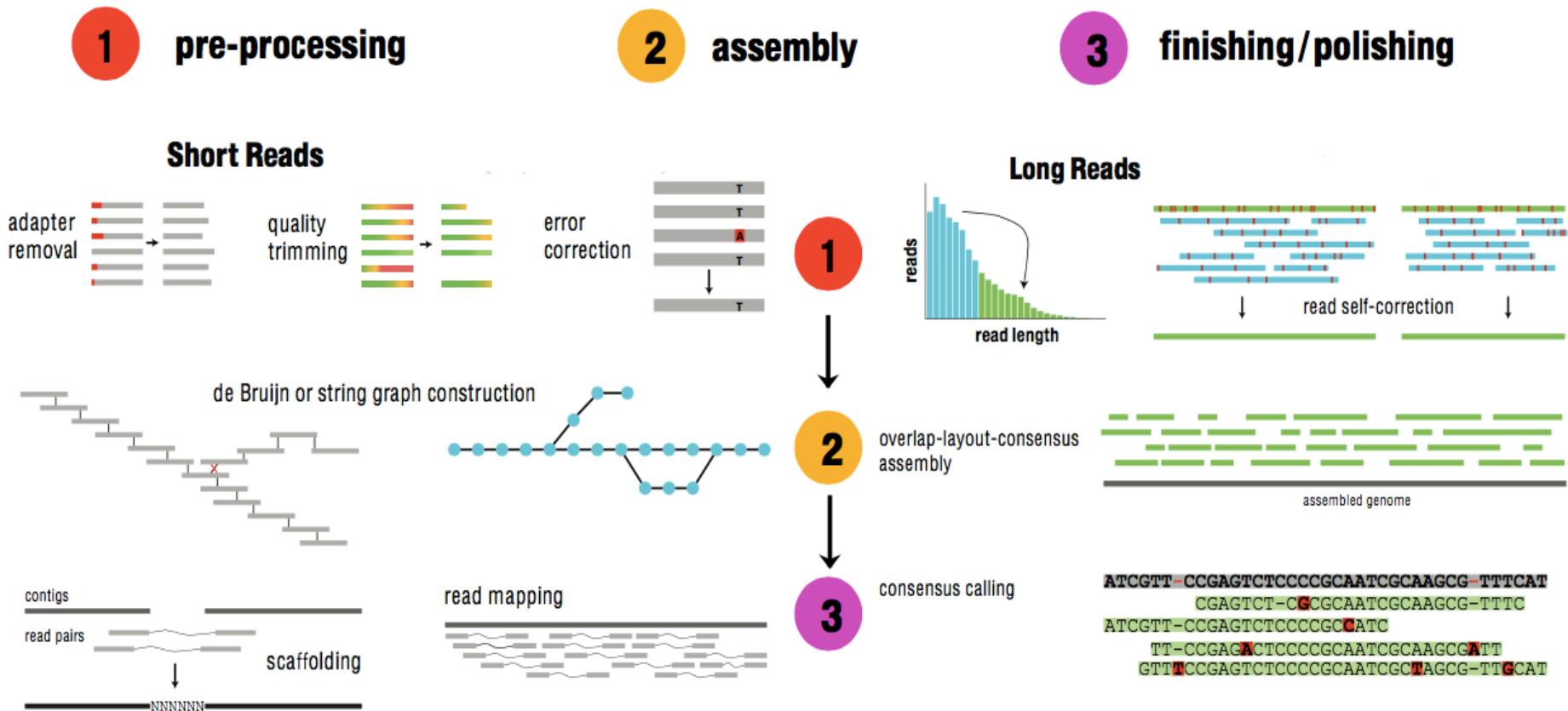
