Table W1. Primer Sequences.

Gene	Primer Sequence or Catalog Number (for TaqMan Assays)
qRT-PCR primer sequences	
CITED1	Forward primer, 5′-AGGATGCCAACCAAGAGATG-3′
	Reverse primer, 5′-TGGTTCCATTTGAGGCTACC-3′
CXXC4	Forward primer, 5′-CAACCCAGCCAAGAAGAAGA-3′
	Reverse primer, 5′-AGATCTGGTGTCCCGTTTTG-3′
DKK1	Forward primer, 5′-TCCGAGGAGAAATTGAGGAA-3′
	Reverse primer, 5′-CCACAGTAACAACGCTGGAA-3′
*KREMEN1**	Hs00230750_m1 (spans exons 2–3 junction)
*PCNA**	Hs00427214_g1 (spans exons 3–4 junction)
*GAPDH**	Hs99999905_m1 (spans exons 3–4 junction)
cDNA sequencing primers for detection of CTNNB1 mutations	
CTNNB1	Forward primer (exons 2–4), 5′-AAAATCCAGCGTGGACAATGG-3′
	Reverse primer (exons 2–4), 5′-TGTGGCAAGTTCTGCATCATC-3′
	Forward primer (exons 1–5), 5′-GGAGGAAGGTCTGAGGAGCAG-3′
	Reverse primer (exons 1–5), 5′-CGATGATGGGAAGGTTATGC-3′

*TaqMan probe–based gene expression analysis assays from Applied Biosystems. Sequences are proprietary, but exon-exon boundaries to which primers and probe are designed are listed.

Table W2a. Gene List for Wnt Pathway RT^2 PCR Array.

Position	Unigene	Refseq	Symbol	Description
A01	Hs.515053	NM_001130	AES	Amino-terminal enhancer of split
A02	Hs.158932	NM_000038	APC	Adenomatous polyposis coli
A03	Hs.592082	NM_003502	AXIN1	Axin 1
A04	Hs.415209	NM_004326	BCL9	B cell CLL/lymphoma 9
A05	Hs.643802	NM_033637	BTRC	β-Transducin repeat containing
A06	Hs.17631	NM_003468	FZD5	Frizzled family receptor 5
A07	Hs.523852	NM_053056	CCND1	Cyclin D1
A08	Hs.376071	NM_001759	CCND2	Cyclin D2
A09	Hs.534307	NM_001760	CCND3	Cyclin D3
A10	Hs.529862	NM_001892	CSNK1A1	Casein kinase 1, α1
A11	Hs.631725	NM_001893	CSNK1D	Casein kinase 1, Δ
A12	Hs.646508	NM_022048	CSNK1G1	Casein kinase 1, γ1
B01	Hs.644056	NM_001895	CSNK2A1	Casein kinase 2, α1 polypeptide
B02	Hs.208597	NM_001328	CTBP1	C-terminal binding protein 1
B03	Hs.501345	NM_022802	CTBP2	C-terminal binding protein 2
B04	Hs.476018	NM_001904	CTNNB1	Catenin (cadherin-associated protein), β1, 88 kDa
B05	Hs.463759	NM_020248	CTNNBIP1	Catenin, β interacting protein 1
B06	Hs.12248	NM_025212	CXXC4	CXXC4
B07	Hs.654934	NM_014992	DAAM1	Dishevelled associated activator of morphogenesis 1
B08	Hs.655626	NM_033425	DIXDC1	DIX domain containing 1
B09	Hs.40499	NM_012242	DKK1	Dickkopf homolog 1 (*Xenopus laevis*)
B10	Hs.74375	NM_004421	DVL1	Dishevelled, dsh homolog 1 (*Drosophila*)
B11	Hs.118640	NM_004422	DVL2	Dishevelled, dsh homolog 2 (*Drosophila*)
B12	Hs.517517	NM_001429	EP300	E1A binding protein p300
C01	Hs.484138	NM_012300	FBXW11	F-box and WD repeat domain containing 11
C02	Hs.494985	NM_012164	FBXW2	F-box and WD repeat domain containing 2
C03	Hs.1755	NM_002007	FGF4	Fibroblast growth factor 4
C04	Hs.283565	NM_005438	FOSL1	FOS-like antigen 1
C05	Hs.663679	NM_003593	FOXN1	Forkhead box N1
C06	Hs.126057	NM_005479	FRAT1	Frequently rearranged in advanced T cell lymphomas
C07	Hs.128453	NM_001463	FRZB	Frizzled-related protein
C08	Hs.36975	NM_000510	FSHB	Follicle stimulating hormone, β polypeptide
C09	Hs.94234	NM_003505	FZD1	Frizzled family receptor 1
C10	Hs.142912	NM_001466	FZD2	Frizzled family receptor 2
C11	Hs.40735	NM_017412	FZD3	Frizzled family receptor 3
C12	Hs.19545	NM_012193	FZD4	Frizzled family receptor 4
D01	Hs.591863	NM_003506	FZD6	Frizzled family receptor 6
D02	Hs.173859	NM_003507	FZD7	Frizzled family receptor 7
D03	Hs.302634	NM_031866	FZD8	Frizzled family receptor 8
D04	Hs.466828	NM_019884	GSK3A	Glycogen synthase kinase 3α
D05	Hs.445733	NM_002093	GSK3B	Glycogen synthase kinase 3β
D06	Hs.714791	NM_002228	JUN	Jun proto-oncogene
D07	Hs.229335	NM_001039570	KREMEN1	Kringle containing transmembrane protein 1
D08	Hs.555947	NM_016269	LEF1	Lymphoid enhancer-binding factor 1
D09	Hs.6347	NM_002335	LRP5	Low density lipoprotein receptor-related protein 5
D10	Hs.584775	NM_002336	LRP6	Low density lipoprotein receptor-related protein 6
D11	Hs.202453	NM_002467	MYC	V-myc myelocytomatosis viral oncogene homolog (avian)
D12	Hs.592059	NM_033119	NKD1	Naked cuticle homolog 1 (*Drosophila*)

