Researchers discover 'dormant' magnetosome genes in non-magnetic bacteria

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Phylogeny, chromosome, and MGCs organization of G2-11. a The maximum likelihood phylogenetic tree based on ribosomal proteins demonstrates the position of G2-11 (highlighted in red) within family *Acetobacteraceae* (highlighted in the yellow box). The *Azospirillaceae* family was used as an outgroup based on the latest *Alphaproteobacteria* phylogeny. Branch length represents the number of base substitutions per site. Values at nodes indicate branch support calculated from 500 replicates using non-parametric bootstrap analysis. Bootstrap values
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