Supplementary information

Supplemental Table 1: GWAS identify MYC as potential risk gene for the development of allergic asthma and multiple sclerosis.

Allergic asthma

Gene	SNP	OR	p-value	Publication
MYC	rs13277355	1.11	1.65x10-10	Pividori, M. et al., 2019

Multiple sclerosis

Gene	SNP	OR	p-value	Publication
MYC	rs4410871	1.09	7.70 x10-09	Gourraud et al., 2012

Supplemental Table 2: Antibodies used for FACS analyses

Antigen	Clone	Company	Fluorochrom
CD62L	MEL-14	BioLegend	AlexaFluor488
CD44	IM7	BioLegend	PE
CD25	3C7	BioLegend	FITC
CD44	IM7	BioLegend	FITC
CD4	RM4-5	BioLegend	APC
CD45	30-F11	BioLegend	BV570
CD4	RM4-5	BioLegend	PacificBlue
PD-1	29F.1A12	BioLegend	PE
CXCR5	L138D7	BioLegend	PE/Cy7
B220	RA3-6B2	BioLegend	FITC
GATA3	16E10A23	BioLegend	APC
IL-4	11B11	BioLegend	PE-Cy7
IL-4	11B11	BioLegend	PE
IL-13	eBio13A	ThermoScientific	AF488
TNFα	MP6-XT22	BioLegend	APC
MYC	D84C12	Cell Signaling	N/A

Suppl. Figure 1
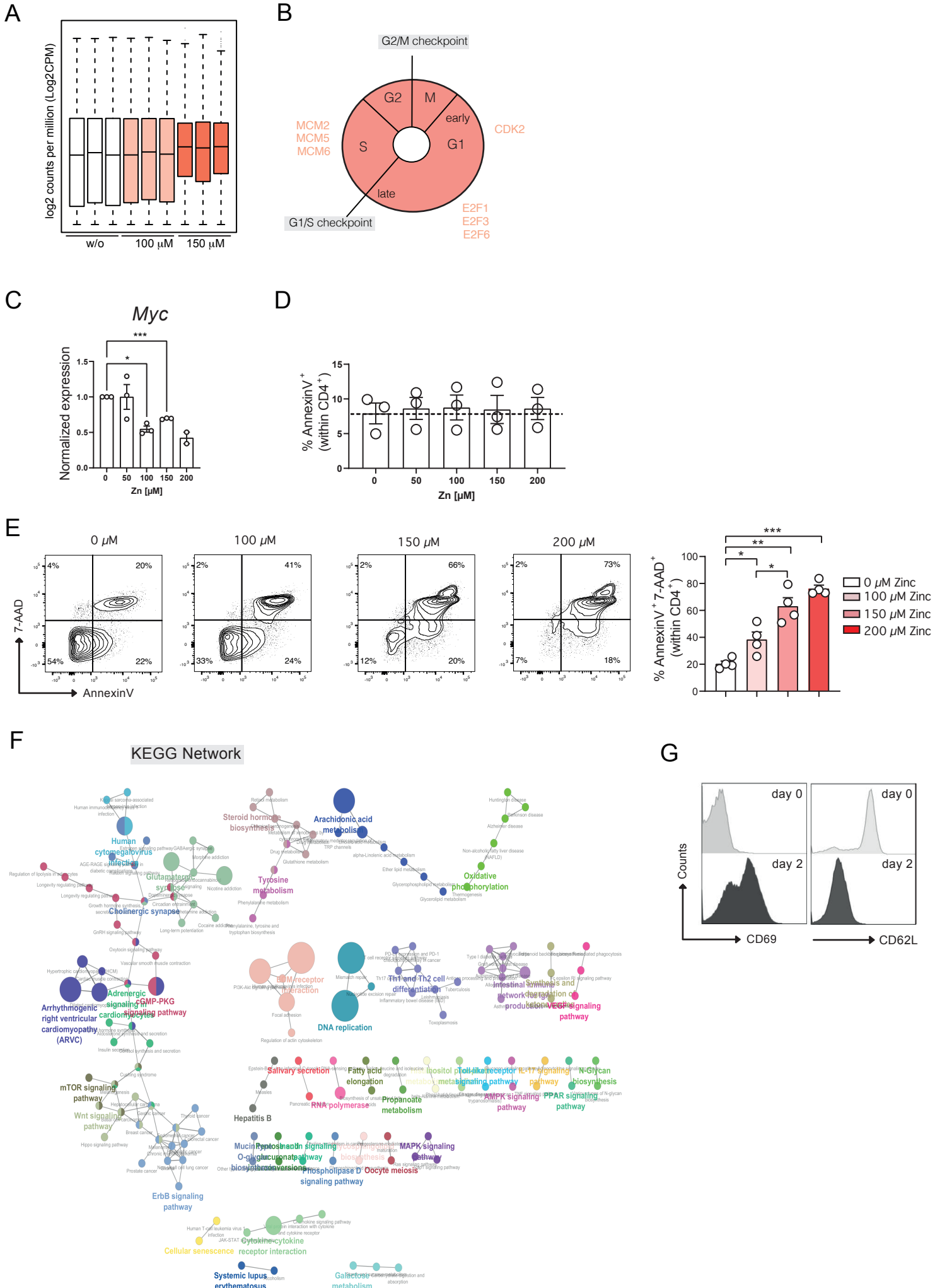
Suppl. Figure 1: High dose zinc aspartate controls gene expression and metabolic fitness of CD4$^+$ T cells.

A, Boxplot showing log2 counts per million of the individual biological samples for RNA seq.

B, Cell cycle phases with the indicated genes out of Figure1E.

C, OT-II TCR tg CD4$^+$ T cells were activated for 6 hrs in the absence and presence of the indicated zinc concentrations. Graphs show normalized gene expression of *Myc* determined by qRT-PCR and using the housekeeping genes *Gapdh*. Data are from 3 mice (except for 200 μM, here 2 mice were analyzed).

D, OT-II TCR tg CD4$^+$ T cells were activated for 6 hrs in the absence and presence of the indicated zinc concentrations and analyzed for early apoptosis using AnnexinV staining and flow cytometry. Data are from 3 mice.

E, OT-II TCR tg CD4$^+$ T cells were activated for 48 hrs in the absence and presence of the indicated zinc concentrations and analyzed for cell death using AnnexinV and 7-AAD staining and flow cytometry. Data are from 4 mice.

F, KEGG network analysis of bulk RNA sequencing data as shown in Figure 1.

G, Representative stainings for CD69 and CD62L of 2D2 TCR tg T cells before and after activation as described in Figure 5E.

RNA sequencing data in A was generated in biological triplicates from 3 mice per group. Data in C and D are from 3 mice. Data in E are from 4 mice. Every dot represents one mouse. Statistical analysis in C-E by one-way ANOVA followed by Tukey's honestly significant difference (HSD) post hoc test for multiple comparisons. $p^* < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$.