

Recap Exercise 3

Example output, HW1

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KmerFinder 2.0 results:								
Hit	Score	z-score	Query Coverage [%]	Template Coverage [%]	Depth	Total Query Coverage [%]	Total Template Coverage [%]	Total Depth
Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus subsp. aureus HO 5096 0412 get sequence	6781	559.2	97.41	97.47	0.97	97.41	97.47	0.97
Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus subsp. aureus MRSA252 get sequence	77	55.3	1.11	1.07	0.01	75.76	73.39	0.73

Overview of best hits according to Kmerfinder

	HO 5096 0412	MSSA476	USA300_FPR3757
P11	X		
P12	X		
P15	X		
P22	X		
P24	X		
P26	X		
HW1	X		
HW2	X		
ERR070035-not-outbreak			X
ERR070041-not-outbreak		X	

Results of NDtree with all ten isolates

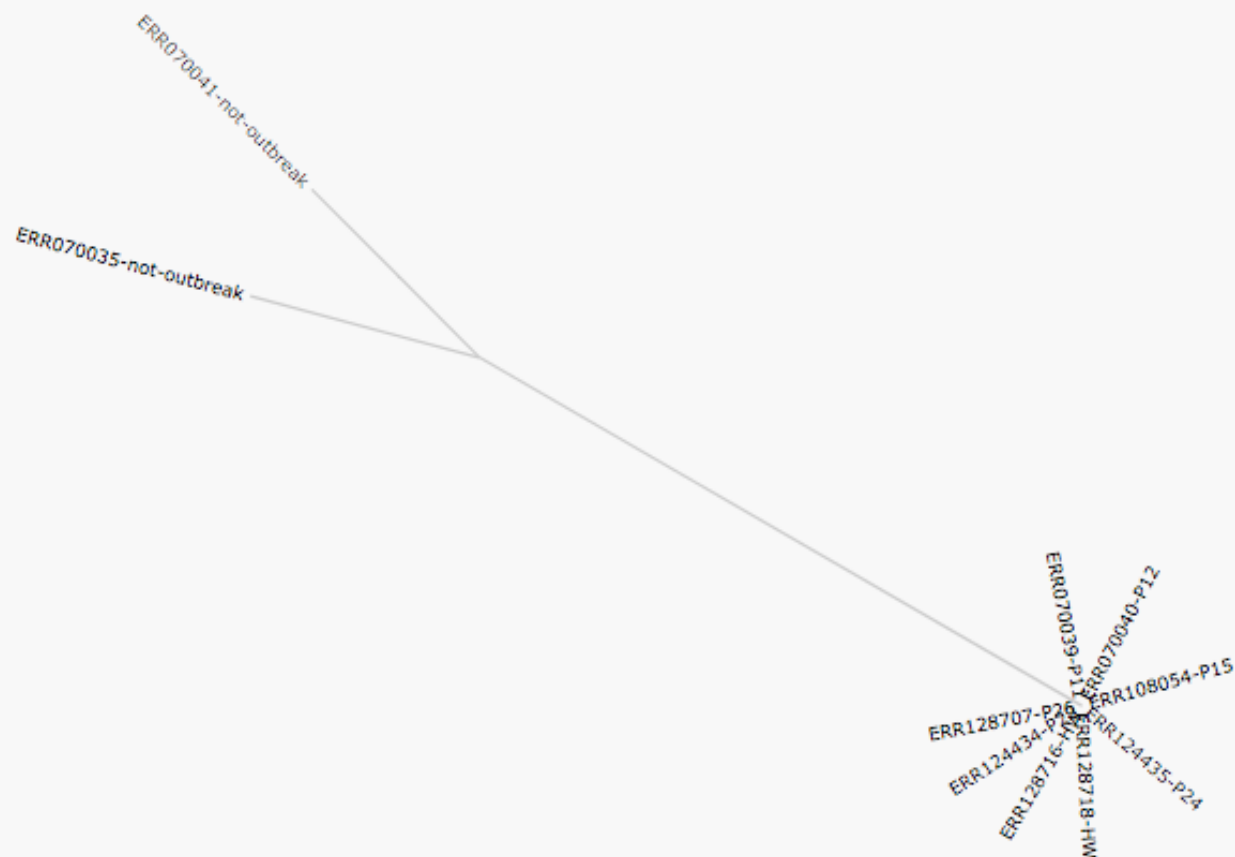
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Click [here](#) to modify the tree in the advanced TreeViewer.

