**Table S1** List of antimicrobial resistance genes and their locations in *A. dhakensis* AMgenome.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| RGI Criteria | ARO Term | Detection Criteria | AMR Gene Family | Drug Class | Resistance Mechanism | % Identity of Matching Region | % Length of Reference Sequence |
| Strict | adeF | protein homolog model | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic, tetracycline antibiotic | antibiotic efflux | 43.71 | 99.06 |
| Strict | rsmA | protein homolog model | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic, diaminopyrimidine antibiotic, phenicol antibiotic | antibiotic efflux | 92.73 | 101.64 |
| Strict | AQU-2 | protein homolog model | AQU beta-lactamase | cephalosporin | antibiotic inactivation | 97.63 | 100.00 |
| Strict | OXA-726 | protein homolog model | OXA beta-lactamase | carbapenem, cephalosporin, penam | antibiotic inactivation | 98.48 | 100.00 |
| Strict | adeF | protein homolog model | resistance-nodulation-cell division (RND) antibiotic efflux pump | fluoroquinolone antibiotic, tetracycline antibiotic | antibiotic efflux | 47.65 | 97.64 |
| Strict | tet(E) | protein homolog model | major facilitator superfamily (MFS) antibiotic efflux pump | tetracycline antibiotic | antibiotic efflux | 99.75 | 100.00 |
| Strict | qacJ | protein homolog model | small multidrug resistance (SMR) antibiotic efflux pump | disinfecting agents and antiseptics | antibiotic efflux | 36.89 | 101.87 |
| Strict | *Escherichia coli* EF-Tu mutants conferring resistance to Pulvomycin | protein variant model | elfamycin resistant EF-Tu | elfamycin antibiotic | antibiotic target alteration | 91.09 | 96.33 |
| Strict | *Escherichia coli* EF-Tu mutants conferring resistance to Pulvomycin | protein variant model | elfamycin resistant EF-Tu | elfamycin antibiotic | antibiotic target alteration | 91.09 | 96.33 |

**Table S2** Summary of putative virulence genes identified in *A. dhakensis* AM

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| VFclass | Virulence factors | Related genes | Contig | Start | End | Length | Strand |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshB* | NODE\_15\_length\_117874\_cov\_109.465029 | 56907 | 57509 | 603 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshC* | NODE\_15\_length\_117874\_cov\_109.465029 | 55891 | 56400 | 510 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshD* | NODE\_15\_length\_117874\_cov\_109.465029 | 55344 | 55904 | 561 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshE* | NODE\_15\_length\_117874\_cov\_109.465030 | 59511 | 61199 | 1689 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshF* | NODE\_15\_length\_117874\_cov\_109.465029 | 57656 | 58117 | 462 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshG* | NODE\_15\_length\_117874\_cov\_109.465029 | 58237 | 59457 | 1221 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshI1* | NODE\_15\_length\_117874\_cov\_109.465029 | 66100 | 66693 | 594 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshI* | NODE\_15\_length\_117874\_cov\_109.465029 | 66794 | 67606 | 813 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshJ* | NODE\_15\_length\_117874\_cov\_109.465029 | 65453 | 66100 | 648 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshK* | NODE\_15\_length\_117874\_cov\_109.465029 | 65134 | 65397 | 264 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshL* | NODE\_15\_length\_117874\_cov\_109.465029 | 63333 | 64985 | 1653 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshM* | NODE\_15\_length\_117874\_cov\_109.465029 | 62350 | 63240 | 891 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshN* | NODE\_15\_length\_117874\_cov\_109.465029 | 61253 | 62353 | 1101 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshO* | NODE\_15\_length\_117874\_cov\_109.465029 | 54514 | 55344 | 831 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshP* | NODE\_15\_length\_117874\_cov\_109.465029 | 54054 | 54524 | 471 | - |
| Adherence | Mannose-sensitive hemagglutinin (Msh) pilus | *mshQ* | NODE\_15\_length\_117874\_cov\_109.465029 | 50413 | 54054 | 3642 | - |
| Adherence | Polar flagella | Undetermined | NODE\_3\_length\_287163\_cov\_99.234731 | 41585 | 42325 | 741 | + |
| Adherence | Polar flagella | Undetermined | NODE\_24\_length\_78570\_cov\_117.161021 | 66966 | 67490 | 525 | + |
| Adherence | Polar flagella | *cheA-2* | NODE\_3\_length\_287163\_cov\_99.234731 | 36646 | 38718 | 2073 | + |
| Adherence | Polar flagella | *cheB-2* | NODE\_3\_length\_287163\_cov\_99.234731 | 38751 | 39860 | 1110 | + |
| Adherence | Polar flagella | *cheR-3* | NODE\_6\_length\_254023\_cov\_96.381750 | 168703 | 169335 | 633 | - |
| Adherence | Polar flagella | *cheV* | NODE\_6\_length\_254023\_cov\_96.381750 | 169546 | 170457 | 912 | - |
| Adherence | Polar flagella | *cheW* | NODE\_3\_length\_287163\_cov\_99.234731 | 42349 | 43191 | 843 | + |
| Adherence | Polar flagella | *cheY* | NODE\_3\_length\_287163\_cov\_99.234731 | 35378 | 35761 | 384 | + |
| Adherence | Polar flagella | *cheZ* | NODE\_3\_length\_287163\_cov\_99.234731 | 35819 | 36514 | 696 | + |
| Adherence | Polar flagella | *flaA* | NODE\_10\_length\_159966\_cov\_92.131898 | 25119 | 25976 | 858 | + |
| Adherence | Polar flagella | *flaB* | NODE\_10\_length\_159966\_cov\_92.131898 | 26610 | 27461 | 852 | + |
| Adherence | Polar flagella | *flaG* | NODE\_10\_length\_159966\_cov\_92.131898 | 27614 | 27943 | 330 | + |
| Adherence | Polar flagella | *flaH* | NODE\_10\_length\_159966\_cov\_92.131898 | 28022 | 29380 | 1359 | + |
| Adherence | Polar flagella | *flaJ* | NODE\_10\_length\_159966\_cov\_92.131898 | 29406 | 29828 | 423 | + |
| Adherence | Polar flagella | *flgA* | NODE\_6\_length\_254023\_cov\_96.381750 | 170704 | 171285 | 582 | + |
| Adherence | Polar flagella | *flgB* | NODE\_6\_length\_254023\_cov\_96.381750 | 168241 | 168639 | 399 | - |
| Adherence | Polar flagella | *flgC* | NODE\_6\_length\_254023\_cov\_96.381750 | 167822 | 168160 | 339 | - |
| Adherence | Polar flagella | *flgD* | NODE\_6\_length\_254023\_cov\_96.381750 | 167078 | 167785 | 708 | - |
