

HAPLOTYPE-RESOLVED CHROMOSOME-LEVEL ASSEMBLY OF EUROPEAN HAZELNUT (*C. AVELLANA*) ‘JEFFERSON’ PROVIDES INSIGHT INTO EASTERN FILBERT BLIGHT



¹Oregon State University, Dept. of Horticulture, Corvallis, OR, USA,
²HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA

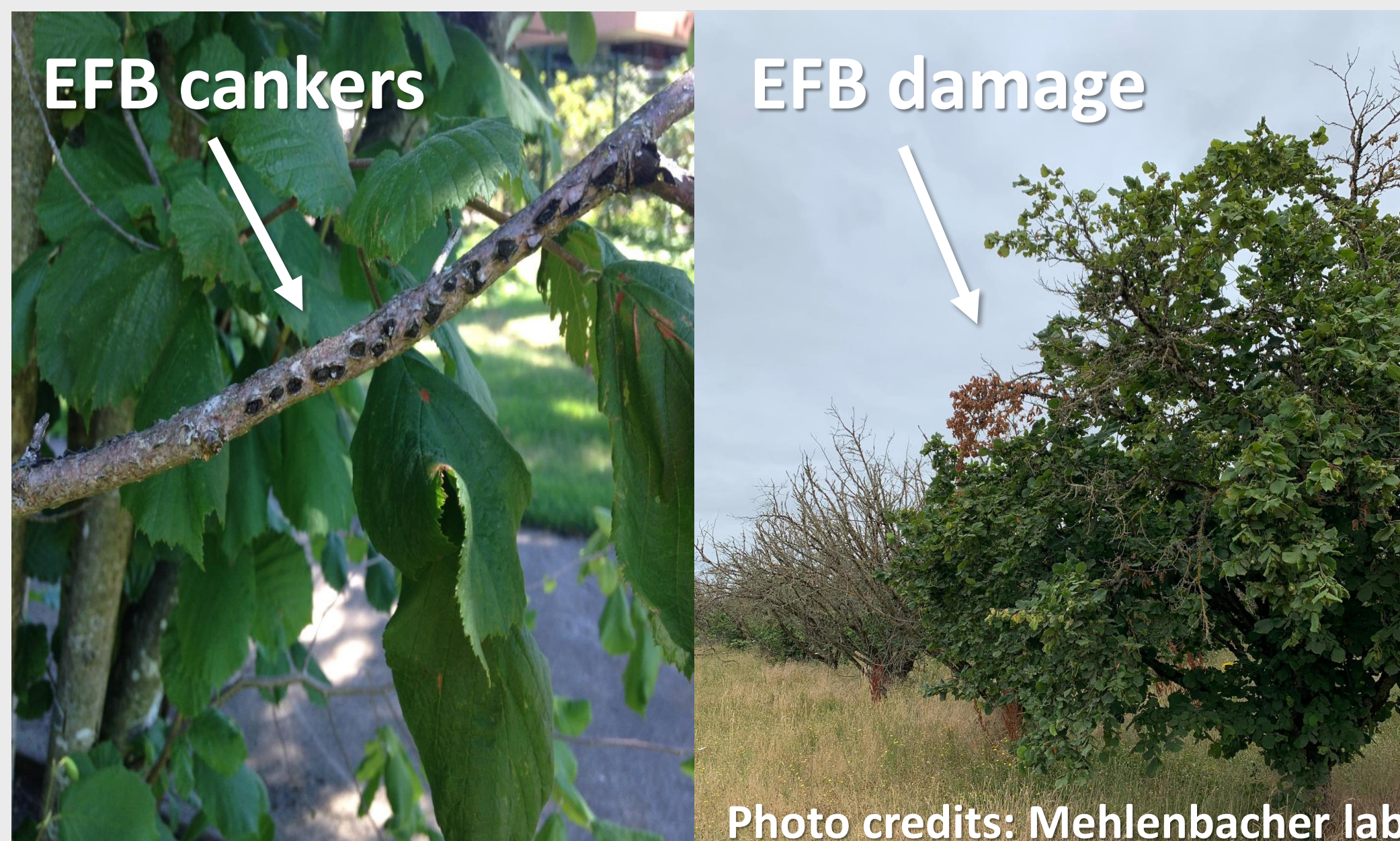
S. Talbot¹, J. Clevenger², J. Snelling¹, S. Mehlenbacher¹, K. Vining¹

