**Table S1: Statistics for the completeness of the *R. proliferus* genome based on 248 CEGs**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | #Prots | %Completeness | - | #Total | Average | %Ortho |
|  | **Complete** | 234 | 94.35 | - | 370 | 1.58 | 38.46 |
|  |  |  |  |  |  |  |  |
| Group | 1 | 59 | 89.39 | - | 91 | 1.58 | 37.29 |
| Group | 2 | 53 | 94.64 | - | 79 | 1.49 | 30.19 |
| Group | 3 | 59 | 96.72 | - | 98 | 1.66 | 44.07 |
| Group | 4 | 63 | 96.92 | - | 102 | 1.62 | 41.27 |
|  |  |  |  |  |  |  |  |
|  | **Partial** | 238 | 95.97 | - | 407 | 1.71 | 43.28 |
|  |  |  |  |  |  |  |  |
| Group | 1 | 61 | 92.42 | - | 102 | 1.67 | 40.98 |
| Group | 2 | 54 | 96.43 | - | 85 | 1.57 | 35.19 |
| Group | 3 | 59 | 96.72 | - | 109 | 1.85 | 49.15 |
| Group | 4 | 64 | 98.46 | - | 111 | 1.73 | 46.88 |

* **Key:**

# Prots = number of 248 ultra-conserved CEGs present in genome

# %Completeness = percentage of 248 ultra-conserved CEGs present

# Total = total number of CEGs present including putative orthologs

# Average = average number of orthologs per CEG

# %Ortho = percentage of detected CEGS that have more than 1 ortholog