

Run started Fri Sep 29 19:59:11 2023 in coassembly mode

SqueezeMeta v1.6.2, March 2023 – (c) J. Tamames, F. Puente-Sánchez  
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Please cite: Tamames & Puente-Sánchez, *Frontiers in Microbiology*  
10.3389 (2019). doi: <https://doi.org/10.3389/fmicb.2018.03349>

Run started for metasqueeze\_test, Fri Sep 29 19:59:11 2023

Project: metasqueeze\_test

Map file: /gpfs1/scratch/jonas/test/test.samples

Fastq directory: /gpfs1/scratch/jonas/test/raw

Command: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/bin/

SqueezeMeta.pl -m coassembly -p metasqueeze\_test -s /gpfs1/scratch/  
jonas/test/test.samples -f /gpfs1/scratch/jonas/test/raw --nopfam  
-miniden 50 -t 60

[0 seconds]: STEP0 -> SqueezeMeta.pl  
COGS; KEGG;

[0 seconds]: STEP1 -> 01.run\_all\_assemblies.pl (megahit)

Preparing files for pair1: cat /gpfs1/scratch/jonas/test/raw/  
SRR1927149\_1.fastq.gz /gpfs1/scratch/jonas/test/raw/  
SRR1929485\_1.fastq.gz > /gpfs1/scratch/jonas/metasqueeze\_test/data/  
raw\_fastq/par1.fastq.gz

Preparing files for pair2: cat /gpfs1/scratch/jonas/test/raw/  
SRR1927149\_2.fastq.gz /gpfs1/scratch/jonas/test/raw/  
SRR1929485\_2.fastq.gz > /gpfs1/scratch/jonas/metasqueeze\_test/data/  
raw\_fastq/par2.fastq.gz

Running assembly with megahit: perl /home/jonas/miniconda3/envs/  
SqueezeMeta\_dev/SqueezeMeta/lib/SqueezeMeta/assembly\_megahit.pl /  
gpfs1/scratch/jonas/metasqueeze\_test metasqueeze\_test /gpfs1/  
scratch/jonas/metasqueeze\_test/data/raw\_fastq/par1.fastq.gz /gpfs1/  
scratch/jonas/metasqueeze\_test/data/raw\_fastq/par2.fastq.gz

2023-09-29 19:59:14 – MEGAHIT v1.2.9

2023-09-29 19:59:14 – Using megahit\_core with POPCNT and BMI2  
support

2023-09-29 19:59:14 – Convert reads to binary library

2023-09-29 20:00:05 – b'INFO sequence/io/sequence\_lib.cpp : 77 –

Lib 0 (/gpfs1/scratch/jonas/metasqueeze\_test/data/raw\_fastq/  
par1.fastq.gz,/gpfs1/scratch/jonas/metasqueeze\_test/data/raw\_fastq/  
par2.fastq.gz): pe, 39159256 reads, 100 max length'

2023-09-29 20:00:05 – b'INFO utils/utils.h : 152 –

Real: 50.8273\tuser: 32.0523\tsys: 6.7292\tmaxrss: 279188'

2023-09-29 20:00:05 – k-max reset to: 119

2023-09-29 20:00:05 – Start assembly. Number of CPU threads 60

2023-09-29 20:00:05 – k list: 21,29,39,59,79,99,119

2023-09-29 20:00:05 – Memory used: 2920879112601

2023-09-29 20:00:05 – Extract solid (k+1)-mers for k = 21

2023-09-29 20:00:34 – Build graph for k = 21

2023-09-29 20:03:10 – Assemble contigs from SDBG for k = 21

2023-09-29 20:08:33 – Local assembly for k = 21

2023-09-29 20:10:11 – Extract iterative edges from k = 21 to 29

2023-09-29 20:11:08 – Build graph for k = 29

2023-09-29 20:11:37 – Assemble contigs from SDBG for k = 29

2023-09-29 20:14:28 - Local assembly for k = 29  
2023-09-29 20:16:32 - Extract iterative edges from k = 29 to 39  
2023-09-29 20:16:52 - Build graph for k = 39  
2023-09-29 20:17:08 - Assemble contigs from SDBG for k = 39  
2023-09-29 20:18:36 - Local assembly for k = 39  
2023-09-29 20:20:59 - Extract iterative edges from k = 39 to 59  
2023-09-29 20:21:09 - Build graph for k = 59  
2023-09-29 20:21:22 - Assemble contigs from SDBG for k = 59  
2023-09-29 20:22:19 - Local assembly for k = 59  
2023-09-29 20:24:56 - Extract iterative edges from k = 59 to 79  
2023-09-29 20:25:02 - Build graph for k = 79  
2023-09-29 20:25:11 - Assemble contigs from SDBG for k = 79  
2023-09-29 20:25:58 - Local assembly for k = 79  
2023-09-29 20:28:31 - Extract iterative edges from k = 79 to 99  
2023-09-29 20:28:35 - Build graph for k = 99  
2023-09-29 20:28:41 - Assemble contigs from SDBG for k = 99  
2023-09-29 20:29:17 - Local assembly for k = 99  
2023-09-29 20:31:38 - Extract iterative edges from k = 99 to 119  
2023-09-29 20:31:42 - Build graph for k = 119  
2023-09-29 20:31:47 - Assemble contigs from SDBG for k = 119  
2023-09-29 20:32:17 - Merging to output final contigs  
2023-09-29 20:32:17 - 241008 contigs, total 212125857 bp, min 200 bp, max 296942 bp, avg 880 bp, N50 1266 bp  
2023-09-29 20:32:17 - ALL DONE. Time elapsed: 1983.296395 seconds  
Running prinseq for selecting contigs longer than 200: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/prinseq-lite.pl -fasta /gpfs1/scratch/jonas/metasqueeze\_test/results/01.metasqueeze\_test.fasta -min\_len 200 -out\_good /gpfs1/scratch/jonas/metasqueeze\_test/results/prinseq; mv /gpfs1/scratch/jonas/metasqueeze\_test/results/prinseq.fasta /gpfs1/scratch/jonas/metasqueeze\_test/results/01.metasqueeze\_test.fasta > /dev/null 2>&1  
Running prinseq for contig statistics: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/prinseq-lite.pl -fasta /gpfs1/scratch/jonas/metasqueeze\_test/results/01.metasqueeze\_test.fasta -stats\_len -stats\_info -stats\_assembly > /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/01.metasqueeze\_test.stats

[33 minutes, 16 seconds]: STEP2 -> 02.rnas.pl  
Running barrnap for Bacteria: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/barrnap --quiet --threads 60 --kingdom bac --reject 0.1 /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/02.metasqueeze\_test.maskedrna.fasta --dbdir /gpfs1/db/squeeze\_meta/v1.6.2/db > /gpfs1/scratch/jonas/metasqueeze\_test/temp/bac.gff  
Running barrnap for Archaea: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/barrnap --quiet --threads 60 --kingdom arc --reject 0.1 /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/02.metasqueeze\_test.maskedrna.fasta --dbdir /gpfs1/db/squeeze\_meta/v1.6.2/db > /gpfs1/scratch/jonas/metasqueeze\_test/temp/arc.gff  
Running barrnap for Eukaryote: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/barrnap --quiet --threads 60 --kingdom euk --reject 0.1 /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/02.metasqueeze\_test.maskedrna.fasta --dbdir /gpfs1/db/

```
squeeze_meta/v1.6.2/db > /gpfs1/scratch/jonas/metasqueeze_test/temp/  
euk.gff
```

```
Running barrnap for Mitochondrial: /home/jonas/miniconda3/envs/  
SqueezeMeta_dev/SqueezeMeta/bin/barrnap --quiet --threads 60 --  
kingdom mito --reject 0.1 /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/02.metasqueeze_test.maskedrna.fasta --dbdir /gpfs1/db/  
squeeze_meta/v1.6.2/db > /gpfs1/scratch/jonas/metasqueeze_test/temp/  
mito.gff
```

```
Running RDP classifier: java -jar /home/jonas/miniconda3/envs/  
SqueezeMeta_dev/SqueezeMeta/lib/classifier/classifier.jar classify /  
gpfs1/scratch/jonas/metasqueeze_test/temp/16S.fasta -o /gpfs1/  
scratch/jonas/metasqueeze_test/temp/16S.out -f filterbyconf
```

```
Running Aragorn: /home/jonas/miniconda3/envs/SqueezeMeta_dev/  
SqueezeMeta/bin/aragorn -w /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/02.metasqueeze_test.maskedrna.fasta -o /gpfs1/scratch/  
jonas/metasqueeze_test/temp/trnas.aragorn
```

```
Creating new gff file: cat /gpfs1/scratch/jonas/metasqueeze_test/  
temp/*gff.mod > /gpfs1/scratch/jonas/metasqueeze_test/temp/  
02.metasqueeze_test.rna.gff
```

```
[34 minutes, 53 seconds]: STEP3 -> 03.run_prodigal.pl
```

```
Running prodigal for predicting ORFs: /home/jonas/miniconda3/envs/  
SqueezeMeta_dev/SqueezeMeta/bin/prodigal -q -m -p meta -i /gpfs1/  
scratch/jonas/metasqueeze_test/intermediate/  
02.metasqueeze_test.maskedrna.fasta -a /gpfs1/scratch/jonas/  
metasqueeze_test/results/03.metasqueeze_test.faa -d /gpfs1/scratch/  
jonas/metasqueeze_test/results/03.metasqueeze_test.fna -f gff -o /  
gpfs1/scratch/jonas/metasqueeze_test/temp/  
02.metasqueeze_test.cds.gff.temp
```

```
[48 minutes, 40 seconds]: STEP4 -> 04.rundiamond.pl
```

```
Diamond block size set to 16 (Free Mem 2853.28 Gb)
```

```
Working with taxonomy database in /gpfs1/db/squeeze_meta/v1.6.2/  
db/nr.dwnd
```

```
Running Diamond for taxa: /home/jonas/miniconda3/envs/  
SqueezeMeta_dev/SqueezeMeta/bin/diamond blastp -q /gpfs1/scratch/  
jonas/metasqueeze_test/results/03.metasqueeze_test.faa -p 60 -d /  
gpfs1/db/squeeze_meta/v1.6.2/db/nr.dwnd -e 0.001 --id 50 -f tab -b  
16 -o /gpfs1/scratch/jonas/metasqueeze_test/intermediate/  
04.metasqueeze_test.nr.diamond > /gpfs1/scratch/jonas/  
metasqueeze_test/temp/diamond.nr.log 2>&1
```

```
Running Diamond for COGs: /home/jonas/miniconda3/envs/  
SqueezeMeta_dev/SqueezeMeta/bin/diamond blastp -q /gpfs1/scratch/  
jonas/metasqueeze_test/results/03.metasqueeze_test.faa -p 60 -d /  
gpfs1/db/squeeze_meta/v1.6.2/db/eggog -e 0.001 --id 50 --quiet -b  
16 -f 6 qseqid qlen sseqid slen pident length evalue bitscore qstart  
qend sstart send -o /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/04.metasqueeze_test.eggog.diamond
```

```
Running Diamond for KEGG: /home/jonas/miniconda3/envs/  
SqueezeMeta_dev/SqueezeMeta/bin/diamond blastp -q /gpfs1/scratch/  
jonas/metasqueeze_test/results/03.metasqueeze_test.faa -p 60 -d /  
gpfs1/db/squeeze_meta/v1.6.2/db/keggdb -e 0.001 --id 50 --quiet -b  
16 -f 6 qseqid qlen sseqid slen pident length evalue bitscore qstart  
qend sstart send -o /gpfs1/scratch/jonas/metasqueeze_test/
```

