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An epigenome browser of the newly assembled genome of the model diatom *Phaeodactylum tricornerutum*

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Rationale of the project

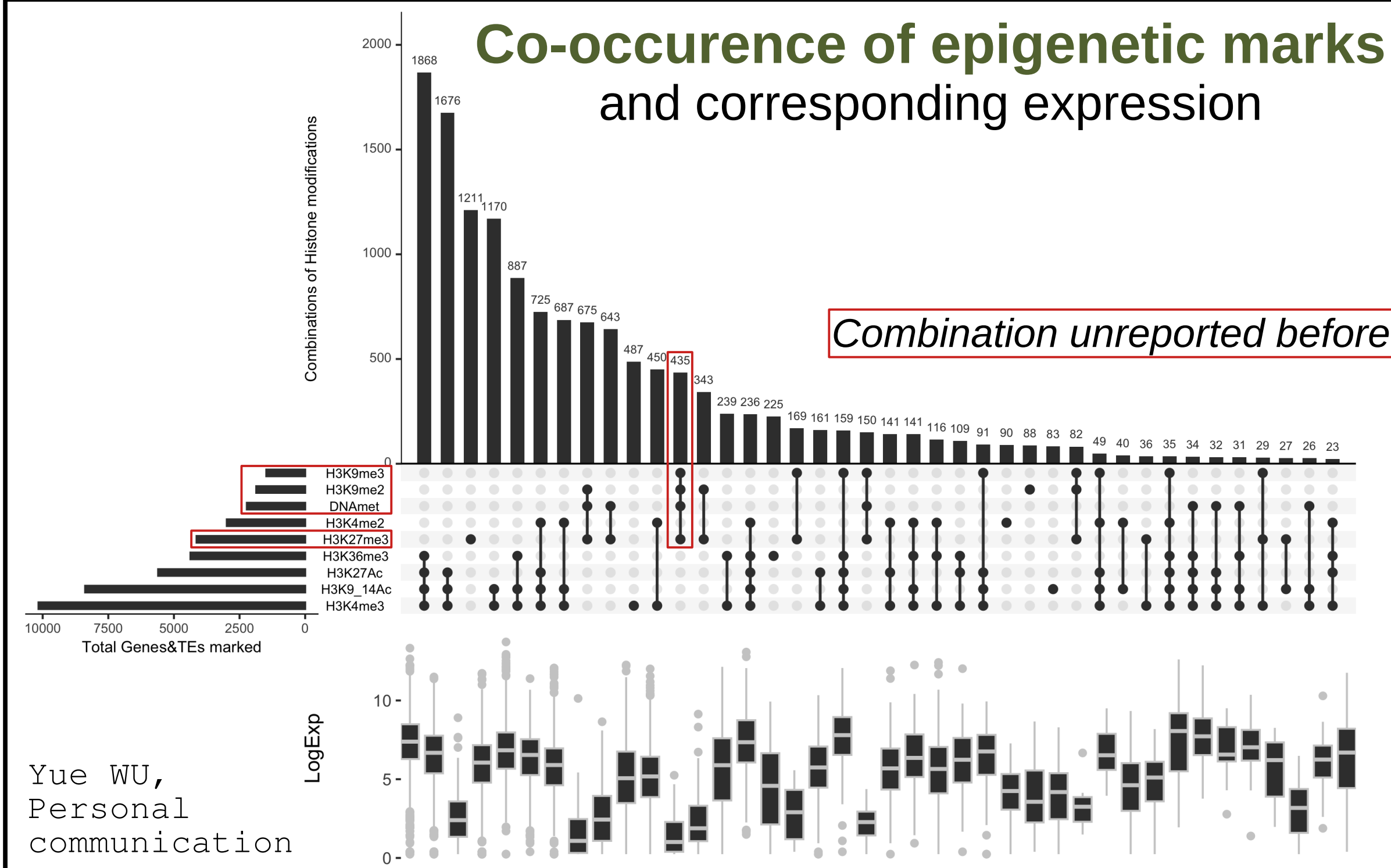
A telomere-to-telomere re-assembly 25 chromosomes – 27.8 Mb

... But few (epigenetic) data available:

- ✓ Transposable Elements (TEs) annotation
- ✓ DNA methylation

- 🔄 Transfer data from fragmented assembly (Phatr3, epigenetic marks)
- 🔄 Update two histone marks annotations with fresh data
- 🔄 Monoclonal vs polyclonal antibodies for H3K9me3 and H3K27me3
- ➕ Add two new histone marks: H3K27Ac and H3K36me3
- 🔔 Release first (epi)Genome Browser to the Research Community

<https://PhaeoEpiView.univ-nantes.fr>



Integrate **YOUR** data!



