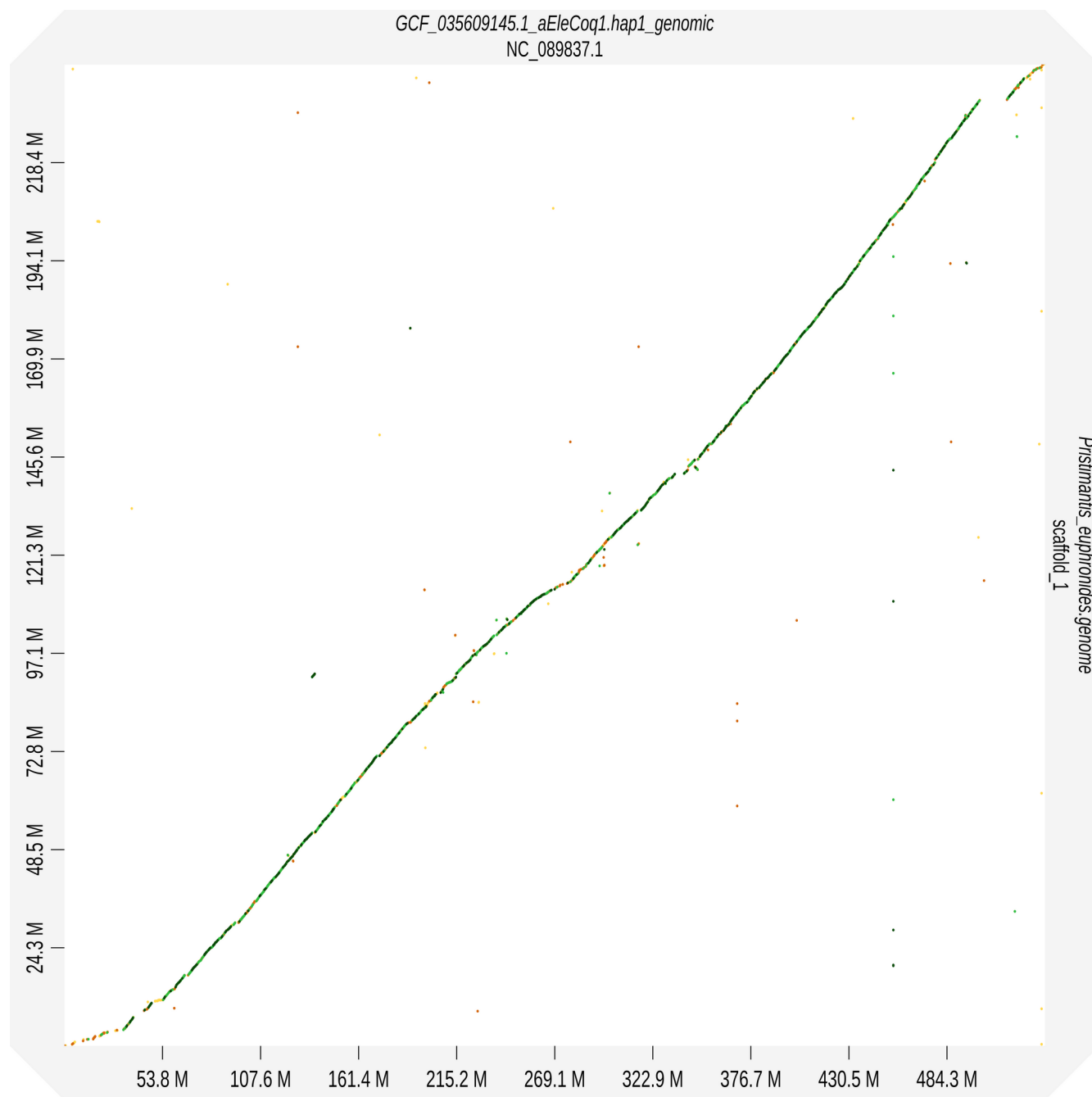


Additional file 8

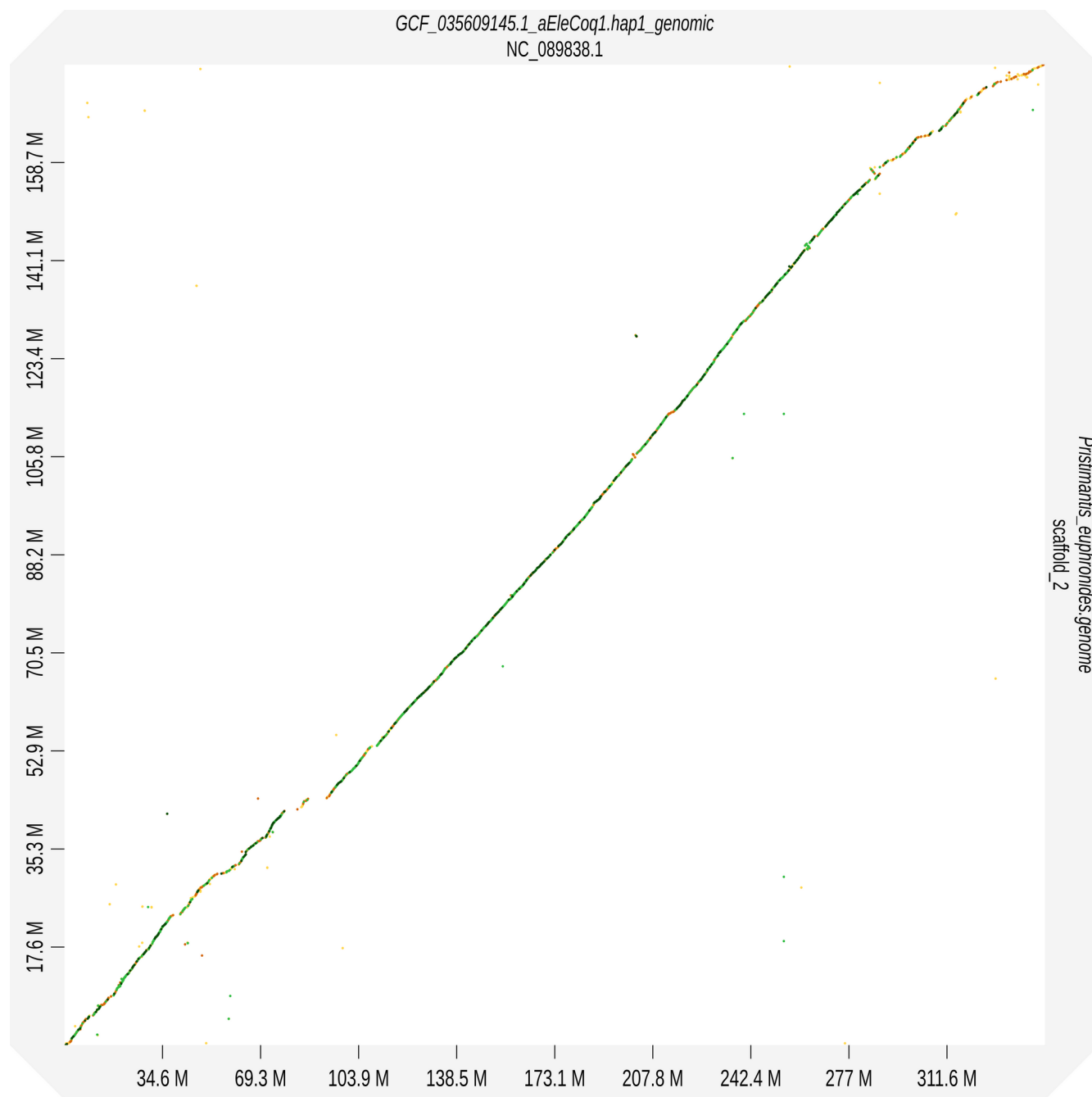
Supplementary results - Evaluation of reference-guided scaffolding

Figure. Scaffolded *Pristimantis