

Supplementary Figures

Title: Sub genome anchored physical frameworks of the allotetraploid Upland cotton (*Gossypium hirsutum* L.) genome, and an approach toward reference-grade assemblies of polyploids

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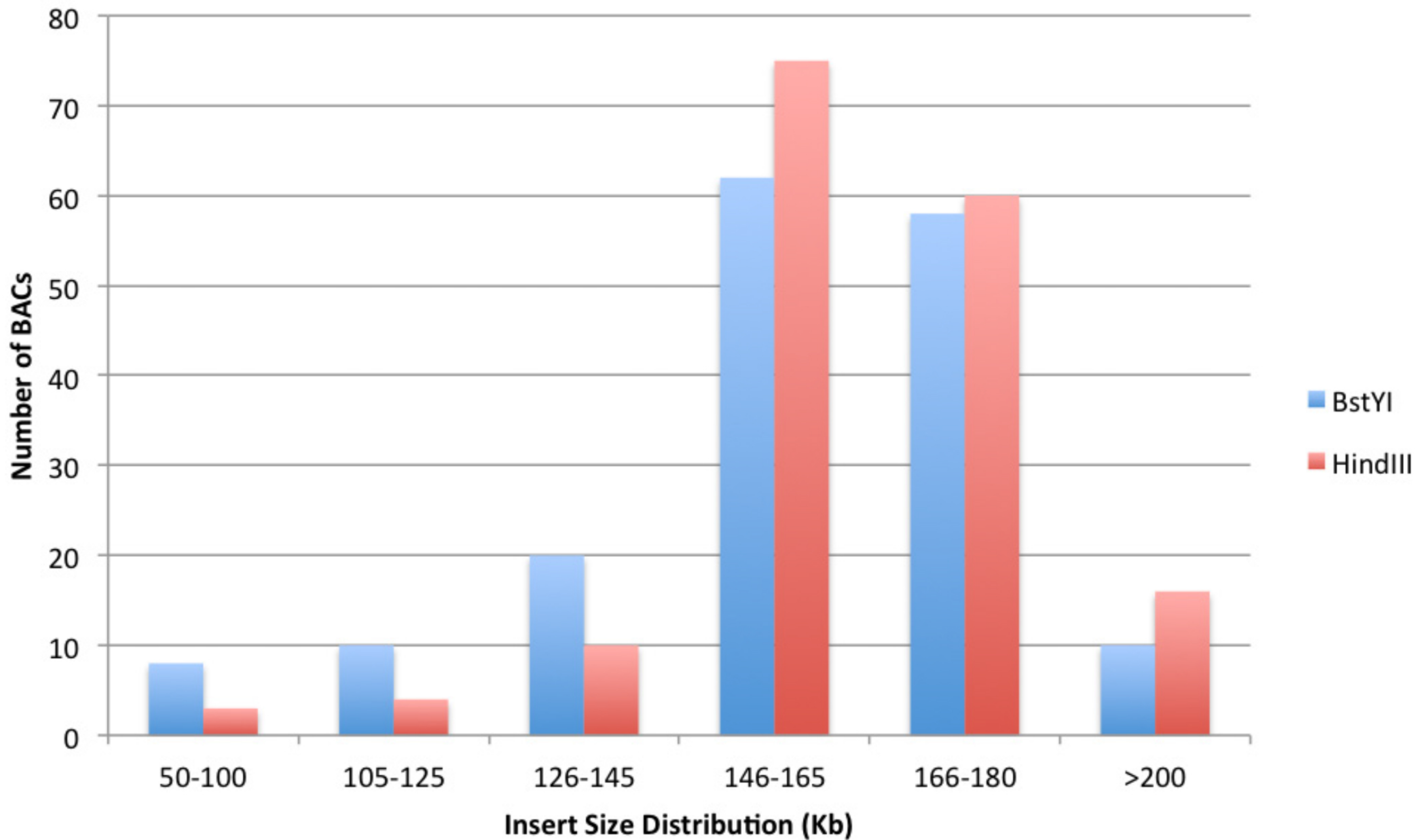
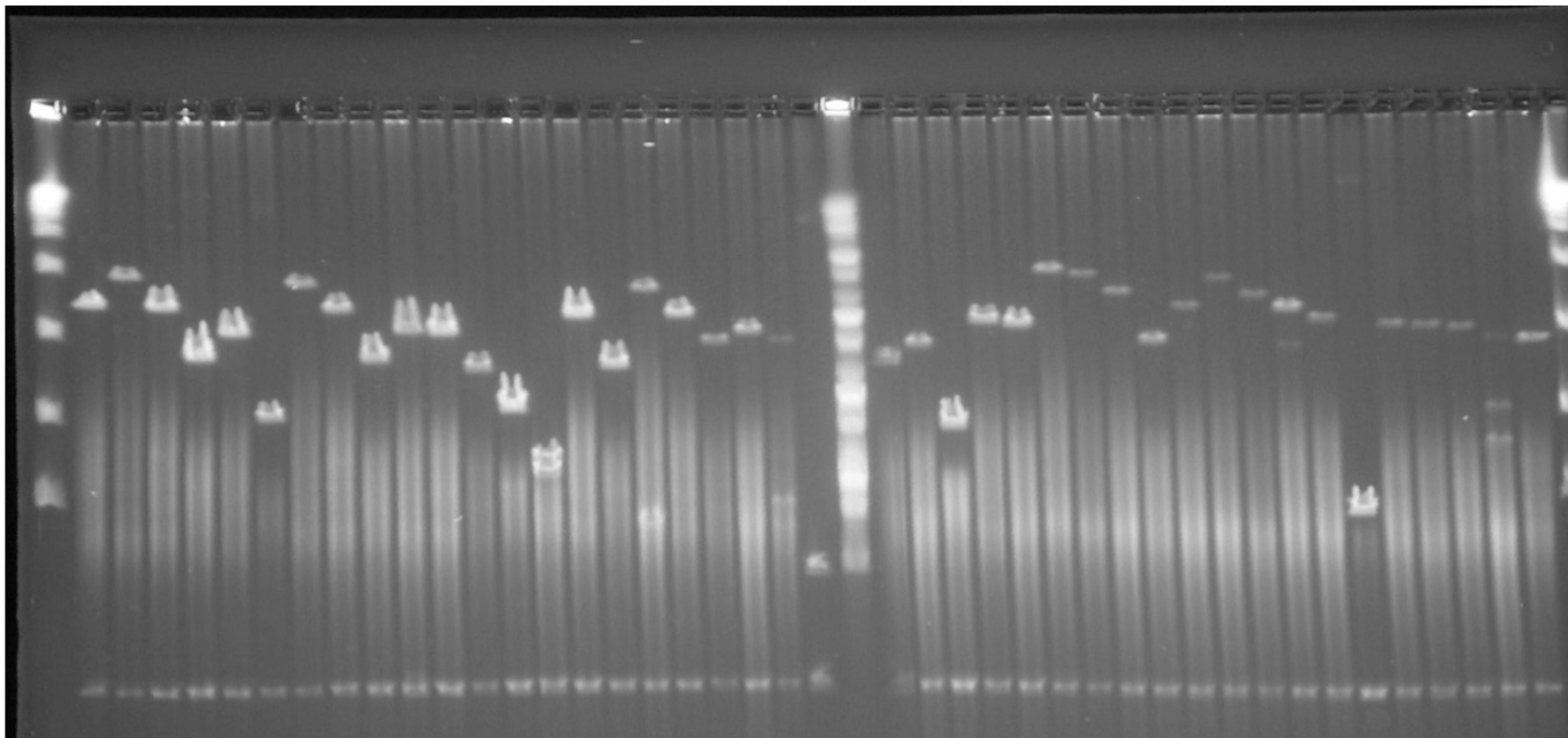
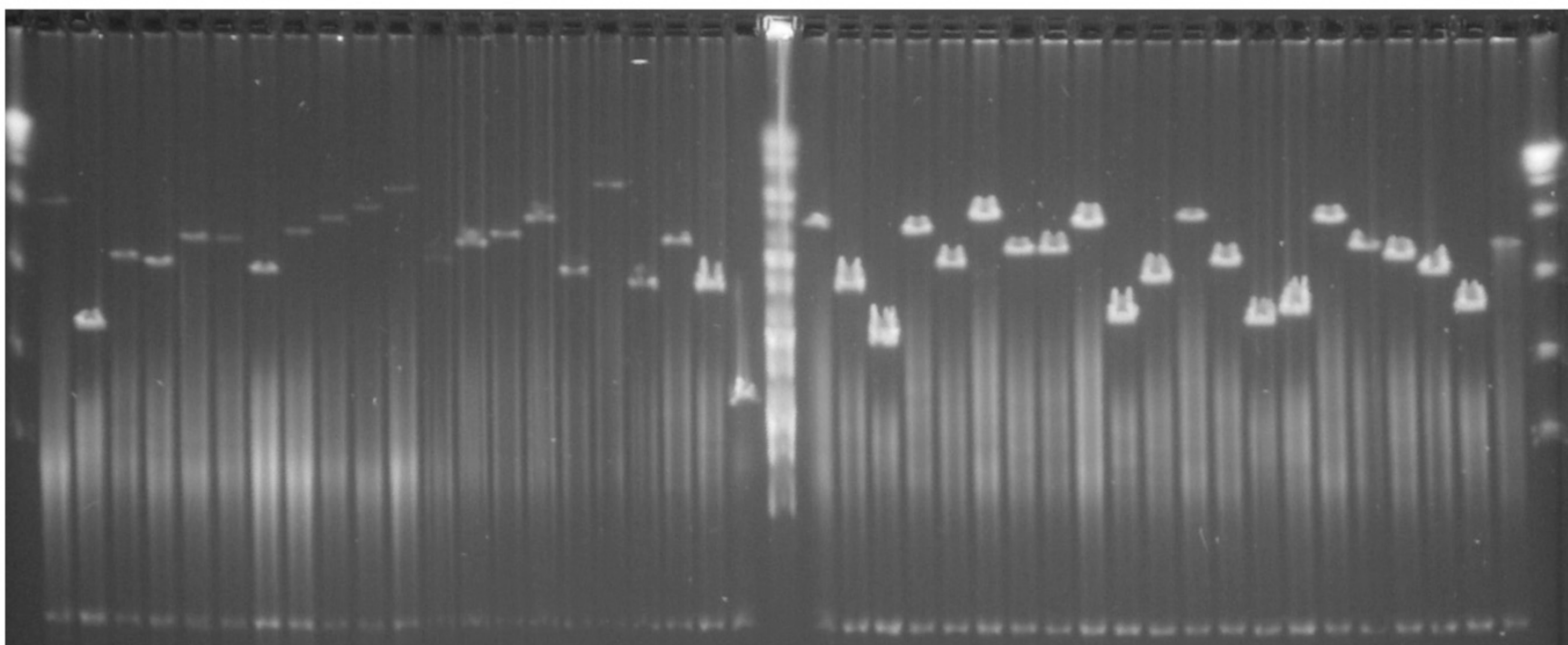


