MagPurix® FFPE DNA Extraction Enables Epigenetic & Genomic Profiling in Pediatric ARMS

Executive Summary

Parameningeal head and neck alveolar rhabdomyosarcoma (ARMS) in infants is a rare, aggressive cancer where standard treatments (such as radiotherapy) are often limited by toxicity. A recent multi-omics study on 10 pediatric ARMS patients used **MagPurix® FFPE DNA Extraction** to turn routine FFPE tumor samples into high-quality DNA for genome-wide methylation and copy-number analysis.

From only 250 ng of MagPurix-extracted DNA per sample, researchers successfully ran Illumina EPIC methylation arrays, generated copy-number profiles, and calculated epigenetic "mitotic clock" scores. These data helped define tumor biology across age groups and supported the identification of CDK9 as a promising therapeutic target in ARMS.

This publication shows how MagPurix® enables advanced genomic and epigenomic studies from difficult pediatric FFPE material, helping translational centers and hospitals unlock more value from archived samples.

Key Findings

1. High-quality DNA from challenging FFPE samples

- Sample type: FFPE tumor tissues from 10 fusion-positive ARMS patients (including infants <1 year).
- Workflow: automated extraction with the MagPurix® FFPE DNA Extraction Kit.
- Outcome: 250 ng of DNA per case was sufficient and reliable for whole-genome methylation analysis on Illumina EPIC arrays.

2. Robust methylation and copy-number data from one workflow

- MagPurix-extracted DNA produced clean, consistent methylation profiles, correctly clustering with reference ARMS cohorts.
- The same EPIC data were used to derive copy-number variation (CNV) and epigenetic mitotic-clock scores, linking higher proliferative history and genomic instability to poorer survival.
- This demonstrates that MagPurix® enables multi-parameter genomic readouts from a single FFPE extraction.

Conclusion

The study demonstrates that MagPurix® FFPE DNA Extraction is a powerful enabler for modern pediatric cancer research:

- Delivers EPIC-grade DNA from limited FFPE tumor samples.
- Supports genome-wide methylation, CNV, and mitotic-clock analyses from one workflow.

- Provides the solid genomic foundation needed to identify and validate new therapeutic targets, such as CDK9 in ARMS.

For hospitals, research centers, and diagnostic partners, MagPurix® offers a robust, automated platform to transform archived FFPE blocks into actionable genomic and epigenomic insights.

Reference

Patrizi, S., Vallese, S., Barresi, S., et al. (2025). Age-linked DNA methylation and gene expression patterns in parameningeal head and neck alveolar rhabdomyosarcoma reveal CDK9 as a promising therapeutic target. *Pharmacological Research*, *216*, 107767.https://doi.org/10.1016/j.phrs.2025.107767