

Table SI. Results of RNA purity and quality testing.

No.	Sample name	Sample type	Concentration c (ng/ μ l)	28S/18S	RIN	Database consolidated
1	HP	RNA	214	1.7	9.3	RNA-Seq
2	HB	RNA	1200	1.8	9.5	RNA-Seq

Table SII. Alignment statistics of tags align to reference genome.

Sample name	Raw read count	Clean read count	Percentage (%)
HB	19,443,590	17,630,686	90.68
HP	22,807,548	21,772,519	95.46

Table SIII. Summary of sequencing data for each sample.

Sample name	Total read	Mapped read	Percentage (%)
HB	17,630,686	16,836,644	95.50
HP	21,772,519	20,907,542	96.03

Table SIV. Transcriptional regulation analysis results (1).

Predicted activation state	Upstream regulator
Inhibited	EPAS1, HIF1A, TGFB1, SMARCA4, VEGFA, TRAP1, PPARG, JUN, IGF1, TGFB2, TNF, NEDD9, CSF1, BMP7, CUL4B, FOXO1, TREM1, BCL, L1, OSM, YBX1, IL6, AR, NUPR1, SOCS1, SYVN1, IL2, POU2F2, F7, ECSIT, CXCL8, P38, MAPK, SELPLG, PRKCD, IGFBP2, PDGF, BB, ERK1/2, GLI1, CCL5, ERG, ERK, IL5, CD40, NFκB (complex), TGM2, CSF2, IFNG
Activated	SPDEF, NEUROG1, HOXD10, COL18A1, UPF2, PRNP, EGLN, miR-34a-5p (and other miRNAs w/seed GGCAGUG), let-7, MGEA5, RABL6, miR-146a-5p (and other miRNAs w/seed GAGAACU) , EFNA1

Table SV. Transcriptional regulation analysis (2).

Upstream regulator	Molecule type	Predicted activation state	Activation z-score	P-value of overlap	Target molecules in dataset
TGFB1	Growth factor	Inhibited	-4.495	0.0000209	AKR1C1/AKR1C2, ANGPTL4, ASPN, BAX, BHLHE40, BMP7, CCL5, CDH1, CDK4, CDKN3, CELSR2, CKS1B, CKS2, CLEC2D, COL6A3, COL7A1, FBN1, FN1, FSTL3, HAS2, IGFBP3, IGFBP5, ITGA1, ITGA2, ITGA3, ITGA5, ITGB2, ITGB3, KDR, KRT7, LAMC2, MAPK8IP3, NRP1, PDGFA, PDGFB, PIK3CD, PLAUR, PLOD2, POLE2, PRSS3, PTGS2, PTHLH, RHOD, SCD, SKI, SMAD7, TNC, VCAN, VEGFA
TNF	Cytokine	Inhibited	-3.674	0.0196	ADORA2A, APLN, BHLHE40, C10orf10, C3, CCL5, CDH1, CFD, CFLAR, DSC3, ETS1, F3, FGG, FN1, G0S2, GNB4, GSTA1, H19, HCAR3, HIVEP1, HSPG2, ICAM1, IDO1, IGF2, ITGA5, ITGB3, JARID2, LAMA3, LAMB3, LAMC2, MUC1, NPM3, NR4A2, OASL, OSMR, PIK3CD, PLAUR, PLOD2, PRDM1, PSME2, PTGES, PTGS1, PTGS2, RFTN1, RPS13, SERPINB9, TNC, TNFRSF6B, VEGFA, WISP1
SPDEF	Transcription regulator	Activated	3.162	0.00202	COL4A5, COL5A2, COL6A1, COL6A2, COL6A3, ITGA3, ITGA5, LAMB2, LAMC1, PLAUR, PTPRF, TNC

Table SVI. Comparisons of RNA-Seq and RT-qPCR results among 20 miRNAs.

miRNA ID	\log_2 ratio (HP/HB) for RNA-Seq	Fold chang (HB/HP) for validation	Upregulated or downregulated (HP/HB)
hsa-let-7a-5p	2.94	1.82	Up
hsa-let-7c-3p	2.23	2.16	Up
hsa-miR-30c-5p	4.59	4.92	Up
hsa-miR-7-1-3p	4.42	4.84	Up
hsa-miR-340-5p	2.97	1.22	Up
hsa-miR-186-5p	2.40	1.68	Up
hsa-miR-21-3p	2.31	1.05	Up
hsa-miR-146b-3p	2.01	1.31	Up
hsa-miR-26a-2-3p	-4.77	-3.34	Down
hsa-miR-423-5p	-4.36	-4.16	Down
hsa-miR-7-5p	-3.88	-1.31	Down
hsa-miR-423-3p	-3.46	-3.60	Down
hsa-miR-191-5p	-2.87	-1.85	Down
hsa-miR-744-5p	-2.81	-2.76	Down
hsa-miR-193a-3p	-2.80	-5.48	Down
hsa-miR-24-3p	-2.59	-5.89	Down
hsa-miR-3529-3p	-2.38	-0.88	Down
hsa-miR-574-5p	-2.32	-1.83	Down
hsa-miR-30c-1-3p	-3.29	-1.74	Down
hsa-let-7f-2-3p	-2.42	-1.52	Down

Table SVII. Comparisons of RNA-Seq and RT-qPCR results among five circRNAs.

circRNA ID	\log_2 ratio (HP/HB) for RNA-Seq	Fold change (HB/HP) for validation	Upregulated or downregulated (HP/HB)
hsa_circ_0059580	-8.495148327	-1.69648	Down
hsa_circ_0067475	-71.71850248	-2.53029	Down
hsa_circ_0007429	-16.8485504	-1.28775	Down
hsa_circ_0002029	11.44313128	1.883067	Up
hsa_circ_0002100	10.96959281	2.201615	Up