**Table 2.** Correlation analysis values of the experimental ***control*** group of several candidate genes involved in metabolism and stress response in tissue of *E. verrucosus* based on the R-script.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *HSP70* | *GDH* | *CS* | *Actin* | *EF* | *GAPDH* | *LDH* | *HADH* | *HK* | *OGDH* | *PK* | *NAKA* | *ATPa* | *PFK1* | *PFK2* | *COX4* | *COX2* |
| *HSP70* | 0 | 0 | 0,830 | 0 | 0,893 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *GDH* | 0 | 0 | 0,643 | 0,652 | 0 | 0,636 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *CS* | 0 | 0 | 0 | 0 | 0,609 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Actin* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,502 | 0 | 0 |
| *EF* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *GAPDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *LDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | -0,617 | 0 | 0 | 0,722 | 0 | 0 | 0,830 | 0,509 | 0 | 0 |
| *HADH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | -0,554 | 0 | 0 | 0 | -0,583 | 0 | 0 | 0 |
| *HK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,740 | 0,505 | 0 | 0 | 0,516 | 0,737 | 0,587 | 0 |
| *OGDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,623 | 0 | 0 | 0,668 | 0,702 | 0,557 | 0 |
| *PK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,846 | 0,655 | 0,504 | 0 |
| *NAKA* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *ATPa* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *PFK1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,738 | 0,584 | 0 |
| *PFK2* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,698 | 0 |
| *COX4* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,671 |
| *COX2* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Genes are set as correlated when Spearman’s p ≥ 0.5.

**Table 3.** Correlation analysis values of the experimental ***treatment*** group of several candidate genes involved in metabolism and stress response in tissue of *E. verrucosus* based on the R-script.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *HSP70* | *GDH* | *CS* | *ACTIN* | *EF* | *GAPDH* | *LDH* | *HADH* | *HK* | *OGDH* | *PK* | *NAKA* | *ATPa* | *PFK1* | *PFK2* | *COX4* | *COX2* |
| *HSP70* | 0 | 0 | 0 | 0 | 0,724 | 0 | 0 | -0,537 | 0 | 0 | 0 | 0 | 0 | 0 | 0,704 | 0 | 0 |
| *GDH* | 0 | 0 | 0,589 | 0 | 0 | 0,513 | 0 | 0 | 0 | 0 | 0 | 0 | 0,529 | 0 | 0 | 0 | 0 |
| *CS* | 0 | 0 | 0 | 0,502 | 0 | 0,764 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *ACTIN* | 0 | 0 | 0 | 0 | 0 | 0,584 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *EF* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *GAPDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *LDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,701 | 0 | 0 | 0 |
| *HADH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | -0,565 | 0 | 0,735 | 0 | 0 | -0,639 | 0 | 0 |
| *HK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *OGDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,709 | 0 | 0 |
| *PK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,649 | 0 | 0 | 0 |
| *NAKA* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | -0,522 | 0 | 0 |
| *ATPa* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *PFK1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *PFK2* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *COX4* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *COX2* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Genes are set as correlated when Spearman’s p ≥ 0.5.

**Table 4.** Correlation analysis values of the experimental ***control*** group of several candidate genes involved in metabolism and stress response in tissue of *E. cyaneus* based on the R-script.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *Actin* | *HSP70* | *CS* | *EF* | *GDH* | *ATPg* | *LDH* | *HADH* | *OGDH* | *HK* | *PFK1* | *PFK2* | *NAKA* | *ATPa* | *COX4* | *PK* |
| *Actin* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,597 | 0 | 0 | 0 | 0 | 0 |
| *HSP70* | 0 | 0 | 0,589 | 0 | 0 | 0,504 | 0 | 0,714 | 0,784 | 0 | 0 | 0 | 0,683 | 0,586 | 0,622 | 0 |
| *CS* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,575 | 0,524 | 0 | 0 | 0 | 0,707 | 0 | 0,542 | 0 |
| *EF* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *GDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *ATPg* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,761 | 0,559 | 0,594 | 0,682 | 0 | 0,518 | 0,683 | 0 | 0 |
| *LDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *HADH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,709 | 0 | 0 | 0 | 0,861 | 0,768 | 0 | 0 |
| *OGDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,617 | 0 | 0 | 0 |
| *HK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,625 | 0 | 0 | 0 | 0 | 0 |
| *PFK1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *PFK2* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *NAKA* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,806 | 0,501 | 0 |
| *ATPa* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *COX4* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *PK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Genes are set as correlated when Spearman’s p ≥ 0.5.

