

Stage 1: Read alignment

- R0 █
- R1 █
- R2 █
- R3 █
- R4 █
- R5 █
- R6 █
- R7 █
- R8 █
- R9 █

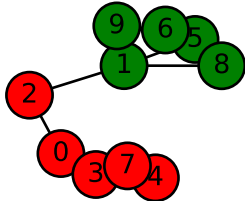


All to all alignment
using suffix tree

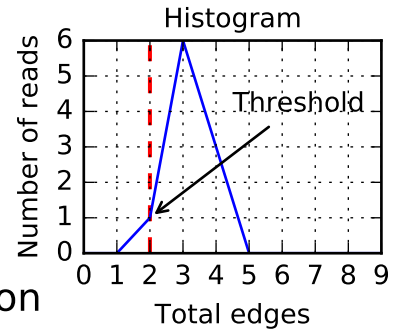


V	E
0	['2', '3', '7', '4']
1	['2', '5', '8', '9']
2	['0', '1']
3	['0', '4', '7']
4	['0', '3', '7']
5	['1', '6', '8', '9']
6	['5', '8', '9']
7	['0', '3', '4']
8	['1', '5', '6']
9	['1', '5', '6']

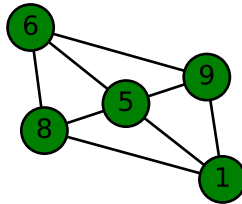
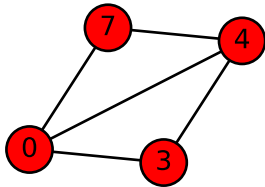
Stage 2: Edges analysis

