

BIOTIA-DX OUTBREAK  
COMPREHENSIVE ANALYSIS RESULTS

| ORDERING                                                                                                                                               | SAMPLE                                                                                                                         | DETAILS                                    |
|--------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------|
| Institution: Example General Hospital<br>Physician: Dr. John Smith<br>Address: 123 Medical Center Dr San Francisco CA 94105<br>Phone Number:<br>Email: | Specimen Type: Blood Sample<br>Collection Date: 2024-01-15<br><br>Received By Lab:<br><br>Run Date:<br>Report Date: 09/24/2025 | Accession Number: GEN2024002<br><br>Notes: |

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Summary

This report contains results of Bacterial Strain Typing by Whole Genome Sequencing performed on isolates. In total, 62 isolates were analyzed with 62 isolates new to this analysis. Isolates were compared to 3 reference genomes.  
All isolates were identified as *Klebsiella pneumoniae* .  
11 sequence types were identified with 10 cgMLST clusters.

Species Identification Analysis Report

Sequence Types are related groups of isolates as determined by MLST. For *Klebsiella pneumoniae* isolates to be given the same sequence type, they must have the same allelic profile. All isolates with a profile in PubMLST are assigned a sequence type, but not all sequence types will have more than one isolate. MLST sequence type assignments are as follows:

- ST 45: SRR34402737 and SRR34402736 .  
ST 147: SRR21822770, SRR21822769, SRR21822763, SRR21822764 , SRR21822756, SRR21822752 , SRR21822758, SRR21822760, SRR21822767 , SRR21822755, SRR21822765 , SRR21822757 , SRR21822762 , SRR21822768 , SRR21822771 , SRR21822766, SRR21822754 , SRR21822759, SRR21822753 , SRR21822761 and SRR21822772 .  
ST 307: SRR34402796, SRR34402800, SRR34402788, SRR34402791 , SRR34402795 , SRR34402798, SRR34402792 , SRR34402790, SRR34402789, SRR34402797 , SRR34402793 , SRR34402799 and SRR34402787.  
ST 20: SRR34402785 and SRR34402786.  
ST 3340: SRR34402807 and SRR34402808 .  
ST 584: SRR34402747 , SRR34402743 , SRR34402744, SRR34402746, SRR34402745 and SRR34402748.  
ST 13: SRR34402810 , SRR34402809 and SRR34402811 .  
ST 25: SRR34402734, SRR34402733 and SRR34402735.  
ST 39: SRR34402749, SRR34402750 and SRR34402784 .  
ST 54: SRR34402803, SRR34402804, SRR34402806 , SRR34402801 and SRR34402802.  
ST 26: SRR34402741 and SRR34402742.

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### cgMLST Analysis Report

#### Description of Complexes

In total, 10 complexes were identified through cgMLST. Isolates in the same cluster are closely genetically related, more so than isolates with only the same sequence type.

For *Klebsiella pneumoniae* isolates to be in the same cluster, there must be fewer than 15 allelic differences between them. Isolates are only assigned a cluster type if more than one isolate is present in the cluster. The following complexes were identified:

**Complex 1:** SRR21822752 , SRR21822753 , SRR21822754 , SRR21822755, SRR21822756, SRR21822758, **SRR21822757** , SRR21822759, SRR21822760, **SRR21822761** , **SRR21822762** , SRR21822763, **SRR21822765** , **SRR21822767** , SRR21822770, **SRR21822771** , SRR21822766, **SRR21822764** and SRR21822769.

**Complex 2:** SRR34402733, SRR34402734 and SRR34402735.

**Complex 3:** **SRR34402736** and SRR34402737.

**Complex 4:** **SRR34402743** , SRR34402744, **SRR34402747** , **SRR34402745** , SRR34402746 and SRR34402748.

**Complex 5:** SRR34402749, **SRR34402750** and **SRR34402784** .

**Complex 6:** **SRR34402785** and SRR34402786.

**Complex 7:** SRR34402787, SRR34402790, SRR34402788, SRR34402789, SRR34402800, **SRR34402793** , **SRR34402791** , **SRR34402792** , **SRR34402795** , SRR34402796, **SRR34402797** , SRR34402798 and **SRR34402799** .

