

Identification and Validation of Necroptosis Landscape on Therapy and Prognosis in Skin Cutaneous Melanoma

Supplement_Figure

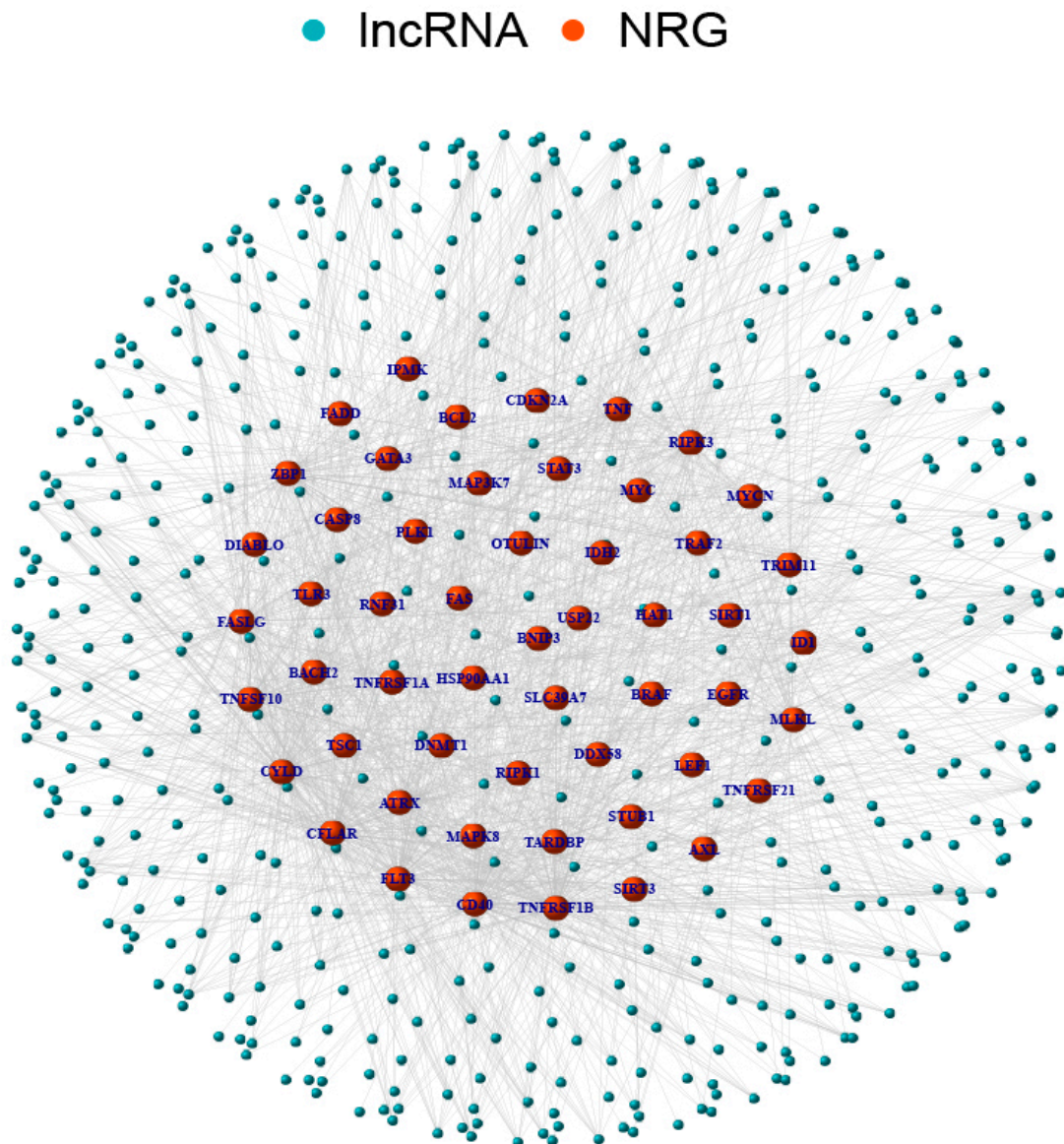


Figure S1 The network between necroptosis genes and lncRNAs in SKCM.
The network between necroptosis genes and lncRNAs in SKCM (green: mRNAs, blue: LncRNAs; correlation coefficients > 0.4 and $p < 0.001$).

