

Figure S1. KEGG pathways of the differentially expressed mRNAs. The abscissa displays the enrichment factor and the ordinate presents the pathway terms with the highest degree of enrichment (the 20 most enriched ones are selected for display). P<0.05 was considered to indicate a statistically significant difference. The colour indicates the P-value with red indicating the most significant enrichment. The size of the dots indicates the number of differentially expressed genes accumulated in the term. KEGG, Kyoto Encyclopedia of Genes and Genomes.

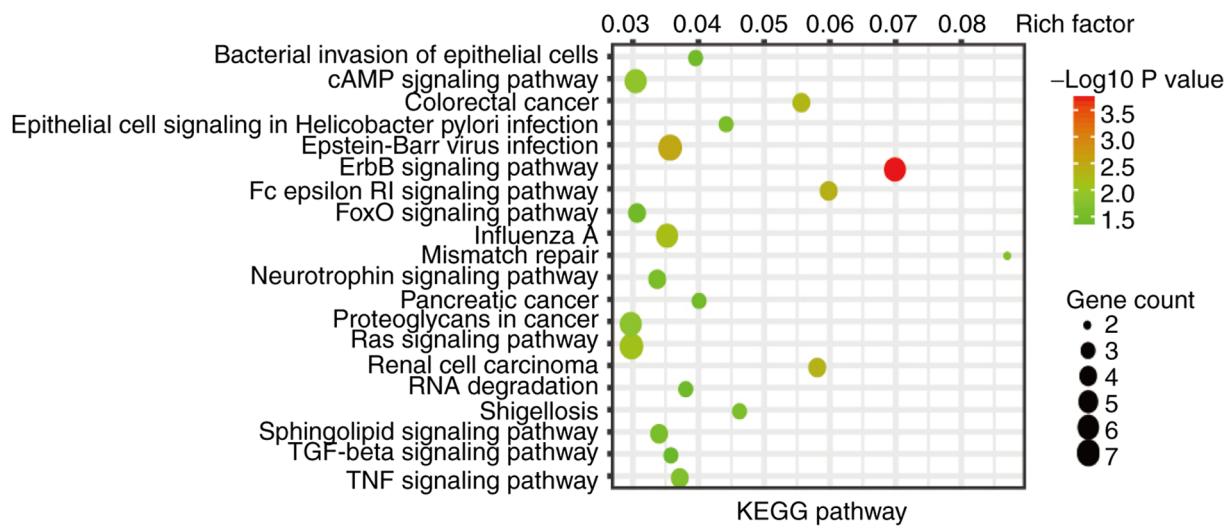


Figure S2. lncRNA-mRNA co-expression network. Construction of the lncRNA-mRNA co-expression network. Triangles represent lncRNAs and circles mRNAs. Red and blue represent up- and downregulated RNAs, respectively. The size of the triangles and circles represents the fold changes of the RNAs. lncRNA, long non-coding RNA.

