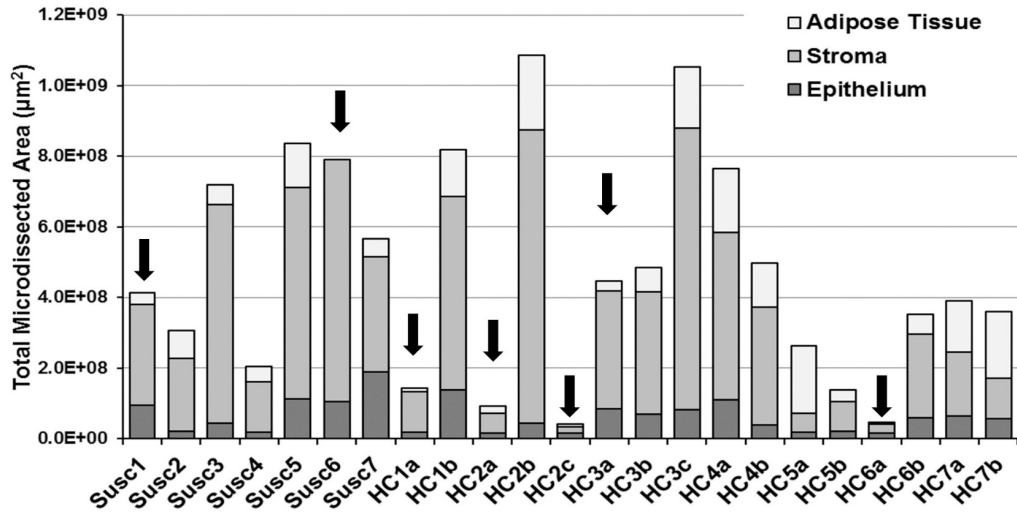
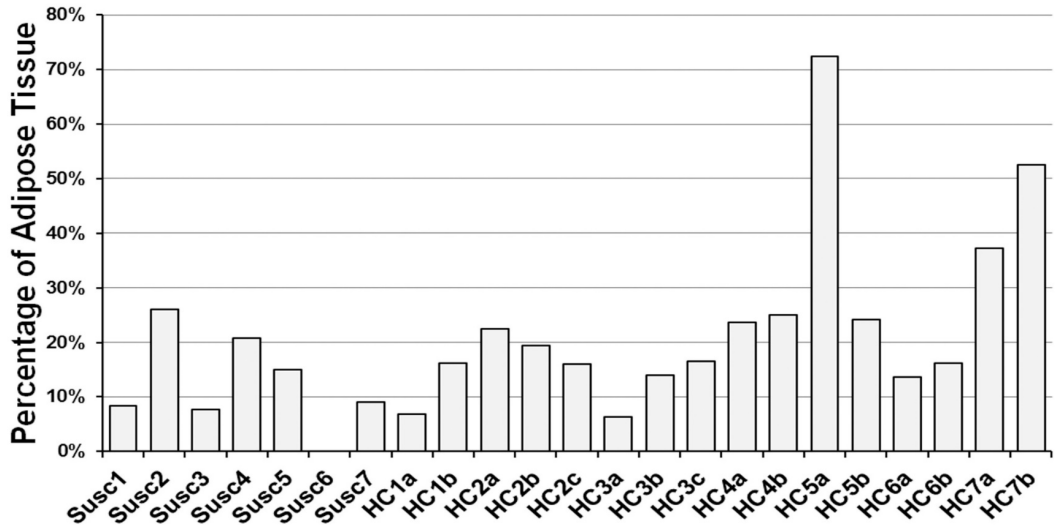
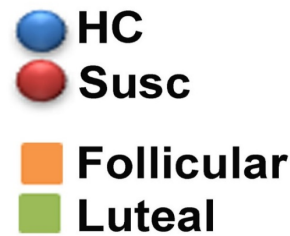
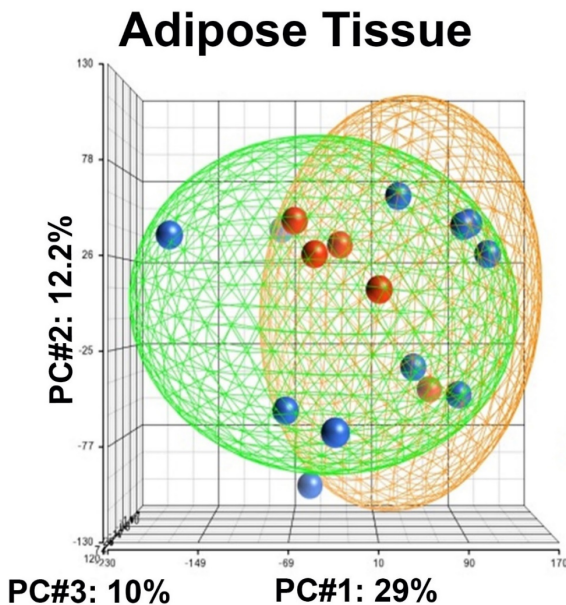
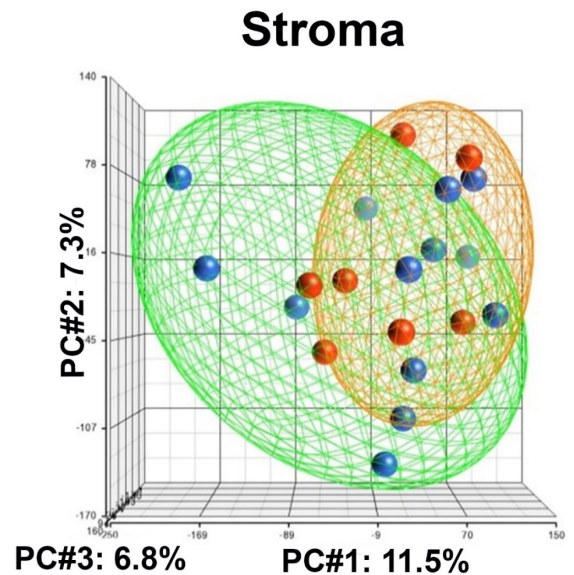
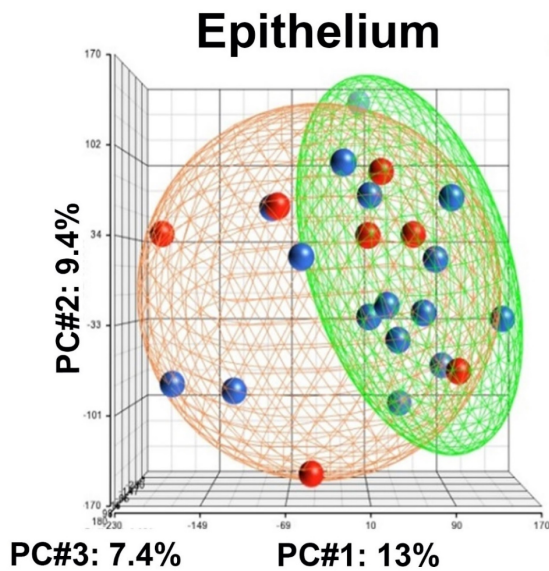
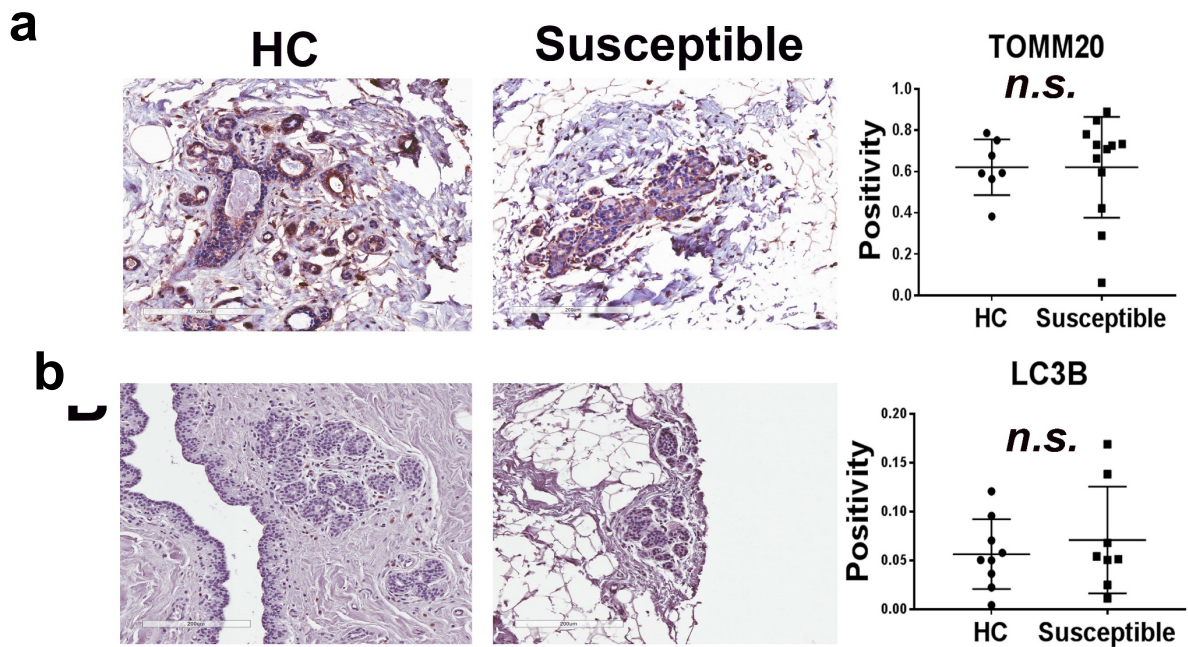


a**b**

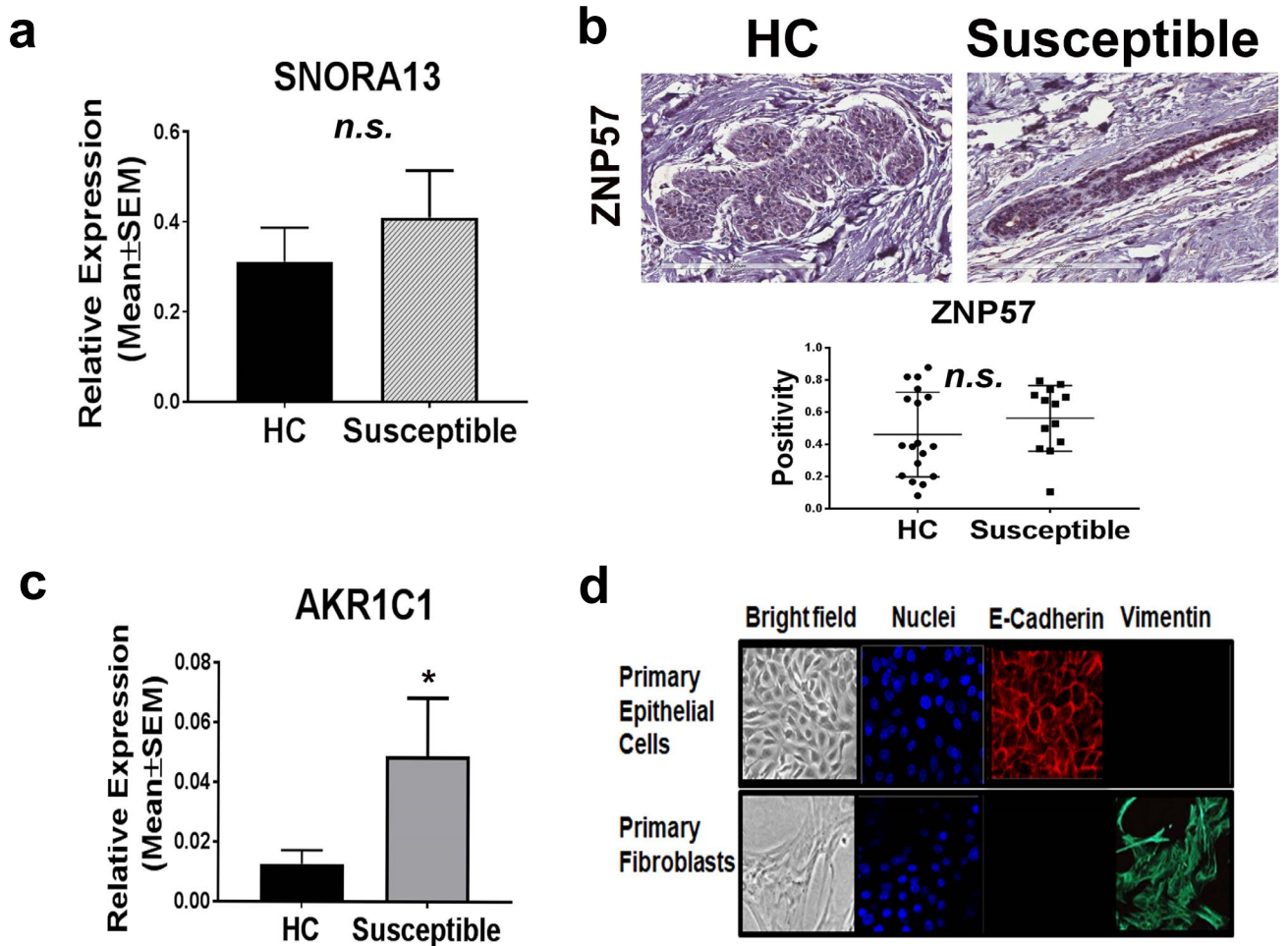
Supplementary Figure 1: Breast tissue microdissection. **a)** Epithelial, stromal and adipose tissue compartments were microdissected from 7 susceptible (Susc) and 16 healthy control (HC) breast tissue samples. Adipose tissue recovered from 6 breast tissue samples (black arrows) was insufficient for the transcriptomic analysis. **b)** Percentage of adipose tissue area in respect of the other tissue compartments in each microdissected sample. In all susceptible samples, the adipose tissue represented only 12.4% (range: 0-26%) of the entire tissue and therefore its influence on the global breast tissue transcriptome is limited.



Supplementary Figure 2: Transcriptome profiling of the microdissected breast compartments. Principal component analysis (PCA) of the transcriptome profile of the microdissected breast epithelium, stroma and adipose tissue from breast tissue cores of susceptible (Susc, red circles) or healthy (HC, blue circles) women at either follicular (orange ellipsoid) or luteal (green ellipsoid) phase of the menstrual cycle.



Supplementary Figure 4: Immunohistochemical evaluation of lipophagy markers. Representative images of the IHC staining with TOMM20 (a) and LC3B (b) antibodies on the paraffin-embedded breast tissue sections (μm) of healthy (HC) and susceptible women are shown on the left. Quantification of the staining, expressed as positivity (ratio of brown positive cells versus total hematoxylin stained nuclei), is shown on the right. Two-tailed t test is used to calculate *p*value *n.s.*: no significant *p*value.



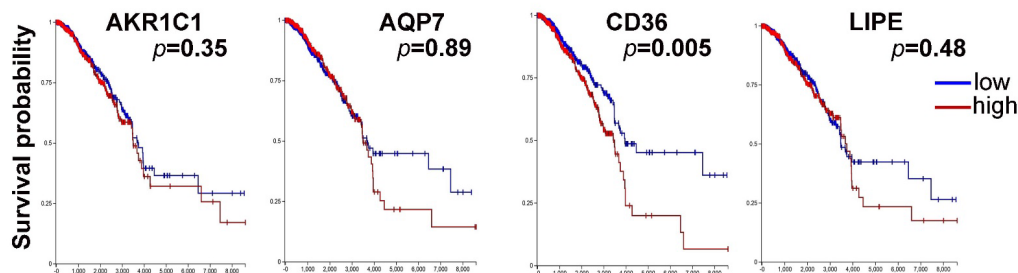
Supplementary Figure 5: Validation of the dysregulation of the selected targets. a) qPCR was used to detect the expression level of SNORA13 in microdissected epithelium from susceptible and healthy control (HC) breast samples. Two-tailed t test is used to calculate *p*value. **b)** IHC staining of ZNP57 in breast tissue sections of susceptible and healthy (HC) women. Matched susceptible and healthy samples were compared using the Wilcoxon matched-pairs signed ranks test. **(c)** Expression of AKR1C1 in the microdissected epithelium was evaluated using qPCR. **d)** Representative images of human primary epithelial cells (left) stained with antibodies for epithelial (E-cadherin, red), mesenchymal (Vimentin, green) lineage and nuclear dye (DAPI, blue). Human primary fibroblast (right) were used as staining control *n.s.*: no significant *p*value; **p*<0.05.

a

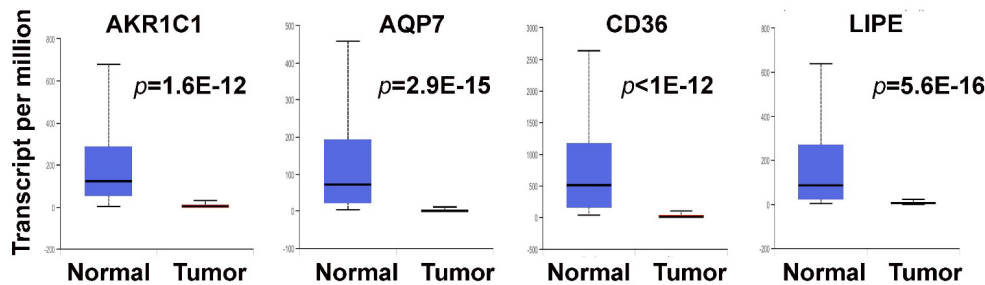
Genomic alteration in AKR1C1, CD36, LIPE and AQP7 genes in Breast Cancer (N=9131, 14 Studies)			
	Cancer Type		
	Invasive Breast Cancer	Breast Cancer	Breast Sarcoma
AKR1C1	2.82%/0.86%*	2.27%/0.16%	
CD36	0.46%/0.46%	0.83%/0.21%	0%/3.7%
LIPE	0.73%/0.36%	0.35%/0.14%	
AQP7	0.91%/0.09%	0.48%/0.1%	

* Amplification frequency/ mutation frequency

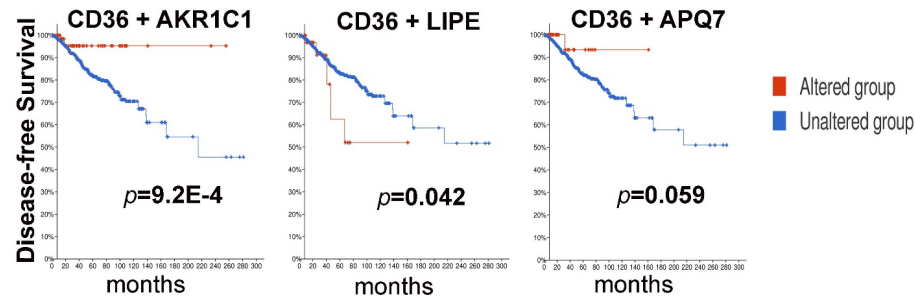
b



c



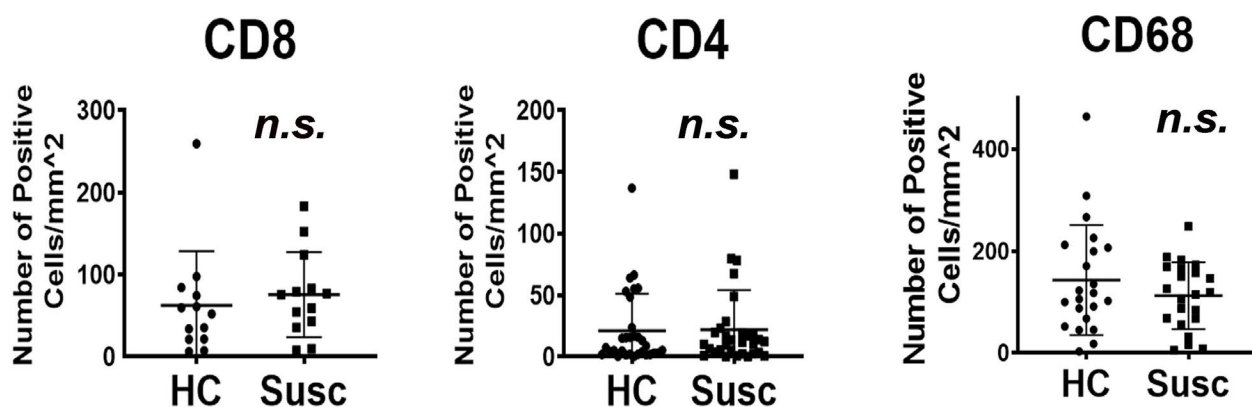
d



e

Mutual Exclusivity analysis of CD36, LIPE, AKR1C1 and AQP7 in Breast Cancer (N=9131, 14 studies)									
A	B	Neither A	Not B	B Not A	Both	Log2 Odds Ratio	p-Value	q-Value	Tendency
AKR1C1	CD36	8812	219	89	11	2.314	<0.001	<0.001	Co-occurrence
CD36	LIPE	8970	94	61	6	>3	<0.001	<0.001	Co-occurrence
LIPE	AQP7	9009	63	55	4	>3	<0.001	0.002	Co-occurrence
AKR1C1	AQP7	8847	225	54	5	1.864	0.016	0.024	Co-occurrence
AKR1C1	LIPE	8839	225	62	5	1.664	0.026	0.032	Co-occurrence
CD36	AQP7	8974	98	57	2	1.684	0.136	0.136	Co-occurrence

Supplementary Figure 6: TCGA analysis of AKR1C1, LIPE, CD36 and AQP7 in breast cancer. Genomic alterations (a), Kaplan Maier curves (b), relation of expression and breast cancer survival rate (c), Kaplan Meier using gene combination (d), and exclusivity analysis (e) were performed by using data from either UALCAN and cBioportal databases.



Supplementary Figure 7: Characterization of the breast stroma and adipose tissue.

IHC staining quantification of CD4, CD8, and CD68 using quPath software. Each dot represents one subject. Comparison between the susceptible and healthy samples was evaluated using a two-sided paired *t*-test.

Supplementary Table 1: Genes differentially expressed between paired susceptible, normal adjacent to tumor (NAT) and contralateral breasts

