

**Supplementary Table 1** The primers of five specific genes and reference gene

CircRNAs	primers	length (bp)
hsa_circRNA_000957	F:5'CTGGATCAGCTAGACTGGATAGT 3' R:5'CCAAACCATAAAGCACAATGTT 3'	133
hsa_circRNA_402437	F:5'CTGGATCAGCTAGACTGGATAGT 3' R:5'CCAAACCATAAAGCACAATGTT 3'	182
hsa_circRNA_091420	F:5'TTATGAACACGTTGGTTGGCTG3' R:5'GGAGAAAGGAAGAGGGAGGGAG3'	88
hsa_circRNA_101798	F:5' GACTTCTCATTCATTCCCG 3' R:5' CACTCCACTTCATGCAGCTGG 3'	96
hsa_circRNA_403250	F:5' CCCTTGATTGAAATCAGCT 3' R:5' ATTGTCACCTTCCAAAACCTT 3'	96
β-actin	F:5' GTGGCCGAGGACTTTGATTG3' R:5' CCTGTAACAACGCATCTCATATT3'	73

**Supplementary Table 2** Microarray analysis of differentially expressed circRNAs in lesional skins of patients with vitiligo compared with healthy skin tissues

CircRNAs	Alias	Source	Regulation	P-value	FC
hsa_circRNA_021714	hsa_circ_0021714	circBase	up	0.03712984	4.1985018
hsa_circRNA_406821		25070500	up	0.046288172	4.1444143
hsa_circRNA_000320	hsa_circ_0000320	circBase	up	0.015848002	4.0351738
hsa_circRNA_404643		25070500	up	0.046711582	3.6513868
hsa_circRNA_104853	hsa_circ_0087861	circBase	up	0.039935583	3.5843878
hsa_circRNA_104852	hsa_circ_0006174	circBase	up	0.03736246	3.2505596
hsa_circRNA_104052	hsa_circ_0008285	circBase	up	0.045260345	2.9990355
hsa_circRNA_102762	hsa_circ_0001030	circBase	up	0.014262897	2.873578
hsa_circRNA_024600	hsa_circ_0024600	circBase	up	0.036434078	2.5701027
hsa_circRNA_101319	hsa_circ_0000524	circBase	up	0.03456983	2.5321638
hsa_circRNA_001795	hsa_circ_0001795	circBase	down	0.042259686	2.4232286
hsa_circRNA_104745	hsa_circ_0005572	circBase	down	0.008380619	2.3879448
hsa_circRNA_067327	hsa_circ_0067327	circBase	down	0.047460972	2.3489956
hsa_circRNA_091420	hsa_circ_0091420	circBase	down	0.027142665	2.1288496
hsa_circRNA_102009	hsa_circ_0042498	circBase	down	0.012632069	2.1119620
hsa_circRNA_404971		25070500	down	0.00028042	2.0930852
hsa_circRNA_405629		25070500	down	5.67309E-05	2.0620139
hsa_circRNA_104974	hsa_circ_0002818	circBase	down	0.000294079	2.0290276
hsa_circRNA_400732		25242744	down	0.011282129	2.0251817
hsa_circRNA_001741	hsa_circ_0001286	circBase	down	0.025836371	1.9358107

Notes: "up" and "down" indicate the upregulated and downregulated circRNAs.

**Supplementary Table 3** Microarray analysis of differentially expressed circRNAs in nonlesional skins of patients with vitiligo compared with healthy skin tissues

CircRNAs	Alias	Source	Regulation	P-value	FC
hsa_circRNA_034642	hsa_circ_0034642	circBase	up	0.037375607	3.2988179
hsa_circRNA_406821		25070500	up	0.037835632	3.0647001
hsa_circRNA_007507	hsa_circ_0007507	circBase	up	0.021286277	2.9470356
hsa_circRNA_006349	hsa_circ_0006349	circBase	up	0.024953348	2.6267721
hsa_circRNA_407249		25070500	up	0.023815484	2.6051557
hsa_circRNA_104193	hsa_circ_0077930	circBase	up	0.038686085	2.4941544
hsa_circRNA_100239	hsa_circ_0012673	circBase	up	0.043052412	2.3047306
hsa_circRNA_406325		25070500	up	0.007347538	2.2945010
hsa_circRNA_031968	hsa_circ_0031968	circBase	up	0.047928631	2.2828710
hsa_circRNA_101128	hsa_circ_0000437	circBase	up	0.044469492	2.2713816
hsa_circRNA_091420	hsa_circ_0091420	circBase	down	0.02544576	2.2719836
hsa_circRNA_103546	hsa_circ_0006517	circBase	down	0.008571479	2.0490085
hsa_circRNA_402437		25242744	down	0.028511703	2.0314534
hsa_circRNA_405629		25070500	down	0.003561857	1.9728884
hsa_circRNA_006668	hsa_circ_0006668	circBase	down	0.03686326	1.9708273
hsa_circRNA_103903	hsa_circ_0008517	circBase	down	0.037914034	1.9576399
hsa_circRNA_102009	hsa_circ_0042498	circBase	down	0.020271167	1.9229992
hsa_circRNA_404905		25070500	down	0.043869591	1.8755044
hsa_circRNA_001226	hsa_circ_0001226	circBase	down	0.009172512	1.8733108
hsa_circRNA_083913	hsa_circ_0083913	circBase	down	0.019582053	1.8672073

Notes: "up" and "down" indicate the upregulated and downregulated circRNAs.

