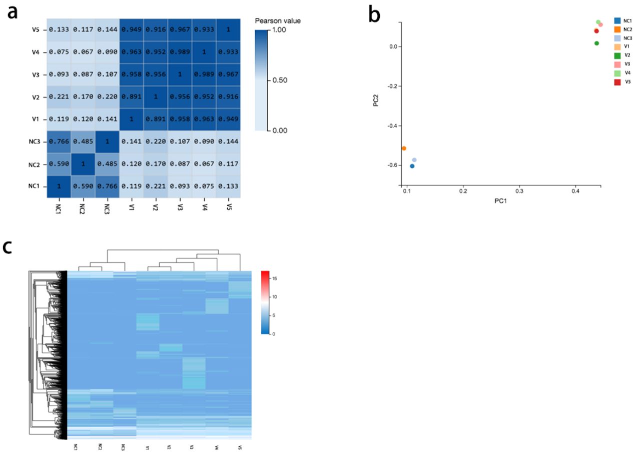

	NC1	NC2	NC3	V1	V2	V3	V4	V5
V5	0.133	0.117	0.144	0.949	0.916	0.967	0.933	1
V4	0.075	0.067	0.090	0.963	0.952	0.989	1	0.933
V3	0.093	0.087	0.107	0.958	0.956	1	0.989	0.967
V2	0.221	0.170	0.220	0.891	1	0.956	0.952	0.916
V1	0.119	0.120	0.141	1	0.891	0.958	0.963	0.949
NC3	0.766	0.485	1	0.141	0.220	0.107	0.090	0.144
NC2	0.590	1	0.485	0.120	0.170	0.087	0.067	0.117
NC1	1	0.590	0.766	0.119	0.221	0.093	0.075	0.133

Figure S1: Details of the transcriptome sequencing of CD8+ T cells from the vitiligo lesional skin and normal controls. a-b. Correlation heatmap and principal components for CD8+ T cells between vitiligo lesional skin and normal controls. c. Clustering heatmap of DEGs in CD8+ T cells between vitiligo lesional skin and normal controls. The X-axis represents the sample. The Y-axis represents the DEGs. *V=Vitiligo, NC=Normal controls.