GeneSymbol	GeneName	NAT vs Contralateral Normal		Susceptible Normal vs Contralateral Normal		Susceptible Normal vs NAT		log2RPKM		Susceptible	Suscep
		PValue	FDR	PValue	FDR	PValue	FDR	Adjacent Norm 1	Adjacent Norm 2		
PPP5K1	diphosphoinositol pentakisphosphate kinase 1	1.9E-05	5.5E-03	1.4E-05	6.7E-04	9.5E-02	3.7E-01	1.38	1.01	-8.36	-8.36
TIMM8A	translocase of inner mitochondrial membrane 8A	5.2E-05	1.2E-02	1.4E-05	6.7E-04	6.8E-02	3.3E-01	3.21	2.86	-6.30	-6.30
FOX1	forkhead box 1	6.8E-05	1.3E-02	9.7E-06	6.7E-04	2.0E-01	4.2E-01	2.99	1.09	-6.65	-6.65
CCDC167	coiled-coil domain containing 167	9.6E-05	1.7E-02	1.8E-05	6.7E-04	1.8E-01	4.1E-01	5.27	3.61	-4.76	-4.76
ZBTB42	zinc finger and BTB domain containing 42	3.1E-04	3.3E-02	9.4E-06	6.7E-04	1.9E-01	4.1E-01	1.61	1.03	-7.27	-7.27
NPL	N-acetylneuraminidase pyruvate lyase	4.9E-04	4.0E-02	3.5E-06	6.7E-04	1.8E-01	4.1E-01	2.17	0.83	-7.11	-7.11
HAUS8	HAUS augmin like complex subunit 8	5.0E-04	4.1E-02	1.7E-05	6.7E-04	4.7E-01	4.9E-01	3.50	1.23	-5.99	-5.99
MRPL33	mitochondrial ribosomal protein L33	1.8E-06	9.5E-04	2.3E-05	6.7E-04	3.1E-01	4.6E-01	5.63	5.13	-4.50	-4.50
SPTBN4	spectrin beta, non-erythrocytic 4	4.0E-04	3.6E-02	2.4E-05	6.7E-04	3.1E-02	2.5E-01	0.45	-0.14	-8.64	-8.64
GATB	glutamyl-tRNA amidotransferase subunit B	5.5E-04	4.2E-02	2.6E-05	6.7E-04	2.5E-01	4.4E-01	0.20	2.63	-6.61	-6.61
ZNF669	zinc finger protein 669	6.4E-05	1.3E-02	3.1E-05	7.5E-04	2.0E-01	4.1E-01	3.13	2.50	-6.44	-6.44
PTRH1	peptidyl-tRNA hydrolase 1 homolog	4.4E-04	3.8E-02	4.2E-05	8.4E-04	2.8E-02	2.5E-01	3.64	2.78	-5.61	-5.61
AP3B2	adaptor related protein complex 3 beta 2 subunit	4.5E-04	3.8E-02	4.0E-05	8.4E-04	1.9E-01	4.1E-01	0.51	-0.06	-8.38	-8.38
ERIC3	glutamate rich 3	1.6E-08	3.4E-05	5.6E-05	8.6E-04	3.6E-01	4.7E-01	3.60	0.10	-8.29	-8.29
CRTAC1	cartilage acidic protein 1	2.5E-04	2.9E-02	5.5E-05	8.6E-04	8.4E-02	3.6E-01	2.42	1.39	-7.07	-7.07
ANKF1	ankyrin repeat and EF-hand domain containing 1	5.2E-04	4.1E-02	5.3E-05	8.6E-04	3.0E-02	2.5E-01	1.90	1.77	-4.32	-4.33
AK7	adenylate kinase 7	5.8E-04	4.3E-02	5.0E-05	8.6E-04	1.8E-03	9.6E-02	1.41	1.32	-7.33	-7.33
PDE6B	phosphodiesterase 6B	1.6E-05	2.1E-02	1.3E-05	9.3E-04	9.1E-02	3.7E-01	2.15	1.56	-7.28	-7.28
LRRRC4C	leucine rich repeat containing 4C	4.6E-04	3.9E-02	6.7E-05	9.3E-04	1.2E-02	1.7E-01	1.26	1.42	-7.35	-7.35
PARP16	poly(ADP-ribose) polymerase family member 16	1.7E-04	2.3E-02	8.4E-05	1.0E-03	5.9E-02	3.2E-01	1.80	1.97	-6.88	-6.88
SLITRK5	SLIT and NTRK like family member 5	2.3E-04	2.7E-02	8.0E-05	1.0E-03	2.9E-02	2.5E-01	1.58	1.22	-7.60	-7.60
LOC101927895	uncharacterized LOC101927895	6.3E-04	4.5E-02	8.3E-05	1.0E-03	2.8E-03	1.2E-01	3.24	3.34	-5.36	-5.36
ZNF385B	zinc finger protein 385B	1.7E-04	2.3E-02	9.6E-05	1.0E-03	3.7E-01	4.7E-01	1.37	0.28	-7.97	-7.97
NSG1	neuronal vesicle trafficking associated 1	4.2E-04	3.7E-02	9.3E-05	1.0E-03	2.0E-02	2.2E-01	1.67	1.88	-6.94	-6.94
ACOT8	acyl-CoA thioesterase 8	2.0E-04	2.6E-02	1.3E-04	1.2E-03	3.9E-02	2.7E-01	3.68	3.13	-5.68	-5.68
LRRRC37A3	leucine rich repeat containing 37 member A3	5.7E-04	4.3E-02	1.2E-04	1.2E-03	3.3E-01	4.6E-01	3.66	1.17	-8.05	-8.05
LIFRA51	LIFR antisense RNA 1	6.6E-04	4.6E-02	1.2E-04	1.2E-03	3.5E-01	4.6E-01	-0.81	1.66	-7.67	-7.67
FANCC	Fanconi anemia complementation group C	3.0E-04	3.2E-02	1.6E-04	1.4E-03	3.2E-01	4.6E-01	-0.63	1.45	-8.00	-8.00
MNNA13	nicotinamide nucleotide adenylyltransferase 3	3.4E-04	3.4E-02	1.6E-04	1.4E-03	3.1E-01	4.6E-01	0.70	2.76	-6.94	-6.94
CADM2	cell adhesion molecule 2	3.7E-04	3.5E-02	1.6E-04	1.4E-03	4.7E-01	4.9E-01	-1.11	0.66	-8.76	-8.76
UBXN8	UBX domain protein 8	4.4E-04	3.8E-02	1.6E-04	1.4E-03	3.4E-01	4.6E-01	3.60	1.48	-5.98	-5.98
RFTN1	raftlin, lipid raft linker 1	1.9E-04	2.5E-02	2.1E-04	1.7E-03	3.3E-01	4.6E-01	2.81	1.55	5.12	5.24
LINC00467	long intergenic non-protein coding RNA 467	5.1E-04	4.1E-02	2.5E-04	2.0E-03	1.7E-01	4.1E-01	2.97	3.65	-5.05	-5.05
ADPRM	ADP-ribose/CDP-alcohol diphosphatase, mannanase	1.3E-04	2.1E-02	3.2E-04	2.4E-03	2.3E-01	4.4E-01	3.23	2.75	-6.05	-6.05
HS2D2	hematopoietic SH2 domain containing	2.9E-04	3.2E-02	3.3E-04	2.4E-03	5.9E-02	3.2E-01	2.33	1.31	-7.13	-7.13
TPRG1	tumor protein p63 regulated 1	1.7E-06	9.5E-04	3.6E-04	2.6E-03	1.1E-01	3.9E-01	2.91	2.50	-7.32	-7.32
NUOFA4	NADH-ubiquinone oxidoreductase complex assembly factor 4	6.6E-05	1.3E-02	4.1E-04	2.8E-03	2.6E-01	4.6E-01	2.41	2.56	-6.72	-6.72
SPR5D2	sphingosine-1-phosphate phosphatase 2	7.9E-05	1.5E-02	4.1E-05	2.9E-03	7.9E-02	3.7E-01	2.33	2.16	-7.83	-7.83
RNF165	ring finger protein 165	9.4E-05	1.7E-02	4.3E-04	2.9E-03	2.4E-01	4.4E-01	1.38	0.39	-8.27	-8.27
CENPW	centromere protein W	3.8E-04	3.5E-02	4.4E-04	2.9E-03	2.4E-01	4.4E-01	1.78	0.72	-7.45	-7.45
MUC15	mucin 15, cell surface associated	1.6E-05	5.1E-03	4.5E-04	2.9E-03	5.0E-01	5.0E-01	3.68	-0.04	-7.21	-7.21
PAK5	p21 (RAC1) activated kinase 5	7.0E-05	1.4E-02	4.8E-04	2.9E-03	1.1E-02	1.7E-01	1.72	1.91	-7.71	-7.71
NXT2	nuclear transport factor 2 like export factor 2	1.6E-04	2.2E-02	4.8E-04	2.9E-03	1.4E-01	4.0E-01	0.67	2.13	-7.02	-7.02
B4GALT6	beta-1,4-galactosyltransferase 6	7.0E-04	4.8E-02	4.8E-04	2.9E-03	9.7E-02	3.7E-01	1.24	1.53	-4.94	-4.95
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	4.0E-04	3.6E-02	5.2E-04	3.0E-03	1.6E-01	4.0E-01	1.40	1.97	-2.67	-2.69
APOD	apolipoprotein D	9.4E-06	3.5E-03	5.6E-04	3.2E-03	2.3E-01	4.4E-01	1.61	9.90	7.94	7.83
ZDHHC13	zinc finger DHHC-type containing 13	1.5E-05	4.7E-03	5.9E-04	3.3E-03	2.5E-01	4.4E-01	2.39	3.33	-6.73	-6.73
ZNF222	zinc finger protein 222	4.5E-04	4.2E-02	6.2E-04	3.4E-03	4.8E-01	4.9E-01	3.31	6.23	-6.23	-6.23
ZNF582	zinc finger protein 582	3.5E-04	3.4E-02	6.7E-04	3.6E-03	2.5E-01	4.5E-01	1.28	1.97	-7.10	-7.10
BID	BH3 interacting domain death agonist	1.6E-04	2.2E-02	7.0E-04	3.6E-03	1.4E-01	4.0E-01	2.07	1.57	-6.86	-6.86
LOC101927045	uncharacterized LOC101927045	7.0E-04	4.8E-02	7.2E-04	3.7E-03	5.0E-01	5.0E-01	1.73	1.86	-6.53	-6.53
CASC2	cancer susceptibility 2 (non-protein coding)	4.3E-04	3.7E-02	7.7E-04	3.9E-03	4.4E-01	4.9E-01	0.31	1.15	-7.83	-7.83
CYB5R2	cytochrome b5 reductase 2	8.5E-05	1.6E-02	8.0E-04	4.0E-03	4.5E-02	2.9E-01	3.09	2.75	-6.45	-6.45
C19orf70	chromosome 19 open reading frame 70	2.2E-05	5.9E-03	8.3E-04	4.0E-03	1.3E-01	4.0E-01	4.38	3.66	-5.59	-5.59
ZFYVE28	zinc finger FYVE-type containing 28	2.2E-04	2.7E-02	8.7E-04	4.1E-03	4.2E-01	4.9E-01	0.05	1.35	-8.00	-8.00
ZNF599	zinc finger protein 599	6.7E-04	4.7E-02	8.7E-04	4.1E-03	1.7E-01	4.1E-01	1.66	1.35	-7.09	-7.09
MKS1	Meckel syndrome, type 1	5.9E-04	4.2E-02	8.9E-04	4.1E-03	3.2E-01	4.6E-01	0.38	2.30	-6.80	-6.80
ESAM	endothelial cell adhesion molecule	7.6E-06	7.6E-04	9.6E-04	4.2E-03	1.2E-01	4.9E-01	1.90	1.38	-6.05	-6.05
ARMC6	armadillo repeat containing 6	3.3E-04	3.4E-02	9.6E-04	4.2E-03	2.9E-01	4.6E-01	2.22	1.29	-6.77	-6.77
DUOX1	dual oxidase 1	3.5E-04	3.4E-02	9.3E-04	4.2E-03	2.7E-01	4.6E-01	1.00	5.00	-7.96	-7.96
ENPEP	glutamyl aminopeptidase	3.9E-04	3.6E-02	1.2E-03	5.2E-03	3.1E-01	4.6E-01	0.76	2.80	4.60	4.40
B4GALT7	beta-1,4-galactosyltransferase 7	6.1E-04	4.5E-02	1.2E-03	5.2E-03	4.5E-01	4.9E-01	2.25	2.01	-6.24	-6.24
LEKR1	leucine, glutamate and lysine rich 1	6.3E-04	4.6E-02	1.4E-03	5.7E-03	1.9E-01	4.1E-01	0.95	0.52	-7.47	-7.47
XDH	xanthine dehydrogenase	1.4E-05	4.5E-03	1.5E-03	5.9E-03	7.4E-02	3.3E-01	1.08	0.80	-7.97	-7.97
EPAS1	endothelial PAS domain protein 1	1.1E-04	1.9E-02	1.5E-03	5.9E-03	1.9E-01	4.1E-01	4.63	4.71	6.82	6.66
RET	ret proto-oncogene	1.1E-04	1.9E-02	1.5E-03	5.9E-03	1.5E-01	4.0E-01	0.76	0.20	-8.21	-8.21
SLC44A3-AS1	SLC44A3 antisense RNA 1	5.9E-04	4.4E-02	1.6E-03	6.1E-03	6.3E-02	3.2E-01	2.74	2.76	-5.86	-5.86
TCEAL5	transcription elongation factor A like 5	1.7E-04	2.6E-02	1.6E-03	6.1E-03	3.8E-01	4.0E-01	3.76	3.45	-5.67	-5.67
LEO1	LEO1 homolog, Par1/RNA polymerase II complex c	4.7E-07	3.5E-04	1.9E-03	7.7E-03	4.0E-02	2.7E-01	5.42	5.31	1.50	1.85
PLXNA3	plexin A3	2.3E-04	2.7E-02	2.1E-03	7.7E-03	3.4E-01	4.6E-01	0.85	1.69	4.13	3.95
TTCA	tetratricopeptide repeat domain 4	6.6E-04	4.6E-02	2.1E-03	7.7E-03	8.5E-02	3.6E-01	1.86	1.81	-6.71	-6.71
MOCOS	molybdenum cofactor sulfurase	2.6E-04	2.9E-02	2.1E-03	7.8E-03	5.0E-01	5.0E-01	0.76	2.38	-7.05	-7.05
LOC100506207	uncharacterized LOC100506207	1.3E-04	2.1E-02	2.2E-03	7.8E-03	6.9E-02	3.3E-01	2.51	2.08	-6.97	-6.97
SMIM22	small integral membrane protein 22	5.9E-04	4.4E-02	2.3E-03	8.0E-03	3.5E-01	4.6E-01	3.62	2.01	-5.61	-5.61
SDHAF3	succinate dehydrogenase complex assembly factor	1.3E-04	2.1E-02	2.4E-03	8.3E-03	2.9E-01	4.6E-01	3.29	1.78	-6.49	-6.49
RAB11FIP4	RAB11 family interacting protein 4	3.2E-06	1.5E-03	2.6E-03	8.9E-03	4.7E-01	4.9E-01	1.83	1.15	-4.61	-4.61
CGREF1	cell growth regulator with EF-hand domain 1	1.6E-04	2.3E-02	2.6E-03	8.9E-03	2.4E-01	4.4E-01	2.11	2.14	-6.88	-6.88
MRPL36	mitochondrial ribosomal protein L36	2.8E-04	2.6E-02	2.8E-03	9.2E-03	2.8E-01	4.6E-01	4.75	3.60	-4.75	-4.75
LINC01473	long intergenic non-protein coding RNA 1473	3.2E-04	3.4E-02	2.8E-03	9.2E-03	1.8E-01	4.1E-01	4.18	4.00	-4.72	-4.72
LINC01481	long intergenic non-protein coding RNA 1481	2.0E-04	2.6E-02	2.9E-03	9.3E-03	3.4E-01	4.6E-01	2.73	3.29	-5.87	-5.87
ROPN1B	rophin associated tail protein 1B	3.8E-04	3.5E-02	2.9E-03	9.3E-03	1.1E-01	4.0E-01	3.67	3.27	-2.47	-2.48
SNAPC2	small nuclear RNA activating complex polypeptide 2	6.0E-04	4.4E-02	3.0E-03	9.6E-03	3.8E-01	4.8E-01	0.69	3.37	-6.21	-6.21
MED21	mediator complex subunit 21	5.5E-05	1.2E-02	3.1E-03	9.9E-03	2.9E-01	4.6E-01	3.78	3.79	-0.75	-0.79
MANE-AS1	NA	3.8E-04	3.5E-02	3.2E-03	9.9E-03	2.9E-01	4.6E-01	1.77	2.15	-6.72	-6.72
DBNDD1	dysbindin domain containing 1	4.7E-04	3.9E-02	3.3E-03	1.0E-02	3.1E-01	4.6E-01	2.30	0.92	-6.96	-6.96
SAXO2	stabilizer of axonemal microtubules 2	7.0E-04	4.8E-02	3.4E-03	1.0E-02	1.9E-01	4.1E-01	0.58	1.55	-7.40	-7.40
FCER1G	Fc fragment of IgE receptor Ig	6.5E-04	4.6E-02	3.6E-03	1.1E-02	5.0E-01	5.0E-01	3.92	3.34	-4.69	-4.69
RNR1	ribonucleoside diphosphate exchange factor 33	3.7E-04	2.4E-02	3.6E-03	1.1E-02	1.3E-01	4.0E-01	3.26	1.50	-7.56	-7.56
AOEC3	amine oxidase, copper containing 3	1.6E									

PLIN1	perilipin 1	6.3E-05	1.3E-02	1.5E-02	3.2E-02	5.8E-02	3.2E-01	1.72	1.98	4.41	5.72	0.80	1.32
CXADR	CXADR, Ig-like cell adhesion molecule	1.8E-04	2.4E-02	1.5E-02	3.2E-02	4.0E-01	4.8E-01	4.00	2.83	0.76	-0.03	3.54	2.91
PTGIS	prostaglandin I2 synthase	3.8E-06	1.7E-03	1.6E-02	3.3E-02	4.3E-01	4.9E-01	2.61	0.38	4.98	4.60	1.87	0.63
SPEG	SPEG complex locus	7.1E-04	4.8E-02	1.7E-02	3.5E-02	6.0E-03	1.6E-01	1.88	1.62	4.44	3.21	0.52	0.59
H2AFY2	H2A histone family member Y2	1.6E-04	2.2E-02	1.7E-02	3.5E-02	3.7E-01	4.7E-01	3.38	3.48	-1.60	-3.49	3.78	2.67
PLN	phospholamban	2.1E-10	6.4E-07	1.7E-02	3.5E-02	6.1E-02	3.2E-01	2.26	0.76	6.72	5.07	-1.19	-3.97
GABPB1-IT1	GABPB1 intronic transcript	8.3E-06	3.8E-03	1.8E-02	3.5E-02	4.7E-01	4.9E-01	2.50	2.16	-2.73	-4.93	1.90	2.85
MYOM1	myomesin 1	1.8E-05	5.4E-03	1.8E-02	3.6E-02	1.8E-02	2.0E-01	1.82	1.42	5.36	3.80	0.58	0.63
ANGPT2	angiotensin 2	1.3E-04	2.1E-02	1.8E-02	3.6E-02	3.7E-02	2.7E-01	0.74	0.52	4.77	3.13	-0.25	-0.90
RHOBTB3	Rho related BTB domain containing 3	5.5E-04	4.2E-02	1.8E-02	3.6E-02	1.7E-02	2.0E-01	4.13	4.03	1.43	2.43	4.59	4.45
ANGPT1	angiotensin 1	1.3E-04	2.1E-02	1.9E-02	3.6E-02	2.5E-01	4.4E-01	1.91	-0.07	5.23	3.53	0.03	0.16
LRRC32	leucine rich repeat containing 32	7.3E-04	4.9E-02	1.9E-02	3.6E-02	2.1E-02	2.2E-01	2.65	2.12	5.48	3.93	0.86	0.32
MREG	melanoregulin	7.3E-08	1.0E-04	1.9E-02	3.7E-02	9.4E-02	3.7E-01	3.98	4.21	0.26	-1.87	4.36	4.80
SLC9A5	solute carrier family 9 member A5	2.0E-06	9.9E-04	1.9E-02	3.7E-02	2.2E-01	4.4E-01	-7.42	-1.81	4.33	2.65	-2.53	-1.18
GCLC	glutamate-cysteine ligase catalytic subunit	3.3E-04	3.4E-02	2.0E-02	3.9E-02	3.9E-01	4.8E-01	3.36	3.04	-1.84	-0.14	3.00	3.27
GLRA3	glycine receptor alpha 3	3.6E-07	2.9E-04	2.1E-02	3.9E-02	3.1E-01	4.6E-01	2.32	2.71	-4.22	-3.33	4.80	1.92
FILIP1L	filamin A interacting protein 1 like	7.7E-06	3.1E-03	2.1E-02	3.9E-02	1.6E-01	4.0E-01	4.17	2.89	6.78	5.42	2.89	2.29
ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1.1E-04	1.9E-02	2.1E-02	3.9E-02	3.3E-01	4.6E-01	1.47	1.93	-4.46	-7.56	1.38	2.78
NRG1	neuregulin 1	9.9E-05	1.8E-02	2.1E-02	3.9E-02	4.2E-01	4.9E-01	1.59	3.72	0.39	-0.65	2.58	2.25
TACO1	translational activator of cytochrome c oxidase I	4.4E-04	3.8E-02	2.1E-02	3.9E-02	2.9E-01	4.6E-01	3.66	2.71	-6.01	-2.92	3.06	2.65
JCHAIN	joining chain of multimeric IgA and IgM	1.9E-10	6.4E-07	2.3E-02	4.1E-02	3.4E-01	4.6E-01	8.83	8.61	5.35	4.65	0.98	7.74
LCP1	lymphocyte cytosolic protein 1	4.7E-04	3.9E-02	2.3E-02	4.2E-02	4.3E-01	4.9E-01	4.36	5.00	1.88	2.87	4.56	4.94
GRIA2	glutamate ionotropic receptor AMPA type subunit 2	2.0E-05	5.8E-03	2.4E-02	4.2E-02	1.3E-01	4.0E-01	1.44	2.79	-8.00	-4.91	0.26	1.34
ANXA3	annexin A3	7.2E-04	4.8E-02	2.4E-02	4.3E-02	4.5E-01	4.9E-01	5.66	5.38	2.64	3.59	5.74	5.22
EHBP1L1	EH domain binding protein 1 like 1	6.4E-04	4.6E-02	2.4E-02	4.3E-02	2.9E-01	4.6E-01	3.25	2.72	5.66	4.66	3.03	3.34
COL5A1	collagen type V alpha 1 chain	1.8E-04	2.4E-02	2.7E-02	4.7E-02	4.8E-01	4.9E-01	3.21	2.46	4.49	5.38	3.07	2.55
RCAN2	regulator of calcineurin 2	2.3E-04	2.7E-02	2.3E-02	4.7E-02	6.9E-02	3.1E-01	3.95	2.02	5.54	3.68	0.89	1.53
LINC00327	long intergenic non-protein coding RNA 327	1.4E-04	2.2E-02	2.7E-02	4.7E-02	1.8E-03	9.6E-02	-6.51	-6.01	1.01	3.62	-3.32	-2.91
LDB3	LIM domain binding 3	5.3E-04	4.2E-02	2.8E-02	4.8E-02	1.5E-02	1.8E-01	0.25	0.75	4.64	2.13	-1.56	-2.24
HBA2	hemoglobin subunit alpha 2	7.1E-06	2.9E-03	2.8E-02	4.8E-02	2.1E-01	4.3E-01	-4.73	-4.73	4.45	5.97	-1.00	-4.73
ST6GAL2	ST6 beta-galactoside alpha-2,6-sialyltransferase 2	4.3E-04	3.7E-02	2.8E-02	4.8E-02	1.3E-02	1.8E-01	-0.13	-0.42	3.68	2.59	0.99	0.74
EGF	epidermal growth factor	4.2E-04	3.7E-02	2.9E-02	4.8E-02	4.6E-01	4.9E-01	1.93	3.35	-2.42	-0.40	2.50	2.96
AEBP1	Ae binding protein 1	1.4E-06	8.6E-04	2.9E-02	4.9E-02	1.3E-01	4.0E-01	5.46	4.56	8.37	6.80	4.46	3.61
IGFBP5	insulin like growth factor binding protein 5	1.7E-06	9.5E-04	3.0E-02	5.1E-02	2.7E-01	4.6E-01	6.73	5.55	9.35	8.04	6.04	5.10
CLEC5A	C-type lectin domain containing 5A	2.3E-05	6.2E-03	3.1E-02	5.1E-02	3.1E-02	2.5E-01	-7.27	-7.27	2.43	2.51	-1.14	-3.67
PDE3A	phosphodiesterase 3A	3.7E-07	2.9E-04	3.1E-02	5.1E-02	1.8E-01	4.1E-01	-1.01	0.01	5.05	3.17	0.20	-1.43
CCOM1	chemokine C1A complex locus 1	5.2E-05	5.9E-03	3.2E-02	5.1E-02	1.2E-04	1.5E-01	-8.21	-8.21	2.22	0.51	-1.78	-1.98
SCGB2A1	secretoglobulin family 2A member 1	2.1E-05	5.9E-03	3.2E-02	5.1E-02	3.3E-01	4.6E-01	3.13	3.93	-4.51	-4.51	2.31	7.25
SCARAS	scavenger receptor class A member 5	1.2E-04	2.0E-02	3.2E-02	5.1E-02	1.3E-01	4.0E-01	3.67	4.63	1.66	0.41	3.33	3.45
AKAP6	A-kinase anchoring protein 6	1.4E-04	2.2E-02	3.1E-02	5.1E-02	4.7E-01	4.9E-01	1.41	1.42	4.47	3.21	1.27	1.54
ADAM33	ADAM metalloproteinase domain 33	1.7E-04	2.3E-02	3.2E-02	5.1E-02	5.4E-02	3.1E-01	3.85	3.24	4.75	6.49	1.15	2.30
SORBS2	sorbin and SH3 domain containing 2	2.1E-04	2.6E-02	3.1E-02	5.1E-02	3.6E-01	4.7E-01	4.25	3.38	6.29	5.35	4.09	3.91
ANKS1B	ankyrin repeat and sterile alpha motif domain contai	2.9E-04	3.2E-02	3.2E-02	5.1E-02	3.6E-01	4.7E-01	2.04	3.06	-2.17	-0.31	2.11	2.54
KCNK2	potassium voltage-gated channel subfamily C mem	3.2E-07	2.9E-04	3.3E-02	5.1E-02	2.2E-01	4.4E-01	3.25	1.86	-4.03	-8.05	1.17	2.26
CLGN	calmagin	1.5E-04	2.2E-02	3.3E-02	5.2E-02	1.5E-01	4.0E-01	1.07	2.41	-2.93	-6.95	2.37	4.39
SYNPO	synaptotagmin	3.8E-04	3.5E-02	3.4E-02	5.2E-02	1.7E-01	4.1E-01	3.13	2.35	5.07	4.34	0.96	0.86
GRPR	regulator of G protein-coupled receptor	1.2E-07	1.4E-04	3.5E-02	5.3E-02	1.7E-01	4.1E-01	3.46	3.20	-6.87	-6.87	3.31	0.87
MYOC	myocilin	6.0E-05	1.3E-02	3.5E-02	5.3E-02	6.1E-02	3.2E-01	-6.48	-6.48	2.18	3.62	-1.41	-4.24
HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2	1.0E-08	2.5E-05	3.5E-02	5.3E-02	3.9E-01	4.8E-01	4.84	2.47	-2.18	-6.75	3.37	4.84
ANK1	ankyrin 1	1.5E-04	2.2E-02	3.5E-02	5.3E-02	1.5E-01	4.0E-01	-8.67	-5.13	0.92	1.46	-5.18	-2.43
FYB2	FYN binding protein 2	2.7E-04	3.0E-02	3.6E-02	5.4E-02	4.1E-01	4.9E-01	1.19	2.77	-3.22	-7.24	1.56	2.91
DUBR	DPPA2 upstream binding RNA	5.0E-04	4.1E-02	3.7E-02	5.5E-02	4.6E-01	4.9E-01	0.05	3.36	5.26	3.89	1.52	2.23
TM2D3	TM2 domain containing 3	3.5E-04	3.4E-02	3.7E-02	5.5E-02	3.3E-02	2.6E-01	4.23	4.70	-0.44	1.35	3.50	3.63
SLFN11	schlafen family member 11	3.6E-04	3.5E-02	3.7E-02	5.5E-02	3.1E-01	4.6E-01	0.92	1.72	3.72	4.75	2.22	1.18
MCAM	melanoma cell adhesion molecule	3.9E-06	1.7E-03	3.8E-02	5.6E-02	2.5E-01	4.4E-01	-6.40	3.81	7.49	6.11	4.27	3.04
PNLDC1	PARN like, ribonuclease domain containing 1	1.1E-04	1.9E-02	3.9E-02	5.7E-02	1.2E-02	1.7E-01	-6.41	-6.41	2.11	3.26	-1.74	0.03
CHMP4C	charged multivesicular body protein 4C	2.9E-04	2.7E-02	3.9E-02	5.7E-02	4.1E-01	4.1E-01	4.15	3.88	-2.31	4.15	4.34	4.00
TFPI2	tissue factor pathway inhibitor 2	2.5E-08	4.3E-05	4.0E-02	5.7E-02	2.9E-01	4.6E-01	4.55	-0.07	-3.63	-2.74	6.80	2.16
ADORA1	adenosine A1 receptor	5.5E-04	4.2E-02	4.0E-02	5.7E-02	1.4E-01	4.0E-01	2.70	1.89	-2.42	-7.00	2.93	2.88
MIR17HG	miR-17-92a-1 cluster host gene	2.1E-04	2.6E-02	4.0E-02	5.8E-02	1.8E-01	4.1E-01	2.04	1.67	-3.20	-7.78	2.05	2.08
CSE1L	chromosome segregation 1 like	3.8E-05	9.0E-03	4.1E-02	5.8E-02	3.3E-01	4.6E-01	4.38	4.88	0.98	2.70	5.19	4.51
PDGFRB	platelet derived growth factor receptor beta	2.6E-04	3.0E-02	4.1E-02	5.8E-02	4.5E-01	4.9E-01	4.63	4.75	7.03	6.12	5.02	4.25
KANK2	KN motif and ankyrin repeat domains 2	7.2E-04	4.8E-02	4.1E-02	5.8E-02	9.5E-02	3.7E-01	4.68	4.33	6.88	5.54	3.92	2.81
ACAN	aggrekan	6.7E-22	1.2E-17	4.2E-02	5.9E-02	6.6E-03	1.6E-01	-8.59	-8.59	5.90	-0.01	-5.77	-6.36
NEBL	nebulin	6.2E-04	4.5E-02	4.4E-02	6.1E-02	7.0E-02	3.3E-01	-3.65	4.07	0.44	2.60	4.31	4.55
BCL2L1	BCL2 like 1	7.4E-04	4.9E-02	4.4E-02	6.1E-02	3.3E-01	4.6E-01	3.78	3.60	1.25	-0.95	3.71	3.55
DRY19L2P4	DRY19L2 pseudogene 4	1.4E-05	1.0E-02	4.4E-02	6.1E-02	2.4E-02	3.3E-01	4.44	3.07	-3.36	-6.46	0.57	-0.30
TJP3	tight junction protein 3	1.2E-05	4.3E-03	4.6E-02	6.2E-02	4.9E-01	5.0E-01	3.55	2.28	-7.19	-2.23	3.20	2.67
MARCKSL1	MARCKS like 1	2.0E-04	2.6E-02	4.6E-02	6.2E-02	1.6E-01	4.0E-01	6.07	5.21	3.97	1.82	6.58	6.04
ZNF79	zinc finger protein 79	3.7E-04	3.5E-02	4.6E-02	6.2E-02	2.8E-01	4.6E-01	3.35	2.51	-6.67	-2.11	2.54	2.73
LAMA5	laminin subunit alpha 5	6.7E-04	4.7E-02	4.6E-02	6.2E-02	1.7E-01	4.1E-01	2.72	2.98	5.33	4.03	2.73	2.61
C10TNF2	C1q and TNF related 2	7.1E-04	4.8E-02	4.5E-02	6.2E-02	1.4E-01	4.0E-01	-3.72	-6.71	1.31	3.45	-1.33	-3.63
FHL5	four and a half LIM domains 5	9.2E-06	3.5E-03	4.8E-02	6.4E-02	1.7E-01	4.1E-01	3.56	0.57	6.79	3.50	0.44	-0.08
PRPF19	pre-mRNA processing factor 19	1.7E-04	2.3E-02	4.9E-02	6.5E-02	4.7E-01	4.9E-01	4.79	4.55	4.03	2.50	4.94	4.34
SORD	sorbitol dehydrogenase	7.6E-04	5.0E-02	5.0E-02	6.6E-02	7.7E-03	1.7E-01	2.20	1.73	-1.44	-6.99	3.83	3.92
PPP1R12B	protein phosphatase 1 regulatory subunit 12B	3.6E-04	3.5E-02	5.0E-02	6.6E-02	3.7E-01	4.7E-01	4.03	3.66	6.44	5.13	3.41	4.00
COL1A2	collagen type I alpha 2 chain	2.3E-04	2.7E-02	5.1E-02	6.7E-02	3.4E-01	4.6E-01	4.76	4.88	7.18	6.20	4.10	4.00
METTL22	methyltransferase like 22	6.9E-04	4.8E-02	5.1E-02	6.7E-02	2.6E-02	2.4E-01	3.41	3.53	-1.55	-6.13	2.59	2.91
CIR1	corepressor interacting with RBPJ, 1	4.4E-05	1.0E-02	5.2E-02	6.8E-02	7.1E-02	3.3E-01	4.67	5.17	2.98	0.09	5.47	5.88
METTL14	methyltransferase like 14	3.4E-04	3.4E-02	5.4E-02	6.9E-02	4.6E-01	4.9E-01	4.02	4.58	2.54	0.61	4.12	4.57
SPEF2	sperm flagellar 2	3.2E-05	7.9E-03	5.6E-02	7.2E-02	3.4E-01	4.6E-01	2.53	3.09	-0.11	-2.73	1.90	3.08
COL5A2	collagen type V alpha 2 chain	6.2E											

