**The process of Next Generation Sequencing**

The tumor DNA was extracted from 10 slides of 15 mm scrolls taken from archived formalin-fixed paraffin-embedded blocks using standard technique (GeneRead DNA FFPE kit, QIAGEN). DNA was profiled by a self-designed targeted panel sequencing assessing 184 genes reported to be frequently mutated in CNS tumors, including common pathological relevant genes in meningiomas as described previously, including *NF2*, *TRAF7*, *KLF4*, *AKT1*, *SMO*, *PIK3CA*, *SMARCE1*, BAP1, *CDKN2A/B*, *TERT-P ARIDIA*, *SUFU*, *SMARCB1*, *POLR2A*, *DMD*, *KMT2C*, *KMC2D* and *PBRM1*. Sequencing was performed by applying a custom hybrid capture approach (Agilent Technologies, CA, USA) on a Miniseq instrument (Illumina, San Diego, CA, USA) with an average coverage of over 500-fold. We performed internal NGS controls for identity check and cross contamination checks to assure the assignment of the correct samples.