120	218	101	7	18.3	ADNP	NM_015339	-	-11831
chr8	141749327	141749510	184	53	7	23.64	PTK2	NM_153831	-	-11828
chr10	104405995	104406174	180	58	10	13.62	TRIM8	NM_030912	+	-11819
chr7	100067282	100067790	509	169	87	6.62	TFR2	NM_003227	-	-11815
chr5	41189613	41189902	290	115	47	6.24	C6	NM_000065	-	-11810
chr11	10786811	10786976	166	46	7	24.4	EIF4G2	NM_001418	-	-11807
chr17	43490647	43492541	1895	1653	144	5.23	NFE2L1	NM_003204	+	-11797
chr1	100969534	100969680	147	93	8	15.07	VCAM1	NM_001078	+	-11796
chr3	185531931	185532589	659	598	68	12.33	EIF4G1	NM_004953	+	-11795
chr1	39810724	39810865	142	54	7	14.64	PABPC4	NM_003819	-	-11791
chr1	200380184	200380380	197	55	8	29.55	ARL8A	NM_138795	-	-11781
chr6	119552547	119552747	201	91	11	8.83	MAN1A1	NM_005907	-	-11780
chr6	133055808	133056193	386	148	41	8.16	VNN1	NM_004666	-	-11769
chr1	53146038	53146258	221	146	26	7.55	ECHDC2	NM_018281	-	-11766
chr1	60143132	60143326	195	62	22	10.47	CYP2J2	NM_000775	-	-11758
chr7	50505243	50505387	145	89	8	35.46	DDC	NM_000790	-	-11758
chr11	2136055	2136189	135	77	11	19.77	INS-IGF2	NM_001042376	-	-11757
chr19	11418873	11419018	146	44	11	6.41	PRKCSH	NM_001001329	+	-11750
chr3	52815330	52815594	265	82	40	5.58	ITIH3	NM_002217	+	-11741
chr15	89290835	89290959	125	64	6	20.92	UNC45A	NM_018671	+	-11741
chr8	124313008	124313144	137	40	6	23.64	C8orf76	NM_032847	-	-11733

chr15	63053978	63054146	169	69	11	47.28	SPG21	NM_016630	-	-11730
chr3	101576590	101576714	125	66	8	35.46	TOMM70A	NM_014820	-	-11716
chrX	152425169	152425314	146	78	25	8.98	BGN	NM_001711	+	-11710
chr11	74551326	74551518	193	86	10	19.78	SLCO2B1	NM_007256	+	-11708
chr11	58478811	58478990	180	120	16	7.91	GLYATL1	NM_080661	+	-11693
chr21	45105446	45105633	188	108	9	19.27	PTTG1IP	NM_004339	-	-11693
chr22	41888907	41889165	259	112	19	10.11	TSPO	NM_000714	+	-11687
chr19	53077047	53077364	318	171	28	9.31	SULT2A1	NM_003167	-	-11682
chr2	43904488	43904796	309	169	20	15.08	ABCG5	NM_022436	-	-11681
chr17	46610485	46610751	267	160	10	14.64	NME2	NM_001018138	+	-11670
chr12	9123087	9123238	152	55	20	13.16	A2M	NM_000014	-	-11668
chr12	49739853	49740009	157	55	11	9.19	LETMD1	NM_015416	+	-11659
chrX	46834024	46834376	353	244	38	5.17	RGN	NM_004683	+	-11658
chr1	120103791	120104179	389	291	104	6.6	HMGCS2	NM_005518	-	-11652
chr5	141295060	141295242	183	128	7	13.94	KIAA0141	NM_014773	+	-11650
chr12	9204169	9204352	184	130	7	11.95	PZP	NM_002864	-	-11649
chr16	57309851	57310182	332	212	22	9.15	GOT2	NM_002080	-	-11647
chr12	7526468	7526667	200	103	10	23.43	CD163	NM_004244	-	-11647
chr12	119659462	119659692	231	151	26	9.18	ACADS	NM_000017	+	-11644
chr4	100356277	100356544	268	146	17	10.79	ADH6	NM_000672	-	-11642
chr7	2372450	2372641	192	59	8	14.06	EIF3S9	NM_001037283	+	-11642
chrX	128712130	128712267	138	52	6	24.4	XPNPEP2	NM_003399	+	-11641
chr14	49316041	49316174	134	84	14	7.19	KLHDC2	NM_014315	+	-11638
chr1	53476544	53476788	245	165	16	7.17	MAGOH	NM_002370	-	-11635
chr19	15895608	15895802	195	77	8	21.96	CYP4F11	NM_021187	-	-11621
chr9	35057887	35058170	284	116	15	12.81	VCP	NM_007126	-	-11610

chr5	68560786	68560933	148	54	6	29.55	MRPS36	NM_033281	+	-11605
chr19	54719559	54719886	328	62	78	5.4	FCGRT	NM_004107	+	-11583
chr5	179326389	179326650	262	89	46	7.29	RNF130	NM_018434	-	-11571
chr2	43979782	43979950	169	120	8	14.85	LRPPRC	NM_133259	-	-11559
chr1	204842967	204843155	189	44	9	23.43	LGTN	NM_006893	-	-11556
chr16	27133484	27133871	388	300	26	10.23	JMJD5	NM_024773	+	-11555
chr1	47387037	47387247	211	62	20	16.48	CYP4A22	NM_001010969	+	-11554
chr9	130135812	130136183	372	258	26	10.89	COQ4	NM_016035	+	-11548
chr19	46539896	46540033	138	93	8	28.16	TGFB1	NM_000660	-	-11543
chr7	26219086	26219388	303	230	18	13.31	CBX3	NM_016587	+	-11540
chr2	242158223	242158396	174	88	14	7.64	BOK	NM_032515	+	-11532
chr11	64631633	64631789	157	87	10	16.09	C11orf2	NM_013265	+	-11531
chr17	37730240	37730399	160	99	8	18.3	STAT3	NM_213662	-	-11531
chr1	12561784	12562056	273	170	30	10.49	DHRS3	NM_004753	-	-11530
chr4	100487901	100488203	303	62	39	11.46	ADH1C	NM_000669	-	-11530
chr16	4372985	4373377	393	323	18	18.98	VASN	NM_138440	+	-11528
chr6	64350359	64351400	1042	615	150	8.62	PTP4A1	NM_003463	+	-11522
chr16	73896409	73896625	217	79	13	9.53	CFDP1	NM_006324	-	-11516
chr11	77468199	77468560	362	236	57	7.29	NDUFC2	NM_004549	-	-11512
chr9	4712509	4712667	159	71	8	21.96	AK3	NM_016282	-	-11510
chr11	62051114	62051455	342	188	14	14.64	AHNAK	NM_001620	-	-11505
chr6	33055497	33055917	421	244	45	6.16	BRD2	NM_005104	+	-11503
chr12	120241863	120242037	175	60	9	12.81	ANAPC5	NM_016237	-	-11494
chr10	85900405	85900656	252	165	30	15.68	GHITM	NM_014394	+	-11492
chr17	2550660	2550901	242	187	12	8.78	KIAA0664	NM_015229	-	-11472
chr19	971753	972120	368	245	20	6.47	C19orf6	NM_001033026	-	-11471

chr17	34173874	34173994	121	61	8	14.17	PSMB3	NM_002795	+	-11467
chrX	131175941	131176199	259	96	11	9.48	RAP2C	NM_021183	-	-11465
chr12	55008273	55008450	178	78	6	15.69	USP52	NM_014871	-	-11463
chr3	48431579	48431723	145	61	9	8.78	PLXNB1	NM_002673	-	-11457
chr12	55786755	55786916	162	92	6	23.43	STAT6	NM_003153	-	-11455
chr12	112325935	112326079	145	84	19	6.79	SDS	NM_006843	-	-11444
chr1	171723422	171724548	1127	264	203	7.7	PRDX6	NM_004905	+	-11440
chr1	159447000	159447166	167	62	15	18.82	NDUFS2	NM_004550	+	-11438
chr2	241827668	241828248	581	129	73	5.44	HDLBP	NM_203346	-	-11432
chr11	65587651	65587813	163	48	9	10.46	SF3B2	NM_006842	+	-11422
chr5	137930125	137930344	220	168	12	14.64	HSPA9	NM_004134	-	-11421
chr2	201396193	201396301	109	55	8	12.77	BZW1	NM_014670	+	-11410
chr1	154496876	154497046	171	114	8	34.16	SMG5	NM_015327	-	-11406
chr16	55974965	55975313	349	141	16	7.66	CX3CL1	NM_002996	+	-11399
chr16	2753005	2754022	1018	148	51	6.19	SRRM2	NM_016333	+	-11368
chr12	119659148	119659414	267	62	24	9.12	ACADS	NM_000017	+	-11366
chr12	45049430	45049603	174	59	8	13.11	SLC38A2	NM_018976	-	-11365
chr1	151884147	151884507	361	61	17	6.61	C1orf77	NM_015607	+	-11359
chr16	1352979	1353285	307	196	30	6.74	GNPTG	NM_032520	+	-11353
chr14	73607585	73607977	393	266	32	7.03	ALDH6A1	NM_005589	-	-11352
chr14	77005171	77005501	331	127	27	8.31	AHSA1	NM_012111	+	-11347
chr6	17719616	17719907	292	114	34	8.02	FAM8A1	NM_016255	+	-11343
chr17	1511671	1512016	346	50	15	12.55	PRPF8	NM_006445	-	-11343
chr3	38150427	38150545	119	60	14	12.2	ACAA1	NM_001607	-	-11335
chr12	49739447	49739679	233	125	11	14.64	LETMD1	NM_015416	+	-11329
chr8	64101256	64101521	266	67	17	8.76	GGH	NM_003878	-	-11325

chr14	50181227	50181405	179	119	6	19.52	SAV1	NM_021818	-	-11296
chr10	112632758	112632880	123	62	7	25.62	PDCD4	NM_014456	+	-11295
chr1	205355364	205355522	159	64	27	6.98	C4BPA	NM_000715	+	-11293
chr3	10142948	10143624	677	522	60	10.67	C3orf10	NM_018462	+	-11292
chr1	239738522	239738817	296	158	22	8.67	FH	NM_000143	-	-11290
chr7	89881805	89882007	203	61	11	14.23	CLDN12	NM_012129	+	-11276
chr20	32342866	32342993	128	55	8	12.81	AHCY	NM_000687	-	-11257
chr1	22022367	22022588	222	133	13	7.58	LDLRAD2	NM_001013693	+	-11244
chr19	52951740	52951856	117	59	17	7.28	GLTSCR2	NM_015710	+	-11237
chr16	70665648	70665860	213	94	34	8.42	HPR	NM_020995	+	-11235
chr22	39982641	39982793	153	94	6	29.55	RANGAP1	NM_002883	-	-11233
chr20	52268964	52269134	171	60	8	12.52	PFDN4	NM_002623	+	-11226
chr1	120103151	120103748	598	174	115	8.76	HMGCS2	NM_005518	-	-11221
chr16	57309592	57309755	164	79	28	5.87	GOT2	NM_002080	-	-11220
chr12	9203790	9203920	131	61	9	15.34	PZP	NM_002864	-	-11217
chr19	47491568	47491860	293	166	17	12.87	CIC	NM_015125	+	-11204
chr5	78412242	78412541	300	77	34	7.81	BHMT2	NM_017614	+	-11203
chr4	185924651	185924939	289	191	31	6.7	ACSL1	NM_001995	-	-11196
chr1	247110156	247110343	188	59	11	12.81	ZNF672	NM_024836	+	-11191
chr6	2904370	2904574	205	96	8	11.71	SERPINB6	NM_004568	-	-11183
chr6	160033678	160033926	249	63	39	5.77	SOD2	NM_000636	-	-11182
chr5	95259862	95260030	169	126	6	20.92	ELL2	NM_012081	-	-11178
chr5	162876154	162876330	177	55	11	20.73	MAT2B	NM_013283	+	-11168
chr1	154256420	154256625	206	62	13	10.56	SSR2	NM_003145	-	-11162
chr5	179069480	179069689	210	53	16	7.69	CANX	NM_001024649	+	-11154
chrX	70387176	70387351	176	55	6	16.27	ZMYM3	NM_201599	-	-11153

chr4	39187736	39187922	187	137	8	17.57	UGDH	NM_003359	-	-11152
chr7	65188921	65189408	488	306	29	19.03	ASL	NM_001024943	+	-11140
chr4	57039464	57039653	190	56	7	12.73	SRP72	NM_006947	+	-11135
chr10	35535807	35535969	163	94	6	20.19	CREM	NM_182721	+	-11134
chr11	60868183	60868352	170	77	26	6.04	DAK	NM_015533	+	-11123
chr6	170697106	170697249	144	60	11	21.08	PSMB1	NM_002793	-	-11116
chr6	160130350	160130630	281	130	12	14.4	TCP1	NM_001008897	-	-11110
chr19	4619590	4619674	85	43	7	41.37	C19orf10	NM_019107	-	-11109
chr6	131946122	131947160	1039	590	288	6.66	ARG1	NM_000045	+	-11103
chr10	7881111	7881201	91	46	6	17.57	ATP5C1	NM_001001973	+	-11103
chr12	6560455	6560611	157	99	9	13.79	CHD4	NM_001273	-	-11102
chr3	9961436	9961593	158	62	8	10.46	CRELD1	NM_001031717	+	-11088
chr14	102673287	102673502	216	106	16	14.64	TNFAIP2	NM_006291	+	-11086
chr1	12561318	12561600	283	88	48	6.37	DHRS3	NM_004753	-	-11074
chr11	65059981	65060197	217	118	11	11.56	SCYL1	NM_020680	+	-11074
chr16	20466808	20467038	231	178	18	10.15	ACSM2	NM_182617	-	-11069
chr19	4115477	4115693	217	99	16	22.24	CREB3L3	NM_032607	+	-11065
chr12	51740842	51741163	322	206	14	12.55	TENC1	NM_170754	+	-11062
chr3	172207529	172207878	350	181	29	12.81	SLC2A2	NM_000340	-	-11048
chr19	4241476	4241703	228	175	14	13.35	SHD	NM_020209	+	-11045
chr14	73596146	73597243	1098	374	122	6.83	C14orf45	NM_025057	+	-11034
chr11	69175594	69176083	490	235	28	5.02	CCND1	NM_053056	+	-11030
chr6	43146980	43147182	203	49	10	15.02	KLC4	NM_201522	+	-11023
chr1	158590541	158590701	161	60	8	16.5	NCSTN	NM_015331	+	-11015
chr6	17718891	17719573	683	237	43	6.92	FAM8A1	NM_016255	+	-11009
chr10	7880871	7881104	234	123	12	13.7	ATP5C1	NM_001001973	+	-11006

chr10	43211912	43212075	164	82	11	9.6	HNRPF	NM_004966	-	-11005
chr16	29891754	29891882	129	75	11	9.44	LOC124446	NM_194280	+	-10998
chr4	109893428	109893638	211	153	8	15.45	AGXT2L1	NM_031279	-	-10986
chr17	31171392	31171583	192	111	9	16.87	TAF15	NM_003487	+	-10983
chr3	187851678	187851823	146	72	18	7.48	FETUB	NM_014375	+	-10981
chr17	4571139	4571517	379	319	24	7.4	ARRB2	NM_004313	+	-10980
chr8	30050938	30051148	211	98	22	7.21	TMEM66	NM_016127	-	-10975
chr19	41308399	41308702	304	62	22	9.79	CKAP1	NM_001281	+	-10975
chr22	35017974	35018243	270	172	29	6.11	MYH9	NM_002473	-	-10972
chr14	104317447	104317703	257	112	13	8.78	AKT1	NM_005163	-	-10970
chr6	133055027	133055384	358	217	49	5.24	VNN1	NM_004666	-	-10960
chr2	198070036	198070506	471	59	17	8.62	HSPD1	NM_002156	-	-10952
chr1	22021328	22022281	954	126	56	7.32	LDLRAD2	NM_001013693	+	-10937
chr19	38388004	38388263	260	52	12	9.55	LRP3	NM_002333	+	-10934
chr11	124955176	124955434	259	61	16	8.53	EI24	NM_001007277	+	-10927
chr2	231448602	231448789	188	58	8	13.76	ITM2C	NM_001012514	+	-10925
chr17	44274057	44274292	236	134	10	10.46	CALCOCO2	NM_005831	+	-10922
chr12	55453862	55454289	428	321	90	5.57	HSD17B6	NM_003725	+	-10915
chr12	111839714	111840015	302	101	17	11.79	OAS1	NM_002534	+	-10894
chr10	135036714	135036869	156	88	40	6.85	ECHS1	NM_004092	-	-10890
chr8	125631175	125631421	247	58	37	5.42	NDUFB9	NM_005005	+	-10886
chr2	71159679	71159838	160	62	6	20.92	NAGK	NM_017567	+	-10884
chr4	187396326	187396543	218	138	19	8.3	KLKB1	NM_000892	+	-10878
chr19	15451107	15451329	223	129	49	5.31	PGLYRP2	NM_052890	-	-10867
chr10	50623268	50623580	313	256	22	6.87	OGDHL	NM_018245	-	-10864
chr6	159117434	159117626	193	60	8	35.34	VIL2	NM_003379	-	-10861

chr10	85899769	85900024	256	159	30	10.62	GHITM	NM_014394	+	-10860
chr21	43357076	43357225	150	62	17	7.69	CBS	NM_000071	-	-10854
chr1	45760065	45760148	84	43	6	35.46	PRDX1	NM_002574	-	-10854
chr2	27583465	27584053	589	415	28	8.62	GCKR	NM_001486	+	-10844
chr14	102672833	102673240	408	340	23	6.83	TNFAIP2	NM_006291	+	-10824
chr2	127902380	127903306	927	559	273	5.76	PROC	NM_000312	+	-10820
chr19	1369185	1369402	218	162	8	41.37	DAZAP1	NM_170711	+	-10819
chr6	33162374	33162555	182	101	33	5.81	HLA-DPB1	NM_002121	+	-10818
chr17	15831308	15831419	112	57	6	35.46	SWS1	NM_001042698	-	-10818
chr19	40461891	40462550	660	514	64	7.85	USF2	NM_003367	+	-10815
chr9	19116048	19116573	526	183	79	7.98	ADFP	NM_001122	-	-10814
chr11	65587065	65587201	137	82	16	7.02	SF3B2	NM_006842	+	-10810
chr3	153025123	153025356	234	132	57	7.91	AADAC	NM_001086	+	-10806
chr14	50452288	50452480	193	68	13	12.72	PYGL	NM_002863	-	-10794
chr3	123776510	123776748	239	103	17	7	DTX3L	NM_138287	+	-10793
chr17	39648578	39648720	143	58	10	16.75	UBTF	NM_014233	-	-10793
chr10	13370345	13370594	250	193	54	5.49	PHYH	NM_001037537	-	-10792
chr4	100487192	100487462	271	119	43	8.87	ADH1C	NM_000669	-	-10789
chr16	70665293	70665406	114	58	23	5.48	HPR	NM_020995	+	-10781
chr1	15782262	15782507	246	115	24	6.3	AGMAT	NM_024758	-	-10769
chr22	25262251	25262473	223	152	13	6.53	TPST2	NM_001008566	-	-10758
chr19	7618594	7618774	181	120	12	9.28	STXBP2	NM_006949	+	-10754
chr17	45538233	45538446	214	52	16	19.52	PDK2	NM_002611	+	-10752
chr10	123717162	123717347	186	42	8	10.89	C10orf86	NM_017615	-	-10749
chr10	96698832	96699177	346	178	64	5.95	CYP2C9	NM_000771	+	-10748
chr11	65132317	65132542	226	145	14	9.93	MAP3K11	NM_002419	-	-10740

chr11	113825865	113826122	258	200	13	21.96	REXO2	NM_015523	+	-10736
chr2	215998064	215998363	300	66	44	14.43	FN1	NM_054034	-	-10734
chr9	129615857	129616060	204	62	15	14.64	FPGS	NM_001018078	+	-10732
chr22	45053127	45053253	127	56	9	14.88	FLJ20699	NM_017931	+	-10729
chr15	77011671	77011890	220	161	12	14.49	CTSH	NM_004390	-	-10728
chr9	103172992	103173601	610	473	105	6.5	BAAT	NM_001701	-	-10712
chrX	70430788	70430901	114	58	7	25.62	NONO	NM_007363	+	-10710
chr1	205339672	205339958	287	196	52	11.35	C4BPB	NM_001017367	+	-10708
chr20	61064628	61065203	576	272	30	5.9	C20orf59	NM_022082	+	-10700
chr6	49517512	49517655	144	84	12	36.6	MUT	NM_000255	-	-10698
chr22	29133396	29133627	232	111	30	8.49	SEC14L2	NM_012429	+	-10695
chr17	35863579	35863895	317	217	51	5.53	IGFBP4	NM_001552	+	-10694
chr4	100426972	100427239	268	156	41	16.19	ADH1A	NM_000667	-	-10693
chr16	1310110	1310320	211	96	9	12.2	UBE2I	NM_003345	+	-10682
chr20	43397826	43398020	195	59	16	8.57	SDC4	NM_002999	-	-10676
chr7	100066350	100066650	301	158	37	5.98	TFR2	NM_003227	-	-10675
chr5	68559822	68559999	178	139	8	29.55	MRPS36	NM_033281	+	-10671
chr20	32342212	32342391	180	52	9	10.98	AHCY	NM_000687	-	-10655
chr3	197438265	197438433	169	71	11	22.27	OSTalpha	NM_152672	+	-10654
chr17	619844	619973	130	61	11	9.52	C17orf25	NM_016080	-	-10652
chr1	39809516	39809715	200	62	9	23.43	PABPC4	NM_003819	-	-10641
chr7	42933506	42933616	111	56	10	16.25	PSMA2	NM_002787	-	-10628
chr16	401876	402468	593	292	53	7.96	DECR2	NM_020664	+	-10610
chr12	56178499	56178727	229	87	10	23.47	MARS	NM_004990	+	-10610
chr6	160473209	160473450	242	113	60	6.02	SLC22A1	NM_153187	+	-10598
chr1	2323398	2323662	265	174	17	13.58	RER1	NM_007033	+	-10589

chr3	50227958	50228293	336	83	40	16.4	SLC38A3	NM_006841	+	-10585
chr11	237317	237560	244	63	13	23.83	PSMD13	NM_002817	+	-10584
chr14	63762227	63762472	246	62	14	9.76	SYNE2	NM_182910	+	-10570
chr11	107507819	107508024	206	60	17	22.62	ACAT1	NM_000019	+	-10557
chr11	34427304	34427592	289	138	44	9.87	CAT	NM_001752	+	-10539
chr15	56968909	56969075	167	105	8	11.44	SLTM	NM_001013843	-	-10539
chr1	111803673	111803801	129	58	9	15.11	ATP5F1	NM_001688	+	-10536
chr19	40841270	40841527	258	178	32	5.98	COX6B1	NM_001863	+	-10533
chr14	77004551	77004687	137	62	6	28.16	AHSA1	NM_012111	+	-10533
chr14	93850051	93850870	820	275	168	5.25	SERPINA6	NM_001756	-	-10532
chr12	45455076	45455342	267	94	31	29.97	SLC38A4	NM_018018	-	-10532
chr22	31123933	31124095	163	104	11	16.71	C22orf28	NM_014306	-	-10527
chr1	149504244	149504345	102	52	9	13.44	PSMD4	NM_153822	+	-10525
chr3	52797023	52797168	146	79	50	5.34	ITIH1	NM_002215	+	-10521
chr2	27737356	27737702	347	156	13	12.2	SUPT7L	NM_014860	-	-10520
chr4	187434385	187434629	245	68	13	10.76	F11	NM_000128	+	-10518
chr12	52401497	52401687	191	56	8	20.92	CALCOCO1	NM_020898	-	-10518
chr2	27173851	27174140	290	76	72	6.04	KHK	NM_000221	+	-10517
chr13	47558433	47558609	177	56	6	23.64	MED4	NM_014166	-	-10517
chr16	20709425	20709519	95	48	9	12.52	EXOD1	NM_080663	-	-10503
chr2	55063058	55063331	274	197	30	10.53	RTN4	NM_007008	-	-10499
chr19	10024204	10024657	454	70	19	13.29	LOC388503	NM_001013640	+	-10499
chrX	138450812	138451050	239	130	19	12.83	F9	NM_000133	+	-10490
chr19	54106218	54106341	124	67	17	43.38	NUCB1	NM_006184	+	-10489
chr10	105128022	105128197	176	120	6	19.52	TAF5	NM_006951	+	-10484
chr1	153536490	153536735	246	61	16	7.2	PKLR	NM_181871	-	-10482

chr4	74576434	74576787	354	217	64	6.26	AFM	NM_001133	+	-10462
chr2	73325163	73325366	204	59	13	6.97	CCT7	NM_001009570	+	-10454
chr21	26029019	26029114	96	49	9	12.65	ATP5J	NM_001003696	-	-10452
chrX	106060154	106060734	581	179	34	5.49	CLDN2	NM_020384	+	-10445
chr3	121839968	121840147	180	103	37	5.27	HGD	NM_000187	-	-10442
chr1	202377054	202377252	199	94	18	7.28	ETNK2	NM_018208	-	-10439
chr19	60888560	60888836	277	149	23	10.54	EPN1	NM_013333	+	-10433
chr2	165259003	165259934	932	128	45	8.19	COBLL1	NM_014900	-	-10429
chr1	53144204	53144914	711	631	52	7.96	ECHDC2	NM_018281	-	-10422
chr9	129910730	129911072	343	228	39	6.8	SLC25A25	NM_001006643	+	-10416
chr6	31616056	31616389	334	182	14	9.78	BAT1	NM_004640	-	-10413
chr6	64347811	64350281	2471	1443	282	10.57	PTP4A1	NM_003463	+	-10403
chr12	21590526	21590788	263	132	11	35.46	GYS2	NM_021957	-	-10399
chr15	41836138	41836264	127	79	8	13.02	PDIA3	NM_005313	+	-10383
chr1	201186717	201186945	229	48	16	26.82	ADIPOR1	NM_015999	-	-10370
chr2	10111045	10111493	449	127	18	8.78	KLF11	NM_003597	+	-10361
chr14	22113778	22113996	219	127	30	6.41	DAD1	NM_001344	-	-10350
chr2	63679813	63679971	159	49	11	8.15	MDH1	NM_005917	+	-10346
chr14	51536174	51536288	115	58	6	25.84	C14orf166	NM_016039	+	-10346
chr16	31109085	31109296	212	119	20	18.62	FUS	NM_001010850	+	-10343
chr9	129627355	129627457	103	52	6	29.28	ENG	NM_000118	-	-10341
chr19	41332539	41333092	554	369	77	5.75	CAPNS1	NM_001003962	+	-10335
chr21	34820808	34820986	179	52	16	13.1	DSCR1	NM_203418	-	-10331
chr16	54404290	54404593	304	151	89	5.19	CES1	NM_001025194	-	-10327
chr11	65059277	65059448	172	113	10	12.55	SCYL1	NM_020680	+	-10325
chr4	166478392	166478585	194	80	23	8.05	SC4MOL	NM_006745	+	-10318

chr17	64596579	64596758	180	42	7	13.31	ABCA6	NM_080284	-	-10317
chr1	75973045	75973185	141	80	8	12.39	ACADM	NM_000016	+	-10316
chr7	102735239	102735424	186	127	8	16.34	PMPCB	NM_004279	+	-10316
chr2	74573807	74574038	232	138	9	16.53	TTC31	NM_022492	+	-10315
chr1	226947444	226947804	361	146	19	8.46	RHOU	NM_021205	+	-10313
chr10	90973420	90973611	192	55	9	28.34	LIPA	NM_000235	-	-10300
chr14	89942378	89943423	1046	218	57	5.57	CALM1	NM_006888	+	-10298
chr7	95060923	95061044	122	62	6	16.89	PKD4	NM_002612	-	-10296
chr6	32044590	32044848	259	130	12	12.55	SKIV2L	NM_006929	+	-10289
chr4	88453881	88454252	372	179	59	8.76	HSD17B13	NM_178135	-	-10288
chr9	35056648	35056847	200	61	13	11.71	VCP	NM_007126	-	-10287
chr2	219957308	219957447	140	55	6	22.88	DNPEP	NM_012100	-	-10287
chr1	26996822	26997353	532	164	23	8.9	PIGV	NM_017837	+	-10281
chrX	46973033	46973338	306	131	13	14.64	PCTK1	NM_006201	+	-10280
chr3	171177428	171177551	124	49	8	12.71	TLOC1	NM_003262	+	-10278
chr10	135200415	135201133	719	258	296	5.26	CYP2E1	NM_000773	+	-10277
chr16	66830058	66830227	170	62	9	17.08	RBM35B	NM_024939	-	-10277
chr19	18513464	18513836	373	172	31	6.01	FKBP8	NM_012181	-	-10269
chr6	43256820	43257164	345	156	25	12.63	SRF	NM_003131	+	-10267
chr7	97758952	97759188	237	90	12	10.25	BRI3	NM_015379	+	-10266
chr17	77639565	77639766	202	44	15	11.87	FASN	NM_004104	-	-10263
chr14	76867150	76867709	560	394	107	6.56	GSTZ1	NM_001513	+	-10251
chr19	8344658	8345260	603	308	40	7.06	ANGPTL4	NM_001039667	+	-10250
chr9	123151137	123151425	289	211	21	8.46	STOM	NM_198194	-	-10248
chr8	17776129	17776426	298	105	66	5.58	FGL1	NM_147203	-	-10245
chr8	11747509	11747681	173	79	25	9.29	CTSB	NM_001908	-	-10237

chr11	101906539	101906685	147	61	18	8.07	MMP7	NM_002423	-	-10236
chr12	6441447	6441744	298	176	16	11.63	TAPBPL	NM_018009	+	-10234
chr10	5488532	5488772	241	100	12	13.01	NET1	NM_005863	+	-10227
chr16	65535221	65536069	849	161	133	9.88	CES2	NM_003869	+	-10222
chr1	19283550	19283807	258	199	14	15.11	ZUBR1	NM_020765	-	-10219
chr7	22828746	22828994	249	156	39	11.46	TOMM7	NM_019059	-	-10216
chr21	33847177	33847432	256	121	11	15.69	SON	NM_032195	+	-10213
chr9	116399652	116400019	368	163	28	6.47	ATP6V1G1	NM_004888	+	-10205
chr8	42378469	42378728	260	205	15	30.03	VDAC3	NM_005662	+	-10182
chr1	54279989	54280111	123	62	14	12.61	TMEM59	NM_004872	-	-10173
chr3	52217118	52217355	238	143	44	7.36	ALAS1	NM_000688	+	-10172
chr16	1809098	1809275	178	117	19	5.73	HAGH	NM_001040427	-	-10170
chr1	89355904	89356066	163	112	6	15.15	GBP2	NM_004120	-	-10169
chr14	77004185	77004320	136	61	11	41.83	AHSA1	NM_012111	+	-10166
chr22	35755182	35755810	629	532	216	6.18	MPST	NM_001013436	+	-10163
chr20	3128964	3129174	211	95	17	9.27	C20orf116	NM_023935	-	-10157
chr5	67631840	67632352	513	146	26	8.37	PIK3R1	NM_181504	+	-10102
chr14	64630158	64630314	157	106	7	18.3	MAX	NM_145114	-	-10099
chr20	55579269	55579635	367	292	18	6.45	PCK1	NM_002591	+	-10093
chr1	93809803	93810028	226	94	7	19.52	BCAR3	NM_003567	-	-10091
chr11	65131674	65131892	219	58	15	9.62	MAP3K11	NM_002419	-	-10090
chr4	159822797	159823032	236	61	18	13.82	ETFDH	NM_004453	+	-10087
chr19	945211	945410	200	85	10	9.76	WDR18	NM_024100	+	-10083
chr17	71459088	71459270	183	83	13	7.14	ACOX1	NM_004035	-	-10082
chr6	43855793	43856010	218	60	9	13.31	VEGFA	NM_001025369	+	-10080
chr7	30440541	30440747	207	74	8	22.88	CARD4	NM_006092	-	-10073

chr2	241166129	241166841	713	580	44	8.7	RNPEPL1	NM_018226	+	-10065
chr4	113787941	113788125	185	127	9	41.37	LARP7	NM_015454	+	-10065
chr19	11417202	11417328	127	67	9	14.88	PRKCSH	NM_001001329	+	-10060
chr12	10265644	10266812	1169	1054	91	6.86	GABARAPL1	NM_031412	+	-10057
chr10	7795124	7795296	173	88	39	5.43	ITIH2	NM_002216	+	-10055
chr12	54818219	54818371	153	59	7	17.57	FAM62A	NM_015292	+	-10051
chr6	43014552	43014965	414	340	23	7.79	TNRC5	NM_183010	+	-10045
chr15	72915721	72916044	324	126	13	11.86	CPLX3	NM_001030005	+	-10041
chr1	184542134	184542634	501	442	27	6.6	PRG4	NM_005807	+	-10034
chr1	158451180	158451779	600	148	36	5.65	PEA15	NM_003768	+	-10029
chr2	150144202	150144425	224	56	12	26.24	C2orf25	NM_015702	-	-10028
chr19	55082498	55082666	169	108	9	17.32	TBC1D17	NM_024682	+	-10026
chr16	31108839	31108977	139	59	16	10.18	FUS	NM_001010850	+	-10024
chr9	129597992	129598163	172	63	6	19.52	CDK9	NM_001261	+	-10006
chr7	140052805	140052949	145	73	11	9.55	NDUFB2	NM_004546	+	-10000
chr7	6606249	6606439	191	131	8	11.19	C7orf26	NM_024067	+	-10000
chr10	104613451	104614000	550	287	28	8.95	C10orf32	NM_144591	+	-9992
chr5	281340	281438	99	50	10	14.49	SDHA	NM_004168	+	-9992
chr6	131945842	131946041	200	138	43	6.07	ARG1	NM_000045	+	-9984
chr6	114373861	114374000	140	84	8	22.28	HDAC2	NM_001527	-	-9979
chr9	129909393	129910632	1240	767	93	5.86	SLC25A25	NM_001006643	+	-9976
chr8	71657955	71658196	242	94	21	6.5	TRAM1	NM_014294	-	-9970
chr9	33110399	33110610	212	61	11	9.31	B4GALT1	NM_001497	-	-9969
chr19	987127	987254	128	67	9	30.82	CNN2	NM_004368	+	-9957
chr22	48991159	48991490	332	232	24	8.51	SELO	NM_031454	+	-9956
chrX	152423245	152423559	315	201	41	5.32	BGN	NM_001711	+	-9955

chr19	1209344	1209494	151	62	7	12.2	MIDN	NM_177401	+	-9943
chr1	11005020	11005207	188	128	9	10.93	TARDBP	NM_007375	+	-9942
chrX	47315215	47315392	178	120	7	12.2	ARAF	NM_001654	+	-9942
chr20	47173074	47173217	144	69	11	9.49	STAU1	NM_001037328	-	-9933
chr16	31418111	31418246	136	80	9	14.64	C16orf58	NM_022744	-	-9931
chr19	2061706	2061915	210	150	10	12.3	AP3D1	NM_003938	-	-9922
chr1	219036634	219036814	181	89	15	32.21	MOSC1	NM_022746	+	-9921
chr1	11656538	11656686	149	88	6	14.64	FBXO6	NM_018438	+	-9919
chr15	79401787	79401978	192	60	7	19.26	STARD5	NM_181900	-	-9910
chr15	72933971	72934150	180	50	6	22.52	SCAMP2	NM_005697	-	-9901
chr19	53674194	53674324	131	54	8	25.62	PSCD2	NM_004228	+	-9901
chr11	33003753	33004193	441	275	19	12.91	DEPDC7	NM_139160	+	-9890
chr7	75355615	75356141	527	181	39	10.14	RHBDD2	NM_001040456	+	-9889
chr16	20338026	20338244	219	61	20	5.88	FLJ20581	NM_017888	+	-9888
chr13	40271208	40271480	273	216	12	11.99	SLC25A15	NM_014252	+	-9884
chr16	67912465	67912669	205	84	8	14.64	VPS4A	NM_013245	+	-9882
chr22	35801113	35801300	188	113	16	11.01	TMPRSS6	NM_153609	-	-9876
chr17	38248093	38248817	725	558	34	7.72	PSME3	NM_005789	+	-9869
chr14	23662207	23663725	1519	155	177	8.99	WDR23	NM_025230	+	-9865
chr22	35246572	35246695	124	68	7	17.93	EIF3S7	NM_003753	-	-9852
chr11	6418450	6418862	413	297	153	5.5	HPX	NM_000613	-	-9845
chr12	55006661	55006828	168	58	8	12.2	USP52	NM_014871	-	-9841
chr19	15893835	15894020	186	80	9	16.34	CYP4F11	NM_021187	-	-9839
chr19	40461415	40461572	158	87	19	10.25	USF2	NM_003367	+	-9837
chr7	42932648	42932824	177	83	17	10.37	PSMA2	NM_002787	-	-9836
chr20	3128617	3128845	229	82	11	11.73	C20orf116	NM_023935	-	-9828

chr17	37728548	37728693	146	89	9	11.39	STAT3	NM_213662	-	-9825
chr2	234633751	234633903	153	76	31	5.04	SPP2	NM_006944	+	-9819
chr16	2751896	2752468	573	141	30	5.03	SRRM2	NM_016333	+	-9814
chr8	22488110	22488970	861	356	89	5.04	SORBS3	NM_001018003	+	-9811
chr7	97758617	97758727	111	56	14	11.38	BRI3	NM_015379	+	-9805
chr3	172206404	172206630	227	129	34	7.64	SLC2A2	NM_000340	-	-9800
chr10	74446622	74446783	162	46	6	29.55	P4HA1	NM_000917	-	-9796
chr12	25248814	25249211	398	143	19	6.99	LYRM5	NM_001001660	+	-9795
chr3	144028978	144029181	204	156	11	29.87	PCOLCE2	NM_013363	-	-9780
chr17	34172170	34172306	137	59	15	8.69	PSMB3	NM_002795	+	-9779
chr11	65131303	65131577	275	58	13	12.2	MAP3K11	NM_002419	-	-9775
chr11	75116133	75116353	221	110	18	8.09	MOGAT2	NM_025098	+	-9772
chr17	37232270	37232497	228	109	7	18.3	FKBP10	NM_021939	+	-9771
chr6	4070424	4070694	271	129	33	8.66	PECI	NM_206836	-	-9768
chr12	9121116	9121321	206	140	32	6.79	A2M	NM_000014	-	-9751
chr9	138686545	138686953	409	300	16	8.78	EGFL7	NM_016215	+	-9751
chr8	143814850	143815372	523	403	24	8.93	C8orf55	NM_016647	+	-9750
chr2	215997093	215997377	285	103	33	6.1	FN1	NM_054034	-	-9748
chr14	95080046	95080817	772	201	75	7.86	GLRX5	NM_016417	+	-9742
chr3	195606158	195606580	423	56	25	13.18	GP5	NM_004488	-	-9742
chr16	401284	401599	316	262	18	13.88	DECR2	NM_020664	+	-9741
chr3	185589842	185590294	453	353	38	6.08	CHRD	NM_003741	+	-9740
chr5	78410934	78411069	136	75	9	11.71	BHMT2	NM_017614	+	-9731
chr11	47246683	47247035	353	247	29	5.64	NR1H3	NM_005693	+	-9727
chr11	63070122	63070573	452	320	32	8.6	RARRES3	NM_004585	+	-9718
chr7	65072691	65072822	132	62	8	13.53	GUSB	NM_000181	-	-9713

chr10	52245782	52246042	261	100	14	12.81	ACF	NM_138933	-	-9710
chr14	73595539	73595918	380	267	29	6.07	C14orf45	NM_025057	+	-9709
chr15	73737697	73738109	413	104	19	7.26	SH3PX3	NM_153271	+	-9707
chr12	45047711	45047933	223	50	11	8.78	SLC38A2	NM_018976	-	-9695
chr1	53143188	53144184	997	158	74	9.94	ECHDC2	NM_018281	-	-9692
chr16	88289487	88290270	784	457	61	10.6	CDK10	NM_003674	+	-9692
chr9	74168531	74168882	352	186	16	7.32	ZFAND5	NM_006007	-	-9686
chr19	17492728	17493113	386	240	18	8.48	PGLS	NM_012088	+	-9682
chr16	31108484	31108634	151	60	16	8.84	FUS	NM_001010850	+	-9681
chr2	224539800	224540058	259	61	13	11.38	MRPL44	NM_022915	+	-9681
chr16	30690658	30690810	153	47	6	15.02	RNF40	NM_014771	+	-9680
chr1	26028562	26028940	379	77	19	8.32	FAM54B	NM_019557	+	-9670
chr15	99750940	99751145	206	58	11	9.05	PCSK6	NM_138322	-	-9670
chr5	89856652	89856865	214	96	10	18.8	LYSMD3	NM_198273	-	-9663
chr2	241466003	241466491	489	202	115	8.22	AGXT	NM_000030	+	-9657
chr10	99436644	99436816	173	128	8	10.46	AVPI1	NM_021732	-	-9644
chr16	21881574	21881747	174	54	12	11.46	UQCRC2	NM_003366	+	-9638
chr19	59661315	59661844	530	89	21	16.73	LENG8	NM_052925	+	-9633
chr11	16726222	16726392	171	44	6	29.55	C11orf58	NM_014267	+	-9623
chr19	4635677	4635855	179	61	7	18.3	DPP9	NM_139159	-	-9619
chr9	34989149	34989396	248	49	21	7.26	DNAJB5	NM_012266	+	-9612
chr14	77253574	77253799	226	59	22	19.85	C14orf156	NM_031210	+	-9612
chr4	109770636	109770806	171	72	6	14.64	RPL34	NM_033625	+	-9609
chr2	166979235	166979391	157	48	6	23.64	SCN7A	NM_002976	-	-9607
chr3	50227080	50227314	235	62	27	7.65	SLC38A3	NM_006841	+	-9606
chr16	70167285	70167859	575	125	66	5.11	TAT	NM_000353	-	-9605

chr6	24822504	24822748	245	125	9	19.1	C6orf62	NM_030939	-	-9603
chr1	115070334	115070662	329	117	21	17.66	CSDE1	NM_001007553	-	-9602
chr6	131945375	131945654	280	131	52	10.41	ARG1	NM_000045	+	-9597
chr13	28140588	28140847	260	103	14	13.96	POMP	NM_015932	+	-9597
chr11	62241015	62241304	290	159	21	12.74	GNG3	NM_012202	+	-9596
chr2	197974344	197974536	193	99	13	7.54	SF3B1	NM_012433	-	-9592
chr3	127553396	127553738	343	213	17	8.37	KLF15	NM_014079	-	-9571
chr16	29890226	29890447	222	138	34	8.13	LOC124446	NM_194280	+	-9563
chr17	22654576	22654781	206	80	10	15.08	WSB1	NM_015626	+	-9549
chr5	78452743	78452980	238	125	41	5.23	BHMT	NM_001713	+	-9542
chr17	77638826	77639041	216	59	13	8.54	FASN	NM_004104	-	-9538
chr19	4303916	4304109	194	71	9	17.04	FLJ14981	NM_032868	+	-9534
chr12	122680923	122681054	132	71	6	29.55	EIF2B1	NM_001414	-	-9532
chr19	51068227	51068882	656	572	73	7.47	FOXA3	NM_004497	+	-9525
chr19	51804161	51805875	1715	1589	164	7.05	CALM3	NM_005184	+	-9524
chr10	85898477	85898669	193	69	14	19.64	GHITM	NM_014394	+	-9505
chr9	37421961	37422176	216	116	73	5.89	GRHPR	NM_012203	+	-9470
chr13	113008794	113008937	144	83	21	9.49	LAMP1	NM_005561	+	-9468
chr18	673248	673380	133	61	10	47.28	ENOSF1	NM_017512	-	-9466
chr15	78241626	78241854	229	74	18	10.9	FAH	NM_000137	+	-9459
chr2	201168242	201168430	189	73	11	21.96	AOX1	NM_001159	+	-9455
chr7	75524640	75524769	130	73	10	17.13	MDH2	NM_005918	+	-9441
chr12	45047503	45047674	172	55	10	10.25	SLC38A2	NM_018976	-	-9436
chr3	150382344	150382653	310	210	35	7.68	CP	NM_000096	-	-9430
chr5	149482825	149483005	181	91	6	20.19	PDGFRB	NM_002609	-	-9411
chrX	129100170	129100399	230	155	13	10.1	AIFM1	NM_004208	-	-9380

chr5	43334340	43334627	288	201	23	6.75	HMGCS1	NM_002130	-	-9373
chr6	33053121	33053778	658	604	49	9.76	BRD2	NM_005104	+	-9364
chr1	150054051	150054531	481	123	34	5.63	RORC	NM_001001523	-	-9359
chr1	7953517	7953735	219	75	24	11.22	PARK7	NM_007262	+	-9356
chr9	122763557	122763787	231	62	26	7.89	C5	NM_001735	-	-9351
chr3	127314289	127314447	159	89	35	20.18	ALDH1L1	NM_012190	-	-9350
chr19	47064902	47065170	269	110	26	7.88	RPS19	NM_001022	+	-9343
chr16	55590104	55590253	150	38	6	14.64	NOD27	NM_032206	+	-9343
chr17	1620961	1621339	379	183	67	6.62	SERPINF1	NM_002615	+	-9331
chr5	150009441	150009760	320	60	12	9.76	SYNPO	NM_007286	+	-9328
chr22	40312010	40312185	176	94	9	14.64	PMM1	NM_002676	-	-9328
chr21	31962636	31963120	485	130	223	5.39	SOD1	NM_000454	+	-9315
chr3	52812888	52813161	274	147	49	8.42	ITIH3	NM_002217	+	-9308
chr9	80111044	80111186	143	58	13	10.47	PSAT1	NM_021154	+	-9308
chr10	96697563	96697728	166	102	34	6.08	CYP2C9	NM_000771	+	-9299
chr1	54279015	54279228	214	61	19	17.75	TMEM59	NM_004872	-	-9290
chr14	59690414	59690539	126	61	11	9.22	DHRS7	NM_016029	-	-9288
chr14	23184202	23184700	499	391	49	6.78	DHRS2	NM_005794	+	-9279
chrX	19281090	19281246	157	62	9	16.09	PDHA1	NM_000284	+	-9275
chr17	23706949	23707055	107	54	8	12.53	POLDIP2	NM_015584	-	-9269
chr22	35800569	35800690	122	62	8	39.04	TMPRSS6	NM_153609	-	-9266
chr9	130892147	130892488	342	282	18	10.01	DOLPP1	NM_020438	+	-9262
chr17	7993497	7993771	275	118	12	10.46	PER1	NM_002616	-	-9257
chr3	185383934	185384580	647	522	72	9	AP2M1	NM_001025205	+	-9253
chr13	40413057	40413414	358	105	12	10.48	ELF1	NM_172373	-	-9250
chr3	172205762	172206074	313	68	45	6.72	SLC2A2	NM_000340	-	-9244

chr21	43355471	43355614	144	59	17	7.38	CBS	NM_000071	-	-9243
chr3	9818326	9818468	143	94	8	16.8	ARPC4	NM_005718	+	-9242
chr3	50226827	50226947	121	61	17	11.85	SLC38A3	NM_006841	+	-9239
chr11	60446979	60447488	510	151	32	5.97	TMEM109	NM_024092	+	-9236
chr1	167759041	167759257	217	138	26	8.47	F5	NM_000130	-	-9225
chr10	96795451	96795738	288	208	59	5.87	CYP2C8	NM_000770	-	-9219
chrX	16781755	16781912	158	50	8	13.88	RBBP7	NM_002893	-	-9215
chr1	52036485	52036675	191	134	14	7.46	NRD1	NM_002525	-	-9205
chr21	46390140	46390322	183	102	42	7.73	FTCD	NM_206965	-	-9201
chr17	2547950	2548626	677	194	40	5.83	KIAA0664	NM_015229	-	-9197
chr17	77638497	77638699	203	119	18	9.91	FASN	NM_004104	-	-9196
chr19	47275372	47275553	182	125	6	17.22	ZNF574	NM_022752	+	-9196
chr16	31107949	31108147	199	71	13	9.71	FUS	NM_001010850	+	-9194
chr3	195605621	195606026	406	138	25	13.37	GP5	NM_004488	-	-9188
chr6	143866730	143867116	387	134	18	11.33	FUCA2	NM_032020	-	-9178
chr10	69770923	69771061	139	83	11	13.31	HNRPH3	NM_012207	+	-9177
chr2	113656911	113657204	294	187	12	12.2	PSD4	NM_012455	+	-9174
chr1	17226818	17226985	168	70	25	5.23	SDHB	NM_003000	-	-9172
chr20	60915350	60915788	439	293	36	5.36	OGFR	NM_007346	+	-9167
chr11	117689604	117689824	221	128	8	15.25	CD3E	NM_000733	+	-9163
chr19	3710746	3710931	186	147	7	19.52	APBA3	NM_004886	-	-9161
chr1	43419651	43419770	120	61	6	21.96	WDR65	NM_152498	+	-9158
chr17	23678753	23679403	651	497	40	6.35	TMEM97	NM_014573	+	-9156
chr1	10390656	10390825	170	115	6	20.92	PGD	NM_002631	+	-9154
chr19	55055057	55055380	324	130	25	8.7	PTOV1	NM_017432	+	-9153
chr11	1934023	1934258	236	111	27	7.49	MRPL23	NM_021134	+	-9145

chr14	23838641	23838785	145	72	15	8.49	DHRS1	NM_138452	-	-9140
chr10	5237712	5237936	225	58	13	12.08	AKR1C4	NM_001818	+	-9139
chr9	33024226	33024342	117	59	13	11.13	DNAJA1	NM_001539	+	-9134
chr13	30617708	30617897	190	74	10	36.6	HSPH1	NM_006644	-	-9133
chr8	64099008	64099327	320	233	21	9.37	GGH	NM_003878	-	-9131
chr10	69235324	69235564	241	120	12	12.35	DNAJC12	NM_021800	-	-9131
chr14	23642192	23642451	260	77	40	8.48	PCK2	NM_004563	+	-9129
chr21	39108566	39108836	271	144	26	6.24	ETS2	NM_005239	+	-9118
chr10	82030301	82030673	373	190	41	7.8	MAT1A	NM_000429	-	-9117
chr9	74714197	74714523	327	184	72	6.7	ALDH1A1	NM_000689	-	-9116
chr10	93557019	93557164	146	103	7	17.57	TNKS2	NM_025235	+	-9116
chr9	123150013	123150272	260	202	16	19.03	STOM	NM_198194	-	-9095
chr4	83967544	83967930	387	220	26	9.44	SEC31A	NM_001077208	-	-9092
chr20	32764630	32764899	270	106	36	8.4	TP53INP2	NM_021202	+	-9091
chr1	205338040	205338341	302	149	53	10.02	C4BPB	NM_001017367	+	-9091
chr14	73594785	73595296	512	204	62	5.21	C14orf45	NM_025057	+	-9087
chr6	31614849	31615062	214	114	11	12.53	BAT1	NM_004640	-	-9086
chr7	150128251	150128405	155	101	18	7.63	TMEM176B	NM_014020	-	-9082
chr6	49515853	49516037	185	61	26	5.42	MUT	NM_000255	-	-9080
chr16	57307398	57307614	217	71	32	7.72	GOT2	NM_002080	-	-9079
chr19	4050174	4050402	229	173	14	8.94	MAP2K2	NM_030662	-	-9074
chr3	38148073	38148273	201	48	17	12.33	ACAA1	NM_001607	-	-9063
chr10	75231136	75231550	415	355	22	12.81	KIAA0913	NM_015037	+	-9056
chr11	125652666	125653312	647	62	46	5.68	FOXRED1	NM_017547	+	-9048
chr12	64825873	64826032	160	78	6	22.52	TMBIM4	NM_016056	-	-9048
chr16	4802067	4802247	181	129	7	29.55	N-PAC	NM_032569	-	-9042

chr2	85673822	85674082	261	58	12	9.76	VAMP5	NM_006634	+	-9041
chr10	81913783	81913899	117	59	11	18.84	ANXA11	NM_001157	-	-9040
chr20	19955434	19955579	146	57	9	14.96	NAT5	NM_181527	+	-9037
chr7	2369809	2370033	225	78	8	16.47	EIF3S9	NM_001037283	+	-9034
chr19	59661103	59661241	139	78	6	21.53	LENG8	NM_052925	+	-9030
chr6	43013803	43013944	142	52	13	13.18	TNRC5	NM_183010	+	-9024
chr22	36542763	36542921	159	53	9	14.64	GCAT	NM_014291	+	-9021
chr5	10339434	10339714	281	134	34	12.34	CMBL	NM_138809	-	-9007
chr1	47176184	47176440	257	172	35	9.58	CYP4A11	NM_000778	-	-9006
chr2	197973626	197973947	322	211	26	7.66	SF3B1	NM_012433	-	-9003
chr5	151111438	151111574	137	60	19	7.22	ATOX1	NM_004045	-	-8998
chr5	178982657	178982781	125	54	7	15.41	HNRPH1	NM_005520	-	-8996
chr15	89221750	89221878	129	59	11	9.09	FURIN	NM_002569	+	-8990
chr7	148339855	148340070	216	75	21	5.27	PDIA4	NM_004911	-	-8982
chr5	150009115	150009409	295	135	13	12.2	SYNPO	NM_007286	+	-8977
chr5	67630838	67631224	387	270	23	8.37	PIK3R1	NM_181504	+	-8974
chrX	46946986	46947212	227	57	13	14.64	UBE1	NM_003334	+	-8974
chr15	89237507	89237679	173	115	9	14.64	FES	NM_002005	+	-8967
chr22	40793058	40793295	238	180	11	8.71	NAGA	NM_000262	-	-8965
chr12	2782814	2783375	562	218	51	7.13	FKBP4	NM_002014	+	-8962
chr15	73008500	73008631	132	74	14	8.37	COX5A	NM_004255	-	-8960
chr2	85431333	85431688	356	295	25	26.06	RETSAT	NM_017750	-	-8956
chr2	10109804	10110086	283	132	12	10.36	KLF11	NM_003597	+	-8954
chr4	110890080	110890252	173	79	39	8.16	CFI	NM_000204	-	-8952
chr1	205352822	205353178	357	274	61	8.42	C4BPA	NM_000715	+	-8949
chr16	30675898	30676186	289	233	14	12.69	PHKG2	NM_000294	+	-8949

chr1	32469260	32469499	240	115	16	11.71	EIF3S2	NM_003757	+	-8942
chr19	17212475	17212629	155	81	10	18.15	NR2F6	NM_005234	-	-8935
chr19	18900213	18900427	215	152	11	7.87	DDX49	NM_019070	+	-8934
chr19	12871293	12871901	609	290	46	8.92	GCDH	NM_000159	+	-8928
chr14	22448478	22448622	145	90	6	29.55	RBM23	NM_018107	-	-8928
chr2	241463858	241465761	1904	1828	312	7.88	AGXT	NM_000030	+	-8927
chrX	106058377	106059205	829	308	42	9.32	CLDN2	NM_020384	+	-8916
chr22	31209864	31210138	275	51	13	8.05	FBXO7	NM_001033024	+	-8915
chr22	36294761	36295359	599	467	58	7.42	CDC42EP1	NM_007061	+	-8913
chr22	41353537	41353672	136	62	12	8.96	CYB5R3	NM_007326	-	-8908
chr1	23517570	23517769	200	98	8	11.71	HNRPR	NM_005826	-	-8906
chr19	38565134	38565350	217	52	13	7.41	CEBPG	NM_001806	+	-8902
chr7	44398447	44398616	170	126	7	18.3	NUDCD3	NM_015332	-	-8901
chr7	26206650	26206891	242	181	31	5.15	HNRPA2B1	NM_002137	-	-8900
chr19	44091166	44091352	187	129	8	24.4	NFKBIB	NM_002503	+	-8898
chr11	124953160	124953385	226	129	10	17.43	EI24	NM_001007277	+	-8878
chr19	19244952	19245048	97	49	6	25.84	TM6SF2	NM_001001524	-	-8875
chr11	5676152	5676368	217	156	10	17.57	TRIM22	NM_006074	+	-8874
chr4	9693658	9693914	257	127	21	9.03	WDR1	NM_005112	-	-8854
chr14	89941210	89941977	768	409	76	6.75	CALM1	NM_006888	+	-8852
chr10	27449365	27449521	157	100	10	20.69	YME1L1	NM_139313	-	-8850
chr12	112087944	112088217	274	128	9	29.55	DDX54	NM_024072	-	-8849
chr2	127901127	127901312	186	73	37	5.94	PROC	NM_000312	+	-8826
chr20	32763357	32764625	1269	789	90	7.32	TP53INP2	NM_021202	+	-8817
chr14	22384291	22384439	149	59	6	16.64	MMP14	NM_004995	+	-8807
chr12	94899876	94900075	200	61	8	11.71	HAL	NM_002108	-	-8803

chr8	30771252	30771464	213	62	8	18.71	PPP2CB	NM_001009552	-	-8796
chrX	51661958	51662223	266	52	23	5.56	MAGED1	NM_001005333	+	-8786
chr17	40576544	40577356	813	611	68	5.69	ACBD4	NM_024722	+	-8777
chr11	111471071	111471598	528	470	32	17.01	SDHD	NM_003002	+	-8767
chr16	68852369	68852556	188	111	8	13.76	AARS	NM_001605	-	-8759
chr11	1739092	1739318	227	77	49	6.65	CTSD	NM_001909	-	-8758
chr3	150381544	150381979	436	84	27	7.3	CP	NM_000096	-	-8756
chr2	27117139	27118076	938	430	66	5.78	FLJ20254	NM_017727	+	-8751
chr17	61646657	61647361	705	618	280	5.13	APOH	NM_000042	-	-8748
chr22	35245375	35245584	210	84	10	29.28	EIF3S7	NM_003753	-	-8741
chr3	185529344	185529516	173	86	16	7.6	EIF4G1	NM_004953	+	-8722
chr17	77297397	77298494	1098	586	143	6.62	SLC25A10	NM_012140	+	-8719
chr1	226402967	226403322	356	197	52	7.17	GUK1	NM_000858	+	-8718
chr17	38314730	38315058	329	195	34	8.32	G6PC	NM_000151	+	-8718
chr16	56601354	56601518	165	117	6	23.64	C16orf57	NM_024598	+	-8713
chr16	57119898	57120066	169	55	8	12.37	CNOT1	NM_016284	-	-8710
chr14	23641781	23642031	251	70	32	8.08	PCK2	NM_004563	+	-8709
chr11	65801071	65801335	265	222	16	13.58	RAB1B	NM_030981	+	-8704
chr1	53142894	53143186	293	75	41	6.43	ECHDC2	NM_018281	-	-8694
chr18	3245723	3246216	494	216	45	9.16	MRCL3	NM_006471	+	-8689
chr3	195604990	195605517	528	60	39	12.88	GP5	NM_004488	-	-8679
chr6	170694589	170694808	220	83	27	10.58	PSMB1	NM_002793	-	-8675
chr10	135066168	135066281	114	58	8	23.43	MTG1	NM_138384	+	-8671
chr17	45987822	45988224	403	164	19	7.08	SPATA20	NM_022827	+	-8664
chr3	52215573	52215846	274	116	61	5.35	ALAS1	NM_000688	+	-8663
chr7	100565695	100565822	128	62	20	5.93	SERPINE1	NM_000602	+	-8651

chr19	15095176	15095430	255	119	9	14.64	ILVBL	NM_176826	-	-8644
chr19	38564883	38565087	205	155	10	11.39	CEBPG	NM_001806	+	-8639
chr6	33149138	33149409	272	199	16	6.97	HLA-DPA1	NM_033554	-	-8638
chr6	38760116	38760319	204	116	13	39.42	GLO1	NM_006708	-	-8622
chr6	36762324	36763084	761	688	82	6.53	CDKN1A	NM_000389	+	-8620
chr5	42843892	42844355	464	212	154	7.73	SEPP1	NM_005410	-	-8616
chr7	107359848	107360108	261	47	11	9.55	LAMB1	NM_002291	-	-8610
chr1	239735854	239736135	282	143	30	5.78	FH	NM_000143	-	-8608
chr6	30701739	30702182	444	358	37	7.8	MRPS18B	NM_014046	+	-8598
chr10	82029895	82030150	256	93	64	7.08	MAT1A	NM_000429	-	-8594
chr4	100485020	100485262	243	180	77	5.1	ADH1C	NM_000669	-	-8589
chr5	176457143	176457743	601	96	63	6.02	FGFR4	NM_022963	+	-8587
chr1	78251632	78251809	178	52	11	12.55	DNAJB4	NM_007034	+	-8586
chr3	49116792	49116942	151	53	8	23.29	QARS	NM_005051	-	-8573
chr5	150387612	150388761	1150	1090	249	5.14	GPX3	NM_002084	+	-8570
chr17	37949586	37950035	450	316	31	5.86	NAGLU	NM_000263	+	-8559
chr19	53073990	53074240	251	169	51	7.74	SULT2A1	NM_003167	-	-8558
chr1	76032770	76033019	250	98	13	8.54	RABGGTB	NM_004582	+	-8546
chr1	159474438	159474611	174	53	16	8.49	NR1I3	NM_001077478	-	-8530
chr6	160471007	160471374	368	186	31	14.62	SLC22A1	NM_153187	+	-8522
chr3	58161701	58161914	214	153	17	7.83	DNASE1L3	NM_004944	-	-8521
chr21	39107999	39108226	228	132	15	18.36	ETS2	NM_005239	+	-8508
chr2	197973213	197973447	235	60	20	5.73	SF3B1	NM_012433	-	-8503
chr8	11745778	11745943	166	93	34	5.05	CTSB	NM_001908	-	-8499
chr6	24611491	24611654	164	111	9	29.28	ALDH5A1	NM_001080	+	-8479
chr4	100424554	100425022	469	183	160	5.81	ADH1A	NM_000667	-	-8476

