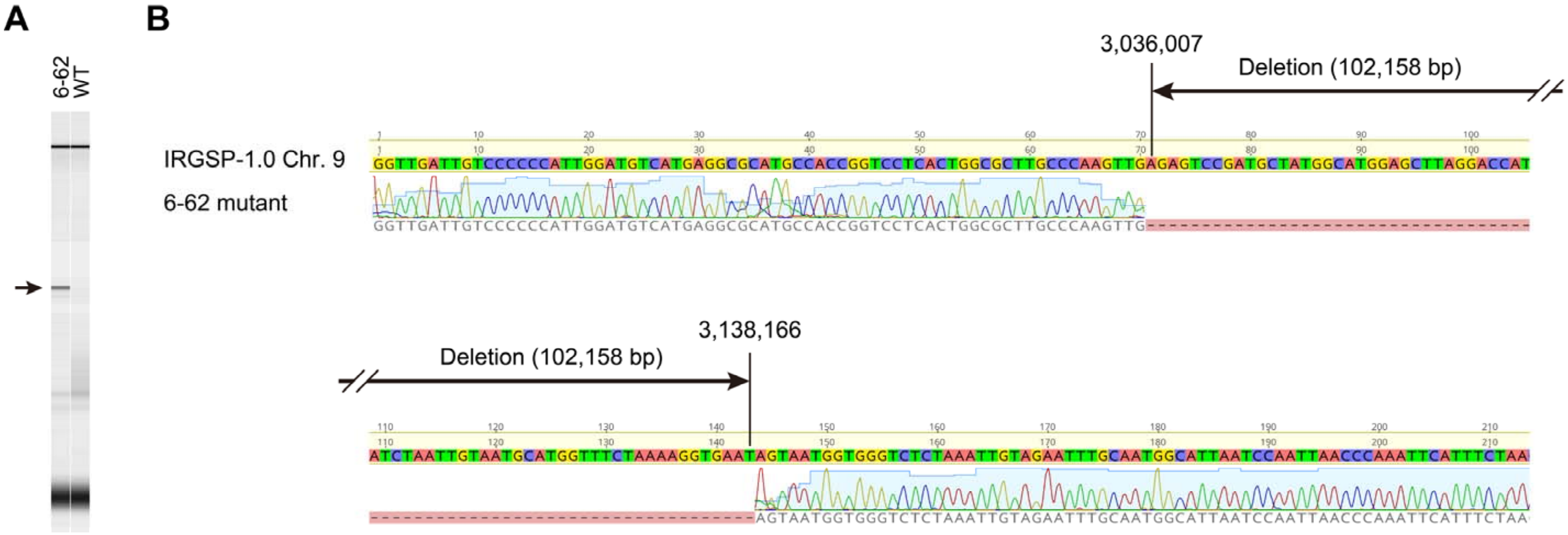

**Figure S1. Confirmation of a large (102,158 bp) deletion in the 6-62 mutant**

A: a pair of PCR primers were designed upstream and downstream of the deletion, and subjected for amplification from genomic DNA from the 6-62 mutant and wild-type Nipponbare. The arrow indicates the 303 bp band expected in the 6-62 mutant. B: A schematic drawing of the structure and flanks of the deletion. Comparison between PCR-direct sequencing of the amplified DNA fragment and the reference Nipponbare genomic sequence indicated that the deletion spans 102,158 bp in length and has no filler sequence.