Table W2a. (*continued*)

Position	Unigene	Refseq	Symbol	Description
E01	Hs.208759	NM_016231	NLK	Nemo-like kinase
E02	Hs.643588	NM_000325	PITX2	Paired-like homeodomain 2
E03	Hs.386453	NM_022825	PORCN	Porcupine homolog (*Drosophila*)
E04	Hs.483408	NM_002715	PPP2CA	Protein phosphatase 2, catalytic subunit, α isozyme
E05	Hs.467192	NM_014225	PPP2R1A	Protein phosphatase 2, regulatory subunit A, α
E06	Hs.256587	NM_015617	PYGO1	Pygopus homolog 1 (*Drosophila*)
E07	Hs.647774	NM_021205	RHOU	Ras homolog gene family, member U
E08	Hs.401388	NM_021627	SENP2	SUMO1/sentrin/SMT3 specific peptidase 2
E09	Hs.713546	NM_003012	SFRP1	Secreted frizzled-related protein 1
E10	Hs.658169	NM_003014	SFRP4	Secreted frizzled-related protein 4
E11	Hs.500822	NM_022039	FBXW4	F-box and WD repeat domain containing 4
E12	Hs.728760	NM_004252	SLC9A3R1	Solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
F01	Hs.98367	NM_022454	SOX17	SRY (sex determining region Y)–box 17
F02	Hs.389457	NM_003181	T	T, brachyury homolog (mouse)
F03	Hs.573153	NM_003202	TCF7	Transcription factor 7 (T cell specific, HMG box)
F04	Hs.516297	NM_031283	TCF7L1	Transcription factor 7–like 1 (T cell–specific, HMG box)
F05	Hs.197320	NM_005077	TLE1	Transducin-like enhancer of split 1 (E(sp1) homolog, *Drosophila*)
F06	Hs.332173	NM_003260	TLE2	Transducin-like enhancer of split 2 (E(sp1) homolog, *Drosophila*)
F07	Hs.284122	NM_007191	WIF1	WNT inhibitory factor 1
F08	Hs.492974	NM_003882	WISP1	WNT1 inducible signaling pathway protein 1
F09	Hs.248164	NM_005430	WNT1	Wingless-type MMTV integration site family, member 1
F10	Hs.121540	NM_025216	WNT10A	Wingless-type MMTV integration site family, member 10A
F11	Hs.108219	NM_004626	WNT11	Wingless-type MMTV integration site family, member 11
F12	Hs.272375	NM_057168	WNT16	Wingless-type MMTV integration site family, member 16
G01	Hs.567356	NM_003391	WNT2	Wingless-type MMTV integration site family member 2
G02	Hs.258575	NM_004185	WNT2B	Wingless-type MMTV integration site family, member 2B
G03	Hs.445884	NM_030753	WNT3	Wingless-type MMTV integration site family, member 3
G04	Hs.336930	NM_033131	WNT3A	Wingless-type MMTV integration site family, member 3A
G05	Hs.25766	NM_030761	WNT4	Wingless-type MMTV integration site family, member 4
G06	Hs.696364	NM_003392	WNT5A	Wingless-type MMTV integration site family, member 5A
G07	Hs.306051	NM_032642	WNT5B	Wingless-type MMTV integration site family, member 5B
G08	Hs.29764	NM_006522	WNT6	Wingless-type MMTV integration site family, member 6
G09	Hs.72290	NM_004625	WNT7A	Wingless-type MMTV integration site family, member 7A
G10	Hs.512714	NM_058238	WNT7B	Wingless-type MMTV integration site family, member 7B
G11	Hs.591274	NM_058244	WNT8A	Wingless-type MMTV integration site family, member 8A
G12	Hs.149504	NM_003395	WNT9A	Wingless-type MMTV integration site family, member 9A
H01	Hs.534255	NM_004048	B2M	β-2-microglobulin
H02	Hs.412707	NM_000194	HPRT1	Hypoxanthine phosphoribosyltransferase 1
H03	Hs.728776	NM_012423	RPL13A	Ribosomal protein L13a
H04	Hs.592355	NM_002046	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
H05	Hs.520640	NM_001101	ACTB	Actin, β
H06	N/A	SA_00105	HGDC	Human genomic DNA contamination
H07	N/A	SA_00104	RTC	RT control
H08	N/A	SA_00104	RTC	RT control
H09	N/A	SA_00104	RTC	RT control
H10	N/A	SA_00103	PPC	Positive PCR control
H11	N/A	SA_00103	PPC	Positive PCR control
H12	N/A	SA_00103	PPC	Positive PCR control

Table W2b. Average C_t.

