

Table S1. PCR primers

Primer	Primer Sequence (5'-3')*	Chromosome Location	Amplicon Length (bp)
<i>GJB2U_F</i>	TATTATTAGTATTGATTTTTTTTTTGAAAAATTGG	chr13:20194345-20194494	150
<i>GJB2U_R</i>	AACAAACACTCCCTCTTAACT		
<i>GJB2L_F</i>	GGGGTTTTGTTTTTTTATGAGTAGATAT	chr13:20194339-20194514	175
<i>GJB2L_R</i>	TACCACCATTATTAACATTAACCTTTTCC		
<i>HOXA9U_F</i>	GGGGGGGAAGTATAGTTATTTAA	chr7:27165541-27165695	155
<i>HOXA9U_R</i>	ACTTTTACTATAAAAATTATAACTACAAAACATC		
<i>HOXA9L_F</i>	GGTTTTTGTTATAAAAATTATGATTGTAAA	chr7:27165544-27165692	153
<i>HOXA9L_R</i>	AAAAAAATACAATCACCTAATAAATTAC		
<i>MEOX2U_F</i>	GGTAGGGTTTTGAAGTTGTTATTTG	chr7:15687782-15687891	110
<i>MEOX2U_R</i>	ACATAACTATTCTCCTACTCATTAC		
<i>MEOX2L_F</i>	GGGTTTAGGGTAGAATAGGTGATTATAGAT	chr7:15687784-1568951	168
<i>MEOX2L_R</i>	CAAAACTTTAAACTACTACTTACTTAAC		
<i>OLIG3U_F</i>	GTGTGGAGATTTTGGAGAGTTTG	chr6:137493892-137494036	145
<i>OLIG3U_R</i>	CAAAACCTACAACAATTAAACTAAAAAT		
<i>OLIG3L_F</i>	ATTTATAGTAGTTGAGGTTGAAGATTA	chr6:137493785-137493932	148
<i>OLIG3L_R</i>	AACAAAAATATAACCATCTTAAAAAACTTAC		
<i>PON3U_F</i>	GGAATTTAGGATTTTTGTAAAGGTTAGA	chr7:95396727-95396826	150
<i>PON3U_R</i>	AAAACACCAAAATCAAAAAACAAATTCCT		
<i>PON3L_F</i>	AAGAAGGTTAGGAGATAGGTT	chr7:95396728-95396871	144
<i>PON3L_R</i>	AAACTCCCAACTTCTACAAAACC		
<i>RASSF1L_F</i>	GGATGTGGGGATTTTTTTTTTTTAGTATAGTAAAG	chr3:50341043-50341160	118
<i>RASSF1L_R</i>	CCTCCTCACACCCACC		
<i>TFAP2BU_F</i>	AGGTTTAATAATTTTATTTTAAATTGTTT	chr6:50817519-50817675	157
<i>TFAP2BU_R</i>	CCATCCCCTCTATTTTCTACT		
<i>TFAP2BL_F</i>	TGTTTTTTTATTTTTTTTATAGGGTG	chr6:50817523-50817665	143
<i>TFAP2BL_R</i>	TTAATAACTTCCACCCCAAATT		
<i>Lambda516</i>	AGGAAGAGGATGGTGTAGTAATTAATAAGA	chrL:2560-2984	425
<i>Lambda517</i>	AACAAACTACATCCACACTTTCACCTC		

U, Upper or Watson strand; L, Lower or Crick strand; bp, base pairs; *human sequences based on Genome Reference Consortium Human Build 38 patch release 12