Supplementary Material

Loss of interleukin-1 beta is not protective in the lupus-prone NZM2328 mouse model

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1 Supplementary Figures and Tables

1.1 Supplementary Figures

Supplementary Figure 1

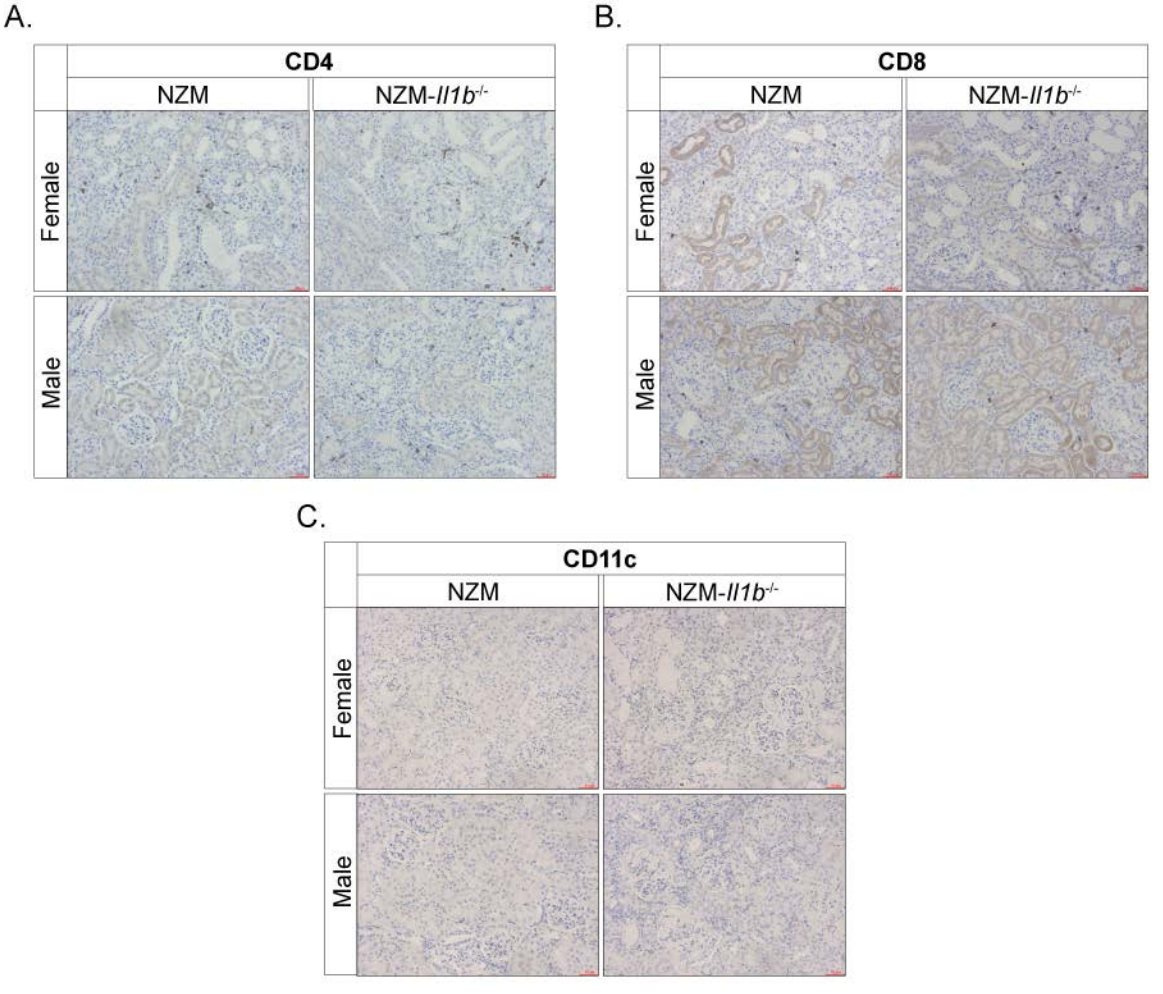
Supplementary Figure 2

Supplementary Figure 3

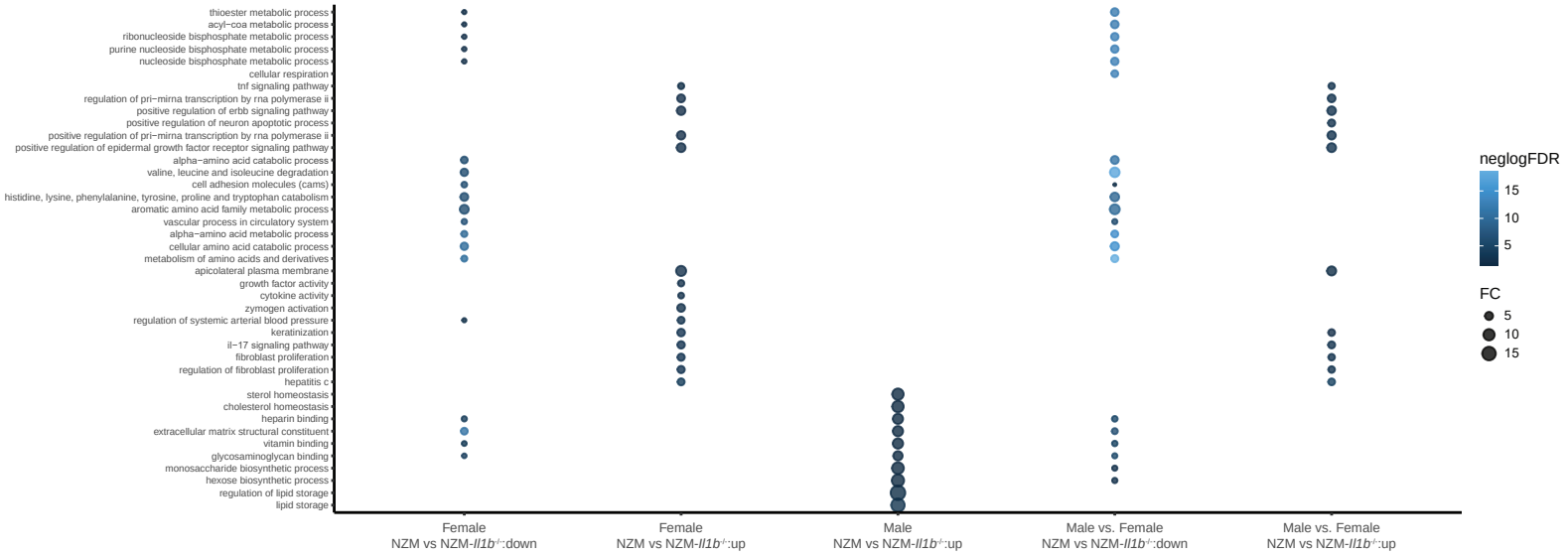
1.2 Supplementary Tables

Supplementary Table 1

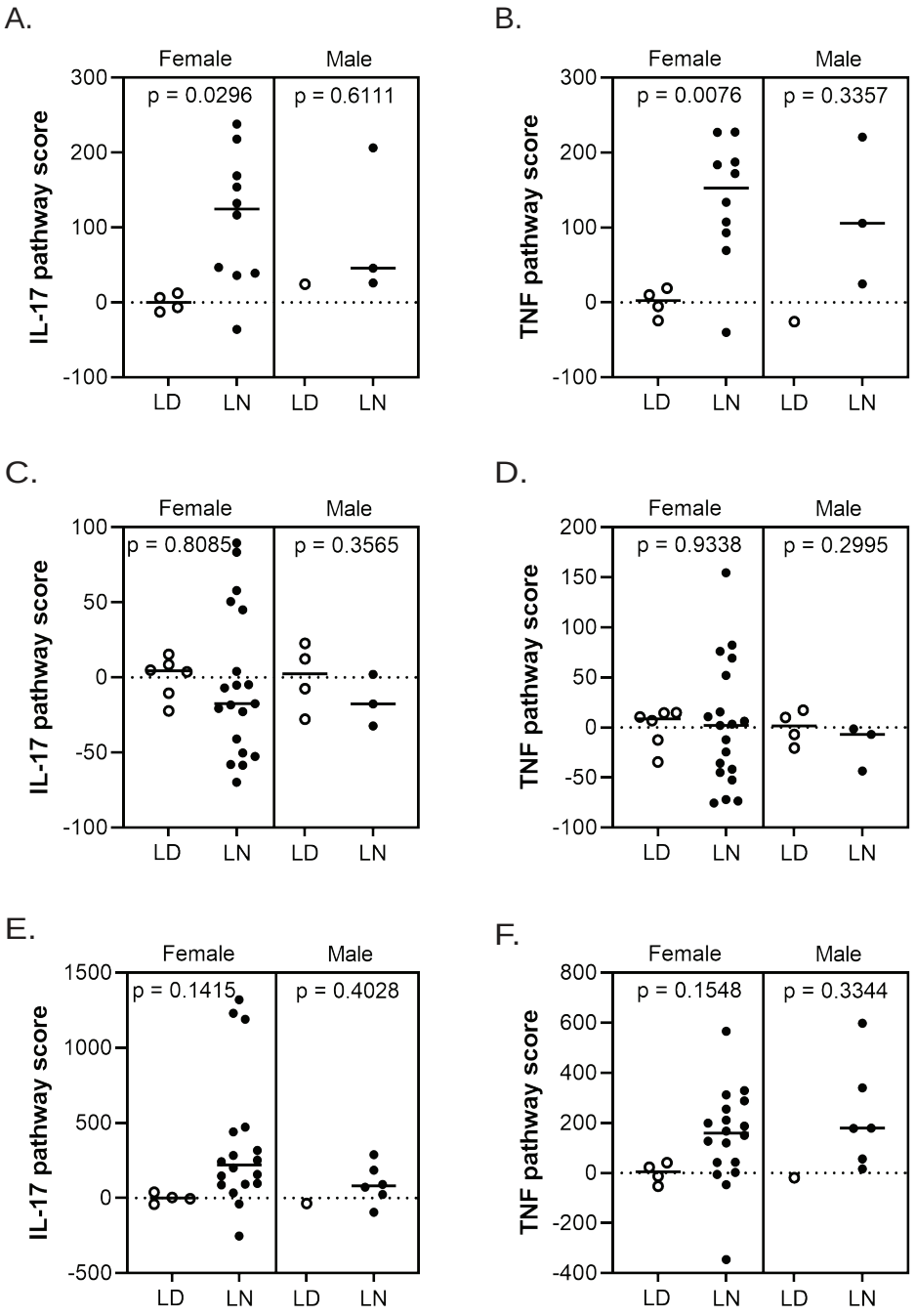
Supplementary Table 2



Supplementary Figure 1. Representative images of kidneys stained with (**A**) CD4, (**B**) CD8, and (**C**) CD11c.



