

Association among downstream taste signaling genes, oral microbiome, and severe early childhood caries

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Table S1. List of primers used.

Gene	Forward	Reverse	Amplicon length
GNAI2_1	AATCAAACCTCAGCAAGTCATCCG	CTCTTGCAACTAGCCCTCTGTG	341
GNAI2_2	CGCAGTCGCTCGGAACT	GTCAAAGTCCTTGTCTGGGGATT	318
GNAI2_3	GGAACCACCACAGCTCTGAAT	CCTTTCCTGCCCTTTCTCTGG	316
GNAI2_4	CCATGTCCAGAAAGCTGAAGTGT	GGCCACAGTGGTCAAGGTAA	346
GNAI2_5	GCTGGTGGGAAGGTTAGTTCTG	GACCTGCTTCAGAGAAGGGAAAA	336
GNAI2_6	TTCTGAGAAGCAGAAGGACCC	GAAACCTTTTGGGAGGTGGGAGA	329
GNAI2_7	GGTACATTCTTCAACTGCCTGA	AGGCCTTGGTTAACAGTCATCG	340
GNAI2_8	CAGGGTCCAGCTAAGGAAGC	GTTCACTAGGTGGTGAGGATGTG	340
GNAI2_9	ACCTGAGAAATGGGGTAGAAAGC	GTGAACCACTTGTGTTGCAGAT	342
GNAI2_10	CTATGACTTGGTGCTAGCTGAGG	CTACTTGGGACAAGAAGCAACCC	326
GNAI2_11	CCTTGCTGCACACGTAGGAT	CTTAGTTCTTCCCCAGCACCC	329
GNAQ_1	CAGAGTCCAGGACGGCAATAAAT	AAAGTGTCCCTCTTGTCTCTTGG	342
GNAQ_2	TGGGGTTTGGAGACAAAACCTAT	CCAACACAGGGCTACAAAACTG	342
GNAQ_3	ACTCCATTCCCCACACCCTA	ATTTTCCCTAAGTTTGTAAAGTAGTGC	308
GNAQ_4	GTAATCAAGGCATAAAAGCTGGG	TTTCCACAGACTCCTCTACCACT	326
GNAQ_5	CCTCCACATGGAAGTAAAGAGAA	AGACCAGTATATGAAGGAAGGTGTT	322
GNAQ_6	TATTTCCAAACCCCCCTATGCAC	TGTGGTCTGATGAGCTGCTATTG	334
GNAQ_7	CAAGGATGGTGGGCTGGG	TGTGTGCGCGCTGTGAG	250
GNAS_1	CTGCAGAGCCAGAGGG	AGGGACAGCTCAAGGTCT	337
GNAS_2	TCCGGCGCCAGGTAT	TCTGGGGCTCCTGAGTG	349
GNAS_3	GCCCAAGCACTCCACCTTC	GTGGGCAACTAACCTGAATCCAT	347
GNAS_4	CGAAGAGATGGAGACCGAAC	TTCTGGTGGAGGGCTGTAT	340
GNAS_5	AGCCTGGATTCCCCAGT	CCCCAAATCCTTCTCCATCAAG	345
GNAS_6	TCCCAGACCTTGCTCCA	CCCGTGAAGTTAGAAGGAGG	349
GNAS_7	GCCTCCCCTCTGGGTC	GAGAGGGTACTTTTCTCCCT	311
GNAS_8	GAAGCAGCAGAGATGGAAGGAG	GCATCTGGATCGGCTGGG	332
GNAS_9	ATTCGCAGCCGATCCC	GATGGATCTTGCGTCTGG	311
GNAS_10	CAGGGGCTCCCACTGC	ATCCGGAGGTCCCATCG	282
GNAS_11	GGCCAGACGCAAGATCCAT	GGGACTCTCAGATCGACCGAA	316
GNAS_12	CAACTTACTCCGAACTTTCTC	CCCCTAGCCCCACCAG	339
GNAS_13	TCCTTGCCGAGGAGCC	CGTGGCCCGGTAGACCT	251
GNAS_14	GTGTTTGGTTTTTGCATGTTGCT	AGAGCCCTTCCCAGGATTTTCTA	341
GNAS_15	CAGAAAGGCGACCTAAGAATTGC	TGTATGCCAATATGGCTGATGGT	340
GNAS_16	GTGGTGGAGTGGCTATTTCTCAT	TCATCGTTTAAGGTCAGGTAGCA	328