| Adherence | Polar flagella | *flgE* | NODE\_6\_length\_254023\_cov\_96.381750 | 165733 | 167067 | 1335 | - |
| Adherence | Polar flagella | *flgF* | NODE\_6\_length\_254023\_cov\_96.381750 | 164836 | 165582 | 747 | - |
| Adherence | Polar flagella | *flgG* | NODE\_6\_length\_254023\_cov\_96.381750 | 164033 | 164821 | 789 | - |
| Adherence | Polar flagella | *flgH* | NODE\_6\_length\_254023\_cov\_96.381750 | 163347 | 164003 | 657 | - |
| Adherence | Polar flagella | *flgI* | NODE\_6\_length\_254023\_cov\_96.381750 | 162241 | 163287 | 1047 | - |
| Adherence | Polar flagella | *flgJ* | NODE\_6\_length\_254023\_cov\_96.381750 | 161102 | 162193 | 1092 | - |
| Adherence | Polar flagella | *flgK* | NODE\_6\_length\_254023\_cov\_96.381750 | 159098 | 161062 | 1965 | - |
| Adherence | Polar flagella | *flgL* | NODE\_6\_length\_254023\_cov\_96.381750 | 157885 | 159075 | 1191 | - |
| Adherence | Polar flagella | *flgM* | NODE\_6\_length\_254023\_cov\_96.381750 | 171375 | 171695 | 321 | + |
| Adherence | Polar flagella | *flgN* | NODE\_6\_length\_254023\_cov\_96.381750 | 171692 | 172108 | 417 | + |
| Adherence | Polar flagella | *flhA* | NODE\_3\_length\_287163\_cov\_99.234731 | 30164 | 32248 | 2085 | + |
| Adherence | Polar flagella | *flhB* | NODE\_3\_length\_287163\_cov\_99.234731 | 28908 | 30038 | 1131 | + |
| Adherence | Polar flagella | *flhF* | NODE\_3\_length\_287163\_cov\_99.234731 | 32265 | 33677 | 1413 | + |
| Adherence | Polar flagella | *flhG* | NODE\_3\_length\_287163\_cov\_99.234731 | 33679 | 34554 | 876 | + |
| Adherence | Polar flagella | *fliA* | NODE\_3\_length\_287163\_cov\_99.234731 | 34568 | 35266 | 699 | + |
| Adherence | Polar flagella | *fliE* | NODE\_3\_length\_287163\_cov\_99.234731 | 16428 | 16745 | 318 | + |
| Adherence | Polar flagella | *fliF* | NODE\_3\_length\_287163\_cov\_99.234731 | 16801 | 18513 | 1713 | + |
| Adherence | Polar flagella | *fliG* | NODE\_3\_length\_287163\_cov\_99.234731 | 18506 | 19567 | 1062 | + |
| Adherence | Polar flagella | *fliH* | NODE\_3\_length\_287163\_cov\_99.234731 | 19632 | 20438 | 807 | + |
| Adherence | Polar flagella | *fliI* | NODE\_3\_length\_287163\_cov\_99.234731 | 20568 | 21833 | 1266 | + |
| Adherence | Polar flagella | *fliJ* | NODE\_3\_length\_287163\_cov\_99.234731 | 21875 | 22300 | 426 | + |
| Adherence | Polar flagella | *fliK* | NODE\_3\_length\_287163\_cov\_99.234731 | 22392 | 24398 | 2007 | + |
| Adherence | Polar flagella | *fliL* | NODE\_3\_length\_287163\_cov\_99.234731 | 24456 | 24974 | 519 | + |
| Adherence | Polar flagella | *fliM* | NODE\_3\_length\_287163\_cov\_99.234731 | 24984 | 26054 | 1071 | + |
| Adherence | Polar flagella | *fliN* | NODE\_3\_length\_287163\_cov\_99.234731 | 26106 | 26498 | 393 | + |
| Adherence | Polar flagella | *fliO* | NODE\_3\_length\_287163\_cov\_99.234731 | 26495 | 26878 | 384 | + |
| Adherence | Polar flagella | *fliP* | NODE\_3\_length\_287163\_cov\_99.234731 | 26865 | 27644 | 780 | + |
| Adherence | Polar flagella | *fliQ* | NODE\_3\_length\_287163\_cov\_99.234731 | 27672 | 27941 | 270 | + |
