

Supplemental information

**The quality of energy- and macronutrient-balanced
diets regulates host susceptibility
to influenza in mice**

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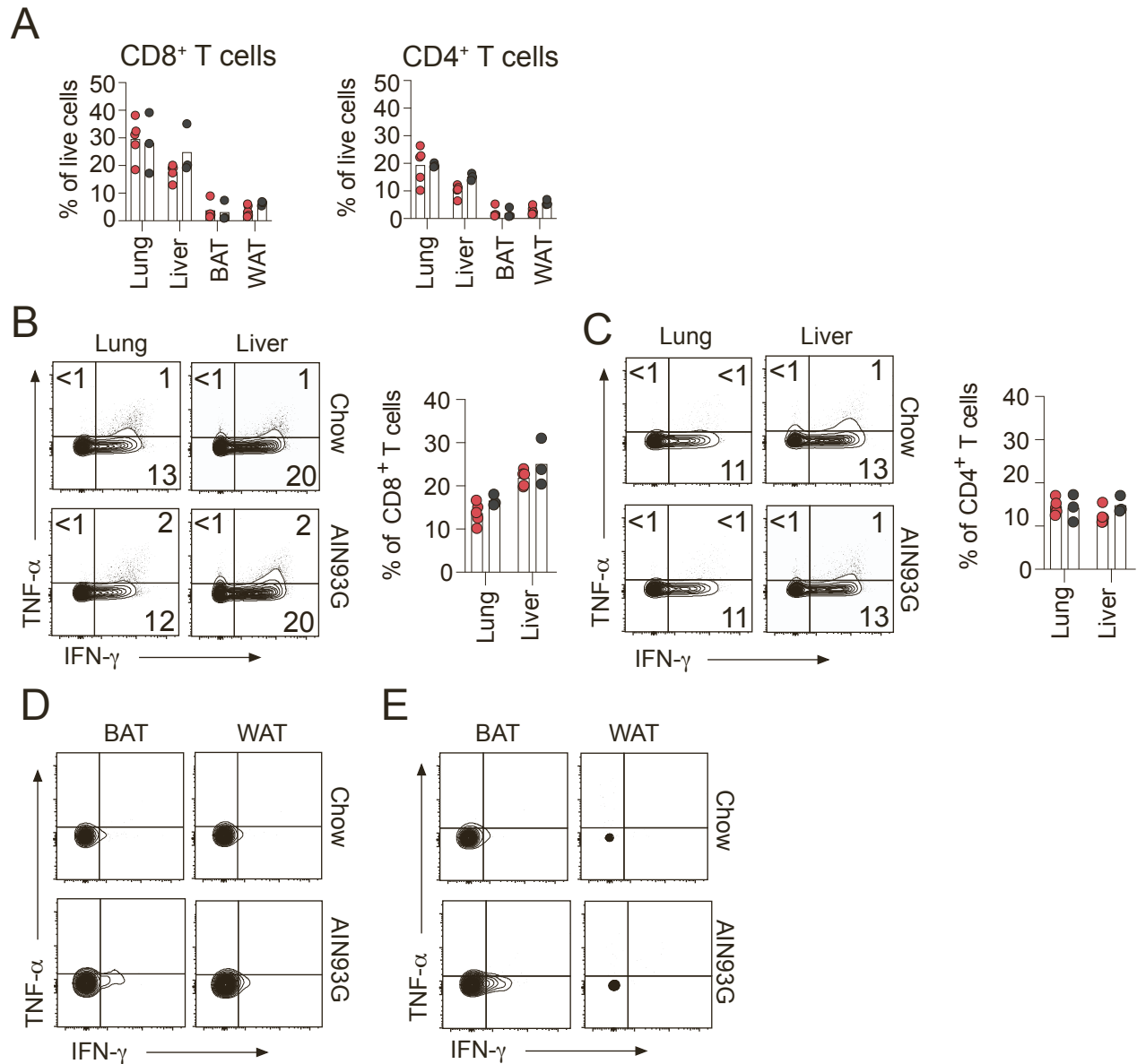


Figure S1. IFN- γ expression and production in non-lymphoid organs of IAV-infected chow and AIN93G fed mice. Mice ($n = 5$) fed with chow (red symbols) or AIN93G (black symbols) diets ad libitum for 3 wks were inoculated i.n. with 5 PFU IAV and various tissues harvested at day 9 p.i. **(A)** Percentage of CD4⁺ and CD8⁺ T cells in total live cells in the lung, liver, BAT and WAT determined by flow cytometry. Symbols represent individual mice, and bars denote group mean. **(B - E)** Single cell suspension prepared from the various tissues of infected mice were stimulated with soluble anti-CD3 mAb for 5 hours ex vivo before intracellular cytokine staining. Representative flow cytometry plots (left) and summary data (right) of the percentage of IFN- γ producing **(B)** CD8⁺ and **(C)** CD4⁺ T cells in lung and liver. Representative flow cytometry plots showing intracellular cytokine staining in **(D)** CD8⁺ and **(E)** CD4⁺ T cells in BAT and WAT.

