

# PolkaPox

Advanced Molecular Detection  
Southeast Region Bioinformatics

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# Overview

## Purpose:

- This Nextflow pipeline processes the raw Illumina orthopoxvirus sequencing reads to generate standardized outputs that consist of consensus genomes, variant calls, assemblies, and quality metrics for downstream genomic analysis.

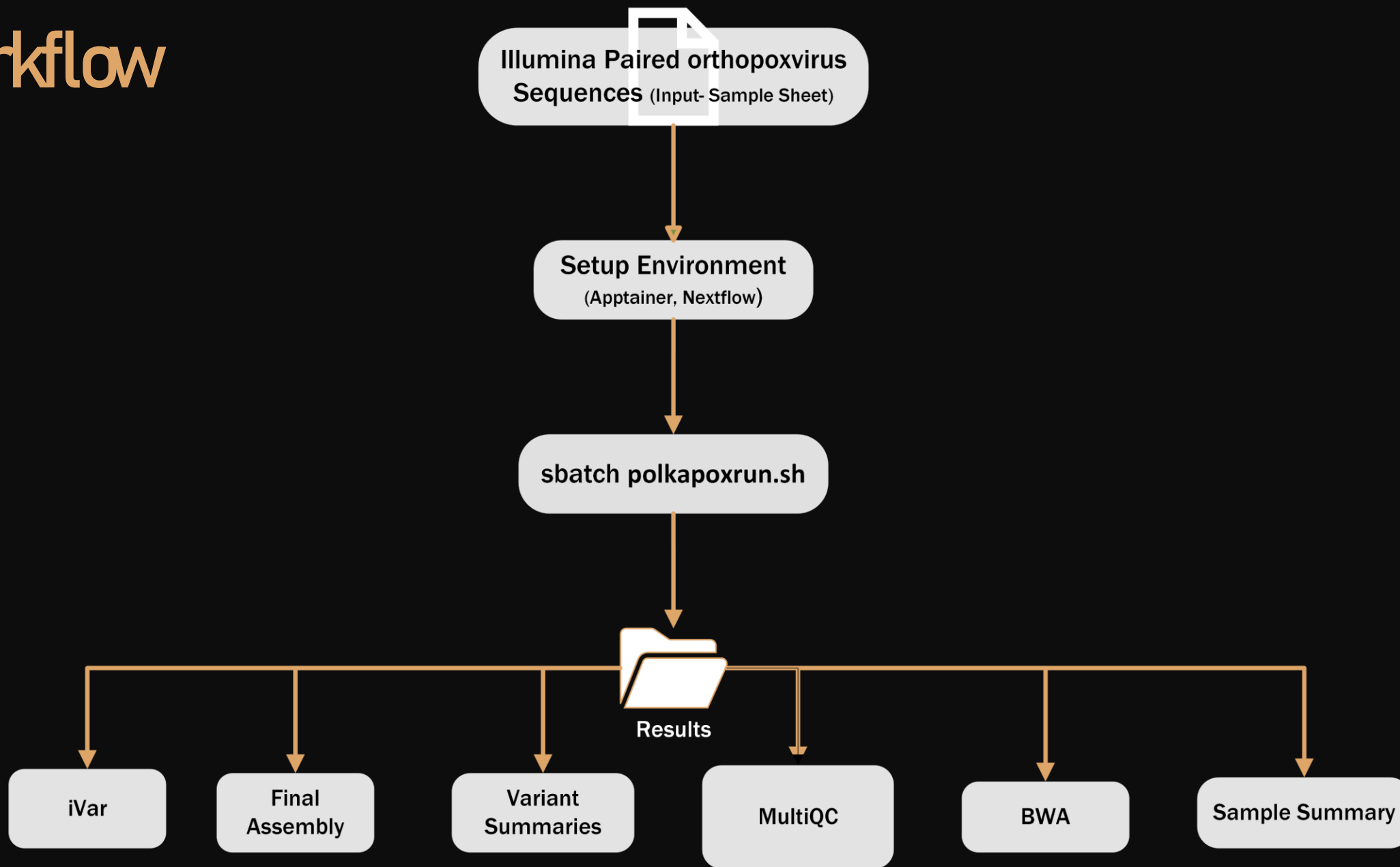
## Usage:

- It enables public health laboratories to integrate these outputs into workflows for outbreak investigation, phylogenetic analysis, and genomic surveillance across multiple samples.

## Dependencies:

- Nextflow and Apptainer/Singularity.

# Workflow

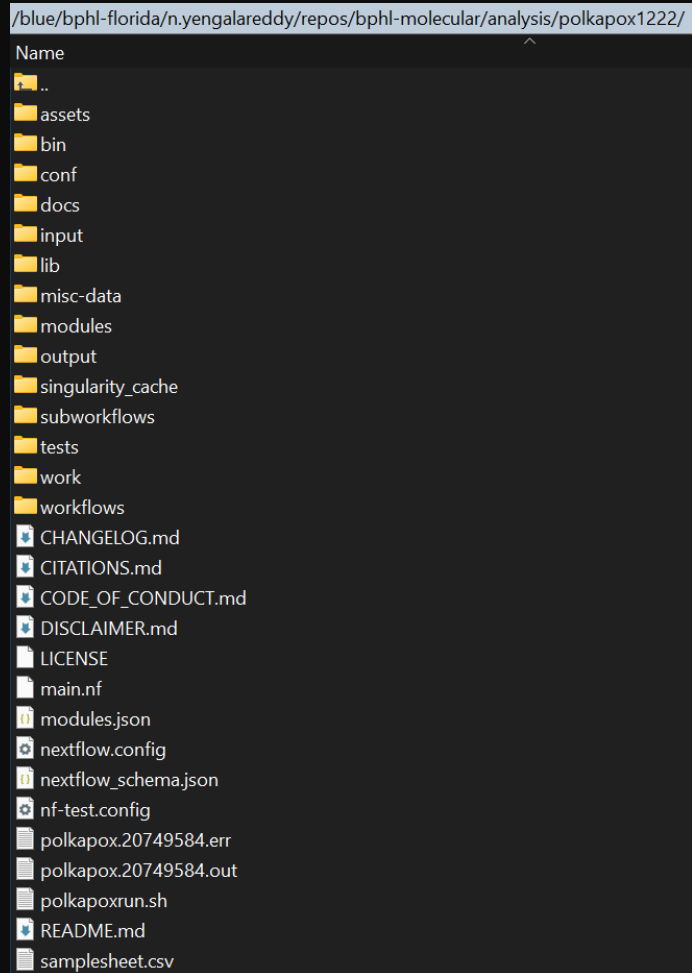


# Application

## Objective

Use raw Illumina orthopoxvirus sequencing reads with PolkaPox to generate consensus genomes, SNV calls, and assembly outputs to support genomic surveillance and outbreak analysis.

