

Table SII. Pathway analysis of putative targets of miRNAs dysregulated in vitiligo

miRNA and targets (n) ^a	Functional group ID, name and genes in the functional group, n ^b	Putative targets in the functional group
miR-99b (40)	HP:0001000, abnormality of skin pigmentation, 39	LIFR, FGFR3, PTPN11
miR-125b (221)	GO:0033059, cellular pigmentation, 54	BCL2, VPS33A, SS18
	HP:0001000, abnormality of skin pigmentation, 268	LIFR, ALDH3A2
	KEGG:04916, melanogenesis, 101	DVL3, MAPK3
miR-155 (438)	GO:0030318, melanocyte differentiation, 28	MEF2A, SOX10, TYRP1
	GO:0042470, melanosome, 109	RAB5C, SDCBP, SYPL1, SYTL2, TMEM33, TYRP1, YWHAE, YWHAZ
	KEGG:04916, melanogenesis, 101	CREB1, GNAS, GSK3B, TCF7L2, TYRP1
miR-199a-3p (321)	GO:0042470, melanosome, 109	SYTL2, TMEM33, YWHAE, NAP1L1, CALU, SYPL1, SLC2A1
	GO:0030318, melanocyte differentiation, 28	ZEB2
	GO:0032400, melanosome localization, 30	VPS33A
	HP:0001000, abnormality of skin pigmentation, 268	STK11, SRD5A3, PDGFRA, KIAA0319L, FOS, ALDH3A2, SPRED1
	HP:0007440, generalized hyperpigmentation, 24	ALDH3A2
miR-145 (377)	GO:0051403, stress-activated MAPK cascade, 246	ARL6IP5, CRKL, DAB2, DUSP6, FOXO1, FZD4, FZD7, HIPK2, MAP2K4, MAP3K11, MAP3K2, MAP4K2, MAP4K4, NRAS, PDCD4, ZEB2, TAOK1, TNFRSF19
	GO:0007254, JNK cascade, 192	CRKL, DAB2, FZD4, FZD7, HIPK2, MAP2K4, MAP3K11, MAP3K2, MAP4K2, MAP4K4, NRAS, PDCD4, ZEB2, TAOK1, TNFRSF19
	KEGG:04350, TGF-beta signalling pathway, 80	ACV1B, ACV2A, INHBB, RPS6KB1, SMAD3, SMAD4, SMAD5, SP1, TGFB2

^aNumber of predicted putative direct targets expressed in the skin shown in parenthesis. ^bPathways with significant overlap ($p < 0.05$) with the predicted targets are presented.