

Table S1. Statistics of assembly sequences from metatranscriptomic sequencing data of three major fungal pathogens of rice.

Sample	Raw reads	Clean reads	Total contigs	Viral-related contigs
<i>M. oryzae</i>	2.16×10^8	2.11×10^8	116,736	79
<i>U. virens</i>	2.88×10^8	2.84×10^8	106,131	593
<i>R. solani</i>	7.82×10^7	7.70×10^7	99,590	10