BACKGROUND

- Glioblastoma, IDH-wildtype (GBM) is the most common malignant tumor of the human central nervous system with a poor prognosis.
- The distribution of copy number variations and the molecular targeted therapy are unknown.
- Therefore, it is important to understand the somatic copy number genome profile of Chinese adult glioblastoma patients.

RESULTS

- Copy number variations was observed in 1871 of 2839 glioblastoma samples (65.9%) (Fig 1). The six most common genes with copy number variation were CDKN2A (48.8%), CDKN2B (47.1%), EGFR (24.3%), PTEN (17.1%), CDK4 (11.3%), PDGFRA (9.3%) (Fig 2).
- Patients with EGFR amplification often carried CDKN2A (16.2%), CDKN2B (15.4%) and PTEN (7.0%), while patients with PDGFRA amplification often carried KIT (7.54%), CDKN2A (6.1%) and KDR (5.9%). MDM2 (7.0%), CDKN2A (6.0%) and CDKN2B (6.2%) were common copy number variants in the CDK4-amplification group.

CONCLUSIONS

- In our GBM patients, 65.9% present copy number variations RB1 cell-cycle, TP53, and RTK pathways are common signaling pathway alterations. CDKN2A/B deletion had the highest incidence and were enriched in EGFR-amplified patient.
- The high frequency of copy number variations in RB1 cell-cycle pathways in glioblastoma suggests that it may be a direction for targeted therapy.