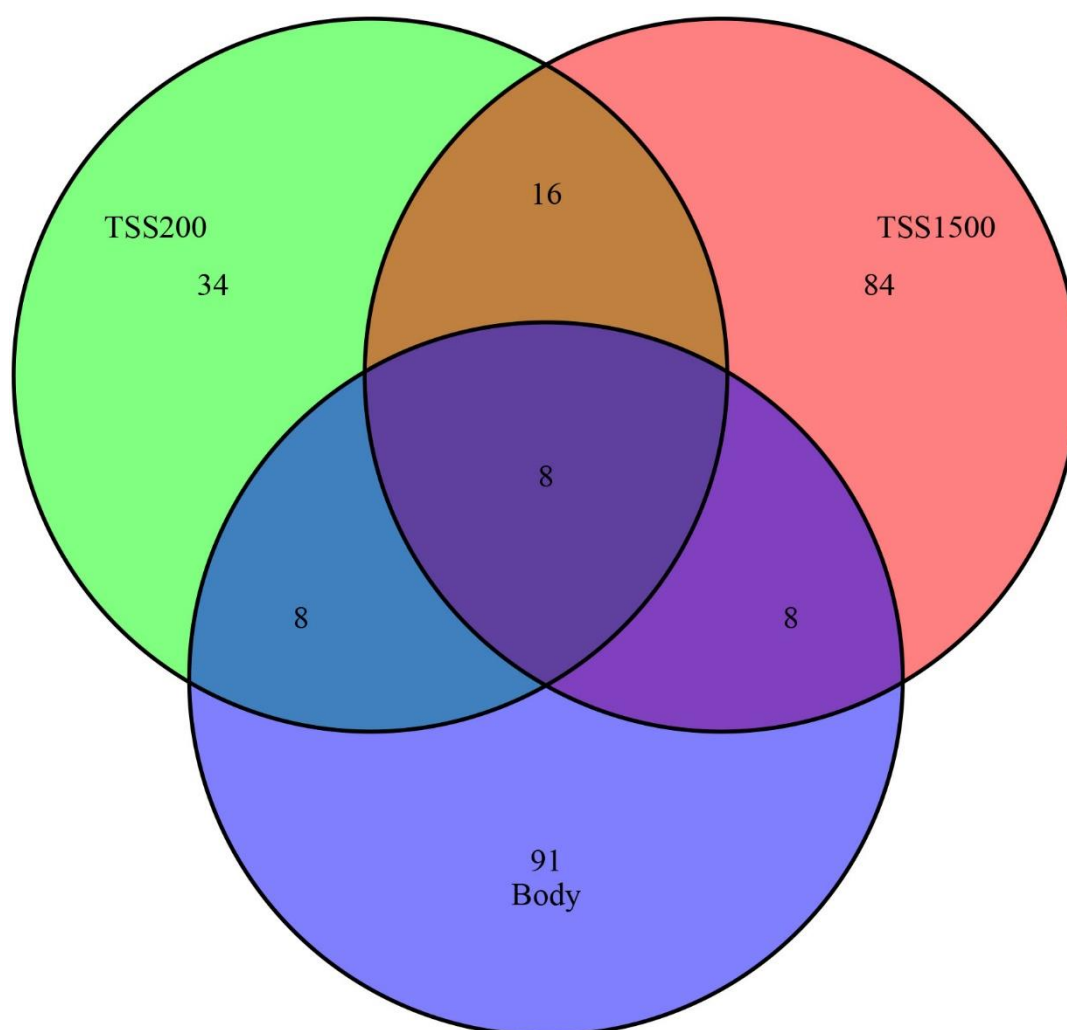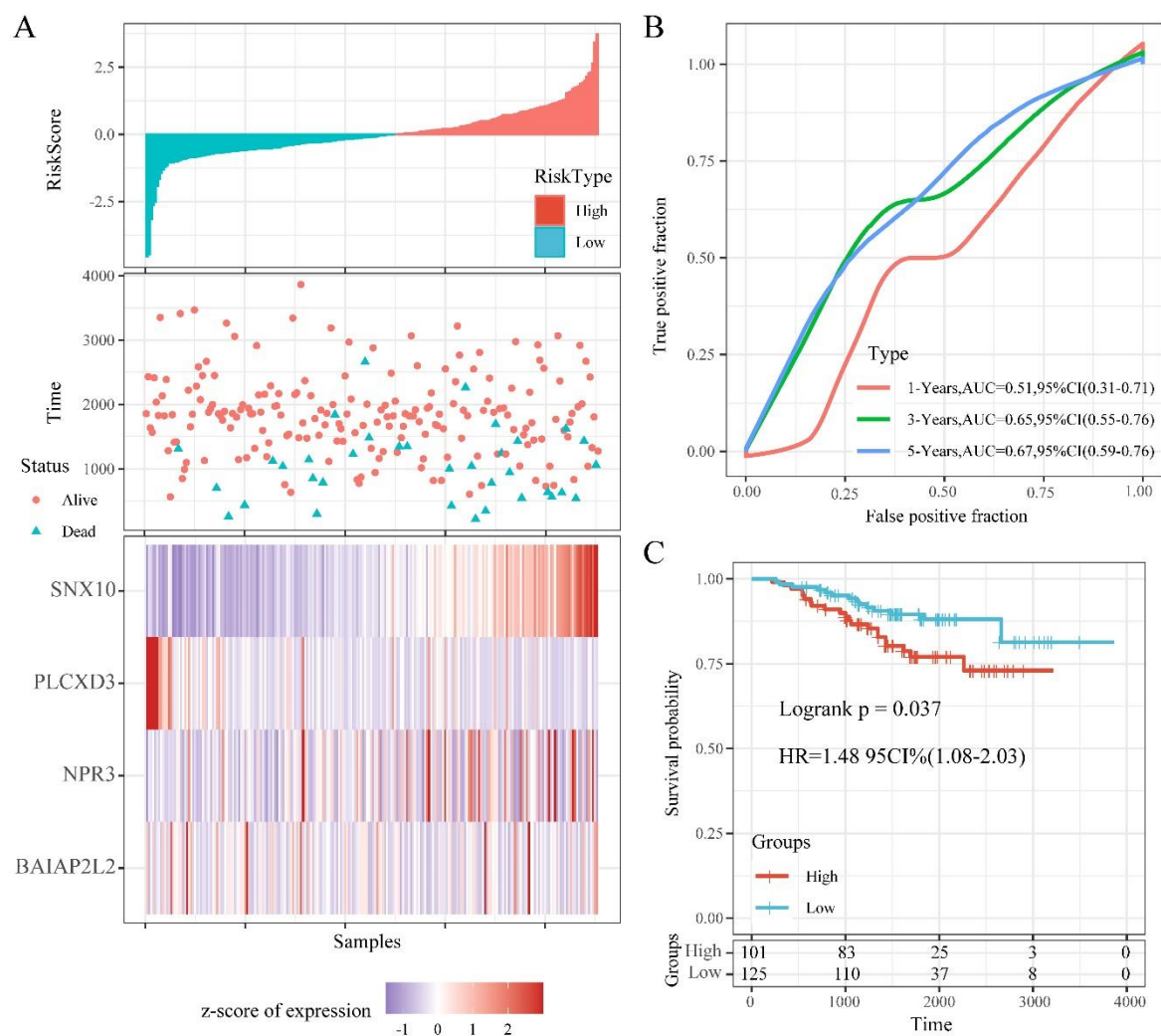*Supplementary Materials*

Combined Methylome and Transcriptome Analyses Reveals Potential Therapeutic Targets for EGFR Wild Type Lung Cancers with Low PD-L1 Expression

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Figure S1. Venn mapping showing the intersection of DMEGs in TSS200, TSS1500 and gene body.

Figure S2. The relationship between RiskScore and patient outcome in the validation cohort (from GEO). (**A**) Each patient's RiskScore, survival time and status, and the expression of 4 DMEGs. The horizontal axis represents the samples, and the vertical axis represents RiskScores, OS, and immune-related gene expression, respectively. (**B**) 1-, 3-, and 5-years ROC analysis of prognosis classification for RiskScore. (**C**) KM survival analysis of patients with high RiskScore vs low RiskScore.
