

**Supplementary Table S1.** Total number of raw reads, high-quality reads per sample, and their mapping rate within *Deschampsia antarctica* transcriptome

| <i>Sample</i> | <i>raw reads</i> | <i>High quality reads</i> | <i>Mapped reads</i> | <i>Mapping rate (%)</i> |
|---------------|------------------|---------------------------|---------------------|-------------------------|
| E1            | 20,456,461       | 19,637,272                | 16,946,758          | 86.30                   |
| E2            | 20,911,828       | 20,089,989                | 17,323,597          | 86.23                   |
| E3            | 24,332,760       | 23,472,782                | 20,437,217          | 87.07                   |
| F1            | 24,659,473       | 23,781,109                | 20,747,380          | 87.24                   |
| F2            | 24,947,240       | 24,390,972                | 21,318,883          | 87.40                   |
| F3            | 23,132,517       | 22,642,675                | 19,845,043          | 87.64                   |
| G1            | 24,107,540       | 23,523,818                | 20,374,801          | 86.61                   |
| G2            | 23,367,878       | 22,862,486                | 19,854,336          | 86.84                   |
| G3            | 24,445,058       | 23,813,002                | 20,645,369          | 86.70                   |
| H1            | 30,212,625       | 29,515,612                | 25,920,826          | 87.82                   |
| H2            | 19,821,101       | 19,300,281                | 16,630,192          | 86.17                   |
| H3            | 22,739,157       | 22,268,592                | 19,435,836          | 87.28                   |

**Supplementary Table S2.** *De novo* transcriptome assembly of *Deschampsia antarctica* by RNA-Seq

| <i>Metric</i>             | <i>D. antartica transcriptome</i> |
|---------------------------|-----------------------------------|
| Trinity transcripts       | 193,333                           |
| <b>Trinity "genes"</b>    | <b>84,162</b>                     |
| GC (%)                    | 47.65                             |
| Contig N50 (bp)           | 2,255                             |
| Median contig length (bp) | 1,127                             |
| Average contig (bp)       | 1,533                             |
| Total assembled bases     | 296,554,700                       |

**Supplementary Table S3.** Assessment of completeness of the *Deschampsia antarctica de novo* assembly using BUSCO\*.

| <i>Summary BUSCO statistics</i> |              |              |
|---------------------------------|--------------|--------------|
| <b>Complete BUSCOs</b>          | <b>1,549</b> | <b>95.9%</b> |
| Complete and single-copy BUSCOs | 288          | 17.8%        |
| Complete and duplicate BUSCOs   | 1,261        | 78.1%        |
| Fragmented BUSCOs               | 31           | 1.9%         |
| Missing BUSCOs                  | 34           | 2.2%         |
| Total BUSCO genes *             | 1,614        | 100.0%       |

