The **MIQE** guidelines: **Minimum** Information for Publication of Quantitative Real-Time PCR Experiments

MIQE checklist for authors, reviewers, and editors.^a

| ITEM TO CHECK | IMPORTANCE |
|---|------------|
| EXPERIMENTAL DESIGN | |
| Definition of experimental and control groups | E |
| Number within each group | E |
| Assay carried out by the core or investigator's laboratory? | D |
| Acknowledgment of authors' contributions | D |
| SAMPLE | |
| Description | E |
| Volume/mass of sample processes | D |
| Micro dissection or macrodissection | E |
| Processing procedure | E |
| If frozen, how and how quickly? | E |
| If fixed, with what and how quickly? | E |
| Sample storage conditions and duration (especially for FFPE ^b samples) | E |
| NUCLEIC ACID EXTRACTION | |
| Procedure and/or instrumentation | E |
| Name of kit and details of any modifications | E |
| Source of additional reagents used | D |
| Details of DNase or RNase treatment | E |
| Contamination assessment (DNA or RNA) | E |
| Nucleic acid quantification | E |
| Instrument and method | E |
| Purity (A ₂₆₀ /A ₂₈₀) | D |
| Yield | D |
| RNA integrity:method/instrument | E |
| RIN/RQI or C_q of 3'and 5' transcripts | Е |
| Electrophoresis traces | D |
| Inhibition testing (C_q dilutions, spike, or other) | E |
| REVERSE TRANSCRIPTION | |
| Complete reaction conditions | E |
| Amount of RNA and reaction volume | E |
| Priming oligonucleotide (if using GSP) and concentration | E |
| Reverse transcriptase and concentration | E |
| Temperature and time | E |

| TEM TO CHECK | IMPORTANCE | ITEM TO CHECK | IMPORTANCE |
|--|---|---|------------|
| XPERIMENTAL DESIGN | | qPCR PROTOCOL | |
| Definition of experimental and control groups | E | Complete reaction conditions | E |
| lumber within each group | Е | Reaction volume and amount of cDNA/DNA | E |
| ssay carried out by the core or investigator's laboratory? | D | Primer, (probe), Mg ² +, and dNTP concentrations | E |
| cknowledgment of authors' contributions | D | Polymerase identity and concentration | Е |
| AMPLE | | Buffer/kit identity and manufacturer | E |
| Description | E | Exact chemical composition of the buffer | D |
| /olume/mass of sample processes | D | Additives (SYBR Green I, DMSO, and so forth) | F |
| Aicro dissection or macrodissection | F | Manufacturer of plates/tubes and catalog number | D |
| | с Г | | Б |
| Processing procedure | E | Complete thermocycling parameters | E |
| frozen, how and how quickly? | E | Reaction set up (manual/robotic) | D |
| f fixed, with what and how quickly? | E | Manufacturer of qPCR instrument | E |
| ample storage conditions and duration (especially for FFPE ^b samples) | E | qPCR VALIDATION | |
| UCLEIC ACID EXTRACTION | | Evidence of optimisation (from gradients) | D |
| Procedure and/or instrumentation | E | Specificity (gel, sequence, melt, or digest) | E |
| lame of kit and details of any modifications | E | For SYBR Green I, C_q of the NTC | E |
| ource of additional reagents used | D | Calibration curves with slope and y intercept | Е |
| etails of DNase or RNase treatment | E | PCR efficiency calculated from slope | E |
| ontamination assessment (DNA or RNA) | E | Cls for PCR efficiency or SE | D |
| lucleic acid quantification | E | r ² of calibration curve | E |
| nstrument and method | E | Linear dynamic range | F |
| urity (A ₂₆₀ /A ₂₈₀) | n | C_{α} variation at LOD | F |
| (ield | D | Cls throughout range | |
| | | | D |
| RNA integrity:method/instrument | E | Evidence for LOD | E |
| RIN/RQI or C_q of 3'and 5' transcripts | E | If multiplex, efficiency and LOD of each assay | E |
| Electrophoresis traces | D | DATA ANALYSIS | |
| hhibition testing (C_q dilutions, spike, or other) | E | qPCR analysis program (source, version) | E |
| EVERSE TRANSCRIPTION | | Method of C_q determination | E |
| Complete reaction conditions | E | Outlier identification and disposition | E |
| mount of RNA and reaction volume | E | Results for NTCs | E |
| riming oligonucleotide (if using GSP) and concentration | E | Justification of number and choice of reference genes | E |
| Reverse transcriptase and concentration | Е | Description of normalisation method | Е |
| emperature and time | Е | Number and concordance of biological replicates | D |
| Nanufacturer of reagents and catalogue numbers | D | Number and stage (reverse transcription or qPCR) of technical replicates | F |
| C_{α} s with and without reverse transcription | Dc | Repeatability (intra assay variation) | E |
| | | | L |
| Storage conditions of cDNA | D | Reproducibility (interassay variation, CV) | D |
| PCR TARGET INFORMATION | | Power analysis | D |
| ene symbol | E | Statistical methods for results significance | E |
| equence accession number | E | Software (source, version) | E |
| ocation of amplicon | D | C _q or raw data submission with RDML | D |
| Amplicon length | E | | |
| nsilico specificity screen (BLAST, and soon) | E | | |
| seudogenes, retropseudogenes, or other homologs? | D | | |
| equence alignment | D | | |
| econdary structure analysis of amplicon | D | | |
| ocation of each primer by exon or intron (if applicable) | E | | |
| /hat splice variants are targeted? | F | | |
| PCR OLIGONUCLEOTIDES | | | |
| rimer sequences | E | | |
| | | | |
| TPrimer D B identification number | U | | |
| robe sequences | Dª | | |
| ocation and identity of any modifications | E | | 1 0 1 0 m |
| lanufacturer of oligonucleotides | D | | - ALA |
| urification method | D | | |
| | //// | | 3 9/1/1 |
| | | | |
| a All occontial information (E) must be submitted with the menuscript Desirchle information (D) at the | submitted if available. If primare are from DTD | r DR information on gPCP target aligonucleatides and and an environment is susible from that survey | |
| ^a All essential information (E) must be submitted with the manuscript. Desirable information (D) should be ^b FFPE, formalin-fixed, paraffin-embedded; RIN, RNA integrity number; RQI, RNA quality indicator; GSP, get | | | the second |
| Assessing the absence of DNA with ano-reverse transcription assay is essential when first extracting RN | | | |
| Disclosure of the probe sequence is highly desirable and strongly encouraged; however, because not all | | | |
| | | | |

Primerdesign products are compliant with the **MIQE** guidelines

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P R I M E R $D \equiv S \mid G \mid N$