Robust quantification of *the SMN* gene copy number by real-time TaqMan PCR

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In the published original article, Table 1, there is an error in the sequence of the SMN probe. Letter “C” in the sixth position should be changed to “A”.

The correct sequence should read:

FAM-ACA AAA TCA AAA AGA AGG AAG GTG
CTC ACA-MGBNFQ.

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Table 1 PCR primers, TaqMan probes, and nonextending oligonucleotides (blockers) for SMN1, SMN2, and CFTR

Component	Sequence	Number of bases
Primers		
SMN1-ex7F-3g	TTC CTT TAT TTT CCT TAC AGG GTg ^b TC ^a	26
SMN2-ex7F-3g	TTC CTT TAT TTT CCT TAC AGG GTg ^b TT ^a	26
SMN-ex7R	GCT GGC AGA CTT ACT CCT TAA TTT AA	26
CFTR-F	TAG GAA GTC ACC AAA GCA GTA CAG C	25
CFTR-R	AGC TAT TCT CAT CTG CAT TCC AAT G	25
Probes		
SMN probe	FAM-ACA AAA TCA AAA AGA AGG AAG GTG CTC ACA-MGBNFQ	30
CFTR probe	VIC-TAT GAC CCG GAT AAC AAG GAG GAA CGC TC-MGBNFQ	29
Blockers		
SMN1 blocker	ATT TTC CTT ACA GGG TTT CAG ACA AAA TCA AAA-PO ₄	33
SMN2 blocker	ATT TTC CTT ACA GGG TTT TAG ACA AAA TCA AAA-PO ₄	33

^a The SMN forward primers distinguished between SMN1 and SMN2 by ending on the nucleotide difference (C/T) at position 6 in exon 7.

^b A mismatch T→G was added at the −3 position from the 3' end of both SMN1 and SMN2 forward primers to achieve allele specificity.