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Supplementary methods

SNAI2 quantification in human tumors

The expression of SNAI2 in the human tumor epithelium and stroma was analyzed semiquantitatively employing a three-point scale. SNAI2 expression in the epithelium was considered intense positive when it was detected in virtually all the tumor nuclei examined (always more than 75%). In contrast, it was considered focal positive when observed in less than 75% of the tumor nuclei (there were no tumors with negative expression of Snai2 in the epithelium). The stroma was considered to express SNAI2 (positive) when nuclear staining was evident at 4x magnification. Focal stromal staining (focal positive) was considered when there was occasional staining of fibroblasts (less than 50% evident at 20x magnification). When no staining was observed, the stroma was considered to be negative for SNAI2 expression. We evaluated HER2-positive (+++) and HER2-negative tumors. ER+ tumors were considered those with more than 10% positive cells. Ki-67 cut-off was considered in 15% of positive cells. PR+ tumors were those with more than 5% positive cells. The slides were all evaluated by two pathologists (MMAH and SFG) who were unaware of the clinical status of the patients.

Immunohistochemistry in mouse tissues

To analyze the protein expression in mouse tumors, tumor sections (3 µm) were deparaffinized and processed to detect cleaved CASPASE-3 after microwaving the tissue in citrate buffer (pH 6) to achieve antigen retrieval. The anti-Ki-67 (MAD020310Q, Master Diagnostica, Granada, Spain), anti-ERBB2 (Abcam, catalog number ab2428), anti-phospho-ERBB2 (Tyr1248) (Abcam, catalog number ab47755), anti-SNAI1/SNAIL (Abcam, ab53519), and cleaved CASPASE-3 (Asp175; Cell Signaling) primary antibodies were used at a 1:50 dilution in the Ventana Discovery automated

immunohistochemistry research slide-staining system (Tucson, AZ85755). Ki-67, ERBB2, phospho-ERBB2(Tyr1248) and SNAI1/SNAIL expressing cells in tumors were quantified with the ARIOL-slide scanner software on tissue-array sections of tumors from *Snai2* WT^{*ErbB2*} and *Snai2* KO^{*ErbB2*} nulliparous and parous mice (10 tumors from each group), each stained in triplicate.

MEF generation

To generate MEFs, embryos from *Snai2* WT^{ErbB2+} and *Snai2* KO^{ErbB2+} mice were isolated on day E13.5 of pregnancy. The embryo's head, limbs and most of the internal organs were removed, the tissue was minced and trypsinized for 30 min, and the cells recovered were seeded in culture dishes with 15 mL of complete DMEM. Once confluent, the MEFs were split at a ratio of 1:3, passaged twice and frozen or expanded for the different studies.

Cancer-associated fibroblasts

Human fibroblasts and CAFs were obtained using a co-implantation breast tumor xenograft model, as described previously (29). Briefly, primary mammary hNFs were isolated from reduction mammoplasty tissue and immortalized with hTERT, the catalytic subunit of the telomerase holoenzyme. Retroviral constructs encoding GFP and the puromycin-resistance protein were also introduced into these fibroblasts. Mouse CAFs were obtained from tumors by flow cytometry, as indicated above.

ELISA

The phosphorylated and total AKT2 or AKT3, and the total ERK, were measured using Sandwich ELISA Kits: pAKT2(Ser474) [catalog number 7932]; total AKT2 [catalog number 7930]; pAKT3(Ser472) [catalog number 7942]; total AKT3 [catalog number

7934]; and total ERK1/2 [catalog number 7050]. The levels of phosphorylated and total AKT1, and of phosphorylated ERK were measured using the ELISA Sandwich Antibody Pair, and by coating a 96-well Microtest Plate (BD Falcon, catalog number 353077) with capture antibody according to the manufacturer's instructions (Pathscan Cell Signaling Technology): pAKT (Thr308) [catalog number 7144]; pAKT1 (Ser473) [catalog number 7143]; total AKT1 [catalog number 7142]; pERK (Thr202/Tyr204) [catalog number 7246]. Absorbance was measured at 450 nm on a Synergy-4 Microplate Reader (Biotek). All assays using proteins from tumors were carried out with 5 μg of protein and serial dilutions (1:2) of the protein extracted from each tumor sample were assayed on each plate (3-50 μg) to control for inter-assay variability.

Protein analyses

The proteins in the tumor samples were analyzed in western blots. Extracting proteins from the frozen tumor tissue in RIPA buffer (150 mM NaCl, 1% [v/v] NP40, 50 mM Tris-HCl [pH 8.0], 0.1% [v/v] SDS, 1 mM EDTA, 0.5% [w/v] Deoxycholate) containing protease and phosphatase inhibitor cocktails (Roche, Basel, Switzerland). The proteins were quantified with a BCA Protein Assay Kit (Thermo Fisher Scientific Inc., catalog number 23228, Waltham, MA USA), resolved by SDS-PAGE and transferred to polyvinylidene difluoride membranes (Immobilon-P, Millipore, Darmstadt, Germany) that were then probed with the following primary antibodies: anti-phospho-AKT1(Ser473, D9E, catalog number 3787); anti-AKT1 (2H10, catalog number 2967); anti-TUBULIN (DM1A, catalog number T6199: Sigma, St Louis, MO, USA); anti-CYCLIN D1 (C-20, sc-717: Santa Cruz, Dallas, TX, USA); anti- α SMA (E184, Abcam, catalog number ab32575), anti-SNAI2 (C19G17, Cell Signaling, catalog number 9584); anti-GAPDH (Sigma, catalog number G8795), anti-FAP (Abcam, catalog number ab53066); anti-S100A4 (Abcam, catalog number ab-27957); anti-ACTIN (C4, Santa Cruz Biotechnology, catalog number sc-47778); anti-ERBB2 (Abcam, catalog number

ab2428); anti-phospho-ERBB2(Tyr1248) (Abcam, catalog number ab47755); anti-HSP90 (4F10, Santa Cruz Biotechnology, sc-69703) and anti-SDF1 (D32F9, Cell Signaling, catalog number 3530). Antibody binding was detected with horseradish peroxidase-conjugated anti-mouse, anti-rabbit or anti-goat secondary antibodies (1:10,000 dilution: BIO-RAD, Berkeley, CA, USA), which were visualized by enhanced chemiluminescence (ECL, Thermo Scientific). The phosphorylated and total AKT2 or AKT3, and the total ERK, were measured by ELISA, as described in the supplementary methods.

Cytokine and growth factor quantification

The cytokines and growth factors in tumor protein lysates were quantified by Luminex technology using Luminex xMAP kits and the Milliplex MAP Angiogenesis/Growth Factor Magnetic Bead Panel (#MAGPMAG-24K, Millipore), assessing: angiopoietin-2, sFASL, amphiregulin, betacellulin, EGF, endoglin, endothelin, FGF-2, follistatin, G-CSF, HGF, IL-1 β , IL-6, IL-17A, KC, leptin, MIP-1 α , MCP-1, PLGF-2, prolactin, sALK-1, sCD31/PECAM 1, SDF-1, VEGF-A, VEGF-C, VEGF-D and TNF α . TGF β 1, TGF β 2 and TGF β 3 were measured using the Milliplex MAP TGF β Magnetic Bead 3 Plex Kit (#TGFMAG64K-03, Millipore). Protein lysates were prepared in lysis buffer (#43-040, Millipore) and passed through a 0.65 µm filter (Ultrafree-MC-DV, #UFC30DV00, Millipore). Each protein was quantified following the manufacturer's instructions and the amount of protein lysate loaded was optimized for each assay: 20 µg for #MAGPMAG-24K and 13.5 µg for TGFMAG64K-03.

The cytokine levels in the culture supernatant from CAFs were quantified using a membrane panel and analyzed following the manufacturer's recommendations (Proteome Profiler[™] Mouse Cytokine R&D Systems ARY006), incubating the membranes with the supernatant from CAFs isolated from *Snai*² WT^{ErbB2+} and *Snai*²

KO^{*ErbB2+*} tumors after six days of growth. This arrays screened for the relative levels of 40 different cytokines and chemokines, and their relative expression was quantified with Quantity One software.

Flow Cytometry and cell sorting

For tumors from *Snai2* WT^{ErbB2+} and *Snai2* KO^{ErbB2+} mice, flow cytometry was used to analyze the stromal composition and immune cell infiltration, and to sort epithelial, endothelial cells and fibroblasts. Tumors were dissected out from female mice and after mechanical dissociation with two scalpels (Swann-Morton, catalog number 0511, Sheffield, United Kingdom), the tissue was digested with collagenase (600 units/mL: Sigma, C2674, St Louis, MO, USA) and hyaluronidase (200 units/ml: Sigma, H3506, St Louis, MO, USA) in culture medium (DMEM/F12, 10% FBS, 1% penicillin/streptomycin, 1% Glutamine). The tissue was digested for 2 hours at 37 °C to analyze infiltrating immune cells, or for 6 hours to sort and quantify the endothelial cells and fibroblasts.

Stromal leukocytes were quantified by flow cytometry. To quantify infiltrating immune cell populations, cell suspensions were stained with anti-B220-FITC (Becton Dickinson #553088), CD4-PE (Becton Dickinson #553048), CD8-PE (Becton Dickinson #553033) and CD45-APC (Becton Dickinson #559864), and the different CD45+ populations were analyzed on an AccuriC6 FACS apparatus (Becton Dickinson). Tumor cells were stained with anti-EpCAM to identify epithelial cells (Immunostep #M236PC7), anti-CD31-FITC to identify endothelial cells (Beckton Dickinson #553372), and anti-CD140-PE to identify fibroblasts (eBioscience #12-140-81), and they were then sorted on a FACS Aria III apparatus (Becton Dickinson). The cells were incubated with antibodies for 30 minutes at 4 °C, washed with 2% FBS in PBS (phosphate-buffered saline, wash buffer), and

resuspended in wash buffer with 1 μ M SYTOX blue to exclude dead cells from the analysis.

RNA extraction, cDNA synthesis and QPCR

Total RNA was isolated using the TRIZOL Reagent (Invitrogen, Carlsbad, CA) and cDNAs were synthesized from equal amounts of RNA using the Transcriptor First-strand cDNA synthesis kit (Roche) to quantify *Snai2* expression. For the TaqMan assays, the primer and probe mixes were obtained from Applied Biosystems (*Snai2* #Mm00441531 1, *Gapdh* #Mm99999915 g1).

Gelatin zymography

Gelatinase activity was assessed as described previously (68). The cell culture supernatants were collected and centrifuged at 1,500 rpm for 5 minutes and the cell-free supernatant was mixed with 2x sample buffer (non-reducing conditions) and separated for 1 hour on gels at 4 °C (10% polyacrylamide, 0.1% gelatin). The subsequent enzymatic reaction was performed at 37 °C overnight, visualizing the gelatinase activity using specific staining solutions and destaining in an acetic acid-methanol-dH₂O solution (1:3:6). The gels were then analyzed semi-quantitatively using ImageJ software.

Cell-migration/invasion assay

Cell migration was assayed in Boyden chambers, using a Falcon cell-culture insert with an 8 μ m pore-size polyethylene terephthalate membrane (Millipore). The cells were recovered by trypsinization and counted, and cell suspensions containing 5-10×10⁴ cells in 300 μ l of serum-free medium were added to the upper chamber, with 500 μ l of the appropriate medium added to the lower chamber. The transwells were incubated for 24 hours at 37 °C, after which the cells on the inside of the transwell inserts were removed with a cotton swab, while those on the underside of the insert fixed and stained. Photographs were taken of five random fields, and the cells were counted to calculate the proportion of transmigrated cells. The invasion was assayed using Boyden chambers with Matrigel (Cell Biolabs, #CBA-110).

QPCR reagents and conditions

A reaction mixture (20 μ L) containing 9 μ L of the cDNA template and 10 μ L of the TagMan Universal PCR master mix was amplified as follows: denaturation at 95 °C for 10 min, and 36 cycles at 95 °C for 15 s and 60 °C for 60 s. Gene expression was quantified in CD140⁺ sorted cells, synthesizing cDNAs as described above and preamplifying for 12 cycles using the SsoAdvanced PreAmp Supermix (Bio-Rad) containing specific primers. The pre-amplification product was then used as a template in the qPCR reactions with PerfeCTa SYBR® Green SuperMix Reagent and amplified using the following program: denaturation at 95°C for 10 min, and 40 cycles at 95 °C for 15 s and 59 °C for 60 s. The primers used were: Cxcl1 Forward (CCCAAACCGAAGTCATAGCCA) and Reverse (TTCTCCGTTACTTGGGGACAC), (TCGCCCATCATCAAGTTCCC) Mmp2 Forward and Reverse (CCTTGGGGCAGCCATAGAAA), *Mmp9* Forward (TTCCCCAAAGACCTGAAAACCT) (AAAGCCGGCCGTAGAGACT), and Reverse Sdf1 Forward (GAGAGCCACATCGCCAGAGC) and Reverse (GGATCCACTTTAATTTCGGGTCAA) (TGCACCACCAACTGCTTAG) and Gapdh Forward and Reverse (GGATGCAGGGATGATGTTC), human SDF1 Forward (CTAGTCAAGTGCGTCCACGA) and Reverse (GGACACACCACAGCACAAAC). QPCR results were analyzed by the $\Delta\Delta$ CT method.

Fig. S1. Expression of SNAI2 in HER2-positive tumors from patients. (**A**) Different levels of SNAI2 expression in the epithelium and stroma of human ERBB2-positive tumors determined by immunohistochemistry. (**a**) Epithelium with focal SNAI2. (**b**) Epithelium expressing SNAI2. (**c**) Stroma with focal SNAI2. (**d**) Stroma expressing SNAI2. (**e**) SNAI2 negative stroma. See the material and methods for more details.

Supplementary Figure S1

A



Fig. S2. Metastasis capability and ERBB2 expression in tumors from nulliparous and parous *SNAI2* WT ^{ErbB2} and *SNAI2* KO ^{ErbB2} mice. (A) Detection of SNAI2 in mouse embryonic fibroblasts (MEFs) and mammary glands in western blots. (B) Comparison of the absolute number of metastasis in nulliparous mice considering all mice with breast cancer. (C) The same comparison in the parous female mice. (D) Comparison of the absolute number of metastasis in nulliparous mice considering only tumors that metastasized. (E) The same comparison in parous mice. A Student's T-test was used for panels B-D. (F) Detection of pERBB2 and total ERBB2 in tumors assessed by western blots. (G) Quantification of ERBB2 and phospho-ERBB2 expression in tumors from both *Snai2* WT^{Erbb2} and *Snai2* KO^{Erbb2} nulliparous and parous female mice assessed by immunohistochemistry and quantified by the Ariol system. (H) SNAI2 expression in hCAF control (scrambled siRNA) and SNAI2-depleted cells with a different pool of two siRNAs (siRNA#2) (a different siRNA to that shown in Figure 2i) analyzed by immunoblotting. (I) Migration of MDA-MB-231 cells in the presence of conditioned medium from control or *SNAI2*-depleted hCAFs with the siRNA#2 (N=3).

Supplementary Figure S2



Control RNAi SNAI2 RNAi#2

Fig. S3. Tumor growth rate and white blood cell infiltration in breast tumors from Snai2 WT^{ErbB2} and Snai2 KO^{ErbB2} mice.

(A) Comparison of the growth rate of tumors from Snai2 WT^{ErbB2} and Snai2 KO^{ErbB2} nulliparous and parous mice. Mann-Whitney *U* test. (B) SNAI2 expression in CAF control and SNAI2-depleted cells analyzed by immunoblotting to show that the cells from which the conditioned medium (hCM) were collected, did not express SNAI2. (C, D) The proportion of intratumoral CD31⁺ cells was quantified by flow cytometry. Mann-Whitney U-test. (E) KC expression analyzed by multiplex bead array (Luminex, 10 tumors per group were studied). Unpaired t-test. (F) Quantification of different intratumoral leukocyte subpopulations by flow cytometry. Mann-Whitney *U* test. (G) Detail of the expression of SNAI1/SNAIL in breast tumors from *Snai2* WT^{Erbb2} and *Snai2* KO^{Erbb2} mice by immunohistochemistry. SNAI1/SNAIL was expressed in the epithelial and stromal compartments (See also Table S6).

Supplementary Figure S3



Fig. S4. ERK and ERK1/2(T185/Y187: pERK1/2) levels in tumors derived from *Snai2*WT^{ErbB2+} and *Snai2* KO^{ErbB2+} mice. (A and B) In nulliparous mice: (A) Total ERK1/2; (B)
pERK1/2. (C and D) In parous mice: (C) total ERK1/2; (D) pERK1/2. The assays were carried out by ELISA (N = 20 mice per group were analyzed, Mann-Whitney *U* test). (E)
Detection of total ERK1/2 and pERK1/2 by western blots of selected tumors (weaker and stronger expression) to confirm the sensitivity of the technique (N = 4 mice per group).
(F) SNAI2 expression in CAF control and SNAI2-depleted cells analyzed by immunoblotting to show that SNAI2-targeting siRNA efficiently reduced the expression of SNAI2. (G) hCAFs cells were treated with control or *SNAI2* siRNA#2 for two days and then co-cultured in transwell inserts with BT474 cells for two days before analyzing the ERK and AKT signaling pathways in BT474 cells by western blots.

Supplementary Figure 4



Fig. S5. Correlation between the AKT and ERK tumor levels, and survival in: (A) Snai2 WT $^{ErbB2++}$ parous mice and (B) Snai2 KO $^{ErbB2++}$ parous mice. The assays were carried out by ELISA (N = 20 mice per group, Spearman's Rank Order Correlation test).

Supplementary Figure S5



Fig. S6. Supernatant from CAF cells influences tumor cell migration by altering cytokine production. (A) Densitometric quantification of cytokine arrays using ImageJ software. (B) Relative *Mmp2* mRNA expression in mCAFs isolated from tumors developed by parous mice (WT, N =8; KO, N =9: Mann-Whitney U test). (C) Relative *Cxcl1* and *Sdf1* mRNA expression in mCAFs from tumors developed by nulliparous mice (WT, N =8; KO, N =9: Mann-Whitney U test). (C) Relative *Cxcl1* and *Sdf1* mRNA expression in mCAFs from tumors developed by nulliparous mice (WT, N =8; KO, N =9: Mann-Whitney U test). (D) *Mmp2* and *Mmp9* mRNA expression was quantified in the same samples as in panel C. (Mann-Whitney U test). (E) pSMAD2, pSMAD3, total SMAD2/3 and SNAI2 expression were analyzed in the same samples as in panel F. (F) Effect of SDF1 treatment (10 ng/ml) on MDA-MB-231 cell migration (unpaired t-test). (G) Migration of MDA-MB-231 cells in the presence of exogenous SDF1 (N=3, ANOVA).
(H) Absence of correlation between the mRNA levels of stromal *SNAI2* and stromal *CXCL1* (Pearson's tests).

Supplementary Figure S6





D













Supplementary Table S1. Evaluation of the survival of patients with strong and weak tumor *SNAI2* expression in different subtypes of breast cancer. Data were obtained with the Kaplan-Meier plotter (30). Breast cancer subtypes were defined based on the 2013 St Gallen criteria, using the expression of ER1, HER2 and Ki67: Luminal A tumors are defined as ER-positive (ER+), HER2-negative (HER-) and Ki67 low; Luminal B tumors are defined as ER+, HER- and Ki67 high, or ER+, HER+; Basal breast cancer is defined as ER-, HER-; and finally, HER2-enriched tumors as ER-, HER+. (Log Rank test, see also Figure 1A-F).

Tumor	subtype	StGallen difinition	SNAI2 ex	pression	Patients (n)	P- value
			Low	High		
All tumors		n.a.	1976	1975	3951	0.3
	Luminal A	ER+, HER2-, Ki67 low	966	967	1933	1
	Luminal B	ER+, HER2-, Ki67 high or ER+, HER2+	574	575	1149	0.2
Intrinsic subtypes		HER2+, ER+	57	57	114	0.06
	Basal	ER-, HER2-	309	309	618	0.09
	HER2-enriched	ER-, HER2+	126	125	251	0.56
	Basal-like 1	n.a.	86	38	124	0.78
	Basal-like 2	n.a.	38	38	76	0.67
	Immunomoduladory	n.a.	102	101	203	0.82
Pletenpol subtypes	Mesenchymal	n.a.	88	89	177	0.69
	Mesenchymal stem-like	n.a.	32	31	63	0.55
	Luminal androgen-receptor	n.a.	49	37	86	0.16

Supplementary Table S2. Clinical and histopathological characteristics of tumors from patients with ERBB2-positive breast
cancerevaluated by immunohistochemistry. CPR, Complete Pathological Response (see alsoFigure 1K-N).

Case number	Age at	Tumor stage	KI67 (%)	HER2	PR (%)	FR %	SN	AI2	Time of Follo	Relapse /	Type of relapse or progression
Case number	diagnosis	after surgery	1007 (76)	TIEN2	FIX (70)	ER /	Epithelial	Stromal	up (weeks)	Progression	Type of relapse of progression
1	57	pT1cN0	10	3	<5	40	-	+	269.7	No	
2	49	pT2N1	50	3	-	-	+ focal	+	222.4	Yes	Local and distance relapse
3	28	pT1cN0	10	3	90	90	+	+	263.1	No	
4	59	pT1aN1	20	3	-	-	-	+ focal	261.1	No	
5	39	pT2N0	10	3	1	75	+ focal	+	816.7	Yes	Local relapse
6	52	pT1bN0	12	3	60	50	+	+	259.0	No	
7	37	pT1cN1	20	3	75	90	+ focal	+ focal	255.9	No	
8	56	pT2N3	20	3	-	-	-	+ focal	253.7	No	
9	48	pT3N2	5	3	<5	50	+ focal	-	251.6	No	
10	35	pT2N2	2	3	-	-	+ focal	+	281.9	Yes	Distant metastasis
11	75	pT2N1	30	3	70	90	+	+	250.7	No	
12	81	pT2N3	1	3	50	50	+ focal	+	129.9	No	
13	65	pTisN0	<5	3	-	-	+	+	474.1	Yes	Local relapse
14	50	pT1aN1	25	3	<5	90	-	+	216.0	No	
15	47	ypT1cN1	20	3	80	90	+ focal	+ focal	164.7	No	
16	58	ypT0N0	30	3	-	-	+	+ focal	199.0	No	
17	86	pT3N3M1	70	3	-	<10	+ focal	+	185.7	Yes	Metastasis at diagnosis
18	48	pT3N3M0	30	3		70	+ focal	+ focal	169.3	Yes	Distant metastasis
19	84	pT1cN0M0	1	3	-	70	+	-	190.0	No	
20	44	pT2N0	10	3	-	-	+ focal	+	416.3	Yes	Local relapse
21	91	pT2N0	20	3		90	+		167.7	Ves	Local and ganglionar relapse
21	47	pT2N0	5	3		90			178.0	No	Local and gangional relapse
22	47	p12N0	40	3	-	90			00.4	No	Distant matastasia
23	70	p14N2a	40	3	-	-			90.4	res	Evitua Intelia
24	91	yp TUNU	5	3	50	100	+ local	+	n.a.	n.a.	Exitus ietails
25	72	plisNU	5	3	70	100	-	+ tocal	195.7	No	
20	12	pT I DNU	10	3		-	+ local	+ local	210.0	NO	
27	42	pT3N2a	20	3	75	90	+	+ tocal	198.0	No	
28	58	pT1cN0	20	3	75	90	+	-	846.4	No	
29	49	pT2pNmic	70	3	-	100	+ tocal	+	191.7	No	
30	60	pTisN0M0	40	3	-	<10	+ focal	+	847.0	Yes	Local relapse
31	63	pT1bN0	10	3	-	-	+ focal	+	716.1	Yes	Local relapse
32	38	ypT0N0	20	3	<1	80	+ focal	+	114.1	No	
33	30	ypT1cN1	25	3	-	50	+ focal	+	140.1	No	
34	42	cT2N2M1	30	3	<1	90	+ focal	+ focal	150.0	No	
35	91	pT2N0	50	3	-	20	+	-	169.0	Yes	Local relapse
36	57	pT1aN0	30	3	-	5	+ focal	+ focal	83.7	No	
37	68	pT1cN0	15	3	-	50	+	+	58.7	No	
38	50	ypT1bypNmic	60	3	-	-	+	+	37.7	No	
39	54	cT4N3M1	40	3	-	5	+	+ focal	67.0	Yes	Metastasis at diagnosis
40	48	ypT2N0	5	3	-	90	+ focal	-	82.7	No	
41	53	CPR	50	3	-	70	+	+	66.0	No	
42	79	pT1cN2	30	3	-	90	+	+	85.1	No	
43	47	ypT2N0	35	3	-	90	+	+ focal	6.1	No	
44	61	yPTx,pN2a	40	3	-	-	+ focal	+ focal	28.1	No	
45	67	ypT1cN0	5	3	-	5	+ focal	-	53.0	No	
46	83	pT2N0M0	30	3	-	90	+ focal	+ focal	49.0	No	
47	93	pT2Nmic	70	3	-	-	+	+ focal	3.4	No	
48	35	pT2N1M0	30	3	-	-	+ focal	+ focal	574.0	Yes	Local and axilar relapse
49	35	pT2N1M0	10	3	-	-	+ focal	+	50.0	No	
50	60	mpT2 pN3a	5	3	-	50	+	-	38.7	Vac	Dietant metaetaeie

Supplementary Table S3. Linear models for SNAI2 and Ki67. The "glm" function of the R "stats" package was used to fit generalized linear models (logistic regression) (see also Figure 10). A.) Stromal SNAI2. B.) Epithelial SNAI2.

