

## Supplementary material

### **Genomic Insights into **Novel Extremotolerant** Bacteria Isolated from the NASA Phoenix Mission Spacecraft Assembly Facility**

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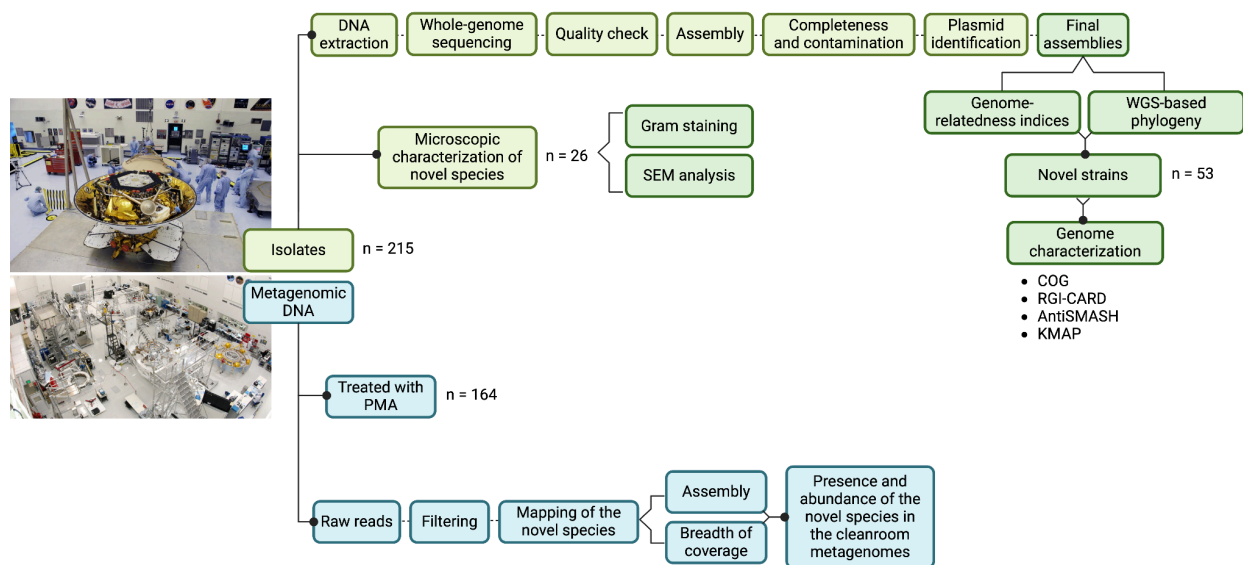
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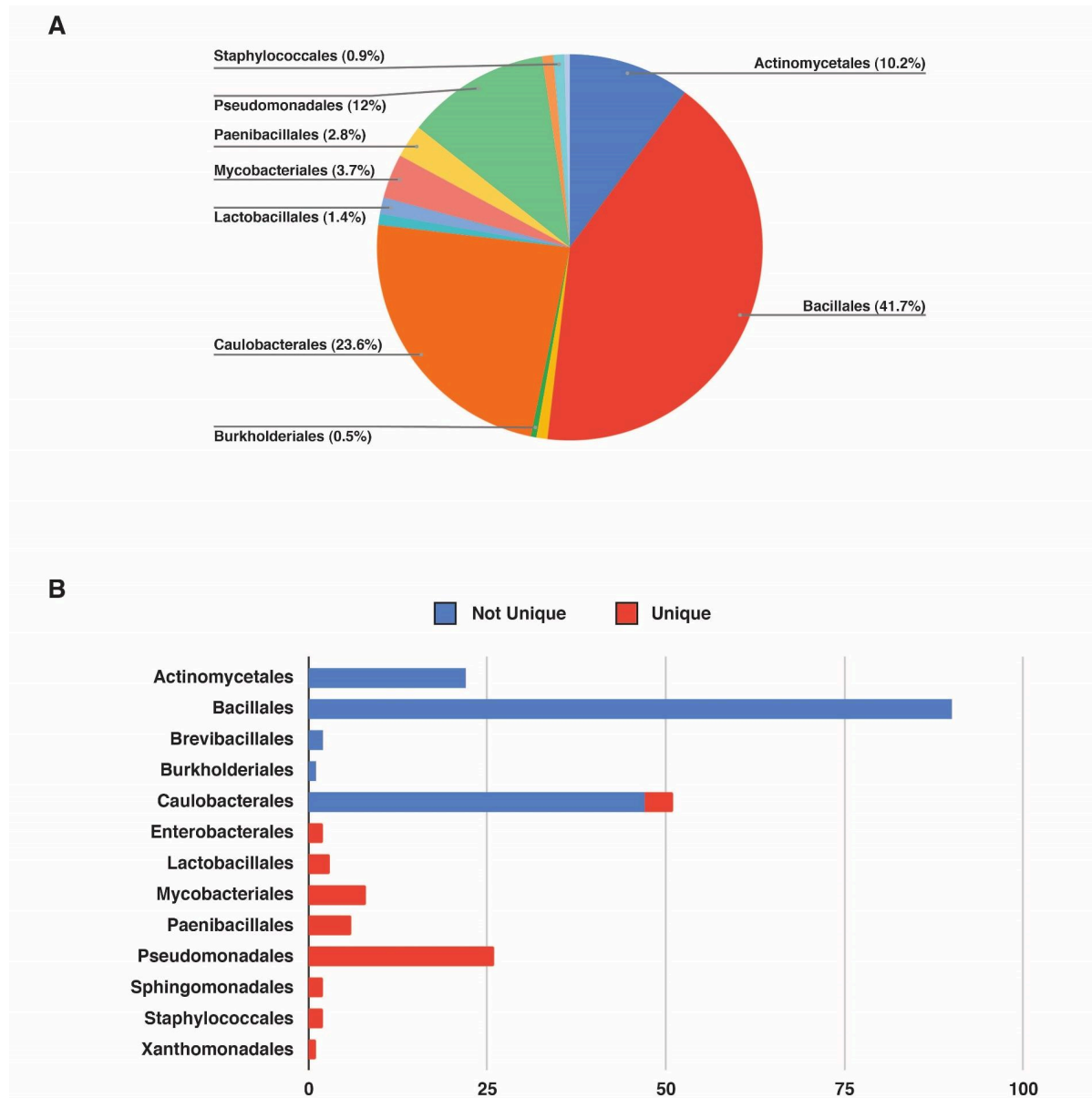
kjvenkat1955@gmail.com