chr1	115069281	115069533	253	145	19	17.29	CSDE1	NM_001007553	-	-8473
chr6	32011657	32011941	285	113	50	6.78	C2	NM_000063	+	-8469
chr12	131782529	131782723	195	104	24	9.14	PXMP2	NM_018663	+	-8459
chr7	37920295	37920520	226	102	8	16.54	SFRP4	NM_003014	-	-8453
chr16	55531273	55531700	428	235	48	5.92	HERPUD1	NM_001010989	+	-8452
chr14	67221470	67221714	245	193	11	8.97	RDH11	NM_016026	-	-8444
chr4	187432207	187432554	348	168	25	9.34	F11	NM_000128	+	-8443
chr16	45555940	45556237	298	138	12	15.27	DNAJA2	NM_005880	-	-8442
chrX	51661398	51661876	479	323	44	7.01	MAGED1	NM_001005333	+	-8439
chr1	93398276	93398428	153	64	7	14.64	TMED5	NM_016040	-	-8430
chr6	43854077	43854345	269	134	18	14.44	VEGFA	NM_001025369	+	-8415
chr17	70528541	70528787	247	108	11	10.98	ICT1	NM_001545	+	-8413
chr17	71457384	71457600	217	55	11	11.71	ACOX1	NM_004035	-	-8412
chr4	70749715	70749931	217	123	11	18.3	SULT1E1	NM_005420	-	-8412
chr11	614798	614985	188	62	16	8.26	MUCDHL	NM_021924	-	-8409
chr5	40803454	40803633	180	62	9	16.64	PRKAA1	NM_006251	-	-8395
chr3	10166540	10166710	171	121	6	19.52	VHL	NM_000551	+	-8392
chr16	65534044	65534231	188	83	43	6.35	CES2	NM_003869	+	-8384
chr11	65129998	65130163	166	62	12	20.92	MAP3K11	NM_002419	-	-8361
chr2	27513103	27513328	226	89	9	16.89	NRBP1	NM_013392	+	-8352
chr11	65800411	65800967	557	223	33	8.78	RAB1B	NM_030981	+	-8336
chr12	48799961	48800496	536	417	46	6.73	C12orf62	NM_032901	+	-8330
chr17	31168806	31168929	124	55	6	24.4	TAF15	NM_003487	+	-8329
chr10	50620866	50621038	173	105	19	16.46	OGDHL	NM_018245	-	-8322
chr11	86197252	86197527	276	166	10	17.57	PRSS23	NM_007173	+	-8317
chr10	22658253	22658458	206	54	9	21.96	BMI1	NM_005180	+	-8313

chr12	6915877	6916052	176	126	6	24.4	ATN1	NM_001940	+	-8312
chr2	234632166	234632383	218	138	39	9.22	SPP2	NM_006944	+	-8299
chr20	17550324	17550620	297	93	22	5.59	RRBP1	NM_001042576	-	-8298
chr1	39272624	39272885	262	122	27	9.32	NDUFS5	NM_004552	+	-8293
chr9	138433083	138433215	133	57	8	12.81	PMPCA	NM_015160	+	-8279
chr19	45565443	45565665	223	84	10	21.96	PLD3	NM_012268	+	-8277
chr1	245538355	245538522	168	121	6	24.4	ZNF496	NM_032752	-	-8277
chr6	131942784	131944317	1534	1347	178	13.01	ARG1	NM_000045	+	-8260
chr19	38564472	38564707	236	129	13	10.25	CEBPG	NM_001806	+	-8259
chr14	102878721	102879244	524	75	54	7.81	EIF5	NM_183004	+	-8256
chr17	77637397	77637758	362	275	20	7.54	FASN	NM_004104	-	-8255
chr22	35799495	35799673	179	70	13	7.86	TMPRSS6	NM_153609	-	-8249
chr14	22383747	22383874	128	79	6	15.25	MMP14	NM_004995	+	-8242
chr2	197973007	197973185	179	56	18	15.77	SF3B1	NM_012433	-	-8241
chr19	44671015	44671132	118	60	6	21.96	TIMM50	NM_001001563	+	-8241
chr12	47953227	47953369	143	91	8	12.56	TUBA6	NM_032704	+	-8238
chr5	179323052	179323317	266	95	23	20.77	RNF130	NM_018434	-	-8238
chr15	43254689	43254942	254	61	18	11.16	SHF	NM_138356	-	-8237
chr2	225051118	225051342	225	139	9	19.77	CUL3	NM_003590	-	-8230
chr2	21081401	21086031	4631	171	1549	5.26	APOB	NM_000384	-	-8225
chr4	155752913	155753396	484	296	123	7.72	FGG	NM_021870	-	-8218
chr5	135318362	135318714	353	67	42	6.89	LECT2	NM_002302	-	-8216
chr16	1807126	1807318	193	85	32	5.18	HAGH	NM_001040427	-	-8213
chr19	2060064	2060198	135	83	7	12.2	AP3D1	NM_003938	-	-8205
chr1	109754076	109754205	130	69	9	27.89	PSMA5	NM_002790	-	-8205
chr2	234341582	234341861	280	134	105	5.26	UGT1A1	NM_000463	+	-8204

chr14	102466728	102466950	223	61	16	7.35	AMN	NM_030943	+	-8204
chr10	106012705	106012868	164	76	24	5.4	GSTO1	NM_004832	+	-8201
chr1	171721102	171721306	205	148	46	6	PRDX6	NM_004905	+	-8198
chr22	36392162	36392871	710	223	41	6.41	PDXP	NM_020315	+	-8189
chr11	66217274	66217485	212	57	8	18.89	SPTBN2	NM_006946	-	-8187
chr11	614524	614759	236	137	13	9.76	MUCDHL	NM_021924	-	-8183
chrX	118261124	118262472	1349	1003	331	5.71	PGRMC1	NM_006667	+	-8182
chr12	97519061	97519712	652	354	94	6.27	SLC25A3	NM_002635	+	-8179
chr16	27151710	27151995	286	157	10	25.62	NSMCE1	NM_145080	-	-8179
chr19	56548178	56548384	207	147	45	6.61	ETFB	NM_001014763	-	-8164
chr1	243073197	243073422	226	94	10	16.27	FAM36A	NM_198076	+	-8161
chr2	85430679	85430891	213	159	17	7.02	RETSAT	NM_017750	-	-8159
chr11	63068647	63068994	348	220	31	7.64	RARRES3	NM_004585	+	-8139
chr15	89256387	89256556	170	53	8	12.44	MAN2A2	NM_006122	+	-8133
chr3	127690807	127690941	135	62	11	8.89	UROC1	NM_144639	-	-8128
chr16	3655965	3656164	200	140	14	10.25	TRAP1	NM_016292	-	-8125
chr8	126517377	126519861	2485	2282	566	6.24	TRIB1	NM_025195	+	-8117
chr12	44607091	44607295	205	104	7	14.64	SFRS2IP	NM_004719	-	-8113
chr22	35015068	35015371	304	75	29	9.54	MYH9	NM_002473	-	-8100
chr9	131436130	131436354	225	124	9	13.18	C9orf32	NM_014064	+	-8099
chr6	7834720	7834850	131	57	10	15.34	TXNDC5	NM_030810	-	-8098
chr10	127509993	127510188	196	137	8	14.35	BCCIP	NM_078468	+	-8084
chr2	241824619	241824895	277	171	32	7.21	HDLBP	NM_203346	-	-8079
chr19	52041003	52041341	339	192	26	12.9	AP2S1	NM_004069	-	-8079
chr11	62091443	62091724	282	47	28	6.42	EEF1G	NM_001404	-	-8076
chr12	123382847	123382988	142	52	7	24.4	NCOR2	NM_006312	-	-8074

chr19	15094526	15094859	334	60	15	14.67	ILVBL	NM_176826	-	-8073
chr5	43332755	43333325	571	157	32	8.36	HMGCS1	NM_002130	-	-8071
chr1	76032387	76032544	158	102	8	17.57	RABGGTB	NM_004582	+	-8071
chr3	130459029	130459202	174	47	6	24.4	COPG	NM_016128	+	-8060
chr3	49116235	49116412	178	122	7	16.27	QARS	NM_005051	-	-8043
chr2	219954921	219955194	274	105	12	23.43	DNPEP	NM_012100	-	-8034
chr9	34651473	34651950	478	149	24	10.5	IL11RA	NM_004512	+	-8019
chr17	23705592	23705805	214	106	14	14.1	POLDIP2	NM_015584	-	-8019
chr9	130891045	130891243	199	134	8	14.57	DOLPP1	NM_020438	+	-8017
chr9	129908427	129908663	237	190	13	6.94	SLC25A25	NM_001006643	+	-8007
chr11	62412397	62412861	465	312	28	30.64	SLC3A2	NM_001013251	+	-7999
chr20	11854339	11854562	224	120	9	25.84	BTBD3	NM_014962	+	-7998
chr20	36416083	36416295	213	65	20	20.27	LBP	NM_004139	+	-7997
chr7	2368807	2368995	189	73	11	9.69	EIF3S9	NM_001037283	+	-7996
chr17	39785534	39786007	474	372	52	6.94	GRN	NM_002087	+	-7991
chr22	18250857	18251023	167	53	7	23.64	TXNRD2	NM_006440	-	-7984
chr17	70528184	70528357	174	120	8	9.76	ICT1	NM_001545	+	-7983
chr11	94343774	94343912	139	83	9	14.25	HSPC148	NM_016403	-	-7982
chr2	31418533	31418667	135	77	7	21.43	XDH	NM_000379	-	-7976
chr6	10838816	10839292	477	259	37	6.98	TMEM14C	NM_016462	+	-7969
chr19	531384	531503	120	61	11	10.74	BSG	NM_001728	+	-7967
chr12	90070979	90071131	153	86	33	7.56	DCN	NM_133504	-	-7965
chr12	122516250	122516566	317	60	12	7.32	U1SNRNPBP	NM_180699	+	-7963
chr7	56094723	56094831	109	55	6	19.97	CCT6A	NM_001009186	+	-7960
chr14	22383425	22383591	167	84	7	15.25	MMP14	NM_004995	+	-7959
chr1	35429529	35429745	217	157	11	10.9	SFPQ	NM_005066	-	-7956

chr5	1378855	1378955	101	51	7	40.99	CLPTM1L	NM_030782	-	-7949
chr5	78336748	78337127	380	184	24	16.69	DMGDH	NM_013391	-	-7942
chr2	27855783	27856020	238	184	14	12.2	MRPL33	NM_004891	+	-7933
chr11	67574787	67574952	166	61	15	13.31	TCIRG1	NM_006053	+	-7930
chr7	100062711	100063903	1193	470	196	5.9	TFR2	NM_003227	-	-7928
chr16	65402099	65402210	112	57	6	25.1	APPBP1	NM_001018160	-	-7928
chr12	55029398	55029575	178	119	8	25.62	STAT2	NM_005419	-	-7925
chr3	52214802	52215106	305	207	48	5.81	ALAS1	NM_000688	+	-7923
chr6	160139059	160139408	350	189	20	7.69	MRPL18	NM_014161	+	-7921
chr11	60422580	60422696	117	59	7	17.08	PRPF19	NM_014502	-	-7914
chr1	1244522	1244735	214	57	8	14.64	CPSF3L	NM_017871	-	-7908
chrX	153317223	153318075	853	297	60	8.33	ATP6AP1	NM_001183	+	-7904
chr17	77616776	77616942	167	59	9	39.42	DUS1L	NM_022156	-	-7902
chr16	31408343	31409830	1488	57	122	7.43	SLC5A2	NM_003041	+	-7891
chr3	185394001	185394467	467	62	26	6.84	ABCF3	NM_018358	+	-7888
chr3	150380477	150381109	633	253	33	6.1	CP	NM_000096	-	-7886
chr5	150468189	150468340	152	96	14	8.16	ANXA6	NM_001155	-	-7880
chr6	53247885	53248027	143	59	7	13.73	ELOVL5	NM_021814	-	-7873
chr3	120878719	120878931	213	65	20	16.63	COX17	NM_005694	-	-7870
chr22	37468277	37468544	268	62	20	7.85	UNC84B	NM_015374	-	-7864
chr16	65533422	65533709	288	192	47	8.11	CES2	NM_003869	+	-7862
chr17	19500274	19500501	228	130	26	5.25	ALDH3A2	NM_001031806	+	-7846
chr3	52828410	52829882	1473	1373	403	7.53	ITIH4	NM_002218	-	-7836
chr14	22572395	22572735	341	283	24	21.63	PSMB5	NM_002797	-	-7835
chr9	80109491	80109703	213	70	16	13.51	PSAT1	NM_021154	+	-7825
chr5	41185665	41185915	251	180	22	14.7	C6	NM_000065	-	-7823

chr11	65070466	65070672	207	105	11	9.76	LTBP3	NM_021070	-	-7821
chr20	60209243	60209457	215	95	10	14.64	GTPBP5	NM_015666	+	-7810
chr20	62172021	62172255	235	102	8	13.31	TCEA2	NM_003195	+	-7802
chr17	53522210	53523590	1381	812	151	8.21	DYNLL2	NM_080677	+	-7793
chr19	942971	943119	149	46	6	18.3	WDR18	NM_024100	+	-7792
chr9	130904493	130904686	194	126	22	6.63	CRAT	NM_004003	-	-7791
chr7	107906868	107907090	223	130	10	10.46	PNPLA8	NM_015723	-	-7784
chr17	43380814	43381688	875	212	103	5.06	PNPO	NM_018129	+	-7773
chr15	72976942	72977233	292	47	15	10.69	MPI	NM_002435	+	-7771
chr12	51584802	51585002	201	106	23	5.89	KRT8	NM_002273	-	-7765
chr12	49611842	49612563	722	183	213	5.93	METTL7A	NM_014033	+	-7763
chr11	117784931	117785072	142	62	22	7.28	ATP5L	NM_006476	+	-7759
chr15	72835730	72835994	265	169	64	5.43	CYP1A2	NM_000761	+	-7758
chr2	43900560	43900866	307	64	19	22.47	ABCG5	NM_022436	-	-7751
chr18	41925646	41925843	198	107	22	8.7	ATP5A1	NM_004046	-	-7736
chr3	185528298	185528529	232	98	25	14.72	EIF4G1	NM_004953	+	-7735
chr17	46593463	46593646	184	126	14	28.34	NME1	NM_198175	+	-7728
chr7	94879555	94879837	283	153	19	11.05	PON2	NM_000305	-	-7727
chrX	153667673	153667886	214	154	9	12.53	MPP1	NM_002436	-	-7725
chr10	27448248	27448395	148	91	6	22.88	YME1L1	NM_139313	-	-7724
chr7	149208154	149208711	558	344	59	5.45	ATP6V0E2	NM_145230	+	-7722
chr22	39503155	39503302	148	56	6	24.4	SLC25A17	NM_006358	-	-7716
chr15	88136287	88136837	551	457	106	6.79	ANPEP	NM_001150	-	-7708
chr11	65583796	65584098	303	115	17	11.92	SF3B2	NM_006842	+	-7707
chr4	185921235	185921449	215	117	26	7.87	ACSL1	NM_001995	-	-7706
chr12	7145757	7145996	240	97	15	12.3	C1RL	NM_016546	-	-7705

chr2	27170817	27171319	503	113	72	9.1	KHK	NM_000221	+	-7696
chr17	7103597	7103962	366	268	17	18.76	C17orf81	NM_203413	+	-7688
chr14	20014389	20015085	697	175	54	8.63	NP	NM_000270	+	-7681
chr22	31121034	31121244	211	82	15	8.24	C22orf28	NM_014306	-	-7676
chr1	37812536	37812676	141	88	8	10.32	GNL2	NM_013285	-	-7672
chr20	10341250	10341504	255	122	9	11.71	MKKS	NM_018848	-	-7672
chr12	68273004	68273138	135	79	10	17.79	CCT2	NM_006431	+	-7664
chr17	6952795	6953024	230	91	54	20.2	ASGR2	NM_080914	-	-7660
chr8	26668546	26669242	697	174	36	8.75	ADRA1A	NM_033303	-	-7659
chr7	94834520	94834777	258	155	18	9.07	PON3	NM_000940	-	-7656
chr16	75385	75821	437	223	28	8.23	MPG	NM_001015052	+	-7653
chr15	38492411	38492618	208	129	20	21.32	IVD	NM_002225	+	-7641
chr14	58182066	58182252	187	90	6	23.64	DACT1	NM_016651	+	-7641
chr17	15883449	15883622	174	59	7	35.46	NCOR1	NM_006311	-	-7639
chr4	37269406	37269884	479	60	23	6.01	C4orf19	NM_018302	+	-7635
chr6	30629180	30629301	122	62	6	29.28	GNL1	NM_005275	-	-7627
chr3	125939243	125939528	286	132	12	20.94	UMPS	NM_000373	+	-7626
chr2	219859157	219859901	745	653	60	10.91	DNAJB2	NM_006736	+	-7618
chr14	77001610	77001770	161	62	9	14.64	AHSA1	NM_012111	+	-7616
chr11	6415902	6416611	710	334	195	8.51	HPX	NM_000613	-	-7594
chr3	185579009	185580052	1044	851	52	5.1	THPO	NM_000460	-	-7586
chr8	27517610	27517953	344	182	114	7.03	CLU	NM_203339	-	-7585
chr11	62821600	62821798	199	93	12	19.52	SLC22A10	NM_001039752	+	-7585
chr8	145130701	145130899	199	95	11	12.81	PARP10	NM_032789	-	-7584
chr17	77636665	77637067	403	346	25	9.76	FASN	NM_004104	-	-7564
chr10	80783451	80784787	1337	381	153	5.53	PPIF	NM_005729	+	-7562

chr1	2486562	2486714	153	53	6	16.89	TNFRSF14	NM_003820	-	-7562
chr1	200250891	200251253	363	113	14	8.86	ELF3	NM_004433	+	-7558
chr19	63597841	63598001	161	77	31	12.96	RPS5	NM_001009	+	-7554
chr20	32763035	32763355	321	185	18	8.02	TP53INP2	NM_021202	+	-7547
chr11	85024728	85024855	128	57	6	18.3	TMEM126B	NM_018480	+	-7546
chr2	220079222	220079405	184	126	13	10.65	GMPPA	NM_205847	+	-7533
chr4	48589529	48589692	164	81	18	8.4	OCIAD2	NM_001014446	-	-7529
chr20	43960394	43961132	739	381	75	9.88	PPGB	NM_000308	+	-7520
chr17	16193954	16194093	140	79	6	14.64	PRR6	NM_181716	-	-7520
chr1	109043317	109044167	851	59	38	12.46	PRPF38B	NM_018061	+	-7507
chr15	78239795	78239898	104	53	8	18.89	FAH	NM_000137	+	-7503
chr1	62842809	62843269	461	241	112	5.43	ANGPTL3	NM_014495	+	-7495
chr17	39785229	39785506	278	179	31	6.33	GRN	NM_002087	+	-7490
chr11	101903377	101903938	562	398	77	5.41	MMP7	NM_002423	-	-7489
chr22	45049808	45050013	206	56	13	10.56	FLJ20699	NM_017931	+	-7489
chr4	109889839	109890136	298	156	19	6.98	AGXT2L1	NM_031279	-	-7484
chr2	20319267	20319414	148	96	7	14.64	PUM2	NM_015317	-	-7481
chr3	191513334	191513665	332	70	23	6.94	CLDN1	NM_021101	-	-7469
chr7	142795727	142795950	224	58	14	20.33	ZYX	NM_001010972	+	-7469
chr7	44128147	44128276	130	53	8	20.5	POLD2	NM_006230	-	-7465
chr9	112053403	112053585	183	124	20	16.08	TXN	NM_003329	-	-7455
chr14	104314034	104314186	153	58	9	15.68	AKT1	NM_005163	-	-7453
chr22	36391796	36392132	337	196	21	7.88	PDXP	NM_020315	+	-7450
chr14	73603814	73604065	252	60	30	6.85	ALDH6A1	NM_005589	-	-7440
chr1	11644688	11644939	252	204	13	8.78	FBXO44	NM_001014765	+	-7439
chr11	118427411	118427536	126	78	7	10.46	HYOU1	NM_006389	-	-7427

chr19	8342009	8342436	428	173	23	12.53	ANGPTL4	NM_001039667	+	-7426
chr12	176810	176938	129	72	6	19.52	SLC6A12	NM_003044	-	-7426
chr2	208816352	208816617	266	149	23	29.21	IDH1	NM_005896	-	-7419
chr16	84397761	84398110	350	177	91	5	COX4I1	NM_001861	+	-7414
chr14	57788572	57788753	182	53	11	9.33	PSMA3	NM_002788	+	-7408
chr14	102466030	102466148	119	60	11	9.58	AMN	NM_030943	+	-7402
chr9	133396254	133396413	160	99	8	16.4	UCK1	NM_031432	-	-7402
chr1	159442765	159443126	362	195	22	7.95	NDUFS2	NM_004550	+	-7398
chr21	43353483	43353761	279	177	22	9.8	CBS	NM_000071	-	-7390
chr6	90417201	90417339	139	56	9	20.5	MDN1	NM_014611	-	-7388
chr1	2486381	2486537	157	55	6	22.52	TNFRSF14	NM_003820	-	-7385
chr12	6370066	6370999	934	712	79	7.41	LTBR	NM_002342	+	-7382
chr5	125915598	125915727	130	57	9	23.43	ALDH7A1	NM_001182	-	-7380
chr1	205336238	205336625	388	297	32	11.36	C4BPB	NM_001017367	+	-7375
chr12	48789455	48791437	1983	602	298	5.04	GPD1	NM_005276	+	-7370
chr2	201433088	201433347	260	62	20	5.71	CLK1	NM_004071	-	-7370
chr12	55158223	55158354	132	58	11	8.7	GLS2	NM_013267	-	-7351
chr5	162804001	162804504	504	323	31	6.64	CCNG1	NM_004060	+	-7350
chr1	176171950	176172213	264	168	11	20.92	LZTR2	NM_033127	-	-7349
chr6	7833910	7834099	190	130	9	30.14	TXNDC5	NM_030810	-	-7347
chr8	6722725	6722853	129	63	22	6.3	DEFB1	NM_005218	-	-7343
chr20	56907347	56907505	159	78	8	13.97	GNAS	NM_001077488	+	-7342
chr19	6319533	6319789	257	86	18	6.58	CLPP	NM_006012	+	-7327
chr9	115195524	115195737	214	157	21	10.97	ALAD	NM_001003945	-	-7324
chr7	98851696	98851863	168	51	13	7.38	BUD31	NM_003910	+	-7316
chr2	232034491	232035012	522	98	42	7.05	NCL	NM_005381	-	-7309

chr3	15584346	15584547	202	83	9	12.55	HACL1	NM_012260	-	-7302
chr19	43991210	43991448	239	97	16	6.12	LGALS4	NM_006149	-	-7294
chr19	44131041	44131173	133	60	6	22.88	FBXO17	NM_148169	-	-7292
chr9	113372172	113372354	183	74	33	6.97	LTB4DH	NM_012212	-	-7281
chr12	6710421	6710757	337	234	15	7.99	COPS7A	NM_016319	+	-7276
chr5	42842708	42843012	305	88	99	5.25	SEPP1	NM_005410	-	-7273
chr17	71272626	71272876	251	191	22	6.3	GALK1	NM_000154	-	-7264
chr21	34817678	34817918	241	61	27	5.54	DSCR1	NM_203418	-	-7263
chr7	1166137	1166329	193	87	13	28.26	ZFAND2A	NM_182491	-	-7260
chr7	65070062	65070356	295	144	18	11.88	GUSB	NM_000181	-	-7247
chr5	176966893	176967024	132	74	6	19.26	B4GALT7	NM_007255	+	-7247
chr10	11831480	11831634	155	95	16	7.38	ECHDC3	NM_024693	+	-7246
chr8	145130298	145130553	256	120	11	11.24	PARP10	NM_032789	-	-7238
chr15	22758330	22758461	132	76	11	19.33	SNURF	NM_022804	+	-7234
chr11	60421901	60422004	104	53	8	12.18	PRPF19	NM_014502	-	-7222
chr12	9118401	9118791	391	83	88	5.72	A2M	NM_000014	-	-7221
chr7	141091746	141091862	117	59	9	15.42	SSBP1	NM_003143	+	-7218
chr12	54684062	54684523	462	325	28	7.32	SUOX	NM_000456	+	-7214
chr3	142946697	142946953	257	138	16	11.29	RNF7	NM_183237	+	-7213
chr20	32762337	32763015	679	480	41	10.03	TP53INP2	NM_021202	+	-7207
chr19	50669540	50670297	758	573	42	7.68	FOSB	NM_006732	+	-7205
chr12	7045184	7045479	296	91	92	5.87	C1S	NM_001734	+	-7198
chr19	55079727	55079831	105	53	8	29.28	TBC1D17	NM_024682	+	-7191
chr19	53584631	53584825	195	70	18	31.41	KDELRL1	NM_006801	-	-7187
chr4	89122647	89123009	363	162	18	9.3	SPP1	NM_001040058	+	-7184
chr17	45917435	45918370	936	819	52	5.22	RSAD1	NM_018346	+	-7182

chr22	35014224	35014446	223	123	28	10.45	MYH9	NM_002473	-	-7175
chr3	185527640	185527966	327	154	37	5.59	EIF4G1	NM_004953	+	-7172
chr9	37419681	37419874	194	109	33	6.53	GRHPR	NM_012203	+	-7168
chr12	51986706	51986914	209	58	10	9.15	C12orf10	NM_021640	+	-7166
chr19	530499	530699	201	59	20	5.4	BSG	NM_001728	+	-7163
chr1	26993856	26994229	374	206	16	11.39	PIGV	NM_017837	+	-7157
chr7	149207534	149208141	608	164	43	6.28	ATP6V0E2	NM_145230	+	-7152
chr17	69947998	69948573	576	487	42	6.49	GPRC5C	NM_018653	+	-7143
chr7	142795357	142795620	264	159	10	15.15	ZYX	NM_001010972	+	-7139
chr4	37268970	37269383	414	295	18	8.78	C4orf19	NM_018302	+	-7134
chr1	115068010	115068188	179	52	15	15.21	CSDE1	NM_001007553	-	-7128
chr11	56991782	56992041	260	160	12	9.52	RTN4RL2	NM_178570	+	-7127
chr4	9692068	9692186	119	60	8	19.52	WDR1	NM_005112	-	-7126
chr17	17356526	17356728	203	89	17	6.69	PEMT	NM_148173	-	-7125
chr10	17318270	17318427	158	87	32	6.94	VIM	NM_003380	+	-7124
chr22	22952611	22952754	144	83	10	14.76	GGTLA1	NM_004121	-	-7116
chr1	1317598	1318067	470	137	27	8.26	CCNL2	NM_001039577	-	-7113
chr1	19280406	19280698	293	111	20	11.44	ZUBR1	NM_020765	-	-7110
chr7	102732031	102732211	181	121	10	25.62	PMPCB	NM_004279	+	-7103
chr1	178125047	178125144	98	50	6	29.28	TOR1AIP1	NM_015602	+	-7102
chr1	1149057	1149250	194	96	18	12.31	SDF4	NM_016176	-	-7099
chr1	158458976	158459211	236	178	12	10.98	WDR42A	NM_015726	-	-7083
chr20	1054141	1054325	185	100	14	9.03	PSMF1	NM_178579	+	-7081
chr1	29353808	29354027	220	160	10	16.11	SFRS4	NM_005626	-	-7076
chr6	160138291	160138562	272	125	20	5.31	MRPL18	NM_014161	+	-7075
chr19	11414200	11414342	143	60	22	7.54	PRKCSH	NM_001001329	+	-7074

chr1	184554196	184554480	285	139	13	12.52	TPR	NM_003292	-	-7070
chr11	70829917	70830177	261	164	26	10.7	DHCR7	NM_001360	-	-7067
chr19	43808484	43808624	141	62	13	7.57	EIF3S12	NM_013234	+	-7063
chr11	6588207	6588840	634	548	52	8.62	ILK	NM_001014795	+	-7058
chr19	9832327	9832450	124	63	6	14.94	OLFM2	NM_058164	-	-7056
chr15	73442026	73442232	207	105	7	10.21	MAN2C1	NM_006715	-	-7046
chr6	43096379	43096993	615	168	48	6	KLHDC3	NM_057161	+	-7039
chr11	65583287	65583428	142	56	11	17.34	SF3B2	NM_006842	+	-7037
chr22	23228074	23228283	210	75	19	10.45	UPB1	NM_016327	+	-7033
chr17	21142277	21142405	129	85	6	17.85	MAP2K3	NM_002756	+	-7032
chr7	1099672	1099993	322	213	15	6.66	GPR30	NM_001039966	+	-7025
chr19	63515402	63515577	176	132	6	17.57	LOC113386	NM_138781	+	-7023
chr12	54917180	54917911	732	650	107	9.29	SLC39A5	NM_173596	+	-7018
chr4	185920535	185920755	221	79	36	7.77	ACSL1	NM_001995	-	-7012
chr2	27579876	27580219	344	53	17	10.07	GCKR	NM_001486	+	-7010
chr5	180603229	180603541	313	133	77	7.33	GNB2L1	NM_006098	-	-7008
chr13	20619318	20619690	373	73	25	6.24	SAP18	NM_005870	+	-7006
chr5	176768629	176768751	123	62	13	15.23	F12	NM_000505	-	-7005
chr17	4848869	4849003	135	61	7	14.64	KIF1C	NM_006612	+	-7004
chr7	54794264	54794427	164	109	8	23.29	SEC61G	NM_001012456	-	-6993
chr2	241823559	241823797	239	59	28	7.39	HDLBP	NM_203346	-	-6981
chr6	32904365	32904563	199	142	8	14.57	TAP2	NM_018833	-	-6976
chr14	104251853	104252187	335	182	18	10.98	C14orf173	NM_022489	+	-6975
chr19	55053095	55053201	107	54	8	20.92	PTOV1	NM_017432	+	-6974
chr14	89939941	89940097	157	102	11	9.19	CALM1	NM_006888	+	-6972
chrX	99777210	99777422	213	62	19	10.4	TSPAN6	NM_003270	-	-6972

chr9	96411915	96412207	293	208	68	5	FBP1	NM_000507	-	-6970
chr5	179065290	179065504	215	62	14	14.17	CANX	NM_001024649	+	-6969
chr17	38312977	38313308	332	153	33	8.26	G6PC	NM_000151	+	-6968
chr2	9538867	9539086	220	109	12	9.66	LOC285148	NM_001039613	+	-6966
chr1	159472852	159473046	195	136	18	10.47	NR1I3	NM_001077478	-	-6965
chr10	120923997	120924170	174	61	9	20.19	PRDX3	NM_006793	-	-6965
chr1	153373209	153373934	726	431	92	10.12	EFNA1	NM_004428	+	-6962
chr19	2279284	2279483	200	144	12	56.31	LSM7	NM_016199	-	-6962
chr19	46048045	46048242	198	83	51	5.27	CYP2A6	NM_000762	-	-6959
chr2	234340310	234340595	286	214	52	5.41	UGT1A1	NM_000463	+	-6938
chr6	32009900	32010403	504	89	49	7.04	C2	NM_000063	+	-6931
chr19	10064015	10064929	915	658	80	6.95	FLJ11286	NM_018381	+	-6921
chr15	78239130	78239315	186	86	29	10.89	FAH	NM_000137	+	-6920
chr11	45790119	45790827	709	270	45	5.54	SLC35C1	NM_018389	+	-6916
chr14	94104194	94104447	254	152	52	6.56	SERPINA4	NM_006215	+	-6912
chr6	139274119	139274220	102	52	6	29.28	REPS1	NM_031922	-	-6907
chr1	218994852	218995194	343	180	21	8.37	MOSC2	NM_017898	+	-6896
chr16	65532511	65532720	210	61	29	8.84	CES2	NM_003869	+	-6873
chr22	37467403	37467552	150	94	10	22.1	UNC84B	NM_015374	-	-6872
chr1	224621806	224621998	193	90	9	30.14	PARP1	NM_001618	-	-6870
chr9	133395683	133395872	190	120	8	13.91	UCK1	NM_031432	-	-6861
chrX	153316851	153317029	179	62	10	10.46	ATP6AP1	NM_001183	+	-6858
chr11	57015254	57015440	187	130	17	8.21	SLC43A1	NM_003627	-	-6857
chr19	40989172	40989582	411	61	40	11.28	PRODH2	NM_021232	-	-6851
chr1	62842205	62842624	420	191	97	5.15	ANGPTL3	NM_014495	+	-6850
chr19	55052949	55053072	124	60	9	14.52	PTOV1	NM_017432	+	-6845

chr5	178980452	178980629	178	124	11	11.71	HNRPH1	NM_005520	-	-6844
chr9	136918811	136919320	510	85	29	6.72	FCN2	NM_004108	+	-6842
chr9	115900431	115900580	150	89	6	20.33	KIF12	NM_138424	-	-6841
chr17	77635656	77636335	680	159	62	11.31	FASN	NM_004104	-	-6832
chr2	17715174	17715367	194	107	8	17.04	SMC6	NM_024624	-	-6806
chr12	49610776	49611602	827	264	108	9.78	METTL7A	NM_014033	+	-6802
chr16	30001563	30001686	124	62	8	17.67	PPP4C	NM_002720	+	-6802
chr10	101153195	101153416	222	109	37	8.36	GOT1	NM_002079	-	-6799
chr20	34673831	34674372	542	138	53	7.94	C20orf24	NM_018840	+	-6792
chr15	88434696	88435008	313	143	24	10.69	IDH2	NM_002168	-	-6791
chr16	88287185	88287368	184	40	8	16.27	CDK10	NM_003674	+	-6790
chr10	135197117	135197645	529	195	189	6.98	CYP2E1	NM_000773	+	-6789
chr3	9806384	9806601	218	60	11	11.17	TADA3L	NM_133480	-	-6789
chr21	45100435	45100727	293	233	22	18.59	PTTG1IP	NM_004339	-	-6787
chr19	46079800	46079950	151	105	7	29.28	CYP2A7	NM_000764	-	-6766
chr2	201432635	201432740	106	54	11	15.49	CLK1	NM_004071	-	-6763
chr7	6591160	6591427	268	208	19	9.81	ZDHHC4	NM_018106	+	-6761
chr14	73603147	73603384	238	158	28	6.97	ALDH6A1	NM_005589	-	-6759
chr7	100563594	100563928	335	252	30	12.26	SERPINE1	NM_000602	+	-6757
chr10	75228763	75229251	489	410	25	14.32	KIAA0913	NM_015037	+	-6757
chr12	6710074	6710233	160	111	7	17.43	COPS7A	NM_016319	+	-6752
chr14	38719985	38720895	911	766	66	5.56	PNN	NM_002687	+	-6745
chr14	23660390	23660603	214	97	22	7.52	WDR23	NM_025230	+	-6743
chr17	43380305	43380654	350	205	34	5.91	PNPO	NM_018129	+	-6739
chr19	19242809	19242911	103	52	6	23.12	TM6SF2	NM_001001524	-	-6738
chr12	107486717	107487244	528	85	35	5.8	ISCU	NM_213595	+	-6733

chr9	139602914	139603076	163	55	6	29.55	ZMYND19	NM_138462	-	-6725
chr5	162803234	162803878	645	573	32	6.03	CCNG1	NM_004060	+	-6724
chr19	18510006	18510290	285	159	21	7.65	FKBP8	NM_012181	-	-6723
chr3	38145763	38145926	164	81	28	6.52	ACAA1	NM_001607	-	-6716
chr5	115174661	115175042	382	211	34	11.88	CDO1	NM_001801	-	-6712
chr10	69768249	69768577	329	61	19	12.85	HNRPH3	NM_012207	+	-6693
chr4	88450401	88450653	253	118	30	9.26	HSD17B13	NM_178135	-	-6689
chr5	177570128	177570801	674	126	44	6.58	HNRPAB	NM_004499	+	-6688
chr8	11743909	11744123	215	155	36	6.93	CTSB	NM_001908	-	-6679
chr1	210854887	210855292	406	271	24	8.49	ATF3	NM_004024	+	-6676
chr1	239733948	239734195	248	103	28	14.52	FH	NM_000143	-	-6668
chr16	30958739	30959067	329	171	16	14.64	STX4	NM_004604	+	-6664
chr8	87560234	87560355	122	62	7	39.42	FAM82B	NM_016033	-	-6661
chr1	26025703	26025925	223	60	10	14.64	FAM54B	NM_019557	+	-6655
chr9	35052970	35053213	244	85	12	12.46	VCP	NM_007126	-	-6653
chr2	119911169	119912562	1394	118	101	5.74	TMEM37	NM_183240	+	-6647
chr2	241823195	241823455	261	73	26	8.12	HDLBP	NM_203346	-	-6639
chr16	638074	638487	414	183	31	6.67	C16orf14	NM_138418	+	-6638
chr20	33683837	33684019	183	134	8	12.2	CPNE1	NM_003915	-	-6638
chr12	45044432	45044875	444	133	32	9.39	SLC38A2	NM_018976	-	-6637
chr20	33599607	33599826	220	146	18	13.96	ERGIC3	NM_015966	+	-6635
chr8	19725682	19725828	147	62	7	17.57	INTS10	NM_018142	+	-6631
chr19	16162804	16163862	1059	1000	80	7.75	FAM32A	NM_014077	+	-6628
chr1	109975621	109976198	578	285	37	8.46	AMPD2	NM_203404	+	-6627
chr14	94123420	94124187	768	580	145	5.41	SERPINA5	NM_000624	+	-6624
chr5	6431523	6431662	140	55	7	24.4	MED10	NM_032286	-	-6623

chr2	27452875	27453510	636	147	42	7.16	SNX17	NM_014748	+	-6618
chr2	241463175	241463451	277	80	96	6.89	AGXT	NM_000030	+	-6617
chr2	197971329	197971559	231	154	17	10.15	SF3B1	NM_012433	-	-6615
chr4	39183244	39183385	142	51	6	18.3	UGDH	NM_003359	-	-6615
chr9	33248913	33249084	172	101	9	17.63	BAG1	NM_004323	-	-6613
chr15	72834074	72834831	758	363	148	5.55	CYP1A2	NM_000761	+	-6595
chr6	160029124	160029338	215	77	22	6.3	SOD2	NM_000636	-	-6594
chr11	62363384	62363552	169	62	6	24.4	WDR74	NM_018093	-	-6593
chr14	20561223	20561351	129	60	13	7.55	NDRG2	NM_201538	-	-6589
chr1	166160342	166160523	182	39	7	20.43	BRP44	NM_015415	-	-6589
chr10	135032401	135032556	156	77	51	5.58	ECHS1	NM_004092	-	-6577
chr11	204636	205096	461	372	33	7.36	RIC8A	NM_021932	+	-6567
chr14	102668832	102668983	152	56	11	15.58	TNFAIP2	NM_006291	+	-6567
chr11	71397967	71398124	158	102	7	12.46	NUMA1	NM_006185	-	-6566
chr19	60863690	60863793	104	53	6	21.96	U2AF2	NM_001012478	+	-6566
chr7	100590520	100591049	530	82	21	5.17	AP1S1	NM_057089	+	-6563
chr17	37525080	37525215	136	43	6	15.41	GCN5L2	NM_021078	-	-6559
chr4	157050621	157050852	232	64	48	6.19	TDO2	NM_005651	+	-6556
chr2	63676014	63676177	164	114	9	16.81	MDH1	NM_005917	+	-6552
chr12	97517841	97518084	244	142	30	5.36	SLC25A3	NM_002635	+	-6551
chr1	195219701	195219881	181	140	8	13.25	CFHR5	NM_030787	+	-6551
chr8	26667884	26668130	247	115	19	8.24	ADRA1A	NM_033303	-	-6547
chr11	66123431	66123812	382	165	25	20.51	CCS	NM_005125	+	-6547
chr7	100062298	100062504	207	69	63	5.05	TFR2	NM_003227	-	-6529
chrX	153331920	153332228	309	195	14	10.98	FAM50A	NM_004699	+	-6527
chr9	138431306	138431456	151	90	7	22.88	PMPCA	NM_015160	+	-6520

chr1	167756252	167756549	298	167	23	8.73	F5	NM_000130	-	-6517
chr17	64592746	64592955	210	152	19	6.15	ABCA6	NM_080284	-	-6514
chr2	113606606	113608122	1517	1223	159	7.84	IL1RN	NM_173842	+	-6514
chr15	88615989	88616410	422	257	26	10.14	NGRN	NM_001033088	+	-6512
chr7	100653930	100654210	281	157	68	5.63	ZNHIT1	NM_006349	+	-6506
chr6	43011305	43011426	122	62	8	22.52	TNRC5	NM_183010	+	-6506
chr12	112320693	112321139	447	69	44	8.56	SDS	NM_006843	-	-6504
chrX	99776823	99776944	122	62	9	16.08	TSPAN6	NM_003270	-	-6494
chr1	24007195	24007445	251	161	33	8.92	HMGCL	NM_000191	-	-6491
chr9	127043098	127043437	340	177	33	7.82	HSPA5	NM_005347	-	-6483
chr11	67013346	67013570	225	83	11	19.71	AIP	NM_003977	+	-6474
chr11	2113152	2113391	240	151	29	8.03	IGF2	NM_000612	-	-6468
chr4	77060054	77060298	245	104	8	13.62	ASAH1	NM_014435	-	-6465
chr8	99190037	99190200	164	69	26	6.86	HRSP12	NM_005836	-	-6458
chrX	138446709	138447017	309	250	28	27.14	F9	NM_000133	+	-6457
chr5	137925182	137925368	187	65	14	9.13	HSPA9	NM_004134	-	-6445
chr1	15777945	15778177	233	84	21	5.69	AGMAT	NM_024758	-	-6439
chr22	18335956	18336507	552	279	118	5.77	COMT	NM_007310	+	-6438
chr16	3654310	3654474	165	88	10	17.22	TRAP1	NM_016292	-	-6435
chr2	188057673	188057984	312	209	18	6.4	TFPI	NM_001032281	-	-6433
chr3	52810022	52810274	253	67	49	5.32	ITIH3	NM_002217	+	-6421
chr3	185381308	185381740	433	363	33	7.49	AP2M1	NM_001025205	+	-6413
chrX	19469986	19470163	178	76	6	17.73	SH3KBP1	NM_001024666	-	-6413
chr13	46249572	46249803	232	141	31	6.37	ESD	NM_001984	-	-6411
chr19	3933220	3933457	238	80	57	6.5	EEF2	NM_001961	-	-6403
chr15	62241249	62241469	221	101	36	11.09	PIIB	NM_000942	-	-6402

chr10	96792477	96792919	443	279	149	5.11	CYP2C8	NM_000770	-	-6400
chr16	84396823	84397093	271	113	35	6.52	COX4I1	NM_001861	+	-6397
chr1	158458262	158458525	264	155	11	11.26	WDR42A	NM_015726	-	-6397
chr1	23586331	23586538	208	140	20	11.42	TCEA3	NM_003196	-	-6397
chr1	85563009	85563145	137	45	6	17.22	DDAH1	NM_012137	-	-6389
chr11	1736754	1736934	181	120	43	5.3	CTSD	NM_001909	-	-6374
chr3	172203035	172203203	169	96	20	9.28	SLC2A2	NM_000340	-	-6373
chr19	7740027	7740446	420	281	25	11.27	CLEC4M	NM_214677	+	-6366
chr12	48438712	48438864	153	60	27	6.16	TEGT	NM_003217	+	-6353
chr6	32009360	32009814	455	140	62	7.93	C2	NM_000063	+	-6342
chr1	159472181	159472423	243	124	22	9.25	NR1I3	NM_001077478	-	-6342
chr3	52826984	52828383	1400	205	269	10.2	ITIH4	NM_002218	-	-6337
chr16	23505908	23506174	267	177	19	15.64	NDUFAB1	NM_005003	-	-6336
chr1	202372838	202373149	312	145	20	20.56	ETNK2	NM_018208	-	-6336
chr1	35847408	35847661	254	147	23	8.93	PSMB2	NM_002794	-	-6335
chr17	1598619	1599213	595	90	113	9.47	SERPINF2	NM_000934	+	-6334
chr3	140551718	140551884	167	62	8	17.12	MRPS22	NM_020191	+	-6334
chr19	41328718	41329087	370	57	29	10.83	CAPNS1	NM_001003962	+	-6330
chr8	146083477	146083663	187	128	6	23.64	ZNF250	NM_021061	-	-6324
chr4	3419639	3419841	203	115	37	6.27	HGFAC	NM_001528	+	-6318
chr11	814518	815214	697	579	63	5.91	PNPLA2	NM_020376	+	-6313
chr5	177574338	177574502	165	112	7	14.08	AGXT2L2	NM_153373	-	-6306
chr10	54201226	54201449	224	136	14	9.84	MBL2	NM_000242	-	-6303
chrX	53582523	53582777	255	155	11	23.61	HUWE1	NM_031407	-	-6301
chr6	44328763	44329125	363	59	33	5.8	HSP90AB1	NM_007355	+	-6299
chr2	218978237	218979017	781	318	79	5.9	CTDSP1	NM_021198	+	-6296

chr14	23777639	23778236	598	59	37	14.01	GMPR2	NM_016576	+	-6294
chrX	153324655	153325005	351	243	25	11.31	GDI1	NM_001493	+	-6291
chr17	71271573	71271899	327	157	24	11.17	GALK1	NM_000154	-	-6287
chr3	187990161	187990340	180	124	11	10.54	EIF4A2	NM_001967	+	-6286
chr11	10781311	10781454	144	83	12	9.49	EIF4G2	NM_001418	-	-6285
chr6	30682227	30682440	214	126	11	15.41	PPP1R10	NM_002714	-	-6279
chr2	238546450	238546713	264	128	8	29.55	UBE2F	NM_080678	+	-6275
chrX	46828749	46828986	238	115	31	6.53	RGN	NM_004683	+	-6268
chr17	6534804	6535027	224	84	27	8.2	SLC13A5	NM_177550	-	-6263
chr19	17489505	17489681	177	62	11	11.66	PGLS	NM_012088	+	-6250
chr4	83569403	83569620	218	61	16	20.75	HNRPDL	NM_031372	-	-6250
chr15	88135137	88135376	240	161	46	5.39	ANPEP	NM_001150	-	-6247
chrX	40398563	40398748	186	128	8	14.64	CRSP2	NM_004229	-	-6247
chr12	55637146	55637726	581	107	95	5.67	RDH16	NM_003708	-	-6241
chr16	29886823	29887121	299	91	45	11.67	LOC124446	NM_194280	+	-6237
chr4	89872182	89872361	180	57	12	18.45	FAM13A1	NM_001015045	-	-6233
chr2	150140455	150140628	174	114	8	10.19	C2orf25	NM_015702	-	-6231
chr4	74572290	74572537	248	89	21	18.02	AFM	NM_001133	+	-6212
chr2	232033646	232033909	264	62	27	8.83	NCL	NM_005381	-	-6206
chr10	17317158	17317507	350	189	74	5.12	VIM	NM_003380	+	-6204
chr2	242406460	242406940	481	96	30	5.76	NEU4	NM_080741	+	-6195
chr17	18094851	18095063	213	56	9	18.71	FLII	NM_002018	-	-6184
chr5	151027216	151027389	174	77	16	14.08	SPARC	NM_003118	-	-6183
chr10	3817086	3817422	337	141	17	8.63	KLF6	NM_001300	-	-6182
chr17	2545401	2545610	210	93	15	10.98	KIAA0664	NM_015229	-	-6181
chr12	6369517	6369797	281	228	14	8.93	LTBR	NM_002342	+	-6180

chr19	4110645	4110808	164	104	8	12.01	CREB3L3	NM_032607	+	-6180
chr7	65184149	65184446	298	190	26	8.18	ASL	NM_001024943	+	-6178
chr2	96301594	96301788	195	47	9	13.56	WDR39	NM_004804	+	-6178
chr20	24897530	24897757	228	148	25	7.79	C20orf3	NM_020531	-	-6177
chr12	48438253	48438684	432	226	55	10.96	TEGT	NM_003217	+	-6173
chr7	100653650	100653876	227	68	32	6.66	ZNHIT1	NM_006349	+	-6172
chr17	38184513	38185151	639	543	33	7.48	VPS25	NM_032353	+	-6172
chr2	197970951	197971116	166	95	19	8.91	SF3B1	NM_012433	-	-6172
chr16	18707743	18707946	204	161	13	16.43	RPS15A	NM_001019	-	-6168
chr12	108502013	108502166	154	60	7	24.4	MVK	NM_000431	+	-6167
chr11	490372	490675	304	247	19	10.01	RNH1	NM_002939	-	-6164
chr2	215993624	215993792	169	62	22	5.66	FN1	NM_054034	-	-6163
chr2	38830083	38830406	324	151	24	10.44	SFRS7	NM_001031684	-	-6158
chr6	43379532	43380131	600	318	67	8.5	SLC22A7	NM_006672	+	-6156
chr12	50737009	50737606	598	509	53	7.59	NR4A1	NM_002135	+	-6149
chr17	1506677	1506822	146	85	10	20.5	PRPF8	NM_006445	-	-6149
chr17	77534713	77534863	151	59	11	53.19	ASPSCR1	NM_024083	+	-6149
chr5	52817693	52818498	806	514	105	5.72	FST	NM_006350	+	-6147
chr17	6951022	6951510	489	82	104	6.8	ASGR2	NM_080914	-	-6146
chr12	112085387	112085505	119	60	7	30.14	DDX54	NM_024072	-	-6137
chr19	38562368	38562584	217	92	17	8.47	CEBPG	NM_001806	+	-6136
chr19	50668722	50669226	505	59	29	7.39	FOSB	NM_006732	+	-6134
chr3	185586502	185586684	183	103	11	10.72	CHRD	NM_003741	+	-6130
chr11	10781111	10781296	186	95	18	14.28	EIF4G2	NM_001418	-	-6127
chr11	65582368	65582515	148	54	8	14.64	SF3B2	NM_006842	+	-6124
chr19	52979341	52979768	428	174	32	5.22	SEPW1	NM_003009	+	-6115

chr11	62154647	62154989	343	163	26	6.7	GANAB	NM_198334	-	-6111
chr3	129827394	129827611	218	73	31	7.75	RPN1	NM_002950	-	-6109
chr11	6414821	6415124	304	114	142	5.23	HPX	NM_000613	-	-6107
chr19	63753313	63753746	434	86	30	5.72	TRIM28	NM_005762	+	-6099
chr18	53424839	53424991	153	58	6	23.64	NARS	NM_004539	-	-6098
chr11	14489001	14489096	96	49	7	34.16	PSMA1	NM_002786	-	-6098
chr9	127042781	127043043	263	164	24	7.7	HSPA5	NM_005347	-	-6089
chr20	17876145	17876321	177	125	8	9.76	SNX5	NM_014426	-	-6076
chr4	3419301	3419598	298	166	30	8.24	HGFAC	NM_001528	+	-6075
chr14	23639034	23639393	360	183	56	6.15	PCK2	NM_001018073	+	-6071
chr22	34112691	34113147	457	327	20	11.71	HMOX1	NM_002133	+	-6061
chr22	27526282	27526591	310	62	37	5.94	XBP1	NM_005080	-	-6043
chr16	73049265	73049399	135	75	6	18.3	GLG1	NM_012201	-	-6043
chr5	130528666	130528924	259	119	41	5.48	HINT1	NM_005340	-	-6042
chr3	121803671	121803846	176	130	11	12.88	NDUFB4	NM_004547	+	-6029
chr14	23835554	23835672	119	60	15	13.73	DHRS1	NM_138452	-	-6027
chr11	60863102	60863251	150	57	12	9.88	DAK	NM_015533	+	-6022
chr11	67560484	67560700	217	84	28	5.3	NDUFS8	NM_002496	+	-6016
chr10	69767571	69767891	321	130	13	6.27	HNRPH3	NM_012207	+	-6007
chr12	7044014	7044285	272	136	83	5.11	C1S	NM_001734	+	-6004
chr17	4800829	4801162	334	245	35	6.39	ENO3	NM_001976	+	-6004
chr9	135223954	135224160	207	62	20	9.09	SURF4	NM_033161	-	-5999
chr17	7023104	7023470	367	194	52	8.24	ASGR1	NM_001671	-	-5994
chr2	101264771	101264970	200	142	11	10.25	RNF149	NM_173647	-	-5986
chr17	1506449	1506659	211	60	15	21.3	PRPF8	NM_006445	-	-5986
chr2	85625643	85625780	138	53	11	15.41	MAT2A	NM_005911	+	-5982

chr17	24100459	24101148	690	269	39	7.32	TRAF4	NM_004295	+	-5976
chr16	70605885	70606102	218	91	11	21.35	DHODH	NM_001025193	+	-5959
chr3	150378826	150379176	351	145	56	6.48	CP	NM_000096	-	-5953
chr1	89296381	89296545	165	82	9	14.49	GBP1	NM_002053	-	-5952
chr22	35242674	35242792	119	60	8	19.52	EIF3S7	NM_003753	-	-5949
chr12	54916436	54916837	402	59	51	7.15	SLC39A5	NM_173596	+	-5944
chr14	93652512	93652772	261	128	31	5.25	IFI27	NM_005532	+	-5941
chr2	232033428	232033644	217	74	17	14.83	NCL	NM_005381	-	-5941
chr19	11413003	11413209	207	130	16	15.15	PRKCSH	NM_001001329	+	-5941
chr9	130902608	130902830	223	132	22	7.84	CRAT	NM_004003	-	-5935
chr2	208814878	208815128	251	193	33	6.43	IDH1	NM_005896	-	-5930
chr3	52212848	52213111	264	135	38	8.12	ALAS1	NM_000688	+	-5928
chr14	99864804	99865356	553	71	87	8.1	C14orf68	NM_207117	+	-5925
chr19	5543764	5543928	165	77	9	20.92	SAFB2	NM_014649	-	-5918
chr3	52809570	52809767	198	114	44	8.12	ITIH3	NM_002217	+	-5914
chr22	36291998	36292353	356	113	24	7.45	CDC42EP1	NM_007061	+	-5907
chr11	116160314	116160391	78	40	6	25.84	ZNF259	NM_003904	-	-5905
chr3	187989174	187989957	784	728	76	7.49	EIF4A2	NM_001967	+	-5903
chr11	828109	828852	744	575	92	5.27	CD151	NM_001039490	+	-5901
chr2	204012416	204012685	270	62	19	11.26	RAPH1	NM_213589	-	-5900
chr21	37924388	37924556	169	116	6	29.55	KCNJ6	NM_002240	-	-5900
chr15	88014201	88014497	297	169	13	15.22	PLIN	NM_002666	-	-5895
chr12	9198471	9198597	127	58	8	14.64	PZP	NM_002864	-	-5894
chr18	41923771	41924000	230	102	20	11.79	ATP5A1	NM_004046	-	-5893
chr20	60317085	60317313	229	121	21	5.59	ADRM1	NM_007002	+	-5892
chr1	1316339	1316845	507	61	40	11.56	CCNL2	NM_001039577	-	-5891

chr3	9986394	9986524	131	52	7	14.64	TMEM111	NM_018447	-	-5888
chr16	20461756	20461856	101	51	9	13.31	ACSM2	NM_182617	-	-5887
chr12	112085106	112085252	147	62	7	21.53	DDX54	NM_024072	-	-5884
chr3	47435845	47436064	220	58	11	12.88	SCAP	NM_012235	-	-5877
chr19	41328525	41328632	108	55	8	12.65	CAPNS1	NM_001003962	+	-5875
chr16	70163912	70164124	213	129	31	8.32	TAT	NM_000353	-	-5870
chr17	45571804	45571963	160	58	9	31.37	PPP1R9B	NM_032595	-	-5865
chrX	47401846	47402003	158	106	11	10.65	UXT	NM_153477	-	-5864
chr17	77634919	77635358	440	85	32	5.07	FASN	NM_004104	-	-5855
chr4	110886715	110887152	438	191	117	5.46	CFI	NM_000204	-	-5852
chr15	70428534	70428683	150	100	7	19.52	HEXA	NM_000520	-	-5851
chr7	150133603	150134630	1028	813	175	6.35	TMEM176A	NM_018487	+	-5844
chr18	3243213	3243369	157	62	16	11.49	MRCL3	NM_006471	+	-5842
chr16	30873302	30873755	454	78	32	11.39	TMEM142C	NM_152288	+	-5840
chr5	35039638	35039801	164	54	8	16.81	AGXT2	NM_031900	-	-5839
chr14	94103038	94103373	336	174	76	5.12	SERPINA4	NM_006215	+	-5838
chr12	55323874	55324061	188	58	25	8.26	ATP5B	NM_001686	-	-5836
chr1	28533786	28533967	182	123	6	23.64	MED18	NM_017638	+	-5832
chr11	32567614	32567793	180	125	9	18.45	PCID1	NM_006360	+	-5827
chr19	38561881	38562274	394	150	22	9.76	CEBPG	NM_001806	+	-5826
chr11	64657001	64657152	152	98	8	14.04	SYVN1	NM_032431	-	-5824
chr5	176696721	176697165	445	99	51	7.38	LMAN2	NM_006816	-	-5809
chr15	26035404	26035593	190	100	8	11.13	HERC2	NM_004667	-	-5809
chr21	34203234	34203425	192	96	24	8.43	ATP5O	NM_001697	-	-5798
chr22	36685276	36685457	182	90	19	6.4	POLR2F	NM_021974	+	-5794
chr11	117638376	117638631	256	152	11	17.57	EVA1	NM_144765	-	-5792

chr3	52791938	52792423	486	181	174	5.36	ITIH1	NM_002215	+	-5776
chr3	144025045	144025177	133	74	7	24.4	PCOLCE2	NM_013363	-	-5776
chr14	20560383	20560527	145	62	22	10.08	NDRG2	NM_201538	-	-5765
chr3	48874885	48875132	248	155	18	14.52	SLC25A20	NM_000387	-	-5764
chr7	100043487	100043687	201	99	20	8.83	PCOLCE	NM_002593	+	-5762
chr16	397414	397618	205	138	11	24.4	DECR2	NM_020664	+	-5760
chr4	184668695	184668962	268	148	12	21.96	ING2	NM_001564	+	-5749
chr16	663666	663881	216	58	10	14.64	RHOT2	NM_138769	+	-5748
chr20	41524910	41525664	755	655	57	6.03	SFRS6	NM_006275	+	-5733
chr17	61643345	61644346	1002	85	319	8.09	APOH	NM_000042	-	-5733
chr6	138459180	138459346	167	50	12	8.56	PERP	NM_022121	-	-5728
chr2	38829569	38829975	407	311	23	9.01	SFRS7	NM_001031684	-	-5727
chr5	157151270	157151598	329	122	17	14.45	CLINT1	NM_014666	-	-5724
chr11	67136397	67136700	304	149	28	8.9	NDUFV1	NM_007103	+	-5718
chr2	241162349	241162488	140	59	7	15.97	RNPEPL1	NM_018226	+	-5712
chr3	51997806	51998306	501	295	112	6.54	ACY1	NM_000666	+	-5704
chr16	8900406	8900554	149	73	6	22.52	USP7	NM_003470	-	-5704
chr8	30768237	30768370	134	88	8	10.98	PPP2CB	NM_001009552	-	-5702
chr3	52301282	52302612	1331	1157	265	6.14	GLYCTK	NM_145262	+	-5701
chr22	37466198	37466377	180	62	13	12.2	UNC84B	NM_015374	-	-5697
chr16	637415	637543	129	52	8	11.39	C16orf14	NM_138418	+	-5694
chr11	45893869	45893992	124	55	7	15.69	PEX16	NM_004813	-	-5692
chr15	88134667	88134816	150	73	29	6.1	ANPEP	NM_001150	-	-5687
chr20	60207158	60207323	166	61	7	22.88	GTPBP5	NM_015666	+	-5676
chr4	3418992	3419188	197	107	39	5.99	HGFAC	NM_001528	+	-5665
chr12	68033943	68034091	149	99	7	29.55	LYZ	NM_000239	+	-5661

chr4	155748782	155750837	2056	348	660	7.33	FGG	NM_021870	-	-5659
chr4	39234436	39234603	168	62	11	8.61	C4orf34	NM_174921	-	-5659
chr6	32025783	32027405	1623	1187	652	5.18	CFB	NM_001710	+	-5654
chr19	59070044	59070245	202	146	8	14.79	MYADM	NM_001020818	+	-5653
chr2	63675077	63675264	188	132	10	16.52	MDH1	NM_005917	+	-5639
chr20	33335576	33335776	201	86	15	8.83	ITGB4BP	NM_181468	-	-5638
chr12	50918635	50918858	224	137	17	12.3	KRT7	NM_005556	+	-5638
chr18	41923527	41923742	216	124	31	6.32	ATP5A1	NM_004046	-	-5635
chr1	94415935	94416111	177	122	9	9.15	ARHGAP29	NM_004815	-	-5630
chr22	35796880	35797053	174	98	18	16.56	TMPRSS6	NM_153609	-	-5629
chr16	70163464	70163880	417	191	37	8.88	TAT	NM_000353	-	-5626
chr12	7179667	7179859	193	58	9	23.29	CLSTN3	NM_014718	+	-5626
chr4	24143643	24143810	168	76	8	12.3	DHX15	NM_001358	-	-5623
chr1	21424319	21424559	241	144	13	14.11	ECE1	NM_001397	-	-5621
chr9	126160815	126161175	361	281	30	5.29	PSMB7	NM_002799	-	-5610
chr12	101761431	101761844	414	182	59	7.83	PAH	NM_000277	-	-5610
chr9	4675024	4675175	152	101	9	13.35	CDC37L1	NM_017913	+	-5610
chr12	49609954	49610406	453	61	81	6.63	METTL7A	NM_014033	+	-5606
chr10	85894592	85894768	177	79	18	16.84	GHITM	NM_014394	+	-5604
chr11	814275	814497	223	60	16	9.41	PNPLA2	NM_020376	+	-5596
chr12	2779823	2779991	169	51	9	12.37	FKBP4	NM_002014	+	-5578
chr10	94444857	94445255	399	238	29	5.31	HHEX	NM_002729	+	-5576
chr2	232033089	232033279	191	120	10	10.46	NCL	NM_005381	-	-5576
chr2	73320345	73320483	139	56	11	39.93	CCT7	NM_001009570	+	-5571
chr17	43378910	43379478	569	128	32	6.82	PNPO	NM_018129	+	-5563
chr6	56436299	56436555	257	118	14	8.78	DST	NM_015548	-	-5560

