



The increasing number of citations of the MIQE guidelines (minimum information for publication of quantitative real-time PCR experiments, Bustin et al. 2009) demonstrates a growing emphasis on standardized experimental practice for qPCR.

The SYBR-based [StellARray[®] qPCR Array system](#) from Lonza offers a simple and reliable system for gene expression analysis that meets the MIQE standards and makes it easier for qPCR users to compare and publish their results.

Essential MIQE Guideline:	StellARray™ Array Provides:
qPCR target information	
Gene symbol	Provided online
Sequence accession number	Amplicon context sequence provided
Amplicon length	Amplicon context sequence provided
In silico specificity screen	Performed for every primer
Location of each primer	Amplicon context sequence provided
Which splice variants are targeted?	In amplicon context sequence
qPCR oligonucleotides	
Primer or amplicon context sequence	Amplicon context sequence provided
Manufacturer of oligos	Integrated DNA Technologies
Purification method	Salt free
qPCR validation	
Specificity (gel, sequence, melt)	Pre-validation qPCR run for each array and melt curve checked
Cq of NTC	No NTC necessary on plate because primers are pre-validated
Calibration curve with slope and y intercept r ² of calibration curve linear dynamic range	Gene regulations are calculated via relative quantification; no calibration curve on the

	array is needed.
PCR efficiency calculated from slope	Slope can be generated with analysis tools provided
Cq variation at LOD	Not more than 5% within replicates
Evidence for LOD	Can be calculated with data provided
Data analysis	
qPCR analysis program	GPR™ Data analysis tool
Method of Cq determination	Provided by instrument manufacturer
Outlier identification and disposition	Predefined cycle cutoff (Cq=37.5)
Results for NTC	Can be calculated with data provided
Justification of number and choice of reference genes	Ten most stable reference genes are proofed via ANOVA based normalizer calculation (via GPR™)
Description of normalization method	GPR™ algorithm (Akilesh et al. 2003)
Number and stage of technical replicates	Dependant on your experiment setup.
Repeatability (intraassay variation)	Can be calculated with data provided; SD for Cq variance or copy number variance
Statistical method for results significance	Standard T-test
Software (source, version)	Provided by instrument manufacturer

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