\*Database: embriophyte\_odb10

\*BUSCO: Benchmarking Universal Single-Copy Orthologs

**Supplementary Table S4.** List of primers used for qRT-PCR analysis.

| <i>Gene</i>                 | <i>Transcript name</i>                                   | <i>Primers</i> |                       | <i>Amplicon (pb)</i> |
|-----------------------------|--|----------------|-----------------------|----------------------|
|                             |  | <i>Type</i>    | <i>Sequence 5'-3'</i> |                      |
| <b>PAB2</b>                 | <i>Polyadenylate-binding protein2</i>                    | FW             | TGGGAGCAACACCAGGTCTC  | 160                  |
|                             |  | RW             | CCTCCAGTTGCTCCTCGCAT  |                      |
| <b>IF4E4</b>                | <i>Eukaryotic translation initiation factor4</i>         | FW             | CACCTCGCTCAAGAAGGGCT  | 159                  |
|                             |  | RW             | CCATTTGCGCACTCTGGGTC  |                      |
| <b>MYB2</b>                 | <i>Transcription factor MYB2</i>                         | FW             | ACCTGAGACGGCAGCTCTTG  | 184                  |
|                             |  | RW             | CACGAGAGGGACTCGAGCAG  |                      |
| <b>DRE1A</b><br><b>CBF3</b> | <i>Dehydration-responsive element-binding protein 1A</i> | FW             | GGTCCGCGTAGTACGATCCC  | 106                  |
|                             |  | RW             | GACGGTTTGTTCGAGGTGCC  |                      |
| <b>DRE1D</b><br><b>CBF4</b> | <i>Dehydration-responsive element-binding protein 1D</i> | FW             | GACAACGTCCTTCACAGCCG  | 160                  |
|                             |  | RW             | GTGCCTCAACTTCGCCGACT  |                      |
| <b>DHN1</b>                 | <i>Dehydrin 1</i>  | FW             | TCCAGCCGATGAAGGACGAC  | 175                  |
|                             |  | RW             | GTCTGCTGTTGCTGCTGCTC  |                      |
| <b>SPSA4</b>                | <i>Sucrose phosphate synthase A4</i>                     | FW             | TCCGGTGAACCTGAGCCAAC  | 138                  |
|                             |  | RW             | GCGTGGTGTCTAGCTGCTATG |                      |
| <b>SUS4</b>                 | <i>Sucrose synthase 4</i>                                | FW             | ACGTACAGCGTCCACAGAGA  | 173                  |
|                             |  | RW             | TGTCCAGCGAGTGGTGAAC   |                      |
| <b>RGLG5</b>                | <i>E3 ubiquitin-protein ligase 5</i>                     | FW             | CGGAGCTTGACGCAATAGG   | 122                  |
|                             |  | RW             | GCATCGCCGAATCCAAAGCA  |                      |
| <b>CAX1</b>                 | <i>Vacuolar cation/proton exchanger 1</i>                | FW             | CAGAAGAGGGAGGTGCCGAG  | 96                   |
|                             |  | RW             | CGCGCTCATGGAGGGTAAGA  |                      |

|              |   |    |                       |     |
|--------------|---|----|-----------------------|-----|
| <b>U73B3</b> | <i>UDP-glycosyltransferase 73B3</i>                     | FW | CGCATTTCATCGAGCGGTACG | 118 |
|              |   | RW | GACGGCTGCGTTATTGCCTC  |     |
| <b>OAT</b>   | <i>Ornithine aminotransferase</i>                       | FW | GGTAAGTGCAGTTCTCGCGG  | 109 |
|              |   | RW | TGATGCAACTGCCACAGCAC  |     |
| <b>DXS1</b>  | <i>1-deoxy-D-xylulose-5-phosphate synthase 1</i>        | FW | AAGATGACGTCGGAGCGGAG  | 163 |
|              |   | RW | GGTCCTGCATTTCTGCGTCG  |     |
| <b>PSBP2</b> | <i>Oxygen-evolving enhancer protein 2</i>               | FW | GTGGTGGACGGGAAGCAGTA  | 165 |
|              |   | RW | CTTCTTCGCGCCCTTGAACC  |     |
| <b>ILL2</b>  | <i>IAA-amino acid hydrolase ILR1-like 2</i>             | FW | CGTAGCGACGGTCTCGAAGT  | 177 |
|              |   | RW | TGCTTCTCGAACGAGGGCTT  |     |
| <b>RBCS1</b> | <i>Ribulose biphosphate carboxylase small subunit 1</i> | FW | TTACTTGCCACCGCTCACCA  | 109 |
|              |   | RW | ACGGAACACAAACCCGACCT  |     |
| <b>FBA5</b>  | <i>Fructose-bisphosphate aldolase 5</i>                 | FW | CACCCTCCTCAAGCCCAACA  | 182 |
|              |   | RW | TCATGGCGTCCAGGTTCTCC  |     |
| <b>TPT</b>   | <i>Triose phosphate/phosphate translocator</i>          | FW | ACGCTCCTGAAGCTGCTCTT  | 143 |
|              |   | RW | TGGGTAGCCGCTGCATTGAA  |     |