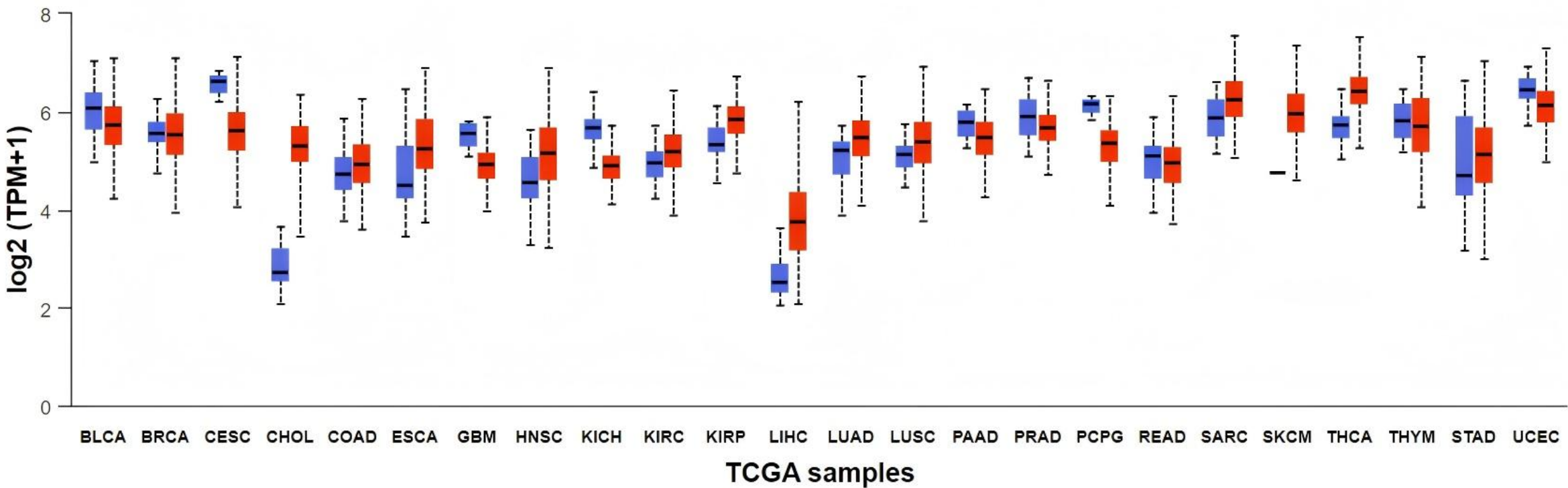
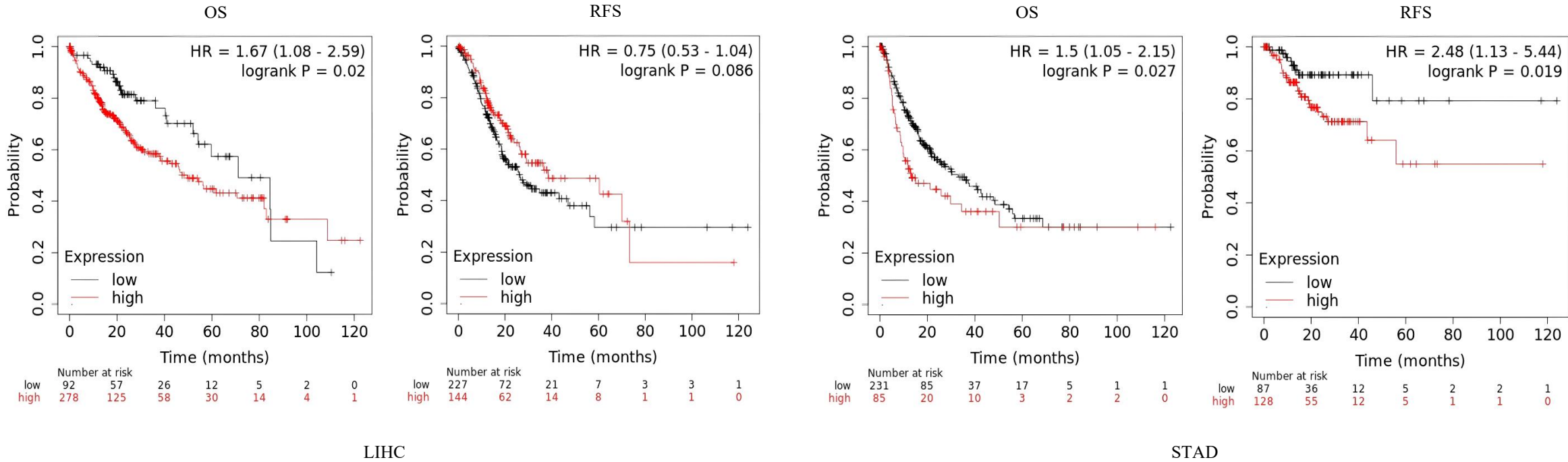


A

Expression of LZTS2 across TCGA cancers (with tumor and normal samples)

