RELATIVE EXPRESSION OF CANCER-RELATED GENES IN Delta IgTRKB HCM-1 COMPARED TO GFP-HCM-1

Fold Change (comparing ΔIgTrkB HCM-1 to GFP HCM-1)

		Group 1					
Position	**Symbol**	**Fold Change**	**95% CI**	**Comments**	**P Value**	**Fold Regulatio**	**Comments**
A01	Akt1	0.6711	(0.51, 0.83)	OKAY	0.033147	-1.4901	OKAY
A02	Angpt1	12.2545	(4.07, 20.44)	OKAY	0.003952	12.2545	OKAY
A03	Apaf1	0.8603	(0.79, 0.93)	OKAY	0.021533	-1.1623	OKAY
A04	Atm	0.88	(0.68, 1.08)	OKAY	0.327008	-1.1364	OKAY
A05	Bad	0.6361	(0.54, 0.73)	OKAY	0.00434	-1.572	OKAY
A06	Bax	0.6677	(0.53, 0.80)	OKAY	0.023795	-1.4976	OKAY
A07	Bcl2	0.3496	(0.29, 0.41)	OKAY	0.000206	-2.8607	OKAY
A08	Bcl2l1	0.4178	(0.35, 0.49)	OKAY	0.000418	-2.3933	OKAY
A09	Birc5	0.6936	(0.63, 0.76)	OKAY	0.002713	-1.4417	OKAY
A10	Brca1	0.8585	(0.70, 1.01)	OKAY	0.160047	-1.1649	OKAY
A11	Casp8	0.8993	(0.87, 0.93)	OKAY	0.005277	-1.112	OKAY
A12	Ccnd1	331.0042	294.74, 367.27	A	0	331.0042	A
B01	Ccne1	0.2792	(0.25, 0.31)	OKAY	0.000213	-3.5812	OKAY
B02	Cdc25a	1.0062	(0.80, 1.22)	OKAY	0.985934	1.0062	OKAY
B03	Cdh1	0.6477	(0.48, 0.82)	OKAY	0.034125	-1.544	OKAY
B04	Cdk2	0.7285	(0.64, 0.81)	OKAY	0.003601	-1.3728	OKAY
B05	Cdk4	0.8427	(0.65, 1.03)	OKAY	0.204136	-1.1867	OKAY
B06	Cdkn1a	0.6605	(0.63, 0.70)	OKAY	0.000064	-1.514	OKAY
B07	Cdkn2a	0.984	(0.90, 1.07)	OKAY	0.721688	-1.0163	OKAY
B08	Cflar	0.7249	(0.65, 0.80)	OKAY	0.004653	-1.3796	OKAY
B09	Chek2	1.2659	(1.08, 1.45)	OKAY	0.037384	1.2659	OKAY
B10	Col18a1	1.3365	(0.65, 2.02)	OKAY	0.342765	1.3365	OKAY
B11	Ctnnb1	0.6716	(0.59, 0.76)	OKAY	0.006962	-1.4891	OKAY
B12	E2f1	0.832	(0.70, 0.96)	OKAY	0.086664	-1.202	OKAY
C01	Egfr	0.6948	(0.53, 0.86)	C	0.056255	-1.4394	C
C02	Ets2	0.3158	(0.27, 0.36)	OKAY	0.000017	-3.1663	OKAY
C03	Fgf1	3.81	(3.20, 4.42)	OKAY	0.000097	3.81	OKAY
C04	Fgfr2	0.0778	(0.06, 0.10)	OKAY	0.000009	-12.8596	OKAY
C05	Figf	1.5599	(1.03, 2.09)	B	0.081262	1.5599	B
C06	Fos	0.3314	(0.29, 0.37)	OKAY	0.000072	-3.0172	OKAY
C07	Grb2	0.463	(0.43, 0.49)	OKAY	0.000009	-2.1598	OKAY
C08	Hgf	28.8628	(15.25, 42.48)	A	0.008818	28.8628	A