**Table 5.** Correlation analysis values of the experimental ***treatment*** group of several candidate genes involved in metabolism and stress response in tissue of *E. cyaneus* based on the R-script.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *Actin* | *HSP70* | *CS* | *EF* | *GDH* | *ATPg* | *LDH* | *HADH* | *OGDH* | *HK* | *PFK1* | *PFK2* | *NAKA* | *ATPa* | *COX4* | *PK* |
| *Actin* | 0 | 0,667 | 0 | 0 | 0 | 0,726 | 0 | 0 | 0,667 | 0 | 0 | 0,648 | 0 | 0 | 0,526 | 0 |
| *HSP70* | 0 | 0 | 0 | 0 | 0 | 0,709 | -0,535 | 0 | 0,883 | 0 | 0 | 0,714 | 0 | 0 | 0 | 0 |
| *CS* | 0 | 0 | 0 | 0,535 | 0 | 0 | 0,577 | 0,694 | 0 | 0 | 0 | 0 | 0,780 | 0 | 0,516 | 0 |
| *EF* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *GDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,503 | 0 |
| *ATPg* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,671 | 0,742 | 0,658 | 0,669 | 0 | 0 | 0 | 0,550 |
| *LDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | -0,595 | -0,630 | 0 | 0 | 0,593 | 0 | 0 | 0 |
| *HADH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,812 | 0,659 | 0 | 0 |
| *OGDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,552 | 0 | 0,703 | 0 | 0 | 0 | 0 |
| *HK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,668 | 0,608 | 0 | 0 | 0 | 0,711 |
| *PFK1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,647 |
| *PFK2* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *NAKA* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,638 | 0 | 0 |
| *ATPa* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *COX4* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *PK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Genes are set as correlated when Spearman’s p ≥ 0.5.

**Table 6.** Correlation analysis values of the experimental ***control*** group of several candidate genes involved in metabolism and stress response in tissue of *G. lacustris* based on the R-script.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *Actin* | *HSP70* | *EF* | *GDH* | *ATPg* | *GAPDH* | *HK* | *NAKA* | *PFK* | *CS* | *COX4* | *PK* | *HADH* | *LDH* |
| *Actin* | 0 | 0 | 0 | 0 | 0 | 0,549 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *HSP70* | 0 | 0 | 0,726 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *EF* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,584 | 0 | 0 | 0 | 0 |
| *GDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *ATPg* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,647 | 0 | 0 | 0 | 0 | 0,808 | 0,569 |
| *GAPDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,638 | 0 | 0 |
| *HK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *NAKA* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,592 | 0 |
| *PFK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *CS* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,778 | 0 | 0 | 0 |
| *COX4* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,599 | 0,652 | 0 |
| *PK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,502 | 0,623 |
| *HADH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,526 |
| *LDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Genes are set as correlated when Spearman’s p ≥ 0.5.

**Table 7.** Correlation analysis values of the experimental ***treatment*** group of several candidate genes involved in metabolism and stress response in tissue of *G. lacustris* based on the R-script.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *Actin* | *HSP70* | *EF* | *GDH* | *ATPg* | *GAPDH* | *HK* | *NAKA* | *PFK* | *CS* | *COX4* | *PK* | *HADH* | *LDH* |
| *Actin* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *HSP70* | 0 | 0 | 0,685 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *EF* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,545 | 0,577 | 0 | 0 | 0 |
| *GDH* | 0 | 0 | 0 | 0 | 0 | 0,689 | 0 | 0 | 0 | 0,549 | 0,610 | 0,685 | 0 | 0 |
| *ATPg* | 0 | 0 | 0 | 0 | 0 | 0,528 | 0 | 0 | 0,537 | 0 | 0,512 | 0,595 | 0,731 | 0,712 |
| *GAPDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,658 | 0,829 | 0 | 0 |
| *HK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *NAKA* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,669 | 0 |
| *PFK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,576 | 0 |
| *CS* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,687 | 0 | 0 | 0 |
| *COX4* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,729 | 0 | 0 |
| *PK* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,588 | 0,578 |
| *HADH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,659 |
| *LDH* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Genes are set as correlated when Spearman’s p ≥ 0.5.