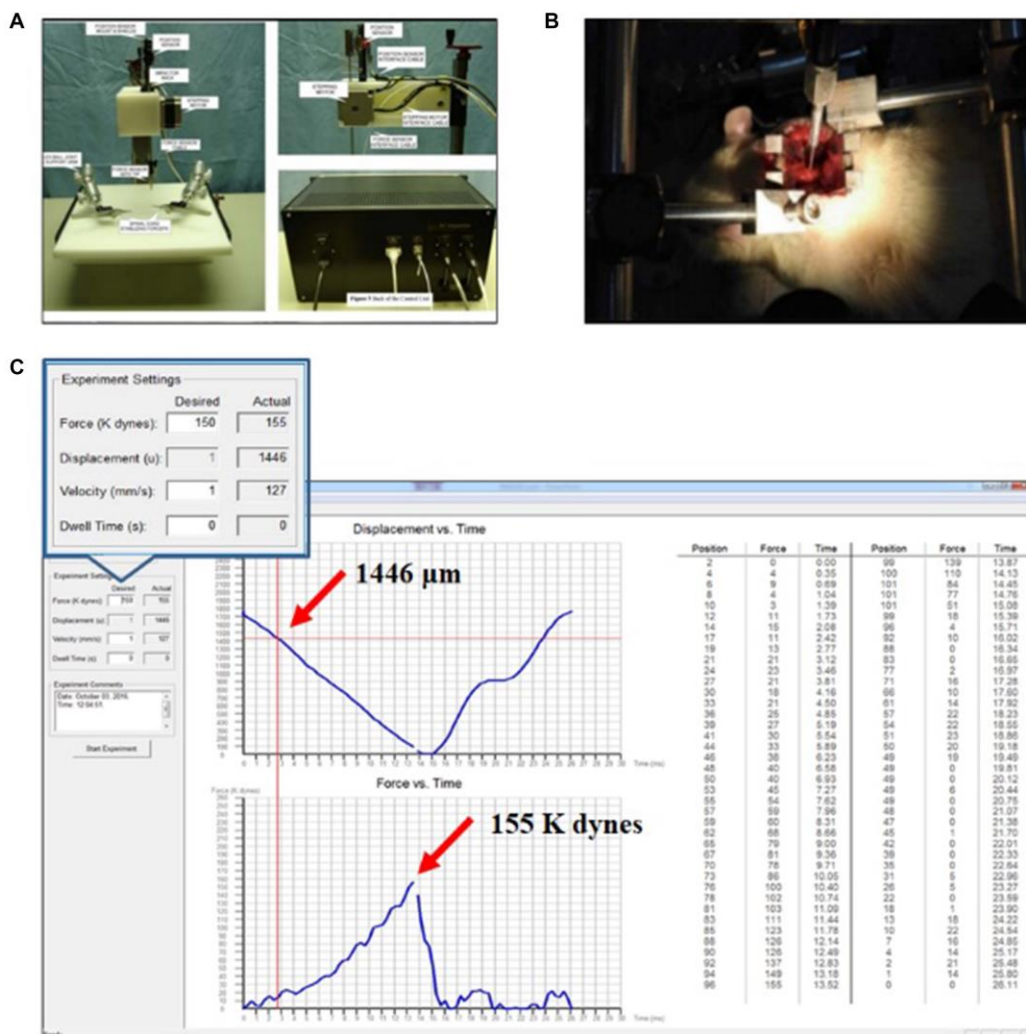
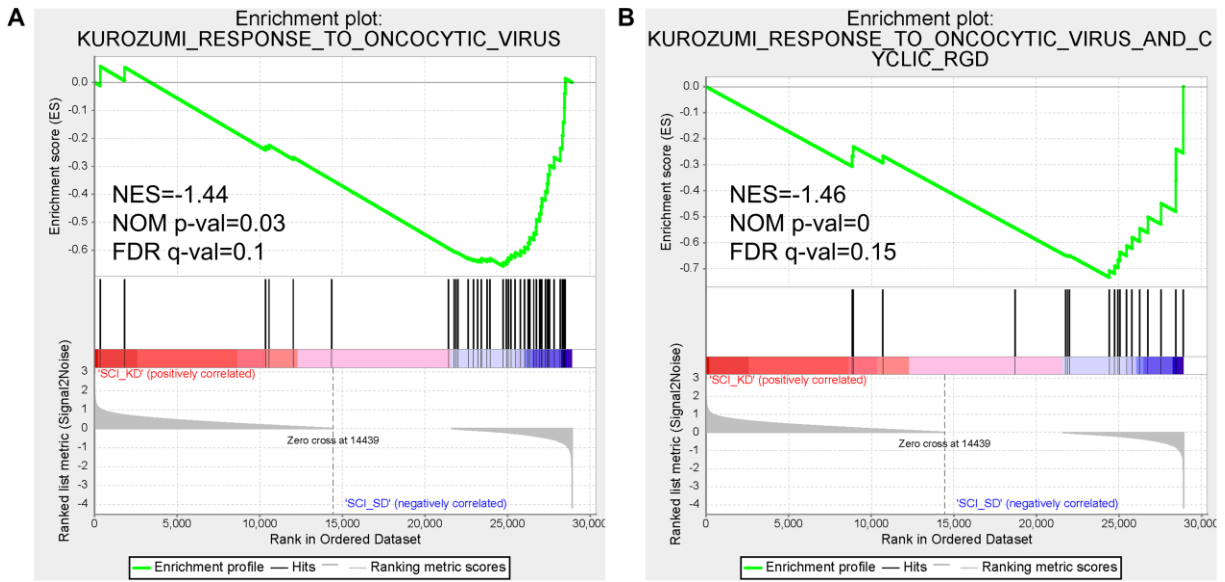


