

File S5. Alignment of *GJA1* cDNA and *GJA1P1* that shows the residues that can discriminate the two sequences. The residues without vertical line are mismatches between them. Despite three mismatches in the PCR primer pair, *GJA1P1* was amplified by the primers (File S4). The amplicon only from *GJA1P1* can be digested by ApeI.

Accession No. of *GJA1* and *GJA1P1* are NM_000165.5 and NG_003029.5, respectively.

Yellow, *GJA1* F and R primer binding sites; Gray, residues that mismatch PCR primers; Cyan, ApeI site

GJA1	1	AAAAGCTTTTACGAGGTATCAGCACTTTTCTTTTCATTAGGGGGAAGGCGTGAGGAAAGTA	60
GJA1P1	1	A--GCTTTTACGAGGTATCAGCACTTTTCTTTTCATT-GGGGGAAGGTGTGAGGAAAGTA	56
GJA1	61	CCAAACAGCAGCGGAGTTTTAACTTTAAATAGACAGGTCTGAGTGCCTGAACTTGCCTT	120
GJA1P1	57	ACAAACAGCAGCGGAGTTTTAACTTTAAATAGACAGGTCTGAGTGCCTGAATTTGCCTT	116
GJA1	121	TTCATTTTACTTCATCCTCCAAGGAGTTCAATCACTTGGCGTGACTTCACTACTTTTAAAG	180
GJA1P1	117	TTCATTTTACTTCATCCTCCAAGGAGTTCAATCACCTGGCGTGACTTCACTTCTTTTAAAG	176
GJA1	181	CAAAAGAGTGGTGCCCAAGCAACATGGGTGACTGGAGCGCCTTAGGCCAACTCCTTGACA	240
GJA1P1	177	CAAAAGAGTGGTGCCCAAGCAACATGCGTGACTGGAGCACTTAGGCCAACTCCTTGACA	236
GJA1	241	AGGTTCAAGCCTACTCAACTGCTGGAGGGAAGGTGTGGCTGTCAGTACTTTTCATTTTCC	300
GJA1P1	237	AGGTTCAAGCCTACTTAACTGCTGGAGGGAAGGTGTGGCTGTCAGTACTTTTCATTTTCC	296
GJA1	301	GAATCCTGCTGCTGGGGACAGCGGTTGAGTCAGCCTGGGGAGATGAGCAGTCTGCCTTTC	360
GJA1P1	297	AAATCCTGCTGCTGAAGACAGTGGTTGAGTCAGCCTGGGGAGATGAGCAGTCTGCCTTTC	356
GJA1	361	GTTGTAACACTCAGCAACCTGGTTGTGAAAATGTCTGCTATGACAAGTCTTTCCCAATCT	420
GJA1P1	357	GTTGTAACACTCAGCAACCTGGTTGTGAAAATGTCTGCTATGACAAGTCTTTCCCAATCT	416
GJA1	421	CTCATGTGCGCTTCTGGGTCTGCAGATCATATTTGTGTCTGTACCCACACTCTTGTACC	480
GJA1P1	417	CTCATGTGCGCTTCTGGGTCTGCAGATCATATTTGTGTCTGTACCCATACTCTTGTACC	476
GJA1	481	TGGCTCATGTGTTCTATGTGATGCGAAAGGAAGAGAACTGAACAAGAAAGAGGAAGAAC	540
GJA1P1	477	TGGCTCATGTGTTCTATGTGATGCAAAAGGAAGAGAACTGAACAAGAAAGAGGAGGAAC	536
GJA1	541	TCAAGGTTGCCCAAACCTGATGGTGTCAATGTGGACATGCACTTGAAGCAGATTGAGATAA	600
GJA1P1	537	TCAAGGTTGCCCAAACCTGATGGTGTCAATGTGGAGATGCACTTGAAGCAGATTGAGATAA	596
GJA1	601	AGAAGTTCAAGTACGGTATTGAAGAGCATGGTAAGGTGAAAATGCGAGGGGGGTTGCTGC	660
GJA1P1	597	AGAAGTTCAAGTATGGTATTGAAGAGCATGGTAAGGTGAAAATGCAAGGGGGGTTGCTGC	656
GJA1	661	GAACCTACATCATCAGTATCCTCTTCAAGTCTATCTTTGAGGTGGCCTTCTTGCTGATCC	720
GJA1P1	657	GAACCTACATCATCAGTATCCTCTTCAAGTCTATCTTTGAGGTGACCTT---GCTGATCC	713
GJA1	721	AGTGGTACATCTATGGATTTCAGCTTGAGTGCTGTTTACACTTGCAAAAGAGATCCCTGCC	780
GJA1P1	714	AGTGGTACATCTATGGATTTCAGCTTGAGTGCTGTTTACACTTGCAAAAGAGATCCCTGCC	773
GJA1	781	CACATCAGGTGGACTGTTTCTCTCTCGCCCCACGGAGAAAACCATCTTCATCATCTTCA	840
GJA1P1	774	CACATCAGGTGGACTGCTTCTCTCTTGCCCCATGGAGAAAACCATCTTCATCATCTTCA	833
GJA1	841	TGCTGGTGGTGTCTTGGTGTCCCTGGCCTTGAATATCATTGAACTCTTCTATGTTTCT	900
GJA1P1	834	TGCTGGTGGTGTCTTGGTGTCCCTGGCCTTGAATATCATTGAACTCTTCTACGTTTCT	893

