Supplemental Figures for:

Trio-binned genomes of the woodrats *Neotoma bryanti* and *Neotoma lepida* reveal novel gene islands and rapid copy number evolution of xenobiotic metabolizing genes

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Figure S1: Alignments of assemblies used to resolve the CYP2 region in *Neotoma lepida*. Alignments of the (**A**) 6.58 Mb and 11.98 Mb contigs from the 40× assembly and (**B**) 13.63 Mb contig from the all reads (AR) assembly against the 18.55 Mb sequence produced by merging the three contigs with quickmerge 0.3. Note that the 13.63 Mb contig is composed of sequence contained in both contigs from the 40× assembly. (**C**) Alignment of the four CYP2 contigs from the *N. lepida* Canu assembly that appear to compose the entirety of this sequence (Nlep_tig00001124, Nlep_tig00001166, Nlep_tig00001922 and Nlep_tig00418827). (**D**) Alignment of the remaining three CYP2 contigs from the Canu assembly that appear to be potential repetitive sequences or assembly errors (Nlep_tig00004740, Nlep_tig00010068 and Nlep_tig00418826). These contigs align to the same region as that occupied by Nlep_tig00418827 (top). These plots use a minimum cluster size of 2,500.
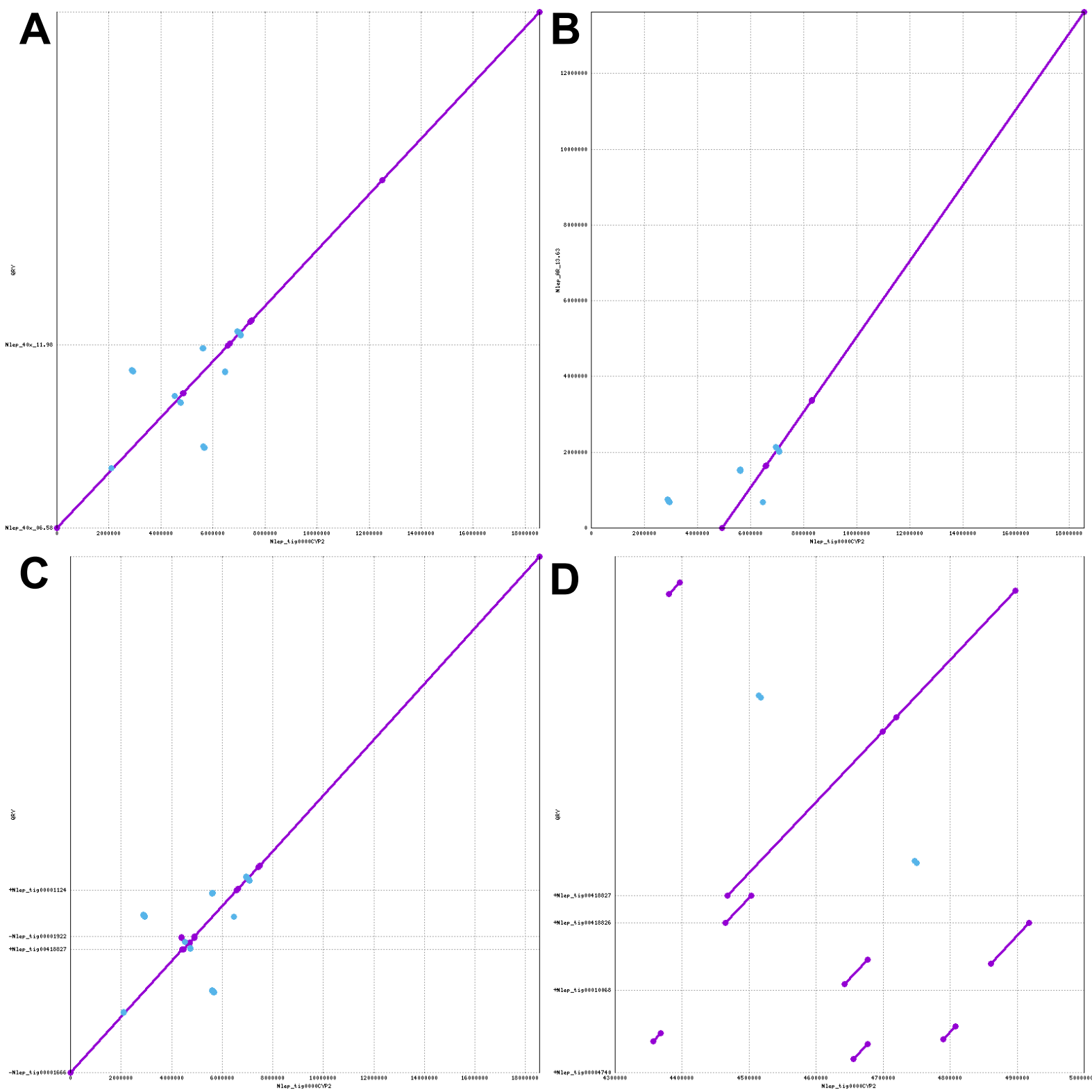
A

Neotoma bryanti 25−mer frequency spectrum
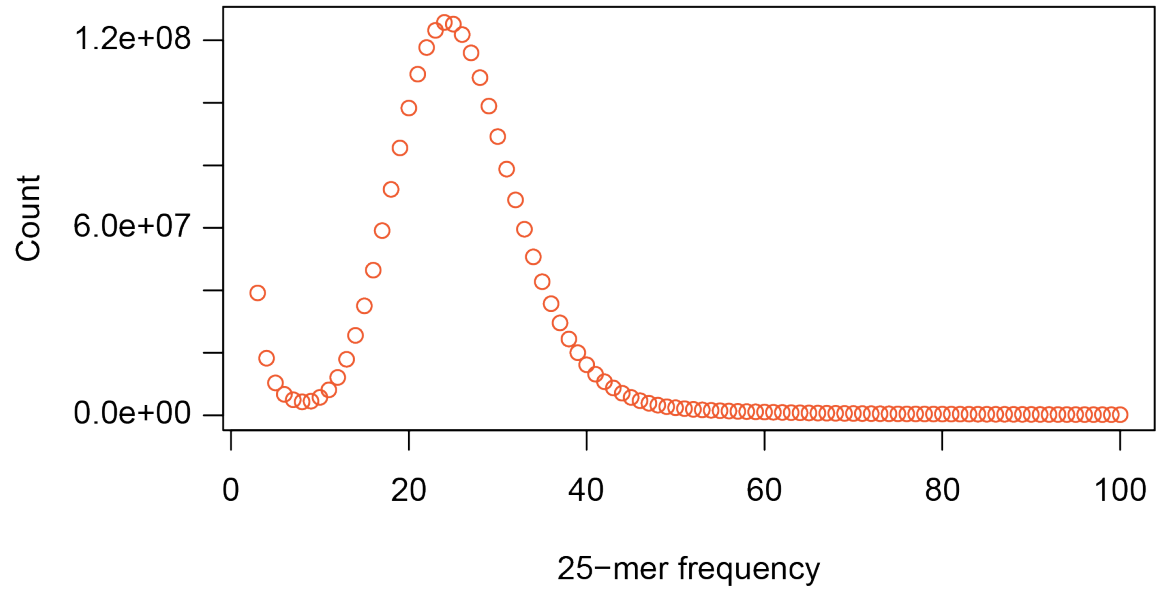
B

Neotoma lepida 25−mer frequency spectrum
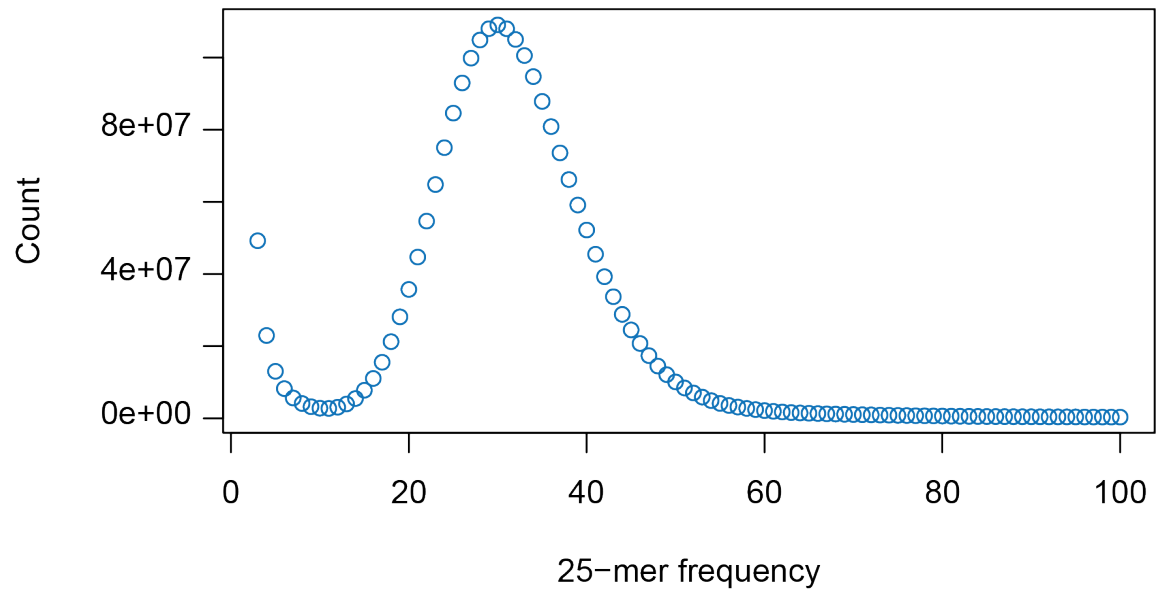
Figure S2: 25-mer frequency spectra for the partitioned *Neotoma bryanti* and *Neotoma lepida* reads. 25-mer spectra counts generated by Jellyfish 2.3.0 are shown for **(A)** *N. bryanti* and **(B)** *N. lepida*.

Figure S3: *Neotoma bryanti* contigs aligned against *Peromyscus leucopus* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 250.
