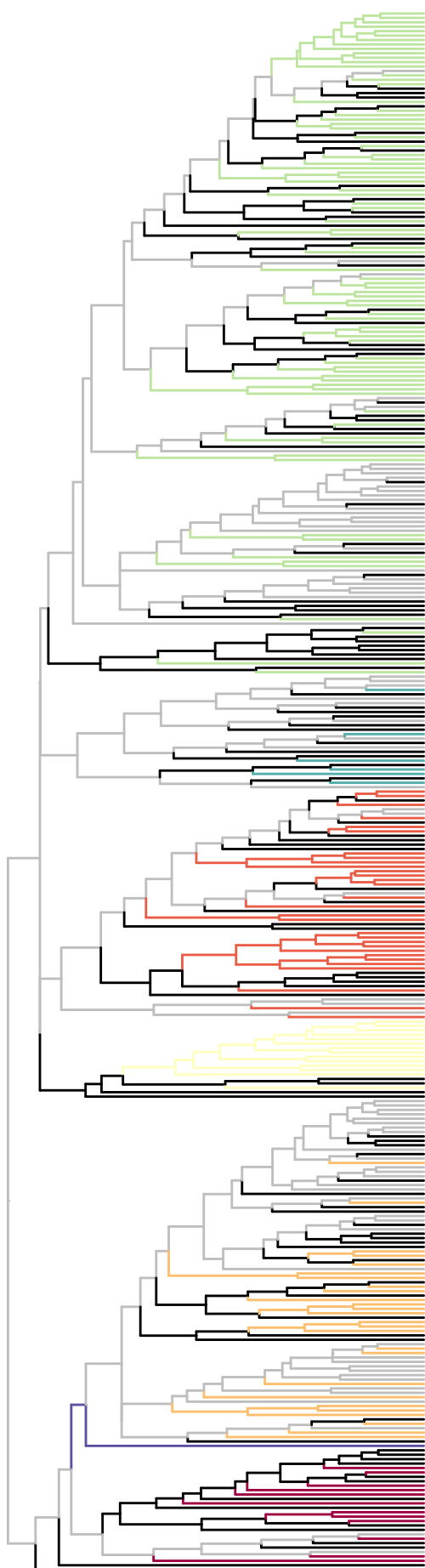


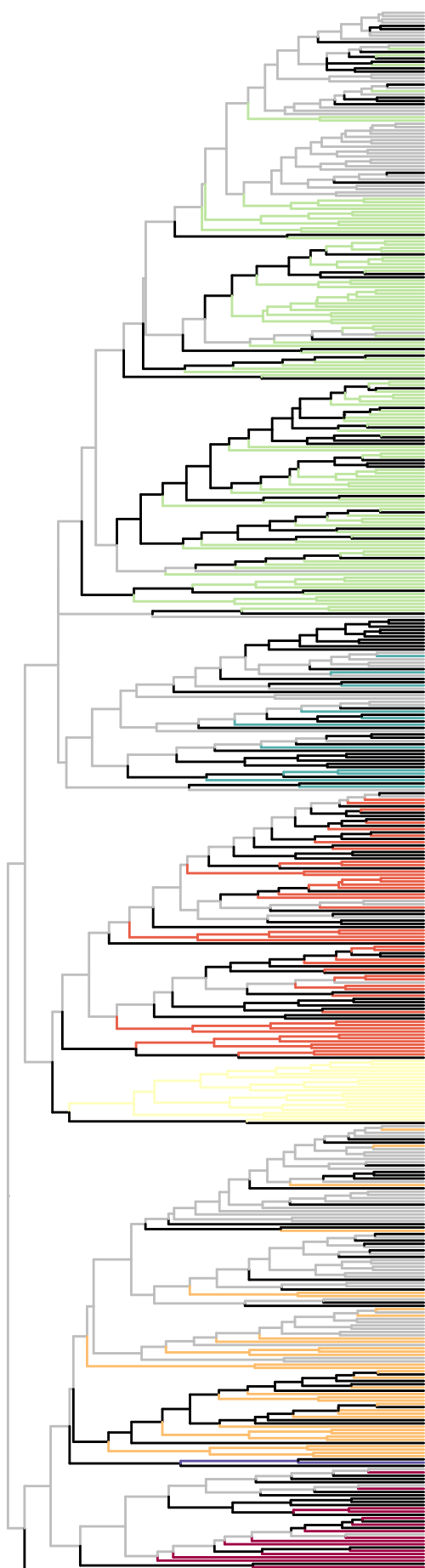
OTU similarity = 91percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

