

Supplemental methods

Animal maintenance. Animals were maintained according to protocols approved by the Institutional Animal Care and Use Committee at the Cincinnati Children's Hospital Medical Center. Mice were housed in a pathogen-free barrier facility in humidity and temperature-controlled rooms on a 12:12 h light/dark cycle and were allowed food and water *ad libitum*.

MicroCT imaging and tumor count and volume measurement. After mice were sacrificed by administration of a lethal dose of sodium pentobarbital, the mouse lungs were inflated with 1-2 cc of air and used for scanning by the ImTek microCT system (ImTek Inc., Knoxville, TN) at the Imaging Research Center at Cincinnati Children's Hospital Medical Center. Tumor counts and volume were collected from the microCT scans using Amira 5.4.6 Software (Visage Imaging, Inc., San Diego, CA). The microCT scan from each animal was analyzed for tumor number and location. Tumor volume was determined by marking the perimeter of the tumor in successive oblique slices.

Antibody information. Antibodies used were mouse MAB anti-NKX2-1/TTF-1 (1:500; WMAB-8G7G31, Seven Hills Bioreagents, Cincinnati, OH), mouse MAB anti-CK7 (cytokeratin 7 [RCK105]) (1:1000; ab9021, Abcam, Cambridge, MA), guinea pig anti-CK20 (cytokeratin 20) (1:200; BP5080, Acris, San Diego, CA), rabbit anti-NKX2-1/TTF-1 (1:1000; WRAB-1231, Seven Hills Bioreagents), rabbit anti-MUC2 (1:100; sc-15334, Santa Cruz Biotechnology, Santa Cruz, CA), mouse MAB anti-MUC5AC (45M1) (1:1000; ab3649, Abcam), rabbit anti-MUC5B (1:100; sc-20119, Santa Cruz

Biotechnology), guinea pig anti-AGR2 (1:1000) generated in this laboratory, goat anti-FOXA2 (1:100; sc-6554, Santa Cruz Biotechnology), goat anti-FOXA3 (1:200; sc-5361, Santa Cruz Biotechnology), guinea pig anti-SPDEF (1:1000) generated in this laboratory, mouse MAB anti-FLAG (1:1000; F3165, Sigma-Aldrich), mouse MAB anti-Ki-67 (MIB-1) (1:100 for immunofluorescence; M7240, Dako, Carpinteria, CA), rabbit anti-FLAG (1:200 for immunofluorescence; F7425, Sigma-Aldrich, St. Louis, MO), rat MAB anti-PAX9 (1:2000; ab28538, Abcam) and guinea pig anti-NKX2-8 (1:10000) generated in this laboratory.

Cell lines. Human lung cancer cell line H2122 (KRAS^{G12C}), A549 (KRAS^{G12S}), H441 (KRAS^{G12V}), H358 (KRAS^{G12C}), H2009 (KRAS^{G12A}), H23 (KRAS^{G12C}), HCC827 (EGFR^{E746_A750del}), H1650 (EGFR^{E746_A750del}) and H1975 (EGFR^{L858R}; EGFR^{T790M}) were obtained from the American Type Culture Collection (Manassas, VA). Human lung cancer cell line H3255 (EGFR^{L858R}) was obtained from National Cancer Institute Division of Cancer Treatment and Diagnosis Tumor/Cell line repository (Frederick, MD). Human lung cancer cell line PC9 (EGFR^{E746_A750del}) was obtained from Immunobiological Laboratories Co (Takasaki, Gunma, Japan).

Gene Ontology analysis. Gene Ontology analysis was performed using DAVID (Database for Annotation, Visualization, and Integrated Discovery; ref. 1, 2). A gene ontology term was considered to be overly represented when p-value < 0.01 and gene hits > 20.

Quantitative RT-PCR. Quantitative RT-PCR (qRT-PCR) was performed on a 7300 real-time PCR system (Applied Biosystems, Foster City, CA) with the TaqMan probes *MUC5AC* (Hs00873651_mH), *MUC5B* (Hs00861595_m1), and *NKX2-1* (Hs00163037_m1), and normalized to endogenous *GAPDH* mRNA (Hs99999905_m1).

Infection of HBEC3 cells with *Nkx2-1*-expressing lentivirus. hTERT, CDK4-immortalized human bronchial epithelial cells (HBEC3 cells) were kindly provided by JD Minna (3). Lentivirus infection was performed with viral vector containing *Flag*-tagged *Nkx2-1* as previously described (4).

Immunoblot assays. Immunoblot assays were performed on whole cell extracts of A549 cells using rabbit anti-NKX2-1 antibody (1:5000; cat# WRAB-1231, Seven Hills Bioreagents), rabbit anti-cleaved PARP (Asp214) antibody (1:2500; cat# 5625, Cell Signaling Technology, Danvers, MA), rabbit anti-FOSL1 (Fra-1) antibody (1:5000; cat# sc-183X, Santa Cruz Biotechnology), and rabbit anti-ACTA1 (1:2500; A2066, Sigma-Aldrich) as described previously (5).

Transient transfection assays. Human lung papillary adenocarcinoma NCI-H441 cells were maintained according to protocols from ATCC (Manassas, VA). One day before transfection, cells were plated in six-well plates at 0.4×10^6 cells/well. DNA mixtures containing expression vectors (1 μ g each), including pcDNA3.Nkx2-1/TTF-1 (5), pcDNA3.NKX2-8 (subcloned from pENTR[tm]221.NKX2-8 [Clone ID IOH26042,

Invitrogen/Life Technologies, Grand Island, NY)), pCMV5.Cebpa (6), pRC/CMV.Foxa2 (7) or pcDNA3.Foxj1 (subcloned from CMV.HFH-3/Foxj1 vector [8]), 1 µg each of AP-1 luciferase reporter construct (Signal AP1 Reporter [luc] Kit: CCS-011L, SABioscience/Qiagen, Valencia, CA) and CMV.β-galactosidase were added to each well of the cells transfected with Lipofectamine 2000 (cat# 11668-019, Invitrogen/Life Technologies). After 24 h, the transfected H441 cells were harvested, and AP-1 luciferase and β-galactosidase activities were determined as previously described (9). Relative light units indicating AP-1 activity are expressed as mean +/- SD of luciferase activity normalized to β-galactosidase in triplicate wells. The results are representative of three repeated experiments.

Treatment of Nkx2-1-expressing A549 cells with cisplatin. Lentiviral *Nkx2-1*-expressing and control A549 cells were treated with cisplatin (cis-Diammineplatinum[II] dichloride, product number P4394, Sigma-Aldrich; 0 to 20 µM final concentration). Cisplatin was dissolved in saline. Seventy-two hours after treatment, the MTS assay (cat# G3580, Promega, Madison, WI) was used according to manufacturer's protocols to measure cell viability.

Treatment of A549 cells with PMA. Control or *Nkx2-1*-expressing virus-infected A549 cells were treated with PMA (AP-1 inducer; Phorbol 12-myristate 13-acetate, cat# P1585, Sigma-Aldrich) at a final concentration of 10 ng/ml. Twenty-four hours after treatment, cells were harvested for quantitative RT-PCR assay for *FGFR1* mRNA using TaqMan probe (Hs00915142_m1) as described previously (4).

Motif frequency analysis. Motif frequency analysis (Supplemental Figure 9, A and B) of the roughly 30 million sequence reads was performed by subtracting adjusted control-data counts from test-counts as follows: an individual count represents the presence of a given k-mer and a matching reverse complement partner k-mer. K-mers not partnered with a reverse complement k-mer were ignored. To account for the difference between the number of test reads (nt) and the number of control reads (nc), control counts were adjusted by multiplying with (nt/nc).

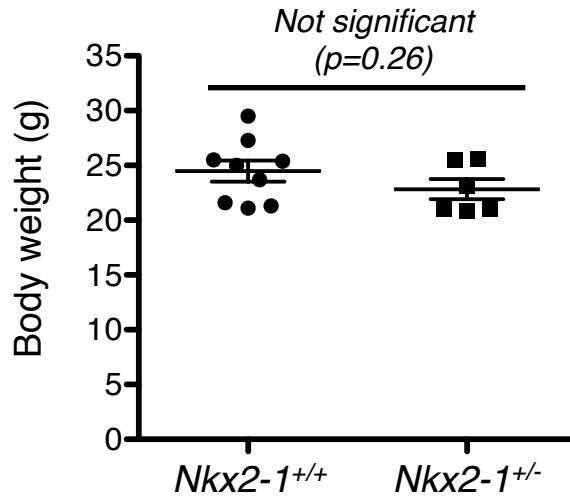
Soft agar colony formation assays. *Nkx2-1*-expressing A549 cells were developed previously (4). *FOSL1*-expressing lentiviral vector was made by inserting *FOSL1* cDNA (obtained from Open Biosystems/Thermo Scientific, Lafayette, CO) into the PGK-IRES-EGFP and packaged to generate the *FOSL1*-expressing lentivirus. Lentivirus infection was performed as described previously (4). Control, *NKX2-1*, *FOSL1* or *NKX2-1/FOSL1*-expressing A549 cells (1×10^4) were mixed with the DMEM media in 0.4% agar, plated on the top of 0.5% agar base, and covered with F-12K media containing 10% FCS. Cultures were maintained at 37°C in the 5% CO₂ incubator for two weeks. The number of anchorage-independent colonies was counted in five random fields.

References

1. Huang da W, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nat Protoc.* 2009;4(1):44-57.

2. Huang da W, Sherman BT, Lempicki RA. Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. *Nucleic Acids Res.* 2009;37(1):1-13.
3. Ramirez RD, Sheridan S, Girard L, Sato M, Kim Y, Pollack J, Peyton M, Zou Y, Kurie JM, Dimaio JM, Milchgrub S, Smith AL, Souza RF, Gilbey L, Zhang X, Gandia K, Vaughan MB, Wright WE, Gazdar AF, Shay JW, Minna JD. Immortalization of human bronchial epithelial cells in the absence of viral oncoproteins. *Cancer Res.* 2004;64(24):9027-9034.
4. Maeda Y, Chen G, Xu Y, Haitchi HM, Du L, Keiser AR, Howarth PH, Davies DE, Holgate ST, Whitsett JA. Airway epithelial transcription factor NK2 homeobox 1 inhibits mucous cell metaplasia and Th2 inflammation. *Am J Respir Crit Care Med.* 2011;184(4):421-429.
5. Maeda Y, Hunter TC, Loudy DE, Davé V, Schreiber V, Whitsett JA. PARP-2 interacts with TTF-1 and regulates expression of surfactant protein-B. *J Biol Chem.* 2006;281(14):9600-9606.
6. Martis PC, Whitsett JA, Xu Y, Perl AK, Wan H, Ikegami M. C/EBPalpha is required for lung maturation at birth. *Development.* 2006;133(6):1155-1164.
7. Wan H, Kaestner KH, Ang SL, Ikegami M, Finkelman FD, Stahlman MT, Fulkerson PC, Rothenberg ME, Whitsett JA. Foxa2 regulates alveolarization and goblet cell hyperplasia. *Development.* 2004;131(4):953-964.
8. Overdier DG, Ye H, Peterson RS, Clevidence DE, Costa RH. The winged helix transcriptional activator HFH-3 is expressed in the distal tubules of embryonic and adult mouse kidney. *J Biol Chem.* 1997;272(21):13725-13730.

9. Fukazawa T, Maeda Y, Sladek FM, Owen-Schaub LB. Development of a cancer-targeted tissue-specific promoter system. *Cancer Res.* 2004;64(1):363-369.



