Extended Data Table 1. Differential gene signatures of Seurat-defined CD8 Tconv clusters 1-8. The top 25 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 below significance. Genes shared or indicative of shared functional state between clusters 1-2 (blue), clusters 3-4 (red), and clusters 5-8 (green) are highlighted. *Tconv, T conventional cell; FC, fold change.*

	Quiescent/inactive						Cytotoxic/proliferative						Innate-like											
	CD8 Tconv cluster 1			CD8 Tconv cluster 2			CD8 Tconv cluster 3			CD8 Tconv cluster 4			CD8 Tconv cluster 5			CD8 Tconv cluster 6			CD8 Tconv cluster 7			CD8 Tconv cluster 8		
Rank	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**	**Gene**	**Log2FC**	**p value**
1	DCD	11.4	1.7E-04	CMC1	2.7	2.2E-29	TYMS	4.8	4.0E-37	HIST1H2AI	4.9	7.7E-24	S100A8	5.6	9.2E-47	CST3	4.9	1.8E-11	IDO1	7.5	6.0E-66	TYROBP	5.1	3.0E-15
2	MUCL1	6.7	1.5E-02	LTB	2.5	1.8E-25	STMN1	3.3	5.4E-22	MKI67	4.7	1.0E-22	CST3	5.3	1.2E-41	S100A8	4.5	4.6E-09	CXCL10	7.4	1.2E-68	XCL1	4.8	1.1E-08
3	XIST	1.9	6.2E-03	FOS	2.4	2.8E-23	KLRC1	3.0	3.6E-19	CENPF	4.0	8.6E-15	S100A9	5.1	2.2E-36	TYROBP	3.8	9.7E-06	SERPING1	7.3	4.7E-66	XCL2	4.6	4.3E-05
4	MALAT1	1.8	1.3E-02	IL7R	2.2	1.8E-19	TRAV12-3	3.0	1.4E-18	HIST1H4C	3.3	5.0E-09	TYROBP	4.8	5.0E-31	FCER1G	3.3	6.4E-04	IL1R2	7.3	9.4E-62	FCER1G	4.2	6.8E-08
5	NEAT1	1.7	2.0E-02	DUSP1	1.9	7.4E-14	GNLY	2.9	2.2E-18	HIST1H1E	3.2	9.1E-09	LYZ	4.7	1.2E-27	TRAV27	2.9	1.8E-02	MARCKS	7.2	4.3E-59	KLRB1	4.0	7.3E-07
6	CTSD	1.7	2.7E-02	HSPA1A	1.8	5.7E-11	TRBV9	2.8	2.6E-17	STMN1	3.1	6.5E-08	FCER1G	4.3	1.4E-22	IFITM3	2.2	3.0E-01	THBS1	7.0	3.2E-58	CMC1	3.6	6.8E-05
7	GRK2	1.4	8.2E-02	ZFP36	1.8	6.9E-13	TUBA1B	2.7	1.3E-16	HIST1H1D	3.0	2.8E-07	AIF1	3.6	3.7E-13	FOS	2.1	3.0E-01	SERPINA1	6.9	3.8E-53	AREG	2.7	5.2E-02
8	MACF1	1.4	8.7E-02	JUNB	1.7	2.6E-11	GALNT2	2.4	5.8E-14	HIST1H1C	2.8	3.8E-06	GLUL	3.3	1.1E-10	HIST1H2AI	1.6	7.9E-01	C15orf48	6.8	7.5E-52	FOS	2.5	9.8E-02
9	AKNA	1.4	9.0E-02	DUSP2	1.6	5.1E-10	TRBV4-1	2.1	3.0E-10	CEBPD	2.7	2.2E-05	FOS	2.9	2.2E-07	HLA-DPA1	1.3	1.0E+00	SPI1	6.6	3.3E-48	KLRD1	2.0	5.8E-01
10	NLRC3	1.4	9.6E-02	DNAJB1	1.5	2.1E-08	TUBB	2.0	4.6E-10	LINC01871	2.2	3.7E-03	IFITM3	2.6	6.0E-06	CTSB	1.2	1.0E+00	S100A8	6.6	1.1E-50	DUSP1	2.0	4.3E-01
