Project MILESTONE 275735 – Final Report- Figures

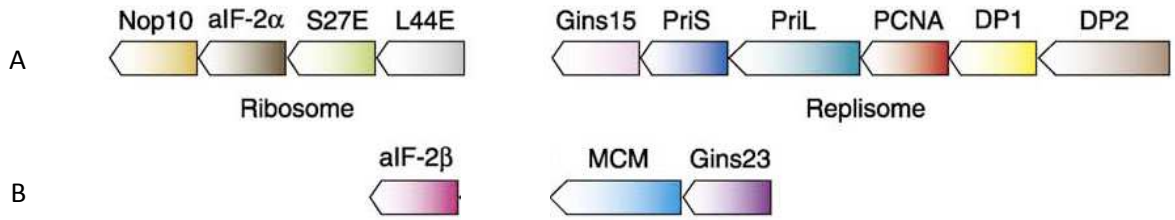

Figure 1: Genes grouped within clusters in archaeal genomes
This figure illustrates the conserved genomic environment of the two clusters of DNA replication and translation genes across different archaeal genomes. (**A**) A set of genes encoding three DNA replication proteins (orange; gins15, priS and PCNA; names are indicated above each gene) are often contiguous to four genes coding for proteins implicated in translation (blue; L44E, S27E, and the α subunit of the initiation factor aIF-2) or in the maturation process of the ribosome (Nop10). Only the most representative genomic neighborhoods are shown, but various alternative versions of this gene cluster are present in archaeal genomes. The gene encoding the large subunit of the DNA primase PriL is sometimes observed in this gene association. An alternative version of this cluster, including the two genes encoding the archaeal DNA polymerase D (DP1 and DP2), is present in the genome of *Candidatus Korarchaeum* cryptofilum.
(**B**) Another genomic association between one or two DNA replication genes (mcm and gins23) and a gene encoding the β subunit of the initiation factor (aIF-2β) has been observed in a few euryarchaeal genomes. The genes encoding MCM and Gins23 are contiguous in the majority of archaeal genomes that harbour a clear gins23 homologue, except in most genomes of Thermoproteales. In a few euryarchaeal genomes, the pair of genes mcm-gins23 or only the mcm gene colocalize with aIF-2β.

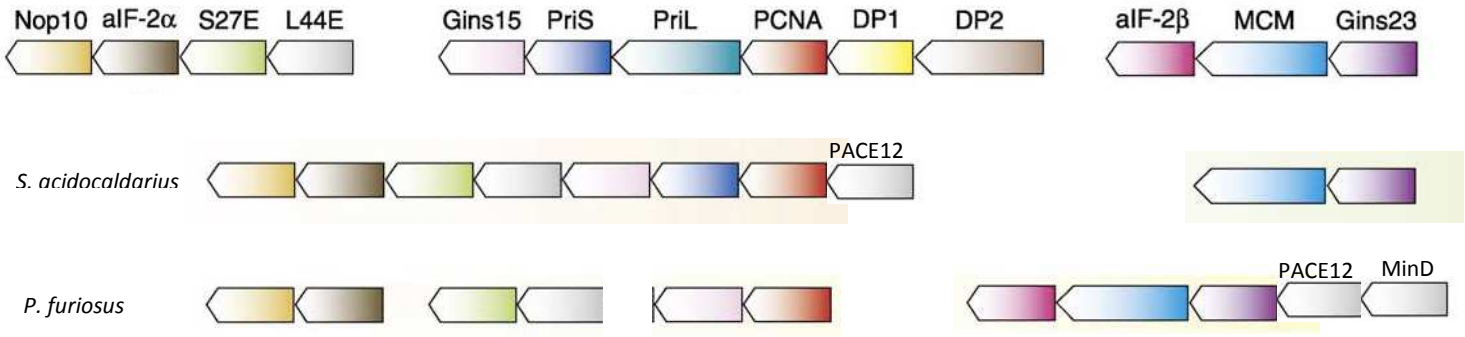

Figure 2: Transcriptional units of the clusters
This figure shows the operons obtained by RT-PCR experiments. The 2 clusters are shown on the first line; the operons seen in *S. acidocaldarius* and *P. furiosus* are shown with the same color

code for each genes. The genes *PACE12* and *minD* are also represented because they are part of the operons.