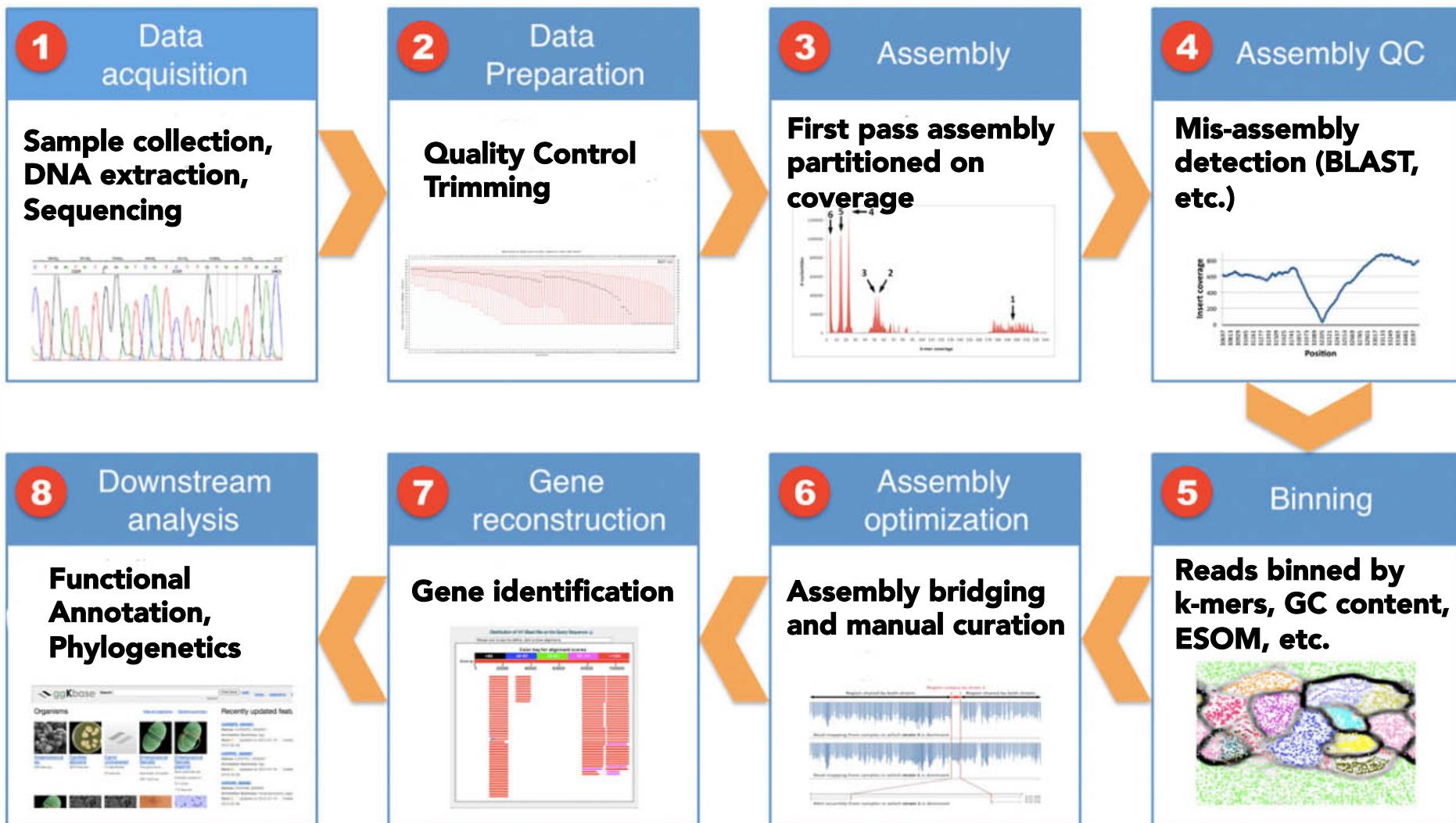