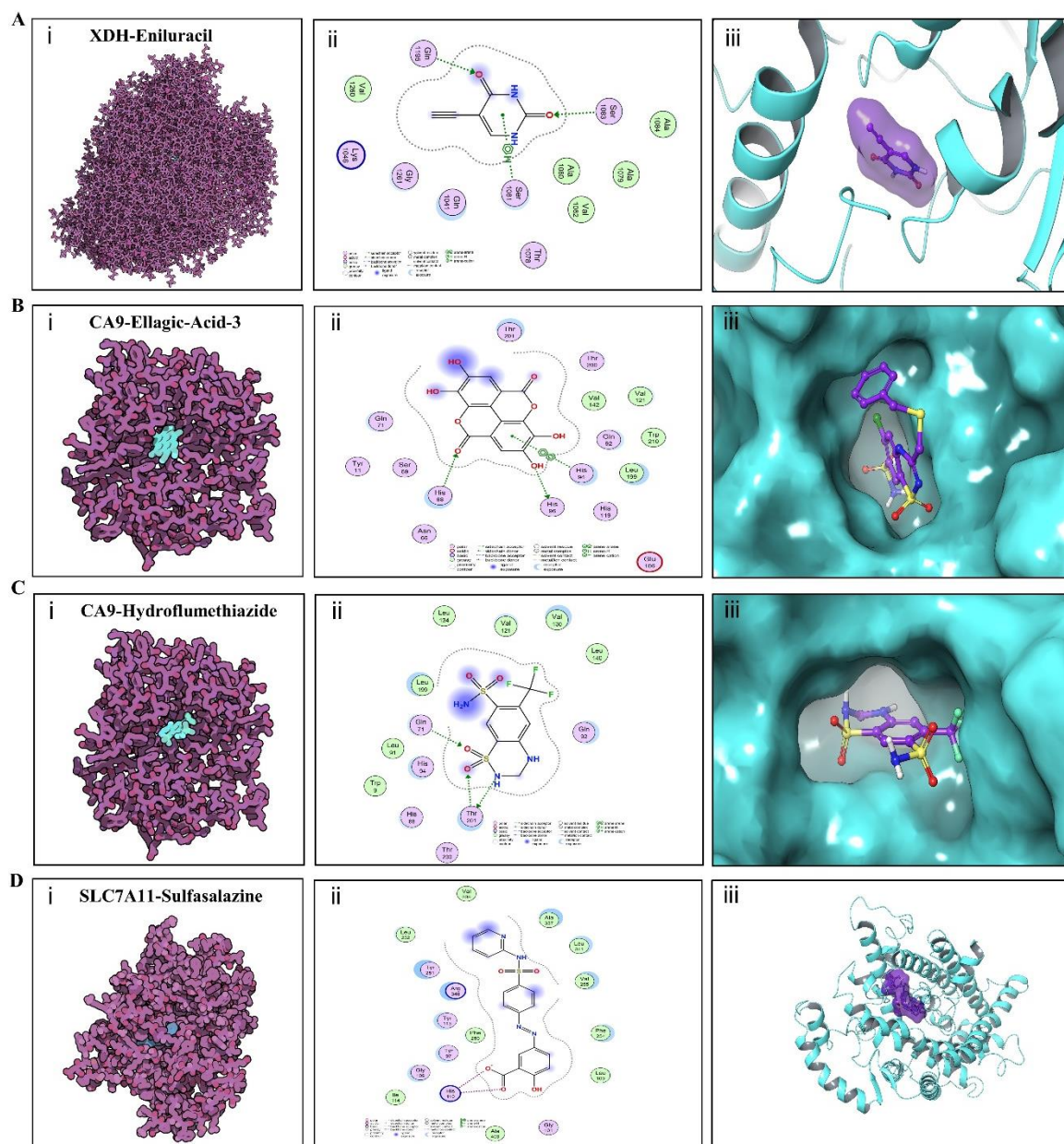
Figure S3. Binding mode of screened drugs to their targets by molecular docking. (**A**) Binding mode of XDH-Eniluracil complex. (**B**) Binding mode of CA9-(Ellagic-Acid-3) complex. (**C**) Binding mode of CA9-Hydroflumethiazide complex. (**D**) Binding mode of SLC7A11-Sulfasalazine complex. (**i**), Cartoon representation, overlay of the crystal structures of small molecule compounds and their targets were illustrated by Molecule of the Month feature. (**ii**), 2D interactions of compounds and their targets. (**iii**) 3D structures of binding interface were showed by PyMOL software.