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*Barcelona  
Supercomputing  
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*Centro Nacional de Supercomputación*



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BARCELONA

## 12th BSC SO Doctoral Symposium

# Pervasive horizontal transfer and extensive gene duplication shape Asgard archaeal genomes

**Saioa Manzano-Morales**

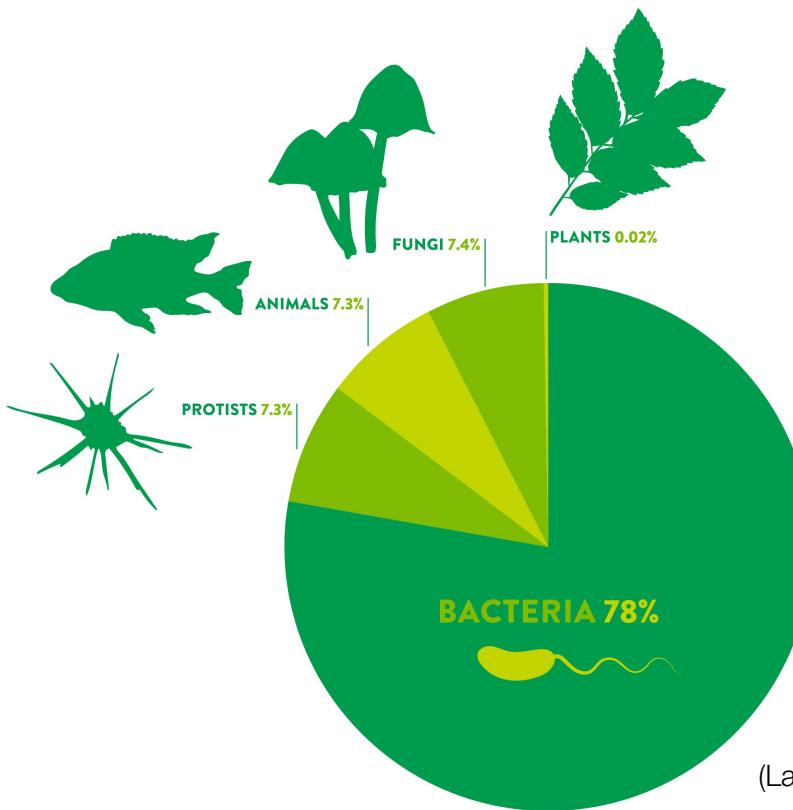
Toni Gabaldón

Comparative Genomics - Life Sciences  
Barcelona Supercomputing Center

# Eukaryotes are cool...

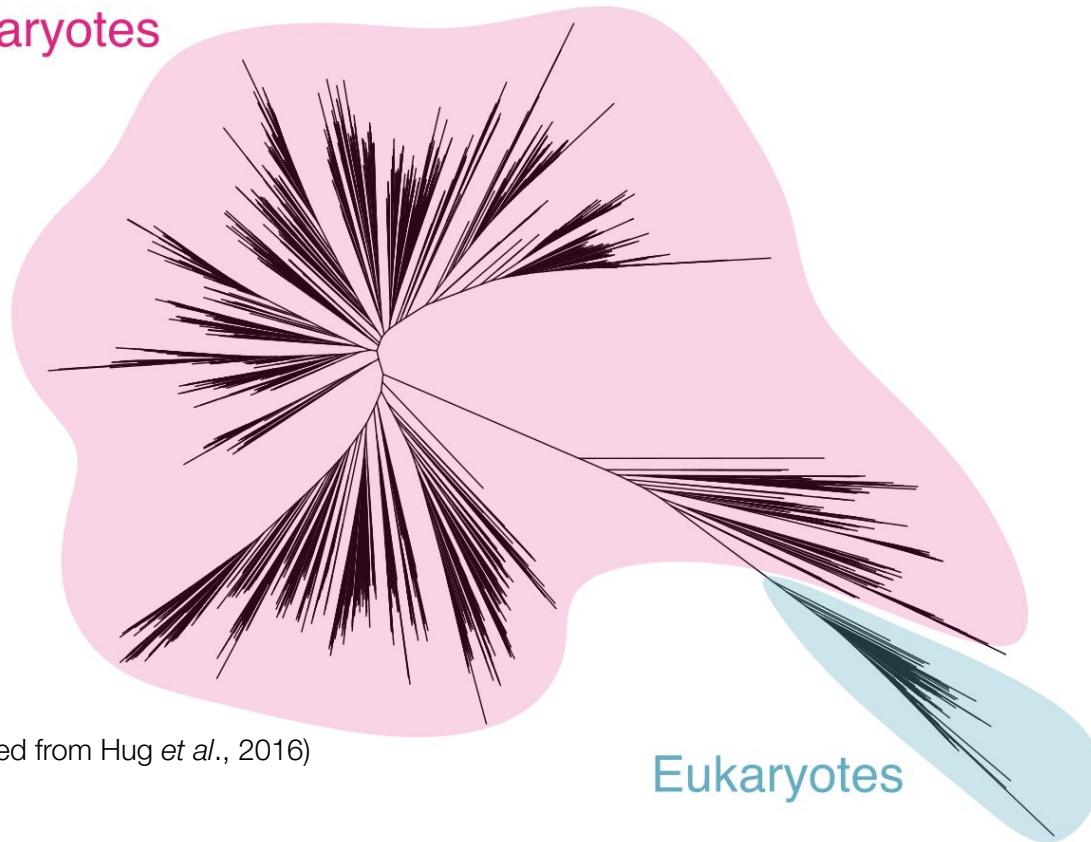


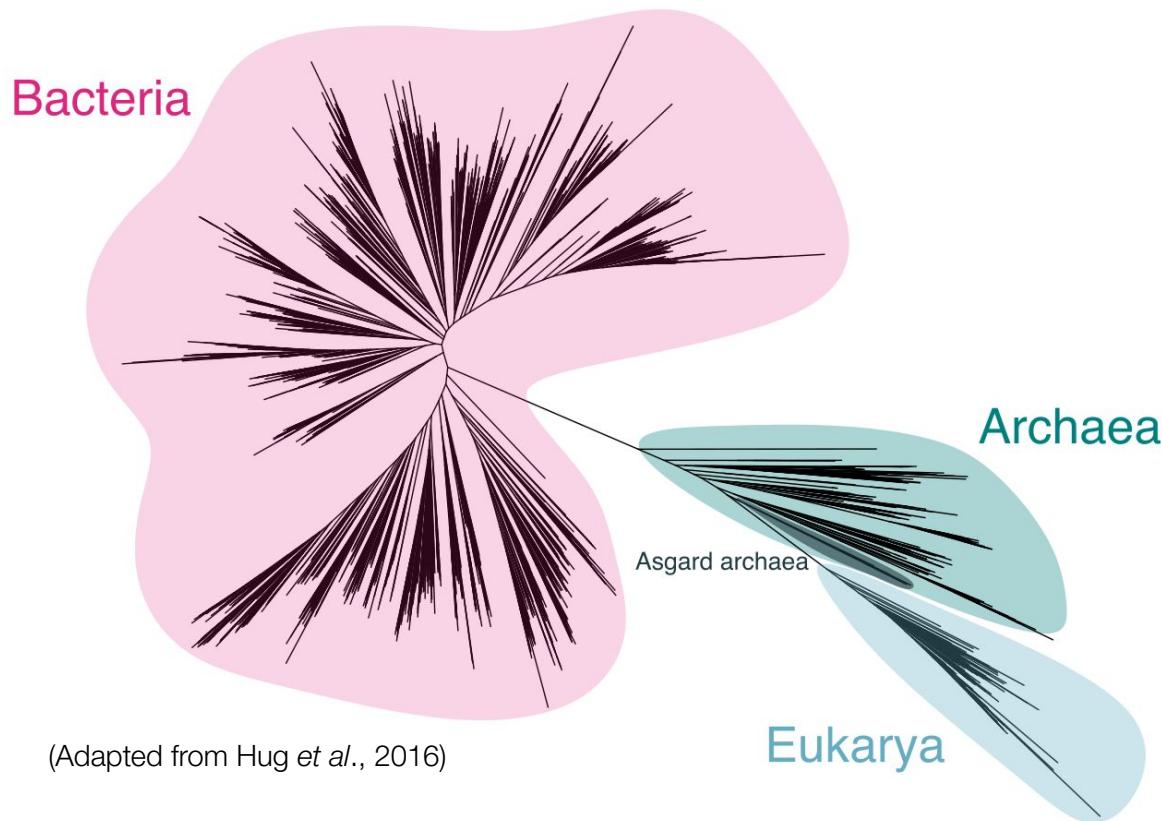
... but the vast majority of life on Earth is prokaryotic!

