

PhyloPHoeNlx

Advanced Molecular Detection

Southeast Region Bioinformatics

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Updates

Nov 28, 2025

- 2026 Needs Assessment Surveys

Overview

Purpose:

- This nextflow pipeline is used to generate reference-based phylogenies from PHoeNIx outputs using core-genome SNVs for molecular epidemiology and relatedness analysis.

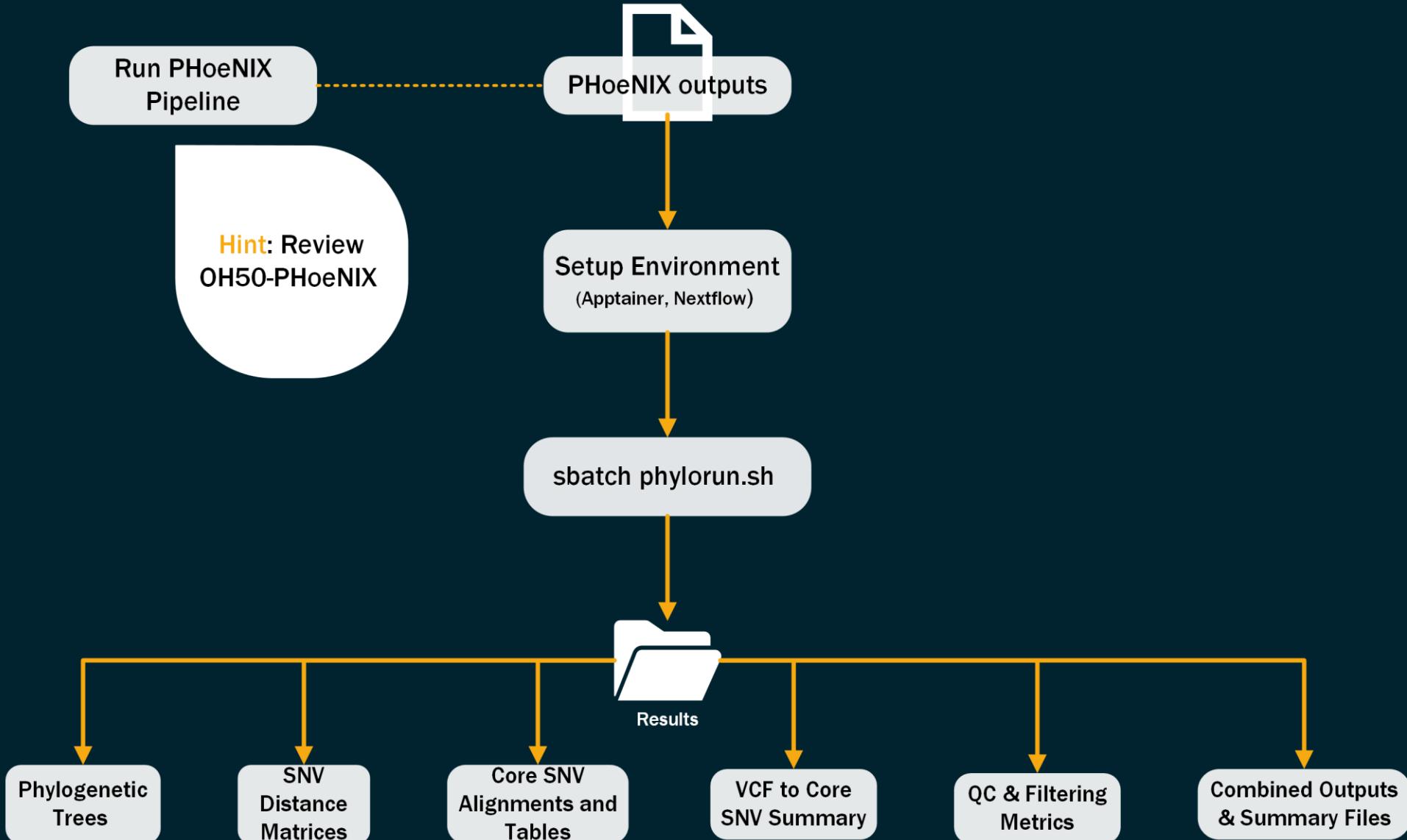
Usage:

- Can be used by public health labs to create per-ST and combined isolate phylogenies, SNV matrices, QC summaries for outbreak detection, surveillance and genome clustering.

Dependencies:

- Nextflow
- Apptainer/Singularity

Workflow



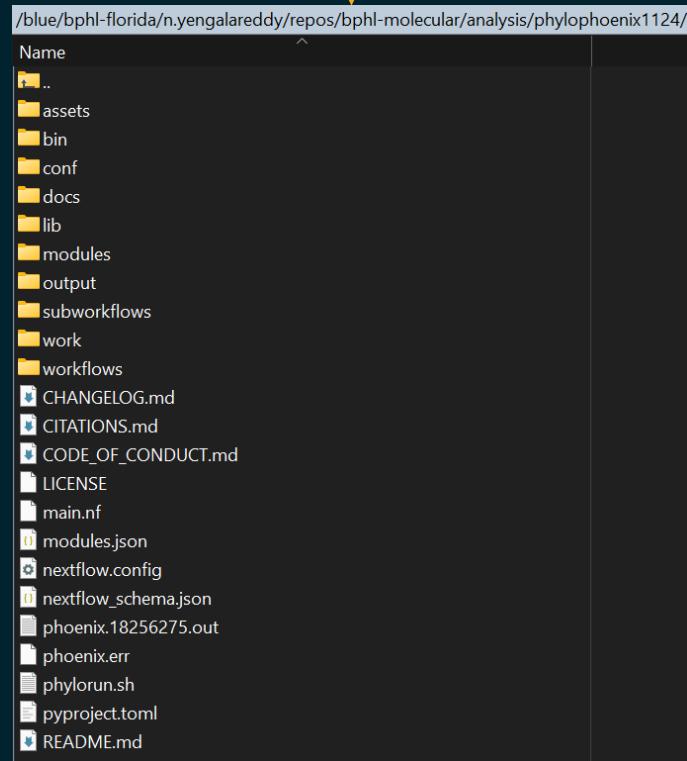
Application

Objective-

Use PHoeNIX output data with PhlyoPHoeNIX to generate SNVs, core genome alignment and phylogenetic trees.

