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Supplemental information

Chronic stress primes innate immune responses in mice and humans

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Supplementary Materials

Fig. S1. Body Weight, Blood Glucose, Total Cholesterol, Triglycerides and Insulin Levels of Control and Stressed mice

Fig. S2 Akt-PI3K Signaling Pathway in Monocytes from Stress and Control Mice

Fig. S3. Fatty Acid Oxidation Pathway in Monocytes from Stress and Control Mice

Fig. S4. Stress Alters the Human Blood Transcriptional Profile

Fig. S5. Basal cytokine production in monocyte purified PBMCs from low stress and high stress subjects.

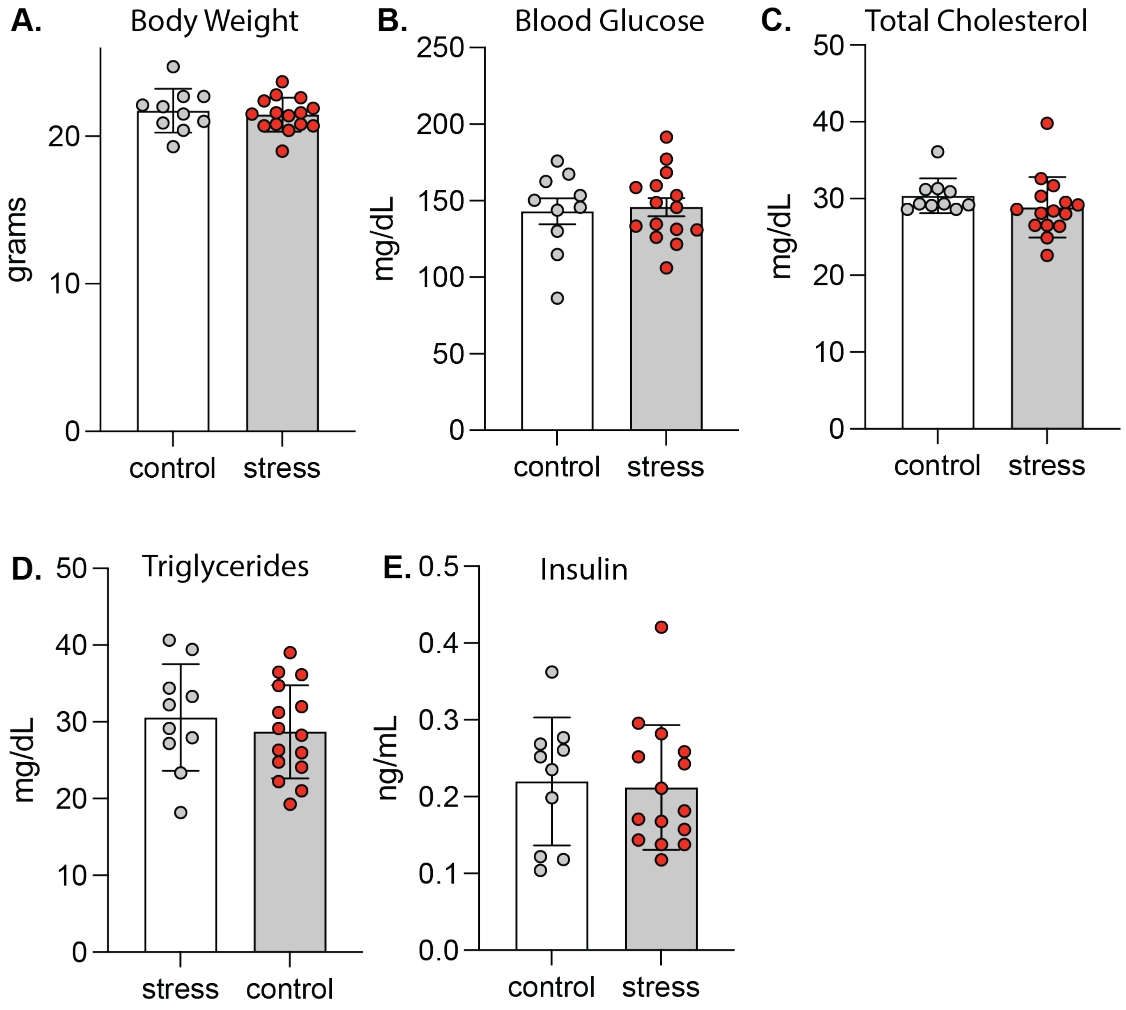


Fig. S1. Body Weight, Blood Glucose, Total Cholesterol, Triglycerides and Insulin Levels of Control and Stressed mice. Related to figure 1.

