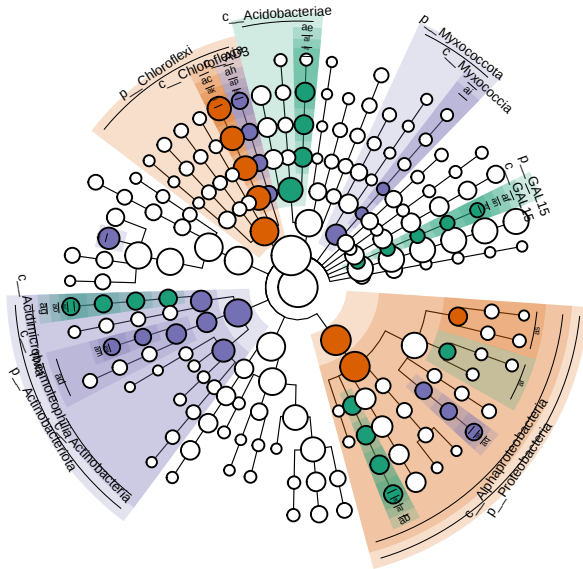




- | | |
|--|--|
|  ab: o__norank_c__Alphaproteobacteria |  aq: f__Hyphomicrobiaceae |
|  ac: o__Chloroflexales |  ar: f__Rhizobiaceae |
|  ad: o__Gaiellales |  as: f__Xanthobacteraceae |
|  ae: o__Acidobacteriales |  at: g__norank_c__Alphaproteobacteria |
|  af: o__GAL15 |  au: g__norank_f__Roseiflexaceae |
|  ag: o__Microtrichales |  av: g__norank_o__Acidobacteriales |
|  ah: o__AD3 |  aw: g__Gaiella |
|  ai: o__Myxococcales |  ax: g__DEV008 |
|  aj: f__norank_c__Alphaproteobacteria |  ay: g__GAL15 |
|  ak: f__Roseiflexaceae |  az: g__CL500-29_marine_group |
|  al: f__norank_o__Acidobacteriales |  bc: g__AD3 |
|  am: f__Gaiellaceae |  bd: g__Hyphomicrobium |
|  an: f__GAL15 |  be: s__norank_c__Alphaproteobacteria |
|  ao: f__Ilumatobacteraceae |  bf: s__metagenome_g__CL500-29_marine_group |
|  ap: f__AD3 |  bg: s__norank_g__Hyphomicrobium |