Appendix 2. Exon specific probes in each kit of MLPA of *COL2A1* and *COL11A1.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Chr. Pos. | Genbank exon | LPO | RPO |
| *COL2A1* | 12q13.11 | 1 | TGCCTGCCTGCCTGCTTTCCA | TGCGTCCCTCAGCATCCTTCTCCCCGGCCCG |
| *COL2A1* | 12q13.11 | 24 | TCAAGATGGTCTGGCAGGTCCCAA | GGTGAGTGGGAGAAGAGGGGCTGGGGTCCCT |
| *COL2A1* | 12q13.11 | 16 | CAGGGTCCTCGTGGCCTGCCTGGTGA | AAGAGGACGGACTGGCCCTGCTGGCGCTGCG |
| *COL2A1* | 12q13.11 | 17 | GGCACCTCTCATGGTCACTTCCTTCT | TGCTCACAGGGTGCCCGAGGCAACGATGG |
| *COL2A1* | 12q13.11 | 4 | TGGCTTACTCGGCTTAATCCTGTGAATGTT | TCATGTTTCAGGGACAGAAAGGAGAACCTGGAGACATCAAGGAT |
| *COL2A1* | 12q13.11 | 10 | TAGCAGTTTATAGGGATTGACCTGGTATCCTCA | TTTTACTTTTTAGGGGCCTCAAGGATTTCAAGGCAAT |
| *COL2A1* | 12q13.11 | 43 | GGTCTGGCTGGTCAGAGAGGCAT | CGTCGGTCTGCCTGGGCAACGTGGTGAGAGAG |
| *COL2A1* | 12q13.11 | 6 | TCCTTCAGGGACCTGCAGGGGAACAA | GGACCCAGAGGGGATCGTGGTGACAAAGGTGAAAAAGTGAGTAAAA |
| *COL2A1* | 12q13.11 | 23 | GTCGGTCCCCCTGGAGAAAGAGTTAAGTGA | ATGTGGAGGCTCCATCCCATGGGGCCTGTGAC |
| *COL2A1* | 12q13.11 | 46 | GGACCTTCTGTTCCTGTCTCTTCTGGAACA | TTCTTCTCTGAGCCTGAGACCTCTCTCCTGACAGGGT |
| *COL2A1* | 12q13.11 | 1 | CTCCCATGTCTTTTCCGTCCTTGGTCT | AGGGCTCTCGGCCTGCGCCTCTGCAAACACC |
| *COL2A1* | 12q13.11 | 49 | CTGCCTCTTCCTTCTACACAGGGTCCTT | CTGGAGACCAAGGTGCTTCTGGTCCTGCTGGTCCTTCT |
| *COL2A1* | 12q13.11 | 14 | GCGAAGTCTGATTGAACATTTTCTCTTGTTCCCT | AGGGTTATCCAGGCCTGGACGGTGCTAAGGGAGAG |
| *COL2A1* | 12q13.11 | 51 | GCAAGAACCCTGCTCGCACCTGCAGA | GACCTGAAACTCTGCCACCCTGAGTGGAAGAGTGGTAAGCT |
| *COL2A1* | 12q13.11 | 20 | GACCCTGAAAAGGGAGACATTGTCAAATAAGCAGC | AAAGAATGAACCCCAACCACCTCCAGCCCTCC |
| *COL2A1* | 12q13.11 | 25 | CCGTCACATGGTATCCCACTGACTCCCTGTGTACCCTTG | TAGGGAGCCCCTGGAGAGCGAGGGCCCAGTGGTCT |
| *COL2A1* | 12q13.11 | 29 | CAGGAAATGGAGCTCAGCTGGGGTACCGTGGAGGTC | TGGAAACTCTGGGCCAGAAGTACCTTTGCCCAATCCTAGGG |
| *COL2A1* | 12q13.11 | 8 | CAGATGGCTGGAGGATTTGATGAA | AAGGCTGGTGGCGCCCAGTTGGGAGTAATGCAAGGACCAA |
| *COL2A1* | 12q13.11 | 35 | GCTGCTGGACTGCTGGGCATT | AGGATCCTAGCCCTGCACCCAGGAGAGCAGGAGAGAG |
| *COL2A1* | 12q13.11 | 27 | TCTGGTGAAGATGGTCGTCCTGGA | CCTCCAGGTCCTCAGGGGGCTCGTGGGCA |
| *COL2A1* | 12q13.11 | 53 | CTAGCTCCCTGCTGCCCCAGTACCCT | TGAGGTCCTTGAACCATGAACTCTTGGCAGCCCCT |
