Supplementary Data

Global Oct4 target gene analysis reveals novel downstream *PTEN* and *TNC* genes required for drug-resistance and metastasis in lung cancer

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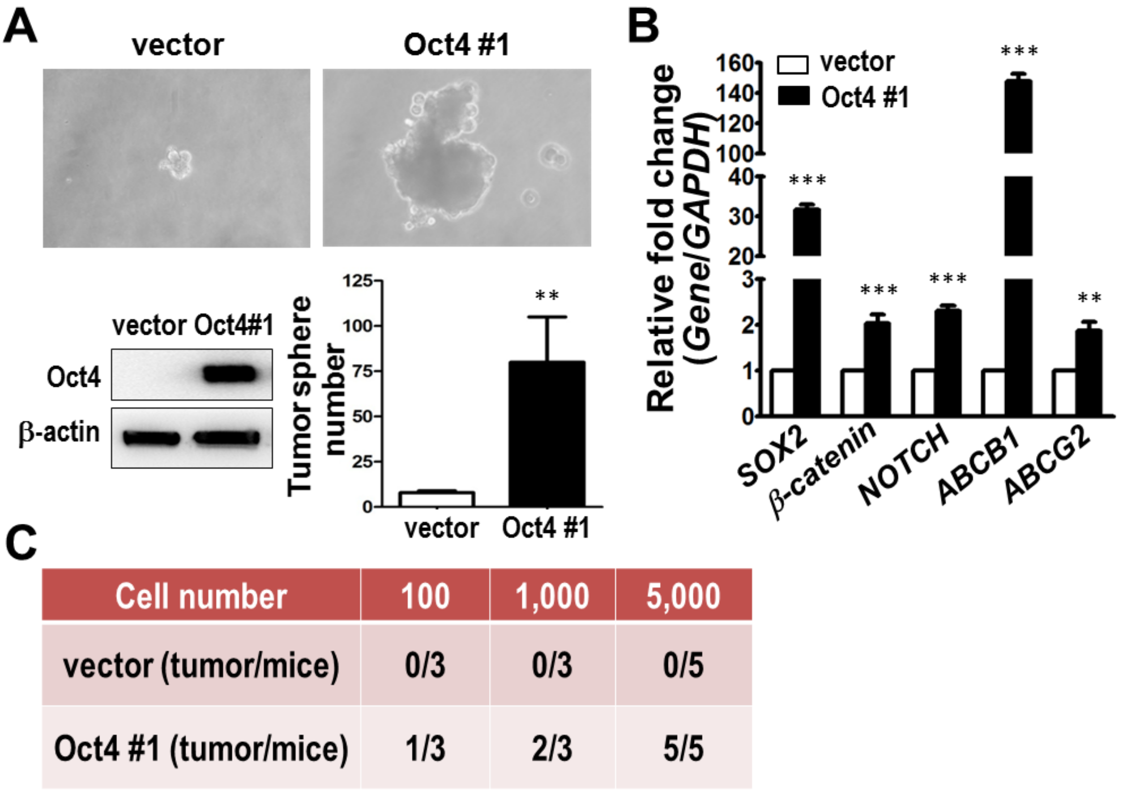
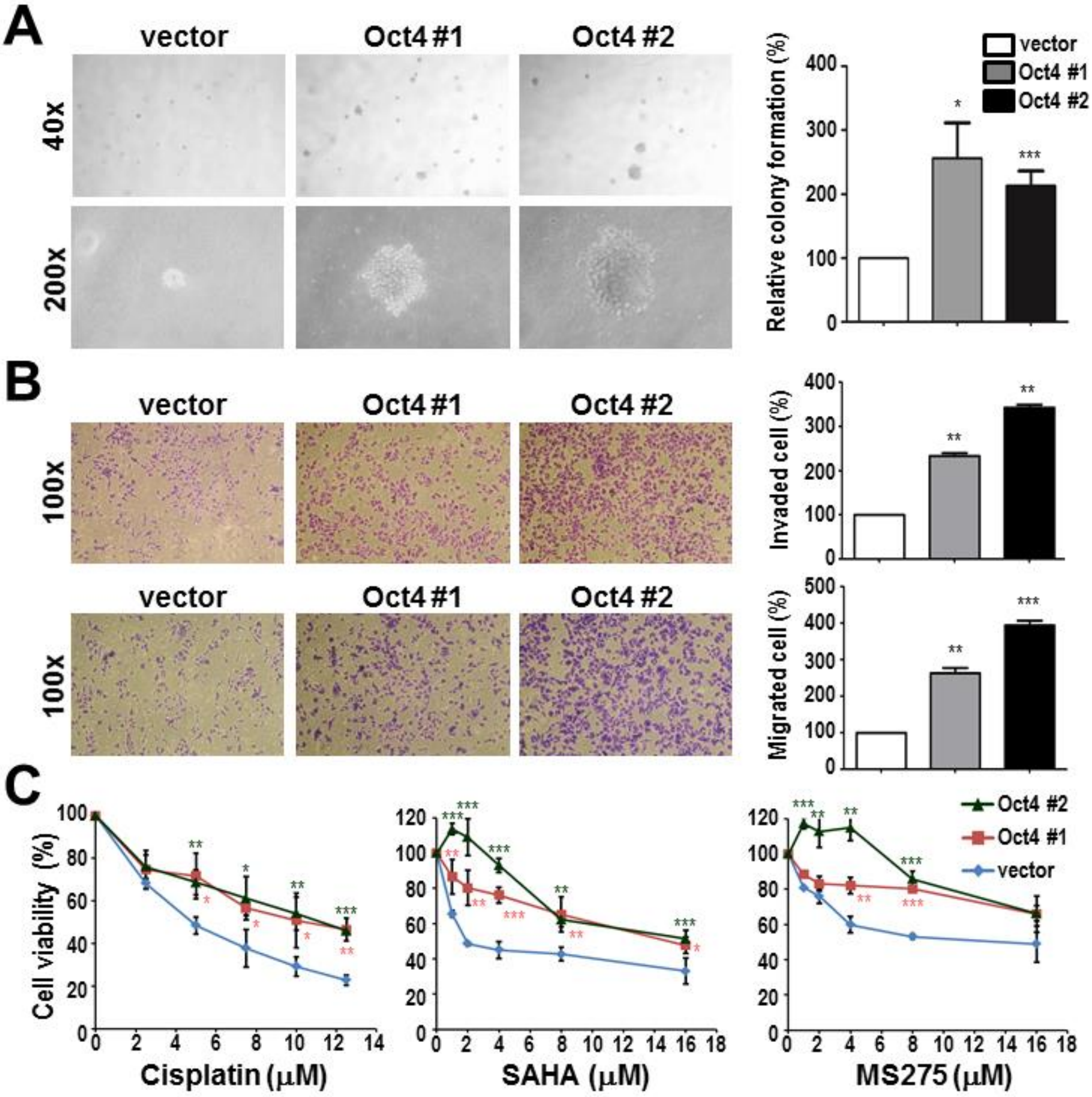


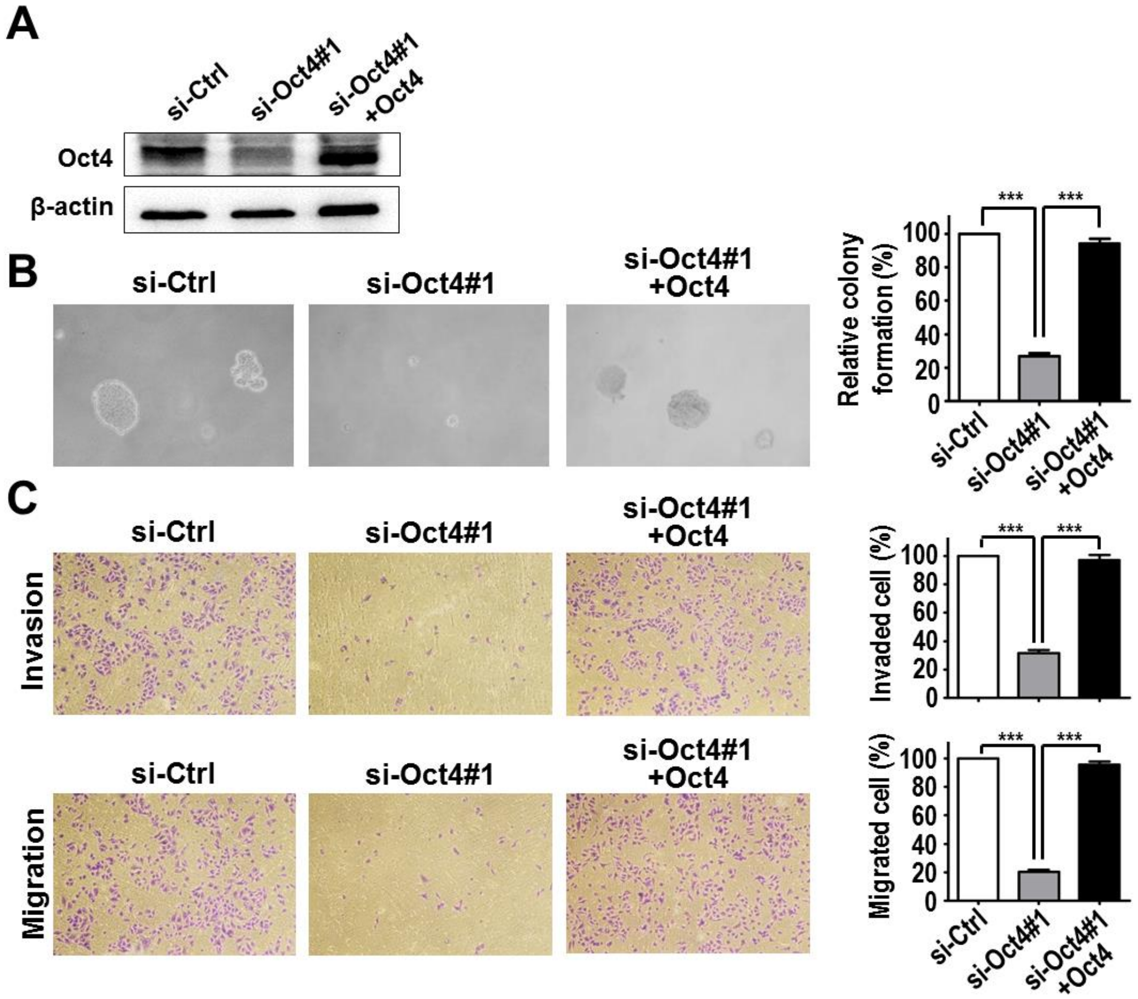
Cell number	100	1,000	5,000
vector (tumor/mice)	0/3	0/3	0/5
Oct4 #1 (tumor/mice)	1/3	2/3	5/5

Supplementary Figure S1. Ectopic expression of Oct4 induces self-renewal and stemness-related gene expression in lung cancer cells.
(A) *In vitro* tumor sphere formation assay of A549 lung cancer cells stably expressing Flag-tagged Oct4 (Oct4#1) or empty vector (vector) photographed (top panel) and quantified (lower right panel). The immunoblots confirmed the Oct4 expression in A549 stable clones (lower left panel). **(B)** qRT-PCR analysis of stemness-related genes of stable cells expressing Oct4 compared to vector control cells. *GAPDH* was used as internal control. Data are mean ±s.e.m. (n = 3). *P* values determined using two-tailed Student's *t*-test. **, *P*<0.01; ***, *P*<0.001. **(C)** *In vivo* tumor formation assay using limited cell number (100, 1000, and 5000 cells) of vector and stable cells expressing Oct4. Cells were mixed with matrigel and subcutaneously injected into BALB/c nude mice. Tumor incidence of mice was analyzed at 8 weeks after implantation.



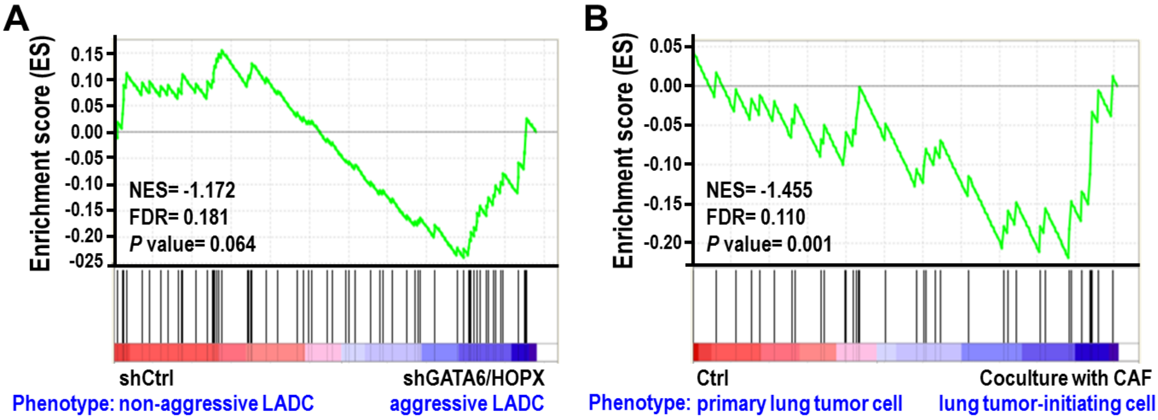
Supplementary Figure S2. Ectopic expression of Oct4 induces anchorage-independent growth, cell motility and drug resistance in lung cancer cells.

(A) Anchorage-independent growth analysis of A549 lung cancer cells stably expressing Flag-Oct4 (Oct4#1 and Oct4#2) or empty vector (vector). Results from one representative experiment are shown (left panel). Original magnification is indicated. The colony number was quantified (right panel). **(B)** Transwell invasion (top panel) and migration (lower panel) analysis of A549 stable clones (vector, Oct4#1, and Oct4#2). Results from one representative experiment are shown (left panels). Original magnification is indicated. The relative migrated and invaded cells were quantified (right panels). **(C)** MTT assay was performed using A549 stable clones (vector, Oct4#1, and Oct4#2) treated with different concentration of cytotoxic drug cisplatin or histone deacetylase inhibitors, SAHA and MS275, for 48 h. Data are mean ±s.e.m. (n = 3). *P* values determined using two-tailed Student's *t*-test. *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$.

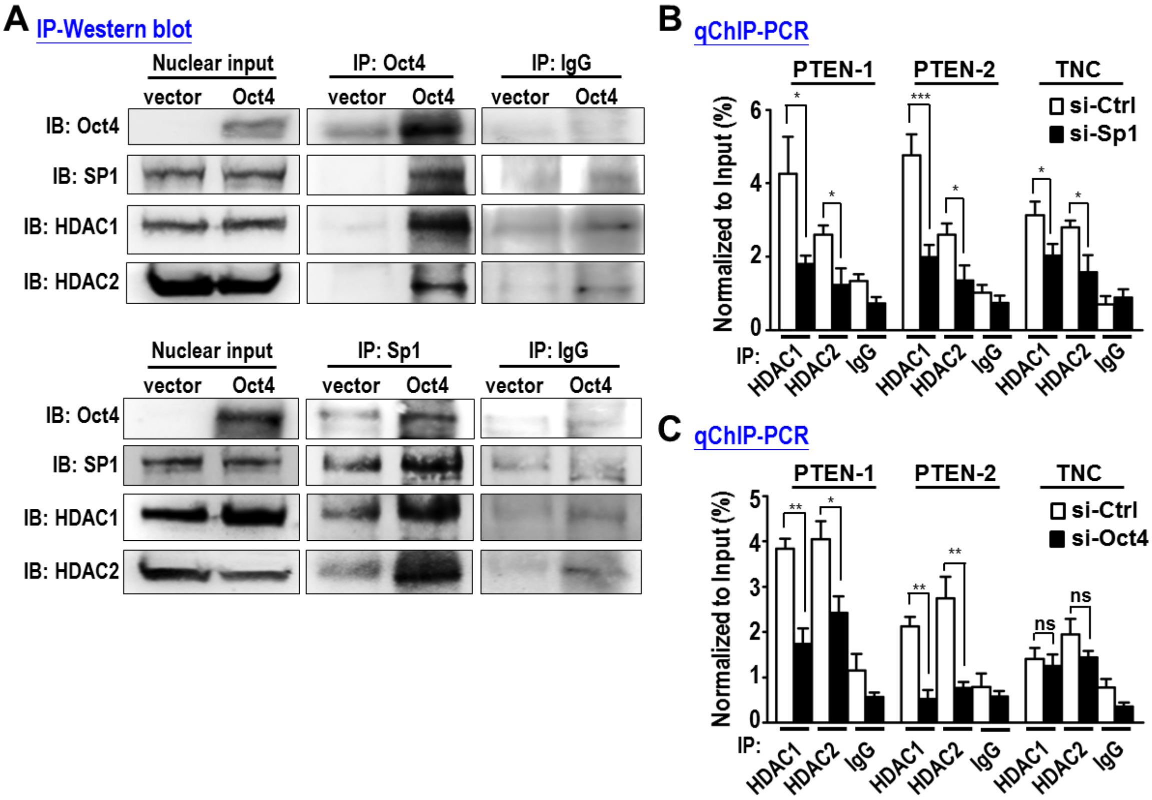


Supplementary Figure S3. Re-enforced Oct4 expression restores the effects of si-Oct4 on cell growth and motility in A549 lung cancer cells.

(A) A549 lung cancer cells were transiently transfected with control (si-Ctrl) or Oct4 (si-Oct4#1) siRNAs for 24 h, followed by ectopic Oct4 expression (+Oct4) for another 24 h. Cells were then subjected to Western blot analysis of Oct4 protein level. β-actin was used as internal control. **(B)** Anchorage-independent growth analysis of A549 cells from (A). Results from one representative experiment are shown (left panel). Original magnification × 100. The colony number was quantified (right panel). **(C)** Transwell invasion (top panel) and migration (lower panel) analysis of A549 cells from (A). Results from one representative experiment are shown (left panels). Original magnification × 100. The relative invaded and migrated cells were quantified (right panels). Data are mean ±s.e.m. (n = 3). *P* values determined using two-tailed Student's t-test. ***, *P*<0.001.

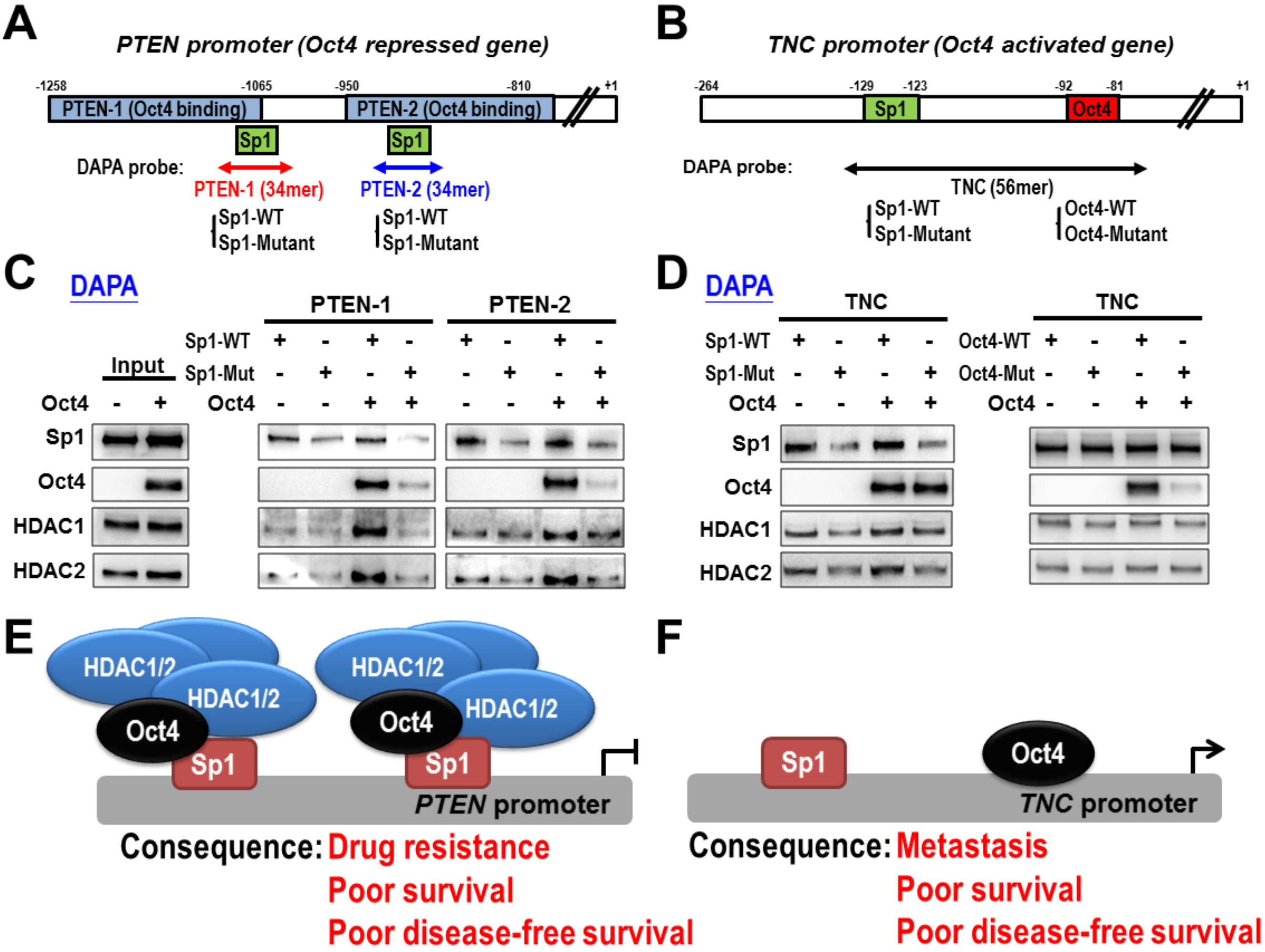


Supplementary Figure S4. Gene set enrichment analysis (GSEA) of the correlation between Oct4-target genes and aggressive gene signatures of lung cancer. Oct4-target gene set comprising Oct4-bound top 150, promoter-associated, and enhancer-associated genes were used in GSEA to assess the correlation to **(A)** an aggressive gene signature of lung adenocarcinoma (LADC) by knocking down of both *GATA6* and *HOPX* genes (27) and **(B)** a gene signature of lung tumor-initiating cells promoting by co-culturing with cancer-associated fibroblasts (CAFs) (28). NES, normalized enrichment score; FDR, false discovery rate. *P* values determined using a random permutation test.



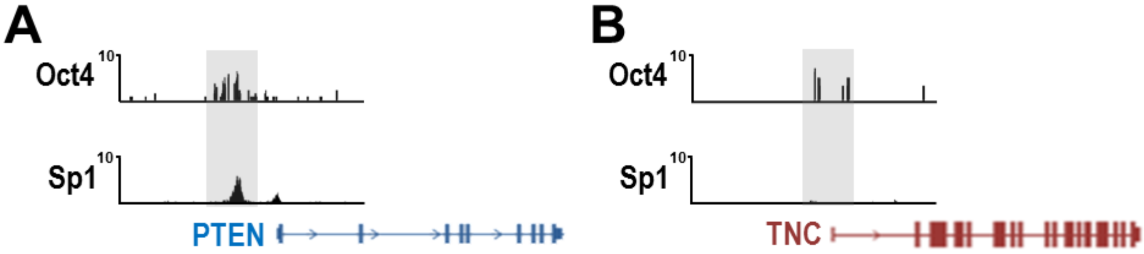
Supplementary Figure S5. Oct4 forms a complex with Sp1 and HDAC1/2 in the presence of *PTEN* promoter, but not *TNC* promoter.

(A) Nuclear lysates of A549 cells stably expressing Oct4 (Oct4) or control (vector) were immunoprecipitated (IP) using anti-Oct4 (upper) or anti-Sp1 (lower) antibody. The immunoprecipitated proteins were analyzed by immunoblot (IB) using indicated antibodies. Normal IgG served as negative control. **(B** and **C)** qChIP-PCR analysis of HDAC1 and HDAC2 occupancies at *PTEN* and *TNC* promoters in A549 cells stably expressing Oct4 after knockdown of Sp1 (si-Sp1) **(B)** or Oct4 (si-Oct4) **(C)** compared to si-control (si-Ctrl). ns, non-significant. Data are mean ±s.e.m. (n = 3). *P* values determined using two-tailed Student’s *t*-test. *, *P*<0.05; **, *P*<0.01; ***, *P*<0.001.

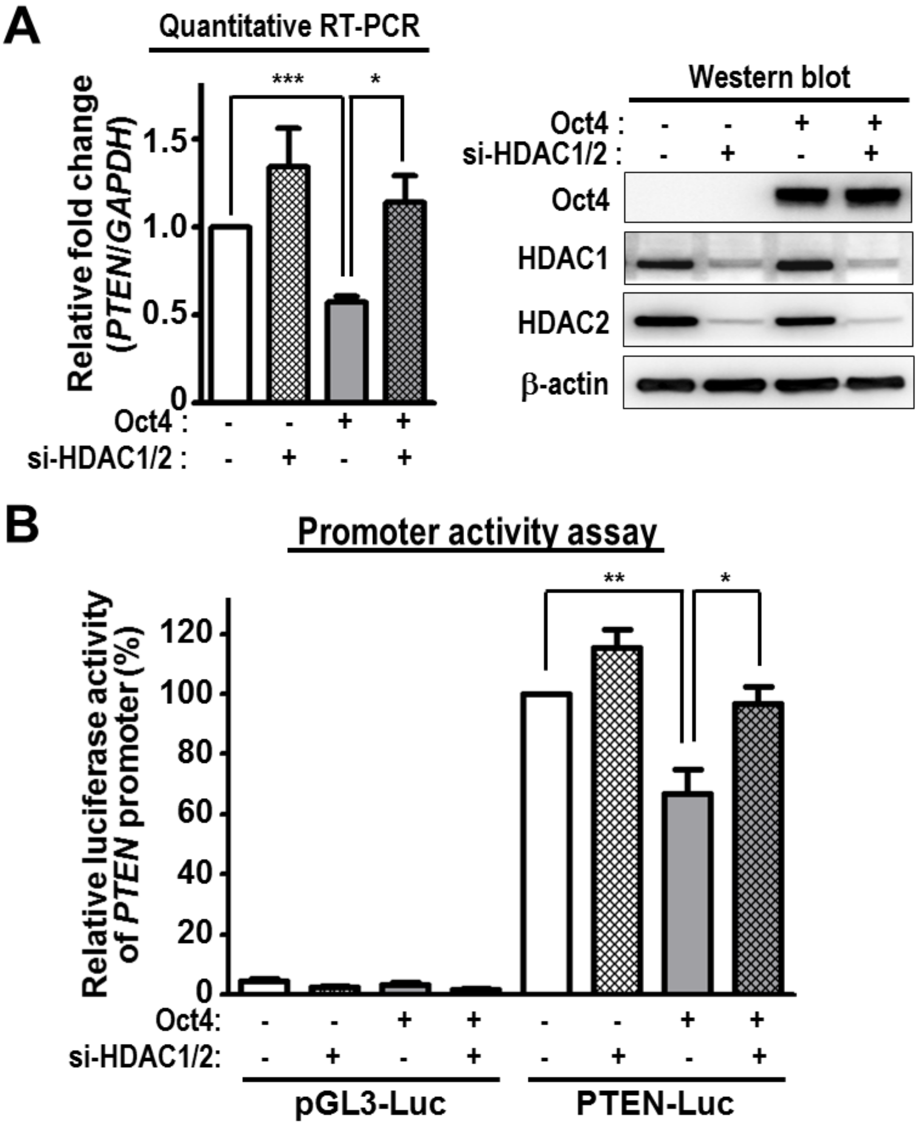


Supplementary Figure S6. Differential targeting of Oct4 and Sp1 at *PTEN* and *TNC* promoter.

(A and B) Promoter regions of *PTEN* **(A)** and *TNC* **(B)** were analyzed. Oct4 ChIP-seq regions (blue; PTEN-1 and PTEN-2), Sp1 binding site (green), and Oct4 binding site (red) are shown in boxes. DAPA probes containing wild-type (WT) and mutant (Mut) Sp1 or Oct4 binding sites were indicated by double headed arrow. The length of DAPA probe was indicated in parentheses. **(C)** DAPA assay showed that Oct4-mediated recruitment of the HDAC1/2 complex to *PTEN* promoter required Sp1 protein to serve as a platform. DAPA assay was performed using DNA probes (PTEN-1 and PTEN-2) containing WT or Mut Sp1 binding site in parental A549 cells upon Oct4 overexpression. **(D)** DAPA assay showed that Oct4 bound to *TNC* promoter in an Sp1-independent manner and did not recruit the HDAC1/2 complex. DAPA assay was performed using DNA probes (TNC) containing WT or Mut Sp1 binding site (left) and Oct4 binding site (right) in parental A549 cells upon Oct4 overexpression. **(E and F)** Working models of differential targeting of Oct4, Sp1, and HDAC1/2 complex at *PTEN* **(E)** and *TNC* **(F)** promoters in relation to cancer progression. All experiments were performed at least three times. Results from one representative experiment are shown.

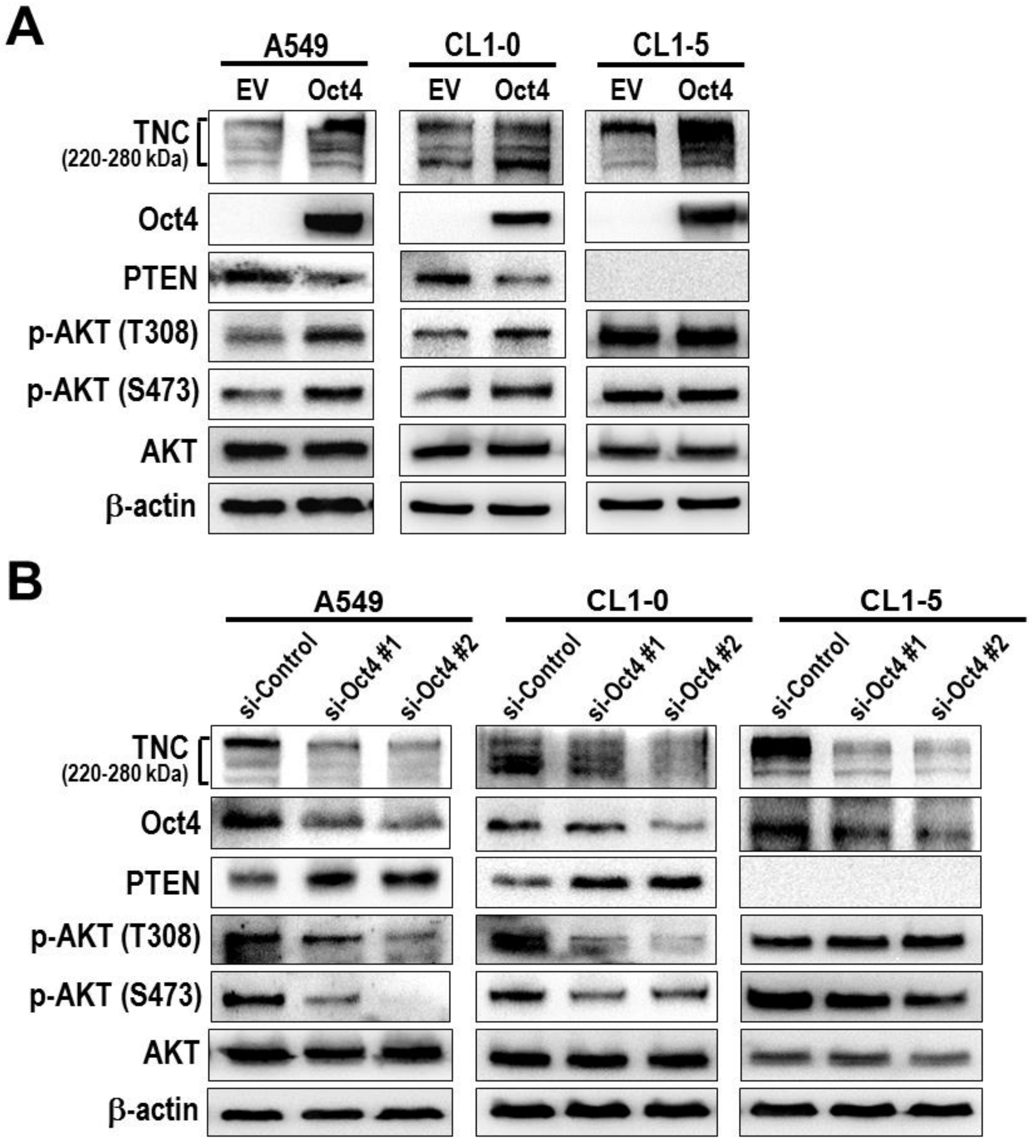


Supplementary Figure S7. Coordinative binding of Oct4 and Sp1 at *PTEN* promoter, but not *TNC* promoter. Configurations of Oct4 binding (data from our Oct4 ChIP-seq) and Sp1 binding (data from the Sp1 ChIP-seq of A549 lung cancer cells in ENCODE datasets) peaks at promoters of *PTEN* **(A)** and *TNC* **(B)** genes.

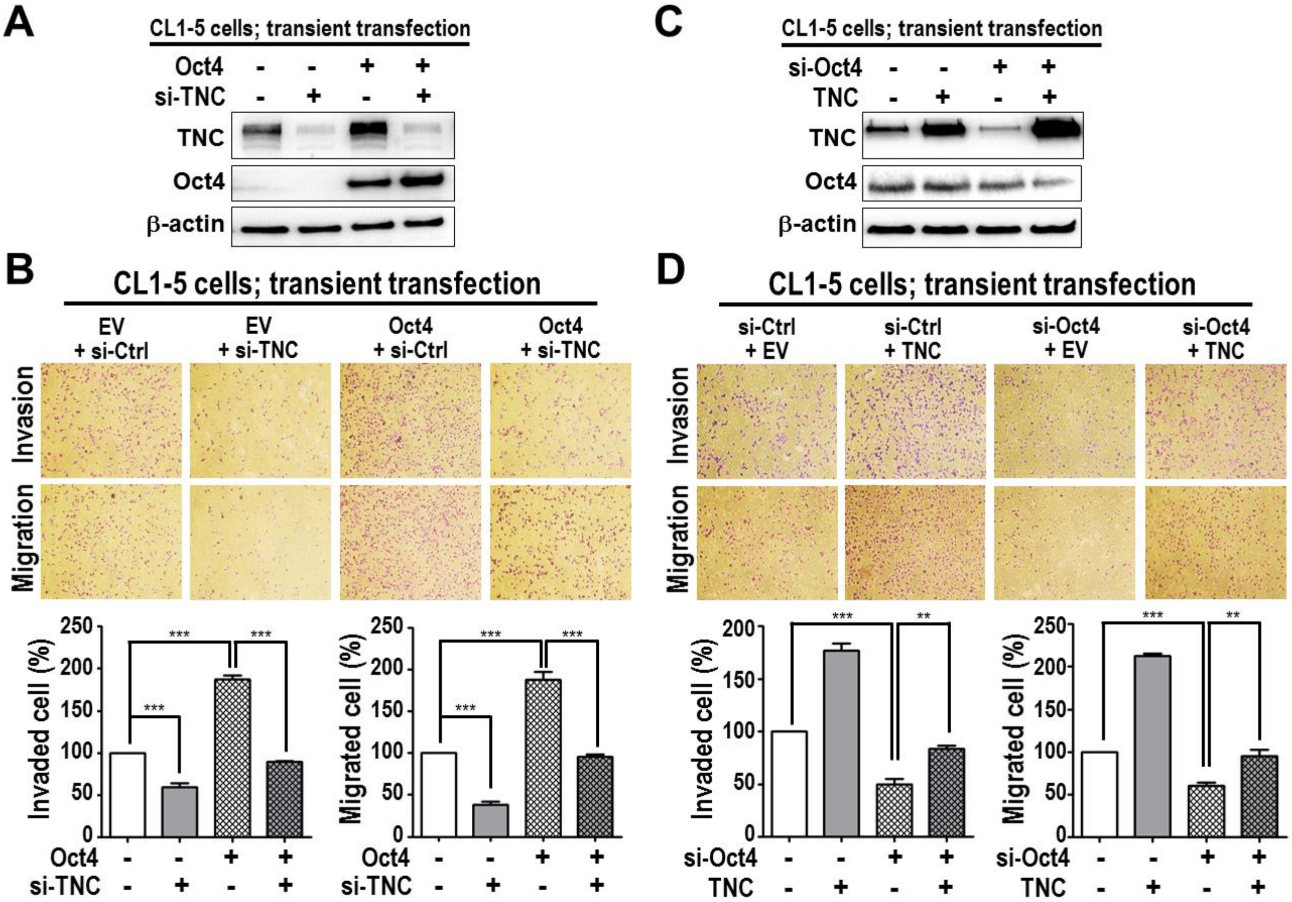


Supplementary Figure S8. Oct4 transcriptionally represses *PTEN* in an HDAC1/2-dependent manner.

(A) qRT-PCR analysis of *PTEN* mRNA expression in A549 cells overexpressing Oct4 (Oct4) and/or knockdown of HDAC1/2 (si-HDAC1/2) (left). Western blot analysis confirmed the efficiency of Oct4 overexpression and HDAC1/2 knockdown (right). **(B)** Dual luciferase activity assays were performed using wild-type *PTEN* promoter (-1352 ~ +141 region) in A549 cells upon overexpression of Oct4 (Oct4) and/or knockdown of HDAC1/2 (si-HDAC1/2). Data are mean ±s.e.m. (n = 3). *P* values determined using two-tailed Student's *t*-test. *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$.



Supplementary Figure S9. Oct4 induces TNC protein expression, while decreases PTEN protein level and increases AKT phosphorylation in lung cancer cell lines. **(A)** A549, CL1-0, and CL1-5 lung cancer cells were transiently transfected with empty vector (EV) and Flag-Oct4 (Oct4) for 24 h and then subjected to Western blot analysis of TNC, PTEN, and AKT phosphorylation levels. β-actin was used as internal control. **(B)** A549, CL1-0, and CL1-5 lung cancer cells were transiently transfected with control (si-Control) and Oct4 (si-Oct4#1 and si-Oct4#2) siRNAs for 48 h and then subjected to Western blot analysis of TNC, PTEN, AKT and AKT phosphorylation levels. β-actin was used as internal control. All experiments were performed at least three times. Results from one representative experiment are shown.



Supplementary Figure S10. TNC expression is required for Oct4-mediated cancer invasion/migration.

(A and **B)** CL1-5 cells were transiently transfected with empty vector (EV) or Oct4 expression vector (Oct4), followed by knockdown of TNC (si-TNC) or control (si-Ctrl). Cells were then subjected to Western blot analysis of TNC protein level **(A)** and transwell invasion/migration assay **(B)**. **(C** and **D)** CL1-5 cells with transient Oct4 (si-Oct4) or control (si-Ctrl) knocked down were transfected with TNC expression vector (TNC) or empty vector (EV). Cells were then subjected to Western blot analysis of TNC protein level **(C)** and transwell invasion/migration assay **(D)**. Representative image of transwell invasion/migration assay (**B** and **D**, upper) and quantitation (**B** and **D**, lower) are shown. Original magnification × 100. Data are mean ±s.e.m. (n = 3). *P* values determined using two-tailed Student's *t*-test. **, *P*<0.01; ***, *P*<0.001.

Supplementary Table S1. The plasmids and their characteristics used in the current study.

Plasmid	**Target**	**Insert (bp)**	**Function**	**Source**
pPyCAGIP vector	None	0	Vector control	From Dr. Ying Jin*
pPyCAGIP-Flag-Oct4	Wild type Oct4	1083	Overexpression	From Dr. Ying Jin*
SFB-tagged vector	None	0	Vector control	From Dr. Maddika†
SFB-tagged-PTEN	Wild type PTEN	1212	Overexpression	From Dr. Maddika†
pCMVscript vector	None	0	Vector control	From Dr. Pringle§
pCMVscript-TNC	Wild type TNC	6606	Overexpression	From Dr. Pringle§
pCDNA3-HA-Neo	None	0	Vector control	From Dr. Hung‡
pCDNA3-HA-Sp1	Wild type Sp1	2358	Overexpression	From Dr. Hung‡
pGL3-Basic vector	None	0	Vector control	Promega
pGL3-TNC promoter	*TNC* promoter (-176 ~ +94)	270	Promoter activity assay	Homemade
pGL3-PTEN promoter	*PTEN* promoter (-1352 ~ +141)	1493	Promoter activity assay	Homemade

* Plasmid was kindly provided by Dr. Ying Jin from Shanghai Stem Cell Institute, Shanghai Jiao Tong University School of Medicine, Shanghai, China.

† Plasmid was kindly provided by Dr. Subbareddy Maddika at Laboratory of Cell Death & Cell Survival, Centre for DNA Fingerprinting and Diagnostics (CDFD), Nampally, India.

§ Plasmid was kindly provided by Dr. J Howard Pringle at Department of Cancer Studies and Molecular Medicine, Infirmary Close, University of Leicester, Leicester, UK.

‡ Plasmid was kindly provided by Dr. Jan-Jong Hung at Institute of Biosignal Transduction, College of Bioscience and Biotechnology, National Cheng-Kung University, Tainan, Taiwan.

Supplementary Table S2. siRNA sequences used in the current study.

RNAi	Function	Double-stranded RNA sequences (5'→ 3')	Source
Oct4-HSS109091 (si-Oct4#1)	Knock-down Oct4	AUC UGC UGC AGU GUG GGU UUC GGG C GCC CGA AAC CCA CAC UGC AGC AGA U	Invitrogen
Oct4 siRNA (si-Oct4#2)	Knock-down Oct4	AGC AGC UUG GGC UCG AGA AdTdT UUC UCG AGC CCA AGC UGC UdTdT	Invitrogen
Sp1-HSS110106	Knock-down Sp1	GGA ACA UCA CCU UGC UAC CUG UCA A UUG ACA GGU AGC AAG GUG AUG UUC C	Invitrogen
HDAC1-HSS103017	Knock-down HDAC1	UAC UUU AGC AGU UCC AGG AUG GCC A UGG CCA UCC UGG AAC UGC UAA AGU A	Invitrogen
HDAC2-HSS142909	Knock-down HDAC2	UUU AGC AUG ACC UUU GAC UGU UAG A UCU AAC AGU CAA AGG UCA UGC UAA A	Invitrogen
AKT1-HSS100345	Knock-down AKT1	AUU CUU GAG GAG GAA GUA GCG UGG C GCC ACG CUA CUU CCU CCU CAA GAA U	Invitrogen
PTEN-L003023-00-0020 SMART pool	Knock-down PTEN	GAU CAG CAU ACA CAA AUU A GAC UUA GAC UUG ACC UAU A GAU CUU GAC CAA UGG CUA A CGA UAG CAU UUG CAG UAU A	Dharmacon
TNC-HSS105145	Knock-down TNC	UUU CUC GGC UGU CAG GAG GAC AUU G CAA UGU CCU CCU GAC AGC CGA GAA A	Invitrogen

Supplementary Table S3. The antibodies and their reaction condition used in the current study.

Target	kDa	Raised In	Application	Dilution	Source	Catalog No.
AKT	60	Rabbit	Western blot	1:1000	Cell signaling	9272
AKT Thr308 phosphorylation	60	Rabbit	Western blot	1:500	Cell signaling	2965
AKT Ser473 phosphorylation	60	Rabbit	Western blot	1:1000	Cell signaling	9272
β-actin	43	Mouse	Western blot	1:5000	Abcam	ab-6276
Bad	25	Mouse	Western blot	1:500	Santa Cruz	sc-8044
Bak	30	Rabbit	Western blot	1:500	Santa Cruz	sc-7873
Bcl-2	26	Mouse	Western blot	1:500	Santa Cruz	sc-7382
Bcl-XL	30	Mouse	Western blot	1:500	Santa Cruz	sc-8392
Caspase 3 Cleaved form	17 19	Rabbit	Western blot	1:500	Cell signaling	9661
GFP-Tag	30	Rabbit	Western blot	1:1000	GeneTex	GTX26556
GSK3β	46	Rabbit	Western blot	1:1000	Cell signaling	9315

Target	kDa	Raised In	Application	Dilution	Source	Catalog No.
GSK3β Ser9 phosphorylation	46	Rabbit	Western blot	1:2000	Novus Biologicals	NB 100-81948
HA-Tag	--*	Rabbit	ChIP[†]	1:100	GeneTex	GTX29110
HDAC1	65	Rabbit	Western blot ChIP[†]	1:2000 1:100	Abcam	ab-7028
HDAC2	65	Rabbit	Western blot ChIP[†]	1:2000 1:100	Abcam	ab-7029
Histone H3 K9K14 acetylation	17	Rabbit	Western blot	1:2000	Millipore	06-599
Oct4	43	Rabbit	Western blot Immunohistochemistry ChIP[†]	1:2000 1:200 1:30	Abcam	ab-19857
Oct4	43	Mouse	Western blot Immunoprecipitation	1:500 1:125	Santa Cruz	sc-5279
PTEN	54	Rabbit	Western blot Immunohistochemistry	1:1000 1:50	Cell signaling	9559

Target	kDa	Raised In	Application	Dilution	Source	Catalog No.
Sp1	95	Rabbit	Western blot Immunoprecipitation	1:1000	Millipore	07-645
Sp1	95	Rabbit	ChIP[†]	1:100	Active Motif	39058
TNC	220-280	Rabbit	Western blot Immunohistochemistry	1:500 1:100	Santa Cruz	sc-20932

***** --, Molecular weight is variable.

[†] ChIP, chromatin-immunoprecipitation.

Supplementary Table S4. The primers and DNA probes used in the current study.

Gene	Primer	Sequences (5’→ 3’)	Application*	PCR size (bp)	Tm (°C)
GAPDH mRNA	Forward	GAG TCA ACG GAT TTG GTC GT	qRT-PCR	238	60
	Reverse	TTG ATT TTG GAG GGA TCT CG			
TNC mRNA	Forward	TGG GAG ATC ATC TTC CGG AAT	qRT-PCR	150	60
	Reverse	CCC CGG GTA TTG TTT TTC ACT			
HDAC4 mRNA	Forward	AAT CTG AAC CAC TGC ATT TCC A	qRT-PCR	123	60
	Reverse	CAG GAC CGG GTG GTT ATA GGA			
MAPK4 mRNA	Forward	TGC TCC TTT CCC CCA ATA ACT	qRT-PCR	200	60
	Reverse	GCT GAC AAA GGA AGG CAT CAC			
PAX6 mRNA	Forward	TAA TCG AAG GGC CAA ATG GA	qRT-PCR	130	60
	Reverse	GGG TTG TGG AAT TGG TTG GT			
EOMES mRNA	Forward	CTG CCT ACC AAA ACA CCG ATA TT	qRT-PCR	200	60
	Reverse	GGT CTG TGG CAC GGT TCT CT			
JARID2 mRNA	Forward	ACA AAG GCG TCC TCA ATG ACT T	qRT-PCR	150	60
	Reverse	GCC TCC AGT ACT CTT GCT CGA T			
HNRNPUL1 mRNA	Forward	AAG TCC ACC AAT AGC CGG TTT	qRT-PCR	130	60
	Reverse	CCA TCC ACT TTC CAT TCT TGG TA			
LAMB1 mRNA	Forward	ACA ACC AGG TGG TGT CAT TAT CAC	qRT-PCR	130	60
	Reverse	ACG TCG CTA TCA GAG GAG GTG TA			
PLEC mRNA	Forward	GGA GGA TGC GTT TCC ACA AG	qRT-PCR	151	60
	Reverse	TGC AGA ATG ATT GTC CAG ATG AG			

Gene	Primer	Sequences (5’→ 3’)	Application*	PCR size (bp)	Tm (℃)
CAD mRNA	Forward	TGG AAC TGC TTT TCG ATA TCT TTC T	qRT-PCR	150	60
	Reverse	CCT TTC GTG GTG GTG GAA GT			
GSK3A mRNA	Forward	AAA GCT CAC CCC TGG ACA AA	qRT-PCR	150	60
	Reverse	CAG ACA TCG CAG TTC ATC AAA GA			
PRKDC mRNA	Forward	ACT GGA TCC TCG GGA TTG G	qRT-PCR	150	60
	Reverse	GAG TTA GCC GAA AAG GCA TCA			
USP47 mRNA	Forward	CAG CAT GAT GTA CAA GAA CTA TGC A	qRT-PCR	150	60
	Reverse	TCG CCA GCC CTC ATA ACC			
PTEN mRNA	Forward	CGA CGG GAA GAC AAG TTC AT	qRT-PCR	163	60
	Reverse	AGG TTT CCT CTG GTC CTG GT			
DKK3 mRNA	Forward	GGT CTT TTC AGA GAC AGT TAT CAC ATC T	qRT-PCR	124	60
	Reverse	GGTGTACTGGAAGCTGGCAAA			
FBXO31 mRNA	Forward	GCG AAA ACT TGC GGA AGC T	qRT-PCR	121	60
	Reverse	CCT CCG TAT GGC CCG ATA T			
MAT1A mRNA	Forward	GTG CAT GCC CCT CAC CAT	qRT-PCR	122	60
	Reverse	TGT ACT GAA CTG TCA CCT GAG TCT TAG A			
FOXO4 mRNA	Forward	CTT TGA GCC AGA TCC CTG AG	qRT-PCR	344	60
	Reverse	TTC CAA CAG CAT TGC TCA TC			
CASZ1 mRNA	Forward	CCA TCG ACC CCT CCT TTA CA	qRT-PCR	150	60
	Reverse	CAA ACT CTC GTA GCA GGT CCT AGA A			

Gene	Primer	Sequences (5’→ 3’)	Application*	PCR size (bp)	Tm (℃)
CELF2 mRNA	Forward	GAG CCT TAC GGA GCC GTC TA	qRT-PCR	200	60
	Reverse	TTG GAC TTT TCA CTA TCT GCA GGT T			
PDZD2 mRNA	Forward	TAA GCA AAG TCC ACG CCA TCT	qRT-PCR	120	60
	Reverse	TGC TGC GTG CTA TGA CTT CAT			
CDH15 mRNA	Forward	CCT ACC CCC TGG TTC AGA TCA	qRT-PCR	131	60
	Reverse	GAA GAC CTT CCC TGT GAA CTT GTC			
IL21R mRNA	Forward	CCT GAA GAC CCA TCC ATT GTG	qRT-PCR	120	60
	Reverse	GCA CCC ACC CAT TTC TTG AA			
RAB37 mRNA	Forward	AGG CCT TGC TTC TGC TGT ATG	qRT-PCR	120	60
	Reverse	TGT TGC CTA GCA GCA TGA TCA			
SOX11 mRNA	Forward	TGT ACA TAT GTT GTG GGT TTA AGA GTC TT	qRT-PCR	190	60
	Reverse	TGT CAT GCT GAA AAC TGC TCT AAA A			
TRAPPC9 mRNA	Forward	ATG AAA AGC TTG CTG GGT CAG A	qRT-PCR	120	60
	Reverse	TCC TTG AAC CCA CTG GAA ATC T			
HTRA3 mRNA	Forward	GAG TTC CAA GAC AAG CAG ATC AAA	qRT-PCR	150	60
	Reverse	CGC AAC CTC TTG CAC ATA AAT TC			
SDC1 mRNA	Forward	CAC ACT CCC CAC ACA GAG GAT	qRT-PCR	124	60
	Reverse	CCG AGG TTT CAA AGG TGA AGT C			
VASH1 mRNA	Forward	ACA TCA GAG AGC TGC AGT ACA ATC A	qRT-PCR	120	60
	Reverse	TGA TTG GCA GGG CCT CTT T			

Gene	Primer	Sequences (5’→ 3’)	Application*	PCR size (bp)	Tm (℃)
TNC	Forward	CCA GGC ATC CGT CTC ACA AT	qChIP-PCR	150	60
	Reverse	CTC GGC CAG GGA AGG AA			
HDAC4	Forward	GCA CAA AAT AGA AAG AAC AGA AGC AA	qChIP-PCR	150	60
	Reverse	TGC GTG AGC CAG TGA TGA G			
MAPK4	Forward	TAC ATC CAC TCC GCC AAC GT	qChIP-PCR	150	60
	Reverse	CAT TCC AGC CAG ACA TAC CTT GT			
PAX6	Forward	TGC ATT TGC CTC CAG ACT TG	qChIP-PCR	150	60
	Reverse	TGC AGC GAC TAA GGA GGA ATC			
EOMES	Forward	ACC ACA GCA GCA CCA ACA TC	qChIP-PCR	120	60
	Reverse	CGC GAA CAC ACA CAT CAA AAA			
JARID2	Forward	GAG CTG CTC AAG TGC CAG ATG	qChIP-PCR	142	60
	Reverse	GGA GGA AGC ACA CCC TGT TC			
CAD	Forward	GGT GCG ACT TTG CGC TAT TC	qChIP-PCR	120	60
	Reverse	GCC GCA GCT CAG AGA AGG T			
GSK3A	Forward	GCT CAG CTT GTC GTA ATT CAT CTG	qChIP-PCR	167	60
	Reverse	TCC AGC TGT GGC ACT TTA TCC			
USP47	Forward	TGT AGT AGG CTG GAA GAA ATT GCA T	qChIP-PCR	167	60
	Reverse	ACT TGG TGC AAA AAT GAC TGA ATC			
POU5F1	Forward	AGG TGA CCA CTT CCC CAT CAG	qChIP-PCR	129	60
	Reverse	ACC CCT GGT GCC GTG AA			

Gene	**Primer**	**Sequences (5’→ 3’)**	**Application***	**PCR size (bp)**	**Tm (℃)**
PTEN	Forward	CCC CGA GCA AAG GAA GAA G	qChIP-PCR	150	60
	Reverse	AGG GTT CAA AAG GAG GTG GAA			
DKK3	Forward	TTT CCT GCC TGA TTG GAG AGA	qChIP-PCR	132	60
	Reverse	GGA GCA GTG GAA GGG AAG TG			
FBXO31	Forward	GAC AGG GAC ACA CAG AGT CAC TAT TC	qChIP-PCR	150	60
	Reverse	TCA GGC ACC TGC CAA GTT G			
FOXO4	Forward	AGG GCG AGG GAC TGG ACT T	qChIP-PCR	150	60
	Reverse	AGG AGC TCT GGC TAC CAC TTG T			
CASZ1	Forward	TGC GTT GGA GCT GAG GTC TA	qChIP-PCR	153	60
	Reverse	CGG CGT TTA TAT TTT AGG GAA GAA			
IL21R	Forward	GGG CTG TGG TGA GGA ATG TG	qChIP-PCR	126	60
	Reverse	GGT CTC TGT TCT TGG CCA TGA			
RAB37	Forward	GGG ACT GCC TGA CCT TGT TG	qChIP-PCR	126	60
	Reverse	TGA GCA AAC GAT GCC AGC TA			
HTRA3	Forward	AAC CCC CAG ACC ACG TTG T	qChIP-PCR	150	60
	Reverse	CAT CCT TCC CCA GGC AGT T			
SDC1	Forward	CCC AGC CCC AGA CTG TAT GT	qChIP-PCR	150	60
	Reverse	AGC CAA TCC TAC GGT GCA TT			
VASH1	Forward	AGA GAG GAG GCT CAG CAA GGT	qChIP-PCR	150	60
	Reverse	GCA TAG CAC CCC TAG AGG AAA G			

Gene	**Primer**	**Sequences (5'→ 3')**	**Application***	**PCR size (bp)**	**Tm (℃)**
PTEN-1 promoter	Forward	CGA CTG TGG CCC GTG TAT C	qChIP-PCR	100	60
	Reverse	AAA GTA CGG AAC GGT AGG AAG CT			
PTEN-2 promoter	Forward	CTT TCC ACT CAA CCC GGT AA	qChIP-PCR	145	60
	Reverse	GGA GTC AAG CTC GGT TCT CA			
PTEN-1 Sp1 site mutant	Sense	TAGGTCTCCTCAACCAACCCACTCGCTGGG	Site-direct mutagenesis	--[†]	61
	Antisense	CCCAGCGAGTGGGTTGGTTGAGGAGACCTA			
PTEN-2 Sp1 site mutant	Sense	AGGGGGGGTTGGGCTAGG	Site-direct mutagenesis	--[†]	61
	Antisense	CCTAGCCCAACCCCCCCT			
TNC Sp1 site mutant	Sense	GTCGGGGGTTGGCAGGCGGGA	Site-direct mutagenesis	--[†]	61
	Antisense	TCCCGCCTGCCAACCCCCGAC			
TNC Oct4 site mutant	Sense	GCCATAAATTGTCCCCAAATGGGTTCC	Site-direct mutagenesis	--[†]	50
	Antisense	GGAACCCATTTGGGGACAATTTATGGC			

***** qRT-PCR, quantitative reverse-transcriptase polymer chain reaction; qChIP-PCR, quantitative chromatin-immunoprecipitation coupled with polymer chain reaction.

[†] --, Not applicable.

Supplementary Table S5. The DAPA probes used in the current study.

Name	**Primer***	**Sequences (5'→ 3')**
PTEN-1	Sense	TAGGTCTCCTCGCCCCGCCCACTCGCTGGGCTGC
Sp1-WT	Antisense (Biotin)	GCAGCCCAGCGAGTGGGCGGGGCGAGGAGACCTA
PTEN-1	Sense	TAGGTCTCCTCACACAACCCACTCGCTGGTCTGC
Sp1-Mut	Antisense (Biotin)	GCAGACCAGCGAGTGGGTTGTGTGAGGAGACCTA
PTEN-2	Sense (Biotin)	CGGCCAAGGGGGGGCGGGGCTAGGTGGTCTCTGA
Sp1-WT	Antisense	TCAGAGACCACCTAGCCCCGCCCCCCCTTGGCCG
PTEN-2	Sense (Biotin)	CGGCCAAGGGGGGGTTGGGCTAGGTGGTCTCTGA
Sp1-Mut	Antisense	TCAGAGACCACCTAGCCCAACCCCCCCTTGGCCG
TNC	Sense (Biotin)	GTCGGGGGCGGGCAGGCGGGAATTCCTACTTTCGCCATAAATTGTATGCAAATGGG
Sp1-WT	Antisense	CCCATTTGCATACAATTTATGGCGAAAGTAGGAATTCCCGCCTGCCCGCCCCCGAC
TNC	Sense (Biotin)	GTCGGGGGTTGGCAGGCGGGAATTCCTACTTTCGCCATAAATTGTATGCAAATGGG
Sp1-Mut	Antisense	CCCATTTGCATACAATTTATGGCGAAAGTAGGAATTCCCGCCTGCCAACCCCCGAC
TNC	Sense (Biotin)	GTCGGGGGCGGGCAGGCGGGAATTCCTACTTTCGCCATAAATTGTATGCAAATGGG
Oct4-WT	Antisense	CCCATTTGCATACAATTTATGGCGAAAGTAGGAATTCCCGCCTGCCCGCCCCCGAC
TNC	Sense (Biotin)	GTCGGGGGCGGGCAGGCGGGAATTCCTACTTTCGCCATAAATTGTCCCCAACTGGG
Oct4-Mut	Antisense	CCCAGTTGGGGACAATTTATGGCGAAAGTAGGAATTCCCGCCTGCCCGCCCCCGAC

***** Biotin was labeled at 5' end of either sense or antisense probe.

Supplementary Table S6. Clinical characteristics of Oct4, PTEN, and TNC expression in lung cancer patients enrolled in this study.

Total patient number (N= 133)

Characteristics*	Oct4 protein Normal expression 41 (30.8%) N (%)	 Overexpression 92 (69.2%) N (%)	*P*-value†
Age			
<60	15 (39.5)	23 (60.5)	0.172
≥60	26 (27.4)	69 (72.6)	
Sex			
Male	30 (32.3)	63 (67.7)	0.586
Female	11 (27.5)	29 (72.5)	
Smoke			
Yes	21 (30.9)	47 (69.1)	0.540
No	15 (36.6)	26 (63.4)	
Tumor type			
ADC	34 (35.1)	63 (64.9)	0.193
SCC	5 (22.7)	17 (77.3)	
Others	2 (14.3)	12 (85.7)	
Tumor stage			
I & II	30 (36.1)	53 (63.9)	0.087
III & IV	11 (22.0)	39 (78.0)	
T status			
T1	12 (50.0)	12 (50.0)	0.006
T2	19 (21.1)	71 (78.9)	
T3	6 (54.5)	5 (45.5)	
T4	4 (50.0)	4 (50.0)	
N status			
N0	26 (40.0)	39 (60.0)	0.025
N1-2	15 (22.1)	53 (77.9)	
M status			
M0	39 (31.7)	84 (68.3)	0.441
M1	2 (20.0)	8 (80.0)	

	PTEN protein		
	Normal expression 52 (39.1%)	Low expression 81 (60.9%)	
Characteristics*	N (%)	N (%)	*P*-value[†]
Age			
<60	21 (55.3)	17 (44.7)	0.016
≥60	31 (32.6)	64 (67.4)	
Sex			
Male	31 (33.3)	62 (66.7)	0.038
Female	21 (52.5)	19 (47.5)	
Smoke			
Yes	22 (32.4)	46 (67.6)	0.028
No	22 (53.7)	19 (46.3)	
Tumor type			
ADC	44 (45.4)	53 (54.6)	0.052
SCC	5 (22.7)	17 (77.3)	
Others	3 (21.4)	11 (78.6)	
Tumor stage			
I & II	34 (41.0)	49 (59.0)	0.570
III & IV	18 (36.0)	32 (64.0)	
T status			
T1	14 (58.3)	10 (41.7)	0.060
T2	29 (32.2)	61 (67.8)	
T3	4 (36.4)	7 (63.6)	
T4	5 (62.5)	3 (37.5)	
N status			
N0	29 (44.6)	36 (55.4)	0.202
N1-2	23 (33.8)	45 (66.2)	
M status			
M0	47 (38.2)	76 (61.8)	0.463
M1	5 (50.0)	5 (50.0)	

	TNC protein		
	Normal expression 55 (41.4%)	Overexpression 78 (58.6%)	
Characteristics*	N (%)	N (%)	*P*-value†
Age			
<60	17 (44.7)	21 (55.3)	0.616
$\geq$60	38 (40.0)	57 (60.0)	
Sex			
Male	39 (41.9)	54 (58.6)	0.835
Female	16 (40.0)	24 (60.0)	
Smoke			
Yes	27 (39.7)	41 (60.3)	0.746
No	15 (36.6)	26 (63.4)	
Tumor type			
ADC	37 (38.1)	60 (61.9)	0.178
SCC	13 (59.1)	9 (40.9)	
Others	5 (35.7)	9 (64.3)	
Tumor stage			
I & II	39 (47.0)	44 (53.0)	0.089
III & IV	16 (32.0)	34 (68.0)	
T status			
T1	10 (41.7)	14 (58.3)	0.942
T2	36 (40.0)	54 (60.0)	
T3	5 (45.5)	6 (54.5)	
T4	4 (50.0)	4 (50.0)	
N status			
N0	36 (55.4)	29 (44.6)	0.001
N1-2	19 (27.9)	49 (72.1)	
M status			
M0	53 (43.1)	70 (56.9)	0.154
M1	2 (20.0)	8 (80.0)	

***** ADC: adenocarcinoma, SCC: squamous cell carcinoma, T describes the size of the tumor, N describes regional lymph nodes, M describes distant metastasis.

† The *P* values were determined by the Pearson $\chi 2$ test.

Supplementary Table S7. The 5,380 regions identified with high confidence in two independent experiments by ChIP-seq analysis taken from control and Oct4 expressing A549 cells.

Chr no.	Region	Length	FDR (%)	# Reads	# Forward reads	# Reverse reads	Normalized difference	Wilcoxon filter p-value	5' gene	3' gene	Common Oct4-target genes identified by Boyer *et al.*, 2005
chr1	+(1453533..1454469)	936	0.06522	24	16	8	0.3333333	0.00072543	ATAD3A	C1orf70	
chr1	+(1459561..1460086)	525	1.94055	9	3	6	0.3333333	0.048	ATAD3A	C1orf70	
chr1	+(1653685..1654210)	525	1.94055	13	6	7	0.0769231	0.00757922	MMP23A_dup1	CDK11B	
chr1	+(1669471..1670152)	681	0.01616	25	12	13	0.04	8.7329E-05	CDK11A	SLC35E2	
chr1	+(1687507..1688207)	700	0.22348	10	6	4	0.2	0.005	SLC35E2	NADK	
chr1	+(2114015..2114523)	508	0.94117	8	4	4	0	0.014	PRKCZ	C1orf86	
chr1	+(2541920..2542620)	700	0.46268	9	6	3	0.3333333	0.012	C1orf93	MMEL1	
chr1	+(3239084..3239768)	684	0.46268	9	6	3	0.3333333	0.012	MIR4251	ARHGEF16	
chr1	+(3339077..3339777)	700	4.18167	9	6	3	0.3333333	0.988	MIR4251	ARHGEF16	
chr1	+(3454542..3455242)	700	0.22348	15	8	7	0.0666667	0.67828558	ARHGEF16	MEGF6	
chr1	+(3742766..3743296)	530	0.94117	11	4	7	0.2727273	0.012	LRRC47	KIAA0562	
chr1	+(3820885..3821411)	526	1.94055	10	3	7	0.4	0.008	LOC100133612	LOC284661	
chr1	+(4033143..4033973)	830	0.00319	18	8	10	0.1111111	0.00018964	LOC100133612	LOC284661	
chr1	+(6259007..6259705)	698	0.22348	12	4	8	0.3333333	0.077	CHD5	RPL22	
chr1	+(6326405..6327090)	685	4.18167	6	3	3	0	0.05	GPR153	ACOT7	
chr1	+(6501725..6502227)	502	1.94055	10	3	7	0.4	0.008	MIR4252	TNFRSF25	
chr1	+(6505625..6506142)	517	4.18167	6	4	2	0.3333333	0.067	MIR4252	TNFRSF25	
chr1	+(6522533..6523099)	566	1.94055	10	4	6	0.2	0.033	MIR4252	TNFRSF25	
chr1	+(6644507..6645047)	540	1.94055	7	3	4	0.1428571	0.029	ZBTB48	KLHL21	
chr1	+(7157981..7158523)	542	1.94055	7	3	4	0.1428571	0.029	CAMTA1	VAMP3	
chr1	+(7468051..7468751)	700	0.46268	9	3	6	0.3333333	0.012	CAMTA1	VAMP3	
chr1	+(9775605..9776118)	513	0.94117	9	4	5	0.1111111	0.143	C1orf200	CLSTN1	
chr1	+(10719411..10720031)	620	1.94055	9	6	3	0.3333333	0.048	PEX14	CASZ1	
chr1	+(11316869..11317569)	700	0.22348	10	6	4	0.2	0.005	EXOSC10	MTOR	
chr1	+(11345573..11346161)	588	1.94055	10	5	5	0	0.0081468	UBIAD1	PTCHD2	
chr1	+(11893536..11894038)	502	4.18167	12	5	7	0.1666667	0.97882147	CLCN6	NPPA	
chr1	+(12032658..12033251)	593	1.94055	10	3	7	0.4	0.992	PLOD1	MFN2	
chr1	+(12300817..12301512)	695	4.18167	6	3	3	0	0.05	VPS13D	SNORA59A	
chr1	+(12339459..12340056)	597	0.94117	11	6	5	0.0909091	0.00308495	VPS13D	SNORA59A	

chr1	+(13670343..13670924)	581	0.81155	22	11	11	0	0.04702034	PRAMEF9_dup2	PRAMEF14_dup2	
chr1	+(13695656..13696162)	506	2.6965	41	20	21	0.0243902	0.0028488	PRAMEF14_dup2	PRAMEF18_dup2	
chr1	+(13746944..13747558)	614	0.11833	20	14	6	0.4	0.1611498	PRAMEF21_dup2	LRRC38	
chr1	+(14761075..14761775)	700	0.22348	10	7	3	0.4	0.008	PRDM2	KAZ	
chr1	+(15279089..15279654)	565	1.94055	7	3	4	0.1428571	0.029	KAZ	C1orf126	
chr1	+(16458376..16458907)	531	4.18167	7	4	3	0.1428571	0.029	FAM131C	EPHA2	
chr1	+(16484804..16485324)	520	4.18167	6	4	2	0.3333333	0.067	EPHA2	ARHGEF19	
chr1	+(16502040..16502665)	625	0.46268	9	5	4	0.1111111	0.008	EPHA2	ARHGEF19	
chr1	+(16735355..16735990)	635	0.94117	11	5	6	0.0909091	0.70805879	C1orf144	SPATA21	
chr1	+(16901107..16901632)	525	1.58044	16	6	10	0.25	0.06444254	MIR3675_dup1	NBPF1	
chr1	+(16906895..16908220)	1325	0.00351	91	50	41	0.0989011	0.00310968	MIR3675_dup1	NBPF1	
chr1	+(16911802..16912324)	522	0.18837	36	19	17	0.0555556	0.00072478	MIR3675_dup1	NBPF1	
chr1	+(16915323..16915913)	590	0.3601	55	26	29	0.0545455	0.05463001	MIR3675_dup1	NBPF1	
chr1	+(16918108..16918987)	879	0.06522	25	12	13	0.04	0.00055009	MIR3675_dup1	NBPF1	
chr1	+(17084049..17084569)	520	4.18167	22	12	10	0.0909091	0.83868573	ESPNP	MST1P9	
chr1	+(17087324..17087836)	512	4.18167	11	4	7	0.2727273	0.324	ESPNP	MST1P9	
chr1	+(17318530..17319087)	557	0.94117	10	3	7	0.4	0.258	MFAP2	ATP13A2	
chr1	+(17814027..17814641)	614	1.94055	7	4	3	0.1428571	0.029	RCC2	ARHGEF10L	
chr1	+(17993395..17994321)	926	0.46268	15	6	9	0.2	0.00073136	ARHGEF10L	ACTL8	
chr1	+(18010730..18011430)	700	1.94055	12	6	6	0	0.97266803	ARHGEF10L	ACTL8	
chr1	+(18020948..18021648)	700	0.22348	10	6	4	0.2	0.005	ARHGEF10L	ACTL8	
chr1	+(18700510..18701210)	700	4.18167	10	4	6	0.2	0.995	IGSF21	KLHDC7A	
chr1	+(18962570..18963087)	517	4.18167	6	3	3	0	0.05	PAX7	TAS1R2	v
chr1	+(19950648..19951284)	636	0.11833	11	4	7	0.2727273	0.003	C1orf151	NBL1	
chr1	+(19980179..19980799)	620	0.94117	8	5	3	0.25	0.018	NBL1	HTR6	
chr1	+(20666303..20667003)	700	0.46268	9	3	6	0.3333333	0.012	VWA5B1	LOC339505	
chr1	+(20668322..20669022)	700	4.18167	10	4	6	0.2	0.995	VWA5B1	LOC339505	
chr1	+(21851347..21852047)	700	0.46268	9	3	6	0.3333333	0.012	ALPL	RAP1GAP	
chr1	+(22324302..22324836)	534	4.18167	14	8	6	0.1428571	0.01943355	CELA3B	CELA3A	
chr1	+(22336215..22336858)	643	1.10834	45	15	30	0.3333333	0.00120778	CELA3A	HSPC157	
chr1	+(22412736..22413277)	541	0.46268	12	4	8	0.3333333	0.467	CDC42	WNT4	
chr1	+(22450910..22452120)	1210	4.18167	12	6	6	0	0.99802612	CDC42	WNT4	
chr1	+(22504605..22505182)	577	1.94055	7	4	3	0.1428571	0.029	WNT4	ZBTB40	
chr1	+(22834654..22835233)	579	1.94055	8	5	3	0.25	0.018	ZBTB40	EPHA8	

chr1	+(22847891..22848406)	515	4.18167	6	3	3	0	0.05	ZBTB40	EPHA8	
chr1	+(23101584..23102087)	503	4.18167	8	4	4	0	0.014	EPHB2	MIR4253	
chr1	+(23710443..23710985)	542	4.18167	6	3	3	0	0.05	C1orf213	TCEA3	
chr1	+(24289414..24289979)	565	4.18167	7	4	3	0.1428571	0.114	PNRC2	SRSF10	
chr1	+(26079836..26080530)	694	1.94055	10	7	3	0.4	0.992	MAN1C1	SEPN1	
chr1	+(26523854..26524494)	640	0.94117	8	5	3	0.25	0.018	CATSPER4	CCDC21	
chr1	+(27237548..27238066)	518	0.22348	13	4	9	0.3846154	0.003	GPATCH3	NR0B2	
chr1	+(27268969..27269663)	694	0.22348	10	7	3	0.4	0.008	NUDC	C1orf172	
chr1	+(27277229..27277734)	505	4.18167	6	2	4	0.3333333	0.067	NUDC	C1orf172	
chr1	+(27464335..27465038)	703	0.94117	13	8	5	0.2307692	0.0017074	FAM46B	SLC9A1	
chr1	+(27815563..27816263)	700	0.11833	11	7	4	0.2727273	0.003	GPR3	WASF2	
chr1	+(27848979..27849677)	698	1.94055	10	7	3	0.4	0.992	WASF2	AHDC1	
chr1	+(27995270..27996050)	780	0.01075	23	10	13	0.1304348	0.00078107	FGR	IFI6	
chr1	+(28075510..28076076)	566	4.18167	11	6	5	0.0909091	0.10062131	FAM76A	STX12	
chr1	+(28450392..28451031)	639	4.18167	6	2	4	0.3333333	0.067	LOC653566	PTAFR	
chr1	+(28476831..28477345)	514	0.94117	9	5	4	0.1111111	0.008	LOC653566	PTAFR	
chr1	+(29161998..29162846)	848	0.00097	21	12	9	0.1428571	6.2118E-05	OPRD1	EPB41	
chr1	+(32047530..32048230)	700	0.94117	13	5	8	0.2307692	0.9982926	TINAGL1	HCRTR1	
chr1	+(32280224..32280761)	537	1.94055	7	3	4	0.1428571	0.029	MIR4254	SPOCD1	
chr1	+(32377084..32377661)	577	0.46268	14	8	6	0.1428571	0.01006838	SPOCD1	PTP4A2	
chr1	+(32496927..32497507)	580	0.94117	9	4	5	0.1111111	0.008	KHDRBS1	TMEM39B	
chr1	+(32689333..32689946)	613	4.18167	11	5	6	0.0909091	0.03394459	EIF3I	MTMR9LP	
chr1	+(33245456..33246127)	671	4.18167	6	4	2	0.3333333	0.067	KIAA1522	YARS	
chr1	+(33333780..33334480)	700	1.94055	12	7	5	0.1666667	0.99775837	S100PBP	FNDC5	
chr1	+(33489727..33490270)	543	1.94055	10	4	6	0.2	0.019	RNF19B	AK2	
chr1	+(34002239..34002770)	531	4.18167	10	4	6	0.2	0.005	ZSCAN20	CSMD2	
chr1	+(35369960..35370493)	533	4.18167	7	3	4	0.1428571	0.029	C1orf212	DLGAP3	
chr1	+(36831658..36832334)	676	4.18167	6	4	2	0.3333333	0.067	FAM176B	STK40	
chr1	+(40735426..40735941)	515	4.18167	9	5	4	0.1111111	0.032	ZMPSTE24	COL9A2	v
chr1	+(41234614..41235918)	1304	1.94055	16	9	7	0.125	0.00062229	MIR30C1	KCNQ4	
chr1	+(42657237..42657761)	524	4.18167	9	6	3	0.3333333	0.012	GUCA2A	FOXJ3	
chr1	+(43317785..43318380)	595	1.94055	10	4	6	0.2	0.238	ZNF691	SLC2A1	
chr1	+(43352523..43353223)	700	0.46268	13	9	4	0.3846154	0.926	ZNF691	SLC2A1	
chr1	+(43365903..43366575)	672	4.18167	6	4	2	0.3333333	0.067	ZNF691	SLC2A1	

chr1	+(43686908..43687441)	533	1.94055	10	3	7	0.4	0.008	WDR65	TMEM125
chr1	+(43888706..43889406)	700	0.11833	11	4	7	0.2727273	0.003	C1orf84	KIAA0467
chr1	+(43912802..43913620)	818	1.94055	17	10	7	0.1764706	0.04855487	KIAA0467	HYI
chr1	+(43941234..43941770)	536	0.46268	9	4	5	0.1111111	0.008	HYI	PTPRF
chr1	+(44068725..44069425)	700	0.22348	14	9	5	0.2857143	0.96406968	PTPRF	KDM4A
chr1	+(44426722..44427250)	528	1.94055	9	6	3	0.3333333	0.012	IPO13	DPH2
chr1	+(44429631..44430134)	503	4.18167	8	3	5	0.25	0.071	IPO13	DPH2
chr1	+(44684996..44685658)	662	0.94117	9	5	4	0.1111111	0.008	DMAP1	ERI3
chr1	+(45278032..45278732)	700	0.11833	13	6	7	0.0769231	0.15865525	BTBD19	PTCH2
chr1	+(45485491..45485997)	506	4.18167	6	2	4	0.3333333	0.067	UROD	ZSWIM5
chr1	+(45876848..45877544)	696	4.18167	9	3	6	0.3333333	0.012	TOE1	TESK2
chr1	+(46527379..46528460)	1081	0.06522	20	13	7	0.3	0.99885903	MAST2	PIK3R3
chr1	+(46662895..46663735)	840	0.02727	20	6	14	0.4	0.000266	TSPAN1	POMGNT1
chr1	+(46745939..46746490)	551	4.18167	8	5	3	0.25	0.286	RAD54L	LRRC41
chr1	+(46868672..46869185)	513	4.18167	6	2	4	0.3333333	0.067	FAAH	DMBX1
chr1	+(46941628..46942328)	700	0.46268	9	3	6	0.3333333	0.012	FAAH	DMBX1
chr1	+(47725860..47726380)	520	1.94055	11	5	6	0.0909091	0.00881105	TAL1	STIL
chr1	+(48049695..48050383)	688	4.18167	6	2	4	0.3333333	0.067	FOXD2	LOC388630
chr1	+(48276179..48276875)	696	4.18167	6	2	4	0.3333333	0.067	FOXD2	LOC388630
chr1	+(51754135..51754714)	579	4.18167	8	4	4	0	0.343	RNF11	TTC39A
chr1	+(51829337..51829875)	538	4.18167	9	5	4	0.1111111	0.008	TTC39A	EPS15
chr1	+(52275968..52276485)	517	1.94055	12	7	5	0.1666667	0.01417552	OSBPL9	NRD1
chr1	+(52746679..52747379)	700	1.94055	10	3	7	0.4	0.992	ZFYVE9	CC2D1B
chr1	+(52902438..52902988)	550	1.94055	11	7	4	0.2727273	0.794	PRPF38A	ZCCHC11
chr1	+(55249451..55250085)	634	0.22348	10	4	6	0.2	0.005	PARS2	TTC22
chr1	+(58456258..58456843)	585	4.18167	6	3	3	0	0.05	C8B	DAB1
chr1	+(59666329..59666843)	514	4.18167	6	4	2	0.3333333	0.067	LOC729467	FGGY
chr1	+(59849337..59850477)	1140	1.94055	13	6	7	0.0769231	0.0013499	FGGY	HOOK1
chr1	+(62340456..62341519)	1063	0.46268	17	8	9	0.0588235	0.99647318	INADL	L1TD1
chr1	+(62738693..62739307)	614	0.46268	9	3	6	0.3333333	0.012	L1TD1	KANK4
chr1	+(63005103..63005703)	600	1.94055	9	4	5	0.1111111	0.008	USP1	DOCK7
chr1	+(63070140..63070706)	566	0.46268	9	3	6	0.3333333	0.012	USP1	DOCK7
chr1	+(65831565..65832086)	521	4.18167	10	5	5	0	0.45840747	DNAJC6	LEPROT
chr1	+(65857967..65858486)	519	4.18167	9	4	5	0.1111111	0.857	DNAJC6	LEPROT

chr1	+(65897330..65897833)	503	4.18167	6	4	2	0.3333333	0.067	LEPR	PDE4B
chr1	+(66826969..66827641)	672	0.02727	14	6	8	0.1428571	0.00097289	PDE4B	SGIP1
chr1	+(67105205..67105743)	538	1.94055	11	5	6	0.0909091	0.00881105	MIR3117	TCTEX1D1
chr1	+(67147640..67148476)	836	0.22348	16	9	7	0.125	0.00062229	MIR3117	TCTEX1D1
chr1	+(67154707..67155274)	567	1.94055	12	5	7	0.1666667	0.28488218	MIR3117	TCTEX1D1
chr1	+(67840050..67840585)	535	4.18167	6	3	3	0	0.05	IL12RB2	SERBP1
chr1	+(68948132..68948634)	502	4.18167	6	3	3	0	0.05	RPE65	DEPDC1
chr1	+(70624910..70625426)	516	1.94055	9	5	4	0.1111111	0.008	PIN1P1	LRRC40
chr1	+(74507005..74507514)	509	4.18167	15	5	10	0.3333333	0.54873837	NEGR1	LRRIQ3
chr1	+(75065177..75065731)	554	4.18167	9	4	5	0.1111111	0.095	TNNI3K	C1orf173
chr1	+(75072003..75072653)	650	0.06522	21	9	12	0.1428571	0.11349721	TNNI3K	C1orf173
chr1	+(76198167..76198775)	608	0.94117	11	5	6	0.0909091	0.29194121	ACADM	RABGGTB
chr1	+(78007463..78008163)	700	0.06522	12	7	5	0.1666667	0.00224163	AK5	ZZZ3
chr1	+(79126048..79126551)	503	4.18167	7	4	3	0.1428571	0.029	IFI44	ELTD1
chr1	+(84640332..84640964)	632	4.18167	9	3	6	0.3333333	0.048	PRKACB	SAMD13
chr1	+(86157104..86157804)	700	0.94117	12	4	8	0.3333333	0.024	CYR61	ZNHIT6
chr1	+(86591103..86591647)	544	4.18167	10	5	5	0	0.08726268	ZNHIT6	COL24A1
chr1	+(89338546..89339246)	700	1.94055	10	3	7	0.4	0.992	PKN2	GTF2B
chr1	+(90179806..90180333)	527	1.94055	7	3	4	0.1428571	0.029	LRRC8C	LRRC8D
chr1	+(90287471..90288171)	700	0.11833	11	5	6	0.0909091	0.00308495	LRRC8D	GEMIN8P4
chr1	+(91404709..91405228)	519	4.18167	10	6	4	0.2	0.543	BARHL2	ZNF644
chr1	+(91795384..91795929)	545	1.94055	8	5	3	0.25	0.071	ZNF644	HFM1
chr1	+(92763283..92763787)	504	4.18167	11	7	4	0.2727273	0.055	C1orf146	GLMN
chr1	+(93312592..93313141)	549	4.18167	7	3	4	0.1428571	0.029	SNORA66	FAM69A
chr1	+(94943652..94944283)	631	4.18167	10	4	6	0.2	0.086	ABCD3	F3
chr1	+(95367076..95367590)	514	4.18167	8	4	4	0	0.014	SLC44A3	CNN3
chr1	+(95711888..95712410)	522	1.94055	9	5	4	0.1111111	0.056	RWDD3	FLJ31662
chr1	+(98293430..98293964)	534	4.18167	6	3	3	0	0.05	PTBP2	DPYD
chr1	+(101704989..101705680)	691	1.94055	13	9	4	0.3846154	0.001	S1PR1	OLFM3
chr1	+(101706636..101707311)	675	4.18167	11	4	7	0.2727273	0.115	S1PR1	OLFM3
chr1	+(103386871..103387392)	521	1.94055	8	3	5	0.25	0.018	HEJ1	COL11A1
chr1	+(104117585..104118087)	502	0.46268	17	8	9	0.0588235	0.80676188	LOC648740	AMY2A
chr1	+(108993384..108993885)	501	4.18167	13	6	7	0.0769231	0.01606229	NBPF6	FAM102B
chr1	+(108997996..108998712)	716	1.58044	47	19	28	0.1914894	0.00295193	NBPF6	FAM102B

chr1	+(109000426..109001054)	628	1.97271	31	21	10	0.3548387	0.00712404	NBPF6	FAM102B	
chr1	+(109242396..109242930)	534	4.18167	10	6	4	0.2	0.019	PRPF38B	FNDC7	
chr1	+(110200386..110200916)	530	1.94055	14	7	7	0	0.2031169	GSTM4	GSTM2	
chr1	+(110201167..110201712)	545	0.94117	16	7	9	0.125	0.01500531	GSTM4	GSTM2	
chr1	+(110231728..110232266)	538	1.94055	10	7	3	0.4	0.033	GSTM1	GSTM5	
chr1	+(110255366..110255929)	563	4.18167	10	4	6	0.2	0.762	GSTM5	GSTM3	
chr1	+(112345119..112345819)	700	1.94055	10	3	7	0.4	0.992	DDX20	KCND3	
chr1	+(115005657..115006304)	647	0.94117	14	5	9	0.2857143	0.15865525	SYT6	TRIM33	
chr1	+(115110546..115111100)	554	1.94055	10	5	5	0	0.0081468	TRIM33	BCAS2	
chr1	+(115342543..115343682)	1139	0.46268	17	8	9	0.0588235	0.999734	SIKE1	SYCP1	
chr1	+(115455524..115456040)	516	1.94055	12	5	7	0.1666667	0.00591469	SYCP1	TSHB	
chr1	+(117297203..117297803)	600	4.18167	8	3	5	0.25	0.036	CD2	PTGFRN	
chr1	+(117663162..117663807)	645	1.94055	8	3	5	0.25	0.018	MIR942	TRIM45	
chr1	+(117991867..117992948)	1081	1.94055	14	7	7	0	0.99912744	MAN1A2	FAM46C	
chr1	+(118558438..118559064)	626	0.94117	11	7	4	0.2727273	0.021	WDR3	SPAG17	
chr1	+(144094172..144094700)	528	2.08944	35	18	17	0.0285714	0.00020658	SRGAP2P2	LOC728855_dup1	
chr1	+(144224007..144224512)	505	4.18167	9	6	3	0.3333333	0.452	SRGAP2P2	LOC728855_dup1	
chr1	+(144814477..144815056)	579	0.02727	23	14	9	0.2173913	0.00587169	LOC653513	PDE4DIP	
chr1	+(144917654..144918190)	536	0.46268	9	5	4	0.1111111	0.008	LOC653513	PDE4DIP	
chr1	+(144954893..144955577)	684	0.46268	13	6	7	0.0769231	0.00213737	LOC653513	PDE4DIP	
chr1	+(145296307..145296845)	538	1.49578	27	12	15	0.1111111	0.00420773	NBPF10	HFE2	
chr1	+(145336755..145337273)	518	1.94055	13	9	4	0.3846154	0.025	NBPF10	HFE2	
chr1	+(145366504..145367059)	555	1.94055	11	4	7	0.2727273	0.006	NBPF10	HFE2	
chr1	+(145538576..145539189)	613	4.18167	6	4	2	0.3333333	0.067	ITGA10	ANKRD35	
chr1	+(147468429..147468997)	568	1.94055	12	5	7	0.1666667	0.71511782	GPR89C_dup2	PDZK1P1_dup2	
chr1	+(147475698..147476244)	546	1.94055	11	4	7	0.2727273	0.264	GPR89C_dup2	PDZK1P1_dup2	
chr1	+(148751597..148752138)	541	4.13675	23	14	9	0.2173913	0.00988246	NBPF16_dup2	PPIAL4D_dup2	
chr1	+(148805700..148806208)	508	3.62933	29	10	19	0.3103448	0.00065948	NBPF16_dup2	PPIAL4D_dup2	
chr1	+(149857700..149858258)	558	4.18167	12	7	5	0.1666667	0.14557611	HIST2H4B_dup2	HIST2H2BE	v
chr1	+(150471741..150472262)	521	4.18167	6	2	4	0.3333333	0.067	TARS2	ECM1	
chr1	+(150477966..150478613)	647	1.94055	7	4	3	0.1428571	0.029	TARS2	ECM1	
chr1	+(150774126..150774826)	700	0.46268	10	3	7	0.4	0.258	CTSS	CTSK	
chr1	+(150825012..150825530)	518	4.18167	9	3	6	0.3333333	0.048	CTSK	ARNT	
chr1	+(150955534..150956231)	697	0.94117	13	8	5	0.2307692	0.01405402	ANXA9	FAM63A	

