Table S2. Lipoproteins exhibiting identical nucleotide and amino acid sequence in early and late strain types and their amino acid identity across sequenced genomes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Early Clone | Late Clone | Protein | % Identity1 | Number of Genomes2 |
| NMY220\_0089 | NMY233\_0073 | putative lipoprotein | 96.5 | 19 |
| NMY220\_0090 | NMY233\_0074 | mltA family protein | 99.2 | 19 |
| NMY220\_0092 | NMY233\_0076 | putative lipoprotein | 99.6 | 20 |
| NMY220\_0108 | NMY233\_0090 | putative lipoprotein | 97.5 | 20 |
| NMY220\_0116 | NMY233\_0098 | capsule polysaccharide export outer membrane protein CtrA | 99.3 | 20 |
| NMY220\_0148 | NMY233\_0130 | putative lipoprotein | 97.7 | 19 |
| NMY220\_0244 | NMY233\_0226 | lipoprotein, SmpA/OmlA family | 95.0 | 20 |
| NMY220\_0317 | NMY233\_0298 | putative thiol:disulfide interchange protein DsbA | 99.3 | 20 |
| NMY220\_0334 | NMY233\_0316 | DSBA thioredoxin domain protein | 99.1 | 20 |
| NMY220\_0533 | NMY233\_0506 | protease Do | 98.4 | 20 |
| NMY220\_0581 | NMY233\_0556 | nosL protein | 99.5 | 20 |
| NMY220\_0749 | NMY233\_0724 | putative lipoprotein | 97.4 | 20 |
| NMY220\_0775 | NMY233\_0750 | L-cystine ABC transporter, periplasmic L-cystine-binding protein | 98.6 | 20 |
| NMY220\_0870 | NMY233\_0859 | cytochrome c, class II | 97.0 | 19 |
| NMY220\_0938 | NMY233\_0924 | putative lipoprotein | 99.8 | 20 |
| NMY220\_0973 | NMY233\_0977 | putative lipoprotein | 99.9 | 20 |
| NMY220\_0984 | NMY233\_0988 | putative lipoprotein | 99.2 | 20 |
| NMY220\_0989 | NMY233\_0992 | gamma-glutamyltransferase | 99.1 | 20 |
| NMY220\_0991 | NMY233\_0994 | fructose-1,6-bisphosphatase | 97.7 | 20 |
| NMY220\_1050 | NMY233\_1054 | putative lipoprotein | 92.4 | 9 |
| NMY220\_1067 | NMY233\_1070 | putative lipoprotein | 98.9 | 20 |
| NMY220\_1069 | NMY233\_1072 | CsgG family protein | 98.2 | 20 |
| NMY220\_1225 | NMY233\_1212 | creA protein | 98.5 | 20 |
| NMY220\_1363 | NMY233\_1342 | LysM domain/M23 peptidase domain protein | 96.4 | 20 |
| NMY220\_1397 | NMY233\_1375 | putative lipoprotein | 91.4 | 20 |
| NMY220\_1399 | NMY233\_1377 | outer membrane autotransporter3 | 71.0 | 20 |
| NMY220\_1407 | NMY233\_1385 | Azurin | 98.9 | 20 |
| NMY220\_1447 | NMY233\_1426 | integral membrane protein | 94.4 | 20 |
| NMY220\_1457 | NMY233\_1433 | putative membrane protein | 99.5 | 20 |
| NMY220\_1458 | NMY233\_1434 | putative periplasmic putrescene-binding ABC transporter, | 99.5 | 20 |
| NMY220\_1608 | NMY233\_1584 | type IV pilus assembly protein PilP | 97.9 | 20 |
| NMY220\_1651 | NMY233\_1628 | carbamoyl-phosphate synthase, large subunit | 99.5 | 20 |
| NMY220\_1665 | NMY233\_1641 | factor H binding protein | 85.4 | 20 |
| NMY220\_1674 | NMY233\_1650 | putative ABC transporter, periplasmic iron-binding protein | 99.7 | 20 |
| NMY220\_1690 | NMY233\_1663 | lipoprotein Mlp | 98.7 | 20 |
| NMY220\_1732 | NMY233\_1707 | putative lipoprotein | 99.4 | 15 |
| NMY220\_1738 | NMY233\_1713 | transglycosylase SLT domain protein | 97.9 | 19 |
| NMY220\_1767 | NMY233\_1742 | putative lipoprotein | 97.5 | 20 |
| NMY220\_1779 | NMY233\_1755 | iron chelate ABC transporter, periplasmic iron chelate-binding protein3 | 97.9 | 20 |
| NMY220\_1781 | NMY233\_1757 | iron chelate ABC transporter, permease protein | 97.7 | 20 |
| NMY220\_1876 | NMY233\_1855 | phospholipid-binding domain protein | 99.8 | 20 |
| NMY220\_1888 | NMY233\_1867 | putative lipoprotein, MafA family | 98.5 | 17 |
| NMY220\_1914 | NMY233\_1891 | phospholipase, patatin family | 99.5 | 20 |

1 % amino acid identity across 22 sequenced genomes (includes NM220 and NM233)

2 Number of sequenced genomes in addition to NM220 and NM233 containing this locus

3 Identical nucleotide sequence, leading gap