Genome of Antarctic-endemic Copepod and Evolutionary Adaptation to Extreme Environments

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Abstract

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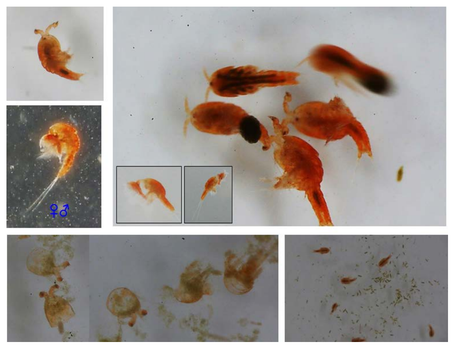

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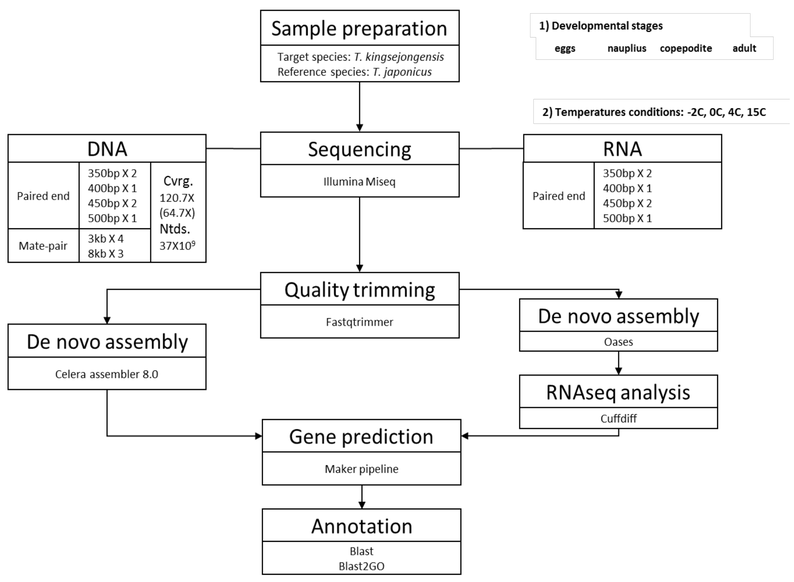

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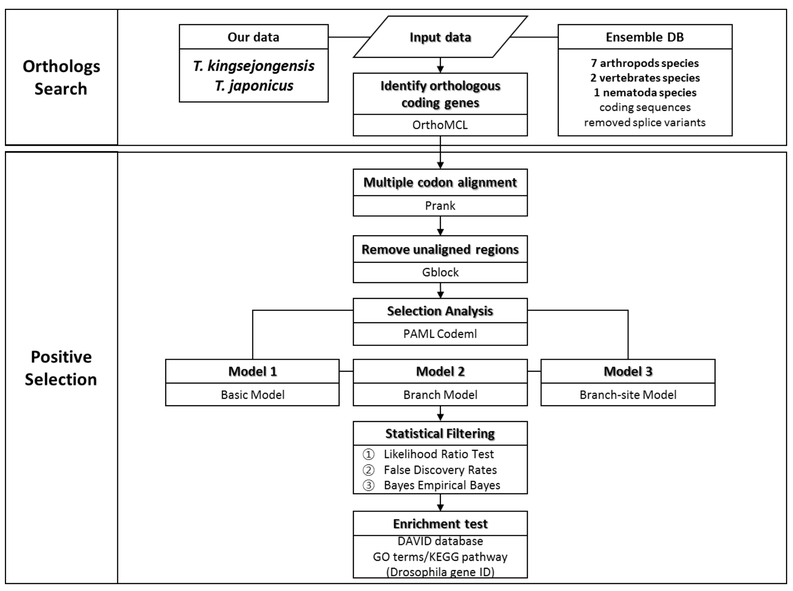

