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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table 1:** A summary of select categories taken from the visualization of enriched GO terms created by the ‘rrvgo’ package across all 9 maSigPro clusters of genes significantly affected by the hypoxia time course. | | | | | | | | | |
| **Broad GO Term Processes** | **Clusters enriched for term** | | | | | | | | |
| **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** |
| **Immune response** | **X** |  |  | **X** | **X** | **X** |  |  |  |
| **Hormone, steroid, or estrogen regulation** | **X** |  |  | **X** | **X** |  |  | **X** |  |
| **Oxidative stress response** | **X** |  |  |  |  |  |  | **X** |  |
| **Cell detoxification or nitrogen-compound metabolism** |  |  | **X** |  |  | **X** |  | **X** | **X** |
| **Glucose homeostasis, glycolysis, and related pathways\*** | **X** | **X** | **X** | **X** | **X** |  |  | **X** | **X** |
| **Mitochondrial-specific targeting and OXPHOS** | **X** |  |  |  | **X** | **X** |  |  |  |
| **Apoptosis** | **X** | **X** |  | **X** |  | **X** |  |  |  |
| **DNA damage repair** |  | **X** |  |  |  | **X** |  |  |  |
| **Unfolded protein response** | **X** |  |  | **X** |  | **X** |  | **X** | **X** |
| **Response to external stimuli or stress** | **X** | **X** |  | **X** |  | **X** | **X** |  |  |
| **Heat or cold response** | **X** |  |  |  |  |  |  | **X** |  |
| **Nervous system regulation and retinal response** | **X** | **X** |  | **X** | **X** |  | **X** | **X** |  |
| **Circadian rhythm or clock regulation** | **X** |  |  |  |  |  |  |  |  |
| **Pigment storage** |  |  |  |  |  |  |  |  | **X** |
| **Regulation of sperm or egg development** | **X** |  |  |  |  |  |  | **X** |  |
| **Iron ion, calcium ion, or other metabolite homeostasis** | **X** | **X** |  | **X** | **X** | **X** |  |  |  |
| **Lipid or fatty-acid homeostasis** | **X** | **X** |  | **X** |  | **X** | **X** | **X** | **X** |
| **BMP signaling pathway** |  |  |  |  | **X** |  |  |  |  |
| **\*Includes fructose, pentose-phosphate, sucrose and carbohydrate, TCA, and pyruvate pathways** | | | | | | | | | |

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| --- | --- | --- | --- |
| **Table 2**: Total number of *T. californicus* genes curated under biological functions of interest. | | | |
| **Function or pathway** | **Total** | **# Significant (maSigPro)** | **Clusters** |
| Glycolysis | 58 genes | 15 genes | 2, 3, 4, 5, 6, 7, 8 |
| Fructose and mannose metabolism | 22 genes | 7 genes | 2, 4, 6, 8, 9 |
| Starch and sucrose metabolism | 54 genes | 20 genes | 2, 3, 8 |
| Pentose phosphate pathway | 22 genes | 8 genes | 1, 2, 3, 6, 8 |
| Pyruvate metabolism | 40 genes | 9 genes | 1, 2, 3, 5, 6, 7, 8 |
| TCA cycle | 26 genes | 2 genes | 1, 2 |
| Response to oxygen (GO Term) | 1022 genes | 108 genes | 1, 2, 3, 4, 5, 6, 7, 8, 9 |
| Antioxidants | 44 genes | 12 genes | 1, 2, 3, 4, 5, 6, 7, 8 |
| Mitochondria-targeted | 613 genes | 47 genes | 1, 2, 3, 4, 5, 6, 7, 8 |
| Carotenoid and pigment genes | 26 genes | 10 genes | 1, 2, 6, 7, 8 |
| Chitin, cuticle, and exoskeleton | 224 genes | 52 genes | 1, 2, 3, 4, 5, 6, 7, 8 |
| The totals for glycolysis and related pathways (fructose, starch/sucrose, pentose phosphate, pyruvate, and TCA) also include genes that are known to be present in two or more of these pathways. Likewise, there is probable overlap in the genes in the antioxidant, mitochondria targeted, response to oxygen, and carotenoid pathways. | | | |