| *COL2A1* | 12q13.11 | 54 | CAGAAACAACACAATCCGTTGCAAACCCAA | AGGACCCAAGTACTTTCCAATCTCAGTCACTCTAGGACTCTGC |
| *COL2A1* | 12q13.11 | 39 | CCAGGGTTTTAGCCTGCCCCTCAT | TCACCTGCTTCCTCCTTCCCATTATAGGGTGCTGATGGCC |
| *COL2A1* | 12q13.11 | 13 | GGTGCTCGTGGTTTCCCAGGA | ACCCCAGGCCTTCCTGGTGTCAAAGGTCACAGAGTAAGTATCACGG |
| *COL2A1* | 12q13.11 | 52 | CCTGTGCCTGTCTGAGCCCCCATGGGTGCTGCCTCT | TCCCCCTGCAGGAGACTACTGGATTGACCCCAACCAAGGCTGCACCTTGGACGCCA |
| *COL2A1* | 12q13.11 | 2 | CTGTGTGCAGGATGGGCAGAGGTATAATGATAA | GGATGTGTGGAAGCCGGAGCCCTGCCGGATCTGT |
| *COL2A1* | 12q13.11 | 31 | CCAAACTCACTCCTTTGCTAACGCTTGTCACT | TCGGCTTCTAGGGACTTCCTGGCCCTCCTGGTCCCCCAGGT |
| *COL2A1* | 12q13.11 | 54 | CCTCCGTTCTGTAGGCATGCCCAA | ATAGCAGTCCTAAGGACTTCTTCTGTTGATTTTTCAACCGAGAGTAAGGACA |
| *COL11A1* | 01p21.1 | 29 | TTCCACAGGGAGCAGATGGTGTCA | GAGGTCTCAAGGGATCTAAAGGTGAAAAGGT |
| *COL11A1* | 01p21.1 | 34 | TGTCTTTGCTAGGGAGTAGCTGGCAAA | CCAGGCCCTCGGGGTCAGCGTGGTCCAACGG |
| *COL11A1* | 01p21.1 | 63 | CTCTCTCTTCTTTCTAACAGGGACCCG | CTGGCCAGAAAGGTGACAGTGGTCTTCCAGGGCCTCC |
| *COL11A1* | 01p21.1 | 27 | TCATCCTGGGAAAGAAGGCCAGTCTGGAGA | AAAGGGGGCTCTGGTAGGTTCCAAAGTATCCATTTAAATGTCC |
| *COL11A1* | 01p21.1 | 3 | TCAGGTGGAACTTTCCCAGAAGACTT | TTCAATACTATTTACAGTAAAACCAAAAAAAGGAATTCAGTCTTTCC |
| *COL11A1* | 01p21.1 | 41 | TGACGATGTTTATTATATTCTTTAGGGTGATCCAGGTCCTCA | AGGTATCTCAGGGAAAGATGGACCAGCAGGATTACGTGGT |
| *COL11A1* | 01p21.1 | 22 | GAGGTTTGCTGGGTCCAAGGGGA | ACTCCAGGAGCTCCAGGGCAGCCTGTATG |
| *COL11A1* | 01p21.1 | 42 | TCACTTTTCCTAGGGTGCACCTGGACTGAAAGGA | GGGGAAGGTCCCCAGGGCCCACCAGGTCCAGTTGTAA |
| *COL11A1* | 01p21.1 | 54 | TAGATGGTGTTGGTGGTGACAAGGGTGAAGATGGA | GATCCTGGTCAACCGGTGAGTAAATGCACTA |
| *COL11A1* | 01p21.1 | 67 | GCTGGTGCAAATGACATTCCTGAAACTTCTGAC | TGCCTCTGCTCGGCAAAATTTCACCTACCACTGTCATCAGTCA |
| *COL11A1* | 01p21.1 | 1 | GAGAGGAAAGGGCTAGAGACACGAAGAACG | CAAACCATCAAATTTAGAAGAAAAAGCCCTTTGACTTTTTCCC |
| *COL11A1* | 01p21.1 | Intr.24 | GTCCAATTGGTCCTCCTGGTGAAAAA | GTAAGTTACTCTGTTGTTCTCGTAAAGCCTGGTGAACATGT |
| *COL11A1* | 01p21.1 | 9 | CAAAGAAATAGACGGCAGGGATTCTG | ATCTTCTGGTAGATGGAGATTTAGGCGAATATGATTTTTATGAA |
| *COL11A1* | 01p21.1 | 50 | GTTGGTTCAGTTGGTGGTGTTGGAGAA | AAGGTAAATATGTTAGTGACACACAGTTTGAAACAGCATGAAT |