intermediate/04.metasqueeze\_test.kegg.diamond

[2 hours, 5 minutes, 12 seconds]: STEP6 -> 06.lca.pl

Splitting Diamond file

Total lines in Diamond: 7359947; Allocating 122665 in 60 threads

Opening file 1 in line (estimated in 122665)  
Opening file 2 in line 122666 (estimated in 122665)  
Opening file 3 in line 245354 (estimated in 245330)  
Opening file 4 in line 368001 (estimated in 367995)  
Opening file 5 in line 490666 (estimated in 490660)  
Opening file 6 in line 613330 (estimated in 613325)  
Opening file 7 in line 736011 (estimated in 735990)  
Opening file 8 in line 858667 (estimated in 858655)  
Opening file 9 in line 981342 (estimated in 981320)  
Opening file 10 in line 1104006 (estimated in 1103985)  
Opening file 11 in line 1226657 (estimated in 1226650)  
Opening file 12 in line 1349337 (estimated in 1349315)  
Opening file 13 in line 1471988 (estimated in 1471980)  
Opening file 14 in line 1594668 (estimated in 1594645)  
Opening file 15 in line 1717329 (estimated in 1717310)  
Opening file 16 in line 1839977 (estimated in 1839975)  
Opening file 17 in line 1962649 (estimated in 1962640)  
Opening file 18 in line 2085311 (estimated in 2085305)  
Opening file 19 in line 2207979 (estimated in 2207970)  
Opening file 20 in line 2330645 (estimated in 2330635)  
Opening file 21 in line 2453318 (estimated in 2453300)  
Opening file 22 in line 2575971 (estimated in 2575965)  
Opening file 23 in line 2698637 (estimated in 2698630)  
Opening file 24 in line 2821316 (estimated in 2821295)  
Opening file 25 in line 2943976 (estimated in 2943960)  
Opening file 26 in line 3066643 (estimated in 3066625)  
Opening file 27 in line 3189293 (estimated in 3189290)  
Opening file 28 in line 3311965 (estimated in 3311955)  
Opening file 29 in line 3434627 (estimated in 3434620)  
Opening file 30 in line 3557289 (estimated in 3557285)  
Opening file 31 in line 3679974 (estimated in 3679950)  
Opening file 32 in line 3802618 (estimated in 3802615)  
Opening file 33 in line 3925282 (estimated in 3925280)  
Opening file 34 in line 4047965 (estimated in 4047945)  
Opening file 35 in line 4170615 (estimated in 4170610)  
Opening file 36 in line 4293290 (estimated in 4293275)  
Opening file 37 in line 4415947 (estimated in 4415940)  
Opening file 38 in line 4538606 (estimated in 4538605)  
Opening file 39 in line 4661291 (estimated in 4661270)  
Opening file 40 in line 4783948 (estimated in 4783935)  
Opening file 41 in line 4906608 (estimated in 4906600)  
Opening file 42 in line 5029266 (estimated in 5029265)  
Opening file 43 in line 5151945 (estimated in 5151930)  
Opening file 44 in line 5274615 (estimated in 5274595)  
Opening file 45 in line 5397284 (estimated in 5397260)  
Opening file 46 in line 5519943 (estimated in 5519925)  
Opening file 47 in line 5642609 (estimated in 5642590)  
Opening file 48 in line 5765259 (estimated in 5765255)  
Opening file 49 in line 5887941 (estimated in 5887920)

Opening file 50 in line 6010603 (estimated in 6010585)  
Opening file 51 in line 6133258 (estimated in 6133250)  
Opening file 52 in line 6255936 (estimated in 6255915)  
Opening file 53 in line 6378598 (estimated in 6378580)  
Opening file 54 in line 6501264 (estimated in 6501245)  
Opening file 55 in line 6623926 (estimated in 6623910)  
Opening file 56 in line 6746595 (estimated in 6746575)  
Opening file 57 in line 6869247 (estimated in 6869240)  
Opening file 58 in line 6991930 (estimated in 6991905)  
Opening file 59 in line 7114588 (estimated in 7114570)  
Opening file 60 in line 7237249 (estimated in 7237235)  
Opening file 61 in line 7359923 (estimated in 7359900)

Starting multithread LCA in 60 threads

Starting thread 10

Starting thread 6

Starting thread 53

Starting thread 11

Starting thread 28

Starting thread 21

Starting thread 9

Starting thread 23

Starting thread 41

Starting thread 2

Starting thread 8

Starting thread 15

Starting thread 39

Starting thread 58

Starting thread 12

Starting thread 1

Starting thread 34

Starting thread 14

Starting thread 25

Starting thread 27

Starting thread 29

Starting thread 54

Starting thread 3

Starting thread 56

Starting thread 33

Starting thread 18

Starting thread 5

Starting thread 44

Starting thread 43

Starting thread 32

Starting thread 35

Starting thread 46

Starting thread 4

Starting thread 7

Starting thread 59

Starting thread 16

Starting thread 20

Starting thread 51

Starting thread 24

Starting thread 38

Starting thread 19

Starting thread 37  
Starting thread 17  
Starting thread 60  
Starting thread 57  
Starting thread 13  
Starting thread 31  
Starting thread 40  
Starting thread 50  
Starting thread 22  
Starting thread 45  
Starting thread 30  
Starting thread 26  
Starting thread 52  
Starting thread 47  
Starting thread 49  
Starting thread 36  
Starting thread 55  
Starting thread 42  
Starting thread 48

Creating /gpfs1/scratch/jonas/metasqueeze\_test/results/

06.metasqueeze\_test.fun3.tax.wranks file: cat /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_1.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_2.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_3.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_4.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_5.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_6.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_7.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_8.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_9.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_10.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_11.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_12.wranks /gpfs1/scratch/jonas/  
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metasqueeze\_test/temp/fun3tax\_15.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_16.wranks /gpfs1/scratch/jonas/  
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metasqueeze\_test/temp/fun3tax\_27.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_28.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_29.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_30.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_31.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_32.wranks /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/fun3tax\_33.wranks /gpfs1/scratch/jonas/

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metasqueeze_test/temp/fun3tax_34.wranks /gpfs1/scratch/jonas/  
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metasqueeze_test/temp/fun3tax_47.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_48.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_49.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_50.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_51.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_52.wranks /gpfs1/scratch/jonas/  
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metasqueeze_test/temp/fun3tax_57.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_58.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_59.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_60.wranks > /gpfs1/scratch/jonas/  
metasqueeze_test/results/06.metasqueeze_test.fun3.tax.wranks  
  Creating /gpfs1/scratch/jonas/metasqueeze_test/results/  
06.metasqueeze_test.fun3.tax.noidfilter.wranks file: cat /gpfs1/  
scratch/jonas/metasqueeze_test/temp/fun3tax_1.noidfilter.wranks /  
gpfs1/scratch/jonas/metasqueeze_test/temp/  
fun3tax_2.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/  
temp/fun3tax_3.noidfilter.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_4.noidfilter.wranks /gpfs1/scratch/  
jonas/metasqueeze_test/temp/fun3tax_5.noidfilter.wranks /gpfs1/  
scratch/jonas/metasqueeze_test/temp/fun3tax_6.noidfilter.wranks /  
gpfs1/scratch/jonas/metasqueeze_test/temp/  
fun3tax_7.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/  
temp/fun3tax_8.noidfilter.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_9.noidfilter.wranks /gpfs1/scratch/  
jonas/metasqueeze_test/temp/fun3tax_10.noidfilter.wranks /gpfs1/  
scratch/jonas/metasqueeze_test/temp/fun3tax_11.noidfilter.wranks /  
gpfs1/scratch/jonas/metasqueeze_test/temp/  
fun3tax_12.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/  
temp/fun3tax_13.noidfilter.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_14.noidfilter.wranks /gpfs1/scratch/  
jonas/metasqueeze_test/temp/fun3tax_15.noidfilter.wranks /gpfs1/  
scratch/jonas/metasqueeze_test/temp/fun3tax_16.noidfilter.wranks /  
gpfs1/scratch/jonas/metasqueeze_test/temp/  
fun3tax_17.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/  
temp/fun3tax_18.noidfilter.wranks /gpfs1/scratch/jonas/  
metasqueeze_test/temp/fun3tax_19.noidfilter.wranks /gpfs1/scratch/  
jonas/metasqueeze_test/temp/fun3tax_20.noidfilter.wranks /gpfs1/
```