ITGA1	integrin subunit alpha 1	5.5E-04	4.2E-02	2.6E-01	2.7E-01	1.4E-01	4.0E-01	3.53	3.88	6.74	4.05	4.68	3.92
ALB	albumin	5.7E-04	4.3E-02	2.6E-01	2.7E-01	4.3E-01	4.9E-01	3.72	1.52	2.79	7.53	5.51	-1.92
TNC	tenascin C	5.4E-05	1.2E-02	2.6E-01	2.7E-01	3.5E-01	4.6E-01	4.45	3.01	6.77	4.35	5.41	3.24
DIO2	iodothyronine deiodinase 2	6.1E-06	2.5E-03	2.8E-01	2.9E-01	1.2E-01	4.0E-01	-0.53	0.25	3.45	0.73	6.48	1.54
VCAN	versican	1.8E-06	9.5E-04	2.9E-01	3.0E-01	2.2E-01	4.4E-01	3.47	3.48	7.87	3.26	4.63	3.45
LINC02344	long intergenic non-protein coding RNA 2344	3.4E-04	3.4E-02	4.1E-01	4.1E-01	1.1E-03	9.6E-02	-4.35	-4.35	-4.35	6.48	2.18	2.84
CP	ceruloplasmin	1.9E-07	1.8E-04	4.5E-01	4.5E-01	3.0E-01	4.6E-01	4.55	-1.60	5.77	2.71	6.04	1.62
TEX41	testis expressed 41 (non-protein coding)	4.2E-04	3.7E-02	4.7E-01	4.7E-01	8.0E-04	9.6E-02	-7.71	-7.71	3.21	-7.71	-2.56	-2.95
LINC01268	long intergenic non-protein coding RNA 1268	2.4E-04	2.8E-02	4.8E-01	4.9E-01	1.3E-02	1.7E-01	-6.91	-6.91	4.24	-6.91	-2.03	-0.14
ECEL1	endothelin converting enzyme like 1	4.2E-04	3.7E-02	4.9E-01	4.9E-01	9.4E-03	1.7E-01	-6.98	-6.98	3.54	-3.90	0.60	-1.25

Supplementary Table 2: Demographics of the study cohort: Susceptible and healthy control (HC) breast tissues were analyzed by immunohistochemistry

	Age at Donation_ran ge	BMI* range	Racial background [#]	Menopausal status ^{**}	BC*** History	Family History of BC	BC Type	Collection year	Year of diagnosis	ER	PR	HER2
Susceptible 9	56-60	>35	White	post	No	Yes (sisiter)	Invasive	2014	2014	+	+	-
Susceptible 8	51-55	20-25	White	pre	No	No	DCIS	2011	2012	+	+	+
Susceptible 38	51-55	>35	AfrAm	post	No	No	DCIS	2012	2017	N/A	N/A	N/A
Susceptible 37	51-55	31-35	AfrAm	post	No	Yes (mother)	N/A	2010	2013	N/A	N/A	N/A
Susceptible 36	36-40	31-35	AfrAm	pre	No	NA	DCIS, Invasive	2012	2014	-	-	-
Susceptible 35	61-65	26-30	AfrAm	post	No	No	N/A	2012	2012	N/A	N/A	N/A
Susceptible 34	36-40	26-30	White	pre	No	No	DCIS	2014	2018	+	+	-
Susceptible 33	61-65	31-35	White	post	No	Yes (sister)	Invasive	2012	2017	+	+	-
Susceptible 32	56-60	31-35	White	post	No	No	DCIS	2012	2017	+	+	-
Susceptible 31	51-55	20-25	White	post	No	No	DCIS	2011	2012	+	-	-
Susceptible 30	41-45	26-30	AfrAm	pre	No	Yes (mother)	Invasive	2012	2017	+	+	-
Susceptible 29	30-35	20-25	White	pre	No	No	Invasive, DCIS, IDC	2010	2017	-	-	+
Susceptible 28	66-70	26-30	White	post	No	Yes (mother, sister)	Invasive, DCIS, IDC	2010	2017	+	N/A	+
Susceptible 27	66-70	26-30	White	post	No	Yes (sister)	DCIS	2014	2016	+	-	-
Susceptible 26	61-65	20-25	White	post	No	Yes (mother)	DCIS	2014	2017	N/A	N/A	N/A
Susceptible 25	56-60	26-30	White	post	No	No	Invasive	2015	2015	-	-	+
Susceptible 24	51-55	>35	White	post	No	No	DCIS	2011	2017	N/A	N/A	N/A
Susceptible 23	41-45	26-30	White	post	No	No	Invasive	2010	2017	-	-	-
Susceptible 22	51-55	31-35	White	post	No	Yes (mother)	DCIS	2011	2016	+	+	-
Susceptible 21	61-65	26-30	White	post	No	No	Invasive, DCIS, IDC	2010	2016	-	-	-
Susceptible 20	46-50	31-35	White	pre	No	No	DCIS	2009	2016	-	-	-
Susceptible 19	46-50	31-35	White	pre	No	No	Invasive	2013	2017	-	-	+
Susceptible 18	66-70	<20	White	post	No	Yes (mother)	DCIS	2014	2015	+	-	-
Susceptible 17	56-60	26-30	White	post	No	No	Invasive	2011	2016	+	+	+
Susceptible 16	61-65	31-35	White	post	No	Yes (Mother)	Invasive	2010	2015	+	-	-
Susceptible 15	36-40	31-35	White	pre	No	No	Invasive	2011	2015	+	+	-
Susceptible 14	56-60	26-30	White	post	No	Yes (mother)	Invasive/ DCIS	2012	2016	+	+	-
Susceptible 13	56-60	31-35	White	post	No	No	DCIS	2011	2014	+	+	-
Susceptible 12	56-60	26-30	White	post	No	No	DCIS	2014	2014	-	-	+
Susceptible 11	>70	26-30	White	post	No	No	Invasive	2009	2012	-	-	-
Susceptible 10	56-60	26-30	White	post	No	No	DCIS	2012	2012	+	-	-
HC9	56-60	31-35	White	pre	No	Yes (Mother)		2011				
HC8	51-55	26-30	White	post	No	No		2012				
HC38	51-55	31-35	AfrAm	post	No	No		2012				
HC37	51-55	31-35	AfrAm	post	No	Yes (mother)		2012				
HC36	36-40	31-35	AfrAm	pre	No	No		2012				
HC35	61-65	26-30	AfrAm	post	No	Yes (mother)		2016				
HC34	36-40	20-25	White	pre	No	No		2016				
HC33	61-65	31-35	White	post	No	No		2013				
HC32	51-55	31-35	White	post	No	No		2013				
HC31	51-55	26-30	White	post	No	No		2012				
HC30	41-45	26-30	AfrAm	pre	No	No		2012				
HC29	30-35	20-25	White	pre	No	No		2012				
HC28	66-70	26-30	White	post	No	No		2011				
HC27	66-70	26-30	White	post	No	No		2013				
HC26	66-70	20-25	White	post	No	No		2013				
HC25	51-55	26-30	White	post	No	No		2014				
HC24	51-55	31-35	White	post	No	No		2011				
HC23	41-45	31-35	White	post	No	No		2010				
HC22	51-55	31-35	White	post	No	No		2010				
HC21	61-65	26-30	White	post	No	Yes (mother, sister)		2016				
HC20	46-50	31-35	White	pre	No	Yes (sisters)		2012				
HC19	46-50	31-35	White	pre	No	No		2014				
HC18	66-70	20-25	White	post	No	Yes (mother)		2014				
HC17	56-60	26-30	White	post	No	No		2010				
HC16	61-65	26-30	White	post	No	No		2010				
HC15	36-40	>35	White	pre	No	No		2014				
HC14	56-60	26-30	White	post	No	Yes (sister)		2013				
HC13	56-60	>35	White	post	No	Yes (Mother)		2010				
HC12	56-60	26-30	White	post	No	No		2009				
HC11	>70	26-30	White	post	No	No		2012				
HC10	56-60	26-30	White	post	No	No		2014				

*BMI: Body Mass Index; #: White: Caucasian, AfrAm: African American; **pre: premenopausal, post: postmenopausal; ** BC: Breast Cancer; #N/A: Not Available; DCIS: Ductal Carcinoma *In Situ*; IDC: Invasive Ductal Carcinoma; ILC: Infiltrating Lobular Carcinoma.

Supplementary Table 3: List of genes differentially expressed in the microdissected breast epithelium, stroma and adipose tissue between healthy women at either luteal (*italic*) or follicular (underlined) phase of the menstrual cycle.

Reason for removal	Gene Symbol	Gene Name	pvalue	K01049	K010434	K010287	K010581	K010278	K010472	K010589	K010474	K010588	K010475	K010587	K010476	K010586	K010477	K010585	K010478	K010584	K010479	K010583	K010480	K010582	K010481	K010581	K010482	K010580	K010483	K010579	K010484	K010578	K010485	K010577	K010486	K010576	K010487	K010575	K010488	K010574	K010489	K010573	K010490	K010572	K010491	K010571	K010492	K010570	K010493	K010569	K010494	K010568	K010495	K010567	K010496	K010566	K010497	K010565	K010498	K010564	K010499	K010563	K010500	K010491	K010559	K010492	K010558	K010493	K010557	K010494	K010556	K010495	K010555	K010496	K010554	K010497	K010553	K010498	K010552	K010499	K010551	K010501	K010491	K010549	K010492	K010548	K010493	K010547	K010494	K010546	K010495	K010545	K010496	K010544	K010497	K010543	K010498	K010542	K010499	K010541	K010502	K010491	K010519	K010492	K010518	K010493	K010517	K010494	K010516	K010495	K010515	K010496	K010514	K010497	K010513	K010498	K010512	K010499	K010511	K010503	K010491	K010509	K010492	K010508	K010493	K010507	K010494	K010506	K010495	K010505	K010496	K010504	K010497	K010503	K010498	K010502	K010499	K010501	K010506	K010491	K010499	K010498	K010497	K010496	K010495	K010494	K010493	K010492	K010491	K010490	K010489	K010488	K010487	K010486	K010485	K010484	K010483	K010482	K010481	K010480	K010479	K010478	K010477	K010476	K010475	K010474	K010473	K010472	K010471	K010470	K010469	K010468	K010467	K010466	K010465	K010464	K010463	K010462	K010461	K010460	K010459	K010458	K010457	K010456	K010455	K010454	K010453	K010452	K010451	K010450	K010449	K010448	K010447	K010446	K010445	K010444	K010443	K010442	K010441	K010440	K010439	K010438	K010437	K010436	K010435	K010434	K010433	K010432	K010431	K010430	K010429	K010428	K010427	K010426	K010425	K010424	K010423	K010422	K010421	K010420	K010419	K010418	K010417	K010416	K010415	K010414	K010413	K010412	K010411	K010410	K010409	K010408	K010407	K010406	K010405	K010404	K010403	K010402	K010401	K010400	K010399	K010398	K010397	K010396	K010395	K010394	K010393	K010392	K010391	K010390	K010389	K010388	K010387	K010386	K010385	K010384	K010383	K010382	K010381	K010380	K010379	K010378	K010377	K010376	K010375	K010374	K010373	K010372	K010371	K010370	K010369	K010368	K010367	K010366	K010365	K010364	K010363	K010362	K010361	K010360	K010359	K010358	K010357	K010356	K010355	K010354	K010353	K010352	K010351	K010350	K010349	K010348	K010347	K010346	K010345	K010344	K010343	K010342	K010341	K010340	K010339	K010338	K010337	K010336	K010335	K010334	K010333	K010332	K010331	K010330	K010329	K010328	K010327	K010326	K010325	K010324	K010323	K010322	K010321	K010320	K010319	K010318	K010317	K010316	K010315	K010314	K010313	K010312	K010311	K010310	K010309	K010308																																																																																																																																																																																																																																																																																																																																																																																																																																			
Microdissected Tissue	Change between Metastasis Phases	HLA-H	major histocompatibility complex, class II (pseudogene)	1.8E-03	239	158	158	330	270	194	75	264	111	939	461	275	519	467	421	286																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											</

*unpaired two-tails t-test *p*-value

Supplementary Table 4: Breast Epithelium-specific differentially expressed genes between susceptible and healthy control breast.

Symbol	geneName	FC*	log2FC	PValue	FDR
AQP7	aquaporin 7	2.49	1.32	1.16E-05	0.001
AKR1C1	aldo-keto reductase family 1 member C1	4.34	2.12	1.18E-05	0.001
XIRP2	xin actin binding repeat containing 2	7.36	2.88	2.44E-05	0.002
SIM1	single-minded family bHLH transcription factor 1	5.44	2.44	6.23E-05	0.003
RBP4	retinol binding protein 4	3.66	1.87	2.77E-04	0.010
PLIN1	perilipin 1	3.92	1.97	3.10E-04	0.010
SORCS1	sortilin related VPS10 domain containing receptor 1	3.01	1.59	3.72E-04	0.010
ZFP57	ZFP57 zinc finger protein	-28.97	-4.86	3.76E-04	0.010
LIPE	lipase E, hormone sensitive type	2.19	1.13	4.42E-04	0.010
MAPK10	mitogen-activated protein kinase 10	2.12	1.09	4.43E-04	0.010
GATA2-AS1	GATA2 antisense RNA 1	2.27	1.18	5.40E-04	0.010
SLED1	proteoglycan 3 pseudogene	2.98	1.58	6.72E-04	0.010
G0S2	G0/G1 switch 2	2.93	1.55	6.73E-04	0.010
CIDEA	cell death-inducing DFFA-like effector a	3.60	1.85	6.85E-04	0.010
NAV3	neuron navigator 3	1.38	0.47	7.01E-04	0.010
STAB2	stabilin 2	2.43	1.28	7.34E-04	0.010
ACVR1C	activin A receptor type 1C	2.19	1.13	1.01E-03	0.013
MYH2	myosin heavy chain 2	6.88	2.78	1.06E-03	0.013
RPS16P5	ribosomal protein S16 pseudogene 5	2.54	1.34	1.32E-03	0.015
FAM221B	family with sequence similarity 221 member B	2.75	1.46	1.56E-03	0.017
CRTC3-AS1	CRTC3 antisense RNA 1	-1.87	-0.90	1.64E-03	0.017
GABRE	gamma-aminobutyric acid type A receptor epsilon subunit	2.21	1.14	1.80E-03	0.018
TNNC2	troponin C2, fast skeletal type	2.37	1.24	1.82E-03	0.018
ADIPOQ	adiponectin, C1Q and collagen domain containing	3.82	1.93	1.93E-03	0.018
INO80B	INO80 complex subunit B	1.87	0.91	2.01E-03	0.018
AQP7P1	aquaporin 7 pseudogene 1	2.06	1.04	2.30E-03	0.020
ACTA1	actin, alpha 1, skeletal muscle	5.40	2.43	2.41E-03	0.020
LOC10192696	uncharacterized LOC101926960	4.33	2.12	2.63E-03	0.020
PLIN4	perilipin 4	2.53	1.34	2.66E-03	0.020
SLC19A3	solute carrier family 19 member 3	3.33	1.74	2.67E-03	0.020
GPD1	glycerol-3-phosphate dehydrogenase 1	2.92	1.55	3.19E-03	0.023
GRIA1	glutamate ionotropic receptor AMPA type subunit 1	2.89	1.53	3.43E-03	0.024
ABCC6	ATP binding cassette subfamily C member 6	2.13	1.09	3.52E-03	0.024
TRHDE-AS1	TRHDE antisense RNA 1	3.86	1.95	4.01E-03	0.025
MYOZ2	myozenin 2	2.13	1.09	4.05E-03	0.025
TUSC5	tumor suppressor candidate 5	4.07	2.03	4.09E-03	0.025
CD36	CD36 molecule	1.72	0.79	4.25E-03	0.026
NOVA1	NOVA alternative splicing regulator 1	1.58	0.66	4.81E-03	0.028
FABP4	fatty acid binding protein 4	2.22	1.15	5.55E-03	0.031
SDS	serine dehydratase	2.42	1.27	5.82E-03	0.031
SNORA13	small nucleolar RNA, H/ACA box 13	-4.30	-2.10	6.11E-03	0.031
FAM86C2P	family with sequence similarity 86, member A pseudogene	-1.42	-0.50	6.13E-03	0.031
TRAF5	TNF receptor associated factor 5	1.40	0.49	6.48E-03	0.031
KLRF1	killer cell lectin like receptor F1	2.38	1.25	6.50E-03	0.031
LOC10192796	uncharacterized LOC101927969	2.12	1.08	6.81E-03	0.031
SLC5A4	solute carrier family 5 member 4	2.01	1.01	6.85E-03	0.031
SAA4	serum amyloid A4, constitutive	-2.46	-1.30	6.86E-03	0.031
HEPACAM	hepatic and glial cell adhesion molecule	2.38	1.25	7.18E-03	0.031
SLC30A1	solute carrier family 30 member 1	1.29	0.36	7.25E-03	0.031
KLB	klotho beta	2.19	1.13	7.44E-03	0.031
FAM214A	family with sequence similarity 214 member A	1.64	0.72	7.48E-03	0.031
SLC4A10	solute carrier family 4 member 10	2.77	1.47	7.81E-03	0.031
SLC2A1-AS1	SLC2A1 antisense RNA 1	2.11	1.07	8.07E-03	0.031
MMP27	matrix metalloproteinase 27	-2.85	-1.51	8.08E-03	0.031
F8	coagulation factor VIII	1.30	0.38	8.22E-03	0.031

PAQR5	progesterone and adiponectin receptor family member 5	1.92	0.94	8.28E-03	0.031
FN3KRP	fructosamine 3 kinase related protein	-1.36	-0.44	8.29E-03	0.031
PCAT19	prostate cancer associated transcript 19 (non-protein coding)	1.51	0.60	8.36E-03	0.031
CBR3-AS1	CBR3 antisense RNA 1	1.71	0.77	8.36E-03	0.031
TMEM229B	transmembrane protein 229B	-1.71	-0.77	8.43E-03	0.031
TSPAN11	tetraspanin 11	-1.72	-0.78	8.58E-03	0.031
DLEU1	deleted in lymphocytic leukemia 1	1.55	0.63	8.74E-03	0.031
PCCA	propionyl-CoA carboxylase alpha subunit	1.34	0.42	9.04E-03	0.031
TPRXL	tetrapeptide repeat homeobox like	1.85	0.89	9.07E-03	0.031
NR5A2	nuclear receptor subfamily 5 group A member 2	1.53	0.61	9.67E-03	0.032
APOB	apolipoprotein B	3.02	1.60	9.73E-03	0.032
TEKT4P2	tektin 4 pseudogene 2	-1.60	-0.68	9.77E-03	0.032
MIR3619	microRNA 3619	1.94	0.95	1.01E-02	0.032
RAET1E-AS1	RAET1E antisense RNA 1	-1.91	-0.93	1.02E-02	0.032
HSD17B13	hydroxysteroid 17-beta dehydrogenase 13	1.83	0.87	1.02E-02	0.032
EMX2	empty spiracles homeobox 2	-2.11	-1.08	1.02E-02	0.032
KCNMA1	potassium calcium-activated channel subfamily M alpha 1	1.52	0.61	1.06E-02	0.032
CPEB2	cytoplasmic polyadenylation element binding protein 2	1.33	0.41	1.06E-02	0.032
CXCR6	C-X-C motif chemokine receptor 6	-1.74	-0.80	1.09E-02	0.033
GYG2	glycogenin 2	1.79	0.84	1.13E-02	0.033
LILRA1	leukocyte immunoglobulin like receptor A1	-1.93	-0.95	1.13E-02	0.033
FAM169A	family with sequence similarity 169 member A	1.36	0.45	1.14E-02	0.033
CPNE5	copine 5	-1.78	-0.83	1.17E-02	0.033
KC6	keratoconus gene 6	5.30	2.41	1.24E-02	0.035
TRIM5	tripartite motif containing 5	-1.24	-0.31	1.26E-02	0.035
LOC10272335	uncharacterized LOC102723354	1.75	0.80	1.27E-02	0.035
LEP	leptin	3.76	1.91	1.33E-02	0.036
GUCY1A3	guanylate cyclase 1 soluble subunit alpha	-1.44	-0.52	1.40E-02	0.036
FAM129C	family with sequence similarity 129 member C	2.44	1.29	1.44E-02	0.036
CPA4	carboxypeptidase A4	-1.81	-0.86	1.44E-02	0.036
PCDHAC1	protocadherin alpha subfamily C, 1	1.75	0.81	1.44E-02	0.036
ARMCX4	armadillo repeat containing, X-linked 4	1.47	0.56	1.45E-02	0.036
C19orf18	chromosome 19 open reading frame 18	1.62	0.70	1.45E-02	0.036
SLC26A7	solute carrier family 26 member 7	1.67	0.74	1.47E-02	0.036
SARDH	sarcosine dehydrogenase	-1.44	-0.52	1.47E-02	0.036
C19orf73	chromosome 19 open reading frame 73	1.57	0.65	1.54E-02	0.037
RGPD4	RANBP2-like and GRIP domain containing 4	-2.12	-1.09	1.54E-02	0.037
COLCA1	colorectal cancer associated 1	1.58	0.66	1.60E-02	0.038
LPL	lipoprotein lipase	1.79	0.84	1.61E-02	0.038
MIR548N	microRNA 548n	2.06	1.05	1.63E-02	0.038
NIPAL3	NIPA like domain containing 3	-1.28	-0.36	1.67E-02	0.038
RAB38	RAB38, member RAS oncogene family	-1.35	-0.43	1.69E-02	0.038
ST6GALNAC5	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	-1.79	-0.84	1.71E-02	0.038
ZNF876P	zinc finger protein 876, pseudogene	1.33	0.41	1.72E-02	0.038
ALDH1L1	aldehyde dehydrogenase 1 family member L1	1.69	0.76	1.74E-02	0.038
CLDN19	claudin 19	1.46	0.55	1.75E-02	0.038
RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	1.67	0.74	1.77E-02	0.038
HCG27	HLA complex group 27 (non-protein coding)	1.72	0.78	1.78E-02	0.038
LINC01132	long intergenic non-protein coding RNA 1132	-1.72	-0.78	1.79E-02	0.038
PTH2R	parathyroid hormone 2 receptor	1.61	0.69	1.88E-02	0.039
C15orf57	chromosome 15 open reading frame 57	-1.23	-0.29	1.89E-02	0.039
KCND2	potassium voltage-gated channel subfamily D member 2	1.86	0.89	1.89E-02	0.039
RNF24	ring finger protein 24	-1.26	-0.33	1.92E-02	0.040
COL8A2	collagen type VIII alpha 2 chain	-1.36	-0.44	1.96E-02	0.040
CEP19	centrosomal protein 19	-1.46	-0.54	1.99E-02	0.040
C1orf21	chromosome 1 open reading frame 21	1.39	0.48	2.02E-02	0.040
ARMCX2	armadillo repeat containing, X-linked 2	-1.21	-0.28	2.04E-02	0.040
HTR7P1	5-hydroxytryptamine receptor 7 pseudogene 1	1.31	0.39	2.05E-02	0.040
WDYHV1	WDYHV motif containing 1	1.34	0.42	2.07E-02	0.040

GUCY1B3	guanylate cyclase 1 soluble subunit beta	-1.37	-0.45	2.14E-02	0.040
DHRS12	dehydrogenase/reductase 12	1.26	0.33	2.16E-02	0.040
SLC41A2	solute carrier family 41 member 2	1.50	0.59	2.17E-02	0.040
TESPA1	thymocyte expressed, positive selection associated 1	1.53	0.61	2.18E-02	0.040
PDE2A	phosphodiesterase 2A	1.47	0.56	2.20E-02	0.040
LINC01296	long intergenic non-protein coding RNA 1296	1.78	0.84	2.20E-02	0.040
CHST6	carbohydrate sulfotransferase 6	-2.24	-1.16	2.21E-02	0.040
PDE3B	phosphodiesterase 3B	1.47	0.56	2.25E-02	0.040
ANP32A-IT1	ANP32A intronic transcript 1	1.49	0.58	2.29E-02	0.040
ZNF793-AS1	ZNF793 antisense RNA 1 (head to head)	1.75	0.81	2.32E-02	0.040
LOC728730	uncharacterized LOC728730	1.28	0.36	2.33E-02	0.040
NPIPB11	nuclear pore complex interacting protein family member B11	1.67	0.74	2.34E-02	0.040
LOC10099663	killer cell lectin like receptor F1	2.37	1.25	2.38E-02	0.040
ADRA2A	adrenoceptor alpha 2A	1.87	0.91	2.38E-02	0.040
IRX6	iroquois homeobox 6	1.91	0.93	2.39E-02	0.040
HIF1A-AS1	HIF1A antisense RNA 1	-1.87	-0.90	2.40E-02	0.040
YEATS2	YEATS domain containing 2	-1.18	-0.24	2.46E-02	0.040
TIMP4	TIMP metalloproteinase inhibitor 4	1.73	0.79	2.49E-02	0.040
PLEKHD1	pleckstrin homology and coiled-coil domain containing D1	1.99	1.00	2.50E-02	0.040
GATA2	GATA binding protein 2	1.60	0.68	2.51E-02	0.040
LOC440300	chondroitin sulfate proteoglycan 4 pseudogene	1.71	0.77	2.52E-02	0.040
SPRN	shadow of prion protein homolog (zebrafish)	-1.89	-0.92	2.52E-02	0.040
KLHL7-AS1	KLHL7 antisense RNA 1 (head to head)	-1.95	-0.96	2.52E-02	0.040
SLC25A33	solute carrier family 25 member 33	1.28	0.36	2.53E-02	0.040
GPRIN2	G protein regulated inducer of neurite outgrowth 2	-1.40	-0.48	2.55E-02	0.040
ELOVL5	ELOVL fatty acid elongase 5	1.84	0.88	2.55E-02	0.040
PPP1R15B	protein phosphatase 1 regulatory subunit 15B	1.17	0.22	2.55E-02	0.040
HDC	histidine decarboxylase	2.18	1.12	2.61E-02	0.040
PIGL	phosphatidylinositol glycan anchor biosynthesis class L	1.41	0.50	2.62E-02	0.040
KLF9	Kruppel like factor 9	1.23	0.30	2.64E-02	0.040
SKAP1	src kinase associated phosphoprotein 1	-1.37	-0.46	2.67E-02	0.040
CIDEC	cell death inducing DFFA like effector c	3.01	1.59	2.67E-02	0.040
LOC10192806	uncharacterized LOC101928069	-1.48	-0.57	2.68E-02	0.040
LOC642236	NA	1.67	0.74	2.75E-02	0.041
TMEM132C	transmembrane protein 132C	1.75	0.80	2.78E-02	0.041
CYP39A1	cytochrome P450 family 39 subfamily A member 1	-1.39	-0.48	2.79E-02	0.041
PHC1	polyhomeotic homolog 1	1.22	0.29	2.87E-02	0.042
HRASLS5	HRAS like suppressor family member 5	1.34	0.42	2.87E-02	0.042
SORD	sorbitol dehydrogenase	1.84	0.88	2.88E-02	0.042
FZD4	frizzled class receptor 4	1.26	0.34	2.91E-02	0.042
IFITM10	interferon induced transmembrane protein 10	1.56	0.64	2.91E-02	0.042
LRRN3	leucine rich repeat neuronal 3	-1.48	-0.56	2.93E-02	0.042
FREM2	FRAS1 related extracellular matrix protein 2	-1.60	-0.67	2.99E-02	0.042
CD8A	CD8a molecule	-1.41	-0.50	3.04E-02	0.042
SLC25A30-AS	SLC25A30 antisense RNA 1	1.64	0.71	3.07E-02	0.042
THSD1	thrombospondin type 1 domain containing 1	1.24	0.31	3.08E-02	0.042
KCNIP2	potassium voltage-gated channel interacting protein 2	1.75	0.81	3.17E-02	0.042
THEM4	thioesterase superfamily member 4	1.29	0.36	3.18E-02	0.042
CHRN2	cholinergic receptor nicotinic beta 2 subunit	1.46	0.55	3.18E-02	0.042
FAM81B	family with sequence similarity 81 member B	2.03	1.02	3.19E-02	0.042
SMO	smoothened, frizzled class receptor	-1.32	-0.41	3.20E-02	0.042
RGS22	regulator of G-protein signaling 22	1.59	0.67	3.20E-02	0.042
MAPK8	mitogen-activated protein kinase 8	1.26	0.34	3.20E-02	0.042
PPID	peptidylprolyl isomerase D	-1.20	-0.27	3.20E-02	0.042
ANKRD29	ankyrin repeat domain 29	1.34	0.42	3.21E-02	0.042
POU5F1P5	POU class 5 homeobox 1 pseudogene 5	1.71	0.77	3.21E-02	0.042
RNF130	ring finger protein 130	-1.20	-0.26	3.25E-02	0.042
TPSAB1	tryptase alpha/beta 1	2.08	1.06	3.30E-02	0.042
CXCR5	C-X-C motif chemokine receptor 5	2.29	1.20	3.32E-02	0.042

