

Online resource 4: Average CNV loads of cerebellar and reference glioma methylation classes

methylation class	cerebellar tumors		reference tumors*		p value CNV loads
	n	average CNV load	n	average CNV load	
MC GBM MES	4	4.05*10 ⁸	127	4.60*10 ⁸	0.727
MC GBM MID	11	1.11*10 ⁹	23	6.46*10 ⁸	0.053
MC GBM MYCN	3	1.13*10 ⁹	18	1.07*10 ⁹	0.761
MC GBM RTK I	8	6.10*10 ⁸	72	7.49*10 ⁸	0.261
MC GBM RTK II	2	4.40*10 ⁸	171	6.23*10 ⁸	n.a.
MC GBM RTK III	1	2.13*10 ⁹	9	5.38*10 ⁸	n.a.
MC DMG K27**	6	6.08*10 ⁸	33	5.82*10 ⁸	0.894
MC A IDH**	6	3.22*10 ⁸	32	8.11*10 ⁸	5.10*10 ⁻⁶
MC AAP	25	4.41*10 ⁸	16	3.83*10 ⁸	0.571
MC HGNET BCOR	1	0	14	1.29*10 ⁸	n.a.
MC PA PF	2	2.30*10 ⁸	109	8.35*10 ⁷	n.a.

Methylation classes and average CNV loads of 86 cerebellar tumors with the histological diagnosis of glioblastoma in comparison to 624 reference tumors. CNV – copy number variation, MC - methylation class, A IDH – IDH mutant glioma, AAP – anaplastic astrocytoma with piloid features, HGNET BCOR – high grade neuroepithelial tumor with BCOR alteration, PA PF - low grade glioma, pilocytic astrocytoma GBM MID/MES/RTK I/RTK II/RTK III/MYCN – glioblastoma IDH wildtype subclasses midline/mesenchymal/RTK I/II/III/MYCN, DMG K27 – diffuse midline glioma H3 K27M mutant

*All reference tumors are of supratentorial localization, except for MC PA PF.

** Frequencies of these tumors in the cerebellum may be biased depending on the supplier diagnosis, the date of diagnosis and the availability and application of antibodies/sequencing methods detecting IDH and histone mutations.

Reinhardt et al., Acta Neuropathologica: “Tumors diagnosed as cerebellar glioblastoma comprise distinct molecular entities”, correspondence: andreas.vondeimling@med.uni-heidelberg.de