chr1	+(151400499..151401045)	546	1.94055	15	7	8	0.0666667	0.12357999	PSMB4	POGZ
chr1	+(151546978..151547525)	547	4.18167	10	7	3	0.4	0.333	MIR554	SNX27
chr1	+(152082713..152083261)	548	0.81155	16	11	5	0.375	0.00540184	TCHHL1	TCHH
chr1	+(152127649..152128202)	553	1.06787	44	21	23	0.0454545	0.01989223	TCHH	RPTN
chr1	+(152128216..152128806)	590	1.06787	48	24	24	0	0.12838031	TCHH	RPTN
chr1	+(152193377..152194222)	845	0.22348	21	14	7	0.3333333	0.18532499	RPTN	HRNR
chr1	+(152277393..152278102)	709	0.06522	18	10	8	0.1111111	0.04568697	HRNR	FLG
chr1	+(152278570..152280037)	1467	0.03638	123	68	55	0.1056911	0.83938281	HRNR	FLG
chr1	+(152280806..152281506)	700	0.00653	51	34	17	0.3333333	0.01625815	HRNR	FLG
chr1	+(152282651..152283178)	527	0.60327	21	10	11	0.047619	0.00458753	HRNR	FLG
chr1	+(152284812..152285336)	524	0.22348	15	10	5	0.3333333	0.13517207	HRNR	FLG
chr1	+(152323315..152323818)	503	4.18167	14	6	8	0.1428571	0.25930251	FLG	FLG2
chr1	+(152326198..152326827)	629	0.22348	15	7	8	0.0666667	0.04128965	FLG	FLG2
chr1	+(152327793..152328644)	851	0.46268	33	18	15	0.0909091	0.25759059	FLG	FLG2
chr1	+(152328767..152329317)	550	4.18167	17	6	11	0.2941176	0.3815123	FLG	FLG2
chr1	+(152883160..152883704)	544	4.18167	7	4	3	0.1428571	0.057	IVL	SPRR4
chr1	+(153065837..153066431)	594	4.18167	10	4	6	0.2	0.086	SPRR2B	SPRR2E
chr1	+(153538135..153538835)	700	1.94055	10	3	7	0.4	0.992	S100A3	S100A2
chr1	+(153570085..153570712)	627	4.18167	6	4	2	0.3333333	0.067	S100A2	S100A16
chr1	+(153580459..153581006)	547	4.18167	12	6	6	0	0.16833419	S100A2	S100A16
chr1	+(153719538..153720057)	519	0.94117	13	9	4	0.3846154	0.099	INTS3	SLC27A3
chr1	+(153912744..153913273)	529	0.22348	13	9	4	0.3846154	0.006	GATAD2B	DENND4B
chr1	+(153916552..153917117)	565	0.46268	9	5	4	0.1111111	0.008	GATAD2B	DENND4B
chr1	+(154312803..154313320)	517	1.94055	11	7	4	0.2727273	0.324	ATP8B2	IL6R
chr1	+(154315323..154316132)	809	1.94055	15	7	8	0.0666667	0.14881073	ATP8B2	IL6R
chr1	+(154437306..154437812)	506	4.18167	10	4	6	0.2	0.457	IL6R	SHE
chr1	+(154814282..154814982)	700	0.22348	11	5	6	0.0909091	0.05017413	ADAR	KCNN3
chr1	+(154842060..154842572)	512	4.18167	10	6	4	0.2	0.129	ADAR	KCNN3
chr1	+(154881613..154882313)	700	0.11833	11	6	5	0.0909091	0.00308495	KCNN3	PMVK
chr1	+(155011702..155012402)	700	1.94055	11	6	5	0.0909091	0.94982587	DCST1	ADAM15
chr1	+(155018372..155018898)	526	4.18167	6	3	3	0	0.05	DCST1	ADAM15
chr1	+(155186693..155187351)	658	4.18167	9	4	5	0.1111111	0.095	MTX1	GBAP1
chr1	+(155257952..155258549)	597	4.18167	10	4	6	0.2	0.305	HCN3	PKLR
chr1	+(155307923..155308577)	654	1.94055	8	3	5	0.25	0.018	RUSC1	ASH1L

chr1	+(155448563..155449146)	583	4.18167	10	6	4	0.2	0.033	RUSC1	ASH1L
chr1	+(155629711..155630605)	894	4.18167	19	10	9	0.0526316	0.46746266	MSTO1	YY1AP1
chr1	+(155717113..155717651)	538	0.94117	27	14	13	0.037037	0.5	MSTO2P	GON4L
chr1	+(155718904..155719437)	533	0.11833	23	11	12	0.0434783	0.45101732	MSTO2P	GON4L
chr1	+(155720256..155720844)	588	0.02727	20	13	7	0.3	0.01465918	MSTO2P	GON4L
chr1	+(155735853..155736541)	688	0.04473	24	12	12	0	0.00395589	MSTO2P	GON4L
chr1	+(155896637..155897155)	518	4.18167	6	4	2	0.3333333	0.067	RIT1	KIAA0907
chr1	+(156146410..156147088)	678	1.94055	13	6	7	0.0769231	0.0992714	SEMA4A	SLC25A44
chr1	+(156169492..156170192)	700	0.94117	11	4	7	0.2727273	0.464	SLC25A44	PMF1
chr1	+(156221060..156221610)	550	4.18167	6	4	2	0.3333333	0.067	PAQR6	SMG5
chr1	+(156347871..156348387)	516	4.18167	8	4	4	0	0.014	RHBG	C1orf61
chr1	+(156556482..156557179)	697	0.94117	9	6	3	0.3333333	0.274	TTC24	APOA1BP
chr1	+(156562052..156562559)	507	1.94055	10	6	4	0.2	0.033	APOA1BP	GPATCH4
chr1	+(156701932..156702469)	537	4.18167	6	3	3	0	0.05	C1orf66	MRPL24
chr1	+(156811437..156812047)	610	0.06522	15	9	6	0.2	0.00160811	NTRK1	INSRR
chr1	+(156844118..156844700)	582	0.94117	12	7	5	0.1666667	0.00926649	INSRR	PEAR1
chr1	+(158587660..158588245)	585	1.94055	10	6	4	0.2	0.005	OR10Z1	SPTA1
chr1	+(159894746..159895377)	631	4.18167	6	3	3	0	0.05	CCDC19	TAGLN2
chr1	+(160011315..160011914)	599	0.94117	15	7	8	0.0666667	0.01862128	PIGM	KCNJ10
chr1	+(160133896..160134400)	504	4.18167	10	4	6	0.2	0.005	ATP1A4	CASQ1
chr1	+(160325642..160326420)	778	4.18167	13	9	4	0.3846154	0.053	NCSTN	NHLH1
chr1	+(160380049..160380749)	700	0.46268	9	6	3	0.3333333	0.012	VANGL2	SLAMF6
chr1	+(161026001..161026659)	658	0.94117	8	4	4	0	0.014	USF1	ARHGAP30
chr1	+(161167318..161167839)	521	1.94055	12	5	7	0.1666667	0.34237168	B4GALT3	ADAMTS4
chr1	+(161228762..161229409)	647	4.18167	6	4	2	0.3333333	0.067	PCP4L1	MPZ
chr1	+(161599237..161599771)	534	4.18167	9	3	6	0.3333333	0.048	HSPA7	FCGR3B
chr1	+(161632898..161633423)	525	1.94055	12	6	6	0	0.1000924	FCGR3B	FCGR2B
chr1	+(161641003..161641519)	516	0.46268	25	16	9	0.28	0.05031556	FCGR2B	RPL31P11
chr1	+(161642573..161643130)	557	0.22348	13	9	4	0.3846154	0.006	FCGR2B	RPL31P11
chr1	+(161829789..161830290)	501	4.18167	9	3	6	0.3333333	0.012	ATF6	OLFML2B
chr1	+(162326494..162327194)	700	0.22348	10	5	5	0	0.00451172	MIR556	C1orf111
chr1	+(162343736..162344413)	677	0.94117	14	8	6	0.1428571	0.39812671	MIR556	C1orf111
chr1	+(162482239..162482807)	568	4.18167	11	4	7	0.2727273	0.082	UHMK1	UAP1
chr1	+(162567159..162567798)	639	0.22348	10	5	5	0	0.00451172	UAP1	DDR2

chr1	+(162740140..162740645)	505	4.18167	11	7	4	0.2727273	0.206	DDR2	HSD17B7	
chr1	+(162825345..162825906)	561	4.18167	9	6	3	0.3333333	0.19	HSD17B7	C1orf110	
chr1	+(164618962..164619665)	703	0.01616	16	7	9	0.125	0.00042755	PBX1	LMX1A	
chr1	+(165876761..165877286)	525	4.18167	6	4	2	0.3333333	0.067	UCK2	MIR3658	
chr1	+(167023722..167025496)	1774	1.94055	26	13	13	0	0.22856236	MAEL	GPA33	
chr1	+(167617480..167618851)	1371	1.94055	13	6	7	0.0769231	0.0013499	RCSD1	MPZL1	
chr1	+(167672247..167672875)	628	0.22348	10	4	6	0.2	0.005	RCSD1	MPZL1	
chr1	+(167742321..167743380)	1059	4.18167	13	6	7	0.0769231	0.0013499	MPZL1	ADCY10	
chr1	+(167764348..167765003)	655	0.46268	9	4	5	0.1111111	0.008	MPZL1	ADCY10	
chr1	+(168013750..168014350)	600	1.94055	8	3	5	0.25	0.018	DCAF6	GPR161	
chr1	+(169510225..169510733)	508	4.22001	34	19	15	0.1176471	0.05726672	SLC19A2	F5	
chr1	+(169679431..169679935)	504	4.18167	9	5	4	0.1111111	0.008	SELP	SELL	
chr1	+(169761537..169762076)	539	4.18167	8	3	5	0.25	0.196	SELE	C1orf156	
chr1	+(169798279..169798788)	509	4.18167	6	2	4	0.3333333	0.067	C1orf112	SCYL3	
chr1	+(171250991..171251567)	576	4.18167	9	3	6	0.3333333	0.19	FMO1	FMO4	
chr1	+(171486564..171487086)	522	4.18167	7	4	3	0.1428571	0.029	BAT2L2	MYOC	
chr1	+(171501519..171502157)	638	0.22348	15	7	8	0.0666667	0.01394527	BAT2L2	MYOC	
chr1	+(171560486..171561015)	529	4.18167	8	4	4	0	0.343	BAT2L2	MYOC	
chr1	+(171569897..171570468)	571	0.94117	8	4	4	0	0.014	BAT2L2	MYOC	
chr1	+(171953309..171953885)	576	4.18167	6	3	3	0	0.05	DNM3	MIR214	
chr1	+(172526651..172527302)	651	1.94055	12	7	5	0.1666667	0.53235847	C1orf9	FASLG	
chr1	+(173628316..173628916)	600	4.18167	11	6	5	0.0909091	0.00308495	SLC9A11	ANKRD45	
chr1	+(173714093..173714631)	538	4.18167	6	4	2	0.3333333	0.067	KLHL20	CENPL	
chr1	+(173799393..173800090)	697	0.46268	16	11	5	0.375	0.05022464	DARS2	LOC100506046	
chr1	+(175691011..175691663)	652	4.18167	9	6	3	0.3333333	0.012	KIAA0040	TNR	
chr1	+(176873360..176873967)	607	0.94117	8	4	4	0	0.014	PAPPA2	ASTN1	
chr1	+(177015248..177015948)	700	0.22348	10	3	7	0.4	0.008	PAPPA2	ASTN1	
chr1	+(178716253..178716757)	504	0.94117	12	4	8	0.3333333	0.055	RALGPS2	ANGPTL1	
chr1	+(179054732..179055238)	506	4.18167	11	5	6	0.0909091	0.10062131	TOR3A	ABL2	
chr1	+(180065348..180065950)	602	1.94055	11	4	7	0.2727273	0.158	CEP350	QSOX1	
chr1	+(180202907..180203415)	508	0.94117	8	4	4	0	0.014	LHX4	ACBD6	
chr1	+(181700030..181700730)	700	4.18167	8	3	5	0.25	0.018	CACNA1E	ZNF648	
chr1	+(186905638..186906992)	1354	1.94055	14	7	7	0	0.99912744	PLA2G4A	FAM5C	v
chr1	+(193116760..193117314)	554	4.18167	8	3	5	0.25	0.036	MIR1278	B3GALT2	

chr1	+(196800534..196801100)	566	1.94055	21	14	7	0.3333333	0.00288676	CFHR1	CFHR4
chr1	+(196883534..196884512)	978	0.01075	33	11	22	0.3333333	0.18987487	CFHR4	CFHR2
chr1	+(198681871..198682381)	510	4.18167	10	4	6	0.2	0.005	PTPRC	MIR181B1
chr1	+(200534338..200535001)	663	0.94117	11	5	6	0.0909091	0.00881105	ZNF281	KIF14
chr1	+(200959702..200960402)	700	0.06522	17	8	9	0.0588235	0.19323812	C1orf106	KIF21B
chr1	+(201061038..201061738)	700	0.94117	9	6	3	0.3333333	0.274	KIF21B	CACNA1S
chr1	+(201072535..201073087)	552	4.18167	11	5	6	0.0909091	0.03394459	KIF21B	CACNA1S
chr1	+(201253652..201254427)	775	0.01616	14	9	5	0.2857143	0.0013499	PKP1	TNNT2
chr1	+(201300821..201301515)	694	0.46268	9	3	6	0.3333333	0.012	PKP1	TNNT2
chr1	+(202092055..202092651)	596	0.06522	16	5	11	0.375	0.14091036	GPR37L1	ARL8A
chr1	+(202146096..202146640)	544	1.94055	7	3	4	0.1428571	0.029	PTPRVP	LGR6
chr1	+(202152005..202152709)	704	0.46268	13	9	4	0.3846154	0.001	PTPRVP	LGR6
chr1	+(202287854..202288526)	672	0.94117	11	4	7	0.2727273	0.206	LGR6	UBE2T
chr1	+(203052734..203053434)	700	0.11833	16	5	11	0.375	0.19775658	PPFIA4	MYOG
chr1	+(203054834..203055482)	648	0.11833	11	5	6	0.0909091	0.00308495	PPFIA4	MYOG
chr1	+(203134106..203134716)	610	4.18167	6	4	2	0.3333333	0.067	ADORA1	MYBPH
chr1	+(203455668..203456368)	700	0.46268	9	3	6	0.3333333	0.012	PRELP	OPTC
chr1	+(204228457..204229063)	606	4.18167	12	4	8	0.3333333	0.341	GOLT1A	PLEKHA6
chr1	+(204506978..204507578)	600	4.18167	9	6	3	0.3333333	0.131	MDM4	LRRN2
chr1	+(204587618..204588467)	849	1.94055	13	4	9	0.3846154	0.02	MDM4	LRRN2
chr1	+(204760654..204761354)	700	0.22348	15	5	10	0.3333333	0.99890018	LRRN2	NFASC
chr1	+(204944177..204944691)	514	4.18167	6	3	3	0	0.05	NFASC	CNTN2
chr1	+(204966200..204966760)	560	0.46268	10	4	6	0.2	0.005	NFASC	CNTN2
chr1	+(205018609..205019227)	618	0.46268	9	4	5	0.1111111	0.008	CNTN2	TMEM81
chr1	+(205487661..205488361)	700	0.11833	15	5	10	0.3333333	0.27014569	CDK18	LOC284578
chr1	+(205495612..205496160)	548	4.18167	6	4	2	0.3333333	0.067	CDK18	LOC284578
chr1	+(205817009..205817516)	507	1.94055	10	7	3	0.4	0.008	SLC41A1	PM20D1
chr1	+(206318919..206319450)	531	0.22348	13	5	8	0.2307692	0.0017074	CTSE	SRGAP2
chr1	+(206324999..206325619)	620	1.94055	11	6	5	0.0909091	0.00308495	CTSE	SRGAP2
chr1	+(206515756..206516714)	958	0.22348	61	38	23	0.2459016	0.00733301	CTSE	SRGAP2
chr1	+(206579696..206580281)	585	3.70843	30	15	15	0	0.00016671	SRGAP2	IKBKE
chr1	+(206642851..206644117)	1266	4.18167	12	6	6	0	0.00197388	SRGAP2	IKBKE
chr1	+(206651002..206651926)	924	0.02727	22	14	8	0.2727273	0.97200196	IKBKE	RASSF5
chr1	+(206776273..206776858)	585	4.18167	12	6	6	0	0.96091545	RASSF5	LGTN

chr1	+(206831363..206832059)	696	4.18167	11	5	6	0.0909091	0.99691505	DYRK3	MAPKAPK2
chr1	+(206905073..206905609)	536	1.58044	13	4	9	0.3846154	0.001	MAPKAPK2	IL10
chr1	+(207072389..207072965)	576	0.46268	9	4	5	0.1111111	0.008	IL24	FAIM3
chr1	+(207104904..207105409)	505	4.18167	12	7	5	0.1666667	0.53235847	FAIM3	PIGR
chr1	+(207731772..207732341)	569	4.18167	12	6	6	0	0.07477068	CR1	CR1L
chr1	+(207733966..207734495)	529	4.18167	16	8	8	0	0.70024491	CR1	CR1L
chr1	+(207741186..207741722)	536	1.94055	9	6	3	0.3333333	0.048	CR1	CR1L
chr1	+(207743223..207743727)	504	4.18167	13	6	7	0.0769231	0.07656373	CR1	CR1L
chr1	+(207753671..207754181)	510	4.18167	9	6	3	0.3333333	0.274	CR1	CR1L
chr1	+(207828261..207828812)	551	4.18167	6	4	2	0.3333333	0.067	CR1L	CD46
chr1	+(211033964..211034487)	523	4.18167	6	3	3	0	0.05	HHAT	KCNH1
chr1	+(211976436..211977051)	615	0.46268	9	4	5	0.1111111	0.008	NEK2	LPGAT1
chr1	+(214505111..214505678)	567	4.18167	6	4	2	0.3333333	0.067	SMYD2	PTPN14
chr1	+(214802023..214802542)	519	0.94117	13	5	8	0.2307692	0.00958624	CENPF	KCNK2
chr1	+(214824770..214825308)	538	0.94117	15	7	8	0.0666667	0.08245742	CENPF	KCNK2
chr1	+(215802112..215802644)	532	4.18167	11	6	5	0.0909091	0.05017413	KCTD3	USH2A
chr1	+(215823690..215824233)	543	4.18167	6	4	2	0.3333333	0.067	KCTD3	USH2A
chr1	+(217207831..217208373)	542	4.18167	6	2	4	0.3333333	0.067	USH2A	ESRRG
chr1	+(217312766..217313894)	1128	4.18167	12	6	6	0	0.00197388	ESRRG	GPATCH2
chr1	+(220174482..220174999)	517	1.94055	12	7	5	0.1666667	0.00224163	SLC30A10	EPRS
chr1	+(220363047..220363549)	502	4.18167	10	5	5	0	0.03790009	MIR194-1	RAB3GAP2
chr1	+(220375444..220376023)	579	0.94117	12	8	4	0.3333333	0.99671074	MIR194-1	RAB3GAP2
chr1	+(220754139..220754836)	697	0.94117	12	7	5	0.1666667	0.00926649	MARK1	C1orf115
chr1	+(220969813..220970483)	670	0.46268	9	4	5	0.1111111	0.008	MOSC1	HLX
chr1	+(223396582..223397226)	644	0.94117	8	3	5	0.25	0.018	TLR5	SUSD4
chr1	+(223400789..223401304)	515	4.18167	9	3	6	0.3333333	0.988	TLR5	SUSD4
chr1	+(223943258..223943910)	652	1.94055	10	7	3	0.4	0.258	CAPN2	TP53BP2
chr1	+(223959158..223959845)	687	4.18167	9	3	6	0.3333333	0.024	CAPN2	TP53BP2
chr1	+(225155007..225155532)	525	0.22348	10	6	4	0.2	0.005	DNAH14	LBR
chr1	+(225452908..225453414)	506	4.18167	9	4	5	0.1111111	0.032	DNAH14	LBR
chr1	+(226061740..226062414)	674	0.94117	12	4	8	0.3333333	0.00328926	EPHX1	TMEM63A
chr1	+(226587951..226588651)	700	0.94117	12	4	8	0.3333333	0.00328926	LIN9	PARP1
chr1	+(226871660..226872511)	851	0.06522	12	6	6	0	0.00197388	C1orf95	ITPKB
chr1	+(226987267..226987967)	700	1.94055	11	4	7	0.2727273	0.997	ITPKB	PSEN2

chr1	+(227075620..227076197)	577	4.18167	8	3	5	0.25	0.036	PSEN2	ADCK3
chr1	+(227127875..227128488)	613	1.94055	7	3	4	0.1428571	0.029	PSEN2	ADCK3
chr1	+(227452422..227452975)	553	4.18167	9	5	4	0.1111111	0.032	ADCK3	CDC42BPA
chr1	+(227668628..227670012)	1384	1.94055	15	8	7	0.0666667	0.00059687	CDC42BPA	ZNF678
chr1	+(228204502..228205202)	700	0.22348	13	5	8	0.2307692	0.0017074	WNT3A	ARF1
chr1	+(228272209..228272909)	700	0.22348	10	3	7	0.4	0.008	ARF1	MIR3620
chr1	+(228431929..228432432)	503	4.18167	10	5	5	0	0.12529603	OBSCN	TRIM11
chr1	+(228459729..228460268)	539	0.94117	9	6	3	0.3333333	0.012	OBSCN	TRIM11
chr1	+(228476129..228476741)	612	1.94055	10	4	6	0.2	0.019	OBSCN	TRIM11
chr1	+(228553928..228554431)	503	1.94055	8	4	4	0	0.014	OBSCN	TRIM11
chr1	+(229567079..229567621)	542	0.46268	13	8	5	0.2307692	0.00641335	C1orf96	ACTA1
chr1	+(230020456..230020991)	535	1.94055	10	3	7	0.4	0.008	URB2	GALNT2
chr1	+(230385776..230386413)	637	4.18167	10	4	6	0.2	0.01	GALNT2	PGBD5
chr1	+(230416388..230416910)	522	4.18167	10	6	4	0.2	0.005	GALNT2	PGBD5
chr1	+(230454840..230456110)	1270	0.94117	16	8	8	0	0.99961123	GALNT2	PGBD5
chr1	+(230479927..230480627)	700	0.46268	9	3	6	0.3333333	0.012	GALNT2	PGBD5
chr1	+(231156523..231157110)	587	0.94117	8	4	4	0	0.014	ARV1	FAM89A
chr1	+(231696643..231697490)	847	0.94117	22	12	10	0.0909091	0.62918298	TSNAX-DISC1	LOC100287814
chr1	+(232538768..232539270)	502	4.18167	7	3	4	0.1428571	0.029	DISC2	SIPA1L2
chr1	+(232550262..232550785)	523	0.94117	9	3	6	0.3333333	0.083	DISC2	SIPA1L2
chr1	+(235772687..235773893)	1206	4.18167	12	6	6	0	0.00197388	B3GALNT2	GNG4
chr1	+(235897391..235897896)	505	4.18167	8	5	3	0.25	0.018	GNG4	LYST
chr1	+(235940371..235940882)	511	4.18167	9	5	4	0.1111111	0.548	GNG4	LYST
chr1	+(236176492..236177145)	653	0.46268	10	5	5	0	0.00451172	MIR1537	NID1
chr1	+(236751201..236751752)	551	4.18167	7	3	4	0.1428571	0.029	LOC100287902	HEATR1
chr1	+(236922831..236923337)	506	4.18167	6	4	2	0.3333333	0.067	ACTN2	MTR
chr1	+(237059051..237059815)	764	0.00319	20	11	9	0.1	8.472E-05	MTR	RYR2
chr1	+(237527427..237527989)	562	0.11833	18	11	7	0.2222222	0.0002444	RYR2	LOC100130331
chr1	+(237733855..237735129)	1274	0.46268	16	10	6	0.25	0.99943095	RYR2	LOC100130331
chr1	+(237791258..237792147)	889	0.00319	19	11	8	0.1578947	0.00013997	RYR2	LOC100130331
chr1	+(237801647..237802627)	980	0.94117	21	13	8	0.2380952	0.00236841	RYR2	LOC100130331
chr1	+(237958326..237958858)	532	1.94055	8	5	3	0.25	0.018	RYR2	LOC100130331
chr1	+(237969229..237969739)	510	4.18167	10	4	6	0.2	0.057	RYR2	LOC100130331
chr1	+(240491734..240492421)	687	0.46268	9	3	6	0.3333333	0.012	FMN2	GREM2

chr1	+(241031773..241032301)	528	1.94055	11	7	4	0.2727273	0.206	GREM2	RGS7	
chr1	+(241307813..241308377)	564	4.18167	10	4	6	0.2	0.995	GREM2	RGS7	
chr1	+(243449318..243449819)	501	4.18167	12	5	7	0.1666667	0.08373231	SDCCAG8	AKT3	
chr1	+(243578867..243579455)	588	0.11833	13	5	8	0.2307692	0.02851994	SDCCAG8	AKT3	
chr1	+(243623274..243624180)	906	0.94117	15	8	7	0.0666667	0.00059687	SDCCAG8	AKT3	
chr1	+(243776791..243777481)	690	0.22348	17	9	8	0.0588235	0.00037875	SDCCAG8	AKT3	
chr1	+(244220144..244220664)	520	1.94055	11	5	6	0.0909091	0.02230486	ZNF238	C1orf100	
chr1	+(244852357..244852860)	503	1.94055	12	5	7	0.1666667	0.40377055	PPPDE1	FAM36A	
chr1	+(245332192..245332737)	545	0.46268	9	4	5	0.1111111	0.008	KIF26B	SMYD3	
chr1	+(245333283..245333873)	590	4.18167	6	4	2	0.3333333	0.067	KIF26B	SMYD3	
chr1	+(246155950..246157089)	1139	0.02727	21	13	8	0.2380952	0.99991702	KIF26B	SMYD3	
chr1	+(246739076..246740712)	1636	0.11833	25	14	11	0.12	0.99998753	CNST	SCCPDH	
chr1	+(247023984..247024595)	611	4.18167	6	2	4	0.3333333	0.067	LOC149134	AHCTF1	
chr1	+(247025332..247026016)	684	0.94117	12	7	5	0.1666667	0.53235847	LOC149134	AHCTF1	
chr1	+(247057689..247058258)	569	4.18167	10	4	6	0.2	0.005	LOC149134	AHCTF1	
chr1	+(248099444..248100115)	671	0.94117	8	4	4	0	0.014	OR2T8	OR2L13	
chr1	+(248246735..248247274)	539	0.22348	19	9	10	0.0526316	0.95679462	OR2L3	OR2M1P	
chr1	+(248262645..248263297)	652	4.18167	13	5	8	0.2307692	0.02021199	OR2L3	OR2M1P	
chr1	+(248343618..248344162)	544	1.94055	13	9	4	0.3846154	0.53	OR2M2	OR2M3	v
chr1	+(248366092..248366604)	512	4.18167	17	11	6	0.2941176	0.42034633	OR2M2	OR2M3	v
chr1	+(248402582..248403114)	532	0.94117	12	5	7	0.1666667	0.01417552	OR2M4	OR2T33	
chr2	+(464665..465187)	522	4.63887	6	3	3	0	0.05	FAM150B	TMEM18	
chr2	+(565078..565765)	687	0.64523	9	5	4	0.1111111	0.008	FAM150B	TMEM18	
chr2	+(669421..669983)	562	1.21424	9	6	3	0.3333333	0.012	FAM150B	TMEM18	
chr2	+(1421533..1422211)	678	4.63887	6	3	3	0	0.05	TPO	PXDN	
chr2	+(1566169..1566866)	697	0.325	10	6	4	0.2	0.005	TPO	PXDN	
chr2	+(1724547..1725247)	700	0.64523	9	3	6	0.3333333	0.012	TPO	PXDN	
chr2	+(1991020..1991720)	700	0.18049	12	5	7	0.1666667	0.00224163	PXDN	MYT1L	
chr2	+(1997790..1998344)	554	2.33844	7	3	4	0.1428571	0.029	PXDN	MYT1L	
chr2	+(2760688..2761310)	622	2.33844	7	4	3	0.1428571	0.029	LOC730811	TSSC1	
chr2	+(2796186..2797028)	842	0.08723	21	9	12	0.1428571	0.00525762	LOC730811	TSSC1	
chr2	+(2799187..2799887)	700	0.325	10	4	6	0.2	0.005	LOC730811	TSSC1	
chr2	+(2838850..2839550)	700	1.21424	13	8	5	0.2307692	0.0017074	LOC730811	TSSC1	
chr2	+(2853340..2853971)	631	0.04989	13	9	4	0.3846154	0.001	LOC730811	TSSC1	

chr2	+(3038819..3039521)	702	0.18049	12	8	4	0.3333333	0.99671074	LOC730811	TSSC1
chr2	+(3044800..3045372)	572	2.33844	10	7	3	0.4	0.992	LOC730811	TSSC1
chr2	+(3058530..3059089)	559	4.63887	6	2	4	0.3333333	0.067	LOC730811	TSSC1
chr2	+(3212311..3212832)	521	2.33844	9	3	6	0.3333333	0.083	LOC730811	TSSC1
chr2	+(3254758..3255317)	559	4.63887	6	3	3	0	0.05	LOC730811	TSSC1
chr2	+(3260379..3261329)	950	3.0624	23	10	13	0.1304348	2.7755E-05	LOC730811	TSSC1
chr2	+(3267073..3267662)	589	2.33844	7	3	4	0.1428571	0.029	LOC730811	TSSC1
chr2	+(3288247..3288760)	513	2.33844	7	4	3	0.1428571	0.029	LOC730811	TSSC1
chr2	+(3298917..3299730)	813	0.18049	12	7	5	0.1666667	0.00224163	LOC730811	TSSC1
chr2	+(3309171..3309871)	700	0.64523	13	9	4	0.3846154	0.999	LOC730811	TSSC1
chr2	+(3681416..3682116)	700	0.18049	11	5	6	0.0909091	0.00308495	COLEC11	ALLC
chr2	+(5350891..5351672)	781	0.0149	15	8	7	0.0666667	0.00059687	LOC727982	SOX11
chr2	+(5835029..5835533)	504	4.63887	10	6	4	0.2	0.176	SOX11	LOC150622
chr2	+(6105161..6105663)	502	4.63887	6	4	2	0.3333333	0.067	LOC150622	LOC400940
chr2	+(9034712..9035306)	594	1.21424	8	4	4	0	0.014	KIDINS220	MBOAT2
chr2	+(9398852..9399551)	699	0.325	10	7	3	0.4	0.008	ASAP2	ITGB1BP1
chr2	+(9463035..9463579)	544	4.63887	6	2	4	0.3333333	0.067	ASAP2	ITGB1BP1
chr2	+(9573827..9574328)	501	4.63887	7	4	3	0.1428571	0.029	CPSF3	IAH1
chr2	+(9576130..9576647)	517	4.63887	9	4	5	0.1111111	0.143	CPSF3	IAH1
chr2	+(10199763..10200384)	621	2.33844	7	3	4	0.1428571	0.029	KLF11	CYS1
chr2	+(10260191..10260925)	734	0.18049	18	10	8	0.1111111	0.0038429	CYS1	RRM2
chr2	+(10262673..10263278)	605	4.63887	7	3	4	0.1428571	0.029	CYS1	RRM2
chr2	+(10281750..10282326)	576	4.63887	8	5	3	0.25	0.125	C2orf48	MIR4261
chr2	+(10283202..10283891)	689	4.63887	6	3	3	0	0.05	C2orf48	MIR4261
chr2	+(10284706..10285406)	700	0.64523	9	3	6	0.3333333	0.012	C2orf48	MIR4261
chr2	+(11358874..11359383)	509	4.63887	9	5	4	0.1111111	0.032	PQLC3	ROCK2
chr2	+(11397238..11397739)	501	2.33844	7	3	4	0.1428571	0.029	PQLC3	ROCK2
chr2	+(11448237..11448833)	596	2.33844	11	5	6	0.0909091	0.10062131	PQLC3	ROCK2
chr2	+(11730860..11731501)	641	4.63887	7	4	3	0.1428571	0.2	GREB1	NTSR2
chr2	+(11732810..11733358)	548	2.33844	7	4	3	0.1428571	0.029	GREB1	NTSR2
chr2	+(11924553..11925332)	779	0.03019	14	6	8	0.1428571	0.00097289	LPIN1	MIR4262
chr2	+(15731477..15732539)	1062	0.64523	22	8	14	0.2727273	0.01447835	NBAS	DDX1
chr2	+(15760947..15761470)	523	4.63887	6	4	2	0.3333333	0.067	DDX1	MYCNOS
chr2	+(15947854..15949033)	1179	1.21424	14	7	7	0	0.98732634	DDX1	MYCNOS

chr2	+(17695076..17695624)	548	1.21424	10	3	7	0.4	0.008	FAM49A	RAD51AP2	
chr2	+(17864509..17865202)	693	0.64523	13	4	9	0.3846154	0.02	VSNL1	SMC6	
chr2	+(19556159..19556707)	548	2.33844	11	5	6	0.0909091	0.81934478	NT5C1B	OSR1	v
chr2	+(19853037..19853737)	700	0.325	11	4	7	0.2727273	0.003	OSR1	FLJ12334	v
chr2	+(20078213..20078913)	700	1.21424	11	7	4	0.2727273	0.003	FLJ12334	TTC32	
chr2	+(20101283..20101922)	639	0.08723	12	8	4	0.3333333	0.99671074	FLJ12334	TTC32	
chr2	+(20305268..20306510)	1242	0.08723	23	12	11	0.0434783	0.99997567	LAPTM4A	SDC1	
chr2	+(20404064..20404764)	700	1.21424	11	6	5	0.0909091	0.00308495	LAPTM4A	SDC1	
chr2	+(20412432..20413426)	994	2.33844	16	7	9	0.125	0.13318996	LAPTM4A	SDC1	
chr2	+(20454415..20455003)	588	2.33844	11	5	6	0.0909091	0.00308495	SDC1	PUM2	
chr2	+(21102055..21102770)	715	0.00246	20	11	9	0.1	0.00172235	C2orf43	APOB	
chr2	+(21245502..21246007)	505	4.63887	6	2	4	0.3333333	0.067	C2orf43	APOB	
chr2	+(21251169..21251744)	575	4.63887	10	6	4	0.2	0.086	C2orf43	APOB	
chr2	+(21362564..21363073)	509	4.63887	10	4	6	0.2	0.129	APOB	KLHL29	
chr2	+(23437431..23438131)	700	0.08723	13	5	8	0.2307692	0.0017074	APOB	KLHL29	
chr2	+(23609340..23609856)	516	2.33844	7	4	3	0.1428571	0.029	KLHL29	ATAD2B	
chr2	+(23679592..23680315)	723	1.21424	14	8	6	0.1428571	0.00097289	KLHL29	ATAD2B	
chr2	+(23712677..23713339)	662	2.33844	10	4	6	0.2	0.457	KLHL29	ATAD2B	
chr2	+(23771780..23772480)	700	0.64523	12	8	4	0.3333333	0.99671074	KLHL29	ATAD2B	
chr2	+(23834019..23834719)	700	0.00954	16	5	11	0.375	0.0009184	KLHL29	ATAD2B	
chr2	+(24432387..24433004)	617	4.63887	8	3	5	0.25	0.018	C2orf84	ITSN2	
chr2	+(25083370..25083887)	517	4.63887	9	5	4	0.1111111	0.635	CENPO	ADCY3	
chr2	+(25213884..25214508)	624	2.33844	11	5	6	0.0909091	0.00308495	LOC729723	EFR3B	
chr2	+(25513806..25514400)	594	4.63887	6	4	2	0.3333333	0.067	POMC	DNMT3A	
chr2	+(25519064..25520045)	981	0.18049	20	12	8	0.2	0.26854699	POMC	DNMT3A	
chr2	+(25994205..25994810)	605	4.63887	10	6	4	0.2	0.019	DTNB	ASXL2	
chr2	+(26532561..26533091)	530	2.33844	10	3	7	0.4	0.008	HADHB	GPR113	
chr2	+(26705016..26705865)	849	0.04989	19	6	13	0.3684211	0.00327517	C2orf39	OTOF	
chr2	+(26784347..26784948)	601	4.63887	6	2	4	0.3333333	0.067	OTOF	C2orf70	
chr2	+(26799714..26800627)	913	2.33844	13	5	8	0.2307692	0.92838254	C2orf70	CIB4	
chr2	+(26852124..26852778)	654	4.63887	6	2	4	0.3333333	0.067	C2orf70	CIB4	
chr2	+(26943225..26944443)	1218	0.64523	15	9	6	0.2	0.99926864	KCNK3	C2orf18	
chr2	+(27033094..27033794)	700	0.64523	9	3	6	0.3333333	0.012	CENPA	DPYSL5	
chr2	+(27121201..27121702)	501	3.0624	19	6	13	0.3684211	0.98870655	DPYSL5	MAPRE3	

chr2	+(27263247..27263788)	541	4.63887	10	7	3	0.4	0.008	TMEM214	AGBL5	
chr2	+(27360280..27360789)	509	2.33844	8	3	5	0.25	0.286	PREB	C2orf53	
chr2	+(27423228..27423772)	544	2.33844	8	4	4	0	0.171	TCF23	SLC5A6	
chr2	+(27465496..27466535)	1039	0.08723	18	10	8	0.1111111	0.96221971	CAD	SLC30A3	
chr2	+(27804685..27805237)	552	1.21424	17	7	10	0.1764706	0.1207833	C2orf16	ZNF512	
chr2	+(27887872..27888381)	509	4.63887	7	3	4	0.1428571	0.029	SLC4A1AP	MRPL33	v
chr2	+(28544998..28545698)	700	0.325	12	4	8	0.3333333	0.00328926	MIR4263	FOSL2	
chr2	+(28561072..28562047)	975	0.64523	15	9	6	0.2	0.00073136	MIR4263	FOSL2	
chr2	+(29296613..29297232)	619	2.33844	14	9	5	0.2857143	0.42074029	FAM179A	C2orf71	
chr2	+(29452277..29452975)	698	0.325	14	7	7	0	0.67263958	CLIP4	ALK	
chr2	+(31146993..31147510)	517	4.63887	11	6	5	0.0909091	0.29194121	CAPN13	GALNT14	
chr2	+(32191308..32191830)	522	1.21424	8	5	3	0.25	0.018	SRD5A2	MEMO1	
chr2	+(32427731..32428297)	566	4.63887	8	4	4	0	0.443	SLC30A6	NLRC4	
chr2	+(32875027..32875573)	546	1.21424	12	8	4	0.3333333	0.99671074	TTC27	LOC285045	
chr2	+(33572027..33572953)	926	1.21424	15	8	7	0.0666667	0.24372665	LTBP1	RASGRP3	
chr2	+(33813305..33813864)	559	4.63887	6	2	4	0.3333333	0.067	RASGRP3	FAM98A	
chr2	+(36805758..36806272)	514	4.63887	8	4	4	0	0.014	CRIM1	FEZ2	
chr2	+(37113729..37114238)	509	3.0624	16	11	5	0.375	0.05022464	VIT	STRN	
chr2	+(37129572..37130108)	536	4.63887	6	4	2	0.3333333	0.067	VIT	STRN	
chr2	+(37310783..37311470)	687	2.33844	7	3	4	0.1428571	0.029	STRN	HEATR5B	
chr2	+(37455448..37456053)	605	2.33844	9	3	6	0.3333333	0.452	SULT6B1	CEBPZ	
chr2	+(39192869..39193978)	1109	0.64523	15	9	6	0.2	0.99890848	LOC375196	SOS1	
chr2	+(42580142..42580644)	502	4.63887	6	2	4	0.3333333	0.067	EML4	COX7A2L	
chr2	+(42587611..42588311)	700	2.33844	11	4	7	0.2727273	0.997	EML4	COX7A2L	
chr2	+(42676446..42677146)	700	2.33844	12	5	7	0.1666667	0.00224163	COX7A2L	KCNG3	
chr2	+(43793283..43793813)	530	0.64523	13	5	8	0.2307692	0.05367327	LOC100129726	THADA	
chr2	+(43819099..43819647)	548	2.33844	8	5	3	0.25	0.071	LOC100129726	THADA	
chr2	+(43980572..43981128)	556	4.63887	8	3	5	0.25	0.018	LOC728819	DYNC2LI1	
chr2	+(44201035..44201566)	531	2.33844	10	6	4	0.2	0.019	ABCG8	LRPPRC	
chr2	+(44457561..44458102)	541	2.33844	10	7	3	0.4	0.058	PPM1B	SLC3A1	
chr2	+(45879946..45880646)	700	4.63887	11	6	5	0.0909091	0.99691505	PRKCE	EPAS1	
chr2	+(46788730..46789545)	815	0.03019	14	7	7	0	0.00087256	RHOQ	PIGF	
chr2	+(46985981..46986584)	603	4.63887	12	5	7	0.1666667	0.40377055	SOCS5	LOC388948	
chr2	+(47135939..47136475)	536	4.63887	6	2	4	0.3333333	0.067	LOC100134259	MCFD2	

chr2	+(47183612..47184298)	686	1.21424	9	4	5	0.1111111	0.016	TTC7A	C2orf61	
chr2	+(47185766..47186357)	591	4.63887	8	4	4	0	0.443	TTC7A	C2orf61	
chr2	+(47213507..47214094)	587	1.21424	8	4	4	0	0.014	TTC7A	C2orf61	
chr2	+(47215897..47216490)	593	0.64523	13	5	8	0.2307692	0.0017074	TTC7A	C2orf61	
chr2	+(47880776..47881670)	894	0.08723	17	9	8	0.0588235	0.000266	KCNK12	MSH6	
chr2	+(48033342..48033878)	536	1.21424	8	5	3	0.25	0.018	MSH6	FBXO11	
chr2	+(48915137..48915688)	551	4.63887	8	4	4	0	0.057	GTF2A1L	LHCGR	
chr2	+(54021310..54021819)	509	4.63887	7	4	3	0.1428571	0.029	ASB3	LOC100302652	
chr2	+(54114398..54114921)	523	4.63887	12	8	4	0.3333333	0.533	GPR75	PSME4	
chr2	+(55105284..55105984)	700	0.18049	11	4	7	0.2727273	0.003	EML6	RTN4	
chr2	+(55253710..55254225)	515	4.63887	6	3	3	0	0.05	EML6	RTN4	
chr2	+(55535918..55536458)	540	1.21424	15	5	10	0.3333333	0.13517207	PRORSD1P	CCDC88A	
chr2	+(61148742..61149327)	585	4.63887	7	4	3	0.1428571	0.2	REL	PUS10	
chr2	+(61652360..61652944)	584	4.63887	6	4	2	0.3333333	0.067	AHSA2	USP34	
chr2	+(61715539..61716071)	532	2.33844	10	5	5	0	0.01414006	SNORA70B	XPO1	
chr2	+(61719273..61719783)	510	4.63887	11	7	4	0.2727273	0.536	SNORA70B	XPO1	
chr2	+(61958710..61959484)	774	0.04989	13	6	7	0.0769231	0.0013499	XPO1	FAM161A	
chr2	+(62067178..62067729)	551	2.33844	14	7	7	0	0.24110135	XPO1	FAM161A	
chr2	+(63651140..63651840)	700	2.33844	14	7	7	0	0.00087256	DBIL5P2	C2orf86	
chr2	+(65237402..65237973)	571	4.63887	7	3	4	0.1428571	0.029	SLC1A4	CEP68	
chr2	+(67631527..67632406)	879	4.63887	13	7	6	0.0769231	0.95676186	ETAA1	C1D	
chr2	+(67960419..67961283)	864	1.21424	14	6	8	0.1428571	0.00097289	ETAA1	C1D	
chr2	+(68429672..68430325)	653	0.64523	9	5	4	0.1111111	0.008	PNO1	PPP3R1	
chr2	+(69409393..69409967)	574	0.18049	13	4	9	0.3846154	0.001	MIR3126	GFPT1	
chr2	+(69745847..69746428)	581	0.325	10	7	3	0.4	0.008	NFU1	AAK1	
chr2	+(69834933..69835911)	978	1.21424	15	8	7	0.0666667	0.00059687	NFU1	AAK1	
chr2	+(70213194..70213872)	678	4.63887	6	2	4	0.3333333	0.067	ASPRV1	LOC400960	
chr2	+(71012336..71012978)	642	0.64523	10	3	7	0.4	0.058	ADD2	FIGLA	
chr2	+(71039371..71039889)	518	4.63887	6	2	4	0.3333333	0.067	FIGLA	CLEC4F	
chr2	+(71792412..71793025)	613	0.64523	10	5	5	0	0.00451172	DYSF	CYP26B1	v
chr2	+(71869688..71870189)	501	2.33844	7	4	3	0.1428571	0.029	DYSF	CYP26B1	v
chr2	+(72109980..72110933)	953	0.325	16	6	10	0.25	0.00056905	DYSF	CYP26B1	v
chr2	+(72250752..72251820)	1068	4.63887	12	8	4	0.3333333	0.99671074	DYSF	CYP26B1	v
chr2	+(72361910..72362769)	859	4.63887	12	7	5	0.1666667	0.00224163	DYSF	CYP26B1	v

chr2	+(72370808..72371736)	928	0.64523	18	9	9	0	0.15493978	DYSF	CYP26B1	v
chr2	+(72410908..72411529)	621	4.63887	6	4	2	0.3333333	0.067	CYP26B1	EXOC6B	v
chr2	+(72460275..72461331)	1056	1.21424	20	11	9	0.1	0.45463452	CYP26B1	EXOC6B	v
chr2	+(72808627..72809327)	700	0.18049	11	6	5	0.0909091	0.00308495	CYP26B1	EXOC6B	v
chr2	+(73312285..73312985)	700	4.63887	9	6	3	0.3333333	0.988	SFXN5	RAB11FIP5	
chr2	+(73718320..73719490)	1170	1.21424	18	9	9	0	0.0015476	ALMS1	NAT8	
chr2	+(74372150..74372665)	515	2.33844	9	6	3	0.3333333	0.012	TET3	BOLA3	
chr2	+(74649929..74650436)	507	4.63887	6	3	3	0	0.05	WDR54	RTKN	
chr2	+(74687309..74687842)	533	0.64523	13	9	4	0.3846154	0.793	WBP1	MOGS	
chr2	+(74718276..74718780)	504	4.63887	10	5	5	0	0.02360089	TTC31	LBX2	
chr2	+(74855288..74855857)	569	0.64523	13	8	5	0.2307692	0.01405402	DOK1	C2orf65	
chr2	+(85292138..85292819)	681	4.63887	6	4	2	0.3333333	0.067	KCMF1	TCF7L1	v
chr2	+(85418425..85419203)	778	0.08723	12	6	6	0	0.00197388	TCF7L1	TGOLN2	v
chr2	+(85482359..85483059)	700	1.21424	10	3	7	0.4	0.008	TCF7L1	TGOLN2	v
chr2	+(85604122..85604822)	700	0.325	10	6	4	0.2	0.005	ELMOD3	CAPG	
chr2	+(85613659..85614359)	700	0.64523	10	3	7	0.4	0.258	ELMOD3	CAPG	
chr2	+(85661815..85662345)	530	4.63887	10	5	5	0	0.03790009	CAPG	SH2D6	
chr2	+(85672656..85673356)	700	0.64523	10	4	6	0.2	0.005	SH2D6	MAT2A	
chr2	+(85702692..85703392)	700	2.33844	9	3	6	0.3333333	0.012	SH2D6	MAT2A	
chr2	+(86278427..86279098)	671	2.33844	10	3	7	0.4	0.008	LOC90784	POLR1A	
chr2	+(86683535..86684049)	514	4.63887	12	6	6	0	0.05465729	KDM3A	VPS24	
chr2	+(86704854..86705374)	520	4.63887	10	7	3	0.4	0.008	KDM3A	VPS24	
chr2	+(88485921..88487057)	1136	1.21424	16	8	8	0	0.99961123	THNSL2	FOXI3	
chr2	+(89055609..89056143)	534	1.21424	8	5	3	0.25	0.018	RPIA	ANKRD36BP2	
chr2	+(89103789..89104378)	589	2.44321	42	28	14	0.3333333	7.5688E-05	ANKRD36BP2	LOC654342	
chr2	+(89148963..89149608)	645	4.63887	6	4	2	0.3333333	0.067	ANKRD36BP2	LOC654342	
chr2	+(89416855..89417434)	579	1.21424	16	10	6	0.25	0.74240941	ANKRD36BP2	LOC654342	
chr2	+(89512605..89513107)	502	4.63887	13	8	5	0.2307692	0.38484897	ANKRD36BP2	LOC654342	
chr2	+(89533676..89534249)	573	1.21424	16	10	6	0.25	0.58586873	ANKRD36BP2	LOC654342	
chr2	+(90160265..90160878)	613	4.63887	8	3	5	0.25	0.018	ANKRD36BP2	LOC654342	
chr2	+(91760286..91760985)	699	1.21424	12	8	4	0.3333333	0.99671074	ANKRD36BP2	LOC654342	
chr2	+(91762913..91763477)	564	2.33844	12	4	8	0.3333333	0.923	ANKRD36BP2	LOC654342	
chr2	+(91766199..91767131)	932	1.56697	44	25	19	0.1363636	2.1111E-07	ANKRD36BP2	LOC654342	
chr2	+(91778390..91778943)	553	1.21424	8	4	4	0	0.014	ANKRD36BP2	LOC654342	

chr2	+(91801078..91801778)	700	4.63887	9	6	3	0.3333333	0.988	ANKRD36BP2	LOC654342
chr2	+(91806491..91807247)	756	1.21424	14	6	8	0.1428571	0.00097289	ANKRD36BP2	LOC654342
chr2	+(91808791..91809326)	535	4.63887	11	5	6	0.0909091	0.29194121	ANKRD36BP2	LOC654342
chr2	+(95501392..95501902)	510	4.63887	10	4	6	0.2	0.005	ACTR3BP2	ANKRD20B
chr2	+(95522274..95523067)	793	0.00027	33	19	14	0.1515152	2.6355E-05	ACTR3BP2	ANKRD20B
chr2	+(95965244..95965789)	545	2.33844	7	4	3	0.1428571	0.029	KCNIP3	FAHD2A
chr2	+(95997252..95997786)	534	2.33844	7	3	4	0.1428571	0.029	KCNIP3	FAHD2A
chr2	+(96520822..96521335)	513	4.63887	10	5	5	0	0.23235105	TRIM43	LOC729234
chr2	+(96521481..96522004)	523	0.41287	23	14	9	0.2173913	0.00052702	TRIM43	LOC729234
chr2	+(96686626..96687137)	511	4.63887	8	5	3	0.25	0.036	LOC729234	GPAT2
chr2	+(96829038..96829853)	815	4.63887	12	6	6	0	0.00197388	DUSP2	STARD7
chr2	+(96860916..96861608)	692	0.325	13	8	5	0.2307692	0.02021199	DUSP2	STARD7
chr2	+(96943798..96944309)	511	4.63887	12	5	7	0.1666667	0.11161257	CIAO1	SNRNP200
chr2	+(97267902..97268411)	509	4.63887	9	6	3	0.3333333	0.726	ARID5A	KIAA1310
chr2	+(97545633..97546901)	1268	1.21424	14	6	8	0.1428571	0.00097289	SEMA4C	FAM178B
chr2	+(97616681..97617207)	526	0.64523	12	4	8	0.3333333	0.00328926	SEMA4C	FAM178B
chr2	+(97711725..97712280)	555	1.56697	26	9	17	0.3076923	0.00116275	FAM178B	FAHD2B
chr2	+(97877457..97877960)	503	4.63887	11	6	5	0.0909091	0.18065522	ANKRD36	ANKRD36B
chr2	+(97883050..97883560)	510	4.63887	10	5	5	0	0.05859256	ANKRD36	ANKRD36B
chr2	+(98041753..98042280)	527	4.63887	9	3	6	0.3333333	0.19	ANKRD36	ANKRD36B
chr2	+(98139722..98140250)	528	1.21424	11	7	4	0.2727273	0.115	ANKRD36	ANKRD36B
chr2	+(98169681..98170210)	529	2.33844	14	7	7	0	0.07085998	ANKRD36	ANKRD36B
chr2	+(99012201..99012716)	515	4.63887	7	3	4	0.1428571	0.029	CNGA3	INPP4A
chr2	+(99187584..99188474)	890	0.03019	14	8	6	0.1428571	0.00097289	INPP4A	C2orf64
chr2	+(99274267..99275150)	883	1.21424	14	5	9	0.2857143	0.0013499	UNC50	MGAT4A
chr2	+(99499651..99500351)	700	0.04989	15	5	10	0.3333333	0.00109982	MGAT4A	C2orf55
chr2	+(99634619..99635266)	647	4.63887	10	6	4	0.2	0.033	C2orf55	TSGA10
chr2	+(100081081..100081646)	565	4.63887	9	4	5	0.1111111	0.008	EIF5B	REV1
chr2	+(100486528..100487560)	1032	2.33844	13	9	4	0.3846154	0.926	REV1	AFF3
chr2	+(100759824..100760802)	978	2.33844	13	7	6	0.0769231	0.0013499	AFF3	LONRF2
chr2	+(100763661..100764361)	700	0.08723	12	4	8	0.3333333	0.00328926	AFF3	LONRF2
chr2	+(101182797..101183318)	521	4.63887	8	4	4	0	0.057	PDCL3	NPAS2
chr2	+(101437462..101437977)	515	4.63887	9	6	3	0.3333333	0.083	NPAS2	RPL31
chr2	+(102644083..102645068)	985	1.21424	15	7	8	0.0666667	0.00059687	IL1R2	IL1R1

chr2	+(105709640..105710555)	915	0.64523	18	7	11	0.2222222	0.00047372	MRPS9	GPR45
chr2	+(106987283..106987816)	533	4.63887	8	5	3	0.25	0.071	UXS1	PLGLA
chr2	+(107004083..107004585)	502	4.63887	11	6	5	0.0909091	0.07206352	PLGLA	RGPD3
chr2	+(107032076..107032578)	502	2.90131	23	12	11	0.0434783	0.00011092	PLGLA	RGPD3
chr2	+(107073022..107073987)	965	0.325	27	13	14	0.037037	4.2364E-05	PLGLA	RGPD3
chr2	+(107093739..107094288)	549	4.63887	6	3	3	0	0.05	RGPD3	ST6GAL2
chr2	+(107197062..107197702)	640	0.64523	9	5	4	0.1111111	0.008	RGPD3	ST6GAL2
chr2	+(108475235..108475752)	517	0.325	21	11	10	0.047619	0.00059928	RGPD4	SLC5A7
chr2	+(108477066..108477716)	650	2.90131	39	27	12	0.3846154	1.3393E-05	RGPD4	SLC5A7
chr2	+(108486873..108487560)	687	0.37718	42	13	29	0.3809524	2.5917E-06	RGPD4	SLC5A7
chr2	+(108488951..108489467)	516	4.63887	6	4	2	0.3333333	0.067	RGPD4	SLC5A7
chr2	+(109102055..109102638)	583	0.325	17	10	7	0.1764706	0.02021199	GCC2	LIMS1
chr2	+(109113085..109113598)	513	2.33844	12	5	7	0.1666667	0.03090926	GCC2	LIMS1
chr2	+(109275989..109276535)	546	2.33844	9	6	3	0.3333333	0.012	LIMS1	RANBP2
chr2	+(109347652..109348209)	557	0.00954	28	11	17	0.2142857	6.7686E-06	RANBP2	CCDC138
chr2	+(109365153..109365688)	535	1.56697	41	23	18	0.1219512	1.5058E-07	RANBP2	CCDC138
chr2	+(109367375..109368281)	906	0.24703	69	34	35	0.0144928	0.00239696	RANBP2	CCDC138
chr2	+(109369155..109369731)	576	2.44321	51	23	28	0.0980392	7.7726E-10	RANBP2	CCDC138
chr2	+(109370064..109370573)	509	4.6845	47	16	31	0.3191489	0.00021194	RANBP2	CCDC138
chr2	+(109371421..109372174)	753	0.08723	30	16	14	0.0666667	0.01111601	RANBP2	CCDC138
chr2	+(109388852..109389364)	512	4.63887	8	5	3	0.25	0.196	RANBP2	CCDC138
chr2	+(109900163..109900863)	700	2.33844	12	6	6	0	0.97266803	MIR4265	MIR4266
chr2	+(110068597..110069874)	1277	0.325	17	10	7	0.1764706	0.00031815	MIR4266	41162
chr2	+(110604957..110606021)	1064	0.08723	38	15	23	0.2105263	0.06202446	RGPD6_dup1	LIMS3_dup1
chr2	+(110663093..110663628)	535	1.21424	16	10	6	0.25	0.00056905	LIMS3-LOC440895_d	LOC100288570_dup1
chr2	+(111281000..111281560)	560	1.15269	36	20	16	0.1111111	4.7264E-07	LIMS3_dup2	RGPD6_dup2
chr2	+(112252194..112252736)	542	4.63887	11	7	4	0.2727273	0.206	BCL2L11	LOC541471
chr2	+(112416926..112417549)	623	0.08723	12	5	7	0.1666667	0.00224163	LOC541471	ANAPC1
chr2	+(112545441..112546326)	885	0.325	19	11	8	0.1578947	0.00013997	LOC541471	ANAPC1
chr2	+(112549978..112550482)	504	1.21424	12	8	4	0.3333333	0.99671074	LOC541471	ANAPC1
chr2	+(112607978..112608481)	503	4.63887	10	4	6	0.2	0.695	LOC541471	ANAPC1
chr2	+(112777907..112778513)	606	4.63887	10	4	6	0.2	0.129	MERTK	TMEM87B
chr2	+(112824361..112824864)	503	4.63887	6	4	2	0.3333333	0.067	TMEM87B	FBLN7
chr2	+(112897719..112898239)	520	2.33844	7	3	4	0.1428571	0.029	FBLN7	ZC3H8

chr2	+(113057317..113057951)	634	4.63887	11	6	5	0.0909091	0.13666084	ZC3H6	RGPD8
chr2	+(113145406..113145923)	517	2.33844	11	4	7	0.2727273	0.003	ZC3H6	RGPD8
chr2	+(113146361..113146958)	597	1.34515	26	11	15	0.1538462	0.00040765	ZC3H6	RGPD8
chr2	+(113155581..113156085)	504	4.63887	23	7	16	0.3913043	0.98083343	ZC3H6	RGPD8
chr2	+(113156373..113157351)	978	0.17743	66	36	30	0.0909091	2.3569E-05	ZC3H6	RGPD8
chr2	+(113159271..113159773)	502	4.6845	58	33	25	0.137931	9.6996E-08	ZC3H6	RGPD8
chr2	+(113163500..113164005)	505	3.30444	55	35	20	0.2727273	0.00130894	ZC3H6	RGPD8
chr2	+(113258439..113259126)	687	1.21424	16	6	10	0.25	0.00056905	TTL	POLR1B
chr2	+(113959554..113960185)	631	2.33844	7	3	4	0.1428571	0.029	IL1RN	LOC440839
chr2	+(114709121..114709626)	505	4.63887	10	6	4	0.2	0.129	ACTR3	LOC100499194
chr2	+(119739711..119740213)	502	1.21424	11	4	7	0.2727273	0.115	MARCO	C1QL2
chr2	+(119777491..119778042)	551	4.63887	6	2	4	0.3333333	0.067	MARCO	C1QL2
chr2	+(120903596..120904135)	539	0.08723	12	7	5	0.1666667	0.00224163	EPB41L5	TMEM185B
chr2	+(121319817..121320517)	700	0.64523	10	7	3	0.4	0.008	LOC84931	GLI2
chr2	+(121673823..121674523)	700	0.08723	13	5	8	0.2307692	0.01405402	GLI2	TFCP2L1
chr2	+(121710263..121710793)	530	1.21424	12	5	7	0.1666667	0.00224163	GLI2	TFCP2L1
chr2	+(121713191..121713805)	614	1.21424	8	5	3	0.25	0.018	GLI2	TFCP2L1
chr2	+(121722902..121723583)	681	4.63887	7	3	4	0.1428571	0.029	GLI2	TFCP2L1
chr2	+(121728048..121728748)	700	0.18049	12	7	5	0.1666667	0.00224163	GLI2	TFCP2L1
chr2	+(121741358..121742058)	700	2.33844	10	3	7	0.4	0.992	GLI2	TFCP2L1
chr2	+(121789191..121789995)	804	0.03019	26	14	12	0.0769231	7.784E-06	GLI2	TFCP2L1
chr2	+(121957854..121958786)	932	2.33844	14	7	7	0	0.00087256	GLI2	TFCP2L1
chr2	+(127555539..127556239)	700	0.08723	12	4	8	0.3333333	0.00328926	GYPC	BIN1
chr2	+(127580364..127581062)	698	2.33844	11	7	4	0.2727273	0.997	GYPC	BIN1
chr2	+(127812462..127813162)	700	4.63887	11	6	5	0.0909091	0.00308495	GYPC	BIN1
chr2	+(128323142..128323841)	699	0.325	10	6	4	0.2	0.005	MYO7B	LIMS2
chr2	+(128396869..128397569)	700	0.64523	9	3	6	0.3333333	0.012	MYO7B	LIMS2
chr2	+(128944862..128945380)	518	4.63887	7	3	4	0.1428571	0.057	UGGT1	HS6ST1
chr2	+(128982851..128983657)	806	0.00954	16	9	7	0.125	0.00042755	UGGT1	HS6ST1
chr2	+(130899715..130900218)	503	4.63887	6	4	2	0.3333333	0.067	LOC285103	CCDC74B
chr2	+(131116233..131116933)	700	1.21424	9	5	4	0.1111111	0.008	PTPN18	CFC1B_dup1
chr2	+(131139784..131140471)	687	0.325	10	6	4	0.2	0.005	PTPN18	CFC1B_dup1
chr2	+(131232119..131232635)	516	3.61997	67	33	34	0.0149254	0.00147804	PTPN18	CFC1B_dup1
chr2	+(131888318..131888957)	639	4.63887	8	4	4	0	0.014	PLEKHB2	POTEE

chr2	+(132020923..132021855)	932	0.54048	36	18	18	0	0.000155	POTEE	LOC440910
chr2	+(132239965..132240647)	682	0.64523	15	10	5	0.3333333	0.00998223	TUBA3D	MZT2A
chr2	+(132285554..132286239)	685	1.21424	9	6	3	0.3333333	0.012	CCDC74A	POTEKP
chr2	+(132366484..132367064)	580	4.63887	9	3	6	0.3333333	0.274	POTEKP	C2orf27A
chr2	+(132369060..132369585)	525	2.38223	33	16	17	0.030303	0.00031072	POTEKP	C2orf27A
chr2	+(132911985..132912499)	514	0.64523	22	15	7	0.3636364	0.00010748	C2orf27B	ANKRD30BL
chr2	+(133010541..133011060)	519	4.63887	6	2	4	0.3333333	0.067	C2orf27B	ANKRD30BL
chr2	+(133011569..133012142)	573	0.64523	25	16	9	0.28	2.2889E-05	C2orf27B	ANKRD30BL
chr2	+(133540133..133540775)	642	2.33844	10	4	6	0.2	0.086	LYPD1	NCKAP5
chr2	+(134525632..134526753)	1121	2.33844	13	7	6	0.0769231	0.98393771	NCKAP5	MIR3679
chr2	+(136028828..136029390)	562	4.63887	10	7	3	0.4	0.667	RAB3GAP1	ZRANB3
chr2	+(136268944..136269462)	518	4.63887	10	4	6	0.2	0.457	RAB3GAP1	ZRANB3
chr2	+(136398809..136399325)	516	2.33844	10	3	7	0.4	0.092	R3HDM1	MIR128-1
chr2	+(136594072..136594581)	509	4.63887	11	5	6	0.0909091	0.64249967	UBXN4	LCT
chr2	+(138738694..138739198)	504	4.63887	8	3	5	0.25	0.018	HNMT	SPOPL
chr2	+(152396706..152397385)	679	1.21424	10	7	3	0.4	0.133	RIF1	NEB
chr2	+(152459837..152460387)	550	0.64523	14	8	6	0.1428571	0.00225435	RIF1	NEB
chr2	+(152541204..152541731)	527	1.21424	10	5	5	0	0.00451172	RIF1	NEB
chr2	+(152552770..152553296)	526	4.63887	9	3	6	0.3333333	0.357	RIF1	NEB
chr2	+(153526588..153527122)	534	1.21424	11	5	6	0.0909091	0.29194121	FMNL2	PRPF40A
chr2	+(153537364..153537880)	516	2.33844	10	3	7	0.4	0.092	FMNL2	PRPF40A
chr2	+(159530107..159530626)	519	4.63887	11	4	7	0.2727273	0.206	PKP4	DAPL1
chr2	+(159572169..159572757)	588	4.63887	6	4	2	0.3333333	0.067	PKP4	DAPL1
chr2	+(160257135..160257650)	515	2.33844	12	7	5	0.1666667	0.01417552	WDSUB1	BAZ2B
chr2	+(160709668..160710197)	529	0.325	16	7	9	0.125	0.00062229	CD302	LY75-CD302
chr2	+(160713670..160715020)	1350	2.33844	13	7	6	0.0769231	0.0013499	CD302	LY75-CD302
chr2	+(160734828..160735348)	520	4.63887	8	5	3	0.25	0.125	CD302	LY75-CD302
chr2	+(162059856..162060407)	551	4.63887	9	3	6	0.3333333	0.19	TANK	PSMD14
chr2	+(162060922..162061437)	515	4.63887	10	4	6	0.2	0.057	TANK	PSMD14
chr2	+(162357279..162358002)	723	0.02589	39	17	22	0.1282051	9.4871E-06	TBR1	SLC4A10
chr2	+(162361611..162362245)	634	0.08723	23	10	13	0.1304348	0.59795967	TBR1	SLC4A10
chr2	+(162362428..162362982)	554	0.325	24	11	13	0.0833333	0.74738082	TBR1	SLC4A10
chr2	+(162834016..162834647)	631	0.02619	21	7	14	0.3333333	0.00012828	SLC4A10	DPP4
chr2	+(163039559..163040259)	700	2.33844	11	4	7	0.2727273	0.003	GCG	FAP

chr2	+(163082901..163083588)	687	0.325	14	5	9	0.2857143	0.00466119	GCG	FAP
chr2	+(165971797..165972304)	507	4.63887	9	5	4	0.1111111	0.008	SLC38A11	SCN3A
chr2	+(166768913..166769565)	652	1.21424	16	5	11	0.375	0.0009184	GALNT3	TTC21B
chr2	+(166848405..166848913)	508	4.63887	8	4	4	0	0.343	TTC21B	SCN1A
chr2	+(167133407..167133986)	579	0.325	15	8	7	0.0666667	0.01031878	SCN1A	SCN9A
chr2	+(167262451..167262962)	511	2.33844	9	4	5	0.1111111	0.095	SCN9A	SCN7A
chr2	+(167321950..167322475)	525	4.63887	12	5	7	0.1666667	0.06144014	SCN9A	SCN7A
chr2	+(168023289..168024519)	1230	0.08723	21	12	9	0.1428571	6.2118E-05	XIRP2	B3GALT1
chr2	+(168104137..168104662)	525	4.63887	8	4	4	0	0.1	XIRP2	B3GALT1
chr2	+(168570896..168571791)	895	0.325	33	13	20	0.2121212	0.15992096	XIRP2	B3GALT1
chr2	+(169873142..169873717)	575	2.33844	17	7	10	0.1764706	0.21748358	G6PC2	ABCB11
chr2	+(170028175..170028827)	652	2.33844	7	4	3	0.1428571	0.029	DHRS9	LRP2
chr2	+(170034209..170034735)	526	0.325	12	8	4	0.3333333	0.99671074	DHRS9	LRP2
chr2	+(170070006..170070520)	514	4.63887	10	4	6	0.2	0.381	DHRS9	LRP2
chr2	+(170133987..170134671)	684	0.64523	10	4	6	0.2	0.01	DHRS9	LRP2
chr2	+(170353995..170354683)	688	0.64523	12	6	6	0	0.02733197	BBS5	KBTBD10
chr2	+(170402208..170403272)	1064	0.04989	20	13	7	0.3	0.0002107	KBTBD10	FASTKD1
chr2	+(170671621..170672169)	548	2.33844	12	5	7	0.1666667	0.00591469	SSB	METTL5
chr2	+(171702168..171702687)	519	4.63887	12	8	4	0.3333333	0.341	GAD1	GORASP2
chr2	+(171911357..171912006)	649	1.21424	8	3	5	0.25	0.018	GORASP2	TLK1
chr2	+(171939143..171939657)	514	4.63887	6	3	3	0	0.05	GORASP2	TLK1
chr2	+(172304988..172305528)	540	4.63887	7	3	4	0.1428571	0.029	DCAF17	CYBRD1
chr2	+(173338654..173339191)	537	4.63887	6	2	4	0.3333333	0.067	ITGA6	PDK1
chr2	+(173429499..173430067)	568	0.325	14	9	5	0.2857143	0.03593032	PDK1	LOC91149
chr2	+(173656571..173657416)	845	0.03019	14	7	7	0	0.00087256	RAPGEF4	ZAK
chr2	+(173908201..173908709)	508	2.33844	10	3	7	0.4	0.992	RAPGEF4	ZAK
chr2	+(175093640..175094164)	524	4.63887	9	3	6	0.3333333	0.024	SP3	OLA1
chr2	+(177486962..177487622)	660	0.64523	9	4	5	0.1111111	0.008	MIR1246	HNRNPA3
chr2	+(177860441..177861597)	1156	2.33844	13	6	7	0.0769231	0.0013499	MIR1246	HNRNPA3
chr2	+(177995501..177996051)	550	4.63887	10	5	5	0	0.00451172	MIR1246	HNRNPA3
chr2	+(178081110..178081625)	515	1.9017	21	7	14	0.3333333	0.02620672	HNRNPA3	NFE2L2
chr2	+(178082233..178082758)	525	2.33844	11	7	4	0.2727273	0.006	HNRNPA3	NFE2L2
chr2	+(178096508..178097135)	627	2.33844	11	7	4	0.2727273	0.206	HNRNPA3	NFE2L2
chr2	+(178481496..178482033)	537	1.9017	22	12	10	0.0909091	0.00880376	TTC30B	TTC30A

chr2	+(179395161..179395802)	641	0.325	16	7	9	0.125	0.07650334	PLEKHA3	TTN
chr2	+(179427181..179427685)	504	4.63887	11	6	5	0.0909091	0.07206352	PLEKHA3	TTN
chr2	+(179432909..179433512)	603	2.33844	11	4	7	0.2727273	0.394	PLEKHA3	TTN
chr2	+(179514154..179514812)	658	1.21424	9	6	3	0.3333333	0.024	PLEKHA3	TTN
chr2	+(179516283..179516797)	514	4.63887	9	5	4	0.1111111	0.365	PLEKHA3	TTN
chr2	+(179527970..179528564)	594	0.0149	31	15	16	0.0322581	0.27661498	PLEKHA3	TTN
chr2	+(179554105..179554712)	607	4.63887	9	6	3	0.3333333	0.048	PLEKHA3	TTN
chr2	+(179560494..179561018)	524	2.33844	9	4	5	0.1111111	0.095	PLEKHA3	TTN
chr2	+(179565791..179566301)	510	4.63887	8	5	3	0.25	0.018	PLEKHA3	TTN
chr2	+(179701832..179702359)	527	4.63887	7	4	3	0.1428571	0.2	TTN	CCDC141
chr2	+(182275445..182276145)	700	0.00954	16	10	6	0.25	0.00056905	UBE2E3	ITGA4
chr2	+(182360059..182360577)	518	4.63887	11	6	5	0.0909091	0.10062131	ITGA4	CERKL
chr2	+(182763541..182764102)	561	2.33844	11	7	4	0.2727273	0.394	SSFA2	PPP1R1C
chr2	+(182775200..182775765)	565	4.63887	10	6	4	0.2	0.057	SSFA2	PPP1R1C
chr2	+(185803402..185804004)	602	4.63887	11	7	4	0.2727273	0.082	ZNF804A	FSIP2
chr2	+(187370032..187370573)	541	4.63887	9	3	6	0.3333333	0.452	ZC3H15	ITGAV
chr2	+(187486938..187487452)	514	4.63887	6	2	4	0.3333333	0.067	ITGAV	FAM171B
chr2	+(188216771..188217387)	616	2.33844	9	5	4	0.1111111	0.143	ZSWIM2	CALCRL
chr2	+(188267367..188268083)	716	0.04989	13	7	6	0.0769231	0.0013499	ZSWIM2	CALCRL
chr2	+(190531054..190531707)	653	4.63887	10	7	3	0.4	0.983	ASNSD1	ANKAR
chr2	+(192280920..192281459)	539	4.63887	11	6	5	0.0909091	0.35750033	MYO1B	OBFC2A
chr2	+(192546558..192547123)	565	4.63887	9	6	3	0.3333333	0.012	OBFC2A	SDPR
chr2	+(196681490..196682022)	532	4.63887	11	6	5	0.0909091	0.05017413	SLC39A10	DNAH7
chr2	+(197729504..197730019)	515	0.64523	10	3	7	0.4	0.008	C2orf66	PGAP1
chr2	+(198269388..198270107)	719	1.21424	13	5	8	0.2307692	0.00420773	ANKRD44	SF3B1
chr2	+(198404694..198405226)	532	2.33844	14	9	5	0.2857143	0.10263725	MOBKL3	RFTN2
chr2	+(198646314..198646833)	519	4.63887	10	4	6	0.2	0.057	MARS2	BOLL
chr2	+(198649868..198650422)	554	4.63887	6	3	3	0	0.05	MARS2	BOLL
chr2	+(198931283..198931983)	700	0.64523	13	4	9	0.3846154	0.999	PLCL1	SATB2
chr2	+(198950583..198951088)	505	4.63887	10	4	6	0.2	0.129	PLCL1	SATB2
chr2	+(200063779..200064449)	670	2.33844	7	4	3	0.1428571	0.029	PLCL1	SATB2
chr2	+(200820045..200820591)	546	2.33844	7	3	4	0.1428571	0.029	C2orf69	C2orf60
chr2	+(201488405..201489060)	655	1.21424	9	6	3	0.3333333	0.024	AOX1	AOX2P
chr2	+(201861953..201862473)	520	4.63887	9	3	6	0.3333333	0.012	ORC2	FAM126B

chr2	+(202276459..202276965)	506	2.33844	10	7	3	0.4	0.017	ALS2CR12	TRAK2	
chr2	+(202319275..202319800)	525	1.21424	11	5	6	0.0909091	0.00308495	STRADB	ALS2CR11	
chr2	+(202337401..202338093)	692	1.21424	12	6	6	0	0.03908455	STRADB	ALS2CR11	
chr2	+(202534257..202534784)	527	4.63887	8	3	5	0.25	0.036	ALS2CR4	MPP4	
chr2	+(202625418..202625936)	518	1.21424	10	4	6	0.2	0.129	MPP4	ALS2	
chr2	+(203991382..203991892)	510	4.63887	8	5	3	0.25	0.018	NBEAL1	CYP20A1	
chr2	+(204052880..204053385)	505	2.33844	10	3	7	0.4	0.008	NBEAL1	CYP20A1	
chr2	+(204510715..204511399)	684	4.63887	7	3	4	0.1428571	0.029	RAPH1	CD28	
chr2	+(204594214..204594774)	560	2.33844	7	4	3	0.1428571	0.029	CD28	CTLA4	
chr2	+(204735779..204736479)	700	1.21424	14	9	5	0.2857143	0.04779036	CTLA4	ICOS	
chr2	+(207075025..207075725)	700	0.0149	15	5	10	0.3333333	0.00109982	SNORA41	GPR1	
chr2	+(207577059..207578238)	1179	1.21424	16	8	8	0	0.99961123	LOC200726	DYTN	
chr2	+(208865595..208866156)	561	1.21424	9	6	3	0.3333333	0.048	FZD5	PLEKHM3	
chr2	+(214239556..214240097)	541	2.33844	9	5	4	0.1111111	0.008	SPAG16	VWC2L	
chr2	+(214721161..214721732)	571	0.64523	9	5	4	0.1111111	0.008	SPAG16	VWC2L	
chr2	+(216203195..216203895)	700	2.33844	11	5	6	0.0909091	0.01422987	ATIC	FN1	
chr2	+(216239712..216240252)	540	4.63887	6	2	4	0.3333333	0.067	ATIC	FN1	
chr2	+(217068667..217069252)	585	4.63887	9	3	6	0.3333333	0.012	XRCC5	40972	
chr2	+(218669096..218669651)	555	4.63887	6	3	3	0	0.05	DIRC3	TNS1	
chr2	+(218694155..218694691)	536	4.63887	6	3	3	0	0.05	DIRC3	TNS1	
chr2	+(218712922..218713658)	736	2.33844	13	6	7	0.0769231	0.0013499	DIRC3	TNS1	
chr2	+(219029590..219030141)	551	4.63887	7	3	4	0.1428571	0.029	CXCR2	CXCR1	
chr2	+(219609697..219610216)	519	2.33844	7	4	3	0.1428571	0.029	TTLL4	CYP27A1	
chr2	+(220115630..220116138)	508	0.64523	14	9	5	0.2857143	0.00981533	STK16	TUBA4A	
chr2	+(220298749..220299331)	582	1.21424	11	7	4	0.2727273	0.021	DES	SPEG	
chr2	+(220316201..220316901)	700	0.04989	13	4	9	0.3846154	0.001	SPEG	GMPPA	v
chr2	+(220348572..220349126)	554	2.33844	8	5	3	0.25	0.018	SPEG	GMPPA	v
chr2	+(220355278..220356129)	851	0.0149	20	9	11	0.1	0.36621995	SPEG	GMPPA	v
chr2	+(220370253..220370951)	698	0.64523	10	6	4	0.2	0.057	GMPPA	ACCN4	v
chr2	+(220480866..220481433)	567	4.63887	6	3	3	0	0.05	STK11IP	SLC4A3	
chr2	+(223511535..223512066)	531	1.34515	37	23	14	0.2432432	0.04848081	SGPP2	FARSB	
chr2	+(225653355..225653885)	530	2.33844	10	3	7	0.4	0.667	CUL3	DOCK10	
chr2	+(228117691..228118218)	527	2.33844	11	6	5	0.0909091	0.05017413	COL4A3	MFF	
chr2	+(228278935..228279635)	700	0.325	10	6	4	0.2	0.005	TM4SF20	AGFG1	

chr2	+(228356077..228356614)	537	4.63887	8	3	5	0.25	0.036	AGFG1	C2orf83
chr2	+(228883442..228884142)	700	2.33844	9	3	6	0.3333333	0.726	WDR69	SPHKAP
chr2	+(230311621..230312321)	700	2.33844	10	3	7	0.4	0.008	PID1	DNER
chr2	+(230723902..230724570)	668	0.04989	20	13	7	0.3	0.00148122	DNER	TRIP12
chr2	+(230910211..230910808)	597	4.63887	11	5	6	0.0909091	0.81934478	FBXO36	SLC16A14
chr2	+(231022570..231023079)	509	4.63887	6	2	4	0.3333333	0.067	SLC16A14	SP110
chr2	+(231116985..231117497)	512	4.63887	6	2	4	0.3333333	0.067	SP140	SP140L
chr2	+(231254457..231254980)	523	4.63887	7	4	3	0.1428571	0.029	SP140L	SP100
chr2	+(231265937..231266569)	632	0.17743	44	17	27	0.2272727	8.4458E-06	SP140L	SP100
chr2	+(231650338..231651025)	687	4.63887	6	4	2	0.3333333	0.067	CAB39	ITM2C
chr2	+(232576273..232576859)	586	4.63887	9	3	6	0.3333333	0.012	PTMA	MIR1244-1
chr2	+(233096540..233097151)	611	2.33844	9	3	6	0.3333333	0.274	DIS3L2	ALPP
chr2	+(233193433..233194133)	700	4.63887	9	6	3	0.3333333	0.988	DIS3L2	ALPP
chr2	+(233246552..233247245)	693	1.21424	12	8	4	0.3333333	0.99671074	ALPP	ECEL1P2
chr2	+(233273758..233274275)	517	4.63887	9	5	4	0.1111111	0.206	ALPPL2	ALPI
chr2	+(233371183..233371918)	735	0.04989	16	6	10	0.25	0.00056905	ECEL1	LOC646960
chr2	+(233389920..233390603)	683	4.63887	6	3	3	0	0.05	LOC646960	CHRND
chr2	+(233632847..233633482)	635	4.63887	9	6	3	0.3333333	0.274	GIGYF2	KCNJ13
chr2	+(233697201..233697743)	542	4.63887	9	3	6	0.3333333	0.988	KCNJ13	C2orf82
chr2	+(233700212..233700715)	503	2.33844	7	4	3	0.1428571	0.029	KCNJ13	C2orf82
chr2	+(233701974..233702702)	728	0.04989	13	7	6	0.0769231	0.0013499	KCNJ13	C2orf82
chr2	+(233839180..233839711)	531	1.39784	20	12	8	0.2	0.00131091	C2orf82	NGEF
chr2	+(235430324..235431024)	700	4.63887	10	4	6	0.2	0.995	ARL4C	SH3BP4
chr2	+(235748395..235748905)	510	1.21424	8	3	5	0.25	0.018	ARL4C	SH3BP4
chr2	+(235890945..235891645)	700	0.18049	13	9	4	0.3846154	0.001	SH3BP4	AGAP1
chr2	+(235907395..235908095)	700	0.08723	13	7	6	0.0769231	0.02275014	SH3BP4	AGAP1
chr2	+(236336506..236337160)	654	1.21424	8	5	3	0.25	0.018	SH3BP4	AGAP1
chr2	+(236570224..236570863)	639	4.63887	8	3	5	0.25	0.5	AGAP1	GBX2
chr2	+(237262845..237263545)	700	0.325	10	7	3	0.4	0.008	ASB18	IQCA1
chr2	+(237411221..237411874)	653	0.64523	9	5	4	0.1111111	0.008	ASB18	IQCA1
chr2	+(238161321..238162021)	700	0.64523	11	7	4	0.2727273	0.003	COPS8	COL6A3
chr2	+(238320649..238321209)	560	0.325	10	4	6	0.2	0.005	COPS8	COL6A3
chr2	+(238345539..238346239)	700	0.04989	13	8	5	0.2307692	0.0017074	COL6A3	MLPH
chr2	+(238946503..238947060)	557	2.33844	7	4	3	0.1428571	0.029	UBE2F	SCLY

chr2	+(239165283..239165890)	607	2.33844	7	4	3	0.1428571	0.029	HES6	PER2
chr2	+(240063334..240064034)	700	0.18049	11	5	6	0.0909091	0.00308495	FLJ43879	HDAC4
chr2	+(240299072..240299772)	700	2.33844	12	7	5	0.1666667	0.00224163	FLJ43879	HDAC4
chr2	+(240418754..240419454)	700	1.21424	13	8	5	0.2307692	0.0017074	MIR4269	NDUFA10
chr2	+(240423789..240424489)	700	0.04989	13	5	8	0.2307692	0.0017074	MIR4269	NDUFA10
chr2	+(240455557..240456257)	700	0.325	10	7	3	0.4	0.008	MIR4269	NDUFA10
chr2	+(240559127..240559827)	700	0.325	10	7	3	0.4	0.008	MIR4269	NDUFA10
chr2	+(240685489..240686109)	620	4.63887	6	3	3	0	0.05	MIR4269	NDUFA10
chr2	+(240922888..240923452)	564	1.21424	9	4	5	0.1111111	0.008	MIR4269	NDUFA10
chr2	+(240972329..240973178)	849	0.00139	24	9	15	0.25	0.00786861	OR6B2	PRR21
chr2	+(240980969..240981956)	987	2.33844	19	8	11	0.1578947	0.25444141	OR6B2	PRR21
chr2	+(240985036..240985558)	522	4.63887	14	8	6	0.1428571	0.92220982	PRR21	OR6B3
chr2	+(241068856..241069813)	957	2.33844	13	7	6	0.0769231	0.98393771	OR6B3	MYEOV2
chr2	+(241106847..241107547)	700	4.63887	9	3	6	0.3333333	0.012	OTOS	GPC1
chr2	+(241287849..241288444)	595	4.63887	6	3	3	0	0.05	OTOS	GPC1
chr2	+(241369915..241371036)	1121	4.63887	12	6	6	0	0.99802612	OTOS	GPC1
chr2	+(241387901..241388454)	553	4.63887	9	6	3	0.3333333	0.012	GPC1	PP14571
chr2	+(241403053..241404145)	1092	4.63887	13	6	7	0.0769231	0.02275014	MIR149	ANKMY1
chr2	+(241406429..241407129)	700	1.21424	9	3	6	0.3333333	0.012	MIR149	ANKMY1
chr2	+(241450687..241451205)	518	0.325	10	3	7	0.4	0.008	MIR149	ANKMY1
chr2	+(241565270..241565882)	612	2.33844	12	5	7	0.1666667	0.18587565	GPR35	AQP12B
chr2	+(241666137..241666812)	675	1.21424	10	3	7	0.4	0.017	AQP12A	KIF1A
chr2	+(241695753..241696278)	525	1.21424	8	3	5	0.25	0.018	AQP12A	KIF1A
chr2	+(241707233..241707918)	685	4.63887	6	2	4	0.3333333	0.067	AQP12A	KIF1A
chr2	+(241758143..241758693)	550	4.63887	6	4	2	0.3333333	0.067	AQP12A	KIF1A
chr2	+(241816602..241817217)	615	2.33844	7	4	3	0.1428571	0.029	AGXT	C2orf54
chr2	+(241936148..241936793)	645	0.64523	9	6	3	0.3333333	0.012	LOC200772	SNED1
chr2	+(241974077..241974962)	885	1.21424	13	5	8	0.2307692	0.0394913	SNED1	MTERFD2
chr2	+(242009361..242009864)	503	1.21424	8	3	5	0.25	0.018	SNED1	MTERFD2
chr2	+(242075149..242075849)	700	0.325	15	10	5	0.3333333	0.00715294	MTERFD2	PASK
chr2	+(242148132..242148832)	700	0.04989	16	7	9	0.125	0.31691947	ANO7	HDLBP
chr2	+(242179106..242179721)	615	0.64523	10	5	5	0	0.02360089	ANO7	HDLBP
chr2	+(242651290..242651842)	552	4.63887	10	6	4	0.2	0.762	ING5	D2HGDH
chr2	+(242658348..242658941)	593	2.33844	7	4	3	0.1428571	0.029	ING5	D2HGDH

chr2	+(242683010..242683595)	585	2.33844	7	4	3	0.1428571	0.029	D2HGDH	GAL3ST2
chr2	+(242752245..242753737)	1492	2.33844	22	15	7	0.3636364	0.00010748	NEU4	PDCD1
chr3	+(440485..441008)	523	3.63011	8	5	3	0.25	0.018	CHL1	CNTN6
chr3	+(586935..588113)	1178	0.091	18	7	11	0.2222222	0.9997556	CHL1	CNTN6
chr3	+(900566..901266)	700	0.74291	12	4	8	0.3333333	0.893	CHL1	CNTN6
chr3	+(4354848..4355391)	543	1.68843	9	4	5	0.1111111	0.143	SETMAR	SUMF1
chr3	+(4486469..4487691)	1222	0.091	17	6	11	0.2941176	0.00045556	SETMAR	SUMF1
chr3	+(4732643..4733174)	531	3.63011	8	5	3	0.25	0.036	ITPR1	EGOT
chr3	+(4770035..4770735)	700	1.68843	12	5	7	0.1666667	0.99775837	ITPR1	EGOT
chr3	+(5164016..5164652)	636	0.091	16	8	8	0	0.00038877	ARL8B	EDEM1
chr3	+(8595900..8596412)	512	1.68843	7	3	4	0.1428571	0.029	LMCD1	LOH3CR2A
chr3	+(8677084..8677784)	700	0.04455	12	8	4	0.3333333	0.99671074	LOH3CR2A	C3orf32
chr3	+(8683075..8684128)	1053	3.63011	12	6	6	0	0.99802612	LOH3CR2A	C3orf32
chr3	+(9054683..9055373)	690	3.63011	11	5	6	0.0909091	0.13666084	RAD18	SRGAP3
chr3	+(9487055..9487627)	572	0.74291	9	3	6	0.3333333	0.024	SETD5	LHFPL4
chr3	+(9798036..9798710)	674	1.68843	12	5	7	0.1666667	0.08373231	OGG1	CAMK1
chr3	+(9984952..9985461)	509	3.63011	6	4	2	0.3333333	0.067	CRELD1	PRRT3
chr3	+(9985858..9986380)	522	0.74291	9	5	4	0.1111111	0.008	CRELD1	PRRT3
chr3	+(10381560..10382074)	514	1.68843	7	3	4	0.1428571	0.029	SEC13	ATP2B2
chr3	+(10954212..10954789)	577	0.74291	12	8	4	0.3333333	0.99671074	SLC6A11	SLC6A1
chr3	+(10976678..10977389)	711	0.04455	13	8	5	0.2307692	0.0394913	SLC6A11	SLC6A1
chr3	+(11007705..11008405)	700	0.74291	10	4	6	0.2	0.005	SLC6A11	SLC6A1
chr3	+(11651818..11652397)	579	3.63011	6	2	4	0.3333333	0.067	ATG7	VGLL4
chr3	+(12360825..12361521)	696	3.63011	10	6	4	0.2	0.005	PPARG	TSEN2
chr3	+(12637205..12637809)	604	3.63011	6	3	3	0	0.05	MKRN2	RAF1
chr3	+(12947992..12948546)	554	3.63011	7	4	3	0.1428571	0.314	SNORA7A	IQSEC1
chr3	+(12973010..12973710)	700	0.18343	10	3	7	0.4	0.008	SNORA7A	IQSEC1
chr3	+(12989196..12989896)	700	3.63011	11	6	5	0.0909091	0.99691505	SNORA7A	IQSEC1
chr3	+(13019738..13020291)	553	0.74291	8	5	3	0.25	0.018	SNORA7A	IQSEC1
chr3	+(13138682..13139382)	700	0.36666	13	9	4	0.3846154	0.207	IQSEC1	NUP210
chr3	+(13175021..13175522)	501	3.63011	8	4	4	0	0.014	IQSEC1	NUP210
chr3	+(13181982..13182627)	645	3.63011	10	4	6	0.2	0.057	IQSEC1	NUP210
chr3	+(13240003..13240889)	886	0.18343	16	7	9	0.125	0.00042755	IQSEC1	NUP210
chr3	+(13256432..13257406)	974	3.63011	12	6	6	0	0.00197388	IQSEC1	NUP210

