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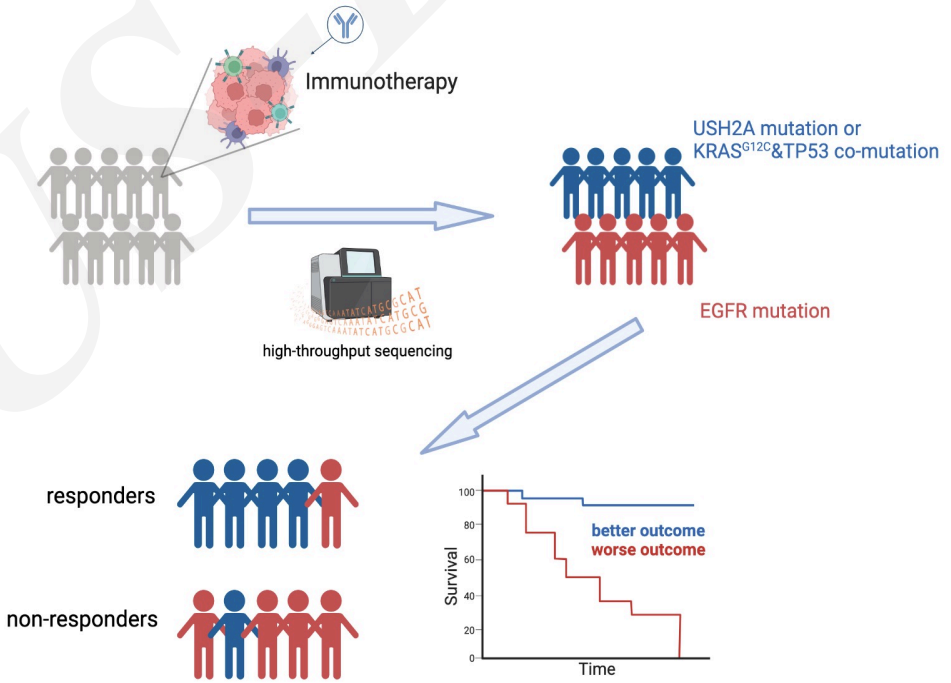
USH2A mutation and specific driver mutation subtypes are associated with clinical efficacy of immune checkpoint inhibitors in lung cancer

Key words: Immune Checkpoint Inhibitors, Lung cancer, USH2A missense mutations, $KRAS^{G12C}$ mutation combined with TP53 mutation, EGFR mutations

Research Summary

This study aimed to identify subtypes of genomic variants associated with the efficacy of immune checkpoint inhibitors (ICIs) based on previous publication, and summarized the conclusion as follows:

- A total of 1546 lung cancer patients with available genomic variation data were included from 14 studies.
- USH2A missense mutations, $KRAS^{G12C}$ mutation combined with TP53 mutation were associated with better efficacy and survival outcomes
- EGFR classical mutations irrespective of combination with $EGFR^{T790M}$ showed the opposite role



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Innovation points

HighLights of this work:

- Individual patient-level analyses with published clinical study data to examine the genomic features correlated with clinical and survival outcomes
- $KRAS^{G12C}$-TP53 co-mutation was correlated with significantly favorable outcomes
- Patients with EGFR classical activating mutations (including L858R missense mutation, exon 19 in-frame deletion) were related to worse outcomes, irrespective of combination with T790M mutation
- Patients harboring USH2A missense mutation showed significantly favorable clinical benefit and prolonged survival