	•					S	tromal SNA	12							
	А.	Estimate	Std. Error	z value	Pr(> z)	Min	1Q	Median	3Q	Max	AIC	N			
	Intercept	10 296	0.521	1 976	0.0481										
All tumors	Ki-67	1 204	0.8002	1 505	0.1325	-21 612	0.4512	0.4512	0.7815	0.7815	45 613	50			
50	Intercept	1 792	1.08	1 659	0.0971										
EK-	Ki-67	18 774	5 345 908	0.004	0.9972	-197 277	0.00005	0.00005	0.55525	0.55525	97 416	18			
ER+	Intercept	0.6931	0.6124	1 132	0.258										
	Ki-67	10 415	0.8759	1 189	0.234	-19 479	0.5701	0.5701	0.6527	0.9005	36 185	32			
FR+PR+	Intercept	20.57	7929.26	0.003	0.996										
Little	Ki-67	-19.18	7929.26	-0.002	0.996	-179 412	0.00005	0.00005	0.66805	0.66805	9 004	10			
ER+PR-	Intercept	-0.2877	0.7638	-0.377	0.706										
	Ki-67	21 595	10 772	2 005	0.045	-20 074	-0.6597	0.535	0.535	13 018	25 341	22			
			Epithelial SNAI2												
	В.	Epithelial SNAI2													
		Estimate	Std. Error	z value	Pr(> z)	Min	1Q	Median	3Q	Max	AIC	N			
All tumors	Intercept	214 007	0.74751	2 863	0.0042										
	Ki-67	0.09353	0.96319	0.097	0.9226	-21 612	0.4512	0.4512	0.4717	0.4717	36 499	50			
EB	Intercept	19.57	4064.63	0.005	0.996										
EK-	Ki-67	-18.06	4064.63	-0.004	0.996	-184 648	0.00008	0.3168	0.63352	0.63352	14 431	18			
	Interest	40.004	0.7740	0.070	0.0077										
ER+	Ki-67	1 335	12 855	1 039	0.0377	-24 478	0.3203	0.3203	0.6039	0.6039	22 754	32			
	14.01	1000	12 000	1 000	0.200	21410	0.0200	0.0200	0.0000	0.0000	22 104				
ER+PR+	Intercept	1 386	1 118	1.24	0.215										
	Ki-67	19.18	7 929 263	0.002	0.998	-179 412	0.00005	0.00005	0.66805	0.66805	9 004	10			
ER+PR-	Intercept	17 918	10 801	1 659	0.0971										
	Ki-67	0.8473	1 496	0.566	0.5711	-23 272	0.3715	0.3715	0.5093	0.5553	17.09	22			

Supplementary Table S4. Differential expression analysis between nulliparous and parous Snai2 WT ErbB2 mice. The 602 gene probe set was obtained from a SAM test with a cut-off of

FDR = 0.05 (≈5% false positives). Overexpressed genes are shown in red and inhibited genes are shown in green.

Image: Section 1, 17:2002 A.10002-50 0.20170 1.10002-1001 and Resent servand-rower. 14th 1 Image: Section 1, 17:2002 A.2012-50 0.20170 1.00002-1001 and Resent servand-rower. 14th 1 Image: Section 1, 10:0002 A.2012-50 0.20170 1.00002-000 and Resent servand-rower. 14th 1 Image: Section 1, 10:0002 A.2012-50 0.20170 1.00002-000 and Resent servand-rower. 14th 1 Image: Section 1, 10:0002 A.2012-50 0.20170 1.10002-000 and Resent servand-rower. 14th 1 Image: Section 1, 10:0002 A.2012-50 0.20170 1.10002-00 and Resent servand-rower. 14th 1 Image: Section 1, 10:0002 A.2012-50 0.20170 1.0012-00 and Resent servand-rower. 14th 1 Image: Section 1, 10:0002 A.2012-50 0.20170 A.2012-50 A.2012-50 A.2012-50 Image: Section 1, 10:0002 A.2012-50 0.20170 A.2012-50 A.2012-50 A.2012-50 Image: Section 1, 10:0002 A.2012-50 0.20170 A.2012-50 A.2012-50 A.2012-50 Image: Section 1, 10:00002 A.2012-50 0.20170		Probeset ID	d-value	p-value	q-value	R fold	Genename	Description
Image: Proceeding of the second sec	1	10459241	13.1721062	2.0089E-05	0.0321007	1.8114672	Afap1I1	actin filament associated protein 1-like 1
Image: Second	2	10507885	11.9890864	3.05353E-05 6.42849E-06	0.0321007	1.6596438	Mycop Digap1	c-myc binding protein discs. Jarge (Drosophila) homolog-associated protein 1
Image: Section (C) 19980 (C) 19990 (C) 1999	4	10420837	10.9937752	4.74101E-05	0.0321007	1.409892	Extl3	exostoses (multiple)-like 3
	5	10513268	12.5177867	2.49104E-05	0.0321007	1.4905297	AI314180	expressed sequence Al314180
Image: Proceeding of the state of	6	10471360	11.2524334	4.25888E-05	0.0321007	1.2579993	Golga2	golgi autoantigen, golgin subfamily a, 2
Image: 1. Process of Process 1. Process 2. Construct of Automation Process Automatic Procest Process Automatic Process Automatic Process Automati	7	10595371	-11.651576	3.69638E-05	0.0321007	0.6919971	Hmgn3	high mobility group nucleosomal binding domain 3
International system Control of the system Control of the system Control of the system ID 0014501 11200000 11200000 11200000 11200000 112000000 112000000 112000000 112000000 112000000 112000000 1120000000 1120000000 11200000000000000000000000000000000000	8	10514008	15.0390282	9.04274E-00 3.45531E-05	0.0321007	1.7721342	Jak'i Miin	Janus Kinase I migration and invasion inhibitory protein
III. Excelose Interaction Int	10	10510972	11.8686858	3.2946E-05	0.0321007	1.5161356	Pank4	pantothenate kinase 4
10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10 10<	11	10514558	-13.489281	1.76784E-05	0.0321007	0.6919462	Gm12696	predicted gene 12696
10 1000000000000000000000000000000000000	12	10421021	-17.669108	5.62493E-06	0.0321007	0.7086152	Gm6878	predicted gene 6878
Biology Construction Construction Construction Biology Construction Construction Construction Construction Construction Biology Construction Construction Construction Construction Construction Construction Biology Construction Constructi	13	10485429	14.9975159	1.2857E-05	0.0321007	1.3806702	Pdhx Revol	pyruvate dehydrogenase complex, component X
Image: 1 Constrained and Status (Status) Constrained and Status (Status) Constrained and Status (Status) Image: 1 Status (Status) Status (Status) Status (Status) Status (Status) Image: 1 Status (Status) Status (Status) Status (Status) Status (Status) Image: 1 Status (Status) Status (Status) Status (Status) Status (Status) Image: 1 Status (Status) Status (Status) Status (Status) Status) Image: 1 Status (Status) Status) Status (Status) Status) Status (Status) Image: 1 Status (Status) Status) Status (Status) Status) Status) Status) Image: 1 Status (Status) Status) Status (Status) Status) Status (Status) Status) Image: 1 Status (Status) Status (Status) <td>14</td> <td>10554129</td> <td>-14.866541</td> <td>1.36605E-05</td> <td>0.0321007</td> <td>0.4167378</td> <td>B130024G19Rik</td> <td>RIKEN cDNA B130024G19 gene</td>	14	10554129	-14.866541	1.36605E-05	0.0321007	0.4167378	B130024G19Rik	RIKEN cDNA B130024G19 gene
17 051270 77830504 0.1781020 0.1782020 0.1782020 0.1782020 0.1782020 0.1782020 0.1782020 0.1782020 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.17820200 0.178202000 0.1782020000000000000000000000000000000000	16	10504926	15.3322532	1.12499E-05	0.0321007	1.5528957	Rnf20	ring finger protein 20
18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18<	17	10515700	17.9630504	4.01781E-06	0.0321007	1.50994	Szt2	seizure threshold 2
Biology 11000000 11000000 11000000 11000000 11000000 11000000 11000000 11000000 11000000 1100000000000000000000000000000000000	18	10515729	12.8695286	2.24997E-05	0.0321007	1.5026044	Szt2	seizure threshold 2
1 0000000 1.4400000 1.4400000 1.4400000 1.4400000000000000000000000000000000000	20	10515716	11.0538585	4.90200E-05	0.0321007	2 0530492	SZIZ Ttc39a	tetratriconentide reneat domain 39A
28 1007094 120284 221264 221204 PRA langestery/fundress 1 PRA langestery/fundress 1 28 100124 1123844 2320145 2201000 1488857 1148857 1148857 28 1001240 12374847 2201716 1688070 1488857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148857 1148877 1148877 1148877 1148877 1148877 1148877 1148877 1148877 1148877 1148877 1148877 1148877 11488777 1148877 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578 11488578	21	10532839	-14.829202	1.44641E-05	0.0321007	0.4657279	Trpv4	transient receptor potential cation channel, subfamily V, member 4
20 1054229 11750408 3.555274.55 0.0071007 1.546007 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00. 117911.00.	22	10507804	12.0821412	2.81246E-05	0.0321007	1.7510043	Trit1	tRNA isopentenyltransferase 1
6 5000000 10.0000000 1.00000000 1.000000000000000000000000000000000000	23	10516229	11.7383499	3.53567E-05	0.0321007	1.3466567	Utp11I	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)
10 1000000000000000000000000000000000000	24	10399407	12 176/055	1.04403E-05	0.0321007	17.91217	VSNIT Zc3bav1	VISININ-IIKE I zinc finger CCCH type, antiviral 1
27 0004465 7.1897464 4.21787.00 0.022107 1.406650 Composition of the comparison of th	26	10516007	13.4591002	1.84819E-05	0.0321007	1.4626186	Zmpste24	zinc metallopeptidase. STE24
28 100/0014 10.27726-08 0.0222157 1.466405 Cph 1014 Operation 1054 30 1017775 6.545305 0.0022167 1.001201 Operation 1054 30 1015005 0.755274 0.001248 0.001111 0.001211 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111 0.00111	27	10514985	17.8971494	4.82137E-06	0.0321007	1.6666366	Zyg11b	zyg-ll family member B, cell cycle regulator
-29 VUYE r/T 6.5455002 VUVE I/T ACIA-recorded to record a concentra succeding. Sector 2 (seeledin Archibite) 10 VUYE r/T 6.5552077 VUVE I/T ACIA-recorded to record a concentra succeding. Sector 2 (seeledin Archibite) 10 VUYE r/T 6.5552077 VUVE r/T ACIA-recorded to record a concentra succeding. Sector 2 (seeledin Archibite) 10 VUYE r/T 6.5552077 VUVE r/T ACIA-record a concentra succeding. Sector 2 (seeledin Archibite) 10 VUYE r/T 6.555207 VUVE r/T ACIA-record a concentra succeding. Sector 2 (seeledin Archibite) 10 VUYE r/T 6.555207 VUYE r/T F.555207 VUYE r/T F.555	28	10510814	10.775626	5.14279E-05	0.0322157	1.4646645	Cep104	centrosomal protein 104
No. District Structure of a control Structure of a control Structure of a control 201 1000710 20101071 Control Contro Contro	29	10478776	8.63435062	0.000168748	0.0331183	1.6045149	Artget2	AUP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
12 1948/10 6.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.0001548 0.00015	31	10592023	9,75697976	9,1606F-05	0.0331183	1,4036022	Rere	arryiou beta (rs4) precursor-line protein 2 arginine glutamic acid dipeptide (RE) repeats
38 10013381 10013381 10013381 10013381 10013381 10013381 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 00001338 0	32	10498710	-8.8181013	0.00015348	0.0331183	0.1690807	Bche	butyrylcholinesterase
41 Considering (AAB escot protein 1) 51 Decode 10, 7079866 75.8644-56 0.033118 1.027527 Construct and the complex should gamma 1 51 Decode 20, 7079866 75.8644-56 0.033118 1.027527 Construct and the complex should gamma 1 51 Decode 20, 7078866 75.8644-56 0.033118 1.028262 Decode 20, 708464 Decode 20, 708464 Decode 20, 708464 Decode 20, 708464 51 Decode 20, 708464 51 Decode 20, 708444 Decode 20, 708464 Decode 20, 708464 Decode 20, 708464 Decode 20, 708464 51 Decode 20, 708444 Decode 20, 708474 Decode 20, 7084744 Decode 20, 7084744 Decode 20, 7084744 51 Decode 20, 7084744 Decode	33	10513583	10.3611971	7.07134E-05	0.0331183	1.5019706	Cdc26	cell division cycle 26
str up:Acc20 V./Ymm39 J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity J. More Complexity J. More Complexity J. More Complexity 1000200 J. More Complexity	34	10606513	-8.7790401	0.000158302	0.0331183	0.8540778	Chm	choroidermia (RAB escort protein 1)
10000000 100000000 1000000000000000000000000000000000000	35	10420225	10.7079696	5.78564E-05 0.000125356	0.0331183	1.2027628	Cong1	cnymase 1, Mast Cell coatomer protein complex, subunit gamma 1
18 10191997 10.587245 0.5877845 0.03118 1.1412426 Disk Disk <thdisk< th=""> Disk <thdis< td=""><td>37</td><td>10507309</td><td>10.4653717</td><td>6.74992E-05</td><td>0.0331183</td><td>1.4648839</td><td>Ccdc17</td><td>colled-coil domain containing 17</td></thdis<></thdisk<>	37	10507309	10.4653717	6.74992E-05	0.0331183	1.4648839	Ccdc17	colled-coil domain containing 17
38 1050942 10.52226 0.207786 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554 0.0001554	38	10518957	10.5873611	6.18742E-05	0.0331183	1.316945	Dffb	DNA fragmentation factor, beta subunit
40 1088468 8.075428 0.000105534 0.00010554 0.00010554 0.00010554 0.00010545 0.0001054 41 1005026 10.600254 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00010841 0.00011871 0.00011871 0.00011871 0.00011871 0.00011871 0.00011871 0.00011871 0.00011871 <td>39</td> <td>10509542</td> <td>10.582236</td> <td>6.26778E-05</td> <td>0.0331183</td> <td>1.4448265</td> <td>Ddost</td> <td>dolichyl-di-phosphooligosaccharide-protein glycotransferase</td>	39	10509542	10.582236	6.26778E-05	0.0331183	1.4448265	Ddost	dolichyl-di-phosphooligosaccharide-protein glycotransferase
10 1042288 1054288 1054288 1054288 1054288 1054288 1054288 1054288 1054288 1054288 1054288 1054288 1055877 9.4322917 0.00013588 10503118 1555786 1055878 1055877 9.4322917 0.00013588 0.00013588 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055878 1055888 1055878 1055878 1055888 1055878 105588 1055878 1055878 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 1055888 105588 1055888 1055888 105588 1055888 1055888 105588888	40	10588495	8.67675428	0.000165534	0.0331183	1.5889151	Dusp7	dual specificity phosphatase 7
13 1091305 10.997295 2.589254 2.589217 41 1050377 9.4322017 0.000108481 0.500172 France 45 10505966 3.089177 0.000108471 0.0001323181 15561404 France 46 10405464 8.711482 0.000126371 0.0331183 15693404 France G protein-coupded receptor kinase 6 47 10386851 8.818450 0.000126371 0.0331183 1.782471 France G protein-coupded receptor kinase 6 48 10469682 9.5348607 0.0031181 1.7824721 France France G protein-coupde differentiation associated (S. cerevisiae) 49 10507262 9.2722086 0.000115713 0.0331183 1.721746 Lugz	41	10452980	8 91649578	0.000143837	0.0331183	1 9098375	Ephaz Fif2ak2	eukarvotic translation initiation factor 2-alpha kinase 2
44 1505737 9.4520917 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013268 0.00013267 0.033118 1.984104 Hasasso Departmenting (partments) 40 1038682 0.313487 0.00015674 0.0331188 1.972421 KiT1 Partments) Departmenting (partments) 51 1050728 9.7220086 0.00015747 0.0331188 1.272747 Inv1 Hasasso Eurona Dipper protin 2 51 1050726 9.7220086 0.00015748 0.0331188 1.276147 Kim1a Visite (K-specific demating 4 51 1050726 9.838817-6 0.0331188 1.761447 Kim1a Visite (K-specific demating 4 A 51 1050726 9.0331188 1.761447 Kim1a Visite (K-specific demating 4 A 51 1050726 9.0331181 1.7614428 Visite K-specific demating 4 <td>43</td> <td>10510365</td> <td>10.6976254</td> <td>5.866E-05</td> <td>0.0331183</td> <td>1.5187966</td> <td>Exosc10</td> <td>exosome component 10</td>	43	10510365	10.6976254	5.866E-05	0.0331183	1.5187966	Exosc10	exosome component 10
46 10606880 e.0096173 0.000122980 0.0331185 1.6860404 Fait Fait-associated factor 1 47 10386651 a.8.184452 0.000122910 0.0331185 1.9.64121 Installatio (Borotin-coupled receptor kinase 6 1 47 10386651 a.8.184452 0.00012270 0.0331185 1.0.6227453 Installation 1	44	10508737	9.43220912	0.000108481	0.0331183	1.5561727	Eya3	eyes absent 3 homolog (Drosophila)
1440-54-1 8.11142-63 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112677 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112678 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688 0.000112688	45	10506989	9.0895173	0.000132588	0.0331183	1.6569404	Faf1	Fas-associated factor 1
Her Indelega Display Display <thdisplay< th=""> <thdisplay< th=""> <thdisp< td=""><td>46</td><td>10405464</td><td>8.7118426</td><td>0.000162319</td><td>0.0331183</td><td>1.3863103</td><td>Grkb He3et3b1</td><td>G protein-coupled receptor kinase b</td></thdisp<></thdisplay<></thdisplay<>	46	10405464	8.7118426	0.000162319	0.0331183	1.3863103	Grkb He3et3b1	G protein-coupled receptor kinase b
Inspace Inspace <t< td=""><td>48</td><td>10466932</td><td>9.21211305</td><td>0.000120534</td><td>0.0331183</td><td>1.7389714</td><td>Insl6</td><td>insulin-like 6</td></t<>	48	10466932	9.21211305	0.000120534	0.0331183	1.7389714	Insl6	insulin-like 6
50 10505880 P.3520665 0.00015604 0.0331183 1.6997678 [K112 Incline rich repeat containing 41 51 1055733 P.3833331 0.000157486 0.0331183 1.6281797 [Linka repeat containing 41 52 10517465 9.7388626 0.0331183 1.6281471 [Linka repeat containing 41 54 10517420 9.90849404 0.000112746 0.0331183 1.634462 [Linka repeat containing 41 54 10517420 9.90849404 0.000122446 0.0331183 1.684462 [Linka repeat containing 41 56 10507520 1.8840412 0.000122446 0.0331183 1.684003 [Integet mediator complex subunt 8 56 10506220 0.8863137 0.000113301 0.4460030 [Integet containing 41 Integet containing 41 56 10506220 0.8985137 0.000113301 0.4460030 [Integet containing 41 Integet containing 41 56 10506220 0.8985137 0.000113301 0.000113010 [Integet containing 41 Integet containing 41 57 1050569 1.0044151 8.18337460 0.0331183 1.7298427 <t< td=""><td>49</td><td>10508883</td><td>9.13494677</td><td>0.000130177</td><td>0.0331183</td><td>1.5752423</td><td>Kdf1</td><td>keratinocyte differentiation factor 1</td></t<>	49	10508883	9.13494677	0.000130177	0.0331183	1.5752423	Kdf1	keratinocyte differentiation factor 1
1 1080/2381 24/220868 0.000115/13 0.0331183 1.626174/ Lincols apportation of the state of th	50	10506880	8.78520695	0.000156694	0.0331183	1.6997678	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)
S3 19517445 9 67348524 0 883115.05 17 631417 Long Long <thlong< th=""> Long <thlon< td=""><td>51</td><td>10507238</td><td>9.27220986</td><td>0.000115713</td><td>0.0331183</td><td>1.6261797</td><td>LITC41</td><td>leucine rich repeat containing 41</td></thlon<></thlong<>	51	10507238	9.27220986	0.000115713	0.0331183	1.6261797	LITC41	leucine rich repeat containing 41
54 10517425 8 bode14404 0.000144641 0.0331183 1 564868 Lypac Inscription 55 10507529 9.18840412 0.000122945 0.0331183 1.7073842 Investment interpoint	53	10517465	9.57368626	9.88381E-05	0.0331183	1.7631417	Kdm1a	Ivsine (K)-specific demethylase 1A
55 10510305 10.06895615 8.03561E-05 0.0331183 1.7072842_Mtor mechanistic target of rapamycin (serine/thronine kinase) 56 1050729 9.1884442 0.000170355 0.0331183 1.846221 Med3 mitochondiral ibosomal protein L50 57 10596925 9.32562124 0.00011055 0.0331183 1.546227 Mag3k6 mitochondiral ibosomal protein kinase kinase kinase finase	54	10517425	8.90649404	0.000144641	0.0331183	1.654858	Lypla2	lysophospholipase 2
66 100/07/29 918940412 CU001/22/49 0.0031183 1.846003 MmpElo mitochondrai ribosomal protein L50 57 10510829 9.06883137 0.000173391 0.0331183 1.546002 MmpElo mitochondrai ribosomal protein L50 58 1050829 9.3262214 0.00011695 0.0331183 1.258442 NADH dehydrogenase (ubiquince) 1 alpha subcomplex, assembly factor 3 60 10356312 8.9764722 0.00011695 0.0331183 1.758852 Opioid growth factor receptor 61 10479411 8.5511665 0.000151873 0.0331183 1.059773 Pleixhon poioid growth factor receptor 62 1055051 8.8704E-56 0.0331183 1.059773 Pleixhon poioid growth factor receptor 63 10550549 9.830488 8.3704E-56 0.0331183 1.059773 Pleixhon pleixhon<	55	10510305	10.0695615	8.03561E-05	0.0331183	1.7073642	Mtor	mechanistic target of rapamycin (serine/threonine kinase)
Open Notice Open Notice Open Notice Open Notice 06 10050625 9.3286173 0.00017330 0.0331183 1.5466267 MagAd6 mitogen-activated protein Kinase Kin	56	10507529	9.18840412	0.000122945	0.0331183	1.684/21	Med8 Mrp150	mediator complex subunit 8
1099025 9.35/62/124 0.000111695 0.0331183 1.25/6442 NADE 60 1035612 -8.9764/722 0.000167944 0.0331183 1.776885 Ogf opiold growth factor receptor 61 10473411 8.65216602 0.000167944 0.0331183 1.776885 Ogf opiold growth factor receptor 62 10615061 8.82896507 0.0001516734 0.0331183 1.1579773 Pleft peldodytcan recognition protein 1 64 1056516 8.673016 0.00016337 0.0331183 1.0579773 Pleft pleckstrin homology domain containing, family B (evectins) member 1 65 10655061 8.673016 0.0016337 0.0331183 1.6573778 Pleft pleckstrin homology domain containing, family B (evectins) member 1 66 10429843 9.2030488 8.35704E.05 0.0331183 1.550389 Angef101 RanBP-type and C3HC4-type Zins finger containing 1 Recetins / mascing 1 67 10439774 8.863193 0.00011427 0.0331183 1.3524257 1104147 0.0031183 1.3526257	58	10508829	9.06883137	0.000133391	0.0331183	1.5469267	Map3k6	mitocionaria noosonar protein 250 mitogen-activated protein kinase kinase kinase 6
60 10356312 8/9764722 0.000140623 0.0331183 0.7969327 Ncl nucleolin 61 1047411 8.6516602 0.000151873 0.0331183 1.6397359 Osbpl9 oxysterol binding protein-like 9 62 10515051 8.8288687 0.000126159 0.0331183 1.0497174 pectodioglycan recognition protein 1 64 10565669 1.004151 8.1693242.0 0.00126159 0.0331183 1.067737 66 1042943 9.3030488 8.357044.0 0.0331183 1.4597379 66 1042943 9.3030488 8.357044.0 0.0331183 1.459739 67 10488549 9.92041754 8.517756-05 0.0331183 1.4592399 Partial Partial Partial 1.656606 0.00114127 0.0331183 1.3592397 Reken DNA 1600014C1070 pare Partial 1.0566735 9.4639533 0.0001677 0.331183 1.92245170 Rinken DNA 1600014C1010 pare 71 10567735 9.4639533 0.000146505 0.0331183 1.927272172 Stzz	59	10596925	9.35262124	0.000111695	0.0331183	1.2584842	Ndufaf3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3
101/19411 8.62216602 0.000167944 0.0031183 1.776885[Ogfr opioid growth factor receptor 62 1055508 9.700241573 0.0331183 1.095795 oxysterol binding protein-like 9 63 1055509 1.0.044151 8.19633E-05 0.0331183 0.0961 Pdytyp peptidodyxcan recognition protein 1 64 10555910 8.6730316 0.000166337 0.0331183 1.0617499 Plethbi placenta expressed transcript 1 65 10429843 9.3030488 8.57775 0.0331183 1.3557773 Rbck1 RanB-Sybe and C3/FC4-type zinc finger containing 1 66 10517744 9.0680085 0.00015107 0.0331183 1.355773 Rbck1 RanB-Sybe and C3/FC4-type zinc finger containing 1 67 104437171 8.3344333 0.00015107 0.0331183 1.3252717 Rbck1 RitEN eDNA 1700093.21 gene 70 10437171 8.386319138 0.0001477 0.0331183 0.24272 Szt2 seizure threshold 2 71 1055731 0.335843 0.0001477 0.0331183 1.502272 Szt2 seizure threshold 2 74	60	10356312	-8.9764722	0.000140623	0.0331183	0.7963927	Ncl	nucleolin
Vac Notified in the second of th	61	10479411	8.65216602	0.000167944	0.0331183	1.776885	Ogfr Ochol0	opioid growth factor receptor
Image: Application of the second se	63	10515051	-10 044151	8.19633E-05	0.0331183	0.0961	Palvrp1	peptidoglycan recognition protein 1
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or 10400291 9.520411241 0.5311103 1.50371731R00K1 rKathB+3p6 and C-3HC4-1ype Zinc Tinger Containing 1 68 10517744 9.0680095 0.000134195 0.0331183 1.550399 Arhgef101 Rho guanine nucleoide exchange factor (GEF) 10-like 69 10552252 8.97368072 0.000114127 0.0331183 1.2022625 1700093J21 Ren RiKEN cDNA 1700093J21 gene 70 10467735 9.4639533 0.000107677 0.0331183 2.2637517 Rnf213 ring finger protein 213 73 10515731 10.3687295 7.1517E-05 0.0331183 1.3075272 Szt2 seizure threshold 2 74 10515649 10.1185807 7.79455E-05 0.0331183 1.341152 Szt2 seizure threshold 2 76 10515737 9.55244538 0.000116106 0.0331183 1.39071001 Shroom family member 1 71 10376007 8.62815563 0.000164551 0.0331183 1.9071001 Shroom family member 1 78 10404675 -9.6672151 9.94416E-05 0.0331183 1.9071001 <	66	10429843	9.93030488	8.35704E-05	0.0331183	1.4995393	Parp10	poly (ADP-ribose) polymerase family, member 10
Sector Sector Sector Sector Sector 69 10552252 8.97386072 0.000141421 I.3528307 I600014C100 gene 70 10437171 8.83844333 0.00015107 0.0331183 1.2022625 I100033121 RIKEN cDNA 1600014C100 gene 71 10567735 9.4639533 0.00017677 0.0331183 2.637517 Rnf213 ring finger protein 213 73 10515731 10.3587295 7.1517E-05 0.0331183 1.5075272 Szt2 seizure threshold 2 74 10615649 10.1158507 7.79455E-05 0.0331183 1.31707188 Szt2 seizure threshold 2 75 10515737 9.55264538 0.000114406 0.0331183 1.5102695 Szt2 seizure threshold 2 76 10515737 9.55264538 0.000116416 0.0331183 1.5102695 Szt2 seizure threshold 2 77 10376007 8.62815563 0.000116416 0.0331183 1.5102695 Szt2 seizure threshold 2 77 10376078	07 88	10488594	9.92041754	0.01/10E-05	0.0331183	1.5057773	Arhaef10l	Rho quanine nucleotide exchange factor (GEF) 10-like
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71 10567735 -9.4639533 0.000107677 0.0331183 0.9245197[3110040M04Rik RIKEN cDNA 3110040M04 gene 72 10383196 8.66319138 0.000148659 0.0331183 2.637517 Rnf213 ring finger protein 213 73 10515731 10.3587295 7.1517E-05 0.0331183 1.5075272 Stz seizure threshold 2 74 10515649 10.1188607 7.79455E-05 0.0331183 1.341152 Stz seizure threshold 2 75 10515737 9.2524538 0.000114106 0.0331183 1.502695 Stz seizure threshold 2 76 10517649 9.26541563 0.0001149551 0.0331183 1.502695 Stz seizure threshold 2 77 10376007 8.62815663 0.000169551 0.0331183 0.7103743 Snmp48 small nuclear ribonucleoprotein 48 (U11/U12) 78 10404675 9.5672151 9.96416E-05 0.0331183 0.7103743 Snmp48 small nuclear RNA activating complex, polypeptide 3 80 10550734 9.51209546 0.00016463 0.0331183 1.562895 Suf43 sufait gene 4 Sufait gene	70	10437171	8.83844333	0.00015107	0.0331183	1.2032625	1700093J21Rik	RIKEN cDNA 1700093J21 gene
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No. 100/1001/1000/1200 No.0001/200 No.0001/200 No.0001/200 SetZure futneshold 2 74 100515649 10.1158507 7.794555-05 0.0331183 1.4707188 SetZure threshold 2 75 10515737 9.55264538 0.000101249 0.0331183 1.5102695 SetZure threshold 2 76 10515735 9.28543774 0.000146951 0.0331183 1.9071001 Shroom family member 1 77 10376007 8.62815563 0.00016551 0.0331183 1.9071001 Shroom family member 1 78 10404675 9.964168-05 0.0331183 1.7367443 Snapc3 small nuclear ribonucleoprotein 48 (U11/U12) 79 10505630 8.71865701 0.000161516 0.0331183 1.613245 Sf3a3 splicing factor 3a, subunit 3 80 10507914 9.51205463 8.6705961 0.00013829 0.0331183 1.562885 Surfat surfati gene 4 82 10554863 8.6705961 0.00013659 0.0031183 1.562882 Syntaxin 12 83 1056982 <t< td=""><td>72</td><td>10383196</td><td>8.86319138</td><td>0.000148659</td><td>0.0331183</td><td>2.637517</td><td>Knf213 Szt2</td><td>ring ringer protein 213 seizure threshold 2</td></t<>	72	10383196	8.86319138	0.000148659	0.0331183	2.637517	Knf213 Szt2	ring ringer protein 213 seizure threshold 2
75 10515737 9.55264538 0.000101249 0.0331183 1.3341152 Szt2 seizure threshold 2 76 10515735 9.28543774 0.000114106 0.0331183 1.5102695 Szt2 seizure threshold 2 77 10376007 8.62815563 0.000169551 0.0331183 1.9071001 Shroom family member 1 78 10404675 9.5672151 9.96416E-05 0.0331183 0.7103743 Smmp48 small nuclear ribonucleoprotein 48 (U11/U12) 79 10505630 8.71865701 0.000161516 0.0331183 1.6173245 Sfsaa splicing factor 3a, subunit 3 80 10507914 9.51209546 0.00014463 0.0331183 1.562885 Surf4 surfeit gene 4 82 10554863 9.6705961 0.000161741 0.0331183 1.562885 Surf4 surfeit gene 4 83 10516982 9.29026738 0.000113020 0.0331183 1.580723 Str12 syntaxin 12 84 10448593 9.54816059 0.000103659 0.0331183 1.2928807	74	10515649	10.1158507	7.79455E-05	0.0331183	1.4707188	Szt2	seizure threshold 2
76 10515735 9.28543774 0.000114106 0.0331183 1.5102695 Szt2 seizure threshold 2 77 10376007 8.62815653 0.000169551 0.0331183 1.9071001 Shroom family member 1 78 10404675 9.5672151 9.96416E-05 0.0331183 0.7103743 Snrop48 small nuclear ribonucleoprotein 48 (U11/U12) 79 10505630 8.71865701 0.000161516 0.0331183 1.7367443 Snapc3 small nuclear ribonucleoprotein 48 (U11/U12) 80 10507914 9.51209546 0.000104463 0.0331183 1.562889 support support 81 10481147 8.97673274 0.00013982 0.0331183 1.562889 Support synaptotagmin-like 2 82 10554863 9.6705961 0.00011302 0.0331183 1.2945878 Traf7 TNF receptor-associated factor 7 84 10448593 9.5481059 0.00011302 0.0331183 1.2928507 Tmem160 transmembrane protein 160 85 10550316 9.5487372 0.000110288	75	10515737	9.55264538	0.000101249	0.0331183	1.3341152	Szt2	seizure threshold 2
// 103/000/ 8.0231563 0.000169551 0.0331183 1.90/1001 Shroom family member 1 78 10404675 -9.5672151 9.96416E-05 0.0331183 0.7103743 Smmp48 small nuclear ribonucleoprotein 48 (U11/U12) 79 10505630 8.71865701 0.000161516 0.0331183 1.567443 Snapc3 small nuclear RNA activating complex, polypeptide 3 80 10507914 9.51209546 0.000104463 0.0331183 1.562880 Suffast synaptotagmin-like 2 81 1048147 8.97673274 0.00013822 0.0331183 1.562880 Synaptotagmin-like 2 82 10554863 -8.6705961 0.000113022 0.0331183 1.562892 Syt12 synaptotagmin-like 2 83 10516982 9.29026738 0.000113020 0.0331183 1.2928507 Tmef160 transmembrane protein 160 84 10448593 9.54816059 0.000110388 1.364831 Tmt112 tRNA methyltransferase 11-2 87 10518642 9.4145545 0.00011088 1.3976341 Vps13d vacuolar protein sorting 13 D (yeast) 88 10518642	76	10515735	9.28543774	0.000114106	0.0331183	1.5102695	Szt2	seizure threshold 2
ro 100000013 5:300102000 0:0031163 0:100000000 Sinal nuclear RNA activating complex, polypeptide 3 79 100505630 8:71865701 0:000104463 0:0331183 1:6113245 Sf3a3 splicing factor 3a, subunit 3 80 100507914 9:51209546 0:000104463 0:0331183 1:6113245 Sf3a3 splicing factor 3a, subunit 3 81 10481147 8:97673274 0:00013822 0:0331183 1:562880 Surf 4 surfeit gene 4 82 10554863 -8:6705961 0:000167141 0:0331183 0:4629362 Syll2 synaptotagmin-like 2 83 10516982 9:29026738 0:000113020 0:0331183 1:2945878 Traf7 TNF receptor-associated factor 7 84 10448593 9:54816059 0:000103659 0:0331183 1:2926507 Tmen160 transmembrane protein 160 86 10461012 9:4185345 0:000110288 0:0331183 1:5362541 be4b ubiquitination factor E48 88 10518228 9:25719268 0:00011732 0:03311	77	10376007	8.62815563	0.000169551	0.0331183	1.9071001	Shroom1	shroom family member 1
Non-transmission Non-transmission Non-transmission Non-transmission 80 10007914 9.51209546 0.00010463 0.0331183 1.613245 St3a3 splicing factor 3a, subunit 3 subunit 3 81 10481147 8.97673274 0.00013882 0.0331183 1.562889 Surfa superior 82 10554863 -8.6705961 0.000167141 0.0331183 1.562889 Surfa superior superior <td< td=""><td>79</td><td>10404075</td><td>8.71865701</td><td>0.000161516</td><td>0.0331183</td><td>1.7367443</td><td>Shimp40 Shapc3</td><td>small nuclear RNA activating complex, polypeptide 3</td></td<>	79	10404075	8.71865701	0.000161516	0.0331183	1.7367443	Shimp40 Shapc3	small nuclear RNA activating complex, polypeptide 3
81 10481147 8.97673274 0.00013982 0.0331183 1.562889 Surf4 surfeit gene 4 82 10554863 -8.6705961 0.000167141 0.0331183 0.4629362 Syntaxin 12 83 10516982 9.29026738 0.000103659 0.0331183 1.5600723 Sk12 syntaxin 12 84 10448593 9.54816059 0.000102656 0.0331183 1.2928507 Tmem160 85 10550316 9.54873732 0.000102856 0.0331183 1.3228507 Tmem160 86 10461012 9.41583091 0.000109284 0.0331183 1.3228507 Tmem160 87 10518642 9.4145545 0.000110088 0.0331183 1.3262541 Ube4b ubiquitination factor E4B 88 10518242 9.25719268 0.00011732 0.0331183 1.3976341 Vps13d vacuolar protein sorting 13 D (yeast) 89 105399421 -9.8638117 8.59811E-05 0.0331183 1.618357 Vipf1 Vipf domain famity, member 1 90 10506668 10.7289079 5.46422E-05 0.0331183 1.4862889 Zb	_80	10507914	9.51209546	0.000104463	0.0331183	1.6113245	Sf3a3	splicing factor 3a, subunit 3
82 10554863 -8.6705961 0.000167141 0.0331183 0.4629362 Syll synaptotagmin-like 2 83 10516962 9.29026738 0.000113302 0.0331183 1.5800723 Skil syntaxin 12 84 10448593 9.54816059 0.000103659 0.0331183 1.2928507 Tmem160 transmebrane protein 160 85 10461012 9.41583091 0.000109284 0.0331183 1.32928507 Tmem160 transmebrane protein 160 86 10461012 9.41583091 0.000109284 0.0331183 1.364831 Trmt112 tRNA methyltransferase 11-2 87 10518642 9.4145545 0.00011732 0.0331183 1.3676341 Vps13d vacuolar protein sorting 13 D (yeast) 88 10518228 9.25719268 0.00011732 0.0331183 1.3763241 Vps13d vacuolar protein sorting 13 D (yeast) 89 105399421 -9.8638117 8.59811E-05 0.0331183 1.618357 Vipf1 Vip1 domain family, member 1 90 10506668 10.7289079 5.	81	10481147	8.97673274	0.00013982	0.0331183	1.562889	Surf4	surfeit gene 4
os tos tosol s.sucoros 0.0011302 0.031183 1.300/2.3181 syntaxin 12 84 10448593 9.54816059 0.000110302 0.0331183 1.2945878 Traf7 TNF receptor-associated factor 7 85 10560376 9.5487372 0.000102856 0.0331183 1.2928507 Tmem160 transmerbrane protein 160 86 10461012 9.41583091 0.000102856 0.0331183 1.3228507 Tmem160 transmerbrane protein 160 86 10461012 9.41563091 0.000110284 0.0331183 1.364281 Trmt112 tRNA methyltransferase 11-2 87 10518642 9.4145545 0.00011732 0.0331183 1.362541 Ube4b ubiquitination factor E4B 88 10518228 9.25719268 0.00011732 0.0331183 0.705222 Mycn v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) 90 10509668 10.7289079 5.46422E-05 0.0331183 1.486289 Zbtb17 zinc finger and BTB domain containing 17	82	10554863	-8.6705961	0.000167141	0.0331183	0.4629362	Sytl2	synaptotagmin-like 2
85 10550316 9.54873792 0.000102856 0.0331183 1.2292507 Timen160 86 10461012 9.41583091 0.000109284 0.0331183 1.2292507 Timen160 transmembrane protein 160 86 10461012 9.41583091 0.000109284 0.0331183 1.32928507 Timen160 transmembrane protein 160 87 10518642 9.4145545 0.000117028 0.0331183 1.362541 Ube4b ubiquitination factor E4B 88 10518228 9.25719268 0.00011732 0.0331183 1.3763241 Vps13d vacuolar protein sorting 13 D (yeast) 89 10399421 -9.8638117 8.59811E-05 0.0331183 1.618357 Vipf1 Vip1 domain family, member 1 90 10509998 10.4428993 6.91063E-05 0.0331183 1.486289 Zbb17 zinc finger and BTB domain containing 17	83	10516982	9.29026738	0.000113302	0.0331183	1.5800723	SIX12 Traf7	Syntaxin 12 TNF recentor-associated factor 7
86 10461012 9.41583091 0.000109284 0.0331183 1.364831 Trmt112 tRNA methyltransferase 11-2 87 10518642 9.4145545 0.000110088 0.0331183 1.5362541 Ube4b ubiquitination factor E4B 88 10518228 9.25719268 0.00011732 0.0331183 1.3976341 Vps13d vacuolar protein sorting 13 D (yeast) 89 10399421 -9.8638117 8.59811E-05 0.0331183 0.705222 Mycn V-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) 90 105096688 10.7289079 5.46422E-05 0.0331183 1.4862889 Zbtb17 zinc finger and BTB domain containing 17	85	10550316	9.54873792	0.000102856	0.0331183	1.2928507	Tmem160	transmembrane protein 160
87 10518642 9.4145545 0.000110088 0.0331183 1.5362541 Ube4b ubiquitination factor E4B 88 10518228 9.25719268 0.00011732 0.0331183 1.976341 Vps13d vacuolar protein sorting 13 D (yeast) 89 10399421 -9.8638117 8.59811E-05 0.0331183 0.705222 Mycn V-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) 90 10506668 10.7289079 5.46422E-05 0.0331183 1.486289 Zbtb17 Zinc finger and BTB domain containing 17	86	10461012	9.41583091	0.000109284	0.0331183	1.364831	Trmt112	tRNA methyltransferase 11-2
88 10518228 9.25/19208 0.00011732 0.0331183 1.39/63411ps13d vacualar protein sorting 13 D (yeast) 89 10399421 -9.8638117 8.59811E-05 0.0331183 0.705222 Mycn v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) 90 10506668 10.7298079 5.46422E-05 0.0331183 1.618357 Yip1 domain family, member 1 91 1050998 10.4428993 6.91063E-05 0.0331183 1.486289 Zbtb17 zinc finger and BTB domain containing 17	87	10518642	9.4145545	0.000110088	0.0331183	1.5362541	Ube4b	ubiquitination factor E4B
Op 10556668 10.7289079 5.46422405 0.0331183 1.618357 Yip1 Yip10min family, member 1 91 10506668 10.7289079 5.46422405 0.0331183 1.486289 Zbb17 zinc finger and BTB domain containing 17	88	10200424	9.25/19268	0.00011732	0.0331183	1.3976341	Vps13d Mycn	vacuolar protein sorting 13 D (yeast)
91 10509998 10.4428993 6.91063E-05 0.0331183 1.4862889 Zbtb17 zinc finger and BTB domain containing 17	90	10506668	10.7289079	5.46422E-05	0.0331183	1.618357	Yipf1	Yip1 domain family, member 1
	91	10509998	10.4428993	6.91063E-05	0.0331183	1.4862889	Zbtb17	zinc finger and BTB domain containing 17

