

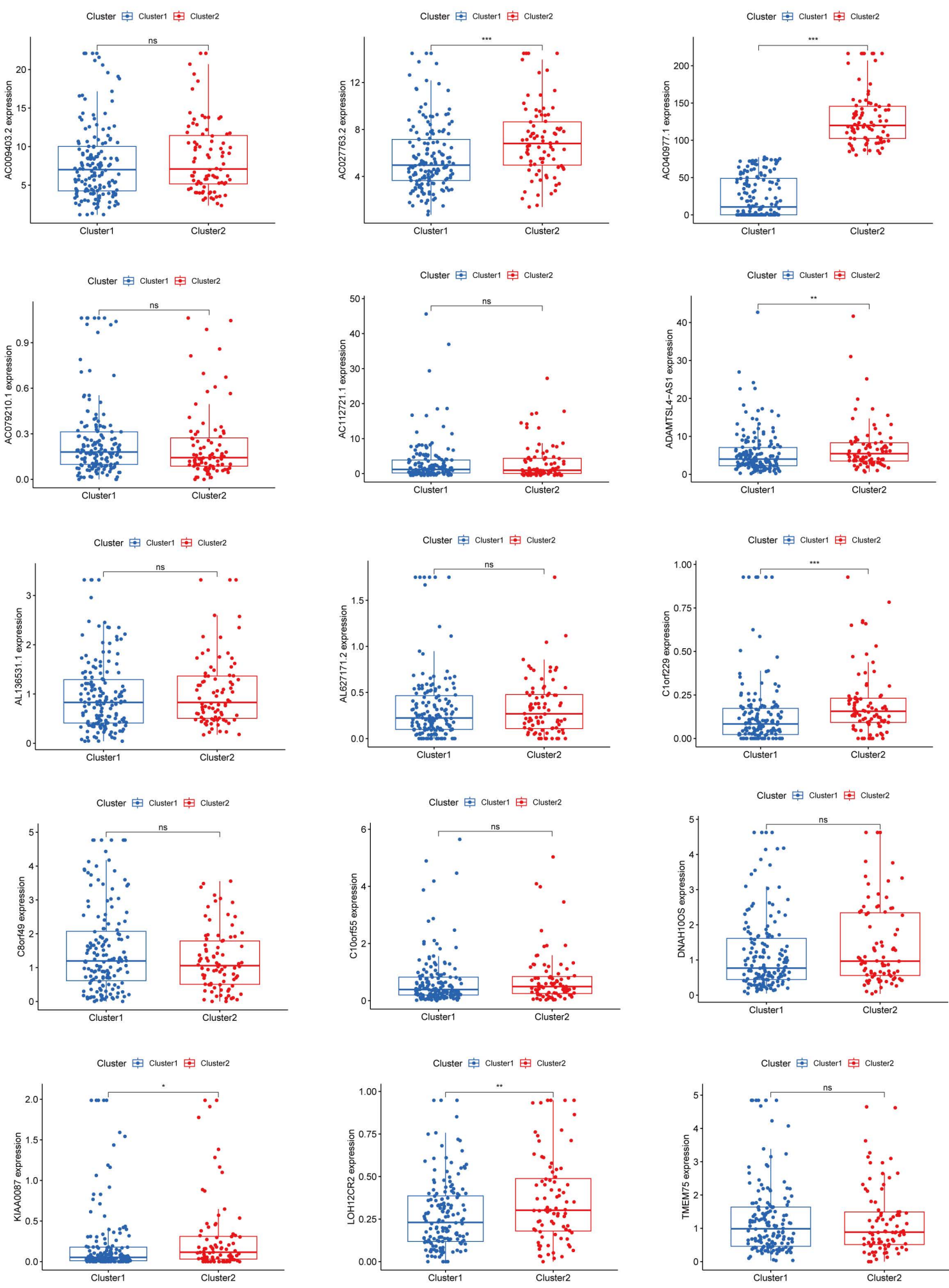
**Figure S1** Differential expression of 19 SR-lncRNAs between clusters

