**S1 Table.** Quality assessment for reference transcriptomes of *Suillus* spp. FASTQ Quality Trimmer v1.0.0 was used to trim and quality filter reads (cutoff for quality scores <28). *Suillus* strain IDs (in parentheses) provided for RNASeq sample ID (e.g. S6\_16) and fungal strain ID (e.g. EM31). Additional information for sample IDs is described in Dataset S1, Table 1 and S3 Table.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample ID | *S. americanus* (S6\_16; EM31) | *S. granulatus* (S9\_3; EM37) | *S. spraguei* (S8\_7; EM27) | *S. decipiens* (S11\_13; EM49) |
| No. total reads | 30,321,196 | 31,841,968 | 24,710,538 | 31,609,240 |
| No. filtered reads1 | 28,015,666 | 28,777,616 | 22,453,880 | 28,981,020 |
| No. contigs | 19,123 | 15,724 | 18,898 | 16,871 |
| Mean length of contigs (bp) | 995 | 1,124 | 993 | 1019 |
| Max length of contigs (bp) | 9,840 | 9,840 | 9,840 | 9,840 |
| N50 length of contigs (bp) | 1,693 | 2,094 | 1,752 | 1,727 |
| No. contigs ≥ 500 bp | 10,508 | 8,755 | 9,907 | 9,316 |