52	10570963	-9.190257	0.000122141	0.0331183	0.9064918	Zmat4	zinc finger, matrin type 4
93	10371603	-8.5535218	0.000175176	0.0331971	0.8890669	Gm6653	predicted gene 6653
94	10515012	8.58893818	0.000172766	0.0331971	1.3657554	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A
95	10489127	8.56009805	0.000174373	0.0331971	1.2539191	Rbl1	retinoblastoma-like 1 (p107)
96	10411287	8.5215632	0.000177587	0.0333735	1.4311153	Btf3l4	basic transcription factor 3-like 4
97	10431229	-8,4854246	0.000184016	0.0342958	0.601381	Celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
98	10572378	-8 3727501	0.000200087	0.0350164	0.3143347	Comp	cartilage oligomeric matrix protein
99	10414661	-8.3366018	0.000203301	0.0350164	0.8502977	Hk1	hexokinase 1
100	10513020	8 31983539	0.000205712	0.0350164	1 6633143	lkhkan	inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-associated protein
101	10514830	8 3426047	0.000202112	0.0350164	1 6934189	Ttc4	terration on happen gent polypointe of manager in Dicense, kindee complex descended protein
102	10508468	8 42417063	0.000192855	0.0350164	1 4441017	Tmem234	transmembrane protein 234
102	10517312	8 41387802	0.000102000	0.0350164	1 4422663	Tmem57	transmembrane protein 57
103	10500370	8 32288407	0.000100000	0.0350164	1 4821152	Hen/8	ubiquiti specific particles 48
104	10309379	0.32200497	0.000204908	0.0350104	1.4021102	Osp40 Calat4	ubiquiui specific pepiluase 40
105	10300030	0.31032930	0.000200515	0.0350104	1.3792007	Gaint4	DDF-N-acety-apha-D-galactosamme.polypeptide N-acety/galactosammy/inansierase 4
100	104/0//4	0.1794930	0.00022339	0.0301322	1.5713004	Angelz	ADP-indexitian factor guarante nucleorade-exchange factor 2 (breieldin A-inhibited)
107	10510452	8.11618399	0.000229819	0.0361322	1.5133088	Dita Ditaia14	DNA fragmentation factor, alpha subunit
108	10510604	8.04157485	0.000245086	0.0361322	1.6268481	Dhajci i	Dnag (Hsp40) nomolog, subtamily C, member 11
109	10515528	8.16126/77	0.000226604	0.0361322	1.3478193	Dpn2	DPH2 nomolog (S. cerevisiae)
110	10481909	7.94267567	0.00025955	0.0361322	1.3468512	FDXW2	F-box and WD-40 domain protein 2
111	10508019	8.0598769	0.000242676	0.0361322	1.5351475	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)
112	10533720	7.93637441	0.000261157	0.0361322	1.7242791	Hcar2	hydroxycarboxylic acid receptor 2
113	10513397	8.22204446	0.000217765	0.0361322	1.6610459	Inip	INTS3 and NABP interacting protein
114	10507218	7.92241069	0.000262765	0.0361322	1.8614835	Mknk1	MAP kinase-interacting serine/threonine kinase 1
115	10597648	8.07616558	0.000239461	0.0361322	1.3562011	Myd88	myeloid differentiation primary response gene 88
116	10394392	8.04079745	0.000246693	0.0361322	1.5675456	Nfyc	nuclear transcription factor-Y gamma
117	10518546	8.08223463	0.00023464	0.0361322	1.4625788	Pex14	peroxisomal biogenesis factor 14
118	10474028	8.18041583	0.000222587	0.0361322	1.3965483	Pex16	peroxisomal biogenesis factor 16
119	10497399	-8.0010356	0.000253925	0.0361322	0.6239982	Pde7a	phosphodiesterase 7A
120	10405866	-8.0704692	0.000241068	0.0361322	0.6711832	Gm10139	predicted gene 10139
121	10519096	8.01736251	0.000251515	0.0361322	1.637015	Rer1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)
122	10383194	7.94460511	0.000258747	0.0361322	2.2139404	Rnf213	ring finger protein 213
123	10515733	8.15060698	0.000227408	0.0361322	1.5551542	Szt2	seizure threshold 2
124	10481457	8.08624293	0.000232229	0.0361322	1.4113076	Sh3glb2	SH3-domain GRB2-like endophilin B2
125	10513952	7.93620574	0.000261961	0.0361322	1.4329411	Tmem261	transmembrane protein 261
126	10535231	8.0766318	0.000238658	0.0361322	1.6237844	Ttyh3	tweety homolog 3 (Drosophila)
127	10383200	7.91061816	0.000265979	0.0362427	2.3715297	Rnf213	ring finger protein 213
128	10444068	7.90975163	0.000266782	0.0362427	1.7045197	Tapbp	TAP binding protein
129	10537463	-7.8752621	0.000271604	0.0366742	0.8287651	Agk	acylglycerol kinase
130	10508805	7.86721165	0.000273211	0.0366742	1.594074	Wasf2	WAS protein family, member 2
131	10516393	7.77381781	0.000290889	0.0370526	1.5269343	38200	argonaute RISC catalytic subunit 4
132	10508454	7.77761403	0.000289282	0.0370526	1.5302709	Bsdc1	BSD domain containing 1
133	10517250	7.74682014	0.000294103	0.0370526	3.5753377	Extl1	exostoses (multiple)-like 1
134	10394971	7.76767301	0.000291693	0.0370526	1.2411067	Klf11	Kruppel-like factor 11
135	10507213	7.83387231	0.00028205	0.0370526	1,4404692	Mob3c	MOB kinase activator 3C
136	10383198	7.83773191	0.000279639	0.0370526	2.3641792	Rnf213	ring finger protein 213
137	10516666	7.82626999	0.000283657	0.0370526	1,7493571	Txlna	taxilin alpha
138	10517443	7.81504928	0.000286068	0.0370526	1.4530487	Tceb3	transcription elongation factor B (SIII), polypeptide 3
139	10512766	7.81716856	0.000285264	0.0370526	2,6814182	Trim14	tripartite motif-containing 14
140	10446986	-7.6996746	0.000303746	0.0373202	0.5778747	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)
141	10508182	7.71073216	0.000301336	0.0373202	1.6215104	Psmb2	proteasome (prosome, macropain) subunit, beta type 2
142	10515072	7,70837996	0.000302139	0.0373202	1.5342323	Rnf11	ring finger protein 11
143	10383202	7.69854877	0.00030455	0.0373202	2.2980061	Rnf213	ring finger protein 213
144	10471201	7.66507785	0.000309371	0.0374958	1.3310932	Abl1	c-abl oncogene 1. non-receptor tyrosine kinase
145	10588836	7 65219946	0.000312585	0.0374958	1.5880168	Gmpph	GDP-mannose pyrophosphorylase B
146	10546661	-7 6399143	0.000316603	0.037571	0.5817561	Foxn1	forkhead hox P1
140	10471571	7 63758578	0.000317407	0.037571	1 5060814	Mankan1	mitogen-activated protein kinase associated protein 1
	10516427	7 63637476	0.00031821	0.037571	1 6547352	Ncdn	metrophilip in the second se
148	10385081	-7 6065274	0.000320621	0.0376584	0 7331383	Ann32-ns	acidic (leucine-rich) nuclear phosphoprotein 32 family, pseudogene
148		1.0000214		0.0010004	0.0740400		Clear de lieu de la contra la contra de la c
148 149 150	10524631	7 58271902	0.000331871	0.0379816	287411479		Z-5 Olidoadenviate synthetase-like 1
148 149 150	10503001	7.58271902	0.000331871	0.0379816	2.8740429	Mecr	2-5 oligoadenyiate synthetase-like 1 mitochondrial trans-2-enovi-CoA reductase
148 149 150 151	10503001 10524631 10508686 10584827	7.58271902 7.58806939	0.000331871 0.000328657 0.000327853	0.0379816 0.0379816 0.0379816	2.8740429 1.4666625 0.5190104	Mecr Mpzl2	2-3 oligoadenyiate synthetase-like 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2
148 149 150 151 152 153	10503081 10524631 10508686 10584827 10515337	7.58271902 7.58806939 -7.591761 7.57676547	0.000331871 0.000328657 0.000327853 0.000333478	0.0379816 0.0379816 0.0379816 0.0379816	2.8740429 1.4666625 0.5190104 1.5446351	Mecr Mpzl2 Nasp	2-> oligoadenyiate synthetase-link i mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoanticenic sperm protein (bistone-binding)
148 149 150 151 152 153 154	10524631 10508686 10584827 10515337 10584870	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463	0.000331871 0.000328657 0.000327853 0.000333478 0.000331067	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366	Mecr Mpzl2 Nasp Tmprss13	2-> oligoadenyiate synthetase-line 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13
148 149 150 151 152 153 154 155	10524631 10508686 10584827 10515337 10584870 10517028	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638	0.000331871 0.000328657 0.000327853 0.000333478 0.000333478 0.000331067	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189	Mecr Mpzl2 Nasp Tmprss13 Tmem222	2-5 oligoadenyiate synthetase-like 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222
148 149 150 151 152 153 154 155 156	10524631 10524631 10508686 10584827 10515337 10584870 10517028 10383365	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585	0.000331871 0.000328657 0.000327853 0.000333478 0.000331067 0.00032946	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922	Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hos	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGE-regulated tyrosine kinase substrate
148 149 150 151 152 153 154 155 156 157	10524631 10524631 10508686 10584827 10515337 10584870 10517028 10383365	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593	0.000331871 0.000328657 0.000327853 0.000331871 0.000331871 0.000331877 0.00032946 0.000349549 0.000349549	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452609	Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane proteiase, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B
148 149 150 151 152 153 154 155 156 157 158	10524631 10524631 10508686 10584827 10515337 10584870 10517028 10383365 10518585 10508893	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53624593	0.000331871 0.000328657 0.000327853 0.000331871 0.00033478 0.000331067 0.00032946 0.000349549 0.000349549 0.000345531	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466540	Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrrd1	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane proteinse, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B pardilysin, N-ardinipe dibasic convertase, NRD convertase 1
148 149 150 151 152 153 154 155 156 157 158	10524631 10524631 10584827 1051534870 10517028 10383365 105176885 10518685 10506893 10407372	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53536973 7.53536973	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.000349549 0.000349549 0.000345531 0.000344729	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853274	Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150	2-5 oligoadenyiate synthetase-line 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted opene 5150
148 149 150 151 152 153 154 155 156 157 158 159	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10383365 10518585 10508893 10497372	7.58271902 7.588069399 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53536973 7.53536973 7.53618705 7.53618705	0.000331871 0.000328657 0.000327853 0.000333478 0.000339478 0.00032946 0.000349549 0.000349549 0.000345531 0.000345531	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494	Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Svrsf4	2 - 5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/ardioine-rich splicing factor 4
148 149 150 151 152 153 154 155 156 157 158 159 160 161	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10517028 10517028 10518585 10506893 10497372 10506893	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53624593 7.53618705 7.53150827 7.53387604	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.000349549 0.000349549 0.000345531 0.000345531 0.0003447139 0.000344728	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.353371 1.5164494 1.6360198	Macr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Sic9a1	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardliysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger) member 1
148 149 150 151 152 153 154 155 156 157 158 159 160 161	10524631 10524631 10524631 1051834827 10515337 10584870 10517028 10584870 10517028 10584870 10518585 10506893 10497372 10508697 10508697	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53624593 7.53536973 7.53536973 7.53350827 7.53337694	0.000331871 0.000328657 0.000327853 0.000331067 0.000331067 0.000349549 0.000349549 0.000345531 0.000345531 0.000345531 0.000347139 0.000346335	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198	Macr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 TmemSPa	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protein 232 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A
148 149 150 151 152 153 154 155 156 157 158 159 160 161 162	10524631 10524631 10584827 10515337 10584870 10517028 10518585 10518585 10506893 1049737 10508697 10508860 10517328	7.58271902 7.58806939 7.591761 7.57676547 7.58690638 7.58690638 7.52745585 7.53624593 7.53624593 7.53624593 7.53618705 7.53150827 7.53387694 7.55644818 7.55644818	0.000331871 0.000328657 0.000327853 0.000333478 0.000339478 0.000339478 0.000349549 0.000349549 0.000349549 0.000344531 0.000347139 0.000347139 0.000346335 0.000339103	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198 1.4721908	Macr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A enoulfment and cell motility 1
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148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10517028 10517028 10518585 10506893 10497372 10506897 10506890 10517328 10403842 10515590 10515590	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58690638 7.53624593 7.53618705 7.53618705 7.53150827 7.53387694 7.55644818 7.51510851 7.49803381	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.000349549 0.000349549 0.000349531 0.000345531 0.0003447139 0.000346335 0.00035567 0.00035574	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.8833371 1.5164494 1.6360198 1.4721908 1.4721908 1.2602456 1.5139241 2.6366909	Gash Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Bnf213	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A rion finder protein 213
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1488 1499 1500 1511 1522 1533 154 1555 1566 1577 1588 1599 1600 1611 1622 1633 1644 1656 1666	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10518585 10518585 10518585 10506893 10497372 10508697 10508697 10508697 10508697 10508860 10515590 10383212 10515590	7.58271902 7.58806939 7.591761 7.57676547 7.58497463 7.58690638 7.52745585 7.53624593 7.53624593 7.53624593 7.53618705 7.53150827 7.53387694 7.55644818 7.55150851 7.49803381 7.59047092 7.49863172	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.000349549 0.000349549 0.000349549 0.000345531 0.000345531 0.000347139 0.000346355 0.000356781 0.000356781 0.000355774	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038263 0.0383137 0.0383137 0.0383137	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.3853371 1.5164494 1.6360198 1.4721908 1.2602456 1.5133241 2.6366992 1.2675096	Gash Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atnaf1	2 -> oligoadenyiate synthetase-linke 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial E1 complex assembly factor 1
1488 1499 1500 1511 1522 1533 154 1555 1566 1577 1588 1599 1600 1611 1622 1633 1644 1655 1667 1677	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10517028 10518685 10506893 10497372 10508690 10517328 10403842 10517328 10403842 10515590 10383212 10514896 10507203	7.58271902 7.58806939 -7.591761 7.57676547 7.58437463 7.58437463 7.5274585 7.53624593 7.53536973 7.53536973 7.53536973 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.53150827 7.	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.000349549 0.000349549 0.000345531 0.000345531 0.0003457139 0.000346735 0.000359103 0.000355174 0.000355174 0.000355978 0.000361292	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.0383137 0.0383137 0.0383137	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.3452698 1.3452698 1.3452699 1.3853371 1.5164494 1.6360198 1.2602456 1.5139241 2.6366992 1.2675096 1.6234067 1.4151649	Gash Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atpaf1 Atpaf1	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardliysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial F1 complex assembly factor 1
$\frac{1488}{1499}$	10524631 10524631 10524631 10518387 1051837 10584870 10517028 10517028 10518585 10506893 10497372 10506893 10497372 10508690 10517328 10403842 10517328 10403842 10514896 10507203 10509203	7.58271902 7.58806939 7.591761 7.57676547 7.58437463 7.58690638 7.53624593 7.53536973 7.53618705 7.53150827 7.53387694 7.55310851 7.49803381 7.49803122 7.4887683 7.48187683 7.48162794 7.3646560	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.000349549 0.000349549 0.000349531 0.000345531 0.0003447139 0.0003447139 0.00034531 0.00035671 0.000355677 0.000356778 0.000356779 0.000356798	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.0383137 0.0383137 0.0383137 0.0383137	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198 1.4721908 1.4721908 1.4721908 1.2602456 1.5139241 2.6366992 1.2675096 1.6234067 1.4151643	Gash Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kiffb Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atpaf1 Atpaf1 Dnaih12	2 -5 oligoadenyiate synthetase-linke 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 18 nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial F1 complex assembly factor 1 ATPase type 13A2 Data (Hendth) begingen generation
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$\frac{1488}{1499}$	10524631 10524631 10584827 10515337 10584870 10517028 10518585 10518585 10506893 10497372 10508697 10508697 10508697 10508697 10508860 10517328 10403842 10515590 10383212 10514896 10507203 10509868 1036392 10450069 10507961	7.58271902 7.58806939 7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53536973 7.53548705 7.53150827 7.53387694 7.55644818 7.51510851 7.49803381 7.49863172 7.48187683 7.48162794 7.39417956 7.3944023 7.48142794 7.3944795	0.000331871 0.000328657 0.000327853 0.000333478 0.000333478 0.000339478 0.000339478 0.000349549 0.000349549 0.000345531 0.00034535 0.000347139 0.000346335 0.00035677 0.000355174 0.000355978 0.000355978 0.000361603 0.00036799 0.000361603 0.00037563 0.00037563 0.00037563 0.00037563	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0384651 0.0384651 0.0388078 0.0388078 0.0388078	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198 1.4721908 1.4721908 1.4721908 1.2602456 1.5139241 2.6366992 1.2675096 1.6234067 1.4151643 1.1224096 1.63982329 1.4955282 1.304951 0.5002525	Masin Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kiftb Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atpaf1 Atpaf2 Dnajb12 H2-K2 Mtf1 Ptprj Atpd3	2-5 oligoadenyiate synthetase-linke 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial F1 complex assembly factor 1 ATP ase type 13A2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein tyrosine phosphatase, receptor type, J adducin 3 (comma)
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$\frac{1488}{1499}$	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10517028 10517028 10518685 10506893 10497372 10508680 10517328 10403842 10515590 10383212 10514896 10507203 10509868 10363392 10450069 1050766 10507603	7.58271902 7.58806939 7.591761 7.57676547 7.58437463 7.558069038 7.52745585 7.53624593 7.53618705 7.53618705 7.53150827 7.53387694 7.5564818 7.5564818 7.5564818 7.5564818 7.5564818 7.49803381 7.49803381 7.49863172 7.48187683 7.48187683 7.48187683 7.48187683 7.4941926 7.3944023 7.42213926 -7.371237 7.33850449	0.000331871 0.000328657 0.000327853 0.000331067 0.00032946 0.00032946 0.000349549 0.000345531 0.000345531 0.000345531 0.0003457139 0.000346739 0.000356781 0.000355774 0.000356781 0.000356789 0.000356779 0.00035677 0.000356781 0.00035678 0.00037642 0.00037642 0.00037642 0.000370442 0.000408209	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0384651 0.0384651 0.0384078 0.0388078 0.0388078 0.0388078	2.8749429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198 1.4721908 1.42602456 1.5139241 2.6366992 1.2675096 1.6234067 1.4151643 1.1224096 1.6982329 1.4955282 1.304951 0.5903582 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893 1.4046893	Gash Mecr Mpzl2 Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atpa13a2 Dnajb12 H2-K2 Mtf1 Ptprj Add3 Acase2	2-5 oligoadenyiate synthetase-link 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane proteins 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP asynthase mitochondrial F1 complex assembly factor 1 ATPase type 13A2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein tyrosine phosphatase, receptor type, J adducin 3 (gamma) aldo-keto reductase family 1, member A1 (aldehyde reductase)
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$\frac{1488}{1499}$	10524631 10524631 10524631 10584827 10515337 10584870 10517028 10518585 10518585 10506893 10497372 10508697 10508697 10508697 10508680 10517528 10403842 10515590 10383212 10515590 1053221 10509688 10507203 10507261 10484888 10463911 10515352 10509178	7.58271902 7.58806939 7.591761 7.57676547 7.58437463 7.58690638 7.52745585 7.53624593 7.53624593 7.5356873 7.53618705 7.53150827 7.53564818 7.53150827 7.53644818 7.49803381 7.49803172 7.48162794 7.39450591 7.3944023 7.42213926 -7.317123 7.33850449 7.27408167 7.23930601	0.000331871 0.000328657 0.000328657 0.000328657 0.000331067 0.00033478 0.00033478 0.000349549 0.000349549 0.000349549 0.000344728 0.000344728 0.000344728 0.000344739 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.000356781 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.00037667 0.000367 0.000367 0.000367 0.000367 0.000367 0.00037667 0.00037667 0.000367 0.000367 0.000367 0.000367 0.000367 0.000367 0.0000367 0.000367 0.000367 0.000367 0.0000367 0.00000000000000000000000000000000000	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0388078 0.0388078 0.0388078 0.0388946 0.0388946 0.0388946	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198 1.4721908 1.4721908 1.2602456 1.5139241 2.6366992 1.2675096 1.6234067 1.4151643 1.1224096 1.6982329 1.304951 0.5903582 1.304951 0.5903582 1.4046893 1.9373643 1.9373643	Masin Mecr Masp Tmprss13 Tmem222 Hgs Kiffb Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atpa11 Atp13a2 Dnajb12 H2-K2 Mtf1 Ptprj Add3 Akr1a1 Asap3 37834	2-5 oligoadenyiate synthetase-linke 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 1B nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial F1 complex assembly factor 1 ATPase type 13A2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein tyrosine phosphatase, receptor type, J adducin 3 (gamma) aldo-keto reductase family 1, member A1 (aldehyde reductase) ATPAR HSPA (bomain, ankyrin repeat and PH domain 3 argonaute RISC catalytic subunit 3 ATP and these with the service divide factor a factor f
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$\frac{1488}{1499}$	10524631 10524631 10524631 10524631 10584827 10515337 10584870 10517028 10518585 10518585 10506893 10497372 10508697 10508697 10508697 10508697 10508697 10508697 10508860 10517328 10403842 10515590 10533212 10515590 10533212 10450069 10507203 10507203 10507203 10507203 10507203 10507203 10507203 1055322 10509178 10516348 10476319 10470381 10478799 10542310 1054685 10346303 10487359 1056685 10346333	7.58271902 7.58806939 7.591761 7.57676547 7.58437463 7.58690638 7.53624593 7.53624593 7.53624593 7.53618705 7.53618705 7.53618705 7.53618705 7.53618705 7.5364818 7.53610851 7.49803381 7.51510851 7.49803172 7.48182794 7.39450591 7.39450591 7.3945059 7.3945059 7.3946092 7.29464509 7.29464509 7.3946092 7.3946092 7.3346092 7.3346092 7.3346092 7.3346092 7.3346092 7.334703091 7.33772054 7.33107109 7.29454684	0.000331871 0.000328657 0.000328657 0.000328657 0.000328657 0.000331067 0.00032946 0.000349549 0.000349549 0.00034535 0.000344728 0.000344728 0.000344728 0.000356781 0.000356781 0.000356781 0.000356781 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00035678 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00037687 0.00040788 0.00040778 0.00040778 0.00040778 0.000407578 0.00039659	0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.0379816 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.038266 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.0383137 0.038846 0.0388078 0.0388078 0.0388078 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946 0.0388946	2.8740429 1.4666625 0.5190104 1.5446351 1.7715366 1.4886189 1.0710922 1.8452698 1.6466549 1.3853371 1.5164494 1.6360198 1.4721908 1.4721908 1.4721908 1.4721908 1.4721908 1.4725096 1.6234067 1.4151643 1.1224096 1.63942329 1.4955282 1.304951 0.5903582 1.4046893 1.9373643 1.5564384 1.7082485 1.5300661 1.2515279 0.7075075 1.8700558 0.7542481 1.6221629 1.655257 1.5956261	Basin Mecr Masp Nasp Tmprss13 Tmem222 Hgs Kif1b Nrd1 Gm5150 Srsf4 Slc9a1 Tmem50a Elmo1 Kdm4a Rnf213 Tceanc2 Atpaf1 Atp13a2 Dnajb12 H2-K2 Mtf1 Ptprj Add3 Atpaf1 Cacfd1 Cascf1 Cascf1 Cdsn1b Eif4e3 Hspe1 Itprip11 Miz2 Naaa	2-3 oligoadenyiate synthetase-like 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane proteia 222 HGF-regulated tyrosine kinase substrate kinesin family member 18 nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP seytipes 13A2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein tyrosine phosphatase, receptor type, J adducin 3 (gamma) aldo-keto reductase family 1, member A1 (aldehyde reductase) ATFAS type. SHA2 ATP Synthase mitochondrial F1 complex assembly factor 1 ATPAS type. JAA2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein tyrosine phosphatase, receptor type, J adducin 3 (gamma) aldo-keto reductase family 1, member A1 (aldehyde reductase) ATGAP with SH3 domain, ankyrin repeat and PH domain 3 argonaute RISC catalytic subunit 3 ATP synthase mitochondrial F1 complex assembly factor 1 calcium channel flower domain containing 1 chromosome segregation 1-like (S. cerevisiae) cyclin-dependent kinase inhibitor 1B eukaryotic translation initiation factor 4E member 3 heat shock protein 1 (chaperonin 10) inositol 1,4,5-triphosphate receptor interacting protein-like 1 mesoderm induction early response 1 homolog (Xenopus laevis MX dynami-like GTPase 2 N-acylethanolamine acid amidase
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Dnajb12 H2-K2 Mtf1 Ptprj Add3 Akr1a1 Asag3 37834 Atpaf1 Cacfd1 Cse11 Cdkn1b Elf4e3 Hspe1 Mizer1 Maza Nsua4 <td>2-5 oligoadehylate synthetase-like 1 mitochondrial trans-2-enoyl-CoA reductase myelin protein zero-like 2 nuclear autoantigenic sperm protein (histone-binding) transmembrane protease, serine 13 transmembrane protein 222 HGF-regulated tyrosine kinase substrate kinesin family member 18 nardilysin, N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial F1 complex assembly factor 1 ATPase type 13A2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein 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N-arginine dibasic convertase, NRD convertase 1 predicted gene 5150 serine/arginine-rich splicing factor 4 solute carrier family 9 (sodium/hydrogen exchanger), member 1 transmembrane protein 50A engulfment and cell motility 1 lysine (K)-specific demethylase 4A ring finger protein 213 transcription elongation factor A (SII) N-terminal and central domain containing 2 ATP synthase mitochondrial F1 complex assembly factor 1 ATPase type 13A2 DnaJ (Hsp40) homolog, subfamily B, member 12 histocompatibility 2, K region locus 2 metal response element binding transcription factor 1 protein tyrosine phosphatase, receptor type, J adducin 3 (gamma) aldo-keto reductase family 1, member A1 (aldehyde reductase) ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 argonaute RISC catalytic subunit 3 ATP synthase mitochondrial F1 complex assembly factor 1 calcium channel flower domain containing 1 chromosome segregation 1-like (S. cerevisiae) ocyclin-dependent kinase inhibitor 1B eukaryotic translation 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130	10383206	7.30158214	0.000413834	0.0388946	2.4082888	Rnf213	ring finger protein 213
191	10456717	-7.3253465	0.000404995	0.0388946	0.6627768	Snord58b	small nucleolar RNA. C/D box 58B
192	10544732	-7.3390977	0.00039937	0.0388946	0.5655842	Skap2	src family associated phosphoprotein 2
193	10545720	-7 266206	0.00042428	0.0388946	0.8710797	Stambo	STAM binding protein
194	10509023	7.32919117	0.000401781	0.0388946	1.5343537	Svf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)
195	10506870	7 27551949	0.00042187	0.0388946	1 8639093	Txndc12	thoredoxin domain containing 12 (endoplasmic reticulum)
196	10507677	7 26093249	0.000430709	0.0392993	1 5836706	Hiven3	human immunodeficiency virus type Lenhancer binding protein 3
107	10/82220	7 25411031	0.000433923	0.0302003	1 2804225	Pemh7	naman mining provide sport of the sport of t
108	10516206	7.26002150	0.000433316	0.0302003	1 3026063	Thran3	by role as one (prosone, massopan) subtrini, beta type 7
190	10310290	7.20002139	0.000432310	0.0392993	1.3920003	Thiapo DhyE9	Infriduction for the solution of the solution
199	10391207	7.23032071	0.000439546	0.0393220	2.0930332	DIIX30	DEAT (ASP-Git-A-TIS) box polypeptide 30
200	10462460	7.24170303	0.000437941	0.0393220	1.3930407		metrymaionic aciduna (cobalanni denciency) colo type, with homocystinuna
201	10510982	7.23989351	0.000438745	0.0393226	1.5844681	Pex10	peroxisomal biogenesis factor 10
202	10514398	7.20702469	0.000444369	0.0394532	1.5560658	Caap1	caspase activity and apoptosis inhibitor 1
203	10383214	7.20005445	0.00044678	0.0395117	2.2883236	Rnf213	ring finger protein 213
204	10480121	7.18177982	0.000452405	0.039811	1.6681647	Fam188a	family with sequence similarity 188, member A
205	10507299	7.14887531	0.000457226	0.039811	1.3698646	Gpbp1I1	GC-rich promoter binding protein 1-like 1
206	10566144	7.16075271	0.000455619	0.039811	1.9715863	Trim21	tripartite motif-containing 21
207	10540622	7.14385468	0.000461244	0.0399919	1.2391526	Brpf1	bromodomain and PHD finger containing. 1
208	10420316	-7 1388189	0.000462851	0.0399919	0 8448114	Gm10873	predicted gene 10873
200	10383233	7 13586011	0.000466066	0.040116	2 1978507	Rnf213	ring finger professor
210	10446136	7.0630067	0.000487762	0.040656	0.7015725	Catepord	rang mgor protein 2 ro
210	10455472	7.06762022	0.000407702	0.040656	1 2020216	Don2	
211	10400472	7.00702933	0.000403331	0.040050	1.2039210		DCF2 decapping enzyme homolog (S. cereviside)
212	10508190	7.07828681	0.000483744	0.040656	1.6093811	AU040320	expressed sequence AU040320
213	10506298	7.06915538	0.000484548	0.040656	1.5336105	Leprot	leptin receptor overlapping transcript
214	10383168	7.06606849	0.000486155	0.040656	2.1537995	Rnf213	ring finger protein 213
215	10517243	7.04681387	0.000493387	0.0408228	1.462245	Pdik1I	PDLIM1 interacting kinase 1 like
216	10508619	7.04534527	0.00049419	0.0408228	1.4738906	Pum1	pumilio RNA-binding family member 1
217	10384940	-7.0407375	0.000498208	0.0410045	0.7224565	Erlec1	endoplasmic reticulum lectin 1
218	10385926	6.9910209	0.000512672	0.0413193	1.2345732	Cdc42se2	CDC42 small effector 2
219	10454564	6.97950011	0.00051669	0.0413193	1.2009843	Ercc3	excision repair cross-complementing rodent repair deficiency, complementation group 3
220	10561498	-6.9913392	0.000511065	0.0413193	0.6494816	Papl	iron/zinc purple acid phospatase-like
221	10534324	7.02125369	0.00050544	0.0413193	1.5003519	Limk1	LIM-domain containing, protein kinase
222	10374703	6,99860925	0.000509458	0.0413193	1.3664808	Pnpt1	polyribonucleotide nucleotidyltransferase 1
222	10383152	6 98494453	0.000515083	0.0413103	2 3091519	Rnf213	ring finger protein 213
224	10521667	-6 9051050	0.0005/28222	0.0413449	0 4048866	Bst1	hone marrow stromal cell antigen 1
224	10521007	6 87706670	0.000564680	0.0412440	1 5120000	Ebna1ba2	ERNA1 binding protein 2
220	1000/00/	0.01120012	0.0005644	0.0413448	1.0100009	Epita tupz Eam16062	family with sequence similarity 160, member P2
220	10421394	0.00933043	0.000500041	0.0413440	1.2259659		lamily with sequence similarity 100, member b2
227	10603151	-6.9553233	0.000526333	0.0413448	0.544998	Сртьр	giycoprotein mob
228	10483110	6.92973475	0.000537583	0.0413448	2.8771594	ltih1	Interteron induced with helicase C domain 1
229	10469289	6.89647322	0.000551243	0.0413448	1.8419616	ll15ra	interleukin 15 receptor, alpha chain
230	10492355	-6.9265867	0.000539993	0.0413448	0.1110699	Mme	membrane metallo endopeptidase
231	10406614	-6.9253646	0.0005416	0.0413448	0.6961461	Mtx3	metaxin 3
232	10501909	-6.8678717	0.000564904	0.0413448	0.7805685	Mettl14	methyltransferase like 14
233	10515295	6.94139275	0.000533565	0.0413448	1.9280461	Mast2	microtubule associated serine/threonine kinase 2
234	10354054	6.90968601	0.000548029	0.0413448	1.5353056	Mitd1	MIT, microtubule interacting and transport, domain containing 1
235	10415408	-6.9487368	0.000528743	0.0413448	0.3167655	Nynrin	NYN domain and retroviral integrase containing
236	10516576	6.93968096	0.000535172	0.0413448	1,4246277	Rbbp4	retinoblastoma binding protein 4
237	10508392	6 88760033	0.000555261	0.0413448	1 9594409	Rnf19b	ring finger protein 198
238	10505008	6 88298937	0.000556868	0.0413448	1 4942676	Slc44a1	solute carrier family 44 member 1
239	10443110	-6.9495872	0.00052794	0.0413448	0 7558806	Syngap1	synaptic Ras GIPase activating protein 1 homolog (rat)
240	10508135	6 93181337	0.000535975	0.0413448	1 587252	Trannc3	trafficing protein particle complex 3
240	10466374	6.0268121	0.00053010	0.0413448	1 6062538	TIO	transducin like enhancer of split 4 homolog of Drosophila E(spl)
241	10516950	6.05/12120	0.00053313	0.0413440	1.0002330	Vtbdf2	The domain family 2
040	10010009	0.90412129	0.000527150	0.0413440	1.4307030		
242	40540405		0.000550054	0.0440440	4 400000		
242 243	10516435	6.89106505	0.000553654	0.0413448	1.490989	Z111y1114	
242 243 244	10516435 10401564	6.85977339	0.000553654 0.000569725	0.0413448	1.490989	Arel1	apoptosis resistant E3 ubiquitin protein ligase 1
242 243 244 245	10516435 10401564 10516640	6.89106505 6.85977339 6.83723858	0.000553654 0.000569725 0.000576957	0.0413448 0.0413627 0.0413627	1.490989 1.5040197 1.7914203	Arel1 Eif3i	apoptosis resistant E3 ubiquitin protein ligase 1 eukaryotic translation initiation factor 3, subunit I
242 243 244 245 246	10516435 10401564 10516640 10514466	6.89106505 6.85977339 6.83723858 6.83573131	0.000553654 0.000569725 0.000576957 0.000577761	0.0413448 0.0413627 0.0413627 0.0413627	1.490989 1.5040197 1.7914203 1.5161916	Arel1 Eif3i	apoptosis resistant E3 ubiquitin protein ligase 1 eukaryotic translation initiation factor 3, subunit I jun proto-oncogene
242 243 244 245 246 247	10516435 10401564 10516640 10514466 10415413	6.89106505 6.85977339 6.83723858 6.83573131 -6.843228	0.000553654 0.000569725 0.000576957 0.000577761 0.000573743	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627	1.490989 1.5040197 1.7914203 1.5161916 0.2871578	Arel1 Eif3i Jun Nynrin	apoptosis resistant E3 ubiquitin protein ligase 1 eukaryotic translation initiation factor 3, subunit 1 jun proto-oncogene NYN domain and retroviral integrase containing
242 243 244 245 246 247 248	10516435 10401564 10516640 10514466 10415413 10598279	6.89106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883	0.000553654 0.000569725 0.000576957 0.000577761 0.000573743 0.000617135	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725	Arel1 Eif3i Jun Nynrin Akap4	An iniger, M IN-WEAPE 4 apoptosis resistant E3 ubiquitin protein ligase 1 eukaryotic translation initiation factor 3, subunit I jun proto-oncogene NYN domain and retroviral integrase containing A kinase (PRKA) anchor protein 4
242 243 244 245 246 247 248 249	10516435 10401564 10516640 10514466 10415413 10598279 10494322	6.89106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321	0.000553654 0.000569725 0.000576957 0.000577761 0.000573743 0.000617135 0.000617939	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312	Arel1 Eif3i Jun Nynrin Akap4 Anp32e	A kinase (RKK) and retroviral integrase containing A kinase (RKK) and retroviral integrase (RKK) and RKK) and RKK (RKK) and RKK
242 243 244 245 246 247 248 249 250	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10435676	6.89106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682	0.000553654 0.000569725 0.000576957 0.000577761 0.000573743 0.000617135 0.000617939 0.000605885	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312 0.8541321	Zinyma Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b	A kinase (PRKA) anchor protein 4 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E glycogen synthase kinase 3 beta
242 243 244 245 246 247 248 249 250 251	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10435676 10434719	6.89106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682 -6.7428496	0.000553654 0.000569725 0.000576957 0.000577761 0.000573743 0.000617135 0.000617939 0.000605885 0.000616332	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312 0.8541321 0.889362	Zhiyina Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1	A kinase (PRKA) anchor protein ligase 1 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E glycogen 9 kininogen 1
242 243 244 245 246 247 248 249 250 251 252	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10435676 10434719 10502778	6.89106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682 -6.7428496 -6.7382896	0.000553654 0.000569725 0.000576957 0.000577761 0.000577743 0.000617135 0.000617135 0.000615885 0.000616332 0.000618342	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312 0.8541321 0.889362 0.6622789	Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1 Lphn2	Alic iniger, MTNP-WP 4 apoptosis resistant E3 ubiquitin protein ligase 1 eukaryotic translation initiation factor 3, subunit 1 jun proto-oncogene NYN domain and retroviral integrase containing A kinase (PRKA) anchor protein 4 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E glycogen synthase kinase 3 beta kininogen 1 latrophilin 2