IL27RA	interleukin 27 receptor subunit alpha	-1.33	-0.41	3.32E-02	0.042
NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	1.54	0.63	3.33E-02	0.042
MMRN1	multimerin 1	2.33	1.22	3.38E-02	0.043
LTBP1	latent transforming growth factor beta binding protein 1	-1.34	-0.42	3.44E-02	0.043
SDC2	syndecan 2	-1.32	-0.40	3.49E-02	0.043
COLCA2	colorectal cancer associated 2	1.52	0.60	3.60E-02	0.044
THOC6	THO complex 6	-1.28	-0.36	3.62E-02	0.044
PCDHB13	protocadherin beta 13	1.30	0.38	3.62E-02	0.044
TBP	TATA-box binding protein	1.20	0.26	3.66E-02	0.045
ACACB	acetyl-CoA carboxylase beta	1.34	0.42	3.67E-02	0.045
GPX3	glutathione peroxidase 3	1.51	0.59	3.79E-02	0.045
LINC01465	long intergenic non-protein coding RNA 1465	1.49	0.57	3.80E-02	0.045
LOC401052	uncharacterized LOC401052	1.44	0.53	3.80E-02	0.045
MURC	muscle related coiled-coil protein	-1.69	-0.75	3.82E-02	0.045
OXER1	oxoeicosanoid receptor 1	1.54	0.62	3.83E-02	0.045
LOC10012951	uncharacterized LOC100129518	1.58	0.66	3.83E-02	0.045
AMH	anti-Mullerian hormone	1.98	0.98	3.85E-02	0.045
RAPGEF3	Rap guanine nucleotide exchange factor 3	1.41	0.50	3.90E-02	0.045
ZMAT4	zinc finger matrix-type 4	1.77	0.83	3.90E-02	0.045
FAM181B	family with sequence similarity 181 member B	-1.55	-0.63	3.98E-02	0.046
STYK1	serine/threonine/tyrosine kinase 1	1.67	0.74	3.99E-02	0.046
PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	1.38	0.46	4.01E-02	0.046
FAM90A1	family with sequence similarity 90 member A1	-1.62	-0.70	4.08E-02	0.046
ROR2	receptor tyrosine kinase like orphan receptor 2	-1.30	-0.38	4.15E-02	0.046
PRDM1	PR/SET domain 1	-1.26	-0.33	4.15E-02	0.046
EMP1	epithelial membrane protein 1	1.39	0.48	4.16E-02	0.046
MUC3A	mucin 3A, cell surface associated	1.51	0.59	4.16E-02	0.046
UNC119B	unc-119 lipid binding chaperone B	-1.16	-0.21	4.16E-02	0.046
AIM2	absent in melanoma 2	1.75	0.80	4.17E-02	0.046
MYO16	myosin XVI	2.17	1.12	4.18E-02	0.046
CGNL1	cingulin like 1	-1.21	-0.28	4.19E-02	0.046
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	1.43	0.52	4.24E-02	0.046
MIR24-1	microRNA 24-1	1.81	0.86	4.26E-02	0.046
HEY2	hes related family bHLH transcription factor with YRPW motif 2	-1.39	-0.47	4.32E-02	0.046
LOC10013134	RAD52 motif containing 1 pseudogene	1.62	0.70	4.34E-02	0.046
SPTLC3	serine palmitoyltransferase long chain base subunit 3	-1.21	-0.28	4.42E-02	0.047
SSTR2	somatostatin receptor 2	1.78	0.83	4.45E-02	0.047
ANAPC13	anaphase promoting complex subunit 13	1.20	0.26	4.46E-02	0.047
ABCB5	ATP binding cassette subfamily B member 5	1.96	0.97	4.47E-02	0.047
NRIP2	nuclear receptor interacting protein 2	-1.50	-0.58	4.52E-02	0.047
PCOLCE2	procollagen C-endopeptidase enhancer 2	2.30	1.20	4.54E-02	0.047
BTNL9	butyrophilin like 9	1.45	0.54	4.54E-02	0.047
EFNB3	ephrin B3	-1.25	-0.33	4.68E-02	0.048
HOXD3	homeobox D3	1.49	0.57	4.77E-02	0.049
SNX29P2	sorting nexin 29 pseudogene 2	1.44	0.53	4.82E-02	0.049
PPARG	peroxisome proliferator activated receptor gamma	1.37	0.45	4.93E-02	0.050
LINC00612	long intergenic non-protein coding RNA 612	1.61	0.68	4.95E-02	0.050
EMX2OS	EMX2 opposite strand/antisense RNA	-1.59	-0.67	4.96E-02	0.050
LOC10028863	OTU deubiquitinase 7A pseudogene	-1.61	-0.69	4.96E-02	0.050

*FC: Fold Change of Susceptible sample versus healthy control

Supplementary Table 5: List of genes differentially expressed in breast stroma in susceptible versus healthy breasts

Symbol	geneName	FC*	log2FC	PValue	FDR
MIR6079	microRNA 6079	2.64	1.40	1.3E-05	0.007
ANKRD36BP2	ankyrin repeat domain 36B pseudogene 2	-2.10	-1.07	2.1E-05	0.007
RFTN1	raftlin, lipid raft linker 1	1.39	0.47	5.7E-05	0.013
LOC283710	uncharacterized LOC283710	-3.80	-1.93	1.2E-04	0.013
LRGUK	leucine rich repeats and guanylate kinase domain containing	-2.30	-1.20	1.2E-04	0.013
TBX5	T-box 5	-1.67	-0.74	1.4E-04	0.013
GAS2	growth arrest specific 2	-2.43	-1.28	1.6E-04	0.013
WNT10A	Wnt family member 10A	-2.13	-1.09	1.7E-04	0.013
SLC15A2	solute carrier family 15 member 2	-1.65	-0.72	1.8E-04	0.013
PDK1	pyruvate dehydrogenase kinase 1	-1.53	-0.61	2.0E-04	0.013
FAM46C	family with sequence similarity 46 member C	-2.46	-1.30	2.1E-04	0.013
HIST1H4D	histone cluster 1 H4 family member d	-1.63	-0.71	2.9E-04	0.015
DERL3	derlin 3	-2.14	-1.10	2.9E-04	0.015
BLNK	B-cell linker	-1.43	-0.52	3.0E-04	0.015
PIM2	Pim-2 proto-oncogene, serine/threonine kinase	-1.97	-0.98	3.2E-04	0.015
GPR15	G protein-coupled receptor 15	-6.62	-2.73	3.4E-04	0.015
MAPK10	mitogen-activated protein kinase 10	1.60	0.67	4.1E-04	0.016
SYNJ1	synaptojanin 1	-1.30	-0.38	4.5E-04	0.017
CD38	CD38 molecule	-1.85	-0.89	4.8E-04	0.017
PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	1.42	0.50	5.5E-04	0.019
SLC17A9	solute carrier family 17 member 9	-1.68	-0.75	6.9E-04	0.020
TCEANC2	transcription elongation factor A N-terminal and central domain containin	-1.31	-0.39	7.7E-04	0.020
DDIT4	DNA damage inducible transcript 4	1.72	0.78	7.8E-04	0.020
FADS3	fatty acid desaturase 3	1.50	0.59	7.8E-04	0.020
C6orf165	NA	-3.02	-1.59	8.0E-04	0.020
LINC01504	long intergenic non-protein coding RNA 1504	-3.04	-1.60	8.2E-04	0.020
TCAP	titin-cap	2.61	1.39	8.6E-04	0.020
LOC100128593	uncharacterized LOC100128593	-2.29	-1.19	9.3E-04	0.020
LOC100506725	uncharacterized LOC100506725	-2.56	-1.36	9.3E-04	0.020
HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1	-1.32	-0.40	9.4E-04	0.020
SCRN2	secernin 2	1.37	0.45	1.0E-03	0.020
TSSK4	testis specific serine kinase 4	-2.05	-1.03	1.0E-03	0.020
ALDH1L1	aldehyde dehydrogenase 1 family member L1	2.71	1.44	1.0E-03	0.020
TNNC2	troponin C2, fast skeletal type	2.88	1.53	1.1E-03	0.020
GINS2	GINS complex subunit 2	-2.40	-1.27	1.1E-03	0.020
TIAM1	T-cell lymphoma invasion and metastasis 1	-1.35	-0.43	1.1E-03	0.020
SARDH	sarcosine dehydrogenase	-1.51	-0.59	1.1E-03	0.020
NLRP11	NLR family pyrin domain containing 11	-6.95	-2.80	1.2E-03	0.020
TNFRSF18	TNF receptor superfamily member 18	-3.38	-1.76	1.2E-03	0.020
SLC7A10	solute carrier family 7 member 10	3.28	1.71	1.2E-03	0.020
ZBP1	Z-DNA binding protein 1	-1.94	-0.96	1.3E-03	0.020
FAH	fumarylacetoacetate hydrolase	1.82	0.86	1.3E-03	0.020
SLC10A7	solute carrier family 10 member 7	-1.34	-0.42	1.3E-03	0.020
AQP7P1	aquaporin 7 pseudogene 1	2.24	1.16	1.3E-03	0.020
KCNA3	potassium voltage-gated channel subfamily A member 3	-1.83	-0.87	1.4E-03	0.020
ALOX12	arachidonate 12-lipoxygenase, 12S type	-3.71	-1.89	1.4E-03	0.020
OIP5-AS1	OIP5 antisense RNA 1	-1.27	-0.34	1.4E-03	0.020
LOC729737	uncharacterized LOC729737	-1.98	-0.99	1.4E-03	0.020
KANSL1L	KAT8 regulatory NSL complex subunit 1 like	-1.37	-0.45	1.4E-03	0.020
C15orf57	chromosome 15 open reading frame 57	-1.34	-0.42	1.5E-03	0.020
ELOVL5	ELOVL fatty acid elongase 5	1.58	0.66	1.6E-03	0.021
DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides 1	-1.98	-0.99	1.6E-03	0.021
GIPC1	GIPC PDZ domain containing family member 1	1.28	0.36	1.7E-03	0.022
MZB1	marginal zone B and B1 cell specific protein	-1.86	-0.90	1.8E-03	0.022
LOC101930071	uncharacterized LOC101930071	1.91	0.94	1.9E-03	0.023
LOC101927318	uncharacterized LOC101927318	-6.40	-2.68	1.9E-03	0.023
IRF4	interferon regulatory factor 4	-1.71	-0.77	1.9E-03	0.023
CYP20A1	cytochrome P450 family 20 subfamily A member 1	-1.28	-0.35	1.9E-03	0.023
LRRC32	leucine rich repeat containing 32	1.34	0.42	2.0E-03	0.023
MAP7D1	MAP7 domain containing 1	1.34	0.42	2.0E-03	0.023
TNNT1	troponin T1, slow skeletal type	4.82	2.27	2.0E-03	0.023
ESRRA	estrogen related receptor alpha	1.33	0.42	2.2E-03	0.024
FAAHP1	fatty acid amide hydrolase pseudogene 1	-3.42	-1.77	2.3E-03	0.024

LY75	lymphocyte antigen 75	-2.19	-1.13	2.3E-03	0.024
DAPK2	death associated protein kinase 2	1.56	0.64	2.4E-03	0.024
KLHL6	kelch like family member 6	-1.55	-0.63	2.4E-03	0.024
TET2	tet methylcytosine dioxygenase 2	-1.21	-0.27	2.5E-03	0.024
PTTG2	pituitary tumor-transforming 2	-2.59	-1.37	2.5E-03	0.024
NPR1	natriuretic peptide receptor 1	1.33	0.41	2.5E-03	0.024
LOC102723766	uncharacterized LOC102723766	-1.99	-0.99	2.5E-03	0.024
PTPRM	protein tyrosine phosphatase, receptor type M	1.29	0.37	2.5E-03	0.024
SNRNP35	small nuclear ribonucleoprotein U11/U12 subunit 35	1.25	0.32	2.6E-03	0.024
RSPH9	radial spoke head 9 homolog	-2.79	-1.48	2.7E-03	0.024
FZD4	frizzled class receptor 4	1.39	0.48	2.7E-03	0.024
COLCA2	colorectal cancer associated 2	1.54	0.62	2.7E-03	0.024
MFSD2A	major facilitator superfamily domain containing 2A	-2.83	-1.50	2.7E-03	0.024
GPR63	G protein-coupled receptor 63	-2.17	-1.12	2.7E-03	0.024
HK2	hexokinase 2	1.99	0.99	2.7E-03	0.024
LINC00648	long intergenic non-protein coding RNA 648	2.89	1.53	2.8E-03	0.024
FRMD4A	FERM domain containing 4A	1.34	0.42	2.8E-03	0.024
NGLY1	N-glycanase 1	-1.24	-0.32	2.9E-03	0.024
TSPAN15	tetraspanin 15	1.47	0.55	2.9E-03	0.024
FCRL5	Fc receptor like 5	-2.00	-1.00	3.1E-03	0.025
SPAG4	sperm associated antigen 4	-2.06	-1.05	3.3E-03	0.027
LINC01230	long intergenic non-protein coding RNA 1230	3.05	1.61	3.4E-03	0.027
P2RY13	purinergic receptor P2Y13	-2.15	-1.10	3.5E-03	0.027
ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	1.47	0.55	3.5E-03	0.027
PHLDA3	pleckstrin homology like domain family A member 3	1.41	0.50	3.5E-03	0.027
MT1X	metallothionein 1X	1.77	0.83	3.6E-03	0.027
CPO	carboxypeptidase O	-2.23	-1.16	3.6E-03	0.027
COL25A1	collagen type XXV alpha 1 chain	1.42	0.51	3.6E-03	0.027
AJAP1	adherens junctions associated protein 1	1.90	0.93	3.7E-03	0.027
UBAC2-AS1	UBAC2 antisense RNA 1	1.83	0.87	3.8E-03	0.028
PLEKHS1	pleckstrin homology domain containing S1	-2.32	-1.21	3.9E-03	0.028
CTNBP1	catenin beta interacting protein 1	1.29	0.37	3.9E-03	0.028
MDF1	MyoD family inhibitor	1.83	0.88	3.9E-03	0.028
EAF2	ELL associated factor 2	-1.54	-0.62	4.0E-03	0.028
TLE4	transducin like enhancer of split 4	-1.23	-0.30	4.0E-03	0.028
FAM213A	family with sequence similarity 213 member A	1.59	0.67	4.2E-03	0.029
IL6R	interleukin 6 receptor	-1.34	-0.43	4.2E-03	0.029
SPATS2	spermatogenesis associated serine rich 2	-1.34	-0.42	4.4E-03	0.029
CCR2	C-C motif chemokine receptor 2	-2.16	-1.11	4.4E-03	0.029
ZNF740	zinc finger protein 740	1.19	0.25	4.4E-03	0.029
RACGAP1	Rac GTPase activating protein 1	-1.57	-0.65	4.4E-03	0.029
FABP4	fatty acid binding protein 4	2.30	1.20	4.6E-03	0.030
PHLDB1	pleckstrin homology like domain family B member 1	1.33	0.41	4.7E-03	0.030
OSBPL3	oxysterol binding protein like 3	-1.25	-0.32	4.8E-03	0.030
PLA2G16	phospholipase A2 group XVI	1.69	0.76	4.9E-03	0.030
ETFB	electron transfer flavoprotein beta subunit	1.42	0.51	4.9E-03	0.030
CCSAP	centriole, cilia and spindle associated protein	-1.28	-0.35	5.1E-03	0.030
FGD5P1	FYVE, RhoGEF and PH domain containing 5 pseudogene 1	1.68	0.75	5.2E-03	0.030
APOBEC3F	apolipoprotein B mRNA editing enzyme catalytic subunit 3F	-1.30	-0.38	5.2E-03	0.030
ZNF818P	zinc finger protein 818, pseudogene	-1.47	-0.56	5.3E-03	0.030
RBM17	RNA binding motif protein 17	1.16	0.21	5.3E-03	0.030
AOC3	amine oxidase, copper containing 3	1.67	0.74	5.3E-03	0.030
PABPN1	poly(A) binding protein nuclear 1	1.36	0.45	5.3E-03	0.030
RHOB	ras homolog family member B	1.35	0.43	5.4E-03	0.030
PLGRKT	plasminogen receptor with a C-terminal lysine	1.38	0.46	5.4E-03	0.030
NAT8L	N-acetyltransferase 8 like	2.54	1.35	5.4E-03	0.030
DNALI1	dynein axonemal light intermediate chain 1	1.32	0.40	5.4E-03	0.030
SIM1	single-minded family bHLH transcription factor 1	2.97	1.57	5.4E-03	0.030
LRP4	LDL receptor related protein 4	-1.38	-0.46	5.4E-03	0.030
LINC00324	long intergenic non-protein coding RNA 324	-1.43	-0.52	5.5E-03	0.030
QRICH2	glutamine rich 2	-1.45	-0.54	5.5E-03	0.030
DUSP4	dual specificity phosphatase 4	1.90	0.92	5.5E-03	0.030
DHX34	DEAH-box helicase 34	-1.30	-0.38	5.7E-03	0.031
DCUN1D3	defective in cullin neddylation 1 domain containing 3	1.44	0.53	5.7E-03	0.031
MUC15	mucin 15, cell surface associated	-3.27	-1.71	6.0E-03	0.031
PIM3	Pim-3 proto-oncogene, serine/threonine kinase	1.39	0.47	6.0E-03	0.031

VPS72	vacuolar protein sorting 72 homolog	1.19	0.25	6.0E-03	0.031
TMEM74B	transmembrane protein 74B	1.78	0.84	6.0E-03	0.031
ADIPOQ-AS1	ADIPOQ antisense RNA 1	2.91	1.54	6.1E-03	0.031
TXNDC11	thioredoxin domain containing 11	-1.28	-0.36	6.1E-03	0.031
SLAMF7	SLAM family member 7	-1.76	-0.81	6.1E-03	0.031
ACAA1	acetyl-CoA acyltransferase 1	1.24	0.31	6.2E-03	0.031
APOBEC3B	apolipoprotein B mRNA editing enzyme catalytic subunit 3B	-2.55	-1.35	6.2E-03	0.031
LOC102724927	uncharacterized LOC102724927	-2.15	-1.11	6.4E-03	0.032
ARL4A	ADP ribosylation factor like GTPase 4A	-1.51	-0.59	6.4E-03	0.032
STYXL1	serine/threonine/tyrosine interacting like 1	-1.43	-0.52	6.4E-03	0.032
MRPL41	mitochondrial ribosomal protein L41	1.40	0.49	6.4E-03	0.032
HIST1H2BF	histone cluster 1 H2B family member f	-1.80	-0.85	6.5E-03	0.032
ZNF571	zinc finger protein 571	-1.34	-0.42	7.1E-03	0.034
MTRNR2L8	MT-RNR2-like 8	-1.86	-0.90	7.4E-03	0.034
MRAS	muscle RAS oncogene homolog	1.44	0.52	7.4E-03	0.034
CTNS	cystinosis, lysosomal cystine transporter	-1.27	-0.35	7.4E-03	0.034
PPIL3	peptidylprolyl isomerase like 3	-1.35	-0.43	7.4E-03	0.034
PHKG1	phosphorylase kinase catalytic subunit gamma 1	1.59	0.67	7.5E-03	0.034
IGFBP3	insulin like growth factor binding protein 3	1.37	0.45	7.5E-03	0.034
BRPF1	bromodomain and PHD finger containing 1	1.21	0.27	7.6E-03	0.034
GLDC	glycine decarboxylase	-2.24	-1.16	7.6E-03	0.034
TSTD3	thiosulfate sulfurtransferase (rhodanese)-like domain containing 3	-1.33	-0.41	7.6E-03	0.034
FRG1B	NA	1.26	0.33	7.6E-03	0.034
GPCPD1	glycerophosphocholine phosphodiesterase 1	-1.23	-0.29	7.8E-03	0.034
PEX5	peroxisomal biogenesis factor 5	1.20	0.26	7.8E-03	0.034
BOK	BOK, BCL2 family apoptosis regulator	1.66	0.73	7.9E-03	0.034
SNORD37	small nucleolar RNA, C/D box 37	-1.83	-0.87	7.9E-03	0.034
LOC202181	SUMO interacting motifs containing 1 pseudogene	-1.25	-0.32	8.0E-03	0.034
LHFPL1	lipoma HMGIC fusion partner-like 1	-2.71	-1.44	8.0E-03	0.034
NFKBIA	NFKB inhibitor alpha	1.22	0.28	8.1E-03	0.034
ADCY6	adenylate cyclase 6	1.35	0.43	8.1E-03	0.034
CYB5A	cytochrome b5 type A	1.58	0.66	8.1E-03	0.034
HIST2H2BF	histone cluster 2 H2B family member f	-1.54	-0.63	8.1E-03	0.034
ZNF778	zinc finger protein 778	-1.24	-0.31	8.2E-03	0.034
CDC37	cell division cycle 37	1.23	0.30	8.3E-03	0.034
MYL2	myosin light chain 2	5.55	2.47	8.4E-03	0.034
PPIF	peptidylprolyl isomerase F	1.29	0.36	8.4E-03	0.034
NDUFA4L2	NDUFA4, mitochondrial complex associated like 2	1.44	0.53	8.4E-03	0.034
NOC2L	NOC2 like nucleolar associated transcriptional repressor	1.23	0.29	8.5E-03	0.034
AAMP	angio associated migratory cell protein	1.25	0.32	8.5E-03	0.034
DDAH2	dimethylarginine dimethylaminohydrolase 2	1.35	0.43	8.6E-03	0.035
BOP1	block of proliferation 1	1.44	0.53	8.7E-03	0.035
PCSK4	proprotein convertase subtilisin/kexin type 4	-1.97	-0.98	8.8E-03	0.035
GFOD1	glucose-fructose oxidoreductase domain containing 1	1.43	0.52	8.8E-03	0.035
CDR1	cerebellar degeneration related protein 1	2.36	1.24	8.8E-03	0.035
TFIP11	tuftelin interacting protein 11	1.22	0.29	8.9E-03	0.035
STX2	syntaxin 2	-1.29	-0.37	9.1E-03	0.035
UNG	uracil DNA glycosylase	1.26	0.33	9.1E-03	0.035
SHCBP1	SHC binding and spindle associated 1	2.23	1.15	9.3E-03	0.035
CENPQ	centromere protein Q	-1.51	-0.60	9.3E-03	0.035
CCR5	C-C motif chemokine receptor 5 (gene/pseudogene)	-1.99	-0.99	9.4E-03	0.035
AIFM2	apoptosis inducing factor, mitochondria associated 2	1.52	0.61	9.4E-03	0.035
CXorf21	chromosome X open reading frame 21	-1.88	-0.91	9.4E-03	0.035
PI4K2B	phosphatidylinositol 4-kinase type 2 beta	-1.22	-0.29	9.4E-03	0.035
GRAMD1B	GRAM domain containing 1B	-1.43	-0.51	9.5E-03	0.035
WBP4	WW domain binding protein 4	1.22	0.29	9.5E-03	0.035
AHR	aryl hydrocarbon receptor	-1.29	-0.37	9.6E-03	0.035
PDK2	pyruvate dehydrogenase kinase 2	1.29	0.37	9.7E-03	0.035
ANKRD20A5P	ankyrin repeat domain 20 family member A5, pseudogene	-1.45	-0.53	9.8E-03	0.035
POLH	DNA polymerase eta	-1.27	-0.34	9.9E-03	0.035
CCDC144NL	coiled-coil domain containing 144 family, N-terminal like	2.80	1.49	9.9E-03	0.035
DECR1	2,4-dienoyl-CoA reductase 1, mitochondrial	1.24	0.31	1.0E-02	0.035
FTSJ3	FtsJ homolog 3	1.24	0.31	1.0E-02	0.035
BMS1P20	BMS1, ribosome biogenesis factor pseudogene 20	-1.27	-0.35	1.0E-02	0.035
SLC2A4RG	SLC2A4 regulator	1.20	0.27	1.0E-02	0.035
RMDN3	regulator of microtubule dynamics 3	1.30	0.37	1.0E-02	0.035