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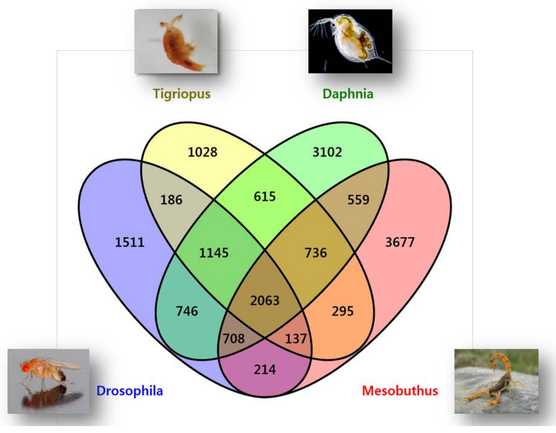

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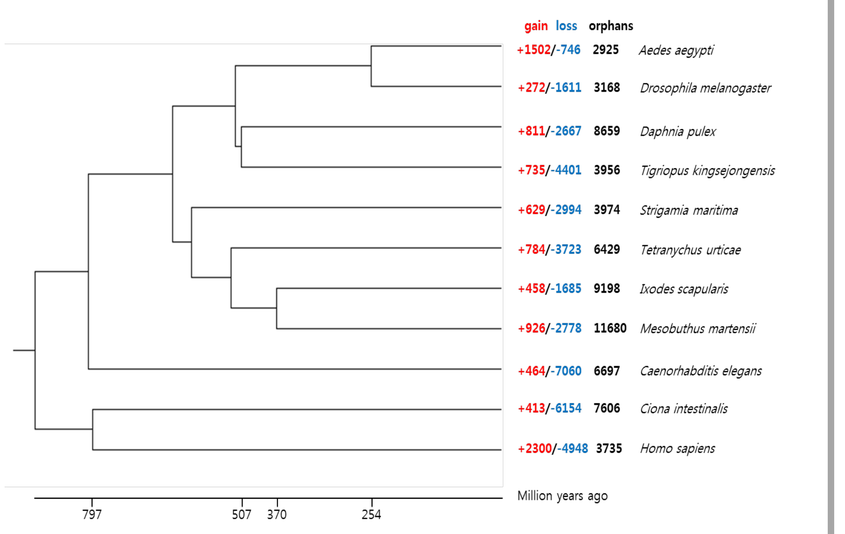

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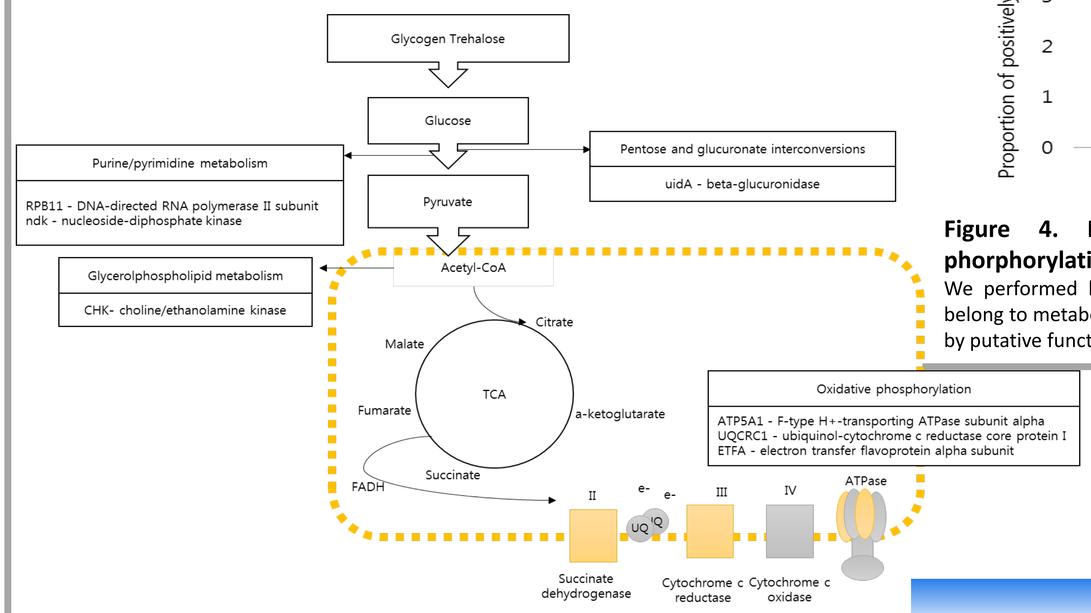