# Application Cont.



```
cd /blue/bphl-<state>/<user>/repos/bphl-molecular/
```

```
git clone https://github.com/CDCgov/polkapox
```

```
mkdir analysis/
```

```
cd analysis/
```

```
cp /blue/bphl-<state>/<user>/repos/bphl-molecular/polkapox/
```



# Application Cont.

```
sample,fastq_1,fastq_2
SRR23873768,input/SRR23873768_R1.fastq.gz,input/SRR23873768_R2.fastq.gz
SRR23873769,input/SRR23873769_R1.fastq.gz,input/SRR23873769_R2.fastq.gz
SRR23873770,input/SRR23873770_R1.fastq.gz,input/SRR23873770_R2.fastq.gz
SRR23873771,input/SRR23873771_R1.fastq.gz,input/SRR23873771_R2.fastq.gz
SRR23873772,input/SRR23873772_R1.fastq.gz,input/SRR23873772_R2.fastq.gz
SRR23873773,input/SRR23873773_R1.fastq.gz,input/SRR23873773_R2.fastq.gz
SRR23873774,input/SRR23873774_R1.fastq.gz,input/SRR23873774_R2.fastq.gz
SRR23873775,input/SRR23873775_R1.fastq.gz,input/SRR23873775_R2.fastq.gz
SRR23873776,input/SRR23873776_R1.fastq.gz,input/SRR23873776_R2.fastq.gz
SRR23873777,input/SRR23873777_R1.fastq.gz,input/SRR23873777_R2.fastq.gz
SRR23873778,input/SRR23873778_R1.fastq.gz,input/SRR23873778_R2.fastq.gz
SRR23873779,input/SRR23873779_R1.fastq.gz,input/SRR23873779_R2.fastq.gz
SRR23873780,input/SRR23873780_R1.fastq.gz,input/SRR23873780_R2.fastq.gz
```

```
GNU nano 5.6.1 polkapoxrun.sh
#!/bin/bash
#SBATCH --account=bphl-umbrella
#SBATCH --qos=bphl-umbrella
#SBATCH --job-name=polkapox_run
#SBATCH --mail-type=END,FAIL
#SBATCH --mail-user=nikhil.yengala@flhealth.gov
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=16
#SBATCH --mem=128G
#SBATCH --time=48:00:00
#SBATCH --output=polkapox.%j.out
#SBATCH --error=polkapox.%j.err

# Load Nextflow

module load nextflow

# Pathways

BASE=/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222
INPUT=$BASE/samplesheet.csv
OUTDIR=$BASE/output

mkdir -p "$OUTDIR"

# Singularity/Apptainer cache

export NXF_SINGULARITY_CACHEDIR=$BASE/singularity_cache
mkdir -p "$NXF_SINGULARITY_CACHEDIR"

# Run PolkaPox

nextflow run /blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/main.nf \
  --input "$INPUT" \
  --outdir "$OUTDIR" \
  --workflow full \
  --profile singularity \
  --threads $SLURM_CPUS_PER_TASK
```

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/

Name

- ..
- assets
- bin
- conf
- docs
- input
- lib
- misc-data
- modules
- output
- singularity\_cache
- subworkflows
- tests
- work
- workflows
- CHANGELOG.md
- CITATIONS.md
- CODE\_OF\_CONDUCT.md
- DISCLAIMER.md
- LICENSE
- main.nf
- modules.json
- nextflow.config
- nextflow\_schema.json
- nf-test.config
- polkapox.20749584.err
- polkapox.20749584.out
- polkapoxrun.sh
- README.md
- samplesheet.csv

# Application Cont.

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name  
..  
bandage  
bwa  
fastp  
final\_assembly  
graph\_recon  
graph\_recon\_mapping  
ivar  
kraken2  
multiqc  
mummer  
pipeline\_info  
quast  
samtools  
seqtk  
unicycler  
variant\_summaries  
sample\_summary.tsv

sample	reference	total_raw	opt_read	opt_perce	human_pe	unclass	kraken_db	kraken	tax_filtered	re_percent	ri_percent	ajc	q30_rate	d_percent	map_percent	ri_average	d_count	20x_n	config	assembly_n50	unicymapped	ri_percent	ri_orientation	sequence	itr_length	gfa_status	gfa_notes	total_snps	F13L_SNP	E9L_SNP	corrected	corrected	corrected	final_asse	optx_read	optx_re
SRR23873 MPKV-UK	548926	1062936	97.17	1.99	0.83	s3://io-pe-10242,10;	984906	92.89901	2.171344	0.956691	1.36189	1063280	100	670	195048	8	189521	158372	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1990	0	14	NA	NA				/blue/bphl/flbue/bphl/flbue/b		
SRR23873 MPKV-UK	525568	1030964	96.12	0.71	1.17	s3://io-pe-10242,10;	961869	93.29443	1.999138	0.343111	0.956892	1.75016	1020318	99.99	649	193546	6	189528	136113	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1530	0	20	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	721192	1425540	96.83	0.02	1.15	s3://io-pe-10242,10;	1259170	88.32933	3.15283	0.34151	0.939077	1.59296	1341578	100	853	193743	10	188645	28720	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1607	0	14	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	681736	1341134	96.36	0.85	0.99	s3://io-pe-10242,10;	1249194	93.14461	1.995028	0.34139	0.958823	1.72317	1345460	100	843	195029	14	189470	116351	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1548	0	11	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	510937	1009132	96.66	0.13	1.22	s3://io-pe-10242,10;	989142	98.11632	0.870521	0.339158	0.98514	2.28839	1067515	99.99	671	193388	0	NA	NA	Unknown	Unknown	Unknown	FAIL	Issue with	1962	0	14	NA	NA				/blue/bphl/flbue/bphl/flbue/b			
SRR23873 MPKV-UK	473019	917240	96.96	2.14	0.9	s3://io-pe-10242,10;	899978	98.11805	1.015438	0.339912	0.983912	1.68854	180761	99.99	608	195227	4	190380	184275	999978	91.75	2 + 4 - 3 +	196517	6121	PASS	Graph suc	1974	0	17		1	0			/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	495481	981036	99	0.14	0.86	s3://io-pe-10242,10;	962910	98.15236	0.962452	0.339996	0.984359	1.80055	1045676	100	652	195079	6	189892	148207	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1861	0	14	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	554142	1096430	96.93	0.02	1.05	s3://io-pe-10242,10;	1075936	98.13084	0.971517	0.340481	0.984562	2.39669	1159957	100	733	194422	9	189207	72377	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	2026	0	17	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	559978	1103420	98.52	0.04	1.44	s3://io-pe-10242,10;	1083402	98.18582	0.870385	0.340782	0.985178	2.35849	1188600	99.99	736	193948	8	189118	129737	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1778	0	14	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	969641	1704166	87.88	0.09	12.03	s3://io-pe-10242,10;	1327432	77.89335	4.081879	0.335789	0.950439	2.77098	1404007	99.99	700	193485	0	NA	NA	Unknown	Unknown	Unknown	FAIL	Issue with	2206	0	17	NA	NA				/blue/bphl/flbue/bphl/flbue/b			
SRR23873 MPKV-UK	582721	1151542	98.81	0.04	1.15	s3://io-pe-10242,10;	1126674	97.84046	0.980456	0.344198	0.981795	2.78375	1223793	99.99	766	193933	7	188587	109124	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	2248	0	12	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	601944	1185568	96.48	0.34	1.19	s3://io-pe-10242,10;	1163430	98.13271	0.951105	0.3444	0.985524	3.06797	1255696	99.99	789	195166	9	189650	110722	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1872	0	20	NA	NA				/blue/bphl/flbue/bphl/flbue/b	
SRR23873 MPKV-UK	513383	1016214	98.97	0.03	1	s3://io-pe-10242,10;	977734	96.2134	1.302088	0.344754	0.977058	2.28715	1043356	100	649	194682	8	189759	177658	NA	NA	Unknown	Unknown	Unknown	FAIL	WARNING:	1910	0	13	NA	NA				/blue/bphl/flbue/bphl/flbue/b	