Application Cont.

```
cd /blue/bphl-<state>/<user>/repos/bphl-molecular/  
  
git clone https://github.com/CDCgov/phylophoenix  
  
mkdir analysis/  
  
cd analysis/  
  
cp /blue/bphl-<state>/<user>/repos/bphl-molecular/phylophoenix/
```



Application Cont.

```
/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output/
```

Name
..
J4
J7
J8
J9
J17
J36
J40
J52
J100
J102
J120
J217
J414
J756
J762
J780
multiqc
pipeline_info
Directory_samplesheet.csv
Phoenix_Summary.tsv
phx_output_GRIPHin_Summary.tsv
phx_output_GRIPHin_Summary.xlsx

```
GNU nano 5.6.1 phylorun.sh
```

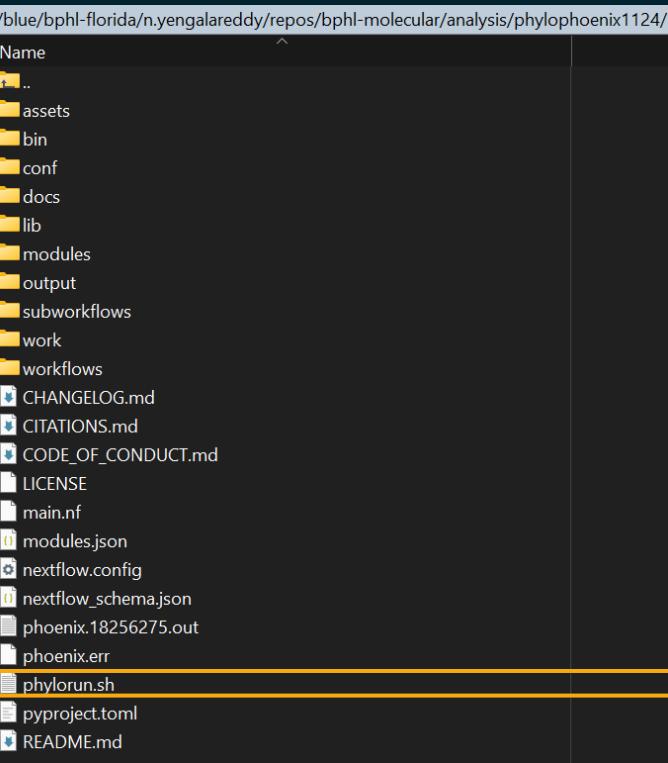
```
#!/bin/bash
#SBATCH --account=bphl-umbrella
#SBATCH --qos=bphl-umbrella
#SBATCH --job-name=Phylophoenix
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=10
#SBATCH --mem=256gb
#SBATCH --time=48:00:00
#SBATCH --output=phoenix.%j.out
#SBATCH --error=phoenix.err
#SBATCH --mail-user=nikhil.yengala@flhealth.gov
#SBATCH --mail-type=FAIL,END

#Load packages
module purge
module load nextflow
module load apptainer

#Cache
export NXF_APPTAINER_CACHEDIR="/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/.apptainer_cache"
export NXF_WORK="/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/work"
export TEMP="/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/scratch/tmp"

#Pathways
[INDIR="/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output"
OUTDIR="/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output"

#Run Code
nextflow run cdcgov/phylophoenix \
-profile singularity \
--indir "$INDIR" \
--by_st \
--outdir "$OUTDIR"
```



Application Cont.

SNVPhyl Summary

WGS_ID	Parent_Folder	Data_Location	SNV Metrics	Minimum_QC_Chr	Minimum_QC_Issues	Warnings	Alerts	Raw_Q30_R1	Total_Raw_Reads	Paired_Truncated_Reads	Total_Truncated_Reads	Estimated_Truncated_Coverage	Scaffold	Average_Q30_R1	
J4	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (14.22%)	coverage >100x(130.18x)	94.04	86.82	3,399,434	2,946,464	3,122,418	130.18	50.46	179
J7	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (16.87%), High scaffold count 200-500 (246)	93.41	85.50	2,176,320	1,852,286	1,976,454	80.52	50.46	246	
J8	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (17.96%), High scaffold count 200-500 (294)	92.44	88.14	2,738,936	2,400,072	2,528,177	100.44	50.31	294	
J9	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (7.71%)	93.95	82.47	2,631,834	2,161,400	2,352,199	109.14	50.71	57	
J17	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (15.96%), High scaffold count 200-500 (267)	93.28	85.82	2,418,604	2,071,012	2,205,606	89.77	50.53	267	
J36	/blue/bphl-florida/phx/output	PASS					90.24	81.23	2,329,860	2,138,345	2,286,586	86.57	57.51	51	
J40	/blue/bphl-florida/phx/output	PASS					90.44	81.33	1,588,860	1,380,798	1,415,518	60.20	51.11	70	
J52	/blue/bphl-florida/phx/output	PASS					94.64	82.86	3,086,434	3,584,824	3,791,309	119.70	50.45	137	
J100	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (16.20%), FastANI coverage is <90%	93.89	84.75	2,153,930	1,818,424	1,950,807	87.21	50.57	99	
J102	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (11.17%)	92.05	79.29	2,155,290	1,771,506	1,925,033	69.61	50.81	67	
J120	/blue/bphl-florida/phx/output	PASS				Average Q30 of raw R1 reads <90.00%	88.45	76.44	2,245,352	1,895,040	2,031,148	54.22	50.43	128	
J217	/blue/bphl-florida/phx/output	PASS					97.24	92.38	1,750,586	1,571,496	1,638,543	93.49	39.01	65	
J414	/blue/bphl-florida/phx/output	PASS				<70% of reads assigned to top genera hit (33.70%), High scaffold count 200-500 (215)	93.48	85.19	2,956,942	2,509,928	2,685,208	108.15	50.28	215	
J756	/blue/bphl-florida/phx/output	PASS					93.20	76.25	1,948,216	1,470,394	1,671,624	70.98	52.03	73	
J762	/blue/bphl-florida/phx/output	PASS					90.07	85.93	1,292,508	1,112,848	1,180,250	46.55	51.88	923	
J780	/blue/bphl-florida/phx/output	PASS	FAIL	High scaffold count >500 (923)		Average Q30 of raw R1 reads <90.00%, High scaffold count 200-500 (268)	89.62	86.62	1,614,562	1,395,998	1,476,162	58.76	51.74	268	