242 243 244 245 246 247 248 249 250 251 252 253	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10436676 10434719 10502778 105247410	6.85977339 6.83723858 6.83723858 6.83723858 6.83273131 -6.843228 -6.7415883 -6.7415883 -6.7405321 -6.7681682 -6.7428496 -6.7382896 -6.744857	0.000553654 0.000569725 0.0005769725 0.000577761 0.000573743 0.000617135 0.000617399 0.00061885 0.000618322 0.000618742 0.000615528	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312 0.8541321 0.859362 0.6622789 0.869534	Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1 Lphn2 Mug1	A kinase (NTN=4ybe 4 apoptosis resistant E3 ubiquitin protein ligase 1 eukaryotic translation initiation factor 3, subunit 1 jun proto-oncogene NYN domain and retroviral integrase containing A kinase (PRKA) anchor protein 4 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E glycogen synthase kinase 3 beta kininogen 1 latrophilin 2 murinoglobulin 1
242 243 244 245 246 247 248 249 250 251 252 253 254	10516435 10401564 10516640 10514466 10415413 10598279 10494322 1043676 10434719 10502778 10541410 10541410	6.83106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682 -6.7428496 -6.7382896 -6.7382897 6.79285744	0.000553654 0.000569725 0.000576957 0.000577761 0.000577743 0.000617135 0.000617399 0.000605885 0.000618742 0.000618742 0.000618528 0.000618528	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 0.2871578 0.9070725 0.7096312 0.8541321 0.859362 0.6622789 0.869534 1.4381887	Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1 Lphn2 Mug1 Sema4d	A kinase (PKKA) and retroviral integrase containing eukaryotic translation initiation factor 3, subunit I jun proto-oncogene NYN domain and retroviral integrase containing A kinase (PRKA) anchor protein 4 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E glycogen synthase kinase 3 beta kininogen 1 latrophilin 2 murinoglobulin 1 sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)
242 243 244 245 246 247 248 249 250 251 252 253 254 255	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10435676 10434719 10502778 10541410 10409240 10367224	6.8370505 6.83723858 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682 -6.7428496 -6.7382896 -6.74857 6.79285744 6.77882373	0.000553654 0.000569725 0.000576957 0.000577761 0.000573743 0.000617135 0.000617352 0.000618322 0.000618322 0.000618528 0.000618528 0.000618528 0.000596243 0.00060026	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.7096312 0.8541321 0.85934 0.6622789 0.869534 1.4381887 3.1443313	Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1 Lphn2 Mug1 Sema4d Stat2	
242 243 244 245 246 247 248 249 250 251 252 253 254 255 256	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10435676 10434719 10502778 10541410 10409240 10367224 10470768	6.83106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7415883 -6.7428496 -6.7382896 -6.74857 6.79285744 6.77882373 6.77043398	0.000553654 0.000569725 0.000576957 0.000577761 0.000577761 0.000617135 0.000617399 0.000618322 0.000618322 0.000618342 0.000618528 0.000596243 0.00060026 0.00060026	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312 0.8541321 0.859342 0.6622789 0.869534 1.4381887 3.1443313	Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1 Lphn2 Mug1 Sema4d Stat2 Um1	
242 243 244 245 246 247 248 250 251 252 253 254 255 256 257	10516435 10401564 10516640 10514466 10415413 10598279 10494322 1043676 10434719 10502778 105541410 10409240 10367224 10470762	6.83106505 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682 -6.7428496 -6.7382896 -6.7428497 6.79285744 6.779285744 6.77043398 6.77043398	0.000553654 0.000569725 0.000576957 0.000577761 0.000577743 0.000617135 0.000617939 0.000605885 0.000616322 0.000616322 0.000616528 0.000615528 0.000603243 0.000603243 0.000603475	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.8541321 0.889362 0.6622789 0.869534 1.4381887 3.1443313 1.3774313 0.2047604	Zhiyimi Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Kng1 Lphn2 Mug1 Sema4d Stat2 Umn1 Unc79	A kinase (PRKA) anchor protein ligase 1 eukaryotic translation initiation factor 3, subunit 1 jun proto-oncogene NYN domain and retroviral integrase containing A kinase (PRKA) anchor protein 4 acidic (leucine-rich) nuclear phosphoprotein 32 family, member E glycogen synthase kinase 3 beta kininogen 1 latrophilin 2 murinoglobulin 1 sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) signal transducer and activator of transcription 2 ubiquitin related modifier 1 homolog (S. cerevisiae) une-79 homolog (C. elegans)
242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258	10516435 10401564 10516640 10514466 10415413 10598279 10494322 10436676 10434719 10502778 10541410 10409240 10367224 10470768 10470768	6.85977339 6.85977339 6.83723858 6.83573131 -6.843228 -6.7415883 -6.7405321 -6.7681682 -6.74857 6.7928574 6.77828574 6.77928574 6.77928574 6.77928574 6.77752024	0.000553654 0.000569725 0.00057761 0.000577761 0.000577743 0.000617135 0.00061735 0.00061532 0.000616332 0.000618742 0.000618742 0.000605843 0.000602643 0.000603475 0.00060164 0.0006034590	0.0413448 0.0413627 0.0413627 0.0413627 0.0413627 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022 0.0419022	1.490989 1.5040197 1.7914203 1.5161916 0.2871578 0.9070725 0.7096312 0.8541321 0.889362 0.6622789 0.869534 1.4381887 1.3774313 0.2047604 1.577322	Zhiyimi Arel1 Eif3i Jun Nynrin Akap4 Anp32e Gsk3b Knq1 Lphn2 Mug1 Sema4d Stat2 Urm1 Unc79 Arfgef2	
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280	10517060	6 5313824	0.000716777	0.043231	1 3341442	Nude	nuclear distribution gene C homolog (Aspergillus)
	10383012	6.52852106	0.00071758	0.043231	1 30/0713	Dae1	hosphatidy/dycerophosphate sufface 1
200	10514070	6 52822400	0.000718384	0.043231	1.6752651	2310067E10Dik	DIVENI CDNA 2310067E19 cone
290	10514070	0.52622409	0.000716364	0.043231	1.07 32031	2010007E19Rik	
291	10502395	-6.5459273	0.000711955	0.043231	0.9146519	4930579F01Rik	RIKEN CDNA 49305/9F01 gene
292	10505064	6.52234142	0.000719991	0.043231	1.5700788	Tmem38b	transmembrane protein 38B
293	10442396	-6.4946214	0.000732044	0.0432925	0.612824	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3
294	10505044	6.49923689	0.000729634	0.0432925	1.5331561	Fktn	fukutin
295	10600504	-6.5006265	0.00072883	0.0432925	0.6534496	Fundc2	FUN14 domain containing 2
296	10505282	6.49225819	0.000733652	0.0432925	1.6431826	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
297	10513195	6 49718835	0.000731241	0.0432925	1 1399376	Txn1	thioredoxin 1
298	10509218	6 49077776	0.000735259	0.0432925	1 5231434	Zfn46	zinc finger protein 46
200	10423134	6 5017562	0.000727223	0.0432025	0.7375132	Zipito	zine finger BNA binding protein
299	10420104	-0.3017302 6.47076055	0.000727223	0.0432925	1.2060442	Zii Dankû	
300	104/020/	0.47070955	0.000746509	0.0433665	1.3209442	Palikz	paniorienaie kinase z
301	10508608	6.47095125	0.000745705	0.0433885	1.5424859	Peti	penta-EF hand domain containing 1
302	10374934	6.47475887	0.000742491	0.0433885	1.346326	Psme4	proteasome (prosome, macropain) activator subunit 4
303	10515698	6.47313404	0.000744098	0.0433885	1.3804444	Szt2	seizure threshold 2
304	10501608	6.47365502	0.000743294	0.0433885	1.8144491	Vcam1	vascular cell adhesion molecule 1
305	10442625	6.46555572	0.000752937	0.0436306	1.4982142	Igfals	insulin-like growth factor binding protein, acid labile subunit
306	10441601	6.46381967	0.000754544	0.0436306	1.7252397	Tagap	T cell activation Rho GTPase activating protein
307	10605571	-6.4469756	0.00076258	0.0437587	0.5665126	Gvk	alvcerol kinase
308	10428192	-6.4514024	0.000760169	0.0437587	0.7470607	Pabpc1	poly(A) binding protein, cytoplasmic 1
309	10490632	6 43536843	0.000765794	0.0437631	2 3433827	Helz2	belicase with zinc finger 2 transcriptional coactivator
310	10518113	6 42859443	0.000770615	0.0437631	1 6720880	Kazn	kazrin perinjakin interacting protein
311	10460036	-6 421173	0.000775437	0.0437631	0.7550302	Nrarn	Notch-regulated ankyrin repeat protein
212	10403530	6 42272926	0.000769205	0.0437631	1.0957949	Olfr1040	Alforder regulated anyth repeat potent
312	10404077	0.43272020	0.000708203	0.0437031	1.0007040	Ulli 1049	Silactory receptor 1049
313	10404187	-0.4229504	0.000774633	0.043/631	0.0310103		tyrosyr-brivk priosprioulesterase z
314	10589596	6.40614346	0.000782669	0.043842	1.1845861		colled-coll domain containing 12
315	10597564	-6.4044267	0.000783472	0.043842	0.7707576	Cmc1	COX assembly mitochondrial protein 1
316	10518857	6.3934133	0.000785883	0.043868	1.2542564	Zbtb48	zinc finger and BTB domain containing 48
317	10471953	6.38161852	0.000793115	0.0439465	1.3236552	Acvr2a	activin receptor IIA
318	10487871	6.36215257	0.000805169	0.0439465	1.383565	Cenpb	centromere protein B
319	10442870	-6.3732311	0.000799544	0.0439465	0.9207504	Ccdc78	coiled-coil domain containing 78
320	10355152	-6.3742177	0.000797936	0.0439465	0.6453239	Fzd5	frizzled homolog 5 (Drosophila)
321	10488879	6.36079827	0.000806776	0.0439465	1.5048914	Gss	dutathione synthetase
322	10506004	6.37804457	0.000706320	0.0430465	1 4760050	Hook1	hook homolog 1 (Drosophila)
300	10276022	6 2057404	0.000700240	0.0420465	0.8260590	Kif3a	kinesin familu member 3A
323	10376033	-0.303/124	0.000792312	0.0439405	0.0209589		
324	10480921	0.3/02/6	0.000801151	0.0439405	1.4340046		quiesun go suntyutyi oxidase z
325	10586064	-0.35/4494	0.000810793	0.043953	0.7879897	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
326	10516678	6.35754666	0.000809186	0.043953	1.5789803	Kpna6	karyopherin (importin) alpha 6
327	10498345	6.35070375	0.000814008	0.0439595	1.154839	Gpr171	G protein-coupled receptor 171
328	10495854	-6.3489198	0.000814811	0.0439595	0.2955719	Prss12	protease, serine 12 neurotrypsin (motopsin)
329	10478778	6.32527887	0.000831686	0.0442161	1.6382598	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
330	10454369	-6.3247996	0.00083249	0.0442161	0.5082382	Fhod3	formin homology 2 domain containing 3
331	10373313	-6.3276709	0.000829275	0.0442161	0.5027652	Nab2	Nafi-A binding protein 2
332	10383210	6 32691577	0.000830079	0.0442161	2 4807145	Rnf213	ring finger protein 213
333	10516551	6 3230684	0.000833203	0.0442161	1 3301554	S100php	S100P binding protein
224	10210331	6.3230004	0.000033233	0.0442101	1.0091004	Orfod2	a coordinating protein
334	10394062	0.30773700	0.000643739	0.0443244	1.4077001	Oglous	2-oxogiutatate and inon-dependent oxygenase domain containing 5
335	10507190	6.28709828	0.000854186	0.0443244	1.6198813	Efcab14	EF-hand calcium binding domain 14
336	10587284	-6.296517	0.000850972	0.0443244	0.4961895	EIOVI5	ELOVE family member 5, elongation of long chain fatty acids (yeast)
337	10495685	-6.3009038	0.000848561	0.0443244	0.6847547	Arhgap29	Rho GTPase activating protein 29
338	10490225	6.28671352	0.000854989	0.0443244	1.5063731	Slmo2	slowmo homolog 2 (Drosophila)
339	10443080	-6.28985	0.000853382	0.0443244	0.7975485	Syngap1	synaptic Ras GTPase activating protein 1 homolog (rat)
340	10519007	6.30193121	0.000846954	0.0443244	1.7072276	Tprgl	transformation related protein 63 regulated like
341	10457489	-6.316974	0.000837311	0.0443244	0.8651114	Tmem241	transmembrane protein 241
342	10348889	-6 277925	0.000862221	0.0443932	0 7371807	D2hadh	D-2-hydroxyglutarate dehydrogenase
343	10516994	6 28016431	0.000861418	0.0443932	1 3651775	Fam76a	family with sequence similarity 76 member A
344	10514884	6 28251606	0.000860614	0.0443032	1 527638	Mrpl37	mitochondrial ribosomal protein L 37
345	10524588	6.27061050	0.000867043	0.0444014	1 3/30753	Ankrd13a	ankurin reneat domain 13a
246	10509711	6.26129016	0.0000070669	0.0444220	1.0400700	Tof12	TAE12 DNA notworked II TATA box binding protein (TPD) approvided factor
247	10460495	6.25000426	0.000072000	0.0444233	1.4010323	TdHZ Zdhbo24	The figure DHC domain containing 24
347	10400400	0.25009430	0.0006799	0.0440912	1.1022471	ZUNNCZ4	zinc inger, DHHC domain containing 24
348	10514054	0.2413/806	0.000005505		1 184074	INFID	nuclear factor I/D
-4/10	10488697		0.000885525	0.0446756	4 4000707	Dia - 10	nuclear factor I/B
043	4054555	0.22040084	0.000885525	0.0452025	1.1698725	Plagl2	nuclear factor I/B pleiomorphic adenoma gene-like 2
350	10515739	6.22893858	0.000885525 0.000899989 0.000898382	0.0452025	1.1698725	Plagl2 Szt2	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2
350 351	10515739 10509246	6.22893858 6.22492771	0.000885525 0.000899989 0.000898382 0.000902399	0.0448738 0.0452025 0.0452025 0.0452228	1.1698725 1.3381465 1.5077833	Plagl2 Szt2 Luzp1	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1
350 351 352	10515739 10509246 10372488	6.22893858 6.22492771 6.21965366	0.000885525 0.000899989 0.000898382 0.000902399 0.000907221	0.0448738 0.0452025 0.0452025 0.0452228 0.0453637	1.1698725 1.3381465 1.5077833 1.1967262	Plagl2 Szt2 Luzp1 Tmem19	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19
350 351 352 353	10515739 10509246 10372488 10543551	6.22646684 6.22893858 6.22492771 6.21965366 6.20761498	0.000885525 0.000899989 0.000898382 0.000902399 0.000907221 0.000916864	0.0448736 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161	Plagl2 Szt2 Luzp1 Tmem19 Rbm28	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28
350 351 352 353 354	10515739 10509246 10372488 10543551 10450145	6.22646684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546	0.000885525 0.000899989 0.000898382 0.000902399 0.000907221 0.000916864 0.000919274	0.0448738 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0456626	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)
350 351 352 353 354 355	10515739 10509246 10372488 10543551 10450145 10518473	6.22646664 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223	0.000885525 0.000899989 0.000898382 0.000902399 0.000907221 0.000918864 0.000919274 0.000923292	0.0448736 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0456626 0.0457614	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567	Plagl2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbx06	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6
350 351 352 353 354 355 356	10515739 10509246 10372488 10543551 10450145 10518473 10542317	6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1799948	0.000885525 0.000899889 0.0009983822 0.000907221 0.000907221 0.000916864 0.000912274 0.000923292 0.000934542	0.0448736 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0456626 0.0457614 0.0459127	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599	Plagl2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B
350 351 352 353 354 355 356 357	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770	6.228408858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1799948 -6.1793264	0.000885525 0.000899899 0.000898382 0.000902399 0.000907221 0.000916864 0.000919274 0.000918274 0.000934542 0.000936953	0.0448736 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0456626 0.0457614 0.0459127 0.0459127	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357
354 350 351 352 353 354 355 356 357 358	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872	6.22840884 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1799948 -6.1793264 -6.1818048	0.000885525 0.00089989 0.000898382 0.000902399 0.000907221 0.000918664 0.000919274 0.000932292 0.000934542 0.00093653 0.000930524	0.0445938 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0456626 0.0457614 0.0459127 0.0459127	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene
354 350 351 352 353 354 355 356 357 358 359	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10531199	0.22040084 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1799948 -6.1799948 -6.1793264 -6.1818048 -6.1748807	0.000885525 0.00089989 0.000898382 0.000902399 0.000907221 0.00091274 0.000919274 0.000934542 0.000934542 0.000930524 0.000930524	0.0448736 0.0452025 0.0452025 0.0452025 0.0452628 0.0453637 0.0456626 0.0457614 0.0459127 0.0459127 0.0459127	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.9562617 0.9562617 0.8969244 0.5790358	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik	nuclear factor I/B plejomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene
354 350 351 352 353 354 355 356 357 358 359 360	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10531199 10543306	0.22040634 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1799948 -6.1793264 -6.1818048 -6.1748807 -6.1716344	0.000885525 0.00089989 0.0008998989 0.000902399 0.000907221 0.000918864 0.000918274 0.000932292 0.000934542 0.00093653 0.000930524 0.000930524 0.000941774 0.000944185	0.0452025 0.0452025 0.0452025 0.0452025 0.0453637 0.0456626 0.0457614 0.0456626 0.0457614 0.0459127 0.0459127 0.0459702 0.0459702	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 0.529348	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12
354 350 351 352 353 354 355 356 355 356 357 358 359 360 361	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10531199 10543306	6.22404684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1748807 -6.1716344 6.16235519	0.000885525 0.00089989 0.000898382 0.000902399 0.000907221 0.000912274 0.000912274 0.000932292 0.000934542 0.00093454 0.000930524 0.000930524 0.000941774 0.000941774	0.0448736 0.0452025 0.0452025 0.0452025 0.0452025 0.0453637 0.0456626 0.0457614 0.0459626 0.04557614 0.0459127 0.0459127 0.0459127 0.0459833 0.0460845	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain famity. member 9
3543 350 351 352 353 354 355 356 357 358 359 360 361 362	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10573128	6.22446684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1818048 -6.1748807 -6.1716344 6.16235219 6.1551004	0.000885525 0.00089989 0.0008998989 0.000902399 0.000902399 0.000912274 0.000919274 0.000919274 0.000934542 0.000934542 0.000934542 0.000930524 0.000941774 0.000941774 0.000944185 0.000948202	0.04436736 0.0452025 0.0452025 0.0452025 0.0456434 0.0456634 0.0456636 0.0457614 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459702 0.0459883 0.0460845	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.9562617 0.9562617 0.8969244 0.5790358 0.529348 1.9519451	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cope	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxyneptidase E
354 350 351 352 353 354 355 356 357 358 359 360 361 362 362	10515739 10509246 10372488 10543551 10450145 1054873 10542317 10471770 10574872 10574872 10574872 10574874 10574892 105743306	6.22446684 6.22893858 6.22493858 6.20761498 6.20183546 6.19545223 -6.1799948 -6.1793264 -6.1716344 6.16235219 -6.1551994	0.000885525 0.00089989 0.0008998989 0.000902399 0.000907221 0.000918864 0.000919274 0.00093692 0.00093653 0.00093653 0.00093653 0.000936542 0.0009484202 0.000944185 0.000944185	0.04450736 0.0452025 0.0452025 0.0452025 0.0452228 0.0453637 0.0456626 0.0457614 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459883 0.0460845 0.0461552	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.5953599 0.9562617 0.8969244 0.5790358 1.9519451 0.1094794 1.4066127	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 0130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1
354 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364	10515739 10509246 10372488 10543551 10450145 10542317 10471770 10574872 10531199 10543306 10573128 10578904 10480652 10578904	0.22446684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793244 -6.1818048 -6.1793264 -6.1716344 -6.1716344 -6.17235219 -6.1551994 6.14513589	0.000885525 0.00089989 0.0008998989 0.000898382 0.000907221 0.00091884 0.000912274 0.000932522 0.000934542 0.00093653 0.000930524 0.000930524 0.000941774 0.000944185 0.000948202 0.000958424	0.04436736 0.0452025 0.0452025 0.0452025 0.045228 0.0453637 0.0456634 0.0456636 0.0457614 0.0459127 0.0459127 0.0459127 0.0459127 0.0459783 0.0460845 0.0461552 0.0461552	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.4060127 1.660027	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Prace	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 120050E23 gene tetraspanin 12 TBC1 domain famity, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C
354 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 364	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10573128 10578904 10480652 10507894	0.22046684 6.2293858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1716344 6.16235219 6.1551994 6.14513589 6.1551994	0.000885525 0.00089989 0.0008998989 0.000898382 0.000902399 0.00091221 0.000912274 0.000912274 0.000935242 0.000934542 0.000934542 0.000941774 0.000941774 0.000941774 0.0009418202 0.000957845 0.000957845	0.04436736 0.0452025 0.0452025 0.0452025 0.0456434 0.0456634 0.0456634 0.0456634 0.04556127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459125 0.0461552 0.0461552	1.1698725 1.3081465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.4060127 1.6360037	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdbb	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C suscinate debydrogeneae complex_evitural P_iron suffar (In)
3543 3551 3552 3553 3554 3555 3556 3557 3558 3559 3600 3611 3622 3631 3642 3633 3644 3655	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10573128 1057894 10507894 10509858	6.22446684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 6.1793264 -6.1793264 -6.1716344 6.16235219 -6.1551994 6.14513589 6.15500591 6.15500591	0.000885525 0.00089989 0.0008998989 0.000902399 0.000907221 0.000918864 0.000919274 0.000918274 0.00093653 0.00093653 0.00093653 0.00094774 0.00094775 0.00094775 0.00095823 0.000958434 0.000956238	0.04450736 0.0452025 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0456626 0.0457614 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459883 0.0460845 0.0461552 0.0461552	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 1.9519451 0.1094794 1.4060127 1.6360037 1.7201131 0.206022	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (lp)
343 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 364 365 364 365 364 365	10515739 10509246 10372488 10543551 10450145 10518473 10542317 10471770 10574872 10574872 10574872 10574872 10574872 10574874 10578904 10573128 10578904 10509858 10456411	0.22446684 6.2293858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793244 -6.1818048 -6.1793264 -6.1716344 -6.1716344 6.16235219 -6.1551994 6.1551994 6.15086711 -6.15200591 -6.1429868	0.000885525 0.00089989 0.000898382 0.000902399 0.00091221 0.00091884 0.000912274 0.00093252 0.000934542 0.00093653 0.000930524 0.000941774 0.000944175 0.000948202 0.000957845 0.000955834 0.000955834 0.000955834	0.04446736 0.0452025 0.0452025 0.0452025 0.045228 0.0453637 0.0456634 0.0456634 0.0455612 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.045983 0.0460845 0.0461552 0.0461552 0.0461552	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562517 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.6360037 1.7201131 0.3193604	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (Ip) NYN domain and retroviral integrase containing
3543 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 366 366 366	10515739 10509246 10372488 10543551 104450145 10518473 10542317 10471770 10574872 10531199 10543306 10573128 10578904 10480652 10507894 10480652 10507894	0.220406034 6.2293858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1818048 -6.1716344 6.16235219 6.1551994 6.14513589 6.15086711 6.15000591 -6.1429868 6.1306699	0.000885525 0.00089989 0.000898382 0.000902399 0.000902399 0.00091221 0.000912274 0.000932292 0.000934542 0.00093653 0.00093653 0.000930524 0.000941774 0.000941774 0.000941774 0.000957845 0.000957845 0.000955843 0.00095638 0.000961059 0.000971506	0.04450735 0.0452025 0.0452025 0.0452025 0.045228 0.0456434 0.0456634 0.0456636 0.0457614 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459125 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552	1.1698725 1.3081465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 1.05790358 0.529348 1.9519451 0.1094794 1.4060127 1.7201131 0.3193604 1.2415719	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cryclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (lp) NYN domain and retroviral integrase containing regulator of G-protein signaling 3
350 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 365 366 367 368	10515739 10509246 10372488 10543651 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10573128 1057894 1057894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057894 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 1057897 10507894 10507894 10507894 10507897 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 105078	6.22496684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1799948 -6.1793264 -6.1818048 -6.1718344 6.16235219 -6.1551994 6.1551994 6.1551994 6.1551994 6.1551994 6.1551994 6.1500591 -6.1529868 6.1306699 6.12571014	0.000885525 0.00089989 0.0008998989 0.000902399 0.000907221 0.000918864 0.000919274 0.000918274 0.00093653 0.00093653 0.00093653 0.000945424 0.000944185 0.000944185 0.00095434 0.000957845 0.000956238 0.000956238 0.000951596 0.000971506 0.000977934	0.04450736 0.0452025 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.04559127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459883 0.0460845 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.5953599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.4060127 1.6360037 1.7201131 0.3193604 1.2415719 1.96199	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3 Rps6ka1	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (lp) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1
353 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 366 366 366 366 366 366 366 366	10515739 10509246 10372488 10543551 10450145 10542317 10471770 10574872 10574872 10574872 10574872 10574872 10574872 10574874 10574874 10573128 10573128 10577894 10509858 10415411 10505326 10517116 10517716	0.22046684 6.2293858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1793264 -6.1716344 -6.1716344 -6.1551994 6.1551994 6.1551994 6.15086711 -6.1500591 -6.1429868 6.1306699 -6.12571014 6.13061409	0.000885525 0.00089989 0.000898382 0.000902399 0.000912214 0.000918274 0.000912274 0.00093524 0.00093553 0.000930524 0.000930524 0.000941774 0.000941774 0.000958434 0.000957845 0.000956338 0.00095634 0.00095634 0.000957845 0.000957845 0.000957845 0.000957835 0.000977934 0.000977934	0.0446736 0.0452025 0.0452025 0.0452025 0.0452238 0.04556434 0.0456634 0.04556434 0.04559127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459883 0.0460845 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552 0.0463101 0.0463101	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.4060127 1.6360037 1.7201131 0.3193604 1.2597174	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3 Rps6ka1 Slc35d2	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 0130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (Ip) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1 solute carrier family 35, member D2
353 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 366 367 368 369 370	10515739 10509246 10372488 10643651 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10578904 10578904 10509858 10507894 10415411 10509326 10517116 10410078 10510391	0.22446684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1818048 -6.1716344 6.16235219 6.1551994 6.14513589 6.15086711 6.1429868 6.1306699 6.13271014	0.000885525 0.00089989 0.0008998989 0.000898382 0.000907221 0.000912274 0.000912274 0.000932292 0.000934542 0.00093653 0.00093653 0.00093653 0.000958434 0.000957845 0.000956238 0.000956238 0.000971506 0.000971506 0.000971506	0.04450130 0.0452025 0.0452025 0.0452025 0.0452225 0.0452225 0.0452225 0.0452225 0.0452225 0.0452225 0.0452227 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459702 0.04639702 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552	1.1698725 1.308725 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.4060127 1.7201131 0.3193604 1.2415719 1.2597174 1.7102531	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3 Rps6ka1 Slc35d2 Srm	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (lp) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1 solute carrier family 35, member D2 spermidine synthase
353 350 351 352 353 354 355 356 355 356 357 358 359 360 361 362 363 364 365 366 366 366 366 367 368 369 370 370	10515739 10509246 10372488 10643651 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10573128 1057894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10578978 10507897 10507897 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 10507894 1050784 1050784 1050784 1050784 1050784 1050784 1	6.22046684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1818048 -6.1748807 -6.1716344 6.16235219 6.1551994 6.14513589 6.15086711 6.1500591 -6.1429868 6.13006599 6.12571014 6.13478113 6.12267305	0.000885525 0.00089989 0.0008998989 0.000902399 0.000907221 0.000918864 0.000919274 0.000918274 0.00093653 0.00093653 0.00093653 0.0009365434 0.00095474 0.000957845 0.000957845 0.000957845 0.000957845 0.000957845 0.000957845 0.000957845 0.000957845 0.000957845 0.000957845 0.00097734 0.00097734 0.00097734 0.00097738	0.04450736 0.0452025 0.0452025 0.0452025 0.0452228 0.0453637 0.0456434 0.0455626 0.0457614 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.045152 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552 0.0463101 0.0463101 0.0463101	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.5953599 0.9562617 0.8969244 0.5790358 0.529348 1.9519451 0.1094794 1.4060127 1.6360037 1.7201131 0.3193604 1.2415719 1.96199 1.2597174 1.7102531 3.573465	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3 Rps6ka1 Slc35d2 Srm Tap1 	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (lp) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1 solute carrier family 35, member D2 spermidine synthase transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
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350 350 351 352 353 354 355 356 355 356 355 356 355 356 355 356 360 361 362 363 364 365 366 366 366 366 366 366 366 366 367 370 371 372 373 374 375	10515739 10509246 10372488 10543551 10450145 1054873 10542317 10471770 10574872 10574872 10574872 10574872 10574872 1057484 1057489 1057484 10509858 10415411 10505326 10517316 1051739 10514255	0.22040684 6.2293858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1818048 -6.1793264 -6.1716344 -6.1716344 -6.1716344 -6.1551994 6.1551994 6.1551994 6.1551994 6.15086711 6.1500591 -6.1429868 6.1306699 6.1306490 6.13071014 6.13041409 6.13478113 6.12267305 -6.1345311 6.09883174 6.109823174	0.000885525 0.00089989 0.00089989 0.000898382 0.000902399 0.000912274 0.000912274 0.000912274 0.000930524 0.000930524 0.000930524 0.000930524 0.000930524 0.000941774 0.000941759 0.000956334 0.000956334 0.000956334 0.00095634 0.000957845 0.000957845 0.000977384 0.000977384 0.000977384 0.000977384 0.000967838 0.0009648291 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.00096486 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.0009646 0.000966 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.000096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.00096 0.000096 0.000096 0.0000000000	0.04436736 0.0452025 0.0452025 0.0452025 0.0452263 0.04556434 0.04556434 0.04556434 0.04559127 0.04559127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0465922 0.0461552 0.0461552 0.0461552 0.0461552 0.0461552 0.0463101 0.0463101 0.0463101 0.0463101 0.0463101 0.0463101	1.1698725 1.3381465 1.5077833 1.1967262 1.1236161 3.4009238 1.456567 0.5953599 0.9562617 0.8969244 0.5790358 1.9519451 0.1094794 1.4060127 1.6360037 1.7201131 0.3193604 1.2415719 1.2597174 1.7102531 3.573465 0.7040215 1.6832344 1.505685	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3 Rps6ka1 Slc35d2 Srm Tap1 Tspyl2 Adar Dennd4c Milt3	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 0130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (Ip) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1 solute carrier family 35, member D2 spermidine synthase transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) TSPV-like 2 adenosine deaminase, RNA-specific DENN/MADD domain containing 4C mveloid/Winphold or mixed-lineage leukemia (trithoray homolog, Dresonhila)
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protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B olfactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA 130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (lp) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1 solute carrier family 35, member D2 spermidine synthase transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) TSPV-like 2 adenosine deaminase, RNA-specific DENN/MADD domain containing 4C mveloid/lymphold or mixed-lineage leukemia (trithorax homolog, Drosophila) SPARC related modular calcium binding 2 synaptogyrin 1 alveolar soft part sarcoma chromosome region, candidate 1 (human) elaC homolog 2 (E. coli) eukaryotic translation initiation factor 4 gamma, 3 isoprenylcysteine carboxyl methyltransferase mitochondrial fission regulator 1-like nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 interacting protein
343 350 351 352 353 353 353 354 355 356 357 358 357 358 357 358 357 358 369 360 361 362 363 364 365 366 366 366 366 366 366 370 371 372 373 374 377 378 377 377 378 377 378 380 381 382 383 384	10515739 10509246 10372488 10643651 10450145 10518473 10542317 10471770 10574872 10531199 10543306 10578904 10578904 10578904 10578904 10578904 10578904 10578904 10507894 10507894 10517216 1051725 10605749 10517253 10605749 10517253 10383456 10517263 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 10517768 105177768 105177768 105177777777777777777777777777777777777	0.22404684 6.22893858 6.22492771 6.21965366 6.20761498 6.20183546 6.19545223 -6.1793264 -6.1793264 -6.1818048 -6.1718344 -6.1718344 -6.1718344 -6.172184807 -6.1551994 6.16235219 -6.1551994 6.14513589 6.12571014 6.1306699 6.12571014 6.13478113 6.1267305 -6.145311 6.09883174 6.1092879 -6.1145977 6.06880422 6.06128469 6.080519 6.06012635 5.06664741 6.05787685	0.000885525 0.00089989 0.0008998989 0.000898382 0.000902399 0.00091221 0.000912274 0.000912274 0.00093524 0.00093524 0.00093653 0.000930524 0.000930524 0.00093653 0.000941274 0.000941274 0.000958434 0.000956338 0.000956338 0.000956338 0.000956338 0.000956338 0.00095634 0.000957845 0.000957845 0.000957845 0.000971506 0.000971506 0.000971506 0.00097488 0.000961059 0.000961059 0.000961059 0.00096165 0.00098291 0.00096238 0.000986391 0.000986391 0.000986391 0.0009963166 0.0010924541 0.001024541 0.001024541 0.001026148 0.001026148 0.001026148 0.001026148	0.04450736 0.0452025 0.0452025 0.0452025 0.0452025 0.0452025 0.0452025 0.0452025 0.0452025 0.0452025 0.0452025 0.0452027 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0459127 0.0465120 0.0461552 0.0461552 0.0461552 0.0461552 0.04661552 0.0463101 0.0463101 0.0463101 0.0463101 0.0463101 0.0463101 0.0463101 0.0464266 0.0464266 0.0464266 0.0466289 0.0466289 0.0466289 0.0466289	1.1698725 1.3381465 1.3077833 1.967262 1.1236161 3.4009238 1.456567 0.593599 0.9562617 0.8969244 1.65690358 0.529348 1.9519451 0.1094794 1.4060127 1.6360037 1.7201131 3.573465 0.7040215 1.7102531 3.573465 1.7535813 2.1850513 2.1850513 1.7830632 1.4460316 1.5641282 1.2815409 1.5401294	Plagi2 Szt2 Luzp1 Tmem19 Rbm28 Psmb9 Fbxo6 Cdkn1b Olfr357 4933405L10Rik D130050E23Rik Tspan12 Tbc1d9 Cpe Ndor1 Rragc Sdhb Nynrin Rgs3 Rps6ka1 Slc35d2 Srm Tap1 Tspyl2 Adar Dennd4c Mili3 Smoc2 Syngr1 Aspscr1 Elac2 Elri4g3 Icmt Mtfr11 Nfac2ip Nfyc	nuclear factor I/B pleiomorphic adenoma gene-like 2 seizure threshold 2 leucine zipper protein 1 transmembrane protein 19 RNA binding motif protein 28 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) F-box protein 6 cyclin-dependent kinase inhibitor 1B offactory receptor 357 RIKEN cDNA 4933405L10 gene RIKEN cDNA 4933405L10 gene RIKEN cDNA D130050E23 gene tetraspanin 12 TBC1 domain family, member 9 carboxypeptidase E NADPH dependent diflavin oxidoreductase 1 Ras-related GTP binding C succinate dehydrogenase complex, subunit B, iron sulfur (Ip) NYN domain and retroviral integrase containing regulator of G-protein signaling 3 ribosomal protein S6 kinase polypeptide 1 solute carrier family 35, member D2 spermidine synthase transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) TSPY-like 2 adenosine deaminase, RNA-specific DENN/MADD domain containing 4C myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) SPARC related modular calcium binding 2 synaptogyrin 1 alveolar soft part sarcoma chromosome region, candidate 1 (human) elaC homolog 2 (E. coli) eukaryotic translation initiation factor 4 gamma, 3 isoprenylcysteine carboxyl methyltransferase mitochondrial fission regulator 1-like nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 interacting protein nuclear transcription factor-Y gamma