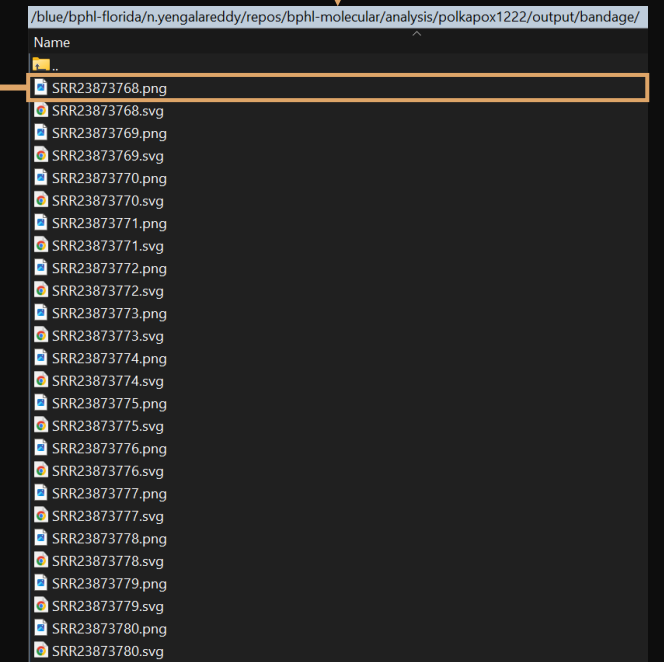
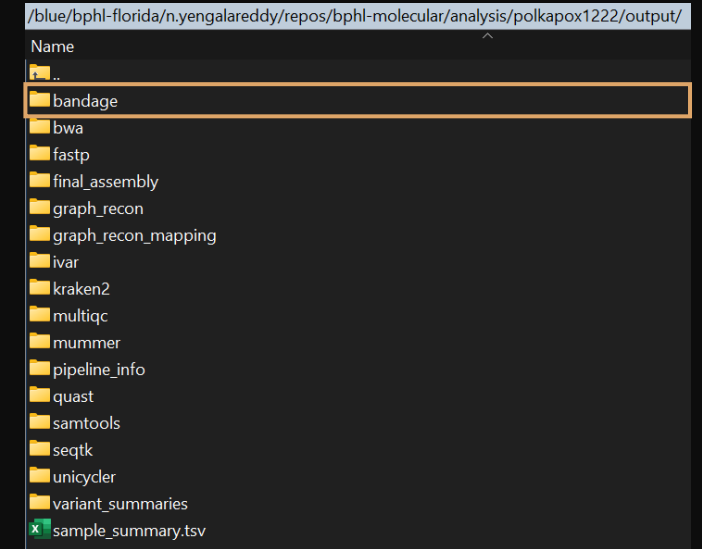
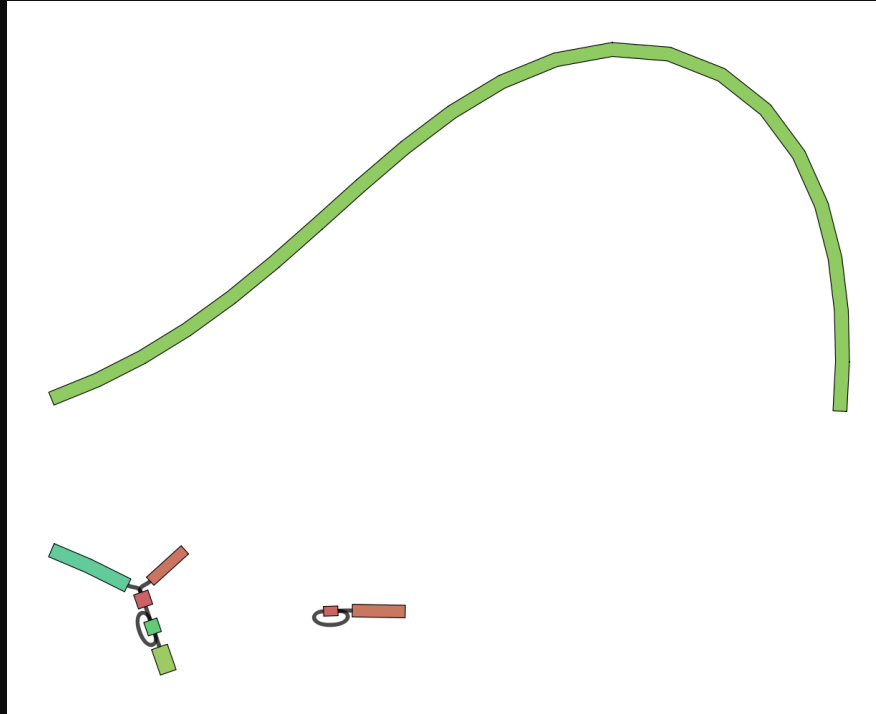
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/

Name  
..  
assets  
bin  
conf  
docs  
input  
lib  
misc-data  
modules  
output  
singularity\_cache  
subworkflows  
tests  
work  
workflows  
CHANGELOG.md  
CITATIONS.md  
CODE\_OF\_CONDUCT.md  
DISCLAIMER.md  
LICENSE  
main.nf  
modules.json  
nextflow.config  
nextflow\_schema.json  
nf-test.config  
polkapox.20749584.err  
polkapox.20749584.out  
polkapoxrun.sh  
README.md  
samplesheet.csv

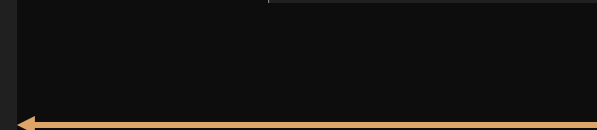
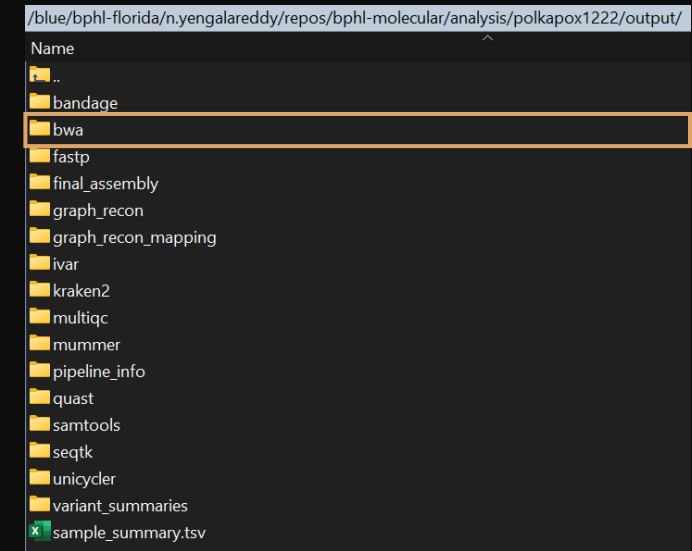
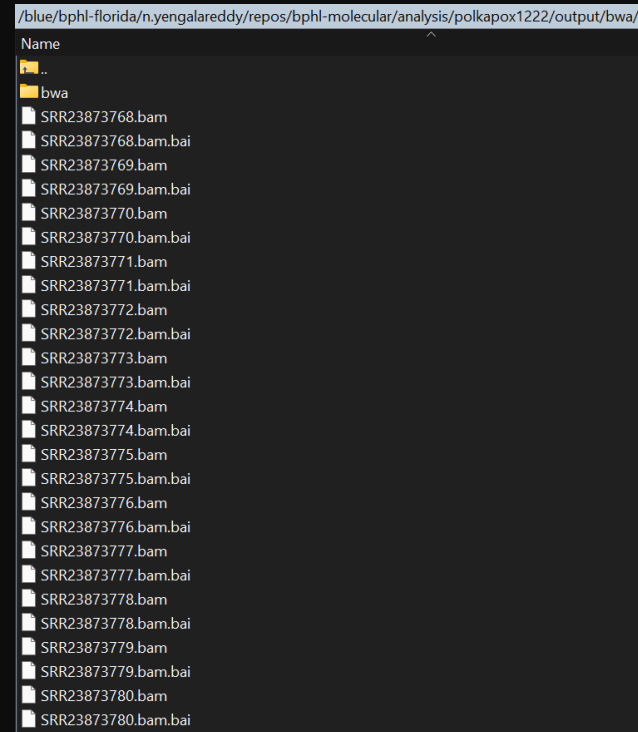
sbatch polkapoxrun.sh



