

# Recap Exercise 3

# Example output, P11

## Center for Genomic Epidemiology

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### KmerFinder-3.0 Server - Results

KmerFinder 3.0 results:

Template	Num	Score	Expected	Template length	query_coverage	Coverage	Depth	tot_query_coverage
NZ_CP007659.1 Staphylococcus aureus subsp. aureus strain H-EMRSA-15, complete genome	3711	118239	1	123423	96.72	96.67	0.96	96.72
NZ_LS483324.1 Staphylococcus aureus strain NCTC10344 genome assembly, chromosome: 1	3980	2028	46	122530	1.66	1.65	0.02	76.90

# Overview of best hits according to Kmerfinder

	H-EMRSA-15	MSSA476	USA300_TCH1516
P11	X		
P12	X		
P15	X		
P22	X		
P24	X		
P26	X		
HW1	X		
HW2	X		
ERR070035-not-outbreak			X
ERR070041-not-outbreak		X	



ncbi complete genome NZ\_CP007659.1



Alle

Videoer

Billeder

Maps

Shopping

Mere

Indstillinger

Værktøjer

Ca. 38.500 resultater (0,48 sekunder)

### CP007659 - Nucleotide Result - NCBI

<https://www.ncbi.nlm.nih.gov/nucleotide?term=CP007659> - Oversæt denne side

1. Staphylococcus aureus subsp. aureus strain H-EMRSA-15, complete genome 2,846,320 bp circular DNA NZ\_CP007659.1 GI:749295050 2. Staphylococcus ...

Du har besøgt denne side den 26-08-18.

### NZ\_CP007659.1 - NCBI

[https://www.ncbi.nlm.nih.gov/nucleotide/NZ\\_CP007659](https://www.ncbi.nlm.nih.gov/nucleotide/NZ_CP007659) - Oversæt denne side

Staphylococcus aureus subsp. aureus strain H-EMRSA-15, complete genome 2,846,320 bp circular DNA NZ\_CP007659.1 GI:749295050.

Du har besøgt denne side den 26-08-18.

### Genomes - Genome - NCBI

<https://www.ncbi.nlm.nih.gov> > NCBI > Genomes & Maps ▾ Oversæt denne side

Items 1 - 100 of 9567 - ... 19988, SAMN02604235 · PRJNA237 · GCA\_000013425.1, Complete Genome, 2.82136 ..... chromosome:NZ\_CP007659.1/CP007659.1 ...

Nucleotide   Help

[Learn more](#) about upcoming changes to the Nucleotide, EST, and GSS databases.

GenBank

Send to:

Change region shown

- Format
- Summary
- GenBank
- GenBank (full)
- FASTA
- FASTA (text)
- Graphics
- ASN.1
- Revision History
- Accession List
- GI List

## Staphylococcus aureus subsp. aureus strain H-EMRSA-15, complete genome

Customize view

- Basic Features
  - Default features
  - Gene, RNA, and CDS features only
- Features added by NCBI
  - 2836 conserved domains
- Display options
  - Show sequence
  - Show reverse complement

2846320 bp DNA circular BCT 07-JUL-2014  
Staphylococcus aureus subsp. aureus strain H-EMRSA-15, complete

VERSION CP007659.1  
DBLINK BioProject: [PRJNA246435](#)  
BioSample: [SAMN02767598](#)  
KEYWORDS .  
SOURCE Staphylococcus aureus subsp. aureus  
ORGANISM [Staphylococcus aureus subsp. aureus](#)  
Bacteria; Firmicutes; Bacilli; Bacillales; Staphylococcaceae;  
Staphylococcus.  
REFERENCE 1 (bases 1 to 2846320)  
AUTHORS Sabirova,J.S., Xavier,B.B., Hernalsteens,J.P., De Greve,H.,  
Ieven,M., Goossens,H. and Malhotra-Kumar,S.  
TITLE Complete Genome Sequences of Two Prolific Biofilm-Forming  
Staphylococcus aureus Isolates Belonging to USA300 and EMRSA-15

