

Table 1 Suppl. The sequences of PCR primers used in this study.

| Transcript ID          | Gene symbol          | Primer  | Sequence (5'-3')         |
|------------------------|----------------------|---------|--------------------------|
| TRINITY_DN194873_c2_g1 | <i>polyubiquitin</i> | Forward | CGCACCTTGGCTGACTACA      |
|                        |                      | Reverse | AACAACCAGACCATGCAACA     |
| TRINITY_DN194873_c2_g1 | <i>WRKY28</i>        | Forward | CACCATAACCCATCACCCTG     |
|                        |                      | Reverse | CCAAGGATGAAGCACCACC      |
| TRINITY_DN194376_c3_g3 | <i>ERF114</i>        | Forward | TGCTTTCATACAGCCGACCAA    |
|                        |                      | Reverse | CGGATGTTATGCCTCCACAG     |
| TRINITY_DN194844_c2_g6 | <i>SDIR1</i>         | Forward | TTGAAGGCATTCGGTATTATGG   |
|                        |                      | Reverse | CGAGGTGGTGTTCGCTATTGTG   |
| TRINITY_DN191945_c3_g1 | <i>SWEET1</i>        | Forward | ATCTTCGGATTGCTTGGACG     |
|                        |                      | Reverse | TTATCTGCTGTGGCTGTGGG     |
| TRINITY_DN197182_c0_g2 | <i>MDH7</i>          | Forward | AAAGTCGATTCCCTTCTGAATGGA |
|                        |                      | Reverse | TAGTGGACTGCATACCTGATCTTG |
| TRINITY_DN194872_c3_g1 | <i>CRRSP4</i>        | Forward | GCTTCCTTGGTGGCAAATCC     |
|                        |                      | Reverse | GCAAGATGGTGCTTATCGTTCC   |
| TRINITY_DN195272_c0_g7 | <i>PEPC1</i>         | Forward | GTAGCTATGCTGCAATGATGGC   |
|                        |                      | Reverse | CATCACATTGGTGGGGAGTGTA   |
| TRINITY_DN194359_c8_g1 | <i>GSTU7</i>         | Forward | AAAGCAGTCTATAAGACCACCCTG |
|                        |                      | Reverse | ATATCAGTGGATGCTTTTCTGGGT |

Table 2 Suppl. Summary of the high-throughput transcriptome sequencing data in *Mesembryanthemum crystallinum* (ice plant) root.

| Sample ID | Group           | Total reads | Total base     | GC (%) | Q20 (%) | Q30 (%) |
|-----------|-----------------|-------------|----------------|--------|---------|---------|
| CK-1      | Control         | 28 536 597  | 8 560 979 100  | 46.34  | 97.29   | 93.28   |
| CK-2      | Control         | 24 455 378  | 7 336 613 400  | 46.41  | 97.25   | 93.24   |
| CK-3      | Control         | 24 190 275  | 7 257 082 500  | 45.87  | 97.25   | 93.29   |
| 50 mM-1   | Low alkalinity  | 26 723 132  | 8 016 939 600  | 46.56  | 97.05   | 92.95   |
| 50 mM-2   | Low alkalinity  | 36 955 318  | 11 086 595 400 | 46.42  | 97.30   | 93.33   |
| 50 mM-3   | Low alkalinity  | 29 110 742  | 8 733 222 600  | 46.33  | 97.17   | 92.98   |
| 90 mM-1   | High alkalinity | 27 146 763  | 8 144 028 900  | 46.27  | 97.03   | 92.72   |
| 90 mM-2   | High alkalinity | 26 143 882  | 7 843 164 600  | 46.83  | 97.23   | 93.19   |
| 90 mM-3   | High alkalinity | 24 850 590  | 7 455 177 000  | 46.40  | 97.33   | 93.47   |

Q20 - phred-like quality scores at Q20 level, Q30 phred-like quality scores at Q30 level.