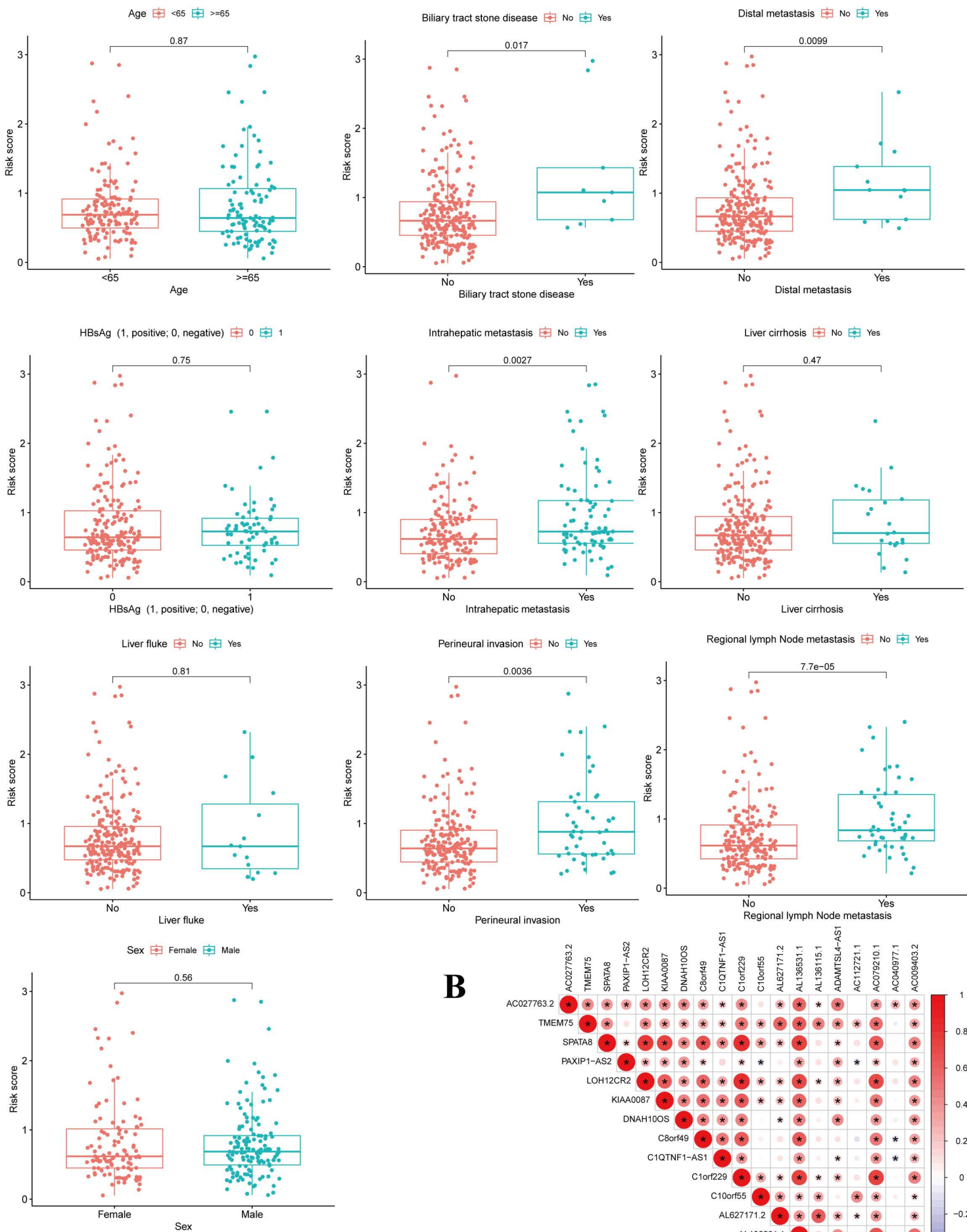
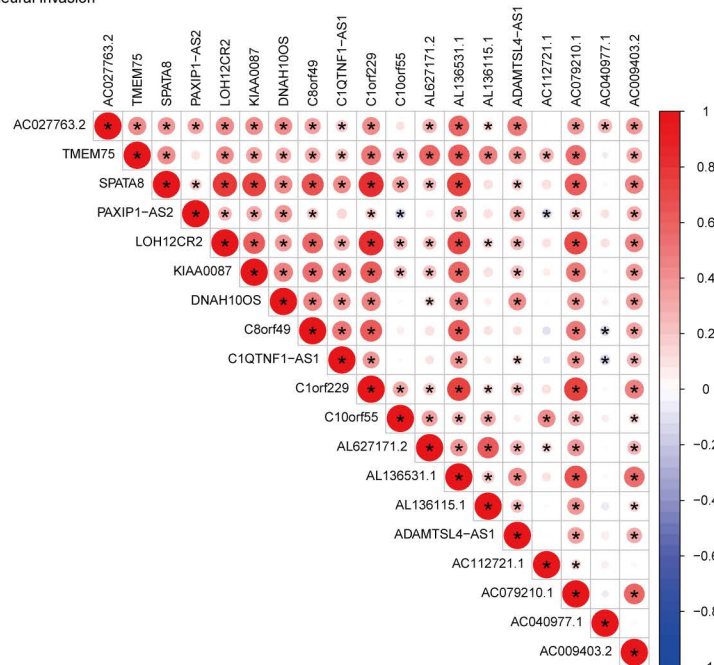
**Figure S2** (A) Relationship between clinical characteristics and SRLS scores. (B) Co-expression relationships between 20 SR-lncRNAs.