Cells in **YELLOW** denote isolates outside of 30-100x coverage
Cells in **ORANGE** denote "Big 5" carbapenemase gene (i.e., blaKPC, blaNDM, 48-like, blaVIM, and blaIMP) or an acquired blaOXA gene, please confirm what AR Lab Network HAI/AR WGS priority these meet.
Cells in **RED** denote isolates that failed one or more auto failure triggers (cov < 30, assembly ratio stdev > 2.58, assembly length < 1Mbps)
*Using Antibiotic Resistance Gene Database RegGANNCB1_20240229(XNT/98AA/90G-[98NT/90])S (ResFinder, ARG-ANNOT, NCBI Bacterial Antimicrobial Resistance Reference Gene Database) using output thresholds ([98AA/90G-[98NT/90])S); gene matches from S:(SRST2) with [%Nuc_Identity, %Coverage], or from G:(GAMMA) with [%Nuc_Identity, %AA_Identity, %Coverage]; GAMMA gene matches indicate association with CDC-compiled rfb, iucD, pag-344, rmpA, and rmpA2 hypervirulence gene database (HyperVirulence_20220414); gene matches noted with [%Nuc_Identity, %AA_Identity, %Coverage].
**Using the plasmid incompatibility replicons plasmidfinder database (PF-Replicons_20240124/[95NT/60]) using output thresholds [95NT/60]; replicon matches noted with [%Nuc_Identity, %Coverage].
DISCLAIMER: These data are preliminary and subject to change. The identification methods used and the data summarized are for public health surveillance or investigational purposes only and must NOT be communicated to the patient, their care provider, or placed in the patient's medical record. These results should NOT be used for diagnosis, treatment, or assessment of individual patient health or management.

Reviewed by: Date:

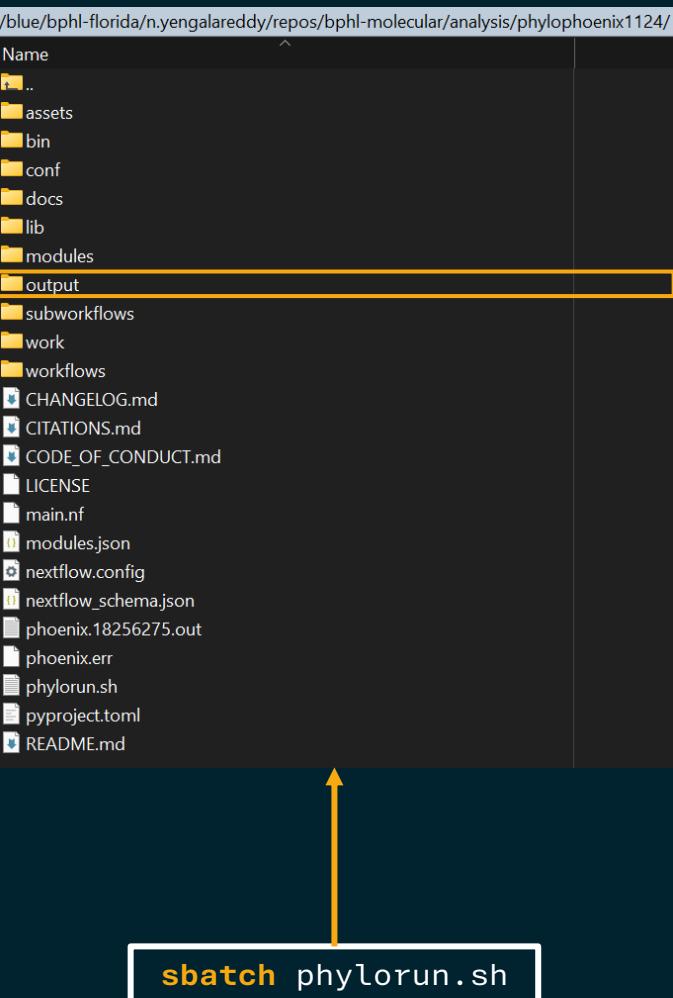
SNVPhyl Analysis: SNV Matrices

All_Isolates J100 SNVPhyl cc0.1%

WGS_ID	J120	J217	J102	J36	J756	J780	J4	J40	J52	J8	J17	J7	J9	J414	J1
J120	0	64	49	46	46	46	45	42	45	39	38	37	37	37	36
J217	64	0	61	58	58	51	51	48	48	45	44	43	43	43	42
J102	49	61	0	3	0	27	25	23	24	22	19	20	20	18	19
J36	46	58	3	0	24	24	22	20	20	21	19	17	17	15	16
J756	46	51	27	24	22	4	0	16	17	13	12	11	11	11	10
J780	45	51	25	22	20	17	0	16	17	13	12	11	11	11	10
J4	42	48	23	20	16	16	0	16	3	4	4	5	5	6	
J40	45	48	24	21	17	17	16	0	13	12	11	11	11	10	
J52	39	45	22	19	13	13	3	13	0	3	4	4	4	3	
J8	38	44	19	16	12	12	4	12	3	0	3	3	1	2	
J17	37	43	20	17	11	11	5	11	4	3	0	0	2	1	
J7	37	43	20	17	11	11	5	11	4	3	0	0	2	1	
J9	37	43	18	15	11	11	5	11	4	1	2	2	0	1	
J414	36	42	19	16	10	10	6	10	3	2	1	1	1	0	
J100*	36	42	19	16	10	10	6	10	3	2	1	1	1	0	

ST10
J52
SNVPhyl cc88.81%

WGS_ID J4 J52*



Application Cont.

File structure and output files:

WGS_ID	J120	J217	J102	J36	J756	J780	J4	J40	J52	J8	J17	J7	J9	J414	J100*	
J120		0	64	49	46	46	45	42	45	39	38	37	37	37	36	36
J217	64	0	61	58	51	51	51	48	48	45	44	43	43	43	42	42
J102	49	61	0	3	27	25	23	24	22	21	19	20	20	18	19	19
J36	46	58	3	0	24	22	20	16	17	19	16	17	17	15	16	16
J756	46	51	27	24	0	4	16	17	13	12	11	11	11	10	10	
J780	45	51	25	22	4	0	16	17	13	12	11	11	11	10	10	
J4	42	48	23	20	16	16	0	16	3	4	5	5	5	6	6	
J40	45	48	24	21	17	17	16	0	13	12	11	11	11	10	10	
J52	39	45	22	19	13	13	3	13	0	3	4	4	4	3	3	
J8	38	44	19	16	12	12	4	12	3	0	3	3	1	2	2	
J17	37	43	20	17	11	11	5	11	4	3	0	0	2	1	1	
J7	37	43	20	17	11	11	5	11	4	3	0	0	2	1	1	
J9	37	43	18	15	11	11	5	11	4	1	2	2	0	1	1	
J414	36	42	19	16	10	10	6	10	3	2	1	1	1	0	0	
J100*	36	42	19	16	10	10	6	10	3	2	1	1	1	0	0	

Application Cont.

