

Supplementary Material:

Table S1. List of primers used in this study.

| Primer name | Primer sequence (5' to 3') |
|----------------------------|-----------------------------------|
| SEQ0546 transcript qPCR F1 | CTAGTGTAGCAGAAACAAC |
| SEQ0546 transcript qPCR R1 | CAGCTGCACCATAATTG |
| SEQ0938 transcript qPCR F1 | GTATGCTAGGAATGATG |
| SEQ0938 transcript qPCR R1 | GCTCAGTTTGACTTAG |
| SEQ0999 transcript qPCR F1 | CCATATCTTGCTCATC |
| SEQ0999 transcript qPCR R1 | CAAACCACCAATGCAG |
| SEQ0269 transcript qPCR F1 | GTGTTTCAGCAGCAAACC |
| SEQ0269 transcript qPCR R1 | CACATAGTCTTCAATGCG |
| SEQ0270 transcript qPCR F1 | GCATATCGCCAATCAAG |
| SEQ0270 transcript qPCR R1 | CATTGCTATAAGCGCTTG |
| SEQ0271 transcript qPCR F1 | CATTCAATTCATCGTCGAG |
| SEQ0271 transcript qPCR R1 | GAGCTCGAAGTTGGAGTC |
| SEQ1728 transcript qPCR F1 | CAGATACGTACAATACAAATGATG |
| SEQ1728 transcript qPCR R1 | CTTCTATTATCTAAAATTTTCGTC |
| SEQ2190 transcript qPCR F1 | GCGAAAGAGGAAGCTAAGAC |
| SEQ2190 transcript qPCR R1 | CTTTATCAGCCGTAGCTTG |
| SEQ0402 transcript qPCR F1 | CAGCGACTACCCTAGCAG |
| SEQ0402 transcript qPCR R1 | CATTTTTAAGCTCGTTAGCG |
| SEQ1817 transcript qPCR F1 | GCTCCTGCACCGAAAG |
| SEQ1817 transcript qPCR R1 | CTAAAGAATGGATGGCTTGC |
| gyrA forward | CTATGAAGCGATGGTCCGTATGG |
| gyrA reverse | CCATAGAACCAAAGTTTCCATGACC |

Table S2. List of genes that were significantly differentially transcribed from transcriptome sequencing between the reduced capsule and mucoid colony phenotypes of *Se1691*.

| Gene ID | Description | Functional Group | Mean fold change in reduced capsule compared to mucoid | Q value |
|----------|--|----------------------|--|---------|
| SEQ_0044 | Aldehyde-alcohol dehydrogenase 2 [includes: alcohol dehydrogenase; acetaldehyde dehydrogenase] (<i>adhE</i>) | Nutrient metabolism | 6.32 | 0.0493 |
| SEQ_0090 | Putative collagen-like surface-anchored protein | Surface anchored | 3.76 | 0.0015 |
| SEQ_0103 | Putative membrane protein | Membrane protein | 2.86 | 0.0298 |
| SEQ_0203 | Putative exported protein | Secreted protein | 2.31 | 0.0482 |
| SEQ_0225 | Putative exported protein | Secreted protein | -8.10 | 0.0015 |
| SEQ_0231 | Putative Mga-like regulatory protein | Regulator | -3.05 | 0.0015 |
| SEQ_0256 | Putative cell surface-anchored protein | Surface anchored | -5.99 | 0.0015 |
| SEQ_0257 | Putative carbohydrate-binding exported protein | Nutrient acquisition | -2.42 | 0.0285 |
| SEQ_0269 | Hyaluronan synthase | Capsule production | -4.68 | 0.0015 |
| SEQ_0270 | UDP-glucose 6-dehydrogenase | Capsule production | -3.95 | 0.0015 |
| SEQ_0271 | UTP--glucose-1-phosphate uridylyltransferase 1 | Capsule production | -2.21 | 0.0285 |
| SEQ_0280 | Putative collagen-like cell surface-anchored protein | Surface anchored | 4.60 | 0.0433 |
| SEQ_0281 | Putative membrane protein | Membrane protein | 2.39 | 0.0120 |
| SEQ_0282 | Putative glucitol/sorbitol-specific phosphotransferase system (PTS), IIA component | Nutrient acquisition | 5.91 | 0.0290 |
| SEQ_0315 | Putative N-acetylmannosamine-6-phosphate 2-epimerase | Nutrient metabolism | -6.01 | 0.0466 |