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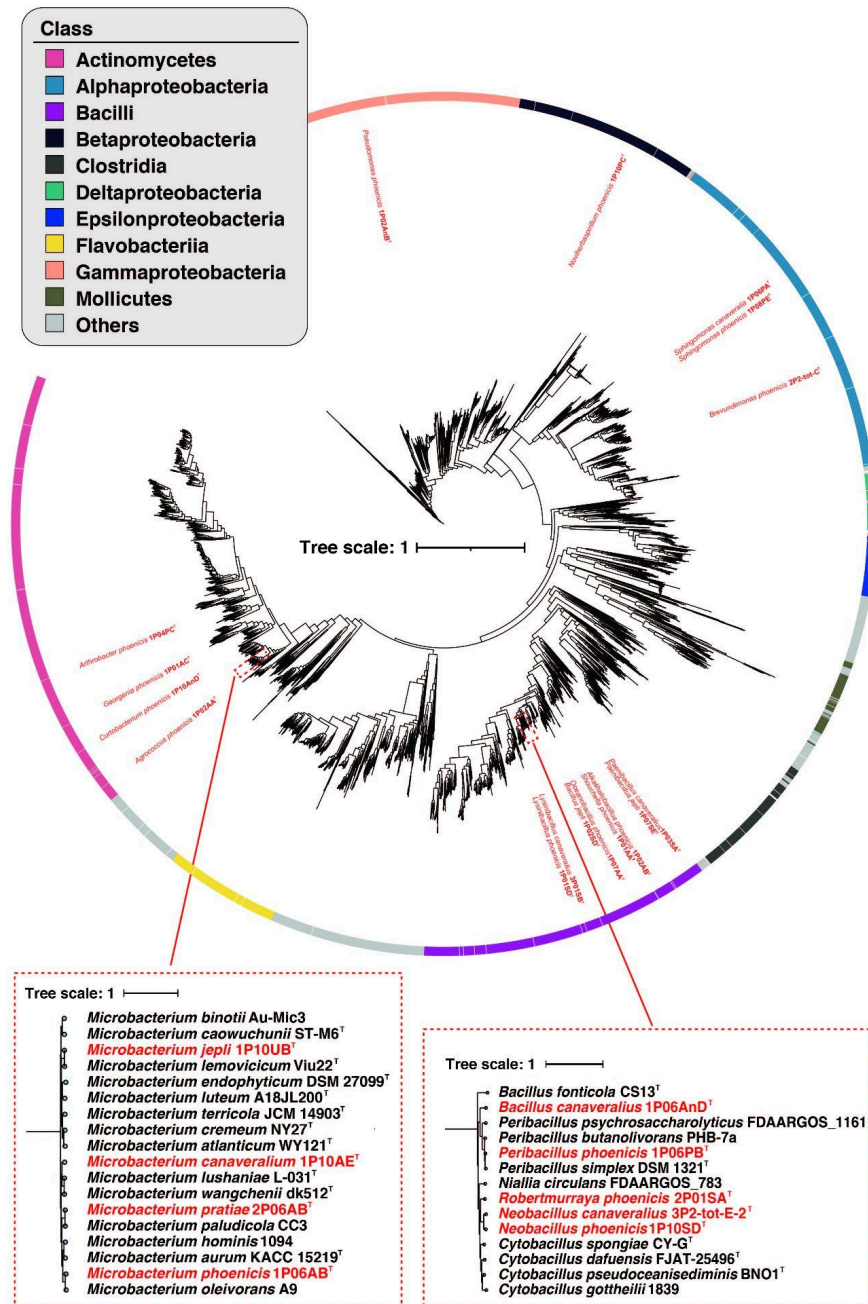
## SUPPLEMENTARY FIGURES



