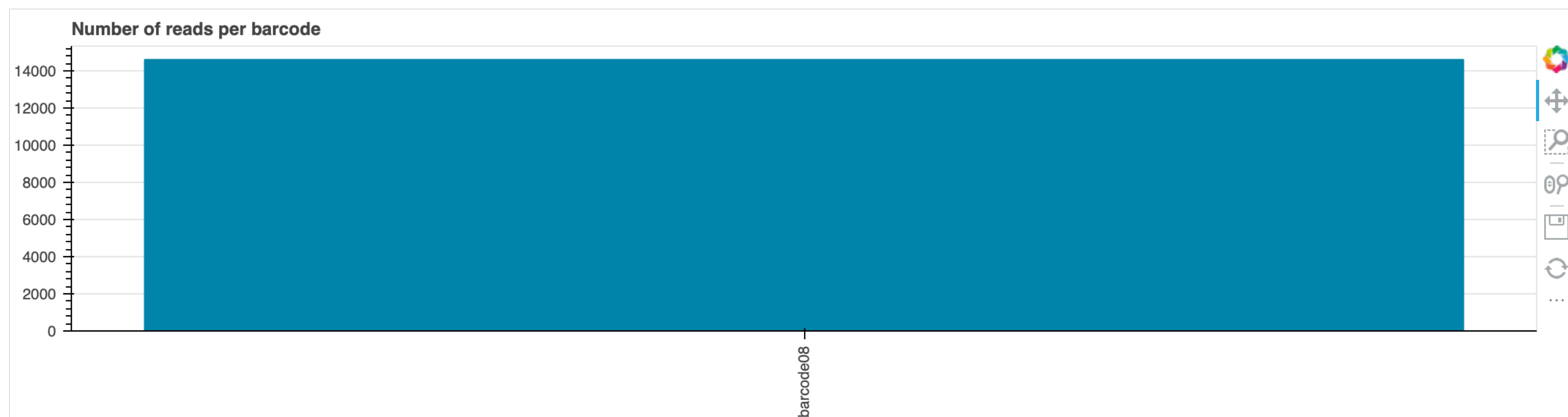


Clone Validation Report

Results generated through the wf-clone-validation Nextflow workflow provided by Oxford Nanopore Technologies.

Summary



Sample status

10 entries per page

Search...

Sample	pass/failed reason	Length
barcode08	Completed successfully	12259

Showing 1 to 1 of 1 entries

Assemblies

For each assembly, read length statistics are displayed as well as a pLannotate plot, and quality plots. A feature table provides descriptions of the annotated sequence.

Unfilled features on the plannote plots are incomplete features; the sequence match in the plasmid covers less than 95% of the full length of the feature in the database. These elements may be leftover fragments from earlier cloning steps used to create a plasmid. If they include only a small fraction of the feature, they likely do not still have the annotated function. However, even small feature fragments may affect plasmid function if they result in cryptic gene expression or are inadvertently combined with other elements during later cloning steps.