# Application Cont.



# Application Cont.



# Application Cont.

## fastp report

Summary	
General	
fastp version:	0.23.2 ( <a href="https://github.com/OpenGene/fastp">https://github.com/OpenGene/fastp</a> )
sequencing:	paired end (150 cycles + 150 cycles)
mean length before filtering:	133bp, 134bp
mean length after filtering:	134bp, 133bp
duplication rate:	1.361888%
Insert size peak:	147
Before filtering	
total reads:	1.062936 M
total bases:	142.285948 M
Q20 bases:	134.469849 M (94.506767%)
Q30 bases:	133.099677 M (93.543796%)
GC content:	34.212179%
After filtering	
total reads:	984.906000 K
total bases:	132.044826 M
Q20 bases:	127.392773 M (96.476914%)
Q30 bases:	126.326067 M (95.669078%)
GC content:	34.127395%
Filtering result	
reads passed filters:	984.906000 K (92.659012%)
reads corrected:	32.991000 K (3.103762%)
bases corrected:	44.029000 K (0.030944%)
reads with low quality:	67.566000 K (6.356545%)
reads with too many N:	0 (0.000000%)
reads too short:	10.464000 K (0.984443%)

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name

..

bandage

bwa

fastp

final\_assembly

graph\_recon

graph\_recon\_mapping

ivar

kraken2

multiqc

mummer

pipeline\_info

quast

samtools

seqtk

unicycler

variant\_summaries

sample\_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/fastp/

Name

..

SRR23873768.fastp.html

SRR23873768.fastp.json

SRR23873768.fastp.log

SRR23873768\_1.fastp.fastq.gz

SRR23873768\_2.fastp.fastq.gz

SRR23873769.fastp.html

SRR23873769.fastp.json

SRR23873769.fastp.log

SRR23873769\_1.fastp.fastq.gz

SRR23873769\_2.fastp.fastq.gz

SRR23873770.fastp.html

SRR23873770.fastp.json

SRR23873770.fastp.log

SRR23873770\_1.fastp.fastq.gz

SRR23873770\_2.fastp.fastq.gz

SRR23873771.fastp.html

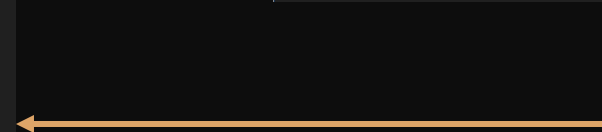
SRR23873771.fastp.json

SRR23873771.fastp.log

# Application Cont.

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/final_assembly/
Name
..
SRR23873768.draft.fa
SRR23873769.draft.fa
SRR23873770.draft.fa
SRR23873771.draft.fa
SRR23873773.final.fa
SRR23873774.draft.fa
SRR23873775.draft.fa
SRR23873776.draft.fa
SRR23873778.draft.fa
SRR23873779.draft.fa
SRR23873780.draft.fa
```

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/
Name
..
bandage
bwa
fastp
final_assembly
graph_recon
graph_recon_mapping
ivar
kraken2
multiqc
mummer
pipeline_info
quast
samtools
seqtk
unicycler
variant_summaries
sample_summary.tsv
```



# Application Cont.

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/graph\_recon/

Name

..

SRR23873768.assembly.log

SRR23873768.assembly.summary

SRR23873768.contigs.fasta

SRR23873769.assembly.log

SRR23873769.assembly.summary

SRR23873769.contigs.fasta

SRR23873770.assembly.log

SRR23873770.assembly.summary

SRR23873770.contigs.fasta

SRR23873771.assembly.log

SRR23873771.assembly.summary

SRR23873771.contigs.fasta

SRR23873772.assembly.log

SRR23873772.assembly.summary

SRR23873773.assembly.log

SRR23873773.assembly.summary

SRR23873773.assembly\_asm.fasta

SRR23873773.contigs.fasta

SRR23873774.assembly.log

SRR23873774.assembly.summary

SRR23873774.contigs.fasta

SRR23873775.assembly.log

SRR23873775.assembly.summary

SRR23873775.contigs.fasta

SRR23873776.assembly.log

SRR23873776.assembly.summary

SRR23873776.contigs.fasta

SRR23873777.assembly.log

SRR23873777.assembly.summary

SRR23873778.assembly.log

SRR23873778.assembly.summary

SRR23873778.contigs.fasta

SRR23873779.assembly.log

SRR23873779.assembly.summary

SRR23873779.contigs.fasta

SRR23873780.assembly.log

SRR23873780.assembly.summary

SRR23873780.contigs.fasta

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name

..

bandage

bwa

fastp

final\_assembly

graph\_recon

graph\_recon\_mapping

ivar

kraken2

multiqc

mummer

pipeline\_info

quast

samtools

seqtk

unicycler

variant\_summaries

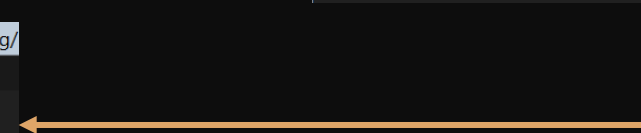
sample\_summary.tsv



# Application Cont.

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/graph_recon_mapping/  
Name  
..  
SRR23873773.bam  
SRR23873773.bam.bai  
SRR23873773.denovo.flagstat
```

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/  
Name  
..  
bandage  
bwa  
fastp  
final_assembly  
graph_recon  
graph_recon_mapping  
ivar  
kraken2  
multiqc  
mummer  
pipeline_info  
quast  
samtools  
seqtk  
unicycler  
variant_summaries  
x sample_summary.tsv
```



# Application Cont.

REGION	POS	REF	ALT	REF_DP	REF_RV	REF_QUAL	ALT_DP	ALT_RV	ALT_QUAL	ALT_FREQ	TOTAL_DP	PVAL	PASS	GFF_FEAT	REF_COD	REF_AA	ALT_COD	ALT_AA
MT903344	784	G	T	40	2	52	1	0	75	0.02439	41	0.401961	FALSE	NA	NA	NA	NA	NA
MT903344	787	G	T	44	3	51	1	0	77	0.022222	45	0.412844	FALSE	NA	NA	NA	NA	NA
MT903344	790	T	G	81	3	53	1	0	29	0.012195	82	0.645905	FALSE	NA	NA	NA	NA	NA
MT903344	801	A	T	90	2	59	1	0	33	0.010989	91	0.372951	FALSE	NA	NA	NA	NA	NA
MT903344	858	T	A	134	5	66	2	0	36	0.014706	136	0.132319	FALSE	cds-QNP1	TTT	F	TTA	L
MT903344	964	A	T	139	25	59	2	1	38	0.014184	141	0.148577	FALSE	cds-QNP1	ACA	T	TCA	S
MT903344	1233	T	G	99	23	58	1	0	37	0.01	100	0.383142	FALSE	cds-QNP1	AGT	S	AGG	R
MT903344	1271	G	A	0	0	0	92	23	58	1	92	3.36E-68	TRUE	cds-QNP1	TGA	*	TAA	*
MT903344	1292	A	G	88	21	59	1	0	32	0.011236	89	0.380342	FALSE	cds-QNP1	GAA	E	GGA	G
MT903344	1316	G	A	89	18	56	1	0	76	0.011111	90	0.386266	FALSE	cds-QNP1	CGC	R	CAC	H
MT903344	1323	C	A	85	20	56	1	0	77	0.011628	86	0.387387	FALSE	cds-QNP1	GAC	D	GAA	E
MT903344	1326	T	C	80	19	58	1	0	34	0.012195	82	0.383886	FALSE	cds-QNP1	GAT	D	GAC	D
MT903344	1326	T	A	80	19	58	1	0	78	0.012195	82	0.383886	FALSE	cds-QNP1	GAT	D	GAA	E
MT903344	1327	A	G	81	20	56	1	0	78	0.012195	82	0.388626	FALSE	cds-QNP1	AGT	S	GGT	G
MT903344	1328	G	T	83	20	57	1	0	75	0.011905	84	0.394366	FALSE	cds-QNP1	AGT	S	ATT	I
MT903344	1355	A	G	87	18	56	1	1	39	0.011364	88	0.4	FALSE	cds-QNP1	TAC	Y	TGC	C
MT903344	1390	T	C	96	14	60	2	1	57	0.020408	98	0.144486	FALSE	cds-QNP1	TGT	C	CGT	R
MT903344	1405	G	A	95	13	61	1	0	73	0.010417	96	0.373541	FALSE	cds-QNP1	GGA	G	AGA	R
MT903344	1605	T	G	94	24	59	1	1	31	0.010526	95	0.384615	FALSE	NA	NA	NA	NA	NA
MT903344	1606	G	A	96	25	60	1	1	20	0.010309	97	0.62451	FALSE	NA	NA	NA	NA	NA
MT903344	1615	G	T	93	26	59	1	1	33	0.010638	94	0.390041	FALSE	NA	NA	NA	NA	NA
MT903344	1622	C	A	94	22	59	1	1	37	0.010526	95	0.381526	FALSE	NA	NA	NA	NA	NA
MT903344	1626	C	T	93	22	60	3	1	51	0.030928	97	0.056205	FALSE	NA	NA	NA	NA	NA
MT903344	1626	C	A	93	22	60	1	1	34	0.010309	97	0.380567	FALSE	NA	NA	NA	NA	NA
MT903344	1642	T	G	96	22	57	3	2	51	0.030303	99	0.06096	FALSE	NA	NA	NA	NA	NA
MT903344	1648	T	A	94	16	59	3	2	38	0.030928	97	0.059425	FALSE	NA	NA	NA	NA	NA
MT903344	1649	A	C	90	17	60	1	0	39	0.010989	91	0.387234	FALSE	NA	NA	NA	NA	NA
MT903344	1653	T	A	88	14	60	3	2	50	0.032967	91	0.055456	FALSE	NA	NA	NA	NA	NA
MT903344	1672	T	A	88	13	59	1	1	37	0.011236	89	0.385281	FALSE	NA	NA	NA	NA	NA
MT903344	1702	A	G	84	17	59	1	0	34	0.011765	85	0.381166	FALSE	NA	NA	NA	NA	NA