```
scratch/jonas/metasqueeze_test/temp/fun3tax_21.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_22.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_23.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_24.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_25.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_26.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_27.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_28.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_29.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_30.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_31.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_32.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_33.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_34.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_35.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_36.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_37.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_38.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_39.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_40.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_41.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_42.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_43.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_44.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_45.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_46.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_47.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_48.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_49.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_50.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_51.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_52.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_53.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_54.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_55.noidfilter.wranks /gpfs1/
scratch/jonas/metasqueeze_test/temp/fun3tax_56.noidfilter.wranks /
gpfs1/scratch/jonas/metasqueeze_test/temp/
fun3tax_57.noidfilter.wranks /gpfs1/scratch/jonas/metasqueeze_test/
temp/fun3tax_58.noidfilter.wranks /gpfs1/scratch/jonas/
metasqueeze_test/temp/fun3tax_59.noidfilter.wranks /gpfs1/scratch/
jonas/metasqueeze_test/temp/fun3tax_60.noidfilter.wranks > /gpfs1/
scratch/jonas/metasqueeze_test/results/
06.metasqueeze_test.fun3.tax.noidfilter.wranks
  Removing temporaty diamond files in /gpfs1/scratch/jonas/
metasqueeze_test/temp
```

[4 hours, 44 minutes, 48 seconds]: STEP7 -> 07.fun3assign.pl



Reading COGs hits from /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/04.metasqueeze\_test.eggnog.diamond

Output in /gpfs1/scratch/jonas/metasqueeze\_test/results/07.metasqueeze\_test.fun3.cog

Reading KEGG hits from /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/04.metasqueeze\_test.kegg.diamond

Output in /gpfs1/scratch/jonas/metasqueeze\_test/results/07.metasqueeze\_test.fun3.kegg

[4 hours, 45 minutes, 3 seconds]: STEP9 -> 09.summarycontigs3.pl

Reading taxa for genes from /gpfs1/scratch/jonas/metasqueeze\_test/results/06.metasqueeze\_test.fun3.tax.wranks

Writing output to /gpfs1/scratch/jonas/metasqueeze\_test/temp/09.metasqueeze\_test.allorfs and /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/09.metasqueeze\_test.contiglog

Reading taxa for genes from /gpfs1/scratch/jonas/metasqueeze\_test/results/06.metasqueeze\_test.fun3.tax.noidfilter.wranks

Writing output to /gpfs1/scratch/jonas/metasqueeze\_test/temp/09.metasqueeze\_test.allorfs.noidfilter and /gpfs1/scratch/jonas/metasqueeze\_test/intermediate/09.metasqueeze\_test.contiglog.noidfilter

[4 hours, 46 minutes, 7 seconds]: STEP10 -> 10.mapsamples.pl

Creating Bowtie reference: python3 /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/bowtie2/bowtie2-build --quiet /gpfs1/scratch/jonas/metasqueeze\_test/results/01.metasqueeze\_test.fasta /gpfs1/scratch/jonas/metasqueeze\_test/data/metasqueeze\_test.bowtie

Getting raw reads for SRR1927149: cp /gpfs1/scratch/jonas/test/raw/SRR1927149\_1.fastq.gz /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1927149.current\_1.gz; cp /gpfs1/scratch/jonas/test/raw/SRR1927149\_2.fastq.gz /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1927149.current\_2.gz;

Aligning with bowtie: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/bowtie2/bowtie2 -x /gpfs1/scratch/jonas/metasqueeze\_test/data/metasqueeze\_test.bowtie -1 /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1927149.current\_1.gz -2 /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1927149.current\_2.gz --quiet -p 60 -S /gpfs1/scratch/jonas/metasqueeze\_test/data/bam/metasqueeze\_test.SRR1927149.sam --very-sensitive-local

Calling sqm\_counter: Sample SRR1927149, BAM /gpfs1/scratch/jonas/metasqueeze\_test/data/bam/metasqueeze\_test.SRR1927149.bam, Number of reads 29669622, GFF /gpfs1/scratch/jonas/metasqueeze\_test/results/03.metasqueeze\_test.gff

Getting raw reads for SRR1929485: cp /gpfs1/scratch/jonas/test/raw/SRR1929485\_1.fastq.gz /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1929485.current\_1.gz; cp /gpfs1/scratch/jonas/test/raw/SRR1929485\_2.fastq.gz /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1929485.current\_2.gz;

Aligning with bowtie: /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/bowtie2/bowtie2 -x /gpfs1/scratch/jonas/metasqueeze\_test/data/metasqueeze\_test.bowtie -1 /gpfs1/scratch/jonas/metasqueeze\_test/temp/metasqueeze\_test.SRR1929485.current\_1.gz

```
-2 /gpfs1/scratch/jonas/metasqueeze_test/temp/  
metasqueeze_test.SRR1929485.current_2.gz --quiet -p 60 -S /gpfs1/  
scratch/jonas/metasqueeze_test/data/bam/  
metasqueeze_test.SRR1929485.sam --very-sensitive-local  
Calling sqm_counter: Sample SRR1929485, BAM /gpfs1/scratch/jonas/  
metasqueeze_test/data/bam/metasqueeze_test.SRR1929485.bam, Number of  
reads 9489634, GFF /gpfs1/scratch/jonas/metasqueeze_test/results/  
03.metasqueeze_test.gff  
Sorting mapcount table: sort -T /gpfs1/scratch/jonas/  
metasqueeze_test/temp -t _ -k 2 -k 3 -n /gpfs1/scratch/jonas/  
metasqueeze_test/intermediate/10.metasqueeze_test.mapcount > /gpfs1/  
scratch/jonas/metasqueeze_test/temp/mapcount.temp; mv /gpfs1/  
scratch/jonas/metasqueeze_test/temp/mapcount.temp /gpfs1/scratch/  
jonas/metasqueeze_test/intermediate/10.metasqueeze_test.mapcount
```

```
[5 hours, 0 minutes, 2 seconds]: STEP11 -> 11.mcount.pl  
Reading contig length from /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/01.metasqueeze_test.lon  
Reading contig taxa from /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/09.metasqueeze_test.contiglog  
Reading contig coverages from /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/10.metasqueeze_test.contigcov  
Writing output to /gpfs1/scratch/jonas/metasqueeze_test/results/  
11.metasqueeze_test.mcount
```

```
[5 hours, 0 minutes, 12 seconds]: STEP12 -> 12.funcover.pl  
Creating cog coverage output in /gpfs1/scratch/jonas/  
metasqueeze_test/results/12.metasqueeze_test.cog.funcover  
Creating kegg coverage output in /gpfs1/scratch/jonas/  
metasqueeze_test/results/12.metasqueeze_test.kegg.funcover  
Creating cog raw reads output in /gpfs1/scratch/jonas/  
metasqueeze_test/ext_tables/12.metasqueeze_test.cog.stamp  
Creating kegg raw reads output in /gpfs1/scratch/jonas/  
metasqueeze_test/ext_tables/12.metasqueeze_test.kegg.stamp
```

```
[5 hours, 0 minutes, 31 seconds]: STEP13 -> 13.mergeannot2.pl  
Creating table in /gpfs1/scratch/jonas/metasqueeze_test/results/  
13.metasqueeze_test.orftable  
Reading GFF in /gpfs1/scratch/jonas/metasqueeze_test/results/  
03.metasqueeze_test.gff  
Reading Diamond hits from /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/04.metasqueeze_test.nr.diamond  
Reading aa sequences from /gpfs1/scratch/jonas/metasqueeze_test/  
results/03.metasqueeze_test.faa  
Reading nt sequences  
Reading rRNA sequences  
Reading tRNA/tmRNA sequences from /gpfs1/scratch/jonas/  
metasqueeze_test/results/02.metasqueeze_test.trnas  
Reading ORF information from /gpfs1/scratch/jonas/  
metasqueeze_test/results/06.metasqueeze_test.fun3.tax.wranks  
Calculating GC content for genes using /gpfs1/scratch/jonas/  
metasqueeze_test/results/03.metasqueeze_test.fna  
Calculating GC content for RNAs using /gpfs1/scratch/jonas/  
metasqueeze_test/results/02.metasqueeze_test.rnas
```

```
Reading contig information from /gpfs1/scratch/jonas/
metasqueeze_test/intermediate/09.metasqueeze_test.contiglog
Reading KEGG annotations from /gpfs1/scratch/jonas/
metasqueeze_test/results/07.metasqueeze_test.fun3.kegg
Reading COGs annotations from /gpfs1/scratch/jonas/
metasqueeze_test/results/07.metasqueeze_test.fun3.cog
Reading RPKMs and Coverages from /gpfs1/scratch/jonas/
metasqueeze_test/intermediate/10.metasqueeze_test.mapcount
GENE TABLE CREATED: /gpfs1/scratch/jonas/metasqueeze_test/results/
13.metasqueeze_test.orftable
[5 hours, 1 minutes, 35 seconds]: STEP14 -> 14.runbinning.pl
```

## RUNNING concoct

```
Cutting contigs in pieces!: python3 /home/jonas/miniconda3/envs/
SqueezeMeta_dev/SqueezeMeta/bin/CONCOCT-1.1.0/scripts/
cut_up_fasta.py /gpfs1/scratch/jonas/metasqueeze_test/results/
01.metasqueeze_test.fasta -c 10000 -o 0 --merge_last -b /gpfs1/
scratch/jonas/metasqueeze_test/temp/metasqueeze_test.contigs.bed > /
gpfs1/scratch/jonas/metasqueeze_test/temp/
metasqueeze_test.choppedcontigs.fasta
```

```
Creating abundance table: PATH=/home/jonas/miniconda3/envs/
SqueezeMeta_dev/SqueezeMeta/bin:$PATH python3 /home/jonas/
miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/CONCOCT-1.1.0/
scripts/concoct_coverage_table.py /gpfs1/scratch/jonas/
metasqueeze_test/temp/metasqueeze_test.contigs.bed /gpfs1/scratch/
jonas/metasqueeze_test/data/bam/metasqueeze_test.SRR1929485.bam /
gpfs1/scratch/jonas/metasqueeze_test/data/bam/
metasqueeze_test.SRR1927149.bam > /gpfs1/scratch/jonas/
metasqueeze_test/intermediate/binners/concoct/coverage_table.tsv
```

```
Running concoct: OMP_THREAD_LIMIT=60 python3 /home/jonas/
miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/CONCOCT-1.1.0/bin/
concoct --composition_file /gpfs1/scratch/jonas/metasqueeze_test/
temp/metasqueeze_test.choppedcontigs.fasta --coverage_file /gpfs1/
scratch/jonas/metasqueeze_test/intermediate/binners/concoct/
coverage_table.tsv --threads 60 -b /gpfs1/scratch/jonas/
metasqueeze_test/intermediate/binners/concoct/concoct_int/ > /dev/
null 2>&1
```

