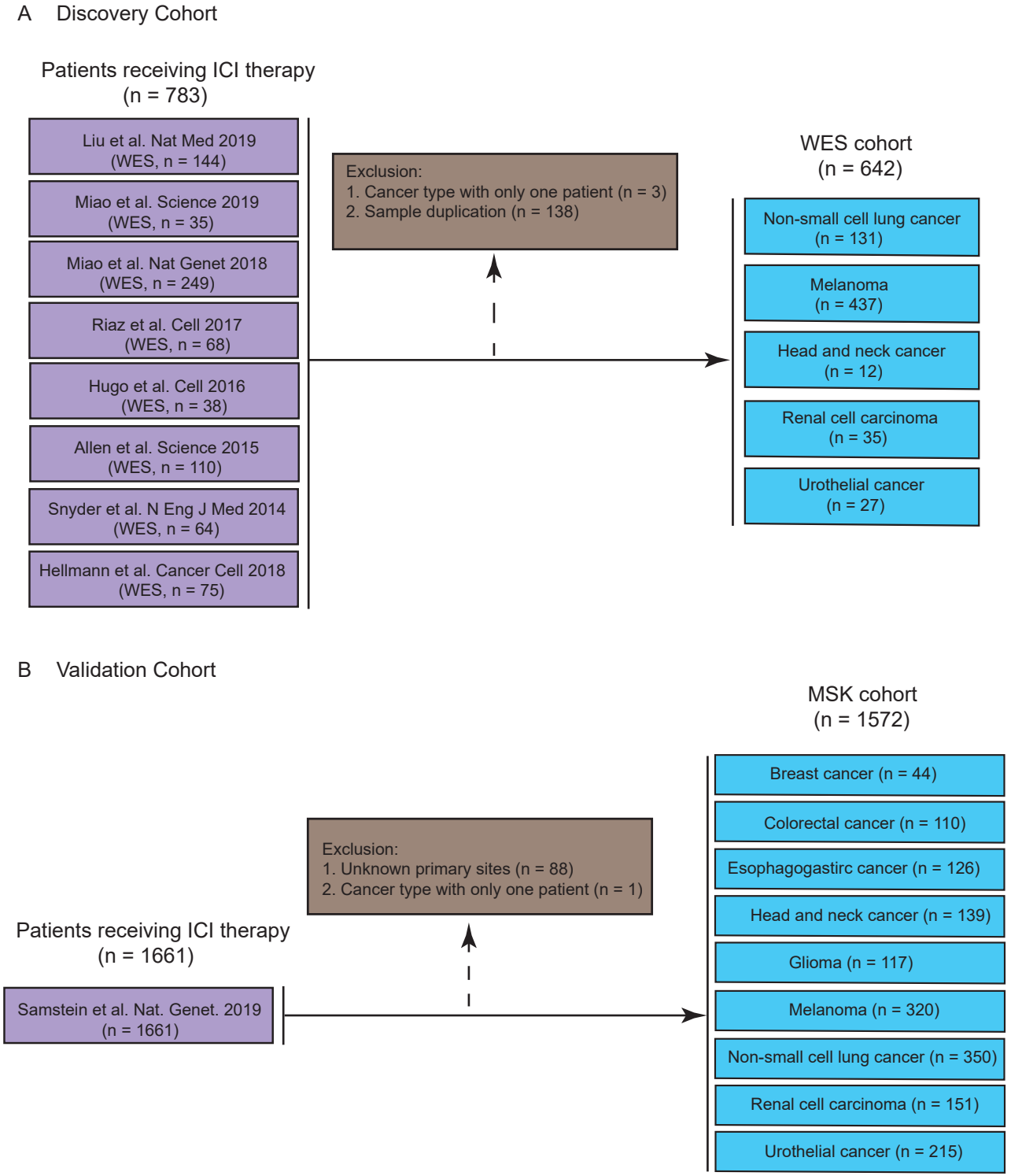

Figure S1. The inclusion and exclusion of the discovery and validation cohorts.