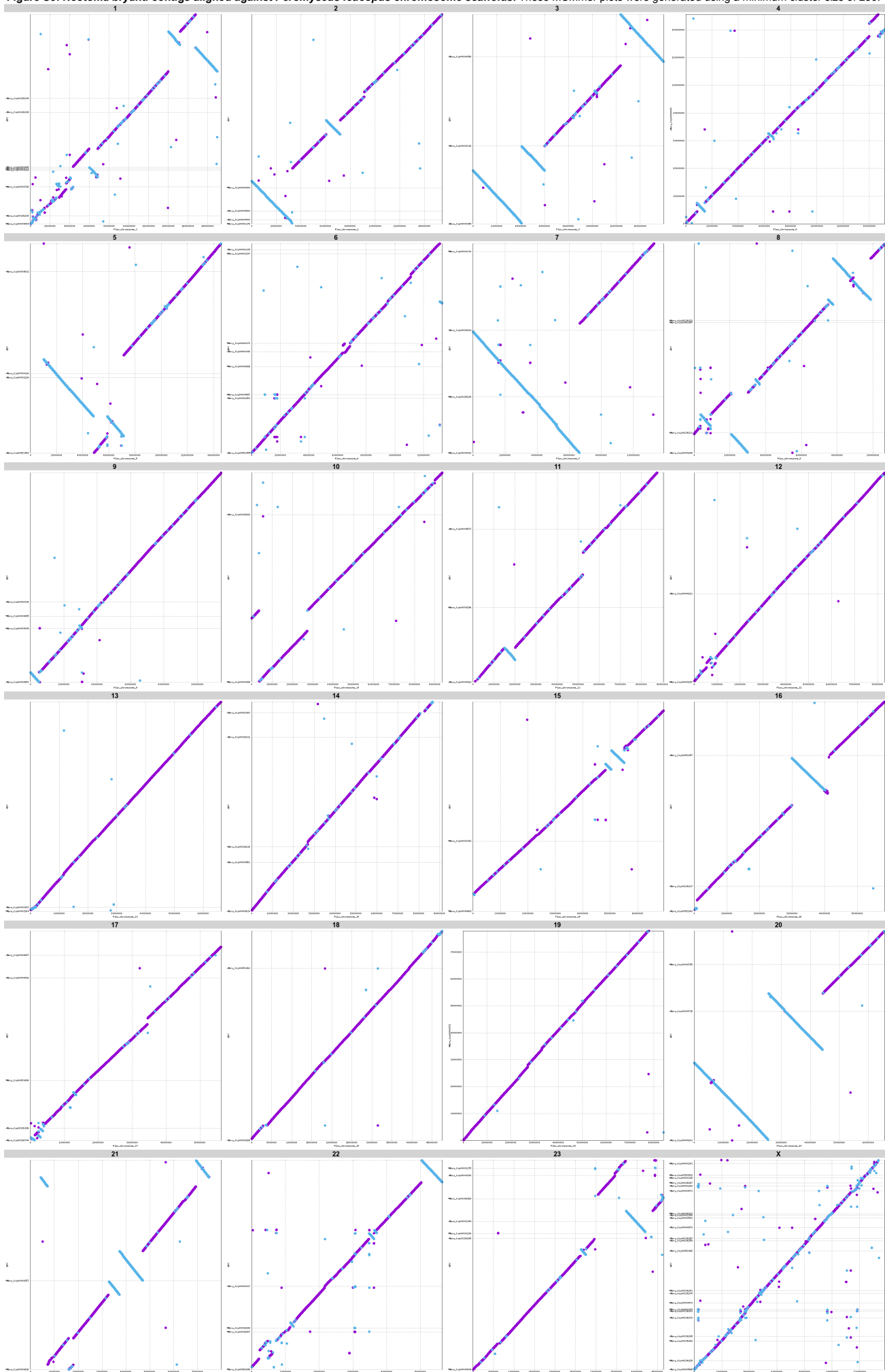
Figure S4: *Neotoma bryanti* contigs aligned against *Peromyscus maniculatus* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 250.
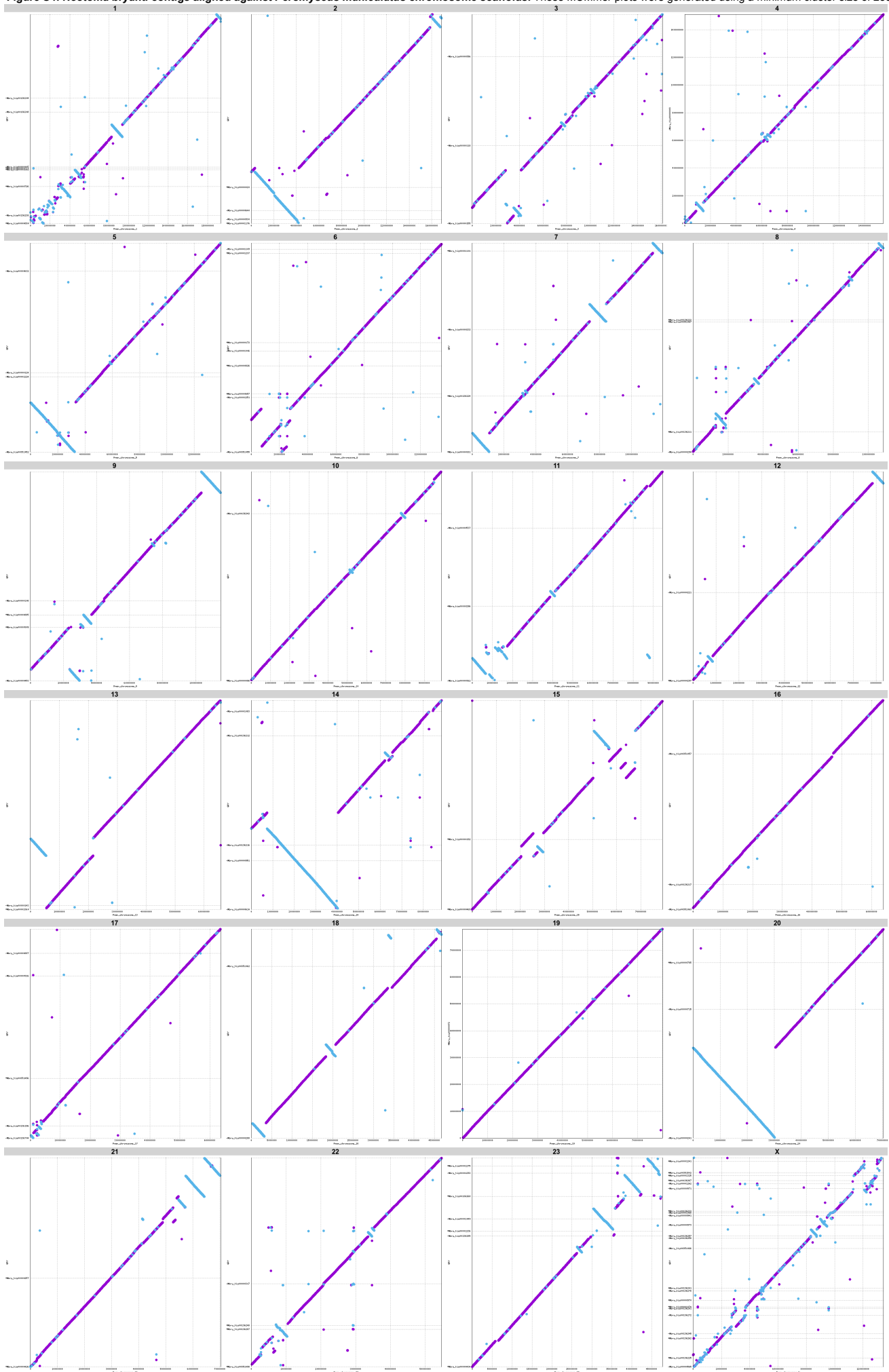
Figure S5: *Neotoma bryanti* contigs aligned