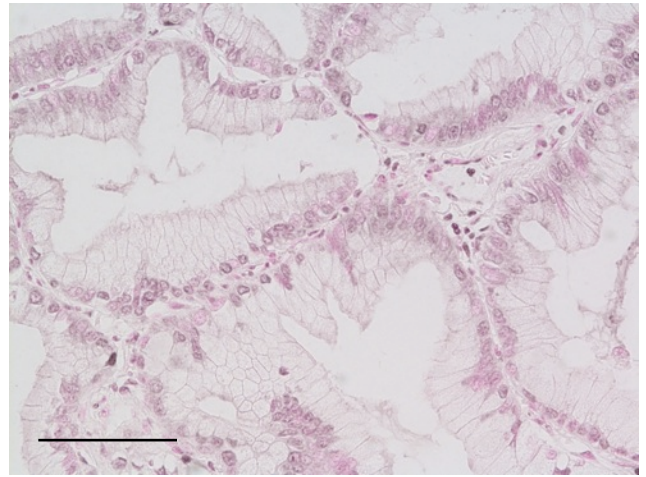
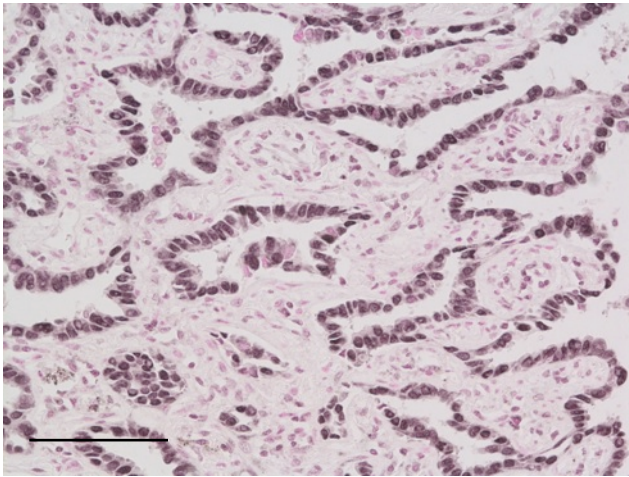
Supplemental Figure 1

Haploinsufficiency of *Nkx2-1* did not influence body weight of mice. The average body weight of *Nkx2-1^{+/+}* mice (n=9) was similar to that of *Nkx2-1^{+/-}* mice (n=6) two months after doxycycline administration. Results are expressed as mean \pm SEM.

Nonmucinous
lung adenocarcinoma
(human)

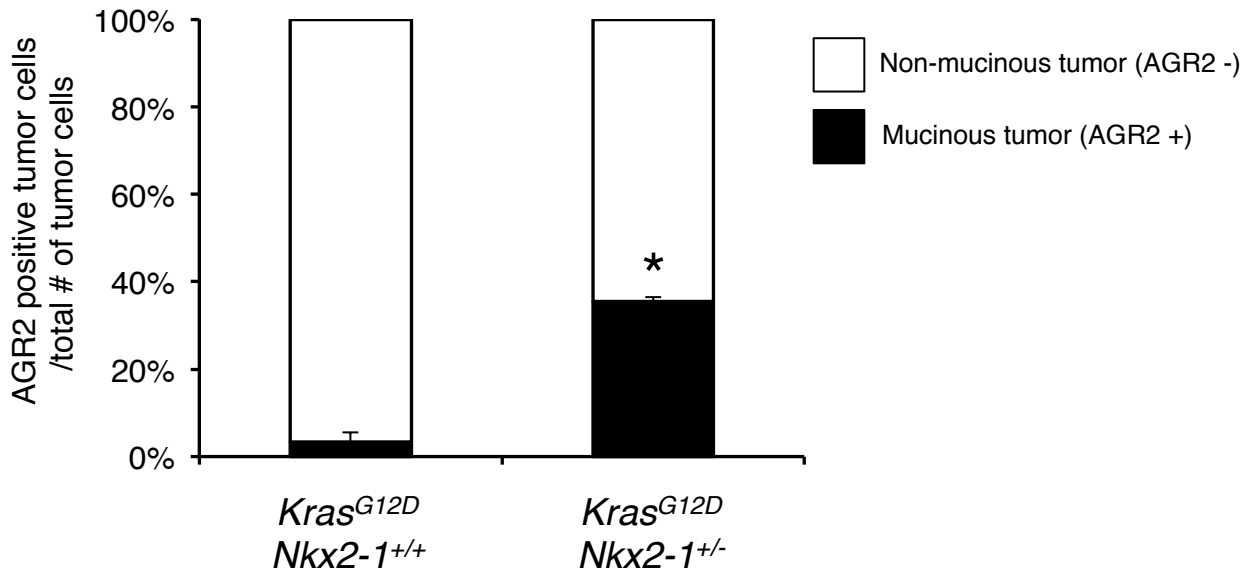
Mucinous adenocarcinoma
of the lung (human)

NKX2-1



Supplemental Figure 2

Lack of NKX2-1 staining in mucinous adenocarcinoma of the lung. Human lung sections were stained for NKX2-1. Nuclear NKX2-1 staining in nonmucinous adenocarcinoma (left panel, patient #7, see Patient Information in Supplemental Table 1) was not expressed in mucinous adenocarcinoma (right panel, patient #4, see Supplemental Table 1). Scale bars: 100 μ m.



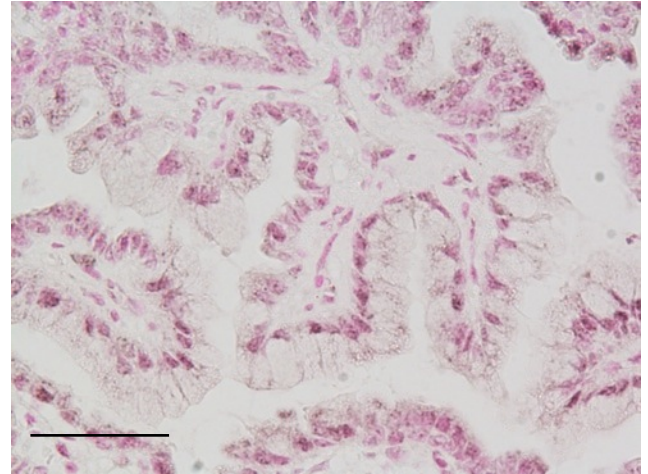
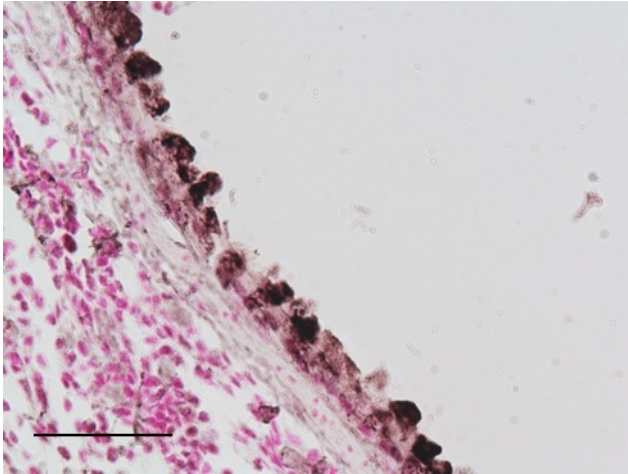
Supplemental Figure 3

Heterogeneous types of lung tumors developed in the *Kras^{G12D};Nkx2-1^{+/-}* mice. Lung sections of *Kras^{G12D};Nkx2-1^{+/+}* (n=3) and *Kras^{G12D};Nkx2-1^{+/-}* (n=4) mice were stained for AGR2, an intracellular goblet cell marker. Cell counts of >400 lung tumor cells per lung section were obtained, and the number of AGR2-positive cells was counted per total number of lung tumor cells. 35% of lung tumors were mucinous tumors stained with AGR2 in the *Kras^{G12D};Nkx2-1^{+/-}* mice, while 3% of lung tumors were stained with AGR2 in the *Kras^{G12D};Nkx2-1^{+/+}* mice, *p<0.01. Results are expressed as mean +/- SD.

HDM challenged
(asthma)

Kras^{G12D}/*Nkx2-1*^{+/-}
(mucinous adenocarcinoma)

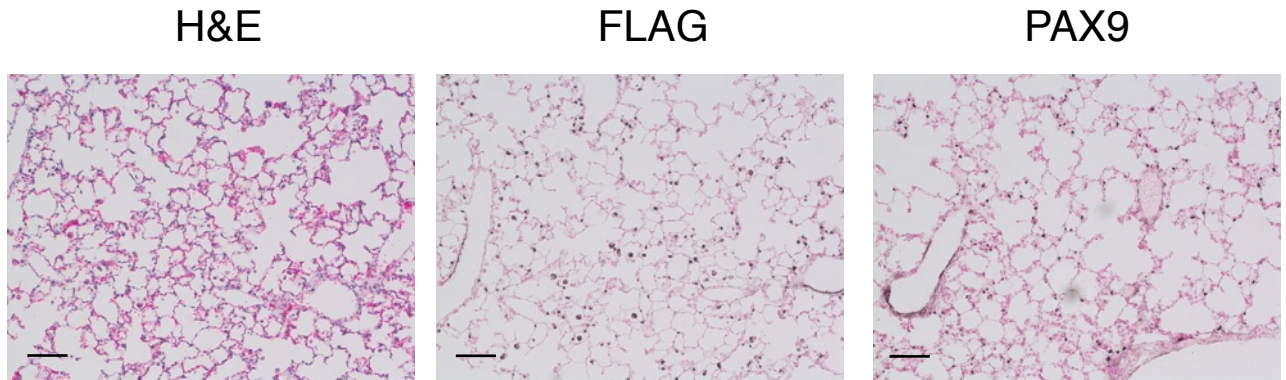
SPDEF



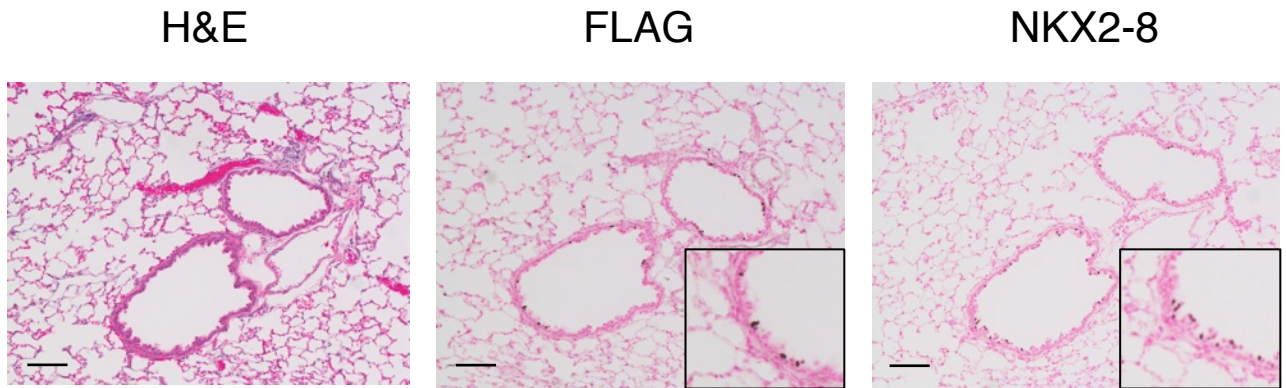
Supplemental Figure 4

SPDEF staining in allergen-induced goblet cell metaplasia but not in mucinous adenocarcinoma in *Kras*^{G12D}/*Nkx2-1*^{+/-} mice. SPDEF is expressed in airway goblet cells induced by HDM (House Dust Mite – allergen; left panel). Tumor associated goblet cells did not stain for SPDEF (n=6, right panel). Scale bars: 50 μ m.

A *Scgb1a1-rtTA*;[*tetO*]-*Flag-Nkx2-1*;[*tetO*]-*PAX9*

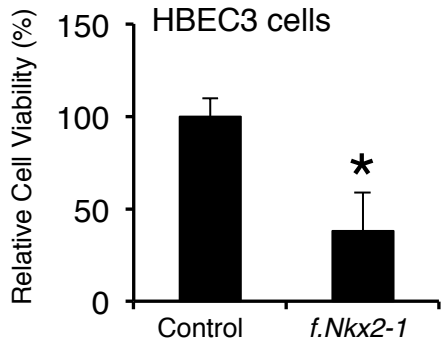
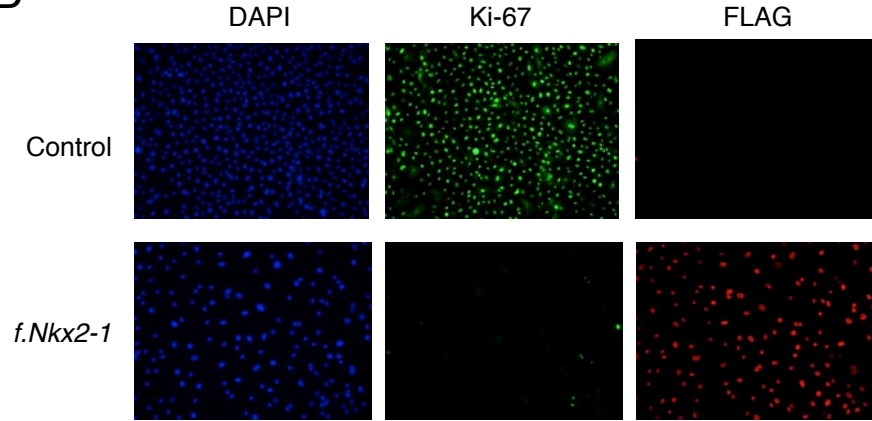


B *Scgb1a1-rtTA*;[*tetO*]-*Flag-Nkx2-1*;[*tetO*]-*NKX2-8*



Supplemental Figure 5

Combinatorial expression of NKX2-1 with PAX9 or NKX2-1 with NKX2-8 did not induce lung tumors. (A) Lung sections were stained with H&E, FLAG (detecting FLAG-NKX2-1) or PAX9. Co-expression of FLAG-tagged NKX2-1 and PAX9 in lungs of the *Scgb1a1-rtTA*;[*tetO*]-*Flag-Nkx2-1*;[*tetO*]-*PAX9* triple transgenic mice did not induce lung tumors after four months of doxycycline administration, n=4. (B) Tissue was stained with H&E, FLAG or NKX2-8. Co-expression of FLAG-NKX2-1 and NKX2-8 in lungs of the *Scgb1a1-rtTA*;[*tetO*]-*Flag-Nkx2-1*;[*tetO*]-*NKX2-8* triple transgenic mice did not induce lung tumors after four months of doxycycline administration, n=5. Scale bars: 100 μ m.

