Supplementary Figures

Association of *EYS* mutations with immune checkpoint inhibitor outcome and response in melanoma and non-small cell lung cancer

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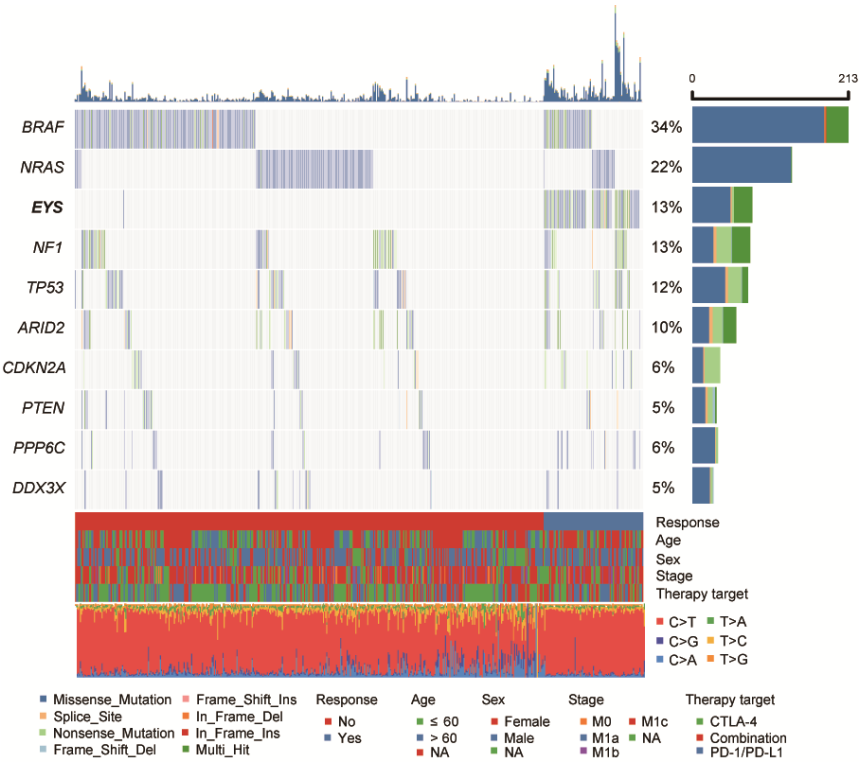

Figure S1. Waterfall plot of *EYS* mutations in SKCM patients with mutation information for specific genes.

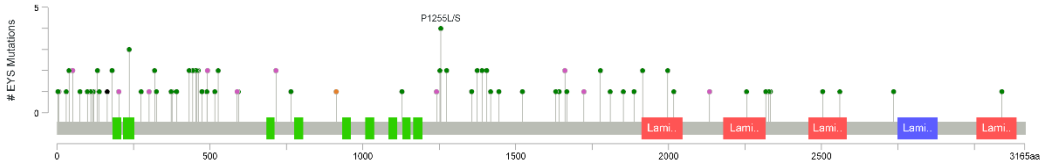

Figure S2. Amino acid modifications associated with altered *EYS* mutations in SKCM patients.

