Table S1. Identity and ADS activity levels of plaque bacterial strains [Huang et al., 2015].

STUDY CODE	ACCESSION NUMBER	HOT NO.✚	CLOSEST RELATIVE	SOURCE	ADS ACTIVITY (Mean ±SD)
			Streptococcus gordonii DL1	Lab strain	339.3±33.0
			arcA-deficient strains of *S. gordonii*	Lab strain	0
Streptococcus parasanguinis A1	KF733681.1	721	*Streptococcus parasanguinis* ChDC B356	CF	688.0±57.1*
Streptococcus intermedius A2	KF733728.1	644	*Streptococcus intermedius* ChDC B589	CF	390.1±17.3*
Streptococcus intermedius A3	KF733728.1	644	*Streptococcus intermedius* ChDC B589	CF	476.9±43.8*
Streptococcus intermedius A4	KF733728.1	644	*Streptococcus intermedius* ChDC B589	CF	233.1±15.7
Streptococcus intermedius A5	KF733728.1	644	*Streptococcus intermedius* ChDC B589	CF	252.85±61.79
Streptococcus intermedius A6	KF733728.1	644	*Streptococcus intermedius* ChDC B589	CF	237.5±11.5
Streptococcus gordonii A7	CP000725.1	622	*Streptococcus gordonii* str. Challis substr. CH1□	CA	283.3±5.2
Streptococcus gordonii A8	NR_074516.1	622	*Streptococcus gordonii* str. Challis substr. CH1	CF	431.9±15.4*
Streptococcus gordonii A9	NR_115242.1	622	*Streptococcus gordonii* ATCC 10558	CA	244.8±10.7
Streptococcus gordonii A10	NR_115242.1	622	*Streptococcus gordonii* ATCC 10558	CA	241.3±15.9
Streptococcus gordonii A11	NR_115242.1	622	*Streptococcus gordonii* ATCC 10558	CF	354.8±20.9*
Streptococcus australis A12	NR_036936.1	073	*Streptococcus australis* AI-1★	CF	309.2±1.4
Streptococcus australis A13	NR_036936.1	073	*Streptococcus australis* AI-1★	CF	287.3±12.7
Streptococcus sanguinis A14	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	129.0±5.6
Streptococcus sanguinis A15	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	119.7±3.7
Streptococcus sanguinis A16	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	129.1±10.4
Streptococcus sanguinis A17	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	94.1±4.3
Streptococcus sanguinis A18	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	107.1±9.1
Streptococcus sanguinis A19	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	98.0±5.7
Streptococcus sanguinis A20	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	93.1±1.4
Streptococcus sanguinis A21	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	116.8±14.0
Streptococcus sanguinis A22	CP000387.1	758	*Streptococcus sanguinis* SK36	CF	88.9±10.0
Streptococcus sanguinis A23	NR_113260.1	758	*Streptococcus sanguinis* SK1284_K2-1	CA	127.6±1.1
Streptococcus sanguinis A24	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	45.2±6.0
Streptococcus sanguinis A25	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	50.2±3.4
Streptococcus sanguinis A26	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	46.0±0.3
Streptococcus sanguinis A27	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	63.4±0.0
Streptococcus sanguinis A28	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	56.4±13.0
Streptococcus sanguinis A29	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	187.1±20.3
Streptococcus sanguinis A30	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	173.3±4.0
Streptococcus sanguinis A31	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	246.2±2.4
Streptococcus sanguinis A32	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	227.3±0.0
Streptococcus sanguinis A33	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	199.2±8.3
Streptococcus sanguinis A34	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	200.6±14.6
Streptococcus sanguinis A35	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	201.9±15.2
Streptococcus sanguinis A36	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	263.4±29.9
Streptococcus sanguinis A37	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	227.9±89.7
Streptococcus sanguinis A38	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	167.7±9.9
Streptococcus sanguinis A39	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	198.1±5.1
Streptococcus sanguinis A40	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	212.5±0.6
Streptococcus sanguinis A41	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	144.0±10.0

Streptococcus sanguinis A42	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	190.1±10.6
Streptococcus sanguinis A43	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	106.4±4.0
Streptococcus sanguinis A44	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CF	104.3±4.1
Streptococcus sanguinis A45	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CA	161.3±3.3
Streptococcus sanguinis A46	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CA	169.8±6.4
Streptococcus sanguinis A47	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CA	221.3±4.8
Streptococcus sanguinis A48	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CA	136.9±4.3
Streptococcus sanguinis A49	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CA	238.2±31.1
Streptococcus sanguinis A50	NR_113260.1	758	*Streptococcus sanguinis* JCM 5708	CA	182.0±39.3
Streptococcus sanguinis A51	KF733682.1	758	*Streptococcus sanguinis* ChDC B357	CF	250.8±1.3
Streptococcus cristatus A52	NR_115274.1	578	*Streptococcus cristatus* ATCC 51100	CA	187.5±41.4
Streptococcus cristatus A53	NR_115274.1	578	*Streptococcus cristatus* ATCC 51100	CA	129.2±31.6
Streptococcus cristatus A54	GU470899.1	578	*Streptococcus cristatus* F0329	CA	160.0±26.2
Streptococcus cristatus A55	GU470899.1	578	*Streptococcus cristatus* F0329	CA	159.0±9.1
Streptococcus cristatus A56	GU470899.1	578	*Streptococcus cristatus* F0329	CA	185.9±41.8

