

Table S1. Enriched GO terms of first mRNA neighbors of NONHSAT212577.1.

GO-Term	P-Value	Enrichment score
TAP1 binding	1.26E-04	33.33
MHC class Ib protein binding	1.26E-04	33.33
peptide-transporting ATPase activity	1.26E-04	33.33

Table S2. Enriched KEGG pathways of first mRNA neighbors of NONHSAT212577.1.

GO-Term	P-Value	Enrichment score
Sulfur metabolism	3.42E-02	10.00
Axon guidance	2.20E-02	1.71
ABC transporters	1.05E-02	4.44
Phagosome	1.57E-02	1.95
Antigen processing and presentation	2.89E-02	2.60
Primary immunodeficiency	7.17E-03	5.41

Table S3. Enriched GO terms of first mRNA neighbors of NONHSAT083203.2.

GO-Term	P-Value	Enrichment score
positive regulation of mesenchymal cell apoptotic process	7.16E-06	100.00
embryonic nail plate morphogenesis	2.14E-05	66.67
activation of meiosis	2.14E-05	66.67
frontal suture morphogenesis	4.28E-05	50.00
BMP signaling pathway involved in heart development	1.07E-04	33.33
embryonic forelimb morphogenesis	9.56E-05	9.09
negative regulation of peptidase activity	8.38E-05	2.22
cellular response to growth factor stimulus	6.69E-05	1.34
circulatory system development	1.11E-05	1.19
anatomical structure formation involved in morphogenesis	1.43E-05	1.16
cellular component morphogenesis	1.08E-04	1.02

Table S4. Enriched KEGG pathways of first mRNA neighbors of NONHSAT083203.2.

GO-Term	P-Value	Enrichment score
ECM-receptor interaction	2.74E-03	3.66
VEGF signaling pathway	1.76E-02	3.39
Small cell lung cancer	3.40E-02	2.38
Hematopoietic cell lineage	4.42E-02	2.06
Proteoglycans in cancer	4.89E-03	1.97
Focal adhesion	3.06E-02	1.51
MicroRNAs in cancer	1.86E-02	1.34
PI3K-Akt signaling pathway	2.88E-02	1.17

Table S5. Enriched GO terms of first mRNA neighbors of NONHSAT193031.1.

GO-Term	P-Value	Enrichment score
diphosphoinositol polyphosphate catabolic process	1.90E-03	100.00
cellular response to non-ionic osmotic stress	1.90E-03	100.00
ovarian follicle rupture	1.90E-03	100.00
positive regulation of fructose 1,6-bisphosphate metabolic process	1.90E-03	100.00
positive regulation of fructose 1,6-bisphosphate 1-phosphatase activity	1.90E-03	100.00
positive regulation of platelet-derived growth factor production	3.79E-03	50.00
positive regulation of adrenergic receptor signaling pathway involved in heart process	3.79E-03	50.00
positive regulation of tumor necrosis factor (ligand) superfamily member 11 production	3.79E-03	50.00
regulation of homologous chromosome segregation	3.79E-03	50.00
CD8-positive, alpha-beta T cell differentiation involved in immune response	3.79E-03	50.00
retrograde trans-synaptic signaling by nitric oxide	3.79E-03	50.00
positive regulation of fibroblast growth factor production	5.69E-03	33.33
negative regulation of adrenergic receptor signaling pathway involved in heart process	5.69E-03	33.33
syncytiotrophoblast cell differentiation involved in labyrinthine layer development	5.69E-03	33.33
negative regulation of synaptic transmission, dopaminergic	5.69E-03	33.33
positive regulation of calcidiol 1-monooxygenase activity	5.69E-03	33.33
Spemann organizer formation	7.58E-03	25.00
negative regulation of glomerular mesangial cell proliferation	7.58E-03	25.00
diadenosine pentaphosphate catabolic process	9.46E-03	20.00
diadenosine hexaphosphate catabolic process	9.46E-03	20.00
adenosine 5'-(hexahydrogen pentaphosphate) catabolic process	9.46E-03	20.00
regulation of chorionic trophoblast cell proliferation	9.46E-03	20.00
positive regulation of interleukin-23 production	9.46E-03	20.00
chorionic trophoblast cell differentiation	1.13E-02	16.67
regulation of neuronal action potential	1.13E-02	16.67
cellular response to interleukin-18	1.13E-02	16.67
optic nerve morphogenesis	1.13E-02	16.67
positive regulation of interleukin-12 biosynthetic process	1.13E-02	16.67
positive regulation of core promoter binding	1.13E-02	16.67
positive regulation of natural killer cell chemotaxis	1.13E-02	16.67
positive regulation of cell migration involved in sprouting angiogenesis	1.32E-02	14.29
positive regulation of prostaglandin biosynthetic process	1.32E-02	14.29
negative regulation of RIG-I signaling pathway	1.32E-02	14.29
positive regulation of killing of cells of other organism	1.32E-02	14.29
negative regulation of mitochondrial membrane permeability	1.32E-02	14.29
negative regulation of myelination	1.32E-02	14.29