		Average C_t		SD	
		Control Group	Group 1	Control Group	Group 1
A01	AES	24.35	24.48	0.645497	0.320156
A02	APC	30.4	30.45	0.774597	0.911043
A03	AXIN1	25.43	26.28	0.464579	0.330404
A04	BCL9	26.88	27.38	0.780491	0.512348
A05	BTRC	26.88	26.43	0.727438	0.670199
A06	FZD5	23.85	23.65	0.675771	0.6245
A07	CCND1	24.98	25.4	0.556028	0.804156
A08	CCND2	34.88	34.25	0.25	0.818535
A09	CCND3	28.4	28.7	0.316228	0.547723
A10	CSNK1A1	23.7	23.38	1.089342	0.434933
A11	CSNK1D	23.15	23.35	0.718795	0.173205
A12	CSNK1G1	31.23	31.2	0.377492	0.812404
B01	CSNK2A1	23.65	23.85	0.443471	0.310913
B02	CTBP1	22.7	23.08	0.522813	0.457347
B03	CTBP2	28.75	28.88	0.932738	1.212092
B04	CTNNB1	22.13	22.28	0.639661	0.492443
B05	CTNNBIP1	27.58	28.53	1.212092	0.623832
B06	CXXC4	32.38	30.9	1.078193	0.616441
B07	DAAM1	25.45	25.93	1.008299	0.655108
B08	DIXDC1	27.03	27.48	0.644851	0.670199
B09	DKK1	20.75	21.65	0.81035	1.567376
B10	DVL1	24.9	24.75	0.571548	0.5
B11	DVL2	29.33	29.1	0.411299	0.469042
B12	EP300	24.95	24.9	0.925563	0.739369
C01	FBXW11	25.93	25.95	0.579511	0.288675
C02	FBXW2	28.7	28.8	0.503322	0.707107
C03	FGF4	35	35	0	0
C04	FOSL1	29.25	29.25	0.404145	0.412311
C05	FOXN1	33.7	34.78	1.536229	0.45
C06	FRAT1	28.75	28.65	0.785281	0.723418
C07	FRZB	28.13	31.2	1.007886	4.436215
C08	FSHB	34.93	35	0.15	0
C09	FZD1	30.3	30.1	0.909212	1.042433
C10	FZD2	35	35	0	0
C11	FZD3	27.48	27.53	0.85	0.221736
C12	FZD4	26.73	27.5	0.780491	0.983192
D01	FZD6	25.23	25.13	0.607591	0.442531
D02	FZD7	27.38	27.3	0.639661	0.469042
D03	FZD8	33.15	33.5	0.714143	0.57735
D04	GSK3A	25.78	26.08	0.464579	0.298608
D05	GSK3B	23.6	23.6	0.716473	0.559762
D06	JUN	26.4	26.35	0.752773	0.704746
D07	KREMEN1	28.73	28.1	0.531507	0.216025
D08	LEF1	25.23	25.43	0.499166	0.680074
D09	LRP5	25.68	25.93	0.330404	0.262996
D10	LRP6	24.75	24.68	0.750555	0.567891
D11	MYC	25.33	25.73	0.629153	0.30957
D12	NKD1	23.8	23.7	0.326599	0.469042
E01	NLK	26.3	26.2	0.668331	0.588784
E02	PITX2	28.1	27.83	0.983192	0.780491
E03	PORCN	27.9	28.18	0.559762	0.320156
E04	PPP2CA	26.7	26.83	0.432049	0.531507
E05	PPP2R1A	22.23	22.48	0.411299	0.320156
E06	PYGO1	28	28	0.535413	0.374166
E07	RHOU	23.78	24.18	0.537742	0.377492
E08	SENP2	25.2	25.48	0.496655	0.4272
E09	SFRP1	34.7	35	0.6	0
E10	SFRP4	29.83	30.58	0.914239	0.618466
E11	FBXW4	25.85	25.83	0.704746	0.585235
E12	SLC9A3R1	21.15	21.43	0.420317	0.35
F01	SOX17	35	35	0	0
F02	T	33.4	33.45	1.202775	0.619139
F03	TCF7	30.5	30.73	0.535413	0.377492
F04	TCF7L1	29.33	28.83	0.846069	0.287228
F05	TLE1	24.95	24.8	0.544671	0.648074
F06	TLE2	34.68	34.9	0.65	0.2
F07	WIF1	34.6	35	0.8	0
F08	WISP1	35	35	0	0
F09	WNT1	34.43	35	1.15	0
F10	WNT10A	32.65	33.53	2.977135	1.839157
F11	WNT11	30.58	32.03	0.411299	2.075853
F12	WNT16	34.2	33.75	1.28841	1.452584
G01	WNT2	35	35	0	0
G02	WNT2B	30.68	30.68	0.899537	1.652019
G03	WNT3	27.23	27.45	0.75	0.479583
G04	WNT3A	35	35	0	0
G05	WNT4	32.85	33.73	1.3	0.895824
G06	WNT5A	29.13	29.43	0.809835	0.537742
G07	WNT5B	34.73	35	0.377492	0
G08	WNT6	35	34.83	0	0.35
G09	WNT7A	35	35	0	0
G10	WNT7B	35	35	0	0
G11	WNT8A	35	34.95	0	0.1
G12	WNT9A	35	35	0	0
H01	B2M	21.05	21.55	0.519615	0.404145
H02	HPRT1	24.35	24.7	0.550757	0.637704
H03	RPL13A	19.73	19.55	0.55	0.369685
H04	GAPDH	16.58	16.65	0.660177	0.532291
H05	ACTB	19.13	18.95	0.655108	0.568624
H06	HGDC	35	35	0	0
H07	RTC	21.93	22.83	0.359398	0.330404
H08	RTC	22.43	23.4	0.368556	0.294392
H09	RTC	22.15	23.08	0.387298	0.499166
H10	PPC	18.65	19.23	0.493288	0.298608
H11	PPC	18.58	19.08	0.457347	0.330404
H12	PPC	18.3	18.78	0.391578	0.262996

Table W2c. Average ΔC_t.