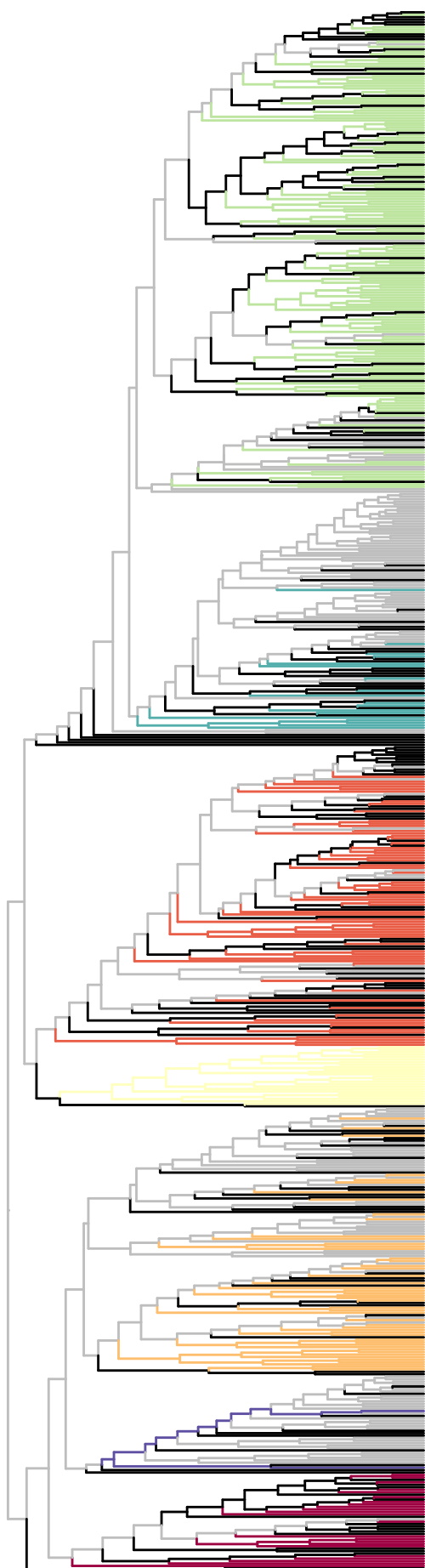
OTU similarity = 92percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

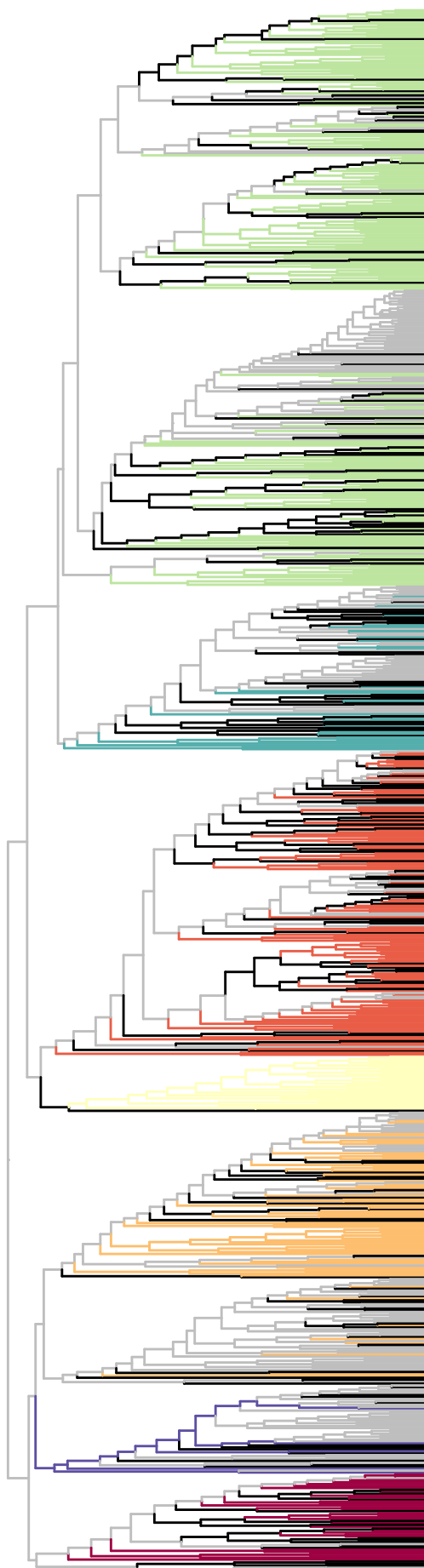
OTU similarity = 93percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