positive regulation of brown fat cell differentiation	1.32E-02	14.29
positive regulation of interleukin-6 biosynthetic process	1.51E-02	12.50
regulation of protein ADP-ribosylation	1.51E-02	12.50
neutrophil apoptotic process	1.70E-02	11.11
positive regulation of MHC class II biosynthetic process	1.70E-02	11.11
positive regulation of fever generation	1.70E-02	11.11
ADP transport	1.70E-02	11.11
negative regulation of intrinsic apoptotic signaling pathway in response to osmotic stress	1.70E-02	11.11
positive regulation of smooth muscle cell apoptotic process	1.70E-02	11.11
regulation of calcium ion transmembrane transport via high voltage-gated calcium channel	1.70E-02	11.11
positive regulation of synaptic plasticity	1.88E-02	10.00
response to fructose	1.88E-02	10.00
positive regulation of isotype switching to IgG isotypes	1.88E-02	10.00
vacuolar proton-transporting V-type ATPase complex assembly	2.07E-02	9.09
positive regulation of tyrosine phosphorylation of Stat1 protein	2.07E-02	9.09
maintenance of protein location in mitochondrion	2.07E-02	9.09
positive regulation of chemokine biosynthetic process	2.07E-02	9.09
ATP transport	2.07E-02	9.09
cyclooxygenase pathway	2.07E-02	9.09
branching involved in labyrinthine layer morphogenesis	2.26E-02	8.33
exogenous drug catabolic process	2.44E-02	7.69
immunological synapse formation	2.44E-02	7.69
positive regulation of guanylate cyclase activity	2.63E-02	7.14
negative regulation of smooth muscle contraction	2.63E-02	7.14
arginine catabolic process	2.63E-02	7.14
positive regulation of exosomal secretion	2.81E-02	6.67
peptidyl-cysteine S-nitrosylation	2.81E-02	6.67
regulation of the force of heart contraction	1.78E-03	6.06
positive regulation of T cell cytokine production	3.18E-02	5.88
anterior/posterior axis specification, embryo	3.18E-02	5.88
response to manganese ion	3.37E-02	5.56
positive regulation of transforming growth factor beta production	3.37E-02	5.56
pinocytosis	3.55E-02	5.26
negative regulation of growth of symbiont in host	3.55E-02	5.26
regulation of bicellular tight junction assembly	3.55E-02	5.26
regulation of mRNA 3'-end processing	3.92E-02	4.76
cellular response to fluid shear stress	3.92E-02	4.76
neurotransmitter biosynthetic process	3.92E-02	4.76
positive regulation of sodium ion transmembrane transport	3.92E-02	4.76
regulation of interferon-gamma-mediated signaling pathway	4.10E-02	4.55
positive regulation of interleukin-1 beta secretion	4.10E-02	4.55
central nervous system projection neuron axonogenesis	4.28E-02	4.35