000	40540405	0.00000504	0.004000054	0.0400000	4 5000005	011	
380	10519105	6.06000524	0.001026951	0.0466289	1.5030805	SKI	ski sarcoma virai oncogene nomolog (avian)
387	10537428	6.0553809	0.001034184	0.0466444	1.3799677	Rab19	RAB19, member RAS oncogene family
388	10416566	6.04812321	0.001040612	0.0468195	2.2998566	Epsti1	epithelial stromal interaction 1 (breast)
389	10505172	6 01061969	0.00106954	0.0472932	1 5916766	Dnaic25	Dna.l (Hsp40) homolog, subfamily C, member 25
300	10506170	6.01037085	0.001062308	0.0472032	1 472503	Efcab7	EE hand calcium hinding domain 7
201	10500110	0.01001000	0.001002300	0.0472002	4 0007000	Detd	En - hand gradetin this returned to
391	10507764	0.01320349	0.001000737	0.0472932	1.3037923	Ppli	painitoy-protein thoesterase 1
392	10514405	6.01891334	0.001063915	0.0472932	1.7995666	Plaa	phospholipase A2, activating protein
393	10452639	6.00366553	0.001076772	0.0473618	1.1987415	Myl12b	myosin, light chain 12B, regulatory
394	10505000	6.00058455	0.001081594	0.0473618	1.612446	Nipsnap3b	nipsnap homolog 3B (C. elegans)
395	10515688	6 00540222	0.001075165	0.0473618	1 3680778	Szt2	seizure threshold 2
306	10404380	5 00178633	0.001091236	0.0474904	1 2510003	Duen22	dual specificity phosphatase 22
207	10404000	5.00000054	0.001007265	0.0474004	1.2010000	Manhal	dual specificace bate A basecard like
397	10477900	5.90033051	0.001097665	0.0474904	1.2009092		marinosidase, bela A, iysosomal-like
398	10511007	5.99173464	0.00109204	0.0474904	1.3885787	2610002J02Rik	RIKEN cDNA 2610002J02 gene
399	10541089	5.98601433	0.001099272	0.0474904	1.4062414	2900097C17Rik	RIKEN cDNA 2900097C17 gene
400	10368101	5.97459633	0.001109718	0.0475558	1.4275995	Arfgef3	ARFGEF family member 3
401	10518069	5.96239485	0.0011282	0.0475558	1.6402824	Efhd2	EF hand domain containing 2
402	10383409	5 9729575	0.001110522	0.0475558	1 1730418	Gcar	
403	10506058	5.0646664	0.001123370	0.0475558	1 //22/31	Inadi	JaaD like (Drosphile)
403	10500056	5.9040004	0.001123379	0.0475556	1.4422431		
404	10507933	5.97035264	0.001115343	0.0475558	1.5747587	Inpp5b	Inositol polyphosphate-5-phosphatase B
405	10508036	5.96357105	0.001125789	0.0475558	1.3146205	Snip1	Smad nuclear interacting protein 1
406	10518774	5.9530116	0.001133825	0.0476149	1.3869134	Park7	Parkinson disease (autosomal recessive, early onset) 7
407	10383208	5.95828267	0.001132218	0.0476149	2.4464676	Rnf213	ring finger protein 213
408	10513082	5 9488473	0.00113945	0.0477622	1 266881	Tmem245	ransmembrane protein 245
400	10516371	5 03122460	0.001157032	0.0470702	1 5568556	3710/	argonauta PICC establistic subunit 1
403	10510571	5.93122403	0.001107932	0.0479702	1.0000000	0-10	
410	10010/12	0.924008/4	0.001101146	0.04/9/02	1.0311245		SCILUIC UNCONUU Z
411	10346191	5.92273693	0.001162753	0.0479702	2.6232112	SIATI	signal transducer and activator of transcription 1
412	10515994	5.93270396	0.001157128	0.0479702	1.4199182	Smap2	small ArtGAP 2
413	10515385	5.92945374	0.001159539	0.0479702	1.5940317	Urod	uroporphyrinogen decarboxylase
414	10514319	5,91102846	0.0011732	0.0480167	1.2212035	Kihi9	kelch-like 9
415	10373629	5 91430714	0.001160085	0.0480167	1 0703475	Olfr798	olfactory receptor 798
110	10274020	5.01010200	0.001103300	0.0400004	1 3000040	Gna11	guanine nucleotide binding protein, alpha 11
410	10371230	5.91010328	0.00110101	0.0400281	1.3090912		guanne nucleotiue pinuing protein, alpha 11
417	10358637	5.89951542	0.001181235	0.0481707	1.19/1166	HIMCN 1	nemicenun 1
418	10409294	5.89775953	0.001183646	0.0481819	1.1872077	Sptlc1	serine palmitoyltransferase, long chain base subunit 1
419	10481772	5.87963195	0.001204539	0.0483236	2.0915407	Garnl3	GTPase activating RANGAP domain-like 3
420	10557211	5.88426275	0.001202128	0.0483236	1.4777988	Rbbp6	retinoblastoma binding protein 6
121	10527252	5 87252662	0.001208556	0.0483336	1 35/350	Ttc26	tetratricopentide repeat domain 26
422	1051/128	5 80206031	0.001100878	0.0483236	2 7456033	Tto30b	tetraticopolitide repeat domain 20
402	10506145	5.00200001	0.001100070	0.0403230	1.2460204	Tmom240	
423	10520145	5.00500199	0.001202931	0.0463230	1.3409321		transmerniorane protein 240
424	10510844	5.80050208	0.001212574	0.048377	1.520791	wrap73	vvD repeat containing, antisense to Trp73
425	10480999	5.85253344	0.001225431	0.0484611	1.3708282	Sdccag3	serologically defined colon cancer antigen 3
426	10480672	5.85232717	0.001226235	0.0484611	1.3719298	Ssna1	Sjogren's syndrome nuclear autoantigen 1
427	10478590	5.85071102	0.001227038	0.0484611	1.6150578	Zswim1	zinc finger SWIM-type containing 1
428	10505791	5.8426529	0.001238288	0.0485967	1.6043358	Focad	focadhesin
429	10383245	5.84600198	0.001235074	0.0485967	1.1386606	Rptor	regulatory associated protein of MTOR, complex 1
430	10515326	5 84234358	0.001239092	0.0485967	1 3867849	Tmem69	transmembrane protein 69
431	10472589	5 83873694	0.001243913	0.0486167	1 3387224	Phospho2	phosphatase orphan 2
432	10478772	5 82855404	0.001255966	0.0488218	1 5570774	Arfaef?	ADP-rithosylation factor quanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
133	10303055	5 70626774	0.001284805	0.0400432	1.2661866	Due1	dibudouriding synthase 1 like (S. cerusica)
400	10550333	5.0020074	0.001204093	0.0490432	1.2001000	Eom175b	amy dound in e synthase raike (3. cerevisiae)
404	10330274	5.00333323	0.001202404	0.0430432	1.1113/31		Tarning with sequence similarity 175, member D
125	10667060		1111110160	0 0400422	1 1 1 60007		furin (naired basic amine cold cleaving onzyme)
435	10564960	5.00404744	0.00128168	0.0490432	1.4468807	Furin	furin (paired basic amino acid cleaving enzyme)
435 436	10564960	5.79046434	0.00128168	0.0490432	1.4468807	Furin Kihi6	furin (paired basic amino acid cleaving enzyme) kelch-like 6
435 436 437	10564960 10438445 10515702	5.79046434 5.80194894	0.00128168 0.001289716 0.001283288	0.0490432 0.0490432 0.0490432	1.4468807 1.5131492 1.5431545	Furin Kihi6 Szt2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2
435 436 437 438	10564960 10438445 10515702 10586242	5.79046434 5.79046434 5.80194894 5.77993247	0.00128168 0.001289716 0.001283288 0.001300162	0.0490432 0.0490432 0.0490432 0.049061	1.4468807 1.5131492 1.5431545 1.2454296	Furin Kihi6 Szt2 Dennd4a	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A
435 436 437 438 439	10564960 10438445 10515702 10586242 10568988	5.80404744 5.79046434 5.80194894 5.77993247 5.72180526	0.00128168 0.001289716 0.001283288 0.001300162 0.00136284	0.0490432 0.0490432 0.0490432 0.049061 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585	Furin Kihl6 Szt2 Dennd4a Bet11	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like
435 436 437 438 439 440	10564960 10438445 10515702 10586242 10568988 10510034	5.80404744 5.79046434 5.80194894 5.77993247 5.72180526 5.71428829	0.00128168 0.001289716 0.001283288 0.001300162 0.00136284 0.001369269	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9
435 436 437 438 439 440 441	10564960 10438445 10515702 10586242 10568988 10510034 10506843	5.79046434 5.79046434 5.77993247 5.72180526 5.71428829 5.75941423	0.00128168 0.001289716 0.001283288 0.001300162 0.00136284 0.001369269 0.001323466	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711	Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B
435 436 437 438 439 440 441 442	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268	5.790464744 5.79046434 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067	0.00128168 0.001289716 0.001283288 0.001300162 0.00136284 0.001369269 0.001323466 0.001355608	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301	Kihl6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila)
435 436 437 438 439 440 441 442 443	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147	5.790464744 5.79046434 5.80194894 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539	0.00128168 0.001289716 0.001283288 0.001300162 0.00136284 0.001369269 0.001323466 0.001355608 0.001334715	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643	Furin Kihl6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP
435 436 437 438 439 440 441 442 443 444	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774	5.790464744 5.79046434 5.80194894 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.74657539	0.00128168 0.001289716 0.001289716 0.001283288 0.001300162 0.001369269 0.001323466 0.001355608 0.001334715 0.001334715	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451	Furin Kihilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Ntbf2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2
435 436 437 438 439 440 441 442 443 444 445	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337	5.790464744 5.79046434 5.80194894 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74664928	0.00128168 0.001283716 0.001283288 0.001300162 0.00136284 0.00136284 0.001323466 0.001323466 0.0013234715 0.001334715	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252	Furin Kihl6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Res12	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 reculator of G-protein signaling 12
435 436 437 438 439 440 441 442 443 444 445 446	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337	5.790464744 5.79046434 5.70194894 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74264928	0.00128168 0.001283716 0.001283288 0.001300162 0.00136284 0.00136269 0.001323466 0.001355608 0.001334715 0.001378911 0.001337891	0.0490432 0.0490432 0.0490432 0.0490613 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 ceizure threshold 2
435 436 437 438 439 440 441 442 443 444 445 446 447	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690	3.50404744 5.79046434 5.7993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74264928 5.73225486	0.00128168 0.001283288 0.001383288 0.001300162 0.001369269 0.001369269 0.001334715 0.001378911 0.00133793 0.001349883	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.8475301 1.8475301 1.845531 1.305451 1.4410252 1.4282895	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 ceizure threshold 2
435 436 437 438 439 440 441 442 443 444 445 446 447 446	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710	3.8040744 5.79046434 5.7993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74264928 5.73225486 5.73225486	0.00128168 0.001283716 0.001283288 0.001300162 0.00136284 0.00136269 0.001323466 0.001323466 0.001334715 0.0013793 0.0013793 0.001354804 0.001354804	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504	Furin Kihl6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2
435 436 437 438 439 440 441 442 443 444 445 446 447 448	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 406555	3.8040744 5.79046434 5.7793247 5.72180526 5.74280526 5.7428829 5.75941423 5.72549067 5.74264928 5.70603657 5.74264928 5.73225486 5.73225486 5.72783411 5.73792316	0.00128168 0.001283716 0.001283288 0.001300162 0.001369269 0.0013560269 0.001354608 0.001334715 0.001337931 0.001337931 0.001349983 0.001354804 0.001343555	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.7457301 1.7854643 1.305451 1.4410252 1.3406504 1.3623079	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx3 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Szt2 Stx35	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 time/torganeticate delte
435 436 437 438 439 440 441 442 443 444 445 446 447 447 448 449	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 10600301	3.50404744 5.79046434 5.79046434 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74264928 5.73225486 5.72783411 5.73792316 5.73792316	0.00128168 0.001283288 0.001383288 0.001300162 0.00136284 0.00136269 0.001323466 0.001334715 0.001378911 0.00133793 0.001354804 0.001354804 0.001354804	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223883 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.3406504 1.3623079 1.1834382	Furin Kihilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Szt3 Sik35 Ssr4	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10521337 10515690 10515710 10476033 10600301 10508269	3.8040744 5.79046434 5.7993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74264928 5.73225486 5.73225486 5.73225486 5.73225486 5.7312749 5.73420091	0.00128168 0.001283288 0.001283288 0.001300162 0.00136284 0.00136284 0.001323466 0.001323466 0.001334715 0.001334713 0.00133793 0.001349983 0.001349983 0.001344984 0.001344555 0.00133108	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.283834 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.1834382 1.3099763	Furin Kihl6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx3I Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Stx35 Ssr4 Smim12	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 1060030 10508269 10584034	3.50404744 5.79046434 5.77993247 5.72180526 5.74280526 5.7428829 5.75941423 5.72549067 5.74264928 5.73225486 5.73225486 5.73225486 5.73723411 5.73792316 5.73792316 5.73112749 5.74329499	0.00128168 0.001283716 0.001283288 0.001300162 0.001369269 0.001369269 0.001355608 0.001337415 0.001337911 0.001379911 0.00134983 0.001354804 0.001354804 0.001354804 0.00135159 0.00133108	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.1834382 1.3099763 1.2787461	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX3 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 StX35 Ssr4 Smim12 Snx19	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 10600301 1058269 105884034 10357917	3.50404744 5.79046434 5.79046434 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.74667539 5.74264928 5.732254841 5.7372341 5.73792316 5.73112749 5.74820091 5.74254124	0.00128168 0.001283288 0.001383288 0.001300162 0.001369269 0.001369269 0.001334715 0.001378911 0.001378911 0.0013793 0.00134983 0.001343555 0.00135159 0.0013317126 0.0013317426	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4410252 1.3406504 1.3623079 1.1834382 1.3099763 1.2787461 1.1714838	Furin Kihlé Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 StX35 Ssr4 Smr19 Tmem183a	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 softing a sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmembrane protein 183A
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453	10564960 10438445 10515702 10586242 10568988 1051034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 10600301 10508269 10584034 10384034	3.30404744 5.79046434 5.7909247 5.72180526 5.71428829 5.75941423 5.72649067 5.74667539 5.7603657 5.74264928 5.73225486 5.722783411 5.73792316 5.73112749 5.74820991 5.74329499 5.72254124 5.62768869	0.00128168 0.001283288 0.001283288 0.001300162 0.00136284 0.00136284 0.001323466 0.001323466 0.001334715 0.0013793 0.0013793 0.001354804 0.001337126 0.001361233 0.001361233 0.001390161	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.834382 1.3099763 1.2787461 1.7114838 4.138261	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Stx35 Ssr4 Smim12 Snx19 Tmem183a Cmpk2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sording nexin 19 transmembrane protein 183A cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial_
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 1060030 10555710 10476033 1060030 105584034 10357917 10395039 10458355	3.6040744 5.79046434 5.7793247 5.72180526 5.71428829 5.75941423 5.72549067 5.74264928 5.732254966 5.7322549 5.7322549 5.7322549 5.7322549 5.7322549 5.7322549 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.68529853	0.00128168 0.001283716 0.001283288 0.001300162 0.001369269 0.001356068 0.001356068 0.00133715 0.001378911 0.001378911 0.00134983 0.001354804 0.001354804 0.001354804 0.001333108 0.001331126 0.001337126 0.00139161 0.00140784	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495691 0.0496691	1.4468807 1.5131492 1.5431545 1.2454296 1.225885 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.834382 1.309763 1.2787461 1.2787461 1.27876704	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX3 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Stx35 Ssr4 Smim12 Snx19 Tmem183a Cmpk2 Apbb3	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmembrane protein 183A cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3
435 436 437 438 439 440 441 442 443 444 445 446 447 446 447 448 449 450 451 452 453 454 455	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515690 10515690 105584034 10508269 10584034 10357917 10395039 10458355 10518031	3.50404744 5.79046434 5.7909247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.74657539 5.74264928 5.73225486 5.732783411 5.73792316 5.732793416 5.732793416 5.7329499 5.74254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.73254124 5.7355555555555555555555555555555555555	0.00128168 0.001283288 0.001383288 0.001300162 0.001369269 0.001369269 0.001334715 0.001378911 0.001378911 0.001378911 0.00134555 0.001354804 0.001343555 0.00135159 0.001337126 0.001337126 0.001337126 0.001337126 0.00139161 0.001426321	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.360504 1.360504 1.3623079 1.1834382 1.3099763 1.2787461 1.1714838 4.138261 1.2376704 1.6140621	Furin Kihilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Sik35 Ssr4 Smx19 Tmem183a Cmpk2 Apbb3 Dnajc16	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seiner/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmembrane protein 183A cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3 DnaJ (Hsp40) homolog, subfamily C, member 16
435 436 437 438 439 440 441 442 443 444 445 444 445 446 447 448 449 450 451 452 453 454 455 456	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 10600301 10508269 10584034 10357917 10395039 10458355 10518031 10381408	3.50404744 5.79046434 5.79046434 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.74667539 5.74264928 5.73225486 5.72783411 5.73792316 5.73792316 5.73712749 5.7482091 5.7482094 5.72254124 5.69768869 5.66797534	0.00128168 0.001283288 0.001283288 0.001300162 0.00136284 0.00136289 0.001323466 0.001335608 0.00133715 0.001378911 0.00133793 0.001354804 0.001343555 0.00135159 0.00133108 0.00133123 0.001361233 0.001390161 0.001427829	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.1834382 1.3099763 1.2787461 1.2787461 1.2376704 1.6140621 1.7740171	Furin Klhilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Stx35 Ssr4 Smin12 Snx19 Tmem183a Cmpk2 Apbb3 Dnajc16 Ifi35	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmembrane protein 183A cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3 DnaJ (Hsp40) homolog, subfamily C, member 16 interferon-induced protein 35
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 456 456 456	10564960 10438445 10515702 10586242 10568988 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 1060030 10515710 10476033 1060030 10555710 10476033 10508269 10584034 10357917 10395039 10458355 10518031 10381408 10419731	3.6040744 5.79046434 5.79046434 5.77993247 5.72180526 5.74280526 5.7428829 5.75941423 5.72549067 5.74264928 5.732254966 5.7322549 5.7322549 5.7322549 5.7322549 5.7322549 5.7322549 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.7432949 5.7432949 5.7432949 5.74494949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7444949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.7424949 5.74444 5.74449 5.74449 5.74449 5.74449 5.744949 5.744949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.7444949 5.744494949 5.7444949494949 5.7	0.00128168 0.001283716 0.001283288 0.001300162 0.001369269 0.001356608 0.001334715 0.001334715 0.001334715 0.001349983 0.001349983 0.001354804 0.001354804 0.001333108 0.001333108 0.00133126 0.001337126 0.00139161 0.001426321 0.001426321 0.001427929 0.001423911	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495691 0.0498267 0.0498267	1.4466807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.834382 1.3099763 1.2787461 1.714838 4.138261 1.2376704 1.6140621 1.7740171 1.3441224	Furin Kihi6 Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2 Stx35 Ssr4 Ssr4 Smim12 Snx19 Tmem183a Cmpk2 Apbb3 Dnajc16 Ifi35 Nrbf2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 colled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmembrane protein 183A cytdine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3 DnaJ (Hsp40) homolog, subfamily C, member 16 interferon-induced protein 35 nuclear receptor binding factor 2
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 457	10564960 10438445 10515702 10586242 10568988 1051034 10506843 10439268 10509147 10369774 10521337 10515690 10515690 10515690 105584034 10367917 10395039 10458355 10518031 10381408 10419731	3.6040744 5.79046434 5.7909247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.74657539 5.74657539 5.74264928 5.73225486 5.732783411 5.73792316 5.73112749 5.74820091 5.742254124 5.68768863 5.68529853 5.666739083 5.666739083 5.666739083	0.00128168 0.001283288 0.001300162 0.001369269 0.001369269 0.001369269 0.001334715 0.001378911 0.001378911 0.001378911 0.00134555 0.00135159 0.00133108 0.00133108 0.001331126 0.001331126 0.001337126 0.001337126 0.001337126 0.001337126 0.001337126 0.001337126 0.001337126 0.00132123 0.001427929 0.001423911	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495267 0.0498267 0.0498267	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.3406504 1.3623079 1.1834382 1.3099763 1.2787461 1.2787461 1.2787461 1.2376704 1.6140621 1.7740171 1.3441224	Furin Kihilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Szt2 Sik35 Ssr4 Smx19 Tmem183a Cmpk2 Apbb3 Dnajc16 Ifi35 Nrbf2 Nrbf2	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmembrane protein 183A cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3 DnaJ (Hsp40) homolog, subfamily C, member 16 interferon-induced protein 35 nuclear receptor binding factor 2
435 436 437 438 439 440 441 442 443 444 445 447 448 449 450 451 452 453 454 455 456 455 456 457 8458	10564960 10438445 10515702 10586242 10568988 1051034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 10600301 1058269 10584034 10357917 10395039 10458355 10518031 10381408 10419731 10419729	3.60404744 5.79046434 5.79046434 5.77993247 5.72180526 5.71428829 5.75941423 5.72549067 5.74657539 5.70603657 5.74264928 5.73225486 5.72783411 5.73792316 5.73712749 5.74820991 5.72254124 5.69768869 5.72254124 5.667763083 5.66797534 5.66797534 5.66797534	0.00128168 0.001283288 0.001383288 0.001300162 0.00136284 0.00136284 0.001323466 0.001334715 0.00133793 0.00133793 0.001354804 0.001337126 0.00133108 0.00133108 0.00133123 0.001361233 0.001361233 0.001427929 0.001423911 0.001423911 0.001423911	0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495267 0.0498267 0.0498267	1.4468807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.3406504 1.3623079 1.1834382 1.3099763 1.7748741 1.3787461 1.2376704 1.1714838 4.138261 1.2376704 1.17740171 1.3441224 1.3441224 1.340272	Furin Klhilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b Dtx31 Gale Nrbf2 Rgs12 Szt2 Szt2 Szt2 Szt2 Szt2 Szt2 Sik35 Ssr4 Smin12 Snx19 Tmem183a Cmpk2 Apbb3 Dnajc16 Ifi35 Nrbf2 Nrbf2 Pdcl	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure thr
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$\begin{array}{r} 4356\\ 436\\ 437\\ 438\\ 439\\ 440\\ 441\\ 442\\ 443\\ 444\\ 445\\ 445\\ 446\\ 447\\ 445\\ 445\\ 445\\ 456\\ 457\\ 458\\ 459\\ 460\\ 461\\ 462\\ 463\\ 459\\ 460\\ 461\\ 465\\ 446\\ 466\\ 469\\ 470\\ 471\\ 472\\ 473\\ 474\\ 475\\ \end{array}$	10564960 10438445 10515702 10586242 10568243 10510034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 1060030 10515710 10476033 1060030 10555710 10484034 1035917 10395039 10458355 10518031 10482139 10482359 10488450 10482509 10482509 10482509 10482509 1048557 10515708 10348194 10550112 1047780 10457780 10463557 10514779 10463557	3.6040744 5.79046434 5.79046434 5.7909247 5.72180526 5.71428829 5.75941423 5.72549067 5.742657539 5.70603657 5.74264928 5.732254866 5.732783411 5.73292316 5.732254826 5.732783411 5.73292316 5.732254826 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.74329499 5.66597534 5.666979534 5.666949163 5.666949163 5.666949163 5.666949163 5.66795083 5.66785007 5.66898513 5.658908513 5.65420452 5.67454814 5.658986513 5.65420452 5.67454814 5.658986513 5.65420452 5.66342633 5.61310858 5.6042089 5.61310858 5.6042089 5.59261019 5.59220681	0.00128168 0.001283716 0.001283288 0.001300162 0.001362269 0.001356269 0.001356668 0.001334715 0.001378911 0.001337911 0.00133793 0.001349983 0.001354804 0.001354804 0.00133408 0.00133408 0.00133408 0.00133408 0.001354233 0.00140784 0.001426321 0.001426321 0.001423911 0.001426321 0.001423911 0.001426321 0.001423911 0.001426321 0.001445635 0.001445685 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.0014456857 0.001490606 0.001490822 0.00146178 0.001490606 0.001490625 0.001490625 0.001450249 0.001500249 0.001500249 0.001500249	0.0490432 0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0501247 0.0501247 0.0501588 0.0501992 0.05008699 0.0508699 0.0509021	1.4466807 1.5131492 1.5431545 1.2454296 1.223585 1.2838341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4410252 1.4410252 1.44282995 1.3406504 1.3623079 1.1834382 1.3099763 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.2787461 1.27579329 1.6885293 2.5308649 1.4710122 1.9440074 1.011598 2.2696384 1.2625219 1.5632322	Furin Klhilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX3 Gale Nrbf2 Rgs12 Szt2 StX35 Ssr4 Ssr4 Ssr4 StX5 Ssr4 Ssr4 Smim12 Snx19 Tmem183a Cmpk2 Apbb3 Dnajc16 Ifi35 Nrbf2 Pla2g4c Rbm43 Znfx1 Dapk3 Psma7 Szt2 Efhd1 Usp1 Notch1 Sult2a6 Map1Ic3a Gbf1 Prkaa2 Garem Spsb3 Slfn4	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 coiled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 3 proteasome (prosome, macropain) subunit, alpha type 7 seizure threshold 2 EF hand domain containing 1 ubiquitin specific peptidase 1 notch 1 sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 6 microtubule-associated protein 1 light chain 3 alpha goli-specific brefeld n-k-resistance factor 1 protein kinase, AMP-activated, alpha 2 catalytic subunit GRB2 associated, requiator of MAPK1 splA/vjanodine receptor domain and SOCS box containing 3 schlafen 4
$\begin{array}{r} 4356\\ 436\\ 437\\ 438\\ 439\\ 440\\ 447\\ 448\\ 449\\ 444\\ 447\\ 448\\ 449\\ 445\\ 446\\ 447\\ 455\\ 456\\ 457\\ 458\\ 459\\ 456\\ 457\\ 458\\ 459\\ 461\\ 462\\ 463\\ 466\\ 467\\ 468\\ 466\\ 467\\ 468\\ 469\\ 470\\ 472\\ 473\\ 474\\ 475\\ 476\\ 476\\ 476\\ 476\\ 476\\ 476\\ 476\\ 476$	10564960 10438445 10515702 10586242 10568988 1051034 10506843 10439268 10509147 10369774 10521337 10515690 10515710 10476033 10600301 105084034 10357917 10350269 10584034 10357917 1035035 10518031 10419729 10482139 1045033 10419729 1048255 10489850 10368005 10490370 105157788 10348194 10560122 10477637 10514779 10457780 1042780 10457780 1045780 1045780	3.50404744 5.79046434 5.790426434 5.7909247 5.72180526 5.7428829 5.75941423 5.72549067 5.74264928 5.732549067 5.74264928 5.73225486 5.7322548 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.73792316 5.74264928 5.74264928 5.668797534 5.6697534 5.66979534 5.66979534 5.66979534 5.66979534 5.66979534 5.66979534 5.66949163 5.66949163 5.66494163 5.66494163 5.66494163 5.66496388 5.66420452 5.6383859 5.61634463 5.61310858 5.60422768 5.60222089 5.59220881 5.58920289	0.00128168 0.001283288 0.001383288 0.001383288 0.001383288 0.001369269 0.001369269 0.0013323466 0.0013355608 0.00133715 0.00133793 0.00134983 0.001343555 0.001337126 0.001331126 0.001331126 0.001337126 0.00142321 0.00142321 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.001423911 0.00142391 0.001445807 0.001445807 0.00144587 0.00144587 0.00145883 0.00145883 0.00145883 0.00145883 0.00145883 0.001504267 0.001504267 0.00150249 0.001512303 0.001521142	0.0490432 0.0490432 0.0490432 0.0490432 0.049061 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495163 0.0495267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0498267 0.0501588 0.05015889 0.0501992 0.0508593 0.0508593 0.0508593	1.4468807 1.5131492 1.5431545 1.2454296 1.223685 1.2388341 1.7158711 1.8475301 1.7854643 1.305451 1.4410252 1.4282895 1.304504 1.3623079 1.834382 1.3099763 1.3099763 1.2787461 1.7114838 4.138261 1.2787461 1.276704 1.6140621 1.7740171 1.3441224 1.3409772 1.5451578329 1.0198588 1.3147786 1.2896384 1.2019588 1.3147786 1.2896384 1.2696384 1.2696384 1.2673692 1.5451578 2.1694978 1.5551578	Furin Kihilé Szt2 Dennd4a Bet11 Casp9 Cc2d1b DtX31 Gale Nrbf2 Rgs12 Szt2 StX35 Ssr4 Smim12 Sm19 Tmem183a Cmpk2 Apbb3 Dnajc16 Ifi35 Nrbf2 Nrbf2 Nrbf2 Pdcl Pla2q4c Rbm43 Znfx1 Dapk3 Psma7 Szt2 Efhd1 Usp1 Notch1 Sult2a6 Map1Ic3a Gbf1 Prkaa2 Garem Spsb3 Slfn4 Mydgf	furin (paired basic amino acid cleaving enzyme) kelch-like 6 seizure threshold 2 DENN/MADD domain containing 4A blocked early in transport 1 homolog (S. cerevisiae)-like caspase 9 colled-coil and C2 domain containing 1B deltex 3-like (Drosophila) galactose-4-epimerase, UDP nuclear receptor binding factor 2 regulator of G-protein signaling 12 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 seizure threshold 2 serine/threonine kinase 35 signal sequence receptor, delta small integral membrane protein 12 sorting nexin 19 transmebrane protein 183A cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3 DhaJ (Hsp40) homolog, subfamily C, member 16 interferon-induced protein 35 nuclear receptor binding factor 2 phosducin-like phospholipase A2, group IVC (cytosolic, calcium-independent) RNA binding motif protein 43 zinc finger, NFX1-type containing 1 death-associated protein 1 seizure threshold 2 EF hand domain containing 1 ubiquitin specific peptidase 1 notch 1 sulfortansferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 6 microtubule-associated protein 1 light chain 3 alpha golg-specific brefeldin A-resistance factor 1 protein MP-activated, alpha 2 catalytic subunit GR2 associated, requilator of MAPK1 spik/ryanodine receptor domain and SOCS box containing 3 schlafen 4 myeloid derived growth factor
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cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial amyloid beta (A4) precursor protein-binding, family B, member 3 DnaJ (Hsp40) homolog, subfamily C, member 16 interferon-induced protein 35 nuclear receptor binding factor 2 phosducin-like phospholipase A2, group IVC (cytosolic, calcium-independent) RNA binding motif protein 43 zinc finger, NFX1-type containing 1 death-associated protein Kinase 3 proteasome (prosome, macropalin) subunit, alpha type 7 seizure threshold 2 EF hand domain containing 1 ubiquitin specific peptidase 1 notch 1 sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 6 microtubule-associated protein 1 light chain 3 alpha golgi-specific brefeldin A-resistance factor 1 protein kinase, AMP-activated, alpha 2 catalytic subunit GR82 associated, regulator of MAPK1 splA/yanodine receptor domain and SOCS box containing 3 schlafen 4 myeloid derived growth factor bone marrow stromal cell antigen 2 cytochrome b-561 C-type lectin domain family