Table 3 Suppl. The list of the 832 consistently upregulated genes in response to both high and low alkalinities. – as separate file

Table 4 Suppl. The list of the 131 consistently downregulated genes in response to both high and low alkalinities. – as separate file

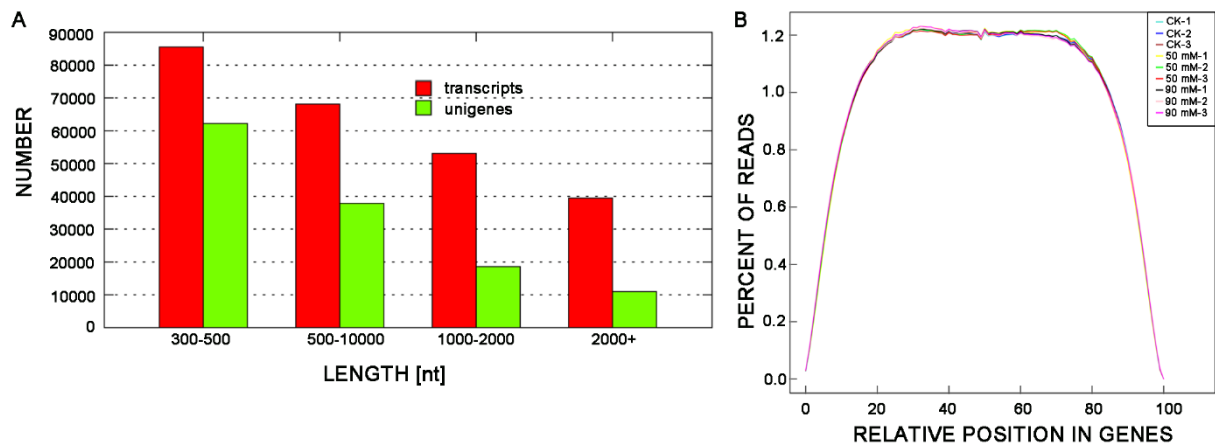


Fig. 1 Suppl. Summary and preliminary analysis of the RNA-seq data in *M. crystallinum* root. *A* - the length distribution of transcripts and unigenes. Most genes were in the length between 300 - 1000 bp. *B* - analysis and distribution of mapped reads on mRNA.

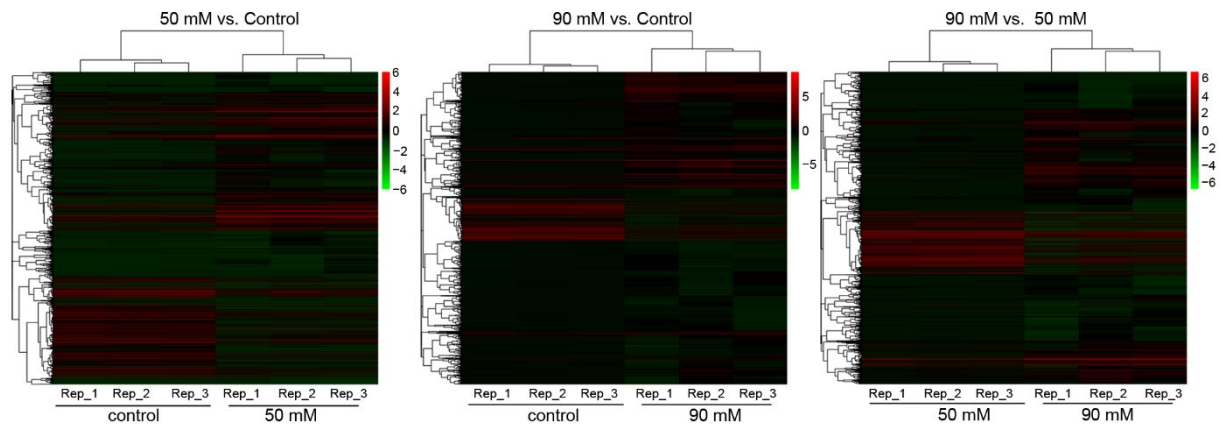


Fig. 2 Suppl. The heatmap clustering of the differentially expressed genes in *M. crystallinum* root in response to alkaline stress.

