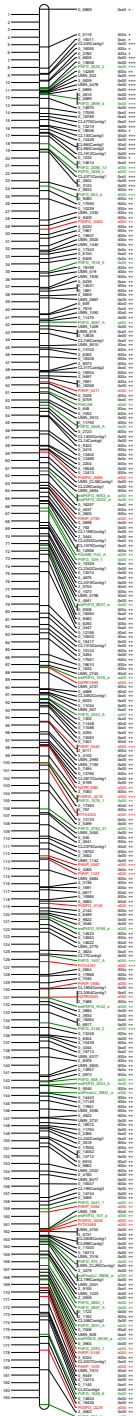
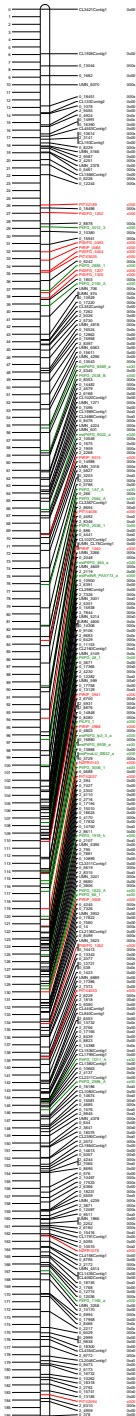
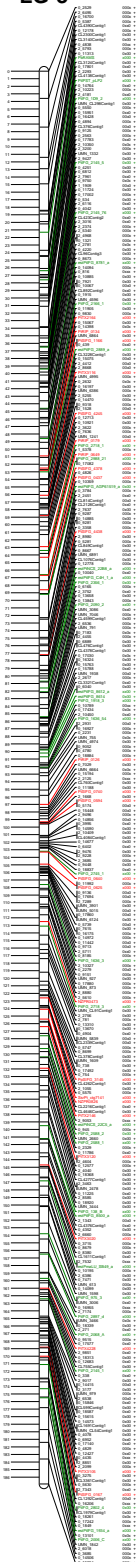
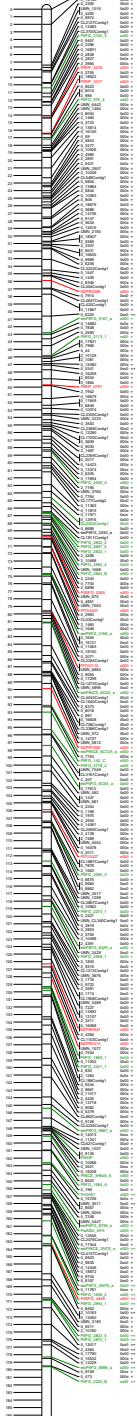
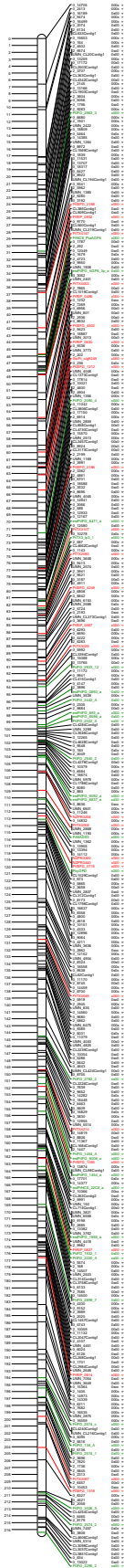
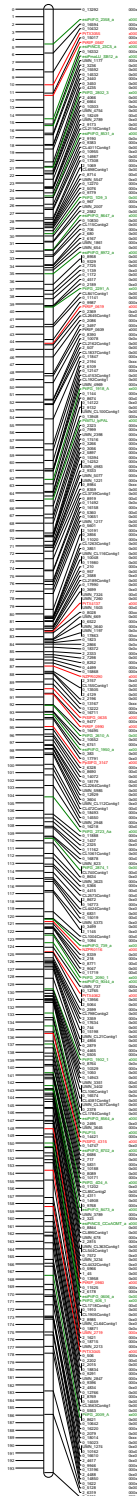
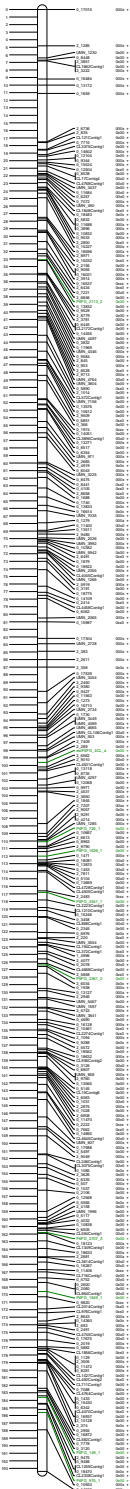


