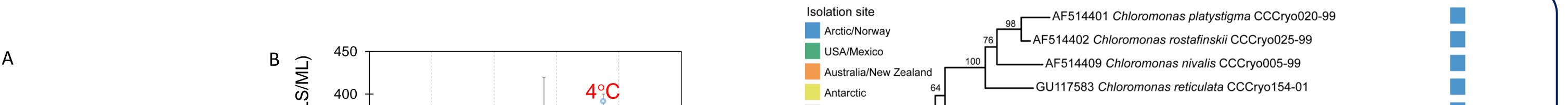
Temperature-dependent Transcriptome Analysis of the Arctic Chlamydomonas sp.

Jungeun Lee^{*}, Sanghee Kim, Sung mi Cho, Hyun Park Korea Polar Research Institute, Incheon, Korea, (jelee@kopri.re.kr)



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 Artic 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.





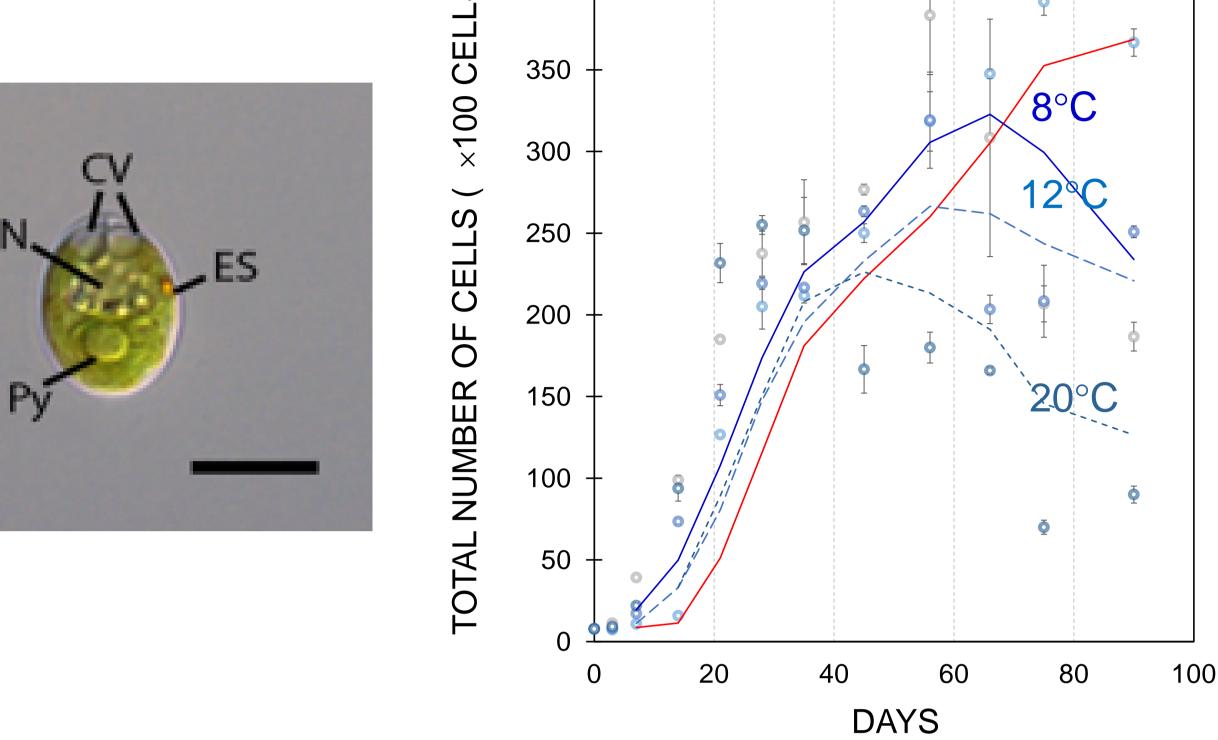


Figure. Cell morphology (A) and growth pattern of KNF24 with temperature (B), A: Cp = chloroplast, CV = contractile vacuole, ES = eyespot, F = flagellum, Py = pyrenoid, S = starch. Scale bars = 10 μ m

