



Article

Implementation of methylation profiling of central nervous system tumors at largest public health center in Brazil

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SUPPLEMENTARY MATERIAL

Classification of Tumors Using the "NGS Neuropathology" Platform

Researchers at the University of Heidelberg in Germany have developed a classification platform based on the methylome of CNS tumors using deep learning algorithms. The "Platform for Next Generation Neuropathology" is available at <https://www.molecularneuropathology.org/mnp/> [3,4]. Epigenomic data obtained by the bead array technique (Illumina®) with the Human Methylation 450 BeadChip or EPIC BeadChip (in .idat file format) can be submitted to the platform, where an automatic comparison to a reference cohort comprising over 2,800 tumors from major recognized CNS entities is performed. Using a classification score ranging from 0 to 1, the platform indicates the similarity to one of the included classes. All class prediction scores theoretically add up to 1. For a classification to be confirmed, the methylation class score must be above 0.9 [3,4].

With the same array data submitted to the classifier for correlation with tumor entities, it is possible to obtain a graph with CNV estimates and the methylation status of the *MGMT* gene promoter, which can be classified as "methylated," "non-methylated," or "undeterminable" [3,4]. Cases with an "undeterminable" classification result are submitted to pyrosequencing, which frequently resolves the classification. The results

of the classifier for "methylated" and "non-methylated" statuses show high concordance with *MGMT* pyrosequencing results [3,4].

When data are uploaded, there is the possibility to consent for their use in further classifier development. Thus, this platform can function as a worldwide cooperative network to continually identify and track tumor classes, potentially adding new entities to the catalog of known human cancers since its use is free of charge [3,4].