		Average ΔC_t [C_t (GOI) – Average C_t (HKG)]		SD	
		Control Group	Group 1	Control Group	Group 1
A01	AES	4.383333	4.458333	0.551429	0.464579
A02	APC	10.433333	10.433333	0.438009	0.514242
A03	AXIN1	5.458333	6.258333	0.574376	0.512348
A04	BCL9	6.908333	7.358333	0.448351	0.403113
A05	BTRC	6.908333	6.408333	0.593405	0.481029
A06	FZD5	3.883333	3.633333	0.475706	0.316228
A07	CCND1	5.008333	5.383333	0.242479	0.404145
A08	CCND2	14.908333	14.233333	0.460575	0.684755
A09	CCND3	8.433333	8.683333	0.222777	0.31798
A10	CSNK1A1	3.733333	3.358333	0.833111	0.485627
A11	CSNK1D	3.183333	3.333333	0.439275	0.253859
A12	CSNK1G1	11.258333	11.183333	0.260164	0.420317
B01	CSNK2A1	3.683333	3.833333	0.244192	0.124722
B02	CTBP1	2.733333	3.058333	0.479197	0.514512
B03	CTBP2	8.783333	8.858333	0.684484	0.899537
B04	CTNNB1	2.158333	2.258333	0.341429	0.452462
B05	CTNNBIP1	7.608333	8.508333	1.0847	0.594652
B06	CXXC4	12.408333	10.883333	0.869813	0.738617
B07	DAAM1	5.483333	5.908333	0.654613	0.262996
B08	DIXDC1	7.058333	7.458333	0.412198	0.492443
B09	DKK1	0.783333	1.633333	0.630403	1.61314
B10	DVL1	4.933333	4.733333	0.448041	0.221108
B11	DVL2	9.358333	9.083333	0.21322	0.088192
B12	EP300	4.983333	4.883333	0.684484	0.574456
C01	FBXW11	5.958333	5.933333	0.490936	0.226078
C02	FBXW2	8.733333	8.783333	0.136083	0.440959
C03	FGF4	15.033333	14.983333	0.372181	0.412311
C04	FOSL1	9.283333	9.233333	0.19341	0.377124
C05	FOXN1	13.733333	14.758333	1.243948	0.471699
C06	FRAT1	8.783333	8.633333	0.664719	0.694422
C07	FRZB	8.158333	11.183333	0.678983	4.205948
C08	FSHB	14.958333	14.983333	0.409494	0.412311
C09	FZD1	10.333333	10.083333	0.822372	1.173314
C10	FZD2	15.033333	14.983333	0.372181	0.412311
C11	FZD3	7.508333	7.508333	0.578232	0.432371
C12	FZD4	6.758333	7.483333	0.525903	0.635085
D01	FZD6	5.258333	5.108333	0.438326	0.313138
D02	FZD7	7.408333	7.283333	0.56462	0.552771
D03	FZD8	13.183333	13.483333	1.027222	0.724952
D04	GSK3A	5.808333	6.058333	0.247019	0.287228
D05	GSK3B	3.633333	3.583333	0.445554	0.218581
D06	JUN	6.433333	6.333333	0.476873	0.454606
D07	KREMEN1	8.758333	8.083333	0.344668	0.338296
D08	LEF1	5.258333	5.408333	0.27672	0.718215
D09	LRP5	5.708333	5.908333	0.172938	0.195078
D10	LRP6	4.783333	4.658333	0.482662	0.211476
D11	MYC	5.358333	5.708333	0.568543	0.413991
D12	NKD1	3.833333	3.683333	0.306715	0.247207
E01	NLK	6.333333	6.183333	0.52985	0.422953
E02	PITX2	8.133333	7.808333	0.894841	0.822091
E03	PORCN	7.933333	8.158333	0.552436	0.330404
E04	PPP2CA	6.733333	6.808333	0.098131	0.183333
E05	PPP2R1A	2.258333	2.458333	0.303529	0.397562
E06	PYGO1	8.033333	7.983333	0.306715	0.310913
E07	RHOU	3.808333	4.158333	0.378472	0.183333
E08	SENP2	5.233333	5.458333	0.476873	0.254406
E09	SFRP1	14.733333	14.983333	0.313877	0.412311
E10	SFRP4	9.858333	10.558333	0.655673	0.206155
E11	FBXW4	5.883333	5.808333	0.599691	0.476387
E12	SLC9A3R1	1.183333	1.408333	0.270117	0.294863
F01	SOX17	15.033333	14.983333	0.372181	0.412311
F02	T	13.433333	13.433333	0.855483	0.507718
F03	TCF7	10.533333	10.708333	0.320878	0.705731
F04	TCF7L1	9.358333	8.808333	0.572438	0.236291
F05	TLE1	4.983333	4.783333	0.345875	0.425572
F06	TLE2	14.708333	14.883333	0.357331	0.378594
F07	WIF1	14.633333	14.983333	0.495162	0.412311
F08	WISP1	15.033333	14.983333	0.372181	0.412311
F09	WNT1	14.458333	14.983333	0.833278	0.412311
F10	WNT10A	12.683333	13.508333	2.646941	1.631717
F11	WNT11	10.608333	12.008333	0.395694	1.678044
F12	WNT16	14.233333	13.733333	1.015801	1.244544
G01	WNT2	15.033333	14.983333	0.372181	0.412311
G02	WNT2B	10.708333	10.658333	0.699934	1.279865
G03	WNT3	7.258333	7.433333	0.606371	0.418994
G04	WNT3A	15.033333	14.983333	0.372181	0.412311
G05	WNT4	12.883333	13.708333	1.143905	0.820738
G06	WNT5A	9.158333	9.408333	0.554694	0.305959
G07	WNT5B	14.758333	14.983333	0.707827	0.412311
G08	WNT6	15.033333	14.808333	0.372181	0.419325
G09	WNT7A	15.033333	14.983333	0.372181	0.412311
G10	WNT7B	15.033333	14.983333	0.372181	0.412311
G11	WNT8A	15.033333	14.933333	0.372181	0.394405
G12	WNT9A	15.033333	14.983333	0.372181	0.412311
H01	B2M	1.083333	1.533333	0.402308	0.169967
H02	HPRT1	4.383333	4.683333	0.361581	0.51099
H03	RPL13A	−0.241667	−0.466667	0.242479	0.235702
H04	GAPDH	−3.391667	−3.366667	0.29234	0.323179
H05	ACTB	−0.841667	−1.066667	0.604535	0.169967
H06	HGDC	15.033333	14.983333	0.372181	0.412311
H07	RTC	1.958333	2.808333	0.602695	0.56001
H08	RTC	2.458333	3.383333	0.598996	0.465475
H09	RTC	2.183333	3.058333	0.586578	0.700991
H10	PPC	−1.316667	−0.791667	0.355382	0.471699
H11	PPC	−1.391667	−0.941667	0.21322	0.533594
H12	PPC	−1.666667	−1.241667	0.237268	0.485627

Table W2d. $2^{-\text{Average}(\Delta\text{Ct})}$.

