

Supplementary Figures

Figure S1. Cell-type composition, marker gene validation and NLRP3 pathway activation in mouse DRG.

Figure S2. Supervised machine-learning analysis of SGC versus other cell types within the injured DRG.

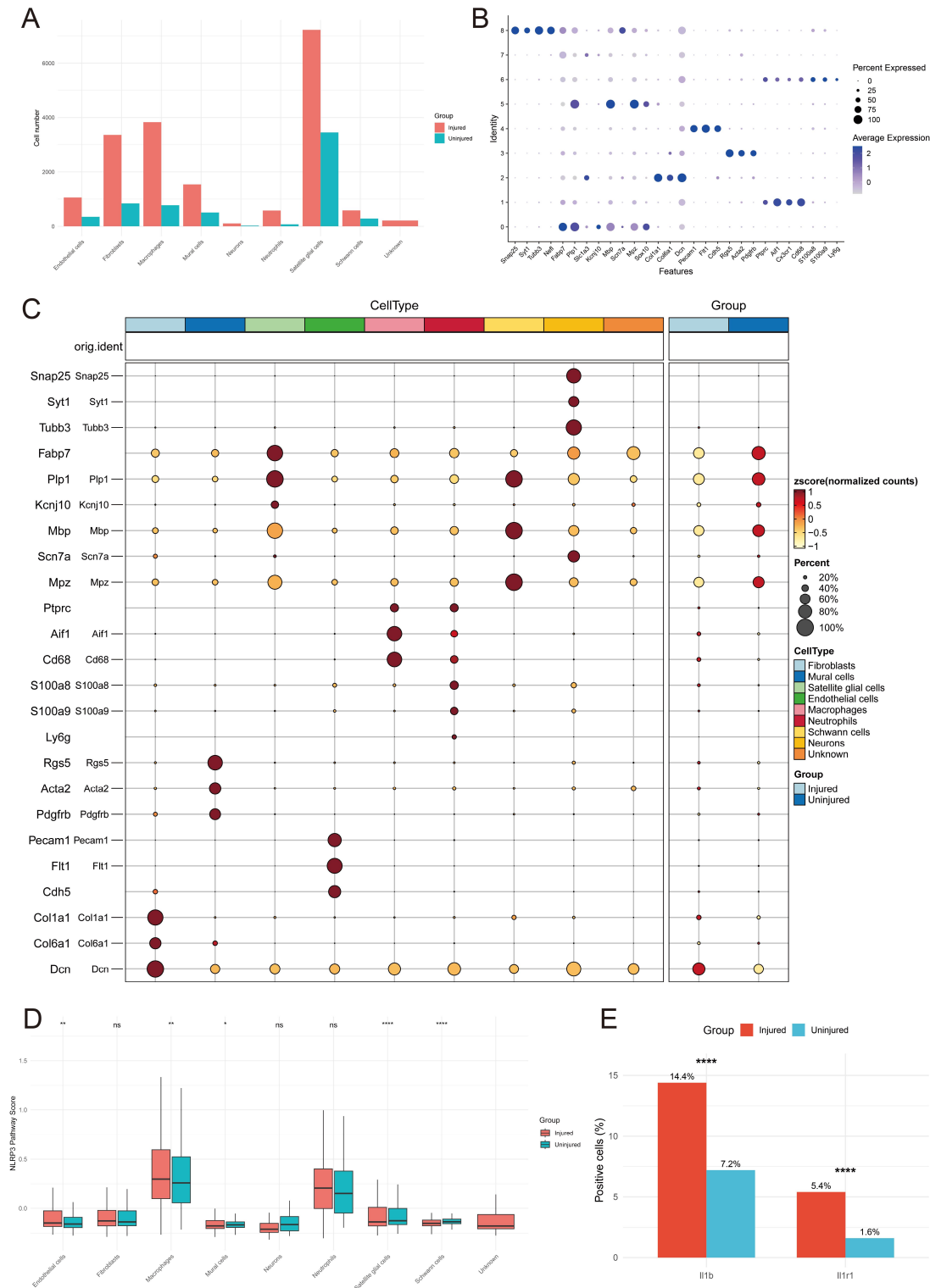


Figure S1. Cell-type composition, marker gene validation and NLRP3 pathway activation in mouse DRG.

(A) Bar plot showing the number of cells per cell type in Injured and Uninjured groups. Pink and green denote Injured and Uninjured groups, respectively. (B) Dot plot showing the expression of

canonical cell marker genes across nine annotated cell types. Dot size represents the percentage of expressing cells (Percent Expressed), and color gradient indicates z-score-normalized average expression level (Average Expression). (C) Dot plot showing the expression patterns of canonical cell marker genes across cell types and groups. The y-axis represents cell marker genes, and the x-axis represents groups. Two annotation bars are shown at the top: the first indicates cell type (CellType, nine annotated cell types) and the second indicates group (Group, Injured and Uninjured). Dot size represents the percentage of cells expressing the gene, and color gradient indicates z-score-normalized average expression level. The left panel displays marker gene expression across nine annotated cell types to validate cell-type annotation: for example, *Snap25*, *Syt1* and *Tubb3* were specifically expressed in neurons. The right panel displays the expression of the same marker genes between Injured and Uninjured groups to assess injury-induced changes in cell-type-specific marker gene expression. For example, satellite glial cell/Schwann cell markers such as *Fabp7*, *Plp1* and *Mbp* showed stronger expression in the Injured group, suggesting glial cell activation after injury. (D) Box plot showing NLRP3 pathway scores across cell types in Injured and Uninjured groups. Statistical significance was determined by Wilcoxon rank-sum test (* $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$; ns, not significant). (E) Bar plot showing the proportion of Il1b- and Il1r1-positive cells in Injured and Uninjured groups. The proportion of Il1b-positive cells was 14.4% in the Injured group versus 7.2% in the Uninjured group; the proportion of Il1r1-positive cells was 5.4% in the Injured group versus 1.6% in the Uninjured group (**** $p < 0.0001$).

