Estimated size: 4 Mb
Assembly: 3.6 Mb in 39 contigs

Final assembly

- Contig 1: 1.5 Mb
- Contig 2: 1.1 Mb
- Contig 3: 0.9 Mb
- Contig 4: 15 kb
- Contig 5: 8 kb
- Contig 6: 1 kb
- Contig 7: 780 bp
- Contig 8: 541 bp

N50: 1.1 Mb. Contigs equal or larger than this represent 50% of the total assembly size; (L50: 2)

NG50: Similar to N50, but based on estimated genome size;

Discarded contigs

- Contig 9: 451 bp
- Contig 10: 325 bp
- Contig 11: 312 bp
- Contig 12: 301 bp
- ... Contig 39: 71 bp

Size cutoff: 500bp

Contigs smaller than cutoff size are not reported
Kmer distribution

Reads ➔ K-mer count table

<table>
<thead>
<tr>
<th>K-mer</th>
<th>Copies</th>
</tr>
</thead>
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</tr>
<tr>
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<td>26</td>
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<tr>
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<tr>
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<td>212</td>
</tr>
</tbody>
</table>

Diagram:
- Single copy: 25
- 12
- 25
All Weill and Qatar employees can request for NetID.

All Cornell collaborators can apply for sponsored NetID.

See details at:
https://it.cornell.edu/netids/how-request-sponsored-netid

https://biohpc.cornell.edu/lab/doc/parallel_exercise1.html
Storage

/workdir: physically located on each BioHPC computer

/home: shared network drive, do not compute large files directly

BioHPC file server (lustre)

Network drive

/home
/programs
/shared_data

/workdir: physically located on each BioHPC computer

/home: shared network drive, do not compute large files directly

Bioculogin
Bioculogin2
Bioculogin3

BioHPC file server (lustre)

Network drive

/home
/programs
/shared_data
“screen” or “tmux”

If your software takes long time to finish, you need to run it under “screen” persistent session.