

Gene	Position (GRCh37/hg19)	Forward sequence (5'->3')	Reverse sequence (5'->3')	Amplicon size
<i>COL3A1</i>	chr2:189851842	ACCACATCTTTTGGCACACA	GCTACCATTTTCTTTTCCAACC	358
<i>COL3A1</i>	chr2:189855743	GCACTTTCTAGTTTTTCATGTTTTCC	TTCAAGTTGTCATTTTTTCATGG	440
<i>COL3A1</i>	chr2:189858779	TGATTCTTTTGACCACATTTCA	CAAAATGCAAAGAAGCCAGT	274
<i>COL3A1</i>	chr2:189861933	TGATTAGTTATTGCCCTTTGAGG	TGAGGTCCAGTTTCACCATTC	259
<i>COL3A1</i>	chr2:189863424	TCTAGGGCTTGCCTGGTACA	TGCTCTATAACCTGCTGAAGAAGG	513
<i>COL3A1</i>	chr2:189864023	TAGTTCCCACCCAGCTGTTC	CCTTGCAGACCAGGAGTACC	400
<i>COL5A2</i>	chr2:189899700	AATTGCCCCAGTTCTAGTG	CGCTTATGGAGACCACCAAT	330
<i>COL5A2</i>	chr2:189899755	AATTGCCCCAGTTCTAGTG	CGCTTATGGAGACCACCAAT	330
<i>COL5A2</i>	chr2:189901388	AGCAAAACCTTGTTTATGCAAT	CCCTCTGTTAATTCTTTTGGAGA	447
<i>COL5A2</i>	chr2:189904234	AGCCGCCTGATCTTCAGTAA	GACCACCCCATCTAGTTACAA	294
<i>COL5A2</i>	chr2:189904265	AGCCGCCTGATCTTCAGTAA	GACCACCCCATCTAGTTACAA	294
<i>COL5A2</i>	chr2:189907975	GCCAGGAAGACCCTGAAGAC	TTTTTCAGTGATCACCTACCATT	312
<i>COL5A2</i>	chr2:189909952	CAAGCTTGAGGAATTCATATTTTT	ACACATGGACATTTGCCTGA	343
<i>COL5A2</i>	chr2:189915371	GAGACTCAAAAATTAATGTCCCTACA	ACGGATGAGCTGTTTTCCACC	445
<i>COL5A2</i>	chr2:189918622	GTCTCAAAGGAGCCTCCAAA	TCCTACACAGTGACCAATGTCC	361
<i>COL5A2</i>	chr2:189931144	ACTGAACTGTGCAGGGAACC	GACTTCGTAAATTAGGCTTCCAA	311
<i>COL5A2</i>	chr2:189940142	GCATGTGGTGAGTGCTCTGT	AACTGAGTGAGGGTTATTGTCAGTT	279
<i>COL5A2</i>	chr2:190044330	ATGGCAAACCTACCATCCTC	TAAAGCTGCATCGCTTGAAA	296
<i>COL7A1</i>	chr3:48607731	CCCTGGATGGTGACATTAGG	GCCTCTGGACTCAAAGGAGA	312
<i>COL7A1</i>	chr3:48608574	ACTCCCTCTTCCCTCCTGTGG	AGCCCGTGTCTGAACTCTGT	311
<i>COL7A1</i>	chr3:48609817	GACAGAGGTCAGGAGGCAAC	CCACAAGCCTGTTTCCAAAT	446
<i>COL7A1</i>	chr3:48612300	GAGGGGACTCTATGGAAGG	GTGTGCCATAACCCTGGAAT	343
<i>COL7A1</i>	chr3:48613087	CCTGCAGGAGTGAAGAGAG	TCAAGGTGGGTGTTTAGGG	333
<i>COL7A1</i>	chr3:48614349	GCACCCTGAGACCTCAGAAA	TGTTTGGGCTGATGTGAGTC	264
<i>COL7A1</i>	chr3:48619925	TGTGGAGAGAGGATAGGAGCA	GGACCAGGAGTGGGACTTTT	229
<i>COL7A1</i>	chr3:48621017	GATGGAGCAGTGTTGATGA	CCCCTGGAAAGAAAGGAGAA	264