against *Peromyscus nasutus* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 250.
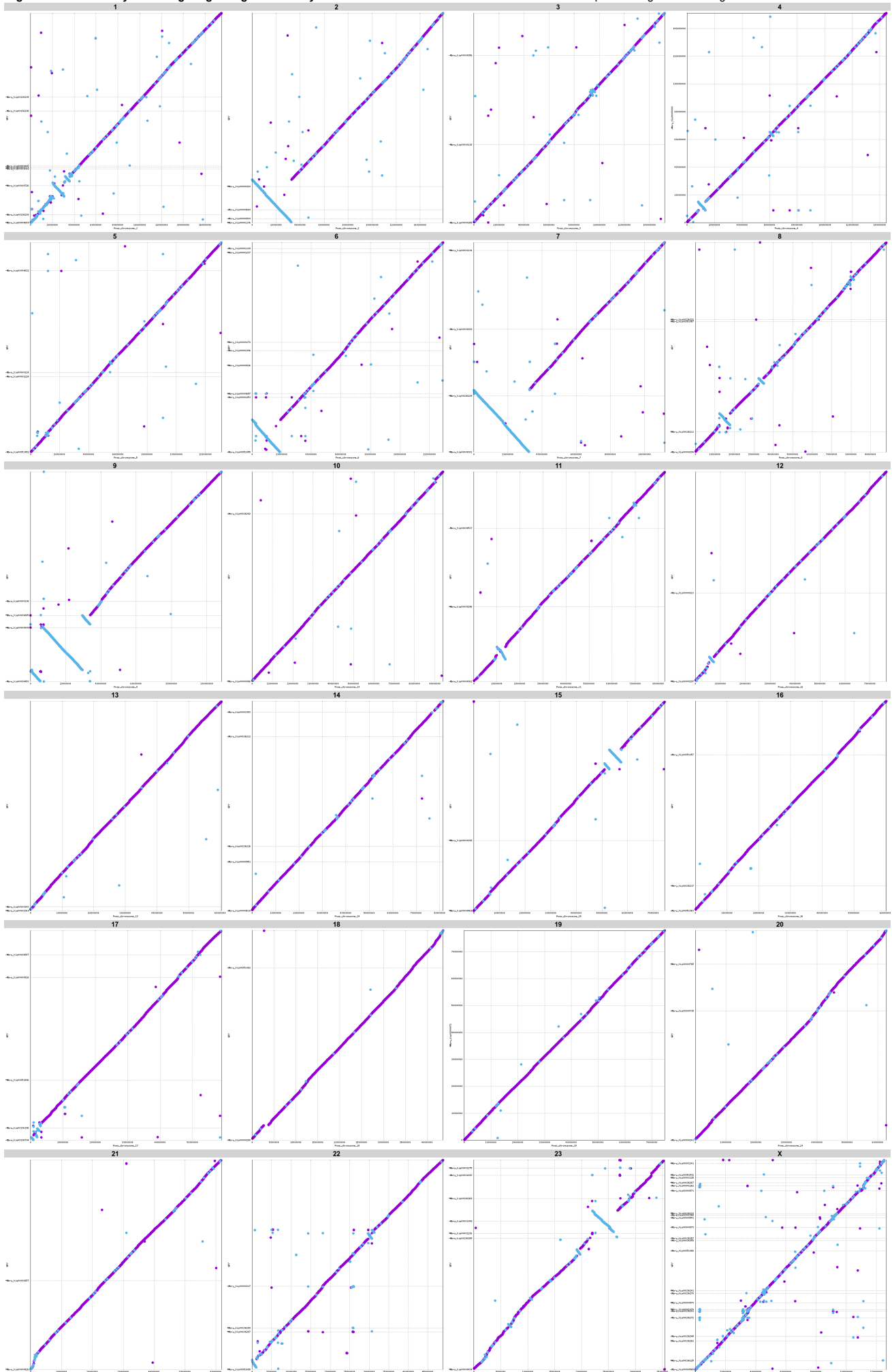
Figure S6: *Neotoma lepida* contigs aligned against *Peromyscus leucopus* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 250.