SUPPLEMENTARY FIGURES

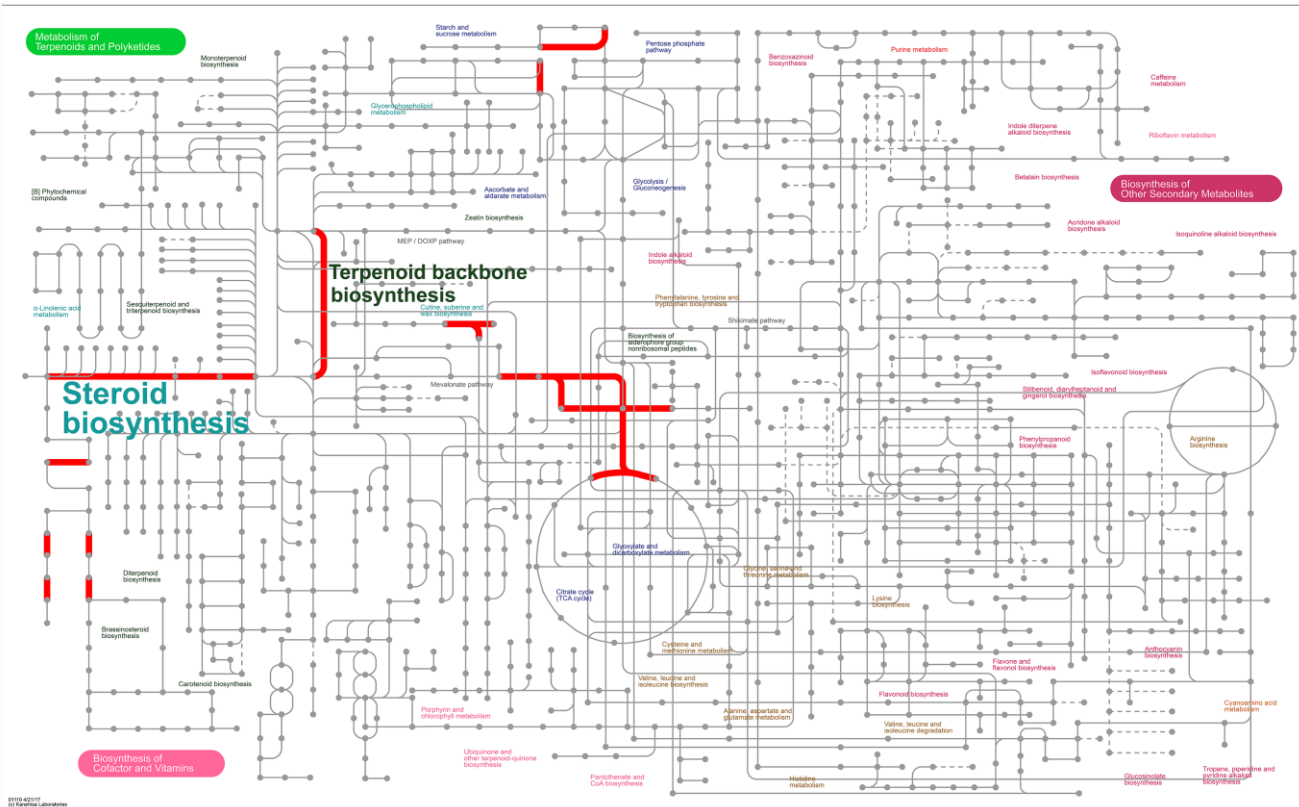


Supplementary Figure 1. Verification of C7 spinal cord hemi-contusion models. (A) Representative images of Infinite Horizon impactor. **(B)** Representative images of C6-T1 vertebrae fixed in a frame tilted at a 25.0° angle. **(C)** Representative images of monitoring data after striking by the Infinite Horizon impactor.