CCNJL	cyclin J like	-1.46	-0.55	1.0E-02	0.035
BLCAP	bladder cancer associated protein	1.22	0.28	1.0E-02	0.035
RBP7	retinol binding protein 7	1.70	0.76	1.0E-02	0.035
TLR1	toll like receptor 1	-1.66	-0.73	1.0E-02	0.035
LOC101926975	uncharacterized LOC101926975	2.63	1.39	1.0E-02	0.035
CXorf65	chromosome X open reading frame 65	2.09	1.06	1.0E-02	0.035
RGS3	regulator of G-protein signaling 3	1.34	0.42	1.0E-02	0.035
HN1	hematological and neurological expressed 1	-1.41	-0.50	1.0E-02	0.035
GATA2	GATA binding protein 2	1.29	0.37	1.0E-02	0.035
FAM212B	family with sequence similarity 212 member B	1.36	0.44	1.0E-02	0.035
CARS	cysteinyl-tRNA synthetase	1.19	0.25	1.0E-02	0.035
FAM50A	family with sequence similarity 50 member A	1.21	0.28	1.1E-02	0.035
ANGPT4	angiopoietin 4	2.04	1.03	1.1E-02	0.035
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2	1.95	0.96	1.1E-02	0.035
C20orf27	chromosome 20 open reading frame 27	1.34	0.43	1.1E-02	0.035
PLIN1	perilipin 1	2.46	1.30	1.1E-02	0.035
ANKRD2	ankyrin repeat domain 2	3.25	1.70	1.1E-02	0.035
RBP5	retinol binding protein 5	1.68	0.75	1.1E-02	0.035
E2F2	E2F transcription factor 2	-3.06	-1.61	1.1E-02	0.035
EVI2A	ecotropic viral integration site 2A	-1.83	-0.87	1.1E-02	0.035
LMCD1	LIM and cysteine rich domains 1	1.27	0.34	1.1E-02	0.035
KIAA0125	NA	-1.76	-0.82	1.1E-02	0.035
TLR7	toll like receptor 7	-1.71	-0.78	1.1E-02	0.035
ABCD2	ATP binding cassette subfamily D member 2	1.75	0.81	1.1E-02	0.035
TYRO3	TYRO3 protein tyrosine kinase	1.64	0.72	1.2E-02	0.035
ACO1	aconitase 1	1.40	0.48	1.2E-02	0.035
IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gam	1.25	0.32	1.2E-02	0.035
ATP1A2	ATPase Na+/K+ transporting subunit alpha 2	2.14	1.10	1.2E-02	0.035
RBP4	retinol binding protein 4	2.90	1.54	1.2E-02	0.035
KIF22	kinesin family member 22	1.26	0.33	1.2E-02	0.035
NBPF1	neuroblastoma breakpoint family member 1	-1.32	-0.40	1.2E-02	0.035
RUNX1-IT1	RUNX1 intronic transcript 1	-1.95	-0.96	1.2E-02	0.035
TSSC4	tumor suppressing subtransferable candidate 4	1.36	0.45	1.2E-02	0.035
TMEM150A	transmembrane protein 150A	-1.32	-0.40	1.2E-02	0.035
LRRC57	leucine rich repeat containing 57	-1.22	-0.29	1.2E-02	0.036
CCDC42B	NA	-2.73	-1.45	1.2E-02	0.036
ZNF215	zinc finger protein 215	-1.75	-0.81	1.2E-02	0.036
GAS2L3	growth arrest specific 2 like 3	-1.54	-0.62	1.2E-02	0.036
DNAL1	dynein axonemal light chain 1	-1.21	-0.28	1.2E-02	0.036
C14orf180	chromosome 14 open reading frame 180	2.53	1.34	1.2E-02	0.036
RALY-AS1	RALY antisense RNA 1	-1.92	-0.94	1.3E-02	0.036
VTRNA1-1	vault RNA 1-1	-1.67	-0.74	1.3E-02	0.036
HINT2	histidine triad nucleotide binding protein 2	1.38	0.47	1.3E-02	0.036
ITGA7	integrin subunit alpha 7	1.63	0.71	1.3E-02	0.036
PRKAB1	protein kinase AMP-activated non-catalytic subunit beta 1	1.20	0.26	1.3E-02	0.036
GBE1	1,4-alpha-glucan branching enzyme 1	1.36	0.44	1.3E-02	0.036
MIR5091	microRNA 5091	1.82	0.86	1.3E-02	0.036
CATSPER2P1	cation channel sperm associated 2 pseudogene 1	1.56	0.64	1.3E-02	0.036
EMX2OS	EMX2 opposite strand/antisense RNA	-1.63	-0.71	1.3E-02	0.036
DTX1	deltex E3 ubiquitin ligase 1	1.46	0.55	1.3E-02	0.036
MEA1	male-enhanced antigen 1	1.27	0.35	1.3E-02	0.036
FERMT1	fermitin family member 1	-1.74	-0.80	1.3E-02	0.036
MYH7	myosin heavy chain 7	6.45	2.69	1.3E-02	0.036
FAM185A	family with sequence similarity 185 member A	-1.22	-0.28	1.3E-02	0.036
CDH5	cadherin 5	1.31	0.39	1.3E-02	0.036
QDPR	quinoid dihydropteridine reductase	1.36	0.44	1.4E-02	0.036
AKR1C3	aldo-keto reductase family 1 member C3	1.45	0.53	1.4E-02	0.036
CYP39A1	cytochrome P450 family 39 subfamily A member 1	-1.50	-0.58	1.4E-02	0.036
HSD17B13	hydroxysteroid 17-beta dehydrogenase 13	2.09	1.06	1.4E-02	0.036
FRMD3	FERM domain containing 3	1.28	0.35	1.4E-02	0.036
P2RY10	purinergic receptor P2Y10	-2.27	-1.18	1.4E-02	0.036
AGAP1-IT1	AGAP1 intronic transcript 1	1.47	0.56	1.4E-02	0.036
NNMT	nicotinamide N-methyltransferase	1.35	0.43	1.4E-02	0.036
PCED1B-AS1	PCED1B antisense RNA 1	-1.68	-0.75	1.4E-02	0.036
ZBTB16	zinc finger and BTB domain containing 16	1.76	0.82	1.4E-02	0.036
PTP4A3	protein tyrosine phosphatase type IVA, member 3	1.72	0.79	1.4E-02	0.036

SLC9C1	solute carrier family 9 member C1	-2.49	-1.31	1.4E-02	0.036
RRH	retinal pigment epithelium-derived rhodopsin homolog	-1.70	-0.77	1.5E-02	0.036
SIGLEC10	sialic acid binding Ig like lectin 10	-1.93	-0.95	1.5E-02	0.036
ZNF205-AS1	ZNF205 antisense RNA 1	1.60	0.68	1.5E-02	0.036
TEKT4P2	tektin 4 pseudogene 2	-1.60	-0.68	1.5E-02	0.036
TSG1	tumor suppressor TSG1	-4.13	-2.05	1.5E-02	0.036
LRRC3	leucine rich repeat containing 3	1.75	0.81	1.5E-02	0.036
LOC441666	zinc finger protein 91 pseudogene	-1.38	-0.47	1.5E-02	0.036
REPIN1	replication initiator 1	1.17	0.23	1.5E-02	0.036
DUSP28	dual specificity phosphatase 28	1.47	0.56	1.5E-02	0.036
STK38	serine/threonine kinase 38	-1.16	-0.21	1.5E-02	0.036
SLC5A4	solute carrier family 5 member 4	1.72	0.78	1.5E-02	0.036
BAALC	brain and acute leukemia, cytoplasmic	1.52	0.61	1.5E-02	0.036
OSGIN2	oxidative stress induced growth inhibitor family member 2	1.32	0.40	1.5E-02	0.036
LAX1	lymphocyte transmembrane adaptor 1	-1.47	-0.56	1.5E-02	0.036
ZGPAT	zinc finger CCCH-type and G-patch domain containing	1.26	0.33	1.5E-02	0.036
GCOM1	GRINL1A complex locus 1	1.50	0.59	1.6E-02	0.036
ST6GALNAC6	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	1.18	0.24	1.6E-02	0.036
FAXC	failed axon connections homolog	-1.69	-0.76	1.6E-02	0.036
RPGR	retinitis pigmentosa GTPase regulator	1.38	0.46	1.6E-02	0.036
APOE	apolipoprotein E	1.50	0.59	1.6E-02	0.036
DOC2A	double C2 domain alpha	-3.52	-1.81	1.6E-02	0.036
ZNF812	NA	-2.09	-1.06	1.6E-02	0.036
PDZD2	PDZ domain containing 2	1.46	0.55	1.6E-02	0.036
NCF1B	neutrophil cytosolic factor 1B pseudogene	-1.73	-0.79	1.6E-02	0.036
CD36	CD36 molecule	1.72	0.78	1.6E-02	0.036
KNTC1	kinetochore associated 1	-1.29	-0.36	1.6E-02	0.036
GHR	growth hormone receptor	1.57	0.65	1.6E-02	0.036
SLC2A12	solute carrier family 2 member 12	-1.63	-0.71	1.6E-02	0.036
TMEM37	transmembrane protein 37	2.01	1.01	1.6E-02	0.036
ACVR1C	activin A receptor type 1C	2.35	1.23	1.6E-02	0.036
ADCY3	adenylate cyclase 3	1.23	0.30	1.6E-02	0.036
NT5C2	5'-nucleotidase, cytosolic II	-1.15	-0.20	1.6E-02	0.036
PLA2G2A	phospholipase A2 group IIA	3.16	1.66	1.6E-02	0.036
CSDC2	cold shock domain containing C2	1.76	0.81	1.6E-02	0.036
PTGFR	prostaglandin F receptor	-1.55	-0.63	1.6E-02	0.036
TINAGL1	tubulointerstitial nephritis antigen like 1	1.43	0.52	1.6E-02	0.036
ACSL6	acyl-CoA synthetase long-chain family member 6	-2.01	-1.01	1.7E-02	0.036
GAS5	growth arrest specific 5 (non-protein coding)	-1.30	-0.38	1.7E-02	0.036
NPEPL1	aminopeptidase-like 1	1.40	0.49	1.7E-02	0.036
MIR1304	microRNA 1304	-2.00	-1.00	1.7E-02	0.036
HIPK1-AS1	HIPK1 antisense RNA 1	-1.80	-0.85	1.7E-02	0.036
CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	1.49	0.58	1.7E-02	0.036
SLC46A1	solute carrier family 46 member 1	-1.21	-0.27	1.7E-02	0.036
FRG1	FSHD region gene 1	1.21	0.27	1.7E-02	0.036
PRR11	proline rich 11	-1.69	-0.76	1.7E-02	0.036
ZNF587	zinc finger protein 587	-1.28	-0.36	1.7E-02	0.036
SAA1	serum amyloid A1	3.17	1.66	1.7E-02	0.036
PPP1R12C	protein phosphatase 1 regulatory subunit 12C	1.24	0.31	1.7E-02	0.036
DBNL	drebrin like	1.19	0.26	1.7E-02	0.036
TUBA3D	tubulin alpha 3d	3.24	1.70	1.7E-02	0.036
JAKMIP1	janus kinase and microtubule interacting protein 1	-2.33	-1.22	1.7E-02	0.036
SLC15A4	solute carrier family 15 member 4	-1.18	-0.24	1.7E-02	0.036
JCHAIN	joining chain of multimeric IgA and IgM	-1.89	-0.92	1.7E-02	0.036
FASN	fatty acid synthase	1.88	0.91	1.7E-02	0.036
CASS4	Cas scaffolding protein family member 4	-1.68	-0.75	1.7E-02	0.036
NMUR1	neuromedin U receptor 1	1.90	0.93	1.7E-02	0.036
RETSAT	retinol saturase	1.65	0.72	1.7E-02	0.036
PPARG	peroxisome proliferator activated receptor gamma	1.40	0.49	1.7E-02	0.036
VAMP5	vesicle associated membrane protein 5	1.30	0.38	1.7E-02	0.036
RPS17	ribosomal protein S17	-1.61	-0.69	1.7E-02	0.036
TTC39C-AS1	TTC39C antisense RNA 1	1.78	0.83	1.7E-02	0.036
AKR1C1	aldo-keto reductase family 1 member C1	1.62	0.70	1.7E-02	0.036
GYG2	glycogenin 2	2.25	1.17	1.7E-02	0.036
ABLIM3	actin binding LIM protein family member 3	1.30	0.38	1.8E-02	0.036
PSMB6	proteasome subunit beta 6	1.33	0.41	1.8E-02	0.036

PABPC1L	poly(A) binding protein cytoplasmic 1 like	-1.44	-0.53	1.8E-02	0.036
CEBPA	CCAAT/enhancer binding protein alpha	1.72	0.78	1.8E-02	0.036
RAB3D	RAB3D, member RAS oncogene family	-1.22	-0.28	1.8E-02	0.036
LYPLA2	lysophospholipase II	1.24	0.31	1.8E-02	0.036
LOC389641	uncharacterized LOC389641	-2.15	-1.10	1.8E-02	0.036
LPL	lipoprotein lipase	2.19	1.13	1.8E-02	0.037
TRIM35	tripartite motif containing 35	1.19	0.25	1.8E-02	0.037
PPM1K	protein phosphatase, Mg2+/Mn2+ dependent 1K	-1.25	-0.32	1.8E-02	0.037
BAD	BCL2 associated agonist of cell death	1.24	0.31	1.8E-02	0.037
OTUD7B	OTU deubiquitinase 7B	1.20	0.26	1.8E-02	0.037
SSRP1	structure specific recognition protein 1	1.17	0.22	1.8E-02	0.037
ZNF566	zinc finger protein 566	-1.22	-0.28	1.8E-02	0.037
MGLL	monoglyceride lipase	1.41	0.49	1.9E-02	0.037
LRRC37BP1	leucine rich repeat containing 37B pseudogene 1	-1.21	-0.27	1.9E-02	0.037
CASP4	caspase 4	-1.18	-0.24	1.9E-02	0.037
SNORD95	small nucleolar RNA, C/D box 95	-1.47	-0.55	1.9E-02	0.037
PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-1.22	-0.29	1.9E-02	0.037
HSH2D	hematopoietic SH2 domain containing	-1.57	-0.65	1.9E-02	0.037
ACACB	acetyl-CoA carboxylase beta	1.58	0.66	1.9E-02	0.037
DNAJA4	DnaJ heat shock protein family (Hsp40) member A4	1.21	0.27	1.9E-02	0.038
TM4SF18	transmembrane 4 L six family member 18	1.28	0.35	1.9E-02	0.038
HEPACAM	hepatic and glial cell adhesion molecule	2.24	1.16	1.9E-02	0.038
NAIP	NLR family apoptosis inhibitory protein	-1.38	-0.47	1.9E-02	0.038
PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	2.17	1.12	1.9E-02	0.038
NCF4	neutrophil cytosolic factor 4	-1.40	-0.48	2.0E-02	0.038
LAT2	linker for activation of T-cells family member 2	-1.59	-0.67	2.0E-02	0.038
C16orf74	chromosome 16 open reading frame 74	-1.65	-0.72	2.0E-02	0.038
C15orf40	chromosome 15 open reading frame 40	-1.30	-0.38	2.0E-02	0.038
AFG3L2	AFG3 like matrix AAA peptidase subunit 2	1.15	0.20	2.0E-02	0.038
IPMK	inositol polyphosphate multikinase	-1.27	-0.35	2.0E-02	0.038
HECTD3	HECT domain E3 ubiquitin protein ligase 3	1.18	0.23	2.0E-02	0.038
ALDH4A1	aldehyde dehydrogenase 4 family member A1	1.55	0.63	2.0E-02	0.038
SDC1	syndecan 1	-1.39	-0.48	2.0E-02	0.038
G0S2	G0/G1 switch 2	2.33	1.22	2.0E-02	0.038
ZNF519	zinc finger protein 519	-1.25	-0.32	2.0E-02	0.038
CCNB1	cyclin B1	-1.36	-0.45	2.0E-02	0.038
ADIPOQ	adiponectin, C1Q and collagen domain containing	2.24	1.16	2.0E-02	0.039
ENDOU	endonuclease, poly(U) specific	1.68	0.75	2.1E-02	0.039
MIR652	microRNA 652	2.42	1.28	2.1E-02	0.039
GALNT15	polypeptide N-acetylgalactosaminyltransferase 15	1.51	0.59	2.1E-02	0.039
ATXN1L	ataxin 1 like	1.16	0.22	2.1E-02	0.039
COL16A1	collagen type XVI alpha 1 chain	1.32	0.40	2.1E-02	0.039
KCTD21-AS1	KCTD21 antisense RNA 1	-1.66	-0.73	2.1E-02	0.039
AKAP8	A-kinase anchoring protein 8	1.19	0.25	2.1E-02	0.039
SLC29A4	solute carrier family 29 member 4	1.96	0.97	2.1E-02	0.039
TUSC5	tumor suppressor candidate 5	2.22	1.15	2.1E-02	0.039
PPP1R1A	protein phosphatase 1 regulatory inhibitor subunit 1A	2.27	1.18	2.1E-02	0.039
VTI1B	vesicle transport through interaction with t-SNAREs 1B	1.26	0.33	2.1E-02	0.039
TK1	thymidine kinase 1	-2.11	-1.08	2.1E-02	0.039
SAP30BP	SAP30 binding protein	1.17	0.22	2.1E-02	0.039
FKBPL	FK506 binding protein like	-1.58	-0.66	2.1E-02	0.039
DPY19L2P3	DPY19L2 pseudogene 3	-2.06	-1.04	2.1E-02	0.039
CRIP3	cysteine rich protein 3	-1.79	-0.84	2.2E-02	0.039
RGPD4	RANBP2-like and GRIP domain containing 4	-1.95	-0.96	2.2E-02	0.039
U2AF1L4	U2 small nuclear RNA auxiliary factor 1 like 4	1.36	0.44	2.2E-02	0.039
PALMD	palmelphin	1.35	0.43	2.2E-02	0.039
ROBO4	roundabout guidance receptor 4	1.29	0.36	2.2E-02	0.039
GPR176	G protein-coupled receptor 176	1.37	0.45	2.2E-02	0.039
HOXA1	homeobox A1	1.45	0.54	2.2E-02	0.039
MIRLET7I	microRNA let-7i	1.63	0.70	2.2E-02	0.039
UBXN1	UBX domain protein 1	1.18	0.24	2.2E-02	0.039
C2CD2	C2 calcium dependent domain containing 2	1.29	0.36	2.2E-02	0.039
ZBTB41	zinc finger and BTB domain containing 41	-1.18	-0.24	2.2E-02	0.039
POU2AF1	POU class 2 associating factor 1	-1.53	-0.61	2.2E-02	0.039
PDE2A	phosphodiesterase 2A	1.35	0.43	2.3E-02	0.039
KLF15	Kruppel like factor 15	1.68	0.75	2.3E-02	0.039

SNORA30	small nucleolar RNA, H/ACA box 30	-1.85	-0.89	2.3E-02	0.039
LIMCH1	LIM and calponin homology domains 1	1.37	0.46	2.3E-02	0.040
SNORD2	small nucleolar RNA, C/D box 2	-1.47	-0.55	2.3E-02	0.040
SLC7A6OS	solute carrier family 7 member 6 opposite strand	1.18	0.24	2.3E-02	0.040
GPD1	glycerol-3-phosphate dehydrogenase 1	2.27	1.18	2.3E-02	0.040
KLRC1	killer cell lectin like receptor C1	-2.28	-1.19	2.3E-02	0.040
APOL6	apolipoprotein L6	1.29	0.37	2.3E-02	0.040
KCNN2	potassium calcium-activated channel subfamily N member 2	-1.93	-0.95	2.3E-02	0.040
APMAP	adipocyte plasma membrane associated protein	1.28	0.35	2.3E-02	0.040
OR52N4	olfactory receptor family 52 subfamily N member 4 (gene/pseudogene)	2.50	1.32	2.3E-02	0.040
ZNF850	zinc finger protein 850	-1.22	-0.29	2.3E-02	0.040
ZNF383	zinc finger protein 383	-1.20	-0.26	2.3E-02	0.040
MDH1B	malate dehydrogenase 1B	-1.61	-0.69	2.4E-02	0.040
MRPL40	mitochondrial ribosomal protein L40	1.25	0.32	2.4E-02	0.040
SAA2	serum amyloid A2	3.19	1.67	2.4E-02	0.040
KCNIP2	potassium voltage-gated channel interacting protein 2	1.95	0.96	2.4E-02	0.040
CH25H	cholesterol 25-hydroxylase	-1.65	-0.72	2.4E-02	0.040
LOC100506136	uncharacterized LOC100506136	-1.55	-0.63	2.4E-02	0.040
INF2	inverted formin, FH2 and WH2 domain containing	1.26	0.33	2.4E-02	0.040
PUS7L	pseudouridylate synthase 7 like	-1.20	-0.26	2.4E-02	0.040
PLIN2	perilipin 2	1.30	0.38	2.4E-02	0.040
HOXB-AS1	HOXB cluster antisense RNA 1	1.36	0.44	2.4E-02	0.040
DTX3L	deltex E3 ubiquitin ligase 3L	-1.16	-0.21	2.4E-02	0.040
HEY1	hes related family bHLH transcription factor with YRPW motif 1	1.40	0.48	2.4E-02	0.040
MGA	MGA, MAX dimerization protein	-1.14	-0.18	2.4E-02	0.040
NANOS1	nanos C2HC-type zinc finger 1	1.43	0.51	2.4E-02	0.040
NUGGC	nuclear GTPase, germinal center associated	-1.59	-0.67	2.4E-02	0.040
MIR3064	microRNA 3064	-1.47	-0.56	2.4E-02	0.040
ZNF775	zinc finger protein 775	1.31	0.39	2.4E-02	0.040
PRKAR2B	protein kinase cAMP-dependent type II regulatory subunit beta	1.85	0.89	2.5E-02	0.040
IDS	iduronate 2-sulfatase	-1.19	-0.26	2.5E-02	0.040
LOC100506127	putative uncharacterized protein FLJ37770-like	-1.30	-0.37	2.5E-02	0.040
APIP	APAF1 interacting protein	1.28	0.36	2.5E-02	0.040
DHRS3	dehydrogenase/reductase 3	1.32	0.40	2.5E-02	0.040
CEP89	centrosomal protein 89	-1.18	-0.23	2.5E-02	0.040
LRRC47	leucine rich repeat containing 47	1.16	0.21	2.5E-02	0.040
SNAI1	snail family transcriptional repressor 1	1.52	0.61	2.5E-02	0.040
FAM89A	family with sequence similarity 89 member A	1.52	0.60	2.5E-02	0.040
STON1	stonin 1	1.24	0.31	2.5E-02	0.040
CEP97	centrosomal protein 97	-1.20	-0.27	2.5E-02	0.040
SEL1L3	SEL1L family member 3	-1.30	-0.38	2.5E-02	0.040
ORMDL3	ORMDL sphingolipid biosynthesis regulator 3	1.31	0.39	2.5E-02	0.040
LYRM7	LYR motif containing 7	-1.22	-0.28	2.6E-02	0.040
NIPSNAP3B	nipsnap homolog 3B	1.38	0.46	2.6E-02	0.040
SNORD36C	small nucleolar RNA, C/D box 36C	-1.52	-0.61	2.6E-02	0.040
PRICKLE2-AS3	PRICKLE2 antisense RNA 3	-1.62	-0.69	2.6E-02	0.040
LOC101929066	uncharacterized LOC101929066	-1.76	-0.82	2.6E-02	0.040
PTGER4	prostaglandin E receptor 4	-1.35	-0.43	2.6E-02	0.040
METTL8	methyltransferase like 8	-1.19	-0.25	2.6E-02	0.040
NOD2	nucleotide binding oligomerization domain containing 2	-1.70	-0.76	2.6E-02	0.040
MIR590	microRNA 590	1.61	0.69	2.6E-02	0.040
TSPAN6	tetraspanin 6	1.26	0.33	2.6E-02	0.040
C2orf44	NA	-1.29	-0.37	2.6E-02	0.040
ITPK1	inositol-tetrakisphosphate 1-kinase	1.27	0.34	2.6E-02	0.040
SNORD59A	small nucleolar RNA, C/D box 59A	-1.71	-0.78	2.7E-02	0.040
FABP5	fatty acid binding protein 5	1.50	0.59	2.7E-02	0.040
DNAJB12	DnaJ heat shock protein family (Hsp40) member B12	1.14	0.19	2.7E-02	0.040
TOX2	TOX high mobility group box family member 2	1.47	0.55	2.7E-02	0.040
SLC19A3	solute carrier family 19 member 3	2.53	1.34	2.7E-02	0.041
NFKBIL1	NFKB inhibitor like 1	1.27	0.34	2.7E-02	0.041
ANO3	anoctamin 3	1.75	0.81	2.7E-02	0.041
PMEPA1	prostate transmembrane protein, androgen induced 1	1.39	0.47	2.7E-02	0.041
RGS16	regulator of G-protein signaling 16	1.47	0.55	2.7E-02	0.041
RAB36	RAB36, member RAS oncogene family	-1.42	-0.50	2.7E-02	0.041
KMT2E-AS1	KMT2E antisense RNA 1 (head to head)	1.23	0.30	2.7E-02	0.041
APOB	apolipoprotein B	2.55	1.35	2.7E-02	0.041

MT01	mitochondrial tRNA translation optimization 1	-1.20	-0.27	2.7E-02	0.041
AMIGO1	adhesion molecule with Ig like domain 1	1.28	0.35	2.7E-02	0.041
FAM210A	family with sequence similarity 210 member A	-1.23	-0.30	2.7E-02	0.041
TMEM88	transmembrane protein 88	1.36	0.45	2.8E-02	0.041
MEOX1	mesenchyme homeobox 1	1.40	0.49	2.8E-02	0.041
LMNB1	lamin B1	-1.43	-0.52	2.8E-02	0.041
ZNF101	zinc finger protein 101	-1.32	-0.40	2.8E-02	0.041
LOC101928324	uncharacterized LOC101928324	-1.57	-0.65	2.8E-02	0.041
SCARB1	scavenger receptor class B member 1	1.32	0.40	2.8E-02	0.041
ZNF581	zinc finger protein 581	-1.29	-0.37	2.8E-02	0.041
SCARNA1	small Cajal body-specific RNA 1	-1.43	-0.52	2.8E-02	0.041
CD300LG	CD300 molecule like family member g	1.67	0.74	2.8E-02	0.041
ZNF418	zinc finger protein 418	1.30	0.38	2.8E-02	0.041
GRM7	glutamate metabotropic receptor 7	-2.03	-1.02	2.8E-02	0.041
RIC8B	RIC8 guanine nucleotide exchange factor B	-1.17	-0.23	2.8E-02	0.041
PDRG1	p53 and DNA damage regulated 1	1.26	0.33	2.9E-02	0.041
AKAP1	A-kinase anchoring protein 1	1.29	0.37	2.9E-02	0.041
LOC100130357	uncharacterized LOC100130357	-1.47	-0.56	2.9E-02	0.041
LOC441155	zinc finger CCCH-type domain-containing-like	1.63	0.70	2.9E-02	0.041
MIR7641-2	microRNA 7641-2	-1.55	-0.63	2.9E-02	0.041
PALM	paralemmin	1.26	0.33	2.9E-02	0.041
ZNF513	zinc finger protein 513	1.36	0.44	2.9E-02	0.041
RCAN3	RCAN family member 3	-1.29	-0.37	2.9E-02	0.041
MLXIPL	MLX interacting protein like	2.14	1.10	2.9E-02	0.041
TMEM259	transmembrane protein 259	1.16	0.22	2.9E-02	0.042
MIR223	microRNA 223	-2.43	-1.28	2.9E-02	0.042
ECM2	extracellular matrix protein 2	1.35	0.43	2.9E-02	0.042
PNPLA2	patatin like phospholipase domain containing 2	1.61	0.69	3.0E-02	0.042
SCG2	secretogranin II	2.34	1.23	3.0E-02	0.042
SEMA3G	semaphorin 3G	1.41	0.49	3.0E-02	0.042
VWF	von Willebrand factor	1.27	0.35	3.0E-02	0.042
APOBEC3G	apolipoprotein B mRNA editing enzyme catalytic subunit 3G	-1.31	-0.38	3.0E-02	0.042
CCDC12	coiled-coil domain containing 12	1.18	0.24	3.0E-02	0.042
EPHX1	epoxide hydrolase 1	1.29	0.37	3.0E-02	0.042
ADCK3	NA	1.40	0.49	3.0E-02	0.042
EPAS1	endothelial PAS domain protein 1	1.30	0.38	3.0E-02	0.042
GFM2	G elongation factor mitochondrial 2	-1.18	-0.24	3.0E-02	0.042
C19orf12	chromosome 19 open reading frame 12	1.25	0.33	3.1E-02	0.042
CUTC	cutC copper transporter	1.16	0.21	3.1E-02	0.042
RXRB	retinoid X receptor beta	1.19	0.26	3.1E-02	0.042
CEACAM21	carcinoembryonic antigen related cell adhesion molecule 21	-1.71	-0.77	3.1E-02	0.042
CWC25	CWC25 spliceosome associated protein homolog	1.14	0.19	3.1E-02	0.042
CYP4F22	cytochrome P450 family 4 subfamily F member 22	2.21	1.14	3.1E-02	0.042
SRSF4	serine and arginine rich splicing factor 4	1.16	0.22	3.1E-02	0.042
ETFDH	electron transfer flavoprotein dehydrogenase	1.26	0.34	3.1E-02	0.042
ASPH	aspartate beta-hydroxylase	1.25	0.32	3.1E-02	0.042
NR2F6	nuclear receptor subfamily 2 group F member 6	1.28	0.35	3.1E-02	0.042
SLC25A20	solute carrier family 25 member 20	1.40	0.49	3.1E-02	0.042
TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	1.22	0.28	3.1E-02	0.042
RAD1	RAD1 checkpoint DNA exonuclease	-1.16	-0.22	3.1E-02	0.042
C7orf31	chromosome 7 open reading frame 31	-1.32	-0.40	3.1E-02	0.042
PRDX6	peroxiredoxin 6	1.32	0.40	3.2E-02	0.042
SQSTM1	sequestosome 1	1.16	0.22	3.2E-02	0.042
POC1B	POC1 centriolar protein B	-1.24	-0.31	3.2E-02	0.042
PDE8B	phosphodiesterase 8B	1.46	0.54	3.2E-02	0.042
ZNF821	zinc finger protein 821	1.31	0.39	3.2E-02	0.042
GNAI1	G protein subunit alpha i1	1.41	0.49	3.2E-02	0.042
VAX2	ventral anterior homeobox 2	1.57	0.65	3.2E-02	0.043
ALOX5	arachidonate 5-lipoxygenase	-1.38	-0.46	3.2E-02	0.043
SLC46A3	solute carrier family 46 member 3	-1.28	-0.35	3.2E-02	0.043
CD8A	CD8a molecule	-1.72	-0.78	3.2E-02	0.043
PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma	-1.38	-0.46	3.2E-02	0.043
HARS	histidyl-tRNA synthetase	1.15	0.20	3.2E-02	0.043
CYP4V2	cytochrome P450 family 4 subfamily V member 2	-1.24	-0.31	3.3E-02	0.043
HOXC4	homeobox C4	-1.39	-0.48	3.3E-02	0.043
PSTK	phosphoseryl-tRNA kinase	-1.43	-0.52	3.3E-02	0.043