euphronides* genome aligned to *Eleutherodactylus coqui* by chromosome. D-Genies v1.5.0 [1] dotplots showing individual scaffold-to-chromosome alignments extracted via the query and target selection interface. Panels A–M: scaffold_1 through scaffold_13 aligned to their corresponding *E. coqui* haplotype 1 chromosomes (RefSeq ID: GCF_035609145.1). Color reflects nucleotide identity in percentage (%) using the default D-Genies scale: white (0%), yellow (1-24%), orange (25-49%), light green (50-74%), and dark green (75-100%).

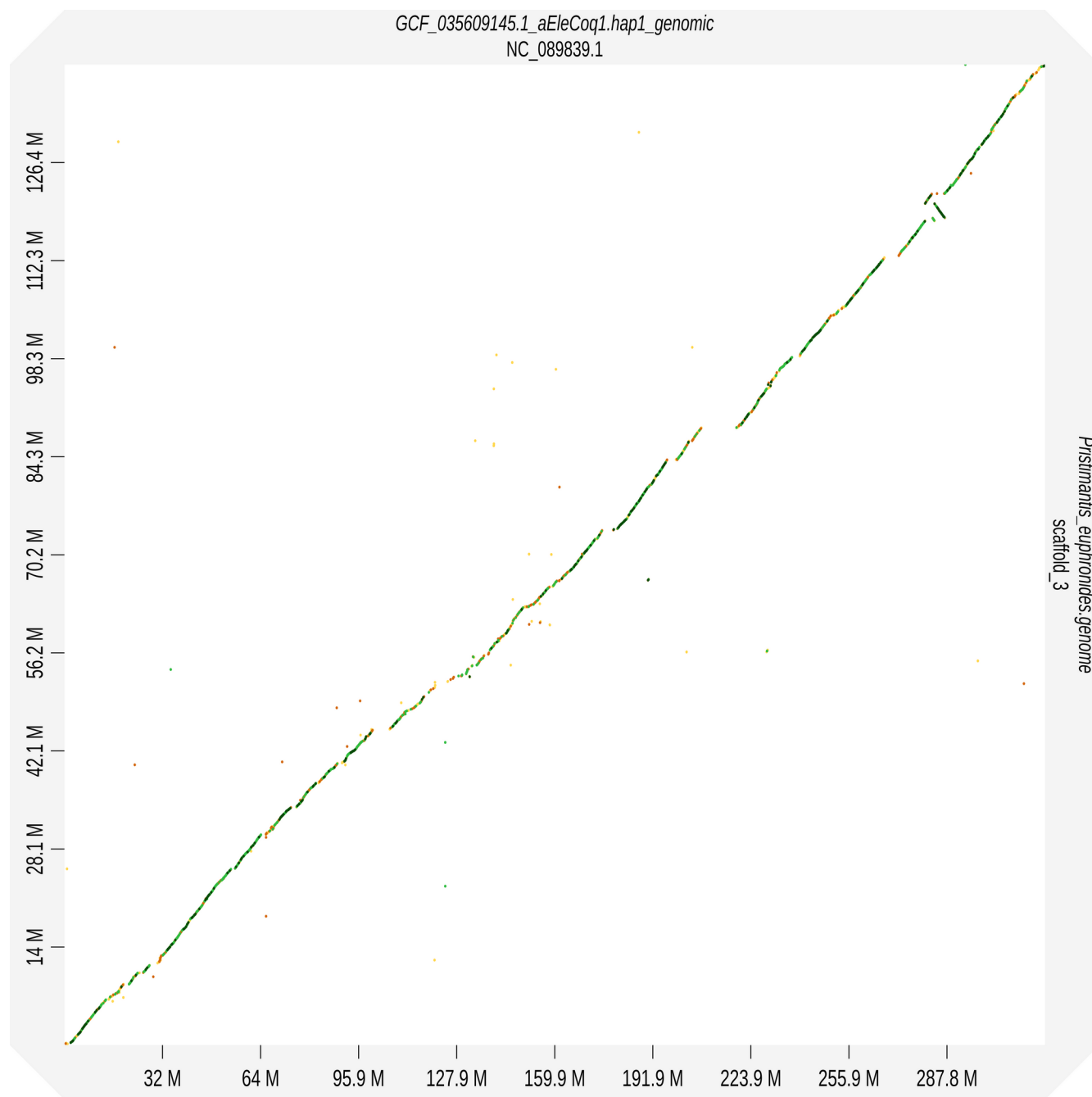
A



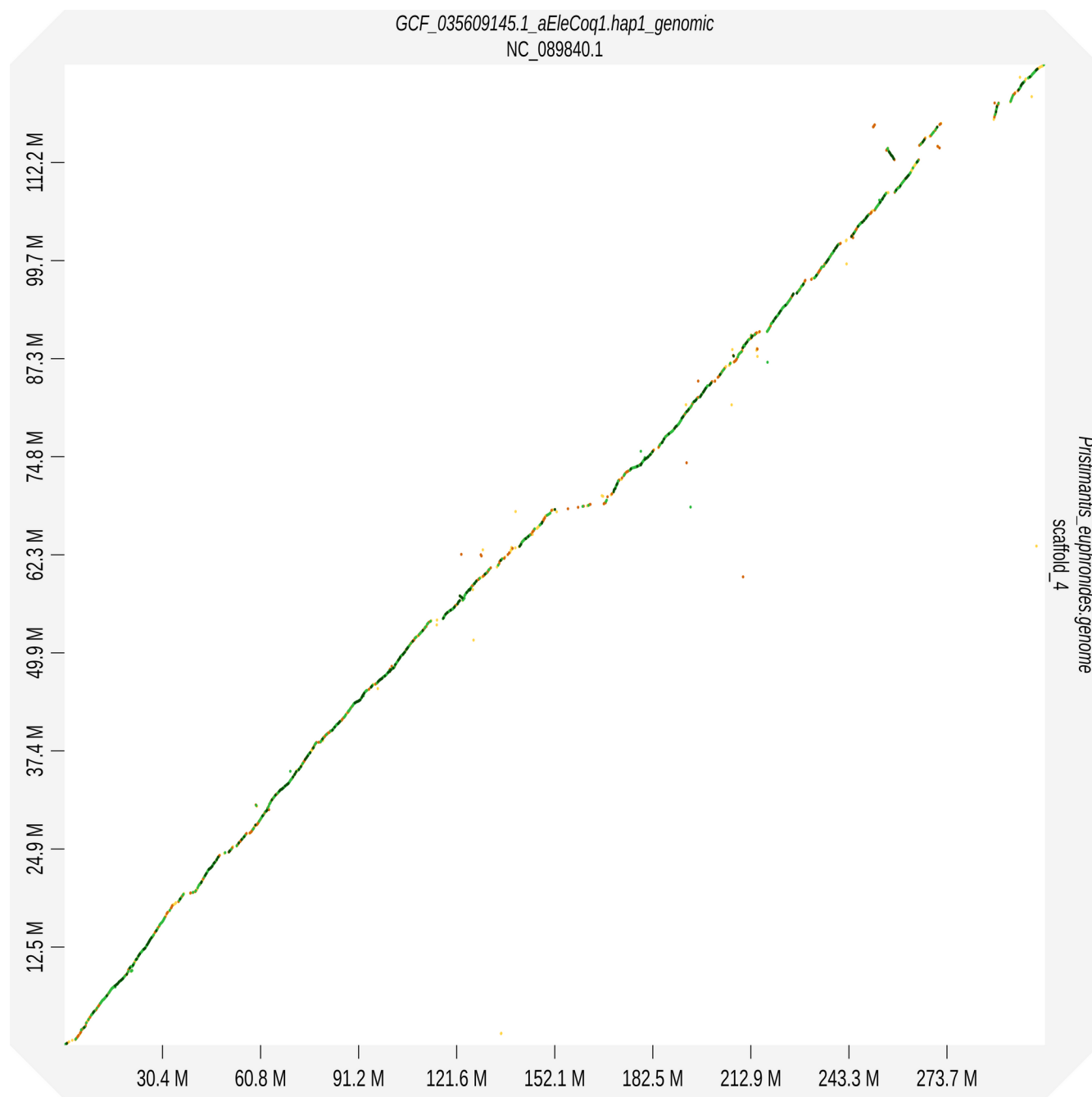
B