A**B****Supplemental Figure 6**

NKX2-1 inhibited growth of immortalized human bronchial epithelial cells (HBEC3 cells). **(A)** HBEC3 cells were infected with *Flag*-tagged *Nkx2-1* (*f.Nkx2-1*)-expressing or control lentivirus. Five days after infection, cell viability was measured by MTS assay. NKX2-1 significantly inhibited viability of HBEC3 cells (n=8), *p<0.01 compared to control. Results are expressed as mean +/- SD. **(B)** Immunocytochemistry was performed using the HBEC3 cells infected with *Nkx2-1* (*f.Nkx2-1*)-expressing or control lentivirus for five days. Paraformaldehyde-fixed cells in chamber slides were stained with anti-Ki-67 (green) and anti-FLAG (red) antibodies. Ki-67 was observed in control HBEC3 cells (top panels) but greatly reduced in *Nkx2-1*-expressing HBEC3 cells (bottom panels).

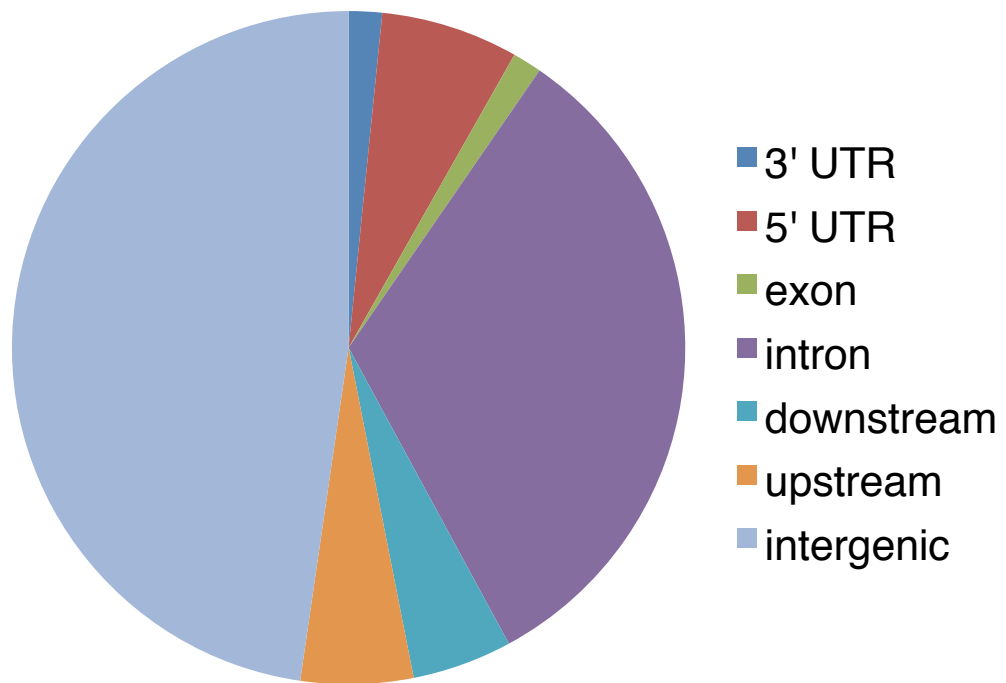
Gene Ontology (Genes down-regulated by NKX2-1)	# of Genes	P-Value
response to wounding	33	1.57E-05
cell adhesion	39	2.84E-05
biological adhesion	39	2.86E-05
intracellular signaling cascade	58	5.18E-05
protein kinase cascade	23	4.25E-04
regulation of cell proliferation	38	6.33E-04
enzyme linked receptor protein signaling pathway	20	0.002270795
cation transport	27	0.003992612
chemical homeostasis	25	0.005823608
metal ion transport	23	0.007314137

Gene Ontology (Genes up-regulated by NKX2-1)	# of Genes	P-Value
response to wounding	29	5.42E-05
positive regulation of cell proliferation	23	3.20E-04
immune response	32	4.11E-04
regulation of cell proliferation	35	4.42E-04
cell motion	22	0.004186382
regulation of programmed cell death	32	0.005293003
regulation of cell death	32	0.005502395
regulation of apoptosis	31	0.008264431
positive regulation of transcription, DNA-dependent	21	0.009087936

Supplemental Figure 7

Gene ontology analysis of the mRNAs regulated by NKX2-1. mRNA microarray data from control and *Nkx2-1*-expressing A549 lung carcinoma cells (Figure 7A) was subjected to gene ontology analysis using the DAVID algorithm. A gene ontology term was considered to be overly represented when p-value < 0.01 and gene hits > 20. Genes down-regulated by NKX2-1 were associated with two groups of genes: 1) intracellular signaling cascade, protein kinase cascade and enzyme linked receptor protein signaling pathways and 2) cell or biological adhesion. Genes up-regulated by NKX2-1 were associated with two groups of genes: 1) programmed cell death or apoptosis and 2) immune response. Genes associated with wounding response and cell proliferation were seen in both NKX2-1 down-regulated and up-regulated groups. NKX2-1 increases and decreases multiple groups of genes to reduce tumorigenesis in A549 cells.

NKX2-1 peak locations on the whole genome

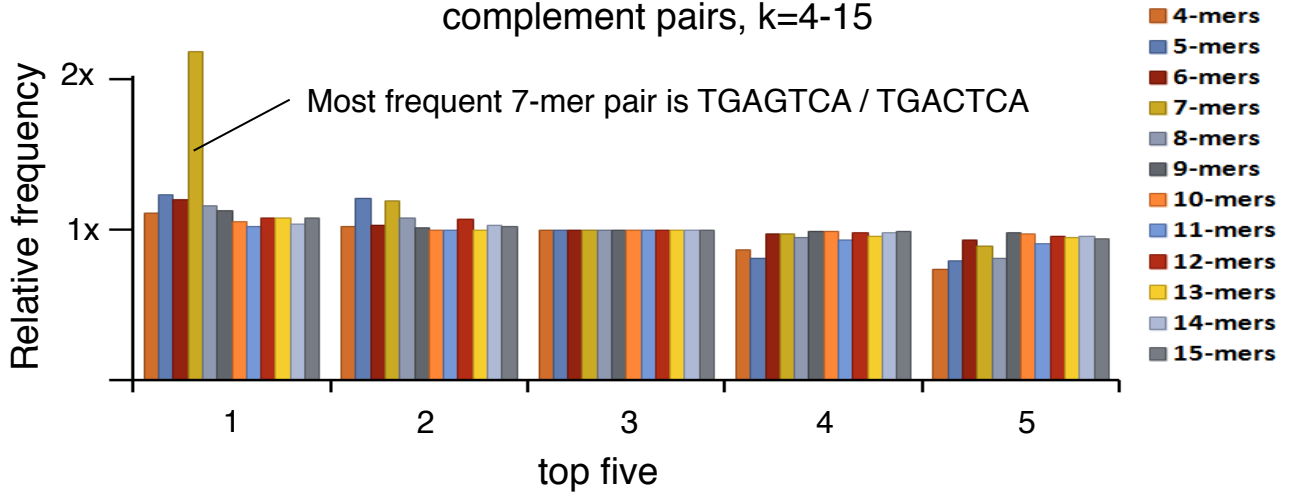


Supplemental Figure 8

NKX2-1 binding peaks were distributed widely throughout the genome. CisGenome software was used to detect NKX2-1 enriched peaks and map the peaks to the nearest TSS (Transcription Start Site). Shown is the distribution of the top 1000 peaks of NKX2-1 binding sites. The "upstream" and "downstream" are defined as 10 kb of 5' or 3' flanking sequence. NKX2-1 was largely associated with intergenic, intron and 5' UTR regions.

A

NKX2-1 ChIP-seq data:
Relative frequency of k-mer + reverse
complement pairs, k=4-15



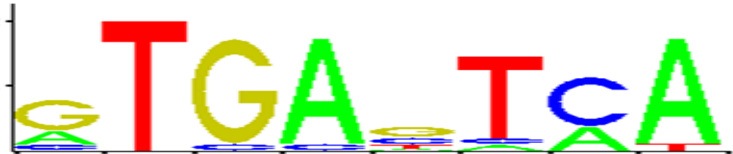
B

15 most frequent 7-mer pairs		
rank	count	7-mer / reverse complement
1	415288	TGAGTCA / TGACTCA
2	227797	GAGTCAT / ATGACTC
3	190194	TCAAGTG / CACTTGA
4	185501	CTCAAGT / ACTTGAG
5	169624	TGAGTGG / CCACTCA
6	168281	GGAGTGG / CCACTCC
7	165258	TTGAGTG / CACTCAA
8	156275	TGGAGTG / CACTCCA
9	150904	ATGAGTC / GACTCAT
10	147532	GAGTCAC / GTGACTC
11	142297	TCTCAAG / CTTGAGA
12	141014	AGTCATC / GATGACT
13	134473	GTGAGTC / GACTCAC
14	133176	GAGTGGT / ACCACTC
15	125743	ACTCAAG / CTTGAGT

C Enriched motif from NKX2-1 ChIP-seq data



D AP-1 consensus motif from JASPAR database



Supplemental Figure 9

NKX2-1 binding to CAAG/CTTG and TGAGTCA/TGACTCA. (A) Using NKX2-1 ChIP-seq data, for each value of k (k=4-15), the number of occurrences of all possible k-mers paired with their reverse complements were computed, sorted, and normalized to the 3rd most frequent k-mer. A 7-mer pair with relatively high frequency was observed. (B) The most frequent 7-mer pair (TGAGTCA/TGACTCA, pink) is a known AP-1 binding motif. Other frequently observed 7-mer pairs were similar to the AP-1 motif (yellow) or to the NKX2-1 binding motif (CAAG/CTTG, blue). (C and D) A consensus motif computed by CisGenome from NKX2-1 ChIP-seq data (C) is consistent with the AP-1 consensus motif in the JASPAR database (see D; <http://jaspar.cgb.ki.se/>).

	distance to TSS	distance to TES	location	TGAnTCA (AP-1 site)	CAAG/CTTG (NKX2-1 site)
AGR2	-5662	-18134	TSS upstream		Yes
ALDH3A1	-4004	-14450	TSS upstream		Yes
ANXA8 ANXA8L1 ANXA8L2	10775	-5366	intron	Yes	Yes
BCAS1	2079	-125146	5'UTR	Yes	Yes
BMPR1B	320047	-80417	5'UTR	Yes	Yes
CD14	-5765	-7458	TSS upstream		Yes
CLMN	119270	-18699	intron	Yes	Yes
CP	41882	-7658	intron	Yes	Yes
EHF	18607	-21806	5'UTR	Yes	Yes
ELF3	-3615	-10231	TSS upstream		Yes
GPR120	28	-20914	5'UTR		Yes
HNF4A	-2649	-32754	TSS upstream	Yes	Yes
IQGAP2	207026	-97780	intron		
ITGB4	28609	-7773	intron		Yes
ITIH2	45114	-1132	intron		Yes
KRT18	782	-3059	intron	Yes	Yes
LCN2	12993	8991	TES downstream	Yes	Yes
MGAT4A	113564	1546	TES downstream	Yes	Yes
MLPH	15147	-52935	intron	Yes	Yes
MUC5AC	-3571	-112773	TSS upstream	Yes	
MUC5B					
RASSF9					
RBP4	2993	-6406	intron		
RDH10	11960	-18289	intron		Yes
SCARA3	-9152	-48112	TSS upstream		Yes
SERPINE1	13271	1104	TES downstream		Yes
SOX2	-147	-2646	TSS upstream		
TC2N	8780	-78831	5'UTR	Yes	
TNS4	19854	-5918	intron		
WDR52					

Supplemental Figure 10

AP-1 binding motif (TGAnTCA) was seen in the NKX2-1 ChIP-seq peaks associated with the NKX2-1-targeted genes induced in the mouse mucinous lung tumor. 13 genes out of the 30 genes contained AP-1 binding motif. Shown are the NKX2-1-targeted genes induced in the mucinous tumor (See Figure 6, highlighted in red and green), location of NKX2-1 ChIP-seq peaks and existence (Yes) of the AP-1 and NKX2-1 motifs. TSS, Transcription Start Site; TES, Transcription End Site.