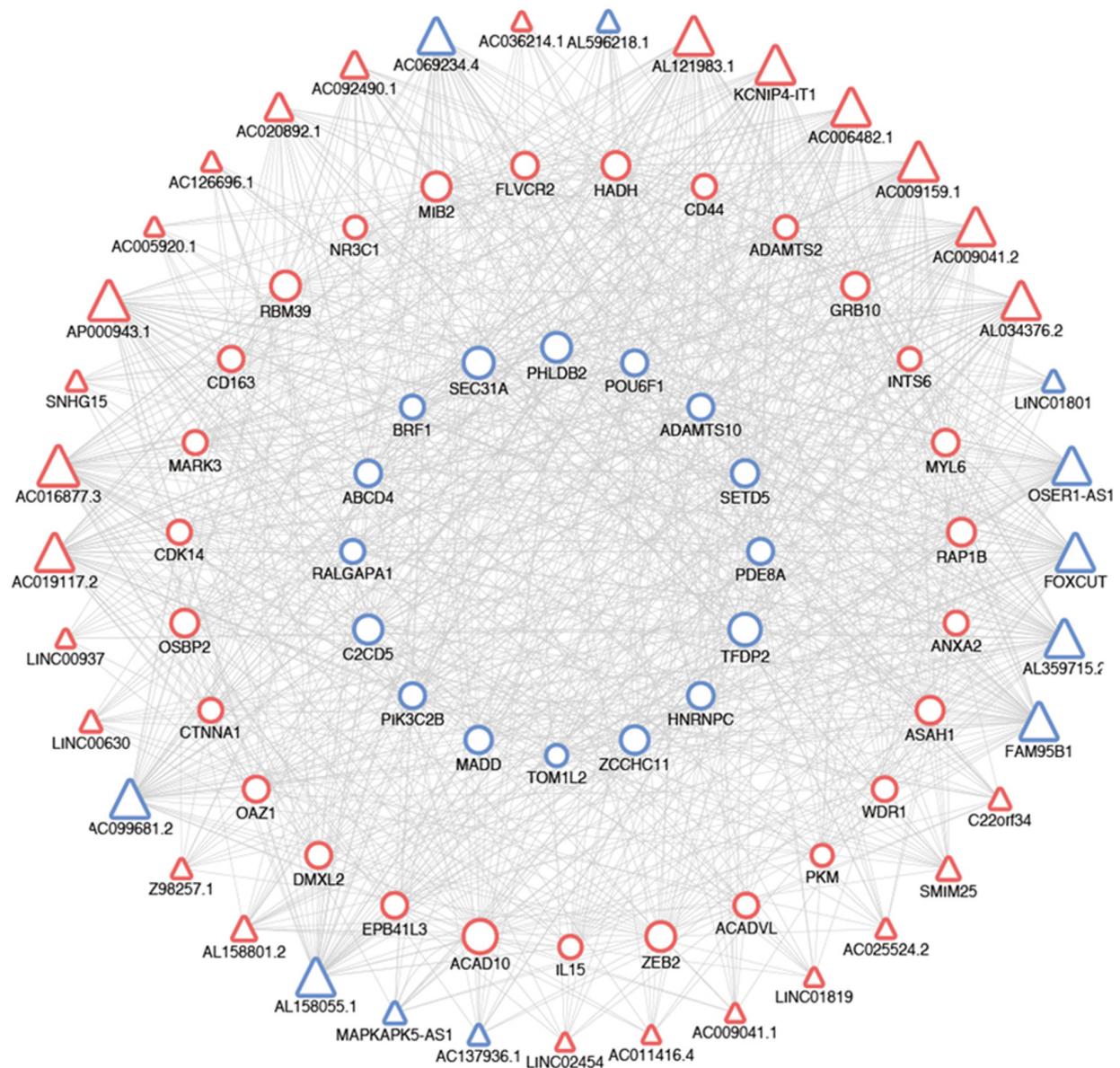


Table SI. Enriched Kyoto Encyclopedia of Genes and Genomes pathways of differentially expressed long non-coding RNAs.

Pathway ID	Pathway name	FDR
hsa04640	Hematopoietic cell lineage	0.0342
hsa04657	IL-17 signaling pathway	0.0040
hsa04658	Th1 and Th2 cell differentiation	0.0039
hsa04659	Th17 cell differentiation	0.0014
hsa04668	TNF signaling pathway	0.0337
hsa04672	Intestinal immune network for IgA production	0.0014
hsa04940	Type I diabetes mellitus	0.0143
hsa04978	Mineral absorption	0.0003
hsa05140	Leishmaniasis	0.0064
hsa05145	Toxoplasmosis	0.0143
hsa05166	HTLV-I infection	0.0040
hsa05168	Herpes simplex infection	0.0191
hsa05169	Epstein-Barr virus infection	0.0342
hsa05310	Asthma	0.0112
hsa05321	Inflammatory bowel disease	0.0003
hsa05332	Graft-versus-host disease	0.0004
hsa00051	Fructose and mannose metabolism	0.0007
hsa00190	Oxidative phosphorylation	0.0131
hsa00230	Purine metabolism	0.0410
hsa00240	Pyrimidine metabolism	0.0038
hsa00310	Lysine degradation	0.0140
hsa00510	N-Glycan biosynthesis	0.0370
hsa00514	Other types of O-glycan biosynthesis	0.0112
hsa00515	Mannose type O-glycan biosynthesis	0.0331
hsa00520	Amino sugar and nucleotide sugar metabolism	0.0037
hsa00562	Inositol phosphate metabolism	0.0112
hsa00730	Thiamine metabolism	0.0135
hsa00970	Aminoacyl-tRNA biosynthesis	0.0079
hsa01521	EGFR tyrosine kinase inhibitor resistance	0.0040
hsa01522	Endocrine resistance	0.0159
hsa01524	Platinum drug resistance	0.0258
hsa03013	RNA transport	0.0042
hsa03015	mRNA surveillance pathway	0.0286
hsa03018	RNA degradation	0.0159
hsa03040	Spliceosome	0.0001
hsa03050	Proteasome	0.0358
hsa03410	Base excision repair	0.0033
hsa03420	Nucleotide excision repair	0.0018
hsa03430	Mismatch repair	0.0331
hsa03440	Homologous recombination	0.0053
hsa03450	Non-homologous end-joining	0.0252
hsa03460	Fanconi anemia pathway	0.0331
hsa04010	MAPK signaling pathway	0.0125
hsa04012	ErbB signaling pathway	0.0191
hsa04064	NF-kappa B signaling pathway	0.0220
hsa04066	HIF-1 signaling pathway	0.0040
hsa04068	FoxO signaling pathway	0.0008
hsa04070	Phosphatidylinositol signaling system	0.0346
hsa04071	Sphingolipid signaling pathway	0.0001
hsa04072	Phospholipase D signaling pathway	0.0038
hsa04110	Cell cycle	0.0001
hsa04114	Oocyte meiosis	0.0217
hsa04115	p53 signaling pathway	0.0005
hsa04120	Ubiquitin mediated proteolysis	0.0001

Table SI. Continued.