Supplementary Figure 2. Pathway analysis of differentially expressed genes between NZM and NZM-*Il1b*$^{-/-}$ kidneys highlighted the TNF ($p=7.59x10^{-5}$) and IL-17 signaling ($p=1.21x10^{-6}$) pathways among the top regulated pathways.



Supplementary Figure 3. RNA-sequencing gene expression analysis of **(A)** IL-17 and **(B)** TNF pathway scores in the glomerular compartment of human lupus nephritis (LN) and healthy living donor (LD) biopsies: IL-17 and TNF signaling pathway scores were significantly higher in female LN (n=10) compared to LD controls (n=4) (p=0.0296 and 0.0076 respectively), but not in males (n=1 LD and 3 LN) (p=0.6111 and 0.3357 respectively). Microarray gene expression analysis of **(C)** IL-17 and **(D)** TNF pathway scores in the tubulointerstitial compartment of human LN and LD biopsies: IL-17 and TNF signaling pathway scores were not significantly different in female LN (n=19) compared to LD controls (n=6) (0.8085 and 0.9338, respectively) or in males (n=4 LD and n=3 LN) (p=0.3565 and 0.2995, respectively). RNA-sequencing gene expression analysis of **(E)** IL-17 and **(F)** TNF pathway scores in the tubulointerstitial compartment of human LN and LD biopsies: IL-17 and TNF signaling pathway scores were not significantly different in female LN (n=18) compared to LD controls (n=4) (p=0.1415 and 0.1548, respectively) or in males (n=1 LD and 6 LN) (p=0.4028 and 0.3344, respectively).