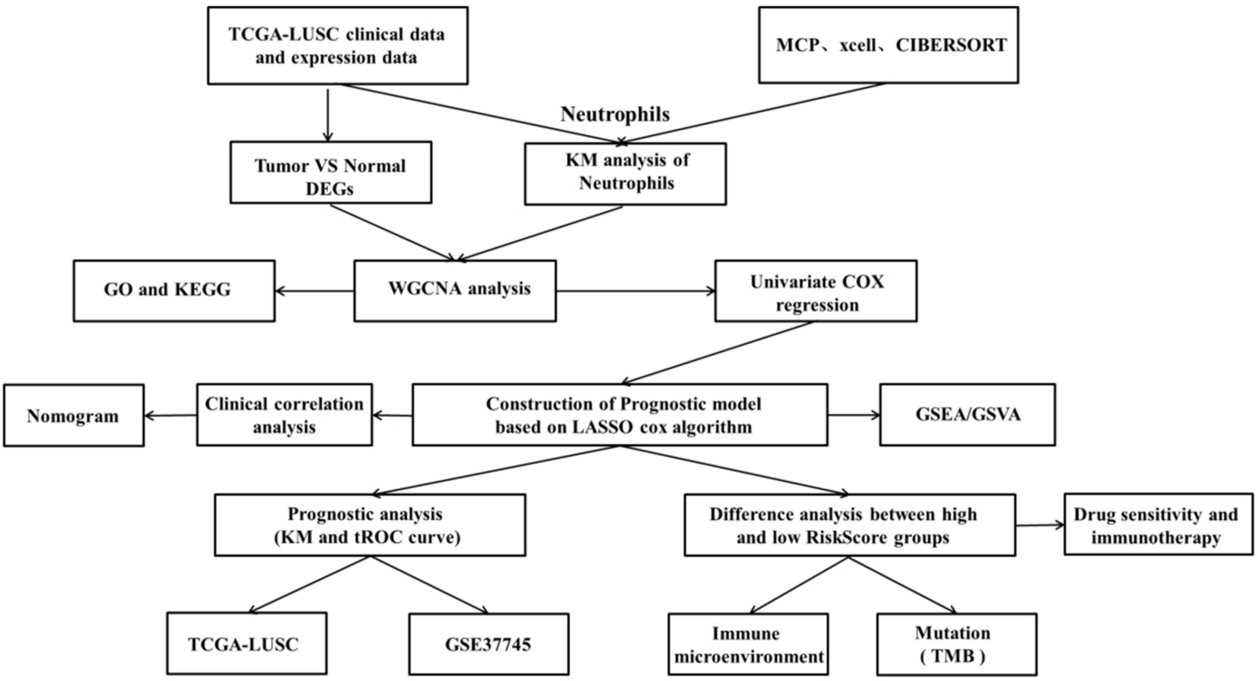

Figure S1 The workflow of this study. TCGA, The Cancer Genome Atlas; LUSC, lung squamous cell carcinoma; MCP, microenvironment cell populations; DEGs, differentially expressed genes; KM, Kaplan-Meier; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; WGCNA, weighted gene co-expression network analysis; LASSO, least absolute shrinkage and selection operator; GSEA, gene set enrichment analysis; GSVA, gene set variation analysis; tROC, time-dependent receiver operating characteristic; TMB, tumor mutation burden.

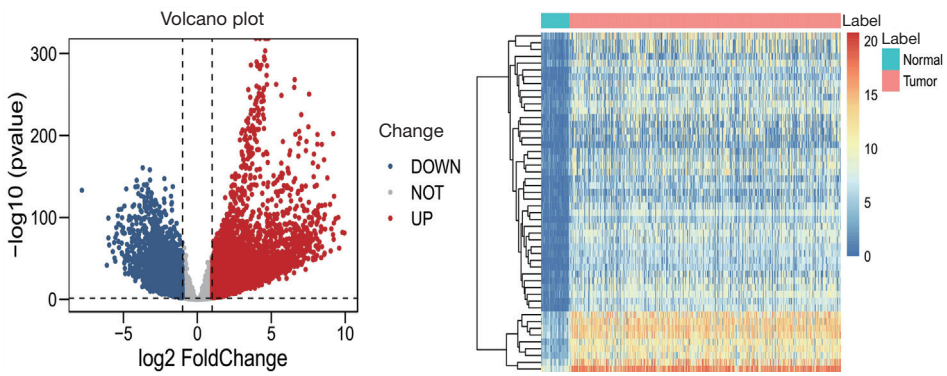

Figure S2 Comparison of neutrophil-related gene expression between lung cancer and normal tissue samples. Right: the adjacent color bar of the heat map indicates the expression level, with red indicating higher expression and blue indicating lower expression.