Pathway ID	Pathway name	FDR
hsa04130	SNARE interactions in vesicular transport	0.0252
hsa04136	Autophagy - other eukaryotes	0.0358
hsa04137	Mitophagy - animal	0.0004
hsa04140	Autophagy - animal	0.0001
hsa04141	Protein processing in endoplasmic reticulum	0.0001
hsa04142	Lysosome	0.0008
hsa04144	Endocytosis	0.0000
hsa04145	Phagosome	0.0038
hsa04150	mTOR signaling pathway	0.0036
hsa04151	PI3K-Akt signaling pathway	0.0307
hsa04152	AMPK signaling pathway	0.0008
hsa04210	Apoptosis	0.0010
hsa04211	Longevity regulating pathway - mammal	0.0036
hsa04215	Apoptosis - multiple species	0.0305
hsa04216	Ferroptosis	0.0066
hsa04218	Cellular senescence	0.0000
hsa04360	Axon guidance	0.0344
hsa04370	VEGF signaling pathway	0.0009
hsa04371	Apelin signaling pathway	0.0038
hsa04380	Osteoclast differentiation	0.0000
hsa04510	Focal adhesion	0.0005
hsa04520	Adherens junction	0.0007
hsa04611	Platelet activation	0.0005
hsa04621	NOD-like receptor signaling pathway	0.0031
hsa04658	Th1 and Th2 cell differentiation	0.0327
hsa04659	Th17 cell differentiation	0.0003
hsa04660	T cell receptor signaling pathway	0.0048
hsa04662	B cell receptor signaling pathway	0.0008
hsa04664	Fc epsilon RI signaling pathway	0.0003
hsa04666	Fc gamma R-mediated phagocytosis	0.0007
hsa04668	TNF signaling pathway	0.0358
hsa04722	Neurotrophin signaling pathway	0.0005
hsa04730	Long-term depression	0.0451
hsa04810	Regulation of actin cytoskeleton	0.1030
hsa04910	Insulin signaling pathway	0.0095
hsa04914	Progesterone-mediated oocyte maturation	0.0159
hsa04915	Estrogen signaling pathway	0.0314
hsa04919	Thyroid hormone signaling pathway	0.0225
hsa04922	Glucagon signaling pathway	0.0473
hsa04926	Relaxin signaling pathway	0.0258
hsa04931	Insulin resistance	0.0409
hsa04932	Non-alcoholic fatty liver disease	0.0062
hsa04933	AGE-RAGE signaling pathway in diabetic complications	0.0280
hsa04962	Vasopressin-regulated water reabsorption	0.0079
hsa05010	Alzheimers disease	0.0056
hsa05012	Parkinsons disease	0.0112
hsa05016	Huntingtons disease	0.0004
hsa05100	Bacterial invasion of epithelial cells	0.0007
hsa05120	Epithelial cell signaling in <i>Helicobacter pylori</i> infection	0.0130
hsa05131	Shigellosis	0.0008
hsa05132	Salmonella infection	0.0008
hsa05133	Pertussis	0.0436
hsa05134	Legionellosis	0.0286
hsa05140	Leishmaniasis	0.0158

Table SI. Continued.

Pathway ID	Pathway name	FDR
hsa05142	Chagas disease (American trypanosomiasis)	0.0018
hsa05145	Toxoplasmosis	0.0014
hsa05152	Tuberculosis	0.0038
hsa05161	Hepatitis B	0.0007
hsa05165	Human papillomavirus infection	0.0008
hsa05166	HTLV-I infection	0.0001
hsa05167	Kaposi's sarcoma-associated herpesvirus infection	0.0008
hsa05168	Herpes simplex infection	0.0040
hsa05169	Epstein-Barr virus infection	0.0008
hsa05200	Pathways in cancer	0.0082
hsa05203	Viral carcinogenesis	0.0008
hsa05205	Proteoglycans in cancer	0.0056
hsa05210	Colorectal cancer	0.0013
hsa05211	Renal cell carcinoma	0.0005
hsa05212	Pancreatic cancer	0.0004
hsa05213	Endometrial cancer	0.0036
hsa05214	Glioma	0.0078
hsa05215	Prostate cancer	0.0008
hsa05219	Bladder cancer	0.0346
hsa05220	Chronic myeloid leukemia	0.0003
hsa05221	Acute myeloid leukemia	0.0039
hsa05222	Small cell lung cancer	0.0036
hsa05223	Non-small cell lung cancer	0.0017
hsa05230	Central carbon metabolism in cancer	0.0105
hsa05231	Choline metabolism in cancer	0.0090
hsa05416	Viral myocarditis	0.0451

Hsa, Homo sapiens; FDR, false discovery rate.