Domestication and Divergence of Saccharomyces cerevisiae Beer Yeasts

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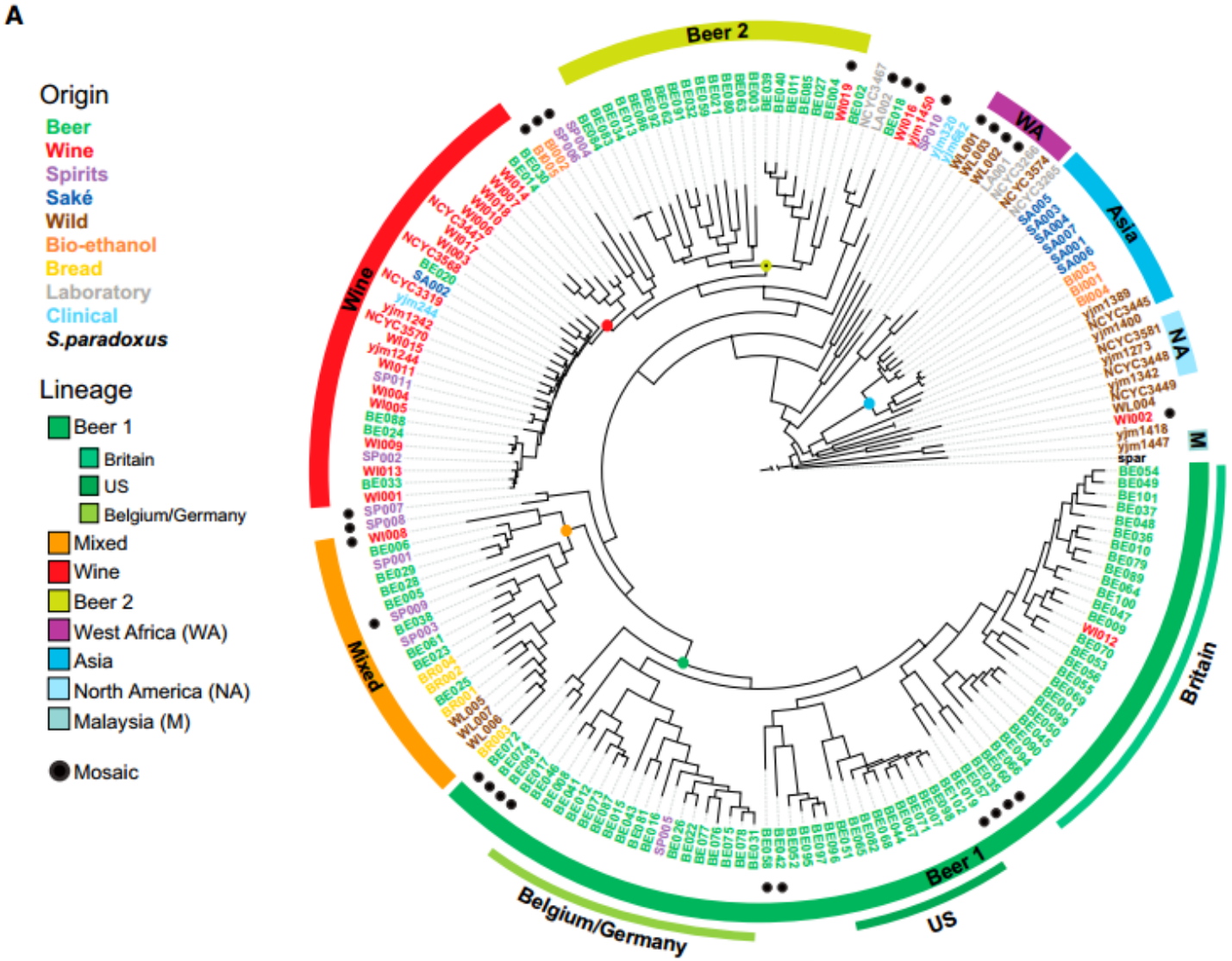
INTRODUCTION

Whereas domestication of livestock, pets, and crops is well documented, it is still unclear to what extent microbes associated with the production of food have also undergone human selection and where the plethora of industrial strains originates from. Here, we present the genomes and phenomes of 157 industrial Saccharomyces cerevisiae yeasts. Our analyses reveal that today's industrial yeasts can be divided into five sublineages that are genetically and phenotypically separated from wild strains and originate from only a few ancestors through complex patterns of domestication and local divergence. Large-scale phenotyping and genome analysis further show strong industry-specific selection for stress tolerance, sugar utilization, and flavor production, while the sexual cycle and other phenotypes related to survival in nature show decay, particularly in beer yeasts. Together, these results shed light on the origins, evolutionary history, and phenotypic diversity of industrial yeasts and provide a resource for further selection of superior strains.

Experimental procedure

- DNA Extraction
- Library Prep and Whole Genome Sequencing
- De Novo Assembly
- Annotation
- Core Genome Analysis and Identification of Single Copy Genes
- Reference-Based Alignments and Variant Calling
- Phylogenetic Analyses
- Population Structure and Diversity Analysis
- Time Divergence Estimate
- Copy-Number Variation Analysis
- Character Evolution Analysis
- Determination of Cell Ploidy
- Phenotypic Analysis
- Development of Artificial Hybrids