484	10506030	5 54760413	0.001582212	0.0517678	1 6203374	Ene15	enidermal growth factor recentor nathway substrate 15
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400	10313277	5.55577401	0.001571700	0.0517078	1.0490421	Luiap i	ieucine noi auapioi protein i
487	10478401	5.54384829	0.00158623	0.0517678	1.3095355		tocopherol (alpha) transfer protein-like
488	10481320	5.5408767	0.001592659	0.0519025	1.4672895	Gtf3c4	general transcription factor IIIC, polypeptide 4
489	10501164	5.52917609	0.001606319	0.0520308	1.434469	Csf1	colony stimulating factor 1 (macrophage)
490	10506415	5.53526818	0.001601498	0.0520308	1.7634984	Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)
491	10383192	5.53268093	0.001603909	0.0520308	2.2612419	Rnf213	ring finger protein 213
492	10359181	5 52803494	0.00160873	0.0520308	1 9342182	Tor3a	torsin family 3 member A
102	10516778	5 52/10073	0.001611044	0.0520308	1 4561535	Zcchc17	zinc finger. CCHC domain containing 17
404	10505622	5.52415510	0.001620622	0.0520500	1.0040202		
494	10000020	5.51596516	0.001029022	0.052054	1.9040203		
495	10379262	5.51674585	0.001628819	0.052054	1.4752164	NTI	
496	10489368	5.51240592	0.001639265	0.0522141	1.7976796	Fitm2	tat storage-inducing transmembrane protein 2
497	10516051	5.4874684	0.001680247	0.052774	1.4715536	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)
498	10509930	5.4875325	0.001679443	0.052774	1.5853739	Fbxo42	F-box protein 42
499	10479335	5.48956546	0.001675425	0.052774	1.3506545	Osbpl2	oxysterol binding protein-like 2
500	10485342	5,48958681	0.001674622	0.052774	1.2104517	Ttc17	tetratricopeptide repeat domain 17
501	10515368	5 48426551	0.001686675	0.0529023	1 3904422	Toe1	target of EGR1 member 1 (nuclear)
502	10514500	5 47704434	0.001701043	0.0531350	1 3201383	Dock7	adjoint of outprinsing 7
502	10424779	5.47194434	0.001701943	0.0531555	1.3291303	Duck/	
503	10434778	5.471824	0.001713193	0.0533157	2.243513	Rtp4	receptor transporter protein 4
504	10489904	5.47093673	0.0017148	0.0533157	1.3627393	Spata2	spermatogenesis associated 2
505	10496580	5.46615804	0.001722032	0.0533435	3.0231481	Gbp3	guanylate binding protein 3
506	10382470	5.46417248	0.00172605	0.0533463	1.1652357	Tmem104	transmembrane protein 104
507	10478077	5.45842168	0.001731675	0.0533491	1.3641267	Ralgapb	Ral GTPase activating protein, beta subunit (non-catalytic)
508	10467149	5.45443785	0.001736496	0.0533779	1.5721743	2010002M12Rik	RIKEN cDNA 2010002M12 gene
509	10378068	5 45189674	0.00173971	0.0533779	2 4215605	Xaf1	XIAP associated factor 1
510	10462621	5 44188711	0.001747746	0.0535516	5 3000886	1830012016Dik	Jiken cDNA 1830012016 gene
510	10402021	5.44100711	0.001772656	0.0535510	1.4040406	Code22	
511	10400100	5.429/0012	0.0017722001	0.053011	1.4042130		DIFEN -DNA 4020500N02 mm
512	1053/426	0.431630/5	0.001767031	0.053611	1.4065218	4930599N23RIK	RINEIN CUINA 4930099INZ3 gene
513	10360589	5.42654549	0.001775871	0.053612	1.1384724	ANCITI	AT nook containing transcription factor 1
514	10507931	5.42424849	0.001778281	0.053613	1.1636318	Mir697	microRNA 697
515	10379530	5.40543443	0.001806406	0.0536506	1.5547047	Ccl12	chemokine (C-C motif) ligand 12
516	10577838	5.40327427	0.00180962	0.0536506	2.1007332	Ddhd2	DDHD domain containing 2
517	10468992	5.40305833	0.001810424	0.0536506	1.5677801	Frmd4a	FERM domain containing 4A
518	10516706	5 4023/167	0.001812024	0.0536506	1 3156929	Khdrhs1	KH domain containing RNA hinding signal transduction associated 1
510	10510700	5.40234107	0.001012031	0.0530500	1.0100000	ModOlO	MAD2 mitotic errect deficient like 2
519	10510286	0.41406598	0.001792745	0.0530506	1.0049387		minotic arrest delicient-like z
5 <u>2</u> 0	10518385	0.41184135	0.00179837	0.0536506	1.0001/48		
521	10500911	5.40918638	0.001802388	0.0536506	1.5862113	Mov10	Moloney leukemia virus 10
522	10550237	5.41404851	0.001793549	0.0536506	1.1451498	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha
523	10394627	5.4007717	0.001812834	0.0536506	1.3618954	Nbas	neuroblastoma amplified sequence
524	10513381	5.41348585	0.001795156	0.0536506	1.3876838	Ptbp3	polypyrimidine tract binding protein 3
525	10464924	5 40554459	0.001805602	0.0536506	1 1641486	Rab1b	RAB1B member RAS oncogene family
526	10566067	5 41491367	0.001701042	0.0536506	1 1450048	Rnf121	ting figure protein 121
527	10502701	5 30375278	0.001820067	0.0537236	3 3360021	IfiAA	interferen induced protein 44
527	10502791	5.39373276	0.001020007	0.0537230	3.3300021	11144	
528	10540860	5.37821930	0.00184578	0.0540816	1.1464509	Alg/	autophagy related 7
529	10508151	5.38376239	0.001840156	0.0540816	1.3263543	Clspn	claspin
530	10462623	5.38441467	0.001837745	0.0540816	4.4430261	lfit1	interferon-induced protein with tetratricopeptide repeats 1
531	10515613	5.38056055	0.00184337	0.0540816	1.6118892	Ptprf	protein tyrosine phosphatase, receptor type, F
532	10515046	5.36348654	0.00186587	0.0542239	1.3530138	Btf3l4	basic transcription factor 3-like 4
533	10403273	5.35725956	0.001878727	0.0544572	1,4509987	Asb13	ankyrin repeat and SOCS box-containing 13
534	10508042	5 33640593	0.001925333	0.0551689	1 3258168	Meaf6	MYST/Esa1-associated factor 6
535	10518679	5 34023511	0.001016404	0.0551689	1 5874401	Nmnat1	nicotinamide nucleotide adenvivitransferase 1
535	10240724	5 2252004	0.001027744	0.0551690	1.0515165	Dah20	DAP20 member DAS encoder single
530	10349724	5.3352004	0.001927744	0.0551069	1.9515105	Rab29	RADZ9, member RAS offcogene family
537	10515844	5.33693213	0.001923726	0.0551689	1.4547014	Zfp691	Zinc finger protein 691
538	10410173	5.32718826	0.001940601	0.0552564	1.2269215	Hiatl1	hippocampus abundant transcript-like 1
539	10444991	5.32578904	0.001945422	0.0553238	1.3520879	Gm6034	predicted gene 6034
540	10481870	5.32221857	0.001953458	0.0554824	1.3558359	Gapvd1	GTPase activating protein and VPS9 domains 1
541	10481654	5.31749557	0.0019631	0.0555464	1.4549995	Fpgs	folylpolyglutamyl synthetase
542	10510422	5.31221263	0.001971136	0.0556341	1.7810604	Casz1	castor zinc finger 1
543	10500406	5 30975434	0.00197435	0.0556552	1 1425616	Cd160	CD160 antigen
544	10348424	5 29947435	0.001983180	0.055765	1 176969	Sh3bp4	SH3-domain binding protein 4
515	10505747	5 20272052	0.00100000	0.055904	1 670/040	Rrana	Res-related GTP hinding A
5/6	10270622	5 20204774	0.001006046	0.0000001	1 8280206	Slfn1	echlafon 1
540	10319033	5.23334114	0.001990040	0.0000001	1.0203230	Died	ormanon i bridaina integrator 1
347	10454580	0.200052/3	0.002008903	0.0559262	1.2/8540/	DIII I D0=+40	pringing integrator i
548	10498367	5.28845104	0.002004886	0.0559262	1.7369804	P2ry13	purinergic receptor P2Y, G-protein coupled 13
549	10448676	5.2850585	0.002011314	0.0559262	1.3783356	SIc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
550	10460085	5.27837729	0.002028189	0.0561651	1.3420549	Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)
551	10393926	5.27060193	0.002038635	0.0561938	1.2163763	Dcxr	dicarbonyl L-xylulose reductase
552	10505587	5.26508903	0.002048278	0.0561938	1.3620205	Kdm4c	lysine (K)-specific demethylase 4C
553	10363379	5.26920697	0.002041849	0.0561938	1.2446471	Micu1	mitochondrial calcium uptake 1
554	10517436	5.26573911	0.002045867	0.0561938	1,4825182	Pithd1	PITH (C-terminal proteasome-interacting domain of thioredoxin-like) domain containing 1
555	10515481	5 25465872	0.002065056	0.0562221	1 2948746	Dman1	DNA methyltransferase 1-associated protein 1
556	10574009	5 25502015	0.002061020	0.0562221	5 2010015	NIrc5	NI R family, CARD domain containing 5
550	10/25/57	5.25552015	0.002001339	0.056002221	1 700/550	Parn0	noly (ADD ribose) polymerase family, member 0
007	10430407	0.2000202	0.002002/42	0.0002221	1.1004008	r aipa T0-	poly (Dor - noose) polymerase ranniy, member 9
558	104/1519	0.20996307	0.002056314	0.0562221	1.5835265		torsin family 2, member A
559	10533304	5.2418769	0.002087652	0.0565177	1.8322372		TRAF type zinc tinger domain containing 1
560	10388861	5.23085993	0.002104527	0.0567456	1.3630948	1 mem199	transmembrane protein 199
561	10450325	5.22071823	0.00212542	0.0569498	3.852683	Cfb	complement factor B
562	10475630	5.21134723	0.002140688	0.0569498	1.240071	Galk2	galactokinase 2
563	10574151	5.21415091	0.002133455	0.0569498	3.5663089	NIrc5	NLR family, CARD domain containing 5
564	10353524	5.21100863	0.002141491	0.0569498	1.8990569	Oafrl1	opioid growth factor receptor-like 1
565	10516974	5,21182401	0.002139884	0.0569498	1.5708193	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8
566	10500107	5 20220707	0.002150160	0.0570405	1 /1/2012	Fuca1	fucneidase alnhal - 1 tissue
500	10009127	5.20022101	0.002109109	0.0070495	1.4140013	i uua i Mirrio OC	nuovaiuaao, alpha-L- 1, uaaut miteehendrial rikeeemel matein 200
00/	10476189	5.19882584	0.002168009	0.0570495	1.373142		
568	10508649	5.20131199	0.002163991	0.0570495	1.3309919	Gm23/11	predicted gene, 23/11
569	10508647	5.20131199	0.002163991	0.0570495	1.3309919	Gm23711	predicted gene, 23711
570	10508112	5.19913904	0.002166401	0.0570495	1.4157609	Lsm10	U7 snRNP-specific Sm-like protein LSM10
571	10359405	5.19579394	0.002176044	0.0571276	1.1636365	Klhl20	kelch-like 20
572	10477090	5.18380511	0.002198544	0.0573843	1.4546735	Tbc1d20	TBC1 domain family, member 20
573	10513551	5,18267422	0.002204169	0.0574646	1.5285438	Fkbp15	FK506 binding protein 15
574	10517000	5 17212537	0.002217820	0.0574706	1 3081679	Arid1a	AT rich interactive domain 1A (SWI-like)
575	1051747	5 1650/666	0.002211029	0.0574700	1 /7/000	Dhdde	debydrodolichyl dinhoenhate synthase
5/5	10017147	5.10094000	0.002223083	0.0074700	1.4/4239	Darm14	uchyurouolionyi ulphosphate synthase
5/6	10439249	0.10894961	0.002224258	0.05/4/06	∠.8031911	marp14	poly (ADP-ribose) polymerase ramily, member 14
577	10515461	5.16759927	0.002226669	0.0574706	1.4708668	Rnf220	ring tinger protein 220
578	10445758	5.16910815	0.002223454	0.0574706	1.1999262	Treml4	triggering receptor expressed on myeloid cells-like 4
		5 15828315	0.002245151	0.0576626	1 836026	Pink1	PTEN induced putative kinase 1
579	10517600	0.10020010	0.002210101	0.0010020	1.000020		
579 580	10517600 10354233	5.15773233	0.002247561	0.0576626	1.283994	Tgfbrap1	transforming growth factor, beta receptor associated protein 1

