

Table S1 Primers utilized in this study.

		Forward (5'→3')	Reverse (5'→3')	AT	PS	Reference
<i>DLX5</i> sequencing	Exon 1-1	CCCAGACATCAGAGCCTT	GCTGAAGACTCGGGCAAAGT	60	651	This report
	Exon 1-2	GTTTGACAGAAGGGTCCCA	CTCCACAGGGCTCTCCTACT	60	545	This report
	Exon 2	CTATTTGAGGCCCTTCCGCA	CTTGCTTTCAACCCGCGAAA	65	542	This report
	Exon 3	CCCAGAGGTCCGAAGATGC	TGCCTTGTGGATCTCTGCA	63	875	This report
<i>TP63</i> sequencing	Exon 1	TCCCGGCTTATATCTATATATA	GACACATTCATAATACACAAGGCAC	60	220	1
	Exon 2	TCCACTTGGGTTTTCATGATAGAG	GTAAGCAATATTTTGACCACCCAC	60	300	1
	Exon 3	GCTTTAGTAAACAACAGCATG	GAAAAGACAGGTTTAAACAGAGC	60	281	1
	Exon 3-1	GAGAGAGAGGGACTTGAGTTCTG	GACCGAGAACCAGCAAATACG	60	261	1
	Exon 4	GGCTAATATTGGGGTTTCTGG	GGGGTCAGGTATGTGCGT	60	321	1
	Exon 5	CCTGTTGGTTCTCTCCTTCCT	TCAAACAAAATGCCACAG	60	306	1
	Exon 6	CCACCAACATCCTGTTTCATGC	GTCTACTCAGTCCATAGAGGTGTTG	60	257	1
	Exon 7	GAAGGAACAACGTCAGTTAAACCC	AAAGCAGCCACGATTTCACTTTGCC	60	245	1
	Exon 8	GTGGTAGATCTTCAGGGGACTTTC	CCAACATCTGGAGAAGATTC	60	263	1
	Exon 9	GCTTTAGAAGTGTTCAGG	ACACCTCCTTTCCCATTGTC	60	237	1
	Exon 10	TGAGGATTGACCACACTTCTAAC	CATCAATCACCTATTGTCTGATC	60	287	1
	Exon 11	TGCTCACCATTATTTCCATGTTTGTG	TCACAGAGTCTTGTCTTAAGC	60	257	1
	Exon 12	GGACTATAACAGTATCCGCCC	CAAGATGGACCACTGGGATG	60	294	1
	Exon 13	CTTATCTCGCCAATGCAGTTGG	AACTACAAGGCGGTTGTCTATCAG	60	241	1
	Exon 14	GGGAATGATAGGATGCTGTGG	AAGATTAAGCAGGAGTGCTT	60	449	1
Exon 15	GATGAAGTCCTAGGCCTTC	GGAAATACAACACACACT	60	205	1	
<i>WNT10B</i> sequencing	Exon 2	GTGTCTGATTGGGCAAGGTT	CTCATTGCTTAGAGCCCTGG	60	491	1
	Exon 3	GGAGAGTTGGAGGGGTCTG	GAAACCATCCCTTCCCGC	64	405	1
	Exon 4	TGCCTGTCAACCTTACCTCC	TAACCAGGCCTAAAAGCTG	60	470	1
	Exon 5	TGTGCCTCTGTGTTCTGTCC	GAAATCAGAGCAAAGGGCTG	60	598	1
	<i>BHLHA9</i> sequencing	Exon 1-1	AGAGGGCAGAGGGCAGAG	CGTGGCACTCCAGGTGTC	65	469
Exon 1-2		CAAGAGGCTCTCCAAGATCG	CCAAGACGCCTTTGCAGT	60	498	This report
Exon 1-3		GGCTGGCAGCTGGACTATAA	AGGATCCTGAGCCTTTCTGG	60	235	This report
7,406 bp sequencing		CGTGATTCTCCACTGTTACCTGTTTGTTCCTT	CCACATATAAGTCATCTTGGAGAATGGACACGAT	66	7,406	This report
FISH probe		CAGAAGTAAATACATACACTCTGCTTCTAATGC	ATCCAAGTTGAGATGTAATAACACACAAGACAT	66	8259	This report
Fusion point analysis	P1/P2	TCATTGTATGGTAATAGCCTAGACACAGATCC	CCGATATCGTGTGTTTATAGTGTTCCTG	66	2195	This report
	P3/P4	AATGTGGTTGAGACCCAGGC	CACACTGGATGGGAAGGACC	60	418	This report
	P5/P6	CTCAGCCAGGTGAAGAGGAC	CGAGGATCCTTTGTTTGTCT	60	214	This report
	RNaseP	CCTGGTACATGCCACTGATG	AGTGTAGAGGGCAAGCCAGA	60	213	2
	Microsatellite analysis	<i>D17S1174</i>	AGGGGAATCGCTTAAACCC	TTGGAGACATGGCAGGGAAC	60	387
Southern blot analysis	Probe 1	GACGGATAACAAGGACCGTG	TTTGGAGAGTTGATACAGCG	58	611	This report
	Probe 2	CTTATCCAGAGCCTACACAAC	CCTTTTCTGGAGAATACTC	55	241	This report
	Probe 3	CACTCTGCTTCTAATGCC	TTTTGGTTGGGCTGACTC	58	504	This report
	Probe 4	AGGCTGTGACACAGACCAC	GCCCCCTTACTTCTTTCAG	58	447	This report
	Probe 5	GTCAGGAGGCTACTCTCAC	AGAGTAGCCCTGGCACGAG	58	533	
Methylation analysis		CCTGGGAGAGAAGGAGGCTCAGG	TGGGCATTTTCTTTGCTTTTACTGACC	514		This report
Mouse expression study		CAAGAGGCTCTCCAAGATCG	CAGCATATGCCCTCAGATCA			This report

AT: annealing temperature (°C); and PS: product size (bp).

References

- Ugur SA et al.: Hum Mol Genet 2008, **17**:2644–2653.
- Wu X et al.: Breast Cancer Res 2012, **14**: R73.