

Microbial community and metabolic pathway succession driven by changed nutrient inputs in tailings: effects of different nutrients on tailing remediation

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Fig caption:

Fig. S1 The qRT-PCR results of microbial biomass with universal primers.

Fig. S2 Alpha diversity index of microbial community

Fig. S3 The heat map of the key microbes in different experiment treatment

Fig. S4 Visualization the differences of sulfur metabolism genes that differed significantly ($p < 0.05$) by box plot

Fig. S5 Microbial community of remediation experiment on the natural conditions

Fig. S6 Remediation experiment of tailings on the natural conditions

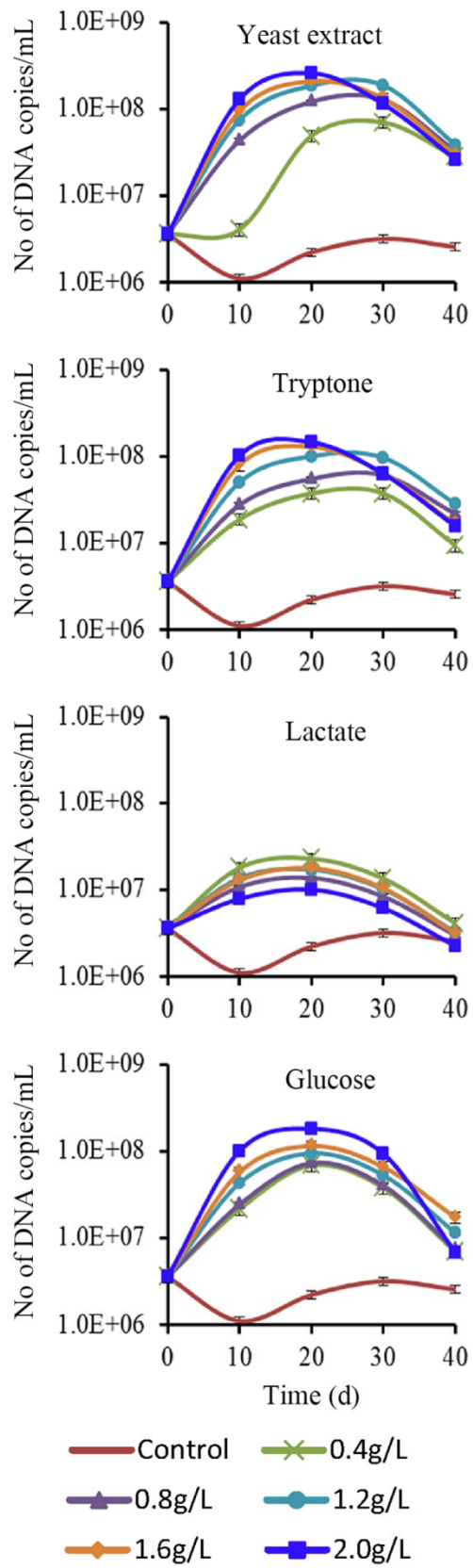


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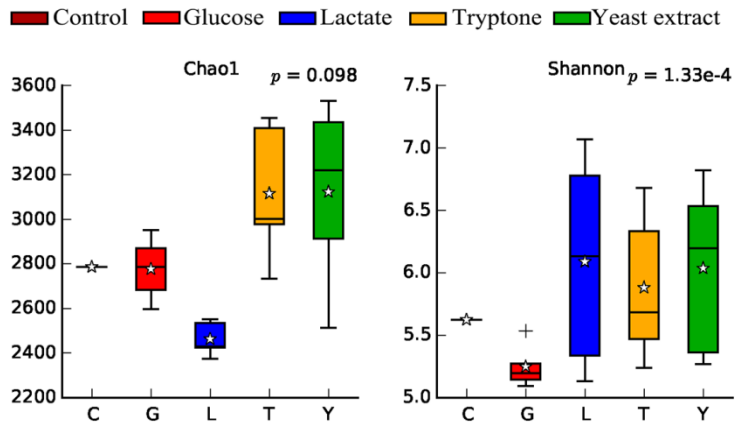