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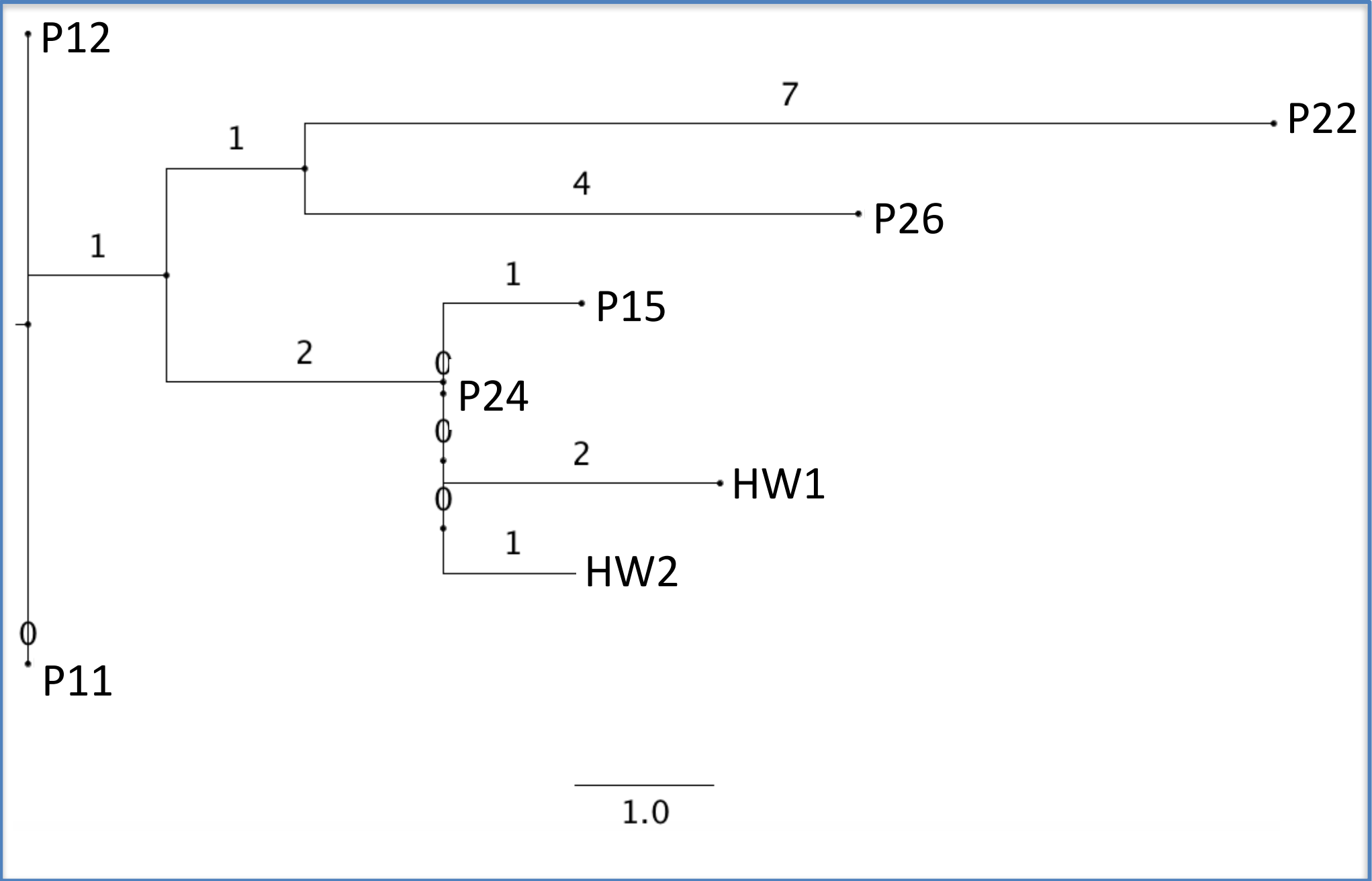
dist.mat.gz