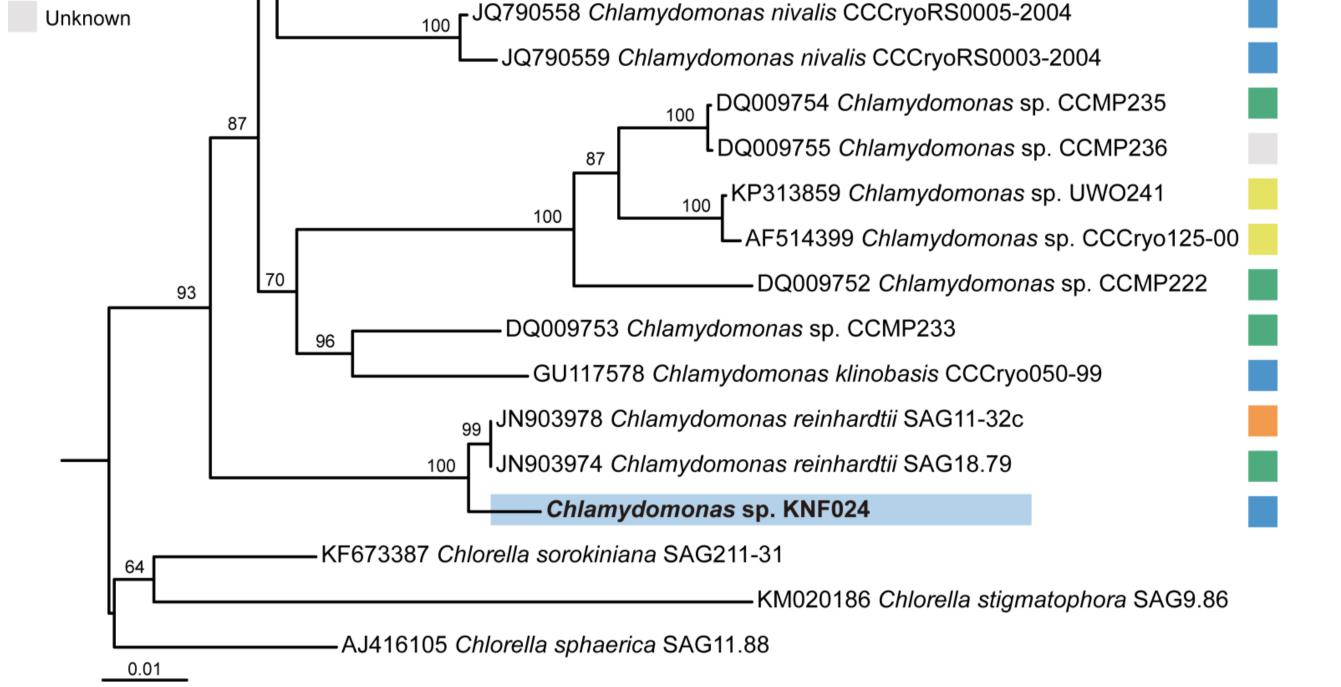
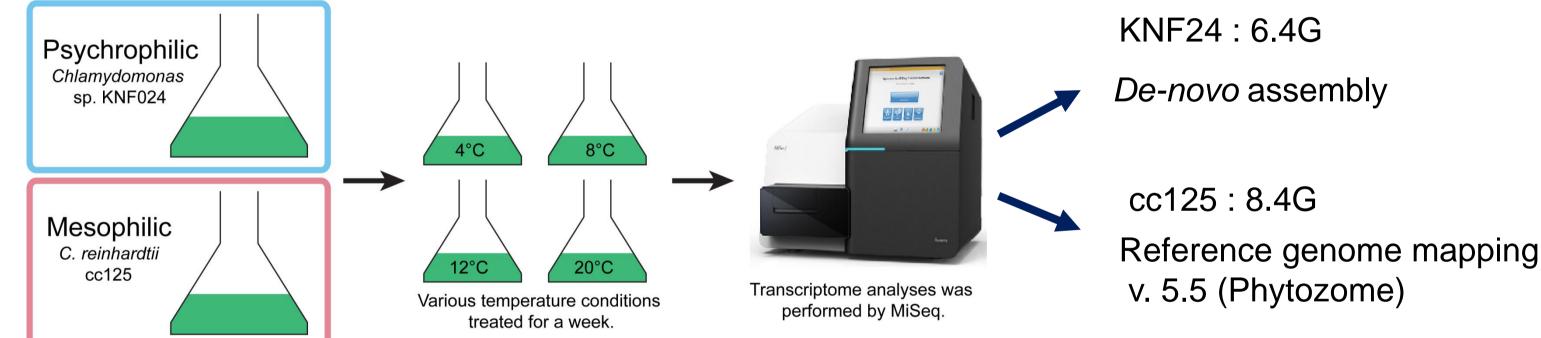
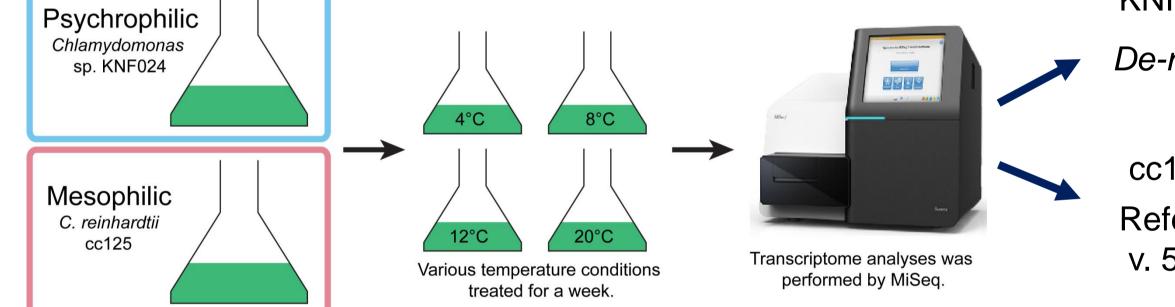