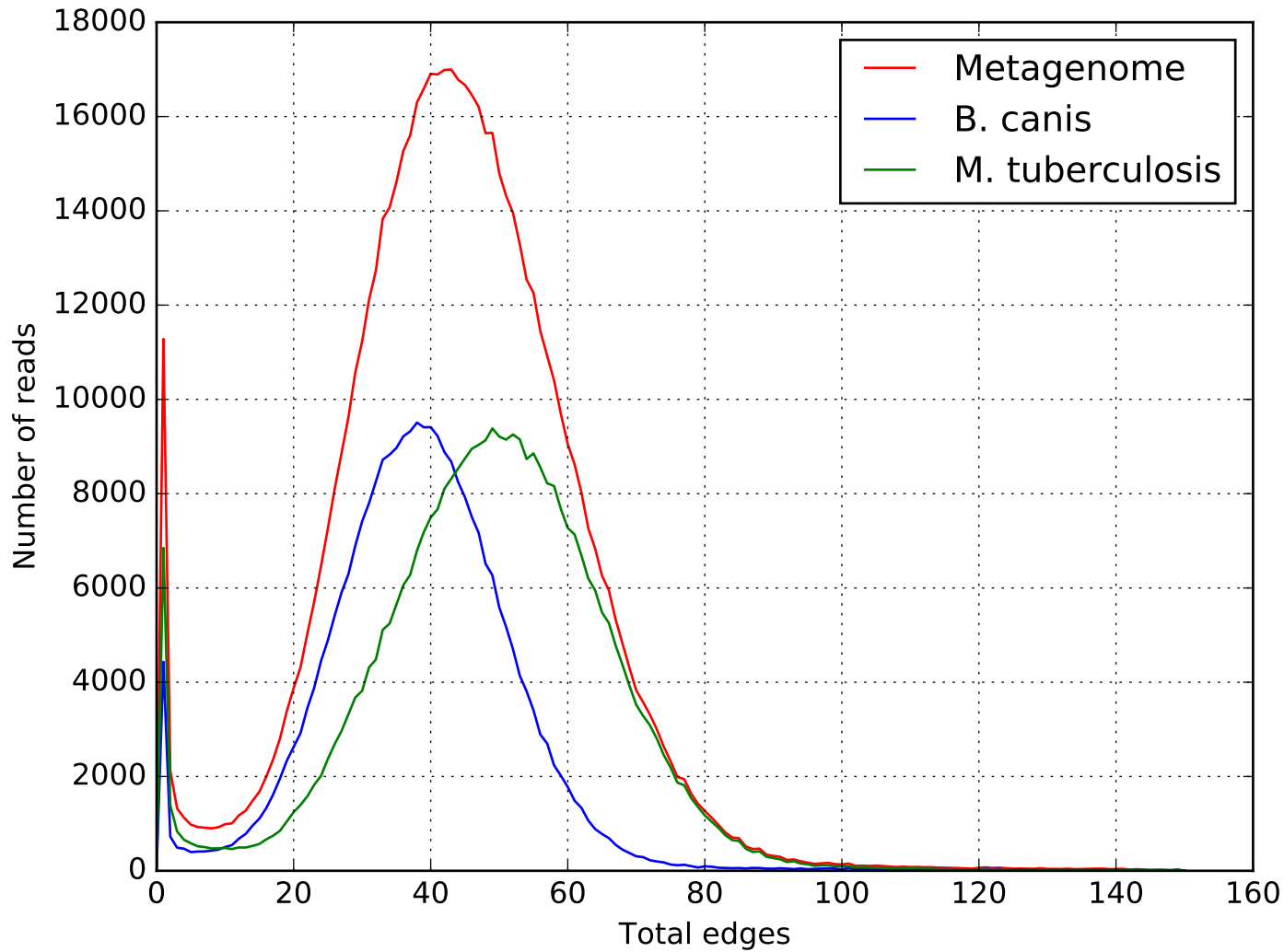


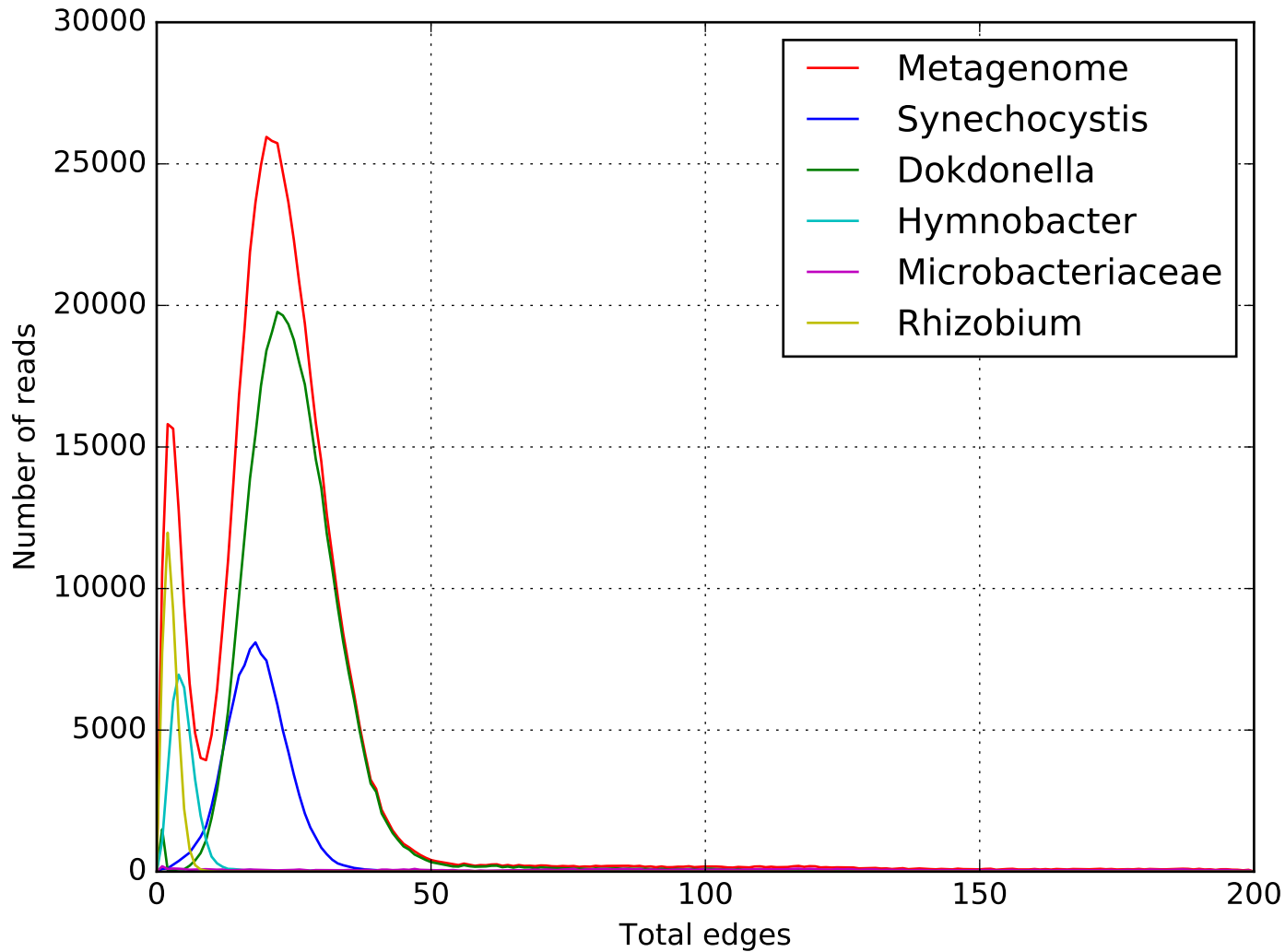
$G=(V,E)$
 V =Reads
 E =Reads alignments