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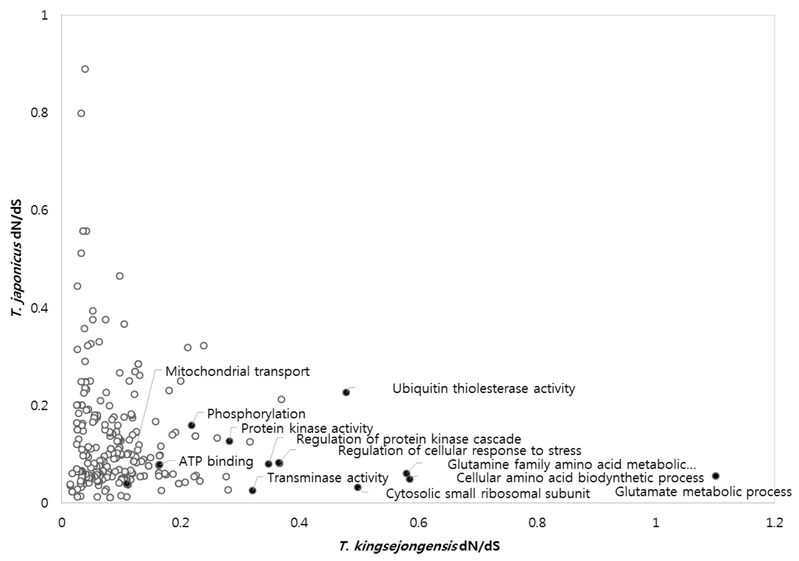

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3. Positively Selected Genes

Table 1. Enriched GO categories identified by PSGs from the *T. kingsejongensis*.

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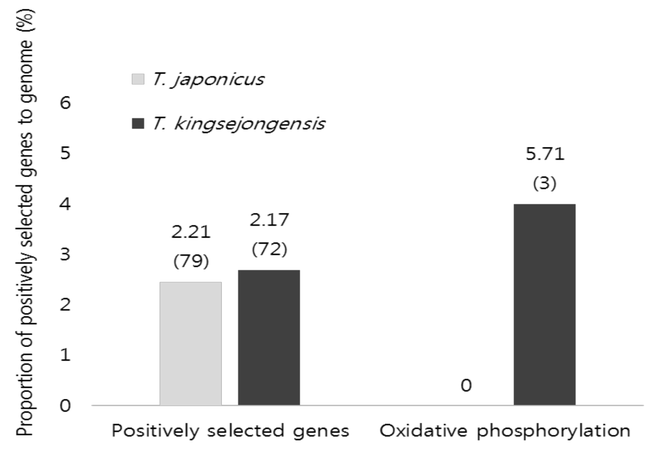

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Positively Selected Genes Involved in Metabolic Pathways

ATP synthase have a catalytic core composed of two catalytic domains alpha (ATP5A) and beta (ATP5B) subunits and these undergo a subsequent conformational changes and form ATP from ADP. Generally, mtDNA- and nuclear- encoded mitochondrial genes especially enzymes from the OxPhos pathway are highly conserved even between the distantly related species [1,2]. In that respect, mutations in mitochondrial genes are known to be lead to variety of negative effects including increased oxidative stress, reduction in body mass and survival, metabolic disorders [3]. However, polymorphism of ATP5A reported in ovenbirds is result in higher individual fitness leading by increased body mass [4] implying possible role in environmental adaptations. Additionally, UQCRC1 polymorphism in human is significantly associated with body lipid accumulation [5] and ETF polymorphism also discovered in human altered resistance to thermal stability of enzyme activity [6]. As *T. kingsejongenesis* face extreme conditions, especially constant low temperatures and seasonal food scarcity similar with other Antarctic invertebrates, efficient energy production, adequate energy sources to save and cold tolerance mechanisms is important for organisms living in high altitude. Additionally, we found four PSGs belong in metabolic pathways: nucleotide, lipid, and carbohydrate metabolic pathways.