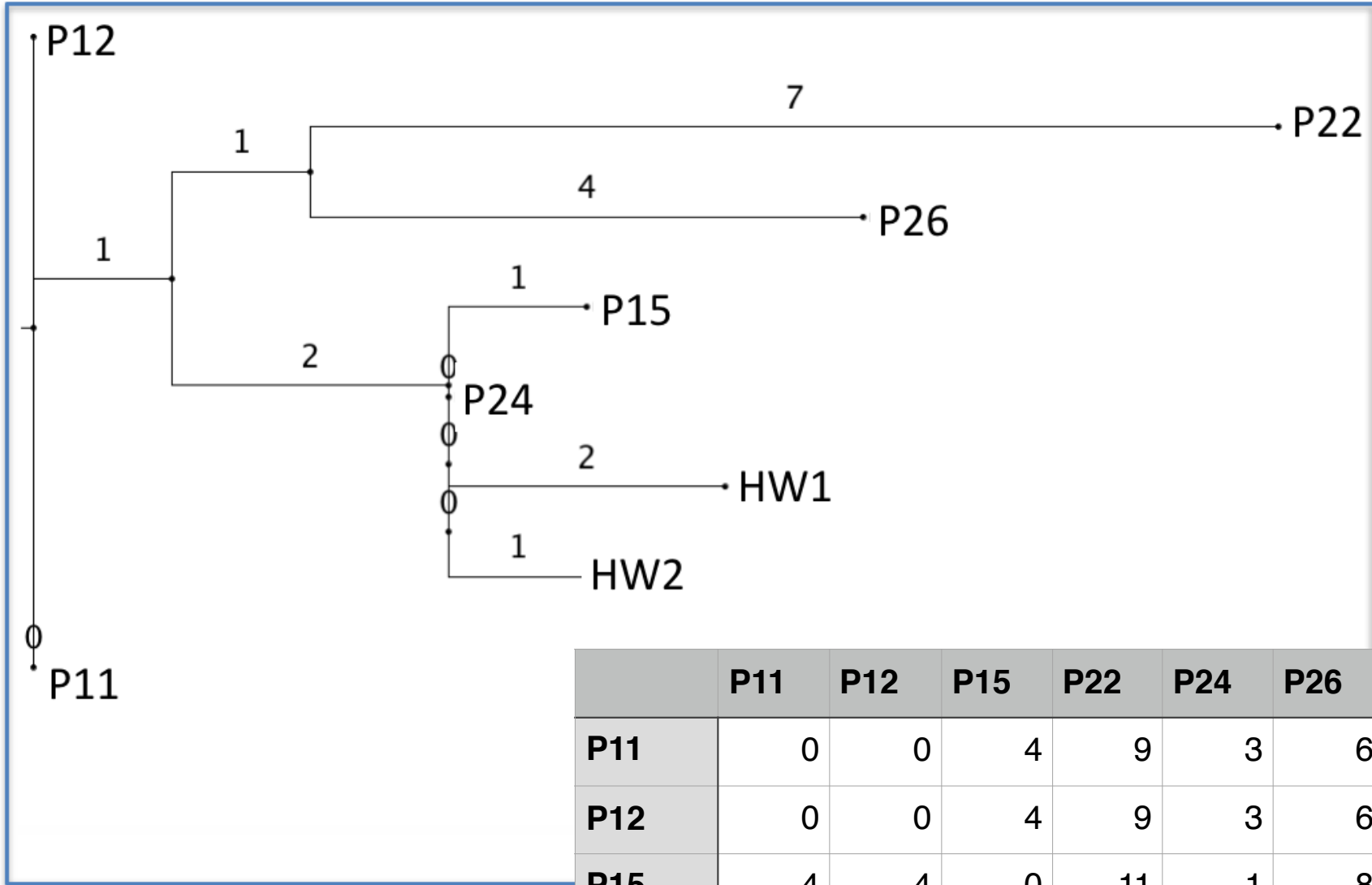
distance.txt.gz

tree.upgma.newick.gz

tree.nj.newick.gz

NDtree, NJ tree





	P11	P12	P15	P22	P24	P26	HW1	HW2
P11	0	0	4	9	3	6	5	4
P12	0	0	4	9	3	6	5	4
P15	4	4	0	11	1	8	3	2
P22	9	9	11	0	10	11	12	11
P24	3	3	1	10	0	7	2	1
P26	6	6	8	11	7	0	9	8
HW1	5	5	3	12	2	9	0	3
HW2	4	4	2	11	1	8	3	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 ^a		References
	wg/cgMLST (allele)	SNPs	
<i>Acinetobacter baumannii</i>	≤8	≤3	[25,26]
<i>Brucella</i> spp.	Epidemiologic validation in progress ^b		http://www.app
<i>Campylobacter coli</i> , <i>C. jejuni</i>	≤14	≤15	[27,28]
<i>Cronobacter</i> spp.	Epidemiologic validation in progress ^b		http://www.app
<i>Clostridium difficile</i>	Epidemiologic validation in progress ^b	≤4	[29], http://www.maths.com/appl
