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Institute of Pathology Heidelberg

Surgical Neuropathology Report

N/25/001191	Kostadinova Todorova, Sofia	*01.05.2020	

Entry: 01.04.2025 **Exit:** 10.04.25 - / HF-HF

Analysis
EPIC-Analysis

Clinical data

Supplier:	University Hospital Tsaritsa Yoanna – ISUL, Sofia, Bulgaria.
Supplier's diagnosis:	Classic Medulloblastoma
Localisation:	IV. ventricle
Manifestation:	Primary tumor
Request for	EPIC array

Material
We received 1 paraffin embedded tissue sample with an external ID of 276/25 (our N25-1191). Tumor cell content approx. 80%. Internal Tumor DNA ID: 447102.

Method
Analysis using Illumina Human Methylation EPIC Array and internal classifier V12.8.

Findings

Classification „brain tumor classifier“	Methylation subclass „Medulloblastoma, Non WNT/non SHH, Group 3 Subtype, Subclass III“	
Version „brain tumor classifier“	V12.8	Score: 0,93

Copy number variations: Indication of isochromosome 17q and other chromosomal

	changes
MGMT promoter:	Unmethylated

Comment:
DNA methylation analysis is a recently developed diagnostic method that was evaluated in several studies (PMID 29539639, 28314689, 30786920, 31786093, 29967940) and which is recommended from international committees for brain tumor diagnostics (PMID 32307792, 32502305, 34185076). Prospective trials for generation of long-term data are ongoing. Studies also show added value for sarcoma diagnostics, which is currently undergoing validation (u.a. PMID 33047515, 33479225, 29881993, 32352245).

Molecular Diagnosis:
Methylation subclass „Medulloblastoma, Non WNT/non SHH, Group 3 Subtype, Subclass III“

Ph. Sievers, MD

F. K. Aras, MD

Enclosure

Methylation profiling report

dkfz. GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION

Heidelberg University Hospital

MolecularNeuropathology.org

Supplier information

Sample identifier:	447102
Sentrix ID:	209273590110_R05C01
Material type:	DNA-FFPE
Gender:	NA
Supplier diagnosis:	-

Automatic prediction		
Array type:	EPICv2	
Material type:	DNA-FFPE	✓
Gender:	unknown	!

Legend: ✓ Ok | ! Supplier information or prediction not available | ✗ Warning, missmatch of prediction and supplier information

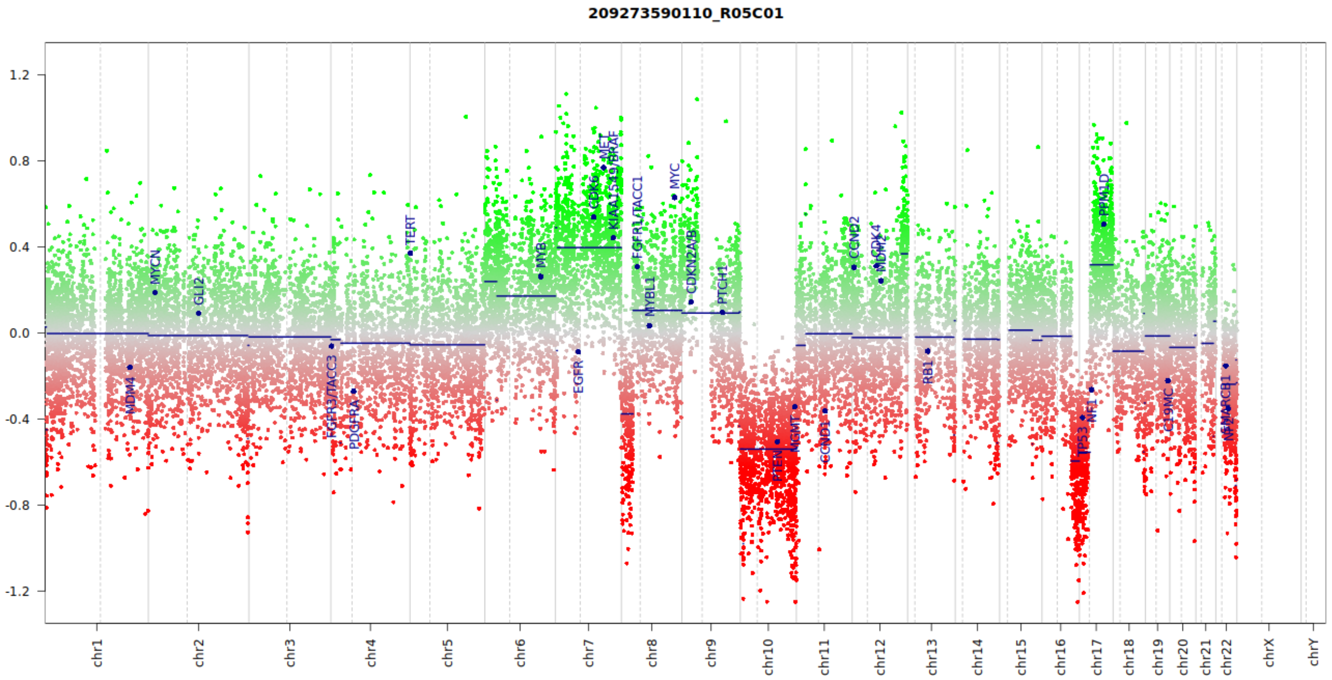
Version 12.8 of the brain classifier results (12.8)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Medulloblastoma	0.99	match	✓
Medulloblastoma Non Wnt/non Shh Activated	0.99	match	✓
Medulloblastoma Group 3	0.99	match	✓
Mc Medulloblastoma, Non Wnt/non Shh, Group 3 Subtype, Subclass III	0.93	match	✓
Mc Medulloblastoma, Non Wnt/non Shh, Group 3 Subtype, Subclass Iv	0.05	no match	✗
Mc Medulloblastoma, Non Wnt/non Shh, Group 3	0.00	no match	✗

			Subtype, Subclass Ii			
			Mc Medulloblastoma, Non Wnt/non Shh, Group 3 Subtype, Subclass I	0.00	no match	✗

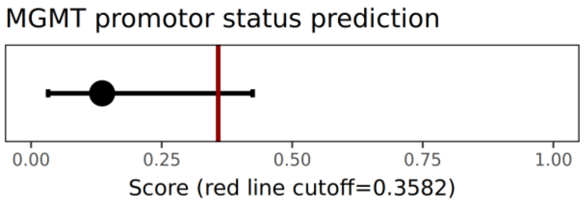
Legend: ✓ Match (score >= 0.9) ✗ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases.

Copy number variation profile



Depiction of chromosome 1 to 22 (the values for chromosome X/Y aren't shown). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment. (see Hovestadt & Zapatka, http://www.bioconductor.org/packages/devel/bioc/html/conumee.html)

MGMT promotor methylation (MGMT-STP27)



Status	Estimated	CI lower	CI upper
unmethylated	0.13594	0.03251	0.42417

(see Bady et al, J Mol Diagn 2016; 18(3):350-61)

Disclaimer

Classification using methylation profiling is a research tool under development, it is not verified and has not been clinically validated. Implementation of the results in a clinical setting is in the sole responsibility of the treating physician.