**Complex 8:** **SRR34402801** , SRR34402802, SRR34402803, SRR34402804 and **SRR34402806** .

**Complex 9:** **SRR34402807** and **SRR34402808** .

**Complex 10:** SRR34402809, **SRR34402810** and **SRR34402811** .

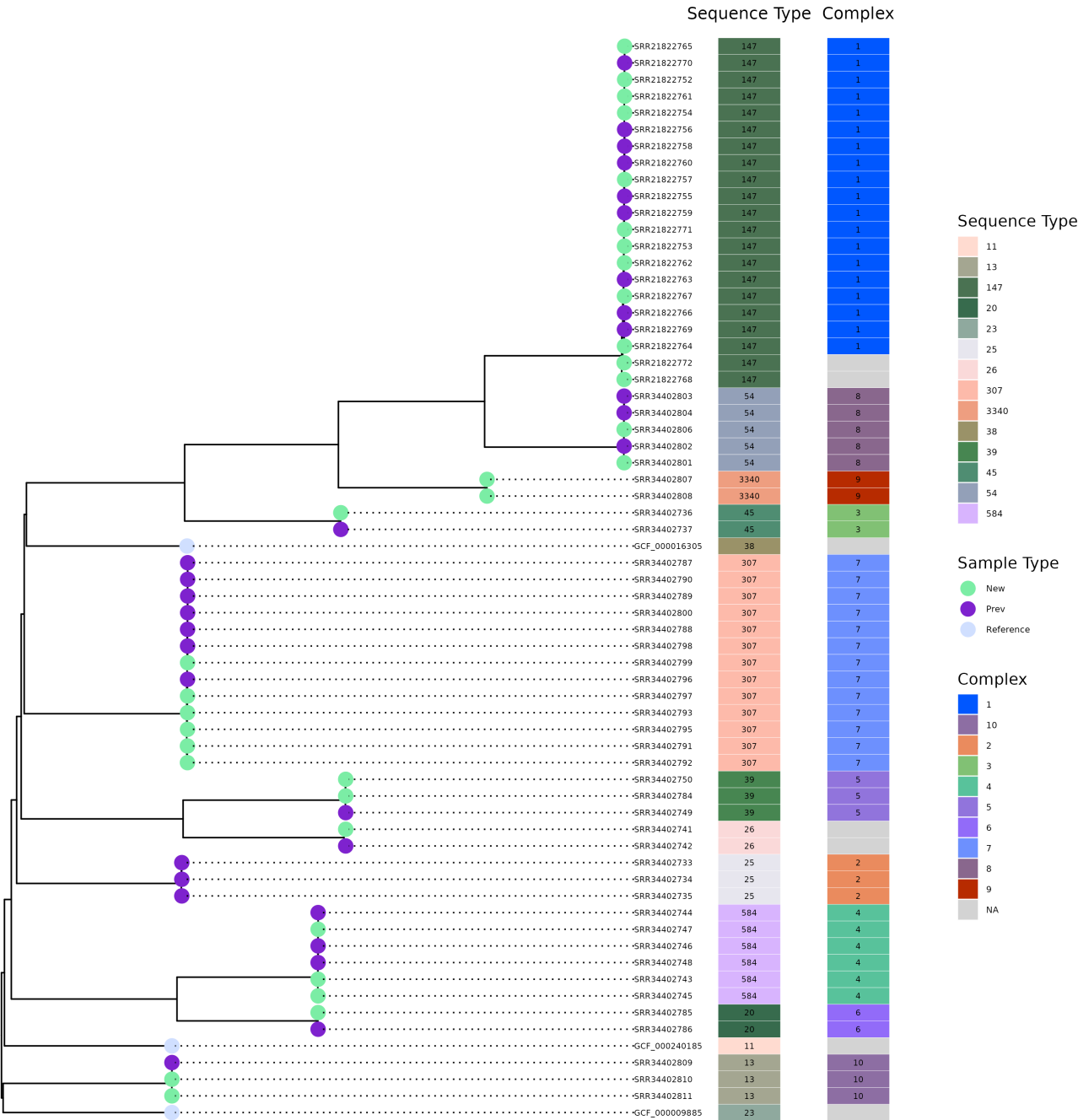
The following samples were not grouped into any complex:

**SRR21822768** , **SRR21822772** , **SRR34402741** , SRR34402742.

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Phylogenetic Tree of Profile Distances

UPGMA tree built from allelic distance matrix including three reference genomes.