chr3	+(13376477..13376996)	519	1.68843	7	4	3	0.1428571	0.029	IQSEC1	NUP210	
chr3	+(13417452..13418152)	700	0.36666	10	4	6	0.2	0.01	IQSEC1	NUP210	
chr3	+(13438184..13438877)	693	3.63011	11	5	6	0.0909091	0.99691505	IQSEC1	NUP210	
chr3	+(13624832..13626164)	1332	0.091	20	9	11	0.1	0.00172235	FBLN2	LOC285375	
chr3	+(13660980..13661558)	578	1.68843	9	5	4	0.1111111	0.008	FBLN2	LOC285375	
chr3	+(13675825..13676525)	700	0.00277	16	5	11	0.375	0.0009184	FBLN2	LOC285375	
chr3	+(13678415..13679115)	700	0.091	14	9	5	0.2857143	0.15865525	FBLN2	LOC285375	
chr3	+(14197409..14198201)	792	0.74291	14	5	9	0.2857143	0.04779036	TMEM43	XPC	
chr3	+(14513606..14514205)	599	3.63011	9	6	3	0.3333333	0.024	SLC6A6	GRIP2	
chr3	+(14514467..14515190)	723	0.01005	20	6	14	0.4	0.000266	SLC6A6	GRIP2	
chr3	+(14519689..14520190)	501	3.63011	13	7	6	0.0769231	0.01606229	SLC6A6	GRIP2	
chr3	+(14537972..14538668)	696	0.74291	13	8	5	0.2307692	0.9982926	SLC6A6	GRIP2	
chr3	+(14553216..14553826)	610	3.63011	6	2	4	0.3333333	0.067	SLC6A6	GRIP2	
chr3	+(14713374..14713995)	621	0.74291	8	4	4	0	0.014	C3orf19	C3orf20	
chr3	+(15025759..15026459)	700	3.63011	11	5	6	0.0909091	0.99691505	NR2C2	MRPS25	
chr3	+(15218912..15219637)	725	0.04455	12	6	6	0	0.00197388	ZFYVE20	COL6A4P1	
chr3	+(15349789..15350420)	631	3.63011	6	2	4	0.3333333	0.067	CAPN7	SH3BP5	
chr3	+(15643321..15644003)	682	3.63011	14	6	8	0.1428571	0.78071098	BTD	ANKRD28	
chr3	+(16219526..16220216)	690	0.36666	9	3	6	0.3333333	0.012	GALNTL2	DPH3	
chr3	+(19432090..19432616)	526	3.63011	6	4	2	0.3333333	0.067	KCNH8	EFHB	
chr3	+(19864670..19865291)	621	3.63011	7	4	3	0.1428571	0.314	KCNH8	EFHB	
chr3	+(21456131..21456722)	591	3.63011	6	3	3	0	0.05	VENTXP7	ZNF385D	
chr3	+(21552369..21552954)	585	0.36666	14	9	5	0.2857143	0.42074029	VENTXP7	ZNF385D	
chr3	+(23123084..23123784)	700	0.02052	13	8	5	0.2307692	0.0017074	ZNF385D	UBE2E2	
chr3	+(23958404..23958959)	555	0.36666	9	4	5	0.1111111	0.008	UBE2E1	NKIRAS1	
chr3	+(23997252..23997779)	527	3.63011	9	4	5	0.1111111	0.008	NR1D2	LOC152024	
chr3	+(24486134..24486731)	597	1.68843	7	3	4	0.1428571	0.029	LOC152024	THRB	
chr3	+(25796454..25796985)	531	3.63011	8	4	4	0	0.014	TOP2B	NGLY1	
chr3	+(26727030..26728110)	1080	0.18343	19	10	9	0.0526316	0.00011928	LRRC3B	NEK10	
chr3	+(27527732..27528273)	541	0.36666	11	4	7	0.2727273	0.003	SLC4A7	EOMES	v
chr3	+(27761311..27761843)	532	0.74291	13	5	8	0.2307692	0.0017074	SLC4A7	EOMES	v
chr3	+(28520157..28520746)	589	0.36666	10	4	6	0.2	0.01	ZCWPW2	RBMS3	
chr3	+(31621294..31621796)	502	3.63011	12	7	5	0.1666667	0.18587565	STT3B	OSBPL10	
chr3	+(32364223..32364801)	578	3.63011	10	4	6	0.2	0.943	CMTM8	CMTM7	

chr3	+(32398654..32399218)	564	1.68843	7	3	4	0.1428571	0.029	CMTM8	CMTM7
chr3	+(33649892..33650501)	609	0.74291	12	8	4	0.3333333	0.184	UBP1	CLASP2
chr3	+(33907739..33908244)	505	0.74291	10	6	4	0.2	0.129	PDCD6IP	ARPP21
chr3	+(33951932..33952632)	700	0.091	11	7	4	0.2727273	0.003	PDCD6IP	ARPP21
chr3	+(36779299..36779939)	640	3.63011	12	8	4	0.3333333	0.404	STAC	DCLK3
chr3	+(37053038..37053571)	533	1.68843	11	7	4	0.2727273	0.006	MLH1	LRRFIP2
chr3	+(37124900..37125488)	588	1.68843	9	6	3	0.3333333	0.012	MLH1	LRRFIP2
chr3	+(37175929..37176434)	505	3.63011	9	3	6	0.3333333	0.19	MLH1	LRRFIP2
chr3	+(37388434..37388966)	532	3.63011	12	8	4	0.3333333	0.99671074	GOLGA4	C3orf35
chr3	+(38167687..38169101)	1414	0.091	26	8	18	0.3846154	3.1671E-05	DLEC1	ACAA1
chr3	+(38349734..38350330)	596	3.63011	6	3	3	0	0.05	SLC22A14	XYLB
chr3	+(38354788..38355480)	692	0.36666	9	5	4	0.1111111	0.008	SLC22A14	XYLB
chr3	+(38515254..38515915)	661	3.63011	6	2	4	0.3333333	0.067	ACVR2B	EXOG
chr3	+(38611645..38612345)	700	0.18343	10	4	6	0.2	0.005	EXOG	SCN5A
chr3	+(38670552..38671243)	691	0.18343	15	5	10	0.3333333	0.5	EXOG	SCN5A
chr3	+(38739183..38739772)	589	0.18343	13	6	7	0.0769231	0.01606229	SCN5A	SCN10A
chr3	+(38763350..38764512)	1162	1.68843	14	6	8	0.1428571	0.00097289	SCN5A	SCN10A
chr3	+(38797006..38797528)	522	3.63011	14	8	6	0.1428571	0.00097289	SCN5A	SCN10A
chr3	+(39142294..39142914)	620	0.74291	11	7	4	0.2727273	0.006	WDR48	GORASP1
chr3	+(39153326..39154052)	726	1.68843	14	7	7	0	0.01267366	TTC21A	CSRNP1
chr3	+(39169802..39170306)	504	0.36666	10	3	7	0.4	0.033	TTC21A	CSRNP1
chr3	+(39185134..39185834)	700	0.091	12	7	5	0.1666667	0.03090926	TTC21A	CSRNP1
chr3	+(39195425..39196125)	700	0.091	13	4	9	0.3846154	0.47	CSRNP1	XIRP1
chr3	+(39374138..39374653)	515	1.68843	12	8	4	0.3333333	0.404	CCR8	SLC25A38
chr3	+(39537958..39538609)	651	1.68843	7	3	4	0.1428571	0.029	MOBP	MYRIP
chr3	+(42576556..42577071)	515	3.63011	12	4	8	0.3333333	0.285	VIPR1	SEC22C
chr3	+(44621474..44622007)	533	3.63011	6	3	3	0	0.05	ZNF167	ZNF660
chr3	+(44776266..44776821)	555	3.63011	8	3	5	0.25	0.196	ZNF501	KIAA1143
chr3	+(47098214..47098852)	638	0.36666	11	4	7	0.2727273	0.264	NRADDP	SETD2
chr3	+(47384855..47385553)	698	1.68843	7	4	3	0.1428571	0.029	KLHL18	PTPN23
chr3	+(47742625..47743174)	549	3.63011	8	5	3	0.25	0.286	CSPG5	SMARCC1
chr3	+(47755719..47756242)	523	0.36666	14	8	6	0.1428571	0.00491164	CSPG5	SMARCC1
chr3	+(47910769..47911908)	1139	0.04455	19	6	13	0.3684211	0.00190008	MIR1226	MAP4
chr3	+(47912251..47912783)	532	3.63011	6	3	3	0	0.05	MIR1226	MAP4

chr3	+(48447780..48448480)	700	0.36666	10	7	3	0.4	0.008	FBXW12	PLXNB1
chr3	+(48450420..48451040)	620	0.74291	9	6	3	0.3333333	0.012	FBXW12	PLXNB1
chr3	+(48473807..48474372)	565	1.68843	9	5	4	0.1111111	0.008	PLXNB1	CCDC51
chr3	+(48510189..48510799)	610	3.63011	6	4	2	0.3333333	0.067	TREX1	SHISA5
chr3	+(48588219..48588748)	529	0.74291	8	4	4	0	0.014	SHISA5	PFKFB4
chr3	+(49073915..49074613)	698	0.36666	9	6	3	0.3333333	0.012	IMPDH2	QRICH1
chr3	+(49278522..49279217)	695	1.68843	10	7	3	0.4	0.058	CCDC36	C3orf62
chr3	+(49722811..49723346)	535	0.18343	15	10	5	0.3333333	0.04320538	APEH	MST1
chr3	+(49749872..49750421)	549	3.63011	6	2	4	0.3333333	0.067	RNF123	AMIGO3
chr3	+(49836316..49836838)	522	1.68843	10	5	5	0	0.05859256	IP6K1	CDHR4
chr3	+(50401848..50402548)	700	0.091	12	5	7	0.1666667	0.00224163	TMEM115	CACNA2D2
chr3	+(50418358..50418907)	549	3.63011	9	4	5	0.1111111	0.008	TMEM115	CACNA2D2
chr3	+(50526948..50528071)	1123	0.74291	16	8	8	0	0.97064629	TMEM115	CACNA2D2
chr3	+(50604278..50604978)	700	0.18343	11	5	6	0.0909091	0.00308495	CACNA2D2	C3orf18
chr3	+(51411578..51412278)	700	0.36666	14	5	9	0.2857143	0.00981533	DOCK3	MANF
chr3	+(52153804..52154715)	911	0.36666	18	9	9	0	0.00017429	C3orf74	POC1A
chr3	+(52281538..52282098)	560	1.68843	7	3	4	0.1428571	0.029	PPM1M	WDR82
chr3	+(52427242..52427776)	534	3.66733	16	11	5	0.375	0.0009184	DNAH1	BAP1
chr3	+(52524622..52525128)	506	3.63011	7	4	3	0.1428571	0.057	NISCH	STAB1
chr3	+(52555003..52555605)	602	3.63011	6	3	3	0	0.05	STAB1	NT5DC2
chr3	+(52780606..52781117)	511	3.63011	9	4	5	0.1111111	0.008	SPCS1	NEK4
chr3	+(52955565..52956091)	526	3.63011	8	4	4	0	0.014	TMEM110	SFMBT1
chr3	+(52964795..52965311)	516	3.63011	7	3	4	0.1428571	0.029	TMEM110	SFMBT1
chr3	+(53223096..53224177)	1081	0.74291	15	8	7	0.0666667	0.99245637	PRKCD	TKT
chr3	+(55041597..55042171)	574	3.63011	6	4	2	0.3333333	0.067	LRTM1	WNT5A
chr3	+(56716112..56716739)	627	3.63011	9	3	6	0.3333333	0.988	CCDC66	C3orf63
chr3	+(57847540..57848064)	524	3.63011	9	4	5	0.1111111	0.095	SLMAP	FLNB
chr3	+(58067177..58067877)	700	0.091	12	8	4	0.3333333	0.024	FLNB	DNASE1L3
chr3	+(65350496..65351049)	553	0.36666	17	9	8	0.0588235	0.000266	MIR548A2	MAGI1
chr3	+(69056560..69057245)	685	1.68843	10	7	3	0.4	0.258	FAM19A4	C3orf64
chr3	+(69150690..69151390)	700	0.74291	11	4	7	0.2727273	0.003	ARL6IP5	LMOD3
chr3	+(70317159..70317665)	506	0.74291	8	5	3	0.25	0.018	MITF	FOXP1
chr3	+(71378036..71378736)	700	0.091	11	6	5	0.0909091	0.00308495	MITF	FOXP1
chr3	+(71384820..71385428)	608	3.63011	6	3	3	0	0.05	MITF	FOXP1

chr3	+(72873305..72873863)	558	3.63011	6	4	2	0.3333333	0.067	RYBP	SHQ1
chr3	+(75714558..75715093)	535	2.57182	32	20	12	0.25	0.00080823	FRG2C	ZNF717
chr3	+(75719523..75720076)	553	0.18343	13	7	6	0.0769231	0.0992714	FRG2C	ZNF717
chr3	+(75790448..75790987)	539	3.63011	13	9	4	0.3846154	0.355	FRG2C	ZNF717
chr3	+(87289634..87290163)	529	0.36666	12	4	8	0.3333333	0.00328926	CHMP2B	POU1F1
chr3	+(93560398..93560989)	591	0.36666	9	5	4	0.1111111	0.008	EPHA3	PROS1
chr3	+(93624735..93625243)	508	3.63011	8	4	4	0	0.1	EPHA3	PROS1
chr3	+(93794808..93795404)	596	0.74291	12	5	7	0.1666667	0.01417552	NSUN3	LOC255025
chr3	+(94593514..94594130)	616	3.63011	6	2	4	0.3333333	0.067	NSUN3	LOC255025
chr3	+(96706453..96706979)	526	3.63011	10	6	4	0.2	0.305	EPHA6	ARL6
chr3	+(97679816..97680516)	700	0.04455	12	4	8	0.3333333	0.00328926	ARL6	MINA
chr3	+(98188745..98189367)	622	0.36666	16	8	8	0	0.01371158	OR5K1	OR5K2
chr3	+(98216350..98216854)	504	3.63011	11	5	6	0.0909091	0.57243393	OR5K1	OR5K2
chr3	+(99566844..99567383)	539	1.68843	16	10	6	0.25	0.00851093	DCBLD2	MIR548G
chr3	+(99569228..99569735)	507	1.68843	12	6	6	0	0.05465729	DCBLD2	MIR548G
chr3	+(100104886..100105415)	529	1.68843	7	4	3	0.1428571	0.029	NIT2	TOMM70A
chr3	+(100438719..100439391)	672	1.68843	11	7	4	0.2727273	0.158	TFG	ABI3BP
chr3	+(101383957..101384533)	576	3.63011	8	3	5	0.25	0.286	PCNP	ZBTB11
chr3	+(107798564..107799115)	551	3.63011	8	3	5	0.25	0.286	LOC285205	CD47
chr3	+(108147435..108148043)	608	1.68843	11	6	5	0.0909091	0.29194121	HHLA2	MYH15
chr3	+(108279199..108279767)	568	3.63011	11	5	6	0.0909091	0.10062131	MYH15	KIAA1524
chr3	+(108408249..108408759)	510	3.63011	6	4	2	0.3333333	0.067	DZIP3	RETNLB
chr3	+(112256799..112257330)	531	0.74291	11	4	7	0.2727273	0.012	BTLA	ATG3
chr3	+(112262902..112263602)	700	0.74291	13	9	4	0.3846154	0.98	BTLA	ATG3
chr3	+(113120000..113120504)	504	3.63011	8	3	5	0.25	0.286	BOC	WDR52
chr3	+(113172171..113172682)	511	3.63011	10	7	3	0.4	0.058	WDR52	SPICE1
chr3	+(113516902..113517428)	526	3.63011	7	3	4	0.1428571	0.029	ATP6V1A	GRAMD1C
chr3	+(118865368..118866029)	661	1.68843	7	3	4	0.1428571	0.029	C3orf30	UPK1B
chr3	+(119064078..119064768)	690	0.74291	10	6	4	0.2	0.005	ARHGAP31	TMEM39A
chr3	+(120719038..120720432)	1394	0.00483	24	10	14	0.1666667	0.8792167	STXBP5L	POLQ
chr3	+(122003391..122003914)	523	3.63011	8	4	4	0	0.014	CASR	CSTA
chr3	+(122639836..122640356)	520	1.68843	7	3	4	0.1428571	0.029	LOC100129550	SEMA5B
chr3	+(123412078..123412650)	572	3.63011	6	2	4	0.3333333	0.067	PTPLB	MYLK
chr3	+(123512615..123513264)	649	3.63011	9	3	6	0.3333333	0.988	PTPLB	MYLK

chr3	+(124488119..124488666)	547	0.74291	8	5	3	0.25	0.018	UMPS	ITGB5	
chr3	+(124636398..124637090)	692	3.63011	10	6	4	0.2	0.005	ITGB5	MUC13	
chr3	+(125283566..125284099)	533	0.74291	15	5	10	0.3333333	0.99890018	SNX4	OSBPL11	
chr3	+(125422076..125422645)	569	3.63011	9	4	5	0.1111111	0.008	OSBPL11	MIR548I1	
chr3	+(125647328..125647876)	548	1.68843	11	5	6	0.0909091	0.10062131	LOC100125556	ALG1L	
chr3	+(126295624..126296324)	700	1.68843	11	4	7	0.2727273	0.003	C3orf22	TXNRD3IT1	
chr3	+(126651322..126651860)	538	0.18343	10	5	5	0	0.00451172	CHCHD6	PLXNA1	
chr3	+(126726445..126727145)	700	0.091	11	5	6	0.0909091	0.00308495	PLXNA1	TPRA1	
chr3	+(126748512..126749666)	1154	1.68843	15	7	8	0.0666667	0.94740374	PLXNA1	TPRA1	
chr3	+(127509939..127510639)	700	3.63011	10	6	4	0.2	0.995	ABTB1	MGLL	
chr3	+(128119240..128119940)	700	1.68843	12	5	7	0.1666667	0.99775837	MIR1280	DNAJB8	
chr3	+(128627196..128627896)	700	8.9E-05	20	14	6	0.4	0.000266	ACAD9	KIAA1257	
chr3	+(128749423..128749957)	534	3.63011	9	6	3	0.3333333	0.274	CCDC48	GP9	
chr3	+(129152743..129153283)	540	3.63011	9	4	5	0.1111111	0.032	C3orf25	MBD4	
chr3	+(129275695..129276307)	612	0.74291	9	3	6	0.3333333	0.024	H1FOO	PLXND1	
chr3	+(129306096..129306796)	700	0.36666	14	9	5	0.2857143	0.9986501	H1FOO	PLXND1	
chr3	+(129338256..129338771)	515	0.36666	10	4	6	0.2	0.057	PLXND1	TMCC1	v
chr3	+(129389545..129390048)	503	3.63011	9	6	3	0.3333333	0.024	PLXND1	TMCC1	
chr3	+(129818150..129818737)	587	0.01005	20	14	6	0.4	0.40228547	ALG1L2	LOC729375	
chr3	+(130107479..130108107)	628	1.68843	10	4	6	0.2	0.086	COL6A5	COL6A6	
chr3	+(130159385..130159915)	530	3.63011	8	5	3	0.25	0.286	COL6A5	COL6A6	
chr3	+(130345242..130345848)	606	3.63011	12	6	6	0	0.01248734	COL6A6	PIK3R4	
chr3	+(131220180..131220863)	683	0.04455	15	5	10	0.3333333	0.00109982	NUDT16	MRPL3	
chr3	+(132241731..132242249)	518	1.68843	11	4	7	0.2727273	0.082	DNAJC13	ACAD11	
chr3	+(132400298..132401216)	918	0.36666	15	6	9	0.2	0.98305257	UBA5	NPHP3	
chr3	+(133190826..133191495)	669	3.63011	8	3	5	0.25	0.018	BFSP2	CDV3	
chr3	+(133211128..133211650)	522	0.74291	8	4	4	0	0.014	BFSP2	CDV3	
chr3	+(133557649..133558349)	700	0.36666	10	7	3	0.4	0.058	SRPRB	RAB6B	
chr3	+(134080179..134080879)	700	0.36666	11	4	7	0.2727273	0.003	RYK	AMOTL2	
chr3	+(134644448..134644981)	533	3.63011	7	4	3	0.1428571	0.029	EPHB1	PPP2R3A	v
chr3	+(135796928..135797561)	633	0.04455	16	6	10	0.25	0.00056905	PPP2R3A	MSL2	v
chr3	+(136455425..136455942)	517	3.63011	9	6	3	0.3333333	0.357	PCCB	STAG1	
chr3	+(141274353..141274860)	507	3.63011	10	4	6	0.2	0.005	RASA2	RNF7	
chr3	+(141438233..141438933)	700	1.68843	10	7	3	0.4	0.992	RASA2	RNF7	

chr3	+(141905067..141905592)	525	3.63011	9	5	4	0.1111111	0.016	TFDP2	GK5	
chr3	+(142486147..142487544)	1397	1.68843	14	7	7	0	0.99912744	TRPC1	PCOLCE2	
chr3	+(142745574..142746080)	506	3.63011	12	6	6	0	0.00520281	SR140	CHST2	
chr3	+(143434807..143435667)	860	0.00063	22	12	10	0.0909091	3.8063E-05	CHST2	SLC9A9	
chr3	+(143692199..143692709)	510	3.63011	6	4	2	0.3333333	0.067	C3orf58	PLOD2	
chr3	+(146303701..146304203)	502	3.63011	7	3	4	0.1428571	0.057	PLSCR1	PLSCR5	
chr3	+(146962569..146963107)	538	3.63011	6	3	3	0	0.05	PLSCR5	ZIC4	v
chr3	+(147111503..147112200)	697	3.63011	9	6	3	0.3333333	0.988	PLSCR5	ZIC4	v
chr3	+(148552243..148552943)	700	0.18343	16	10	6	0.25	0.99538163	CPB1	CPA3	v
chr3	+(151160258..151160957)	699	3.63011	10	7	3	0.4	0.058	P2RY12	IGSF10	
chr3	+(151164593..151165113)	520	0.18343	12	8	4	0.3333333	0.99671074	P2RY12	IGSF10	
chr3	+(152255412..152256110)	698	0.091	11	6	5	0.0909091	0.00308495	TMEM14E	P2RY1	
chr3	+(152553725..152554277)	552	3.63011	10	4	6	0.2	0.005	P2RY1	RAP2B	
chr3	+(152846744..152847252)	508	3.63011	6	3	3	0	0.05	P2RY1	RAP2B	
chr3	+(155545697..155546218)	521	3.63011	12	6	6	0	0.0186865	C3orf33	SLC33A1	
chr3	+(156893884..156894444)	560	0.36666	9	5	4	0.1111111	0.008	CCNL1	VEPH1	
chr3	+(157081810..157082328)	518	3.63011	12	6	6	0	0.21166982	CCNL1	VEPH1	
chr3	+(164410632..164411249)	617	3.63011	6	2	4	0.3333333	0.067	LOC647107	SI	
chr3	+(164756774..164757316)	542	3.63011	9	6	3	0.3333333	0.012	LOC647107	SI	
chr3	+(170744203..170744704)	501	1.68843	9	5	4	0.1111111	0.008	EIF5A2	SLC2A2	
chr3	+(171057052..171057986)	934	0.18343	16	6	10	0.25	0.00056905	SLC2A2	TNIK	
chr3	+(171332125..171332825)	700	0.04455	12	7	5	0.1666667	0.00224163	MIR569	PLD1	
chr3	+(179407653..179408257)	604	3.63011	11	5	6	0.0909091	0.05017413	USP13	PEX5L	
chr3	+(180702263..180702836)	573	0.74291	9	4	5	0.1111111	0.032	FXR1	DNAJC19	
chr3	+(183029232..183029870)	638	3.63011	10	6	4	0.2	0.033	LAMP3	MCF2L2	
chr3	+(183056439..183056952)	513	3.63011	6	4	2	0.3333333	0.067	LAMP3	MCF2L2	
chr3	+(183209950..183210601)	651	3.63011	9	3	6	0.3333333	0.024	B3GNT5	KLHL6	
chr3	+(183682791..183683295)	504	0.74291	15	9	6	0.2	0.31867594	PARL	ABCC5	
chr3	+(184069346..184070568)	1222	0.04455	19	7	12	0.2631579	0.99980713	FAM131A	CLCN2	
chr3	+(184071289..184071971)	682	1.68843	8	4	4	0	0.171	FAM131A	CLCN2	
chr3	+(184297309..184297862)	553	3.63011	6	2	4	0.3333333	0.067	EPHB3	MAGEF1	
chr3	+(184612437..184612942)	505	3.63011	7	4	3	0.1428571	0.029	VPS8	C3orf70	
chr3	+(184963528..184964214)	686	0.74291	9	5	4	0.1111111	0.016	C3orf70	EHHADH	
chr3	+(188423467..188424167)	700	0.18343	10	4	6	0.2	0.005	FLJ42393	TPRG1	

chr3	+(194083912..194084424)	512	3.63011	8	4	4	0	0.014	CPN2	LRRC15
chr3	+(195438833..195439416)	583	3.63011	9	6	3	0.3333333	0.012	MIR570	MUC20
chr3	+(195447527..195448028)	501	3.63011	9	3	6	0.3333333	0.131	MIR570	MUC20
chr3	+(195506741..195507268)	527	2.38872	34	18	16	0.0588235	0.15851131	MUC20	MUC4
chr3	+(195507762..195508293)	531	2.57182	34	20	14	0.1764706	0.00715294	MUC20	MUC4
chr3	+(195512800..195513393)	593	0.87094	53	35	18	0.3207547	0.19381167	MUC20	MUC4
chr3	+(195664573..195665115)	542	3.63011	9	4	5	0.1111111	0.008	TNK2	SDHAP1
chr3	+(195691938..195692443)	505	3.63011	9	3	6	0.3333333	0.012	TNK2	SDHAP1
chr3	+(195954793..195955401)	608	0.74291	13	7	6	0.0769231	0.84134475	OSTalpha	PCYT1A
chr3	+(196385655..196386355)	700	0.18343	15	5	10	0.3333333	0.99890018	LRRC33	C3orf34
chr3	+(197836701..197837228)	527	3.63011	9	3	6	0.3333333	0.012	LOC348840	FAM157A
chr3	+(197847041..197847673)	632	1.68843	12	4	8	0.3333333	0.285	LOC348840	FAM157A
chr3	+(197894388..197894982)	594	3.39201	49	19	30	0.2244898	5.2068E-07	FAM157A	
chr4	+(337427..338121)	694	0.14315	14	8	6	0.1428571	0.00225435	ZNF141	ABCA11P
chr4	+(420377..420974)	597	1.42588	9	5	4	0.1111111	0.016	ZNF141	ABCA11P
chr4	+(515507..516079)	572	0.64584	16	8	8	0	0.6236431	PIGG	PDE6B
chr4	+(524116..524769)	653	1.42588	10	7	3	0.4	0.033	PIGG	PDE6B
chr4	+(884268..885250)	982	0.64584	15	10	5	0.3333333	0.88966432	CPLX1	GAK
chr4	+(905379..906933)	1554	0.32738	24	8	16	0.3333333	0.99995558	CPLX1	GAK
chr4	+(1074949..1075595)	646	1.42588	10	3	7	0.4	0.333	FGFRL1	RNF212
chr4	+(1186782..1187426)	644	3.26113	6	2	4	0.3333333	0.067	TMED11P	SPON2
chr4	+(1283869..1284569)	700	0.64584	13	5	8	0.2307692	0.9982926	MAEA	KIAA1530
chr4	+(1310139..1310862)	723	0.00937	17	7	10	0.1764706	0.08592868	MAEA	KIAA1530
chr4	+(1348360..1348871)	511	1.42588	7	3	4	0.1428571	0.029	KIAA1530	CRIPAK
chr4	+(1374267..1374901)	634	1.42588	7	3	4	0.1428571	0.029	KIAA1530	CRIPAK
chr4	+(1387971..1388614)	643	0.03083	23	10	13	0.1304348	0.94656814	CRIPAK	FAM53A
chr4	+(1482400..1483100)	700	0.32738	9	6	3	0.3333333	0.012	CRIPAK	FAM53A
chr4	+(1619538..1620110)	572	3.26113	7	3	4	0.1428571	0.029	CRIPAK	FAM53A
chr4	+(1734044..1734744)	700	1.42588	11	4	7	0.2727273	0.997	TACC3	FGFR3
chr4	+(2410905..2411604)	699	0.32738	9	4	5	0.1111111	0.008	MXD4	ZFYVE28
chr4	+(2453206..2453811)	605	3.26113	6	3	3	0	0.05	LOC402160	RNF4
chr4	+(2701426..2701952)	526	3.26113	10	5	5	0	0.12529603	FAM193A	TNIP2
chr4	+(2830435..2831135)	700	0.02116	13	9	4	0.3846154	0.001	SH3BP2	ADD1
chr4	+(2931884..2932398)	514	3.26113	6	3	3	0	0.05	ADD1	MFSD10

chr4	+(2934448..2934988)	540	3.26113	8	4	4	0	0.014	ADD1	MFSD10
chr4	+(2945603..2946200)	597	1.42588	9	3	6	0.3333333	0.012	C4orf10	NOP14
chr4	+(3134398..3135029)	631	0.14315	10	7	3	0.4	0.008	HTT	C4orf44
chr4	+(3225088..3225788)	700	0.14315	11	4	7	0.2727273	0.003	HTT	C4orf44
chr4	+(3439244..3439944)	700	0.06643	11	6	5	0.0909091	0.00308495	RGS12	HGFAC
chr4	+(3838267..3839121)	854	0.32738	16	11	5	0.375	0.97629081	ADRA2C	LOC348926
chr4	+(3944877..3945387)	510	1.42588	15	9	6	0.2	0.00073136	ADRA2C	LOC348926
chr4	+(4164142..4164750)	608	3.26113	6	2	4	0.3333333	0.067	LOC348926	OTOP1
chr4	+(4281019..4281536)	517	3.26113	10	7	3	0.4	0.133	TMEM128	LYAR
chr4	+(5627165..5627666)	501	3.26113	10	4	6	0.2	0.005	C4orf6	EVC2
chr4	+(5844361..5844883)	522	1.42588	7	4	3	0.1428571	0.029	EVC	CRMP1
chr4	+(6082682..6083955)	1273	1.42588	13	6	7	0.0769231	0.9986501	CRMP1	JAKMIP1
chr4	+(6149183..6149702)	519	1.42588	7	4	3	0.1428571	0.029	CRMP1	JAKMIP1
chr4	+(6586794..6587315)	521	1.42588	7	3	4	0.1428571	0.029	MAN2B2	MRFAP1
chr4	+(7770526..7771047)	521	1.42588	7	3	4	0.1428571	0.029	AFAP1-AS1	AFAP1
chr4	+(8051844..8052496)	652	0.06643	11	7	4	0.2727273	0.003	AFAP1	ABLIM2
chr4	+(8081232..8082406)	1174	0.64584	16	8	8	0	0.00038877	AFAP1	ABLIM2
chr4	+(8114090..8114776)	686	1.42588	10	7	3	0.4	0.992	AFAP1	ABLIM2
chr4	+(8178303..8178862)	559	1.42588	10	3	7	0.4	0.992	ABLIM2	SH3TC1
chr4	+(8220628..8221318)	690	0.06643	15	9	6	0.2	0.00921106	SH3TC1	HTRA3
chr4	+(8274082..8274785)	703	0.00937	14	8	6	0.1428571	0.00097289	HTRA3	ACOX3
chr4	+(8279229..8280228)	999	0.64584	14	8	6	0.1428571	0.00097289	HTRA3	ACOX3
chr4	+(9261120..9261645)	525	3.26113	12	7	5	0.1666667	0.18587565	USP17_dup3	USP17_dup4
chr4	+(9265318..9265948)	630	0.64584	20	7	13	0.3	0.00050347	USP17_dup3	USP17_dup4
chr4	+(9269287..9269870)	583	3.26113	11	5	6	0.0909091	0.18065522	USP17_dup3	USP17_dup4
chr4	+(9327730..9328231)	501	4.06502	27	18	9	0.3333333	0.01982494	USP17_dup4	USP17_dup5
chr4	+(9342188..9342849)	661	0.97025	21	8	13	0.2380952	0.00092257	USP17_dup6	USP17_dup7
chr4	+(9345886..9346406)	520	3.26113	12	8	4	0.3333333	0.024	USP17_dup6	USP17_dup7
chr4	+(9347144..9347677)	533	1.42588	10	5	5	0	0.05859256	USP17_dup6	USP17_dup7
chr4	+(9365731..9366239)	508	1.42588	18	9	9	0	0.13484495	USP17_dup9	USP17L6P
chr4	+(9945245..9946090)	845	0.00937	14	6	8	0.1428571	0.00097289	DRD5	SLC2A9
chr4	+(13612537..13613145)	608	1.42588	13	7	6	0.0769231	0.0013499	LOC285548	BOD1L
chr4	+(16504049..16504749)	700	0.32738	12	8	4	0.3333333	0.008	FLJ39653	LDB2
chr4	+(17624988..17625561)	573	3.26113	8	3	5	0.25	0.071	MED28	FAM184B

chr4	+(17816375..17817007)	632	0.64584	11	7	4	0.2727273	0.012	NCAPG	LCORL
chr4	+(17842035..17842537)	502	3.26113	8	4	4	0	0.014	NCAPG	LCORL
chr4	+(17885491..17886016)	525	1.42588	15	5	10	0.3333333	0.9669037	NCAPG	LCORL
chr4	+(17964401..17965049)	648	0.14315	14	7	7	0	0.00300561	NCAPG	LCORL
chr4	+(39846051..39846639)	588	0.64584	9	6	3	0.3333333	0.012	UBE2K	PDS5A
chr4	+(40034993..40035505)	512	0.14315	10	5	5	0	0.00451172	PDS5A	LOC344967
chr4	+(40788192..40788710)	518	0.14315	20	9	11	0.1	0.15252943	NSUN7	APBB2
chr4	+(42582969..42583669)	700	3.26113	10	4	6	0.2	0.995	SHISA3	ATP8A1
chr4	+(47601408..47601930)	522	3.26113	6	3	3	0	0.05	ATP10D	CORIN
chr4	+(48529767..48530271)	504	3.26113	7	3	4	0.1428571	0.2	ZAR1	FRYL
chr4	+(54384989..54385626)	637	1.42588	7	3	4	0.1428571	0.029	FIP1L1	LNX1
chr4	+(56229952..56230572)	620	0.64584	16	9	7	0.125	0.11174712	SRD5A3	TMEM165
chr4	+(57302720..57303373)	653	0.00501	15	8	7	0.0666667	0.00059687	PAICS	SRP72
chr4	+(57352321..57352847)	526	3.26113	6	3	3	0	0.05	SRP72	ARL9
chr4	+(59663327..59664027)	700	0.64584	13	8	5	0.2307692	0.0017074	LOC255130	LPHN3
chr4	+(62935984..62936665)	681	1.42588	9	4	5	0.1111111	0.032	LPHN3	TECRL
chr4	+(68338080..68338590)	510	3.26113	7	3	4	0.1428571	0.029	LOC100144602	CENPC1
chr4	+(68377804..68378311)	507	3.26113	11	5	6	0.0909091	0.5	LOC100144602	CENPC1
chr4	+(68384881..68385445)	564	1.42588	12	5	7	0.1666667	0.06144014	LOC100144602	CENPC1
chr4	+(69362003..69362917)	914	3.26113	14	7	7	0	0.2826494	TMPRSS11E	UGT2B17
chr4	+(71274923..71275451)	528	3.26113	9	4	5	0.1111111	0.032	PROL1	MUC7
chr4	+(71346784..71347353)	569	0.25864	40	19	21	0.05	0.58048319	MUC7	AMTN
chr4	+(72338234..72338888)	654	0.64584	9	3	6	0.3333333	0.012	SLC4A4	GC
chr4	+(74285694..74286267)	573	3.26113	6	2	4	0.3333333	0.067	ALB	AFP
chr4	+(75484662..75485212)	550	1.42588	10	7	3	0.4	0.258	AREG_dup2	BTC
chr4	+(75675614..75676190)	576	0.64584	9	5	4	0.1111111	0.008	AREG_dup2	BTC
chr4	+(78808198..78808728)	530	3.26113	7	3	4	0.1428571	0.029	MRPL1	FRAS1
chr4	+(79102219..79102722)	503	3.26113	14	9	5	0.2857143	0.63055866	FRAS1	ANXA3
chr4	+(79202119..79202731)	612	1.42588	11	4	7	0.2727273	0.464	FRAS1	ANXA3
chr4	+(79368898..79369651)	753	0.64584	13	6	7	0.0769231	0.005064	FRAS1	ANXA3
chr4	+(83680099..83680682)	583	3.26113	6	2	4	0.3333333	0.067	C4orf11	SCD5
chr4	+(84190844..84191401)	557	0.64584	10	7	3	0.4	0.033	PLAC8	COQ2
chr4	+(84383464..84384253)	789	0.00032	28	15	13	0.0714286	5.9919E-05	MRPS18C	FAM175A
chr4	+(87666206..87666716)	510	3.26113	11	6	5	0.0909091	0.01422987	PTPN13	SLC10A6

chr4	+(88278281..88278782)	501	3.26113	7	4	3	0.1428571	0.029	HSD17B13	HSD17B11
chr4	+(88310287..88310888)	601	3.26113	6	3	3	0	0.05	HSD17B13	HSD17B11
chr4	+(88535180..88535705)	525	4.06502	27	10	17	0.2592593	0.04389915	DSPP	DMP1
chr4	+(88536358..88537243)	885	0.10874	146	90	56	0.2328767	0.9407998	DSPP	DMP1
chr4	+(88537382..88538061)	679	0.18652	43	29	14	0.3488372	0.07700791	DSPP	DMP1
chr4	+(88978943..88979449)	506	3.26113	10	4	6	0.2	0.033	PKD2	ABCG2
chr4	+(92108734..92109259)	525	3.26113	6	2	4	0.3333333	0.067	TMSL3	GRID2
chr4	+(100273675..100274185)	510	1.42588	11	6	5	0.0909091	0.02230486	ADH1B	ADH1C
chr4	+(100450840..100451540)	700	3.26113	11	6	5	0.0909091	0.10062131	C4orf17	RG9MTD2
chr4	+(100851493..100852002)	509	3.26113	9	4	5	0.1111111	0.016	MAPKSP1	DNAJB14
chr4	+(100867498..100868006)	508	3.26113	6	4	2	0.3333333	0.067	MAPKSP1	DNAJB14
chr4	+(102019339..102019886)	547	0.32738	15	10	5	0.3333333	0.01374317	EMCN	PPP3CA
chr4	+(103555695..103556395)	700	0.14315	13	9	4	0.3846154	0.01	NFKB1	MANBA
chr4	+(103610394..103611057)	663	1.42588	11	4	7	0.2727273	0.003	NFKB1	MANBA
chr4	+(103910797..103911369)	572	1.42588	8	5	3	0.25	0.018	CISD2	NHEDC1
chr4	+(104070075..104070593)	518	3.26113	9	4	5	0.1111111	0.056	BDH2	CENPE
chr4	+(106159215..106159724)	509	3.26113	11	6	5	0.0909091	0.42756607	TET2	PPA2
chr4	+(106317174..106317692)	518	3.26113	6	2	4	0.3333333	0.067	TET2	PPA2
chr4	+(109588104..109588644)	540	0.64584	15	8	7	0.0666667	0.00388698	OSTC	AGXT2L1
chr4	+(120176589..120177176)	587	1.42588	7	4	3	0.1428571	0.029	USP53	C4orf3
chr4	+(120194618..120195129)	511	3.26113	12	5	7	0.1666667	0.18587565	USP53	C4orf3
chr4	+(122774004..122774544)	540	1.42588	9	6	3	0.3333333	0.012	CCNA2	BBS7
chr4	+(123855131..123855679)	548	3.26113	7	4	3	0.1428571	0.114	SPATA5	SPRY1
chr4	+(130030210..130030752)	542	3.26113	7	3	4	0.1428571	0.029	C4orf33	PCDH10
chr4	+(139992602..139993375)	773	3.26113	12	6	6	0	0.00815459	CCRN4L	ELF2
chr4	+(141300346..141300879)	533	3.26113	13	5	8	0.2307692	0.27909232	LOC100129858	CLGN
chr4	+(141448425..141448974)	549	3.26113	9	4	5	0.1111111	0.056	ELMOD2	UCP1
chr4	+(144940420..144940923)	503	3.26113	13	6	7	0.0769231	0.01606229	GYPE	GYPB
chr4	+(145061806..145062323)	517	0.64584	16	8	8	0	0.02935371	GYPB	GYPA
chr4	+(145561103..145562113)	1010	0.64584	15	8	7	0.0666667	0.00059687	GYPA	HHIP
chr4	+(145567665..145568191)	526	1.42588	9	4	5	0.1111111	0.008	HHIP	ANAPC10
chr4	+(148809222..148810455)	1233	0.06643	17	11	6	0.2941176	0.00045556	ARHGAP10	NR3C2
chr4	+(151829397..151829929)	532	3.26113	9	5	4	0.1111111	0.056	DCLK2	LRBA
chr4	+(152096031..152096536)	505	3.26113	13	8	5	0.2307692	0.98594598	SNORD73A	SH3D19

chr4	+(152179715..152180521)	806	0.00501	15	8	7	0.0666667	0.00059687	SH3D19	PRSS48
chr4	+(153332209..153332961)	752	0.32738	19	8	11	0.1578947	0.01949431	PET112L	FBXW7
chr4	+(153897901..153898601)	700	1.42588	10	7	3	0.4	0.008	FHDC1	TRIM2
chr4	+(154556486..154557186)	700	1.42588	13	7	6	0.0769231	0.005064	KIAA0922	TLR2
chr4	+(155241567..155242196)	629	1.42588	11	4	7	0.2727273	0.021	SFRP2	DCHS2
chr4	+(157693576..157694243)	667	1.42588	9	3	6	0.3333333	0.726	CTSO	PDGFC
chr4	+(157731822..157732421)	599	1.42588	8	4	4	0	0.014	CTSO	PDGFC
chr4	+(164085423..164085982)	559	3.26113	10	6	4	0.2	0.176	FSTL5	NAF1
chr4	+(164440371..164440979)	608	1.42588	8	5	3	0.25	0.071	C4orf43	40969
chr4	+(165110796..165111347)	551	3.26113	10	7	3	0.4	0.258	C4orf43	40969
chr4	+(165848712..165849263)	551	1.42588	13	6	7	0.0769231	0.05804158	ANP32C	TRIM61
chr4	+(165879919..165880437)	518	3.26113	10	6	4	0.2	0.086	ANP32C	TRIM61
chr4	+(166199839..166200594)	755	1.42588	17	11	6	0.2941176	0.34383645	KLHL2	GK3P
chr4	+(166200602..166201144)	542	0.32738	16	9	7	0.125	0.88825288	KLHL2	GK3P
chr4	+(166232529..166233039)	510	1.42588	14	8	6	0.1428571	0.01943355	GK3P	SC4MOL
chr4	+(169085110..169085645)	535	3.26113	8	4	4	0	0.014	ANXA10	DDX60
chr4	+(169095320..169096008)	688	0.64584	8	4	4	0	0.014	ANXA10	DDX60
chr4	+(170601068..170601575)	507	1.42588	11	5	6	0.0909091	0.00529357	CLCN3	C4orf27
chr4	+(173301214..173301723)	509	3.26113	9	5	4	0.1111111	0.095	GALNTL6	GALNT7
chr4	+(184588212..184588721)	509	1.42588	10	7	3	0.4	0.033	C4orf41	STOX2
chr4	+(184728717..184729266)	549	0.32738	11	7	4	0.2727273	0.158	C4orf41	STOX2
chr4	+(184931991..184932691)	700	0.00937	21	14	7	0.3333333	0.00288676	STOX2	ENPP6
chr4	+(185606481..185607103)	622	0.32738	17	11	6	0.2941176	0.06583401	CCDC111	MLF1IP
chr4	+(185634084..185634743)	659	0.64584	8	4	4	0	0.014	CCDC111	MLF1IP
chr4	+(186111454..186111965)	511	3.26113	10	5	5	0	0.00451172	SLC25A4	KIAA1430
chr4	+(186510810..186511326)	516	3.26113	8	5	3	0.25	0.286	PDLIM3	SORBS2
chr4	+(186536000..186536528)	528	0.32738	12	8	4	0.3333333	0.014	PDLIM3	SORBS2
chr4	+(186544686..186545263)	577	3.26113	6	4	2	0.3333333	0.067	PDLIM3	SORBS2
chr4	+(186598120..186598630)	510	1.42588	10	5	5	0	0.0081468	PDLIM3	SORBS2
chr4	+(186999866..187000432)	566	1.42588	8	3	5	0.25	0.018	TLR3	FAM149A
chr4	+(187074560..187075107)	547	0.14315	13	9	4	0.3846154	0.001	FAM149A	CYP4V2
chr4	+(187350999..187351699)	700	0.14315	10	7	3	0.4	0.008	F11	LOC285441
chr4	+(188925856..188926556)	700	0.14315	12	8	4	0.3333333	0.024	ZFP42	TRIML2
chr4	+(190873360..190873864)	504	1.42588	12	7	5	0.1666667	0.34237168	FRG1	TUBB4Q

chr4	+(190878291..190878972)	681	0.06889	39	23	16	0.1794872	2.1444E-06	FRG1	TUBB4Q
chr5	+(154635..155335)	700	0.05995	13	6	7	0.0769231	0.00332094	PLEKHG4B	LRRC14B
chr5	+(223220..223731)	511	0.01049	19	6	13	0.3684211	0.0003125	SDHA	PDCD6
chr5	+(231083..231703)	620	2.83731	9	6	3	0.3333333	0.869	SDHA	PDCD6
chr5	+(319126..319641)	515	0.26306	9	5	4	0.1111111	0.008	AHRR	LOC100310782
chr5	+(427426..428126)	700	1.33407	9	4	5	0.1111111	0.008	LOC100310782	C5orf55
chr5	+(479581..480256)	675	0.26306	10	5	5	0	0.01414006	LOC25845	SLC9A3
chr5	+(509817..510722)	905	0.61213	15	8	7	0.0666667	0.00059687	LOC25845	SLC9A3
chr5	+(557870..558570)	700	1.33407	12	5	7	0.1666667	0.00224163	SLC9A3	CEP72
chr5	+(627637..628310)	673	0.11662	10	5	5	0	0.00451172	CEP72	TPPP
chr5	+(665301..665956)	655	0.11662	11	7	4	0.2727273	0.082	CEP72	TPPP
chr5	+(685378..686078)	700	0.61213	12	8	4	0.3333333	0.976	CEP72	TPPP
chr5	+(825047..825734)	687	0.26306	9	6	3	0.3333333	0.012	TPPP	ZDHHC11
chr5	+(886582..887136)	554	2.83731	8	5	3	0.25	0.125	ZDHHC11	BRD9
chr5	+(992369..992938)	569	0.61213	8	3	5	0.25	0.018	TRIP13	NKD2
chr5	+(1010727..1011427)	700	0.11662	10	4	6	0.2	0.005	NKD2	SLC12A7
chr5	+(1068926..1069626)	700	2.83731	10	4	6	0.2	0.005	NKD2	SLC12A7
chr5	+(1101178..1101878)	700	0.02552	12	7	5	0.1666667	0.00224163	NKD2	SLC12A7
chr5	+(1167853..1168547)	694	2.83731	10	4	6	0.2	0.995	SLC12A7	SLC6A19
chr5	+(1226315..1226932)	617	2.83731	8	3	5	0.25	0.018	SLC6A18	TERT
chr5	+(1230968..1231831)	863	0.05995	14	7	7	0	0.08985625	SLC6A18	TERT
chr5	+(1240260..1240836)	576	0.26306	12	8	4	0.3333333	0.533	SLC6A18	TERT
chr5	+(1271259..1271846)	587	0.11662	15	8	7	0.0666667	0.00059687	SLC6A18	TERT
chr5	+(1282022..1282737)	715	3E-07	27	10	17	0.2592593	9.8696E-06	SLC6A18	TERT
chr5	+(1393018..1393636)	618	0.61213	8	5	3	0.25	0.018	CLPTM1L	SLC6A3
chr5	+(1493069..1493997)	928	0.26306	16	6	10	0.25	0.00056905	SLC6A3	LPCAT1
chr5	+(1509328..1509836)	508	2.83731	9	5	4	0.1111111	0.008	SLC6A3	LPCAT1
chr5	+(1570050..1570673)	623	2.39506	13	7	6	0.0769231	0.0013499	LPCAT1	SDHAP3
chr5	+(1626668..1627291)	623	2.83731	6	2	4	0.3333333	0.067	SDHAP3	LOC728613
chr5	+(4648371..4649071)	700	1.33407	11	4	7	0.2727273	0.997	IRX1	LOC340094
chr5	+(5034624..5035324)	700	0.01049	16	9	7	0.125	0.31691947	LOC340094	ADAMTS16
chr5	+(6235935..6236635)	700	0.05995	11	5	6	0.0909091	0.00308495	KIAA0947	FLJ33360
chr5	+(6319040..6319740)	700	0.11662	10	4	6	0.2	0.005	KIAA0947	FLJ33360
chr5	+(6361250..6361950)	700	0.00503	14	9	5	0.2857143	0.0013499	FLJ33360	MED10

chr5	+(6491376..6492006)	630	0.00503	14	6	8	0.1428571	0.00097289	UBE2QL1	LOC255167	
chr5	+(6609699..6610321)	622	1.33407	10	5	5	0	0.00451172	LOC255167	NSUN2	
chr5	+(7599020..7599720)	700	0.02552	12	7	5	0.1666667	0.00224163	ADCY2	C5orf49	
chr5	+(9630017..9630711)	694	0.26306	23	7	16	0.3913043	0.1425247	SNORD123	TAS2R1	
chr5	+(11240317..11240992)	675	0.26306	10	4	6	0.2	0.005	DAP	CTNND2	
chr5	+(12292420..12292992)	572	0.61213	8	5	3	0.25	0.018	CTNND2	TAG	
chr5	+(12488527..12489127)	600	2.83731	6	3	3	0	0.05	CTNND2	TAG	
chr5	+(14359106..14359640)	534	1.33407	10	3	7	0.4	0.008	TRIO	FAM105A	
chr5	+(14703163..14704283)	1120	0.61213	15	7	8	0.0666667	0.99940313	FAM105B	ANKH	
chr5	+(14797340..14798206)	866	0.26306	19	9	10	0.0526316	0.01688149	FAM105B	ANKH	
chr5	+(15734930..15735596)	666	2.83731	6	3	3	0	0.05	FBXL7	40979	
chr5	+(28927128..28927828)	700	0.11662	13	6	7	0.0769231	0.0992714	LOC729862	CDH6	
chr5	+(31750402..31751102)	700	2.83731	10	6	4	0.2	0.005	C5orf22	PDZD2	
chr5	+(31940214..31940892)	678	2.83731	9	6	3	0.3333333	0.988	MIR4279	GOLPH3	
chr5	+(32403815..32404395)	580	0.61213	10	3	7	0.4	0.008	MTMR12	ZFR	
chr5	+(34945894..34946442)	548	1.33407	8	5	3	0.25	0.125	DNAJC21	AGXT2	
chr5	+(35324605..35325196)	591	2.83731	6	3	3	0	0.05	PRLR	SPEF2	
chr5	+(35705432..35706010)	578	2.83731	9	3	6	0.3333333	0.024	SPEF2	IL7R	
chr5	+(35874407..35874908)	501	2.83731	12	4	8	0.3333333	0.024	IL7R	CAPSL	
chr5	+(36035695..36036234)	539	1.67066	18	11	7	0.2222222	0.0469197	UGT3A1	UGT3A2	
chr5	+(36265330..36265833)	503	2.83731	7	3	4	0.1428571	0.314	C5orf33	RANBP3L	
chr5	+(37000653..37001160)	507	1.33407	15	8	7	0.0666667	0.01031878	NIPBL	C5orf42	
chr5	+(37021909..37022432)	523	2.83731	6	2	4	0.3333333	0.067	NIPBL	C5orf42	
chr5	+(37291661..37292261)	600	1.33407	8	5	3	0.25	0.018	C5orf42	NUP155	v
chr5	+(38511805..38512315)	510	2.83731	6	4	2	0.3333333	0.067	EGFLAM	LIFR	
chr5	+(38949773..38950669)	896	2.83731	20	10	10	0	0.08680868	OSMR	RICTOR	
chr5	+(42336965..42337571)	606	1.33407	7	4	3	0.1428571	0.029	FBXO4	GHR	
chr5	+(42582473..42583124)	651	2.83731	6	4	2	0.3333333	0.067	GHR	CCDC152	
chr5	+(43659063..43659638)	575	2.83731	7	3	4	0.1428571	0.029	NNT	FGF10	
chr5	+(49695477..49695979)	502	2.83731	6	4	2	0.3333333	0.067	HCN1	EMB	
chr5	+(50111038..50111574)	536	0.61213	8	3	5	0.25	0.018	PARP8	ISL1	
chr5	+(54720683..54721322)	639	2.83731	6	4	2	0.3333333	0.067	SKIV2L2	PPAP2A	v
chr5	+(58271466..58272166)	700	0.15683	15	6	9	0.2	0.00073136	RAB3C	PDE4D	
chr5	+(58292897..58293868)	971	0.00188	25	15	10	0.2	1.5895E-05	RAB3C	PDE4D	

chr5	+(60859837..60861019)	1182	0.02552	18	6	12	0.3333333	0.99962648	ZSWIM6	FLJ37543
chr5	+(60982471..60983079)	608	1.33407	9	4	5	0.1111111	0.016	FLJ37543	KIF2A
chr5	+(61653830..61654447)	617	0.61213	12	6	6	0	0.07477068	KIF2A	DIMT1L
chr5	+(61779596..61780293)	697	0.26306	11	6	5	0.0909091	0.01422987	IPO11	LRRC70
chr5	+(61876793..61877442)	649	0.61213	9	3	6	0.3333333	0.012	LRRC70	HTR1A
chr5	+(63626629..63627874)	1245	0.11662	20	10	10	0	7.8526E-05	RNF180	RGS7BP
chr5	+(63802062..63802751)	689	1.33407	10	3	7	0.4	0.258	RNF180	RGS7BP
chr5	+(64082214..64082716)	502	2.83731	9	6	3	0.3333333	0.024	CWC27	ADAMTS6
chr5	+(64181048..64181562)	514	1.33407	11	6	5	0.0909091	0.00881105	CWC27	ADAMTS6
chr5	+(64748632..64749146)	514	2.83731	10	6	4	0.2	0.005	CWC27	ADAMTS6
chr5	+(65370673..65371280)	607	0.11662	12	4	8	0.3333333	0.00328926	LOC100303749	SREK1
chr5	+(65798804..65799380)	576	2.83731	6	3	3	0	0.05	SREK1	MAST4
chr5	+(66456075..66456610)	535	0.61213	8	4	4	0	0.014	MAST4	CD180
chr5	+(66460838..66461597)	759	0.11662	15	8	7	0.0666667	0.00059687	MAST4	CD180
chr5	+(67634578..67635418)	840	0.00188	15	9	6	0.2	0.00073136	PIK3R1	SLC30A5
chr5	+(68370603..68371247)	644	1.33407	9	6	3	0.3333333	0.274	PIK3R1	SLC30A5
chr5	+(68411800..68412308)	508	2.83731	9	5	4	0.1111111	0.452	SLC30A5	CCNB1
chr5	+(69715932..69716549)	617	1.67066	22	15	7	0.3636364	0.01878678	GTF2H2B	SMA5
chr5	+(69717200..69717715)	515	0.26306	14	6	8	0.1428571	0.00097289	GTF2H2B	SMA5
chr5	+(69729790..69730476)	686	0.05995	17	8	9	0.0588235	0.06182886	GTF2H2B	SMA5
chr5	+(69737088..69737863)	775	2.5E-05	49	30	19	0.2244898	1.4452E-06	GTF2H2B	SMA5
chr5	+(70212555..70213419)	864	0.12647	58	31	27	0.0689655	7.9852E-09	SERF1B_dup2	SMN1_dup2
chr5	+(70234528..70235125)	597	0.61698	48	33	15	0.375	1.3778E-05	SMN2_dup2	NAIP
chr5	+(70240340..70240890)	550	4.35408	20	10	10	0	7.8526E-05	SMN2_dup2	NAIP
chr5	+(70241458..70242129)	671	0.14093	30	12	18	0.2	0.00115184	SMN2_dup2	NAIP
chr5	+(70840239..70840783)	544	2.83731	10	6	4	0.2	0.967	BDP1	MCCC2
chr5	+(70945705..70946210)	505	0.61213	9	5	4	0.1111111	0.008	MCCC2	CARTPT
chr5	+(71295652..71296350)	698	0.61213	8	3	5	0.25	0.018	CARTPT	MAP1B
chr5	+(71491230..71491774)	544	1.33407	16	6	10	0.25	0.45681333	MAP1B	MRPS27
chr5	+(71648157..71648857)	700	2.83731	15	5	10	0.3333333	0.5	PTCD2	ZNF366
chr5	+(71739635..71740251)	616	1.33407	12	6	6	0	0.16833419	PTCD2	ZNF366
chr5	+(71756536..71757091)	555	2.83731	10	7	3	0.4	0.333	PTCD2	ZNF366
chr5	+(72192646..72193173)	527	0.61213	12	7	5	0.1666667	0.34237168	TNPO1	FCHO2
chr5	+(72743508..72744034)	526	2.83731	6	4	2	0.3333333	0.067	TMEM174	FOXD1

chr5	+(75884349..75885028)	679	1.33407	11	7	4	0.2727273	0.158	IQGAP2	F2RL2	
chr5	+(76760355..76760954)	599	2.83731	11	7	4	0.2727273	0.003	PDE8B	WDR41	
chr5	+(77788303..77788833)	530	0.61213	8	3	5	0.25	0.018	SCAMP1	LHFPL2	
chr5	+(78925648..78926223)	575	0.61213	8	3	5	0.25	0.018	PAPD4	CMYA5	
chr5	+(79374457..79375029)	572	2.83731	9	3	6	0.3333333	0.548	THBS4	SERINC5	
chr5	+(80370767..80371991)	1224	2.83731	12	6	6	0	0.99802612	RASGRF2	RNU5E	v
chr5	+(85578378..85579234)	856	0.11662	23	11	12	0.0434783	0.00044452	NBPF22P	COX7C	
chr5	+(85580528..85581208)	680	0.00753	30	19	11	0.2666667	0.01843193	NBPF22P	COX7C	
chr5	+(85588502..85589270)	768	0.5982	35	13	22	0.2571429	0.00094598	NBPF22P	COX7C	
chr5	+(85591790..85592611)	821	1.33407	13	5	8	0.2307692	0.00420773	NBPF22P	COX7C	
chr5	+(89920656..89921203)	547	1.33407	8	3	5	0.25	0.286	GPR98	ARRDC3	
chr5	+(93929385..93929902)	517	2.83731	9	5	4	0.1111111	0.056	POU5F2	C5orf36	
chr5	+(95087688..95088197)	509	1.33407	10	7	3	0.4	0.192	RHOBTB3	GLRX	
chr5	+(95158029..95158555)	526	2.83731	10	6	4	0.2	0.381	RHOBTB3	GLRX	
chr5	+(95249292..95249813)	521	0.61213	10	4	6	0.2	0.005	C5orf27	ELL2	
chr5	+(101590692..101591329)	637	2.83731	6	3	3	0	0.05	ST8SIA4	SLCO4C1	
chr5	+(101592684..101593233)	549	1.33407	9	5	4	0.1111111	0.032	ST8SIA4	SLCO4C1	
chr5	+(102285230..102285748)	518	2.83731	13	8	5	0.2307692	0.27909232	PAM	GIN1	
chr5	+(102432669..102433183)	514	0.61213	12	6	6	0	0.00520281	PAM	GIN1	
chr5	+(102440107..102440619)	512	2.83731	8	4	4	0	0.1	PAM	GIN1	
chr5	+(102468949..102469502)	553	2.83731	10	5	5	0	0.17360382	PPIP5K2	C5orf30	
chr5	+(102613103..102613608)	505	2.83731	9	6	3	0.3333333	0.048	C5orf30	NUDT12	
chr5	+(108713696..108714354)	658	1.33407	13	8	5	0.2307692	0.1207833	FER	PJA2	
chr5	+(109120367..109120884)	517	0.61213	10	6	4	0.2	0.457	MAN2A1	LOC100289673	
chr5	+(109200653..109201176)	523	1.33407	9	5	4	0.1111111	0.095	MAN2A1	LOC100289673	
chr5	+(109904099..109904691)	592	0.61213	12	8	4	0.3333333	0.014	LOC100289673	TMEM232	
chr5	+(110784451..110785123)	672	0.61213	13	5	8	0.2307692	0.02021199	CAMK4	STARD4	
chr5	+(111610735..111611248)	513	1.33407	9	5	4	0.1111111	0.008	SNORA13	EPB41L4A	
chr5	+(112203047..112203595)	548	2.83731	13	6	7	0.0769231	0.01606229	SRP19	REEP5	
chr5	+(112367187..112367887)	700	0.61213	9	3	6	0.3333333	0.012	DCP2	MCC	
chr5	+(113822531..113823053)	522	2.83731	7	4	3	0.1428571	0.057	KCNN2	TRIM36	v
chr5	+(116273175..116273875)	700	0.00188	15	5	10	0.3333333	0.00109982	SEMA6A	DTWD2	
chr5	+(118309998..118310633)	635	3.40873	46	28	18	0.2173913	2.8027E-05	SEMA6A	DTWD2	
chr5	+(118512877..118513413)	536	1.33407	8	3	5	0.25	0.018	DMXL1	TNFAIP8	

chr5	+(118969719..118970378)	659	0.26306	10	5	5	0	0.00451172	FAM170A	PRR16	
chr5	+(121760868..121761381)	513	2.83731	8	4	4	0	0.029	SNCAIP	SNX2	
chr5	+(122361326..122362026)	700	0.26306	10	7	3	0.4	0.008	SNX24	PPIC	
chr5	+(122736573..122737123)	550	1.33407	7	4	3	0.1428571	0.029	PRDM6	CEP120	
chr5	+(122758261..122759581)	1320	0.02552	20	8	12	0.2	0.53074856	PRDM6	CEP120	
chr5	+(122911330..122912030)	700	0.69282	20	13	7	0.3	0.03128691	CSNK1G3	ZNF608	
chr5	+(122990828..122991331)	503	0.61213	8	4	4	0	0.014	CSNK1G3	ZNF608	
chr5	+(123982952..123984009)	1057	2.39506	33	20	13	0.2121212	0.0044495	CSNK1G3	ZNF608	
chr5	+(125758437..125759137)	700	0.61213	12	4	8	0.3333333	0.00328926	GRAMD3	ALDH7A1	
chr5	+(125941697..125942397)	700	0.11662	10	6	4	0.2	0.005	PHAX	C5orf48	
chr5	+(126860029..126860530)	501	2.83731	10	5	5	0	0.45840747	PRRC1	CTXN3	
chr5	+(128301812..128302351)	539	2.83731	9	4	5	0.1111111	0.206	SLC27A6	ISOC1	
chr5	+(128324099..128324659)	560	0.99425	20	9	11	0.1	0.00062137	SLC27A6	ISOC1	
chr5	+(130777754..130778313)	559	2.83731	9	3	6	0.3333333	0.048	CDC42SE2	RAPGEF6	
chr5	+(132159111..132159866)	755	0.00188	22	13	9	0.1818182	0.00226938	ANKRD43	SHROOM1	
chr5	+(132233645..132234188)	543	2.83731	6	4	2	0.3333333	0.067	LEAP2	AFF4	
chr5	+(132784005..132784554)	549	0.61213	8	5	3	0.25	0.018	HSPA4	FSTL4	
chr5	+(132829179..132829718)	539	2.83731	6	3	3	0	0.05	HSPA4	FSTL4	
chr5	+(133278313..133279013)	700	0.01049	13	5	8	0.2307692	0.0017074	MIR1289-2	C5orf15	
chr5	+(133295178..133295686)	508	2.83731	10	3	7	0.4	0.092	MIR1289-2	C5orf15	
chr5	+(133324423..133325733)	1310	2.83731	12	6	6	0	0.00197388	C5orf15	VDAC1	
chr5	+(133888939..133889639)	700	0.05995	11	7	4	0.2727273	0.003	PHF15	SAR1B	
chr5	+(133890103..133890702)	599	0.26306	9	4	5	0.1111111	0.008	PHF15	SAR1B	
chr5	+(133931622..133932319)	697	2.83731	6	4	2	0.3333333	0.067	PHF15	SAR1B	
chr5	+(134191994..134192498)	504	2.83731	7	3	4	0.1428571	0.029	C5orf24	TXNDC15	
chr5	+(134259507..134260481)	974	0.05995	30	14	16	0.0666667	0.02300038	PCBD2	CATSPER3	
chr5	+(136602237..136602743)	506	2.83731	6	2	4	0.3333333	0.067	TRPC7	SPOCK1	
chr5	+(137677185..137677748)	563	1.33407	11	4	7	0.2727273	0.082	FAM53C	KDM3B	
chr5	+(138208715..138209309)	594	0.61213	13	8	5	0.2307692	0.1207833	CTNNA1	LRRTM2	
chr5	+(138261992..138262670)	678	0.26306	9	5	4	0.1111111	0.008	LRRTM2	SIL1	
chr5	+(138717256..138717778)	522	0.26306	13	4	9	0.3846154	0.413	PAIP2	SLC23A1	
chr5	+(139216307..139216946)	639	0.61213	9	6	3	0.3333333	0.083	PSD2	NRG2	
chr5	+(139745089..139746007)	918	2.83731	15	9	6	0.2	0.00666417	SLC4A9	ANKHD1	v
chr5	+(139844172..139844859)	687	1.33407	10	7	3	0.4	0.192	ANKHD1-EIF4EBP3	EIF4EBP3	

chr5	+(139908918..139909516)	598	0.05995	13	5	8	0.2307692	0.00420773	ANKHD1-EIF4EBP3	EIF4EBP3
chr5	+(140167492..140168538)	1046	1.33407	17	8	9	0.0588235	0.0014273	PCDHA1	PCDHA2
chr5	+(140207744..140208247)	503	2.83731	7	3	4	0.1428571	0.057	PCDHA6	PCDHA7
chr5	+(140228397..140229457)	1060	0.02552	47	24	23	0.0212766	0.01272351	PCDHA9	PCDHA10
chr5	+(140230057..140230559)	502	2.83731	9	3	6	0.3333333	0.19	PCDHA9	PCDHA10
chr5	+(140593613..140594217)	604	0.12647	48	25	23	0.0416667	0.00509406	PCDHB13	PCDHB14
chr5	+(140745507..140746168)	661	0.26306	11	7	4	0.2727273	0.115	PCDHGA5	PCDHGB3
chr5	+(140777461..140777986)	525	1.92865	26	11	15	0.1538462	0.00198556	PCDHGA8	PCDHGB5
chr5	+(140779778..140780307)	529	0.61213	15	6	9	0.2	0.20469774	PCDHGB5	PCDHGA9
chr5	+(140868875..140869384)	509	2.83731	9	4	5	0.1111111	0.365	PCDHGC5	DIAPH1
chr5	+(140870119..140871161)	1042	1.33407	16	9	7	0.125	0.00251538	PCDHGC5	DIAPH1
chr5	+(141035145..141035776)	631	2.83731	8	3	5	0.25	0.5	FCHSD1	ARAP3
chr5	+(141052999..141053713)	714	0.00503	19	13	6	0.3684211	0.03275061	FCHSD1	ARAP3
chr5	+(143191443..143192136)	693	0.11662	17	6	11	0.2941176	0.00064968	NR3C1	HMHB1
chr5	+(144405449..144406122)	673	0.61213	8	4	4	0	0.014	KCTD16	PRELID2
chr5	+(145202435..145202937)	502	2.83731	7	3	4	0.1428571	0.029	KCTD16	PRELID2
chr5	+(145383289..145383833)	544	2.83731	6	4	2	0.3333333	0.067	SH3RF2	PLAC8L1
chr5	+(145664171..145664700)	529	2.83731	9	4	5	0.1111111	0.016	RBM27	POU4F3
chr5	+(148245331..148245913)	582	0.11662	10	7	3	0.4	0.008	ADRB2	SH3TC2
chr5	+(148420694..148421296)	602	0.26306	10	4	6	0.2	0.086	ADRB2	SH3TC2
chr5	+(148618709..148619313)	604	0.61213	11	4	7	0.2727273	0.003	ABLIM3	AFAP1L1
chr5	+(148761295..148761895)	600	0.61213	9	5	4	0.1111111	0.008	IL17B	LOC728264
chr5	+(148784889..148785452)	563	0.02552	12	8	4	0.3333333	0.99671074	IL17B	LOC728264
chr5	+(148808523..148809223)	700	1.33407	11	7	4	0.2727273	0.997	MIR143	MIR145
chr5	+(149242490..149243019)	529	2.83731	6	2	4	0.3333333	0.067	PPARGC1B	PDE6A
chr5	+(149276029..149277152)	1123	0.05995	21	12	9	0.1428571	0.99946051	PPARGC1B	PDE6A
chr5	+(149488647..149489177)	530	2.83731	6	3	3	0	0.05	HMGXB3	CSF1R
chr5	+(149757027..149757727)	700	0.01049	13	8	5	0.2307692	0.0017074	TCOF1	CD74
chr5	+(149758685..149759376)	691	1.33407	10	7	3	0.4	0.008	TCOF1	CD74
chr5	+(150020702..150021402)	700	0.11662	10	3	7	0.4	0.008	SYNPO	MYOZ3
chr5	+(150027648..150028192)	544	2.83731	6	4	2	0.3333333	0.067	SYNPO	MYOZ3
chr5	+(150030483..150031408)	925	0.11662	23	10	13	0.1304348	0.96395138	SYNPO	MYOZ3
chr5	+(152206838..152208215)	1377	0.02552	18	6	12	0.3333333	0.00037352	NMUR2	GRIA1
chr5	+(153078161..153078861)	700	0.11662	10	3	7	0.4	0.008	GRIA1	FAM114A2

chr5	+(153856074..153856612)	538	2.83731	6	3	3	0	0.05	SAP30L	HAND1	v
chr5	+(156531306..156531913)	607	2.83731	6	4	2	0.3333333	0.067	HAVCR1	HAVCR2	
chr5	+(156820353..156820931)	578	0.26306	9	4	5	0.1111111	0.008	C5orf40	NIPAL4	
chr5	+(157001394..157002007)	613	0.05995	11	7	4	0.2727273	0.003	NIPAL4	ADAM19	
chr5	+(157216325..157216901)	576	1.33407	11	7	4	0.2727273	0.606	LSM11	CLINT1	
chr5	+(158523876..158524474)	598	1.33407	7	3	4	0.1428571	0.029	CLINT1	EBF1	
chr5	+(160016428..160016938)	510	2.83731	6	4	2	0.3333333	0.067	MIR146A	ATP10B	
chr5	+(161524419..161525063)	644	0.26306	9	4	5	0.1111111	0.008	GABRG2	CCNG1	
chr5	+(161580060..161580661)	601	0.61213	15	7	8	0.0666667	0.06623179	GABRG2	CCNG1	
chr5	+(164022067..164022662)	595	2.83731	6	3	3	0	0.05	MAT2B	ODZ2	
chr5	+(165809166..165809675)	509	1.33407	9	5	4	0.1111111	0.032	MAT2B	ODZ2	
chr5	+(166069996..166070498)	502	1.33407	8	3	5	0.25	0.018	MAT2B	ODZ2	
chr5	+(167400351..167401051)	700	0.26306	13	4	9	0.3846154	0.999	ODZ2	WWC1	
chr5	+(167469692..167470336)	644	2.83731	6	2	4	0.3333333	0.067	ODZ2	WWC1	
chr5	+(167581681..167582525)	844	0.11662	15	10	5	0.3333333	0.00109982	ODZ2	WWC1	
chr5	+(167671208..167671905)	697	0.11662	10	3	7	0.4	0.008	ODZ2	WWC1	
chr5	+(167914346..167914854)	508	0.26306	9	5	4	0.1111111	0.008	RARS	FBLL1	
chr5	+(167928581..167929281)	700	0.11662	12	4	8	0.3333333	0.00328926	RARS	FBLL1	
chr5	+(167992888..167993497)	609	2.83731	9	6	3	0.3333333	0.131	FBLL1	PANK3	
chr5	+(168233093..168233764)	671	0.11662	12	5	7	0.1666667	0.00224163	MIR103-1AS	SLIT3	
chr5	+(169812206..169812890)	684	2.83731	6	3	3	0	0.05	KCNIP1	KCNMB1	
chr5	+(169864915..169865884)	969	2.83731	12	4	8	0.3333333	0.00328926	KCNMB1	GABRP	
chr5	+(171595880..171596445)	565	2.83731	6	2	4	0.3333333	0.067	FBXW11	STK10	
chr5	+(173530818..173531426)	608	2.83731	10	4	6	0.2	0.695	HMP19	MSX2	
chr5	+(173689145..173689756)	611	2.83731	6	3	3	0	0.05	HMP19	MSX2	
chr5	+(173864491..173865398)	907	1.33407	13	7	6	0.0769231	0.0013499	HMP19	MSX2	
chr5	+(175717983..175718669)	686	0.61213	8	4	4	0	0.014	C5orf25	KIAA1191	
chr5	+(175972762..175973569)	807	0.05995	12	8	4	0.3333333	0.99671074	CDHR2	GPRIN1	
chr5	+(176001920..176002728)	808	0.26306	20	8	12	0.2	0.96796124	CDHR2	GPRIN1	
chr5	+(176021180..176022959)	1779	0.61213	24	11	13	0.0833333	0.46537358	CDHR2	GPRIN1	
chr5	+(176335308..176335816)	508	2.83731	9	4	5	0.1111111	0.032	HK3	UIMC1	
chr5	+(176339531..176340122)	591	2.83731	6	2	4	0.3333333	0.067	HK3	UIMC1	
chr5	+(176729752..176730370)	618	0.11662	11	5	6	0.0909091	0.03394459	NSD1	RAB24	
chr5	+(176832142..176833099)	957	2.83731	15	6	9	0.2	0.03854994	PFN3	F12	

chr5	+(176856069..176856622)	553	2.83731	6	2	4	0.3333333	0.067	GRK6	PRR7	
chr5	+(177163202..177163793)	591	2.83731	12	6	6	0	0.21166982	LOC202181	FAM153A	
chr5	+(177238921..177239621)	700	0.05995	11	6	5	0.0909091	0.00308495	FAM153A	LOC728554	
chr5	+(177461684..177462400)	716	0.5982	48	21	27	0.125	2.893E-07	FAM153C	N4BP3	
chr5	+(177465748..177466296)	548	1.29796	32	22	10	0.375	0.34216639	FAM153C	N4BP3	
chr5	+(177468686..177469704)	1018	0.14093	52	30	22	0.1538462	0.00016332	FAM153C	N4BP3	
chr5	+(177473489..177474001)	512	2.83731	29	19	10	0.3103448	0.99490709	FAM153C	N4BP3	
chr5	+(177707348..177708020)	672	1.33407	10	7	3	0.4	0.992	AGXT2L2	COL23A1	
chr5	+(177905192..177905892)	700	0.05995	11	4	7	0.2727273	0.003	AGXT2L2	COL23A1	
chr5	+(178011878..178013226)	1348	0.00011	82	56	26	0.3658537	1	AGXT2L2	COL23A1	
chr5	+(178016368..178017696)	1328	0.61213	15	8	7	0.0666667	0.00059687	AGXT2L2	COL23A1	
chr5	+(178556911..178557458)	547	0.61213	8	5	3	0.25	0.018	ZNF354C	ADAMTS2	
chr5	+(178562641..178563334)	693	2.83731	9	6	3	0.3333333	0.988	ZNF354C	ADAMTS2	
chr5	+(178644911..178645422)	511	0.61213	8	5	3	0.25	0.018	ZNF354C	ADAMTS2	
chr5	+(178724872..178725598)	726	0.01049	13	6	7	0.0769231	0.0013499	ZNF354C	ADAMTS2	
chr5	+(178749659..178750184)	525	1.33407	7	3	4	0.1428571	0.029	ZNF354C	ADAMTS2	
chr5	+(178795069..178795779)	710	0.0018	16	10	6	0.25	0.00056905	ADAMTS2	RUFY1	
chr5	+(178883204..178883904)	700	0.11662	10	4	6	0.2	0.005	ADAMTS2	RUFY1	
chr5	+(179044822..179045386)	564	2.83731	8	5	3	0.25	0.071	RUFY1	HNRNPH1	
chr5	+(179150354..179150966)	612	0.61213	10	4	6	0.2	0.019	CANX	MAML1	
chr5	+(179264370..179264883)	513	0.61213	11	5	6	0.0909091	0.00881105	SQSTM1	C5orf45	
chr5	+(179778291..179779486)	1195	2.83731	12	6	6	0	0.00197388	MAPK9	GFPT2	
chr5	+(180017502..180018202)	700	2.83731	9	6	3	0.3333333	0.012	CNOT6	SCGB3A1	
chr5	+(180045124..180046188)	1064	0.61213	15	8	7	0.0666667	0.99940313	SCGB3A1	FLT4	
chr6	+(302365..302885)	520	3.30942	6	2	4	0.3333333	0.067	DUSP22	IRF4	
chr6	+(3093848..3094548)	700	0.15779	11	4	7	0.2727273	0.003	RIPK1	BPHL	
chr6	+(3292474..3293168)	694	0.15779	10	5	5	0	0.00451172	PSMG4	SLC22A23	
chr6	+(3311898..3313242)	1344	3.30942	12	6	6	0	0.99802612	PSMG4	SLC22A23	
chr6	+(3321701..3322215)	514	1.57131	7	4	3	0.1428571	0.029	PSMG4	SLC22A23	
chr6	+(4903603..4904303)	700	1.57131	10	3	7	0.4	0.942	CDYL	RPP40	v
chr6	+(5652647..5653171)	524	0.68762	8	5	3	0.25	0.018	FARS2	NRN1	
chr6	+(5710446..5711105)	659	3.30942	9	4	5	0.1111111	0.857	FARS2	NRN1	
chr6	+(6219395..6220093)	698	3.30942	10	6	4	0.2	0.995	NRN1	F13A1	
chr6	+(6518908..6519454)	546	0.68762	8	4	4	0	0.014	F13A1	LY86-AS1	

chr6	+(8417010..8417710)	700	0.02086	20	14	6	0.4	0.31034536	SCARNA27	SLC35B3	
chr6	+(8430186..8430785)	599	1.57131	10	7	3	0.4	0.008	SCARNA27	SLC35B3	
chr6	+(10983276..10983976)	700	3.30942	9	3	6	0.3333333	0.726	SYCP2L	ELOVL2	
chr6	+(12684581..12685281)	700	0.68762	13	5	8	0.2307692	0.9982926	EDN1	PHACTR1	
chr6	+(13229760..13230621)	861	0.0008	18	12	6	0.3333333	0.00037352	PHACTR1	TBC1D7	
chr6	+(15486075..15486793)	718	0.03399	12	6	6	0	0.00197388	JARID2	DTNBP1	v
chr6	+(15652077..15652600)	523	3.30942	11	7	4	0.2727273	0.003	JARID2	DTNBP1	v
chr6	+(15759781..15760481)	700	3.30942	10	4	6	0.2	0.005	DTNBP1	MYLIP	
chr6	+(17771228..17771928)	700	3.30942	9	6	3	0.3333333	0.726	NUP153	KIF13A	
chr6	+(18459591..18460107)	516	3.30942	8	4	4	0	0.343	RNF144B	MIR548A1	
chr6	+(24643741..24644910)	1169	0.08005	17	6	11	0.2941176	0.99954444	ALDH5A1	KIAA0319	
chr6	+(25521540..25522172)	632	3.30942	6	2	4	0.3333333	0.067	LRRC16A	SCGN	
chr6	+(25850618..25851220)	602	0.32535	12	4	8	0.3333333	0.077	SLC17A1	SLC17A3	
chr6	+(27879508..27880088)	580	0.68762	11	5	6	0.0909091	0.05017413	HIST1H2BO	OR2B2	
chr6	+(29141630..29142164)	534	0.15779	15	9	6	0.2	0.02256348	OR2J2	OR14J1	
chr6	+(29912115..29913152)	1037	1.57131	21	13	8	0.2380952	0.10913309	HLA-A	HCG9	
chr6	+(29975569..29976361)	792	3.30942	15	6	9	0.2	0.1728893	HCG9	ZNRD1-AS1	
chr6	+(30514845..30515358)	513	0.32535	12	4	8	0.3333333	0.004	HLA-E	GNL1	
chr6	+(30671766..30673137)	1371	0.32535	50	28	22	0.12	0.15474517	NRM	MDC1	
chr6	+(30859161..30859722)	561	0.15779	15	5	10	0.3333333	0.99890018	DDR1	GTF2H4	
chr6	+(30917023..30917731)	708	0.00497	53	17	36	0.3584906	0.35156157	DPCR1	MUC21	
chr6	+(30918670..30919333)	663	4.09809	30	17	13	0.1333333	0.01556664	DPCR1	MUC21	
chr6	+(31132072..31134301)	2229	1.1E-34	519	360	159	0.3872832	0.09193238	TCF19	POU5F1	
chr6	+(31137546..31138903)	1357	4E-209	2140	966	1174	0.0971963	0.90111116	TCF19	POU5F1	
chr6	+(31595440..31595978)	538	0.68762	14	8	6	0.1428571	0.98056645	SNORA38	BAT3	
chr6	+(31603893..31604593)	700	0.68762	12	7	5	0.1666667	0.14557611	SNORA38	BAT3	
chr6	+(31639346..31639954)	608	3.30942	9	3	6	0.3333333	0.726	LY6G5B	LY6G5C	
chr6	+(31777934..31778448)	514	3.30942	15	5	10	0.3333333	0.72985431	LSM2	HSPA1L	
chr6	+(31797631..31798266)	635	0.68762	18	11	7	0.2222222	0.12879966	HSPA1B	C6orf48	
chr6	+(31868753..31869257)	504	4.09809	13	6	7	0.0769231	0.00332094	EHMT2	ZBTB12	
chr6	+(31984003..31984571)	568	1.57131	13	8	5	0.2307692	0.55819127	C4B_dup2	CYP21A2_dup2	
chr6	+(31992008..31993011)	1003	1.57131	17	7	10	0.1764706	0.31279262	C4B_dup2	CYP21A2_dup2	
chr6	+(32008029..32008649)	620	3.30942	11	5	6	0.0909091	0.70805879	CYP21A2_dup2	TNXB_dup2	
chr6	+(32017493..32018024)	531	3.30942	6	2	4	0.3333333	0.067	CYP21A2_dup2	TNXB_dup2	

chr6	+(32261230..32261850)	620	1.57131	18	10	8	0.1111111	0.67157329	NOTCH4	C6orf10
chr6	+(32336320..32336900)	580	1.57131	10	4	6	0.2	0.01	NOTCH4	C6orf10
chr6	+(33154044..33154556)	512	1.57131	10	3	7	0.4	0.033	HLA-DPB2	COL11A2
chr6	+(33380257..33380840)	583	1.57131	10	3	7	0.4	0.033	PHF1	CUTA
chr6	+(33619708..33620373)	665	3.30942	6	2	4	0.3333333	0.067	ITPR3	C6orf125
chr6	+(33661897..33662597)	700	0.08005	11	6	5	0.0909091	0.00308495	ITPR3	C6orf125
chr6	+(34003666..34004171)	505	1.57131	8	5	3	0.25	0.018	MIR1275	GRM4
chr6	+(34488137..34489396)	1259	0.02086	20	9	11	0.1	0.84747057	PACSIN1	SPDEF
chr6	+(35478636..35479188)	552	3.30942	6	2	4	0.3333333	0.067	TEAD3	TULP1
chr6	+(36261953..36262468)	515	0.32535	9	4	5	0.1111111	0.008	PNPLA1	C6orf222
chr6	+(36709411..36709989)	578	1.57131	8	4	4	0	0.014	CDKN1A	CPNE5
chr6	+(36945625..36946167)	542	1.57131	8	5	3	0.25	0.018	PI16	MTCH1
chr6	+(39891732..39892527)	795	0.00026	19	8	11	0.1578947	0.00013997	DAAM2	MOCS1
chr6	+(41203863..41204563)	700	0.03399	12	7	5	0.1666667	0.00224163	TREML4	TREML2P1
chr6	+(41248430..41249038)	608	0.68762	9	3	6	0.3333333	0.012	TREML2P1	TREM1
chr6	+(42123157..42123768)	611	0.68762	10	7	3	0.4	0.017	GUCA1A	GUCA1B
chr6	+(42235687..42236387)	700	0.02086	19	7	12	0.2631579	0.30604494	MRPS10	TRERF1
chr6	+(42664715..42665681)	966	0.08005	17	11	6	0.2941176	0.18285615	UBR2	PRPH2
chr6	+(42975551..42976125)	574	3.30942	13	5	8	0.2307692	0.8792167	PPP2R5D	MEA1
chr6	+(43006274..43007253)	979	0.32535	15	9	6	0.2	0.99926864	RRP36	CUL7
chr6	+(43222532..43223046)	514	3.30942	8	4	4	0	0.014	TTBK1	SLC22A7
chr6	+(43416802..43417332)	530	3.30942	7	4	3	0.1428571	0.057	ABCC10	DLK2
chr6	+(43648653..43649434)	781	0.68762	15	6	9	0.2	0.8271107	RSPH9	MRPS18A
chr6	+(44373739..44374510)	771	1.57131	13	5	8	0.2307692	0.07161746	CDC5L	SUPT3H
chr6	+(44497846..44498546)	700	0.15779	10	6	4	0.2	0.005	CDC5L	SUPT3H
chr6	+(45459326..45459844)	518	3.30942	12	6	6	0	0.13116584	RUNX2	CLIC5
chr6	+(46107268..46107868)	600	3.30942	7	3	4	0.1428571	0.314	ENPP4	ENPP5
chr6	+(46132913..46133470)	557	3.30942	10	5	5	0	0.02360089	ENPP4	ENPP5
chr6	+(47253845..47254372)	527	3.30942	9	4	5	0.1111111	0.032	GPR110	TNFRSF21
chr6	+(55374419..55374923)	504	3.30942	6	2	4	0.3333333	0.067	GFRAL	HMGCLL1
chr6	+(56373110..56373626)	516	3.30942	14	7	7	0	0.32736042	COL21A1	DST
chr6	+(56420244..56420786)	542	3.30942	13	8	5	0.2307692	0.07161746	COL21A1	DST
chr6	+(56464647..56465212)	565	1.57131	7	3	4	0.1428571	0.029	COL21A1	DST
chr6	+(56955315..56955920)	605	0.03399	19	7	12	0.2631579	0.01730528	ZNF451	BAG2

chr6	+(57374162..57374782)	620	3.30942	6	4	2	0.3333333	0.067	PRIM2	GUSBP4
chr6	+(64408031..64408798)	767	0.68762	13	8	5	0.2307692	0.02851994	PHF3	EYS
chr6	+(66204585..66205285)	700	1.57131	11	6	5	0.0909091	0.00308495	PHF3	EYS
chr6	+(68851343..68851889)	546	1.57131	7	3	4	0.1428571	0.029	MCART3P	BAI3
chr6	+(69577227..69577824)	597	1.57131	7	3	4	0.1428571	0.029	BAI3	LMBRD1
chr6	+(70461995..70462502)	507	3.30942	9	5	4	0.1111111	0.008	BAI3	LMBRD1
chr6	+(74072860..74073509)	649	1.57131	10	4	6	0.2	0.305	C6orf221	OOEP
chr6	+(74466126..74466648)	522	3.30942	8	5	3	0.25	0.018	CD109	COL12A1
chr6	+(80744806..80745317)	511	3.30942	9	4	5	0.1111111	0.206	TTK	BCKDHB
chr6	+(80775759..80776424)	665	0.68762	16	10	6	0.25	0.19277332	TTK	BCKDHB
chr6	+(84650108..84650643)	535	1.57131	10	6	4	0.2	0.005	CYB5R4	MRAP2
chr6	+(84862153..84862686)	533	3.30942	7	3	4	0.1428571	0.2	MRAP2	KIAA1009
chr6	+(90359585..90360120)	535	3.30942	7	4	3	0.1428571	0.029	LYRM2	MDN1
chr6	+(90374058..90374601)	543	1.57131	8	5	3	0.25	0.018	LYRM2	MDN1
chr6	+(94120307..94120834)	527	3.30942	9	4	5	0.1111111	0.278	MAP3K7	EPHA7
chr6	+(110746014..110746518)	504	3.30942	8	5	3	0.25	0.018	DDO	SLC22A16
chr6	+(111318366..111318935)	569	3.30942	6	3	3	0	0.05	RPF2	GSTM2P1
chr6	+(117010263..117010793)	530	3.30942	10	4	6	0.2	0.005	KPNA5	FAM162B
chr6	+(117638156..117638735)	579	1.57131	8	4	4	0	0.014	VGLL2	ROS1
chr6	+(118588089..118588667)	578	0.68762	12	8	4	0.3333333	0.014	SLC35F1	C6orf204
chr6	+(119136009..119136680)	671	0.03399	21	13	8	0.2380952	0.2128337	PLN	MCM9
chr6	+(119182113..119182709)	596	3.30942	6	2	4	0.3333333	0.067	PLN	MCM9
chr6	+(123576722..123577229)	507	3.30942	8	4	4	0	0.171	CLVS2	TRDN
chr6	+(123833169..123833675)	506	3.30942	6	2	4	0.3333333	0.067	CLVS2	TRDN
chr6	+(129478802..129479388)	586	3.30942	7	4	3	0.1428571	0.029	LAMA2	ARHGAP18
chr6	+(132859462..132859966)	504	3.30942	11	6	5	0.0909091	0.07206352	TAAR9	TAAR8
chr6	+(135653044..135653728)	684	0.15779	10	5	5	0	0.00451172	MYB	AHI1
chr6	+(136469814..136470585)	771	0.68762	14	6	8	0.1428571	0.00097289	PDE7B	FAM54A
chr6	+(136590473..136590978)	505	3.30942	9	6	3	0.3333333	0.048	FAM54A	BCLAF1
chr6	+(138835905..138836605)	700	0.15779	11	5	6	0.0909091	0.05017413	HEBP2	NHSL1
chr6	+(143081149..143081849)	700	1.57131	13	6	7	0.0769231	0.03164542	LOC153910	HIVEP2
chr6	+(144207622..144208160)	538	3.30942	8	4	4	0	0.1	C6orf94	PLAGL1
chr6	+(144510208..144510780)	572	1.57131	12	5	7	0.1666667	0.14557611	STX11	UTRN
chr6	+(146266436..146266978)	542	3.30942	8	5	3	0.25	0.286	FBXO30	SHPRH