# Assembling One Genome Can Be Difficult

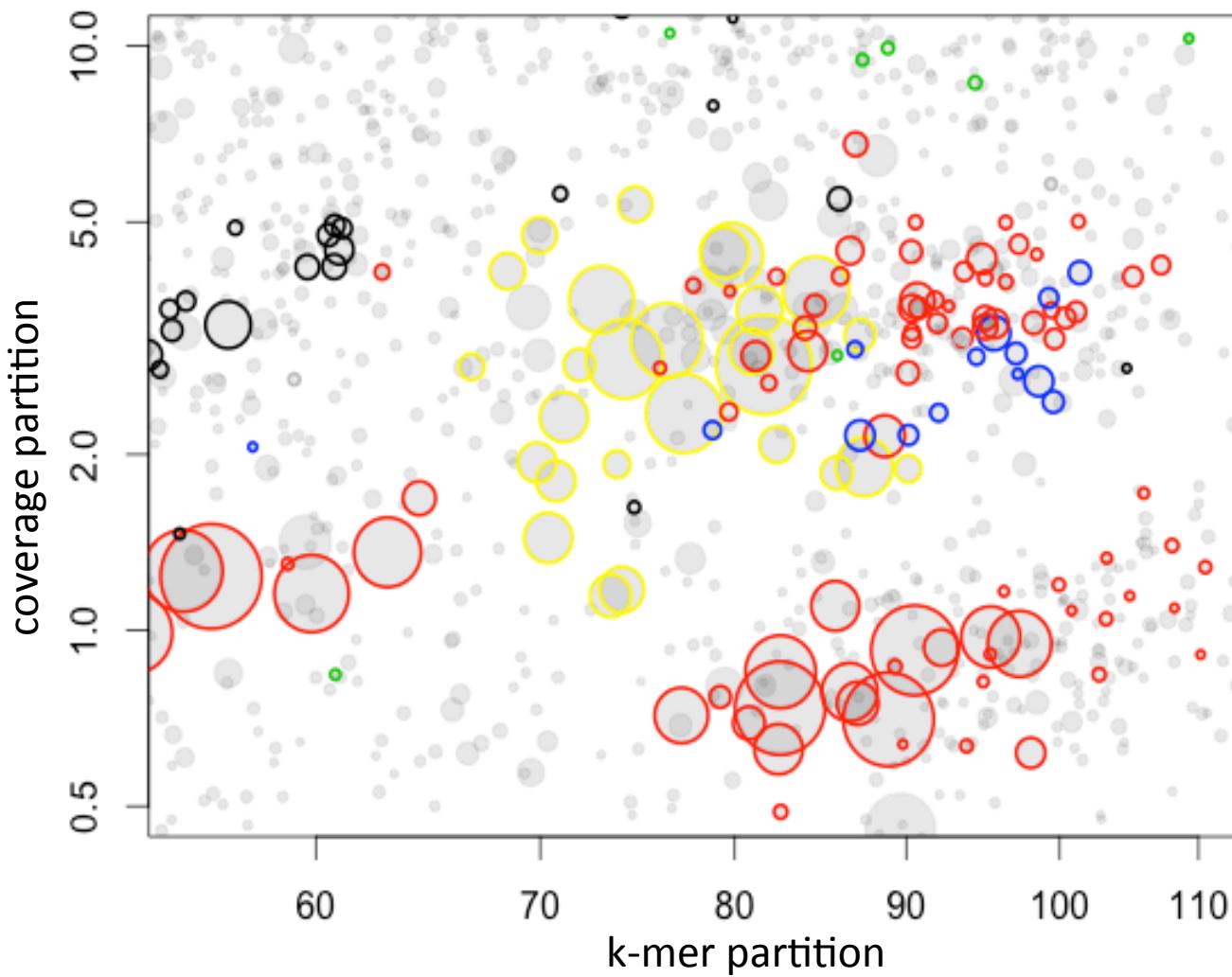


# Metagenome assembly strategy to capture long contigs from environmental sequences



Modified from Sharon *et al.* 2013 Genome Research; Crusoe *et al.* *in prep* khmer protocols