Figure S2

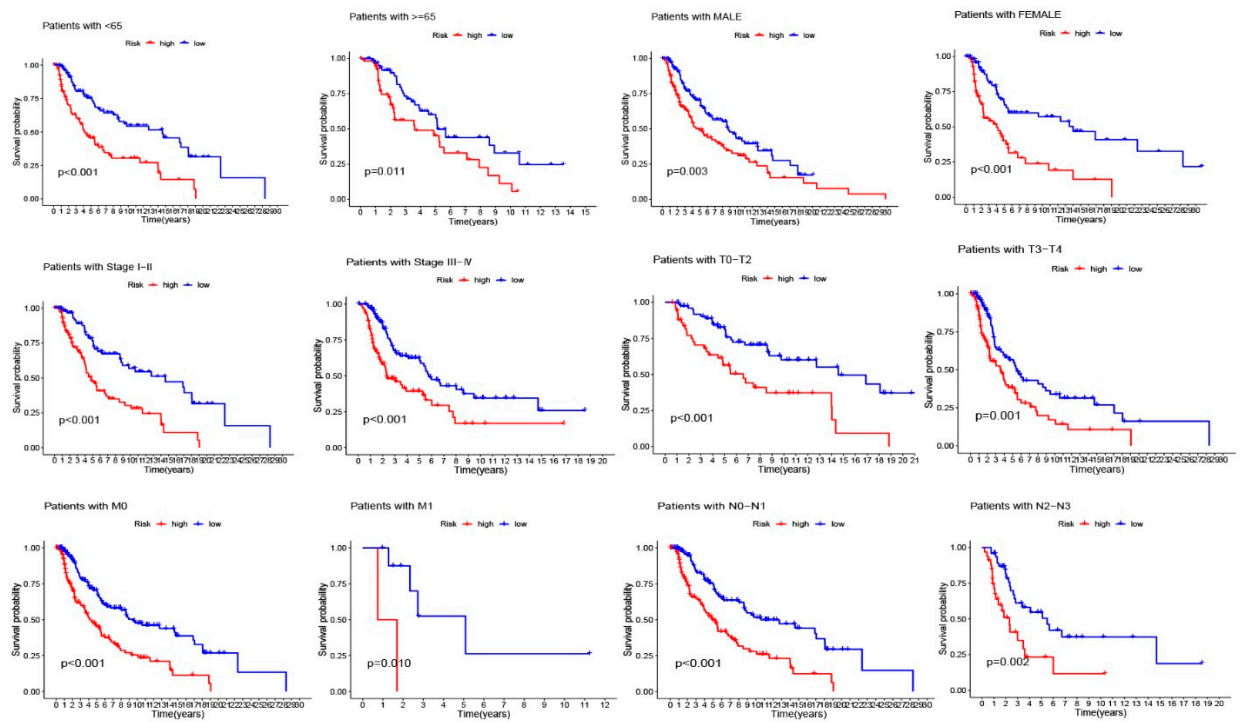
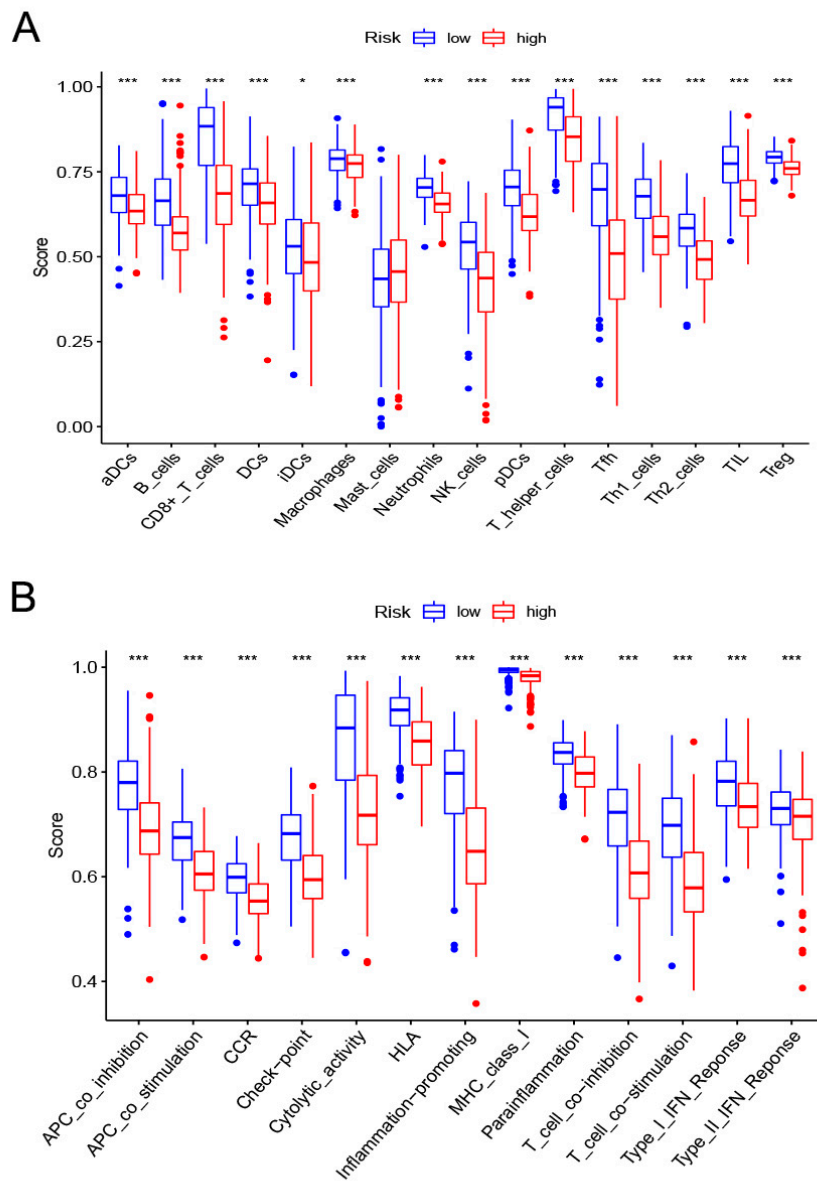


