Supplementary Material

# Supplementary Figures and Tables

## Supplementary Figures



**Supplementary Figure1.** Go functional annotation of succinylated proteins.(A)CK22/CK0. (B) RL22/RL0.



**Supplementary Figure2.** Significant enrichment of succinylated proteins in KEGG pathways in RL22/CK22. (A) Oxidative phosphorylation pathway.(B) Nitrogen metabolism.(C) TCA cycle. (D) Ribosome.

## SupplementaryTables

**Supplementary Table 1.** Real-time PCR primers for *nif* genes.

|  |  |  |
| --- | --- | --- |
| Gene | Primer sequences | |
| Forward primer(5′–3′) | Reverse primer(5′–3′) |
| 16S rRNA | CACTGGAACTGAGACACG | CCGGTGCTTATTCTGTCG |
| *nifA* | ATCCACACCGACTCGGAAG | GCGATGAACGGCATTTCC |
| *nifH* | CATGGAAGCCGAAGACGAG | GAGATGGGGAACTCGGTG |
| *nifD* | TCCAACAAGAAGTCCCAGC | GTGGTGCCGATGTAGTAG |
| *nifK* | GCACCACCCAGGAAGAG | ATCGGGATGTTCAGCTTC |

**Supplemental Table 2.**List of identified lysine succinylated proteins and sites.

**Supplemental Table 3.**Differentially expressed statistics.

**Supplemental Table 4.**The numbers of identified modification sites.

**Supplemental Table 5.** GO and Subcellular Classify of succinylated proteins.

**Supplemental Table 6.**GO Classify of succinylated proteins in CK22/CK0.

**Supplemental Table 7.**GO Classify of succinylated proteins in RL22/RL0.

**Supplemental Table 8.**Enrichment analysis of succinylated proteins.

**Supplemental Table 9.** Protein-protein interaction network for succinylated proteins.

**Supplementary Table10.** The identified succinylated proteins related to the nitrogen fixation system.

|  |  |  |  |
| --- | --- | --- | --- |
| Modified protein | Position | Ratio | Modified sequences |
| NifD | 330 | 0.59 | KCEEVIAK(1)YKPEWEAVVAK |
| 341 | 0.65 | PEWEAVVAK(1)YRPR |
| 433 | 1.55 | FIFQK(1)MGIPFR |
| NifK | 300 | 1.75 | DAPNALSTVLLQPWQLEK(0.969)TKK |
| NifF | 3 | 1.54 | AK(1)IGLFFGSNTGK |
| 160 | 2.10 | FVGLALDLDNQSGK(1)TDER |