

Extended Data Table 3. Differential gene signatures of CD8 Tconv expressing dominantly expanded TCR compared to other TCR in affected skin or blister fluid. The genes that show significant (Wilcoxon rank sum test, Benjamini Hochberg adjusted $p < 0.05$) increased expression above the threshold for fold-change ($0.6 \log_2 FC$) are shown. Genes shared in the signature of dominantly-expanded TCR+ Tconv between affected skin and blister fluid highlighted blue. *TCR*, T-cell receptor; *FDR adj p*, False discovery rate adjusted p -value; *FC*, fold change; *Tconv*, T conventional cell.

Rank	Dominant TCR in affected skin			Dominant TCR in Blister fluid		
	Gene	FDR adj p	log2FC	Gene	FDR adj p	log2FC
1	GNLY	1.0E-06	2.7	GNLY	1.5E-118	1.9
2	GZMB	6.1E-04	1.6	LAG3	6.5E-175	1.5
3	KLRC1	3.6E-16	1.4	TIGIT	6.0E-142	1.3
4	GALNT2	3.3E-07	1.4	KLRC1	1.6E-158	1.3
5	LAG3	2.6E-07	1.3	GZMB	7.7E-65	1.1
6	BATF	5.8E-08	1.3	PRF1	1.9E-119	1.1
7	PRF1	2.5E-03	1.2	PHLDA1	3.3E-150	1.0
8	DUSP4	5.2E-06	1.2	GALNT2	6.3E-123	1.0
9	PTMS	2.6E-06	1.1	FCGR3A	8.0E-90	1.0
10	FCGR3A	1.2E-03	1.0	ACP5	8.9E-100	1.0
11	TIGIT	2.3E-03	1.0	NGK7	9.1E-102	1.0
12	ACP5	2.8E-06	1.0	HAVCR2	1.3E-95	0.9
13	LYST	2.1E-05	1.0	IGFLR1	4.4E-120	0.9
14	HAVCR2	3.2E-05	0.9	GAPDH	3.8E-108	0.8
15	CD27	2.1E-02	0.9	ENTPD1	2.3E-115	0.8
16	MT1E	2.9E-03	0.9	KLRD1	1.0E-61	0.8
17	LAYN	2.0E-09	0.9	LYST	3.7E-87	0.8
18	RAB27A	2.5E-05	0.9	PTMS	1.5E-79	0.8
19	SNX9	4.0E-04	0.9	TNFRSF1B	2.0E-74	0.8
20	GAPDH	1.5E-06	0.9	HMOX1	2.6E-145	0.8
21	TNFRSF9	9.4E-10	0.9	PKM	4.7E-63	0.8
22	CD59	8.6E-06	0.9	LAYN	3.7E-138	0.8
23	AHI1	1.1E-05	0.9	SIRPG	1.1E-73	0.7
24	PKM	1.5E-02	0.8	CCL4	5.0E-23	0.7
25	PHLDA1	2.6E-02	0.8	CD27	1.4E-66	0.7
26	CBLB	1.4E-02	0.8	TNFRSF9	8.5E-134	0.7
27	MTSS1	1.2E-08	0.8	CBLB	7.3E-67	0.7
28	HMOX1	1.2E-09	0.8	CCL3	5.7E-68	0.7
29	ENTPD1	2.6E-07	0.8	AD000671.2	4.7E-93	0.7
30	AD000671.2	1.2E-03	0.8	ADGRG1	1.1E-128	0.7
31	CTLA4	1.8E-05	0.8	CD63	3.3E-59	0.7
32	CD70	2.2E-10	0.7	LSP1	3.1E-86	0.7
33	LSP1	1.6E-03	0.7	CD8A	1.5E-42	0.7
34	PPM1G	2.0E-02	0.7	S100A4	1.3E-50	0.7
35	APOBEC3C	4.4E-02	0.6	LINC01943	1.6E-82	0.7
36	CD38	2.5E-03	0.6	SERPINB1	2.8E-53	0.6
37				LINC01871	2.9E-42	0.6
38				RHOB	5.2E-129	0.6
39				RAB27A	3.9E-61	0.6
40				DUSP4	7.4E-83	0.6
41				AC017002.3	5.0E-92	0.6
42				NEAT1	5.9E-31	0.6
43				IFNG	4.1E-60	0.6
44				SNX9	4.3E-92	0.6
45				ITGA4	1.8E-48	0.6
46				PGAM1	4.0E-48	0.6
47				CTLA4	1.9E-65	0.6