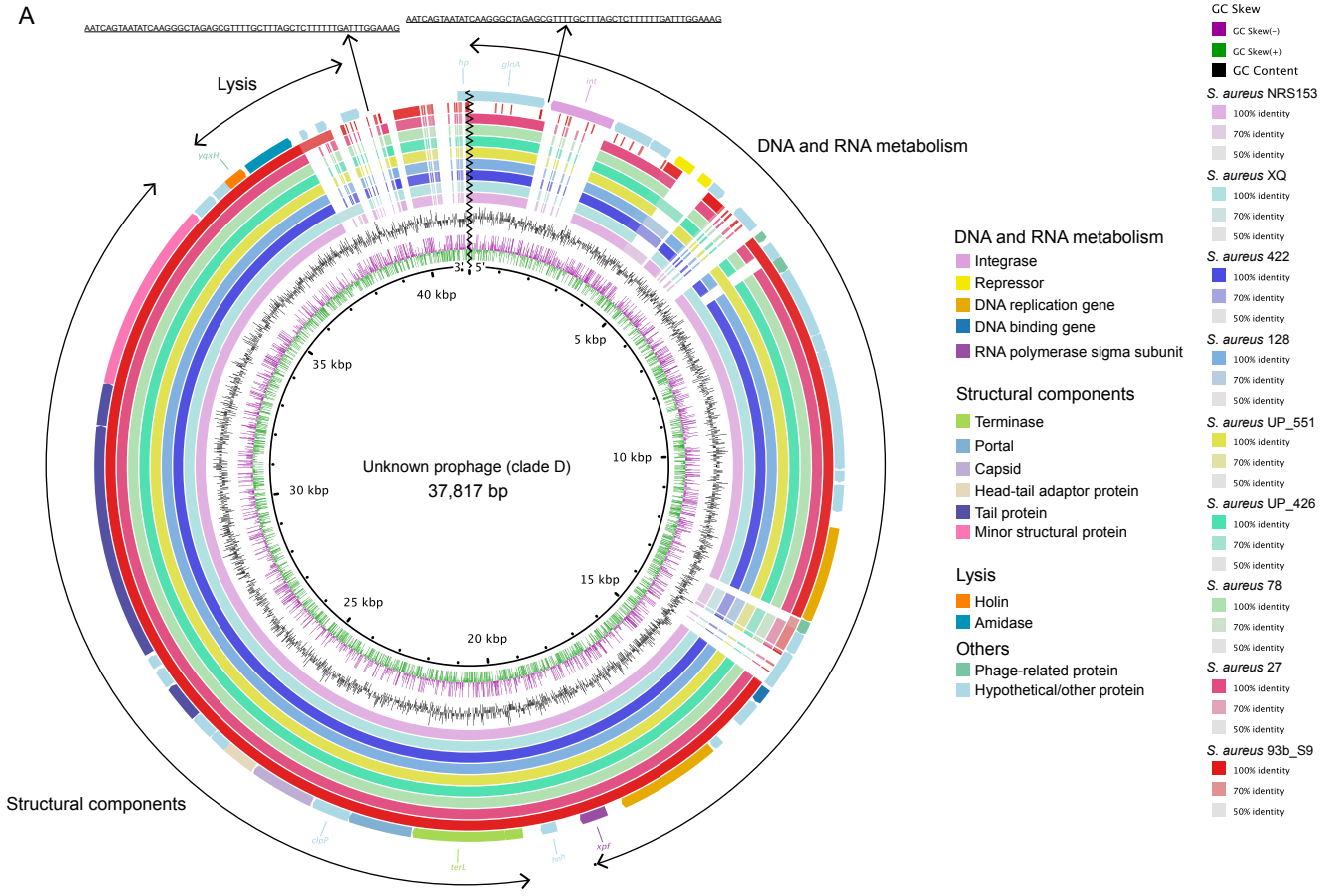
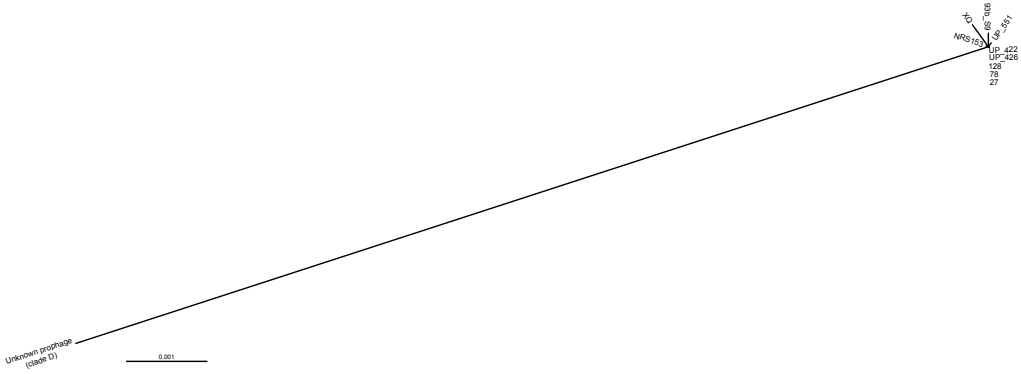
A


AATCAGTAATATCAAGGGCTAGAGCGTTTTTGCTTTAGCTCTTTTTTGATTTGGAAAG
AATCAGTAATATCAAGGGCTAGAGCGTTTTTGCTTTAGCTCTTTTTTGATTTGGAAAG
Lysis
DNA and RNA metabolism
Structural components
hp
glnA
int
yqxH
clpP
terL
nsh
xpf
3'
5'
40 kbp
5 kbp
35 kbp
10 kbp
30 kbp
15 kbp
25 kbp
20 kbp
Unknown prophage (clade D)
37,817 bp
GC Skew
GC Skew(−)
GC Skew(+)
GC Content
S. aureus NRS153
100% identity
70% identity
50% identity
S. aureus XQ
100% identity
70% identity
50% identity
S. aureus 422
100% identity
70% identity
50% identity
S. aureus 128
100% identity
70% identity
50% identity
S. aureus UP_551
100% identity
70% identity
50% identity
S. aureus UP_426
100% identity
70% identity
50% identity
S. aureus 78
100% identity
70% identity
50% identity
S. aureus 27
100% identity
70% identity
50% identity
S. aureus 93b_S9
100% identity
70% identity
50% identity
DNA and RNA metabolism
Integrase
Repressor
DNA replication gene
DNA binding gene
RNA polymerase sigma subunit
Structural components
Terminase
Portal
Capsid
Head-tail adaptor protein
Tail protein
Minor structural protein
Lysis
Holin
Amidase
Others
Phage-related protein
Hypothetical/other protein

B


Unknown prophage (clade D)
0.001
NRS153
XQ
93b_S9
UP_551
UP_422
UP_426
128
78
27