Analyze this sequence

- Run BLAST
- Pick Primers
- Highlight Sequence Features

Related information

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Nucleotide

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FASTA

# Staphylococcus aureus subsp. aureus strain H-EMRSA-15, comp

GenBank: CP007659.1

[GenBank](#) [Graphics](#)

>CP007659.1 Staphylococcus aureus subsp. aureus strain H-EMRSA-15, complete genome

```

CGATTAAGATAGAAATACACGATGCGAGCAATCAAAATTTTCATAACATCACCATGAGTTTGGTCCGAAGC
ATGAGTGTTTACAAATGTTTGAATACCTTATACAGTTCTTATACATACTTTATAAAATTTTCCCAAGCTG
TTTTGATACACTCACTAACAGATACTCTATAGAAGGAAAAGTTATCCACTTATGCACATTTACAGTTTTC
AGAATGTGGATAATTAGAAATTACACACAAAGTTATACTATTTTTAGCAACATATTCACAGGTATTTGA
CATATAGAGAACTGAAAAAGTATAATTGTGTGGATAAGTCGTCCAACTCATGATTTTATAAGGATTTATT
TATTGATATTTACATAAAAATACTGTGCATAACTAATAAGCAGGATAAAAGTTATCCACTGATTGTTATTA
ACTTGTGGATAATTATTAACATGGTGTGTTTAGAAGTTATCCACGGCTGTTATTTTTGTGTATAACTTAA
AAATTTAAGAAAGATGGAGTAAATTTATGTCCGAAAAAGAAATTTGGGAAAAAGTCTTGAATTTGCTCA
AGAAAAATTATCAGCTGTAAGTTACTCAACTTTCCTAAAAGATACTGAACTTTACACGATCAAAGATGGT
GAAGCTATCGTATTATCGAGTATTCCTTTAATGCAAATTTGGTAAATCAAATATGCTGAAATTTATCC
AAGCAATCTTATTTGATGTTGTAGGCTATGAAGTAAACCTCACTTTTACTACTGAAGAATTAGCAAA
TTATAGTAATAATGAACTGCTACTCCAAAAGAAACAACAAACCTTCTACTGAAACAACCTGAGGATAAT
CATGTGCTTGGTAGAGAGCAATTCATGCCCATAACACATTTGACACTTTTGTAAATAGGACCTGGTAACC
GCTTCCACATGCAGCGAGTTTAGCTGTGGCCGAAGCACCAGCCAAAGCGTACAATCCATTATTTATCTA
TGGAGGTGTTGGTTTAGGAAAAACCCATTTAATGCATGCCATTTGGTCATCATGTTTATAGATAATAATCCA
GATGCCAAAGTGATTTACACATCAAGTGAAAAATTCACAAATGAATTTATTAATCAATACGTGATAACG
AAGGTGAAGCTTTCAGAGAAAGATATCGTAATATCGACGTCTTATTAATCGATGATATTCAGTTCATACA
AAATAAAGTACAAAACAAGAAGATTTTTCTATACTTTTTAATGAATTCATCAGAATAACAAGCAAATA

```

Send to:

- Complete Record
- Coding Sequences
- Gene Features

**Choose Destination**

- File
- Clipboard
- Collections
- Analysis Tool

Change region shown

View

sequence

[Pick Primers](#)

[Highlight Sequence Features](#)

### Related information

[Assembly](#)

[BioProject](#)

[BioSample](#)

[Protein](#)

[PubMed](#)

[Taxonomy](#)