Figure S1. BAC insert size distribution of the restriction-derived TM-1 BAC libraries, GH_TBb and GH_TBh.

GH_TBb



GH_TBh



GH_TBr

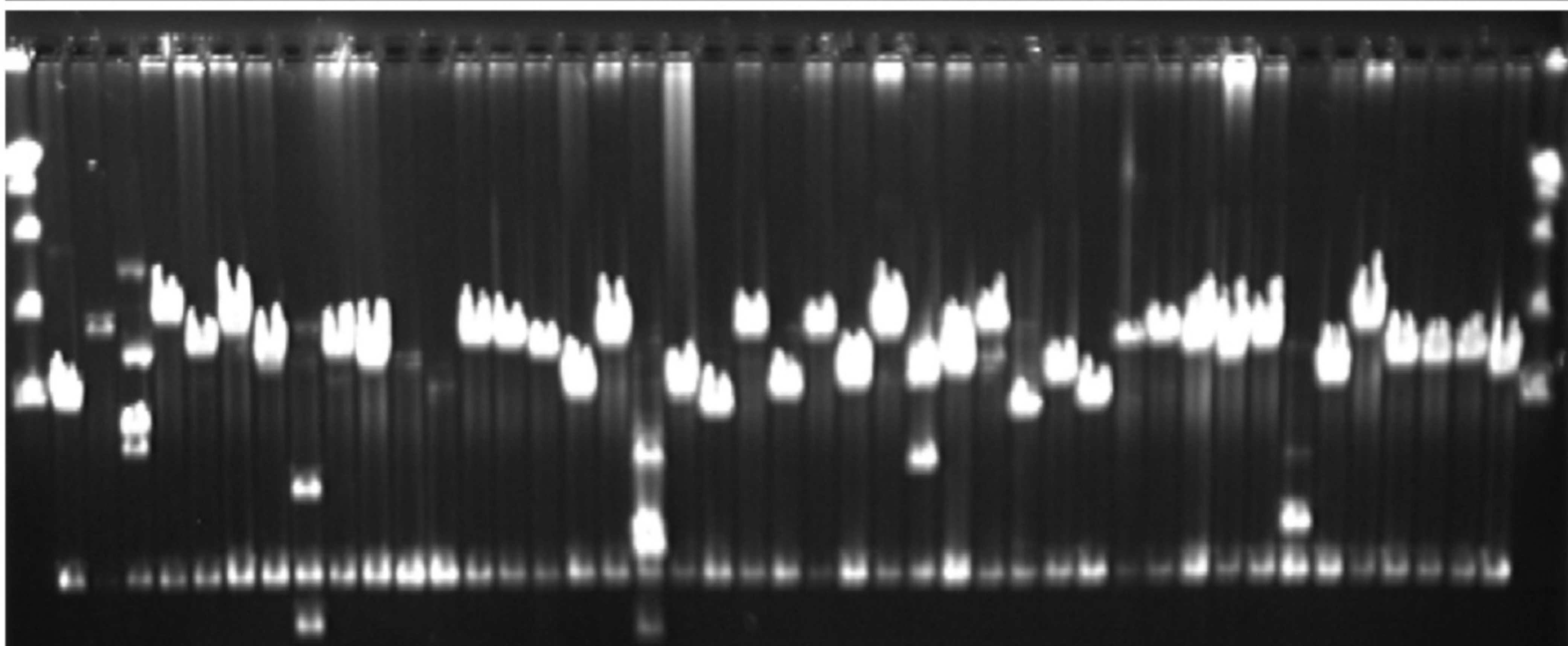


Figure S2. Figure S2 A-C. Pulsed-field gel electrophoresis of random *NotI* digested TM-1 BACs from GH_TBb, GH_TBh, and GH_TBr. The 2 outermost lanes contain Lambda ladder PFG marker (NEB) and the middle lane contains Lambda midrange PFG marker (NEB).