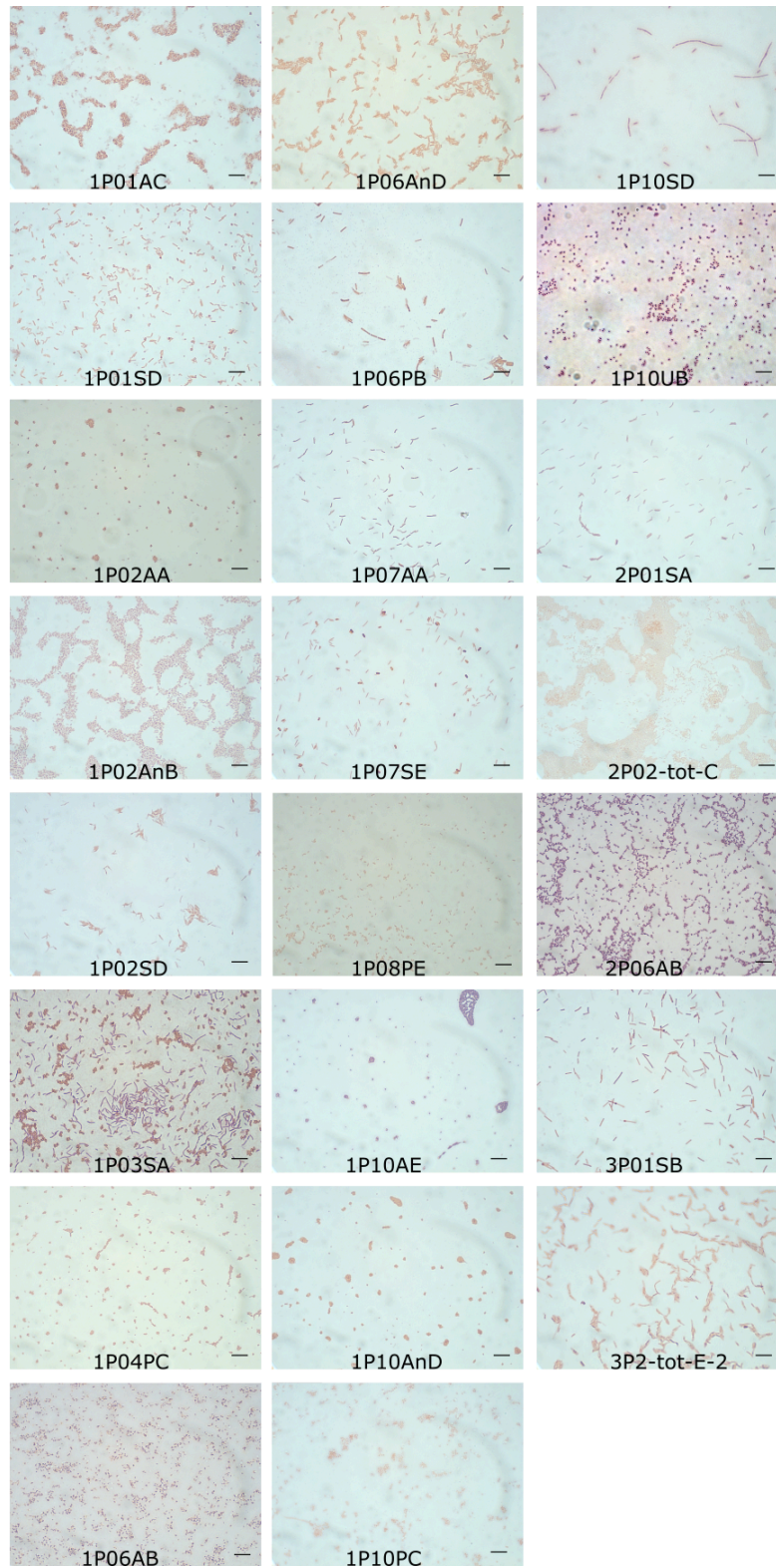
**Supplementary Figure S1.** A schematic flow chart of the experimental design and analyses used to describe 53 novel strains from the Phoenix mission spacecraft assembly facility, and to evaluate their persistence in the cleanrooms through metagenomic analysis.



