

Appendix

Lymphopenia drives T cell exhaustion in immunodeficient STING gain-of-function mice

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CD4⁺

Signature details	Size (number of genes)	NES	Nom p-value	FDR q-value
PID TCR PATHWAY	64	1.61	0.008	0.050
BIOCARTA TCR PATHWAY	44	1.66	0.007	0.032
REACTOME TCR SIGNALING	112	1.39	0.027	0.167

CD8⁺

Signature details	Size (number of genes)	NES	Nom p-value	FDR q-value
PID TCR PATHWAY	64	1.34	0.061	0.191
BIOCARTA TCR PATHWAY	44	1.39	0.060	0.145
REACTOME TCR SIGNALING	112	1.49	0.006	0.079

Appendix Table S1. GSEA signatures.

NES: normalized enrichment score.

Nom p-value: Nominal p-value

FDR q-value: False Discovery Rate q-value

CD4⁺

Gene	Locus	Control mice – FPKM Mean	STING GOF mice – FPKM Mean	Fold change (STING GOF/control)	p value	q value
<i>cd3e</i>	chr9:44998742-45009590	443.883	684.158	0.624149	0.00005	0.000397557
<i>il7r</i>	chr15:9506158-9529876	189.951	65.0465	-1.54608	0.00005	0.000397557
<i>cdkn1b</i>	chr6:134920400-134925525	108.714	89.3016	-0.283779	0.025	0.0789669
<i>bcl2</i>	chr1:106538178-106714290	44.0479	51.3457	0.22117	0.1275	0.269564
<i>gfi1</i>	chr5:107716654-107725805	8.02892	17.9484	1.16058	0.00005	0.000397557
<i>socs1</i>	chr16:10783808-10785536	17.496	32.3648	0.887397	0.00015	0.00107805

CD8⁺

Gene	Locus	Control mice – FPKM Mean	STING GOF mice – FPKM Mean	Fold change (STING GOF/control)	p value	q value
<i>cd3e</i>	chr9:44998742-45009590	491.595	578.488	0.234817	0.04835	0.136132
<i>il7r</i>	chr15:9506158-9529876	253.798	124.345	-1.02933	0.00005	0.000423756
<i>cdkn1b</i>	chr6:134920400-134925525	86.0948	65.1919	-0.401234	0.0014	0.00782091
<i>bcl2</i>	chr1:106538178-106714290	51.4897	80.2689	0.640556	0.00005	0.000423756
<i>gfi1</i>	chr5:107716654-107725805	6.8492	12.5575	0.874541	0.0001	0.000799047
<i>socs1</i>	chr16:10783808-10785536	18.4175	32.9478	0.839101	0.0001	0.000799047

Appendix Table S2. Data of RNA-seq analysis for selected genes.

Data are represented as the mean for FPKM for each group of mice, with the results of the statistical test.