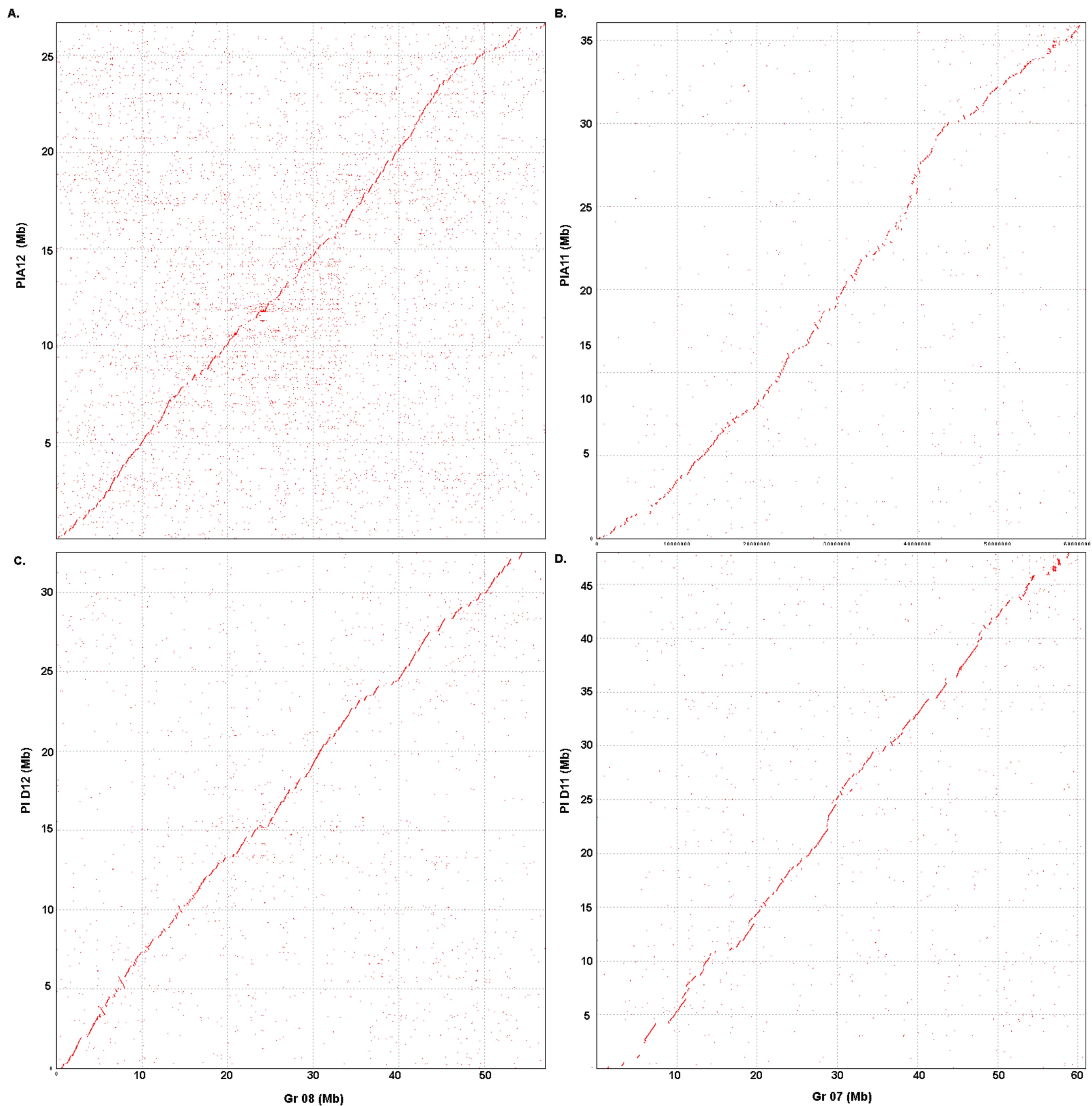


Figure S4. A. Dot plot alignment between *Gossypium hirsutum* chromosome A12 and *Gossypium raimondii* Chromosome 08. B. Dot plot alignment between *Gossypium hirsutum* D12 and *Gossypium raimondii* Chromosome 08.

