

# MNP Methylation Profiling Report (mnp.v12epicv2)

01 August, 2024

## Sample Information

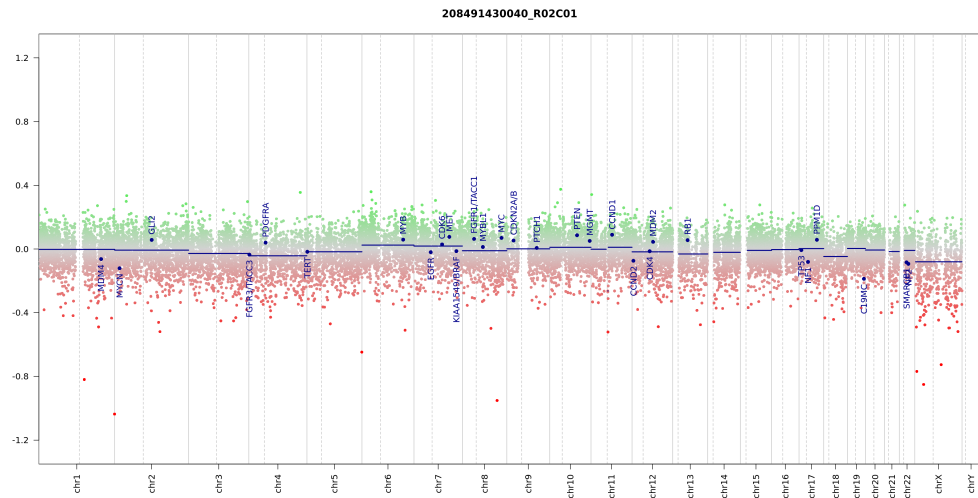
ID	Sentrix ID	Array type	Material type	Gender
NH24-2554	208491430040_R02C01	IlluminaHumanMethylationEPICv2	Frozen	Male

## Brain Tumor Methylation Classifier

	predicted	maxscore
super family	Circumscribed astrocytic tumours	0.9527
family	subependymal giant cell astrocytoma	0.9526
class	subependymal giant cell astrocytoma	0.9526
subclass	Subependymal giant cell astrocytoma	0.9526

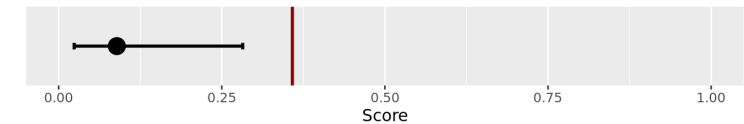
Detailed class descriptions are available at [www.molecularneuropathology.org](http://www.molecularneuropathology.org)

## Copy Number Variation Profile



Depiction of chromosome 1 to 22 (and X/Y if automatic prediction was successful). 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 Prediction



Status	Estimated	CI_Lower	CI_Upper	Cutoff
unmethylated	0.0892154	0.0238343	0.2821136	0.3582

see: Pierre Bady, Davide Sciuscio, Annie-Claire Diserens et al. *MGMT methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status*. Acta Neuropathologica, p.547-560, Number 4, 2012.

## Reference

### DNA methylation-based classification of central nervous system tumours

David Capper, David T. W. Jones, Martin Sill, Volker Hovestadt, Daniel Schrimpf, Dominik Sturm, Christian Koelsche, Felix Sahm, Lukas Chavez, David E. Reuss, Ann Kathrin Kratz, Annika K. Wefers, Kristin Huang, Kristian W. Pajtler, Leonille Schweizer, Damian Stichel, Adriana Olar, Nils W. Engel, Kerstin Lindenberg, Patrick N. Harter, Anne K. Braczynski, Karl H. Plate, Hildegard Dohmen, Boyan K. Garvalov, Roland Coras, Annett Hölsken, Ekkehard Hoyer, Melanie Bewerunge-Hudler, Matthias Schick, Roger Fischer, Rudi Beschner, Jens Schittenhelm, Ori Staszewski, Khalida Wani, Pascale Varlet, Melanie Pages, Petra Temming, Dietmar Lohmann, Florian Selt, Hendrik Witt, Till Milde, Olaf Witt, Eleonora Aronica, Felice Giangaspero, Elisabeth Rushing, Wolfram Scheurlen, Christoph Geisenberger, Fausto J. Rodriguez, Albert Becker, Matthias Preusser, Christine Haberler, Rolf Bjerkvig, Jane Cryan, Michael Farrell, Martina Deckert, Jürgen Hench, Stephan Frank, Jonathan Serrano, Kasthuri Kannan, Aristotelis Tsirigos, Wolfgang Brück, Silvia Hofer, Stefanie Brehmer, Marcel Seiz-Rosenhagen, Daniel Hänggi, Volkmar Hans, Stephanie Rozsnoki, Jordan R. Hansford, Patricia Kohlfhof, Bjarne W. Kristensen, Matt Lechner, Beatriz Lopes, Christian Mawrin, Ralf Ketter, Andreas Kulozik, Ziad Khatib, Frank Heppner, Arend Koch, Anne Jouvett, Catherine Keohane, Helmut Mühleisen, Wolf Mueller, Ute Pohl, Marco Prinz, Axel Benner, Marc Zapatka, Nicholas G. Gottardo, Pablo Hernández Driever, Christof M. Kramm, Hermann L. Müller, Stefan Rutkowski, Katja von Hoff, Michael C. Frühwald, Astrid Gnekow, Gudrun Fleischhack, Stephan Toppelt, Gabriele Calaminus, Camilla-Maria Monoranu, Arie Perry, Chris Jones, Thomas S. Jacques, Bernhard Radlwimmer, Marco Gessi, Torsten Pietsch, Johannes Schramm, Gabriele Schackert, Manfred Westphal, Guido Reifenberger, Pieter Wesseling, Michael Weller, Vincent Peter Collins, Ingmar Blümcke, Martin Bendszus, Jürgen Debus, Annie Huang, Nada Jabado, Paul A. Northcott, Werner Paulus, Amar Gajjar, Giles W. Robinson, Michael D. Taylor, Zane Jaunmuktane, Marina Ryzhova, Michael Platten, Andreas Unterberg, Wolfgang Wick, Matthias A. Karajannis, Michel Mittelbronn, Till Acker, Christian Hartmann, Kenneth Aldape, Ulrich Schüller, Rolf Buslei, Peter Lichter, Marcel Kool, Christel Herold-Mende, David W. Ellison, Martin Hasselblatt, Matija Snuderl, Sebastian Brandner, Andrey Korshunov, Andreas von Deimling & Stefan M. Pfister



**Classification using methylation arrays is a research tool under development, 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.**