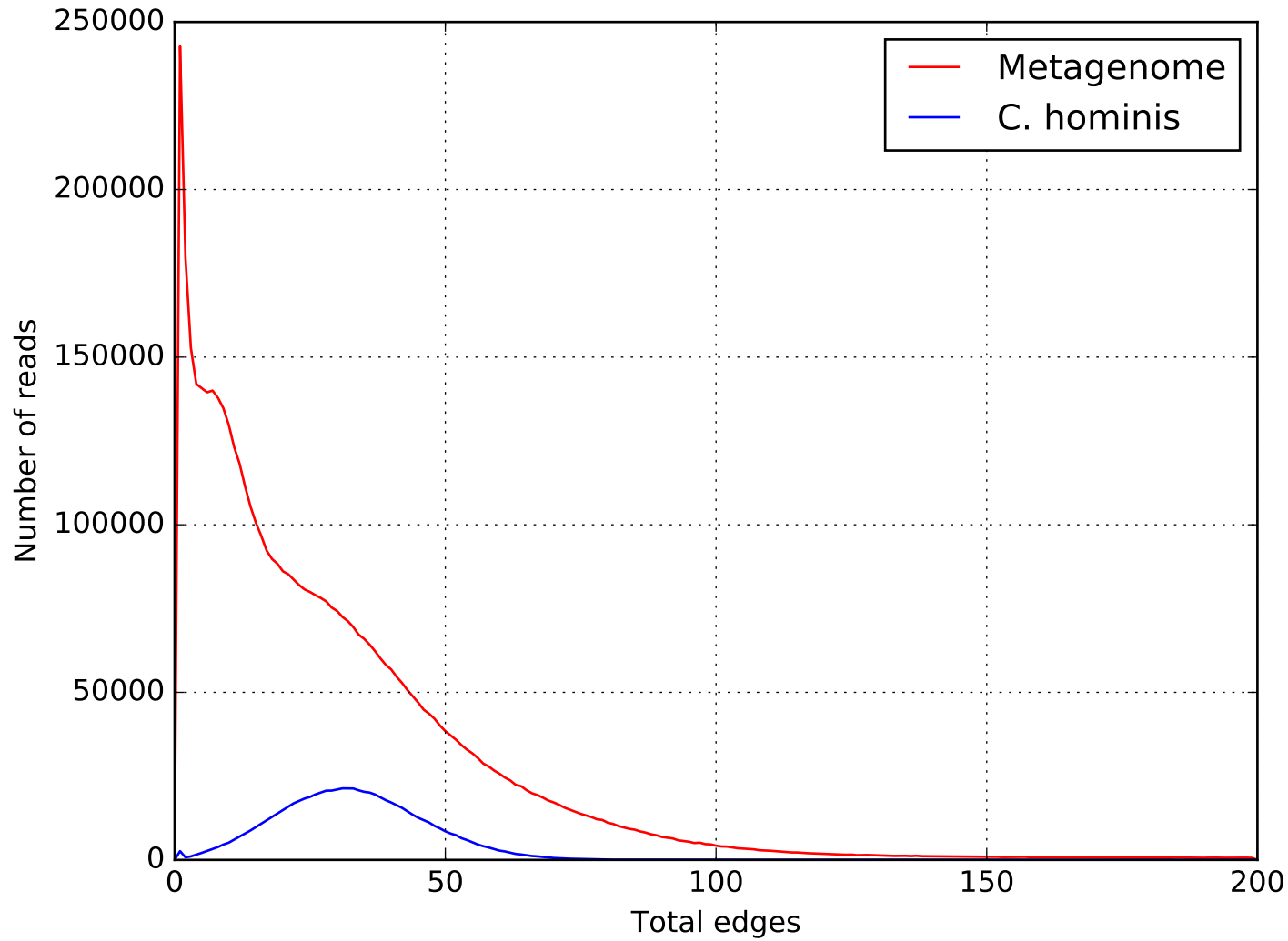


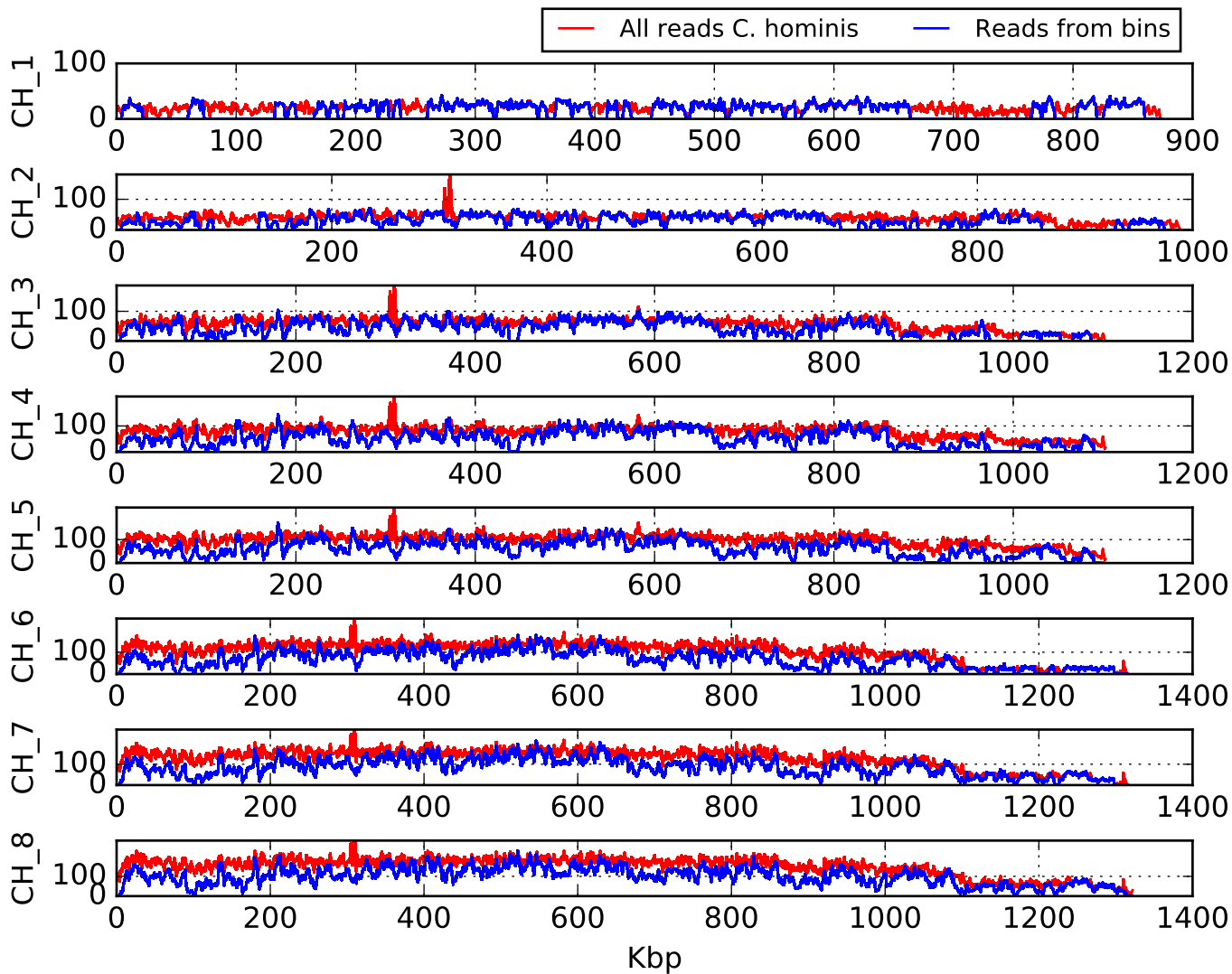
Stage 3: Graph traversal and bin generation