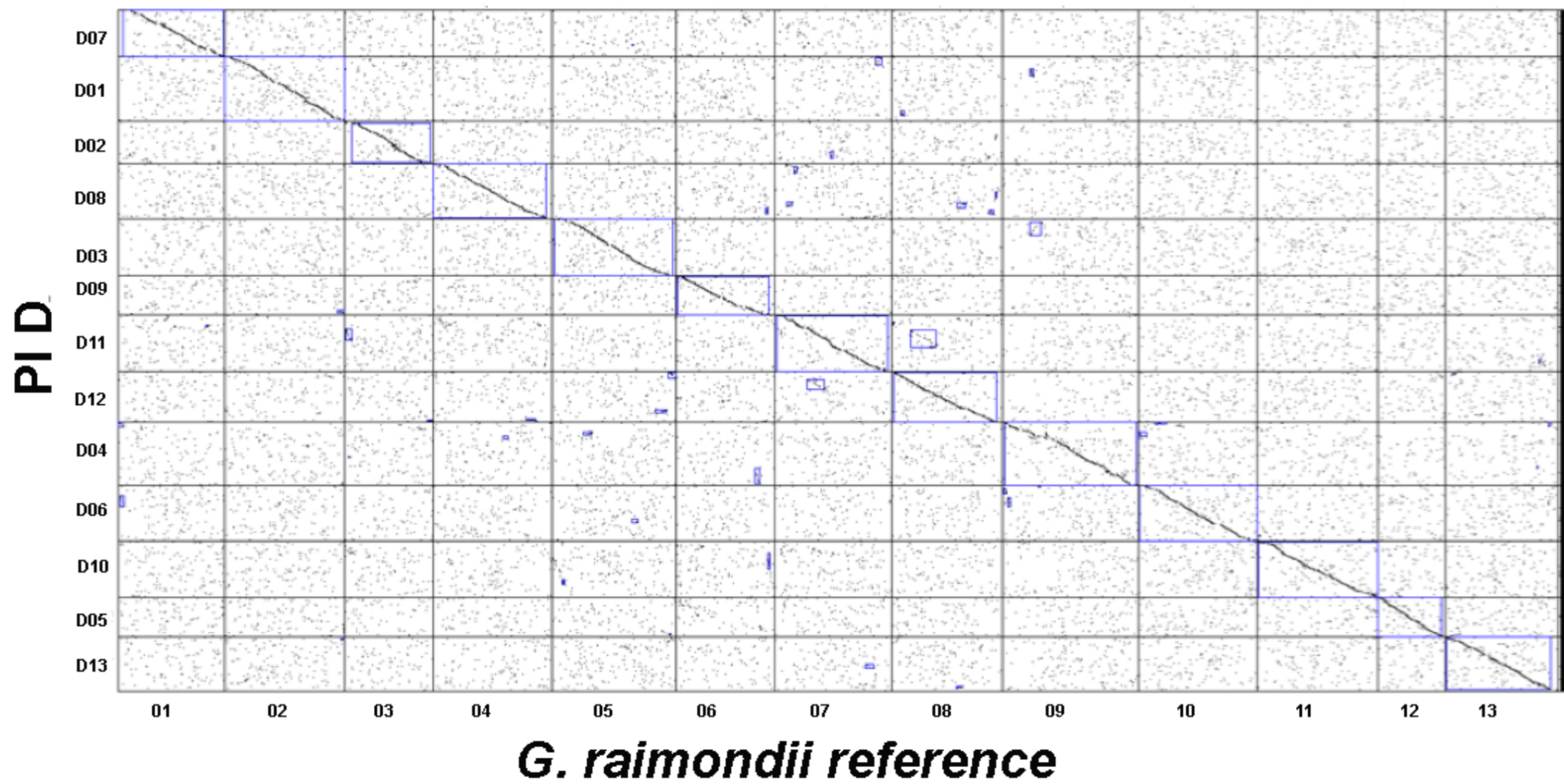
