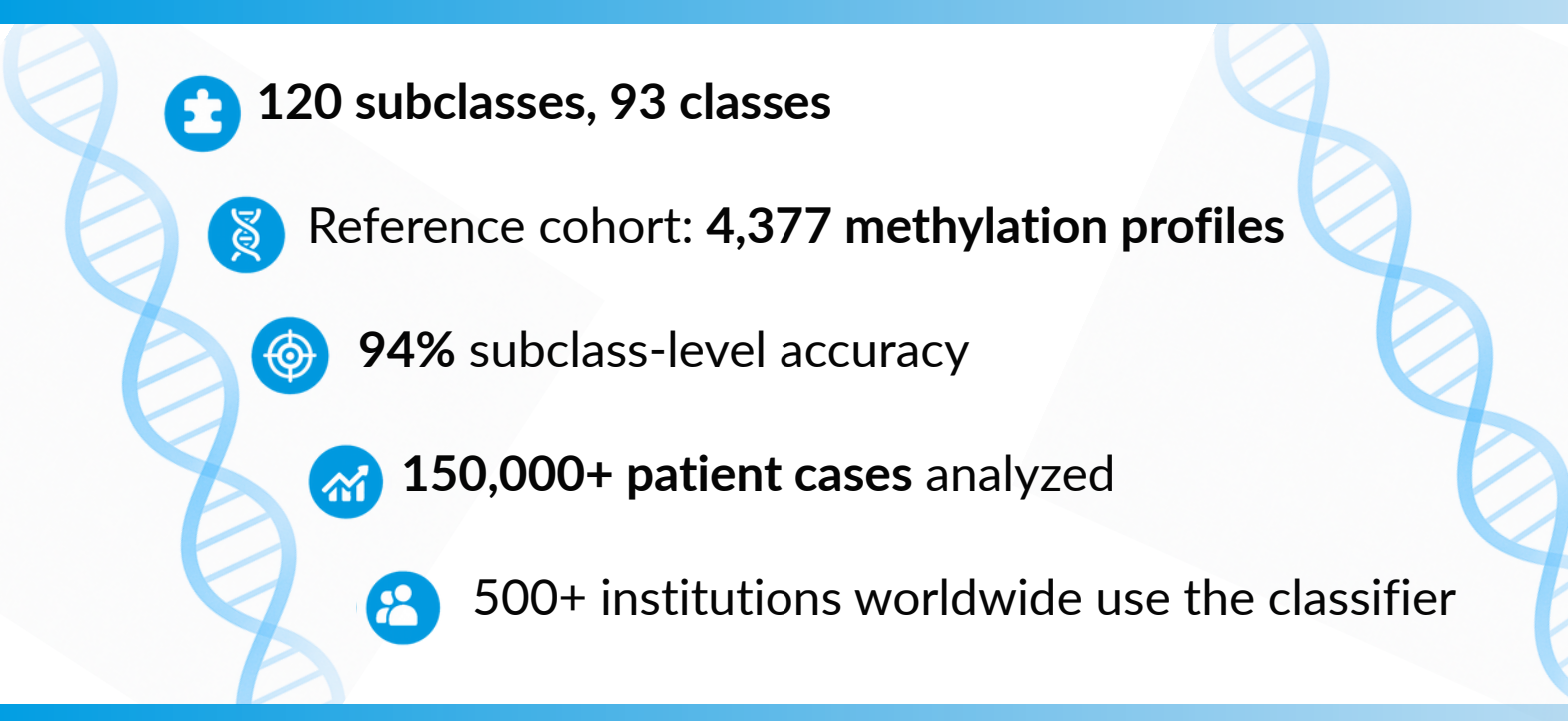


Epignostix Sarcoma Methylation Classifier

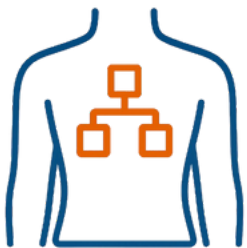
Version 13.1

Released: June 2025

- 
-  **120 subclasses, 93 classes**
 -  **Reference cohort: 4,377 methylation profiles**
 -  **94% subclass-level accuracy**
 -  **150,000+ patient cases analyzed**
 -  **500+ institutions worldwide use the classifier**

Comprehensive Methylation Profiling Report

Tumor Classification



- Calibrated score based on a **two-tier hierarchical structure**.
- Includes **evidence-level annotations** to support alignment with **WHO Classification of Tumours of Soft Tissue and Bone**



Copy Number Variation (CNV) Profile

29 tumor relevant gene regions are highlighted.



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/sarcoma-methylation-classifier/>



On-premise version for routine use



Compatible with standard laptops
An installation guide is included.



