Table S1. Primers and DHPLC conditions for alternate *PKHD1* exons

		Primer sequences		Genomic DNA nucleotide		DHPLC conditions	
Exon	**Size (*bp*)**	**Forward (5'-3')**	**Reward (5'-3')**	**From**	**To**	**Temp.**	**Initial % buffer B**
20a (20)	261	GGATGTGGACTCCTCACTACG	AATCCTCCCAGCTGACTGAA	33325	33585	58.6, 62	56, 54
32a (32A)	353	CCACAGGTGCTATGAATTC	GTGACTACTGGTGTTGCTG	61321	61673	61, 63.7	57, 56
32a (32B)	365	AAGGCTTCACTTTCATGTATGAA	CCTCACAGTAAGTATGGTCC	61628	61992	59, 60.6	61, 59
32b (32D)	367	CTTCCTTGCAATGTAAACTTTT	GATACCAAAGTCCATCTACCTC	62332	62698	57.9, 58.9	59, 59
32b (32E)	441	CTCATCCGGTGCATTGTTC	CCAGAAGTGAAAGGAGCTACCA	62626	63066	58, 62	60, 55
32c (32E)	441	CTCATCCGGTGCATTGTTC	CCAGAAGTGAAAGGAGCTACCA	62626	63066	58, 62	60, 55
38/38a (38.1)	327	TGGGGTTTGGGTAGCTGTAG	CCAAGGCCATGAGACTGTTT	157391	157717	57.6, 59.6	58, 55
38/38a (38.2)	348	GCAGGATGGTGGAGCTTTTA	GCAGACACTTGGCATTTTCA	157589	157936	56.3, 57	60, 59
39a/39b (38)	332	AAATTATCTGGACAACTTTTCCTC	AGACCCCAATACAAATGTCCA	175001	175332	59, 60.5	58, 56
39b (39.1)	445	GGTACTGAGTGTCAGCTTGGC	CAGCCACCCAATTCTCTGTAA	175247	175691	54.9, 55.9	60, 59
39b (39)	278	TTTGGAGTGATGTCCTCAGTTCT	GCAATGCCATCTATCATCAGAC	175612	175889	57, 59.5	57, 55
39b (39.2)	328	CTCACTAATGAGAGGGAGAAGC	TTCTTTAATAGAAATATTTTCCCCAGA	175757	176084	57.3	57
41a (40)	286	CATGCTTTAGGTTCTCTGGACTTT	TGCCTTAAACATGGGAGAAA	178101	178386	58.5, 60.5, 61.5	57, 56, 54
41a (41.1)	400	GAGCTATGAGAGGTAAGGGGGT	CACAAAGCTAGTAAGTGGTAGAGAGACA	178319	178718	56.4	60
41a (41.2)	381	GATTCTGGAACAGGCAGTCC	TTCTGTTTTTCTGATTCTGATCTTG	178598	178978	57.8, 58.8	59, 58
44a (43)	258	TCAAGGGTGTTGAGTTGAGTACA	TTGAGAAAGAACTTTATGCCCTC	183819	184076	56.9, 58.9	56, 54
51a/51b (50)	300	TGATGGGGTTCCTTACTAAATGA	TGGTGATTTCTGACTATGTGCTC	239591	239890	58.3, 59.3, 60.3	57, 56, 55
60a (59)	285	GTGGCTGGTGGTTTATATG	GGGTTTGAAGAATTGCCAAG	340670	340954	54.1, 57.4, 58.7	57, 55, 52
62.1	378	TGTCCTGAGACCTTTTTCCTTC	TAAAGGGAATGGTGAGGGTG	343981	344358	55.7, 57.2	60, 58
62.2	377	CCTGGGAGTCATCTTTTATTTTTC	CAAACGCCCTGATGTAGTGA	344268	344644	55.5, 58.1	60, 57
62.3	440	CGCCTTTTACTTACTTATCCTGG	CAGCAAACTCTTCTGGCTGG	344570	345009	54.7, 57.5	60, 57
63	328	CCACAGTCTGTTGGATGAAAAA	TCTGGGTGAGTAGTTTTTGTACG	346942	347269	54.2, 56.5	58, 56
64.1	341	AAACTTGTGTTTAGAGAGAAAATTGTG	TCTCTTGAGACAGTGACCAGAA	405320	405660	56.7, 57.2	58, 57
64.2	323	TTCTTGTCCATCTTTGGTTGG	GAGGTGGTGAACTACAAGCCA	405578	405900	57.5, 58	58.57
64.3	349	TGCGTATAGCTGTGTTCCAA	TGAGTTAAAGAGAACACTGAAGGG	405815	406163	55.8, 56.7, 58.5	58, 57, 55
64.4	339	CATGCTTGATTAAGGCTACTGG	TTCACTGCTGTGGAATGTCA	406098	406436	56, 57.2, 58.8	59, 58, 56
64.5	326	AAGCTGATCTTGGGAAAGGA	GAACCAGTAGGGGGACAGAA	406365	406690	56.1, 57.4	58, 57
64.6	346	AACCCCAATTCACAACCAAC	TGGACAGTAATCAACATGAACAA	406630	406975	53.5, 55.5	58, 56
66a (62)	273	AATGGATTGTGGAAAATTGCT	GGCTGAATGCTACATGCTACTT	438315	438587	55.3, 57.3	56, 55
71a (67B)	394	TGCAAGAGACTGGGAACTGG	CTGGGAACATTCTGCCTTTC	468285	468678	61.1, 62.4	57, 56

GenBank NM_138694.2, AY129465

Primers of the longest *PKHD1* ORF amplifying (parts of) alternate exons are given in parentheses.

Predicted exons not included in the longest ORF are shown in bold type.