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name

..

bandage

bwa

fastp

final\_assembly

graph\_recon

graph\_recon\_mapping

ivar

kraken2

multiqc

mummer

pipeline\_info

quast

samtools

seqtk

unicycler

variant\_summaries

sample\_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/ivar/

Name

..

SRR23873768.bwa.fa

SRR23873768.bwa.mpileup

SRR23873768.ivar.tsv

SRR23873768.ivar.vcf

SRR23873769.bwa.fa

SRR23873769.bwa.mpileup

SRR23873769.ivar.tsv

SRR23873769.ivar.vcf

SRR23873770.bwa.fa

SRR23873770.bwa.mpileup

SRR23873770.ivar.tsv

SRR23873770.ivar.vcf

SRR23873771.bwa.fa

SRR23873771.bwa.mpileup

SRR23873771.ivar.tsv

SRR23873771.ivar.vcf

SRR23873772.bwa.fa

SRR23873772.bwa.mpileup

SRR23873772.ivar.tsv

SRR23873772.ivar.vcf

SRR23873773.bwa.fa

SRR23873773.bwa.mpileup

SRR23873773.ivar.tsv

SRR23873773.ivar.vcf

SRR23873774.bwa.fa

SRR23873774.bwa.mpileup

# Application Cont.

0.83	4564	4564	U	0	unclassified
99.17	542362	0	R	1	root
97.17	531468	0	D	10239	Viruses
97.17	531468	0	D1	2732004	Varidnaviria
97.17	531468	0	K	2732005	Bamfordvirae
97.17	531468	0	P	2732007	Nucleocytoviricota
97.17	531468	0	C	2732525	Pokkesviricetes
97.17	531468	0	O	2732527	Chitovirales
97.17	531468	0	F	10240	Poxviridae
97.17	531468	0	F1	10241	Chordopoxvirinae
97.17	531468	130901	G	10242	Orthopoxvirus
66.23	362206	362206	S	10244	Monkeypox virus
1.04	10590	8228	S	10245	Vaccinia virus
0.43	2362	2362	S1	397342	Horsepox virus
0.96	5274	5274	S	2200830	Orthopoxvirus akhmetapox
0.93	5099	5099	S	12643	Ectromelia virus
0.89	4861	4861	S	10243	Cowpox virus
0.52	2865	2865	S	10255	Variola virus
0.47	2593	0	G1	347814	unclassified Orthopoxvirus
0.47	2593	2593	S	2602439	Borealpox virus
0.44	2413	2413	S	28873	Camelpox virus
0.30	1660	1660	S	28871	Taterapox virus
0.29	1572	1572	S	28874	Volepox virus
0.17	932	932	S	10256	Raccoonpox virus
0.09	502	502	S	160796	Skunkpox virus
1.99	10894	0	R1	131567	cellular organisms
1.99	10894	0	D	2759	Eukaryota
1.99	10894	0	D1	33154	Opisthokonta
1.99	10894	0	K	33208	Metazoa
1.99	10894	0	K1	6072	Eumetazoa
1.99	10894	0	K2	33213	Bilateria
1.99	10894	0	K3	33511	Deuterostomia
1.99	10894	0	P	7711	Chordata
1.99	10894	0	P1	89593	Cranialia
1.99	10894	0	P2	7742	Vertebrata
1.99	10894	0	P3	7776	Gnathostomata
1.99	10894	0	P4	117570	Teleostomi
1.99	10894	0	P5	117571	Euteleostomi
1.99	10894	0	P6	8287	Sarcopterygii
1.99	10894	0	P7	1338369	Dipnotetrapodomorpha
1.99	10894	0	P8	32523	Tetrapoda
1.99	10894	0	P9	32524	Amniota
1.99	10894	0	C	40674	Mammalia
1.99	10894	0	C1	32525	Theria
1.99	10894	0	C2	9347	Eutheria
1.99	10894	0	C3	1437010	Boreoeutheria
1.99	10894	0	C4	314146	Euarchotheria
1.99	10894	0	O	9443	Primates
1.99	10894	0	O1	376913	Haplorrhini
1.99	10894	0	O2	314293	Simiiformes
1.99	10894	0	O3	9526	Catarrhini
1.99	10894	0	O4	314295	Hominidae
1.99	10894	0	F	9604	Homininae
1.99	10894	0	F1	207598	Homininae
1.99	10894	0	G	9605	Homo
1.99	10894	10894	S	9606	Homo sapiens

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/	
Name	
..	
bandage	
bwa	
fastp	
final_assembly	
graph_recon	
graph_recon_mapping	
ivar	
kraken2	
multiqc	
mummer	
pipeline_info	
quast	
samtools	
seqtk	
unicycler	
variant_summaries	
sample_summary.tsv	

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/kraken2/	
Name	
..	
SRR23873768.classified_1.fastq.gz	
SRR23873768.classified_2.fastq.gz	
SRR23873768.kraken2.classifiedreads.txt	
SRR23873768.kraken2.report.txt	
SRR23873769.classified_1.fastq.gz	
SRR23873769.classified_2.fastq.gz	
SRR23873769.kraken2.classifiedreads.txt	
SRR23873769.kraken2.report.txt	
SRR23873770.classified_1.fastq.gz	
SRR23873770.classified_2.fastq.gz	
SRR23873770.kraken2.classifiedreads.txt	
SRR23873770.kraken2.report.txt	
SRR23873771.classified_1.fastq.gz	
SRR23873771.classified_2.fastq.gz	
SRR23873771.kraken2.classifiedreads.txt	
SRR23873771.kraken2.report.txt	
SRR23873772.classified_1.fastq.gz	
SRR23873772.classified_2.fastq.gz	
SRR23873772.kraken2.classifiedreads.txt	
SRR23873772.kraken2.report.txt	
SRR23873773.classified_1.fastq.gz	
SRR23873773.classified_2.fastq.gz	
SRR23873773.kraken2.classifiedreads.txt	
SRR23873773.kraken2.report.txt	



# Application Cont.

MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

This report has been generated by the [polkapox](#) analysis pipeline. For information about how to interpret these results, please see the [documentation](#).

