

# Temperature-dependent Transcriptome Analysis of the Arctic *Chlamydomonas* sp.

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*Chlamydomonas* sp. is widely present in the Earth's aquatic ecosystem and is worth as a model species based on environmental factors related to environmental stresses. As a part of a study on the environmental adaptation mechanisms that exist in polar *Chlamydomonas*, we selected an Arctic *Chlamydomonas* sp. strain from the KOPRI culture collection of polar microorganisms (KCCPM, KNF0024), which had been isolated from ice-covered freshwater from the Arctic. This strain shows psychrophilic growth. To explore its adaptation strategy in freezing environments and identify the genes related cold acclimation, we investigated its temperature-dependent transcriptome changes. Uni-gene sets of this strain were established through *de-novo* assembly. The assembled contigs were annotated and functionally classified according to the biological functions. We examined the candidate target genes whose expression differs in accordance with the temperature, clustered them by expression patterns. In addition, we compared the temperature-dependent transcriptome response between this Arctic *Chlamydomonas* sp. with those of *Chlamydomonas reinhardtii*, a mesophilic species. This dataset would be a valuable resource to understand the molecular mechanism behind *Chlamydomonas*' adaptation under extreme and changing environment.

## Characteristics of Arctic *Chlamydomonas* sp.

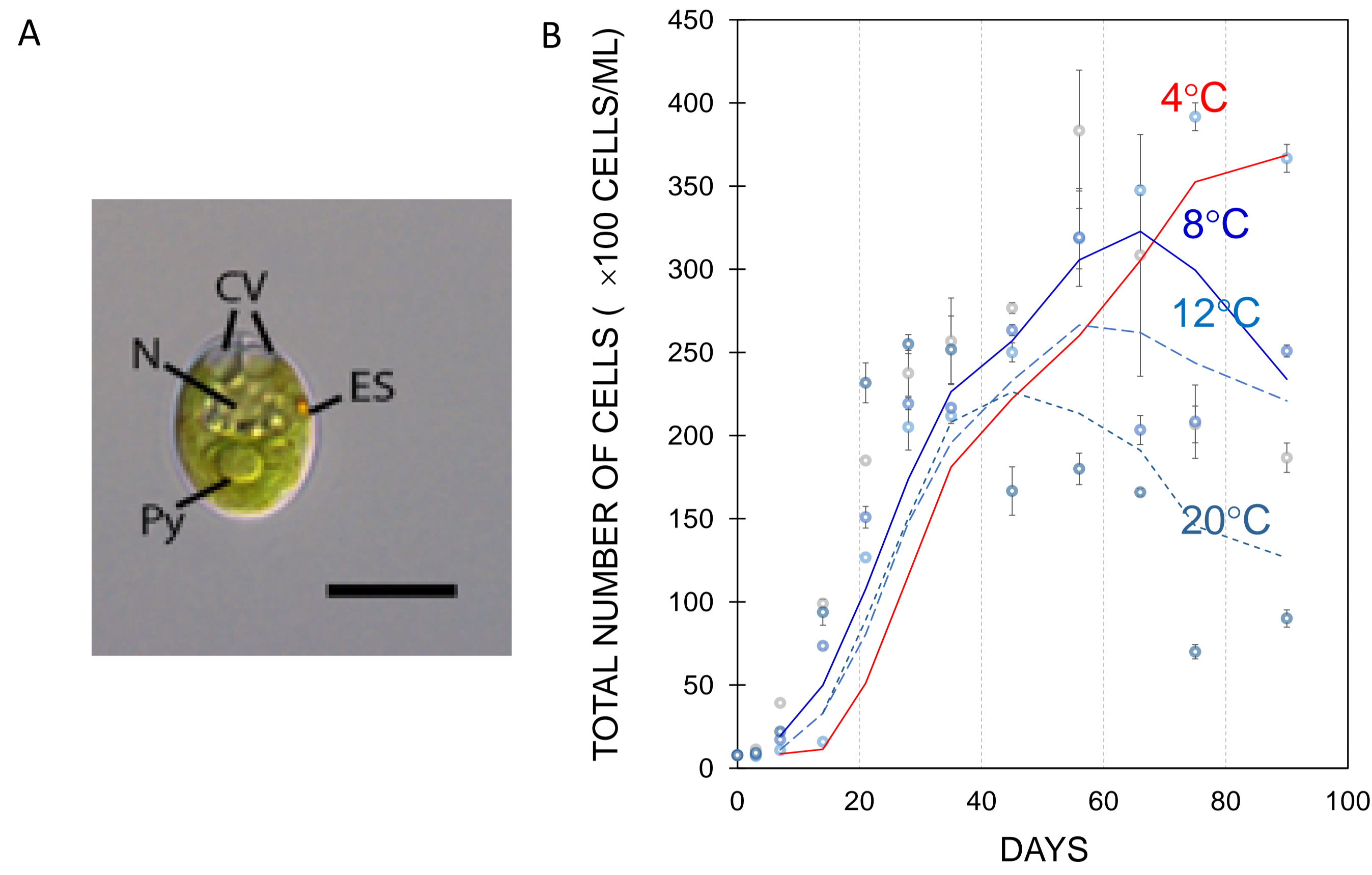


Figure. Cell morphology (A) and growth pattern of KNF24 with temperature (B), A: Cp = chloroplast, CV = contractile vacuole, ES = eyespot, F = flagellum, Py = pyrenoid, S = starch. Scale bars = 10µm