一、Niche and Geography Drive Diversification



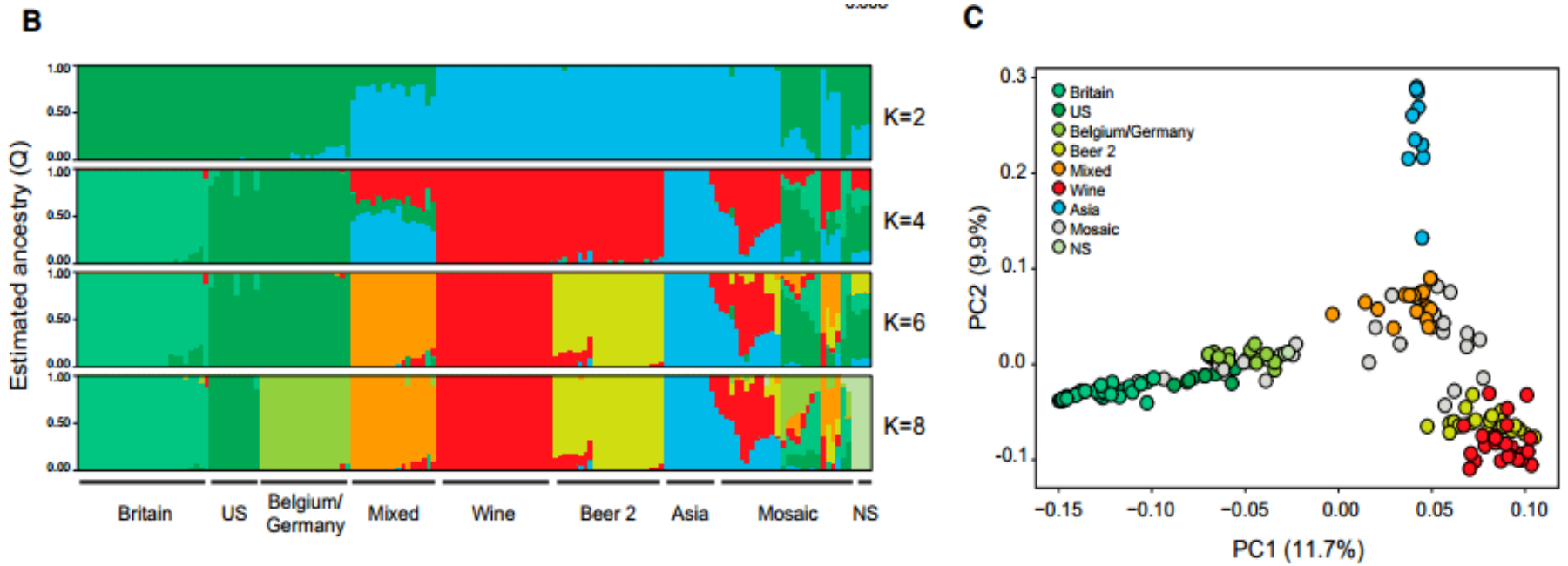
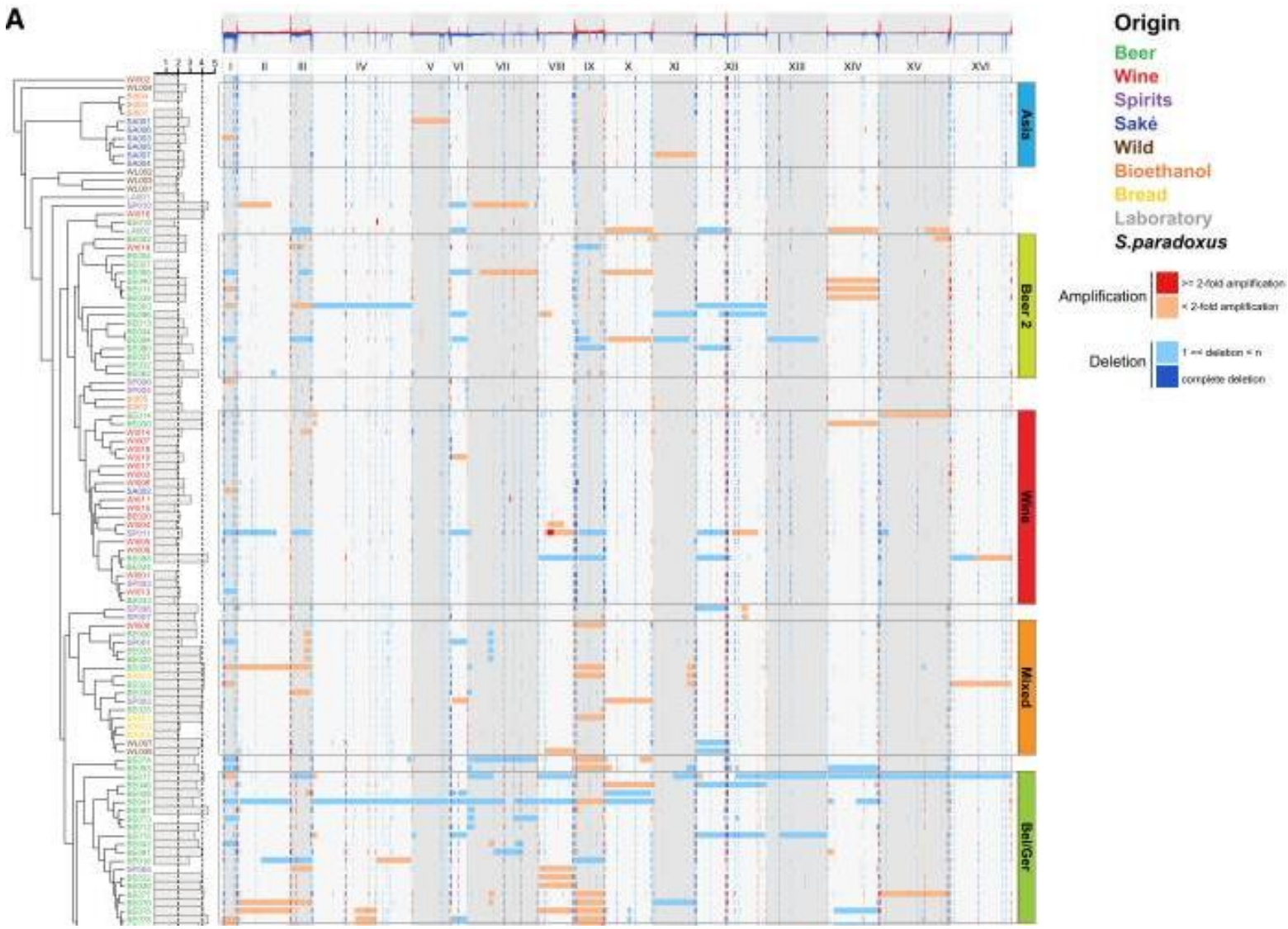