https://dx.doi.org/10.21037/tlcr-24-411

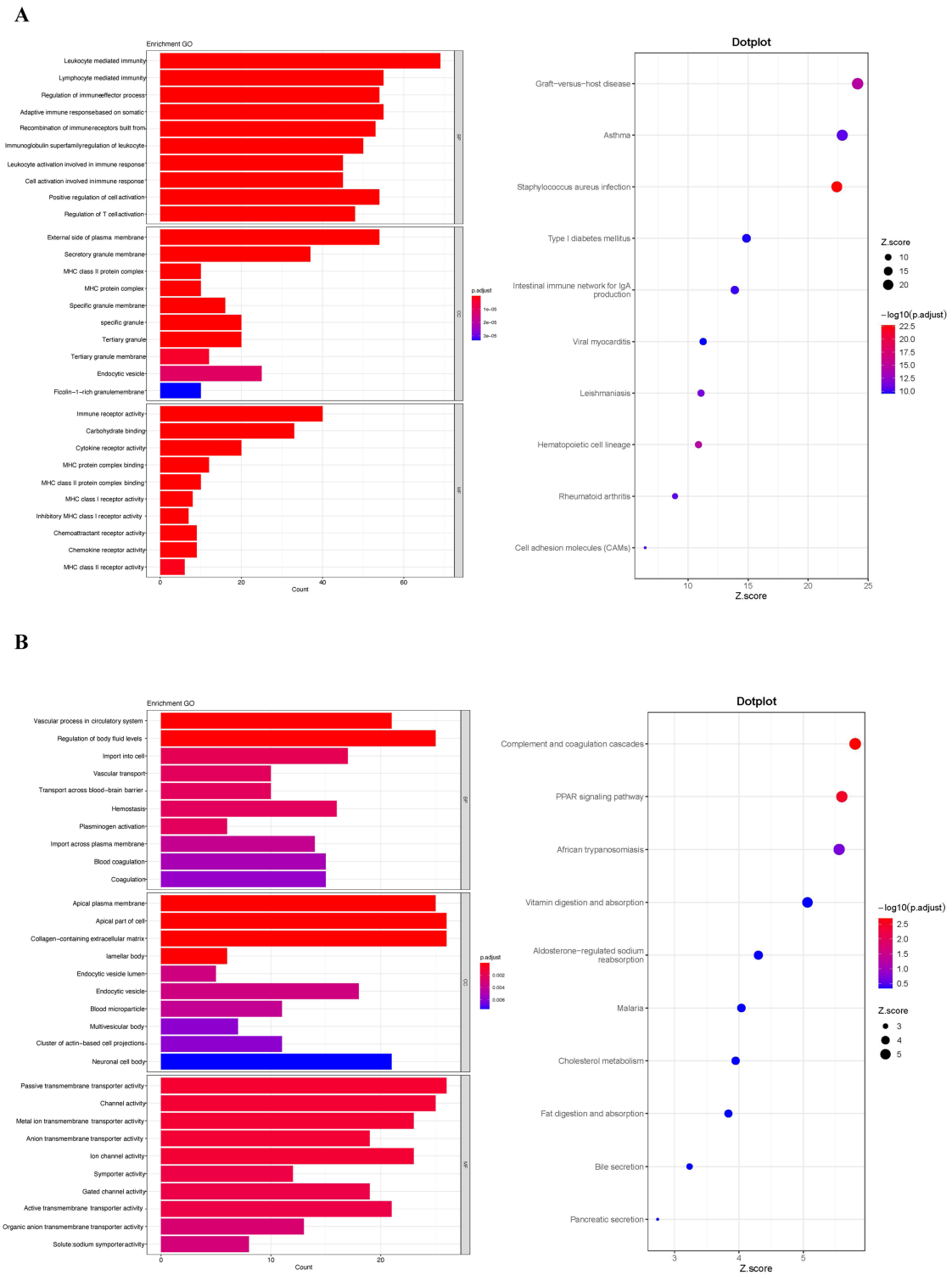

Figure S3 Annotation of the related path (GO BP) of the blue module (A) and yellow modules (B). GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function.