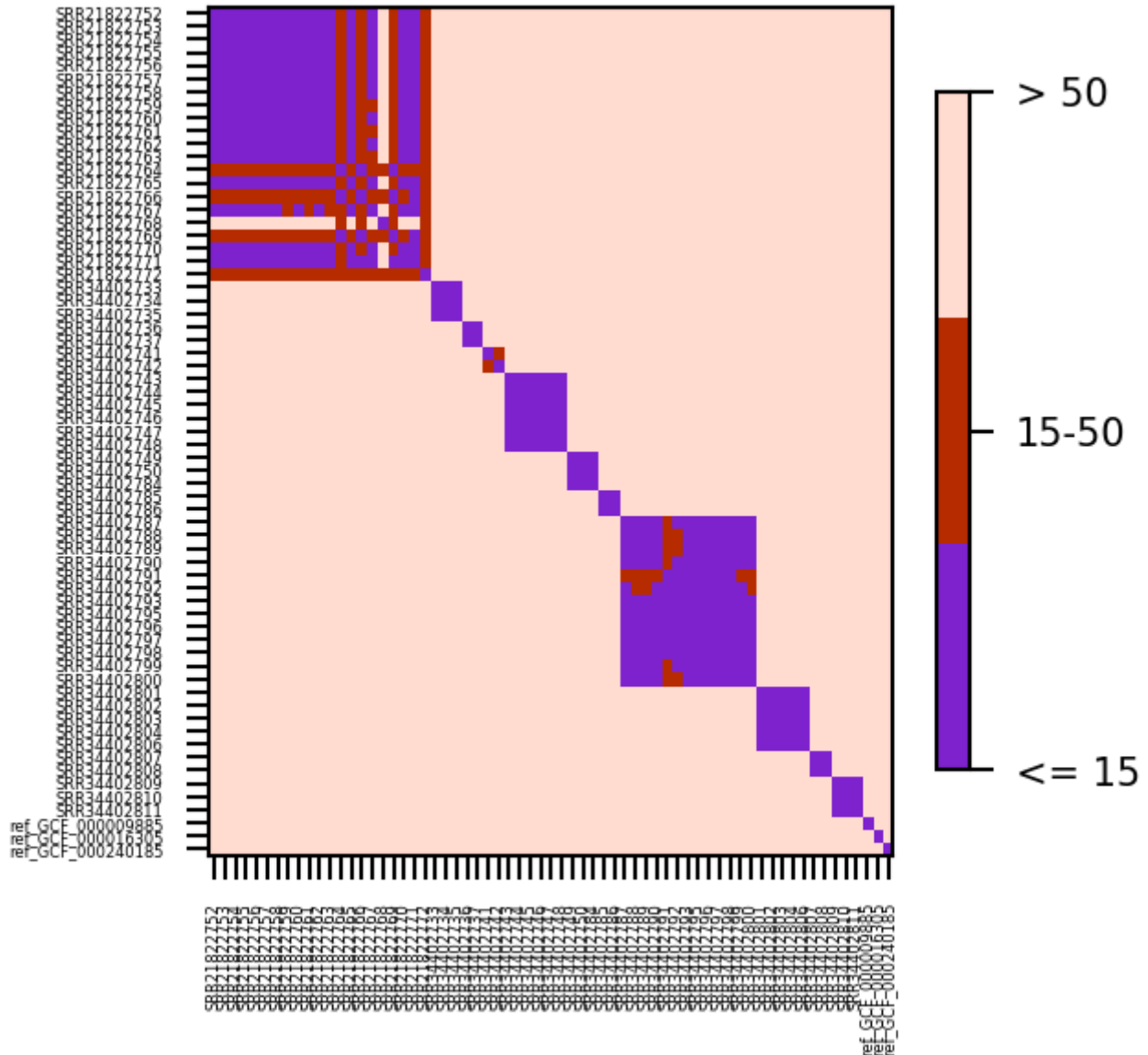


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## COMPREHENSIVE ANALYSIS RESULTS

### Heatmap of Profile Distances

Each cell represents the allelic distance between two samples. The distances are grouped into three bins:  $\leq 15$ ,  $15 < 50$ , and  $> 50$ , where 15 is the species-specific base threshold for *klebsiella\_pneumoniae* cgMLST analysis. The heatmap is colored according to the distance between samples, with darker colors indicating a smaller allelic distance indicating a closer relationship.



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### Result Interpretation Table

| Sample Name | Sequence Type | Complex Type |
|-------------|---------------|--------------|
| SRR21822752 | 147           | 1            |
| SRR21822753 | 147           | 1            |
| SRR21822754 | 147           | 1            |
| SRR21822755 | 147           | 1            |
| SRR21822756 | 147           | 1            |
| SRR21822757 | 147           | 1            |
| SRR21822758 | 147           | 1            |
| SRR21822759 | 147           | 1            |
| SRR21822760 | 147           | 1            |
| SRR21822761 | 147           | 1            |
| SRR21822762 | 147           | 1            |
| SRR21822763 | 147           | 1            |
| SRR21822764 | 147           | 1            |
| SRR21822765 | 147           | 1            |
| SRR21822766 | 147           | 1            |
| SRR21822767 | 147           | 1            |
| SRR21822768 | 147           | -            |
| SRR21822769 | 147           | 1            |
| SRR21822770 | 147           | 1            |
| SRR21822771 | 147           | 1            |
| SRR21822772 | 147           | -            |
| SRR34402733 | 25            | 2            |

