Research and development opportunities in red alder (*Alnus rubra* Bong.).

NCGR
National Center for Genome Resources
Callum Bell

CSUN
Jeremy Yoder

Portland State
UNIVERSITY
Daniel Ballhorn

Red alder: *Alnus rubra* Bong.

Goals for this meeting

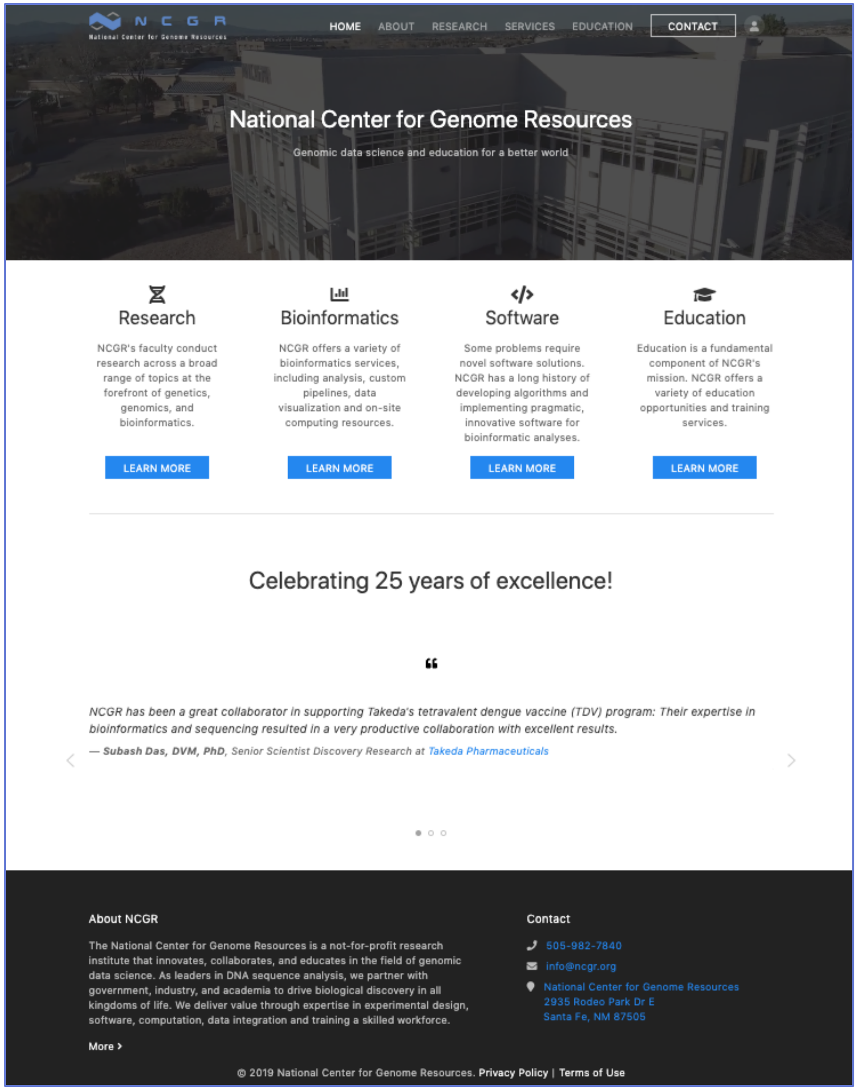
- Bring awareness of our work to broader red alder community
- Become better integrated with others in the field
- Discover value of our research materials, especially the provenance trial
- Explore funding sources
- Build an alliance aimed at further work
- Introductions


NCGR

NCGR History

- New Mexico non profit
- Formed in 1994
- Software and database support for the DOE human genome project
- Research
- Bioinformatics
- Software
- Education

www.ncgr.org



National Center for Genome Resources

Genomic data science and education for a better world

Research

NCGR's faculty conduct research across a broad range of topics at the forefront of genetics, genomics, and bioinformatics.

Bioinformatics

NCGR offers a variety of bioinformatics services, including analysis, custom pipelines, data visualization and on-site computing resources.

Software

Some problems require novel software solutions. NCGR has a long history of developing algorithms and implementing pragmatic, innovative software for bioinformatic analyses.

Education

Education is a fundamental component of NCGR's mission. NCGR offers a variety of education opportunities and training services.

Celebrating 25 years of excellence!

“

NCGR has been a great collaborator in supporting Takeda's tetravalent dengue vaccine (TDV) program: Their expertise in bioinformatics and sequencing resulted in a very productive collaboration with excellent results.

*— **Subash Das, DVM, PhD**, Senior Scientist Discovery Research at Takeda Pharmaceuticals*

About NCGR

The National Center for Genome Resources is a not-for-profit research institute that innovates, collaborates, and educates in the field of genomic data science. As leaders in DNA sequence analysis, we partner with government, industry, and academia to drive biological discovery in all kingdoms of life. We deliver value through expertise in experimental design, software, computation, data integration and training a skilled workforce.

More ›

Contact

☎ 505-982-7840
✉ info@ncgr.org
National Center for Genome Resources
2935 Rodeo Park Dr E
Santa Fe, NM 87505

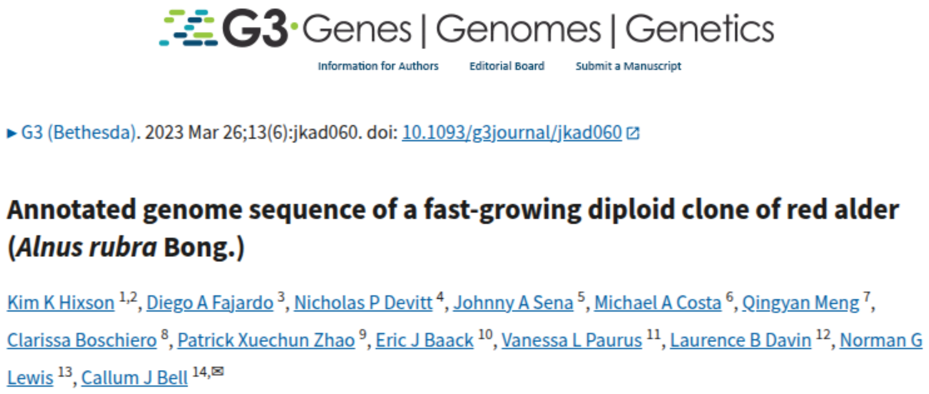
WASHINGTON STATE UNIVERSITY

Norman G. Lewis

Deciphering the molecular basis of elite red alder lines and their Frankia alni symbionts (NSF award 1547842)

Research materials all owned by Weyerhaeuser and licensed to WSU:

- Red alder clone collection
- Frankia strains and root nodules
- Provenance trial



G3 Genes | Genomes | Genetics

Information for Authors Editorial Board Submit a Manuscript

▸ G3 (Bethesda). 2023 Mar 26;13(6):jkad060. doi: 10.1093/g3journal/jkad060

Annotated genome sequence of a fast-growing diploid clone of red alder (*Alnus rubra* Bong.)

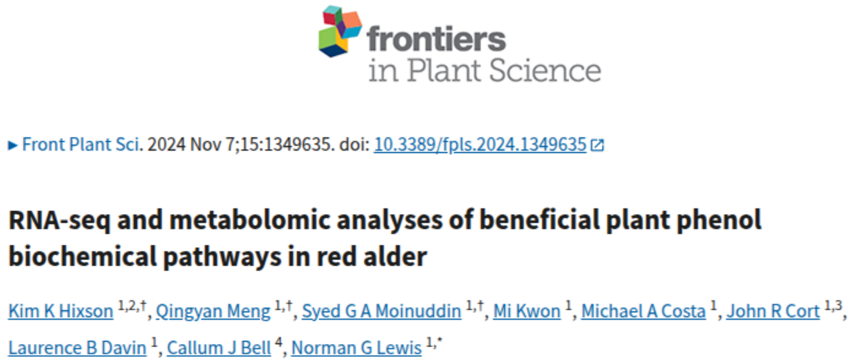
Kim K Hixson [1,2], Diego A Fajardo [3], Nicholas P Devitt [4], Johnny A Sena [5], Michael A Costa [6], Qingyan Meng [7], Clarissa Boschiero [8], Patrick Xuechun Zhao [9], Eric J Baack [10], Vanessa L Paurus [11], Laurence B Davin [12], Norman G Lewis [13], Callum J Bell [14,✉]

SCIENTIFIC DATA

▸ Sci Data. 2024 Dec 18;11:1343. doi: 10.1038/s41597-024-04131-0

A root nodule microbiome sequencing data set from red alder (*Alnus rubra* Bong.)

Callum J Bell [1,✉], Johnny A Sena [1], Diego A Fajardo [1], Evan M Lavelle [1], Michael A Costa [2], Barrington Herman [3], Laurence B Davin [2], Norman G Lewis [2], Alison M Berry [4]

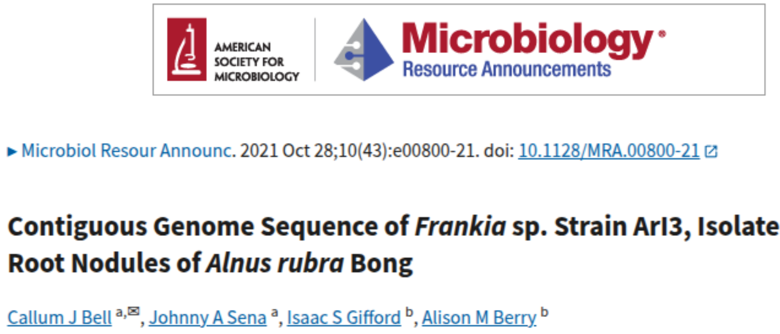


frontiers in Plant Science

▸ Front Plant Sci. 2024 Nov 7;15:1349635. doi: 10.3389/fpls.2024.1349635

RNA-seq and metabolomic analyses of beneficial plant phenol biochemical pathways in red alder

Kim K Hixson [1,2,†], Qingyan Meng [1,†], Syed G A Moinuddin [1,†], Mi Kwon [1], Michael A Costa [1], John R Cort [1,3], Laurence B Davin [1], Callum J Bell [4], Norman G Lewis [1,*]



AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

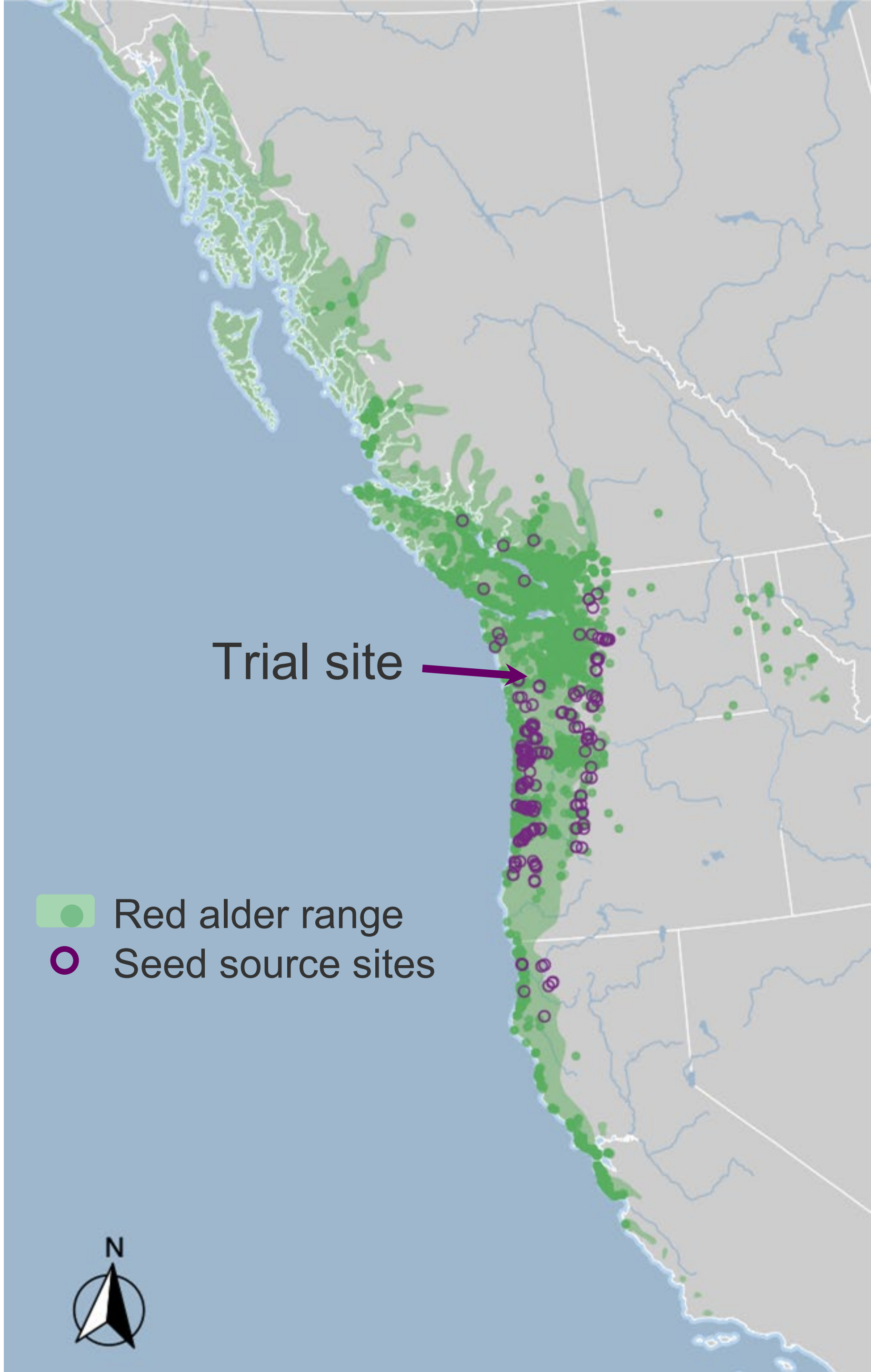
▸ Microbiol Resour Announc. 2021 Oct 28;10(43):e00800-21. doi: 10.1128/MRA.00800-21

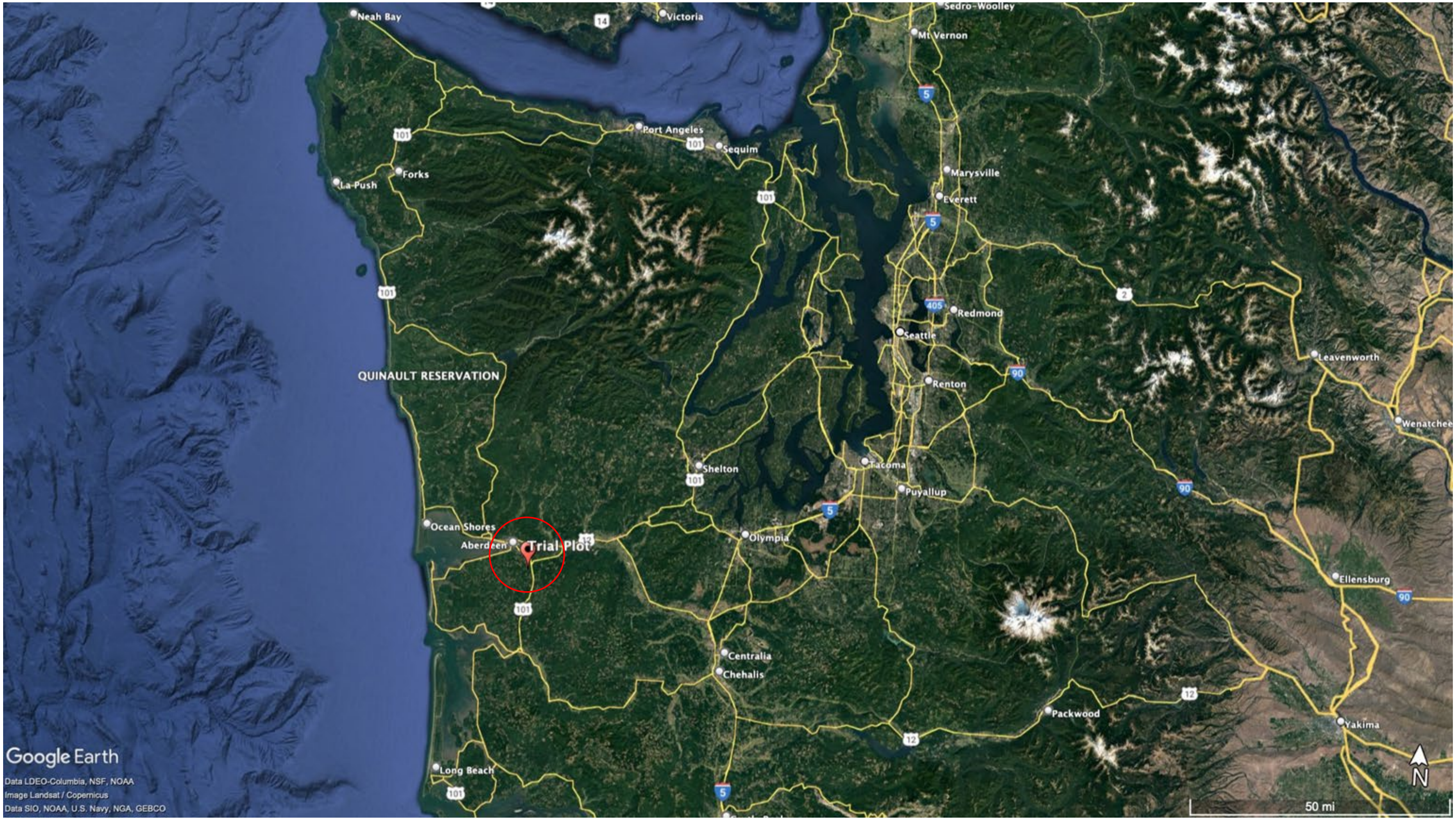
Contiguous Genome Sequence of *Frankia* sp. Strain ArI3, Isolated from Root Nodules of *Alnus rubra* Bong

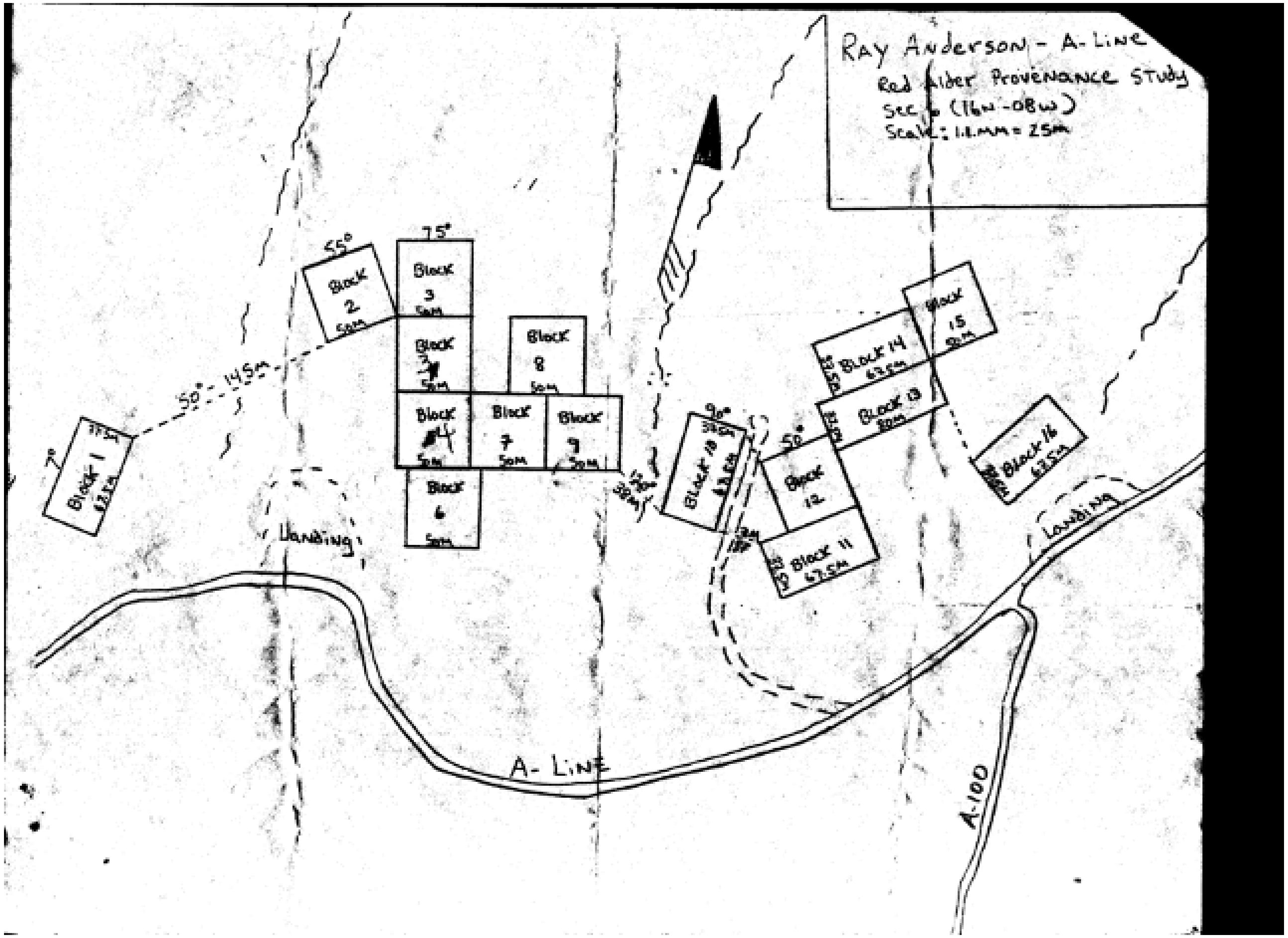
Callum J Bell [a,✉], Johnny A Sena [a], Isaac S Gifford [b], Alison M Berry [b]