Fig. S2 Alpha diversity index of microbial community

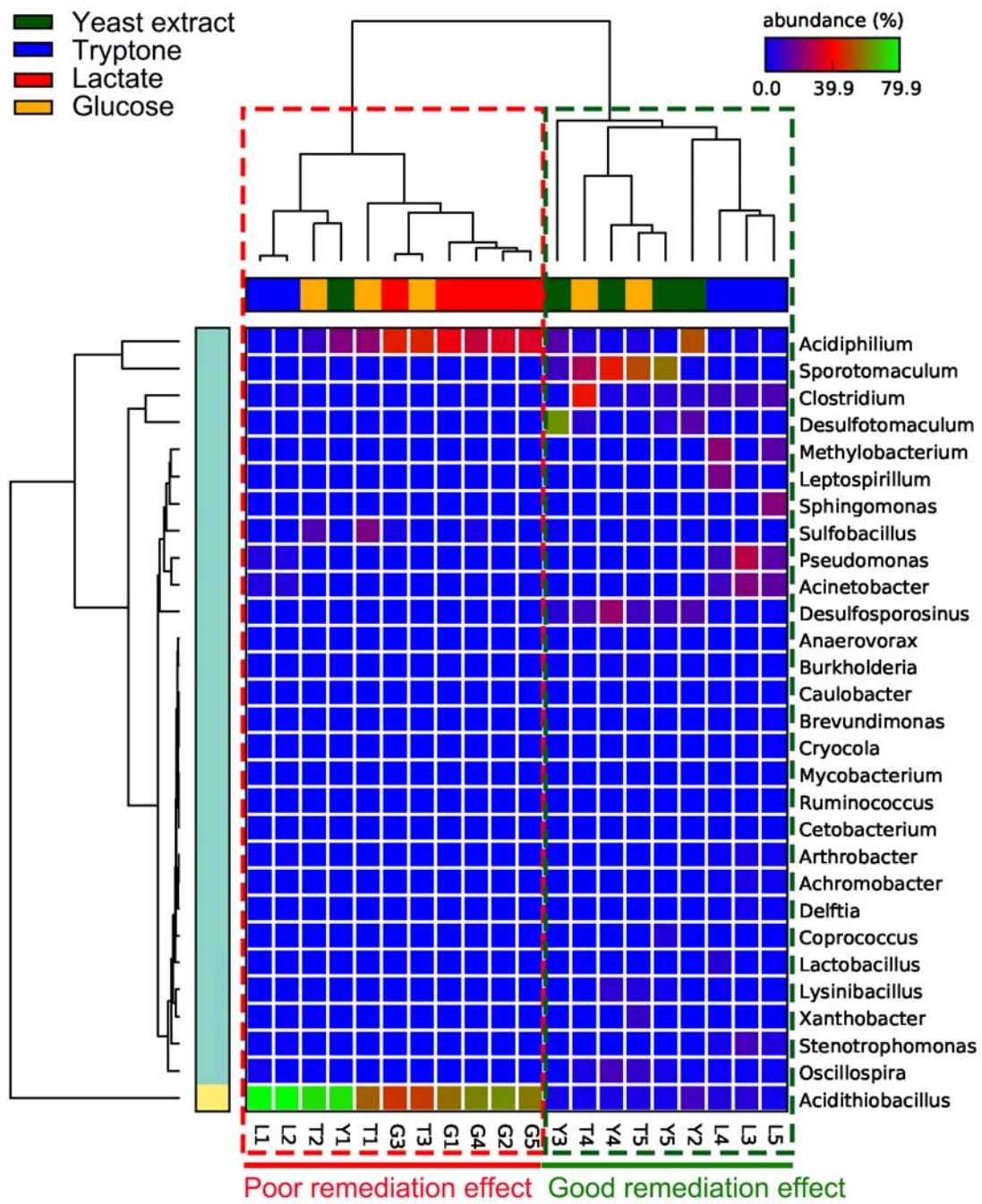


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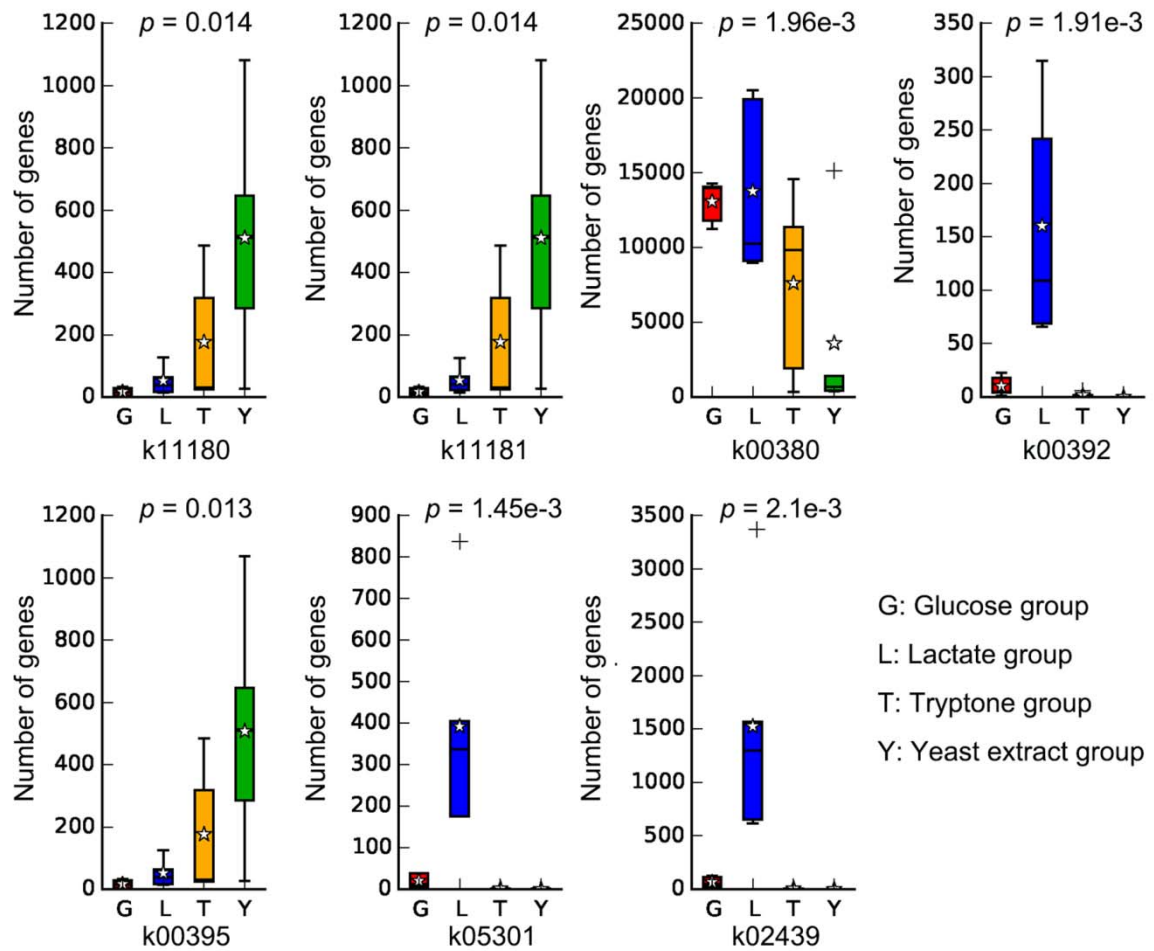