INTRODUCTION

- European hazelnut (*Corylus avellana*) is grown in the Oregon Willamette Valley, representing 97% of USA hazelnut production
- Eastern filbert blight, (EFB), a fungal disease caused by *Anisogramma anomala*, reduces yield and ultimately results in plant death
- Emerging strains of EFB threaten to overwhelm current qualitative resistance in commercial cultivars
- The identification of EFB resistance genes and development of linked DNA markers would facilitate their use in breeding new resistant cultivars

- ‘Jefferson’ has been the focus of genome resource development
- EFB resistance in ‘Jefferson’ is conferred by the cultivar ‘Gasaway’, characterized as a dominant allele at a single locus mapped to a ~130 Kb region of linkage group 6
- Version 4 (V4) of ‘Jefferson’, is a haplotype-resolved chromosome-level trio hifiasm assembly generated using PacBio HiFi, Hi-C, and parental Illumina reads
- Structural and functional genome annotation by BRAKER and OmicsBox

Figure 1. Oregon State University cultivar release *C. avellana* cv. ‘Jefferson’ carries a single dominant allele for eastern filbert blight resistance



‘JEFFERSON’ HI-C CONTACT MAPS DIFFERENTIATE CHROMOSOMAL HAPLOTYPES

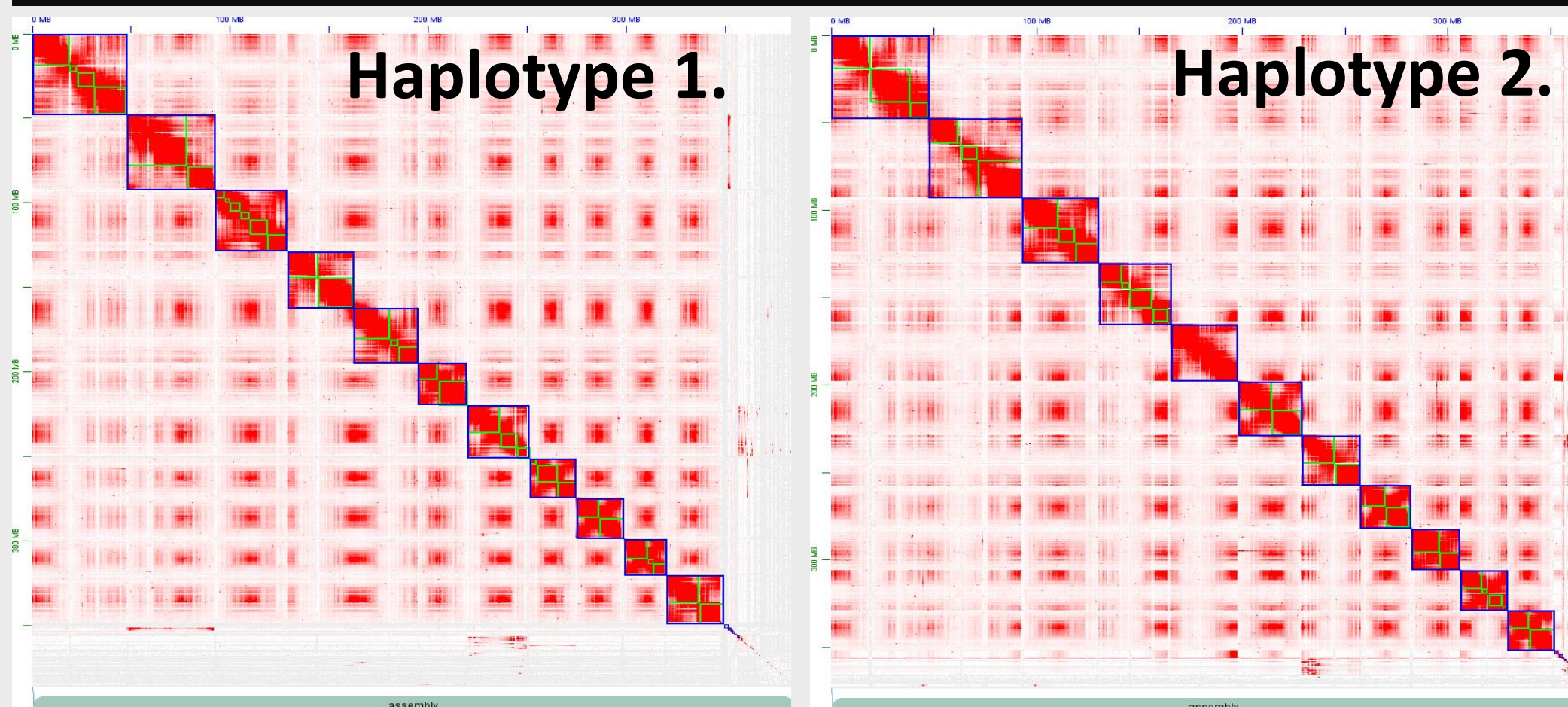


Figure 2. Hi-C contact maps of ‘Jefferson’ haplotypes

ITERATIVE IMPROVEMENT OF THE ‘JEFFERSON’ REFERENCE GENOME

Table 1. Comparison of ‘Jefferson’ genome assembly metrics

	“Jeff V1”	“Jeff V3”	“Jeff V4 Haplotype 1”	“Jeff V4 Haplotype 2”	“Tombul” (Lucas et al., 2021)
Total Scaffold number	36,641	701	11	11	11
Length (Mbp)	345.5	559	349.7	352	369.7
N50 (Mbp)	0.1745	49.8	32.5	32.4	36.6
Largest contig (Mbp)	0.0215	72.27	48.25	47.6	50.95
#N's per 100 Kbp	NA	18.32	1.26	1.19	476.68
GC (%)	NA	35.98	36.36	36.34	35.91
Genes Annotated	29,850	34,982	30,808	30,889	27,270