| Adherence | Polar flagella | *fliR* | NODE\_3\_length\_287163\_cov\_99.234731 | 28015 | 28782 | 768 | + |
| Adherence | Polar flagella | *flmD* | NODE\_24\_length\_78570\_cov\_117.161021 | 64848 | 66104 | 1257 | - |
| Adherence | Polar flagella | *flmH* | NODE\_24\_length\_78570\_cov\_117.161021 | 67720 | 68469 | 750 | + |
| Adherence | Polar flagella | *flrA* | NODE\_6\_length\_254023\_cov\_96.381750 | 149056 | 150402 | 1347 | - |
| Adherence | Polar flagella | *flrB* | NODE\_6\_length\_254023\_cov\_96.381750 | 147915 | 148949 | 1035 | - |
| Adherence | Polar flagella | *flrC* | NODE\_6\_length\_254023\_cov\_96.381750 | 146495 | 147838 | 1344 | - |
| Adherence | Polar flagella | *maf-1* | NODE\_10\_length\_159966\_cov\_92.131898 | 30132 | 32219 | 2088 | + |
| Adherence | Polar flagella | *maf-2* | NODE\_24\_length\_78570\_cov\_117.161021 | 62507 | 63802 | 1296 | - |
| Adherence | Polar flagella | *motX* | NODE\_1\_length\_322842\_cov\_106.555829 | 230245 | 230838 | 594 | + |
| Adherence | Polar flagella | *motY* | NODE\_2\_length\_289620\_cov\_91.052424 | 54128 | 54961 | 834 | + |
| Adherence | Polar flagella | *nueA* | NODE\_24\_length\_78570\_cov\_117.161021 | 66094 | 66789 | 696 | - |
| Adherence | Polar flagella | *nueB* | NODE\_24\_length\_78570\_cov\_117.161021 | 63795 | 64841 | 1047 | - |
| Adherence | Polar flagella | *pomA2* | NODE\_5\_length\_257795\_cov\_102.337846 | 119403 | 120119 | 717 | - |
| Adherence | Polar flagella | *pomA* | NODE\_3\_length\_287163\_cov\_99.234731 | 39863 | 40600 | 738 | + |
| Adherence | Polar flagella | *pomB2* | NODE\_5\_length\_257795\_cov\_102.337846 | 118498 | 119352 | 855 | - |
| Adherence | Polar flagella | *pomB2* | NODE\_10\_length\_159966\_cov\_92.131898 | 118360 | 119235 | 876 | - |
| Adherence | Polar flagella | *pomB* | NODE\_3\_length\_287163\_cov\_99.234731 | 40603 | 41526 | 924 | + |
| Adherence | Tap type IV pili | *tapB* | NODE\_9\_length\_184585\_cov\_110.417711 | 116596 | 118188 | 1593 | + |
| Adherence | Tap type IV pili | *tapC* | NODE\_9\_length\_184585\_cov\_110.417711 | 118301 | 119545 | 1245 | + |
| Adherence | Tap type IV pili | *tapD* | NODE\_9\_length\_184585\_cov\_110.417711 | 119568 | 120440 | 873 | + |
| Adherence | Tap type IV pili | *tapF* | NODE\_10\_length\_159966\_cov\_92.131898 | 84715 | 85476 | 762 | + |
| Adherence | Tap type IV pili | *tapM* | NODE\_14\_length\_123275\_cov\_100.634678 | 95 | 1078 | 984 | + |
| Adherence | Tap type IV pili | *tapN* | NODE\_14\_length\_123275\_cov\_100.634678 | 1066 | 1644 | 579 | + |
| Adherence | Tap type IV pili | *tapO* | NODE\_14\_length\_123275\_cov\_100.634678 | 1641 | 2240 | 600 | + |
| Adherence | Tap type IV pili | *tapP* | NODE\_14\_length\_123275\_cov\_100.634678 | 2270 | 2767 | 498 | + |
| Adherence | Tap type IV pili | *tapQ* | NODE\_14\_length\_123275\_cov\_100.634678 | 2814 | 4985 | 2172 | + |
| Adherence | Tap type IV pili | *tapT* | NODE\_8\_length\_215741\_cov\_106.565131 | 81902 | 82858 | 957 | - |
| Adherence | Tap type IV pili | *tapU* | NODE\_8\_length\_215741\_cov\_106.565131 | 80764 | 81873 | 1110 | - |