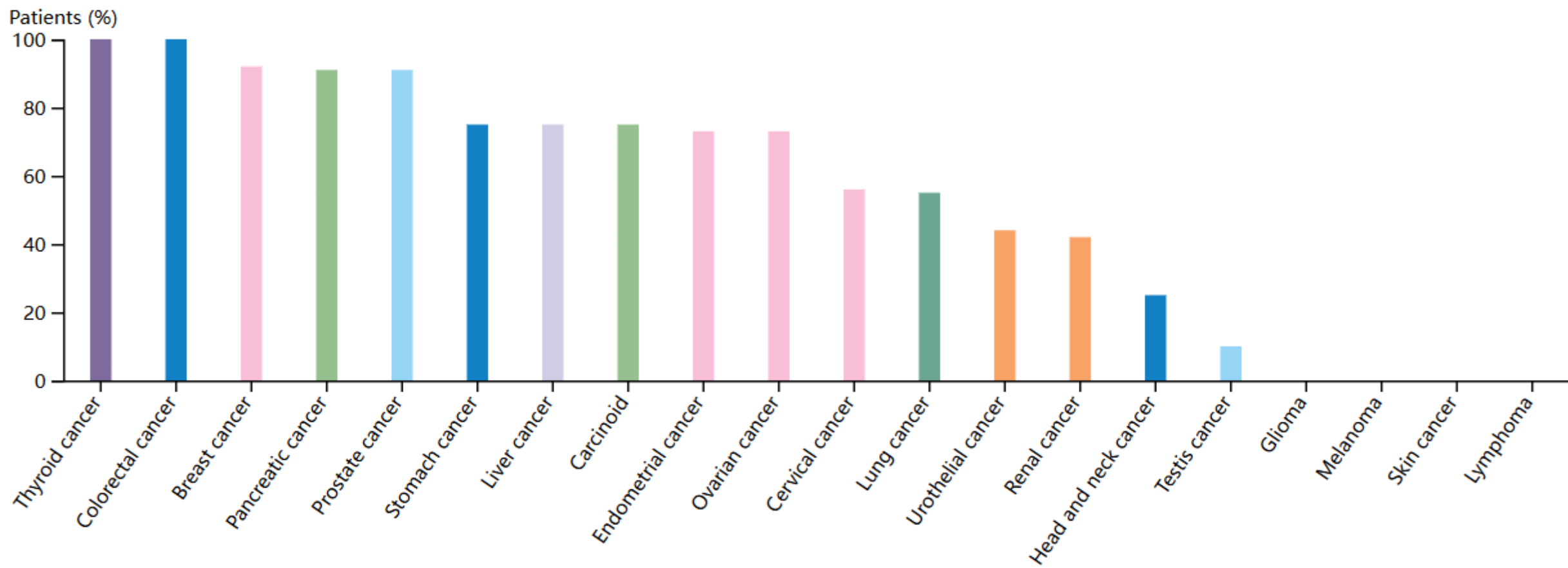


B

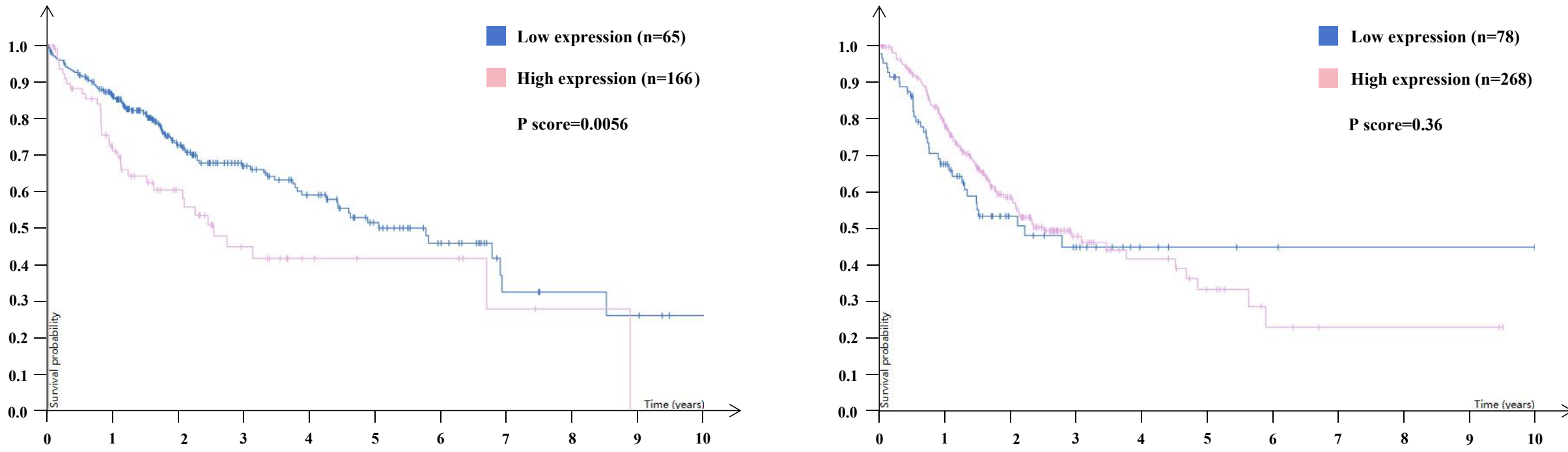


Supplementary Figure 1. Expression and prognostic values of LZTS2. (A) Expression levels of LZTS2 across tumor and normal tissues in various TCGA cancer types via UALCAN. (B) OS and RFS curves stratified by LZTS2 expression in LIHC and STAD patients from KM plotter (survival analysis was performed on batch-corrected expression data).