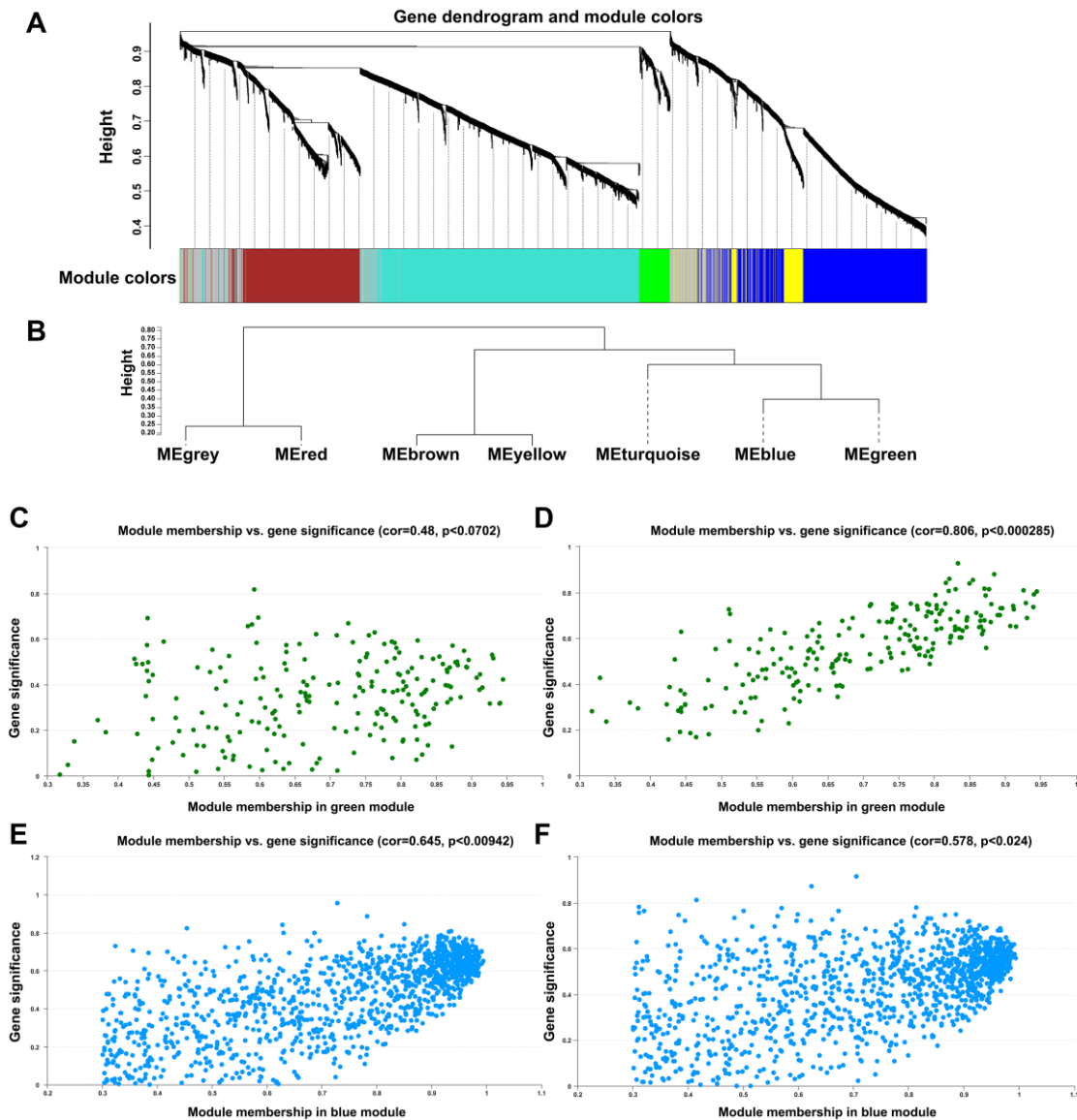


Supplementary Figure 2. GSEA showing that SCI_KD and D are significantly negatively correlated with inflammatory cytokines and their receptors, and the NES values are -1.44 (A) and -1.46 (B), respectively.