| Adherence | Tap type IV pili | *tapV* | NODE\_2\_length\_289620\_cov\_91.052424 | 5100 | 7256 | 2157 | + |
| Adherence | Tap type IV pili | *tapW* | NODE\_6\_length\_254023\_cov\_96.381750 | 55611 | 56735 | 1125 | + |
| Adherence | Tap type IV pili | *tapY1* | NODE\_1\_length\_322842\_cov\_106.555829 | 258870 | 262190 | 3321 | + |
| Adherence | Tap type IV pili | *tppA* | NODE\_1\_length\_322842\_cov\_106.555829 | 262193 | 262600 | 408 | + |
| Adherence | Tap type IV pili | *tppB* | NODE\_1\_length\_322842\_cov\_106.555829 | 256836 | 257249 | 414 | + |
| Adherence | Tap type IV pili | *tppE* | NODE\_1\_length\_322842\_cov\_106.555829 | 256435 | 256839 | 405 | + |
| Adherence | Tap type IV pili | *tppF* | NODE\_8\_length\_215741\_cov\_106.565131 | 52922 | 53539 | 618 | - |
| Adherence | Type I fimbriae | *fimA* | NODE\_1\_length\_322842\_cov\_106.555829 | 74901 | 75278 | 378 | + |
| Adherence | Type I fimbriae | *fimC* | NODE\_1\_length\_322842\_cov\_106.555829 | 75892 | 78369 | 2478 | + |
| Adherence | Type I fimbriae | *fimD* | NODE\_1\_length\_322842\_cov\_106.555829 | 78380 | 79111 | 732 | + |
| Adherence | Type I fimbriae | *fimE* | NODE\_1\_length\_322842\_cov\_106.555829 | 79677 | 80144 | 468 | + |
| Adherence | Type I fimbriae | *fimF* | NODE\_1\_length\_322842\_cov\_106.555829 | 80168 | 80707 | 540 | + |
| Adherence | Accessory colonization factor(Vibrio) | *acfC* | NODE\_14\_length\_123275\_cov\_100.634678 | 24393 | 25127 | 735 | - |
| Secretion system | T2SS | *exeA* | NODE\_9\_length\_184585\_cov\_110.417711 | 29955 | 31598 | 1644 | + |
| Secretion system | T2SS | *exeB* | NODE\_9\_length\_184585\_cov\_110.417711 | 31598 | 32281 | 684 | + |
| Secretion system | T2SS | *exeC* | NODE\_1\_length\_322842\_cov\_106.555829 | 124766 | 125581 | 816 | + |
| Secretion system | T2SS | *exeD* | NODE\_1\_length\_322842\_cov\_106.555829 | 125603 | 127636 | 2034 | + |
| Secretion system | T2SS | *exeE* | NODE\_1\_length\_322842\_cov\_106.555829 | 127636 | 129141 | 1506 | + |
| Secretion system | T2SS | *exeF* | NODE\_1\_length\_322842\_cov\_106.555829 | 129143 | 130363 | 1221 | + |
| Secretion system | T2SS | *exeG* | NODE\_1\_length\_322842\_cov\_106.555829 | 130515 | 130946 | 432 | + |
| Secretion system | T2SS | *exeH* | NODE\_1\_length\_322842\_cov\_106.555829 | 131110 | 131661 | 552 | + |
| Secretion system | T2SS | *exeI* | NODE\_1\_length\_322842\_cov\_106.555829 | 131658 | 132017 | 360 | + |
| Secretion system | T2SS | *exeJ* | NODE\_1\_length\_322842\_cov\_106.555829 | 132062 | 132709 | 648 | + |
| Secretion system | T2SS | *exeK* | NODE\_1\_length\_322842\_cov\_106.555829 | 132856 | 133824 | 969 | + |
| Secretion system | T2SS | *exeL* | NODE\_1\_length\_322842\_cov\_106.555829 | 133944 | 135128 | 1185 | + |
| Secretion system | T2SS | *exeM* | NODE\_1\_length\_322842\_cov\_106.555829 | 135125 | 135616 | 492 | + |
| Secretion system | T2SS | *exeN* | NODE\_1\_length\_322842\_cov\_106.555829 | 135678 | 136433 | 756 | + |
| Secretion system | T6SS | *hcp* | NODE\_7\_length\_222130\_cov\_100.899006 | 25500 | 26018 | 519 | + |