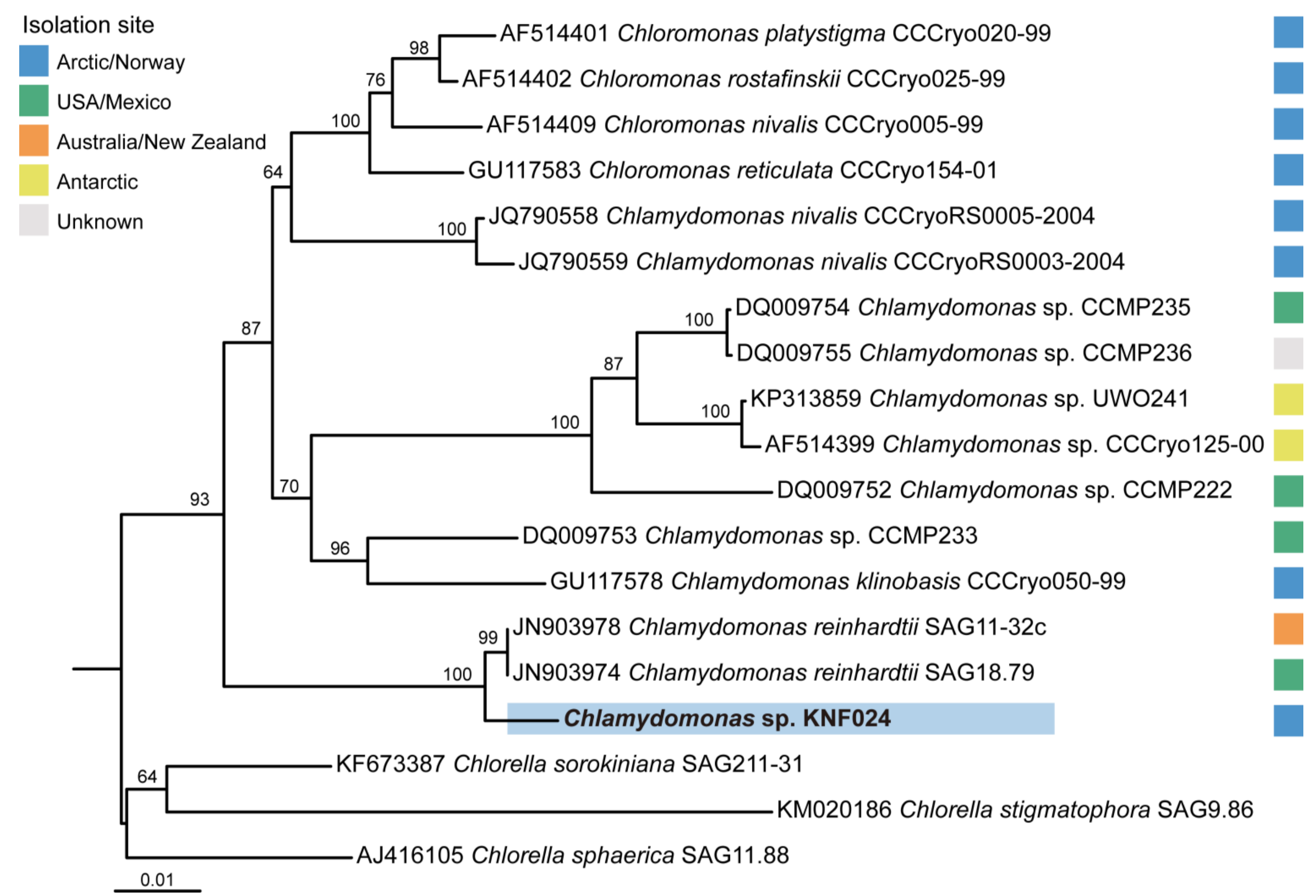
