

1. What is the species of the five unknown samples ?

- ☐ *Salmonella enterica*
- ☒ *Escherichia coli*
- ☐ *Vibrio cholera*
- ☐ *Campylobacter jejuni*

2. Which samples have the same ST-type ? (please chose all options that have the same ST-type)

- ☒ 1
- ☐ 4
- ☒ 2
- ☒ 3

3. Which unknown samples contain plasmid ? (please chose one or more correct options)

☒ 1

☐ 2

☒ 3

☐ 4

☒ 5

4. Which samples **DO NOT** contain genes conferred to beta-lactam resistance ? (please chose one or more correct options)

☒ 4

☐ 3

☒ 2

☐ 1

5. Why do you need a reference genome for construct SNP phylogenetic tree ?

- ☐ To do reference based assembly
- ☐ To include in phylogenetic tree
- ☒ To identify SNPs
- ☐ To identify genes

6. Which unknown sample is the most distantly related strain ?

- ☐ 1
- ☐ 2
- ☐ 3
- ☒ 4
- ☐ 5

7. From the answer of question 6. Why is the strain the most distantly related ? (please chose one or more correct options)

- ☒ It has the most number of SNPs differences
- ☒ In SNP phylogenetic tree, It's clustered far away from other samples
- ☐ It is different species
- ☒ It has different ST type

8. Which unknown samples are outbreak strains (clonal strains) ? (please chose one or more correct options)

- ☒ 1
- ☐ 2
- ☒ 3
- ☐ 4
- ☒ 5

9. From the question 8. Why did you make decision that those strains are outbreak or clonal ? (please chose one or more correct options)

- ☐ They have different ST-type
- ☒ They have the same ST-type
- ☒ They have the same resistance profile
- ☒ They are clustered closely in phylogenetic tree and have much lower number of SNP differences compared to other non-outbreak strains.

10. One of the strains has the same ST-type as the three outbreak strains. Why is that strain not part of the outbreak ? (please chose one or more correct options)

- ☒ It doesn't have any plasmids
- ☒ It has relatively high number of SNP differences compared to outbreak strains
- ☒ It has different resistance profile
- ☐ It is different species