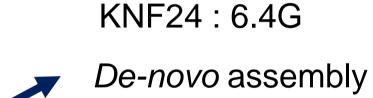
Figure. Neighbor-Joining tree of *Chlamydomonas* sp. KNF024 and closely related genus Chloromonas (Chlorophyceae) inferred from 18S rRNA sequences (1190 nt, 19 taxa). Numbers above branches indicated NJ bootstrap value (>50%). The genus *Chlororella* (Trebouxiophyceae) served as outgroup taxa. Color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

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

Workflow







C.Reinharditi

(8,855)

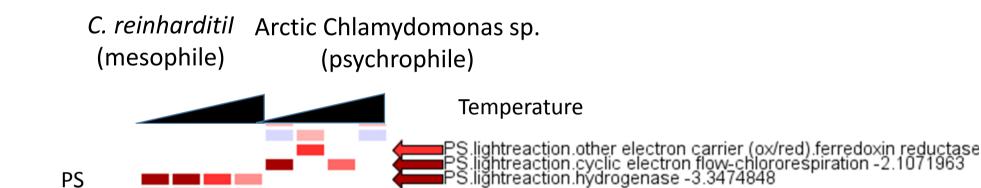
2,136

550

1.374

4,803

Comparison of transcriptome dynamics between mesophilic C.reinharditii and the arctic Chlamydomonas sp.



Characterization of arctic Chlamydomonas sp. transcriptome

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

Acanthamoeba castellanii

Volvox carteri f nagariensis

Green alga)

32%

Gene count

others

Chlamydomonas reinhardtii

(Green alga)

46%

(Amoebae).