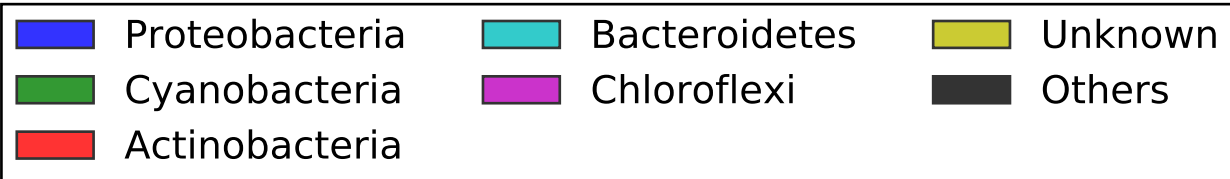
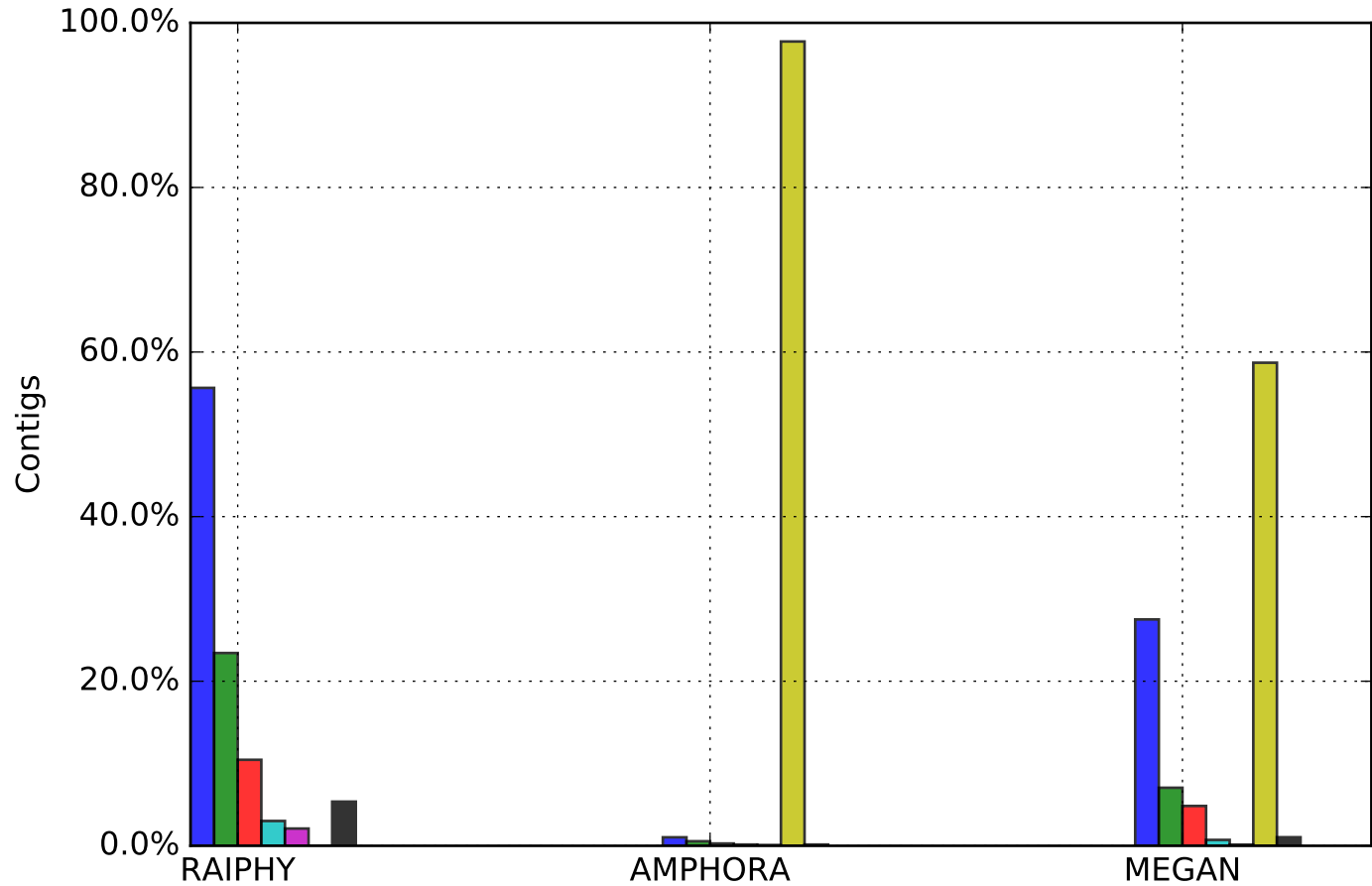