Genes

- Chr-by-chr liftover of Phatr3 annotation: 12,178 → 11,739
- 439 missing genes, among which 295 were duplicated ✓
- Validation
 - Gene lengths difference: mostly below ± 0.1% ✓
 - Gene expression difference: mostly below ± 0.1% ✓

Transposable Elements

- EDTA annotation, published with assembly (Giguere et al, 2022)
- Similar figures to what was previously published
 - Phatr3: 3705 copies of TEs, 3.373 Mbp
 - EDTA: 3190 copies of TEs, 3.276 Mbp

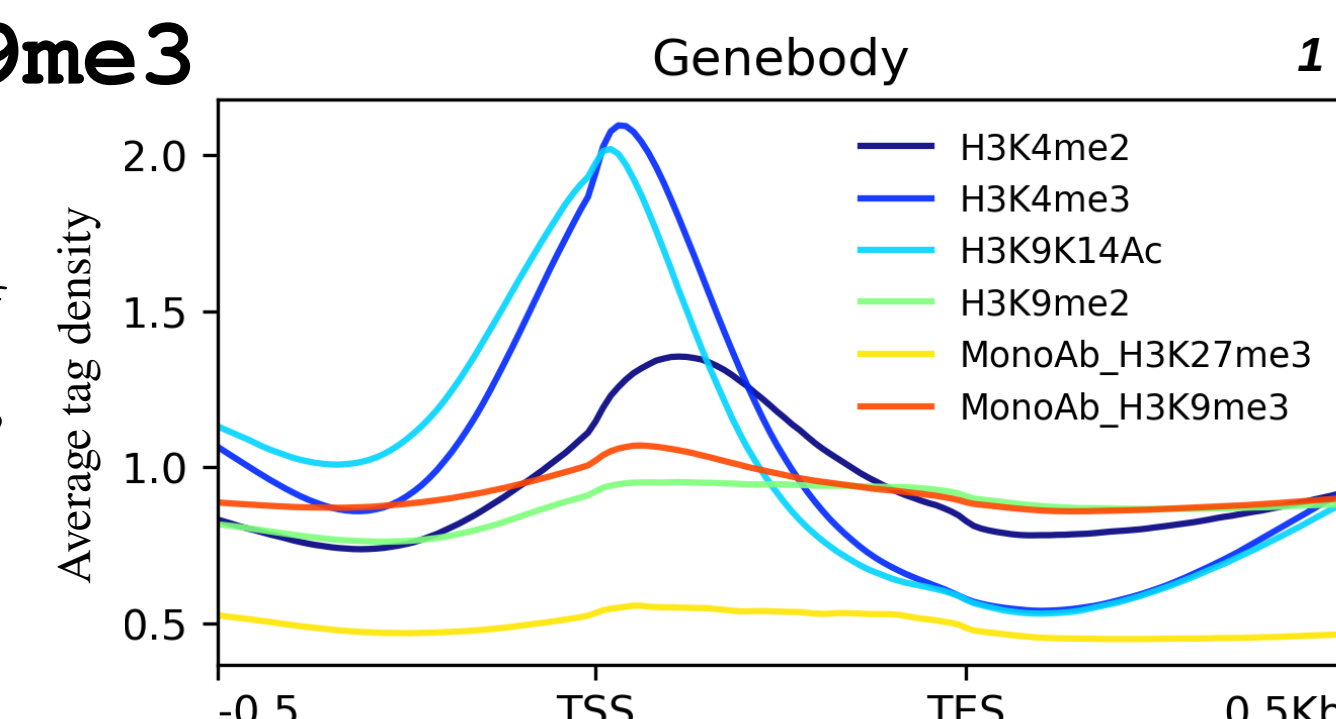
Expression

- Unstranded RNAseq from previous study (Murik et al, 2018)
 - Early growth: ~500K cells/mL
 - Late growth: ~1M cells/mL

Histone Marks

- Five permissive marks
 - H3K4me3, H3K9/K14Ac, H3K4me2, H3K27Ac, H3K36me3
- Three repressive marks
 - H3K27me3, H3K9me2, H3K9me3

Right: enrichment profiles of H3K4me2, H3K4me3, H3K9_14Ac, H3K9me2, H3K9me3 (MonoAb), H3K27me3 (MonoAb) along genes (upstream TSS, coding region, downstream TES).