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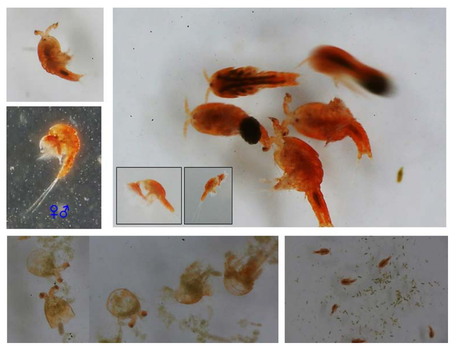

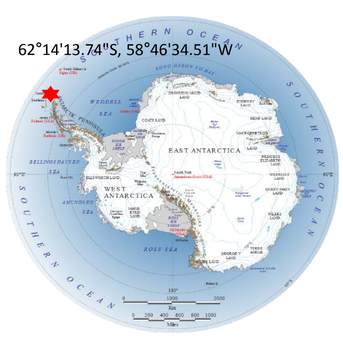

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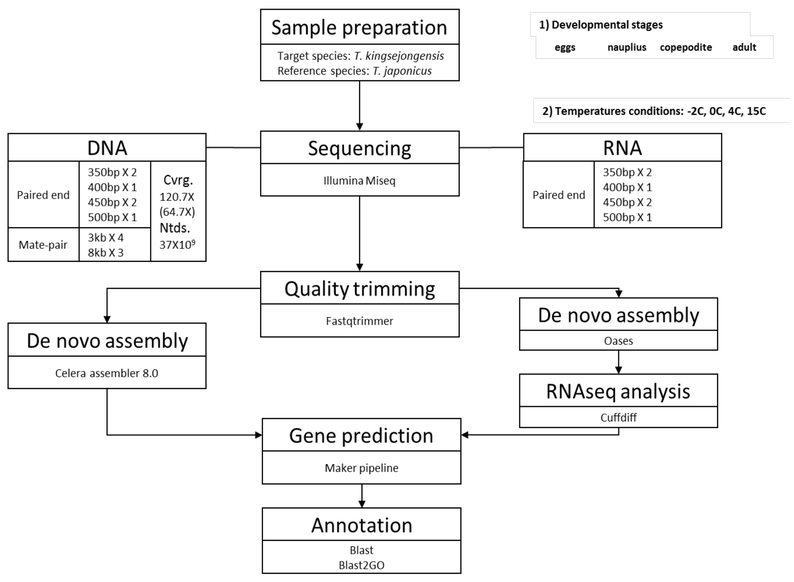