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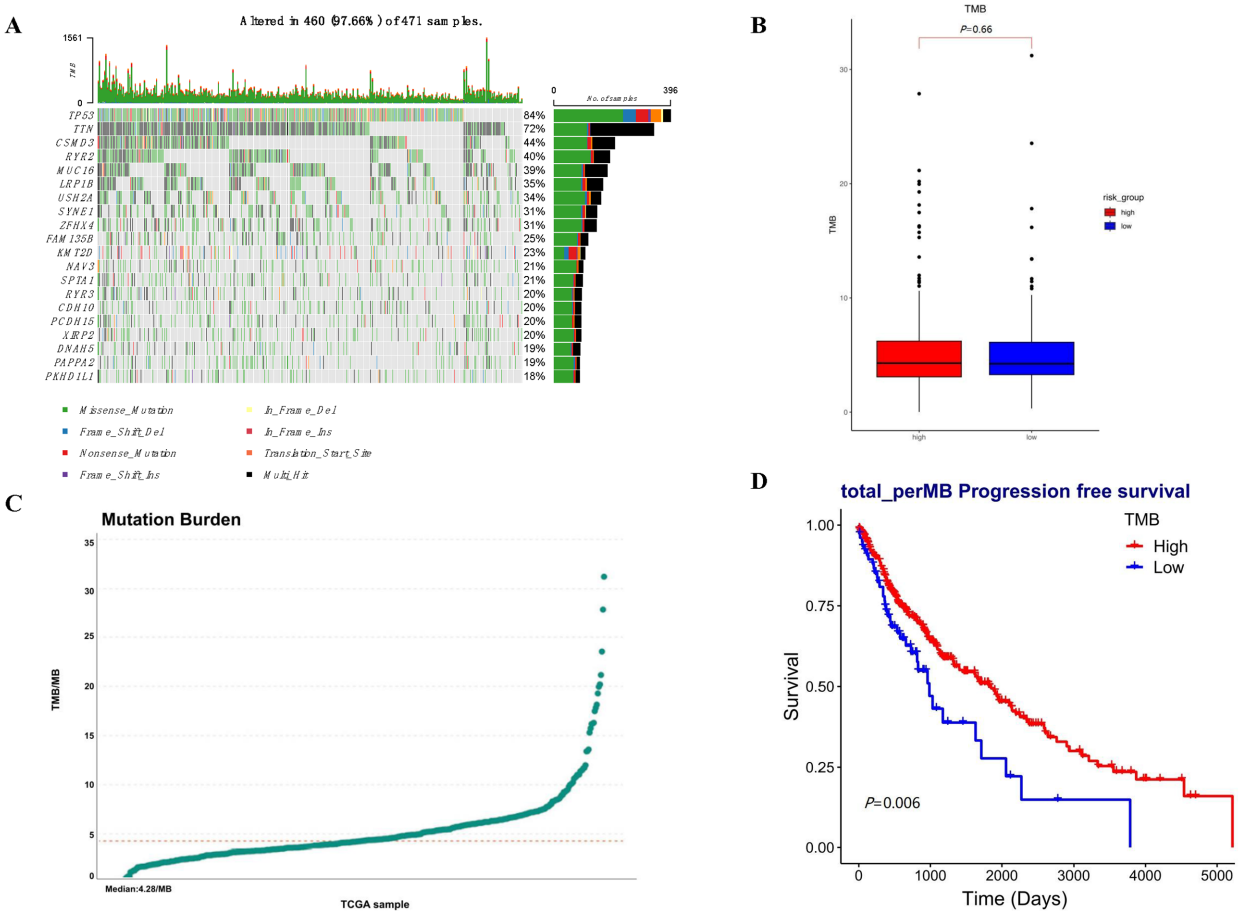

Figure S4 Analysis of the genetic mutations. (A) The 20 most frequently mutated genes. (B) Correlation between the risk group and TMB. (C) TMB sorting of all the samples. (D) Prognostic difference between the TMB-high and TMB-low groups. TMB, tumor mutation burden; TCGA, The Cancer Genome Atlas.