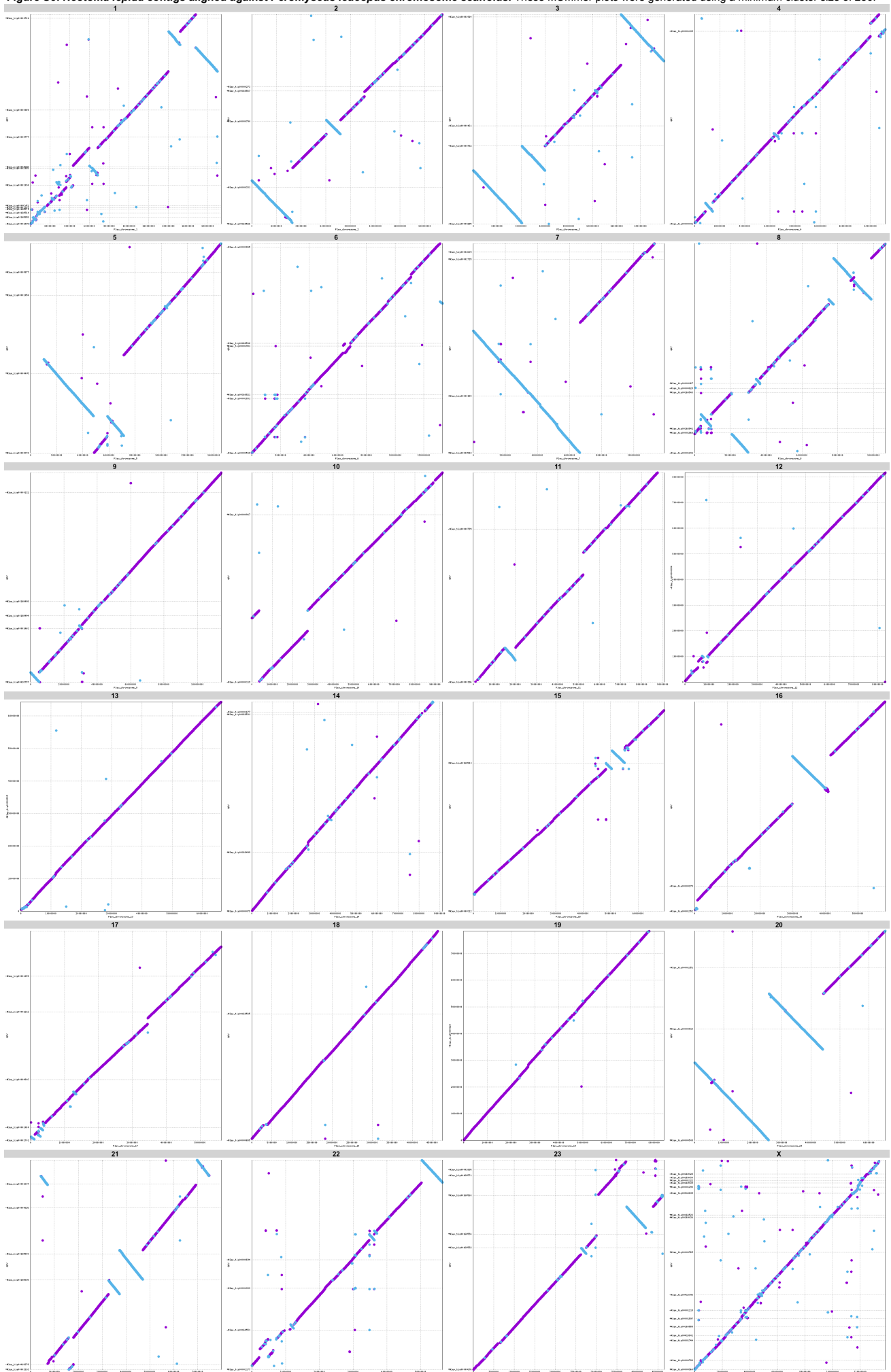
Figure S7: *Neotoma lepida* contigs aligned against *Peromyscus maniculatus* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 250.