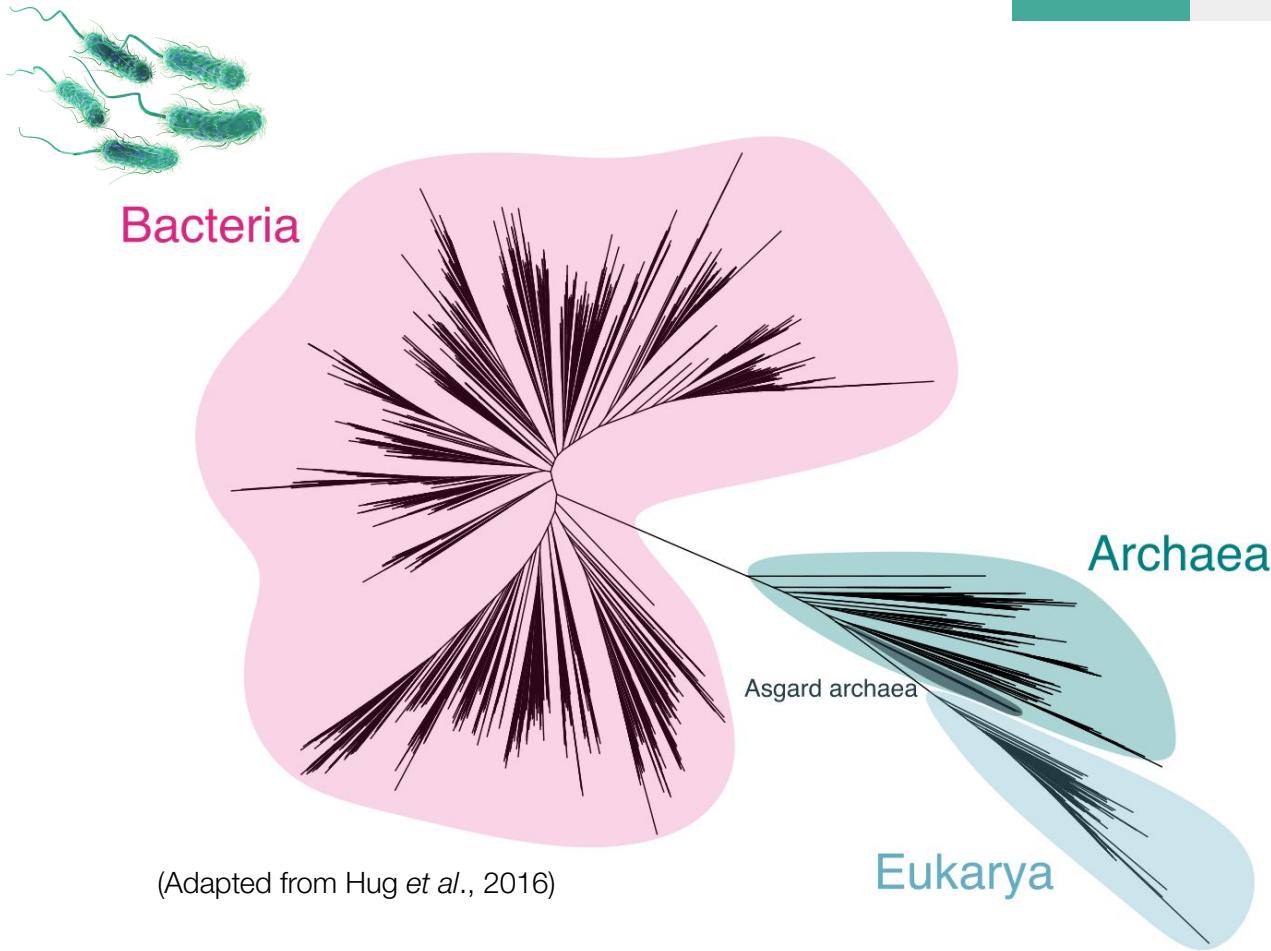


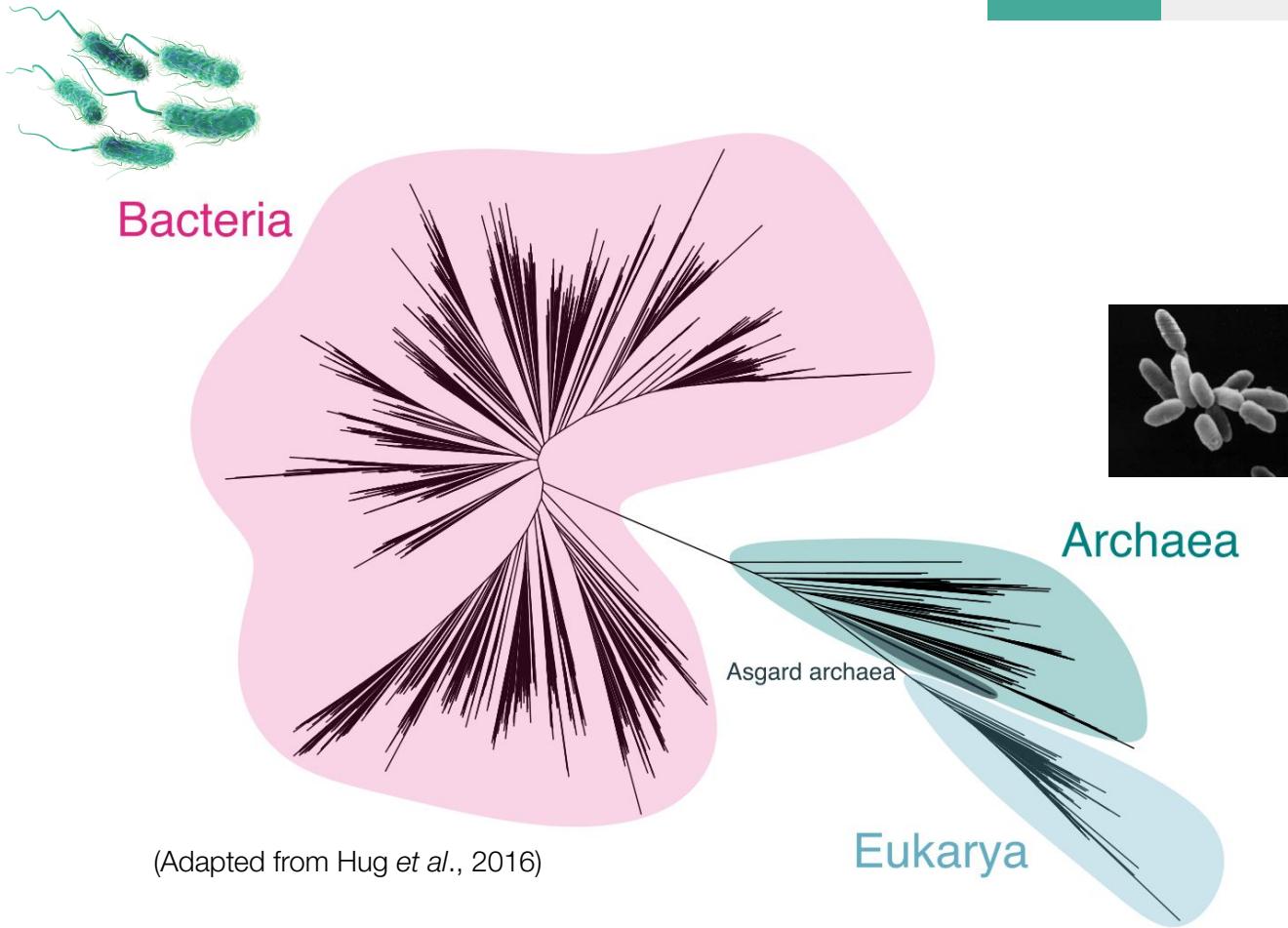
(Lanson *et al.* 2017)