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C09	Icam1	0.8024	(0.64, 0.96)	OKAY	0.09479	-1.2462	OKAY
C10	Ifna1	0.5962	(0.43, 0.76)	OKAY	0.031622	-1.6773	OKAY
C11	Ifnb1	0.6948	(0.53, 0.86)	C	0.056255	-1.4394	C
C12	Igf1	1.2033	(0.99, 1.42)	OKAY	0.110241	1.2033	OKAY
D01	Itga2	2.0379	(0.00001, 4.42)	B	0.240529	2.0379	B
D02	Itga3	3.2204	(2.84, 3.60)	OKAY	0.000003	3.2204	OKAY
D03	Itga4	2.6461	(2.29, 3.01)	OKAY	0.000616	2.6461	OKAY
D04	Itgav	0.7198	(0.49, 0.95)	OKAY	0.103062	-1.3892	OKAY
D05	Itgb1	0.8033	(0.75, 0.86)	OKAY	0.003023	-1.2449	OKAY
D06	Itgb3	1.3199	(1.13, 1.51)	OKAY	0.014714	1.3199	OKAY
D07	Jun	0.6971	(0.62, 0.78)	OKAY	0.005623	-1.4344	OKAY
D08	Kiss1	0.8025	(0.45, 1.16)	B	0.44723	-1.2461	B
D09	Map2k1	0.9434	(0.80, 1.09)	OKAY	0.49754	-1.06	OKAY
D10	Mcam	0.8277	(0.78, 0.88)	OKAY	0.004231	-1.2082	OKAY
D11	Mdm2	0.4271	(0.40, 0.46)	OKAY	0.000028	-2.3412	OKAY
D12	Met	1.5722	(1.42, 1.72)	OKAY	0.000925	1.5722	OKAY
E01	Mmp2	1.2279	(1.00, 1.46)	OKAY	0.115956	1.2279	OKAY
E02	Mmp9	2.7324	(0.38, 5.08)	B	0.099061	2.7324	B
E03	Mta1	0.8157	(0.71, 0.92)	OKAY	0.044843	-1.2259	OKAY
E04	Mta2	0.6971	(0.63, 0.76)	OKAY	0.003718	-1.4345	OKAY
E05	Muc1	4.8839	(3.71, 6.05)	OKAY	0.00003	4.8839	OKAY
E06	Myc	1.2005	(0.00001, 2.56)	B	0.729366	1.2005	B
E07	Ncam1	0.9485	(0.64, 1.26)	OKAY	0.747884	-1.0543	OKAY
E08	Nfkb1	0.9427	(0.82, 1.07)	OKAY	0.45719	-1.0608	OKAY
E09	Nfkbia	0.7632	(0.64, 0.88)	OKAY	0.025716	-1.3103	OKAY
E10	Nme1	0.9041	(0.86, 0.95)	OKAY	0.012676	-1.1061	OKAY
E11	Pdgfa	0.4972	(0.32, 0.67)	OKAY	0.014808	-2.0111	OKAY
E12	Pdgfb	0.6596	(0.57, 0.75)	A	0.002921	-1.5162	A
F01	Pik3r1	0.5227	(0.46, 0.58)	OKAY	0.000261	-1.9131	OKAY
F02	Plau	0.3997	(0.29, 0.51)	A	0.010559	-2.502	A
F03	Plaur	0.8447	(0.75, 0.94)	OKAY	0.03657	-1.1839	OKAY
F04	Pten	0.5849	(0.54, 0.63)	OKAY	0.000285	-1.7098	OKAY
F05	Raf1	0.6613	(0.55, 0.78)	OKAY	0.018242	-1.5121	OKAY
F06	Rb1	0.5646	(0.51, 0.62)	OKAY	0.000464	-1.771	OKAY
F07	S100a4	0.5091	(0.45, 0.57)	OKAY	0.00049	-1.9641	OKAY