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|             |     |   |
|-------------|-----|---|
| SRR34402734 | 25  | 2 |
| SRR34402735 | 25  | 2 |
| SRR34402736 | 45  | 3 |
| SRR34402737 | 45  | 3 |
| SRR34402741 | 26  | - |
| SRR34402742 | 26  | - |
| SRR34402743 | 584 | 4 |
| SRR34402744 | 584 | 4 |
| SRR34402745 | 584 | 4 |
| SRR34402746 | 584 | 4 |
| SRR34402747 | 584 | 4 |
| SRR34402748 | 584 | 4 |
| SRR34402749 | 39  | 5 |
| SRR34402750 | 39  | 5 |
| SRR34402784 | 39  | 5 |
| SRR34402785 | 20  | 6 |
| SRR34402786 | 20  | 6 |
| SRR34402787 | 307 | 7 |
| SRR34402788 | 307 | 7 |
| SRR34402789 | 307 | 7 |
| SRR34402790 | 307 | 7 |
| SRR34402791 | 307 | 7 |
| SRR34402792 | 307 | 7 |
| SRR34402793 | 307 | 7 |
| SRR34402795 | 307 | 7 |

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|               |      |    |
|---------------|------|----|
| SRR34402796   | 307  | 7  |
| SRR34402797   | 307  | 7  |
| SRR34402798   | 307  | 7  |
| SRR34402799   | 307  | 7  |
| SRR34402800   | 307  | 7  |
| SRR34402801   | 54   | 8  |
| SRR34402802   | 54   | 8  |
| SRR34402803   | 54   | 8  |
| SRR34402804   | 54   | 8  |
| SRR34402806   | 54   | 8  |
| SRR34402807   | 3340 | 9  |
| SRR34402808   | 3340 | 9  |
| SRR34402809   | 13   | 10 |
| SRR34402810   | 13   | 10 |
| SRR34402811   | 13   | 10 |
| GCF_000009885 | 23   | -  |
| GCF_000016305 | 38   | -  |
| GCF_000240185 | 11   | -  |

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### Detailed Analysis Results

Isolates **SRR21822752**, **SRR21822753**, **SRR21822754**, **SRR21822755**, **SRR21822756**, **SRR21822758**, **SRR21822757**, **SRR21822759**, **SRR21822760**, **SRR21822761**, **SRR21822762**, **SRR21822763**, **SRR21822765**, **SRR21822767**, **SRR21822770**, **SRR21822771**, **SRR21822766**, **SRR21822764** and **SRR21822769** form a complex and are closely related to each other.

Isolates **SRR34402733**, **SRR34402734** and **SRR34402735** form a complex and are closely related to each other.

Isolates **SRR34402736** and **SRR34402737** form a complex and are closely related to each other.

Isolates **SRR34402743**, **SRR34402744**, **SRR34402747**, **SRR34402745**, **SRR34402746** and **SRR34402748** form a complex and are closely related to each other.

Isolates **SRR34402749**, **SRR34402750** and **SRR34402784** form a complex and are closely related to each other.

Isolates **SRR34402785** and **SRR34402786** form a complex and are closely related to each other.

Isolates **SRR34402787**, **SRR34402790**, **SRR34402788**, **SRR34402789**, **SRR34402800**, **SRR34402793**, **SRR34402791**, **SRR34402792**, **SRR34402795**, **SRR34402796**, **SRR34402797**, **SRR34402798** and **SRR34402799** form a complex and are closely related to each other.

Isolates **SRR34402801**, **SRR34402802**, **SRR34402803**, **SRR34402804** and **SRR34402806** form a complex and are closely related to each other.

Isolates **SRR34402807** and **SRR34402808** form a complex and are closely related to each other.

Isolates **SRR34402809**, **SRR34402810** and **SRR34402811** form a complex and are closely related to each other.

Isolates **SRR21822768**, **SRR21822772**, **SRR34402741** and **SRR34402742** were not closely related to any other isolate.

### Methodology

Whole Genome Sequencing libraries were generated from normalized genomic DNA and sequenced on an Illumina NextSeq550. Genome assembly and species typing were performed using BIOTIA-DX ISOLATE. Sequence type for each isolate was determined using multi locus sequence type (MLST), for *Klebsiella pneumoniae* this consists of comparing 7 genomic sites. Sequence type Isolate relatedness was determined by core genome multi locus sequencing typing (cgMLST), for *Klebsiella pneumoniae* this consists of comparing 3699 genomic sites which are found in >95% of all known *Klebsiella pneumoniae* genomes.

Pairwise allelic distances between isolates were grouped into a tree using unweighted pair group method with arithmetic mean (UPGMA). Pairs of isolates with 15 or fewer allelic differences were considered possibly related and pairs of isolates with less than 50 allelic differences were considered closely related.



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### References

This report made use of PubMLST (<https://pubmlst.org/>) developed by Keith Jolley (Jolley et al. Wellcome Open Res 2018, 3:124 [version 1; referees: 2 approved]) and sited at the University of Oxford. The development of that website was funded by the Wellcome Trust