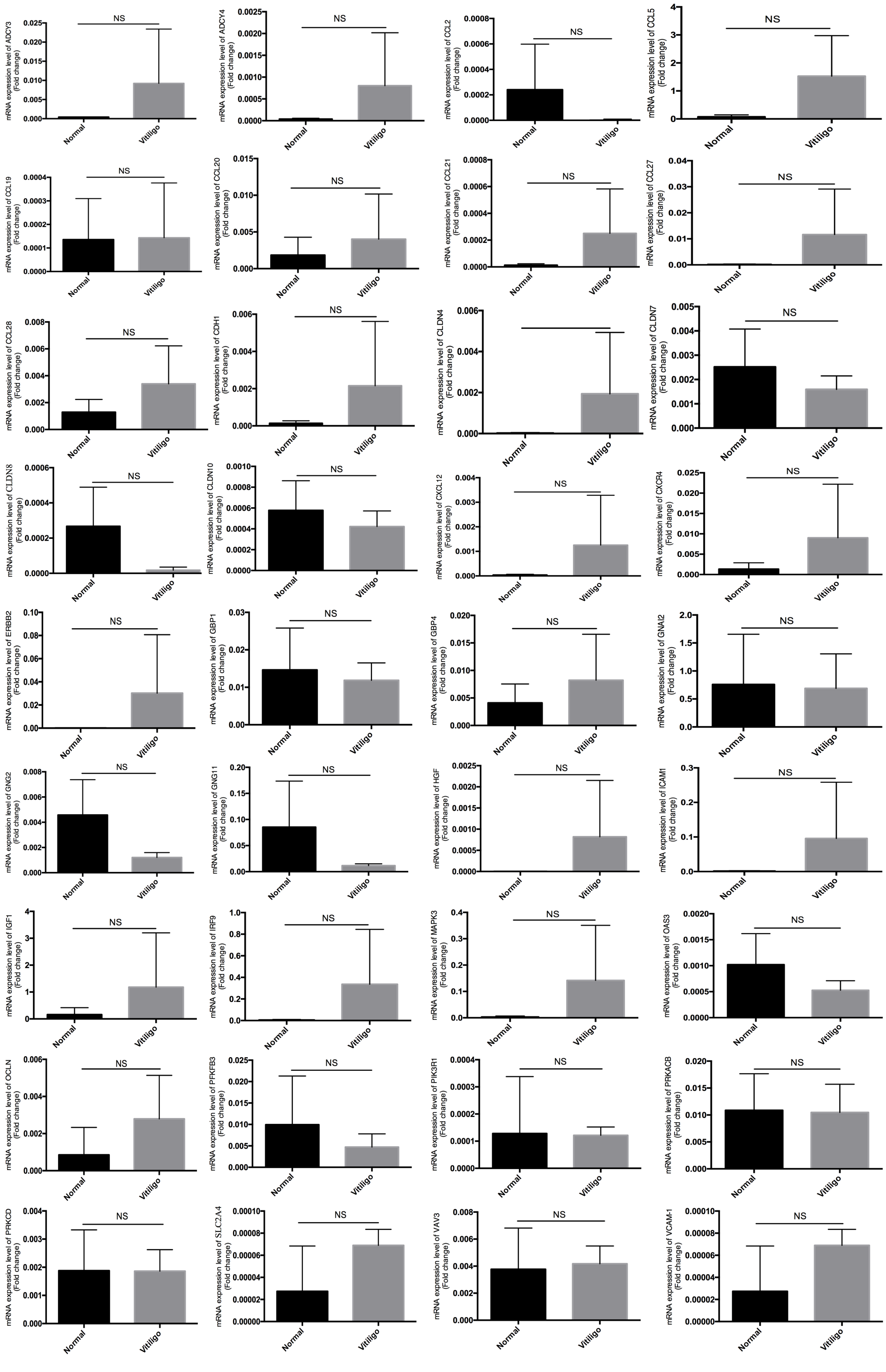

Figure S2: Validation of 36 DEGs by RT-qPCR. NS=non-significance.

Table S1. The list of primers and reference sequences in RT-qPCR

Primer name	Primer sequence (5’ to 3’)
ADCY3-F	GGACCAGCAGCAGTTCAA
ADCY3-R	AAGCCGCAGATGCAGTAG
CCL2-F	TAGCAGCCACCTTCATTC
CCL2-R	CTTCTTTGGGACACTTGC
CCL5-F	AGCCCTCGCTGTCATCCT
CCL5-R	GGCAATGTAGGCAAAGCAG
CCL19-F	TTCTCATCAAGGATGGCT
CCL19-R	CTCTGGATGATGCGTTCTA
CCL20-F	ACCGTATTCTTCATCCTAA
CCL20-R	TTCACCCAAGTCTGTTTT
CCL21-F	GGAAGATTCCCGCCAAGG
CCL21-R	AGCTGCTGCACCCAGAGC
CCL27-F	TCCTGAGCCCAGACCCTA
CCL27-R	GCAGTTCCACCTGGATGAC
CCL28-F	GCTCCTGGAAAGAGTGAATATGTG
CCL28-R	GTATGGTTGTGCGGGCTGAC
CDH1-F	CTTGGTCTACGCCTGGGACT
CDH1-R	TTGGGAAATGTGAGCAATTCTG
CLDN4-F	CCTTCATCGGCAGCAACA
CLDN4-R	CAGCAGCGAGTCGTACACCTT
CXCL12-F	AAGGTCGTGGTCGTGCTG
CXCL12-R	CCACTTTAGCTTCGGGTCA
CXCR4-F	TGACACTCCCGCCCAATA
CXCR4-R	CCCTGAGCCCATTTCCTC
ADCY4-F	TGCTAGTGACAAACAGGCCC
ADCY4-R	GGACACATTGGGAGCTTGGA
ERBB2-F	CAGAGGCTGCGGATTGTG
ERBB2-R	TGTTCAGCGGGTCTCCAT
F2RL1-F	GAAACTTAAAATTCAGGAGCAA
F2RL1-R	GAAAACTCATCCACAGAAAAGA

