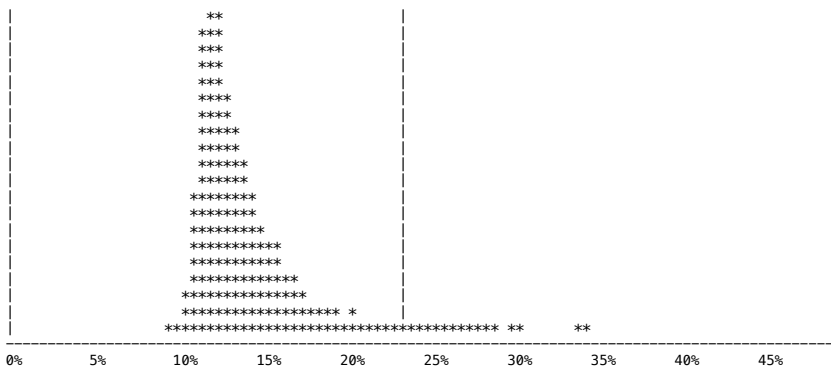


```

[2020-05-28 15:06:00] root: INFO: Starting Flye 2.6-release
[2020-05-28 15:06:00] root: DEBUG: Cmd: /software/shared/apps/x86_64/flye/2.6.0/bin//flye --nano-raw 40parent_g344.fasta --threads 5 --genome-size 110m --min-overlap 5000 --debug --out-dir /scratch/scgenes/chlamy/40parent/output_flye_P40_g3.4.4_4865318
[2020-05-28 15:06:00] root: DEBUG: Python version: 3.6.5 (default, Aug 17 2018, 13:29:29)
[GCC 6.3.0]
[2020-05-28 15:06:00] root: INFO: >>>STAGE: configure
[2020-05-28 15:06:00] root: INFO: Configuring run
[2020-05-28 15:06:39] root: INFO: Total read length: 5436436201
[2020-05-28 15:06:39] root: INFO: Input genome size: 110000000
[2020-05-28 15:06:39] root: INFO: Estimated coverage: 49
[2020-05-28 15:06:39] root: INFO: Reads N50/N90: 44262 / 14090
[2020-05-28 15:06:39] root: INFO: Selected minimum overlap: 5000
[2020-05-28 15:06:39] root: INFO: Selected k-mer size: 17
[2020-05-28 15:06:39] root: INFO: >>>STAGE: assembly
[2020-05-28 15:06:39] root: INFO: Assembling disjointigs
[2020-05-28 15:06:39] root: DEBUG: -----Begin assembly log-----
[2020-05-28 15:06:39] root: DEBUG: Running: flye-assemble --reads 40parent_g344.fasta --out-asm /scratch/scgenes/chlamy/40parent/output_flye_P40_g3.4.4_4865318/00-assembly/draft_assembly.fasta --genome-size 110000000 --config /shared/clsoft/apps/x86_64/flye/2.6.0/flye/config/bin_cfg/asm_raw_reads.cfg --log /scratch/scgenes/chlamy/40parent/output_flye_P40_g3.4.4_4865318/flye.log --threads 5 --debug --min-ovlp 5000 --kmer 17
[2020-05-28 15:06:39] DEBUG: Build date: Oct 15 2019 10:20:10
[2020-05-28 15:06:39] DEBUG: Total RAM: 503 Gb
[2020-05-28 15:06:39] DEBUG: Available RAM: 494 Gb
[2020-05-28 15:06:39] DEBUG: Total CPUs: 64
[2020-05-28 15:06:39] DEBUG: Parameters:
[2020-05-28 15:06:39] DEBUG:     big_genome_threshold=29000000
[2020-05-28 15:06:39] DEBUG:     low_cutoff_warning=1
[2020-05-28 15:06:39] DEBUG:     hard_min_coverage_rate=10
[2020-05-28 15:06:39] DEBUG:     assemble_kmer_sample=1
[2020-05-28 15:06:39] DEBUG:     repeat_graph_kmer_sample=1
[2020-05-28 15:06:39] DEBUG:     read_align_kmer_sample=1
[2020-05-28 15:06:39] DEBUG:     maximum_jump=1500
[2020-05-28 15:06:39] DEBUG:     maximum_overhang=1500
[2020-05-28 15:06:39] DEBUG:     repeat_kmer_rate=100
[2020-05-28 15:06:39] DEBUG:     assemble_ovlp_relative_divergence=0.10
[2020-05-28 15:06:39] DEBUG:     repeat_graph_ovlp_divergence=0.15
[2020-05-28 15:06:39] DEBUG:     read_align_ovlp_divergence=0.25
[2020-05-28 15:06:39] DEBUG:     max_coverage_drop_rate=5
[2020-05-28 15:06:39] DEBUG:     chimera_window=100
[2020-05-28 15:06:39] DEBUG:     min_reads_in_disjointig=4
[2020-05-28 15:06:39] DEBUG:     max_inner_reads=10
[2020-05-28 15:06:39] DEBUG:     max_inner_fraction=0.25
[2020-05-28 15:06:39] DEBUG:     add_unassembled_reads=0
