Figure S1. Construction of ceRNA network. Triangular green nodes denote miRNAs. Diamond-shaped red nodes indicate lncRNAs and oval blue nodes indicate mRNAs. ceRNA, competing endogenous RNA; miRNA/miR, microRNA; lnc, long non-coding RNA.



Table SI. Details o	of the Dg and Hg.
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Sample	Sex	Age, years	Usage
Dg 1	Male	70	Microarray
Dg 2	Female	49	Microarray
Dg 3	Male	50	Microarray
Hg 1	Male	62	Microarray
Hg 2	Female	35	Microarray
Hg 3	Female	40	Microarray
Dg 4	Female	81	RT-qPCR
Dg 5	Female	75	RT-qPCR
Dg 6	Male	68	RT-qPCR
Dg 7	Female	64	RT-qPCR
Dg 8	Male	61	RT-qPCR
Hg 4	Male	40	RT-qPCR
Hg 5	Male	48	RT-qPCR
Hg 6	Female	46	RT-qPCR
Hg 7	Female	49	RT-qPCR
Hg 8	Male	45	RT-qPCR
Dg 9	Male	60	RT-qPCR, Western blotting
Dg 10	Male	50	RT-qPCR, Western blotting
Dg 11	Female	49	RT-qPCR, Western blotting
Dg 12	Female	70	RT-qPCR, Western blotting
Dg 13	Male	64	RT-qPCR. Western blotting
Dg 14	Male	61	RT-qPCR, Western blotting
Dg 15	Male	50	RT-qPCR, Western blotting
Dg 16	Male	40	RT-qPCR, Western blotting
Dg 17	Male	81	RT-qPCR, Western blotting
Dg 18	Female	49	RT-qPCR, Western blotting
Dg 19	Female	43	RT-qPCR, Western blotting
Hg 9	Female	45	RT-qPCR. Western blotting
Hg 10	Female	40	RT-qPCR, Western blotting
Hg 11	Male	17	RT-qPCR, Western blotting
Hg 12	Male	36	RT-qPCR. Western blotting
Hg 13	Male	42	RT-qPCR. Western blotting
Hg 14	Female	35	RT-qPCR. Western blotting
Hg 15	Male	31	RT-qPCR. Western blotting
Hg 16	Female	42	RT-qPCR. Western blotting
Hg 17	Female	31	RT-qPCR. Western blotting
Hg 18	Female	45	RT-gPCR. Western blotting
Hg 19	Male	36	RT-gPCR. Western blotting
		20	iti qi citi, mesterii biotinig

Dg, degeneration group; Hg, healthy group; RT-qPCR, reverse transcription-quantitative PCR.

Table SII. Specific primer sequences for reverse transcription-quantiative PCR.

RNA	Forward primer $(5' \rightarrow 3')$	Reverse primer $(5' \rightarrow 3')$
miR-20a-5p	GCCCGCTAAAGTGCTTATAGTG	GCTGTCAACGATACGCTACGT
ITGB8	TGTGTTCAAGAGGATTTCATTTCAG	AGCCTTTGCTTATTAAATTGGAAAC
ENST00000548900	TACCAGCTGATGAAGGCATCT	CTTGTAAGCTCATCTGCCTCAG
lnc-MYBPC1-1:1	CGGGTTGCGAGTACACTTGA	TGTAATGCCAAACGCGAACG
Inc-ARL13A-1:1	TCAAGCCACTAGACCTAACTTCA	GGCAGGGTAGCACTGCTTTA
lnc-KANSL1L-1:1	CTGTAATCGCAGCACTTTGG	GGGTCTCACTTTGTTGCCTA
Inc-DNAJB6-3:1	TGGGTGGGAATTGGTATCTC	TCATTGCATTGCAGGGACT
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
β-actin	CTCCCTGGAGAAGAGCTACGAGC	CCAGGAAGGAAGGCTGGAAGAG
miR, microRNA; lnc, long no	on-coding RNA; ITGB8, integrin subunit β 8.	

Table SIII. Top 20 of GO biological process enrichment analysis for differentially expressed genes (P<0.05).

