Additional File 11, Table S8: *Streptococcus anginosus* genes with a match to the virulence gene database.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| db\_ref | Region | PIDa | % HSPb | Gene Name | Description |
| **gi|32812823\*** | **SAIN\_1627** | **SANR\_1894** | **97** | **100.0** | ***gap*dh** | **glyceraldehyde 3-phosphate dehydrogenase** |
| **gi|16151617** | **SAIN\_0997** | **SANR\_1074** | **95** | **100.0** | ***eno*** | **alpha-enolas** |
| **gi|1881547** | **SAIN\_0666** | **SANR\_0675** | **93** | **98.9** | ***cps19f*O**  | **capsular polysaccharide biosynthesis**  |
| **gi|1881546** | **SAIN\_0657** | **SANR\_0666** | **91** | **99.4** | ***cps19f*N**  | **capsular polysaccharide biosynthesis**  |
| **gi|1881544** | **SAIN\_0655** | **SANR\_0664** | **90** | **99.7** | ***cps19f*L** | **capsular polysaccharide biosynthesis**  |
| **gi|1881545** | **SAIN\_0656** | **SANR\_0665** | **90** | **99.5** | ***cps19f*M** | **capsular polysaccharide biosynthesis**  |
| **VFG0964** | **SAIN\_1619** | **SANR\_1886** | **86** | **97.4** | ***has*C** | **UDP-glucose pyrophosphorylase** |
| **VFG1359** | **SAIN\_0244** | **SANR\_0284** | **83** | **100.0** | ***psa*A** |  **manganese ABC transporter** |
| **gi|253559383** | **SAIN\_0537** | **SANR\_0554** | **80** | **99.7** | ***sil*E** | **Streptococcal invasion locus** |
| **VFG0959** | **SAIN\_0616** | **SANR\_0625** | **75** | **99.8** | ***fbp***  | **Fibronectin binding protein** |
| **VFG1330** | **SAIN\_1064** | **SANR\_1155** | **62** | **99.7** | ***lmb*** |  **laminin-binding surface protein** |
| **gi|22797659** | **SAIN\_1534** | **SANR\_1773** | **59** | **81.3** | ***pul*A**  |  **pullulanase** |
| **gi|253559382** | **SAIN\_0538** | **SANR\_0555** | **54** | **99.3** | ***sil*D**  | **Streptococcal invasion locus** |
| **gi|253559378** | **SAIN\_0541** | **SANR\_1817** | **52** | **98.4** | ***sil*A**  | **Streptococcal invasion locus** |
| **gi|6002654** | **SAIN\_1370** | **SANR\_1594** | **46** | **99.1** | ***csr*R** | **response regulator** |
| **gi|11245963** | **SAIN\_1156** | **SANR\_0814** | **44** | **88.6** | ***sal*X** | **salivaricin A gene** |
| gi|253559384 | SAIN\_0549 | SANR\_0567 | 43 | 51.3 | *blp*M | Streptococcal invasion locus |
| **gi|4886774** | **SAIN\_0266** | **SANR\_0306** | **42** | **86.4** | ***cyl*Z** |  **cyl gene cluster** |
| **gi|253559379** | **SAIN\_0540** | **SANR\_0557** | **41** | **84.0** | ***sil*B** | **Streptococcal invasion locus** |
| **gi|253559380** | **SAIN\_0539** | **SANR\_0556** | **41** | **55.1** | ***sil*CR** | **Streptococcal invasion locus** |
| **gi|4886772** | **SAIN\_0263** | **SANR\_0303** | **38** | **95.1** | ***cyl*G** |  **cyl gene cluster** |
| gi|8825620 | NA | SANR\_0369 | 68 | 99.2 | *sagC* | Streptolysin-S operon |
| gi|3283389 | NA | SANR\_0368 | 64 | 99.4 | *sagB* | Streptolysin-S operon |
| VFG1364 | NA | SANR\_1718 | 63 | 97.0 | *hyl*  |  hyaluronidase |
| VFG0977 | NA | SANR\_0367 | 83 | 68.5 | *sagA* | Streptolysin-S operon |
| gi|1161270 | NA | SANR\_1810 | 39 | 96.7 | *spx*B  |  pyruvate oxidase |
| gi|209559120 | NA | SANR\_0370 | 80 | 100.0 | *sagD* | Streptolysin S biosynthesis protein |
| gi|209559121 | NA | SANR\_0371 | 46 | 98.2 | *sagE*  | Streptolysin S self-immunity protein  |
| gi|209559122 | NA | SANR\_0372 | 37 | 91.4 | *sagF*  | Streptolysin S biosynthesis protein |
| gi|209559123 | NA | SANR\_0373 | 72 | 100.0 | *sagG* | Streptolysin S export ATP-binding protein  |
| gi|209559124 | NA | SANR\_0374 | 73 | 99.7 | *sagH* |  Streptolysin S export transmembrane protein |
| gi|209559125 | NA | SANR\_0375 | 69 | 99.2 | *sagI*  | Streptolysin S export transmembrane protein  |
| gi|209559600 | NA | SANR\_0893 | 47 | 89.2 | *inlA* | Internalin A protein |
| gi|1161270 | SAIN\_1574 | NA | 97 | 100.0 | spxB  |  pyruvate oxidase |
| VFG1366 | SAIN\_1729 | NA | 71 | 100.0 | *cps4*B | capsular polysaccharide biosynthesis protein |
| VFG1368 | SAIN\_1727 | NA | 68 | 97.4 | *cps4*D | capsular polysaccharide biosynthesis protein |
| gi|485275 | SAIN\_1730 | NA | 64 | 98.6 | *cps19f*A | capsular polysaccharide biosynthesis operon |
| VFG1367 | SAIN\_1728 | NA | 64 | 99.1 | *cps4*C | capsular polysaccharide biosynthesis protein |
| gi|257348146 | SAIN\_1710 | NA | 62 | 56.3 | *pav*B | adhesion |
| VFG1373 | SAIN\_1479 | NA | 58 | 94.0 | *cpns4*I | capsular polysaccharide biosynthesis protein |
| gi|485279 | SAIN\_1726 | NA | 56 | 98.2 | *cps19f*E | capsular polysaccharide biosynthesis operon |
| gi|4886775 | SAIN\_0499 | NA | 38 | 87.4 | *cyl*A |  cyl gene cluster |

**\*Bolded items are conserved in all sequenced SAG strains from this study**

aPercent coverage of protein from SAG compared to best match in NCBI database using BlastX

bPID is equal to the percent protein identity for the best match using BlastX from NCBI