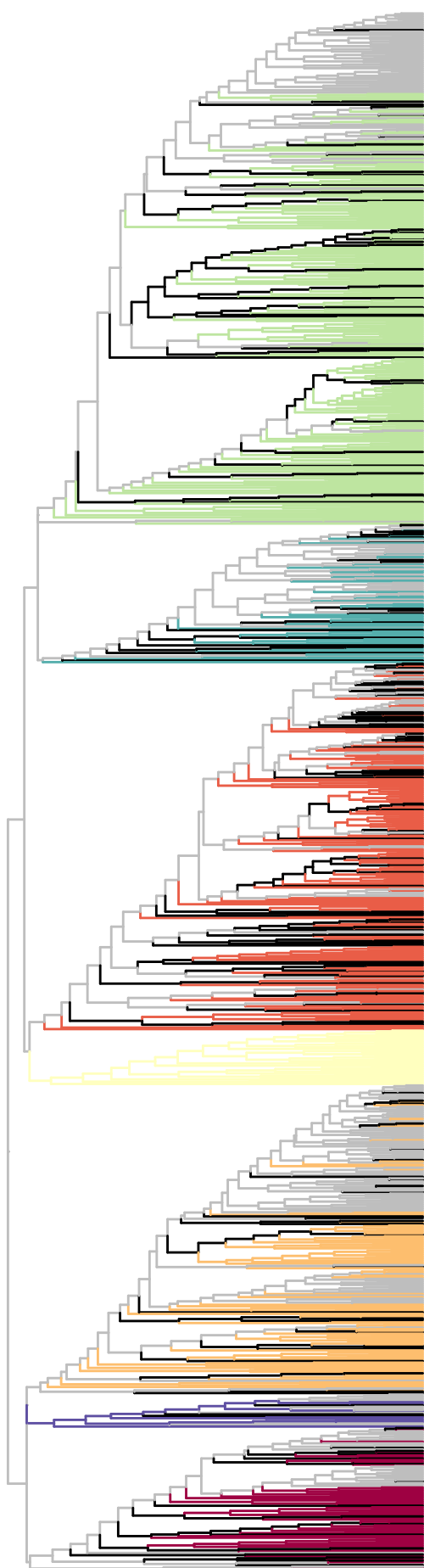
OTU similarity = 94percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

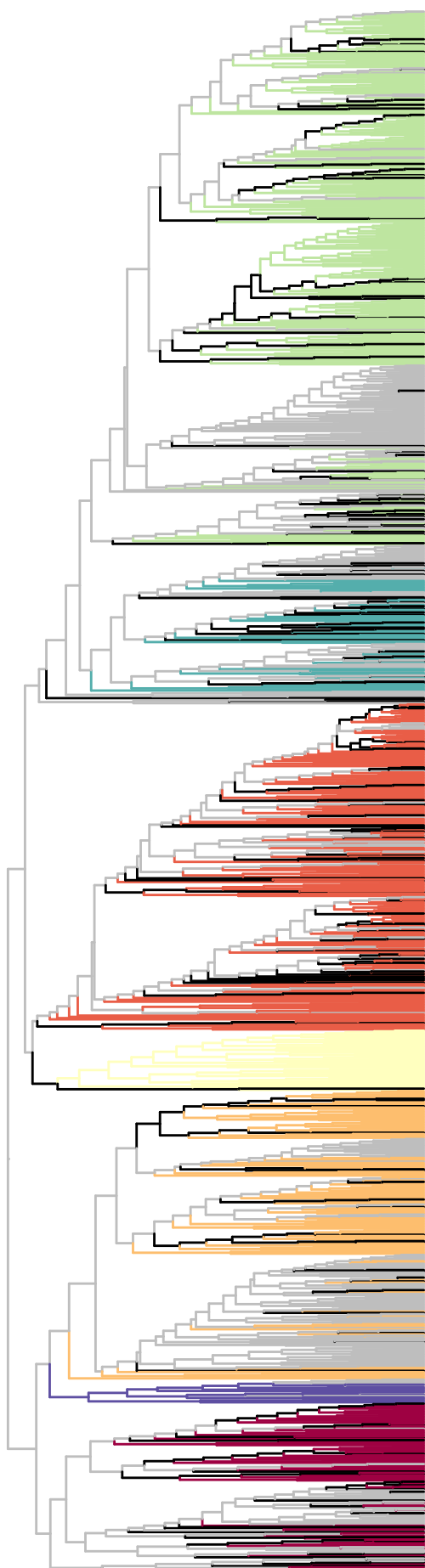
OTU similarity = 95percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