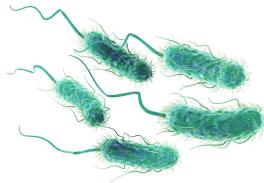
## Prokaryotes



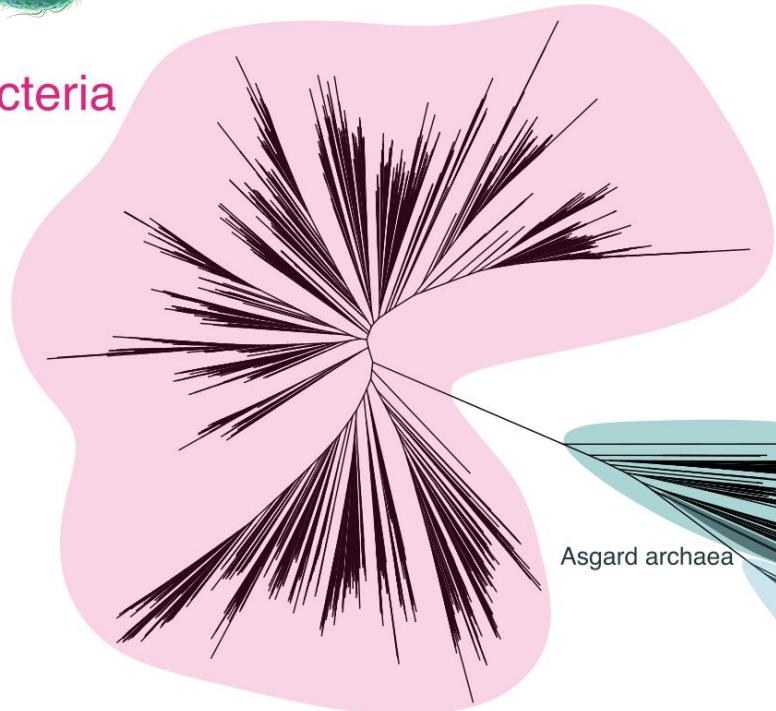








Bacteria



(Adapted from Hug et al., 2016)

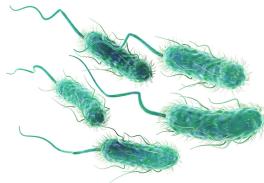


Archaea

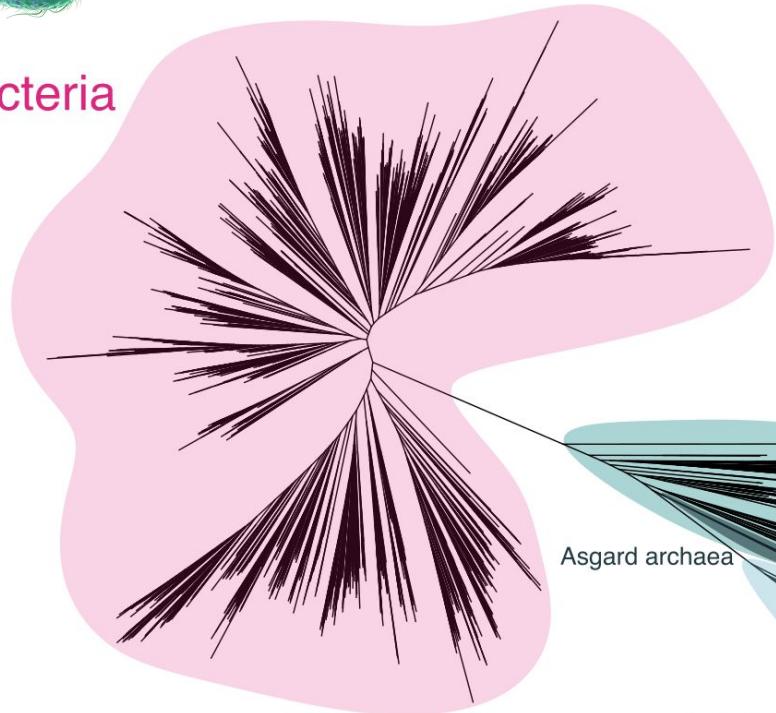
Asgard archaea

Eukarya





Bacteria



(Adapted from Hug et al., 2016)



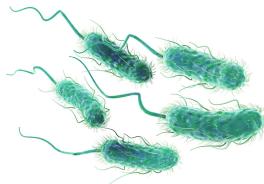
Archaea



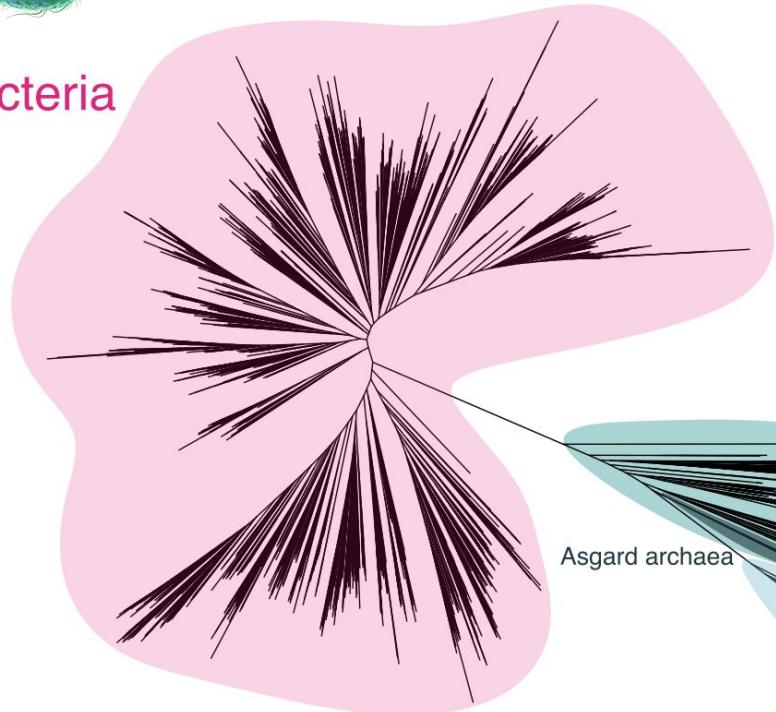
Asgard archaea

Eukarya





Bacteria



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Archaea

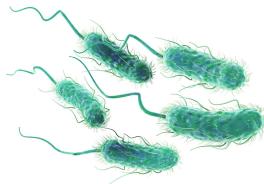


Asgard archaea

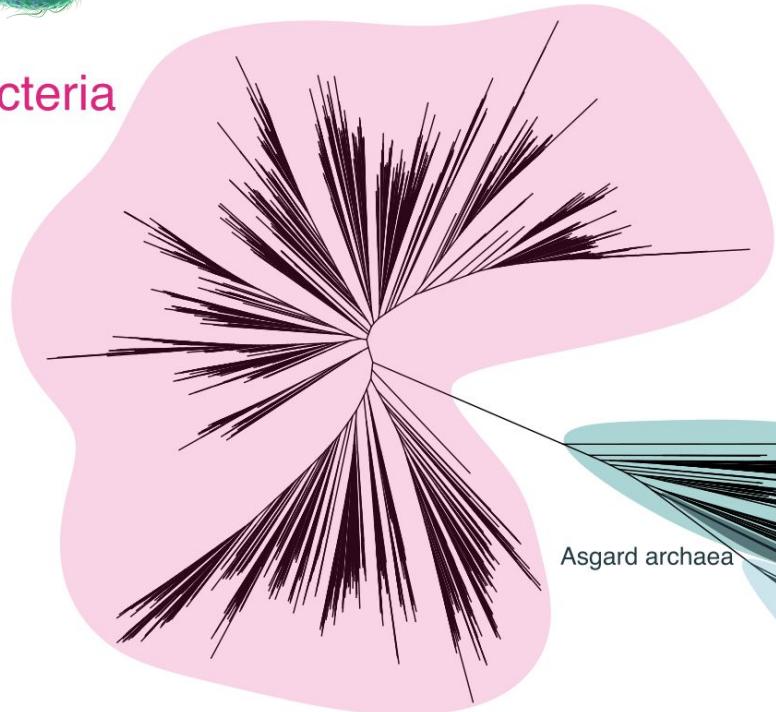


Eukarya





Bacteria



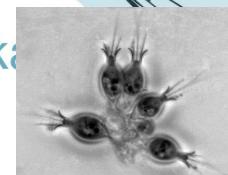
(Adapted from Hug et al., 2016)