GJA1	901	TCAAGGGCGTTAAGGATCGGGTTAAGGGAAAGAGCGACCCCTTACCATGCGACCAGTGGTG	960
GJA1P1	894	TCAAGGGCGTTAAGGATTGGGTTAAGGGAAAGAGCGACCCCTTACCATGCGACCACTGGCC	953
GJA1	961	CGCTGAGCCCTGCCAAAGACTGTGGGTCTCAAAAAATATGCTTATTTCAATGGCTGCTCCT	1020
GJA1P1	954	CGCTGAGCCCCGCCAAAGACTGTGGGTCTCAAAAAATATGCTTATTTCAATGGCTGCTCCT	1013
GJA1	1021	CACCAACCGCTCCCCCTCTCGCCTATGTCTCCTCCTGGGTACAAGCTGGTTACTGGCGACA	1080
GJA1P1	1014	CACCAACTGCTCCCCCTCTCGCCTATGTCTCTTCCTGGGTACAAGCTGGTTAATGGCGACA	1073
GJA1	1081	GAAACAATTCTTCTTGCCGCAATTACAACAAGCAAGTGAGCAAAACTGGGGCTAATT	1140
GJA1P1	1074	GAAACAATTCTTCTTGCCGCAATTACGACAAGCAAGTGAGCAAAACTGGGGCTAATT	1133
GJA1	1141	ACAGTGCAGAACAAAATCGAATGGGGCAGGCGGGAAGCACCATCTCTAACTCCCACGCAC	1200
GJA1P1	1134	ACAGTGCAGAACAAAATCGAATGGGGCAGGCGGGAAGCACCATCTCTAACTCCCACGCAC	1193
GJA1	1201	AGCCTTTTGATTTCCCCGATGATAACCAGAATTCTAAAAAACTAGCTGCTGGACATGAAT	1260
GJA1P1	1194	AGCCTTTTGATTTCCCCGATGATAACCAGAATTCTAAAAAACTAGCTGCTGGACATGAAC	1253
GJA1	1261	TACAGCCACTAGCCATTGTGGACCAGCGACCTTCAAGCAGAGCCAGCAGTCGTGCCAGCA	1320
GJA1P1	1254	TACAGCCACTAGCCATTGTGGACCAGCAACCTTCAAGCAGAGCCAGCAGTCGTGCCAGCA	1313
GJA1	1321	GCAGACCTCGGCCTGATGACCTGGAGATCTAGATACAGGCTTGAAAGCATCAAGATTCCA	1380
GJA1P1	1314	GCAGGCCTCAGCCTGATGACCTGGAGATCTAGATACAGGCTTGAAAGTATCAAGATTTCCT	1373
GJA1	1381	CTCAATTGTGGAGAAGAAAAAAGGTGCTGTAGAAAGTGACCCAGGTGTTAATTTTGATCC	1440
GJA1P1	1374	CTCACTTGTGGAGAAGAAAAAAGGTGCTGTAGAAAGTGACCCAGGTGTTAATTTTGATCC	1433
GJA1	1441	GGTGGAGGTGGTACTCAACAGCCTTATTCATGAGGCTTAGAAAAACACAAAGACATTAGAA	1500
GJA1P1	1434	GGTGGAGGTGGTATTCAACAGTCTTATTCATGAGGCTTAGAAAAACACAAAGACATTAGAA	1493
GJA1	1501	TACCTAGGTTCACTGGGGGTGTATGGGGTAGATGGGTGGAGAGGGAGGGGATAAGAGAGG	1560
GJA1P1	1494	TACCTAGGTTCACTGGGGGTGTATGGGGTAGATGGGTGGAGAGGGAGGGGATAAGAGAGG	1553
GJA1	1561	TGCATGTTGGTATTTAAAGTAGTGGATTCAAAGAACTTAGATTATAAATAAGAGTTCCAT	1620
GJA1P1	1554	TGCATATTGGTATTTAAAGTAGTGGATTCAAAAACTTAGATTATAAATAAGAGTTCCAT	1613
GJA1	1621	TAGGTGATACATAGATAAGGGCTTTTTCTCCCCGAAACACCCCTAAGAATGGTTCTGTG	1680
GJA1P1	1614	TACATGATACATAGATTAGGGCTTTTTCTCCAGCAAAACACCCCTAAGAATGGTTCTGGG	1673
GJA1	1681	TATGTGAATGAGCGGGTGGTAATTGTGGCTAAATATTTTGTTTTACCAAGAACTGAAA	1740
GJA1P1	1674	TATGTGAATGAGTGGGTGGTAATTGTGGCTAAATATTTTGTTTTACCAAGAACTGAAA	1733
GJA1	1741	TAATTCTGGCCAGGAATAAATACTTCCTGAACATCTTAGGTCTTTTCAACAAGAAAAAGA	1800
GJA1P1	1734	TAATTCTGGCCAGGAATAAATACTTCCTGAACATCTTAGGTCTTTTCAACAAGAAAAAGA	1793
GJA1	1801	CAGAGGATTGTCTTTAAGTCCCTGCTAAAACATTCCATTGTTAAAAATTTGCACTTTGAAG	1860
GJA1P1	1794	CAGAGGATTGTCTTTAAGTCCCTGCTAAAACATTCCATTGTTAAAAATTTGCACTTTGAAG	1853
GJA1	1861	GTAAGCTTTCTAGGCCTGACCCTCCAGGTGTCAATGGACTTGTGCTACTATATTTTTTTTA	1920
GJA1P1	1854	GTTAGCTTTCTAGGCCTGACCCTCCAGGTGTCAATGGACTTGTGCTACTATATTTTTTTTA	1913

