Supplementary materials

1. Supplementary Figures

Figure S1. K-means analysis of significantly different metabolites
Figure S2. O2PLS model analysis of transcriptome and metabolome a: transcriptome loading plot; b: metabolome loading plot. The distance from each point to the origin point meant the correlation of these transcripts or metabolites with the other omics. The top 10 genes and metabolites that influenced the other omics were indicated in figure S4 a & b respectively.
Figure S3. KEGG enrichment pathway analysis. (A) KEGG enrichment pathway of MMA2 vs. MCA10; (B) MMA2 vs. MMA4; (C) MMA4 vs. MCA10.
Figure S4. The fifty most enriched GO terms when analyzing DEGs between MMA4 and MCA10
Figure S5. The cytoscape of STRING interactions of the cold acclimation induced proteins. The genes gradually up-regulated during cold acclimation were analyzed with STRING database. A total of 598 proteins were mapped into the database of Arabidopsis thaliana, and their STRING interactions with a medium confidence were further revealed by the Cytoscape. GSR2, Glutamine synthetase cytosolic isozyme 1; NOA1, nitric oxide associated protein 1; DOX1, α-dioxygenase gene1; RCD1-like, radical-induced cell death1-like, DREB2A, dehydration-responsive element-binding protein 2A; SERK1, Somatic embryogenesis receptor-like kinase 1.
## 2. Supplementary Tables

**Table S1** Regeneration of embryogenic tissue (ET) from cryo-preserved tissue following various pretreatments on the basis of cryo-vials. Mean ± SD, n = 4.

| Treatment | Vials in test | R1 | R2 | R 3 | R 4 | Total | Percentage (%) |
|-----------|---------------|----|----|-----|-----|-------|----------------|
| MMA0      |               | 3  | 3  | 3   | 3   | 12    | 0.00±0.00      |
|           | Vials of ET regeneration | 0  | 0  | 0   | 0   | 0     |                |
| MMA2      |               | 3  | 3  | 3   | 3   | 12    | 0.00±0.00      |
|           | Vials of ET regeneration | 0  | 0  | 0   | 0   | 0     |                |
| MMA4      |               | 3  | 3  | 3   | 3   | 12    | 8.33±16.65     |
|           | Vials of ET regeneration | 0  | 0  | 0   | 1   | 1     |                |
| MCA2      |               | 3  | 3  | 3   | 3   | 12    | 8.33±16.65     |
|           | Vials of ET regeneration | 0  | 0  | 0   | 1   | 1     |                |
| MCA4      |               | 3  | 3  | 3   | 3   | 12    | 24.98±16.65    |
|           | Vials of ET regeneration | 0  | 1  | 1   | 1   | 3     |                |
| MCA10     |               | 3  | 3  | 2   | 3   | 11    | 91.68±16.65    |
|           | Vials of ET regeneration | 3  | 3  | 2   | 3   | 11    |                |
Table S2 Tissue survival rate and embryogenicity before and/or after cryo-preservation in *Picea glauca*. Significant differences are indicated by different letters ($P < 0.05$). Mean ± SD, $n > 5$.

| Treatment | Survival rate after cryo-treatment (%) | Embryogenicity (%) | Before cryo-treatment | After cryo-treatment |
|-----------|----------------------------------------|--------------------|-----------------------|---------------------|
| MMA0      | 0.00±0.00 (c)                          | 100.0±0.00 (a)     |                       | 0.00±0.00 (b)       |
| MMA2      | 0.00±0.00 (c)                          | 100.0±0.00 (a)     |                       | 0.00±0.00 (b)       |
| MMA4      | 100.00±0.00 (a)                        | 0.00±0.00 (b)      |                       | 4.15±6.49 (b)       |
| MCA2      | 36.73±14.93 (b)                        | 100.0±0.00 (a)     |                       | 2.00±4.90 (b)       |
| MCA4      | 41.37±12.37 (b)                        | 100.0±0.00 (a)     |                       | 4.77±7.41 (b)       |
| MCA10     | 100.00±0.00 (a)                        | 100.0±0.00 (a)     |                       | 29.29±13.17 (a)     |
| Primers | sequences |
|---------|-----------|
| tubulin-F | TGAACTTAATACGAACAGGAA |
| tubulin-R | TTAGTCAGGTTGGCATTC |
| NOS-F | GCCTTGAGTACATACATTAG |
| NOS-R | GACCTATGATGGTGTGGAT |
| ABI5-F | TTCAAGCACAAGAATCAA |
| ABI5-R | CCATTAGAGGACAGCAT |
| ABI3-1F | GAAGGATTGAGGAAGAGAC |
| ABI3-1R | TTACAGCCAGAAGAGACT |
| DOX-1F | CGTGATAATGTGCTTTGA |
| DOX-1R | TGAGTGGGAGATATTGTAAT |
| RCD1-1F | GCAACCTATCTCCAACAATC |
| RCD1-1R | CCTACGGGCTTATATGAAATACA |
| RCD1-2F | TCGCAGAAGAAGTGAATG |
| RCD1-2R | TGAATATGGAAGTGAAAGACA |
| PLT-F | GGTGTATTACTTGCCATCAG |
| PLT-R | CGGTTCACCTCAGGACTT |
| NCA-F | GGACTATTGGATGGTGAAT |
| NCA-R | TGTTGTGTTGGGAAGGATT |
| GLP-1F | CAGATCAGCGACAAAGTAG |
| GLP-1R | GCGGATGATGGACATT |
| GLP-3F | GTTGTGGGAGATCAATGTT |
| GLP-3R | GAAATCTTGGTGTCATC |
| ALBUMIN-F | TAAGTGACGAACAGAAGA |
| ALMUMIN-R | GGTGAGCATTGAAATGAGAG |
| Vicilline-F | GGAAGCATTACCGTATTTG |
| Vicilline-R | GGAAGGTCTCTGAACTTTT |
| thaumin-F | CAAGGTGATCTCTCAAGGG |
| thaumin-R | GGAAGTTCACACTCAATGG |
| DMR2-F | TGATTGAGAAGAGATGTT |
| DMR2-R | CTGCCACCAATAATGAGA |
| PAL-1F | AAGTCCTCGTAGATGGAAT |
| PAL-1R | GATAATACCTCCAGAAGCAT |