



Polymorphic STRs represent unique genetic signals beyond SNPs associated with climate adaptation in *Marchantia polymorpha*

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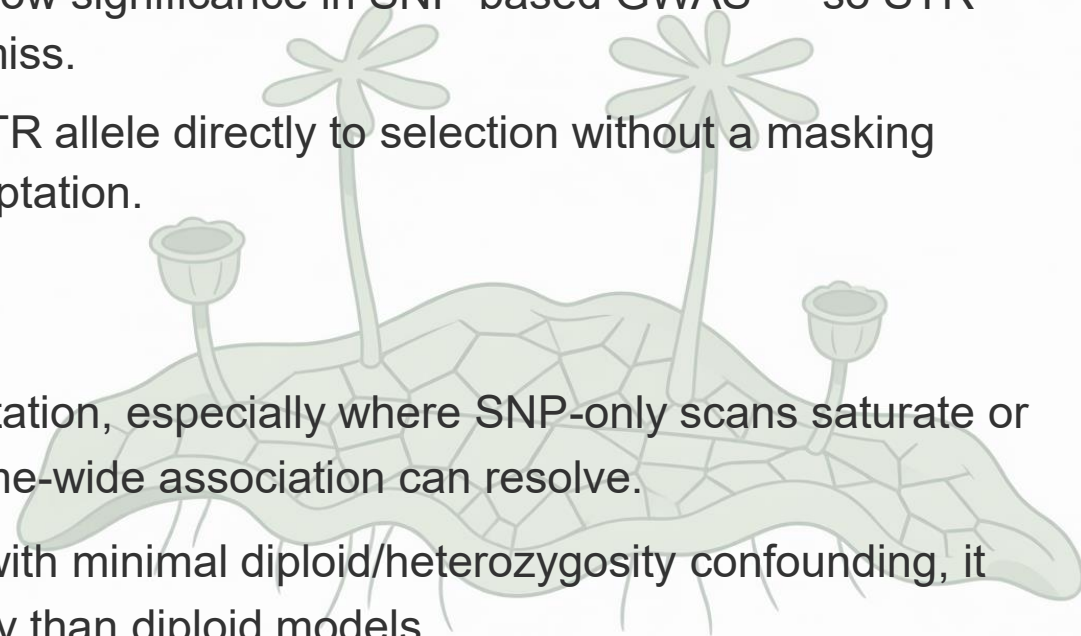
Highlight

Key Findings

- First population-genomic map of pSTRs in bryophytes: 29,084 high-confidence pSTRs catalogued across 78 non-clonal *Marchantia polymorpha* accessions from Europe, Japan and North America, revealing clear genetic divergence between European and Japanese populations.
- Genome-wide association links many pSTR repeat-number changes to temperature-related climate variables, suggesting STRs may help liverworts adapt to local climates.
- pSTR analysis detects candidate adaptive loci that fall below significance in SNP-based GWAS — so STR repeat variation adds genetic information that SNP scans miss.
- *Marchantia*'s haploid-dominant life cycle exposes each STR allele directly to selection without a masking second copy — an ideal system to study repeat-based adaptation.