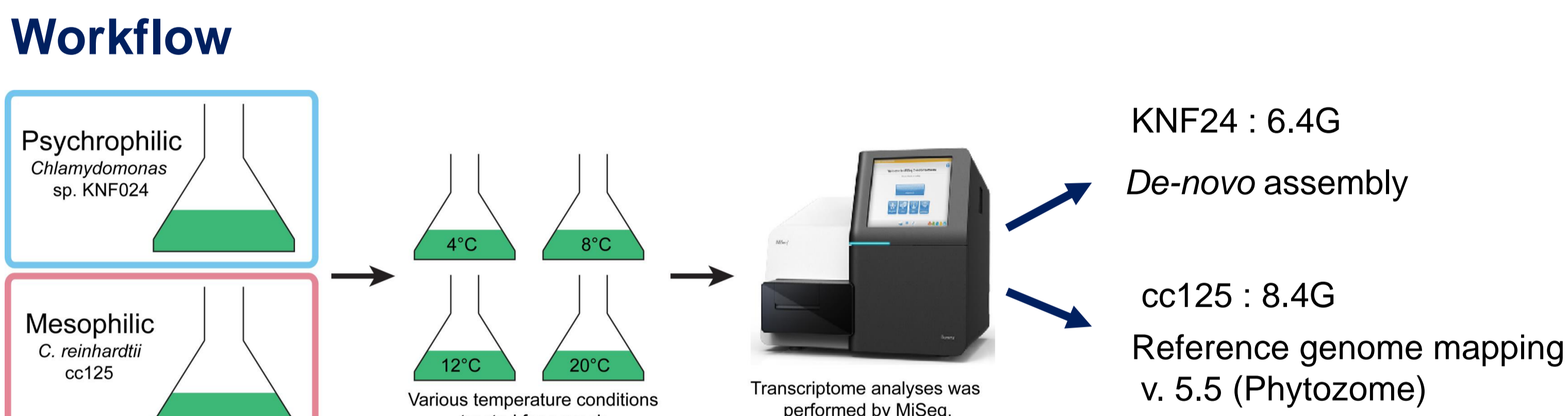