negative regulation of myoblast differentiation	4.28E-02	4.35
labyrinthine layer blood vessel development	4.28E-02	4.35
decidualization	4.46E-02	4.17
positive regulation of osteoclast differentiation	4.46E-02	4.17
nitric oxide biosynthetic process	3.69E-04	4.05
retinal ganglion cell axon guidance	4.64E-02	4.00
positive regulation of NF-kappaB import into nucleus	4.64E-02	4.00
response to lithium ion	4.83E-02	3.85
positive regulation of protein deacetylation	4.83E-02	3.85
lactation	5.59E-03	3.39
regulation of mitophagy	5.97E-03	3.28
unsaturated fatty acid biosynthetic process	7.58E-03	2.90
positive regulation of lymphocyte mediated immunity	9.36E-03	2.60
female gamete generation	1.51E-03	2.50
positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1.01E-02	2.50
positive regulation of production of molecular mediator of immune response	1.06E-02	2.44
NAD metabolic process	1.08E-02	2.41
camera-type eye morphogenesis	1.91E-02	1.79
regulation of smooth muscle cell proliferation	2.27E-02	1.63
reactive oxygen species metabolic process	1.59E-03	1.49
establishment of protein localization to mitochondrion	7.27E-03	1.43
positive regulation of synaptic transmission	2.97E-02	1.41
regulation of blood vessel diameter	3.01E-02	1.40
synapse assembly	3.53E-02	1.28
response to temperature stimulus	1.08E-02	1.23
negative regulation of multi-organism process	3.86E-02	1.22
mitochondrial transport	3.61E-03	1.19
regulation of JNK cascade	4.25E-02	1.16
cell chemotaxis	1.58E-02	1.07
positive regulation of intracellular protein transport	1.60E-02	1.07
autophagy	1.96E-03	1.04
regulation of blood circulation	1.80E-02	1.02
positive regulation of cytokine production	7.78E-03	0.96
maintenance of location	2.19E-02	0.95
muscle contraction	2.81E-02	0.86
protein import	2.83E-02	0.86
response to metal ion	2.87E-02	0.85
coenzyme metabolic process	3.00E-02	0.84
positive regulation of cellular catabolic process	3.40E-02	0.80
ossification	3.87E-02	0.76
regulation of cellular catabolic process	7.99E-03	0.75

calcium ion transport	4.17E-02	0.74
establishment of protein localization to organelle	1.03E-02	0.70
blood vessel development	2.97E-02	0.64
developmental process involved in reproduction	4.03E-02	0.58
negative regulation of cell proliferation	4.29E-02	0.57
carboxylic acid metabolic process	4.49E-02	0.48
positive regulation of cellular component organization	2.94E-02	0.48
cell-cell signaling	3.50E-02	0.42
cellular catabolic process	4.99E-02	0.39

Table S6. Enriched KEGG pathways of first mRNA neighbors of NONHSAT193031.1.

GO-Term	P-Value	Enrichment score
Neomycin, kanamycin and gentamicin biosynthesis	9.70E-03	20.00
Arginine biosynthesis	4.01E-02	4.76
Biosynthesis of unsaturated fatty acids	4.39E-02	4.35
Histidine metabolism	4.57E-02	4.17
Arginine and proline metabolism	4.08E-03	4.00
Leishmaniasis	8.54E-03	2.73
IL-17 signaling pathway	1.36E-02	2.15
HIF-1 signaling pathway	1.59E-02	1.98

Table S7. Enriched GO terms of first mRNA neighbors of NONHSAT035952.2.

GO-Term	P-Value	Enrichment score
conditioned place preference	1.61E-03	100.00
immunoglobulin transcytosis in epithelial cells mediated by polymeric	3.22E-03	50.00
immunoglobulin receptor		
dTMP biosynthetic process	3.22E-03	50.00
glycine biosynthetic process from serine	3.22E-03	50.00
adenylate cyclase-inhibiting opioid receptor signaling pathway	3.22E-03	50.00
post-translational protein acetylation	4.83E-03	33.33
mesenchymal stem cell proliferation	6.43E-03	25.00
negative regulation of luteinizing hormone secretion	6.43E-03	25.00
carnitine biosynthetic process	8.03E-03	20.00
primary lung bud formation	8.03E-03	20.00
L-serine catabolic process	8.03E-03	20.00
positive regulation of dopamine secretion	9.63E-03	16.67
negative regulation of RIG-I signaling pathway	1.12E-02	14.29
bud elongation involved in lung branching	1.12E-02	14.29
regulation of aerobic respiration	1.12E-02	14.29
tetrahydrofolate interconversion	1.60E-02	10.00
embryonic viscerocranium morphogenesis	1.76E-02	9.09
inner cell mass cell proliferation	1.92E-02	8.33

