Supplemental Figures

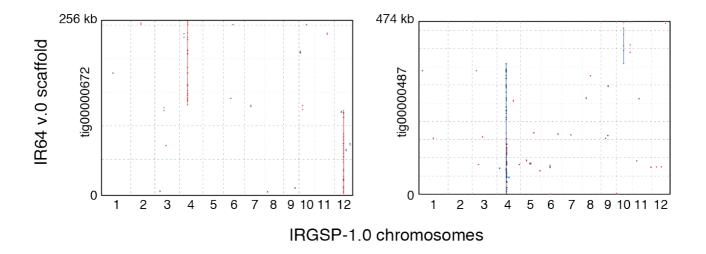


Figure S1. Genome alignment between IRGSP-1.0 genome and IR64 scaffolds. Red and blue dots represent forward and reverse alignments, respectively.

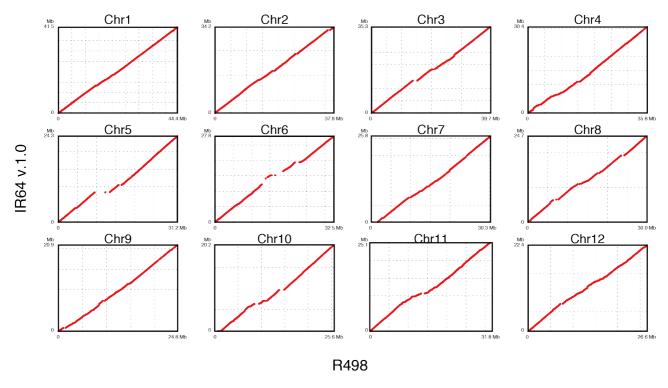


Figure S2. Chromosome alignments between R498 and IR64 v.1.0.

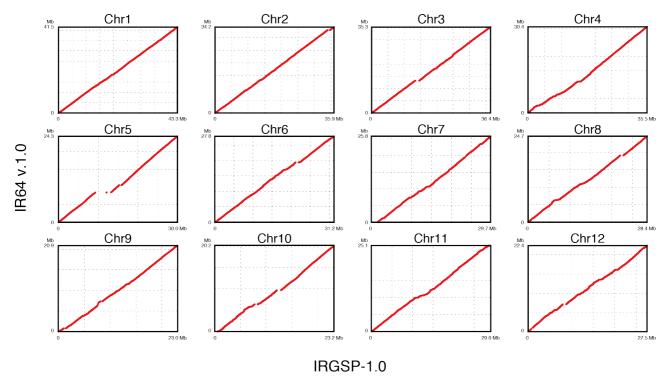


Figure S3. Chromosome alignments between IRGSP-1.0 and IR64 v.1.0.

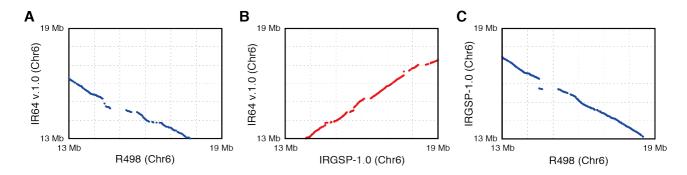


Figure S4. Chromosome alignments of chromosome 6 from 13 Mbp to 19 Mbp.

A) R498 versus IR64 v.1.0, B) IRGSP-1.0 versus IR64 v.1.0 and C) R498 versus IRGSP-1.0.

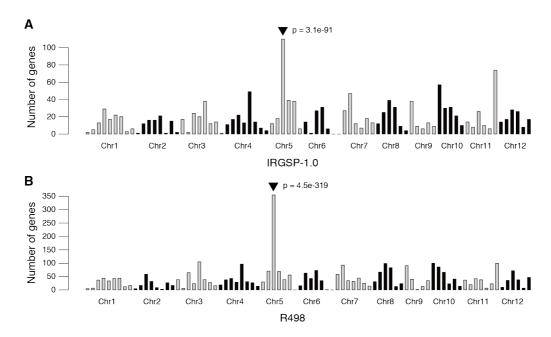


Figure S5. Chromosomal distribution of genes mapped on IR64 v.1.0 unanchored sequences. A) IRGSP-1.0, B) R498. Arrowheads indicate locations of the alignment gaps in chromosome 5. Enrichment test results (one-tailed p-values) are indicated.

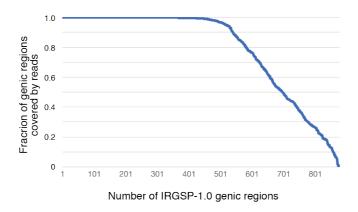


Figure S6. Fraction of missing genic regions in IR64 covered by paired-end reads obtained from linked-read sequencing of IR64 genome.

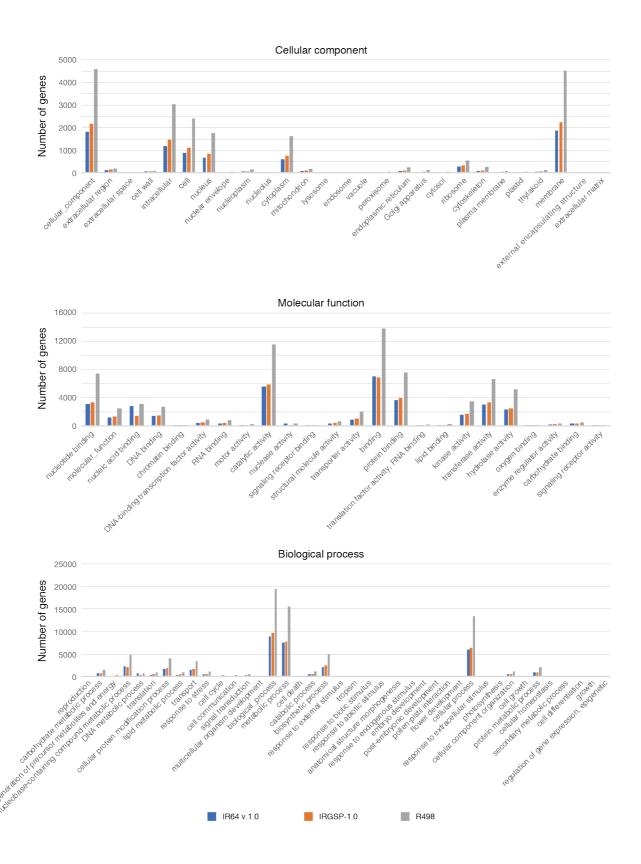


Figure S7. Distribution of gene ontologies.