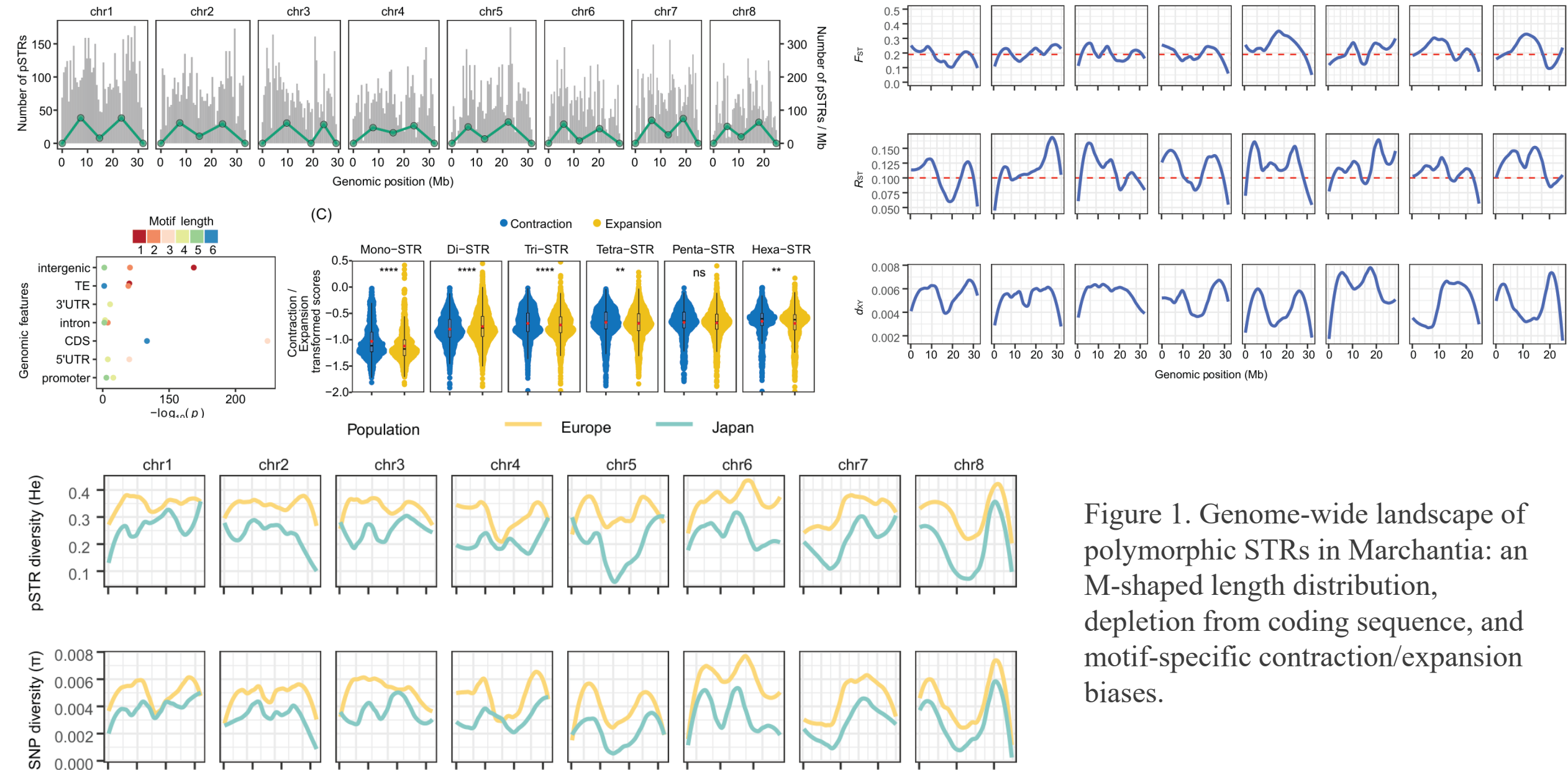
Scientific Significance

- pSTRs open a complementary window onto climate adaptation, especially where SNP-only scans saturate or miss functionally relevant repeats — extending what genome-wide association can resolve.
- The haploid liverwort offers a clean genetic background: with minimal diploid/heterozygosity confounding, it lets us study the STR-repeat–environment link more directly than diploid models.