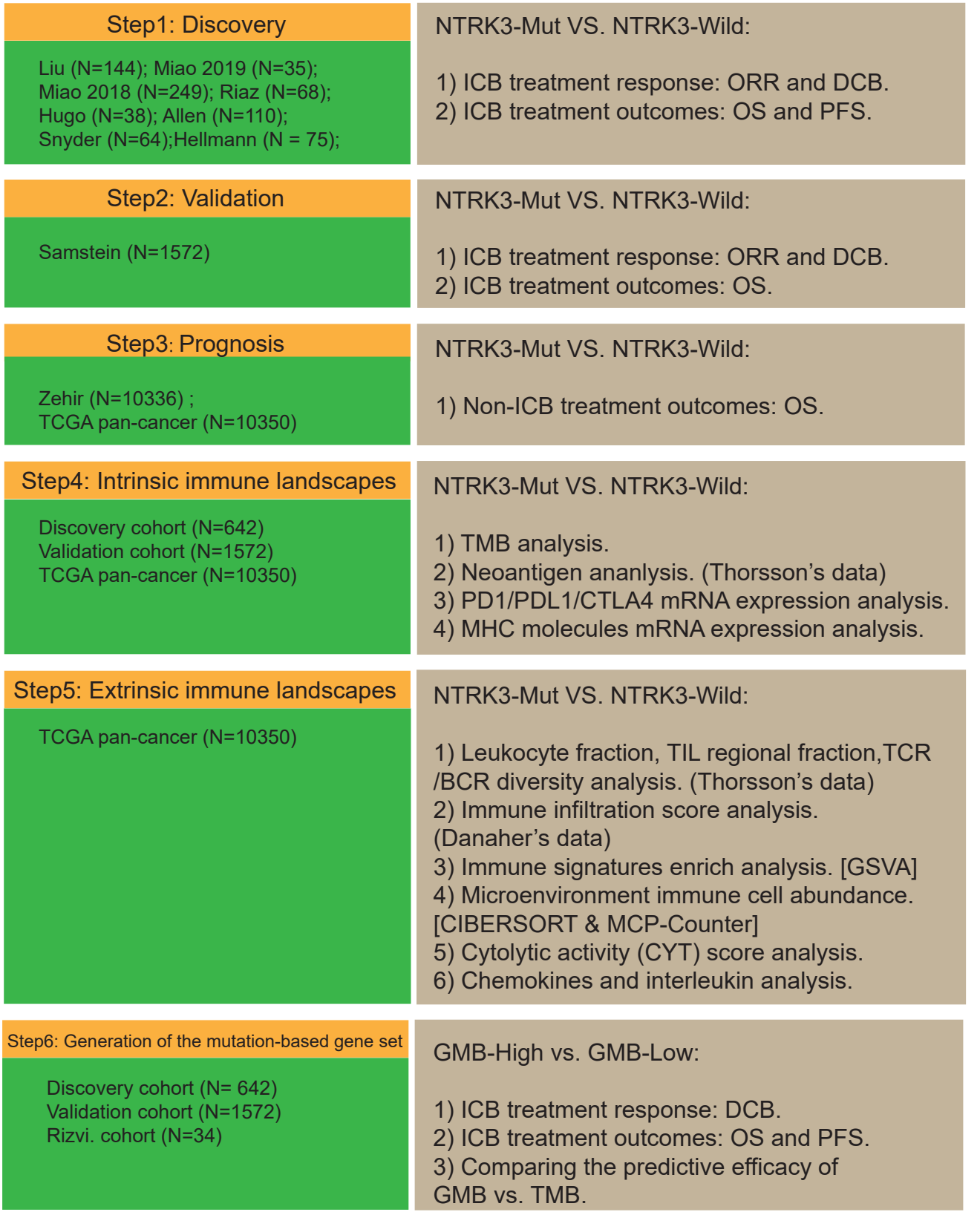

Figure S2. The flow chart of this study.