Weyerhaeuser provenance trial

- 350 original trees
- Seed collected from each tree
- Open pollinated
- 16 half-siblings from each tree
- Planted in a common location
- Randomized into 16 blocks




Neah Bay
Victoria
Sedro-Woolley
Mt Vernon
Port Angeles
Sequim
Forks
La-Push
Marysville
Everett
Redmond
Seattle
Renton
Leavenworth
Wenatchee
QUINAULT RESERVATION
Shelton
Tacoma
Puyallup
Ocean Shores
Aberdeen
Trial Plot
Olympia
Ellensburg
Centralia
Chehalis
Packwood
Yakima
Long Beach
101
5
405
90
2
12
14
Google Earth
Data LDEO-Columbia, NSF, NOAA
Image Landsat / Copernicus
Data SIO, NOAA, U.S. Navy, NGA, GEBCO
N
50 mi


Ray Anderson - A-Line
Red Alder Provenance Study
Sec 6 (16N-08W)
Scale: 1.1 mm = 25m
Block 1
37.5m
62.5m
7°
50° - 145m
Block 2
50m
55°
Block 3
50m
75°
Block 4
50m
Block 5
50m
Block 6
50m
Block 7
50m
Block 8
50m
Block 9
50m
Block 10
37.5m
62.5m
90°
Block 11
62.5m
37.5m
Block 12
50°
Block 13
80m
Block 14
62.5m
37.5m
Block 15
50m
Block 16
62.5m
Landing
Landing
A-Line
A-100


Ray Anderson's


Google Earth
N
900 ft


Google Earth
Data SIO, NOAA, U.S. Navy, NGA, GEBCO
Data LDEO-Columbia, NSF, NOAA
N
300 ft

Study genetic variation by GBS (Genotyping by Sequencing)

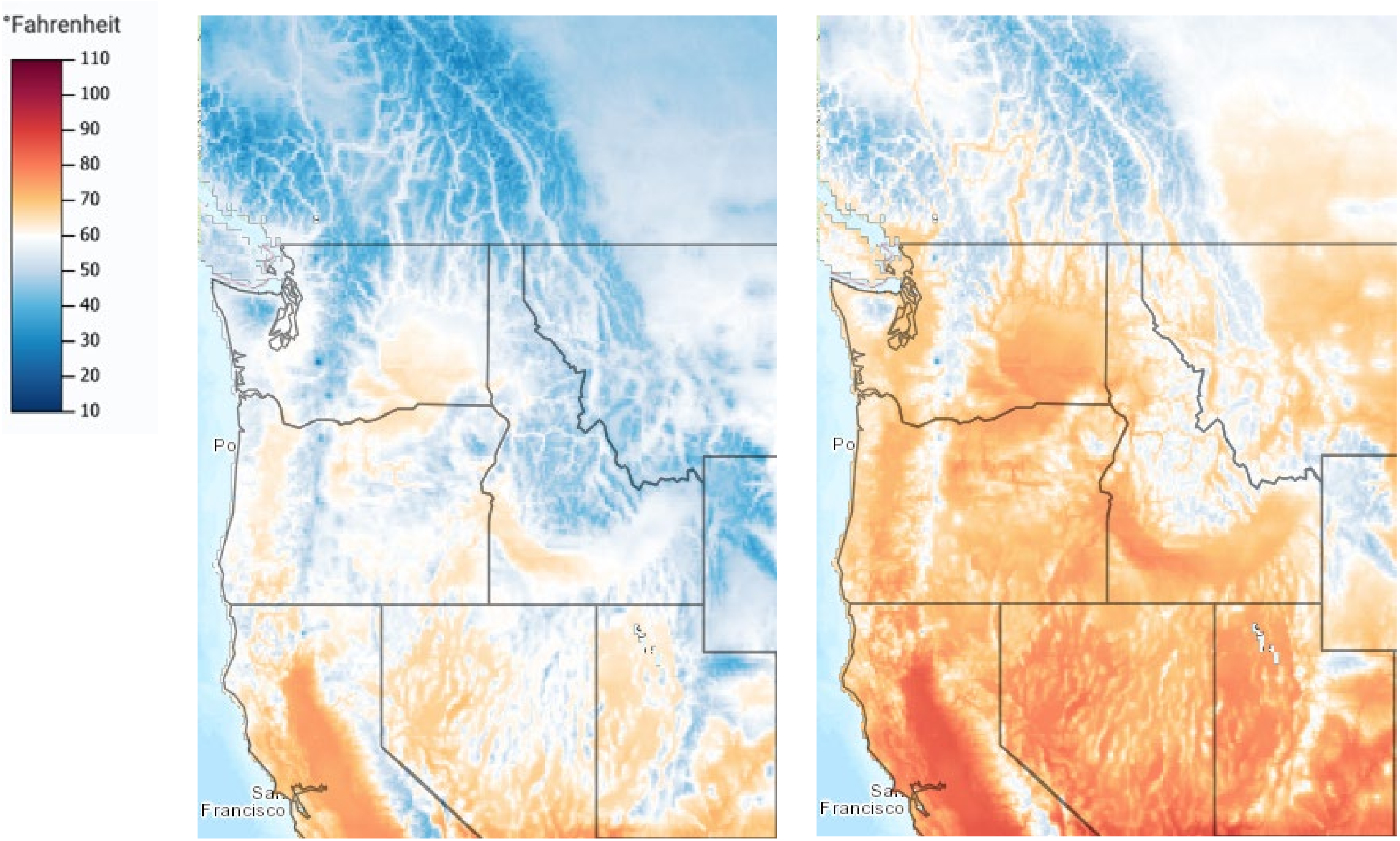
- Locate the trees
- Sample the best and worst growing tree from each family of 16
- Leaf DNA extraction
- 523 trees passed QC
- ApeK1 digestion
- 7.6 M 101 bp reads per sample
- SNP calling with FreeBayes
- 501,933 SNPs
- Combined data with Ballhorn lab

Analysis of GBS data

- GWAS for growth traits
  - Height
  - Diameter at Breast Height (DBH)
  - Estimated volume
  - Best/worst grower in family
- Genotype-Environment associations
  - Precipitation
  - Temperature
  - Soil variables

Climate models

CMIP5 (Coupled Model Intercomparison Project Phase 5)

