1 Supplemental Figures

- 2
- 3 Figure S1



4 Figure S1: Growth of *S. sanguinis* SK36 and *P. aeruginosa* PAO1 in coculture. (A

and B) The dilution series of S. sanguinis SK36 from an OD_{600} of 0.1 (Ss 1 = undiluted) 5 6 and the response of each indicated dilution (1:10, 1:100) to coculture with *P. aeruginosa* 7 PAO1 (A) and the corresponding *P. aeruginosa* PAO1 (PAO1) biofilm growth in coculture with each S. sanguinis dilution (B). The data shown in Figure 1A and Figure 8 9 S1 panels A and B are from the same experiments. Each bar represents an average of 10 three biological replicates with three technical replicates. Error bars represent SD. ns, not significant, **, P < 0.01 by repeated measures two-tailed student's *t*-test (A) or 11 12 repeated measures one-way analysis of variance (ANOVA) with Dunnett's post-test using PAO1 as the control (B). 13

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Figure S2: Coculture growth kinetics of *S. sanguinis* and *P. aeruginosa* PAO1 and PA14 over 24 hours. (A and B) The growth kinetics of the indicated bacterial species in coculture was investigated over 24 hours, with *S. sanguinis* biofilm and planktonic growth from coculture with *P. aeruginosa* PA14 and PAO1 (A), and the corresponding *P. aeruginosa* PA14 and PAO1 biofilm and planktonic growth (B). The data shown in Figure 1B and Figure S2 panels A and B are from the same experiments. Each time point represents the average of three biological replicates and three technical replicates.





26 Figure S3: All oral Streptococcus spp. tested in coculture with P. aeruginosa

27 **PAO1 and the corresponding** *P. aeruginosa* growth. (A) Coculture biofilm growth of

every oral *Streptococcus spp.* strain tested here with *P. aeruginosa* PAO1.

29 Streptococcus spp. are indicated by their strain number and correspond to the following

30 strains: S. anginosus C238, S. anginosus 5535, S. intermedius 4807, S. intermedius

31 7156, S. constellatus 4808, S. constellatus 7155, S. oralis ATCC35037, S.

32 parasanguinis ATCC15912, S. pneumoniae D39, S. peroris ATCC700780, S. oralis

33 7404, S. salivarius JIM8777, S. salivarius JIM8780, and S. salivarius 7402. (B) The

34 growth of *P. aeruginosa* PAO1 in coculture with each oral *Streptococcus spp.* strain

tested here. The data shown in Figure S3A and B, and Figure 1C are from the same

36 experiments. Each bar represents the average of three biological replicates with three

technical replicates. ns, not significant, *, P < 0.05, **, P < 0.01 by repeated measures

38 two-tailed student's *t*-test (A) or by repeated measures ANOVA with Dunnett's posttest

using PAO1 as the control (B).



Figure S4: S. sanguinis SK36 planktonic growth, and P. aeruginosa biofilm and 41 planktonic growth corresponding to Figure 1. (A to C) Coculture experiments were 42 conducted with S. sanguinis SK36 with different P. aeruginosa clinical and laboratory 43 44 strains to investigate the effects on S. sanguinis planktonic growth (A), and P. 45 aeruginosa biofilm (B) and P. aeruginosa planktonic growth (C). The data shown in Figure 1D and Figure S4 panels A to C are from the same experiments. Bars represent 46 the average of three biological replicates with three technical replicates. Error bars 47 indicate SD. ns, not significant, *, P < 0.05, **, P < 0.01, ***, P < 0.001 by repeated 48

- measures ANOVA with Dunnett's posttest for multiple comparisons using Ss only as the
 control (A), or by repeated measures two-tailed student's *t*-test (B and C). (D) *S. sanguinis* SK36 was tested in coculture with *P. aeruginosa* PA14 in the indicated rich
- 52 media. The error bars indicate the standard deviation. ns, not significant, *, P < 0.05 by
- 53 paired two-tailed student's *t*-test.

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Figure S5: *P. aeruginosa* catalase mutants do not have a defect in *S. sanguinis* 57 SK36 growth enhancement. (A) S. sanguinis SK36 biofilm growth data from coculture 58 59 with *P. aeruginosa* PA14 $\Delta katA$, $\Delta katB$, and $\Delta katAB$ mutants. (B) Corresponding *P.* aeruginosa biofilm growth data indicates no significant growth defects of *P. aeruginosa* 60 61 catalase mutants in coculture with S. sanguinis SK36. Bars represent the average of 62 three biological replicates with three technical replicates. Error bars indicate SD. ns, not significant by repeated measures ANOVA with Dunnett's post-test for multiple 63 64 comparisons using Ss only as the positive control (A) and by repeated measures 65 ANOVA with Tukey's post-test for multiple comparisons (B).

66 Figure S6



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Figure S6: The *P. aeruginosa* PA14 \triangle *dbpA* mutant does not have a defect in S. *sanguinis* SK36 growth enhancement. (A) *S. sanguinis* SK36 biofilm growth data from coculture with the *P. aeruginosa* PA14 *dbpA*::*TnM* and the \triangle *dbpA* mutants. (B) *P. aeruginosa* biofilm growth data from coculture with *S. sanguinis* SK36. Bars represent the average of four biological replicates with three technical replicates. Error bars indicate SD. ns, not significant, *, P < 0.05 by repeated measures ANOVA with Dunnett's posttest for multiple comparisons using Ss + PA14 as the control condition.

