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# Strategies to Minimize Variability Between Individual qPCR Reactions

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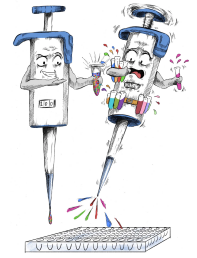
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**We use this protocol and it's working**

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## Abstract

Precise pipetting is paramount for generating precise and reliable qPCR results. Despite meticulous pipetting, significant variability can arise in qPCR, even between technical replicates. While some variability is expected in samples with low target concentrations, it is concerning in samples with high target concentrations. To maintain data integrity, it is generally recommended to discard data with a discrepancy of more than 0.2-0.5 Ct values between technical replicates, in particular when the Ct values are below 30 [Anonymous, 2019].

This protocol provides approaches to reduce this variability through an optimized pipetting strategy. Central to this strategy is the use of pipetting schemes and built-in redundancies in the workflow keeping track of individual pipetting steps.

## Attachments

**02\_setting\_qPCR\_assa...**

677KB

## Image Attribution

For permission to use the image and to contact the creator of the image, irod, please contact [gregor.blaha@ucr.edu](mailto:gregor.blaha@ucr.edu)



## Protocol references

Anonymous, 2019. Tips, Tricks & Best Practices, The Ultimate qPCR Assay Design Guide. Bio-Rad - Bulletin 6894 Ver B | 19-2076 NASD

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