Exophiala dermatitidis (Black yeast)

1%

Cladophialophora carrionii

(Black fungus)

1%

Monosiga brevicollis (Choanoflagellate)

Salpingoeca rosetta

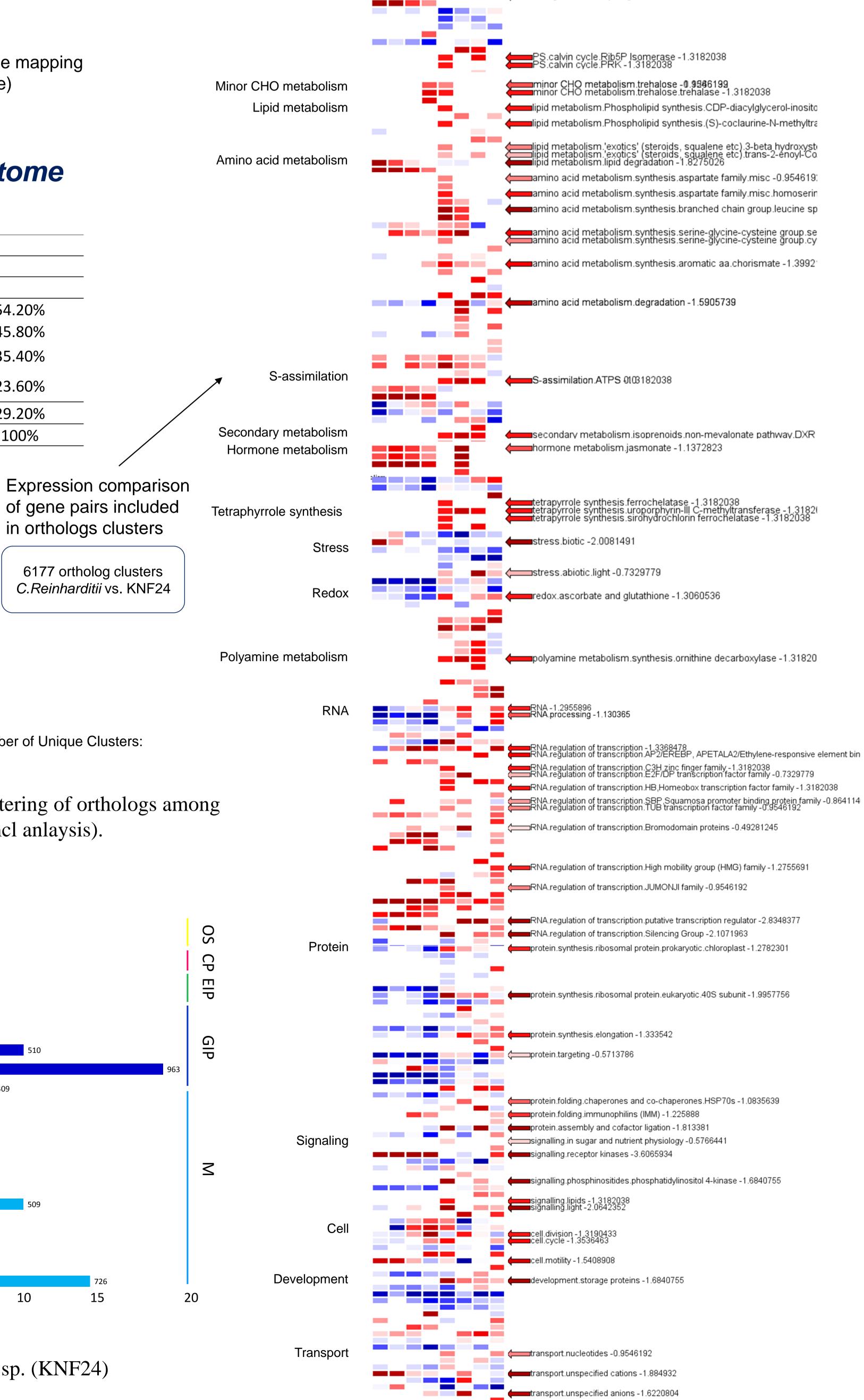
(Choanoflagellate)