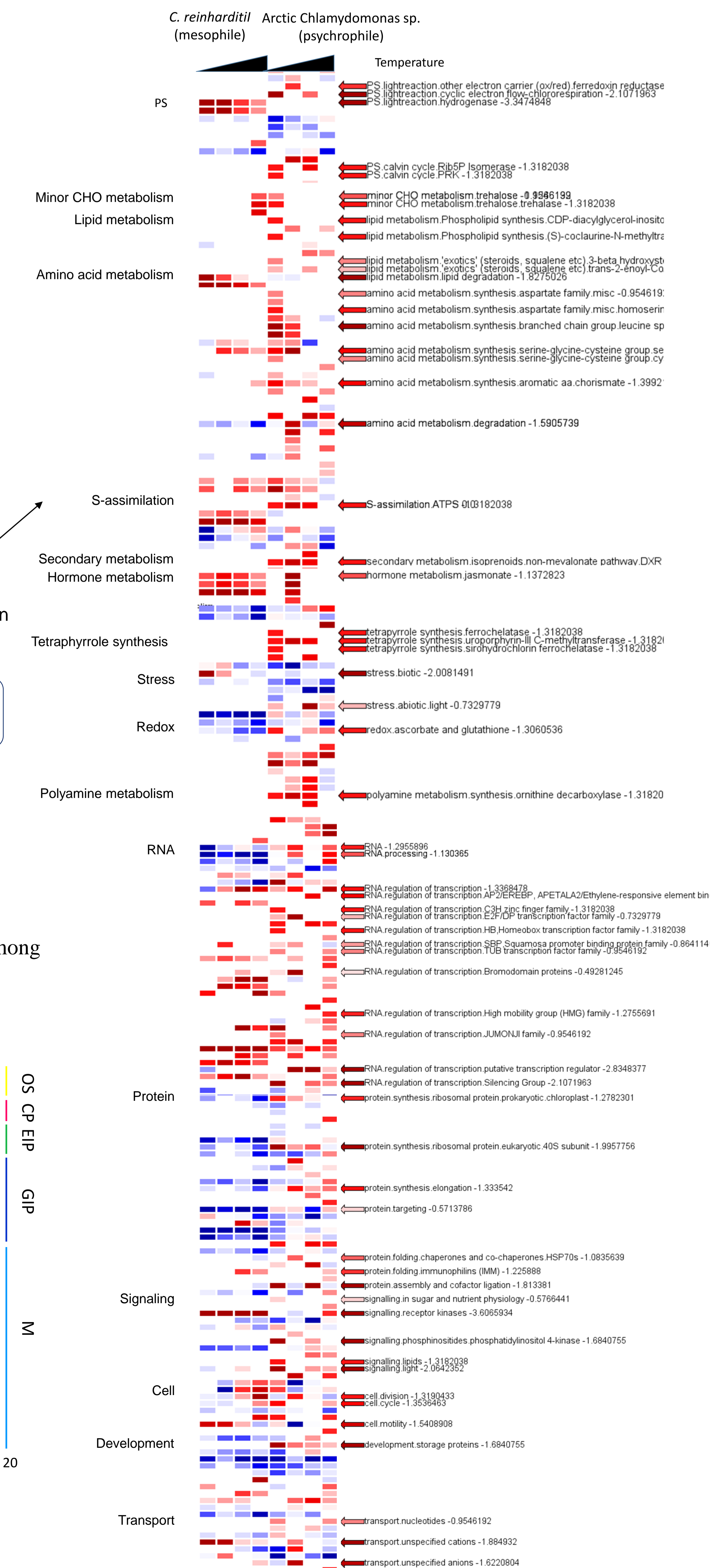


