

Dissecting genetic mechanisms of differential locomotion, depression, and allodynia after spinal cord injury in three mouse strains

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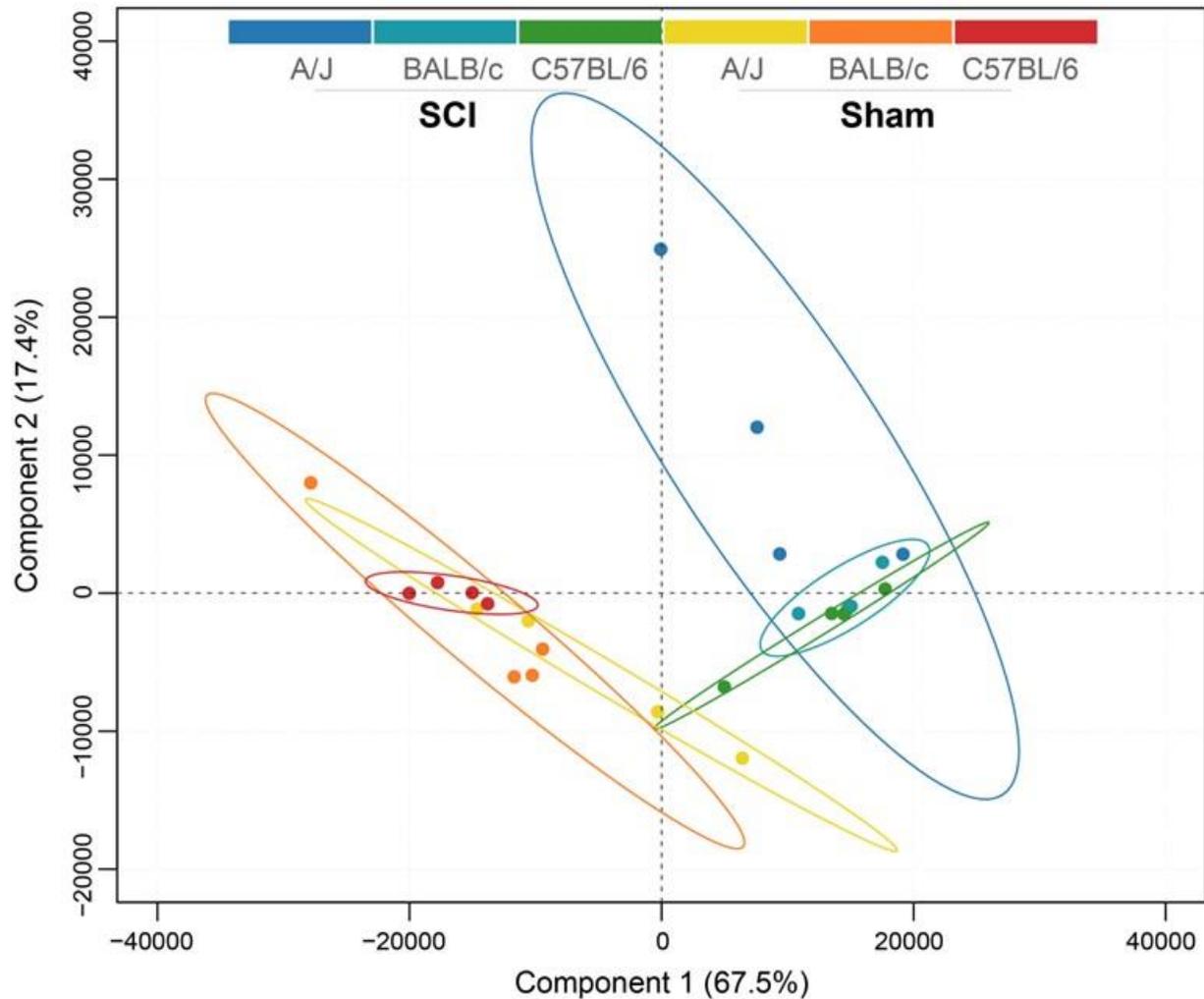
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Supplementary Information

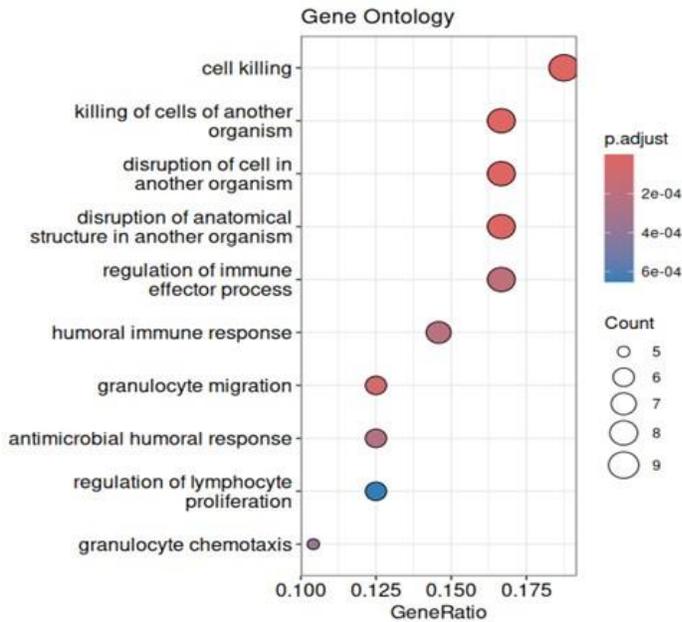
Supplemental Information includes Supplemental two figures and figure legends.