The 56 ADS-positive strains identified had greater than 99% sequence similarity with their assigned bacterial taxa, as derived from their database accession numbers. HOT = Human oral taxon ID from the Human Oral Microbiome Database. ADS activity was expressed as nanomoles of citrulline generated perminute per milligram of protein. An asterisk (*) indicates that the bacterial strain expressed higher ADS activity than *S. gordonii* DL1. SD = Standard deviation.

[1] The closest relative strains to *S. gordonii* A7 are *Streptococcus* sp. JCM 5703 and *S. gordonii* strain Challis substrain CH1.

[2] The closest relative strains to *S. australis* A12 and A13 are *S. australis* AI-1, but also *Streptococcus rubneri* LMG 27207 (accession No.: NR_109720.1). Because A12 and A13 were collected from dental plaque and are ADS-positive, whereas the *S. rubneri* strain in the database is an ADS-negative throat isolate, A12 and A13 will be considered herein as strains of *S. australis*.

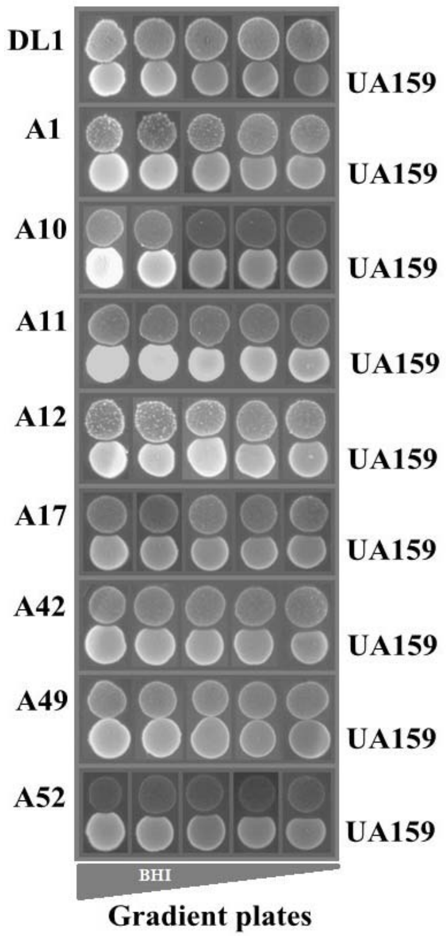

Figure S1. Growth inhibition of arginolytic strains on *S. mutans* UA159 using gradient BHI plates. Arginolytic strains were spotted first, and *S. mutans* was spotted 24 hr later.

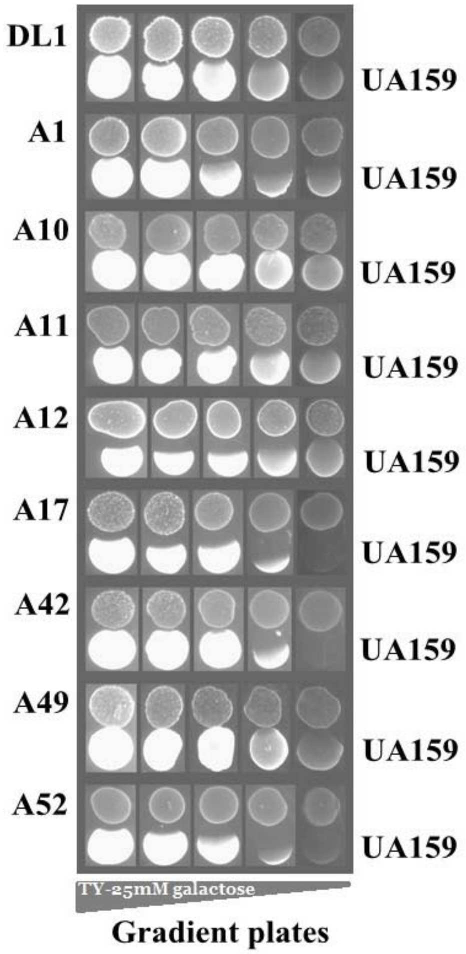

Figure S2. Growth inhibition of arginolytic strains on *S. mutans* UA159 using gradient TY-25mM galactose plates. Arginolytic strains were spotted first, and *S. mutans* was spotted 24 h later.