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|----------|---|-------------------------|--------|--------|
| SEQ_0316 | Sugar phosphotransferase system (PTS), IIBC component | Nutrient acquisition | -3.87 | 0.0015 |
| SEQ_0317 | Putative glucose-specific phosphotransferase system (PTS), IIBC component | Nutrient acquisition | -4.27 | 0.0015 |
| SEQ_0320 | Putative N-acetylmannosamine-6-phosphate 2-epimerase (pseudogene) | Nutrient metabolism | -8.22 | 0.0015 |
| SEQ_0321 | Extracellular solute-binding lipoprotein | Nutrient acquisition | -11.03 | 0.0015 |
| SEQ_0322 | Putative transport system permease | Nutrient acquisition | -10.34 | 0.0015 |
| SEQ_0323 | Putative transport system permease | Nutrient acquisition | -9.18 | 0.0015 |
| SEQ_0324 | Conserved hypothetical protein | Nutrient acquisition | -8.44 | 0.0015 |
| SEQ_0325 | Putative membrane protein | Nutrient acquisition | -7.31 | 0.0015 |
| SEQ_0326 | Putative N-acetylneuraminate lyase | Nutrient metabolism | -7.54 | 0.0015 |
| SEQ_0327 | ROK family protein | Regulator | -6.65 | 0.0015 |
| SEQ_0329 | Putative transcription regulator | Regulator | -7.22 | 0.0015 |
| SEQ_0350 | MerR family regulatory protein | Regulator | -8.05 | 0.0015 |
| SEQ_0351 | Putative glutamine synthetase | Amino acid biosynthesis | -5.96 | 0.0015 |
| SEQ_0352 | Putative peptide binding protein | Nutrient acquisition | -6.08 | 0.0015 |
| SEQ_0353 | Di-tripeptide transport system permease protein | Nutrient acquisition | -3.98 | 0.0015 |
| SEQ_0354 | Di-tripeptide transporter permease protein | Nutrient acquisition | -3.90 | 0.0015 |
| SEQ_0355 | Di-tripeptide transporter ATP-binding protein | Nutrient acquisition | -3.89 | 0.0015 |
| SEQ_0356 | Di-tripeptide transporter ATP-binding protein | Nutrient acquisition | -3.98 | 0.0081 |
| SEQ_0377 | Putative protein F2 like fibronectin-binding protein (pseudogene) FNZ | Secreted protein | -3.35 | 0.0466 |
| SEQ_0378 | Putative regulatory | Regulator | -4.32 | 0.0015 |

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| | protein-RofA related | | | |
| SEQ_0382 | Hypothetical protein | Hypothetical | 2.28 | 0.0408 |
| SEQ_0402 | Putative cell surface-anchored protein | Surface anchored | 3.94 | 0.0055 |
| SEQ_0430 | Sucrose-6-phosphate hydrolase | Nutrient metabolism | 2.19 | 0.0493 |
| SEQ_0490 | Putative membrane protein | Membrane protein | -5.63 | 0.0015 |
| SEQ_0504 | Putative exported protein | Secreted protein | -4.93 | 0.0015 |
| SEQ_0546 | Streptolysin S precursor | Pathogenicity/adaptation/chaperones | -4.60 | 0.0015 |
| SEQ_0671 | Probable potassium transport system protein | Nutrient acquisition | -3.59 | 0.0015 |
| SEQ_0696 | DNA/RNA non-specific endonuclease | Pathogenicity/adaptation/chaperones | -2.21 | 0.0224 |
| SEQ_0721 | Immunoglobulin G-binding protein G precursor (IgG-binding protein G) LPXTG | Surface anchored | -2.35 | 0.0179 |
| SEQ_0817 | Hypothetical phage protein | Phage | -2.14 | 0.0168 |
| SEQ_0855 | Putative collagen-like surface-anchored protein | Surface anchored | 4.83 | 0.0234 |
| SEQ_0862 | GntR family regulatory protein | Regulator | -4.22 | 0.0015 |
| SEQ_0866 | Beta-galactosidase 3 | Pseudogene | -3.83 | 0.0042 |
| SEQ_0896 | Putative exported protein | Secreted protein | 3.43 | 0.0015 |
| SEQ_0931 | Putative permease | Nutrient acquisition | -9.03 | 0.0015 |
| SEQ_0932 | ABC transporter ATP-binding protein | Nutrient acquisition | -8.97 | 0.0015 |
| SEQ_0938 | Immunoglobulin G-endopeptidase (<i>ideS</i>) / Mac/ Secreted immunoglobulin binding protein (Sib38) | Pathogenicity/adaptation/chaperones | 4.62 | 0.0015 |
| SEQ_0947 | Conserved hypothetical protein | Hypothetical | 16.56 | 0.0015 |
| SEQ_0948 | Putative membrane protein | Membrane protein | 6.46 | 0.0015 |
| SEQ_0949 | Putative exported protein | Secreted protein | 15.15 | 0.0015 |
| SEQ_0950 | Conserved hypothetical protein | Hypothetical | 7.80 | 0.0015 |
| SEQ_0951 | Glycosyl transferase family protein | Glycosylation | 2.93 | 0.0015 |
| SEQ_0999 | <i>ideE</i> ; IgG endopeptidase | Pathogenicity/adaptation/chaperones | 2.88 | 0.0015 |