GJA1	1921	TTCTTGGTATCAGTTTAAAATTCAGACAAGGCCACAGAATAAGATTTTCCATGCATTTG	1980
GJA1P1	1914	TTCTTGGTATCAGTTTAAAATTCAGACAAGGCCACAGAATAAGATTTTCCATGCATTTG	1973
GJA1	1981	CAAAT-----ACGTATATTCTTTTTCCATCCACTTGCACAAATATCATTACCATC	2029
GJA1P1	1974	AAAATCTCAGCATTATACATATATT--TTTTCCATCCACTTGCACCATATCATTACCATC	2031
GJA1	2030	ACTTTTTTCATCATTCCTCAGCTACTACTCACATTCATTTAATGGTTTCTGTAAACATTTT	2089
GJA1P1	2032	ACTTTTTTCATCATTCCTCAGCTACTACTCACATTCATTTAATGGTTTCTGTAAACATTTT	2091
GJA1	2090	TAAGACAGTTGGGATGTCACTTAACATTTTTTTT---TTGAGCTAAAGTCAGGGAATCAA	2146
GJA1P1	2092	TAAGACAGTTGGGATGTCACTTAACATTTTTTTTCTTTTGAGCTAGAGTCAGGGAATCAA	2151
GJA1	2147	GCCATGCTTAATATTTAACAATCACTTATATGTGTGTCGAAGAGTTTGTGTTTGTTGTCA	2206
GJA1P1	2152	GCCATGCTTAATATTTAACAGTCACTTGTATGTGTGTGGAAG--TTTGTGTTTGTTGTCA	2209
GJA1	2207	TGTATTGGTACAAGCAGATACAGTATAAACTCACAAACACAGATTTGAAAAATAATGCACA	2266
GJA1P1	2210	TGTATTGGTACAAGCAGATACAGTACAAACTCACAAACACAGATTTGAAAAATAATGCACA	2269
GJA1	2267	TATGGTGTTCAAATTTGAACCTTTCTCATGGATTTTTGTGGTGTGGGCCAATATGGTGT	2326
GJA1P1	2270	TACAGTGTTCAAATTTGAACCTTTCTCATGGATTTTTGTGGTGTGGGCCAATACGGTGT	2329
GJA1	2327	TACATTATATAATTCCTGCTGTGGCAAGTAAAGCACACTTTTTTTTT-CTCCTAAAATGT	2385
GJA1P1	2330	TACATTATATAATTCCTGCTGTGGCAAGTAAACACACTTTTTTTTTTCTCCTAAAATGT	2389
GJA1	2386	TTTTCCCTGTGTATCCTATTATGGATACTGGTTTTGTTAATTATGATTCTTTATTTTCTC	2445
GJA1P1	2390	TTTTCCCCGTGTATCCTATTACGGATACTAGTTTTGTTAATTATGATTCTTTATTTTCTC	2449
GJA1	2446	TCCTTTTTTTTAGGATATAGCAGTAATGCTATTACTGAAATGAATTTCTTTTTCTGAAAT	2505
GJA1P1	2450	TCTTTTTTTTAGGATATAGCAGTAATGCTATTACTGAAATGAATTTCTTTCTCTGAAAT	2509