Supplemental Table 1

Patient information

	Sex	Age	Histology	Alcian blue staining	MUC5AC	NKX2-1
1	F	75	Adenocarcinoma	Positive (intracytoplasmic mucin)	Positive	Negative
2	M	74	Adenocarcinoma	Positive (mucin pools within airspaces)	Positive	Positive
3	F	73	Adenocarcinoma	Positive (intracytoplasmic mucin)	Positive	Negative
4	F	75	Adenocarcinoma	Positive (intracytoplasmic mucin)	Positive	Negative
5	F	44	Adenocarcinoma	Positive (intracytoplasmic mucin)	Positive	Negative
6	M	56	Adenocarcinoma	Positive (mucin pools within airspaces)	Positive	Positive
7	F	65	Adenocarcinoma	Negative	Negative	Positive

Supplemental Table 2

Listed are genes induced in mouse mucinous tumors. Microarray analysis was performed using mRNAs isolated from lungs of control and *Kras*^{G12D};*Nkx2-1*^{+/-} (mucinous tumor model) mice, n=3 for each group. Shown are mRNAs with a more than 2.0-fold change and with less than 5% FDR.

Fold Change	Gene Symbol
-3.0	Rapgef4
-2.3	Emr4
-2.3	Acox1
-2.2	Pon1
-2.2	Gcom1
-2.1	Car3
-2.1	Bmp6
-2.1	Ednrb
-2.0	Nkg7
-2.0	Edil3
2.0	AK129341
2.0	Saa3
2.0	4930529M08Rik
2.0	Trp63
2.0	Dnahc10
2.0	Hnf4a
2.0	1700028P14Rik
2.0	Itga7
2.0	Gm1661
2.0	Krt19
2.0	Celsr1
2.0	Il13ra1
2.0	Pla2g1b
2.0	Srd5a1
2.0	E230008N13Rik
2.0	lqcg
2.0	Plch1
2.0	Tanc2
2.0	Slc38a4
2.0	Fam81b
2.0	Nek5
2.0	4930451C15Rik
2.1	Rdh10
2.1	Coro2a
2.1	Ccdc39ITtc14
2.1	4930529M08Rik
2.1	Spf2
2.1	Dnahc6
2.1	Ak7
2.1	Gabre
2.1	Cwh43
2.1	4922501L14Rik
2.1	Gm626
2.1	Dnahc7b

2.1	AU021092
2.1	Lox
2.1	Wdr72
2.1	Cckar
2.1	Aspa
2.1	Lrriq1
2.1	4930485B16Rik
2.1	Dnahc6
2.1	Bcas1
2.1	1700007K13Rik
2.1	Spag6
2.1	Dnahc5
2.1	Spef2
2.1	D19Ert652e
2.1	Ctsk
2.1	Gm626
2.1	Trpv6
2.1	Ect2 LOC100045792
2.1	Plek2
2.1	Gdpd2
2.1	Nme5
2.1	Epcam
2.1	Slc10a5
2.1	Dynlrb2
2.1	4930485B16Rik
2.1	Dnahc3
2.1	Sfrp1
2.1	LOC382693 Gm16710
2.1	D19Ert652e
2.1	Ptges
2.2	Car13
2.2	Wdr52
2.2	Fam166b
2.2	Itgbl1
2.2	4930529M08Rik
2.2	Dnahc6
2.2	Onecut2
2.2	Iqgap2
2.2	Syt5
2.2	Lbp
2.2	Rassf9
2.2	Igk-V28 Gm7202 Igk-V21-4 Igkv6-25 Gm16939
2.2	Spata18
2.2	Cp
2.2	E230008N13Rik
2.2	AU021034
2.2	Ugt2b34
2.2	Ect2 LOC100045792
2.2	D19Ert652e

2.2	Spats2
2.2	Al428936
2.2	5330417C22Rik
2.2	4930529M08Rik
2.2	Lrrc48
2.2	Ckmt1
2.2	Mt2
2.2	Dnahc3
2.2	Gm626
2.2	Cfi
2.2	Liph
2.2	Prrg4
2.2	Gsta4
2.2	E230008N13Rik
2.2	E230008N13Rik
2.2	B3galt2
2.3	Mapk13
2.3	Meig1
2.3	4833427G06Rik
2.3	Cetn4
2.3	Galnt3
2.3	Gprc5c
2.3	Igf1
2.3	Dnahc12
2.3	Mboat1
2.3	Pax9
2.3	Spef2
2.3	Rsph4a
2.3	Hes6
2.3	Slco1a5
2.3	Fam154b
2.3	Lad1
2.3	Gm626
2.3	Clip4
2.3	1110032A04Rik
2.3	Mpzl2
2.3	Spef2
2.3	Clmn
2.3	Slc28a3
2.3	Ch11
2.3	Ibsp
2.3	Mgat4a
2.3	Rpr11Gm8760Ilgkv4-71
2.3	Spef2
2.4	Ifitm1Gm7676
2.4	Fam84a
2.4	Wdr49
2.4	Zfp750
2.4	Akr1b8

2.4	Gm626
2.4	Fbxl13Lrrc17
2.4	Dnahc12
2.4	1700003M02Rik
2.4	Slc38a11
2.4	Prm1
2.4	Itgb4
2.4	Mall
2.4	Cd24a
2.4	Spef2
2.4	Gm626
2.4	D19Ertid652e
2.4	Rgs5
2.4	Gm410
2.4	Muc3
2.4	Prom1
2.4	Kcne3
2.4	LOC382693IGm16710
2.5	Gpr120
2.5	Spef2
2.5	Sorbs2
2.5	Bmpr1b
2.5	Atp6v1b1
2.5	Timp1
2.5	Dpcr1
2.5	Tnip3
2.5	Esrp1
2.5	Ppil6ISmpd2
2.5	Dnahc3
2.5	Kcnrg
2.5	Capsl
2.5	Gm1077
2.5	Basp1
2.5	Msln
2.5	Spef2
2.5	Creb3l1
2.5	Ntrk2
2.6	Golm1
2.6	Rgs22
2.6	Raly1
2.6	Areg
2.6	Krt18
2.6	Cd177
2.6	Egln3
2.6	Gabrp
2.6	Gm12695
2.6	Tmem212
2.6	Rgs5
2.6	Serpina9

2.6	Aldh3a1
2.6	Trf
2.6	Spef2
2.6	Tc2n
2.7	Fetub
2.7	Prg4
2.7	Atp10b
2.7	Tmem232
2.7	Efcab1
2.7	Rbp4
2.7	Fermt1
2.7	Spef2
2.7	Col15a1
2.7	Ptgr1
2.7	Me1
2.8	Fxyd3llgi4
2.8	Ighg
2.8	Gm626
2.8	Vill
2.8	Spef2
2.8	Serpine1
2.8	Ptprz1
2.8	Cd14
2.8	Naaladl2
2.8	Ereg
2.9	Mfsd4
2.9	Gm70
2.9	Ces1f
2.9	Foxq1
2.9	Clic6
2.9	Acpp
2.9	Me1
2.9	Slc44a4
3.0	Mlph
3.0	BC048546
3.0	Enpp1
3.0	Gm16970Igh-VX24
3.0	Orm2
3.0	Mgst2
3.0	Muc4
3.0	Lcn2
3.1	Sntn
3.1	Alox15
3.1	Gm626
3.2	Tns4
3.2	Manea
3.2	Slc16a12
3.3	Alox12e
3.3	Cldn2

3.3	Cdhr4
3.3	Elf3
3.3	Sytl5
3.4	Agr3
3.5	AA467197Mir147
3.5	Adamdec1
3.6	Serpib5
3.6	Lgals4Lgals6
3.6	Sox2
3.6	Rnf128
3.6	Chad
3.6	Adam8
3.7	Sytl5
3.7	Abp1
3.7	Gsto1
3.8	Pglyrp1
3.8	Mcpt2
3.8	Krt20
3.9	Lrg1
3.9	Anxa10
4.0	Refbp2
4.0	Ehf
4.0	Itih4
4.1	Prss35
4.1	Cdhr1
4.2	IghgLOC100045391
4.2	Psp
4.2	Aqp4
4.4	Lrrc26
4.5	Ly6d
4.5	Tspan1
4.6	Naaladl2
4.6	Anxa8
4.7	Gm1418
4.9	Vtcn1
4.9	Scara3
5.0	Reg1
5.1	Fut2
5.1	St8sia6
5.2	Orm1
5.4	Cxcl17
5.6	Itih2
5.6	Muc5ac
6.0	Adam28
6.0	Scgb3a1
6.5	Clu
6.9	LOC100046275
6.9	Tmc5
7.0	2210407C18Rik

7.5	Oit1
7.6	LOC100046275
7.7	Retnla
8.0	Chi3l4
8.6	Pigr
8.9	Vsig1
9.9	Plunc
10.1	Sprr2a1 Sprr2a3
10.1	Sprr2a1 Sprr2a3
11.1	Muc5b
13.4	U46068
14.3	Sprr2a1 Sprr2a2 Sprr2a3
16.6	Tff2
18.8	Agr2
28.9	Reg3g
37.1	Gp2
49.9	Ltf
59.5	Dmbt1

Supplemental Table 3

Listed are the locations of NKX2-1 binding sites in genes regulated by NKX2-1. Results were obtained by combining mRNA microarray and ChIP-seq analysis of A549 lung carcinoma cells. Microarray analysis was performed on lentiviral *Nkx2-1*-expressing and control A549 cells. Selection was based on more than 2.0-fold change with less than 5% FDR. ChIP-seq analysis was performed on lentiviral *Nkx2-1*-expressing A549 cells. The locations of ChIP-seq peaks relative to the TSS (Transcription Start Site) or TES (Transcription End Site) are shown. Upstream and downstream were defined as 10 kb regions flanking the TSS and TES of the gene.

Fold Change	Gene Symbol	distance_to_TSS	distance_to_TES	location
-78.6	NTS			
-72.5	CNTN1			
-39.8	UPK1B			
-34.6	PTGS2			
-28.8	BICC1	119271	-196670	intron
-28.1	TMEM47			
-27.0	MMP7	-3872	-14110	TSS_upstream
-21.6	MTUS1	125801	-31321	intron
-20.9	NR5A2	137105	-12673	intron
-20.4	TM4SF4	-4359	-32993	TSS_upstream
-20.2	CFH			
-19.8	PLA2G4A			
-19.1	THSD7A			
-17.0	PDE3A	311778	94	TES_downstream
-16.8	DAB2			
-16.1	VCAN	2457	-108172	5'UTR
-15.2	HGD	54078	-234	exon
-15.2	HGD	54078	-234	exon
-15.2	TNS4	19854	-5918	intron
-14.6	CNTNAP3 CNTNAP3B	325	-215209	intron
-14.6	CNTNAP3 CNTNAP3B	325	-215209	intron
-14.6	C5	103179	5241	TES_downstream
-14.5	CNTNAP3 CNTNAP3B	325	-215209	intron
-14.4	GPRIN3			
-12.7	DCDC2 KAAG1	134755	-51541	intron
-12.5	PCDH9	314593	-612908	intron
-12.2	AGR2	-5662	-18134	TSS_upstream
-11.6	INPP4B			
-11.4	FGL1			
-10.9	CNTNAP3 CNTNAP3B IRP11-138L21.1	325	-215209	intron
-10.8	F2RL2	13065	5133	TES_downstream
-10.7	FGA			
-10.5	C3	-2813	-45628	TSS_upstream
-10.5	BAMBI			
-10.5	CNTNAP3 IRP11-138L21.1 CNTNAP3B	325	-215209	intron
-10.4	FLRT3			
-10.3	CLMN	119270	-18699	intron
-10.2	C12orf27	9520	7066	TES_downstream
-10.1	SLC7A7	-4178	-46816	TSS_upstream
-9.9	CDK6	70081	-158913	intron