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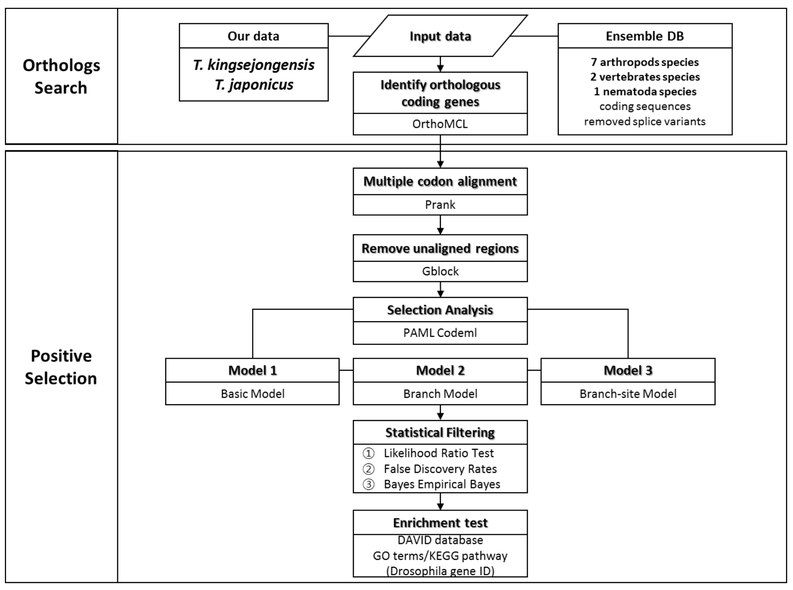

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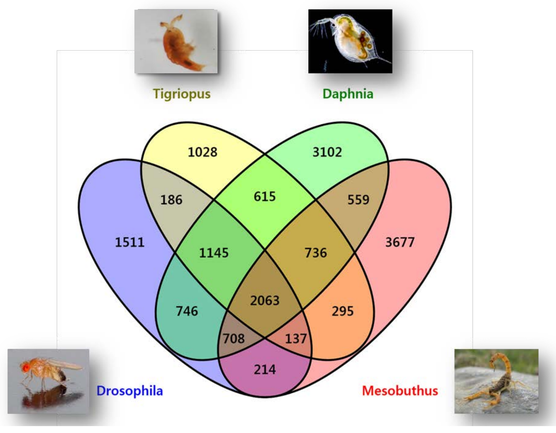

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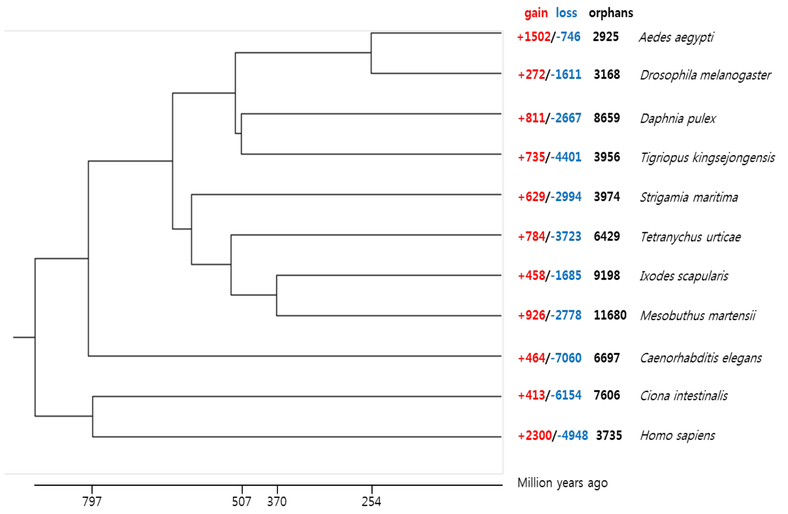