# Results of NDtree with all ten isolates

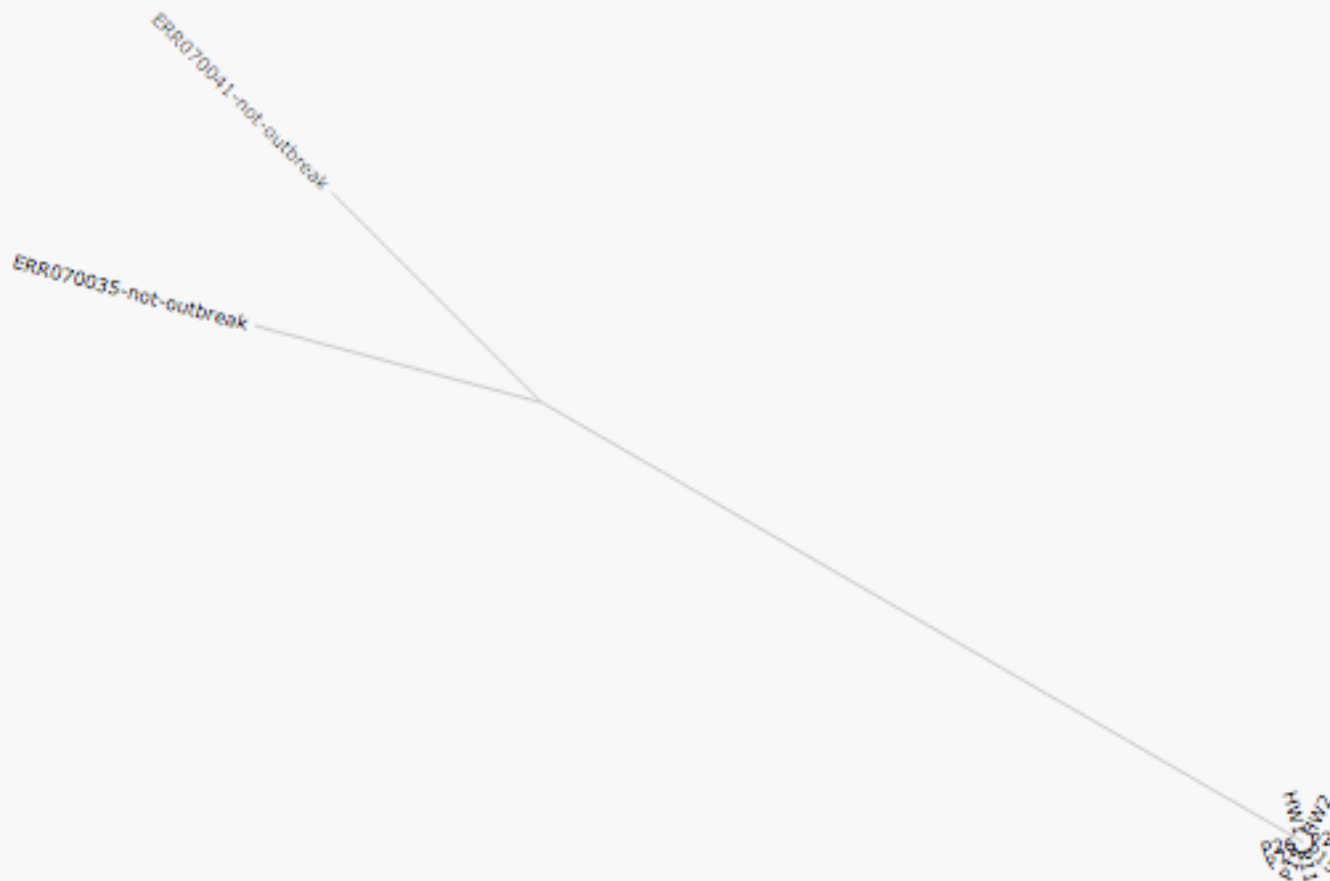
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Download as PNG

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Click [here](#) to modify the tree in the advanced TreeViewer.

