|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Method for transcriptome assembly  | #transcripts | # of Open reading frames (ORFs) | % of Open reading frames (ORFs) | N50 | Shortest transcript | Longesttranscript | % of sequences that aligned  |
| *De novo* only with trinity | 874,457 | 57,557 | 6.5 | 804 | 224 | 29,623 | Not applicable |
| Weddell seal genome guided and *de novo with* trinity  | 1,383,525 | 67,643 | 4.9 | 1,135 | 224 | 27,818 | 76.51% |
| Weddell seal transcriptome guided and *de novo* with trinity | 32,856 | 21,646 | 65.9 | 1,994 | 224 | 54,385 | 27.43% |