Supplementary Table II **MLPA probes.**

Probe name	Cytoband	Size (bp)	5′ half-probe[a]	3′ half-probe[b]	Comment	SD
GABRA	4p12	84	CAGCCTGTTGTCATAACCATCG	AGCAAACTGTCCAGGATGCG	Pilot	
RELN2	7q22.1	87	CAGCATTACGGAATGAAGGTCA	CCACAAGAAGTGGCTTCACAACC	Control	0.04
KRTAP2-1	17q21.2	93	CCCGGAACGCGTAACTCACCTT	CTGAAAAAGTCACACTCCCATTTCTCTAC	A	0.05
UQCRQ	5q31.1	93	CACAGTCACCGATCCGGTTGACTCGTT	CGTCATTTCCGGCAAGGTTGGAAG	GDF9	0.08
C5IGS1	5q31.1	96	GCTTTTCCACATGCCTTAGAAGTTTCAGC	AAGCACCTAGCGAACATCTTAATCC	GDF9	0.04
SH3GL3	15q25.2	96	GAACCTGAGGCCAGCTCTAACCAGTCTT	TCATGGATGCATACACCTGCCTGCAG	A	0
C2ORF67	2q34	99	CAAATCGTCATCAGAGCTGCTATCAGTTGCA	TCGGAATCCAAACCCTCTTCAACATG	A	0.03
C5IGS2	5q35.1	99	GTAGACAAAGGAGGTGGTGCAAGAGCGCAAA	ACTACTTCATGGGGAGGACGTCTCAG	GDF9	0.05
CXIGS1	Xp22.33	99	CAAAATTAACTGTAGGATTCCATTTTCTGC	ATCTACACATCACTGGCATAGGCTCTG		
DAX1	Xp21.2	102	GCAGCCTCAGCGGGCCTGTTGAAGACGCTG	CGCTTCGTCAAGTACTTGCCCTGCTTCCAG	Control	nd
KRTAP2-3	17q21.2	102	GATCCTCAAGCACGAATTCAACAATAACAT	CCTATCTATTTCCCCACATAATTATGCAGC	A	0.03
PCLN1[c]	3q28	105	GACACAAGGSGTGTAAAATGCACG	TTTCAGGGTGTGTTTGCATATGATTTAATCAATCAGTATG	Control	0.04
CACNA1C_3	12p13.33	108	CTCCTTCAGGTCTTGATTTCAGAAGGACTGGGGC	AGTTTGCTCAAGATCCCAAGTTCATCGAGGTC		
DNAH6	2p11.2	108	GTTTCCTGAGTGACTTTCCACCAGCTGTAAAGC	AAACTGCATCAAGCATTGTAGAAGCCTCAGTTG	A	0.03
GDF9_exon2-1	5q31.1	108	CCTTCCATCAGTGGAACTGCTATTTAACCTGGAT	CGCATTACTACCGTTGAACACTTACTCAAGTC	GDF9	0.09
GDF9_exon1-1	5q31.1	111	GCAGCTGATAACACCTTATTTAGCCAATTT	GTTAATTAGATACAGATTTACTTGGTTATTTAGCTTTCC	GDF9	0.04
KRTAP2-4	17q21.2	111	GTGGACTTTGCAAACACATTCTACAACCTGATGG	TTTTTACTGCTCAAACTGTCACCATCATCTTTTGC	A	0.04
SH3GL3_2	15q25.2	111	CTTTGCTGGGATAATATGCAATCAAGCTAATAGGTGCC	TTACCTGGACCTCCCAACAGGTAATAAATGG		
SMARCC1	3p21.31	111	CCTGCCAAAGGTGATCAGAGTCGATCAGTTGA	CCTTGGGGAAGATAATGTGACAGAGCAGACCAATCAC		
C5IGS5	5q31.1	114	GTATACTAATTCTCCTTGTTAACTAGCATATATAAATCAATCG	AGTCACACAGAACAATATAACATTTGTCC	GDF9	0.08
TJP3	19p13.3	114	CCCGTGGCCGACATTGCTATGCAGAAGTTGACT	GCTGAGATGCCTGACCAGTTTGAAATCGCAGGTGAGAAG	A	0.02
C2IGS12	2q34	117	GAGTGGAGACCACCTGGACAGTGACAGAGATCACTCATT	CCCCAGAAAGGTAGCATTATGACTTCAATTCCCATC		
C2IGS13	2p16.2	117	CTCTATTGCTATCCTCCATGGCCTGGAGAACGAATGCA	GGCCTCTTTCTCTTCTACCTATGCAAGATAAGAAATG		
GDF9_exon1-2	5q31.1	117	GCCTCCTTCCCGCGCTTTTCAAAG	TTCTATCTGTTGGGCGAGGTGGGTCACCTAGGCTGCAGCCAGACTCCAGAG	GDF9	0.03
P2RY8	Xp22.33	117	GCTACTACCACGTGTACAAGCTCACGCTGTGTCTCA	GCTGCCTCAACAACTGTCTGGACCCGTTTGTTTATTAC	A	0.03
KRTAP2-2	17q21.2	120	CATACTAGCTCACACTATGCATTGAAGACACCTTTT	CAGACCAACCACAGATGAGAAATACTTTTCCTAGGACTCCAG	A	0.02
SRY	Yp11.31	120	GAATGCGAAACTCAGAGATCAGCAAGCAGCTGGGA	TACCAGTGGAAAATGCTTACTGAAGCCGAAAAATGGCCATTCG	Control	nd
C15IGS2	15q26.2	123	GGAATATCCCATCGTTACTTAGGTGTCAATATGTGTAT	CAGATGACTGGATTAGTATTTTAAAACAGCAATGGCAAAGAAG		
CSPG5	3p21.31	123	GCCTGCTTGACTTATACGATGATTTCACCCCCTTCGATGAATCT	GATTTCTACCCCACCACATCCTTTTATGATGACTTGG	A	0.03
D.NAH6_2	2p11.2	123	GTCACACCTACACCCTGCAGGAATTTAA	GGCCGCACAAGTCATACGGCTAGCAGAGGTAACAAATTTTGTCTATAAGAATC		
GDF9_exon2-2	5q31.1	123	CTTCCCATCACCGTCACCGCAGAGGTCAGGAAACTGTCAGTT	CTGAATTGAAGAAGCCCTTGGGCCCAGCTTCCTTCAATC	GDF9	0.02
C5IGS4	5q31.1	126	CCCATTCATGCTCAAGGTCTTCACATACAAAGCAAGAGATGGCTT	CTAAGGGTTCTAACCACTCTGATGTTTTAAGCATGTGTC	GDF9	0.04
KRTAP2-3_2	17q21.2	126	GTGGAGTCTCTCATCTGATCCAGAAGGGGTAGAAGAGTCTGC	ACAAGCTTCTGTGCACCTGGGAATGTTTCGTGCGTTGAGAGG		
TSPYL6	2p16.2	126	GTGGTTGAGGGGACATGTCAGACCCTATCCTCAT	GGCAAGGTTAATATGTTGGTGTTCTTGACAAGTACCAGGCTTTCTCAGCC	A	0.03

