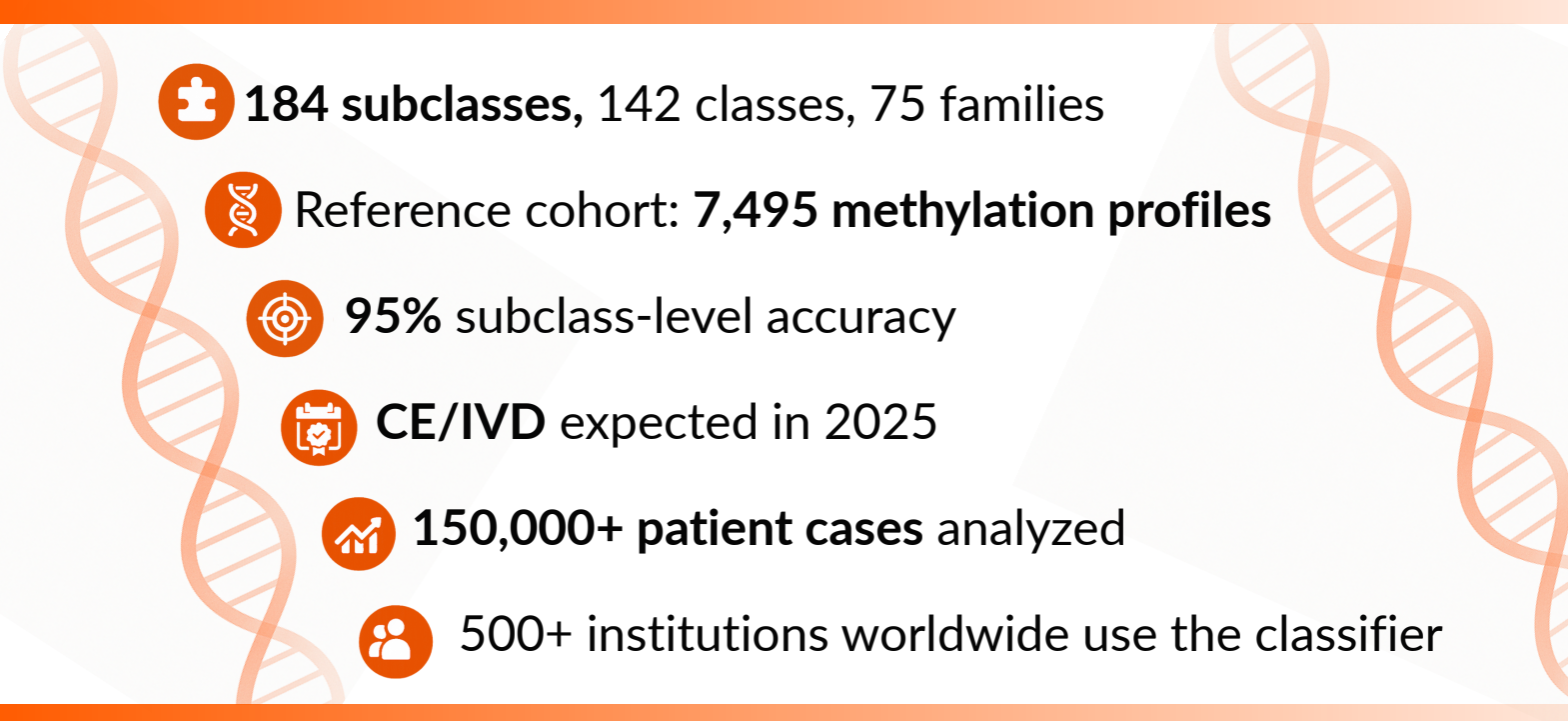


Epignostix CNS Tumor Methylation Classifier

Version 12.8

Released: April 2025

- 
-  **184 subclasses, 142 classes, 75 families**
 -  **Reference cohort: 7,495 methylation profiles**
 -  **95% subclass-level accuracy**
 -  **CE/IVD expected in 2025**
 -  **150,000+ patient cases analyzed**
 -  **500+ institutions worldwide use the classifier**

Comprehensive Methylation Profiling Report



Tumor Classification

- Calibrated score based on a **four-tier hierarchical structure**.
- Includes **evidence-level annotations** to support alignment with **WHO CNS tumor classification**.



Copy Number Variation (CNV) Profile

29 CNS tumor relevant gene regions are highlighted.



MGMT Promoter Methylation (MGMT-STP27)



Quality Control Metrics

- **21 metrics** derived from Illumina Methylation Array control probes.
- Overall array quality assessed using **three core criteria**.



Learn more at:

<https://epignostix.com/our-technology/our-technology-cns-tumor-classifier/>



On-premise version for routine use



Compatible with standard laptops
An installation guide is included.