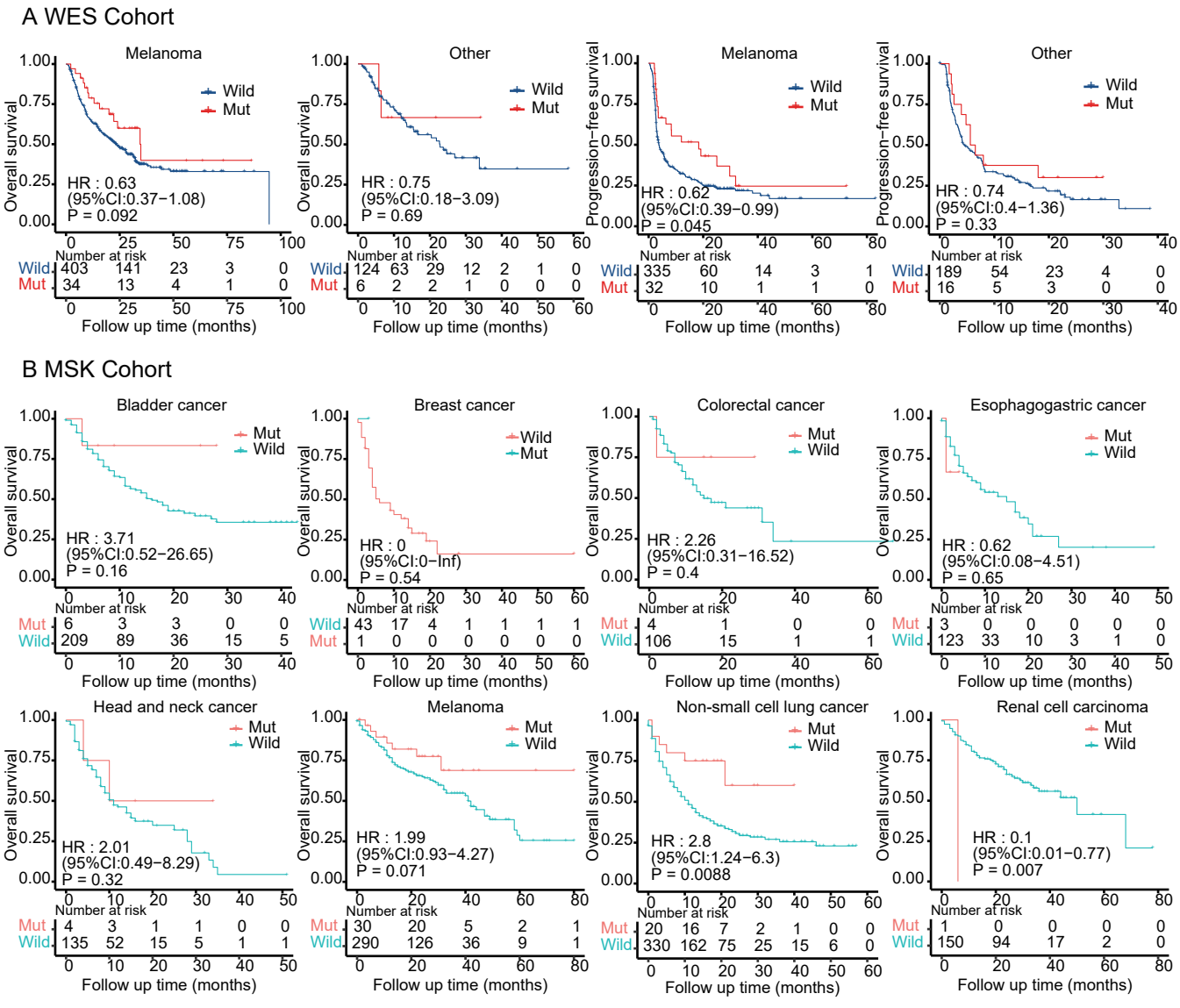

Figure S3. Subgroup survival analyses of different cancer types in the WES and MSK cohorts.