RB1 ex23	13q14.2	129	GTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCT	AGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTTCACC	Control	0.03
CREBBP	16p13.3	131	CCAGACCCACCCAGGCCTCCTCAATAGTAACTCTGGCCATAGCTTAAT	TAATCAGGCTTCACAAGGGCAGGCGCAAGTCATGAATGGATC	Control	0.03
CACNA1C	12p13.3	132	CTGTGTGCATATGTCCTGCCCGTGTATATGCACCCACACCATGTGCCCG	TGCACACCAGTGACTACGCAGTCCCCCCTTTCTGGTTTAGC	A	0.03
C15IGS1	15q26.2	135	CCTACTTTTTCTGACACTGTGCTATGTTTTGAATTCTGTAGGAATCC	TTGGCGGAAGTTGCCTTCAGCATTTTAGGCCTGTCTAAACAGGTAG		
CACNA1C_2	12p13.33	135	GATGATTTGTAAACACACAGTCCTGTGCAGAAAGATCCCCTTCAGGAGG	TGTCTCCAGCATCCCAAAGCTGTGCGCACCTTCTCTTTTCCTGC		

Bp, basepair; SD, Standard deviation in probe validation; A, included in an MLPA kit for screening of array-CGH findings; GDF9, included in the MLPA kit for *GDF9* analysis; nd, not determined.

[a] The 5′ half-probes are preceded by the universal tag sequence GGGTTCCCTAAGGGTTGGA.

[b] The 3′ half-probes are followed by the universal tag sequence TCTAGATTGGATCTTGCTGGCAC.

[c] From Stern *et al*. (2004).