**Table S1. Summary of read data for *P. cheesemanii* stress transcriptome.**

| **Library** | **Raw reads** | **Clean reads** | **Raw data (GB)** | **Clean data (GB)** |
| --- | --- | --- | --- | --- |
| **Control** | 115,407,011 | 115,383,228 | 32.24 | 32.24 |
| **UV-B** | 99,224,069 | 99,204,290 | 27.72 | 27.72 |
| **Cold** | 111,242,384 | 111,202,228 | 31.08 | 31.07 |
| **Salt** | 111,282,532 | 111,236,246 | 31.09 | 31.08 |
| **Total** | 437,155,996 | 437,025,992 | 122.13 | 122.11 |

**Table S2. Assessment of transcriptome assemblies generated by multiple assemblers.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **k-mer size** | **Bowtie (%)** | **Complete BUSCOs (%)** | **Fragmented BUSCOs (%)** | **Missing BUSCOs (%)** |
| **Velvet/Oases** | k55 | 88.21 | 92.7 | 4.5 | 2.8 |
| k65 | 87.84 | 96.1 | 1.9 | 2 |
| k75 | 87.56 | 97.1 | 1.3 | 1.6 |
| k85 | 86.64 | 96.9 | 1.4 | 1.7 |
| k95 | 85.9 | 96.4 | 2.1 | 1.5 |
| **Trans-ABySS** | k51 | 90.79 | 92.5 | 4.4 | 3.1 |
| k53 | 90.88 | 92.8 | 4.4 | 2.8 |
| k55 | 90.98 | 93.1 | 4 | 2.9 |
| k57 | 91.08 | 93.8 | 3.5 | 2.7 |
| k59 | 91.4 | 94.3 | 3.5 | 2.2 |
| k61 | 91.21 | 94 | 3.5 | 2.5 |
| k63 | 91.25 | 94.1 | 3.5 | 2.4 |
| **Trinity** | k19 | 88.81 | 59.9 | 24.4 | 15.7 |
| k21 | 88.72 | 84.5 | 9.4 | 6.1 |
| k23 | 88.62 | 89.4 | 7.2 | 3.4 |
| k25 | 88.26 | 86.3 | 8 | 5.7 |
| k27 | 88.68 | 87 | 7.4 | 5.6 |
| k29 | 89.41 | 88.1 | 8.1 | 3.8 |
| k31 | 89.86 | 88.6 | 7.1 | 4.3 |

**Table S3. Summary statistics for transcriptome assembly.**

|  |  |
| --- | --- |
| **Assembly** |  |
| Trans-ABySS transcripts (combined 7 assemblies) | 318,111 |
| CAP3 transcripts | 223,341 |
| EvidentialGene transcripts | 67,905 |
| EvidentialGene genes | 45,911 |
| Minimum transcript length (bp) | 200 |
| Longest transcript length (bp) | 18,443 |
| Final size of assembly (bp) | 107,064,440 |