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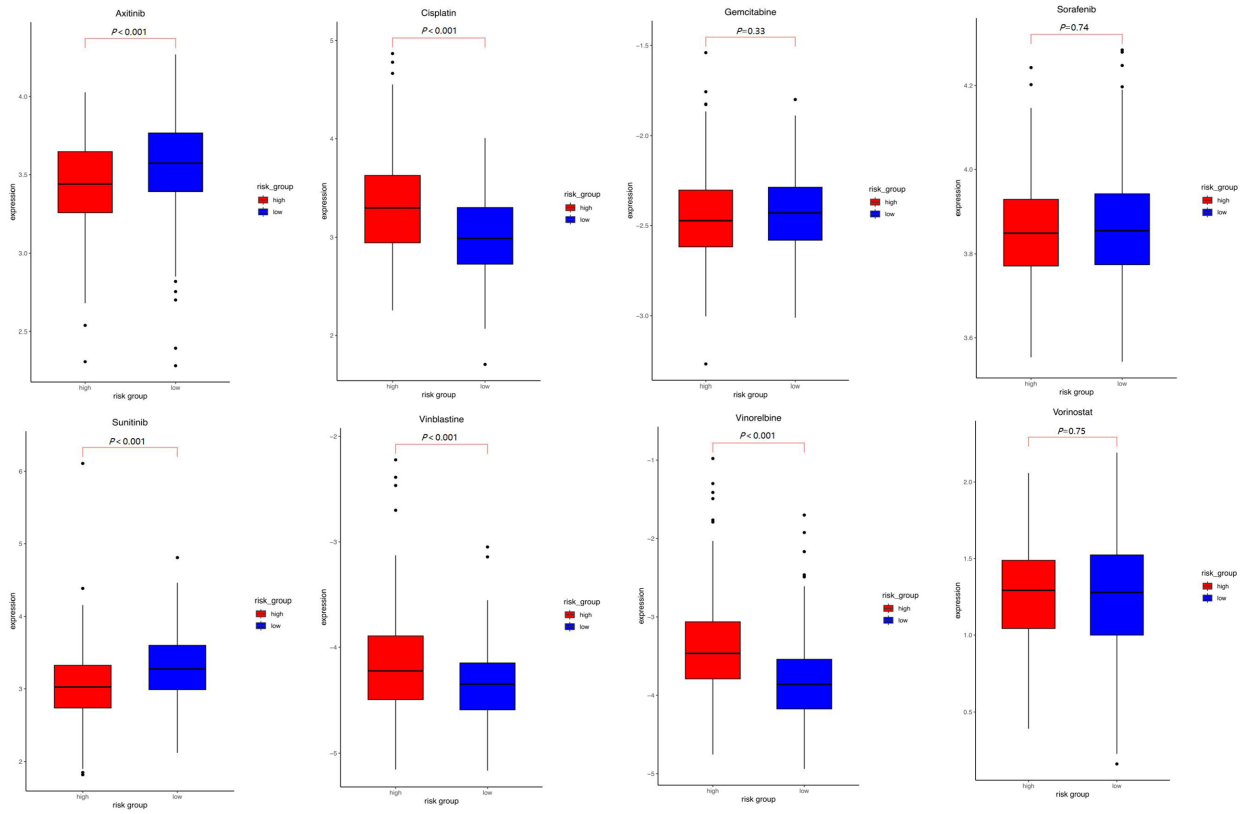

Figure S5 Difference in drug sensitivity between the high- and low-risk groups.

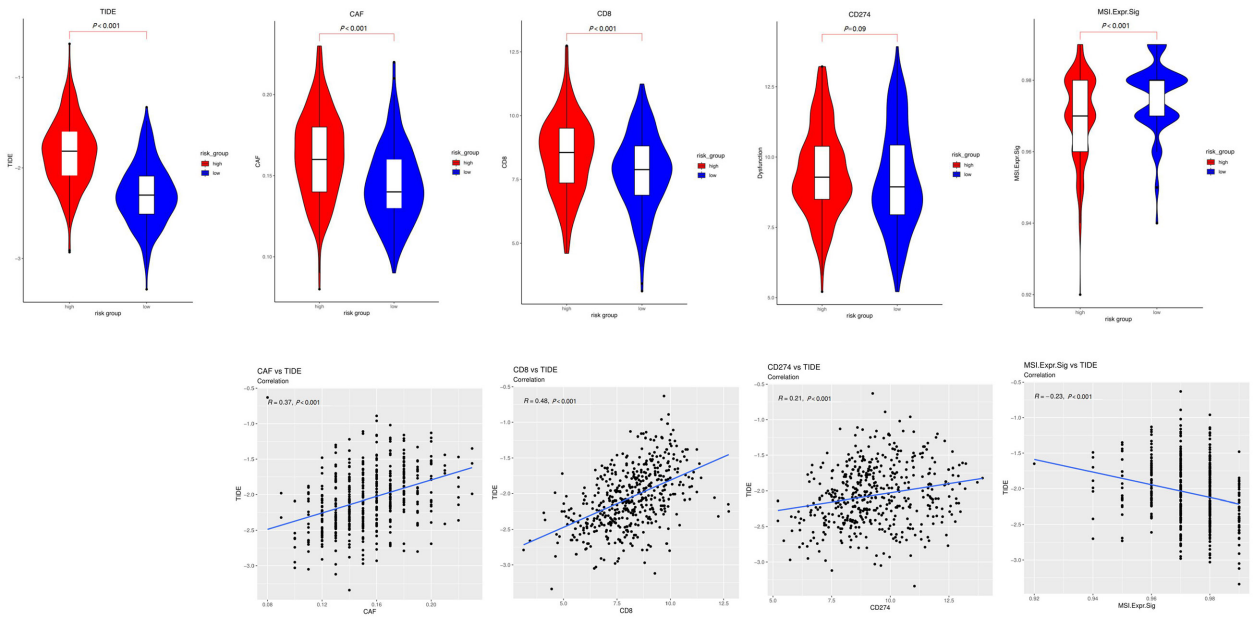

Figure S6 Analysis of TIDE. TIDE, Tumor Immune Dysfunction and Exclusion; CAF, cancer-associated fibroblasts; MSI, microsatellite instability; expr., expression; sig, significant.

https://dx.doi.org/10.21037/tlcr-24-411