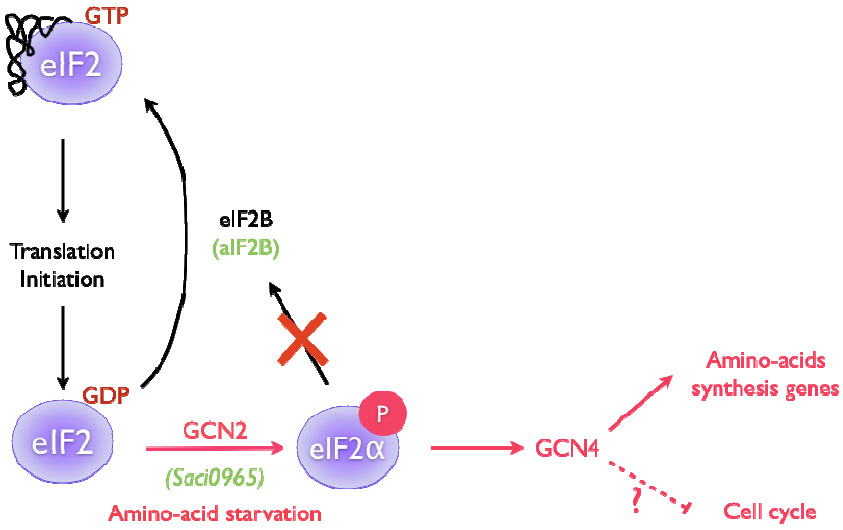

Figure 3: General amino-acids control in Eukaryotes
Initiation of translation in eukaryotes happens after binding of the initiation complex eIF2 to GTP and $tRNA^{i}$. After initiation, GTP is hydrolyzed in GDP, which is regenerated into GTP by eIF2B. In case of amino-acid starvation, empty tRNAs activate the kinase activity of GCN2, which phosphorylates the α subunit of eIF2. This stabilizes its binding to eIF2B and inhibits the regeneration activity of eIF2B, preventing any new initiation. Expression of GCN4 is activated at the same time in yeast. Yeast gene names are written in red, and their equivalents in *S. acidocaldarius* in green.

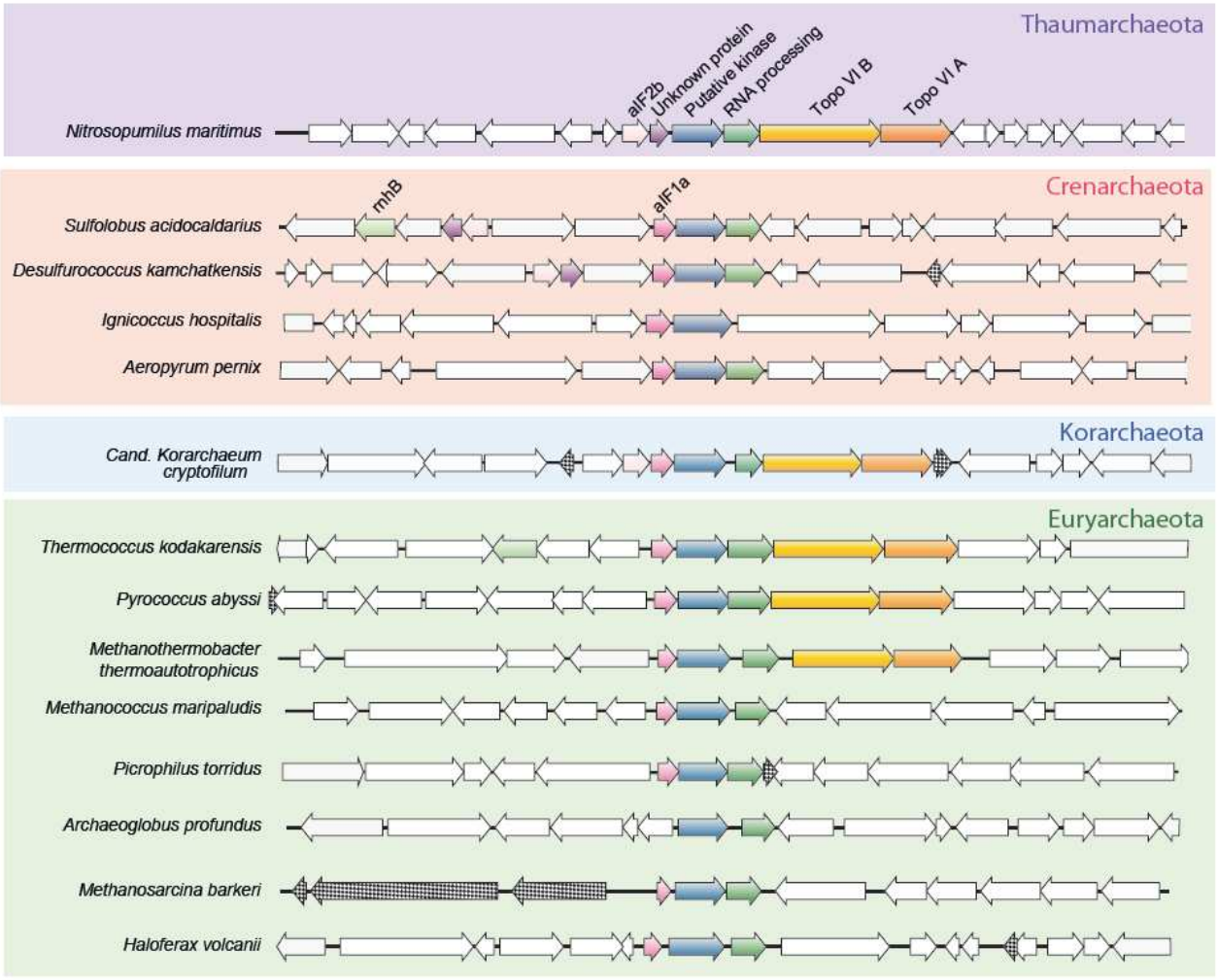

Figure 4: Genomic context and conservation of the putative kinase Saci0965

Saci0965 sequence (blue) was searched for in representative archaeal genomes for the 4 main phyla, and in all of them was found clustering with RNA processing genes (green) and translation initiation subunits of aIF1 and aIF2 complexes (pink). The chart was generated with Absynte software (http://archaea.u-psud.fr/absynte).