Supplemental Table 3. Preamplification uniformly decreases cycle threshold values without biasing relative quantification values.*

Mean Cycle Threshold†

Transcript	NO PREAMP‡	PREAMP‡
Hsp70_1	21.078	9.017
Hsp70_2	25.424	12.998
Hsp70_5	20.362	7.936
Hsp70_6	28.883	16.268
Hsp70_8	20.676	7.974
Hsp70_1L	29.685	17.145
Hsp70_9	21.831	9.023
EpoR	25.065	12.676
Hmbs	25.194	12.721

Relative Quantification§

Transcript	NO PREAMP‡	PREAMP‡	FOLD
Hsp70_1	17.334	13.038	1.330
Hsp70_2	0.853	0.826	1.033
Hsp70_5	28.482	27.577	1.033
Hsp70_6	0.078	0.086	1.104
Hsp70_8	22.913	26.861	1.172
Hsp70_1L	0.044	0.047	1.048
Hsp70_9	10.288	12.977	1.261
EpoR	1.094	1.032	1.060

* Preamplification was performed using the Taqman preamplification multiplex system (ABI). A variation in relative quantification ≤ 2.82 fold represents acceptable uniformity. The observed variation is less than 1.34 fold for all transcripts.

† Values are the mean of triplicate PCR determinations. The coefficient of variance of triplicate determinations is <4% for all samples.

‡ Values were obtained using cDNA derived from a universal human RNA standard (Stratagene) that was either unamplified (NO PREAMP) or preamplified for 14 cycles (PREAMP).

§ Values are normalized to the reference gene *Hmbs*.

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