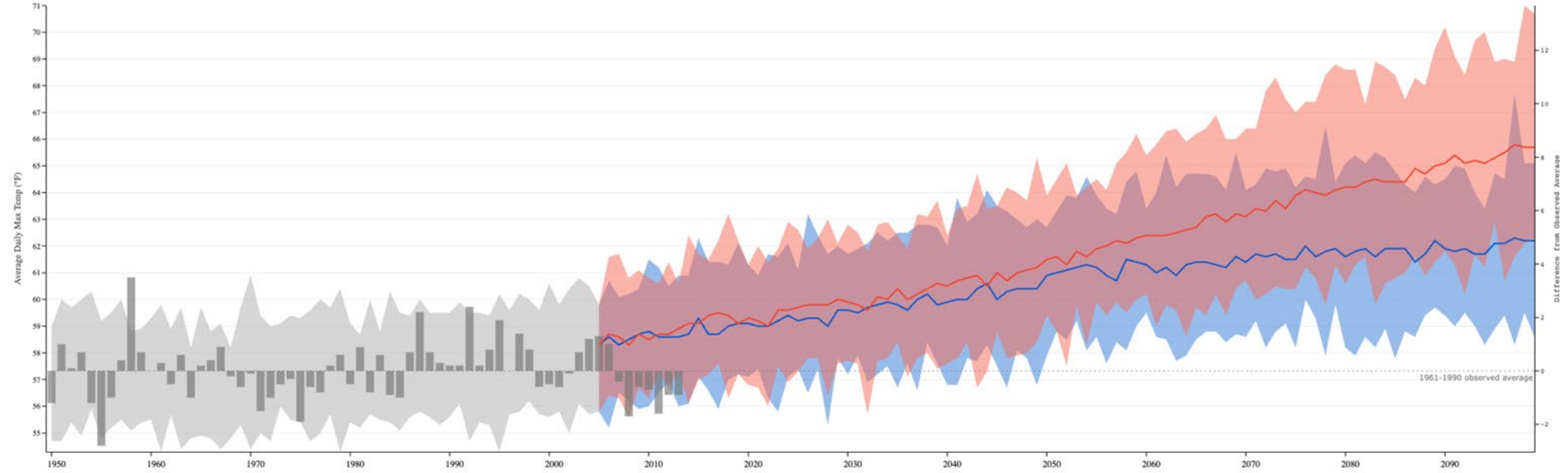


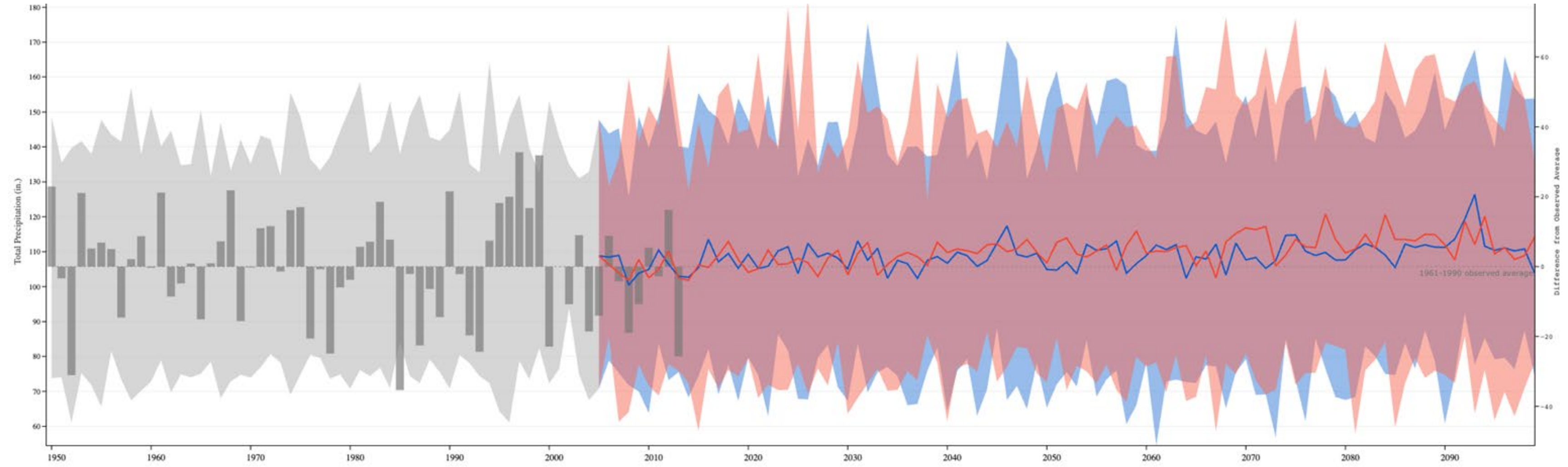
1961-1990 mean

2099, high emissions scenario

Climate models

Aberdeen, Washington

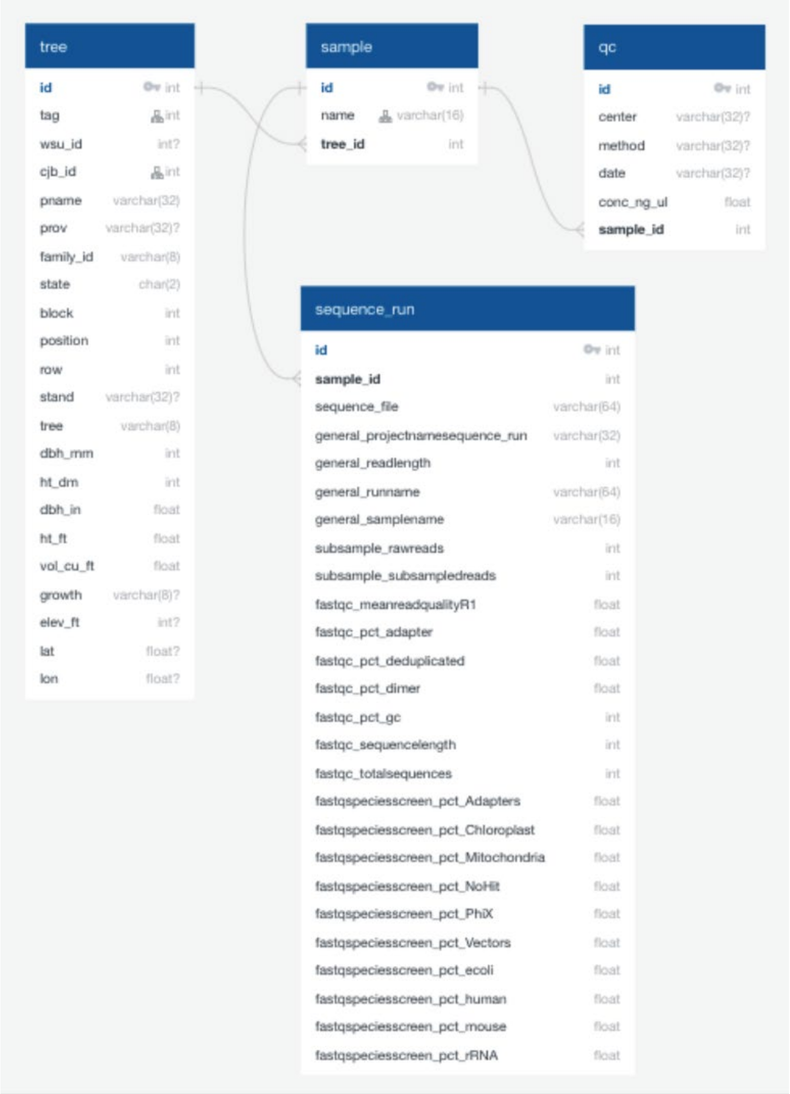




Data from the U.S. Climate Resilience Toolkit Climate Explorer


55

Provenance trial database

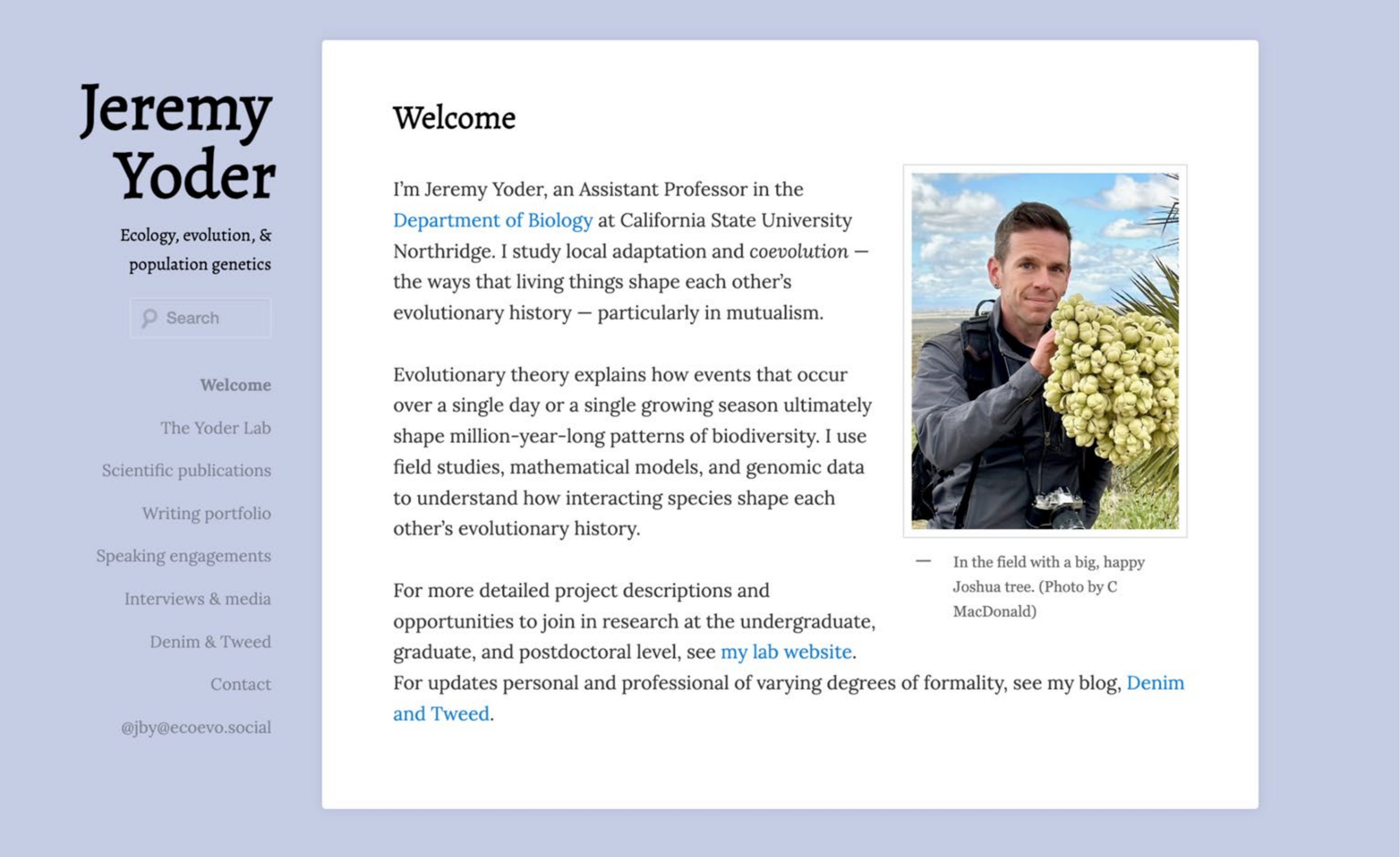


tree	
id	🔑 int
tag	int
wsu_id	int?
cjb_id	int
pname	varchar(32)
prov	varchar(32)?
family_id	varchar(8)
state	char(2)
block	int
position	int
row	int
stand	varchar(32)?
tree	varchar(8)
dbh_mm	int
ht_dm	int
dbh_in	float
ht_ft	float
vol_cu_ft	float
growth	varchar(8)?
elev_ft	int?
lat	float?
lon	float?

sample	
id	🔑 int
name	varchar(16)
tree_id	int

qc	
id	🔑 int
center	varchar(32)?
method	varchar(32)?
date	varchar(32)?
conc_ng_ul	float
sample_id	int

sequence_run	
id	🔑 int
sample_id	int
sequence_file	varchar(64)
general_projectnamesequence_run	varchar(32)
general_readlength	int
general_runname	varchar(64)
general_samplename	varchar(16)
subsample_rawreads	int
subsample_subsampledreads	int
fastqc_meanreadqualityR1	float
fastqc_pct_adapter	float
fastqc_pct_deduplicated	float
fastqc_pct_dimer	float
fastqc_pct_gc	int
fastqc_sequencelength	int
fastqc_totalsequences	int
fastqspeciesscreen_pct_Adapters	float
fastqspeciesscreen_pct_Chloroplast	float
fastqspeciesscreen_pct_Mitochondria	float
fastqspeciesscreen_pct_NoHit	float
fastqspeciesscreen_pct_PhiX	float
fastqspeciesscreen_pct_Vectors	float
fastqspeciesscreen_pct_ecoli	float
fastqspeciesscreen_pct_human	float
fastqspeciesscreen_pct_mouse	float
fastqspeciesscreen_pct_rRNA	float



Jeremy Yoder

Ecology, evolution, & population genetics

Welcome

I'm Jeremy Yoder, an Assistant Professor in the Department of Biology at California State University Northridge. I study local adaptation and *coevolution* — the ways that living things shape each other's evolutionary history — particularly in mutualism.

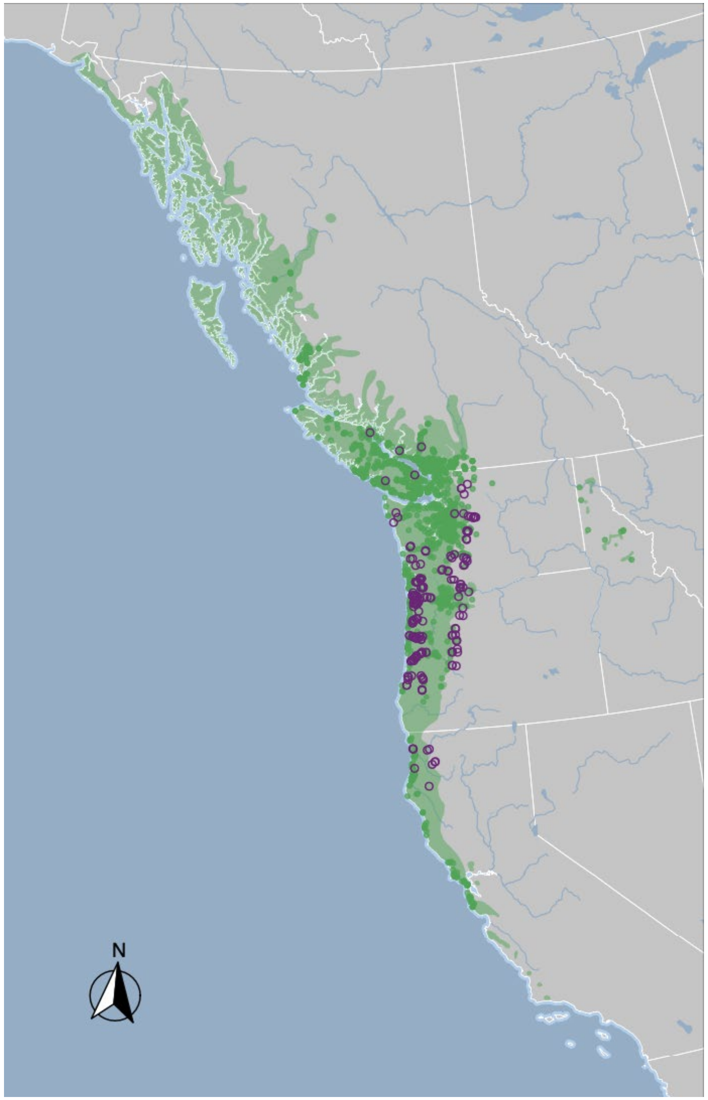
Evolutionary theory explains how events that occur over a single day or a single growing season ultimately shape million-year-long patterns of biodiversity. I use field studies, mathematical models, and genomic data to understand how interacting species shape each other's evolutionary history.