RNAseq replicates



Supplementary Figure 1. Transcriptional profiles in the spinal cord tissue are dysregulated in three mouse strains at 8 weeks after moderate/severe SCI. Bulk RNA-seq was performed on sham or injured spinal cord tissue from A/J, BALB/C, and C57BL/6 mice. Principal component analysis (PCA) of all normalized gene counts revealed a clear separation of sham and SCI samples into individual groups across the first two principal components. n=4 mice/group.

A. Cluster 5: Highly upregulated in all the three strains



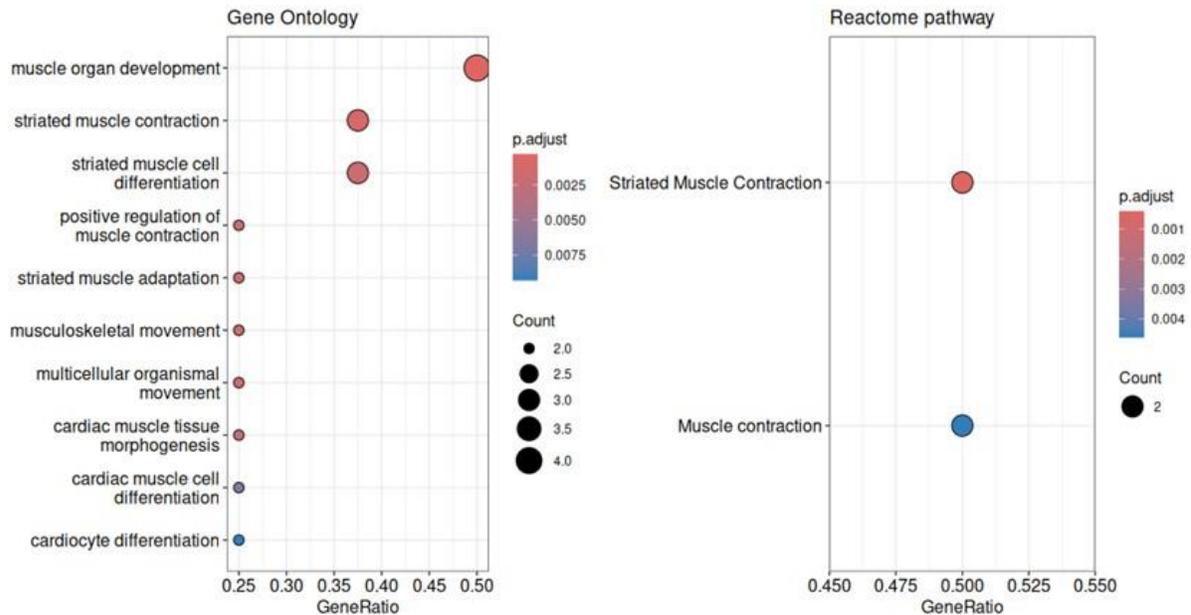
Immune genes:

C6, Cd22, Clec7a, Cxcl1, H2-M2, Lgals3, Lilrb4b, Tnfsf18

B. Cluster 2: Upregulated in the other strains, but not in A/J mice

There is no particular enrichment of GO or pathway terms in this cluster.

C. Cluster 9: Downregulated ONLY in BALB/c



D. Cluster 7: Downregulated genes with the injury.

The genes in this cluster are about 50% more downregulated in C57BL/6.

Supplementary Figure 2. Gene ontology (GO) analysis showed the results for cluster 5, 2, 9, and 7, respectively. (A-B) GO analysis of cluster 5 (**A**) showed highly upregulated immune genes in response to injury in all three mouse strains. Cluster 2 (**B**) showed upregulated genes in the other strains, but not in A/J mice. **(C-D)** GO analysis of cluster 9 (**C**) showed downregulated genes in BALB/c mice. Cluster 7 (**D**) showed downregulated genes in all three mouse strains after SCI. Dot sizes indicate the number of genes with the enriched GO terms, and colors indicate the significance levels. Gene ratio on x-axis (A, C) indicates % of genes in a GO term compared to the total number of genes in that category. GO terms are abbreviated for brevity. n=4 mice/group.