

# C. macellaria assembly

## hifiasm code

```
module load hifiasm/0.16.1hifiasm  
-o trio2 -t 32 -1 pat.yak -2 mat.yak cell2_filt.fasta
```

Busco diptera_odb10.2019-11-20 n = 3285 number of genomes: 56
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Low coverage (10-20X)	Method/sample	Length	Contigs	Single-copy	Duplicated	Fragmented	Missing
	trio_cell2	548,820,781	250	98.3	0.5	0.5	0.7
trio_cell2_purged	537,270,425	122	98.3	0.4	0.5	0.8	

switch error rate	W	0.006394
hamming error rate	H	0.004622
Total mat-pat error rate	N	0.006452

High coverage (70-80X)	Method/sample	Length	Contigs	Single-copy	Duplicated	Fragmented	Missing
	trio_cell2	542,178,613	195	98.3	0.4	0.5	0.8
trio_cell2_purged	532,641,740	105	98.3	0.4	0.5	0.8	

**Wow. Much lower.** 

switch error rate	W	0.00036
hamming error rate	H	0.000311
Total mat-pat error rate	N	0.000313