-9.7	MUC5BIMUC5AC			
-9.4	PPYR1	10066	5281	TES_downstream
-9.3	CPLX2	45040	-42373	5'UTR
-9.3	PLEKHH2	40111	-90575	intron
-9.0	GRB14	960	-128067	intron
-8.7	TM4SF20	12072	-5076	intron
-8.7	MGAM			
-8.6	C21orf63	71023	-31922	intron
-8.2	HSPA2	4589	1823	TES_downstream
-8.1	POF1B	35948	-66405	intron
-8.1	TLE4			
-7.9	GPRC5B	34376	8520	TES_downstream
-7.9	CYP1B1	5123	-3454	exon
-7.8	HLA-DMB	-83	-6485	TSS_upstream
-7.7	TC2N	8780	-78831	5'UTR
-7.6	NEO1	218350	-34318	intron
-7.5	CYP4F11	23201	705	TES_downstream
-7.4	SLPI	6481	4154	TES_downstream
-7.3	CNKSR2			
-7.3	IQGAP2	207026	-97780	intron
-7.3	ALDH3A1	-4004	-14450	TSS_upstream
-7.2	FAM111B	-108	-20336	TSS_upstream
-7.1	CA12	-6475	-64819	TSS_upstream
-7.1	CP	41882	-7658	intron
-7.1	BMPR1B	320047	-80417	5'UTR
-7.0	SLC16A7			
-7.0	SEMA3A	105842	-130710	intron
-6.9	AADAC	2464	-11952	intron
-6.8	FGB			
-6.7	ALX1			
-6.7	LPAR1	133190	-31119	intron
-6.7	BAAT	15537	-9050	intron
-6.6	C14orf105	926	-23055	intron
-6.6	PLD5	56923	-378803	5'UTR
-6.6	FAM107B			
-6.6	HLA-DMB	-83	-6485	TSS_upstream
-6.6	ODZ3	254613	-224427	intron
-6.5	FBN2	59935	-220198	intron
-6.4	SERPINE2	21670	-34760	5'UTR
-6.2	SRGN	19022	2285	TES_downstream
-6.1	STEAP2			
-6.1	PDE8B	215594	-926	exon
-6.0	RERG	27229	-86357	intron
-5.7	EPB41L4A	198010	-58685	intron
-5.7	NRXN3	354632	-1106033	intron
-5.6	AKAP12	29541	-89017	intron
-5.5	CDCA7L	6442	-38582	intron
-5.5	LRRK2	127737	-16534	intron
-5.4	APOH	-44	-17452	TSS_upstream

-5.4	CDH17	90840	9419	TES_downstream
-5.4	NBEA	232769	-497647	intron
-5.3	AKR1C3	-4293	-17601	TSS_upstream
-5.3	PRICKLE2	36206	-95398	intron
-5.3	PRKD1			
-5.2	CCND3	5177	-1703	exon
-5.2	ELOVL7	60076	-32408	intron
-5.2	SAMD9			
-5.2	CYP4F3			
-5.1	RSPO3	61677	-16457	intron
-5.1	DOK4	22060	7547	TES_downstream
-5.1	ELMO1	231011	-363539	intron
-5.1	LOC554202			
-5.0	ITGB4	28609	-7773	intron
-5.0	AKR1B10	681	-13140	intron
-5.0	ATP2B1			
-5.0	C11orf9	-4971	-40839	TSS_upstream
-5.0	LHX8			
-4.9	RASSF9			
-4.8	SLC7A2	39639	7852	TES_downstream
-4.7	LRRC6	68438	-34927	intron
-4.7	RDH10	11960	-18289	intron
-4.7	STEAP1	11386	935	TES_downstream
-4.7	SLC12A2	115617	9721	TES_downstream
-4.7	VGLL3			
-4.6	DAPK1	116069	-94723	intron
-4.6	C7orf68	8191	5604	TES_downstream
-4.6	PDE7B	184316	-159558	intron
-4.5	CPS1	20999	-101504	intron
-4.5	RHOBTB1	58358	-16475	3'UTR
-4.5	GAL3ST1	-8074	-18326	TSS_upstream
-4.5	MNS1			
-4.5	GLP2R	54569	-9072	intron
-4.5	DCBLD2	12408	-93310	intron
-4.4	SMOC1	106657	-46283	intron
-4.4	FSTL1			
-4.4	UPK3B	7480	-9972	3'UTR
-4.4	NIPAL2			
-4.3	SULT2B1	-7193	-30883	TSS_upstream
-4.3	ANKRD30A	80415	-26295	intron
-4.3	STRA6	6445	-16965	intron
-4.2	SERPINE1	13271	1104	TES_downstream
-4.2	SIK1			
-4.2	ANXA8L1 ANXA8L2	10693	-5361	intron
-4.2	SPP1			
-4.1	PLSCR4	23616	-35224	5'UTR
-4.1	GPR56	5206	-31319	5'UTR
-4.0	CXXC5	22149	-12230	5'UTR
-4.0	TRIML2	-6317	-20298	TSS_upstream

-4.0	TFPI2			
-3.9	MGAT4A	113564	1546	TES_downstream
-3.9	HSPA1AIHSPA1B	1909	-517	exon
-3.9	LPHN2	121668	-70356	intron
-3.9	HSPA1AIHSPA1B	1909	-517	exon
-3.9	B4GALT4	-2423	-31579	TSS_upstream
-3.9	LIN7A	99094	-41429	intron
-3.9	SULF2	-417	-129074	TSS_upstream
-3.9	RAP1GAP	30681	-42466	5'UTR
-3.8	VTN			
-3.8	PDE1C			
-3.8	PLCB1	115254	-636995	intron
-3.8	HSPA1BIHSPA1A	1813	-706	exon
-3.8	HSPA1BIHSPA1A	1813	-706	exon
-3.7	SLC46A3	-9875	-28805	TSS_upstream
-3.7	HKDC1	48566	1311	TES_downstream
-3.7	TMTC2	329341	-117788	intron
-3.7	hCG_1776007	21238	-371897	5'UTR
-3.7	RGL1	-2133	-294590	TSS_upstream
-3.7	HSPA1BIHSPA1A	1813	-706	exon
-3.7	ALPK2	25039	-122666	intron
-3.7	SORL1	12489	-169021	intron
-3.6	CA8	47229	-45302	intron
-3.6	COL5A2	87980	-59983	intron
-3.6	OLR1			
-3.6	DKK1	5009	1634	TES_downstream
-3.6	TMEM27	45454	7751	TES_downstream
-3.6	PTPRM	806386	-33158	intron
-3.6	FXYD2	-441	-5110	TSS_upstream
-3.6	RNF43	22906	-40985	intron
-3.6	ROBO1	170409	-251812	intron
-3.6	CD14	-5765	-7458	TSS_upstream
-3.6	ARHGAP24	245766	-281772	intron
-3.6	HMGCS1	-2105	-26206	TSS_upstream
-3.5	FAM113B			
-3.5	EHF	18607	-21806	5'UTR
-3.5	C5orf13	-105	-28048	TSS_upstream
-3.5	ADAMTS9	19915	-152117	intron
-3.5	ST8SIA4	30737	-65610	intron
-3.5	ZNF827	129932	-47783	intron
-3.5	TSKU	1515	-13397	5'UTR
-3.4	SGCD	373058	-67971	intron
-3.4	SCARA3	-9152	-48112	TSS_upstream
-3.4	FRMD3	185698	-105343	intron
-3.4	WIPF1	28082	-46922	5'UTR
-3.4	GABARAPL1	-564	-10797	TSS_upstream
-3.4	THBS1			
-3.4	NOVA1			
-3.4	SLFN11			

-3.4	SPATA17	125430	-110359	intron
-3.3	MAP7	128667	-79252	intron
-3.3	PDGFRL	34024	-31898	intron
-3.3	STK32B	314073	-135125	intron
-3.3	PLXND1	57207	5681	TES_downstream
-3.3	SLC22A3	76150	-30438	intron
-3.3	GATSL1IGATSL2	8267	-51453	intron
-3.3	GATSL1IGATSL2	8267	-51453	intron
-3.3	RTN4RL2	-7914	-23958	TSS_upstream
-3.3	BCAS1	2079	-125146	5'UTR
-3.3	PPFIBP2	36799	-103189	intron
-3.2	CCNE2	-618	-15644	TSS_upstream
-3.2	SVEP1			
-3.2	SOX2	-147	-2646	TSS_upstream
-3.2	PTPN13	92932	-127926	intron
-3.2	TNFAIP2	10436	-676	3'UTR
-3.2	FHL1			
-3.2	KIAA1244ILOC202451	19247	-163495	intron
-3.2	INSL4	-594	-3141	TSS_upstream
-3.2	FGFR4			
-3.2	C5orf23			
-3.2	RBP4	2993	-6406	intron
-3.2	MRAP2			
-3.2	UNC13D	5373	-12115	intron
-3.1	HPGD	31717	-747	3'UTR
-3.1	ARHGAP18	47770	-85359	intron
-3.1	ARID5B	126657	-68603	intron
-3.1	ZNF608	100755	-7440	exon
-3.1	TGFBR3	131737	-74148	intron
-3.1	CES1			
-3.1	EDN1	7546	649	TES_downstream
-3.1	FGFR1	22902	-34793	intron
-3.1	KRT8	8468	571	TES_downstream
-3.0	BACE2			
-3.0	CLGN			
-3.0	FAM111A	-1602	-11859	TSS_upstream
-3.0	KCTD1	13174	-81348	5'UTR
-3.0	SLC9A2	89234	-2407	3'UTR
-3.0	FRAS1	42651	-444048	intron
-3.0	ADD3	74264	-53345	5'UTR
-3.0	CMIP	209325	-57265	intron
-3.0	RHPN2	12374	-73951	intron
-3.0	DCBLD1	15780	-71418	intron
-3.0	PLEKHA6	35994	-105068	5'UTR
-3.0	SH3BP4	75672	-28056	5'UTR
-3.0	SHANK2	606108	-15738	intron
-3.0	CPNE4	81944	-418316	5'UTR
-2.9	OLFML3	-405	-3250	TSS_upstream
-2.9	PDGFD	240502	-16610	intron

-2.9	HSPG2ILDLRAD2	79200	-35812	intron
-2.9	ALDH1A1	4519	-47862	intron
-2.9	CHST11	60072	-241033	intron
-2.9	ELF3	-3615	-10231	TSS_upstream
-2.9	BTBD11	34578	-306644	intron
-2.9	ZNF704	201241	-35006	intron
-2.9	FMN2	47515	-335783	intron
-2.9	LHFP	-494	-260820	TSS_upstream
-2.9	RGNEF	59867	-225677	intron
-2.9	LST-3TM12IELMOD3ISLCO1B3	10770	-63638	intron
-2.9	RIBC2			
-2.9	PDK3			
-2.9	SH3BGRL2	-25	-72394	TSS_upstream
-2.9	CPPED1	127944	-16143	intron
-2.8	IQCK	95222	-45857	intron
-2.8	FAM38B2			
-2.8	GLIPR1IKRR1	-138	-21340	TSS_upstream
-2.8	CD38	13919	-56856	intron
-2.8	C19orf21			
-2.8	KCNAB2	33820	-40323	intron
-2.8	SCD5	82960	-86360	intron
-2.8	ADAM23	178207	3898	TES_downstream
-2.8	HMOX1	20113	7006	TES_downstream
-2.8	SEMA4GIMRPL43	-1011	-14097	TSS_upstream
-2.8	ABCA12	135801	-71083	intron
-2.7	E2F7	3985	-40348	intron
-2.7	ARHGAP23	15381	-39602	intron
-2.7	GATS			
-2.7	SNORD114-3			
-2.7	SLCO1B1			
-2.7	ANXA13	53947	-2665	intron
-2.7	PGM2L1	67802	-339	3'UTR
-2.7	KIAA1147	47553	2130	TES_downstream
-2.7	SLFN13			
-2.7	CRIP2	-8981	-14350	TSS_upstream
-2.7	FSTL3			
-2.7	SLITRK6			
-2.7	CDH6	27479	-103962	5'UTR
-2.7	NID2	53346	-11079	intron
-2.7	PRAME	-6879	-18451	TSS_upstream
-2.7	GLIS3	276408	-51647	intron
-2.7	SEMA3E	209874	-75228	intron
-2.7	CCDC146	66	-172519	5'UTR
-2.7	SNAP25	36423	-52165	5'UTR
-2.7	PDLIM5	55737	-160601	intron
-2.7	TSPAN13	35574	4766	TES_downstream
-2.6	PDZD8	14212	-78119	intron
-2.6	CPEB4	56044	-15937	intron
-2.6	RND3	15005	-4463	intron