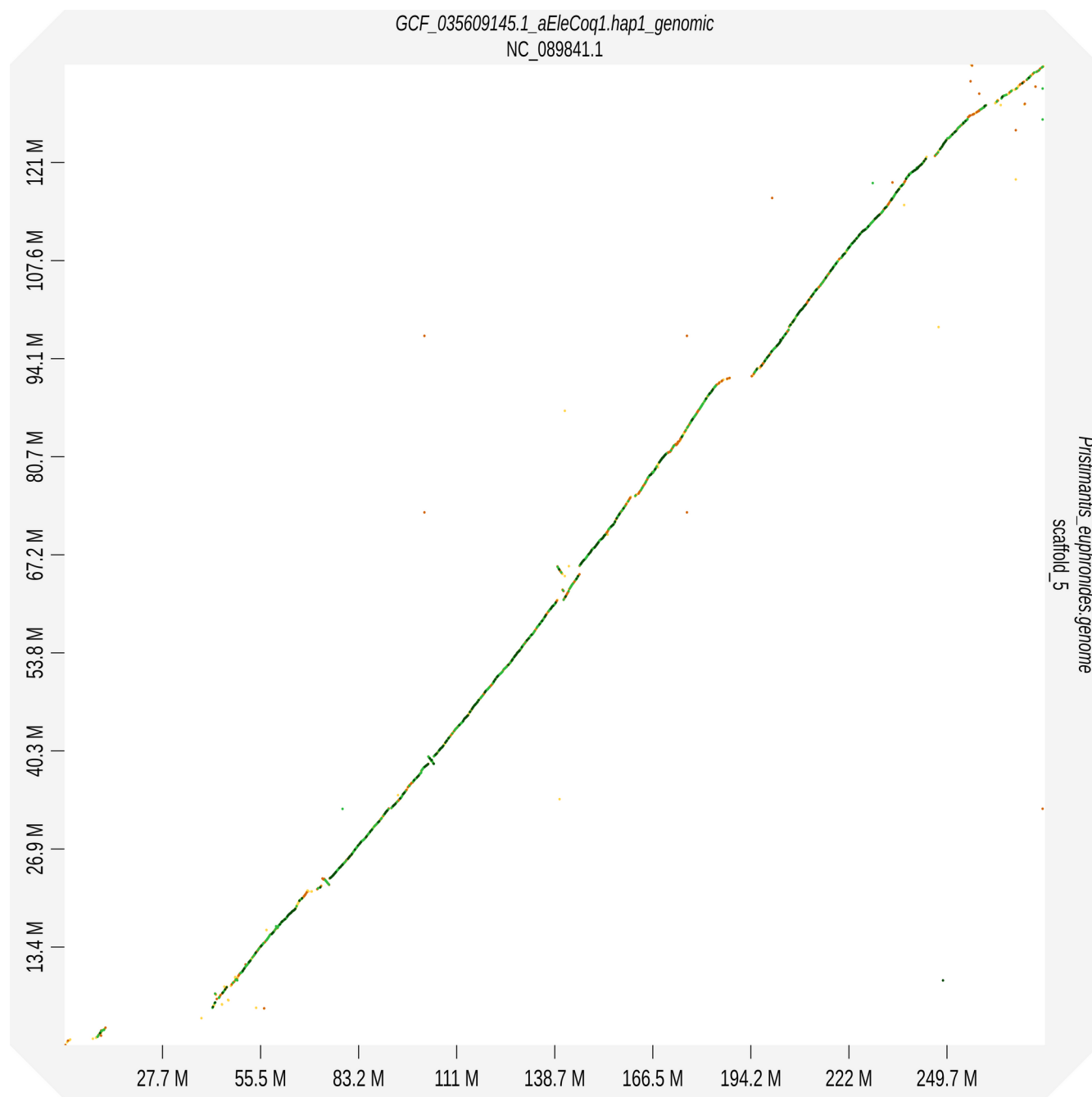
C



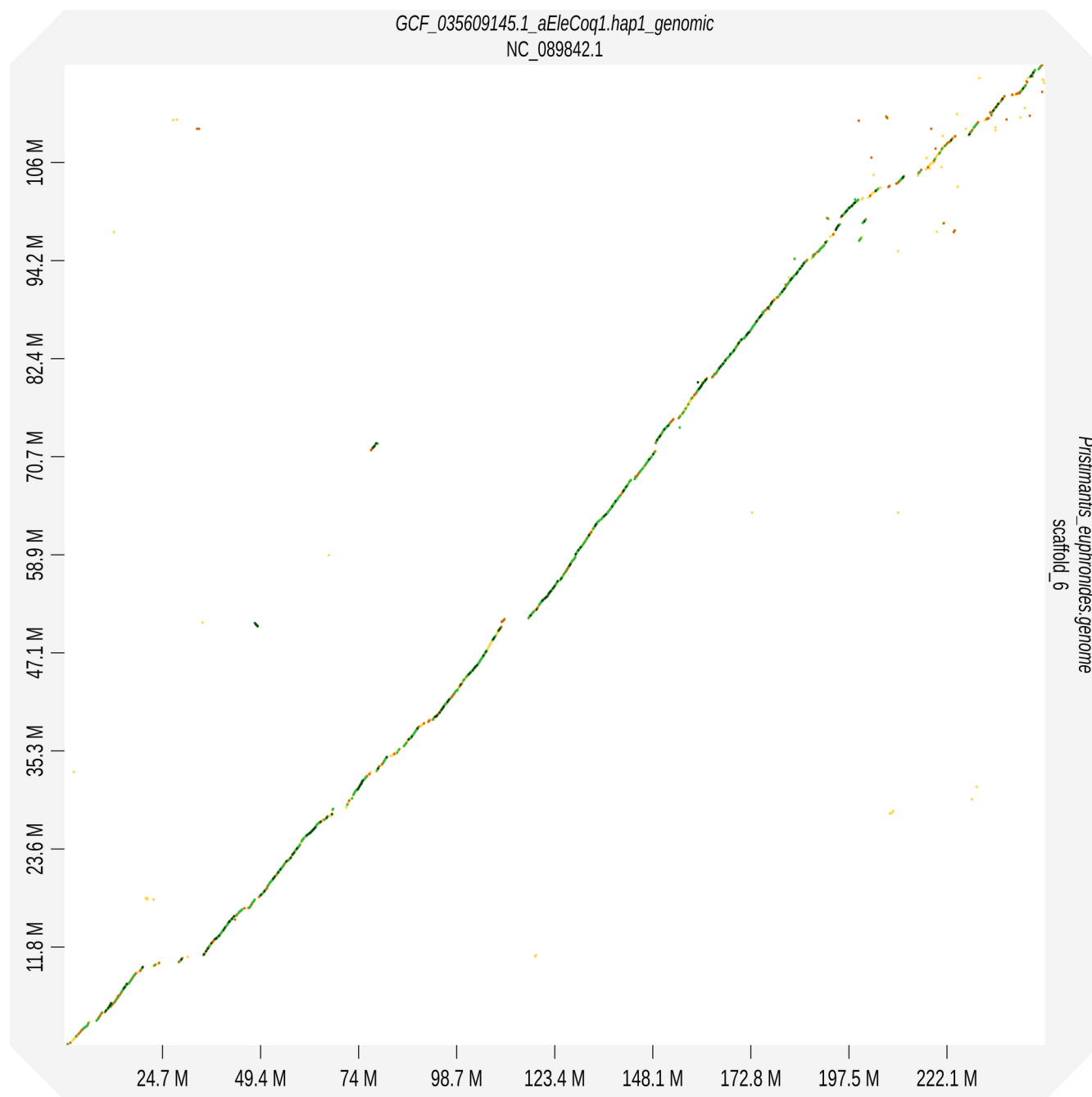
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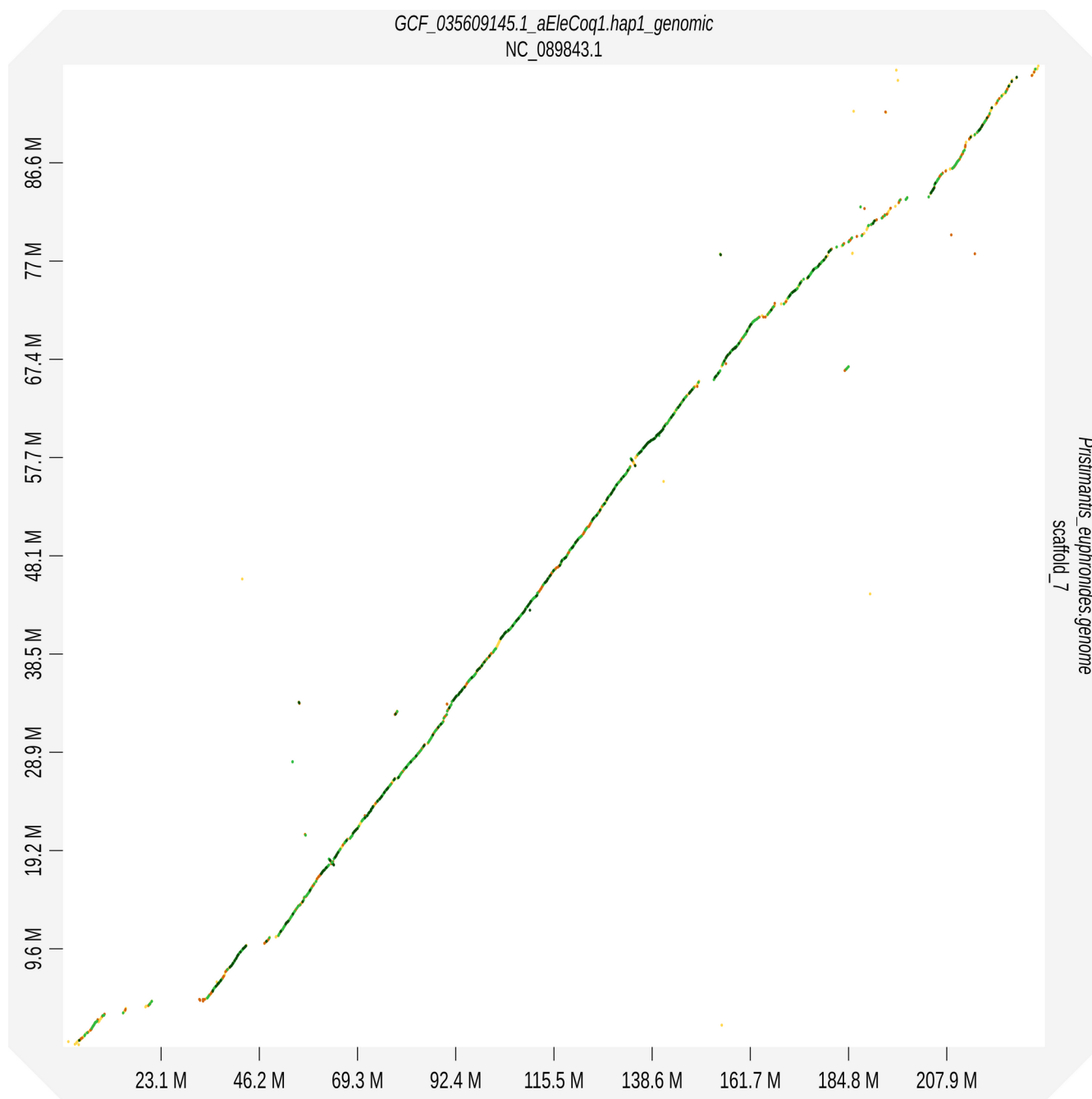
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