GNAS_17	CTCCTAACTGACATGGTGCAATA	GGGGCTAAGGCCACACAAG	350
GNAS_18	CAAGTGTCTGGTCACATAGGGAAC	TAGAACTTTCTGCCAGTGGGGTA	348
GNAS_19	CAAATTGATGTGAGCGCTGTGAA	ACAGTTGGCTTACTGGAAGTTGA	327
GNAS_20	TGGCTTTGGTGAGATCCATTGAC	CCCTAACACACAGAAGCAAAGC	327
GNAS_21	CTCTGGAATAACCAGCTGTCCTC	TGGGCGGTCACTCCAC	338
GNAS_22	AACAACAGGTTTGTGGAGTGACC	AAAAGAACCACCGCAATGAACAG	334
GNAS_23	GAGAAGCAAGAAAAACGCACTCC	ACACTGGATGTGCGTGAATAAA	339
GNAS_24	TATGACATCAGAGGCTGGCTGAC	CCTATGGTGGGTGATTAAGTCT	346
GNASE01_1	CAGCGCAACGAGGAGAAG	AGACAGAGCCCGCGAAC	100
GNAT3_1	ACTAAACACGTCATACAGCACCT	GCAGGAACTACATCAAGAACCAG	250
GNAT3_2	TGATTAGAAAAGCCACAGTCTT	TGACCGTTGCCTTTATGATTTTGC	327
GNAT3_3	CCAGTTTGGATCATAAAGATAACTCA	AATCCTACCCATTCTCATTCTG	324
GNAT3_4	TGTTGAGCATCATGAACAAGGAT	CCTCAATGCACATTTTGGAGGAT	328
GNAT3_5	GGCTAGAGCTTTTCTCCATGAGG	CCTGGTTTCTCAAACGCAAAGT	348
GNAT3_6	AATCTCATTATGTCACCTGTTC	CTTTATGCAATGGCAAATACCCT	322
GNAT3_7	GCTGCTGAGTCATTGAGCTGATA	GGCATCATCCAGCCATGAAAAAC	336
GNAT3_8	TTATGGCTCAAACTCTATTGCAG	TGTATGGTCAAAATTCCTTTTAATG	321
GNAT3_9	TTGCACAGGAACTATGACCACTC	CCAGACTTCACCACTATGCAGTT	346
GNAT3_10	TCAGGTTTTTGAAAGCAAAAGGGA	GCTAGGTACTTCAGCAGAGCATT	263
PLCB2_1	GGGCTGAACCTCCTTGCTAAAT	TCCGAACATGGATATTGGGCATC	349
PLCB2_2	GACCCACAGTGAAGGATGATG	TGTCTGTGTTGCCTGATTCTCT	255
PLCB2_3	CATCTCCTAAGGGCAAAGTCAGG	CCTGCCCTATGTTGGATTCTCA	315
PLCB2_4	CTTCCACCTGAAGTGGGGTC	CTTCTCGCCAAGCTTACTTCCTC	347
PLCB2_5	CCAACTCTCGCAGCTCCTTC	GGTGTGGAGGAGGCGAAC	324
PLCB2_6	TTTAAAGGGAAGTGCCTGTGGG	GAAGTCTGTGAAGCTCAAGGAGG	329
PLCB2_7	CTTCTGTGTAGGGAGAGCAGGT	GTTGGGGTGGGATCCAGATG	344
PLCB2_8	CTGGAAGTCTCCCTGTCTT	CTTGGGTCCTAGGCTGTGTG	315
PLCB2_9	ACTGTTCTGCCCTACTCCTTACA	ACCATGTTCTCACACTGATGCTG	335
PLCB2_10	GAGCTGCCTTGTCTTACTTCTCT	AGAACGAATGCTTCAGCTCTAGG	348
PLCB2_11	TTTCCAGGATATCAGGGGAGGG	AATGGAGGAAATGGAGACTGGG	335
PLCB2_12	TGCATTCTACCCCCAAATTCTCA	GTTAGGTTCTCTGGTGCAGATG	337
PLCB2_13	CTTGTTGTAGCTGTCCCTGAGTT	GAGGCATCTCTATAGGCCAGAGG	339
PLCB2_14	CTGACTCCGTGGCTGGATATTTA	TAAGAAGATGCAGTCGGATGAGG	349
PLCB2_15	AGAAGAGGGGAGGGCAAAGAA	GGTGAGTCGGGGAGGACTAT	348
PLCB2_16	ACATACAGCTCTGTGCGCACT	CTGGTAATAAGGAGCTCAGGCTAT	339
PLCB2_17	CAAGTGAACCCTAGCATCCTCTG	ATCACCTAAGGCCTCATGTTCT	342
PLCB2_18	GAACATGAGGCCTAGGGTGATT	TGTGTGATTGAAACTAGGCAGGG	325