#Chromos	Position	Status	Reference	J102	J120	J17	J217	J36	J4	J40	J414	J52	J7	J756	J780	J8	J9
J100_10_le	749	filtered-co	A	-	-	-	-	-	G	A	-	-	-	-	-	-	-
J100_10_le	1706	filtered-co	A	-	-	-	-	-	G	G	-	-	-	-	-	-	-
J100_10_le	5147	filtered-co	A	-	-	-	-	-	G	G	-	-	-	-	-	-	-
J100_10_le	6452	filtered-co	T	-	-	-	-	-	C	C	-	-	-	-	-	-	-
J100_10_le	6658	filtered-co	G	-	-	-	-	-	G	A	-	-	-	-	-	-	-
J100_10_le	6671	filtered-co	A	-	-	-	-	-	A	T	-	-	-	-	-	-	-
J100_10_le	6738	filtered-co	T	-	-	-	-	-	G	G	-	-	-	-	-	-	-
J100_10_le	9018	filtered-co	T	-	-	-	-	-	T	G	-	-	-	-	-	-	-
J100_10_le	9290	filtered-co	C	-	-	-	-	-	C	T	-	-	-	-	-	-	-
J100_10_le	9684	filtered-co	C	-	-	-	-	-	T	C	-	-	-	-	-	-	-
J100_10_le	10601	filtered-co	G	-	-	-	-	-	G	T	-	-	-	-	-	-	-
J100_10_le	11260	filtered-co	T	-	-	-	-	-	C	C	-	-	-	-	-	-	-
J100_10_le	11787	filtered-co	C	-	-	-	-	-	C	T	-	-	-	-	-	-	-
J100_10_le	11883	filtered-co	C	-	-	-	-	-	C	T	-	-	-	-	-	-	-
J100_10_le	12944	filtered-inv	T	-	-	-	-	-	C	T	-	-	-	-	-	-	-
J100_10_le	12947	filtered-inv	G	-	-	-	-	-	C	G	-	-	-	-	-	-	-
J100_10_le	12953	filtered-inv	T	-	-	-	-	-	C	T	T	-	-	-	-	-	-
J100_10_le	12956	filtered-inv	T	-	-	-	-	-	C	T	T	-	-	-	-	-	-
J100_10_le	12959	filtered-inv	C	-	-	-	-	-	T	C	C	-	-	-	-	-	-
J100_10_le	12963	filtered-inv	A	-	-	-	-	-	C	A	A	-	-	-	-	-	-
J100_10_le	12964	filtered-inv	A	-	-	-	-	-	G	A	A	-	-	-	-	-	-
J100_10_le	12965	filtered-inv	A	-	-	-	-	-	G	A	A	-	-	-	-	-	-
J100_10_le	12966	filtered-inv	C	-	-	-	-	-	T	C	C	-	-	-	-	-	-
J100_10_le	12968	filtered-inv	T	-	-	-	-	-	G	T	T	-	-	-	-	-	-
J100_10_le	12971	filtered-inv	G	-	-	-	-	-	A	G	G	-	-	-	-	-	-
J100_10_le	12975	filtered-inv	A	-	-	-	-	-	C	A	A	-	-	-	-	-	-
J100_10_le	12977	filtered-inv	G	-	-	-	-	-	T	G	G	-	-	-	-	-	-

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/All_Isolates/

Name
..
J4
J7
J8
J9
J17
J36
J40
J52
J102
J120
J217
J414
J756
J780
All_Isolates_centroid.info.txt
All_Isolates_filtered_density_all.txt
All_Isolates_snvAlignment.phy
All_Isolates_snvMatrix.tsv
All_Isolates_SNVPhy.newick
All_Isolates_snvTable.tsv
All_Isolates_vcf2core.tsv
filterStats.txt
mappingQuality.txt



Application Cont.

#Reference name	Total length	Total invalid and excluded positions	Total valid and included positions	Total valid and included positions in core genome	Percentage of valid and included positions in core genome	Percentage of all positions that are valid, included, and part of the core genome
J100_10_length_191265	191265	109214	82051	190	0.23	0.1
J100_11_length_173813	173813	116481	57332	23	0.04	0.01
J100_12_length_133152	133152	80088	53064	16	0.03	0.01
J100_13_length_128238	128238	86058	42180	63	0.15	0.05
J100_14_length_114931	114931	80951	33980	2	0.01	0
J100_15_length_114793	114793	68452	46341	104	0.22	0.09
J100_16_length_114641	114641	51838	62803	0	0	0
J100_17_length_95134	95134	68305	26829	22	0.08	0.02
J100_18_length_91901	91901	63242	28659	44	0.15	0.05
J100_19_length_86809	86809	67086	19723	6	0.03	0.01
J100_20_length_327680	327680	225843	101837	138	0.14	0.04
J100_21_length_82107	82107	53336	28771	47	0.16	0.06
J100_22_length_75146	75146	44221	30925	58	0.19	0.06
J100_23_length_70543	70543	47604	22939	11	0.05	0.02
J100_24_length_68720	68720	48477	20243	0	0	0
J100_25_length_66768	66768	38783	27985	0	0	0
J100_26_length_62572	62572	31784	30788	0	0	0
J100_27_length_57922	57922	27967	29955	0	0	0
J100_28_length_53668	53668	33064	20604	21	0.1	0.04
J100_29_length_48808	48808	25250	23558	2	0.01	0
J100_30_length_318649	318649	155357	163292	194	0.12	0.06
J100_31_length_46747	46747	31052	15695	0	0	0
J100_32_length_45795	45795	23140	22655	0	0	0
J100_33_length_42887	42887	25841	17046	0	0	0
J100_34_length_41499	41499	16797	24702	208	0.84	0.5
J100_35_length_39482	39482	19558	19924	3	0.02	0.01
J100_36_length_31040	31040	21578	9462	576	6.09	1.86
J100_37_length_30247	30247	11434	18813	0	0	0
J100_38_length_30012	30012	16379	13633	0	0	0
J100_39_length_27925	27925	3116	24809	0	0	0
J100_40_length_25793	25793	7476	18317	0	0	0
J100_41_length_302869	302869	197955	104914	30	0.03	0.01
J100_42_length_25578	25578	11650	13928	0	0	0
J100_43_length_22745	22745	9279	13466	0	0	0
J100_44_length_19410	19410	1318	18092	0	0	0
J100_45_length_18534	18534	10248	8286	0	0	0
J100_46_length_13400	13400	3190	10210	0	0	0
J100_47_length_11905	11905	N/A	11905	0	0	0
J100_48_length_11357	11357	959	10398	0	0	0
J100_49_length_9095	9095	224	8871	0	0	0
J100_50_length_6370	6370	5239	1131	0	0	0
J100_51_length_6105	6105	2172	3933	0	0	0
J100_52_length_5850	5850	1043	4807	0	0	0