# Metagenomic Binning

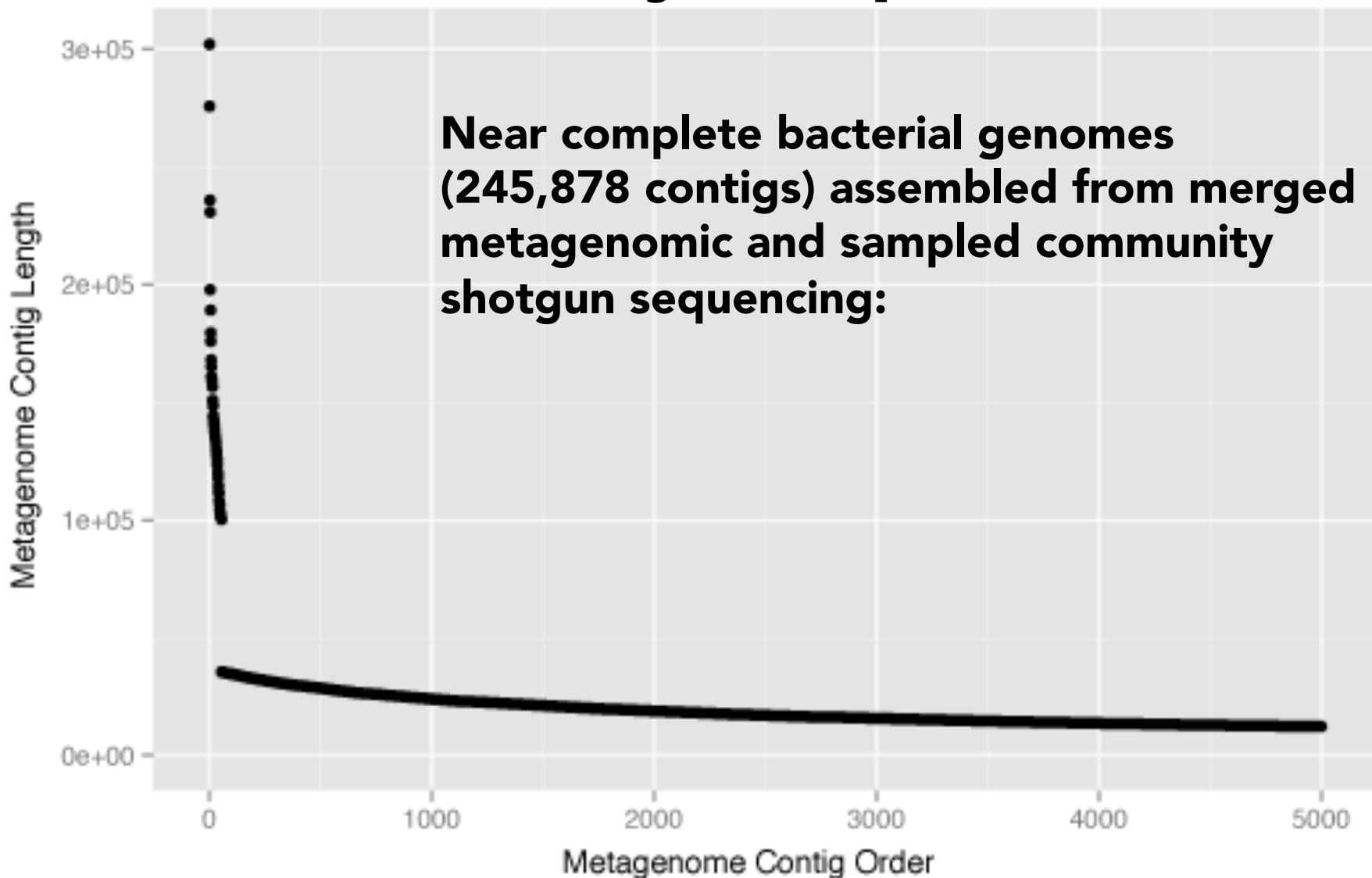


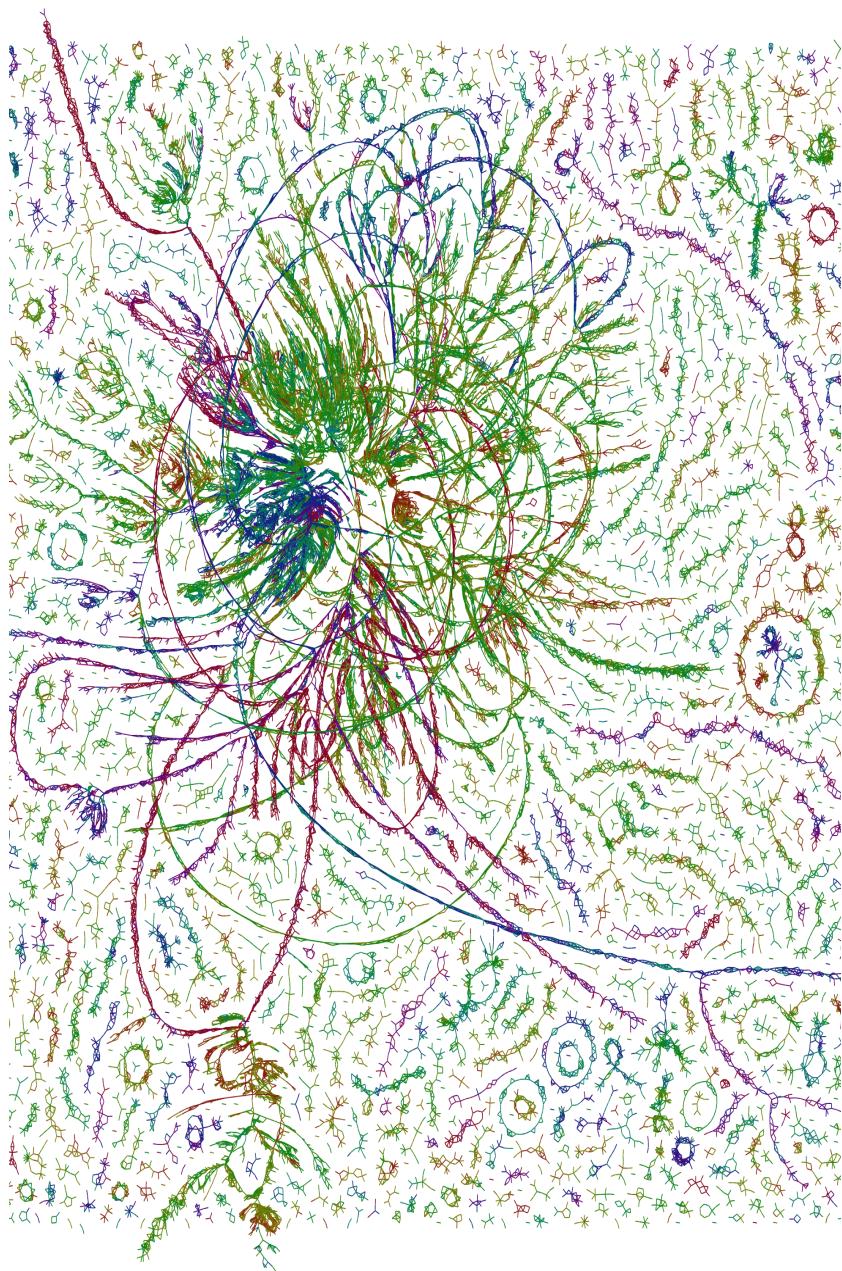
On “simple” Beetle (ALB) gut metagenome, we could use read binning to select for specific reads to assemble:

Able to capture 2433 “yeast-like” contigs with maximum of 39443 bp pre-scaffolding.