CDKN2B	cyclin dependent kinase inhibitor 2B	1.62	0.69	3.3E-02	0.043
MX2	MX dynamin like GTPase 2	-1.27	-0.35	3.3E-02	0.043
AMOTL2	angiominin like 2	1.32	0.40	3.3E-02	0.043
TMEM69	transmembrane protein 69	-1.18	-0.24	3.3E-02	0.043
SLC27A5	solute carrier family 27 member 5	1.32	0.40	3.3E-02	0.043
NSUN4	NOP2/Sun RNA methyltransferase family member 4	-1.20	-0.26	3.4E-02	0.043
MARC1	mitochondrial amidoxime reducing component 1	1.83	0.87	3.4E-02	0.043
GNAO1	G protein subunit alpha o1	-1.50	-0.59	3.4E-02	0.043
NOSTRIN	nitric oxide synthase trafficking	1.35	0.43	3.4E-02	0.043
KCNQ1	potassium voltage-gated channel subfamily Q member 1	-1.38	-0.47	3.4E-02	0.043
STRN4	striatin 4	1.14	0.19	3.4E-02	0.043
PDGFB	platelet derived growth factor subunit B	1.34	0.42	3.4E-02	0.043
MAOA	monoamine oxidase A	1.62	0.70	3.4E-02	0.043
DMRT3	doublesex and mab-3 related transcription factor 3	1.54	0.62	3.4E-02	0.044
ILVBL	ilvB acetolactate synthase like	1.20	0.26	3.4E-02	0.044
CXCL3	C-X-C motif chemokine ligand 3	-1.94	-0.95	3.4E-02	0.044
LINC00996	long intergenic non-protein coding RNA 996	-1.63	-0.70	3.5E-02	0.044
C1orf35	chromosome 1 open reading frame 35	1.25	0.32	3.5E-02	0.044
LINS	NA	-1.25	-0.33	3.5E-02	0.044
CCNB1IP1	cyclin B1 interacting protein 1	-1.23	-0.30	3.5E-02	0.044
LOC100505549	uncharacterized LOC100505549	-1.34	-0.43	3.5E-02	0.044
MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	1.24	0.31	3.5E-02	0.044
LOC100506474	uncharacterized LOC100506474	1.68	0.75	3.5E-02	0.044
ZNF561	zinc finger protein 561	-1.19	-0.25	3.5E-02	0.044
PDCD2L	programmed cell death 2 like	1.24	0.31	3.5E-02	0.044
PHLDB2	pleckstrin homology like domain family B member 2	1.27	0.35	3.5E-02	0.044
CAPN2	calpain 2	1.16	0.22	3.6E-02	0.044
DHRS4L2	dehydrogenase/reductase 4 like 2	1.27	0.34	3.6E-02	0.044
LOC101928370	uncharacterized LOC101928370	1.43	0.51	3.6E-02	0.044
MMD	monocyte to macrophage differentiation associated	1.78	0.83	3.6E-02	0.044
CPNE5	copine 5	-1.39	-0.48	3.6E-02	0.044
LGI4	leucine rich repeat LGI family member 4	1.42	0.51	3.6E-02	0.044
EMC6	ER membrane protein complex subunit 6	1.36	0.45	3.6E-02	0.045
STBD1	starch binding domain 1	1.84	0.88	3.6E-02	0.045
SNORD56	small nucleolar RNA, C/D box 56	-1.70	-0.77	3.6E-02	0.045
FPGT	fucose-1-phosphate guanylyltransferase	-1.28	-0.36	3.7E-02	0.045
RGS14	regulator of G-protein signaling 14	-1.31	-0.39	3.7E-02	0.045
ESYT1	extended synaptotagmin 1	1.25	0.32	3.7E-02	0.045
CARD8-AS1	CARD8 antisense RNA 1	-1.40	-0.48	3.7E-02	0.045
APAF1	apoptotic peptidase activating factor 1	-1.25	-0.32	3.7E-02	0.045
CS	citrate synthase	1.29	0.36	3.7E-02	0.045
COL13A1	collagen type XIII alpha 1 chain	1.49	0.57	3.7E-02	0.045
AOC4P	amine oxidase, copper containing 4, pseudogene	1.85	0.89	3.7E-02	0.045
FAM86JP	family with sequence similarity 86, member A pseudogene	-1.94	-0.96	3.7E-02	0.045
NOP9	NOP9 nucleolar protein	1.16	0.21	3.7E-02	0.045
CPT1C	carnitine palmitoyltransferase 1C	-1.40	-0.48	3.8E-02	0.045
CAV1	caveolin 1	1.27	0.34	3.8E-02	0.045
LOC730183	uncharacterized LOC730183	1.57	0.66	3.8E-02	0.045
GJA4	gap junction protein alpha 4	1.42	0.51	3.8E-02	0.045
RBM45	RNA binding motif protein 45	-1.22	-0.29	3.8E-02	0.045
PTPRVP	protein tyrosine phosphatase, receptor type V, pseudogene	-1.69	-0.76	3.8E-02	0.045
ZNF219	zinc finger protein 219	1.26	0.33	3.8E-02	0.045
FLJ42627	uncharacterized LOC645644	-1.52	-0.60	3.8E-02	0.045
COL4A2	collagen type IV alpha 2 chain	1.36	0.44	3.8E-02	0.045
LRRTM2	leucine rich repeat transmembrane neuronal 2	1.42	0.51	3.9E-02	0.045
CDK9	cyclin dependent kinase 9	1.19	0.25	3.9E-02	0.045
LOC101928489	uncharacterized LOC101928489	-1.69	-0.76	3.9E-02	0.045
ZNF225	zinc finger protein 225	-1.15	-0.20	3.9E-02	0.045
SNORD59B	small nucleolar RNA, C/D box 59B	-1.72	-0.78	3.9E-02	0.045
MIR1254-1	microRNA 1254-1	-1.69	-0.76	3.9E-02	0.045
KLHL3	kelch like family member 3	1.25	0.32	3.9E-02	0.045
ZNF235	zinc finger protein 235	-1.20	-0.26	3.9E-02	0.045
PFAS	phosphoribosylformylglycinamide synthase	1.21	0.27	3.9E-02	0.046
PHF20	PHD finger protein 20	-1.14	-0.19	4.0E-02	0.046
GPT2	glutamic--pyruvic transaminase 2	1.57	0.65	4.0E-02	0.046
LINC01232	long intergenic non-protein coding RNA 1232	-1.55	-0.63	4.0E-02	0.046

RNU6-2	RNA, U6 small nuclear 2	-1.37	-0.45	4.0E-02	0.046
CCDC120	coiled-coil domain containing 120	-1.36	-0.44	4.0E-02	0.046
ZRANB2-AS1	ZRANB2 antisense RNA 1	1.63	0.71	4.0E-02	0.046
RAB26	RAB26, member RAS oncogene family	-2.00	-1.00	4.0E-02	0.046
EID2B	EP300 interacting inhibitor of differentiation 2B	-1.31	-0.39	4.1E-02	0.047
PTH2R	parathyroid hormone 2 receptor	1.66	0.73	4.1E-02	0.047
BTN2A3P	butyrophilin subfamily 2 member A3, pseudogene	-1.29	-0.36	4.1E-02	0.047
SHISA3	shisa family member 3	-1.75	-0.81	4.1E-02	0.047
VPS8	VPS8, CORVET complex subunit	-1.16	-0.22	4.1E-02	0.047
CTIF	cap binding complex dependent translation initiation factor	1.25	0.32	4.1E-02	0.047
TNIP1	TNFAIP3 interacting protein 1	1.19	0.25	4.1E-02	0.047
SWSAP1	SWIM-type zinc finger 7 associated protein 1	-1.47	-0.55	4.1E-02	0.047
TAF11	TATA-box binding protein associated factor 11	1.22	0.29	4.1E-02	0.047
BAIAP2L2	BAI1 associated protein 2 like 2	1.53	0.61	4.2E-02	0.047
SPN	sialophorin	-1.52	-0.61	4.2E-02	0.047
AQP7P3	aquaporin 7 pseudogene 3	2.10	1.07	4.2E-02	0.047
LZTS2	leucine zipper tumor suppressor 2	1.17	0.23	4.2E-02	0.047
WDR60	WD repeat domain 60	1.17	0.22	4.2E-02	0.047
BTNL9	butyrophilin like 9	1.63	0.70	4.2E-02	0.047
ANO2	anoctamin 2	1.40	0.49	4.2E-02	0.047
CA4	carbonic anhydrase 4	1.79	0.84	4.2E-02	0.047
PRKRIP1	PRKR interacting protein 1 (IL11 inducible)	1.26	0.33	4.2E-02	0.047
AQP7	aquaporin 7	1.89	0.92	4.2E-02	0.047
CHKB-AS1	CHKB antisense RNA 1 (head to head)	-1.35	-0.43	4.2E-02	0.047
CDC23	cell division cycle 23	-1.15	-0.21	4.2E-02	0.047
CYTIP	cytohesin 1 interacting protein	-1.59	-0.67	4.2E-02	0.047
SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	1.36	0.45	4.2E-02	0.047
MEI1	meiotic double-stranded break formation protein 1	-1.50	-0.59	4.3E-02	0.047
HP09053	uncharacterized LOC101929357	-2.08	-1.06	4.3E-02	0.047
TXNL4B	thioredoxin like 4B	-1.21	-0.28	4.3E-02	0.047
XCR1	X-C motif chemokine receptor 1	-2.57	-1.36	4.3E-02	0.047
AKR1E2	aldo-keto reductase family 1 member E2	1.28	0.35	4.3E-02	0.047
MKNK2	MAP kinase interacting serine/threonine kinase 2	1.18	0.23	4.3E-02	0.047
CCDC168	coiled-coil domain containing 168	-1.71	-0.77	4.3E-02	0.047
RAB3IP	RAB3A interacting protein	-1.38	-0.46	4.3E-02	0.047
MAP3K6	mitogen-activated protein kinase kinase kinase 6	1.26	0.33	4.3E-02	0.047
C17orf100	chromosome 17 open reading frame 100	-1.50	-0.58	4.3E-02	0.047
CFAP45	cilia and flagella associated protein 45	1.50	0.59	4.3E-02	0.047
CDO1	cysteine dioxygenase type 1	1.46	0.55	4.3E-02	0.047
FAM96A	family with sequence similarity 96 member A	-1.17	-0.23	4.4E-02	0.047
PMS1	PMS1 homolog 1, mismatch repair system component	-1.19	-0.25	4.4E-02	0.047
PHOSPHO2	phosphatase, orphan 2	-1.37	-0.46	4.4E-02	0.047
TIGD4	tigger transposable element derived 4	-1.57	-0.65	4.4E-02	0.047
ZNF557	zinc finger protein 557	-1.14	-0.19	4.4E-02	0.047
SLC45A4	solute carrier family 45 member 4	-1.20	-0.26	4.4E-02	0.047
ADAT1	adenosine deaminase, tRNA specific 1	-1.18	-0.24	4.4E-02	0.047
GSE1	Gse1 coiled-coil protein	1.18	0.24	4.4E-02	0.048
INIP	INTS3 and NABP interacting protein	-1.22	-0.29	4.4E-02	0.048
MIR7161	microRNA 7161	1.93	0.95	4.4E-02	0.048
MIR5586	microRNA 5586	-1.88	-0.91	4.5E-02	0.048
LOC101927550	uncharacterized LOC101927550	-1.35	-0.43	4.5E-02	0.048
KMO	kynurenine 3-monooxygenase	-1.73	-0.79	4.5E-02	0.048
FNDC3A	fibronectin type III domain containing 3A	-1.12	-0.17	4.5E-02	0.048
RDH16	retinol dehydrogenase 16 (all-trans)	1.50	0.59	4.5E-02	0.048
LIPE	lipase E, hormone sensitive type	1.96	0.97	4.5E-02	0.048
LOC101926960	uncharacterized LOC101926960	2.24	1.16	4.5E-02	0.048
SOX2-OT	SOX2 overlapping transcript	-1.88	-0.91	4.5E-02	0.048
PTRF	polymerase I and transcript release factor	1.26	0.33	4.5E-02	0.048
BIN2	bridging integrator 2	-1.45	-0.54	4.6E-02	0.048
NFU1	NFU1 iron-sulfur cluster scaffold	1.24	0.31	4.6E-02	0.048
RSRP1	arginine and serine rich protein 1	-1.17	-0.23	4.6E-02	0.048
KANK3	KN motif and ankyrin repeat domains 3	1.37	0.45	4.6E-02	0.048
PTTG1	pituitary tumor-transforming 1	-1.75	-0.81	4.6E-02	0.048
GCAT	glycine C-acetyltransferase	-1.50	-0.58	4.6E-02	0.048
AGAP5	ArfGAP with GTPase domain, ankyrin repeat and PH domain 5	-1.26	-0.34	4.6E-02	0.048
ISCA2	iron-sulfur cluster assembly 2	1.25	0.32	4.6E-02	0.048

LINC00426	long intergenic non-protein coding RNA 426	-1.82	-0.87	4.6E-02	0.048
EDEM1	ER degradation enhancing alpha-mannosidase like protein 1	-1.12	-0.17	4.6E-02	0.048
COPRS	coordinator of PRMT5 and differentiation stimulator	1.21	0.28	4.6E-02	0.048
FGF2	fibroblast growth factor 2	1.26	0.34	4.6E-02	0.048
PMM1	phosphomannomutase 1	1.26	0.33	4.7E-02	0.048
SIAH2	siah E3 ubiquitin protein ligase 2	-1.24	-0.31	4.7E-02	0.048
CLDND2	claudin domain containing 2	1.62	0.70	4.7E-02	0.048
NUDT6	nudix hydrolase 6	1.24	0.31	4.7E-02	0.048
C1QTNF9B-AS	C1QTNF9B antisense RNA 1	-1.80	-0.85	4.7E-02	0.049
ADGRF5	adhesion G protein-coupled receptor F5	1.27	0.35	4.7E-02	0.049
ANGPTL4	angiopoietin like 4	1.90	0.93	4.7E-02	0.049
SKAP1	src kinase associated phosphoprotein 1	-1.42	-0.51	4.7E-02	0.049
MIR623	microRNA 623	-1.99	-1.00	4.8E-02	0.049
GALR1	galanin receptor 1	2.21	1.15	4.8E-02	0.049
SNCG	synuclein gamma	1.47	0.56	4.8E-02	0.049
MIR126	microRNA 126	1.90	0.92	4.8E-02	0.049
SIAE	sialic acid acetyltransferase	1.18	0.24	4.8E-02	0.049
MIR6809	microRNA 6809	1.46	0.55	4.8E-02	0.049
TMED1	transmembrane p24 trafficking protein 1	1.28	0.35	4.8E-02	0.049
KLHL5	kelch like family member 5	1.13	0.18	4.8E-02	0.049
ZNF266	zinc finger protein 266	-1.27	-0.35	4.8E-02	0.049
ADIPOR2	adiponectin receptor 2	1.18	0.23	4.9E-02	0.049
DRAP1	DR1 associated protein 1	1.28	0.35	4.9E-02	0.049
FASTKD3	FAST kinase domains 3	-1.24	-0.31	4.9E-02	0.049
RILP	Rab interacting lysosomal protein	1.23	0.30	4.9E-02	0.049
SNORD96A	small nucleolar RNA, C/D box 96A	-1.44	-0.52	5.0E-02	0.050
PTS	6-pyruvoyltetrahydropterin synthase	1.25	0.32	5.0E-02	0.050
HIST1H4E	histone cluster 1 H4 family member e	-1.22	-0.29	5.0E-02	0.050

* FC: Fold Change

Supplementary Table 6: List of genes differentially expressed in breast adipose tissue in susceptible versus healthy breasts.

Symbol	geneName	FC	log2FC	PValue	FDR
LOC101929680	uncharacterized LOC101929680	6.76	2.76	9.3E-06	0.001
C19orf35	chromosome 19 open reading frame 35	-6.25	-2.64	3.6E-04	0.013
LINC00667	long intergenic non-protein coding RNA 667	1.71	0.78	4.2E-04	0.013
ZKSCAN2	zinc finger with KRAB and SCAN domains 2	1.46	0.54	5.4E-04	0.013
CPA4	carboxypeptidase A4	-6.15	-2.62	5.8E-04	0.013
FCHO1	FCH domain only 1	-2.67	-1.41	5.8E-04	0.013
IDH2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial	1.67	0.74	8.3E-04	0.013
CES4A	carboxylesterase 4A	-2.09	-1.06	8.3E-04	0.013
RIMS2	regulating synaptic membrane exocytosis 2	9.54	3.25	8.4E-04	0.013
SPTB	spectrin beta, erythrocytic	2.50	1.32	8.8E-04	0.013
CAMK2B	calcium/calmodulin dependent protein kinase II beta	-4.86	-2.28	1.0E-03	0.014
NTS	neurotensin	7.33	2.87	1.6E-03	0.020
BRIP1	BRCA1 interacting protein C-terminal helicase 1	2.07	1.05	2.1E-03	0.020
ETV2	ETS variant 2	3.64	1.87	2.1E-03	0.020
SNORD85	NA	-2.16	-1.11	2.2E-03	0.020
FAM46C	family with sequence similarity 46 member C	-2.42	-1.28	2.5E-03	0.020
GADD45B	growth arrest and DNA damage inducible beta	1.64	0.72	2.6E-03	0.020
ASGR1	asialoglycoprotein receptor 1	-4.19	-2.07	2.7E-03	0.020
SNORD58A	small nucleolar RNA, C/D box 58A	-1.75	-0.81	2.7E-03	0.020
ZDHHC11	zinc finger DHHC-type containing 11	-2.09	-1.06	2.8E-03	0.020
MAMLD1	mastermind like domain containing 1	1.44	0.52	3.1E-03	0.022
APOBEC3G	apolipoprotein B mRNA editing enzyme catalytic subun	-1.73	-0.79	3.5E-03	0.023
SLC6A13	solute carrier family 6 member 13	3.67	1.88	3.6E-03	0.023
KLF9	Kruppel like factor 9	1.53	0.61	3.9E-03	0.023
UCP3	uncoupling protein 3	-2.45	-1.29	3.9E-03	0.023
DPYSL4	dihydropyrimidinase like 4	-2.83	-1.50	4.1E-03	0.023
SCP2	sterol carrier protein 2	1.51	0.59	4.2E-03	0.023
FKBP5	FK506 binding protein 5	1.94	0.96	4.4E-03	0.023
RTN1	reticulon 1	1.69	0.76	5.0E-03	0.025
ADCY10	adenylate cyclase 10, soluble	3.48	1.80	5.1E-03	0.025
PPIL6	peptidylprolyl isomerase like 6	-1.72	-0.78	5.3E-03	0.025
TSNAXIP1	translin associated factor X interacting protein 1	-2.53	-1.34	5.5E-03	0.025
TMEM91	transmembrane protein 91	-1.74	-0.80	5.6E-03	0.025
LOC100507639	uncharacterized LOC100507639	4.32	2.11	5.8E-03	0.025
AP4M1	adaptor related protein complex 4 mu 1 subunit	-1.54	-0.62	6.0E-03	0.025
LINC00324	long intergenic non-protein coding RNA 324	-1.83	-0.87	6.7E-03	0.027
GRIA1	glutamate ionotropic receptor AMPA type subunit 1	2.68	1.42	7.6E-03	0.030
BLNK	B-cell linker	-1.79	-0.84	7.9E-03	0.030
LOC105376360	uncharacterized LOC105376360	5.37	2.42	8.1E-03	0.030
SLC22A14	solute carrier family 22 member 14	-4.65	-2.22	8.1E-03	0.030
GALNT13	polypeptide N-acetylgalactosaminyltransferase 13	2.15	1.11	8.2E-03	0.030
CYP26C1	cytochrome P450 family 26 subfamily C member 1	-4.50	-2.17	8.7E-03	0.031
CERS6	ceramide synthase 6	1.32	0.40	9.1E-03	0.031
KLHL6	kelch like family member 6	-1.55	-0.63	9.5E-03	0.031
MIR5690	microRNA 5690	3.51	1.81	9.5E-03	0.031
NFKBIA	NFkB inhibitor alpha	1.40	0.48	1.0E-02	0.031
LIPG	lipase G, endothelial type	-5.31	-2.41	1.0E-02	0.031
C8orf89	chromosome 8 open reading frame 89	-3.70	-1.89	1.0E-02	0.031
CHURC1	churchill domain containing 1	1.33	0.41	1.0E-02	0.031
KCTD14	potassium channel tetramerization domain containing 1	-6.16	-2.62	1.1E-02	0.031
SLC27A2	solute carrier family 27 member 2	3.84	1.94	1.1E-02	0.031
FIGN	fidgetin, microtubule severing factor	1.65	0.72	1.1E-02	0.031

MFI2-AS1	MFI2 antisense RNA 1	-1.92	-0.94	1.1E-02	0.031
CA13	carbonic anhydrase 13	-2.09	-1.07	1.1E-02	0.031
LIFR	leukemia inhibitory factor receptor alpha	1.43	0.52	1.2E-02	0.031
MT1X	metallothionein 1X	2.00	1.00	1.2E-02	0.031
USP6NL	USP6 N-terminal like	1.44	0.53	1.2E-02	0.031
FOXN2	forkhead box N2	1.47	0.56	1.3E-02	0.032
DIRC3	disrupted in renal carcinoma 3	1.51	0.59	1.3E-02	0.034
ADRB3	adrenoceptor beta 3	4.74	2.24	1.4E-02	0.036
CD27	CD27 molecule	-3.48	-1.80	1.5E-02	0.036
ZNF677	zinc finger protein 677	1.38	0.46	1.6E-02	0.037
LINC00312	long intergenic non-protein coding RNA 312	1.59	0.67	1.6E-02	0.038
GLUL	glutamate-ammonia ligase	1.91	0.93	1.6E-02	0.038
LINC00562	long intergenic non-protein coding RNA 562	1.97	0.98	1.7E-02	0.038
TMEM132C	transmembrane protein 132C	1.47	0.55	1.7E-02	0.038
AMIGO1	adhesion molecule with Ig like domain 1	1.56	0.64	1.7E-02	0.038
SLC16A5	solute carrier family 16 member 5	-1.58	-0.66	1.8E-02	0.038
SMOC1	SPARC related modular calcium binding 1	2.47	1.30	1.8E-02	0.038
CCDC150	coiled-coil domain containing 150	-1.82	-0.86	1.8E-02	0.038
SLC38A3	solute carrier family 38 member 3	3.31	1.73	1.9E-02	0.038
TSGA10	testis specific 10	1.53	0.62	1.9E-02	0.038
THRB	thyroid hormone receptor beta	1.34	0.42	1.9E-02	0.038
SNORA16B	small nucleolar RNA, H/ACA box 16B	-2.51	-1.33	1.9E-02	0.038
ACVR1C	activin A receptor type 1C	2.06	1.04	1.9E-02	0.038
MIR921	microRNA 921	-3.51	-1.81	2.0E-02	0.038
DNAH6	dynein axonemal heavy chain 6	2.10	1.07	2.0E-02	0.038
SEN3	SUMO1/sentrin/SMT3 specific peptidase 3	2.07	1.05	2.0E-02	0.038
BPIFB2	BPI fold containing family B member 2	4.92	2.30	2.1E-02	0.039
DENND1C	DENN domain containing 1C	-1.70	-0.77	2.1E-02	0.040
RPS10P7	ribosomal protein S10 pseudogene 7	-3.57	-1.84	2.3E-02	0.041
KLHL8	kelch like family member 8	1.33	0.42	2.3E-02	0.041
SNORD74	small nucleolar RNA, C/D box 74	-2.61	-1.38	2.3E-02	0.041
CYP2B7P	cytochrome P450 family 2 subfamily B member 7, pseudogene	2.27	1.18	2.3E-02	0.041
MIR21	microRNA 21	2.29	1.20	2.3E-02	0.041
LOC105747689	uncharacterized LOC105747689	2.00	1.00	2.4E-02	0.041
SAA4	serum amyloid A4, constitutive	4.64	2.21	2.4E-02	0.041
KANSL1-AS1	KANSL1 antisense RNA 1	2.13	1.09	2.5E-02	0.042
COL8A1	collagen type VIII alpha 1 chain	2.27	1.18	2.6E-02	0.042
PRKAG2-AS1	PRKAG2 antisense RNA 1	2.61	1.38	2.7E-02	0.044
LOC101927237	uncharacterized LOC101927237	2.55	1.35	2.7E-02	0.044
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	1.67	0.74	2.8E-02	0.044
NUDT9	nudix hydrolase 9	1.27	0.34	2.8E-02	0.044
NPPA-AS1	NPPA antisense RNA 1	-2.62	-1.39	2.8E-02	0.044
LOC642361	uncharacterized LOC642361	1.58	0.66	2.8E-02	0.044
HCG22	HLA complex group 22	2.51	1.33	2.8E-02	0.044
SHC3	SHC adaptor protein 3	-1.83	-0.87	3.0E-02	0.045
SPATA9	spermatogenesis associated 9	2.14	1.10	3.0E-02	0.046
TMED6	transmembrane p24 trafficking protein 6	-2.08	-1.06	3.1E-02	0.046
TMEM218	transmembrane protein 218	1.40	0.49	3.1E-02	0.046
FKBP1B	FK506 binding protein 1B	-1.91	-0.93	3.1E-02	0.046
SBF2-AS1	SBF2 antisense RNA 1	1.58	0.66	3.2E-02	0.046
CPT1B	carnitine palmitoyltransferase 1B	2.39	1.26	3.4E-02	0.049
NRIP1	nuclear receptor interacting protein 1	1.41	0.49	3.5E-02	0.049
C14orf39	chromosome 14 open reading frame 39	1.90	0.92	3.6E-02	0.049
ATG16L2	autophagy related 16 like 2	-1.54	-0.63	3.6E-02	0.049
DARS-AS1	DARS antisense RNA 1	2.28	1.19	3.6E-02	0.049
MIR548AR	microRNA 548ar	1.96	0.97	3.7E-02	0.049