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/All_Isolates/

Name
..
J4
J7
J8
J9
J17
J36
J40
J52
J102
J120
J217
J414
J756
J780
All_Isolates_centroid.info.txt
All_Isolates_filtered_density_all.txt
All_Isolates_snvAlignment.phy
All_Isolates_snvMatrix.tsv
All_Isolates_SNPhyl.newick
All_Isolates_snvTable.tsv
All_Isolates_vcf2core.tsv
filterStats.txt
mappingQuality.txt



Application Cont.

Chromosome	Genomes	J217	J120	J102	J40	J36	J780	J756	J52	J414	J9	J7	J8	J17	J4	
J100_10_length_191265	ALL	35525	35355	33313	8774	8699	7712	5036	4039	832	793	612	513	503	468	461
Total number of N's and -'s		98.67	98.19	92.52	24.37	24.16	21.42	13.99	11.22	2.31	2.20	1.70	1.42	1.40	1.30	1.28
Total percent of N's and -'s																
Total number of unfiltered variants in chromosome:		36005														
Chromosome	Genomes	J217	J120	J102	J36	J40	J780	J756	J414	J9	J17	J7	J8	J52	J4	
J100_11_length_173813	ALL	37901	37803	35905	11162	10650	10388	6839	3466	325	293	148	112	109	79	71
Total number of N's and -'s		99.17	98.92	93.95	29.21	27.87	27.18	17.90	9.07	0.85	0.77	0.39	0.29	0.29	0.21	0.19
Total percent of N's and -'s																
Total number of unfiltered variants in chromosome:		38217														
Chromosome	Genomes	J217	J120	J102	J36	J40	J780	J756	J4	J52	J414	J8	J7	J9	J17	
J100_12_length_133152	ALL	26000	25882	24319	6396	5933	5633	3419	2934	18	17	16	8	6	6	4
Total number of N's and -'s		99.32	98.87	92.90	24.43	22.66	21.52	13.06	11.21	0.07	0.06	0.06	0.03	0.02	0.02	0.02
Total percent of N's and -'s																
Total number of unfiltered variants in chromosome:		26179														
Chromosome	Genomes	J217	J120	J102	J36	J40	J780	J756	J4	J52	J414	J7	J8	J17	J4	J52
J100_13_length_128238	ALL	27986	27487	26819	5817	5459	5069	1821	1611	66	56	55	13	13	12	11
Total number of N's and -'s		99.18	97.41	95.04	20.61	19.35	17.96	6.45	5.71	0.23	0.20	0.19	0.05	0.05	0.04	0.04
Total percent of N's and -'s																
Total number of unfiltered variants in chromosome:		28218														
Chromosome	Genomes	J217	J120	J102	J36	J40	J780	J756	J9	J4	J414	J17	J7	J8	J52	
J100_14_length_114931	ALL	24393	24204	23379	8981	8536	6413	3243	3099	1153	1113	400	297	296	278	188
Total number of N's and -'s		99.24	98.47	95.11	36.54	34.73	26.09	13.19	12.61	4.69	4.53	1.63	1.21	1.20	1.13	0.76
Total percent of N's and -'s																
Total number of unfiltered variants in chromosome:		24581														
Chromosome	Genomes	J217	J120	J780	J102	J40	J756	J36	J414	J4	J9	J52	J17	J7	J8	
J100_15_length_114793	ALL	20924	20843	20213	5134	4146	4059	3826	3634	2157	693	385	287	276	130	90
Total number of N's and -'s		97.23	96.85	93.92	23.86	19.26	18.86	17.78	16.89	10.02	3.22	1.79	1.33	1.28	0.60	0.42
Total percent of N's and -'s																
Total number of unfiltered variants in chromosome:		21521														

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/All_Isolates/

Name
..
J4
J7
J8
J9
J17
J36
J40
J52
J102
J120
J217
J414
J756
J780
All_Isolates_centroid.info.txt
All_Isolates_filtered_density_all.txt
All_Isolates_snvAlignment.phy
All_Isolates_snvMatrix.tsv
All_Isolates_SNVPhyl.newick
All_Isolates_snvTable.tsv
All_Isolates_vcf2core.tsv
filterStats.txt
mappingQuality.txt



Application Cont.

```
=====Reference Mapping Quality=====
NUMBER OF BP's IN REFERENCE GENOME: 4882908
MINIMUM DEPTH: 10
MINIMUM MAPPING: 80
bam4 : 1.37%
bam2 : 3.72%
bam1 : 48.58%
bam5 : 48.77%
bam6 : 51.39%
bam10 : 57.64%
bam11 : 57.78%
```

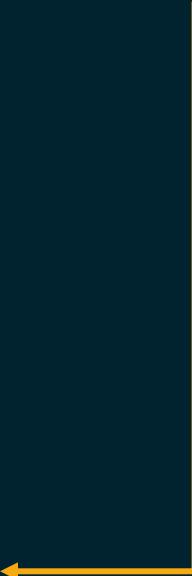
Name	
..	
J4	
J7	
J8	
J9	
J17	
J36	
J40	
J52	
J102	
J120	
J217	
J414	
J756	
J780	
All_Isolates_centroid.info.txt	
All_Isolates_filtered_density_all.txt	
All_Isolates_snvAlignment.phy	
All_Isolates_snvMatrix.tsv	
All_Isolates_SNVPhyl.newick	
All_Isolates_snvTable.tsv	
All_Isolates_vcf2core.tsv	
filterStats.txt	
mappingQuality.txt	



