

Figure S1. Association of *RIPK3* with sarcoma survival in TARGET. (A) *RIPK3* log<sub>2</sub>(TPM+1) expression data were separated into higher (red dot) or lower (blue dot) groups (upper panel) or into live (red dot) or dead (blue dot) groups (lower panel). (B) Kaplan-Meier analysis according to *RIPK3* expression revealed no significant difference. (C) Receiver operating curve analysis for 1, 3 and 5 years. *RIPK3*, receptor interacting serine/threonine kinase 3; exp, expression; TPM, transcripts per million; AUC, area under the curve.

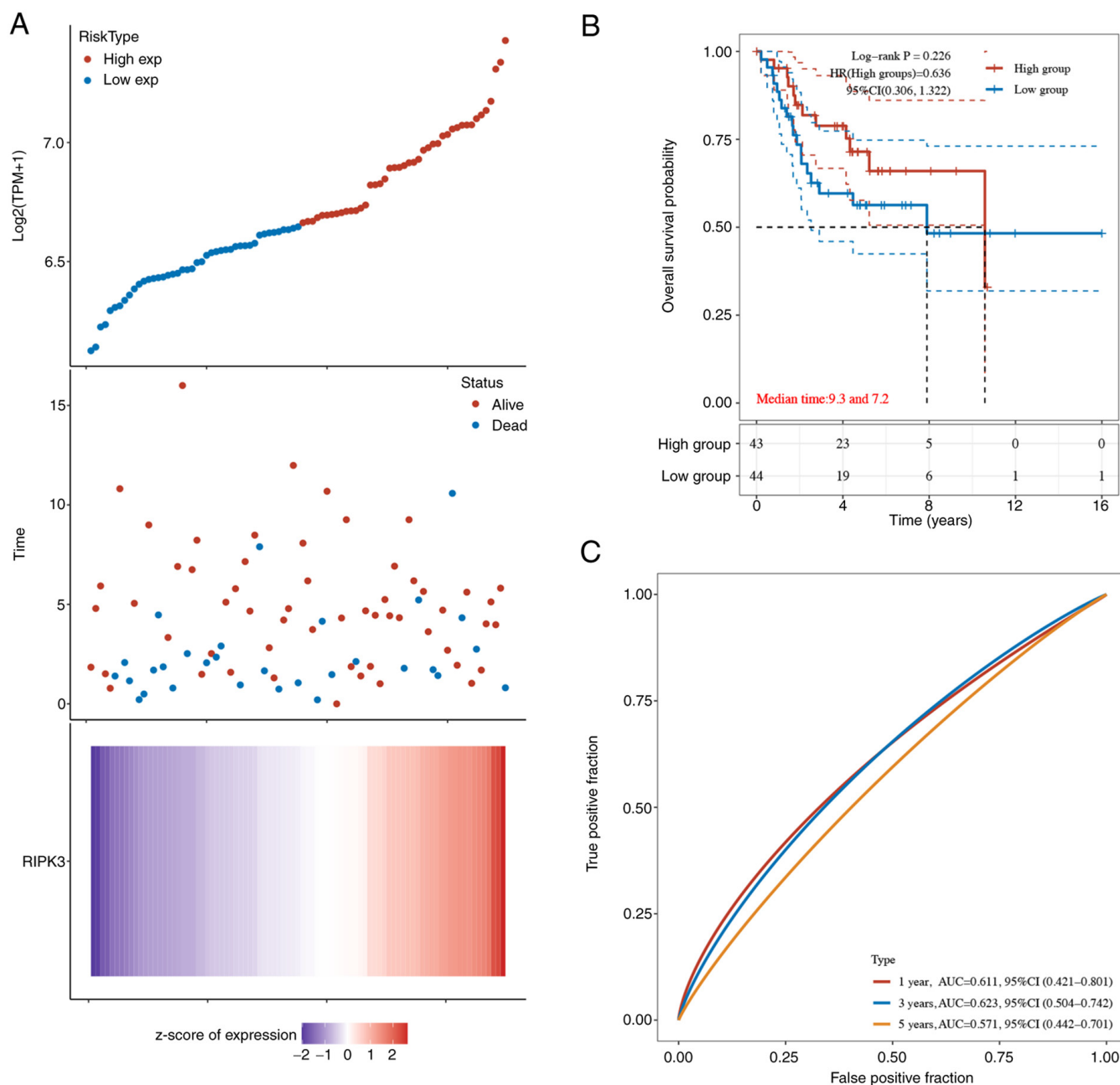


Figure S2. Survival analysis according to *RIPK1*, *RIPK2* and *RIPK4* expression in the (A) TCGA and (B) TARGET datasets. *RIPK*, receptor interacting serine/threonine kinase; TCGA, The Cancer Genome Atlas; TARGET, Therapeutically Applicable Research To Generate Effective Treatments.