PTPN4	protein tyrosine phosphatase, non-receptor type 4	1.27	0.35	3.8E-02	0.049
FBXO16	F-box protein 16	-4.60	-2.20	3.8E-02	0.049
AMOTL2	angiomin like 2	1.58	0.66	3.9E-02	0.049
PEX10	peroxisomal biogenesis factor 10	1.34	0.42	3.9E-02	0.049
KCNJ2	potassium voltage-gated channel subfamily J member 2	-1.77	-0.82	3.9E-02	0.049
LINC01277	long intergenic non-protein coding RNA 1277	2.96	1.57	3.9E-02	0.049
PAX3	paired box 3	2.45	1.29	4.0E-02	0.049
LONRF1	LON peptidase N-terminal domain and ring finger 1	1.28	0.36	4.0E-02	0.049
DGKI	diacylglycerol kinase iota	1.44	0.53	4.2E-02	0.049
SNORD56	small nucleolar RNA, C/D box 56	-1.90	-0.93	4.2E-02	0.049
PKD1L2	polycystin 1 like 2 (gene/pseudogene)	2.02	1.01	4.3E-02	0.049
EFNA5	ephrin A5	1.45	0.54	4.3E-02	0.049
LOC100126784	uncharacterized LOC100126784	-2.95	-1.56	4.3E-02	0.049
VSTM4	V-set and transmembrane domain containing 4	1.35	0.43	4.3E-02	0.049
SIM1	single-minded family bHLH transcription factor 1	2.94	1.55	4.3E-02	0.049
ANO3	anoctamin 3	1.79	0.84	4.3E-02	0.049
AXIN2	axin 2	1.54	0.62	4.4E-02	0.049
LOC100287015	uncharacterized LOC100287015	-1.77	-0.83	4.4E-02	0.049
LOC728730	uncharacterized LOC728730	1.57	0.65	4.4E-02	0.049
DNAL4	dynein axonemal light chain 4	1.36	0.44	4.4E-02	0.049
FBXL17	F-box and leucine rich repeat protein 17	1.24	0.31	4.4E-02	0.049
PGBD4	piggyBac transposable element derived 4	1.64	0.72	4.5E-02	0.049
DTX3	deltex E3 ubiquitin ligase 3	-1.62	-0.70	4.5E-02	0.049
MIR7-1	microRNA 7-1	-5.14	-2.36	4.5E-02	0.049
KLHDC10	kelch domain containing 10	1.24	0.31	4.7E-02	0.049
LOC101927932	uncharacterized LOC101927932	1.94	0.96	4.7E-02	0.049
GZMM	granzyme M	-3.68	-1.88	4.7E-02	0.049
FMO2	flavin containing monooxygenase 2	1.69	0.75	4.7E-02	0.049
IRAK3	interleukin 1 receptor associated kinase 3	1.27	0.35	4.7E-02	0.049
SYTL1	synaptotagmin like 1	-2.11	-1.08	4.8E-02	0.049
PCDHB7	protocadherin beta 7	1.36	0.45	4.8E-02	0.049
MS4A1	membrane spanning 4-domains A1	2.22	1.15	4.8E-02	0.049
TIPIN	TIMELESS interacting protein	1.51	0.60	4.8E-02	0.049
LOC100506551	uncharacterized LOC100506551	2.54	1.34	4.8E-02	0.049
LOC101927865	uncharacterized LOC101927865	1.71	0.77	4.8E-02	0.049
CENPH	centromere protein H	1.57	0.65	4.8E-02	0.049
RGS22	regulator of G-protein signaling 22	1.55	0.63	4.8E-02	0.049
RRS1-AS1	RRS1 antisense RNA 1 (head to head)	1.63	0.70	4.9E-02	0.049
RAI2	retinoic acid induced 2	1.37	0.45	5.0E-02	0.050
LIN7A	lin-7 homolog A, crumbs cell polarity complex component	1.59	0.67	5.0E-02	0.050

*FC: Fold Change

Supplementary Table 7: Canonical pathway analysis of the microdissected breast epithelium RNAseq dataset

	Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Upregulated Genes	PPAR signaling pathway	4.95	0.06	PPARG,APOB,LPL,MAPK8,MAPK10,NR5A2,RBP4
	Adipogenesis pathway	3.79	0.04	PPARG,FZD4,LEP,PLIN1,LPL,FABP4
	AMPK Signaling	3.47	0.03	LEP,ACACB,ADRA2A,CHRNA2,ADIPOQ,LIPE,KLB
	PPAR α /RXR α Activation	3.11	0.03	GPD1,CD36,LPL,ADIPOQ,MAPK8,ACVR1C
	TR/RXR Activation	2.53	0.04	KLF9,AKR1C1/AKR1C2,PDE3B,KLB
	Paxillin Signaling	2.31	0.04	MAPK8,MAPK10,KLB,ACTA1
	LXR/RXR Activation	2.21	0.03	APOB,CD36,LPL,RBP4
	Insulin signaling pathway	1.98	0.03	PDE3B,MAPK8,LIPE,KLB
	cAMP-mediated signaling	1.91	0.02	PDE2A,ADRA2A,PDE3B,RAPGEF3,PKIA
	Retinol Biosynthesis	1.58	0.05	LPL,LIPE
Downregulated Genes	Metalloproteases Inhibition	2.43	0.05	MMP27,SDC2
	PCP pathway	2.05	0.03	ROR2,SMO
	Th1/Th2 Activation	2.04	0.02	CXCR6,IL27RA,CD8A

Supplementary Table 8: Ingenuity network analysis of the microdissected breast epithelium-related RNAseq dataset: upregulated (Up) and downregulated (Down) genes are analyzed together or separately

ID	Analysis	Molecules in Network	Score	Focus	Top Diseases and Functions
1	Epithelium Up and Down	ACACB,Adipokine,AMH,C/ebp,CIDEc,Cpla2,CPT1,CXCR5,ERK1/2,F8,FABP,G0S2,GPRIN2,GUC	31	18	Connective Tissue Development and Function, Lipid Metabolism, Small Molecule Biochemistry
2	Epithelium Up and Down	ACAC,ADIPOQ,AIM2,AKR1C1/AKR1C2,CD36,Collagen Alpha1,Collagen type I,EFNB3,ELOVL5,F	29	17	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry
3	Epithelium Up and Down	26s Proteasome,ACTA1,AMPK,APOB,Cg,DHRS12,EMX2,FSH,Gsk3,Hdac,Histone h3,Histone H4	29	17	Endocrine System Disorders, Metabolic Disease, Cardiovascular Disease
4	Epithelium Up and Down	ABCB5,ABCB6,AKR1C1/AKR1C2,ALDH1L1,CCS,CDH1,CHRNB2,CHST6,CT3F,CTSG,FAM129	29	17	Cancer, Organismal Injury and Abnormalities, Reproductive System Disease
5	Epithelium Up and Down	AR,ARMCX2,Ca2+,CGNL1,creatine,DNAse1,etaidic acid,FGF23,GHSR,GSKB,H19,HEPACAM,I	22	14	Connective Tissue Disorders, Organismal Injury and Abnormalities, Skeletal and Muscular Disorders
6	Epithelium Up and Down	ACVR1C,Akt,Alp,BCR (complex),CIDEA,CPA4,DLEU1,E2f,EMP1,Fritzzled,HDC,IFN Beta,IgG,I	20	13	Cellular Movement, Reproductive System Development and Function, Organ Morphology
7	Epithelium Up and Down	ADCY,ADRB,AQP7,Beta Arrestin,Calcineurin protein(s),CaMKII,Cofilin,COL8A2,collagen,Creb,cvt	20	13	Cell Morphology, Organ Morphology, Skeletal and Muscular System Development and Function
8	Epithelium Up and Down	ADRA2A,Ap1,Collagen(s),CXCR6,estrogen receptor,Focal adhesion kinase,FZD4,G protein alpha,	20	13	Cardiovascular Disease, Gastrointestinal Disease, Hepatic System Disease
9	Epithelium Up and Down	ANKRD29,APOBEC3G,APP,BTNL9,C19orf18,CAVIN4,CH3/Chik,CLDN16,CLDN19,CLIC5,FAN	20	13	Neurological Disease, Organismal Injury and Abnormalities, Hematological Disease
10	Epithelium Up and Down	Akr1b7,APOA1,ApoC3,C1orf21,CDCA7,CDH3,COL11A1,COL12A1,CYP39A1,CYP4A22,dihydrote	20	13	Connective Tissue Development and Function, Tissue Morphology, Cancer
11	Epithelium Up and Down	Actin,AIM2,ANG,ARPP21,ATF6,caspase,CD3,CD8A,CLCN1,cvtokine,EMX2OS,FAS,FYB2,GATA,	18	12	Cell Death and Survival, Cancer, Hereditary Disorder
12	Epithelium Up and Down	ANAPC13,AREG,ARRB2,CCDC32,CDCA2,CDK4,CMKLR1,CPEB2,DRD3,Endothelin,FLFR4,FO	16	11	Endocrine System Development and Function, Molecular Transport, Small Molecule Biochemistry
13	Epithelium Up and Down	ACA11,BICD2,C19orf73,Calmmodulin,CD32,CEP19,CEP85,COMMD2,CPNE5,EPB4,FL2,EXOC	16	11	Cellular Development, Cellular Growth and Proliferation, Embryonic Development
14	Epithelium Up and Down	ARMCX4,DPACT1,PDE4DIP	2	1	Developmental Disorder, Hereditary Disorder, Immunological Disease
ID	Analysis	Molecules in Network	Score	Focus	Top Diseases and Functions
1	Epithelium Up	ABCC6,ACAC,ACACB,Adipokine,AMH,CD36,CIDEc,Cpla2,CPT1,CXCR5,ERK1/2,FABP,FABP4,I	41	21	Lipid Metabolism, Small Molecule Biochemistry, Connective Tissue Development and Function
2	Epithelium Up	ABCB5,Acas1b,Akr1b7,AKR1C4,AKR1C1/AKR1C2,ALDH1L1,AREG,C1orf21,Ca2+,CDH1,CPEB,	29	16	Lipid Metabolism, Small Molecule Biochemistry, Developmental Disorder
3	Epithelium Up	ACVR1C,ADCY,ADRB,AIM2,AKR1C1/AKR1C2,C/ebp,Calcineurin protein(s),CaMKII,collagen,Coll	24	14	Cell Morphology, Organ Morphology, Skeletal and Muscular System Development and Function
4	Epithelium Up	acetic acid,ANKRD29,ARRB2,BTNL9,C9orf116,CAMK2N2,CLEC10A,cvtokine,FAM221B,FAM81E	24	14	Cellular Compromise, Cellular Development, Cellular Growth and Proliferation
5	Epithelium Up	beta-estradiol,C19orf73,FAM214A,GABRP,GATA2,GPX3,Gypa,HEPACAM,HGFAC,Iip1,Kap,KR'	22	13	Infectious Diseases, Nervous System Development and Function, Cancer
6	Epithelium Up	APP,ATF6,C19orf18,CLDN19,CLIC5,creatine,FAM129C,FCHO1,GSK3B,LYG2,HNT2,HDXA9,H	22	13	Hematological System Development and Function, Hematopoiesis, Lymphoid Tissue Structure and Development
7	Epithelium Up	ADIPOQ,Akt,Alp,AMPK,AQP7,CIDEA,Cofilin,Collagen type I,ELOVL5,EMP1,GFPI,IFN Beta,IgG,Ik	20	12	Cell Morphology, Connective Tissue Development and Function, Tissue Morphology
8	Epithelium Up	26s Proteasome,ACTA1,Actin,caspase,Cq,cytochrome C,DHRS12,F,Actin,FSH,FZD4,GNRH,Gsk	20	12	Skeletal and Muscular System Development and Function, Cellular Assembly and Organization, Cellular Development
9	Epithelium Up	3,5-diiodothyronine,A1CF,AADAC,Alpha 1 antitrypsin,ANAPC13,ANGPTL3,APOA1,APOA5,APOB	12	8	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry
10	Epithelium Up	ADRA2A,Ap1,BCR (complex),Beta Arrestin,CD3,CHRNB2,Collagen(s),DLEU1,E2f,ERK,estrogen r	10	7	Neurological Disease, Skeletal and Muscular Disorders, Cancer
11	Epithelium Up	ARMCX4,DPACT1,PDE4DIP	2	1	Developmental Disorder, Hereditary Disorder, Immunological Disease
ID	Analysis	Molecules in Network	Score	Focus	Top Diseases and Functions
1	Epithelium Down	5'-methylthiadenosine,CD3,CD8A,CPA4,CXCR6,EFNB3,EMX2,ERK,GPR18,GUCY1A1,GUCY1E	42	18	Cardiovascular System Development and Function, Embryonic Development, Organ Development
2	Epithelium Down	APP,AR,ARMCX2,BRD3,Ca2+,CALB2,CAVIN4,CEP19,COLA46,COL8A2,DNMT1,EGFL6,ESR1,I	30	14	Gene Expression, DNA Replication, Recombination, and Repair, Organ Morphology
3	Epithelium Down	5'-methylthiadenosine,CCDC32,COND1,CHST6,CYP39A1,DLK1,DNMT1,ESR2,FGF2,GATA4,gf	25	12	Gene Expression, Cellular Development, Cellular Growth and Proliferation
4	Epithelium Down	AAAS,ARL1,ARL2,BICD2,CCDC47,CDCA2,CGNL1,CHMP1A,CHMP2A,CPNE5,DNMT1,EED,FAI	11	6	Cell Cycle, DNA Replication, Recombination, and Repair, Molecular Transport
5	Epithelium Down	EMX2OS,NFYB	2	1	Cellular Development, Gene Expression, Cancer
6	Epithelium Down	FAS,HLA-B,HLA-B27,LILRA1,LILRA3	2	1	Dermatological Diseases and Conditions, Organismal Injury and Abnormalities, Gastrointestinal Disease

Supplementary Table 9: List of canonical pathways linked with the genes differentially expressed between susceptible and matched healthy control breast stroma samples

	Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
UPREGULATED	PPARα/RXRα Activation	7.61	0.09	GPD1,PRKAB1,ACAA1,CD36,ADCY3,ADCY6,ADIPOQ,IKBKG,GHR,PRKAR2B,NFKBIA,FASN,LPL,MRAS,ADIPOR2,ACVR1C
	RAR Activation	6.49	0.08	DHRS3,AKR1C3,ADCY3,ADCY6,TNIP1,PRKAR2B,RBP7,RDH16,IGFBP3,MAPK10,NR2F6,RBP5,RXRB,ZBTB16,RBP4
	Retinol Biosynthesis	5.45	0.17	DHRS3,RBP7,AKR1C3,LPL,LIPE,RBP5,PNPLA2
	FXR/RXR Activation	5.34	0.09	APOE,SLC27A5,MLXIPL,APOB,SCARB1,FASN,SAA1,LPL,MAPK10,SAA2,RBP4
	LXR/RXR Activation	4.69	0.08	APOE,MLXIPL,APOB,FASN,CD36,SAA1,LPL,SAA2,RXRB,RBP4
	Relaxin Signaling	3.71	0.06	PDE2A,IKBKG,NFKBIA,PRKAR2B,NPR1,ADCY3,MRAS,ADCY6,GNAI1,PDE8B
	Protein Kinase A Signaling	3.22	0.04	PDE2A,MYL2,AKAP8,BAD,ADCY3,GNAI1,ADCY6,LIPE,PTPRM,IKBKG,PRKAR2B,NFKBIA,DUSP4,PDE8B,AKAP1,PHKG1
	Triacylglycerol Degradation	2.86	0.09	LPL,LIPE,MGLL,PNPLA2,PRDX6
DOWNREGULATED	Anti-viral Immunity	4.16	0.38	APOBEC3B,APOBEC3G,TK1
	TREM1 Signaling	2.86	0.07	CXCL3,NOD2,TLR1,TLR7,LAT2
	Eicosanoid Signaling	2.2	0.06	PTGFR,ALOX12,ALOX5,PTGER4
	Granzyme B Signaling	1.89	0.13	APAF1,IL1MB1
	Th1 Pathway	1.78	0.04	CCR5,PIK3CG,IL6R,CD8A,KLRC1
	G-Protein Coupled Receptor Signaling	1.48	0.03	GRM7,P2RY13,PIK3CG,GNAO1,RGS14,PTGER4,XCR1
	Mitotic Roles of Polo-Like Kinase	1.45	0.05	PTTG1,CDC23,CENB1
	cAMP-mediated signaling	1.4	0.03	GRM7,P2RY13,GNAO1,RGS14,PTGER4,XCR1
	Th1 and Th2 Activation Pathway	1.28	0.03	CCR5,PIK3CG,IL6R,CD8A,KLRC1

Supplementary Table 10: Ingenuity network analysis of the microdissected breast stroma-related RNAseq dataset: upregulated (Up) and downregulated (Down) genes are analyzed together or separately

ID	Analysis	Molecules in Network	Score	Focus % Top Diseases and Functions
1	Stroma Up and Down	ASPH,BAALC,Csblp300,CCDC12,CCDC120,CD37,CDK9,CEP97,CQO8A,DMRT3,EAZF2,FR	46	30 Gene Expression, Developmental Disorder, Hereditary Disorder
2	Stroma Up and Down	ACVR1C,Alpha tubulin,AMOTL2,APOBEC3B,APOBEC3F,APOBEC3G,B-cell receptor,CCN1L	41	28 Antimicrobial Response, RNA Post-Transcriptional Modification, Cell Signaling
3	Stroma Up and Down	26s Proteasome,AAMP,AIFM2,C4A,CEBPA,CYP39A1,EPHX1,estrogen receptor,FAM212B,FA	37	36 Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function
4	Stroma Up and Down	AFG3L2,AKAP,AKAP1,AK,ANGPTL4,CDK4R,CYP19,ELOV5,FADS3,FNDC3A,GIS2,GRAM	35	25 Lipid Metabolism, Small Molecule Biochemistry, Infectious Diseases
5	Stroma Up and Down	ACAC,AKR,APAF1,APIP,BOP1,Cdk,CDKN2B,CFAP206,CPT11,CPT1C,Cyclin A,Cyclin D,Cycl	35	25 Cell Cycle, DNA Replication, Recombination, and Repair, Endocrine System Disorders
6	Stroma Up and Down	ABLIM3,Actin,ADCY3,Alpha Actinin,Alpha catenin,Cadherin,Calmodulin,CAV1,CAVIN1,CDH5,	33	24 Connective Tissue Disorders, Developmental Disorder, Hereditary Disorder
7	Stroma Up and Down	ACAD5,APC (complex),chemokine receptor,chemotactin,COL13A1,COL16A1,COL25A1,COL	31	23 Cancer, Connective Tissue Disorders, Organismal Injury and Abnormalities
8	Stroma Up and Down	ADIPQO,ADIPOR2,AGPAT2,AMPK,CCDO1,Colin,CYBSA,cytochrome C,cytochrome-c oxidase	31	23 Lipid Metabolism, Small Molecule Biochemistry, Connective Tissue Disorders
9	Stroma Up and Down	ABCD2,ACAA1,AKR1C3,AKR1C2,ANO3,DHRS3,ECM2,FABP,GAS2,JUN,JUNB,JUN	29	22 Endocrine System Development and Function, Lipid Metabolism, Small Molecule Biochemistry
10	Stroma Up and Down	20s proteasome,ADCI,ANGPT1,ANKRD2,ATP1A2,Atia1,Natriuretic Peptide,Collagen,Alpha 1	27	21 Developmental Disorder, Small Molecule Biochemistry, Hereditary Disorder
11	Stroma Up and Down	Adaptor protein 2,ADGRF5,CCR2,CCR5,chemokine FZD4,G protein alphaI,G protein beta 1	23	19 Behavior, Organismal Injury and Abnormalities, Tissue Morphology
12	Stroma Up and Down	AKAP8,ACCA3,ACOP7,Cdc2,CH25H,CYTP,DUSP4,Em,ETFDDH,Gamma tubulin,GLDC,HOXC4	25	20 Humoral Immune Response, Protein Synthesis, Developmental Disorder
13	Stroma Up and Down	ACACB,ACSLE6,ALOX5,ALOX12,APOB,BCR (complex),BLNK,CD36,CD33,ouros,Collagen,hoce	23	19 Lipid Metabolism, Small Molecule Biochemistry, Energy Production
14	Stroma Up and Down	Adaptor protein 2,ADGRF5,CCR2,CCR5,chemokine FZD4,G protein alphaI,G protein beta 1	23	19 Behavior, Organismal Injury and Abnormalities, Tissue Morphology
15	Stroma Up and Down	ALT,APOE,C11orf12,Complement,CXCL3,cytokine,DNAJA4,FAH,GOT,HARS,hemoglobin,HIS	23	19 Organismal Injury and Abnormalities, Digestive System Development and Function, Hepatic System Development and Function
16	Stroma Up and Down	14-3-3,ADRB,ARL4A,BAD,BOK,Calineurin protein(s),CaMKII,Caspase 3/7,CUTC,CxorF21,DE	21	18 Hematological System Development and Function, Hematopoiesis, Humoral Immune Response
17	Stroma Up and Down	CD38,CD5A,Chuk,IKKb,Ikba,IGAS,GCAT,GFOD1,Itf,IPN,alphanbeta,IPN,Beta,IPN,hoce,1,Ifr	21	18 Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking
18	Stroma Up and Down	ACVR1C,APMAP,ATAD2,ATPase,ATXN1L,COPRS,DOX1,FAM210A,FXO24,FNBP1,HIST17	21	18 Cardiac Dilation, Cardiovascular Disease, Hereditary Disorder
19	Stroma Up and Down	Alo,calcain,CAPN2,Collagen(s),EDEMI,ESY71,FERMT1,FGF2,HEY1,HIF1,Intein,Laminin (c	20	17 Organismal Development, Cellular Development, Cellular Growth and Proliferation
20	Stroma Up and Down	ALDH4A1,ANO2,APP,BCAT2,beta-estradiol,C16orf7,CDCA7,CDRI,COL13A1,DNA1,DNALH1	20	17 Cellular Assembly and Organization, Cell-To-Cell Signaling and Interaction, Inflammatory Response
21	Stroma Up and Down	ABCD2,ACOT4,ADAT1,BCL2L1,CASS4,CEP98,CETNL,CRK,CYP3A7,FRMD4A,GYS2,HBP1,	20	17 Cell Morphology, Cellular Function and Maintenance, Connective Tissue Development and Function
22	Stroma Up and Down	ADGRE1,AGAP5 (includes others),BIN2,Caln1 (includes others),CCDC32,CD44,DAPK2,DAP	18	16 Cell Signaling, Nucleic Acid Metabolism, Small Molecule Biochemistry
23	Stroma Up and Down	ADCT,ADCY6,Ampa Receptor,C-C chemokine receptor,CASP4,CTNNBIP1,G protein,G orde	16	15 Cell Signaling, Molecular Transport, Nucleic Acid Metabolism
24	Stroma Up and Down	ALDH4A1,ALOX12,APP,ARNGEF5,BCAT2,C1orf5,C7orf51,CCDC144NL,COL13,CDN3,CEL	16	15 Hematological Disease, Metabolic Disease, Cellular Compromise
25	Stroma Up and Down	ACACB,ADAM11,ADAM22,ADAM23,C2CD2,CD8B,CFAP45,CREB3L2,DCUN1D3,ELAVL1,FA	16	16 Nervous System Development and Function, Developmental Disorder, Hereditary Disorder
ID	Analysis	Molecules in Network	Score	Focus % Top Diseases and Functions
1	Stroma Up	ACVR1C,AMOTL2,ASPH,Cadherin,CCDC12,CDH5,COL13A1,CQO8A,CTNNBIP1,DTX1,ERK	51	29 Developmental Disorder, Embryonic Development, Organismal Development
2	Stroma Up	ADIPQO,ADIPOR2,APOE,AQP7,Atrial Natriuretic Peptide,ATXN1,Lchmotrovesin,DD	45	27 Carbohydrate Metabolism, Connective Tissue Disorders, Organismal Injury and Abnormalities
3	Stroma Up	Actin,Alpha catenin,APOLE,BAALC,C16orf12,caspase,CD3,CD37,CK2,cytokine,DMRT3,ESY	34	32 Cell Death and Survival, Dermatological Diseases and Conditions, Developmental Disorder
4	Stroma Up	AFG3L2,AKAP,AKAP1,AK,ANGPTL4,CDK4R,CYP19,ELOV5,FADS3,FNDC3A,GIS2,GRAM	35	25 Lipid Metabolism, Small Molecule Biochemistry, Developmental Disorder
5	Stroma Up	ACAP,AKAP1,AK,ALT,ANGPTL4,CD36,CDK4R,CYP19,DOIT4,ELOVL5,FASN,FXR,ligand-FX	32	21
6	Stroma Up	ABCD2,ACAA1,ACAC,ACACB,AKR1C3,AKR1C1,AKR1C2,ANO3,CPT1,DHRS3,FABP,GOS2J	30	20 Energy Production, Lipid Metabolism, Small Molecule Biochemistry
7	Stroma Up	26s Proteasome,AFG3L2,Alpha tubulin,BOP1,BOPF1,C4A,CDK3,CEBPA,CDSC2,Cdin,AHA	27	19 Cell Cycle, Connective Tissue Development and Function, Cell Morphology
8	Stroma Up	7beta-hydroxysterol,ABLIM3,APP,BCL2,C16orf12,Ca2+,D-serine,DNAJB12,DRAP1,ECM	27	19 Skeletal and Muscular System Development and Function, Cell Morphology, Renal and Urological System Development and Function
9	Stroma Up	AMGO1,AOC3,COL16A1,COL25A1,COL4A2,collagen,Collagen type I,Collagen type IV,Collag	24	17 Organismal Development, Cancer, Organismal Injury and Abnormalities
10	Stroma Up	ADGRE1,ADGRV1,AFM2,APOBEC3B,ATP1A2,CD300,G,CEP55,CWC25,FANCD2,F7S1J3	22	16 Protein Trafficking, Hereditary Disorder, Ophthalmic Disease
11	Stroma Up	AAMP,ADCY,Ampa Receptor,CAMK8,Cdk,Chuk,Ikba,Ikba,Collagen,Alpha1,Cyclin D,EZ1,ETI	20	15 Developmental Disorder, Endocrine System Disorders, Hereditary Disorder
12	Stroma Up	ADAM11,ADAM2,APP,APMAP,ASAP2,BLCP,C2CD2,C3orf62,CFAP45,DCUN1D3,DSP28	20	15 Connective Tissue Disorders, Developmental Disorder, Hereditary Disorder
13	Stroma Up	ADGRF5,AGT1R1,ANO2,BCAT2,beta-estradiol,CDCA7,CDRI,CLDN2,CMLK1,COPRS,CRE	20	15 Post-Translational Modification, Cell-To-Cell Signaling and Interaction, Nervous System Development and Function
14	Stroma Up	ADGRF5,ALDH11,CDD4,CTRB2,CUTC,D-erythro-C16-ceramide,DICER1,ENDOU1,F11,FRM	20	15 Cardiovascular System Development and Function, Cell-To-Cell Signaling and Interaction, Hematological System Development and Function
15	Stroma Up	ADCY3,ADGRF5,AKAP8,AMPKAp1,Calmodulin,CAPN2,CAV1,CS,DAPK2,estrogen receptor,J	18	14 Cell Signaling, Nucleic Acid Metabolism, Small Molecule Biochemistry
16	Stroma Up	ALDH1B1,ALDH4A1,C3orf116,CAMK2N2,C17F,DHRS4,DHRS4L2,DNAJ5,EPHX1,FKBP5,as	18	14 Cell Morphology, Hematological Disease, Metabolic Disease
17	Stroma Up	14-3-3,ADCY6,ADRB,BAD,BOK,Calineurin protein(s),CD33,ouros,CDO1,Cc,Creb,DBNL,DUS	16	13 Cell Death and Survival, Embryonic Development, Cellular Growth and Proliferation
18	Stroma Up	ALAP1,ANXA9,ARL4D,ATPSPQ,C2orf27,CDK2N2B,CHCHD10,COL12A1,CTNNB1,Cyclin D1I	16	13 Connective Tissue Development and Function, Skeletal and Muscular System Development and Function, Tissue Development
19	Stroma Up	ADPGK,AGRN,APP,ATM,C1orf35,CARS,CCDC144NL,CCNB1P1,CNNG2,CRHR2,DAPPI1,DF	15	12 Nervous System Development and Function, Organ Morphology, Tissue Morphology
20	Stroma Up	Alo,BCR (complex),CAVIN1,Complement,CYBSA,cytochrome C,cytochrome-c oxidase,EGLN,	13	11 Developmental Disorder, Gastrointestinal Disease, Hematological Disease
21	Stroma Up	FAM89A,UBXN2B	2	1 Cell Cycle, Cellular Assembly and Organization, Cancer
22	Stroma Up	BTNL9,STAT1	2	1 Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function
23	Stroma Up	ABL1,TMEM74B	2	1 Cancer, Cardiovascular Disease, Cellular Assembly and Organization
24	Stroma Up	MIR5091,mirR-5091 (miRNAs w/seed CGGAGAC)	2	1
25	Stroma Up	MIR6079,mirR-6079 (miRNAs w/seed UGAGAGC)	2	1
ID	Analysis	Molecules in Network	Score	Focus % Top Diseases and Functions
1	Stroma Down	AHR,AKAPAF1,APC (complex),CCNB1,CCNB1P1,CD38,Cdc2,CDK23,Cyclin A,Cyclin D,Cyc	37	22 Cell Cycle, Cell Death and Survival, Hepatic System Development and Function
2	Stroma Down	B-cell receptor,BCR (complex),BLNK,CH25H,DAP11,Ecdatin,ERK1/2,FCLRL5,HOXD4,HS42D	33	20 Humoral Immune Response, Protein Synthesis, Cell-To-Cell Signaling and Interaction
3	Stroma Down	ALOX5,CCR2,CCR5,chemokine,chemokine receptor,Coflin,Collagen type I,Collagen(s),CXCL	30	19 Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking
4	Stroma Down	ADGRF5,APP,C1orf51,CPO,CYP20A1,DNA11,DOCK2A,DOCK2B,DYNLT1,FAS1D3,Gozr,GIP	26	17 Cell-To-Cell Signaling and Interaction, Cell Death and Survival, Cellular Compromise
5	Stroma Down	AGAP5 (includes others),ALOX12,ARMT1,ATAD2,beta-estradiol,C16orf74,CCDC32,OPT1C,C	26	17 Lipid Metabolism, Small Molecule Biochemistry, Organ Morphology
6	Stroma Down	ADM,ACSLE6,ARL4A,CASS4,COL24,CCNB1,CEP98,CNR1,CRK,ECM2,GCAT,GFPM2,GPR84,G	26	17 Cell-To-Cell Signaling and Interaction, Dermatological Diseases and Conditions, Organismal Injury and Abnormalities
7	Stroma Down	APOBEC3B,APOBEC3F,APOBEC3G,C-C chemokine receptor,CASP4,CD8A,cytidine deamin	24	16 Antimicrobial Response, Inflammatory Response, Cell Signaling
8	Stroma Down	14-3-3,Actin,ALOX12,Alpha tubulin,CYTIIP,ERK,F,FERMT1,GAS2,GAS2L3,HDLH	24	16 Cancer, Endocrine System Disorders, Gastrointestinal Disease
9	Stroma Down	ACOK3,ADAT1,CHK6-AS1,Couo,T1DAPK2,E2F4,E2F7,FBXW2,FGT,GINS2,HIF1A,HIST2H	24	16 Cellular Function and Maintenance, Cell Cycle, Cancer
10	Stroma Down	AFM2,ALOX12,BCL2L1,CCSAP,CC74,CTNS,CYP39A1,ED2B,ENMD2G5,ESR1,GRB2,HBP1	24	16 Cellular Growth and Proliferation, Cell Cycle, Tissue Morphology
11	Stroma Down	ADCY,ADRB,AMPK,Calmodulin,Ca,CPNE5,Creb,FNDC3A,G protein alphaI,G protein beta 1	22	15 Cancer, Dermatological Diseases and Conditions, Organismal Injury and Abnormalities
12	Stroma Down	26s Proteasome,ALOX12,AP1,caspase,CD3,CYP4V2,F5H,GLDC,HDL-cholesterol,HIST1H4D	22	15 Nucleic Acid Metabolism, Small Molecule Biochemistry, Cellular Development
13	Stroma Down	ADAT1,ANKRD49,APH1A,CAMK2N1,DPIY184,DTXSL,ELAVL1,EVD2,FAM210A,FAMNC,Gf	22	15 Developmental Disorder, Hereditary Disorder, Neurological Disease
14	Stroma Down	12-hydroxycoccaltetraenoic acid,ALOX12,APOB,BIN2,CEP97,DEE1,EGFR,ERN1,F2,F	18	13 Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral Metabolism
15	Stroma Down	ADCYAP1,CCDC120,CCDC168,Ccl6,CEACAM,CEACAM21,CENPO,CFAP206,CREBBP,CUL	16	12 Cellular Development, Behavior, Cancer
16	Stroma Down	ME1,NEDD8	2	1 Post-Translational Modification, Cell Cycle, Reproductive System Development and Function
17	Stroma Down	KANS1,LOFTN	2	1 Cell Death and Survival, Cell Morphology, Cellular Function and Maintenance
18	Stroma Down	miR-92a-3p (and other miRNAs w/seed AUUGGAC),OIP5-AS1	2	1 Cancer, Organismal Injury and Abnormalities, Gastrointestinal Disease
19	Stroma Down	mi-1254,miR-1254 (and other miRNAs w/seed GCGUUGA)	2	1
20	Stroma Down	mi-7641,miR-7641 (miRNAs w/seed UGAUUCU)	2	1
21	Stroma Down	NALP,NLRP11	2	1 Cancer, Gastrointestinal Disease, Hepatic System Disease
22	Stroma Down	MIR5586,miR-5586-3p (miRNAs w/seed AGAGUGUA),miR-5586-5a (miRNAs w/seed AUCCAC	2	1
23	Stroma Down	mi-3064,miR-3064-3p (miRNAs w/seed GCCACAC),miR-3064-3p (miRNAs w/seed UGGCCAC	1	1