A

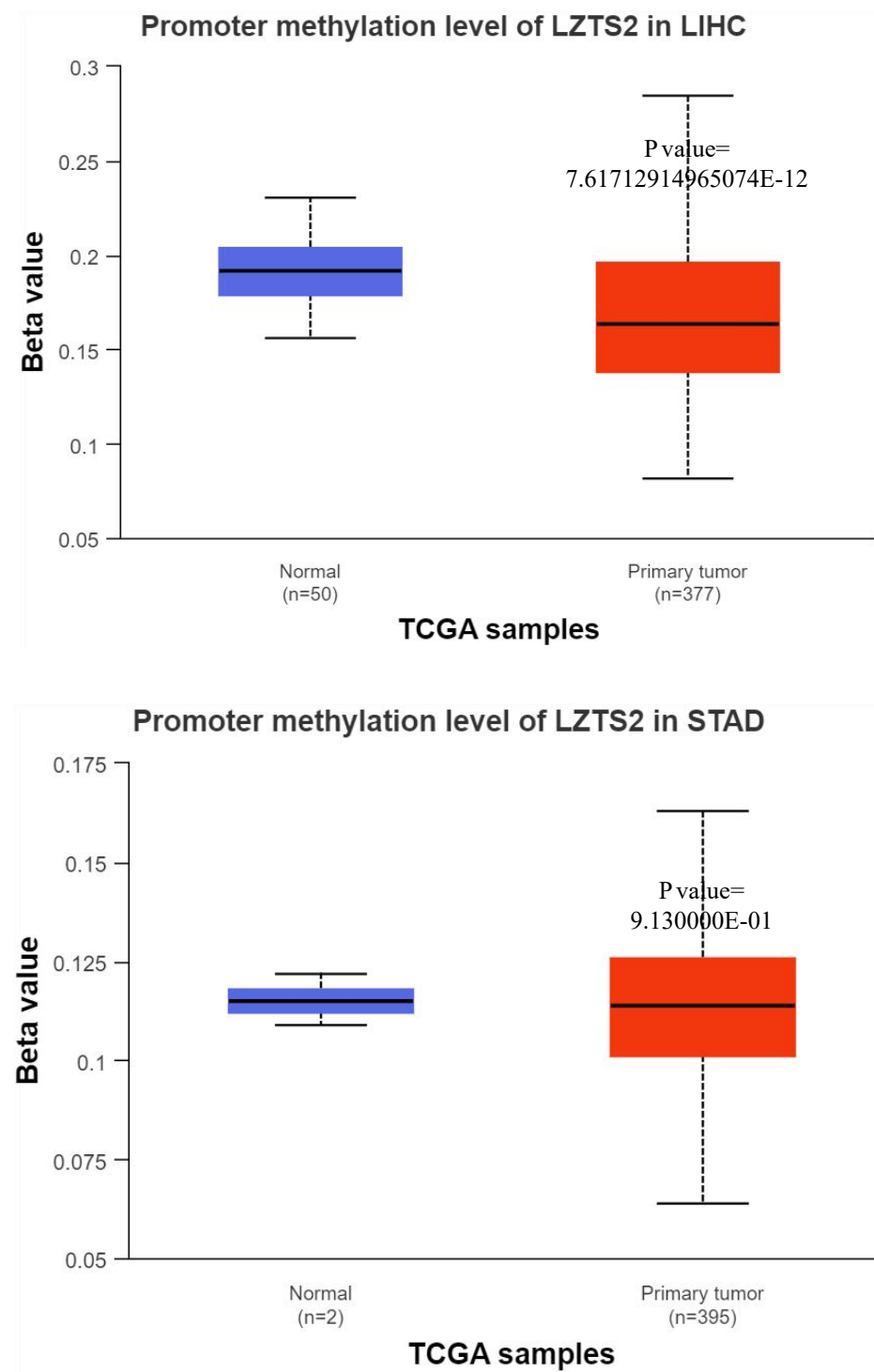


B



Supplementary Figure 2. Expression and survival analysis of LZTS2. (A) Protein expression of LZTS2 in human tissues as analyzed by the HPA. (B) Survival analysis of LZTS2 expression in LIHC and STAD based on data from the HPA.