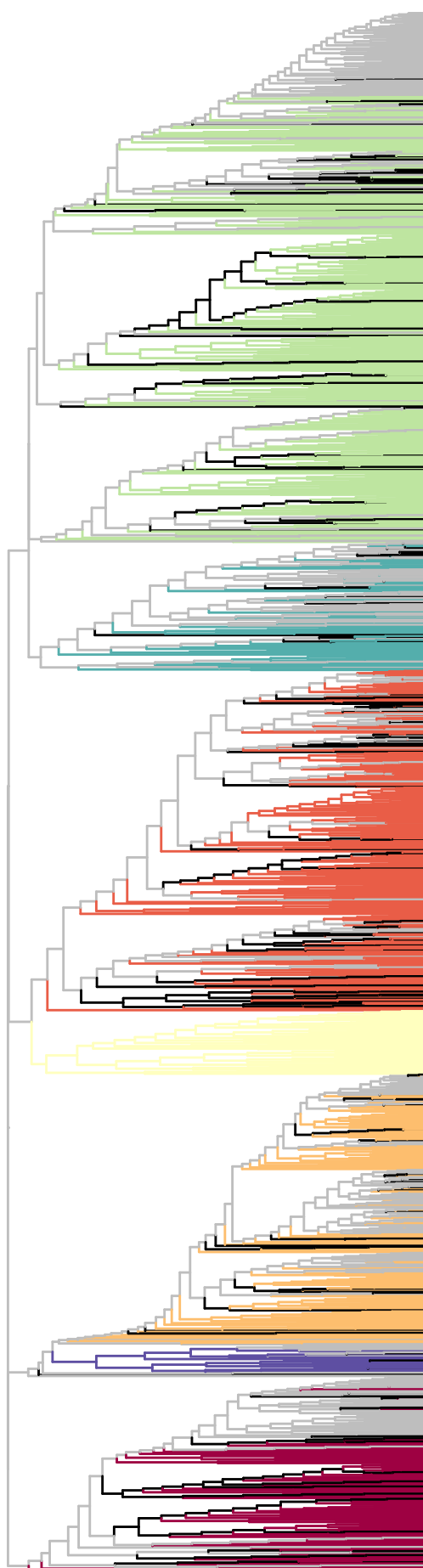
OTU similarity = 96percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