77 Figure S7



Figure S7: The *P. aeruginosa* PA14 *pqsL*::*Tn*M mutant does not have a growth
defect compared to wild-type *P. aeruginosa* PA14. *P. aeruginosa* PA14 biofilm
growth data from coculture with *S. sanguinis* SK36. The data shown in Figure S7 and
Figure 2B are from the same experiments. Bars represent the average of three
biological replicates with three technical replicates. Error bars indicate SD. ns, not
significant by repeated measures ANOVA with Dunnett's posttest for multiple
comparisons using *P. aeruginosa* PA14 only as the control condition.



Figure S8: S. sanguinis SK36 planktonic growth in coculture with the P. 86 aeruginosa PA14 pgs mutant strains, and the corresponding *P. aeruginosa pgs* 87 mutant strain biofilm and planktonic viable counts. (A to C) S. sanguinis SK36 88 89 planktonic growth from coculture with *P. aeruginosa* PA14 PQS biosynthetic mutants (A) and the corresponding P. aeruginosa PQS biosynthetic mutants' biofilm (B) and 90 91 planktonic growth data (C). The data shown in Figure 3B and Figure S8 panels A-C are 92 from the same experiments. Bars represent the average of three biological replicates and three technical replicates. Error bars indicate SD. *, P < 0.05, ***, P < 0.001 by 93 repeated measures ANOVA with Dunnett's posttest for multiple comparisons using Ss 94 only as the control condition (A) or by repeated measures ANOVA with Tukey's posttest 95 for multiple comparisons (B and C). 96





Figure S9: Quantifying growth from complementation studies. (A) S. sanguinis 99 SK36 planktonic growth data from coculture with wild type *P. aeruginosa* PA14, the 100 101 $\Delta pqsL$ mutant, complementation strain and vector control. (B and C) There is no 102 significant difference in P. aeruginosa biofilm (B) and planktonic (C) cells recovered from coculture with S. sanguinis SK36. The data shown in Figure 3C and Figure S9 103 panels A-C are from the same experiments. Bars represent three biological replicates 104 with three technical replicates. Error bars indicate SD. ns, not significant, **, P < 0.01, 105 106 by repeated measures ANOVA with Tukey's posttest for multiple comparisons.



- 108 Figure S10: There is no significant difference between the growth of *P*.
- 109 *aeruginosa* strains in the presence of different *Streptococcus* spp. Growth of the
- 110 wild-type and mutant *P. aeruginosa* strains in the presence of different *Streptococcus*
- spp. The data shown in Figures 3D and Figure S10 are from the same experiments.
- Bars represent three biological replicates with three technical replicates. Error bars
- indicate SD. ns, not significant by repeated measures ANOVA with Tukey's posttest for
- 114 multiple comparisons.
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117 Figure S11



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- 119 Figure S11: There is no significant difference between the growth of *P*.
- 120 *aeruginosa* PA14 wild type and mutant strains in coculture with *S. sanguinis*
- 121 **SK36.** Growth of the wild type and mutant *P. aeruginosa* PA14 as biofilms from
- 122 coculture with *S. sanguinis* SK36 (Ss). The data shown in Figures 4A and Figure S11
- are from the same experiments. Bars represent three biological replicates with three
- technical replicates. Error bars indicate SD. ns, not significant by repeated measures
- 125 ANOVA with Tukey's posttest for multiple comparisons.

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S. sanguinis SK36

129 **Figure S12: Complementation analysis.** Shown is the complementation analysis of

- the $\triangle pqsLpvdApchE$ mutant in coculture with S. sanguinis SK36. Introducing the
- pMQ72 plasmid carrying the *pchE* gene (pMQ72-*pchE*) but not the vector control
- 132 (pMQ72) restores the reduced viability of S. sanguinis SK36 observed for the $\Delta pqsL$
- 133 mutant. ***, P < 0.001 comparing $\Delta pqsL\Delta pvdA\Delta pchE/pMQ72$ to
- 134 $\Delta pqsL\Delta pvdA\Delta pchE/pMQ72-pqsE$. Significance was determined with a one-way ANOVA
- 135 followed by Tukey's multiple comparison. There was no significant difference (ns)
- 136 between the $\Delta pqsL$ mutant and the $\Delta pqsL\Delta pvdA\Delta pchE/pMQ72-pqsE$ strain using this
- 137 same test.



Figure S13: Growth under anaerobic conditions. (A) S. sanguinis SK36 planktonic 139 growth increases upon coculture with P. aeruginosa PA14 in anaerobic conditions. (B 140 141 and C) *P. aeruginosa* biofilm (B) and planktonic growth in coculture with *S. sanguinis* SK36 in anaerobic conditions are lower (C) compared to P. aeruginosa grown in air. 142 The data in Figure 4B and Figure S13 panels A-C are from the same experiments. Bars 143 144 represent the average of three biological replicates with three technical replicates. Error bars indicate SD. ns, not significant, *, P < 0.05, **, P < 0.01, ***, P < 0.001 by repeated 145 measures two-tailed student's *t*-test. 146 147





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ns

ApgsL + Ssx_1129

vpqsL + Ssx_

ApqsL + Ss

ApgsL + Ssx_0256 ApqsL + Ssx_0686 ApqsL + Ssx_1578 1581 ApqsL + Ssx_1744

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- the control (A) or with Tukey's posttest for multiple comparisons (B and C). 160

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Figure S14