

Supplementary information

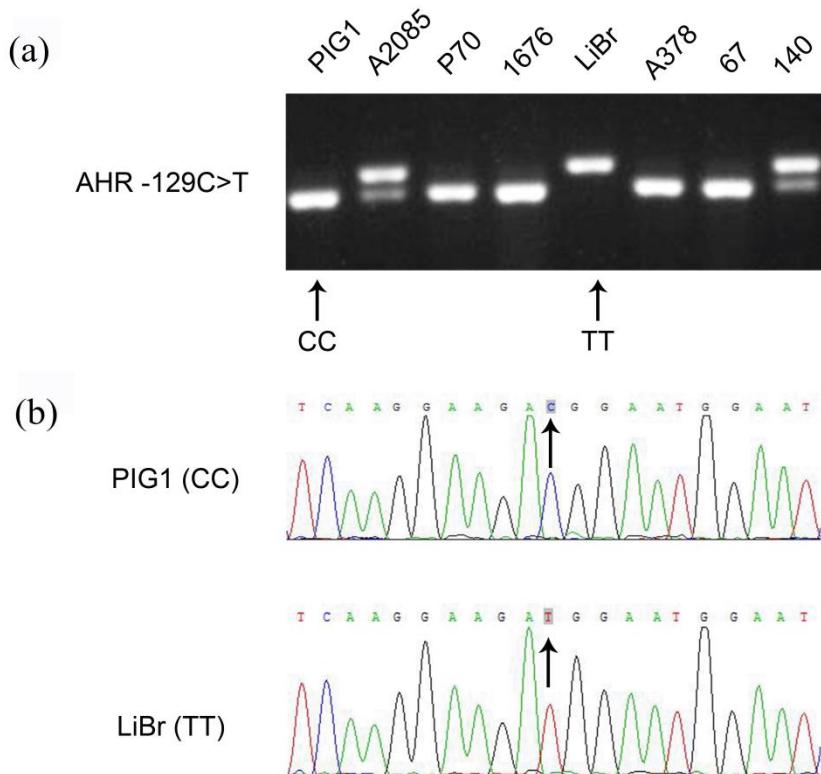
***AHR* promoter variant modulates its transcription and downstream effectors by allele-specific *AHR*-SP1 interaction functioning as a genetic marker for vitiligo**

Xiaowen Wang^{1,2}, Kai Li^{1,2}, Ling Liu^{1,2}, Qiong Shi¹, Pu Song¹, Zhe Jian¹, Sen Guo¹, Gang Wang¹, Chunying Li^{1*} & Tianwen Gao^{1*}

¹Department of Dermatology, Xijing Hospital, Fourth Military Medical University, Xi'an, Shaanxi, China

²Xiaowen Wang, Kai Li and Ling Liu contributed equally to this work.

Supplementary Fig. S1 Genotypes and sequence analysis of *AHR* -129C>T variation in PIG1 and LiBr cells. (a) Genotyping the -129C>T polymorphism in normal human melanocyte cell line (PIG1) and various human melanoma cell lines (A2085, P70 1676, LiBr, A378, 67 and 140). (b) Sequencing the *AHR* polymerase chain reaction products of PIG1 and LiBr cells.



Supplementary Table S1. Primary information for disease duration, onset age and body surface area of vitiligo patients.

Patient ID	Disease duration (month)	Onset age (year)	Body surface area (%)
1	180	8	1.0
2	480	22	80.0
3	84	33	5.0
4	312	13	73.0
5	168	10	1.0
6	120	18	2.5
7	12	47	1.0
8	60	10	22.5
9	120	9	0.5
10	36	24	2.0
11	84	40	4.0
12	144	45	8.0
13	180	17	9.0
14	73	12	0.5
15	25	20	1.0
16	20	16	7.0
17	72	19	4.0

Supplementary Table S2. Primer sequences used for ChIP assay and real-time quantitative PCR amplification.

Assay	Gene	Primer sequences (5'→3')		Product size (bp)
		Forward primer	Reverse primer	
ChIP	<i>AHR</i>	CCCTCAAGGAAGACGGA	CCGGCTGAATAGCAGGAG	122
		ATGG	CA	
RT-PCR	<i>SPI</i>	ACATCACCTACGCCAGT	TCTATGCCGCTTCCAAGG	101
		CGC	AT	
	<i>ACTB</i>	ATGATGACACAGCAGGT	TTGCCATACACTTCCCAC	190
		GGA	A	
		TCATGAAGTGTGACGTG	CAGGAGGAGCAATGATCT	156
		GACATC	TGATCT	