Figure S2 Kaplan-Meier analysis in clinicopathological features.
Kaplan-Meier survival curves of OS prognostic value stratified by age, gender, stage, T, M, or N between low- and high-risk groups in the entire set.

Figure S3



FigureS3 The ssGSEA analysis between high- and low-risk group.
The ssGSEA scores of immune cells and immune functions between high- and low-risk group (* $p < 0.05$, *** $p < 0.001$).

Figure S4

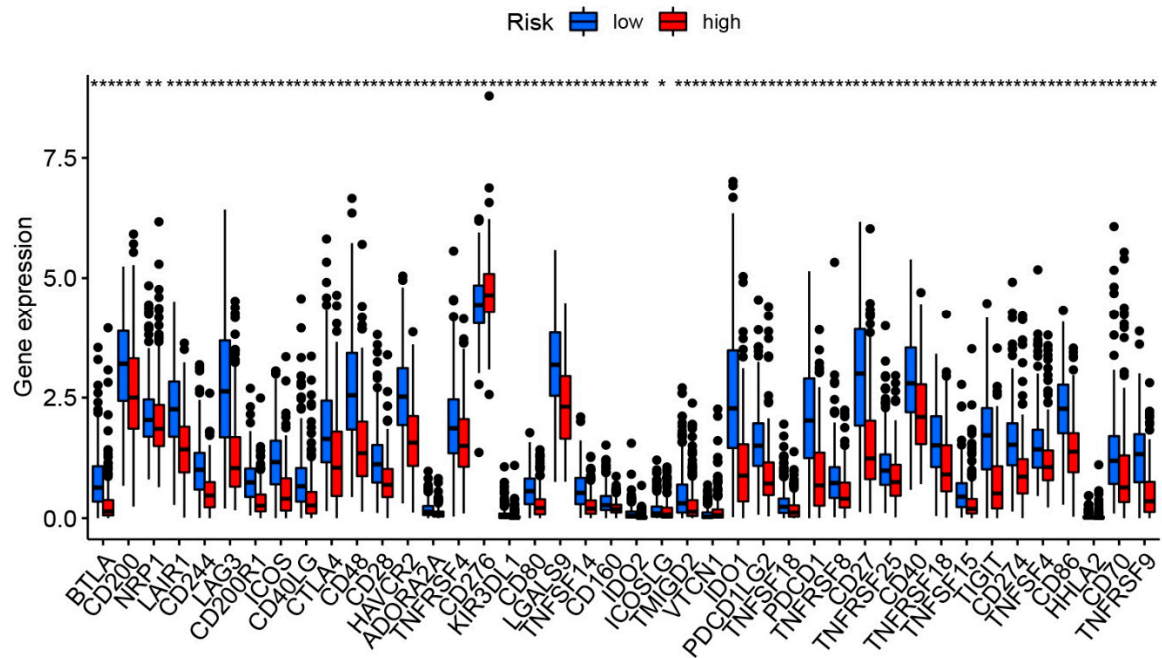
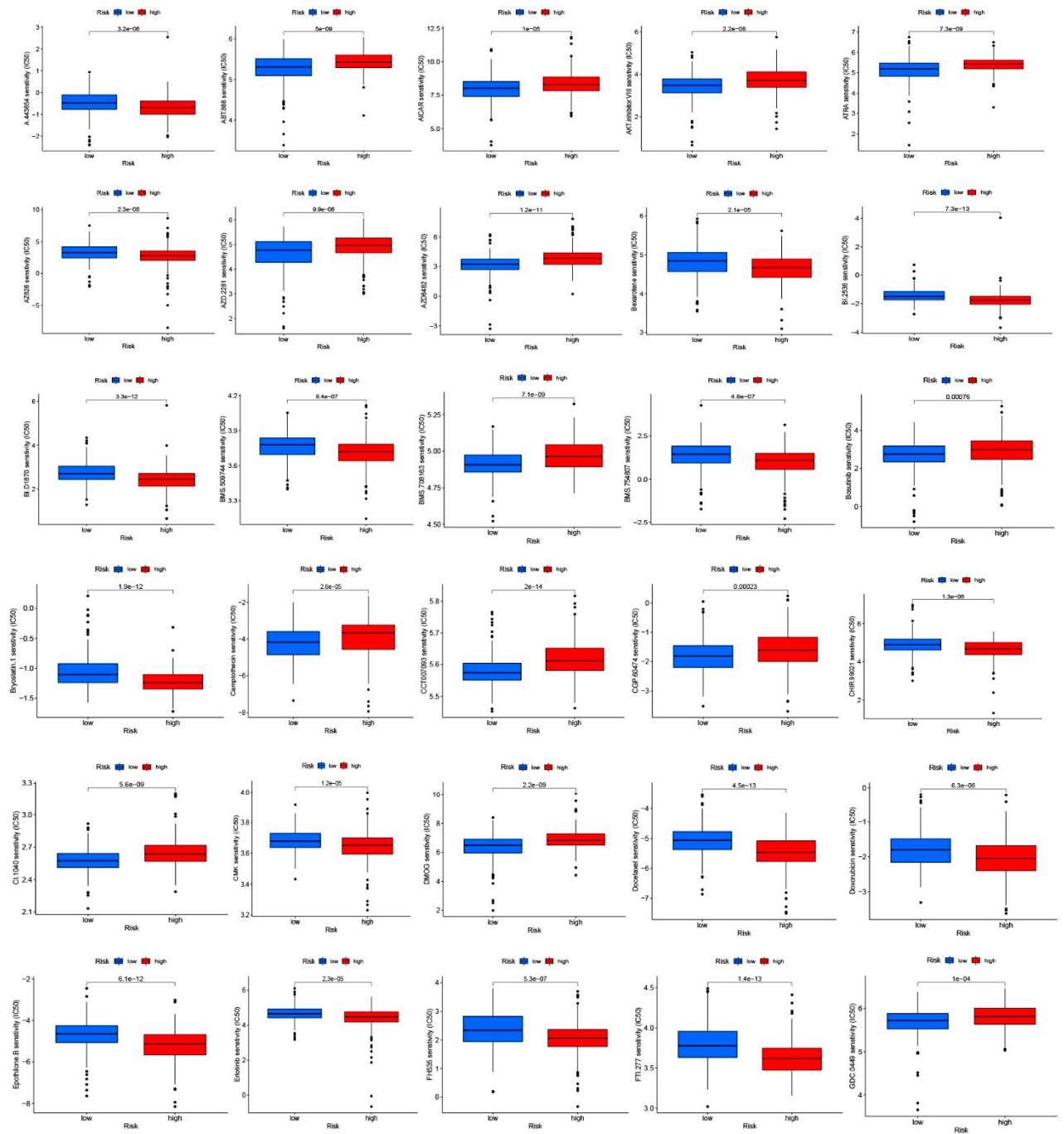