**Supplementary Figure S2.** Taxonomic distribution of isolated species. A. Order-level classification of 215 isolated species, showing their phylogenetic diversity. B. Proportion of novel species within each order, highlighting the contribution of this study to the discovery of novel species in each taxonomic group.



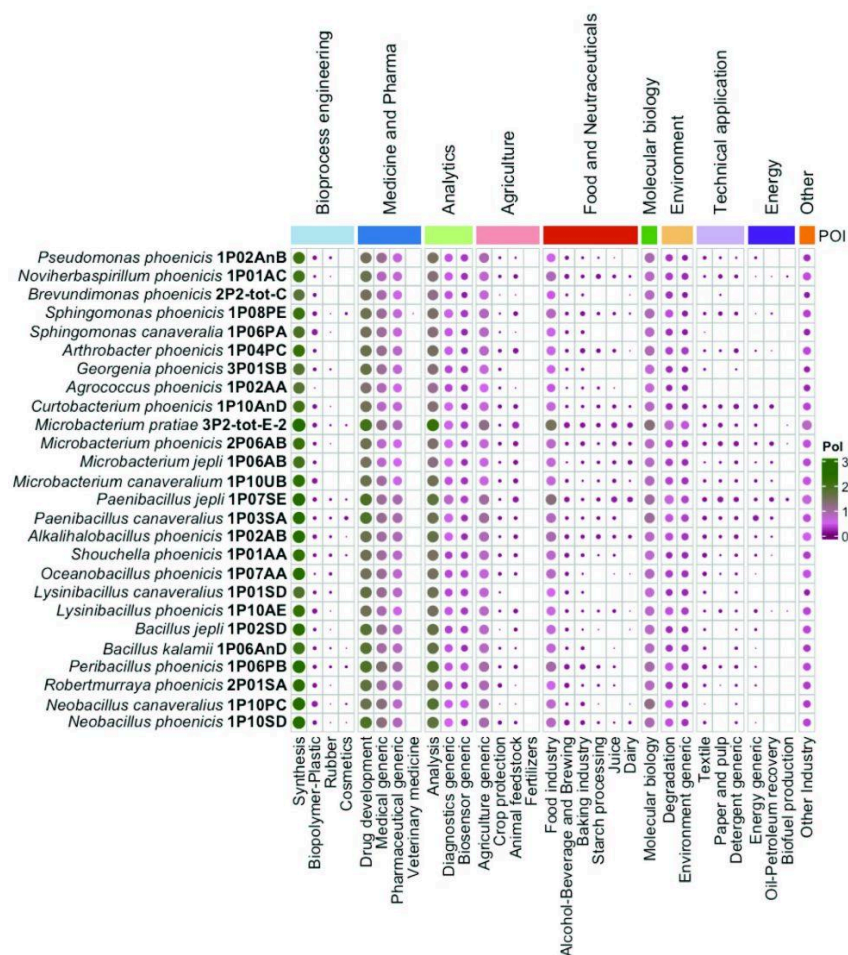
**Supplementary Figure S3.** A bacterial tree of life containing the 26 novel species isolated from Phoenix mission spacecraft based on 4,441 complete, non-anomalous representative genomes of Bacteria from the NCBI Reference Sequence database and built using the 16 SCG-set as previously described in Hug *et al.* (2016).