Figure 1. Phylogeny and Population Structure of Industrial S. cerevisiae Strains

二、Remarkable Structural Variation in Beer Yeasts



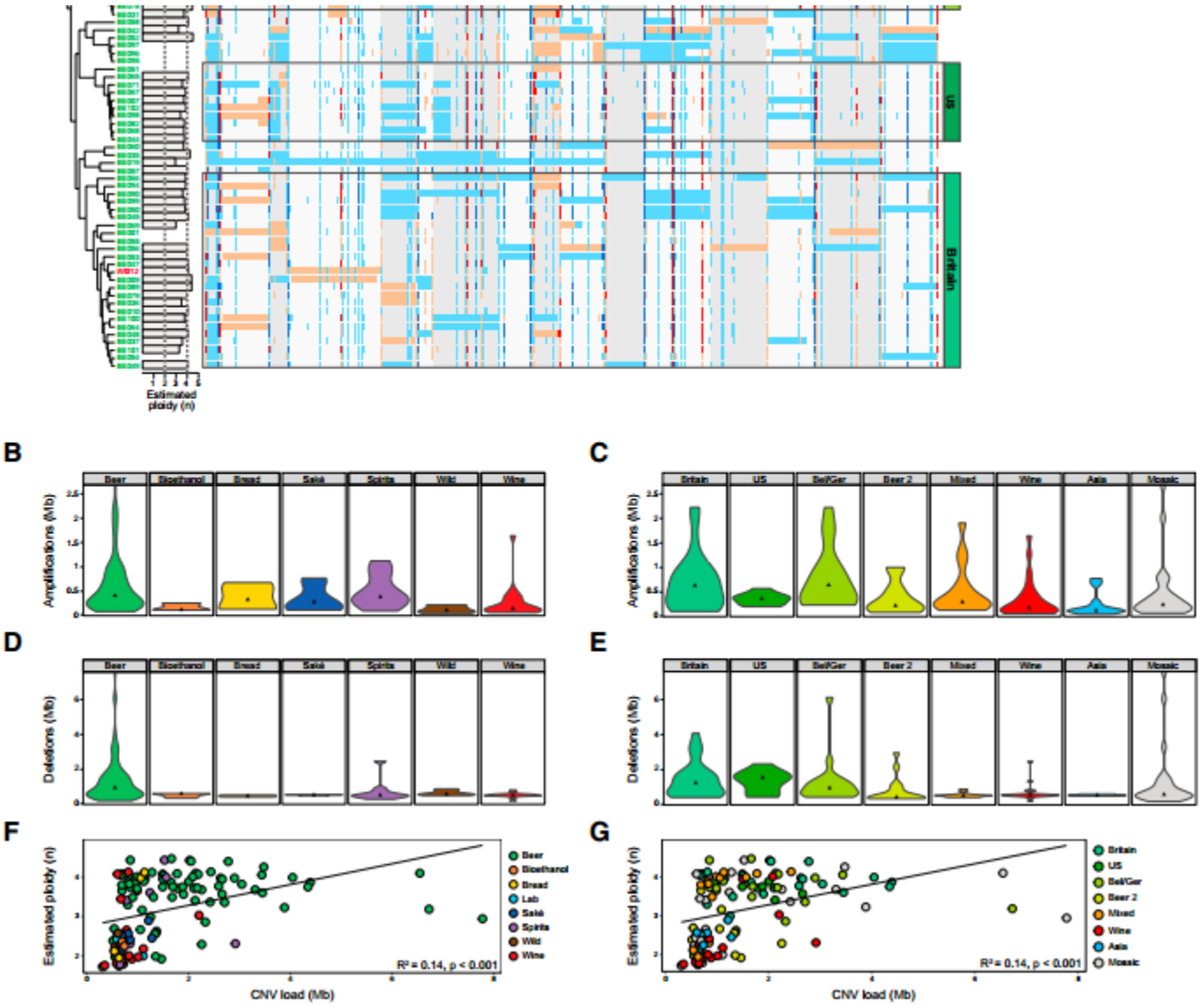
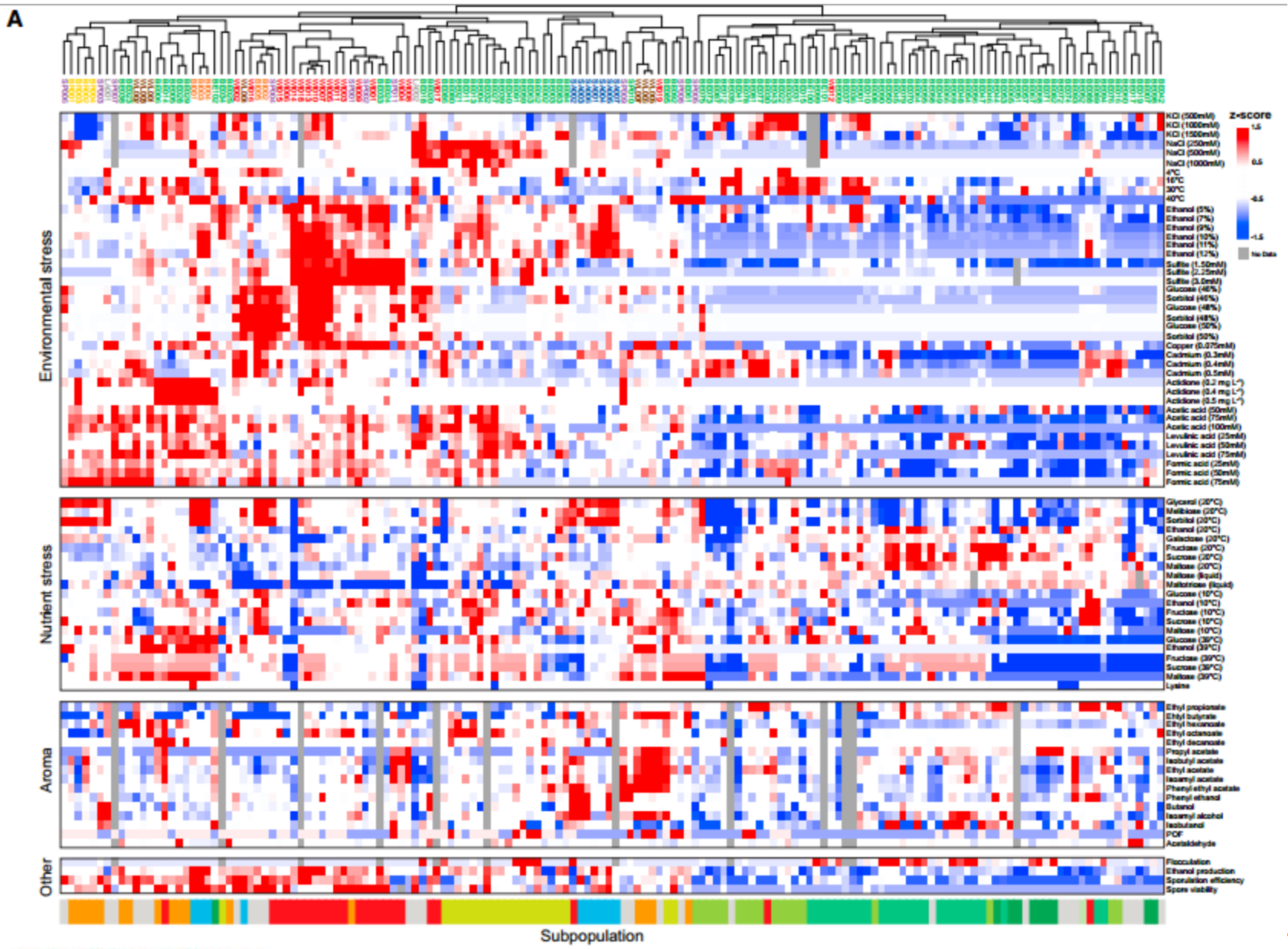


