**Table S3**. Enriched functions in *C. baileyi* N-rich proteins.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **molecular function** | |  |  |  |  |  |  |  | |
| ID | Name | Bgd count | Result count | % of bgd | Fold enrichment | Odds ratio | Benjamini\* | Bonferroni |
| GO:0003700 | transcription factor activity, sequence-specific DNA binding | 15 | 3 | 20 | 15.06 | 17.07 | *0.005681* | *0.011363* |
| GO:0001071 | nucleic acid binding transcription factor activity | 15 | 3 | 20 | 15.06 | 17.07 | *0.005681* | *0.011363* |
| GO:0070566 | adenylyltransferase activity | 1 | 1 | 100 | 75.29 | 78.52 | *0.029772* | 0.208404 |
| GO:1901682 | sulfur compound transmembrane transporter activity | 1 | 1 | 100 | 75.29 | 78.52 | *0.029772* | 0.208404 |
| GO:0004652 | polynucleotide adenylyltransferase activity | 1 | 1 | 100 | 75.29 | 78.52 | *0.029772* | 0.208404 |
| GO:0015116 | sulfate transmembrane transporter activity | 1 | 1 | 100 | 75.29 | 78.52 | *0.029772* | 0.208404 |
| GO:0015103 | inorganic anion transmembrane transporter activity | 1 | 1 | 100 | 75.29 | 78.52 | *0.029772* | 0.208404 |
| GO:0001671 | ATPase activator activity | 2 | 1 | 50 | 37.65 | 39.24 | *0.038831* | 0.310644 |
|  |  |  |  |  |  |  |  |  |
| **cellular function** | |  |  |  |  |  |  |  | |
| ID | Name | Bgd count | Result count | % of bgd | Fold enrichment | Odds ratio | Benjamini | Bonferroni |
| GO:1903506 | regulation of nucleic acid-templated transcription | 34 | 3 | 8.8 | 6.64 | 7.45 | *0.024575* | 0.218151 |
| GO:0051252 | regulation of RNA metabolic process | 34 | 3 | 8.8 | 6.64 | 7.45 | *0.024575* | 0.218151 |
| GO:2001141 | regulation of RNA biosynthetic process | 34 | 3 | 8.8 | 6.64 | 7.45 | *0.024575* | 0.218151 |
| GO:0006355 | regulation of transcription, DNA-templated | 34 | 3 | 8.8 | 6.64 | 7.45 | *0.024575* | 0.218151 |
| GO:0010468 | regulation of gene expression | 35 | 3 | 8.6 | 6.45 | 7.23 | *0.024575* | 0.234821 |
| GO:0019219 | regulation of nucleobase-containing compound metabol proc | 36 | 3 | 8.3 | 6.27 | 7.03 | *0.024575* | 0.252211 |
| GO:0051171 | regulation of nitrogen compound metabolic process | 37 | 3 | 8.1 | 6.1 | 6.83 | *0.024575* | 0.270327 |
| GO:0010556 | regulation of macromolecule biosynthetic process | 37 | 3 | 8.1 | 6.1 | 6.83 | *0.024575* | 0.270327 |
| GO:0031326 | regulation of cellular biosynthetic process | 37 | 3 | 8.1 | 6.1 | 6.83 | *0.024575* | 0.270327 |
| GO:0009889 | regulation of biosynthetic process | 37 | 3 | 8.1 | 6.1 | 6.83 | *0.024575* | 0.270327 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 37 | 3 | 8.1 | 6.1 | 6.83 | *0.024575* | 0.270327 |
| GO:0031323 | regulation of cellular metabolic process | 43 | 3 | 7 | 5.25 | 5.86 | *0.027498* | 0.394474 |
| GO:0060255 | regulation of macromolecule metabolic process | 46 | 3 | 6.5 | 4.91 | 5.47 | *0.027498* | 0.466606 |
| GO:0080090 | regulation of primary metabolic process | 46 | 3 | 6.5 | 4.91 | 5.47 | *0.027498* | 0.466606 |
| GO:0019222 | regulation of metabolic process | 47 | 3 | 6.4 | 4.81 | 5.35 | *0.027498* | 0.492149 |
| GO:0072348 | sulfur compound transport | 1 | 1 | 100 | 75.29 | 78.52 | *0.027498* | 0.494958 |
| GO:0015698 | inorganic anion transport | 1 | 1 | 100 | 75.29 | 78.52 | *0.027498* | 0.494958 |
| GO:0008272 | sulfate transport | 1 | 1 | 100 | 75.29 | 78.52 | *0.027498* | 0.494958 |
| GO:0043631 | RNA polyadenylation | 2 | 1 | 50 | 37.65 | 39.24 | *0.038831* | 0.73778 |

\* Significant values are italicized.