— In the field with a big, happy Joshua tree. (Photo by C MacDonald)

For more detailed project descriptions and opportunities to join in research at the undergraduate, graduate, and postdoctoral level, see my lab website.
For updates personal and professional of varying degrees of formality, see my blog, Denim and Tweed.

https://lab.jbyoder.org/

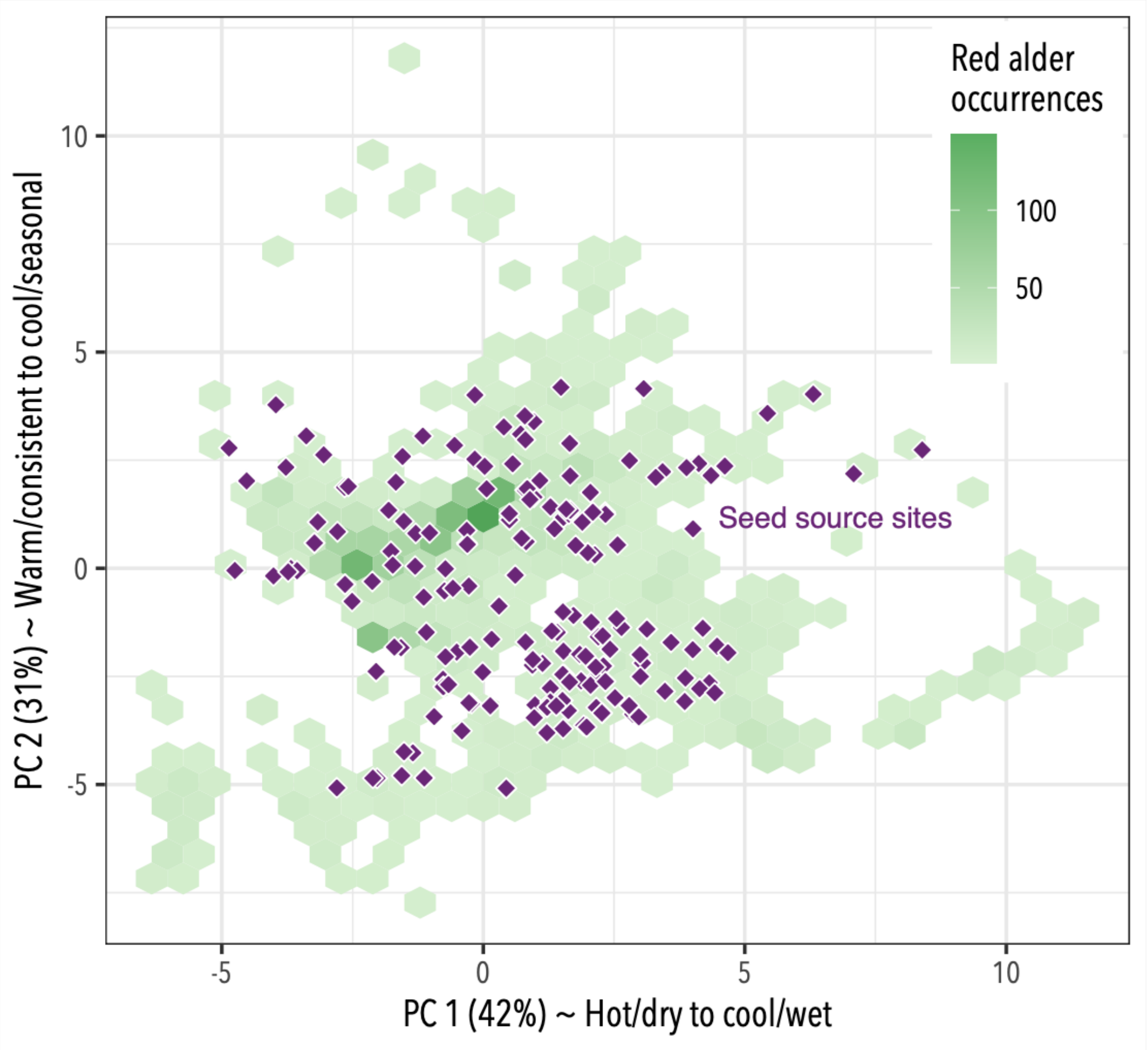
Range representation



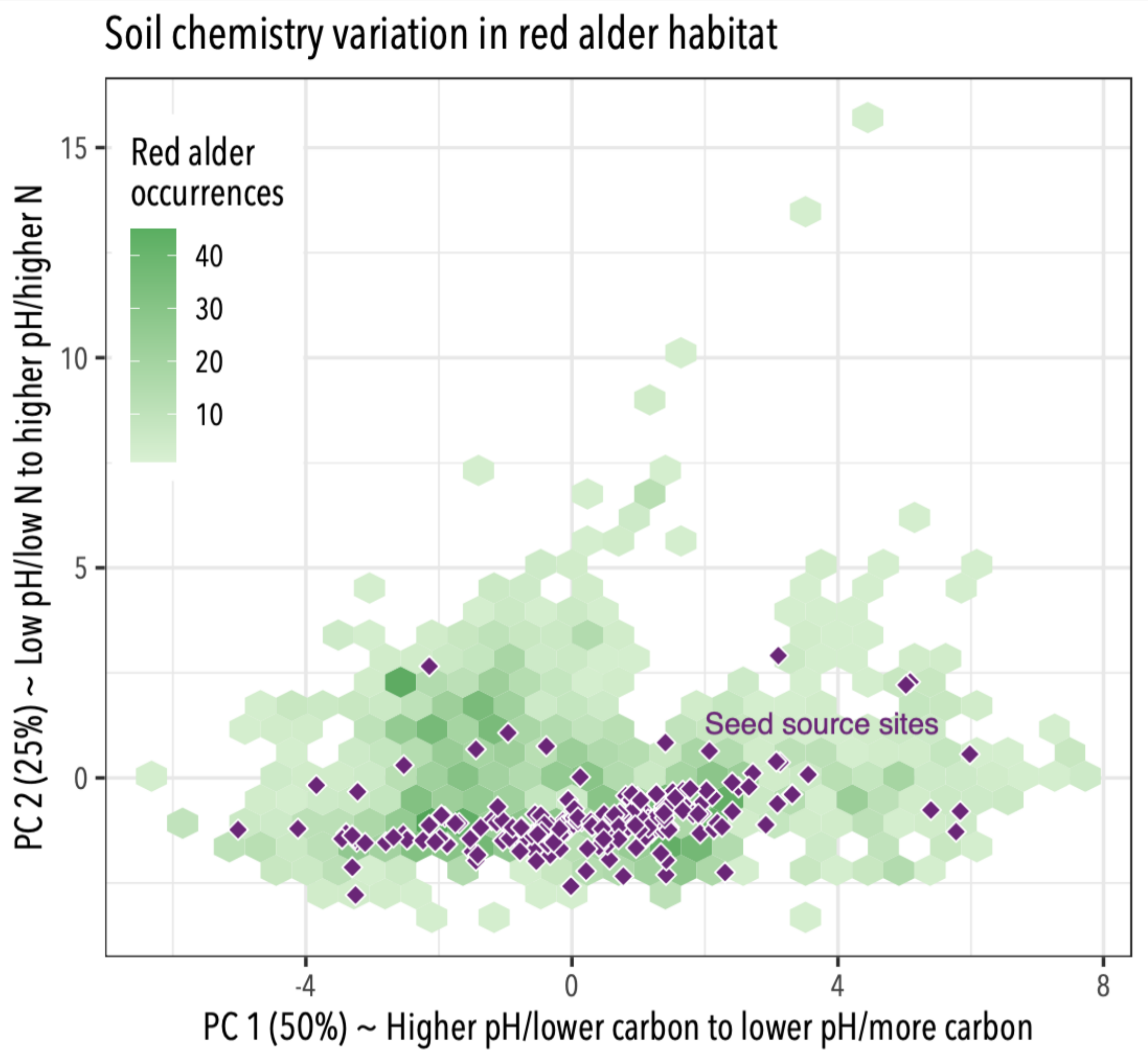
- Green contour: USDA
- Green dots: GBIF occurrences
- Purple dots: our provenances