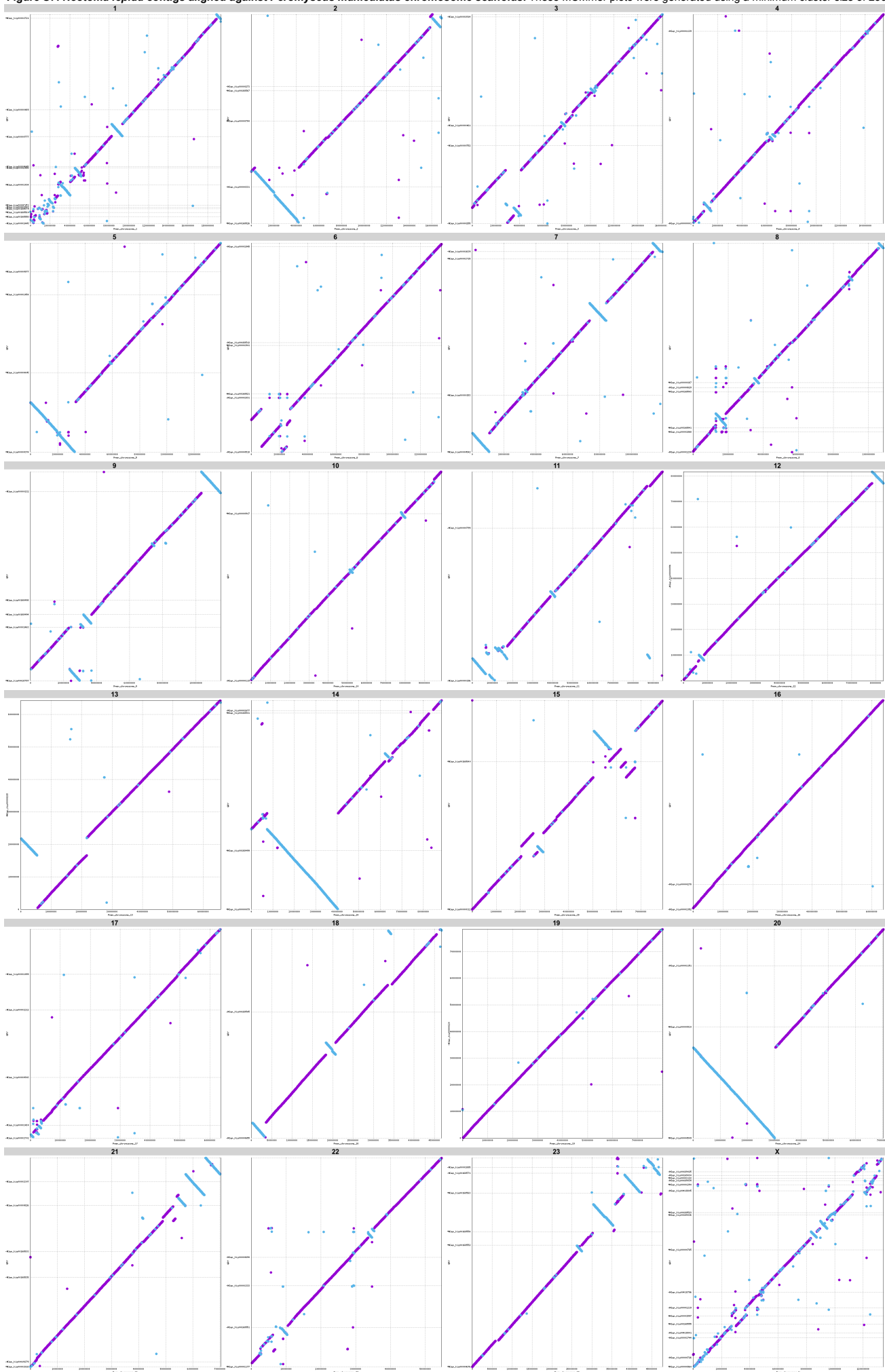
Figure S8: *Neotoma lepida* contigs aligned against *Peromyscus nasutus* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 250.
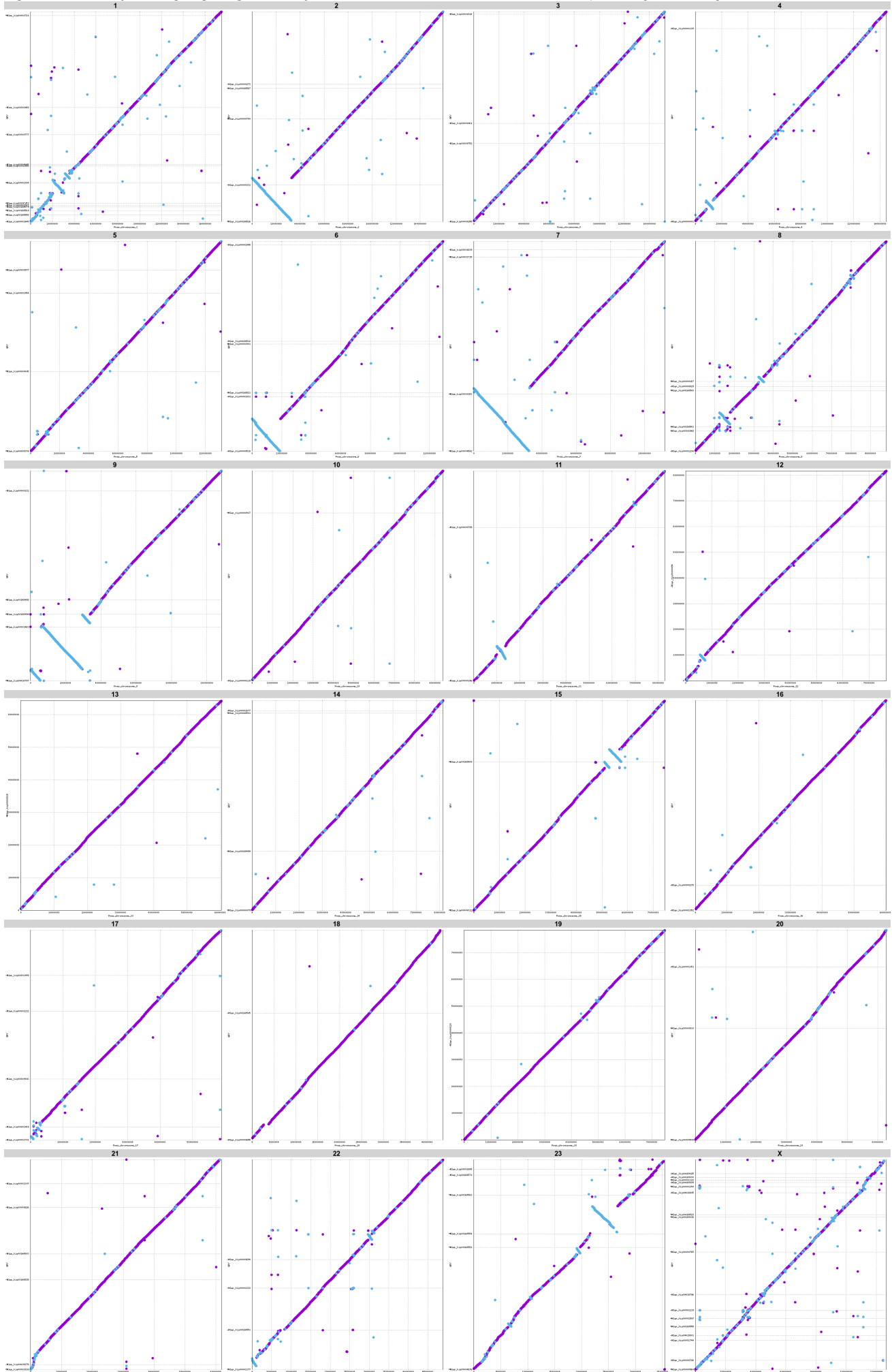
Figure S9: *Neotoma bryanti* contigs aligned against *Neotoma