

Tree scale: 1

Phylum

- Cyanobacteria
- Deinococcota
- Proteobacteria
- Archaea
- Latescibacterota
- Patescibacteria
- Acidobacteriota
- Actinobacteriota
- Bacteroidota
- Chloroflexota
- Dormibacterota
- Eremiobacterota
- Other
- Desulfobacterota
- Firmicutes
- Nitrospirota
- Planctomycetota
- Verrucomicrobiota
- Methylomirabilota

Branch colour (RuBisCO form)

- Form II
- Form III
- Form IA
- Form IB
- Form IC
- Form ID
- Form IE
- Form IV

Site

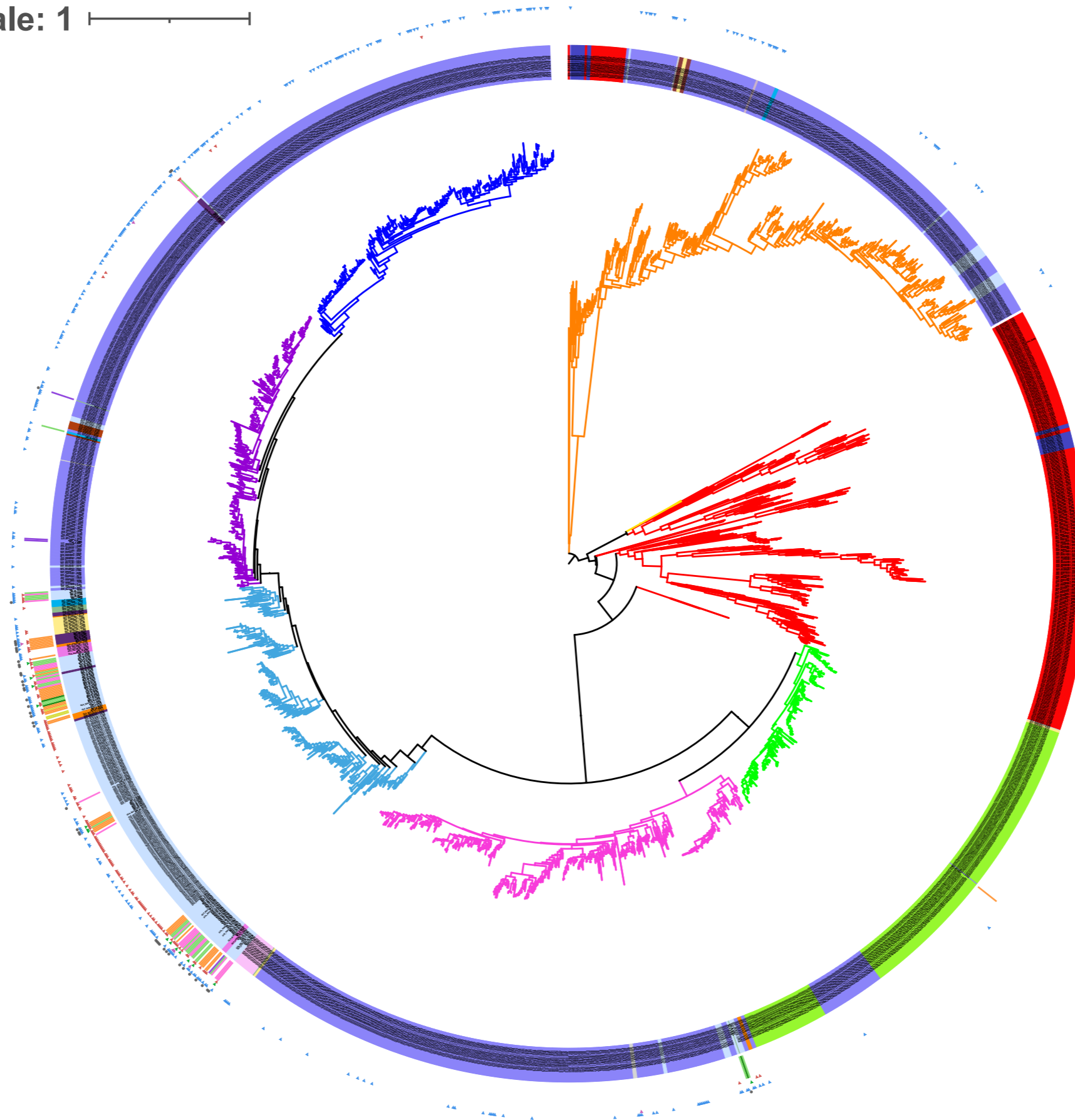
- Tibetan Plateau
- Mitchell Peninsula
- The Ridge
- New Harbour
- Spitsbergen Svalbard
- Alexandra Fjord Highlands

H2 and CO oxidation genes

- hhyL*
- hhmL*
- hylL*
- coxL*

MAG Quality

- >50% complete, <10% contaminated



Supplementary 19: Maximum likelihood phylogenetic tree of RuBisCO gene sequences obtained from our MAGs and over 3000 published genomes. Leaves are coloured to represent phylum, while coloured branches show RuBisCO form. MAGs assembled in this study are classified according to the site where they are most abundant, and our medium to high quality MAGs are indicated by a grey outer circle. Genomes which harboured additional trace gas oxidation genes, including the high affinity groups 1h-[NiFe]-hydrogenase (*hhyL*), 1m-[NiFe]-hydrogenase (*hhmL*), 1l-[NiFe]-hydrogenase (*hylL*) and/or aerobic carbon monoxide dehydrogenase (*coxL*) with an active-site loop are indicated by outer triangles, coloured red, green, pink, and blue, respectively. Bootstrap values >90% are depicted as filled circles on branches; 1000 ultrafast bootstrap iterations were applied.