GO biological process	GO	Count	P-value
Regulation of multicellular organismal	GO:0051239	69	4.71x10 ⁻⁰⁷
process			
Ossification	GO:0001503	15	1.06x10 ⁻⁰⁶
Skeletal system development	GO:0001501	21	1.27x10 ⁻⁰⁶
Extracellular matrix organization	GO:0030198	17	1.43x10 ⁻⁰⁶
Extracellular structure organization	GO:0043062	17	1.48x10 ⁻⁰⁶
Regulation of multicellular organismal	GO:2000026	50	1.73x10 ⁻⁰⁶
development			
Animal organ development	GO:0048513	67	3.56x10 ⁻⁰⁶
System development	GO:0048731	85	3.71x10 ⁻⁰⁶
Anatomical structure morphogenesis	GO:0009653	50	5.51x10 ⁻⁰⁶
Skeletal system morphogenesis	GO:0048705	13	1.16x10 ⁻⁰⁵
Regulation of developmental process	GO:0050793	56	1.19x10 ⁻⁰⁵
Animal organ morphogenesis	GO:0009887	29	1.32×10^{-05}
Multicellular organism development	GO:0007275	91	1.45x10 ⁻⁰⁵
Bone morphogenesis	GO:0060349	9	1.69x10 ⁻⁰⁵
Tube development	GO:0035295	26	1.79x10 ⁻⁰⁵
Multicellular organismal process	GO:0032501	115	3.75x10 ⁻⁰⁵
Collagen fibril organization	GO:0030199	6	4.11x10 ⁻⁰⁵
Bone development	GO:0060348	11	5.30x10 ⁻⁰⁵
Nucleic acid metabolic process	GO:0090304	9	5.33x10 ⁻⁰⁵
Mesenchyme development	GO:0060485	11	8.63x10 ⁻⁰⁵
GO, Gene Ontology			

GO, Gene Ontology.

Table SIV. Top 20 of GO molecular function enrichment analysis for differentially expressed genes (P<0.05).

GO molecular function	GO	Count	P-value
Glycosaminoglycan binding	GO:0005539	16	5.21x10 ⁻⁰⁸
Hemoglobin binding	GO:0030492	5	4.06x10 ⁻⁰⁷
Extracellular matrix structural constituent	GO:0005201	11	8.27x10 ⁻⁰⁶
Heparin binding	GO:0008201	11	1.26x10 ⁻⁰⁵
Sulfur compound binding	GO:1901681	12	8.52x10 ⁻⁰⁵
Serine-type endopeptidase activity	GO:0004252	9	3.26x10 ⁻⁰⁴
Signaling receptor binding	GO:0005102	36	6.44x10 ⁻⁰⁴
Serine-type peptidase activity	GO:0008236	9	7.44x10 ⁻⁰⁴
Organic cyclic compound binding	GO:0097159	50	7.87x10 ⁻⁰⁴
Hydrolase activity, acting on acid	GO:0016825	9	8.83x10 ⁻⁰⁴
phosphorus-nitrogen bonds			
Serine hydrolase activity	GO:0017171	9	8.83x10 ⁻⁰⁴
Growth factor activity	GO:0008083	8	1.04x10 ⁻⁰³
Receptor ligand activity	GO:0048018	15	1.05x10 ⁻⁰³
Structural molecule activity	GO:0005198	19	1.11x10 ⁻⁰³
Signaling receptor activator activity	GO:0030546	15	1.17×10^{-03}
Heterocyclic compound binding	GO:1901363	50	1.25x10 ⁻⁰³
Endopeptidase activity	GO:0004175	14	1.46x10 ⁻⁰³
Chloride transmembrane transporter activity	GO:0015108	6	1.63x10 ⁻⁰³
Metalloendopeptidase activity	GO:0004222	6	1.88x10 ⁻⁰³
Integrin binding	GO:0005178	7	1.93x10 ⁻⁰³

GO, Gene Ontology.

Table SV. Top 20 of GO cellular component enrichment analysis for differentially expressed genes (P<0.05).

GO cellular component	GO	Count	P-value
Extracellular region	GO:0005576	105	1.15x10 ⁻¹³
Extracellular space	GO:0005615	78	3.78x10 ⁻⁰⁹
Specific granule lumen	GO:0035580	10	$1.28 \mathrm{x} 10^{-08}$
Extracellular matrix	GO:0031012	25	$1.53 \mathrm{x} 10^{-08}$
Collagen-containing	GO:0062023	21	4.96x10 ⁻⁰⁸
extracellular matrix			
Specific granule	GO:0042581	12	$1.04 \mathrm{x} 10^{-06}$
Nucleus	GO:0005634	60	6.35x10 ⁻⁰⁵
Phagocytic vesicle lumen	GO:0097013	3	8.81x10 ⁻⁰⁵
Secretory vesicle	GO:0099503	27	1.63x10 ⁻⁰⁴
Endocytic vesicle lumen	GO:0071682	4	$1.70 \mathrm{x} 10^{-04}$
Secretory granule lumen	GO:0034774	13	1.83x10 ⁻⁰⁴
Cytoplasmic vesicle lumen	GO:0060205	13	2.05x10 ⁻⁰⁴
Vesicle lumen	GO:0031983	13	2.18x10 ⁻⁰⁴
Endocytic vesicle	GO:0030139	13	2.30x10 ⁻⁰⁴
Cellular anatomical entity	GO:0110165	240	2.49x10 ⁻⁰⁴
Extracellular exosome	GO:0070062	44	2.93x10 ⁻⁰⁴
Phagocytic vesicle	GO:0045335	8	3.12x10 ⁻⁰⁴
Secretory granule	GO:0030141	23	3.25x10 ⁻⁰⁴
Extracellular vesicle	GO:1903561	44	3.28x10 ⁻⁰⁴
Extracellular organelle	GO:0043230	44	3.38x10 ⁻⁰⁴

GO, Gene Ontolgy.