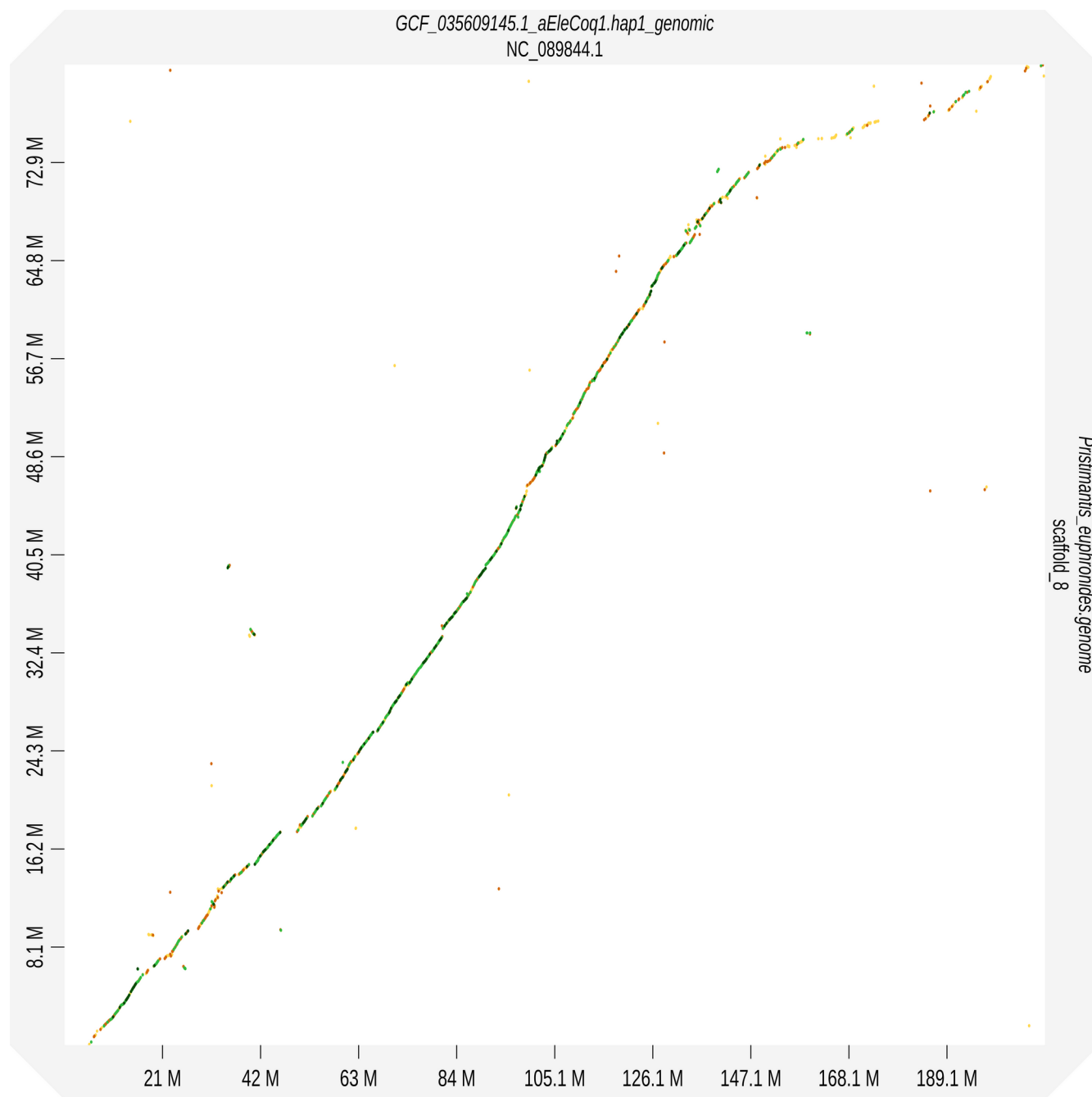
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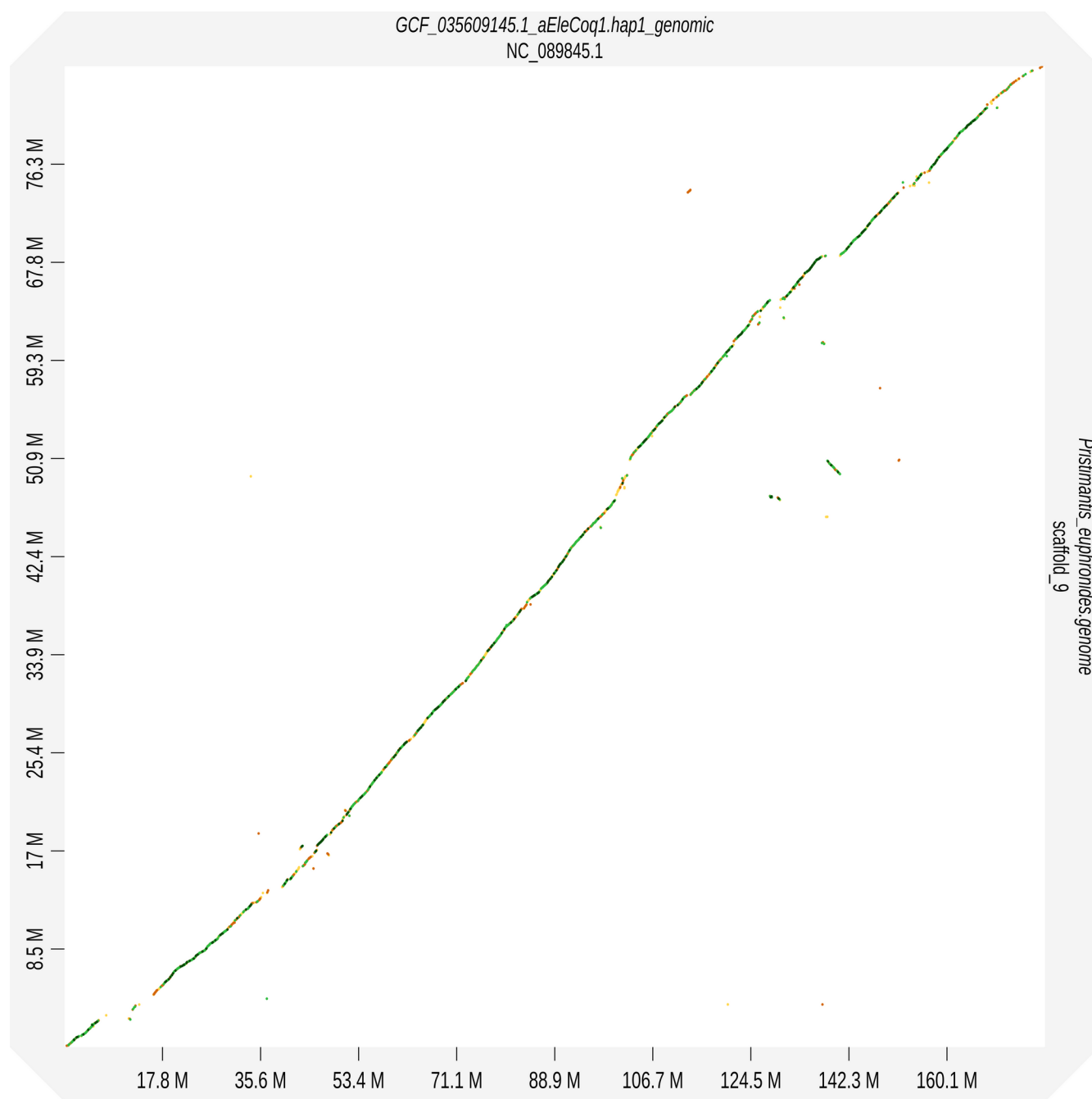
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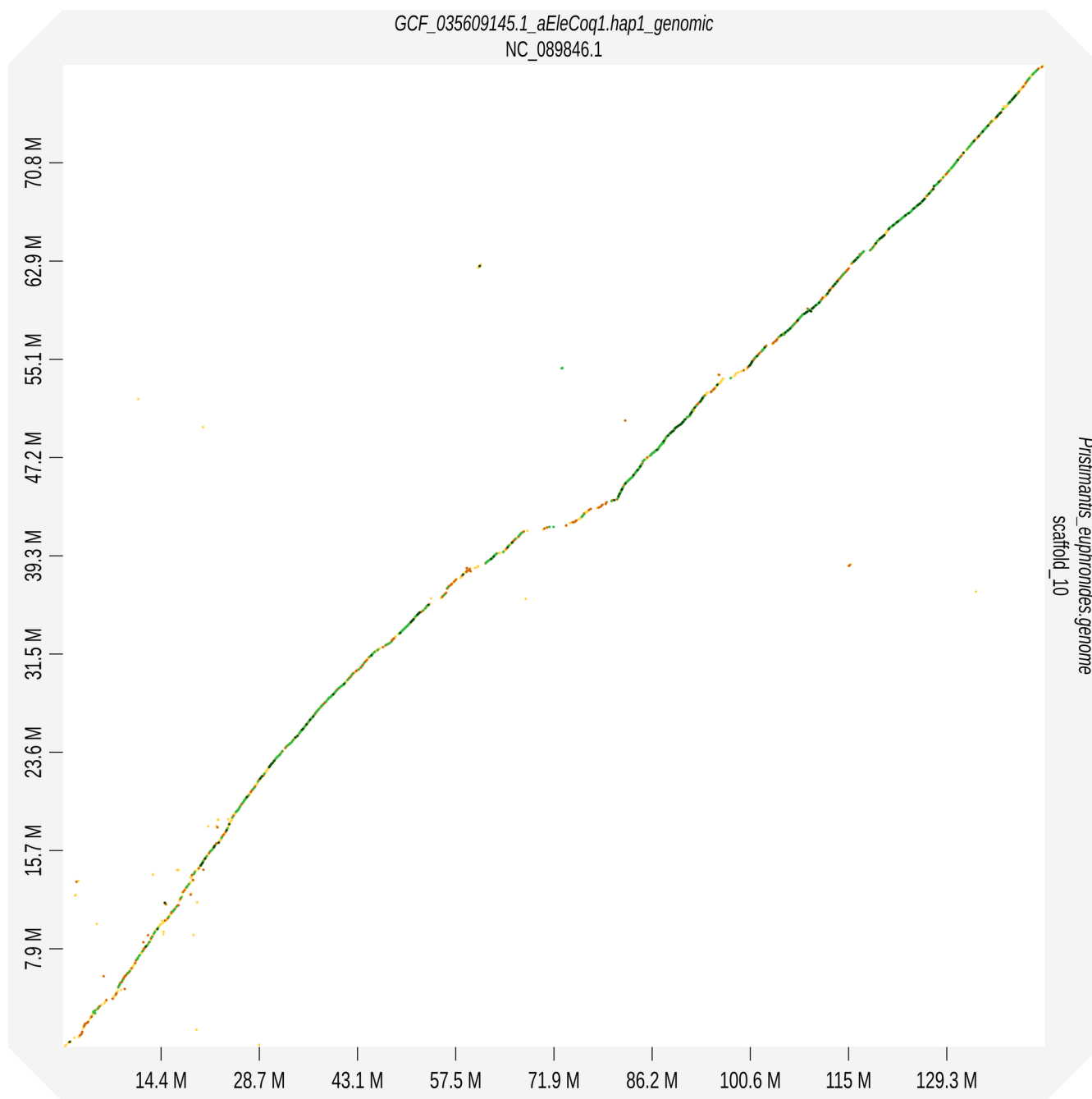