chr6	+(147123666..147124198)	532	3.30942	9	3	6	0.3333333	0.012	C6orf103	LOC729176	
chr6	+(149769260..149769960)	700	0.32535	9	3	6	0.3333333	0.012	SUMO4	ZC3H12D	
chr6	+(150004549..150005078)	529	1.57131	16	10	6	0.25	0.41413127	KATNA1	LATS1	
chr6	+(150239477..150239989)	512	1.57131	17	7	10	0.1764706	0.0017074	RAET1E	RAET1G	
chr6	+(150240468..150241039)	571	1.57131	16	10	6	0.25	0.09652953	RAET1E	RAET1G	
chr6	+(150390060..150390635)	575	3.30942	8	4	4	0	0.443	RAET1L	ULBP3	
chr6	+(151266298..151266844)	546	0.68762	8	4	4	0	0.014	MTHFD1L	AKAP12	
chr6	+(152449934..152450550)	616	0.68762	8	5	3	0.25	0.018	ESR1	SYNE1	
chr6	+(152488612..152489312)	700	0.32535	11	4	7	0.2727273	0.115	ESR1	SYNE1	
chr6	+(152598914..152599651)	737	0.03399	12	6	6	0	0.00197388	ESR1	SYNE1	
chr6	+(158260917..158261605)	688	0.68762	8	5	3	0.25	0.018	SNX9	SYNJ2	
chr6	+(158986080..158987102)	1022	0.0008	32	10	22	0.375	0.03681914	TMEM181	DYNLT1	
chr6	+(159045388..159045939)	551	3.30942	6	3	3	0	0.05	TMEM181	DYNLT1	
chr6	+(159048985..159049623)	638	3.30942	6	4	2	0.3333333	0.067	TMEM181	DYNLT1	
chr6	+(159083959..159084499)	540	3.30942	6	3	3	0	0.05	SYTL3	MIR3918	
chr6	+(160558016..160558554)	538	3.30942	6	3	3	0	0.05	SLC22A1	SLC22A2	
chr6	+(160976739..160977666)	927	3.30942	19	13	6	0.3684211	0.06798093	LPAL2	LPA	
chr6	+(161127898..161129291)	1393	0.08917	39	17	22	0.1282051	0.52258566	PLG	MAP3K4	
chr6	+(166737774..166738347)	573	0.08005	12	8	4	0.3333333	0.99671074	PRR18	SFT2D1	
chr6	+(167591530..167592215)	685	0.50599	31	20	11	0.2903226	6.1615E-05	TCP10L2	UNC93A	
chr6	+(167814931..167815633)	702	0.03399	17	9	8	0.0588235	0.000266	TCP10	C6orf123	
chr6	+(168139012..168139613)	601	3.30942	6	2	4	0.3333333	0.067	TCP10	C6orf123	
chr6	+(168192844..168193463)	619	1.57131	7	3	4	0.1428571	0.029	TCP10	C6orf123	
chr6	+(168343795..168344313)	518	1.57131	10	7	3	0.4	0.058	MLLT4	HGC6.3	
chr6	+(168365999..168367248)	1249	1.57131	13	6	7	0.0769231	0.9986501	MLLT4	HGC6.3	
chr6	+(168376756..168377758)	1002	0.03248	47	24	23	0.0212766	0.05523257	MLLT4	HGC6.3	
chr6	+(169008676..169009321)	645	0.68762	8	3	5	0.25	0.018	SMOC2	THBS2	v
chr6	+(169284458..169285267)	809	0.02086	13	7	6	0.0769231	0.0013499	SMOC2	THBS2	v
chr6	+(169637042..169637672)	630	3.30942	6	4	2	0.3333333	0.067	SMOC2	THBS2	v
chr6	+(170615967..170616530)	563	0.68762	8	5	3	0.25	0.018	FAM120B	PSMB1	
chr6	+(170765164..170766215)	1051	0.03399	18	12	6	0.3333333	0.99962648	FAM120B	PSMB1	
chr7	+(46255..46787)	532	2.79191	6	4	2	0.3333333	0.067		FAM20C	
chr7	+(178984..179567)	583	2.79191	10	6	4	0.2	0.543		FAM20C	
chr7	+(297198..297898)	700	1.18321	10	3	7	0.4	0.742	FAM20C	LOC100288524	

chr7	+(301548..302348)	800	0.00174	19	9	10	0.0526316	0.00011928	FAM20C	LOC100288524	
chr7	+(692349..693141)	792	0.13075	15	8	7	0.0666667	0.00059687	FLJ44511	PRKAR1B	
chr7	+(787538..788069)	531	2.79191	7	4	3	0.1428571	0.029	HEATR2	SUN1	
chr7	+(791697..793811)	2114	0.00691	49	23	26	0.0612245	0.01242448	HEATR2	SUN1	
chr7	+(887921..888584)	663	0.5931	13	6	7	0.0769231	0.00213737	SUN1	GET4	
chr7	+(895569..896554)	985	0.00691	22	13	9	0.1818182	0.00095082	SUN1	GET4	
chr7	+(930217..930809)	592	0.27893	12	8	4	0.3333333	0.024	GET4	ADAP1	
chr7	+(948923..949623)	700	1.18321	10	3	7	0.4	0.742	GET4	ADAP1	
chr7	+(1325595..1326184)	589	0.27893	13	4	9	0.3846154	0.999	UNCX	MICALL2	
chr7	+(1364385..1365400)	1015	1.18321	13	7	6	0.0769231	0.9986501	UNCX	MICALL2	
chr7	+(1458255..1458843)	588	0.02846	12	5	7	0.1666667	0.00224163	UNCX	MICALL2	
chr7	+(1481292..1482167)	875	0.05401	19	13	6	0.3684211	0.78504691	UNCX	MICALL2	
chr7	+(1672013..1672713)	700	0.05401	11	5	6	0.0909091	0.00308495	TFAMP1	ELFN1	
chr7	+(1735380..1736550)	1170	0.13075	20	8	12	0.2	0.00025847	TFAMP1	ELFN1	
chr7	+(1780657..1781357)	700	0.13075	10	3	7	0.4	0.008	ELFN1	MAD1L1	v
chr7	+(1887834..1888351)	517	0.5931	11	5	6	0.0909091	0.00308495	ELFN1	MAD1L1	v
chr7	+(1933744..1934424)	680	2.79191	9	6	3	0.3333333	0.988	ELFN1	MAD1L1	v
chr7	+(2017793..2018352)	559	2.79191	6	2	4	0.3333333	0.067	ELFN1	MAD1L1	v
chr7	+(2076720..2077420)	700	0.02846	12	8	4	0.3333333	0.99671074	ELFN1	MAD1L1	v
chr7	+(2160848..2161380)	532	0.5931	8	4	4	0	0.014	ELFN1	MAD1L1	v
chr7	+(2181665..2182317)	652	2.79191	6	4	2	0.3333333	0.067	ELFN1	MAD1L1	v
chr7	+(2416049..2416749)	700	0.13075	10	7	3	0.4	0.008	EIF3B	CHST12	
chr7	+(2556591..2557144)	553	0.5931	12	8	4	0.3333333	0.715	LFNG	C7orf27	
chr7	+(2632459..2632968)	509	0.5931	9	3	6	0.3333333	0.012	IQCE	TTYH3	
chr7	+(2738774..2739443)	669	2.79191	11	5	6	0.0909091	0.96605541	AMZ1	GNA12	
chr7	+(2740685..2741200)	515	1.18321	7	4	3	0.1428571	0.029	AMZ1	GNA12	
chr7	+(2910794..2911494)	700	0.13075	10	7	3	0.4	0.008	GNA12	CARD11	
chr7	+(2976593..2977392)	799	2.79191	12	7	5	0.1666667	0.00224163	GNA12	CARD11	
chr7	+(3995137..3995808)	671	1.18321	12	7	5	0.1666667	0.00224163	SDK1	FOXK1	
chr7	+(4167525..4168746)	1221	0.05401	31	18	13	0.1612903	1.1008E-05	SDK1	FOXK1	
chr7	+(4245368..4246494)	1126	1.18321	15	6	9	0.2	0.00335832	SDK1	FOXK1	
chr7	+(4754620..4755311)	691	0.05401	11	7	4	0.2727273	0.003	FOXK1	KIAA0415	
chr7	+(5025888..5026527)	639	1.18321	10	4	6	0.2	0.005	RNF216L	RBAK	
chr7	+(5343154..5343771)	617	2.79191	6	4	2	0.3333333	0.067	SLC29A4	TNRC18	

chr7	+(5415311..5416011)	700	0.05401	11	5	6	0.0909091	0.00308495	SLC29A4	TNRC18
chr7	+(5568014..5568570)	556	2.79191	10	6	4	0.2	0.238	MIR589	ACTB
chr7	+(5780835..5781463)	628	0.01316	16	9	7	0.125	0.18413054	FSCN1	RNF216
chr7	+(6439460..6439996)	536	1.18321	10	7	3	0.4	0.008	RAC1	DAGLB
chr7	+(6620081..6620688)	607	0.5931	13	7	6	0.0769231	0.01113549	ZDHHC4	C7orf26
chr7	+(12414120..12414756)	636	1.18321	10	7	3	0.4	0.017	TMEM106B	VWDE
chr7	+(12728176..12728677)	501	4.30823	25	8	17	0.36	0.22442991	ARL4A	ETV1
chr7	+(13091224..13091924)	700	2.79191	10	4	6	0.2	0.995	ARL4A	ETV1
chr7	+(16598370..16598932)	562	0.5931	10	7	3	0.4	0.033	LOC100129335	ANKMY2
chr7	+(23741446..23741983)	537	2.79191	9	5	4	0.1111111	0.032	C7orf46	STK31
chr7	+(29989148..29989848)	700	1.18321	12	5	7	0.1666667	0.99775837	WIPF3	SCRN1
chr7	+(30027804..30028590)	786	1.18321	13	7	6	0.0769231	0.0013499	WIPF3	SCRN1
chr7	+(30885249..30885911)	662	0.13075	10	5	5	0	0.00451172	FAM188B	AQP1
chr7	+(33055105..33055620)	515	2.79191	10	5	5	0	0.0081468	FKBP9	NT5C3
chr7	+(34013889..34014414)	525	2.79191	8	4	4	0	0.1	BMPER	AAA1
chr7	+(34707481..34708181)	700	0.05401	11	4	7	0.2727273	0.003	BMPER	AAA1
chr7	+(35919509..35920015)	506	2.79191	11	6	5	0.0909091	0.18065522	41159	EEPD1
chr7	+(36005601..36006535)	934	0.5931	19	8	11	0.1578947	0.00085126	41159	EEPD1
chr7	+(36193674..36194870)	1196	0.13075	18	10	8	0.1111111	0.99981036	EEPD1	KIAA0895
chr7	+(36238357..36238906)	549	2.79191	6	4	2	0.3333333	0.067	EEPD1	KIAA0895
chr7	+(36344834..36345423)	589	0.5931	8	5	3	0.25	0.018	EEPD1	KIAA0895
chr7	+(36396698..36397319)	621	2.79191	12	7	5	0.1666667	0.11161257	EEPD1	KIAA0895
chr7	+(36664185..36664712)	527	1.18321	7	3	4	0.1428571	0.029	ANLN	AOAH
chr7	+(36934138..36934813)	675	1.18321	11	6	5	0.0909091	0.02230486	AOAH	ELMO1
chr7	+(39873103..39873626)	523	2.79191	11	6	5	0.0909091	0.07206352	NCRNA00265	CDK13
chr7	+(39893937..39894548)	611	1.18321	11	4	7	0.2727273	0.324	NCRNA00265	CDK13
chr7	+(40109862..40110561)	699	0.01316	13	9	4	0.3846154	0.001	CDK13	C7orf11
chr7	+(44116039..44116733)	694	1.18321	10	7	3	0.4	0.258	PGAM2	POLM
chr7	+(44260996..44262203)	1207	2.79191	12	4	8	0.3333333	0.00328926	YKT6	CAMK2B
chr7	+(44415531..44416231)	700	0.27893	9	3	6	0.3333333	0.012	CAMK2B	NUDCD3
chr7	+(44431798..44432474)	676	0.27893	10	4	6	0.2	0.005	CAMK2B	NUDCD3
chr7	+(45094188..45094755)	567	1.18321	7	3	4	0.1428571	0.029	CCM2	NACAD
chr7	+(45122730..45123252)	522	2.79191	6	4	2	0.3333333	0.067	CCM2	NACAD
chr7	+(45143812..45144478)	666	0.5931	11	6	5	0.0909091	0.01422987	NACAD	TBRG4

chr7	+(45614743..45615257)	514	0.5931	8	3	5	0.25	0.018	ADCY1	SEPT7P2
chr7	+(45667017..45667523)	506	0.5931	8	5	3	0.25	0.018	ADCY1	SEPT7P2
chr7	+(45718985..45719572)	587	1.18321	10	3	7	0.4	0.333	ADCY1	SEPT7P2
chr7	+(46116472..46117170)	698	2.79191	11	6	5	0.0909091	0.00308495	IGFBP3	TNS3
chr7	+(47502585..47503271)	686	2.79191	6	3	3	0	0.05	IGFBP3	TNS3
chr7	+(47548857..47549452)	595	0.13075	10	5	5	0	0.00451172	IGFBP3	TNS3
chr7	+(48284820..48285457)	637	1.18321	10	6	4	0.2	0.005	ABCA13	CDC14C
chr7	+(50721707..50722229)	522	1.18321	7	4	3	0.1428571	0.029	LOC100129427	GRB10
chr7	+(50733556..50734256)	700	0.13075	10	4	6	0.2	0.005	LOC100129427	GRB10
chr7	+(54609965..54610665)	700	0.5931	10	3	7	0.4	0.742	HPVC1	VSTM2A
chr7	+(55219108..55219808)	700	0.02846	12	4	8	0.3333333	0.00328926	EGFR	LANCL2
chr7	+(55345847..55346547)	700	0.13075	15	10	5	0.3333333	0.00109982	EGFR	LANCL2
chr7	+(55473638..55474328)	690	1.18321	7	3	4	0.1428571	0.029	LANCL2	VOPP1
chr7	+(55506278..55507035)	757	0.0026	17	8	9	0.0588235	0.000266	LANCL2	VOPP1
chr7	+(57514394..57515094)	700	0.13075	10	7	3	0.4	0.008	ZNF716	LOC643955
chr7	+(57545017..57545524)	507	1.18321	14	6	8	0.1428571	0.65073232	ZNF716	LOC643955
chr7	+(57701440..57701948)	508	1.18321	10	3	7	0.4	0.008	ZNF716	LOC643955
chr7	+(57706425..57707083)	658	0.5931	12	4	8	0.3333333	0.715	ZNF716	LOC643955
chr7	+(61073281..61073862)	581	2.79191	16	5	11	0.375	0.01010547	ZNF716	LOC643955
chr7	+(61744799..61745338)	539	1.49865	15	5	10	0.3333333	0.0330963	ZNF716	LOC643955
chr7	+(62752098..62752635)	537	1.18321	13	5	8	0.2307692	0.05367327	ZNF716	LOC643955
chr7	+(62758437..62758969)	532	0.05401	22	12	10	0.0909091	0.0061114	ZNF716	LOC643955
chr7	+(64274686..64275386)	700	2.79191	11	5	6	0.0909091	0.99691505	ZNF138	LOC168474
chr7	+(64852724..64853345)	621	2.79191	9	6	3	0.3333333	0.012	ZNF92	INTS4L2
chr7	+(64863880..64864576)	696	1.18321	11	7	4	0.2727273	0.158	ZNF92	INTS4L2
chr7	+(70254350..70255264)	914	0.5931	15	7	8	0.0666667	0.00059687	AUTS2	WBSCR17
chr7	+(72360767..72361272)	505	2.79191	9	3	6	0.3333333	0.012	POM121	NSUN5P2
chr7	+(72383902..72385155)	1253	1.18321	13	6	7	0.0769231	0.0013499	POM121	NSUN5P2
chr7	+(72409003..72409546)	543	0.5931	13	7	6	0.0769231	0.02275014	POM121	NSUN5P2
chr7	+(72415855..72416453)	598	2.79191	6	4	2	0.3333333	0.067	POM121	NSUN5P2
chr7	+(73100634..73101215)	581	2.79191	11	5	6	0.0909091	0.13666084	WBSCR22	STX1A
chr7	+(73105011..73105522)	511	0.27893	14	5	9	0.2857143	0.01938279	WBSCR22	STX1A
chr7	+(73119878..73120578)	700	0.27893	10	7	3	0.4	0.008	WBSCR22	STX1A
chr7	+(73423753..73424273)	520	0.27893	9	4	5	0.1111111	0.008	WBSCR28	ELN

chr7	+(73470535..73471046)	511	1.18321	8	5	3	0.25	0.125	ELN	LIMK1
chr7	+(73474315..73474821)	506	1.18321	9	6	3	0.3333333	0.024	ELN	LIMK1
chr7	+(73477705..73478239)	534	0.44463	18	11	7	0.2222222	0.00819715	ELN	LIMK1
chr7	+(73480826..73481398)	572	2.79191	6	3	3	0	0.05	ELN	LIMK1
chr7	+(73507431..73507950)	519	1.18321	7	3	4	0.1428571	0.029	LIMK1	EIF4H
chr7	+(73535932..73536480)	548	2.79191	6	3	3	0	0.05	LIMK1	EIF4H
chr7	+(74162409..74162952)	543	1.18321	12	7	5	0.1666667	0.01417552	GTF2I	NCF1
chr7	+(74172906..74173591)	685	0.05401	22	15	7	0.3636364	0.00052306	GTF2I	NCF1
chr7	+(74236898..74237501)	603	1.18321	24	13	11	0.0833333	0.72851692	NCF1	GTF2IRD2
chr7	+(74300229..74301187)	958	0.03508	56	30	26	0.0714286	0.0573788	GTF2IRD2	STAG3L2
chr7	+(75441942..75443067)	1125	1.18321	14	7	7	0	0.99912744	CCL26	CCL24
chr7	+(75695377..75695962)	585	2.79191	10	6	4	0.2	0.005	MDH2	SRRM3
chr7	+(75757706..75758250)	544	2.79191	8	3	5	0.25	0.036	MDH2	SRRM3
chr7	+(76142550..76143085)	535	1.18321	7	3	4	0.1428571	0.029	UPK3B	LOC100133091
chr7	+(76459913..76461014)	1101	0.5931	16	8	8	0	0.00038877	POMZP3	PMS2P11
chr7	+(76619114..76620109)	995	0.13075	21	10	11	0.047619	0.00458753	PMS2P11	LOC100132832
chr7	+(78782193..78782893)	700	1.18321	11	4	7	0.2727273	0.003	PHTF2	MAGI2
chr7	+(80374009..80374531)	522	1.18321	11	4	7	0.2727273	0.012	CD36	SEMA3C
chr7	+(80678922..80679622)	700	0.05401	11	4	7	0.2727273	0.003	SEMA3C	HGF
chr7	+(82545789..82546297)	508	2.79191	10	5	5	0	0.30075407	CACNA2D1	PCLO
chr7	+(82581752..82582288)	536	1.18321	12	8	4	0.3333333	0.024	CACNA2D1	PCLO
chr7	+(82763710..82765078)	1368	0.00691	51	25	26	0.0196078	0.29238704	CACNA2D1	PCLO
chr7	+(82784966..82785482)	516	1.18321	13	6	7	0.0769231	0.04323814	CACNA2D1	PCLO
chr7	+(86994503..86995014)	511	2.79191	6	4	2	0.3333333	0.067	CROT	ABCB4
chr7	+(89791266..89791774)	508	2.79191	10	7	3	0.4	0.058	STEAP1	STEAP2
chr7	+(90007182..90007800)	618	1.18321	11	6	5	0.0909091	0.07206352	GTPBP10	CLDN12
chr7	+(90042469..90043039)	570	0.27893	10	3	7	0.4	0.008	CLDN12	CDK14
chr7	+(91756633..91757139)	506	0.5931	15	8	7	0.0666667	0.01394527	AKAP9	CYP51A1
chr7	+(92731749..92732251)	502	2.79191	10	7	3	0.4	0.192	CDK6	SAMD9
chr7	+(92760798..92761351)	553	2.79191	10	6	4	0.2	0.238	SAMD9	SAMD9L
chr7	+(94156137..94156986)	849	2.79191	12	7	5	0.1666667	0.53235847	CASD1	SGCE
chr7	+(94916037..94916689)	652	0.27893	23	8	15	0.3043478	0.00097289	PPP1R9A	PON1
chr7	+(95606560..95607119)	559	2.79191	9	4	5	0.1111111	0.032	DYNC1I1	SLC25A13
chr7	+(97598681..97599452)	771	0.13075	29	14	15	0.0344828	0.0072619	ASNS	MGC72080

chr7	+(98513223..98513770)	547	2.79191	6	3	3	0	0.05	MIR3609	SMURF1
chr7	+(98693421..98693997)	576	2.79191	6	3	3	0	0.05	MIR3609	SMURF1
chr7	+(98870754..98871454)	700	1.18321	11	7	4	0.2727273	0.997	KPNA7	MYH16
chr7	+(99688277..99688857)	580	2.79191	10	3	7	0.4	0.667	COPS6	MCM7
chr7	+(99694840..99695471)	631	0.5931	11	4	7	0.2727273	0.003	COPS6	MCM7
chr7	+(99704436..99705136)	700	0.05401	16	5	11	0.375	0.38850387	AP4M1	TAF6
chr7	+(99794610..99795769)	1159	0.00691	61	28	33	0.0819672	0.0011298	STAG3	GATS
chr7	+(100210404..100210934)	530	2.79191	6	4	2	0.3333333	0.067	MOSPD3	TFR2
chr7	+(100349548..100350101)	553	0.49228	35	17	18	0.0285714	0.11738184	ZAN	EPHB4
chr7	+(100663776..100664476)	700	0.5931	12	8	4	0.3333333	0.99671074	MUC17	TRIM56
chr7	+(100684056..100684990)	934	2.79191	16	11	5	0.375	0.19775658	MUC17	TRIM56
chr7	+(100732967..100733472)	505	2.79191	6	4	2	0.3333333	0.067	TRIM56	SERPINE1
chr7	+(101041595..101042295)	700	0.05401	11	7	4	0.2727273	0.003	EMID2	MYL10
chr7	+(101242265..101242965)	700	1.18321	10	4	6	0.2	0.871	EMID2	MYL10
chr7	+(101287410..101288053)	643	0.13075	11	5	6	0.0909091	0.00308495	MYL10	CUX1
chr7	+(101481623..101482808)	1185	0.27893	20	11	9	0.1	8.472E-05	CUX1	SH2B2
chr7	+(101913473..101914498)	1025	0.5931	14	8	6	0.1428571	0.99902711	CUX1	SH2B2
chr7	+(101952081..101952781)	700	0.02846	16	5	11	0.375	0.07837268	MIR4285	SPDYE6
chr7	+(101989077..101989582)	505	1.18321	10	7	3	0.4	0.992	MIR4285	SPDYE6
chr7	+(102230526..102231129)	603	0.49228	24	11	13	0.0833333	7.3868E-05	SPDYE2_dup1	RASA4
chr7	+(102236241..102236753)	512	2.79191	13	4	9	0.3846154	0.074	SPDYE2_dup1	RASA4
chr7	+(102251494..102252020)	526	2.79191	10	7	3	0.4	0.667	SPDYE2_dup1	RASA4
chr7	+(102389485..102389999)	514	2.79191	10	6	4	0.2	0.057	FAM185A	FBXL13
chr7	+(102450655..102451739)	1084	0.5931	14	6	8	0.1428571	0.00097289	FAM185A	FBXL13
chr7	+(102962850..102963357)	507	0.5931	10	7	3	0.4	0.092	PMPCB	DNAJC2
chr7	+(104783442..104783953)	511	2.79191	9	4	5	0.1111111	0.095	MLL5	SRPK2
chr7	+(104829555..104830933)	1378	0.5931	15	7	8	0.0666667	0.99940313	MLL5	SRPK2
chr7	+(104971841..104972870)	1029	1.18321	13	6	7	0.0769231	0.0013499	MLL5	SRPK2
chr7	+(105445674..105446355)	681	2.79191	9	6	3	0.3333333	0.012	EFCAB10	ATXN7L1
chr7	+(105517336..105517947)	611	0.5931	8	3	5	0.25	0.018	ATXN7L1	CDHR3
chr7	+(106509681..106510200)	519	2.79191	6	2	4	0.3333333	0.067	PIK3CG	PRKAR2B
chr7	+(106938425..106938931)	506	2.79191	8	4	4	0	0.029	HBP1	COG5
chr7	+(107571471..107572228)	757	0.00691	17	7	10	0.1764706	0.0006399	DLD	LAMB1
chr7	+(117289876..117290398)	522	1.18321	7	3	4	0.1428571	0.029	CFTR	CTTNBP2

chr7	+(117431653..117432277)	624	0.27893	17	6	11	0.2941176	0.00448627	CFTR	CTTNBP2	
chr7	+(124404691..124405212)	521	0.13075	10	5	5	0	0.00451172	TMEM229A	GPR37	
chr7	+(127975613..127976217)	604	0.01316	22	12	10	0.0909091	0.00150257	LEP	RBM28	
chr7	+(128452004..128453088)	1084	0.5931	19	7	12	0.2631579	0.02126124	CCDC136	FLNC	
chr7	+(128767327..128767832)	505	2.79191	6	2	4	0.3333333	0.067	LOC407835	TSPAN33	
chr7	+(131191204..131191705)	501	2.79191	6	3	3	0	0.05	MKLN1	PODXL	
chr7	+(131192368..131193068)	700	2.79191	11	5	6	0.0909091	0.99691505	MKLN1	PODXL	
chr7	+(131574087..131575402)	1315	1.18321	13	7	6	0.0769231	0.9986501	PODXL	PLXNA4	
chr7	+(131814601..131815551)	950	0.5931	17	11	6	0.2941176	0.00045556	PODXL	PLXNA4	
chr7	+(132070891..132071591)	700	0.02846	12	6	6	0	0.00197388	PODXL	PLXNA4	
chr7	+(133087469..133087977)	508	1.18321	10	3	7	0.4	0.008	EXOC4	LRGUK	
chr7	+(133830051..133830751)	700	0.27893	9	6	3	0.3333333	0.012	LRGUK	SLC35B4	
chr7	+(134618332..134618889)	557	2.79191	15	7	8	0.0666667	0.5	CALD1	AGBL3	
chr7	+(134632176..134632704)	528	0.01316	13	7	6	0.0769231	0.0013499	CALD1	AGBL3	
chr7	+(135386203..135386724)	521	2.79191	9	3	6	0.3333333	0.048	PL-5283	SLC13A4	
chr7	+(136622860..136623462)	602	1.18321	13	4	9	0.3846154	0.999	MIR490	PTN	
chr7	+(137792109..137792629)	520	2.79191	6	4	2	0.3333333	0.067	AKR1D1	TRIM24	
chr7	+(138088277..138088803)	526	2.79191	12	6	6	0	0.02733197	AKR1D1	TRIM24	
chr7	+(138188890..138189547)	657	2.79191	9	6	3	0.3333333	0.012	TRIM24	SVOPL	
chr7	+(138330407..138331079)	672	1.18321	7	4	3	0.1428571	0.029	TRIM24	SVOPL	
chr7	+(138587793..138588534)	741	0.01316	15	10	5	0.3333333	0.0330963	TMEM213	KIAA1549	
chr7	+(139164044..139165129)	1085	0.13075	17	6	11	0.2941176	0.8861	LOC100129148	KLRG2	
chr7	+(139704295..139704995)	700	0.01316	13	4	9	0.3846154	0.001	TBXAS1	PARP12	
chr7	+(139826462..139827162)	700	0.13075	12	4	8	0.3333333	0.00328926	PARP12	JHDM1D	
chr7	+(140300828..140301367)	539	2.79191	10	4	6	0.2	0.129	MKRN1	DENND2A	
chr7	+(141095659..141096290)	631	2.79191	6	3	3	0	0.05	LOC100131199	AGK	
chr7	+(141490395..141490898)	503	1.18321	15	5	10	0.3333333	0.54873837	TAS2R5	PRSS37	
chr7	+(142479475..142480146)	671	0.02846	12	8	4	0.3333333	0.99671074	TRY6	PRSS2	
chr7	+(143021252..143021806)	554	0.27893	13	6	7	0.0769231	0.03164542	CLCN1	FAM131B	
chr7	+(143086735..143087320)	585	1.18321	7	4	3	0.1428571	0.029	ZYX	EPHA1	v
chr7	+(143094274..143094817)	543	0.13075	12	5	7	0.1666667	0.18587565	ZYX	EPHA1	v
chr7	+(143792185..143792718)	533	2.79191	9	3	6	0.3333333	0.083	OR2A25	OR2A12	
chr7	+(144060288..144060813)	525	1.88159	32	14	18	0.125	0.00438241	ARHGEF5	NOBOX	
chr7	+(148946652..148947476)	824	0.5931	14	8	6	0.1428571	0.00491164	ZNF212	ZNF783	

chr7	+(149424482..149425182)	700	2.79191	11	5	6	0.0909091	0.00308495	KRBA1	ZNF467
chr7	+(149494560..149495109)	549	0.27893	9	5	4	0.1111111	0.008	SSPO	ZNF862
chr7	+(149505309..149506009)	700	0.27893	9	3	6	0.3333333	0.012	SSPO	ZNF862
chr7	+(149519420..149519953)	533	1.18321	8	5	3	0.25	0.125	SSPO	ZNF862
chr7	+(150673874..150674416)	542	2.79191	6	2	4	0.3333333	0.067	ABP1	KCNH2
chr7	+(150697505..150698045)	540	2.79191	9	3	6	0.3333333	0.452	NOS3	ATG9B
chr7	+(150768887..150769499)	612	2.79191	6	2	4	0.3333333	0.067	SLC4A2	FASTK
chr7	+(150819455..150820096)	641	1.18321	7	4	3	0.1428571	0.029	AGAP3	GBX1
chr7	+(151093960..151094660)	700	0.13075	10	7	3	0.4	0.008	NUB1	WDR86
chr7	+(151134353..151135053)	700	1.18321	11	7	4	0.2727273	0.003	LOC100131176	CRYGN
chr7	+(151269474..151269992)	518	2.79191	9	5	4	0.1111111	0.032	RHEB	PRKAG2
chr7	+(151335853..151336889)	1036	0.5931	14	8	6	0.1428571	0.00097289	RHEB	PRKAG2
chr7	+(151879054..151879697)	643	1.18321	12	7	5	0.1666667	0.53235847	GALNT11	MLL3
chr7	+(151902082..151902715)	633	1.18321	9	6	3	0.3333333	0.048	GALNT11	MLL3
chr7	+(151918687..151919281)	594	1.18321	11	5	6	0.0909091	0.01422987	GALNT11	MLL3
chr7	+(152513598..152514110)	512	1.18321	11	7	4	0.2727273	0.006	ACTR3B	DPP6
chr7	+(153855756..153856351)	595	0.5931	8	4	4	0	0.014	DPP6	LOC100132707
chr7	+(154187318..154187853)	535	2.79191	6	3	3	0	0.05	DPP6	LOC100132707
chr7	+(154702543..154703504)	961	0.13075	20	14	6	0.4	0.000266	DPP6	LOC100132707
chr7	+(157224663..157225211)	548	1.18321	7	3	4	0.1428571	0.029	DNAJB6	PTPRN2
chr7	+(157264517..157265153)	636	0.13075	10	3	7	0.4	0.008	DNAJB6	PTPRN2
chr7	+(157334262..157334962)	700	1.18321	11	4	7	0.2727273	0.997	DNAJB6	PTPRN2
chr7	+(157413838..157414453)	615	0.5931	9	5	4	0.1111111	0.008	DNAJB6	PTPRN2
chr7	+(157500540..157501401)	861	0.0026	18	9	9	0	0.00017429	DNAJB6	PTPRN2
chr7	+(157506989..157508166)	1177	0.27893	17	9	8	0.0588235	0.999734	DNAJB6	PTPRN2
chr7	+(157623478..157624178)	700	2.79191	10	4	6	0.2	0.005	DNAJB6	PTPRN2
chr7	+(157735202..157735705)	503	2.79191	6	4	2	0.3333333	0.067	DNAJB6	PTPRN2
chr7	+(157756931..157758131)	1200	1.18321	13	7	6	0.0769231	0.9986501	DNAJB6	PTPRN2
chr7	+(157860355..157861486)	1131	0.13075	17	7	10	0.1764706	0.99968185	DNAJB6	PTPRN2
chr7	+(157869799..157870434)	635	1.18321	8	5	3	0.25	0.125	DNAJB6	PTPRN2
chr7	+(157958854..157959734)	880	0.01316	18	7	11	0.2222222	0.00216645	DNAJB6	PTPRN2
chr7	+(158140737..158141842)	1105	0.01316	21	9	12	0.1428571	0.33490768	DNAJB6	PTPRN2
chr7	+(158248613..158249313)	700	1.18321	11	5	6	0.0909091	0.00308495	DNAJB6	PTPRN2
chr7	+(158672198..158672739)	541	2.79191	6	3	3	0	0.05	WDR60	LOC154822

chr7	+(158821895..158822442)	547	1.18321	7	3	4	0.1428571	0.029	VIPR2		
chr8	+(232913..233613)	700	0.02297	12	4	8	0.3333333	0.00328926	ZNF596	FBXO25	
chr8	+(408154..408712)	558	2.46595	8	5	3	0.25	0.036	FBXO25	C8orf42	
chr8	+(640092..640696)	604	2.46595	6	3	3	0	0.05	C8orf42	ERICH1	
chr8	+(677478..678327)	849	0.47176	15	7	8	0.0666667	0.00059687	C8orf42	ERICH1	
chr8	+(751100..752281)	1181	0.47176	18	7	11	0.2222222	0.99783355	ERICH1	LOC286083	
chr8	+(1130662..1131214)	552	1.07955	7	3	4	0.1428571	0.029	ERICH1	LOC286083	
chr8	+(1206020..1206829)	809	0.00017	18	7	11	0.2222222	0.0002444	ERICH1	LOC286083	
chr8	+(1269197..1269805)	608	0.10114	17	10	7	0.1764706	0.68720738	LOC286083	DLGAP2	
chr8	+(1286871..1287980)	1109	1.07955	14	7	7	0	0.98732634	LOC286083	DLGAP2	
chr8	+(1472823..1473521)	698	1.07955	12	7	5	0.1666667	0.99775837	DLGAP2	CLN8	
chr8	+(1496416..1497076)	660	1.07955	11	4	7	0.2727273	0.003	DLGAP2	CLN8	
chr8	+(1724308..1725008)	700	1.07955	10	3	7	0.4	0.992	CLN8	MIR596	
chr8	+(2003429..2004128)	699	0.23896	9	6	3	0.3333333	0.012	MYOM2	CSMD1	
chr8	+(2196703..2197272)	569	2.46595	6	2	4	0.3333333	0.067	MYOM2	CSMD1	
chr8	+(2225225..2225925)	700	0.04466	15	5	10	0.3333333	0.80436636	MYOM2	CSMD1	
chr8	+(3216141..3217226)	1085	1.07955	13	6	7	0.0769231	0.9986501	MYOM2	CSMD1	
chr8	+(3951582..3952282)	700	0.23896	13	9	4	0.3846154	0.999	MYOM2	CSMD1	
chr8	+(5146047..5146927)	880	0.00982	13	6	7	0.0769231	0.0013499	CSMD1	MCPH1	
chr8	+(7190581..7191785)	1204	0.00184	34	20	14	0.1764706	0.86098912	FAM90A20	FAM66B	
chr8	+(7195461..7196158)	697	0.25246	35	23	12	0.3142857	0.01194461	FAM90A20	FAM66B	
chr8	+(7199378..7200035)	657	0.04466	12	7	5	0.1666667	0.00224163	FAM90A20	FAM66B	
chr8	+(7835071..7835640)	569	2.46595	11	4	7	0.2727273	0.206	FAM66E	DEFB109P1B_dup2	
chr8	+(8234234..8234849)	615	0.04466	15	10	5	0.3333333	0.0330963	FLJ10661	SGK223	
chr8	+(8348304..8349004)	700	0.47176	12	4	8	0.3333333	0.00328926	SGK223	CLDN23	
chr8	+(8873660..8874225)	565	2.46595	7	3	4	0.1428571	0.029	ERI1	PPP1R3B	
chr8	+(10466424..10467049)	625	0.10114	12	7	5	0.1666667	0.28488218	PRSS55	RP1L1	
chr8	+(10467135..10467982)	847	0.00297	23	15	8	0.3043478	0.02640376	PRSS55	RP1L1	
chr8	+(11420567..11421158)	591	2.46595	9	3	6	0.3333333	0.726	BLK	GATA4	v
chr8	+(11554718..11555317)	599	1.07955	7	4	3	0.1428571	0.029	BLK	GATA4	v
chr8	+(11593641..11594535)	894	0.00297	21	8	13	0.2380952	8.2983E-05	GATA4	NEIL2	v
chr8	+(11614228..11614918)	690	1.07955	9	5	4	0.1111111	0.095	GATA4	NEIL2	v
chr8	+(12232522..12233072)	550	0.23896	14	5	9	0.2857143	0.00981533	FAM66A	DEFB109P1	
chr8	+(12283041..12284015)	974	0.0104	61	31	30	0.0163934	3.422E-05	FAM90A25P	FAM86B2	

chr8	+(12286329..12287002)	673	0.25246	31	19	12	0.2258065	0.00371808	FAM90A25P	FAM86B2
chr8	+(13218206..13218906)	700	0.23896	9	6	3	0.3333333	0.012	C8orf79	DLC1
chr8	+(13356984..13357556)	572	2.46595	8	5	3	0.25	0.393	C8orf79	DLC1
chr8	+(17488335..17489008)	673	2.46595	9	4	5	0.1111111	0.857	PDGFRL	MTUS1
chr8	+(18079319..18080019)	700	0.04508	18	11	7	0.2222222	0.00216645	NAT1	NAT2
chr8	+(19440050..19440750)	700	0.00982	13	4	9	0.3846154	0.001	SH2D4A	CSGALNACT1
chr8	+(21956572..21957114)	542	1.07955	12	6	6	0	0.02733197	FAM160B2	NUDT18
chr8	+(21987000..21987682)	682	1.07955	7	3	4	0.1428571	0.029	NUDT18	HR
chr8	+(21991940..21992640)	700	0.23896	13	4	9	0.3846154	0.999	HR	REEP4
chr8	+(22005242..22005795)	553	1.07955	7	4	3	0.1428571	0.029	REEP4	LGI3
chr8	+(22461962..22462526)	564	2.46595	12	6	6	0	0.00197388	C8orf58	KIAA1967
chr8	+(22477730..22478335)	605	0.23896	9	4	5	0.1111111	0.008	KIAA1967	BIN3
chr8	+(22575821..22576496)	675	1.07955	7	3	4	0.1428571	0.029	EGR3	PEBP4
chr8	+(22974224..22974725)	501	2.46595	10	5	5	0	0.0081468	TNFRSF10C	TNFRSF10D
chr8	+(23057057..23057843)	786	0.23896	17	9	8	0.0588235	0.000266	TNFRSF10D	TNFRSF10A
chr8	+(23240341..23240956)	615	1.07955	8	5	3	0.25	0.018	R3HCC1	LOXL2
chr8	+(27155799..27156434)	635	0.10114	10	6	4	0.2	0.005	STMN4	TRIM35
chr8	+(27641298..27641814)	516	2.46595	6	3	3	0	0.05	ESCO2	PBK
chr8	+(27737099..27737682)	583	2.46595	6	3	3	0	0.05	PBK	SCARA5
chr8	+(28207532..28208232)	700	0.23896	12	6	6	0	0.5	PNOC	ZNF395
chr8	+(28360506..28361025)	519	0.47176	13	8	5	0.2307692	0.18988774	FZD3	MIR4288
chr8	+(28633194..28634114)	920	0.10114	17	10	7	0.1764706	0.00031815	EXTL3	INTS9
chr8	+(30942618..30943159)	541	2.46595	12	6	6	0	0.13116584	WRN	NRG1
chr8	+(33360796..33361315)	519	2.46595	13	4	9	0.3846154	0.47	MAK16	C8orf41
chr8	+(35382738..35383273)	535	2.46595	11	5	6	0.0909091	0.70805879	UNC5D	KCNU1
chr8	+(36408387..36409086)	699	2.46595	9	6	3	0.3333333	0.988	UNC5D	KCNU1
chr8	+(36793101..36793634)	533	2.46595	7	3	4	0.1428571	0.029	KCNU1	ZNF703
chr8	+(37472507..37473102)	595	0.10114	10	5	5	0	0.00451172	KCNU1	ZNF703
chr8	+(37601618..37602645)	1027	0.23896	17	7	10	0.1764706	0.99910455	ERLIN2	LOC728024
chr8	+(37645118..37646066)	948	0.02297	18	6	12	0.3333333	0.00037352	PROSC	GPR124
chr8	+(37678239..37678798)	559	2.46595	6	4	2	0.3333333	0.067	GPR124	BRF2
chr8	+(37718883..37719491)	608	0.10114	10	7	3	0.4	0.008	BRF2	RAB11FIP1
chr8	+(37731879..37732534)	655	0.23896	10	6	4	0.2	0.019	BRF2	RAB11FIP1
chr8	+(37762369..37762945)	576	2.46595	6	3	3	0	0.05	RAB11FIP1	GOT1L1

chr8	+(37901123..37902268)	1145	0.47176	14	7	7	0	0.98732634	EIF4EBP1	ASH2L	
chr8	+(38066352..38067029)	677	0.47176	10	5	5	0	0.05859256	BAG4	DDHD2	
chr8	+(39775520..39776056)	536	2.46595	6	3	3	0	0.05	IDO1	IDO2	
chr8	+(41552394..41552925)	531	2.46595	6	4	2	0.3333333	0.067	NKX6-3	ANK1	
chr8	+(41685417..41686101)	684	0.00982	13	6	7	0.0769231	0.0013499	NKX6-3	ANK1	
chr8	+(42182220..42182858)	638	1.07955	9	3	6	0.3333333	0.012	IKBKB	POLB	
chr8	+(42292098..42293230)	1132	2.46595	15	10	5	0.3333333	0.99284706	VDAC3	SLC20A2	
chr8	+(42587101..42587669)	568	2.46595	9	5	4	0.1111111	0.032	CHRNB3	CHRNA6	
chr8	+(42828042..42828552)	510	2.46595	9	3	6	0.3333333	0.452	HOOK3	FNTA	
chr8	+(48641516..48642043)	527	2.46595	12	7	5	0.1666667	0.08373231	KIAA0146	CEBPD	
chr8	+(48744395..48744910)	515	2.46595	7	3	4	0.1428571	0.029	CEBPD	PRKDC	
chr8	+(48887041..48887741)	700	0.47176	13	4	9	0.3846154	0.207	MCM4	UBE2V2	
chr8	+(51786222..51787448)	1226	0.47176	14	8	6	0.1428571	0.99902711	SNTG1	PXDNL	
chr8	+(52665168..52665868)	700	0.10114	11	4	7	0.2727273	0.003	SNTG1	PXDNL	
chr8	+(53084538..53085065)	527	2.46595	8	4	4	0	0.014	PCMTD1	ST18	
chr8	+(54642258..54642958)	700	0.23896	9	6	3	0.3333333	0.012	OPRK1	ATP6V1H	
chr8	+(56675227..56675736)	509	1.07955	8	4	4	0	0.057	SBF1P1	TMEM68	
chr8	+(56698852..56699452)	600	0.47176	9	4	5	0.1111111	0.008	TGS1	LYN	
chr8	+(59059716..59060247)	531	2.46595	11	5	6	0.0909091	0.42756607	FAM110B	UBXN2B	
chr8	+(61693702..61694213)	511	1.07955	9	6	3	0.3333333	0.274	CHD7	LOC100130298	
chr8	+(63662816..63663469)	653	0.47176	8	3	5	0.25	0.018	NKAIN3	LOC643763	
chr8	+(63985171..63985695)	524	1.07955	7	4	3	0.1428571	0.029	GGH	TTPA	
chr8	+(64048686..64049280)	594	0.47176	9	4	5	0.1111111	0.008	TTPA	YTHDF3	
chr8	+(66651555..66652117)	562	1.07955	8	5	3	0.25	0.018	MTFR1	PDE7A	
chr8	+(67755501..67756013)	512	2.46595	8	3	5	0.25	0.018	PTTG3P	C8orf45	
chr8	+(72942029..72942704)	675	0.47176	12	8	4	0.3333333	0.596	LOC100132891	TRPA1	
chr8	+(73117369..73117887)	518	2.46595	9	5	4	0.1111111	0.056	TRPA1	LOC392232	
chr8	+(73926000..73926504)	504	0.47176	13	8	5	0.2307692	0.0017074	TERF1	C8orf84	
chr8	+(77775833..77776452)	619	2.46595	9	3	6	0.3333333	0.988	ZFHX4	PEX2	
chr8	+(80548939..80549533)	594	1.07955	10	7	3	0.4	0.133	STMN2	HEY1	
chr8	+(81430689..81431201)	512	2.46595	8	5	3	0.25	0.125	ZBTB10	ZNF704	
chr8	+(81507012..81507517)	505	2.46595	10	5	5	0	0.08726268	ZBTB10	ZNF704	
chr8	+(86389108..86389757)	649	2.46595	9	4	5	0.1111111	0.008	CA2	REXO1L2P_dup1	v
chr8	+(87755534..87756092)	558	1.07955	8	4	4	0	0.014	CPNE3	CNGB3	

chr8	+(92085760..92086457)	697	0.10114	10	6	4	0.2	0.005	OTUD6B	LRRC69	
chr8	+(92114751..92115421)	670	0.02297	14	5	9	0.2857143	0.0020741	OTUD6B	LRRC69	
chr8	+(92147731..92148232)	501	2.46595	7	3	4	0.1428571	0.029	LRRC69	SLC26A7	
chr8	+(92170792..92171313)	521	0.10114	15	8	7	0.0666667	0.01031878	LRRC69	SLC26A7	
chr8	+(95448571..95449146)	575	0.47176	12	8	4	0.3333333	0.036	GEM	RAD54B	v
chr8	+(95879119..95879620)	501	2.46595	7	3	4	0.1428571	0.2	INTS8	CCNE2	
chr8	+(98698690..98699203)	513	2.46595	10	4	6	0.2	0.033	MTDH	LAPTM4B	
chr8	+(98700900..98701763)	863	1.07955	14	7	7	0	0.00087256	MTDH	LAPTM4B	
chr8	+(98993133..98994447)	1314	0.04466	17	11	6	0.2941176	0.99954444	MATN2	RPL30	
chr8	+(99242721..99243421)	700	1.07955	10	3	7	0.4	0.008	POP1	NIPAL2	
chr8	+(99662320..99663253)	933	0.47176	14	5	9	0.2857143	0.0013499	KCNS2	STK3	
chr8	+(99961341..99962002)	661	0.47176	9	5	4	0.1111111	0.008	OSR2	VPS13B	v
chr8	+(100578569..100579186)	617	2.46595	7	4	3	0.1428571	0.029	MIR875	COX6C	
chr8	+(101075601..101076110)	509	0.97106	19	10	9	0.0526316	0.0604097	COX6C	RGS22	
chr8	+(101196389..101197088)	699	2.46595	9	3	6	0.3333333	0.988	SPAG1	RNF19A	
chr8	+(101281923..101282433)	510	2.46595	6	2	4	0.3333333	0.067	SPAG1	RNF19A	
chr8	+(101470337..101470847)	510	0.02297	12	4	8	0.3333333	0.00328926	RNF19A	ANKRD46	
chr8	+(110509031..110509547)	516	2.46595	7	4	3	0.1428571	0.114	PKHD1L1	EBAG9	
chr8	+(117862605..117863135)	530	1.07955	10	4	6	0.2	0.01	UTP23	RAD21	
chr8	+(118169758..118170267)	509	2.5843	14	6	8	0.1428571	0.00491164	SLC30A8	MED30	
chr8	+(124266332..124267032)	700	1.07955	13	6	7	0.0769231	0.38754848	C8orf76	ZHX1	
chr8	+(125565179..125566120)	941	2.46595	12	6	6	0	0.00197388	NDUFB9	MTSS1	
chr8	+(125636285..125636985)	700	1.07955	11	4	7	0.2727273	0.003	NDUFB9	MTSS1	
chr8	+(126448388..126448985)	597	2.46595	7	4	3	0.1428571	0.314	TRIB1	FAM84B	
chr8	+(126653823..126654483)	660	2.46595	6	2	4	0.3333333	0.067	TRIB1	FAM84B	
chr8	+(126776377..126777077)	700	2.46595	9	3	6	0.3333333	0.988	TRIB1	FAM84B	
chr8	+(127521993..127522607)	614	2.46595	6	3	3	0	0.05	TRIB1	FAM84B	
chr8	+(128427893..128429629)	1736	4.2E-34	453	231	222	0.0198675	0.77966238	POU5F1B	LOC727677	
chr8	+(128833191..128834269)	1078	2.46595	12	6	6	0	0.99802612	MIR1204	MIR1205	
chr8	+(130993090..130993790)	700	1.07955	12	5	7	0.1666667	0.99775837	FAM49B	ASAP1	
chr8	+(130994834..130995381)	547	0.47176	8	4	4	0	0.014	FAM49B	ASAP1	
chr8	+(131022983..131023683)	700	0.23896	9	3	6	0.3333333	0.012	FAM49B	ASAP1	
chr8	+(131063635..131064284)	649	0.23896	9	4	5	0.1111111	0.008	FAM49B	ASAP1	
chr8	+(131068624..131069275)	651	1.07955	11	7	4	0.2727273	0.997	FAM49B	ASAP1	

chr8	+(131098270..131098802)	532	2.46595	6	3	3	0	0.05	FAM49B	ASAP1
chr8	+(133363676..133364291)	615	2.46595	6	3	3	0	0.05	HHLA1	KCNQ3
chr8	+(133426037..133426737)	700	0.10114	15	10	5	0.3333333	0.99890018	HHLA1	KCNQ3
chr8	+(133504841..133505826)	985	0.23896	17	8	9	0.0588235	0.000266	KCNQ3	HPYR1
chr8	+(134237587..134238278)	691	2.46595	9	6	3	0.3333333	0.012	WISP1	NDRG1
chr8	+(134296198..134296759)	561	2.46595	10	5	5	0	0.94140744	WISP1	NDRG1
chr8	+(134368228..134368844)	616	0.47176	8	4	4	0	0.014	NDRG1	ST3GAL1
chr8	+(134471940..134472490)	550	1.07955	12	7	5	0.1666667	0.28488218	NDRG1	ST3GAL1
chr8	+(134496974..134497555)	581	2.46595	6	2	4	0.3333333	0.067	NDRG1	ST3GAL1
chr8	+(134623251..134624237)	986	2.46595	12	6	6	0	0.99802612	ST3GAL1	ZFAT
chr8	+(135141162..135142194)	1032	0.23896	15	9	6	0.2	0.00073136	ST3GAL1	ZFAT
chr8	+(135470503..135471399)	896	0.00063	23	10	13	0.1304348	2.7755E-05	ST3GAL1	ZFAT
chr8	+(139726106..139726672)	566	0.47176	8	4	4	0	0.014	FAM135B	COL22A1
chr8	+(140613030..140613730)	700	0.23896	10	5	5	0	0.00451172	COL22A1	KCNK9
chr8	+(140669282..140669805)	523	2.46595	6	4	2	0.3333333	0.067	COL22A1	KCNK9
chr8	+(140694110..140694807)	697	2.46595	13	9	4	0.3846154	0.999	COL22A1	KCNK9
chr8	+(140749699..140750237)	538	0.47176	9	6	3	0.3333333	0.083	KCNK9	TRAPPC9
chr8	+(140755246..140755875)	629	0.23896	9	4	5	0.1111111	0.008	KCNK9	TRAPPC9
chr8	+(140845452..140846152)	700	0.00011	19	13	6	0.3684211	0.0003125	KCNK9	TRAPPC9
chr8	+(141047958..141048628)	670	2.46595	6	3	3	0	0.05	KCNK9	TRAPPC9
chr8	+(141057785..141058379)	594	0.10114	10	5	5	0	0.00451172	KCNK9	TRAPPC9
chr8	+(141060287..141060940)	653	2.46595	6	3	3	0	0.05	KCNK9	TRAPPC9
chr8	+(141079703..141080403)	700	0.02297	12	5	7	0.1666667	0.00224163	KCNK9	TRAPPC9
chr8	+(141562235..141562935)	700	0.02297	12	8	4	0.3333333	0.99671074	CHRAC1	EIF2C2
chr8	+(141588461..141588980)	519	0.23896	9	5	4	0.1111111	0.008	CHRAC1	EIF2C2
chr8	+(141615329..141615982)	653	2.46595	9	6	3	0.3333333	0.548	CHRAC1	EIF2C2
chr8	+(142186338..142186953)	615	0.10114	10	7	3	0.4	0.008	DENND3	SLC45A4
chr8	+(142194922..142195622)	700	0.10114	10	6	4	0.2	0.005	DENND3	SLC45A4
chr8	+(142490539..142491209)	670	0.47176	8	4	4	0	0.014	PTP4A3	FLJ43860
chr8	+(142559073..142559757)	684	2.46595	9	6	3	0.3333333	0.274	FLJ43860	NCRNA00051
chr8	+(142595258..142596163)	905	2.46595	14	5	9	0.2857143	0.36944134	FLJ43860	NCRNA00051
chr8	+(142686324..142686984)	660	0.23896	9	3	6	0.3333333	0.012	FLJ43860	NCRNA00051
chr8	+(142729280..142730693)	1413	0.23896	23	10	13	0.1304348	0.85412612	FLJ43860	NCRNA00051
chr8	+(142823425..142823986)	561	1.07955	7	3	4	0.1428571	0.029	FLJ43860	NCRNA00051

chr8	+(142867159..142867859)	700	0.47176	11	6	5	0.0909091	0.02230486	FLJ43860	NCRNA00051
chr8	+(142974749..142975449)	700	0.23896	10	3	7	0.4	0.008	FLJ43860	NCRNA00051
chr8	+(143023346..143023912)	566	2.46595	6	4	2	0.3333333	0.067	FLJ43860	NCRNA00051
chr8	+(143058964..143059952)	988	2.46595	12	6	6	0	0.00197388	FLJ43860	NCRNA00051
chr8	+(143100353..143101053)	700	0.04466	11	7	4	0.2727273	0.003	FLJ43860	NCRNA00051
chr8	+(143104774..143105333)	559	2.46595	9	3	6	0.3333333	0.988	FLJ43860	NCRNA00051
chr8	+(143241596..143242102)	506	1.07955	7	3	4	0.1428571	0.029	FLJ43860	NCRNA00051
chr8	+(143277785..143278325)	540	1.07955	7	3	4	0.1428571	0.029	FLJ43860	NCRNA00051
chr8	+(143319694..143320286)	592	2.46595	6	4	2	0.3333333	0.067	NCRNA00051	TSNARE1
chr8	+(143363547..143364172)	625	0.47176	8	5	3	0.25	0.018	NCRNA00051	TSNARE1
chr8	+(143369652..143370175)	523	1.07955	7	4	3	0.1428571	0.029	NCRNA00051	TSNARE1
chr8	+(143498582..143499161)	579	1.07955	7	4	3	0.1428571	0.029	TSNARE1	BAI1
chr8	+(143573068..143573647)	579	0.47176	12	8	4	0.3333333	0.99671074	BAI1	ARC
chr8	+(143582486..143583015)	529	2.46595	6	2	4	0.3333333	0.067	BAI1	ARC
chr8	+(143615899..143616445)	546	0.23896	9	4	5	0.1111111	0.008	BAI1	ARC
chr8	+(143630071..143630771)	700	0.04466	11	6	5	0.0909091	0.00308495	BAI1	ARC
chr8	+(143636238..143636938)	700	0.00982	13	9	4	0.3846154	0.001	BAI1	ARC
chr8	+(143644837..143645462)	625	2.46595	11	5	6	0.0909091	0.94982587	BAI1	ARC
chr8	+(143691976..143692671)	695	2.46595	10	6	4	0.2	0.995	BAI1	ARC
chr8	+(143759819..143760613)	794	0.00184	16	6	10	0.25	0.00056905	PSCA	LY6K
chr8	+(143816417..143817105)	688	0.23896	13	9	4	0.3846154	0.001	C8orf55	SLURP1
chr8	+(144095043..144095550)	507	0.47176	8	3	5	0.25	0.018	CYP11B2	LOC100133669
chr8	+(144095797..144096950)	1153	1.07955	16	5	11	0.375	0.85908964	CYP11B2	LOC100133669
chr8	+(144296517..144297343)	826	0.00011	21	12	9	0.1428571	0.00053949	GPIHBP1	ZFP41
chr8	+(144354307..144355073)	766	0.00982	13	7	6	0.0769231	0.0013499	GLI4	ZNF696
chr8	+(144458360..144458924)	564	0.04466	12	7	5	0.1666667	0.00224163	RHPN1	MAFA
chr8	+(144462377..144463005)	628	1.07955	7	4	3	0.1428571	0.029	RHPN1	MAFA
chr8	+(144505569..144506269)	700	0.00017	22	8	14	0.2727273	6.6151E-05	RHPN1	MAFA
chr8	+(144653668..144654368)	700	0.47176	10	3	7	0.4	0.742	GSDMD	C8orf73
chr8	+(144662549..144663060)	511	2.46595	9	3	6	0.3333333	0.083	NAPRT1	EEF1D
chr8	+(144667677..144668272)	595	2.46595	6	3	3	0	0.05	NAPRT1	EEF1D
chr8	+(144776456..144777069)	613	2.46595	6	4	2	0.3333333	0.067	ZNF707	BREA2
chr8	+(144778623..144779208)	585	0.10114	10	7	3	0.4	0.008	ZNF707	BREA2
chr8	+(144795107..144795807)	700	1.07955	10	7	3	0.4	0.992	LOC100130274	MAPK15

chr8	+(144799111..144799905)	794	1.07955	13	7	6	0.0769231	0.15865525	MAPK15	FAM83H	
chr8	+(144917317..144917873)	556	0.23896	9	4	5	0.1111111	0.008	PUF60	NRBP2	
chr8	+(145030744..145031340)	596	2.46595	6	4	2	0.3333333	0.067	EPPK1	PLEC	
chr8	+(145057724..145058304)	580	2.46595	6	4	2	0.3333333	0.067	MIR661	PARP10	
chr8	+(145150968..145151491)	523	2.46595	6	2	4	0.3333333	0.067	CYC1	SHARPIN	
chr8	+(145254746..145255446)	700	0.10114	12	8	4	0.3333333	0.533	HEATR7A	SCXA_dup1	
chr8	+(145534408..145534941)	533	2.46595	12	6	6	0	0.99802612	HSF1	DGAT1	
chr8	+(145558388..145559459)	1071	0.04466	18	12	6	0.3333333	0.00744336	DGAT1	SCRT1	
chr8	+(145632868..145633434)	566	2.46595	11	5	6	0.0909091	0.05017413	ADCK5	CPSF1	
chr8	+(145637185..145637964)	779	0.00011	23	11	12	0.0434783	0.03241909	MIR1234	SLC39A4	
chr8	+(145649871..145651124)	1253	0.10114	17	6	11	0.2941176	0.9966722	SLC39A4	VPS28	
chr8	+(145735949..145736544)	595	0.23896	9	5	4	0.1111111	0.008	MFSD3	RECQL4	
chr8	+(145775956..145776487)	531	1.07955	7	4	3	0.1428571	0.029	MGC70857	ARHGAP39	
chr8	+(145779889..145780589)	700	0.02297	13	9	4	0.3846154	0.001	MGC70857	ARHGAP39	
chr8	+(145783507..145784207)	700	0.04466	11	5	6	0.0909091	0.00308495	MGC70857	ARHGAP39	
chr8	+(145806026..145806725)	699	0.23896	13	4	9	0.3846154	0.001	MGC70857	ARHGAP39	
chr8	+(145903974..145904479)	505	2.46595	6	2	4	0.3333333	0.067	ARHGAP39	ZNF251	
chr9	+(354204..355020)	816	7.5E-05	32	18	14	0.125	8.4923E-07	DOCK8	KANK1	
chr9	+(390211..390720)	509	3.54521	9	4	5	0.1111111	0.278	DOCK8	KANK1	
chr9	+(1959988..1960688)	700	0.06099	12	4	8	0.3333333	0.00328926	DMRT2	SMARCA2	
chr9	+(2191096..2191618)	522	3.54521	6	3	3	0	0.05	SMARCA2	FLJ35024	
chr9	+(2838290..2838834)	544	1.65224	8	5	3	0.25	0.018	KCNV2	KIAA0020	
chr9	+(6507103..6507839)	736	0.0022	17	11	6	0.2941176	0.00045556	UHRF2	GLDC	v
chr9	+(6577974..6579097)	1123	0.43546	15	6	9	0.2	0.00073136	UHRF2	GLDC	v
chr9	+(8834877..8835577)	700	0.93087	9	3	6	0.3333333	0.012	C9orf123	PTPRD	
chr9	+(10651150..10651698)	548	1.65224	7	3	4	0.1428571	0.029	PTPRD	TYRP1	
chr9	+(12657623..12658323)	700	3.54521	10	4	6	0.2	0.995	PTPRD	TYRP1	
chr9	+(16106857..16107557)	700	0.06099	12	5	7	0.1666667	0.00224163	C9orf93	BNC2	
chr9	+(16668030..16668558)	528	3.54521	6	2	4	0.3333333	0.067	C9orf93	BNC2	
chr9	+(16713457..16714141)	684	3.54521	6	3	3	0	0.05	C9orf93	BNC2	
chr9	+(17415846..17416358)	512	3.54521	8	4	4	0	0.014	CNTLN	SH3GL2	
chr9	+(19102556..19103256)	700	0.21815	15	5	10	0.3333333	0.99890018	RRAGA	HAUS6	
chr9	+(20413579..20414587)	1008	3.54521	26	10	16	0.2307692	0.29908073	SLC24A2	MLLT3	
chr9	+(21206074..21206586)	512	3.54521	12	5	7	0.1666667	0.00926649	IFNA7	IFNA10	

chr9	+(21206950..21207519)	569	1.65224	17	8	9	0.0588235	0.03375409	IFNA7	IFNA10
chr9	+(21217074..21217593)	519	3.54521	11	4	7	0.2727273	0.006	IFNA10	IFNA16
chr9	+(21409269..21409771)	502	3.54521	13	8	5	0.2307692	0.23210716	IFNA8	IFNA1
chr9	+(32549977..32550677)	700	3.54521	11	6	5	0.0909091	0.00308495	DDX58	TOPORS
chr9	+(33797452..33798227)	775	0.0022	25	8	17	0.36	0.01798855	PRSS3	UBE2R2
chr9	+(34234003..34234596)	593	1.65224	10	3	7	0.4	0.092	UBAP1	KIF24
chr9	+(34570288..34571754)	1466	0.01435	22	14	8	0.2727273	0.99993385	ENHO	CNTFR
chr9	+(34834094..34834931)	837	2.13968	40	24	16	0.2	0.0031363	C9orf144B	C9orf144
chr9	+(34835054..34835560)	506	3.54521	12	6	6	0	0.05465729	C9orf144B	C9orf144
chr9	+(35377011..35377711)	700	3.54521	9	3	6	0.3333333	0.274	UNC13B	ATP8B5P
chr9	+(35605397..35606544)	1147	0.93087	16	10	6	0.25	0.99538163	TESK1	CD72
chr9	+(35697559..35698259)	700	0.06099	15	5	10	0.3333333	0.00242438	TPM2	TLN1
chr9	+(35737671..35738178)	507	3.54521	6	2	4	0.3333333	0.067	CREB3	GBA2
chr9	+(36724715..36725352)	637	3.54521	6	2	4	0.3333333	0.067	MELK	PAX5
chr9	+(36800009..36800536)	527	0.93087	8	5	3	0.25	0.018	MELK	PAX5
chr9	+(36835766..36836624)	858	0.06099	12	6	6	0	0.00197388	MELK	PAX5
chr9	+(36873844..36874544)	700	0.11433	11	7	4	0.2727273	0.003	MELK	PAX5
chr9	+(36891196..36891698)	502	3.54521	9	6	3	0.3333333	0.917	MELK	PAX5
chr9	+(37024440..37025051)	611	0.11433	11	4	7	0.2727273	0.003	MELK	PAX5
chr9	+(37440801..37441368)	567	3.54521	9	5	4	0.1111111	0.452	GRHPR	ZBTB5
chr9	+(37887577..37888188)	611	0.06099	18	6	12	0.3333333	0.01561431	DCAF10	MCART1
chr9	+(37997630..37998160)	530	3.54521	7	4	3	0.1428571	0.029	MCART1	SHB
chr9	+(38003191..38003722)	531	1.65224	7	4	3	0.1428571	0.029	MCART1	SHB
chr9	+(38018623..38019323)	700	0.43546	14	5	9	0.2857143	0.9986501	MCART1	SHB
chr9	+(38397998..38398525)	527	3.54521	13	6	7	0.0769231	0.0013499	ALDH1B1	IGFBPL1
chr9	+(38441804..38442408)	604	3.54521	6	2	4	0.3333333	0.067	IGFBPL1	ANKRD18A
chr9	+(38488554..38489102)	548	0.93087	8	4	4	0	0.014	IGFBPL1	ANKRD18A
chr9	+(38619715..38620248)	533	1.65224	8	4	4	0	0.014	IGFBPL1	ANKRD18A
chr9	+(39890054..39890583)	529	0.93087	18	9	9	0	0.00592447	FAM75A2_dup2	FAM74A1
chr9	+(40772617..40773377)	760	0.21815	39	22	17	0.1282051	0.06666885	FAM74A3	ZNF658
chr9	+(41591713..41592270)	557	3.54521	19	12	7	0.2631579	0.82372893	FAM75A5_dup2	LOC653501_dup2
chr9	+(65617426..65617941)	515	1.84713	46	22	24	0.0434783	0.03568014	FAM75A7_dup3	LOC442421
chr9	+(66500309..66500914)	605	3.54521	14	8	6	0.1428571	0.96464942	LOC442421	LOC100133920_dup1
chr9	+(66513516..66514715)	1199	1.65224	27	14	13	0.037037	0.34893059	LOC442421	LOC100133920_dup1

chr9	+(66516755..66517257)	502	3.85533	23	11	12	0.0434783	0.01561612	LOC442421	LOC100133920_dup1
chr9	+(66837026..66837641)	615	3.54521	6	4	2	0.3333333	0.067	LOC442421	LOC100133920_dup1
chr9	+(67938494..67939157)	663	0.43546	15	9	6	0.2	0.00335832	ANKRD20A3_dup3	LOC642236
chr9	+(68435506..68436118)	612	1.65224	9	3	6	0.3333333	0.024	ANKRD20A3_dup3	LOC642236
chr9	+(68455294..68455893)	599	1.65224	10	7	3	0.4	0.008	LOC642236	LOC100132352
chr9	+(69067538..69068146)	608	3.26016	26	8	18	0.3846154	0.00530092	LOC100132352	PGM5P2
chr9	+(69081857..69082358)	501	1.65224	11	5	6	0.0909091	0.18065522	LOC100132352	PGM5P2
chr9	+(69381708..69382608)	900	1.65224	19	12	7	0.2631579	0.00019287	CBWD6	ANKRD20A4
chr9	+(70176190..70176701)	511	3.54521	10	6	4	0.2	0.033	LOC100133920_dup2	FOXD4L5
chr9	+(70428507..70429304)	797	0.21815	26	17	9	0.3076923	0.00233044	FOXD4L5	FOXD4L2_dup2
chr9	+(70482815..70483770)	955	0.01946	54	25	29	0.0740741	2.4258E-06	FOXD4L4_dup2	CBWD3_dup1
chr9	+(70484150..70484652)	502	1.91123	69	46	23	0.3333333	3.767E-05	FOXD4L4_dup2	CBWD3_dup1
chr9	+(70486408..70486958)	550	3.26016	34	16	18	0.0588235	0.00259687	FOXD4L4_dup2	CBWD3_dup1
chr9	+(70488471..70489464)	993	2.69852	52	29	23	0.1153846	0.15766002	FOXD4L4_dup2	CBWD3_dup1
chr9	+(70862214..70862924)	710	0.22442	112	60	52	0.0714286	5.5511E-17	CBWD3_dup2	FOXD4L3
chr9	+(70871600..70872297)	697	0.02892	32	21	11	0.3125	2.8233E-05	CBWD3_dup2	FOXD4L3
chr9	+(71668990..71669503)	513	0.93087	8	4	4	0	0.014	FXN	TJP2
chr9	+(71731288..71731988)	700	1.65224	10	7	3	0.4	0.992	FXN	TJP2
chr9	+(74804998..74805555)	557	0.93087	8	4	4	0	0.014	GDA	ZFAND5
chr9	+(75393672..75394193)	521	1.65224	7	4	3	0.1428571	0.029	TMC1	ALDH1A1
chr9	+(75420050..75420599)	549	3.54521	9	4	5	0.1111111	0.095	TMC1	ALDH1A1
chr9	+(77353915..77354426)	511	0.21815	15	5	10	0.3333333	0.00164431	RORB	TRPM6
chr9	+(79933157..79933678)	521	3.54521	6	3	3	0	0.05	VPS13A	GNA14
chr9	+(80157705..80158379)	674	3.54521	10	6	4	0.2	0.995	VPS13A	GNA14
chr9	+(84558337..84558853)	516	2.28983	17	6	11	0.2941176	0.00599235	FAM75D4	FAM75D3
chr9	+(84560161..84561283)	1122	1.65224	46	31	15	0.3478261	0.10079032	FAM75D3	FAM75D1
chr9	+(84562134..84562642)	508	3.54521	14	6	8	0.1428571	0.84915021	FAM75D3	FAM75D1
chr9	+(84606847..84607483)	636	0.43546	12	8	4	0.3333333	0.014	FAM75D1	RASEF
chr9	+(84607697..84608504)	807	0.93087	18	12	6	0.3333333	0.03757785	FAM75D1	RASEF
chr9	+(84676392..84676893)	501	3.26016	23	12	11	0.0434783	3.1608E-05	FAM75D1	RASEF
chr9	+(84677064..84677619)	555	0.93087	12	5	7	0.1666667	0.00224163	FAM75D1	RASEF
chr9	+(85597403..85597911)	508	3.54521	11	6	5	0.0909091	0.00308495	FAM75D1	RASEF
chr9	+(86239064..86240388)	1324	0.43546	15	9	6	0.2	0.99926864	C9orf103	UBQLN1
chr9	+(86452017..86452617)	600	0.21815	18	12	6	0.3333333	0.96947765	GKAP1	KIF27

chr9	+(86466922..86467538)	616	1.65224	7	4	3	0.1428571	0.029	GKAP1	KIF27	
chr9	+(87366767..87367422)	655	3.54521	14	6	8	0.1428571	0.01943355	NTRK2	AGTPBP1	
chr9	+(87863472..87864054)	582	3.54521	6	4	2	0.3333333	0.067	NTRK2	AGTPBP1	
chr9	+(88960409..88960914)	505	3.54521	7	4	3	0.1428571	0.029	ISCA1	ZCCHC6	
chr9	+(90130432..90131543)	1111	1.65224	15	7	8	0.0666667	0.00059687	DAPK1	CTSL1	
chr9	+(90219602..90220281)	679	0.43546	9	4	5	0.1111111	0.008	DAPK1	CTSL1	
chr9	+(90245166..90246239)	1073	1.65224	13	8	5	0.2307692	0.0017074	DAPK1	CTSL1	
chr9	+(95055635..95056280)	645	0.43546	14	7	7	0	0.08985625	C9orf44	IARS	
chr9	+(95888329..95888928)	599	0.21815	10	5	5	0	0.00451172	C9orf89	NINJ1	
chr9	+(95993754..95994317)	563	1.65224	9	5	4	0.1111111	0.548	WNK2	C9orf129	
chr9	+(96407694..96408309)	615	0.21815	15	7	8	0.0666667	0.91754258	PHF2	MIR4291	
chr9	+(96408721..96409243)	522	1.65224	7	3	4	0.1428571	0.029	PHF2	MIR4291	
chr9	+(97203107..97203617)	510	3.54521	11	7	4	0.2727273	0.082	HIATL1	FBP2	
chr9	+(97207155..97207691)	536	3.54521	8	5	3	0.25	0.018	HIATL1	FBP2	
chr9	+(97882883..97883575)	692	3.54521	6	3	3	0	0.05	MIR24-1	FANCC	
chr9	+(97992319..97993017)	698	0.43546	13	9	4	0.3846154	0.999	MIR24-1	FANCC	
chr9	+(98161565..98162265)	700	0.21815	10	6	4	0.2	0.005	FANCC	PTCH1	
chr9	+(99285584..99286095)	511	3.54521	11	6	5	0.0909091	0.57243393	HABP4	CDC14B	v
chr9	+(99606996..99607643)	647	3.54521	9	6	3	0.3333333	0.012	ZNF510	ZNF782	
chr9	+(99961827..99962328)	501	3.54521	12	6	6	0	0.13116584	LOC340508	ZNF322B	
chr9	+(100053367..100053904)	537	3.54521	6	4	2	0.3333333	0.067	LOC57653	C9orf174	
chr9	+(100833599..100834299)	700	1.65224	12	5	7	0.1666667	0.99775837	NANS	TRIM14	
chr9	+(100861948..100862536)	588	0.93087	8	3	5	0.25	0.018	NANS	TRIM14	
chr9	+(101055964..101056649)	685	0.21815	11	6	5	0.0909091	0.03394459	TBC1D2	GABBR2	
chr9	+(101533060..101533697)	637	0.43546	9	4	5	0.1111111	0.008	GABBR2	ANKS6	
chr9	+(101715580..101716278)	698	0.21815	10	5	5	0	0.00451172	COL15A1	TGFBR1	
chr9	+(101746539..101747239)	700	0.93087	12	4	8	0.3333333	0.00328926	COL15A1	TGFBR1	
chr9	+(101984469..101985247)	778	0.21815	19	10	9	0.0526316	0.00011928	ALG2	SEC61B	
chr9	+(107379512..107380030)	518	1.65224	12	5	7	0.1666667	0.04407898	OR13C2	OR13C9	
chr9	+(108123309..108123965)	656	0.43546	11	6	5	0.0909091	0.00529357	SLC44A1	FSD1L	
chr9	+(108286060..108286565)	505	3.54521	15	9	6	0.2	0.88070358	FSD1L	FKTN	
chr9	+(108520290..108520905)	615	3.54521	6	3	3	0	0.05	TMEM38B	ZNF462	
chr9	+(109686843..109687364)	521	1.65224	9	5	4	0.1111111	0.032	ZNF462	MIR548Q	
chr9	+(111950278..111950872)	594	0.43546	9	5	4	0.1111111	0.008	C9orf4	EPB41L4B	

chr9	+(112017656..112018177)	521	3.54521	6	4	2	0.3333333	0.067	C9orf4	EPB41L4B	
chr9	+(113169423..113169958)	535	1.65224	10	5	5	0	0.23235105	TXNDC8	SVEP1	
chr9	+(113703783..113704482)	699	0.93087	10	7	3	0.4	0.008	MUSK	LPAR1	
chr9	+(114173078..114173768)	690	3.54521	9	6	3	0.3333333	0.048	OR2K2	KIAA0368	
chr9	+(114688999..114689669)	670	3.54521	6	2	4	0.3333333	0.067	UGCG	MIR3134	
chr9	+(115805744..115806653)	909	0.93087	16	5	11	0.375	0.26661423	ZNF883	ZFP37	
chr9	+(115811718..115812877)	1159	3.54521	13	7	6	0.0769231	0.98393771	ZNF883	ZFP37	
chr9	+(115983531..115984092)	561	0.43546	14	8	6	0.1428571	0.00097289	SLC31A2	FKBP15	
chr9	+(116696888..116697431)	543	1.65224	7	3	4	0.1428571	0.029	ZNF618	AMBP	
chr9	+(116811163..116811787)	624	0.11433	11	6	5	0.0909091	0.00308495	ZNF618	AMBP	
chr9	+(116924614..116925177)	563	0.93087	9	3	6	0.3333333	0.131	COL27A1	MIR455	
chr9	+(117094899..117095567)	668	3.26016	32	15	17	0.0625	0.00047617	ORM2	AKNA	
chr9	+(117129520..117130218)	698	0.01435	14	6	8	0.1428571	0.00097289	ORM2	AKNA	
chr9	+(117145464..117145977)	513	1.65224	8	3	5	0.25	0.018	ORM2	AKNA	
chr9	+(117797967..117798602)	635	3.54521	10	4	6	0.2	0.129	TNFSF8	TNC	v
chr9	+(119858090..119858641)	551	3.54521	7	3	4	0.1428571	0.029	PAPPA	ASTN2	
chr9	+(120155042..120156422)	1380	1.65224	13	7	6	0.0769231	0.9986501	PAPPA	ASTN2	
chr9	+(123667522..123668613)	1091	0.43546	18	11	7	0.2222222	0.0002444	PHF19	TRAF1	
chr9	+(124343914..124344598)	684	3.54521	10	6	4	0.2	0.995	DAB2IP	TTLL11	
chr9	+(126132770..126133276)	506	3.54521	6	3	3	0	0.05	CRB2	DENND1A	
chr9	+(126142134..126142834)	700	0.11433	11	6	5	0.0909091	0.00308495	CRB2	DENND1A	
chr9	+(126199512..126200022)	510	0.43546	9	5	4	0.1111111	0.008	CRB2	DENND1A	
chr9	+(126346328..126346965)	637	1.65224	7	3	4	0.1428571	0.029	CRB2	DENND1A	
chr9	+(127224846..127225546)	700	0.11433	11	5	6	0.0909091	0.00308495	GPR144	NR5A1	
chr9	+(127617344..127618356)	1012	0.06099	25	9	16	0.28	0.99610283	WDR38	RPL35	
chr9	+(127683874..127684470)	596	3.54521	9	6	3	0.3333333	0.012	ARPC5L	GOLGA1	
chr9	+(127950254..127950954)	700	0.11433	11	5	6	0.0909091	0.00308495	SCAI	PPP6C	
chr9	+(127982310..127983009)	699	0.93087	10	6	4	0.2	0.01	RABEPK	HSPA5	
chr9	+(127998935..127999490)	555	0.93087	12	5	7	0.1666667	0.34237168	RABEPK	HSPA5	
chr9	+(128749560..128750080)	520	3.54521	7	4	3	0.1428571	0.029	PBX3	FAM125B	
chr9	+(128953715..128954620)	905	0.11433	18	9	9	0	0.00017429	PBX3	FAM125B	
chr9	+(129105104..129105777)	673	0.43546	9	4	5	0.1111111	0.008	FAM125B	LMX1B	
chr9	+(129378743..129379289)	546	3.54521	6	2	4	0.3333333	0.067	LMX1B	ZBTB43	
chr9	+(129434606..129435306)	700	0.21815	10	7	3	0.4	0.008	LMX1B	ZBTB43	

chr9	+(129599896..129600431)	535	1.65224	10	6	4	0.2	0.019	ZBTB43	ZBTB34
chr9	+(129648480..129649049)	569	0.93087	8	5	3	0.25	0.018	ZBTB34	RALGPS1
chr9	+(129884002..129884625)	623	1.65224	11	4	7	0.2727273	0.394	RALGPS1	ANGPTL2
chr9	+(129957130..129957830)	700	0.21815	15	8	7	0.0666667	0.79105652	ANGPTL2	GARNL3
chr9	+(129971327..129972011)	684	0.43546	11	7	4	0.2727273	0.536	ANGPTL2	GARNL3
chr9	+(130080662..130081249)	587	0.93087	8	4	4	0	0.014	GARNL3	SLC2A8
chr9	+(130287033..130287733)	700	0.93087	10	4	6	0.2	0.005	LRSAM1	FAM129B
chr9	+(130501528..130502038)	510	3.54521	6	2	4	0.3333333	0.067	TOR2A	SH2D3C
chr9	+(130633777..130634461)	684	0.43546	14	7	7	0	0.91014375	ENG	AK1
chr9	+(130649002..130649560)	558	1.65224	11	7	4	0.2727273	0.115	AK1	ST6GALNAC6
chr9	+(130690867..130691516)	649	0.06099	13	5	8	0.2307692	0.0394913	ST6GALNAC4	PIP5KL1
chr9	+(131004976..131005611)	635	3.54521	6	3	3	0	0.05	DNM1	MIR199B
chr9	+(131019704..131020245)	541	1.65224	7	3	4	0.1428571	0.029	MIR3154	GOLGA2
chr9	+(131035904..131036410)	506	0.93087	12	4	8	0.3333333	0.00328926	MIR3154	GOLGA2
chr9	+(131570167..131570702)	535	0.06099	13	8	5	0.2307692	0.0394913	TBC1D13	ENDOG
chr9	+(131582261..131582888)	627	3.54521	6	2	4	0.3333333	0.067	ENDOG	C9orf114
chr9	+(131661007..131662055)	1048	0.11433	21	14	7	0.3333333	0.00012828	LRRC8A	PHYHD1
chr9	+(131669764..131670356)	592	1.65224	12	4	8	0.3333333	0.00328926	LRRC8A	PHYHD1
chr9	+(131719094..131719602)	508	3.54521	6	3	3	0	0.05	NUP188	SH3GLB2
chr9	+(131798465..131799165)	700	0.06099	12	5	7	0.1666667	0.00224163	SH3GLB2	FAM73B
chr9	+(131825121..131826233)	1112	0.43546	18	11	7	0.2222222	0.99713007	FAM73B	DOLPP1
chr9	+(132184777..132185340)	563	0.43546	9	5	4	0.1111111	0.008	C9orf106	C9orf50
chr9	+(132189785..132191109)	1324	1.65224	15	7	8	0.0666667	0.00059687	C9orf106	C9orf50
chr9	+(132366418..132367118)	700	1.65224	10	7	3	0.4	0.992	C9orf106	C9orf50
chr9	+(132376270..132376921)	651	0.43546	9	4	5	0.1111111	0.008	C9orf106	C9orf50
chr9	+(132619840..132620540)	700	0.02892	16	11	5	0.375	0.61149613	USP20	FNBP1
chr9	+(132905685..132906271)	586	0.43546	9	5	4	0.1111111	0.008	GPR107	NCS1
chr9	+(132939372..132940544)	1172	1.65224	15	8	7	0.0666667	0.99245637	NCS1	ASS1
chr9	+(133057559..133058942)	1383	0.02892	26	9	17	0.3076923	1.869E-05	NCS1	ASS1
chr9	+(133226509..133227067)	558	3.54521	6	4	2	0.3333333	0.067	NCS1	ASS1
chr9	+(133356658..133357358)	700	0.43546	14	5	9	0.2857143	0.00981533	ASS1	LOC100272217
chr9	+(133730083..133730783)	700	0.06099	13	4	9	0.3846154	0.001	ABL1	QRFP
chr9	+(133777648..133778476)	828	0.00701	16	6	10	0.25	0.00056905	QRFP	FIBCD1
chr9	+(134019686..134020205)	519	1.65224	8	3	5	0.25	0.018	NUP214	FAM78A

chr9	+(134039112..134039636)	524	3.54521	8	3	5	0.25	0.018	NUP214	FAM78A
chr9	+(134396673..134397242)	569	3.54521	10	6	4	0.2	0.033	POMT1	UCK1
chr9	+(134466988..134467526)	538	3.54521	7	3	4	0.1428571	0.029	UCK1	RAPGEF1
chr9	+(134526139..134526769)	630	3.54521	9	6	3	0.3333333	0.274	UCK1	RAPGEF1
chr9	+(134616163..134616746)	583	0.06099	12	5	7	0.1666667	0.00224163	RAPGEF1	MED27
chr9	+(134620490..134621190)	700	0.43546	9	6	3	0.3333333	0.012	RAPGEF1	MED27
chr9	+(135202697..135203209)	512	1.65224	13	9	4	0.3846154	0.207	NTNG2	SETX
chr9	+(135276866..135277566)	700	0.21815	18	11	7	0.2222222	0.14881787	SETX	TTF1
chr9	+(135733217..135733917)	700	3.54521	9	3	6	0.3333333	0.988	GTF3C4	C9orf98
chr9	+(135772274..135772799)	525	3.54521	9	3	6	0.3333333	0.083	C9orf9	TSC1
chr9	+(136279709..136280214)	505	3.54521	8	4	4	0	0.014	C9orf96	REXO4
chr9	+(136405501..136406309)	808	0.06099	18	7	11	0.2222222	0.17081484	ADAMTSL2	FAM163B
chr9	+(136410463..136410984)	521	0.93087	8	5	3	0.25	0.018	ADAMTSL2	FAM163B
chr9	+(136482947..136483529)	582	3.54521	7	3	4	0.1428571	0.029	FAM163B	DBH
chr9	+(136520614..136521283)	669	0.11433	13	7	6	0.0769231	0.0013499	DBH	SARDH
chr9	+(136679045..136679687)	642	0.93087	8	4	4	0	0.014	SARDH	VAV2
chr9	+(136733845..136734448)	603	1.65224	7	3	4	0.1428571	0.029	SARDH	VAV2
chr9	+(136811177..136811685)	508	0.43546	9	4	5	0.1111111	0.008	SARDH	VAV2
chr9	+(136813281..136813844)	563	3.54521	10	6	4	0.2	0.005	SARDH	VAV2
chr9	+(136814086..136814647)	561	1.65224	7	4	3	0.1428571	0.029	SARDH	VAV2
chr9	+(137414681..137415381)	700	0.11433	11	4	7	0.2727273	0.003	RXRA	COL5A1
chr9	+(137433189..137433696)	507	3.54521	6	2	4	0.3333333	0.067	RXRA	COL5A1
chr9	+(137453695..137454342)	647	0.93087	8	3	5	0.25	0.018	RXRA	COL5A1
chr9	+(137490499..137491159)	660	0.93087	8	3	5	0.25	0.018	RXRA	COL5A1
chr9	+(137586445..137587133)	688	3.54521	6	4	2	0.3333333	0.067	COL5A1	MIR3689A
chr9	+(137612582..137613111)	529	0.93087	8	3	5	0.25	0.018	COL5A1	MIR3689A
chr9	+(137673786..137674486)	700	0.06099	13	9	4	0.3846154	0.02	COL5A1	MIR3689A
chr9	+(137675006..137675583)	577	3.54521	6	3	3	0	0.05	COL5A1	MIR3689A
chr9	+(137681528..137682228)	700	0.21815	10	4	6	0.2	0.005	COL5A1	MIR3689A
chr9	+(137727791..137728491)	700	3.54521	9	6	3	0.3333333	0.012	COL5A1	MIR3689A
chr9	+(137735953..137736471)	518	1.65224	10	7	3	0.4	0.008	COL5A1	MIR3689A
chr9	+(138676980..138677680)	700	1.65224	10	7	3	0.4	0.008	KCNT1	CAMSAP1
chr9	+(138714608..138715171)	563	3.54521	9	6	3	0.3333333	0.012	KCNT1	CAMSAP1
chr9	+(138972851..138973541)	690	0.43546	9	6	3	0.3333333	0.012	UBAC1	NACC2

chr9	+(139077431..139078081)	650	0.02892	13	7	6	0.0769231	0.0013499	C9orf69	LHX3
chr9	+(139090402..139091639)	1237	0.43546	18	11	7	0.2222222	0.01324732	C9orf69	LHX3
chr9	+(139292868..139293420)	552	0.11433	12	6	6	0	0.00197388	CARD9	SNAPC4
chr9	+(139329160..139329860)	700	1.65224	12	4	8	0.3333333	0.055	PMPCA	INPP5E
chr9	+(139348704..139349462)	758	0.93087	13	9	4	0.3846154	0.099	INPP5E	SEC16A
chr9	+(139398999..139399579)	580	3.54521	9	3	6	0.3333333	0.452	C9orf163	NOTCH1
chr9	+(139415693..139416714)	1021	1.65224	14	7	7	0	0.99912744	C9orf163	NOTCH1
chr9	+(139442753..139443288)	535	1.65224	9	5	4	0.1111111	0.548	NOTCH1	EGFL7
chr9	+(139557636..139558171)	535	0.93087	14	5	9	0.2857143	0.00981533	EGFL7	MIR126
chr9	+(139752794..139753372)	578	1.65224	9	6	3	0.3333333	0.274	MAMDC4	EDF1
chr9	+(139753482..139754693)	1211	0.93087	16	9	7	0.125	0.99524777	MAMDC4	EDF1
chr9	+(139785016..139785576)	560	0.43546	14	5	9	0.2857143	0.9986501	TRAF2	FBXW5
chr9	+(139944565..139945337)	772	0.01871	52	32	20	0.2307692	0.73875166	NPDC1	ENTPD2
chr9	+(140052382..140052897)	515	3.54521	9	3	6	0.3333333	0.917	GRIN1	LRRC26
chr9	+(140082284..140083147)	863	3.54521	12	6	6	0	0.00197388	MIR3621	ANAPC2
chr9	+(140088050..140088750)	700	0.11433	12	6	6	0	0.00197388	SSNA1	TPRN
chr9	+(140243003..140243996)	993	0.21815	17	6	11	0.2941176	0.95623415	NRARP	EXD3
chr9	+(140277698..140278398)	700	0.11433	13	4	9	0.3846154	0.074	NRARP	EXD3
chr9	+(140326107..140326802)	695	1.65224	11	7	4	0.2727273	0.997	NOXA1	ENTPD8
chr9	+(140350574..140351145)	571	3.54521	10	5	5	0	0.00451172	ENTPD8	NELF
chr9	+(140359198..140359898)	700	0.11433	16	5	11	0.375	0.9990816	NELF	PNPLA7
chr9	+(140400433..140401782)	1349	0.02892	22	12	10	0.0909091	0.74517426	NELF	PNPLA7
chr9	+(140687134..140687735)	601	3.54521	6	4	2	0.3333333	0.067	FLJ40292	MIR602
chr9	+(140782916..140783765)	849	0.21815	19	11	8	0.1578947	0.00662147	CACNA1B	TUBBP5
chr9	+(140798626..140799169)	543	3.54521	6	4	2	0.3333333	0.067	CACNA1B	TUBBP5
chr10	+(267056..267570)	514	0.28001	16	9	7	0.125	0.00042755	ZMYND11	DIP2C
chr10	+(375242..375904)	662	0.55496	12	8	4	0.3333333	0.024	ZMYND11	DIP2C
chr10	+(410119..410933)	814	0.01727	15	5	10	0.3333333	0.00109982	ZMYND11	DIP2C
chr10	+(461494..462041)	547	2.7175	6	3	3	0	0.05	ZMYND11	DIP2C
chr10	+(931403..931920)	517	2.7175	6	4	2	0.3333333	0.067	C10orf108	LARP4B
chr10	+(1043170..1043870)	700	2.7175	9	6	3	0.3333333	0.988	GTPBP4	IDI2
chr10	+(1284428..1285100)	672	0.55496	8	4	4	0	0.014	NCRNA00200	ADARB2
chr10	+(1787554..1788714)	1160	0.55496	14	6	8	0.1428571	0.00097289	NCRNA00168	PFKP
chr10	+(1994537..1995237)	700	0.28001	9	6	3	0.3333333	0.012	NCRNA00168	PFKP