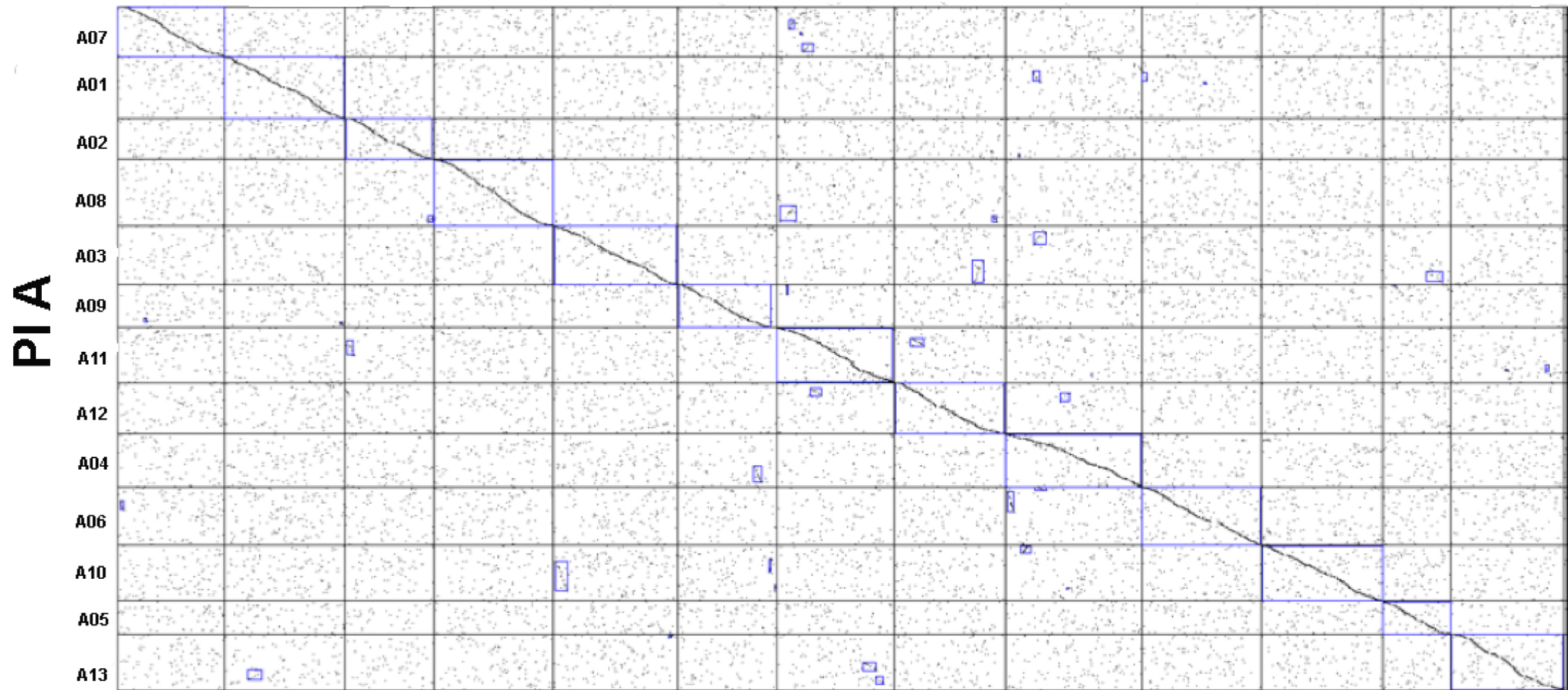