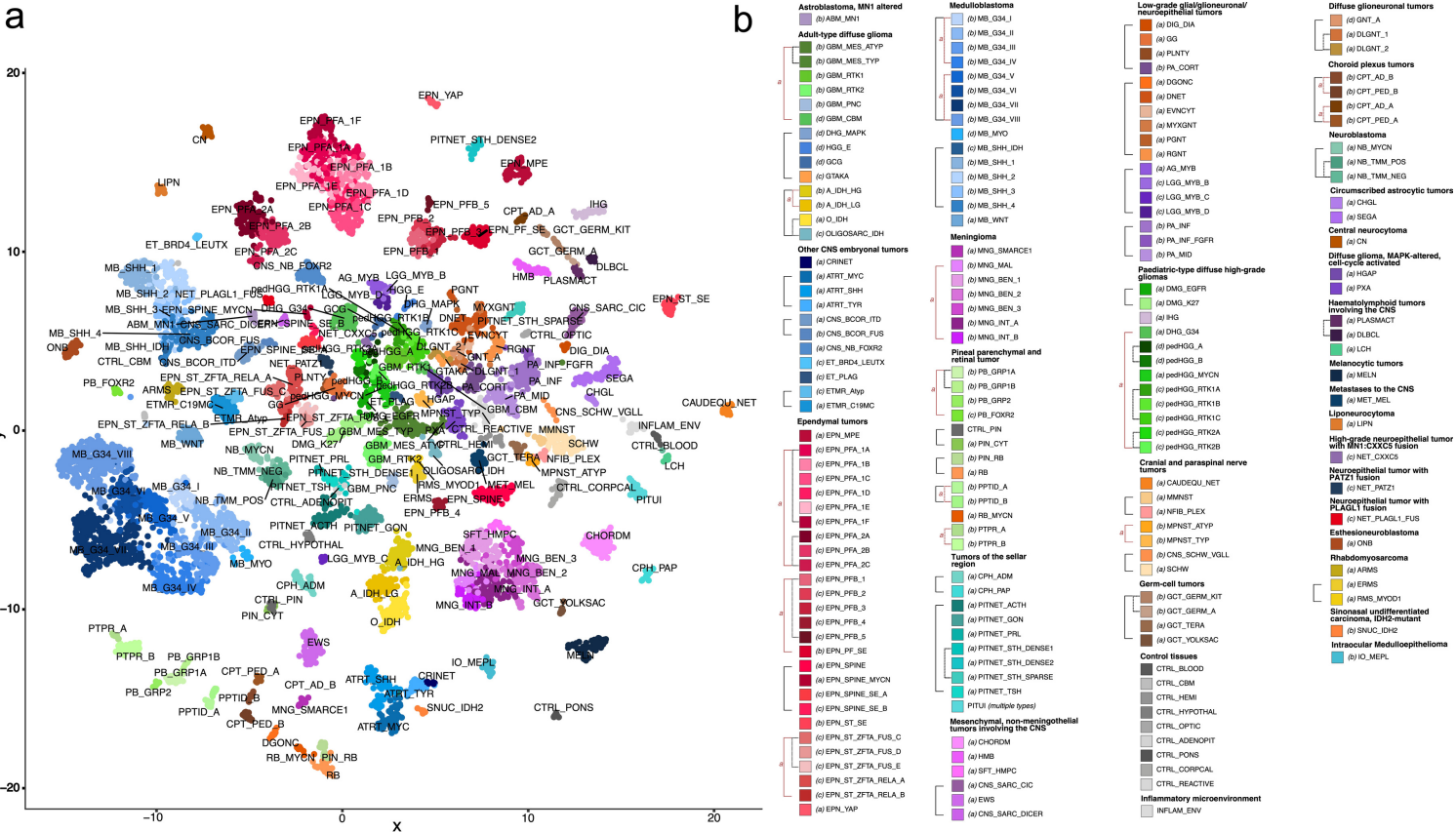
RUO Platform freely accessible for
academic research and scientific use



Register here:
<https://app.epignostix.com/>



Contact for more information
info@epignostix.com



(a) UMAP projection of 7,495 samples used for training the v12.8 classifier (b) Legend indicating color code for each subclass shown in (a). Letters in round brackets before abbreviation of the subclass indicate 'evidence level' for the respective subclass.
Level a - Tumor type/subtype identical to WHO 2021;
Level b - Large single or more than one smaller dataset published describing the type/subtype as molecularly and/or clinically distinct, or the methylation class represents a distinct fraction of an established WHO 2021 tumor class;
Level c - Single small dataset or case series;
Level d - solely based on clusters in tSNE/UMAP.

Sill M. et al., medRxiv (2025)



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