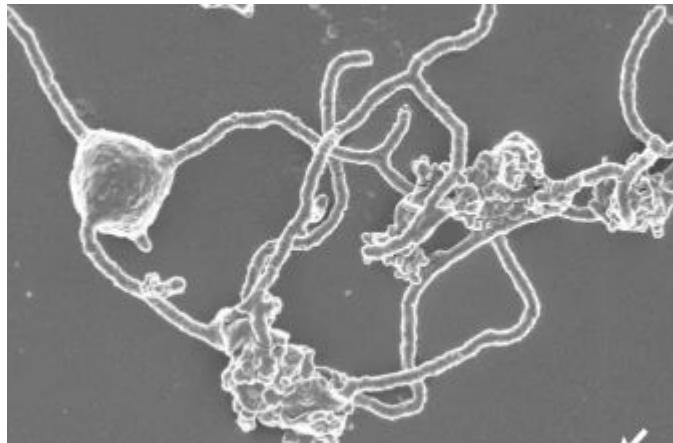
Archaea



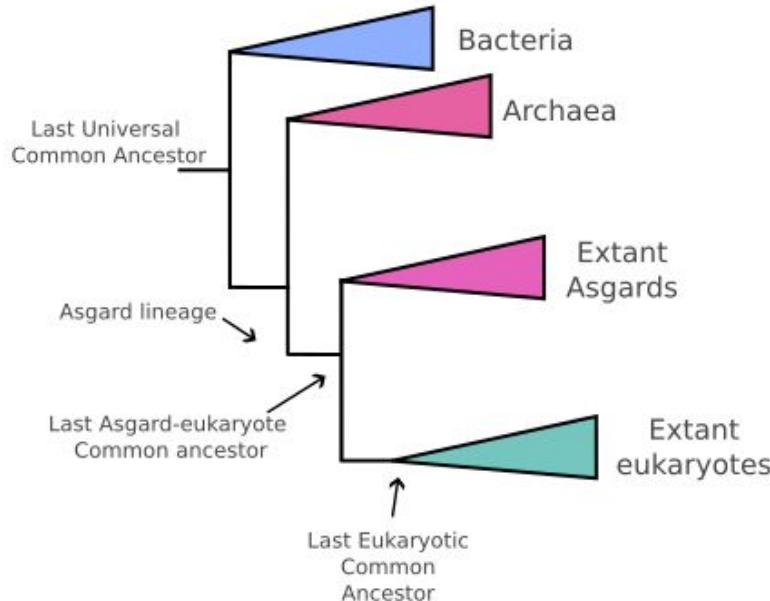
Euka



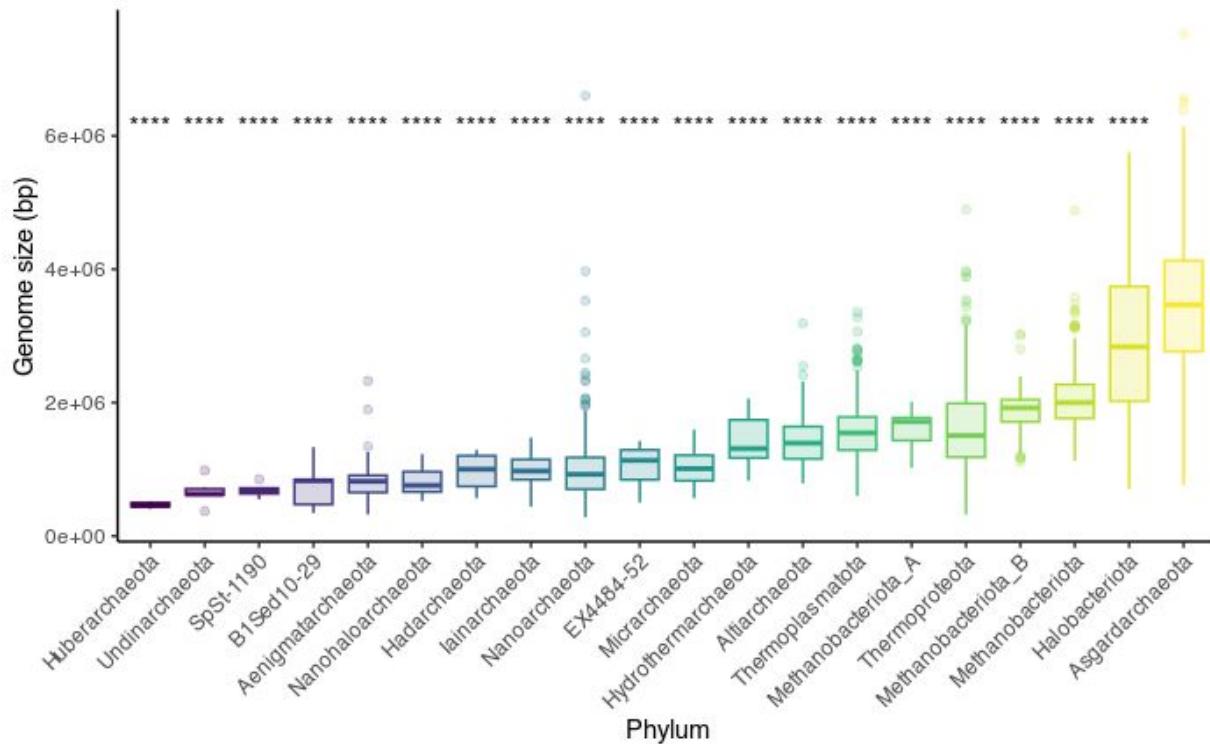
# Asgard archaea have a unique phylogenetic placement



(Imachi *et al.* 2020)