### Downloads:

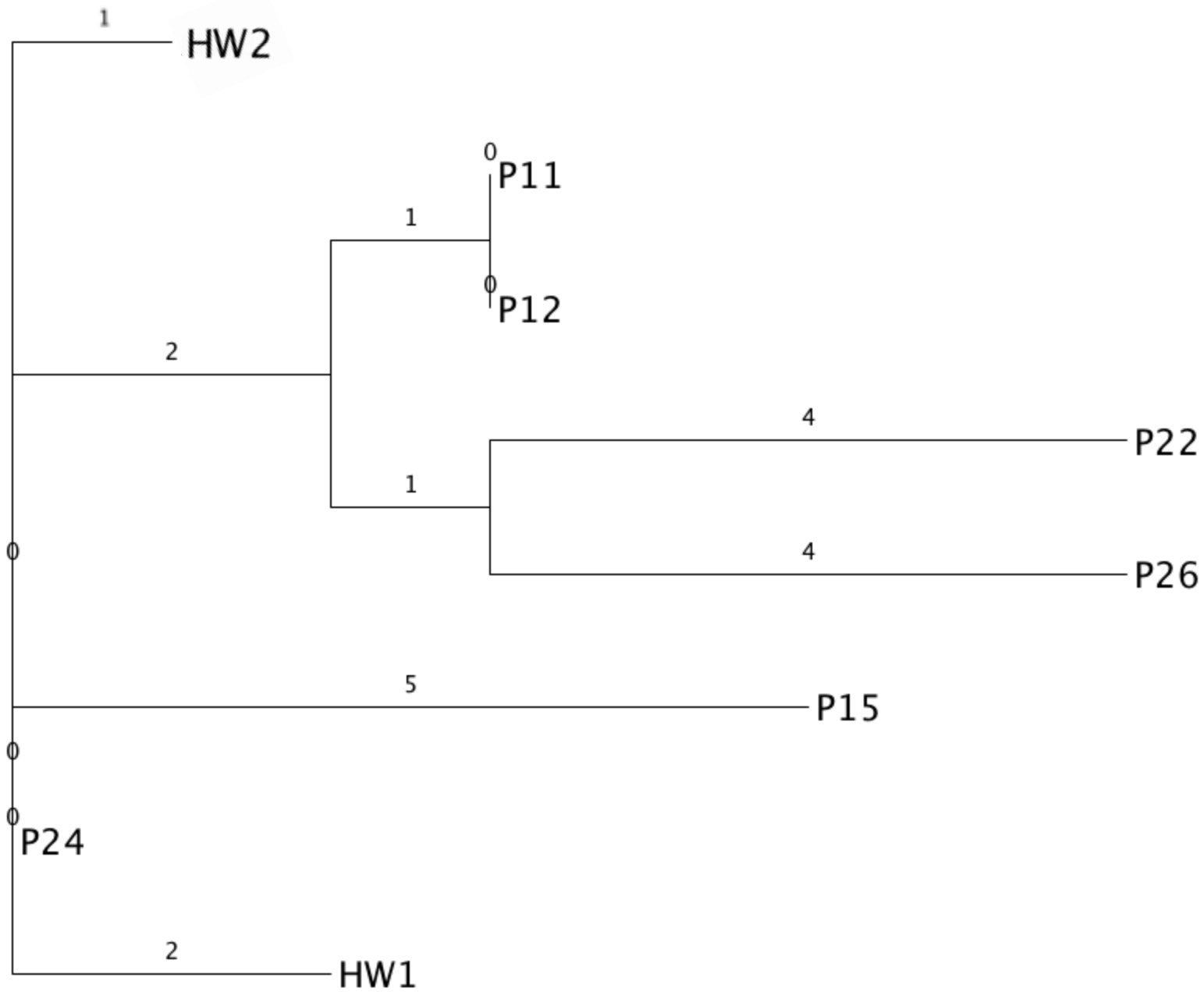
dist.mat.gz

distance.txt.gz

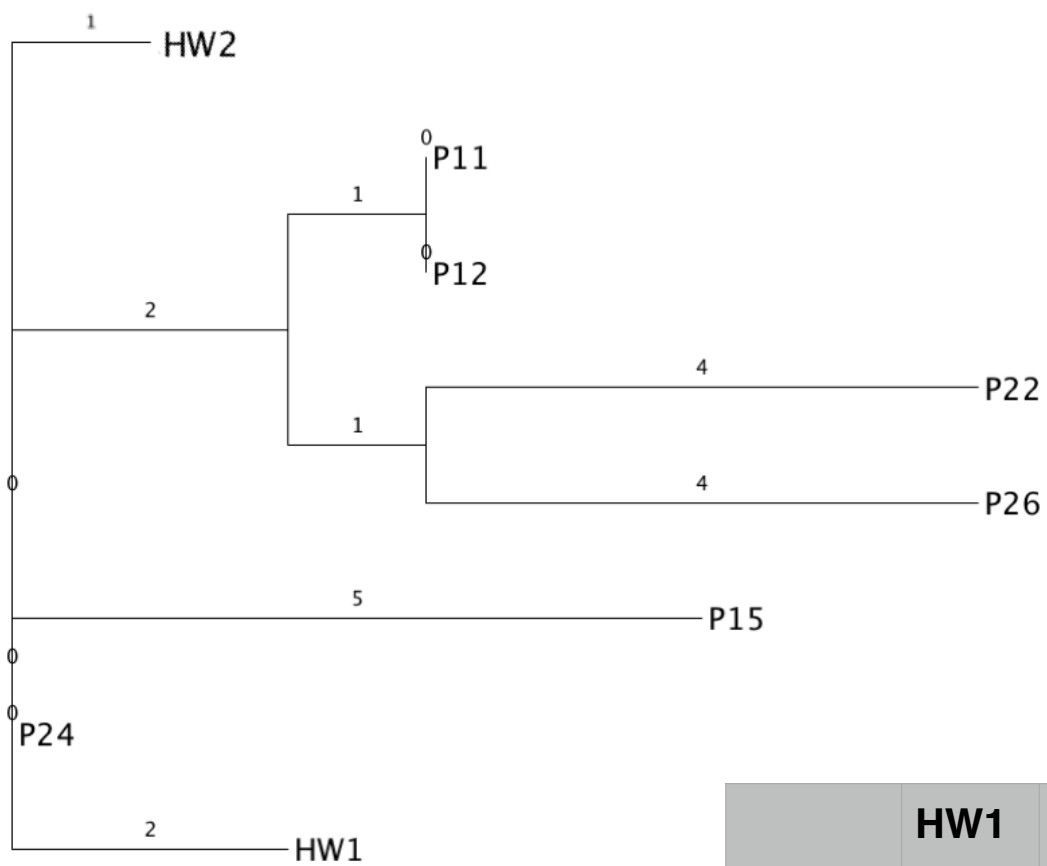
tree.upgma.newick.gz

tree.nj.newick.gz

# NDtree, NJ tree







	HW1	HW2	P11	P12	P15	P22	P24	P26
HW1	0	3	5	5	7	9	2	9
HW2	3	0	4	4	6	8	1	8
P11	5	4	0	0	8	6	3	6
P12	5	4	0	0	8	6	3	6
P15	7	6	8	8	0	12	5	12
P22	9	8	6	6	12	0	7	8
P24	2	1	3	3	5	7	0	7
P26	9	8	6	6	12	8	7	0

Max distance among isolates: 12 (HW1-P22)

**Table 1**

Examples of relatedness criteria for wg/cgMLST and SNP typing schemes of representative clinically relevant bacteria