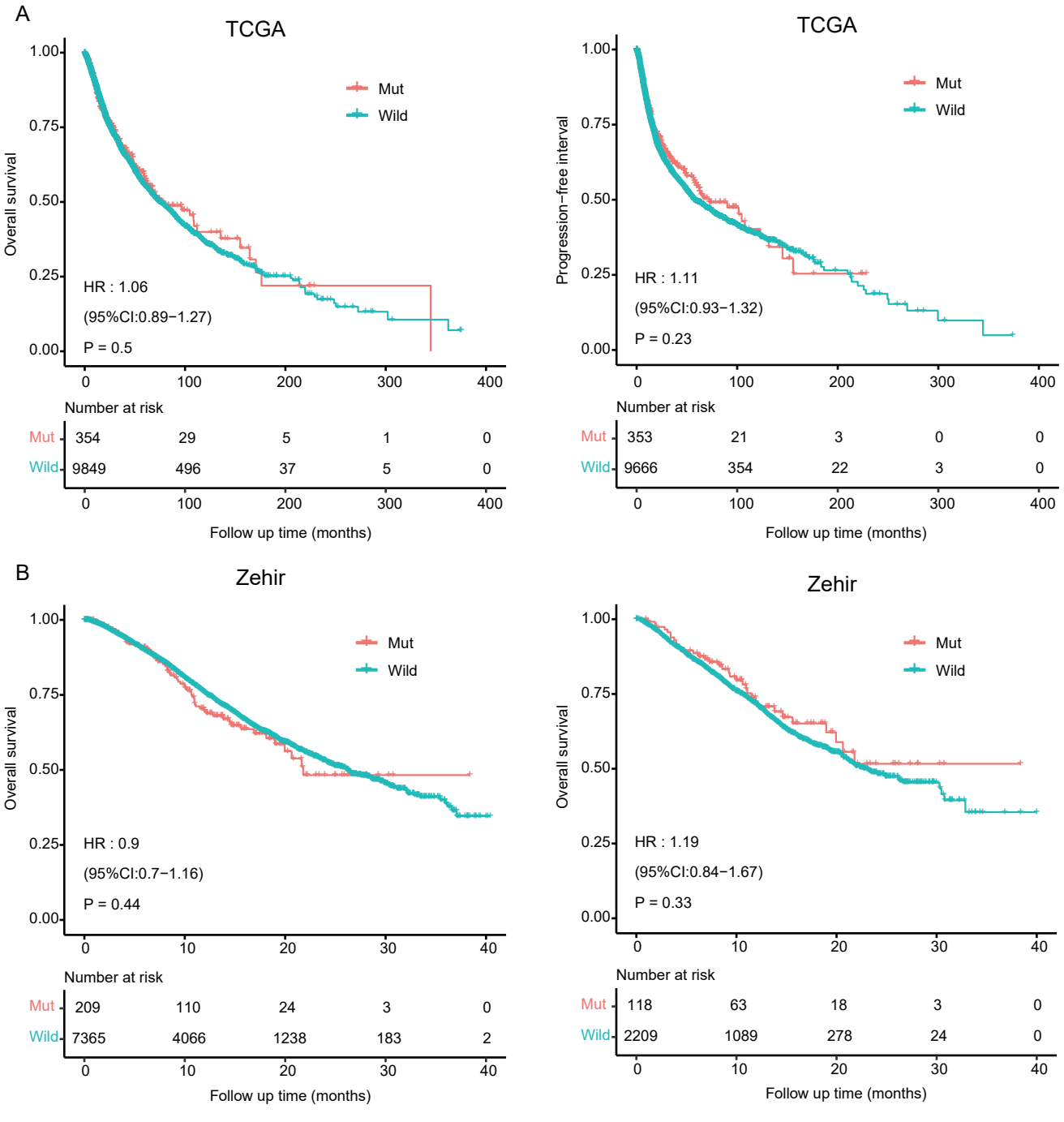

Figure S4. The survival analysis of NTRK3 mutation in the TCGA (A) and Zehir (B) cohorts.

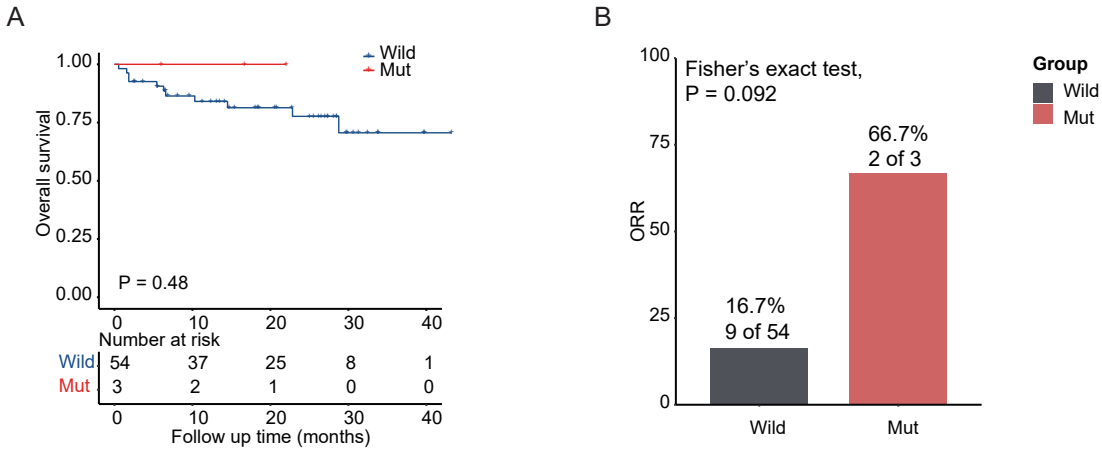

Figure S5. The association between NTRK3-Mut, overall survival and response in the internel cohorts (n = 57).