Chlorella variabilis

(Green alga)

circadian rhythm

Sequencing output	It from KNF24 I	ibraries		
Assembly		Blast		
#Unigenes	55 <i>,</i> 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 <i>,</i> 894	100%





KNF24

(7,246)

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

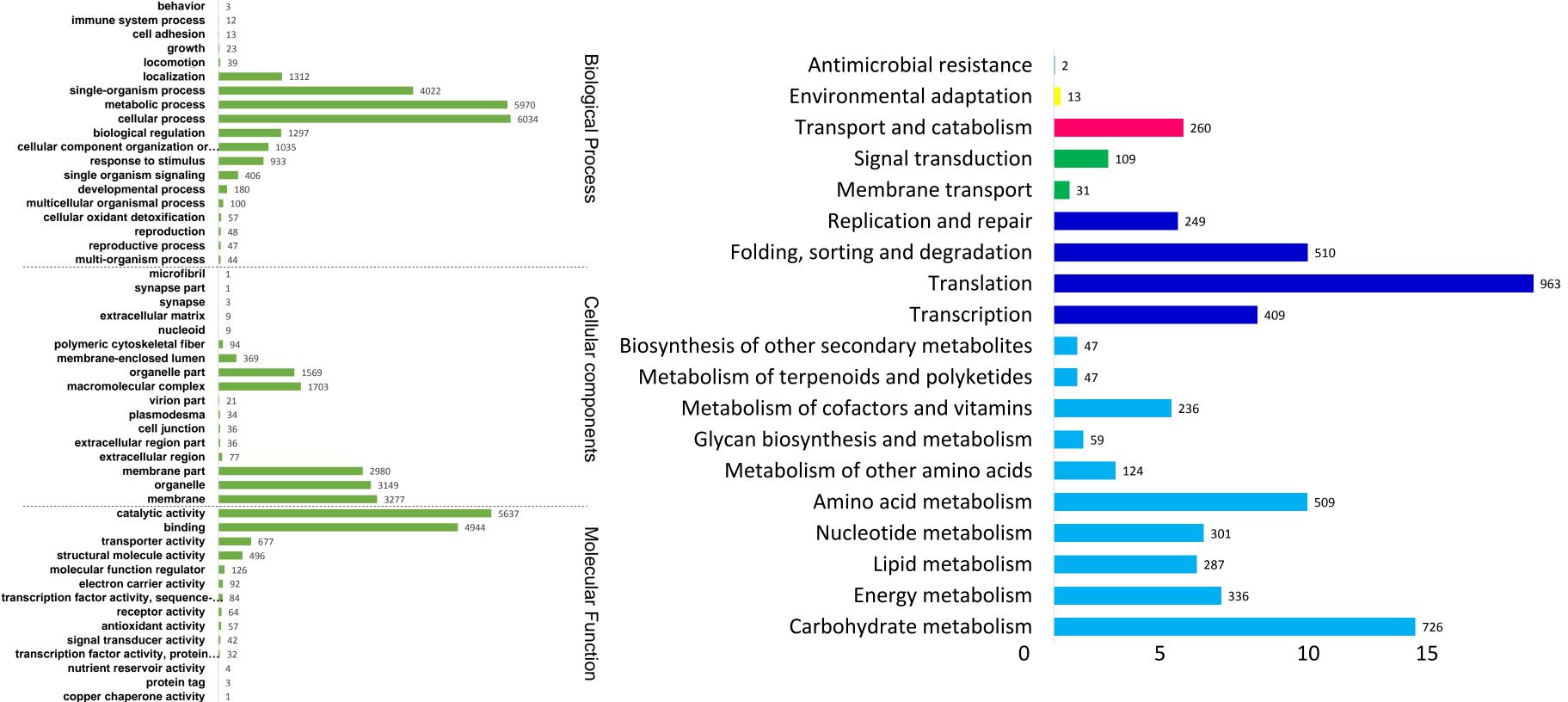


Figure. Functional classification of annotated unigenes of the Arctic *Chlamydomonas* sp. (KNF24) Left: Gene Ontology, Right: KEGG orthologs