GJA1	2506	GTAATCATTGATGCTTGAATGATAGAATTTTAGTACTGTAAACAGGCTTTAGTCATTAAT	2565
GJA1P1	2510	GTAATCACTGATGCTTGAATGACAGAATTTTAGTACTGTAAACAGGCTTTAGTCATTAAT	2569
GJA1	2566	GTGAGAGACTTAGAAAAAATGCTTAGAGTGGA-----CTATTAAATGTGCCTAAATGAAT	2620
GJA1P1	2570	GTGAGAGACTTAGAAAAAATGCTTAGAGTGAGTGACTATTAAACGTGCCTAAATGAAT	2629
GJA1	2621	TTTGCAGTAACTGGTATTCTTGGGTTTTCC-TACTTAATACACAGTAATTCAGAACTTGT	2679
GJA1P1	2630	TTTGCAGTAACTGGTATTCTTGGGTTTGCCTACTTAATACACAGTAATTCAGAACTTGT	2689
GJA1	2680	ATTCTATTATGAGTTTAGCAGTCTTTTGGAGTGACCAGCAACTTTGATGTTTGCACTAAG	2739
GJA1P1	2690	ATTCT----GAGTTTAACAGTCTTTTGGAGTGACCAGCAACTTTGATGTTTGCACTAAG	2744
GJA1	2740	ATTTTATTTTGAATGCAAGAGAGGTTGAAAGAGGATTCAGTAGTACACATACAATAATT	2799
GJA1P1	2745	ATTTTATTTTGAATGCAAGAGAGGTTGAAAGAGGATTCAGTAGTACACATACAATAATT	2804
GJA1	2800	TATTTGAACTATATGTTGAAGACATCTACCAGTTTCTCCAAATGCCTTTTTTAAACTCA	2859
GJA1P1	2805	TATTTGAACTATATGCTGAAGACATCTACCAGTTTCTCCAAATGCCTTTTTTAAACTCA	2864
GJA1	2860	TCACAGAAGATTGGTGAAAATGCTGAGTATGACACTTTTCTTCTTGCATGCATGTCAGCT	2919
GJA1P1	2865	TCACAGACGACTGGTGAAAATGCTGAGTATGACACTTTTCTACTTGCATG----TCAGCT	2920

GJA1	2920	ACATAAACAGTTTTGTACAATGAAAATTACTAATTTGTTTGACATTCCATGTTAAACTAC	2979
GJA1P1	2921	ACATAAACAGTTTTGTACAATGAAAATTACTAATTTGTTTGACATTCCATGTTAAACTAT	2980
GJA1	2980	GGTCATGTTTCAGCTTCATTGCATGTAATGTAGACCTAGTCCATCAGATCATGTGTTCTGG	3039
GJA1P1	2981	GGTCATGTTTCAGCTTCACTGCATGTAATGTAGACCTTGTCCATCAGATCATGTGTTCTGG	3040
GJA1	3040	AGAGTGTTCTTTATTCAATAAAAGTTTTTAATTTAGTATAAACATA	3083
GJA1P1	3041	AGAGTGTTCTTTATTCAATA--GTTTTAATTTAGCAT	3075