retinal metabolic process	1.92E-02	8.33
lymphangiogenesis	2.55E-02	6.25
maintenance of protein location in nucleus	2.55E-02	6.25
nose development	2.55E-02	6.25
neuron cell-cell adhesion	2.55E-02	6.25
protein localization to chromatin	2.86E-02	5.56
folic acid metabolic process	2.86E-02	5.56
positive regulation of p38MAPK cascade	2.86E-02	5.56
estrous cycle	2.86E-02	5.56
positive regulation of dendrite extension	2.86E-02	5.56
maternal behavior	3.18E-02	5.00
sensory perception of temperature stimulus	3.18E-02	5.00
regulation of mRNA 3'-end processing	3.33E-02	4.76
regulation of energy homeostasis	3.33E-02	4.76
positive regulation of potassium ion transmembrane transport	4.26E-02	3.70
stem cell development	4.46E-03	3.23
synaptic vesicle endocytosis	4.88E-02	3.23
calcium ion-regulated exocytosis of neurotransmitter	4.88E-02	3.23
nucleoside monophosphate biosynthetic process	1.17E-02	1.96
protein tetramerization	1.98E-02	1.48
learning	2.39E-02	1.34
adult behavior	2.75E-02	1.24
carboxylic acid biosynthetic process	1.63E-02	0.90
signal release	3.64E-02	0.66
inorganic ion transmembrane transport	3.85E-02	0.50

Table S8. Enriched KEGG pathways of first mRNA neighbors of NONHSAT035952.2.

GO-Term	P-Value	Enrichment score
Steroid biosynthesis	3.02E-02	5.00
One carbon pool by folate	6.67E-02	5.00
Glyoxylate and dicarboxylate metabolism	6.67E-02	3.57
mRNA surveillance pathway	8.08E-03	2.20

Table S9. LncRNAs, miRNAs and mRNAs in ceRNA networks of co-expressed modules.

Module 1			Module 2		
lncRNAs	miRNAs	mRNAs	lncRNAs	miRNAs	mRNAs
NONHSAT19 3031.1	hsa-miR-1273f	NUDT3	NONHSAT053 761.2	hsa-miR-3926	ADAMTS8
NONHSAT08 3203.2	hsa-miR-4708-5p	TRIM33	NONHSAT035 952.2	hsa-miR-7847-3p	COL4A3BP
NONHSAT02 5064.2	hsa-miR-6088	ZNF460		hsa-miR-3612	HMGCS1

hsa-miR-4770	SLC25A24	hsa-miR-650	METTL7A
hsa-miR-143-3p	TOMM22	hsa-miR-6880-5p	MSMO1
hsa-miR-548aw	SLC24A4	hsa-miR-345-5p	NRXN3
hsa-miR-527	VMA21		NTRK3
hsa-miR-518a-5p	CCDC36		RGS9BP
hsa-miR-5579-3p	GREB1		RNF125
hsa-miR-4275	TAF8		TIFA
hsa-miR-24-3p	SHISA2		TMEM254
hsa-miR-2467-5p	PTPN14		TRPM6
hsa-miR-4327	SCRG1		ZNF611
hsa-miR-3192-5p	DDX11		
hsa-miR-1273h-5p	ESCO2		
hsa-miR-149-3p	ZNF117		
hsa-miR-30b-3p	FAM208A		
hsa-miR-3689a-3p	BEST3		
hsa-miR-3689b-3p	TNXB		
hsa-miR-3689c	TRIM65		
hsa-miR-4728-5p	WFDC8		
hsa-miR-6779-5p	NGFR		
hsa-miR-6780a-5p	LSG1		
hsa-miR-6785-5p	SGCD		
hsa-miR-6799-5p	RNF213		
hsa-miR-6883-5p	TRUB1		
hsa-miR-7106-5p	DNAH3		
hsa-miR-5196-5p	TCAIM		
hsa-miR-4747-5p	TLE1		
hsa-miR-146a-5p			
hsa-miR-146b-5p			
hsa-miR-6758-3p			
hsa-miR-204-3p			
hsa-miR-4646-5p			
hsa-miR-1207-3p			
hsa-miR-1301-3p			
hsa-miR-4480			
hsa-miR-150-5p			
hsa-miR-4713-5p			
hsa-miR-942-5p			
hsa-miR-4738-3p			
hsa-miR-4641			
hsa-miR-3202			
hsa-miR-548g-3p			
hsa-miR-15a-3p			
hsa-miR-4790-3p			
hsa-miR-3166			

hsa-miR-1324
hsa-miR-6829-5p
hsa-miR-2116-3p

Figure legends

Figure S1. The global lncRNA-miRNA-mRNA triple network.

The global triple network was comprised of 19422 lncRNAs, 2599 miRNAs, and 15050 mRNAs, and there were 756280 edges in all. The blue concave quadrilateral represents lncRNA, the pink ellipse represents miRNA, and the green diamond represents mRNA.

Figure S1

