

Table S3

	p
Frameshift (n=84) versus other (n=88)	0.169796
Missense (n=14) versus other (n=158)	0.163241
Nonsense (n=14) versus other (n=158)	0.050943
Splice (n=46) versus other (n=126)	0.605297
Structural variation (n=14) versus other (n=158)	0.402844
Structural variation, nonsense or frameshift PVs (n=112) versus missense or splicing PVs (n=60)	0.872893

Table S3. Risk of medulloblastoma according to the *SUFU* PV. Chi-square test depending on the type of variation or the expected protein effects of the *SUFU* gene

p-values <0.05 were considered statistically significant

PVs : pathogenic variants