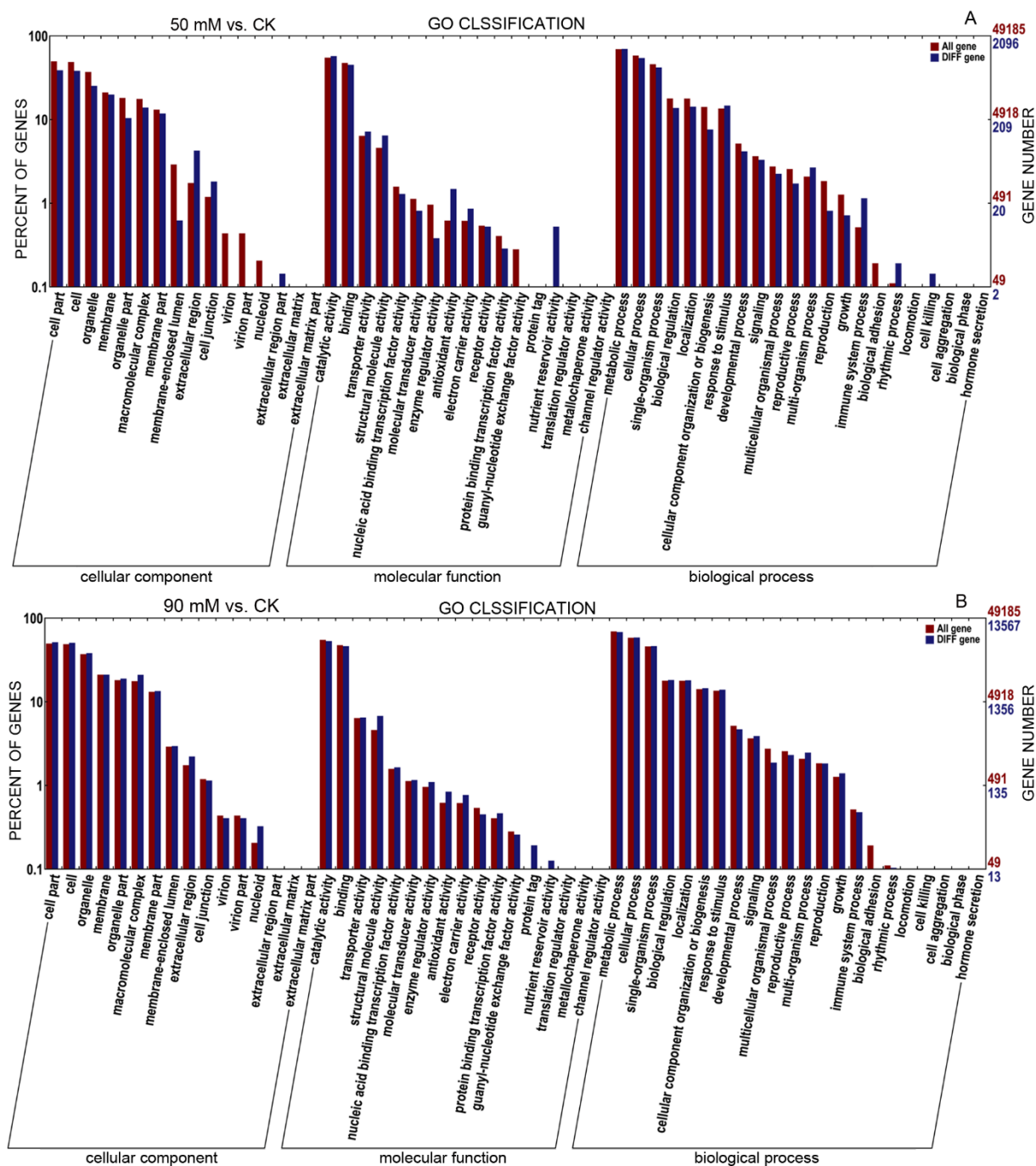


Fig. 3 Suppl. The result of the Gene Ontology enrichment analysis for the differentially expressed genes (DEGs) in *M. crystallinum* root in response to alkaline stress. *A* and *B* - the functional categories associated with the DEGs in *M. crystallinum* root in response to low (50 mM NaHCO<sub>3</sub>, pH 7.5) and high alkaline stress (90 mM NaHCO<sub>3</sub>, pH 9.5), respectively. The value above the column indicates the gene number enriched in corresponding category.

