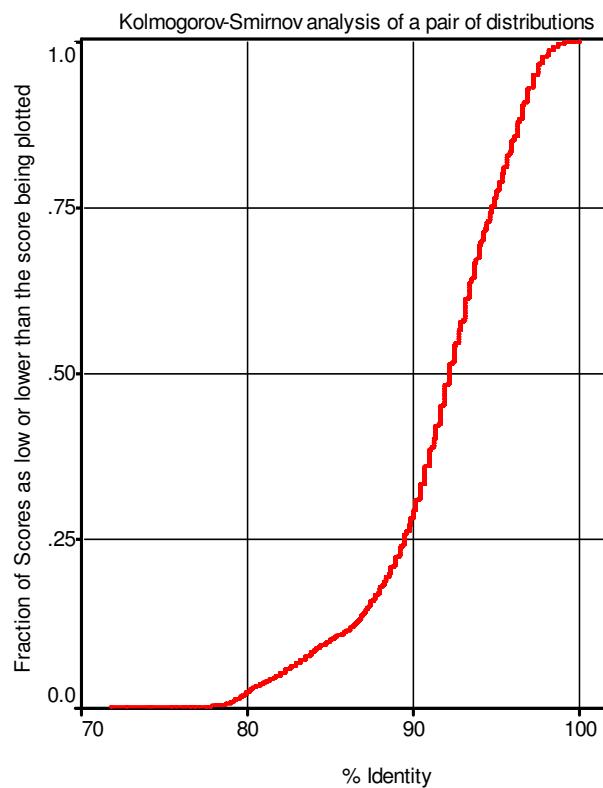
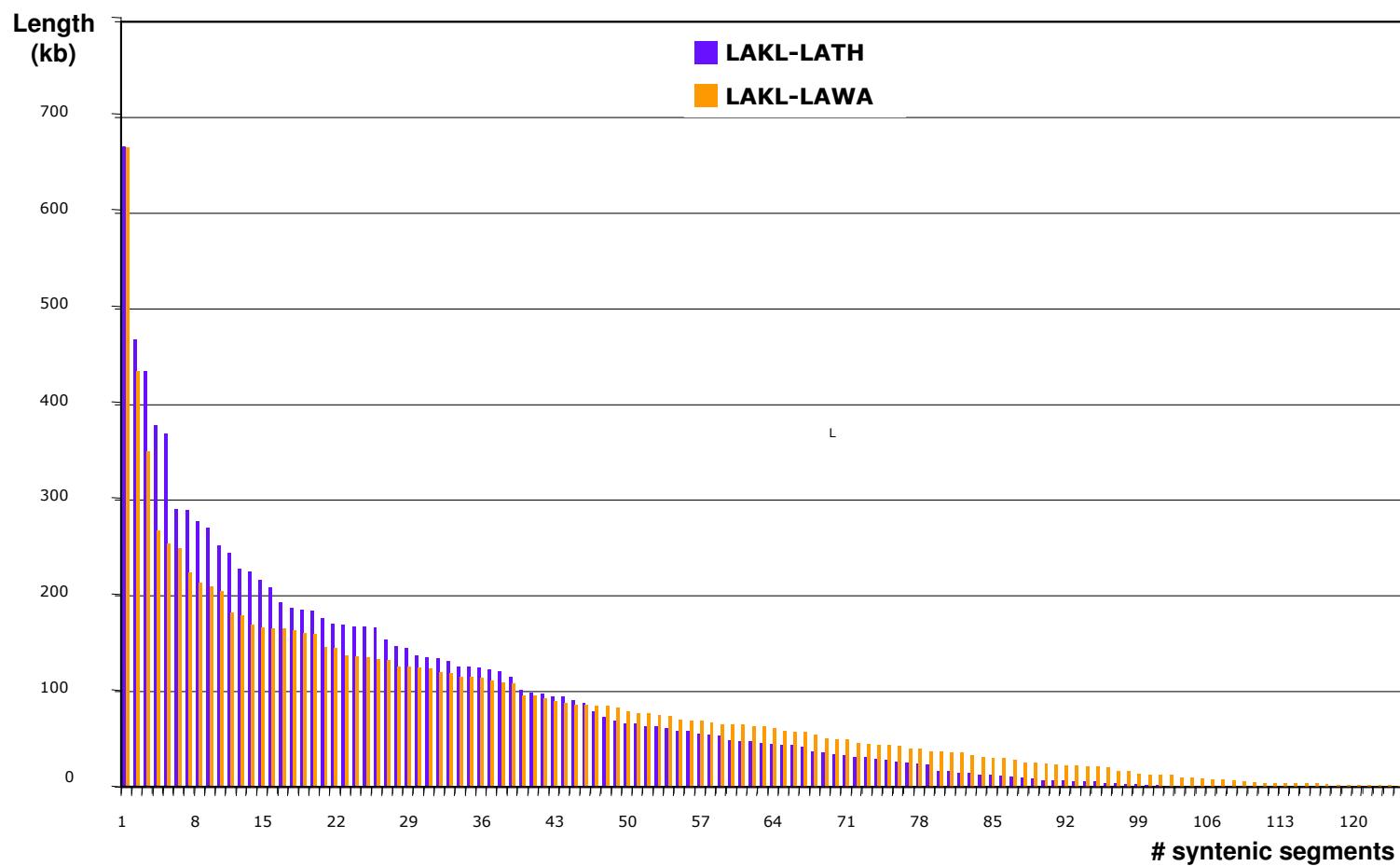


Supplemental Figure 1: Intron pattern of genes encoded by C-left and the rest of the genome. Values below arrows indicate minimal and maximal sizes, average size (av) and median (med). Note that the two patterns are slightly different. Introns of C_left are longer than those of the rest of the genome and 5' splice sites (5'ss), 3' splice sites (3'ss) and branch points (BP) are more conserved.



Supplemental Figure S2: Nucleotide conservation of LTRs. A total of 163 LTR sequences were aligned using MAFFT. The pairwise conservation ranged from 71 to 100%. About 70% of the LTRs diverge from one another by less than 10%.



Supplemental Figure S3: Size distribution of syntenic segments between the genomes of *L. kluyveri* and *L. thermotolerans* (LAKL-LATH, blue bars) and the genomes of *L. kluyveri* and *L. waltii* (LAKL-LAWA, orange bars). Segments are ordered according to their length in kilobases (kb) from the largest to the smallest.