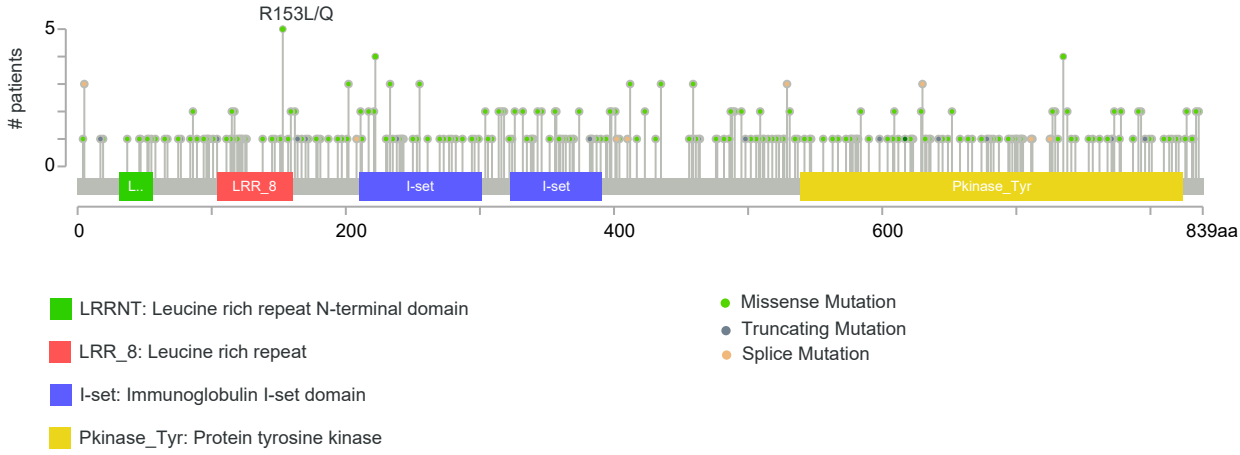

Figure S6. The mutation landscape of NTRK3 genome.