Organism	Relatedness threshold <sup>a</sup>		References
	wg/cgMLST (allele)	SNPs	
<i>Acinetobacter baumannii</i>	≤8	≤3	[25,26]
<i>Brucella</i> spp.	Epidemiologic validation in progress <sup>b</sup>		<a href="http://www.app">http://www.app</a>
<i>Campylobacter coli</i> , <i>C. jejuni</i>	≤14	≤15	[27,28]
<i>Cronobacter</i> spp.	Epidemiologic validation in progress <sup>b</sup>		<a href="http://www.app">http://www.app</a>
<i>Clostridium difficile</i>	Epidemiologic validation in progress <sup>b</sup>	≤4	[29], <a href="http://www.maths.com/appl">http://www.maths.com/appl</a>
<i>Enterococcus faecium</i>	≤20	≤16	[30]
<i>Enterococcus raffinosus</i>	Epidemiologic validation in progress <sup>b</sup>		<a href="http://www.app">http://www.app</a>
<i>Escherichia coli</i>	≤10	≤10	[31,32], <a href="https://">https://</a>
<i>Francisella tularensis</i>	≤1	≤2	[33,34]
<i>Klebsiella oxytoca</i>	Epidemiologic validation in progress <sup>b</sup>		<a href="http://www.app">http://www.app</a>
<i>Klebsiella pneumonia</i>	≤10	≤18	[35,36]
<i>Legionella pneumophila</i>	≤4	≤15	[37]
<i>Listeria monocytogenes</i>	≤10	≤3	[38,39]
<i>Mycobacterium abscessus</i>		≤30	[40]
<i>Mycobacterium tuberculosis</i>	≤12	≤12	[41]
<i>Neisseria gonorrhoeae</i>	Epidemiologic validation in progress <sup>b</sup>	≤14	[42], <a href="http://www">http://www</a>
<i>Neisseria meningitidis</i>	Epidemiologic validation in progress <sup>b</sup>		<a href="http://www.cgn">http://www.cgn</a>
<i>Pseudomonas aeruginosa</i>	≤14	≤37	[31,43]
<i>Salmonella dublin</i>	Epidemiologic validation in progress <sup>b</sup>	≤13	[44], <a href="https://ent">https://ent</a>
<i>Salmonella enterica</i>	Epidemiologic validation in progress <sup>b</sup>	≤4	[45], <a href="http://www.maths.com/appl">http://www.maths.com/appl</a>
<i>Salmonella typhimurium</i>	Epidemiologic validation in progress <sup>b</sup>	≤2	[46], <a href="https://ent">https://ent</a>
<i>Staphylococcus aureus</i>	≤24	≤15	[47,48]
<i>Streptococcus suis</i>		≤21	[49]
<i>Vibrio parahaemolyticus</i>	≤10		[50]
<i>Yersinia</i> spp.	0		[51]

# CSIPhylogeny, distance matrix that includes the two non-outbreak strains

	<b>ERR070035- not- outbreak</b>	<b>ERR07004 1-not- outbreak</b>	<b>HW-1</b>	<b>HW-2</b>	<b>P11</b>	<b>P12</b>	<b>P15</b>	<b>P22</b>	<b>P24</b>	<b>P26</b>
<b>ERR070035- not- outbreak</b>	0	10114	15617	15614	15613	15612	15616	15614	15616	15613
<b>ERR070041- not- outbreak</b>	10114	0	15421	15418	15417	15416	15420	15418	15420	15417
<b>HW-1</b>	15617	15421	0	7	8	11	9	13	9	12
<b>HW-2</b>	15614	15418	7	0	5	8	4	10	4	9
<b>P11</b>	15613	15417	8	5	0	5	7	9	7	8
<b>P12</b>	15612	15416	11	8	5	0	8	8	10	9
<b>P15</b>	15616	15420	9	4	7	8	0	10	6	11
<b>P22</b>	15614	15418	13	10	9	8	10	0	12	9
<b>P24</b>	15616	15420	9	4	7	10	6	12	0	11
<b>P26</b>	15613	15417	12	9	8	9	11	9	11	0