| Secretion system | T6SS | *hcp* | NODE\_10\_length\_159966\_cov\_92.131898 | 155119 | 155637 | 519 | + |
| Secretion system | T6SS | *vgrG1* | NODE\_7\_length\_222130\_cov\_100.899006 | 26503 | 28545 | 2043 | + |
| Secretion system | T6SS | *vgrG3* | NODE\_10\_length\_159966\_cov\_92.131898 | 155901 | 157949 | 2049 | + |
| Toxin | Aerolysin AerA | *aerA* | NODE\_15\_length\_117874\_cov\_109.465029 | 11048 | 11929 | 882 | - |
| Toxin | Extracellular hemolysin AHH1 | *ahh1* | NODE\_3\_length\_287163\_cov\_99.234731 | 159636 | 161501 | 1866 | + |
| Toxin | Hemolysin HlyA | *hlyA* | NODE\_6\_length\_254023\_cov\_96.381750 | 128340 | 129659 | 1320 | - |
| Toxin | Hemolysin III | Undetermined | NODE\_27\_length\_58979\_cov\_104.850124 | 40383 | 41018 | 636 | - |
| Toxin | The repeat in toxin (RTX) | *rtxA* | NODE\_22\_length\_85969\_cov\_100.510234 | 69488 | 83560 | 14073 | + |
| Toxin | The repeat in toxin (RTX) | *rtxB* | NODE\_22\_length\_85969\_cov\_100.510234 | 66195 | 68084 | 1890 | - |
| Toxin | The repeat in toxin (RTX) | *rtxC* | NODE\_22\_length\_85969\_cov\_100.510234 | 69246 | 69470 | 225 | + |
| Toxin | The repeat in toxin (RTX) | *rtxD* | NODE\_22\_length\_85969\_cov\_100.510234 | 64834 | 66198 | 1365 | - |
| Toxin | The repeat in toxin (RTX) | *rtxE* | NODE\_22\_length\_85969\_cov\_100.510234 | 62672 | 64837 | 2166 | - |
| Toxin | The repeat in toxin (RTX) | *rtxH* | NODE\_22\_length\_85969\_cov\_100.510234 | 68659 | 68988 | 330 | + |
| Toxin | Thermostable hemolysin (TH) | Undetermined | NODE\_5\_length\_257795\_cov\_102.337846 | 28463 | 29143 | 681 | + |
| Toxin | Exotoxin A (ETA)(Pseudomonas) | *toxA* | NODE\_23\_length\_83985\_cov\_94.684678 | 78831 | 80678 | 1848 | + |
| Immune evasion | Capsule(Acinetobacter) | *-* | NODE\_6\_length\_254023\_cov\_96.381750 | 211039 | 212172 | 1134 | - |
| Immune evasion | Polysaccharide capsule(Bacillus) | *galU* | NODE\_23\_length\_83985\_cov\_94.684678 | 112 | 948 | 837 | + |
| Iron uptake | Acinetobactin(Acinetobacter) | *basB* | NODE\_31\_length\_42802\_cov\_112.281709 | 30177 | 31700 | 1524 | + |
| Iron uptake | Acinetobactin(Acinetobacter) | *basG* | NODE\_31\_length\_42802\_cov\_112.281709 | 37992 | 39191 | 1200 | + |

**Table S3** Prophage information of *A. dhakensis* AM

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Region | Region length (kb) | Completeness | Region Position | Most common phage | GC content (%) |
| 1 | 8.4 | incomplete | NODE\_4\_length\_272632\_cov\_89.380820 | PHAGE\_Bacill\_G\_NC\_023719(2) | 64.60 |
| 2 | 7.5 | incomplete | NODE\_9\_length\_184585\_cov\_110.417711 | PHAGE\_Serrat\_CHI14\_NC\_041996(1) | 59.12 |
| 3 | 8 | incomplete | NODE\_16\_length\_114246\_cov\_116.032347 | PHAGE\_Bacill\_vB\_BanS\_Tsamsa\_NC\_023007(2) | 63.27 |
| 4 | 13.6 | incomplete | NODE\_17\_length\_108745\_cov\_105.362103 | PHAGE\_Klebsi\_ST13\_OXA48phi12.1\_NC\_049453(4) | 60.27 |
| 5 | 13.6 | incomplete | NODE\_21\_length\_91290\_cov\_97.438304 | PHAGE\_Bacill\_G\_NC\_023719(2) | 62.24 |