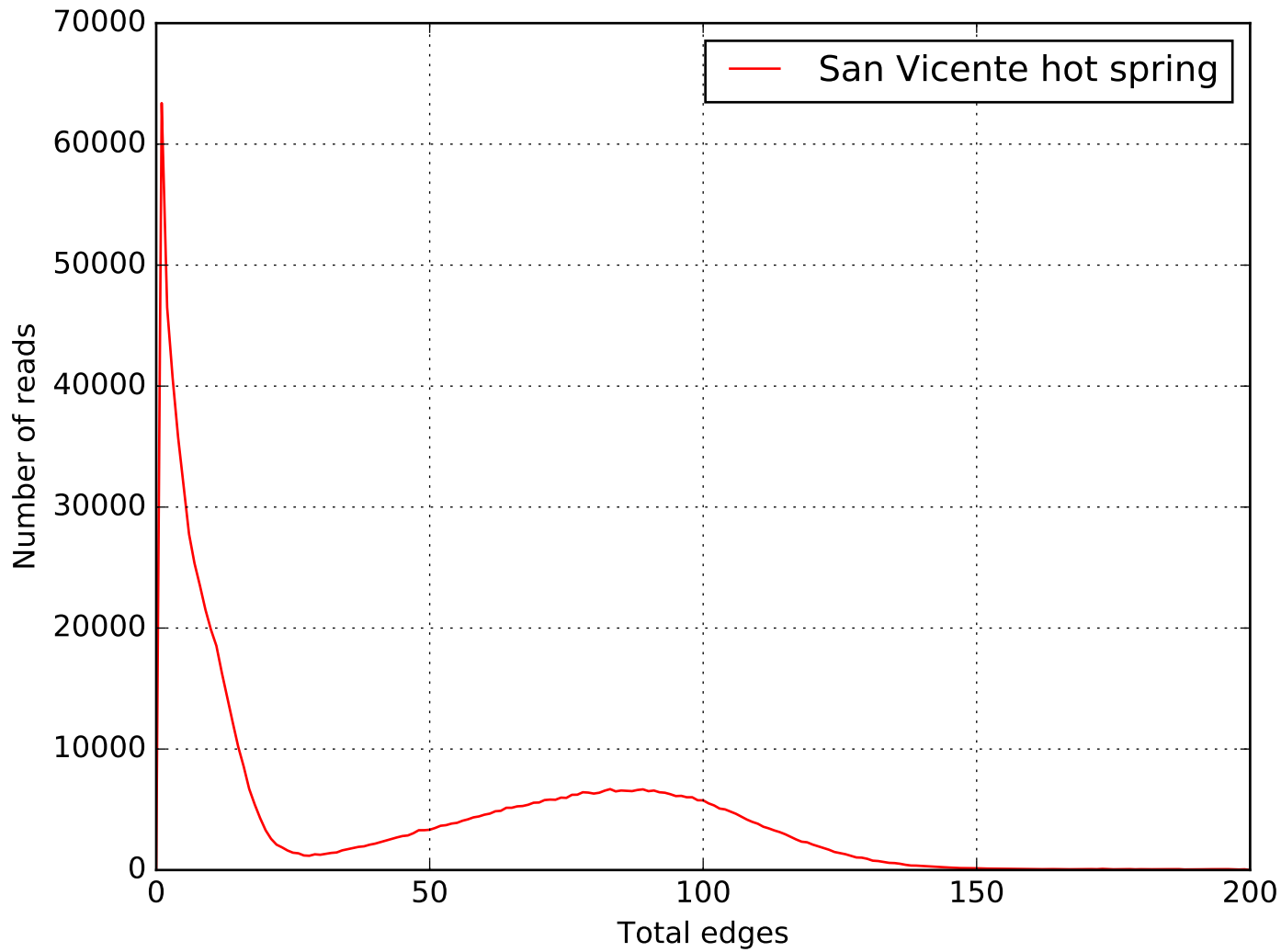


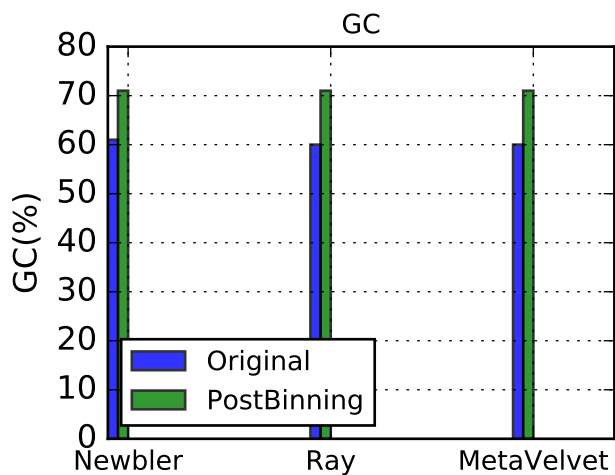
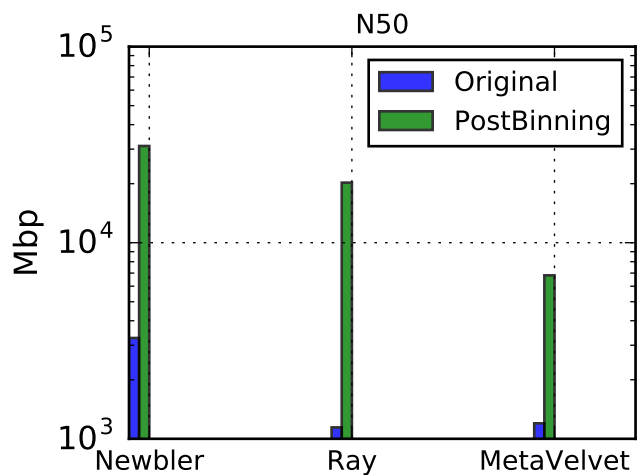
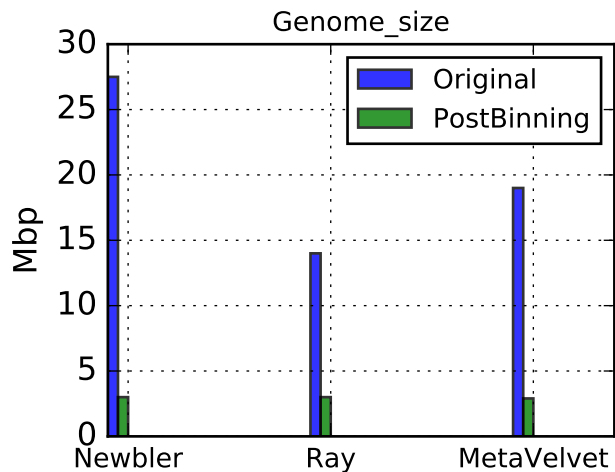
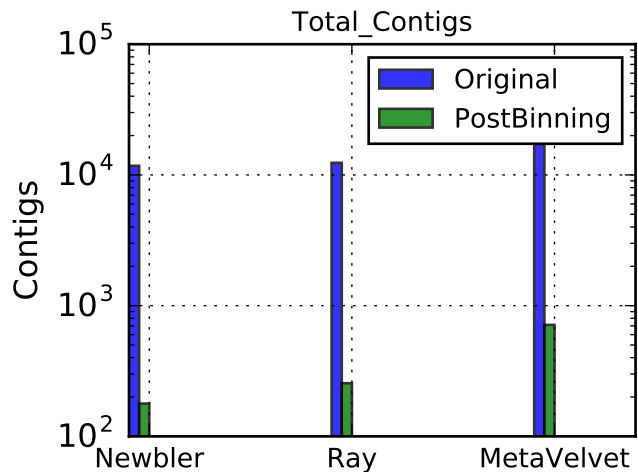