Global Biodiversity Information Facility

BioCLIM 30 year average PCA



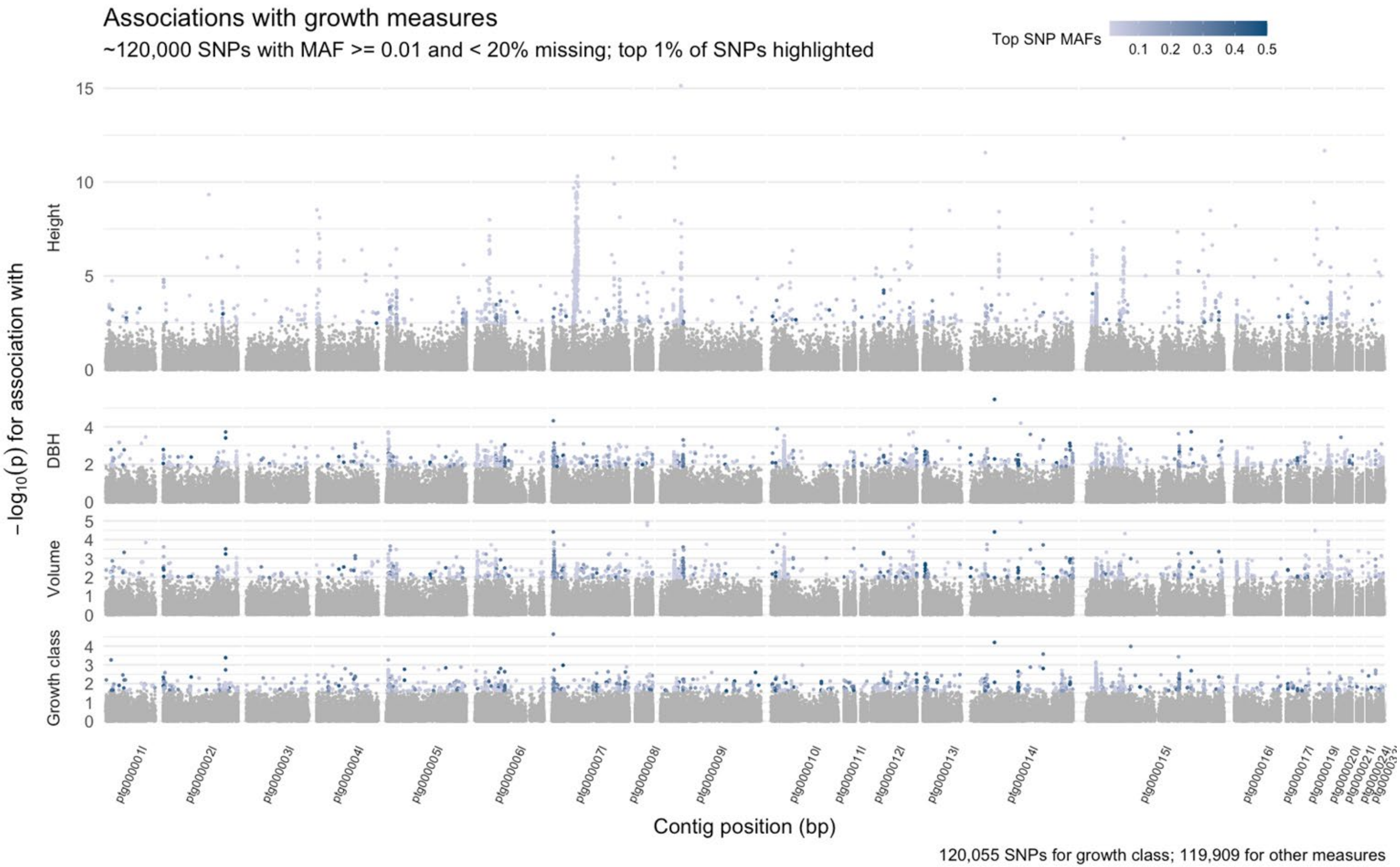
Soil chemistry PCA

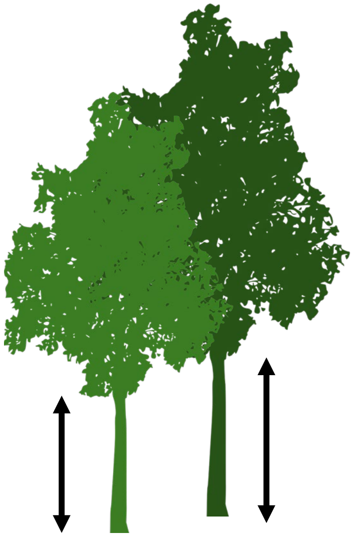


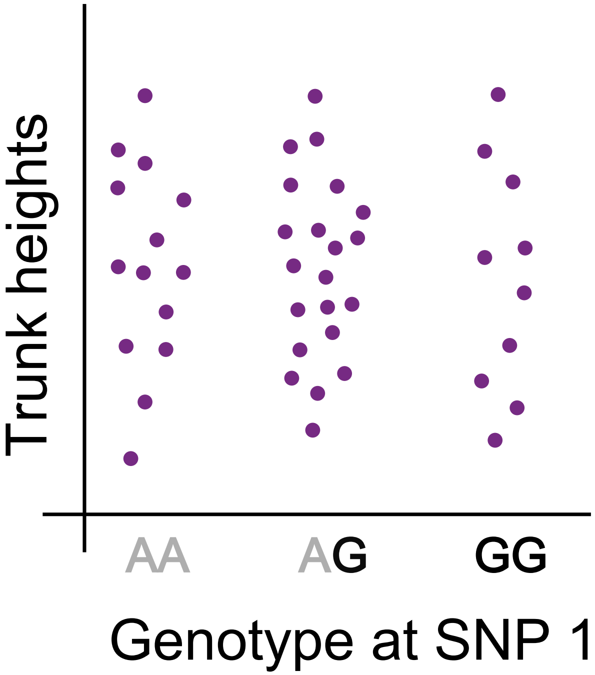
Gene-Environment GWAS

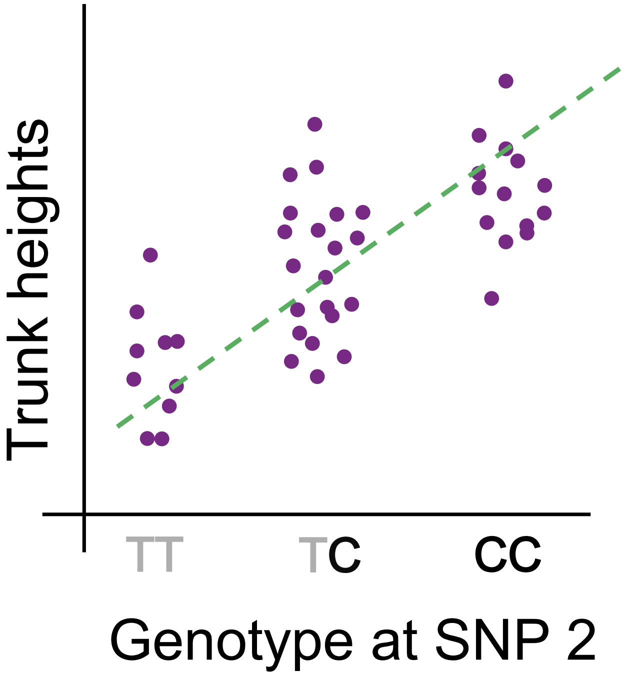
Climate PC1: warmer/drier; PC2: more coastal/temperate
Soil PC1: higher pH/lower SOC; PC2: lower N, lower pH