chr12	90026006	90026914	909	727	75	5.15	LUM	NM_002345	-	-5551
chr9	38385726	38388251	2526	1616	304	5.52	ALDH1B1	NM_000692	+	-5550
chr1	149608792	149608946	155	60	13	9.08	SELENBP1	NM_003944	-	-5542
chr21	46438880	46439000	121	61	8	29.28	LSS	NM_002340	-	-5532
chr9	19110795	19111277	483	216	164	5.81	ADFP	NM_001122	-	-5518
chrX	47401509	47401653	145	89	15	25.1	UXT	NM_153477	-	-5514
chr2	218977244	218978232	989	776	68	8.78	CTDSP1	NM_021198	+	-5511
chr11	6587101	6587288	188	69	14	13.51	ILK	NM_001014795	+	-5506
chr11	116580043	116580751	709	156	50	11.2	TAGLN	NM_001001522	+	-5502
chr17	39783329	39783510	182	57	13	10.14	GRN	NM_002087	+	-5494
chr12	54995846	54995977	132	74	7	14.17	TMEM4	NM_014255	-	-5494
chr9	33020419	33020701	283	177	33	8.8	DNAJA1	NM_001539	+	-5493
chr7	100674838	100675105	268	192	18	10.79	FIS1	NM_016068	-	-5491
chr11	10780149	10780659	511	62	43	6.55	EIF4G2	NM_001418	-	-5490
chr2	96300587	96301099	513	383	25	10.01	WDR39	NM_004804	+	-5489
chr14	23638486	23638810	325	230	52	5.47	PCK2	NM_001018073	+	-5488
chr7	100043205	100043412	208	137	22	7.61	PCOLCE	NM_002593	+	-5487
chr1	153531513	153531739	227	171	23	12.19	PKLR	NM_181871	-	-5486
chr5	43330528	43330736	209	133	15	10.38	HMGCS1	NM_002130	-	-5482
chr2	74447074	74447271	198	51	11	17.67	DCTN1	NM_023019	-	-5482
chr16	28909139	28909349	211	120	8	18.3	LAT	NM_001014987	+	-5462
chr1	150050415	150050631	217	45	12	8.29	RORC	NM_001001523	-	-5459
chr1	1677780	1677993	214	109	9	12.2	NADK	NM_023018	-	-5456
chr17	7067634	7069328	1695	1625	475	7.87	ACADVL	NM_000018	+	-5452
chr12	55323415	55323676	262	166	52	7.03	ATP5B	NM_001686	-	-5451
chr14	20560042	20560210	169	61	29	8.41	NDRG2	NM_201538	-	-5448

chr8	22484359	22484598	240	70	17	10.54	SORBS3	NM_001018003	+	-5439
chr14	68329363	68329558	196	62	25	6.1	ZFP36L1	NM_004926	-	-5431
chr3	158353485	158353712	228	61	11	9.35	CCNL1	NM_020307	-	-5431
chr12	6708655	6708910	256	208	14	24.4	COPS7A	NM_016319	+	-5429
chr15	43445814	43446042	229	106	80	5.24	GATM	NM_001482	-	-5427
chr19	18876557	18876749	193	85	8	16.95	COPE	NM_007263	-	-5426
chr20	32336893	32337161	269	197	18	7.88	AHCY	NM_000687	-	-5425
chr3	49024984	49025252	269	117	12	8.13	WDR6	NM_018031	+	-5423
chr2	119846173	119846549	377	295	94	6.81	DBI	NM_020548	+	-5420
chr12	7043360	7043695	336	81	90	6.29	C1S	NM_001734	+	-5414
chr7	99407182	99407700	519	227	203	5.34	AZGP1	NM_001185	-	-5413
chr4	74571526	74571737	212	110	40	5.38	AFM	NM_001133	+	-5412
chr8	145697691	145698326	636	579	56	5.48	PPP1R16A	NM_032902	+	-5410
chr2	219755589	219756606	1018	542	57	5.09	C2orf17	NM_024293	+	-5409
chr7	100113934	100114713	780	403	68	5.71	GNB2	NM_005273	+	-5403
chr3	135012612	135012760	149	99	6	23.64	SRPRB	NM_021203	+	-5394
chr15	38490084	38490370	287	168	17	18.91	IVD	NM_002225	+	-5393
chr8	141595774	141595977	204	97	7	22.52	CHRA1	NM_017444	+	-5392
chr3	58158571	58158784	214	86	23	8.77	DNASE1L3	NM_004944	-	-5391
chr11	68420547	68420713	167	116	9	14.64	MRPL21	NM_181515	-	-5391
chr3	5000233	5001594	1362	77	118	6.34	BHLHB2	NM_003670	+	-5387
chr11	67136161	67136352	192	88	18	5.62	NDUFV1	NM_007103	+	-5370
chr11	58239283	58239499	217	153	21	11.91	GLYAT	NM_005838	-	-5361
chr2	241461044	241462193	1150	1082	274	8.97	AGXT	NM_000030	+	-5359
chr19	54285530	54285631	102	52	7	17.08	SNRP70	NM_001009820	+	-5355
chr14	93824355	93824757	403	261	53	5.9	SERPINA10	NM_016186	-	-5353

chr3	185525942	185526135	194	56	16	7.57	EIF4G1	NM_004953	+	-5341
chr1	163903152	163903412	261	97	18	12.74	ALDH9A1	NM_000696	-	-5340
chr4	155708176	155708934	759	139	316	5.26	FGB	NM_005141	+	-5339
chr19	8287394	8287567	174	54	12	25.48	NDUFA7	NM_005001	-	-5334
chr9	89535744	89536132	389	162	54	6	CTSL	NM_001912	+	-5333
chr11	116666795	116666955	161	59	8	12.55	BACE1	NM_012104	-	-5329
chr19	1447261	1447489	229	73	45	8.38	REEP6	NM_138393	+	-5325
chr4	70385454	70385780	327	121	56	8.3	UGT2B4	NM_021139	-	-5308
chr17	71453385	71454494	1110	1051	95	5.27	ACOX1	NM_004035	-	-5306
chr1	165781974	165782180	207	122	20	7.27	CREG1	NM_003851	-	-5304
chr6	31610909	31611280	372	311	20	9.99	BAT1	NM_004640	-	-5304
chr5	178978498	178979089	592	459	43	10.4	HNRPH1	NM_005520	-	-5304
chr19	12867995	12868270	276	61	24	8.89	GCDH	NM_000159	+	-5297
chr2	215938381	215938718	338	158	113	5.54	FN1	NM_002026	-	-5293
chr7	148336187	148336374	188	90	23	5.96	PDIA4	NM_004911	-	-5286
chr20	43392396	43392626	231	130	32	5.64	SDC4	NM_002999	-	-5282
chr19	56545371	56545502	132	62	22	7.73	ETFB	NM_001014763	-	-5282
chr7	94877134	94877391	258	81	20	5.67	PON2	NM_000305	-	-5281
chr20	35245990	35246163	174	116	13	53.19	RPN2	NM_002951	+	-5276
chr3	150378208	150378498	291	205	83	9.59	CP	NM_000096	-	-5275
chr1	54443550	54443699	150	59	12	10.98	MRPL37	NM_016491	+	-5272
chr14	22310284	22310841	558	347	50	8.17	OXA1L	NM_005015	+	-5271
chr11	813955	814172	218	111	19	18.3	PNPLA2	NM_020376	+	-5271
chr17	7022419	7022743	325	175	42	8.96	ASGR1	NM_001671	-	-5267
chr7	42943428	42943728	301	242	23	7.05	MRPL32	NM_031903	+	-5265
chr2	201389991	201390156	166	116	6	22.88	BZW1	NM_014670	+	-5265

chr17	37946624	37946734	111	56	6	17.57	NAGLU	NM_000263	+	-5258
chr1	15776747	15776990	244	140	30	6.12	AGMAT	NM_024758	-	-5252
chr8	64141031	64141232	202	60	20	17.74	TPPA	NM_000370	-	-5248
chr17	59931246	59931442	197	56	25	6.25	DDX5	NM_004396	-	-5241
chr22	35796460	35796664	205	153	11	9.89	TMPRSS6	NM_153609	-	-5240
chr19	46078232	46078424	193	59	8	14.13	CYP2A7	NM_000764	-	-5240
chr6	86385706	86385894	189	61	11	21.96	SYNCRIP	NM_006372	-	-5237
chr11	118405128	118405509	382	94	30	5.08	SLC37A4	NM_001467	-	-5234
chr22	37465676	37465914	239	62	16	11.37	UNC84B	NM_015374	-	-5234
chr17	64759473	64759620	148	89	7	21.96	ABCA5	NM_018672	-	-5234
chr19	7934459	7934689	231	77	13	7.89	ELAVL1	NM_001419	-	-5232
chr17	7421862	7422010	149	50	11	13.07	EIF4A1	NM_001416	+	-5230
chr12	7172521	7172782	262	132	43	8.95	RBP5	NM_031491	-	-5228
chr10	50617704	50617940	237	106	13	10.05	OGDHL	NM_018245	-	-5224
chr7	45923321	45923596	276	100	46	7.07	IGFBP3	NM_000598	-	-5222
chr3	20001512	20001679	168	109	8	17.22	C3orf48	NM_144714	-	-5222
chr16	2143397	2143872	476	48	20	5.58	RAB26	NM_014353	+	-5221
chr3	135684335	135684457	123	62	6	24.4	ANAPC13	NM_015391	-	-5218
chr3	101541354	101541474	121	61	8	23.43	NIT2	NM_020202	+	-5217
chr1	183537147	183537361	215	109	9	8.37	IVNS1ABP	NM_006469	-	-5215
chr19	59069625	59069807	183	122	8	19.26	MYADM	NM_001020818	+	-5215
chr17	23702792	23702994	203	92	20	19.52	POLDIP2	NM_015584	-	-5208
chr5	86730874	86731042	169	121	6	22.88	CCNH	NM_001239	-	-5204
chr12	123833168	123833320	153	96	11	16.5	SCARB1	NM_005505	-	-5192
chr22	35750045	35750838	794	600	113	7.75	MPST	NM_001013436	+	-5191
chr3	121834588	121834894	307	232	58	5.62	HGD	NM_000187	-	-5189

chr7	6035069	6035178	110	56	8	16.5	EIF2AK1	NM_014413	-	-5188
chr10	135015473	135016085	613	110	202	5.28	PRAP1	NM_145202	+	-5185
chr7	42927964	42928171	208	58	9	21.3	PSMA2	NM_002787	-	-5183
chr14	23705112	23705439	328	127	23	8.64	ISGF3G	NM_006084	+	-5178
chr12	6732345	6732606	262	113	22	6.03	MLF2	NM_005439	-	-5176
chr9	94928525	94928772	248	124	12	9.08	NINJ1	NM_004148	-	-5172
chr16	30672234	30672401	168	114	6	23.64	PHKG2	NM_000294	+	-5164
chr11	62290584	62290754	171	78	12	32.94	POLR2G	NM_002696	+	-5164
chr5	90705252	90705458	207	152	14	10.35	ARRDC3	NM_020801	-	-5161
chr14	22864161	22864396	236	158	13	9.76	PABPN1	NM_004643	+	-5160
chr9	35051570	35051720	151	56	11	10.14	VCP	NM_007126	-	-5160
chr14	20559789	20559918	130	60	16	7.14	NDRG2	NM_201538	-	-5156
chr20	33682238	33682537	300	252	15	10.98	CPNE1	NM_003915	-	-5156
chr2	38829216	38829401	186	62	14	13.62	SFRS7	NM_001031684	-	-5153
chr1	120097302	120097678	377	178	91	8.09	HMGCS2	NM_005518	-	-5151
chr12	107802897	107803142	246	94	14	12.61	DAO	NM_001917	+	-5147
chr12	6955099	6955399	301	162	15	15.02	EMG1	NM_006331	+	-5146
chr10	5131531	5131711	181	50	12	14.58	AKR1C3	NM_003739	+	-5144
chr9	136917433	136917620	188	57	10	22.97	FCN2	NM_004108	+	-5142
chr6	44327725	44327964	240	53	32	6.64	HSP90AB1	NM_007355	+	-5138
chr1	1365211	1365907	697	562	39	5.4	VWA1	NM_022834	+	-5136
chr19	54100709	54100984	276	199	26	10.1	NUCB1	NM_006184	+	-5132
chr2	88208346	88208755	410	302	123	7.08	FABP1	NM_001443	-	-5131
chr20	42422572	42422985	414	151	21	12.12	HNF4A	NM_001030004	+	-5131
chr11	611557	611705	149	68	20	6.54	MUCDHL	NM_021924	-	-5129
chr4	17193041	17193153	113	57	6	24.4	LAP3	NM_015907	+	-5129

chr17	46603941	46604208	268	61	20	9.42	NME2	NM_001018138	+	-5127
chr10	11829331	11829515	185	116	20	60.29	ECHDC3	NM_024693	+	-5127
chr17	37946473	37946600	128	75	6	17.43	NAGLU	NM_000263	+	-5124
chr1	3536078	3536534	457	186	43	8.18	FAM79A	NM_182752	+	-5119
chr2	53950057	53950193	137	53	9	14.04	PSME4	NM_014614	-	-5119
chr11	118130611	118130734	124	52	6	18.3	DDX6	NM_004397	-	-5112
chr1	54274785	54275048	264	141	18	12.56	TMEM59	NM_004872	-	-5110
chr17	77634342	77634612	271	170	26	5.46	FASN	NM_004104	-	-5109
chr1	159394872	159395275	404	173	37	10.74	UFC1	NM_016406	+	-5103
chr16	1777892	1778062	171	116	12	11.27	NUBP2	NM_012225	+	-5103
chr22	40256690	40256853	164	80	8	14.41	POLR3H	NM_138338	-	-5101
chr7	154725260	154725568	309	216	28	7.24	INSIG1	NM_198337	+	-5093
chr3	185525730	185525875	146	90	15	10.61	EIF4G1	NM_004953	+	-5081
chr19	1339829	1339980	152	62	12	24.48	NDUFS7	NM_024407	+	-5075
chr11	116159389	116159560	172	118	6	17.22	ZNF259	NM_003904	-	-5074
chr2	20100546	20100965	420	96	39	9.66	LAPTM4A	NM_014713	-	-5072
chr3	185568608	185568959	352	102	17	14.64	POLR2H	NM_006232	+	-5072
chr12	12766182	12766640	459	310	21	9.41	CDKN1B	NM_004064	+	-5065
chr9	129621976	129622174	199	60	10	13.56	ENG	NM_000118	-	-5058
chr12	55914274	55914873	600	402	101	5.77	SHMT2	NM_005412	+	-5055
chr9	122759369	122759486	118	60	20	11.52	C5	NM_001735	-	-5050
chr3	184220598	184220747	150	89	9	22.77	MCCC1	NM_020166	-	-5046
chr17	4799911	4800202	292	95	32	5.99	ENO3	NM_001976	+	-5044
chr6	30800651	30801176	526	242	39	5.6	TUBB	NM_178014	+	-5041
chr19	10367595	10367839	245	137	16	8.37	CDC37	NM_007065	-	-5031
chr4	83568216	83568400	185	126	12	8.78	HNRPDL	NM_031372	-	-5030

chr7	100561885	100562196	312	58	26	8.57	SERPINE1	NM_000602	+	-5025
chr1	12555326	12555550	225	75	39	6.82	DHRS3	NM_004753	-	-5024
chr7	50498317	50498650	334	274	18	19.56	DDC	NM_000790	-	-5021
chr16	82403769	82404112	344	287	29	9.44	HSBP1	NM_001537	+	-5019
chr7	87677188	87677385	198	138	13	20.29	SRI	NM_003130	-	-5018
chrX	57639832	57639998	167	115	6	19.52	ZXDB	NM_007157	+	-5005
chr1	62840476	62840773	298	130	45	9.35	ANGPTL3	NM_014495	+	-4999
chr6	33156369	33156732	364	271	34	6.66	HLA-DPB1	NM_002121	+	-4995
chr14	23638075	23638315	241	96	43	10.14	PCK2	NM_001018073	+	-4993
chr5	177568918	177569105	188	53	10	11.56	HNRPAB	NM_004499	+	-4992
chr10	99521154	99521493	340	121	14	10.46	SFRP5	NM_003015	-	-4986
chr22	25222717	25222882	166	105	7	25.24	TFIP11	NM_001008697	-	-4986
chr20	5048323	5048585	263	147	11	30.8	PCNA	NM_182649	-	-4986
chr3	187817644	187818564	921	145	197	8.81	AHSG	NM_001622	+	-4984
chr4	185918412	185918724	313	169	49	5.46	ACSL1	NM_001995	-	-4981
chr17	71270365	71270591	227	137	29	10.65	GALK1	NM_000154	-	-4979
chr11	57013277	57013560	284	138	16	8.32	SLC43A1	NM_003627	-	-4977
chr11	813684	813878	195	62	10	8.51	PNPLA2	NM_020376	+	-4977
chr16	3652785	3653013	229	172	17	12.29	TRAP1	NM_016292	-	-4974
chr19	6317169	6317428	260	156	14	38.07	CLPP	NM_006012	+	-4966
chr3	188452107	188452255	149	96	10	16.73	MASP1	NM_001031849	-	-4954
chr8	128822077	128822450	374	151	20	9.13	MYC	NM_002467	+	-4953
chr5	42840379	42840691	313	198	90	7.98	SEPP1	NM_005410	-	-4952
chr3	187988757	187989004	248	115	17	8.13	EIF4A2	NM_001967	+	-4950
chr19	5647683	5647792	110	56	9	14.49	LONP1	NM_004793	-	-4947
chr1	153530887	153531193	307	144	25	5.78	PKLR	NM_181871	-	-4940

chr1	184537334	184537537	204	82	9	22.52	PRG4	NM_005807	+	-4937
chr14	50446337	50446622	286	94	36	6.8	PYGL	NM_002863	-	-4936
chr17	2544147	2544357	211	118	15	10.1	KIAA0664	NM_015229	-	-4928
chr16	31103760	31103881	122	62	8	14.29	FUS	NM_001010850	+	-4928
chr14	23733759	23734011	253	129	8	14.82	TM9SF1	NM_001014842	-	-4927
chr10	82025734	82026479	746	497	98	6.79	MAT1A	NM_000429	-	-4923
chr20	41524503	41524854	352	91	23	7.36	SFRS6	NM_006275	+	-4923
chr12	49923676	49923814	139	56	24	7.46	DAZAP2	NM_014764	+	-4922
chr11	611331	611496	166	57	13	9.35	MUCDHL	NM_021924	-	-4920
chr12	51582010	51582153	144	50	11	10.54	KRT8	NM_002273	-	-4916
chr9	35726657	35727228	572	415	26	6.27	CREB3	NM_006368	+	-4912
chr16	73048102	73048259	158	38	6	18.3	GLG1	NM_012201	-	-4903
chr7	26202525	26202890	366	65	71	6.8	HNRPA2B1	NM_002137	-	-4899
chr12	54915498	54915790	293	213	22	11.87	SLC39A5	NM_173596	+	-4897
chr11	32566695	32566862	168	122	9	12.81	PCID1	NM_006360	+	-4896
chr19	3718248	3718566	319	100	33	5.06	MRPL54	NM_172251	+	-4895
chr2	201430673	201430872	200	151	16	5.86	CLK1	NM_004071	-	-4895
chr7	75350941	75351145	205	147	9	15.01	RHBDD2	NM_001040456	+	-4893
chr5	135397364	135397489	126	57	7	23.12	TGFBI	NM_000358	+	-4893
chr3	102887357	102887514	158	79	13	12.72	RPL24	NM_000986	-	-4891
chr1	43407112	43407330	219	124	9	22.44	EBNA1BP2	NM_006824	-	-4888
chr20	60316028	60316307	280	178	23	12.3	ADRM1	NM_007002	+	-4886
chr1	45753889	45754178	290	128	40	7.43	PRDX1	NM_002574	-	-4884
chr14	69308320	69308468	149	88	20	8.73	SFRS5	NM_006925	+	-4882
chr9	115898506	115898615	110	56	6	17.57	KIF12	NM_138424	-	-4876
chr11	66377262	66377444	183	123	14	14.74	PC	NM_022172	-	-4872

chr11	74955493	74955687	195	138	9	17.13	SERPINH1	NM_001235	+	-4870
chr19	965171	965512	342	58	25	6.26	C19orf6	NM_001033026	-	-4863
chr19	43561644	43561923	280	195	21	8.2	PSMD8	NM_002812	+	-4863
chr19	7491381	7491936	556	343	40	12.79	ZNF358	NM_018083	+	-4862
chr17	37977065	37977449	385	73	20	11.27	MLX	NM_170607	+	-4846
chr14	59685801	59686080	280	185	32	9.57	DHRS7	NM_016029	-	-4829
chr1	232810802	232811466	665	274	32	5.11	IRF2BP2	NM_001077397	-	-4827
chr6	30568884	30570076	1193	1021	193	6.73	HLA-E	NM_005516	+	-4827
chrX	54487895	54488401	507	211	30	6.07	TSR2	NM_058163	+	-4824
chr12	94895785	94896093	309	143	14	11.71	HAL	NM_002108	-	-4821
chr17	77634066	77634323	258	57	27	5.04	FASN	NM_004104	-	-4820
chr19	54877000	54877173	174	61	7	35.46	PRMT1	NM_001536	+	-4819
chr12	9116165	9116388	224	121	56	5.55	A2M	NM_000014	-	-4818
chr6	21706550	21706766	217	157	9	12.2	SOX4	NM_003107	+	-4816
chr7	45894559	45899298	4740	3557	744	8.42	IGFBP1	NM_000596	+	-4815
chr15	88432574	88433026	453	342	57	6.63	IDH2	NM_002168	-	-4809
chr5	43329859	43330060	202	123	23	8.03	HMGCS1	NM_002130	-	-4806
chr17	59930795	59931005	211	62	23	10.82	DDX5	NM_004396	-	-4804
chr16	1771367	1771513	147	65	8	16.89	SPSB3	NM_080861	-	-4799
chr20	47167728	47168081	354	61	30	5.83	STAU1	NM_001037328	-	-4797
chr12	6312770	6312980	211	131	20	6.8	TNFRSF1A	NM_001065	-	-4796
chr1	219031436	219031687	252	120	12	22.14	MOSC1	NM_022746	+	-4794
chr5	180601074	180601323	250	120	55	5.05	GNB2L1	NM_006098	-	-4790
chr1	74948375	74948560	186	109	11	10.89	CRYZ	NM_001889	-	-4789
chr3	126652834	126652972	139	66	9	14.25	SNX4	NM_003794	-	-4788
chr6	64344218	64344664	447	167	38	6	PTP4A1	NM_003463	+	-4786

chr2	27113922	27114108	187	61	10	18.63	FLJ20254	NM_017727	+	-4783
chr7	150132773	150133559	787	181	237	6.16	TMEM176A	NM_018487	+	-4773
chr10	85893712	85893935	224	95	16	8.2	GHITM	NM_014394	+	-4771
chr6	43094583	43094725	143	58	11	16.47	KLHDC3	NM_057161	+	-4771
chr2	127896946	127897254	309	170	25	7.11	PROC	NM_000312	+	-4768
chr20	42565872	42566077	206	131	9	14.64	SERINC3	NM_006811	-	-4763
chr3	52808357	52808615	259	130	37	8.63	ITIH3	NM_002217	+	-4762
chr12	74709855	74710246	392	89	33	10.66	PHLDA1	NM_007350	-	-4752
chr22	37465234	37465430	197	105	13	9.61	UNC84B	NM_015374	-	-4750
chr19	45021492	45021686	195	61	8	16.89	FBL	NM_001436	-	-4749
chr2	72971908	72972799	892	649	68	5.53	SPR	NM_003124	+	-4744
chr20	43429630	43429856	227	57	12	9.32	SYS1	NM_033542	+	-4742
chr7	94769430	94769661	232	109	48	5	PON1	NM_000446	-	-4738
chr12	45449335	45449542	208	98	27	7.23	SLC38A4	NM_018018	-	-4732
chr12	109418205	109418445	241	144	11	17.64	VPS29	NM_016226	-	-4732
chr12	55322488	55322949	462	275	55	6.37	ATP5B	NM_001686	-	-4724
chr6	36674566	36674867	302	167	13	7.37	SFRS3	NM_003017	+	-4724
chr11	74792723	74792931	209	54	34	5.86	RPS3	NM_001005	+	-4722
chr9	127041515	127041668	154	70	26	5.51	HSPA5	NM_005347	-	-4714
chr12	49922404	49923606	1203	1034	135	5.53	DAZAP2	NM_014764	+	-4714
chr11	611076	611290	215	140	25	12.46	MUCDHL	NM_021924	-	-4714
chr1	148817826	148818373	548	156	46	9.22	MCL1	NM_182763	-	-4713
chr16	29988642	29989251	610	559	53	7.88	ALDOA	NM_184041	+	-4707
chr16	16155966	16156198	233	150	15	9.1	ABCC6	NM_001171	-	-4707
chr17	40584885	40585172	288	159	14	14.76	HEXIM1	NM_006460	+	-4706
chr22	35011843	35011971	129	62	16	6.61	MYH9	NM_002473	-	-4700

chr12	107485050	107485211	162	106	8	14.64	ISCU	NM_213595	+	-4700
chr11	489029	489208	180	121	14	9.22	RNH1	NM_002939	-	-4697
chr1	20836930	20837230	301	87	23	8.81	PINK1	NM_032409	+	-4696
chr9	35599725	35599974	250	139	12	13.07	TESK1	NM_006285	+	-4694
chr3	49188567	49188756	190	54	8	9.76	KLHDC8B	NM_173546	+	-4685
chr6	37048387	37048577	191	139	9	13.07	MTCH1	NM_014341	-	-4682
chr17	71513411	71513691	281	199	14	8.23	CDK3	NM_001258	+	-4678
chr17	24099616	24099848	233	128	11	10.23	TRAF4	NM_004295	+	-4676
chr5	179160924	179161385	462	55	32	6.76	MGAT4B	NM_054013	-	-4675
chr11	67135346	67135657	312	172	27	10.66	NDUFV1	NM_007103	+	-4675
chr2	215937809	215938098	290	121	78	7.43	FN1	NM_002026	-	-4673
chr19	17487979	17488099	121	61	6	27.45	PGLS	NM_012088	+	-4668
chr14	69307643	69308248	606	232	83	5.15	SFRS5	NM_006925	+	-4662
chr1	114110464	114110637	174	58	7	11.71	RSBN1	NM_018364	-	-4660
chr21	45017903	45018042	140	103	6	16.27	UBE2G2	NM_182688	-	-4659
chrX	153323172	153323372	201	129	9	10.46	GDI1	NM_001493	+	-4658
chr10	27445133	27445329	197	106	9	20.19	YME1L1	NM_139313	-	-4658
chr16	1992229	1992426	198	144	10	35.46	ZNF598	NM_178167	-	-4658
chr10	17315570	17315960	391	60	41	5.34	VIM	NM_003380	+	-4657
chr5	138314798	138314967	170	117	9	17.08	SIL1	NM_001037633	-	-4657
chr6	37250233	37250619	387	120	17	13.22	PIM1	NM_002648	+	-4656
chr7	99087970	99088408	439	259	38	8.36	CYP3A5	NM_000777	-	-4655
chr22	40788788	40788981	194	107	9	17.04	NAGA	NM_000262	-	-4651
chrX	18825219	18825445	227	62	8	11.26	PHKA2	NM_000292	-	-4646
chr3	45047307	45047418	112	57	6	20.92	CLEC3B	NM_003278	+	-4645
chr1	93394422	93394641	220	77	15	27.45	TMED5	NM_016040	-	-4643

chr22	27524956	27525182	227	149	25	10.45	XBP1	NM_005080	-	-4634
chr5	52816534	52816980	447	162	64	10.75	FST	NM_006350	+	-4629
chr16	29781645	29781808	164	59	8	12.2	CDIPT	NM_006319	-	-4629
chr11	68285607	68285772	166	92	10	17.48	CPT1A	NM_001876	-	-4628
chr14	37751426	37751582	157	54	6	18.3	SSTR1	NM_001049	+	-4628
chr16	29729029	29729980	952	606	110	8.09	MAZ	NM_001042539	+	-4625
chr2	26271466	26271624	159	83	22	5.82	HADHA	NM_000182	-	-4616
chr19	59069022	59069207	186	126	9	14.64	MYADM	NM_001020818	+	-4615
chr19	54687033	54687287	255	196	23	6.4	RPL13A	NM_012423	+	-4611
chr16	19037641	19037808	168	108	6	11.87	LOC162073	NM_001034841	+	-4603
chr7	108001448	108002191	744	435	57	6.63	DNAJB9	NM_012328	+	-4600
chrX	48345110	48345441	332	159	16	14.58	WDR13	NM_017883	+	-4597
chr17	4799451	4799754	304	137	31	7.57	ENO3	NM_001976	+	-4596
chr19	11213339	11213720	382	237	54	5.59	LOC55908	NM_018687	+	-4595
chr11	71396020	71396153	134	61	7	17.57	NUMA1	NM_006185	-	-4595
chr11	2111227	2111515	289	202	37	5.48	IGF2	NM_000612	-	-4592
chr5	81609188	81609486	299	215	65	6.65	RPS23	NM_001025	-	-4590
chr12	9196629	9197290	662	118	41	11.63	PZP	NM_002864	-	-4587
chr7	100673988	100674183	196	72	24	6.22	FIS1	NM_016068	-	-4569
chr7	100113636	100113878	243	133	25	6.1	GNB2	NM_005273	+	-4568
chr19	38574038	38574266	229	63	22	13.41	PEPD	NM_000285	-	-4568
chr19	5647076	5647409	334	61	16	8.56	LONP1	NM_004793	-	-4564
chr12	54994873	54995044	172	79	13	8.39	TMEM4	NM_014255	-	-4561
chr2	240718941	240719201	261	117	24	22.93	MYEOV2	NM_138336	-	-4549
chr3	20000847	20000999	153	40	7	19.52	C3orf48	NM_144714	-	-4542
chr17	6884501	6884966	466	75	36	14.78	SLC16A13	NM_201566	+	-4541

chr14	22850178	22850416	239	122	9	22.88	BCL2L2	NM_004050	+	-4541
chr15	72832492	72832776	285	147	31	13.56	CYP1A2	NM_000761	+	-4540
chr5	177572529	177572734	206	145	21	11.31	AGXT2L2	NM_153373	-	-4538
chr4	155729973	155730412	440	144	206	5.61	FGA	NM_021871	-	-4534
chr2	85662135	85662758	624	332	62	7.69	VAMP8	NM_003761	+	-4531
chr16	366131	366384	254	62	11	14.64	TMEM8	NM_021259	-	-4524
chr20	41523874	41524453	580	235	28	7.32	SFRS6	NM_006275	+	-4522
chr6	21706190	21706472	283	185	12	8.29	SOX4	NM_003107	+	-4522
chr7	100640341	100640483	143	42	6	14.64	PLOD3	NM_001084	-	-4505
chr3	38158292	38159510	1219	1014	82	8.18	MYD88	NM_002468	+	-4502
chr11	77456335	77457054	720	612	189	5.12	THRSP	NM_003251	+	-4500
chr1	167754209	167754532	324	143	35	5.76	F5	NM_000130	-	-4500
chr2	232031973	232032203	231	68	16	17.79	NCL	NM_005381	-	-4500
chr19	52687067	52687201	135	74	14	7.25	NAPA	NM_003827	-	-4499
chr20	36412608	36412796	189	131	15	15.22	LBP	NM_004139	+	-4498
chr19	50886965	50887049	85	43	9	11.2	SNRPD2	NM_177542	-	-4492
chr17	34614229	34614545	317	141	31	8.44	RPL19	NM_000981	+	-4484
chr1	3535586	3535890	305	209	16	6.7	FAM79A	NM_182752	+	-4475
chr7	86873535	86873770	236	53	23	6.91	ABCB4	NM_018850	-	-4474
chr1	120096446	120096997	552	328	119	8.21	HMGCS2	NM_005518	-	-4470
chr14	73109852	73110001	150	59	6	14.64	ACOT2	NM_006821	+	-4470
chr3	25810664	25811038	375	255	17	9.61	OXSM	NM_017897	+	-4464
chr5	141287845	141288053	209	112	8	15.41	KIAA0141	NM_014773	+	-4461
chr1	53456692	53456821	130	54	6	16.27	C1orf123	NM_017887	-	-4460
chr19	1446280	1446622	343	61	79	5.19	REEP6	NM_138393	+	-4458
chr17	39782294	39782470	177	89	12	14.64	GRN	NM_002087	+	-4454

chr15	73439510	73439640	131	53	7	16.57	MAN2C1	NM_006715	-	-4454
chr1	22846301	22847186	886	622	125	5.06	C1QC	NM_172369	+	-4453
chr10	134947330	134947578	249	135	8	18.89	TUBGCP2	NM_006659	-	-4451
chr4	77449319	77451282	1964	1602	148	6.94	GENX-3414	NM_003943	+	-4450
chr14	23637232	23637770	539	81	68	7.1	PCK2	NM_001018073	+	-4448
chr2	242087404	242087547	144	60	10	24.4	STK25	NM_006374	-	-4442
chr7	56103723	56103851	129	54	8	11.33	SUMF2	NM_001042468	+	-4441
chr4	74570273	74570761	489	237	56	5.97	AFM	NM_001133	+	-4436
chr9	138691682	138691850	169	89	12	11.13	AGPAT2	NM_001012727	-	-4435
chr1	62839927	62840207	281	166	29	7.48	ANGPTL3	NM_014495	+	-4433
chr17	7431449	7432284	836	492	72	5.3	MPDU1	NM_004870	+	-4431
chr3	151746509	151746891	383	116	44	9.97	SERP1	NM_014445	-	-4421
chr12	16401781	16402036	256	81	58	8.39	MGST1	NM_145764	+	-4419
chr3	49024029	49024234	206	80	10	15.41	WDR6	NM_018031	+	-4405
chr19	13124892	13126684	1793	1548	178	6.56	IER2	NM_004907	+	-4403
chr1	144127646	144129034	1389	1167	193	8.26	HFE2	NM_213653	+	-4400
chr4	17101388	17101516	129	59	8	11.92	QDPR	NM_000320	-	-4396
chr1	222643861	222644211	351	299	16	8.57	WDR26	NM_025160	-	-4395
chr16	29781441	29781571	131	58	7	15.15	CDIPT	NM_006319	-	-4392
chr17	39441375	39441943	569	294	28	8.33	NAGS	NM_153006	+	-4386
chr6	32934102	32934300	199	60	13	6.8	PSMB9	NM_002800	+	-4385
chr9	115192480	115192798	319	59	21	7.84	ALAD	NM_001003945	-	-4385
chr6	49511118	49511338	221	115	27	6.11	MUT	NM_000255	-	-4381
chr1	11013370	11013548	179	65	11	10.48	MASP2	NM_006610	-	-4381
chr17	59262815	59262922	108	55	11	10.74	PSMC5	NM_002805	+	-4381
chr12	2778503	2778793	291	50	17	14.91	FKBP4	NM_002014	+	-4380

chr2	197968997	197969321	325	221	31	5.95	SF3B1	NM_012433	-	-4377
chr17	1596966	1597250	285	178	56	5.31	SERPINF2	NM_000934	+	-4371
chr1	151877396	151877517	122	62	7	20.5	C1orf77	NM_015607	+	-4369
chr22	34983290	34983437	148	58	15	47.58	APOL1	NM_145343	+	-4368
chr20	23566191	23566658	468	129	92	7.34	CST3	NM_000099	-	-4365
chr7	95054980	95055110	131	62	11	10.53	PDK4	NM_002612	-	-4362
chr10	96437528	96437715	188	84	11	14.64	CYP2C18	NM_000772	+	-4348
chr19	18149654	18149925	272	114	42	6.64	IFI30	NM_006332	+	-4347
chr3	49428548	49428980	433	275	29	6.34	TCTA	NM_022171	+	-4338
chr4	3417551	3417861	311	59	53	7.01	HGFAC	NM_001528	+	-4338
chr16	66535337	66535621	285	135	30	6.26	LCAT	NM_000229	-	-4334
chr2	96308032	96308128	97	49	7	20.5	ASCC3L1	NM_014014	-	-4327
chr6	43094076	43094278	203	59	11	12.55	KLHDC3	NM_057161	+	-4324
chr20	42420696	42422164	1469	217	102	8.96	HNF4A	NM_001030004	+	-4310
chr11	67134977	67135290	314	231	26	7.15	NDUFV1	NM_007103	+	-4308
chr3	185379354	185379634	281	112	26	14.64	AP2M1	NM_001025205	+	-4307
chr6	43591600	43591848	249	62	22	5.21	YIPF3	NM_015388	-	-4306
chr7	142674793	142674990	198	130	29	5.8	GSTK1	NM_015917	+	-4305
chr16	21876261	21876414	154	95	10	14.64	UQCRC2	NM_003366	+	-4305
chr9	130624296	130624900	605	389	51	10.22	ENDOG	NM_004435	+	-4301
chr19	46005825	46006103	279	110	16	7.99	EGLN2	NM_017555	+	-4286
chr12	15668504	15668625	122	62	6	23.12	EPS8	NM_004447	-	-4283
chr10	105347912	105348056	145	79	6	13.94	SH3PXD2A	NM_014631	-	-4281
chr19	53069651	53069958	308	209	94	5.39	SULT2A1	NM_003167	-	-4276
chr16	78189702	78190001	300	255	17	7.88	MAF	NM_005360	-	-4270
chr1	159439841	159439998	158	50	11	9.25	NDUFS2	NM_004550	+	-4270

chr14	93591091	93591289	199	56	14	23.31	DDX24	NM_020414	-	-4268
chr16	47064	47282	219	158	10	12.2	C16orf33	NM_024571	+	-4266
chr19	10366905	10367069	165	55	13	7.25	CDC37	NM_007065	-	-4261
chr16	31103047	31103211	165	53	9	10.46	FUS	NM_001010850	+	-4258
chr17	1909125	1909270	146	103	6	15.41	HIC1	NM_006497	+	-4258
chr17	77398361	77398580	220	113	54	6.95	P4HB	NM_000918	-	-4255
chr10	102734181	102735376	1196	730	83	9.63	MRPL43	NM_176793	-	-4253
chr6	43377799	43378223	425	224	79	5.99	SLC22A7	NM_006672	+	-4248
chr5	133524541	133524715	175	119	9	20.5	SKP1A	NM_170679	-	-4248
chr1	152018440	152018637	198	102	10	17.08	SLC27A3	NM_024330	+	-4246
chr9	123950228	123950405	178	66	10	12.55	NDUFA8	NM_014222	-	-4245
chr3	10321719	10321854	136	52	8	28.47	SEC13L1	NM_030673	-	-4238
chr7	99869357	99869693	337	233	25	9.05	BCDIN3	NM_019606	+	-4229
chr19	17207307	17207921	615	45	33	12.01	NR2F6	NM_005234	-	-4227
chr7	94831000	94831347	348	190	61	5.28	PON3	NM_000940	-	-4226
chr7	73287792	73287994	203	133	7	16.27	RFC2	NM_002914	-	-4225
chr8	125624506	125624754	249	94	45	6.73	NDUFB9	NM_005005	+	-4219
chr17	37971443	37971836	394	170	29	8.24	COASY	NM_001042529	+	-4219
chr10	134976300	134976630	331	60	28	6.46	ZNF511	NM_145806	+	-4218
chr15	83232936	83233134	199	148	11	23.31	SLC28A1	NM_201651	+	-4218
chr9	19109627	19109968	342	156	62	5.01	ADFP	NM_001122	-	-4209
chrX	118258288	118258497	210	83	38	7.86	PGRMC1	NM_006667	+	-4207
chr2	61952707	61952972	266	74	19	7.79	CCT4	NM_006430	-	-4206
chr16	31030669	31031452	784	370	64	5.99	BCKDK	NM_005881	+	-4204
chr1	47379818	47379895	78	40	6	22.52	CYP4A22	NM_001010969	+	-4202
chr17	4799093	4799357	265	186	29	10.57	ENO3	NM_001976	+	-4199

chr17	24099170	24099370	201	61	11	8.83	TRAF4	NM_004295	+	-4198
chr7	72649448	72649655	208	75	17	6.89	MLXIPL	NM_032951	-	-4196
chr17	43407390	43407608	219	133	9	12.2	CDK5RAP3	NM_025197	+	-4181
chr11	94443601	94443881	281	128	12	12.34	SFRS2B	NM_032102	+	-4178
chr17	39782010	39782192	183	100	12	10.72	GRN	NM_002087	+	-4176
chr17	39513651	39513815	165	129	8	15.91	HDAC5	NM_001015053	-	-4169
chr17	40584356	40584634	279	225	12	9.45	HEXIM1	NM_006460	+	-4168
chr1	27572198	27572357	160	90	8	14.06	FCN3	NM_003665	-	-4168
chr16	74223076	74223298	223	167	13	7.62	KARS	NM_005548	-	-4167
chr10	80781181	80781388	208	129	14	18.27	PPIF	NM_005729	+	-4163
chr12	26383335	26383714	380	240	20	12.81	ITPR2	NM_002223	-	-4161
chr9	37909588	37910054	467	229	19	6.84	SHB	NM_003028	-	-4159
chr14	99863175	99863589	415	248	58	7.6	C14orf68	NM_207117	+	-4158
chr17	77284547	77284967	421	109	46	5.48	MRPL12	NM_002949	+	-4156
chr19	3527879	3528096	218	57	9	22.34	HMG20B	NM_006339	+	-4154
chr11	64612082	64612421	340	104	13	6.64	ZFPL1	NM_006782	+	-4152
chr1	1253800	1254157	358	55	18	12.2	MGC10334	NM_001029885	+	-4152
chr11	488444	488661	218	45	16	7.32	RNH1	NM_002939	-	-4150
chr15	32167534	32167655	122	62	8	14.29	C15orf24	NM_020154	-	-4139
chr1	2316968	2317212	245	188	14	14.35	RER1	NM_007033	+	-4139
chr22	34983078	34983200	123	62	8	14.41	APOL1	NM_145343	+	-4131
chr2	109733156	109733327	172	53	7	12.2	ANKRD57	NM_023016	+	-4128
chr8	144769884	144770059	176	96	10	18.04	TSTA3	NM_003313	-	-4127
chr1	149294009	149294195	187	128	8	12.84	CDC42SE1	NM_001038707	-	-4125
chr20	44184279	44184437	159	101	6	19.52	CD40	NM_152854	+	-4125
chr1	23894748	23895004	257	179	53	8.42	RPL11	NM_000975	+	-4124

chr19	59301912	59302093	182	61	19	22.65	NDUFA3	NM_004542	+	-4122
chr8	101788288	101788438	151	98	13	12.16	PABPC1	NM_002568	-	-4119
chr14	73132087	73132276	190	72	7	18.3	ACOT4	NM_152331	+	-4114
chr3	52300645	52301021	377	258	39	8.07	GLYCTK	NM_145262	+	-4110
chr17	71357186	71357483	298	138	19	20.62	WBP2	NM_012478	-	-4108
chr16	70162066	70162358	293	76	32	7.02	TAT	NM_000353	-	-4104
chr22	35011099	35011364	266	120	34	6.49	MYH9	NM_002473	-	-4093
chr11	118404123	118404367	245	143	15	13.43	SLC37A4	NM_001467	-	-4092
chr3	95078483	95078737	255	127	28	5.87	PROS1	NM_000313	-	-4091
chr11	57126061	57126370	310	88	117	5.55	SERPING1	NM_001032295	+	-4090
chr2	10844858	10845057	200	114	24	5.12	PDIA6	NM_005742	-	-4088
chr1	1331033	1331245	213	59	10	20.27	MRPL20	NM_017971	-	-4086
chr3	51401366	51401824	459	125	43	7.24	ARMET	NM_006010	+	-4082
chr14	38718044	38718227	184	125	17	13.47	PNN	NM_002687	+	-4077
chr14	104310610	104310807	198	88	22	17.39	AKT1	NM_005163	-	-4074
chr6	32717042	32717232	191	62	7	24.4	HLA-DQA1	NM_002122	+	-4072
chrX	153322632	153322785	154	94	8	8.13	GDI1	NM_001493	+	-4071
chr2	96307698	96307867	170	50	8	14.93	ASCC3L1	NM_014014	-	-4066
chr14	102874839	102875049	211	70	14	10.85	EIF5	NM_183004	+	-4061
chr19	12706104	12706510	407	280	36	6.95	C19orf43	NM_024038	-	-4056
chr1	144152573	144153992	1420	1012	215	7.09	TXNIP	NM_006472	+	-4054
chr1	148817316	148817713	398	220	50	8.26	MCL1	NM_182763	-	-4053
chr10	4999348	4999506	159	59	9	15.07	AKR1C1	NM_001353	+	-4053
chr19	3930679	3931106	428	337	117	5.07	EEF2	NM_001961	-	-4052
chr22	37464437	37464731	295	191	21	7.77	UNC84B	NM_015374	-	-4051
chr3	15068713	15069073	361	209	24	5.29	MRPS25	NM_022497	-	-4050

chr1	45753111	45753344	234	84	51	5.71	PRDX1	NM_002574	-	-4050
chr1	17221668	17221849	182	76	27	5.06	SDHB	NM_003000	-	-4036
chr2	200532165	200532320	156	103	6	22.88	C2orf47	NM_024520	+	-4036
chr1	159465979	159466490	512	187	47	20.35	TOMM40L	NM_032174	+	-4034
chr9	34640344	34640667	324	69	27	7.45	GALT	NM_000155	+	-4033
chr6	33351776	33351861	86	44	6	23.12	RPS18	NM_022551	+	-4032
chr1	1710350	1710620	271	66	15	13.49	GNB1	NM_002074	-	-4031
chr19	13749844	13750286	443	376	45	10.38	C19orf53	NM_014047	+	-4030
chr2	85426621	85426762	142	56	10	11.66	RETSAT	NM_017750	-	-4030
chr17	45983456	45983588	133	77	6	18.3	SPATA20	NM_022827	+	-4028
chr17	17353457	17353625	169	95	26	6.01	PEMT	NM_148173	-	-4022
chr2	201429634	201429993	360	108	29	8.57	CLK1	NM_004071	-	-4016
chr19	18875064	18875338	275	135	18	24.16	COPE	NM_007263	-	-4015
chr12	51979240	51979515	276	210	51	7.79	PFDN5	NM_002624	+	-4014
chr5	176765547	176765758	212	83	45	11.73	F12	NM_000505	-	-4012
chr11	63762379	63762848	470	322	34	6.31	VEGFB	NM_003377	+	-4007
chr4	77003881	77004051	171	72	6	18.3	PPEF2	NM_006239	-	-4000
chr3	58469617	58469896	280	113	39	7.32	ACOX2	NM_003500	-	-3993
chr1	7997800	7998374	575	417	63	8.13	ERRFI1	NM_018948	-	-3993
chr17	59929777	59930191	415	361	46	5.29	DDX5	NM_004396	-	-3990
chr19	10090531	10090671	141	70	11	9.29	EIF3S4	NM_003755	-	-3981
chr9	85776788	85776891	104	53	8	24.4	HNRPK	NM_031263	-	-3980
chr1	149207996	149208250	255	120	33	8.4	LASS2	NM_022075	-	-3977
chr4	100420303	100420522	220	86	73	5.4	ADH1A	NM_000667	-	-3976
chr6	8362091	8362280	190	122	8	11.13	SLC35B3	NM_015948	-	-3975
chr3	49700269	49700367	99	50	8	12.87	MST1	NM_020998	-	-3975

chr9	137535504	137536348	845	668	45	9.28	MRPS2	NM_016034	+	-3974
chr12	10040721	10040902	182	50	8	15.99	CLEC1B	NM_016509	-	-3972
chr3	4999466	5000178	713	214	45	6.42	BHLHB2	NM_003670	+	-3971
chr16	31013378	31013643	266	146	10	20.43	VKORC1	NM_024006	-	-3967
chr16	29988297	29988507	211	151	23	8.5	ALDOA	NM_184041	+	-3963
chr4	155706950	155707556	607	209	224	5.44	FGB	NM_005141	+	-3961
chr6	122809965	122810152	188	60	16	6.88	SERINC1	NM_020755	-	-3961
chr17	43569572	43569761	190	96	9	16.69	SKAP1	NM_003726	-	-3961
chr9	129904409	129904612	204	143	10	20.91	SLC25A25	NM_001006643	+	-3956
chr16	30907389	30907986	598	484	54	8.17	HSD3B7	NM_025193	+	-3954
chrX	53131947	53132238	292	126	11	12.2	TSPYL2	NM_022117	+	-3952
chr7	100113006	100113253	248	184	16	8.9	GNB2	NM_005273	+	-3943
chr1	177321475	177321676	202	45	8	11.71	TOR3A	NM_022371	+	-3942
chr17	37168190	37168330	141	82	8	12.39	JUP	NM_002230	-	-3941
chr3	51996030	51996540	511	439	60	6.91	ACY1	NM_000666	+	-3938
chr17	19496430	19496593	164	60	8	12.55	ALDH3A2	NM_001031806	+	-3938
chr8	30043817	30044108	292	66	27	6.65	TMEM66	NM_016127	-	-3935
chr11	59102204	59102380	177	122	9	8.93	OSBP	NM_002556	-	-3934
chr17	7020794	7021405	612	272	104	6.67	ASGR1	NM_001671	-	-3929
chr3	88187289	88187721	433	330	24	7.4	CGGBP1	NM_001008390	-	-3926
chr1	75966658	75966795	138	77	10	16.16	ACADM	NM_000016	+	-3926
chr16	28745678	28745839	162	51	6	28.16	ATXN2L	NM_145714	+	-3925
chr12	102851844	102852237	394	57	35	5.77	HSP90B1	NM_003299	+	-3919
chr1	180621990	180622209	220	58	23	5.57	GLUL	NM_001033056	-	-3918
chr16	20459523	20459884	362	60	28	11.93	ACSM2	NM_182617	-	-3915
chr16	87240993	87241110	118	60	15	12.96	CYBA	NM_000101	-	-3912

chr5	176954851	176955720	870	725	105	6.89	TMED9	NM_017510	+	-3902
chr5	137830354	137832980	2627	2159	471	6.85	EGR1	NM_001964	+	-3901
chr8	101788073	101788218	146	87	8	12.83	PABPC1	NM_002568	-	-3899
chr19	55050021	55050125	105	53	8	30.82	PTOV1	NM_017432	+	-3898
chr9	139025225	139025396	172	118	12	18.3	ABCA2	NM_001606	-	-3890
chr6	43591300	43591431	132	71	9	10.65	YIPF3	NM_015388	-	-3889
chr19	1223215	1224234	1020	656	90	6.83	CIRBP	NM_001280	+	-3888
chr9	96408812	96409111	300	171	77	5.72	FBP1	NM_000507	-	-3874
chr11	10778535	10779042	508	385	39	6.38	EIF4G2	NM_001418	-	-3873
chrX	152716975	152717157	183	60	35	6.85	SSR4	NM_006280	+	-3870
chr1	115064679	115064930	252	143	28	8.3	CSDE1	NM_001007553	-	-3870
chr17	77633162	77633368	207	89	25	9.4	FASN	NM_004104	-	-3865
chr1	24047740	24048024	285	56	13	14.6	FUCA1	NM_000147	-	-3864
chr15	79058412	79059010	599	374	32	10.23	MESDC2	NM_015154	-	-3861
chr7	123356273	123356423	151	62	7	16.57	SPAM1	NM_153189	+	-3859
chr6	30799436	30799992	557	446	31	5.93	TUBB	NM_178014	+	-3857
chr1	42697885	42698615	731	632	42	6.81	PPCS	NM_024664	+	-3856
chr19	4315044	4315221	178	106	8	14.64	SH3GL1	NM_003025	-	-3854
chr11	610288	610428	141	57	12	11.34	MUCDHL	NM_021924	-	-3852
chr17	6883736	6884277	542	396	30	12.7	SLC16A13	NM_201566	+	-3852
chr12	50734354	50735307	954	237	76	7.26	NR4A1	NM_002135	+	-3850
chr8	144715260	144715481	222	60	14	9.41	GSDMDC1	NM_024736	+	-3847
chr10	22648867	22649147	281	127	16	12.34	COMMD3	NM_012071	+	-3843
chr16	65529419	65529689	271	120	42	7.09	CES2	NM_003869	+	-3842
chr8	96010832	96011211	380	236	19	6.56	TP53INP1	NM_033285	-	-3835
chr10	121326580	121326804	225	59	10	10.98	TIAL1	NM_001033925	-	-3835

chr19	12651259	12651368	110	56	8	12.88	DHPS	NM_001930	-	-3835
chr7	150132280	150132619	340	164	52	10	TMEM176A	NM_018487	+	-3833
chr21	43349972	43350203	232	71	21	9.62	CBS	NM_000071	-	-3832
chr15	94678587	94678781	195	153	9	17.13	NR2F2	NM_021005	+	-3832
chr1	19485300	19485473	174	58	14	9.34	AKR7A3	NM_012067	-	-3830
chr22	43970386	43970615	230	100	11	10.46	C22orf9	NM_015264	-	-3829
chr3	151746163	151746293	131	58	16	7.19	SERP1	NM_014445	-	-3823
chr14	50445283	50445509	227	79	17	11.08	PYGL	NM_002863	-	-3823
chr1	11012767	11012989	223	102	9	13.51	MASP2	NM_006610	-	-3822
chr1	62839245	62839592	348	158	27	8.28	ANGPTL3	NM_014495	+	-3818
chr3	187987589	187987871	283	121	22	11.74	EIF4A2	NM_001967	+	-3817
chr10	4999096	4999269	174	116	23	10.19	AKR1C1	NM_001353	+	-3816
chr1	156070807	156071144	338	158	19	9.9	CD5L	NM_005894	-	-3815
chr5	52815634	52816163	530	189	35	5.37	FST	NM_006350	+	-3812
chr15	64573265	64573531	267	59	11	18.3	SNAPC5	NM_006049	-	-3812
chr21	43190084	43190257	174	102	11	11.46	NDUFV3	NM_001001503	+	-3811
chr12	55154601	55154813	213	62	20	6.86	GLS2	NM_013267	-	-3810
chr17	59262133	59262351	219	163	17	8.82	PSMC5	NM_002805	+	-3810
chr7	6472207	6472603	397	208	34	7.1	KDELR2	NM_006854	-	-3809
chr2	208812733	208813004	272	159	36	7.24	IDH1	NM_005896	-	-3806
chr11	18461997	18462233	237	86	11	24.29	TSG101	NM_006292	-	-3799
chr1	153370485	153370767	283	203	30	12.43	EFNA1	NM_004428	+	-3795
chr10	113903052	113903404	353	125	27	7.75	GPAM	NM_020918	-	-3793
chr21	43465295	43466001	707	321	48	7.53	CRYAA	NM_000394	+	-3792
chr1	1253328	1253794	467	140	25	14.64	MGC10334	NM_001029885	+	-3789
chr9	103226560	103227261	702	439	298	5.59	ALDOB	NM_000035	-	-3782

chr2	130820517	130820738	222	114	12	7.32	IMP4	NM_033416	+	-3780
chr9	130813712	130813913	202	85	8	14.64	SH3GLB2	NM_020145	-	-3779
chr12	56503262	56503754	493	59	24	6.27	CTDSP2	NM_005730	-	-3777
chr14	21039699	21039898	200	84	7	19.26	METTL3	NM_019852	-	-3776
chr9	129591299	129591931	633	577	39	7.13	CDK9	NM_001261	+	-3774
chr12	26382839	26383327	489	153	20	10.46	ITPR2	NM_002223	-	-3774
chr12	45448234	45448574	341	161	20	10.81	SLC38A4	NM_018018	-	-3764
chr3	42890235	42892451	2217	944	228	6.8	CYP8B1	NM_004391	-	-3763
chr7	148138980	148139167	188	146	7	12.46	EZH2	NM_004456	-	-3760
chr17	37238573	37238744	172	60	13	6.72	NT5C3L	NM_052935	-	-3758
chr9	126158744	126159323	580	246	61	8.88	PSMB7	NM_002799	-	-3758
chr17	77293416	77293518	103	52	8	12.33	SLC25A10	NM_012140	+	-3743
chr2	188040645	188040946	302	241	26	5.9	TFPI	NM_006287	-	-3742
chr19	60881708	60882143	436	191	27	9.58	EPN1	NM_013333	+	-3740
chr11	63845597	63845879	283	86	37	6.4	PRDX5	NM_012094	+	-3735
chr3	49699986	49700127	142	46	10	13.58	MST1	NM_020998	-	-3735
chr17	73698621	73698767	147	89	11	10.76	AFMID	NM_001010982	+	-3730
chr15	88431646	88431947	302	75	37	13.31	IDH2	NM_002168	-	-3730
chr3	140562626	140562853	228	168	12	10.01	COPB2	NM_004766	-	-3729
chr19	964234	964368	135	77	14	12.85	C19orf6	NM_001033026	-	-3719
chr3	127308571	127308815	245	167	46	5.12	ALDH1L1	NM_012190	-	-3718
chr12	7041740	7041998	259	150	61	6.55	C1S	NM_001734	+	-3717
chr17	39202347	39202731	385	329	21	12.35	DUSP3	NM_004090	-	-3716
chr19	54099422	54099563	142	62	13	24.95	NUCB1	NM_006184	+	-3711
chr21	44381461	44381632	172	92	19	10.91	C21orf33	NM_004649	+	-3709
chr3	150376510	150376929	420	250	55	8.82	CP	NM_000096	-	-3706

chr5	176764909	176765451	543	87	66	12.28	F12	NM_000505	-	-3705
chr2	190136538	190137266	729	595	58	9.42	SLC40A1	NM_014585	-	-3704
chr3	52300001	52300613	613	117	50	5.82	GLYCTK	NM_145262	+	-3702
chr16	70161657	70161956	300	116	33	8.78	TAT	NM_000353	-	-3702
chr9	89534292	89534500	209	140	19	12.67	CTSL	NM_001912	+	-3701
chr19	4108018	4108328	311	102	23	9.11	CREB3L3	NM_032607	+	-3700
chr20	5938428	5938578	151	93	12	22.11	CRLS1	NM_019095	+	-3700
chr4	71058074	71058242	169	99	6	12.2	LOC401137	NM_214711	+	-3699
chr11	6192645	6192851	207	113	7	18.89	C11orf56	NM_032127	-	-3699
chr2	27112840	27113023	184	47	9	12.2	FLJ20254	NM_017727	+	-3698
chr20	61844651	61845351	701	159	105	6.21	SLC2A4RG	NM_020062	+	-3697
chr14	49308088	49308232	145	57	7	21.53	KLHDC2	NM_014315	+	-3696
chr1	154294608	154294921	314	230	28	6.9	MAPBPIP	NM_014017	+	-3693
chr4	3416787	3417216	430	60	45	13.38	HGFAC	NM_001528	+	-3693
chr1	202437373	202437600	228	80	18	11.13	GOLT1A	NM_198447	-	-3690
chr17	77458934	77459070	137	61	9	13.01	PCYT2	NM_002861	-	-3687
chr19	1229784	1230233	450	180	34	13.18	C19orf24	NM_017914	+	-3683
chr7	72648632	72649141	510	84	38	9.19	MLXIPL	NM_032951	-	-3682
chr10	126079380	126079542	163	109	8	14.32	OAT	NM_000274	-	-3681
chr12	54399534	54399767	234	60	35	5.82	BLOC1S1	NM_001487	+	-3680
chr1	158455440	158455805	366	82	17	7.38	WDR42A	NM_015726	-	-3677
chr11	67134427	67134656	230	143	32	6.73	NDUFV1	NM_007103	+	-3674
chr10	73249218	73249729	512	409	113	5.85	PSAP	NM_002778	-	-3668
chr5	151106009	151106244	236	146	33	6.14	ATOX1	NM_004045	-	-3668
chr20	57040682	57040796	115	58	20	6.73	ATP5E	NM_006886	-	-3668
chr19	52117050	52117439	390	270	18	8.54	GRLF1	NM_004491	+	-3667