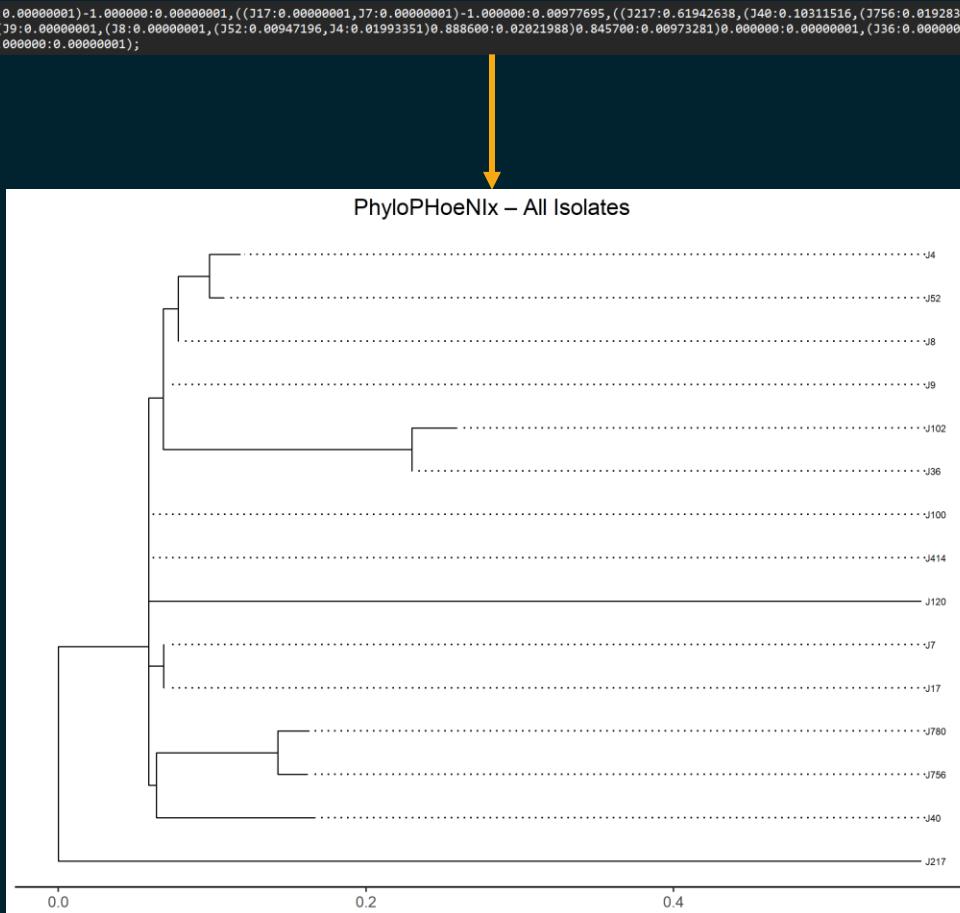
Application Cont.

/.../bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/All_Isolates/J4/	
Name	
..	
J4.bam	
J4_consolidated.vcf	
J4_filtered_density.txt	
J4_freebayes_filtered.vcf.gz	
J4_mpileup.vcf.gz	
J4_sorted.bam	

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/All_Isolates/	
Name	
..	
J4	
J7	
J8	
J9	
J17	
J36	
J40	
J52	
J102	
J120	
J217	
J414	
J756	
J780	
All_Isolates_centroid.info.txt	
All_Isolates_filtered_density_all.txt	
All_Isolates_snvAlignment.phy	
All_Isolates_snvMatrix.tsv	
All_Isolates_SNVPhyl.newick	
All_Isolates_snvTable.tsv	
All_Isolates_vcf2core.tsv	
filterStats.txt	
mappingQuality.txt	



Application Cont.



/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/All_Isolates/

Name
..
J4
J7
J8
J9
J17
J36
J40
J52
J102
J120
J217
J414
J756
J780
All_Isolates_centroid.info.txt
All_Isolates_filtered_density_all.txt
All_Isolates_snvAlignment.phy
All_Isolates_snvMatrix.tsv
All_Isolates_SNVPhyl.newick
All_Isolates_snvTable.tsv
All_Isolates_vcf2core.tsv
filterStats.txt
mappingQuality.txt

Application Cont.

The screenshot shows a file browser interface with two main panes. The left pane displays a list of files under the path `./..bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/pipeline_info/`. The right pane shows a detailed view of the `pipeline_info` folder at the path `/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/`. A yellow box highlights the `execution_report_2025-11-12_14-03-56.html` file in the left list, and a yellow arrow points from it to the corresponding entry in the right pane's tree view. Another yellow arrow points from the right pane's tree view down to a screenshot of a Nextflow workflow report.

`./..bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/pipeline_info/`

Name

- `execution_report_2025-11-12_14-03-56.html`
- `execution_timeline_2025-11-12_14-03-56.html`
- `execution_trace_2025-11-12_14-03-56.txt`
- `pipeline_dag_2025-11-12_14-03-56.html`
- `samplesheet.valid.csv`
- `software_versions.yml`

`/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/`

Name

- ..
- All_Isolates
- `pipeline_info`
- `ST_SampleSheets`
- `ST10`
- `ST11`
- `Directory_samplesheet.csv`
- `SNVPhyl_GRiPhin_Summary.xlsx`
- `versions.yml`

Nextflow workflow report
[big_mayer]

Workflow execution completed successfully!

Run times
12-Nov-2025 14:03:56 - 12-Nov-2025 15:29:39 (duration: **1h 25m 43s**)

333 succeeded

Nextflow command

```
nextflow run cdcgov/phylophoenix -profile singularity --indir /blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output --by_st --outdir /blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output
```

CPU-Hours 11.9

Launch directory `/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124`

Work directory `/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/work`

Project directory `/home/n.yengalareddy/.nextflow/assets/cdcgov/phylophoenix`

Script name `main.nf`

Script ID `e9c85f4e8c871beaf6a40d48efa67f25`

Workflow session `430bc40d-ea7d-4a17-b421-7cea67a7b76c`

Workflow repository <https://github.com/cdcgov/phylophoenix>, revision `main` (commit hash `5c7094818477a3263d5a9f9c3cabcf73ba221ee`)

Workflow profile singularity

Nextflow version version 25.04.7, build 5955 (08-09-2025 13:29 UTC)

Application Cont.