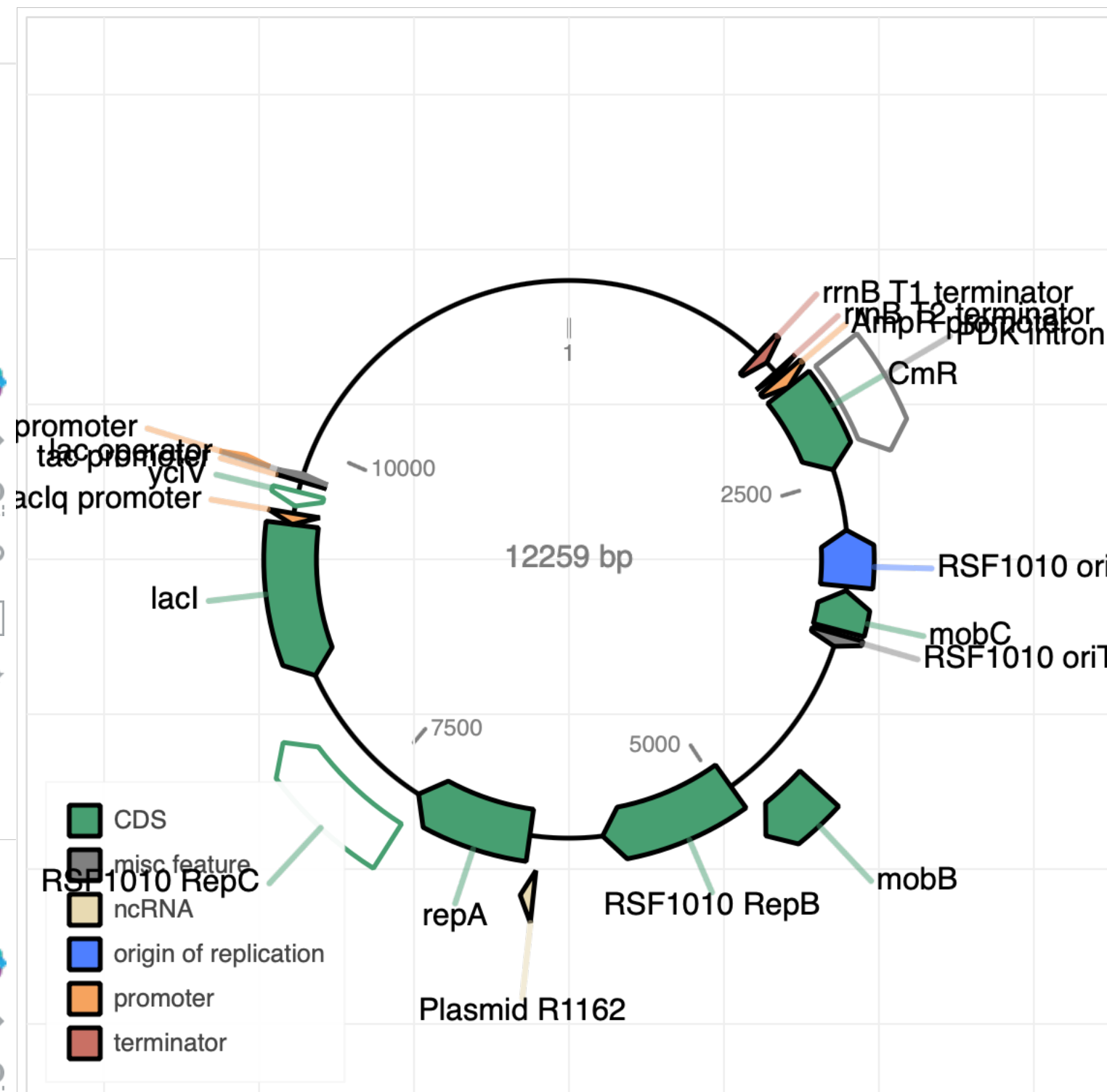
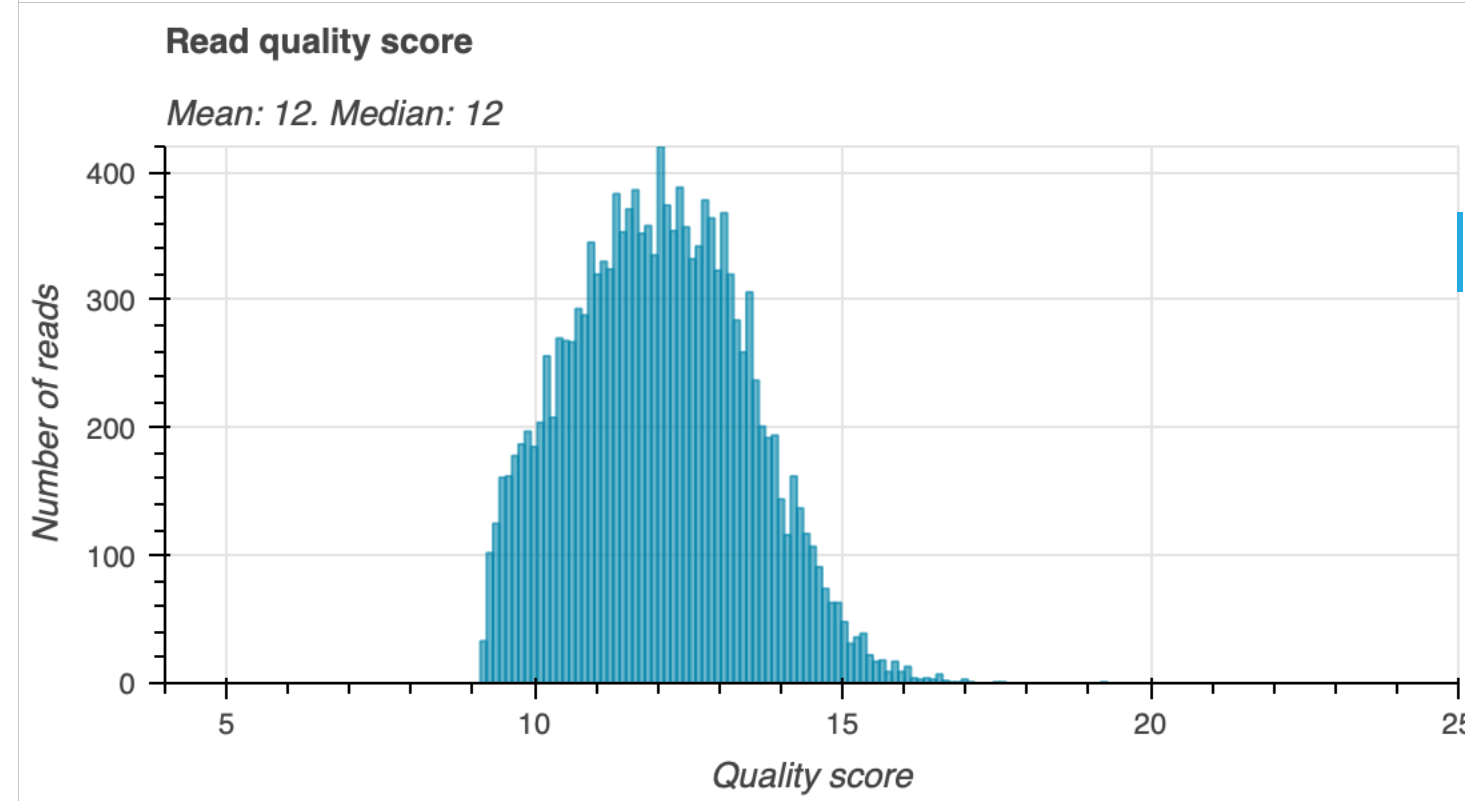