```
Merging clusters: python3 /home/jonas/miniconda3/envs/
SqueezeMeta_dev/SqueezeMeta/bin/CONCOCT-1.1.0/scripts/
merge_cutup_clustering.py /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/binners/concoct/concoct_int/clustering_gt1000.csv > /
gpfs1/scratch/jonas/metasqueeze_test/intermediate/binners/concoct/
concoct_int/clustering_merged.csv 2> /dev/null
```

```
Extracting final bins: python3 /home/jonas/miniconda3/envs/
SqueezeMeta_dev/SqueezeMeta/bin/CONCOCT-1.1.0/scripts/
extract_fasta_bins.py /gpfs1/scratch/jonas/metasqueeze_test/results/
01.metasqueeze_test.fasta /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/binners/concoct/concoct_int/clustering_merged.csv --
output_path /gpfs1/scratch/jonas/metasqueeze_test/intermediate/
binners/concoct > /dev/null 2>&1
```

```
Creating coverage file in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/binners/metabat2/contigs.depth.txt
```

```
Output depth matrix to /gpfs1/scratch/jonas/metasqueeze_test/
```

```
intermediate/binners/metabat2/contigs.depth.txt.PROV
Output matrix to /gpfs1/scratch/jonas/metasqueeze_test/intermediate/
binners/metabat2/contigs.depth.txt.PROV
Opening 2 bams
Consolidating headers
Processing bam files
Thread 0 finished: metasqueeze_test.SRR1929485.bam with 9489634
reads and 4549780 readsWellMapped
Thread 1 finished: metasqueeze_test.SRR1927149.bam with 29669622
reads and 21089581 readsWellMapped
Creating depth matrix file: /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/binners/metabat2/contigs.depth.txt.PROV
Closing most bam files
Closing last bam file
Finished
Running metabat2 : metabat2 -t 60 -i /gpfs1/scratch/jonas/
metasqueeze_test/temp/bincontigs.fasta -a /gpfs1/scratch/jonas/
metasqueeze_test/intermediate/binners/metabat2/contigs.depth.txt
-o /gpfs1/scratch/jonas/metasqueeze_test/intermediate/binners/
metabat2/metabat2 --saveTNF saved_1500.tnf --saveDistance
saved_1500.dist
[5 hours, 16 minutes, 11 seconds]: STEP15 -> 15.dastool.pl
Creating abundance file in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/binners/DAS/concoct.table
Creating abundance file in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/binners/DAS/metabat2.table
Running DAS Tool for concoct,metabat2: LD_LIBRARY_PATH=/home/jonas/
miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/lib PATH=/home/jonas/
miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:$PATH /home/jonas/
miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/DAS_Tool/DAS_Tool
-i /gpfs1/scratch/jonas/metasqueeze_test/intermediate/binners/DAS/
concoct.table,/gpfs1/scratch/jonas/metasqueeze_test/intermediate/
binners/DAS/metabat2.table -l concoct,metabat2 -c /gpfs1/scratch/
jonas/metasqueeze_test/results/01.metasqueeze_test.fasta --
write_bins 1 --score_threshold 0 --search_engine diamond -t 60 -o /
gpfs1/scratch/jonas/metasqueeze_test/intermediate/binners/DAS/
metasqueeze_test --db_directory /gpfs1/db/squeeze_meta/v1.6.2/db
[5 hours, 17 minutes, 20 seconds]: STEP16 -> 16.addtax2.pl
  Reading taxonomic assignments for contigs from /gpfs1/scratch/
jonas/metasqueeze_test/intermediate/09.metasqueeze_test.contiglog
  Looking for bins in /gpfs1/scratch/jonas/metasqueeze_test/results/
bins
  Output created in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/16.metasqueeze_test.bintax
[5 hours, 19 minutes, 33 seconds]: STEP17 -> 17.checkM_batch.pl
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set family Prevotellaceae /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Prevotellaceae.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*

\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Marker set for Prevotellaceae contains 553 marker genes arranged in 298 sets.

Marker set inferred from 69 reference genomes.

Marker set for Bacteroidales contains 402 marker genes arranged in 267 sets.

Marker set inferred from 210 reference genomes.

Marker set for Bacteroidia contains 401 marker genes arranged in 266 sets.

Marker set inferred from 211 reference genomes.

Marker set for Bacteroidetes contains 286 marker genes arranged in 195 sets.

Marker set inferred from 419 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Prevotellaceae.ms

```
{ Current stage: 0:00:03.648 || Total: 0:00:03.648 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.104.fa_sub.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotellaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

```
{ Current stage: 0:01:19.799 || Total: 0:01:19.799 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.942 || Total: 0:01:20.741 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
```

```
Finished processing 0 of 1 (0.00%) bins.
```

```
Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.357 || Total: 0:01:21.099 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotellaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****  
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
```

```
Parsing HMM hits to marker genes:
```

```
Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.092 || Total: 0:00:00.092 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set genus Treponema /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Treponema.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - taxon_set] Generate taxonomic-specific marker set.
```

```
*****  
*****
```

```
Marker set for Treponema contains 326 marker genes arranged in 173 sets.
```

```
Marker set inferred from 28 reference genomes.
```

```
Marker set for Spirochaetaceae contains 235 marker genes arranged in 124 sets.
```

```
Marker set inferred from 56 reference genomes.
```

```
Marker set for Spirochaetales contains 218 marker genes arranged
```

in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Spirochaetia contains 218 marker genes arranged in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Spirochaetes contains 218 marker genes arranged in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Treponema.ms

```
{ Current stage: 0:00:03.638 || Total: 0:00:03.638 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.6.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Treponema.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - analyze] Identifying marker genes in bins.

```
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

```
{ Current stage: 0:00:33.469 || Total: 0:00:33.469 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.398 || Total: 0:00:33.868 }
```

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.334 || Total: 0:00:34.203 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
```

```
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Treponema.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.
Parsing HMM hits to marker genes:
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.066 || Total: 0:00:00.066 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set class Lentisphaeria /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Lentisphaeria.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Unrecognized taxon: Lentisphaeria (in rank class):

```
{ Current stage: 0:00:03.878 || Total: 0:00:03.878 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set phylum Lentisphaerae /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Lentisphaerae.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```



Unrecognized taxon: Lentisphaerae (in rank phylum):

```
{ Current stage: 0:00:03.509 || Total: 0:00:03.509 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set domain Bacteria /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Bacteria.ms >> /gpfs1/scratch/
jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Bacteria.ms

```
{ Current stage: 0:00:03.607 || Total: 0:00:03.607 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.64.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:00:24.905 || Total: 0:00:24.905 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.399 || Total: 0:00:25.305 }
```

```
Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.243 || Total: 0:00:25.548 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****  
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.067 || Total: 0:00:00.067 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set order Aeromonadales /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Aeromonadales.ms >> /gpfs1/  
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - taxon_set] Generate taxonomic-specific marker set.
```

```
*****  
*****
```

```
Marker set for Aeromonadales contains 456 marker genes arranged in  
237 sets.
```

```
Marker set inferred from 23 reference genomes.
```

```
Marker set for Gammaproteobacteria contains 280 marker genes  
arranged in 178 sets.
```

```
Marker set inferred from 1167 reference genomes.
```

```
Marker set for Proteobacteria contains 182 marker genes arranged  
in 119 sets.
```

Marker set inferred from 2343 reference genomes.  
Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Aeromonadales.ms

```
{ Current stage: 0:00:03.623 || Total: 0:00:03.623 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.77.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Aeromonadales.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.
```

```
{ Current stage: 0:01:17.168 || Total: 0:01:17.168 }
```

```
Parsing HMM hits to marker genes:  
  Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.538 || Total: 0:01:17.707 }
```

```
Calculating genome statistics for 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.378 || Total: 0:01:18.085 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Aeromonadales.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.181 || Total: 0:00:00.181 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set genus Prevotella /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Prevotella.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Marker set for Prevotella contains 522 marker genes arranged in  
281 sets.

Marker set inferred from 65 reference genomes.

Marker set for Prevotellaceae contains 553 marker genes arranged  
in 298 sets.

Marker set inferred from 69 reference genomes.

Marker set for Bacteroidales contains 402 marker genes arranged in  
267 sets.

Marker set inferred from 210 reference genomes.

Marker set for Bacteroidia contains 401 marker genes arranged in  
266 sets.

Marker set inferred from 211 reference genomes.

Marker set for Bacteroidetes contains 286 marker genes arranged in  
195 sets.

Marker set inferred from 419 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Prevotella.ms

```
{ Current stage: 0:00:03.678 || Total: 0:00:03.678 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x metabat2.5.fa_sub.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - analyze] Identifying marker genes in bins.

```
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:00:39.614 || Total: 0:00:39.614 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.362 || Total: 0:00:39.977 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.328 || Total: 0:00:40.305 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - qa] Tabulating genome statistics.

```
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.067 || Total: 0:00:00.067 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set family Rikenellaceae /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Rikenellaceae.ms >> /gpfs1/  
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Marker set for Rikenellaceae contains 648 marker genes arranged in  
386 sets.  
Marker set inferred from 6 reference genomes.  
Marker set for Bacteroidales contains 402 marker genes arranged in  
267 sets.  
Marker set inferred from 210 reference genomes.  
Marker set for Bacteroidia contains 401 marker genes arranged in  
266 sets.  
Marker set inferred from 211 reference genomes.  
Marker set for Bacteroidetes contains 286 marker genes arranged in  
195 sets.  
Marker set inferred from 419 reference genomes.  
Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.  
Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Rikenellaceae.ms

```
{ Current stage: 0:00:03.641 || Total: 0:00:03.641 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x metabat2.13.fa_sub.contigs.fa /gpfs1/  
scratch/jonas/metasqueeze_test/data/checkm_markers/  
Rikenellaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/results/  
bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /  
gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.
```

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:01:31.679 || Total: 0:01:31.679 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:03.328 || Total: 0:01:35.008 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.387 || Total: 0:01:35.396 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Rikenellaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.170 || Total: 0:00:00.170 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set class Clostridia /gpfs1/scratch/jonas/
```

```
metasqueeze_test/data/checkm_markers/Clostridia.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

```
Marker set for Clostridia contains 196 marker genes arranged in 110 sets.  
Marker set inferred from 446 reference genomes.  
Marker set for Firmicutes contains 172 marker genes arranged in 99 sets.  
Marker set inferred from 1349 reference genomes.  
Marker set for Bacteria contains 104 marker genes arranged in 58 sets.  
Marker set inferred from 5449 reference genomes.
```

```
Marker set written to: /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms
```

```
{ Current stage: 0:00:03.624 || Total: 0:00:03.624 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.31.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.
```

```
{ Current stage: 0:00:38.490 || Total: 0:00:38.490 }
```

```
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.674 || Total: 0:00:39.165 }
```



Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.361 || Total: 0:00:39.526 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.162 || Total: 0:00:00.162 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.9.fa_sub.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:00:37.598 || Total: 0:00:37.598 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.693 || Total: 0:00:38.292 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.358 || Total: 0:00:38.650 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.152 || Total: 0:00:00.152 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set genus Brachyspira /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Brachyspira.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Marker set for Brachyspira contains 783 marker genes arranged in 458 sets.

Marker set inferred from 10 reference genomes.

Marker set for Brachyspiraceae contains 783 marker genes arranged in 458 sets.

Marker set inferred from 10 reference genomes.

Marker set for Spirochaetales contains 218 marker genes arranged in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Spirochaetia contains 218 marker genes arranged in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Spirochaetes contains 218 marker genes arranged in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Brachyspira.ms

{ Current stage: 0:00:03.582 || Total: 0:00:03.582 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.1.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Brachyspira.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

[CheckM - analyze] Identifying marker genes in bins.