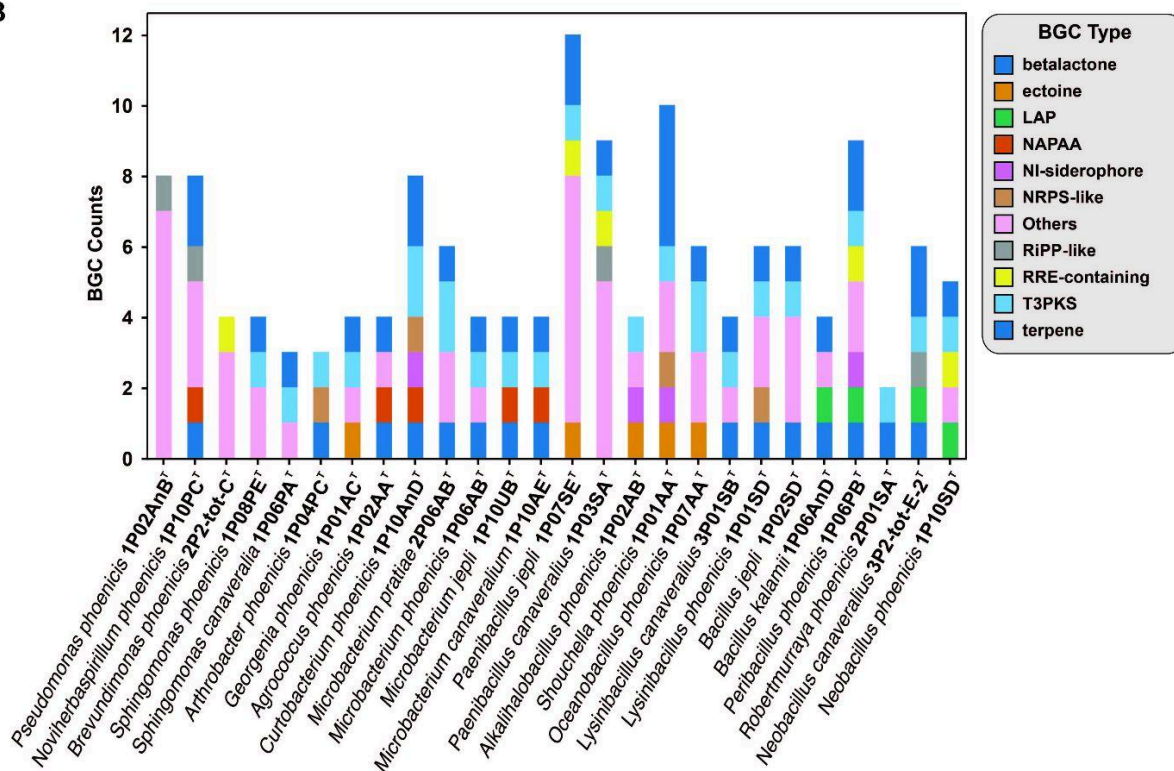
**Supplementary Figure S4.** Gram-staining images of the novel species isolated from Phoenix spacecraft mission.



A



B



**Supplementary Figure S5:** A. Identification of Proteins of Interest (PoI) using KMAP with applications in various industries, leveraging the unique functional capabilities of novel species from NASA cleanrooms. B. Secondary metabolite-producing biosynthetic gene clusters of novel Phoenix spacecraft bacterial species identified by AntiSMASH.