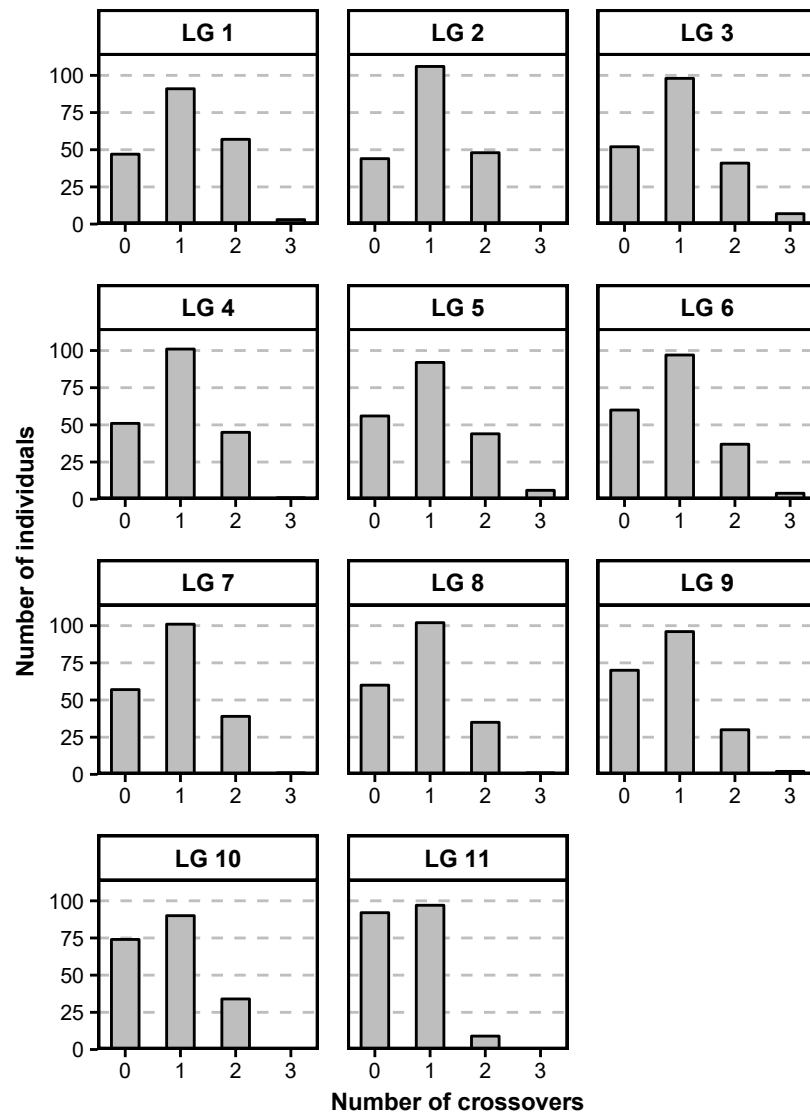
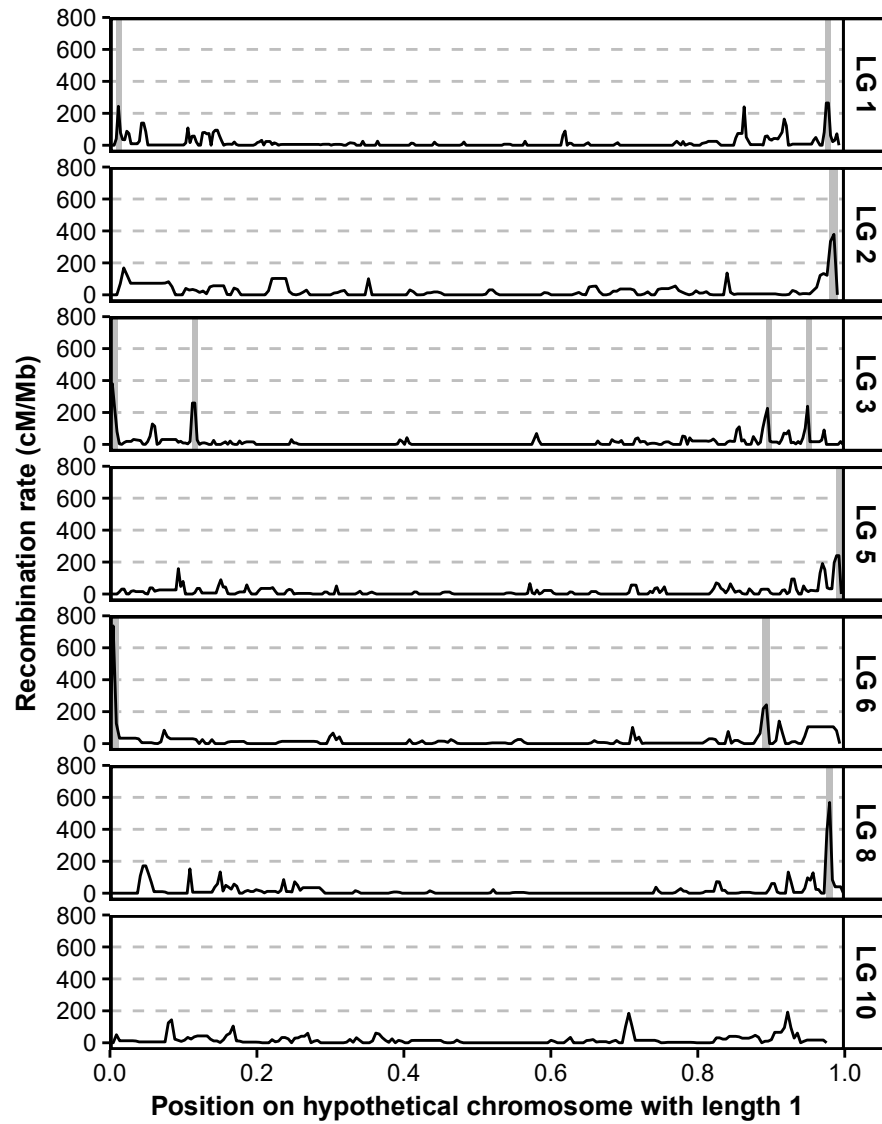


