TABLE S1 Bacterial strains and plasmid used in this study

Strain	Relevant Characteristics	Source
S. gordonii strains:		
CH1	Parental strain Challis, sequenced	(1)
KS1	Kan^r derivative of CH1	(2)
KS1Ω*abpA*	*abpA*-deficient derivative of KS1 made by inserting *tet*(M) encoding Tc^r; Kan^r	(2)
KS1Ω*abpA*/pFS001	KS1Ω*abpA* transformed with pFS001; Kan^r, Tc^r, Em^r,	This study
Plasmids:		
pVA749	Plasmid for complementation, Em^r	(3)
pFS001	pVA749 carrying *abpA* and its promoter 285 bp upstream from the translational start site	This study

* r, resistance; Kan, kanamycin; Tc, tetracycline; Em, erythromycin.

1. **Tardif G, Sulavik MC, Jones GW, Clewell DB.** 1989. Spontaneous switching of the sucrose-promoted colony phenotype in *Streptococcus sanguis*. Infect Immun **57**:3945-3948.
2. **Tanzer JM, Thompson A, Sharma K, Vickerman MM, Haase EM, Scannapieco FA.** 2012. *Streptococcus mutans* out-competes *Streptococcus gordonii* in vivo. J Dent Res **91**:513-519.
3. **Macrina FL, Tobian JA, Jones KR, Evans RP, Clewell DB.** 1981. Molecular cloning in the streptococci. pp. 195-210. *In* A. Hollander, R. DeMoss, S. Kaplan, J. Konisky, D. Savage,

and R. Wolfe (ed.), Genetic engineering of microorganisms for chemicals. Plenum Publishing Corp., New York.

TABLE S2 Primers used in this study

Primer name	Primer sequence (5' to 3')	Target and purpose
Hind3C'abpAF	ATAAGCTTCAGAAGCAATAATTCGTATCCATG	*Hind*III underlined. Construction of *abpA* complemented strain
Hind3C'abpAR	ATAAGCTTCTTATTTGGAGCCTTCTTAGTTTG	*Hind*III underlined. Construction of *abpA* complemented strain
pVA749-F	CTCGCGCTCTAAACGCTCTA	Plasmid pVA749
pVA749-R	GGCAGTTGAAAGTCAGCACC	Plasmid pVA749
gyrA-F	GCGGATTGTTGTAACCGAGT	*gyrA*, endogenous control qRT-PCR
gyrA-R	ACGGACACCCTCACGATTAG	*gyrA*, endogenous control qRT-PCR
srtB-F	GAATGAGCCTTACATGGGGA	*srtB*, qRT-PCR
srtB-R	TACTTCCACGAGCATGACCA	*srtB*, qRT-PCR
SGO_0100-F	CTGAGGTTTCGCCCTCAACT	SGO_0100, qRT-PCR
SGO_0100-R	TAACTGCTGACCAGACTGCG	SGO_0100, qRT-PCR
SGO_0101-F	TTGGCTGCCATTCGTTACCA	SGO_0101, qRT-PCR
SGO_0101-R	GACTGGCTCCAAAGGTCACA	SGO_0101, qRT-PCR
SGO_0102-F	ACAGTTGCAGTCGGTCTGAG	SGO_0102, qRT-PCR
SGO_0102-R	TTATCCCTTGTCACCACCGC	SGO_0102, qRT-PCR
SGO_0103-F	GTCTCAGCACCTTCCGTTCA	SGO_0103, qRT-PCR

SGO_0103-R	TACGCGCCAAGGAAGTAGGA	SGO_0103, qRT-PCR
SGO_0104-F	ACGGAGCACCTGCTGTTATC	SGO_0104, qRT-PCR
SGO_0104-R	CAGTCAGCAAGGAAGGCAGA	SGO_0104, qRT-PCR
SGO_1174-F	CTGCCCAAGCTGGTACTTCA	SGO_1174, qRT-PCR
SGO_1174-R	CCACCAAGGCGAAGAAGAGT	SGO_1174, qRT-PCR
SGO_1175-F	TGGACAAGGTTCAGCCCAAG	SGO_1175, qRT-PCR
SGO_1175-R	TTTATCAGCCAGTTGTGCAT	SGO_1175, qRT-PCR
SGO_1176-F	AGAGCGGGCCTTTTCTAACC	SGO_1176, qRT-PCR
SGO_1176-R	TAGGACGGGTGAAACTTGGC	SGO_1176, qRT-PCR
SGO_1177-F	GGGCTTCCTGGTGCTCTATC	SGO_1177, qRT-PCR
SGO_1177-R	AACGTTGGAGACACAACCGA	SGO_1177, qRT-PCR
SGO_1178-F	GCAGCCTGCTCTAATCAAAAA	SGO_1178, qRT-PCR
SGO_1178-R	TCAGACATCATAGAAGAGTCCTTC	SGO_1178, qRT-PCR
SGO_1179-F	TCGGATCAGCCGAAAACGAT	SGO_1179, qRT-PCR
SGO_1179-R	ACCAAGGGGCATAGACCACT	SGO_1179, qRT-PCR

TABLE S6 Primers used for the gene junction amplification in RT-PCR of the gene clusters SGO_1173-1180 and SGO_2103-2106

Primer name	Primer sequence (5' to 3')
SGO_1173/1174-F	ACTCTTCTTCGCCTTGGTGG
SGO_1173/1174-R	AATCGAACCGTTCTGGGCTT
SGO_1174/1175-F	CATGCACAACTGGCTGATCC
SGO_1174/1175-R	CTTGCTCAGTGTGGAGGTGG
SGO_1175/1176-F	GCCAAGTTTCACCCGTCCTA
SGO_1175/1176-R	TTTCTCTGGCTAGCTTGGCT
SGO_1176/1177-F	ATTTTGGGCTTCCTGGTGCT
SGO_1176/1177-R	TACACCCCAGAAACAGCCAC
SGO_1177/1178-F	CGCTACACTTACAATCGCTGG
SGO_1177/1178-R	GATAGAGCACCAGGAAGCCC
SGO_1178/1179-F	GCTCTTCAGGGAGGTTTGCT
SGO_1178/1179-R	TGAATCACTTGACTTCATTTCGTCT
SGO_1179/1180-F	CGTGTGGAAACCTCTCGGAA
SGO_1179/1180-R	AGCACCAGCCCCATATCCTA
SGO_2103/2104-F	TCGGACTAGCTTCGATGGAGA
SGO_2103/2104-R	CCACAGCCTCATACCAGTGA
SGO_2104/2105-F	GTTGAAGGTGGAAGCCACAA
SGO_2104/2105-R	CAGCTGCAACAGCAACAACA
SGO_2105/2106-F	AGCAGGTGCAGTTGATGTGT
SGO_2105/2106-R	GTATGCGCCGTCGTTGTTAC