Figure. Neighbor-Joining tree of *Chlamydomonas* sp. KNF024 and closely related genus *Chloromonas* (Chlorophyceae) inferred from 18S rRNA sequences (1190 nt, 19 taxa). Numbers above branches indicated NJ bootstrap value (>50%). The genus *Chlororella* (Trebouxiophyceae) served as outgroup taxa. Color boxes indicates isolation site of each strain.

## RNA-seq analysis to study temperature response of arctic *Chlamydomonas* sp.



## Comparison of transcriptome dynamics between mesophilic *C.reinhardtii* and the arctic *Chlamydomonas* sp.



## Characterization of arctic *Chlamydomonas* sp. transcriptome

Table. *De novo* assembly and annotation of KNF24 transcriptome

Sequencing output from KNF24 libraries			
Assembly		Blast	
#Unigenes	55,894	Blast2GO	
Ave	1,376	Without Blast Hits	30,313 54.20%
N75	392	Blast Results only	25,581 45.80%
N50	751	Mapping Results only	19,784 35.40%
N25	1,663	Annotated Sequences	13,216 23.60%
Minimum	95	UniProt result	16,321 29.20%
Maximum	13,916	Total Sequences	55,894 100%

### Expression comparison of gene pairs included in orthologs clusters

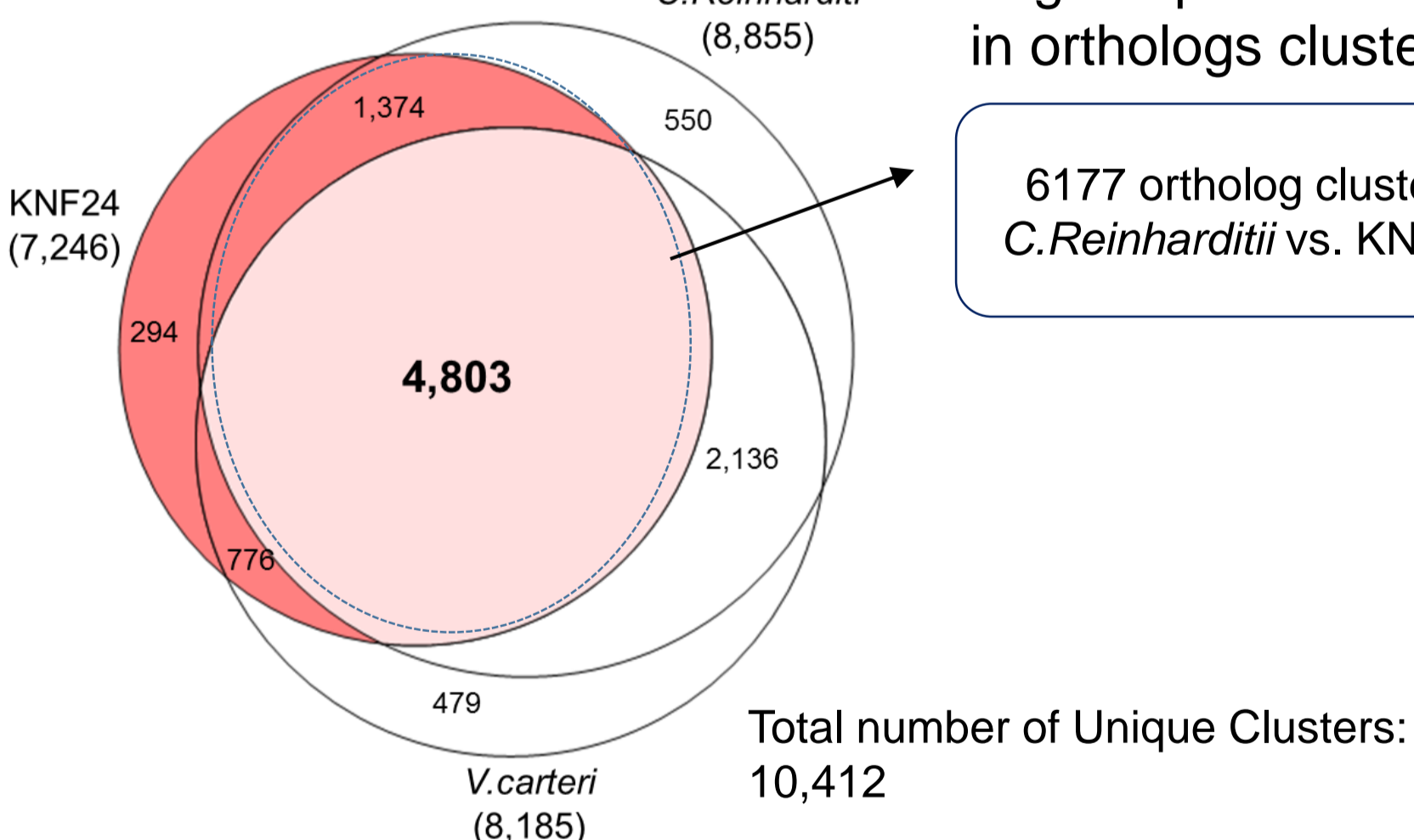


Figure. Top hit species distribution of assembled contigs with blast results (A) and clustering of orthologs among *C.reinhardtii*, *Volvox carteri* and the arctic *Chlamydomonas* sp. (KNF24) (by Orthomcl analysis).

