





Kbase Log


 **KBbase**
PREDICTIVE BIOLOGY


Narrative Navigator


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[SRP064501](#)
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[SRP387165](#)
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[SRP108595](#)
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[SRP358279](#)
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Shared with: [Kevin Thomas Paul](#).


Data


Preview


 SRR5855488_assembly
Assembly


 SRR5855487_assembly
Assembly

 SRR5855484_MEGAHIT.assembly
Assembly

 SRR5855497_MEGAHIT.assembly
Assembly

 SRR5855498_MEGAHIT.assembly
Assembly

 SRR5255491_MEGAHIT.assembly
Assembly

 SRR5255486_MEGAHIT.assembly
Assembly

<https://narrative.kbase.us/narratives/169651/1/31>

Workflow

Welcome to the Narrative

DATA Import Paired-End Reads from Web - v1.0.12
Import a Paired-End Library into your Narrative as a Reads object.

Reset Finished with **success** at Feb 1, 2024 at 4:50pm

View Configure Info Job Status Result

Finished with **success** at Feb 1, 2024 at 4:50pm
Ran for 2h 28m
Queued for 14s

> Logs

Assess Read Quality with FastQC - v0.12.1
A quality control application for high throughput sequence data.

Reset Finished with success at Feb 1, 2024 at 10:14pm

View Configure Info Job Status Result

Objects
No objects created

Report
View report in separate window
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FastQC Report

Summary

- Basic Statistics
- Per base sequence quality
- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
- Per base N content
- Sequence Length Distribution
- Sequence Duplication Levels

Basic Statistics

Measure	Value
Filename	SRR5855486_169368_1_rev.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1616951
Total Bases	2.3 Gbp
Sequences flagged as poor quality	0
Sequence length	146
N/C	47

Produced by **fastqc** (version 0.12.1)

Links

MEGA-HIT Assemble Reads with MEGA-HIT v12.9
Assemble metagenomic reads using the MEGA-HIT assembler.

Reset Finished with success at Feb 2, 2024 at 3:58pm

View Configure Info Job Status Result

Objects
Created Object Name Type Description
SRR5855486_1_MEGA-HIT assembly Assembly Assembled contigs

Showing 1 to 1 of 1 entries

Report
View report in separate window

Statistics without reference SRR5855486_1 assembly

# contigs	49467
# contigs (>= 0 bp)	49467
# contigs (>= 1000 bp)	49467
# contigs (>= 10000 bp)	533
# contigs (>= 100000 bp)	0
# contigs (>= 1000000 bp)	0
Largest contig	87419
Total length	90386932
Total length (>= 0 bp)	90386932
Total length (>= 1000 bp)	90386932
Total length (>= 10000 bp)	10945832
Total length (>= 100000 bp)	0
Total length (>= 1000000 bp)	0
N50	1499
N75	1234
L50	12376
L75	28968
GC (%)	46.85
Mismatches	
# N's	0
# N's per 100 kbp	0

Plot: Cumulative length No GC content

100 Mbp

90 80 70 60 50 40 30 20

100 Mbp

SRR5855486_1 assembly

> Summary

Links

Trimomatic Trim Reads with Trimmomatic - v0.36
Trim paired- or single-end Illumina reads with Trimmomatic.

Reset Finished with success at Feb 2, 2024 at 2:15pm

View Configure Info Job Status Result

Objects
Created Object Name Type Description
SRR5855486_trimmed_paired PairedEndLibrary Trimmed Reads
SRR5855486_trimmed_unpaired_fwd SingleEndLibrary Trimmed Unpaired Forward Reads
SRR5855486_trimmed_unpaired_rev SingleEndLibrary Trimmed Unpaired Reverse Reads

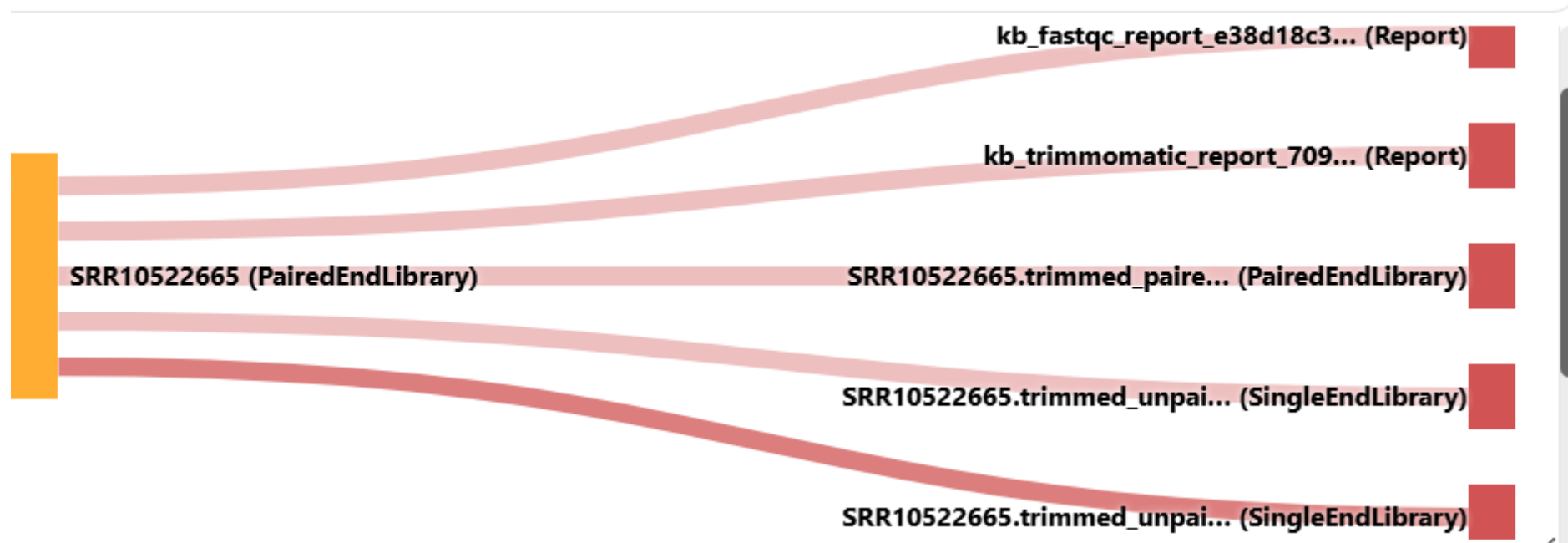
Showing 1 to 3 of 3 entries

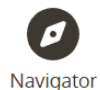
Report
View report in separate window

TRIMMOMATIC RESULTS FOR SRR5855486 (object 169368/3/1)

Input Read Pairs	1516951	(100.0%)
Both Surviving	1516731	(100.0%)
Forward Only Surviving	200	(0.0%)
Reverse Only Surviving	20	(0.0%)
Dropped	0	(0.0%)

General Flow of each Dataset





SRR10522665.assembly

KBaseGenomeAnnotations.Assembly-5.1

Saved Feb 12, 2024 by kentaccis



Copy

Data View

Object Overview

Provenance

Related Data

Linked Samples



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search

#	Id	Contig Length (bp)	GC (%)
1	k141_100001	5,245	38.70
2	k141_100006	1,766	33.35
3	k141_100020	1,912	41.42
4	k141_100021	1,301	29.13
5	k141_100028	1,130	31.77
6	k141_10004	1,268	30.68
7	k141_100051	1,378	36.58