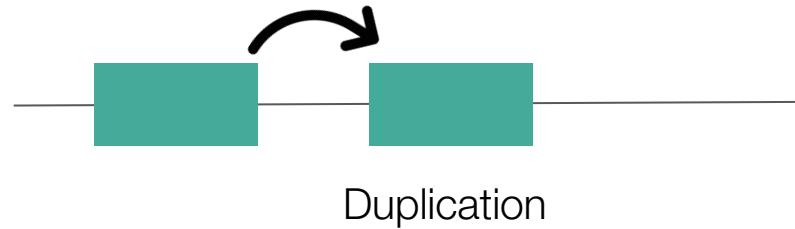


# Asgard genome size is significantly larger than other archaea



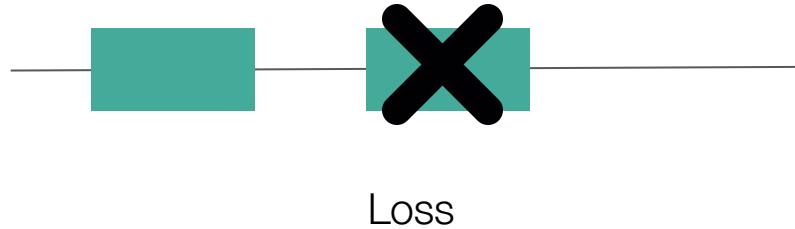
# Genome evolution

Increase

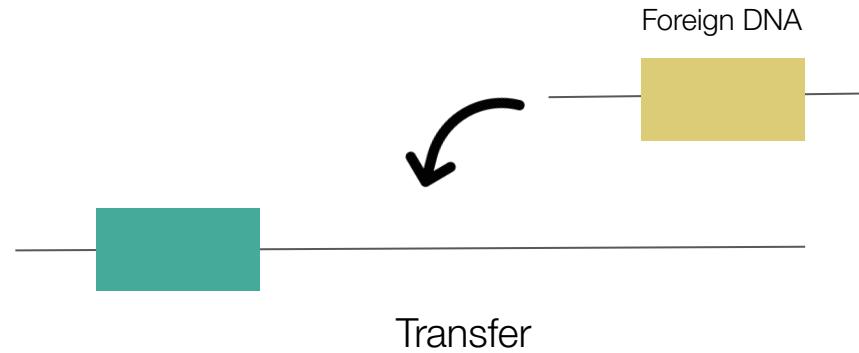


Duplication

Decrease



Loss



Transfer

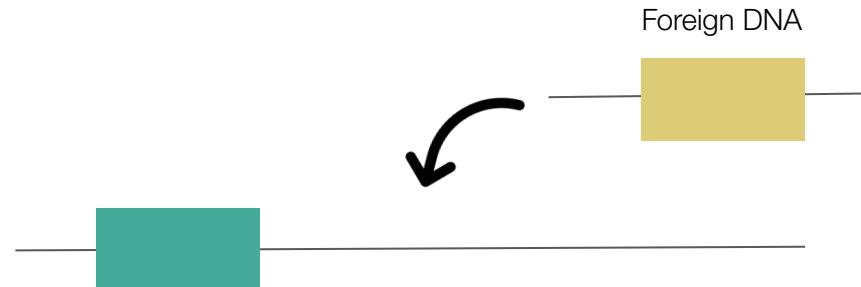
# Genome evolution

Increase



Duplication

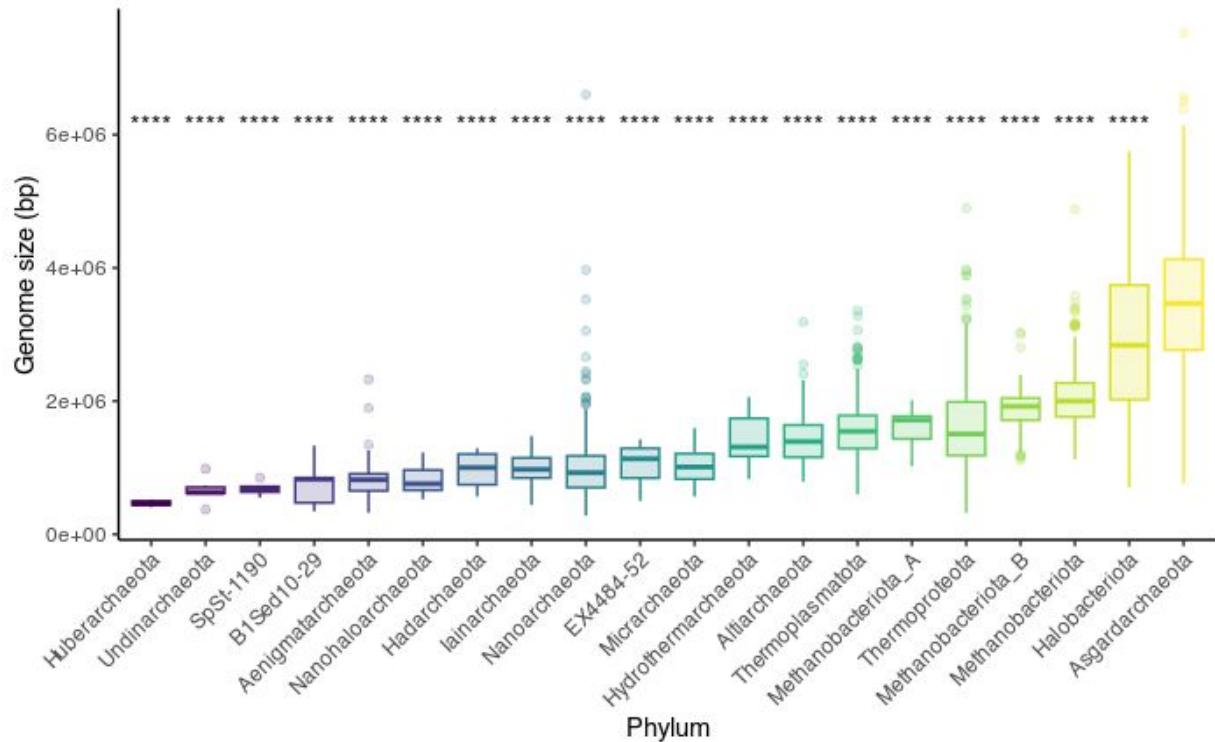
Common in **eukaryotes**



Transfer

Common in **prokaryotes**

# Asgard genome size is significantly larger than other archaea

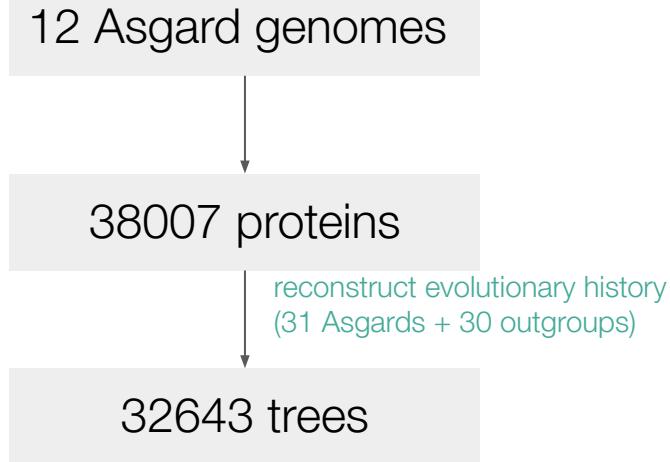


Did Asgards **expand** their genome in a **prokaryote-like** or **eukaryote-like** manner?

# Phylogenomics workflow

12 Asgard genomes

# Phylogenomics workflow



# Phylogenomics workflow

12 Asgard genomes



38007 proteins

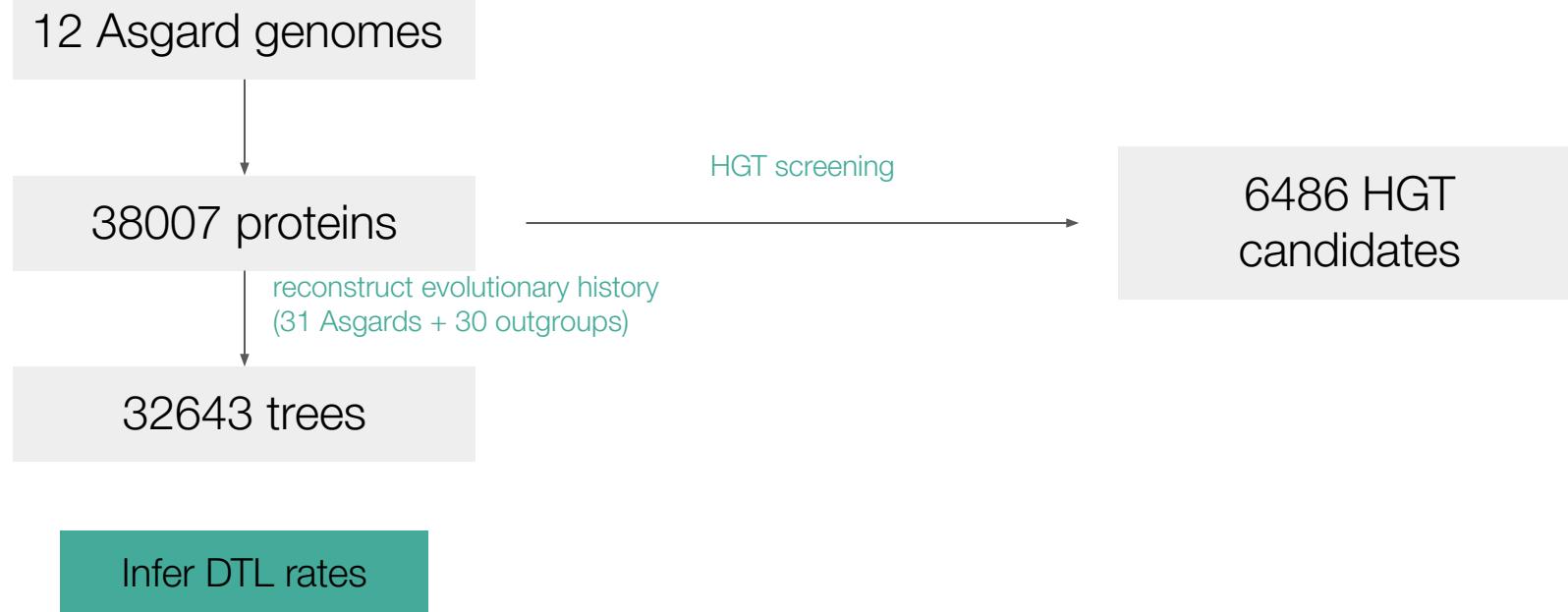


reconstruct evolutionary history  
(31 Asgards + 30 outgroups)