chr12	6749275	6749460	186	123	53	5.45	PTMS	NM_002824	+	-3659
chr2	96307286	96307459	174	57	9	12.74	ASCC3L1	NM_014014	-	-3658
chr3	23936198	23937296	1099	169	147	5.1	RPL15	NM_002948	+	-3654
chr10	135029448	135029630	183	99	80	5.46	ECHS1	NM_004092	-	-3651
chr15	38846728	38847227	500	61	54	13.01	GCHFR	NM_005258	+	-3651
chr19	10086662	10086845	184	123	18	8.76	P2RY11	NM_002566	+	-3649
chr1	149290211	149290523	313	136	13	7.32	C1orf56	NM_017860	+	-3641
chr22	40809070	40809284	215	104	25	8.81	C22orf32	NM_033318	+	-3640
chr22	23269769	23270047	279	184	15	9.06	C22orf13	NM_031444	-	-3638
chr6	32518919	32519260	342	152	65	5.01	HLA-DRA	NM_019111	+	-3636
chr6	4064400	4064560	161	75	23	6.73	PECI	NM_206836	-	-3634
chr16	8898335	8898483	149	95	8	21.81	USP7	NM_003470	-	-3633
chr10	50616222	50616348	127	55	11	12.2	OGDHL	NM_018245	-	-3632
chr18	11876922	11877105	184	76	7	18.3	MPPE1	NM_023075	-	-3632
chr14	104293964	104294177	214	93	24	15.67	SIVA	NM_006427	+	-3631
chr6	32024937	32025381	445	125	158	5.19	CFB	NM_001710	+	-3630
chr5	43328709	43328875	167	60	15	8.97	HMGCS1	NM_002130	-	-3621
chr19	44571416	44571731	316	54	18	9.76	PAF1	NM_019088	-	-3620
chr2	113605091	113605227	137	73	12	12.2	IL1RN	NM_173842	+	-3619
chr1	232809433	232810257	825	152	87	5.03	IRF2BP2	NM_001077397	-	-3618
chr20	61043300	61043503	204	86	11	8.78	C20orf11	NM_017896	+	-3618
chr10	3810012	3811805	1794	244	185	8.37	KLF6	NM_001008490	-	-3617
chr12	55913224	55913434	211	62	24	5.74	SHMT2	NM_005412	+	-3616
chr16	30105870	30106038	169	108	7	14.64	CORO1A	NM_007074	+	-3612
chr10	74808697	74808817	121	61	8	14.17	ANXA7	NM_001156	-	-3608
chr21	39487511	39487625	115	58	6	17.57	BRWD1	NM_033656	-	-3607

chr5	170750902	170750998	97	49	8	29.28	NPM1	NM_001037738	+	-3596
chr1	32149866	32149972	107	54	8	20.92	PTP4A2	NM_080391	-	-3593
chr12	54408983	54409089	107	54	15	13.56	CD63	NM_001780	-	-3592
chr17	77632766	77633093	328	152	28	8.13	FASN	NM_004104	-	-3590
chr6	33279277	33280166	890	695	77	5.84	SLC39A7	NM_006979	+	-3586
chr15	94678338	94678535	198	108	8	10.85	NR2F2	NM_021005	+	-3586
chr6	28346339	28346456	118	60	6	17.57	ZNF187	NM_001023560	+	-3585
chr6	43377161	43377558	398	176	34	9.3	SLC22A7	NM_006672	+	-3583
chr19	40325449	40325813	365	59	46	8.74	FXVD1	NM_005031	+	-3582
chr6	43138638	43138928	291	191	13	12.78	KLC4	NM_138343	+	-3579
chr19	34885031	34885213	183	123	9	13.4	C19orf12	NM_001031726	-	-3579
chr22	37464105	37464259	155	87	16	15.55	UNC84B	NM_015374	-	-3579
chr7	100041214	100041503	290	142	15	8.49	PCOLCE	NM_002593	+	-3578
chr16	2233321	2233470	150	62	24	13.31	DCI	NM_001919	-	-3572
chr2	220075343	220075444	102	52	7	18.3	GMPPA	NM_205847	+	-3572
chr6	30568454	30568819	366	240	54	5.95	HLA-E	NM_005516	+	-3570
chr9	138880432	138880622	191	82	26	6.29	EDF1	NM_153200	-	-3569
chr19	54070818	54071057	240	180	12	12.3	PPP1R15A	NM_014330	+	-3568
chr19	18148938	18149145	208	87	18	7.61	IFI30	NM_006332	+	-3567
chr7	72739242	72739400	159	99	6	18.89	WBSCR22	NM_017528	+	-3567
chr22	17803164	17803597	434	98	51	9	MRPL40	NM_003776	+	-3562
chr17	40571938	40572140	203	78	13	9.91	ACBD4	NM_024722	+	-3561
chr8	144731401	144731657	257	183	17	8.47	NAPRT1	NM_145201	-	-3559
chr19	11317706	11318011	306	193	21	10.75	UNQ501	NM_198536	-	-3554
chr3	53238053	53238260	208	102	11	10.66	TKT	NM_001064	-	-3548
chr19	60659518	60659714	197	82	19	10.1	ISOC2	NM_024710	-	-3547

chr11	118403498	118403821	324	266	20	10.46	SLC37A4	NM_001467	-	-3546
chr2	85401130	85402202	1073	918	55	7.48	TGOLN2	NM_006464	-	-3545
chr22	48743382	48743708	327	146	25	6.84	PIM3	NM_001001852	+	-3544
chr9	127040230	127040495	266	62	33	8.28	HSPA5	NM_005347	-	-3541
chr3	153017840	153018089	250	191	64	5.29	AADAC	NM_001086	+	-3539
chr7	7646468	7646638	171	102	9	15.02	RPA3	NM_002947	-	-3537
chr7	108000582	108001125	544	489	35	9.73	DNAJB9	NM_012328	+	-3534
chr1	35425144	35425320	177	118	10	11.39	SFPQ	NM_005066	-	-3531
chr3	52241064	52241197	134	57	6	22.88	TWF2	NM_007284	-	-3531
chr5	162816541	162816694	154	94	7	24.4	NUDCD2	NM_145266	-	-3530
chr2	42851012	42851262	251	165	29	14.09	HAAO	NM_012205	-	-3529
chr6	76007557	76007744	188	111	26	11.56	COX7A2	NM_001865	-	-3522
chr22	38258344	38258563	220	69	10	30.82	RPS19BP1	NM_194326	-	-3520
chr11	826244	826468	225	169	20	9.22	CD151	NM_001039490	+	-3517
chr17	2542835	2542941	107	54	10	14.35	KIAA0664	NM_015229	-	-3512
chr5	95252032	95252362	331	257	15	9.76	ELL2	NM_012081	-	-3510
chr6	44325989	44326330	342	163	18	6.01	HSP90AB1	NM_007355	+	-3504
chr2	31414006	31414195	190	132	12	8.35	XDH	NM_000379	-	-3504
chr17	77612409	77612544	136	56	13	21.47	DUS1L	NM_022156	-	-3504
chr2	204009892	204010288	397	257	25	8.02	RAPH1	NM_213589	-	-3503
chr6	43039024	43039974	951	368	129	9.53	GNMT	NM_018960	+	-3497
chr11	71394726	71395055	330	201	12	15.58	NUMA1	NM_006185	-	-3497
chr2	27450177	27450388	212	159	9	10.31	SNX17	NM_014748	+	-3496
chr19	7490191	7490565	375	260	17	7.32	ZNF358	NM_018083	+	-3491
chr6	43093264	43093444	181	123	11	12.81	KLHDC3	NM_057161	+	-3490
chr8	99126231	99126605	375	222	64	6.77	RPL30	NM_000989	-	-3487

chr19	50611904	50612018	115	58	6	35.46	ERCC1	NM_202001	-	-3486
chr10	13362962	13363279	318	117	67	6.21	PHYH	NM_001037537	-	-3477
chr2	96283285	96283516	232	143	11	10.77	TMEM127	NM_017849	-	-3476
chr1	101478185	101478517	333	274	14	14.64	EDG1	NM_001400	+	-3475
chr2	85622964	85623271	308	58	14	7.32	MAT2A	NM_005911	+	-3473
chrX	51656519	51656907	389	302	28	7.32	MAGED1	NM_001005333	+	-3470
chr14	69306752	69307050	299	241	24	8.76	SFRS5	NM_006925	+	-3464
chr10	94826940	94827119	180	44	10	15.81	CYP26A1	NM_000783	+	-3463
chr17	7987798	7987976	179	76	10	12.55	PER1	NM_002616	-	-3462
chr20	2767242	2767431	190	57	11	14.64	FAM113A	NM_022760	-	-3461
chr1	149207475	149207730	256	110	24	6.43	LASS2	NM_022075	-	-3457
chr22	22709362	22709597	236	109	13	12.09	GSTT1	NM_000853	-	-3457
chr16	78188836	78189186	351	130	21	6.85	MAF	NM_005360	-	-3455
chr9	129965528	129965810	283	128	12	8.29	C9orf16	NM_024112	+	-3451
chr5	137922170	137922369	200	57	14	12.69	HSPA9	NM_004134	-	-3446
chr15	99664939	99665098	160	81	13	7.03	PCSK6	NM_002570	-	-3442
chrX	2866132	2866283	152	93	8	13.35	ARSE	NM_000047	-	-3432
chr8	126514707	126515173	467	130	38	6.57	TRIB1	NM_025195	+	-3429
chr1	45253574	45253841	268	100	50	5.31	UROD	NM_000374	+	-3425
chr5	130526142	130526306	165	71	32	5.31	HINT1	NM_005340	-	-3424
chr11	62039955	62043374	3420	314	364	7.69	AHNAK	NM_001620	-	-3424
chr20	23282630	23282793	164	61	6	24.4	NXT1	NM_013248	+	-3421
chr9	115191525	115191832	308	62	28	9.58	ALAD	NM_001003945	-	-3419
chr17	1503851	1504089	239	108	22	9.62	PRPF8	NM_006445	-	-3416
chrX	7829997	7830209	213	145	17	17.15	PNPLA4	NM_004650	-	-3406
chr7	44521834	44522065	232	132	9	12	NPC1L1	NM_013389	-	-3405

chr12	9642360	9642538	179	129	11	14.64	KLRB1	NM_002258	-	-3401
chr9	129620198	129620514	317	87	23	12.76	ENG	NM_000118	-	-3398
chr14	23685558	23685807	250	47	11	16.27	PSME2	NM_002818	-	-3393
chr9	135521667	135521897	231	60	18	7.44	SARDH	NM_007101	-	-3391
chr2	96307076	96307190	115	58	8	23.43	ASCC3L1	NM_014014	-	-3389
chr10	113902293	113902996	704	76	43	5.81	GPAM	NM_020918	-	-3385
chr10	102276730	102276872	143	55	11	10.47	NDUFB8	NM_005004	-	-3385
chr1	154548485	154548759	275	61	21	13.42	CCT3	NM_001008800	-	-3384
chr8	11740451	11740823	373	190	59	7.4	CTSB	NM_001908	-	-3379
chr22	40855662	40855824	163	84	30	5.67	CYP2D6	NM_000106	-	-3378
chr11	65382122	65382240	119	60	22	6.39	CFL1	NM_005507	-	-3378
chr1	44216165	44216565	401	242	39	5.09	ATP6V0B	NM_004047	+	-3377
chr11	65811836	65812004	169	59	11	18.82	YIF1A	NM_020470	-	-3377
chr1	152216258	152216744	487	247	31	6.42	JTB	NM_006694	-	-3374
chr20	61448318	61448480	163	61	8	21.96	CHRNA4	NM_000744	-	-3372
chr10	96691307	96691790	484	316	89	5.37	CYP2C9	NM_000771	+	-3361
chr2	218976201	218976415	215	68	18	5.67	CTDSP1	NM_182642	+	-3358
chr10	81831585	81831758	174	47	6	24.4	C10orf57	NM_025125	+	-3353
chr3	58391431	58391747	317	62	25	9.28	PDHB	NM_000925	-	-3350
chr1	200246905	200247045	141	54	8	12.39	ELF3	NM_004433	+	-3350
chr3	49111550	49111718	169	57	15	10.98	QARS	NM_005051	-	-3349
chr11	608592	609923	1332	940	104	8.13	MUCDHL	NM_021924	-	-3347
chr11	73366562	73366710	149	72	7	14.64	UCP2	NM_003355	-	-3347
chr12	54841229	54841712	484	303	98	7.09	MYL6	NM_021019	+	-3346
chr6	90096162	90096409	248	123	12	10.89	UBE2J1	NM_016021	-	-3346
chr6	31347732	31347851	120	61	13	8.65	HLA-C	NM_002117	-	-3343

chr12	48435661	48435846	186	84	48	5.45	TEGT	NM_003217	+	-3335
chr17	38309450	38309671	222	93	30	5.85	G6PC	NM_000151	+	-3331
chr13	43908624	43908987	364	191	24	11.99	TSC22D1	NM_006022	-	-3327
chr16	28764715	28764938	224	60	19	9.02	TUFM	NM_003321	-	-3326
chr9	37415898	37416030	133	73	30	5.65	GRHPR	NM_012203	+	-3324
chr7	150407498	150407961	464	138	21	8.15	FASTK	NM_006712	-	-3321
chr1	19454027	19454203	177	116	6	13.73	C1orf33	NM_016183	+	-3318
chr20	41522860	41523245	386	162	30	11.3	SFRS6	NM_006275	+	-3314
chr11	32565125	32565280	156	89	9	20.5	PCID1	NM_006360	+	-3314
chr1	154703184	154703451	268	163	12	10.98	MEF2D	NM_005920	-	-3308
chr22	40254463	40255053	591	320	32	12.11	POLR3H	NM_138338	-	-3301
chr17	77292896	77293072	177	56	12	11.66	SLC25A10	NM_012140	+	-3297
chr3	185445952	185446105	154	71	8	14.94	ALG3	NM_005787	-	-3295
chr22	29305741	29305907	167	59	8	21.53	PES1	NM_014303	-	-3295
chr1	158455248	158455418	171	101	13	9.76	WDR42A	NM_015726	-	-3290
chr3	38142038	38142498	461	76	127	5.71	ACAA1	NM_001607	-	-3288
chr1	152514750	152514948	199	135	21	12.63	HAX1	NM_001018837	+	-3286
chr14	74815874	74818568	2695	2224	438	7.12	FOS	NM_005252	+	-3285
chr1	59019665	59022336	2672	621	556	5.76	JUN	NM_002228	-	-3284
chr3	102766501	102766685	185	124	6	19.52	RG9MTD1	NM_017819	+	-3284
chr3	10320698	10320895	198	62	15	26.09	SEC13L1	NM_030673	-	-3279
chr16	29987616	29987817	202	58	13	7.89	ALDOA	NM_184041	+	-3273
chr12	6947813	6948049	237	105	21	7.63	PHB2	NM_007273	-	-3272
chr17	7477241	7477486	246	133	12	12.61	SHBG	NM_001040	+	-3271
chr4	100479734	100479939	206	145	76	5.35	ADH1C	NM_000669	-	-3266
chr10	105141920	105142069	150	78	19	10.25	USMG5	NM_032747	-	-3266

chr5	43328228	43328519	292	156	29	6.41	HMGCS1	NM_002130	-	-3265
chr3	9909504	9910533	1030	517	72	10.07	JAGN1	NM_032492	+	-3262
chr19	10460844	10461055	212	157	11	8.13	KEAP1	NM_012289	-	-3260
chr19	50140213	50140593	381	111	98	6.62	APOC4	NM_001646	+	-3259
chr12	55778549	55778720	172	72	9	14.64	STAT6	NM_003153	-	-3259
chr22	49291326	49291503	178	58	8	13.03	TMEM153	NM_033200	-	-3258
chrX	53240393	53240636	244	193	12	14.17	JARID1C	NM_004187	-	-3258
chr9	36207022	36207697	676	94	42	6.8	GNE	NM_005476	-	-3257
chr1	46873258	46874252	995	131	79	7.28	ATPAF1	NM_001042546	-	-3253
chr2	160336520	160336852	333	58	30	8.94	CD302	NM_014880	-	-3243
chr6	169847123	169847420	298	181	17	6.54	C6orf120	NM_001029863	+	-3239
chr10	104426483	104426712	230	115	8	11.71	ARL3	NM_004311	-	-3234
chr9	72192248	72192560	313	160	17	6.87	KLF9	NM_001206	-	-3226
chr17	72244548	72245019	472	121	23	10.1	SFRS2	NM_003016	-	-3226
chr17	35333789	35334045	257	60	17	6.44	ORMDL3	NM_139280	-	-3224
chr9	129310522	129310653	132	74	8	14.64	C9orf88	NM_022833	-	-3214
chr17	36040422	36040719	298	148	14	17.45	SMARCE1	NM_003079	-	-3212
chr11	64421704	64421805	102	52	6	17.57	KIAA0404	NM_015104	-	-3211
chr10	3813814	3814449	636	172	71	6.86	KLF6	NM_001300	-	-3209
chr20	60148215	60148394	180	65	21	10.54	PSMA7	NM_002792	-	-3209
chr12	52963793	52963963	171	132	8	12.52	HNRPA1	NM_002136	+	-3209
chr21	36366566	36367358	793	417	190	7.12	CBR1	NM_001757	+	-3204
chr14	49432519	49432791	273	110	11	10.98	ARF6	NM_001663	+	-3203
chr14	34943372	34943667	296	142	19	9.75	NFKBIA	NM_020529	-	-3200
chr4	175650879	175651154	276	115	18	26.28	HPGD	NM_000860	-	-3199
chr19	59301012	59301166	155	99	11	47.06	NDUFA3	NM_004542	+	-3195

chr20	36411330	36411491	162	102	12	41.18	LBP	NM_004139	+	-3193
chr10	74681536	74681799	264	89	13	13.53	MRPS16	NM_016065	-	-3191
chr11	72146452	72146610	159	77	40	6.21	STARD10	NM_006645	-	-3188
chr16	73706225	73706444	220	62	18	15.69	LDHD	NM_153486	-	-3185
chr10	104622189	104622383	195	138	9	14.28	AS3MT	NM_020682	+	-3184
chr19	41325784	41325934	151	57	10	13.18	CAPNS1	NM_001003962	+	-3177
chr1	202457363	202457778	416	146	18	12.18	PLEKHA6	NM_014935	-	-3174
chr16	30906747	30907205	459	209	32	7.39	HSD3B7	NM_025193	+	-3173
chr9	129925809	129925965	157	101	7	26.62	PTGES2	NM_025072	-	-3172
chr17	43273064	43273227	164	50	9	14.41	SCRN2	NM_138355	-	-3171
chr8	145233958	145234460	503	298	27	5.73	MAF1	NM_032272	+	-3168
chr7	100305874	100306052	179	103	8	14.64	TRIP6	NM_003302	+	-3167
chr8	145212455	145212672	218	147	13	8.54	GPAA1	NM_003801	+	-3161
chr16	1931241	1931395	155	46	9	11.35	SEPX1	NM_016332	-	-3161
chr20	42560816	42561437	622	258	31	6.83	SERINC3	NM_198941	-	-3160
chrX	153663132	153663319	188	135	8	24.4	MPP1	NM_002436	-	-3158
chr6	31347361	31347662	302	80	47	7.02	HLA-C	NM_002117	-	-3154
chr11	65244710	65244869	160	53	7	17.57	RNASEH2C	NM_032193	-	-3148
chr3	51995297	51995748	452	62	46	8.82	ACY1	NM_000666	+	-3146
chr8	145702897	145703376	480	256	55	12.65	GPT	NM_005309	+	-3144
chr17	40583363	40583601	239	60	12	7.99	HEXIM1	NM_006460	+	-3135
chr3	50314469	50315457	989	219	64	5.79	HYAL1	NM_153286	-	-3133
chr19	40985729	40985864	136	76	6	17.02	PRODH2	NM_021232	-	-3133
chrX	55189197	55189392	196	84	9	20.09	FAM104B	NM_138362	-	-3133
chr1	201179537	201179707	171	68	8	14.64	ADIPOR1	NM_015999	-	-3132
chr4	3416350	3416648	299	62	26	10.57	HGFAC	NM_001528	+	-3125

chrX	56609732	56609918	187	111	6	16.89	UBQLN2	NM_013444	+	-3122
chr7	72648349	72648580	232	123	22	5.37	MLXIPL	NM_032951	-	-3121
chr1	8846445	8846770	326	212	50	5.64	ENO1	NM_001428	-	-3121
chr14	104309742	104309851	110	56	9	18.05	AKT1	NM_005163	-	-3118
chr21	44576202	44576371	170	99	8	12.44	C21orf2	NM_004928	-	-3117
chr17	31337703	31337912	210	106	23	8.61	CCL14	NM_032963	-	-3108
chr10	3172863	3173025	163	109	9	14.32	PITRM1	NM_014889	-	-3106
chr5	10333322	10333812	491	297	65	7.84	CMBL	NM_138809	-	-3105
chr10	22088013	22088587	575	131	25	7.22	DNAJC1	NM_022365	-	-3104
chr7	47284185	47284377	193	59	10	13.62	TNS3	NM_022748	-	-3100
chr12	45040706	45041336	631	523	80	7.78	SLC38A2	NM_018976	-	-3098
chr3	51683305	51683424	120	61	8	14.06	TEX264	NM_015926	+	-3095
chr4	100263747	100266948	3202	3114	588	11.02	ADH4	NM_000670	-	-3092
chr19	5645756	5645936	181	57	12	16.47	LONP1	NM_004793	-	-3091
chr6	32657496	32657612	117	59	9	11.98	HLA-DRB1	NM_002124	-	-3086
chr11	111258292	111258559	268	136	10	24.4	C11orf1	NM_022761	+	-3085
chr9	122982950	122983320	371	219	20	8.69	RAB14	NM_016322	-	-3084
chr2	24869513	24869725	213	102	11	15.59	LOC391356	NM_001013663	-	-3084
chr12	56502584	56503059	476	365	20	5.81	CTDSP2	NM_005730	-	-3082
chr14	20010295	20010486	192	60	9	21.53	NP	NM_000270	+	-3082
chr1	159356921	159357595	675	504	41	5.93	NIT1	NM_005600	+	-3081
chr1	20177447	20177598	152	55	11	18.82	PLA2G2A	NM_000300	-	-3081
chr15	72831125	72831314	190	87	33	10.33	CYP1A2	NM_000761	+	-3078
chr19	40325194	40325308	115	58	19	10.66	FXYD1	NM_005031	+	-3077
chr6	31958393	31958591	199	99	9	17.48	EHMT2	NM_006709	-	-3074
chr7	44123692	44123883	192	114	13	10.98	POLD2	NM_006230	-	-3072

chr10	44818797	44818998	202	59	11	17.57	ZNF22	NM_006963	+	-3071
chr2	127895310	127895556	247	120	51	6.99	PROC	NM_000312	+	-3070
chr17	19495384	19495724	341	229	23	7.13	ALDH3A2	NM_001031806	+	-3069
chr19	15089723	15089854	132	78	9	13.53	ILVBL	NM_176826	-	-3068
chr10	105346706	105346842	137	79	6	15.25	SH3PXD2A	NM_014631	-	-3067
chr2	238150602	238150769	168	86	11	15.69	RAB17	NM_022449	-	-3066
chr22	49367121	49367317	197	148	8	14.42	CHKB	NM_005198	-	-3065
chr3	50366178	50366364	187	69	9	11.87	CYB561D2	NM_007022	+	-3064
chr5	52815009	52815414	406	273	31	9.51	FST	NM_006350	+	-3063
chr11	66925096	66925290	195	111	24	10.71	PPP1CA	NM_001008709	-	-3063
chr4	77301363	77301970	608	526	36	7.53	SCARB2	NM_005506	-	-3053
chrX	48643408	48643535	128	68	8	13.12	PQBP1	NM_001032384	+	-3053
chrX	23711672	23714273	2602	2373	585	6.49	SAT1	NM_002970	+	-3049
chr17	78289656	78289845	190	143	8	29.55	FN3K	NM_022158	+	-3049
chr1	22837928	22838751	824	718	130	6.77	C1QA	NM_015991	+	-3047
chr2	208812059	208812235	177	67	23	7.77	IDH1	NM_005896	-	-3037
chr3	149942157	149943312	1156	420	66	7.32	AGTR1	NM_032049	+	-3036
chr1	93392613	93393033	421	227	21	12.81	TMED5	NM_016040	-	-3035
chr1	1252727	1253038	312	118	16	10.98	MGC10334	NM_001029885	+	-3033
chr17	77632324	77632532	209	150	31	8.27	FASN	NM_004104	-	-3029
chr6	31432460	31432658	199	59	18	9.76	HLA-B	NM_005514	-	-3029
chr7	148333920	148334110	191	131	16	8.48	PDIA4	NM_004911	-	-3022
chr17	15878787	15879004	218	159	14	17.55	NCOR1	NM_006311	-	-3021
chr12	54408303	54408514	212	62	21	7.76	CD63	NM_001780	-	-3017
chr11	63844689	63845159	471	118	60	9.58	PRDX5	NM_012094	+	-3015
chr12	9114282	9114577	296	121	58	6.43	A2M	NM_000014	-	-3007

chr17	43406258	43406434	177	92	8	15.55	CDK5RAP3	NM_025197	+	-3007
chr14	69305975	69306592	618	468	50	5.85	SFRS5	NM_006925	+	-3006
chr7	94829906	94830125	220	139	20	10.25	PON3	NM_000940	-	-3004
chr7	128292693	128293136	444	283	21	11.7	ATP6V1F	NM_004231	+	-3003
chr1	67925930	67926468	539	277	40	6.41	GADD45A	NM_001924	+	-2998
chr1	109276490	109276647	158	97	7	14.08	CLCC1	NM_015127	-	-2995
chr11	811626	811895	270	172	16	6.92	PNPLA2	NM_020376	+	-2994
chr11	57078505	57078696	192	98	15	25.3	UBE2L6	NM_004223	-	-2992
chr19	12928672	12928961	290	51	16	7.43	GADD45GIP1	NM_052850	-	-2989
chr1	239730339	239730516	178	58	14	29.28	FH	NM_000143	-	-2989
chr17	71356228	71356360	133	77	9	15.58	WBP2	NM_012478	-	-2985
chr16	23385810	23386125	316	131	12	11.71	GGA2	NM_015044	-	-2981
chr8	96009244	96010355	1112	168	64	8.06	TP53INP1	NM_033285	-	-2979
chr10	104231745	104231954	210	151	9	10.46	ACTR1A	NM_005736	-	-2978
chr7	100587326	100587461	136	82	7	19.97	AP1S1	NM_001283	+	-2975
chr12	54363788	54364659	872	554	92	5.77	METTL7B	NM_152637	+	-2974
chr9	34639294	34639604	311	178	25	6.26	GALT	NM_000155	+	-2970
chr14	22600374	22600585	212	103	14	8.28	ACIN1	NM_014977	-	-2970
chr19	17200518	17201020	503	303	38	18.41	OCEL1	NM_024578	+	-2966
chrX	46825382	46825683	302	188	33	10.5	RGN	NM_004683	+	-2965
chr20	61844121	61844615	495	98	42	5.01	SLC2A4RG	NM_020062	+	-2961
chr11	111116612	111116775	164	55	8	10.46	PPP2R1B	NM_002716	-	-2961
chr6	133047144	133047380	237	162	24	5.45	VNN1	NM_004666	-	-2956
chr11	802757	802886	130	62	32	5.02	RPLP2	NM_001004	+	-2951
chr3	46516825	46517439	615	473	38	5.15	RTP3	NM_031440	+	-2951
chr16	56352436	56352582	147	94	7	12.2	KIFC3	NM_005550	-	-2951

chr2	27729894	27730132	239	116	10	14.64	SUPT7L	NM_014860	-	-2950
chr11	63512655	63512850	196	136	8	17.22	OTUB1	NM_017670	+	-2950
chr4	76789661	76789939	279	132	14	8.54	G3BP2	NM_012297	-	-2949
chr1	148815828	148816607	780	435	107	5.22	MCL1	NM_182763	-	-2947
chr11	14485764	14485940	177	99	8	12.96	PSMA1	NM_002786	-	-2942
chr6	31717510	31717735	226	101	13	9.76	BAT3	NM_004639	-	-2939
chr15	43443339	43443548	210	136	79	5.16	GATM	NM_001482	-	-2933
chr10	102276052	102276418	367	170	29	9.55	NDUFB8	NM_005004	-	-2931
chrX	152716090	152716216	127	61	20	8.83	SSR4	NM_006280	+	-2929
chr3	187920490	187920741	252	158	76	5.19	KNG1	NM_000893	+	-2928
chr17	18174594	18174845	252	70	31	12.12	SHMT1	NM_004169	-	-2926
chr12	2777152	2777338	187	135	9	22.52	FKBP4	NM_002014	+	-2925
chr11	7466080	7466253	174	130	7	24.4	OLFML1	NM_198474	+	-2923
chr3	186391757	186394029	2273	487	325	6.83	EHHADH	NM_001966	-	-2922
chr16	87453803	87453925	123	62	13	23.41	TRAPPC2L	NM_016209	+	-2917
chr8	125634328	125635126	799	151	47	6.58	MTSS1	NM_014751	-	-2915
chr20	61447867	61448023	157	56	6	15.41	CHRNA4	NM_000744	-	-2915
chr3	49820099	49820551	453	139	17	17.69	UBE1L	NM_003335	-	-2909
chr19	11316910	11317365	456	146	76	6.95	UNQ501	NM_198536	-	-2908
chr14	21038899	21039026	128	49	7	17.57	METTTL3	NM_019852	-	-2904
chr19	60658772	60659068	297	158	27	5.8	ISOC2	NM_024710	-	-2901
chr19	53406049	53406225	177	60	7	14.64	CARD8	NM_014959	-	-2901
chr12	9195453	9195603	151	54	8	13.85	PZP	NM_002864	-	-2900
chr6	31744187	31744532	346	187	27	11.82	CSNK2B	NM_001320	+	-2897
chr12	68268214	68268370	157	55	6	18.3	CCT2	NM_006431	+	-2896
chr10	44187876	44188507	632	169	30	5.69	CXCL12	NM_000609	-	-2895

chr6	31608518	31608871	354	60	17	9.76	BAT1	NM_004640	-	-2895
chr17	40583042	40583353	312	112	18	6.85	HEXIM1	NM_006460	+	-2887
chr2	85622506	85622682	177	61	9	20.73	MAT2A	NM_005911	+	-2884
chr2	218839814	218839979	166	60	12	13.37	AAMP	NM_001087	-	-2883
chr9	35650992	35651191	200	140	14	14.64	CCDC107	NM_174923	+	-2881
chr14	68324760	68327005	2246	506	346	7.63	ZFP36L1	NM_004926	-	-2878
chr3	52299136	52299788	653	526	76	6.83	GLYCTK	NM_145262	+	-2877
chr8	145212186	145212387	202	60	13	16.73	GPAA1	NM_003801	+	-2876
chr22	28056363	28056545	183	110	8	13.07	AP1B1	NM_001127	-	-2875
chr10	102733746	102733995	250	129	14	9.55	MRPL43	NM_176793	-	-2872
chr8	68120551	68120737	187	138	9	19.17	COPS5	NM_006837	-	-2866
chr19	2688088	2688388	301	152	12	8.81	SLC39A3	NM_213568	-	-2864
chr19	3006641	3006769	129	61	18	11.85	AES	NM_001130	-	-2862
chr6	32518182	32518485	304	199	58	5.86	HLA-DRA	NM_019111	+	-2861
chr7	149701295	149702047	753	555	64	9.55	REPIN1	NM_014374	+	-2857
chr7	42941105	42941320	216	98	19	37.96	MRPL32	NM_031903	+	-2857
chr19	44570806	44570966	161	61	9	10.98	PAF1	NM_019088	-	-2855
chr1	115063718	115063913	196	88	23	8.61	CSDE1	NM_001007553	-	-2853
chr1	85820664	85821899	1236	1084	154	5.37	CYR61	NM_001554	+	-2852
chr3	172199534	172199682	149	60	27	12.86	SLC2A2	NM_000340	-	-2852
chr5	137116465	137117824	1360	126	92	7.99	HNRPA0	NM_006805	-	-2851
chrX	43513396	43513652	257	186	22	13.17	MAOB	NM_000898	-	-2851
chr11	67110351	67110711	361	298	26	5.95	GSTP1	NM_000852	+	-2850
chr14	77246923	77247033	111	56	8	13	C14orf156	NM_031210	+	-2846
chr1	158514935	158516069	1135	386	101	8.31	PEX19	NM_002857	-	-2844
chr11	58236696	58236978	283	224	45	7.91	GLYAT	NM_005838	-	-2840

chr16	28527146	28527251	106	54	9	13.97	SULT1A1	NM_177530	-	-2833
chr17	45618994	45619286	293	112	22	8.58	COL1A1	NM_000088	-	-2829
chr19	52976363	52976480	118	60	9	14.64	SEPW1	NM_003009	+	-2827
chr12	21844199	21844417	219	142	9	14.64	ABCC9	NM_020297	-	-2825
chr11	62313941	62314297	357	70	25	7.47	LOC374395	NM_199337	+	-2823
chr5	151023821	151024028	208	132	26	8.12	SPARC	NM_003118	-	-2822
chr5	176763443	176764564	1122	513	212	5.08	F12	NM_000505	-	-2818
chr11	63063536	63063673	138	88	6	18.3	RARRES3	NM_004585	+	-2818
chr7	23513565	23513743	179	46	7	13.94	TRA2A	NM_013293	-	-2817
chr19	2708267	2708525	259	109	10	18.3	SGTA	NM_003021	-	-2814
chr16	31039158	31039301	144	54	8	25.62	MYST1	NM_032188	+	-2814
chr7	150121919	150122136	218	139	55	5.23	TMEM176B	NM_014020	-	-2813
chr14	23846807	23847046	240	124	35	6.44	CIDEB	NM_014430	-	-2812
chr7	72648093	72648270	178	119	16	5.49	MLXIPL	NM_032951	-	-2811
chr16	28764142	28764422	281	61	27	9.99	TUFM	NM_003321	-	-2810
chr14	23677698	23678021	324	173	54	6.64	PSME1	NM_176783	+	-2804
chr5	133562660	133562851	192	104	14	9.84	PPP2CA	NM_002715	-	-2804
chr12	51978072	51978299	228	87	29	8.16	PFDN5	NM_002624	+	-2798
chr17	45802802	45803016	215	94	11	17.57	MRPL27	NM_148570	-	-2789
chr7	45920824	45921162	339	157	43	7.13	IGFBP3	NM_000598	-	-2788
chr1	159234555	159235393	839	95	52	6.91	F11R	NM_016946	-	-2786
chr9	19108299	19108544	246	62	53	5.01	ADFP	NM_001122	-	-2785
chr9	89533297	89533584	288	233	14	8.29	CTSL	NM_001912	+	-2785
chr11	118402860	118403058	199	122	15	8.93	SLC37A4	NM_001467	-	-2783
chr17	59261206	59261323	118	60	9	11.77	PSMC5	NM_002805	+	-2782
chr3	187816119	187816360	242	110	110	5.13	AHSG	NM_001622	+	-2780

chr4	3415813	3416294	482	137	50	9.62	HGFAC	NM_001528	+	-2771
chr10	4997969	4998222	254	177	28	12.75	AKR1C1	NM_001353	+	-2769
chr1	158454732	158454896	165	60	17	9.66	WDR42A	NM_015726	-	-2768
chr10	14602783	14603330	548	148	31	10.65	FAM107B	NM_031453	-	-2766
chr1	11905279	11905475	197	110	8	14.42	KIAA2013	NM_138346	-	-2764
chr8	145062944	145064068	1125	138	54	6.03	PLEC1	NM_201384	-	-2760
chr20	2795077	2795351	275	127	16	20.92	VPS16	NM_080414	+	-2759
chr16	56352148	56352388	241	187	13	10.59	KIFC3	NM_005550	-	-2757
chr1	16143587	16143704	118	60	6	30.29	ZBTB17	NM_003443	-	-2752
chr11	66924719	66924976	258	197	20	10.07	PPP1CA	NM_001008709	-	-2749
chrX	47371141	47371318	178	42	6	20.33	CFP	NM_002621	-	-2747
chr17	4797686	4797905	220	120	23	20.92	ENO3	NM_001976	+	-2747
chr1	158330225	158330507	283	173	12	11.65	IGSF8	NM_052868	-	-2746
chr2	120155728	120155969	242	62	10	17.57	TMEM177	NM_030577	+	-2745
chr3	53237337	53237454	118	60	6	16.89	TKT	NM_001064	-	-2742
chr5	177566682	177566854	173	45	9	12.66	HNRPAB	NM_004499	+	-2741
chr5	90702619	90703036	418	178	33	10.49	ARRDC3	NM_020801	-	-2739
chr20	44414116	44414323	208	116	8	12.18	SLC35C2	NM_015945	-	-2739
chr14	69314697	69315042	346	262	62	8.27	SLC10A1	NM_003049	-	-2738
chr6	31346807	31347243	437	275	42	8.1	HLA-C	NM_002117	-	-2735
chr17	2542040	2542163	124	60	10	10.29	KIAA0664	NM_015229	-	-2734
chr1	20853199	20853574	376	207	23	14.31	DDOST	NM_005216	-	-2728
chr22	29060085	29060699	615	556	31	6.3	SF3A1	NM_001005409	-	-2723
chr2	198062149	198062276	128	58	15	8.75	HSPD1	NM_002156	-	-2722
chr1	113047773	113047993	221	85	15	14.94	RHOC	NM_001042679	-	-2722
chr14	94099554	94100255	702	597	176	5.67	SERPINA4	NM_006215	+	-2720

chr4	74568791	74569038	248	135	29	7.26	AFM	NM_001133	+	-2713
chr4	170147739	170148029	291	130	13	9.94	CBR4	NM_032783	-	-2713
chr7	75796445	75796764	320	50	16	8.87	YWHAG	NM_012479	-	-2712
chr1	57169975	57170183	209	134	38	6.31	C8B	NM_000066	-	-2711
chr22	18245606	18245748	143	76	9	12.56	TXNRD2	NM_006440	-	-2709
chr6	31431821	31432337	517	198	42	7.96	HLA-B	NM_005514	-	-2708
chr17	7098749	7098982	234	60	13	7.99	C17orf81	NM_203413	+	-2708
chr1	3533893	3534120	228	108	12	10.01	FAM79A	NM_182752	+	-2705
chr1	39266957	39267293	337	177	38	9.32	NDUFS5	NM_004552	+	-2701
chr9	35049009	35049259	251	100	35	6.12	VCP	NM_007126	-	-2699
chr13	45527877	45528021	145	73	26	6.98	CPB2	NM_001872	-	-2698
chr16	671683	672813	1131	940	112	7.16	STUB1	NM_005861	+	-2698
chr19	3716146	3716363	218	90	17	7.18	MRPL54	NM_172251	+	-2692
chr16	54955315	54955554	240	60	17	9.37	AMFR	NM_001144	-	-2689
chr16	88156934	88157316	383	238	51	5.33	RPL13	NM_033251	+	-2685
chr1	144126624	144127319	696	415	39	5.76	HFE2	NM_213653	+	-2685
chr19	17377080	17377439	360	273	53	8.66	BST2	NM_004335	-	-2684
chr11	59163308	59163451	144	60	7	14.64	FLJ36874	NM_152716	-	-2682
chr2	204008709	204009464	756	414	44	9.25	RAPH1	NM_213589	-	-2679
chr1	156069590	156070008	419	202	28	10.22	CD5L	NM_005894	-	-2679
chr22	23267612	23269086	1475	227	103	7.2	C22orf13	NM_031444	-	-2677
chr12	56137754	56138039	286	119	24	14.66	INHBE	NM_031479	+	-2677
chr1	158528157	158528360	204	145	14	15.97	COPA	NM_004371	-	-2675
chr12	7139640	7140965	1326	1014	110	5.03	C1RL	NM_016546	-	-2674
chr3	185523286	185523467	182	80	17	11.09	EIF4G1	NM_004953	+	-2673
chr16	87453545	87453679	135	76	9	15.81	TRAPPC2L	NM_016209	+	-2671

chr1	120094813	120095191	379	185	111	5.91	HMGCS2	NM_005518	-	-2664
chr19	6325804	6326104	301	137	18	8.81	ALKBH7	NM_032306	+	-2661
chr7	1161601	1161729	129	61	8	13.22	ZFAND2A	NM_182491	-	-2660
chr11	59100847	59101104	258	86	15	8.37	OSBP	NM_002556	-	-2658
chr3	49431699	49431873	175	59	9	12.73	AMT	NM_000481	-	-2658
chr10	81907363	81907517	155	91	15	22.69	ANXA11	NM_001157	-	-2658
chr11	47239601	47239964	364	181	15	19.1	NR1H3	NM_005693	+	-2656
chr8	144730522	144730753	232	101	17	9.69	NAPRT1	NM_145201	-	-2655
chr2	27729484	27729833	350	192	15	8.54	SUPT7L	NM_014860	-	-2651
chr1	232808623	232809289	667	428	50	6.71	IRF2BP2	NM_001077397	-	-2650
chr10	96788650	96789168	519	88	107	9.72	CYP2C8	NM_000770	-	-2649
chr1	153548576	153548849	274	160	16	27.7	FDPS	NM_002004	+	-2649
chr6	34324627	34324783	157	62	7	24.4	C6orf1	NM_001008703	-	-2648
chr6	34665116	34665690	575	217	36	6.27	C6orf106	NM_022758	-	-2641
chr7	94829550	94829760	211	143	41	6.18	PON3	NM_000940	-	-2639
chr1	67942077	67942373	297	46	12	9.89	GNG12	NM_018841	-	-2637
chr16	78188139	78188368	230	118	10	11.44	MAF	NM_005360	-	-2637
chr10	94442050	94442316	267	178	18	21.43	HHEX	NM_002729	+	-2637
chr1	149605709	149606040	332	209	42	6.25	SELENBP1	NM_003944	-	-2636
chr1	205331591	205331885	295	115	52	8.33	C4BPB	NM_001017367	+	-2635
chr11	56825854	56826309	456	61	27	6.68	TNKS1BP1	NM_033396	-	-2630
chr9	85468611	85468794	184	130	10	14.64	UBQLN1	NM_053067	-	-2628
chr10	96689878	96691056	1179	507	143	5.86	CYP2C9	NM_000771	+	-2627
chr17	77631849	77632129	281	61	35	6.58	FASN	NM_004104	-	-2626
chr22	28495661	28495980	320	148	46	6.02	UCRC	NM_001003684	+	-2623
chr12	122032938	122033454	517	420	66	6.36	ARL6IP4	NM_001002252	+	-2622

chr1	26519249	26519615	367	311	21	12.54	CD52	NM_001803	+	-2618
chr17	7065929	7066493	565	122	112	8.27	ACADVL	NM_000018	+	-2617
chr20	339103	339370	268	168	18	6.87	RBCK1	NM_006462	+	-2615
chr19	10324598	10324817	220	164	9	12.88	TYK2	NM_003331	-	-2609
chr12	202561	202659	99	50	6	25.84	SLC6A13	NM_016615	-	-2608
chr21	44380359	44380527	169	110	12	12.37	C21orf33	NM_004649	+	-2604
chr2	224532664	224532977	314	210	13	11.49	MRPL44	NM_022915	+	-2600
chr11	116199028	116199227	200	140	10	14.23	APOA4	NM_000482	-	-2600
chr2	27209499	27209729	231	86	13	7.89	PREB	NM_013388	-	-2599
chr8	145138376	145138802	427	314	56	6.83	GRINA	NM_000837	+	-2589
chr17	37810050	37810588	539	417	25	7.32	PTRF	NM_012232	-	-2588
chr19	16492173	16492293	121	61	8	13.01	CHERP	NM_006387	-	-2588
chrX	152621473	152621730	258	152	13	11.33	BCAP31	NM_005745	-	-2584
chr20	61839966	61841017	1052	599	139	6.76	LIME1	NM_017806	+	-2579
chr9	122982325	122982814	490	278	29	7.17	RAB14	NM_016322	-	-2578
chr2	218845528	218845934	407	71	30	10.73	PNKD	NM_001077399	+	-2576
chr15	20509641	20509769	129	70	6	18.3	CYFIP1	NM_001033028	+	-2574
chr10	33508488	33509004	517	112	22	5.63	NRP1	NM_003873	-	-2570
chr3	49110405	49110938	534	128	42	9.12	QARS	NM_005051	-	-2569
chr9	34638672	34639203	532	191	33	10.33	GALT	NM_000155	+	-2569
chr11	33683390	33683699	310	146	17	9.09	CD59	NM_000611	-	-2566
chr5	32827041	32827262	222	102	9	9.76	C5orf23	NM_024563	+	-2561
chr16	45403	45577	175	116	8	17.94	C16orf33	NM_024571	+	-2561
chr12	55023892	55024210	319	55	22	7.47	STAT2	NM_005419	-	-2560
chr3	129823672	129824060	389	213	54	6.76	RPN1	NM_002950	-	-2558
chr14	34250983	34251957	975	421	64	7.56	CFL2	NM_021914	-	-2557

chr6	32023405	32024307	903	806	238	5.07	CFB	NM_001710	+	-2556
chr8	64092594	64092746	153	94	17	9.71	GGH	NM_003878	-	-2550
chr13	20967279	20967389	111	56	7	39.42	EFHA1	NM_152726	-	-2550
chr17	71451095	71451736	642	244	53	7	ACOX1	NM_004035	-	-2548
chr4	83565604	83565916	313	204	15	13.31	HNRPD1	NM_031372	-	-2546
chr17	72226181	72226549	369	137	13	10.81	PTDSR	NM_015167	-	-2545
chr10	123708984	123709141	158	58	10	10.98	C10orf86	NM_017615	-	-2543
chr17	4121627	4121804	178	96	12	11.71	UBE2G1	NM_003342	-	-2542
chr4	39503153	39503420	268	155	12	21.96	SCC-112	NM_015200	-	-2542
chr1	224176539	224176744	206	147	8	10.1	PYCR2	NM_013328	-	-2541
chr8	9035053	9035452	400	298	28	10.85	PPP1R3B	NM_024607	-	-2537
chr17	2541813	2541964	152	99	12	9.41	KIAA0664	NM_015229	-	-2535
chr6	109796301	109796945	645	560	42	5.31	CD164	NM_006016	-	-2530
chr12	102850740	102850847	108	55	11	17.39	HSP90B1	NM_003299	+	-2529
chrX	38550074	38550544	471	185	22	11.03	MID1IP1	NM_021242	+	-2528
chr11	71393914	71394086	173	83	9	14.17	NUMA1	NM_006185	-	-2528
chr12	6632069	6632232	164	62	8	10.46	ING4	NM_016162	-	-2526
chr3	151744408	151744995	588	525	56	14.35	SERP1	NM_014445	-	-2525
chr19	12865283	12865497	215	161	16	10.49	GCDH	NM_000159	+	-2524
chr17	70827979	70828275	297	59	18	7.99	GRB2	NM_203506	-	-2523
chr17	40582285	40582987	703	573	34	9.76	HEXIM1	NM_006460	+	-2521
chr5	112242070	112242491	422	297	37	6.18	REEP5	NM_005669	-	-2512
chr18	49985367	49985553	187	127	8	35.46	MBD2	NM_015832	-	-2509
chr2	198061902	198062062	161	110	17	8.25	HSPD1	NM_002156	-	-2508
chr15	72830569	72830742	174	85	43	5.49	CYP1A2	NM_000761	+	-2506
chr16	57300708	57301041	334	217	37	7.34	GOT2	NM_002080	-	-2506

chr11	113673773	113674247	475	194	90	7.2	NNMT	NM_006169	+	-2503
chr19	34883932	34884137	206	148	10	8.13	C19orf12	NM_001031726	-	-2503
chr19	15886586	15886681	96	49	6	16.89	CYP4F11	NM_021187	-	-2500
chr22	17545232	17545591	360	86	30	7.25	SLC25A1	NM_005984	-	-2497
chr12	119386108	119386350	243	119	15	13.42	SFRS9	NM_003769	-	-2497
chr11	59163121	59163264	144	56	8	14.76	FLJ36874	NM_152716	-	-2495
chr6	43038764	43038971	208	103	44	8.03	GNMT	NM_018960	+	-2494
chr16	1989979	1990262	284	61	12	24.4	ZNF598	NM_178167	-	-2494
chr17	59926166	59928692	2527	666	361	5	DDX5	NM_004396	-	-2491
chr4	1689702	1689968	267	136	10	12.55	TMEM129	NM_138385	-	-2491
chr22	40329249	40329367	119	60	9	32.94	D15Wsu75e	NM_015704	-	-2486
chr19	1195062	1195228	167	109	26	5.81	ATP5D	NM_001001975	+	-2480
chr12	91063291	91063505	215	69	21	9.67	BTG1	NM_001731	-	-2472
chr19	63703383	63703988	606	450	117	7.55	SLC27A5	NM_012254	-	-2471
chr19	5847896	5848151	256	87	26	11.78	NDUFA11	NM_175614	-	-2466
chr8	81112011	81112126	116	59	6	16.89	TPD52	NM_001025252	-	-2465
chr4	74827285	74827602	318	153	18	9.01	IL8	NM_000584	+	-2464
chr1	27112466	27113028	563	465	30	8.24	NR0B2	NM_021969	-	-2463
chr19	54069521	54069951	431	147	20	7.36	PPP1R15A	NM_014330	+	-2462
chr3	157743363	157743700	338	60	13	8.25	SSR3	NM_007107	-	-2462
chr16	87405719	87405840	122	62	8	14.29	APRT	NM_000485	-	-2461
chr10	90965658	90965771	114	58	7	15.53	LIPA	NM_000235	-	-2460
chr15	63044691	63044869	179	61	16	9.61	SPG21	NM_016630	-	-2453
chr13	49135184	49135316	133	72	9	15.58	EBPL	NM_032565	-	-2453
chr6	43131989	43132196	208	151	13	13.7	MRPL2	NM_015950	-	-2452
chr12	48786314	48786518	205	100	28	6.75	GPD1	NM_005276	+	-2451

chr1	28804460	28804648	189	53	7	16.64	TAF12	NM_005644	-	-2449
chr17	77093850	77094039	190	129	28	6.35	ACTG1	NM_001614	-	-2446
chr17	72243811	72244237	427	141	31	5.12	SFRS2	NM_003016	-	-2444
chr22	40807855	40808088	234	113	16	18.84	C22orf32	NM_033318	+	-2444
chr11	66374702	66375014	313	59	23	7.32	PC	NM_022172	-	-2442
chr15	61234801	61235027	227	143	18	7.98	RPS27L	NM_015920	-	-2435
chr19	4296724	4297010	287	59	17	9.8	FLJ14981	NM_032868	+	-2435
chr14	23677380	23677651	272	196	30	7.32	PSME1	NM_176783	+	-2434
chr7	148333150	148333519	370	127	51	8.33	PDIA4	NM_004911	-	-2431
chr6	11293729	11293949	221	101	11	11.71	NEDD9	NM_006403	-	-2430
chr11	67110131	67110289	159	61	14	6.21	GSTP1	NM_000852	+	-2428
chr16	8856271	8856726	456	192	50	5.56	CARHSP1	NM_001042476	-	-2424
chr19	1550392	1550593	202	127	46	7.53	UQCR	NM_006830	-	-2420
chr20	61843643	61844072	430	360	41	5.93	SLC2A4RG	NM_020062	+	-2418
chr14	23846345	23846651	307	196	41	6.92	CIDEB	NM_014430	-	-2417
chr9	139257755	139257947	193	60	17	7.77	TUBB2C	NM_006088	+	-2416
chr5	14764241	14764433	193	111	12	9.89	ANKH	NM_054027	-	-2415
chr17	77457611	77457797	187	61	11	11.56	PCYT2	NM_002861	-	-2414
chr19	4398451	4398667	217	136	13	8.47	UBXD1	NM_025241	-	-2407
chr6	99957086	99957328	243	127	15	15.32	C6orf111	NM_032870	-	-2405
chr3	127307236	127307501	266	129	86	5.84	ALDH1L1	NM_012190	-	-2404
chr21	44020506	44020663	158	62	13	20.82	CSTB	NM_000100	-	-2404
chr9	123104076	123104301	226	86	8	21.69	GSN	NM_000177	+	-2402
chr1	153255615	153255947	333	218	19	13.01	ZBTB7B	NM_015872	+	-2400
chrX	76970746	76970919	174	62	7	17.57	KFZp564K14	NM_032121	-	-2400
chr3	49431437	49431614	178	60	11	7.82	AMT	NM_000481	-	-2399

chr10	80779406	80779623	218	82	10	11.12	PPIF	NM_005729	+	-2398
chr2	177805366	177805678	313	102	20	7.75	NFE2L2	NM_006164	-	-2394
chr8	145223886	145224377	492	108	63	7.32	CYC1	NM_001916	+	-2391
chr6	32918714	32918865	152	101	10	11.65	PSMB8	NM_148919	-	-2389
chr4	185915953	185916130	178	62	31	5.35	ACSL1	NM_001995	-	-2387
chr17	39639901	39640312	412	336	23	18.1	UBTF	NM_014233	-	-2385
chr12	105158072	105158303	232	174	12	15.07	CKAP4	NM_006825	-	-2382
chr6	139737284	139737472	189	55	13	13.73	CITED2	NM_006079	-	-2381
chr5	177566238	177566490	253	122	10	17.57	HNRPAB	NM_004499	+	-2377
chr6	7234855	7235177	323	159	16	11.03	SSR1	NM_003144	-	-2375
chr10	43201953	43203444	1492	823	147	5.29	HNRPF	NM_004966	-	-2374
chr1	8845865	8846022	158	62	32	6.25	ENO1	NM_001428	-	-2373
chr6	31893363	31893686	324	254	42	5.04	HSPA1A	NM_005345	+	-2371
chr18	41920338	41920478	141	62	26	6.19	ATP5A1	NM_004046	-	-2371
chr4	57594096	57594373	278	88	53	6.27	IGFBP7	NM_001553	-	-2371
chr17	17954833	17955112	280	182	16	8.2	MYO15A	NM_016239	+	-2368
chr4	39134411	39134507	97	49	9	12.78	RPL9	NM_001024921	-	-2366
chr5	172127757	172130069	2313	1502	536	6.64	DUSP1	NM_004417	-	-2363
chr19	59388902	59389272	371	193	20	8.15	TSEN34	NM_001077446	+	-2357
chr22	40854701	40854800	100	51	19	6.95	CYP2D6	NM_000106	-	-2354
chr12	108498210	108498352	143	52	9	16.75	MVK	NM_000431	+	-2353
chr12	101758244	101758586	343	158	67	7.13	PAH	NM_000277	-	-2352
chr6	31733710	31734000	291	173	57	6.39	APOM	NM_019101	+	-2351
chr12	21851525	21851725	201	115	10	17.66	ABCC9	NM_020298	-	-2351
chr1	158527735	158528034	300	135	15	11.98	COPA	NM_004371	-	-2349
chr8	59567496	59567637	142	60	8	24.4	CYP7A1	NM_000780	-	-2346

chr7	149668411	149668694	284	222	101	5.35	RARRES2	NM_002889	-	-2343
chr1	11029522	11029785	264	172	39	5.48	MASP2	NM_139208	-	-2343
chr1	157950751	157951044	294	200	38	6.77	CRP	NM_000567	-	-2341
chr9	89532987	89533139	153	73	19	7.17	CTSL	NM_001912	+	-2340
chr8	103909906	103910051	146	89	9	11.71	AZIN1	NM_015878	-	-2339
chr11	73365521	73365700	180	67	9	19.97	UCP2	NM_003355	-	-2337
chr9	135218181	135220497	2317	307	336	7.7	SURF4	NM_033161	-	-2336
chr5	180598640	180598869	230	101	33	8.98	GNB2L1	NM_006098	-	-2336
chr17	4648538	4648747	210	137	37	8.35	PSMB6	NM_002798	+	-2333
chrX	47370701	47370902	202	138	8	11.83	CFP	NM_002621	-	-2331
chr17	17658286	17658439	154	54	13	10.46	SREBF1	NM_001005291	-	-2329
chr6	119543164	119543295	132	72	12	10.63	MAN1A1	NM_005907	-	-2328
chr19	12911842	12912746	905	770	258	6.4	CALR	NM_004343	+	-2324
chr21	46383204	46383442	239	57	28	8.31	FTCD	NM_206965	-	-2321
chr14	93589088	93589342	255	111	13	8.71	DDX24	NM_020414	-	-2321
chr10	88720201	88720486	286	179	31	5.76	C10orf116	NM_006829	+	-2319
chr17	2541604	2541747	144	88	11	10.54	KIAA0664	NM_015229	-	-2318
chr17	71588700	71589220	521	130	31	7.63	LGICZ1	NM_180990	+	-2317
chr19	40984820	40985047	228	166	21	15.86	PRODH2	NM_021232	-	-2316
chr2	8740823	8741875	1053	498	85	6.27	ID2	NM_002166	+	-2312
chr11	1732689	1732870	182	90	41	6.3	CTSD	NM_001909	-	-2310
chr11	27345792	27346394	603	208	37	5.27	LGR4	NM_018490	-	-2309
chr11	75108640	75108885	246	201	15	8.4	MOGAT2	NM_025098	+	-2304
chr13	30610917	30611068	152	114	8	11.13	HSPH1	NM_006644	-	-2304
chr19	19238313	19238475	163	100	10	18.3	TM6SF2	NM_001001524	-	-2302
chr7	95051894	95053049	1156	243	100	5.12	PDK4	NM_002612	-	-2301

chrX	48267043	48267496	454	316	68	5.54	EBP	NM_006579	+	-2296
chr3	52412193	52412362	170	60	9	9.76	BAP1	NM_004656	-	-2296
chr3	52716722	52717191	470	61	48	7.45	SPCS1	NM_014041	+	-2295
chr6	30144954	30145201	248	131	11	12.55	PPP1R11	NM_021959	+	-2291
chr17	77611033	77611330	298	155	20	14.18	DUS1L	NM_022156	-	-2290
chr19	47154719	47154964	246	168	18	7.2	RABAC1	NM_006423	-	-2287
chr19	6332686	6332862	177	62	8	29.55	GTF2F1	NM_002096	-	-2282
chr1	154980560	154980806	247	160	43	5.92	HDGF	NM_004494	-	-2281
chr12	55042766	55042902	137	57	16	6.02	APOF	NM_001638	-	-2281
chr9	103162554	103165161	2608	2091	593	6.11	BAAT	NM_001701	-	-2272
chr6	33278648	33278848	201	57	20	7.65	SLC39A7	NM_006979	+	-2268
chr13	29238535	29238811	277	105	12	14.19	UBL3	NM_007106	-	-2268
chr12	55394633	55394753	121	61	16	7.09	NACA	NM_005594	-	-2267
chr17	1594902	1595146	245	173	30	8.8	SERPINF2	NM_000934	+	-2267
chr5	140007229	140007408	180	121	25	5.27	NDUFA2	NM_002488	-	-2266
chr4	101090357	101090529	173	61	9	17.73	H2AFZ	NM_002106	-	-2263
chr20	41521836	41522192	357	301	14	12.5	SFRS6	NM_006275	+	-2261
chr1	43625057	43625243	187	92	8	13.69	MED8	NM_001001653	-	-2259
chr1	154547344	154547632	289	74	26	5.64	CCT3	NM_001008800	-	-2257
chr8	124096659	124097022	364	103	25	5.33	DERL1	NM_024295	-	-2254
chr8	81111702	81111915	214	154	9	14.64	TPD52	NM_001025252	-	-2254
chr5	140679697	140680494	798	140	33	8.13	TAF7	NM_005642	-	-2253
chr12	45038621	45040490	1870	675	426	5.17	SLC38A2	NM_018976	-	-2252
chr2	105322519	105322696	178	122	6	18.89	C2orf49	NM_024093	+	-2252
chr22	23283604	23283868	265	95	19	8.73	SNRPD3	NM_004175	+	-2251
chr4	186744881	186745840	960	158	50	9.09	SORBS2	NM_003603	-	-2248

chr1	144151628	144152183	556	433	59	5.04	TXNIP	NM_006472	+	-2245
chr10	85891189	85891408	220	114	29	6.9	GHITM	NM_014394	+	-2244
chr12	94920848	94920983	136	79	12	9.96	LTA4H	NM_000895	-	-2242
chr11	65445382	65445544	163	103	10	16.71	DRAP1	NM_006442	+	-2241
chr14	23655953	23656099	147	92	8	15.07	WDR23	NM_025230	+	-2239
chr20	2976357	2976911	555	342	51	6.38	MRPS26	NM_030811	+	-2237
chr12	55911747	55912054	308	113	24	12.39	SHMT2	NM_005412	+	-2236
chr4	89867588	89868363	776	610	49	7.32	FAM13A1	NM_001015045	-	-2235
chr1	89347937	89348131	195	65	9	15.69	GBP2	NM_004120	-	-2234
chr2	175751116	175751468	353	225	52	6.99	ATP5G3	NM_001002258	-	-2232
chrX	105165735	105166079	345	268	52	5.37	SERPINA7	NM_000354	-	-2227
chr20	2588900	2589269	370	316	22	12.64	IDH3B	NM_174855	-	-2227
chr2	97630876	97631176	301	165	33	6.37	COX5B	NM_001862	+	-2224
chr16	1951453	1951753	301	108	33	11.11	NDUFB10	NM_004548	+	-2221
chr19	45018948	45019158	211	153	14	20.08	FBL	NM_001436	-	-2221
chr16	29727387	29727572	186	79	15	11.44	MAZ	NM_001042539	+	-2217
chr3	130372553	130373337	785	151	81	5.59	CNBP	NM_003418	-	-2215
chr17	53923573	53924111	539	151	24	5.86	MTMR4	NM_004687	-	-2215
chr11	68280147	68280880	734	61	70	5.61	CPT1A	NM_001031847	-	-2214
chr6	136621589	136621896	308	186	16	7.32	BCLAF1	NM_014739	-	-2203
chrX	70360247	70362001	1755	1437	442	5.41	GJB1	NM_000166	+	-2201
chr17	16188564	16188774	211	132	8	18.54	PRR6	NM_181716	-	-2201
chr1	204833577	204833800	224	142	14	29.52	LGTM	NM_006893	-	-2201
chr4	3415540	3415723	184	54	16	8.08	HGFAC	NM_001528	+	-2200
chr10	113899620	113901809	2190	389	372	6.1	GPAM	NM_020918	-	-2198
chr1	152822836	152823356	521	112	31	6.89	ADAR	NM_001111	-	-2198