		$2^{-\text{Average}(\Delta\text{Ct})}$	
		Control Group	Group 1
A01	AES	0.047917	0.045489
A02	APC	0.000723	0.000723
A03	AXIN1	0.022745	0.013063
A04	BCL9	0.008325	0.006094
A05	BTRC	0.008325	0.011773
A06	FZD5	0.067764	0.080586
A07	CCND1	0.03107	0.023958
A08	CCND2	0.000033	0.000052
A09	CCND3	0.002893	0.002433
A10	CSNK1A1	0.075189	0.097508
A11	CSNK1D	0.110083	0.099213
A12	CSNK1G1	0.000408	0.00043
B01	CSNK2A1	0.077841	0.070154
B02	CTBP1	0.150378	0.120047
B03	CTBP2	0.00227	0.002155
B04	CTNNB1	0.224015	0.209013
B05	CTNNBIP1	0.005125	0.002746
B06	CXXC4	0.000184	0.000529
B07	DAAM1	0.022354	0.01665
B08	DIXDC1	0.007503	0.005686
B09	DKK1	0.581023	0.322343
B10	DVL1	0.032728	0.037595
B11	DVL2	0.001524	0.001844
B12	EP300	0.031613	0.033882
C01	FBXW11	0.016083	0.016364
C02	FBXW2	0.00235	0.00227
C03	FGF4	0.00003	0.000031
C04	FOSL1	0.001605	0.001661
C05	FOXN1	0.000073	0.000036
C06	FRAT1	0.00227	0.002518
C07	FRZB	0.0035	0.00043
C08	FSHB	0.000031	0.000031
C09	FZD1	0.000775	0.000922
C10	FZD2	0.00003	0.000031
C11	FZD3	0.005492	0.005492
C12	FZD4	0.009237	0.005588
D01	FZD6	0.026127	0.028989
D02	FZD7	0.005887	0.006419
D03	FZD8	0.000108	0.000087
D04	GSK3A	0.017845	0.015006
D05	GSK3B	0.080586	0.083427
D06	JUN	0.011571	0.012402
D07	KREMEN1	0.002309	0.003687
D08	LEF1	0.026127	0.023547
D09	LRP5	0.019126	0.01665
D10	LRP6	0.036314	0.039601
D11	MYC	0.024377	0.019126
D12	NKD1	0.070154	0.077841
E01	NLK	0.012402	0.01376
E02	PITX2	0.003561	0.004461
E03	PORCN	0.004091	0.0035
E04	PPP2CA	0.009399	0.008923
E05	PPP2R1A	0.209013	0.181957
E06	PYGO1	0.003817	0.003952
E07	RHOU	0.07138	0.056004
E08	SENP2	0.026583	0.022745
E09	SFRP1	0.000037	0.000031
E10	SFRP4	0.001077	0.000663
E11	FBXW4	0.016941	0.017845
E12	SLC9A3R1	0.440333	0.376747
F01	SOX17	0.00003	0.000031
F02	T	0.00009	0.00009
F03	TCF7	0.000675	0.000598
F04	TCF7L1	0.001524	0.002231
F05	TLE1	0.031613	0.036314
F06	TLE2	0.000037	0.000033
F07	WIF1	0.000039	0.000031
F08	WISP1	0.00003	0.000031
F09	WNT1	0.000044	0.000031
F10	WNT10A	0.000152	0.000086
F11	WNT11	0.000641	0.000243
F12	WNT16	0.000052	0.000073
G01	WNT2	0.00003	0.000031
G02	WNT2B	0.000598	0.000619
G03	WNT3	0.006532	0.005786
G04	WNT3A	0.00003	0.000031
G05	WNT4	0.000132	0.000075
G06	WNT5A	0.00175	0.001472
G07	WNT5B	0.000036	0.000031
G08	WNT6	0.00003	0.000035
G09	WNT7A	0.00003	0.000031
G10	WNT7B	0.00003	0.000031
G11	WNT8A	0.00003	0.000032
G12	WNT9A	0.00003	0.000031
H01	B2M	0.471937	0.345478
H02	HPRT1	0.047917	0.03892
H03	RPL13A	1.182358	1.381913
H04	GAPDH	10.495265	10.314962
H05	ACTB	1.792119	2.094588
H06	HGDC	0.00003	0.000031
H07	RTC	0.257326	0.14276
H08	RTC	0.181957	0.095833
H09	RTC	0.220166	0.120047
H10	PPC	2.490899	1.731073
H11	PPC	2.623816	1.920746
H12	PPC	3.174802	2.364716

Table W2e. Fold Change.

