Figure Captions

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## Figure 1 (figures/fig1-tree/tree-abbrev.pdf)

Phylogenetic placement of the SAGs and MAGs within the acI lineage, relative to other sequenced actinobacterial genomes in the class Actinobacteria (Gao and Gupta 2012). The tree was built using RAxML (Stamatakis 2014) from a concatenated alignment of single-copy marker genes (Darling et al. 2014). The class Acidimicrobiia forms the outgroup.

## Figure 2a(b) (figures/fig2-sampling/completeness-2.svg and figures/fig2-sampling/completeness-1.svg)

Mean estimated completeness of tribe(clade)-level population genomes. For each tribe(clade), genomes were randomly sampled (with replacement) from the set of all genomes belonging to that tribe(clade). Completeness was estimated using single-copy marker genes (Parks et al. 2015). Error bars represent the 95% confidence estimated from 1000 iterations.

## Supplementary Figure 1 (figures/fig1-tree/tree-full.pdf)

Phylogenetic placement of the SAGs and MAGs within the acI lineage, relative to other sequenced actinobacterial genomes in the class Actinobacteria (Gao and Gupta 2012). The tree was built using RAxML (Stamatakis 2014) from a concatenated alignment of single-copy marker genes (Darling et al. 2014). The class Acidimicrobiia forms the outgroup.

## References

Darling, Aaron E, Guillaume Jospin, Eric Lowe, Frederick A Matsen, Holly M Bik, and Jonathan A Eisen. 2014. “PhyloSift: phylogenetic analysis of genomes and metagenomes.” *PeerJ* 2 (January): e243. [doi:10.7717/peerj.243](http://doi.org/10.7717/peerj.243).

Gao, Beile, and Radhey S Gupta. 2012. “Phylogenetic Framework and Molecular Signatures for the Main Clades of the Phylum Actinobacteria.” *Microbiology and Molecular Biology Reviews* 76 (1): 66–112. [doi:10.1128/MMBR.05011-11](http://doi.org/10.1128/MMBR.05011-11).

Parks, Donovan H, Michael Imelfort, Connor T Skennerton, Phil Hugenholtz, and Gene W Tyson. 2015. “CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes.” *Genome Research* 25 (7): 1043–55. [doi:10.1101/gr.186072.114.Freely](http://doi.org/10.1101/gr.186072.114.Freely).

Stamatakis, Alexandros. 2014. “RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies.” *Bioinformatics* 30 (9): 1312–13. [doi:10.1093/bioinformatics/btu033](http://doi.org/10.1093/bioinformatics/btu033).