chr16	23385100	23385338	239	123	8	14	GGA2	NM_015044	-	-2194
chr6	133087413	133087813	401	296	16	13.7	VNN3	NM_018399	-	-2192
chr3	127684879	127685004	126	73	9	14.64	UROC1	NM_144639	-	-2191
chr17	7425452	7425716	265	207	32	14.64	CD68	NM_001040059	+	-2187
chr9	111043596	111044020	425	270	20	7.47	EPB41L4B	NM_018424	-	-2186
chr9	127038944	127039137	194	120	38	7.81	HSPA5	NM_005347	-	-2183
chr8	145621864	145621988	125	67	13	10.98	VPS28	NM_016208	-	-2181
chr14	69305586	69305766	181	123	18	9.01	SFRS5	NM_006925	+	-2180
chr3	49135143	49135730	588	148	34	6.16	LAMB2	NM_002292	-	-2179
chr2	229598613	229599111	499	57	25	10.25	FLJ20701	NM_017933	-	-2178
chr19	54010090	54010260	171	93	12	10.01	DHRS10	NM_016246	-	-2175
chr19	40453701	40453910	210	150	12	15.09	USF2	NM_003367	+	-2175
chr16	20330273	20330531	259	205	17	17.08	FLJ20581	NM_017888	+	-2175
chr11	69166979	69167226	248	59	13	10.89	CCND1	NM_053056	+	-2173
chr8	105462212	105462999	788	446	84	12.65	DPYS	NM_001385	-	-2171
chr20	43388478	43389514	1037	798	162	7.12	SDC4	NM_002999	-	-2170
chr9	7788374	7788661	288	122	11	10.54	C9orf123	NM_033428	-	-2169
chr4	75183676	75183785	110	56	11	12.58	CXCL2	NM_002089	-	-2166
chrX	101025888	101026082	195	139	8	18.3	ZMAT1	NM_032441	-	-2164
chr13	109205966	109206347	382	258	18	11.05	IRS2	NM_003749	-	-2163
chr19	1222323	1222506	184	61	20	7.63	CIRBP	NM_001280	+	-2160
chr1	94412237	94412640	404	345	19	8.87	ARHGAP29	NM_004815	-	-2159
chr18	41920044	41920264	221	144	33	6.18	ATP5A1	NM_004046	-	-2157
chr8	145180109	145180309	201	142	12	8.83	OPLAH	NM_017570	-	-2154
chr16	65820386	65820696	311	252	24	6.5	HSPC171	NM_014187	+	-2153
chr2	20264043	20266192	2150	62	441	5.31	SDC1	NM_002997	-	-2152

chrX	149687015	149687619	605	321	25	13.85	CD99L2	NM_031462	-	-2152
chr10	74680416	74680759	344	172	18	7.05	MRPS16	NM_016065	-	-2151
chrX	51654913	51655585	673	522	36	7.66	MAGED1	NM_001005333	+	-2148
chr19	60658063	60658310	248	169	17	13.31	ISOC2	NM_024710	-	-2143
chr2	84506045	84506307	263	157	31	16.37	SUCLG1	NM_003849	-	-2143
chr2	216517728	216517914	187	131	8	34.16	MREG	NM_018000	-	-2142
chr1	1143993	1144291	299	173	22	10.46	SDF4	NM_016176	-	-2140
chr12	54840036	54840505	470	105	93	6.72	MYL6	NM_021019	+	-2139
chr11	60888297	60888569	273	221	12	23.98	TMEM138	NM_016464	+	-2138
chr9	135210408	135210622	215	159	11	18.3	SURF1	NM_003172	-	-2136
chr4	89232446	89232575	130	66	9	25.62	ABCG2	NM_004827	-	-2135
chr22	22439964	22440151	188	127	23	7.47	C22orf16	NM_213720	-	-2130
chr19	2428405	2429262	858	506	111	7.36	GADD45B	NM_015675	+	-2128
chr1	101476972	101477170	199	126	8	11.65	EDG1	NM_001400	+	-2128
chr1	228906539	228907015	477	85	121	6.37	AGT	NM_000029	-	-2124
chr20	44621734	44621993	260	161	12	14.64	SLC13A3	NM_022829	-	-2124
chr19	2222359	2222642	284	148	31	10.3	OAZ1	NM_004152	+	-2123
chr21	46435445	46435589	145	59	8	12.81	LSS	NM_002340	-	-2121
chr5	176953744	176953933	190	86	20	7.65	TMED9	NM_017510	+	-2115
chr17	77396285	77396438	154	65	46	5.04	P4HB	NM_000918	-	-2113
chr20	42559814	42560384	571	217	33	5.32	SERINC3	NM_198941	-	-2107
chrX	153262756	153263086	331	277	19	9.69	EMD	NM_000117	+	-2106
chr22	39552461	39552652	192	144	13	11.24	ST13	NM_003932	-	-2106
chr17	37969502	37969723	222	62	11	17.08	COASY	NM_001042529	+	-2106
chr11	94441533	94441808	276	172	12	13.56	SFRS2B	NM_032102	+	-2105
chr7	149700785	149701293	509	325	30	7.32	REPIN1	NM_014374	+	-2103

chr6	32918400	32918579	180	119	10	12.5	PSMB8	NM_148919	-	-2103
chr17	71285939	71286212	274	159	22	7.35	H3F3B	NM_005324	-	-2101
chr22	37209331	37211490	2160	377	305	5.65	DDX17	NM_030881	-	-2100
chrX	54854122	54854315	194	102	8	14.2	MAGED2	NM_201222	+	-2098
chr4	155745390	155747275	1886	226	507	6.45	FGG	NM_021870	-	-2097
chr9	129670367	129670585	219	113	9	10.46	AK1	NM_000476	-	-2096
chr9	139257226	139257622	397	354	24	5.09	TUBB2C	NM_006088	+	-2091
chr15	88179328	88179880	553	428	28	14.57	AP3S2	NM_005829	-	-2088
chr3	52805455	52805940	486	414	48	6.37	ITIH3	NM_002217	+	-2087
chr12	45446136	45446895	760	287	143	5.45	SLC38A4	NM_018018	-	-2085
chr1	166155817	166156014	198	70	26	5.15	BRP44	NM_015415	-	-2080
chrX	2864769	2864930	162	59	23	8.54	ARSE	NM_000047	-	-2079
chr2	151033495	151035031	1537	283	146	5.01	RND3	NM_005168	-	-2077
chr16	31029028	31029325	298	248	16	9.85	BCKDK	NM_005881	+	-2077
chr4	15773798	15774093	296	215	19	13.01	FLJ90013	NM_153365	-	-2077
chr8	144729941	144730173	233	112	27	7.8	NAPRT1	NM_145201	-	-2075
chr22	20328180	20328613	434	240	24	7.26	SDF2L1	NM_022044	+	-2072
chr1	149206171	149206344	174	62	34	5.56	LASS2	NM_022075	-	-2071
chr11	759128	759291	164	111	6	18.3	PDDC1	NM_182612	-	-2068
chr3	191506156	191508263	2108	439	326	6.7	CLDN1	NM_021101	-	-2067
chr17	45815278	45815663	386	213	16	7.47	LRRC59	NM_018509	-	-2065
chr13	19660737	19661673	937	329	46	7.81	GJB2	NM_004004	-	-2065
chr22	40304756	40304922	167	57	7	29.28	PMM1	NM_002676	-	-2065
chr8	145137840	145138277	438	284	70	7.92	GRINA	NM_000837	+	-2064
chr3	195338500	195338691	192	56	8	13.07	HES1	NM_005524	+	-2064
chr9	129309266	129309498	233	87	11	10.9	C9orf88	NM_022833	-	-2059

chr11	59099651	59100499	849	238	54	8.29	OSBP	NM_002556	-	-2053
chr1	20852612	20852899	288	143	20	15.34	DDOST	NM_005216	-	-2053
chr4	122810469	122810647	179	129	9	14.64	ANXA5	NM_001154	-	-2050
chr19	10364739	10364856	118	60	9	18.82	CDC37	NM_007065	-	-2048
chr16	73704962	73705306	345	87	24	8.71	LDHD	NM_153486	-	-2047
chr5	178975713	178975832	120	61	12	16.89	HNRPH1	NM_005520	-	-2047
chr19	40433036	40433444	409	131	50	7.98	LSR	NM_015925	+	-2046
chrX	102728734	102729119	386	204	26	7.32	TCEAL4	NM_001006935	+	-2045
chr7	107999380	107999636	257	140	12	14.64	DNAJB9	NM_012328	+	-2045
chr2	20313736	20313975	240	187	11	8.32	PUM2	NM_015317	-	-2042
chr3	47868884	47869226	343	82	17	7.32	MAP4	NM_030884	-	-2037
chr5	140007005	140007176	172	101	25	6.48	NDUFA2	NM_002488	-	-2034
chr8	101604085	101604211	127	54	6	24.4	ANKRD46	NM_198401	-	-2034
chr17	7986295	7986546	252	91	15	17.34	PER1	NM_002616	-	-2032
chrY	19613590	19613943	354	77	14	8.13	CD24	NM_013230	-	-2030
chr4	77300471	77300945	475	329	34	7.67	SCARB2	NM_005506	-	-2028
chr12	56212247	56212387	141	48	8	14.45	DCTN2	NM_006400	-	-2027
chr10	73704630	73705705	1076	469	56	5.25	DDIT4	NM_019058	+	-2023
chr5	140874793	140876794	2002	62	181	6.28	DIAPH1	NM_005219	-	-2022
chr1	169328395	169328680	286	85	27	6.98	FMO3	NM_001002294	+	-2021
chr1	148813658	148815681	2024	299	396	7.23	MCL1	NM_182763	-	-2021
chr1	158453681	158454147	467	97	37	5.7	WDR42A	NM_015726	-	-2019
chr3	158349755	158350299	545	275	34	7.98	CCNL1	NM_020307	-	-2018
chr14	93842140	93842355	216	92	58	5.06	SERPINA6	NM_001756	-	-2017
chrX	38549557	38550033	477	132	21	6.66	MID1IP1	NM_021242	+	-2017
chr5	148188182	148188365	184	128	8	11.71	ADRB2	NM_000024	+	-2017

chr9	73489686	73490118	433	272	25	12.68	TMEM2	NM_013390	-	-2016
chr19	63549950	63550370	421	212	155	6.02	A1BG	NM_130786	-	-2015
chr17	4648218	4648422	205	100	25	6.86	PSMB6	NM_002798	+	-2008
chr2	219794066	219794354	289	118	13	8.46	ATG9A	NM_001077198	-	-2008
chr1	207946656	207946819	164	62	45	8	HSD11B1	NM_005525	+	-2006
chr17	43271792	43272061	270	212	13	6.59	SCRN2	NM_138355	-	-2005
chrX	152715058	152715290	233	59	29	14.5	SSR4	NM_006280	+	-2003
chr21	46382760	46383122	363	129	61	6.45	FTCD	NM_206965	-	-2001
chr7	47282064	47283277	1214	91	67	6.91	TNS3	NM_022748	-	-2000
chr6	166700169	166700397	229	175	20	8.38	BRP44L	NM_016098	-	-1998
chr16	70160094	70160250	157	74	21	7.57	TAT	NM_000353	-	-1996
chr2	27208951	27209124	174	87	13	7.64	PREB	NM_013388	-	-1994
chr16	1780380	1782415	2036	853	261	8.05	IGFALS	NM_004970	-	-1994
chr14	81009033	81009637	605	337	39	6.13	SEL1L	NM_005065	-	-1992
chr4	6694356	6695335	980	535	152	7.32	MRFAP1	NM_033296	+	-1990
chr19	8336813	8337000	188	99	8	11.01	ANGPTL4	NM_001039667	+	-1990
chr17	4583083	4583460	378	242	22	16.6	MED11	NM_001001683	+	-1989
chr7	26199631	26199977	347	140	44	11.2	HNRPA2B1	NM_002137	-	-1986
chr22	49312846	49313035	190	119	11	15.02	ECGF1	NM_001953	-	-1986
chr12	6310003	6310168	166	60	13	6.48	TNFRSF1A	NM_001065	-	-1984
chr4	186302922	186303373	452	130	18	13.24	SLC25A4	NM_001151	+	-1982
chr10	103535962	103536179	218	161	13	5.32	MGEA5	NM_012215	-	-1981
chr5	32161602	32162560	959	96	75	5.4	GOLPH3	NM_022130	-	-1980
chr7	40140388	40140847	460	132	29	10.98	C7orf11	NM_138701	-	-1980
chr19	7653112	7653742	631	514	55	6.16	TRAPPC5	NM_001042461	+	-1979
chr1	11029076	11029421	346	238	50	6.4	MASP2	NM_139208	-	-1979

chr3	39159837	39160327	491	223	31	6.59	AXUD1	NM_033027	-	-1977
chr11	66373961	66374549	589	141	54	7.05	PC	NM_022172	-	-1977
chr16	3011997	3012337	341	58	14	9.76	TNFRSF12A	NM_016639	+	-1977
chr22	38040656	38040807	152	72	41	5.65	RPL3	NM_000967	-	-1974
chr9	32447101	32447272	172	114	7	23.43	DDX58	NM_014314	-	-1972
chr12	6925174	6925432	259	81	31	5.31	C12orf57	NM_138425	+	-1969
chr20	17544094	17544290	197	64	16	10.1	RRBP1	NM_001042576	-	-1968
chr16	66421200	66421529	330	223	14	14.64	CENPT	NM_025082	-	-1967
chr1	33247734	33248137	404	265	17	11.83	AK2	NM_013411	-	-1965
chr3	51994412	51994561	150	77	19	8.24	ACY1	NM_000666	+	-1959
chr1	153184726	153185134	409	285	19	7.32	PBXIP1	NM_020524	-	-1955
chr19	18545417	18545567	151	101	13	7.37	UBA52	NM_001033930	+	-1954
chr17	43375674	43375869	196	58	8	17.98	PNPO	NM_018129	+	-1954
chr12	120161613	120161831	219	65	9	8.37	CAMKK2	NM_172226	-	-1952
chr19	55125733	55126217	485	131	138	5.94	ATF5	NM_012068	+	-1946
chr17	77631283	77631448	166	77	25	6.89	FASN	NM_004104	-	-1945
chr17	39511378	39511591	214	155	16	34.68	HDAC5	NM_001015053	-	-1945
chr4	110883076	110883244	169	88	34	5.36	CFI	NM_000204	-	-1944
chr16	1768434	1768657	224	59	11	9.35	SPSB3	NM_080861	-	-1943
chr19	53579284	53579579	296	115	30	8.05	KDELRL1	NM_006801	-	-1941
chr13	30610496	30610698	203	144	9	15.69	HSPH1	NM_006644	-	-1934
chr3	40327946	40328107	162	108	13	24.4	EIF1B	NM_005875	+	-1931
chr1	157948706	157950633	1928	111	501	6.19	CRP	NM_000567	-	-1930
chr3	151743257	151744400	1144	277	90	7.73	SERP1	NM_014445	-	-1930
chr19	5644566	5644774	209	105	12	7.44	LONP1	NM_004793	-	-1929
chr1	45252149	45252345	197	140	13	7.69	UROD	NM_000374	+	-1929

chr12	111830873	111831044	172	118	6	15.41	OAS1	NM_002534	+	-1923
chr1	152789158	152789591	434	374	27	7.41	UBE2Q1	NM_017582	-	-1917
chr9	130112974	130113133	160	59	6	22.88	TRUB2	NM_015679	-	-1917
chr19	1222123	1222260	138	62	15	7.93	CIRBP	NM_001280	+	-1914
chr8	8598828	8598989	162	44	6	14.64	CLDN23	NM_194284	+	-1914
chr6	43375320	43375885	566	89	96	5.39	SLC22A7	NM_006672	+	-1910
chr7	123110715	123111146	432	138	16	5.86	WASL	NM_003941	-	-1910
chr11	6591507	6592485	979	415	72	7.76	TPP1	NM_000391	-	-1910
chr19	15851571	15851743	173	53	11	8.87	CYP4F2	NM_001082	-	-1910
chr5	115169883	115170240	358	197	48	9.36	CDO1	NM_001801	-	-1910
chr15	49804276	49804463	188	51	9	13.76	LYSMD2	NM_153374	-	-1910
chr9	138807074	138807535	462	139	43	5.07	TMEM141	NM_032928	+	-1908
chr9	33102304	33102549	246	95	15	8.67	B4GALT1	NM_001497	-	-1908
chr1	119227077	119229095	2019	199	164	6.06	TBX15	NM_152380	-	-1907
chr4	157065924	157066626	703	150	36	5.49	CTSO	NM_001334	-	-1899
chr19	46042630	46043182	553	454	59	6.54	CYP2A6	NM_000762	-	-1899
chr17	6858180	6858585	406	308	77	5.7	MGC71993	NM_001004333	+	-1897
chr17	39639493	39639824	332	109	16	7.32	UBTF	NM_014233	-	-1897
chr17	29608042	29608305	264	136	13	11.39	CCL2	NM_002982	+	-1897
chr1	1311751	1312846	1096	740	91	6.44	CCNL2	NM_001039577	-	-1892
chr19	962368	962540	173	53	12	7.32	C19orf6	NM_001033026	-	-1891
chr12	30674906	30675078	173	101	7	14.64	IPO8	NM_006390	-	-1889
chr10	54196804	54197030	227	58	11	8.13	MBL2	NM_000242	-	-1884
chr17	7065468	7065760	293	188	51	9.92	ACADVL	NM_000018	+	-1884
chr1	27569895	27570072	178	111	19	9.56	FCN3	NM_003665	-	-1883
chr1	149640202	149640547	346	205	36	10.54	PSMB4	NM_002796	+	-1883

chr16	74159439	74159628	190	134	11	9.74	GABARAPL2	NM_007285	+	-1879
chr1	159356236	159356392	157	60	10	14.97	NIT1	NM_005600	+	-1878
chr1	159338457	159338845	389	80	16	15.19	PFDN2	NM_012394	-	-1875
chr3	132584747	132585271	525	116	25	15.37	NUDT16	NM_152395	+	-1875
chr5	43325734	43327128	1395	1021	147	5.84	HMGCS1	NM_002130	-	-1874
chr11	57266846	57267171	326	145	33	8.75	C11orf31	NM_170746	+	-1874
chr3	48613114	48613308	195	94	42	5	UQCRC1	NM_003365	-	-1873
chr19	18251563	18253443	1881	64	380	5.88	JUND	NM_005354	-	-1873
chr7	142672135	142672555	421	133	45	7.09	GSTK1	NM_015917	+	-1870
chr15	38845299	38845445	147	93	11	9.69	GCHFR	NM_005258	+	-1869
chr1	226362511	226362872	362	118	19	20.19	MRPL55	NM_181462	-	-1869
chr9	135206639	135206756	118	60	30	6.48	RPL7A	NM_000972	+	-1867
chr2	171558458	171558678	221	97	8	12.94	TLK1	NM_012290	-	-1863
chr18	2908299	2908852	554	431	38	6.37	LPIN2	NM_014646	-	-1860
chr10	73764254	73764453	200	69	8	22.88	DNAJB12	NM_001002762	-	-1860
chr3	128892099	128892459	361	50	21	8.54	MGLL	NM_007283	-	-1859
chr2	65168989	65169349	361	284	35	9.98	RAB1A	NM_004161	-	-1857
chr1	158329322	158329617	296	226	15	11.56	IGSF8	NM_052868	-	-1856
chr19	40453448	40453590	143	60	19	10.47	USF2	NM_003367	+	-1855
chr19	11548040	11548330	291	136	12	10.98	ACP5	NM_001611	-	-1854
chr3	149941799	149942129	331	41	13	8.37	AGTR1	NM_032049	+	-1853
chr1	159467504	159467933	430	87	29	6.3	NR1I3	NM_001077478	-	-1852
chr17	76840586	76841119	534	409	31	12.51	MGC15523	NM_138570	-	-1852
chr20	35580311	35581082	772	564	40	6.46	BLCAP	NM_006698	-	-1849
chr6	122807093	122808040	948	859	93	6.51	SERINC1	NM_020755	-	-1849
chr2	96215667	96216180	514	125	24	7.53	STARD7	NM_020151	-	-1849

chr2	20097459	20097742	284	159	29	10.4	LAPTM4A	NM_014713	-	-1849
chr12	47809554	47809680	127	54	6	14.64	K-ALPHA-1	NM_006082	-	-1848
chr6	7234420	7234649	230	73	10	10.46	SSR1	NM_003144	-	-1847
chr21	34810684	34812501	1818	106	387	6.22	DSCR1	NM_203418	-	-1846
chr1	85558134	85558602	469	243	24	6.83	DDAH1	NM_012137	-	-1846
chr14	69305245	69305431	187	62	23	6.26	SFRS5	NM_006925	+	-1845
chr20	4782603	4782842	240	161	12	7.79	SLC23A2	NM_005116	-	-1841
chr12	53260959	53261140	182	103	41	8.59	PPP1R1A	NM_006741	-	-1841
chr1	115062762	115062900	139	59	13	11.67	CSDE1	NM_001007553	-	-1840
chr17	77588542	77588884	343	130	63	5.02	DCXR	NM_016286	-	-1838
chr5	57787146	57787406	261	158	18	9.41	PLK2	NM_006622	-	-1838
chr16	74220800	74220969	170	111	18	18.67	KARS	NM_005548	-	-1838
chr19	55708331	55708508	178	118	23	7.3	LOC554235	NM_001024656	-	-1833
chr22	40786011	40786163	153	92	7	12.2	NAGA	NM_000262	-	-1833
chr11	111115398	111115645	248	140	10	12.55	PPP2R1B	NM_002716	-	-1831
chr12	119687036	119687246	211	127	7	24.4	SPPL3	NM_139015	-	-1828
chr2	160333635	160335436	1802	396	157	6.6	CD302	NM_014880	-	-1827
chr2	26268661	26268835	175	54	17	10.25	HADHA	NM_000182	-	-1827
chr17	17340006	17340304	299	211	13	12.2	RASD1	NM_016084	-	-1825
chr22	18244565	18244863	299	167	18	24.08	TXNRD2	NM_006440	-	-1824
chr17	24108729	24108945	217	59	7	20.92	C17orf63	NM_018182	-	-1823
chr1	1673515	1674358	844	185	48	6.18	NADK	NM_023018	-	-1821
chr8	110417510	110417632	123	62	17	15.31	ENY2	NM_020189	+	-1821
chr2	53946711	53946895	185	113	12	22.28	PSME4	NM_014614	-	-1821
chr11	65527686	65527940	255	96	15	11.2	BANF1	NM_003860	+	-1815
chr1	35093277	35093522	246	69	16	8.1	C1orf212	NM_138428	-	-1812

chr10	71730368	71730543	176	124	6	19.52	LRRC20	NM_207119	-	-1809
chr15	41873099	41873611	513	225	97	6.87	SERF2	NM_001018108	+	-1804
chr1	26480135	26480602	468	178	54	7.38	SH3BGRL3	NM_031286	+	-1803
chr1	1707447	1708388	942	834	70	7.8	GNB1	NM_002074	-	-1799
chr1	154980054	154980323	270	53	26	6.05	HDGF	NM_004494	-	-1798
chr5	34025022	34025458	437	304	34	5.03	AMACR	NM_014324	-	-1796
chr20	48241487	48242577	1091	895	135	10.51	CEBPB	NM_005194	+	-1795
chr6	30730491	30730679	189	49	8	16.64	DHX16	NM_003587	-	-1794
chr9	93211206	93212942	1737	692	184	6.27	NFIL3	NM_005384	-	-1793
chrX	153327341	153327492	152	102	7	13.56	FAM50A	NM_004699	+	-1791
chr7	99403583	99404075	493	370	194	5.14	AZGP1	NM_001185	-	-1788
chr11	122435013	122435198	186	138	19	6.81	HSPA8	NM_006597	-	-1788
chr12	122032064	122032618	555	251	67	6.19	ARL6IP4	NM_001002252	+	-1786
chr2	69407540	69407696	157	57	7	18.3	GFPT1	NM_002056	-	-1786
chr6	4062435	4062710	276	203	44	7.22	PECI	NM_206836	-	-1784
chr3	48485749	48485982	234	54	11	9.15	SCOTIN	NM_016479	-	-1782
chr20	57038751	57038908	158	64	34	5.91	ATP5E	NM_006886	-	-1780
chr20	43955249	43955383	135	59	9	13.85	PPGB	NM_000308	+	-1771
chr17	70745883	70746060	178	118	6	16.27	GGA3	NM_014001	-	-1771
chr20	1372176	1372582	407	83	18	14.64	NSFL1C	NM_182483	-	-1770
chr1	1143680	1143920	241	109	27	8.57	SDF4	NM_016176	-	-1769
chr15	72829096	72830004	909	706	181	7.1	CYP1A2	NM_000761	+	-1768
chr19	17199686	17199819	134	78	8	15.53	OCEL1	NM_024578	+	-1765
chr10	93379518	93379944	427	174	26	7.88	PPP1R3C	NM_005398	-	-1764
chr2	47242360	47242571	212	111	14	14.02	CALM2	NM_001743	-	-1763
chr7	72734556	72734943	388	69	21	8.52	WBSCR18	NM_032317	-	-1760

chr19	12763315	12765068	1754	1447	187	5.63	JUNB	NM_002229	+	-1759
chr10	72314893	72315030	138	76	31	9.77	PCBD1	NM_000281	-	-1758
chr5	157146845	157147631	787	456	62	14.4	CLINT1	NM_014666	-	-1757
chr11	65097850	65098150	301	166	13	7.34	FAM89B	NM_152832	+	-1755
chr6	31345950	31346262	313	139	36	6.87	HLA-C	NM_002117	-	-1754
chr2	165059119	165059330	212	145	14	10.35	GRB14	NM_004490	-	-1752
chr1	89371468	89371809	342	216	17	11.68	GBP7	NM_207398	-	-1752
chr11	59331774	59331938	165	61	7	16.89	MRPL16	NM_017840	-	-1749
chr4	122810183	122810345	163	73	13	7.16	ANXA5	NM_001154	-	-1748
chr17	4782806	4783095	290	139	16	9.76	SLC25A11	NM_003562	-	-1747
chr10	71581466	71581719	254	56	12	10.46	SAR1A	NM_020150	-	-1746
chr20	23563877	23564036	160	86	47	5.93	CST3	NM_000099	-	-1743
chr4	39502412	39502621	210	128	9	23.12	SCC-112	NM_015200	-	-1743
chr8	145223204	145223725	522	92	50	5.21	CYC1	NM_001916	+	-1739
chr9	110670812	110671360	549	155	25	6.66	IKBKAP	NM_003640	-	-1739
chr7	23306989	23307202	214	46	15	10.97	C7orf30	NM_138446	+	-1738
chr10	3808909	3809922	1014	173	190	5.32	KLF6	NM_001008490	-	-1734
chr3	147271520	147271650	131	50	8	11.51	PLOD2	NM_000935	-	-1733
chr7	99866969	99867196	228	95	10	12.2	BCDIN3	NM_019606	+	-1732
chr9	138960675	138961261	587	426	84	9.88	C8G	NM_000606	+	-1728
chr10	27525609	27525876	268	125	10	14.64	ACBD5	NM_145698	-	-1727
chr19	47444911	47445287	377	85	20	7.32	ERF	NM_006494	-	-1726
chr11	77458553	77458773	221	58	38	5.39	NDUFC2	NM_004549	-	-1725
chr18	75763441	75765198	1758	178	213	8.73	PQLC1	NM_025078	-	-1723
chr4	152262314	152262608	295	103	17	8.64	SH3D19	NM_001009555	-	-1720
chr11	194367	194643	277	141	12	11.39	BET1L	NM_016526	-	-1720

chr3	195338121	195338347	227	116	9	16.89	HES1	NM_005524	+	-1720
chr15	46958990	46959298	309	129	17	7.92	EID1	NM_014335	+	-1717
chr17	17657622	17657826	205	53	16	9.3	SREBF1	NM_001005291	-	-1716
chr12	109415187	109415427	241	163	23	15.88	VPS29	NM_016226	-	-1714
chr11	1253113	1253888	776	270	50	7.3	TOLLIP	NM_019009	-	-1711
chr3	48870925	48871078	154	95	18	7.33	SLC25A20	NM_000387	-	-1710
chr19	54692894	54693153	260	154	71	5.18	RPS11	NM_001015	+	-1708
chr7	127017347	127017459	113	57	15	8.27	ARF5	NM_001662	+	-1707
chr22	40253257	40253459	203	59	13	11.89	POLR3H	NM_138338	-	-1707
chr2	177803509	177804990	1482	340	114	5.13	NFE2L2	NM_006164	-	-1706
chr5	1104637	1105201	565	173	27	16.54	SLC12A7	NM_006598	-	-1702
chr6	31430846	31431330	485	62	128	5.13	HLA-B	NM_005514	-	-1701
chr9	89532330	89532499	170	62	16	8.3	CTSL	NM_001912	+	-1700
chr7	75771262	75771558	297	252	17	13.05	HSPB1	NM_001540	+	-1700
chr6	44324388	44324526	139	80	11	17.22	HSP90AB1	NM_007355	+	-1700
chr1	200369980	200370297	318	75	12	7.32	ARL8A	NM_138795	-	-1698
chr22	37460677	37462377	1701	112	205	6.32	UNC84B	NM_015374	-	-1697
chr2	659506	659671	166	56	7	18.3	TMEM18	NM_152834	-	-1697
chr16	18711023	18712187	1165	909	116	8.77	ARL6IP1	NM_015161	-	-1696
chr8	96008488	96009071	584	517	42	6.91	TP53INP1	NM_033285	-	-1695
chr10	44192855	44194210	1356	125	194	5.22	CXCL12	NM_199168	-	-1694
chr12	49920379	49920584	206	95	19	8.44	DAZAP2	NM_014764	+	-1692
chr12	108478888	108479350	463	88	65	5.55	MMAB	NM_052845	-	-1689
chr17	77092805	77093282	478	225	64	6.04	ACTG1	NM_001614	-	-1689
chr12	48028806	48028996	191	54	7	16.73	FLJ13236	NM_024902	+	-1689
chrX	120010586	120010830	245	181	23	7.17	GLUD2	NM_012084	+	-1688

chr19	44114866	44115121	256	97	12	11.39	MRPS12	NM_021107	+	-1688
chr16	4685011	4685403	393	120	14	14.64	NUDT16L1	NM_032349	+	-1687
chr3	161702116	161702338	223	106	9	16.32	KPNA4	NM_002268	-	-1681
chr11	46698845	46699010	166	107	28	8.2	F2	NM_000506	+	-1680
chr22	40812990	40813156	167	84	19	32.03	NDUFA6	NM_002490	-	-1680
chr9	139256816	139257208	393	198	27	6.47	TUBB2C	NM_006088	+	-1677
chr1	238720780	238721172	393	299	19	6.9	GREM2	NM_022469	-	-1675
chr11	101772330	101773940	1611	212	173	5.31	TMEM123	NM_052932	-	-1673
chr1	45251829	45252088	260	157	26	13.2	UROD	NM_000374	+	-1672
chr2	55630533	55630689	157	101	6	14.64	SMEK2	NM_020463	-	-1671
chr16	28457570	28457831	262	167	29	7.67	NUPR1	NM_001042483	-	-1669
chr19	5644309	5644512	204	72	14	7.96	LONP1	NM_004793	-	-1667
chr9	115210835	115211008	174	78	8	12.74	POLE3	NM_017443	-	-1667
chr5	125909922	125910014	93	47	6	29.28	ALDH7A1	NM_001182	-	-1667
chr21	45509780	45509936	157	98	6	14.64	POFUT2	NM_133635	-	-1665
chr6	53471297	53471764	468	276	41	6.85	GCLC	NM_001498	-	-1664
chr12	119385080	119385516	437	274	18	8.13	SFRS9	NM_003769	-	-1663
chr2	217246280	217246734	455	127	22	11.39	IGFBP5	NM_000599	-	-1661
chr16	8896356	8896510	155	97	8	9.89	USP7	NM_003470	-	-1660
chr12	55040903	55042280	1378	575	281	5.42	APOF	NM_001638	-	-1659
chr14	49158336	49158897	562	159	31	8.61	MGAT2	NM_001015883	+	-1659
chr5	175707156	175707332	177	103	10	14.64	KIAA1191	NM_020444	-	-1659
chr1	27569662	27569848	187	96	22	32.94	FCN3	NM_003665	-	-1659
chr20	60312824	60313079	256	200	15	8.75	ADRM1	NM_007002	+	-1658
chr20	29715939	29717580	1642	179	104	8.48	BCL2L1	NM_001191	-	-1657
chrX	118891274	118891418	145	75	28	8.49	NDUFA1	NM_004541	+	-1657

chr11	85347299	85347787	489	157	30	5.01	PICALM	NM_001008660	-	-1654
chr17	4639775	4640647	873	802	80	9.13	LOC388323	NM_001014985	+	-1654
chr9	122755804	122756089	286	106	37	6.28	C5	NM_001735	-	-1653
chr10	22646817	22646955	139	92	7	17.57	COMMD3	NM_012071	+	-1651
chr1	158164903	158165104	202	62	7	27.11	IGSF9	NM_020789	-	-1649
chr14	23676740	23676864	125	60	21	7.32	PSME1	NM_176783	+	-1647
chr20	36191479	36191925	447	164	21	7.32	TGM2	NM_004613	-	-1647
chr17	39753958	39754168	211	73	14	12.73	SLC25A39	NM_016016	-	-1647
chr11	47596705	47597090	386	261	38	13.73	MTCH2	NM_014342	-	-1647
chrX	18822229	18822445	217	91	9	16.27	PHKA2	NM_000292	-	-1646
chr8	124095455	124096412	958	808	45	7.32	DERL1	NM_024295	-	-1644
chr7	150130160	150130428	269	136	53	8.08	TMEM176A	NM_018487	+	-1642
chr17	23698341	23699427	1087	264	134	6.57	POLDIP2	NM_015584	-	-1641
chr6	33376751	33377092	342	61	18	9.15	TAPBP	NM_003190	-	-1641
chr7	45918463	45920014	1552	189	514	5.55	IGFBP3	NM_000598	-	-1640
chr17	6528758	6530401	1644	71	279	5.83	SLC13A5	NM_177550	-	-1637
chr2	27569757	27569888	132	65	9	12.5	FNDC4	NM_022823	-	-1634
chr2	70168217	70169837	1621	310	240	6.16	PCBP1	NM_006196	+	-1633
chr16	46952823	46953578	756	437	40	6.51	SIAH1	NM_001006610	-	-1632
chrX	118487679	118488064	386	251	31	6.68	SLC25A5	NM_001152	+	-1628
chr13	26909241	26909410	170	62	11	19.97	MTIF3	NM_152912	-	-1628
chr17	7471595	7471905	311	74	44	6.37	SAT2	NM_133491	-	-1625
chr4	159850470	159851353	884	650	47	5.55	PPID	NM_005038	-	-1624
chr12	112316020	112316258	239	127	20	9.25	SDS	NM_006843	-	-1623
chr14	22511200	22511871	672	62	29	6.66	JUB	NM_198086	-	-1622
chr12	74706669	74707116	448	387	26	13.01	PHLDA1	NM_007350	-	-1622

chr11	6454406	6455122	717	616	39	6.46	ARFIP2	NM_012402	-	-1619
chr19	14064933	14065127	195	60	13	7.61	PRKACA	NM_207518	-	-1619
chr2	190134414	190135180	767	626	57	9.27	SLC40A1	NM_014585	-	-1618
chr3	151942596	151943216	621	136	51	6.97	SIAH2	NM_005067	-	-1616
chr22	34953337	34953818	482	138	33	7.94	APOL2	NM_030882	-	-1616
chr10	5722231	5722452	222	119	11	11.38	ASB13	NM_024701	-	-1616
chr17	53954079	53954229	151	54	10	8.54	37138	NM_004574	-	-1615
chr12	32836403	32836569	167	61	6	14.64	PKP2	NM_001005242	-	-1615
chr3	48612916	48613048	133	59	18	6.62	UQCRC1	NM_003365	-	-1613
chr1	152822048	152822771	724	144	42	7.32	ADAR	NM_001111	-	-1613
chr5	36230464	36231185	722	534	68	5.81	C5orf33	NM_153013	-	-1612
chr12	55149076	55150238	1163	244	86	6.69	SPRYD4	NM_207344	+	-1610
chr5	180151310	180151760	451	95	34	7.92	MGAT1	NM_002406	-	-1608
chr8	12986628	12986848	221	57	12	10.65	DLC1	NM_006094	-	-1606
chrX	102817617	102818691	1075	385	95	5.69	MORF4L2	NM_012286	-	-1603
chr6	135280856	135281821	966	747	127	5.34	ALDH8A1	NM_022568	-	-1600
chr1	150045187	150046772	1586	304	170	5.72	RORC	NM_001001523	-	-1600
chr5	90700724	90701896	1173	958	77	9.47	ARRDC3	NM_020801	-	-1599
chr9	129744108	129744278	171	54	8	12.2	FAM102A	NM_203305	-	-1597
chr17	71450112	71450783	672	263	69	5.1	ACOX1	NM_004035	-	-1595
chr9	19039729	19040966	1238	791	88	6.66	RRAGA	NM_006570	+	-1595
chr1	113046715	113046862	148	60	14	9.76	RHOC	NM_001042679	-	-1591
chr11	46722960	46723248	289	151	17	6.1	CKAP5	NM_001008938	-	-1589
chr22	45460165	45460559	395	43	16	8.37	CERK	NM_182661	-	-1588
chr14	104246651	104246800	150	52	6	19.26	C14orf173	NM_022489	+	-1588
chr12	54401743	54402074	332	273	20	7.23	RDH5	NM_002905	+	-1587

chr11	5204740	5204858	119	60	7	41.37	HBB	NM_000518	-	-1587
chr11	60858617	60858815	199	109	28	6.66	DAK	NM_015533	+	-1586
chr20	2391735	2391866	132	58	9	19.52	SNRPB	NM_198216	-	-1586
chr2	39067891	39068052	162	89	6	17.22	SOS1	NM_005633	-	-1583
chr5	179222188	179223260	1073	413	59	7.81	TBC1D9B	NM_015043	-	-1582
chr17	59579820	59580109	290	131	13	12.55	TEX2	NM_018469	-	-1582
chr11	47558660	47558787	128	62	8	12.81	NDUFS3	NM_004551	+	-1580
chr11	66088926	66089088	163	62	19	11.93	CTSF	NM_003793	-	-1577
chr7	44122235	44122387	153	75	13	10.03	POLD2	NM_006230	-	-1576
chr6	32917877	32918051	175	71	16	7.05	PSMB8	NM_148919	-	-1575
chr11	607954	608149	196	117	27	6.1	MUCDHL	NM_021924	-	-1573
chr22	48699790	48699920	131	75	7	10.46	CRELD2	NM_024324	+	-1573
chr12	6956930	6957181	252	197	13	11.39	MBOAT5	NM_005768	-	-1573
chr5	176762743	176763318	576	224	116	8	F12	NM_000505	-	-1572
chr1	19070515	19072083	1569	323	351	5.47	ALDH4A1	NM_003748	-	-1571
chr20	41521091	41521502	412	360	24	13.66	SFRS6	NM_006275	+	-1571
chr11	2381546	2381668	123	62	6	21.96	TSSC4	NM_005706	+	-1570
chr14	67213863	67214839	977	222	67	7.95	RDH11	NM_016026	-	-1569
chr7	150410094	150410670	577	297	31	9.65	TMUB1	NM_031434	-	-1565
chr22	40853446	40854007	562	404	99	8.04	CYP2D6	NM_000106	-	-1561
chr2	218838530	218838656	127	61	15	23.83	AAMP	NM_001087	-	-1560
chr2	150135809	150135955	147	86	11	8.61	C2orf25	NM_015702	-	-1558
chr4	88444519	88445521	1003	483	293	5.01	HSD17B13	NM_178135	-	-1557
chr16	70158835	70159809	975	366	221	5.88	TAT	NM_000353	-	-1555
chr14	104308102	104308286	185	61	13	13.54	AKT1	NM_005163	-	-1553
chr1	33247089	33247724	636	167	35	10.86	AK2	NM_013411	-	-1552

chr11	65870741	65870970	230	60	11	23.57	B3GNT1	NM_006876	-	-1551
chr17	37719644	37720416	773	203	46	5.58	STAT3	NM_213662	-	-1548
chr10	14601564	14602111	548	127	40	7.13	FAM107B	NM_031453	-	-1547
chr11	67786235	67786927	693	219	37	5.99	C11orf24	NM_022338	-	-1545
chr7	100304217	100304430	214	153	9	18.3	TRIP6	NM_003302	+	-1545
chr10	50614071	50614260	190	112	19	9.94	OGDHL	NM_018245	-	-1544
chr1	154974736	154975261	526	77	43	10.26	MRPL24	NM_024540	-	-1544
chr13	28173574	28173761	188	111	13	12.39	LOC283537	NM_181785	-	-1542
chr11	60927909	60928319	411	220	19	6.66	FLJ12529	NM_024811	-	-1541
chr17	18173245	18173459	215	115	20	7.55	SHMT1	NM_004169	-	-1540
chr1	85820138	85820586	449	365	35	5.86	CYR61	NM_001554	+	-1539
chr5	177565426	177565652	227	173	15	24.92	HNRPAB	NM_004499	+	-1539
chr4	74160290	74160902	613	211	27	7.69	ANKRD17	NM_032217	-	-1536
chr17	76833404	76834928	1525	362	114	6.7	MGC15523	NM_001037984	-	-1535
chr1	159355597	159356049	453	392	25	15.69	NIT1	NM_005600	+	-1535
chr11	2247601	2247839	239	111	9	17.5	ASCL2	NM_005170	-	-1535
chr19	46529883	46530020	138	81	6	14.64	TGFB1	NM_000660	-	-1530
chr2	31411670	31412220	551	264	34	7.33	XDH	NM_000379	-	-1529
chr7	99794879	99795090	212	103	10	10.46	PILRB	NM_178238	+	-1529
chr22	35007298	35008799	1502	472	213	8.65	MYH9	NM_002473	-	-1528
chr7	100558377	100558695	319	184	18	9.34	SERPINE1	NM_000602	+	-1524
chr11	60824851	60825021	171	57	11	8.76	DDB1	NM_001923	-	-1522
chr2	220113017	220113440	424	246	17	11.39	CHPF	NM_024536	-	-1519
chr16	55218110	55218603	494	324	85	6.43	MT1E	NM_175617	+	-1518
chrX	106843143	106844630	1488	375	152	7.26	TSC22D3	NM_001015881	-	-1518
chr22	41596894	41597239	346	219	20	11.98	PACSIN2	NM_007229	-	-1518

chr11	66923592	66923745	154	62	13	14.38	PPP1CA	NM_001008709	-	-1518
chr1	120256747	120257217	471	109	29	5.02	NOTCH2	NM_024408	-	-1517
chr17	39438906	39439070	165	72	9	14.49	NAGS	NM_153006	+	-1513
chr9	87832048	87832389	342	88	12	10.01	GOLPH2	NM_016548	-	-1510
chr14	49430753	49431095	343	61	20	7.32	ARF6	NM_001663	+	-1507
chr11	61314519	61314685	167	106	24	5.2	C11orf10	NM_014206	-	-1505
chr5	179157227	179158214	988	592	98	5.78	MGAT4B	NM_054013	-	-1504
chr4	40121578	40122000	423	106	22	9.01	FLJ20273	NM_019027	-	-1503
chr16	28525648	28525919	272	214	14	9.29	SULT1A1	NM_177530	-	-1501
chr15	63198091	63198271	181	88	6	14.64	PDCD7	NM_005707	-	-1501
chr17	2539434	2540928	1495	109	138	8.01	KIAA0664	NM_015229	-	-1499
chr17	4522796	4522981	186	107	7	12.2	PELP1	NM_014389	-	-1499
chr10	91333650	91334225	576	215	42	6.97	PANK1	NM_138316	-	-1497
chr17	74478846	74480428	1583	558	195	6.16	LGALS3BP	NM_005567	-	-1496
chr10	135191883	135192352	470	171	220	6.27	CYP2E1	NM_000773	+	-1496
chr14	91653574	91653718	145	64	21	7.64	NDUFB1	NM_004545	-	-1496
chr17	45814424	45815093	670	329	38	14.28	LRRC59	NM_018509	-	-1495
chr3	128890910	128892094	1185	218	87	10.79	MGLL	NM_007283	-	-1494
chr1	167751186	167751525	340	174	51	7.82	F5	NM_000130	-	-1493
chr20	61623314	61624068	755	248	59	6.63	C20orf149	NM_024299	+	-1492
chr9	127240741	127240986	246	112	9	14.64	MAPKAP1	NM_001006620	-	-1492
chr20	7910872	7911206	335	227	16	9.81	TXNDC13	NM_021156	-	-1491
chr17	7775766	7775882	117	59	9	15.42	TRAPPC1	NM_021210	-	-1491
chr16	66267210	66267434	225	113	10	14.64	GFOD2	NM_030819	-	-1490
chr1	222641171	222641306	136	62	7	19.1	WDR26	NM_025160	-	-1490
chr16	8896140	8896337	198	51	10	15.83	USP7	NM_003470	-	-1487

chr14	23757160	23757397	238	85	16	11.32	NEDD8	NM_006156	-	-1486
chr3	47868021	47868674	654	169	38	10.33	MAP4	NM_030884	-	-1485
chr11	397046	397200	155	60	10	11.26	SIGIRR	NM_021805	-	-1485
chr17	40569906	40570064	159	57	12	13.31	ACBD4	NM_024722	+	-1485
chr2	659310	659456	147	90	7	18.3	TMEM18	NM_152834	-	-1482
chr13	27095217	27095508	292	81	20	12.83	POLR1D	NM_015972	+	-1480
chr3	185521780	185522273	494	358	30	5.06	EIF4G1	NM_004953	+	-1479
chr7	56138124	56138231	108	55	9	14.23	CHCHD2	NM_016139	-	-1470
chr8	145701442	145701700	259	159	24	8.61	GPT	NM_005309	+	-1468
chr7	94765295	94766388	1094	820	294	5.83	PON1	NM_000446	-	-1465
chr2	232028861	232029167	307	185	27	14.38	NCL	NM_005381	-	-1464
chr19	2377566	2378079	514	60	47	12.04	TIMM13	NM_012458	-	-1458
chr9	93834557	93834704	148	84	8	17.57	SPTLC1	NM_006415	-	-1457
chr19	52034488	52034718	231	107	20	5.07	AP2S1	NM_004069	-	-1456
chrX	71410266	71410634	369	260	46	5.94	RPS4X	NM_001007	-	-1456
chr15	99661592	99663110	1519	173	191	6.5	PCSK6	NM_002570	-	-1454
chr4	89866964	89867582	619	84	35	6.59	FAM13A1	NM_001015045	-	-1454
chr17	12837718	12837887	170	118	6	17.22	ELAC2	NM_018127	-	-1453
chr2	218847227	218848612	1386	211	115	9.1	TMBIM1	NM_022152	-	-1452
chr6	7826773	7828203	1431	298	174	8.69	TXNDC5	NM_030810	-	-1451
chr3	161701839	161702108	270	132	10	14.64	KPNA4	NM_002268	-	-1451
chr21	45050697	45051408	712	176	39	10.42	SUMO3	NM_006936	-	-1449
chrX	2832015	2833459	1445	89	142	9.14	ARSD	NM_001669	-	-1448
chr6	160020210	160021586	1377	1100	190	6.52	SOD2	NM_001024465	-	-1446
chrX	102499305	102499478	174	61	8	14.64	WBP5	NM_001006612	+	-1443
chr16	56706193	56706439	247	99	11	10.98	C16orf80	NM_013242	-	-1442

chr8	82734030	82734192	163	117	7	19.52	IMPA1	NM_005536	-	-1442
chr9	34542698	34542871	174	56	8	15.29	CNTFR	NM_001842	-	-1441
chr3	52208228	52208622	395	220	41	5.78	ALAS1	NM_000688	+	-1439
chr5	180597630	180597971	342	193	58	6.81	GNB2L1	NM_006098	-	-1438
chr6	52765515	52765784	270	149	48	9.75	GSTA1	NM_145740	-	-1437
chr9	123142246	123142610	365	167	33	6.68	STOM	NM_198194	-	-1433
chr6	31606757	31607408	652	365	31	9.01	BAT1	NM_004640	-	-1432
chr10	61459432	61459595	164	103	6	22.52	ANK3	NM_001149	-	-1430
chr1	36375892	36376190	299	170	11	13.13	TRAPPC3	NM_014408	-	-1429
chr17	10558512	10558790	279	86	19	7.35	LOC388335	NM_001004313	-	-1426
chr12	21810172	21810581	410	258	28	7.99	KCNJ8	NM_004982	-	-1425
chr3	134776548	134776687	140	88	6	24.4	CDV3	NM_017548	+	-1424
chr10	88800932	88801645	714	398	124	6.48	GLUD1	NM_005271	-	-1423
chr11	69177394	69178446	1053	808	96	5.68	FLJ42258	NM_001004327	-	-1422
chr11	70823122	70824527	1406	641	158	6.73	DHCR7	NM_001360	-	-1417
chr3	32498107	32499223	1117	283	112	5.84	CMTM6	NM_017801	-	-1416
chr14	23845350	23845650	301	186	61	12.78	CIDEB	NM_014430	-	-1416
chr10	27525142	27525564	423	93	19	12.39	ACBD5	NM_145698	-	-1415
chr4	39501953	39502293	341	194	12	20.33	SCC-112	NM_015200	-	-1415
chr3	150676293	150676537	245	83	28	11.79	TM4SF4	NM_004617	+	-1414
chr11	1731583	1731973	391	76	98	5.79	CTSD	NM_001909	-	-1413
chr3	48485306	48485612	307	193	17	8.99	SCOTIN	NM_016479	-	-1412
chr19	40929359	40929743	385	305	21	10.15	PSENN	NM_172341	+	-1410
chr19	4105874	4106038	165	105	6	15.69	CREB3L3	NM_032607	+	-1410
chr9	72190088	72190742	655	160	27	5.75	KLF9	NM_001206	-	-1408
chr2	42843930	42844549	620	257	30	6.6	OXER1	NM_148962	-	-1404

chr14	92476952	92477364	413	111	20	12.81	ITPK1	NM_014216	-	-1404
chr3	150373832	150374626	795	207	101	5.6	CP	NM_000096	-	-1403
chr2	98583417	98583696	280	116	11	10.25	MGC52110	NM_001008215	-	-1399
chr1	44893108	44893487	380	283	18	11.13	TMEM53	NM_024587	-	-1399
chr15	77002373	77002560	188	92	19	8.26	CTSH	NM_004390	-	-1398
chr21	46434511	46434864	354	295	17	10.37	LSS	NM_002340	-	-1396
chr3	114851085	114851320	236	100	10	25.84	KIAA2018	NM_001009899	-	-1396
chr1	33561795	33563205	1411	701	103	12.39	PHC2	NM_004427	-	-1395
chr13	43905676	43907052	1377	706	120	5.54	TSC22D1	NM_006022	-	-1392
chr1	154978996	154979914	919	84	124	5.01	HDGF	NM_004494	-	-1389
chr17	77418898	77420275	1378	852	155	6.18	ARHGDI	NM_004309	-	-1389
chrX	53238266	53238766	501	132	22	6.11	JARID1C	NM_004187	-	-1388
chr19	14486969	14487967	999	246	71	7.67	DNAJB1	NM_006145	-	-1386
chr14	20890698	20890861	164	116	6	23.64	SUPT16H	NM_007192	-	-1384
chr6	133045278	133045807	530	61	48	7.32	VNN1	NM_004666	-	-1383
chr16	625537	625812	276	134	11	12.12	MGC13114	NM_001040165	-	-1383
chr9	137533489	137533757	269	111	12	15.25	MRPS2	NM_016034	+	-1383
chr22	37857927	37858115	189	61	10	14.64	CBX7	NM_175709	-	-1382
chr2	218838358	218838478	121	61	12	17.57	AAMP	NM_001087	-	-1382
chr9	85465649	85466079	431	53	23	11.71	UBQLN1	NM_013438	-	-1381
chr13	109205247	109205563	317	113	18	7.32	IRS2	NM_003749	-	-1379
chr10	75212836	75213212	377	198	21	12.42	CHCHD1	NM_203298	+	-1379
chr1	1238016	1238206	191	139	8	13.94	CPSF3L	NM_017871	-	-1379
chr16	18724704	18725053	350	60	15	7.32	SMG1	NM_015092	-	-1377
chr4	140647647	140648018	372	201	22	5.69	SETD7	NM_030648	-	-1376
chr3	120633635	120633766	132	73	7	21.96	TMEM39A	NM_018266	-	-1376

chr16	73044040	73044729	690	370	36	8.98	GLG1	NM_012201	-	-1373
chr12	119649193	119649420	228	137	37	5.29	ACADS	NM_000017	+	-1372
chr19	45432747	45432926	180	125	11	17.57	AKT2	NM_001626	-	-1371
chr6	52724259	52724508	250	115	50	5.97	GSTA2	NM_000846	-	-1369
chr13	102217678	102217835	158	84	11	18.51	C13orf27	NM_138779	-	-1368
chr20	62165687	62165820	134	76	7	14.64	TCEA2	NM_003195	+	-1367
chr3	195843855	195844175	321	266	15	14.64	LSG1	NM_018385	-	-1367
chr19	4474216	4474911	696	259	42	6.11	LSDP5	NM_001013706	-	-1366
chr19	54281454	54281642	189	124	20	8.3	SNRP70	NM_001009820	+	-1366
chr21	26174761	26176097	1337	983	224	5.62	APP	NM_000484	-	-1365
chr3	42889876	42890053	178	57	31	7.82	CYP8B1	NM_004391	-	-1365
chr2	217072850	217073129	280	133	36	9.78	RPL37A	NM_000998	+	-1365
chr14	34941289	34941830	542	306	56	6.54	NFKBIA	NM_020529	-	-1363
chr10	100167131	100167308	178	60	9	12.55	HPS1	NM_000195	-	-1363
chr19	5630614	5630795	182	52	7	23.64	P117	NM_205767	-	-1363
chr1	159467093	159467443	351	198	26	8.28	NR1I3	NM_001077478	-	-1362
chr14	98934984	98935198	215	129	9	17.08	SETD3	NM_032233	-	-1362
chr9	130898082	130898256	175	89	20	5.55	CRAT	NM_004003	-	-1361
chr6	24814184	24814503	320	179	25	8.03	C6orf62	NM_030939	-	-1358
chr2	218376486	218377109	624	130	30	7.83	TNS1	NM_022648	-	-1353
chr12	91061112	91062384	1273	254	197	6.36	BTG1	NM_001731	-	-1351
chr3	3087609	3087773	165	104	6	27.11	IL5RA	NM_000564	-	-1351
chr6	159107358	159108114	757	89	45	7.71	VIL2	NM_003379	-	-1349
chr18	59149871	59150161	291	55	12	7.32	FVT1	NM_002035	-	-1348
chr12	63394566	63394838	273	226	13	9.32	GNS	NM_002076	-	-1348
chr16	69252779	69253955	1177	233	75	8.62	LOC92154	NM_138383	-	-1347

chr12	7139073	7139638	566	403	57	10.36	C1RL	NM_016546	-	-1347
chr8	103731309	103731533	225	62	11	12.2	KLF10	NM_001032282	-	-1345
chr1	20682501	20682809	309	210	23	5.82	CAMK2N1	NM_018584	-	-1338
chr6	43374810	43375313	504	333	46	7.51	SLC22A7	NM_006672	+	-1338
chr7	98831626	98831862	237	88	16	26.35	PDAP1	NM_014891	-	-1338
chr1	223657040	223657163	124	60	8	12.71	LBR	NM_002296	-	-1336
chr9	129308092	129308772	681	194	33	7.32	C9orf88	NM_022833	-	-1333
chr1	11038431	11038568	138	94	6	22.52	SRM	NM_003132	-	-1333
chr12	6309189	6309516	328	233	25	6.17	TNFRSF1A	NM_001065	-	-1332
chr19	4276239	4276371	133	43	9	15.58	STAP2	NM_001013841	-	-1331
chr2	215933757	215934752	996	789	335	5.34	FN1	NM_002026	-	-1327
chr20	61446208	61446433	226	100	10	19.85	CHRNA4	NM_000744	-	-1325
chr6	99955067	99956247	1181	528	60	6.37	C6orf111	NM_032870	-	-1324
chr11	118420290	118421433	1144	421	91	7.93	HYOU1	NM_006389	-	-1324
chr10	44185585	44186935	1351	186	114	6.06	CXCL12	NM_000609	-	-1323
chr5	14763067	14763336	270	116	16	6.92	ANKH	NM_054027	-	-1318
chr16	29726403	29726672	270	60	21	7.32	MAZ	NM_001042539	+	-1317
chr2	206697102	206697362	261	88	17	21.02	NDUFS1	NM_005006	-	-1314
chr3	99781927	99782294	368	155	16	9.43	CPOX	NM_000097	-	-1313
chr2	31603602	31604471	870	193	50	5.58	SRD5A2	NM_000348	-	-1312
chr4	21998959	21999407	449	249	26	9.01	GPR125	NM_145290	-	-1311
chr1	151847092	151847301	210	149	17	16.73	S100A16	NM_080388	-	-1311
chr1	56733412	56734330	919	415	92	8.97	PPAP2B	NM_003713	-	-1308
chr20	365112	365430	319	61	13	6.23	TBC1D20	NM_144628	-	-1305
chr8	125632225	125633516	1292	836	109	8.03	MTSS1	NM_014751	-	-1305
chr1	149639836	149639969	134	61	21	9.32	PSMB4	NM_002796	+	-1305

chr6	119541987	119542272	286	163	13	9.67	MAN1A1	NM_005907	-	-1305
chr21	45093927	45095244	1318	154	133	5.47	PTTG1IP	NM_004339	-	-1304
chr8	134318617	134319898	1282	152	89	7.82	NDRG1	NM_006096	-	-1303
chr17	7064442	7065179	738	414	101	8.44	ACADVL	NM_000018	+	-1303
chr9	85774030	85774214	185	129	11	13.54	HNRPK	NM_031263	-	-1303
chr2	136589374	136589692	319	145	16	21.02	CXCR4	NM_001008540	-	-1303
chr16	55225167	55225374	208	62	43	6.64	MT1M	NM_176870	+	-1302
chr2	119842172	119842431	260	123	34	6.8	DBI	NM_020548	+	-1302
chr6	11089644	11090282	639	307	26	8.02	ELOVL2	NM_017770	-	-1302
chr17	77629503	77630804	1302	419	141	5.17	FASN	NM_004104	-	-1301
chr15	62766846	62768128	1283	132	87	7.77	OAZ2	NM_002537	-	-1300
chr17	77970937	77971158	222	92	7	19.52	HEXDC	NM_173620	+	-1299
chr6	76020444	76020666	223	100	18	10.98	TMEM30A	NM_018247	-	-1298
chr13	20649074	20649666	593	368	68	10.31	MRP63	NM_024026	+	-1295
chr19	54708924	54709597	674	416	110	5.92	FCGRT	NM_004107	+	-1294
chr3	49134358	49134845	488	118	44	7.14	LAMB2	NM_002292	-	-1294
chr20	3713205	3713792	588	393	32	8.61	CENPB	NM_001810	-	-1293
chr12	55776482	55776753	272	116	18	6.41	STAT6	NM_003153	-	-1292
chr1	148504444	148505714	1271	561	122	6.89	APH1A	NM_001077628	-	-1292
chr3	50301258	50301416	159	61	8	11.56	IFRD2	NM_006764	-	-1292
chr1	115061846	115062349	504	139	30	7.38	CSDE1	NM_001007553	-	-1289
chr11	118685430	118685732	303	117	12	9.76	MCAM	NM_006500	-	-1288
chr2	165250654	165250790	137	77	14	12.03	COBLL1	NM_014900	-	-1285
chrX	47327733	47327917	185	78	23	5.03	TIMP1	NM_003254	+	-1284
chr18	2907048	2908276	1229	489	115	5.69	LPIN2	NM_014646	-	-1284
chr11	396761	396999	239	181	19	12.39	SIGIRR	NM_021805	-	-1284

chr16	358487	358679	193	56	11	15.07	MRPL28	NM_006428	-	-1283
chr6	33493214	33493577	364	81	34	7.99	CUTA	NM_001014837	-	-1281
chr19	17375917	17376035	119	60	15	9.98	BST2	NM_004335	-	-1280
chr1	165777589	165778154	566	505	53	7.1	CREG1	NM_003851	-	-1278
chr17	77456531	77456661	131	74	14	7.67	PCYT2	NM_002861	-	-1278
chr2	96215430	96215607	178	62	10	12.81	STARD7	NM_020151	-	-1276
chr2	241817899	241818091	193	131	36	5.14	HDLBP	NM_203346	-	-1275
chr3	173706390	173707433	1044	958	86	5.46	TNFSF10	NM_003810	-	-1275
chr11	63756475	63756937	463	350	23	7.91	DNAJC4	NM_005528	+	-1274
chr3	49371591	49372857	1267	202	149	6.18	RHOA	NM_001664	-	-1273
chr14	102872127	102872261	135	62	8	15.3	EIF5	NM_183004	+	-1273
chr17	31328588	31328920	333	237	28	5.48	CCL16	NM_004590	-	-1272
chr11	17053499	17053787	289	229	24	9.47	RPS13	NM_001017	-	-1272
chr4	129411654	129412019	366	209	22	8.57	PGRMC2	NM_006320	-	-1271
chr1	199720095	199720551	457	370	31	5.02	CSRP1	NM_004078	-	-1269
chr8	48812028	48813297	1270	262	252	7.21	CEBPD	NM_005195	-	-1269
chr19	6365367	6365627	261	79	16	8.37	KHSRP	NM_003685	-	-1269
chr19	46042387	46042549	163	89	70	5.06	CYP2A6	NM_000762	-	-1266
chr3	147393793	147394080	288	229	13	9.84	PLSCR4	NM_020353	-	-1265
chr11	552427	552711	285	132	13	10.43	RASSF7	NM_003475	+	-1262
chr11	62405957	62406124	168	62	9	17.22	SLC3A2	NM_001013251	+	-1262
chr1	44214327	44214449	123	62	10	15.25	ATP6V0B	NM_004047	+	-1261
chr2	197965917	197966203	287	181	32	5.78	SF3B1	NM_012433	-	-1259
chr11	65415317	65415708	392	164	20	6.7	CCDC85B	NM_006848	+	-1258
chr22	18331071	18331327	257	130	41	7.94	COMT	NM_007310	+	-1258
chr7	75794591	75795310	720	534	44	10.14	YWHAG	NM_012479	-	-1258