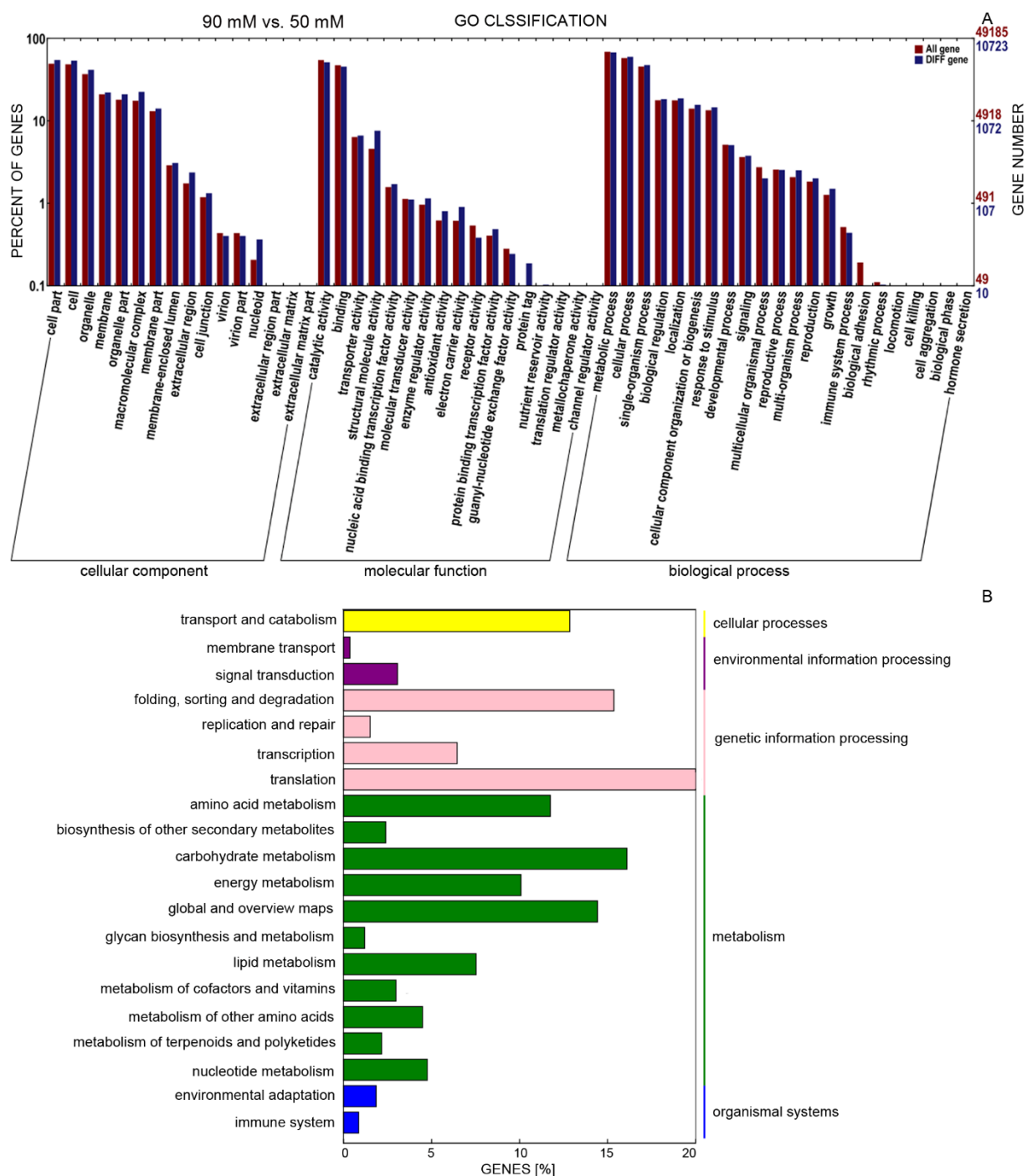


Fig. 4 Suppl. The Gene Ontology terms and pathways for the differentially expressed genes (DEGs) in *M. crystallinum* root between high (90 mM) and low (50 mM) alkalinity-stressed groups. *A* and *B* - the Gene Ontology categories and *KEGG* pathways associated with DEGs in *M. crystallinum* root between high (90 mM NaHCO<sub>3</sub>) and low (50 mM NaHCO<sub>3</sub>) alkalinity-stressed groups. The value above the column indicates the gene number enriched in corresponding category.