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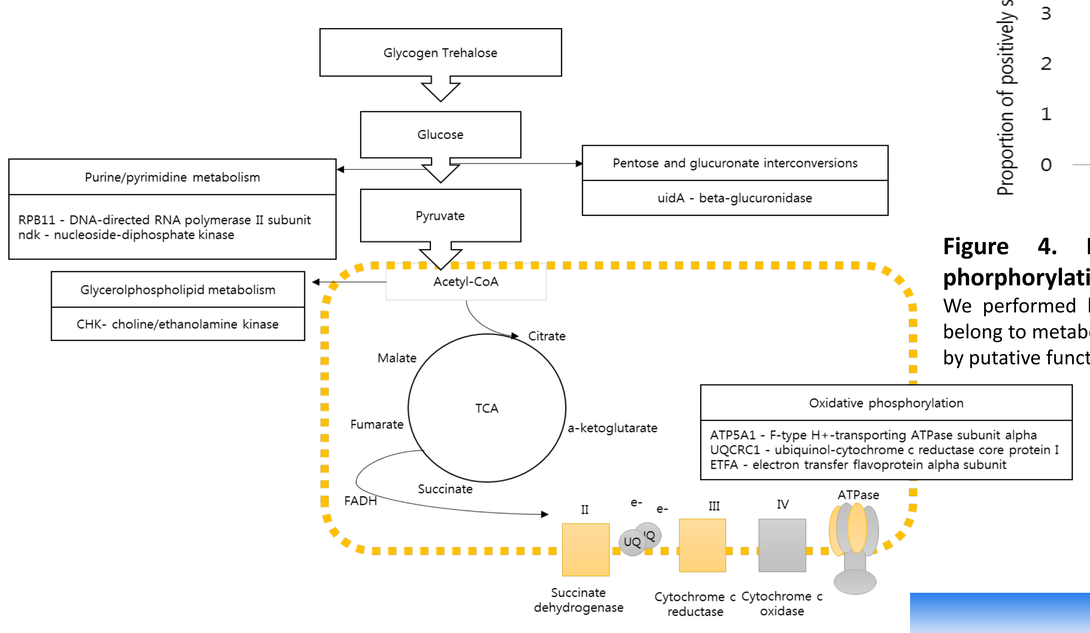

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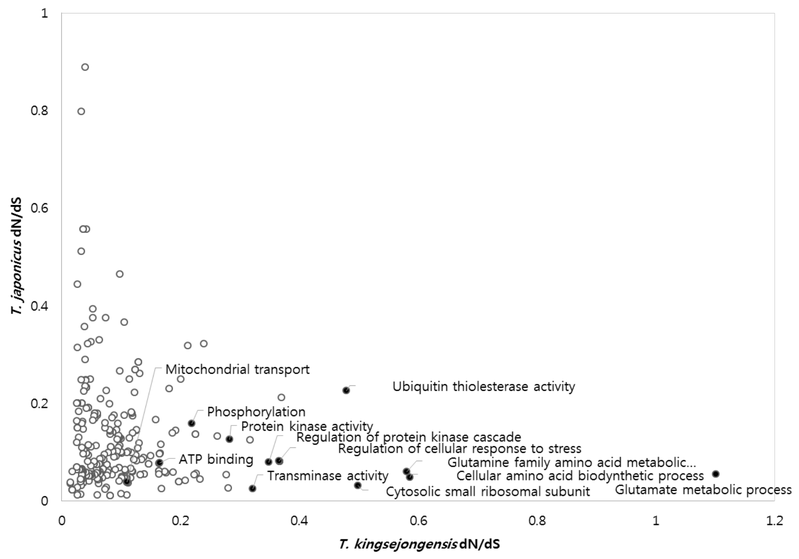

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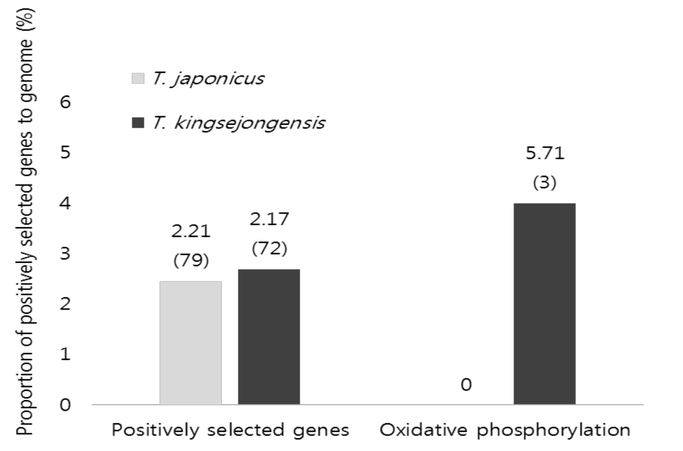

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