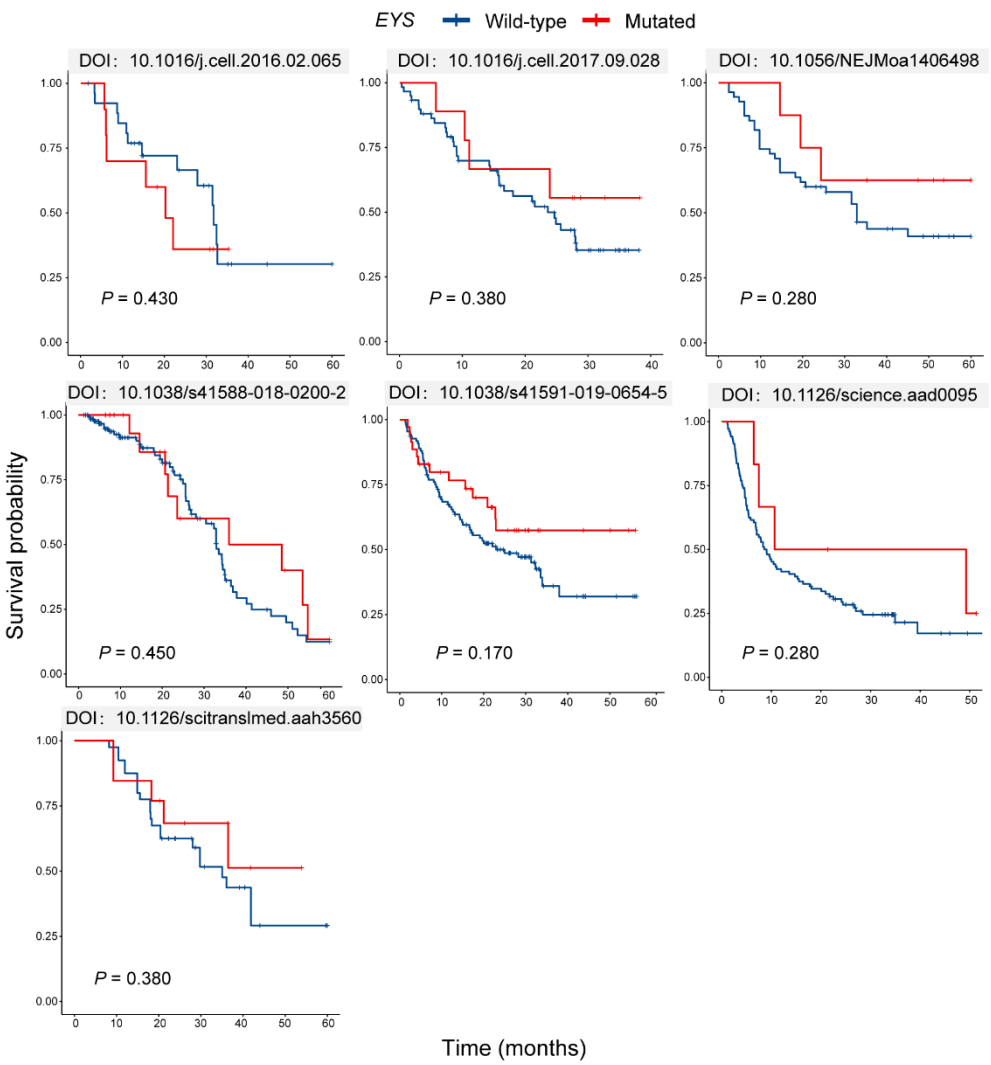

Figure S3. Survival predictive power of *EYS* mutations in a single SKCM cohort.

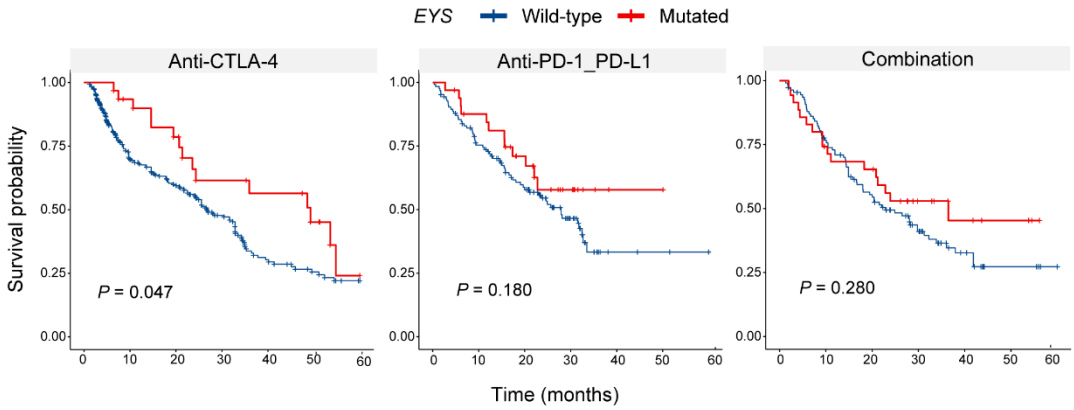

Figure S4. Survival predictive ability of *EYS* mutations in different SKCM ICI treatments.

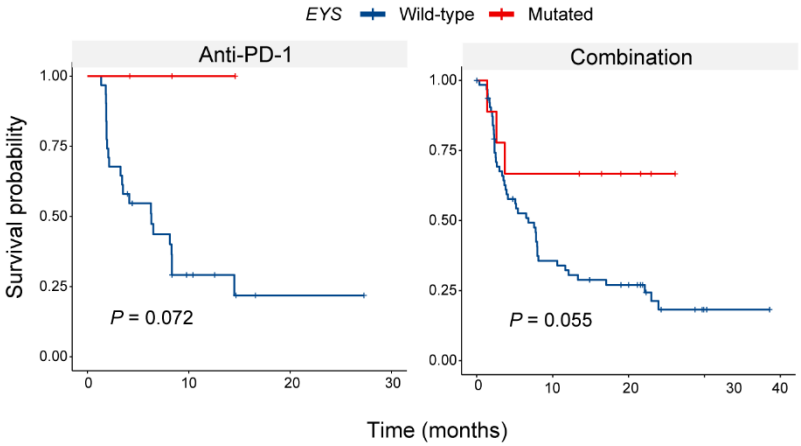

Figure S5. Survival predictive ability of *EYS* mutations in different NSCLC ICI treatments.