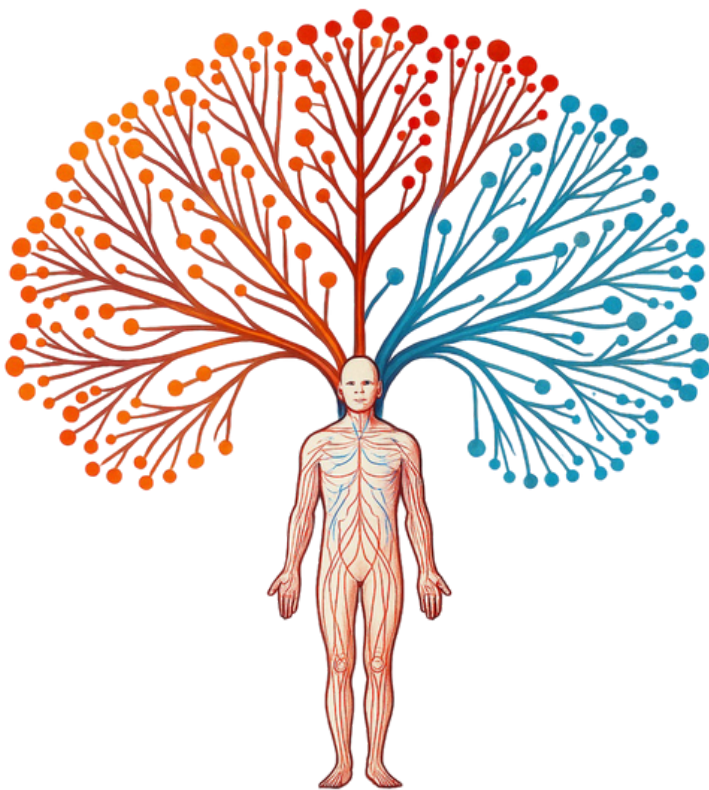
RUO Platform freely accessible for
academic research and scientific use



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



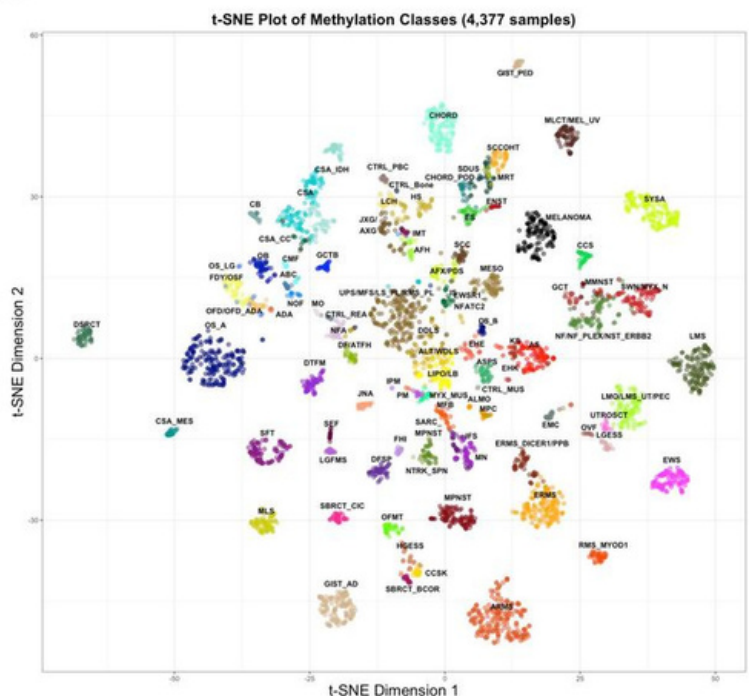
Contact for more information
info@epignostix.com



a



b



Level a - Tumor type/subtype identical to WHO 2020
Level b - Large single or more than 1 smaller dataset published describing the type/subtype as molecularly and/or clinically distinct
Level c - Single small dataset or case series
Level d - solely based on clusters in tSNE/UMAP

Overview of the DNA methylation-based sarcoma reference cohort used for training the v13.1 sarcoma classifier.
(a) Overview of 89 tumour and four control DNA methylation classes included in the v13.1 sarcoma classifier reference cohort. The sarcoma methylation classes are grouped according to the WHO 2020 scheme. Letters in rounded brackets before abbreviation of the class indicate 'evidence level' for the respective class. Full names and further details of the methylation classes are given in supplementary tables 1 and 2. (b) t-SNE projection of complete reference sample set (4377 DNA methylation profiles) used for training the v13.1 sarcoma classifier.

Jäger N. et al., medRxiv (2025)



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