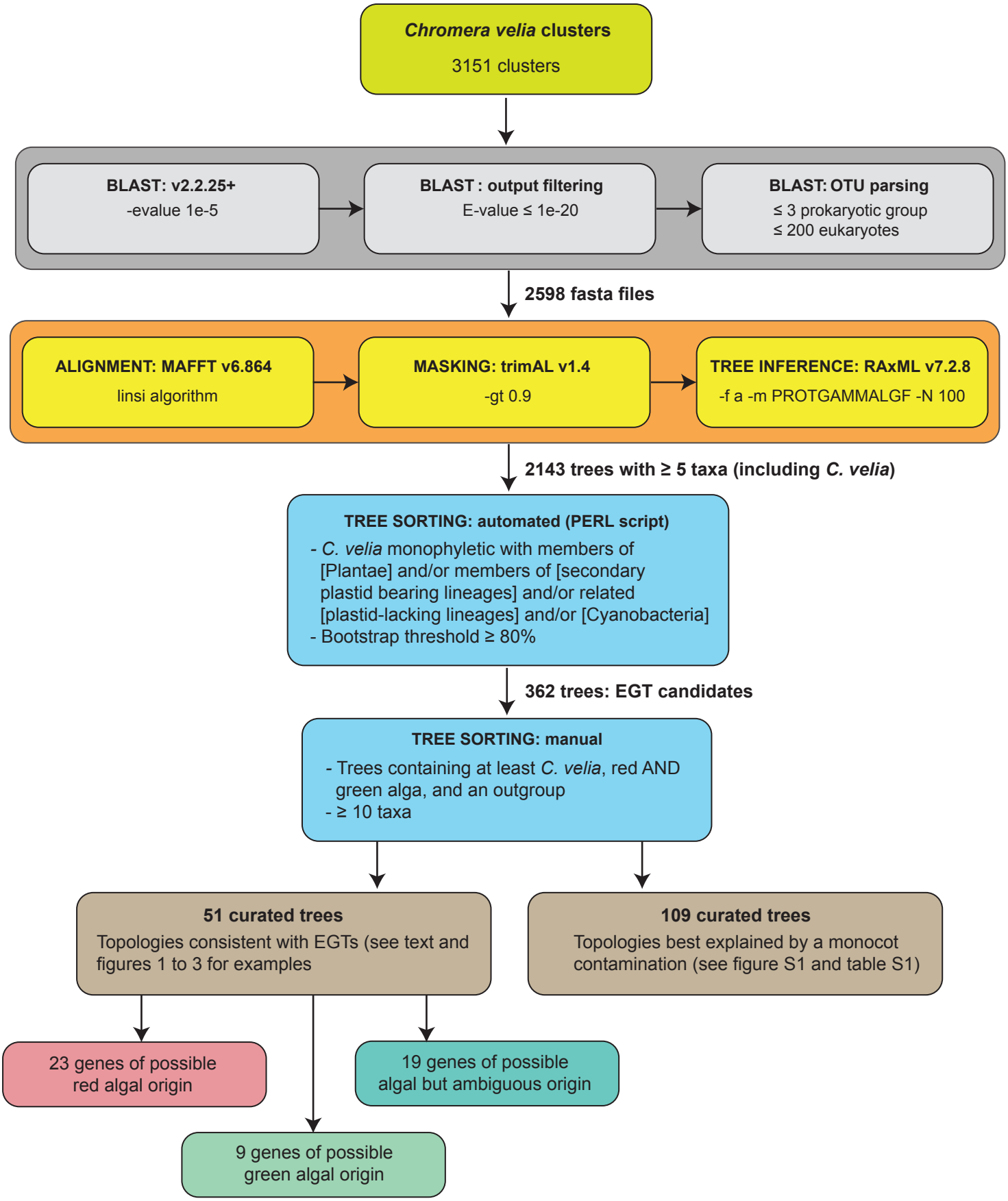
Chromera velia clusters
3151 clusters
BLAST: v2.2.25+
-evalue 1e-5
BLAST : output filtering
E-value ≤ 1e-20
BLAST: OTU parsing
≤ 3 prokaryotic group
≤ 200 eukaryotes
2598 fasta files
ALIGNMENT: MAFFT v6.864
linsi algorithm
MASKING: trimAL v1.4
-gt 0.9
TREE INFERENCE: RAxML v7.2.8
-f a -m PROTGAMMALGF -N 100
2143 trees with ≥ 5 taxa (including *C. velia*)
TREE SORTING: automated (PERL script)
- *C. velia* monophyletic with members of [Plantae] and/or members of [secondary plastid bearing lineages] and/or related [plastid-lacking lineages] and/or [Cyanobacteria]
- Bootstrap threshold ≥ 80%
362 trees: EGT candidates
TREE SORTING: manual
- Trees containing at least *C. velia*, red AND green alga, and an outgroup
- ≥ 10 taxa
51 curated trees
Topologies consistent with EGTs (see text and figures 1 to 3 for examples
109 curated trees
Topologies best explained by a monocot contamination (see figure S1 and table S1)
23 genes of possible red algal origin
19 genes of possible algal but ambiguous origin
9 genes of possible green algal origin