<i>Enterococcus faecium</i>	≤20	≤16	[30]
<i>Enterococcus raffinosus</i>	Epidemiologic validation in progress ^b		http://www.app
<i>Escherichia coli</i>	≤10	≤10	[31,32], https://
<i>Francisella tularensis</i>	≤1	≤2	[33,34]
<i>Klebsiella oxytoca</i>	Epidemiologic validation in progress ^b		http://www.app
<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 ^b	≤14	[42], http://www
<i>Neisseria meningitidis</i>	Epidemiologic validation in progress ^b		http://www.cgn
<i>Pseudomonas aeruginosa</i>	≤14	≤37	[31,43]
<i>Salmonella dublin</i>	Epidemiologic validation in progress ^b	≤13	[44], https://ent
<i>Salmonella enterica</i>	Epidemiologic validation in progress ^b	≤4	[45], http://www.maths.com/appl
<i>Salmonella typhimurium</i>	Epidemiologic validation in progress ^b	≤2	[46], https://ent
<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

	ERR070035- not- outbreak	P11	P12	ERR070041- not- outbreak	P15	P22	P24	P26	HW-1	HW-2
ERR070035- not- outbreak	0	15606	15605	10112	15609	15607	15609	15606	15610	15607
P11	15606	0	5	15414	7	9	7	8	8	5
P12	15605	5	0	15413	8	8	10	9	11	8
ERR070041- not- outbreak	10112	15414	15413	0	15417	15415	15417	15414	15418	15415
P15	15609	7	8	15417	0	10	6	11	9	4
P22	15607	9	8	15415	10	0	12	9	13	10
P24	15609	7	10	15417	6	12	0	11	9	4
P26	15606	8	9	15414	11	9	11	0	12	9
HW-1	15610	8	11	15418	9	13	9	12	0	7
HW-2	15607	5	8	15415	4	10	4	9	7	0

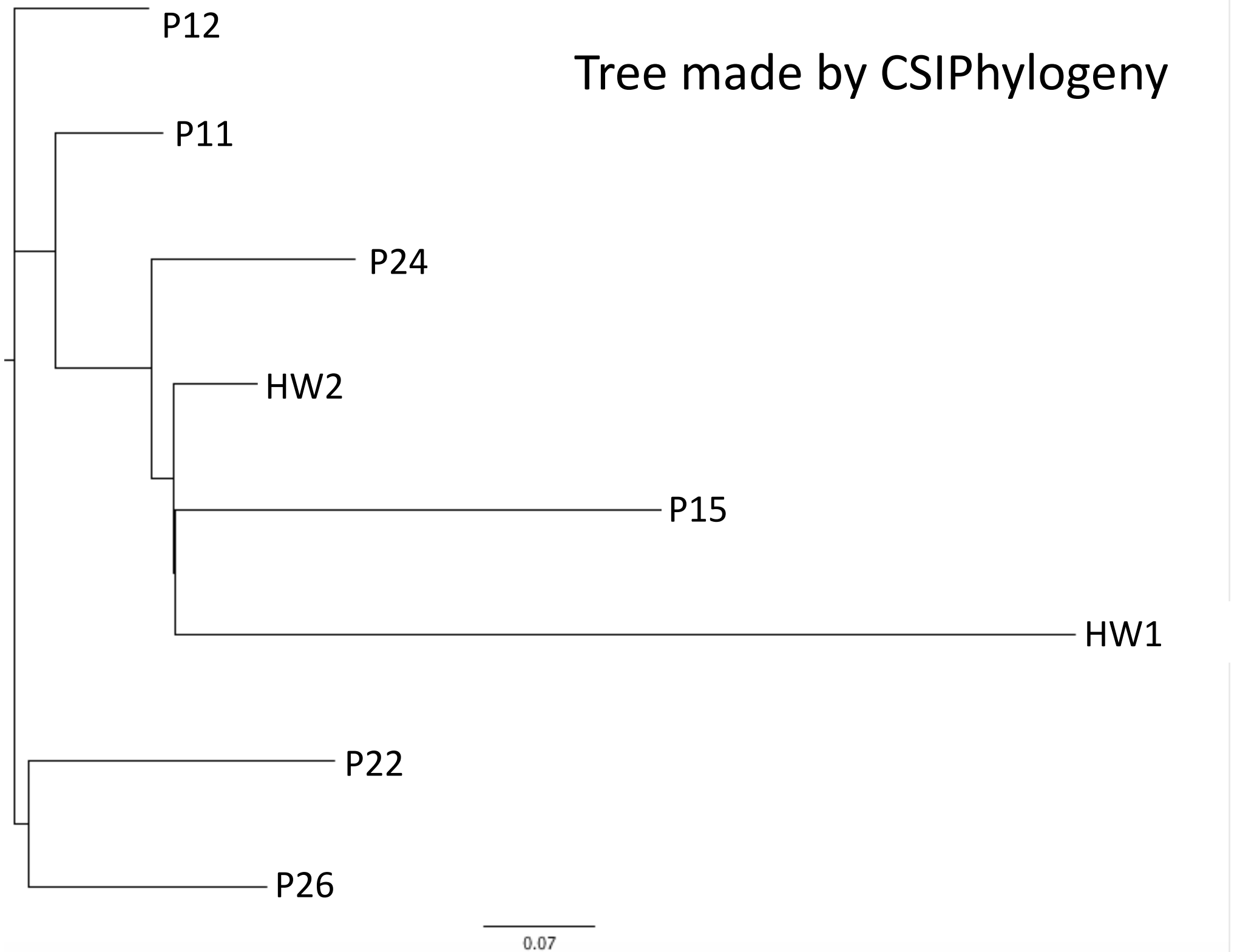
Distance matrix generated when non-outbreak strains were part of analysis
(but have here been deleted for simplicity)

