



FIGURE S2.—Graphical comparison between *O. glaberrima* cv. CG14 BAC OG-BBa0049I08 and the orthologous *O. sativa* cv. Nipponbare genomic segment. Pairwise alignments of the *O. glaberrima* cv. CG14 BAC OG-BBa0049I08 and the respective *O. sativa* cv. Nipponbare orthologous region. Predicted genes (empty boxes) and TEs (dark bars) are shown for each of the sequences. Gray triangles mark the locus *S*₁, as shown in Figure 4. **C:** Nipponbare genes manually corrected. **P:** Partial gene.

#: Pseudogene. The insertion of two LTR retrotransposons are indicated with arrows.