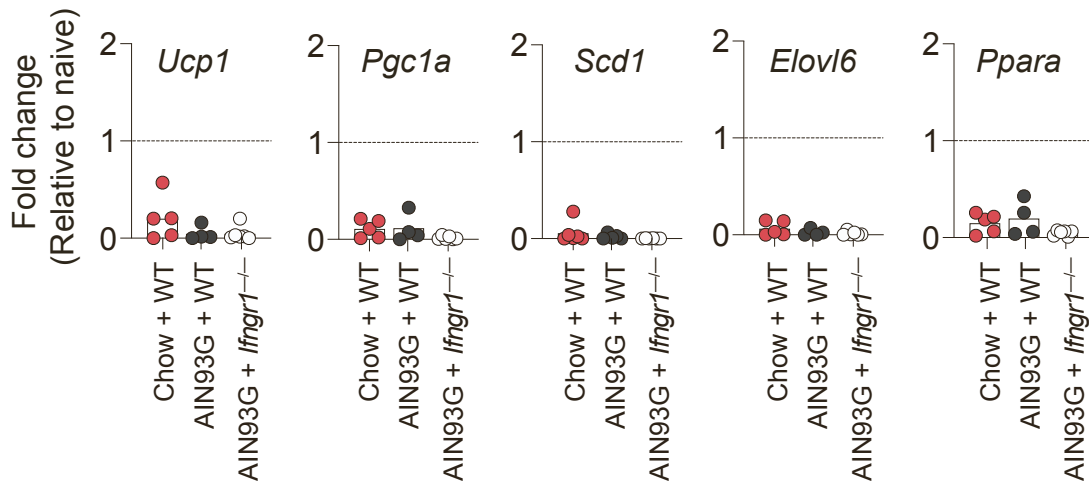


Figure S2. IAV infection downregulates thermogenic genes in the BAT irrespective of diet regime or presence of IFN- γ signalling. WT and *Ifngr1*^{-/-} mice (n = 4 – 5) fed with chow or AIN93G diets ad libitum for 3 weeks were infected with 2.5 PFU IAV i.n.. Data shown are fold change in mRNA expression in the BAT of the infected mice over naïve chow-fed mice as measured by qRT-PCR at day 9 p.i. Symbols represent individual mice and bars denote group mean. Dotted lines indicate the gene expression levels of naïve chow-fed mice.

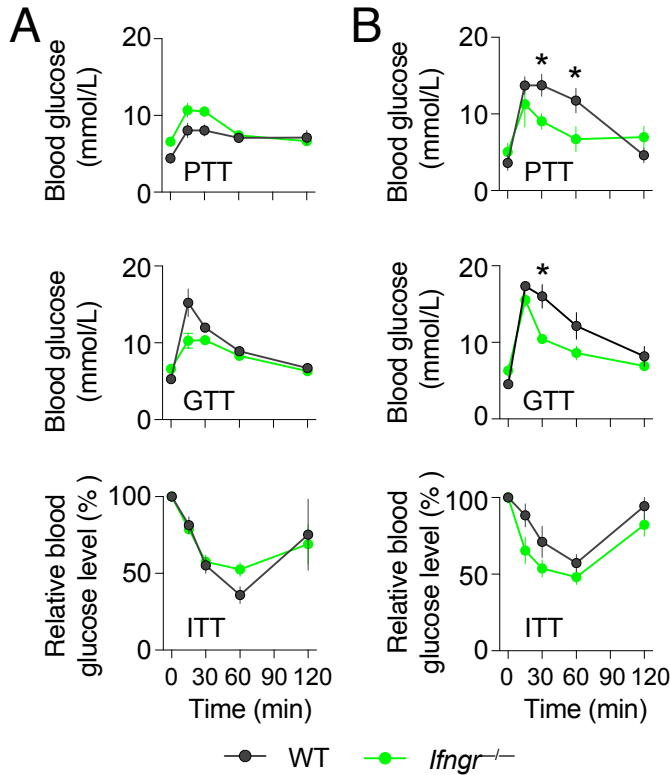


Figure S3. IFN- γ modulates glucose metabolism in IAV-infected AIN93G-fed mice. WT and *Ifngr*^{-/-} mice (n = 5) fed with AIN93G diets for 3 wks were infected with 2.5 PFU IAV i.n.. PTT, GTT, ITT were performed **(A)** before and **(B)** 9 days after IAV infection. Data shown are mean blood glucose levels \pm SD determined in PTT and GTT, or mean percentage \pm SD of baseline glucose levels measured at time 0 in ITT. Statistical analysis was performed using two-way repeated-measures ANOVA. *p < 0.05.

Table S3: List of qRT-PCR primer sequences. Related to STAR Methods

Gene	Forward (5')	Reverse (3')
18S	GTAACCCGTTGAACCCCAT	CCATCCAATCGGTAGTAGCG
Elovl6	TCAGCAAAGCACCCGAAC	AGCGACCATGTCTTTGTAGGAG
IAV NP	CAGCCTAATCAGACCAAATG	TACCTGCTTCTCAGTTCAAG
Ifna	TGCAACCCTCCTAGACTCATT	CCAGCAGGGCGTCTTCCT
Ifnb	ATGAGTGGTGGTTGCAGGC	TGACCTTTCAAATGCAGTAGA
Ifng	ACAATGAACGCTACACACTGCAT	TGGCAGTAACAGCCAGAAACA
Il1b	CAACCAACAAGTGATATTCTCCATG	GATCCACACTCTCCAGCTGCA
Nos2	CAGCTGGGCTGTACAAACCTT	CATTGGAAGTGAAGCGTTTCG
Pgc1a	GGACATGTGCAGCCAAGACTCT	CACTTCAATCCACCCAGAAAGCT
Ppara	TATGGAGTGACATAGAGTGTGCT	CCACTTCAATCCACCCAGAAAG
Scd1	TTCTTGCGATACACTCTGGTGC	CGGGATTGAATGTTCTTGTCG
Tnfa	AATGGCCTCCCTCTCATCAGTT	CCACTTGGTGGTTTGCTACGA
Ucp1	GTGAAGGTCAGAATGCAAGC	GGCAGTTGCCTAGTGAAAGGT