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F08	Serpinb2	0.6948	(0.53, 0.86)	C	0.056255	-1.4394	C
F09	Serpine1	4.6608	(3.80, 5.52)	OKAY	0.000027	4.6608	OKAY
F10	Tek	2.2423	(1.33, 3.15)	A	0.020516	2.2423	A
F11	Tert	1.32	(0.98, 1.66)	OKAY	0.100349	1.32	OKAY
F12	Tgfb1	0.9707	(0.84, 1.10)	OKAY	0.668129	-1.0302	OKAY
G01	Tgfbr1	0.5698	(0.49, 0.65)	OKAY	0.001248	-1.755	OKAY
G02	Thbs1	0.4721	(0.42, 0.52)	OKAY	0.000563	-2.1183	OKAY
G03	Timp1	0.7597	(0.65, 0.87)	OKAY	0.01583	-1.3163	OKAY
G04	Tnf	1.2705	(0.85, 1.69)	B	0.212688	1.2705	B
G05	Tnfrsf10b	2.9606	(2.37, 3.56)	OKAY	0.000145	2.9606	OKAY
G06	Tnfrsf1a	1.074	(0.83, 1.32)	OKAY	0.615624	1.074	OKAY
G07	Fas	0.72	(0.55, 0.89)	B	0.059538	-1.3889	B
G08	Tp53	0.8027	(0.66, 0.94)	OKAY	0.080759	-1.2458	OKAY
G09	Twist1	38.5679	(23.45, 53.68)	A	0.000015	38.5679	A
G10	Vegfa	4.816	(3.26, 6.37)	OKAY	0.000115	4.816	OKAY
G11	Vegfb	1.8261	(1.53, 2.13)	OKAY	0.005226	1.8261	OKAY
G12	Vegfc	0.2969	(0.05, 0.55)	OKAY	0.018051	-3.3679	OKAY
H01	Rplp1	0.909	(0.85, 0.96)	OKAY	0.034638	-1.1001	OKAY
H02	Hprt1	1.0348	(0.96, 1.11)	OKAY	0.429036	1.0348	OKAY
H03	Rpl13a	1.0249	(0.92, 1.13)	OKAY	0.674153	1.0249	OKAY
H04	Ldha	1.3041	(1.20, 1.41)	OKAY	0.003074	1.3041	OKAY
H05	Actb	0.7955	(0.73, 0.86)	OKAY	0.006687	-1.2571	OKAY
H06	RGDC	0.6512	(0.50, 0.80)	OKAY	0.026663	-1.5356	OKAY
H07	RTC	0.7213	(0.58, 0.87)	OKAY	0.044468	-1.3864	OKAY
H08	RTC	0.6846	(0.55, 0.82)	OKAY	0.029512	-1.4608	OKAY
H09	RTC	0.7065	(0.57, 0.85)	OKAY	0.036775	-1.4154	OKAY
H10	PPC	0.712	(0.51, 0.91)	OKAY	0.089911	-1.4046	OKAY
H11	PPC	0.7281	(0.54, 0.91)	OKAY	0.089716	-1.3735	OKAY
H12	PPC	0.7509	(0.54, 0.97)	OKAY	0.131062	-1.3317	OKAY

Comments:

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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.

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This fold-change result may also have greater variations if p value > 0.05; therefore, it is important to have a sufficient number of biological 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 > 0.05).

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

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

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Fold Change & Fold Regulat

Fold-Change (2^(- Delta Delta Ct)) is the normalized gene expression (2^(- Delta Ct)) in the Test Sample divided the normalized gene expression (2^(- Delta Ct)) in the Control Sample.

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Fold-Regulation represents fold-change results in a biologically meaningful way. Fold-change values greater than one indicate a positive- or an up-regulation, and the fold-regulation is equal to the fold-change.

Fold-change values less than one indicate a negative or down-regulation, and the fold-regulation is the negative inverse of the fold-change.

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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.