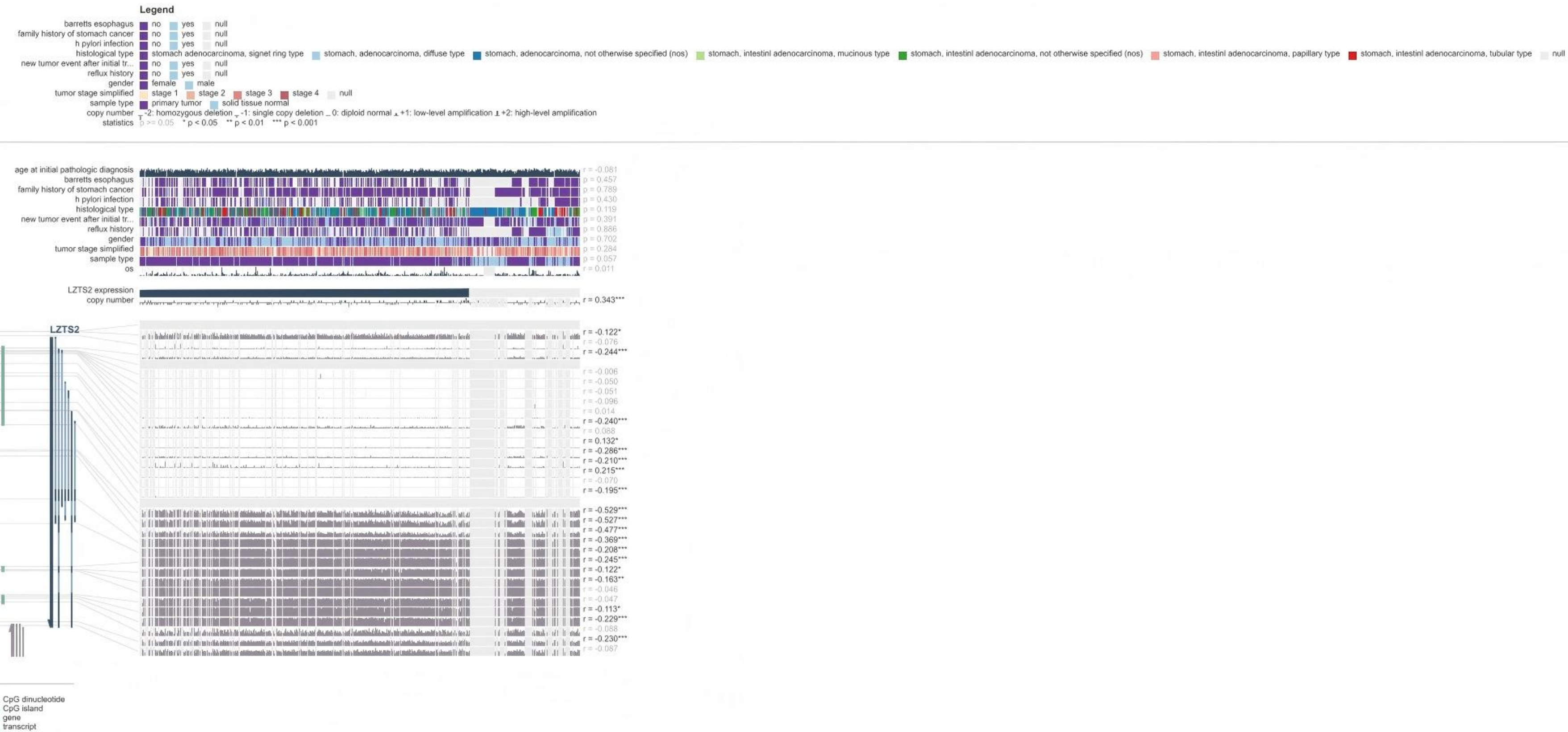
A



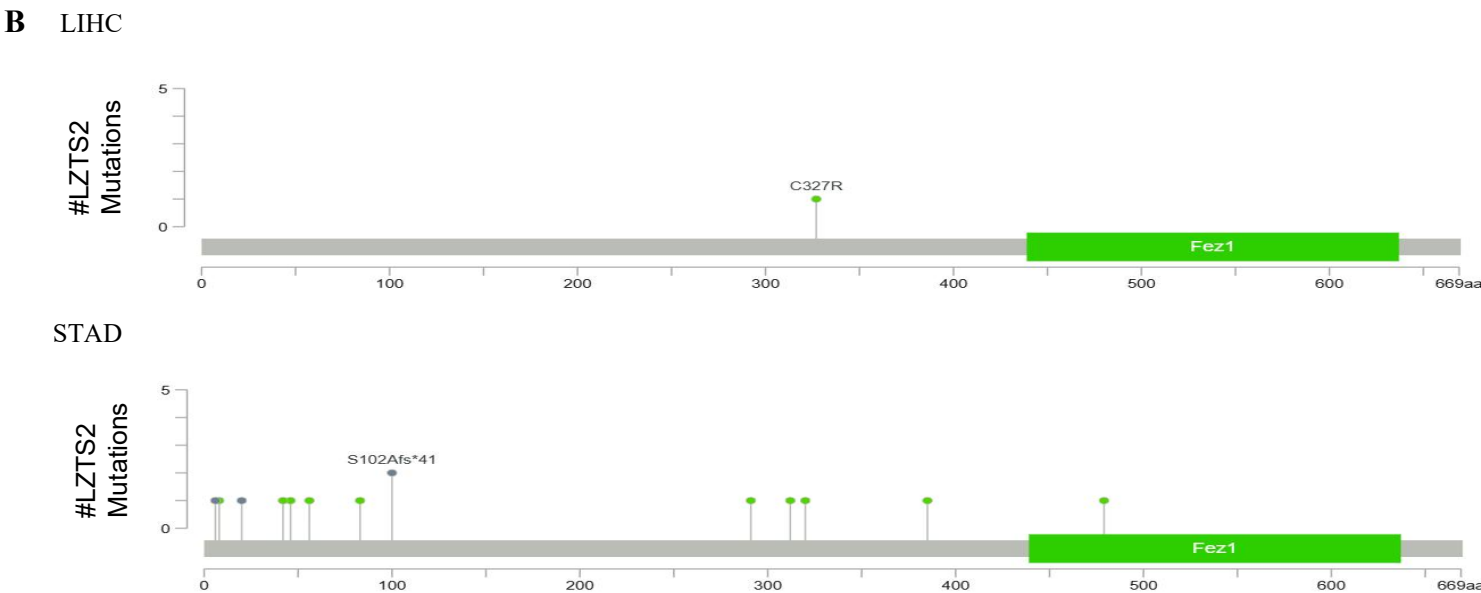
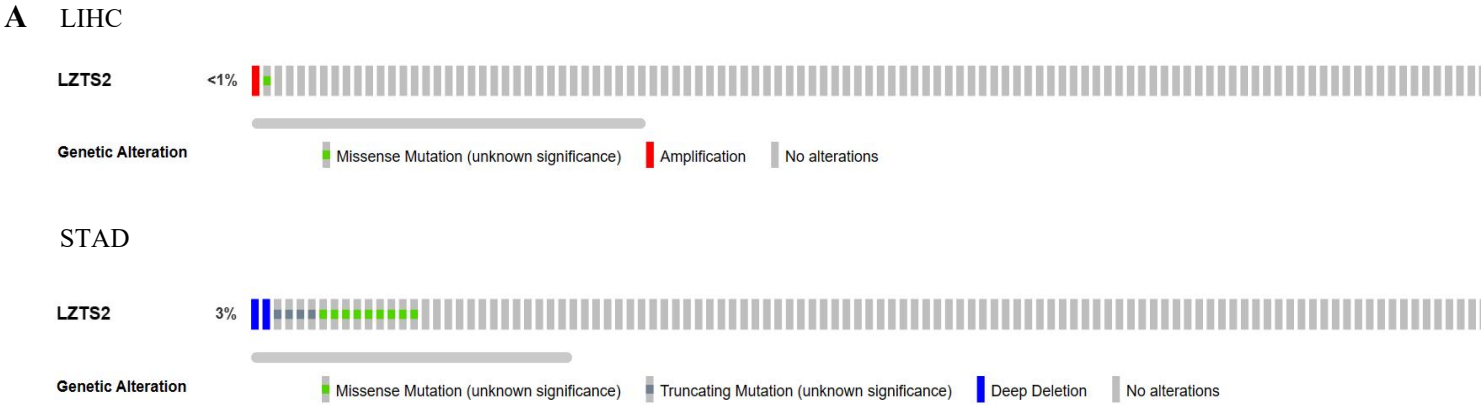
B



C

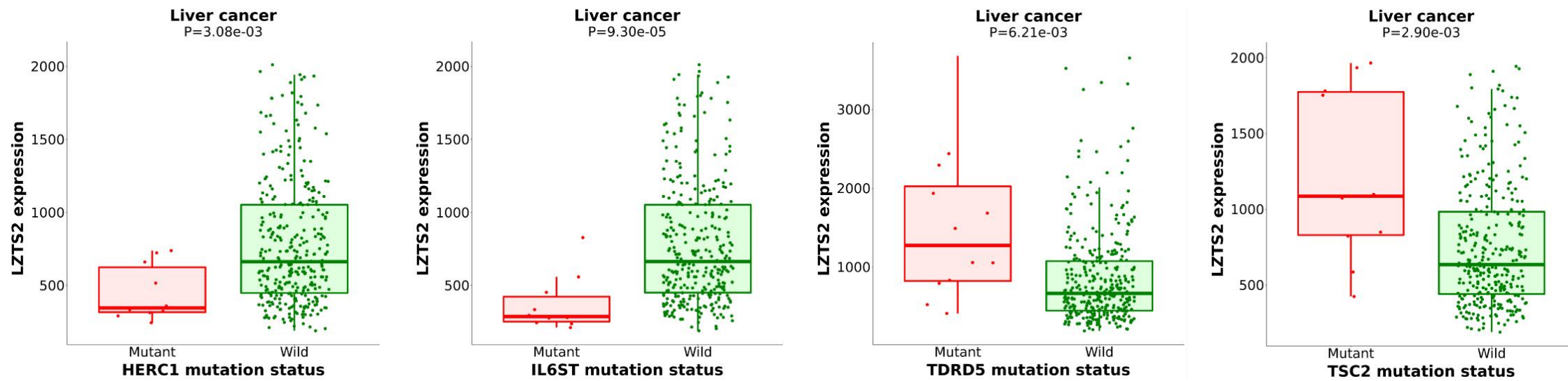


Supplementary Figure 3. LZTS2 promoter methylation levels. (A) Promoter methylation level inquiry via UALCAN (beta values were quantile-normalized, and probes with detection p-values >0.01 were excluded). (B) and (C) Promoter methylation level validation via MEXPRESS.