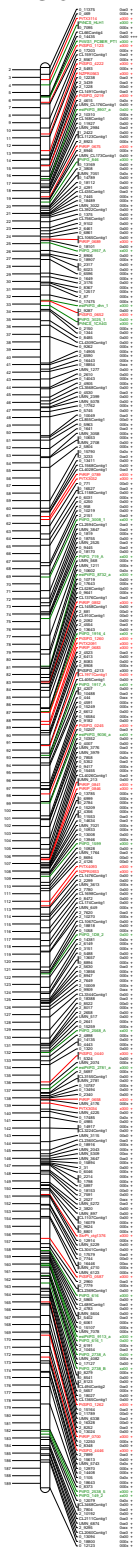
LG-1**LG-2****LG-3****LG-4****LG-5****LG-6**

Consensus map of *Pinus taeda*, 3856 loci in 12 linkage groups. cM positions left of bar, GeneIDs right of bar. Marker types: SNP & PAV (black), SSR (red), ESTP & RFLP (green). Input maps: qtl-base1, qtl-base2, BC1, 10-5; marker segregating (x), marker not seg. (0). cM difference between 95% CI upper & lower bounds of locus position: 0-1 (+), 1-2 (++), 2-3 (+++), 3-4 (++++).

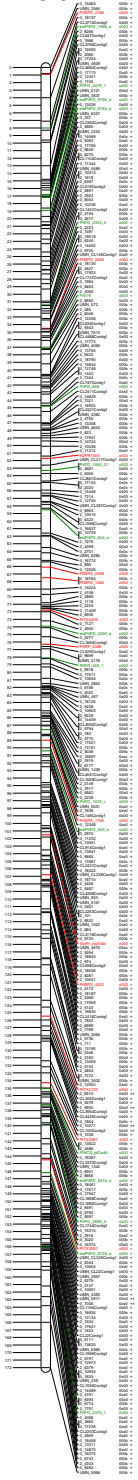
LG-7



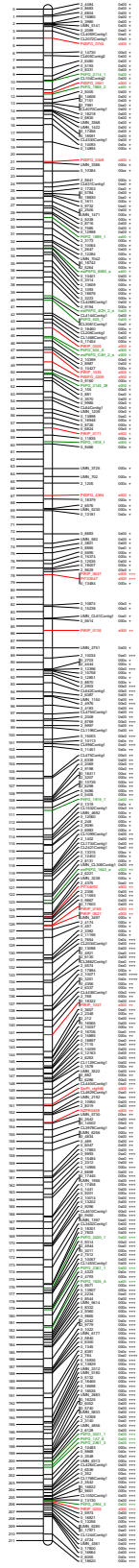
LG-8



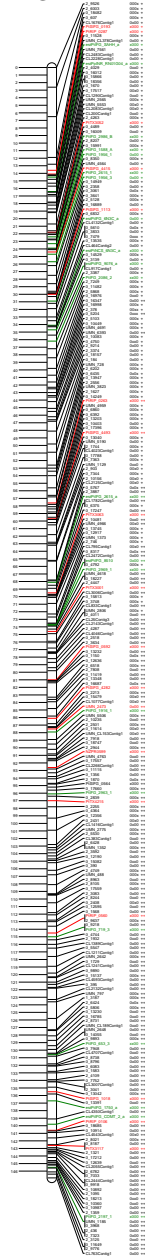
LG-9



LG-10



LG-11



LG-12