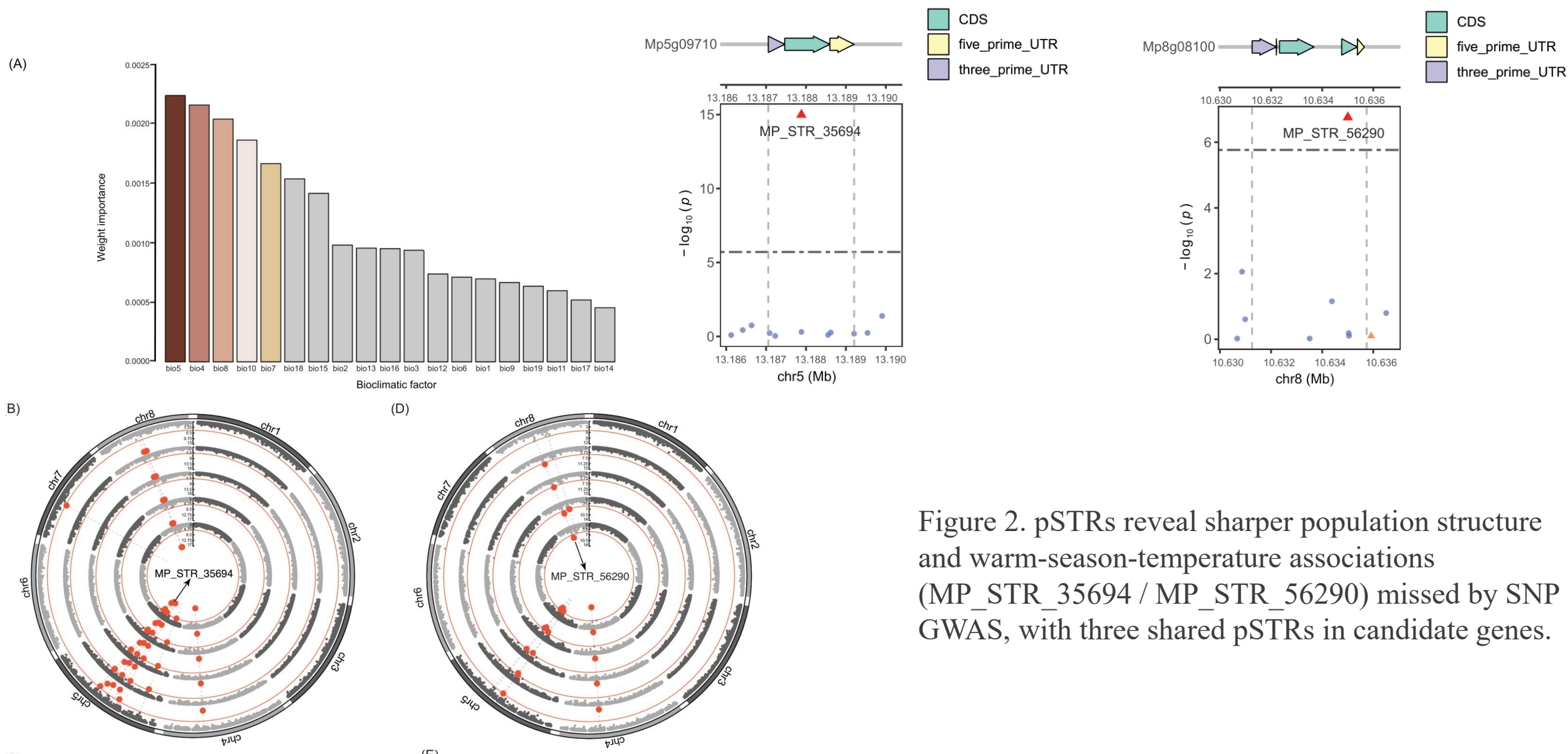


Result: pSTR Landscape & Climate-Adaptive Signals

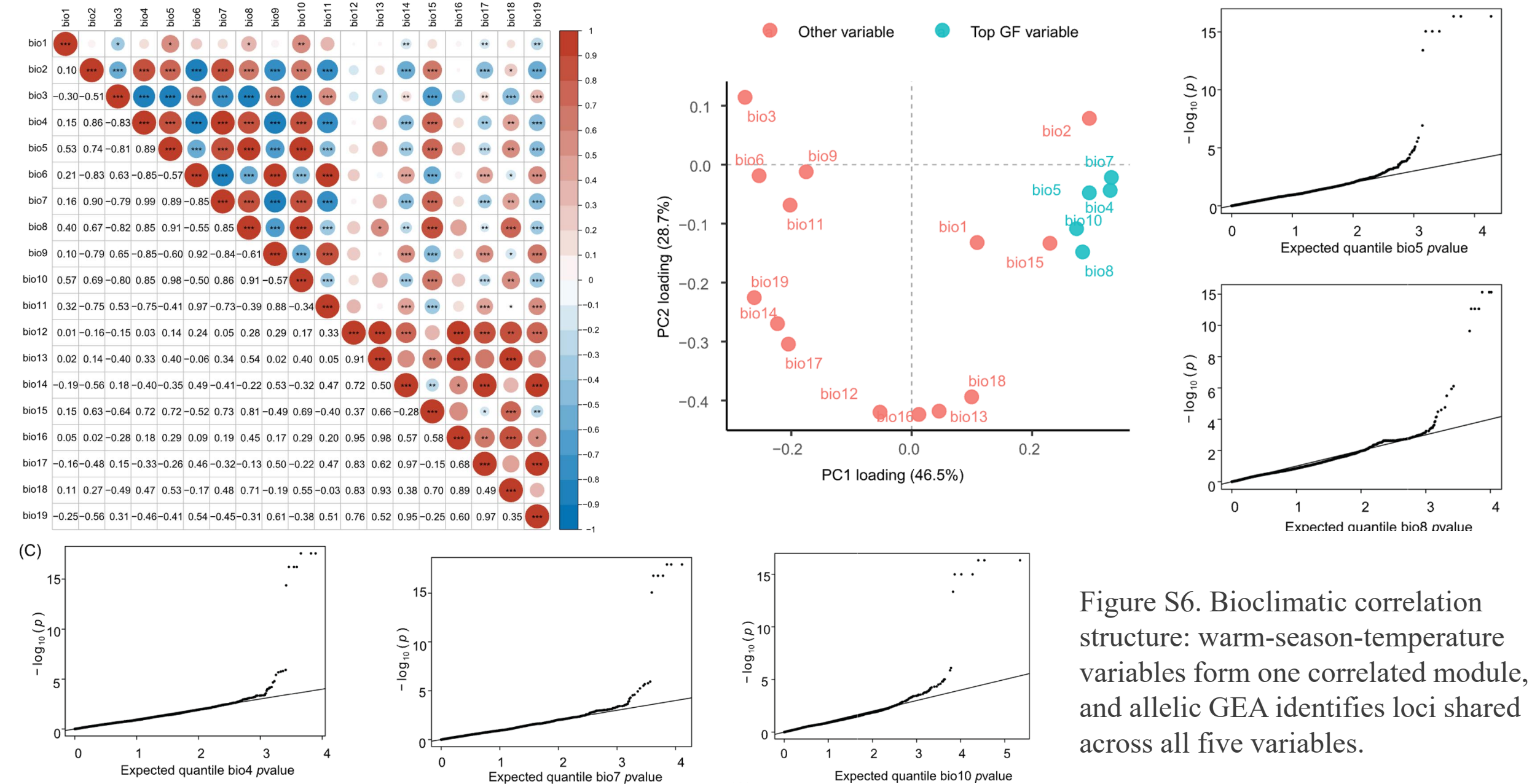




Result: pSTR Landscape & Climate-Adaptive Signals