-2.6	KRT18	782	-3059	intron
-2.6	ADM	-6542	-8823	TSS_upstream
-2.6	LONRF3	30512	-12722	intron
-2.6	S100A3	7359	5434	TES_downstream
-2.6	NNT	62759	-40117	intron
-2.6	PDXK	46247	3038	TES_downstream
-2.6	HLA-DMAIHLA-DMB	11999	7491	TES_downstream
-2.6	HLA-DMAIHLA-DMB	11999	7491	TES_downstream
-2.6	UCP2	-8036	-16209	TSS_upstream
-2.6	LOC100289612			
-2.6	KRT18	782	-3059	intron
-2.6	LRIG1	81720	-39903	intron
-2.6	MAP3K8	4034	-23861	5'UTR
-2.6	COL12A1	106973	-14607	intron
-2.6	FANCI	31581	-41587	intron
-2.5	HEXIM1	11091	6308	TES_downstream
-2.5	NOSTRIN	22572	-39836	intron
-2.5	OSGIN2	-5671	-31668	TSS_upstream
-2.5	NPR3	80435	4848	TES_downstream
-2.5	PLK2	-6937	-13038	TSS_upstream
-2.5	ST3GAL6			
-2.5	SIPA1L2	4893	-112636	intron
-2.5	GINS1	-8423	-49291	TSS_upstream
-2.5	ASAP2	13606	-185312	intron
-2.5	MYO1E	203121	-33386	intron
-2.5	GULP1	1185	-302075	5'UTR
-2.5	SLC4A11	1898	-8411	intron
-2.5	HLA-DMAIHLA-DMB	11999	7491	TES_downstream
-2.5	SERINC5	130020	-14376	intron
-2.5	WDR17	57993	-58840	intron
-2.5	DUSP4	21560	6995	TES_downstream
-2.5	TACC1	-7772	-73595	TSS_upstream
-2.5	SLC29A4	1539	-19602	5'UTR
-2.5	TUBA4A	-6587	-10224	TSS_upstream
-2.5	FOXA1	-36	-5332	TSS_upstream
-2.4	PLSCR1	12403	-17257	intron
-2.4	LARGE	354816	-292537	intron
-2.4	PBK	31999	3790	TES_downstream
-2.4	ADAM12	141002	-233223	intron
-2.4	TGM2	24750	-12084	intron
-2.4	TESC	22276	-38245	intron
-2.4	CACNA1H	29084	-39446	intron
-2.4	MCM10	23269	-26250	intron
-2.4	DKFZP564O0823	115302	-1723	3'UTR
-2.4	OPN3IKMO	31476	-15772	intron
-2.4	SIPA1L3	23432	-277706	5'UTR
-2.4	IGFBP7IPOLR2B	70164	-9129	intron
-2.4	GPR37			
-2.4	GNE	-735	-44784	TSS_upstream

-2.4	TMEM195	235465	-126232	intron
-2.4	TSPAN14	45012	-23340	intron
-2.4	CNNM1	45619	-19610	intron
-2.4	TFCP2L1	30253	-38359	intron
-2.4	SLC22A5	18199	-7702	intron
-2.4	CASP4			
-2.4	TLR3			
-2.4	GDAP1	15907	-808	3'UTR
-2.4	HFE	641	-7319	intron
-2.4	OLFM2	1720	-80955	intron
-2.4	SPA17ISIAE			
-2.4	GATM	-8020	-25676	TSS_upstream
-2.3	CBLB	217512	6735	TES_downstream
-2.3	SCN9A	145947	-34846	intron
-2.3	ANXA8IANXA8L1IANXA8L2	10775	-5366	intron
-2.3	CACNG6	16558	-3818	intron
-2.3	FMN1	241685	-52053	intron
-2.3	IGSF11			
-2.3	EML1	152780	4132	TES_downstream
-2.3	FZD2	-450	-2432	TSS_upstream
-2.3	TMEM37			
-2.3	C1orf106	-2364	-26588	TSS_upstream
-2.3	TLE1	83596	-21400	intron
-2.3	GPR137B	-9032	-75408	TSS_upstream
-2.3	CPEB2	3478	-62774	exon
-2.3	TEX9	17756	-62671	intron
-2.3	AMN1IC12orf72	-3867	-61902	TSS_upstream
-2.3	TMEM144	399	-44638	5'UTR
-2.3	PIK3C2B	64149	-3566	intron
-2.3	LOH3CR2A			
-2.3	MUC13	5080	-24211	intron
-2.3	MORC4	68142	8665	TES_downstream
-2.3	MAP3K1	1825	-79251	intron
-2.3	SPDEF	-4359	-22870	TSS_upstream
-2.3	PTGFRN	39536	-40747	intron
-2.3	SLC6A15			
-2.3	E2F8	7732	-9157	intron
-2.3	MLF1IP	1836	-38230	intron
-2.3	GLT8D4	57390	-29745	intron
-2.3	ATP1B1	-2772	-28785	TSS_upstream
-2.3	KANK2	-657	-33956	TSS_upstream
-2.3	ANXA8L2IANXA8L1	10830	-5288	intron
-2.3	JAK1	17412	-115869	5'UTR
-2.3	ESCO2	31292	928	TES_downstream
-2.3	FIGN	32413	-95982	intron
-2.3	WWC1	3085	-177156	intron
-2.3	PRKCH	202885	-26295	intron
-2.3	DNAJC15	18013	-67929	intron
-2.3	THRINR1D1	38340	7382	TES_downstream

-2.3	CADM2	186668	-155648	intron
-2.3	TNS3	20674	-243772	5'UTR
-2.3	WNT7BILOC100289775	8683	-48077	intron
-2.3	ANXA4	22598	-61869	5'UTR
-2.2	PCNA	-7557	-19225	TSS_upstream
-2.2	JAM3			
-2.2	PKP2	56905	-49193	intron
-2.2	KCNT2	292474	-90112	exon
-2.2	BMP6	-4961	-159910	TSS_upstream
-2.2	BIN1	41114	-18141	intron
-2.2	C14orf174			
-2.2	C5orf36	256559	-211193	intron
-2.2	BRI3BP	-4494	-36649	TSS_upstream
-2.2	MAST4	153071	-187747	intron
-2.2	KCNV1			
-2.2	SLC41A2	63822	-61374	intron
-2.2	SMAD6	60076	-19585	5'UTR
-2.2	SGK2	-7362	-26897	TSS_upstream
-2.2	EFNA5	126371	-167634	intron
-2.2	TTC39C	34588	-108248	5'UTR
-2.2	KRT81	13824	8224	TES_downstream
-2.2	LMCD1	-3961	-70255	TSS_upstream
-2.2	LGSN	14607	-29418	intron
-2.2	UACA	-4750	-113705	TSS_upstream
-2.2	PRTFDC1	87333	-16646	intron
-2.2	PHACTR2	21508	-201496	intron
-2.2	PBX1	58823	-233420	intron
-2.2	HTR1D	-2153	-4986	TSS_upstream
-2.2	UNQ353ICSNK1G1			
-2.2	RNF157	10515	-87340	intron
-2.2	RNF217	58861	-41282	intron
-2.2	HIP1	194504	-10366	intron
-2.2	SLC6A16	3749	-31831	5'UTR
-2.2	PERP	20660	1642	TES_downstream
-2.2	PLEKHA5	211052	-35631	intron
-2.2	PRDM5	80588	-147495	intron
-2.2	DUSP10	-264	-40959	TSS_upstream
-2.2	MLLT3	52789	-224757	intron
-2.2	CDC25A	8251	-22882	intron
-2.2	KIAA1377	-1896	-87941	TSS_upstream
-2.2	ST3GAL1	72583	-44509	5'UTR
-2.2	GAB1	52892	-84842	intron
-2.1	PTPRK	313495	-238450	intron
-2.1	ZHX2	1824	-191030	5'UTR
-2.1	C1QTNF1	-5926	-31544	TSS_upstream
-2.1	PMEPA1	71406	9829	TES_downstream
-2.1	RNF182			
-2.1	LCN2	12993	8991	TES_downstream
-2.1	HEATR5A	10756	-86430	intron

-2.1	ZWINT			
-2.1	ABCC3	18957	-37887	intron
-2.1	HS6ST1	12971	-40145	intron
-2.1	EIF5A2	-1149	-21370	TSS_upstream
-2.1	PTPLAD2			
-2.1	APLP1	1674	-9623	intron
-2.1	PRPS2	32	-32817	5'UTR
-2.1	IFNE			
-2.1	GNAI1	20085	-64500	intron
-2.1	AKR1C2	9457	-18784	5'UTR
-2.1	POLE2	20585	-24072	intron
-2.1	KRT18	970	-3059	intron
-2.1	EHBP1	118799	-221819	intron
-2.1	DSC3	55231	2503	TES_downstream
-2.1	RTTN	160937	-40982	intron
-2.1	IGF1R	265264	-49733	intron
-2.1	EXO1			
-2.1	APH1B	9776	-21799	intron
-2.1	CDON	2337	-104135	5'UTR
-2.1	CYP24A1	-2784	-23312	TSS_upstream
-2.1	TIMD4	42516	-1457	intron
-2.1	NNMT	23940	7237	TES_downstream
-2.1	NEBL			
-2.1	C12orf75	25261	-15620	intron
-2.1	SUSD1	115456	-19038	intron
-2.1	THRB	348566	-29053	intron
-2.1	LPHN3			
-2.1	ARHGAP29	-2193	-71036	TSS_upstream
-2.1	SYNE2	17242	-356240	5'UTR
-2.1	ITGB3	25567	-33301	intron
-2.1	WDR52			
-2.1	ZNF25			
-2.1	CSGALNACT1	82019	-196402	5'UTR
-2.1	PFKFB3	3235	-29430	intron
-2.1	MGC45800			
-2.1	ASPHD1	2903	-2325	intron
-2.1	GPR120	28	-20914	5'UTR
-2.1	GM2A	26062	8724	TES_downstream
-2.1	HNF4A	-2649	-32754	TSS_upstream
-2.1	EMP1	25623	5518	TES_downstream
-2.1	SUSD2	706	-6924	intron
-2.1	C3orf14			
-2.1	FAM120C	106189	-8766	intron
-2.1	KIAA1522	15263	-17796	intron
-2.0	HSPH1	11242	-14110	intron
-2.0	PPM1L	7054	-307763	intron
-2.0	PLCE1	-5646	-340046	TSS_upstream
-2.0	SIRPA	-1038	-46764	TSS_upstream
-2.0	UNC93B1	-5557	-18575	TSS_upstream

-2.0	RAGE	71606	-4746	intron
-2.0	SKIL	7427	-28048	intron
-2.0	FAM38B	295686	-182831	intron
-2.0	ZNRF3	50285	-123300	5'UTR
-2.0	BST1	-7773	-36995	TSS_upstream
-2.0	LCA5	-7678	-60116	TSS_upstream
-2.0	RTKN2	1966	-73544	intron
-2.0	ANGIRNASE4	-1736	-11743	TSS_upstream
-2.0	KCNJ2			
-2.0	TIPIN			
-2.0	TNFAIP8			
-2.0	TRPS1			
-2.0	AMIGO2	-5391	-8742	TSS_upstream
-2.0	CARHSP1	-9762	-25823	TSS_upstream
-2.0	PDLIM1	54806	1357	TES_downstream
-2.0	GDF15	-218	-3236	TSS_upstream
-2.0	RASSF2	4241	-39380	5'UTR
-2.0	PRICKLE1	62222	-69209	5'UTR
-2.0	FRK	41396	-77832	intron
-2.0	SDK2	36952	-272751	intron
-2.0	B4GALNT1 SLC26A10			
-2.0	TMEM92	-3883	-10894	TSS_upstream
-2.0	COX17	6243	-1628	3'UTR
-2.0	PKD2			
-2.0	PAX7	5050	-100081	intron
-2.0	FHL2	2506	-35890	5'UTR
-2.0	SLC9A3R2	-3263	-15401	TSS_upstream
-2.0	SPATA6	90245	-83322	intron
-2.0	TCTN2	44415	7128	TES_downstream
-2.0	COX17	6243	-1628	3'UTR
-2.0	MLPH	15147	-52935	intron
-2.0	ANKRD5	5253	-16455	intron
-2.0	IVNS1ABP	1461	-19476	5'UTR
-2.0	LASP1	60363	8453	TES_downstream
-2.0	SEC11C	-550	-19486	TSS_upstream
-2.0	BRCA1	20515	-60512	3'UTR
-2.0	KLF13			
-2.0	TNFSF10			
-2.0	LOC100133315			
-2.0	C6orf155	9848	3549	TES_downstream
-2.0	INSIG1	-6561	-19017	TSS_upstream
-2.0	C14orf132	51113	-3358	5'UTR
-2.0	MFAP3L	20554	-19125	exon
-2.0	ITIH2	45114	-1132	intron
-2.0	SLC16A4	2286	-25845	intron
-2.0	TNFRSF10D	7390	-21046	intron
-2.0	GRIN2B	25622	-392990	5'UTR
-2.0	C2CD3	42239	-94345	intron
-2.0	FAM172A	376179	-117793	intron