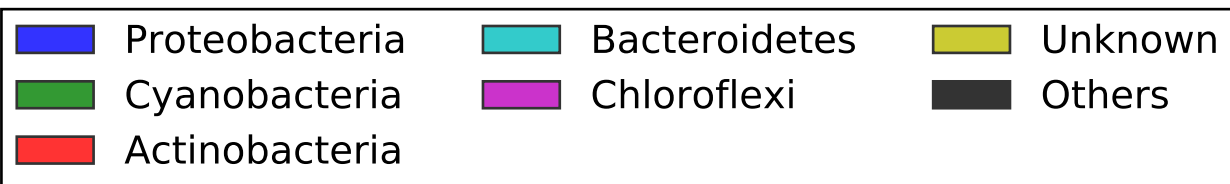
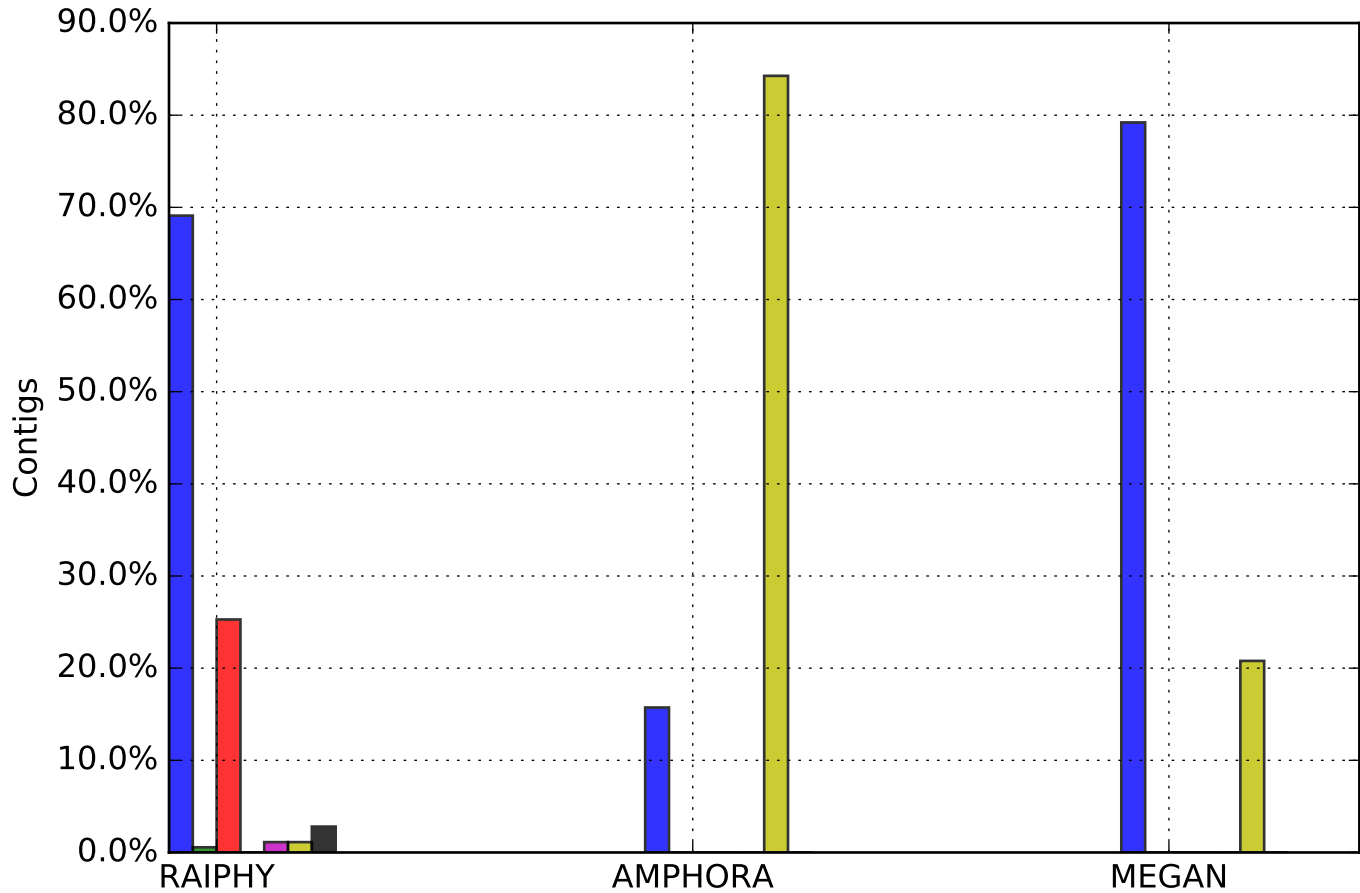


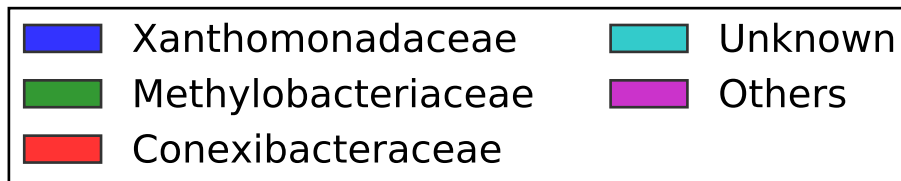
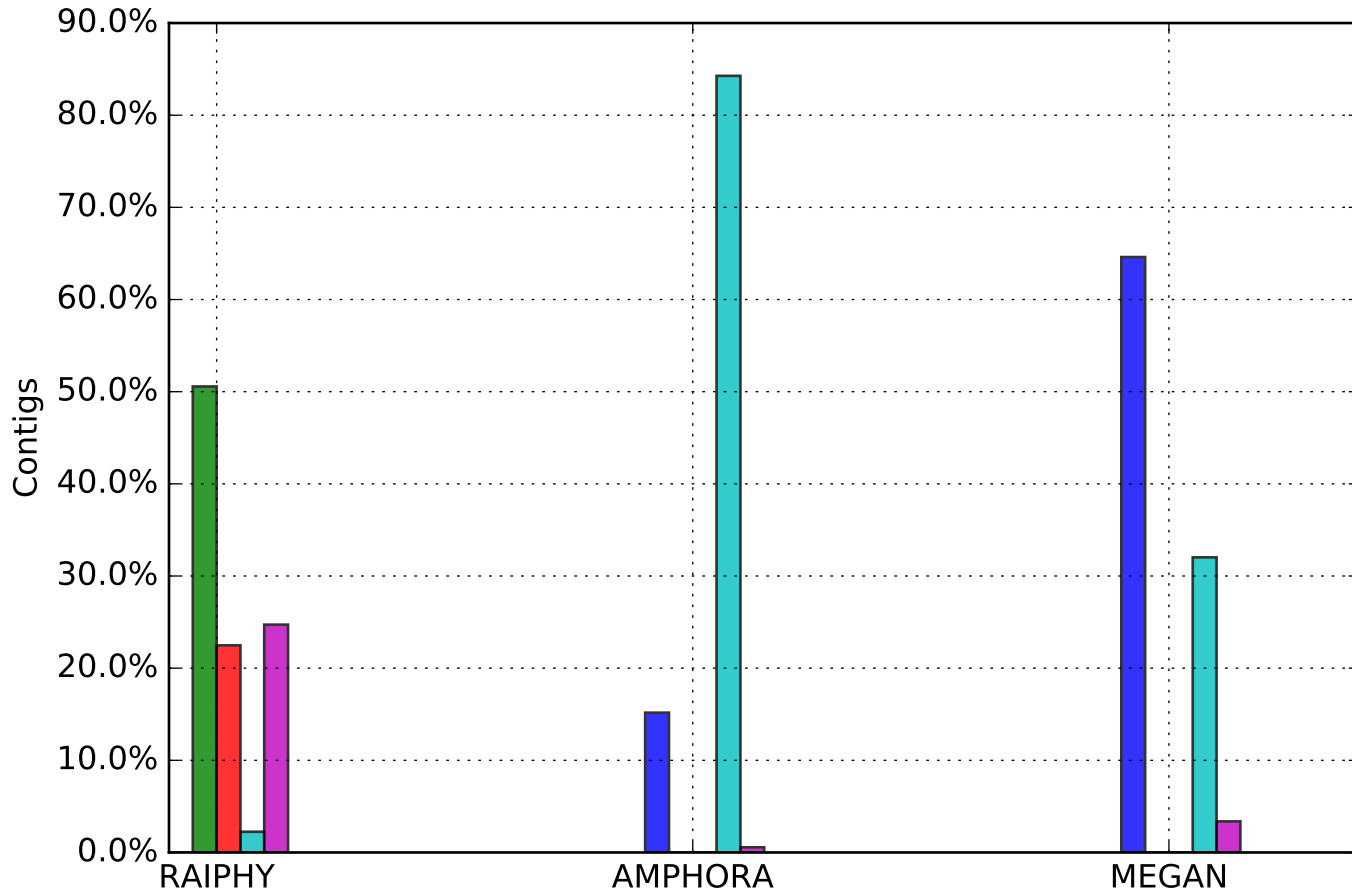