Report generated on 2025-12-12, 01:40 based on data in: `/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/work/c7/26d5d13cf18b5e28369f10244afc89`

Welcome! Not sure where to start?

Watch a tutorial video (6:06)

don't show again

General Statistics

Copy table

Configure Columns

Plot

Showing 13 rows and 13 columns.

Sample Name	M Reads Mapped	N50 (Kbp)	Assembly Length (Mbp)	% Monkeypox virus	% Top 5 Species	% Unclassified	% Duplication	GC content	% PF	% Adap
SRR23873768	1.1	158.4Kbp	0.2Mbp	66.2%	70.9%	0.8%	1.4%	34.1%	92.7%	2.2%
SRR23873769	1.0	136.1Kbp	0.2Mbp	68.4%	72.4%	1.2%	1.8%	34.3%	93.3%	1.9%
SRR23873770	1.3	28.7Kbp	0.2Mbp	68.6%	72.9%	1.1%	1.6%	34.2%	88.3%	3.2%
SRR23873771	1.3	116.4Kbp	0.2Mbp	67.9%	72.4%	1.0%	1.7%	34.1%	93.1%	2.0%
SRR23873772	1.1			68.1%	72.1%	1.2%	2.3%	33.9%	98.1%	0.9%
SRR23873773	1.0	184.3Kbp	0.2Mbp	66.9%	71.3%	0.9%	1.7%	34.0%	98.1%	1.0%
SRR23873774	1.0	148.2Kbp	0.2Mbp	67.6%	72.1%	0.9%	1.8%	34.0%	98.2%	1.0%
SRR23873775	1.2	72.4Kbp	0.2Mbp	65.8%	70.3%	1.0%	2.4%	34.0%	98.1%	1.0%
SRR23873776	1.2	129.7Kbp	0.2Mbp	67.6%	71.9%	1.4%	2.4%	34.1%	98.2%	0.9%
SRR23873777	1.4			50.7%	54.1%	12.0%	2.8%	33.6%	77.9%	4.1%
SRR23873778	1.2	109.1Kbp	0.2Mbp	67.9%	72.0%	1.1%	2.8%	34.4%	97.8%	1.0%
SRR23873779	1.3	110.7Kbp	0.2Mbp	70.2%	74.1%	1.2%	3.1%	34.4%	98.1%	1.0%
SRR23873780	1.0	177.7Kbp	0.2Mbp	67.1%	71.6%	1.0%	2.3%	34.5%	96.2%	1.3%

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name

..

bandage

bwa

fastp

final\_assembly

graph\_recon

graph\_recon\_mapping

ivar

kraken2

multiqc

mummer

pipeline\_info

quast

samtools

seqtk

unicycler

variant\_summaries

sample\_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/multiqc/

Name

..

multiqc\_data

multiqc\_plots

multiqc\_report.html

Advanced Molecular Detection

Southeast Region Bioinformatics

# Application Cont.

NUCIMER

	[REF]	[QRY]
[Sequences]		
TotalSeqs	1	1
AlignedSeqs	1(100.00%)	1(100.00%)
UnalignedSeqs	0(0.00%)	0(0.00%)
[Bases]		
TotalBases	196517	195569
AlignedBases	195208(99.33%)	195208(99.82%)
UnalignedBases	1309(0.67%)	361(0.18%)
[Alignments]		
1-to-1	2	2
TotalLength	195208	195208
AvgLength	97604.00	97604.00
AvgIdentity	99.98	99.98
M-to-M	2	2
TotalLength	195208	195208
AvgLength	97604.00	97604.00
AvgIdentity	99.98	99.98
[Feature Estimates]		
Breakpoints	4	2
Relocations	0	0
Translocations	0	0
Inversions	0	0
Insertions	3	1
InsertionSum	1309	361
InsertionAvg	436.33	361.00
TandemIns	0	0
TandemInsSum	0	0
TandemInsAvg	0.00	0.00

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name
..
bandage
bwa
fastp
final_assembly
graph_recon
graph_recon_mapping
ivar
kraken2
multiqc
mummer
pipeline_info
quast
samtools
seqtk
unicycler
variant_summaries
sample_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/mummer/

Name
..
SRR23873773.report

# Application Cont.

## Nextflow workflow report

[exotic\_khorana]

Workflow execution completed successfully!

**Run times**  
12-Dec-2025 00:06:07 - 12-Dec-2025 01:41:40 (duration: **1h 35m 33s**)

191 succeeded

**Nextflow command**

```
nextflow run /blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/main.nf --input /blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/samplesheet.csv --outdir /blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output --workflow full -profile singularity --threads 16
```

CPU-Hours	18.5
Launch directory	/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222
Work directory	/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/work
Project directory	/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222
Script name	main.nf
Script ID	7fdd575a8e8cc8f58ebd1deea75e8b95
Workflow session	f85d4705-709b-4685-9890-8fa88e19754a
Workflow profile	singularity
Nextflow version	version 25.04.7, build 5955 (08-09-2025 13:29 UTC)

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name
..
bandage
bwa
fastp
final_assembly
graph_recon
graph_recon_mapping
ivar
kraken2
multiqc
mummer
pipeline_info
quast
samtools
seqtk
unicycler
variant_summaries
sample_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/pipeline\_info/

Name
..
execution_report_2025-12-12_00-06-07.html
execution_timeline_2025-12-12_00-06-07.html
execution_trace_2025-12-12_00-06-07.txt
pipeline_dag_2025-12-12_00-06-07.html
samplesheet.valid.csv
software_versions.yml