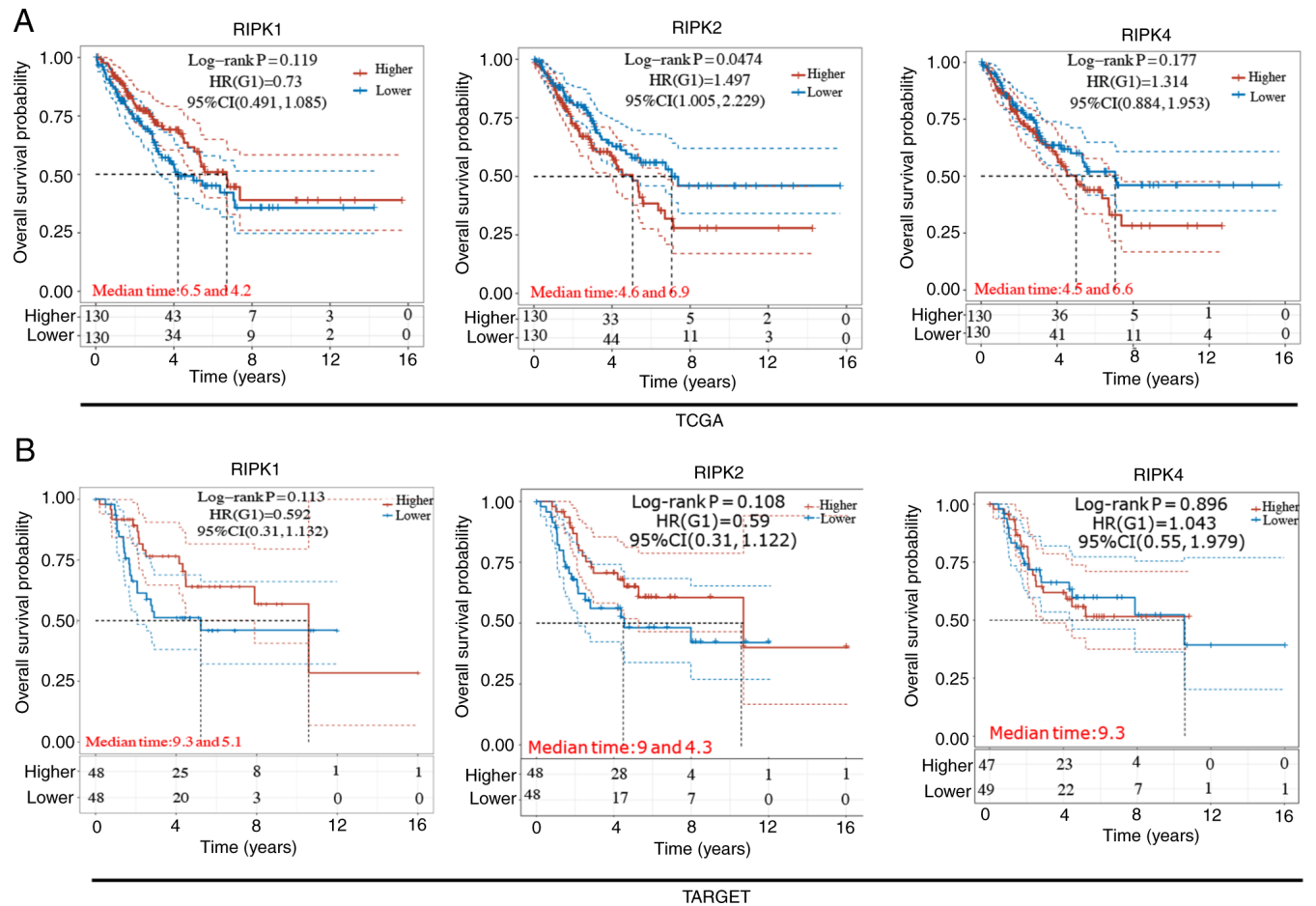


Figure S3. Expression of *TMC8* and *TMEM97* according to *RIPK3* expression level in the Therapeutically Applicable Research To Generate Effective Treatments dataset. (A) *TMC8* was upregulated and (B) *TMEM97* was downregulated in the *RIPK3*<sup>higher</sup> group. The data were analyzed using Wilcoxon rank-sum test. *TMC8*, transmembrane channel like 8; *TMEM97*, transmembrane protein 97; receptor interacting serine/threonine kinase

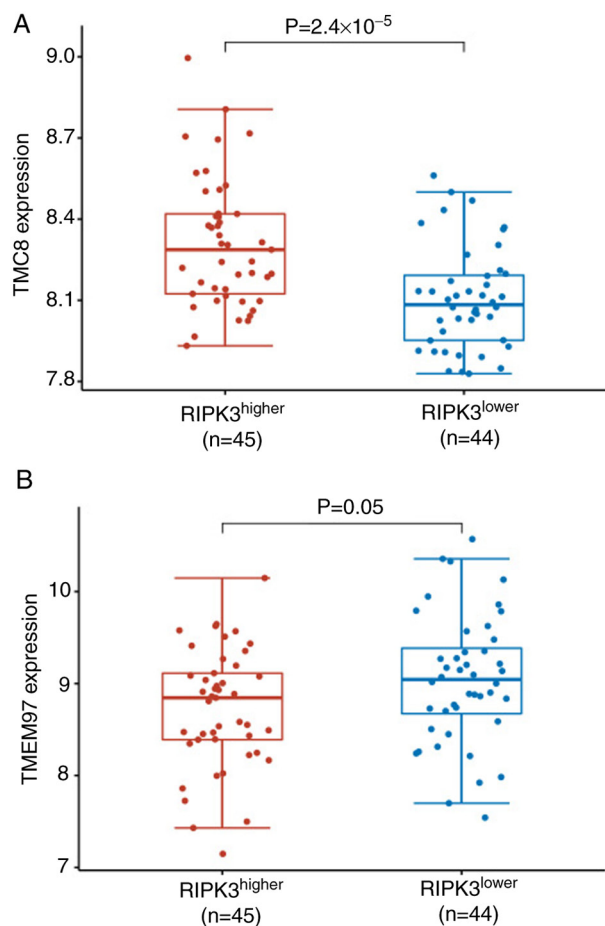


Figure S4. Expression profiles of the *RIPK3*<sup>higher</sup> and *RIPK3*<sup>lower</sup> groups in the Therapeutically Applicable Research To Generate Effective Treatments dataset. (A) Volcano plot of transcriptome sequence data in the *RIPK3*<sup>higher</sup> and *RIPK3*<sup>lower</sup> groups. The red dots represent fold change >2 and FDR adjusted P<0.05, and the blue dots represent fold change <-2 and FDR adjusted P<0.05. (B) Unsupervised hierarchical clustering of 130 *RIPK3*<sup>higher</sup> and 129 *RIPK3*<sup>lower</sup> samples based on the top 50 up- and top 50 downregulated genes. Each column represents a sample, and the differentially expressed genes are listed in rows. (C) KEGG and GO functional annotations of up- and downregulated genes, respectively. *RIPK3*, receptor interacting serine/threonine kinase 3; KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology; FDR, false discovery rate.