Figure S4 The difference of 42 checkpoints expression.
The difference of 42 checkpoints expression between high- and low-risk group (* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Figure S5



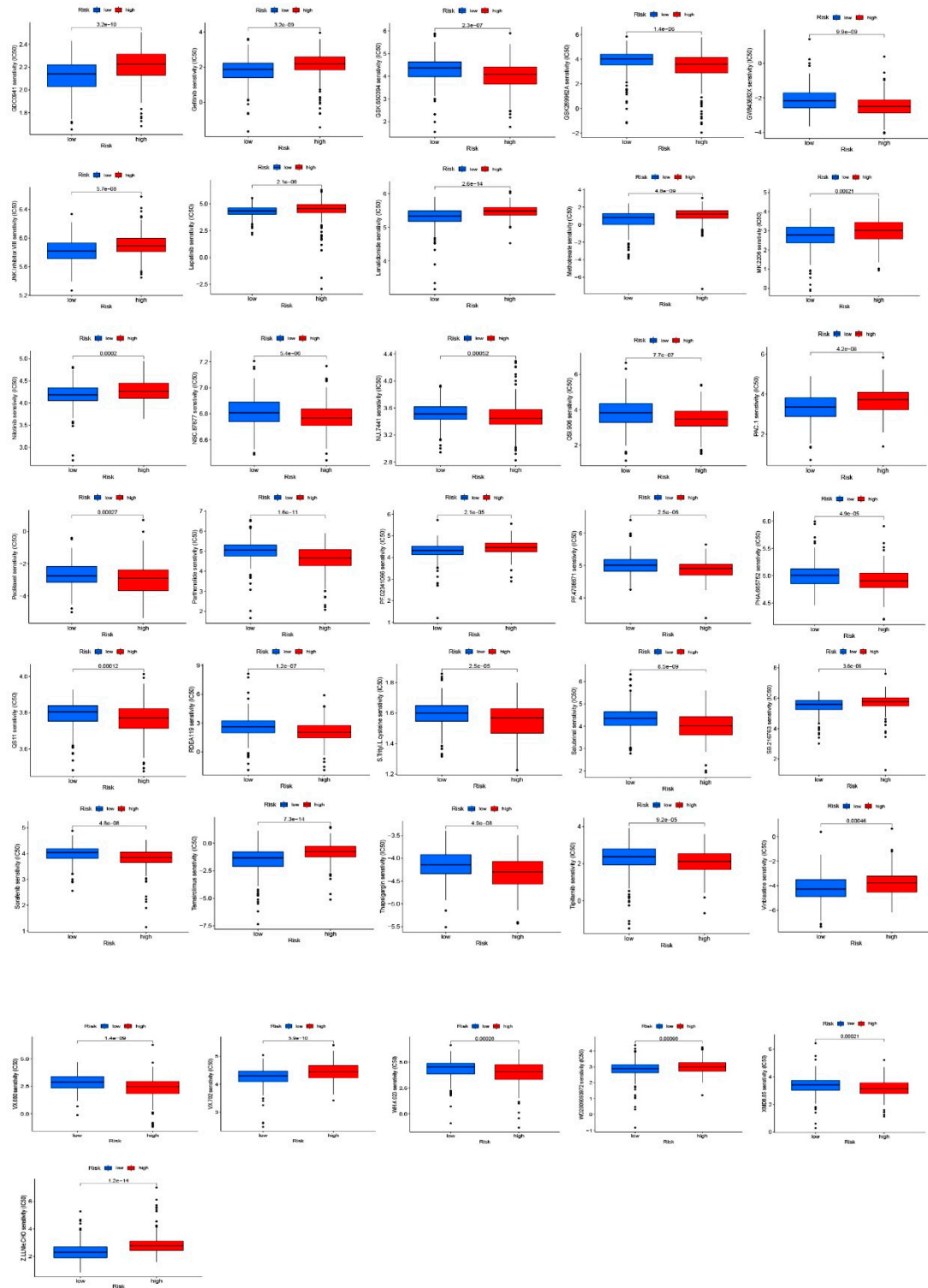


Figure S5 Potential therapeutic medicine of subgroups.