# Application Cont.

Assembly	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873	SRR23873775.contigs
# contigs (	4	6	14	8	5	8	6	10	9	7	9
# contigs (	3	5	8	6	4	7	5	7	7	6	7
# contigs (	1	3	5	4	2	5	3	6	5	4	4
# contigs (	1	3	3	2	1	3	3	5	4	4	3
# contigs (	1	2	2	1	1	2	1	2	3	3	2
# contigs (	1	1	1	1	1	1	1	1	1	1	2
Total lengt	190396	189044	189704	189546	189775	189134	189908	188661	189675	188603	189306
Total lengt	190380	189028	189470	189521	189759	189118	189892	187022	189650	188587	189207
Total lengt	184275	183414	182386	183899	184101	183489	183910	182951	183641	182880	182332
Total lengt	184275	183414	165244	169982	177659	168515	183910	175099	176441	182880	177122
Total lengt	184275	164540	153683	158372	177659	158191	148207	113014	164868	164074	158310
Total lengt	184275	136113	116351	158372	177659	129737	148207	84294	110722	109124	158310
# contigs	3	5	8	6	4	7	5	9	7	6	7
Largest co	184275	136113	116351	158372	177659	129737	148207	84294	110722	109124	85933
Total lengt	190380	189028	189470	189521	189759	189118	189892	188645	189650	188587	189207
Reference	197223	197223	197223	197223	197223	197223	197223	197223	197223	197223	197223
GC (%)	32.94	32.96	32.95	32.95	32.95	32.95	32.94	32.96	32.94	32.94	32.95
Reference	33.02	33.02	33.02	33.02	33.02	33.02	33.02	33.02	33.02	33.02	33.02
N50	184275	136113	116351	158372	177659	129737	148207	28720	110722	109124	72377
NG50	184275	136113	116351	158372	177659	129737	148207	28720	110722	109124	72377
N90	184275	18874	9617	7372	177659	8474	16863	18628	11573	18806	18812
NG90	184275	18874	7525	6545	177659	6500	16863	7852	7200	18806	5210
auN	178484	104267	80404.1	133664	166648	94546.6	119152	49394.8	73484.7	73126.1	68832.9
auNG	172291	99934.9	77243.4	128444	160341	90661.2	114723	47246.4	70663	69924.1	66035.2
L50	1	1	1	1	1	1	1	2	1	1	2
LG50	1	1	1	1	1	1	1	2	1	1	2
L90	1	3	4	3	1	4	3	5	4	4	3
LG90	1	3	5	4	1	5	3	6	5	4	4
# misasse	0	0	0	0	0	0	0	0	0	0	0
# misasse	0	0	0	0	0	0	0	0	0	0	0
Misasse	0	0	0	0	0	0	0	0	0	0	0
# local mis	0	0	0	0	0	0	0	0	0	0	0
# scaffold	0	0	0	0	0	0	0	0	0	0	0
# unalign	0	0	0	0	0	0	0	0	0	0	0
# unalign 0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned	0	0	0	0	0	0	0	0	0	0	0
Genome fr	96.575	95.861	96.114	96.136	96.254	95.93	96.297	95.71	96.205	95.658	95.997
Duplicatio	1	1	1	1	0.999	1	0.999	0.999	1	1	0.999
# N's per 1	0	0	0	0	0	0	0	0	0	0	0
# mismatc	27.31	23.28	21.64	23.74	23.19	21.68	21.6	23.33	23.2	23.86	23.26
# indels pe	3.68	1.59	2.11	2.64	1.58	2.12	3.16	3.18	3.16	2.65	2.64
# genomic 370 + 3 pa 364 + 9 pa 360 + 13 p 366 + 7 pa 368 + 5 pa 362 + 11 p 366 + 7 pa 356 + 19 p 364 + 9 pa 362 + 9 pa 362 + 9 part											
Largest ali	184275	136113	116351	158372	177659	129737	148196	84294	110722	109115	85933
Total align	190380	188973	189470	189521	189718	189102	189823	188620	189650	188578	189206
NA50	184275	136113	116351	158372	177659	129737	148196	28720	110722	109115	72377
NGA50	184275	136113	116351	158372	177659	129737	148196	28720	110722	109115	72377
NA90	184275	18847	9617	7372	177659	8474	16863	18628	11573	18806	18811
NGA90	184275	18847	7525	6545	177659	6500	16863	7852	7200	18806	5210
auNA	178484	104254	80404.1	133664	166646	94545.2	119132	49389.7	73484.7	73115.7	68832.7
auNGA	172291	99921.7	77243.4	128444	160340	90659.8	114704	47241.6	70663	69914.1	66035
LA50	1	1	1	1	1	1	1	2	1	1	2
LGA50	1	1	1	1	1	1	1	2	1	1	2
LA90	1	3	4	3	1	4	3	5	4	4	3
LGA90	1	3	5	4	1	5	3	6	5	4	4

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name
..
bandage
bwa
fastp
final_assembly
graph_recon
graph_recon_mapping
ivar
kraken2
multiqc
mummer
pipeline_info
quast
samtools
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variant_summaries
sample_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/quast/

Name
..
quast
report.tsv

# Application Cont.

MT903344	350	1
MT903344	351	1
MT903344	352	1
MT903344	353	1
MT903344	354	1
MT903344	355	1
MT903344	356	1
MT903344	357	1
MT903344	358	1
MT903344	359	1
MT903344	360	1
MT903344	361	1
MT903344	362	1
MT903344	363	1
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MT903344	368	1
MT903344	369	1
MT903344	370	1
MT903344	371	1
MT903344	372	1
MT903344	373	1
MT903344	374	1
MT903344	375	1
MT903344	376	1
MT903344	377	1

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name

..

bandage

bwa

fastp

final\_assembly

graph\_recon

graph\_recon\_mapping

ivar

kraken2

multiqc

mummer

pipeline\_info

quast

samtools

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variant\_summaries

sample\_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/samtools/

Name

SRR23873768.depth.tsv

SRR23873768.flagstat

SRR23873769.depth.tsv

SRR23873769.flagstat

SRR23873770.depth.tsv

SRR23873770.flagstat

SRR23873771.depth.tsv

SRR23873771.flagstat

SRR23873772.depth.tsv

SRR23873772.flagstat

SRR23873773.depth.tsv

SRR23873773.flagstat

SRR23873774.depth.tsv

SRR23873774.flagstat

SRR23873775.depth.tsv

SRR23873775.flagstat

SRR23873776.depth.tsv

SRR23873776.flagstat

SRR23873777.depth.tsv

SRR23873777.flagstat

SRR23873778.depth.tsv

SRR23873778.flagstat

SRR23873779.depth.tsv

SRR23873779.flagstat

SRR23873780.depth.tsv

SRR23873780.flagstat

# Application Cont.

SRR23873768.1  
SRR23873768.2  
SRR23873768.3  
SRR23873768.4  
SRR23873768.5  
SRR23873768.6  
SRR23873768.7  
SRR23873768.8  
SRR23873768.9  
SRR23873768.10  
SRR23873768.11  
SRR23873768.12  
SRR23873768.13  
SRR23873768.14  
SRR23873768.15  
SRR23873768.16  
SRR23873768.17  
SRR23873768.18  
SRR23873768.19  
SRR23873768.20  
SRR23873768.21  
SRR23873768.22  
SRR23873768.23  
SRR23873768.24  
SRR23873768.25  
SRR23873768.26  
SRR23873768.27  
SRR23873768.28  
SRR23873768.29  
SRR23873768.30  
SRR23873768.31  
SRR23873768.32  
SRR23873768.33  
SRR23873768.34  
SRR23873768.35  
SRR23873768.36  
SRR23873768.37  
SRR23873768.38  
SRR23873768.39  
SRR23873768.40  
SRR23873768.41  
SRR23873768.42  
SRR23873768.43

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name

- ..
- bandage
- bwa
- fastp
- final\_assembly
- graph\_recon
- graph\_recon\_mapping
- ivar
- kraken2
- multiqc
- mummer
- pipeline\_info
- quast
- samtools
- seqtk
- unicycler
- variant\_summaries
- sample\_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/seqtk/

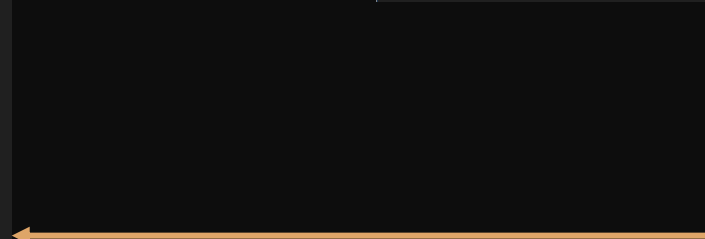
Name

- SRR23873768.opreads.txt
- SRR23873768.1.fq.gz
- SRR23873768.2.fq.gz
- SRR23873769.opreads.txt
- SRR23873769.1.fq.gz
- SRR23873769.2.fq.gz
- SRR23873770.opreads.txt
- SRR23873770.1.fq.gz
- SRR23873770.2.fq.gz
- SRR23873771.opreads.txt
- SRR23873771.1.fq.gz
- SRR23873771.2.fq.gz
- SRR23873772.opreads.txt
- SRR23873772.1.fq.gz
- SRR23873772.2.fq.gz
- SRR23873773.opreads.txt
- SRR23873773.1.fq.gz
- SRR23873773.2.fq.gz
- SRR23873774.opreads.txt
- SRR23873774.1.fq.gz
- SRR23873774.2.fq.gz
- SRR23873775.opreads.txt
- SRR23873775.1.fq.gz
- SRR23873775.2.fq.gz
- SRR23873776.opreads.txt
- SRR23873776.1.fq.gz
- SRR23873776.2.fq.gz
- SRR23873777.opreads.txt
- SRR23873777.1.fq.gz
- SRR23873777.2.fq.gz
- SRR23873778.opreads.txt
- SRR23873778.1.fq.gz
- SRR23873778.2.fq.gz
- SRR23873779.opreads.txt
- SRR23873779.1.fq.gz
- SRR23873779.2.fq.gz
- SRR23873780.opreads.txt
- SRR23873780.1.fq.gz
- SRR23873780.2.fq.gz