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

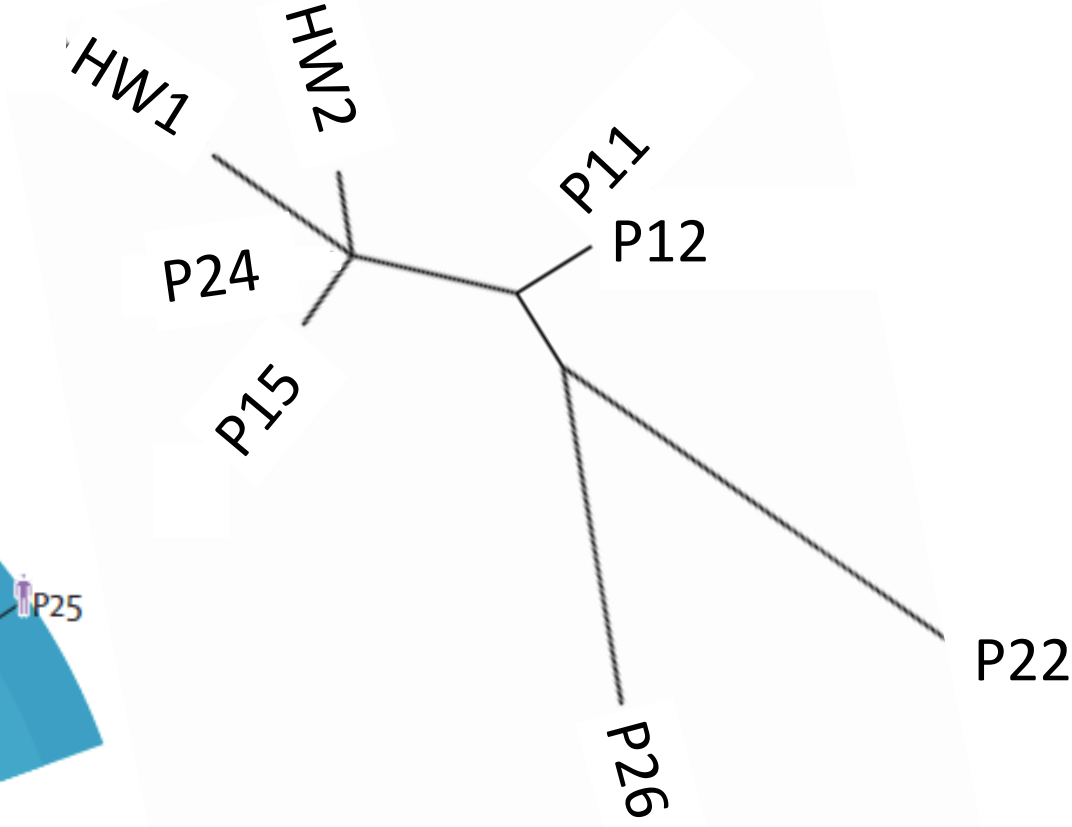
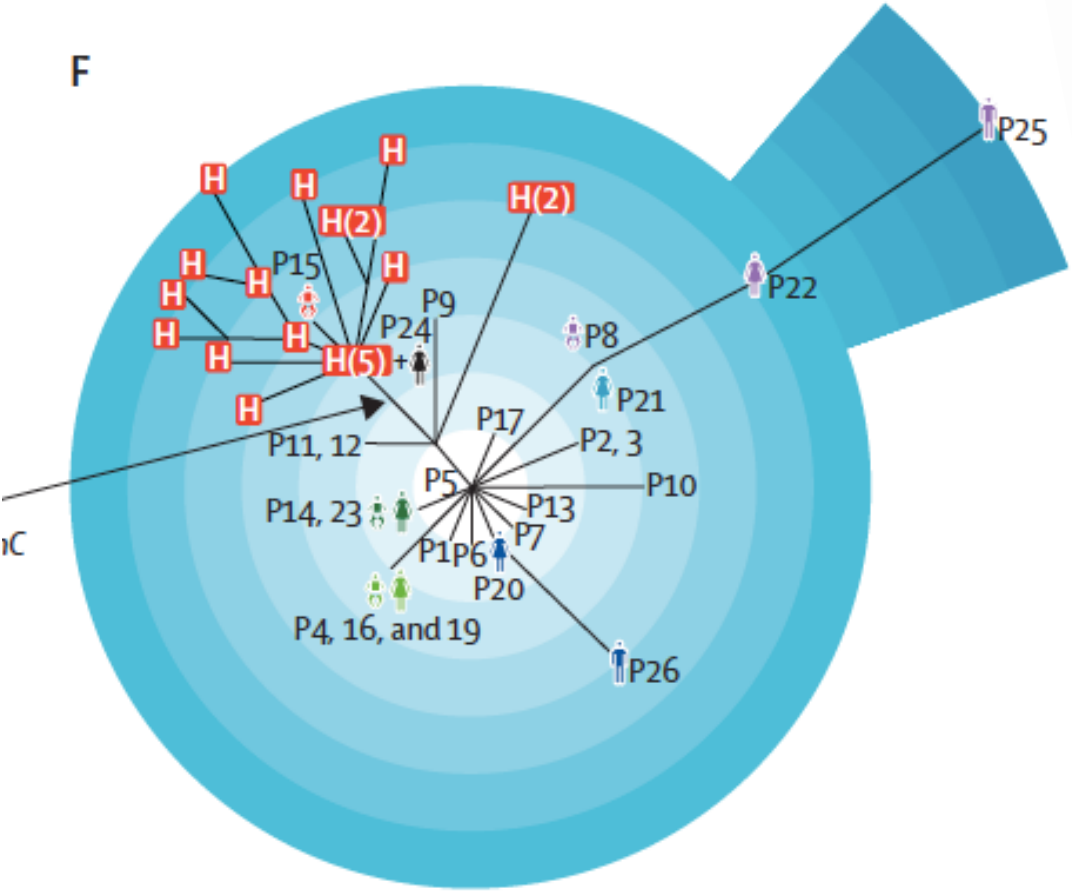
Distance matrix generated when non-outbreak strains are omitted