Growth trait GWAS

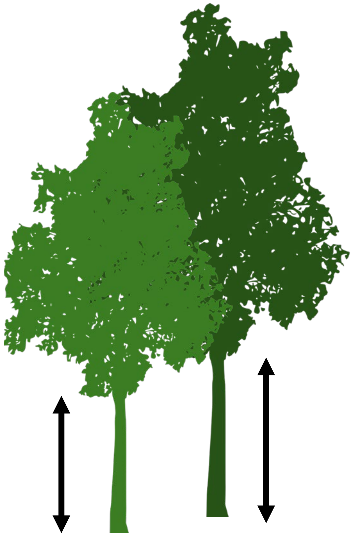


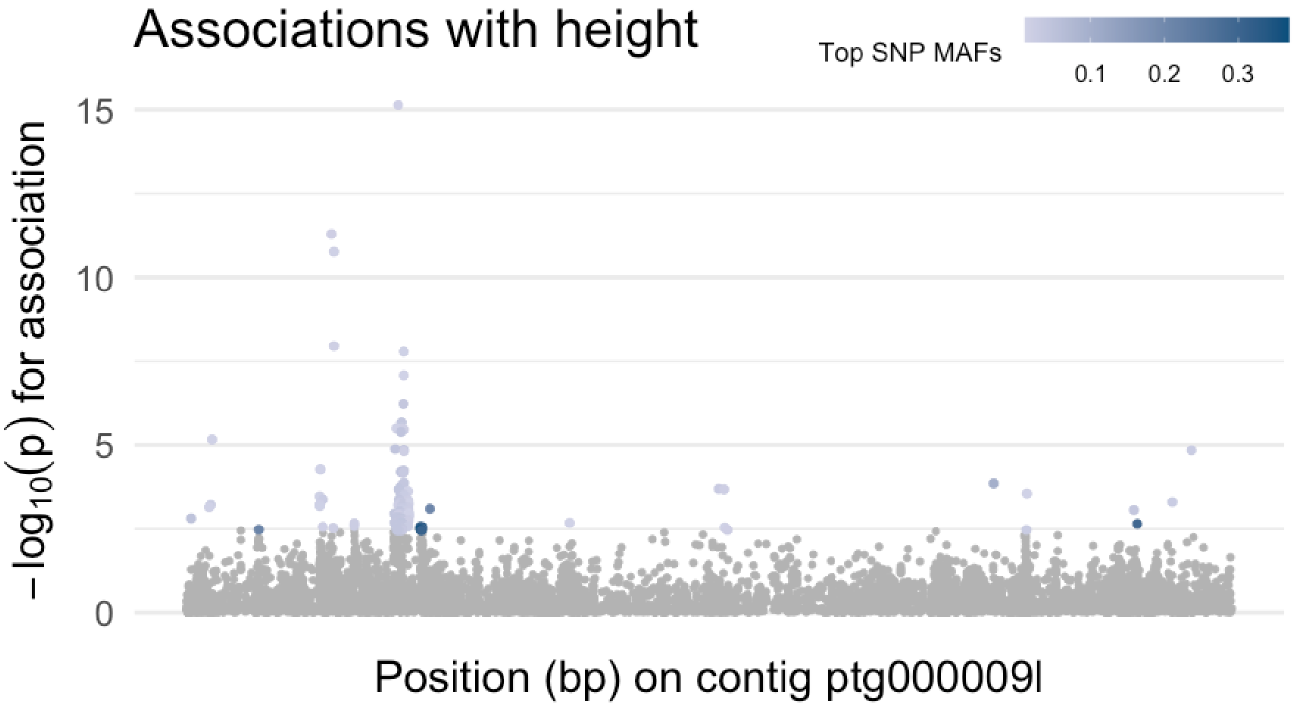


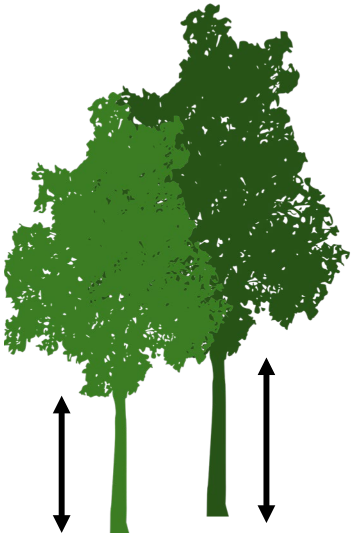


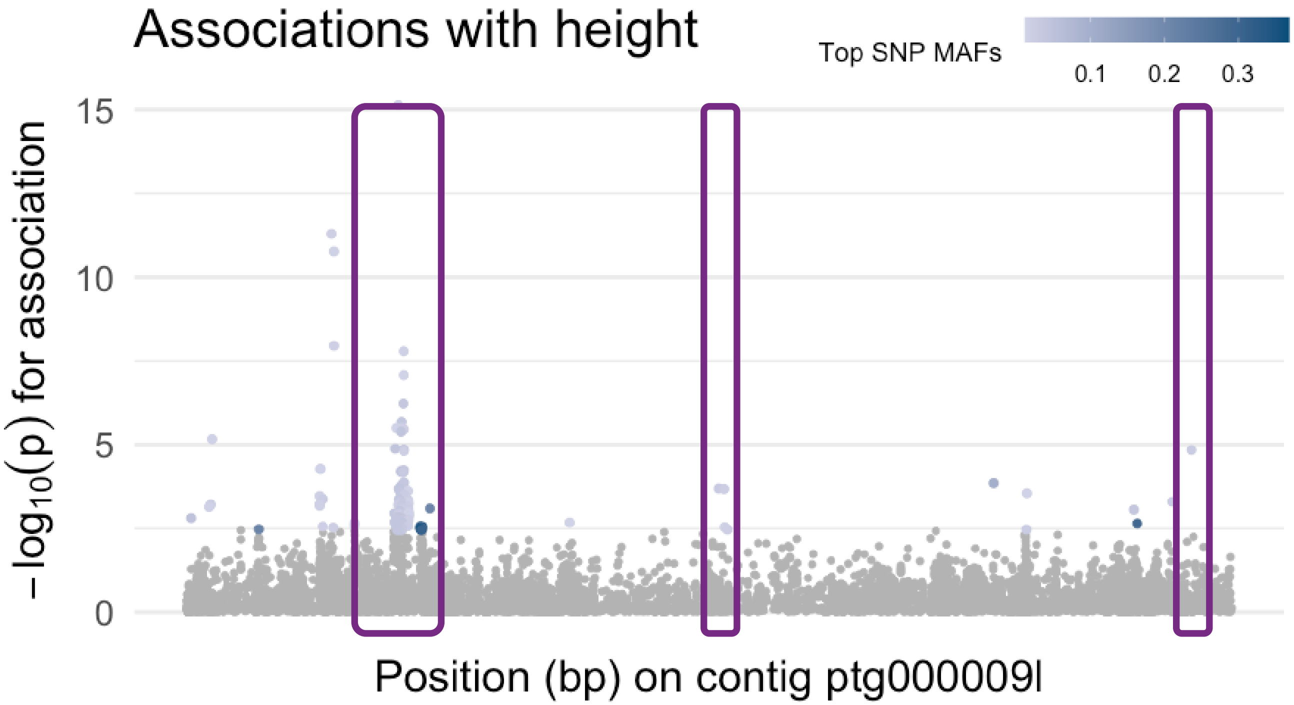


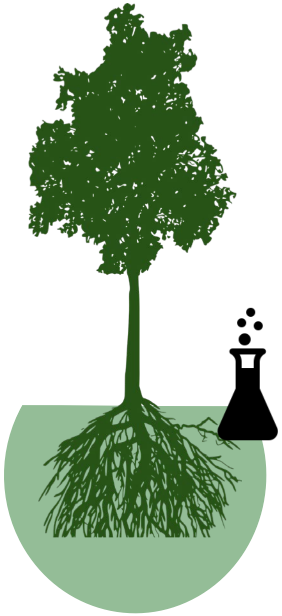
SNP 2 is “associate
with height

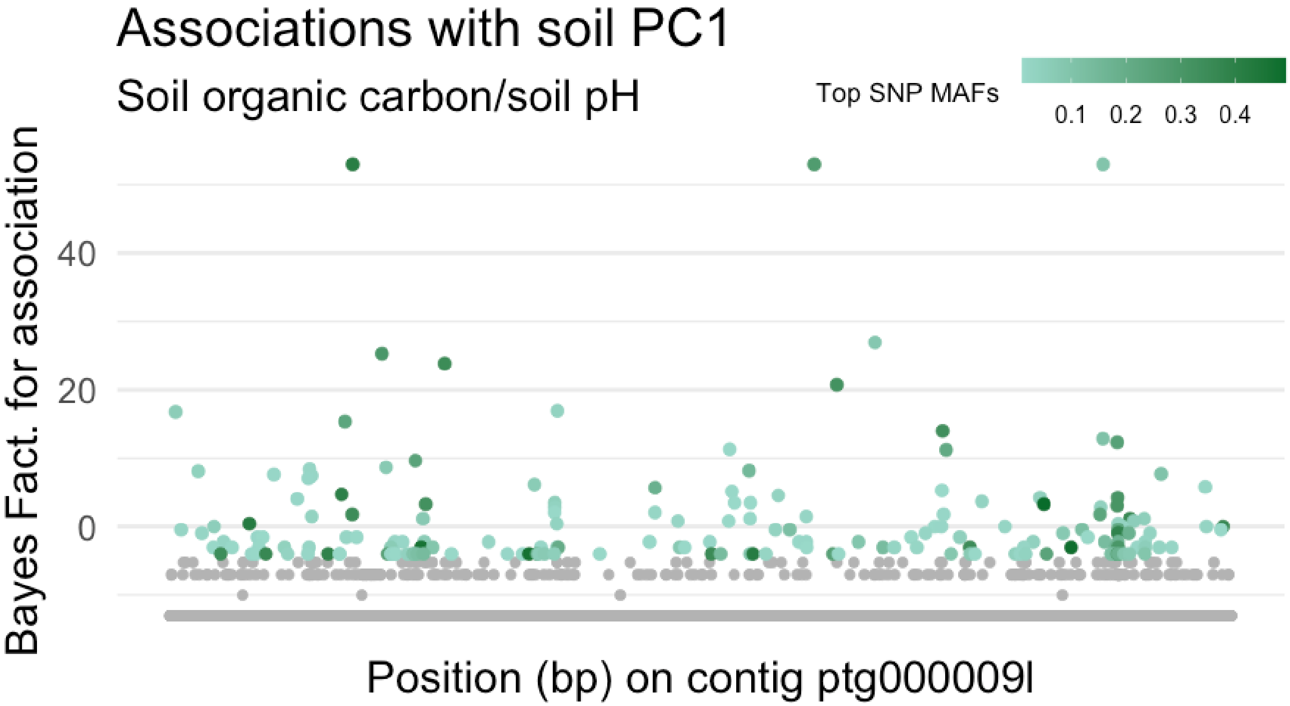



Associations with height
Top SNP MAFs
0.1
0.2
0.3
−log$_{10}$(p) for association
15
10
5
0
Position (bp) on contig ptg000009l



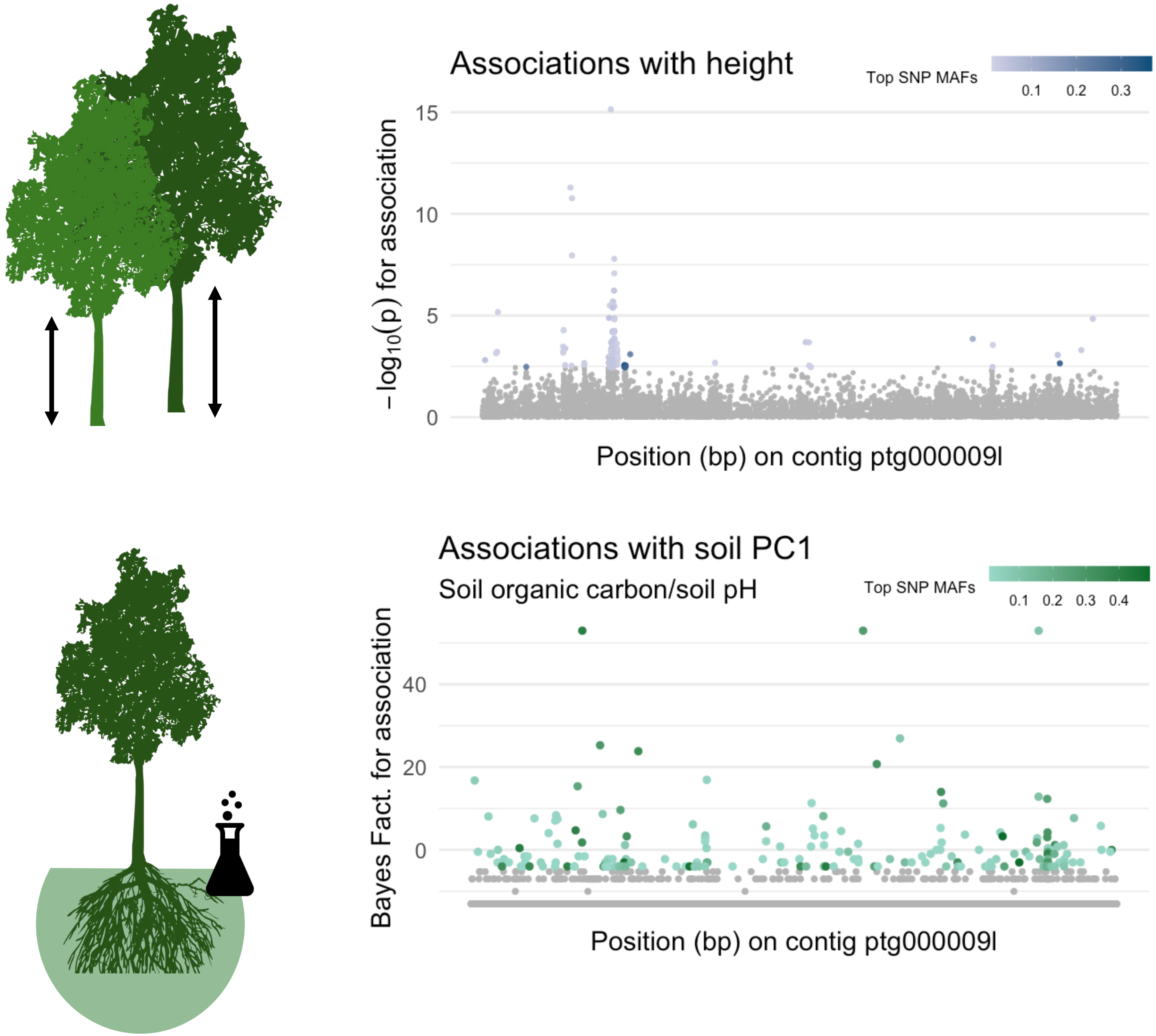

Associations with height
Top SNP MAFs
0.1
0.2
0.3
15
10
5
0
$-\log_{10}(p)$ for association
Position (bp) on contig ptg000009l