chr10	+(2714518..2715433)	915	0.55496	15	6	9	0.2	0.00666417	NCRNA00168	PFKP	
chr10	+(2723903..2724537)	634	1.23598	7	3	4	0.1428571	0.029	NCRNA00168	PFKP	
chr10	+(3166680..3167380)	700	2.7175	13	9	4	0.3846154	0.207	PFKP	PITRM1	
chr10	+(5144453..5144970)	517	2.7175	13	8	5	0.2307692	0.01405402	AKR1C3	AKR1CL1	
chr10	+(5734301..5734998)	697	1.23598	7	4	3	0.1428571	0.029	C10orf18	GDI2	
chr10	+(6065858..6066469)	611	2.7175	9	3	6	0.3333333	0.048	IL15RA	IL2RA	
chr10	+(6067748..6068283)	535	1.23598	8	5	3	0.25	0.018	IL15RA	IL2RA	
chr10	+(6142947..6143787)	840	0.01727	13	7	6	0.0769231	0.0013499	RBM17	PFKFB3	
chr10	+(6184883..6185583)	700	0.05992	11	4	7	0.2727273	0.003	RBM17	PFKFB3	
chr10	+(6263758..6264458)	700	0.02989	12	6	6	0	0.00197388	MIR3155	PRKCQ	
chr10	+(6267866..6268440)	574	2.7175	11	5	6	0.0909091	0.99691505	MIR3155	PRKCQ	
chr10	+(6472129..6473099)	970	0.28001	15	6	9	0.2	0.00073136	MIR3155	PRKCQ	
chr10	+(6885094..6886014)	920	2.7175	12	6	6	0	0.00197388	LOC439949	SFMBT2	
chr10	+(7409447..7410098)	651	2.7175	6	4	2	0.3333333	0.067	LOC439949	SFMBT2	
chr10	+(11312450..11313037)	587	2.7175	9	4	5	0.1111111	0.008	CELF2	USP6NL	
chr10	+(12864431..12865069)	638	2.7175	9	6	3	0.3333333	0.548	CAMK1D	LOC283070	
chr10	+(13782472..13782988)	516	2.7175	10	6	4	0.2	0.005	PRPF18	FRMD4A	
chr10	+(14952148..14952676)	528	0.55496	13	8	5	0.2307692	0.9982926	SUV39H2	DCLRE1C	
chr10	+(14977268..14977783)	515	2.7175	6	2	4	0.3333333	0.067	SUV39H2	DCLRE1C	
chr10	+(14981416..14982075)	659	1.23598	10	3	7	0.4	0.008	SUV39H2	DCLRE1C	
chr10	+(16940676..16941206)	530	0.55496	8	4	4	0	0.014	RSU1	CUBN	
chr10	+(17483699..17484399)	700	2.7175	9	3	6	0.3333333	0.012	VIM	ST8SIA6	
chr10	+(18064847..18065411)	564	0.05992	22	7	15	0.3636364	0.00040653	FAM23A_dup2	MRC1L1_dup2	
chr10	+(18284377..18284892)	515	2.7175	7	3	4	0.1428571	0.029	SLC39A12	CACNB2	
chr10	+(18927895..18928594)	699	2.7175	10	6	4	0.2	0.995	CACNB2	NSUN6	
chr10	+(20453414..20454057)	643	1.23598	7	3	4	0.1428571	0.029	PLXDC2	NEBL	v
chr10	+(20592488..20593412)	924	0.02989	20	12	8	0.2	0.00010641	PLXDC2	NEBL	v
chr10	+(21157418..21157926)	508	2.7175	10	7	3	0.4	0.008	PLXDC2	NEBL	v
chr10	+(23730573..23731099)	526	0.55496	17	6	11	0.2941176	0.01040023	OTUD1	KIAA1217	
chr10	+(24490642..24491263)	621	0.55496	8	5	3	0.25	0.018	KIAA1217	PRINS	
chr10	+(24834527..24835068)	541	2.7175	9	5	4	0.1111111	0.452	MIR603	ARHGAP21	
chr10	+(25786012..25787217)	1205	0.02989	22	10	12	0.0909091	0.99996194	GPR158	MYO3A	
chr10	+(27318013..27318547)	534	1.23598	10	6	4	0.2	0.005	NCRNA00202	ANKRD26	
chr10	+(27324002..27324699)	697	0.02989	15	8	7	0.0666667	0.00131091	NCRNA00202	ANKRD26	

chr10	+(27535451..27535993)	542	1.23598	10	4	6	0.2	0.129	ACBD5	LOC387646
chr10	+(27627557..27628061)	504	2.7175	8	5	3	0.25	0.018	LOC387646	PTCHD3
chr10	+(27815338..27815959)	621	0.55496	10	6	4	0.2	0.005	RAB18	MKX
chr10	+(27897761..27898379)	618	2.7175	6	3	3	0	0.05	RAB18	MKX
chr10	+(29769177..29769783)	606	0.55496	13	4	9	0.3846154	0.038	LOC387647	SVIL
chr10	+(32983489..32983994)	505	2.7175	11	4	7	0.2727273	0.055	C10orf68	ITGB1
chr10	+(33198973..33199617)	644	1.23598	7	3	4	0.1428571	0.029	C10orf68	ITGB1
chr10	+(33541224..33541727)	503	2.7175	6	3	3	0	0.05	ITGB1	NRP1
chr10	+(34206700..34207400)	700	0.12128	10	4	6	0.2	0.005	NRP1	PARD3
chr10	+(36811978..36812610)	632	0.28001	19	9	10	0.0526316	0.3415457	FZD8	ANKRD30A
chr10	+(37440787..37441290)	503	2.7175	10	7	3	0.4	0.033	ANKRD30A	MTRNR2L7
chr10	+(37469943..37470764)	821	0.01241	68	37	31	0.0882353	0.0013572	ANKRD30A	MTRNR2L7
chr10	+(37474282..37474837)	555	1.86846	54	21	33	0.2222222	0.00259801	ANKRD30A	MTRNR2L7
chr10	+(37478218..37478892)	674	0.10713	27	16	11	0.1851852	1.0989E-05	ANKRD30A	MTRNR2L7
chr10	+(37488249..37488754)	505	2.7175	11	5	6	0.0909091	0.13666084	ANKRD30A	MTRNR2L7
chr10	+(37506590..37507274)	684	1.23598	15	7	8	0.0666667	0.99940313	ANKRD30A	MTRNR2L7
chr10	+(37868895..37869432)	537	0.55496	12	8	4	0.3333333	0.107	ANKRD30A	MTRNR2L7
chr10	+(38049009..38049518)	509	1.23598	7	4	3	0.1428571	0.029	MTRNR2L7	ZNF248
chr10	+(38120426..38120950)	524	2.7175	9	5	4	0.1111111	0.365	MTRNR2L7	ZNF248
chr10	+(38241374..38241890)	516	2.7175	10	6	4	0.2	0.305	ZNF248	ZNF25
chr10	+(38598782..38599318)	536	1.23598	10	5	5	0	0.00451172	LOC100129055	HSD17B7P2
chr10	+(38654086..38654648)	562	1.23598	12	5	7	0.1666667	0.11161257	HSD17B7P2	SEPT7L
chr10	+(43087923..43088487)	564	0.28001	15	9	6	0.2	0.06275324	ZNF37BP	ZNF33B
chr10	+(43604295..43604995)	700	0.28001	9	3	6	0.3333333	0.012	RET	CSGALNACT2
chr10	+(43691917..43692481)	564	2.7175	10	6	4	0.2	0.995	CSGALNACT2	RASGEF1A
chr10	+(43808479..43809474)	995	0.02989	18	12	6	0.3333333	0.00037352	RASGEF1A	FXYD4
chr10	+(44922455..44923151)	696	0.28001	9	5	4	0.1111111	0.008	CXCL12	LOC220980
chr10	+(45324528..45325228)	700	0.12128	10	3	7	0.4	0.008	CXCL12	LOC220980
chr10	+(46212992..46213518)	526	1.23598	20	7	13	0.3	0.00015575	ANUBL1	FAM21C
chr10	+(46238676..46239179)	503	2.7175	6	2	4	0.3333333	0.067	FAM21C	AGAP4
chr10	+(46247689..46248365)	676	0.00584	28	13	15	0.0714286	5.9919E-05	FAM21C	AGAP4
chr10	+(46969248..46969948)	700	0.12128	13	6	7	0.0769231	0.33411757	FAM35B	SYT15
chr10	+(47400395..47400939)	544	0.28088	44	21	23	0.0454545	0.00100131	FAM35B2	ANTXRL
chr10	+(47901435..47901939)	504	1.23598	12	7	5	0.1666667	0.14557611	FAM21B_dup1	CTSLL2

chr10	+(47919758..47920261)	503	2.7175	10	3	7	0.4	0.033	FAM21B_dup1	CTSLL2	
chr10	+(47943454..47943967)	513	0.55496	17	9	8	0.0588235	0.00468738	FAM21B_dup1	CTSLL2	
chr10	+(48007119..48007657)	538	0.55496	12	8	4	0.3333333	0.008	FAM21B_dup1	CTSLL2	
chr10	+(48262716..48263588)	872	0.10152	39	17	22	0.1282051	3.3468E-06	ANXA8L1_dup2	ZNF488	
chr10	+(48329358..48329993)	635	2.7175	6	3	3	0	0.05	ANXA8L1_dup2	ZNF488	
chr10	+(48370062..48370589)	527	2.7175	6	2	4	0.3333333	0.067	ZNF488	RBP3	
chr10	+(48390014..48390709)	695	0.28001	10	7	3	0.4	0.058	ZNF488	RBP3	
chr10	+(48771197..48771848)	651	1.23598	10	7	3	0.4	0.017	GDF10	PTPN20A_dup2	
chr10	+(49465288..49465823)	535	1.23598	7	4	3	0.1428571	0.029	FRMPD2P1_dup2	FRMPD2	
chr10	+(49712172..49713339)	1167	0.02989	19	7	12	0.2631579	0.00561494	MAPK8	ARHGAP22	
chr10	+(50038544..50039051)	507	2.7175	6	2	4	0.3333333	0.067	WDFY4	LRRC18	
chr10	+(50966283..50966784)	501	2.7175	8	4	4	0	0.014	C10orf53	OGDHL	
chr10	+(51073139..51073644)	505	2.7175	9	5	4	0.1111111	0.008	OGDHL	PARG	v
chr10	+(51191760..51192262)	502	2.7175	12	5	7	0.1666667	0.02117853	OGDHL	PARG	v
chr10	+(51225616..51226193)	577	2.7175	14	8	6	0.1428571	0.03535058	OGDHL	PARG	v
chr10	+(51291175..51291679)	504	2.7175	9	6	3	0.3333333	0.048	OGDHL	PARG	v
chr10	+(51464723..51465767)	1044	1.23598	33	20	13	0.2121212	0.02542629	LOC728407	AGAP7	
chr10	+(51821389..51821893)	504	2.7175	9	6	3	0.3333333	0.048	AGAP6	FAM21A	
chr10	+(51822480..51822992)	512	2.7175	10	6	4	0.2	0.238	AGAP6	FAM21A	
chr10	+(51844813..51845315)	502	2.7175	19	13	6	0.3684211	0.02183558	FAM21B_dup2	ASAH2	
chr10	+(51851574..51852274)	700	0.01767	38	17	21	0.1052632	1.8555E-05	FAM21B_dup2	ASAH2	
chr10	+(51852556..51853205)	649	0.8428	35	14	21	0.2	0.21933228	FAM21B_dup2	ASAH2	
chr10	+(51853287..51853850)	563	0.8428	24	9	15	0.25	0.01084662	FAM21B_dup2	ASAH2	
chr10	+(51859658..51860305)	647	0.11559	44	21	23	0.0454545	3.0462E-06	FAM21B_dup2	ASAH2	
chr10	+(51873277..51873786)	509	0.55496	19	11	8	0.1578947	0.01038818	FAM21B_dup2	ASAH2	
chr10	+(51877259..51877865)	606	1.13649	20	7	13	0.3	0.06114457	FAM21B_dup2	ASAH2	
chr10	+(51885824..51886386)	562	2.7175	10	6	4	0.2	0.543	FAM21B_dup2	ASAH2	
chr10	+(51887034..51887850)	816	2.7175	18	10	8	0.1111111	0.00821967	FAM21B_dup2	ASAH2	
chr10	+(51889295..51889907)	612	1.23598	13	5	8	0.2307692	0.15275354	FAM21B_dup2	ASAH2	
chr10	+(51890225..51890747)	522	0.55496	12	4	8	0.3333333	0.596	FAM21B_dup2	ASAH2	
chr10	+(51994297..51994798)	501	2.7175	18	6	12	0.3333333	0.01561431	FAM21B_dup2	ASAH2	
chr10	+(52025913..52026430)	517	2.7175	11	4	7	0.2727273	0.036	ASAH2	SGMS1	
chr10	+(55353361..55354004)	643	1.23598	10	5	5	0	0.69924593	MBL2	PCDH15	
chr10	+(55568999..55569558)	559	1.23598	11	7	4	0.2727273	0.264	MBL2	PCDH15	

chr10	+(55581555..55582080)	525	2.7175	9	3	6	0.3333333	0.131	MBL2	PCDH15	
chr10	+(60549246..60549881)	635	2.7175	7	3	4	0.1428571	0.2	LOC728640	PHYHIPL	
chr10	+(61566538..61567047)	509	2.7175	7	3	4	0.1428571	0.029	SLC16A9	CCDC6	v
chr10	+(61946343..61946954)	611	2.7175	6	3	3	0	0.05	C10orf40	ANK3	
chr10	+(62148917..62149419)	502	2.7175	9	3	6	0.3333333	0.131	C10orf40	ANK3	
chr10	+(64573586..64574150)	564	2.7175	10	5	5	0	0.03790009	ADO	EGR2	
chr10	+(67889036..67889656)	620	2.7175	8	3	5	0.25	0.018	ANXA2P3	CTNNA3	v
chr10	+(69594106..69594615)	509	2.7175	6	4	2	0.3333333	0.067	LRRTM3	DNAJC12	
chr10	+(70391878..70392400)	522	1.23598	12	5	7	0.1666667	0.04407898	TET1	CCAR1	
chr10	+(70404274..70405151)	877	0.55496	17	8	9	0.0588235	0.02165407	TET1	CCAR1	
chr10	+(70694394..70694895)	501	2.7175	8	4	4	0	0.014	DDX50	DDX21	v
chr10	+(70742243..70742910)	667	0.28001	13	8	5	0.2307692	0.0017074	DDX21	KIAA1279	v
chr10	+(71630779..71631467)	688	2.7175	6	4	2	0.3333333	0.067	COL13A1	H2AFY2	
chr10	+(71879618..71880584)	966	1.23598	14	6	8	0.1428571	0.00149246	H2AFY2	AIFM2	
chr10	+(73295466..73296048)	582	0.02989	12	5	7	0.1666667	0.00224163	CDH23	C10orf105	
chr10	+(73446429..73446961)	532	2.7175	6	3	3	0	0.05	CDH23	C10orf105	
chr10	+(73495572..73496153)	581	0.05992	11	7	4	0.2727273	0.003	CDH23	C10orf105	
chr10	+(73537407..73537947)	540	0.05992	12	7	5	0.1666667	0.02117853	C10orf54	PSAP	
chr10	+(73569522..73570190)	668	2.7175	8	5	3	0.25	0.714	C10orf54	PSAP	
chr10	+(73759010..73759695)	685	2.7175	6	3	3	0	0.05	CHST3	SPOCK2	
chr10	+(73871295..73871925)	630	0.55496	8	5	3	0.25	0.018	SPOCK2	ASCC1	
chr10	+(74096312..74096927)	615	0.12128	11	6	5	0.0909091	0.00308495	DDIT4	DNAJB12	
chr10	+(74635196..74635896)	700	0.00815	14	5	9	0.2857143	0.0013499	CCDC109A	OIT3	
chr10	+(75394087..75394598)	511	1.23598	8	5	3	0.25	0.018	USP54	MYOZ1	
chr10	+(75404647..75405166)	519	1.23598	9	4	5	0.1111111	0.008	MYOZ1	SYNPO2L	
chr10	+(75435168..75435746)	578	0.02989	23	16	7	0.3913043	0.82521259	SYNPO2L	AGAP5	
chr10	+(75597180..75597880)	700	0.28001	10	3	7	0.4	0.058	NDST2	CAMK2G	
chr10	+(75873564..75874264)	700	0.55496	9	3	6	0.3333333	0.012	VCL	AP3M1	
chr10	+(76804139..76805263)	1124	0.05992	19	11	8	0.1578947	0.99986003	MYST4	DUPD1	
chr10	+(76867488..76868188)	700	0.28001	13	5	8	0.2307692	0.0017074	DUPD1	DUSP13	
chr10	+(77163938..77164546)	608	2.7175	6	3	3	0	0.05	NCRNA00245	C10orf11	
chr10	+(77213998..77214601)	603	0.55496	8	3	5	0.25	0.018	NCRNA00245	C10orf11	
chr10	+(77295384..77295898)	514	2.7175	6	4	2	0.3333333	0.067	NCRNA00245	C10orf11	
chr10	+(77671358..77671918)	560	0.55496	8	3	5	0.25	0.018	C10orf11	KCNMA1	

chr10	+(79168062..79168762)	700	2.7175	8	4	4	0	0.014	C10orf11	KCNMA1
chr10	+(79493207..79493775)	568	0.55496	10	6	4	0.2	0.129	KCNMA1	DLG5
chr10	+(79809679..79810416)	737	0.00815	15	9	6	0.2	0.00073136	RPS24	LOC283050
chr10	+(79813108..79813808)	700	0.05992	13	5	8	0.2307692	0.07161746	RPS24	LOC283050
chr10	+(79915848..79916548)	700	1.23598	12	5	7	0.1666667	0.00224163	RPS24	LOC283050
chr10	+(80146442..80146951)	509	1.23598	7	4	3	0.1428571	0.029	RPS24	LOC283050
chr10	+(80376945..80377621)	676	1.23598	7	4	3	0.1428571	0.029	RPS24	LOC283050
chr10	+(80564505..80565205)	700	0.12128	14	6	8	0.1428571	0.15084979	RPS24	LOC283050
chr10	+(80722260..80722835)	575	0.55496	8	5	3	0.25	0.018	RPS24	LOC283050
chr10	+(80806708..80807408)	700	0.05992	11	7	4	0.2727273	0.003	RPS24	LOC283050
chr10	+(81023045..81024034)	989	0.28001	18	10	8	0.1111111	0.97950364	ZMIZ1	PPIF
chr10	+(81056219..81056747)	528	1.23598	10	4	6	0.2	0.005	ZMIZ1	PPIF
chr10	+(81371887..81372454)	567	0.01727	16	11	5	0.375	0.00134045	SFTPA1	LOC650623
chr10	+(82033792..82034655)	863	0.00815	16	10	6	0.25	0.06444254	ANXA11	MAT1A
chr10	+(82185264..82185820)	556	0.28001	10	5	5	0	0.00451172	C10orf58	TSPAN14
chr10	+(82202475..82203022)	547	0.55496	8	3	5	0.25	0.018	C10orf58	TSPAN14
chr10	+(82265454..82266075)	621	0.12128	16	10	6	0.25	0.00056905	TSPAN14	SH2D4B
chr10	+(85954635..85955236)	601	2.7175	6	3	3	0	0.05	CDHR1	LRIT2
chr10	+(86147103..86147799)	696	1.23598	7	3	4	0.1428571	0.029	FAM190B	GRID1
chr10	+(87546358..87546912)	554	0.05992	11	5	6	0.0909091	0.00308495	FAM190B	GRID1
chr10	+(87978034..87979167)	1133	0.12128	17	10	7	0.1764706	0.00031815	FAM190B	GRID1
chr10	+(88075869..88076569)	700	0.02989	15	8	7	0.0666667	0.20894348	FAM190B	GRID1
chr10	+(88113719..88114957)	1238	0.12128	20	10	10	0	0.7751541	FAM190B	GRID1
chr10	+(88452100..88453305)	1205	0.12128	16	8	8	0	0.00038877	LDB3	BMPR1A
chr10	+(88768391..88769088)	697	0.11137	38	18	20	0.0526316	4.5185E-07	AGAP11	FAM25A
chr10	+(88820178..88820714)	536	2.7175	10	3	7	0.4	0.258	FAM25A	GLUD1
chr10	+(88930426..88931092)	666	0.11559	35	23	12	0.3142857	0.01428384	FAM35A	FAM22A
chr10	+(89621937..89622130)	193	0.00269	59	29	30	0.0169492	0.95525929	CFLP1 (16568)	KILLIN
chr10	+(89622245..89622385)	141	0.19754	13	5	8	0.2307692	0.02851994	CFLP1 (16724)	KILLIN
chr10	+(90966030..90966547)	517	2.7175	9	3	6	0.3333333	0.274	FAS-AS1	CH25H
chr10	+(91532322..91532878)	556	1.23598	10	5	5	0	0.00451172	KIF20B	HTR7
chr10	+(93311909..93313054)	1145	1.23598	14	7	7	0	0.01267366	PCGF5	LOC100188947
chr10	+(93878497..93879197)	700	1.23598	14	8	6	0.1428571	0.15084979	BTAF1	CPEB3
chr10	+(94773832..94774539)	707	2.7175	13	9	4	0.3846154	0.001	EXOC6	CYP26C1

chr10	+(94824983..94825588)	605	0.55496	8	5	3	0.25	0.018	CYP26C1	CYP26A1	
chr10	+(95136919..95137487)	568	1.23598	8	5	3	0.25	0.018	CYP26A1	MYOF	
chr10	+(98823384..98824006)	622	1.23598	12	8	4	0.3333333	0.715	C10orf12	SLIT1	
chr10	+(98825227..98825775)	548	0.28001	9	4	5	0.1111111	0.008	C10orf12	SLIT1	
chr10	+(98848157..98849101)	944	0.28001	18	8	10	0.1111111	0.03778029	C10orf12	SLIT1	
chr10	+(99656291..99656923)	632	1.23598	10	3	7	0.4	0.092	GOLGA7B	CRTAC1	
chr10	+(99734025..99734545)	520	1.23598	7	3	4	0.1428571	0.029	GOLGA7B	CRTAC1	
chr10	+(99738118..99738818)	700	0.55496	13	5	8	0.2307692	0.9982926	GOLGA7B	CRTAC1	
chr10	+(99857901..99858601)	700	1.23598	10	7	3	0.4	0.008	CRTAC1	C10orf28	
chr10	+(101639622..101640152)	530	2.7175	9	6	3	0.3333333	0.083	ABCC2	DNMBP	
chr10	+(102576852..102577552)	700	0.12128	10	4	6	0.2	0.005	PAX2	FAM178A	v
chr10	+(102766169..102766869)	700	0.55496	13	6	7	0.0769231	0.5	LZTS2	PDZD7	
chr10	+(103600926..103601465)	539	0.12128	10	6	4	0.2	0.005	MGEA5	KCNIP2	v
chr10	+(103825952..103826652)	700	0.05992	11	7	4	0.2727273	0.003	HPS6	LDB1	
chr10	+(103828606..103829124)	518	2.7175	6	4	2	0.3333333	0.067	HPS6	LDB1	
chr10	+(103899076..103899584)	508	1.23598	10	6	4	0.2	0.129	PPRC1	NOLC1	
chr10	+(104241313..104241881)	568	2.7175	6	3	3	0	0.05	TMEM180	ACTR1A	
chr10	+(104687050..104687581)	531	2.7175	6	2	4	0.3333333	0.067	CNNM2	NT5C2	
chr10	+(104811146..104811761)	615	0.55496	8	4	4	0	0.014	CNNM2	NT5C2	
chr10	+(105151770..105152302)	532	0.05992	13	5	8	0.2307692	0.00420773	TAF5	USMG5	
chr10	+(105177267..105177816)	549	0.21264	17	11	6	0.2941176	0.00045556	PDCD11	CALHM2	
chr10	+(105232052..105232637)	585	0.55496	8	5	3	0.25	0.018	CALHM1	CALHM3	
chr10	+(105266860..105267456)	596	2.7175	9	3	6	0.3333333	0.012	NEURL	SH3PXD2A	
chr10	+(105333695..105334220)	525	0.28001	9	4	5	0.1111111	0.008	NEURL	SH3PXD2A	
chr10	+(105437778..105438879)	1101	0.12128	19	10	9	0.0526316	0.99988072	NEURL	SH3PXD2A	
chr10	+(105457538..105458101)	563	0.55496	8	3	5	0.25	0.018	NEURL	SH3PXD2A	
chr10	+(105793175..105793847)	672	0.00815	14	6	8	0.1428571	0.00097289	SLK	COL17A1	
chr10	+(105883179..105884280)	1101	1.23598	14	8	6	0.1428571	0.93933236	C10orf78	C10orf79	v
chr10	+(106057056..106057682)	626	2.7175	11	5	6	0.0909091	0.00881105	GSTO2	ITPRIP	
chr10	+(106410361..106411058)	697	0.55496	13	8	5	0.2307692	0.0017074	SORCS3	SORCS1	
chr10	+(116012368..116012921)	553	0.55496	8	3	5	0.25	0.018	VWA2	AFAP1L2	
chr10	+(118620341..118620910)	569	1.23598	11	5	6	0.0909091	0.07206352	HSPA12A	KIAA1598	
chr10	+(118682941..118683641)	700	2.7175	9	6	3	0.3333333	0.988	HSPA12A	KIAA1598	
chr10	+(118689241..118689745)	504	2.7175	9	6	3	0.3333333	0.024	HSPA12A	KIAA1598	

chr10	+(118701995..118702562)	567	0.28001	9	4	5	0.1111111	0.008	HSPA12A	KIAA1598	
chr10	+(119026064..119026744)	680	1.23598	10	3	7	0.4	0.058	SLC18A2	PDZD8	
chr10	+(119262816..119263443)	627	0.28001	9	5	4	0.1111111	0.008	PDZD8	EMX2OS	
chr10	+(121011674..121012374)	700	0.28001	9	6	3	0.3333333	0.012	GRK5	RGS10	
chr10	+(121159139..121160057)	918	0.55496	14	8	6	0.1428571	0.00097289	GRK5	RGS10	
chr10	+(121202432..121203598)	1166	0.12128	18	11	7	0.2222222	0.9997556	GRK5	RGS10	
chr10	+(121372127..121372826)	699	0.28001	14	9	5	0.2857143	0.9986501	TIAL1	BAG3	
chr10	+(121418842..121420039)	1197	0.00031	27	15	12	0.1111111	5.6273E-06	BAG3	INPP5F	
chr10	+(121427288..121427895)	607	0.55496	8	4	4	0	0.014	BAG3	INPP5F	
chr10	+(121713877..121714934)	1057	1.23598	13	6	7	0.0769231	0.9986501	SEC23IP	PPAPDC1A	
chr10	+(122274594..122275294)	700	0.28001	9	4	5	0.1111111	0.008	PPAPDC1A	LOC283089	
chr10	+(122318142..122319230)	1088	0.28001	16	6	10	0.25	0.99538163	PPAPDC1A	LOC283089	
chr10	+(124234991..124235691)	700	0.12128	10	4	6	0.2	0.005	HTRA1	DMBT1	
chr10	+(124349314..124350303)	989	1.23598	23	10	13	0.1304348	0.33210008	DMBT1	C10orf120	
chr10	+(124352826..124353361)	535	4.60097	37	17	20	0.0810811	6.5604E-06	DMBT1	C10orf120	
chr10	+(124353368..124354870)	1502	0.01727	69	35	34	0.0144928	0.06993232	DMBT1	C10orf120	
chr10	+(124355796..124356313)	517	1.23598	10	3	7	0.4	0.008	DMBT1	C10orf120	
chr10	+(124359337..124359897)	560	2.02194	22	12	10	0.0909091	0.00077534	DMBT1	C10orf120	
chr10	+(124360402..124360969)	567	1.23598	8	5	3	0.25	0.071	DMBT1	C10orf120	
chr10	+(124376418..124376919)	501	3.10812	20	8	12	0.2	0.00025847	DMBT1	C10orf120	
chr10	+(124377606..124378276)	670	0.01727	16	10	6	0.25	0.13903784	DMBT1	C10orf120	
chr10	+(124379727..124380342)	615	0.55496	8	3	5	0.25	0.018	DMBT1	C10orf120	
chr10	+(124799927..124800471)	544	2.7175	9	6	3	0.3333333	0.083	ACADSB	HMX3	
chr10	+(124895839..124897049)	1210	0.02989	18	7	11	0.2222222	0.6243719	HMX3	HMX2	
chr10	+(125259079..125259790)	711	0.00815	14	7	7	0	0.00087256	BUB3	GPR26	
chr10	+(125329247..125329838)	591	1.23598	7	4	3	0.1428571	0.029	BUB3	GPR26	
chr10	+(125426180..125426710)	530	2.7175	9	6	3	0.3333333	0.012	GPR26	CPXM2	
chr10	+(125551124..125551683)	559	0.55496	8	5	3	0.25	0.018	GPR26	CPXM2	
chr10	+(125758230..125758930)	700	0.05992	13	8	5	0.2307692	0.0017074	CPXM2	CHST15	
chr10	+(126153326..126153891)	565	0.55496	8	4	4	0	0.014	LHPP	FAM53B	v
chr10	+(126257309..126257880)	571	0.55496	8	5	3	0.25	0.018	LHPP	FAM53B	v
chr10	+(126349865..126350565)	700	0.28001	12	4	8	0.3333333	0.00328926	LHPP	FAM53B	v
chr10	+(126357402..126357948)	546	2.7175	6	4	2	0.3333333	0.067	LHPP	FAM53B	v
chr10	+(126727047..126727679)	632	0.05992	12	4	8	0.3333333	0.107	ZRANB1	CTBP2	

chr10	+(126779517..126780079)	562	1.23598	10	3	7	0.4	0.992	ZRANB1	CTBP2
chr10	+(129869384..129870081)	697	2.7175	10	6	4	0.2	0.995	PTPRE	MKI67
chr10	+(129900737..129901322)	585	1.23598	8	5	3	0.25	0.036	PTPRE	MKI67
chr10	+(129903437..129904082)	645	0.00137	34	20	14	0.1764706	0.04009062	PTPRE	MKI67
chr10	+(129904261..129905131)	870	0.05992	28	12	16	0.1428571	0.00172393	PTPRE	MKI67
chr10	+(129905885..129906818)	933	1.23598	31	15	16	0.0322581	0.11783996	PTPRE	MKI67
chr10	+(129907409..129907931)	522	0.55496	12	8	4	0.3333333	0.77	PTPRE	MKI67
chr10	+(130668930..130669630)	700	0.28001	9	3	6	0.3333333	0.012	MKI67	MGMT
chr10	+(130696485..130697076)	591	1.23598	7	4	3	0.1428571	0.029	MKI67	MGMT
chr10	+(130855868..130856568)	700	1.23598	10	3	7	0.4	0.008	MKI67	MGMT
chr10	+(131314487..131314994)	507	2.7175	6	4	2	0.3333333	0.067	MGMT	EBF3
chr10	+(131391409..131391943)	534	0.00815	14	5	9	0.2857143	0.0013499	MGMT	EBF3
chr10	+(131529391..131529979)	588	1.23598	7	3	4	0.1428571	0.029	MGMT	EBF3
chr10	+(131564929..131565629)	700	1.23598	10	3	7	0.4	0.008	MGMT	EBF3
chr10	+(131723276..131723780)	504	1.23598	8	5	3	0.25	0.018	MGMT	EBF3
chr10	+(132976074..132976679)	605	0.55496	8	5	3	0.25	0.018	MIR378C	TCERG1L
chr10	+(133068882..133069582)	700	0.05992	12	5	7	0.1666667	0.00224163	MIR378C	TCERG1L
chr10	+(133208700..133209248)	548	1.23598	7	4	3	0.1428571	0.029	TCERG1L	PPP2R2D
chr10	+(133331739..133332293)	554	0.55496	8	3	5	0.25	0.018	TCERG1L	PPP2R2D
chr10	+(133470688..133471193)	505	1.23598	7	3	4	0.1428571	0.029	TCERG1L	PPP2R2D
chr10	+(133557813..133558500)	687	0.28001	9	6	3	0.3333333	0.012	TCERG1L	PPP2R2D
chr10	+(133857630..133858727)	1097	1.23598	14	7	7	0	0.00087256	BNIP3	JAKMIP3
chr10	+(133934418..133934927)	509	1.23598	7	4	3	0.1428571	0.029	JAKMIP3	DPYSL4
chr10	+(134058101..134058801)	700	0.12128	10	7	3	0.4	0.008	DPYSL4	STK32C
chr10	+(134445319..134445947)	628	1.23598	10	3	7	0.4	0.992	INPP5A	NKX6-2
chr10	+(134463593..134464119)	526	2.7175	6	4	2	0.3333333	0.067	INPP5A	NKX6-2
chr10	+(134514977..134515677)	700	0.00584	21	13	8	0.2380952	0.82676768	INPP5A	NKX6-2
chr10	+(134516368..134517068)	700	0.00584	15	9	6	0.2	0.00073136	INPP5A	NKX6-2
chr10	+(134567998..134568990)	992	0.05992	19	9	10	0.0526316	0.00011928	INPP5A	NKX6-2
chr10	+(135034921..135035621)	700	1.23598	11	7	4	0.2727273	0.997	KNDC1	UTF1
chr10	+(135037955..135038461)	506	2.7175	6	3	3	0	0.05	KNDC1	UTF1
chr10	+(135120305..135121005)	700	0.02989	12	5	7	0.1666667	0.00224163	ADAM8	TUBGCP2
chr10	+(135439019..135440319)	1300	0.28088	83	41	42	0.0120482	0.004974	SPRNP1	FRG2B
chr11	+(452924..453716)	792	0.0294	12	7	5	0.1666667	0.00224163	PTDSS2	RNH1

chr11	+(594273..594966)	693	2.99724	9	6	3	0.3333333	0.012	PHRF1	IRF7
chr11	+(595778..596477)	699	1.40219	11	7	4	0.2727273	0.997	PHRF1	IRF7
chr11	+(615505..616558)	1053	1.40219	13	6	7	0.0769231	0.9986501	PHRF1	IRF7
chr11	+(621372..621896)	524	2.99724	6	3	3	0	0.05	IRF7	CDHR5
chr11	+(641379..642175)	796	0.66276	14	6	8	0.1428571	0.00097289	DRD4	DEAF1
chr11	+(665590..666259)	669	2.99724	6	4	2	0.3333333	0.067	DRD4	DEAF1
chr11	+(771406..772075)	669	0.66276	9	4	5	0.1111111	0.008	TALDO1	PDDC1
chr11	+(974510..975210)	700	2.99724	9	3	6	0.3333333	0.988	AP2A2	MUC6
chr11	+(997079..997779)	700	0.14182	10	3	7	0.4	0.008	AP2A2	MUC6
chr11	+(1016212..1018981)	2769	0.00223	571	272	299	0.0472855	0.11356778	AP2A2	MUC6
chr11	+(1074389..1074917)	528	0.66276	8	5	3	0.25	0.018	MUC6	MUC2
chr11	+(1092692..1093196)	504	4.29974	77	48	29	0.2467532	0.00531486	MUC2	MUC5B
chr11	+(1102406..1102926)	520	0.66276	8	4	4	0	0.014	MUC2	MUC5B
chr11	+(1122872..1123572)	700	0.08468	11	5	6	0.0909091	0.00308495	MUC2	MUC5B
chr11	+(1154230..1154804)	574	0.66276	8	4	4	0	0.014	MUC2	MUC5B
chr11	+(1263693..1264271)	578	0.14182	15	8	7	0.0666667	0.02457042	MUC5B	TOLLIP
chr11	+(1264405..1264975)	570	0.31019	12	5	7	0.1666667	0.08373231	MUC5B	TOLLIP
chr11	+(1266535..1267036)	501	2.99724	14	9	5	0.2857143	0.27425312	MUC5B	TOLLIP
chr11	+(1269065..1269739)	674	0.03757	44	17	27	0.2272727	0.00478329	MUC5B	TOLLIP
chr11	+(1269867..1270380)	513	0.48299	34	15	19	0.1176471	0.02122725	MUC5B	TOLLIP
chr11	+(1271729..1272283)	554	3.49895	29	12	17	0.1724138	0.14395042	MUC5B	TOLLIP
chr11	+(1331389..1332089)	700	1.40219	11	7	4	0.2727273	0.997	LOC255512	BRSK2
chr11	+(1369791..1370412)	621	2.99724	6	3	3	0	0.05	LOC255512	BRSK2
chr11	+(1382593..1383260)	667	2.99724	6	2	4	0.3333333	0.067	LOC255512	BRSK2
chr11	+(1470279..1470844)	565	0.31019	9	5	4	0.1111111	0.008	BRSK2	MOB2
chr11	+(1605454..1606034)	580	0.31019	15	10	5	0.3333333	0.02502177	BRSK2	MOB2
chr11	+(1717999..1718992)	993	0.07918	40	16	24	0.2	0.05465999	BRSK2	MOB2
chr11	+(1903104..1903804)	700	0.08468	14	7	7	0	0.00087256	MIR4298	TNNT3
chr11	+(1951003..1951682)	679	0.08468	24	11	13	0.0833333	0.88252402	TNNT3	MRPL23
chr11	+(1969231..1969931)	700	0.08468	12	5	7	0.1666667	0.04407898	MRPL23	LOC100133545
chr11	+(1974858..1975397)	539	1.40219	9	5	4	0.1111111	0.365	MRPL23	LOC100133545
chr11	+(2157978..2158482)	504	2.99724	9	6	3	0.3333333	0.988	MIR675	INS-IGF2
chr11	+(2327316..2328003)	687	0.14182	11	7	4	0.2727273	0.006	TSPAN32	CD81
chr11	+(2424644..2425291)	647	1.40219	7	3	4	0.1428571	0.029	TSSC4	TRPM5

chr11	+(2468308..2468812)	504	2.99724	9	3	6	0.3333333	0.012	KCNQ1	KCNQ1OT1	
chr11	+(2932786..2933397)	611	0.66276	8	5	3	0.25	0.018	SLC22A18	PHLDA2	
chr11	+(3024727..3025341)	614	0.14182	10	6	4	0.2	0.005	SNORA54	CARS	
chr11	+(3028681..3029413)	732	0.14182	23	8	15	0.3043478	0.0983528	SNORA54	CARS	
chr11	+(3425787..3426460)	673	0.0294	12	4	8	0.3333333	0.00328926	LOC650368	TRPC2	
chr11	+(4411439..4411942)	503	2.99724	7	4	3	0.1428571	0.314	OR52B4	TRIM21	
chr11	+(4510462..4510971)	509	2.99724	11	5	6	0.0909091	0.35750033	OR52K1	OR52M1	
chr11	+(4615580..4616187)	607	1.40219	12	5	7	0.1666667	0.18587565	OR52I1	TRIM68	
chr11	+(4870009..4870552)	543	2.99724	10	5	5	0	0.69924593	OR51F2	OR51S1	
chr11	+(6220709..6221296)	587	1.40219	10	7	3	0.4	0.033	OR52W1	C11orf42	
chr11	+(7544032..7544688)	656	0.31019	12	5	7	0.1666667	0.00224163	PPFIBP2	CYB5R2	
chr11	+(7596883..7597538)	655	2.99724	6	4	2	0.3333333	0.067	PPFIBP2	CYB5R2	
chr11	+(8017131..8017831)	700	0.66276	9	3	6	0.3333333	0.012	EIF3F	TUB	
chr11	+(8111019..8111643)	624	0.66276	8	4	4	0	0.014	TUB	RIC3	
chr11	+(8350195..8350895)	700	0.66276	8	4	4	0	0.014	LMO1	STK33	
chr11	+(8389062..8389762)	700	2.99724	9	3	6	0.3333333	0.012	LMO1	STK33	
chr11	+(8495973..8496670)	697	0.31019	10	6	4	0.2	0.005	LMO1	STK33	
chr11	+(8751188..8751710)	522	1.40219	10	7	3	0.4	0.008	SNORA45	ST5	
chr11	+(9607868..9608518)	650	1.40219	12	5	7	0.1666667	0.18587565	WEE1	SWAP70	v
chr11	+(10645306..10645980)	674	1.40219	8	5	3	0.25	0.018	LYVE1	MRVI1	
chr11	+(10668904..10670133)	1229	0.08468	19	8	11	0.1578947	0.99986003	LYVE1	MRVI1	
chr11	+(10762082..10762782)	700	0.14182	12	7	5	0.1666667	0.00224163	MRVI1	CTR9	
chr11	+(10818858..10819409)	551	1.40219	11	4	7	0.2727273	0.464	CTR9	EIF4G2	
chr11	+(11924577..11925159)	582	0.66276	12	4	8	0.3333333	0.00328926	USP47	DKK3	
chr11	+(12009767..12010467)	700	0.00341	16	10	6	0.25	0.01502979	USP47	DKK3	
chr11	+(14308509..14309206)	697	2.99724	10	6	4	0.2	0.995	SPON1	RRAS2	
chr11	+(14852121..14852659)	538	1.40219	11	4	7	0.2727273	0.003	PDE3B	CYP2R1	
chr11	+(16071108..16071610)	502	1.40219	9	4	5	0.1111111	0.016	INSC	SOX6	
chr11	+(17112481..17113413)	932	0.08468	17	9	8	0.0588235	0.00352682	RPS13	PIK3C2A	
chr11	+(17171773..17172520)	747	0.66276	12	6	6	0	0.00815459	RPS13	PIK3C2A	
chr11	+(17298568..17299268)	700	0.31019	13	9	4	0.3846154	0.999	NUCB2	DKFZp686O24166	
chr11	+(18104843..18105344)	501	2.99724	8	5	3	0.25	0.018	TPH1	SAAL1	
chr11	+(27389284..27389984)	700	2.99724	11	5	6	0.0909091	0.29194121	CCDC34	LGR4	
chr11	+(31814644..31815234)	590	2.99724	10	4	6	0.2	0.005	ELP4	PAX6	v

chr11	+(33090326..33090855)	529	0.14182	13	4	9	0.3846154	0.001	TCP11L1	NCRNA00294	
chr11	+(33111933..33112497)	564	1.40219	12	6	6	0	0.02733197	NCRNA00294	CSTF3	
chr11	+(34172652..34173835)	1183	0.14182	26	17	9	0.3076923	1.869E-05	NAT10	ABTB2	v
chr11	+(34510472..34511143)	671	0.14182	10	6	4	0.2	0.005	CAT	ELF5	
chr11	+(35685002..35685515)	513	2.99724	8	5	3	0.25	0.5	TRIM44	LDLRAD3	
chr11	+(36598476..36599036)	560	2.99724	8	5	3	0.25	0.196	RAG1	RAG2	
chr11	+(45680634..45681691)	1057	0.0294	18	7	11	0.2222222	0.99362333	SYT13	CHST1	
chr11	+(45948023..45948558)	535	2.99724	9	4	5	0.1111111	0.452	GYLTL1B	PHF21A	v
chr11	+(46000940..46001952)	1012	0.31019	23	10	13	0.1304348	0.86785582	GYLTL1B	PHF21A	v
chr11	+(46275359..46276059)	700	0.31019	13	4	9	0.3846154	0.001	PHF21A	CREB3L1	v
chr11	+(46740507..46741207)	700	1.40219	10	3	7	0.4	0.992	ZNF408	F2	
chr11	+(47306415..47307114)	699	2.99724	11	6	5	0.0909091	0.00308495	MADD	MYBPC3	
chr11	+(47354121..47354772)	651	0.31019	10	6	4	0.2	0.129	MADD	MYBPC3	
chr11	+(47414170..47414870)	700	0.00341	15	8	7	0.0666667	0.00059687	SPI1	SLC39A13	
chr11	+(47431483..47432183)	700	0.01969	13	8	5	0.2307692	0.0017074	SLC39A13	PSMC3	
chr11	+(47506958..47507625)	667	1.40219	7	3	4	0.1428571	0.029	RAPSN	CELF1	
chr11	+(47772385..47773085)	700	0.14182	11	7	4	0.2727273	0.003	AGBL2	FNBP4	
chr11	+(47774287..47774877)	590	2.99724	10	5	5	0	0.02360089	AGBL2	FNBP4	
chr11	+(48119535..48120223)	688	2.99724	8	3	5	0.25	0.393	PTPRJ	OR4B1	
chr11	+(49000173..49000683)	510	0.66276	12	5	7	0.1666667	0.01417552	OR4A47	FOLH1	
chr11	+(49010681..49011187)	506	2.67895	34	22	12	0.2941176	1.4553E-05	OR4A47	FOLH1	
chr11	+(49056437..49056939)	502	2.15276	18	12	6	0.3333333	0.00099831	OR4A47	FOLH1	
chr11	+(49190590..49191287)	697	0.31019	13	9	4	0.3846154	0.003	OR4A47	FOLH1	
chr11	+(55032050..55033104)	1054	0.00341	35	24	11	0.3714286	0.57050785	TRIM48	OR4A16	
chr11	+(57093395..57094479)	1084	0.31019	16	8	8	0	0.95355402	TNKS1BP1	SSRP1	
chr11	+(57126355..57127034)	679	0.0294	12	6	6	0	0.00197388	P2RX3	PRG3	
chr11	+(57234929..57235629)	700	0.66276	10	5	5	0	0.00451172	RTN4RL2	SLC43A1	
chr11	+(57256373..57257014)	641	0.66276	9	4	5	0.1111111	0.008	RTN4RL2	SLC43A1	
chr11	+(57947332..57947885)	553	2.99724	9	4	5	0.1111111	0.032	OR9I1	OR9Q2	
chr11	+(58170189..58170836)	647	1.40219	7	4	3	0.1428571	0.029	OR5B17	OR5B3	
chr11	+(58369241..58369921)	680	2.99724	6	2	4	0.3333333	0.067	ZFP91-CNTF	CNTF	
chr11	+(60785642..60786182)	540	2.99724	6	2	4	0.3333333	0.067	CD6	CD5	
chr11	+(60996004..60996649)	645	0.12171	39	27	12	0.3846154	0.01123944	PGA4	PGA5	
chr11	+(61008526..61009060)	534	1.55669	34	20	14	0.1764706	9.8127E-06	PGA4	PGA5	

chr11	+(61013504..61014025)	521	0.66276	13	7	6	0.0769231	0.01113549	PGA5	VWCE
chr11	+(61017120..61017715)	595	0.08468	25	14	11	0.12	0.00090285	PGA5	VWCE
chr11	+(61018342..61018891)	549	2.99724	8	4	4	0	0.1	PGA5	VWCE
chr11	+(61133297..61133912)	615	0.66276	11	5	6	0.0909091	0.00308495	TMEM138	TMEM216
chr11	+(61292315..61292927)	612	0.66276	14	5	9	0.2857143	0.03593032	LRRC10B	SYT7
chr11	+(61453588..61454882)	1294	1.40219	15	7	8	0.0666667	0.05259626	DAGLA	C11orf9
chr11	+(61492374..61493074)	700	1.40219	8	3	5	0.25	0.018	DAGLA	C11orf9
chr11	+(61528904..61529486)	582	0.66276	12	4	8	0.3333333	0.00328926	DKFZP434K028	C11orf10
chr11	+(61545867..61546529)	662	2.99724	7	4	3	0.1428571	0.029	DKFZP434K028	C11orf10
chr11	+(61623934..61625267)	1333	1.40219	14	7	7	0	0.99912744	FADS2	FADS3
chr11	+(61676201..61676895)	694	0.14182	10	7	3	0.4	0.008	FADS3	RAB3IL1
chr11	+(61725414..61725941)	527	2.99724	6	2	4	0.3333333	0.067	BEST1	FTH1
chr11	+(61729513..61730596)	1083	0.66276	16	8	8	0	0.00316147	BEST1	FTH1
chr11	+(62140242..62140907)	665	1.40219	9	3	6	0.3333333	0.048	ASRGL1	SCGB1A1
chr11	+(62186416..62186979)	563	2.99724	6	2	4	0.3333333	0.067	ASRGL1	SCGB1A1
chr11	+(62289798..62290311)	513	2.99724	9	5	4	0.1111111	0.016	SCGB1A1	AHNAK
chr11	+(62293536..62294052)	516	2.99724	9	4	5	0.1111111	0.452	SCGB1A1	AHNAK
chr11	+(62299542..62300049)	507	2.99724	8	5	3	0.25	0.5	SCGB1A1	AHNAK
chr11	+(62327463..62328043)	580	2.99724	8	4	4	0	0.029	AHNAK	EEF1G
chr11	+(62339605..62340425)	820	0.66276	16	7	9	0.125	0.00042755	AHNAK	EEF1G
chr11	+(62348434..62349064)	630	2.99724	8	5	3	0.25	0.196	EEF1G	TUT1
chr11	+(62483030..62483534)	504	2.99724	10	5	5	0	0.03790009	GNG3	HNRNPUL2
chr11	+(62533759..62534267)	508	2.99724	11	5	6	0.0909091	0.07206352	POLR2G	TAF6L
chr11	+(62540957..62541480)	523	2.99724	6	2	4	0.3333333	0.067	TAF6L	TMEM179B
chr11	+(62545316..62545929)	613	0.31019	11	6	5	0.0909091	0.00529357	TAF6L	TMEM179B
chr11	+(62556551..62557084)	533	2.99724	9	4	5	0.1111111	0.016	TMEM179B	TMEM223
chr11	+(62591536..62592232)	696	0.31019	14	9	5	0.2857143	0.0013499	NXF1	STX5
chr11	+(62592521..62593221)	700	0.31019	11	4	7	0.2727273	0.003	NXF1	STX5
chr11	+(62847211..62847740)	529	2.99724	7	4	3	0.1428571	0.029	SLC22A8	SLC22A24
chr11	+(63312663..63313915)	1252	0.0294	20	6	14	0.4	0.99332621	RARRES3	HRASLS2
chr11	+(63636539..63637239)	700	0.66276	12	8	4	0.3333333	0.99671074	MARK2	RCOR2
chr11	+(63669540..63670063)	523	0.14182	12	5	7	0.1666667	0.00368558	MARK2	RCOR2
chr11	+(63710377..63711077)	700	2.99724	9	3	6	0.3333333	0.012	NAA40	COX8A
chr11	+(63843758..63844809)	1051	0.31019	15	9	6	0.2	0.00073136	OTUB1	MACROD1

chr11	+(63849269..63849794)	525	0.66276	8	5	3	0.25	0.018	OTUB1	MACROD1
chr11	+(64039208..64039907)	699	2.99724	10	6	4	0.2	0.995	PLCB3	BAD
chr11	+(64044048..64044590)	542	2.99724	6	4	2	0.3333333	0.067	PLCB3	BAD
chr11	+(64116045..64116745)	700	1.40219	10	3	7	0.4	0.742	CCDC88B	RPS6KA4
chr11	+(64128319..64128837)	518	0.66276	8	3	5	0.25	0.018	RPS6KA4	MIR1237
chr11	+(64418297..64418997)	700	0.66276	10	7	3	0.4	0.058	SLC22A12	NRXN2
chr11	+(64453109..64453737)	628	0.31019	9	3	6	0.3333333	0.012	SLC22A12	NRXN2
chr11	+(64502501..64503070)	569	2.99724	6	2	4	0.3333333	0.067	NRXN2	RASGRP2
chr11	+(64543685..64544302)	617	2.99724	9	4	5	0.1111111	0.032	PYGM	SF1
chr11	+(64556702..64557701)	999	0.66276	16	9	7	0.125	0.94956952	SF1	MAP4K2
chr11	+(64757534..64758234)	700	0.31019	14	9	5	0.2857143	0.0013499	C11orf85	BATF2
chr11	+(65178723..65179468)	745	0.0294	14	8	6	0.1428571	0.0140929	FRMD8	NEAT1
chr11	+(65311377..65312107)	730	1.40219	13	6	7	0.0769231	0.0013499	SCYL1	LTBP3
chr11	+(65382788..65383488)	700	0.66276	12	5	7	0.1666667	0.00224163	MAP3K11	PCNXL3
chr11	+(65384648..65385593)	945	0.66276	19	10	9	0.0526316	0.94876478	PCNXL3	SIPA1
chr11	+(65396440..65397048)	608	0.00742	17	10	7	0.1764706	0.08592868	PCNXL3	SIPA1
chr11	+(65631335..65632025)	690	0.66276	8	5	3	0.25	0.018	MUS81	EFEMP2
chr11	+(66033694..66034394)	700	0.0294	13	9	4	0.3846154	0.001	KLC2	RAB1B
chr11	+(66106103..66106803)	700	0.31019	12	5	7	0.1666667	0.71511782	RIN1	BRMS1
chr11	+(66138535..66139066)	531	2.99724	6	3	3	0	0.05	B3GNT1	SLC29A2
chr11	+(66181224..66181818)	594	1.40219	7	4	3	0.1428571	0.029	SLC29A2	NPAS4
chr11	+(66333430..66334130)	700	0.66276	9	4	5	0.1111111	0.008	ACTN3	CTSF
chr11	+(66359307..66359977)	670	1.40219	10	7	3	0.4	0.992	CTSF	CCDC87
chr11	+(66370578..66371278)	700	1.40219	12	7	5	0.1666667	0.99775837	CCS	RBM14
chr11	+(66453546..66454450)	904	0.31019	15	9	6	0.2	0.00073136	RBM4B	SPTBN2
chr11	+(66680004..66681029)	1025	0.00742	20	13	7	0.3	0.39075565	RCE1	PC
chr11	+(66809235..66809757)	522	2.99724	6	3	3	0	0.05	SYT12	RHOD
chr11	+(66812970..66813515)	545	2.99724	6	3	3	0	0.05	SYT12	RHOD
chr11	+(67046437..67046958)	521	1.40219	7	4	3	0.1428571	0.029	ADRBK1	ANKRD13D
chr11	+(67133434..67134134)	700	1.40219	12	5	7	0.1666667	0.99775837	POLD4	CLCF1
chr11	+(67158930..67159505)	575	1.40219	11	7	4	0.2727273	0.394	CLCF1	RAD9A
chr11	+(67196398..67197038)	640	1.40219	8	4	4	0	0.171	RPS6KB2	PTPRCAP
chr11	+(67208689..67209284)	595	1.40219	9	3	6	0.3333333	0.274	PTPRCAP	CORO1B
chr11	+(67289683..67290234)	551	1.40219	9	4	5	0.1111111	0.095	CDK2AP2	CABP2

chr11	+(67292825..67294118)	1293	0.14182	19	12	7	0.2631579	0.00019287	CABP2	GSTP1	
chr11	+(67308706..67310040)	1334	0.14182	17	9	8	0.0588235	0.00468738	CABP2	GSTP1	
chr11	+(67310868..67311443)	575	2.99724	7	3	4	0.1428571	0.2	CABP2	GSTP1	
chr11	+(67560591..67561239)	648	0.31019	14	9	5	0.2857143	0.12853715	ALDH3B2	LOC645332	
chr11	+(67792439..67793110)	671	0.14182	10	6	4	0.2	0.005	ALDH3B1	NDUFS8	
chr11	+(67911818..67912920)	1102	2.99724	12	6	6	0	0.99802612	CHKA	SUV420H1	
chr11	+(67926122..67926710)	588	1.40219	8	5	3	0.25	0.018	CHKA	SUV420H1	
chr11	+(68025612..68026312)	700	0.01969	13	5	8	0.2307692	0.0017074	SUV420H1	C11orf24	
chr11	+(68091621..68092765)	1144	0.01969	19	13	6	0.3684211	0.9996875	LRP5	PPP6R3	
chr11	+(68147672..68148193)	521	0.66276	8	3	5	0.25	0.018	LRP5	PPP6R3	
chr11	+(68196539..68197239)	700	2.99724	11	5	6	0.0909091	0.97769514	LRP5	PPP6R3	
chr11	+(68334413..68334930)	517	1.40219	8	5	3	0.25	0.018	PPP6R3	GAL	
chr11	+(68380300..68380947)	647	0.01969	14	5	9	0.2857143	0.0013499	PPP6R3	GAL	
chr11	+(68680193..68680739)	546	0.66276	8	4	4	0	0.014	IGHMBP2	MRGPRD	
chr11	+(69205647..69206209)	562	0.66276	8	5	3	0.25	0.018	MYEOV	CCND1	
chr11	+(69213928..69214571)	643	2.99724	6	2	4	0.3333333	0.067	MYEOV	CCND1	
chr11	+(69291525..69292849)	1324	0.14182	18	8	10	0.1111111	0.00018964	MYEOV	CCND1	
chr11	+(69360529..69361229)	700	0.00019	20	10	10	0	7.8526E-05	MYEOV	CCND1	
chr11	+(69407676..69408335)	659	2.99724	6	3	3	0	0.05	MYEOV	CCND1	
chr11	+(69408346..69408868)	522	1.40219	7	3	4	0.1428571	0.029	MYEOV	CCND1	
chr11	+(69454450..69456065)	1615	1.3E-05	159	93	66	0.1698113	0.20569289	MYEOV	CCND1	
chr11	+(69587978..69588491)	513	0.31019	9	3	6	0.3333333	0.012	FGF19	FGF4	
chr11	+(69623618..69624318)	700	0.0039	21	12	9	0.1428571	0.00014481	FGF4	FGF3	v
chr11	+(69625280..69625978)	698	2.99724	9	4	5	0.1111111	0.857	FGF4	FGF3	v
chr11	+(69636630..69637248)	618	0.66276	8	5	3	0.25	0.018	FGF3	ANO1	v
chr11	+(69649430..69649990)	560	2.99724	6	2	4	0.3333333	0.067	FGF3	ANO1	v
chr11	+(69788688..69789258)	570	1.40219	8	5	3	0.25	0.018	FGF3	ANO1	v
chr11	+(69811508..69812207)	699	0.31019	9	6	3	0.3333333	0.012	FGF3	ANO1	v
chr11	+(70269985..70270685)	700	0.14182	12	7	5	0.1666667	0.28488218	CTTN	SHANK2	
chr11	+(70426509..70427123)	614	0.14182	11	7	4	0.2727273	0.036	CTTN	SHANK2	
chr11	+(70440162..70440868)	706	0.0294	14	9	5	0.2857143	0.0013499	CTTN	SHANK2	
chr11	+(70441491..70442191)	700	0.01969	13	8	5	0.2307692	0.0017074	CTTN	SHANK2	
chr11	+(70514393..70514924)	531	1.40219	11	7	4	0.2727273	0.997	CTTN	SHANK2	
chr11	+(70557407..70558598)	1191	0.66276	14	6	8	0.1428571	0.00097289	CTTN	SHANK2	

chr11	+(70591079..70591814)	735	0.00031	19	10	9	0.0526316	0.00011928	CTTN	SHANK2
chr11	+(70644403..70644945)	542	0.31019	11	6	5	0.0909091	0.00308495	CTTN	SHANK2
chr11	+(70687349..70688049)	700	0.0294	12	8	4	0.3333333	0.99671074	CTTN	SHANK2
chr11	+(70753036..70753736)	700	0.31019	9	3	6	0.3333333	0.012	CTTN	SHANK2
chr11	+(70856215..70856838)	623	0.14182	10	6	4	0.2	0.005	CTTN	SHANK2
chr11	+(71151892..71152508)	616	0.08468	14	9	5	0.2857143	0.00981533	MIR3664	DHCR7
chr11	+(71192487..71193402)	915	0.66276	16	6	10	0.25	0.00119462	NADSYN1	KRTAP5-7
chr11	+(71276267..71276852)	585	0.66276	13	7	6	0.0769231	0.4432015	KRTAP5-9	KRTAP5-10
chr11	+(71293237..71293918)	681	0.31019	19	11	8	0.1578947	0.31014701	KRTAP5-10	KRTAP5-11
chr11	+(71639736..71640436)	700	0.08468	11	7	4	0.2727273	0.003	LOC100133315	RNF121
chr11	+(72004411..72005635)	1224	0.26018	26	11	15	0.1538462	0.01562608	PHOX2A	CLPB
chr11	+(72047126..72048013)	887	0.00085	17	11	6	0.2941176	0.00045556	PHOX2A	CLPB
chr11	+(72294659..72295569)	910	0.66276	14	8	6	0.1428571	0.99902711	CLPB	PDE2A
chr11	+(72380237..72380937)	700	0.08468	11	5	6	0.0909091	0.00308495	CLPB	PDE2A
chr11	+(72945630..72946312)	682	2.99724	8	5	3	0.25	0.018	P2RY2	P2RY6
chr11	+(73026048..73026748)	700	1.40219	14	7	7	0	0.32736042	ARHGEF17	RELT
chr11	+(74687458..74688158)	700	1.40219	13	6	7	0.0769231	0.84134475	SPCS2	NEU3
chr11	+(74910984..74911684)	700	0.08468	12	4	8	0.3333333	0.00328926	SLCO2B1	LOC441617
chr11	+(74953035..74953602)	567	2.99724	9	3	6	0.3333333	0.988	LOC441617	ARRB1
chr11	+(75161666..75162268)	602	1.40219	10	3	7	0.4	0.008	KLHL35	GDPD5
chr11	+(75298299..75298847)	548	0.31019	13	5	8	0.2307692	0.02021199	SERPINH1	MAP6
chr11	+(75946826..75947486)	660	2.99724	10	6	4	0.2	0.005	WNT11	PRKRIR
chr11	+(76010894..76011396)	502	1.40219	7	3	4	0.1428571	0.029	WNT11	PRKRIR
chr11	+(76061672..76062228)	556	1.40219	11	5	6	0.0909091	0.07206352	WNT11	PRKRIR
chr11	+(76062889..76063550)	661	0.66276	18	7	11	0.2222222	0.19478884	WNT11	PRKRIR
chr11	+(76260920..76261421)	501	2.99724	6	4	2	0.3333333	0.067	C11orf30	LRRC32
chr11	+(76300041..76300597)	556	2.99724	11	6	5	0.0909091	0.00308495	C11orf30	LRRC32
chr11	+(76318891..76319438)	547	2.99724	6	2	4	0.3333333	0.067	C11orf30	LRRC32
chr11	+(79119945..79120646)	701	0.08468	12	8	4	0.3333333	0.99671074	NARS2	ODZ4
chr11	+(83877765..83878345)	580	2.99724	7	3	4	0.1428571	0.029	CCDC90B	DLG2
chr11	+(85195201..85195725)	524	1.40219	14	7	7	0	0.99912744	CCDC90B	DLG2
chr11	+(86103336..86103921)	585	0.0294	14	9	5	0.2857143	0.0013499	CCDC81	ME3
chr11	+(89133217..89133880)	663	1.40219	11	7	4	0.2727273	0.206	TYR	NOX4
chr11	+(96117411..96117947)	536	0.14182	15	7	8	0.0666667	0.00544818	MIR1260B	CCDC82

chr11	+(100830355..100830858)	503	2.99724	6	4	2	0.3333333	0.067	ARHGAP42	TMEM133
chr11	+(108044093..108044603)	510	2.99724	10	7	3	0.4	0.033	ACAT1	NPAT
chr11	+(108263818..108264347)	529	2.99724	7	3	4	0.1428571	0.029	ATM	C11orf65
chr11	+(110450914..110451452)	538	0.31019	11	6	5	0.0909091	0.00529357	FDX1	ARHGAP20
chr11	+(111866008..111866511)	503	2.99724	6	4	2	0.3333333	0.067	DIXDC1	DLAT
chr11	+(113629061..113629613)	552	1.40219	9	4	5	0.1111111	0.056	TMPRSS5	ZW10
chr11	+(113928872..113929438)	566	2.99724	6	4	2	0.3333333	0.067	HTR3A	ZBTB16
chr11	+(113934199..113934835)	636	0.66276	8	3	5	0.25	0.018	ZBTB16	NNMT
chr11	+(114014456..114015156)	700	0.00341	15	5	10	0.3333333	0.00109982	ZBTB16	NNMT
chr11	+(117246185..117246780)	595	1.40219	9	4	5	0.1111111	0.016	CEP164	DSCAML1
chr11	+(117367581..117368160)	579	1.40219	7	4	3	0.1428571	0.029	CEP164	DSCAML1
chr11	+(117738930..117740843)	1913	0.08468	24	11	13	0.0833333	1.718E-05	FXYD2	FXYD6
chr11	+(118777615..118778282)	667	1.40219	7	3	4	0.1428571	0.029	CXCR5	BCL9L
chr11	+(120846309..120847681)	1372	1.40219	13	6	7	0.0769231	0.0013499	GRIK4	TBCEL
chr11	+(121007991..121008582)	591	2.99724	7	3	4	0.1428571	0.314	TECTA	SC5DL
chr11	+(121177753..121178373)	620	1.40219	13	8	5	0.2307692	0.92838254	SC5DL	SORL1
chr11	+(121232441..121233030)	589	1.40219	10	7	3	0.4	0.092	SC5DL	SORL1
chr11	+(121367839..121368899)	1060	1.40219	13	7	6	0.0769231	0.0013499	SORL1	LOC399959
chr11	+(122542029..122542729)	700	0.01969	13	4	9	0.3846154	0.001	UBASH3B	CRTAM
chr11	+(122944205..122944716)	511	2.99724	9	6	3	0.3333333	0.19	HSPA8	ASAM
chr11	+(123396400..123397093)	693	0.66276	8	5	3	0.25	0.018	ASAM	GRAMD1B
chr11	+(123439173..123439873)	700	0.0294	12	5	7	0.1666667	0.00224163	GRAMD1B	SCN3B
chr11	+(128842794..128843458)	664	1.40219	17	6	11	0.2941176	0.54002781	TP53AIP1	ARHGAP32
chr11	+(131074366..131075251)	885	0.14182	17	7	10	0.1764706	0.00031815	SNX19	NTM
chr11	+(131684822..131685522)	700	0.00742	14	9	5	0.2857143	0.0013499	NTM	OPCML
chr12	+(90483..90990)	507	3.08111	11	7	4	0.2727273	0.003	LOC100288778	FAM138D
chr12	+(651083..651763)	680	0.29741	9	3	6	0.3333333	0.012	B4GALNT3	NINJ2
chr12	+(1219101..1219602)	501	3.08111	10	4	6	0.2	0.457	ERC1	LOC100292680
chr12	+(1772195..1772834)	639	0.69993	8	4	4	0	0.014	MIR3649	ADIPOR2
chr12	+(1865342..1866554)	1212	0.03249	19	7	12	0.2631579	0.99980713	ADIPOR2	CACNA2D4
chr12	+(1939930..1940610)	680	0.69993	13	7	6	0.0769231	0.00757922	ADIPOR2	CACNA2D4
chr12	+(2714510..2715073)	563	0.29741	12	5	7	0.1666667	0.00368558	CACNA1C	LOC283440
chr12	+(3232156..3232849)	693	0.69993	8	5	3	0.25	0.018	TSPAN9	PRMT8
chr12	+(3298015..3299079)	1064	0.06632	21	11	10	0.047619	0.99994624	TSPAN9	PRMT8

chr12	+(3387753..3388323)	570	3.08111	8	4	4	0	0.443	TSPAN9	PRMT8
chr12	+(3414561..3415261)	700	0.12742	10	4	6	0.2	0.005	TSPAN9	PRMT8
chr12	+(3423251..3423845)	594	3.08111	6	4	2	0.3333333	0.067	TSPAN9	PRMT8
chr12	+(3524877..3525554)	677	1.46883	7	4	3	0.1428571	0.029	TSPAN9	PRMT8
chr12	+(4648724..4649240)	516	0.29741	9	5	4	0.1111111	0.008	RAD51AP1	DYRK4
chr12	+(5694701..5695310)	609	3.08111	9	3	6	0.3333333	0.988	NTF3	ANO2
chr12	+(5983598..5984198)	600	1.46883	7	3	4	0.1428571	0.029	NTF3	ANO2
chr12	+(6092038..6092620)	582	1.46883	7	4	3	0.1428571	0.029	ANO2	VWF
chr12	+(6100737..6101359)	622	1.46883	7	4	3	0.1428571	0.029	ANO2	VWF
chr12	+(6128567..6129098)	531	3.08111	11	7	4	0.2727273	0.036	ANO2	VWF
chr12	+(6228274..6228830)	556	0.69993	8	5	3	0.25	0.018	ANO2	VWF
chr12	+(6324545..6325064)	519	0.69993	8	4	4	0	0.014	CD9	PLEKHG6
chr12	+(6438833..6439754)	921	3.08111	15	9	6	0.2	0.31867594	PLEKHG6	TNFRSF1A
chr12	+(6778952..6779652)	700	0.69993	10	3	7	0.4	0.742	ING4	ZNF384
chr12	+(6940748..6941416)	668	0.12742	10	4	6	0.2	0.005	LEPREL2	GNB3
chr12	+(6949867..6950567)	700	3.08111	9	3	6	0.3333333	0.988	GNB3	CDCA3
chr12	+(6952361..6952947)	586	1.46883	13	9	4	0.3846154	0.355	GNB3	CDCA3
chr12	+(6980714..6981414)	700	0.69993	11	6	5	0.0909091	0.70805879	TPI1	SPSB2
chr12	+(7045867..7046384)	517	3.08111	10	6	4	0.2	0.457	ATN1	C12orf57
chr12	+(7653528..7654076)	548	0.69993	10	6	4	0.2	0.057	CD163L1	CD163
chr12	+(9072186..9072706)	520	3.08111	6	4	2	0.3333333	0.067	PHC1	M6PR
chr12	+(9312511..9313064)	553	3.08111	10	6	4	0.2	0.129	A2M	PZP
chr12	+(10305883..10306583)	700	0.29741	9	3	6	0.3333333	0.012	CLEC7A	OLR1
chr12	+(10319149..10319713)	564	1.46883	10	6	4	0.2	0.005	CLEC7A	OLR1
chr12	+(10370560..10371402)	842	0.03249	15	6	9	0.2	0.00073136	GABARAPL1	KLRD1
chr12	+(11060890..11061428)	538	3.08111	7	4	3	0.1428571	0.2	TAS2R10	PRR4
chr12	+(11214061..11214585)	524	3.08111	12	5	7	0.1666667	0.53235847	TAS2R10	PRR4
chr12	+(11243502..11244102)	600	0.12742	22	8	14	0.2727273	0.12296535	TAS2R10	PRR4
chr12	+(11506080..11507106)	1026	0.64527	69	35	34	0.0144928	0.48085429	PRB4	PRB1
chr12	+(11546133..11547042)	909	0.54621	116	54	62	0.0689655	0.10549031	PRB1	PRB2
chr12	+(12618115..12618815)	700	3.08111	10	4	6	0.2	0.129	LOH12CR1	DUSP16
chr12	+(12763947..12764891)	944	0.00834	21	14	7	0.3333333	0.00017112	DUSP16	CREBL2
chr12	+(18434762..18435273)	511	1.46883	9	3	6	0.3333333	0.012	PIK3C2G	PLCZ1
chr12	+(21294133..21295002)	869	3.08111	12	6	6	0	0.37438702	SLCO1B1	SLCO1A2

chr12	+(21621237..21621751)	514	1.46883	11	4	7	0.2727273	0.006	PYROXD1	RECQL
chr12	+(22624406..22624914)	508	1.46883	10	7	3	0.4	0.033	ST8SIA1	KIAA0528
chr12	+(25313832..25314565)	733	0.00185	18	10	8	0.1111111	0.00018964	LRMP	CASC1
chr12	+(30869371..30869893)	522	3.08111	12	7	5	0.1666667	0.08373231	IPO8	CAPRIN2
chr12	+(31237470..31238016)	546	2.19401	27	18	9	0.3333333	0.00023478	DDX11	FAM60A
chr12	+(31255687..31256522)	835	0.39347	23	15	8	0.3043478	0.00049732	DDX11	FAM60A
chr12	+(32134137..32134742)	605	3.08111	7	3	4	0.1428571	0.029	C12orf35	BICD1
chr12	+(32328110..32328715)	605	1.46883	7	4	3	0.1428571	0.029	BICD1	FGD4
chr12	+(41659665..41660365)	700	0.29741	9	3	6	0.3333333	0.012	PDZRN4	GXYLT1
chr12	+(44770156..44770661)	505	3.08111	7	3	4	0.1428571	0.114	TMEM117	NELL2
chr12	+(44913503..44914019)	516	3.08111	9	5	4	0.1111111	0.056	TMEM117	NELL2
chr12	+(48139179..48139748)	569	0.12742	10	4	6	0.2	0.005	ENDOU	RAPGEF3
chr12	+(48141022..48141747)	725	0.01356	14	8	6	0.1428571	0.01943355	ENDOU	RAPGEF3
chr12	+(48238016..48238687)	671	0.01356	16	10	6	0.25	0.00334766	HDAC7	VDR
chr12	+(48251003..48251659)	656	1.46883	10	6	4	0.2	0.543	HDAC7	VDR
chr12	+(49496630..49497160)	530	3.08111	8	5	3	0.25	0.018	DHH	LMBR1L
chr12	+(49979046..49979664)	618	3.08111	6	3	3	0	0.05	MCRS1	FAM186B
chr12	+(50263787..50264687)	900	0.29741	15	5	10	0.3333333	0.19563364	BCDIN3D	FAIM2
chr12	+(50291323..50292023)	700	0.06632	11	4	7	0.2727273	0.003	BCDIN3D	FAIM2
chr12	+(50323282..50323886)	604	3.08111	6	4	2	0.3333333	0.067	LOC283332	AQP2
chr12	+(50348253..50348949)	696	0.69993	10	7	3	0.4	0.008	AQP2	AQP5
chr12	+(50725337..50725916)	579	3.08111	8	5	3	0.25	0.286	MIR1293	FAM186A
chr12	+(50747725..50748425)	700	0.03249	20	8	12	0.2	0.00677733	MIR1293	FAM186A
chr12	+(50748568..50749124)	556	3.08111	10	6	4	0.2	0.238	MIR1293	FAM186A
chr12	+(51419840..51420410)	570	0.69993	8	5	3	0.25	0.018	HIGD1C	SLC11A2
chr12	+(51688549..51689249)	700	0.69993	12	4	8	0.3333333	0.00328926	SMAGP	BIN2
chr12	+(51882297..51882854)	557	1.46883	9	4	5	0.1111111	0.008	SLC4A8	SCN8A
chr12	+(52080745..52081286)	541	3.08111	7	4	3	0.1428571	0.029	SCN8A	FIGNL2
chr12	+(52200192..52200709)	517	3.08111	11	4	7	0.2727273	0.264	SCN8A	FIGNL2
chr12	+(52565803..52566359)	556	1.46883	8	3	5	0.25	0.125	C12orf44	KRT80
chr12	+(52821723..52822413)	690	1.46883	10	4	6	0.2	0.381	KRT82	KRT75
chr12	+(52884685..52885222)	537	0.69993	12	8	4	0.3333333	0.99671074	KRT6C	KRT6A
chr12	+(52886230..52886822)	592	0.00023	23	16	7	0.3913043	0.000256	KRT6C	KRT6A
chr12	+(53001851..53002470)	619	1.46883	11	7	4	0.2727273	0.158	KRT72	KRT73

chr12	+(53008702..53009260)	558	3.08111	6	4	2	0.3333333	0.067	KRT72	KRT73
chr12	+(53009873..53010433)	560	3.08111	9	3	6	0.3333333	0.048	KRT72	KRT73
chr12	+(53037324..53038024)	700	0.06632	11	7	4	0.2727273	0.003	KRT73	KRT2
chr12	+(53170464..53171108)	644	0.69993	9	6	3	0.3333333	0.012	KRT77	KRT76
chr12	+(53189008..53189759)	751	0.00185	30	11	19	0.2666667	0.00011679	KRT76	KRT3
chr12	+(53205629..53206179)	550	3.08111	13	6	7	0.0769231	0.76247474	KRT3	KRT4
chr12	+(53345249..53345995)	746	0.03249	15	9	6	0.2	0.03854994	KRT18	EIF4B
chr12	+(53427305..53427830)	525	1.46883	14	7	7	0	0.04226675	EIF4B	LOC283335
chr12	+(53440352..53441325)	973	0.69993	14	6	8	0.1428571	0.00097289	EIF4B	LOC283335
chr12	+(53457644..53458344)	700	0.12742	14	6	8	0.1428571	0.84915021	TENC1	SPRYD3
chr12	+(53494343..53495043)	700	0.00388	17	9	8	0.0588235	0.000266	IGFBP6	SOAT2
chr12	+(53590568..53591209)	641	3.08111	6	3	3	0	0.05	ZNF740	ITGB7
chr12	+(53647370..53647933)	563	0.69993	11	7	4	0.2727273	0.158	MFSD5	ESPL1
chr12	+(53898236..53899388)	1152	1.46883	14	7	7	0	0.99912744	TARBP2	NPFF
chr12	+(53928092..53928731)	639	1.46883	9	6	3	0.3333333	0.012	NPFF	ATF7
chr12	+(55042078..55042778)	700	3.08111	10	6	4	0.2	0.005	LACRT	DCD
chr12	+(56087705..56088320)	615	3.08111	8	5	3	0.25	0.393	METTL7B	ITGA7
chr12	+(56558846..56559546)	700	0.12742	11	5	6	0.0909091	0.00308495	MYL6	SMARCC2
chr12	+(56572462..56573062)	600	3.08111	6	4	2	0.3333333	0.067	MYL6	SMARCC2
chr12	+(57000146..57000724)	578	0.29741	12	4	8	0.3333333	0.00328926	RBMS2	BAZ2A
chr12	+(57397825..57398376)	551	1.46883	8	3	5	0.25	0.125	GPR182	ZBTB39
chr12	+(57569075..57569933)	858	1.46883	14	7	7	0	0.99912744	LRP1	MIR1228
chr12	+(57602069..57603346)	1277	0.29741	18	9	9	0	0.88338488	MIR1228	NXPH4
chr12	+(58009307..58009852)	545	3.08111	6	2	4	0.3333333	0.067	ARHGEF25	SLC26A10
chr12	+(58021646..58022291)	645	0.06632	11	5	6	0.0909091	0.00308495	SLC26A10	B4GALNT1
chr12	+(63328197..63328891)	694	0.69993	11	7	4	0.2727273	0.885	MIRLET7I	PPM1H
chr12	+(64823616..64824136)	520	3.08111	9	4	5	0.1111111	0.008	XPOT	TBK1
chr12	+(64889974..64890664)	690	1.46883	10	7	3	0.4	0.058	TBK1	RASSF3
chr12	+(65781775..65782475)	700	0.03249	12	7	5	0.1666667	0.00224163	MSRB3	RPSAP52
chr12	+(69339382..69339938)	556	1.46883	8	5	3	0.25	0.018	MDM2	CPM
chr12	+(70959897..70960481)	584	3.08111	12	7	5	0.1666667	0.06144014	KCNMB4	PTPRB
chr12	+(71065937..71066478)	541	3.08111	12	5	7	0.1666667	0.08373231	PTPRB	PTPRR
chr12	+(71286539..71287069)	530	3.08111	9	6	3	0.3333333	0.81	PTPRB	PTPRR
chr12	+(72092479..72092983)	504	3.08111	8	3	5	0.25	0.018	TMEM19	RAB21

chr12	+(72175446..72175961)	515	3.08111	11	5	6	0.0909091	0.00881105	RAB21	TBC1D15
chr12	+(74934754..74935549)	795	0.06632	12	5	7	0.1666667	0.00224163	ATXN7L3B	KCNC2
chr12	+(75435989..75436493)	504	3.08111	6	2	4	0.3333333	0.067	ATXN7L3B	KCNC2
chr12	+(75714812..75715469)	657	0.12742	17	7	10	0.1764706	0.08592868	KCNC2	CAPS2
chr12	+(77222029..77222543)	514	3.08111	8	3	5	0.25	0.018	ZDHHC17	CSRP2
chr12	+(77240177..77240877)	700	0.69993	12	8	4	0.3333333	0.024	ZDHHC17	CSRP2
chr12	+(77449547..77450052)	505	3.08111	9	5	4	0.1111111	0.095	CSRP2	E2F7
chr12	+(78350443..78351143)	700	0.06632	11	6	5	0.0909091	0.00308495	NAV3	SYT1
chr12	+(80208916..80209616)	700	0.12742	10	4	6	0.2	0.005	PAWR	PPP1R12A
chr12	+(80211015..80211536)	521	1.46883	12	7	5	0.1666667	0.04407898	PAWR	PPP1R12A
chr12	+(82750664..82751170)	506	0.65817	18	10	8	0.1111111	0.00642562	PPFIA2	CCDC59
chr12	+(83098959..83099600)	641	3.08111	6	2	4	0.3333333	0.067	TMTC2	SLC6A15
chr12	+(83515379..83516532)	1153	0.06632	20	11	9	0.1	0.99991528	TMTC2	SLC6A15
chr12	+(86198395..86198988)	593	0.69993	10	7	3	0.4	0.058	ALX1	RASSF9
chr12	+(88442844..88443444)	600	0.42719	19	13	6	0.3684211	0.00327517	C12orf29	CEP290
chr12	+(88473742..88474321)	579	0.29741	10	7	3	0.4	0.008	C12orf29	CEP290
chr12	+(88532737..88533257)	520	3.08111	10	7	3	0.4	0.017	C12orf29	CEP290
chr12	+(89894897..89895400)	503	1.46883	12	7	5	0.1666667	0.18587565	DUSP6	POC1B
chr12	+(93792819..93793335)	516	1.46883	10	4	6	0.2	0.019	NUDT4P1	UBE2N
chr12	+(95365057..95365633)	576	1.46883	10	7	3	0.4	0.033	KRT19P2	NDUFA12
chr12	+(95603473..95604051)	578	3.08111	6	4	2	0.3333333	0.067	NR2C1	FGD6
chr12	+(97168430..97169113)	683	3.08111	7	4	3	0.1428571	0.2	CDK17	NEDD1
chr12	+(97300720..97301525)	805	1.46883	13	7	6	0.0769231	0.0013499	CDK17	NEDD1
chr12	+(97469467..97470612)	1145	1.46883	13	7	6	0.0769231	0.9986501	NEDD1	RMST
chr12	+(98994720..98995246)	526	0.69993	15	8	7	0.0666667	0.00190677	SNORA53	IKBIP
chr12	+(99135045..99135595)	550	1.46883	7	3	4	0.1428571	0.029	APAF1	ANKS1B
chr12	+(100566811..100567375)	564	3.08111	6	2	4	0.3333333	0.067	UHRF1BP1L	GOLGA2B
chr12	+(101472733..101473280)	547	1.46883	7	4	3	0.1428571	0.029	ANO4	SLC5A8
chr12	+(101522713..101523413)	700	0.29741	13	4	9	0.3846154	0.001	ANO4	SLC5A8
chr12	+(102155315..102155851)	536	3.08111	9	6	3	0.3333333	0.274	SYCP3	GNPTAB
chr12	+(102313576..102314207)	631	3.08111	10	5	5	0	0.0081468	DRAM1	CCDC53
chr12	+(104252785..104253308)	523	3.08111	6	2	4	0.3333333	0.067	NT5DC3	GNN
chr12	+(104496546..104497134)	588	3.08111	9	3	6	0.3333333	0.048	HCFC2	NFYB
chr12	+(105124130..105124817)	687	1.46883	7	4	3	0.1428571	0.029	MIR3922	SLC41A2

chr12	+(105845246..105845890)	644	0.12742	10	5	5	0	0.00451172	C12orf75	NUAK1
chr12	+(106460080..106460588)	508	3.08111	10	6	4	0.2	0.005	C12orf75	NUAK1
chr12	+(106760009..106760605)	596	1.46883	9	3	6	0.3333333	0.012	POLR3B	RFX4
chr12	+(107214673..107216036)	1363	0.69993	15	5	10	0.3333333	0.9669037	RIC8B	C12orf23
chr12	+(108013558..108014073)	515	3.08111	8	3	5	0.25	0.714	BTBD11	PWP1
chr12	+(108909917..108910506)	589	3.08111	6	3	3	0	0.05	FICD	SART3
chr12	+(109109612..109110275)	663	3.08111	9	6	3	0.3333333	0.988	SELPLG	CORO1C
chr12	+(109132775..109133475)	700	0.06632	11	6	5	0.0909091	0.00308495	CORO1C	SSH1
chr12	+(109182437..109182938)	501	0.69993	13	7	6	0.0769231	0.84134475	CORO1C	SSH1
chr12	+(109204345..109205001)	656	0.29741	9	4	5	0.1111111	0.008	CORO1C	SSH1
chr12	+(109504876..109505546)	670	1.46883	10	7	3	0.4	0.008	USP30	ALKBH2
chr12	+(109696254..109696938)	684	3.08111	6	2	4	0.3333333	0.067	ACACB	FOXN4
chr12	+(110243147..110244018)	871	4.2E-05	23	7	16	0.3913043	9.1405E-05	MGC14436	TRPV4
chr12	+(110290279..110290817)	538	3.08111	9	5	4	0.1111111	0.056	TRPV4	GLTP
chr12	+(110340472..110340990)	518	0.12742	14	5	9	0.2857143	0.0013499	TCHP	GIT2
chr12	+(111057359..111058035)	676	3.08111	6	4	2	0.3333333	0.067	TCTN1	HVCN1
chr12	+(111087535..111088118)	583	1.46883	7	4	3	0.1428571	0.029	TCTN1	HVCN1
chr12	+(111375767..111376458)	691	1.46883	7	4	3	0.1428571	0.029	LOC100131138	CUX2
chr12	+(111490568..111491174)	606	1.46883	11	7	4	0.2727273	0.003	CUX2	FAM109A
chr12	+(111516365..111516930)	565	0.69993	8	5	3	0.25	0.018	CUX2	FAM109A
chr12	+(111706337..111706877)	540	3.08111	6	4	2	0.3333333	0.067	CUX2	FAM109A
chr12	+(111714367..111715055)	688	3.08111	11	5	6	0.0909091	0.00308495	CUX2	FAM109A
chr12	+(111799387..111800493)	1106	0.03249	21	7	14	0.3333333	0.16605784	CUX2	FAM109A
chr12	+(111926107..111926742)	635	1.46883	10	3	7	0.4	0.033	SH2B3	ATXN2
chr12	+(112614349..112614971)	622	1.46883	11	7	4	0.2727273	0.794	TRAFD1	C12orf51
chr12	+(112926054..112926573)	519	3.08111	8	5	3	0.25	0.018	PTPN11	RPH3A
chr12	+(113541703..113542357)	654	0.12742	10	5	5	0	0.00451172	DTX1	RASAL1
chr12	+(113616856..113617409)	553	0.12742	10	5	5	0	0.00451172	CCDC42B	DDX54
chr12	+(113734412..113734999)	587	3.08111	9	3	6	0.3333333	0.012	TPCN1	SLC24A6
chr12	+(113966282..113966832)	550	0.12742	10	6	4	0.2	0.005	LHX5	RBM19
chr12	+(114123351..114123991)	640	0.29741	9	4	5	0.1111111	0.008	LHX5	RBM19
chr12	+(114200060..114200752)	692	0.69993	8	4	4	0	0.014	LHX5	RBM19
chr12	+(114377235..114378553)	1318	0.69993	18	10	8	0.1111111	0.99981036	LHX5	RBM19
chr12	+(116446467..116447050)	583	0.12742	15	8	7	0.0666667	0.17726974	TBX3	MED13L