Result: Bioclimatic Module & Candidate Gene Expression



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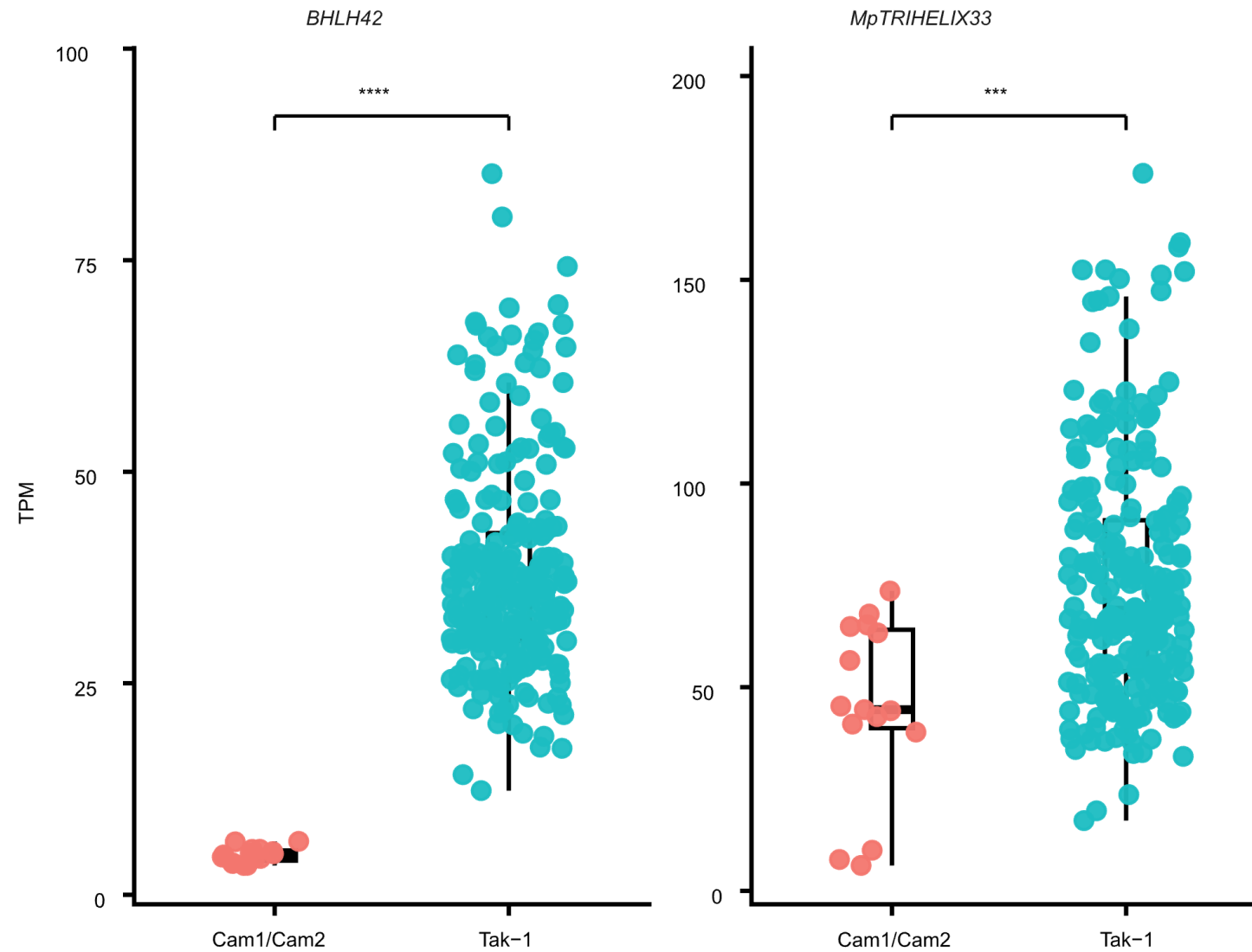