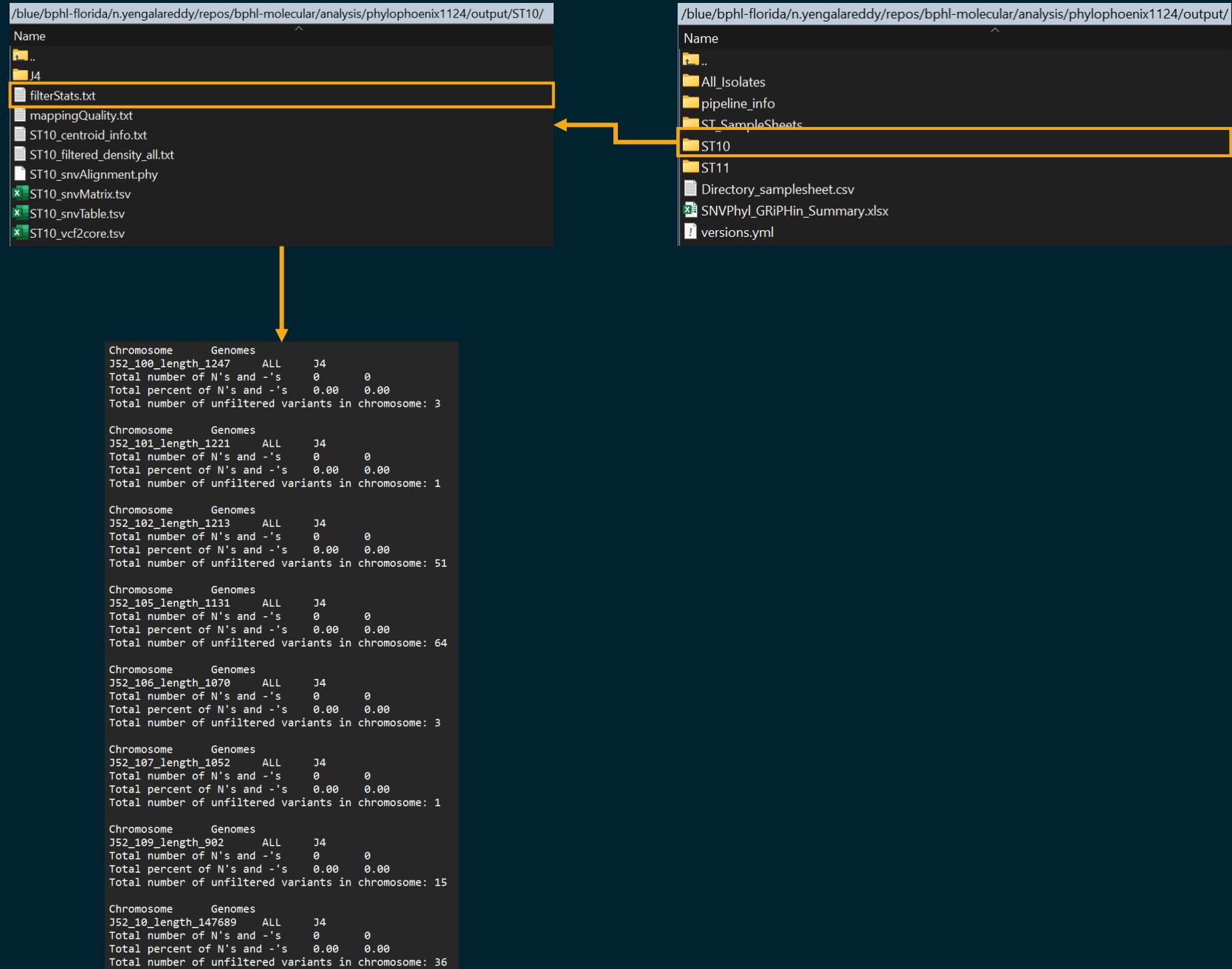
```
|sample,seq_type,assembly_1,assembly_2  
J4_J52,ST10,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output/J4/assembly/J4.filtered.scaffolds.fa.gz,/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/Phoenix0609/phx_output/J52/assembly/J52.filtered.scaffolds.fa.gz
```

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/
Name
..
All_Isolates
pipeline_info
ST_SampleSheets
ST10
ST11
Directory_samplesheet.csv
SNVPhyl_GRiPhin_Summary.xlsx
versions.yml

.../n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/ST_SampleSheets/
Name
..
ST10_samplesheet.csv
ST11_samplesheet.csv



Application Cont.

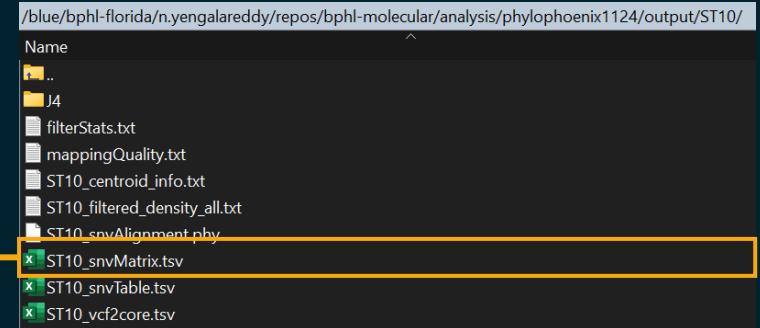


Application Cont.

```
=====Reference Mapping Quality=====
NUMBER OF BP's IN REFERENCE GENOME: 5051000
MINIMUM DEPTH: 10
MINIMUM MAPPING: 80
```

/blue/bphl-florida/n.yengalareddy/repos/bphl-molecular/analysis/phylophoenix1124/output/ST10/
Name
..
J4
filterStats.txt
mappingQuality.txt
ST10_centroid_info.txt
ST10_filtered_density_all.txt
ST10_snvAlignment.phy
x ST10_snvMatrix.tsv
x ST10_snvTable.tsv
x ST10_vcf2core.tsv

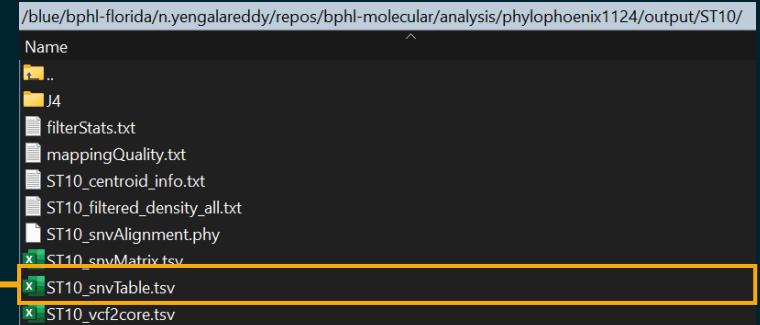
Application Cont.