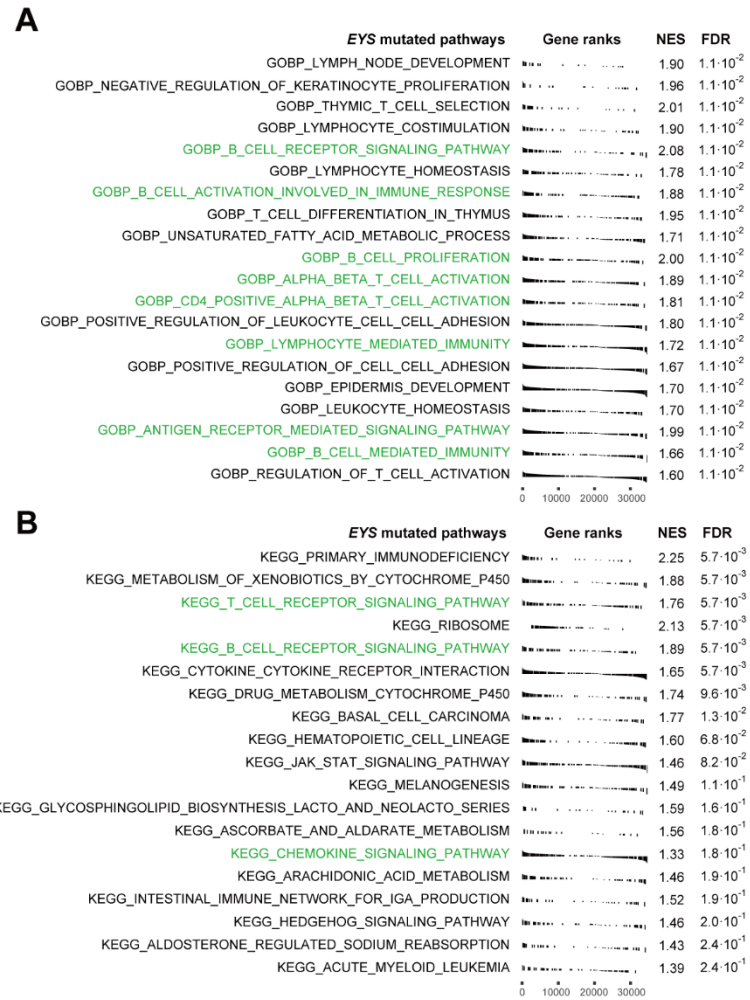

Figure S6. Pathway enrichment analysis results of GSEA in SKCM based on GO and KEGG gene sets in patients with *EYS* mutations.