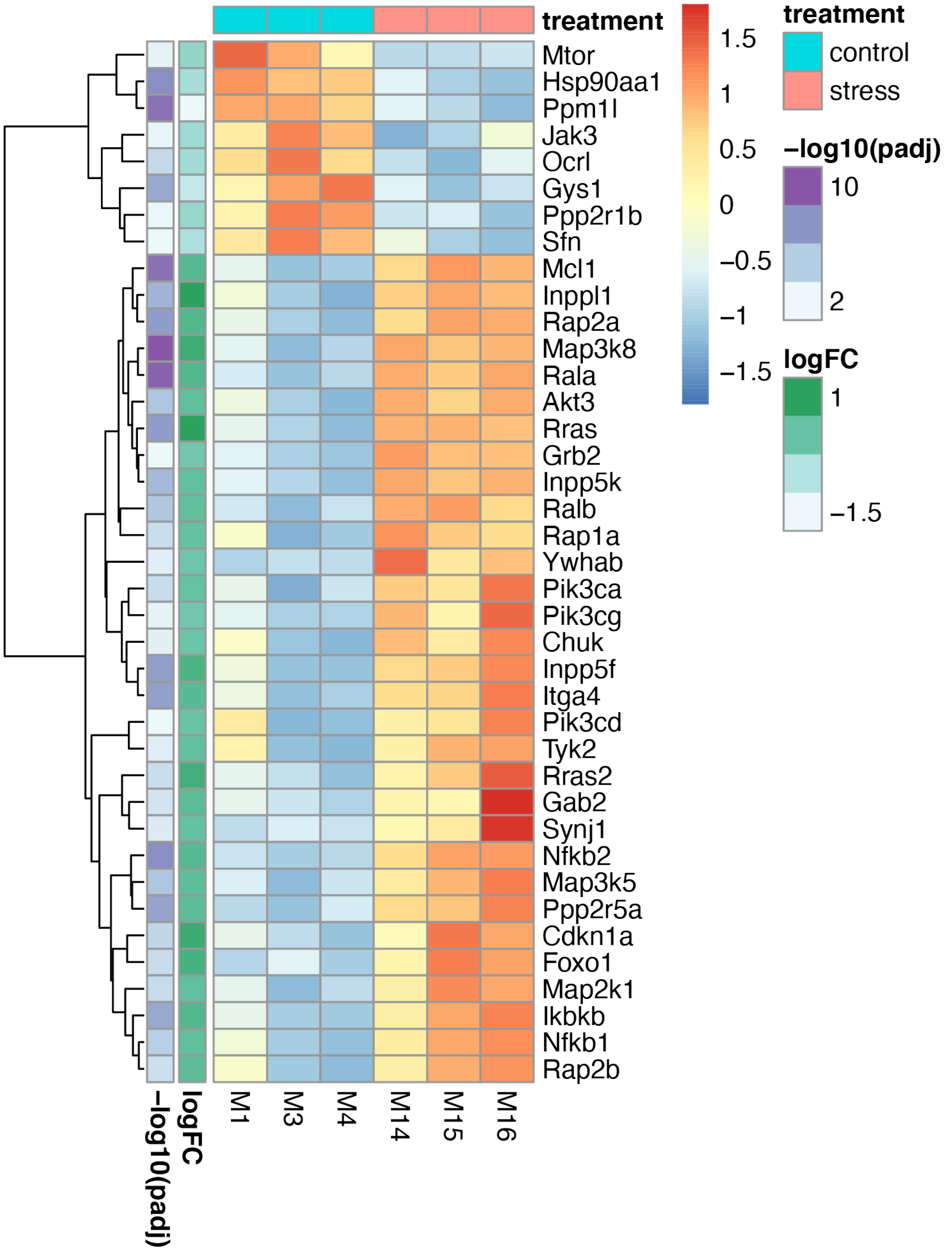


Figure S2. Akt-PI3K Signaling Pathway in Monocytes from Stressed and Control Mice

Heatmap showing the RNA-Seq gene expression profile of the *Akt-PI3K pathway* in monocytes from mice exposed to chronic variable stress and control mice (n = 6, 3 mice per phenotype). Related to figure 4.