-2.0	FAM102B	49979	-28998	intron
-2.0	PDK2	6979	-8747	intron
-2.0	ZNF792			
2.0	CDK7	17828	-24806	intron
2.0	RBMS1	112168	-109487	intron
2.0	MFSD2	4741	-10102	intron
2.0	NR4A3IEWSR1	45913	877	TES_downstream
2.0	EDN2	-1181	-7076	TSS_upstream
2.0	STAMBPL1	12449	-30767	5'UTR
2.0	TMEM106AIFLJ77644	13031	5336	TES_downstream
2.0	SIPA1L1	197658	-12418	intron
2.0	DENND1A			
2.0	NAPSB			
2.0	DDR2	74297	-73712	5'UTR
2.0	H1F0	2036	-292	3'UTR
2.0	SLCO4A1hCG_2018279			
2.0	PCGF1	-3754	-6397	TSS_upstream
2.0	EYA4	186930	-103832	intron
2.0	NFIL3	4469	-10346	5'UTR
2.0	ADAM17	-3383	-69887	TSS_upstream
2.0	LRRFIP1	67926	-86138	intron
2.0	ZNF808			
2.0	VRK2	62396	-50930	intron
2.0	C12orf49	18943	-3304	intron
2.0	NIPAL3	-4770	-61997	TSS_upstream
2.0	RNF19B	16361	-11873	exon
2.0	ST3GAL5	42282	-7604	intron
2.0	FMNL2	80099	-234496	intron
2.0	MCL1	10311	5212	TES_downstream
2.0	IRAK2	8612	-70252	intron
2.0	NRG1	19647	-175393	intron
2.0	EPAS1	38637	-50635	intron
2.0	GSN	9671	-23370	intron
2.0	CBS	25965	3226	TES_downstream
2.0	DEFB136	-8442	-9102	TSS_upstream
2.0	ZC4H2	-1464	-61538	TSS_upstream
2.0	HORMAD1	-3648	-26458	TSS_upstream
2.0	ANKRD13A	43090	3092	TES_downstream
2.0	ZNF616			
2.0	GPSM2ICLCC1	36347	-17093	intron
2.0	CCDC88A	140457	8378	TES_downstream
2.0	TMEM216	-7340	-13798	TSS_upstream
2.0	ZNF614	-220	-15322	TSS_upstream
2.0	RAB27A	48985	-17798	intron
2.0	IL18R1	38203	2085	TES_downstream
2.0	PPA1	2890	-27714	intron
2.0	HINT3	28189	4663	TES_downstream
2.0	BAHD1	8564	-18466	5'UTR
2.0	PIP4K2A	61428	-118308	intron

2.0	DNTTIP1	-8751	-28239	TSS_upstream
2.0	STXBP6	19420	-218367	5'UTR
2.0	TMEM43	9510	-9230	intron
2.0	SGPP2	6228	-128066	intron
2.1	SDC4	-6986	-30119	TSS_upstream
2.1	GJA1IIIFT140	-920	-15047	TSS_upstream
2.1	RHOBTB2	22495	-10285	intron
2.1	SKAP2	-2259	-199910	TSS_upstream
2.1	ASNS	27977	7943	TES_downstream
2.1	UHRF1BP1	-6419	-91914	TSS_upstream
2.1	GPR116	14150	-88283	5'UTR
2.1	CHI3L1	8497	634	TES_downstream
2.1	ZFAND1	12480	-7092	intron
2.1	GALNT13	490024	-92038	intron
2.1	TXNDC17IMED31	1903	-1735	intron
2.1	PHC2	-3106	-55076	TSS_upstream
2.1	TSPAN8	-2771	-35673	TSS_upstream
2.1	IGF2BP2	150127	-31172	intron
2.1	FAHD2BIFAH2AILOC729234			
2.1	IL1R1	5598	-20333	intron
2.1	TMEM106AIFLJ77644	13031	5336	TES_downstream
2.1	SNX21	2155	-7289	intron
2.1	LOC339803			
2.1	NPC2	2759	-10681	intron
2.1	TBX3	-56	-13966	TSS_upstream
2.1	ST7IST7OT3	-2306	-278998	TSS_upstream
2.1	TRERF1	118758	-108356	5'UTR
2.1	LEPREL1	28733	-135656	intron
2.1	SARS	4810	-19435	intron
2.1	ZHX1IC8orf76	11097	-14753	5'UTR
2.1	DSC2	38163	1719	TES_downstream
2.1	FNBP1	45523	-110484	intron
2.1	ABCA3	8697	-56171	5'UTR
2.1	DPYSL3	36435	-26454	intron
2.1	INPP5B	16229	-70131	intron
2.1	MPP7	101217	-129927	intron
2.1	CTH	-630	-28927	TSS_upstream
2.1	ZNF737	36551	8724	TES_downstream
2.1	RBMS3	30532	-693144	intron
2.1	NFKB2	-7282	-14130	TSS_upstream
2.1	WISP2	13640	1074	TES_downstream
2.1	HK1	46344	-85535	intron
2.1	CHAC2	14996	7638	TES_downstream
2.1	PPPDE2	-9809	-29789	TSS_upstream
2.1	FAHD2A			
2.1	OSBPL10	2963	-317957	intron
2.1	ANK2	104165	-229944	intron
2.1	GALNTL4	330161	-20979	intron
2.2	GPR126	74969	-69376	intron

2.2	PDE10A	90559	-244246	intron
2.2	DHRS9	13226	-18154	5'UTR
2.2	GLUL	-4784	-15285	TSS_upstream
2.2	RASGEF1A	2542	-69841	5'UTR
2.2	G0S2			
2.2	C17orf60	7381	4191	TES_downstream
2.2	TMEM173	7142	400	TES_downstream
2.2	ITGA6	13711	-65156	intron
2.2	KIAA1644	3631	-65543	5'UTR
2.2	ZNF160			
2.2	C10orf81			
2.2	PDK1	846	-42235	intron
2.2	HIATL1	45692	-40676	intron
2.2	PGBD5	-4683	-60657	TSS_upstream
2.2	KCTD14	-7780	-15338	TSS_upstream
2.2	ZNF426			
2.2	GFPT2	17965	-34650	intron
2.2	NR4A2	-6138	-14479	TSS_upstream
2.2	NEXN	1275	-54101	5'UTR
2.2	CRLF2	-70	-16706	TSS_upstream
2.2	UPP1	-3571	-23154	TSS_upstream
2.2	MXD1	-7603	-35474	TSS_upstream
2.2	GOT1	9305	-24597	intron
2.2	LONRF2	54795	5354	TES_downstream
2.2	ROR1	144610	-260407	intron
2.2	CKB	9770	6596	TES_downstream
2.2	RAET1E	2547	51	TES_downstream
2.2	ATF3	-7294	-19414	TSS_upstream
2.2	IL27RA	813	-20950	intron
2.2	FOSL2	-1404	-23139	TSS_upstream
2.2	SH3KBP1	104944	-248716	intron
2.2	UBXN10	-4978	-12341	TSS_upstream
2.2	CRISPLD2	613	-88916	5'UTR
2.2	CLIP4	9917	-58453	intron
2.2	CLK1PPIL3	-4433	-16168	TSS_upstream
2.2	PLAUR	-373	-22143	TSS_upstream
2.3	MT1X	9568	7843	TES_downstream
2.3	EDEM1	9091	-23199	intron
2.3	ANKRD1	-2168	-11343	TSS_upstream
2.3	WSCD1	1766	-52045	5'UTR
2.3	FHOD3	472423	-9893	intron
2.3	ATG4A	-3859	-66820	TSS_upstream
2.3	FOXN3	154944	-308033	5'UTR
2.3	SLC6A12	10842	-12398	intron
2.3	IGFBP2	3348	-27681	intron
2.3	TSC22D3	43517	-19040	intron
2.3	PPP1R15A	2201	-1468	exon
2.3	PNPLA4	-325	-28996	TSS_upstream
2.3	CSF1	-9908	-29029	TSS_upstream

2.3	SLIT3	637333	2272	TES_downstream
2.3	FBLN1	18481	-79814	intron
2.3	RPS6KA5	13293	-176533	intron
2.3	TJP2	4511	-76518	intron
2.3	DEFB134	1035	-1235	intron
2.3	PRDM1	11480	-12139	intron
2.3	TUBE1	26	-16864	5'UTR
2.3	DKFZp686O24166			
2.3	RNF41	24829	7411	TES_downstream
2.3	FAM108C1	4748	-55560	intron
2.3	GFPT1	1632	-65845	intron
2.3	HEY1	6848	2996	TES_downstream
2.3	ETS1	11378	-117419	5'UTR
2.3	DNAH11	74567	-284055	intron
2.3	PIP5KL1	-4205	-10166	TSS_upstream
2.3	APBB2	89310	-315280	5'UTR
2.3	SH3RF2	40399	-86352	intron
2.4	GALNT5	3635	-49937	intron
2.4	NFE2L3	18653	-16254	intron
2.4	PPM1E	236068	6768	TES_downstream
2.4	PKN2	14103	-137912	intron
2.4	BLID	7798	6938	TES_downstream
2.4	TP63	68659	-197193	intron
2.4	RBKSILOC100302650	34923	-74034	intron
2.4	CD55	15858	-23634	exon
2.4	GRB10	13834	-189565	5'UTR
2.4	CXCL12	4967	-9968	intron
2.4	LPIN1	12610	-68181	5'UTR
2.4	NR1D2	-3976	-39334	TSS_upstream
2.4	FOXP1	366090	-262313	5'UTR
2.4	SLC1A4	17444	-17097	intron
2.4	KCNMA1	265802	-502416	intron
2.4	EPCAM	7438	-10440	intron
2.4	IL1RAP	2084	-135326	5'UTR
2.4	NCOA7	123199	-17066	intron
2.4	NF-E4			
2.4	ST8SIA6			
2.4	AP1S2ILOC653653	-10000	-39170	TSS_upstream
2.4	FCHO2	73342	-61198	intron
2.4	PXK	50683	-41578	intron
2.4	SVIL	149776	-27848	intron
2.4	SLC4A4	31922	-352878	5'UTR
2.4	STK33	9403	-192682	5'UTR
2.4	WDFY2	1516	-176170	intron
2.4	PITPNM3	30602	-74691	intron
2.4	SYNE1	447384	-68327	intron
2.4	CGNL1	126870	-47345	intron
2.4	CD47	39885	-8109	intron
2.4	LAYN	16142	-4413	intron

2.4	KCNH1	425882	-29918	intron
2.4	ARG2IVT11B	16796	-15059	intron
2.4	PNMA2	-2367	-11654	TSS_upstream
2.4	RUNX2	-104	-222868	TSS_upstream
2.5	DST	411363	-85263	intron
2.5	EFHD2	20059	-389	3'UTR
2.5	CREB3L1	13947	-29795	intron
2.5	SERTAD2	13446	-8844	5'UTR
2.5	ZNF717 LOC100287163			
2.5	CALCB			
2.5	CAB39	65293	-42939	intron
2.5	LYN	119289	-12261	intron
2.5	DMKN	-4690	-21127	TSS_upstream
2.5	SH3BP5	12804	-64943	intron
2.5	VEGFA	14047	-2221	intron
2.5	FBXL13	260290	-1417	intron
2.5	LRRN4	-156	-13425	TSS_upstream
2.5	MTHFD2	7735	-8997	intron
2.5	BCAT1	49458	-88569	intron
2.5	MECOM	41700	-21413	intron
2.5	TPST2	43664	-20709	5'UTR
2.5	IFRD1	-965	-26694	TSS_upstream
2.5	OLFML2B	-606	-41266	TSS_upstream
2.5	ITGA2	52194	-53258	intron
2.5	LRRFIP1	67926	-86138	intron
2.5	SERPINB8	87	-19257	5'UTR
2.5	MOCOS	7545	-73659	intron
2.5	RAB39B			
2.5	CNNM4	26011	-24976	intron
2.5	RRAGD	26995	-20663	intron
2.5	RUNX1	18787	-82101	intron
2.5	ATP6V0A4	13191	-78710	5'UTR
2.5	SCNN1B	62184	-16844	intron
2.6	KRT15	-2805	-8077	TSS_upstream
2.6	MAMLD1	36955	-31771	intron
2.6	GRAMD3	9806	-61176	intron
2.6	GABRG3	263433	-298184	intron
2.6	ALPPL2			
2.6	CAPG			
2.6	B4GALNT2	23471	-13551	intron
2.6	RHOU	5581	-5959	intron
2.6	RAB31	152697	-1628	3'UTR
2.6	MTHFD2	7735	-8997	5'UTR
2.6	TMCC3	5924	-77500	intron
2.6	IL1RL1	22788	-17747	5'UTR
2.6	RIMKLA	43107	-325	3'UTR
2.6	TRERF1	118758	-108356	5'UTR
2.6	MST131			
2.6	ACOX2	-121	-32186	TSS_upstream

