Table 1. MIQE checklist for authors, reviewers, and editors.				
Item to check	Importance	Section/line number, or reason for not reporting		
Experimental design				
Definition of experimental and control groups	Е	Line 125		
Number within each group	E	Line 126		
Assay carried out by the core or investigator's laboratory?	D			
Acknowledgment of authors' contributions	D			
Sample				
Description	Е	Line 126		
Volume/mass of sample processed	D			
Microdissection or macrodissection	Е	Not Applicable		
Processing procedure	Е	Line 126-127		
If frozen, how and how quickly?	E	Line 126-127		
If fixed, with what and how quickly?	E	Not Applicable		
Sample storage conditions and duration (especially for FFPEb same		Line 126-127		
Nucleic acid extraction	P	Elife 120 127		
Procedure and/or instrumentation	Е	Line 127-128		
Name of kit and details of any modifications	E	Line 127-128		
Source of additional reagents used	D	Ellie 127 120		
Details of DNase or RNase treatment	E	Line 127-128		
Contamination assessment (DNA or RNA)	E	Line 127-128		
Nucleic acid quantification	E	Line 127-128		
Instrument and method	E	Line 127-128		
Purity (A260/A280)	D	Ellie 127 120		
Yield	D			
RNA integrity: method/instrument	E	Line 127-128		
RIN/RQI or Cq of 3 and 5 transcripts	E	Not Applicable		
Electrophoresis traces	D	rotrippheusic		
Inhibition testing (Cq dilutions, spike, or other)	E	Not Applicable		
Reverse transcription	<u> </u>	rotrippheusic		
Complete reaction conditions	Е	Line 128		
Amount of RNA and reaction volume	E	Line 128		
Priming oligonucleotide (if using GSP) and concentration	E	Not Applicable		
Reverse transcriptase and concentration	E	Line 128		
Temperature and time	E	Line 128-130		
Manufacturer of reagents and catalogue numbers	D	Line 129		
Cqs with and without reverse transcription	D	Ellie 12)		
Storage conditions of Cdna	D			
qPCR target information				
Gene symbol	Е	Line 134		
Sequence accession number	E	Line 134		
Location of amplicon	D	<u> </u>		
Amplicon length	E	Not Applicable		
In silico specificity screen (BLAST, and so on)	E	Not Applicable		
Pseudogenes, retropseudogenes, or other homologs?	D	1.0011.pp1104010		
Sequence alignment	D			
Sequence alignment				

Location of each primer by exon or intron (if applicable)	Е	Not Applicable
What splice variants are targeted?	E	Not Applicable
qPCR oligonucleotides	L	1 vot / Applicable
Primer sequences	E	Line 134
RTPrimerDB identification number	D	Line 154
Probe sequences	D	
Location and identity of any modifications	E	Not Applicable
Manufacturer of oligonucleotides	D	Not Applicable
Purification method	D D	
qPCR protocol	D	
Complete reaction conditions	E	Line 130-132
Reaction volume and amount of cDNA/DNA	E	Line 130 132
Primer, (probe), Mg2, and dNTP concentrations	E	Line 130-132
Polymerase identity and concentration	E	Not Applicable
Buffer/kit identity and manufacturer	E	Line 130-132
Exact chemical composition of the buffer	D	Eme 130-132
Additives (SYBR Green I, DMSO, and so forth)	E	Line 130-132
Manufacturer of plates/tubes and catalog number	D	Eine 130 132
Complete thermocycling parameters	E	Line 130-132
Reaction setup (manual/robotic)	D	2110 130 132
Manufacturer of qPCR instrument	E	Line 130-132
qPCR validation	L	Emic 130 132
Evidence of optimization (from gradients)	D	
Specificity (gel, sequence, melt, or digest)	E	Not Applicable
For SYBR Green I, Cq of the NTC	E	Not Applicable
Calibration curves with slope and y intercept	E	Not Applicable
PCR efficiency calculated from slope	E	Not Applicable
CIs for PCR efficiency or SE	D	- tot i ippiiousio
r 2 of calibration curve	E	Not Applicable
Linear dynamic range	E	Not Applicable
Cq variation at LOD	E	Not Applicable
CIs throughout range	D	- PF
Evidence for LOD	E	Not Applicable
If multiplex, efficiency and LOD of each assay	E	Not Applicable
Data analysis		PF
qPCR analysis program (source, version)	E	Line 132
Method of Cq determination	E	Line 132
Outlier identification and disposition	E	Line 132-133
Results for NTCs	E	Not Applicable
Justification of number and choice of reference genes	E	Line 132
Description of normalization method	E	Line 133
Number and concordance of biological replicates	D	
Number and stage (reverse transcription or qPCR) of technical repli		Line 133
Repeatability (intraassay variation)	E	Line 133
Reproducibility (interassay variation, CV)	D	
Power analysis	D	
Statistical methods for results significance	E	Line 180-181
Software (source, version)	E	Line 178
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Cq or raw data submission with RDML	D	