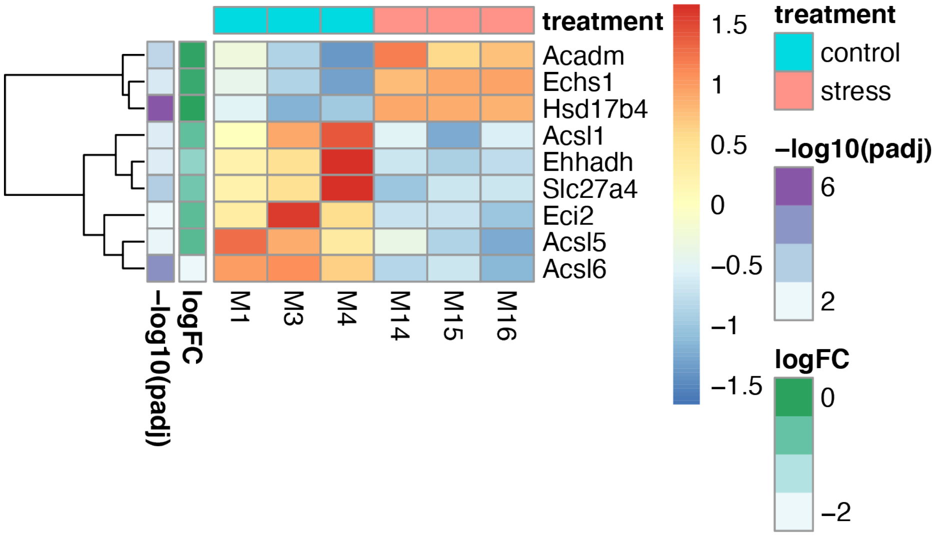
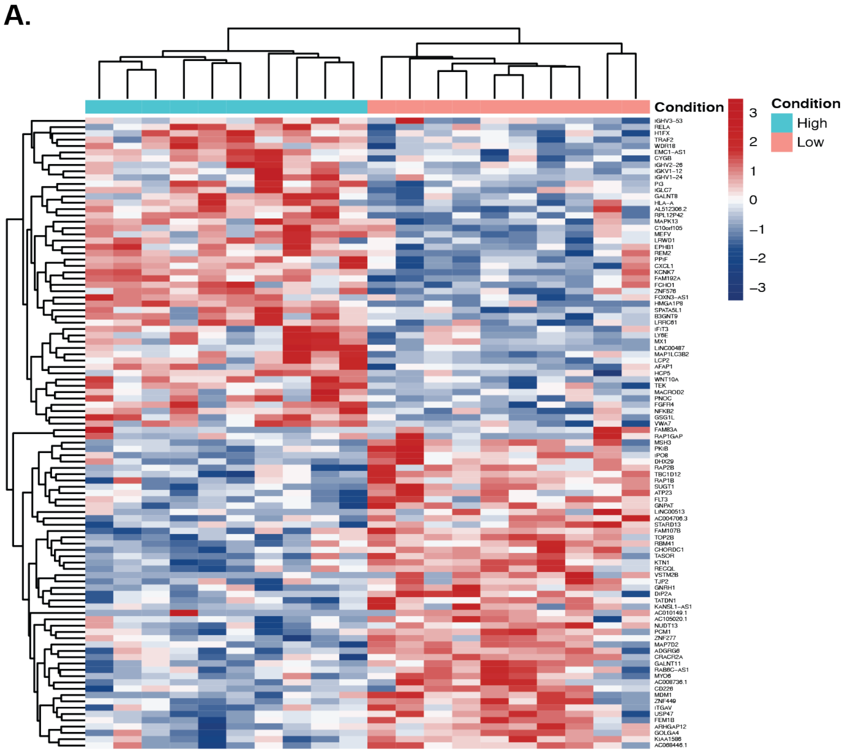


Figure S3. Fatty Acid Oxidation Pathway in Monocytes from Stress and Control Mice

Heatmap showing the RNA-Seq gene expression profile of the *fatty acid oxidation pathway* in monocytes from mice exposed to chronic variable stress and control mice (n = 6, 3 mice per phenotype). Related to figure 4.