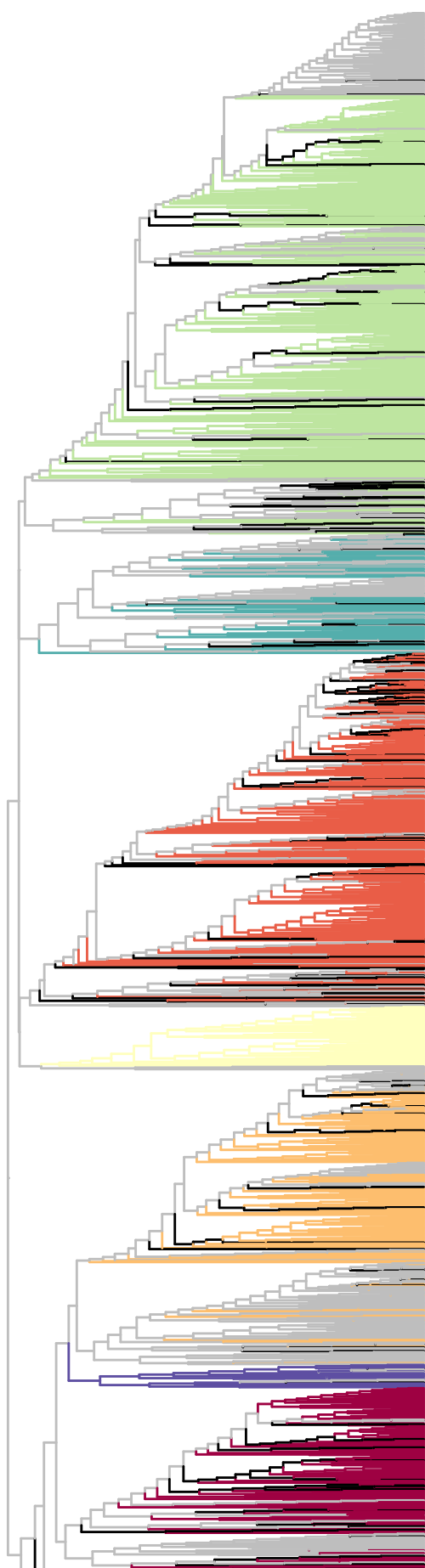
OTU similarity = 97percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