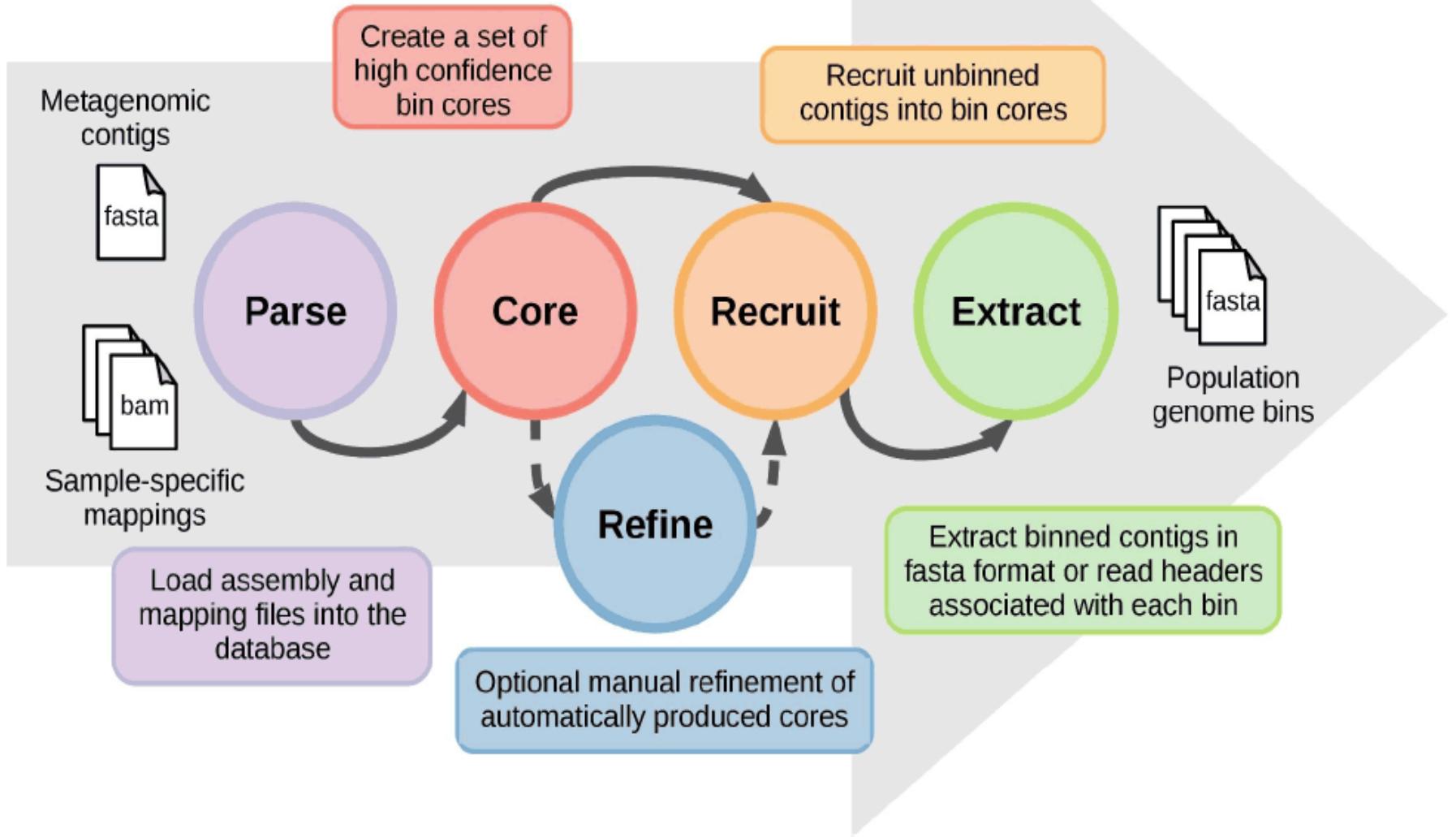
Data from Scully *et al* 2013 PLOS One e73827

# Centralia Sample 13 metagenome assembly (first pass)





Statistic	Number
contigs	539255
contigs ( $\geq$ 1000 bp)	228255
Largest contig (bp)	371898
Total assembly length (bp)	872883788
Total assembly length ( $\geq$ 1000 bp)	658347018
N50	2297
N75	1012
L50	75119
L75	224591
GC(%)	61.54



A photograph of a forest scene. In the foreground, there is a field of dry, golden-brown grass. Behind it stands a dense stand of tall, slender trees, likely birches, characterized by their light-colored, vertically striped bark. The trees are closely packed, creating a rhythmic pattern across the frame. The sky above is a pale, clear blue, suggesting a bright, possibly late afternoon or early morning setting.

**Thank you!**

**Questions?**