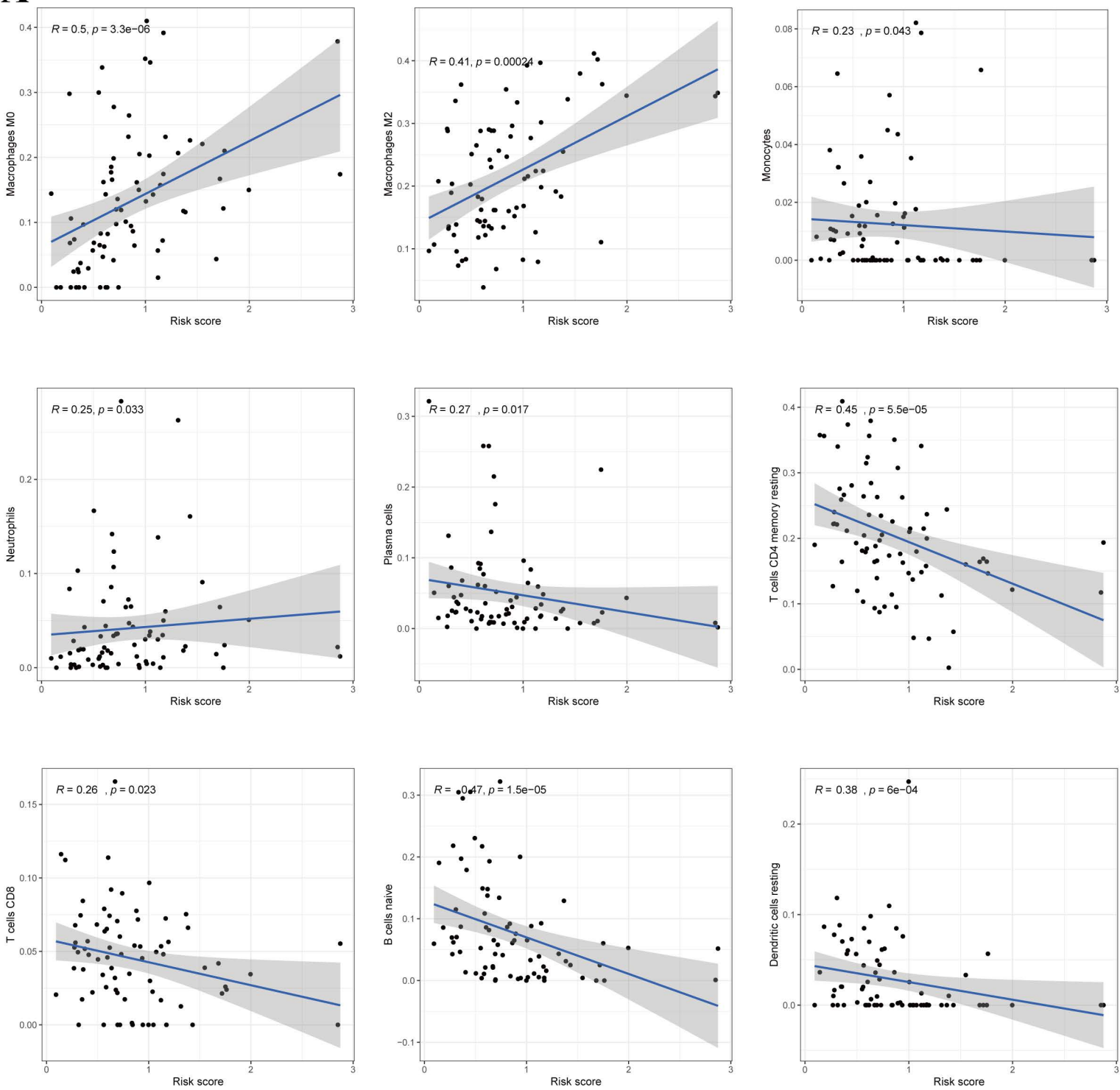
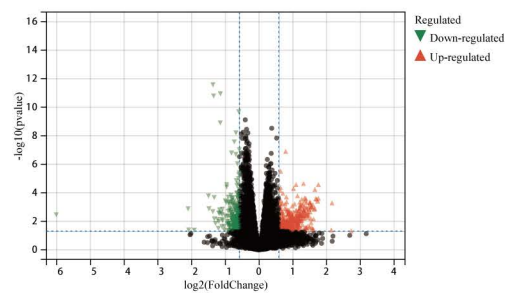
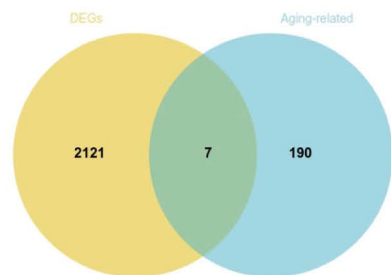
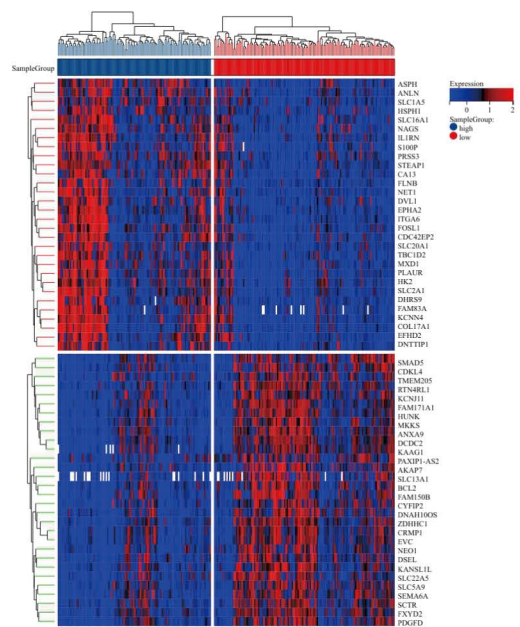
**Figure S3** (A) EPIC algorithm reveals correlation between immune cell infiltration and SRLS scores. (B) Volcano plot showing differential genes between high and low risk groups based on limma package. (C) Venn diagram showing intersection of SRGs with differential genes. (D) Clustering heatmap showing specific up-regulated differential genes vs. down-regulated differential genes.

