

**Supp Table 1.** Primer and probe sequences and distance from transcriptional start site

<b>Primers and Probes</b>	<b>Sequences</b>	<b>Distance to transcriptional start site</b>
APC1 Ext F(2)	AAAACCCTATACCCCACTAC	-142 to +14 Transcript variant 2
APC1 Ext R(2)	GGTTGTATTAATATAGTTATATGT	
APC1 FM	AATACGAACCAAAACGCTCCC	
APC1 FUM	TAAATACAAACCAAAACACTCCC	
APC1 RM	TATGTCGGTTACGTGCGTTTATAT	
APC1 RUM	GTTATATGTTGGTTATGTGTGTTT	
APC1 UM Probe	6FAM-TTCCCATCAAAAACCCACCAATTAAC	
APC1 M Probe	VIC-CCCGTCGAAAACCCGCCGATTA	
BRCA1 Ext F	TATTTTGAGAGGTTGTTGTTTAG	-20 to +226
BRCA1 Ext R	AAACATCACTTAAACCCCTAT	
BRCA1 FM	TTTCGTGGTAACGGAAAAGCG	
BRCA1 FUM	TGGTAATGGAAAAGTGTGGGAA	
BRCA1 RM	CCGTCCAAAAAATCTCAACGAA	
BRCA1 RUM(4)	CCCATCCAAAAAATCTCAACAAA	
BRCA1 UM Probe	6FAM-CTCACACCACACAATCACAATTTTAAT	
BRCA1 M Probe	VIC-CTCACGCCGCGCAATCGCAATTT	
CDH1 Ext F	TAATTTTAGGTTAGAGGGTAT	-182 to +34
CDH1 Ext R	AACTCACAATACTTTACAATTC	
CDH1 FM	AGGGTTATCGCGTTTATGCGAG	
CDH1 FUM	GAGGGTTATTGTGTTTATGTGAG	
CDH1 RM	ACAACCAATCAACAACGCGAAC	
CDH1 RUM	CACAACCAATCAACAACACAAAC	
CDH1 UM Probe	6FAM-CTCCCCAAAACAAAATAACAACCCAC	
CDH1 M Probe	VIC-CCCAAACGAAACTAACGACCCGC	
CYCLIN D2 Ext F	TATTTTTTGTAAGATAGTTTTGAT	-1169 to -880
CYCLIN D2 Ext R	TACAACCTTCTAAAAAATAACCC	
CYCLIN D2 FM	TTTGATTAAGGATGCGTTAGAGTACG	
CYCLIN D2 FUM2	TTAAGGATGTGTTAGAGTATGTG	
CYCLIN D2 RM	ACTTTCTCCCTAAAAACCGACTACG	
CYCLIN D2 RUM2	AAACTTTCTCCCTAAAAACCAACTACAAT	
CCND2 UM Probe	6FAM-AAATCACCACCAACACAATCAACCCTA	
CYCLIN D2 M Probe	VIC-CGCCGCAACACGATCGACCCTA	

<b>Primers and Probes</b>	<b>Sequences</b>	<b>Distance to transcriptional start site</b>
ESR1 Ext F3	TTGGAGGTTTGGGAGTTTAG	-18 to +280 Transcript variant 1
ESR1 Ext R(4)	ACAATAAAACCATCCCAAATAC	
ESR1 FM 2	AGGGCGTTCGTTTTGGGATTG	
ESR1 FUM2	TGGTGGAGGGTGTGTTGTTTTG	
ESR1 RM 2	CGCCGACACGCGAACTCTAA	
ESR1 RUM2	ATCCCACCAACACACAAACTC	
ESR1 UM Probe	6FAM-AATCCAATAAAACCAAACAACCCAACAA	
ESR1 M Probe	VIC-CGATAAAACCGAACGACCCGACGA	
HIN1 Ext R(3)	AAACTACAAAACAAAACCAC	SCGB3A1; -206 to +80
HIN1 Ext F(2)	GTTTGTTAAGAGGAAGTTTT	
HIN1 FM	TAGGGAAGGGGTACGGGTTT	
HIN1-FUM (2)	AAGTTTTTGAGGTTTGGGTAGGGA	
HIN1 RM	CGCTCACGACCGTACCCTAA	
HIN1 RUM (2)	ACCAACCTCACCCACACTCCTA	
HIN1 UM Probe	6FAM-CAACTCCTACTACAACCAACAAACC	
HIN1 M Probe	VIC-ACTCCTACTACGACCGACGAACC	
RAR-□ Ext F	GTAGGAGGGTTATTTTTTGTT	+34 to +269
RAR-□ Ext R(2)	AATTACATTTTCCAACTTACTC	
RAR-□ FM	AGAACGCGAGCGATTGAGTAG	
RAR-□ FUM	TTGAGAATGTGAGTGATTTGAGTAG	
RAR-□ RM	TACAAAAAACCTTCCGAATACGTT	
RAR-□ RUM	TTACAAAAAACCTTCCAAATACATTC	
RAR-□ UM Probe	6FAM-AAATCCTACCCCAACAATACCCAAAC	
RAR-□ M Probe	VIC-ATCCTACCCCGACGATACCCAAAC	
RASSF1A Ext F(2)	GTTTTATAGTTTTTGTATTTAGG	-38 to +160
RASSF1A Ext R(2)	AACTCAATAAACTCAAACCTCCC	
RASSF1A FM	GCGTTGAAGTCGGGGTTC	
RASSF1A FUM	GGTGTGAAGTTGGGGTTTG	
RASSF1A RM	CCCGTACTTCGCTAACTTTAAACG	
RASSF1A RUM	CCCATACTTCACTAACTTTAAAC	
RASSF1A UM Probe	6FAM-CTAACAAACACAAACCAAACAAAACCA	
RASSF1A M Probe	VIC-ACAAACGCGAACCGAACGAAACCA	

<b>Primers and Probes</b>	<b>Sequences</b>	<b>Distance to transcriptional start site</b>
TWIST Ext F(3)	GAGATGAGATATTATTTATTGTG	-415 to -162
TWIST Ext R(4)	CCTCCCAAACCATTCAAAAAC	
TWIST FM	GTTAGGGTTCGGGGGCGTTGTT	
TWIST FUM (3)	GGTTTGGGGGTGTTGTTTGTATG	
TWIST RM	CCGTCGCCTTCCTCCGACGAA	
TWIST RUM (5)	CCATCACCTTCCTCCAACAAAC	
TWIST UM Probe	6FAM-AAACAATTCCTTCCCCACCAAAACA	
TWIST M Probe	VIC-AAACGATTCCTTCCCCGCCGAAA	