Figure 2. Ploidy and Copy-Number Variation in Industrial S. cerevisiae Strains

三、Relaxed Selection on Sex and Survival in Nature



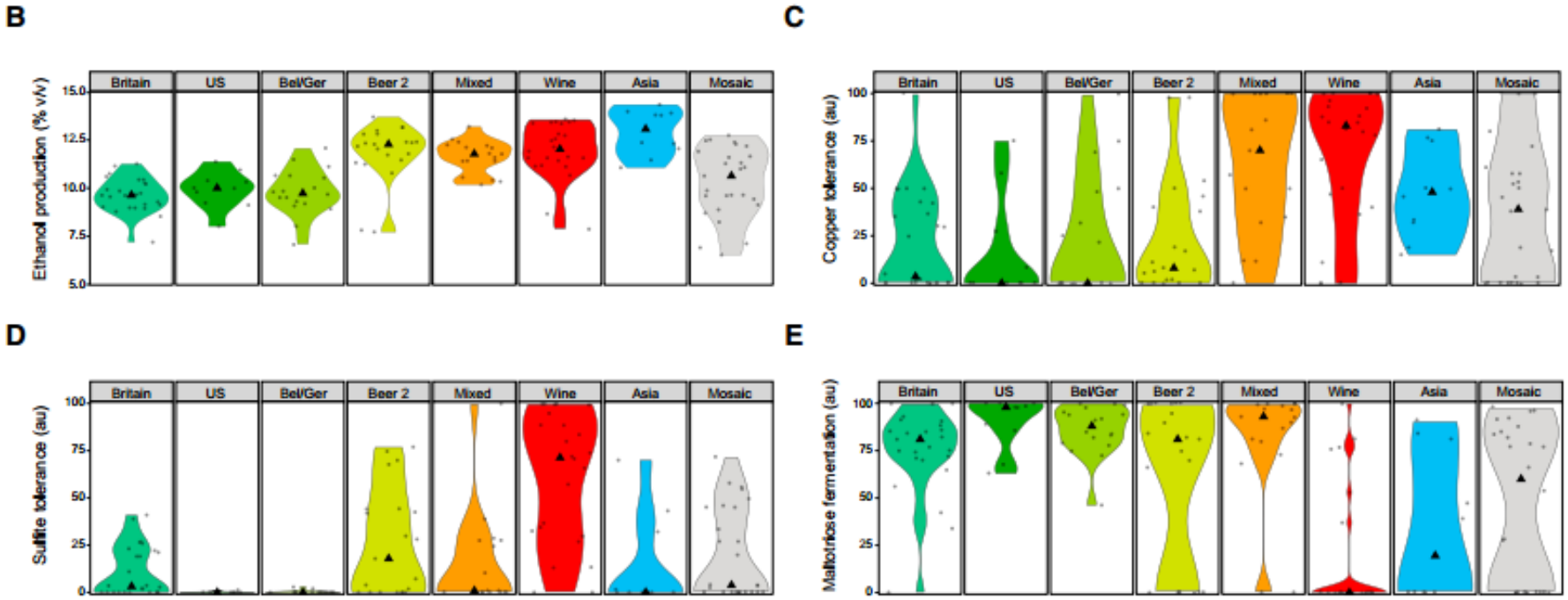
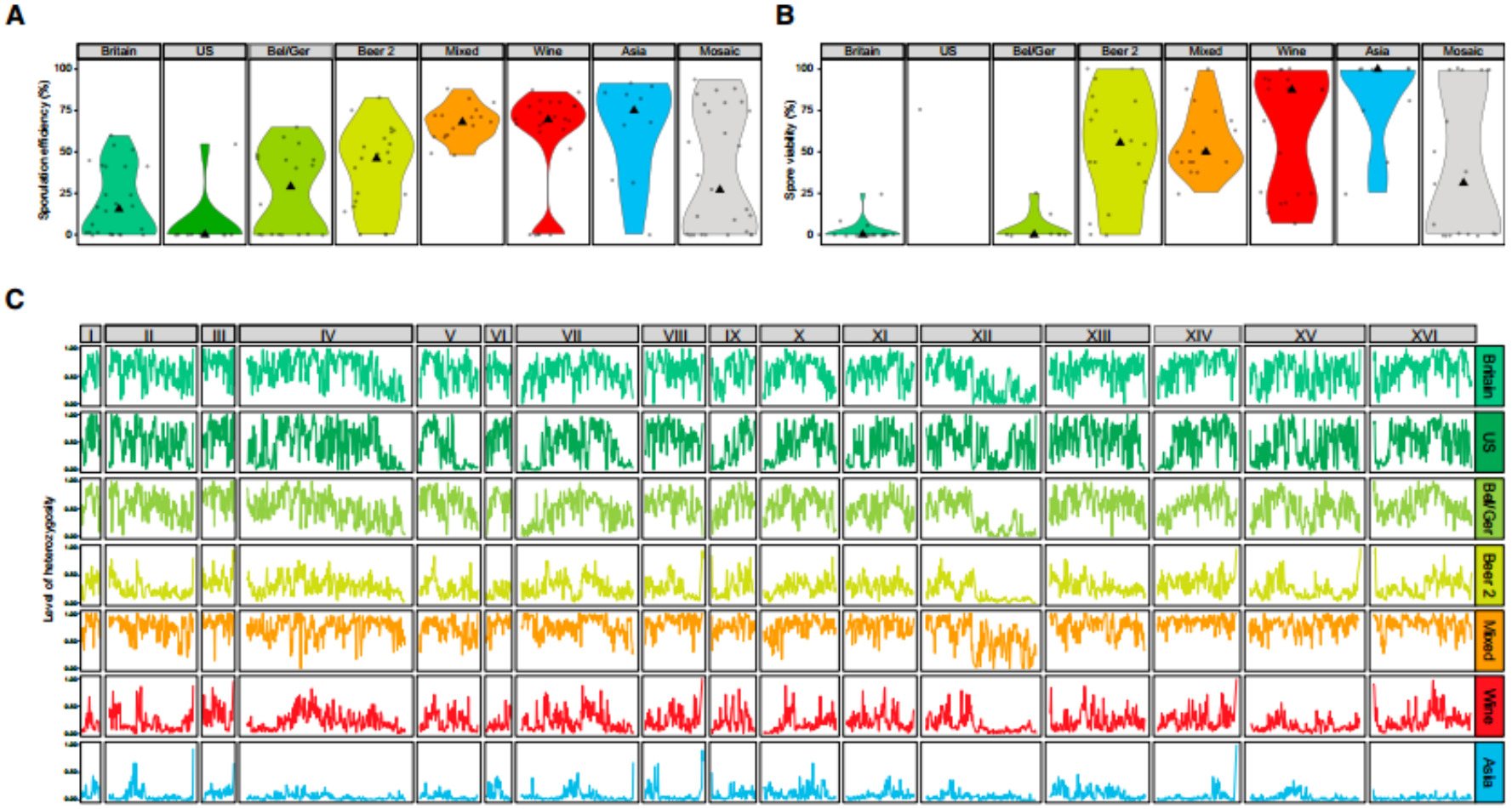


Figure 3. Trait Variation of Industrial S. cerevisiae Strains


A
Britain
US
Bel/Ger
Beer 2
Mixed
Wine
Asia
Mosaic
Sporulation efficiency (%)
100
75
50
25
0
B
Britain
US
Bel/Ger
Beer 2
Mixed
Wine
Asia
Mosaic
Spore viability (%)
100
75
50
25
0
C
I
II
III
IV
V
VI
VII
VIII
IX
X
XI
XII
XIII
XIV
XV
XVI
Level of heterozygosity
Britain
US
Bel/Ger
Beer 2
Mixed
Wine
Asia