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

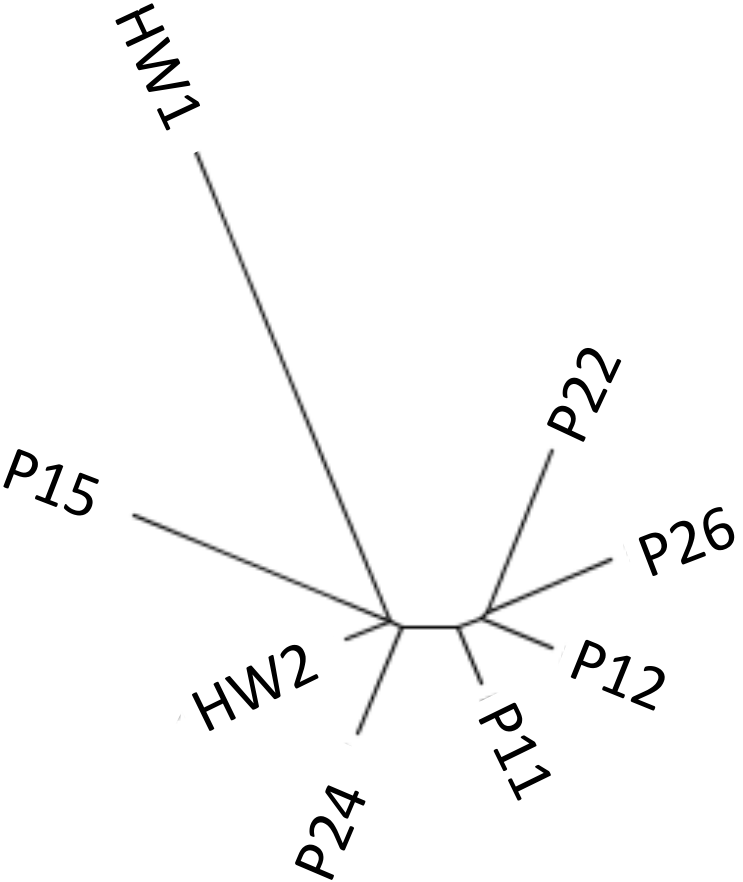
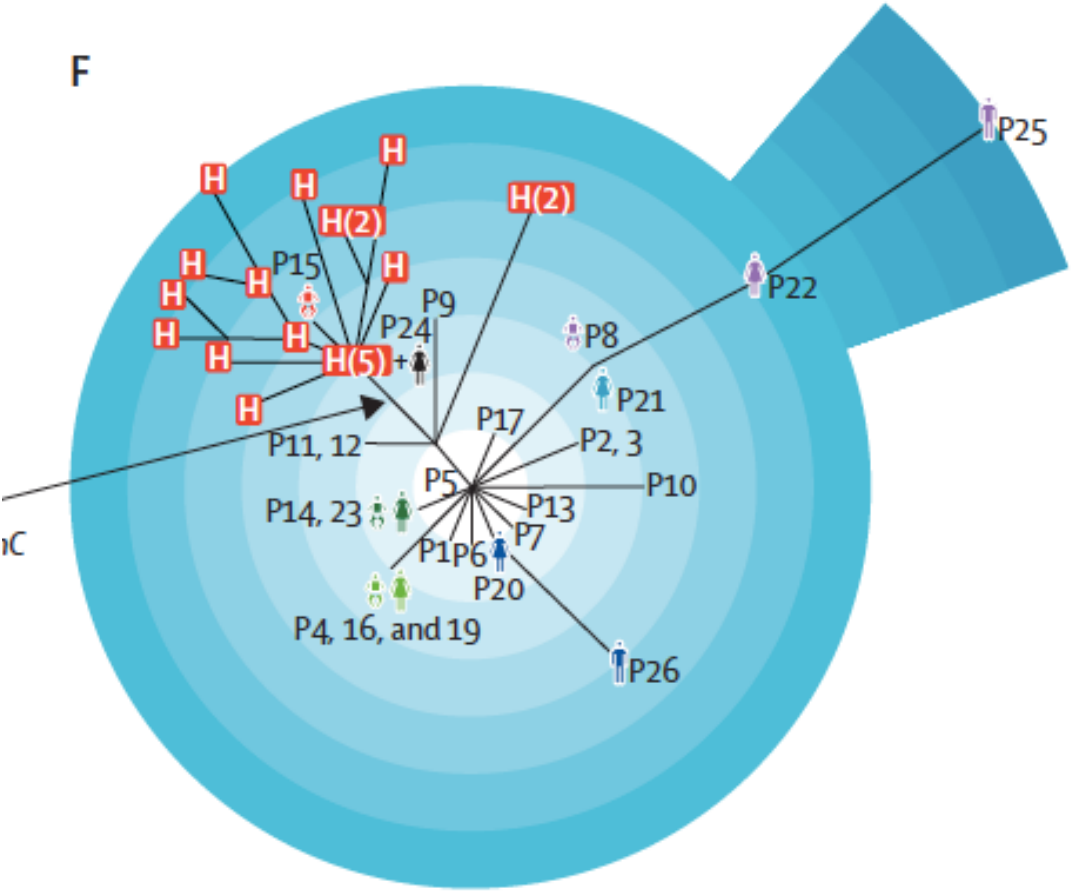
Tree made by CSIPhylogeny



