Figure S1. The Large Gap Mapping tool of CLC was used to identify the new genes by comparison of IRGSP-1.0 Nipponbare with UQ-Nipponbare. The genes from the UQ-Nipponbare were initially mapped to the IRGSP-1.0 Nipponbare genome sequence. After this initial mapping, both the mapped and unmapped genes were then subjected to another round of mapping, this time against the IRGSP-1.0 Nipponbare gene annotation.