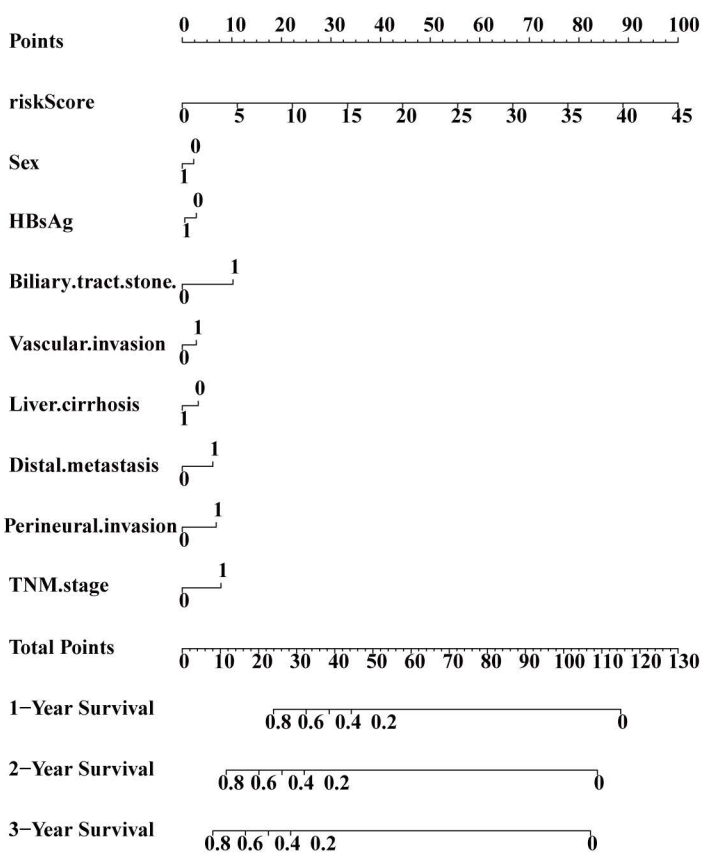
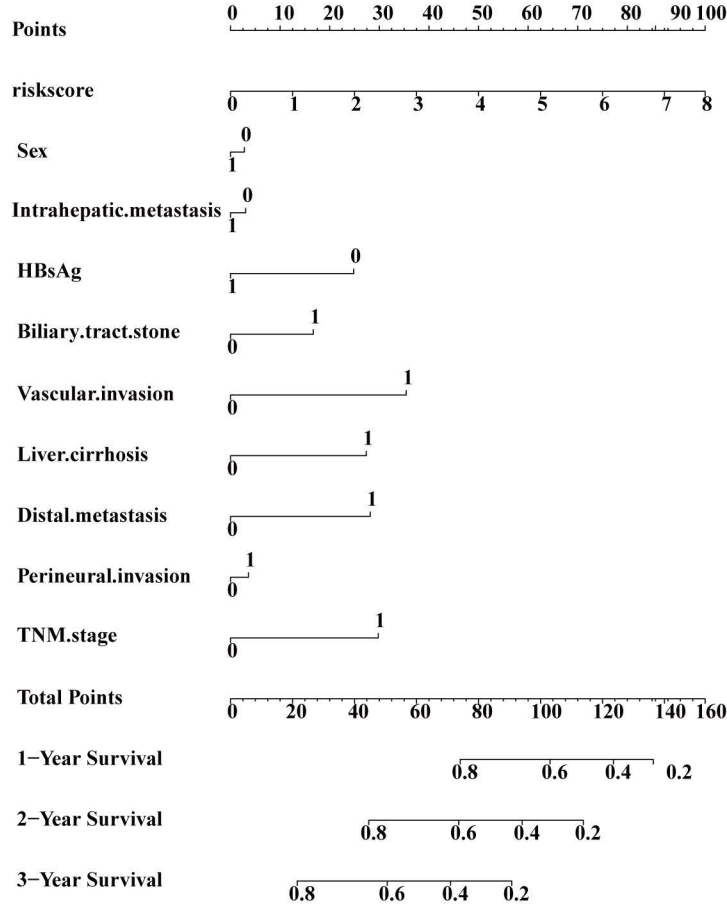
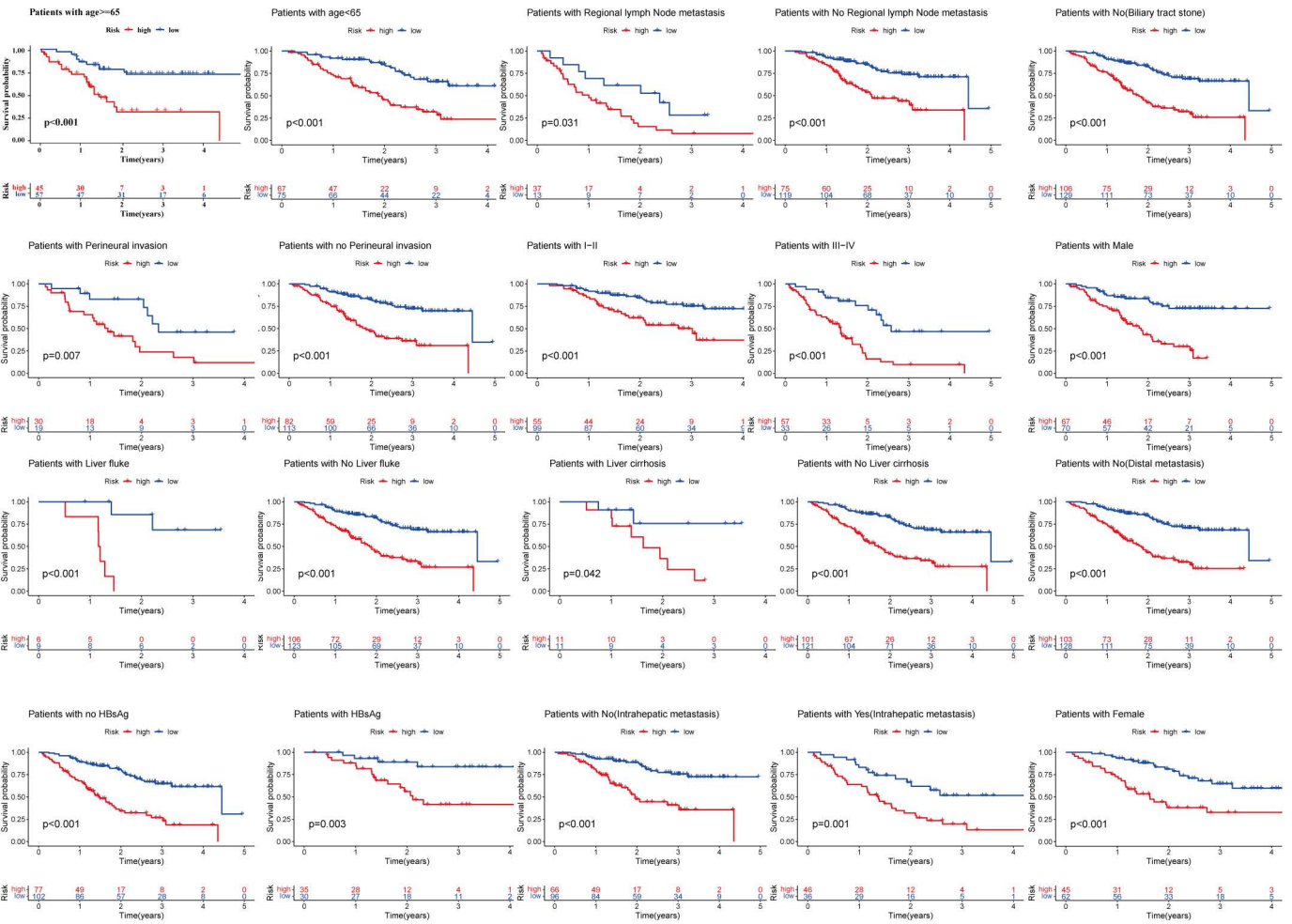
**Figure S4** (A,B) Nomograms developed by combining clinicopathological features and risk score in both test and training cohorts to assess the individual probabilities of 1-year, 2-year, and 3-year survival rates. (C) Subgroup survival analysis to assess the clinical applicability of SRLS.