		Fold Change (Compared to Control Group)		
		Group 1		
		Fold Change	95% CI	Comments
A01	AES	0.9493	(0.48, 1.41)	Okay
A02	APC	1	(0.54, 1.46)	B
A03	AXIN1	0.5743	(0.27, 0.87)	Okay
A04	BCL9	0.732	(0.43, 1.03)	Okay
A05	BTRC	1.4142	(0.68, 2.15)	Okay
A06	FZD5	1.1892	(0.73, 1.65)	Okay
A07	CCND1	0.7711	(0.52, 1.02)	Okay
A08	CCND2	1.5966	(0.70, 2.49)	B
A09	CCND3	0.8409	(0.62, 1.06)	Okay
A10	CSNK1A1	1.2968	(0.45, 2.15)	Okay
A11	CSNK1D	0.9013	(0.59, 1.21)	Okay
A12	CSNK1G1	1.0534	(0.70, 1.41)	B
B01	CSNK2A1	0.9013	(0.73, 1.07)	Okay
B02	CTBP1	0.7983	(0.42, 1.18)	Okay
B03	CTBP2	0.9493	(0.22, 1.68)	Okay
B04	CTNNB1	0.933	(0.57, 1.29)	Okay
B05	CTNNBIP1	0.5359	(0.09, 0.99)	Okay
B06	CXXC4	2.8779	(0.65, 5.11)	Okay
B07	DAAM1	0.7448	(0.39, 1.10)	Okay
B08	DIXDC1	0.7579	(0.43, 1.09)	Okay
B09	DKK1	0.5548	(0.00001, 1.21)	Okay
B10	DVL1	1.1487	(0.76, 1.54)	Okay
B11	DVL2	1.21	(1.02, 1.40)	Okay
B12	EP300	1.0718	(0.42, 1.72)	Okay
C01	FBXW11	1.0175	(0.64, 1.39)	Okay
C02	FBXW2	0.9659	(0.66, 1.27)	Okay
C03	FGF4	1.0353	(0.64, 1.43)	C
C04	FOSL1	1.0353	(0.74, 1.33)	Okay
C05	FOXN1	0.4914	(0.05, 0.94)	B
C06	FRAT1	1.1096	(0.39, 1.83)	Okay
C07	FRZB	0.1229	(0.00001, 0.48)	A
C08	FSHB	0.9828	(0.59, 1.37)	B
C09	FZD1	1.1892	(0.03, 2.35)	B
C10	FZD2	1.0353	(0.64, 1.43)	C
C11	FZD3	1	(0.51, 1.49)	Okay
C12	FZD4	0.605	(0.27, 0.94)	Okay
D01	FZD6	1.1096	(0.70, 1.52)	Okay
D02	FZD7	1.0905	(0.51, 1.68)	Okay
D03	FZD8	0.8123	(0.12, 1.51)	B
D04	GSK3A	0.8409	(0.62, 1.06)	Okay
D05	GSK3B	1.0353	(0.69, 1.38)	Okay
D06	JUN	1.0718	(0.59, 1.55)	Okay
D07	KREMEN1	1.5966	(1.07, 2.12)	Okay
D08	LEF1	0.9013	(0.43, 1.37)	Okay
D09	LRP5	0.8706	(0.72, 1.02)	Okay
D10	LRP6	1.0905	(0.70, 1.48)	Okay
D11	MYC	0.7846	(0.41, 1.16)	Okay
D12	NKD1	1.1096	(0.81, 1.41)	Okay
E01	NLK	1.1096	(0.60, 1.62)	Okay
E02	PITX2	1.2527	(0.22, 2.29)	Okay
E03	PORCN	0.8556	(0.48, 1.23)	Okay
E04	PPP2CA	0.9493	(0.82, 1.08)	Okay
E05	PPP2R1A	0.8706	(0.57, 1.17)	Okay
E06	PYGO1	1.0353	(0.73, 1.34)	Okay
E07	RHOU	0.7846	(0.56, 1.01)	Okay
E08	SENP2	0.8556	(0.54, 1.17)	Okay
E09	SFRP1	0.8409	(0.54, 1.14)	B
E10	SFRP4	0.6156	(0.33, 0.90)	A
E11	FBXW4	1.0534	(0.51, 1.60)	Okay
E12	SLC9A3R1	0.8556	(0.62, 1.09)	Okay
F01	SOX17	1.0353	(0.64, 1.43)	C
F02	T	1	(0.32, 1.68)	B
F03	TCF7	0.8858	(0.42, 1.35)	B
F04	TCF7L1	1.4641	(0.85, 2.08)	Okay
F05	TLE1	1.1487	(0.72, 1.58)	Okay
F06	TLE2	0.8858	(0.57, 1.20)	B
F07	WIF1	0.7846	(0.44, 1.13)	B
F08	WISP1	1.0353	(0.64, 1.43)	C
F09	WNT1	0.695	(0.26, 1.13)	B
F10	WNT10A	0.5645	(0.00001, 1.76)	B
F11	WNT11	0.3789	(0.00001, 0.82)	B
F12	WNT16	1.4142	(0.00001, 2.96)	B
G01	WNT2	1.0353	(0.64, 1.43)	C
G02	WNT2B	1.0353	(0.01, 2.06)	B
G03	WNT3	0.8858	(0.44, 1.33)	Okay
G04	WNT3A	1.0353	(0.64, 1.43)	C
G05	WNT4	0.5645	(0.02, 1.10)	B
G06	WNT5A	0.8409	(0.48, 1.20)	Okay
G07	WNT5B	0.8556	(0.38, 1.33)	B
G08	WNT6	1.1688	(0.72, 1.61)	B
G09	WNT7A	1.0353	(0.64, 1.43)	C
G10	WNT7B	1.0353	(0.64, 1.43)	C
G11	WNT8A	1.0718	(0.68, 1.47)	B
G12	WNT9A	1.0353	(0.64, 1.43)	C
H01	B2M	0.732	(0.51, 0.95)	Okay
H02	HPRT1	0.8123	(0.47, 1.16)	Okay
H03	RPL13A	1.1688	(0.90, 1.44)	Okay
H04	GAPDH	0.9828	(0.69, 1.27)	Okay
H05	ACTB	1.1688	(0.67, 1.67)	Okay
H06	HGDC	1.0353	(0.64, 1.43)	C
H07	RTC	0.5548	(0.24, 0.86)	Okay
H08	RTC	0.5267	(0.26, 0.80)	Okay
H09	RTC	0.5453	(0.21, 0.88)	Okay
H10	PPC	0.695	(0.42, 0.97)	Okay
H11	PPC	0.732	(0.45, 1.02)	Okay
H12	PPC	0.7448	(0.47, 1.02)	Okay

Comments:

A: This gene's average threshold cycle is relatively high (>30) in either the control or the test sample and is reasonably low in the other sample (<30).

These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample, suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result.

This fold-change result may also have greater variations if $P > .05$; therefore, it is important to have a sufficient number of biologic replicates to validate the result for this gene.

B: This gene's average threshold cycle is relatively high (>30), meaning that its relative expression level is low, in both control and test samples, and the P value for the fold change is either unavailable or relatively high ($P > .05$).

This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biologic replicates to validate the result for this gene.

C: This gene's average threshold cycle is either not determined or greater than the defined cutoff value (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and uninterpretable.

Fold change and fold regulation:

Fold change ($2^{-\Delta\Delta C_T}$) is the normalized gene expression ($2^{-\Delta C_T}$) in the test sample divided by the normalized gene expression ($2^{-\Delta C_T}$) in the control sample.