582	10453276 5.15196952	0.002257204	0.057713 1	1.1340274	Thada	thyroid adenoma associated
583	10481164 5.14605432	0.002272472	0.0579719 1	1.9162677	Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6
584	10444821 5.14357012	0.002278097	0.0579802 2	2.3874011	H2-Q5	histocompatibility 2, Q region locus 5
585	10494335 5.13659796	0.002293364	0.0580167 1	1.1153593	Otud7b	OTU domain containing 7B
586	10542414 5.13713513	0.00229015	0.0580167 1	1.2213453	Ptpro	protein tyrosine phosphatase, receptor type, O
587	10510629 5.13153894	0.002304614	0.0580207 1	1.5628865	Nol9	nucleolar protein 9
588	10490150 5.13106397	0.002305418	0.0580207 4	1.4862421	Zbp1	Z-DNA binding protein 1
589	10510270 5.12489598	0.002316667	0.058178	1.696075	Mthfr	5,10-methylenetetrahydrofolate reductase
590	10464128 5.1203741	0.0023239	0.0582572 1	1.4420932	Casp7	caspase 7
591	10566846 5.11628344	0.002329524	0.0582572 1	1.3357373	Dennd5a	DENN/MADD domain containing 5A
592	10516823 5.11742414	0.002327917	0.0582572 1	1.4545914	Epb4.1	erythrocyte protein band 4.1
593	10352097 5.11544693	0.002330328	0.0582572 1	1.1206592	1700016C15Rik	RIKEN cDNA 1700016C15 gene
594	10517559 5.11178887	0.002339167	0.0582887 1	1.3226459	Cdc42	cell division cycle 42
595	10533256 5.10470899	0.002355238	0.0585597 2	2.5163261	Oas1a	2'-5' oligoadenylate synthetase 1A
596	10351163 5.09662979	0.002375327	0.0587999 1	1.1942522	Scyl3	SCY1-like 3 (S. cerevisiae)
597	10517883 5.09398176	0.002380952	0.0588745 1	1.7236847	Necap2	NECAP endocytosis associated 2
598	10517996 5.08698063	0.002393809	0.0590475 1	1.4802193	Plekhm2	pleckstrin homology domain containing, family M (with RUN domain) member 2
599	10405125 5.08361134	0.002405863	0.0591017 1	1.7627607	Fbxw17	F-box and WD-40 domain protein 17
600	10535780 5.07303438	0.002421934	0.0592527 1	1.1526578	Flt3	FMS-like tyrosine kinase 3
601	10429128 5.07195272	0.002423541	0.0592527	1.88872	Sla	src-like adaptor
602	10444056 5.06424246	0.002440416	0.0593416 1	1.2732644	Daxx	Fas death domain-associated protein