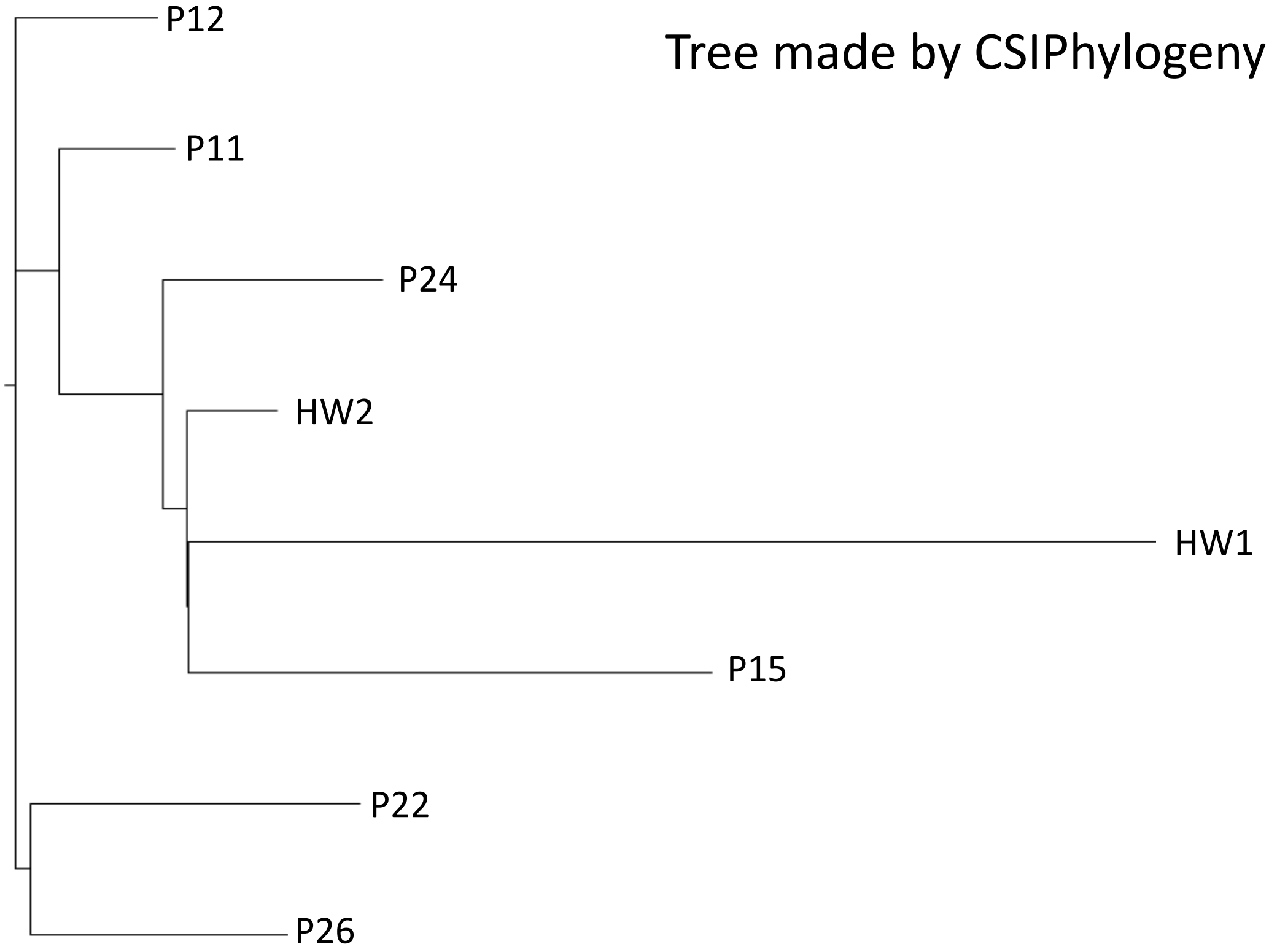
Distance matrix generated when non-outbreak strains were part of analysis  
(but have here been deleted for simplicity)

	HW-1	HW-2	P11	P12	P15	P22	P24	P26
HW-1	0	7	8	11	9	13	9	12
HW-2	7	0	5	8	4	10	4	9
P11	8	5	0	5	7	9	7	8
P12	11	8	5	0	8	8	10	9
P15	9	4	7	8	0	10	6	11
P22	13	10	9	8	10	0	12	9
P24	9	4	7	10	6	12	0	11

