**S1 Table. Statistics for mapped reads and detected genes.**

| | Raw Reads (million pairs) | Length (bp) | Data size (Gbps) | Mapped fragments (poplar) | Detected gene[a] (poplar) | Mapped fragments (fungi) | Detected genes (fungi) |
|---|---|---|---|---|---|---|---|
| **214_High_48 h[b]** | 9.4 | 151 | 2.8 | 3,332,423 | 23,840 | 16,928 | 1,502 |
| **214_High_96 h** | 10.1 | 151 | 3.0 | 4,765,384 | 24,569 | 15,304 | 1,632 |
| **214_Weak_24 h[c]** | 22.7 | 100 | 4.5 | 13,089,007 | 25,596 | 13,339 | 1,087 |
| **895_High_12 h** | 14.4 | 100 | 2.9 | 10,014,506 | 26,474 | 92,717 | 5,250 |
| **895_High_48 h** | 15 | 100 | 3.0 | 10,738,751 | 26,220 | 69,963 | 5,026 |
| **895_High_96 h** | 17.8 | 100 | 3.6 | 11,333,846 | 26,003 | 145,303 | 6,148 |
| **895_Weak_6 h** | 13.1 | 100 | 2.6 | 9,743,550 | 27,040 | 11,504 | 1,338 |
| **895_Weak_24 h** | 11.5 | 100 | 2.3 | 8,071,463 | 26,250 | 10,666 | 1,281 |
| **895_Weak_72 h** | 12.8 | 100 | 2.6 | 8,716,076 | 25,177 | 5,347 | 649 |

[a] The criterion for "detected gene" was that the mapped fragments were not less than 2.

[b] "High" means infected with highly active fungi.

[c] "Weak" means infected with weakly active fungi.