Supplementary Table 11: List of canonical pathway involving the genes differentially expressed in breast adipose tissue between susceptible and matched healthy control samples.

	Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
UPREGULATED	Mitochondrial L-carnitine Shuttle Pathway	2.79	0.118	SLC27A2,CPT1B
	PPAR α /RXR α Activation	2.41	0.0222	NFKBIA,CPT1B,ADCY10,ACVR1C
	Immune response regulation	2.36	0.0326	NFKBIA,IRAK3,ADCY10
	Fatty Acid β -oxidation I	2.24	0.0625	SLC27A2,SCP2
	Glutamate Receptor Signaling	1.76	0.0351	GRIA1,GLUL
	AMPK Signaling	1.38	0.0139	CPT1B,ADRB3,EIF4EBP1
	GABA Receptor Signaling	1.35	0.0211	ADCY10,SLC6A13
	Sumoylation Pathway	1.34	0.0208	NFKBIA,SENP3
	TR/RXR Activation	1.32	0.0204	KLF9,THRB
	ATM Signaling	1.32	0.0204	NFKBIA,GADD45B
DOWNREGULATED	Retinol Biosynthesis	2.67	0.0476	CES4A,LIPG
	Salvage Pathways of Pyrimidine Deoxyribor	1.88	0.125	APOBEC3G
	B Cell Development	1.72	0.0154	BLNK,CAMK2B
	B Cell Receptor Signaling	1.4	0.0104	BLNK,CAMK2B

Supplementary Table 12: Ingenuity network analysis of the microdissected breast adipose tissue-related RNAseq dataset: Upregulated (Up) and downregulated (Down) genes are analyzed together or separately.

ID	Analysis	Molecules in Network	Score	Focus N Top Diseases and Functions
1	Adipose Tissue Up and Down	ACVR1C, ADCY, ADCY10, ADRB3, Akt, AMOTL2, AMPK, AXIN2, c	32	17 Cardiovascular Disease, Cardiac Arrhythmia, Organismal Injury and Abnormalities
2	Adipose Tissue Up and Down	AMIGO1, ASGR1, BCR (complex), BLNK, Calcineurin protein(s), (	30	16 Cell Death and Survival, Tissue Morphology, Cellular Compromise
3	Adipose Tissue Up and Down	ADRB, ANO3, Ap1, APOBEC3G, CaMKII, CERS6, Cq, Ck2, COL6A	30	16 Cellular Function and Maintenance, Molecular Transport, Lipid Metabolism
4	Adipose Tissue Up and Down	ACOX3, ARMC1, ASCC1, BPIFB2, BRIP1, BST1, C21orf59, CCDC	25	14 Cell Morphology, Cellular Function and Maintenance, Cell Death and Survival
5	Adipose Tissue Up and Down	ACOT7, APP, ARMC1, ASCC1, ATXN1, BRCA1, CAMK2B, CHURC	23	13 Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Cellular Assembly and Organization
6	Adipose Tissue Up and Down	AR, ATAD2, beta-estradiol, CES4A, CLCN1, DNAH6, DNAH8, DNA	20	12 Organ Morphology, Reproductive System Development and Function, Cellular Growth and Proliferation
7	Adipose Tissue Up and Down	10-nitrooleate, 22(R)-hydroxycholesterol, AP4M1, ATG16L2, ATP	18	11 Small Molecule Biochemistry, Connective Tissue Development and Function, Tissue Morphology
8	Adipose Tissue Up and Down	26S Proteasome, ACSF3, ADRB3, alpha-hydroxyglutarate, ANK1,	12	8 Organ Morphology, Renal Dilation, Renal and Urological System Development and Function
9	Adipose Tissue Up and Down	mir-921, miR-921 (miRNAs w/seed UAGUGAG)	2	1
10	Adipose Tissue Up and Down	MIR5690, miR-5690 (miRNAs w/seed CAGCUAC)	2	1
11	Adipose Tissue Up and Down	CYP26C, CYP26C1	2	1 Dermatological Diseases and Conditions, Developmental Disorder, Drug Metabolism
12	Adipose Tissue Up and Down	CA13, Carbonic anhydrase	2	1 Ophthalmic Disease, Organismal Injury and Abnormalities, Developmental Disorder
13	Adipose Tissue Up and Down	PARVG, TAL1, WFDC1, ZNF677	2	1 Cardiovascular System Development and Function, Cell Cycle, Cellular Development
ID	Analysis	Molecules in Network	Score	Focus M Top Diseases and Functions
1	Adipose Tissue Up	ADCY10, APP, ATXN1, beta-estradiol, BPIFB2, CFL2, CHURC1, C	41	19 Nucleic Acid Metabolism, RNA Post-Transcriptional Modification, Small Molecule Biochemistry
2	Adipose Tissue Up	ADCY, ADCY10, ADRB, Calcineurin protein(s), CaMKII, Cq, CPT1I	38	18 Amino Acid Metabolism, Cancer, Endocrine System Disorders
3	Adipose Tissue Up	AMIGO1, AR, BRIP1, CCND1, CENPH, COL11A1, COL8A1, COL8	30	15 Psychological Disorders, Cancer, Organismal Injury and Abnormalities
4	Adipose Tissue Up	ACVR1C, AMPK, ANO3, BCR (complex), caspase CD3, CERS6, C	23	12 Lipid Metabolism, Small Molecule Biochemistry, Hereditary Disorder
5	Adipose Tissue Up	ADRB1, ADRB3, adrenoceptor, Akt, AMOTL2, AXIN2, Camkk, CAP	18	10 Cardiac Arrhythmia, Cardiovascular Disease, Organismal Injury and Abnormalities
6	Adipose Tissue Up	AURKA, ZKSCAN2	2	1 Cancer, Cell Cycle, Cell Death and Survival
7	Adipose Tissue Up	PPP1CA, TMEM132C	2	1 Cellular Compromise, Cell-To-Cell Signaling and Interaction, Nervous System Development and Function
8	Adipose Tissue Up	PPP1CC, VSTM4	2	1 Cell Cycle, Cellular Movement, Cancer
9	Adipose Tissue Up	MIR5690, miR-5690 (miRNAs w/seed CAGCUAC)	2	1
10	Adipose Tissue Up	PARVG, TAL1, WFDC1, ZNF677	2	1 Cardiovascular System Development and Function, Cell Cycle, Cellular Development
ID	Analysis	Molecules in Network	Score	Focus M Top Diseases and Functions
1	Adipose Tissue Down	ACOT7, AP4M1, APOBEC3G, APP, ARMC1, ASGR1, BLNK, CAMI	42	17 Cell-To-Cell Signaling and Interaction, Small Molecule Biochemistry, Cell Death and Survival
2	Adipose Tissue Down	22(R)-hydroxycholesterol, ADRB, ASGR1, ATG16L2, CES4A, CHI	36	15 Endocrine System Development and Function, Organ Development, Molecular Transport
3	Adipose Tissue Down	mir-921, miR-921 (miRNAs w/seed UAGUGAG)	3	1
4	Adipose Tissue Down	CYP26C, CYP26C1	3	1 Dermatological Diseases and Conditions, Developmental Disorder, Drug Metabolism
5	Adipose Tissue Down	CA13, Carbonic anhydrase	3	1 Ophthalmic Disease, Organismal Injury and Abnormalities, Developmental Disorder
6	Adipose Tissue Down	CETN1, FBXO16, SKP1	2	1 Hereditary Disorder, Ophthalmic Disease, Organismal Injury and Abnormalities

Supplementary Table 13: Relative leukocyte fractions evaluated by CIBERSORT analysis on the stroma RNAseq dataset.

Input Sample	B cells naive	B cells memory	Plasma cells	T cells CD8	T cells CD4 naive	T cells CD4 memory resting	CD4 memory activated	T cells follicular helper	T cells regulatory (Tregs)	T cells gamma delta	NK cells resting	NK cells activated	Monocytes	Macrophages M0	Macrophages M1	Macrophages M2	Dendritic cells resting	Dendritic cells activated	Mast cells resting	Mast cells activated	Eosinophils	Neutrophils
Susceptible 1	0.150	0	0.162	0.013	0	0.418	0	0	0	0	0.038	0	0.061	0.036	0.052	0	0.009	0	0.061	0	0	0
Susceptible 2	0.139	0	0.299	0	0.043	0.104	0	0.030	0	0	0.003	0.065	0.184	0.029	0.013	0	0.052	0	0.039	0	0	0
Susceptible 3	0.217	0	0.145	0	0	0.132	0	0.002	0.041	0	0	0.030	0.086	0	0.025	0.056	0.075	0	0.191	0	0	0
Susceptible 4	0.116	0	0.188	0.007	0.035	0.080	0	0	0	0	0.040	0.035	0.180	0.018	0.014	0.135	0.023	0	0.129	0	0	0
Susceptible 5	0.177	0	0.138	0.033	0	0.052	0	0	0	0	0	0.093	0.041	0.033	0.021	0.059	0.070	0	0.284	0	0	0
Susceptible 6	0.300	0	0.123	0.062	0.015	0.034	0	0.006	0	0	0.011	0.034	0.134	0	0.020	0.063	0.115	0	0.082	0	0	0
Susceptible 7	0.229	0	0.252	0	0.026	0.225	0	0	0	0	0.035	0.044	0.021	0	0	0.053	0.040	0	0.073	0	0	0
HC 1	0.219	0	0.164	0.010	0	0.106	0	0.008	0	0	0	0.043	0.132	0	0.033	0.095	0.087	0	0.102	0	0	0
HC 2	0.088	0	0.034	0.036	0.031	0.446	0	0	0	0	0	0.109	0.211	0	0	0.015	0	0.011	0.019	0	0	0
HC 3	0.205	0	0.161	0	0.083	0.145	0	0	0	0	0	0.054	0.083	0.002	0.003	0.013	0.137	0	0.113	0	0	0
HC 4	0.129	0	0.186	0.022	0	0.284	0	0	0.005	0	0.016	0.080	0.093	0.014	0.023	0.010	0.010	0	0.128	0	0	0
HC 5	0.081	0	0.071	0.012	0	0.229	0	0	0	0	0.017	0.025	0.247	0	0	0	0.042	0	0.092	0	0	0.184
HC 6	0.075	0	0.086	0.004	0	0.092	0	0.005	0.021	0.001	0	0.039	0.530	0	0.038	0	0.040	0	0.069	0	0	0
HC 7	0.220	0	0.290	0	0.038	0	0.029	0.074	0	0.009	0.019	0	0.034	0.043	0.123	0	0.044	0	0.070	0	0.007	0
HC 8	0.260	0	0.210	0	0	0.110	0	0.006	0	0	0	0.061	0.033	0	0	0.079	0.098	0	0.144	0	0	0
HC 9	0.211	0	0.129	0.011	0	0.137	0	0.032	0	0	0	0.050	0.131	0	0.013	0.098	0.088	0	0.101	0	0	0
HC 10	0.156	0	0.404	0	0.029	0.131	0	0	0	0	0.006	0.052	0.092	0	0	0.041	0	0	0.088	0	0	0
HC 11	0.032	0	0.370	0.002	0	0.257	0	0	0.067	0	0	0.038	0.029	0	0	0	0	0	0.206	0	0	0
HC 12	0.074	0	0.103	0.015	0	0.374	0	0	0.026	0	0.020	0	0.069	0.021	0.029	0.039	0.087	0	0.148	0	0	0
HC 13	0.272	0	0.245	0	0	0.141	0	0.011	0	0	0	0.083	0.019	0.005	0	0.028	0.077	0	0.118	0	0	0
HC 14	0.179	0	0.174	0.060	0.073	0.208	0	0	0	0	0.005	0.046	0.067	0.002	0.013	0.002	0.074	0	0.097	0	0	0
HC 15	0.221	0	0.302	0	0.008	0.149	0	0	0	0	0	0.080	0.045	0	0.015	0.016	0.112	0	0.052	0	0	0
HC 16	0.104	0	0.171	0	0	0.205	0	0	0.014	0	0	0.034	0.083	0.029	0.005	0.038	0.196	0	0.120	0	0	0
p value	0.341		0.873	0.514	0.966	0.478	0.521	0.698	0.766	0.484	0.025	0.622	0.734	0.157	0.852	0.201	0.559	0.521	0.498		0.521	0.521
fold change										3.54												

HC: Healthy Control; RMSE = root mean squared error

Supplementary Table 14: Co-expression analysis of the microdissected epithelium (Epi)-, Stroma- and adipose tissue (Fat)-related data in Susceptible (Susc) and Healthy (HC) samples.

Stroma-HC	Fat-HC	statistic	p value	FDR	beta
KCNF1	GJB1	71.25	1.7E-12	0.00	1.03
KDEL2	STG6ALNAC2	-36.07	3.8E-10	0.03	-1.59
TRAPPC2B	LOC100506388	35.94	3.9E-10	0.03	0.80
GRN	PAPD5	-34.86	5.0E-10	0.03	-0.75
AGTRAP	EMBP1	34.68	5.2E-10	0.03	3.02
METTL21EP	PLAG1	34.40	5.6E-10	0.03	0.88
HIST1H3E	CASP8	34.04	6.1E-10	0.03	0.17
VWA8	RPGR	32.27	9.3E-10	0.04	2.07
FBXL8	LOC100506388	30.16	1.6E-09	0.05	0.75
STAP1	ELP5	-29.93	1.7E-09	0.05	-0.12
SNORA23	TMEM176A	-29.80	1.7E-09	0.05	-0.97
MB1	SH3KBP1	-28.94	2.2E-09	0.06	-1.52
CENPN	LINC00968	28.47	2.5E-09	0.06	4.02
SNORD17	RDH16	27.42	3.4E-09	0.07	1.21
FBXO7	BEGAIN	-27.11	3.7E-09	0.07	-4.65
LOC101929066	KLRD1	26.88	3.9E-09	0.07	1.06
C21orf62-AS1	RORA-AS1	26.78	4.1E-09	0.07	2.03
FAM171A1	ARRDC2	-26.67	4.2E-09	0.07	-1.62
ZNF811	TMEM161A	26.46	4.5E-09	0.07	1.43
RFESD	FBXO48	26.22	4.8E-09	0.07	0.69
LOC101928979	LOC100506388	26.04	5.1E-09	0.07	0.99
RASA4	MIR68	25.77	5.5E-09	0.07	0.33
INADL	SLC37A2	-25.75	5.5E-09	0.07	-1.33
GP2	MEPCE	25.66	5.7E-09	0.07	0.85
JADE1	ISLR	-25.63	5.8E-09	0.07	-1.93
FOXN3-AS1	LOC100506497	25.42	6.2E-09	0.07	1.20
MYOZ1	KIAA0196	25.26	6.5E-09	0.08	0.17
LRG1	SLC25A37	24.92	7.2E-09	0.08	0.57
AKAP9	CREBZF	24.83	7.4E-09	0.08	1.46
HIST1H2AI	KIFC1	24.52	8.2E-09	0.09	1.15
Epi-HC	Stroma-HC	statistic	p value	FDR	beta
COL5A2	COL3A1	13.31	1.0E-09	0.07	1.31
WISP2	WISP2	13.22	1.1E-09	0.07	0.64
TNFSF4	LOC441455	13.15	1.2E-09	0.07	1.87
LAMTOR2	FOXF1	13.10	1.3E-09	0.07	3.45
GSTT1	LOC391322	13.05	1.4E-09	0.07	0.83
HMCN1	COL3A1	12.90	1.6E-09	0.07	2.19
MIR26A2	SHROOM1	12.78	1.8E-09	0.07	0.70
SCN3B	BATF3	12.77	1.8E-09	0.07	0.98
DCST1	ZNF663P	12.65	2.1E-09	0.07	1.29
PTTG2	PILRB	12.21	3.4E-09	0.10	0.72
COL6A3	SPARC	11.96	4.5E-09	0.10	0.73
JADE1	PXYLP1	-11.94	4.6E-09	0.10	-3.75
ARRDC5	C16orf87	11.93	4.7E-09	0.10	0.39
PLIN4	PTPN2	-11.80	5.4E-09	0.10	-0.21
SNORD116-18	SNORD116-18	11.77	5.6E-09	0.10	0.84
SPATA5L1	PMS2P5	11.70	6.1E-09	0.10	1.71
CYP4F24P	CYP4F24P	11.66	6.4E-09	0.10	1.13
DLSTP1	LOC102724190	11.61	6.8E-09	0.10	0.86
RABL2B	PNPLA6	11.59	6.9E-09	0.10	0.63
LINC00906	MIR601	-11.57	7.1E-09	0.10	-3.27
RASSF2	RNVJ11-8	-11.52	7.6E-09	0.10	-2.18
SLC28A1	NHP2L1	11.50	7.7E-09	0.10	0.09
LINC00176	QKI	-11.49	7.8E-09	0.10	-0.12
JADE1	ADAMTS8	-11.42	8.5E-09	0.10	-5.92
RPGR	ATF6B	11.38	8.9E-09	0.10	0.63
Epi-HC	Fat-HC	statistic	p value	FDR	beta
ALDH1L1-AS2	MEAT6	Inf	0.0E+00	0.00	1.83
ADGRG4	UGT2B15	Inf	0.0E+00	0.00	1.87
ALDH1L1-AS2	UGT2B11	Inf	0.0E+00	0.00	3.20
LINC01028	MEAT6	Inf	0.0E+00	0.00	1.83
LINC01028	UGT2B11	Inf	0.0E+00	0.00	3.20
MIR3612	C1QL2	Inf	0.0E+00	0.00	1.35
MIR3612	FLJ31662	Inf	0.0E+00	0.00	1.03
ADGRG4	CRISP3	189812531.25	6.6E-64	0.00	2.19
LOC101928223	MEAT6	189812531.25	6.6E-64	0.00	0.82
LOC101928223	UGT2B11	134217728.00	1.1E-62	0.00	1.44
PGAP1	ZFPM2-AS1	34.94	4.9E-10	0.01	2.77
NOMO1	RFC1	-32.76	8.2E-10	0.02	-0.65
NRXN3	FRMD3	-29.79	1.7E-09	0.04	-1.32
DERL2	NIPSNAP3B	28.74	1.8E-09	0.04	4.62
HM13	RAB40B	28.62	2.4E-09	0.05	1.13
RPL41	AGTR1	26.46	4.5E-09	0.09	1.95
THAP7-AS1	FOXO1	26.13	4.9E-09	0.09	0.79
SLC2A8	YOD1	25.93	5.2E-09	0.09	0.95
GTF2H2C	BCDIN3D-AS1	24.94	7.1E-09	0.12	1.33
RERE	FNTA	-24.23	9.0E-09	0.14	-1.51
CDH1	PYGL	-23.93	9.9E-09	0.15	-1.51
Stroma-Sus	Fat-Sus	statistic	p value	FDR	beta
snps	snps				
SSRP1	HIST2H3D	1689.49	4.6E-10	0.14	7.83
SLC1A2	KLHL20	-832.70	3.8E-09	0.57	-0.15
HS2ST1	ADCY8	698.79	6.5E-09	0.64	14.29
Epi-Susc	Stroma-Susc	statistic	p value	FDR	beta
AKR1B1	COLGALT2	150.69	2.4E-10	0.07	3.50
MIR4523	AARD	-102.06	1.7E-09	0.25	-1.06
ZNF763	APPL1	-81.75	5.2E-09	0.51	-0.37
HSD17B7P2	TRPV2	-72.65	9.4E-09	0.60	-0.48
Epi-Susc	Fat-Susc	statistic	p value	FDR	beta
LOC101926964	CA6	Inf	0.0E+00	0.00	1.43
LOC101926908	CYP24A1	Inf	0.0E+00	0.00	1.44
LOC101926964	CR2	Inf	0.0E+00	0.00	2.59
LOC101926964	FLJ31662	Inf	0.0E+00	0.00	1.43
LOC101926908	KIAA2012	Inf	0.0E+00	0.00	2.84
LOC101926964	LINC01122	Inf	0.0E+00	0.00	2.13
LOC101926964	LINC01132	Inf	0.0E+00	0.00	3.06
LOC101926964	NEBL-AS1	Inf	0.0E+00	0.00	1.43
LOC101926908	TCN1	Inf	0.0E+00	0.00	1.44
LOC101926964	SRMS	Inf	0.0E+00	0.00	3.21
ALDH1L1-AS2	IL22RA1	116235962.09	1.4E-24	0.00	0.66
ALDH1L1-AS2	NUPR1L	116235962.09	1.4E-24	0.00	0.49
LOC101926964	C2CD4D	116235962.09	1.4E-24	0.00	2.32
LOC101926908	CTAGE15	116235962.09	1.4E-24	0.00	1.92
LOC101926964	CEMP1	116235962.09	1.4E-24	0.00	2.32
LOC101926964	FDCSP	116235962.09	1.4E-24	0.00	4.07
LOC101926908	KRT86	116235962.09	1.4E-24	0.00	1.92
LOC101926964	LIPG	116235962.09	1.4E-24	0.00	2.32
LOC101926964	MEAT6	116235962.09	1.4E-24	0.00	3.87
LOC101926964	SIX3	116235962.09	1.4E-24	0.00	2.32
LOC101926908	TNFSF11	116235962.09	1.4E-24	0.00	1.92
LOC101926964	ZSCAN1	116235962.09	1.4E-24	0.00	2.47
LHCGR	SYCE3	1405.28	7.9E-10	0.01	1.43
MAGT1	CYB5D2	-1064.12	1.8E-09	0.02	-0.75
TOB1	FBXO28	682.04	7.0E-09	0.08	0.79