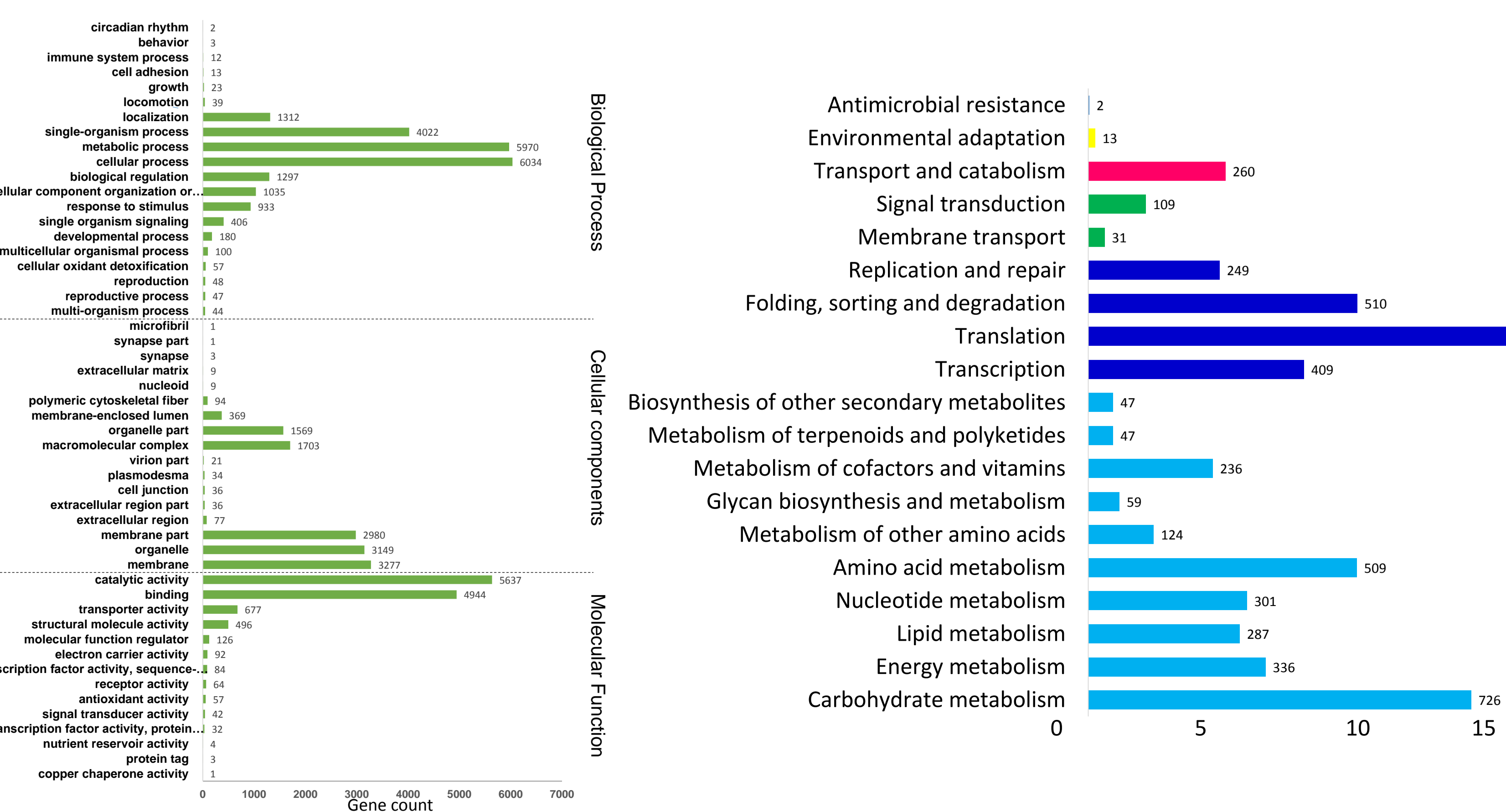


Figure. Functional classification of annotated unigenes of the Arctic *Chlamydomonas* sp. (KNF24) Left: Gene Ontology, Right: KEGG orthologs