Extended Data Table 2. Differential gene signatures of keratinocytes and CD8 Tconv in affected compared to unaffected skin. The genes that show significant (Wilcoxon rank sum test, Benjamini Hochberg adjusted p <0.05) increased expression are shown in order of fold change. Red font indicates genes significantly differentially expressed but below the threshold for fold change (0.6 log2FC, 1.5 actual fold change). *FDR adj p, False discovery rate adjusted p-value; FC, fold change; Tconv, T conventional cell.*

	Keratinocyte signature			**CD8 Tconv signature**		
Rank	**Gene**	**FDR adj p**	**log2FC**	**Gene**	**FDR adj p**	**log2FC**
1	CD74	1.2E-34	2.0	GNLY	2.2E-02	1.3
2	IFITM3	1.2E-22	1.8	CD27	1.7E-05	0.7
3	IFI6	6.3E-34	1.7	LY6E	2.4E-03	0.7
4	IFITM1	2.8E-33	1.6	PSMB9	3.6E-04	0.6
5	HLA-C	8.6E-12	1.3	RNF213	1.4E-03	0.6
6	HLA-B	5.2E-05	1.1	LAG3	1.5E-03	0.6
7	B2M	1.4E-14	1.1	LIMD2	9.1E-03	0.6
8	KRT6B	4.0E-04	1.1	TIGIT	1.1E-02	0.5
9	LY6E	1.3E-04	0.9	GALNT2	4.7E-03	0.5
10	PSME2	1.0E-07	0.8	IFI6	1.1E-02	0.5
11	TMSB10	1.3E-04	0.8	LYST	1.5E-02	0.5
12	CST3	1.3E-04	0.8	XAF1	7.2E-04	0.4
13	DCD	1.5E-04	0.8	GBP2	1.4E-02	0.4
14	STAT1	4.2E-12	0.8	DCD	4.8E-02	0.4
15	VIM	2.1E-04	0.7	ACP5	1.1E-02	0.4
16	GSTP1	3.8E-03	0.7			
17	IFI27	1.3E-09	0.7			
18	CCL4	8.7E-11	0.7			
19	PSME1	1.2E-02	0.7			
20	PSMB9	2.5E-11	0.6			
21	GAPDH	8.7E-08	0.6			