

Chromosome 2

- A de novo deletion underlying spinal muscular atrophy: implications for carrier testing and genetic counseling
- Dual phenotypes in recurrent astrocytoma, IDH-mutant; coexistence of IDH-mutant and IDH-wildtype components: a case report with genetic and epigenetic analysis
- Gliosarcoma: The Distinct Genomic Alterations Identified by Comprehensive Analysis of Copy Number Variations
- Identification of an Immunogenic Medulloblastoma-Specific Fusion Involving *EPC2* and *GULP1*
- Genome-Wide Association Study Identifies Risk Loci for Cluster Headache
- Uniparental isodisomy of chromosome 2 causing *MRPL44*-related multisystem mitochondrial disease
- Duplication 2p16 is associated with perisylvian polymicrogyria
- A C19MC-LIN28A-MYCN Oncogenic Circuit Driven by Hijacked Super-enhancers Is a Distinct Therapeutic Vulnerability in ETMRs: A Lethal Brain Tumor

Chromosome 2 is one of the 23 pairs of chromosomes in humans. People normally have two copies of this chromosome. Chromosome 2 is the second-largest human chromosome, spanning more than 242 million base pairs (the building material of DNA) and representing almost 8% of the total DNA in human cells.

Chromosome 2 contains the HOXD homeobox gene cluster.

There was a distinct DNA copy number variations (CNV) signal in chromosome 2 especially in **Gliosarcoma**. The pathway enrichment of genes with CNV was suggested that the GBM and GSM shared the similar mechanism of tumor development. However, the CNV of some screened genes displayed a disparate form between GBM and GSM, such as **AMP**, **BEND2**, **HDAC6**, **FOXP3**, **ZBTB33**, **TFE3**, and **VEGFD**. It meant that GSM was a distinct subgroup possessing typical **biomarkers**. The pathways and copy number alterations detected in this study may represent key drivers in gliosarcoma **oncogenesis** and may provide a starting point toward targeted oncologic analysis with therapeutic potential ¹⁾

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Cheng CD, Chen C, Wang L, Dong YF, Yang Y, Chen YN, Niu WX, Wang WC, Liu QS, Niu CS. Gliosarcoma: The Distinct Genomic Alterations Identified by Comprehensive Analysis of Copy Number Variations. *Anal Cell Pathol (Amst)*. 2022 Jun 15;2022:2376288. doi: 10.1155/2022/2376288. PMID: 35757013; PMCID: PMC9226978.

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