chr12	+(117465946..117466499)	553	3.08111	6	4	2	0.3333333	0.067	FBXW8	TESC
chr12	+(117723650..117724198)	548	3.08111	9	4	5	0.1111111	0.548	FBXO21	NOS1
chr12	+(117797159..117798325)	1166	0.12742	19	9	10	0.0526316	0.00011928	FBXO21	NOS1
chr12	+(117992823..117993338)	515	3.08111	10	7	3	0.4	0.058	NOS1	KSR2
chr12	+(119909619..119910335)	716	0.29741	17	11	6	0.2941176	0.3815123	CCDC60	TMEM233
chr12	+(120222861..120223561)	700	0.00834	15	9	6	0.2	0.01694743	PRKAB1	CIT
chr12	+(120530067..120531227)	1160	0.29741	17	10	7	0.1764706	0.00089545	CCDC64	RAB35
chr12	+(120534874..120535430)	556	3.08111	9	3	6	0.3333333	0.048	CCDC64	RAB35
chr12	+(120549540..120550240)	700	3.08111	11	6	5	0.0909091	0.00308495	CCDC64	RAB35
chr12	+(120599072..120599577)	505	3.08111	8	3	5	0.25	0.5	RAB35	GCN1L1
chr12	+(120759641..120760215)	574	3.08111	9	3	6	0.3333333	0.024	SIRT4	PLA2G1B
chr12	+(120762602..120763105)	503	3.08111	7	3	4	0.1428571	0.029	SIRT4	PLA2G1B
chr12	+(121435335..121435842)	507	3.08111	9	4	5	0.1111111	0.143	HNF1A	C12orf43
chr12	+(121470827..121471513)	686	3.08111	13	7	6	0.0769231	0.01606229	C12orf43	OASL
chr12	+(121947409..121947976)	567	1.46883	10	7	3	0.4	0.992	RNF34	KDM2B
chr12	+(121968515..121969208)	693	1.46883	7	3	4	0.1428571	0.029	RNF34	KDM2B
chr12	+(122208331..122208973)	642	1.46883	7	3	4	0.1428571	0.029	TMEM120B	RHOF
chr12	+(122252775..122253371)	596	0.69993	9	3	6	0.3333333	0.083	SETD1B	HPD
chr12	+(122691409..122692109)	700	0.29741	12	7	5	0.1666667	0.28488218	B3GNT4	DIABLO
chr12	+(122803660..122804239)	579	1.46883	10	7	3	0.4	0.008	VPS33A	CLIP1
chr12	+(122861971..122862537)	566	1.46883	14	9	5	0.2857143	0.02659758	VPS33A	CLIP1
chr12	+(122957794..122958333)	539	0.12742	10	3	7	0.4	0.008	CLIP1	ZCCHC8
chr12	+(123001525..123002073)	548	0.69993	12	5	7	0.1666667	0.02117853	ZCCHC8	RSRC2
chr12	+(123006560..123007195)	635	1.46883	12	6	6	0	0.16833419	ZCCHC8	RSRC2
chr12	+(123035553..123036229)	676	1.46883	10	3	7	0.4	0.017	KNTC1	GPR109A
chr12	+(123343974..123344623)	649	1.46883	10	6	4	0.2	0.129	HIP1R	VPS37B
chr12	+(123358513..123359213)	700	0.01356	13	6	7	0.0769231	0.0013499	HIP1R	VPS37B
chr12	+(123472009..123472709)	700	3.08111	10	3	7	0.4	0.867	ARL6IP4	PITPNM2
chr12	+(123497062..123497762)	700	0.29741	10	3	7	0.4	0.258	ARL6IP4	PITPNM2
chr12	+(123685920..123686529)	609	1.46883	10	7	3	0.4	0.992	MIR4304	MPHOSPH9
chr12	+(123728752..123729321)	569	3.08111	6	4	2	0.3333333	0.067	C12orf65	CDK2AP1
chr12	+(123950847..123951395)	548	3.08111	11	6	5	0.0909091	0.97769514	SNRNP35	RILPL1
chr12	+(123968567..123969069)	502	3.08111	7	3	4	0.1428571	0.029	SNRNP35	RILPL1
chr12	+(124177035..124177538)	503	3.08111	8	5	3	0.25	0.286	TCTN2	ATP6V0A2

chr12	+(124209419..124210119)	700	0.69993	9	6	3	0.3333333	0.274	ATP6V0A2	DNAH10	
chr12	+(124497485..124498185)	700	0.00834	18	6	12	0.3333333	0.28707454	ZNF664	FAM101A	
chr12	+(124785626..124786270)	644	0.12742	10	3	7	0.4	0.008	FAM101A	NCOR2	
chr12	+(124802436..124803136)	700	1.46883	11	4	7	0.2727273	0.003	FAM101A	NCOR2	
chr12	+(124937497..124938020)	523	0.12742	10	4	6	0.2	0.005	FAM101A	NCOR2	
chr12	+(124942853..124943469)	616	3.08111	11	6	5	0.0909091	0.99691505	FAM101A	NCOR2	
chr12	+(124970651..124971282)	631	0.12742	12	5	7	0.1666667	0.00224163	FAM101A	NCOR2	
chr12	+(125038743..125039443)	700	1.46883	9	4	5	0.1111111	0.008	FAM101A	NCOR2	
chr12	+(125184232..125184932)	700	0.12742	15	5	10	0.3333333	0.00109982	NCOR2	SCARB1	
chr12	+(125291257..125291821)	564	3.08111	6	4	2	0.3333333	0.067	NCOR2	SCARB1	
chr12	+(125398678..125399614)	936	0.29741	15	6	9	0.2	0.00073136	SCARB1	UBC	
chr12	+(128865907..128866571)	664	3.08111	6	2	4	0.3333333	0.067	MIR3612	SLC15A4	
chr12	+(129181338..129182033)	695	3.08111	10	4	6	0.2	0.005	MIR3612	SLC15A4	
chr12	+(129396214..129396761)	547	1.46883	7	3	4	0.1428571	0.029	GLT1D1	TMEM132D	
chr12	+(129462681..129463300)	619	0.29741	9	4	5	0.1111111	0.008	GLT1D1	TMEM132D	
chr12	+(130649959..130650488)	529	3.08111	11	6	5	0.0909091	0.07206352	FZD10	PIWIL1	v
chr12	+(131363607..131364958)	1351	0.12742	16	10	6	0.25	0.99943095	RAN	GPR133	
chr12	+(131436389..131437314)	925	3.08111	12	6	6	0	0.00197388	RAN	GPR133	
chr12	+(131550253..131551537)	1284	0.00388	23	8	15	0.3043478	5.3756E-05	GPR133	LOC116437	
chr12	+(131914662..131915243)	581	3.08111	6	3	3	0	0.05	LOC116437	SFSWAP	
chr12	+(132177391..132178091)	700	0.69993	13	6	7	0.0769231	0.97724986	LOC116437	SFSWAP	
chr12	+(132221223..132222051)	828	3.08111	12	4	8	0.3333333	0.00328926	SFSWAP	MMP17	
chr12	+(132402886..132403586)	700	0.03249	12	8	4	0.3333333	0.99671074	ULK1	PUS1	
chr12	+(132497929..132498596)	667	0.69993	11	7	4	0.2727273	0.115	EP400	SNORA49	
chr12	+(132501983..132502518)	535	4.85899	14	6	8	0.1428571	0.00097289	EP400	SNORA49	
chr12	+(132592594..132593305)	711	0.03249	12	6	6	0	0.00197388	EP400NL	DDX51	
chr12	+(132670868..132672413)	1545	1.46883	19	7	12	0.2631579	0.99980713	NOC4L	GALNT9	
chr12	+(132824361..132825034)	673	0.69993	8	3	5	0.25	0.018	NOC4L	GALNT9	
chr12	+(132844124..132845057)	933	0.01356	24	13	11	0.0833333	0.00035037	NOC4L	GALNT9	
chr12	+(132856746..132857446)	700	0.12742	10	4	6	0.2	0.005	NOC4L	GALNT9	
chr12	+(132890862..132891897)	1035	0.03249	19	7	12	0.2631579	0.99980713	NOC4L	GALNT9	
chr12	+(132939491..132940321)	830	0.00101	17	9	8	0.0588235	0.000266	LOC100130238	FBRSL1	
chr12	+(133013511..133014211)	700	3.08111	11	6	5	0.0909091	0.00308495	LOC100130238	FBRSL1	
chr12	+(133114483..133115183)	700	0.06632	12	4	8	0.3333333	0.00328926	FBRSL1	LOC645277	

chr12	+(133280951..133281453)	502	3.08111	9	4	5	0.1111111	0.008	PXMP2	PGAM5	
chr12	+(133315952..133317168)	1216	0.12742	16	6	10	0.25	0.74240941	PGAM5	ANKLE2	
chr12	+(133445998..133446683)	685	1.46883	8	4	4	0	0.014	GOLGA3	CHFR	
chr12	+(133501828..133502355)	527	1.46883	8	4	4	0	0.171	CHFR	ZNF605	
chr12	+(133521951..133522478)	527	0.29741	11	7	4	0.2727273	0.006	CHFR	ZNF605	
chr13	+(19750829..19751381)	552	2.82415	10	4	6	0.2	0.129	PHF2P1	TUBA3C	
chr13	+(20006470..20007096)	626	2.82415	9	6	3	0.3333333	0.048	LOC100287114	TPTE2	
chr13	+(20117331..20118020)	689	2.82415	6	2	4	0.3333333	0.067	TPTE2	MPHOSPH8	
chr13	+(20276984..20277521)	537	1.26257	10	3	7	0.4	0.033	MPHOSPH8	PSPC1	
chr13	+(20325340..20325992)	652	0.63564	14	9	5	0.2857143	0.04779036	MPHOSPH8	PSPC1	
chr13	+(20579280..20579783)	503	2.82415	9	6	3	0.3333333	0.548	ZMYM2	GJA3	
chr13	+(21233627..21234830)	1203	0.11848	19	9	10	0.0526316	0.99988072	IFT88	IL17D	
chr13	+(21741842..21742432)	590	0.26487	14	5	9	0.2857143	0.27425312	SAP18	SKA3	
chr13	+(21999353..21999887)	534	0.63564	14	6	8	0.1428571	0.15084979	MRP63	ZDHHC20	
chr13	+(24436108..24436839)	731	0.05597	12	5	7	0.1666667	0.00591469	TNFRSF19	MIPEP	
chr13	+(24470799..24471309)	510	2.82415	6	3	3	0	0.05	PCOTH	C1QTNF9B	
chr13	+(24833087..24833709)	622	2.82415	6	3	3	0	0.05	MIR2276	C1QTNF9	
chr13	+(26548360..26549060)	700	2.82415	10	4	6	0.2	0.995	ATP8A2	SHISA2	
chr13	+(28014268..28014776)	508	2.82415	6	2	4	0.3333333	0.067	GTF3A	MTIF3	
chr13	+(30003056..30003566)	510	2.82415	9	6	3	0.3333333	0.012	MTUS2	SLC7A1	
chr13	+(31175907..31176672)	765	0.00952	13	6	7	0.0769231	0.0013499	HMGB1	USPL1	
chr13	+(31191559..31192238)	679	2.82415	6	4	2	0.3333333	0.067	HMGB1	USPL1	
chr13	+(31891360..31892060)	700	0.26487	10	3	7	0.4	0.008	B3GALTL	RXFP2	
chr13	+(32360533..32361161)	628	1.26257	10	7	3	0.4	0.192	RXFP2	EEF1DP3	
chr13	+(32913332..32913944)	612	2.82415	11	4	7	0.2727273	0.082	BRCA2	N4BP2L1	
chr13	+(33016939..33017445)	506	1.26257	8	3	5	0.25	0.018	N4BP2L1	N4BP2L2	
chr13	+(35740092..35740792)	700	0.26487	13	9	4	0.3846154	0.999	NBEA	MAB21L1	v
chr13	+(37678688..37679325)	637	0.11968	23	14	9	0.2173913	0.09293837	FAM48A	CSNK1A1L	
chr13	+(37679368..37680038)	670	0.63564	9	4	5	0.1111111	0.095	FAM48A	CSNK1A1L	
chr13	+(38166117..38166717)	600	2.82415	10	6	4	0.2	0.381	CSNK1A1L	POSTN	
chr13	+(40253907..40254509)	602	0.63564	12	8	4	0.3333333	0.024	MIR4305	FLJ42392	
chr13	+(40794121..40794659)	538	2.82415	6	2	4	0.3333333	0.067	MIR4305	FLJ42392	
chr13	+(41517825..41518327)	502	2.82415	10	4	6	0.2	0.005	MIR621	ELF1	
chr13	+(41566773..41567548)	775	0.05597	14	6	8	0.1428571	0.01943355	MIR621	ELF1	

chr13	+(45515109..45515676)	567	2.82415	10	4	6	0.2	0.057	TSC22D1	NUFIP1
chr13	+(47466254..47466849)	595	2.82415	10	5	5	0	0.00451172	ESD	HTR2A
chr13	+(48523449..48523989)	540	1.26257	8	4	4	0	0.014	HTR2A	SUCLA2
chr13	+(49918086..49918621)	535	1.26257	8	4	4	0	0.014	CDADC1	CAB39L
chr13	+(50254080..50254742)	662	2.82415	10	6	4	0.2	0.005	ARL11	EBPL
chr13	+(52989965..52990521)	556	1.26257	11	6	5	0.0909091	0.03394459	THSD1	VPS36
chr13	+(53233163..53233727)	564	2.82415	6	2	4	0.3333333	0.067	SUGT1	LECT1
chr13	+(73327651..73328175)	524	2.82415	7	3	4	0.1428571	0.029	C13orf34	DIS3
chr13	+(73351250..73351950)	700	0.63564	11	4	7	0.2727273	0.003	C13orf34	DIS3
chr13	+(75814182..75814697)	515	2.20716	31	16	15	0.0322581	0.00011839	LOC338864	CTAGE11P
chr13	+(79190670..79191177)	507	2.82415	11	4	7	0.2727273	0.082	POU4F1	RNF219
chr13	+(79942833..79943502)	669	1.26257	10	7	3	0.4	0.192	RNF219	RBM26
chr13	+(96415914..96416444)	530	0.63564	12	6	6	0	0.02733197	DNAJC3	UGGT2
chr13	+(98642393..98643093)	700	0.63564	10	3	7	0.4	0.033	IPO5	FARP1
chr13	+(99173784..99174386)	602	2.82415	9	3	6	0.3333333	0.048	MIR3170	STK24
chr13	+(99195605..99196520)	915	1.26257	16	9	7	0.125	0.03198447	MIR3170	STK24
chr13	+(99479630..99480304)	674	2.82415	6	4	2	0.3333333	0.067	SLC15A1	DOCK9
chr13	+(101020558..101021139)	581	1.26257	9	6	3	0.3333333	0.012	PCCA	A2LD1
chr13	+(101199593..101200708)	1115	0.63564	16	8	8	0	0.99961123	PCCA	A2LD1
chr13	+(102527318..102527843)	525	2.82415	6	2	4	0.3333333	0.067	ITGBL1	FGF14
chr13	+(103400006..103400508)	502	2.82415	13	6	7	0.0769231	0.23752526	C13orf39	C13orf40
chr13	+(103400973..103401498)	525	1.26257	10	4	6	0.2	0.238	C13orf39	C13orf40
chr13	+(103442191..103442891)	700	2.82415	9	3	6	0.3333333	0.988	C13orf27	KDELC1
chr13	+(107196213..107196733)	520	2.82415	12	4	8	0.3333333	0.00328926	EFNB2	ARGLU1
chr13	+(109758834..109759534)	700	0.02363	12	4	8	0.3333333	0.00328926	MYO16	IRS2
chr13	+(109814099..109814965)	866	0.02363	12	6	6	0	0.00197388	MYO16	IRS2
chr13	+(110855061..110855758)	697	2.82415	9	6	3	0.3333333	0.988	IRS2	COL4A1
chr13	+(111121297..111121989)	692	0.63564	10	3	7	0.4	0.008	COL4A2	RAB20
chr13	+(111304575..111305302)	727	0.00266	15	10	5	0.3333333	0.00109982	CARKD	CARS2
chr13	+(112725595..112726148)	553	2.82415	9	3	6	0.3333333	0.726	SOX1	C13orf28
chr13	+(113445374..113446074)	700	0.26487	9	3	6	0.3333333	0.012	ATP11A	LOC100289410
chr13	+(113571079..113571671)	592	0.26487	9	5	4	0.1111111	0.008	ATP11A	LOC100289410
chr13	+(113592471..113593049)	578	2.82415	10	6	4	0.2	0.543	ATP11A	LOC100289410
chr13	+(113633626..113634350)	724	7.9E-05	23	13	10	0.1304348	0.00025736	MCF2L	F7

chr13	+(114309894..114310549)	655	0.0016	16	7	9	0.125	0.00042755	TFDP1	ATP4B
chr13	+(114549015..114549587)	572	0.63564	8	5	3	0.25	0.018	FAM70B	GAS6
chr13	+(114631889..114632550)	661	1.26257	7	3	4	0.1428571	0.029	FLJ44054	RASA3
chr13	+(114774872..114775443)	571	2.82415	6	4	2	0.3333333	0.067	FLJ44054	RASA3
chr13	+(114823376..114823915)	539	2.82415	8	4	4	0	0.443	FLJ44054	RASA3
chr13	+(114891536..114892065)	529	0.63564	8	4	4	0	0.014	FLJ44054	RASA3
chr14	+(19434041..19434751)	710	0.00434	45	16	29	0.2888889	0.00087441	OR11H12	POTEG
chr14	+(19563062..19564069)	1007	0.2625	35	22	13	0.2571429	0.04391365	POTEG	POTEM
chr14	+(19640834..19642213)	1379	0.2625	16	7	9	0.125	0.99957245	POTEG	POTEM
chr14	+(19806155..19807508)	1353	0.01375	95	43	52	0.0947368	0.64851699	POTEG	POTEM
chr14	+(19855054..19855573)	519	2.74666	10	7	3	0.4	0.5	POTEG	POTEM
chr14	+(20248689..20249346)	657	0.43643	49	24	25	0.0204082	0.18942966	OR4M1	OR4N2
chr14	+(20295529..20296581)	1052	0.18178	46	30	16	0.3043478	0.03787697	OR4M1	OR4N2
chr14	+(20302509..20303090)	581	1.21459	7	4	3	0.1428571	0.029	OR4N2	OR4K2
chr14	+(20711154..20711662)	508	2.74666	10	4	6	0.2	0.457	OR11H4	TTC5
chr14	+(21168212..21168721)	509	2.74666	10	4	6	0.2	0.238	RNASE4	EDDM3A
chr14	+(21519311..21520162)	851	0.00309	15	7	8	0.0666667	0.00059687	RNASE7	RNASE8
chr14	+(21526030..21526621)	591	2.74666	7	4	3	0.1428571	0.029	RNASE7	RNASE8
chr14	+(21569304..21569879)	575	0.53491	8	4	4	0	0.014	ARHGEF40	ZNF219
chr14	+(21895833..21896521)	688	0.2625	17	11	6	0.2941176	0.0222116	SUPT16H	CHD8
chr14	+(21963265..21963774)	509	2.74666	6	2	4	0.3333333	0.067	TOX4	METTL3
chr14	+(21993368..21994026)	658	0.2625	10	6	4	0.2	0.129	METTL3	SALL2
chr14	+(23858105..23858616)	511	2.74666	8	5	3	0.25	0.018	CMTM5	MYH6
chr14	+(23893132..23893774)	642	2.74666	11	6	5	0.0909091	0.70805879	MIR208A	MYH7
chr14	+(23901734..23902235)	501	2.74666	9	5	4	0.1111111	0.056	MIR208A	MYH7
chr14	+(24517633..24518749)	1116	2.52785	45	19	26	0.1555556	7.8231E-07	DHRS4L1	LRRC16B
chr14	+(24521830..24523091)	1261	0.2625	19	8	11	0.1578947	0.02375447	LRRC16B	CPNE6
chr14	+(24569123..24569633)	510	2.74666	7	3	4	0.1428571	0.029	PCK2	DCAF11
chr14	+(24792024..24792623)	599	0.00507	15	7	8	0.0666667	0.00089011	LTB4R	ADCY4
chr14	+(24869007..24869707)	700	0.2625	9	3	6	0.3333333	0.012	NYNRIN	CBLN3
chr14	+(24884882..24885420)	538	1.21459	11	7	4	0.2727273	0.979	NYNRIN	CBLN3
chr14	+(25076469..25077120)	651	2.74666	9	3	6	0.3333333	0.048	CTSG	GZMH
chr14	+(31597751..31598389)	638	1.21459	10	6	4	0.2	0.238	AP4S1	HECTD1
chr14	+(32062260..32062937)	677	0.2625	9	5	4	0.1111111	0.008	NUBPL	C14orf128

chr14	+(34155088..34155788)	700	0.07261	11	7	4	0.2727273	0.003	NPAS3	EGLN3	v
chr14	+(35554793..35555368)	575	0.53491	8	3	5	0.25	0.018	FAM177A1	PPP2R3C	
chr14	+(35777843..35778548)	705	0.00176	19	13	6	0.3684211	0.0003125	PSMA6	NFKBIA	
chr14	+(35815710..35816665)	955	1.21459	16	8	8	0	0.07074106	PSMA6	NFKBIA	
chr14	+(39648407..39648955)	548	0.2625	17	9	8	0.0588235	0.00103778	PNN	MIA2	
chr14	+(39649510..39650028)	518	1.21459	13	6	7	0.0769231	0.84134475	PNN	MIA2	
chr14	+(39684079..39684676)	597	1.21459	10	3	7	0.4	0.583	PNN	MIA2	
chr14	+(39745773..39746571)	798	0.53491	18	8	10	0.1111111	0.00821967	CTAGE5	FBXO33	
chr14	+(39817782..39818304)	522	1.21459	9	3	6	0.3333333	0.19	CTAGE5	FBXO33	
chr14	+(39855347..39855959)	612	1.21459	11	7	4	0.2727273	0.082	CTAGE5	FBXO33	
chr14	+(45506795..45507470)	675	0.07261	11	4	7	0.2727273	0.003	FAM179B	PRPF39	
chr14	+(45605141..45605724)	583	1.21459	12	5	7	0.1666667	0.06144014	FANCM	C14orf106	
chr14	+(45654066..45654643)	577	2.74666	11	5	6	0.0909091	0.02230486	FANCM	C14orf106	
chr14	+(45674944..45675568)	624	2.74666	9	4	5	0.1111111	0.032	FANCM	C14orf106	
chr14	+(45693386..45694067)	681	0.2625	14	6	8	0.1428571	0.01006838	FANCM	C14orf106	
chr14	+(50121332..50121864)	532	2.74666	9	6	3	0.3333333	0.274	C14orf104	POLE2	
chr14	+(50154740..50155966)	1226	0.53491	14	8	6	0.1428571	0.99902711	C14orf104	POLE2	
chr14	+(50192269..50192875)	606	2.74666	9	6	3	0.3333333	0.274	KLHDC1	KLHDC2	
chr14	+(50251078..50251586)	508	1.21459	10	6	4	0.2	0.005	KLHDC2	SDCCAG1	
chr14	+(50294571..50295222)	651	0.01043	23	9	14	0.2173913	0.00278788	KLHDC2	SDCCAG1	
chr14	+(50363102..50363647)	545	0.53491	11	6	5	0.0909091	0.03394459	ARF6	C14orf182	
chr14	+(50612146..50612749)	603	0.12133	15	9	6	0.2	0.03854994	C14orf138	SOS2	
chr14	+(50626322..50626830)	508	2.74666	11	5	6	0.0909091	0.10062131	C14orf138	SOS2	
chr14	+(51131495..51132517)	1022	0.02438	45	24	21	0.0666667	0.02030103	ATL1	SAV1	
chr14	+(51224545..51225054)	509	2.74666	8	3	5	0.25	0.036	SAV1	NIN	
chr14	+(51382149..51382703)	554	0.07261	12	4	8	0.3333333	0.00328926	ABHD12B	PYGL	
chr14	+(51560400..51561511)	1111	1.21459	15	9	6	0.2	0.00666417	PYGL	TRIM9	
chr14	+(51713690..51714214)	524	2.74666	8	5	3	0.25	0.018	TMX1	FRMD6	
chr14	+(53187636..53188145)	509	1.21459	8	4	4	0	0.014	PSMC6	STYX	
chr14	+(55510282..55511615)	1333	0.53491	25	16	9	0.28	0.000224	SOCS4	MAPK1IP1L	
chr14	+(55641867..55642498)	631	2.74666	10	6	4	0.2	0.057	LGALS3	DLGAP5	
chr14	+(58478525..58479125)	600	2.74666	10	4	6	0.2	0.033	SLC35F4	C14orf37	
chr14	+(58770084..58770684)	600	2.74666	9	6	3	0.3333333	0.548	ARID4A	TOMM20L	
chr14	+(58833449..58834150)	701	0.2625	17	8	9	0.0588235	0.06182886	ARID4A	TOMM20L	

chr14	+(59954292..59954954)	662	1.21459	12	7	5	0.1666667	0.00591469	JKAMP	C14orf38
chr14	+(60584948..60585494)	546	0.53491	14	6	8	0.1428571	0.00097289	C14orf135	DHRS7
chr14	+(61234038..61234634)	596	1.21459	7	4	3	0.1428571	0.029	MNAT1	TRMT5
chr14	+(61449153..61449685)	532	1.21459	10	6	4	0.2	0.057	SLC38A6	TMEM30B
chr14	+(61512591..61513291)	700	0.2625	11	7	4	0.2727273	0.003	SLC38A6	TMEM30B
chr14	+(63733444..63733953)	509	1.21459	7	4	3	0.1428571	0.029	RHOJ	GPHB5
chr14	+(63784294..63784851)	557	1.21459	9	3	6	0.3333333	0.274	RHOJ	GPHB5
chr14	+(64613932..64614629)	697	2.74666	9	6	3	0.3333333	0.012	SYNE2	ESR2
chr14	+(65047036..65048120)	1084	0.53491	16	8	8	0	0.00038877	C14orf50	PLEKHG3
chr14	+(65193652..65194871)	1219	0.53491	14	6	8	0.1428571	0.00097289	PLEKHG3	SPTB
chr14	+(65550633..65551184)	551	1.21459	8	4	4	0	0.014	FNTB	MAX
chr14	+(65704719..65705353)	634	0.53491	8	5	3	0.25	0.018	MAX	LOC645431
chr14	+(67671096..67671724)	628	0.53491	11	7	4	0.2727273	0.206	FAM71D	MPP5
chr14	+(68028399..68029037)	638	0.53491	15	9	6	0.2	0.63816319	PLEKHH1	PIGH
chr14	+(68035723..68036282)	559	0.01043	13	8	5	0.2307692	0.0017074	PLEKHH1	PIGH
chr14	+(68252473..68253047)	574	0.12133	10	6	4	0.2	0.005	RDH12	ZFYVE26
chr14	+(68582538..68583058)	520	2.54189	27	16	11	0.1851852	0.16183909	RAD51L1	ZFP36L1
chr14	+(69144691..69145391)	700	0.07261	12	7	5	0.1666667	0.00224163	RAD51L1	ZFP36L1
chr14	+(69560875..69561403)	528	0.53491	8	3	5	0.25	0.018	ACTN1	DCAF5
chr14	+(69792416..69793223)	807	0.00309	16	8	8	0	0.00585934	GALNTL1	ERH
chr14	+(70454358..70454917)	559	2.74666	6	2	4	0.3333333	0.067	SMOC1	SLC8A3
chr14	+(71269441..71269950)	509	0.2625	13	8	5	0.2307692	0.0017074	TTC9	MAP3K9
chr14	+(71500602..71501165)	563	2.74666	9	6	3	0.3333333	0.083	PCNX	SNORD56B
chr14	+(71631734..71632255)	521	1.21459	10	3	7	0.4	0.992	PCNX	SNORD56B
chr14	+(71648013..71648673)	660	2.74666	6	2	4	0.3333333	0.067	PCNX	SNORD56B
chr14	+(71850184..71850806)	622	2.74666	6	4	2	0.3333333	0.067	PCNX	SNORD56B
chr14	+(72944668..72945215)	547	0.53491	8	5	3	0.25	0.018	RGS6	DPF3
chr14	+(73075738..73076438)	700	0.07261	11	4	7	0.2727273	0.003	RGS6	DPF3
chr14	+(73268709..73269296)	587	0.2625	9	4	5	0.1111111	0.008	RGS6	DPF3
chr14	+(73366454..73367028)	574	0.2625	9	5	4	0.1111111	0.008	DPF3	DCAF4
chr14	+(73578763..73579350)	587	2.74666	10	6	4	0.2	0.176	RBM25	PSEN1
chr14	+(73950360..73950938)	578	0.53491	8	3	5	0.25	0.018	NUMB	HEATR4
chr14	+(75078842..75079473)	631	0.2625	9	4	5	0.1111111	0.008	ISCA2	LTBP2
chr14	+(75190067..75190658)	591	2.74666	10	3	7	0.4	0.583	FCF1	YLPM1

chr14	+(75265950..75266472)	522	2.74666	11	4	7	0.2727273	0.676	YLPM1	PROX2
chr14	+(75515181..75515758)	577	0.53491	14	8	6	0.1428571	0.15084979	EIF2B2	MLH3
chr14	+(75989946..75990462)	516	0.53491	8	4	4	0	0.014	BATF	FLVCR2
chr14	+(76965909..76966609)	700	0.2625	11	4	7	0.2727273	0.006	ESRRB	VASH1
chr14	+(77120905..77121605)	700	0.53491	12	8	4	0.3333333	0.99671074	ESRRB	VASH1
chr14	+(77246837..77247452)	615	0.2625	14	7	7	0	0.91014375	VASH1	ANGEL1
chr14	+(77247561..77248145)	584	1.21459	7	4	3	0.1428571	0.029	VASH1	ANGEL1
chr14	+(77687805..77688397)	592	0.2625	13	9	4	0.3846154	0.001	TMEM63C	NGB
chr14	+(77722793..77723357)	564	2.74666	6	2	4	0.3333333	0.067	TMEM63C	NGB
chr14	+(78397842..78398418)	576	2.74666	6	3	3	0	0.05	ADCK1	NRXN3
chr14	+(79075104..79075796)	692	2.74666	11	6	5	0.0909091	0.99691505	NRXN3	DIO2
chr14	+(81743165..81743675)	510	2.74666	7	4	3	0.1428571	0.029	SNORA79	STON2
chr14	+(85997547..85998247)	700	0.07261	14	9	5	0.2857143	0.15865525	FLRT2	GALC
chr14	+(86120996..86121782)	786	1.3E-05	22	13	9	0.1818182	4.6818E-05	FLRT2	GALC
chr14	+(86856665..86857327)	662	2.74666	9	6	3	0.3333333	0.988	FLRT2	GALC
chr14	+(90754207..90754892)	685	0.2625	10	6	4	0.2	0.019	PSMC1	C14orf102
chr14	+(90839659..90841005)	1346	0.12133	18	8	10	0.1111111	0.99981036	C14orf102	CALM1
chr14	+(91000554..91001088)	534	0.07261	11	6	5	0.0909091	0.00308495	LOC400238	TTC7B
chr14	+(91018610..91019310)	700	0.0305	20	11	9	0.1	0.90816507	LOC400238	TTC7B
chr14	+(91019752..91020341)	589	0.53491	8	4	4	0	0.014	LOC400238	TTC7B
chr14	+(91043786..91044319)	533	2.74666	6	4	2	0.3333333	0.067	LOC400238	TTC7B
chr14	+(91404655..91405195)	540	1.21459	7	3	4	0.1428571	0.029	TTC7B	RPS6KA5
chr14	+(91759506..91760111)	605	0.2625	10	5	5	0	0.00451172	GPR68	CCDC88C
chr14	+(91836792..91837435)	643	0.53491	8	5	3	0.25	0.018	GPR68	CCDC88C
chr14	+(91928254..91928794)	540	2.74666	8	4	4	0	0.014	CCDC88C	SMEK1
chr14	+(91931402..91932009)	607	2.74666	6	4	2	0.3333333	0.067	CCDC88C	SMEK1
chr14	+(92493289..92494151)	862	8E-06	43	27	16	0.255814	1.6734E-06	FBLN5	TRIP11
chr14	+(92604300..92605093)	793	0.0305	20	11	9	0.1	0.00438241	CPSF2	SLC24A4
chr14	+(92777415..92778079)	664	0.53491	8	3	5	0.25	0.018	CPSF2	SLC24A4
chr14	+(93081389..93082089)	700	0.12133	10	7	3	0.4	0.008	RIN3	LGMN
chr14	+(93177758..93178265)	507	2.74666	8	3	5	0.25	0.018	RIN3	LGMN
chr14	+(93179849..93180377)	528	2.74666	7	3	4	0.1428571	0.2	RIN3	LGMN
chr14	+(93460542..93461243)	701	0.00507	14	9	5	0.2857143	0.0013499	CHGA	ITPK1
chr14	+(93540103..93540812)	709	0.0305	15	8	7	0.0666667	0.00059687	CHGA	ITPK1

chr14	+(93753105..93753800)	695	1.21459	10	7	3	0.4	0.992	UBR7	BTBD7
chr14	+(94394189..94394696)	507	1.21459	11	7	4	0.2727273	0.536	FAM181A	ASB2
chr14	+(94517312..94517841)	529	2.74666	10	6	4	0.2	0.543	OTUB2	DDX24
chr14	+(94567899..94568599)	700	0.53491	9	5	4	0.1111111	0.008	IFI27L1	IFI27
chr14	+(94593933..94594741)	808	1.21459	15	8	7	0.0666667	0.00273928	IFI27	IFI27L2
chr14	+(94708307..94708863)	556	1.21459	10	4	6	0.2	0.033	PPP4R4	SERPINA10
chr14	+(94731753..94732259)	506	2.74666	9	5	4	0.1111111	0.032	PPP4R4	SERPINA10
chr14	+(95760918..95761522)	604	0.2625	9	5	4	0.1111111	0.008	FLJ45244	CLMN
chr14	+(95864707..95865293)	586	2.74666	10	5	5	0	0.00451172	CLMN	C14orf139
chr14	+(96341048..96342208)	1160	0.53491	14	6	8	0.1428571	0.00097289	TCL1A	C14orf132
chr14	+(96509363..96511219)	1856	0.53491	20	14	6	0.4	0.68965464	C14orf132	BDKRB2
chr14	+(99504614..99505314)	700	0.12133	10	3	7	0.4	0.008	C14orf177	BCL11B
chr14	+(99590699..99591411)	712	0.01043	13	7	6	0.0769231	0.0013499	C14orf177	BCL11B
chr14	+(99696986..99697555)	569	1.21459	7	4	3	0.1428571	0.029	C14orf177	BCL11B
chr14	+(99989752..99990352)	600	1.21459	7	4	3	0.1428571	0.029	CCNK	CCDC85C
chr14	+(100047489..100048153)	664	0.2625	9	4	5	0.1111111	0.008	CCNK	CCDC85C
chr14	+(101029733..101030642)	909	0.2625	15	9	6	0.2	0.00073136	WDR25	BEGAIN
chr14	+(101041697..101042338)	641	2.74666	6	2	4	0.3333333	0.067	BEGAIN	C14orf70
chr14	+(101096338..101097302)	964	1.21459	13	6	7	0.0769231	0.0013499	BEGAIN	C14orf70
chr14	+(101130534..101131075)	541	2.74666	6	4	2	0.3333333	0.067	C14orf70	DLK1
chr14	+(101370668..101371553)	885	0.53491	17	7	10	0.1764706	0.02021199	MEG8	SNORD113-1
chr14	+(102284994..102285532)	538	1.21459	10	3	7	0.4	0.008	PPP2R5C	DYNC1H1
chr14	+(102468821..102469355)	534	2.74666	8	5	3	0.25	0.018	DYNC1H1	HSP90AA1
chr14	+(102751415..102751955)	540	2.74666	6	4	2	0.3333333	0.067	WDR20	RAGE
chr14	+(103218990..103219916)	926	0.53491	14	6	8	0.1428571	0.00097289	RCOR1	TRAF3
chr14	+(103262087..103262743)	656	1.21459	12	5	7	0.1666667	0.99775837	TRAF3	AMN
chr14	+(103338090..103338601)	511	2.74666	6	2	4	0.3333333	0.067	TRAF3	AMN
chr14	+(103342585..103343112)	527	2.74666	7	4	3	0.1428571	0.029	TRAF3	AMN
chr14	+(103399939..103400515)	576	0.12133	10	5	5	0	0.00451172	AMN	CDC42BPB
chr14	+(103915143..103915752)	609	2.74666	9	6	3	0.3333333	0.19	MARK3	CKB
chr14	+(103966831..103967505)	674	2.74666	6	4	2	0.3333333	0.067	MARK3	CKB
chr14	+(103998896..103999447)	551	2.74666	6	2	4	0.3333333	0.067	TRMT61A	BAG5
chr14	+(104010027..104010579)	552	1.21459	8	5	3	0.25	0.018	TRMT61A	BAG5
chr14	+(104178640..104179896)	1256	0.53491	16	6	10	0.25	0.01502979	KLC1	XRCC3

chr14	+(104228948..104229597)	649	2.74666	9	6	3	0.3333333	0.012	ZFYVE21	PPP1R13B
chr14	+(104610408..104611108)	700	2.74666	10	6	4	0.2	0.005	KIF26A	C14orf180
chr14	+(104735769..104736305)	536	0.53491	8	3	5	0.25	0.018	KIF26A	C14orf180
chr14	+(104755110..104756084)	974	2.74666	12	8	4	0.3333333	0.99671074	KIF26A	C14orf180
chr14	+(104983994..104984514)	520	1.21459	7	3	4	0.1428571	0.029	KIF26A	C14orf180
chr14	+(104988228..104988739)	511	0.53491	8	5	3	0.25	0.018	KIF26A	C14orf180
chr14	+(105052549..105053070)	521	2.74666	8	3	5	0.25	0.125	C14orf180	TMEM179
chr14	+(105256092..105256635)	543	2.74666	6	2	4	0.3333333	0.067	SIVA1	AKT1
chr14	+(105410811..105411415)	604	0.53491	15	9	6	0.2	0.11929642	PLD4	AHNAK2
chr14	+(105415011..105415666)	655	1.21459	10	7	3	0.4	0.008	PLD4	AHNAK2
chr14	+(105441150..105441850)	700	1.21459	10	3	7	0.4	0.5	PLD4	AHNAK2
chr14	+(105527107..105527733)	626	0.00507	17	6	11	0.2941176	0.00045556	CDCA4	GPR132
chr14	+(105648392..105648993)	601	0.53491	8	4	4	0	0.014	NUDT14	BRF1
chr14	+(105682146..105683652)	1506	0.2625	24	14	10	0.1666667	4.3705E-05	NUDT14	BRF1
chr14	+(105911100..105911800)	700	0.00507	14	8	6	0.1428571	0.00097289	MTA1	CRIP2
chr14	+(106007254..106007954)	700	1.21459	9	6	3	0.3333333	0.012	TMEM121	KIAA0125
chr14	+(106090788..106091343)	555	2.74666	11	5	6	0.0909091	0.18065522	TMEM121	KIAA0125
chr14	+(106107945..106108458)	513	2.74666	10	6	4	0.2	0.005	TMEM121	KIAA0125
chr14	+(106132955..106133553)	598	1.21459	19	11	8	0.1578947	0.04932381	TMEM121	KIAA0125
chr14	+(106174527..106175035)	508	2.74666	7	4	3	0.1428571	0.029	TMEM121	KIAA0125
chr14	+(106183509..106184127)	618	1.21459	7	4	3	0.1428571	0.029	TMEM121	KIAA0125
chr14	+(106388002..106388684)	682	1.21459	10	3	7	0.4	0.017	KIAA0125	ADAM6
chr15	+(22051915..22052417)	502	4.78021	23	16	7	0.3913043	0.74798207	CXADRP2	POTEB_dup2
chr15	+(22061962..22062939)	977	0.11731	55	27	28	0.0181818	0.02541208	CXADRP2	POTEB_dup2
chr15	+(22063313..22064052)	739	0.01663	79	45	34	0.1392405	9.8773E-09	CXADRP2	POTEB_dup2
chr15	+(22077296..22077943)	647	0.10462	56	26	30	0.0714286	0.01635013	CXADRP2	POTEB_dup2
chr15	+(22082119..22082697)	578	2.9207	33	12	21	0.2727273	0.00394071	CXADRP2	POTEB_dup2
chr15	+(22118287..22118789)	502	2.38943	8	4	4	0	0.014	POTEB_dup2	NF1P1_dup2
chr15	+(22958023..22958851)	828	0.47311	14	6	8	0.1428571	0.00097289	CYFIP1	NIPA2
chr15	+(23014250..23014782)	532	2.38943	6	4	2	0.3333333	0.067	CYFIP1	NIPA2
chr15	+(23075107..23075682)	575	2.38943	6	3	3	0	0.05	NIPA2	NIPA1
chr15	+(23287960..23288478)	518	2.38943	10	6	4	0.2	0.381	GOLGA8IP	HERC2P2
chr15	+(23309927..23310593)	666	0.01044	24	16	8	0.3333333	0.11033568	GOLGA8IP	HERC2P2
chr15	+(23330319..23330823)	504	2.38943	17	7	10	0.1764706	0.38484897	GOLGA8IP	HERC2P2

chr15	+(23466593..23467171)	578	1.13138	7	3	4	0.1428571	0.029	GOLGA8E	MKRN3	
chr15	+(23512395..23513079)	684	1.87258	21	14	7	0.3333333	0.00012828	GOLGA8E	MKRN3	
chr15	+(23572839..23573376)	537	2.38943	15	10	5	0.3333333	0.59675203	GOLGA8E	MKRN3	
chr15	+(23602459..23602989)	530	1.13138	13	8	5	0.2307692	0.0394913	GOLGA8E	MKRN3	
chr15	+(23812407..23812932)	525	2.38943	10	3	7	0.4	0.033	MKRN3	MAGEL2	
chr15	+(25926432..25927185)	753	0.00177	16	11	5	0.375	0.0009184	UBE3A	ATP10A	
chr15	+(27283506..27284123)	617	1.13138	7	3	4	0.1428571	0.029	GABRG3	OCA2	v
chr15	+(27998816..27999367)	551	2.38943	9	3	6	0.3333333	0.012	GABRG3	OCA2	v
chr15	+(28107912..28108611)	699	0.23588	10	7	3	0.4	0.058	GABRG3	OCA2	v
chr15	+(28440975..28441524)	549	0.47311	15	7	8	0.0666667	0.01031878	OCA2	HERC2	
chr15	+(28446299..28446916)	617	1.13138	13	8	5	0.2307692	0.00641335	OCA2	HERC2	
chr15	+(28478217..28478904)	687	0.6732	32	10	22	0.375	0.11129435	OCA2	HERC2	
chr15	+(28483138..28484038)	900	2.38943	17	8	9	0.0588235	0.01344276	OCA2	HERC2	
chr15	+(28505592..28506292)	700	1.13138	10	4	6	0.2	0.005	OCA2	HERC2	
chr15	+(28596167..28596672)	505	3.68894	34	18	16	0.0588235	0.01361483	HERC2	GOLGA8F_dup1	
chr15	+(29129994..29130582)	588	0.47311	8	4	4	0	0.014	LOC646278	APBA2	
chr15	+(29139954..29140652)	698	2.38943	9	6	3	0.3333333	0.988	LOC646278	APBA2	
chr15	+(29283293..29284029)	736	0.01044	15	8	7	0.0666667	0.00059687	APBA2	FAM189A1	
chr15	+(29526092..29526622)	530	2.38943	9	5	4	0.1111111	0.056	APBA2	FAM189A1	
chr15	+(29671625..29672325)	700	0.47311	10	3	7	0.4	0.017	APBA2	FAM189A1	
chr15	+(30874740..30875435)	695	0.1169	38	18	20	0.0526316	7.1114E-08	FAM7A2_dup1	ARHGAP11B	
chr15	+(31266448..31266954)	506	1.13138	10	3	7	0.4	0.008	FAN1	MTMR10	
chr15	+(31342342..31342893)	551	1.13138	13	9	4	0.3846154	0.47	MTMR10	TRPM1	
chr15	+(31557552..31558092)	540	1.13138	9	4	5	0.1111111	0.008	MIR211	KLF13	
chr15	+(31664698..31665291)	593	0.47311	8	4	4	0	0.014	KLF13	OTUD7A	
chr15	+(31745482..31746182)	700	1.13138	14	7	7	0	0.32736042	KLF13	OTUD7A	
chr15	+(31790714..31791862)	1148	0.47311	14	8	6	0.1428571	0.99902711	KLF13	OTUD7A	
chr15	+(32058892..32059496)	604	0.04914	21	11	10	0.047619	0.14542285	OTUD7A	CHRNA7	
chr15	+(32103945..32104633)	688	0.47311	11	4	7	0.2727273	0.394	OTUD7A	CHRNA7	
chr15	+(32107847..32108547)	700	0.02098	12	7	5	0.1666667	0.00224163	OTUD7A	CHRNA7	
chr15	+(32438144..32439441)	1297	0.47311	15	7	8	0.0666667	0.00059687	CHRNA7	FAM7A3_dup2	
chr15	+(32912132..32912757)	625	1.15732	23	16	7	0.3913043	0.00132055	ARHGAP11A	SCG5	
chr15	+(32916234..32916777)	543	0.89935	31	19	12	0.2258065	0.00089581	ARHGAP11A	SCG5	
chr15	+(34149750..34150258)	508	2.38943	7	4	3	0.1428571	0.029	RYR3	AVEN	

chr15	+(34241041..34241741)	700	1.13138	9	3	6	0.3333333	0.012	RYR3	AVEN	
chr15	+(34577620..34578799)	1179	0.01044	21	8	13	0.2380952	0.98976071	TMEM85	SLC12A6	
chr15	+(34823255..34824219)	964	0.00402	31	14	17	0.0967742	0.43692235	MIR1233-2_dup1	GOLGA8B	
chr15	+(34826310..34826815)	505	2.38943	10	6	4	0.2	0.762	MIR1233-2_dup1	GOLGA8B	
chr15	+(35044842..35045381)	539	1.13138	12	4	8	0.3333333	0.341	MIR1233-2_dup2	GJD2	
chr15	+(35082434..35082942)	508	2.38943	6	3	3	0	0.05	GJD2	ACTC1	
chr15	+(35085404..35086047)	643	0.47311	13	8	5	0.2307692	0.00958624	GJD2	ACTC1	
chr15	+(35132836..35133536)	700	0.23588	9	3	6	0.3333333	0.012	ACTC1	AQR	
chr15	+(35232799..35233389)	590	1.13138	9	3	6	0.3333333	0.083	ACTC1	AQR	
chr15	+(37389228..37389763)	535	2.38943	6	4	2	0.3333333	0.067	LOC145845	MEIS2	v
chr15	+(38765553..38766057)	504	0.47311	10	4	6	0.2	0.005	FAM98B	RASGRP1	
chr15	+(40328144..40329034)	890	0.11295	22	11	11	0	0.00391362	EIF2AK4	SRP14	
chr15	+(40582336..40582998)	662	2.38943	11	6	5	0.0909091	0.03394459	LOC100131244	PLCB2	
chr15	+(40897073..40897615)	542	1.13138	9	3	6	0.3333333	0.048	CASC5	RAD51	
chr15	+(40917325..40917843)	518	2.38943	7	3	4	0.1428571	0.029	CASC5	RAD51	
chr15	+(41142557..41143257)	700	0.02098	12	6	6	0	0.00197388	SPINT1	RHOV	
chr15	+(41796570..41797253)	683	0.47311	11	7	4	0.2727273	0.082	ITPKA	LTK	
chr15	+(42128585..42129285)	700	0.02098	13	4	9	0.3846154	0.001	JMJD7-PLA2G4B	PLA2G4B	
chr15	+(42140875..42141575)	700	0.11295	11	7	4	0.2727273	0.115	PLA2G4B	SPTBN5	
chr15	+(42171906..42172469)	563	2.38943	7	4	3	0.1428571	0.029	PLA2G4B	SPTBN5	
chr15	+(42179210..42179726)	516	2.38943	7	3	4	0.1428571	0.029	PLA2G4B	SPTBN5	
chr15	+(43024212..43025390)	1178	1.13138	16	5	11	0.375	0.0009184	STARD9	CDAN1	
chr15	+(44066591..44067136)	545	0.47311	9	4	5	0.1111111	0.095	PDIA3	ELL3	
chr15	+(45428020..45428635)	615	0.11295	14	6	8	0.1428571	0.01943355	DUOX1	SHF	
chr15	+(48543833..48544354)	521	2.38943	9	6	3	0.3333333	0.452	SLC12A1	DUT	
chr15	+(49657925..49658447)	522	1.13138	9	3	6	0.3333333	0.357	LOC100306975	C15orf33	
chr15	+(49926480..49927025)	545	1.13138	15	8	7	0.0666667	0.17726974	DTWD1	ATP8B4	
chr15	+(50350825..50351521)	696	0.11295	10	6	4	0.2	0.005	DTWD1	ATP8B4	
chr15	+(50494499..50495055)	556	1.13138	8	5	3	0.25	0.018	SLC27A2	HDC	
chr15	+(50503763..50504463)	700	0.11295	10	6	4	0.2	0.005	SLC27A2	HDC	
chr15	+(50916089..50916598)	509	1.13138	7	4	3	0.1428571	0.029	USP50	TRPM7	
chr15	+(51020436..51020937)	501	0.23588	9	5	4	0.1111111	0.008	TRPM7	SPPL2A	
chr15	+(51039513..51040108)	595	0.47311	12	7	5	0.1666667	0.00591469	TRPM7	SPPL2A	
chr15	+(52145323..52146023)	700	0.04914	11	6	5	0.0909091	0.00308495	TMOD3	LEO1	

chr15	+(52356567..52357103)	536	0.73895	22	7	15	0.3636364	0.04208177	MAPK6	BCL2L10
chr15	+(52671693..52672348)	655	0.23588	12	5	7	0.1666667	0.04407898	MIR1266	MYO5A
chr15	+(56704266..56704901)	635	0.47311	11	6	5	0.0909091	0.00308495	TEX9	MNS1
chr15	+(57614482..57615090)	608	1.13138	11	4	7	0.2727273	0.003	LOC283663	CGNL1
chr15	+(57710889..57711589)	700	0.11295	10	6	4	0.2	0.005	CGNL1	GCOM1
chr15	+(57831050..57831750)	700	0.11295	10	6	4	0.2	0.005	CGNL1	GCOM1
chr15	+(58271511..58272447)	936	0.04914	18	8	10	0.1111111	0.0038429	GRINL1A	ALDH1A2
chr15	+(59415352..59416052)	700	0.02098	16	6	10	0.25	0.00082904	CCNB2	MYO1E
chr15	+(59435652..59436406)	754	1.13138	13	6	7	0.0769231	0.0013499	CCNB2	MYO1E
chr15	+(59499780..59500286)	506	2.38943	11	7	4	0.2727273	0.324	CCNB2	MYO1E
chr15	+(62242811..62243429)	618	1.13138	10	3	7	0.4	0.017	RORA	VPS13C
chr15	+(62335972..62336489)	517	2.38943	9	3	6	0.3333333	0.19	RORA	VPS13C
chr15	+(62994825..62995364)	539	2.38943	8	3	5	0.25	0.018	TLN2	MIR190
chr15	+(63135315..63136214)	899	7.9E-05	26	11	15	0.1538462	9.2717E-06	MIR190	TPM1
chr15	+(63932827..63933504)	677	2.38943	6	4	2	0.3333333	0.067	FBXL22	HERC1
chr15	+(63966630..63967165)	535	3.0968	14	5	9	0.2857143	0.0013499	FBXL22	HERC1
chr15	+(64422275..64422808)	533	2.38943	6	3	3	0	0.05	SNX1	SNX22
chr15	+(64495066..64495614)	548	2.38943	7	3	4	0.1428571	0.029	PPIB	CSNK1G1
chr15	+(65145855..65146550)	695	2.38943	9	3	6	0.3333333	0.012	PLEKHO2	ANKDD1A
chr15	+(65148620..65149319)	699	0.23588	9	6	3	0.3333333	0.012	PLEKHO2	ANKDD1A
chr15	+(65158918..65160064)	1146	0.11295	17	10	7	0.1764706	0.99968185	PLEKHO2	ANKDD1A
chr15	+(65180634..65181597)	963	0.01044	19	7	12	0.2631579	0.02126124	PLEKHO2	ANKDD1A
chr15	+(65707207..65707846)	639	2.38943	11	5	6	0.0909091	0.64249967	IGDCC3	IGDCC4
chr15	+(65945973..65946514)	541	1.13138	14	7	7	0	0.01750284	SLC24A1	DENND4A
chr15	+(65996757..65997298)	541	0.11295	10	5	5	0	0.00451172	SLC24A1	DENND4A
chr15	+(66251143..66251842)	699	0.47311	12	8	4	0.3333333	0.99671074	RAB11A	MEGF11
chr15	+(66260901..66261534)	633	1.13138	11	4	7	0.2727273	0.997	RAB11A	MEGF11
chr15	+(66304958..66305485)	527	1.13138	7	3	4	0.1428571	0.029	RAB11A	MEGF11
chr15	+(66319075..66320255)	1180	2.38943	12	6	6	0	0.99802612	RAB11A	MEGF11
chr15	+(66388383..66389159)	776	0.00402	14	8	6	0.1428571	0.00097289	RAB11A	MEGF11
chr15	+(66825250..66825758)	508	1.13138	13	6	7	0.0769231	0.00757922	ZWILCH	LCTL
chr15	+(66843566..66844132)	566	2.38943	9	4	5	0.1111111	0.857	ZWILCH	LCTL
chr15	+(67094891..67095479)	588	1.13138	7	4	3	0.1428571	0.029	SMAD6	SMAD3
chr15	+(67134152..67134852)	700	0.11295	10	4	6	0.2	0.005	SMAD6	SMAD3

chr15	+(67158194..67158884)	690	1.13138	12	7	5	0.1666667	0.99775837	SMAD6	SMAD3	
chr15	+(67207553..67208248)	695	2.38943	9	6	3	0.3333333	0.012	SMAD6	SMAD3	
chr15	+(67446592..67447227)	635	2.38943	6	3	3	0	0.05	SMAD3	AAGAB	
chr15	+(67479488..67480419)	931	0.11295	18	8	10	0.1111111	0.07756579	SMAD3	AAGAB	
chr15	+(68127474..68127983)	509	0.23588	10	5	5	0	0.05859256	SKOR1	PIAS1	
chr15	+(68473325..68473960)	635	1.13138	8	3	5	0.25	0.018	PIAS1	CALML4	
chr15	+(68959040..68959571)	531	1.13138	7	4	3	0.1428571	0.029	CORO2B	ANP32A	
chr15	+(69023303..69024003)	700	0.02098	15	8	7	0.0666667	0.00059687	CORO2B	ANP32A	
chr15	+(69635980..69637340)	1360	1.13138	14	7	7	0	0.99912744	PAQR5	KIF23	
chr15	+(70175915..70176615)	700	0.04914	11	6	5	0.0909091	0.00308495	C15orf50	TLE3	v
chr15	+(70345332..70346180)	848	0.03632	17	9	8	0.0588235	0.000266	C15orf50	TLE3	v
chr15	+(72432720..72433302)	582	2.38943	6	2	4	0.3333333	0.067	SENP8	GRAMD2	
chr15	+(72488617..72489317)	700	0.47311	10	4	6	0.2	0.457	SENP8	GRAMD2	
chr15	+(72954337..72954921)	584	0.23588	18	7	11	0.2222222	0.51805927	GOLGA6B	HIGD2B	
chr15	+(72957868..72958467)	599	0.04914	13	8	5	0.2307692	0.00420773	GOLGA6B	HIGD2B	
chr15	+(73615121..73615767)	646	0.23588	9	4	5	0.1111111	0.008	NEO1	HCN4	
chr15	+(74522880..74523408)	528	2.38943	6	2	4	0.3333333	0.067	STRA6	CCDC33	
chr15	+(74543164..74543864)	700	2.38943	10	4	6	0.2	0.995	CCDC33	CYP11A1	
chr15	+(75107218..75107918)	700	0.01044	13	8	5	0.2307692	0.0017074	LMAN1L	CPLX3	
chr15	+(75134372..75134890)	518	2.38943	7	3	4	0.1428571	0.2	CPLX3	ULK3	
chr15	+(75466476..75467757)	1281	0.02098	23	14	9	0.2173913	0.95551349	PPCDC	C15orf39	
chr15	+(75499770..75500312)	542	2.38943	7	4	3	0.1428571	0.029	C15orf39	GOLGA6C	
chr15	+(75554556..75555062)	506	1.13138	13	8	5	0.2307692	0.02851994	GOLGA6C	GOLGA6D	
chr15	+(75558519..75559143)	624	0.1169	38	24	14	0.2631579	4.7363E-05	GOLGA6C	GOLGA6D	
chr15	+(75579843..75580819)	976	0.25429	50	18	32	0.28	7.8568E-05	GOLGA6D	COMMD4	
chr15	+(75648876..75649400)	524	0.47311	9	5	4	0.1111111	0.008	MIR631	MAN2C1	v
chr15	+(75676417..75676941)	524	2.38943	6	2	4	0.3333333	0.067	MAN2C1	SIN3A	v
chr15	+(76031125..76032177)	1052	0.23588	21	12	9	0.1428571	0.9993081	ODF3L1	DNM1P35	
chr15	+(76074790..76075484)	694	0.11295	35	22	13	0.2571429	0.09152246	MIR4313	UBE2Q2	
chr15	+(76171315..76171935)	620	1.13138	9	6	3	0.3333333	0.012	UBE2Q2	FBXO22	
chr15	+(76175470..76175992)	522	1.13138	10	5	5	0	0.00451172	UBE2Q2	FBXO22	
chr15	+(77301754..77302373)	619	2.38943	9	3	6	0.3333333	0.988	PSTPIP1	TSPAN3	
chr15	+(77473914..77474465)	551	1.13138	11	7	4	0.2727273	0.003	TSPAN3	PEAK1	
chr15	+(77914964..77915522)	558	0.11295	13	4	9	0.3846154	0.001	HMG20A	LINGO1	

chr15	+(77936666..77937897)	1231	0.11295	16	9	7	0.125	0.99138242	LINGO1	LOC645752
chr15	+(78020456..78021219)	763	0.02098	12	6	6	0	0.00197388	LINGO1	LOC645752
chr15	+(78189704..78190700)	996	0.23588	19	13	6	0.3684211	0.0089409	LINGO1	LOC645752
chr15	+(78208048..78208592)	544	3.4975	26	16	10	0.2307692	0.00306598	LINGO1	LOC645752
chr15	+(78212176..78212679)	503	2.38943	12	6	6	0	0.0186865	LINGO1	LOC645752
chr15	+(78213706..78214306)	600	0.50121	26	13	13	0	7.3434E-06	LINGO1	LOC645752
chr15	+(78277753..78278339)	586	0.01044	14	6	8	0.1428571	0.01943355	LOC645752	LOC91450
chr15	+(79178342..79178964)	622	0.47311	13	6	7	0.0769231	0.0013499	MORF4L1	CTSH
chr15	+(79315004..79315592)	588	0.23588	9	4	5	0.1111111	0.008	CTSH	RASGRF1
chr15	+(79338862..79339427)	565	2.38943	11	5	6	0.0909091	0.03394459	CTSH	RASGRF1
chr15	+(80451915..80452496)	581	0.47311	9	5	4	0.1111111	0.008	FAH	LOC283688
chr15	+(80472024..80472664)	640	1.13138	7	3	4	0.1428571	0.029	FAH	LOC283688
chr15	+(80709996..80710607)	611	0.23588	9	4	5	0.1111111	0.008	ARNT2	FAM108C1
chr15	+(80772332..80773020)	688	0.47311	8	4	4	0	0.014	ARNT2	FAM108C1
chr15	+(80885963..80886561)	598	2.38943	10	5	5	0	0.82639618	ARNT2	FAM108C1
chr15	+(81170881..81171562)	681	1.13138	9	6	3	0.3333333	0.024	MIR549	MESDC2
chr15	+(83240417..83241551)	1134	0.04914	18	6	12	0.3333333	0.00037352	RPS17_dup2	CPEB1
chr15	+(83795254..83795761)	507	2.38943	9	6	3	0.3333333	0.012	TM6SF1	HDGFRP3
chr15	+(84638923..84639623)	700	0.23588	10	3	7	0.4	0.008	ADAMTSL3	LOC648809
chr15	+(84784373..84785251)	878	0.04914	20	13	7	0.3	0.10967381	LOC648809	LOC440300
chr15	+(85189254..85189765)	511	2.38943	6	3	3	0	0.05	SCAND2	WDR73
chr15	+(85405481..85406323)	842	2.38943	12	6	6	0	0.02733197	ALPK3	SLC28A1
chr15	+(88453180..88453747)	567	0.23588	9	6	3	0.3333333	0.012	NCRNA00052	NTRK3
chr15	+(88678289..88678808)	519	1.13138	10	7	3	0.4	0.992	NCRNA00052	NTRK3
chr15	+(89450805..89451315)	510	2.38943	8	3	5	0.25	0.018	HAPLN3	MFGE8
chr15	+(90984542..90985083)	541	2.38943	6	2	4	0.3333333	0.067	IQGAP1	CRTC3
chr15	+(91016875..91017431)	556	2.38943	8	3	5	0.25	0.036	IQGAP1	CRTC3
chr15	+(91037719..91038369)	650	1.13138	10	6	4	0.2	0.01	IQGAP1	CRTC3
chr15	+(91122299..91122999)	700	0.00402	14	8	6	0.1428571	0.00097289	CRTC3	BLM
chr15	+(91433417..91434563)	1146	0.04914	18	6	12	0.3333333	0.71292546	FES	MAN2A2
chr15	+(91460860..91461775)	915	0.11295	20	10	10	0	0.00630557	MAN2A2	UNC45A
chr15	+(91496906..91497514)	608	2.38943	6	3	3	0	0.05	HDDC3	RCCD1
chr15	+(91552623..91553323)	700	0.02098	13	7	6	0.0769231	0.0013499	PRC1	VPS33B
chr15	+(93587296..93588935)	1639	1.13138	19	12	7	0.2631579	0.43288619	MIR3175	RGMA

chr15	+(100160964..100161601)	637	0.23588	9	5	4	0.1111111	0.008	MEF2A	LYSMD4
chr15	+(100856324..100857024)	700	2.38943	11	5	6	0.0909091	0.99691505	C15orf51	ADAMTS17
chr15	+(100989024..100989724)	700	0.04914	11	6	5	0.0909091	0.00308495	FLJ42289	LASS3
chr15	+(101909891..101910591)	700	0.01044	13	8	5	0.2307692	0.0017074	SNRPA1	PCSK6
chr16	+(239035..239570)	535	1.12325	7	3	4	0.1428571	0.029	HBQ1	LUC7L
chr16	+(458188..458727)	539	2.543	9	5	4	0.1111111	0.008	DECR2	RAB11FIP3
chr16	+(555327..556023)	696	0.55004	8	3	5	0.25	0.018	RAB11FIP3	NCRNA00235
chr16	+(572836..573536)	700	2.543	10	4	6	0.2	0.995	RAB11FIP3	NCRNA00235
chr16	+(651624..652152)	528	2.543	8	3	5	0.25	0.393	RAB40C	WFIKKN1
chr16	+(781068..781768)	700	0.01501	17	10	7	0.1764706	0.00031815	HAGHL	NARFL
chr16	+(906357..907471)	1114	0.55004	15	8	7	0.0666667	0.00059687	PRR25	LMF1
chr16	+(988121..988909)	788	0.00922	20	10	10	0	7.8526E-05	PRR25	LMF1
chr16	+(1168494..1169121)	627	0.55004	8	5	3	0.25	0.018	C1QTNF8	CACNA1H
chr16	+(1173733..1174234)	501	1.12325	7	4	3	0.1428571	0.029	C1QTNF8	CACNA1H
chr16	+(1251069..1251708)	639	1.12325	8	4	4	0	0.014	CACNA1H	TPSG1
chr16	+(1263847..1264448)	601	0.23472	9	6	3	0.3333333	0.012	CACNA1H	TPSG1
chr16	+(1385063..1386006)	943	0.11182	19	9	10	0.0526316	0.99988072	BAIAP3	C16orf42
chr16	+(1459914..1460594)	680	0.11182	11	7	4	0.2727273	0.003	GNPTG	UNKL
chr16	+(1608601..1609205)	604	2.543	6	4	2	0.3333333	0.067	TELO2	IFT140
chr16	+(1617401..1618371)	970	0.23472	16	8	8	0	0.00038877	TELO2	IFT140
chr16	+(1681089..1681697)	608	2.543	6	3	3	0	0.05	CRAMP1L	HN1L
chr16	+(1699875..1700809)	934	0.11182	16	10	6	0.25	0.00056905	CRAMP1L	HN1L
chr16	+(1709591..1710478)	887	2.543	12	5	7	0.1666667	0.00224163	CRAMP1L	HN1L
chr16	+(1841671..1842206)	535	2.543	7	3	4	0.1428571	0.029	NUBP2	IGFALS
chr16	+(2030495..2031032)	537	2.543	8	5	3	0.25	0.036	TBL3	NOXO1
chr16	+(2278460..2279008)	548	2.543	9	3	6	0.3333333	0.988	E4F1	DNASE1L2
chr16	+(2336018..2337200)	1182	0.02629	19	12	7	0.2631579	0.99980713	MIR940	ABCA3
chr16	+(2367736..2368301)	565	1.12325	8	4	4	0	0.1	MIR940	ABCA3
chr16	+(2369663..2370303)	640	0.11182	11	5	6	0.0909091	0.03394459	MIR940	ABCA3
chr16	+(2549023..2549657)	634	0.08266	16	9	7	0.125	0.00042755	TBC1D24	ATP6V0C
chr16	+(2791134..2791834)	700	0.06262	11	4	7	0.2727273	0.003	PRSS27	LOC100128788
chr16	+(2792522..2793114)	592	0.55004	8	3	5	0.25	0.018	PRSS27	LOC100128788
chr16	+(3077915..3078613)	698	1.12325	9	6	3	0.3333333	0.012	THOC6	CCDC64B
chr16	+(3306226..3306854)	628	2.543	7	4	3	0.1428571	0.029	ZNF200	MEFV

chr16	+(3644279..3644979)	700	0.55004	8	3	5	0.25	0.018	NLRC3	SLX4
chr16	+(3650889..3651589)	700	0.11182	15	6	9	0.2	0.00666417	NLRC3	SLX4
chr16	+(3711013..3711880)	867	0.00081	17	9	8	0.0588235	0.000266	DNASE1	TRAP1
chr16	+(3875655..3876355)	700	1.12325	12	5	7	0.1666667	0.00224163	TRAP1	CREBBP
chr16	+(4343862..4344560)	698	2.543	9	6	3	0.3333333	0.012	TFAP4	GLIS2
chr16	+(4387989..4388507)	518	2.543	6	4	2	0.3333333	0.067	GLIS2	PAM16
chr16	+(4572584..4573133)	549	0.23472	9	6	3	0.3333333	0.012	HMOX2	C16orf5
chr16	+(4707727..4708338)	611	2.543	6	3	3	0	0.05	MGRN1	NUDT16L1
chr16	+(4714669..4715327)	658	0.02629	19	12	7	0.2631579	0.02595649	MGRN1	NUDT16L1
chr16	+(4796849..4797549)	700	0.02629	15	9	6	0.2	0.00073136	C16orf71	ZNF500
chr16	+(4848927..4849627)	700	0.02629	18	12	6	0.3333333	0.98770571	LOC440335	ROGDI
chr16	+(4972789..4973489)	700	2.543	9	3	6	0.3333333	0.988	UBN1	PPL
chr16	+(11177137..11177808)	671	0.55004	8	3	5	0.25	0.018	CLEC16A	SOCS1
chr16	+(11285005..11285608)	603	2.543	6	3	3	0	0.05	CLEC16A	SOCS1
chr16	+(11303087..11304367)	1280	0.55004	22	7	15	0.3636364	0.99989252	CLEC16A	SOCS1
chr16	+(11304689..11305220)	531	2.543	6	2	4	0.3333333	0.067	CLEC16A	SOCS1
chr16	+(11362490..11362997)	507	2.543	16	8	8	0	0.17228119	SOCS1	TNP2
chr16	+(11773736..11774334)	598	1.12325	8	4	4	0	0.171	SNN	TXNDC11
chr16	+(11790809..11792026)	1217	1.12325	15	7	8	0.0666667	0.94740374	SNN	TXNDC11
chr16	+(12145499..12146005)	506	2.74678	16	8	8	0	0.33721204	RUNDC2A	SNX29
chr16	+(12298475..12299137)	662	1.12325	8	5	3	0.25	0.125	SNX29	CPPED1
chr16	+(12531650..12532446)	796	0.00422	15	8	7	0.0666667	0.00059687	SNX29	CPPED1
chr16	+(12673796..12674489)	693	2.543	6	3	3	0	0.05	SNX29	CPPED1
chr16	+(12886993..12887693)	700	1.12325	10	7	3	0.4	0.008	SNX29	CPPED1
chr16	+(14136588..14137123)	535	2.543	6	2	4	0.3333333	0.067	ERCC4	MKL2
chr16	+(14294521..14295031)	510	2.543	10	5	5	0	0.30075407	MKL2	MIR193B
chr16	+(15082095..15082601)	506	2.543	7	4	3	0.1428571	0.029	PDXDC1	NTAN1
chr16	+(16336771..16337324)	553	2.1236	42	19	23	0.0952381	0.00175716	NOMO3	MIR3179-1_dup2
chr16	+(16338685..16339259)	574	0.23472	19	10	9	0.0526316	0.07082235	NOMO3	MIR3179-1_dup2
chr16	+(16344634..16345261)	627	2.4667	36	23	13	0.2777778	5.9327E-07	NOMO3	MIR3179-1_dup2
chr16	+(16345903..16346600)	697	0.35077	48	24	24	0	0.00345475	NOMO3	MIR3179-1_dup2
chr16	+(16363776..16365181)	1405	0.05098	100	51	49	0.02	0.00023933	NOMO3	MIR3179-1_dup2
chr16	+(17452137..17452952)	815	0.00097	18	11	7	0.2222222	0.0002444	PKD1P1	XYLT1
chr16	+(20748198..20748829)	631	0.23472	15	7	8	0.0666667	0.03203876	ACSM1	THUMPD1

chr16	+(20974959..20975620)	661	0.23472	9	4	5	0.1111111	0.008	LYRM1	DNAH3
chr16	+(21079484..21080094)	610	0.55004	9	5	4	0.1111111	0.143	LYRM1	DNAH3
chr16	+(21117782..21118292)	510	2.543	11	6	5	0.0909091	0.03394459	LYRM1	DNAH3
chr16	+(21181546..21182208)	662	0.55004	12	6	6	0	0.00815459	TMEM159	ZP2
chr16	+(21808912..21809570)	658	0.11182	15	10	5	0.3333333	0.00109982	OTOA	RRN3P1
chr16	+(22269400..22269961)	561	0.06262	11	6	5	0.0909091	0.00308495	EEF2K	POLR3E
chr16	+(22332846..22333425)	579	1.12325	10	6	4	0.2	0.543	POLR3E	CDR2
chr16	+(22339493..22340019)	526	0.23472	9	5	4	0.1111111	0.008	POLR3E	CDR2
chr16	+(22431917..22432822)	905	1.12325	13	7	6	0.0769231	0.0013499	CDR2	RRN3P3
chr16	+(22579008..22579513)	505	2.74678	22	12	10	0.0909091	0.00343109	LOC653786	MIR548D2
chr16	+(23063682..23064210)	528	2.543	6	4	2	0.3333333	0.067	HS3ST2	USP31
chr16	+(23091177..23091715)	538	2.543	6	2	4	0.3333333	0.067	HS3ST2	USP31
chr16	+(24165909..24166414)	505	0.55004	8	4	4	0	0.014	PRKCB	CACNG3
chr16	+(27219193..27219893)	700	0.06262	11	5	6	0.0909091	0.00308495	JMJD5	NSMCE1
chr16	+(27252586..27253236)	650	0.11182	10	3	7	0.4	0.008	JMJD5	NSMCE1
chr16	+(27413460..27414455)	995	2.543	12	5	7	0.1666667	0.00224163	IL4R	IL21R
chr16	+(27480879..27481453)	574	2.543	9	5	4	0.1111111	0.008	LOC283888	GTF3C1
chr16	+(27561183..27561804)	621	2.543	8	5	3	0.25	0.018	LOC283888	GTF3C1
chr16	+(28112639..28113339)	700	0.11182	13	7	6	0.0769231	0.5	GSG1L	XPO6
chr16	+(28226728..28227237)	509	2.543	6	3	3	0	0.05	XPO6	SBK1
chr16	+(28322828..28323453)	625	2.543	6	2	4	0.3333333	0.067	SBK1	EIF3CL_dup1
chr16	+(28604354..28604902)	548	2.543	11	4	7	0.2727273	0.324	CCDC101	SULT1A2
chr16	+(28619511..28620035)	524	2.543	10	5	5	0	0.05859256	SULT1A2	SULT1A1
chr16	+(29301560..29302073)	513	2.543	6	4	2	0.3333333	0.067	RRN3P2	RUNDC2C
chr16	+(29342392..29343090)	698	2.543	12	6	6	0	0.00815459	RUNDC2C	LOC606724_dup1
chr16	+(29824381..29825024)	643	1.12325	9	5	4	0.1111111	0.143	PRRT2	C16orf53
chr16	+(29875383..29876083)	700	0.02629	16	5	11	0.375	0.96920638	LOC440356	SEZ6L2
chr16	+(29908075..29908634)	559	0.55004	12	5	7	0.1666667	0.00224163	LOC440356	SEZ6L2
chr16	+(30005699..30006355)	656	1.35514	17	9	8	0.0588235	0.00468738	TAOK2	HIRIP3
chr16	+(30080732..30081432)	700	0.55004	9	3	6	0.3333333	0.274	ALDOA	PPP4C
chr16	+(30087885..30088585)	700	0.23472	9	6	3	0.3333333	0.012	PPP4C	TBX6
chr16	+(30129045..30130062)	1017	0.03584	34	17	17	0	0.27333358	GDPD3	MAPK3
chr16	+(30204125..30204654)	529	1.95747	23	12	11	0.0434783	0.00084811	LOC606724_dup2	BOLA2B_dup2
chr16	+(30214123..30214633)	510	0.55004	12	5	7	0.1666667	0.00368558	SULT1A4_dup2	LOC388242_dup2

chr16	+(30304296..30304814)	518	1.02887	16	11	5	0.375	0.00134045	LOC613037	LOC440354_dup2	
chr16	+(30315890..30316401)	511	2.543	11	5	6	0.0909091	0.03394459	LOC613037	LOC440354_dup2	
chr16	+(30529747..30530429)	682	0.06262	15	10	5	0.3333333	0.00109982	ITGAL	ZNF768	
chr16	+(30661858..30662363)	505	0.55004	8	4	4	0	0.014	ZNF689	PRR14	
chr16	+(30667094..30667649)	555	2.543	6	3	3	0	0.05	PRR14	FBRS	
chr16	+(30721220..30721729)	509	2.543	6	2	4	0.3333333	0.067	SRCAP	SNORA30	
chr16	+(30732200..30732793)	593	0.11182	15	10	5	0.3333333	0.35665159	SNORA30	PHKG2	
chr16	+(30913918..30914479)	561	2.543	6	2	4	0.3333333	0.067	CTF1	NCRNA00095	
chr16	+(30972569..30973269)	700	1.12325	12	7	5	0.1666667	0.46764153	SETD1A	HSD3B7	
chr16	+(31089170..31090623)	1453	0.01501	25	11	14	0.12	0.0696889	ZNF646	PRSS53	
chr16	+(31190795..31191492)	697	2.543	10	6	4	0.2	0.995	PRSS36	FUS	v
chr16	+(31201254..31202342)	1088	0.06262	23	14	9	0.2173913	0.01881766	FUS	PYCARD	v
chr16	+(31447176..31447876)	700	0.11182	12	7	5	0.1666667	0.02117853	COX6A2	ZNF843	
chr16	+(31722616..31723316)	700	0.00422	15	10	5	0.3333333	0.00109982	KIAA0664L3	ZNF720	
chr16	+(31770308..31770905)	597	2.543	9	3	6	0.3333333	0.048	ZNF720	ZNF267	
chr16	+(46615551..46616128)	577	2.543	6	4	2	0.3333333	0.067	ANKRD26P1	SHCBP1	
chr16	+(46660396..46660905)	509	2.543	7	4	3	0.1428571	0.029	SHCBP1	VPS35	
chr16	+(49720366..49720905)	539	2.543	6	3	3	0	0.05	C16orf78	ZNF423	
chr16	+(49994334..49995034)	700	0.02629	12	5	7	0.1666667	0.00224163	ZNF423	TMEM188	
chr16	+(50256906..50257428)	522	1.12325	9	4	5	0.1111111	0.016	PAPD5	ADCY7	
chr16	+(50368329..50368989)	660	0.55004	12	4	8	0.3333333	0.008	ADCY7	BRD7	
chr16	+(50436040..50436570)	530	0.23472	9	5	4	0.1111111	0.008	BRD7	NKD1	
chr16	+(53256438..53256992)	554	1.12325	8	3	5	0.25	0.018	CHD9	RBL2	
chr16	+(53307949..53308454)	505	2.543	12	7	5	0.1666667	0.00224163	CHD9	RBL2	
chr16	+(53341277..53341863)	586	2.543	12	8	4	0.3333333	0.99671074	CHD9	RBL2	
chr16	+(55517584..55518098)	514	0.23472	10	5	5	0	0.00451172	MMP2	LPCAT2	v
chr16	+(55536590..55537290)	700	0.11182	11	6	5	0.0909091	0.05017413	MMP2	LPCAT2	v
chr16	+(56358718..56359288)	570	2.543	6	4	2	0.3333333	0.067	MIR3935	AMFR	
chr16	+(56378958..56379618)	660	1.12325	7	4	3	0.1428571	0.029	MIR3935	AMFR	
chr16	+(56667057..56667604)	547	1.12325	8	5	3	0.25	0.286	MT1M	MT1JP	
chr16	+(57111452..57112016)	564	0.11182	10	4	6	0.2	0.005	NLRC5	CPNE2	
chr16	+(57712244..57712911)	667	0.23472	10	7	3	0.4	0.008	GPR97	CCDC135	
chr16	+(57736863..57737687)	824	0.01501	13	7	6	0.0769231	0.0013499	CCDC135	KATNB1	
chr16	+(57848780..57849480)	700	0.06262	11	5	6	0.0909091	0.00308495	KIFC3	CNGB1	

chr16	+(57952935..57953446)	511	1.95747	12	7	5	0.1666667	0.00224163	KIFC3	CNGB1	
chr16	+(58068663..58069215)	552	2.543	9	5	4	0.1111111	0.857	MMP15	C16orf80	
chr16	+(58529153..58530627)	1474	0.23472	24	9	15	0.25	0.9999715	NDRG4	SETD6	
chr16	+(58578960..58579476)	516	2.543	9	3	6	0.3333333	0.012	SETD6	CNOT1	
chr16	+(66462810..66463311)	501	2.543	6	2	4	0.3333333	0.067	BEAN1	TK2	
chr16	+(66562408..66563108)	700	0.06262	16	5	11	0.375	0.9990816	BEAN1	TK2	
chr16	+(66642132..66642797)	665	0.55004	12	8	4	0.3333333	0.893	CMTM3	CMTM4	
chr16	+(67100534..67101049)	515	2.543	11	6	5	0.0909091	0.07206352	CBFB	C16orf70	
chr16	+(67322276..67322974)	698	0.23472	11	7	4	0.2727273	0.082	PLEKHG4	KCTD19	
chr16	+(67449202..67449885)	683	1.12325	7	4	3	0.1428571	0.029	TPPP3	ZDHHC1	
chr16	+(67486599..67487652)	1053	0.02629	21	7	14	0.3333333	0.00288676	HSD11B2	ATP6V0D1	
chr16	+(67488952..67489471)	519	0.55004	8	4	4	0	0.014	HSD11B2	ATP6V0D1	
chr16	+(67576123..67576823)	700	2.543	21	12	9	0.1428571	0.61189735	FAM65A	CTCF	
chr16	+(67762656..67763356)	700	0.17238	18	8	10	0.1111111	0.00018964	GFOD2	RANBP10	
chr16	+(67859128..67859965)	837	0.55004	15	7	8	0.0666667	0.00059687	TSNAXIP1	CENPT	
chr16	+(67924210..67924715)	505	2.543	6	4	2	0.3333333	0.067	NRN1L	PSKH1	
chr16	+(67962478..67963178)	700	0.06262	12	5	7	0.1666667	0.04407898	PSKH1	CTRL	
chr16	+(67964045..67964853)	808	1.12325	15	8	7	0.0666667	0.08245742	PSKH1	CTRL	
chr16	+(67970275..67970833)	558	1.12325	10	5	5	0	0.00451172	CTRL	PSMB10	
chr16	+(67978256..67979217)	961	0.00922	25	11	14	0.12	1.2469E-05	LCAT	SLC12A4	
chr16	+(67985389..67985892)	503	0.55004	9	4	5	0.1111111	0.095	LCAT	SLC12A4	
chr16	+(68025688..68026382)	694	1.95747	12	5	7	0.1666667	0.00224163	DPEP3	DPEP2	
chr16	+(68056905..68057605)	700	0.08266	19	13	6	0.3684211	0.0003125	DPEP2	DDX28	
chr16	+(68264756..68265864)	1108	1.12325	31	14	17	0.0967742	0.00111986	NFATC3	ESRP2	
chr16	+(68718867..68719515)	648	2.543	11	4	7	0.2727273	0.036	CDH3	CDH1	v
chr16	+(68867121..68867648)	527	2.543	6	2	4	0.3333333	0.067	CDH1	TMCO7	v
chr16	+(69095394..69096020)	626	1.12325	10	3	7	0.4	0.992	TMCO7	HAS3	
chr16	+(69143305..69143933)	628	1.12325	9	3	6	0.3333333	0.274	HAS3	CHTF8	
chr16	+(69173659..69174332)	673	1.12325	10	7	3	0.4	0.017	CIRH1A	SNTB2	
chr16	+(69193851..69194551)	700	0.11182	11	7	4	0.2727273	0.003	CIRH1A	SNTB2	
chr16	+(69873675..69874375)	700	0.24322	14	8	6	0.1428571	0.00097289	WWP2	MIR140	
chr16	+(70216158..70216832)	674	0.55004	12	4	8	0.3333333	0.00328926	CLEC18C	LOC729513	
chr16	+(70217509..70218175)	666	1.12325	15	10	5	0.3333333	0.05567345	CLEC18C	LOC729513	
chr16	+(70431963..70432597)	634	0.11182	10	5	5	0	0.00451172	DDX19A	ST3GAL2	

chr16	+(70450881..70451581)	700	0.11182	10	6	4	0.2	0.005	DDX19A	ST3GAL2	
chr16	+(70733825..70734333)	508	0.23472	9	4	5	0.1111111	0.008	MTSS1L	VAC14	
chr16	+(70781242..70782535)	1293	1.12325	18	11	7	0.2222222	0.9997556	MTSS1L	VAC14	
chr16	+(70785292..70785830)	538	2.543	6	4	2	0.3333333	0.067	MTSS1L	VAC14	
chr16	+(70851998..70852574)	576	0.11182	10	5	5	0	0.00451172	LOC100130894	HYDIN	
chr16	+(70891354..70892094)	740	0.23472	12	7	5	0.1666667	0.01417552	LOC100130894	HYDIN	
chr16	+(70913058..70914076)	1018	0.00949	34	22	12	0.2941176	0.34590038	LOC100130894	HYDIN	
chr16	+(70927594..70928219)	625	2.543	10	4	6	0.2	0.005	LOC100130894	HYDIN	
chr16	+(70951903..70952413)	510	1.12325	12	8	4	0.3333333	0.285	LOC100130894	HYDIN	
chr16	+(71007740..71008785)	1045	0.55004	17	6	11	0.2941176	0.01351504	LOC100130894	HYDIN	
chr16	+(71318638..71319143)	505	2.543	9	3	6	0.3333333	0.012	HYDIN	FTSJD1	
chr16	+(71438812..71439347)	535	2.543	6	4	2	0.3333333	0.067	CALB2	ZNF23	
chr16	+(71482361..71482866)	505	2.543	10	4	6	0.2	0.695	CALB2	ZNF23	
chr16	+(71522803..71523503)	700	0.00018	19	13	6	0.3684211	0.0003125	ZNF23	ZNF19	
chr16	+(71795017..71795558)	541	2.543	9	3	6	0.3333333	0.726	SNORA70D	AP1G1	
chr16	+(71977806..71978411)	605	0.55004	14	6	8	0.1428571	0.00335314	KIAA0174	PKD1L3	
chr16	+(72153598..72154271)	673	2.74678	19	7	12	0.2631579	0.00264348	DHX38	PMFBP1	
chr16	+(72204750..72205335)	585	2.543	6	2	4	0.3333333	0.067	DHX38	PMFBP1	
chr16	+(74443073..74443881)	808	0.55004	21	11	10	0.047619	0.06960017	LOC283922	CLEC18B	
chr16	+(74702109..74702674)	565	2.543	9	4	5	0.1111111	0.206	RFWD3	MLKL	
chr16	+(74712596..74713118)	522	2.543	6	2	4	0.3333333	0.067	RFWD3	MLKL	
chr16	+(75351784..75352484)	700	0.55004	9	3	6	0.3333333	0.274	BCAR1	CFDP1	
chr16	+(75563829..75564525)	696	0.55004	10	7	3	0.4	0.008	CHST6	CHST5	v
chr16	+(81094909..81095447)	538	1.12325	9	6	3	0.3333333	0.274	ATMIN	C16orf46	
chr16	+(81410715..81411327)	612	2.543	11	6	5	0.0909091	0.02230486	GAN	CMIP	
chr16	+(81520714..81521409)	695	0.23472	9	6	3	0.3333333	0.012	CMIP	PLCG2	
chr16	+(81730702..81731353)	651	2.543	6	4	2	0.3333333	0.067	CMIP	PLCG2	
chr16	+(81956838..81957449)	611	0.11182	13	5	8	0.2307692	0.23210716	PLCG2	SDR42E1	
chr16	+(82037876..82038576)	700	2.543	10	4	6	0.2	0.995	PLCG2	SDR42E1	
chr16	+(84035237..84035830)	593	2.543	9	6	3	0.3333333	0.012	NECAB2	SLC38A8	
chr16	+(84328457..84329597)	1140	0.11182	17	7	10	0.1764706	0.99968185	WFDC1	ATP2C2	
chr16	+(84426274..84427401)	1127	1.12325	13	7	6	0.0769231	0.9986501	ATP2C2	KIAA1609	
chr16	+(84495168..84495690)	522	1.12325	8	3	5	0.25	0.018	ATP2C2	KIAA1609	
chr16	+(84632462..84633162)	700	0.23472	9	3	6	0.3333333	0.012	KIAA1609	COTL1	

chr16	+(84878133..84878841)	708	0.00081	22	7	15	0.3636364	0.00010748	CRISPLD2	ZDHHC7
chr16	+(84919605..84920545)	940	0.06262	19	11	8	0.1578947	0.00013997	CRISPLD2	ZDHHC7
chr16	+(85139526..85140270)	744	0.02629	15	6	9	0.2	0.00073136	KIAA0513	FAM92B
chr16	+(85214032..85214615)	583	0.23472	9	3	6	0.3333333	0.012	LOC400548	KIAA0182
chr16	+(85215601..85216343)	742	1.12325	14	7	7	0	0.00087256	LOC400548	KIAA0182
chr16	+(85337605..85338124)	519	2.543	6	3	3	0	0.05	LOC400548	KIAA0182
chr16	+(85599875..85600570)	695	2.543	9	6	3	0.3333333	0.988	LOC400548	KIAA0182
chr16	+(85603238..85603762)	524	0.23472	9	4	5	0.1111111	0.008	LOC400548	KIAA0182
chr16	+(85613875..85614443)	568	2.543	13	8	5	0.2307692	0.23210716	LOC400548	KIAA0182
chr16	+(85615164..85615864)	700	0.06262	16	11	5	0.375	0.9990816	LOC400548	KIAA0182
chr16	+(85690722..85691314)	592	2.543	9	6	3	0.3333333	0.988	KIAA0182	GINS2
chr16	+(85814560..85815146)	586	2.543	6	4	2	0.3333333	0.067	MIR1910	COX4NB
chr16	+(86585397..86586097)	700	0.02629	16	6	10	0.25	0.00240046	FOXF1	MTHFSD
chr16	+(87403638..87404506)	868	0.00018	19	6	13	0.3684211	0.0003125	LOC100288525	FBXO31
chr16	+(87741358..87742064)	706	0.01501	13	9	4	0.3846154	0.001	LOC100129637	KLHDC4
chr16	+(87815042..87815742)	700	1.12325	12	7	5	0.1666667	0.00224163	KLHDC4	SLC7A5
chr16	+(87896556..87897107)	551	1.12325	7	3	4	0.1428571	0.029	KLHDC4	SLC7A5
chr16	+(88570055..88570695)	640	1.12325	7	3	4	0.1428571	0.029	ZFPM1	ZC3H18
chr16	+(88626808..88627876)	1068	0.11182	20	10	10	0	7.8526E-05	ZFPM1	ZC3H18
chr16	+(88630580..88631194)	614	0.11182	10	3	7	0.4	0.008	ZFPM1	ZC3H18
chr16	+(88719108..88720260)	1152	0.06262	21	11	10	0.047619	0.28660066	CYBA	MVD
chr16	+(88725397..88725907)	510	2.543	6	2	4	0.3333333	0.067	CYBA	MVD
chr16	+(88827147..88827648)	501	1.12325	7	3	4	0.1428571	0.029	CTU2	FAM38A
chr16	+(88831354..88831958)	604	0.06262	14	5	9	0.2857143	0.15865525	CTU2	FAM38A
chr16	+(88898372..88898985)	613	1.12325	7	4	3	0.1428571	0.029	APRT	GALNS
chr16	+(88946316..88946961)	645	2.543	9	5	4	0.1111111	0.857	PABPN1L	CBFA2T3
chr16	+(89003812..89004346)	534	0.11182	10	7	3	0.4	0.008	PABPN1L	CBFA2T3
chr16	+(89102986..89104239)	1253	0.06262	21	9	12	0.1428571	6.2118E-05	CBFA2T3	ACSF3
chr16	+(89119025..89120202)	1177	0.11182	20	9	11	0.1	8.472E-05	CBFA2T3	ACSF3
chr16	+(89133206..89133870)	664	2.543	6	2	4	0.3333333	0.067	CBFA2T3	ACSF3
chr16	+(89212984..89213496)	512	2.543	6	3	3	0	0.05	ACSF3	C16orf81
chr16	+(89243953..89244608)	655	0.55004	8	4	4	0	0.014	CDH15	ZNF778
chr16	+(89370750..89371350)	600	2.543	6	4	2	0.3333333	0.067	ZNF778	ANKRD11
chr16	+(89379108..89379744)	636	2.543	6	3	3	0	0.05	ZNF778	ANKRD11