# Application Cont.

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/unicycler/
Name
..
SRR23873768.bridges_applied.gfa
SRR23873768.scaffolds.fa.gz
SRR23873768.unicycler.log
SRR23873769.bridges_applied.gfa
SRR23873769.scaffolds.fa.gz
SRR23873769.unicycler.log
SRR23873770.bridges_applied.gfa
SRR23873770.scaffolds.fa.gz
SRR23873770.unicycler.log
SRR23873771.bridges_applied.gfa
SRR23873771.scaffolds.fa.gz
SRR23873771.unicycler.log
SRR23873772.bridges_applied.gfa
SRR23873772.scaffolds.fa.gz
SRR23873772.unicycler.log
SRR23873773.bridges_applied.gfa
SRR23873773.scaffolds.fa.gz
SRR23873773.unicycler.log
SRR23873774.bridges_applied.gfa
SRR23873774.scaffolds.fa.gz
SRR23873774.unicycler.log
SRR23873775.bridges_applied.gfa
SRR23873775.scaffolds.fa.gz
SRR23873775.unicycler.log
SRR23873776.bridges_applied.gfa
SRR23873776.scaffolds.fa.gz
SRR23873776.unicycler.log
SRR23873777.bridges_applied.gfa
SRR23873777.scaffolds.fa.gz
SRR23873777.unicycler.log
SRR23873778.bridges_applied.gfa
SRR23873778.scaffolds.fa.gz
SRR23873778.unicycler.log
SRR23873779.bridges_applied.gfa
SRR23873779.scaffolds.fa.gz
SRR23873779.unicycler.log
SRR23873780.bridges_applied.gfa
SRR23873780.scaffolds.fa.gz
SRR23873780.unicycler.log
```

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/
Name
..
bandage
bwa
fastp
final_assembly
graph_recon
graph_recon_mapping
ivar
kraken2
multiqc
mummer
pipeline_info
quast
samtools
seqtk
unicycler
variant_summaries
sample_summary.tsv
```



# Application Cont.

run	sample	coord	refBase	altBase	totalDP	altDP	altQual	altFreq	altPval	GFFfeature	RefCodon	RefAA	AltCodon	AltAA
/blue/bphl	SRR23873	39148	C	T	547	547	66	1	0	cds-QNP1 CTC	L	CTT	L	
/blue/bphl	SRR23873	39570	A	T	772	14	69	0.018135	5.67E-07	cds-QNP1 CAA	Q	CTA	L	
/blue/bphl	SRR23873	39714	A	G	380	17	60	0.044737	1.89E-08	cds-QNP1 AAA	K	AGA	R	
/blue/bphl	SRR23873	39730	C	T	363	6	54	0.016529	0.002049	cds-QNP1 ATC	I	ATT	I	
/blue/bphl	SRR23873	39933	A	C	271	4	66	0.01476	0.019793	cds-QNP1 CAG	Q	CCG	P	
/blue/bphl	SRR23873	40143	T	G	594	21	73	0.035354	3.54E-10	cds-QNP1 TTC	F	TGC	C	
/blue/bphl	SRR23873	51501	A	T	278	3	39	0.010791	0.04496	cds-QNP1 CAA	Q	CAT	H	
/blue/bphl	SRR23873	51878	C	T	340	6	48	0.017647	0.002429	cds-QNP1 TCC	S	TTC	F	
/blue/bphl	SRR23873	51994	T	G	305	7	44	0.022951	0.000993	cds-QNP1 TTT	F	GTT	V	
/blue/bphl	SRR23873	52094	T	A	320	5	39	0.015625	0.006993	cds-QNP1 ATT	I	AAT	N	
/blue/bphl	SRR23873	52648	A	G	207	3	48	0.014493	0.052829	cds-QNP1 ATG	M	GTG	V	
/blue/bphl	SRR23873	52894	G	A	978	978	63	1	0	cds-QNP1 GAC	D	AAC	N	
/blue/bphl	SRR23873	54126	G	A	999	999	65	1	0	cds-QNP1 GAG	E	GAA	E	
/blue/bphl	SRR23873	39148	C	T	510	510	65	1	0	cds-QNP1 CTC	L	CTT	L	
/blue/bphl	SRR23873	39570	A	T	765	13	68	0.016994	1.60E-06	cds-QNP1 CAA	Q	CTA	L	
/blue/bphl	SRR23873	39611	A	T	681	14	67	0.020558	5.88E-07	cds-QNP1 AGG	R	TGG	W	
/blue/bphl	SRR23873	39714	A	G	335	9	52	0.026866	0.000106	cds-QNP1 AAA	K	AGA	R	
/blue/bphl	SRR23873	39892	T	A	230	6	63	0.026087	0.002249	cds-QNP1 GGT	G	GGA	G	
/blue/bphl	SRR23873	39899	A	T	224	6	57	0.026786	0.002109	cds-QNP1 ATT	I	TTT	F	
/blue/bphl	SRR23873	39906	T	A	208	3	43	0.014423	0.045225	cds-QNP1 ATC	I	AAC	N	
/blue/bphl	SRR23873	40143	T	G	453	9	77	0.019868	8.28E-05	cds-QNP1 TTC	F	TGC	C	
/blue/bphl	SRR23873	51837	A	G	252	3	64	0.011905	0.050291	cds-QNP1 AGA	R	AGG	R	
/blue/bphl	SRR23873	51878	C	T	232	5	53	0.021552	0.007197	cds-QNP1 TCC	S	TTC	F	
/blue/bphl	SRR23873	51882	C	T	233	3	61	0.012876	0.051393	cds-QNP1 TTC	F	TTT	F	
/blue/bphl	SRR23873	52078	C	A	247	8	37	0.032389	0.000333	cds-QNP1 CTC	L	ATC	I	
/blue/bphl	SRR23873	52094	T	A	251	3	38	0.011952	0.052655	cds-QNP1 ATT	I	AAT	N	
/blue/bphl	SRR23873	52480	C	T	126	4	38	0.031746	0.020629	cds-QNP1 CAT	H	TAT	Y	

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/

Name
..
bandage
bwa
fastp
final_assembly
graph_recon
graph_recon_mapping
ivar
kraken2
multiqc
mummer
pipeline_info
quast
samtools
seqtk
unicycler
variant_summaries
sample_summary.tsv

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/polkapox1222/output/variant\_summaries/

Name
all_samples.vcf.summary.txt
SRR23873768_ivar_summary.txt
SRR23873769_ivar_summary.txt
SRR23873770_ivar_summary.txt
SRR23873771_ivar_summary.txt
SRR23873772_ivar_summary.txt
SRR23873773_ivar_summary.txt
SRR23873774_ivar_summary.txt
SRR23873775_ivar_summary.txt
SRR23873776_ivar_summary.txt
SRR23873777_ivar_summary.txt
SRR23873778_ivar_summary.txt
SRR23873779_ivar_summary.txt
SRR23873780_ivar_summary.txt



# Conclusion



Fundamentals of  
PolkaPox



Installation and setup  
of PolkaPox in HPG



Successfully executed  
job query for  
PolkaPox



Generated output files



# Advanced Molecular Detection

## Southeast Region Bioinformatics

# Questions?

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