

Sample selection and deletion

Switch between the current Sample tab and the Import Tab

Bin selection
Resetting of all filters

Show only binned scaffolds (default) or show all scaffolds

Bin name if its saved right now with

Sample Name

Consens-Taxonomy

%GC

Coverage

save Bin

Export all Bins, optionally as fasta files

delete Bin

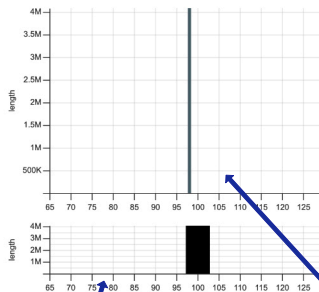
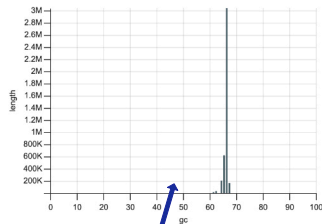
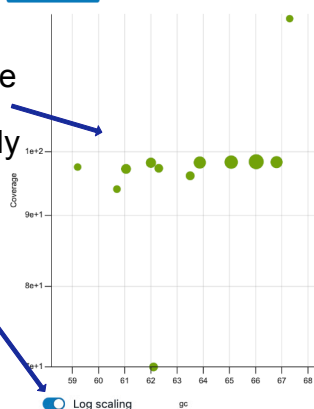
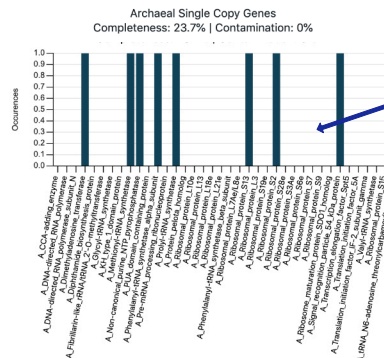
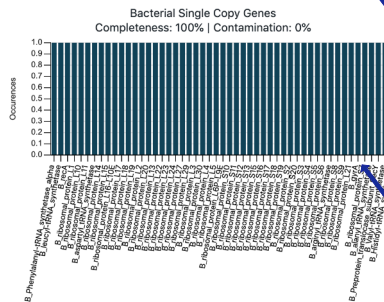
universal bacterial single copy genes

universal archaeal single copy genes

GC vs coverage plot, optionally log10 scaled

Consens-taxonomy distribution across selection

from Domain (inner) to species (outer) circle



Cov-barplot, with teh summed length of scaffolds on the Y-axis

GC-barplot, with the summed length of scaffolds on the Y-axis

Zooming window for the cov-barplot