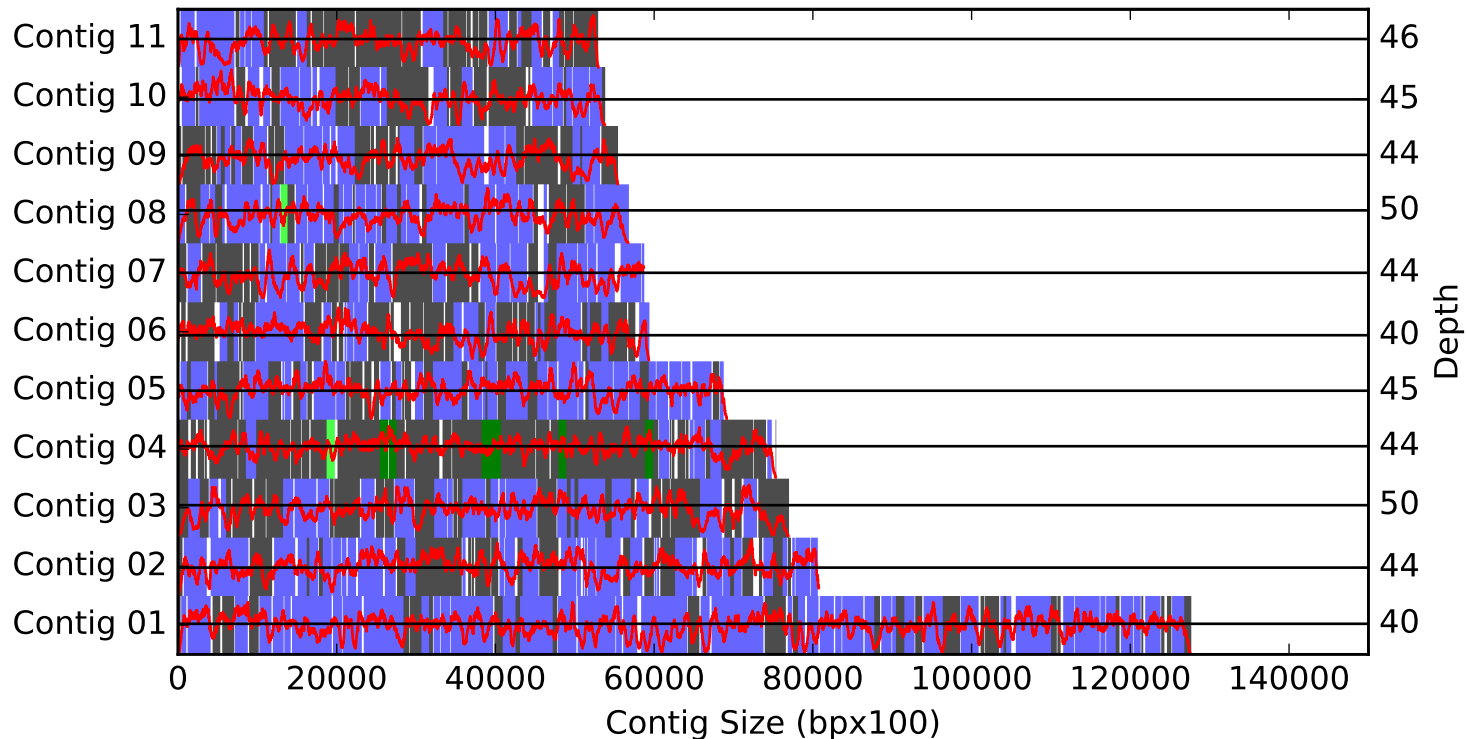


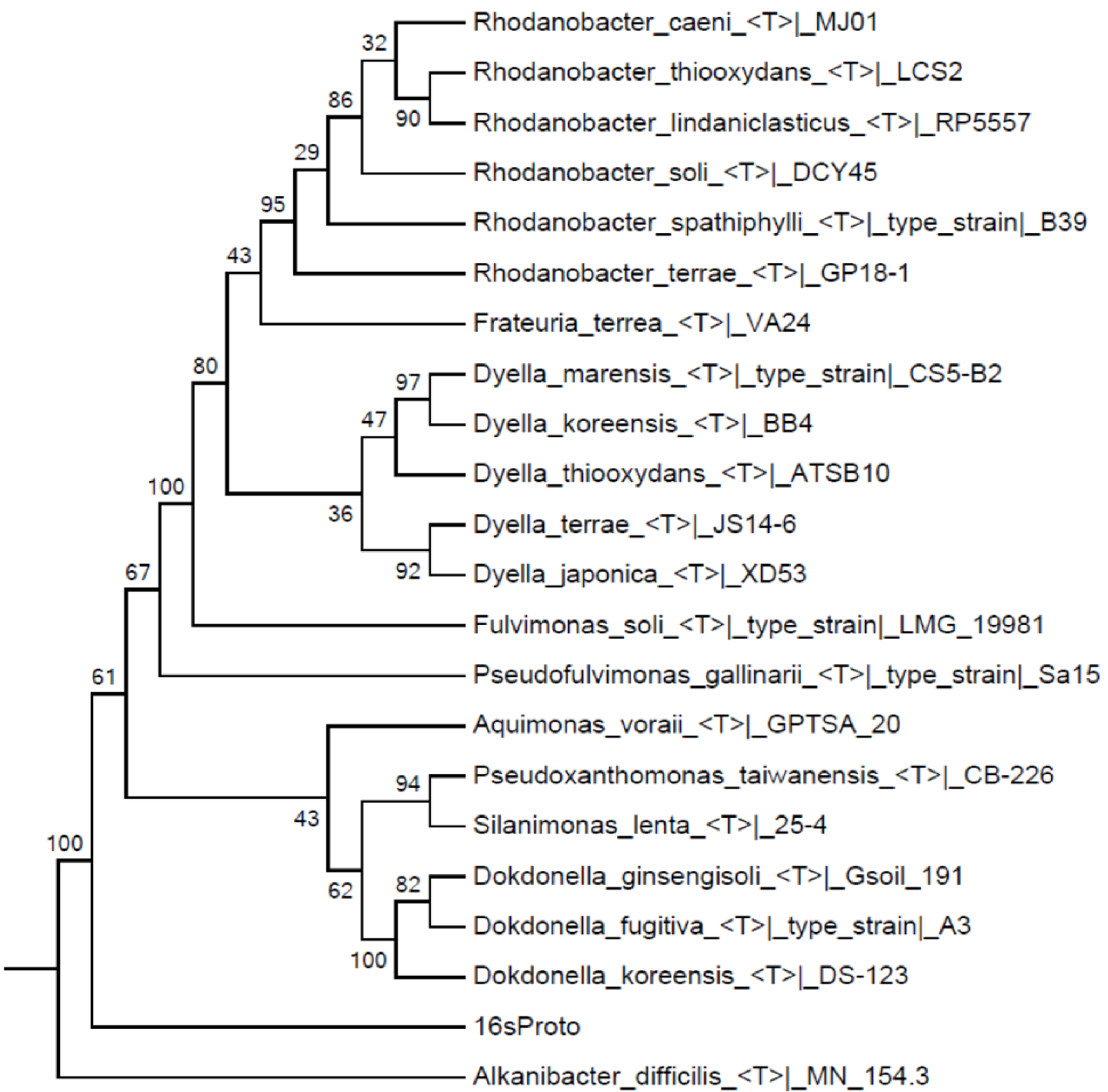