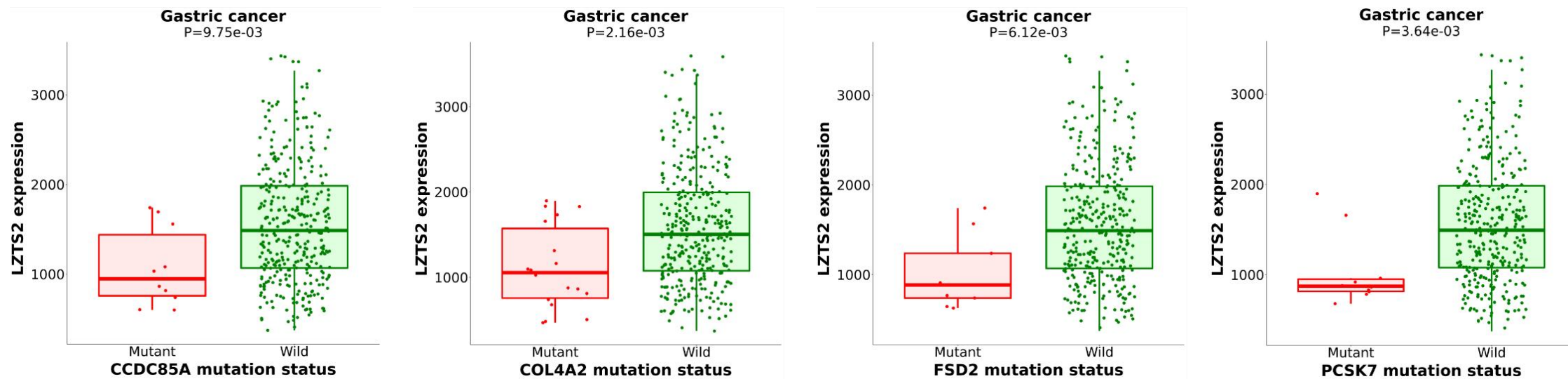


Supplementary Figure 4. Analysis of genetic mutations, CNV alterations, and identification of mutational hotspots of LZTS2 in TCGA LIHC and STAD datasets using cBioPortal. (A) The frequency of genetic alterations and CNVs (mutations, deep amplification, and deep deletion) in LIHC and STAD samples, and (B) Protein architecture of LZTS2 protein showing most frequently observed mutations in TCGA LIHC and STAD samples. A green color region in protein architecture is showing the LZTS domain of LZTS2 protein.

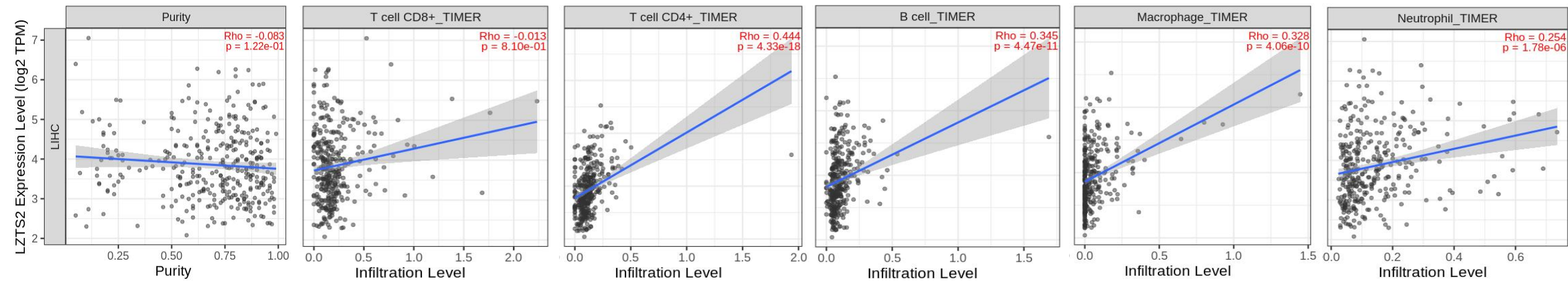
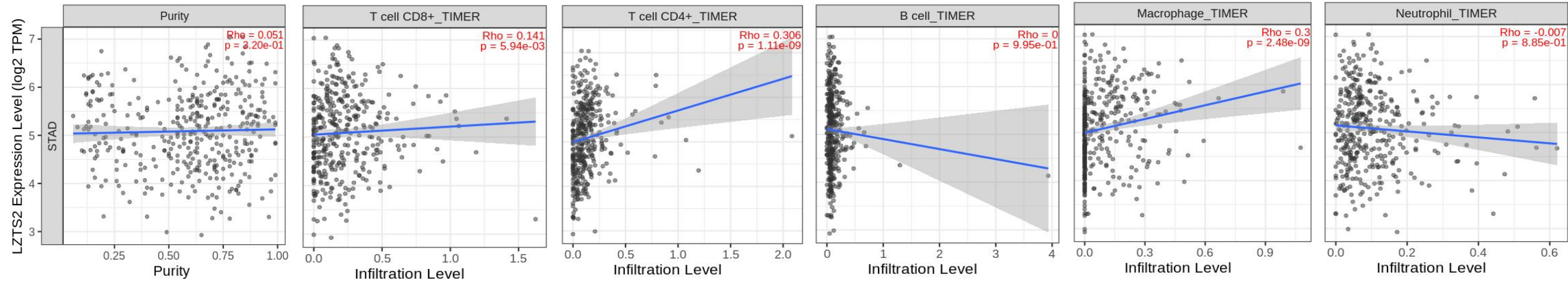
A