2.7	OSTbetaIRASL12	-4838	-8063	TSS_upstream
2.7	AREG	2646	-7207	intron
2.7	ERRFI1	-1882	-16495	TSS_upstream
2.7	CHAC1	3764	683	TES_downstream
2.7	SLC27A2	-8668	-62863	TSS_upstream
2.7	UST	188554	-141300	intron
2.7	MPP5	100704	6190	TES_downstream
2.7	FAM46C	25696	3290	TES_downstream
2.7	NAV2	27919	-380346	intron
2.7	ZBTB10	32302	-3858	exon
2.7	PHLDB2	45057	-71737	intron
2.7	CDC42EP3	30551	1968	TES_downstream
2.7	TMC5	63743	-24632	intron
2.7	SLC12A8	86484	-43643	intron
2.7	MAP2	50097	-104334	5'UTR
2.8	MPZL2	-66	-7445	TSS_upstream
2.8	SDR16C5	19066	-1605	intron
2.8	SPOCK1	293418	-230612	intron
2.8	MCTP1	427354	-150636	intron
2.8	PROS1	4509	-96543	intron
2.8	SGEF	124126	-12341	intron
2.8	FADS3	6006	-12001	intron
2.8	EREG	13590	-10027	intron
2.8	PSD3	49071	-437311	intron
2.8	MT1A	-9703	-11122	TSS_upstream
2.8	MCAM			
2.8	AREG	2646	-7207	intron
2.8	STXBP5	-2308	-185507	TSS_upstream
2.9	VDR	17439	-46053	5'UTR
2.9	ADC	18336	-20944	intron
2.9	SERPINB11	28081	7155	TES_downstream
2.9	CTSS	80	-35671	5'UTR
2.9	SWAP70	16172	-72705	intron
2.9	YPEL2	-3753	-73795	TSS_upstream
2.9	ANTXR2	3927	-167777	intron
2.9	NEK7	96742	-68696	intron
2.9	PSD3	49071	-437311	intron
2.9	FLVCR2	53185	-16387	intron
2.9	ANTXRL	5791	-37421	5'UTR
2.9	DYSF	105147	-127992	intron
2.9	INPP1	36329	8135	TES_downstream
3.0	LRRFIP1	67926	-86138	intron
3.0	ADK	90535	-467559	intron
3.0	GPR64	98977	-34267	intron
3.0	CA13	-5941	-44527	TSS_upstream
3.0	TNMD	6510	-8580	intron
3.0	SEMA4B	26923	-17815	intron
3.0	C11orf86			
3.0	LPCAT1	53901	-8631	intron

3.0	MBOAT2	-7399	-154574	TSS_upstream
3.1	PMAIP1	9158	4812	TES_downstream
3.1	PLEK2	26728	1600	TES_downstream
3.1	PAM	157798	-6091	intron
3.1	LRRFIP1	67926	-86138	intron
3.1	OSBPL6	59201	-142298	5'UTR
3.1	CYCSP6			
3.1	SESN2	-9981	-32976	TSS_upstream
3.1	TNIK	352172	-45733	intron
3.1	MOBKL2B	133975	-70667	intron
3.2	ZNF542ILOC283788			
3.2	CTSB	-9154	-34764	TSS_upstream
3.2	ST6GAL1	132884	-14939	intron
3.2	TMEM163	51221	-212019	intron
3.2	KIAA1462	31800	-1616	3'UTR
3.2	CFLAR	16210	-31901	intron
3.3	JUN	2460	-861	3'UTR
3.3	CSF2RA	15332	-21686	intron
3.3	CSF2RA	15332	-21686	intron
3.3	IL8	-8200	-11356	TSS_upstream
3.3	PPAP2B	76782	-8042	intron
3.4	ATP2B4	25147	-92132	5'UTR
3.4	ARL4D	8322	6172	TES_downstream
3.4	LYST	34670	-171205	5'UTR
3.4	EGR1	-3781	-7604	TSS_upstream
3.4	PROS1	4509	-96543	intron
3.5	CH25H	-4154	-5529	TSS_upstream
3.5	RIMKLB	232	-79037	5'UTR
3.5	CEP70	84629	-15311	intron
3.5	NTM	381713	-44290	intron
3.5	NOS1AP	149219	-151013	intron
3.5	CDCP1	20614	-43530	intron
3.5	STEAP4	38684	8225	TES_downstream
3.5	RIMS2	309099	-443376	intron
3.6	ARNTL	10925	-98560	5'UTR
3.6	FAM126A	-7055	-79938	TSS_upstream
3.6	B3GNT5	2318	-17828	5'UTR
3.6	ZNF91	29644	-8126	intron
3.6	SFTPA2ISFTPA1	538	-4016	5'UTR
3.6	C10orf72	50384	-50842	intron
3.6	SFTPA2ISFTPA1	538	-4016	5'UTR
3.7	PDCD1LG2	11355	-49381	5'UTR
3.7	NT5E	14723	-31471	intron
3.7	OGFRL1	5648	-7846	intron
3.8	FAM176A	-1333	-69981	TSS_upstream
3.8	ABLIM3	13321	-105624	intron
3.9	HRH1	-2204	-128363	TSS_upstream
3.9	MYBL1	45705	-5364	intron
3.9	C1orf116	21676	7441	TES_downstream

3.9	PAG1	109328	-34927	5'UTR
3.9	GRK5	-7347	-255280	TSS_upstream
3.9	DOCK9	169735	-123184	intron
3.9	TMOD1	17454	-82648	5'UTR
4.0	HHIPL2	26369	527	TES_downstream
4.0	NID1	65706	-23634	intron
4.1	ATP11A	101532	-95305	intron
4.1	PLLP	6846	-21716	intron
4.1	FAS	32287	7034	TES_downstream
4.1	FAM40B	4701	-49262	intron
4.1	ZFPM2	205778	-279840	intron
4.2	ZNF724P			
4.2	SYT14	186237	-39856	5'UTR
4.2	EPCAM	7438	-10440	intron
4.2	MYBPH	-2483	-10486	TSS_upstream
4.2	GABBR2	177775	-243034	intron
4.3	EFR3B	12827	-104203	intron
4.3	BDKRB1	-334	-8873	TSS_upstream
4.4	SPARC	-4983	-30481	TSS_upstream
4.4	DDIT3INR1H3	13525	9598	TES_downstream
4.4	FAM71D	2279	-36842	5'UTR
4.4	PCDH19	121071	2450	TES_downstream
4.4	PPP1R3C	508	-4149	intron
4.4	NAMPT	37513	609	TES_downstream
4.4	ALDH1A3	-6559	-43378	TSS_upstream
4.5	IGFBP1	-5909	-11216	TSS_upstream
4.6	TANC1	147279	-116743	intron
4.6	SFTPA1ISFTPA2	-170	-4673	TSS_upstream
4.6	SFTPA1ISFTPA2	-170	-4673	TSS_upstream
4.7	NAMPT	37513	609	TES_downstream
4.7	INHBA			
4.9	LAMP3	31442	-9221	intron
4.9	SMURF2	31361	-86290	intron
4.9	CITED2	2710	322	TES_downstream
4.9	TMEM90B			
5.0	NMNAT2	-9238	-179596	TSS_upstream
5.1	TNC	-9139	-106819	TSS_upstream
5.1	KCNMB4	47213	-17702	intron
5.2	BOC	46700	-28228	intron
5.2	CUGBP2	10441	-320970	intron
5.3	SMPDL3B	-6204	-30362	TSS_upstream
5.3	PLAUIC10orf55	-1962	-8356	TSS_upstream
5.3	SFMBT2	150475	-98726	intron
5.3	RAB11FIP1	27528	-13005	exon
5.4	CRABP2	13100	7135	TES_downstream
5.4	HLF	13529	-46576	intron
5.4	WDR69	15723	-36976	intron
5.6	TIMP3	30523	-31702	intron
5.6	TNFAIP3	5894	-9970	intron

5.7	FAM84B	10991	5212	TES_downstream
5.7	CCNA1	1016	-9593	intron
5.8	LAMC2	52351	-6737	exon
5.9	IFI16	-9107	-54368	TSS_upstream
5.9	NAV1	105300	-73347	intron
5.9	FLJ32810	199693	-103556	intron
6.0	SFRP1	27765	-19749	intron
6.1	TMEM133			
6.1	LAMB3	329	-36130	5'UTR
6.2	MPP1	1227	-25615	intron
6.2	CXCL2	-403	-2636	TSS_upstream
6.2	AHCYL2	214111	8924	TES_downstream
6.2	CMAH	-824	-57578	TSS_upstream
6.4	CHRD1	74551	-47440	intron
6.5	HK2	23693	-36999	intron
6.5	EPHA4	35035	-119226	intron
6.6	SLC16A9	30824	-28303	intron
7.0	GLS	72653	-11576	intron
7.2	STC2	13256	-1524	3'UTR
7.3	KCNQ3	218879	-132868	intron
7.3	DOCK11	41203	-149048	intron
7.4	ABCA8	68783	-19317	intron
7.4	PTPRE	93825	-85012	5'UTR
7.5	GAB3	-9902	-85723	TSS_upstream
7.7	SESN3	2496	-55617	intron
7.7	HBEGF	-612	-14371	TSS_upstream
7.8	BARX2	82919	6627	TES_downstream
7.9	DMBT1	719	-82352	intron
8.0	PLAT	-1356	-34314	TSS_upstream
8.1	SEMA6D	38514	-17219	5'UTR
8.1	DUSP6 LOC100131490	-254	-4711	TSS_upstream
8.3	TNFSF15	6183	-10612	intron
8.3	RGS4	15229	7034	TES_downstream
8.4	IL6	-166	-5019	TSS_upstream
8.6	MMP2	-6831	-34334	TSS_upstream
8.7	VSIG1	-8275	-42488	TSS_upstream
8.8	RPS6KA2	160626	-57246	intron
8.8	FSTL4	92298	-323773	intron
8.9	PITPNC1	13026	-302695	intron
9.0	FAM83A	-3577	-30030	TSS_upstream
9.2	LMO3	42731	-15393	intron
9.8	NCKAP5	242531	-654127	intron
9.8	KRT16 KRT14 LOC400578 IMGC102966			
10.4	EFEMP1	66331	9078	TES_downstream
10.6	MCTP2	8595	-177155	intron
10.9	GFRA2	67396	-29420	intron
11.0	TACR1	58945	-94110	intron
11.1	CCBE1	105294	-158201	intron
11.1	CPM	-8205	-120267	TSS_upstream

11.4	CACNA1E	271784	-46213	exon
12.2	ACSL5	5044	-47137	intron
12.9	KIAA1199	2838	-169449	5'UTR
13.0	STK32A	68821	-80368	intron
15.6	FAM20A	61270	-4567	intron
16.0	MFAP5	4383	-12510	intron
16.4	CLIC2	-14	-58498	TSS_upstream
16.9	SCEL	-1259	-110846	TSS_upstream
18.6	SLCO2A1	2170	-95208	intron
18.7	SLAMF7	22748	7225	TES_downstream
19.1	CEACAM6	22752	6037	TES_downstream
19.5	TNFRSF9	-138	-21117	TSS_upstream
19.5	FAM49A	2121	-111074	5'UTR
20.1	NAPSA	5456	-1740	intron
20.3	EPB41L3	80211	-71387	intron
21.2	ATP8B4	69144	-191839	intron
24.7	TIMP3	30523	-31702	intron
27.0	EDIL3	73011	-369474	intron
27.4	SLC6A14	8276	-16573	intron
31.9	KIT	3955	-78829	intron
33.1	PRUNE2	231703	-63007	intron
35.6	NRK	88189	-47871	intron
36.0	CD274	4891	-13025	5'UTR
42.2	PRUNE2	231703	-63007	intron
45.3	SFTPBIEDNRB	-316	-9640	TSS_upstream
70.4	CDH11	109519	-65715	5'UTR