WGS_ID	J4	J52*
J4	0	5212
J52*	5212	0

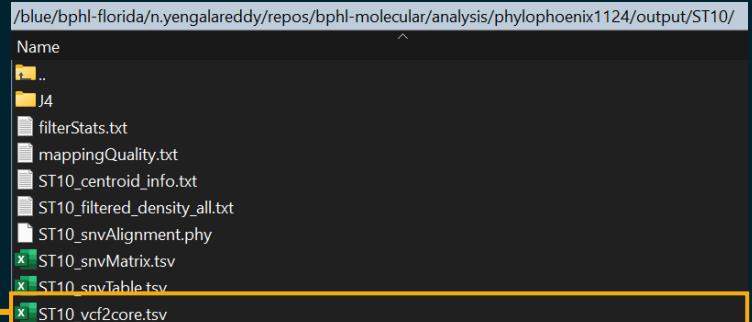
Application Cont.

#Chromosome	Position	Status	Reference	J4
J52_100_length_1247	48	valid	A	T
J52_100_length_1247	286	valid	A	C
J52_100_length_1247	413	filtered-invalid	G	A
J52_101_length_1221	217	valid	A	G
J52_102_length_1213	80	filtered-invalid	A	T
J52_102_length_1213	124	filtered-invalid	G	T
J52_102_length_1213	140	filtered-invalid	G	A
J52_102_length_1213	162	filtered-invalid	A	G
J52_102_length_1213	206	filtered-invalid	C	T
J52_102_length_1213	207	filtered-invalid	A	G
J52_102_length_1213	208	filtered-invalid	A	C
J52_102_length_1213	209	filtered-invalid	C	G
J52_102_length_1213	218	filtered-invalid	T	C
J52_102_length_1213	223	filtered-invalid	A	T
J52_102_length_1213	227	filtered-invalid	A	G
J52_102_length_1213	228	filtered-invalid	A	C
J52_102_length_1213	230	filtered-invalid	T	A
J52_102_length_1213	233	filtered-invalid	G	A
J52_102_length_1213	234	filtered-invalid	C	A
J52_102_length_1213	235	filtered-invalid	A	T
J52_102_length_1213	238	filtered-invalid	C	G
J52_102_length_1213	239	filtered-invalid	G	T
J52_102_length_1213	242	filtered-invalid	T	G
J52_102_length_1213	245	filtered-invalid	T	A
J52_102_length_1213	248	filtered-invalid	A	G
J52_102_length_1213	255	filtered-invalid	C	A
J52_102_length_1213	256	filtered-invalid	T	G
J52_102_length_1213	257	filtered-invalid	G	T
J52_102_length_1213	260	filtered-invalid	G	A
J52_102_length_1213	261	filtered-invalid	A	C
J52_102_length_1213	264	filtered-invalid	T	G
J52_102_length_1213	266	filtered-invalid	T	C



Application Cont.

#Reference name	Total length	Total invalid and excluded positions	Total valid and included positions	Total valid and included positions in core genome	Percentage of valid and included positions in core genome	Percentage of all positions that are valid, included, and part of the core genome	
J52_100_length_1247	1247	906	341	341	100	27.35	
J52_101_length_1221	1221	N/A	1221	1221	100	100	
J52_102_length_1213	1213	324	889	889	100	73.29	
J52_103_length_1191	1191	602	589	1	0.17	0.08	
J52_104_length_1133	1133	N/A	1133	1133	100	100	
J52_105_length_1131	1131	357	774	599	77.39	52.96	
J52_106_length_1070	1070	260	810	0	0	0	
J52_107_length_1052	1052	885	167	30	17.96	2.85	
J52_108_length_1031	1031	N/A	1031	1031	100	100	
J52_109_length_902	902	29	873	806	92.33	89.36	
J52_10_length_147689	147689	608	147081	147081	100	99.59	
J52_110_length_882	882	N/A	882	194	22	22	
J52_111_length_880	880	N/A	880	880	100	100	
J52_112_length_876	876	N/A	876	461	52.63	52.63	
J52_113_length_831	831	N/A	831	808	97.23	97.23	
J52_114_length_755	755	55	700	604	86.29	80	
J52_115_length_747	747	747	0	0 NaN	0	0	
J52_116_length_747	747	747	0	0 NaN	0	0	
J52_117_length_733	733	698	35	35	100	4.77	
J52_118_length_708	708	N/A	708	708	100	100	
J52_119_length_683	683	65	618	390	63.11	57.1	
J52_11_length_142687	142687	1335	141352	139501	98.69	97.77	
J52_120_length_648	648	N/A	648	648	100	100	
J52_121_length_635	635	N/A	635	634	99.84	99.84	
J52_122_length_621	621	381	240	0	0	0	
J52_123_length_610	610	610	0	0 NaN	0	0	
J52_124_length_601	601	N/A	601	473	78.7	78.7	
J52_125_length_597	597	N/A	597	347	58.12	58.12	
J52_126_length_573	573	573	0	0 NaN	0	0	
J52_127_length_573	573	9	564	529	93.79	92.32	
J52_128_length_573	573	573	0	0 NaN	0	0	
J52_129_length_566	566	440	126	0	0	0	
J52_12_length_130470	130470	8182	122288	110624	90.46	84.79	
J52_130_length_565	565	N/A	565	564	99.82	99.82	
J52_131_length_562	562	562	0	0 NaN	0	0	
J52_132_length_545	545	N/A	545	0	0	0	
J52_133_length_538	538	125	413	395	95.64	73.42	
J52_134_length_534	534	398	136	136	100	25.47	



Conclusion

-  Fundamentals of PhyloPHoeNIx
-  Installation and setup of PhyloPHoeNIx in HPG
-  Successfully executed job query for PhyloPHoeNIx
-  Generated output files



Advanced Molecular Detection

Southeast Region Bioinformatics

Questions?

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