B

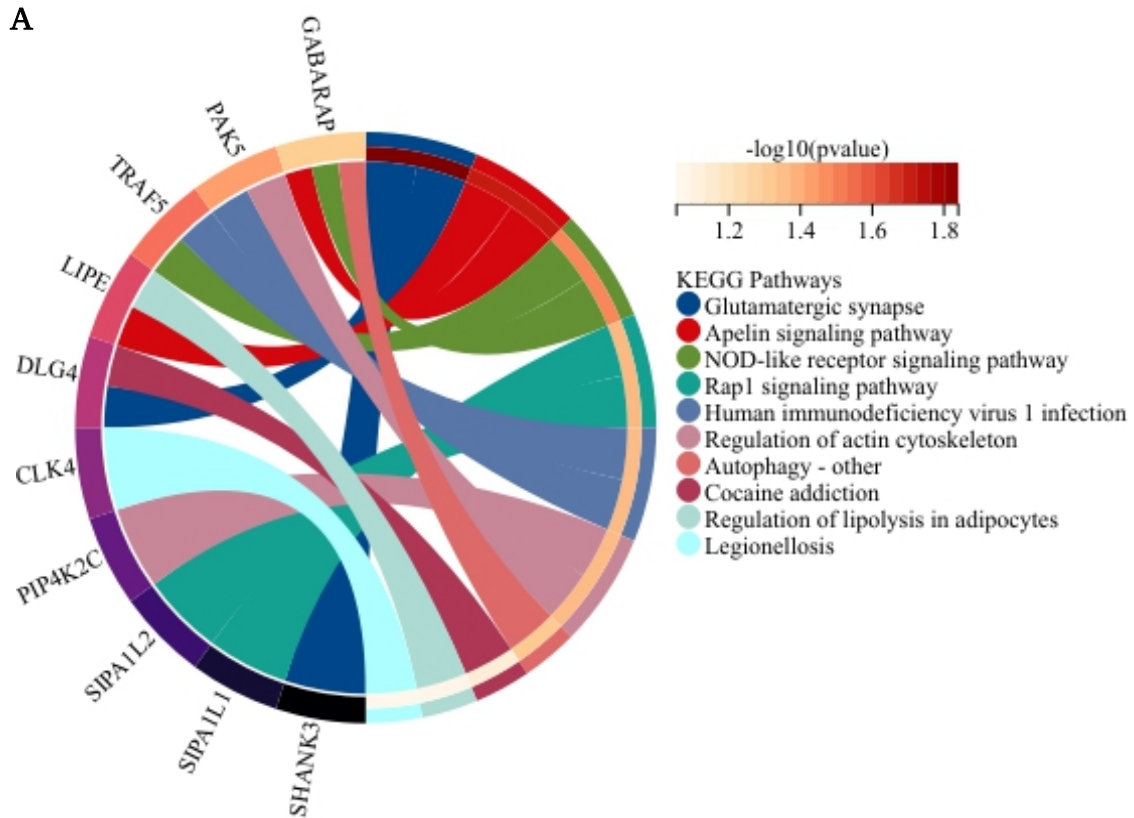


Supplementary Figure 5 . Correlations among mutant genes and LZTS2 overexpression in LIHC and STAD samples obtained via MuTarget. (A) A list of top 4 positively correlated genes with LZTS2 overexpression in LIHC, and **(B)** A list of top 4 positively correlated genes with LZTS2 overexpression in STAD. Green color box whisker plots showing LZTS2 expression in wild type samples while red color box whisker plots showing LZTS2 expression in mutantsamples for a specific gene.

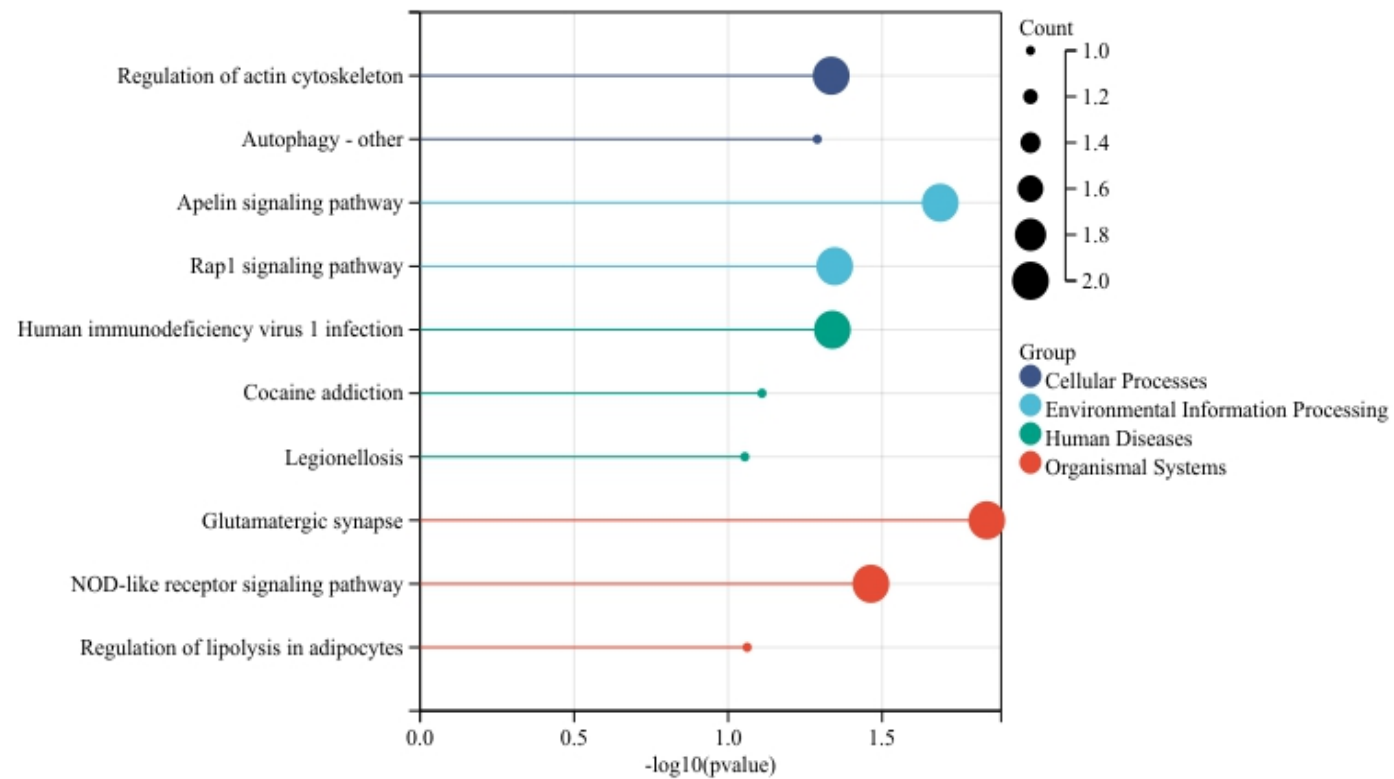
A**B**

Supplementary Figure 6. Correlation analysis between tumor purity, different immune cells infiltration level, and LZTS2 expression in LIHC and STAD. (A) A correlation analysis between CD4+ T cells, CD8+ T cells, B cells, macrophages, and neutrophils immune cells infiltration and LZTS2 expression in LIHC, and (B) A correlation analysis between CD4+ T cells, CD8+ T cells, B cells, macrophages, and neutrophils immune cells infiltration and LZTS2 expression in STAD.