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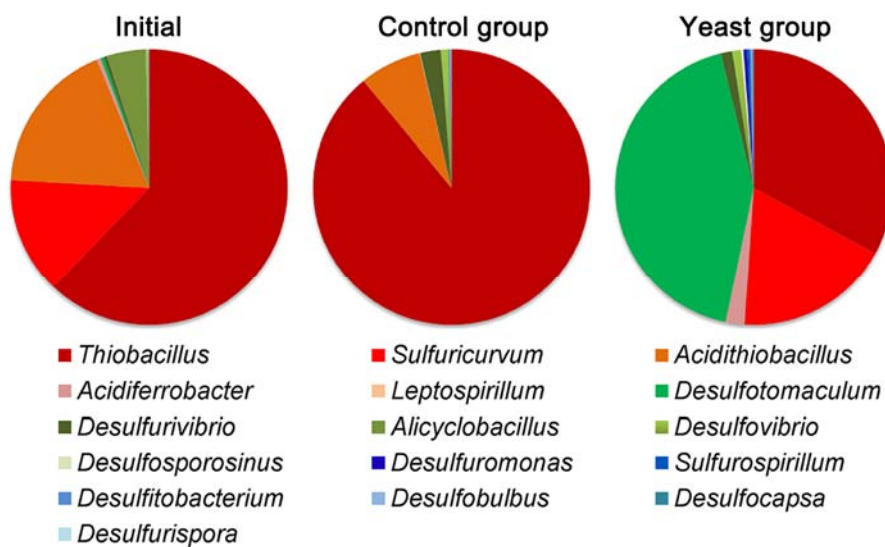


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