```
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:01:11.857 || Total: 0:01:11.857 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.434 || Total: 0:01:12.292 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.372 || Total: 0:01:12.664 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Brachyspira.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - qa] Tabulating genome statistics.

```
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.091 || Total: 0:00:00.091 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set order Bacteroidales /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Bacteroidales.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

```
*****
*****
```

Marker set for Bacteroidales contains 402 marker genes arranged in  
267 sets.

Marker set inferred from 210 reference genomes.

Marker set for Bacteroidia contains 401 marker genes arranged in  
266 sets.

Marker set inferred from 211 reference genomes.

Marker set for Bacteroidetes contains 286 marker genes arranged in  
195 sets.

Marker set inferred from 419 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Bacteroidales.ms

```
{ Current stage: 0:00:03.632 || Total: 0:00:03.632 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.45.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Bacteroidales.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:59.168 || Total: 0:00:59.168 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:04.421 || Total: 0:01:03.589 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.362 || Total: 0:01:03.951 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Bacteroidales.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.154 || Total: 0:00:00.154 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm taxon\_set order Spirochaetales /gpfs1/scratch/jonas/  
metasqueeze\_test/data/checkm\_markers/Spirochaetales.ms >> /gpfs1/  
scratch/jonas/metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Marker set for Spirochaetales contains 218 marker genes arranged  
in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Spirochaetia contains 218 marker genes arranged in  
127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Spirochaetes contains 218 marker genes arranged in  
127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Spirochaetales.ms

{ Current stage: 0:00:03.659 || Total: 0:00:03.659 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.71.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze\_test/data/checkm\_markers/Spirochaetales.ms /gpfs1/  
scratch/jonas/metasqueeze\_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/checkm\_batch >> /gpfs1/scratch/jonas/  
metasqueeze\_test/syslog 2>&1

\*\*\*\*\*

```
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:43.652 || Total: 0:00:43.652 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.506 || Total: 0:00:44.158 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.347 || Total: 0:00:44.506 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Spirochaetales.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.163 || Total: 0:00:00.163 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
```

```
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.47.fa_sub.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:27.699 || Total: 0:00:27.699 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:03.149 || Total: 0:00:30.848 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.363 || Total: 0:00:31.212 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```



QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.118 || Total: 0:00:00.118 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.20.fa_sub.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.
```

```
{ Current stage: 0:00:20.607 || Total: 0:00:20.607 }
```

```
Parsing HMM hits to marker genes:  
  Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.415 || Total: 0:00:21.023 }
```

```
Calculating genome statistics for 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.312 || Total: 0:00:21.335 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.074 || Total: 0:00:00.074 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set family Oscillospiraceae /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Oscillospiraceae.ms >> /gpfs1/  
scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Unrecognized taxon: Oscillospiraceae (in rank family):

{ Current stage: 0:00:03.663 || Total: 0:00:03.663 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.25.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:36.622 || Total: 0:00:36.622 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.777 || Total: 0:00:37.400 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.342 || Total: 0:00:37.742 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.162 || Total: 0:00:00.162 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.75.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Bacteroidales.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:51.195 || Total: 0:00:51.195 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.419 || Total: 0:00:51.614 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.300 || Total: 0:00:51.915 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Bacteroidales.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.123 || Total: 0:00:00.123 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.18.fa_sub.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
```

\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:01:12.422 || Total: 0:01:12.422 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.654 || Total: 0:01:13.076 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.344 || Total: 0:01:13.420 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.145 || Total: 0:00:00.145 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
```

```
checkm analyze -t 60 -x metabat2.8.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:20.635 || Total: 0:00:20.635 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.402 || Total: 0:00:21.038 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.376 || Total: 0:00:21.414 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
```

temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.070 || Total: 0:00:00.070 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.81.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Bacteroidales.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.
```

```
{ Current stage: 0:00:49.925 || Total: 0:00:49.925 }
```

```
Parsing HMM hits to marker genes:  
  Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.480 || Total: 0:00:50.405 }
```

```
Calculating genome statistics for 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.360 || Total: 0:00:50.766 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Bacteroidales.ms /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.101 || Total: 0:00:00.101 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.103.fa_sub.contigs.fa /gpfs1/
scratch/jonas/metasqueeze_test/data/checkm_markers/
Bacteroidales.ms /gpfs1/scratch/jonas/metasqueeze_test/results/
bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /
gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:45.285 || Total: 0:00:45.285 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.496 || Total: 0:00:45.781 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.337 || Total: 0:00:46.119 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Bacteroidales.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
```



```
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.094 || Total: 0:00:00.094 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set family Succinivibrionaceae /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Succinivibrionaceae.ms >> /  
gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Marker set for Succinivibrionaceae contains 637 marker genes  
arranged in 317 sets.

Marker set inferred from 6 reference genomes.

Marker set for Aeromonadales contains 456 marker genes arranged in  
237 sets.

Marker set inferred from 23 reference genomes.

Marker set for Gammaproteobacteria contains 280 marker genes  
arranged in 178 sets.

Marker set inferred from 1167 reference genomes.

Marker set for Proteobacteria contains 182 marker genes arranged  
in 119 sets.

Marker set inferred from 2343 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Succinivibrionaceae.ms

{ Current stage: 0:00:03.602 || Total: 0:00:03.602 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
```

```
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.84.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Succinivibrionaceae.ms /
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:01:30.702 || Total: 0:01:30.702 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:01.883 || Total: 0:01:32.585 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.383 || Total: 0:01:32.969 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Succinivibrionaceae.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.246 || Total: 0:00:00.246 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set genus Alistipes /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Alistipes.ms >> /gpfs1/scratch/  
jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Marker set for Alistipes contains 703 marker genes arranged in 335 sets.

Marker set inferred from 5 reference genomes.

Marker set for Rikenellaceae contains 648 marker genes arranged in 386 sets.

Marker set inferred from 6 reference genomes.

Marker set for Bacteroidales contains 402 marker genes arranged in 267 sets.

Marker set inferred from 210 reference genomes.

Marker set for Bacteroidia contains 401 marker genes arranged in 266 sets.

Marker set inferred from 211 reference genomes.

Marker set for Bacteroidetes contains 286 marker genes arranged in 195 sets.

Marker set inferred from 419 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Alistipes.ms

```
{ Current stage: 0:00:03.651 || Total: 0:00:03.651 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x metabat2.18.fa_sub.contigs.fa /gpfs1/  
scratch/jonas/metasqueeze_test/data/checkm_markers/Alistipes.ms /  
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/  
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:01:12.699 || Total: 0:01:12.699 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.569 || Total: 0:01:13.268 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.371 || Total: 0:01:13.639 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Alistipes.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.122 || Total: 0:00:00.122 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
```

```
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set family Elusimicrobiaceae /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Elusimicrobiaceae.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Unrecognized taxon: Elusimicrobiaceae (in rank family):

```
{ Current stage: 0:00:03.613 || Total: 0:00:03.613 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/ppplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set order Elusimicrobiales /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Elusimicrobiales.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Unrecognized taxon: Elusimicrobiales (in rank order):

```
{ Current stage: 0:00:03.609 || Total: 0:00:03.609 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/ppplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set class Elusimicrobia /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Elusimicrobia.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Unrecognized taxon: Elusimicrobia (in rank class):

```
{ Current stage: 0:00:03.654 || Total: 0:00:03.654 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/ppplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set phylum Elusimicrobia /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Elusimicrobia.ms >> /gpfs1/
```

scratch/jonas/metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Unrecognized taxon: Elusimicrobia (in rank phylum):

{ Current stage: 0:00:03.617 || Total: 0:00:03.617 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.16.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze\_test/data/checkm\_markers/Bacteria.ms /gpfs1/  
scratch/jonas/metasqueeze\_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/checkm\_batch >> /gpfs1/scratch/jonas/  
metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:22.740 || Total: 0:00:22.740 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.411 || Total: 0:00:23.152 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.338 || Total: 0:00:23.491 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_batch -f /gpfs1/scratch/jonas/metasqueeze\_test/temp/

```
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****  
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
```

```
Parsing HMM hits to marker genes:
```

```
Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.096 || Total: 0:00:00.096 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x metabat2.22.fa_sub.contigs.fa /gpfs1/  
scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /  
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/  
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
```

```
Finished processing 0 of 1 (0.00%) bins.
```

```
Finished processing 1 of 1 (100.00%) bins.
```

```
Saving HMM info to file.
```

```
{ Current stage: 0:01:21.237 || Total: 0:01:21.237 }
```

```
Parsing HMM hits to marker genes:
```

```
Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
Aligning marker genes with multiple hits in a single bin:
```

```
Finished processing 0 of 1 (0.00%) bins.
```

```
Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:02.460 || Total: 0:01:23.697 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
```

```
Finished processing 0 of 1 (0.00%) bins.
```

```
Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.275 || Total: 0:01:23.972 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.193 || Total: 0:00:00.193 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set family Lachnospiraceae /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Lachnospiraceae.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Marker set for Lachnospiraceae contains 312 marker genes arranged in 160 sets.  
Marker set inferred from 86 reference genomes.  
Marker set for Clostridiales contains 202 marker genes arranged in 114 sets.  
Marker set inferred from 395 reference genomes.  
Marker set for Clostridia contains 196 marker genes arranged in 110 sets.  
Marker set inferred from 446 reference genomes.  
Marker set for Firmicutes contains 172 marker genes arranged in 99 sets.  
Marker set inferred from 1349 reference genomes.  
Marker set for Bacteria contains 104 marker genes arranged in 58 sets.  
Marker set inferred from 5449 reference genomes.



Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Lachnospiraceae.ms

