

Appendix 3

Primers used to amplify a paralogue specific probe for use in Northern blot, Dot blot and Southern blot analyses. 'T' stands for the annealing temperature.

<i>Gene</i>	<i>Primer</i>	<i>Sequence</i>	<i>T</i> (°C)	<i>Size</i> (bp)
AIF1	F	TGACCATGCTGATGTATGAGGAAAAAGCGA	62	200
	R	GATCTGGAGGAGGGGGTAAT		
AIF1-L	F	TGACCATGTTAAGGGAGGAGAGCAAGCA	62	251
	R	CTGAGCCCTTAGCCAGAGAA		
BRD2	F	TGACCATGGAGGGATGCAGGGACATTT	62	411
	R	AACAAAGACAGTCCAGGGGA		
BRDT	F	TGACCATGGGGTACCATTGATATGACCCTT	62	199
	R	CTGTTTAATCATTTTATAGAGCAGTCA		
BRD3	F	TGACCATGGACAGATGGATGTCGCACAC	62	425
	R	CAAATGACAAGGACAATGCG		
BRD4	F	TGACCATGGTGAAAGGGACAGGACTCCA	65	508
	R	CAGTGAGAAGCATGCTGTGG		
C4	F	TGACCATGAGAGATGACTCCGCGTCTGT	65	395
	R	ATTCTCCTTCTGCCCCAGAT		
C3	F	TGACCATGCATTCCCCACTCCAGATAA	65	214
	R	ACATGAAGGTGAGGCAGGTC		
C5	F	TGACCATGTTGCACTTATGGACTCCTGTTG	65	352
	R	GATCAGTTTCCTGTTTCCTTGGT		
CLIC1	F	TGACCATGAAGTACCGGGGATTCACCAT	65	310
	R	CTTCCCTCATCCCCTCTTC		
CLIC4	F	TGACCATGGGAGATGGAGTCTGAATGGA	65	384
	R	AATGGGTTTAAGGGCACAGA		
CLIC3	F	TGACCATGGTACGCCGCTACCTGGAC	65	153
	R	CCCGACAAAGATGCCTTTATT		
CLIC5	F	TGACCATGTGTTGATGCCAAAATACCCA	65	427
	R	GACCACCTCCTAAATGTGGC		
CLIC6	F	TGACCATGTGTGGCCAAGAAGTACAGAGAT	65	146
	R	TTGCAACATCTGAATATGCG		
CLIC2	F	TGACCATGGAATTCTCAGGAGTCTGGCG	65	350
	R	GCAGTGGTTTGCCATACAGA		
GPX5	F	TGACCATGTAGCAATGGGGTCACAGTCA	65	277
	R	TCCTCTCCAGGTGCCATAAC		
GPX4	F	TGACCATGTCCACAAGTGTGTGGCCC	65	186
	R	CACAAGGTAGCCAGGGGTG		
GPX3	F	TGACCATGAACCCAAAGGAAAAACCAGC	62	451
	R	GAGTCTCAAGCCAGTGGACC		
GPX1	F	TGACCATGTCTCTCGAGAAGTGCAGGT	65	439
	R	ACTGGGATCAACAGGACCAG		
GPX2	F	TGACCATGTCTCTACTCCATCCAGTCCTGA	62	256
	R	CTTCACGCCTCTCAGACACC		
NOTCH4	F	TGACCATGCATTA AAAAGGCAGGCTGGAA	65	475
	R	CATCCCCACAGTGGAGTTCT		
NOTCH2	F	TGACCATGATGAGGAGGACAACACTGCC	65	395
	R	GCATCACAGCCAATTGCTTA		
NOTCH1	F	TGACCATGCAATACTGCATCCATGGCCT	65	244

	R	GTCCCTGAGCAACCATCTGT		
NOTCH3	F	TGACCATGATGTTCCATAGCCTTGCTGG	65	294
	R	GGGAATTCAGCTACACAGGG		
PBX2	F	TGACCATGGCAGGGCTGGACTCAGTAAT	62	409
	R	CACTTCCAACCTGTCCCAGT		
PBX1	F	TGACCATGCAGGAGGGAGGGTTTCTCTC	62	267
	R	TCAGTGATATGAGAGAGGGCG		
PBX3	F	TGACCATGCGAGTGTGGAAACATTGGGGT	62	325
	R	TCAATCCAGGGTGTAAATCCA		
PBX4	F	TGACCATGGTTTGGGGGATAAGCAGGAA	62	286
	R	GAAAATCTGTGCCAGTCCT		
RXRB	F	TGACCATGAAGAAATGCCAGTGGTGGAG	62	263
	R	AAAGGAGCCCCAAAGAGAAG		
RXRG	F	TGACCATGTCCTGACTAATCCCAGAGGG	62	215
	R	CATAGCCTGCGGAAACTT		
RXRA	F	TGACCATGTATACTTGGATATGGCGGGG	65	299
	R	CGGAGAAGCCACTTCACAGT		
TUBB_6p21.3	F	TGACCATGAGAGCAACATGAACGACCTG	65	200
	R	TGGAGGGAGATTGAAAGTGG		
TUBB2_18p11.3	F	TGACCATG TTCCTTCTTGAACCCTGGTG	65	225
	R	TTTATTTTGTGGCCCCTCAG		
TUBB5_19p13.3	F	TGACCATGCTGAATCCCCTCTGACTCCA	65	293
	R	CCTCTCTCCTCACAGGCAC		
TUBB4QL_10p15.3	F	TGACCATGACAGCATCTGGTTTTGCCTC	65	130
	R	CCACTGGAATGCTTGTTCCT		
TUBB4_16q24.3	F	TGACCATGCAGCTGGAGTGAGAGGCAG	65	201
	R	GCCTGGAGCTGCAATAAGAC		
TUBB1_20q13.3	F	TGACCATGTGCACTCACCATTAGCTTCG	65	396
	R	TAGTCAGGCACCTGGCTCTT		