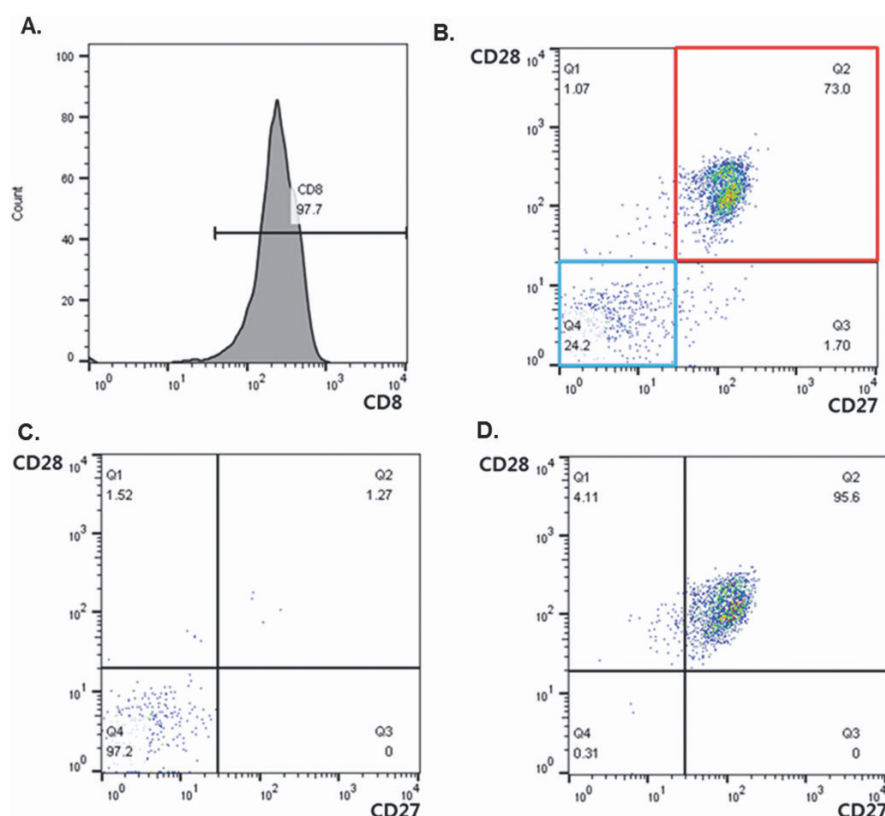




Supplementary Fig. S1. Representative purities of CD8⁺CD27⁻CD28⁻ and CD8⁺CD27⁺CD28⁺ T cells.

A, B. CD8⁺ T cells analysed after CD8⁺ T cell positive selection. **C.** Purity of CD8⁺CD27⁻CD28⁻ cells after sorting. **D.** Purity of CD8⁺CD27⁺CD28⁺ cells after sorting.

Supplementary Table S1. Top biological functions of differentially expressed genes between Behçet's disease patients and healthy controls as presented by Ingenuity Pathway Analysis (IPA).

Biological functions	<i>p</i> -value	Number of molecules
Disease and disorders:		
Cancer	1.30E-03 - 1.48E-25	997
Organismal injury and abnormalities	1.33E-03 - 1.48E-25	1012
Dermatological diseases and conditions	9.09E-04 - 1.50E-20	620
Gastrointestinal disease	1.33E-03 - 1.05E-19	932
Reproductive system disease	7.38E-04 - 2.16E-13	633
Molecular and cellular functions:		
Cellular movement	1.29E-03 - 9.33E-11	256
Cell-to-cell signaling and interaction	1.30E-03 - 2.68E-07	232
Molecular transport	8.52E-04 - 2.70E-06	161
Cellular function and maintenance	1.33E-03 - 6.48E-06	296
Cellular assembly and organization	1.17E-03 - 8.77E-06	200
Physiological system development and function:		
Immune cell trafficking	1.29E-03 - 6.70E-09	127
Haematological system development and function	1.33E-03 - 5.21E-08	192
Nervous system development and function	1.30E-03 - 2.68E-07	186
Tissue development	1.33E-03 - 4.58E-06	234
Cardiovascular system development and function	1.30E-03 - 7.73E-06	146

Top biological functions of differentially expressed genes between Behçet's disease patients and healthy controls in this study provided by Ingenuity Pathway Analysis (IPA®). The *p*-value was determined by comparing the number of genes found in each category with the number of known genes within the IPA software system.

Supplementary Table S2. Top ten genes based on the order of expression fold change in CD8⁺ T cells of CD27⁺CD28⁺ subset compared to CD27⁻CD28⁻ subset.**a. Behçet's disease patients.**

Gene ID	Gene Symbol	Description	log ₂ fold change of RNA sequencing
7757	ZNF208	zinc finger protein 208	58.2
57412	AS3MT	arsenite methyltransferase	47.4
100129316	LOC100129316	uncharacterised LOC100129316	-42.6
1240	CMKLR1	chemerin chemokine-like receptor 1	-43.4
140469	MYO3B	myosin IIIB	-44.3
5097	PCDH1	protocadherin 1	-47.2
9936	CD302	CD302 molecule	-48.9
353345	GPR141	G protein-coupled receptor 141	-56.1
51314	NME8	NME/NM23 family member 8	-69.6
153090	DAB2	DAB2 interacting protein	-107.8

b. Healthy controls

Gene ID	Gene Symbol	Description	log ₂ fold change of RNA sequencing
50944	SHANK1	SH3 and multiple ankyrin repeat domains 1	171.7
4681	NBL1	neuroblastoma 1, DAN family BMP antagonist	143.0
57412	AS3MT	arsenite methyltransferase	123.3
9934	P2RY14	purinergic receptor P2Y14	121.8
100616394	MIR4444-1	microRNA 4444-1	-83.9
23022	PALLD	palladin, cytoskeletal associated protein	-93.4
1240	CMKLR1	chemerin chemokine-like receptor 1	-106.3
353345	GPR141	G protein-coupled receptor 141	-110.7
51314	NME8	NME/NM23 family member 8	-112.5
5097	PCDH1	protocadherin 1	-116.2

Summary of top ten up- and down-regulated genes found in CD8⁺ T cells of CD27⁺CD28⁺ subset compared to CD27⁻CD28⁻ subset. Positive and negative fold change values indicate up-regulation and down-regulation, respectively, of gene expression in CD8⁺CD27⁺CD28⁺ T cells relative to CD8⁺CD27⁻CD28⁻ T cells.