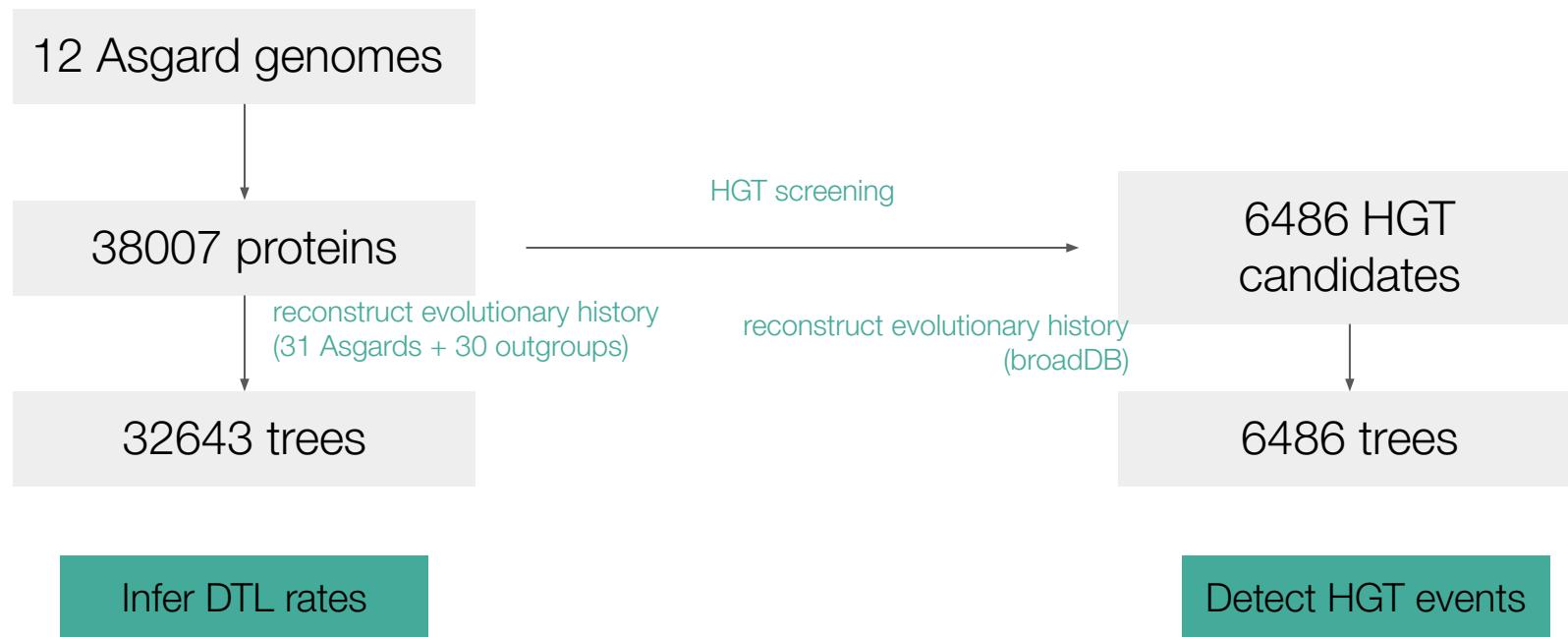
32643 trees

Infer DTL rates

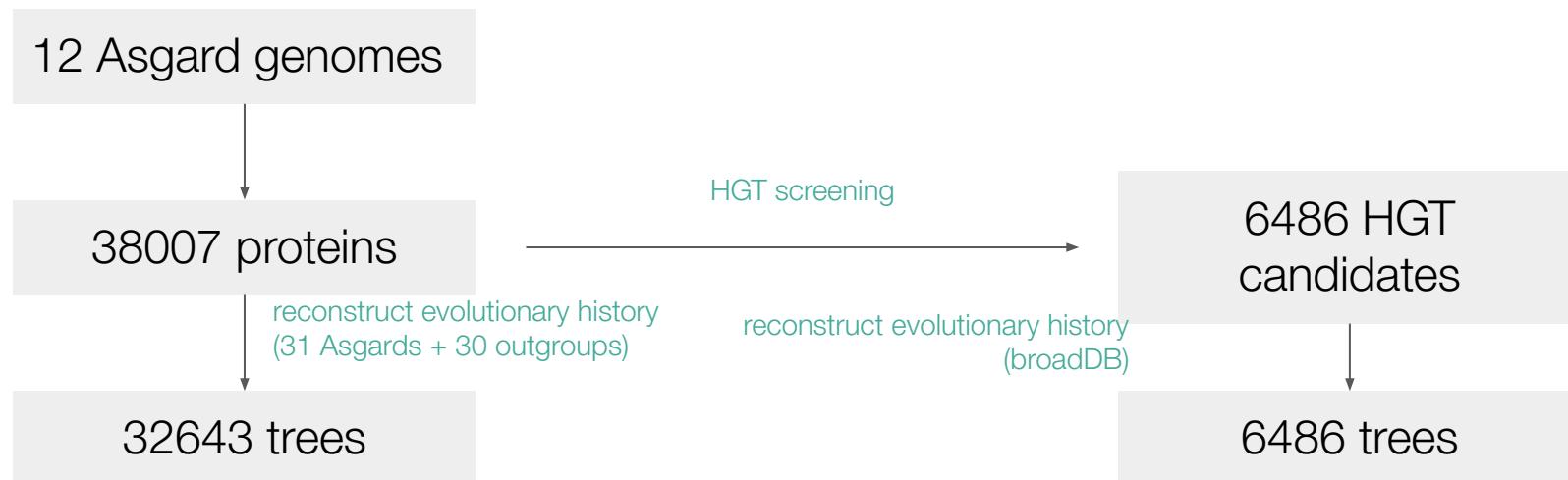
# Phylogenomics workflow



# Phylogenomics workflow



# Phylogenomics workflow

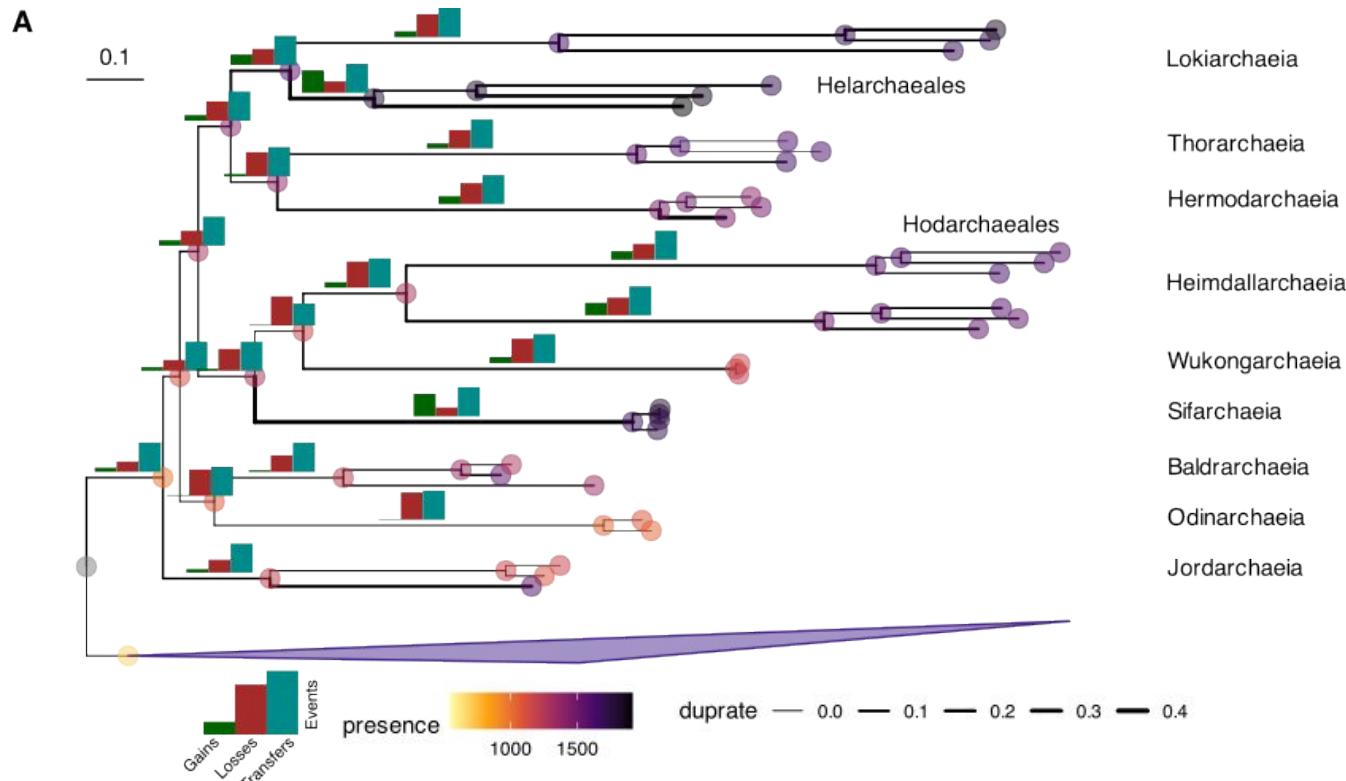


Infer DTL rates

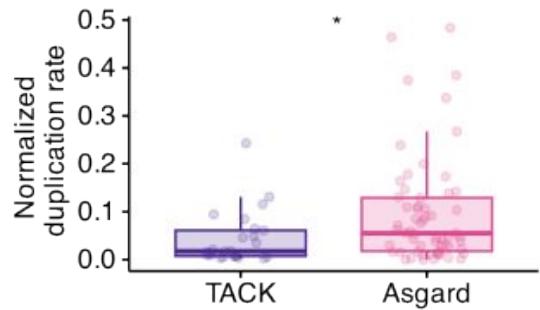
Detect HGT events

**1 tree = 2h x 4 CPU**

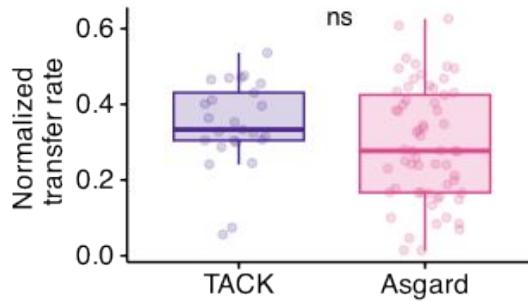
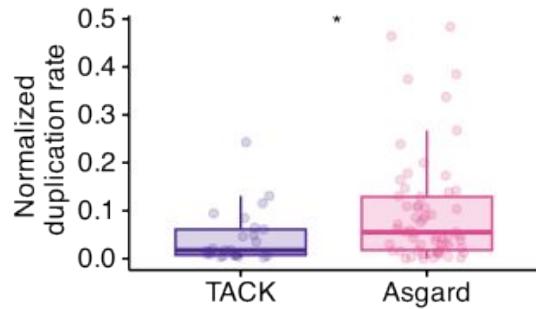
# Duplication/loss played a part in the development of the lineages



**Asgard archaea have significantly higher duplication rates than their prokaryotic sisters...**

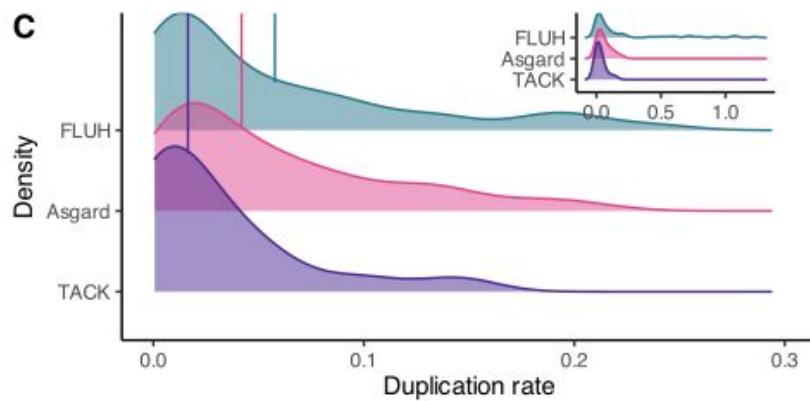