IMPROVED GENE ANNOTATION

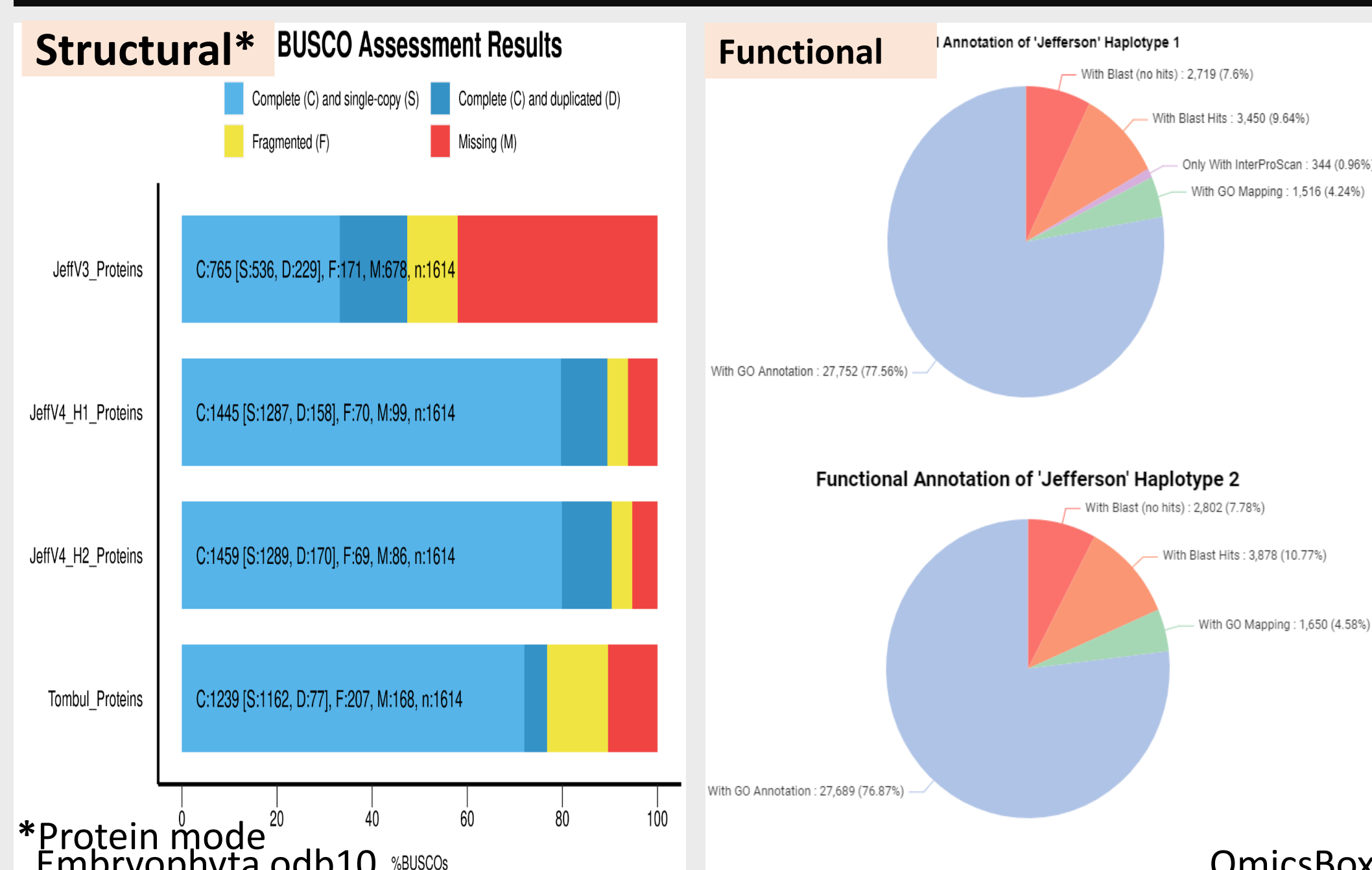


Figure 3. ‘Jefferson’ genome annotation metrics

SYNTENIC ‘JEFFERSON’ HAPLOTYPES

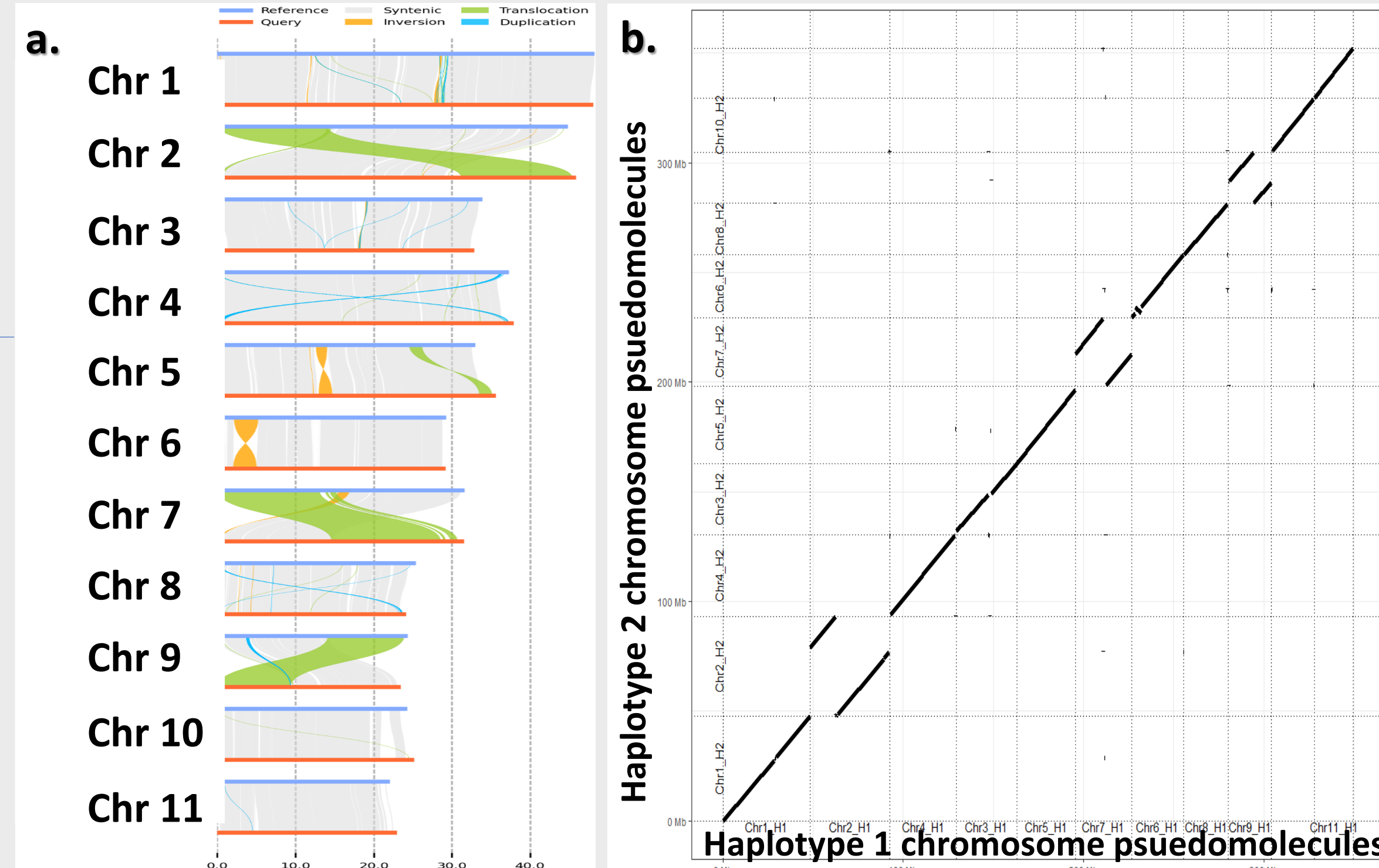


Figure 4. Visualizing ‘Jefferson’ V4 aligned haplotype genome assemblies
a. Synteny plot alignment of ‘Jefferson’ haplotypes (pafr)
b. Dotplot showing alignment of ‘Jefferson’ haplotypes

