

Genome assembly metadata

☐ Genome Assembly structured comment is in the contig .sqn file(s)

Assembly date ?

← the date you carried out the assembly

★ Assembly method ?

SPAdes

▴ ▾

★ Version or Date program was run ?

3.12.0

Delete



+ Add another assembly method

← run `spades.py -v` to find this out

Assembly name ?

Al4-7

← leave this blank

i If you have a meaningful assembly name like UCLA_Agam_2.1 ([see naming recommendations](#)), please provide it here, otherwise we will auto-generate it.

★ Genome coverage ?

80

← you calculated this in protocol 3

★ Sequencing Technology ?

Illumina MiSeq

▴ ▾

Delete



+ Add another sequencing technology