Potential therapeutic medicine of subgroups (all $p < 0.001$).

Figure S6

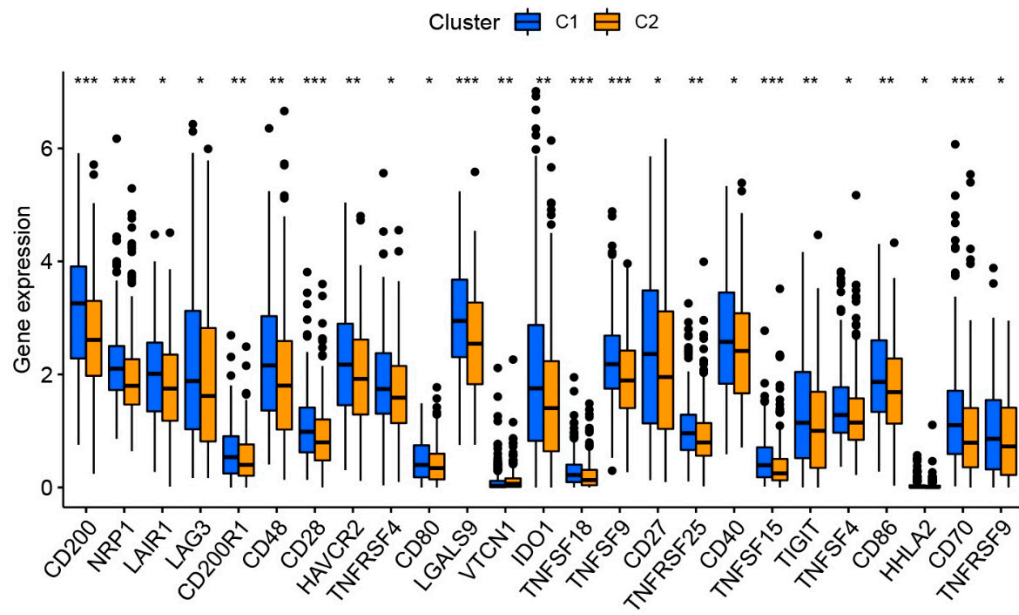


Figure S6 The difference of 25 checkpoints expression in different clusters.
The difference of 25 checkpoints expression in different clusters (* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Figure S7