‘JEFFERSON’ CHROMOSOMAL FEATURES AND RESISTANCE GENE DISTRIBUTION

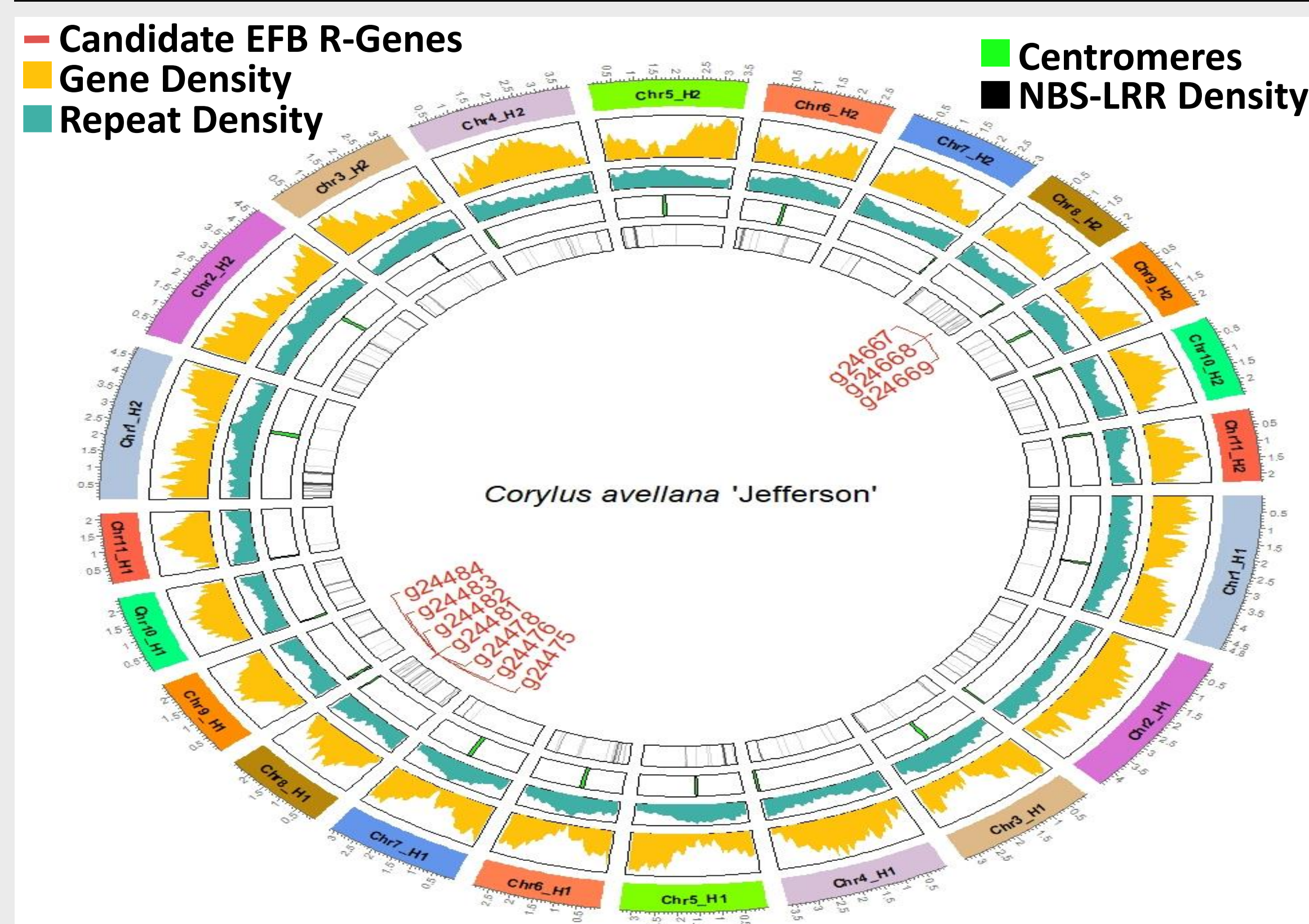


Figure 5. Circos plot of ‘Jefferson’ V4 haplotypes

PAIRED R-GENE CANDIDATES ARE TIGHTLY LINKED ON HAPLOTYPE 1

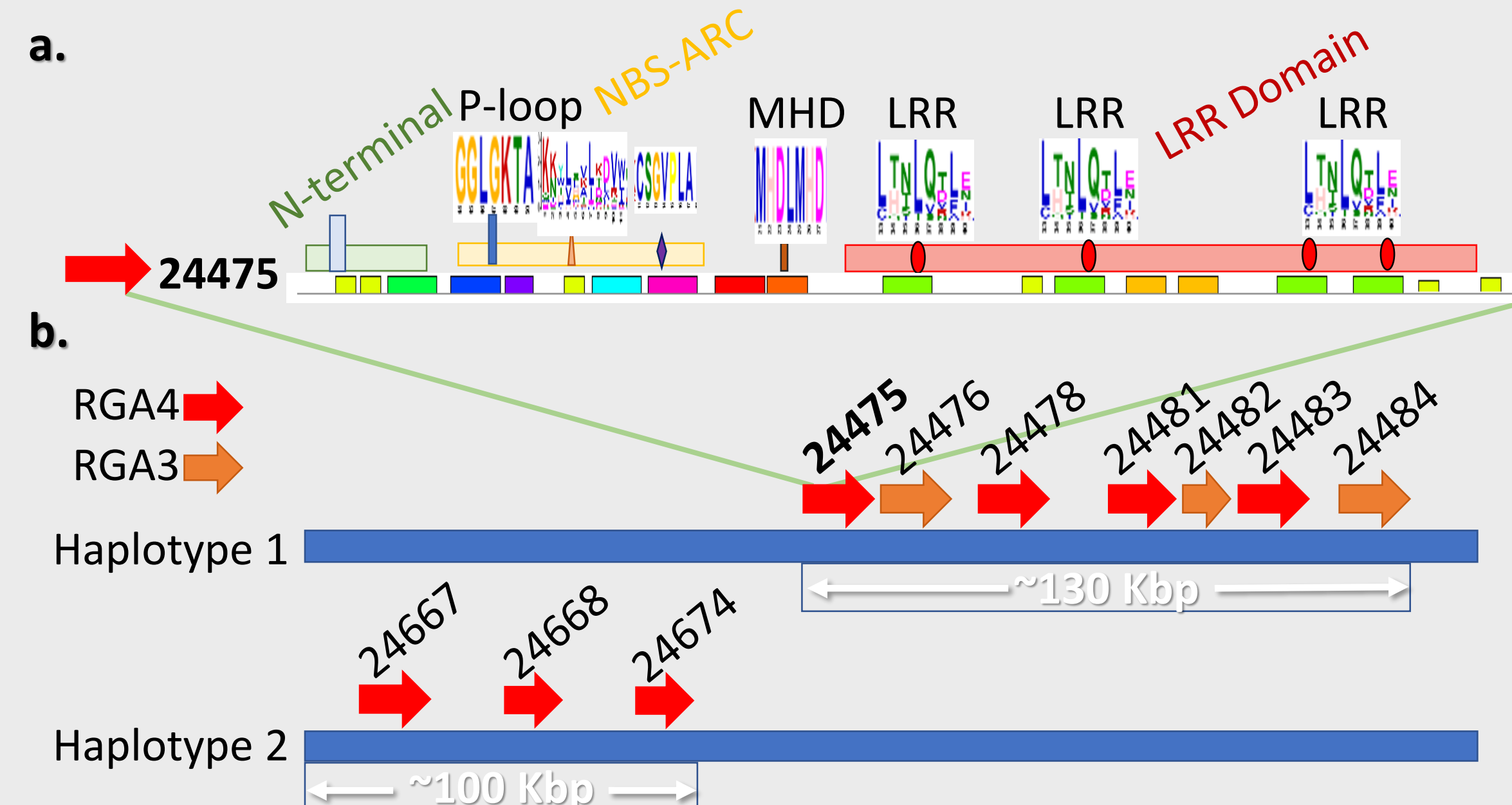


Figure 6. Visualizing putative EFB R-gene candidates
a. Protein motifs of an R-gene candidate identified by MEME
b. Putative EFB R-gene distribution in ‘Jefferson’ chromosome 8 haplotypes

CONCLUSIONS & FUTURE RESEARCH

- ‘Jefferson’ V4 is a haplotype-resolved chromosome-level genome assembly that is higher quality than previously published assemblies
- Haplotype phasing will improve molecular marker accuracy for putative EFB R-gene candidates
- Comparative genomics efforts are underway to explore gene synteny and allelic diversity among other EFB resistance sources