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|----------|---|-------------------------------------|--------|--------|
| SEQ_1001 | Putative exported protein | Secreted protein | 3.63 | 0.0015 |
| SEQ_1278 | Putative surface-anchored 5'-nucleotidase | Surface anchored | -3.66 | 0.0015 |
| SEQ_1281 | ABC transporter, ATP-binding/permease protein (pseudogene) | Pseudogene | -3.64 | 0.0043 |
| SEQ_1283 | ABC transporter, ATP-binding/permease protein | Nutrient acquisition | -3.55 | 0.0029 |
| SEQ_1291 | Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase family protein | Nutrient acquisition | -23.48 | 0.0015 |
| SEQ_1328 | Hypothetical protein (pseudogene) | Pseudogene | 2.46 | 0.0015 |
| SEQ_1345 | Transport system membrane protein | Nutrient acquisition | 2.26 | 0.0068 |
| SEQ_1346 | Extracellular solute-binding protein | Nutrient acquisition | 2.40 | 0.0015 |
| SEQ_1351 | Conserved hypothetical protein | Hypothetical | -6.75 | 0.0015 |
| SEQ_1352 | LysR family regulatory protein | Regulator | -2.34 | 0.0029 |
| SEQ_1375 | Sugar phosphotransferase system (PTS), mannose/fructose family, IIA component | Nutrient acquisition | 2.67 | 0.0055 |
| SEQ_1505 | Putative exported protein | Secreted protein | 6.32 | 0.0015 |
| SEQ_1543 | Putative exported protein | Secreted protein | 3.80 | 0.0015 |
| SEQ_1548 | Putative alkaline phosphatase synthesis sensor protein | Regulator | -3.40 | 0.0015 |
| SEQ_1549 | Alkaline phosphatase synthesis transcriptional regulatory protein | Regulator | -3.46 | 0.0343 |
| SEQ_1654 | Conserved hypothetical protein | Hypothetical | -3.31 | 0.0015 |
| SEQ_1661 | Metal-dependent transcriptional regulator | Regulator | -2.11 | 0.0336 |
| SEQ_1728 | Exotoxin L precursor, <i>seeL</i> | Pathogenicity/adaptation/chaperones | -4.71 | 0.0015 |
| SEQ_1768 | Putative cysteine synthase | Amino acid biosynthesis | 2.45 | 0.0015 |
| SEQ_1800 | Putative exported protein | Secreted protein | -8.16 | 0.0015 |

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|----------|--|-------------------------------------|--------|--------|
| SEQ_1817 | Collagen-like surface-anchored protein | Surface anchored | 4.15 | 0.0015 |
| SEQ_1821 | Putative lipoprotein | Nutrient acquisition | -13.75 | 0.0015 |
| SEQ_1903 | Extracellular solute-binding protein | Nutrient acquisition | -2.15 | 0.0427 |
| SEQ_1941 | Putative membrane protein | Membrane protein | 3.80 | 0.0015 |
| SEQ_1949 | Putative secreted alpha-amylase | Nutrient acquisition | 2.31 | 0.0317 |
| SEQ_1957 | Streptococcal histidine triad protein | Nutrient acquisition | -6.04 | 0.0015 |
| SEQ_1958 | Laminin binding protein | Nutrient acquisition | -8.05 | 0.0015 |
| SEQ_1959 | Putative cell surface-anchored protein | Surface anchored | 3.67 | 0.0015 |
| SEQ_1960 | Conserved hypothetical protein | Hypothetical | -4.55 | 0.0015 |
| SEQ_1977 | Type I restriction-modification system M protein | DNA modification | -2.07 | 0.0290 |
| SEQ_2010 | Thioredoxin (pseudogene) | Pseudogene | -2.95 | 0.0015 |
| SEQ_2014 | Streptokinase | Pathogenicity/adaptation/chaperones | -3.52 | 0.0015 |
| SEQ_2125 | ABC transporter ATP-binding protein | Nutrient acquisition | -2.65 | 0.0015 |
| SEQ_2126 | Transport system permease protein | Nutrient acquisition | -2.33 | 0.0215 |
| SEQ_2127 | Putative lipoprotein | Nutrient acquisition | -2.34 | 0.0144 |
| SEQ_2128 | Putative lipoprotein | Nutrient acquisition | -2.24 | 0.0267 |
| SEQ_2180 | Putative cell surface-anchored protein | Surface anchored | 4.24 | 0.0015 |
| SEQ_2190 | Putative cell surface-anchored protein | Surface anchored | 4.75 | 0.0015 |
| SEQ_2196 | PadR family regulatory protein | Regulator | -8.31 | 0.0015 |
| SEQ_2197 | Hypothetical protein | Hypothetical | -6.89 | 0.0015 |
| SEQ_2198 | Hypothetical protein | Hypothetical | -5.35 | 0.0015 |
| peg 1573 | Mobile element protein | Phage | 3.62 | 0.0015 |
| peg 1265 | Hypothetical protein | Hypothetical | 5.67 | 0.0015 |
| peg 1583 | N-acetylmannosamine-6-phosphate 2-epimerase | Nutrient metabolism | -6.70 | 0.0029 |
| peg 1601 | N-acetylmannosamine-6-phosphate 2-epimerase | Nutrient metabolism | -17.44 | 0.0053 |

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|----------|----------------------|--------------|-------|--------|
| peg 1647 | Hypothetical protein | Hypothetical | -7.17 | 0.0015 |
| peg 1771 | Hypothetical protein | Hypothetical | -3.91 | 0.0229 |