ACCSCIENCE PUBLISHING

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ORIGINAL RESEARCH ARTICLE

Identifying the roles of hub gene in keloid formation using single-cell transcriptomics

Supplementary Files

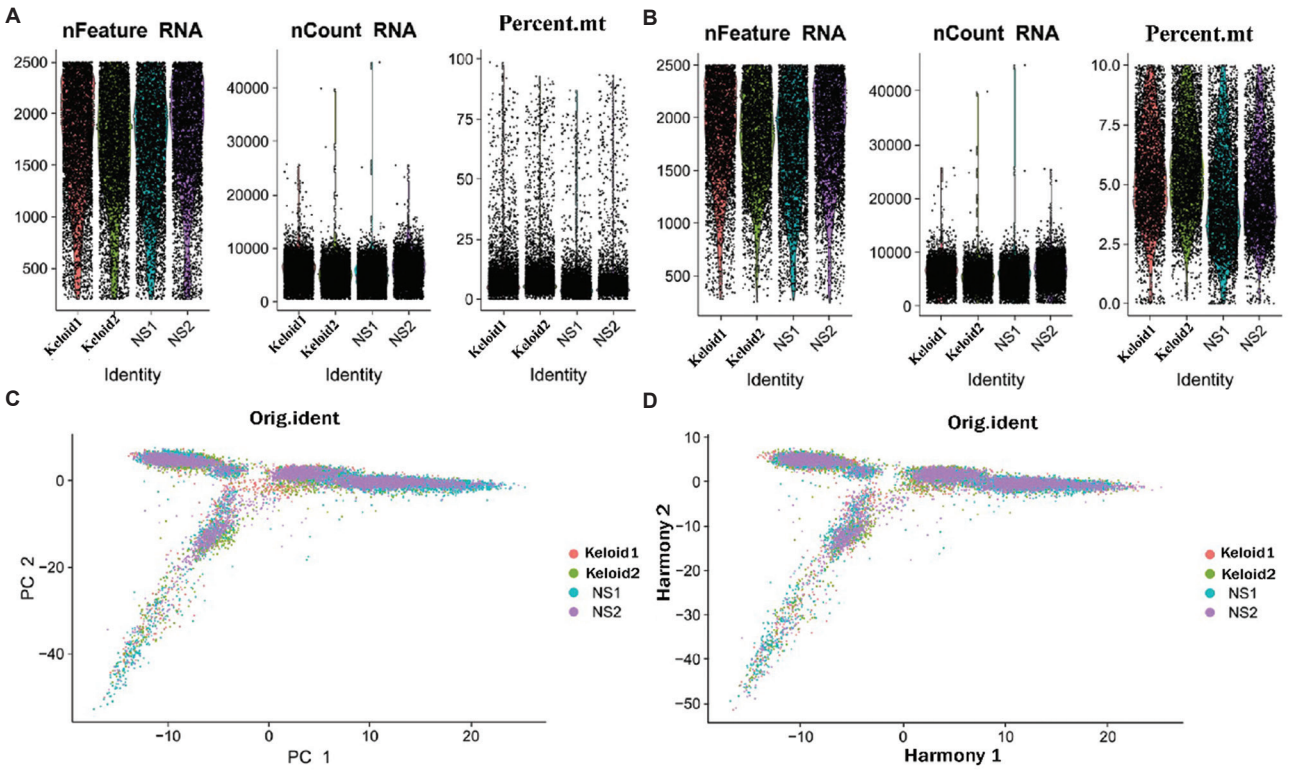

Figure S1. Quality control and batch effect correction of transcriptomic data. (A) Scatter plot of GSE163973 before quality control; (B) scatter plot of GSE163973 after quality control; (C) principal component analysis of GSE163973; and (D) scatter plot of GSE163973 following batch effect removal
Abbreviations: NS: Normal skin; PC: Principal component

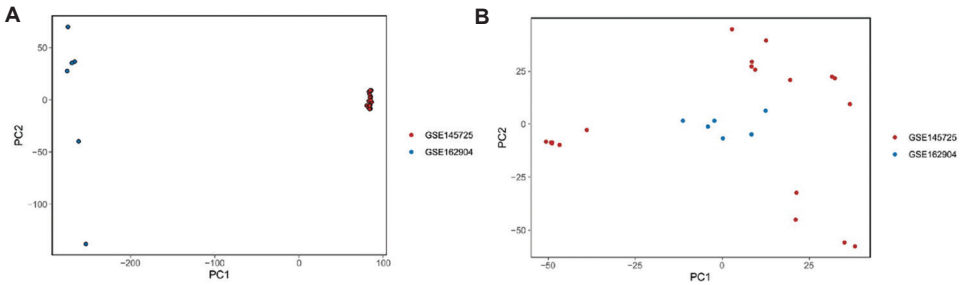

Figure S2. Batch effect correction and principal component analysis of multi-omics data. (A) Scatter plot of GSE145725 and GSE162904 before effect removal; and (B) scatterplot of GSE145725 and GSE162904 following batch effect removal
Abbreviation: PC: Principal component

Table S1. Hub genes for key fibroblast subpopulations

EFEMP2	FTL	FBN1	NUCB1	GSTP1	TMSB10	PLAC9	FCGRT	GRN	SSR4
CTSK	PRDX4	RCN3	GPX3	IGFBP4	CTSD	SERPINF1	FTH1	P4HB	PPIB
SERF2	CD63	WISP2	RPL5	RPL18	RPL29	SSFA2	RPL12	RPS8	RPL30
RPL19	NUMB	MGST3	RPS23	RPS14	RPL18A	RAPGEF2	RPS12	RPL11	RPL10A
RPL41	RPS2	RPL7A	ADM	RPS18	GUK1	CPXM1	TSPAN13	ANTXR1	PERP
PLXDC2	BGN	HMCN2	SULF2	TPM4	MMP23B	COL6A2	FAP	ADAM12	COMP
C12ORF75	HTRA1	ARL4C	NREP	HMCN1	ASPN	FNDC1	LRRC15	ELN	SMOC2
PLA2G2A	RPL32	VPS28	EDIL3	THBS4					

Table S2. Eight hub genes of the keloid formation gene signature

Gene	Coefficient	95% confidence interval	*p*-value
Intercept	−91.23656757		
GUK1	1.660697015	0.66 – 2.66	0.05
BGN	1.465902028	0.87 – 2.06	0.01
MGST3	0.801550282	0.40 – 1.20	0.03
ADM	1.229477648	0.43 – 2.03	0.05
RAPGEF2	−0.629911361	−1.03 – −0.23	0.02
VPS28	3.713383386	2.51 – 4.91	0.02
NUMB	2.387227582	1.00 – 3.77	0.05
SSFA2	−0.115439332	−0.32 – 0.09	0.01