

Table S3 Summary of RNA-seq reads and mapping statistics.

| Sample | Replication | ^a Total clean reads | ^b Mapping to Ina168 reference genome | b /a *100 (%) |
|---------|-------------|--------------------------------|---|---------------|
| Conidia | -1 | 3,787,507 | 3,712,988 | 98.0% |
| | -2 | 4,278,481 | 3,927,887 | 91.8% |
| | -3 | 4,566,448 | 4,354,557 | 95.4% |
| 12 hpi | -1 | 21,911,609 | 205,875 | 0.9% |
| | -2 | 18,863,494 | 443,718 | 2.4% |
| | -3 | 21,067,292 | 746,316 | 3.5% |
| 24 hpi | -1 | 18,336,408 | 273,898 | 1.5% |
| | -2 | 16,535,399 | 454,551 | 2.7% |
| | -3 | 17,890,040 | 531,192 | 3.0% |
| 36 hpi | -1 | 23,380,354 | 1,427,532 | 6.1% |
| | -2 | 16,869,313 | 1,225,044 | 7.3% |
| | -3 | 21,487,630 | 2,579,929 | 12.0% |
| 48 hpi | -1 | 11,155,133 | 2,285,789 | 20.5% |
| | -2 | 10,045,391 | 3,754,649 | 37.4% |
| | -3 | 9,699,083 | 2,789,260 | 28.8% |