chr16	+(89454947..89455517)	570	0.55004	8	3	5	0.25	0.018	ZNF778	ANKRD11
chr16	+(89617511..89618169)	658	0.55004	8	3	5	0.25	0.018	SPG7	RPL13
chr16	+(89623218..89623728)	510	2.543	9	5	4	0.1111111	0.548	SPG7	RPL13
chr16	+(89849064..89849600)	536	2.543	11	5	6	0.0909091	0.42756607	ZNF276	FANCA
chr16	+(89970395..89971050)	655	1.12325	8	5	3	0.25	0.018	TCF25	MC1R
chr16	+(90124496..90125006)	510	2.543	10	5	5	0	0.03790009	LOC100130015	PRDM7
chr16	+(90161513..90162015)	502	1.12325	11	4	7	0.2727273	0.012	PRDM7	
chr16	+(90170779..90171308)	529	1.12325	10	4	6	0.2	0.019	PRDM7	
chr17	+(94538..95351)	813	0.00099	18	6	12	0.3333333	0.00037352	DOC2B	RPH3AL
chr17	+(96258..96868)	610	1.42674	7	3	4	0.1428571	0.029	DOC2B	RPH3AL
chr17	+(101400..102081)	681	0.17344	10	7	3	0.4	0.008	DOC2B	RPH3AL
chr17	+(123138..123640)	502	3.12167	6	4	2	0.3333333	0.067	DOC2B	RPH3AL
chr17	+(133438..134138)	700	0.70612	9	6	3	0.3333333	0.274	DOC2B	RPH3AL
chr17	+(147230..148245)	1015	0.70612	14	8	6	0.1428571	0.99902711	DOC2B	RPH3AL
chr17	+(177835..178535)	700	1.42674	11	7	4	0.2727273	0.997	DOC2B	RPH3AL
chr17	+(435862..436402)	540	0.70612	10	3	7	0.4	0.742	FAM101B	VPS53
chr17	+(694560..695081)	521	0.17344	17	7	10	0.1764706	0.31279262	RNMTL1	NXN
chr17	+(728825..729429)	604	0.70612	8	4	4	0	0.014	RNMTL1	NXN
chr17	+(773016..773585)	569	3.12167	6	4	2	0.3333333	0.067	RNMTL1	NXN
chr17	+(915968..916668)	700	0.70612	12	5	7	0.1666667	0.00224163	TIMM22	ABR
chr17	+(984007..984685)	678	0.70612	14	8	6	0.1428571	0.00097289	TIMM22	ABR
chr17	+(994333..995482)	1149	0.70612	19	9	10	0.0526316	0.00072543	TIMM22	ABR
chr17	+(1031563..1032263)	700	3.12167	10	4	6	0.2	0.995	TIMM22	ABR
chr17	+(1472713..1473835)	1122	0.04228	18	11	7	0.2222222	0.0002444	PITPNA	SLC43A2
chr17	+(1496344..1496953)	609	0.01781	13	9	4	0.3846154	0.001	PITPNA	SLC43A2
chr17	+(1531561..1532092)	531	3.12167	6	2	4	0.3333333	0.067	PITPNA	SLC43A2
chr17	+(1761023..1761525)	502	0.70612	10	4	6	0.2	0.005	RPA1	RTN4RL1
chr17	+(2699741..2700398)	657	3.12167	10	6	4	0.2	0.457	RAP1GAP2	OR1D5
chr17	+(2760060..2760683)	623	1.42674	7	4	3	0.1428571	0.029	RAP1GAP2	OR1D5
chr17	+(2768950..2769545)	595	0.70612	8	4	4	0	0.014	RAP1GAP2	OR1D5
chr17	+(2787105..2787690)	585	0.32584	9	5	4	0.1111111	0.008	RAP1GAP2	OR1D5
chr17	+(2801667..2802269)	602	0.70612	8	4	4	0	0.014	RAP1GAP2	OR1D5
chr17	+(2823984..2824684)	700	0.32584	9	6	3	0.3333333	0.012	RAP1GAP2	OR1D5
chr17	+(3548360..3549007)	647	0.32584	9	4	5	0.1111111	0.008	CTNS	TAX1BP3

chr17	+(3584272..3584834)	562	0.70612	8	5	3	0.25	0.018	TMEM93	P2RX5	
chr17	+(3592680..3593435)	755	0.01033	18	11	7	0.2222222	0.00216645	TMEM93	P2RX5	
chr17	+(3785886..3786430)	544	1.42674	8	4	4	0	0.171	C17orf85	CAMKK1	
chr17	+(3817376..3817965)	589	0.17344	10	4	6	0.2	0.005	CAMKK1	P2RX1	
chr17	+(4442608..4443123)	515	3.12167	6	2	4	0.3333333	0.067	SPNS2	MYBBP1A	
chr17	+(4448817..4449624)	807	0.01033	22	9	13	0.1818182	0.30824348	SPNS2	MYBBP1A	
chr17	+(4478921..4479535)	614	0.09029	15	6	9	0.2	0.85557782	GGT6	SMTNL2	
chr17	+(4505931..4506568)	637	0.32584	9	5	4	0.1111111	0.008	SMTNL2	ALOX15	
chr17	+(4797401..4798101)	700	0.01781	13	9	4	0.3846154	0.001	MINK1	CHRNE	v
chr17	+(4805601..4806175)	574	0.70612	10	7	3	0.4	0.017	MINK1	CHRNE	v
chr17	+(4842603..4843291)	688	1.42674	9	6	3	0.3333333	0.048	GP1BA	SLC25A11	
chr17	+(5045256..5045900)	644	0.70612	12	6	6	0	0.00520281	USP6	ZNF594	
chr17	+(5048651..5049161)	510	3.12167	8	5	3	0.25	0.196	USP6	ZNF594	
chr17	+(5049218..5049786)	568	0.70612	10	7	3	0.4	0.008	USP6	ZNF594	
chr17	+(5075943..5076489)	546	1.42674	11	4	7	0.2727273	0.003	USP6	ZNF594	
chr17	+(6349510..6350210)	700	1.42674	10	3	7	0.4	0.992	FAM64A	PITPNM3	
chr17	+(6390939..6391635)	696	3.12167	9	6	3	0.3333333	0.988	FAM64A	PITPNM3	
chr17	+(6458160..6458715)	555	0.70612	8	4	4	0	0.014	FAM64A	PITPNM3	
chr17	+(6462669..6463391)	722	0.00438	15	8	7	0.0666667	0.00059687	PITPNM3	KIAA0753	
chr17	+(7130596..7131171)	575	3.12167	8	4	4	0	0.171	MIR324	DVL2	
chr17	+(7190378..7191078)	700	0.32584	10	4	6	0.2	0.005	SLC2A4	YBX2	
chr17	+(7196862..7197541)	679	0.70612	12	4	8	0.3333333	0.976	SLC2A4	YBX2	
chr17	+(7393122..7393822)	700	0.09029	11	6	5	0.0909091	0.00308495	POLR2A	TNFSF12	
chr17	+(7416262..7416861)	599	1.13024	28	15	13	0.0714286	0.01129689	POLR2A	TNFSF12	
chr17	+(7464430..7464943)	513	0.70612	8	3	5	0.25	0.018	TNFSF13	SENP3	
chr17	+(7466349..7467466)	1117	0.70612	16	7	9	0.125	0.00042755	SENP3	EIF4A1	
chr17	+(7480378..7480879)	501	2.28029	12	5	7	0.1666667	0.02117853	SNORD10	SNORA67	
chr17	+(7483147..7483793)	646	0.01781	19	7	12	0.2631579	0.0020296	CD68	MPDU1	
chr17	+(7491452..7492037)	585	0.32584	10	5	5	0	0.00451172	MPDU1	SOX15	
chr17	+(7554413..7555145)	732	0.04228	15	5	10	0.3333333	0.0330963	ATP1B2	TP53	
chr17	+(7576562..7577115)	553	3.12167	9	4	5	0.1111111	0.206	ATP1B2	TP53	
chr17	+(7695948..7696547)	599	1.42674	7	3	4	0.1428571	0.029	RPL29P2	KDM6B	
chr17	+(7718107..7718807)	700	0.17344	10	4	6	0.2	0.005	RPL29P2	KDM6B	
chr17	+(8166156..8166711)	555	3.12167	9	5	4	0.1111111	0.032	PFAS	SLC25A35	

chr17	+(9007878..9008412)	534	3.12167	8	5	3	0.25	0.018	NTN1	STX8
chr17	+(9085692..9086392)	700	0.01781	16	9	7	0.125	0.13318996	NTN1	STX8
chr17	+(9114085..9114785)	700	0.17344	14	6	8	0.1428571	0.84915021	NTN1	STX8
chr17	+(9232858..9233558)	700	0.09029	11	7	4	0.2727273	0.003	NTN1	STX8
chr17	+(9503080..9503642)	562	3.12167	6	2	4	0.3333333	0.067	WDR16	USP43
chr17	+(9596100..9596752)	652	3.12167	8	3	5	0.25	0.036	USP43	DHRS7C
chr17	+(9775141..9776293)	1152	3.12167	12	6	6	0	0.00197388	GLP2R	RCVRN
chr17	+(10000182..10000882)	700	3.12167	11	6	5	0.0909091	0.99691505	RCVRN	GAS7
chr17	+(10206405..10207081)	676	2.28029	17	9	8	0.0588235	0.00194621	GAS7	MYH13
chr17	+(10303762..10304462)	700	0.70612	13	9	4	0.3846154	0.926	MYH13	MYH8
chr17	+(12897453..12898046)	593	1.42674	9	3	6	0.3333333	0.012	ARHGAP44	ELAC2
chr17	+(12900306..12901006)	700	0.70612	10	4	6	0.2	0.005	ARHGAP44	ELAC2
chr17	+(15612911..15614100)	1189	0.70612	18	10	8	0.1111111	0.00168325	ZNF286A	TBC1D26
chr17	+(16068064..16068631)	567	0.70612	10	5	5	0	0.0081468	TTC19	NCOR1
chr17	+(16285423..16285970)	547	0.70612	16	6	10	0.25	0.45681333	UBB	TRPV2
chr17	+(16611971..16612671)	700	0.81546	41	25	16	0.2195122	0.0325841	CCDC144A	LOC162632
chr17	+(16631031..16631533)	502	3.12167	13	6	7	0.0769231	0.00213737	CCDC144A	LOC162632
chr17	+(16701350..16701864)	514	3.12167	8	4	4	0	0.057	FAM106C	KRT16P2
chr17	+(16978664..16979844)	1180	1.42674	13	5	8	0.2307692	0.0017074	MPRIP	PLD6
chr17	+(17010599..17011396)	797	0.17344	16	9	7	0.125	0.00042755	MPRIP	PLD6
chr17	+(17039471..17039991)	520	3.12167	6	2	4	0.3333333	0.067	MPRIP	PLD6
chr17	+(17064427..17065015)	588	3.12167	6	2	4	0.3333333	0.067	MPRIP	PLD6
chr17	+(17105902..17106428)	526	1.42674	8	5	3	0.25	0.125	MPRIP	PLD6
chr17	+(17506638..17507280)	642	1.42674	7	4	3	0.1428571	0.029	PEMT	RAI1
chr17	+(17512717..17513252)	535	3.12167	6	3	3	0	0.05	PEMT	RAI1
chr17	+(17555038..17556376)	1338	0.00438	24	9	15	0.25	0.9999715	PEMT	RAI1
chr17	+(17626070..17626663)	593	3.12167	7	3	4	0.1428571	0.2	RAI1	SMCR5
chr17	+(18000980..18002172)	1192	0.70612	15	7	8	0.0666667	0.98968122	DRG2	MYO15A
chr17	+(18039572..18040107)	535	3.12167	6	2	4	0.3333333	0.067	MYO15A	ALKBH5
chr17	+(18137919..18138469)	550	3.12167	7	3	4	0.1428571	0.029	LLGL1	FLII
chr17	+(18486367..18486878)	511	3.12167	15	9	6	0.2	0.00160811	FAM106A	CCDC144B
chr17	+(18850441..18851577)	1136	1.42674	13	7	6	0.0769231	0.9986501	PRPSAP2	SLC5A10
chr17	+(18917405..18918508)	1103	0.70612	18	9	9	0	0.0015476	FAM83G	GRAP
chr17	+(19284943..19285476)	533	1.42674	9	5	4	0.1111111	0.008	MAPK7	MFAP4

chr17	+(19646284..19646984)	700	0.09029	16	11	5	0.375	0.0009184	SLC47A2	ALDH3A1	
chr17	+(20015018..20015570)	552	1.42674	9	5	4	0.1111111	0.008	SPECC1	CCDC144C	
chr17	+(20134968..20135652)	684	0.17344	11	7	4	0.2727273	0.003	SPECC1	CCDC144C	
chr17	+(20241193..20241722)	529	2.0662	24	10	14	0.1666667	0.00296128	CCDC144C	LGALS9B	
chr17	+(20254354..20254894)	540	2.0662	25	9	16	0.28	0.67469352	CCDC144C	LGALS9B	
chr17	+(20261067..20261591)	524	1.74239	38	20	18	0.0526316	0.00425452	CCDC144C	LGALS9B	
chr17	+(20265274..20266030)	756	2.75008	38	16	22	0.1578947	0.0011624	CCDC144C	LGALS9B	
chr17	+(20266080..20266600)	520	0.70612	12	7	5	0.1666667	0.00591469	CCDC144C	LGALS9B	
chr17	+(20304139..20305002)	863	0.55542	43	26	17	0.2093023	1.5022E-05	CCDC144C	LGALS9B	
chr17	+(20321291..20321803)	512	1.42674	11	6	5	0.0909091	0.00529357	CCDC144C	LGALS9B	
chr17	+(20641060..20641575)	515	3.12167	6	4	2	0.3333333	0.067	CDRT15L2	CCDC144NL	
chr17	+(20683781..20684478)	697	0.32584	9	6	3	0.3333333	0.012	CDRT15L2	CCDC144NL	
chr17	+(20768577..20769269)	692	0.32584	12	6	6	0	0.00197388	CDRT15L2	CCDC144NL	
chr17	+(21075154..21075655)	501	0.70612	10	5	5	0	0.05859256	DHRS7B	TMEM11	
chr17	+(21192303..21193454)	1151	0.70612	19	7	12	0.2631579	0.72294343	MAP2K3	KCNJ12	
chr17	+(21199842..21200517)	675	1.42674	7	4	3	0.1428571	0.029	MAP2K3	KCNJ12	
chr17	+(21210346..21210908)	562	0.70612	8	5	3	0.25	0.018	MAP2K3	KCNJ12	
chr17	+(21240741..21241379)	638	1.42674	7	4	3	0.1428571	0.029	MAP2K3	KCNJ12	
chr17	+(21317085..21317652)	567	1.42674	12	6	6	0	0.97266803	KCNJ18	C17orf51	
chr17	+(21317706..21318437)	731	0.00387	16	7	9	0.125	0.00042755	KCNJ18	C17orf51	
chr17	+(21318947..21319666)	719	0.04228	14	9	5	0.2857143	0.00981533	KCNJ18	C17orf51	
chr17	+(26955241..26955748)	507	3.12167	6	4	2	0.3333333	0.067	SGK494	KIAA0100	
chr17	+(27075295..27076044)	749	0.32584	17	10	7	0.1764706	0.00314259	TRAF4	C17orf63	
chr17	+(27208141..27208656)	515	1.42674	13	7	6	0.0769231	0.97724986	MIR144	FLOT2	
chr17	+(27208779..27209297)	518	2.28029	12	6	6	0	0.00197388	MIR144	FLOT2	
chr17	+(27228085..27228673)	588	0.70612	12	7	5	0.1666667	0.59622945	FLOT2	DHRS13	
chr17	+(27381221..27381873)	652	0.70612	11	5	6	0.0909091	0.00308495	PIPOX	MYO18A	v
chr17	+(27407598..27408475)	877	0.00211	18	10	8	0.1111111	0.00223263	PIPOX	MYO18A	v
chr17	+(27419579..27420175)	596	0.70612	9	6	3	0.3333333	0.012	PIPOX	MYO18A	v
chr17	+(27426319..27427083)	764	0.04228	12	7	5	0.1666667	0.00224163	PIPOX	MYO18A	v
chr17	+(27930103..27930803)	700	0.09029	11	6	5	0.0909091	0.00308495	ANKRD13B	CORO6	
chr17	+(28326528..28327133)	605	3.12167	10	4	6	0.2	0.033	EFCAB5	CCDC55	
chr17	+(28506178..28506685)	507	3.12167	15	6	9	0.2	0.00335832	MIR3184	SLC6A4	
chr17	+(28549349..28550049)	700	0.32584	13	4	9	0.3846154	0.001	MIR3184	SLC6A4	

chr17	+(28562914..28563426)	512	1.42674	7	3	4	0.1428571	0.029	MIR3184	SLC6A4
chr17	+(29557407..29557912)	505	3.12167	9	4	5	0.1111111	0.008	NF1	OMG
chr17	+(29631868..29632389)	521	2.93322	31	13	18	0.1612903	0.00411951	OMG	EVI2B
chr17	+(30266911..30267604)	693	0.11087	44	17	27	0.2272727	0.01210858	SUZ12	LRRC37B
chr17	+(30351690..30352193)	503	3.12167	16	6	10	0.25	0.00240046	LRRC37B	SH3GL1P1
chr17	+(30354137..30355405)	1268	0.10809	42	27	15	0.2857143	0.83753418	LRRC37B	SH3GL1P1
chr17	+(30362335..30362856)	521	0.32584	18	12	6	0.3333333	0.00247894	LRRC37B	SH3GL1P1
chr17	+(30421564..30422258)	694	0.04228	38	25	13	0.3157895	0.00607612	SH3GL1P1	RHOT1
chr17	+(30519985..30520558)	573	0.32584	13	7	6	0.0769231	0.0013499	ARGFXP2	RHBDL3
chr17	+(30824672..30825863)	1191	0.32584	16	6	10	0.25	0.02544691	CDK5R1	MYO1D
chr17	+(32924674..32925374)	700	0.32584	10	4	6	0.2	0.129	TMEM132E	CCT6B
chr17	+(33806126..33806650)	524	3.12167	7	4	3	0.1428571	0.029	SLFN13	SLFN12L
chr17	+(34149466..34149981)	515	1.42674	11	4	7	0.2727273	0.979	TAF15	C17orf66
chr17	+(34417275..34417853)	578	3.12167	10	6	4	0.2	0.129	CCL18	CCL3
chr17	+(34584287..34584845)	558	0.32584	11	4	7	0.2727273	0.003	CCL4L2_dup1	TBC1D3C_dup1
chr17	+(34624469..34625106)	637	1.42674	10	4	6	0.2	0.005	TBC1D3C_dup1	CCL3L3_dup2
chr17	+(34625369..34625880)	511	2.0662	32	10	22	0.375	0.00014824	TBC1D3C_dup1	CCL3L3_dup2
chr17	+(35878683..35879253)	570	0.17344	11	6	5	0.0909091	0.00308495	DUSP14	SYNRG
chr17	+(36635536..36636062)	526	3.12167	17	10	7	0.1764706	0.72090768	ARHGAP23	SRCIN1
chr17	+(36909111..36909962)	851	0.00024	22	15	7	0.3636364	0.00410387	PSMB3	PIP4K2B
chr17	+(36922697..36923202)	505	1.42674	7	4	3	0.1428571	0.029	PSMB3	PIP4K2B
chr17	+(36942453..36943153)	700	0.70612	9	6	3	0.3333333	0.012	PSMB3	PIP4K2B
chr17	+(37070987..37071935)	948	0.04228	22	7	15	0.3636364	0.00018558	LASP1	FBXO47
chr17	+(37110964..37111475)	511	3.12167	8	5	3	0.25	0.018	LASP1	FBXO47
chr17	+(37195602..37196136)	534	0.70612	13	6	7	0.0769231	0.00332094	FLJ43826	LOC100131347
chr17	+(37221789..37222350)	561	0.32584	9	5	4	0.1111111	0.008	LOC100131347	PLXDC1
chr17	+(37565973..37566499)	526	0.70612	9	4	5	0.1111111	0.008	FBXL20	MED1
chr17	+(37818007..37818933)	926	0.32584	17	9	8	0.0588235	0.000266	STARD3	TCAP
chr17	+(37872854..37873554)	700	3.12167	9	6	3	0.3333333	0.988	ERBB2	C17orf37
chr17	+(38100503..38101078)	575	1.42674	7	4	3	0.1428571	0.029	LOC728129	GSDMA
chr17	+(38129549..38130155)	606	1.42674	13	6	7	0.0769231	0.97724986	GSDMA	PSMD3
chr17	+(38307131..38307679)	548	0.32584	9	6	3	0.3333333	0.012	CASC3	RAPGEFL1
chr17	+(38402699..38403373)	674	0.32584	9	5	4	0.1111111	0.008	WIPF2	CDC6
chr17	+(38487413..38488007)	594	3.12167	9	6	3	0.3333333	0.81	RARA	GJD3

chr17	+(38504476..38505027)	551	0.70612	9	4	5	0.1111111	0.056	RARA	GJD3	
chr17	+(38567444..38567957)	513	3.12167	7	3	4	0.1428571	0.029	GJD3	TOP2A	v
chr17	+(38643234..38643743)	509	1.42674	15	6	9	0.2	0.03854994	IGFBP4	TNS4	
chr17	+(39305223..39305758)	535	3.12167	9	4	5	0.1111111	0.095	KRTAP4-12	KRTAP4-5	
chr17	+(39766417..39767106)	689	1.42674	9	6	3	0.3333333	0.274	KRT14	KRT16	
chr17	+(39768068..39768854)	786	0.32584	30	10	20	0.3333333	0.00160122	KRT14	KRT16	
chr17	+(39776627..39777723)	1096	0.00438	35	24	11	0.3714286	0.02750442	KRT16	KRT17	
chr17	+(39913496..39913998)	502	3.12167	6	3	3	0	0.05	HAP1	JUP	v
chr17	+(40125206..40125906)	700	3.12167	9	3	6	0.3333333	0.012	CNP	DNAJC7	
chr17	+(40330599..40331281)	682	0.70612	8	4	4	0	0.014	RAB5C	KCNH4	
chr17	+(40452762..40453314)	552	0.70612	8	4	4	0	0.014	STAT5A	STAT3	
chr17	+(40725063..40725581)	518	1.42674	9	4	5	0.1111111	0.056	MLX	PSMC3IP	
chr17	+(41208877..41209444)	567	0.32584	16	11	5	0.375	0.02370919	RND2	BRCA1	
chr17	+(41400071..41400876)	805	2.6E-10	81	37	44	0.0864198	9.2586E-07	TMEM106A	LOC100130581	
chr17	+(41464567..41465071)	504	1.42674	11	7	4	0.2727273	0.003	TMEM106A	LOC100130581	
chr17	+(41465988..41466509)	521	0.32584	25	17	8	0.36	0.67940706	TMEM106A	LOC100130581	
chr17	+(41477242..41478409)	1167	1.42674	15	5	10	0.3333333	0.27014569	ARL4D	MIR2117	
chr17	+(42056081..42056781)	700	0.17344	10	4	6	0.2	0.005	PPY	PYY	
chr17	+(42090083..42090688)	605	0.09029	18	10	8	0.1111111	0.00642562	NAGS	TMEM101	
chr17	+(42169429..42170308)	879	1.42674	14	5	9	0.2857143	0.0020741	G6PC3	HDAC5	
chr17	+(42273495..42274000)	505	3.12167	6	3	3	0	0.05	TMUB2	ATXN7L3	
chr17	+(42325374..42326074)	700	0.32584	13	8	5	0.2307692	0.0017074	UBTF	SLC4A1	
chr17	+(42391485..42392130)	645	3.12167	6	4	2	0.3333333	0.067	RUNDC3A	SLC25A39	
chr17	+(42397557..42398092)	535	3.12167	9	6	3	0.3333333	0.548	RUNDC3A	SLC25A39	
chr17	+(42422887..42423709)	822	0.01033	16	6	10	0.25	0.02544691	GRN	FAM171A2	
chr17	+(42475177..42475703)	526	3.12167	9	3	6	0.3333333	0.024	ITGA2B	GPATCH8	
chr17	+(42526177..42526877)	700	3.12167	9	3	6	0.3333333	0.988	ITGA2B	GPATCH8	
chr17	+(42785967..42786597)	630	1.42674	12	6	6	0	0.00197388	CCDC43	DBF4B	
chr17	+(42824402..42824972)	570	1.42674	8	4	4	0	0.014	DBF4B	ADAM11	
chr17	+(42987418..42987929)	511	1.42674	12	8	4	0.3333333	0.99671074	CCDC103	GFAP	
chr17	+(42990670..42991206)	536	3.12167	8	3	5	0.25	0.5	CCDC103	GFAP	
chr17	+(43205089..43205789)	700	0.09029	18	7	11	0.2222222	0.9997556	NMT1	PLCD3	
chr17	+(43332323..43332884)	561	0.17344	14	5	9	0.2857143	0.00313484	LOC100133991	C17orf46	
chr17	+(44053155..44054233)	1078	0.01781	25	12	13	0.04	1.1045E-05	LOC100130148	STH	

chr17	+(44376966..44377498)	532	1.42674	12	8	4	0.3333333	0.024	LRRC37A	ARL17A_dup1	
chr17	+(44590804..44591449)	645	0.70612	14	7	7	0	0.05511153	LRRC37A2	ARL17A_dup2	
chr17	+(44591957..44592630)	673	1.42674	18	7	11	0.2222222	0.03168284	LRRC37A2	ARL17A_dup2	
chr17	+(44618028..44618580)	552	1.74239	34	18	16	0.0588235	1.0983E-05	LRRC37A2	ARL17A_dup2	
chr17	+(44626268..44627468)	1200	0.11087	51	28	23	0.0980392	0.0018882	LRRC37A2	ARL17A_dup2	
chr17	+(44630536..44631232)	696	0.01781	25	13	12	0.04	0.00967052	LRRC37A2	ARL17A_dup2	
chr17	+(44632310..44632816)	506	2.75008	24	11	13	0.0833333	0.00296175	LRRC37A2	ARL17A_dup2	
chr17	+(44653431..44653936)	505	2.0662	25	11	14	0.12	0.00012227	LRRC37A2	ARL17A_dup2	
chr17	+(44701438..44702058)	620	0.04228	21	13	8	0.2380952	0.00019363	NSFP1_dup2	WNT3	
chr17	+(44771317..44771828)	511	3.12167	16	6	10	0.25	0.03259822	NSFP1_dup2	WNT3	
chr17	+(44781948..44782629)	681	0.61533	26	14	12	0.0769231	0.06141133	NSFP1_dup2	WNT3	
chr17	+(45265775..45266834)	1059	0.01781	32	10	22	0.375	0.46759709	RPRML	CDC27	
chr17	+(45470168..45470833)	665	3.12167	6	2	4	0.3333333	0.067	C17orf57	LOC100272146	
chr17	+(47916982..47917613)	631	0.70612	9	3	6	0.3333333	0.012	MYST2	TAC4	
chr17	+(47985880..47986503)	623	3.12167	10	6	4	0.2	0.762	TAC4	DLX4	
chr17	+(48185299..48185889)	590	3.12167	6	4	2	0.3333333	0.067	PDK2	SAMD14	
chr17	+(48620008..48620690)	682	0.70612	8	3	5	0.25	0.018	EPN3	SPATA20	
chr17	+(48916802..48917324)	522	3.12167	11	4	7	0.2727273	0.158	WFIKKN2	TOB1	
chr17	+(48922871..48923547)	676	0.32584	9	6	3	0.3333333	0.012	WFIKKN2	TOB1	
chr17	+(49072476..49073068)	592	1.42674	7	4	3	0.1428571	0.029	TOB1	SPAG9	v
chr17	+(49365355..49365941)	586	1.42674	13	7	6	0.0769231	0.19568297	UTP18	CA10	
chr17	+(51710167..51710747)	580	1.42674	7	3	4	0.1428571	0.029	CA10	KIF2B	
chr17	+(51900742..51901306)	564	0.09029	12	6	6	0	0.00197388	KIF2B	TOM1L1	
chr17	+(54921210..54921882)	672	0.17344	14	7	7	0	0.00202049	DGKE	MTVR2	
chr17	+(55074076..55074708)	632	3.12167	6	2	4	0.3333333	0.067	SCPEP1	RNF126P1	
chr17	+(55439055..55439755)	700	0.17344	10	7	3	0.4	0.008	MSI2	MRPS23	
chr17	+(55511298..55511998)	700	0.17344	10	3	7	0.4	0.008	MSI2	MRPS23	
chr17	+(55739797..55740730)	933	1.42674	13	6	7	0.0769231	0.0013499	MSI2	MRPS23	
chr17	+(55856394..55857094)	700	0.04228	12	5	7	0.1666667	0.00224163	MSI2	MRPS23	
chr17	+(56083640..56084150)	510	1.42674	10	7	3	0.4	0.058	VEZF1	SRSF1	
chr17	+(56383214..56383913)	699	1.42674	11	6	5	0.0909091	0.76739559	MPO	BZRAP1	
chr17	+(56676604..56677187)	583	1.42674	10	4	6	0.2	0.005	C17orf47	TEX14	v
chr17	+(57138236..57138746)	510	3.12167	6	3	3	0	0.05	PPM1E	TRIM37	
chr17	+(58937086..58937744)	658	3.12167	6	4	2	0.3333333	0.067	BCAS3	TBX2	

chr17	+(59457036..59457736)	700	0.04228	15	7	8	0.0666667	0.20894348	BCAS3	TBX2
chr17	+(59520958..59521485)	527	0.70612	8	4	4	0	0.014	C17orf82	TBX4
chr17	+(59560490..59561024)	534	3.12167	6	2	4	0.3333333	0.067	TBX4	NACA2
chr17	+(59562717..59563433)	716	0.32584	13	9	4	0.3846154	0.001	TBX4	NACA2
chr17	+(60348301..60348810)	509	3.12167	10	7	3	0.4	0.058	MED13	TBC1D3P2
chr17	+(60362239..60363140)	901	0.70612	29	17	12	0.1724138	0.13414294	TBC1D3P2	EFCAB3
chr17	+(60363154..60363655)	501	2.28029	22	8	14	0.2727273	0.07588612	TBC1D3P2	EFCAB3
chr17	+(60365666..60366207)	541	1.42674	12	7	5	0.1666667	0.18587565	TBC1D3P2	EFCAB3
chr17	+(60368010..60368715)	705	0.1736	73	42	31	0.1506849	1.1553E-11	TBC1D3P2	EFCAB3
chr17	+(60629190..60630226)	1036	0.00438	52	26	26	0	0.04437669	TLK2	MRC2
chr17	+(60630767..60631382)	615	3.12167	7	3	4	0.1428571	0.029	TLK2	MRC2
chr17	+(60768282..60768851)	569	0.70612	8	3	5	0.25	0.018	MRC2	40978
chr17	+(60793353..60794549)	1196	1.42674	13	6	7	0.0769231	0.0013499	MRC2	40978
chr17	+(60794584..60795279)	695	1.42674	9	6	3	0.3333333	0.012	MRC2	40978
chr17	+(61575679..61576595)	916	0.04228	23	11	12	0.0434783	2.4325E-05	ACE	KCNH6
chr17	+(61627907..61628557)	650	1.42674	8	3	5	0.25	0.018	DCAF7	TACO1
chr17	+(61986780..61987293)	513	3.12167	9	3	6	0.3333333	0.012	CSH1	CSHL1
chr17	+(61987425..61988100)	675	0.09029	20	9	11	0.1	0.15252943	CSH1	CSHL1
chr17	+(62033399..62034009)	610	3.12167	9	3	6	0.3333333	0.988	CD79B	SCN4A
chr17	+(62793421..62793987)	566	0.70612	14	8	6	0.1428571	0.99508836	LOC146880	PLEKHM1P
chr17	+(62810860..62811634)	774	0.32584	20	13	7	0.3	0.02165575	LOC146880	PLEKHM1P
chr17	+(62893074..62893608)	534	1.42674	8	5	3	0.25	0.071	MIR4315-2_dup2	LRRC37A3
chr17	+(62952468..62953069)	601	0.70612	9	6	3	0.3333333	0.012	LRRC37A3	AMZ2P1
chr17	+(63010660..63011201)	541	3.12167	9	5	4	0.1111111	0.857	AMZ2P1	GNA13
chr17	+(64750251..64751452)	1201	0.09029	19	11	8	0.1578947	0.99986003	PRKCA	MIR634
chr17	+(64837999..64838585)	586	1.42674	7	4	3	0.1428571	0.029	MIR634	CACNG5
chr17	+(64876534..64877073)	539	0.70612	10	7	3	0.4	0.017	CACNG5	CACNG4
chr17	+(64949519..64950138)	619	3.12167	6	4	2	0.3333333	0.067	CACNG5	CACNG4
chr17	+(65131988..65132499)	511	3.12167	10	6	4	0.2	0.033	CACNG1	HELZ
chr17	+(65490643..65491220)	577	3.12167	9	3	6	0.3333333	0.012	PITPNC1	NOL11
chr17	+(67260605..67261455)	850	0.04228	21	12	9	0.1428571	0.15988353	ABCA10	ABCA5
chr17	+(67532855..67533550)	695	3.12167	6	4	2	0.3333333	0.067	MAP2K6	KCNJ16
chr17	+(67683993..67684550)	557	0.17344	10	5	5	0	0.00451172	MAP2K6	KCNJ16
chr17	+(70557947..70558647)	700	1.42674	10	3	7	0.4	0.992	SOX9	LOC100499467

chr17	+(70568921..70569619)	698	3.12167	11	6	5	0.0909091	0.00308495	SOX9	LOC100499467
chr17	+(71381831..71382528)	697	1.42674	9	3	6	0.3333333	0.131	CDC42EP4	SDK2
chr17	+(71397838..71398409)	571	0.01033	14	9	5	0.2857143	0.0013499	CDC42EP4	SDK2
chr17	+(71417910..71418437)	527	0.70612	12	7	5	0.1666667	0.00224163	CDC42EP4	SDK2
chr17	+(71702433..71702973)	540	3.12167	6	2	4	0.3333333	0.067	SDK2	C17orf54
chr17	+(72217748..72218448)	700	0.17344	14	5	9	0.2857143	0.00981533	TTYH2	DNAI2
chr17	+(72239718..72240678)	960	1.42674	14	7	7	0	0.91014375	TTYH2	DNAI2
chr17	+(72310294..72311472)	1178	0.09029	25	15	10	0.2	0.8540426	DNAI2	KIF19
chr17	+(72728533..72729228)	695	3.12167	7	3	4	0.1428571	0.2	CD300LF	MIR3615
chr17	+(72729848..72730485)	637	1.42674	8	3	5	0.25	0.286	CD300LF	MIR3615
chr17	+(72769015..72769516)	501	0.70612	8	4	4	0	0.014	SLC9A3R1	NAT9
chr17	+(72853506..72854013)	507	0.70612	8	3	5	0.25	0.018	TMEM104	GRIN2C
chr17	+(72944232..72944932)	700	0.04228	12	6	6	0	0.00197388	OTOP3	C17orf28
chr17	+(72947604..72948132)	528	3.12167	6	3	3	0	0.05	OTOP3	C17orf28
chr17	+(73016757..73017265)	508	3.12167	12	6	6	0	0.05465729	ICT1	ATP5H
chr17	+(73671067..73671593)	526	3.12167	11	5	6	0.0909091	0.81934478	SAP30BP	ITGB4
chr17	+(73700273..73701645)	1372	3.12167	15	6	9	0.2	0.96145006	SAP30BP	ITGB4
chr17	+(73725955..73727140)	1185	0.17344	20	13	7	0.3	0.00627746	ITGB4	GALK1
chr17	+(73745948..73746648)	700	0.70612	13	5	8	0.2307692	0.97148006	ITGB4	GALK1
chr17	+(74077761..74078272)	511	3.12167	6	4	2	0.3333333	0.067	ZACN	EXOC7
chr17	+(74274980..74275557)	577	3.12167	8	5	3	0.25	0.018	FAM100B	QRICH2
chr17	+(74737880..74738534)	654	3.12167	7	4	3	0.1428571	0.029	MFSD11	MGAT5B
chr17	+(74836236..74836805)	569	3.12167	6	3	3	0	0.05	MFSD11	MGAT5B
chr17	+(74909043..74909743)	700	3.12167	9	3	6	0.3333333	0.012	MGAT5B	C17orf86
chr17	+(74958050..74958580)	530	3.12167	6	3	3	0	0.05	MGAT5B	C17orf86
chr17	+(75201393..75201925)	532	0.32584	12	5	7	0.1666667	0.18587565	SEC14L1	41161
chr17	+(75398971..75399539)	568	0.04228	12	7	5	0.1666667	0.00224163	MIR4316	FLJ45079
chr17	+(75477306..75477839)	533	1.42674	11	4	7	0.2727273	0.394	MIR4316	FLJ45079
chr17	+(75596925..75597430)	505	3.12167	6	4	2	0.3333333	0.067	MIR4316	FLJ45079
chr17	+(75690478..75691027)	549	0.70612	8	5	3	0.25	0.018	MIR4316	FLJ45079
chr17	+(75869750..75870450)	700	0.17344	12	8	4	0.3333333	0.99671074	MIR4316	FLJ45079
chr17	+(75877638..75878207)	569	0.70612	10	7	3	0.4	0.008	MIR4316	FLJ45079
chr17	+(76045769..76046286)	517	0.32584	9	6	3	0.3333333	0.012	TNRC6C	TMC6
chr17	+(76093367..76094067)	700	0.32584	9	3	6	0.3333333	0.012	TNRC6C	TMC6

chr17	+(76567261..76567961)	700	0.09029	11	5	6	0.0909091	0.00308495	PGS1	DNAH17
chr17	+(77079404..77080076)	672	0.17344	11	4	7	0.2727273	0.003	ENGASE	RBFOX3
chr17	+(77103736..77104255)	519	1.42674	7	4	3	0.1428571	0.029	ENGASE	RBFOX3
chr17	+(77140849..77141549)	700	0.01781	15	9	6	0.2	0.00073136	ENGASE	RBFOX3
chr17	+(77186043..77186654)	611	3.12167	10	3	7	0.4	0.192	ENGASE	RBFOX3
chr17	+(77345272..77345908)	636	3.12167	6	3	3	0	0.05	ENGASE	RBFOX3
chr17	+(77452549..77453102)	553	3.12167	6	4	2	0.3333333	0.067	ENGASE	RBFOX3
chr17	+(77537725..77538349)	624	0.70612	8	5	3	0.25	0.018	RBFOX3	ENPP7
chr17	+(77710472..77711051)	579	0.17344	11	4	7	0.2727273	0.003	ENPP7	CBX2
chr17	+(78117814..78118378)	564	3.12167	6	3	3	0	0.05	GAA	EIF4A3
chr17	+(78190251..78190941)	690	0.70612	13	8	5	0.2307692	0.76789284	CARD14	SGSH
chr17	+(78228197..78228748)	551	1.42674	7	3	4	0.1428571	0.029	SLC26A11	RNF213
chr17	+(78231373..78232073)	700	0.17344	10	6	4	0.2	0.005	SLC26A11	RNF213
chr17	+(78361053..78361657)	604	3.12167	6	4	2	0.3333333	0.067	RNF213	LOC100294362
chr17	+(78403449..78403962)	513	3.12167	6	3	3	0	0.05	FLJ35220	NPTX1
chr17	+(78636829..78638443)	1614	0.32584	23	16	7	0.3913043	0.68000299	RPTOR	CHMP6
chr17	+(78809759..78810459)	700	0.32584	13	4	9	0.3846154	0.999	RPTOR	CHMP6
chr17	+(78828893..78829582)	689	0.70612	10	3	7	0.4	0.742	RPTOR	CHMP6
chr17	+(79029965..79031200)	1235	0.32584	18	12	6	0.3333333	0.99962648	BAIAP2	AATK
chr17	+(79041793..79042402)	609	3.12167	6	2	4	0.3333333	0.067	BAIAP2	AATK
chr17	+(79063707..79064407)	700	3.12167	11	5	6	0.0909091	0.99691505	BAIAP2	AATK
chr17	+(79085659..79086359)	700	3.12167	10	6	4	0.2	0.995	BAIAP2	AATK
chr17	+(79098295..79098828)	533	3.12167	7	3	4	0.1428571	0.029	BAIAP2	AATK
chr17	+(79156834..79157475)	641	3.12167	6	3	3	0	0.05	LOC388428	AZI1
chr17	+(79238943..79239729)	786	0.70612	14	6	8	0.1428571	0.00097289	C17orf89	SLC38A10
chr17	+(79259772..79260471)	699	0.17344	14	9	5	0.2857143	0.0013499	C17orf89	SLC38A10
chr17	+(79636585..79637217)	632	1.42674	7	3	4	0.1428571	0.029	CCDC137	ARL16
chr17	+(80006699..80007225)	526	0.01033	16	7	9	0.125	0.00042755	DCXR	RFNG
chr17	+(80085534..80086234)	700	0.09029	11	4	7	0.2727273	0.003	FASN	CCDC57
chr17	+(80120549..80121102)	553	0.32584	13	4	9	0.3846154	0.001	FASN	CCDC57
chr17	+(80157636..80158159)	523	0.70612	8	5	3	0.25	0.018	FASN	CCDC57
chr17	+(80212959..80213462)	503	1.42674	9	4	5	0.1111111	0.016	SLC16A3	CSNK1D
chr17	+(80255465..80256045)	580	0.32584	9	5	4	0.1111111	0.008	CSNK1D	CD7
chr17	+(80280104..80280756)	652	3.12167	9	6	3	0.3333333	0.726	CD7	SECTM1

chr17	+(80287788..80288398)	610	3.12167	6	2	4	0.3333333	0.067	CD7	SECTM1
chr17	+(80383037..80383728)	691	0.17344	10	7	3	0.4	0.008	HEXDC	C17orf62
chr17	+(80523794..80524437)	643	3.12167	6	2	4	0.3333333	0.067	FOXK2	WDR45L
chr17	+(80559129..80559834)	705	0.04228	14	8	6	0.1428571	0.0140929	FOXK2	WDR45L
chr17	+(80789070..80789649)	579	0.70612	9	6	3	0.3333333	0.012	TBCD	ZNF750
chr17	+(80962553..80963253)	700	0.00211	18	6	12	0.3333333	0.00037352	ZNF750	B3GNTL1
chr18	+(346080..347041)	961	0.97814	14	6	8	0.1428571	0.0983528	THOC1	COLEC12
chr18	+(2752225..2752745)	520	2.05641	10	3	7	0.4	0.258	SMCHD1	EMILIN2
chr18	+(2945583..2946241)	658	0.08524	21	11	10	0.047619	0.6109023	EMILIN2	LPIN2
chr18	+(8337491..8338124)	633	0.01812	12	7	5	0.1666667	0.00224163	PTPRM	LOC100192426
chr18	+(9524390..9525058)	668	0.41893	10	6	4	0.2	0.005	RALBP1	PPP4R1
chr18	+(9588300..9588968)	668	0.97814	8	4	4	0	0.1	RALBP1	PPP4R1
chr18	+(10533394..10533901)	507	2.05641	11	7	4	0.2727273	0.003	NAPG	FAM38B
chr18	+(11533529..11534229)	700	0.0091	13	9	4	0.3846154	0.001	FAM38B	GNAL
chr18	+(11753621..11754149)	528	0.97814	8	5	3	0.25	0.018	GNAL	CHMP1B
chr18	+(12005492..12006192)	700	2.05641	9	6	3	0.3333333	0.012	IMPA2	CIDEA
chr18	+(12075648..12076153)	505	2.05641	16	7	9	0.125	0.05043048	IMPA2	CIDEA
chr18	+(12340012..12340611)	599	2.05641	6	4	2	0.3333333	0.067	TUBB6	AFG3L2
chr18	+(12422932..12423496)	564	2.05641	6	2	4	0.3333333	0.067	SLMO1	SPIRE1
chr18	+(13613407..13614107)	700	0.03999	11	4	7	0.2727273	0.003	C18orf1	C18orf19
chr18	+(14522003..14522604)	601	0.0091	43	27	16	0.255814	7.5505E-08	CXADRP3	POTEC
chr18	+(14523236..14523941)	705	0.00536	71	46	25	0.2957746	1.6418E-11	CXADRP3	POTEC
chr18	+(14537481..14537987)	506	1.49469	31	16	15	0.0322581	0.00133156	CXADRP3	POTEC
chr18	+(14798951..14799458)	507	3.31878	22	13	9	0.1818182	0.0006003	ANKRD30B	MIR3156-2
chr18	+(14812760..14813313)	553	3.31878	18	6	12	0.3333333	0.00037352	ANKRD30B	MIR3156-2
chr18	+(14842533..14843078)	545	2.05641	16	11	5	0.375	0.73338577	MIR3156-2	LOC644669
chr18	+(19995642..19996149)	507	3.31878	22	8	14	0.2727273	0.5	GATA6	CTAGE1
chr18	+(20910589..20911289)	700	0.08524	10	6	4	0.2	0.005	CABLES1	C18orf45
chr18	+(20981419..20982246)	827	0.00054	16	8	8	0	0.00038877	CABLES1	C18orf45
chr18	+(21487383..21488068)	685	0.97814	8	4	4	0	0.029	LAMA3	TTC39C
chr18	+(28721873..28722400)	527	0.97814	11	5	6	0.0909091	0.23260441	DSC2	DSC1
chr18	+(32888796..32889306)	510	2.05641	8	3	5	0.25	0.018	ZNF271	ZNF24
chr18	+(33077559..33078454)	895	0.00807	16	8	8	0	0.04644598	ZNF396	INO80C
chr18	+(34172280..34172940)	660	2.05641	6	3	3	0	0.05	FHOD3	C18orf10

chr18	+(34829704..34830302)	598	0.41893	8	5	3	0.25	0.018	KIAA1328	CELF4
chr18	+(43410785..43411485)	700	0.03999	11	5	6	0.0909091	0.00308495	SIGLEC15	KIAA1632
chr18	+(44435360..44435891)	531	2.05641	9	6	3	0.3333333	0.012	ST8SIA5	PIAS2
chr18	+(45675156..45675856)	700	0.41893	13	5	8	0.2307692	0.9982926	ZBTB7C	KIAA0427
chr18	+(45881179..45881741)	562	2.05641	9	5	4	0.1111111	0.857	ZBTB7C	KIAA0427
chr18	+(46265712..46266235)	523	0.41893	8	5	3	0.25	0.018	KIAA0427	SMAD7
chr18	+(46333612..46334145)	533	0.08524	10	5	5	0	0.00451172	KIAA0427	SMAD7
chr18	+(46377638..46378328)	690	0.97814	11	7	4	0.2727273	0.997	KIAA0427	SMAD7
chr18	+(46521898..46522502)	604	2.05641	6	2	4	0.3333333	0.067	SMAD7	DYM
chr18	+(46892640..46893198)	558	0.41893	8	4	4	0	0.014	SMAD7	DYM
chr18	+(47488419..47488923)	504	0.41893	8	3	5	0.25	0.018	SCARNA17	MYO5B
chr18	+(48190305..48191000)	695	0.00035	20	11	9	0.1	0.0083517	MAPK4	MRO
chr18	+(52601862..52602371)	509	2.05641	8	4	4	0	0.014	RAB27B	CCDC68
chr18	+(55282956..55283637)	681	0.97814	9	3	6	0.3333333	0.083	FECH	NARS
chr18	+(56148984..56149515)	531	2.05641	8	5	3	0.25	0.018	MIR122	ALPK2
chr18	+(56587221..56587767)	546	2.05641	13	8	5	0.2307692	0.15275354	ZNF532	LOC390858
chr18	+(56615132..56615636)	504	2.05641	10	6	4	0.2	0.01	ZNF532	LOC390858
chr18	+(57103142..57103795)	653	0.41893	13	5	8	0.2307692	0.27909232	LMAN1	CCBE1
chr18	+(60036507..60037025)	518	2.05641	6	4	2	0.3333333	0.067	TNFRSF11A	ZCCHC2
chr18	+(60242197..60242811)	614	2.05641	8	4	4	0	0.443	ZCCHC2	PHLPP1
chr18	+(60424932..60425893)	961	0.16965	15	6	9	0.2	0.00073136	PHLPP1	BCL2
chr18	+(67863402..67864240)	838	0.01812	14	5	9	0.2857143	0.0013499	CD226	RTTN
chr18	+(67997104..67997636)	532	2.05641	13	8	5	0.2307692	0.00958624	SOCS6	CBLN2
chr18	+(77207769..77208729)	960	0.97814	13	7	6	0.0769231	0.0013499	NFATC1	CTDP1
chr18	+(77476384..77477576)	1192	0.01812	23	11	12	0.0434783	0.96758091	CTDP1	KCNG2
chr18	+(77674295..77674995)	700	0.08524	15	10	5	0.3333333	0.00109982	KCNG2	PQLC1
chr19	+(110605..111853)	1248	0.00123	186	111	75	0.1935484	7.1696E-05	FAM138F	OR4F17
chr19	+(1006530..1007230)	700	0.14459	10	4	6	0.2	0.005	GRIN3B	C19orf6
chr19	+(1056763..1057271)	508	2.97166	7	4	3	0.1428571	0.029	ABCA7	HMHA1
chr19	+(1065222..1065880)	658	2.97166	6	2	4	0.3333333	0.067	ABCA7	HMHA1
chr19	+(1155898..1156520)	622	2.97166	6	3	3	0	0.05	GPX4	SBNO2
chr19	+(1578350..1579018)	668	2.97166	6	3	3	0	0.05	MEX3D	MBD3
chr19	+(1617245..1617797)	552	2.97166	6	4	2	0.3333333	0.067	UQCR11	TCF3
chr19	+(1708896..1709596)	700	0.04215	13	7	6	0.0769231	0.01606229	TCF3	ONECUT3

chr19	+(2274151..2274851)	700	2.97166	9	3	6	0.3333333	0.988	OAZ1	C19orf35	
chr19	+(3086278..3086802)	524	2.97166	6	2	4	0.3333333	0.067	AES	GNA11	
chr19	+(3115831..3116517)	686	0.61721	8	3	5	0.25	0.018	GNA11	GNA15	
chr19	+(3516063..3516663)	600	1.34748	7	4	3	0.1428571	0.029	FZR1	C19orf28	
chr19	+(3632631..3633780)	1149	0.30033	15	9	6	0.2	0.00073136	C19orf29	PIP5K1C	v
chr19	+(4353782..4354317)	535	2.97166	6	2	4	0.3333333	0.067	MPND	SH3GL1	
chr19	+(4504791..4505491)	700	0.14459	11	4	7	0.2727273	0.003	HDGFRP2	PLIN4	
chr19	+(4512693..4513230)	537	2.97166	6	2	4	0.3333333	0.067	HDGFRP2	PLIN4	
chr19	+(4816079..4816648)	569	1.34748	8	4	4	0	0.014	FEM1A	TICAM1	
chr19	+(4817080..4817589)	509	2.97166	12	4	8	0.3333333	0.184	FEM1A	TICAM1	
chr19	+(5292031..5292665)	634	0.30033	9	6	3	0.3333333	0.012	KDM4B	PTPRS	
chr19	+(5394635..5395138)	503	0.30033	9	5	4	0.1111111	0.008	PTPRS	ZNRF4	
chr19	+(5867103..5867642)	539	2.97166	9	6	3	0.3333333	0.048	FUT3	FUT5	
chr19	+(6213696..6214214)	518	2.97166	6	4	2	0.3333333	0.067	ACSBG2	MLLT1	
chr19	+(6215215..6216278)	1063	0.61721	14	8	6	0.1428571	0.00097289	ACSBG2	MLLT1	
chr19	+(7477305..7477978)	673	0.30033	9	5	4	0.1111111	0.008	ARHGEF18	LOC100128573	
chr19	+(7910332..7910922)	590	1.34748	7	4	3	0.1428571	0.029	EVI5L	FLJ22184	
chr19	+(8005614..8006304)	690	0.04215	13	7	6	0.0769231	0.0013499	CTXN1	TIMM44	
chr19	+(8921786..8922288)	502	2.97166	13	5	8	0.2307692	0.5	OR2Z1	ZNF558	
chr19	+(9203822..9204358)	536	1.34748	11	4	7	0.2727273	0.464	MUC16	OR1M1	
chr19	+(9211418..9212182)	764	0.00374	15	8	7	0.0666667	0.00059687	OR1M1	OR7G2	
chr19	+(10295115..10295815)	700	2.97166	9	3	6	0.3333333	0.988	EIF3G	DNMT1	
chr19	+(10789502..10790163)	661	1.34748	7	4	3	0.1428571	0.029	ILF3	QTRT1	
chr19	+(11323685..11324332)	647	1.34748	9	4	5	0.1111111	0.008	KANK2	DOCK6	
chr19	+(11725363..11725955)	592	0.61721	10	4	6	0.2	0.033	ZNF627	ZNF833P	
chr19	+(12057820..12058339)	519	1.34748	10	6	4	0.2	0.238	ZNF700	ZNF763	
chr19	+(12088025..12088712)	687	1.34748	14	7	7	0	0.57599689	ZNF763	ZNF433	
chr19	+(12184524..12185137)	613	0.61721	10	3	7	0.4	0.033	ZNF844	ZNF788	
chr19	+(12186427..12186972)	545	1.34748	12	5	7	0.1666667	0.11161257	ZNF844	ZNF788	
chr19	+(12574668..12575302)	634	0.61721	9	5	4	0.1111111	0.032	ZNF443	ZNF709	
chr19	+(12575710..12576360)	650	0.61721	11	6	5	0.0909091	0.05017413	ZNF443	ZNF709	
chr19	+(12638302..12638813)	511	2.97166	12	5	7	0.1666667	0.14557611	ZNF709	ZNF564	
chr19	+(13009666..13010306)	640	0.61721	9	5	4	0.1111111	0.095	GCDH	SYCE2	
chr19	+(13113807..13114504)	697	2.97166	9	6	3	0.3333333	0.988	NFIX	LYL1	v

chr19	+(13397154..13397717)	563	2.97166	6	4	2	0.3333333	0.067	IER2	CACNA1A	
chr19	+(14000732..14001279)	547	0.30033	13	6	7	0.0769231	0.01606229	NANOS3	C19orf57	
chr19	+(14011631..14012328)	697	2.97166	9	6	3	0.3333333	0.012	NANOS3	C19orf57	
chr19	+(14579724..14580538)	814	0.87687	18	7	11	0.2222222	0.0002444	PKN1	PTGER1	
chr19	+(15511111..15511650)	539	2.97166	13	9	4	0.3846154	0.793	AKAP8	AKAP8L	
chr19	+(15917802..15918678)	876	0.61721	20	12	8	0.2	0.00677733	OR10H5	OR10H1	
chr19	+(16127328..16127915)	587	0.14459	10	6	4	0.2	0.005	LOC126536	FLJ25328	
chr19	+(17197664..17198629)	965	1.34748	13	6	7	0.0769231	0.0013499	MYO9B	USE1	
chr19	+(17436535..17437077)	542	2.97166	6	2	4	0.3333333	0.067	DDA1	ANO8	
chr19	+(17712376..17712879)	503	2.97166	6	2	4	0.3333333	0.067	GLT25D1	UNC13A	
chr19	+(18376973..18377474)	501	1.3783	20	11	9	0.1	0.00036134	LOC729966	KIAA1683	v
chr19	+(18896959..18897607)	648	1.34748	10	7	3	0.4	0.808	CRTC1	COMP	
chr19	+(19541274..19541821)	547	0.30033	9	4	5	0.1111111	0.008	GATAD2A	TSSK6	
chr19	+(19562765..19563443)	678	2.97166	6	3	3	0	0.05	GATAD2A	TSSK6	
chr19	+(19654294..19655230)	936	0.61721	18	10	8	0.1111111	0.05487232	CILP2	PBX4	
chr19	+(20728228..20728758)	530	2.97166	10	5	5	0	0.45840747	MIR1270-2_dup2	ZNF737	
chr19	+(20808014..20808884)	870	2.97166	18	11	7	0.2222222	0.08019165	ZNF737	ZNF626	
chr19	+(20976298..20976862)	564	2.97166	9	3	6	0.3333333	0.012	ZNF626	ZNF85	
chr19	+(22001739..22002261)	522	1.3783	16	6	10	0.25	0.00170267	LOC641367	ZNF43	
chr19	+(22171398..22171906)	508	3.3319	21	10	11	0.047619	0.00123102	ZNF43	ZNF208	
chr19	+(22585841..22586689)	848	0.61721	16	6	10	0.25	0.06444254	ZNF676	ZNF98	
chr19	+(22835977..22836498)	521	1.34748	17	10	7	0.1764706	0.08592868	ZNF492	ZNF99	
chr19	+(22836551..22837170)	619	0.30033	10	5	5	0	0.00451172	ZNF492	ZNF99	
chr19	+(22880120..22880654)	534	1.34748	7	3	4	0.1428571	0.029	ZNF492	ZNF99	
chr19	+(30198850..30199633)	783	0.00085	17	9	8	0.0588235	0.000266	PLEKHF1	C19orf12	
chr19	+(30222347..30222941)	594	0.61721	9	6	3	0.3333333	0.083	C19orf12	CCNE1	
chr19	+(30311500..30312052)	552	2.97166	8	5	3	0.25	0.018	CCNE1	C19orf2	
chr19	+(30334328..30335501)	1173	1.34748	13	6	7	0.0769231	0.0013499	CCNE1	C19orf2	
chr19	+(30378265..30378855)	590	0.30033	9	5	4	0.1111111	0.008	CCNE1	C19orf2	
chr19	+(30552150..30552850)	700	0.30033	11	5	6	0.0909091	0.18065522	C19orf2	ZNF536	
chr19	+(30568604..30569199)	595	1.34748	12	4	8	0.3333333	0.715	C19orf2	ZNF536	
chr19	+(30582179..30582992)	813	0.00374	23	12	11	0.0434783	0.01819444	C19orf2	ZNF536	
chr19	+(30788561..30789081)	520	0.30033	9	5	4	0.1111111	0.008	C19orf2	ZNF536	
chr19	+(30948695..30949233)	538	0.30033	9	5	4	0.1111111	0.008	ZNF536	DKFZp566F0947	

chr19	+(31026715..31027226)	511	2.97166	6	4	2	0.3333333	0.067	ZNF536	DKFZp566F0947
chr19	+(31036607..31037279)	672	0.04215	12	7	5	0.1666667	0.00224163	ZNF536	DKFZp566F0947
chr19	+(31039229..31039736)	507	2.97166	10	3	7	0.4	0.742	ZNF536	DKFZp566F0947
chr19	+(31117491..31118046)	555	1.34748	10	6	4	0.2	0.543	ZNF536	DKFZp566F0947
chr19	+(31244231..31244931)	700	2.97166	11	5	6	0.0909091	0.99691505	ZNF536	DKFZp566F0947
chr19	+(31349055..31349754)	699	0.30033	15	10	5	0.3333333	0.99890018	ZNF536	DKFZp566F0947
chr19	+(31400742..31401296)	554	2.97166	6	3	3	0	0.05	ZNF536	DKFZp566F0947
chr19	+(31632229..31633123)	894	0.14459	15	6	9	0.2	0.00073136	ZNF536	DKFZp566F0947
chr19	+(31734279..31734906)	627	1.34748	7	4	3	0.1428571	0.029	DKFZp566F0947	TSHZ3
chr19	+(31767259..31767851)	592	0.14459	13	6	7	0.0769231	0.01113549	DKFZp566F0947	TSHZ3
chr19	+(32224175..32224780)	605	1.34748	7	4	3	0.1428571	0.029	TSHZ3	ZNF507
chr19	+(32477328..32477884)	556	1.34748	7	4	3	0.1428571	0.029	TSHZ3	ZNF507
chr19	+(32672455..32673028)	573	2.97166	6	2	4	0.3333333	0.067	TSHZ3	ZNF507
chr19	+(32873142..32873682)	540	1.34748	10	3	7	0.4	0.008	ZNF507	DPY19L3
chr19	+(33107591..33108166)	575	2.97166	6	4	2	0.3333333	0.067	PDCD5	ANKRD27
chr19	+(33110720..33111704)	984	0.30033	15	9	6	0.2	0.00073136	PDCD5	ANKRD27
chr19	+(33119664..33120364)	700	1.34748	13	6	7	0.0769231	0.97724986	PDCD5	ANKRD27
chr19	+(33120873..33122097)	1224	0.61721	21	8	13	0.2380952	0.99991702	PDCD5	ANKRD27
chr19	+(33227367..33228048)	681	0.61721	8	5	3	0.25	0.018	TDRD12	SLC7A9
chr19	+(33319610..33320980)	1370	0.06425	19	11	8	0.1578947	0.00013997	TDRD12	SLC7A9
chr19	+(33352607..33353150)	543	0.61721	9	6	3	0.3333333	0.012	TDRD12	SLC7A9
chr19	+(33430361..33431292)	931	2.97166	13	7	6	0.0769231	0.98393771	SLC7A9	CCDC123
chr19	+(33481122..33481890)	768	0.30033	18	10	8	0.1111111	0.03102776	C19orf40	RHPN2
chr19	+(33490045..33490570)	525	1.34748	10	3	7	0.4	0.908	C19orf40	RHPN2
chr19	+(33576501..33577080)	579	2.97166	8	4	4	0	0.014	GPATCH1	WDR88
chr19	+(33689741..33690688)	947	0.30033	17	8	9	0.0588235	0.000266	LRP3	SLC7A10
chr19	+(33795837..33796530)	693	0.30033	9	6	3	0.3333333	0.012	LOC80054	CEBPG
chr19	+(33862578..33863144)	566	0.0163	13	8	5	0.2307692	0.0017074	LOC80054	CEBPG
chr19	+(33876715..33877250)	535	0.14459	10	3	7	0.4	0.008	CEBPG	PEPD
chr19	+(33887271..33887825)	554	0.61721	8	3	5	0.25	0.018	CEBPG	PEPD
chr19	+(33893989..33894748)	759	0.61721	14	8	6	0.1428571	0.00097289	CEBPG	PEPD
chr19	+(33902038..33902627)	589	0.30033	13	4	9	0.3846154	0.999	CEBPG	PEPD
chr19	+(33903896..33904421)	525	2.97166	11	6	5	0.0909091	0.99691505	CEBPG	PEPD
chr19	+(33951514..33952212)	698	0.55276	13	6	7	0.0769231	0.0013499	CEBPG	PEPD

chr19	+(33995445..33996145)	700	2.97166	10	4	6	0.2	0.005	CEBPG	PEPD
chr19	+(34003925..34004586)	661	0.61721	8	5	3	0.25	0.018	CEBPG	PEPD
chr19	+(34150665..34151333)	668	2.97166	6	2	4	0.3333333	0.067	CHST8	KCTD15
chr19	+(34165585..34166285)	700	0.14459	16	11	5	0.375	0.90368099	CHST8	KCTD15
chr19	+(34214420..34215120)	700	0.00374	15	7	8	0.0666667	0.00059687	CHST8	KCTD15
chr19	+(34838356..34839056)	700	0.14459	11	7	4	0.2727273	0.006	KIAA0355	GPI
chr19	+(34847960..34848534)	574	0.61721	8	5	3	0.25	0.018	KIAA0355	GPI
chr19	+(34870983..34871492)	509	1.34748	7	4	3	0.1428571	0.029	GPI	PDCD2L
chr19	+(34877120..34877732)	612	2.97166	6	3	3	0	0.05	GPI	PDCD2L
chr19	+(34905874..34906574)	700	0.30033	13	9	4	0.3846154	0.001	PDCD2L	UBA2
chr19	+(34977356..34978015)	659	0.14459	10	5	5	0	0.00451172	WTIP	LOC643719
chr19	+(35125695..35126224)	529	2.97166	6	2	4	0.3333333	0.067	SCGBL	ZNF302
chr19	+(35168565..35169488)	923	0.00078	31	10	21	0.3548387	0.85461702	SCGBL	ZNF302
chr19	+(35486565..35487311)	746	0.06425	22	12	10	0.0909091	0.25482574	ZNF792	GRAMD1A
chr19	+(35500789..35501479)	690	0.00078	20	13	7	0.3	0.00015575	GRAMD1A	SCN1B
chr19	+(35512706..35513617)	911	0.30033	18	8	10	0.1111111	0.00223263	GRAMD1A	SCN1B
chr19	+(35523119..35523961)	842	0.0163	20	7	13	0.3	0.00028336	SCN1B	HPN
chr19	+(35533266..35534396)	1130	2.97166	18	8	10	0.1111111	0.99981036	HPN	LOC100128675
chr19	+(35538111..35538768)	657	0.30033	9	6	3	0.3333333	0.012	HPN	LOC100128675
chr19	+(35624770..35625333)	563	2.97166	12	8	4	0.3333333	0.715	FXYD3	LGI4
chr19	+(35635858..35636396)	538	2.97166	6	2	4	0.3333333	0.067	FXYD7	FXYD5
chr19	+(35761821..35762467)	646	2.97166	8	5	3	0.25	0.393	USF2	HAMP
chr19	+(35770882..35771582)	700	0.30033	13	7	6	0.0769231	0.66588243	USF2	HAMP
chr19	+(35811447..35812131)	684	0.0163	16	8	8	0	0.00038877	MAG	CD22
chr19	+(35828892..35829804)	912	0.14459	18	7	11	0.2222222	0.00216645	CD22	FFAR1
chr19	+(35996862..35997563)	701	0.14459	17	10	7	0.1764706	0.31279262	KRTDAP	DMKN
chr19	+(36001481..36002261)	780	1.34748	13	4	9	0.3846154	0.001	KRTDAP	DMKN
chr19	+(36024051..36024719)	668	0.61721	13	5	8	0.2307692	0.9982926	SBSN	GAPDHS
chr19	+(36025943..36027175)	1232	0.06425	19	8	11	0.1578947	0.00013997	GAPDHS	TMEM147
chr19	+(36032606..36033148)	542	2.97166	6	2	4	0.3333333	0.067	GAPDHS	TMEM147
chr19	+(36250629..36251319)	690	0.61721	13	9	4	0.3846154	0.02	C19orf55	ARHGAP33
chr19	+(36356685..36357284)	599	1.34748	8	4	4	0	0.014	KIRREL2	APLP1
chr19	+(36523122..36523729)	607	0.61721	8	4	4	0	0.014	ALKBH6	CLIP3
chr19	+(36592714..36593265)	551	2.97166	6	2	4	0.3333333	0.067	WDR62	POLR2I

chr19	+(36604374..36605165)	791	0.06425	12	6	6	0	0.00197388	WDR62	POLR2I	
chr19	+(37440420..37441066)	646	2.97166	9	3	6	0.3333333	0.012	ZNF568	ZNF420	
chr19	+(37547071..37547667)	596	1.34748	10	7	3	0.4	0.417	ZNF568	ZNF420	
chr19	+(37642991..37644292)	1301	0.30033	30	12	18	0.2	0.14495151	ZNF420	ZNF585A	
chr19	+(37677063..37677571)	508	2.97166	14	6	8	0.1428571	0.39812671	ZNF585A	ZNF585B	
chr19	+(37734063..37734624)	561	1.34748	9	4	5	0.1111111	0.008	ZNF383	LOC284412	
chr19	+(37879753..37880316)	563	2.97166	6	2	4	0.3333333	0.067	ZNF527	ZNF569	v
chr19	+(37893852..37894552)	700	2.97166	11	5	6	0.0909091	0.99691505	ZNF527	ZNF569	v
chr19	+(37922514..37923025)	511	2.97166	6	2	4	0.3333333	0.067	ZNF527	ZNF569	v
chr19	+(37957587..37958206)	619	1.34748	10	4	6	0.2	0.005	ZNF527	ZNF569	v
chr19	+(37958895..37959541)	646	1.34748	11	7	4	0.2727273	0.003	ZNF569	ZNF570	v
chr19	+(38180460..38181160)	700	1.34748	11	7	4	0.2727273	0.997	ZFP30	ZNF781	
chr19	+(38411186..38412927)	1741	0.14459	23	10	13	0.1304348	0.78994366	SIPA1L3	DPF1	
chr19	+(38464235..38465072)	837	0.01114	14	8	6	0.1428571	0.00097289	SIPA1L3	DPF1	
chr19	+(38565719..38566317)	598	1.34748	8	3	5	0.25	0.018	SIPA1L3	DPF1	
chr19	+(38588404..38588972)	568	2.97166	6	4	2	0.3333333	0.067	SIPA1L3	DPF1	
chr19	+(38594443..38595143)	700	0.30033	9	6	3	0.3333333	0.012	SIPA1L3	DPF1	
chr19	+(38797567..38798138)	571	2.97166	6	4	2	0.3333333	0.067	SPINT2	YIF1B	
chr19	+(38808938..38809638)	700	1.34748	12	5	7	0.1666667	0.28488218	C19orf33	KCNK6	
chr19	+(38811089..38811703)	614	2.97166	8	3	5	0.25	0.714	KCNK6	CATSPERG	
chr19	+(38892659..38893430)	771	0.61721	15	8	7	0.0666667	0.00059687	SPRED3	FAM98C	
chr19	+(38895003..38895703)	700	2.97166	10	4	6	0.2	0.995	FAM98C	RASGRP4	
chr19	+(38925719..38926419)	700	1.34748	8	5	3	0.25	0.018	RYR1	MAP4K1	
chr19	+(38997128..38998755)	1627	0.06425	30	11	19	0.2666667	0.00666933	RYR1	MAP4K1	
chr19	+(39001075..39001643)	568	0.14459	12	6	6	0	0.00520281	RYR1	MAP4K1	
chr19	+(39002724..39003368)	644	2.97166	14	5	9	0.2857143	0.63055866	RYR1	MAP4K1	
chr19	+(39073333..39074033)	700	1.34748	12	7	5	0.1666667	0.00224163	RYR1	MAP4K1	
chr19	+(39167180..39167880)	700	0.30033	9	6	3	0.3333333	0.012	ACTN4	CAPN12	
chr19	+(39213065..39213693)	628	0.14459	10	5	5	0	0.00451172	ACTN4	CAPN12	
chr19	+(39218136..39219023)	887	0.00078	18	12	6	0.3333333	0.00037352	ACTN4	CAPN12	
chr19	+(39224324..39225109)	785	0.39994	22	15	7	0.3636364	0.01878678	ACTN4	CAPN12	
chr19	+(39228472..39229126)	654	0.61721	8	5	3	0.25	0.018	ACTN4	CAPN12	
chr19	+(39306152..39306852)	700	0.06425	15	6	9	0.2	0.00073136	LGALS4	ECH1	
chr19	+(39342020..39342584)	564	2.97166	6	4	2	0.3333333	0.067	ECH1	HNRNPL	

chr19	+(39372106..39372652)	546	2.97166	7	3	4	0.1428571	0.029	RINL	SIRT2
chr19	+(39377962..39378561)	599	0.14459	10	7	3	0.4	0.008	RINL	SIRT2
chr19	+(39422837..39424095)	1258	0.00221	35	23	12	0.3142857	0.09331884	MRPS12	FBXO17
chr19	+(39517486..39518186)	700	0.04215	18	7	11	0.2222222	0.00216645	FBXO17	FBXO27
chr19	+(39849226..39849926)	700	0.30033	13	6	7	0.0769231	0.66588243	SAMD4B	PAF1
chr19	+(39898503..39899188)	685	0.06425	15	7	8	0.0666667	0.00059687	ZFP36	PLEKHG2
chr19	+(39948975..39949675)	700	0.30033	10	7	3	0.4	0.058	SUPT5H	TIMM50
chr19	+(39959930..39960478)	548	2.97166	6	3	3	0	0.05	SUPT5H	TIMM50
chr19	+(40224529..40225044)	515	1.34748	7	4	3	0.1428571	0.029	LGALS14	CLC
chr19	+(40317997..40319447)	1450	0.00221	37	13	24	0.2972973	7.5667E-06	LEUTX	DYRK1B
chr19	+(40330789..40331360)	571	0.61721	18	12	6	0.3333333	0.06699686	DYRK1B	FBL
chr19	+(40401968..40402613)	645	3.3319	23	15	8	0.3043478	0.0070857	FBL	FCGBP
chr19	+(40519537..40520157)	620	0.30033	15	7	8	0.0666667	0.01031878	ZNF546	ZNF780B
chr19	+(40580688..40581784)	1096	0.06425	32	15	17	0.0625	0.00017946	ZNF780B	ZNF780A
chr19	+(40671279..40672188)	909	0.00221	24	16	8	0.3333333	4.4425E-05	ZNF780A	MAP3K10
chr19	+(40767972..40768969)	997	0.0163	20	9	11	0.1	0.63378005	CNTD2	AKT2
chr19	+(40774318..40774921)	603	0.14459	10	4	6	0.2	0.005	CNTD2	AKT2
chr19	+(40861478..40862009)	531	2.97166	14	9	5	0.2857143	0.0013499	PLD3	HIPK4
chr19	+(40886989..40887491)	502	2.97166	7	4	3	0.1428571	0.114	PLD3	HIPK4
chr19	+(40902390..40903185)	795	0.30033	18	9	9	0	0.00353832	HIPK4	PRX
chr19	+(40946880..40947907)	1027	0.00035	29	11	18	0.2413793	4.2991E-06	SERTAD1	SERTAD3
chr19	+(40995345..40995862)	517	1.34748	8	5	3	0.25	0.125	SPTBN4	SHKBP1
chr19	+(41095292..41095901)	609	0.30033	9	3	6	0.3333333	0.012	SHKBP1	LTBP4
chr19	+(41096013..41096571)	558	0.61721	10	3	7	0.4	0.008	SHKBP1	LTBP4
chr19	+(41113570..41114071)	501	2.97166	9	6	3	0.3333333	0.19	LTBP4	NUMBL
chr19	+(41129932..41131317)	1385	0.61721	14	8	6	0.1428571	0.00097289	LTBP4	NUMBL
chr19	+(41208138..41208731)	593	2.97166	6	4	2	0.3333333	0.067	NUMBL	ADCK4
chr19	+(41231108..41231808)	700	0.14459	14	5	9	0.2857143	0.0013499	ITPKC	C19orf54
chr19	+(41355956..41356469)	513	2.97166	10	4	6	0.2	0.057	EGLN2	CYP2A6
chr19	+(41628921..41630099)	1178	0.30033	17	10	7	0.1764706	0.00031815	CYP2F1	CYP2S1
chr19	+(41726743..41727388)	645	0.22248	15	5	10	0.3333333	0.00109982	AXL	HNRNPUL1
chr19	+(41729436..41729971)	535	2.97166	6	3	3	0	0.05	AXL	HNRNPUL1
chr19	+(41813669..41814541)	872	0.00221	20	8	12	0.2	0.00010641	HNRNPUL1	CCDC97
chr19	+(41860313..41861182)	869	1.34748	14	9	5	0.2857143	0.0013499	TGFB1	B9D2

chr19	+(41891760..41892681)	921	1.34748	14	8	6	0.1428571	0.00097289	TMEM91	EXOSC5
chr19	+(41909304..41909972)	668	0.14459	10	6	4	0.2	0.005	BCKDHA	B3GNT8
chr19	+(41920686..41921384)	698	0.61721	8	4	4	0	0.014	BCKDHA	B3GNT8
chr19	+(42125434..42126428)	994	0.61721	18	6	12	0.3333333	0.1305271	CEACAM21	CEACAM4
chr19	+(42190456..42191012)	556	1.34748	11	4	7	0.2727273	0.324	CEACAM4	CEACAM7
chr19	+(42239280..42239794)	514	2.97166	6	4	2	0.3333333	0.067	CEACAM5	CEACAM6
chr19	+(42261529..42262359)	830	0.06425	12	5	7	0.1666667	0.00224163	CEACAM6	CEACAM3
chr19	+(42292667..42293367)	700	1.34748	12	5	7	0.1666667	0.00224163	CEACAM6	CEACAM3
chr19	+(42301573..42302108)	535	1.34748	13	7	6	0.0769231	0.03164542	CEACAM3	LYPD4
chr19	+(42318059..42318654)	595	0.00085	17	8	9	0.0588235	0.000266	CEACAM3	LYPD4
chr19	+(42423356..42424479)	1123	0.61721	14	8	6	0.1428571	0.99902711	ARHGEF1	RABAC1
chr19	+(42460466..42461404)	938	0.61721	16	6	10	0.25	0.00056905	ARHGEF1	RABAC1
chr19	+(42479539..42480184)	645	1.34748	10	4	6	0.2	0.005	RABAC1	ATP1A3
chr19	+(42481878..42482565)	687	0.04215	12	5	7	0.1666667	0.00224163	RABAC1	ATP1A3
chr19	+(42566338..42566873)	535	2.97166	6	4	2	0.3333333	0.067	ATP1A3	GRIK5
chr19	+(42569396..42570096)	700	0.30033	12	5	7	0.1666667	0.04407898	ATP1A3	GRIK5
chr19	+(42572906..42573428)	522	2.97166	9	6	3	0.3333333	0.988	GRIK5	ZNF574
chr19	+(42596200..42596775)	575	2.97166	8	4	4	0	0.1	ZNF574	POU2F2
chr19	+(42728015..42728669)	654	1.34748	12	5	7	0.1666667	0.00224163	ZNF526	GSK3A
chr19	+(42737482..42738027)	545	0.61721	8	3	5	0.25	0.018	ZNF526	GSK3A
chr19	+(42838993..42839513)	520	2.97166	6	4	2	0.3333333	0.067	MEGF8	CNFN
chr19	+(42848022..42848718)	696	0.61721	13	9	4	0.3846154	0.02	MEGF8	CNFN
chr19	+(42848791..42849356)	565	0.14459	15	10	5	0.3333333	0.00109982	MEGF8	CNFN
chr19	+(42854834..42855363)	529	2.97166	9	6	3	0.3333333	0.012	MEGF8	CNFN
chr19	+(42906342..42907070)	728	1.34748	20	8	12	0.2	0.00273928	CNFN	LIPE
chr19	+(42910223..42910761)	538	0.61721	11	6	5	0.0909091	0.29194121	CNFN	LIPE
chr19	+(42976765..42977632)	867	0.30033	13	6	7	0.0769231	0.0013499	CXCL17	CEACAM1
chr19	+(43028213..43028913)	700	0.61721	12	6	6	0	0.16833419	CXCL17	CEACAM1
chr19	+(43092670..43093278)	608	0.61721	16	5	11	0.375	0.07837268	CEACAM1	CEACAM8
chr19	+(43096806..43097506)	700	0.00374	15	10	5	0.3333333	0.00109982	CEACAM1	CEACAM8
chr19	+(43165162..43165713)	551	0.14459	10	7	3	0.4	0.008	CEACAM8	PSG3
chr19	+(43268182..43268722)	540	1.34748	11	6	5	0.0909091	0.64249967	PSG3	PSG8
chr19	+(44564360..44564903)	543	1.34748	9	3	6	0.3333333	0.274	ZNF223	ZNF284
chr19	+(44584769..44585469)	700	0.14459	16	6	10	0.25	0.00056905	ZNF284	ZNF224

chr19	+(44598860..44599383)	523	2.97166	6	2	4	0.3333333	0.067	ZNF224	LOC100379224
chr19	+(44604758..44605285)	527	2.97166	9	6	3	0.3333333	0.024	ZNF224	LOC100379224
chr19	+(44890428..44892081)	1653	0.22248	38	26	12	0.3684211	0.57472719	ZFP112	ZNF285
chr19	+(44975902..44976504)	602	0.61721	17	11	6	0.2941176	0.45997219	ZNF229	ZNF180
chr19	+(44981878..44982403)	525	1.34748	9	5	4	0.1111111	0.278	ZNF229	ZNF180
chr19	+(45157398..45158073)	675	0.61721	8	4	4	0	0.014	PVR	CEACAM19
chr19	+(45288947..45289584)	637	2.97166	6	2	4	0.3333333	0.067	CBLC	BCAM
chr19	+(45298417..45298923)	506	1.34748	7	3	4	0.1428571	0.029	CBLC	BCAM
chr19	+(45850564..45851073)	509	2.97166	6	4	2	0.3333333	0.067	KLC3	ERCC2
chr19	+(45920247..45920902)	655	0.0163	13	5	8	0.2307692	0.0017074	CD3EAP	ERCC1
chr19	+(46005860..46006505)	645	2.97166	6	2	4	0.3333333	0.067	PPM1N	VASP
chr19	+(46028920..46029585)	665	0.06425	12	4	8	0.3333333	0.00328926	VASP	OPA3
chr19	+(46060153..46061044)	891	1.34748	13	6	7	0.0769231	0.0013499	VASP	OPA3
chr19	+(46145197..46145896)	699	0.02999	22	11	11	0	3.5526E-05	GPR4	EML2
chr19	+(46289740..46290306)	566	2.97166	6	3	3	0	0.05	DMPK	DMWD
chr19	+(46332100..46333480)	1380	0.04215	20	8	12	0.2	0.00010641	RSPH6A	SYMPK
chr19	+(46832467..46832974)	507	1.34748	8	4	4	0	0.014	HIF3A	PPP5C
chr19	+(47254673..47255229)	556	0.61721	8	4	4	0	0.014	FKRP	SLC1A5
chr19	+(47492485..47493133)	648	0.01114	14	8	6	0.1428571	0.00097289	GRLF1	NPAS1
chr19	+(47592892..47593583)	691	1.34748	10	4	6	0.2	0.005	TMEM160	ZC3H4
chr19	+(47868468..47869162)	694	0.04215	12	6	6	0	0.00197388	DHX34	MEIS3
chr19	+(47873767..47874467)	700	0.30033	9	3	6	0.3333333	0.012	DHX34	MEIS3
chr19	+(48014980..48015500)	520	0.30033	9	5	4	0.1111111	0.008	KPTN	NAPA
chr19	+(48157335..48158035)	700	0.06425	11	7	4	0.2727273	0.003	GLTSCR1	EHD2
chr19	+(48223722..48224263)	541	2.97166	6	3	3	0	0.05	EHD2	GLTSCR2
chr19	+(48305133..48305656)	523	2.94904	14	7	7	0	0.32736042	SEPW1	TPRX1
chr19	+(48525136..48525646)	510	2.97166	8	4	4	0	0.057	ELSPBP1	CABP5
chr19	+(48658460..48659163)	703	1.34748	12	7	5	0.1666667	0.00224163	PLA2G4C	LIG1
chr19	+(48676908..48677467)	559	0.14459	10	7	3	0.4	0.008	LIG1	CARD8
chr19	+(48733770..48734296)	526	2.97166	14	5	9	0.2857143	0.87146285	LIG1	CARD8
chr19	+(48832549..48833215)	666	1.34748	10	6	4	0.2	0.129	EMP3	TMEM143
chr19	+(48945350..48945868)	518	0.61721	8	3	5	0.25	0.018	GRIN2D	GRWD1
chr19	+(48953733..48954246)	513	0.14459	10	7	3	0.4	0.008	GRWD1	KCNJ14
chr19	+(49061834..49062399)	565	2.97166	9	6	3	0.3333333	0.988	SULT2B1	FAM83E

chr19	+(49221322..49221838)	516	2.97166	7	3	4	0.1428571	0.029	FUT2	MAMSTR
chr19	+(49253247..49253854)	607	0.61721	9	3	6	0.3333333	0.012	IZUMO1	FUT1
chr19	+(49298317..49298987)	670	1.34748	7	3	4	0.1428571	0.029	FGF21	BCAT2
chr19	+(49364500..49365041)	541	2.97166	6	4	2	0.3333333	0.067	HSD17B14	PLEKHA4
chr19	+(49477681..49478902)	1221	2.97166	12	5	7	0.1666667	0.00224163	FTL	GYS1
chr19	+(49492739..49493900)	1161	0.61721	21	8	13	0.2380952	0.99811521	FTL	GYS1
chr19	+(49495423..49495940)	517	0.06425	11	7	4	0.2727273	0.003	FTL	GYS1
chr19	+(49608066..49608766)	700	0.14459	10	7	3	0.4	0.008	SNRNP70	LIN7B
chr19	+(49632399..49632940)	541	2.97166	7	3	4	0.1428571	0.029	PPFIA3	HRC
chr19	+(49638877..49639478)	601	0.61721	12	7	5	0.1666667	0.18587565	PPFIA3	HRC
chr19	+(49691945..49692526)	581	2.97166	11	5	6	0.0909091	0.07206352	TRPM4	SLC6A16
chr19	+(49778027..49778542)	515	2.97166	7	3	4	0.1428571	0.314	TRPM4	SLC6A16
chr19	+(50088237..50088857)	620	1.34748	7	4	3	0.1428571	0.029	PRRG2	PRR12
chr19	+(50160902..50161404)	502	1.34748	11	4	7	0.2727273	0.264	SCAF1	IRF3
chr19	+(50184143..50184843)	700	0.30033	9	3	6	0.3333333	0.012	PRMT1	C19orf76
chr19	+(50272368..50273068)	700	1.34748	10	3	7	0.4	0.008	AP2A1	FUZ
chr19	+(50301490..50302185)	695	0.14459	20	14	6	0.4	0.00667379	AP2A1	FUZ
chr19	+(50378982..50379533)	551	0.30033	9	4	5	0.1111111	0.008	PNKP	AKT1S1
chr19	+(50419908..50420415)	507	2.97166	6	3	3	0	0.05	TBC1D17	IL4I1
chr19	+(50485055..50485634)	579	0.04215	13	4	9	0.3846154	0.099	SIGLEC16	VRK3
chr19	+(50755218..50755880)	662	0.30033	9	4	5	0.1111111	0.008	MYH14	KCNC3
chr19	+(50880909..50882697)	1788	0.00035	40	16	24	0.2	0.8652718	NR1H2	POLD1
chr19	+(50909638..50910351)	713	0.0163	13	9	4	0.3846154	0.001	POLD1	SPIB
chr19	+(50926445..50927055)	610	0.30033	11	5	6	0.0909091	0.18065522	SPIB	MYBPC2
chr19	+(51050015..51050580)	565	2.97166	6	3	3	0	0.05	ASPDH	LRRC4B
chr19	+(51197091..51197791)	700	0.04215	12	8	4	0.3333333	0.99671074	LOC342918	SHANK1
chr19	+(51226476..51227024)	548	2.97166	6	4	2	0.3333333	0.067	SHANK1	CLEC11A
chr19	+(52032926..52034107)	1181	0.30033	19	11	8	0.1578947	0.83912483	SIGLEC12	SIGLEC6
chr19	+(52084660..52085197)	537	1.34748	11	6	5	0.0909091	0.01422987	ZNF175	FLJ30403
chr19	+(52783223..52783787)	564	1.34748	7	3	4	0.1428571	0.029	ZNF766	MIR643
chr19	+(52793949..52794459)	510	2.97166	8	4	4	0	0.014	MIR643	ZNF480
chr19	+(53208335..53208874)	539	0.61721	13	4	9	0.3846154	0.074	ZNF83	ZNF611
chr19	+(53270519..53271152)	633	1.34748	12	6	6	0	0.07477068	ZNF611	ZNF600
chr19	+(53454080..53454803)	723	0.61721	16	8	8	0	0.04644598	ZNF321	ZNF816

chr19	+(53603529..53604099)	570	2.97166	6	2	4	0.3333333	0.067	HERV-V2	ZNF160	
chr19	+(53854233..53854809)	576	2.97166	9	6	3	0.3333333	0.19	ZNF845	ZNF525	
chr19	+(54060281..54061426)	1145	2.97166	12	7	5	0.1666667	0.97882147	ZNF331	LOC284379	
chr19	+(54375729..54376282)	553	1.34748	7	4	3	0.1428571	0.029	MYADM	PRKCG	
chr19	+(54410318..54411457)	1139	0.00221	27	17	10	0.2592593	0.0052232	PRKCG	CACNG7	
chr19	+(54454849..54455549)	700	0.14459	10	3	7	0.4	0.008	CACNG7	CACNG8	
chr19	+(54481549..54482249)	700	0.14459	10	7	3	0.4	0.008	CACNG8	MIR935	
chr19	+(54626294..54626848)	554	1.34748	7	3	4	0.1428571	0.029	PRPF31	CNOT3	v
chr19	+(54650605..54651184)	579	0.61721	8	4	4	0	0.014	CNOT3	LENG1	
chr19	+(54755608..54756147)	539	2.97166	6	2	4	0.3333333	0.067	LILRA6	LILRB5	
chr19	+(54780696..54781430)	734	0.00221	22	7	15	0.3636364	0.94363505	LILRB5	LILRB2	
chr19	+(54914749..54915449)	700	2.97166	11	6	5	0.0909091	0.05017413	LAIR1	TTYH1	
chr19	+(54945321..54945939)	618	0.14459	10	5	5	0	0.00451172	TTYH1	LENG8	
chr19	+(54968634..54969332)	698	0.04215	13	6	7	0.0769231	0.0013499	LENG8	LENG9	
chr19	+(55142080..55142607)	527	1.34748	11	6	5	0.0909091	0.18065522	LILRB1	LILRB4	
chr19	+(55262831..55263351)	520	2.97166	10	5	5	0	0.00451172	KIR2DL3	KIR3DP1	
chr19	+(55370117..55370639)	522	0.14459	19	9	10	0.0526316	0.00568463	KIR3DL2	FCAR	
chr19	+(55386397..55386916)	519	2.97166	6	2	4	0.3333333	0.067	FCAR	NCR1	
chr19	+(55538771..55539276)	505	1.34748	10	3	7	0.4	0.008	NLRP2	GP6	
chr19	+(55597027..55597727)	700	0.00221	21	11	10	0.047619	5.3756E-05	EPS8L1	PPP1R12C	
chr19	+(55603294..55603994)	700	0.04215	13	8	5	0.2307692	0.0394913	EPS8L1	PPP1R12C	
chr19	+(55750929..55751466)	537	0.06425	11	7	4	0.2727273	0.003	TMEM86B	PPP6R1	
chr19	+(55831474..55832142)	668	0.30033	11	7	4	0.2727273	0.003	BRSK1	TMEM150B	
chr19	+(55916827..55918066)	1239	0.30033	16	10	6	0.25	0.00056905	RPL28	UBE2S	
chr19	+(55943985..55944685)	700	0.0163	13	8	5	0.2307692	0.0017074	UBE2S	SHISA7	
chr19	+(55950594..55951134)	540	1.34748	7	4	3	0.1428571	0.029	UBE2S	SHISA7	
chr19	+(55991219..55992321)	1102	2.97166	13	7	6	0.0769231	0.0013499	ZNF628	NAT14	
chr19	+(56174830..56175735)	905	0.14459	17	11	6	0.2941176	0.01040023	U2AF2	EPN1	
chr19	+(56179154..56179901)	747	0.00221	19	11	8	0.1578947	0.00147643	U2AF2	EPN1	
chr19	+(56180935..56181499)	564	0.30033	14	6	8	0.1428571	0.00097289	U2AF2	EPN1	
chr19	+(56300134..56300713)	579	2.97166	11	5	6	0.0909091	0.81934478	RFPL4A	NLRP11	
chr19	+(56361111..56361811)	700	0.0163	21	9	12	0.1428571	0.00950824	NLRP4	NLRP13	
chr19	+(56491492..56492335)	843	0.01114	14	8	6	0.1428571	0.00097289	NLRP8	NLRP5	
chr19	+(56531819..56532327)	508	2.97166	9	6	3	0.3333333	0.048	NLRP5	ZNF787	