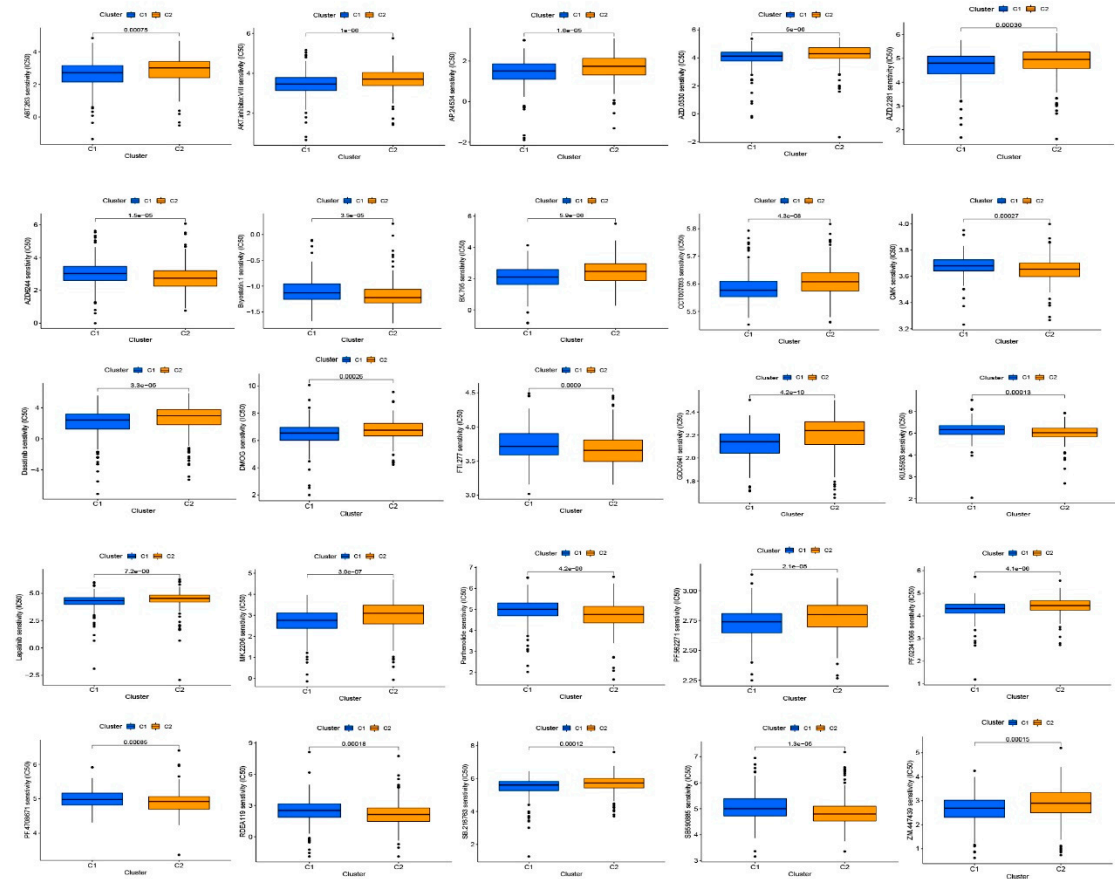


Figure S7 Potential therapeutic medicine in different clusters.
Potential therapeutic medicine in different clusters (all $p < 0.001$).