Assessing the genetic diversity of Cu resistance in mine tailings through high-throughput recovery of full length *copA* genes

Xiaofang Li[1], Yong-Guan Zhu[2], Babak Shaban[3], Timothy J. C. Bruxner[4], Philip L. Bond[5], Longbin Huang[1]*

[1]Centre for Mined Land Rehabilitation, Sustainable Minerals Institute, The University of Queensland, QLD 4072, Australia

[2]Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, 10081, China

[3]Australian Genomics Research Facility, Parkville, Melbourne 3000, Australia

[4]Institute for Molecular Bioscience, The University of Queensland, QLD 4072, Australia

[5]Advanced Water Management Centre, The University of Queensland, QLD 4072, Australia

***Corresponding authors**

Longbin Huang: l.huang@uq.edu.au; also to Yong-Guan Zhu: ygzhu@iue.ac.cn

Running title: Metagenomics for *copA* diversity in mine tailings

Notes:
1-12 Alpha Proteobacteria
13-22 Deta Proteobacteria
23-47 Gamma Proteobacteria
48-54 Delta Proteobateria
55-59 Epsilonproteobacteria
60-74 Firmcutes
75-91 Actinobacteria
92-97 Cyanobacteria
98-110 CFB group bacteria
111-113 Mycoplasmas
114-116 Chlamydias
117-119 Acidobacteriaceae
120-122 GNS bacteria

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>gi|392987295:1790883-1793066 Enterococcus hirae ATCC 9790 chromosome, complete genome_71

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>gi|384133787:390174-392552 Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1 chromosome, complete genome_72

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>gi|339626328:c3356477-3354051 Sulfobacillus acidophilus TPY chromosome, complete genome_73

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>gi|374290092:c400946-398721 Blattabacterium sp. (Cryptocercus punctulatus) str. Cpu chromosome, complete genome101

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>gi|294505815:c2045657-2043036 Salinibacter ruber M8 chromosome, complete genome102

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>gi|110636427:c1729671-1727257 Cytophaga hutchinsonii ATCC 33406 chromosome, complete genome103

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>gi|379728134:2860809-2863028 Saprospira grandis str. Lewin chromosome, complete genome104

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>gi|268315578:1607644-1609509 Rhodothermus marinus DSM 4252 chromosome, complete genome105

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>gi|313205511:1994409-1996637 Riemerella anatipestifer ATCC 11845 = DSM 15868 chromosome, complete genome106

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>gi|327402011:c4250481-4248232 Fluviicola taffensis DSM 16823 chromosome, complete genome107

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>gi|325102757:1876259-1878529 Pedobacter saltans DSM 12145 chromosome, complete genome108

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