<i>COL7A1</i>	chr3:48622510	AGGCCAGAGGCAGAACAGT	TGTTCCACCCCAATAACAC	292
<i>COL7A1</i>	chr3:48623625	TTCTACCAAGAACCCCCAGA	AAGGCTATCATGCAGCCACT	272
<i>COL7A1</i>	chr3:48624040	ACCTCTCAAGGGTTCATCCA	CCTGCTCTGTCATCCTCCTC	367
<i>COL7A1</i>	chr3:48624478	CCTATTGGGTGGTCAGGAGA	GAAGGGCAGAAAGGTGTGTC	290
<i>COL7A1</i>	chr3:48627789	GAGAAGCAAGGGTCTGCAAG	GGTTGTGGTGTGTCAGATGCAA	423
<i>COL7A1</i>	chr3:48628920	TGACAGTTCAGGGCTCAGTG	GCTCTCCAACAGGACCAGAG	305
COL6A5	chr3:130098623	TGGATGTGAAGGAAAATTGC	TTCAGCGTGGAAATTGTCTG	397
COL6A5	chr3:130098639	CTATCCAAGTTGGGAAATCCA	TTCAGCGTGGAAATTGTCTG	274
COL6A5	chr3:130098653	CTATCCAAGTTGGGAAATCCA	TTCAGCGTGGAAATTGTCTG	274
COL6A5	chr3:130098666	CATATGGCAGCAGAAGAGCA	TCATTCTGGAGCTTTTTTCAGG	262
COL6A5	chr3:130104078	TTGACTGATGGGATGTCCAC	ACATCAGGCCTTGTCTCAGC	301
COL6A5	chr3:130104153	TGGGATGTCCACAGACAGAG	CCAGTCTTGGCATTGGTTT	382
COL6A5	chr3:130107482	CAAGGTTCTAGTCAACCAGCTTC	CCAATCTGGGTTTTGTCTGC	322
COL6A5	chr3:130107567	TGCAGGATGTGAAGACATGA	CCCTTGGAGTGGGTGAAGTA	312
COL6A5	chr3:130107599	TGCAGGATGTGAAGACATGA	CCCTTGGAGTGGGTGAAGTA	312
COL6A5	chr3:130107975	GGAGTAGCGCAGGATGATGT	CTGGAGGTCACAGGCATTTT	360
COL6A5	chr3:130114082	ATGGCTCAATTTGGAAGCAA	TCTCCTATGCCCAAACCAG	296
COL6A5	chr3:130124469	CATAGTGCCCATGTGCTTTG	GAAAATGAGGGAGGAAAGGAA	257
COL6A5	chr3:130125119	GGGATTGATGGACTTGATGG	TACCCCTTGCTTCAATCAG	344
COL6A5	chr3:130128898	CACCTCTTATAGCTTGACCCAAA	TCCAAAATAATATCACTTGCCAGA	381
COL6A5	chr3:130132401	TAAGTGCCAGTGTGAAAGC	TGATATGATTCCCAGCACCA	285
COL6A5	chr3:130135644	AGGCTGCATCAAGGAGTTGT	CCTAGACGATGGGTTGATGG	389
COL6A5	chr3:130150310	TTTGCAGGCCAGATTTCTTT	AAACCATGGCAACTCTTGCT	335
COL6A5	chr3:130150464	GAGCTTTAATAAAAACACGGGACA	TGGCTGTTTGACCATTGCTA	317
COL6A5	chr3:130150590	AACTGTCCTGTGGGAGCAAG	TGGCTGTTTGACCATTGCTA	253
COL6A5	chr3:130159330	TGGGAAAGTTCCAGGAGAAA	CTTAGCCCTCAAAGCCATCA	270
COL6A5	chr3:130159640	TGGCTTTGAGGGCTAAGTGT	TCACCATTTTGTGACCAGGA	374
COL6A5	chr3:130187662	AGATTTGGAGGGTGCATCTG	AGGTGGAGGTGTCAGTGGAGTG	371

<i>COL6A5</i>	chr3:130187718	TGCCATGAGTATGGAAATGC	AGGTGGAGGTCAGTGGAGTG	324
<i>COL1A2</i>	chr7:94033892	TTGGGAGAAAAGGAAAAGCA	CAGGTCCTTGGAAACCTTGA	354
<i>COL1A2</i>	chr7:94040384	TTGCAGGGTAGTCCTGGTTC	CAAAAATGCAACTGTCAGCAA	408
<i>COL1A2</i>	chr7:94049737	CAGATTCATCTTTGGTCCATT	GGAAATAAACAGTTACAGCTCTGG	329
<i>VEGFB</i>	chr11:64003467	GCAGGAAAACCAGTGAGGAC	CTCCTGTGCATCAGTCTCCA	360
<i>VEGFB</i>	chr11:64005068	CCCCAGCTCTAGGGAAGACT	CCTTCCCAAACAAACACCAC	331
<i>VEGFB</i>	chr11:64005069	CCCCAGCTCTAGGGAAGACT	CCTTCCCAAACAAACACCAC	331
<i>FLT1</i>	chr13:28885760	AGACAAAATAGGGCAAATGTTA	CCCAATCAATGCCATACTGA	331
<i>FLT2</i>	chr13:28897068	AAAATTTTCAGAGATGCATAGTATGTTG	CCCCTGTGCTAGTTCACGAT	366
<i>FLT3</i>	chr13:28964035	AGAAAACAGCCTTTTTGTTGC	ATGTGCCAAATGGGTTTCAT	339
<i>FLT4</i>	chr13:28971113	CCTGAGAGCAAGGATGAAGG	ACCTTGGTTGTGGCTGACTC	250
<i>FLT5</i>	chr13:28973215	AAGCGCATATGAAGGCAAAT	AGCTGACACCCAGCTTAAA	369
<i>FLT6</i>	chr13:29008200	TTGGCTGCAAGCATAAGAGA	TTGATCCCTGATGGAAAACG	254
<i>FLT7</i>	chr13:29012432	GCCCAGGTGTTTGTAAAGGAA	GGGCCAAATTCAGAGACAAA	389
<i>FLT8</i>	chr13:29012444	GCCCAGGTGTTTGTAAAGGAA	GGGCCAAATTCAGAGACAAA	389