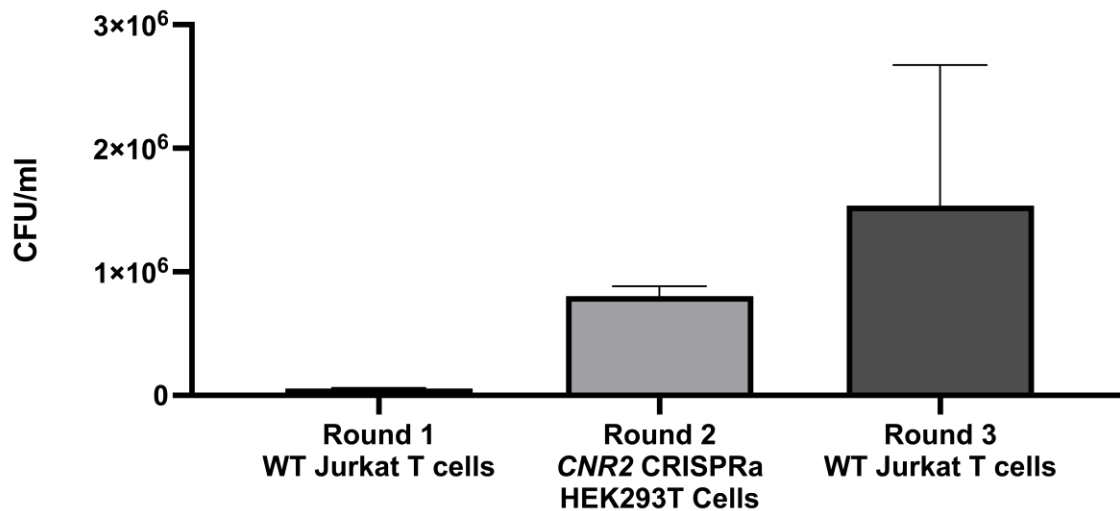
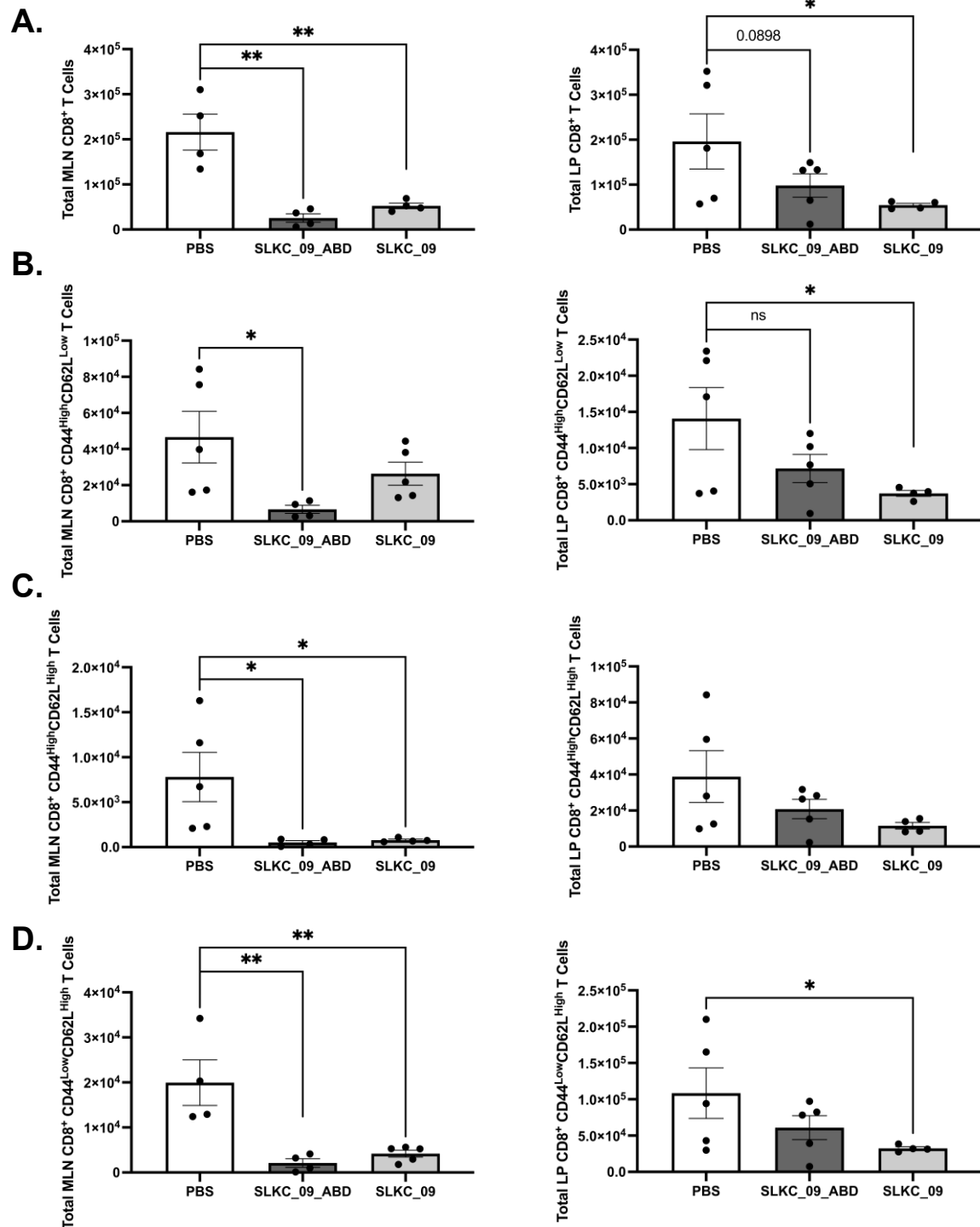




Selection Round	Cell Type	CFU/ml
Round 1	WT Jurkats	56,000 CFU/ml
Round 2	CNR2 CRISPRa HEKs	800,000 CFU/ml
Round 3	WT Jurkats	1.53 million CFU/ml

Supplementary Figure S1: Selection outline utilised for cell surface selection against *CNR2* uses endogenously-expressing and genetically modified overexpressing cell lines for efficient peptide binder amplification. Bar chart and table depicting the CFU/ml values as selection rounds alternate between endogenously *CNR2*-expressing WT Jurkat T cells and genetically modified *CNR2* overexpressing HEK293T cells. (51 words)



Supplementary Figure S2: SLKC_09 and SLKC_09_ABD broadly suppress CD8⁺ T cell subsets across gut-associated lymphoid compartments. Total CD8⁺ T cell numbers were quantified by flow cytometry across four phenotypically defined subpopulations in the mesenteric lymph node (MLN) and intestinal lamina propria (LP) following treatment of TNF^{ΔARE} mice with SLKC_09_ABD or SLKC_09 relative to PBS vehicle control. **(A)** Total CD8⁺ T cells in the MLN and LP. **(B)** Effector CD8⁺CD44^{High}CD62L^{Low} T cells in the MLN and LP. **(C)** Central memory CD8⁺CD44^{High}CD62L^{High} T cells in the MLN and LP. **(D)** Naïve

CD8⁺CD44^{Low}CD62L^{High} T cells in the LP and MLN. Bars represent mean $\pm$ SEM of n = 5 animals per group. Statistical comparisons were made relative to PBS control. * p < 0.05; ** p < 0.01; p values shown where differences trended toward significance. (133 words)