```
{ Current stage: 0:00:03.624 || Total: 0:00:03.624 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.7.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Lachnospiraceae.ms /
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:46.422 || Total: 0:00:46.422 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:01.957 || Total: 0:00:48.380 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.360 || Total: 0:00:48.740 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Lachnospiraceae.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
```

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.202 || Total: 0:00:00.202 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm taxon\_set phylum Firmicutes /gpfs1/scratch/jonas/  
metasqueeze\_test/data/checkm\_markers/Firmicutes.ms >> /gpfs1/  
scratch/jonas/metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Marker set for Firmicutes contains 172 marker genes arranged in 99  
sets.

Marker set inferred from 1349 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Firmicutes.ms

{ Current stage: 0:00:03.564 || Total: 0:00:03.564 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.54.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze\_test/data/checkm\_markers/Firmicutes.ms /gpfs1/  
scratch/jonas/metasqueeze\_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/checkm\_batch >> /gpfs1/scratch/jonas/  
metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:00:29.469 || Total: 0:00:29.469 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.449 || Total: 0:00:29.919 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.350 || Total: 0:00:30.270 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Firmicutes.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.130 || Total: 0:00:00.130 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x metabat2.14.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:37.131 || Total: 0:00:37.131 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.440 || Total: 0:00:37.572 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.260 || Total: 0:00:37.832 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.134 || Total: 0:00:00.134 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
```

```
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.111.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:27.112 || Total: 0:00:27.112 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.418 || Total: 0:00:27.531 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.328 || Total: 0:00:27.859 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.095 || Total: 0:00:00.095 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.98.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Lachnospiraceae.ms /  
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/  
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:00:45.389 || Total: 0:00:45.389 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.775 || Total: 0:00:46.164 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.372 || Total: 0:00:46.537 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Lachnospiraceae.ms /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.181 || Total: 0:00:00.181 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/ppplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm taxon\_set family Oscillospiraceae /gpfs1/scratch/jonas/  
metasqueeze\_test/data/checkm\_markers/Oscillospiraceae.ms >> /gpfs1/  
scratch/jonas/metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Unrecognized taxon: Oscillospiraceae (in rank family):

{ Current stage: 0:00:03.652 || Total: 0:00:03.652 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/ppplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.102.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze\_test/data/checkm\_markers/Clostridia.ms /gpfs1/  
scratch/jonas/metasqueeze\_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/checkm\_batch >> /gpfs1/scratch/jonas/  
metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:21.593 || Total: 0:00:21.593 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.392 || Total: 0:00:21.985 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.345 || Total: 0:00:22.331 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.082 || Total: 0:00:00.082 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.43.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Lachnospiraceae.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:



Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:00:35.493 || Total: 0:00:35.493 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.406 || Total: 0:00:35.899 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.331 || Total: 0:00:36.231 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Lachnospiraceae.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.121 || Total: 0:00:00.121 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.69.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:28.269 || Total: 0:00:28.269 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.974 || Total: 0:00:29.244 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.370 || Total: 0:00:29.614 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.130 || Total: 0:00:00.130 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
```

```
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set phylum Spirochaetes /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Spirochaetes.ms >> /gpfs1/
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Marker set for Spirochaetes contains 218 marker genes arranged in 127 sets.

Marker set inferred from 71 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Spirochaetes.ms

```
{ Current stage: 0:00:03.615 || Total: 0:00:03.615 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.10.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Spirochaetes.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

```
{ Current stage: 0:00:33.941 || Total: 0:00:33.941 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.451 || Total: 0:00:34.392 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.358 || Total: 0:00:34.750 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Spirochaetes.ms /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.129 || Total: 0:00:00.129 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.34.fa_sub.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Alistipes.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:01:20.088 || Total: 0:01:20.088 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:03.414 || Total: 0:01:23.503 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.367 || Total: 0:01:23.870 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Alistipes.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.174 || Total: 0:00:00.174 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.109.fa_sub.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:01:52.326 || Total: 0:01:52.326 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:12.774 || Total: 0:02:05.101 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.393 || Total: 0:02:05.494 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.336 || Total: 0:00:00.336 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set genus Campylobacter /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Campylobacter.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
```

\*\*\*\*\*

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Marker set for Campylobacter contains 598 marker genes arranged in 263 sets.

Marker set inferred from 55 reference genomes.

Marker set for Campylobacteraceae contains 505 marker genes arranged in 274 sets.

Marker set inferred from 66 reference genomes.

Marker set for Campylobacterales contains 458 marker genes arranged in 273 sets.

Marker set inferred from 107 reference genomes.

Marker set for Epsilonproteobacteria contains 445 marker genes arranged in 271 sets.

Marker set inferred from 111 reference genomes.

Marker set for Proteobacteria contains 182 marker genes arranged in 119 sets.

Marker set inferred from 2343 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Campylobacter.ms

```
{ Current stage: 0:00:03.757 || Total: 0:00:03.757 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.94.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Campylobacter.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

```
{ Current stage: 0:00:43.083 || Total: 0:00:43.083 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.408 || Total: 0:00:43.492 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.333 || Total: 0:00:43.825 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Campylobacter.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

[CheckM - qa] Tabulating genome statistics.

```
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.113 || Total: 0:00:00.113 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.95.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotellaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

[CheckM - analyze] Identifying marker genes in bins.

```
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.



Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:01:23.254 || Total: 0:01:23.254 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.811 || Total: 0:01:24.066 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.346 || Total: 0:01:24.412 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotellaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

[CheckM - qa] Tabulating genome statistics.

```
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.214 || Total: 0:00:00.214 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.110.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:36.068 || Total: 0:00:36.068 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.486 || Total: 0:00:36.554 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.307 || Total: 0:00:36.862 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.161 || Total: 0:00:00.161 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
```

```
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x metabat2.32.fa_sub.contigs.fa /gpfs1/
scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:40.572 || Total: 0:00:40.572 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.327 || Total: 0:00:40.900 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.329 || Total: 0:00:41.230 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.116 || Total: 0:00:00.116 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set genus Escherichia /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Escherichia.ms >> /gpfs1/  
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Marker set for Escherichia contains 1212 marker genes arranged in  
320 sets.

Marker set inferred from 27 reference genomes.

Marker set for Enterobacteriaceae contains 297 marker genes  
arranged in 121 sets.

Marker set inferred from 262 reference genomes.

Marker set for Enterobacteriales contains 297 marker genes  
arranged in 121 sets.

Marker set inferred from 262 reference genomes.

Marker set for Gammaproteobacteria contains 280 marker genes  
arranged in 178 sets.

Marker set inferred from 1167 reference genomes.

Marker set for Proteobacteria contains 182 marker genes arranged  
in 119 sets.

Marker set inferred from 2343 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Escherichia.ms

```
{ Current stage: 0:00:03.711 || Total: 0:00:03.711 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.32.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Escherichia.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.
```

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:02:14.596 || Total: 0:02:14.596 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:02.390 || Total: 0:02:16.987 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.399 || Total: 0:02:17.386 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Escherichia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.441 || Total: 0:00:00.441 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set class Alphaproteobacteria /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Alphaproteobacteria.ms >> /
```

```
gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - taxon_set] Generate taxonomic-specific marker set.
```

```
*****  
*****
```

```
Marker set for Alphaproteobacteria contains 225 marker genes  
arranged in 148 sets.
```

```
Marker set inferred from 648 reference genomes.
```

```
Marker set for Proteobacteria contains 182 marker genes arranged  
in 119 sets.
```

```
Marker set inferred from 2343 reference genomes.
```

```
Marker set for Bacteria contains 104 marker genes arranged in 58  
sets.
```

```
Marker set inferred from 5449 reference genomes.
```

```
Marker set written to: /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Alphaproteobacteria.ms
```

```
{ Current stage: 0:00:03.645 || Total: 0:00:03.645 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.106.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Alphaproteobacteria.ms /  
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/  
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
```

```
Finished processing 0 of 1 (0.00%) bins.
```

```
Finished processing 1 of 1 (100.00%) bins.
```

```
Saving HMM info to file.
```

```
{ Current stage: 0:00:28.518 || Total: 0:00:28.518 }
```

```
Parsing HMM hits to marker genes:
```

```
Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
Aligning marker genes with multiple hits in a single bin:
```

```
Finished processing 0 of 1 (0.00%) bins.
```

```
Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.416 || Total: 0:00:28.935 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
```

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.334 || Total: 0:00:29.269 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Alphaproteobacteria.ms /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.122 || Total: 0:00:00.122 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.36.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:00:20.198 || Total: 0:00:20.198 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.414 || Total: 0:00:20.612 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.248 || Total: 0:00:20.861 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.114 || Total: 0:00:00.114 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.13.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:



Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:00:22.830 || Total: 0:00:22.830 }

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.377 || Total: 0:00:23.208 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.326 || Total: 0:00:23.534 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.097 || Total: 0:00:00.097 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set class Negativicutes /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Negativicutes.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

```
Marker set for Negativicutes contains 334 marker genes arranged in 167 sets.
```

```
Marker set inferred from 64 reference genomes.
```

```
Marker set for Firmicutes contains 172 marker genes arranged in 99 sets.
```

```
Marker set inferred from 1349 reference genomes.
```

```
Marker set for Bacteria contains 104 marker genes arranged in 58 sets.
```

```
Marker set inferred from 5449 reference genomes.
```

```
Marker set written to: /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Negativicutes.ms
```

```
{ Current stage: 0:00:03.660 || Total: 0:00:03.660 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.27.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Negativicutes.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:53.494 || Total: 0:00:53.494 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:01.727 || Total: 0:00:55.221 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.356 || Total: 0:00:55.578 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Negativicutes.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - qa] Tabulating genome statistics.

