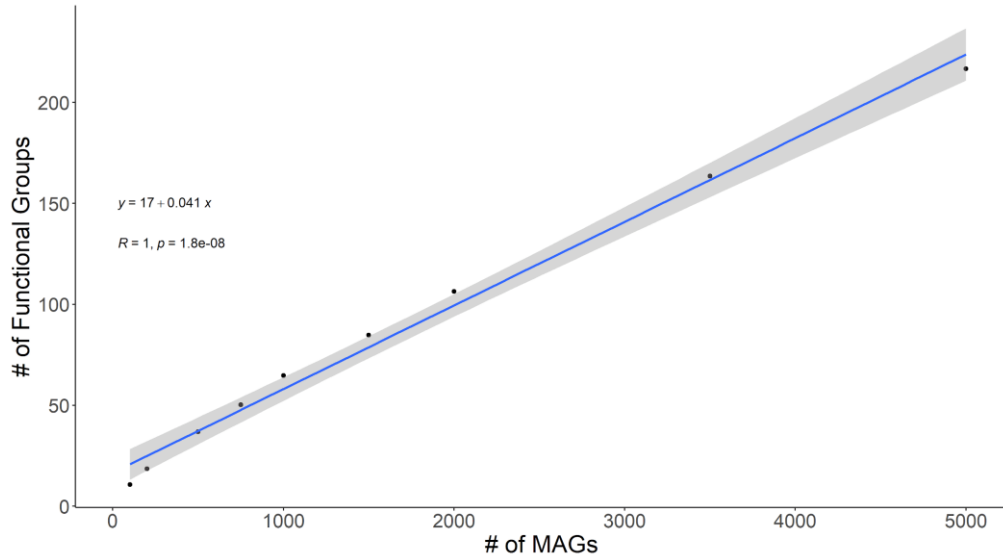
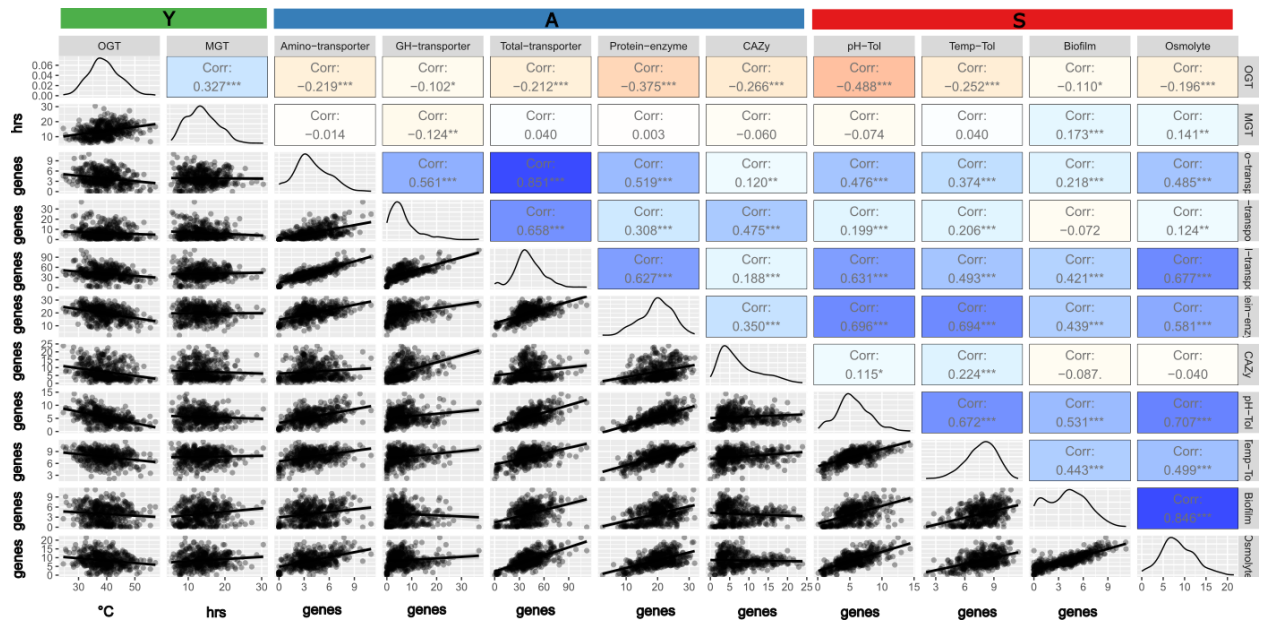