B.

Pathway	P-value
Upregulated	
Interferon Signaling	1.2×10^{-6}
B Cell Development	6.6×10^{-6}
IL-6 Signaling	2.5×10^{-4}
NF-kB Signaling	3.7×10^{-4}

Figure S4. Stress Alters the Human Blood Transcriptional Profile

(A) Heatmap of the top 100 DE transcripts identified by RNA-Seq (Illumina HiSeq4000 Sequencing) of blood of low stress (PSS-4 < 5, n = 10) and high stress (PSS-4 > 5, n = 10) human subjects. Subjects were clustered in hierarchical condition trees with each row representing a single gene and each column an individual subject. **(B)** Canonical pathways upregulated and downregulated by stress as determined by Ingenuity Pathway Analysis of significantly DE transcripts in high stress versus low stress subjects ($p < 0.05$). Related to figure 5.

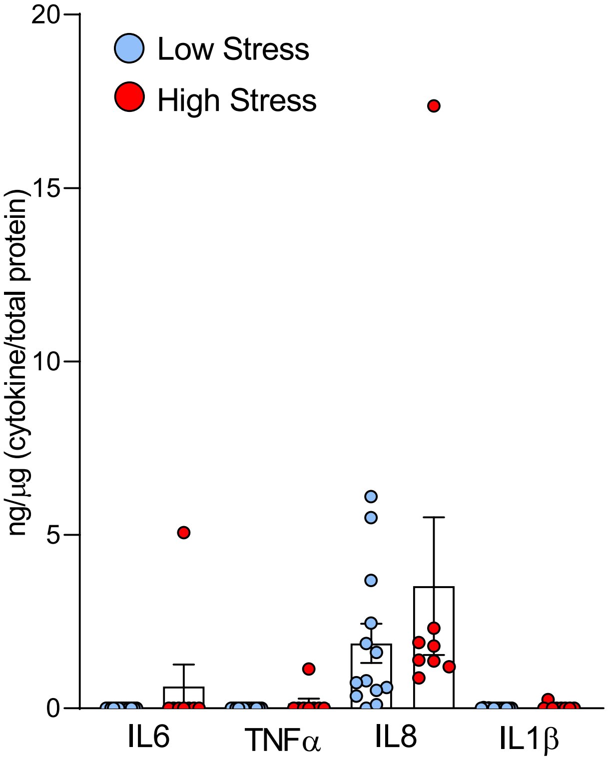


Figure S5. Basal cytokine production in monocyte purified PBMCs from low stress and high stress subjects.

Basal cytokine production in monocyte purified PBMCs from low stress and high stress subjects. Data are mean ± s.e.m. Related to figure 5.

Supplemental Table 6. Demographics of Women for Blood Transcriptome RNA-Seq Analysis. Related to Figure 5.

	Low Stress	**High Stress**
n	15	12
PSS4 score (median, IQR)	3 [2-4]	7.5 [5.5-9]
Age (median, IQR)	64 [61-70]	62.5 [57-70.5]
Race (White, %)	86.7	100.0
BMI	26.7 (23.9, 28.9)	26.6 (23.5, 34.7)
Ethnicity (Hispanic, %)	46.7	58.3
Peak Cardiac Troponin (ng/mL, median, IQR)	2.3 [0.75-13.6]	2.5 [0.36-5]
Diabetes (%)	33.3	33.3
Hypertension (%)	33.3	66.7
Dyslipidemia (%)	66.7	50.0
Smoking (Current, %)	13.3	8.3
Aspirin (%)	86.7	100.0