NDtree results

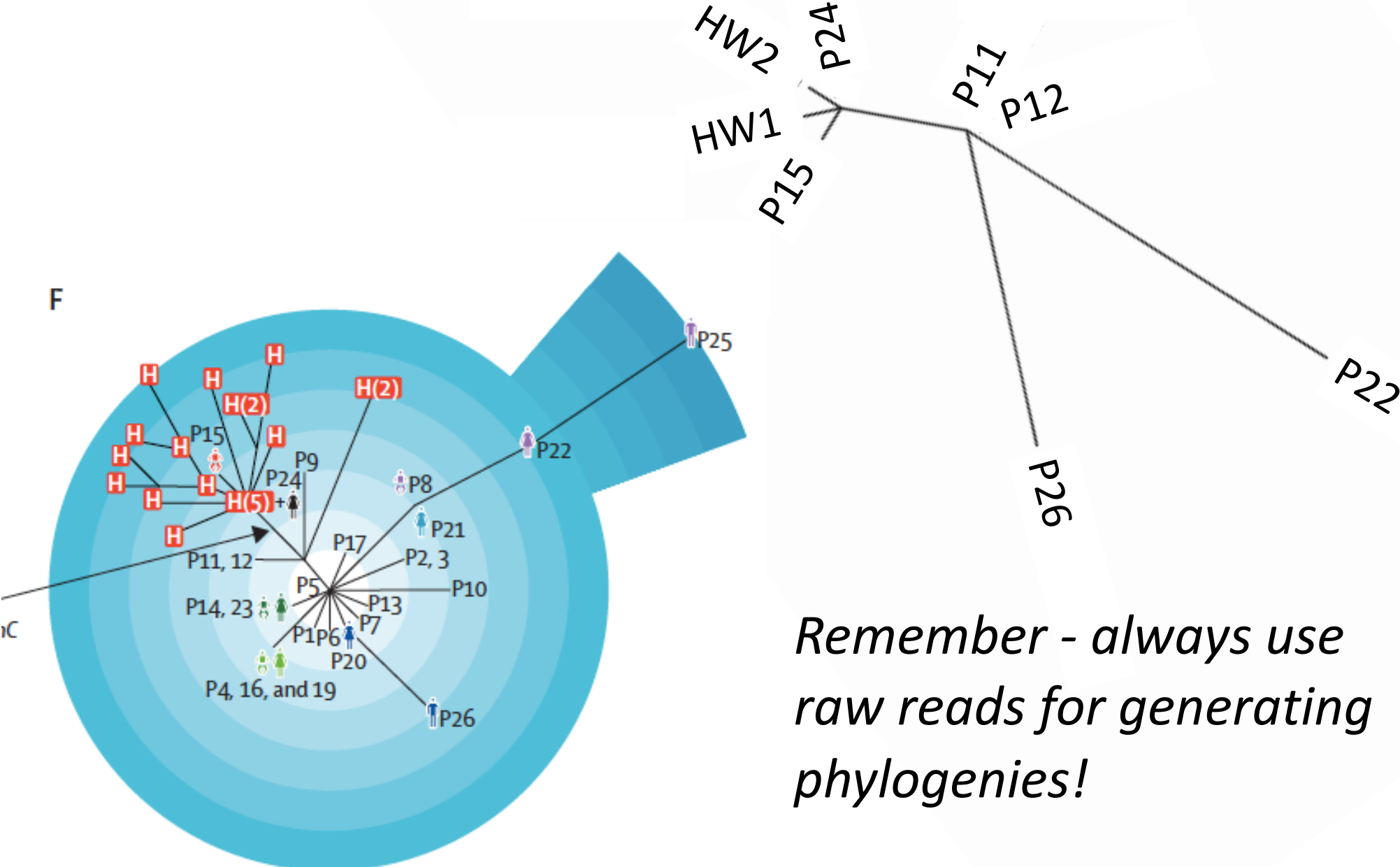


CSIPhylogeny results



Doesn't fit!

CSIPhylogeny results - Raw reads



Remember - always use raw reads for generating phylogenies!