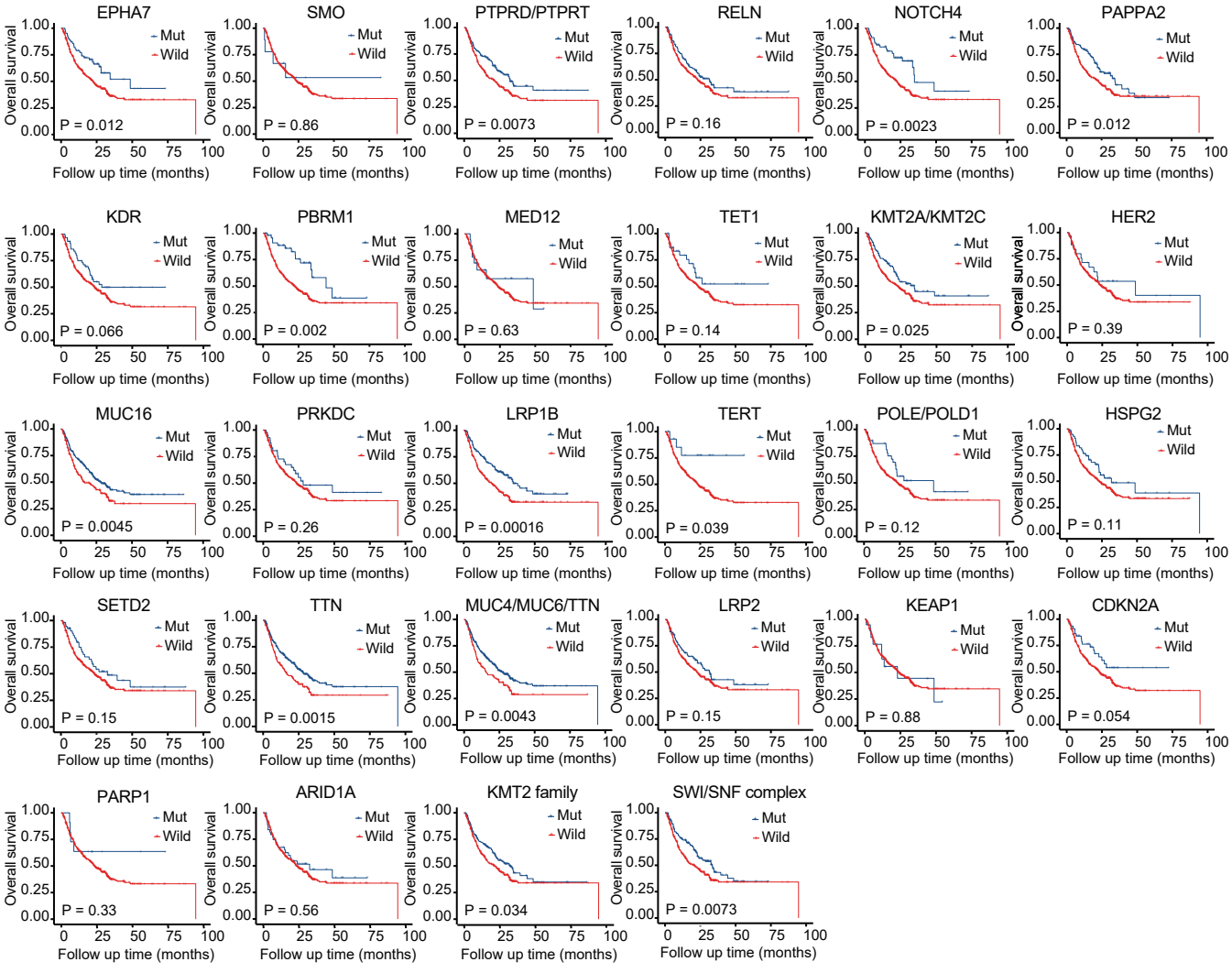

Figure S7. Overall survival analysis of candidate genes in the WES cohort.