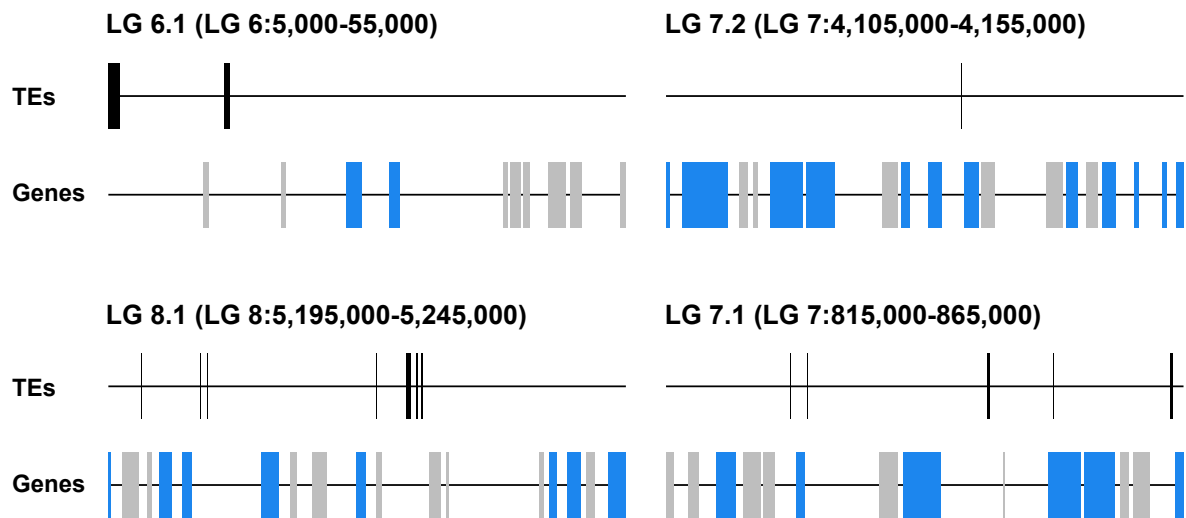
Supplementary Figure S1. Physical distance of consecutive crossover events on each of the pseudochromosomes across the 198 analyzed haploid progeny of *Armillaria ostoyae* strain C15. Because a major part of the left chromosome arm of pseudochromosome LG 11 is likely missing, no panel is shown for this pseudochromosome.



Supplementary Figure S2. Crossover events per pseudochromosome in 198 haploid progeny of the diploid *Armillaria ostoyae* strain C15.



Supplementary Figure S3. Recombination landscape of *Armillaria ostoyae* strain C15 with pseudochromosomes scaled to length 1. Recombination rates were estimated in non-overlapping 20 kb segments. Vertical grey bars indicate the location of recombination hotspots defined as 50 kb windows centered on one or two adjacent 20 kb segments with recombination rates ≥ 200 cM/Mb. A potential recombination hotspot towards the end of LG 1 was not considered a recombination hotspot because of an overlap with an assembly gap. Only chromosomes with telomeres at both ends were included. A version of this figure showing all the chromosomes in their original size is provided as Figure 2.



Supplementary Figure S4. Transposable element and gene composition of the four strongest recombination hotspots (excluding LG11). The strongest hotspot is shown on the top left and the others are arranged in decreasing strength. In the gene trace, annotated genes (i.e. with PFAM annotation) are colored in blue.