11	SYNE2	1.4	9.5E-02	TXNIP	1.3	1.3E-06	ACP5	2.0	5.5E-10	GNLY	2.2	4.2E-03	HLA-DQA1	2.5	5.2E-05	HIST1H1E	1.2	1.0E+00	CST3	6.6	5.2E-52	PPP1R14B	1.8	6.1E-01
12	NKTR	1.4	1.0E-01	CXCR4	1.3	1.5E-06	HIST1H4C	2.0	8.2E-10	HMGB2	2.2	5.4E-03	IFIT3	2.5	5.9E-05	SAT1	1.2	1.0E+00	CD14	6.5	4.0E-46	IL7R	1.8	9.1E-01
13	IKZF3	1.3	1.2E-01	HLA-DPA1	1.3	2.6E-06	HAVCR2	2.0	1.1E-09	TUBA1B	2.0	2.2E-02	HIST1H2AI	2.4	1.7E-04	FTL	1.1	1.0E+00	C1QA	6.4	2.5E-46	IFITM3	1.6	8.0E-01
14	INPP5D	1.3	1.2E-01	HLA-DPB1	1.2	1.1E-05	LGALS1	1.8	8.0E-09	MT1E	1.8	4.1E-02	HIST1H1E	2.0	3.4E-03	HLA-DRA	1.0	1.0E+00	C1QB	6.4	1.4E-45	DUSP2	1.5	9.3E-01
15	RNF213	1.3	1.2E-01	ZFP36L2	1.1	3.2E-05	GZMB	1.8	1.3E-08	IFI27	1.9	5.2E-02	SAT1	1.9	9.9E-03	TXN	1.0	1.0E+00	CTSL	6.3	8.3E-40	TXNIP	1.5	1.0E+00
16	JUND	1.3	1.3E-01	CD6	1.1	3.5E-05	HMGB2	1.8	1.6E-08	ETS1	1.8	7.4E-02	HLA-DRA	1.8	1.7E-02	TNFSF10	0.9	1.0E+00	C1QC	6.3	5.7E-43	ZFP36	1.2	1.0E+00
17	OGA	1.3	1.3E-01	GZMM	1.1	3.8E-05	FABP5	1.8	4.9E-08	MT2A	1.8	9.4E-02	JUND	1.8	2.7E-02	NEAT1	0.9	1.0E+00	S100A9	6.1	4.8E-39	BTG1	1.2	1.0E+00
18	GNAS	1.3	1.3E-01	CD69	1.1	7.4E-05	HMGN2	1.6	4.0E-07	DUT	1.7	9.9E-02	PARP14	1.7	4.5E-02	TYMP	0.9	1.0E+00	TYROBP	5.9	4.2E-37	MBP	1.1	1.0E+00
19	MT-ND1	1.3	1.5E-01	PDCD4	1.1	1.7E-04	H2AFZ	1.6	7.2E-07	SET	1.7	1.1E-01	HLA-DPA1	1.7	4.7E-02	MIF	0.8	1.0E+00	LYZ	5.7	2.5E-32	FGFBP2	1.1	1.0E+00
20	STK10	1.3	1.6E-01	MALAT1	1.0	2.1E-04	IFI27	1.5	1.9E-06	H1FX	1.7	1.4E-01	DUSP1	1.7	5.1E-02	MT-ND6	0.8	1.0E+00	RNASE1	5.6	5.8E-30	PDCD4	1.1	1.0E+00
21	MT-ND6	1.2	1.6E-01	BTG1	1.0	2.8E-04	MT1E	1.5	2.0E-06	H2AFV	1.7	1.5E-01	H1FX	1.6	7.5E-02	LMNA	0.8	1.0E+00	FCER1G	5.5	5.0E-29	HLA-DPB1	1.1	1.0E+00
22	MT-ND2	1.2	1.5E-01	JUN	1.0	6.0E-04	DUT	1.5	2.5E-06	ITGB1	1.7	1.5E-01	CTSB	1.6	8.2E-02	HLA-DRB1	0.8	1.0E+00	C1orf162	5.3	3.1E-25	ZFP36L2	1.0	1.0E+00
23	KMT2A	1.2	1.6E-01	KLF6	1.0	7.0E-04	PRF1	1.4	1.1E-05	LYST	1.5	2.1E-01	HLA-DQB1	1.6	8.9E-02	JUND	0.8	1.0E+00	FGL2	5.1	4.1E-22	HLA-DPA1	1.0	1.0E+00
24	MT-ND4	1.2	1.6E-01	FTH1	0.9	2.9E-03	PTMS	1.4	1.2E-05	MZT2B	1.5	2.2E-01	TNFSF10	1.5	9.1E-02	TRBV28	0.8	1.0E+00	IFIT2	5.0	2.3E-21	DDIT4	1.0	1.0E+00
25	SRRM2	1.2	1.7E-01	LINC02446	0.8	4.8E-03	LAG3	1.4	2.3E-05	IFI16	1.5	2.6E-01	FTL	1.5	9.3E-02	MT-ND4	0.8	1.0E+00	AIF1	4.7	2.3E-17	JUNB	1.0	1.0E+00

🟦 Shared or indicative or clusters 1-2 🟥 Shared or indicative or clusters 3-4 🟩 Shared or indicative or clusters 5-8