RAPID-CNS2 provides a swift and highly flexible alternative to conventional Next-generation sequencing NGS and array-based methods for single-nucleotide variant SNV/InDel analysis, detection of copy number alterations, target gene methylation analysis (e.g. MGMT), and methylation-based classification. The turnaround time of ~5 days for this proof-of-concept study can be further shortened to < 24h by optimizing target sizes and enabling real-time computational analysis. Expected advances in nanopore sequencing and analysis hardware make the prospect of integrative molecular diagnosis in an intra-operative setting a feasible prospect in the future. This low-capital approach would be cost-efficient for low throughput settings or in locations with less sophisticated laboratory infrastructure, and invaluable in cases requiring immediate diagnoses [1)]

1)
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