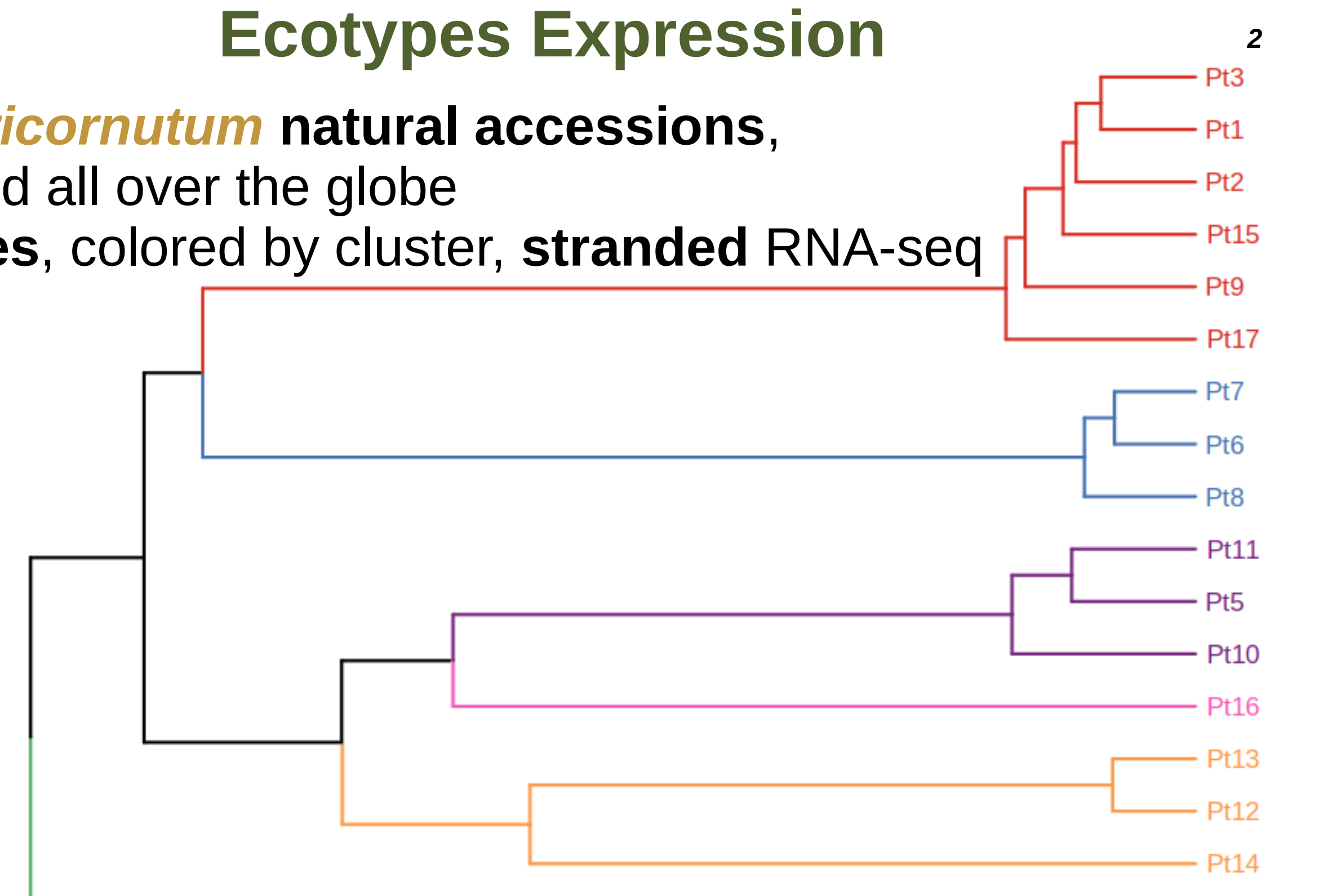


DNA Methylation

- McrBC (Veluchamy et al, 2013), Bisulfite-seq (Hoguin et al, 2021) and Nanopore basecalling (Giguere et al, 2022)

Ecotypes Expression

- 17 *P. tricornerutum* natural accessions, sampled all over the globe
- 6 clades, colored by cluster, stranded RNA-seq



Conclusions

PhaeoEpiView provides accurate, up-to-date genome and epigenome view of epigenetic regulation of genes and TEs. It is intuitive, user-friendly and allows users to upload their own tracks. PhaeoEpiView will contribute to boosting fundamental and applied research in microalgae and single-celled species.

1 Chaumier, Wu et al, Scientific Reports, 2023 (<https://doi.org/10.1038/s41598-023-35403-1>)
 2 Chaumier, Yeng et al, bioRxiv, 2023 (<https://doi.org/10.1101/2023.05.31.543125>)