Figure S7. Candidate gene expression in MarpolBase: MpBHLH42 and MpTRIHILIX33 show higher TPM in the Japanese Tak-1 accession than in Cam-1/Cam-2.



Summary and Outlook

Summary

- First population-genomic pSTR map in a bryophyte, built from 78 non-clonal *Marchantia polymorpha* accessions.
- pSTRs capture climate-adaptive signals that SNP-based GWAS fails to detect.
- Candidate adaptive genes MpBHLH42 and MpTRIHELIX33 stand out as heat-stress-response regulators.

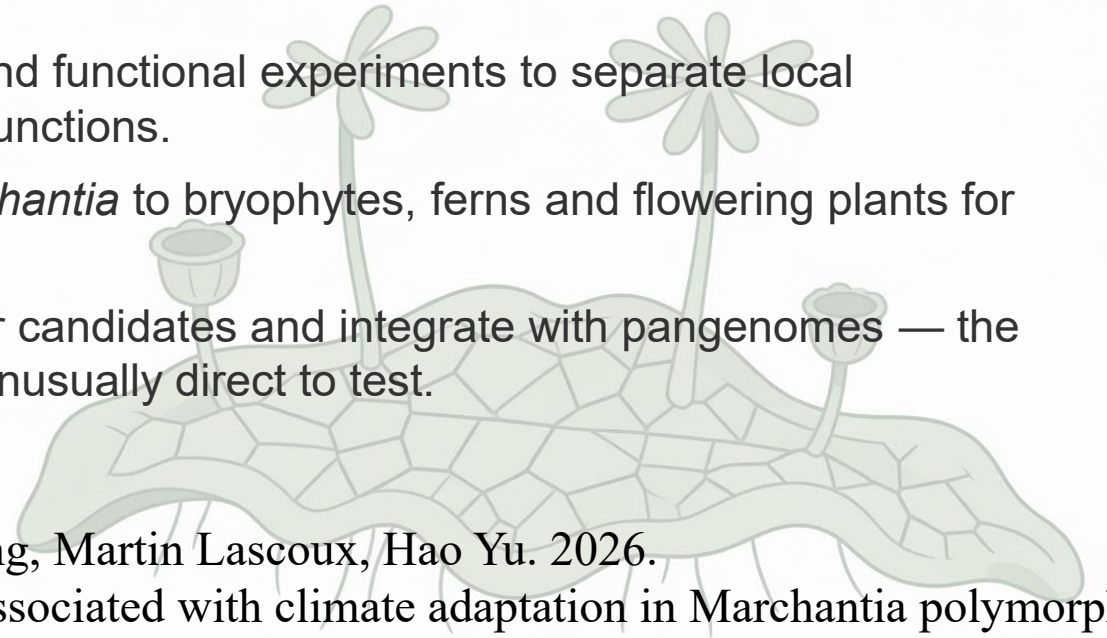
Outlook

- Depth: add samples from intermediate regions/climates and functional experiments to separate local adaptation from population history and validate candidate functions.
- Breadth: extend pSTR population genomics beyond *Marchantia* to bryophytes, ferns and flowering plants for cross-species comparison of repeat-mediated adaptation.
- Close the loop: functionally validate MpBHLH42 and other candidates and integrate with pangenomes — the haploid liverwort model makes the STR–environment link unusually direct to test.

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