A

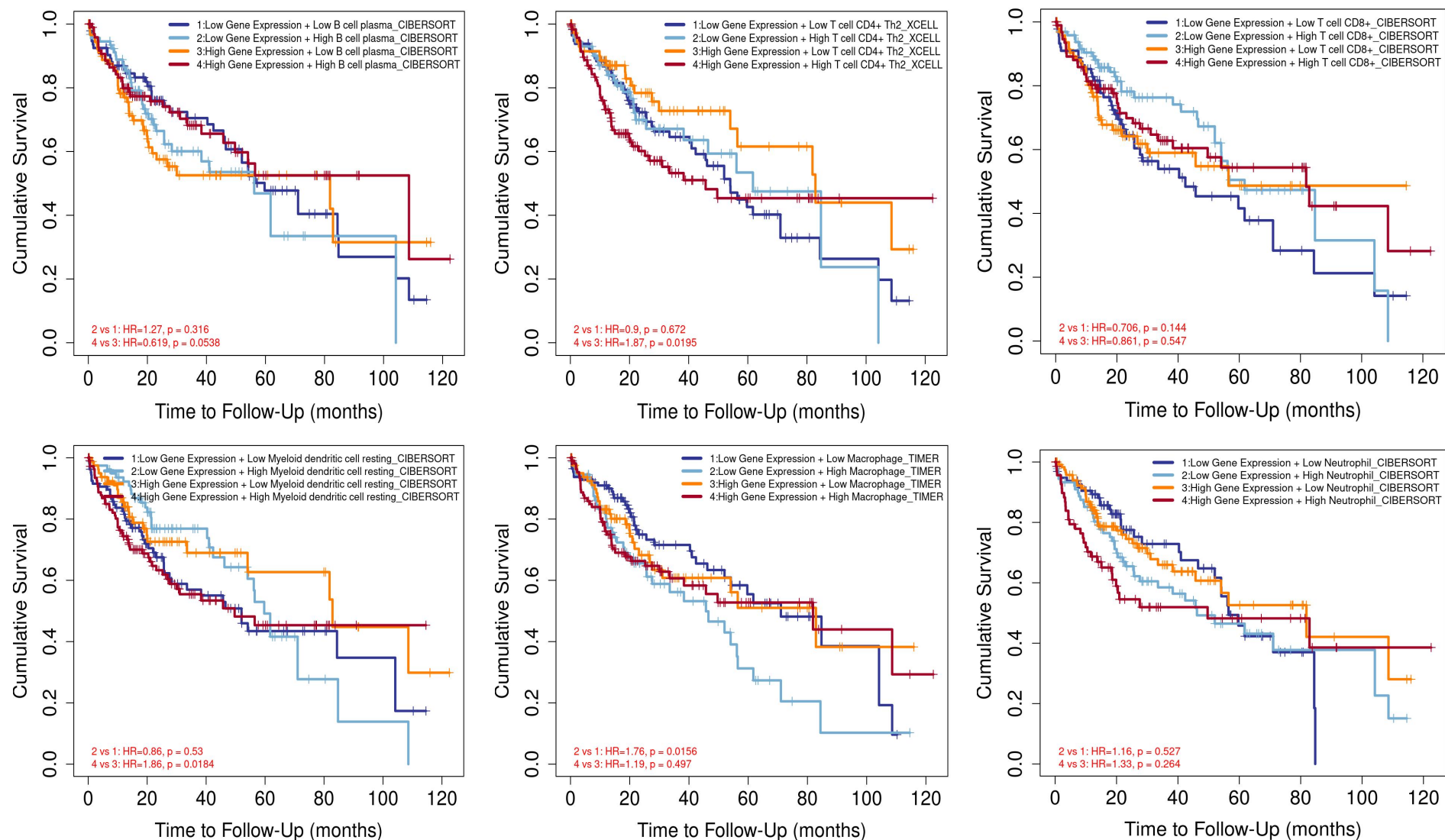


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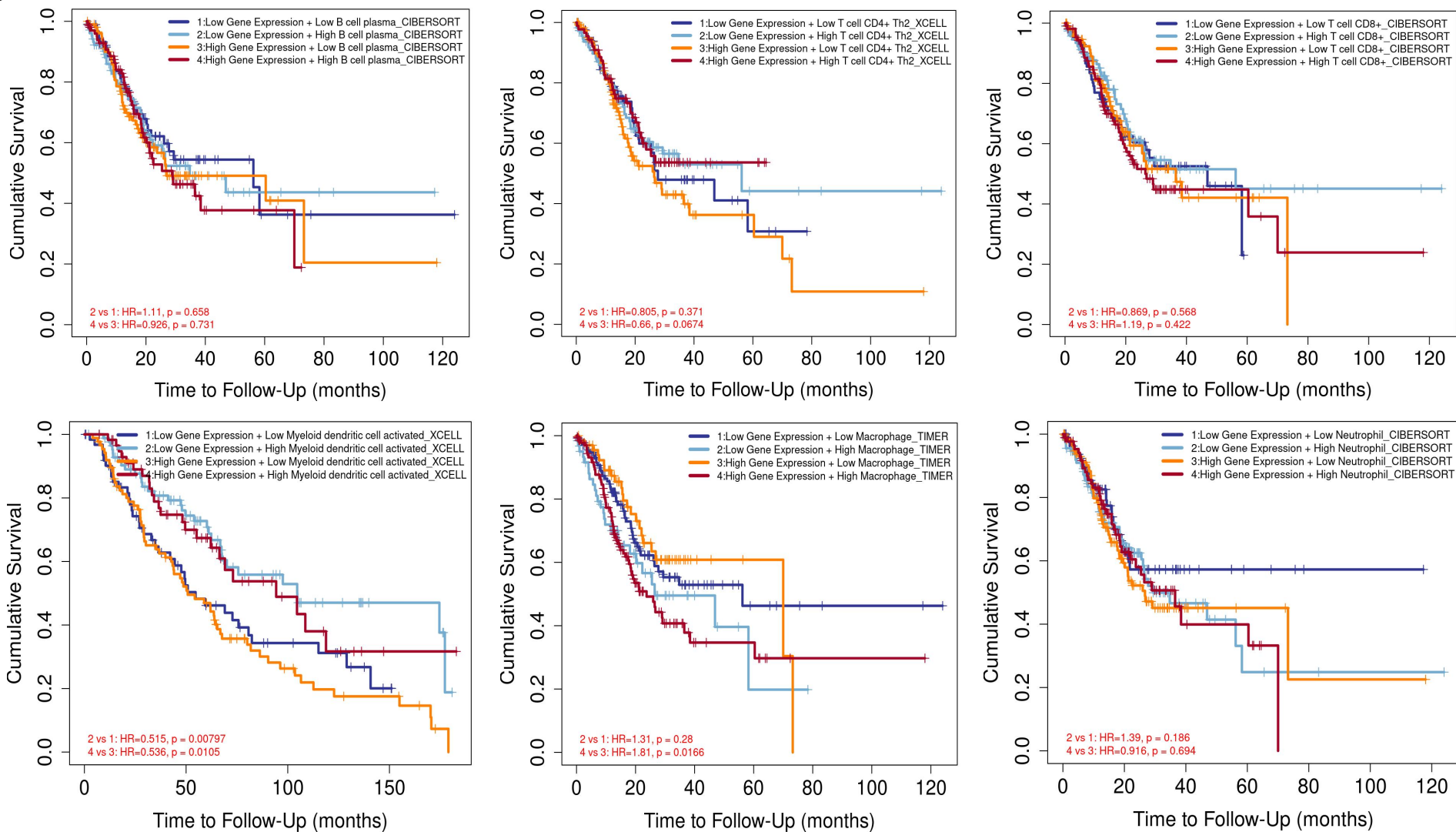


Supplementary Figure 7. GO/KEGG enrichment analysis of LZTS2-related gene function from the STRING database.