chr1	219942185	219942644	460	305	34	6.06	DUSP10	NM_144728	-	-1256
chr4	7113378	7113936	559	434	33	8.18	GRPEL1	NM_025196	-	-1256
chr4	39229808	39230200	393	333	29	9.59	C4orf34	NM_174921	-	-1256
chr2	85677463	85677601	139	58	15	8.14	LOC51255	NM_016494	+	-1254
chr9	139125943	139126065	123	62	8	16.27	DPP7	NM_013379	-	-1252
chr19	43998740	43999154	415	238	50	11.75	ECH1	NM_001398	-	-1251
chr6	108298648	108299465	818	599	49	7.98	SEC63	NM_007214	-	-1250
chr11	71392588	71392804	217	105	12	17.67	NUMA1	NM_006185	-	-1246
chr2	8740228	8740807	580	240	44	8.24	ID2	NM_002166	+	-1244
chr8	145620900	145621051	152	62	14	11.13	VPS28	NM_016208	-	-1244
chr7	72645415	72646701	1287	148	188	7.18	MLXIPL	NM_032951	-	-1242
chr15	46957625	46958822	1198	401	90	5.01	EID1	NM_014335	+	-1241
chr1	202366814	202368054	1241	175	181	6.74	ETNK2	NM_018208	-	-1241
chr6	36570466	36570890	425	377	17	10.46	STK38	NM_007271	-	-1241
chr13	47883947	47884423	477	175	19	6.66	P2RY5	NM_005767	-	-1239
chr6	28979755	28979997	243	91	11	10.46	TRIM27	NM_006510	-	-1239
chr6	117989182	117989365	184	129	7	13.31	GOPC	NM_001017408	-	-1238
chr17	650349	650573	225	144	9	18.3	NXN	NM_022463	-	-1238
chr8	145210582	145210747	166	90	8	12.62	GPAA1	NM_003801	+	-1236
chr11	606616	607811	1196	886	161	7.45	MUCDHL	NM_021924	-	-1235
chr5	39142167	39142347	181	57	7	18.3	FYB	NM_001465	-	-1233
chr17	8133795	8133945	151	101	6	18.3	RANGNRF	NM_016492	+	-1232
chr17	30763289	30763432	144	57	6	17.22	SLFN12	NM_018042	-	-1230
chr3	130516314	130517532	1219	329	108	5.64	H1FX	NM_006026	-	-1228
chr12	94890573	94892500	1928	106	155	7.65	HAL	NM_002108	-	-1228
chr2	88108547	88109067	521	388	25	8.9	KRCC1	NM_016618	-	-1228

chr1	226361996	226362228	233	176	19	5.46	MRPL55	NM_181462	-	-1225
chr11	63767254	63767388	135	77	12	7.91	FKBP2	NM_057092	+	-1225
chr19	2428012	2428356	345	84	35	5.44	GADD45B	NM_015675	+	-1222
chr1	23995767	23995897	131	62	11	9.59	GALE	NM_000403	-	-1222
chr20	33331142	33331358	217	115	19	7.32	ITGB4BP	NM_181468	-	-1220
chr1	26479830	26480019	190	138	12	13.18	SH3BGRL3	NM_031286	+	-1220
chr11	65809739	65809846	108	55	8	12.65	YIF1A	NM_020470	-	-1219
chr3	49430237	49430432	196	60	16	15.78	AMT	NM_000481	-	-1217
chr10	27440418	27440607	190	52	9	23.12	YME1L1	NM_014263	-	-1217
chr1	205330205	205330466	262	157	36	6.14	C4BPB	NM_001017367	+	-1216
chr2	72968979	72969271	293	67	21	17.16	SPR	NM_003124	+	-1216
chr20	29657481	29657968	488	204	45	17.3	ID1	NM_181353	+	-1216
chr9	139463411	139463712	302	175	18	18.82	NELF	NM_015537	-	-1215
chr17	77587046	77588256	1211	97	519	5.42	DCXR	NM_016286	-	-1210
chr1	51593515	51593732	218	87	9	12.2	EPS15	NM_001981	-	-1209
chr14	69304519	69304793	275	142	29	7.48	SFRS5	NM_006925	+	-1207
chr7	98845617	98845754	138	50	6	17.43	BUD31	NM_003910	+	-1207
chr15	72799869	72800149	281	57	13	6.86	CYP1A1	NM_000499	-	-1206
chr15	43440620	43441819	1200	733	451	6.05	GATM	NM_001482	-	-1204
chr21	36365105	36365358	254	74	31	7.44	CBR1	NM_001757	+	-1204
chr1	158453155	158453331	177	117	15	10.19	WDR42A	NM_015726	-	-1203
chr2	3480634	3481898	1265	824	389	5.05	ADI1	NM_018269	-	-1201
chr1	21878297	21878581	285	121	15	9.76	USP48	NM_032236	-	-1201
chr8	105460881	105462029	1149	325	141	11.33	DPYS	NM_001385	-	-1201
chr3	143509106	143509339	234	145	11	24.4	XRN1	NM_019001	-	-1199
chr1	32603544	32604571	1028	270	56	5.99	BSDC1	NM_018045	-	-1198

chr2	46982936	46983716	781	430	42	10.14	MCFD2	NM_139279	-	-1198
chr9	115175544	115176715	1172	103	84	5.72	HDHD3	NM_031219	-	-1197
chr5	132230958	132231414	457	193	96	9.2	UQCRQ	NM_014402	+	-1197
chr12	9112501	9112765	265	163	78	5.87	A2M	NM_000014	-	-1195
chr1	89291544	89291787	244	140	16	9.53	GBP1	NM_002053	-	-1194
chr9	91410725	91410941	217	60	16	11.2	GADD45G	NM_006705	+	-1194
chr19	4397266	4397452	187	127	18	6.84	UBXD1	NM_025241	-	-1192
chr1	218155059	218155419	361	262	16	6.66	SLC30A10	NM_018713	-	-1191
chr16	30807666	30807808	143	94	6	23.64	BCL7C	NM_004765	-	-1190
chr19	9825420	9826583	1164	584	96	7.32	OLFM2	NM_058164	-	-1189
chr9	36205304	36205628	325	230	24	7.14	GNE	NM_005476	-	-1188
chr19	14064343	14064696	354	137	26	7.67	PRKACA	NM_207518	-	-1188
chr8	99537040	99537225	186	120	8	14.64	STK3	NM_006281	-	-1188
chr9	130532963	130533077	115	58	7	34.16	ZYG11BL	NM_006336	-	-1188
chr17	17339356	17339666	311	176	16	8.54	RASD1	NM_016084	-	-1187
chr20	42562362	42562501	140	80	8	13.85	SERINC3	NM_006811	-	-1187
chr20	24891579	24892766	1188	135	194	5.8	C20orf3	NM_020531	-	-1186
chr16	1767764	1767899	136	78	15	11.95	SPSB3	NM_080861	-	-1185
chr4	9685100	9686243	1144	837	109	7.39	WDR1	NM_005112	-	-1183
chr17	37985968	37986242	275	164	13	8.05	LOC162427	NM_178126	-	-1182
chr6	7233618	7233983	366	281	18	8.04	SSR1	NM_003144	-	-1181
chr1	7945364	7945560	197	137	23	23.07	PARK7	NM_007262	+	-1181
chr2	53945910	53946254	345	177	15	7.32	PSME4	NM_014614	-	-1180
chr3	52715837	52716076	240	82	18	18.74	SPCS1	NM_014041	+	-1180
chr22	17544086	17544272	187	92	18	8.21	SLC25A1	NM_005984	-	-1178
chr8	40130122	40131321	1200	716	197	5.37	C8orf4	NM_020130	+	-1176

chr7	127016783	127016927	145	85	20	7.96	ARF5	NM_001662	+	-1175
chr3	67508711	67509010	300	230	15	10.25	SUCLG2	NM_003848	-	-1175
chr17	6857715	6857863	149	57	17	11.63	MGC71993	NM_001004333	+	-1175
chr1	234206627	234206937	311	152	21	9.15	NID1	NM_002508	-	-1174
chr3	199162351	199162621	271	133	35	5.49	RPL35A	NM_000996	+	-1173
chr17	53778419	53778710	292	233	19	14.25	SUPT4H1	NM_003168	-	-1173
chr6	53470490	53471268	779	489	56	9.65	GCLC	NM_001498	-	-1168
chr2	86684770	86685193	424	94	29	6.21	RNF103	NM_005667	-	-1167
chr1	38047467	38047721	255	59	24	8.96	C1orf122	NM_198446	+	-1166
chr3	113807062	113807266	205	146	11	9	CCDC80	NM_199511	-	-1166
chr17	50825953	50826135	183	135	7	11.71	MMD	NM_012329	-	-1163
chr7	95588325	95588630	306	246	40	5.82	SLC25A13	NM_014251	-	-1162
chr8	117928281	117928514	234	122	11	11.99	RAD21	NM_006265	-	-1160
chr1	47168068	47168592	525	281	97	6.33	CYP4A11	NM_000778	-	-1158
chr17	35139961	35140092	132	59	8	11.39	C17orf37	NM_032339	-	-1156
chr12	119384889	119385009	121	61	8	14.28	SFRS9	NM_003769	-	-1156
chr2	162557187	162558156	970	474	63	8.35	DPP4	NM_001935	-	-1154
chrX	153388716	153388853	138	60	6	20.92	FAM3A	NM_021806	-	-1154
chr1	29347382	29348104	723	150	48	8.37	SFRS4	NM_005626	-	-1153
chr3	124814361	124814987	627	276	33	11.8	MYLK	NM_053031	-	-1153
chr6	133086567	133086774	208	118	16	12.18	VNN3	NM_018399	-	-1153
chr14	23701165	23701410	246	157	9	16.27	ISGF3G	NM_006084	+	-1149
chr1	11009204	11010313	1110	146	89	6.88	MASP2	NM_006610	-	-1146
chr8	145062193	145062453	261	92	14	9.15	PLEC1	NM_201384	-	-1145
chr22	48699364	48699492	129	54	6	22.88	CRELD2	NM_024324	+	-1145
chr11	125638056	125639193	1138	276	205	5.34	SRPR	NM_003139	-	-1144

chr1	33101076	33101606	531	348	25	6.83	FNDC5	NM_153756	-	-1143
chr1	207945716	207945955	240	141	63	5.81	HSD11B1	NM_005525	+	-1142
chr8	121619859	121620368	510	305	25	11.2	SNTB1	NM_021021	-	-1142
chr5	139910812	139910978	167	57	8	12.55	SRA1	NM_001035235	-	-1141
chr1	45866154	45866707	554	61	37	6.76	GPBP1L1	NM_021639	-	-1140
chr8	22494819	22495068	250	139	11	12.81	PDLIM2	NM_198042	+	-1140
chr10	69712920	69713561	642	527	63	5.55	MAWBP	NM_022129	-	-1139
chr10	30642745	30642903	159	105	6	10.98	PAPD1	NM_018109	-	-1139
chr11	71487004	71487125	122	62	10	24.4	C11orf59	NM_017907	-	-1139
chr11	62148883	62150016	1134	396	170	5.53	GANAB	NM_198334	-	-1138
chr18	53419807	53420031	225	108	17	9.88	NARS	NM_004539	-	-1138
chr5	176872107	176872322	216	110	10	12.55	DDX41	NM_016222	-	-1138
chr11	47142778	47143565	788	212	49	5.32	ZNF289	NM_032389	-	-1136
chr1	161379399	161379857	459	148	21	11.76	RGS5	NM_003617	-	-1136
chr10	99517291	99517642	352	62	17	9.32	SFRP5	NM_003015	-	-1135
chr16	4599431	4600020	590	60	34	8.24	FAM100A	NM_145253	-	-1134
chr15	57216723	57216989	267	214	13	10.25	MYO1E	NM_004998	-	-1134
chr2	188037849	188038338	490	323	35	10.46	TFPI	NM_006287	-	-1134
chr16	1761295	1761454	160	60	10	8.84	NME3	NM_002513	-	-1132
chr7	44519202	44519790	589	247	41	7.96	NPC1L1	NM_013389	-	-1130
chr9	4701472	4702285	814	163	63	5.16	AK3	NM_016282	-	-1128
chr3	122833847	122834064	218	61	9	15.91	HCLS1	NM_005335	-	-1128
chr17	37968600	37968745	146	56	9	30.03	COASY	NM_001042529	+	-1128
chr3	12600070	12601233	1164	343	88	9.23	RAF1	NM_002880	-	-1126
chr20	48131844	48132195	352	62	16	14.64	UBE2V1	NM_001032288	-	-1126
chr6	43846556	43847055	500	197	31	5.86	VEGFA	NM_001025369	+	-1125

chr19	12619131	12619446	316	261	17	9.25	MAN2B1	NM_000528	-	-1125
chr17	7017984	7018598	615	271	151	5.76	ASGR1	NM_001671	-	-1122
chr19	17277965	17278596	632	330	78	5.34	MRPL34	NM_023937	+	-1120
chr12	40993123	40993275	153	95	6	18.3	ZCRB1	NM_033114	-	-1120
chr3	51977479	51978690	1212	190	176	5.14	ABHD14B	NM_032750	-	-1119
chr6	33380695	33381140	446	307	27	5.22	TAPBP	NM_172209	-	-1117
chr14	104306819	104307850	1032	221	99	6.67	AKT1	NM_005163	-	-1117
chr7	50626160	50626373	214	137	10	11.26	GRB10	NM_001001550	-	-1114
chr1	148138684	148138936	253	93	15	17.08	BOLA1	NM_016074	+	-1112
chr4	657075	657335	261	70	33	9.77	ATP5I	NM_007100	-	-1110
chr20	5029392	5029598	207	148	17	9.85	C20orf30	NM_001009924	-	-1110
chr1	199370859	199371632	774	336	40	7.81	TMEM9	NM_016456	-	-1109
chr12	6472478	6472682	205	60	25	6	MRPL51	NM_016497	-	-1104
chr14	54378813	54379579	767	47	75	6.74	GCH1	NM_001024071	-	-1104
chr3	39425073	39425218	146	100	10	19.24	RPSA	NM_001012321	+	-1104
chr11	59098890	59099548	659	224	44	5.86	OSBP	NM_002556	-	-1102
chr3	101565915	101566100	186	61	8	12.62	TOMM70A	NM_014820	-	-1102
chr20	43387357	43388445	1089	416	217	5.6	SDC4	NM_002999	-	-1101
chr1	93390719	93391099	381	197	19	9.15	TMED5	NM_016040	-	-1101
chr12	7168475	7168654	180	80	26	7.91	RBP5	NM_031491	-	-1100
chr17	72242380	72242893	514	399	42	8.1	SFRS2	NM_003016	-	-1100
chr19	11408194	11408365	172	56	16	7.55	PRKCSH	NM_001001329	+	-1097
chr13	31989778	31990125	348	223	17	10.19	PFAAP5	NM_014887	-	-1095
chr11	27344825	27345179	355	161	23	6.93	LGR4	NM_018490	-	-1094
chr8	144988621	144988995	375	145	20	5.86	NRBP2	NM_178564	-	-1090
chr1	15772332	15772826	495	266	42	6.69	AGMAT	NM_024758	-	-1088

chrX	153359315	153359522	208	152	8	14.64	LAGE3	NM_006014	-	-1088
chr16	87291343	87291495	153	107	7	14.64	RNF166	NM_178841	-	-1086
chr3	58389225	58389482	258	76	16	7.55	PDHB	NM_000925	-	-1085
chr19	1549036	1549258	223	139	66	7.96	UQCR	NM_006830	-	-1085
chr19	960990	961734	745	62	72	8.97	C19orf6	NM_001033026	-	-1085
chr11	57265543	57266382	840	712	76	9.5	C11orf31	NM_170746	+	-1085
chr19	53066336	53066766	431	218	122	5.28	SULT2A1	NM_003167	-	-1084
chr18	55148757	55149171	415	354	27	6.84	LMAN1	NM_005570	-	-1084
chr18	11874351	11874557	207	146	11	18.18	MPPE1	NM_023075	-	-1084
chr5	180150121	180151235	1115	133	138	6.7	MGAT1	NM_002406	-	-1083
chr3	4378603	4378912	310	152	12	11.35	SUMF1	NM_182760	-	-1083
chr1	156067619	156068409	791	506	51	6.43	CD5L	NM_005894	-	-1080
chr6	43588456	43588621	166	53	10	14.64	YIPF3	NM_015388	-	-1079
chr10	98270429	98271497	1069	109	69	8.48	TM9SF3	NM_020123	-	-1078
chr12	27017907	27018466	560	253	28	7.38	TM7SF3	NM_016551	-	-1077
chr19	41178834	41179017	184	58	10	16.73	LOC644096	NM_001042631	+	-1077
chr17	18171973	18172995	1023	466	223	5.46	SHMT1	NM_004169	-	-1076
chr20	36190258	36191353	1096	208	114	6.82	TGM2	NM_004613	-	-1075
chr6	137560531	137561388	858	208	60	5.95	IFNGR1	NM_000416	-	-1074
chr19	18504454	18504641	188	105	31	9.63	FKBP8	NM_012181	-	-1074
chr19	10087630	10087764	135	84	11	11.98	EIF3S4	NM_003755	-	-1074
chr3	50300999	50301198	200	56	10	13.14	IFRD2	NM_006764	-	-1074
chr12	122031628	122031905	278	122	31	5.77	ARL6IP4	NM_001002252	+	-1073
chr13	49172422	49172535	114	58	6	29.28	KPNA3	NM_002267	-	-1073
chr17	7085378	7085534	157	81	21	5.36	GABARAP	NM_007278	-	-1072
chr21	45131017	45131370	354	211	16	12.09	ITGB2	NM_000211	-	-1072

chr11	65809357	65809699	343	128	21	18.41	YIF1A	NM_020470	-	-1072
chr14	34250166	34250471	306	223	19	7.84	CFL2	NM_021914	-	-1071
chr17	38204055	38204249	195	134	19	10.47	CCDC56	NM_001040431	-	-1071
chr9	138954714	138955778	1065	638	82	5.78	FBXW5	NM_018998	-	-1070
chr17	78166357	78166810	454	109	17	9.76	WDR45L	NM_019613	-	-1069
chr2	10841461	10842035	575	139	70	6.39	PDIA6	NM_005742	-	-1066
chr15	88575152	88575547	396	223	38	7.73	CIB1	NM_006384	-	-1066
chr3	48764030	48764161	132	78	6	15.58	PRKAR2A	NM_004157	-	-1065
chr1	939206	939805	600	187	27	5.49	ISG15	NM_005101	+	-1064
chr7	72621962	72622273	312	71	14	11.42	TBL2	NM_012453	-	-1064
chr9	115894686	115894801	116	59	6	17.57	KIF12	NM_138424	-	-1062
chr14	30639333	30640134	802	180	50	6.59	HECTD1	NM_015382	-	-1060
chr3	50312341	50313381	1041	58	164	10.16	HYAL1	NM_153286	-	-1057
chr1	149604273	149604460	188	68	30	11.93	SELENBP1	NM_003944	-	-1056
chr14	102871729	102872043	315	134	17	9.22	EIF5	NM_183004	+	-1055
chr1	152198238	152199262	1025	341	61	6	SLC39A1	NM_014437	-	-1050
chr6	132311560	132312061	502	241	32	7.35	CTGF	NM_001901	-	-1050
chr12	47683234	47683372	139	58	8	14.25	PRKAG1	NM_212461	-	-1050
chr17	18028785	18029062	278	221	16	12.21	ALKBH5	NM_017758	+	-1049
chr17	74182399	74182774	376	62	18	20.5	PSCD1	NM_004762	-	-1049
chr16	43898	44065	168	102	13	24.6	C16orf33	NM_024571	+	-1049
chr6	32917278	32917524	247	62	21	6.03	PSMB8	NM_148919	-	-1048
chr14	21037009	21037169	161	88	9	14.14	METTL3	NM_019852	-	-1047
chr17	5231013	5231189	177	95	9	8.51	NUP88	NM_002532	-	-1046
chr17	71407194	71407364	171	120	15	16.73	MRPL38	NM_032478	-	-1046
chr5	34023701	34024707	1007	521	104	7.56	AMACR	NM_014324	-	-1045

chr4	39177368	39177814	447	126	19	12.81	UGDH	NM_003359	-	-1044
chr17	18089776	18089923	148	56	8	14.64	FLII	NM_002018	-	-1044
chr6	30565987	30566292	306	242	34	5.82	HLA-E	NM_005516	+	-1043
chr6	116704893	116705483	591	358	43	5.99	TSPYL1	NM_003309	-	-1043
chr16	66820758	66820993	236	152	18	7.6	RBM35B	NM_024939	-	-1043
chr16	10534209	10534518	310	55	17	5.86	EMP2	NM_001424	-	-1042
chr11	10284086	10284259	174	59	6	19.52	ADM	NM_001124	+	-1042
chr12	94576363	94576755	393	333	17	11.39	NTN4	NM_021229	-	-1041
chr8	101339280	101339502	223	108	9	10.77	RNF19	NM_015435	-	-1039
chr20	33720585	33721062	478	157	27	7	NFS1	NM_021100	-	-1038
chr7	150119967	150120361	395	184	88	7.82	TMEM176B	NM_014020	-	-1038
chr2	27403103	27403264	162	37	6	15.41	GTF3C2	NM_001035521	-	-1038
chr16	3011252	3011398	147	47	6	17.43	TNFRSF12A	NM_016639	+	-1038
chr11	116196639	116197664	1026	340	77	7.51	APOA4	NM_000482	-	-1037
chr6	117988852	117989162	311	117	12	11.71	GOPC	NM_001017408	-	-1035
chr9	130532753	130532923	171	51	6	23.64	ZYG11BL	NM_006336	-	-1034
chr2	55052850	55053865	1016	805	212	5.61	RTN4	NM_007008	-	-1033
chr10	73797153	73798134	982	135	102	11.76	CBARA1	NM_006077	-	-1031
chr13	98134849	98135088	240	99	7	24.4	SLC15A1	NM_005073	-	-1031
chr9	138959837	138960563	727	185	53	5.44	C8G	NM_000606	+	-1030
chr16	31027869	31028278	410	52	21	12.01	BCKDK	NM_005881	+	-1030
chr20	412152	412367	216	58	9	20.92	CSNK2A1	NM_177560	-	-1030
chr11	62099801	62100125	325	37	12	6.27	TUT1	NM_022830	-	-1029
chr2	219792353	219793374	1022	77	56	7.04	ATG9A	NM_001077198	-	-1028
chr3	10343375	10343772	398	56	19	7.32	ATP2B2	NM_001001331	-	-1028
chr11	85346349	85347160	812	725	58	5.1	PICALM	NM_001008660	-	-1027

chr3	130370956	130372148	1193	766	227	5.6	CNBP	NM_003418	-	-1026
chr20	35579310	35580259	950	186	72	11.5	BLCAP	NM_006698	-	-1026
chr5	134934323	134935299	977	110	67	5.72	CXCL14	NM_004887	-	-1025
chr5	149762307	149762420	114	58	26	5.42	CD74	NM_001025159	-	-1024
chr3	147716445	147716681	237	94	11	13.88	PLSCR1	NM_021105	-	-1024
chrX	39796385	39796583	199	85	8	11.65	BCOR	NM_017745	-	-1023
chr19	1350412	1350629	218	149	30	6.96	GAMT	NM_138924	-	-1022
chr15	75125432	75126408	977	628	75	8.71	TSPAN3	NM_005724	-	-1022
chr1	158452343	158453149	807	150	50	6.71	WDR42A	NM_015726	-	-1021
chr19	1528272	1528698	427	61	22	7.99	MBD3	NM_003926	-	-1021
chr12	54991249	54991503	255	104	32	7	TMEM4	NM_014255	-	-1020
chr7	6030008	6031008	1001	212	112	7.79	EIF2AK1	NM_014413	-	-1018
chr10	1076057	1076983	927	170	107	8.91	IDI1	NM_004508	-	-1018
chr11	64645541	64645693	153	61	30	5.15	FAU	NM_001997	-	-1015
chr20	45719704	45720573	870	813	62	6.07	SULF2	NM_018837	-	-1015
chr12	6728110	6728445	336	262	40	7.19	MLF2	NM_005439	-	-1015
chr1	35422305	35422803	499	419	24	12.5	SFPQ	NM_005066	-	-1014
chr6	38751744	38752710	967	345	87	12.14	GLO1	NM_006708	-	-1013
chr19	54150746	54150939	194	54	9	14.2	BAX	NM_004324	+	-1011
chr15	71640070	71640419	350	46	17	6.66	NPTN	NM_012428	-	-1009
chr1	58813758	58814239	482	328	26	7.06	TACSTD2	NM_002353	-	-1009
chr1	152445778	152446831	1054	268	150	6	C1orf43	NM_138740	-	-1008
chr17	5277653	5277829	177	82	15	12.96	C1QBP	NM_001212	-	-1007
chr7	150129473	150129792	320	149	71	5.77	TMEM176A	NM_018487	+	-1006
chr19	5630324	5630438	115	58	6	35.46	P117	NM_205767	-	-1006
chr12	55775541	55776465	925	308	72	6.07	STAT6	NM_003153	-	-1004

chr11	64288663	64289656	994	85	82	7.62	SF1	NM_201995	-	-1003
chr8	145210289	145210512	224	83	9	16.89	GPAA1	NM_003801	+	-1001
chr1	87100992	87101716	725	342	72	7.57	37149	NM_004261	-	-999
chr11	60927042	60927776	735	131	44	9.41	FLJ12529	NM_024811	-	-998
chr1	37805862	37806002	141	80	7	16.27	GNL2	NM_013285	-	-998
chr5	176664299	176664438	140	70	10	16.4	PX19	NM_013237	+	-998
chr2	241817305	241817813	509	120	93	5.18	HDLBP	NM_203346	-	-997
chr3	169210689	169210921	233	116	19	6.14	GOLPH4	NM_014498	-	-997
chr1	74943811	74944768	958	878	83	8.09	CRYZ	NM_001889	-	-997
chr1	20851204	20851843	640	172	50	8.85	DDOST	NM_005216	-	-997
chr11	6589449	6589645	197	90	20	12.2	TAF10	NM_006284	-	-997
chr3	172196253	172197826	1574	1329	250	6.55	SLC2A2	NM_000340	-	-996
chr16	15062041	15062377	337	52	12	12.2	RRN3	NM_018427	-	-996
chr19	55707183	55707669	487	115	54	6.16	LOC554235	NM_001024656	-	-994
chr19	54692193	54692437	245	175	40	8.3	RPS11	NM_001015	+	-992
chr20	44412146	44412576	431	131	18	9.47	SLC35C2	NM_015945	-	-992
chr3	151941652	151942591	940	209	87	8.52	SIAH2	NM_005067	-	-991
chr3	48484989	48485191	203	54	15	9.47	SCOTIN	NM_016479	-	-991
chr19	7700702	7700842	141	81	10	9.76	CLEC4G	NM_198492	-	-991
chr12	6364440	6364608	169	57	9	12.81	LTBR	NM_002342	+	-991
chrX	55496001	55496250	250	61	12	9.76	MAGEH1	NM_014061	+	-988
chr2	73309454	73309630	177	117	7	19.26	C2orf7	NM_032319	-	-988
chr10	5847095	5848179	1085	268	100	9.93	GDI2	NM_001494	-	-987
chr14	23844146	23845219	1074	383	234	5.44	CIDEB	NM_014430	-	-985
chr2	75573510	75573936	427	333	38	7.71	TMEM166	NM_032181	-	-985
chr12	123828133	123829110	978	312	138	6.19	SCARB1	NM_005505	-	-982

chr1	67940124	67940718	595	116	23	7.47	GNG12	NM_018841	-	-982
chr14	66874549	66875324	776	622	37	9.09	ATP6V1D	NM_015994	-	-982
chr11	67108715	67108843	129	60	10	16.47	GSTP1	NM_000852	+	-982
chrX	84234727	84234936	210	135	8	28.16	SATL1	NM_001012980	-	-981
chr14	93819811	93820384	574	161	74	5.73	SERPINA10	NM_016186	-	-980
chr17	6946112	6946344	233	90	60	5.97	ASGR2	NM_080914	-	-980
chr1	149290535	149291050	516	266	23	6.1	CDC42SE1	NM_001038707	-	-980
chr2	85677138	85677326	189	117	15	17.57	LOC51255	NM_016494	+	-979
chr19	40929159	40929309	151	60	14	14.37	PSENEN	NM_172341	+	-976
chr12	45445578	45445785	208	62	37	5.68	SLC38A4	NM_018018	-	-975
chr19	2684269	2684497	229	180	12	20.12	SLC39A3	NM_144564	-	-973
chr11	193599	193895	297	213	16	7.32	BET1L	NM_016526	-	-972
chr8	59566098	59566261	164	107	8	8.37	CYP7A1	NM_000780	-	-970
chr2	208809732	208810166	435	288	46	6.03	IDH1	NM_005896	-	-968
chr17	71353392	71354342	951	723	95	5.8	WBP2	NM_012478	-	-967
chr9	122618800	122619116	317	36	13	6.19	PSMD5	NM_005047	-	-962
chr11	56930990	56931965	976	178	89	6.57	SLC43A3	NM_014096	-	-961
chr15	51595400	51595615	216	98	14	7.81	WDR72	NM_182758	-	-959
chr1	209985568	209985910	343	51	20	9.04	LPGAT1	NM_014873	-	-959
chr11	67577647	67577862	216	164	9	14.64	CHKA	NM_001277	-	-959
chr6	160021990	160023702	1713	1653	189	8.78	SOD2	NM_000636	-	-958
chr1	115051764	115052065	302	196	15	10.32	NRAS	NM_002524	-	-958
chr11	65887299	65887526	228	129	9	39.42	SLC29A2	NM_001532	-	-958
chrX	53475451	53475886	436	78	60	6.71	HADH2	NM_001037811	-	-956
chr3	49027270	49028392	1123	621	84	7.89	DALRD3	NM_001009996	-	-954
chr19	10895194	10895396	203	55	8	13.56	YIPF2	NM_024029	-	-952

chr19	15850692	15850785	94	48	7	18.3	CYP4F2	NM_001082	-	-952
chr14	22440385	22440643	259	118	13	9.76	RBM23	NM_018107	-	-949
chr2	220112335	220112869	535	128	28	7.32	CHPF	NM_024536	-	-948
chr1	6167791	6168612	822	126	47	7.74	RPL22	NM_000983	-	-945
chr1	26061235	26061507	273	46	13	7.99	PAQR7	NM_178422	-	-945
chr1	163898121	163899016	896	125	122	6.14	ALDH9A1	NM_000696	-	-944
chr9	34601159	34601433	275	140	12	14.64	C9orf23	NM_148178	-	-941
chr11	113672348	113672684	337	122	72	6.71	NNMT	NM_006169	+	-940
chr4	1195271	1196165	895	338	59	6.55	CTBP1	NM_001012614	-	-938
chr2	85398843	85399594	752	376	76	5.9	TGOLN2	NM_006464	-	-937
chr9	34077114	34077322	209	87	12	8.78	WDR40A	NM_015397	-	-937
chr17	37530452	37531460	1009	541	74	9.25	RAB5C	NM_004583	-	-937
chr1	203894149	203894539	391	317	16	12.81	SLC45A3	NM_033102	-	-936
chr11	61039518	61040297	780	633	35	5.71	SYT7	NM_004200	-	-934
chr9	99887188	99887389	202	123	8	14.08	TRIM14	NM_033221	-	-932
chr1	153183199	153184110	912	699	62	6.36	PBXIP1	NM_020524	-	-931
chr15	43247337	43247635	299	138	13	8.76	SHF	NM_138356	-	-930
chr5	150460779	150461390	612	182	53	8.96	ANXA6	NM_001155	-	-930
chr5	32160897	32161508	612	400	52	9.37	GOLPH3	NM_022130	-	-928
chr5	175748964	175749316	353	264	27	7.75	HIGD2A	NM_138820	+	-927
chr19	53811124	53811326	203	60	46	6.54	RPL18	NM_000979	-	-926
chr10	90963316	90964237	922	100	69	6.75	LIPA	NM_000235	-	-926
chr11	64377440	64377709	270	134	12	12.55	EHD1	NM_006795	-	-926
chr3	48869407	48870293	887	79	110	7.21	SLC25A20	NM_000387	-	-925
chrX	48318502	48318704	203	80	14	35.14	RBM3	NM_001017430	+	-925
chr1	6204187	6204765	579	269	28	5.09	ICMT	NM_012405	-	-924

chrX	18821318	18821723	406	58	22	11.39	PHKA2	NM_000292	-	-924
chr10	102736832	102736939	108	55	12	9.49	MRPL43	NM_032112	-	-923
chr11	65869942	65870342	401	296	20	13.7	B3GNT1	NM_006876	-	-923
chr5	150069212	150069422	211	133	11	7.72	DCTN4	NM_016221	-	-920
chr17	32516620	32516960	341	231	12	10.46	ACACA	NM_198838	-	-920
chr5	68697062	68697246	185	83	9	13.54	TAF9	NM_003187	-	-920
chr16	88290642	88291185	544	173	24	14.64	C16orf76	NM_152339	-	-920
chr10	14601187	14601483	297	53	18	10.15	FAM107B	NM_031453	-	-919
chr16	1928257	1929151	895	215	109	5.46	SEPX1	NM_016332	-	-917
chr1	207915383	207916304	922	842	127	6.94	G0S2	NM_015714	+	-917
chr8	26670483	26670746	264	106	15	10.25	ADRA1A	NM_033302	-	-917
chr17	4804036	4804162	127	71	12	12.39	SPAG7	NM_004890	-	-917
chr16	85998106	85998269	164	60	8	13.73	ZCCHC14	NM_015144	-	-917
chr3	72507082	72507355	274	49	13	8.78	RYBP	NM_012234	-	-915
chr1	1142194	1143065	872	103	79	6.38	SDF4	NM_016176	-	-914
chr12	120160402	120160793	392	52	23	7.88	CAMKK2	NM_172226	-	-914
chr16	4501323	4501593	271	115	15	8.54	C16orf5	NM_013399	-	-914
chr1	166931386	166932243	858	89	58	5.23	DPT	NM_001937	-	-913
chr9	131437385	131437615	231	98	12	29.28	ASB6	NM_017873	-	-912
chr17	7984502	7985425	924	258	65	8.12	PER1	NM_002616	-	-911
chr5	133560645	133560956	312	139	25	13.7	PPP2CA	NM_002715	-	-909
chr2	42848481	42848641	161	79	27	5.66	HAAO	NM_012205	-	-908
chr17	64375784	64375933	150	62	9	14.64	ABCA8	NM_007168	-	-908
chr20	4781428	4781908	481	234	29	7.32	SLC23A2	NM_005116	-	-907
chr19	1936447	1937353	907	60	46	10.33	BTBD2	NM_017797	-	-907
chr4	55639970	55640312	343	248	16	6.66	KDR	NM_002253	-	-906

chr10	120917323	120918110	788	360	100	5.91	PRDX3	NM_006793	-	-905
chr7	149666973	149667255	283	92	60	6.22	RARRES2	NM_002889	-	-904
chr3	48687006	48687187	182	124	8	17.08	NCKIPSD	NM_016453	-	-904
chr19	1056072	1056551	480	366	69	6.35	GPX4	NM_001039848	+	-903
chr19	63755241	63755646	406	89	49	7.03	CHMP2A	NM_198426	-	-901
chr17	52320997	52321169	173	52	7	17.57	TRIM25	NM_005082	-	-901
chr11	65122406	65122701	296	59	23	7.75	MAP3K11	NM_002419	-	-899
chr22	40811966	40812374	409	184	42	8.75	NDUFA6	NM_002490	-	-898
chr4	70742297	70742417	121	61	7	20.92	SULT1E1	NM_005420	-	-898
chr9	103192764	103192967	204	144	8	23.64	MRPL50	NM_019051	-	-898
chr19	44124297	44124777	481	92	27	7.04	FBXO17	NM_148169	-	-896
chr3	158348608	158349176	569	163	77	7.19	CCNL1	NM_020307	-	-895
chr1	154529738	154530003	266	100	14	7.79	C1orf85	NM_144580	-	-895
chr12	6308210	6309079	870	73	76	9.26	TNFRSF1A	NM_001065	-	-895
chrX	102395181	102395473	293	111	19	8.58	TCEAL8	NM_001006684	-	-894
chr19	1193450	1193641	192	70	22	7.87	ATP5D	NM_001001975	+	-893
chr6	33492830	33493188	359	232	25	9.76	CUTA	NM_001014837	-	-892
chr5	95249534	95249744	211	59	19	10.3	ELL2	NM_012081	-	-892
chr20	32331772	32332627	856	335	79	7.83	AHCY	NM_000687	-	-891
chr9	114021150	114021428	279	177	11	12.25	ROD1	NM_005156	-	-890
chr2	73022705	73023561	857	200	63	10.98	SFXN5	NM_144579	-	-888
chr13	28172227	28173106	880	187	80	7.36	LOC283537	NM_181785	-	-887
chr1	42695473	42695646	174	123	8	17.43	PPCS	NM_024664	+	-887
chr1	163963182	163964017	836	391	53	6.48	TMCO1	NM_019026	-	-886
chr12	49604823	49605686	864	345	119	7.23	METTL7A	NM_014033	+	-886
chr3	101565017	101565884	868	90	54	15.89	TOMM70A	NM_014820	-	-886

chr10	64597620	64597880	261	134	12	8.78	JMJD1C	NM_004241	-	-885
chr10	101146639	101147500	862	751	125	5.28	GOT1	NM_002079	-	-883
chr12	53075769	53076196	428	164	21	8.36	ITGA5	NM_002205	-	-883
chr22	15998966	15999290	325	177	18	5.71	CECR5	NM_033070	-	-880
chr9	111180422	111181218	797	134	32	5.83	PTPN3	NM_002829	-	-880
chr22	22706827	22707020	194	83	13	13.01	GSTT1	NM_000853	-	-880
chr4	185546384	185546788	405	205	21	8.3	IRF2	NM_002199	-	-879
chr9	35803241	35803837	597	475	46	8.74	HINT2	NM_032593	-	-879
chrX	129091598	129091897	300	91	32	6.59	AIFM1	NM_004208	-	-878
chr14	74017161	74017274	114	58	7	14.64	NPC2	NM_006432	-	-878
chr22	17698918	17699101	184	83	9	14.64	HIRA	NM_003325	-	-878
chr9	129617068	129617993	926	131	79	7.05	ENG	NM_000118	-	-877
chr8	145700761	145701109	349	289	26	7.64	GPT	NM_005309	+	-877
chr3	121596005	121596692	688	267	41	5.33	FSTL1	NM_007085	-	-876
chr21	43346395	43347247	853	134	180	6.04	CBS	NM_000071	-	-876
chr21	45014030	45014259	230	72	13	11.39	UBE2G2	NM_182688	-	-876
chr5	139910227	139910713	487	372	35	12.39	SRA1	NM_001035235	-	-876
chr20	33054431	33054751	321	231	25	12.69	TRPC4AP	NM_015638	-	-876
chr7	72821835	72822138	304	192	15	7.99	CLDN3	NM_001306	-	-875
chr9	12765066	12765886	821	156	48	12.02	C9orf150	NM_203403	+	-875
chr1	202639446	202640017	572	335	39	6.85	PPP1R15B	NM_032833	-	-874
chr19	16618311	16618837	527	173	32	8.61	C19orf42	NM_024104	-	-873
chr3	127544712	127545040	329	61	23	8.67	KLF15	NM_014079	-	-873
chr4	17097141	17097990	850	206	136	5.41	QDPR	NM_000320	-	-870
chr1	19537973	19538729	757	532	57	5.54	CAPZB	NM_004930	-	-870
chr16	73465698	73465841	144	54	7	29.55	WDR59	NM_030581	-	-870

chr22	23266437	23267278	842	393	123	5.87	C22orf13	NM_031444	-	-869
chr3	150231036	150231461	426	94	21	9.76	HLTF	NM_139048	-	-868
chr2	238147731	238148569	839	141	84	5.31	RAB17	NM_022449	-	-866
chr6	43302021	43302212	192	53	14	19.03	C6orf108	NM_006443	-	-866
chr1	152821189	152822023	835	116	79	5.13	ADAR	NM_001111	-	-865
chr11	10775213	10776034	822	124	133	8.42	EIF4G2	NM_001418	-	-865
chr1	24044222	24045022	801	124	80	8.47	FUCA1	NM_000147	-	-862
chr22	22566913	22567425	513	402	110	5.71	MIF	NM_002415	+	-861
chr17	37164413	37165249	837	276	62	6.13	JUP	NM_002230	-	-860
chr12	122672083	122672382	300	140	13	15.37	EIF2B1	NM_001414	-	-860
chr12	12520379	12520956	578	224	25	9.15	DUSP16	NM_030640	-	-859
chr3	58154090	58154251	162	60	21	8.54	DNASE1L3	NM_004944	-	-858
chr2	65167663	65168350	688	147	31	9.98	RAB1A	NM_004161	-	-858
chr20	38748387	38748789	403	108	17	14.75	MAFB	NM_005461	-	-857
chr3	124693461	124693949	489	421	39	7.16	PTPLB	NM_198402	-	-856
chr9	106583541	106583962	422	219	21	12.36	ABCA1	NM_005502	-	-856
chr6	37044361	37044749	389	259	24	5.58	MTCH1	NM_014341	-	-854
chr15	41872327	41872660	334	210	59	8.38	SERF2	NM_001018108	+	-853
chr4	21998208	21998949	742	584	56	8.83	GPR125	NM_145290	-	-853
chr20	22510076	22510674	599	313	36	9.74	FOXA2	NM_021784	-	-852
chr8	52893430	52893552	123	62	6	17.57	PCMTD1	NM_052937	-	-851
chr4	39229305	39229794	490	374	44	9.78	C4orf34	NM_174921	-	-850
chr2	43893445	43893963	519	133	50	11.82	ABCG5	NM_022436	-	-848
chr16	45394040	45394305	266	158	13	9.32	LOC388272	NM_001001436	-	-846
chr12	112314646	112315480	835	286	199	5.42	SDS	NM_006843	-	-845
chr7	150409539	150409949	411	266	25	7.74	TMUB1	NM_031434	-	-844

chr12	47537617	47538043	427	248	22	7.81	RND1	NM_014470	-	-844
chr8	30040085	30041016	932	248	116	5.25	TMEM66	NM_016127	-	-843
chr3	198721570	198721892	323	158	22	5.83	BDH1	NM_004051	-	-841
chr19	568757	569063	307	168	23	14.98	POLRMT	NM_005035	-	-841
chr6	17723945	17724087	143	90	8	14.64	NUP153	NM_005124	-	-840
chr9	130896902	130897734	833	62	121	6.25	CRAT	NM_004003	-	-839
chr9	139256227	139256369	143	57	9	16.75	TUBB2C	NM_006088	+	-838
chr1	151774284	151774536	253	127	28	5.56	S100A6	NM_014624	-	-837
chr3	50300763	50300961	199	115	13	13.18	IFRD2	NM_006764	-	-837
chr3	95075005	95075482	478	99	74	8.27	PROS1	NM_000313	-	-836
chr2	219947757	219947996	240	192	13	12.3	DNPEP	NM_012100	-	-836
chr3	48420279	48421101	823	200	75	6.02	PLXNB1	NM_002673	-	-835
chr12	54911263	54911728	466	292	37	8.68	SLC39A5	NM_173596	+	-835
chr1	31868586	31868892	307	60	17	11.99	PEF1	NM_012392	-	-835
chr5	55272956	55273285	330	209	18	7.73	IL6ST	NM_002184	-	-834
chr3	67508298	67508668	371	265	25	8.61	SUCLG2	NM_003848	-	-833
chr10	74805558	74806040	483	379	30	12.12	ANXA7	NM_001156	-	-831
chr14	64482985	64483118	134	60	6	18.3	RAB15	NM_198686	-	-831
chr9	94298007	94298250	244	96	9	24.4	ECM2	NM_001393	-	-831
chr3	47033314	47033740	427	166	24	17.08	SETD2	NM_014159	-	-830
chr2	37062109	37062486	378	129	17	21.96	KIAA1414	NM_019024	-	-830
chr9	129743121	129743510	390	247	20	6.66	FAM102A	NM_203305	-	-829
chr10	81905292	81905687	396	198	33	6.32	ANXA11	NM_001157	-	-828
chr17	57023289	57023401	113	57	7	17.08	NACAL	NM_199290	-	-826
chrX	99770735	99771275	541	274	37	6.1	TSPAN6	NM_003270	-	-825
chr4	129411065	129411570	506	425	32	5.73	PGRMC2	NM_006320	-	-822

chr7	100662789	100662915	127	78	7	27.45	CLDN15	NM_014343	-	-822
chr6	26021418	26021788	371	190	29	7.24	SLC17A2	NM_005835	-	-820
chr9	138687415	138688233	819	556	138	5.84	AGPAT2	NM_001012727	-	-818
chr11	68278937	68279484	548	401	83	6.35	CPT1A	NM_001031847	-	-818
chr19	14063672	14064325	654	493	54	8.3	PRKACA	NM_207518	-	-817
chr13	110329379	110329704	326	59	20	9.55	ANKRD10	NM_017664	-	-816
chr5	1103511	1104314	804	130	57	9.25	SLC12A7	NM_006598	-	-815
chr3	187841520	187841657	138	55	11	20.2	FETUB	NM_014375	+	-815
chr5	41178025	41178906	882	476	262	5.25	C6	NM_000065	-	-814
chr4	70380493	70381285	793	481	230	6.57	UGT2B4	NM_021139	-	-813
chr8	102000767	102000902	136	58	6	21.53	YWHAZ	NM_145690	-	-813
chr2	190133640	190134374	735	482	96	5.52	SLC40A1	NM_014585	-	-812
chr10	103534125	103535009	885	154	48	5.3	MGEA5	NM_012215	-	-811
chr16	45251722	45251902	181	59	12	13.42	VPS35	NM_018206	-	-811
chr1	151845996	151846800	805	286	71	5.89	S100A16	NM_080388	-	-810
chr9	135617347	135617647	301	100	21	7.32	VAV2	NM_003371	-	-810
chr20	34004880	34005769	890	493	71	8.23	SCAND1	NM_016558	-	-810
chr11	65577055	65577201	147	60	7	21.43	SF3B2	NM_006842	+	-810
chr15	73450943	73451138	196	62	7	14.64	SIN3A	NM_015477	-	-809
chr16	82644893	82645679	787	98	45	6.2	MBTPS1	NM_201268	-	-808
chr1	97316191	97316697	507	221	30	11.13	DPYD	NM_000110	-	-808
chr17	4795848	4795966	119	60	14	12.2	ENO3	NM_001976	+	-808
chr11	118400293	118401081	789	61	144	7.49	SLC37A4	NM_001467	-	-806
chr16	11680509	11681249	741	201	50	7.66	TXNDC11	NM_015914	-	-806
chr1	199719311	199720087	777	242	61	5.46	CSRP1	NM_004078	-	-805
chr11	58233384	58234943	1560	438	250	7.9	GLYAT	NM_005838	-	-805

chr7	97749577	97749724	148	91	21	6.5	BRI3	NM_015379	+	-802
chr7	95587383	95588269	887	398	72	8.02	SLC25A13	NM_014251	-	-801
chr5	133521031	133521267	237	130	16	9.54	SKP1A	NM_170679	-	-800
chr19	52241693	52241807	115	58	6	21.96	TMEM160	NM_017854	-	-800
chr6	133044352	133045223	872	385	143	5.73	VNN1	NM_004666	-	-799
chr12	55150865	55151802	938	535	137	7.32	GLS2	NM_013267	-	-799
chr19	60857701	60858026	326	165	15	7.95	U2AF2	NM_001012478	+	-799
chr6	31935301	31935730	430	281	19	10.49	NEU1	NM_000434	-	-799
chr3	188922480	188922657	178	75	9	12.55	BCL6	NM_138931	-	-799
chr6	158978142	158978290	149	62	9	14.64	DYNLT1	NM_006519	-	-797
chr4	88477102	88477583	482	323	48	6.12	DHRS8	NM_016245	-	-795
chr2	198074043	198074159	117	59	8	13.7	HSPE1	NM_002157	+	-795
chr20	30754467	30754960	494	396	26	16.73	COMMD7	NM_053041	-	-795
chrX	48664901	48665225	325	60	17	11.1	OTUD5	NM_017602	-	-794
chr2	53945519	53945867	349	207	29	6.13	PSME4	NM_014614	-	-793
chr12	108852542	108852784	243	109	9	9.76	GIT2	NM_014776	-	-793
chr1	24000922	24001746	825	188	194	6.23	HMGCL	NM_000191	-	-792
chr3	48701033	48701231	199	143	11	43.92	IHPK2	NM_001005909	-	-791
chr19	2051993	2052782	790	57	52	15.42	AP3D1	NM_003938	-	-789
chrX	149685477	149686255	779	664	45	6.08	CD99L2	NM_031462	-	-788
chr3	185911314	185911636	323	226	18	11.03	MAGEF1	NM_022149	-	-787
chr22	18479853	18480183	331	54	14	8.37	HTF9C	NM_022727	-	-786
chr9	123141184	123141961	778	91	125	6.58	STOM	NM_198194	-	-784
chr6	109794451	109795198	748	454	81	5.53	CD164	NM_006016	-	-783
chr17	24424673	24425447	775	59	57	10.47	TIAF1	NM_004740	-	-783
chr8	144728520	144728881	362	272	35	11.56	NAPRT1	NM_145201	-	-783

chr11	125578115	125578301	187	62	8	20.5	RPUSD4	NM_032795	-	-783
chr1	149604008	149604186	179	99	27	5.24	SELENBP1	NM_003944	-	-782
chr5	134698383	134698751	369	72	25	6.95	H2AFY	NM_138609	-	-782
chr5	132186261	132186692	432	259	23	11.07	SHROOM1	NM_133456	-	-782
chr8	30656550	30656758	209	61	16	13.77	GSR	NM_000637	-	-782
chr6	43412262	43412567	306	191	12	13.94	ZNF318	NM_014345	-	-782
chr17	7096944	7097056	113	57	9	14.89	C17orf81	NM_203413	+	-782
chr5	78329567	78329965	399	171	44	7.3	DMGDH	NM_013391	-	-780
chr19	1988491	1989248	758	82	61	10.54	MKNK2	NM_017572	-	-779
chr3	81622008	81622325	318	258	23	11.64	GBE1	NM_000158	-	-778
chr6	2964690	2964990	301	222	33	6.06	LOC401233	NM_001013680	-	-777
chr4	1687548	1688254	707	432	37	6.37	TMEM129	NM_138385	-	-777
chr10	126076413	126076638	226	147	14	8.78	OAT	NM_000274	-	-777
chr11	62117652	62118027	376	226	22	13.21	MTA2	NM_004739	-	-777
chr2	144862673	144862829	157	102	7	18.77	ZFHX1B	NM_014795	-	-776
chr19	44568607	44568886	280	204	20	7.38	PAF1	NM_019088	-	-775
chr6	31732108	31732424	317	236	52	10.44	APOM	NM_019101	+	-775
chr19	52682716	52683475	760	294	79	5.22	NAPA	NM_003827	-	-773
chr17	77455311	77456156	846	189	89	7.62	PCYT2	NM_002861	-	-773
chr9	33807793	33807952	160	113	6	14.64	UBE2R2	NM_017811	+	-771
chr8	9032929	9033685	757	101	55	6.1	PPP1R3B	NM_024607	-	-770
chrX	119454991	119455162	172	59	7	14.64	LAMP2	NM_013995	-	-770
chr5	57785779	57786337	559	319	28	8.18	PLK2	NM_006622	-	-769
chr19	55064162	55064875	714	548	36	5.86	AKT1S1	NM_032375	-	-767
chr7	26198029	26198757	729	655	130	5.03	HNRPA2B1	NM_002137	-	-766
chr19	17203701	17204460	760	71	94	5.42	NR2F6	NM_005234	-	-766

chr1	219941777	219942154	378	127	29	6.64	DUSP10	NM_144728	-	-766
chr20	2975248	2975439	192	112	11	9.84	MRPS26	NM_030811	+	-765
chr15	63042454	63043180	727	131	77	6.48	SPG21	NM_016630	-	-764
chr22	49311539	49311812	274	59	18	11.71	ECGF1	NM_001953	-	-763
chr19	10058565	10058771	207	151	13	13.64	FLJ11286	NM_018381	+	-763
chr7	72493281	72493440	160	76	8	14.06	BAZ1B	NM_032408	-	-763
chr11	67108488	67108624	137	70	11	25.34	GSTP1	NM_000852	+	-763
chr2	136381330	136381485	156	100	8	15.99	DARS	NM_001349	-	-762
chr11	6659789	6660216	428	59	21	7.31	MRPL17	NM_022061	-	-761
chr6	70443058	70443232	175	57	9	19.52	LMBRD1	NM_018368	-	-761
chr3	39158359	39159109	751	103	65	8.1	AXUD1	NM_033027	-	-759
chr3	48484302	48484957	656	85	56	9.6	SCOTIN	NM_016479	-	-757
chr17	17350250	17350360	111	56	10	16.27	PEMT	NM_148173	-	-757
chr12	54797202	54797395	194	85	8	14.64	RPL41	NM_001035267	+	-755
chr22	17543120	17543846	727	401	98	9.12	SLC25A1	NM_005984	-	-752
chr10	123228242	123228596	355	101	22	6.06	FGFR2	NM_022970	-	-751
chr19	2184674	2184905	232	175	10	10.46	PLEKHJ1	NM_018049	-	-751
chr12	48784619	48784817	199	62	26	5.46	GPD1	NM_005276	+	-750
chr12	169512	170262	751	467	62	6.94	SLC6A12	NM_003044	-	-750
chr12	13019091	13019817	727	342	80	9.63	HEBP1	NM_015987	-	-750
chr22	45043057	45043273	217	54	8	19.06	FLJ20699	NM_017931	+	-749
chr17	4639463	4639741	279	177	20	8.17	LOC388323	NM_001014985	+	-748
chr17	43270635	43270804	170	110	13	13.69	SCRN2	NM_138355	-	-748
chr3	49037327	49037519	193	60	15	19.83	IMPDH2	NM_000884	-	-748
chr1	120092143	120093274	1132	607	520	5.23	HMGCS2	NM_005518	-	-747
chr9	94923618	94924347	730	61	60	5.63	NINJ1	NM_004148	-	-747

chr11	47217460	47218174	715	234	54	7.2	ACP2	NM_001610	-	-746
chr19	44511442	44511587	146	61	9	14.96	GMFG	NM_004877	-	-746
chr16	2167431	2167928	498	118	20	7.29	CASKIN1	NM_020764	-	-744
chr15	73718504	73719234	731	123	53	9.06	IMP3	NM_018285	-	-744
chr6	144457733	144458454	722	91	79	9.87	SF3B5	NM_031287	-	-744
chr17	1561645	1562297	653	509	32	10.25	MGC14376	NM_032895	-	-744
chr11	57008584	57009326	743	60	81	5.64	SLC43A1	NM_003627	-	-743
chr17	59262993	59263919	927	62	59	8.78	SMARCD2	NM_003077	-	-743
chr5	108698675	108699060	386	252	27	6.22	PJA2	NM_014819	-	-742
chr16	85997587	85998094	508	114	24	8.93	ZCCHC14	NM_015144	-	-742
chr17	12837021	12837176	156	55	6	22.88	ELAC2	NM_018127	-	-742
chr11	59330235	59330930	696	203	54	5.66	MRPL16	NM_017840	-	-741
chr1	1298995	1299711	717	303	95	5.38	AURKAIP1	NM_017900	-	-739
chr6	64340383	64340615	233	126	15	7.96	PTP4A1	NM_003463	+	-737
chr19	10457833	10458532	700	254	42	10.25	KEAP1	NM_012289	-	-737
chr6	112499262	112499411	150	98	6	14.64	TUBE1	NM_016262	-	-737
chr10	80812095	80812827	733	101	43	8.78	C10orf56	NM_153367	-	-736
chr1	233339420	233340017	598	417	35	6.25	TOMM20	NM_014765	-	-735
chr15	47207375	47207569	195	60	13	6.66	COPS2	NM_004236	-	-735
chr19	12910920	12911157	238	90	37	7.19	CALR	NM_004343	+	-735
chr14	53963889	53964130	242	61	16	7.32	CNIH	NM_005776	-	-734
chr5	35034286	35034696	411	347	27	8.78	AGXT2	NM_031900	-	-734
chr1	43622779	43622909	131	60	6	15.25	MED8	NM_052877	-	-734
chr1	199617089	199617320	232	122	12	10.19	LAD1	NM_005558	-	-732
chr17	71818977	71819340	364	191	23	7.11	PRPSAP1	NM_002766	-	-731
chr11	76978831	76979058	228	124	8	11.71	AQP11	NM_173039	+	-731

chr15	88027636	88028020	385	59	21	6.41	PEX11A	NM_003847	-	-729
chr6	46625773	46626133	361	103	25	6.8	CYP39A1	NM_016593	-	-729
chr12	45444825	45445539	715	232	148	6.91	SLC38A4	NM_018018	-	-729
chr16	74239708	74239911	204	61	8	11.95	TERF2IP	NM_018975	+	-727
chr13	20965441	20965565	125	47	6	14.64	EFHA1	NM_152726	-	-726
chr10	99186215	99186380	166	58	8	17.01	EXOSC1	NM_016046	-	-724
chr1	21795839	21796025	187	126	7	22.88	RAP1GAP	NM_002885	-	-724
chr10	104229428	104229698	271	196	12	10.46	ACTR1A	NM_005736	-	-722
chr16	15595992	15596466	475	177	25	5.22	KIAA0430	NM_014647	-	-721
chr4	83958781	83959555	775	611	63	5.67	SEC31A	NM_001077208	-	-717
chr6	90410441	90410668	228	139	13	10.01	MDN1	NM_014611	-	-717
chr2	86684309	86684743	435	61	32	10.92	RNF103	NM_005667	-	-717
chr19	43912740	43913385	646	62	52	6.88	CAPN12	NM_144691	-	-714
chr11	33063252	33063424	173	97	8	12.2	CSTF3	NM_001326	-	-714
chr2	96214348	96215044	697	367	46	6	STARD7	NM_020151	-	-713
chr17	71265553	71266325	773	203	106	8.3	GALK1	NM_000154	-	-713
chr17	68791861	68792070	210	95	13	7.99	CDC42EP4	NM_012121	-	-712
chr2	74506538	74507207	670	62	63	11.32	RTKN	NM_001015056	-	-711
chr11	133623903	133624094	192	132	14	7.5	THYN1	NM_001037305	-	-710
chr19	59397087	59397247	161	108	14	9.43	RPS9	NM_001013	+	-710
chr4	106510202	106510393	192	115	24	9.84	PPA2	NM_001034191	-	-710
chr17	37718997	37719578	582	423	54	15.86	STAT3	NM_213662	-	-710
chr4	186743820	186744301	482	231	34	7.76	SORBS2	NM_003603	-	-709
chr19	43998312	43998611	300	78	54	5.94	ECH1	NM_001398	-	-708
chr17	1194617	1195302	686	364	77	6.18	YWHAE	NM_006761	-	-708
chr11	71392036	71392266	231	149	17	7.61	NUMA1	NM_006185	-	-708

chr20	7811651	7812336	686	626	164	5.02	HAO1	NM_017545	-	-706
chr3	123729628	123730167	540	224	27	7.91	PARP9	NM_031458	-	-705
chr17	35853250	35853903	654	577	124	6.32	IGFBP4	NM_001552	+	-702
chr12	54361776	54362387	612	429	44	8.96	METTL7B	NM_152637	+	-702
chr15	99630000	99630613	614	183	32	6.74	SELS	NM_018445	-	-700
chr2	71066621	71067277	657	434	35	7.21	TEX261	NM_144582	-	-700
chr2	27568205	27568954	750	619	46	7.93	FNDC4	NM_022823	-	-700
chr1	167700061	167700490	430	248	23	6.3	SLC19A2	NM_006996	-	-699
chr18	46063202	46063415	214	47	13	8.78	CXXC1	NM_014593	-	-699
chr7	105676406	105676665	260	142	16	8.88	PBEF1	NM_005746	-	-698
chr22	26577750	26578355	606	118	45	9.76	PITPNB	NM_012399	-	-698
chr19	46629120	46629760	641	229	28	7.32	FLJ10241	NM_018035	-	-697
chr9	34511428	34511736	309	211	13	10.98	C9orf165	NM_198573	-	-697
chr1	2479724	2479849	126	71	10	11.71	TNFRSF14	NM_003820	-	-697
chr10	88800655	88800917	263	76	59	6.85	GLUD1	NM_005271	-	-695
chrX	38096748	38096996	249	198	18	16.41	OTC	NM_000531	+	-695
chr4	7112734	7113374	641	506	33	7.32	GRPEL1	NM_025196	-	-694
chr4	6760711	6761029	319	159	29	7.71	MRFAP1L1	NM_152301	-	-694
chr2	217245524	217245767	244	108	10	12.55	IGFBP5	NM_000599	-	-694
chr19	40322754	40322924	171	116	26	6.26	FXVD1	NM_005031	+	-693
chrX	153660288	153660852	565	223	25	31.06	MPP1	NM_002436	-	-691
chr10	13359806	13360492	687	523	151	5.03	PHYH	NM_001037537	-	-690
chr8	28259165	28259712	548	169	29	20.59	ZNF395	NM_018660	-	-690
chr14	64475625	64476313	689	323	78	6.05	GPX2	NM_002083	-	-689
chr17	71449137	71449877	741	295	119	6.56	ACOX1	NM_004035	-	-689
chr5	150068768	150069191	424	170	19	20.5	DCTN4	NM_016221	-	-689