ID	Description	P-value	Count	GeneID
hsa05150	Staphylococcus aureus infection	0.00061	6	HLA-DRB5, DEFA4, HLA-DQB1, C4B, C4A, KRT17
hsa04151	PI3K-Akt signaling pathway	0.005105	10	KITLG, FGF18, THBS3, FGF7, ITGA11,
				GNG2, ITGB8, FGF9, CSH1, GH1
hsa05226	Gastric cancer	0.005705	6	FGF18, FGF7, FZD7, FGF9, JUP, FZD1
hsa05221	Acute myeloid leukemia	0.006083	4	CCNA1, CEBPE, MPO, JUP
hsa05133	Pertussis	0.009454	4	C4BPA, C4B, C4A, C4BPB
hsa04080	Neuroactive ligand-receptor	0.011739	9	TRH, GABRD, EDN2, S1PR1, GABRP, TBXA2R, CSH1,
	interaction			GH1, INSL3
hsa04610	Complement and coagulation cascades	0.013857	4	C4BPA, C4B, C4A, C4BPB
hsa05322	Systemic lupus erythematosus	0.015075	5	HLA-DRB5, HLA-DQB1, C4B, C4A, ELANE
hsa04512	Ectracellular matix-receptor	0.015571	4	DMP1, THBS3, ITGA11, ITGB8
	interaction			
hsa05202	Transcriptional misregulation in	0.016012	6	CCNA1, CEBPE, MPO, ELANE, COMMD3-BMI1, JUP
has04727	cancer	0.01617	4	ADCV1 CARDD CNC2 CARDD
118a04727	Mamphine addiction	0.01017	4	ADCV1 CARRD, CNC2, CARRP
hss03052	Protoin digastion and absorption	0.017413	4	ADC 11, GADKD, GNG2, GADKP COL5A1, SLC7A8, COL2A1, COL5A2
nsa04974	Call adhasis restantia	0.020073	4	ULJAI, SLU/Að, CULJAI, CULJAZ
nsa04514	Cell adhesion molecules	0.022259) 5	HLA-DKBJ, HLA-DQBI, VCAN, HGB8, PIPKF
nsa03224	Breast cancer	0.022239	3	FUF18, FUF7, FZD7, FUF9, FZD1
nsa04916	Melanogenesis	0.024513	4	ADUYI, KIILG, FZD7, FZD1
nsa04145	Phagosome	0.025285	2	HLA-DKB5, HLA-DQB1, THB55, MPO, COLEC12
nsa04015	Kapi signaling pathway	0.027243	6	ADUY1, KIILU, FUF18, FUF7, EVL, FUF9
hsa04725	Cholinergic synapse	0.034091	4	ADUY1, GNG2, KUNJ12, KUNQ5
hsa04014	Ras signaling pathway	0.041318	6	PLA2G2A, KITLG, FGF18, FGF7, GNG2, FGF9

Table SVI. Top 20 of Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis for differentially expressed genes (P<0.05).

Table SVII. Top 20 of GO biological process enrichment analysis for differentially expressed genes in competing endogenous RNA network (P<0.05).

GO biological process	GO	Count	P-value
Animal organ morphogenesis	GO:0009887	16	6.11x10 ⁻⁰⁹
Anatomical structure morphogenesis	GO:0009653	22	2.59x10 ⁻⁰⁸
Extracellular matrix organization	GO:0030198	10	3.84x10 ⁻⁰⁸
Extracellular structure organization	GO:0043062	10	3.95x10 ⁻⁰⁸
Ossification	GO:0001503	9	4.89x10 ⁻⁰⁸
System development	GO:0048731	31	6.46x10 ⁻⁰⁸
Osteoblast differentiation	GO:0001649	7	7.48x10 ⁻⁰⁸
Multicellular organism development	GO:0007275	33	8.21x10 ⁻⁰⁸
Blood vessel development	GO:0001568	11	1.12×10^{-07}
Skeletal system development	GO:0001501	11	1.36x10 ⁻⁰⁷
Regulation of developmental process	GO:0050793	23	1.48x10 ⁻⁰⁷
Vasculature development	GO:0001944	11	1.71x10 ⁻⁰⁷
Blood vessel morphogenesis	GO:0048514	10	2.04x10 ⁻⁰⁷
Cardiovascular system development	GO:0072358	11	2.07x10 ⁻⁰⁷
Tube morphogenesis	GO:0035239	12	2.32x10 ⁻⁰⁷
Negative regulation of developmental process	GO:0051093	14	2.63x10 ⁻⁰⁷
Regulation of multicellular organismal development	GO:2000026	20	2.96x10 ⁻⁰⁷
Negative regulation of cell differentiation	GO:0045596	12	5.06x10 ⁻⁰⁷
tube development	GO:0035295	13	5.13x10 ⁻⁰⁷
Anatomical structure development	GO:0048856	33	5.75x10 ⁻⁰⁷
CO. Cana Ontalagy			