**Figure S5** (A,B) Mutational landscapes of different SRLS subgroups.

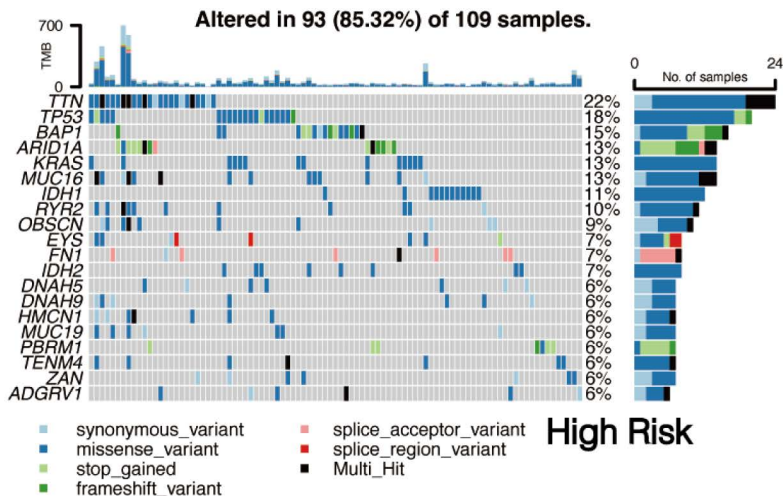


**A****B**

**A****B****C****D**

**A****B****C**

A



B