**Asgard archaea have significantly higher duplication rates than their prokaryotic sisters...**



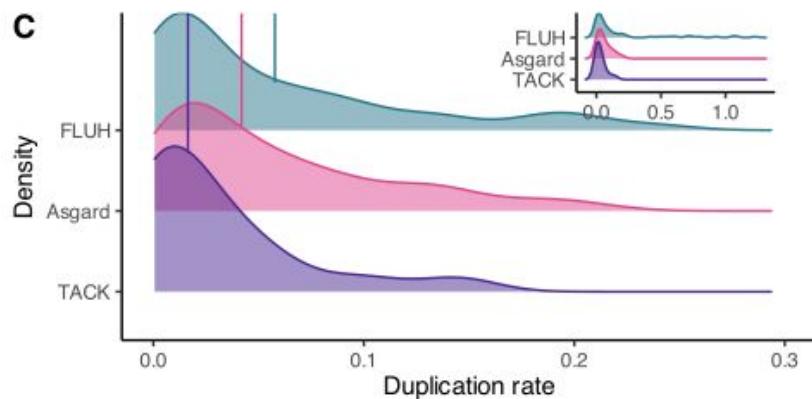
**...despite comparable transfer rates!**

## Asgard duplication rates are an intermediate between “typical” prokaryotes and eukaryotes



FLUH: Free-Living Unicellular Heterotroph (eukaryote)

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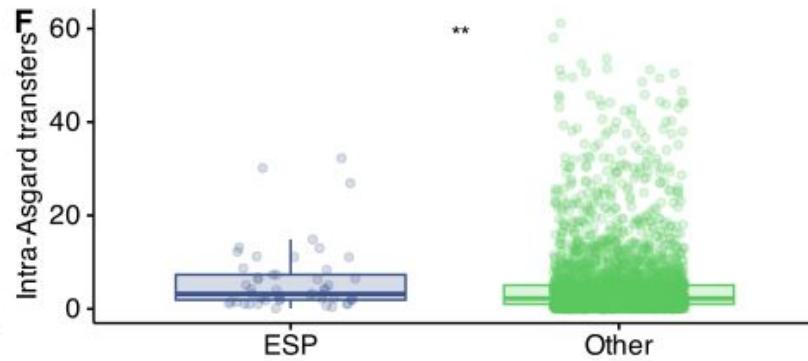


FLUH: Free-Living Unicellular Heterotroph (eukaryote)

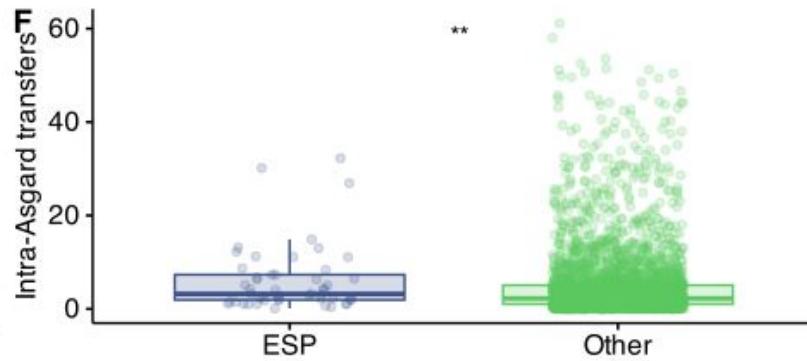
Did Asgards **expand** their genome in a **prokaryote-like** or **eukaryote-like** manner?