lepida* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 2,500.
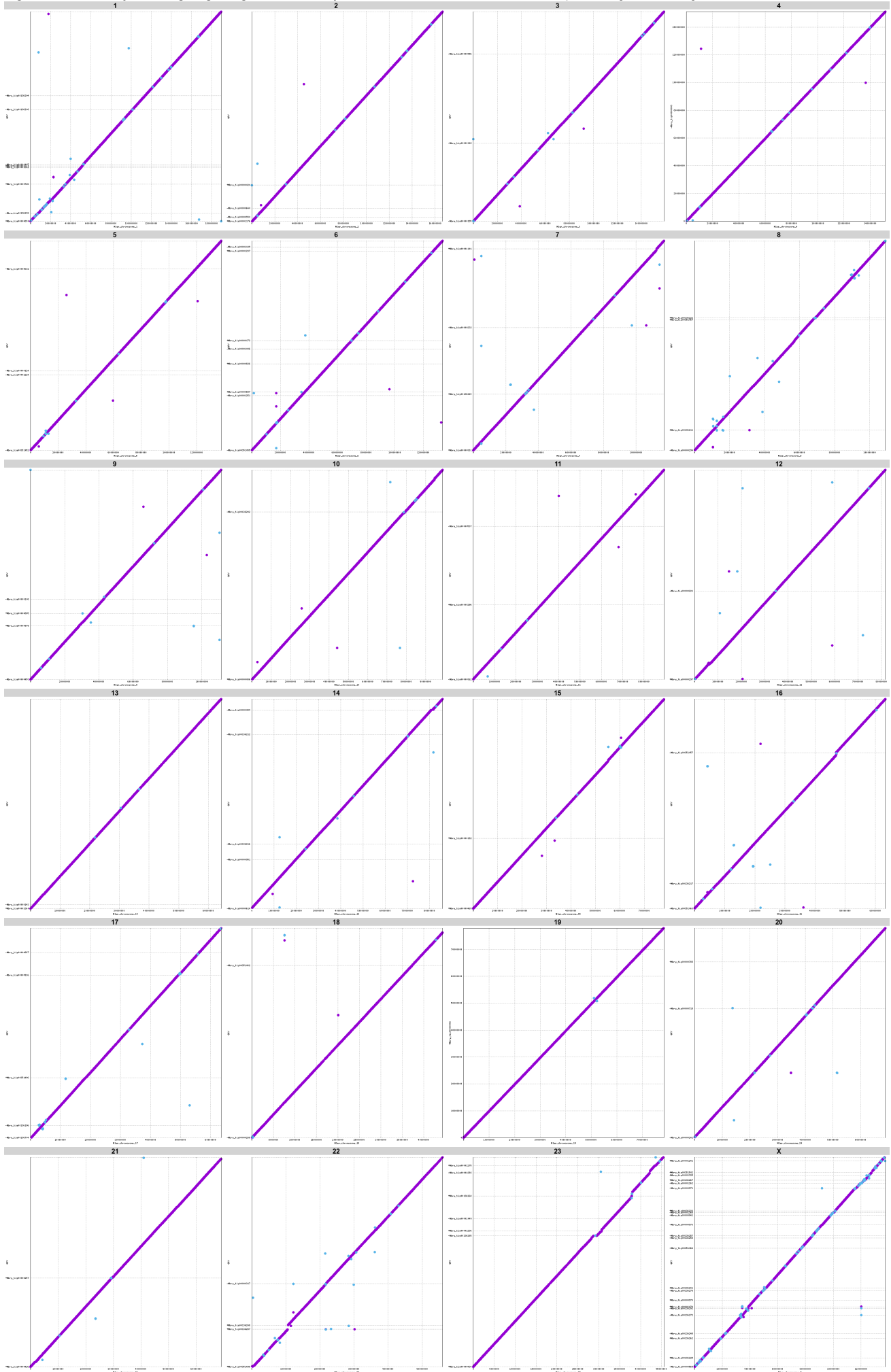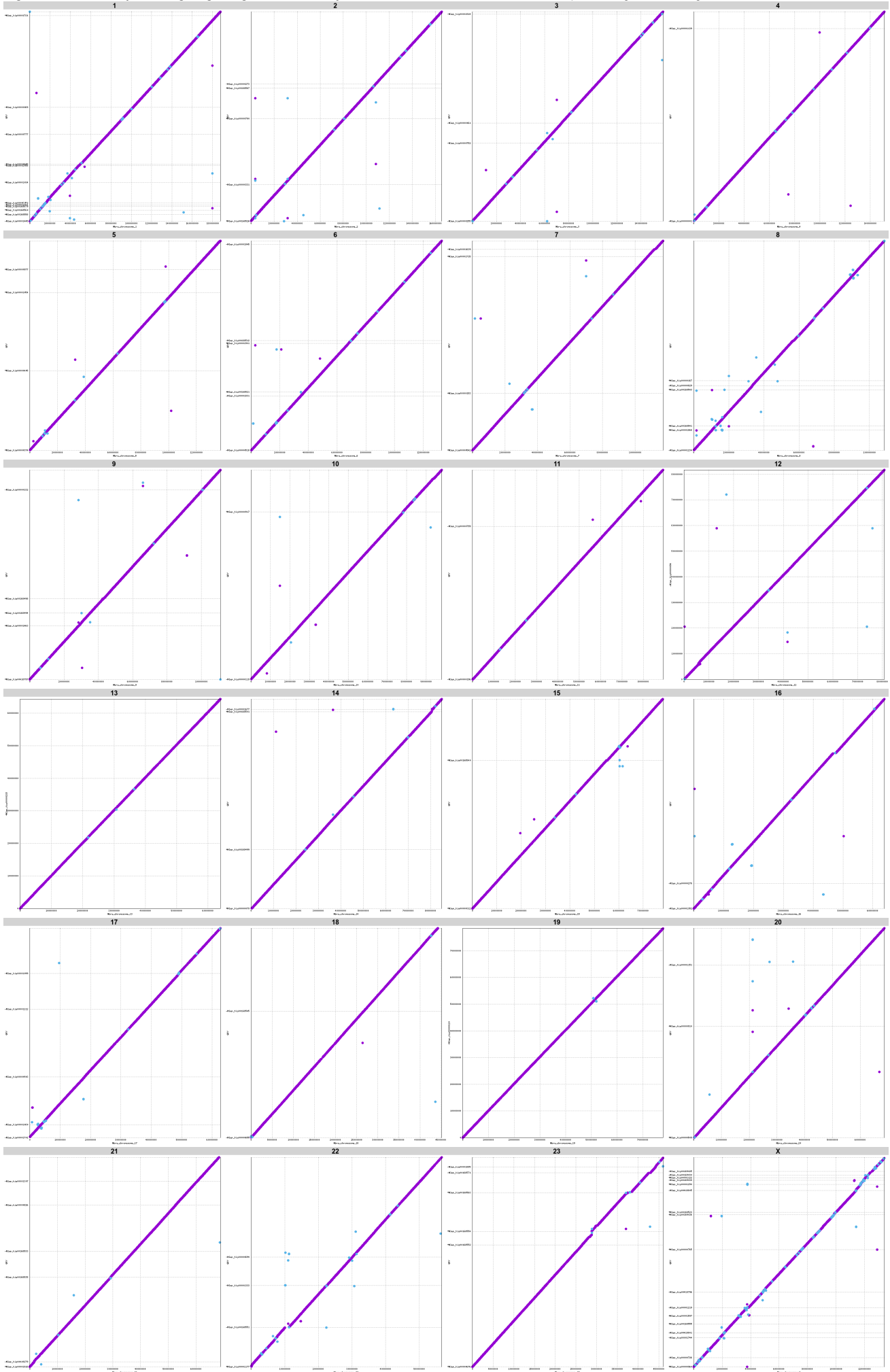
Figure S10: *Neotoma lepida* contigs aligned against *Neotoma bryanti* chromosome scaffolds. These MUMmer plots were generated using a minimum cluster size of 2,500.

Figure S11: Phylogeny of CYP2ABFGST genes. Unrooted phylogeny of the CYP2ABFGST genes from the four rodent species studied, as well as protein sequences of the genes named *CYP2B35*, *CYP2B36*, and *CYP2B37* from Wilderman et al. (2014).