| *COL11A1* | 01p21.1 | 19 | GATGGACTTCCGGGTCTGCCA | GGTGACAAAGGTCACAGGGTAAGATACATCTATTCCT |
| *COL11A1* | 01p21.1 | 12 | GTTTCTCTATAGGGTATTATGGGTCCTCCA | GGTCTACAAGGCCCCACTGGACCCCCTGGTGACC |
| *COL11A1* | 01p21.1 | 8 | CAACTATGGAACAATGGAAAGTTACCAGAC | AGAAGCTCCTAGGCATGTTTCTGGGACAAATGAGGTAATACGT |
| *COL11A1* | 01p21.1 | 45 | CTCTAAGTCAAATCTTTCAATTTCAGGGTGAA | ATTGGTGAGCCGGGACAAAAAGGCAGCAAGGG |
| *COL11A1* | 01p21.1 | 57 | GAAGCAGGTGCAGAAGGTCCTCCTGGA | AAAACCGGCCCAGTCGGTCCTCAGGGACCTGCAGGAA |
| *COL11A1* | 01p21.1 | 36 | CTTTTCTTTTCTTGGTGCCAGGGCACTTCA | GGTGGCGATGGCCCTCCTGGCCCTCCAGGTGAAA |
| *COL11A1* | 01p21.1 | 59 | GACCTCCTGGCTTACCTGGTCTCAAAGGT | GACCCTGGCTCCAAGGGTGAAAAGGTGAGAATAAAAGAATG |
| *COL11A1* | 01p21.1 | 21 | CAATGACAGGGAGAAGATGGAGAAATTGGA | CCAAGAGGTCTTCCAGGTGAAGCTGTAAGCAACTTACTTT |
| *COL11A1* | 01p21.1 | 17 | CAACGGGAAAACCTGGAAAAAGGGTA | TGGCTTATTTTCATTGTGCATTTTGAAGGCATCTGCCATGATCA |
| *COL11A1* | 01p21.1 | 31 | CAAGAGGGGAAGATGGCCCTGAAGGA | CCCAAAGGTCGAGCAGGCCCAACTGGAGACCC |
| *COL11A1* | 01p21.1 | 10 | CATTCAACAGATAAATGGCCATGGTGCAT | ATGGAGAGAAAGGACAGAAAGGAGAACCAGCAGTGGTTGAGCCT |
| *COL11A1* | 01p21.1 | 30 | CCAGGATTCAAAGGTGACATGGGTCTA | AAAGGTGACAGAGTAAGTATAGAGAAAATGTACACCAGTACAC |
| *COL11A1* | 01p21.1 | 52 | CCAAAGGAGAAAGAGGAGAGAAAGGGGAAG | CTGGTCCACCTGGAGCTGCTGGACCTCCAGG |
| *COL11A1* | 01p21.1 | 58 | CCTGGAGCTGCAGGCCAAGATGGACCA | CCTGGTCCTATGGTGAGTAAGATCTTTTCAGTCATTTAAAAAGTGA |
| *COL11A1* | 01p21.1 | 15 | CCACCTGGCCCAATGGGTCTA | ACTGGAAGACCAGGTCCTGTGGTAGGTTACCCCAACAAAG |
| *COL11A1* | 01p21.1 | 4 | TCTTTTTTAGGTGGCATCGGGTAGCAA | TCAGCGTGGAGAAGAAAACTGTGACAATGATTGTTGATTG |
| *COL11A1* | 01p21.1 | 60 | TCTGCCTTTCAAAGGGACATCCTGGTTTAA | TTGGCCTGATTGGTCCTCCAGGAGAACAAGGGGA |
| *COL11A1* | 01p21.1 | 35 | TCTCATCTGCAGGGTCCTCGAGGT | TCAAGAGGTGCAAGAGGTCCCACTGGGAAACCTGGGCCAA |
| *COL11A1* | 01p21.1 | 65 | TGGATTGATCCTAACCAAGGTTGCTCA | GGAGATTCCTTCAAAGTTTACTGTAATTTCACATCTGGTGGTG |
| *COL11A1* | 01p21.1 | 44 | GGAGAGATGGAGTTCAAGGTCCTGTT | GGTCTCCCAGGGCCAGCTGGTCCTGCCGGCTC |
| *COL11A1* | 01p21.1 | 26 | GACCACAAGGAAAACCAGGACTTG | CTGGACTTCCTGGTGCTGATGGGCCTCCTGTAAG |
| *COL11A1* | 01p21.1 | 61 | CCCTTTAAATTGGCTGATTCTCTCTCTAGGGAA | TTCCTGGTCCTGCTGGTCCCTTAGGTCCACCTGG |
| *COL11A1* | 01p21.1 | 18 | GTCACTTCGCTTAATCATGCTGTTGG | CATTATTAGGGTCGTCCAGGTGCAGATGGAGGAAG |