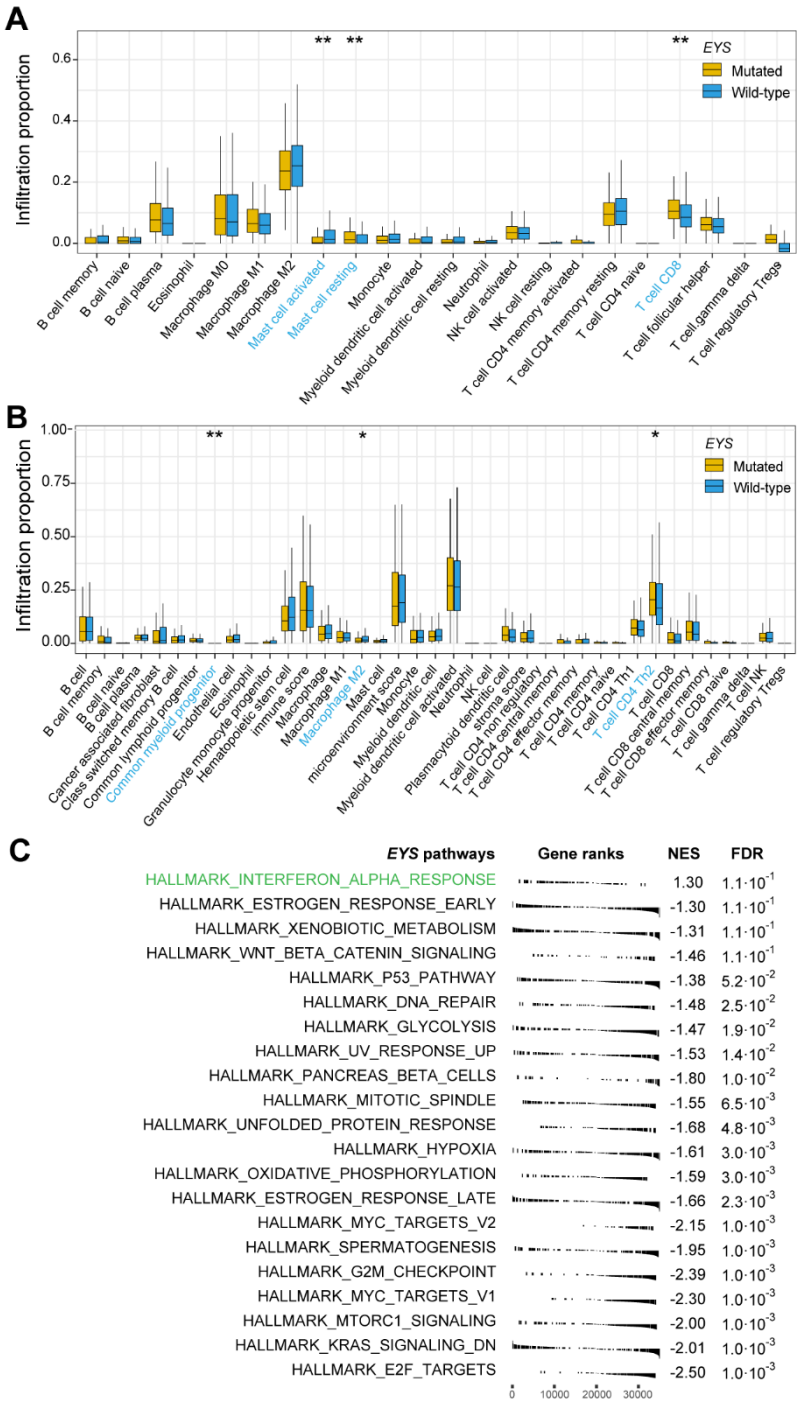

Figure S7. Immune infiltration and molecular pathways associated with *EYS* mutations in NSCLC. (A) Differences in the infiltration levels of 22 immune cells between *EYS*-mutant vs. wild-type patients based on the CIBERSORT algorithm, with significantly different immune cells highlighted in blue. (B) Differential enrichment scores of 64 immune/stromal cells in *EYS*-mutant vs. wild-type patients based on the xCell algorithm. (C) GSEA-based pathway enrichment analysis results of the two subgroups of *EYS* in NSCLC.

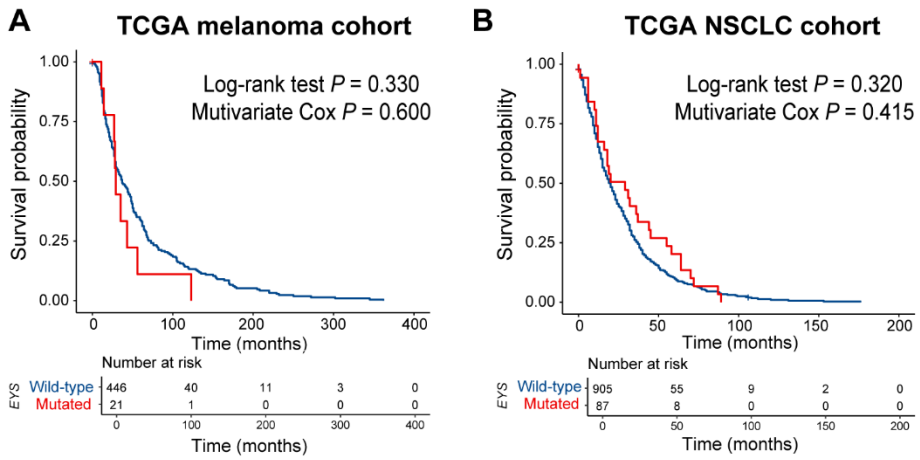

Figure S8. Survival predictive ability of *EYS* mutations in (A) SKCM and (B) NSCLC patients obtained from the TCGA cohort.