chr16	19420535	19421205	671	94	28	8.19	MIR16	NM_016641	-	-688
chr17	4781288	4782036	749	129	52	9.28	SLC25A11	NM_003562	-	-688
chr8	42393204	42393838	635	105	33	5.58	SLC20A2	NM_006749	-	-687
chr21	27130933	27131165	233	148	8	13.65	ADAMTS1	NM_006988	-	-687
chr20	57003632	57004320	689	314	188	5.04	CTSZ	NM_001336	-	-685
chr1	229731584	229731706	123	62	6	17.57	TSNAX	NM_005999	+	-685
chr4	122808823	122809281	459	152	37	6.72	ANXA5	NM_001154	-	-684
chr1	201197807	201198309	503	193	23	6.14	CYB5R1	NM_016243	-	-683
chr5	151021180	151021889	710	198	49	6.78	SPARC	NM_003118	-	-683
chr12	112221522	112221637	116	59	6	17.57	SLC24A6	NM_024959	-	-683
chr9	139566323	139566845	523	415	92	5.1	MRPL41	NM_032477	+	-681
chr5	135310519	135311179	661	457	110	8.27	LECT2	NM_002302	-	-681
chr1	149639086	149639344	259	99	35	5.69	PSMB4	NM_002796	+	-680
chr19	10305822	10306133	312	87	33	6.83	ICAM3	NM_002162	-	-680
chr17	44836418	44837096	679	556	45	9.94	PHB	NM_002634	-	-678
chr6	33348409	33348507	99	50	14	10.15	RPS18	NM_022551	+	-678
chr19	5867672	5867831	160	114	6	18.3	RANBP3	NM_003624	-	-678
chr6	122806208	122806868	661	369	54	7.26	SERINC1	NM_020755	-	-677
chr6	33326401	33326703	303	159	19	13.31	VPS52	NM_022553	-	-676
chr11	65378861	65379537	677	329	72	5.81	CFL1	NM_005507	-	-675
chr7	135262237	135262723	487	396	28	8.32	MTPN	NM_145808	-	-675
chr9	35046466	35047234	769	343	70	5.63	VCP	NM_007126	-	-674
chr9	98122893	98123482	590	102	36	6.91	SLC35D2	NM_007001	-	-673
chr5	133335965	133336178	214	49	11	10.25	VDAC1	NM_003374	-	-673
chr17	18028457	18028686	230	109	9	14.64	ALKBH5	NM_017758	+	-673
chr2	20095928	20096562	635	107	115	6.03	LAPTM4A	NM_014713	-	-669

chr6	108639447	108640079	633	288	59	6.18	SNX3	NM_003795	-	-669
chr12	21580421	21581057	637	514	52	6.69	GYS2	NM_021957	-	-668
chr20	48240800	48241450	651	53	48	9.53	CEBPB	NM_005194	+	-668
chr14	20339545	20340022	478	54	27	5.44	RNASE1	NM_198232	-	-667
chr1	54270201	54270604	404	287	65	7.56	TMEM59	NM_004872	-	-666
chr4	1150661	1151388	728	377	39	8.2	SPON2	NM_012445	-	-666
chr8	145511304	145511428	125	60	9	10.65	DGAT1	NM_012079	-	-666
chr21	15255570	15256092	523	242	34	10.94	NRIP1	NM_003489	-	-666
chr16	73465415	73465637	223	131	8	17.57	WDR59	NM_030581	-	-666
chr7	94872134	94872775	642	193	59	6.27	PON2	NM_000305	-	-665
chr17	70638415	70638583	169	79	8	24.4	NT5C	NM_014595	-	-665
chr5	150389713	150390363	651	460	69	5.2	TNIP1	NM_006058	-	-663
chr12	48433023	48433174	152	55	40	13.8	TEGT	NM_003217	+	-663
chr17	70256334	70257040	707	463	50	5.99	SLC9A3R1	NM_004252	+	-662
chr6	89847199	89847877	679	62	48	9.94	PNRC1	NM_006813	+	-662
chr19	7699864	7700513	650	77	63	11.9	CLEC4G	NM_198492	-	-662
chr2	190754396	190754587	192	62	7	19.52	MGC13057	NM_032321	+	-662
chr22	48698864	48699008	145	85	9	34.45	CRELD2	NM_024324	+	-661
chr3	49429396	49429875	480	102	42	7.91	AMT	NM_000481	-	-660
chr17	53921905	53922555	651	206	38	6.35	MTMR4	NM_004687	-	-659
chr19	41178346	41178599	254	103	9	18.3	LOC644096	NM_001042631	+	-659
chr11	65049676	65049781	106	54	6	24.4	SCYL1	NM_020680	+	-658
chr1	154245404	154246120	717	263	79	5.88	SSR2	NM_003145	-	-657
chr11	6578225	6578386	162	114	6	26.14	KIAA0409	NM_015324	-	-657
chr11	71486046	71486642	597	177	41	6.56	C11orf59	NM_017907	-	-656
chr11	484861	485167	307	58	18	7.19	RNH1	NM_002939	-	-656

chr12	7138473	7138947	475	160	30	7.73	C1RL	NM_016546	-	-656
chr10	21823821	21824083	263	151	15	8.54	C10orf114	NM_001010911	-	-656
chr10	99427191	99427826	636	54	48	7.16	AVPI1	NM_021732	-	-654
chr17	71546893	71547439	547	426	31	7.28	SRP68	NM_014230	-	-654
chr6	33367720	33368068	349	44	15	7.32	RGL2	NM_004761	-	-653
chr11	64418775	64419246	472	136	19	8.37	KIAA0404	NM_015104	-	-652
chr16	1761899	1762548	650	206	56	5.6	MRPS34	NM_023936	-	-651
chr19	2705747	2706361	615	300	35	6.3	SGTA	NM_003021	-	-650
chr3	57532296	57532779	484	85	45	7.09	ARF4	NM_001660	-	-650
chr18	59149050	59149462	413	104	24	6.91	FVT1	NM_002035	-	-649
chr20	29656781	29657401	621	60	48	8.44	ID1	NM_181353	+	-649
chr6	41142610	41143158	549	505	29	10.25	C6orf130	NM_145063	-	-649
chr6	30260245	30260860	616	243	38	6.44	TRIM26	NM_003449	-	-648
chr8	18429483	18429740	258	161	11	17.08	PSD3	NM_206909	-	-648
chr2	96622995	96623284	290	229	16	8.49	FLJ10081	NM_017991	-	-647
chr2	31410624	31411336	713	575	69	6.68	XDH	NM_000379	-	-645
chr3	50330632	50330888	257	123	11	10.46	HYAL2	NM_033158	-	-645
chr17	37807938	37808644	707	509	38	5.39	PTRF	NM_012232	-	-644
chr20	17542310	17542966	657	81	85	10.1	RRBP1	NM_001042576	-	-644
chr2	8739609	8740205	597	230	112	5.76	ID2	NM_002166	+	-642
chr3	49369942	49370256	315	112	39	7.58	GPX1	NM_000581	-	-642
chr2	127522244	127522719	476	379	25	6.97	BIN1	NM_004305	-	-641
chr6	39981618	39981918	301	61	13	10.98	MOCS1	NM_005942	-	-641
chr10	101360291	101360910	620	299	40	8.17	SLC25A28	NM_031212	-	-639
chr2	47240849	47241447	599	208	77	9.19	CALM2	NM_001743	-	-639
chr17	77503979	77504325	347	213	24	10.14	NOTUM	NM_178493	-	-639

chr10	94824099	94824295	197	144	7	15.41	CYP26A1	NM_000783	+	-639
chr11	66372577	66373210	634	394	103	5.91	PC	NM_022172	-	-638
chr10	91333075	91333366	292	116	25	5.96	PANK1	NM_138316	-	-638
chr22	49308876	49309502	627	515	28	7.99	SCO2	NM_005138	-	-638
chr17	35081223	35081538	316	105	23	8.24	PERLD1	NM_033419	-	-637
chr10	105344196	105344412	217	159	11	14.64	SH3PXD2A	NM_014631	-	-637
chr14	23978687	23979449	763	309	52	9.45	C14orf124	NM_020195	-	-636
chr13	45598108	45598694	587	360	40	6.75	LCP1	NM_002298	-	-635
chr12	26379578	26380187	610	382	29	5.36	ITPR2	NM_002223	-	-634
chr1	224615469	224615762	294	168	11	12.55	PARP1	NM_001618	-	-634
chr17	45143014	45143319	306	127	12	8.37	FAM117A	NM_030802	-	-632
chr1	32572109	32572658	550	297	25	6.9	MARCKSL1	NM_023009	-	-631
chr8	102000554	102000720	167	56	8	17.12	YWHAZ	NM_145690	-	-631
chr19	48803451	48803845	395	61	23	13.31	ZNF428	NM_182498	-	-629
chr1	43402882	43403070	189	131	11	16.6	EBNA1BP2	NM_006824	-	-628
chr17	34162934	34163154	221	140	14	25.89	PSMB3	NM_002795	+	-627
chr9	122618597	122618780	184	94	8	14.64	PSMD5	NM_005047	-	-626
chr17	74182254	74182351	98	50	7	24.4	PSCD1	NM_004762	-	-626
chr19	59369085	59369545	461	356	19	8.13	LENG4	NM_024298	-	-625
chr1	89290784	89291218	435	136	25	8.19	GBP1	NM_002053	-	-625
chr17	69711853	69712013	161	55	25	7.07	RPL38	NM_000999	+	-624
chr9	130058376	130058553	178	129	7	24.4	GOLGA2	NM_004486	-	-624
chr19	2427130	2427757	628	458	57	8.17	GADD45B	NM_015675	+	-623
chr3	88184127	88184418	292	154	19	9.41	CGGBP1	NM_001008390	-	-623
chr12	109414137	109414336	200	109	19	9.52	VPS29	NM_016226	-	-623
chr12	9111582	9112192	611	85	102	10.09	A2M	NM_000014	-	-622

chr3	9796677	9797274	598	449	38	9.73	TADA3L	NM_006354	-	-621
chr11	125268918	125269211	294	116	10	9.76	PUS3	NM_031307	-	-621
chr19	1349729	1350227	499	439	82	6.23	GAMT	NM_138924	-	-620
chr7	101900918	101901173	256	135	22	5.35	POLR2J	NM_006234	-	-619
chr6	7233027	7233421	395	210	23	7.71	SSR1	NM_003144	-	-619
chr3	10342877	10343362	486	177	22	8.3	ATP2B2	NM_001001331	-	-618
chr15	53906743	53907040	298	171	13	11.39	NEDD4	NM_198400	-	-618
chr9	85464752	85465315	564	170	35	12.98	UBQLN1	NM_013438	-	-617
chr12	109642465	109642742	278	150	16	6.83	PPP1CC	NM_002710	-	-616
chr13	112880186	112880542	357	44	13	6.97	PCID2	NM_018386	-	-616
chr6	44189387	44189964	578	272	53	5.48	MRPL14	NM_032111	-	-615
chr19	44615646	44616303	658	180	86	7.05	RPS16	NM_001020	-	-615
chr1	36694328	36694574	247	176	14	10.85	MRPS15	NM_031280	-	-615
chr11	72073782	72074375	594	242	48	5.22	CENTD2	NM_015242	-	-613
chr7	2544141	2544653	513	435	24	6.57	C7orf27	NM_152743	-	-613
chr2	96280406	96280653	248	53	14	8.78	TMEM127	NM_017849	-	-613
chr1	149234347	149234785	439	315	22	11.25	FAM63A	NM_018379	-	-613
chr4	140646681	140647253	573	123	30	8.39	SETD7	NM_030648	-	-611
chr9	139203274	139203564	291	117	13	14.91	SSNA1	NM_003731	+	-611
chr1	144150032	144150548	517	365	34	6.99	TXNIP	NM_006472	+	-610
chr20	47683033	47683499	467	111	23	6.27	B4GALT5	NM_004776	-	-608
chr14	37129115	37129549	435	119	19	14.86	FOXA1	NM_004496	-	-608
chr8	99183755	99184349	595	343	162	5.3	HRSP12	NM_005836	-	-607
chr1	152213538	152213976	439	256	73	5.89	JTB	NM_006694	-	-606
chr13	19875813	19876413	601	512	109	7.42	CRYL1	NM_015974	-	-605
chr22	49288198	49288850	653	118	35	8.76	TMEM153	NM_033200	-	-605

chr16	68843704	68844401	698	236	54	8.18	AARS	NM_001605	-	-604
chr7	99140729	99141199	471	266	30	5.52	CYP3A7	NM_000765	-	-603
chr12	74705719	74706097	379	96	23	7.13	PHLDA1	NM_007350	-	-603
chr15	58426873	58427246	374	169	35	7.67	ANXA2	NM_001002857	-	-603
chr7	75769874	75770459	586	406	50	10.72	HSPB1	NM_001540	+	-601
chr6	49507373	49507557	185	113	25	9.21	MUT	NM_000255	-	-600
chr5	68696648	68696926	279	122	11	14.64	TAF9	NM_003187	-	-600
chr17	23924275	23924859	585	173	49	5.14	ALDOC	NM_005165	-	-599
chr16	11549362	11549954	593	281	51	5.97	LITAF	NM_004862	-	-598
chr8	143849772	143850214	443	319	20	7.32	LYNX1	NM_177476	-	-598
chr4	109882730	109883250	521	409	37	10.17	AGXT2L1	NM_031279	-	-598
chr8	101338582	101339060	479	330	30	10.02	RNF19	NM_015435	-	-597
chr12	94576117	94576310	194	141	8	14.64	NTN4	NM_021229	-	-596
chr6	43374015	43374570	556	398	102	6.23	SLC22A7	NM_006672	+	-595
chr2	18599801	18600071	271	182	12	9.92	RDH14	NM_020905	-	-594
chr3	58388476	58388990	515	432	41	7.54	PDHB	NM_000925	-	-593
chr5	38511081	38511415	335	65	19	11.44	LIFR	NM_002310	-	-593
chr2	20681290	20681637	348	220	16	13.01	HS1BP3	NM_022460	-	-593
chr14	69312202	69312896	695	528	169	7.24	SLC10A1	NM_003049	-	-592
chr11	119586969	119587546	578	366	48	11.54	OAF	NM_178507	+	-590
chr17	53435981	53436450	470	72	53	8.47	SFRS1	NM_006924	-	-589
chr10	99334509	99334699	191	84	8	11.19	C10orf65	NM_138413	+	-589
chr2	121812188	121812413	226	81	10	17.08	CLASP1	NM_015282	-	-589
chr1	52027748	52028058	311	157	20	8.05	NRD1	NM_002525	-	-588
chr9	131689304	131689874	571	215	25	8.36	FNBP1	NM_015033	-	-588
chr17	24394240	24394631	392	193	34	10.44	PIPOX	NM_016518	+	-588

chr1	154351379	154351709	331	228	24	10.65	LMNA	NM_005572	+	-588
chr20	29996813	29997007	195	139	8	14.64	PDRG1	NM_030815	-	-588
chr1	62835726	62836361	636	575	81	6.7	ANGPTL3	NM_014495	+	-587
chr14	49304703	49305122	420	293	26	7.91	KLHDC2	NM_014315	+	-586
chr14	64611689	64612182	494	246	22	8.68	MAX	NM_002382	-	-585
chr7	2361447	2361584	138	82	6	18.3	EIF3S9	NM_001037283	+	-585
chr14	34055261	34055470	210	160	12	7.99	C14orf11	NM_018453	-	-584
chr20	47163384	47163867	484	203	46	7.09	STAU1	NM_001037328	-	-583
chr11	66087510	66088094	585	63	67	8.06	CTSF	NM_003793	-	-583
chr1	244954342	244954582	241	54	11	8.82	SCCPDH	NM_016002	+	-582
chr9	130621001	130621181	181	58	8	11.71	ENDOG	NM_004435	+	-582
chr2	150134701	150134978	278	132	19	7.33	C2orf25	NM_015702	-	-581
chr19	1527625	1528258	634	148	40	15.47	MBD3	NM_003926	-	-581
chr2	26110889	26111058	170	112	6	24.4	RAB10	NM_016131	+	-581
chr14	73502777	73503514	738	337	49	6.16	ENTPD5	NM_001249	-	-579
chr10	96987342	96987899	558	102	60	5.72	PDLIM1	NM_020992	-	-578
chr1	153163875	153164410	536	135	59	6.28	PMVK	NM_006556	-	-578
chr2	27207047	27207708	662	436	43	7.32	PREB	NM_013388	-	-578
chr3	133759694	133760253	560	298	55	8.2	ACAD11	NM_032169	-	-578
chr4	6693344	6693922	579	152	52	5.39	MRFAP1	NM_033296	+	-577
chr9	139218546	139218934	389	276	19	5.7	MGC14327	NM_053045	-	-577
chr14	23728269	23728775	507	212	36	5.57	TM9SF1	NM_006405	-	-576
chr9	122754376	122755012	637	172	167	5.79	C5	NM_001735	-	-576
chr1	201414732	201415128	397	278	20	6.98	CHI3L1	NM_001276	-	-576
chr4	100416568	100417121	554	221	111	9.22	ADH1A	NM_000667	-	-575
chr12	105155937	105156495	559	125	33	10.91	CKAP4	NM_006825	-	-574

chr14	74668282	74668497	216	162	10	12.55	TMED10	NM_006827	-	-574
chr1	201176720	201177148	429	296	31	7.32	ADIPOR1	NM_015999	-	-573
chr15	62151981	62152387	407	248	39	14.9	FAM96A	NM_032231	-	-572
chr7	6468010	6469365	1356	1259	153	6.73	KDELRL2	NM_006854	-	-571
chr1	158328207	158328332	126	62	9	11.71	IGSF8	NM_052868	-	-571
chr22	35951228	35951828	601	384	31	11.73	RAC2	NM_002872	-	-571
chr7	139431399	139431587	189	62	11	21.81	KIAA1718	NM_030647	-	-571
chr6	26232603	26232920	318	178	13	9.31	HIST1H2AC	NM_003512	+	-569
chr4	89661463	89661725	263	202	28	7.06	PIGY	NM_001042616	-	-568
chr17	23898177	23898420	244	119	9	21.43	UNC119	NM_054035	-	-568
chr13	31873870	31874380	511	327	36	7.48	CG018	NM_052818	-	-567
chr2	234292195	234292743	549	380	31	9.76	UGT1A4	NM_007120	+	-567
chr6	166698421	166698964	544	454	85	6.42	BRP44L	NM_016098	-	-565
chr12	112221378	112221519	142	62	7	14.64	SLC24A6	NM_024959	-	-565
chr1	65071515	65072058	544	335	66	7.17	JAK1	NM_002227	-	-564
chr3	187117277	187117798	522	244	30	5.94	SFRS10	NM_004593	-	-563
chr17	77609057	77609603	547	493	44	6.41	DUS1L	NM_022156	-	-563
chr11	65121813	65122365	553	57	43	10.8	MAP3K11	NM_002419	-	-563
chr7	42923169	42923551	383	46	14	10.85	PSMA2	NM_002787	-	-563
chr5	175752133	175752625	493	387	28	25.26	CLTB	NM_001834	-	-563
chr14	22564908	22565462	555	134	51	7.04	PSMB5	NM_002797	-	-562
chr12	56135674	56135924	251	105	22	8.08	INHBE	NM_031479	+	-562
chrX	105163850	105164413	564	466	107	6.84	SERPINA7	NM_000354	-	-561
chr19	18278740	18279278	539	223	36	7.23	LSM4	NM_012321	-	-561
chr16	55020960	55021110	151	47	8	12.92	NUDT21	NM_007006	-	-561
chr6	128331618	128332184	567	125	28	8.3	PTPRK	NM_002844	-	-560

chr9	88092514	88093029	516	70	23	21.96	ZCCHC6	NM_024617	-	-560
chr7	40138943	40139426	484	259	35	7.09	C7orf11	NM_138701	-	-559
chr19	44061282	44061598	317	194	18	9.32	SIRT2	NM_030593	-	-559
chr1	12550486	12551084	599	122	156	5.65	DHRS3	NM_004753	-	-558
chr4	157044597	157044854	258	84	32	6.61	TDO2	NM_005651	+	-558
chr10	97355760	97356234	475	142	19	10.25	ALDH18A1	NM_001017423	-	-558
chr3	37069851	37070060	210	154	9	10.46	LRRFIP2	NM_017724	-	-558
chr1	244770880	244771048	169	110	6	24.4	TFB2M	NM_022366	-	-558
chr6	160462851	160463409	559	499	119	5.38	SLC22A1	NM_153187	+	-557
chr7	149666614	149666907	294	102	90	6.46	RARRES2	NM_002889	-	-556
chr2	188037286	188037760	475	305	41	7.45	TFPI	NM_006287	-	-556
chr17	15875451	15876539	1089	121	66	7.97	NCOR1	NM_006311	-	-556
chr3	66512018	66512467	450	121	18	8.61	LRIG1	NM_015541	-	-556
chr2	97638918	97639417	500	62	27	8.54	ACTR1B	NM_005735	-	-555
chr22	18682229	18682356	128	62	8	13.12	DGCR6L	NM_033257	-	-555
chr8	118881047	118881335	289	60	18	8.46	EXT1	NM_000127	-	-553
chr21	44378386	44378476	91	46	6	17.57	C21orf33	NM_004649	+	-553
chr3	186391471	186391659	189	116	40	5.53	EHHADH	NM_001966	-	-552
chr15	38815444	38815929	486	310	27	8.24	FAM82C	NM_018145	-	-552
chr17	12836446	12836983	538	110	27	18.38	ELAC2	NM_018127	-	-549
chr12	51975869	51976049	181	81	26	5.3	PFDN5	NM_002624	+	-548
chr6	138453707	138454166	460	304	42	5.39	PERP	NM_022121	-	-548
chr6	135280170	135280767	598	204	83	6.25	ALDH8A1	NM_022568	-	-546
chr13	42495661	42495907	247	157	15	18.08	DNAJC15	NM_013238	+	-546
chr5	54756574	54756986	413	135	29	6.05	PPAP2A	NM_003711	-	-545
chr12	97511797	97512078	282	135	18	7.43	SLC25A3	NM_002635	+	-545

chr8	42152259	42152456	198	83	7	13.31	PLAT	NM_000930	-	-545
chr10	51262133	51262638	506	268	36	5.39	TIMM23	NM_006327	-	-543
chr12	53259326	53259842	517	247	23	6.66	PPP1R1A	NM_006741	-	-543
chr19	16489923	16490248	326	146	15	7.32	CHERP	NM_006387	-	-543
chr8	30762956	30763211	256	59	15	8.75	PPP2CB	NM_001009552	-	-543
chr8	12985467	12985783	317	101	24	9.28	DLC1	NM_006094	-	-541
chr11	124294380	124294895	516	417	28	6.41	HEPN1	NM_001037558	+	-540
chr16	4599111	4599426	316	152	19	9.32	FAM100A	NM_145253	-	-540
chr1	11037587	11037775	189	57	8	12.2	SRM	NM_003132	-	-540
chr1	111793634	111793805	172	54	10	22.66	ATP5F1	NM_001688	+	-540
chr11	298163	298453	291	110	32	7.24	IFITM2	NM_006435	+	-539
chr1	23509171	23509402	232	154	13	11.89	HNRPR	NM_005826	-	-539
chr2	73308700	73309181	482	135	20	16.47	C2orf7	NM_032319	-	-539
chr18	664017	664452	436	263	25	7.66	ENOSF1	NM_017512	-	-538
chr4	16112639	16112799	161	123	6	19.26	LDB2	NM_001290	-	-538
chr20	33053914	33054412	499	98	29	5.68	TRPC4AP	NM_015638	-	-537
chr1	154529121	154529644	524	104	45	6.58	C1orf85	NM_144580	-	-536
chr16	55523575	55523784	210	51	13	10.76	HERPUD1	NM_001010989	+	-536
chr22	31113580	31114103	524	273	30	6.82	C22orf28	NM_014306	-	-535
chr7	5533304	5533847	544	366	73	7.34	ACTB	NM_001101	-	-535
chr17	37604930	37605256	327	62	16	9.58	STAT5B	NM_012448	-	-535
chr16	1817281	1817758	478	423	20	7	FAHD1	NM_031208	+	-533
chr11	47155836	47156193	358	205	19	9.17	PACSIN3	NM_016223	-	-533
chr16	66819985	66820483	499	203	29	11.26	RBM35B	NM_024939	-	-533
chr8	124330239	124330410	172	119	9	25.62	ZHX1	NM_001017926	-	-533
chr5	137918904	137919455	552	185	51	8.08	HSPA9	NM_004134	-	-532

chr18	42935544	42935944	401	281	17	17.57	IER3IP1	NM_016097	-	-532
chr5	132230394	132230748	355	127	85	6.73	UQCRQ	NM_014402	+	-531
chr22	25251834	25252246	413	233	24	10.88	TPST2	NM_001008566	-	-531
chr11	63793891	63794408	518	104	30	12.13	BAD	NM_004322	-	-531
chr11	27344487	27344616	130	58	12	14.64	LGR4	NM_018490	-	-531
chr17	53404153	53404438	286	116	12	7.32	VEZF1	NM_007146	-	-530
chr1	152220947	152221283	337	208	17	7.4	RAB13	NM_002870	-	-530
chr5	132239203	132239500	298	122	25	8.38	AFF4	NM_014423	-	-530
chr4	81045897	81046278	382	113	24	9.32	ANTXR2	NM_058172	-	-530
chr2	151033036	151033484	449	324	56	9.45	RND3	NM_005168	-	-530
chr15	56217812	56218299	488	246	61	9.89	AQP9	NM_020980	+	-529
chr6	160119613	160120048	436	138	45	7.58	TCP1	NM_001008897	-	-528
chr9	34359228	34359435	208	62	11	10.66	KIAA1161	NM_020702	-	-528
chr11	6189364	6189680	317	52	15	11.6	C11orf56	NM_032127	-	-528
chr4	103771773	103772218	446	175	21	20.5	MANBA	NM_005908	-	-528
chr16	30011139	30011662	524	362	36	5.31	YPEL3	NM_031477	-	-527
chr19	50663486	50663619	134	58	7	21.96	FOSB	NM_006732	+	-527
chr4	187350009	187350194	186	137	7	35.46	CYP4V2	NM_207352	+	-527
chr1	1466946	1467442	497	411	43	7.84	SSU72	NM_014188	-	-526
chr14	49114026	49114328	303	168	11	22.18	RPS29	NM_001030001	-	-526
chr20	1371000	1371337	338	175	16	9.9	NSFL1C	NM_182483	-	-525
chr17	77652587	77653159	573	309	29	11.19	CCDC57	NM_198082	-	-525
chr17	77569869	77570392	524	281	46	5.11	STRA13	NM_144998	-	-524
chr2	218837099	218837620	522	461	37	7.64	AAMP	NM_001087	-	-524
chr2	36633192	36633428	237	174	11	17.93	FEZ2	NM_001042548	-	-524
chr3	49133548	49134073	526	76	61	5.24	LAMB2	NM_002292	-	-522

chr4	75181828	75182141	314	118	41	15.28	CXCL2	NM_002089	-	-522
chrX	152619218	152619667	450	386	42	5.49	BCAP31	NM_005745	-	-521
chr3	151742517	151742991	475	247	33	10.93	SERP1	NM_014445	-	-521
chr14	68916807	68917117	311	55	22	8.2	ERH	NM_004450	-	-519
chr12	119418650	119418760	111	56	14	11.38	DYNLL1	NM_001037495	+	-519
chr3	9774134	9774550	417	152	18	7.33	CAMK1	NM_003656	-	-518
chr11	8671508	8671993	486	237	24	12.81	ST5	NM_213618	-	-518
chr11	62200591	62201065	475	62	23	8.11	LOC51035	NM_015853	-	-517
chr14	91405721	91406023	303	148	19	6.16	FBLN5	NM_006329	-	-515
chrX	102817115	102817602	488	91	42	5.95	MORF4L2	NM_012286	-	-514
chr16	87245943	87246362	420	196	23	12.3	MVD	NM_002461	-	-514
chr3	122865974	122866152	179	121	10	17.08	GOLGB1	NM_004487	-	-513
chr14	69862803	69863050	248	79	18	17.57	C14orf112	NM_016468	-	-513
chrX	18820962	18821310	349	169	19	6.13	PHKA2	NM_000292	-	-511
chr3	121829710	121830216	507	260	135	6.19	HGD	NM_000187	-	-511
chr12	120159938	120160390	453	161	20	7.74	CAMKK2	NM_172226	-	-511
chr7	32493220	32493454	235	60	15	8.03	LSM5	NM_012322	-	-511
chr1	23580202	23580652	451	336	38	9.14	TCEA3	NM_003196	-	-511
chr15	38485334	38485486	153	97	10	17.92	IVD	NM_002225	+	-509
chr19	40431744	40431906	163	94	14	13.13	LSR	NM_015925	+	-508
chr5	176691473	176691863	391	207	37	5.32	LMAN2	NM_006816	-	-507
chr22	22706170	22706646	477	99	63	7.35	GSTT1	NM_000853	-	-506
chr2	234624095	234624589	495	68	73	6.44	SPP2	NM_006944	+	-505
chr14	68324153	68324632	480	164	69	6.77	ZFP36L1	NM_004926	-	-505
chr1	33251239	33251674	436	199	29	7.18	AK2	NM_001625	-	-505
chr8	17545626	17546088	463	254	25	9.49	MTUS1	NM_020749	-	-505

chr13	77367820	77368121	302	172	12	10.46	EDNRB	NM_000115	-	-505
chr3	49037109	49037275	167	108	11	8.54	IMPDH2	NM_000884	-	-504
chr3	126648470	126648688	219	96	8	21.96	SNX4	NM_003794	-	-504
chr4	3484103	3484595	493	285	47	6.26	LRPAP1	NM_002337	-	-503
chrX	153230101	153230592	492	395	36	6.6	FLNA	NM_001456	-	-502
chr1	154974045	154974219	175	60	21	6.66	MRPL24	NM_024540	-	-502
chr6	29799463	29799721	259	58	18	7.58	HLA-F	NM_018950	+	-502
chr17	16186618	16187075	458	290	22	7.66	PRR6	NM_181716	-	-502
chr5	132237212	132237758	547	392	69	8.28	LEAP2	NM_052971	+	-502
chr6	31692138	31692269	132	72	10	18.82	AIF1	NM_032955	+	-502
chr11	125577813	125578020	208	149	10	20.5	RPUSD4	NM_032795	-	-502
chr2	219355098	219355449	352	227	43	5.15	CYP27A1	NM_000784	+	-501
chr6	30565485	30565750	266	208	21	7.79	HLA-E	NM_005516	+	-501
chr1	205168459	205168995	537	262	34	8.65	PIGR	NM_002644	-	-501
chr4	38965751	38965971	221	60	8	14.64	RFC1	NM_002913	-	-501
chr16	2030116	2030316	201	79	21	9.42	NTHL1	NM_002528	-	-500
chr2	165249608	165250005	398	97	23	9.99	COBLL1	NM_014900	-	-500
chr14	22485605	22485777	173	57	10	15.2	C14orf94	NM_017815	-	-500
chr7	65063115	65063607	493	350	45	5.7	GUSB	NM_000181	-	-498
chr6	30018615	30018807	193	134	24	7.67	HLA-A	NM_002116	+	-498
chrX	48771240	48771683	444	99	19	16.25	TFE3	NM_006521	-	-498
chr13	77368737	77369041	305	162	12	21.96	EDNRB	NM_003991	-	-498
chr15	99671090	99671244	155	60	19	5.9	PCSK6	NM_138320	-	-497
chr6	43129968	43130241	274	60	20	6.42	MRPL2	NM_015950	-	-497
chr5	173249082	173249291	210	155	7	13.94	CPEB4	NM_030627	+	-497
chr2	61558772	61559070	299	166	12	23.43	XPO1	NM_003400	-	-497

chr19	819319	819457	139	49	6	29.55	THRAP5	NM_005481	-	-496
chr15	32163578	32164010	433	236	41	11.77	C15orf24	NM_020154	-	-494
chr16	11874117	11874532	416	159	25	8.12	GSPT1	NM_002094	-	-493
chr6	32003715	32003964	250	190	26	7.32	C2	NM_000063	+	-492
chr11	66962377	66962585	209	47	13	8.78	CORO1B	NM_020441	-	-492
chr1	203954010	203954223	214	44	20	11.49	NUCKS1	NM_022731	-	-492
chr17	4784611	4784865	255	199	14	9.84	RNF167	NM_015528	+	-491
chr21	45049950	45050450	501	135	29	13.2	SUMO3	NM_006936	-	-491
chr19	11477780	11478235	456	402	33	20.03	ECSIT	NM_016581	-	-491
chr15	74295667	74296125	459	202	36	7.17	ETFA	NM_000126	-	-490
chr1	93389943	93390487	545	434	34	9.97	TMED5	NM_016040	-	-489
chr1	27568199	27568676	478	73	79	6.74	FCN3	NM_003665	-	-487
chr19	10014388	10014645	258	59	14	6.76	LOC388503	NM_001013640	+	-487
chr12	56115049	56115296	248	146	14	12.2	INHBC	NM_005538	+	-487
chr11	68280907	68281630	724	439	54	6.14	CPT1A	NM_001876	-	-486
chr3	198721060	198721536	477	88	36	6.54	BDH1	NM_004051	-	-485
chr4	184048382	184048723	342	185	19	11.27	DCTD	NM_001921	-	-485
chr14	92240074	92240394	321	62	16	12.53	LGMN	NM_001008530	-	-485
chr19	44568352	44568595	244	129	16	8.78	PAF1	NM_019088	-	-484
chr17	35138894	35139420	527	338	35	8.82	C17orf37	NM_032339	-	-484
chr20	2587050	2587525	476	136	36	5.81	IDH3B	NM_174855	-	-483
chr10	54195256	54195629	374	244	29	6.26	MBL2	NM_000242	-	-483
chr1	16323685	16323902	218	122	9	15.96	EPHA2	NM_004431	-	-483
chr19	15849909	15850315	407	178	34	16.39	CYP4F2	NM_001082	-	-482
chr2	27288620	27288884	265	205	12	17.57	C2orf28	NM_080592	+	-482
chr1	63831702	63832015	314	76	29	5.02	PGM1	NM_002633	+	-481

chr11	65062835	65063331	497	245	26	5.46	LTBP3	NM_021070	-	-480
chr3	53826825	53827160	336	182	23	8.85	CHDH	NM_018397	-	-480
chr1	36560308	36560698	391	123	15	9.54	C1orf78	NM_018166	-	-480
chr3	10317644	10318095	452	150	33	6.62	SEC13L1	NM_030673	-	-479
chr7	75454243	75454721	479	185	42	5.14	TMPIT	NM_031925	-	-478
chr1	154828511	154828659	149	61	11	8.73	APOA1BP	NM_144772	+	-478
chr17	8003271	8003666	396	93	19	14.64	VAMP2	NM_014232	-	-478
chr9	130532218	130532367	150	95	6	14.64	ZYG11BL	NM_006336	-	-478
chr1	45749259	45749771	513	149	87	6.63	PRDX1	NM_002574	-	-477
chr2	237897479	237897877	399	222	19	8.76	COL6A3	NM_004369	-	-477
chr12	54796766	54797115	350	105	16	8.97	RPL41	NM_001035267	+	-475
chr1	148969512	148969652	141	61	7	14.64	CTSS	NM_004079	-	-475
chr15	77001173	77001636	464	400	73	5.36	CTSH	NM_004390	-	-474
chr2	208809392	208809672	281	225	29	5.76	IDH1	NM_005896	-	-474
chr6	30818971	30819429	459	73	32	8.64	IER3	NM_003897	-	-474
chr14	53963653	53963869	217	97	12	11.98	CNIH	NM_005776	-	-473
chr13	20612961	20613157	197	124	21	14.42	SAP18	NM_005870	+	-473
chr11	56823698	56824151	454	314	29	8.55	TNKS1BP1	NM_033396	-	-472
chr1	159275719	159276136	418	276	20	10.05	USF1	NM_207005	-	-471
chr11	57052606	57052982	377	211	27	12.14	TIMM10	NM_012456	-	-471
chr17	45800244	45800698	455	175	40	14.43	MRPL27	NM_148570	-	-471
chrX	16772854	16773167	314	128	18	16.09	RBBP7	NM_002893	-	-470
chr6	33492324	33492765	442	146	68	6.47	CUTA	NM_001014837	-	-469
chr21	45130377	45130765	389	84	23	5.7	ITGB2	NM_000211	-	-467
chr2	201426161	201426444	284	210	25	8.32	CLK1	NM_004071	-	-467
chrX	34555393	34555570	178	58	8	14.64	TMEM47	NM_031442	-	-467

chr8	145700345	145700698	354	220	36	5.53	GPT	NM_005309	+	-466
chr11	800214	800401	188	131	37	6.51	RPLP2	NM_001004	+	-466
chr7	50493902	50494094	193	48	14	7.54	DDC	NM_000790	-	-465
chr3	4377881	4378294	414	296	23	12.12	SUMF1	NM_182760	-	-465
chr22	49410279	49410785	507	98	28	6.6	ARSA	NM_000487	-	-464
chr9	34611421	34611919	499	381	20	6.66	ARID3C	NM_001017363	-	-464
chr6	31344465	31344972	508	310	103	6.78	HLA-C	NM_002117	-	-464
chr4	100446444	100447014	571	351	149	5.36	ADH1B	NM_000668	-	-463
chr21	36364220	36364616	397	129	63	5.56	CBR1	NM_001757	+	-462
chr2	240548846	240549292	447	191	46	6.14	NDUFA10	NM_004544	-	-462
chr11	71391565	71392019	455	116	27	7.61	NUMA1	NM_006185	-	-461
chr1	25441364	25441788	425	172	20	14.64	C1orf63	NM_020317	-	-461
chr6	119540418	119541427	1010	473	83	9.55	MAN1A1	NM_005907	-	-460
chr4	175648119	175648415	297	145	22	9.76	HPGD	NM_000860	-	-460
chr9	72189438	72189793	356	275	20	6.95	KLF9	NM_001206	-	-459
chr16	80626432	80626822	391	214	23	7.63	HSD17B2	NM_002153	+	-459
chr19	54280540	54280734	195	114	23	6.28	SNRP70	NM_001009820	+	-458
chr11	58467580	58467754	175	84	21	7.26	GLYATL1	NM_080661	+	-457
chr22	23281950	23282074	125	62	10	36.6	SNRPD3	NM_004175	+	-457
chrX	153387724	153388155	432	280	20	9.76	FAM3A	NM_021806	-	-456
chr17	7247024	7247476	453	109	45	10.32	C17orf61	NM_152766	-	-456
chr9	130111445	130111672	228	163	12	12.55	TRUB2	NM_015679	-	-456
chr7	123109248	123109691	444	279	33	7.58	WASL	NM_003941	-	-455
chr2	127731505	127731790	286	163	13	10.98	ERCC3	NM_000122	-	-455
chr17	17338494	17338933	440	149	24	9.02	RASD1	NM_016084	-	-454
chr1	148861227	148861677	451	90	62	7.3	ENSA	NM_207045	-	-453

chr16	66526193	66526359	167	108	17	6.72	PSMB10	NM_002801	-	-452
chrX	151746653	151746979	327	129	18	8.38	CETN2	NM_004344	-	-451
chr11	67030613	67030995	383	143	31	12.15	CDK2AP2	NM_005851	-	-451
chr11	2922265	2922686	422	272	22	9.27	NAP1L4	NM_005969	-	-450
chr19	11524863	11525306	444	60	26	17.34	ELOF1	NM_032377	-	-449
chr17	5318382	5318784	403	57	20	5.9	DERL2	NM_016041	-	-448
chr6	31806574	31806786	213	62	22	8.11	CLIC1	NM_001288	-	-448
chr11	124011057	124011351	295	155	22	10.8	SIAE	NM_170601	-	-448
chr8	96007391	96007823	433	59	58	5.76	TP53INP1	NM_033285	-	-447
chr1	1327086	1327606	521	282	60	8.83	MRPL20	NM_017971	-	-447
chr6	30803573	30803938	366	246	23	10.72	FLOT1	NM_005803	-	-447
chr8	145510754	145511209	456	234	41	10.85	DGAT1	NM_012079	-	-447
chr1	1260536	1260967	432	118	30	6.32	DVL1	NM_004421	-	-446
chr20	48131352	48131514	163	92	11	8.35	UBE2V1	NM_001032288	-	-445
chr1	239727670	239727972	303	161	26	13.94	FH	NM_000143	-	-445
chr11	62814004	62814657	654	554	51	6.58	SLC22A10	NM_001039752	+	-444
chr10	106004648	106005111	464	341	32	14.56	GSTO1	NM_004832	+	-444
chr14	102468483	102468911	429	266	25	7.81	CDC42BPB	NM_006035	-	-443
chr3	37004379	37004677	299	137	12	15.69	EPM2AIP1	NM_014805	-	-443
chr22	22438315	22438463	149	88	34	5.55	C22orf16	NM_213720	-	-442
chr19	2184160	2184596	437	145	21	6.4	PLEKHJ1	NM_018049	-	-442
chr9	83388497	83388861	365	60	20	17.08	TLE1	NM_005077	-	-442
chr1	23994703	23995115	413	125	24	6.8	GALE	NM_000403	-	-440
chr8	121619317	121619666	350	56	18	12.46	SNTB1	NM_021021	-	-440
chr19	60433046	60433399	354	293	17	14.64	SAPS1	NM_014931	-	-440
chr19	10322219	10322648	430	163	26	19.52	TYK2	NM_003331	-	-440

chr11	1252247	1252616	370	304	28	5.42	TOLLIP	NM_019009	-	-439
chr17	27203006	27203450	445	85	27	7.33	C17orf79	NM_018405	-	-439
chr1	28435172	28435636	465	351	53	9.36	ATPIF1	NM_178191	+	-439
chr2	31602856	31603598	743	494	48	9.76	SRD5A2	NM_000348	-	-439
chr1	158017687	158017821	135	62	8	12.81	DUSP23	NM_017823	+	-439
chr11	62316274	62316658	385	242	19	16.53	NXF1	NM_006362	-	-439
chr12	55021666	55022087	422	205	27	6.18	STAT2	NM_005419	-	-437
chr18	45262051	45262464	414	235	23	11.71	LOC497661	NM_001035005	-	-437
chr2	27402286	27402661	376	213	18	12.81	GTF3C2	NM_001035521	-	-435
chr19	45638851	45639025	175	57	7	18.3	SERTAD3	NM_013368	-	-435
chr1	19273593	19274022	430	85	42	12.59	ZUBR1	NM_020765	-	-434
chr21	36754939	36755223	285	173	16	8.54	CLDN14	NM_012130	-	-433
chr1	158525623	158526118	496	172	29	10.89	COPA	NM_004371	-	-433
chr12	6944773	6945209	437	90	80	5.66	PHB2	NM_007273	-	-432
chr17	68791374	68791790	417	119	25	7.12	CDC42EP4	NM_012121	-	-432
chr7	47281433	47281709	277	154	16	16.89	TNS3	NM_022748	-	-432
chr18	65822304	65822451	148	53	7	18.3	RTTN	NM_173630	-	-431
chr5	131846691	131847113	423	277	19	6.19	IRF1	NM_002198	-	-430
chr6	158977548	158977922	375	181	20	6.41	DYNLT1	NM_006519	-	-429
chr1	20698649	20698957	309	135	14	11.31	C1orf166	NM_024544	-	-428
chr6	133085618	133086049	432	253	24	18.82	VNN3	NM_018399	-	-428
chr19	19236014	19236600	587	243	38	5.29	TM6SF2	NM_001001524	-	-427
chr14	23829584	23830072	489	215	72	7.16	DHRS1	NM_138452	-	-427
chr1	20174528	20174943	416	86	38	5.66	PLA2G2A	NM_000300	-	-426
chr17	4803347	4803671	325	231	24	6.54	SPAG7	NM_004890	-	-426
chr17	17349603	17350029	427	72	62	6.77	PEMT	NM_148173	-	-426

chr9	6522584	6522891	308	245	20	11.27	GLDC	NM_000170	-	-426
chr17	43270074	43270482	409	256	22	18.3	SCRN2	NM_138355	-	-426
chr17	7774406	7774815	410	213	26	5.34	TRAPPC1	NM_021210	-	-424
chr19	53951174	53951579	406	278	16	7.43	FGF21	NM_019113	+	-424
chr14	23175530	23175845	316	257	16	9.25	DHRS2	NM_005794	+	-424
chr19	52033271	52033686	416	62	43	9.34	AP2S1	NM_004069	-	-424
chr3	52410267	52410490	224	62	13	10.14	BAP1	NM_004656	-	-424
chr10	27440708	27441095	388	334	22	15.15	YME1L1	NM_139313	-	-424
chrX	48715319	48715501	183	139	8	21.96	GRIPAP1	NM_020137	-	-424
chr19	55992818	55993195	378	273	17	9.15	C19orf48	NM_199250	-	-423
chr16	29735623	29735755	133	89	6	19.52	C16orf53	NM_024516	+	-423
chr7	44518660	44519082	423	265	26	5.32	NPC1L1	NM_013389	-	-422
chr15	86803734	86804135	402	226	30	13.24	MRPL46	NM_022163	-	-422
chr11	14435701	14436049	349	199	22	7.15	COPB1	NM_016451	-	-421
chr5	1371011	1371427	417	118	36	12.21	CLPTM1L	NM_030782	-	-421
chr7	100662347	100662514	168	124	6	17.75	CLDN15	NM_014343	-	-421
chr17	4639013	4639413	401	135	28	6.85	LOC388323	NM_001014985	+	-420
chr1	36631700	36632037	338	135	16	9.15	LSM10	NM_032881	-	-420
chr4	153462074	153462280	207	114	10	18.18	FBXW7	NM_018315	-	-420
chr1	218208751	218208983	233	57	15	7.96	EPRS	NM_004446	-	-417
chr3	47430163	47430604	442	231	59	7.96	SCAP	NM_012235	-	-417
chr16	361903	362277	375	129	21	8.78	TMEM8	NM_021259	-	-417
chr18	70071557	70071923	367	225	148	5.2	CYB5A	NM_148923	-	-416
chr19	44019154	44019284	131	56	18	10.87	HNRPL	NM_001533	-	-416
chr19	4041546	4041744	199	121	14	11.65	MAP2K2	NM_030662	-	-416
chr18	9904266	9904370	105	53	7	34.16	VAPA	NM_194434	+	-416

chr3	188418035	188419045	1011	108	62	5.75	MASP1	NM_001879	-	-414
chr9	76865928	76866351	424	161	35	7.76	C9orf95	NM_017881	-	-414
chr19	4626401	4626650	250	202	14	10.98	DPP9	NM_139159	-	-414
chr16	45747053	45747214	162	108	9	12.5	ITFG1	NM_030790	-	-414
chr11	6590557	6590988	432	111	36	5.8	TPP1	NM_000391	-	-413
chr11	65808631	65809040	410	351	39	6	YIF1A	NM_020470	-	-413
chr19	3909678	3909864	187	62	9	12.55	DAPK3	NM_001348	-	-413
chr12	63393519	63393902	384	62	26	9.14	GNS	NM_002076	-	-412
chr1	53134193	53134904	712	437	130	9.75	ECHDC2	NM_018281	-	-412
chr11	113109366	113109531	166	57	8	23.12	ZW10	NM_004724	-	-411
chr1	45240735	45241210	476	341	26	6.97	HECTD3	NM_024602	-	-410
chr2	46982647	46982928	282	133	16	8.26	MCFD2	NM_139279	-	-410
chr6	159106774	159107175	402	305	39	10.3	VIL2	NM_003379	-	-410
chr3	99781274	99781391	118	60	6	17.57	CPOX	NM_000097	-	-410
chr16	65739638	65739915	278	124	12	10.46	MGC4655	NM_033309	-	-409
chr9	33375064	33375357	294	44	12	20.33	AQP7	NM_001170	-	-409
chrX	118254221	118254697	477	262	78	6.63	PGRMC1	NM_006667	+	-407
chr8	64090301	64090602	302	53	25	8.84	GGH	NM_003878	-	-406
chr13	20964984	20965245	262	93	14	11.51	EFHA1	NM_152726	-	-406
chr19	5642858	5643250	393	164	32	6.47	LONP1	NM_004793	-	-405
chr1	43689408	43689820	413	121	34	7.39	HYI	NM_031207	-	-405
chr4	103936231	103936621	391	208	31	5.72	UBE2D3	NM_181892	-	-404
chr2	43304146	43304613	468	119	25	8.22	ZFP36L2	NM_006887	-	-403
chr6	33390260	33390576	317	166	14	12.81	ZBTB22	NM_005453	-	-403
chr1	159390424	159390574	151	57	9	25.62	UFC1	NM_016406	+	-402
chr1	195275108	195275344	237	59	25	8.92	F13B	NM_001994	-	-401

chr12	127843880	127844118	239	124	8	14	SLC15A4	NM_145648	-	-401
chr18	3440386	3440572	187	35	6	22.52	TGIF	NM_003244	+	-401
chr1	153378999	153379392	394	144	32	5.77	DPM3	NM_018973	-	-400
chr2	27386090	27386264	175	95	8	18.3	MPV17	NM_002437	-	-400
chr2	165057604	165057976	373	250	25	8.58	GRB14	NM_004490	-	-398
chr11	62171054	62171295	242	123	9	14.64	INTS5	NM_030628	-	-398
chr22	49311272	49311446	175	62	12	11.53	ECGF1	NM_001953	-	-397
chr4	24732995	24733216	222	96	9	14.64	SLA/LP	NM_153825	-	-397
chr20	5028565	5028885	321	146	18	17.08	C20orf30	NM_001009924	-	-397
chr19	4396019	4396656	638	470	46	6.59	UBXD1	NM_025241	-	-396
chr3	187840870	187841237	368	98	24	8.08	FETUB	NM_014375	+	-395
chr17	7063958	7064270	313	108	30	6.81	ACADVL	NM_000018	+	-394
chr2	183497960	183498244	285	119	13	14.6	NCKAP1	NM_013436	-	-394
chr16	28761604	28762005	402	150	72	6.14	TUFM	NM_003321	-	-393
chr1	223655902	223656220	319	145	17	9.34	LBR	NM_002296	-	-393
chr8	101602356	101602570	215	68	11	20.5	ANKRD46	NM_198401	-	-393
chr11	75157482	75157847	366	62	43	7.14	DGAT2	NM_032564	+	-392
chr5	95175413	95175822	410	176	24	11.01	GLRX	NM_002064	-	-392
chr9	106583233	106583498	266	125	12	11.56	ABCA1	NM_005502	-	-392
chr10	135018620	135019042	423	215	46	7.52	C10orf125	NM_198472	-	-389
chr10	105343996	105344164	169	121	6	17.22	SH3PXD2A	NM_014631	-	-389
chr2	96877721	96877895	175	103	6	17.73	ANKRD39	NM_016466	-	-389
chr10	97413343	97413552	210	59	8	18.3	C10orf61	NM_015631	-	-389
chr17	77872463	77872578	116	59	6	35.46	SECTM1	NM_003004	-	-389
chr17	77134375	77134746	372	319	18	5.63	NPLOC4	NM_017921	-	-388
chr11	60873069	60873243	175	128	12	8.37	CYBASC3	NM_153611	-	-388

chr19	55046410	55046615	206	96	7	18.3	PTOV1	NM_017432	+	-388
chr9	126155589	126155952	364	59	49	6.13	PSMB7	NM_002799	-	-387
chr16	1799041	1799492	452	273	86	7.06	HAGH	NM_001040427	-	-387
chr2	47887638	47887951	314	200	12	11.44	FBXO11	NM_025133	-	-387
chrX	47396352	47396526	175	121	7	14.64	UXT	NM_153477	-	-387
chr14	74815308	74815669	362	162	33	8.94	FOS	NM_005252	+	-386
chr22	37856819	37857119	301	62	19	22.03	CBX7	NM_175709	-	-386
chr13	44808949	44809687	739	169	134	7.03	TPT1	NM_003295	-	-384
chr4	100476320	100477057	738	600	151	8.14	ADH1C	NM_000669	-	-384
chr9	129687421	129687804	384	146	23	8.03	ST6GALNAC6	NM_013443	-	-383
chr2	128112481	128112855	375	75	21	8.24	LIMS2	NM_017980	-	-383
chr19	1226556	1226933	378	246	16	9.69	C19orf24	NM_017914	+	-383
chr3	25735817	25736161	345	68	15	10.46	NGLY1	NM_018297	-	-383
chr10	104394225	104394737	513	235	20	7.32	TRIM8	NM_030912	+	-382
chr10	123227945	123228227	283	155	17	7.32	FGFR2	NM_022970	-	-382
chr14	101884629	101884755	127	48	6	18.3	CINP	NM_032630	-	-382
chr1	120056103	120056413	311	166	27	6.26	PHGDH	NM_006623	+	-381
chr4	69716507	69716698	192	133	17	7.71	UGT2B10	NM_001075	+	-381
chr14	93819429	93819784	356	232	54	6.12	SERPINA10	NM_016186	-	-380
chr1	202433927	202434290	364	184	47	7.99	GOLT1A	NM_198447	-	-380
chr22	22643467	22643940	474	310	144	6.12	DDT	NM_001355	-	-379
chr14	49155371	49155536	166	106	22	6.48	RPL36AL	NM_001001	-	-378
chr12	107563060	107563395	336	249	16	9.84	CORO1C	NM_014325	-	-378
chr3	188921821	188922236	416	224	22	14.21	BCL6	NM_138931	-	-378
chr13	112187565	112187706	142	61	9	47.28	TUBGCP3	NM_006322	-	-378
chr12	120230562	120230920	359	85	31	5.73	ANAPC5	NM_016237	-	-377

chr17	71406321	71406695	375	159	21	6.41	MRPL38	NM_032478	-	-377
chr1	46426971	46427317	347	131	23	7.62	POMGNT1	NM_017739	-	-377
chr11	59160933	59161146	214	157	10	14.64	FLJ36874	NM_152716	-	-377
chr9	101024634	101024766	133	62	19	7.01	SEC61B	NM_006808	+	-376
chr14	23748690	23749004	315	52	15	7.69	CHMP4A	NM_014169	-	-376
chr1	19502937	19503425	489	167	32	10.23	AKR7A2	NM_003689	-	-375
chrX	46822742	46823093	352	122	22	11.6	RGN	NM_004683	+	-375
chr6	32654523	32654900	378	117	42	5.93	HLA-DRB1	NM_002124	-	-374
chr12	15664541	15664716	176	53	7	11.71	EPS8	NM_004447	-	-374
chr9	94258474	94258685	212	59	11	14.64	ASPN	NM_017680	-	-374
chr6	90409814	90410324	511	194	28	8.31	MDN1	NM_014611	-	-373
chr5	137520611	137520857	247	90	9	14.64	BRD8	NM_183359	-	-373
chr18	45563859	45564244	386	258	115	5.65	ACAA2	NM_006111	-	-372
chr1	205329194	205329622	429	314	51	8.57	C4BPB	NM_001017367	+	-372
chr5	141222434	141222773	340	59	16	12.92	PCDH1	NM_002587	-	-372
chr1	54132451	54132819	369	166	24	8.49	DIO1	NM_001039716	+	-371
chr3	187866423	187866861	439	153	158	5.14	HRG	NM_000412	+	-370
chr19	4487701	4488597	897	700	150	6.7	LRG1	NM_052972	-	-370
chr11	9258855	9259149	295	182	14	8.64	TMEM41B	NM_015012	-	-370
chr17	58863477	58863767	291	198	18	9.94	CYB561	NM_001017917	-	-370
chr22	29830774	29831134	361	269	17	10.57	SELM	NM_080430	-	-370
chr3	121797899	121798186	288	63	30	6.56	NDUFB4	NM_004547	+	-369
chr6	32916478	32916844	367	72	40	6.27	PSMB8	NM_148919	-	-368
chr1	71301585	71301930	346	287	17	11.39	ZRANB2	NM_203350	-	-368
chr12	51577373	51577605	233	60	21	12.28	KRT8	NM_002273	-	-368
chr6	31606010	31606344	335	177	17	13.42	BAT1	NM_004640	-	-368

chr2	10840939	10841336	398	208	33	7.32	PDIA6	NM_005742	-	-367
chr8	71648270	71648593	324	179	50	8.19	TRAM1	NM_014294	-	-367
chrX	23711229	23711590	362	151	87	5.3	SAT1	NM_002970	+	-366
chr22	23221299	23221616	318	138	37	10.48	UPB1	NM_016327	+	-366
chr15	70830860	70831128	269	155	10	15.15	ADPGK	NM_031284	-	-366
chr2	100990254	100990487	234	119	11	8.57	TBC1D8	NM_007063	-	-365
chr3	127682725	127683178	454	139	19	11.26	UROC1	NM_144639	-	-365
chr20	33677395	33677745	351	168	18	6.17	CPNE1	NM_003915	-	-364
chr17	17091052	17091229	178	79	11	9.12	COPS3	NM_003653	-	-364
chr22	28514615	28514966	352	166	22	11.6	ASCC2	NM_032204	-	-364
chr19	18357913	18358347	435	268	32	6.37	GDF15	NM_004864	+	-363
chr17	43565816	43566163	348	117	29	6.55	SKAP1	NM_003726	-	-363
chr12	52345240	52345574	335	170	42	7.58	ATP5G2	NM_005176	-	-363
chr11	65440887	65441222	336	105	21	13.12	C11orf68	NM_031450	-	-363
chr16	28017078	28017179	102	52	7	20.5	XPO6	NM_015171	-	-363
chr11	60414809	60415144	336	158	34	5.74	PRPF19	NM_014502	-	-362
chr4	82567212	82567604	393	207	18	8.78	RASGEF1B	NM_152545	-	-362
chr13	30608835	30609126	292	47	16	9.98	HSPH1	NM_006644	-	-362
chr8	144765943	144766292	350	296	24	6.41	TSTA3	NM_003313	-	-360
chr2	130656408	130656532	125	65	10	16.47	FLJ14346	NM_025029	+	-360
chr19	17277653	17277835	183	98	11	10.65	MRPL34	NM_023937	+	-359
chr7	94826893	94827479	587	412	105	7.37	PON3	NM_000940	-	-358
chr17	77242541	77242829	289	208	13	17.57	LOC339229	NM_001039842	-	-358
chr6	33326085	33326385	301	59	14	21.96	VPS52	NM_022553	-	-358
chr3	144019535	144019758	224	127	13	7.65	PCOLCE2	NM_013363	-	-357
chr16	55217204	55217440	237	70	73	6.52	MT1E	NM_175617	+	-355

chr19	8282290	8282588	299	62	24	8.03	NDUFA7	NM_005001	-	-355
chr12	94918816	94919096	281	174	13	8.23	LTA4H	NM_000895	-	-355
chr2	190777681	190777959	279	117	14	9.53	HIBCH	NM_014362	-	-355
chr17	36227920	36228250	331	253	23	12.6	KRT10	NM_000421	-	-355
chr11	62117315	62117605	291	122	16	18.82	MTA2	NM_004739	-	-355
chr6	52722548	52723493	946	764	135	8.86	GSTA2	NM_000846	-	-354
chr14	44654888	44655212	325	185	18	9.52	FKBP3	NM_002013	-	-354
chr2	63922544	63922870	327	61	34	10.37	UGP2	NM_006759	+	-353
chr11	18458597	18458787	191	133	9	16.78	TSG101	NM_006292	-	-353
chr16	83156728	83157058	331	95	17	10.98	COTL1	NM_021149	-	-352
chr17	38306359	38306691	333	62	81	5.98	G6PC	NM_000151	+	-351
chr20	61297270	61297579	310	53	21	8.78	YTHDF1	NM_017798	-	-351
chr16	28418234	28418535	302	153	13	25.62	IL27	NM_145659	-	-351
chr4	152811515	152811800	286	165	13	6.98	PET112L	NM_004564	-	-350
chr10	80777239	80777575	337	177	19	7.4	PPIF	NM_005729	+	-350
chr22	40326802	40327231	430	116	19	9.44	D15Wsu75e	NM_015704	-	-350
chr2	220111944	220112271	328	60	22	9.6	CHPF	NM_024536	-	-350
chr9	130523030	130523329	300	245	15	26.35	ZDHHC12	NM_032799	-	-350
chr9	35089896	35090241	346	76	20	10.13	STOML2	NM_013442	-	-349
chr13	47705302	47705654	353	276	41	6.6	ITM2B	NM_021999	+	-348
chr19	1442165	1442512	348	104	49	7.45	REEP6	NM_138393	+	-348
chr6	31762767	31763062	296	157	17	7.58	BAT5	NM_021160	-	-348
chr12	45038232	45038584	353	137	77	5.69	SLC38A2	NM_018976	-	-346
chr9	89530800	89531145	346	278	22	6.51	CTSL	NM_001912	+	-346
chr6	170686107	170686479	373	200	52	6.67	PSMB1	NM_002793	-	-346
chr11	67152048	67152331	284	61	12	10.4	NUDT8	NM_181843	-	-346