GBP1-F	TGACATACTCCCTGAAGCTG
GBP1-R	GGCCGATCAAAGACAAAG
GBP4-F	TTCTCAGCCCGTGGTGGT
GBP4-R	TGGAGCCCAGAGGGAAGC
HGF-F	GCCATGAATTTGACCTCTA
HGF-R	GCTGACATTTGATGCCACT
HIF1A-F	TACCATCAGCTATTTGCGTG
HIF1A-R	GAGAACCATAACAAAACCATCC
ICAM1-F	CTGCTCGGGGCTCTGTTC
ICAM1-R	AGGAGGTGCTGCATGTCA
IGF1-F	TGCCTGCTCACCTTCACC
IGF1-R	CCATACCCTGTGGGCTTGT
IRF9-F	CAGGCAAGCAGGACTTCC
IRF9-R	GGCGAGTCTTCCAGACAG
MAPK3-F	GGAGGTGGAGATGGTGAAGG
MAPK3-R	GGGCTGATCTTCTTGATGGC
OAS3-F	GCGGGTGCTGAAAACTGT
OAS3-R	GCAGTCGAGGAAGATGACAA
OCLN-F	CAATGGCAAAGTGAATGAC
OCLN-R	CAGGCGAAGTTAATGGAA
PFKFB3-F	CTGACTCGCTACCTCAACTGG
PFKFB3-R	CGGACTTTCATGGCTTCCT
PIK3CB-F	ACCCAGGGGAAAAATTAGAC
PIK3CB-R	ACAATCCCACAAGTGACAGG
PIK3R1-F	ACATTGCCCCGCCTCTTCTTAT
PIK3R1-R	TGTCGTAATTCTGCCAGGTTGC
PRKACB-F	TAGCCAAAGCCAAAGAAGACTT
PRKACB-R	TGACTCTTCCAAATGAACCTGT
PRKCD-F	AGAAGAACAATGGCAAGGC
PRKCD-R	CTCCAGGAAATACTGAACAGAC
SLC2A4-F	ACTGGCCATTGTTATCGGCA
SLC2A4-R	GTCAGGCGCTTCAGACTCTT
CLDN8-F	GTGGATGAATTGCGTGAGGC

CLDN8-R	TAGGTCCGGAGAAAGAGCCA
CLDN10-F	GGAGGCTCCGATAAAGCCAA
CLDN10-R	GCACAGCCCTGACAGTATGA
CLDN7-F	TTTCATCGTGGCAGGTCTTG
CLDN7-R	TGTTGGTAGGGATCAAAGGGT
GNG11-F	CGAAAATGCCTGCCCTTCAC
GNG11-R	TAGACACTTGTTGTCTCTGCAAC
GNAI2-F	TCAACGACTCAGCTGCCTAC
GNAI2-R	CATGCATGCGGTTCATCTCC
GNG2-F	GGAGCTAAGATCTGCCAGTGA
GNG2-R	TCAGGCCCCTCTCAAAGACT
VAV3-F	CACGACTTTCTCGAACACCTAT
VAV3-R	GGCCTTTGTAGATGTCTTCATC
VCAM-1-F	TCCGTCTCATTGACTTGC
VCAM-1-R	TGACTGTGATCGGCTTCC

Table S2. The list of primers and reference sequences in MethylTarget

Primer Name	Primer Sequence
HIF-1α_6F	GGTTGGGTTTTGATAAGTTATTTGAG
HIF-1α_6R	ATATCTTCACRACRAACRACCCCCAAACTC
HIF-1α_7F	GGGTTATAGAGTAGGTTGGGTTTT
HIF-1α_7R	CTCCCCTCCCCTCTCTTC
HIF-1α_8F	GAGGTGGAGGYGGGTTTTT
HIF-1α_8R	CACCCCCATCTCCTTTCTCTT
F2RL1_4F	TTTTTATAGTTAGGAAAGGTAAGGGAGA
F2RL1_4R	CCCCACCCCCTTCCCTAC
F2RL1_5F	AAGAAAGGTTTTTAGTAGTTGGAGAGG
F2RL1_5R	CCTAATCCCCTCCCCCAACT