Figure S3. A dot plot alignment of the *G. hirsutum* TM-1 subgenome specific BES aligned to the *G. raimondii* extant diploid progenitor reference assembly. The BES alignments are relatively colinear and evenly distributed.

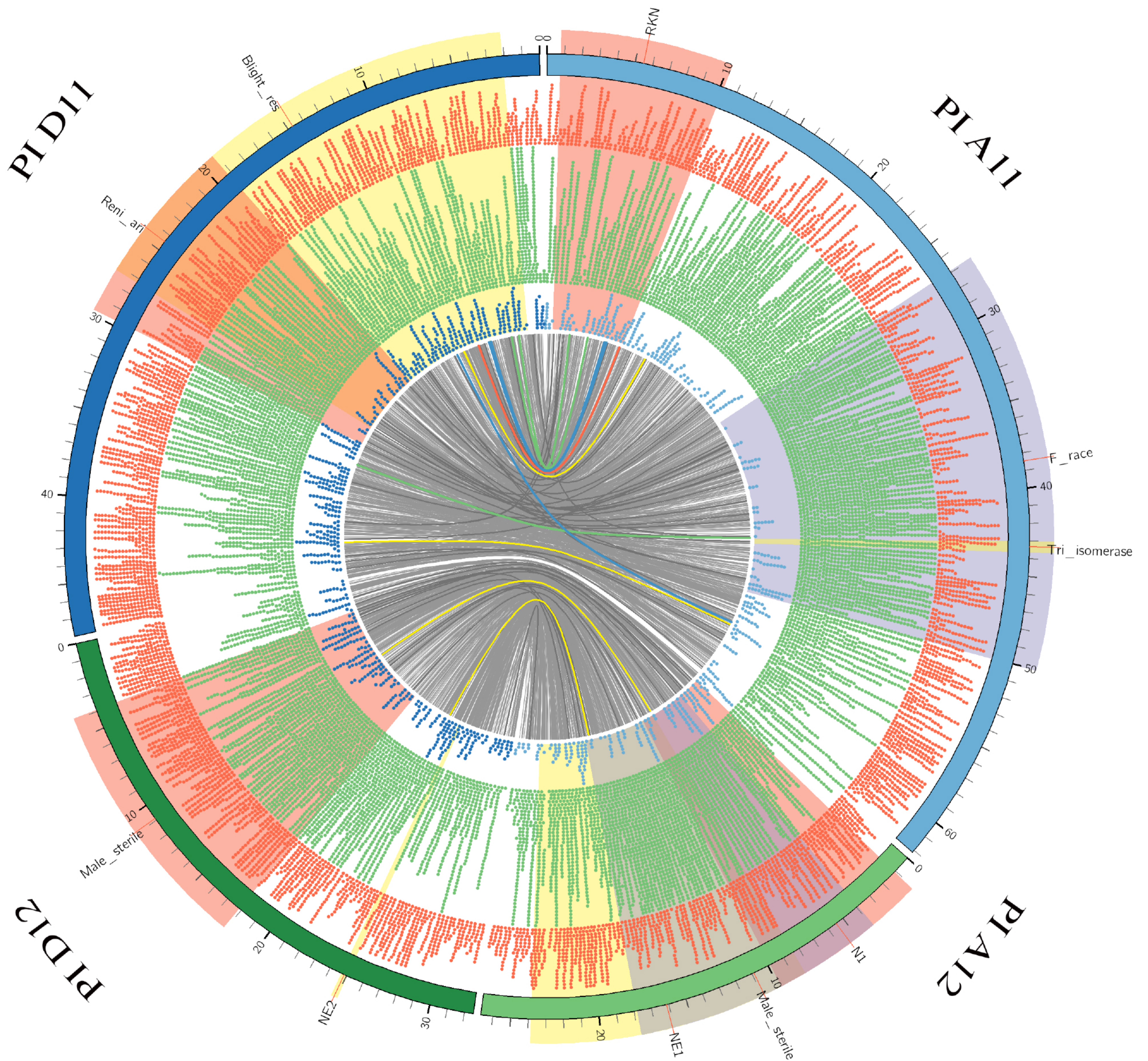


Figure S5. Pseudomolecule alignments of pilot chromosomes A11/D11 and A12/D12 as aligned as homeologous pairs by the inner links. Blue glyphs (internal) are retroelements, green glyphs are *Gypsy* elements, and red glyphs are *Copia* elements. Highlights denote SSR qtl boundaries of qualitative traits.