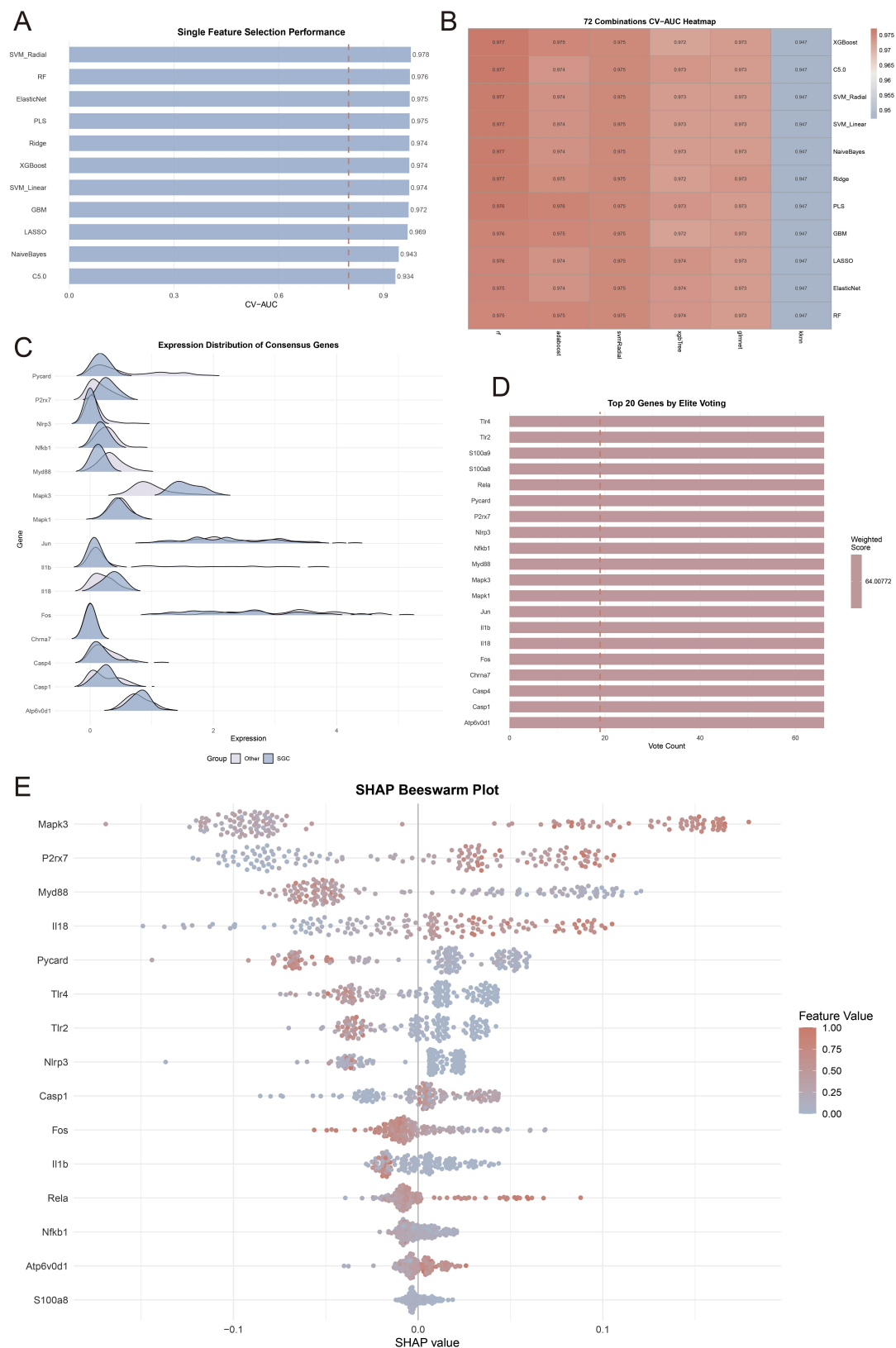


Figure S2. Supervised machine-learning analysis of SGC versus other cell types within the injured DRG.

(A) Bar plot showing the CV-AUC performance of 12 individual feature-selection algorithms. The

red dashed line denotes the pre-defined performance threshold of $CV-AUC = 0.9$ for screening elite model combinations. (B) Heatmap displaying CV-AUC values for all 72 combinations of feature-selection algorithms and downstream classifiers. Color gradient corresponds to the magnitude of CV-AUC. (C) Ridge plot showing the expression distribution of consensus genes between SGC and Other groups. Blue and grey curves denote gene expression in the two groups, respectively. (D) Bar plot of consensus genes ranked by weighted voting scores derived from elite model combinations. The vertical red dashed line indicates the voting threshold for consensus gene inclusion. (E) SHAP beeswarm plot interpreting the contribution of each consensus gene to SGC versus Other classification. Each dot corresponds to a metacell; dot color reflects gene expression value, and horizontal position represents the SHAP value indicating direction and magnitude of predictive effect.