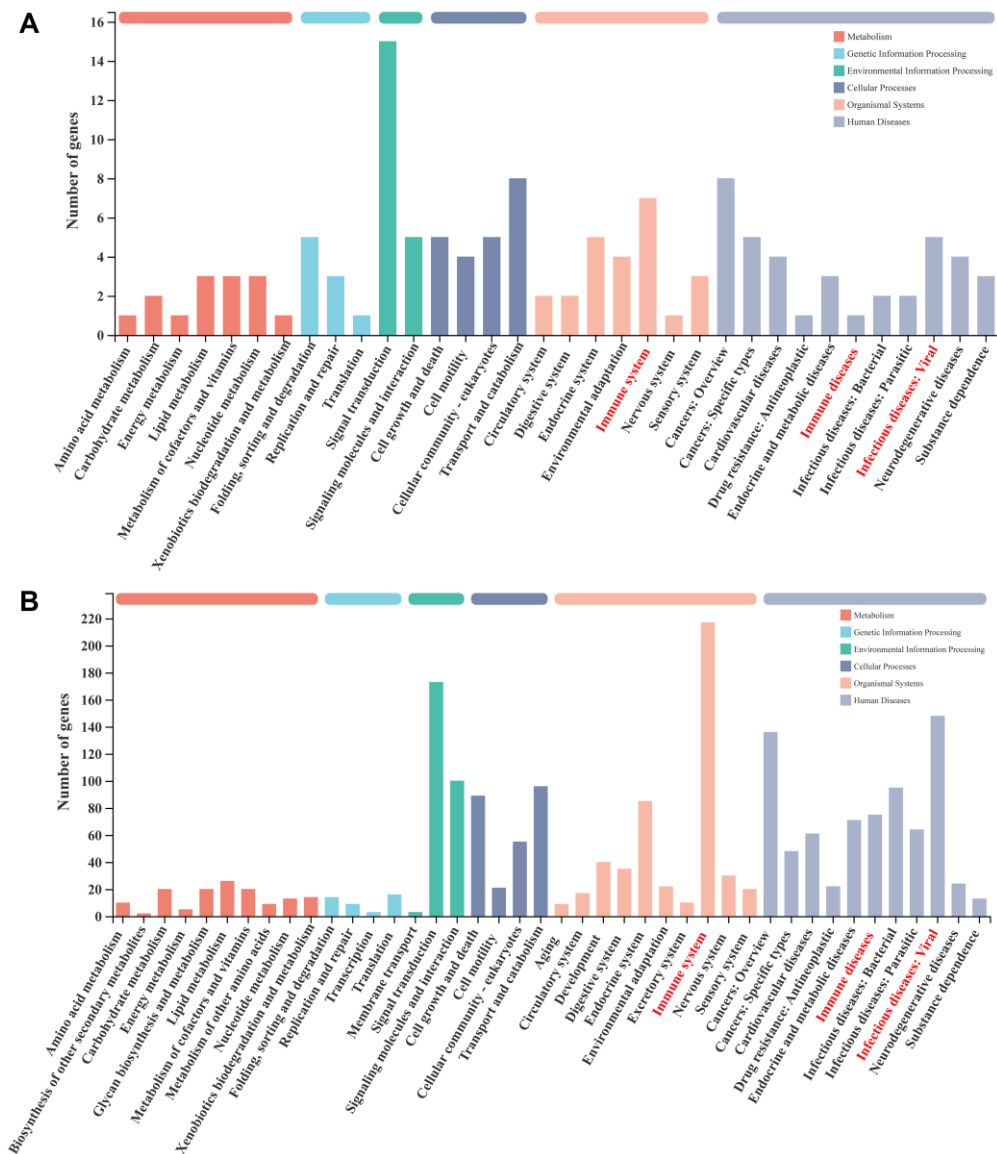
Secondary metabolites



Supplementary Figure 3. Visual analysis of enriched steroid metabolism-related genes using iPath3.0.



Supplementary Figure 4. Visualization of WGCNA analysis features. (A) Module clustering tree diagram display, in which branches represent a module. The closer two modules are branched, the closer the distance between the two modules. (B) Gene clustering tree (dendrogram) obtained by hierarchical clustering based on adjacent dissimilarity. (C–D) MM-GS analysis of the MEgreen module, in which C shows the SCI group, and D shows the Sham group. (E–F) MM-GS analysis of the MEblue module, in which E shows the SCI group, and F shows the Sham group.



Supplementary Figure 5. Analysis of WGCNA module genes by KEGG pathway annotation. (A) The KEGG pathway annotation analysis histogram of the MEgreen module. (B) The KEGG pathway annotation analysis histogram of the MEblue module, in which the red font indicates items with significant changes in the green and blue modules.