**Supplementary Table 4 Microarray analysis of differentially expressed circRNAs in lesional skins compared with nonlesional skins of patients with vitiligo**

CircRNAs	Alias	Source	Regulation	P-value	FC
hsa_circRNA_101604	hsa_circ_0000638	circBase	up	0.004894636	1.8246798
hsa_circRNA_103649	hsa_circ_0001414	circBase	up	0.017846321	1.7289010
hsa_circRNA_407302		25070500	up	0.012914132	1.6755376
hsa_circRNA_102859	hsa_circ_0007967	circBase	up	0.046753252	1.5888567
hsa_circRNA_102060	hsa_circ_0007539	circBase	up	0.023918784	1.5778724
hsa_circRNA_000458	hsa_circ_0000458	circBase	up	0.001735708	1.5694358
hsa_circRNA_101633	hsa_circ_0036629	circBase	up	0.016185331	1.5085626
hsa_circRNA_084861	hsa_circ_0084861	circBase	up	0.028376683	1.5017946
hsa_circRNA_402705		25242744	up	0.016572806	1.4996013
hsa_circRNA_104570	hsa_circ_0004219	circBase	up	0.019948587	1.4940891
hsa_circRNA_000964	hsa_circ_0001653	circBase	down	0.023874165	1.522513
hsa_circRNA_407081		25070500	down	0.031216789	1.4299775
hsa_circRNA_404336		25242744	down	0.014559995	1.3917289
hsa_circRNA_029409	hsa_circ_0029409	circBase	down	0.043008286	1.3202556
hsa_circRNA_047478	hsa_circ_0047478	circBase	down	0.04849399	1.3152305
hsa_circRNA_402353		25242744	down	0.044108607	1.3122114
hsa_circRNA_404689		25070500	down	0.013101564	1.3101354
hsa_circRNA_086760	hsa_circ_0086760	circBase	down	0.040914429	1.2526927
hsa_circRNA_071095	hsa_circ_0071095	circBase	down	0.030447615	1.252526
hsa_circRNA_404517		25070500	down	0.015667077	1.2375248

Notes: "up" and "down" indicate the upregulated and downregulated circRNAs.







**Supplementary Table 6** KEGG pathway analysis of the target mRNAs

#Column "PathwayID" stands for Pathway identifiers used in KEGG  
 #Column "Definition" stands for the definition of the PathwayID  
 #Column "SelectionCounts" stands for the count of the DE genes' entities directly associated with the listed PathwayID  
 #Column "SelectionSize" stands for the count of the DE genes' entities  
 #Column "GeneRatio" stands for the count of chosen background population genes' entities associated with the listed PathwayID  
 #Column "Size" stands for the total number of chosen background population genes' entities  
 #Column "FDR" stands for the false discovery rate of the PathwayID  
 #Column "Enrichment Score" stands for the Enrichment Score value of the PathwayID, it equals " $\log_{10}(\text{Pvalue})$ "  
 #Column "GeneRatio" stands for the Gene Ratio value of the PathwayID, it equals " $\text{SelectionCounts}/\text{SelectionSize}$ "

PathwayID	Definition	Organism	Website	Fisher_PValue	SelectionCounts	SelectionSize	Count	Size	FDR	Enrichment_Score	GeneRatio	Gene
hsa00060	Schiff-aldehyde metabolism - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa00060-19221+9514+5e29+5648	0.000778937	4	54	47	7906	0.0916483	1.554484	0.070704		
hsa00065	Ether lipid metabolism - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa00065-9114+9881+100137049	0.003950331	3	54	47	7906	0.097052	2.403967	0.05556	GALST1 IMD7 PLA2G4B PLA2G4B	
hsa01730	VIFIP1 coupling software - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa01730-9881+100137049+5648	0.007477056	3	54	59	7906	0.0323455	3.126269	0.05556	IMD7 PLA2G4B PLA2G4B SPH2	
hsa00932	alpha-Linolenic acid metabolism - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa00932-9881+100137049	0.01242363	2	54	25	7906	0.9645717	1.908751	0.070707	IMD7 PLA2G4B PLA2G4B	
hsa00933	omega-3 fatty acid metabolism - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa00933-9881+100137049+5648	0.01242363	2	54	26	7906	0.9645717	1.908751	0.070707	IMD7 PLA2G4B PLA2G4B	
hsa04217	Nicotinamide - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04217-8315+8681+100137049+7705	0.0242979	4	54	162	7906	0.9645717	1.614411	0.070707	HST1 IMD7 PLA2G4B PLA2G4B USP7	
hsa04666	Tc gamma R-mediated phagocytosis - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04666-9881+100137049+5648	0.02538077	3	54	65	7906	0.9645717	1.595895	0.070707	IMD7 PLA2G4B PLA2G4B SPH2	
hsa04980	Allotetraploid sodium reabsorption - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa04980-53826+3291	0.02618174	2	54	27	7906	0.9645717	1.583902	0.070707	IMD7 PLA2G4B PLA2G4B SPH2	
hsa05113	Various types of N-glycan biosynthesis - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05113-11251+618	0.02887919	2	54	26	7906	0.9645717	1.579412	0.070707	EXY14 HSD11B2	
hsa05120	Prostaglandin metabolism - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05120-11251+4575+4575	0.02987919	3	54	163	7906	0.9645717	1.579412	0.070707	MAN1B1 EPN1	
hsa05113	Ovarian steroidogenesis - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa05113-9881+100137049	0.04389662	2	54	49	7906	1	1.357559	0.070707	IMD7 PLA2G4B PLA2G4B	
hsa07200	Carbon metabolism - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa07200-2021+5573+10993	0.0454967	1	54	117	7906	1	1.342756	0.070707	GPF OGK88 SDS	
hsa09510	N-Glycan biosynthesis - Homo sapiens (human)	http://www.genome.jp/kegg-bin/show_pathway?hsa09510-11251+6184	0.04553266	2	54	90	7906	1	1.341677	0.070707	MAN1B1 EPN1	