[2020-05-28 15:06:39] DEBUG:     max_separation=500
[2020-05-28 15:06:39] DEBUG:     unique_edge_length=50000
[2020-05-28 15:06:39] DEBUG:     min_repeat_res_support=0.51
[2020-05-28 15:06:39] DEBUG:     out_paths_ratio=5
[2020-05-28 15:06:39] DEBUG:     graph_cov_drop_rate=5
[2020-05-28 15:06:39] DEBUG:     coverage_estimate_window=100
[2020-05-28 15:06:39] DEBUG:     extend_contigs_with_repeats=1
[2020-05-28 15:06:39] DEBUG:     min_read_cov_cutoff=3
[2020-05-28 15:06:39] DEBUG:     short_tip_length=10000
[2020-05-28 15:06:39] DEBUG:     long_tip_length=100000
[2020-05-28 15:06:39] DEBUG:     max_bubble_length=50000
[2020-05-28 15:06:39] DEBUG: Running with k-mer size: 17
[2020-05-28 15:06:39] DEBUG: Running with minimum overlap 5000
[2020-05-28 15:06:39] DEBUG: Metagenome mode: N
[2020-05-28 15:06:39] INFO: Reading sequences
[2020-05-28 15:07:58] DEBUG: Building positional index
[2020-05-28 15:07:58] DEBUG: Total sequence: 5436436201 bp
[2020-05-28 15:07:58] DEBUG: Expected read coverage: 49
[2020-05-28 15:07:58] INFO: Generating solid k-mer index
[2020-05-28 15:07:58] DEBUG: Hard threshold set to 4
[2020-05-28 15:07:58] DEBUG: Started k-mer counting
[2020-05-28 15:20:43] INFO: Counting k-mers (1/2):
[2020-05-28 15:30:34] INFO: Counting k-mers (2/2):
[2020-05-28 15:57:03] DEBUG: Estimated minimum kmer coverage: 5
[2020-05-28 15:57:03] DEBUG: Filtered 71550192 erroneous k-mers
[2020-05-28 15:57:03] DEBUG: Repetitive k-mer frequency: 3049
[2020-05-28 15:57:03] DEBUG: Filtered 5220 repetitive k-mers (4.38253e-05)
[2020-05-28 15:57:03] INFO: Filling index table
[2020-05-28 15:57:09] DEBUG: Sampling rate: 1
[2020-05-28 15:57:09] DEBUG: Solid k-mers: 119104154
[2020-05-28 15:57:09] DEBUG: K-mer index size: 3597317768
[2020-05-28 15:57:09] DEBUG: Mean k-mer frequency: 30.2031
[2020-05-28 16:24:06] DEBUG: Sorting k-mer index
[2020-05-28 16:25:44] DEBUG: Peak RAM usage: 24 Gb
[2020-05-28 16:25:44] DEBUG: Estimating k-mer identity bias
[2020-05-28 16:38:56] DEBUG: Median overlap divergence: 0.134287
[2020-05-28 16:38:56] DEBUG: K-mer estimate bias: 0.057691
[2020-05-28 16:38:56] DEBUG: Max divergence threshold set to 0.234287
[2020-05-28 16:38:56] INFO: Extending reads
[2020-05-28 16:38:56] DEBUG: Estimating overlap coverage
[2020-05-28 17:51:59] INFO: Overlap-based coverage: 698
[2020-05-28 17:51:59] INFO: Median overlap divergence: 0.127709
[2020-05-28 17:51:59] DEBUG: Sequence divergence distribution:

```



Q25 = 0.12, Q50 = 0.13, Q75 = 0.15

```
[2020-05-29 21:47:36] INFO: Assembled 0 disjointigs
[2020-05-29 21:47:46] INFO: Generating sequence
[2020-05-29 21:47:46] DEBUG: Writing FASTA
[2020-05-29 21:47:46] DEBUG: Peak RAM usage: 24 Gb
-----End assembly log-----
[2020-05-29 21:47:48] root: ERROR: No disjointigs were assembled - please check if the read type and genome size parameters are correct
```