Supplementary Table S5. Quantification of angiogenic factors in mammary tumors of nulliparous and parous mice in the presence or absence of SNAI2. Angiogenic factors were quantified in the protein lysate of tumors developed by *Snai2* WT^{erbb2} and *Snai2* KO^{erbb2} mice by a multiplex bead array (Luminex assay): nulliparous mice, N=10 mice per group; parous mice, No=8 mice per group (n.d., non-detectable).

	Nulliparous	s vs. Parous
	WT (p-value)	KO (p-value)
Angiopoietin-2	0.0531	0.7558
G-CSF	0.9645	0.5052
sALK-1	0.7896	0.5043
Leptin	0.1196	0.1682
IL-1B	0.8933	0.3026
EGF	0.4501	0.2667
Endoglin	1	0.6251
FGF-2	0.894	0.5634
Follistatin	0.2667	0.8242
HGF	0.3496	0.8589
sCD31/PECAM-1	0.3986	0.6893
PLGF-2	0.6893	0.8242
KC	0.0561	0.3508
Prolactin	0.8565	0.5036
MIP-1a	0.8239	0.3501
SDF-1	0.1824	0.3281
VEGF-A	0.3508	0.7558
TGFb1	0.5636	0.5634
TGFb2	0.0832	0.5636
TGFb3	0.4501	0.0832
sFasL	n.d.	n.d.
Amphiregulin	n.d.	n.d.
Betacellulin	n.d.	n.d.
IL-6	n.d.	n.d.
Endothelin-1	n.d.	n.d.
IL-17A	n.d.	n.d.
MCP-1	n.d.	n.d.
VEGF-C	n.d.	n.d.
VEGF-D	n.d.	n.d.
ΤΝFα	n.d.	n.d.

Supplementary Table S6. SNAI1 expression and breast cancer in Snai2-deficient mice. A) Comparison between the proportion of SNAI1positive cells in the stroma and epithelium of tumors quantified by immunohistochemistry (IHC) in different groups of mice (Mann-Whitney U test). B) Correlation between the proportion of SNAI1-positive stroma or epithelium cells in the tumors quantified by IHC with survival, tumor latency and the number of metastasis (Spearman's test). C) Comparison between the proportions of SNAI1-positive tumor stroma or epithelium cells quantified by IHC with the presence/absence of metastasis (Mann-Whitney *U* test).

Α.	Tissue zone	Nulliparous/Parous Snai2 WT Erbb2 (N=19)		Snai2 KO ^{Erbb2} (N=20)	p-value
Percentage of SNAI1+ cells		Nulliparous	11.15	23.84	0.05
	Stroma	Parous	37.395	24.26	0.4963
		p-value	0.03738	0.8798	
	Epithelium	Nulliparous	76.59	85.865	0.8065
		Parous	93.24	86.69	0.7624
		p-value	0.3272	0.2568	

В.		Survi	val	Latency		Number of metastasis	
		Snai2 WT Erbb2	Snai2 KO ^{Erbb2}	Snai2 WT Erbb2	Snai2 KO ^{Erbb2}	Snai2 WT Erbb2	Snai2 KO ^{Erbb2}
% of SNAI1+ cells in the stroma							
	N	8	10	8	10	8	10
Nulliparous	p-value	0.4927	0.1869	0.5479	0.6272	0.4226	0.836
	r	-0.2857	0.4545	-0.2515	0.1758	-0.3314	-0.0754
	N	8	10	8	10	8	10
Parous	p-value	0.5653	0.4325	0.4346	0.26	0.5091	0.8792
	r	0.241	-0.2805	0.3234	-0.3939	0.2755	-0.0554
% of SNAI1+ cells in the epithe	əlium						
	N	8	10	8	10	8	10
Nulliparous	p-value	0.5309	0.1276	0.6287	0.1497	0.8852	0.582
	r	0.2619	0.5152	0.2036	0.4909	0.0614	-0.1988
	N	8	10	8	10	8	10
Parous	p-value	0.2829	0.226	0.3652	0.9602	0.9775	0.3771
	r	-0.4338	-0.4207	-0.3713	0.0182	-0.012	-0.3139

с.		Metastasis (yes/no)					
		Snai2 W	T Erbb2	Snai2 KO ^{Erbb2}			
		No	Yes	No	Yes		
% of SNAI1+ cells in the stroma							
	N	3	5	6	4		
Nulliparous	median	18.182	10.952	23.84	26.768		
	p-value	0.4561		0.8312			
	N	1	7	2	8		
Parous	median	5.405	41.463	45.703	24.26		
	p-value	0.2752		0.4334			
% of SNAI1+ cells in the epith	elium						
	N	3	5	6	4		
Nulliparous	median	76.59	76.193	86.196	70.362		
	p-value	0.6547		0.6	698		
	N	1	7	2	8		
Parous	median	16.223	94.391	87.836	86.693		
	p-value	0.2752		0.4334			

Supplementary Table S7. Total and phosphorylated levels of ERK1/2 and AKT in breast

cancer from Snai2 WT^{ErbB2} and Snai2 KO^{ErbB2}, nulliparous and parous mice.

Quantifications were assessed by ELISA. Mean (me) and standard deviation (sd) are shown.

Twenty mice per group were analyzed. Red, significant P-values. T-test.

	Snai2 WT ^{ERBB2}	Snai2 KO ^{ERBB2}	<i>P</i> -value
	(me ± sd)	(me ± sd)	, value
Total ERK 1/2			
Nulliparous Parous	2.9290 ±0.4326 3.2670 ±0.3454	3.0420 ±0.3527 3.4440 ±0.2344	0.3076 < 0.0001
<i>P</i> -value	0.0294	< 0.0001	
pERK 1/2(pT202/Y204) Nulliparous Parous <i>P</i> -value	0.309 ±0.07854 0.3525 ±0.08864 0.0145	0.356 ±0.154 0.658 ±0.2565 0.0006	0.1071 0.0002
Total AKT Nulliparous Parous <i>P</i> -value	0.171 ±0.1468 0.187 ±0.05973 0.5248	0.177 ±0.1613 0.392 ±0.197 0.002	0.528 0.0001
pAKT (T308) Nulliparous Parous <i>P</i> -value	0.219 ±0.04706 0.258 ±0.0759 0.044	0.241 ±0.1269 0.462 ±0.2002 0.0005	0.2846 <mark>0.0001</mark>
pAKT1 (S473) Nulliparous Parous <i>P</i> -value	0.366 ±0.218 0.387 ±0.09257 0.6263	0.397 ±0.2466 0.741 ±0.2649 0.002	0.4142 < 0.0001

Supplementary Table S8. Correlation of total and phosphorylated ERK1/2 and AKT levels

with survival and tumor latency. Protein levels were quantified by ELISA (Spearman's correlation: red: statistically significant values; blue, values with a trend towards significance).

		Survival Latence		ency	
		Snai2 WT ^{ErbB2}	Snai2 KO ^{ErbB2}	Snai2 WT ^{ErbB2}	Snai2 KO ^{ErbB2}
Total ER	K1/2				
Nulliparous	<i>P</i> -value	0.933	0.979	0.758	0.870
	r	-0.020	0.006	-0.073	-0.039
Dereus	Divalue	0.074	0.005	0.764	0.070
Parous	P-value	0.974	0.200	0.701	0.279
	I	-0.006	-0.290	0.075	-0.234
ERK1/2 (pT202/Y204)					
Nulliparous	<i>P</i> -value	0.214	0.411	0.446	0.373
	r	0.291	0.195	0.181	0.211
Parous	<i>P</i> -value	0.976	0.075	0.512	0.009
	r	-0.007	0.406	-0.156	0.566
Total A	KT				
Nulliparous	<i>P</i> -value	0.224	0.139	0.485	0.102
	r	0.285	0.343	0.166	0.376
Daraua	D voluo	0.572	0.046	0.222	0.011
Falous	F-value	0.373	0.010	0.332	0.011
	I	-0.136	0.552	-0.229	0.001
AKT (p]	[308)				
Nulliparous	<i>P</i> -value	0.191	0.242	0.436	0.177
	r	0.305	0.274	0.185	0.314
Parous	<i>P</i> -value	0.771	0.087	0.566	0.014
	r	-0.071	0.403	-0.137	0.552
AKT1 (p	S473)				
Nulliparous	<i>P</i> -value	0.206	0.103	0.427	0.742
	r	0.295	0.375	0.194	0.081
_	- .	0.040			
Parous	P-value	0.913	0.015	0.611	0.002
	r	-0.027	0.536	-0.121	0.657
				1	

Supplementary Table S9. Age of mice used in all experiments involving animals and showed in

the figures across the manuscript. (*) Tissue microarray (TMA) experiments, including the

assessment of Ki-67, Caspase-3, ERBB2, pERBB2 and SNAI1 by immunohistochemistry.

		Nulliparous /	Age	ELISA	Expressio n Array	Tissue
	Conotypo					array
	Genotype	Parous	(weeks)			studies
						(TMA) (*)
1	WT	Nulliparous	68.14	ELISA		TMA
2	WT	Nulliparous	39.43	ELISA		
3	WT	Nulliparous	45.57	ELISA		
4	WT	Nulliparous	44.57	ELISA		
5	WT	Nulliparous	77.57	ELISA		
6	WT	Nulliparous	62.57	ELISA		
7	WT	Nulliparous	40.57	ELISA		
8	WT	Nulliparous	57.57	ELISA		
9	WT	Nulliparous	58.43	ELISA		
10	WT	Nulliparous	40.43	ELISA		
11	WT	Nulliparous	56.43	ELISA		TMA
12	WT	Nulliparous	61.29	ELISA		TMA
13	WT	Nulliparous	51.00	ELISA		TMA
14	WT	Nulliparous	50.29	ELISA		TMA
15	WT	Nulliparous	55.71	ELISA		TMA
16	WT	Nulliparous	67.14	ELISA	ARRAY	
17	WT	Nulliparous	75.14	ELISA	ARRAY	
18	WT	Nulliparous	72.14	ELISA	ARRAY	
19	WT	Nulliparous	71.71	ELISA	ARRAY	TMA
20	WT	Nulliparous	59.14	ELISA		
21	WT	Nulliparous	66.57			TMA
22	WT	Nulliparous	62.43			TMA
23	KO	Nulliparous	59.71	ELISA		
24	KO	Nulliparous	44.29	ELISA		
25	KO	Nulliparous	50.43	ELISA		
26	КО	Nulliparous	49.71	ELISA		
27	КО	Nulliparous	45.00	ELISA		
28	КО	Nulliparous	51.29	ELISA		
29	KO	Nulliparous	55.00	ELISA		TMA
30	KO	Nulliparous	42.29	ELISA		TMA
31	KO	Nulliparous	38.86	ELISA		TMA
32	КО	Nulliparous	38.29	ELISA		TMA
33	KO	Nulliparous	42.71	ELISA		TMA
34	KO	Nulliparous	40.00	ELISA		TMA
35	KO	Nulliparous	77.00	ELISA		
36	KO	Nulliparous	62.71	ELISA	ARRAY	
37	КО	Nulliparous	105.57	ELISA	ARRAY	TMA
38	КО	Nulliparous	93.71	ELISA	ARRAY	TMA
39	КО	Nulliparous	73.14	ELISA		TMA
40	КО	Nulliparous	51.57	ELISA	ARRAY	TMA
41	KO	Nulliparous	44.00	ELISA		
42	КО	Nulliparous	46.00	ELISA		
43	WT	Parous	79.14	ELISA	ARRAY	

44	WT	Parous	42 43	FLISA		
45	WT	Parous	40.43	ELISA		
46	WT	Parous	54.14	ELISA		
47	WT	Parous	43.29	ELISA		
48	WT	Parous	40.43	ELISA		
49	WT	Parous	39.29	ELISA		
50	WT	Parous	58.29	ELISA		
51	WT	Parous	58.29	ELISA		
52	WT	Parous	42.29	ELISA		
53	WT	Parous	44.71	ELISA		TMA
54	WT	Parous	20.00	ELISA		TMA
55	WT	Parous	53.29	ELISA		TMA
56	WT	Parous	53.29	ELISA		TMA
57	WT	Parous	55.14	ELISA		TMA
58	WT	Parous	54.29	ELISA		TMA
59	WT	Parous	64.57	ELISA	ARRAY	
60	WT	Parous	58.29	ELISA	ARRAY	
61	WT	Parous	65.00	ELISA	ARRAY	
62	WT	Parous	54.29	ELISA		
63	KO	Parous	45.14	ELISA		
64	KO	Parous	45.14	ELISA		
65	KO	Parous	50.00	ELISA		
66	KO	Parous	46.14	ELISA		
67	KO	Parous	49.00	ELISA		
68	KO	Parous	46.71	ELISA		TMA
69	KO	Parous	53.57	ELISA		TMA
70	KO	Parous	58.71	ELISA		TMA
71	KO	Parous	47.00	ELISA		TMA
72	KO	Parous	45.86	ELISA		TMA
73	KO	Parous	41.86	ELISA		TMA
74	KO	Parous	38.14	ELISA		TMA
75	KO	Parous	43.00	ELISA		TMA
76	KO	Parous	41.86	ELISA		TMA
77	KO	Parous	36.00	ELISA		TMA
78	KO	Parous	93.00	ELISA	ARRAY	
79	KO	Parous	75.43	ELISA	ARRAY	
80	KO	Parous	60.00	ELISA	ARRAY	
81	KO	Parous	66.00	ELISA	ARRAY	
82	KO	Parous	66.00	ELISA	ARRAY	
83	KO	Parous	57.86			TMA