chr19	+(56622643..56623190)	547	2.97166	9	3	6	0.3333333	0.012	NLRP5	ZNF787
chr19	+(56623355..56623917)	562	0.61721	8	4	4	0	0.014	NLRP5	ZNF787
chr19	+(56629117..56629804)	687	0.0163	13	4	9	0.3846154	0.001	NLRP5	ZNF787
chr19	+(56641701..56642401)	700	0.61721	11	5	6	0.0909091	0.70805879	ZNF787	ZNF444
chr19	+(57133166..57133834)	668	1.34748	16	7	9	0.125	0.68308053	ZNF71	LOC147670
chr19	+(57646284..57647132)	848	0.06425	21	9	12	0.1428571	0.12775441	USP29	ZIM3
chr19	+(57671852..57672518)	666	0.30033	10	6	4	0.2	0.005	ZIM3	DUXA
chr19	+(57766868..57767517)	649	1.34748	14	7	7	0	0.2031169	ZNF805	ZNF460
chr19	+(57768427..57769184)	757	1.34748	20	13	7	0.3	0.16095609	ZNF805	ZNF460
chr19	+(57769936..57770567)	631	0.30033	11	6	5	0.0909091	0.00308495	ZNF805	ZNF460
chr19	+(57773740..57774292)	552	2.97166	8	4	4	0	0.243	ZNF805	ZNF460
chr19	+(58187453..58188025)	572	1.34748	11	5	6	0.0909091	0.01422987	ZSCAN4	ZNF551
chr19	+(58192637..58193892)	1255	1.34748	13	7	6	0.0769231	0.0013499	ZSCAN4	ZNF551
chr19	+(58383874..58384479)	605	1.34748	11	5	6	0.0909091	0.07206352	ZNF587	ZNF814
chr19	+(58385211..58385733)	522	2.97166	11	5	6	0.0909091	0.18065522	ZNF587	ZNF814
chr19	+(58386370..58386898)	528	1.34748	20	7	13	0.3	0.02165575	ZNF587	ZNF814
chr19	+(58388096..58388623)	527	2.97166	8	3	5	0.25	0.036	ZNF587	ZNF814
chr19	+(58554250..58555562)	1312	1.34748	19	6	13	0.3684211	0.9996875	ZSCAN1	ZNF135
chr19	+(58557730..58558239)	509	1.34748	9	5	4	0.1111111	0.008	ZSCAN1	ZNF135
chr19	+(58565255..58565773)	518	1.34748	8	4	4	0	0.014	ZSCAN1	ZNF135
chr19	+(58567998..58568739)	741	0.0163	15	8	7	0.0666667	0.00059687	ZSCAN1	ZNF135
chr19	+(58870162..58870730)	568	0.14459	10	3	7	0.4	0.008	A1BG-AS1	ZNF497
chr19	+(58950994..58951978)	984	2.97166	12	5	7	0.1666667	0.65762832	ZNF584	ZNF132
chr19	+(58966421..58966924)	503	2.97166	10	6	4	0.2	0.457	ZNF324B	ZNF324
chr19	+(59058426..59059126)	700	0.06425	12	8	4	0.3333333	0.99671074	TRIM28	CHMP2A
chr20	+(1629518..1630070)	552	3.4286	18	12	6	0.3333333	0.00247894	SIRPB1	SIRPG
chr20	+(1799999..1800637)	638	0.40887	8	5	3	0.25	0.018	LOC100289473	SIRPA
chr20	+(1822181..1822867)	686	0.00662	13	7	6	0.0769231	0.0013499	LOC100289473	SIRPA
chr20	+(1881358..1881940)	582	0.89571	13	7	6	0.0769231	0.0013499	SIRPA	PDYN
chr20	+(1895607..1896435)	828	0.22026	16	7	9	0.125	0.0018019	SIRPA	PDYN
chr20	+(2276556..2277690)	1134	0.03432	18	11	7	0.2222222	0.00120674	STK35	TGM3
chr20	+(3138450..3139150)	700	0.18556	9	3	6	0.3333333	0.012	AVP	UBOX5
chr20	+(3245089..3245593)	504	2.17504	9	3	6	0.3333333	0.083	SLC4A11	C20orf194
chr20	+(3659841..3660405)	564	0.40887	10	7	3	0.4	0.017	GFRA4	ADAM33

chr20	+(3683492..3684028)	536	0.03432	16	5	11	0.375	0.96920638	ADAM33	SIGLEC1
chr20	+(3687583..3688102)	519	0.01563	13	4	9	0.3846154	0.001	ADAM33	SIGLEC1
chr20	+(3692032..3692696)	664	2.17504	9	5	4	0.1111111	0.857	SIGLEC1	HSPA12B
chr20	+(3765477..3766005)	528	2.17504	12	8	4	0.3333333	0.976	SPEF1	CENPB
chr20	+(3841687..3842387)	700	0.18556	9	3	6	0.3333333	0.012	MAVS	PANK2
chr20	+(4135521..4136100)	579	0.18556	9	5	4	0.1111111	0.008	SMOX	LOC728228
chr20	+(4210972..4211931)	959	0.00662	22	15	7	0.3636364	0.29851354	LOC728228	ADRA1D
chr20	+(4707710..4708240)	530	0.89571	9	4	5	0.1111111	0.008	PRND	PRNT
chr20	+(8626602..8627103)	501	2.17504	6	4	2	0.3333333	0.067	PLCB1	PLCB4
chr20	+(8915989..8916630)	641	0.40887	13	5	8	0.2307692	0.76789284	PLCB1	PLCB4
chr20	+(9632176..9632688)	512	2.17504	6	3	3	0	0.05	C20orf103	PAK7
chr20	+(13397844..13398396)	552	2.17504	6	4	2	0.3333333	0.067	ISM1	TASP1
chr20	+(13762687..13763360)	673	2.17504	9	3	6	0.3333333	0.988	TASP1	ESF1
chr20	+(14099623..14100479)	856	0.12313	14	8	6	0.1428571	0.00097289	MACROD2	FLRT3
chr20	+(14473926..14474440)	514	0.89571	14	9	5	0.2857143	0.02659758	FLRT3	KIF16B
chr20	+(15531737..15532590)	853	0.03432	12	6	6	0	0.00197388	FLRT3	KIF16B
chr20	+(15866398..15866903)	505	2.17504	17	10	7	0.1764706	0.78251642	FLRT3	KIF16B
chr20	+(15991808..15992508)	700	0.18556	13	4	9	0.3846154	0.001	FLRT3	KIF16B
chr20	+(17417216..17417916)	700	0.03432	11	7	4	0.2727273	0.003	PCSK2	BFSP1
chr20	+(17580990..17581950)	960	0.89571	19	11	8	0.1578947	0.4344151	DSTN	RRBP1
chr20	+(17598718..17599282)	564	0.89571	8	4	4	0	0.171	DSTN	RRBP1
chr20	+(17607073..17607761)	688	0.40887	11	7	4	0.2727273	0.003	DSTN	RRBP1
chr20	+(18010875..18011575)	700	0.09429	10	6	4	0.2	0.005	C20orf72	OVOL2
chr20	+(18026823..18027396)	573	0.40887	8	5	3	0.25	0.018	C20orf72	OVOL2
chr20	+(18492740..18493440)	700	0.03432	16	11	5	0.375	0.01804853	SEC23B	LOC388789
chr20	+(18534446..18535144)	698	0.18556	10	7	3	0.4	0.058	SEC23B	LOC388789
chr20	+(18625343..18625948)	605	0.18556	9	4	5	0.1111111	0.008	DTD1	HSPC072
chr20	+(18639248..18639790)	542	2.17504	6	2	4	0.3333333	0.067	DTD1	HSPC072
chr20	+(19519876..19521247)	1371	0.89571	14	7	7	0	0.00087256	LOC100130264	RIN2
chr20	+(20516381..20516914)	533	2.17504	9	6	3	0.3333333	0.988	INSM1	RALGAPA2
chr20	+(20636005..20636636)	631	2.17504	6	3	3	0	0.05	INSM1	RALGAPA2
chr20	+(21000057..21001378)	1321	0.09429	17	10	7	0.1764706	0.00031815	RALGAPA2	PLK1S1
chr20	+(21080976..21081506)	530	0.89571	10	7	3	0.4	0.992	RALGAPA2	PLK1S1
chr20	+(23668523..23669221)	698	0.89571	7	4	3	0.1428571	0.029	CST3	CST4

chr20	+(24115723..24116291)	568	2.17504	10	6	4	0.2	0.005	GGTLC1	TMEM90B
chr20	+(24351805..24352434)	629	2.17504	6	4	2	0.3333333	0.067	GGTLC1	TMEM90B
chr20	+(24431176..24431876)	700	2.17504	10	4	6	0.2	0.995	GGTLC1	TMEM90B
chr20	+(24471171..24471828)	657	2.17504	7	3	4	0.1428571	0.2	TMEM90B	CST7
chr20	+(24733585..24734192)	607	2.17504	6	4	2	0.3333333	0.067	TMEM90B	CST7
chr20	+(24759031..24759669)	638	0.89571	7	4	3	0.1428571	0.029	TMEM90B	CST7
chr20	+(24773813..24775816)	2003	0.40887	22	14	8	0.2727273	6.6151E-05	TMEM90B	CST7
chr20	+(24848329..24848870)	541	0.89571	7	3	4	0.1428571	0.029	TMEM90B	CST7
chr20	+(24948245..24948945)	700	0.01563	12	4	8	0.3333333	0.00328926	CST7	C20orf3
chr20	+(25021430..25022129)	699	0.40887	8	3	5	0.25	0.018	C20orf3	ACSS1
chr20	+(25483480..25484010)	530	0.89571	11	4	7	0.2727273	0.003	GINS1	NINL
chr20	+(25489470..25490361)	891	0.00068	16	10	6	0.25	0.00056905	GINS1	NINL
chr20	+(25603535..25604235)	700	0.89571	10	3	7	0.4	0.008	NINL	NANP
chr20	+(25657383..25657968)	585	0.40887	14	8	6	0.1428571	0.5	NANP	ZNF337
chr20	+(29520348..29520866)	518	0.89571	14	5	9	0.2857143	0.10263725	MIR663	FRG1B
chr20	+(29623776..29624406)	630	0.21922	59	34	25	0.1525424	1.9141E-07	FRG1B	DEFB115
chr20	+(29627833..29628832)	999	0.03556	78	40	38	0.025641	0.06431916	FRG1B	DEFB115
chr20	+(29631133..29632090)	957	0.97277	52	30	22	0.1538462	0.57347056	FRG1B	DEFB115
chr20	+(29633572..29634409)	837	0.15212	61	35	26	0.147541	0.0060634	FRG1B	DEFB115
chr20	+(29653259..29653959)	700	0.03432	12	7	5	0.1666667	0.00224163	FRG1B	DEFB115
chr20	+(30995327..30995847)	520	0.40887	9	4	5	0.1111111	0.008	ASXL1	C20orf112
chr20	+(31049508..31050208)	700	0.09429	10	5	5	0	0.00451172	ASXL1	C20orf112
chr20	+(31109272..31109972)	700	0.40887	9	3	6	0.3333333	0.274	C20orf112	LOC149950
chr20	+(31376554..31377070)	516	2.17504	7	3	4	0.1428571	0.029	DNMT3B	MAPRE1
chr20	+(31427305..31427871)	566	2.17504	7	3	4	0.1428571	0.029	MAPRE1	SUN5
chr20	+(31455141..31455841)	700	0.03432	11	5	6	0.0909091	0.00308495	MAPRE1	SUN5
chr20	+(31485881..31486506)	625	0.89571	8	5	3	0.25	0.018	MAPRE1	SUN5
chr20	+(31572665..31573297)	632	0.89571	9	6	3	0.3333333	0.012	MAPRE1	SUN5
chr20	+(31573466..31574284)	818	0.00662	18	11	7	0.2222222	0.0002444	MAPRE1	SUN5
chr20	+(31673499..31674001)	502	0.40887	8	3	5	0.25	0.018	C20orf186	C20orf70
chr20	+(31678530..31679087)	557	0.18556	9	5	4	0.1111111	0.008	C20orf186	C20orf70
chr20	+(32883043..32883616)	573	0.89571	7	3	4	0.1428571	0.029	ASIP	AHCY
chr20	+(33190114..33190654)	540	2.17504	6	2	4	0.3333333	0.067	MAP1LC3A	PIGU
chr20	+(33337026..33337691)	665	0.18556	12	7	5	0.1666667	0.14557611	TP53INP2	NCOA6

chr20	+(33583006..33584239)	1233	0.40887	22	14	8	0.2727273	0.00133621	MIR499	TRPC4AP
chr20	+(33595100..33595800)	700	0.09429	12	8	4	0.3333333	0.533	MIR499	TRPC4AP
chr20	+(33848104..33848661)	557	0.89571	8	3	5	0.25	0.125	MMP24	EIF6
chr20	+(34187670..34188181)	511	0.89571	7	3	4	0.1428571	0.029	ERGIC3	FER1L4
chr20	+(34437438..34438122)	684	2.17504	10	6	4	0.2	0.995	PHF20	SCAND1
chr20	+(34505080..34505593)	513	2.17504	8	4	4	0	0.057	PHF20	SCAND1
chr20	+(34533212..34533840)	628	0.40887	8	4	4	0	0.014	PHF20	SCAND1
chr20	+(34730184..34730884)	700	3E-05	23	7	16	0.3913043	0.29649005	EPB41L1	C20orf4
chr20	+(34761668..34762368)	700	0.03432	12	6	6	0	0.0186865	EPB41L1	C20orf4
chr20	+(34828097..34828707)	610	0.89571	9	3	6	0.3333333	0.024	C20orf4	DLGAP4
chr20	+(34964368..34965036)	668	0.18556	9	6	3	0.3333333	0.012	C20orf4	DLGAP4
chr20	+(35004869..35005476)	607	0.89571	11	4	7	0.2727273	0.003	DLGAP4	MYL9
chr20	+(35453692..35454392)	700	0.09429	10	4	6	0.2	0.005	DSN1	C20orf117
chr20	+(35835520..35836097)	577	2.17504	7	3	4	0.1428571	0.029	RPN2	GHRH
chr20	+(36547304..36547988)	684	0.18556	9	6	3	0.3333333	0.012	VSTM2L	TTI1
chr20	+(36639947..36640626)	679	2.17504	10	4	6	0.2	0.457	VSTM2L	TTI1
chr20	+(36776347..36776878)	531	0.89571	7	4	3	0.1428571	0.029	RPRD1B	TGM2
chr20	+(36850482..36851389)	907	0.00662	24	15	9	0.25	0.82231968	TGM2	KIAA1755
chr20	+(37049779..37050396)	617	2.17504	6	2	4	0.3333333	0.067	LBP	LOC388796
chr20	+(37121159..37121704)	545	0.89571	10	4	6	0.2	0.005	RALGAPB	ADIG
chr20	+(37193635..37194146)	511	2.17504	8	4	4	0	0.029	RALGAPB	ADIG
chr20	+(37207855..37208555)	700	0.01563	15	8	7	0.0666667	0.00544818	RALGAPB	ADIG
chr20	+(37481468..37481982)	514	2.17504	6	3	3	0	0.05	PPP1R16B	FAM83D
chr20	+(37507199..37508146)	947	0.09429	16	10	6	0.25	0.00056905	PPP1R16B	FAM83D
chr20	+(39830656..39831191)	535	0.89571	10	6	4	0.2	0.033	PLCG1	ZHX3
chr20	+(42340683..42341880)	1197	0.09429	19	8	11	0.1578947	0.62940925	MYBL2	GTSF1L
chr20	+(42345608..42346290)	682	0.40887	8	4	4	0	0.014	MYBL2	GTSF1L
chr20	+(42789104..42789804)	700	0.89571	12	7	5	0.1666667	0.99775837	TOX2	JPH2
chr20	+(43032145..43032766)	621	0.40887	8	5	3	0.25	0.018	HNF4A	MIR3646
chr20	+(43231760..43232460)	700	0.09429	10	3	7	0.4	0.008	PKIG	ADA
chr20	+(43953769..43954411)	642	0.40887	8	5	3	0.25	0.018	RBPJL	SDC4
chr20	+(44505564..44506171)	607	2.17504	6	3	3	0	0.05	ZSWIM3	ZSWIM1
chr20	+(44508313..44509047)	734	0.00662	13	6	7	0.0769231	0.0013499	ZSWIM3	ZSWIM1
chr20	+(44591933..44592997)	1064	0.00662	22	11	11	0	3.5526E-05	PCIF1	ZNF335

chr20	+(45864970..45865627)	657	0.89571	10	7	3	0.4	0.192	MIR3616	ZMYND8
chr20	+(45974285..45974985)	700	0.01563	12	7	5	0.1666667	0.00224163	MIR3616	ZMYND8
chr20	+(46365168..46365720)	552	0.89571	8	4	4	0	0.014	NCOA3	SULF2
chr20	+(46374109..46375325)	1216	0.03432	17	6	11	0.2941176	0.00045556	NCOA3	SULF2
chr20	+(46454031..46454718)	687	2.17504	9	6	3	0.3333333	0.988	SULF2	LOC284749
chr20	+(46485630..46486330)	700	0.40887	12	4	8	0.3333333	0.00328926	SULF2	LOC284749
chr20	+(46508701..46509401)	700	2.17504	11	6	5	0.0909091	0.99691505	SULF2	LOC284749
chr20	+(46584820..46586110)	1290	0.18556	16	9	7	0.125	0.99957245	SULF2	LOC284749
chr20	+(46666903..46667564)	661	0.89571	9	6	3	0.3333333	0.274	SULF2	LOC284749
chr20	+(46789703..46790292)	589	2.17504	6	3	3	0	0.05	SULF2	LOC284749
chr20	+(47714313..47714989)	676	0.09429	12	6	6	0	0.00197388	CSE1L	STAU1
chr20	+(47739575..47740149)	574	0.18556	10	4	6	0.2	0.005	CSE1L	STAU1
chr20	+(47847235..47847944)	709	0.00143	15	5	10	0.3333333	0.00109982	DDX27	ZNFX1
chr20	+(47864494..47865011)	517	0.89571	12	8	4	0.3333333	0.467	DDX27	ZNFX1
chr20	+(47887457..47888313)	856	0.00662	22	11	11	0	0.00057618	DDX27	ZNFX1
chr20	+(47991079..47991715)	636	2.17504	7	4	3	0.1428571	0.029	SNORD12	KCNB1
chr20	+(48439353..48439877)	524	0.89571	10	5	5	0	0.00451172	SLC9A8	SPATA2
chr20	+(48521961..48522465)	504	2.17504	9	5	4	0.1111111	0.056	SLC9A8	SPATA2
chr20	+(48744888..48746113)	1225	0.40887	15	8	7	0.0666667	0.00059687	UBE2V1	TMEM189-UBE2V1
chr20	+(48759233..48759907)	674	0.18556	9	6	3	0.3333333	0.012	UBE2V1	TMEM189-UBE2V1
chr20	+(48762359..48763059)	700	0.00662	13	8	5	0.2307692	0.0017074	UBE2V1	TMEM189-UBE2V1
chr20	+(48766028..48766898)	870	0.00143	15	9	6	0.2	0.00073136	UBE2V1	TMEM189-UBE2V1
chr20	+(49217790..49219095)	1305	0.00068	23	8	15	0.3043478	0.4232253	MIR645	FAM65C
chr20	+(49462222..49462922)	700	2.17504	10	4	6	0.2	0.005	BCAS4	ADNP
chr20	+(49462961..49463632)	671	2.17504	10	4	6	0.2	0.005	BCAS4	ADNP
chr20	+(49503539..49504129)	590	2.17504	6	2	4	0.3333333	0.067	BCAS4	ADNP
chr20	+(49508199..49508899)	700	0.03556	20	6	14	0.4	0.02891344	BCAS4	ADNP
chr20	+(50048544..50049136)	592	0.89571	8	5	3	0.25	0.018	KCNG1	NFATC2
chr20	+(50100959..50101649)	690	2.17504	6	3	3	0	0.05	KCNG1	NFATC2
chr20	+(50224990..50225511)	521	2.17504	9	6	3	0.3333333	0.19	MIR3194	ATP9A
chr20	+(51940337..51940998)	661	0.18556	9	6	3	0.3333333	0.012	TSHZ2	ZNF217
chr20	+(52198837..52199387)	550	2.17504	10	5	5	0	0.23235105	TSHZ2	ZNF217
chr20	+(52636126..52636715)	589	0.40887	8	4	4	0	0.014	SUMO1P1	BCAS1
chr20	+(55071451..55071984)	533	2.17504	9	3	6	0.3333333	0.643	C20orf43	GCNT7

chr20	+(55072339..55073436)	1097	0.00383	20	14	6	0.4	0.999734	C20orf43	GCNT7	
chr20	+(55205471..55206171)	700	0.18556	13	4	9	0.3846154	0.001	TFAP2C	BMP7	v
chr20	+(55619745..55620727)	982	0.89571	13	7	6	0.0769231	0.0013499	TFAP2C	BMP7	v
chr20	+(56273522..56274181)	659	0.40887	8	3	5	0.25	0.018	ZBP1	PMEPA1	
chr20	+(56443631..56444155)	524	2.17504	6	3	3	0	0.05	PMEPA1	C20orf85	
chr20	+(56688758..56689307)	549	0.40887	8	5	3	0.25	0.018	PMEPA1	C20orf85	
chr20	+(56735408..56736050)	642	0.40887	8	4	4	0	0.014	C20orf85	PPP4R1L	
chr20	+(56744392..56745092)	700	0.40887	13	5	8	0.2307692	0.07161746	C20orf85	PPP4R1L	
chr20	+(57035564..57036148)	584	2.17504	6	3	3	0	0.05	VAPB	APCDD1L	
chr20	+(58383144..58383704)	560	0.18556	9	6	3	0.3333333	0.012	PHACTR3	SYCP2	
chr20	+(58419993..58420589)	596	0.40887	13	5	8	0.2307692	0.0017074	PHACTR3	SYCP2	
chr20	+(59069009..59069718)	709	0.00383	14	7	7	0	0.00087256	C20orf197	CDH4	
chr20	+(59378568..59379268)	700	0.03432	11	6	5	0.0909091	0.00308495	C20orf197	CDH4	
chr20	+(59875095..59875948)	853	0.40887	20	8	12	0.2	0.00010641	CDH4	MIR1257	
chr20	+(60083255..60083786)	531	2.17504	6	3	3	0	0.05	CDH4	MIR1257	
chr20	+(60100995..60102374)	1379	0.03432	17	6	11	0.2941176	0.00045556	CDH4	MIR1257	
chr20	+(60302947..60303882)	935	0.89571	15	6	9	0.2	0.03854994	CDH4	MIR1257	
chr20	+(60377715..60378415)	700	0.03432	11	6	5	0.0909091	0.00308495	CDH4	MIR1257	
chr20	+(60429412..60430203)	791	0.03432	16	7	9	0.125	0.02510048	CDH4	MIR1257	
chr20	+(60579480..60580180)	700	0.89571	10	7	3	0.4	0.992	MIR1257	TAF4	
chr20	+(60642473..60642990)	517	0.18556	9	5	4	0.1111111	0.008	TAF4	LSM14B	
chr20	+(60754562..60755234)	672	0.89571	7	3	4	0.1428571	0.029	SS18L1	GTPBP5	
chr20	+(60768113..60768695)	582	2.17504	6	4	2	0.3333333	0.067	GTPBP5	HRH3	
chr20	+(60798383..60798920)	537	2.17504	6	3	3	0	0.05	HRH3	OSBPL2	
chr20	+(60819831..60820355)	524	0.89571	7	4	3	0.1428571	0.029	OSBPL2	ADRM1	
chr20	+(60847965..60848665)	700	0.18556	11	4	7	0.2727273	0.003	OSBPL2	ADRM1	
chr20	+(60886723..60887328)	605	0.89571	12	6	6	0	0.00197388	ADRM1	LAMA5	
chr20	+(60947403..60947979)	576	2.17504	9	3	6	0.3333333	0.012	LAMA5	RPS21	
chr20	+(61167167..61168293)	1126	0.40887	15	8	7	0.0666667	0.99245637	MIR133A2	SLCO4A1	
chr20	+(61196880..61197583)	703	0.01563	12	7	5	0.1666667	0.00224163	MIR133A2	SLCO4A1	
chr20	+(61271304..61272004)	700	2.17504	12	5	7	0.1666667	0.99775837	MIR133A2	SLCO4A1	
chr20	+(61295285..61295806)	521	0.40887	13	8	5	0.2307692	0.0017074	SLCO4A1	LOC100127888	
chr20	+(61387203..61388216)	1013	0.18556	17	8	9	0.0588235	0.000266	NTSR1	C20orf20	
chr20	+(61391244..61391944)	700	0.09429	11	7	4	0.2727273	0.115	NTSR1	C20orf20	

chr20	+(61439160..61439860)	700	0.01563	13	7	6	0.0769231	0.0013499	OGFR	COL9A3
chr20	+(61588888..61589425)	537	2.17504	9	6	3	0.3333333	0.988	SLC17A9	BHLHE23
chr20	+(61839857..61840441)	584	0.09429	10	5	5	0	0.00451172	MIR124-3	YTHDF1
chr20	+(61888906..61889606)	700	0.01563	12	5	7	0.1666667	0.00224163	FLJ16779	ARFGAP1
chr20	+(61900505..61901210)	705	0.09429	14	5	9	0.2857143	0.0013499	FLJ16779	ARFGAP1
chr20	+(62088309..62089334)	1025	0.18556	15	9	6	0.2	0.00073136	CHRNA4	KCNQ2
chr20	+(62094686..62095309)	623	0.89571	8	5	3	0.25	0.125	CHRNA4	KCNQ2
chr20	+(62108717..62109340)	623	0.89571	7	4	3	0.1428571	0.029	KCNQ2	EEF1A2
chr20	+(62129108..62129806)	698	2.17504	10	6	4	0.2	0.995	KCNQ2	EEF1A2
chr20	+(62293899..62294516)	617	0.22026	13	8	5	0.2307692	0.0017074	RTEL1	TNFRSF6B
chr20	+(62387144..62387683)	539	2.17504	6	4	2	0.3333333	0.067	SLC2A4RG	ZBTB46
chr20	+(62681924..62683288)	1364	0.18556	16	7	9	0.125	0.99957245	SOX18	TCEA2
chr20	+(62703177..62703704)	527	0.40887	8	3	5	0.25	0.018	TCEA2	RGS19
chr21	+(9906128..9906831)	703	0.31351	12	5	7	0.1666667	0.04407898	MIR3687	LOC100132288
chr21	+(9911891..9912899)	1008	1.69869	11	5	6	0.0909091	0.99691505	MIR3687	LOC100132288
chr21	+(9954638..9955715)	1077	0.31351	15	7	8	0.0666667	0.00059687	MIR3687	LOC100132288
chr21	+(10213960..10214477)	517	4.76807	7	3	4	0.1428571	0.057	LOC100132288	TPTE
chr21	+(10850869..10851553)	684	0.8348	8	3	5	0.25	0.018	LOC100132288	TPTE
chr21	+(10857386..10857887)	501	1.69869	6	3	3	0	0.05	LOC100132288	TPTE
chr21	+(10933590..10934484)	894	1.5E-05	55	21	34	0.2363636	3.9274E-08	LOC100132288	TPTE
chr21	+(10944460..10945287)	827	0.31351	15	8	7	0.0666667	0.00544818	LOC100132288	TPTE
chr21	+(10959560..10960072)	512	1.69869	12	5	7	0.1666667	0.00368558	LOC100132288	TPTE
chr21	+(10998022..10998550)	528	2.71744	26	15	11	0.1538462	6.8189E-05	TPTE	BAGE2
chr21	+(11015272..11015789)	517	4.7703	19	12	7	0.2631579	0.03148953	TPTE	BAGE2
chr21	+(11020496..11021363)	867	1.24958	49	25	24	0.0204082	0.00090426	TPTE	BAGE2
chr21	+(11026559..11027061)	502	4.7703	20	13	7	0.3	0.00037882	TPTE	BAGE2
chr21	+(11038825..11039689)	864	0.15769	48	23	25	0.0416667	0.01191639	TPTE	BAGE2
chr21	+(11113136..11113654)	518	1.69869	7	4	3	0.1428571	0.029	BAGE	ANKRD30BP2
chr21	+(11139751..11140284)	533	4.76807	5	2	3	0.2	0.1	BAGE	ANKRD30BP2
chr21	+(11143360..11143978)	618	1.69869	10	6	4	0.2	0.762	BAGE	ANKRD30BP2
chr21	+(11144245..11145856)	1611	0.00351	24	15	9	0.25	2.8497E-05	BAGE	ANKRD30BP2
chr21	+(14417467..14417971)	504	3.31233	28	18	10	0.2857143	1.5141E-05	ANKRD30BP2	MIR3156-3
chr21	+(14768309..14768826)	517	1.69869	9	6	3	0.3333333	0.012	ANKRD30BP2	MIR3156-3
chr21	+(14771685..14772230)	545	4.76807	8	5	3	0.25	0.018	ANKRD30BP2	MIR3156-3

chr21	+(14995109..14995617)	508	4.76807	8	5	3	0.25	0.036	POTED	C21orf15
chr21	+(15003001..15003794)	793	0.00257	38	23	15	0.2105263	0.00025149	POTED	C21orf15
chr21	+(15011450..15012066)	616	0.8348	12	6	6	0	0.00815459	POTED	C21orf15
chr21	+(16337050..16337610)	560	0.8348	11	7	4	0.2727273	0.264	SAMSN1	NRIP1
chr21	+(18931112..18931629)	517	0.8348	9	6	3	0.3333333	0.012	CXADR	BTG3
chr21	+(19725876..19726408)	532	4.76807	7	3	4	0.1428571	0.029	CHODL	TMPRSS15
chr21	+(20229855..20230447)	592	1.69869	6	2	4	0.3333333	0.067	TMPRSS15	C21orf131
chr21	+(21112034..21112543)	509	0.8348	10	4	6	0.2	0.129	TMPRSS15	C21orf131
chr21	+(27113695..27114473)	778	1.69869	13	6	7	0.0769231	0.05804158	GABPA	APP
chr21	+(28296453..28296985)	532	4.76807	8	4	4	0	0.057	ADAMTS1	ADAMTS5
chr21	+(30332552..30333103)	551	4.76807	5	2	3	0.2	0.1	N6AMT1	LTN1
chr21	+(31802679..31803185)	506	4.76807	9	4	5	0.1111111	0.365	KRTAP13-4	KRTAP15-1
chr21	+(31812728..31813230)	502	4.76807	6	3	3	0	0.2	KRTAP15-1	KRTAP19-1
chr21	+(33044029..33044576)	547	2.07249	13	7	6	0.0769231	0.12654896	SOD1	SFRS15
chr21	+(33074337..33075374)	1037	0.31351	16	10	6	0.25	0.97455309	SOD1	SFRS15
chr21	+(33948062..33949030)	968	0.31351	15	8	7	0.0666667	0.05259626	C21orf63	TCP10L
chr21	+(33981961..33982527)	566	0.8348	10	5	5	0	0.03790009	TCP10L	C21orf59
chr21	+(34165722..34166546)	824	1.69869	11	5	6	0.0909091	0.57243393	C21orf49	C21orf62
chr21	+(34615759..34616284)	525	0.8348	10	4	6	0.2	0.005	IFNAR2	IL10RB
chr21	+(35470116..35470664)	548	1.69869	6	2	4	0.3333333	0.067	SLC5A3	C21orf82
chr21	+(35472499..35473006)	507	1.69869	9	6	3	0.3333333	0.024	SLC5A3	C21orf82
chr21	+(35475459..35476103)	644	1.69869	11	5	6	0.0909091	0.02230486	SLC5A3	C21orf82
chr21	+(35852773..35853387)	614	4.76807	5	2	3	0.2	0.1	FAM165B	KCNE1
chr21	+(36231385..36232046)	661	1.69869	9	3	6	0.3333333	0.048	NCRNA00160	RUNX1
chr21	+(36264991..36265495)	504	4.76807	5	3	2	0.2	0.1	NCRNA00160	RUNX1
chr21	+(37422465..37423053)	588	1.69869	9	5	4	0.1111111	0.143	MIR802	SETD4
chr21	+(37637178..37637879)	701	0.06448	10	6	4	0.2	0.005	DOPEY2	MORC3
chr21	+(37692106..37692734)	628	0.31351	8	3	5	0.25	0.018	DOPEY2	MORC3
chr21	+(37741544..37742049)	505	4.76807	6	2	4	0.3333333	0.067	MORC3	CHAF1B
chr21	+(37833029..37833549)	520	4.76807	9	4	5	0.1111111	0.008	CHAF1B	CLDN14
chr21	+(37857885..37858414)	529	1.69869	12	6	6	0	0.05465729	CHAF1B	CLDN14
chr21	+(38441656..38442182)	526	4.76807	8	5	3	0.25	0.286	DSCR6	PIGP
chr21	+(38560721..38561324)	603	4.76807	8	5	3	0.25	0.286	TTC3	DSCR9
chr21	+(39811109..39811648)	539	1.69869	6	4	2	0.3333333	0.067	KCNJ15	ERG

chr21	+(40636242..40636809)	567	1.69869	6	2	4	0.3333333	0.067	PSMG1	BRWD1
chr21	+(40667807..40668507)	700	0.8348	10	3	7	0.4	0.058	PSMG1	BRWD1
chr21	+(40759625..40760126)	501	4.76807	6	3	3	0	0.05	WRB	LCA5L
chr21	+(42749480..42749986)	506	1.69869	6	2	4	0.3333333	0.067	MX2	MX1
chr21	+(42774998..42775698)	700	0.06448	11	4	7	0.2727273	0.003	MX2	MX1
chr21	+(42780869..42781459)	590	4.76807	5	3	2	0.2	0.1	MX2	MX1
chr21	+(44474554..44475132)	578	4.76807	5	2	3	0.2	0.1	PKNOX1	CBS
chr21	+(44985162..44985825)	663	0.8348	9	5	4	0.1111111	0.008	C21orf84	HSF2BP
chr21	+(45292767..45293992)	1225	1.69869	11	6	5	0.0909091	0.99691505	AGPAT3	TRAPPC10
chr21	+(45546616..45547127)	511	4.76807	6	2	4	0.3333333	0.067	PWP2	C21orf33
chr21	+(45550084..45551141)	1057	0.00464	19	8	11	0.1578947	0.00013997	PWP2	C21orf33
chr21	+(45752762..45753879)	1117	0.8348	12	5	7	0.1666667	0.40377055	PFKL	C21orf2
chr21	+(45878251..45878952)	701	0.31351	14	9	5	0.2857143	0.15865525	LRRC3	C21orf29
chr21	+(45898675..45899337)	662	4.76807	5	3	2	0.2	0.1	LRRC3	C21orf29
chr21	+(46021313..46021840)	527	0.8348	11	4	7	0.2727273	0.158	LRRC3	C21orf29
chr21	+(46036804..46037319)	515	1.69869	6	4	2	0.3333333	0.067	LRRC3	C21orf29
chr21	+(46057189..46058260)	1071	0.15769	23	12	11	0.0434783	0.75079804	LRRC3	C21orf29
chr21	+(46066296..46066831)	535	0.31351	14	9	5	0.2857143	0.06259688	LRRC3	C21orf29
chr21	+(46069523..46070784)	1261	0.8348	13	7	6	0.0769231	0.0013499	LRRC3	C21orf29
chr21	+(46101678..46102191)	513	0.31351	9	4	5	0.1111111	0.016	LRRC3	C21orf29
chr21	+(46131139..46131670)	531	0.8348	7	3	4	0.1428571	0.029	LRRC3	C21orf29
chr21	+(46338105..46338829)	724	0.01104	12	5	7	0.1666667	0.00224163	PTTG1IP	ITGB2
chr21	+(46367109..46367804)	695	1.69869	10	6	4	0.2	0.995	C21orf70	NCRNA00163
chr21	+(46409087..46409787)	700	0.06448	10	6	4	0.2	0.005	C21orf70	NCRNA00163
chr21	+(46491902..46492478)	576	1.69869	6	2	4	0.3333333	0.067	NCRNA00162	C21orf122
chr21	+(46548086..46548642)	556	4.76807	9	4	5	0.1111111	0.008	ADARB1	POFUT2
chr21	+(46887956..46888516)	560	1.69869	6	4	2	0.3333333	0.067	NCRNA00175	SLC19A1
chr21	+(46943508..46944103)	595	1.69869	6	3	3	0	0.05	NCRNA00175	SLC19A1
chr21	+(46996786..46997328)	542	1.69869	6	3	3	0	0.05	SLC19A1	PCBP3
chr21	+(47025835..47026535)	700	0.06448	12	6	6	0	0.00197388	SLC19A1	PCBP3
chr21	+(47295894..47296490)	596	1.69869	11	7	4	0.2727273	0.036	PCBP3	COL6A1
chr21	+(47570381..47570942)	561	1.69869	6	4	2	0.3333333	0.067	COL6A2	FTCD
chr21	+(47600285..47600804)	519	1.69869	6	4	2	0.3333333	0.067	FTCD	C21orf56
chr21	+(47690244..47690940)	696	0.15769	11	4	7	0.2727273	0.003	MCM3AP-AS1	MCM3AP

chr21	+(47772221..47773266)	1045	1.69869	12	6	6	0	0.00197388	PCNT	DIP2A
chr21	+(47811056..47811756)	700	1.69869	7	3	4	0.1428571	0.029	PCNT	DIP2A
chr21	+(47850312..47850997)	685	1.69869	6	3	3	0	0.05	PCNT	DIP2A
chr22	+(16257918..16258612)	694	0.24081	50	29	21	0.16	1.7457E-09		POTEH
chr22	+(16266570..16267141)	571	0.44654	63	34	29	0.0793651	0.00604053		POTEH
chr22	+(16267780..16268672)	892	0.00438	144	74	70	0.0277778	1.6573E-08		POTEH
chr22	+(16275015..16275681)	666	1.05638	30	17	13	0.1333333	0.00050926		POTEH
chr22	+(16278817..16279504)	687	0.19846	58	24	34	0.1724138	5.3473E-07		POTEH
chr22	+(16282208..16282849)	641	0.19577	73	34	39	0.0684932	0.16799856		POTEH
chr22	+(16345617..16346192)	575	0.95339	10	4	6	0.2	0.005	POTEH	OR11H1
chr22	+(16350256..16350846)	590	3.79571	19	8	11	0.1578947	0.22869527	POTEH	OR11H1
chr22	+(16352608..16353168)	560	1.95252	9	5	4	0.1111111	0.206	POTEH	OR11H1
chr22	+(16353231..16353906)	675	0.95339	10	7	3	0.4	0.008	POTEH	OR11H1
chr22	+(16365744..16366248)	504	3.79571	15	6	9	0.2	0.02256348	POTEH	OR11H1
chr22	+(16448493..16449690)	1197	0.01468	96	63	33	0.3125	0.07733532	POTEH	OR11H1
chr22	+(17621678..17622354)	676	0.0754	10	5	5	0	0.00451172	CECR6	CECR5
chr22	+(18232734..18233434)	700	0.0754	11	4	7	0.2727273	0.003	BCL2L13	BID
chr22	+(18256470..18257152)	682	1.95252	9	6	3	0.3333333	0.988	BCL2L13	BID
chr22	+(18308681..18309381)	700	0.39879	12	6	6	0	0.00197388	MIR3198	MICAL3
chr22	+(19058146..19058870)	724	0.01468	12	6	6	0	0.00197388	DGCR10	DGCR2
chr22	+(19902747..19903297)	550	1.95252	6	2	4	0.3333333	0.067	C22orf29	TXNRD2
chr22	+(19963891..19964483)	592	0.95339	7	3	4	0.1428571	0.029	COMT	ARVCF
chr22	+(20092732..20093483)	751	0.00229	15	8	7	0.0666667	0.00059687	MIR1306	TRMT2A
chr22	+(21779817..21780488)	671	0.95339	7	3	4	0.1428571	0.029	HIC2	PI4KAP2
chr22	+(21838094..21838648)	554	0.95339	10	5	5	0	0.01414006	HIC2	PI4KAP2
chr22	+(21901590..21902116)	526	1.95252	9	5	4	0.1111111	0.032	PI4KAP2	RIMBP3B_dup2
chr22	+(22153079..22153598)	519	1.95252	6	3	3	0	0.05	YPEL1	MAPK1
chr22	+(22218306..22219129)	823	0.00229	15	9	6	0.2	0.00073136	YPEL1	MAPK1
chr22	+(22676819..22677335)	516	0.95339	9	4	5	0.1111111	0.016	LOC96610	ZNF280B
chr22	+(22989928..22990450)	522	1.95252	7	3	4	0.1428571	0.029	GGTLC2	MIR650
chr22	+(23969410..23969972)	562	1.95252	6	2	4	0.3333333	0.067	IGLL1	C22orf43
chr22	+(24483283..24483830)	547	1.95252	6	2	4	0.3333333	0.067	CABIN1	SUSD2
chr22	+(24511515..24512208)	693	1.95252	9	6	3	0.3333333	0.988	CABIN1	SUSD2
chr22	+(24640219..24640794)	575	0.95339	7	3	4	0.1428571	0.029	SUSD2	GGT5

chr22	+(24709143..24709652)	509	1.95252	6	4	2	0.3333333	0.067	SPECC1L	ADORA2A	
chr22	+(25019743..25020364)	621	0.95339	15	10	5	0.3333333	0.00505617	C22orf36	BCRP3	
chr22	+(25024466..25025165)	699	0.06575	35	12	23	0.3142857	0.00413086	C22orf36	BCRP3	
chr22	+(25265354..25265876)	522	1.95252	7	4	3	0.1428571	0.029	SGSM1	TMEM211	
chr22	+(29597631..29598267)	636	0.03801	11	5	6	0.0909091	0.00308495	KREMEN1	EMID1	
chr22	+(29620728..29621277)	549	1.95252	6	2	4	0.3333333	0.067	EMID1	RHBDD3	
chr22	+(29885619..29886178)	559	0.95339	15	8	7	0.0666667	0.08245742	NEFH	THOC5	
chr22	+(29888571..29889121)	550	0.0754	10	5	5	0	0.00451172	NEFH	THOC5	
chr22	+(30189270..30189945)	675	0.0754	10	6	4	0.2	0.005	UQCR10	ASCC2	
chr22	+(32109109..32109794)	685	1.95252	15	6	9	0.2	0.00921106	PISD	C22orf30	
chr22	+(32753836..32754431)	595	0.39879	10	3	7	0.4	0.192	RFPL3	RFPL3S	
chr22	+(33309563..33310097)	534	1.95252	6	2	4	0.3333333	0.067	FBXO7	SYN3	
chr22	+(35659569..35660204)	635	0.95339	9	4	5	0.1111111	0.032	HMGXB4	TOM1	
chr22	+(35942655..35943355)	700	0.16964	13	4	9	0.3846154	0.793	RASD2	MB	
chr22	+(36694681..36695235)	554	1.95252	8	3	5	0.25	0.286	APOL1	MYH9	
chr22	+(37545085..37546077)	992	0.0754	17	7	10	0.1764706	0.00031815	TMPRSS6	IL2RB	
chr22	+(37581027..37581529)	502	0.95339	7	4	3	0.1428571	0.029	IL2RB	C1QTNF6	
chr22	+(37766771..37767404)	633	0.39879	8	5	3	0.25	0.018	CYTH4	ELFN2	
chr22	+(37844059..37844735)	676	1.95252	6	2	4	0.3333333	0.067	ELFN2	MFNG	
chr22	+(38081605..38082770)	1165	1.95252	12	7	5	0.1666667	0.97882147	LGALS1	NOL12	
chr22	+(38779187..38779885)	698	0.16964	9	6	3	0.3333333	0.012	CSNK1E	LOC400927	
chr22	+(38902109..38902809)	700	0.0049	18	10	8	0.1111111	0.23859831	KDELR3	DDX17	
chr22	+(39176849..39177398)	549	0.95339	7	4	3	0.1428571	0.029	SUN2	DNAL4	
chr22	+(39387374..39387892)	518	1.95252	11	4	7	0.2727273	0.021	APOBEC3B	APOBEC3C	
chr22	+(39988117..39989291)	1174	0.01468	19	11	8	0.1578947	0.83912483	CACNA1I	ENTHD1	
chr22	+(40040899..40041540)	641	1.95252	6	4	2	0.3333333	0.067	CACNA1I	ENTHD1	
chr22	+(41572909..41573537)	628	0.95339	11	4	7	0.2727273	0.536	EP300	L3MBTL2	
chr22	+(42072604..42073266)	662	0.95339	17	9	8	0.0588235	0.00352682	XRCC6	NHP2L1	
chr22	+(42388399..42388999)	600	0.39879	9	3	6	0.3333333	0.012	41155	WBP2NL	
chr22	+(42422590..42423373)	783	0.03801	17	11	6	0.2941176	0.06583401	WBP2NL	NAGA	
chr22	+(42606268..42607144)	876	0.01468	26	13	13	0	0.00742745	CYP2D7P1	TCF20	v
chr22	+(42607164..42607844)	680	0.39879	10	7	3	0.4	0.017	CYP2D7P1	TCF20	v
chr22	+(42950837..42951375)	538	3.79571	15	6	9	0.2	0.03854994	SERHL2	RRP7B	
chr22	+(43627026..43627832)	806	0.0049	15	8	7	0.0666667	0.00754363	TTLL12	SCUBE1	

chr22	+(43678743..43679248)	505	0.95339	7	3	4	0.1428571	0.029	TTLL12	SCUBE1
chr22	+(43786698..43787396)	698	0.16964	9	6	3	0.3333333	0.012	SCUBE1	MPPED1
chr22	+(44235345..44235985)	640	0.0754	15	10	5	0.3333333	0.13517207	EFCAB6	SULT4A1
chr22	+(44687316..44688016)	700	1.95252	11	5	6	0.0909091	0.00308495	PARVG	KIAA1644
chr22	+(44848857..44849428)	571	1.95252	6	2	4	0.3333333	0.067	KIAA1644	LDOC1L
chr22	+(45758483..45759224)	741	0.03801	12	6	6	0	0.00197388	FAM118A	SMC1B
chr22	+(45802313..45802846)	533	1.95252	6	4	2	0.3333333	0.067	FAM118A	SMC1B
chr22	+(46273197..46273842)	645	1.95252	6	4	2	0.3333333	0.067	ATXN10	WNT7B
chr22	+(46311456..46312156)	700	0.16964	9	6	3	0.3333333	0.012	ATXN10	WNT7B
chr22	+(46317660..46318184)	524	1.95252	6	2	4	0.3333333	0.067	ATXN10	WNT7B
chr22	+(46752458..46753429)	971	1.95252	12	7	5	0.1666667	0.00926649	TRMU	CELSR1
chr22	+(46769440..46770091)	651	0.0754	13	8	5	0.2307692	0.23210716	TRMU	CELSR1
chr22	+(47036053..47036754)	701	0.00709	13	9	4	0.3846154	0.001	GRAMD4	CERK
chr22	+(47452499..47453002)	503	0.39879	8	4	4	0	0.014	TBC1D22A	FLJ46257
chr22	+(47846215..47846779)	564	0.95339	7	3	4	0.1428571	0.029	TBC1D22A	FLJ46257
chr22	+(50106056..50106756)	700	0.16964	9	3	6	0.3333333	0.012	C22orf34	BRD1
chr22	+(50197239..50198565)	1326	0.39879	17	9	8	0.0588235	0.000266	C22orf34	BRD1
chr22	+(50357668..50358368)	700	0.95339	9	5	4	0.1111111	0.008	PIM3	IL17REL
chr22	+(50551708..50552300)	592	1.95252	9	3	6	0.3333333	0.274	MOV10L1	PANX2
chr22	+(50654777..50655310)	533	1.95252	6	4	2	0.3333333	0.067	SELO	TUBGCP6
chr22	+(50784481..50785174)	693	0.03801	11	6	5	0.0909091	0.00308495	PPP6R2	SBF1
chr22	+(51152572..51153404)	832	0.00229	15	8	7	0.0666667	0.00059687	SHANK3	ACR
chr22	+(51167088..51167738)	650	0.95339	9	4	5	0.1111111	0.365	SHANK3	ACR
chrX	+(3239598..3240368)	770	0.00121	23	11	12	0.0434783	0.24920196	ARSF	MXRA5
chrX	+(3241083..3241610)	527	3.74219	5	3	2	0.2	0.1	ARSF	MXRA5
chrX	+(3363086..3363786)	700	0.073	9	4	5	0.1111111	0.008	MXRA5	PRKX
chrX	+(5223824..5224524)	700	3.74219	8	3	5	0.25	0.125	LOC389906	NLGN4X
chrX	+(5821333..5821841)	508	3.74219	6	2	4	0.3333333	0.4	LOC389906	NLGN4X
chrX	+(7023524..7024055)	531	1.41465	6	3	3	0	0.05	VCX3A	HDHD1
chrX	+(8507483..8508103)	620	1.41465	8	4	4	0	0.014	VCX3B	KAL1
chrX	+(8763241..8763746)	505	0.19635	9	4	5	0.1111111	0.008	KAL1	FAM9A
chrX	+(10085076..10085776)	700	0.52234	8	4	4	0	0.014	WWC3	CLCN4
chrX	+(10165743..10166438)	695	0.073	13	8	5	0.2307692	0.0017074	CLCN4	MID1
chrX	+(10174141..10175203)	1062	1.41465	16	9	7	0.125	0.93758876	CLCN4	MID1

chrX	+(10463483..10464046)	563	3.74219	6	4	2	0.3333333	0.067	CLCN4	MID1
chrX	+(11042884..11043435)	551	0.52234	7	3	4	0.1428571	0.029	MID1	HCCS
chrX	+(11159949..11160498)	549	1.41465	6	3	3	0	0.05	HCCS	ARHGAP6
chrX	+(11781453..11782135)	682	0.52234	12	4	8	0.3333333	0.055	MSL3	FRMPD4
chrX	+(12722205..12722742)	537	1.41465	6	2	4	0.3333333	0.067	FRMPD4	PRPS2
chrX	+(12993095..12993992)	897	1.41465	11	5	6	0.0909091	0.00308495	TLR8	TMSL3
chrX	+(13635675..13636568)	893	0.01092	20	10	10	0	0.00325085	EGFL6	TCEANC
chrX	+(13774597..13775123)	526	4.03702	13	5	8	0.2307692	0.05367327	OFD1	GPM6B
chrX	+(13785984..13786492)	508	4.03702	9	6	3	0.3333333	0.012	OFD1	GPM6B
chrX	+(15408033..15408565)	532	1.41465	7	3	4	0.1428571	0.029	FIGF	PIR
chrX	+(15497559..15498214)	655	0.2884	14	8	6	0.1428571	0.00225435	FIGF	PIR
chrX	+(15838180..15838847)	667	0.52234	11	7	4	0.2727273	0.006	ZRSR2	AP1S2
chrX	+(16716159..16716669)	510	0.52234	7	3	4	0.1428571	0.029	GRPR	CTPS2
chrX	+(16759473..16760130)	657	1.41465	9	3	6	0.3333333	0.012	SYAP1	TXLNG
chrX	+(16855261..16856055)	794	0.03356	14	7	7	0	0.02382272	TXLNG	RBBP7
chrX	+(16863756..16864312)	556	1.41465	6	3	3	0	0.05	TXLNG	RBBP7
chrX	+(16887215..16887764)	549	3.74219	7	4	3	0.1428571	0.057	TXLNG	RBBP7
chrX	+(17080196..17080857)	661	3.74219	8	3	5	0.25	0.286	REPS2	NHS
chrX	+(17083419..17084119)	700	0.03356	10	7	3	0.4	0.008	REPS2	NHS
chrX	+(18341906..18342551)	645	0.52234	9	6	3	0.3333333	0.048	BEND2	SCML2
chrX	+(18356565..18357212)	647	1.41465	13	7	6	0.0769231	0.0992714	BEND2	SCML2
chrX	+(18456012..18456922)	910	0.52234	13	8	5	0.2307692	0.01405402	CDKL5	RS1
chrX	+(18969016..18969716)	700	0.073	13	7	6	0.0769231	0.02275014	LOC100132163	PHKA2
chrX	+(19031598..19032111)	513	3.74219	7	3	4	0.1428571	0.314	PHKA2	GPR64
chrX	+(19041925..19042517)	592	1.41465	9	6	3	0.3333333	0.012	PHKA2	GPR64
chrX	+(20194363..20194881)	518	3.74219	8	4	4	0	0.057	SCARNA9L	RPS6KA3
chrX	+(21366589..21367413)	824	0.00513	12	5	7	0.1666667	0.00224163	RPS6KA3	CNKSR2
chrX	+(21581378..21581912)	534	3.74219	9	5	4	0.1111111	0.278	CNKSR2	KLHL34
chrX	+(21619099..21619860)	761	0.08034	29	19	10	0.3103448	8.4139E-05	CNKSR2	KLHL34
chrX	+(21876340..21876883)	543	0.52234	14	5	9	0.2857143	0.15865525	YY2	SMS
chrX	+(22010462..22010977)	515	3.74219	6	3	3	0	0.05	SMS	PHEX
chrX	+(22235898..22236482)	584	3.74219	5	2	3	0.2	0.1	PHEX	ZNF645
chrX	+(23017364..23018293)	929	0.073	15	10	5	0.3333333	0.00715294	ZNF645	DDX53
chrX	+(23019260..23020742)	1482	0.00513	42	22	20	0.047619	0.00221481	DDX53	PTCHD1

chrX	+(23021230..23021780)	550	3.74219	6	2	4	0.3333333	0.067	DDX53	PTCHD1	
chrX	+(23411386..23411908)	522	3.74219	8	5	3	0.25	0.071	PTCHD1	PRDX4	
chrX	+(24382670..24383193)	523	3.74219	6	4	2	0.3333333	0.133	FAM48B1	PDK3	
chrX	+(24740795..24741594)	799	0.52234	12	5	7	0.1666667	0.00224163	POLA1	SCARNA23	
chrX	+(26213157..26213850)	693	0.19635	15	5	10	0.3333333	0.04320538	MAGEB6	VENTXP1	
chrX	+(27839169..27839866)	697	1.41465	8	4	4	0	0.014	MAGEB10	DCAF8L1	
chrX	+(27998792..27999396)	604	0.19635	13	6	7	0.0769231	0.04323814	MAGEB10	DCAF8L1	
chrX	+(28807227..28807860)	633	1.41465	9	6	3	0.3333333	0.083	IL1RAPL1	MAGEB2	v
chrX	+(30237261..30238539)	1278	3.74219	19	13	6	0.3684211	0.19022756	MAGEB2	MAGEB3	
chrX	+(30648620..30649320)	700	0.073	11	4	7	0.2727273	0.003	CXorf21	GK	
chrX	+(30725163..30726147)	984	0.00024	33	19	14	0.1515152	1.0138E-05	GK	TAB3	
chrX	+(30738847..30739352)	505	1.41465	6	4	2	0.3333333	0.067	GK	TAB3	
chrX	+(30814585..30815285)	700	0.19635	8	3	5	0.25	0.018	GK	TAB3	
chrX	+(30873230..30873733)	503	3.74219	8	3	5	0.25	0.607	GK	TAB3	
chrX	+(32591718..32592251)	533	0.52234	8	4	4	0	0.014	FTHL17	DMD	
chrX	+(33501495..33502004)	509	0.52234	7	3	4	0.1428571	0.029	DMD	FAM47A	
chrX	+(34147932..34148468)	536	3.74219	7	4	3	0.1428571	0.057	DMD	FAM47A	
chrX	+(34181350..34182045)	695	3.74219	9	5	4	0.1111111	0.992	FAM47A	TMEM47	
chrX	+(34812209..34813319)	1110	0.52234	12	5	7	0.1666667	0.00224163	TMEM47	FAM47B	
chrX	+(34961178..34962247)	1069	0.52234	17	11	6	0.2941176	0.65616355	FAM47B	MAGEB16	
chrX	+(35820032..35820587)	555	3.74219	6	4	2	0.3333333	0.133	MAGEB16	CXorf22	
chrX	+(37026549..37027110)	561	0.2884	15	10	5	0.3333333	0.01374317	FAM47C	PRRG1	
chrX	+(37027896..37028701)	805	0.03356	27	17	10	0.2592593	0.09586971	FAM47C	PRRG1	
chrX	+(39714797..39715814)	1017	3.74219	10	5	5	0	0.00451172	MID1IP1	BCOR	
chrX	+(39921720..39922402)	682	1.41465	12	6	6	0	0.01248734	MID1IP1	BCOR	
chrX	+(40157654..40158354)	700	0.073	9	6	3	0.3333333	0.012	BCOR	ATP6AP2	
chrX	+(41074827..41076096)	1269	0.19635	20	10	10	0	0.58970208	USP9X	DDX3X	
chrX	+(41530345..41530982)	637	1.41465	10	4	6	0.2	0.005	NYX	CASK	
chrX	+(41587294..41588551)	1257	0.073	28	15	13	0.0714286	0.21008005	NYX	CASK	
chrX	+(43586627..43587584)	957	0.52234	13	7	6	0.0769231	0.00213737	MAOA	MAOB	
chrX	+(43595242..43595767)	525	3.74219	7	3	4	0.1428571	0.057	MAOA	MAOB	
chrX	+(43887785..43888729)	944	0.52234	12	5	7	0.1666667	0.00224163	NDP	EFHC2	
chrX	+(44107229..44108093)	864	3.74219	10	5	5	0	0.54159253	NDP	EFHC2	
chrX	+(44918118..44918649)	531	1.41465	7	4	3	0.1428571	0.114	KDM6A	CXorf36	

chrX	+(44938479..44939021)	542	3.74219	10	5	5	0	0.23235105	KDM6A	CXorf36
chrX	+(44941731..44942265)	534	3.74219	5	2	3	0.2	0.1	KDM6A	CXorf36
chrX	+(46510295..46510946)	651	1.41465	10	4	6	0.2	0.057	CHST7	SLC9A7
chrX	+(46696169..46696789)	620	3.74219	5	2	3	0.2	0.1	SLC9A7	RP2
chrX	+(47099138..47099762)	624	3.74219	6	2	4	0.3333333	0.133	USP11	ZNF157
chrX	+(47100481..47101041)	560	1.41465	6	3	3	0	0.05	USP11	ZNF157
chrX	+(47158106..47158772)	666	0.52234	7	3	4	0.1428571	0.029	USP11	ZNF157
chrX	+(47447570..47448270)	700	0.03356	10	7	3	0.4	0.008	ARAF	SYN1
chrX	+(47495985..47496536)	551	3.74219	6	2	4	0.3333333	0.067	CFP	ELK1
chrX	+(47919484..47920005)	521	3.74219	5	2	3	0.2	0.1	SPACA5B_dup1	ZNF630
chrX	+(47925978..47926506)	528	1.41465	10	4	6	0.2	0.086	SPACA5B_dup1	ZNF630
chrX	+(47991412..47992366)	954	0.00694	43	28	15	0.3023256	2.5424E-05	SPACA5B_dup2	SSX5
chrX	+(48018449..48019043)	594	0.52234	10	7	3	0.4	0.008	SPACA5B_dup2	SSX5
chrX	+(48023981..48024485)	504	3.74219	11	6	5	0.0909091	0.00308495	SPACA5B_dup2	SSX5
chrX	+(48047087..48047609)	522	1.41465	15	6	9	0.2	0.01257238	SPACA5B_dup2	SSX5
chrX	+(48054055..48054706)	651	0.073	15	8	7	0.0666667	0.02457042	SPACA5B_dup2	SSX5
chrX	+(48071828..48072342)	514	3.74219	15	10	5	0.3333333	0.00505617	SSX5	SSX1
chrX	+(48073944..48074479)	535	0.19635	15	8	7	0.0666667	0.01862128	SSX5	SSX1
chrX	+(48117814..48118468)	654	0.52234	14	5	9	0.2857143	0.0013499	SSX1	SSX3
chrX	+(48136570..48137443)	873	2.9E-07	50	20	30	0.2	8.2434E-07	SSX1	SSX3
chrX	+(48158665..48159279)	614	0.01092	16	5	11	0.375	0.09631901	SSX1	SSX3
chrX	+(48160974..48161692)	718	0.07018	27	15	12	0.1111111	0.02851994	SSX1	SSX3
chrX	+(48162870..48164376)	1506	0.00513	50	24	26	0.04	0.13002633	SSX1	SSX3
chrX	+(48185832..48186453)	621	0.00054	25	15	10	0.2	0.00094715	SSX1	SSX3
chrX	+(48214062..48215102)	1040	0.2884	40	17	23	0.15	0.0083336	SSX1	SSX3
chrX	+(48299542..48300287)	745	0.19635	14	7	7	0	0.00635813	SSX4B_dup2	SLC38A5
chrX	+(48317895..48318508)	613	0.81582	14	6	8	0.1428571	0.00225435	SSX4B_dup2	SLC38A5
chrX	+(48455610..48456685)	1075	0.19635	14	8	6	0.1428571	0.00097289	RBM3	WDR13
chrX	+(48547478..48548061)	583	3.74219	6	2	4	0.3333333	0.067	WAS	SUV39H1
chrX	+(49103836..49104514)	678	1.41465	6	4	2	0.3333333	0.067	CCDC22	FOXP3
chrX	+(49113646..49114250)	604	1.41465	8	3	5	0.25	0.018	CCDC22	FOXP3
chrX	+(50376011..50376530)	519	1.41465	8	5	3	0.25	0.125	DGKK	SHROOM4
chrX	+(52591015..52591532)	517	3.74219	7	3	4	0.1428571	0.029	XAGE1E_dup5	SSX8
chrX	+(52637255..52638214)	959	0.00513	28	18	10	0.2857143	0.00055637	XAGE1E_dup5	SSX8

chrX	+(52639786..52640532)	746	0.19635	19	7	12	0.2631579	0.24948115	XAGE1E_dup5	SSX8
chrX	+(52653671..52654498)	827	0.70173	25	8	17	0.36	0.00368399	SSX8	SSX7
chrX	+(52657178..52657816)	638	1.00556	26	14	12	0.0769231	3.0118E-05	SSX8	SSX7
chrX	+(52658935..52659480)	545	0.19635	12	4	8	0.3333333	0.055	SSX8	SSX7
chrX	+(52661755..52662274)	519	1.41465	14	6	8	0.1428571	0.0070857	SSX8	SSX7
chrX	+(52674039..52675071)	1032	2E-06	49	20	29	0.1836735	0.01807589	SSX8	SSX7
chrX	+(52679143..52679918)	775	0.06317	30	21	9	0.4	0.002028	SSX8	SSX7
chrX	+(52682115..52682894)	779	7.6E-06	39	14	25	0.2820513	3.0238E-05	SSX8	SSX7
chrX	+(52842123..52842634)	511	3.74219	10	4	6	0.2	0.005	XAGE5	XAGE3
chrX	+(52843929..52844468)	539	1.41465	7	3	4	0.1428571	0.029	XAGE5	XAGE3
chrX	+(52891218..52891732)	514	3.74219	9	4	5	0.1111111	0.008	XAGE5	XAGE3
chrX	+(53111895..53112595)	700	0.52234	10	3	7	0.4	0.033	TSPYL2	KDM5C
chrX	+(53116826..53117330)	504	3.74219	6	4	2	0.3333333	0.067	TSPYL2	KDM5C
chrX	+(53387878..53388666)	788	0.19635	15	9	6	0.2	0.00073136	IQSEC2	SMC1A
chrX	+(53438583..53439090)	507	3.74219	6	3	3	0	0.05	IQSEC2	SMC1A
chrX	+(53439963..53440485)	522	1.41465	7	4	3	0.1428571	0.114	IQSEC2	SMC1A
chrX	+(54107159..54107734)	575	3.74219	5	2	3	0.2	0.1	PHF8	FAM120C
chrX	+(54275498..54276031)	533	1.41465	7	4	3	0.1428571	0.2	FAM120C	WNK3
chrX	+(54277793..54278492)	699	0.52234	12	7	5	0.1666667	0.18587565	FAM120C	WNK3
chrX	+(54337377..54337996)	619	3.74219	10	7	3	0.4	0.133	FAM120C	WNK3
chrX	+(54975358..54975859)	501	3.74219	7	3	4	0.1428571	0.314	TRO	PFKFB1
chrX	+(56592036..56592587)	551	1.41465	13	7	6	0.0769231	0.01606229	UBQLN2	LOC550643
chrX	+(56763243..56763870)	627	1.41465	12	6	6	0	0.00197388	LOC550643	LOC442454
chrX	+(57162293..57162983)	690	0.0508	38	20	18	0.0526316	0.03970532	SPIN2B	SPIN2A
chrX	+(57621174..57621803)	629	1.41465	10	5	5	0	0.23235105	ZXDB	ZXDA
chrX	+(57622451..57623186)	735	1.41465	14	8	6	0.1428571	0.5	ZXDB	ZXDA
chrX	+(63443868..63444480)	612	0.073	12	5	7	0.1666667	0.04407898	FAM123B	ASB12
chrX	+(64547706..64548406)	700	0.52234	9	5	4	0.1111111	0.016	ZC4H2	ZC3H12B
chrX	+(64708971..64709553)	582	3.74219	6	4	2	0.3333333	0.067	ZC3H12B	LAS1L
chrX	+(67316509..67317043)	534	1.41465	6	3	3	0	0.05	AR	OPHN1
chrX	+(67433603..67434105)	502	3.74219	10	4	6	0.2	0.619	AR	OPHN1
chrX	+(67459640..67460218)	578	3.74219	5	3	2	0.2	0.1	AR	OPHN1
chrX	+(67940821..67941456)	635	0.52234	9	5	4	0.1111111	0.008	STARD8	EFNB1
chrX	+(68004058..68004595)	537	1.31725	16	9	7	0.125	0.11174712	STARD8	EFNB1

chrX	+(68059062..68059613)	551	0.19635	8	4	4	0	0.014	EFNB1	PJA1
chrX	+(68381325..68381833)	508	3.74219	8	5	3	0.25	0.125	EFNB1	PJA1
chrX	+(68382306..68383467)	1161	3.74219	13	5	8	0.2307692	0.5	EFNB1	PJA1
chrX	+(68420408..68421108)	700	0.073	9	6	3	0.3333333	0.012	PJA1	FAM155B
chrX	+(68434621..68435769)	1148	0.073	17	9	8	0.0588235	0.999734	PJA1	FAM155B
chrX	+(69263381..69263955)	574	1.41465	9	5	4	0.1111111	0.008	MIR676	AWAT2
chrX	+(69499993..69501104)	1111	0.52234	14	6	8	0.1428571	0.12263906	ARR3	RAB41
chrX	+(69503888..69504416)	528	0.52234	8	5	3	0.25	0.125	RAB41	PDZD11
chrX	+(69720157..69720701)	544	1.41465	7	4	3	0.1428571	0.029	DLG3	TEX11
chrX	+(70026145..70026805)	660	1.41465	9	4	5	0.1111111	0.095	DLG3	TEX11
chrX	+(70094100..70094810)	710	0.01092	11	5	6	0.0909091	0.00308495	DLG3	TEX11
chrX	+(70147625..70148159)	534	3.74219	6	4	2	0.3333333	0.267	TEX11	SLC7A3
chrX	+(70212060..70212921)	861	0.03356	11	6	5	0.0909091	0.03394459	SLC7A3	SNX12
chrX	+(70321380..70321999)	619	0.073	10	4	6	0.2	0.005	FOXO4	CXorf65
chrX	+(70493073..70493653)	580	4.03702	8	5	3	0.25	0.018	NLGN3	BCYRN1
chrX	+(70518092..70518625)	533	1.41465	7	4	3	0.1428571	0.029	NLGN3	BCYRN1
chrX	+(70616870..70617541)	671	1.41465	8	3	5	0.25	0.125	NLGN3	BCYRN1
chrX	+(70618207..70618726)	519	1.41465	6	4	2	0.3333333	0.067	NLGN3	BCYRN1
chrX	+(70778270..70779499)	1229	0.52234	14	8	6	0.1428571	0.00097289	NLGN3	BCYRN1
chrX	+(70782746..70783446)	700	1.41465	10	7	3	0.4	0.058	NLGN3	BCYRN1
chrX	+(70889878..70890453)	575	3.74219	7	4	3	0.1428571	0.029	NLGN3	BCYRN1
chrX	+(70934134..70935097)	963	0.073	26	18	8	0.3846154	0.99675777	NLGN3	BCYRN1
chrX	+(71034239..71034939)	700	0.2884	12	7	5	0.1666667	0.00224163	CXorf49_dup2	NHSL2
chrX	+(71093035..71093686)	651	0.52234	12	4	8	0.3333333	0.077	CXorf49_dup2	NHSL2
chrX	+(71363070..71363784)	714	0.073	12	8	4	0.3333333	0.055	RGAG4	FLJ44635
chrX	+(73405605..73406106)	501	3.74219	7	4	3	0.1428571	0.314	NCRNA00183	NCRNA00182
chrX	+(76854791..76855449)	658	4.03702	12	6	6	0	0.00815459	FGF16	ATRX
chrX	+(76871944..76872450)	506	3.74219	10	5	5	0	0.23235105	FGF16	ATRX
chrX	+(77111961..77112655)	694	1.41465	8	5	3	0.25	0.125	ATRX	MAGT1
chrX	+(77528290..77528936)	646	3.74219	9	5	4	0.1111111	0.365	TAF9B	CYSLTR1
chrX	+(79828452..79829063)	611	3.74219	12	7	5	0.1666667	0.71511782	FAM46D	BRWD3
chrX	+(79937828..79938363)	535	3.74219	8	4	4	0	0.057	FAM46D	BRWD3
chrX	+(79947174..79947802)	628	0.52234	10	4	6	0.2	0.057	FAM46D	BRWD3
chrX	+(79972807..79973364)	557	3.74219	8	4	4	0	0.014	FAM46D	BRWD3

chrX	+(79983909..79984609)	700	0.01092	13	4	9	0.3846154	0.001	FAM46D	BRWD3
chrX	+(80310516..80311193)	677	1.41465	6	2	4	0.3333333	0.067	BRWD3	HMGN5
chrX	+(81836421..81836983)	562	0.19635	8	5	3	0.25	0.018	SH3BGRL	POU3F4
chrX	+(82763927..82764927)	1000	0.52234	14	9	5	0.2857143	0.99018467	POU3F4	CYLC1
chrX	+(83588501..83589061)	560	3.74219	6	2	4	0.3333333	0.267	RPS6KA6	HDX
chrX	+(83724103..83724795)	692	0.81582	16	11	5	0.375	0.07837268	RPS6KA6	HDX
chrX	+(85746446..85747146)	700	0.073	13	4	9	0.3846154	0.999	DACH2	KLHL4
chrX	+(85969263..85969874)	611	0.52234	11	5	6	0.0909091	0.02230486	DACH2	KLHL4
chrX	+(90692939..90693446)	507	4.03702	13	8	5	0.2307692	0.02021199	PABPC5	PCDH11X
chrX	+(91137743..91138284)	541	0.52234	14	8	6	0.1428571	0.39812671	PCDH11X	NAP1L3
chrX	+(91873090..91873759)	669	0.19635	15	9	6	0.2	0.00921106	PCDH11X	NAP1L3
chrX	+(92408949..92409477)	528	3.74219	5	2	3	0.2	0.1	PCDH11X	NAP1L3
chrX	+(96122271..96122806)	535	0.52234	8	5	3	0.25	0.018	DIAPH2	RPA4
chrX	+(96167034..96167734)	700	1.41465	10	4	6	0.2	0.033	RPA4	LOC442459
chrX	+(96173354..96173869)	515	0.03356	12	8	4	0.3333333	0.036	RPA4	LOC442459
chrX	+(96185563..96186113)	550	1.44534	11	7	4	0.2727273	0.006	RPA4	LOC442459
chrX	+(96193907..96194410)	503	3.74219	10	5	5	0	0.00451172	RPA4	LOC442459
chrX	+(96638476..96639003)	527	0.52234	10	3	7	0.4	0.417	RPA4	LOC442459
chrX	+(100486279..100486979)	700	1.41465	6	2	4	0.3333333	0.067	DRP2	TAF7L
chrX	+(100536940..100537481)	541	3.74219	10	7	3	0.4	0.192	DRP2	TAF7L
chrX	+(101908907..101909447)	540	3.74219	6	4	2	0.3333333	0.067	GPRASP1	GPRASP2
chrX	+(101912205..101912708)	503	3.74219	7	4	3	0.1428571	0.114	GPRASP1	GPRASP2
chrX	+(101971569..101972081)	512	3.74219	8	4	4	0	0.243	GPRASP2	BHLHB9
chrX	+(102006059..102006578)	519	3.74219	8	3	5	0.25	0.393	BHLHB9	RAB40AL
chrX	+(102006831..102007772)	941	3.74219	35	18	17	0.0285714	0.02779186	BHLHB9	RAB40AL
chrX	+(102333136..102334123)	987	9.2E-05	38	22	16	0.1578947	0.00975386	BEX1	NXF3
chrX	+(102334217..102335286)	1069	0.52234	24	9	15	0.25	0.00158061	BEX1	NXF3
chrX	+(102967054..102967557)	503	3.74219	7	4	3	0.1428571	0.114	MORF4L2	GLRA4
chrX	+(102968404..102968973)	569	1.41465	12	5	7	0.1666667	0.28488218	MORF4L2	GLRA4
chrX	+(103040389..103040906)	517	3.74219	7	3	4	0.1428571	0.2	PLP1	RAB9B
chrX	+(103216122..103216943)	821	0.00023	30	20	10	0.3333333	0.00414961	RAB9B	MIR1256
chrX	+(106105910..106106428)	518	1.41465	6	2	4	0.3333333	0.067	TBC1D8B	RIPPLY1
chrX	+(106113749..106114274)	525	1.41465	9	3	6	0.3333333	0.012	TBC1D8B	RIPPLY1
chrX	+(106185652..106186293)	641	1.41465	6	4	2	0.3333333	0.067	CLDN2	MORC4

chrX	+(106356471..106356989)	518	3.74219	7	4	3	0.1428571	0.029	MORC4	RBM41
chrX	+(106394555..106395255)	700	3.74219	8	3	5	0.25	0.982	RBM41	NUP62CL
chrX	+(106921376..106922076)	700	0.52234	11	7	4	0.2727273	0.997	PRPS1	TSC22D3
chrX	+(106926323..106926910)	587	3.74219	8	4	4	0	0.829	PRPS1	TSC22D3
chrX	+(106959045..106959745)	700	0.19635	8	3	5	0.25	0.018	PRPS1	TSC22D3
chrX	+(107377247..107377886)	639	0.52234	13	6	7	0.0769231	0.00757922	ATG4A	COL4A6
chrX	+(110961114..110961809)	695	0.52234	8	5	3	0.25	0.286	ALG13	TRPC5
chrX	+(111202179..111202879)	700	3.74219	8	5	3	0.25	0.982	ALG13	TRPC5
chrX	+(113965800..113966407)	607	1.41465	9	5	4	0.1111111	0.635	MIR1298	MIR1911
chrX	+(114413831..114414341)	510	1.41465	12	6	6	0	0.2609197	IL13RA2	LRCH2
chrX	+(114609327..114610027)	700	0.073	9	5	4	0.1111111	0.008	LUZP4	PLS3
chrX	+(114874345..114875050)	705	1.41465	10	5	5	0	0.0081468	PLS3	AGTR2
chrX	+(114953061..114953761)	700	0.52234	11	4	7	0.2727273	0.158	PLS3	AGTR2
chrX	+(117521091..117521600)	509	0.52234	10	4	6	0.2	0.019	MIR1277	DOCK11
chrX	+(117699973..117700483)	510	1.41465	13	6	7	0.0769231	0.00757922	DOCK11	IL13RA1
chrX	+(117718457..117719008)	551	0.52234	8	3	5	0.25	0.286	DOCK11	IL13RA1
chrX	+(117732104..117732788)	684	3.74219	8	5	3	0.25	0.982	DOCK11	IL13RA1
chrX	+(117743035..117743792)	757	0.01092	18	9	9	0	0.00017429	DOCK11	IL13RA1
chrX	+(117748412..117748977)	565	1.41465	11	7	4	0.2727273	0.012	DOCK11	IL13RA1
chrX	+(117758182..117758792)	610	4.66385	15	5	10	0.3333333	0.0330963	DOCK11	IL13RA1
chrX	+(117769904..117770577)	673	0.52234	12	5	7	0.1666667	0.85442389	DOCK11	IL13RA1
chrX	+(118139729..118140674)	945	0.52234	13	8	5	0.2307692	0.02021199	LONRF3	KIAA1210
chrX	+(118220470..118221135)	665	1.44534	16	6	10	0.25	0.02544691	LONRF3	KIAA1210
chrX	+(118222794..118223444)	650	1.41465	13	6	7	0.0769231	0.07656373	LONRF3	KIAA1210
chrX	+(118893721..118894419)	698	1.41465	9	4	5	0.1111111	0.095	ANKRD58	RPL39
chrX	+(119572884..119573445)	561	3.74219	5	2	3	0.2	0.1	ATP1B4	LAMP2
chrX	+(119581678..119582306)	628	3.74219	8	5	3	0.25	0.5	ATP1B4	LAMP2
chrX	+(122536699..122537373)	674	1.41465	11	7	4	0.2727273	0.036	GRIA3	THOC2
chrX	+(122747115..122747815)	700	0.03356	13	4	9	0.3846154	0.074	GRIA3	THOC2
chrX	+(122754800..122755508)	708	0.03356	16	7	9	0.125	0.01500531	GRIA3	THOC2
chrX	+(122756593..122757126)	533	3.74219	5	2	3	0.2	0.1	GRIA3	THOC2
chrX	+(122757502..122758080)	578	1.41465	13	7	6	0.0769231	0.28385458	GRIA3	THOC2
chrX	+(123556039..123556616)	577	3.74219	6	3	3	0	0.2	SH2D1A	ODZ1
chrX	+(128700933..128701541)	608	1.41465	8	3	5	0.25	0.018	OCRL	APLN

chrX	+(128788031..128788546)	515	1.41465	6	4	2	0.3333333	0.067	OCRL	APLN	
chrX	+(128880628..128881150)	522	1.41465	9	6	3	0.3333333	0.012	XPNPEP2	SASH3	
chrX	+(129199312..129200012)	700	0.19635	8	5	3	0.25	0.018	BCORL1	ELF4	
chrX	+(129542998..129543516)	518	4.03702	12	4	8	0.3333333	0.00328926	RBMX2	FAM45B	
chrX	+(129629091..129630467)	1376	0.06317	51	17	34	0.3333333	0.11144811	FAM45B	ENOX2	
chrX	+(129630705..129631405)	700	0.00024	33	17	16	0.030303	0.05648728	FAM45B	ENOX2	
chrX	+(129665188..129665888)	700	0.073	9	6	3	0.3333333	0.012	FAM45B	ENOX2	
chrX	+(129790183..129790731)	548	4.03702	12	4	8	0.3333333	0.184	FAM45B	ENOX2	
chrX	+(130408315..130409015)	700	0.19635	12	4	8	0.3333333	0.00328926	ARHGAP36	IGSF1	
chrX	+(130416288..130416840)	552	3.74219	5	3	2	0.2	0.1	ARHGAP36	IGSF1	
chrX	+(130678563..130679197)	634	0.52234	9	5	4	0.1111111	0.206	OR13H1	LOC286467	
chrX	+(133379552..133380166)	614	1.41465	6	4	2	0.3333333	0.067	CCDC160	PHF6	
chrX	+(135312470..135313026)	556	0.19635	11	6	5	0.0909091	0.01422987	FHL1	MAP7D3	
chrX	+(135326405..135326935)	530	3.74219	10	5	5	0	0.03790009	FHL1	MAP7D3	
chrX	+(140982876..140983434)	558	1.41465	8	4	4	0	0.171	MAGEC3	MAGEC1	
chrX	+(140984011..140984998)	987	0.19635	20	6	14	0.4	0.89198971	MAGEC3	MAGEC1	
chrX	+(140994157..140994865)	708	0.81582	30	15	15	0	0.27377615	MAGEC1	MAGEC2	
chrX	+(140995351..140995935)	584	1.41465	9	6	3	0.3333333	0.012	MAGEC1	MAGEC2	
chrX	+(142967073..142968510)	1437	0.03356	40	26	14	0.3	0.93714429	SPANXN2	UBE2NL	
chrX	+(143991440..143992334)	894	0.03356	12	5	7	0.1666667	0.00224163	UBE2NL	SPANXN1	
chrX	+(144255152..144255685)	533	3.74219	8	3	5	0.25	0.018	UBE2NL	SPANXN1	
chrX	+(147003299..147003935)	636	1.41465	8	5	3	0.25	0.286	MIR514-3_dup2	FMR1-AS1	
chrX	+(147013831..147014359)	528	3.74219	9	3	6	0.3333333	0.19	FMR1	FMR1NB	
chrX	+(149943533..149944780)	1247	0.073	16	9	7	0.125	0.00042755	MTMR1	CD99L2	v
chrX	+(149984521..149985045)	524	3.74219	9	5	4	0.1111111	0.206	MTMR1	CD99L2	v
chrX	+(150099616..150100316)	700	0.19635	8	5	3	0.25	0.018	CD99L2	HMGB3	v
chrX	+(150793649..150794327)	678	0.03356	11	7	4	0.2727273	0.036	PASD1	PRRG3	
chrX	+(150844325..150844958)	633	0.52234	8	5	3	0.25	0.018	PASD1	PRRG3	
chrX	+(152127693..152128352)	659	3.74219	6	3	3	0	0.35	ZNF185	PNMA5	
chrX	+(152613609..152614973)	1364	0.073	25	15	10	0.2	0.05384858	ZNF275	ZFP92	
chrX	+(152731261..152731842)	581	1.41465	10	6	4	0.2	0.995	TREX2	HAUS7	
chrX	+(152837075..152837730)	655	3.74219	5	2	3	0.2	0.1	ATP2B3	FAM58A	
chrX	+(152853409..152854328)	919	0.01092	26	18	8	0.3846154	0.13326027	ATP2B3	FAM58A	
chrX	+(152869941..152870474)	533	3.74219	5	3	2	0.2	0.1	FAM58A	DUSP9	

chrX	+(152877670..152878282)	612	1.41465	6	3	3	0	0.05	FAM58A	DUSP9
chrX	+(152935012..152935539)	527	0.52234	12	8	4	0.3333333	0.533	DUSP9	PNCK
chrX	+(152963508..152964083)	575	1.41465	6	4	2	0.3333333	0.067	SLC6A8	BCAP31
chrX	+(152966472..152966982)	510	3.74219	5	2	3	0.2	0.1	SLC6A8	BCAP31
chrX	+(153050568..153051126)	558	3.74219	7	4	3	0.1428571	0.2	SRPK3	IDH3G
chrX	+(153069911..153071011)	1100	0.19635	14	9	5	0.2857143	0.0013499	SSR4	PDZD4
chrX	+(153133660..153134170)	510	3.74219	6	4	2	0.3333333	0.067	PDZD4	L1CAM
chrX	+(153458665..153459206)	541	4.03702	12	4	8	0.3333333	0.055	OPN1MW_dup1	OPN1MW2_dup2
chrX	+(153461007..153461783)	776	3.74219	11	5	6	0.0909091	0.02230486	OPN1MW_dup1	OPN1MW2_dup2
chrX	+(153462802..153463371)	569	0.81582	13	8	5	0.2307692	0.0394913	OPN1MW_dup1	OPN1MW2_dup2
chrX	+(153499777..153500324)	547	4.03702	14	5	9	0.2857143	0.03593032	OPN1MW_dup2	TEX28
chrX	+(153579926..153580427)	501	3.74219	6	3	3	0	0.05	TKTL1	FLNA
chrX	+(153599029..153599721)	692	0.19635	8	5	3	0.25	0.018	TKTL1	FLNA
chrX	+(153663342..153664325)	983	1.41465	12	7	5	0.1666667	0.08373231	ATP6AP1	GDI1
chrX	+(153775366..153776066)	700	1.41465	9	6	3	0.3333333	0.012	FAM3A	G6PD
chrX	+(153880441..153880983)	542	1.41465	10	6	4	0.2	0.057	NCRNA00204_dup2	CTAG2
chrY	+(249158..249779)	621	1.74153	7	4	3	0.1428571	0.029	NCRNA00107	PPP2R3B
chrY	+(272001..272690)	689	0.0116	9	5	4	0.1111111	0.008	NCRNA00107	PPP2R3B
chrY	+(272752..273452)	700	0.00344	10	3	7	0.4	0.008	NCRNA00107	PPP2R3B
chrY	+(273635..274503)	868	1.4E-05	23	9	14	0.2173913	0.2853752	NCRNA00107	PPP2R3B
chrY	+(448173..448873)	700	0.03527	13	5	8	0.2307692	0.0017074	PPP2R3B	SHOX
chrY	+(644513..645419)	906	0.0116	14	9	5	0.2857143	0.0013499	SHOX	CRLF2
chrY	+(760611..761304)	693	0.11116	10	3	7	0.4	0.008	SHOX	CRLF2
chrY	+(920383..920926)	543	1.9736	7	4	3	0.1428571	0.029	SHOX	CRLF2
chrY	+(1277358..1278038)	680	0.00344	22	12	10	0.0909091	0.91692773	SHOX	CRLF2
chrY	+(1351251..1351785)	534	4.16944	9	3	6	0.3333333	0.19	CSF2RA	MIR3690
chrY	+(1364088..1364788)	700	0.03067	20	6	14	0.4	0.01599867	MIR3690	IL3RA
chrY	+(1374005..1374861)	856	0.23333	24	15	9	0.25	0.00106719	MIR3690	IL3RA
chrY	+(1458286..1458883)	597	0.54239	8	5	3	0.25	0.5	IL3RA	SLC25A6
chrY	+(2134697..2135228)	531	1.0295	13	6	7	0.0769231	0.00332094	ASMT	DHRSX
chrY	+(2266980..2267680)	700	0.00032	20	10	10	0	0.00124845	ASMT	DHRSX
chrY	+(2582466..2582967)	501	1.25554	15	8	7	0.0666667	0.02457042	CD99	XGPY2
chrY	+(2590362..2590992)	630	0.95714	18	11	7	0.2222222	0.00120674	CD99	XGPY2
chrY	+(2591191..2591869)	678	0.54239	10	7	3	0.4	0.058	CD99	XGPY2

chrY	+(4966629..4967206)	577	1.74153	7	3	4	0.1428571	0.057	PCDH11Y	TTTY23B_dup1
chrY	+(5368783..5369629)	846	0.03527	17	8	9	0.0588235	0.00807239	PCDH11Y	TTTY23B_dup1
chrY	+(5948971..5949617)	646	0.23029	17	8	9	0.0588235	0.000266	PCDH11Y	TTTY23B_dup1
chrY	+(21115598..21116298)	700	0.03527	12	4	8	0.3333333	0.00328926	NCRNA00185	TTTY14
chrY	+(28740673..28741371)	698	0.54239	9	4	5	0.1111111	0.032	TTTY3_dup2	SPRY3
chrY	+(58831118..58831634)	516	1.74153	8	5	3	0.25	0.196	TTTY3_dup2	SPRY3
chrY	+(58867981..58868528)	547	1.74153	5	2	3	0.2	0.1	TTTY3_dup2	SPRY3
chrY	+(58983156..58984362)	1206	5.3E-06	27	11	16	0.1851852	7.0441E-06	TTTY3_dup2	SPRY3
chrY	+(58993211..58994517)	1306	0.11116	32	10	22	0.375	0.99997604	TTTY3_dup2	SPRY3
chrY	+(59001681..59002245)	564	0.05151	13	4	9	0.3846154	0.02	TTTY3_dup2	SPRY3
chrY	+(59107663..59108485)	822	0.02787	27	12	15	0.1111111	0.04383441	SPRY3	VAMP7
chrY	+(59228106..59228827)	721	0.05403	20	12	8	0.2	0.00215447	VAMP7	IL9R
chrY	+(59230462..59231162)	700	0.0116	10	3	7	0.4	0.008	VAMP7	IL9R

Supplementary Table S8. The correlation between protein expression of Oct4 in relation to PTEN and TNC protein expression in lung cancer patients.*****

Characteristics		Oct4 protein	
		Normal expression	Overexpression
	Total	N (%)	N (%)
Overall	133	41 (30.8)	92 (69.2)
PTEN protein	133		
Normal expression	52	22 (42.3)	18 (57.7)
Low expression	81	19 (23.5)	62 (76.5)$^{\mathbf{0.022}}$
TNC protein	133		
Normal expression	55	30 (54.5)	25 (45.5)
Overexpression	78	11 (14.1)	67 (85.9)$^{\mathbf{<0.001}}$

***** These results were analyzed by the Pearson $\chi 2$ test. The *P* values with significance are shown as superscripts.

Supplementary Table S9. The correlation between protein expression of TNC in relation to both Oct4 and PTEN protein expression levels in lung cancer patients.*

Characteristics		Oct4 and PTEN protein		
		Oct4 Normal expression PTEN Normal expression	Others	Oct4 Overexpression PTEN Low expression
	Total	N (%)	N (%)	N (%)
Overall	133	22 (100)	49 (100)	62 (100)
TNC protein	133			
Normal expression	55	16 (72.7)	20 (40.8)	19 (30.6)
Overexpression	78	6 (27.3)	29 (59.2)	43 (69.4)$^{\mathbf{0.003}}$

***** These results were analyzed by the Pearson $\chi 2$ test. The *P* values with significance are shown as superscripts.