chr1	159232659	159232952	294	133	29	6.15	F11R	NM_016946	-	-345
chr22	39971558	39971905	348	213	22	16.73	RANGAP1	NM_002883	-	-345
chr13	49133050	49133206	157	102	9	9.76	EBPL	NM_032565	-	-343
chr11	2355120	2355465	346	287	35	13.3	CD81	NM_004356	+	-343
chr19	19617093	19617354	262	207	12	17.57	ATP13A1	NM_020410	-	-343
chr10	15293695	15293995	301	155	11	21.69	C10orf38	NM_001010924	-	-343
chr6	32244021	32244309	289	189	15	9.15	AGPAT1	NM_006411	-	-342
chr2	158301417	158301547	131	60	6	14.64	ACVR1	NM_001105	-	-341
chr4	72826274	72826615	342	134	152	5.13	GC	NM_000583	-	-339
chr6	24775245	24775591	347	266	35	8.89	THEM2	NM_018473	+	-338
chr4	157064889	157065065	177	118	14	10.74	CTSO	NM_001334	-	-338
chr12	70289790	70289988	199	104	9	17.57	CCDC131	NM_144982	-	-338
chr21	46381030	46381457	428	157	192	5.65	FTCD	NM_206965	-	-336
chr6	101063519	101063664	146	88	8	17.57	ASCC3	NM_006828	-	-335
chr10	52236471	52236667	197	95	24	21.63	ACF	NM_138933	-	-335
chr7	23305585	23305796	212	153	11	10.86	C7orf30	NM_138446	+	-332
chr15	73435186	73435518	333	173	21	10.97	MAN2C1	NM_006715	-	-332
chr10	12978658	12978961	304	203	18	7.12	CCDC3	NM_031455	-	-331
chr1	166153820	166154265	446	248	68	7.15	BRP44	NM_015415	-	-331
chr2	85629710	85630046	337	117	24	8.22	GGCX	NM_000821	-	-331
chr14	89933149	89933456	308	103	20	13.53	CALM1	NM_006888	+	-331
chr11	47142428	47142759	332	96	22	7.29	ZNF289	NM_032389	-	-330
chr11	69176822	69177354	533	351	53	9.1	FLJ42258	NM_001004327	-	-330
chr12	6471492	6471908	417	237	48	9.16	MRPL51	NM_016497	-	-330
chr19	5845690	5846014	325	63	43	10.38	NDUFA11	NM_175614	-	-329
chr2	241456597	241457162	566	384	125	5.75	AGXT	NM_000030	+	-328

chr3	186391167	186391434	268	94	36	5.43	EHHADH	NM_001966	-	-327
chr1	35421888	35422116	229	61	11	7.32	SFPQ	NM_005066	-	-327
chr12	200118	200378	261	54	16	15.29	SLC6A13	NM_016615	-	-327
chr12	101756267	101756560	294	154	91	5.38	PAH	NM_000277	-	-326
chr16	87237202	87237524	323	70	31	9.46	CYBA	NM_000101	-	-326
chr12	108852121	108852317	197	140	10	10.46	GIT2	NM_014776	-	-326
chr11	67166604	67166926	323	140	23	7.09	ACY3	NM_080658	-	-324
chr5	98218766	98219132	367	266	16	11.81	CHD1	NM_001270	-	-324
chr1	167750036	167750355	320	179	55	5.86	F5	NM_000130	-	-323
chr19	960652	960972	321	120	36	8.88	C19orf6	NM_001033026	-	-323
chr11	107848150	107848380	231	123	8	13.53	KDELC2	NM_153705	-	-323
chr17	31334710	31335126	417	218	61	6.69	CCL14	NM_032963	-	-322
chr11	117629447	117629666	220	124	8	15.91	EVA1	NM_005797	-	-322
chrX	54976320	54976636	317	233	16	37.13	PFKFB1	NM_002625	-	-322
chr19	2220540	2220840	301	135	57	6.49	OAZ1	NM_004152	+	-321
chr19	40322109	40322550	442	215	32	6.47	FXVD1	NM_005031	+	-319
chr8	30555712	30555891	180	123	9	17.08	GTF2E2	NM_002095	-	-318
chr19	45620176	45620573	398	292	20	6.99	SERTAD1	NM_013376	-	-317
chr1	67242451	67242756	306	45	13	7.79	SLC35D1	NM_015139	-	-317
chr1	159336955	159337287	333	162	22	8.13	PFDN2	NM_012394	-	-317
chr11	18223360	18223680	321	74	44	5.33	SAA2	NM_030754	-	-316
chr10	90684768	90685128	361	212	21	11.63	ACTA2	NM_001613	-	-316
chr6	30143065	30143226	162	77	9	17.57	PPP1R11	NM_021959	+	-316
chr20	2390314	2390595	282	90	24	5.9	SNRPB	NM_198216	-	-315
chr18	59207536	59207721	186	59	6	23.64	VPS4B	NM_004869	-	-315
chrX	23595550	23595879	330	271	32	5.37	PRDX4	NM_006406	+	-314

chrX	152848618	152848883	266	103	15	7.79	ARD1A	NM_003491	-	-313
chr4	129410705	129411061	357	119	34	8.08	PGRMC2	NM_006320	-	-313
chr12	54581479	54581776	298	156	13	12.55	WIBG	NM_032345	-	-313
chr8	27646773	27647063	291	169	17	7.81	CCDC25	NM_018246	-	-312
chr4	109130474	109130700	227	78	11	20.5	HADH	NM_005327	+	-312
chr1	224079571	224079907	337	237	85	6.43	EPHX1	NM_000120	+	-309
chr9	34679585	34679876	292	59	27	7.13	CCL19	NM_006274	-	-308
chr19	4311357	4311675	319	114	21	10.14	SH3GL1	NM_003025	-	-308
chr12	69805207	69805451	245	113	13	12.55	TSPAN8	NM_004616	-	-308
chr11	65094661	65094826	166	107	11	20.5	SSSCA1	NM_006396	+	-308
chrX	129091088	129091326	239	178	25	8.16	AIFM1	NM_004208	-	-307
chr22	49364299	49364559	261	94	14	20.5	CHKB	NM_005198	-	-307
chr1	42668784	42668987	204	147	7	24.4	ZMYND12	NM_032257	-	-306
chr17	37098668	37098957	290	62	43	5.04	EIF1	NM_005801	+	-305
chrX	118943163	118943355	193	113	7	29.55	NKAP	NM_024528	-	-304
chr19	53527513	53527730	218	168	10	12.2	TMEM143	NM_018273	-	-303
chr10	69712471	69712724	254	133	35	5.72	MAWBP	NM_022129	-	-302
chr20	2764017	2764272	256	119	12	21.96	FAM113A	NM_022760	-	-302
chr2	96280119	96280341	223	136	11	9.55	TMEM127	NM_017849	-	-301
chr19	18962822	18963003	182	111	7	19.52	SFRS14	NM_014884	-	-301
chr5	125908211	125908645	435	307	27	6.37	ALDH7A1	NM_001182	-	-298
chr1	203893628	203893899	272	132	12	7.96	SLC45A3	NM_033102	-	-296
chr1	17217872	17218109	238	144	26	10.45	SDHB	NM_003000	-	-296
chr19	54830385	54830659	275	156	11	10.98	RRAS	NM_006270	-	-296
chr2	33662251	33662528	278	223	15	12.81	FAM98A	NM_015475	-	-296
chr22	40805659	40805938	280	95	26	8.2	C22orf32	NM_033318	+	-294

chr6	2893397	2893685	289	59	24	13.6	SERPINB6	NM_004568	-	-294
chr19	19227648	19227764	117	59	6	29.28	HAPLN4	NM_023002	-	-294
chr1	31868104	31868350	247	93	11	9.76	PEF1	NM_012392	-	-293
chr3	129927624	129927961	338	146	19	16.5	RAB7	NM_004637	+	-293
chr1	53465256	53465446	191	59	9	19.58	MAGOH	NM_002370	-	-293
chr12	55318234	55318517	284	184	101	6.02	ATP5B	NM_001686	-	-292
chr19	18145618	18145870	253	60	13	17.67	IFI30	NM_006332	+	-292
chr6	82936694	82936965	272	91	26	6.83	IBTK	NM_015525	-	-291
chr13	46243371	46243683	313	123	19	8.25	ESD	NM_001984	-	-291
chr5	74052701	74053078	378	59	22	8.3	GFM2	NM_032380	-	-291
chr19	43801685	43801852	168	67	18	8.61	EIF3S12	NM_013234	+	-291
chr15	51594689	51594947	259	61	22	12.64	WDR72	NM_182758	-	-291
chr2	43311619	43311785	167	62	6	29.55	THADA	NM_022065	-	-291
chr14	20628051	20628365	315	175	19	9.22	ZNF219	NM_016423	-	-290
chr19	50358027	50358315	289	113	15	8.46	TRAPPC6A	NM_024108	-	-289
chr9	139124831	139125101	271	60	28	5.29	DPP7	NM_013379	-	-288
chr14	94117694	94117851	158	61	14	10.02	SERPINA5	NM_000624	+	-288
chr10	133631299	133631481	183	61	15	13.4	BNIP3	NM_004052	-	-288
chr19	41087159	41087432	274	65	31	7.22	TYROBP	NM_003332	-	-287
chr19	10362815	10363095	281	150	17	12.55	CDC37	NM_007065	-	-287
chr1	2479193	2479438	246	92	18	9.6	TNFRSF14	NM_003820	-	-286
chr11	65407923	65408072	150	101	6	18.3	FIBP	NM_004214	-	-285
chr1	53452202	53452645	444	162	37	6.5	C1orf123	NM_017887	-	-284
chr7	42938506	42938747	242	90	14	10.63	MRPL32	NM_031903	+	-284
chr4	39176788	39177052	265	61	18	7.76	UGDH	NM_003359	-	-282
chr9	96901224	96901440	217	51	16	12.71	FANCC	NM_000136	-	-282

chr11	66962179	66962375	197	62	14	14.42	CORO1B	NM_020441	-	-282
chr9	122190954	122191250	297	140	11	29.55	CDK5RAP2	NM_001011649	-	-282
chr3	137451903	137452119	217	159	12	41.37	PCCB	NM_000532	+	-282
chr19	7447763	7448041	279	61	14	12.25	PEX11G	NM_080662	-	-281
chr3	140718967	140719253	287	197	36	6.49	RBP1	NM_002899	-	-280
chr11	484523	484791	269	188	34	12.8	RNH1	NM_002939	-	-280
chr2	72968131	72968335	205	53	8	14.08	SPR	NM_003124	+	-280
chr12	47602062	47602289	228	101	10	16.69	FKBP11	NM_016594	-	-280
chr19	47152678	47152956	279	90	20	6.13	RABAC1	NM_006423	-	-279
chr2	131521935	131522198	264	205	14	10.31	LOC130074	NM_001009993	-	-279
chr6	30796086	30796414	329	61	13	14.45	TUBB	NM_178014	+	-279
chr2	219782861	219783015	155	68	9	9.76	ABCB6	NM_005689	-	-278
chr11	62214356	62214600	245	62	16	16.14	BSCL2	NM_032667	-	-278
chr9	126659971	126660255	285	73	46	5.05	RPL35	NM_007209	-	-277
chr7	99083765	99084030	266	87	37	5.69	CYP3A5	NM_000777	-	-277
chr18	53418895	53419170	276	123	22	6.73	NARS	NM_004539	-	-277
chr19	4294747	4294852	106	54	7	17.08	FLJ14981	NM_032868	+	-277
chr1	40193437	40193673	237	128	9	17.35	MFSD2	NM_032793	+	-277
chrX	152929175	152929427	253	154	11	20.5	IRAK1	NM_001025242	-	-277
chr19	55124212	55124547	336	145	72	5.37	ATF5	NM_012068	+	-276
chr21	33029095	33029277	183	126	6	23.64	C21orf66	NM_016631	-	-276
chr16	2029837	2030091	255	160	25	7.47	NTHL1	NM_002528	-	-275
chr13	110091777	110092034	258	58	13	7.55	FLJ12118	NM_024537	-	-275
chr20	38748017	38748207	191	73	8	11.19	MAFB	NM_005461	-	-275
chr7	44585210	44585562	353	193	21	12.06	TMED4	NM_182547	-	-275
chr5	141468551	141468781	231	95	13	11.84	NDFIP1	NM_030571	+	-274

chr6	39981174	39981550	377	104	15	9.45	MOCS1	NM_005942	-	-273
chr16	3055621	3055935	315	198	20	7.69	IL32	NM_001012632	+	-272
chr12	6955666	6955880	215	144	23	8.66	MBOAT5	NM_005768	-	-272
chr19	52940654	52940891	238	150	11	8.71	GLTSCR2	NM_015710	+	-272
chr19	46189025	46189315	291	146	22	9.37	CYP2B6	NM_000767	+	-272
chr1	15771709	15772010	302	119	29	15.48	AGMAT	NM_024758	-	-272
chr3	9980628	9980908	281	162	20	16.46	TMEM111	NM_018447	-	-272
chr18	52421060	52421321	262	60	18	7.67	TXNL1	NM_004786	-	-271
chr2	86683990	86684297	308	139	18	12.4	RNF103	NM_005667	-	-271
chr1	182926347	182926531	185	54	7	20.92	EDEM3	NM_025191	-	-271
chr2	219823275	219823514	240	107	12	10.54	TUBA1	NM_006000	-	-270
chr19	5538149	5538280	132	72	9	10.65	SAFB2	NM_014649	-	-270
chr19	43984129	43984423	295	104	20	8.64	LGALS4	NM_006149	-	-269
chr1	149048827	149049078	252	197	13	8.78	ARNT	NM_001668	-	-269
chr3	58465870	58466170	301	145	37	8.14	ACOX2	NM_003500	-	-267
chr14	52311726	52311928	203	94	13	13.37	GNPNAT1	NM_198066	-	-267
chr14	88692424	88692544	121	61	6	33.79	CHES1	NM_005197	-	-267
chr2	74607302	74607549	248	132	28	9.08	AUP1	NM_181575	-	-266
chr16	65523491	65523732	242	183	29	9.21	FAM96B	NM_016062	-	-266
chr16	3648050	3648304	255	121	21	13.69	TRAP1	NM_016292	-	-265
chr2	75039375	75039547	173	92	7	14.64	POLE4	NM_019896	+	-265
chr15	89275235	89275425	191	131	11	19.52	HDDC3	NM_198527	-	-265
chr19	46584174	46584382	209	53	8	23.64	EXOSC5	NM_020158	-	-265
chr10	12249636	12249843	208	148	17	6.85	NUDT5	NM_014142	-	-264
chr1	75962998	75963133	136	90	9	46.85	ACADM	NM_000016	+	-264
chr19	46041204	46041546	343	278	80	5.88	CYP2A6	NM_000762	-	-263

chr17	18088923	18089139	217	96	16	7.41	FLII	NM_002018	-	-260
chr12	56374203	56374410	208	91	18	6.7	OS9	NM_001017956	+	-258
chr11	61397607	61397832	226	51	12	17.57	FADS3	NM_021727	-	-258
chr1	145123556	145124718	1163	431	141	9.02	FMO5	NM_001461	-	-257
chr5	35033988	35034219	232	62	13	9.32	AGXT2	NM_031900	-	-257
chr12	111829221	111829378	158	97	10	43.92	OAS1	NM_002534	+	-257
chr9	138876389	138876647	259	171	55	5.06	EDF1	NM_003792	-	-256
chr14	23633375	23633578	204	61	14	16.43	PCK2	NM_001018073	+	-256
chr10	15860259	15860436	178	51	7	29.55	C10orf97	NM_024948	-	-256
chr6	31731588	31731904	317	153	37	6.78	APOM	NM_019101	+	-255
chr16	2504020	2504208	189	108	14	9.22	ATP6V0C	NM_001694	+	-255
chr19	18871329	18871578	250	97	30	11.9	COPE	NM_007263	-	-255
chr17	6485080	6485303	224	84	22	7.22	TXNL5	NM_032731	+	-253
chr17	30360286	30360496	211	61	9	10.17	RFFL	NM_001017368	-	-253
chr17	46151988	46152228	241	81	13	12.35	CROP	NM_006107	+	-253
chr7	95050793	95050999	207	117	33	9.09	PDK4	NM_002612	-	-251
chr17	9094534	9094764	231	115	8	16.91	STX8	NM_004853	-	-251
chr12	55392540	55392736	197	54	15	12.5	NACA	NM_005594	-	-250
chr20	10333960	10334082	123	62	6	21.96	MKKS	NM_018848	-	-250
chrX	15312906	15313095	190	138	9	16.69	PIR	NM_001018109	-	-249
chr1	32252153	32252325	173	122	6	19.52	KHDRBS1	NM_006559	+	-248
chr8	120148770	120148873	104	53	6	29.28	COLEC10	NM_006438	+	-247
chr1	11902699	11902957	259	144	15	10.11	KIAA2013	NM_138346	-	-246
chr19	39547925	39548154	230	170	15	11.79	GPI	NM_000175	+	-246
chr16	10930293	10930494	202	135	14	9.86	DEXI	NM_014015	-	-245
chr19	1803453	1803642	190	56	8	13.91	KLF16	NM_031918	-	-244

chr22	22566580	22566807	228	92	66	5.34	MIF	NM_002415	+	-243
chr3	52002796	52002927	132	71	30	5.8	RPL29	NM_000992	-	-243
chr5	172343436	172343611	176	58	14	9.45	ATP6V0E1	NM_003945	+	-243
chr1	154149518	154149702	185	116	10	12.2	KIAA0907	NM_014949	-	-243
chr14	69303594	69303829	236	88	15	13.94	SFRS5	NM_006925	+	-243
chr15	53260881	53261055	175	114	10	19.52	C15orf15	NM_016304	-	-243
chr16	73043371	73043597	227	106	16	10.14	GLG1	NM_012201	-	-241
chr14	98933867	98934075	209	79	13	10.2	SETD3	NM_032233	-	-239
chr3	51397765	51397981	217	102	8	17.93	ARMET	NM_006010	+	-239
chr2	44356096	44356341	246	124	9	24.4	SLC3A1	NM_000341	+	-239
chr20	1297631	1297861	231	121	17	24.4	FKBP1A	NM_000801	-	-239
chr19	63754756	63754983	228	61	21	6.68	CHMP2A	NM_198426	-	-238
chr1	154828205	154828419	215	67	9	14.08	APOA1BP	NM_144772	+	-238
chr3	49696398	49696629	232	154	56	5.73	MST1	NM_020998	-	-237
chr1	54269956	54270175	220	90	28	9.76	TMEM59	NM_004872	-	-237
chr11	57122188	57122517	330	158	42	14.2	SERPING1	NM_001032295	+	-237
chr10	5478641	5478782	142	55	7	29.28	NET1	NM_005863	+	-237
chr17	69711429	69711625	197	48	16	13.73	RPL38	NM_000999	+	-236
chr1	158163515	158163691	177	55	10	25.62	IGSF9	NM_020789	-	-236
chr11	117212963	117213137	175	58	13	7.69	FXVD6	NM_022003	-	-235
chr16	1760248	1760557	310	221	18	7.81	NME3	NM_002513	-	-235
chr1	145093344	145093545	202	125	11	9.32	PRKAB2	NM_005399	-	-235
chr22	30051836	30052025	190	58	8	13.91	PATZ1	NM_014323	-	-235
chr3	28258131	28258362	232	148	12	20.38	MGC61571	NM_182523	+	-235
chr6	31891316	31891549	234	51	20	7.54	HSPA1A	NM_005345	+	-234
chr20	31410389	31410539	151	101	6	14.64	CDK5RAP1	NM_016082	-	-234

chr15	23133541	23133723	183	122	12	19.52	UBE3A	NM_130838	-	-234
chr3	122865603	122865873	271	145	13	27.89	GOLGB1	NM_004487	-	-234
chr16	28524442	28524651	210	132	19	8.61	SULT1A1	NM_177530	-	-233
chr8	55041823	55041901	79	40	6	21.96	TCEA1	NM_006756	-	-232
chr11	63498563	63498885	323	263	35	5.82	COX8A	NM_004074	+	-231
chr5	132238638	132239201	564	289	60	7.02	AFF4	NM_014423	-	-231
chr11	62099115	62099327	213	84	8	13.07	TUT1	NM_022830	-	-231
chr7	51051426	51051634	209	57	13	14.64	COBL	NM_015198	-	-231
chr2	26110533	26110708	176	60	6	17.22	RAB10	NM_016131	+	-231
chr16	28016870	28017047	178	120	11	20.85	XPO6	NM_015171	-	-231
chr15	67532228	67532442	215	71	41	5.25	RPLP1	NM_001003	+	-230
chr5	175748376	175748618	243	106	22	5.93	HIGD2A	NM_138820	+	-229
chr7	128290160	128290362	203	150	14	10.4	ATP6V1F	NM_004231	+	-229
chr10	75606497	75606677	181	103	6	16.27	ADK	NM_001123	+	-228
chr7	134483399	134483590	192	116	7	16.27	TMEM140	NM_018295	+	-227
chr14	76994225	76994381	157	61	7	28.16	AHSA1	NM_012111	+	-227
chr19	14537901	14538117	217	131	41	6.35	NDUFB7	NM_004146	-	-226
chr5	180596530	180596759	230	81	52	6.73	GNB2L1	NM_006098	-	-226
chr6	31714737	31715022	286	170	25	8.97	BAT3	NM_004639	-	-226
chr5	324796	324961	166	109	8	29.55	PDCD6	NM_013232	+	-226
chr3	48611450	48611660	211	128	51	5.27	UQCRC1	NM_003365	-	-225
chr15	81476226	81476410	185	62	14	8.13	BTBD1	NM_025238	-	-224
chr14	38714171	38714374	204	150	10	17.92	PNN	NM_002687	+	-224
chr1	157824147	157824461	315	204	96	5.54	APCS	NM_001639	+	-222
chr16	20455919	20456191	273	185	29	6.79	ACSM2	NM_182617	-	-222
chr11	62083737	62083870	134	90	7	17.57	EEF1G	NM_001404	-	-222

chrX	63321719	63321941	223	138	9	29.28	FAM123B	NM_152424	-	-219
chr12	7038301	7038499	199	77	48	7.28	C1S	NM_001734	+	-218
chr7	137411778	137411953	176	56	14	11.6	AKR1D1	NM_005989	+	-218
chr1	11027382	11027659	278	127	29	8.65	MASP2	NM_139208	-	-217
chr6	33773236	33773539	304	177	17	13.35	C6orf125	NM_032340	-	-216
chr12	51837804	51837930	127	80	6	15.91	CSAD	NM_015989	-	-216
chr16	4598891	4599101	211	56	17	11.33	FAM100A	NM_145253	-	-215
chr17	6880408	6880639	232	161	14	10.19	SLC16A13	NM_201566	+	-214
chr22	38246532	38246727	196	62	17	10.52	ATF4	NM_001675	+	-213
chr8	125620529	125620748	220	132	22	13.69	NDUFB9	NM_005005	+	-213
chr2	113601550	113601821	272	200	28	27.88	IL1RN	NM_173842	+	-213
chr1	42984668	42984844	177	118	8	12.96	LEPRE1	NM_022356	-	-212
chr7	100037953	100038135	183	54	8	14.64	PCOLCE	NM_002593	+	-210
chr20	60145192	60145395	204	55	19	17.22	PSMA7	NM_002792	-	-210
chr12	52861586	52861727	142	60	7	20.92	SMUG1	NM_014311	-	-209
chr19	523577	523744	168	96	14	13.53	BSG	NM_001728	+	-208
chr4	48582217	48582370	154	83	22	6.39	OCIAD2	NM_001014446	-	-207
chr19	19091484	19091637	154	95	10	18.82	TMEM161A	NM_017814	-	-207
chr1	77934293	77934469	177	101	8	12.2	USP33	NM_201624	-	-206
chr20	30754191	30754371	181	62	17	17.23	COMMD7	NM_053041	-	-206
chr1	153556806	153557080	275	82	39	6.22	C1orf104	NM_001039517	-	-205
chr17	4581441	4581676	236	175	8	20.73	MED11	NM_001001683	+	-205
chr11	113815443	113815590	148	88	7	31.37	REXO2	NM_015523	+	-204
chr17	77117389	77117590	202	59	9	12.55	C17orf70	NM_025161	-	-203
chrX	34555204	34555305	102	52	6	17.57	TMEM47	NM_031442	-	-202
chr17	45133622	45133889	268	186	15	9.16	SLC35B1	NM_005827	-	-201

chr3	52207244	52207384	141	50	8	14.45	ALAS1	NM_000688	+	-201
chrX	47396156	47396339	184	69	15	11.67	UXT	NM_153477	-	-200
chr3	44941701	44941864	164	115	6	14.64	ZDHHC3	NM_016598	-	-200
chr19	38013327	38013460	134	50	6	18.3	SLC7A9	NM_014270	-	-199
chr14	102636274	102636430	157	102	6	17.73	C14orf73	NM_001077594	+	-197
chr11	56757666	56757838	173	113	11	7.88	AGTRL1	NM_005161	-	-196
chr17	7303389	7303618	230	82	11	10.46	ZBTB4	NM_020899	-	-196
chr12	119360315	119360482	168	61	12	11.07	COX6A1	NM_004373	+	-196
chr1	36693983	36694154	172	56	18	10.07	MRPS15	NM_031280	-	-195
chr17	7700675	7700923	249	178	28	8.33	LSMD1	NM_032356	-	-194
chr10	29006478	29006623	146	42	6	20.19	BAMBI	NM_012342	+	-194
chr1	93070201	93070374	174	52	16	9.55	RPL5	NM_000969	+	-193
chr12	54990432	54990675	244	180	14	9.76	TMEM4	NM_014255	-	-192
chr10	111614597	111614705	109	55	6	21.96	XPNPEP1	NM_020383	-	-192
chr14	74197793	74197900	108	55	6	17.57	KIAA0317	NM_001039479	-	-191
chr11	111602344	111602499	156	62	8	22.28	PTS	NM_000317	+	-191
chr14	20222527	20222798	272	214	50	7.66	ANG	NM_001145	+	-190
chr1	158452143	158452318	176	62	21	8.25	WDR42A	NM_015726	-	-190
chr1	9711664	9711856	193	81	11	9.89	CLSTN1	NM_001009566	-	-190
chr14	63924791	63925035	245	115	13	10.76	MTHFD1	NM_005956	+	-190
chr17	1612014	1612197	184	122	20	8.76	SERPINF1	NM_002615	+	-189
chr14	34831360	34831513	154	85	12	11.27	PSMA6	NM_002791	+	-189
chr9	135208486	135208674	189	105	18	6.09	SURF1	NM_003172	-	-188
chr6	76019404	76019556	153	58	12	7.75	TMEM30A	NM_018247	-	-188
chr12	99391815	99391997	183	60	8	10.72	NR1H4	NM_005123	+	-188
chr2	150134410	150134585	176	97	11	17.08	C2orf25	NM_015702	-	-188

chr9	33015299	33015396	98	50	8	32.54	DNAJA1	NM_001539	+	-188
chr6	32003251	32003659	409	192	27	7.81	C2	NM_000063	+	-187
chr3	143508164	143508327	164	113	6	29.55	XRN1	NM_019001	-	-187
chr1	153408541	153408694	154	89	18	7.33	KRTCAP2	NM_173852	-	-186
chr4	140430592	140430727	136	83	13	10.95	NDUFC1	NM_002494	-	-186
chr14	23753005	23753185	181	100	10	18.55	MDP-1	NM_138476	-	-186
chr1	176164566	176165049	484	262	30	7.09	LZTR2	NM_033127	-	-185
chr14	104290577	104290731	155	108	11	24.4	SIVA	NM_006427	+	-185
chr15	57215834	57216039	206	145	17	11.06	MYO1E	NM_004998	-	-184
chr8	145178096	145178339	244	124	10	13.56	OPLAH	NM_017570	-	-184
chr19	5629440	5629616	177	59	13	15.55	P117	NM_205767	-	-184
chr12	102848336	102848501	166	60	16	7.29	HSP90B1	NM_003299	+	-183
chr11	73363364	73363546	183	62	11	8.04	UCP2	NM_003355	-	-183
chr11	63840773	63840926	154	74	14	12.2	HSPC152	NM_016404	-	-183
chr17	77442873	77443077	205	93	9	17.57	ANAPC11	NM_001002245	+	-183
chr3	52786645	52786829	185	103	48	5.76	ITIH1	NM_002215	+	-182
chr2	27573207	27573390	184	90	11	10.78	GCKR	NM_001486	+	-181
chrX	76968546	76968700	155	58	15	15.89	KFZp564K14	NM_032121	-	-181
chr20	36408219	36408478	260	160	23	10.15	LBP	NM_004139	+	-180
chr9	130620617	130620779	163	57	8	16.71	ENDOG	NM_004435	+	-180
chr16	74157817	74157929	113	57	7	32.03	GABARAPL2	NM_007285	+	-180
chr6	52643811	52644020	210	160	8	18.45	TMEM14A	NM_014051	+	-178
chr17	60437316	60437470	155	52	8	11.35	GNA13	NM_006572	-	-175
chr17	37518654	37518831	178	118	8	19.71	GCN5L2	NM_021078	-	-175
chr15	38843591	38843749	159	77	8	13.97	GCHFR	NM_005258	+	-173
chr20	23007997	23008166	170	123	8	14.93	CD93	NM_012072	-	-173

chr1	171713088	171713280	193	109	24	5.65	PRDX6	NM_004905	+	-172
chr2	254938	255043	106	54	8	12.42	ACP1	NM_001040649	+	-172
chrX	152413662	152413775	114	58	11	9.18	BGN	NM_001711	+	-171
chr2	85676391	85676517	127	59	12	10.23	LOC51255	NM_016494	+	-170
chr12	94776870	94777009	140	69	11	18.45	SNRPF	NM_003095	+	-170
chr2	201158975	201159144	170	121	8	12.44	AOX1	NM_001159	+	-169
chr7	56136836	56136930	95	48	9	12.52	CHCHD2	NM_016139	-	-169
chr18	32630083	32630201	119	60	6	17.57	C18orf10	NM_015476	-	-169
chr5	149803970	149804152	183	110	20	8.57	RPS14	NM_001025070	-	-166
chr8	62699669	62699814	146	77	6	14.64	ASPH	NM_032468	-	-166
chr19	12894336	12894458	123	62	9	11.98	FARSLA	NM_004461	-	-165
chr12	49666077	49666208	132	73	7	31.37	SLC11A2	NM_000617	-	-165
chr12	47682323	47682486	164	107	10	11.39	PRKAG1	NM_212461	-	-164
chr19	17187176	17187331	156	95	7	18.3	MDS032	NM_018467	+	-164
chr10	69761855	69762048	194	66	8	22.88	HNRPH3	NM_012207	+	-164
chr5	150540766	150540970	205	115	12	24.01	CCDC69	NM_015621	-	-164
chr19	3909471	3909614	144	83	8	10.98	DAPK3	NM_001348	-	-163
chr5	147184344	147184501	158	52	7	26.14	SPINK1	NM_003122	-	-163
chr13	26907560	26907944	385	148	44	6.3	MTIF3	NM_152912	-	-162
chr6	26232412	26232513	102	52	6	35.46	HIST1H2AC	NM_003512	+	-162
chr11	71964868	71964994	127	44	8	13.02	PDE2A	NM_002599	-	-161
chr4	39376218	39376425	208	154	11	13.7	HIP2	NM_005339	+	-160
chr18	44824194	44824331	138	72	6	19.52	DYM	NM_017653	-	-160
chr17	37234978	37235146	169	58	7	28.34	NT5C3L	NM_052935	-	-160
chr1	70649512	70649700	189	55	7	29.28	CTH	NM_001902	+	-158
chr19	50137284	50137490	207	132	19	11.37	APOC4	NM_001646	+	-156

chr8	144728103	144728252	150	62	22	8.78	NAPRT1	NM_145201	-	-154
chr15	76619870	76619977	108	55	8	12.65	PSMA4	NM_002789	+	-154
chr13	112825125	112825264	140	79	12	11.27	F10	NM_000504	+	-151
chr4	22303651	22303836	186	139	7	16.27	GBA3	NM_020973	+	-149
chr1	53253134	53253344	211	77	73	6.46	SCP2	NM_001007250	+	-147
chr12	56271304	56271470	167	54	7	35.46	PIP5K2C	NM_024779	+	-147
chr16	16150843	16151637	795	265	64	8	ABCC6	NM_001171	-	-146
chr10	5228808	5228941	134	75	23	10.3	AKR1C4	NM_001818	+	-144
chr7	128381845	128382328	484	56	21	7.99	TNPO3	NM_012470	-	-143
chr12	55443376	55443508	133	73	20	7.01	HSD17B6	NM_003725	+	-134
chr2	27163129	27163752	624	519	101	10.34	KHK	NM_000221	+	-129
chr12	48432488	48432639	152	65	36	6.68	TEGT	NM_003217	+	-128
chr22	18309247	18309429	183	45	6	17.73	COMT	NM_000754	+	-121
chr2	27848120	27848208	89	45	6	23.12	MRPL33	NM_004891	+	-121
chr8	86563506	86563617	112	57	7	23.29	CA2	NM_000067	+	-120
chr1	7944266	7944479	214	160	12	12.53	PARK7	NM_007262	+	-100
chr4	78034678	78035205	528	116	22	7.73	ANKRD56	NM_001029870	-	-99
chr6	33010392	33010492	101	51	6	25.1	HLA-DMB	NM_002118	-	-99
chr12	48784045	48784163	119	60	13	11.32	GPD1	NM_005276	+	-96
chr14	94097540	94097627	88	45	9	11.6	SERPINA4	NM_006215	+	-92
chr2	232281488	232281571	84	43	6	35.46	PTMA	NM_002823	+	-92
chr2	219022952	219023253	302	156	17	22.28	USP37	NM_020935	-	-36
chr16	70157067	70158279	1213	188	254	5.73	TAT	NM_000353	-	-25
chr16	49727747	49727853	107	54	8	12.53	SALL1	NM_002968	-	-24
chr19	13115919	13116230	312	62	14	17.57	STX10	NM_003765	-	-6
chr18	55147683	55148059	377	171	21	5.69	LMAN1	NM_005570	-	28

chr5	34022940	34023626	687	354	49	5.33	AMACR	NM_014324	-	36
chr19	44567562	44568074	513	414	22	7.32	PAF1	NM_019088	-	37
chr19	6615348	6615528	181	127	7	19.52	TNFSF14	NM_003807	-	37
chr8	30655454	30655937	484	57	25	7.97	GSR	NM_000637	-	39
chr8	9031181	9032839	1659	264	211	6.12	PPP1R3B	NM_024607	-	76
chr1	153257073	153257503	431	322	24	5.52	DCST2	NM_144622	-	124
chr5	78328715	78329054	340	198	25	9.96	DMGDH	NM_013391	-	131
chr11	65177545	65178259	715	174	49	8.23	RELA	NM_021975	-	133
chr17	34143041	34143538	498	385	63	5.25	PCGF2	NM_007144	-	137
chr5	39408046	39408353	308	143	14	9.76	DAB2	NM_001343	-	149
chr14	73502164	73502773	610	147	38	5.09	ENTPD5	NM_001249	-	162
chr5	55272050	55272279	230	61	11	10.1	IL6ST	NM_002184	-	172
chr1	162795230	162795388	159	106	6	18.3	PBX1	NM_002585	+	172
chr1	210180958	210181144	187	54	6	19.52	INTS7	NM_015434	-	176
chr12	12519132	12519920	789	399	41	7.32	DUSP16	NM_030640	-	177
chr17	71134132	71134339	208	53	8	14.64	RECQL5	NM_004259	-	180
chr19	45431111	45431371	261	161	20	9.47	AKT2	NM_001626	-	184
chr17	24912074	24912250	177	78	11	21.96	LOC116236	NM_198147	-	187
chr14	19881152	19881418	267	124	17	8.8	PARP2	NM_005484	+	194
chr11	117906562	117906932	371	286	59	8.15	TMEM25	NM_032780	+	201
chr3	178221259	178221658	400	76	20	8.78	TBL1XR1	NM_024665	-	209
chr16	49727386	49727619	234	128	14	13.7	SALL1	NM_002968	-	210
chr2	43967986	43968180	195	97	8	18.3	LRPPRC	NM_133259	-	211
chr7	86812329	86812729	401	284	20	8.22	CROT	NM_021151	+	217
chr9	115068644	115068896	253	121	11	18.52	CDC26	NM_139286	-	217
chr4	120437701	120438006	306	57	24	7.47	LOC401152	NM_001001701	-	234

chr22	29214273	29214656	384	57	19	7.03	SEC14L4	NM_174977	-	243
chr6	90409247	90409706	460	201	36	8.66	MDN1	NM_014611	-	245
chr5	133969465	133969773	309	250	14	9.05	SAR1B	NM_001033503	-	245
chr9	34611057	34611203	147	55	8	12.55	ARID3C	NM_001017363	-	252
chr3	53826174	53826420	247	116	13	11.39	CHDH	NM_018397	-	260
chr8	38950363	38950591	229	62	12	23.47	HTRA4	NM_153692	+	262
chr17	72241211	72241500	290	164	15	5.72	SFRS2	NM_003016	-	293
chr13	29931506	29931690	185	139	6	16.73	HMGB1	NM_002128	-	306
chr4	104166122	104166462	341	145	18	7.88	LOC133308	NM_178833	-	337
chr2	43303059	43303870	812	619	58	6.23	ZFP36L2	NM_006887	-	340
chr12	131188493	131188644	152	61	6	23.64	DDX51	NM_175066	-	354
chr11	47549605	47549959	355	246	17	10.4	KBTBD4	NM_016506	-	366
chr18	55146749	55147678	930	173	88	6.76	LMAN1	NM_005570	-	409
chr17	1271189	1271790	602	88	35	9.79	CRK	NM_016823	-	419
chr1	198641376	198641608	233	62	13	18.3	ZNF281	NM_012482	-	441
chr4	100342709	100344453	1745	261	417	6.06	ADH6	NM_000672	-	449
chr10	115871364	115871506	143	66	6	14.64	C10orf118	NM_018017	-	457
chr19	45430082	45431097	1016	91	86	13.16	AKT2	NM_001626	-	458
chr5	36228757	36229107	351	61	52	6.28	C5orf33	NM_153013	-	466
chr7	44584460	44584784	325	163	19	10.47	TMED4	NM_182547	-	503
chr9	71234291	71234507	217	159	8	12.71	APBA1	NM_001163	-	514
chr10	310576	310862	287	151	12	15.91	DIP2C	NM_014974	-	569
chr8	38950070	38950271	202	58	8	14.79	HTRA4	NM_153692	+	582
chr14	74619813	74620139	327	147	15	9.15	NEK9	NM_033116	-	588
chr19	6614809	6614970	162	49	8	14.64	TNFSF14	NM_003807	-	595
chr1	35840575	35840724	150	116	6	19.26	PSMB2	NM_002794	-	602

chr15	66858358	66858646	289	116	16	6.35	ANP32A	NM_006305	-	613
chr7	26197112	26197375	264	109	19	5.37	HNRPA2B1	NM_002137	-	616
chr3	172195648	172196209	562	367	54	5.63	SLC2A2	NM_000340	-	621
chr7	15205652	15205838	187	53	8	15.69	FLJ16237	NM_001004320	-	629
chr2	38375658	38375994	337	277	16	11.09	ARL6IP2	NM_022374	-	633
chr8	23209490	23209717	228	120	10	29.55	LOXL2	NM_002318	-	637
chr11	47444750	47445880	1131	255	61	9.94	CUGBP1	NM_001025596	-	641
chr3	32254188	32254509	322	58	15	17.43	CMTM8	NM_178868	+	665
chr2	169486871	169487016	146	44	7	10.46	ABCB11	NM_003742	-	678
chr11	118731192	118731464	273	58	13	6.66	USP2	NM_004205	-	698
chr20	48939287	48939562	276	150	11	10.98	ADNP	NM_015339	-	727
chr1	166152628	166153202	575	69	35	6.73	BRP44	NM_015415	-	732
chr17	71507819	71508274	456	105	24	6.68	CDK3	NM_001258	+	739
chr3	53825602	53825888	287	143	17	17.22	CHDH	NM_018397	-	792
chr1	94124179	94124365	187	58	9	12.55	GCLM	NM_002061	-	812
chr8	1698259	1698503	245	163	14	10.76	CLN8	NM_018941	+	844
chr7	6467250	6467937	688	122	161	6.34	KDELR2	NM_006854	-	857
chr5	55271208	55271585	378	80	23	9.93	IL6ST	NM_002184	-	866
chr1	99945696	99945974	279	186	15	14.3	FRRS1	NM_001013660	-	872
chr4	39227472	39228047	576	413	35	9.82	C4orf34	NM_174921	-	897
chr15	68128429	68128557	129	53	7	20.92	TLE3	NM_005078	-	915
chr15	88026075	88026362	288	161	11	11.87	PEX11A	NM_003847	-	929
chr14	73501333	73502003	671	501	45	6.37	ENTPD5	NM_001249	-	932
chr12	12518634	12519087	454	128	30	6.65	DUSP16	NM_030640	-	1010
chr7	26196338	26196975	638	198	41	9.87	HNRPA2B1	NM_002137	-	1016
chr19	57308291	57308448	158	103	6	26.14	ZNF616	NM_178523	-	1017

chr2	176497394	176497620	227	140	8	14.64	KIAA1715	NM_030650	-	1035
chr18	45562569	45562805	237	102	15	12.67	ACAA2	NM_006111	-	1067
chr2	169486167	169486627	461	290	21	15.15	ABCB11	NM_003742	-	1067
chr7	121502248	121502341	94	48	8	13.01	AASS	NM_005763	-	1081
chr16	57256522	57256715	194	47	9	14.2	FLJ10815	NM_018231	-	1083
chr2	241815405	241815719	315	56	17	7.44	HDLBP	NM_203346	-	1097
chr1	229566125	229566949	825	149	40	19.33	EGLN1	NM_022051	-	1104
chr2	31601706	31602032	327	59	21	8.24	SRD5A2	NM_000348	-	1127
chr11	118123979	118124448	470	245	28	10.32	DDX6	NM_004397	-	1174
chr19	7588719	7589169	451	89	21	11.01	XAB2	NM_020196	-	1242
chr3	172195291	172195582	292	214	47	6.22	SLC2A2	NM_000340	-	1248
chr1	167748370	167748784	415	349	25	9.72	F5	NM_000130	-	1248
chr1	91918767	91919319	553	166	28	45.05	TGFBR3	NM_003243	-	1255
chr19	6614161	6614290	130	70	7	27.45	TNFSF14	NM_003807	-	1275
chr14	93817787	93818124	338	227	19	7.61	SERPINA10	NM_016186	-	1280
chr8	121617254	121617932	679	64	56	7.81	SNTB1	NM_021021	-	1294
chr1	21417199	21417612	414	103	30	11.71	ECE1	NM_001397	-	1326
chr17	77793873	77794201	329	61	15	7.32	CSNK1D	NM_001893	-	1329
chr18	55146219	55146746	528	214	71	5.65	LMAN1	NM_005570	-	1341
chr2	114186889	114187041	153	108	6	18.3	SLC35F5	NM_025181	-	1361
chr19	10012401	10012789	389	255	17	9.35	LOC388503	NM_001013640	+	1369
chr4	119419928	119420446	519	355	46	11.4	PRSS12	NM_003619	-	1418
chr14	52176608	52176927	320	114	13	18.3	ERO1L	NM_014584	-	1429
chr2	218373964	218374287	324	217	17	8.4	TNS1	NM_022648	-	1469
chr2	31601214	31601680	467	316	25	6.84	SRD5A2	NM_000348	-	1479
chr2	111593296	111593472	177	56	6	19.52	BCL2L11	NM_207002	+	1489

chr22	29212870	29213364	495	82	45	6.59	SEC14L4	NM_174977	-	1535
chr2	169485601	169486146	546	488	25	11.99	ABCB11	NM_003742	-	1548
chr12	61824820	61824922	103	52	7	20.5	AVPR1A	NM_000706	-	1560
chr12	103720633	103720914	282	156	19	7.43	SLC41A2	NM_032148	-	1579
chr7	129258028	129258620	593	153	35	9.01	UBE2H	NM_003344	-	1610
chr12	61824457	61824796	340	197	14	8.3	AVPR1A	NM_000706	-	1686
chr3	172194790	172195137	348	277	39	7.87	SLC2A2	NM_000340	-	1693
chr1	167747898	167748329	432	216	23	11.48	F5	NM_000130	-	1703
chr1	21416329	21417181	853	597	49	10.41	ECE1	NM_001397	-	1757
chr19	60587065	60587352	288	85	15	11.26	RPL28	NM_000991	+	1759
chr4	24730803	24731012	210	113	9	12.2	SLA/LP	NM_153825	-	1807
chr8	64133594	64134151	558	176	29	8.17	TTPA	NM_000370	-	1833
chr11	47444436	47444677	242	89	12	16.73	CUGBP1	NM_001025596	-	1844
chr1	91918557	91918718	162	61	7	28.16	TGFBR3	NM_003243	-	1856
chr5	110859842	110860046	205	62	9	16.89	STARD4	NM_139164	-	1874
chr9	34356709	34356966	258	131	16	13.22	KIAA1161	NM_020702	-	1941
chrX	10373956	10374172	217	107	7	28.16	MID1	NM_000381	-	1993
chr4	39226732	39226946	215	121	13	6.3	C4orf34	NM_174921	-	1998
chr1	209812287	209813003	717	57	40	6.46	SLC30A1	NM_021194	-	2002
chr14	95573261	95573402	142	87	6	29.55	C14orf132	NM_020215	+	2028
chr14	98245480	98245666	187	93	6	23.64	C14orf177	NM_182560	+	2036
chr18	75831453	75831782	330	160	21	9.66	TXNL4A	NM_006701	-	2074
chr10	45270382	45270719	338	221	15	9.76	36958	NM_001002266	-	2103
chr15	91242011	91242314	304	206	19	10.01	CHD2	NM_001042572	+	2108
chr11	47444100	47444396	297	51	13	15.69	CUGBP1	NM_001025596	-	2125
chr2	196707749	196707963	215	98	7	14.64	STK17B	NM_004226	-	2139

chr5	524105	524279	175	122	6	24.4	SLC9A3	NM_004174	-	2145
chr2	218372766	218373605	840	423	65	5.33	TNS1	NM_022648	-	2151
chr5	55270011	55270289	279	169	19	7.81	IL6ST	NM_002184	-	2162
chr10	98267976	98268251	276	125	17	8.08	TM9SF3	NM_020123	-	2168
chr2	114185941	114186189	249	110	8	18.23	SLC35F5	NM_025181	-	2213
chr7	44833302	44833708	407	157	25	5.96	H2AFV	NM_138635	-	2218
chr1	35419184	35419377	194	58	10	11.71	SFPQ	NM_005066	-	2412
chr12	61823893	61824044	152	46	8	10.46	AVPR1A	NM_000706	-	2438
chr1	67239154	67239945	792	322	46	6.51	SLC35D1	NM_015139	-	2494
chr5	55269706	55269947	242	182	17	13.31	IL6ST	NM_002184	-	2504
chr15	88175064	88175269	206	97	7	14.64	AP3S2	NM_005829	-	2523
chr3	48760309	48760540	232	127	11	10.19	PRKAR2A	NM_004157	-	2556
chr16	20773974	20774314	341	52	13	9.76	DCUN1D3	NM_173475	-	2585
chr11	65114134	65114254	121	61	6	17.57	KCNK7	NM_033347	-	2648
chr11	117602641	117602830	190	46	9	20.5	LOC196264	NM_198275	-	2716
chr8	134536289	134537571	1283	131	110	8.14	ST3GAL1	NM_003033	-	2755
chr1	56729977	56730221	245	140	11	12.2	PPAP2B	NM_003713	-	2801
chr1	203949287	203950864	1578	1039	108	7	NUCKS1	NM_022731	-	2867
chr1	9909316	9909480	165	88	9	29.28	LZIC	NM_032368	-	2884
chr1	31115037	31115612	576	393	24	9.84	SDC3	NM_014654	-	2956
chr22	23155848	23156129	282	108	12	14.64	ADORA2A	NM_000675	+	2962
chr4	39225588	39225965	378	88	53	8.51	C4orf34	NM_174921	-	2979
chr1	209811617	209811989	373	176	25	10.01	SLC30A1	NM_021194	-	3016
chr17	17687581	17687814	234	180	12	17.57	TOM1L2	NM_144678	-	3050
chr1	218150373	218151139	767	120	56	10.29	SLC30A10	NM_018713	-	3089
chr18	31166306	31166860	555	181	28	7.22	ZNF24	NM_006965	-	3096

chr4	53935337	53935521	185	50	7	19.52	FIP1L1	NM_030917	+	3098
chr18	51042571	51042839	269	149	11	29.55	TCF4	NM_003199	-	3127
chr1	9909058	9909219	162	91	8	11.86	LZIC	NM_032368	-	3145
chr4	111186496	111186786	291	143	12	10.98	ELOVL6	NM_024090	-	3205
chr7	133459198	133459383	186	54	6	21.53	LRGUK	NM_144648	+	3261
chr4	39225271	39225565	295	133	28	6.72	C4orf34	NM_174921	-	3379
chr22	23155557	23155704	148	101	6	24.4	ADORA2A	NM_000675	+	3387
chr4	171144339	171144645	307	55	13	8.99	MFAP3L	NM_001009554	-	3546
chr12	93995252	93995400	149	97	7	21.96	FGD6	NM_018351	-	3547
chr19	7063297	7064020	724	441	52	5.3	INSR	NM_000208	-	3621
chr7	41691245	41691418	174	60	7	14.64	INHBA	NM_002192	-	3709
chr1	19477826	19477923	98	50	6	21.96	AKR7A3	NM_012067	-	3720
chr8	58033739	58034091	353	153	16	10.98	IMPAD1	NM_017813	-	3730
chr10	71857768	71858317	550	198	37	13.18	NODAL	NM_018055	-	3759
chr11	63148756	63149066	311	230	13	18.21	KFZP564J086	NM_015459	-	3946
chr6	131197606	131198213	608	355	37	6.36	EPB41L2	NM_001431	-	3969
chr1	67237911	67238426	516	219	33	6.87	SLC35D1	NM_015139	-	4013
chr1	35219730	35220336	607	361	26	12.44	ZMYM6	NM_007167	-	4018
chr1	35416678	35417675	998	343	45	6.83	SFPQ	NM_005066	-	4114
chr8	58033247	58033659	413	142	24	8.47	IMPAD1	NM_017813	-	4162
chr11	58228483	58228630	148	102	6	22.18	GLYAT	NM_201648	-	4176
chr6	46201587	46201680	94	48	6	35.46	ENPP4	NM_014936	+	4190
chr14	69904205	69904389	185	58	6	18.3	SYNJ2BP	NM_018373	-	4237
chr9	138038256	138038435	180	54	7	19.52	BTBD14A	NM_144653	-	4590
chr1	67237646	67237830	185	92	20	12.55	SLC35D1	NM_015139	-	4609
chr5	133964922	133965401	480	86	48	5.27	SAR1B	NM_001033503	-	4617

chr18	75829087	75829209	123	62	6	29.28	TXNL4A	NM_006701	-	4647
chr6	31905601	31905974	374	61	40	21.9	C6orf48	NM_001040437	+	4697
chr10	52230995	52231624	630	60	37	5.73	ACF	NM_138933	-	4708
chrX	131334696	131335015	320	140	14	10.98	MBNL3	NM_018388	-	4844
chr3	52549459	52549574	116	59	6	21.96	PB1	NM_018165	-	4849
chr17	44721836	44722358	523	73	25	15.31	ZNF652	NM_014897	-	5126
chrX	131334280	131334583	304	42	15	8.9	MBNL3	NM_018388	-	5276
chr14	69903006	69903349	344	178	18	15.11	SYNJ2BP	NM_018373	-	5277
chr4	70621629	70621936	308	61	17	12.81	SULT1B1	NM_014465	-	5340
chr9	133362287	133362744	458	220	22	8.13	POMT1	NM_001077365	+	5365
chr19	48782296	48782432	137	45	7	14.64	IRGQ	NM_001007561	-	5433
chr15	18842884	18843036	153	108	7	14.64	LOC283755	NM_001024682	-	5521
chr19	48782103	48782262	160	73	7	14.64	IRGQ	NM_001007561	-	5603
chr6	86374747	86375051	305	196	12	13.56	SYNCRIP	NM_006372	-	5606
chr17	15142064	15142209	146	56	6	22.88	TEKT3	NM_031898	-	5646
chr17	44721541	44721756	216	106	10	17.08	ZNF652	NM_014897	-	5728
chrX	131333768	131334087	320	62	22	31.37	MBNL3	NM_018388	-	5772
chr10	52229922	52230482	561	131	50	8.21	ACF	NM_138933	-	5850
chr18	57626646	57627377	732	155	55	7.67	RNF152	NM_173557	-	5906
chr10	117806486	117806918	433	223	29	8.15	GFRA1	NM_145793	-	6024
chr11	56159296	56159474	179	61	6	23.43	OR5AP2	NM_001002925	-	6066
chr1	220902144	220902338	195	138	10	18.82	C1orf80	NM_022831	-	6112
chr1	24748923	24749046	124	52	6	29.55	C1orf130	NM_001010980	+	6142
chr6	7226390	7226653	264	96	13	7.73	SSR1	NM_003144	-	6149
chr8	23203569	23203935	367	83	15	26.14	LOXL2	NM_002318	-	6419
chr10	52229169	52229685	517	128	47	8.04	ACF	NM_138933	-	6647

chr14	22503243	22503426	184	59	6	23.64	JUB	NM_198086	-	6823
chr7	135009493	135009687	195	49	11	9.99	SLC13A4	NM_012450	-	6845
chr17	62497370	62497510	141	61	7	17.57	HELZ	NM_014877	-	7018
chr3	172189041	172189694	654	256	32	9.32	SLC2A2	NM_000340	-	7136
chr2	231622099	231622678	580	323	57	7.08	PSMD1	NM_002807	+	7174
chr5	114567815	114568074	260	144	8	18.3	PGGT1B	NM_005023	-	7401
chr2	231619819	231621843	2025	1896	186	6.61	PSMD1	NM_002807	+	8009
chr9	124647351	124647525	175	87	7	14.64	MNAB	NM_018835	-	8371
chr13	26899236	26899366	131	73	11	45.75	MTIF3	NM_152912	-	8416
chr1	26424676	26424823	148	61	9	17.34	CCDC21	NM_022778	+	8456
chr2	220136323	220136611	289	144	20	16.93	INHA	NM_002191	+	8586
chr4	68592429	68592611	183	136	8	22.88	TMPRSS11F	NM_207407	-	8899
chrY	6829222	6829410	189	43	9	16.6	TBL1Y	NM_033284	+	9316
chr8	33338268	33338452	185	73	7	19.52	FUT10	NM_032664	-	9434
chr1	150638782	150638907	126	45	7	21.96	CRNN	NM_016190	-	9435
chr17	71124218	71124382	165	60	6	23.64	RECQL5	NM_004259	-	10137
chr1	156691481	156691656	176	49	6	22.88	OR10K1	NM_001004473	+	10319
chr19	50126078	50126348	271	63	43	6.1	APOC4	NM_001646	+	10986
chr5	6639866	6640814	949	541	78	7	NSUN2	NM_017755	-	11540
chr6	131190262	131190526	265	186	21	6.47	EPB41L2	NM_001431	-	11656
chr14	22090401	22090710	310	160	14	22.69	DAD1	NM_001344	-	12936
chr5	66500327	66500505	179	131	8	12.2	CD180	NM_005582	-	13366
chr1	220894671	220894828	158	52	11	10.41	C1orf80	NM_022831	-	13622
chr12	11215898	11216150	253	156	19	13.18	TAS2R42	NM_181429	-	13715
chr1	224064445	224064629	185	48	9	21.67	EPHX1	NM_000120	+	14969
chr15	70538236	70538394	159	62	6	22.88	ARIH1	NM_005744	+	15326

chr2	231614245	231614404	160	69	11	10.54	PSMD1	NM_002807	+	15448
chr3	196254127	196254302	176	115	6	18.3	C3orf21	NM_152531	-	16001
chr20	22491644	22493735	2092	694	140	8.51	FOXA2	NM_021784	-	16087
chr4	15297040	15297269	230	130	7	24.4	BST1	NM_004334	+	16469
chr13	27417539	27417638	100	51	12	8.78	CDX2	NM_001265	-	16640
chr14	22086469	22086601	133	50	8	13.63	DAD1	NM_001344	-	17045
chr20	22490369	22491573	1205	128	95	9.52	FOXA2	NM_021784	-	18249
chr3	144142940	144143943	1004	232	59	8.4	PAQR9	NM_198504	-	18822
chr11	65029551	65030070	520	353	48	10.46	SCYL1	NM_020680	+	19053
chr20	22490100	22490356	257	125	19	12.06	FOXA2	NM_021784	-	19466
chr11	65029061	65029448	388	200	28	6.51	SCYL1	NM_020680	+	19675
chr20	22489202	22490065	864	121	81	7.08	FOXA2	NM_021784	-	19757
chr2	46572556	46572703	148	87	6	14.64	ATP6V1E2	NM_080653	-	19788
chr4	101306085	101306247	163	54	6	19.52	DDIT4L	NM_145244	-	19804
chr19	49818982	49819144	163	105	7	19.52	PVR	NM_006505	+	19921
chr2	85599705	85599871	167	52	6	23.64	MAT2A	NM_005911	+	19927
chr2	36416799	36416968	170	122	6	21.53	CRIM1	NM_016441	+	19932
chr7	55808334	55808780	447	299	18	7.85	FLJ44060	NM_207366	-	19950
chr11	65028328	65029056	729	574	41	5.73	SCYL1	NM_020680	+	20067
chr15	46467337	46467526	190	53	7	14.64	FBN1	NM_000138	-	20270
chr3	9493199	9494004	806	254	35	7.99	LHFPL4	NM_198560	-	21041
chr11	65026630	65027642	1013	557	78	5.84	SCYL1	NM_020680	+	21481
chr3	172066810	172066980	171	119	8	15.02	EIF5A2	NM_020390	-	21918
chr4	185523368	185523775	408	59	25	8.96	IRF2	NM_002199	-	22134
chr4	123497225	123497391	167	61	8	14.67	Tenr	NM_139243	+	22226
chr11	65023115	65026463	3349	1628	460	6.2	SCYL1	NM_020680	+	22660

chr3	180740058	180740221	164	60	6	19.52	ACTL6A	NM_004301	+	23180
chr6	119239778	119239936	159	53	6	14.64	ASF1A	NM_014034	+	23691
chr4	44301119	44301267	149	96	6	24.4	YIPF7	NM_182592	-	24185
chr4	189129119	189129306	188	47	10	52.71	ZFP42	NM_174900	+	24612
chr6	129219572	129219719	148	105	6	21.53	LAMA2	NM_000426	+	26315
chr5	95220949	95221610	662	103	88	5.49	ELL2	NM_012081	-	27242
chr3	187089246	187089333	88	45	6	17.57	SFRS10	NM_004593	-	27902
chr1	40371548	40371643	96	49	7	41.37	RLF	NM_012421	+	28004
chr22	39790184	39790277	94	48	6	29.28	EP300	NM_001429	+	28275
chr3	191559719	191559834	116	59	6	25.1	CLDN16	NM_006580	+	28700
chr4	53274504	53274768	265	209	12	11.64	FLJ12684	NM_024534	-	29674
chr9	37079631	37079810	180	113	10	18.45	ZCCHC7	NM_032226	+	30658
chr13	51818272	51818452	181	128	6	29.55	THSD1	NM_018676	-	30852
chr9	37079130	37079342	213	96	9	21.83	ZCCHC7	NM_032226	+	31126
chr6	29631239	29632239	1001	550	102	6.62	OR2H2	NM_007160	+	31422
chr3	19133139	19133312	174	124	6	17.22	KCNH8	NM_144633	+	31708
chr6	29630699	29630972	274	210	18	8.48	OR2H2	NM_007160	+	32689
chr9	37076972	37077440	469	168	21	12.02	ZCCHC7	NM_032226	+	33028
chr6	29629741	29630371	631	61	32	5.18	OR2H2	NM_007160	+	33290
chr6	29628546	29629475	930	138	55	5.49	OR2H2	NM_007160	+	34186
chr2	8230134	8230301	168	99	6	12.2	C2orf46	NM_207358	-	34422
chr9	133332772	133332951	180	125	6	14.64	POMT1	NM_001077365	+	35158
chr19	376086	376252	167	109	12	9.78	C19orf19	NM_182577	-	38107
chr1	91881949	91882172	224	150	12	32.8	TGFBR3	NM_003243	-	38402
chr3	142649073	142649409	337	283	18	14.64	RASA2	NM_006506	+	39206
chr17	31506245	31506394	150	62	6	18.3	CCL3L3	NM_001001437	-	39989

chr19	46148097	46148493	397	113	23	13.08	CYP2B6	NM_000767	+	40550
chr12	109915150	109915317	168	119	6	29.55	CUTL2	NM_015267	+	40894
chr19	373146	373338	193	132	11	17.08	C19orf19	NM_182577	-	41021
chr16	10388778	10389043	266	114	14	23.37	ATF7IP2	NM_024997	+	41182
chr10	63287846	63288018	173	56	6	24.4	ARID5B	NM_032199	+	43430
chr13	90804409	90804594	186	34	6	17.73	GPC5	NM_004466	+	44293
chr18	70208201	70208638	438	88	42	9.62	C18orf51	NM_001044369	-	45304
chr16	76333287	76333573	287	88	13	10.5	KIAA1576	NM_020927	+	46410