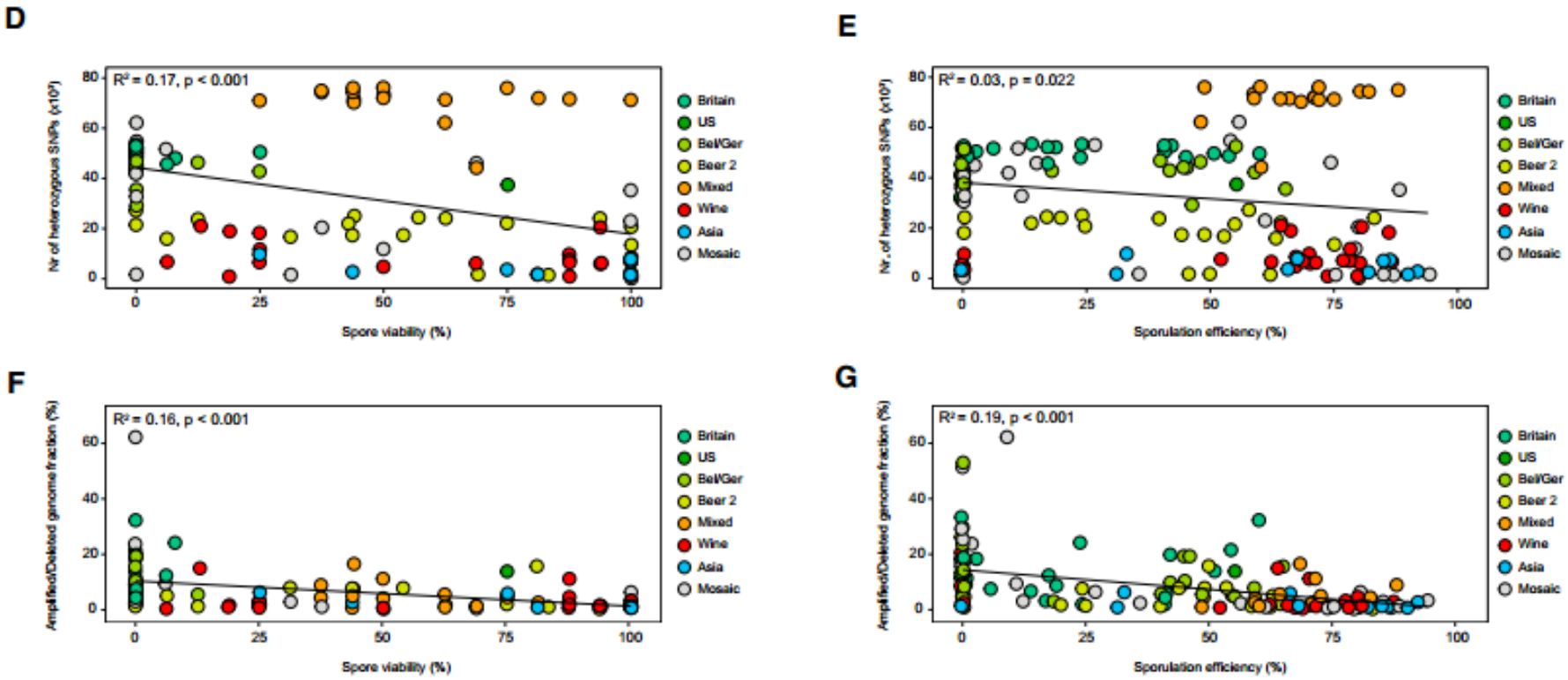
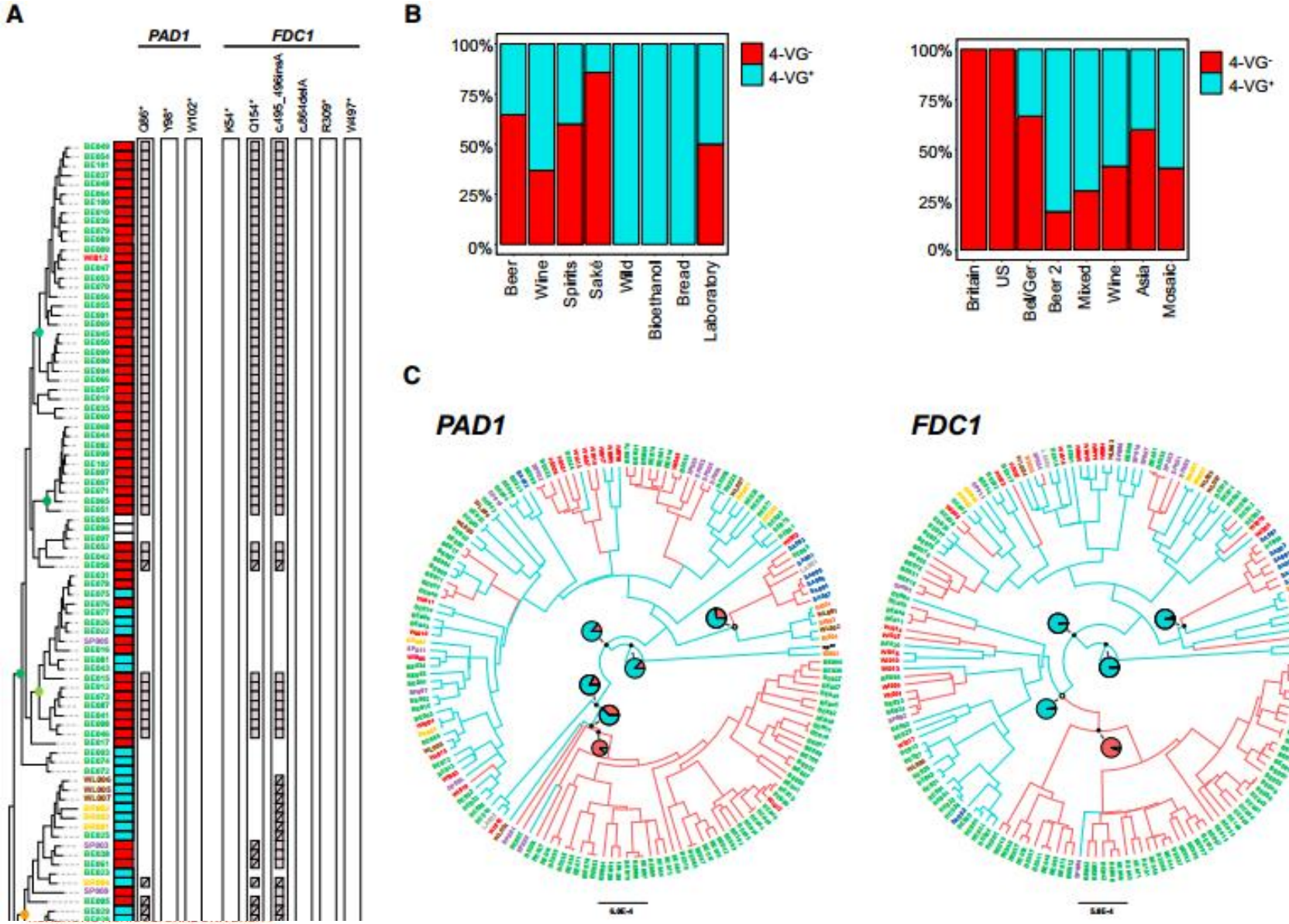