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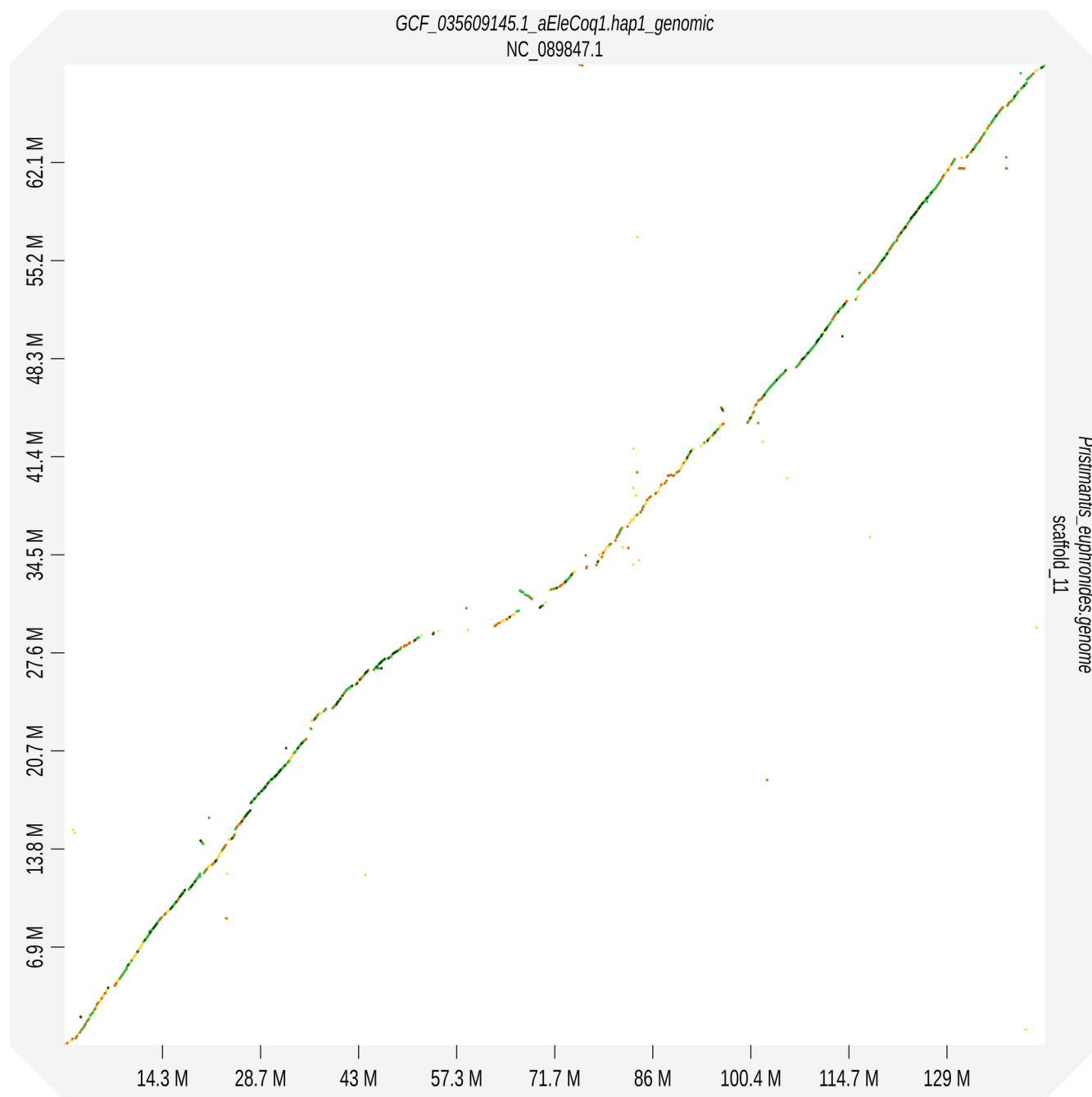
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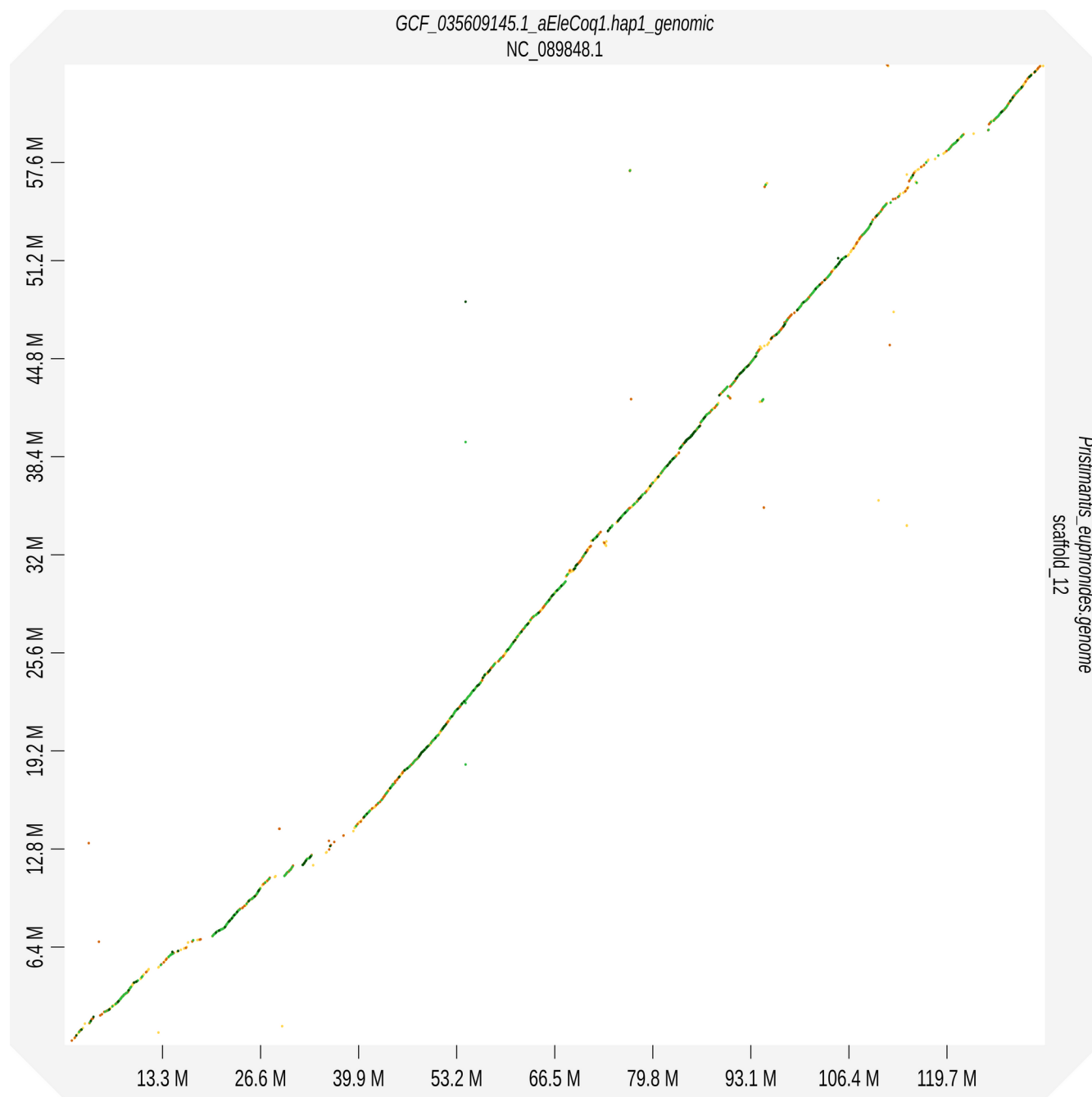