| *COL11A1* | 01p21.1 | 39 | GGCTTTTACAAATAATACTTTGCCTCCTTAGGGA | TTTCAAGGCAAGACCGGCCCTCCTGGGCCAG |
| *COL11A1* | 01p21.1 | 55 | GTGAGGCTGGCCCACCAGGTC | CTCCTGGAAAACGAGTAAGTTTCTTTAATTCTTTATTTGA |
| *COL11A1* | 01p21.1 | 6 | GTATTTTGCCACTAACACAATTGCCTGAT | ATTTTTTCCTTTGCAATGTAGTATGCACCAGAGGATATAATCGA |
| *COL11A1* | 01p21.1 | 62 | GTAGGGTCCTCAAGGCCCAAAGGGTA | ACAAAGGCTCTACTGTAAGTACTTTTCCCTTTGAC |
| *COL11A1* | 01p21.1 | 20 | GGTCCTCCTGGTGATGATGGAAT | GAGGGTATGTTAATACTTCTTTTCTTAAGAAATATTTAAAATTAAAACAT |
| *COL11A1* | 01p21.1 | 68 | GGCTATGAAAAGACTGTCATTGAAATCAATACA | CCAAAAATTGATCAAGTACCTATTGTTGATGTCATGATCAATGACTTTG |
| *COL11A1* | 01p21.1 | 40 | GCTTATCTAATTTAGGGACCAACCGGT | GAGACTGGTCCAATAGGGGAACGTGGGCATCCTG |
| *COL11A1* | 01p21.1 | 37 | CAGGGTCCTCAAGGACCTCAGGGTCCAGTT | GGATTCCCTGGACCAAAAGGCCCTCCTGTAAGTGTCAGAG |
| *COL11A1* | 01p21.1 | 28 | GAGTAGCACTTTCAATTTATTACACGTATAAGTGGT | AATTCATCTATTTCAGGGTCCCCCTGGTCCACAAGGTCCT |
| *COL11A1* | 01p21.1 | 11 | CTTTTCCTGTTATAGGGTATGCTTGTCGAA | GGACCACCAGGACCAGCAGGACCTGCAGTATGTAAATGTT |
| *COL11A1* | 01p21.1 | 38 | CTGCCAGGACACCCTGGGCAACGT | GGGGAGACTGTAAGTGACCTTGTTACTCTTATTAAAAATTTCCATC |
| *COL11A1* | 01p21.1 | 16 | CTTTTTCTCTATAGGGGGGGCCTGGT | TCATCTGGGGCCAAAGGTGAGAGTGGTGATCC |
| *COL11A1* | 01p21.1 | 43 | GTATACTAGGGCTCACCAGGAGAACGTGGG | TCAGCAGGTACAGCTGGCCCAATTGGTTTACCAG |
| *COL11A1* | 01p21.1 | 2 | CACAATTCTCCAGAGGGAATATCAAAAACAACG | GGATTTTGCACAAACAGAAAGAATTCTAAAGGCTCAG |
| *COL11A1* | 01p21.1 | 47 | CAGGTCCTAGAGGACAGCAGGGGA | TGTTTGGGCAAAAAGGTGATGAGGGTGCCAGAGGCTT |
| *COL11A1* | 01p21.1 | 7 | CCAAGAAGAAGAAAAGTTATCAAGCATCAGCAA | AAGCCAAACTAGGGGTAAAGGTAGCGAAGAAAAAGCAATCAAG |
| *COL11A1* | 01p21.1 | 23 | CCATAAATACTTTTTCTTCATTGCAGGGTATGG | CAGGTGTAGATGGCCCCCCAGGACCAAAAGG |
| *COL11A1* | 01p21.1 | 5 | CCAGGGGGACATTCAGCAGTTTTTGATCA | CAGGTGATCCCAAGGCAGCATATGACTACTGTGAGCAT |
| *COL11A1* | 01p21.1 | 49 | CCAAGAGGCCCTCAAGGTCCCAAT | GGAGCTGATGTAAGAACTCTGAAATATATGTTAATTATTTTGAAGT |
| *COL11A1* | 01p21.1 | 64 | CGAGAAGACATACTGAAGGCATGCAAGCAG | ATGCAGATGATAATATTCTTGATTACTCGGATGGAATGGAAGA |

Note: Chr. Pos.= the position of the gene in the chromosome; LPO=the 5' half of the probe; RPO=the 3' half of the probe; Intr.=intron.