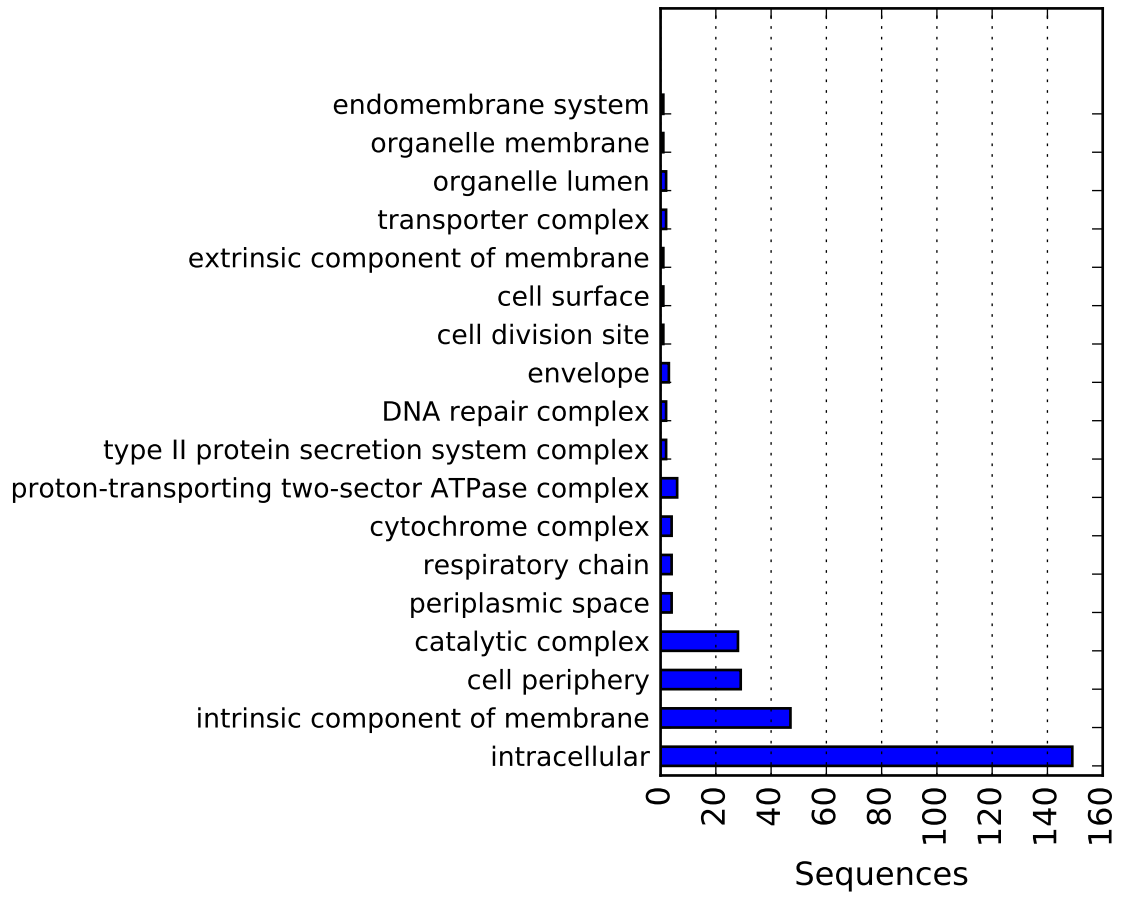








Gene Ontology terms



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