Table S3. Details of CpG regions in HIF-1α and F2RL1 promoter

Target	Position	Chr*	Genome Position	Distance 2TSS*	Type
HIF1A_6	35	14	62162334	216	CG
HIF1A_6	41	14	62162340	222	CG
HIF1A_6	47	14	62162346	228	CG
HIF1A_6	54	14	62162353	235	CG
HIF1A_6	57	14	62162356	238	CG
HIF1A_6	64	14	62162363	245	CG
HIF1A_6	68	14	62162367	249	CG
HIF1A_6	86	14	62162385	267	CG
HIF1A_6	98	14	62162397	279	CG
HIF1A_6	103	14	62162402	284	CG
HIF1A_6	142	14	62162441	323	CG
HIF1A_6	144	14	62162443	325	CG
HIF1A_6	161	14	62162460	342	CG
HIF1A_6	170	14	62162469	351	CG
HIF1A_6	175	14	62162474	356	CG
HIF1A_7	30	14	62162855	737	CG
HIF1A_7	42	14	62162843	725	CG
HIF1A_7	45	14	62162840	722	CG
HIF1A_7	47	14	62162838	720	CG
HIF1A_7	58	14	62162827	709	CG
HIF1A_7	62	14	62162823	705	CG
HIF1A_7	65	14	62162820	702	CG
HIF1A_7	92	14	62162793	675	CG
HIF1A_7	111	14	62162774	656	CG
HIF1A_7	116	14	62162769	651	CG
HIF1A_7	132	14	62162753	635	CG
HIF1A_7	143	14	62162742	624	CG
HIF1A_7	146	14	62162739	621	CG
HIF1A_7	155	14	62162730	612	CG

HIF1A_7	165	14	62162720	602	CG
HIF1A_7	169	14	62162716	598	CG
HIF1A_7	172	14	62162713	595	CG
HIF1A_8	20	14	62162078	-40	CG
HIF1A_8	33	14	62162065	-53	CG
HIF1A_8	37	14	62162061	-57	CG
HIF1A_8	40	14	62162058	-60	CG
HIF1A_8	46	14	62162052	-66	CG
HIF1A_8	69	14	62162029	-89	CG
HIF1A_8	72	14	62162026	-92	CG
HIF1A_8	93	14	62162005	-113	CG
HIF1A_8	117	14	62161981	-137	CG
HIF1A_8	124	14	62161974	-144	CG
HIF1A_8	127	14	62161971	-147	CG
HIF1A_8	133	14	62161965	-153	CG
HIF1A_8	139	14	62161959	-159	CG
HIF1A_8	152	14	62161946	-172	CG
HIF1A_8	155	14	62161943	-175	CG
F2RL1_4	30	5	76114563	-238	CG
F2RL1_4	33	5	76114566	-235	CG
F2RL1_4	38	5	76114571	-230	CG
F2RL1_4	74	5	76114607	-194	CG
F2RL1_4	76	5	76114609	-192	CG
F2RL1_4	102	5	76114635	-166	CG
F2RL1_4	113	5	76114646	-155	CG
F2RL1_4	151	5	76114684	-117	CG
F2RL1_4	161	5	76114694	-107	CG
F2RL1_4	165	5	76114698	-103	CG
F2RL1_4	171	5	76114704	-97	CG
F2RL1_4	178	5	76114711	-90	CG
F2RL1_4	197	5	76114730	-71	CG
F2RL1_4	199	5	76114732	-69	CG
F2RL1_4	205	5	76114738	-63	CG

F2RL1_4	212	5	76114745	-56	CG
F2RL1_4	219	5	76114752	-49	CG
F2RL1_4	227	5	76114760	-41	CG
F2RL1_5	30	5	76115626	825	CG
F2RL1_5	55	5	76115601	800	CG
F2RL1_5	60	5	76115596	795	CG
F2RL1_5	62	5	76115594	793	CG
F2RL1_5	79	5	76115577	776	CG
F2RL1_5	91	5	76115565	764	CG
F2RL1_5	102	5	76115554	753	CG
F2RL1_5	114	5	76115542	741	CG
F2RL1_5	120	5	76115536	735	CG
F2RL1_5	122	5	76115534	733	CG
F2RL1_5	131	5	76115525	724	CG
F2RL1_5	144	5	76115512	711	CG

*Chr=chromosome, TSS= transcriptional start site