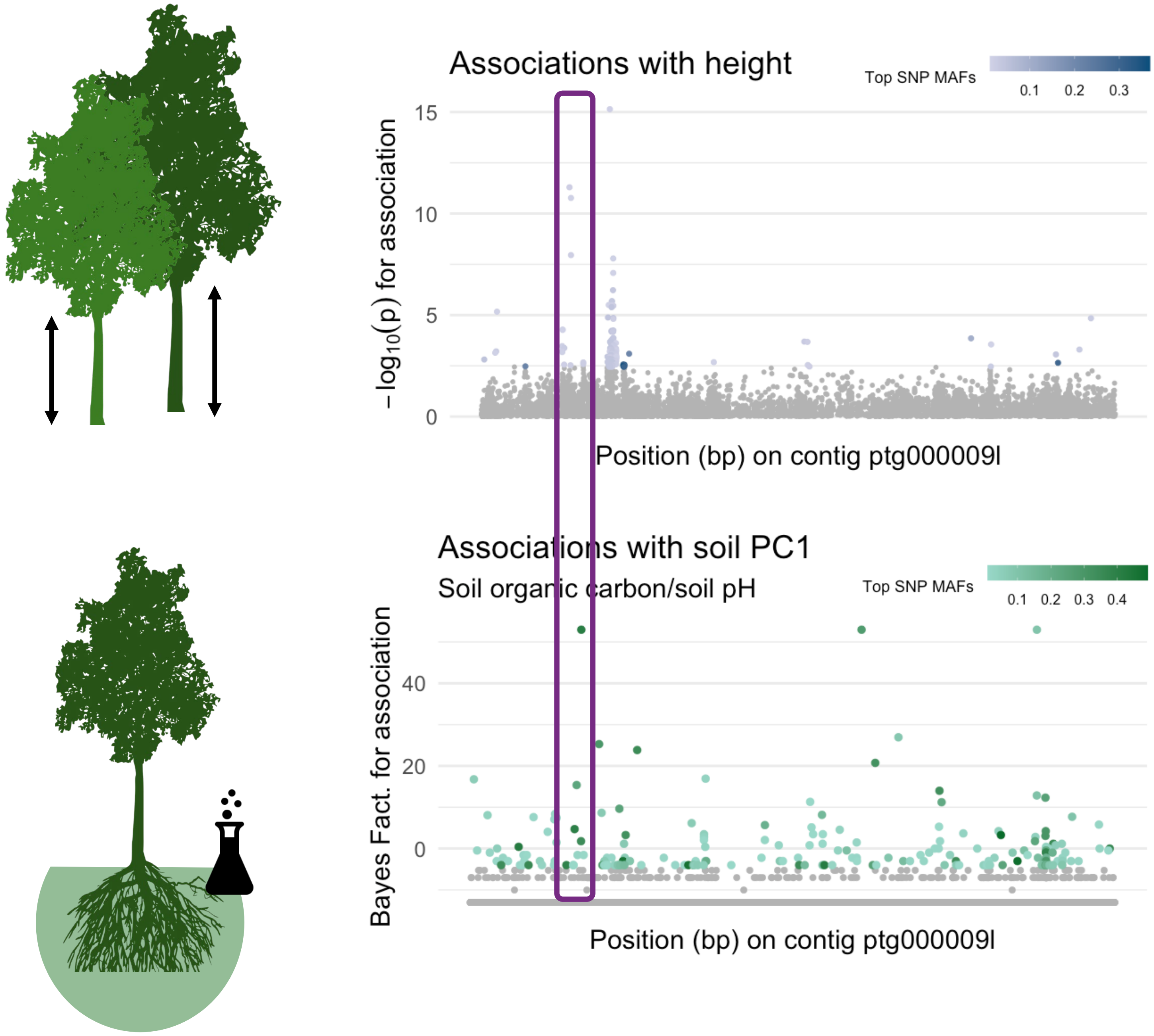


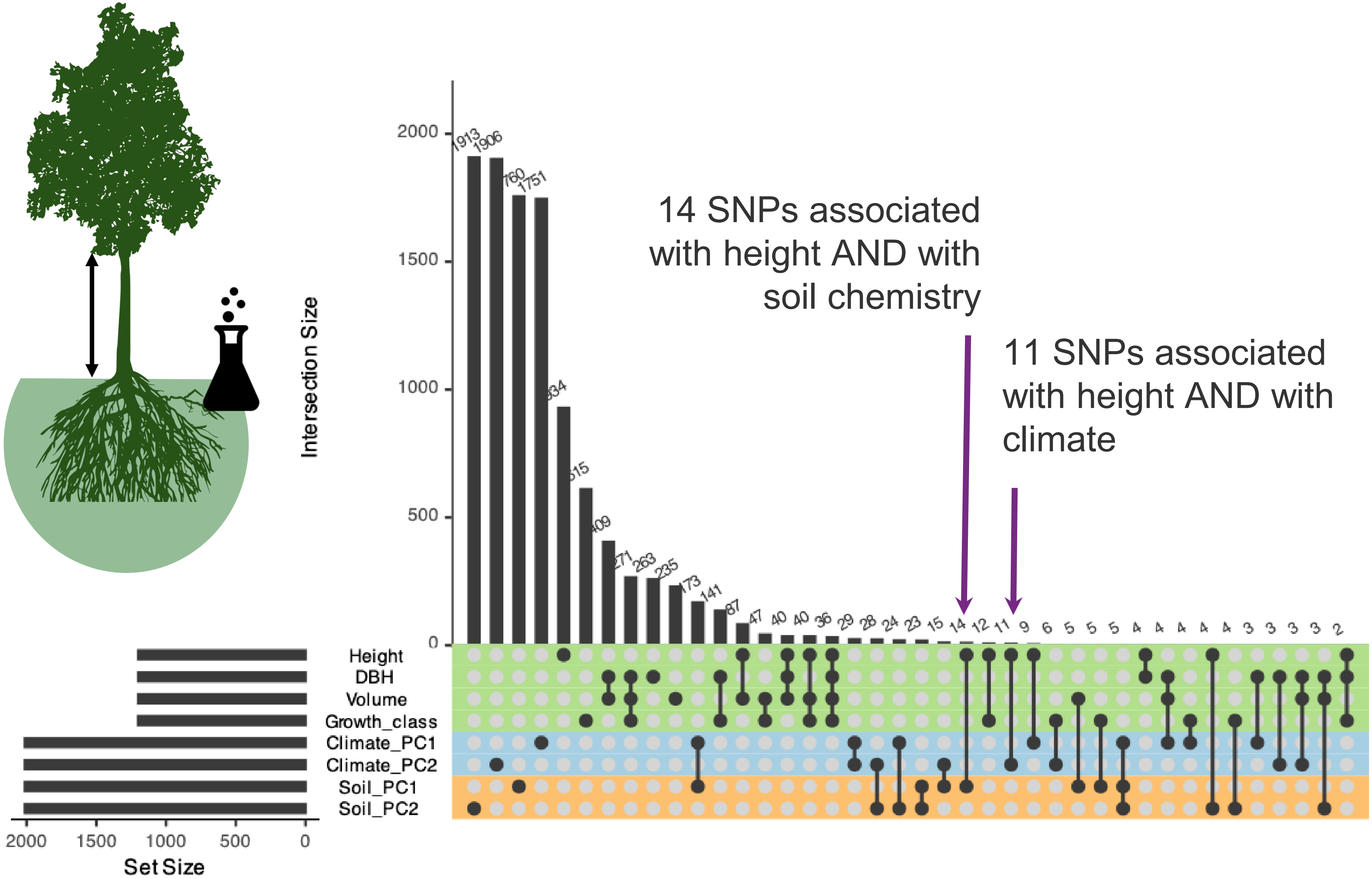


Associations with soil PC1

Soil organic carbon/soil pH


Associations with height
Top SNP MAFs
0.1
0.2
0.3
−log10(p) for association
15
10
5
0
Position (bp) on contig ptg000009l
Associations with soil PC1
Soil organic carbon/soil pH
Top SNP MAFs
0.1
0.2
0.3
0.4
Bayes Fact. for association
40
20
0
Position (bp) on contig ptg000009l

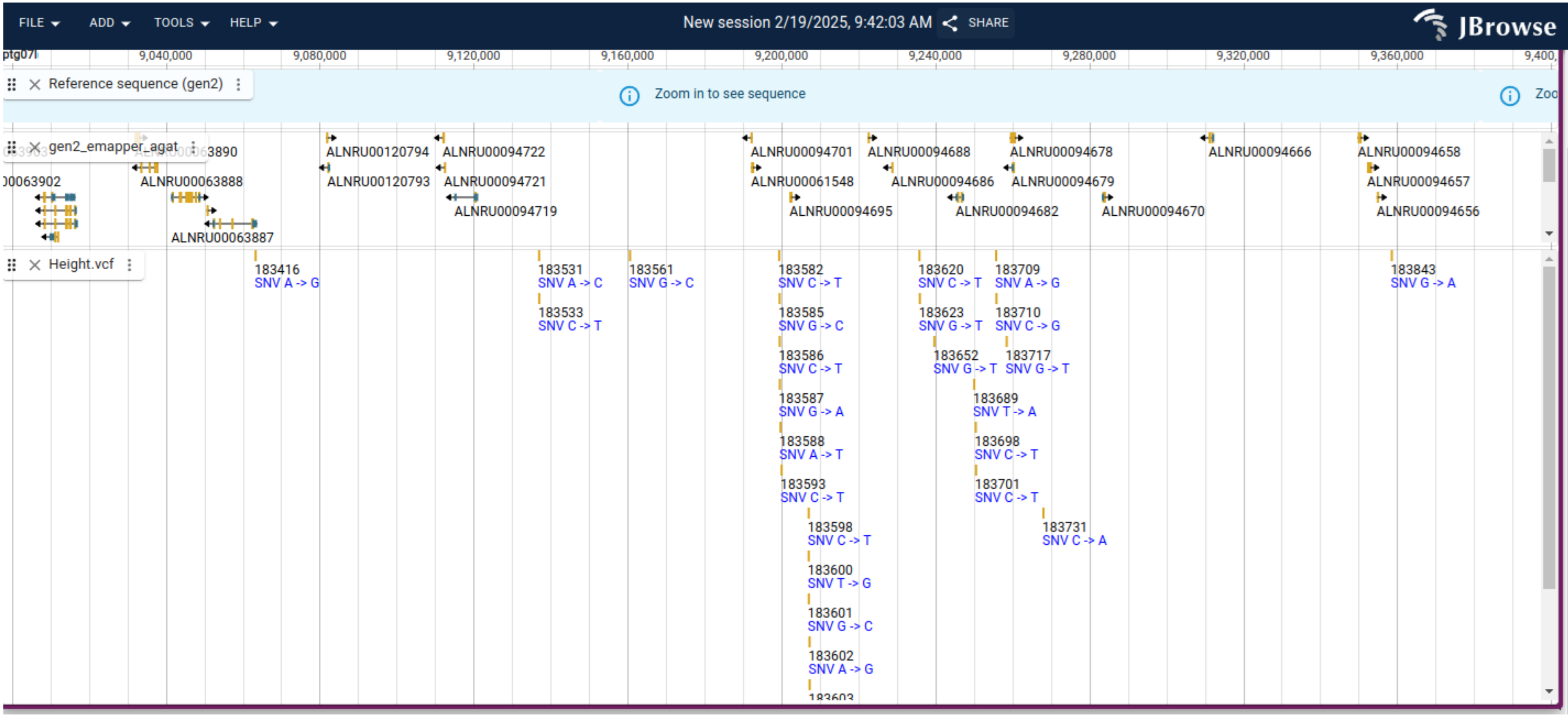

Associations with height
Top SNP MAFs
0.1
0.2
0.3
15
10
5
0
$-\log_{10}(p)$ for association
Position (bp) on contig ptg000009l
Associations with soil PC1
Soil organic carbon/soil pH
Top SNP MAFs
0.1
0.2
0.3
0.4
40
20
0
Bayes Fact. for association
Position (bp) on contig ptg000009l



14 SNPs associated with height AND with soil chemistry

11 SNPs associated with height AND with climate

Finding genes of interest…



Conclusion and discussion of opportunities

- Value of the trial?
- Future of trial site
- Future directions
- Interest in collaboration
- Funding opportunities
- Questions for us

WASHINGTON STATE UNIVERSITY

Norman Lewis
Laurence Davin
Barri Herman
Mike Costa
Syed Moinuddin

Pacific Northwest
NATIONAL LABORATORY

Kim Hixson

NCGR
National Center for Genome Resources

Andy Binns
Diego Fajardo
Johnny Sena
Nico Devitt

CSUN

Jeremy Yoder

Portland State
UNIVERSITY

Daniel Ballhorn
Robyn Dove