```
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/
temp/checkm\_prov.txt

{ Current stage: 0:00:00.216 || Total: 0:00:00.216 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set genus Phascolarctobacterium /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Phascolarctobacterium.ms >> /
gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

```
*****
*****
```

Unrecognized taxon: Phascolarctobacterium (in rank genus):

{ Current stage: 0:00:03.719 || Total: 0:00:03.719 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set family Acidaminococcaceae /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Acidaminococcaceae.ms >> /
gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - taxon\_set] Generate taxonomic-specific marker set.

\*\*\*\*\*  
\*\*\*\*\*

Marker set for Acidaminococcaceae contains 677 marker genes arranged in 256 sets.

Marker set inferred from 7 reference genomes.

Marker set for Selenomonadales contains 334 marker genes arranged in 167 sets.

Marker set inferred from 64 reference genomes.

Marker set for Negativicutes contains 334 marker genes arranged in 167 sets.

Marker set inferred from 64 reference genomes.

Marker set for Firmicutes contains 172 marker genes arranged in 99 sets.

Marker set inferred from 1349 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/checkm\_markers/Acidaminococcaceae.ms

```
{ Current stage: 0:00:03.636 || Total: 0:00:03.636 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.49.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Acidaminococcaceae.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

```
{ Current stage: 0:01:23.260 || Total: 0:01:23.260 }
```

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:29.409 || Total: 0:01:52.669 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.393 || Total: 0:01:53.063 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Acidaminococcaceae.ms /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.430 || Total: 0:00:00.430 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm taxon_set family Oscillospiraceae /gpfs1/scratch/jonas/  
metasqueeze_test/data/checkm_markers/Oscillospiraceae.ms >> /gpfs1/  
scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Unrecognized taxon: Oscillospiraceae (in rank family):

```
{ Current stage: 0:00:03.618 || Total: 0:00:03.618 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.12.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/
```

```
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:39.737 || Total: 0:00:39.737 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.496 || Total: 0:00:40.233 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.366 || Total: 0:00:40.600 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/ppplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.222 || Total: 0:00:00.222 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.74.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Alphaproteobacteria.ms /
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:22.799 || Total: 0:00:22.799 }
```

```
Parsing HMM hits to marker genes:
```

```
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.401 || Total: 0:00:23.201 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
```

```
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.346 || Total: 0:00:23.547 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Alphaproteobacteria.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.134 || Total: 0:00:00.134 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.60.fa_sub.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Alistipes.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:01:35.979 || Total: 0:01:35.979 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:10.681 || Total: 0:01:46.661 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.405 || Total: 0:01:47.066 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Alistipes.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```



```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.304 || Total: 0:00:00.304 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm taxon_set genus Dialister /gpfs1/scratch/jonas/
metasqueeze_test/data/checkm_markers/Dialister.ms >> /gpfs1/scratch/
jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - taxon_set] Generate taxonomic-specific marker set.
*****
*****
```

Marker set for Dialister contains 695 marker genes arranged in 210 sets.

Marker set inferred from 4 reference genomes.

Marker set for Veillonellaceae contains 345 marker genes arranged in 171 sets.

Marker set inferred from 57 reference genomes.

Marker set for Selenomonadales contains 334 marker genes arranged in 167 sets.

Marker set inferred from 64 reference genomes.

Marker set for Negativicutes contains 334 marker genes arranged in 167 sets.

Marker set inferred from 64 reference genomes.

Marker set for Firmicutes contains 172 marker genes arranged in 99 sets.

Marker set inferred from 1349 reference genomes.

Marker set for Bacteria contains 104 marker genes arranged in 58 sets.

Marker set inferred from 5449 reference genomes.

Marker set written to: /gpfs1/scratch/jonas/metasqueeze\_test/data/  
checkm\_markers/Dialister.ms

```
{ Current stage: 0:00:03.737 || Total: 0:00:03.737 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
```

```
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.46.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Dialister.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:01:17.796 || Total: 0:01:17.796 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:02.290 || Total: 0:01:20.087 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.355 || Total: 0:01:20.443 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Dialister.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
```

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.275 || Total: 0:00:00.275 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.113.fa_sub.contigs.fa /gpfs1/
scratch/jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:00:41.669 || Total: 0:00:41.669 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:03.927 || Total: 0:00:45.597 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.399 || Total: 0:00:45.997 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.245 || Total: 0:00:00.245 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.57.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze\_test/data/checkm\_markers/Alphaproteobacteria.ms /  
gpfs1/scratch/jonas/metasqueeze\_test/results/bins /gpfs1/scratch/  
jonas/metasqueeze\_test/temp/checkm\_batch >> /gpfs1/scratch/jonas/  
metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:33.715 || Total: 0:00:33.715 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.446 || Total: 0:00:34.161 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.346 || Total: 0:00:34.508 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze\_test/data/

```
checkm_markers/Alphaproteobacteria.ms /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.181 || Total: 0:00:00.181 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.40.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Prevotellaceae.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:01:12.484 || Total: 0:01:12.484 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:02.597 || Total: 0:01:15.082 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.364 || Total: 0:01:15.446 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Prevotellaceae.ms /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.245 || Total: 0:00:00.245 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x metabat2.15.fa_sub.contigs.fa /gpfs1/
scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:01:17.087 || Total: 0:01:17.087 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:02.058 || Total: 0:01:19.145 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.408 || Total: 0:01:19.554 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.252 || Total: 0:00:00.252 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.82.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

{ Current stage: 0:00:36.157 || Total: 0:00:36.157 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.503 || Total: 0:00:36.661 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.319 || Total: 0:00:36.980 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.243 || Total: 0:00:00.243 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm analyze -t 60 -x concoct.66.fa.contigs.fa /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Treponema.ms /gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
```



```
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:55.893 || Total: 0:00:55.893 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.992 || Total: 0:00:56.886 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.385 || Total: 0:00:57.271 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Treponema.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.250 || Total: 0:00:00.250 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
```

```
checkm analyze -t 60 -x concoct.100.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Prevotella.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:44.280 || Total: 0:00:44.280 }
```

```
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.414 || Total: 0:00:44.694 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.248 || Total: 0:00:44.943 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
Parsing HMM hits to marker genes:
  Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/
```

temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.181 || Total: 0:00:00.181 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.19.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Escherichia.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

```
Identifying marker genes in 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.
```

```
{ Current stage: 0:01:07.516 || Total: 0:01:07.516 }
```

```
Parsing HMM hits to marker genes:  
  Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.409 || Total: 0:01:07.926 }
```

```
Calculating genome statistics for 1 bins with 60 threads:  
  Finished processing 0 of 1 (0.00%) bins.  
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.384 || Total: 0:01:08.311 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Escherichia.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.198 || Total: 0:00:00.198 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.115.fa_sub.contigs.fa /gpfs1/  
scratch/jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /  
gpfs1/scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/  
jonas/metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:28.006 || Total: 0:00:28.006 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:02.779 || Total: 0:00:30.785 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.364 || Total: 0:00:31.149 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - qa] Tabulating genome statistics.
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/
temp/checkm\_prov.txt

{ Current stage: 0:00:00.205 || Total: 0:00:00.205 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.55.fa_sub.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
[CheckM - analyze] Identifying marker genes in bins.
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:20.650 || Total: 0:00:20.650 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.378 || Total: 0:00:21.028 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.308 || Total: 0:00:21.336 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
```

```
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - qa] Tabulating genome statistics.

```
*****
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.152 || Total: 0:00:00.152 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.96.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Treponema.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

[CheckM - analyze] Identifying marker genes in bins.

```
*****
*****
```

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:00:59.345 || Total: 0:00:59.345 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.449 || Total: 0:00:59.794 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.333 || Total: 0:01:00.128 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Treponema.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.260 || Total: 0:00:00.260 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.92.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:00:19.860 || Total: 0:00:19.860 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.408 || Total: 0:00:20.269 }

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.301 || Total: 0:00:20.570 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - qa] Tabulating genome statistics.  
*****  
*****
```

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/temp/checkm\_prov.txt

{ Current stage: 0:00:00.168 || Total: 0:00:00.168 }

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/checkm taxon_set family Oscillospiraceae /gpfs1/scratch/jonas/metasqueeze_test/data/checkm_markers/Oscillospiraceae.ms >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - taxon_set] Generate taxonomic-specific marker set.  
*****  
*****
```

Unrecognized taxon: Oscillospiraceae (in rank family):



```
{ Current stage: 0:00:03.630 || Total: 0:00:03.630 }
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm analyze -t 60 -x concoct.114.fa.contigs.fa /gpfs1/scratch/
jonas/metasqueeze_test/data/checkm_markers/Clostridia.ms /gpfs1/
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/
metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - analyze] Identifying marker genes in bins.
```

```
*****
*****
```

```
Identifying marker genes in 1 bins with 60 threads:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
Saving HMM info to file.
```

```
{ Current stage: 0:00:28.394 || Total: 0:00:28.394 }
```

```
Parsing HMM hits to marker genes:
```

```
  Finished parsing hits for 1 of 1 (100.00%) bins.
Aligning marker genes with multiple hits in a single bin:
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.442 || Total: 0:00:28.836 }
```

```
Calculating genome statistics for 1 bins with 60 threads:
```

```
  Finished processing 0 of 1 (0.00%) bins.
  Finished processing 1 of 1 (100.00%) bins.
```

```
{ Current stage: 0:00:00.328 || Total: 0:00:29.164 }
```

```
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/
checkm_markers/Clostridia.ms /gpfs1/scratch/jonas/metasqueeze_test/
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****
*****
```

```
Calculating AAI between multi-copy marker genes.
```

Reading HMM info from file.  
Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

```
{ Current stage: 0:00:00.192 || Total: 0:00:00.192 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.76.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze_test/data/checkm_markers/Bacteria.ms /gpfs1/  
scratch/jonas/metasqueeze_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze_test/temp/checkm_batch >> /gpfs1/scratch/jonas/  
metasqueeze_test/syslog 2>&1
```

```
*****  
*****  
[CheckM - analyze] Identifying marker genes in bins.  
*****  
*****
```

Identifying marker genes in 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.  
Saving HMM info to file.

```
{ Current stage: 0:01:27.727 || Total: 0:01:27.727 }
```

Parsing HMM hits to marker genes:  
Finished parsing hits for 1 of 1 (100.00%) bins.  
Aligning marker genes with multiple hits in a single bin:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:01.568 || Total: 0:01:29.296 }
```

Calculating genome statistics for 1 bins with 60 threads:  
Finished processing 0 of 1 (0.00%) bins.  
Finished processing 1 of 1 (100.00%) bins.