Figure 4. The Reproductive Lifestyle of Industrial S. cerevisiae Strains


A
PAD1
FDC1
Q66*
Y98*
W102*
K54*
Q154*
c.495_496insA
c.664delA
R309*
W497*
B
100%
75%
50%
25%
0%
4-VG-
4-VG+
Beer
Wine
Spirits
Saké
Wild
Bioethanol
Bread
Laboratory
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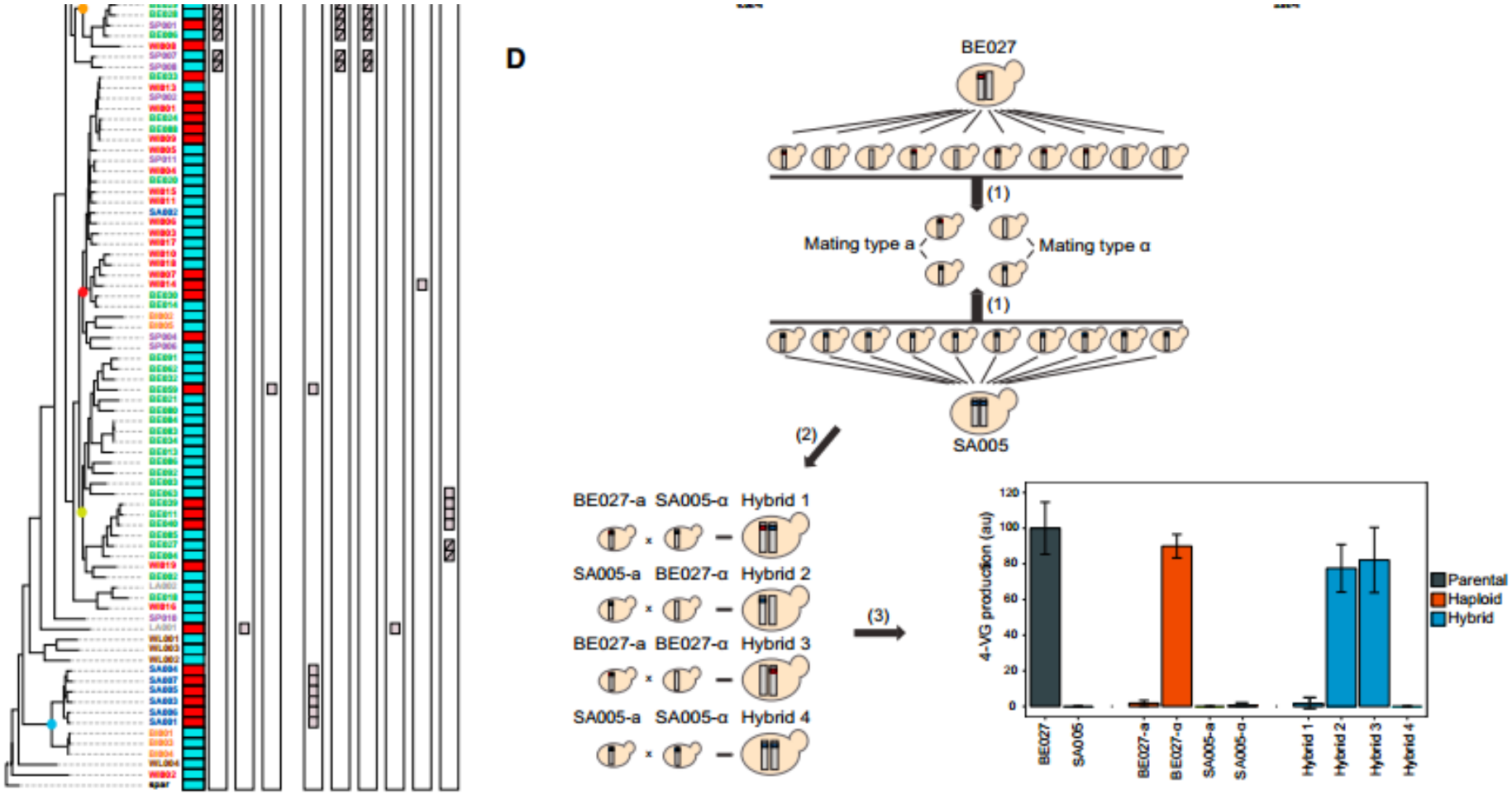
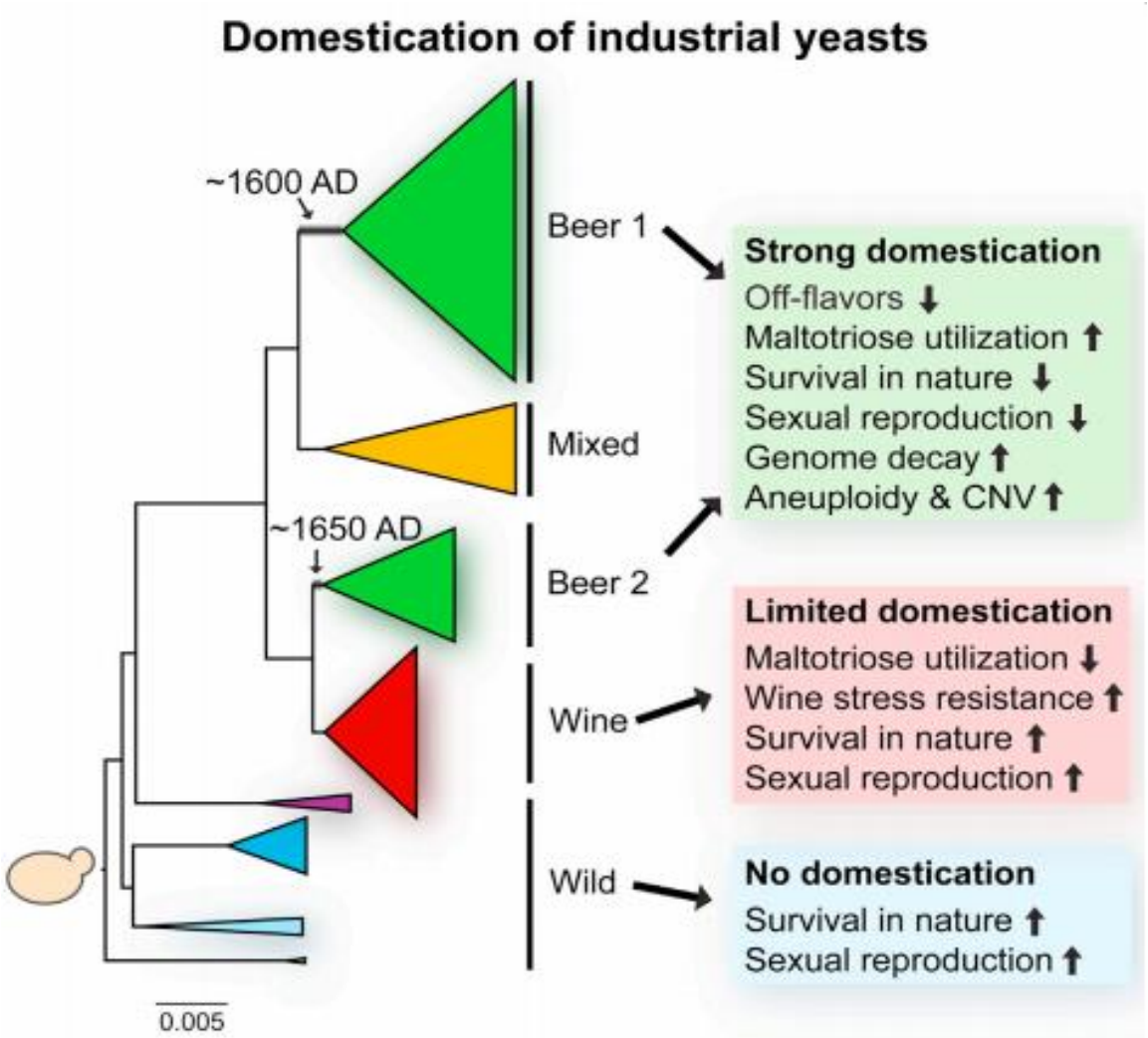


Figure 5. Production of 4-Vinyl Guaiacol by Industrial S. cerevisiae Strains

四、CONCLUSION



一句话总结

通过基因组和表型分析揭示了啤酒酵母和其他酿酒酵母用作酿造啤酒或其他酒精的历史与驯化过程。

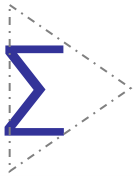
研究亮点

1、对157种酿酒酵母菌（S. cerevisiae）进行了测序；

2、当代的工业酵母起源于很小一部分驯化的酵母；

3、啤酒酵母显示了很强的驯化的基因和表型特征；

4、工业酵母的驯化在时间上比细菌的发现史还早100年。



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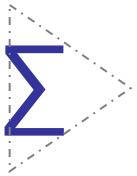

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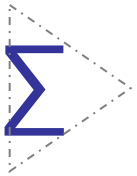

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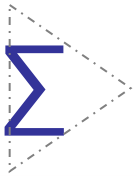

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报告要求

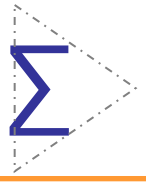
- 报告最后一页，解答三个问题：

  （1）用一句话概括此研究的主要结论或创新点。

  （2）此研究对你有何启发。

  （3）此研究还存在哪些问题可以改进。

目标：归纳总结能力和发现问题能力的培养。



Good Luck!