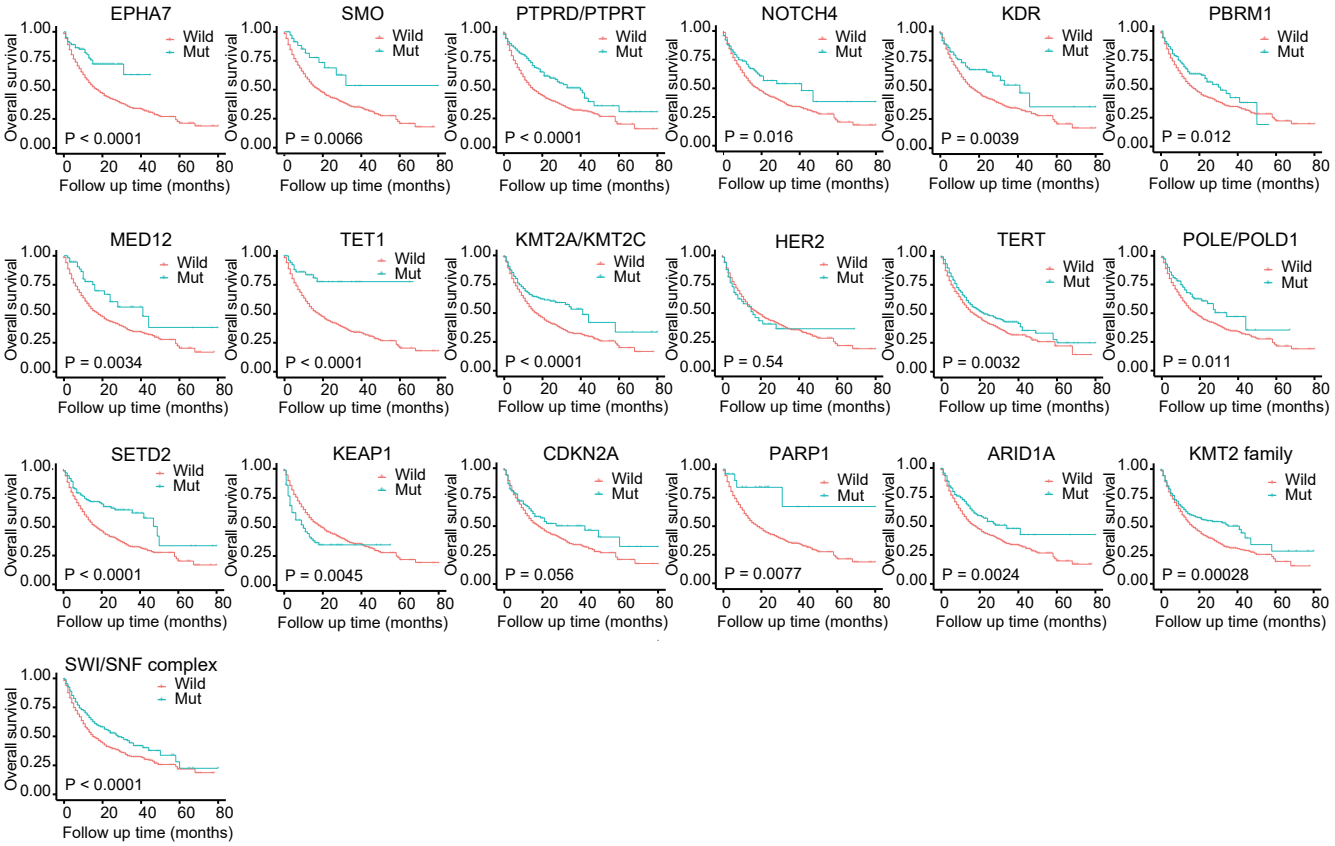

Figure S8. Overall survival analysis of candidate genes in the MSK cohort.