PLCB2_19	CTCTAGCTTCAGCCCTCCAAC	GCCCTGAGAATAACACAGACCAT	347
PLCB2_20	GGAACCCCTGTGAAAGCAGAG	CTCATCGACAAGTATGAGCCCAG	327
PLCB2_21	AGAAACCAGACCATGCCTTCAG	GGATATGGACCTGTGCTCTTCTC	325
PLCB2_22	GTAGGGTTTGGCCTTAGCAT	GCAGGGGCAATAAGGTTACTAT	316
PLCB2_23	GGGGTGACCCTGCTTACAAC	TGTGGTTGATGGACTGTGTTCAAG	297
PLCB2_24	CATTCCTGGCCAAGTTGCTTTCT	CCTTGACGGGCTGCTTTCT	332
PLCB2_25	TGAGAAAGAAAGGCTTTGGGGAG	CCTGGACTTCCTGAGAGACACA	347
PLCB2_26	GATGTTTGACTAGGGCCAGTACG	TCCATCCTAACCATAACCACCAC	328
PLCB2_27	TCAGAAGTCAGGCTTCCCAC	CCATAGGAAGGGGAAGTTGGGTC	343
PLCB2_28	TGTCTGGCCTCAATGATAAGCAG	GAAATGGCATCCCCAATCCTCT	318
PLCB2_29	CATAAACCAATCCTCCCACCCAA	AGAGCAACTAGATTTCTGGAGCA	315
PLCB2E26_1	GGAGCTAAAGGGCGTGGT	GGGGACAGGCCCTGAGA	100
PLCB2E27_1	CAGGATCTCAGGGCCTGTC	GAGTCGGTGAGGGGGTTG	100
RAC1_1	AGGGTACCAATGTGTATGTGGTG	ACAGCAAAACAAATGGTCAAAGA	318
RAC1_2	TCTTGGCACACCTTCTCTAGGAT	TTTACATGGAACCAATCCCACCC	350
RAC1_3	TTGTATGCTTTTGGATCTCTCCG	TTTCATCAAGCAAAACCCCAACC	330
RAC1_4	GTCCAACAAGTCCTTCCCA	AACTAAAAATTCCTAGGCTAAGTG	253
RAC1_5	GGACATCTGTAAAGGAGCGTGTC	TGGTTCCCCAAGAGTACACCAG	337
RAC1_6	GTGGTGTGATCAGAAGAGAGTG	TCTGTAACAAAAAGTTGGCATTGA	328
RAC1E01_1	TGCAGTTTTCTCAGCTTTG	ACCGCCTACGCGAGACC	100
RALB_1	TAGGTTGAAAGCAAATCGCCTCT	AGCTATTCAGAAGCCACCTCAAC	347
RALB_2	AGTGCCCATATGTGGAATTTGTG	GAAAAGGCCAAAAAGCTTCTGGG	345
RALB_3	TCACAAAACCAGGGTTCGTTCTT	GTTCCCTAAAACCCAGCAGATGA	326
RALB_4	TCACAGTGTGAGGTTAACAAAAGAA	TTTGAGTGAATGAAGTCGGGGAG	325