Fold regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than 1 indicate a positive or an up-regulation, and the fold regulation is equal to the fold change. Fold-change values less than 1 indicate a negative or down-regulation, and the fold regulation is the negative inverse of the fold change.

Fold-change and fold-regulation values greater than 2 are indicated in red; fold-change values less than 0.5 and fold-regulation values less than −2 are indicated in blue.

Table W2f. *P* values.

		P Value (Compared to Control Group)
		Group 1
A01	AES	0.792341
A02	APC	0.965095
A03	AXIN1	0.125466
A04	BCL9	0.200823
A05	BTRC	0.198872
A06	FZD5	0.434184
A07	CCND1	0.1434
A08	CCND2	0.130908
A09	CCND3	0.26405
A10	CSNK1A1	0.581515
A11	CSNK1D	0.502102
A12	CSNK1G1	0.690156
B01	CSNK2A1	0.294784
B02	CTBP1	0.379823
B03	CTBP2	0.96217
B04	CTNNB1	0.757378
B05	CTNNBIP1	0.138199
B06	CXXC4	0.043045
B07	DAAM1	0.294942
B08	DIXDC1	0.291973
B09	DKK1	0.746279
B10	DVL1	0.490117
B11	DVL2	0.042473
B12	EP300	0.888903
C01	FBXW11	0.941277
C02	FBXW2	0.995686
C03	FGF4	0.836286
C04	FOSL1	0.714447
C05	FOXN1	0.156795
C06	FRAT1	0.689437
C07	FRZB	0.76046
C08	FSHB	0.954679
C09	FZD1	0.515336
C10	FZD2	0.836286
C11	FZD3	0.922969
C12	FZD4	0.135681
D01	FZD6	0.652247
D02	FZD7	0.769613
D03	FZD8	0.548591
D04	GSK3A	0.225384
D05	GSK3B	0.967886
D06	JUN	0.790172
D07	KREMEN1	0.033755
D08	LEF1	0.90179
D09	LRP5	0.181439
D10	LRP6	0.780073
D11	MYC	0.292486
D12	NKD1	0.506295
E01	NLK	0.693875
E02	PITX2	0.718265
E03	PORCN	0.416707
E04	PPP2CA	0.535224
E05	PPP2R1A	0.475922
E06	PYGO1	0.833288
E07	RHOU	0.114162
E08	SENP2	0.356227
E09	SFRP1	0.441863
E10	SFRP4	0.119764
E11	FBXW4	0.886316
E12	SLC9A3R1	0.288113
F01	SOX17	0.836286
F02	T	0.836247
F03	TCF7	0.879469
F04	TCF7L1	0.126211
F05	TLE1	0.461623
F06	TLE2	0.558308
F07	WIF1	0.357022
F08	WISP1	0.836286
F09	WNT1	0.333883
F10	WNT10A	0.398512
F11	WNT11	0.104759
F12	WNT16	0.495047
G01	WNT2	0.836286
G02	WNT2B	0.690109
G03	WNT3	0.545446
G04	WNT3A	0.836286
G05	WNT4	0.151461
G06	WNT5A	0.380818
G07	WNT5B	0.526959
G08	WNT6	0.428128
G09	WNT7A	0.836286
G10	WNT7B	0.836286
G11	WNT8A	0.713394
G12	WNT9A	0.836286
H01	B2M	0.07127
H02	HPRT1	0.439236
H03	RPL13A	0.214986
H04	GAPDH	0.937356
H05	ACTB	0.727042
H06	HGDC	0.836286
H07	RTC	0.102875
H08	RTC	0.089411
H09	RTC	0.115337
H10	PPC	0.124293
H11	PPC	0.171647
H12	PPC	0.184196

P value:
The *P* values are calculated based on a Student's *t* test of the replicate $2^{-\Delta Ct}$ values for each gene in the control group and treatment groups, and *P* values less than .05 are indicated in red.

Table W2g. Fold Regulation.