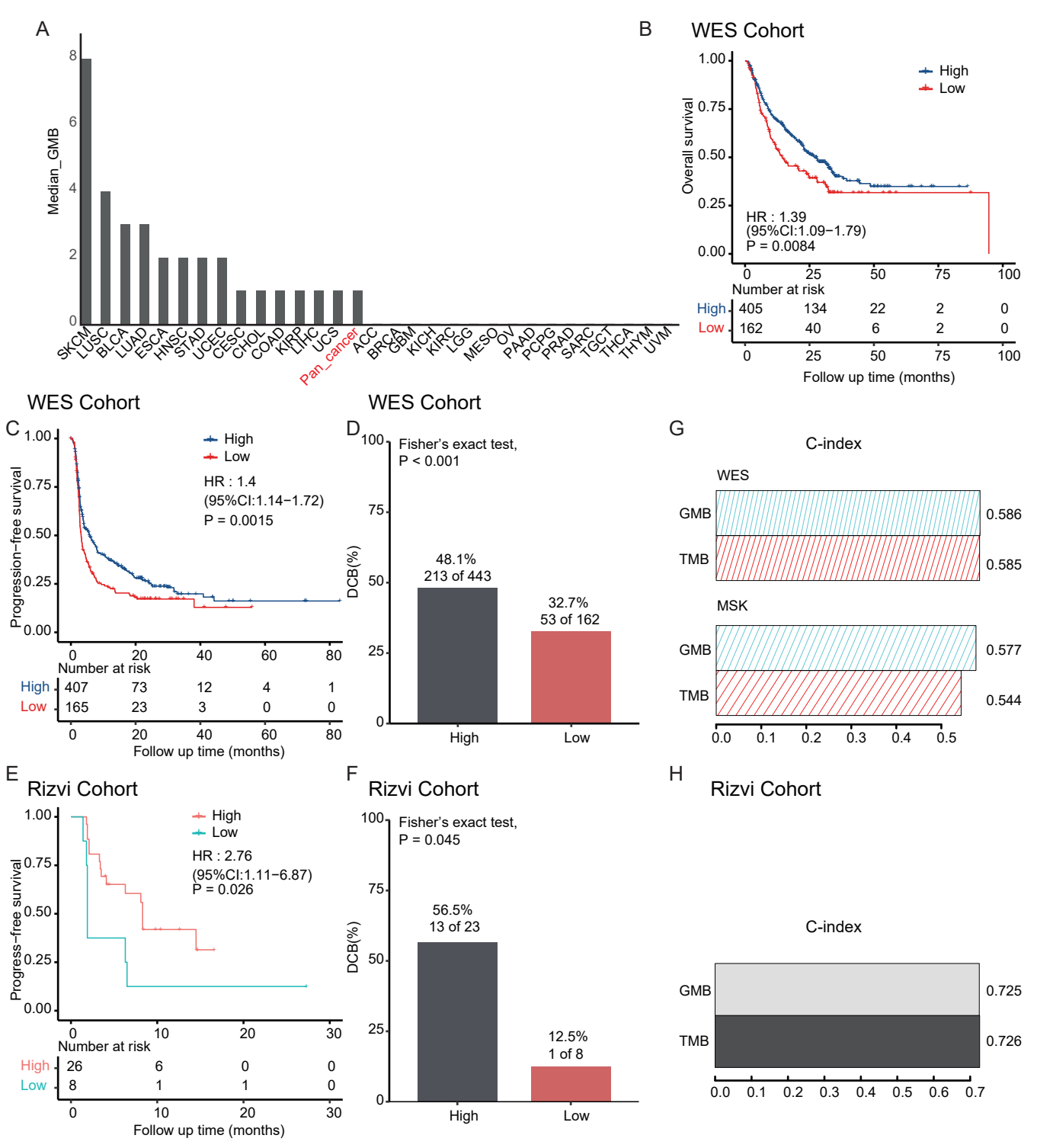

Figure S9. Construction and validation of the mutation-based gene set. (A) The median mutation number of the mutation-based gene set in TCGA solid tumors. (B) Overall survival (OS) analysis of the mutation-based gene set in the WES cohort. (C) Progression-free survival (PFS) analysis of the mutation-based gene set in the WES cohort. (D) Durable clinical benefit (DCB) comparison of the mutation-based gene set in the WES cohort. (E) P-rogression-free survival (PFS) analysis of the mutation-based gene set in the Rizvi cohort. (F) Durable clinical benefit (DCB) comparison of the mutation-based gene set in the Rizvi cohort. (G-H) Comparison of the efficacy between TMB and the mutation-based gene set in the WES, MSK, and Rizvi cohorts.

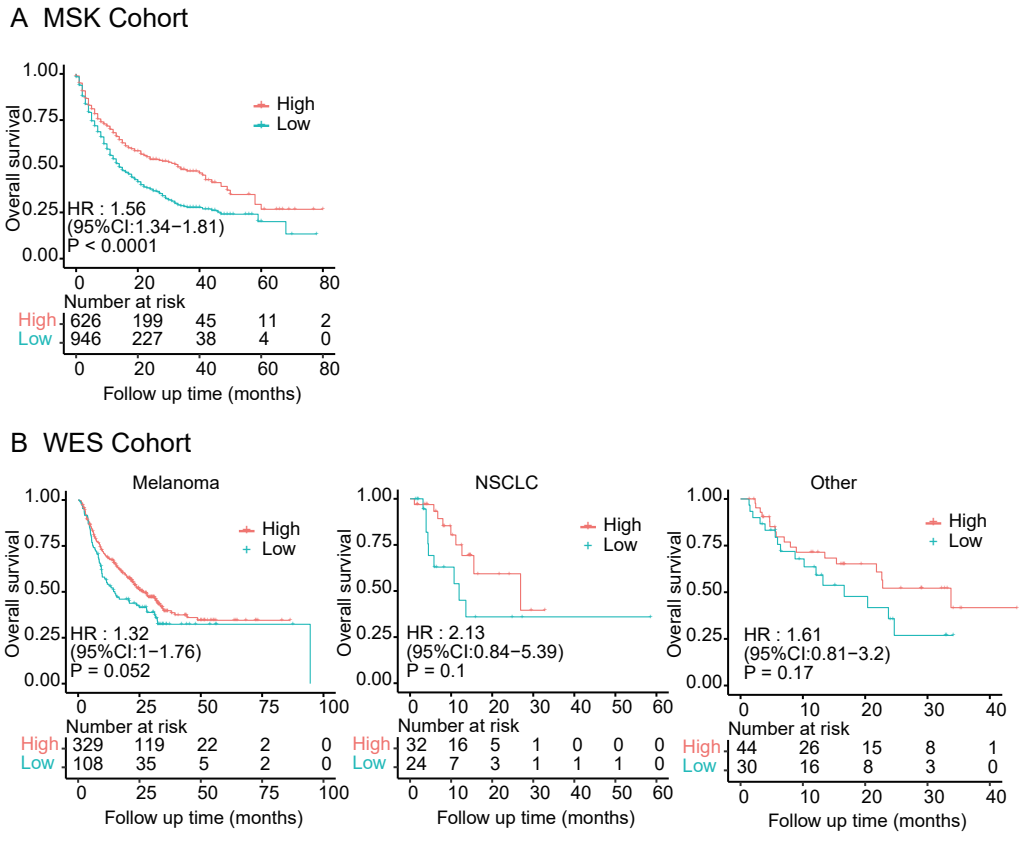

Figure S10. Overall analysis of the mutation-based gene set in the MSK cohort (A) and different types of cancers in the WES cohort (B).