# Y-A+S is the new YAS: Updating microbial life history tradeoffs with comparative genomics - SI

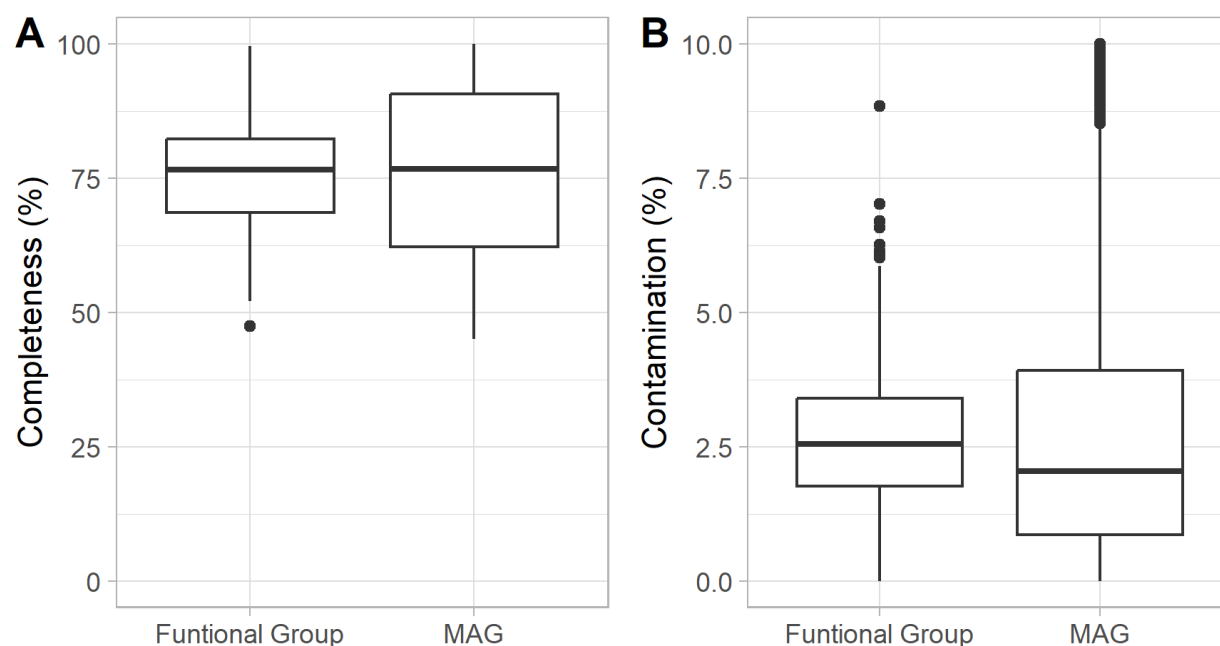
## Supplementary Figures



**Figure S1.** Curve to extrapolate the potential FGs for the entire MAG-to-genes matrix of 27214 MAGs and isolates. We randomly selected 100, 200, 500, 750, 1000, 1500, 2000, 3500, and 5000 MAGs to obtain the maximum number of FGs for each sample size. We repeated the process with 12 different samples per sample size and used the mean value of their FGs to fit a linear model.







**Figure S5.** Summary statistics of MAGs and functional group quality regarding completeness and contamination. All isolates used in this study were of high quality.

## Supplementary Tables

**Table S1.** Publicly available whole-genome sequences from soil isolates from the JGI-IMG portal  
<https://img.jgi.doe.gov/m>

[Table S1.xlsx](#)

**Table S2.** Key for microTrait genes encoding for carbohydrate degradation enzymes

[Table S2.xlsx](#)

**Table S3.** Key for microTrait genes encoding for protein degradation enzymes

[Table S3.xlsx](#)

**Table S4.** Key for microTrait genes encoding for transporters

[Table S4.xlsx](#)

**Table S5.** Key for microTrait genes encoding for osmolytes

[Table S5.xlsx](#)

**Table S6.** Key for microTrait genes encoding for biofilms

[Table\\_S6.xlsx](#)

**Table S7.** Key for microTrait genes encoding for high-temperature resistance

[Table\\_S7.xlsx](#)

**Table S8.** Key for microTrait genes encoding for pH tolerance

[Table\\_S8.xlsx](#)

**Table S9.** Correlations among traits for fast-growing MAGs FGs

[Table\\_S9.xlsx](#)

**Table S10.** Correlations among traits for slow-growing MAGs FGs

[Table\\_S10.xlsx](#)

**Table S11.** Correlations among traits for fast-growing soil isolate FGs

[Table\\_S11.xlsx](#)

**Table S12.** Correlations among traits for slow-growing soil isolate FGs

[Table\\_S12.xlsx](#)

**Table S13.** MAG microTrait output and metadata from the JGI-IMG portal <https://img.jgi.doe.gov/m>

[Table\\_S13.csv](#)

**Table S14.** microTrait output using MAGs from Nelson et al. <sup>2</sup>

[Table\\_S14.csv](#)

**Table S15.** microTrait output using MAGs from Malik et al. <sup>3</sup>

[Table\\_S15.csv](#)

**Table S16.** microTrait output from isolates

[Table\\_S16.csv](#)

**Table S17.** Selected genes to perform functional grouping

[Table\\_S17.xlsx](#)

**Table S18.** Functional groups per MAGs

[Table\\_S18.csv](#)

**Table S19.** Functional groups per isolate

[Table\\_S19.csv](#)

**Table S20.** Aggregate traits for slow-growing MAGs

[Table\\_S20.xlsx](#)

**Table S21.** Aggregate traits for fast-growing MAGs

[Table\\_S21.xlsx](#)

**Table S22.** Aggregate traits for slow and fast-growing isolates

[Table\\_S22.xlsx](#)

**Table S23.** Estimations of CUE for soil isolates

[Table\\_S23.csv](#)

## References

1. Marschmann, G. L. *et al.* Predictions of rhizosphere microbiome dynamics with a genome-informed and trait-based energy budget model. *Nat. Microbiol.* **9**, 421–433 (2024).
2. Nelson, A. R. *et al.* Wildfire-dependent changes in soil microbiome diversity and function. *Nat. Microbiol.* **7**, 1419–1430 (2022).
3. Malik, A. A. *et al.* Bacterial population-level trade-offs between drought tolerance and resource acquisition traits impact decomposition. *ISME J.* wrae224 (2024)  
doi:10.1093/ismejo/wrae224.