GO, Gene Ontology.

Table SVIII. Top 20 of GO molecular function enrichment analysis for differentially expressed genes in competing endogenous RNA network (P<0.05).

GO molecular function	GO	Count	P-value
Glycosaminoglycan binding	GO:0005539	8	3.17x10 ⁻⁰⁷
Extracellular matrix structural constituent	GO:0030492	6	7.50x10 ⁻⁰⁶
Heparin binding	GO:0005201	6	9.74x10 ⁻⁰⁶
Integrin binding	GO:0008201	5	5.10x10 ⁻⁰⁵
Sulfur compound binding	GO:1901681	6	8.08x10 ⁻⁰⁵
Extracellular matrix structural constituent conferring tensile strength	GO:0004252	3	2.42x10 ⁻⁰⁴
Cell adhesion molecule binding	GO:0005102	7	4.63x10 ⁻⁰⁴
Platelet-derived growth factor binding	GO:0008236	2	6.64x10 ⁻⁰⁴
Growth factor binding	GO:0097159	4	6.86x10 ⁻⁰⁴
Binding	GO:0016825	53	9.13x10 ⁻⁰⁴
SMAD binding	GO:0017171	3	1.35x10 ⁻⁰³
Wnt-activated receptor activity	GO:0008083	2	1.37x10 ⁻⁰³
Molecular_function	GO:0048018	57	1.50x10 ⁻⁰³
	GO:0005198		
Signaling receptor binding	GO:0030546	12	1.88x10 ⁻⁰³
Protein binding	GO:1901363	45	2.00x10 ⁻⁰³
Fibronectin binding	GO:0004175	2	3.09x10 ⁻⁰³
Structural molecule activity	GO:0015108	7	3.15x10 ⁻⁰³
Protein-containing complex binding	GO:0004222	9	4.17x10 ⁻⁰³
Wnt-protein binding	GO:0005178	2	4.42×10^{-03}
GO, Gene Ontology.			

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Table SIX. Top 20 of GO cellular component enrichment analysis for differentially expressed genes in competing endogenous RNA network (P<0.05).

GO cellular component	GO	Count	P-value
Extracellular matrix	GO:0031012	10	1.95x10 ⁻⁰⁶
Fibrillar collagen trimer	GO:0005583	3	8.54x10 ⁻⁰⁶
Banded collagen fibril	GO:0098643	3	8.54x10 ⁻⁰⁶
Collagen-containing extracellular	GO:0062023	8	1.65x10 ⁻⁰⁵
matrix			
Extracellular region	GO:0005576	26	3.03x10 ⁻⁰⁵
Complex of collagen trimers	GO:0098644	3	3.73x10 ⁻⁰⁵
Collagen type V trimer	GO:0005588	2	7.26x10 ⁻⁰⁵
Integrin complex	GO:0008305	3	1.18x10 ⁻⁰⁴
Collagen trimer	GO:0005581	4	1.26x10 ⁻⁰⁴
Extracellular space	GO:0005615	21	1.65x10 ⁻⁰⁴
Basement membrane	GO:0005604	4	1.73x10 ⁻⁰⁴
Protein complex involved in cell	GO:0098636	3	1.77x10 ⁻⁰⁴
adhesion			
Endoplasmic reticulum lumen	GO:0005788	6	2.19x10 ⁻⁰⁴
Interstitial matrix	GO:0005614	2	6.51x10 ⁻⁰⁴
Integral component of membrane	GO:0016021	28	8.94x10 ⁻⁰⁴
Focal adhesion	GO:0005925	6	9.57x10 ⁻⁰⁴
Cell-substrate junction	GO:0030055	6	1.04x10 ⁻⁰³
Intrinsic component of membrane	GO:0031224	28	1.05x10 ⁻⁰³
Plasma membrane	GO:0005886	27	1.59x10 ⁻⁰³
Cell periphery	GO:0071944	27	2.78x10 ⁻⁰³
GO, Gene Ontology.			