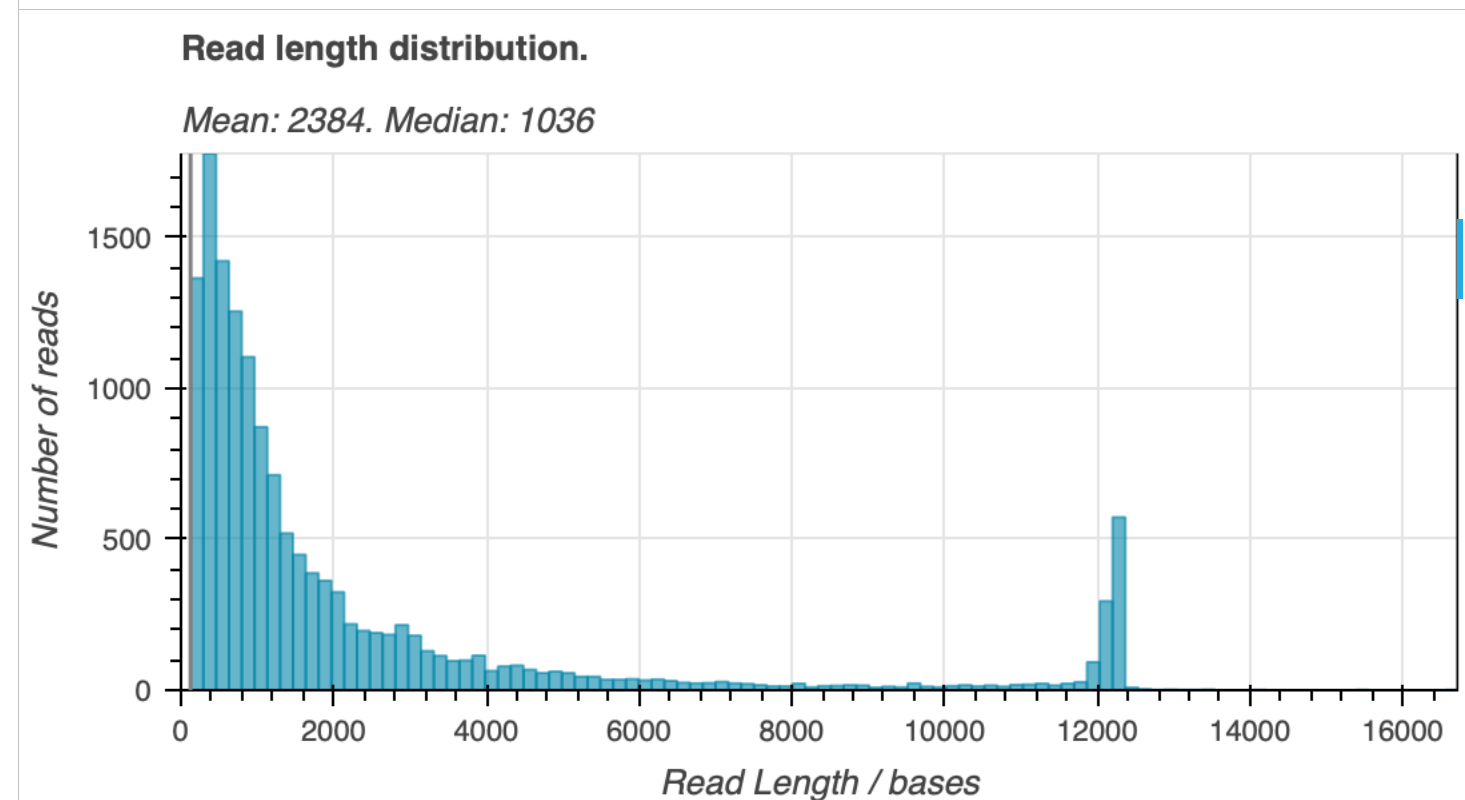
The Plasmid annotation plot and feature table are produced using Plannote.

