# Investigation of ARID1A Mutation and correlation with immunotherapy biomarker in Chinese Head and Neck Cancer Patients

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Abstract 3437

## Background

- AT-rich interactive domain 1A (ARID1A), a gene that encoding a subunit of the BAF (SWI/SNF) chromatin remodeling complex, is correlated with the origination and progress of tumor. Previous research on ARID1A gene revealed that ARID1A deficiency was associated with higher tumor mutation burden (TMB) level and mismatch repair (MMR) in cancer, which might cooperate with immune checkpoint blockade therapy. However, the ARID1A characteristics, its correlation with immunogenic marker, and the predictive value of immunotherapy in head and neck cancer was unknown

## Methods

- An independent cohorts (the MSKCC study cohort) with next generation sequencing (NGS) data from 129 patients with head and neck cancer of pan-cancer, were used to analyze the prognostic effect of ARID1A on immunotherapy. Tumor tissue samples from Chinese head and neck cancer were analyzed using NGS (panel on 381/733-gene). TMB was defined as total number of somatic non-synonymous mutations in coding region. MSI was evaluated by NGS of 500 known MSI loci. PD-L1 expression was evaluated using immunohistochemistry (Dako 22C3).

## Results

- In Chinese patients, genetic mutation of 366 head and neck cancer patients were analyzed using NGS, of which 25 (6.8%) harbored ARID1A$^{mut}$. In head and neck cancer patients with ARID1A$^{mut}$, the most frequently mutated genes were TP53 (72%), followed by CYP2C19 (48%), DPYD (48%), ATM (36%), KMT2C (36%), BRCA1 (32%) and NOTCH1 (32%).

## Results

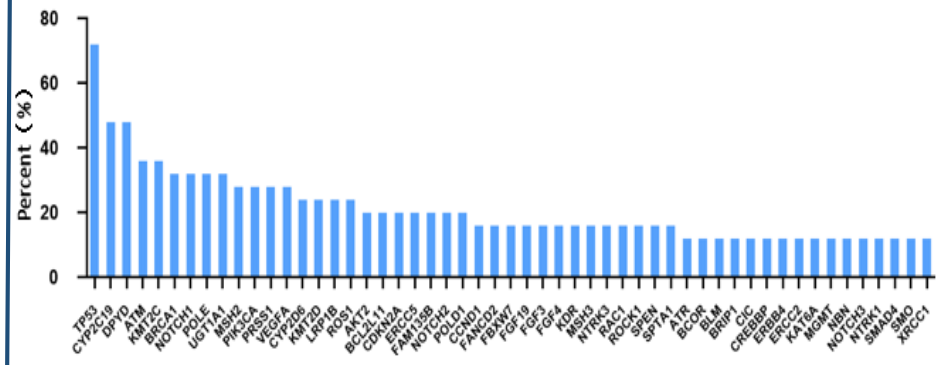


**Figure1. Statistics of other gene mutations in in Chinese head and neck cancer with ARID1A (showing mutation frequency > 10%)**

- ARID1A$^{mut}$ (median, 6.45 Muts/Mb) was associated with higher TMB (P =0.002) than ARID1A$^{wt}$ (median, 5.14 Muts/Mb), which was significant difference. The same as TMB, there was significant difference in MSI between ARID1A$^{mut}$ and ARID1A$^{wt}$ (P＜0.001). But there was no difference in PD-L1 expression between ARID1A$^{mut}$ and ARID1A$^{wt}$ (P =0.71).

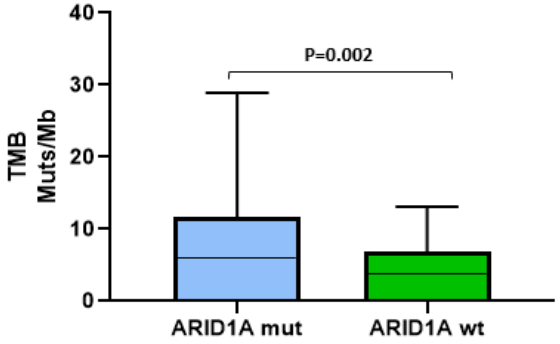


**Figure2. TMB statistics for Chinese patients with ARID1A$^{mut}$ and ARID1A$^{WT}$ in head and neck cancer**

- In MSKCC cohort, there were 10 (7.6%) patients harbored ARID1A mutation. ARID1A mutation (ARID1A$^{mut}$) (median, 8.85 Muts/Mb) was associated with higher TMB (P =0.046) than PALB wild-type (ARID1A$^{wt}$) (median, 5.58 Muts/Mb).

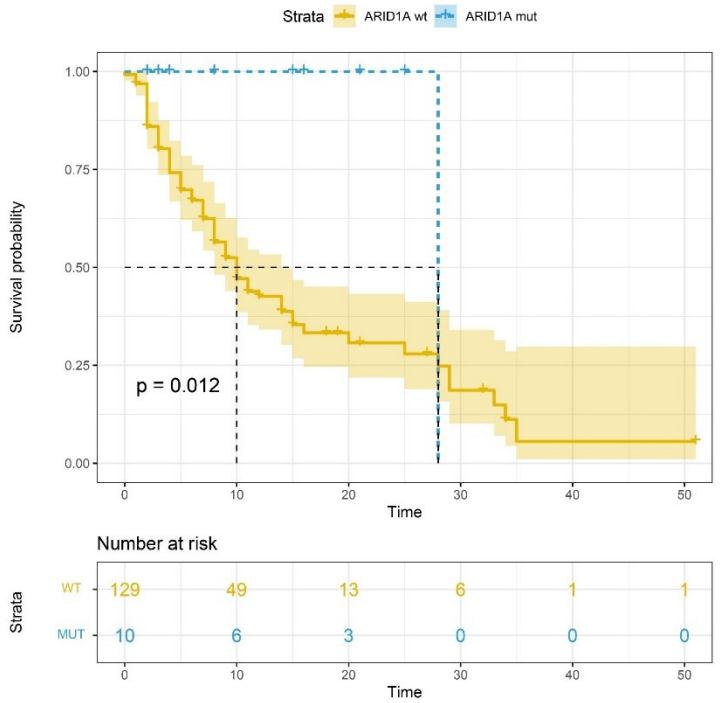


**Figure3. Association between ARID1A statue and the prognosis in head and neck cancer**

## Conclusion

- The results showed that the ARID1A gene had a high correlation with TMB and MSI in head and neck cancer, and might a potential biomarker for immune checkpoint therapy.