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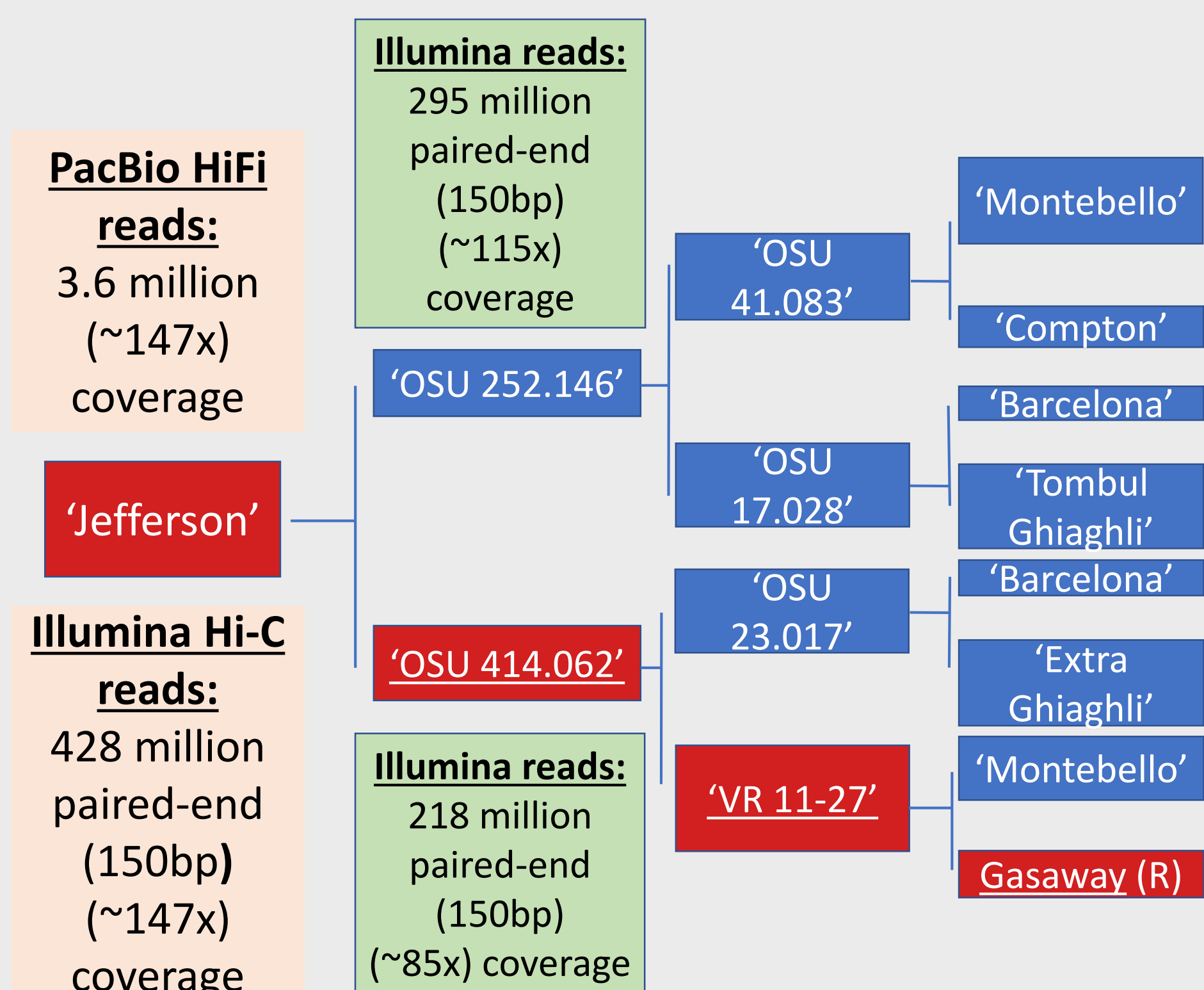


Figure 1. *C. avellana* ‘Jefferson’ pedigree with seq data

References

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