Sample: barcode08

Completed successfully

raw downsampled

14599
No. reads



10 entries per page

Search...

Feature	Database	Identity	Match Length	Description	Start Location	End Location	Length	Strand
RSF1010 RepB	snappgene	100.0%	100.0%	replication protein B of the broad-host-range plasmid RSF1010 (Scholz et al., 1989); repB	4922	5894	972	1
CmR	snappgene	100.0%	100.0%	chloramphenicol acetyltransferase; cat; confers resistance to chloramphenicol	1767	2427	660	1
RSF1010 oriV	snappgene	100.0%	100.0%	replication origin of the broad-host-range plasmid RSF1010; requires the RSF1010 RepA/B/C proteins for replication (Scholz et al., 1989)	2860	3255	395	-1
repA	swissprot	100.0%	100.0%	REPJ_ECOLX - Experimental evidence at protein level: Swiss-Prot protein existence level 1. This protein is involved in regulating the plasmid copy-number. Increasing the level of this protein results in a higher plasmid copy-number. From Escherichia coli.	6404	7241	837	1
lacI	snappgene	99.9%	100.0%	lac repressor; lacI; The lac repressor binds to the lac operator to inhibit transcription in E. coli. This inhibition can be relieved by adding lactose or isopropyl-β-D-thiogalactopyranoside (IPTG).	8356	9439	1083	-1
AmpR promoter	snappgene	100.0%	100.0%	bla	1675	1767	92	1
RSF1010 oriT	snappgene	100.0%	100.0%	origin of transfer of the broad-host-range plasmid RSF1010 (Scholz et al., 1989)	3596	3684	88	1
rrnB T1 terminator	snappgene	100.0%	100.0%	Escherichia coli rrnB; transcription terminator T1 from the E. coli rrnB gene	1451	1538	87	1
RSF1010 RepC	snappgene	99.6%	99.9%	replication protein C of the broad-host-range plasmid RSF1010 (Scholz et al., 1989); repC	7230	8082	853	1
lacIq promoter	snappgene	100.0%	100.0%	lacI (mutant); In the lacIq allele, a single base change in the promoter boosts expression of the lacI gene about 10-fold.	9439	9517	78	-1

Showing 1 to 10 of 19 entries

1 2 >

Software versions

The table below highlights versions of key software used within the analysis.

10 entries per page

Search...

Name	Version
medaka	1.7.1
minimap2	2.24-r1122
sambtools	1.15.1
seqkit	v2.3.0
Tricycler	v0.5.3
porechop	0.2.4
bedtools	v2.30.0
canu	2.2
fastcat	0.3.6
last	from util-linux 2.34

Showing 1 to 10 of 12 entries

1 2 >

Workflow parameters

The table below highlights values of the main parameters used in this analysis.

10 entries per page

Search...

Key	Value
help	False
out_dir	/global/home/groups/fc_fpsdnaseq/20230110/clone-validation/plate1/barcode08
wfversion	v0.2.5
fastq	/global/home/groups/fc_fpsdnaseq/20230110/plate1_tmp/barcode08
db_directory	wf-clone-validation-db
sanitize_fastq	False
threads	4
host_reference	NO_HOST_REF
regions_bedfile	NO_REG_BED
approx_size	7000

Showing 1 to 10 of 31 entries

1 2 3 4 >

About

This report was produced using the [epi2me-labs/wf-clone-validation](#). The workflow can be run using `nextflow epi2me-labs/wf-clone-validation --help`

Version details Revision: master Git Commit: 944a6f9bf676e63080c3971104718224d9d4f3b1

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