OTU similarity = 97.7percent

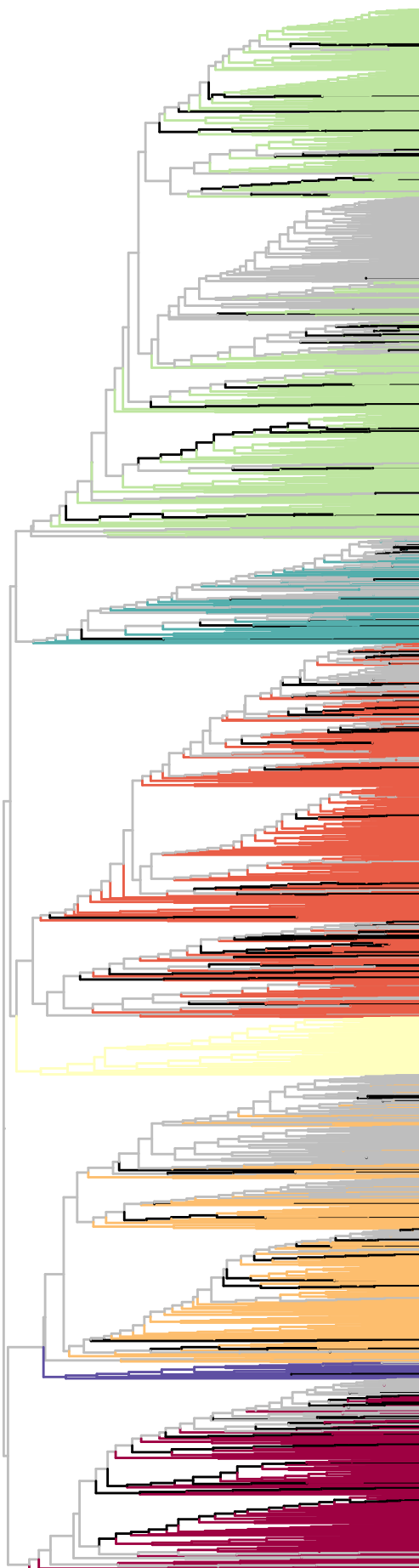


Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae



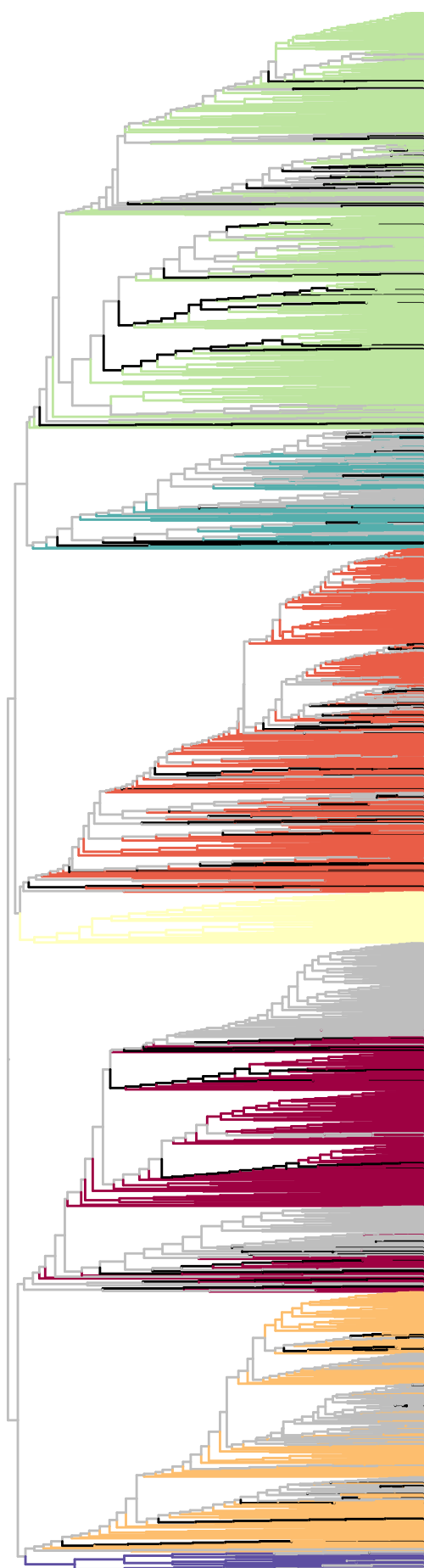
OTU similarity = 98percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

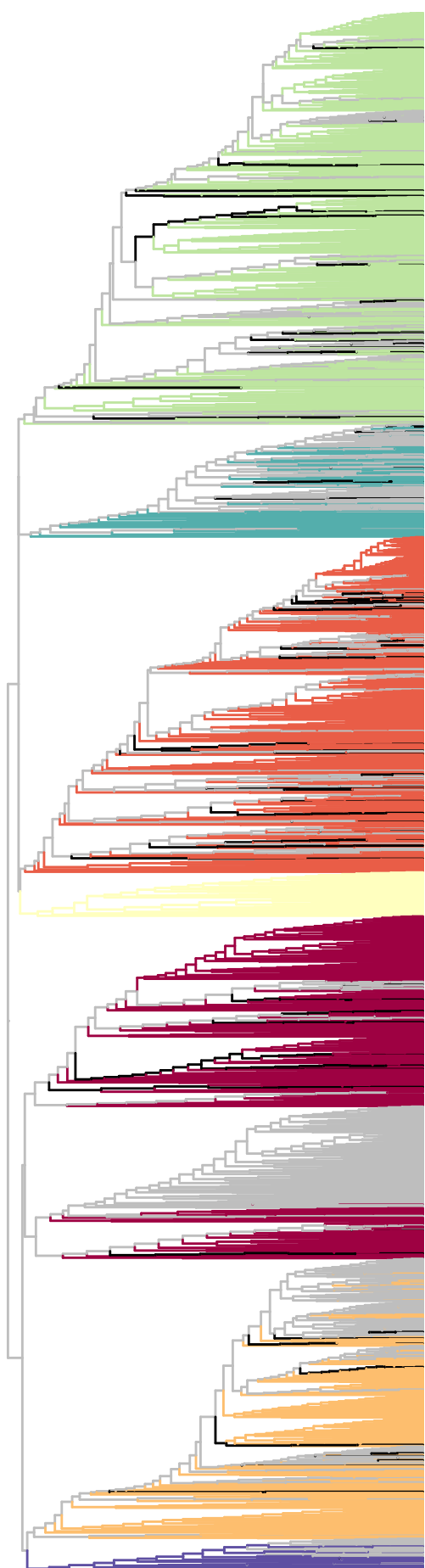
OTU similarity = 99percent



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae

OTU similarity = asv



Family (branch colours)

- Anaeromyxobacteraceae
- Haliangiaceae
- Myxococcaceae
- Nannocystaceae
- Polyangiaceae
- Sandaracinaceae
- uncertain
- unconstrained
- Vulgatibacteraceae