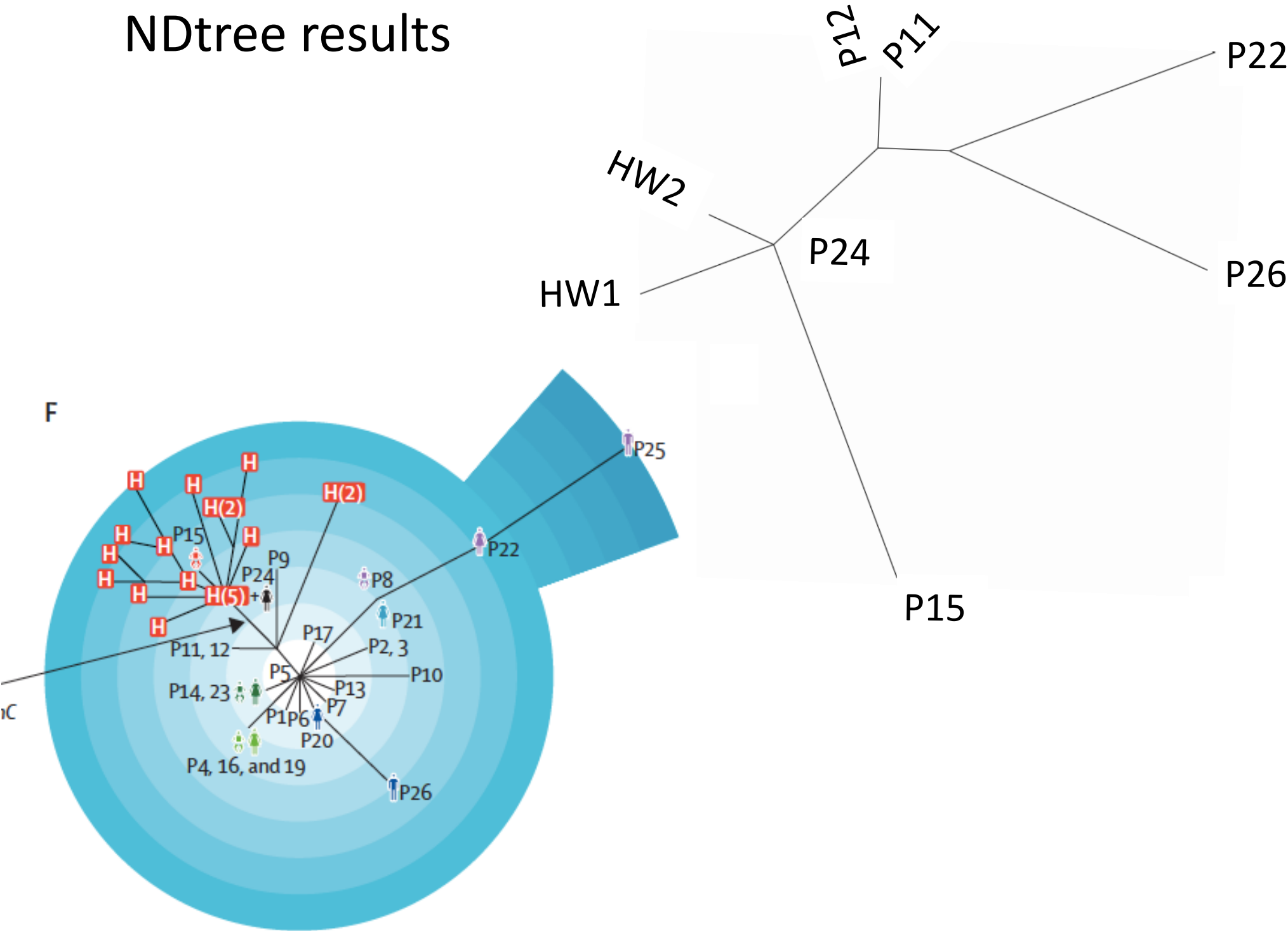
Distance matrix generated when non-outbreak strains are omitted

	HW-1	HW-2	P11	P12	P15	P22	P24	P26
HW-1	0	18	20	22	23	24	20	22
HW-2	18	0	8	10	13	14	8	12
P11	20	8	0	6	17	12	10	10
P12	22	10	6	0	17	10	12	10
P15	23	13	17	17	0	21	17	21
P22	24	14	12	10	21	0	12	12

# Tree made by CSIPhylogeny



# NDtree results



# CSIPhylogeny results