```
{ Current stage: 0:00:00.411 || Total: 0:01:29.707 }  
PATH=/home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/hmmer:  
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Bacteria.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****
```

\*\*\*\*\*

[CheckM - qa] Tabulating genome statistics.

\*\*\*\*\*  
\*\*\*\*\*

Calculating AAI between multi-copy marker genes.

Reading HMM info from file.

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

QA information written to: /gpfs1/scratch/jonas/metasqueeze\_test/  
temp/checkm\_prov.txt

{ Current stage: 0:00:00.309 || Total: 0:00:00.309 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:  
\$PATH /home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/  
checkm analyze -t 60 -x concoct.56.fa.contigs.fa /gpfs1/scratch/  
jonas/metasqueeze\_test/data/checkm\_markers/Prevotella.ms /gpfs1/  
scratch/jonas/metasqueeze\_test/results/bins /gpfs1/scratch/jonas/  
metasqueeze\_test/temp/checkm\_batch >> /gpfs1/scratch/jonas/  
metasqueeze\_test/syslog 2>&1

\*\*\*\*\*  
\*\*\*\*\*

[CheckM - analyze] Identifying marker genes in bins.

\*\*\*\*\*  
\*\*\*\*\*

Identifying marker genes in 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

Saving HMM info to file.

{ Current stage: 0:01:35.404 || Total: 0:01:35.404 }

Parsing HMM hits to marker genes:

Finished parsing hits for 1 of 1 (100.00%) bins.

Aligning marker genes with multiple hits in a single bin:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.735 || Total: 0:01:36.140 }

Calculating genome statistics for 1 bins with 60 threads:

Finished processing 0 of 1 (0.00%) bins.

Finished processing 1 of 1 (100.00%) bins.

{ Current stage: 0:00:00.384 || Total: 0:01:36.524 }

PATH=/home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/pplacer:/  
home/jonas/miniconda3/envs/SqueezeMeta\_dev/SqueezeMeta/bin/hmmer:

```
$PATH /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/  
checkm qa -t 60 /gpfs1/scratch/jonas/metasqueeze_test/data/  
checkm_markers/Prevotella.ms /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_batch -f /gpfs1/scratch/jonas/metasqueeze_test/temp/  
checkm_prov.txt >> /gpfs1/scratch/jonas/metasqueeze_test/syslog 2>&1
```

```
*****  
*****
```

```
[CheckM - qa] Tabulating genome statistics.
```

```
*****  
*****
```

```
Calculating AAI between multi-copy marker genes.
```

```
Reading HMM info from file.
```

```
Parsing HMM hits to marker genes:
```

```
Finished parsing hits for 1 of 1 (100.00%) bins.
```

```
QA information written to: /gpfs1/scratch/jonas/metasqueeze_test/  
temp/checkm_prov.txt
```

```
{ Current stage: 0:00:00.310 || Total: 0:00:00.310 }  
[6 hours, 20 minutes, 43 seconds]: STEP18 -> 18.getbins.pl  
Reading 16S rRNA in contigs from /gpfs1/scratch/jonas/  
metasqueeze_test/results/02.metasqueeze_test.16S.txt  
Creating bin coverage table in /gpfs1/scratch/jonas/  
metasqueeze_test/intermediate/18.metasqueeze_test.bincov  
Creating contigs in bins table in /gpfs1/scratch/jonas/  
metasqueeze_test/intermediate/18.metasqueeze_test.contigsinbins  
Calculating coverages for bins from /gpfs1/scratch/jonas/  
metasqueeze_test/intermediate/10.metasqueeze_test.contigcov  
Creating table in /gpfs1/scratch/jonas/metasqueeze_test/results/  
18.metasqueeze_test.bintable  
[6 hours, 21 minutes, 3 seconds]: STEP19 -> 19.getcontigs.pl  
Reading taxa for contigs information from /gpfs1/scratch/jonas/  
metasqueeze_test/intermediate/09.metasqueeze_test.contiglog  
Reading GC & length from /gpfs1/scratch/jonas/metasqueeze_test/  
results/01.metasqueeze_test.fasta  
Reading number of genes from /gpfs1/scratch/jonas/  
metasqueeze_test/results/03.metasqueeze_test.faa  
Reading coverages from /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/10.metasqueeze_test.contigcov  
Reading bins from /gpfs1/scratch/jonas/metasqueeze_test/  
intermediate/18.metasqueeze_test.contigsinbins  
Creating contig table in /gpfs1/scratch/jonas/metasqueeze_test/  
results/19.metasqueeze_test.contigtable  
[6 hours, 21 minutes, 47 seconds]: STEP20 -> 20.minpath.pl  
Running MinPath for kegg (concoct.1.fa.contigs): python3 /home/  
jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/MinPath1.4.py  
-ko /gpfs1/scratch/jonas/metasqueeze_test/temp/  
concoct.1.fa.contigs.minpath.temp.kegg -map ec2path -report /gpfs1/  
scratch/jonas/metasqueeze_test/temp/  
concoct.1.fa.contigs.kegg.temp.report -details /gpfs1/scratch/jonas/  
metasqueeze_test/temp/concoct.1.fa.contigs.kegg.details > /dev/null
```

concoct.10.fa.contigs concoct.100.fa.contigs concoct.102.fa.contigs  
concoct.103.fa\_sub.contigs concoct.104.fa\_sub.contigs  
concoct.106.fa.contigs concoct.109.fa\_sub.contigs  
concoct.110.fa.contigs concoct.111.fa.contigs  
concoct.113.fa\_sub.contigs concoct.114.fa.contigs  
concoct.115.fa\_sub.contigs concoct.12.fa.contigs  
concoct.13.fa.contigs concoct.16.fa.contigs  
concoct.18.fa\_sub.contigs concoct.19.fa.contigs  
concoct.20.fa\_sub.contigs concoct.25.fa.contigs  
concoct.27.fa.contigs concoct.31.fa.contigs concoct.32.fa.contigs  
concoct.34.fa\_sub.contigs concoct.36.fa.contigs  
concoct.40.fa.contigs concoct.43.fa.contigs concoct.45.fa.contigs  
concoct.46.fa.contigs concoct.47.fa\_sub.contigs  
concoct.49.fa.contigs concoct.54.fa.contigs  
concoct.55.fa\_sub.contigs concoct.56.fa.contigs  
concoct.57.fa.contigs concoct.6.fa.contigs concoct.60.fa\_sub.contigs  
concoct.64.fa.contigs concoct.66.fa.contigs concoct.69.fa.contigs  
concoct.7.fa.contigs concoct.71.fa.contigs concoct.74.fa.contigs  
concoct.75.fa.contigs concoct.76.fa.contigs concoct.77.fa.contigs  
concoct.81.fa.contigs concoct.82.fa.contigs concoct.84.fa.contigs  
concoct.9.fa\_sub.contigs concoct.92.fa.contigs concoct.94.fa.contigs  
concoct.95.fa.contigs concoct.96.fa.contigs concoct.98.fa.contigs  
concoct.99.fa.contigs metabat2.13.fa\_sub.contigs  
metabat2.14.fa.contigs metabat2.15.fa\_sub.contigs  
metabat2.18.fa\_sub.contigs metabat2.22.fa\_sub.contigs  
metabat2.32.fa\_sub.contigs metabat2.5.fa\_sub.contigs  
metabat2.8.fa.contigs

```
Running MinPath for metacyc (concoct.1.fa.contigs): python3 /home/  
jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/bin/MinPath1.4.py  
-any /gpfs1/scratch/jonas/metasqueeze_test/temp/  
concoct.1.fa.contigs.minpath.temp -map ec2path -report /gpfs1/  
scratch/jonas/metasqueeze_test/temp/  
concoct.1.fa.contigs.metacyc.temp.report -details /gpfs1/scratch/  
jonas/metasqueeze_test/temp/concoct.1.fa.contigs.metacyc.details  
> /dev/null
```

concoct.10.fa.contigs concoct.100.fa.contigs concoct.102.fa.contigs  
concoct.103.fa\_sub.contigs concoct.104.fa\_sub.contigs  
concoct.106.fa.contigs concoct.109.fa\_sub.contigs  
concoct.110.fa.contigs concoct.111.fa.contigs  
concoct.113.fa\_sub.contigs concoct.114.fa.contigs  
concoct.115.fa\_sub.contigs concoct.12.fa.contigs  
concoct.13.fa.contigs concoct.16.fa.contigs  
concoct.18.fa\_sub.contigs concoct.19.fa.contigs  
concoct.20.fa\_sub.contigs concoct.25.fa.contigs  
concoct.27.fa.contigs concoct.31.fa.contigs concoct.32.fa.contigs  
concoct.34.fa\_sub.contigs concoct.36.fa.contigs  
concoct.40.fa.contigs concoct.43.fa.contigs concoct.45.fa.contigs  
concoct.46.fa.contigs concoct.47.fa\_sub.contigs  
concoct.49.fa.contigs concoct.54.fa.contigs  
concoct.55.fa\_sub.contigs concoct.56.fa.contigs  
concoct.57.fa.contigs concoct.6.fa.contigs concoct.60.fa\_sub.contigs  
concoct.64.fa.contigs concoct.66.fa.contigs concoct.69.fa.contigs  
concoct.7.fa.contigs concoct.71.fa.contigs concoct.74.fa.contigs  
concoct.75.fa.contigs concoct.76.fa.contigs concoct.77.fa.contigs

concoct.81.fa.contigs concoct.82.fa.contigs concoct.84.fa.contigs  
concoct.9.fa\_sub.contigs concoct.92.fa.contigs concoct.94.fa.contigs  
concoct.95.fa.contigs concoct.96.fa.contigs concoct.98.fa.contigs  
concoct.99.fa.contigs metabat2.13.fa\_sub.contigs  
metabat2.14.fa.contigs metabat2.15.fa\_sub.contigs  
metabat2.18.fa\_sub.contigs metabat2.22.fa\_sub.contigs  
metabat2.32.fa\_sub.contigs metabat2.5.fa\_sub.contigs  
metabat2.8.fa.contigs  
[6 hours, 23 minutes, 58 seconds]: STEP21 -> 21.stats.pl

Deleting temporary files in /gpfs1/scratch/jonas/metasqueeze\_test/  
temp

[6 hours, 24 minutes, 13 seconds]: FINISHED -> Have fun!