Prokaryotic-like in their transfers,  
(almost) “eukaryotic-like” in their  
duplications

# Eukaryotic Signature Proteins are more prone to intra-Asgard gene transfer

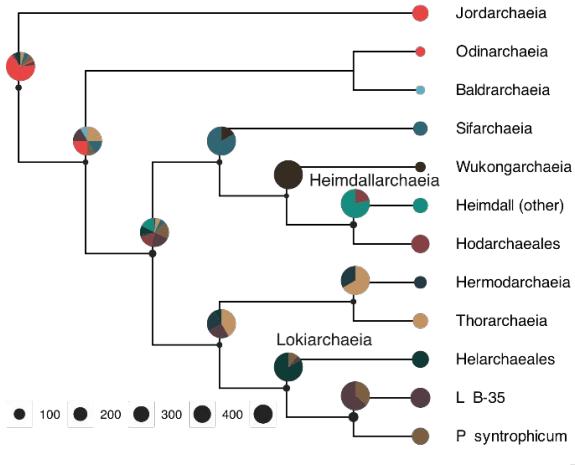


# Eukaryotic Signature Proteins are more prone to intra-Asgard gene transfer

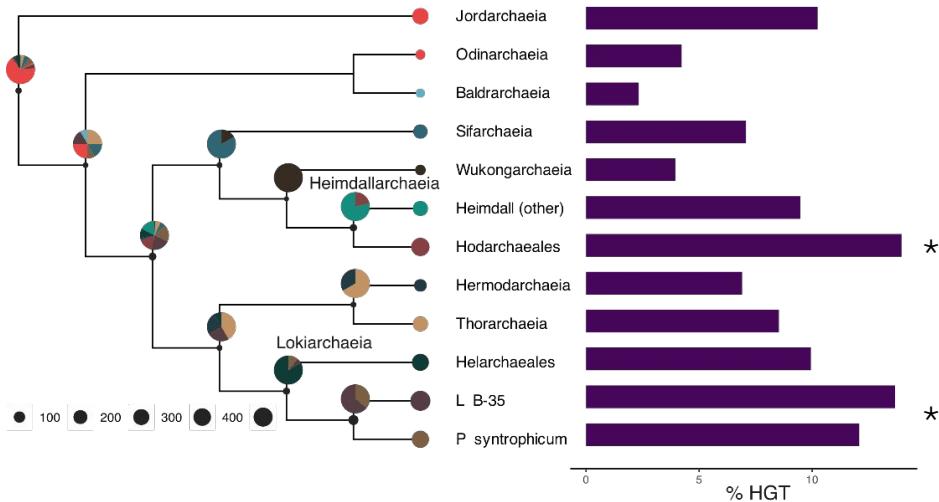


... explaining their patchy distribution across the Asgard tree

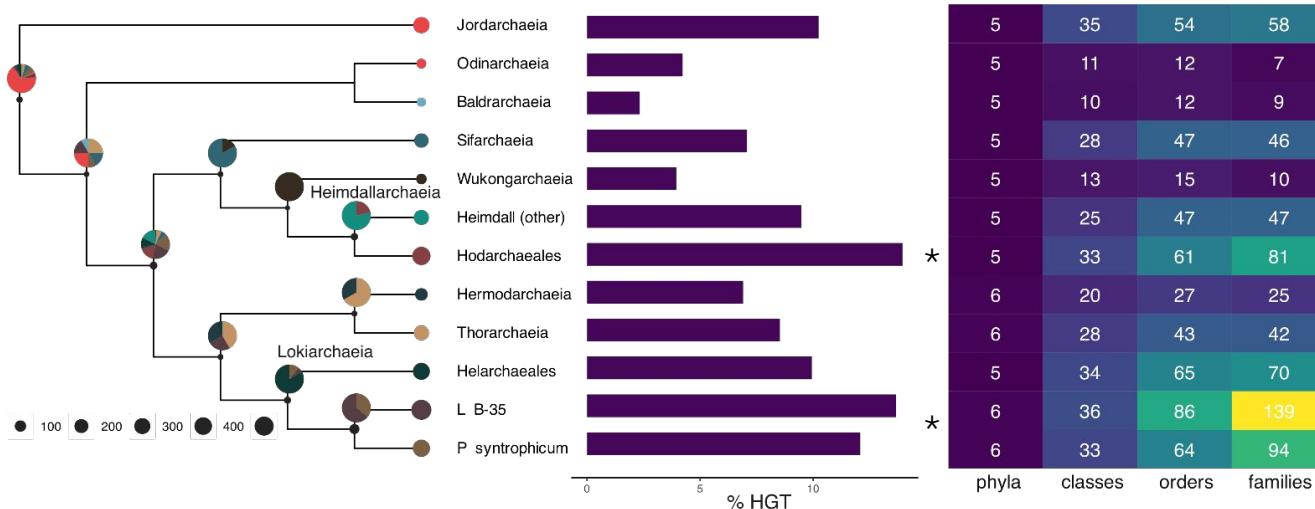
# Bacteria-Asgard HGT has been a constant, on-going process across Asgard evolution...



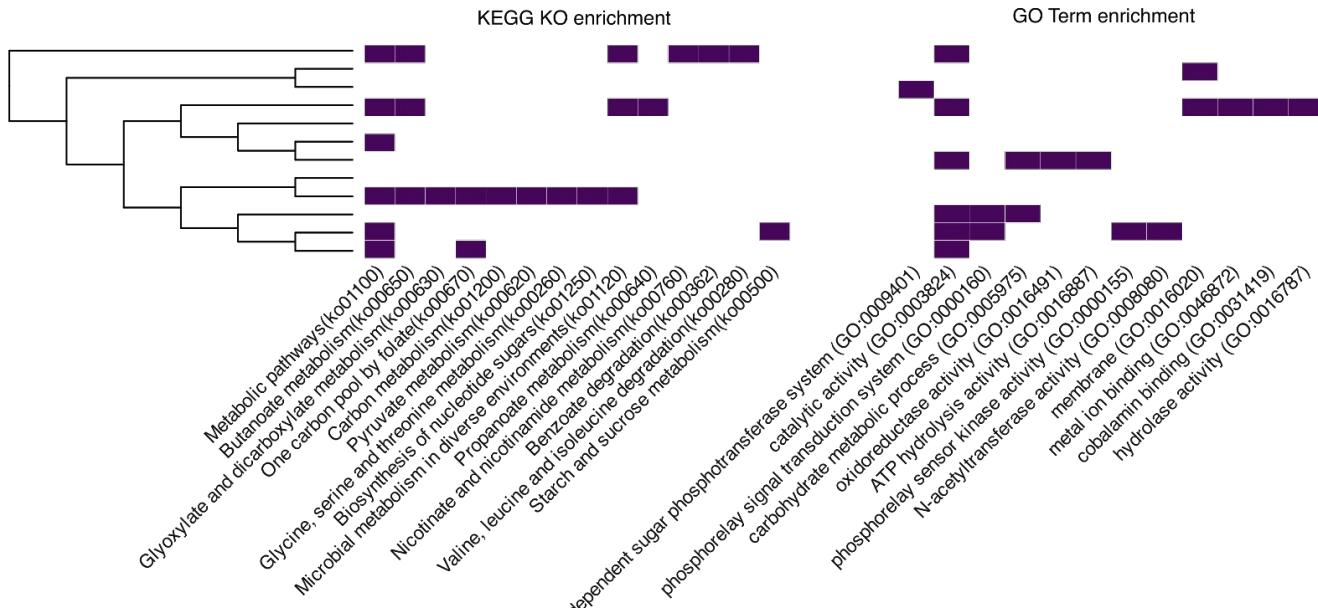
...leading to varying percentages of HGT-derived proteins across lineages...

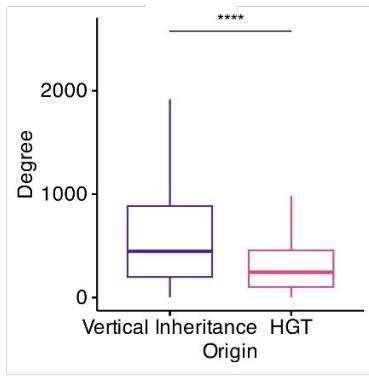


# ...from a variety of sources

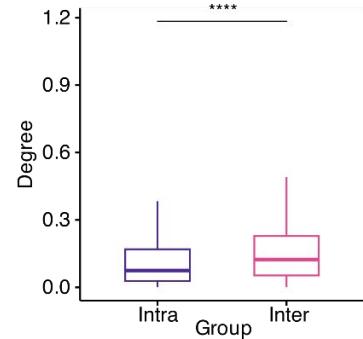


# Genes of bacterial origin are enriched in metabolic functions





**... and are connected to vertically inherited genes rather than being modular**



# Take-home messages

- A role for both **gene duplication** and **gene transfer** in shaping Asgard archaeal genomes

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- Pervasive inter- and intra-domain **horizontal gene transfer** of **metabolic genes**

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- A role for both **gene duplication** and **gene transfer** in shaping Asgard archaeal genomes
- Pervasive inter- and intra-domain **horizontal gene transfer** of **metabolic genes**
- Integration in **PPI** network

# Comparative Genomics

Toni Gabaldón



Marina  
Marcet-Houben



Moisès  
Bernabeu



GORDON AND BETTY  
**MOORE**  
FOUNDATION

GA: 724173

GBMF9742



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SEVERO  
OCHOA



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