A

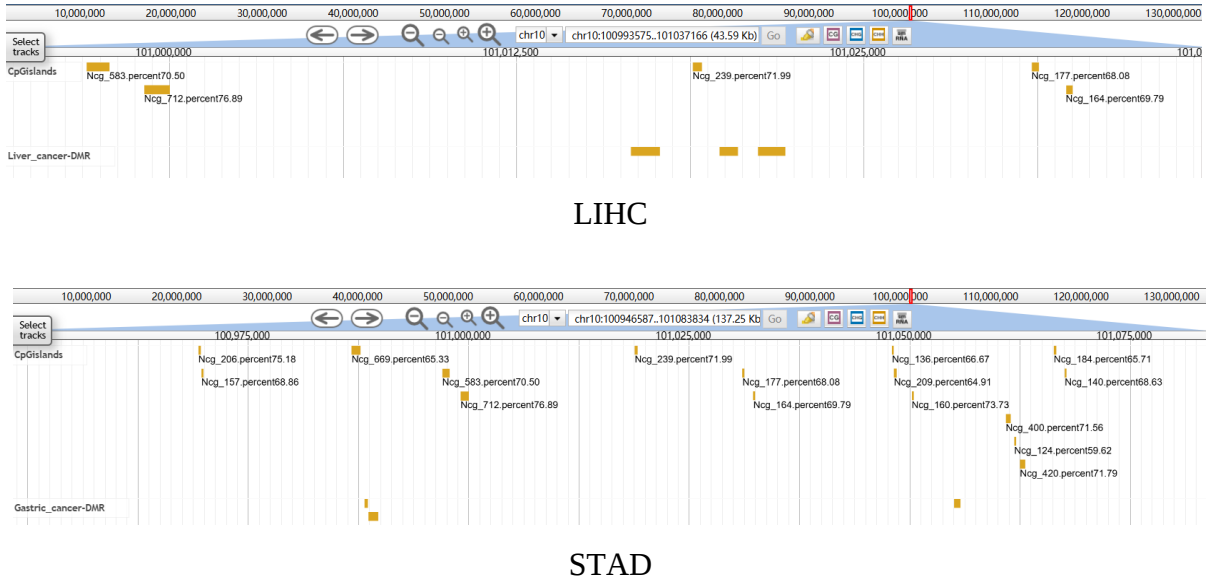


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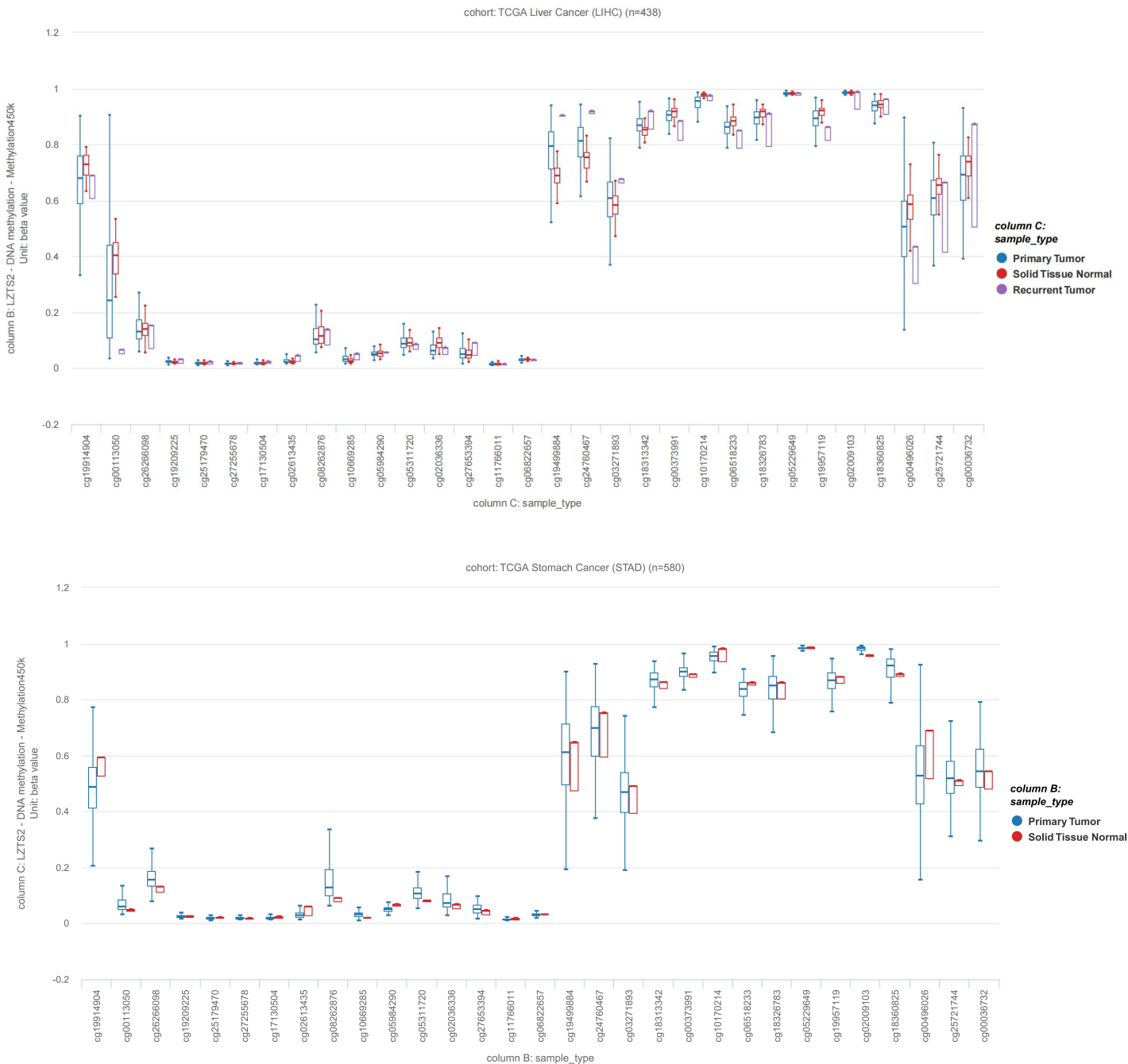


Supplementary Figure 8. Stage-stratified survival analysis with immune infiltration in LIHC and STAD cohorts from TIMER2.0 database. (A) LIHC (B) STAD. Statistical significance determined by log-rank test with Benjamini-Hochberg correction.

A



B



Supplementary Figure 9. Genomic and epigenetic characterization in LIHC and STAD cancers. (A) Chromosomal distribution of genomic loci and variation patterns (data from MethMarkerDB). (B) Methylation beta-value comparisons in LIHC and STAD cohorts (data from UCSC Xena).