		Up-regulation/Down-regulation (Compared to Control Group)	
		Group 1	
		Fold Regulation	Comments
A01	AES	−1.0534	Okay
A02	APC	1	B
A03	AXIN1	−1.7411	Okay
A04	BCL9	−1.366	Okay
A05	BTRC	1.4142	Okay
A06	FZD5	1.1892	Okay
A07	CCND1	−1.2968	Okay
A08	CCND2	1.5966	B
A09	CCND3	−1.1892	Okay
A10	CSNK1A1	1.2968	Okay
A11	CSNK1D	−1.1096	Okay
A12	CSNK1G1	1.0534	B
B01	CSNK2A1	−1.1096	Okay
B02	CTBP1	−1.2527	Okay
B03	CTBP2	−1.0534	Okay
B04	CTNNB1	−1.0718	Okay
B05	CTNNBIP1	−1.8661	Okay
B06	CXXC4	2.8779	Okay
B07	DAAM1	−1.3426	Okay
B08	DIXDC1	−1.3195	Okay
B09	DKK1	−1.8025	Okay
B10	DVL1	1.1487	Okay
B11	DVL2	1.21	Okay
B12	EP300	1.0718	Okay
C01	FBXW11	1.0175	Okay
C02	FBXW2	−1.0353	Okay
C03	FGF4	1.0353	C
C04	FOSL1	1.0353	Okay
C05	FOXN1	−2.035	B
C06	FRAT1	1.1096	Okay
C07	FRZB	−8.1398	A
C08	FSHB	−1.0175	B
C09	FZD1	1.1892	B
C10	FZD2	1.0353	C
C11	FZD3	1	Okay
C12	FZD4	−1.6529	Okay
D01	FZD6	1.1096	Okay
D02	FZD7	1.0905	Okay
D03	FZD8	−1.2311	B
D04	GSK3A	−1.1892	Okay
D05	GSK3B	1.0353	Okay
D06	JUN	1.0718	Okay
D07	KREMEN1	1.5966	Okay
D08	LEF1	−1.1096	Okay
D09	LRP5	−1.1487	Okay
D10	LRP6	1.0905	Okay
D11	MYC	−1.2746	Okay
D12	NKD1	1.1096	Okay
E01	NLK	1.1096	Okay
E02	PITX2	1.2527	Okay
E03	PORCN	−1.1688	Okay
E04	PPP2CA	−1.0534	Okay
E05	PPP2R1A	−1.1487	Okay
E06	PYGO1	1.0353	Okay
E07	RHOU	−1.2746	Okay
E08	SENP2	−1.1688	Okay
E09	SFRP1	−1.1892	B
E10	SFRP4	−1.6245	A
E11	FBXW4	1.0534	Okay
E12	SLC9A3R1	−1.1688	Okay
F01	SOX17	1.0353	C
F02	T	1	B
F03	TCF7	−1.129	B
F04	TCF7L1	1.4641	Okay
F05	TLE1	1.1487	Okay
F06	TLE2	−1.129	B
F07	WIF1	−1.2746	B
F08	WISP1	1.0353	C
F09	WNT1	−1.4389	B
F10	WNT10A	−1.7715	B
F11	WNT11	−2.639	B
F12	WNT16	1.4142	B
G01	WNT2	1.0353	C
G02	WNT2B	1.0353	B
G03	WNT3	−1.129	Okay
G04	WNT3A	1.0353	C
G05	WNT4	−1.7715	B
G06	WNT5A	−1.1892	Okay
G07	WNT5B	−1.1688	B
G08	WNT6	1.1688	B
G09	WNT7A	1.0353	C
G10	WNT7B	1.0353	C
G11	WNT8A	1.0718	B
G12	WNT9A	1.0353	C
H01	B2M	−1.366	Okay
H02	HPRT1	−1.2311	Okay
H03	RPL13A	1.1688	Okay
H04	GAPDH	−1.0175	Okay
H05	ACTB	1.1688	Okay
H06	HGDC	1.0353	C
H07	RTC	−1.8025	Okay
H08	RTC	−1.8987	Okay
H09	RTC	−1.834	Okay
H10	PPC	−1.4389	Okay
H11	PPC	−1.366	Okay
H12	PPC	−1.3426	Okay

Comments:

A: This gene's average threshold cycle is relatively high (>30) in either the control or the test sample and is reasonably low in the other sample (<30).

These data mean that the gene's expression is relatively low in one sample and reasonably detected in the other sample suggesting that the actual fold-change value is at least as large as the calculated and reported fold-change result.

This fold-change result may also have greater variations if $P > .05$; therefore, it is important to have a sufficient number of biologic replicates to validate the result for this gene.

B: This gene's average threshold cycle is relatively high (>30), meaning that its relative expression level is low, in both control and test samples, and the P value for the fold change is either unavailable or relatively high ($P > .05$).

This fold-change result may also have greater variations; therefore, it is important to have a sufficient number of biologic replicates to validate the result for this gene.

C: This gene's average threshold cycle is either not determined or greater than the defined cutoff value (default 35), in both samples meaning that its expression was undetected, making this fold-change result erroneous and uninterpretable.

Fold change and fold regulation:

Fold change ($2^{-\Delta\Delta C_t}$) is the normalized gene expression ($2^{-\Delta C_t}$) in the test sample divided by the normalized gene expression ($2^{-\Delta C_t}$) in the control sample.

Fold regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than 1 indicate a positive or an up-regulation, and the fold regulation is equal to the fold change. Fold-change values less than 1 indicate a negative or down-regulation, and the fold regulation is the negative inverse of the fold change.

Fold-change and fold-regulation values greater than 2 are indicated in red; fold-change values less than 0.5 and fold-regulation values less than −2 are indicated in blue.

Table W3. β-Catenin Mutational Status in Hepatoblastoma Specimens.

Sample	Histology	Mutational Status	CITED1 Densitometry	β-Catenin Densitometry
1	2	2	40.73	1.15
2	1	2	28.97	1.28
3	2	ND	27.79	0.61
4	2	ND	40.36	0.56
5	1	1	39.13	0.2
6	2	2	19.84	0.4
7	1	1	31.18	0.63
8	1	2	7.14	0.34
9	2	1	52.66	0.56
10	1	1	ND	1.77
11	1	ND	40.27	1.42
12	2	2	43.9	1.47
13	2	2	63.69	1.02
14	2	ND	47.42	1.29
15	1	1	9.78	0.28
16	1	2	42.78	1.7
17	2	2	40.82	1.58
18	2	2	18.07	ND
19	2	2	41.59	0.42

Histology 1, fetal; histology 2, EMEF; mutational status 1, wild type; mutational status 2, mutant; ND, not determined.

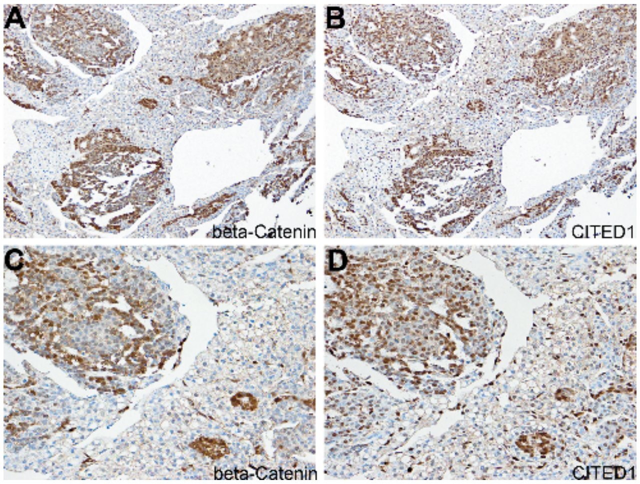

Figure W1. Serial sections immunohistochemically stained for β-catenin and CITED1 reveal expression in similar cell populations (serial sections A and B: original magnification, ×200; serial sections C and D: original magnification, ×400).