J



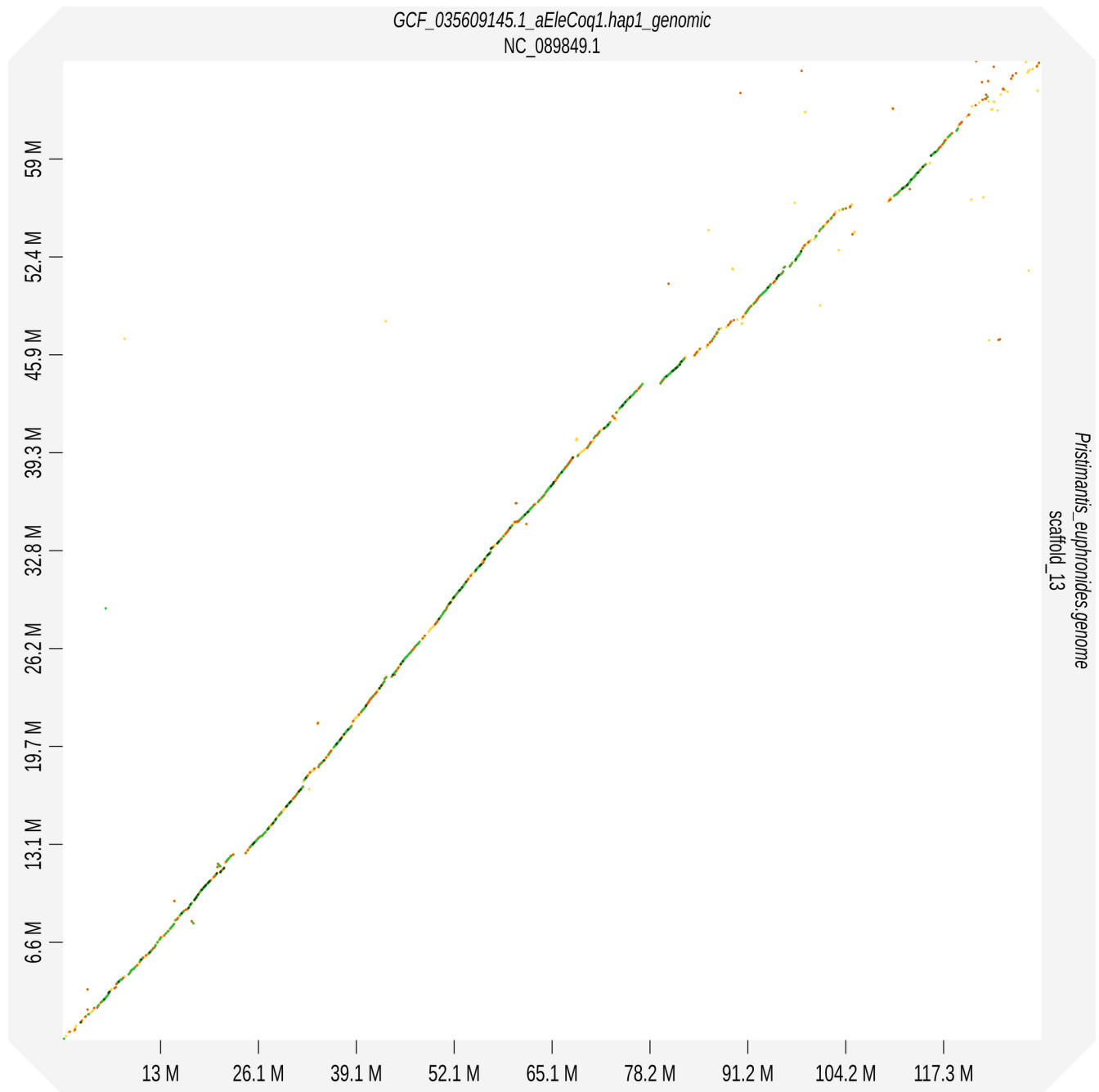
K



L



M



Reference

1. Cabanettes F, Klopp C. D-GENIES: dot plot large genomes in an interactive, efficient and simple way. PeerJ. 2018 Jun 4;6:e4958.