NORMALIZATION ASSISTANT
FREQUENTLY ASKED QUESTIONS

AUTOMATED DNA AND RNA NORMALIZATION FOR EVERYONE IN YOUR LAB
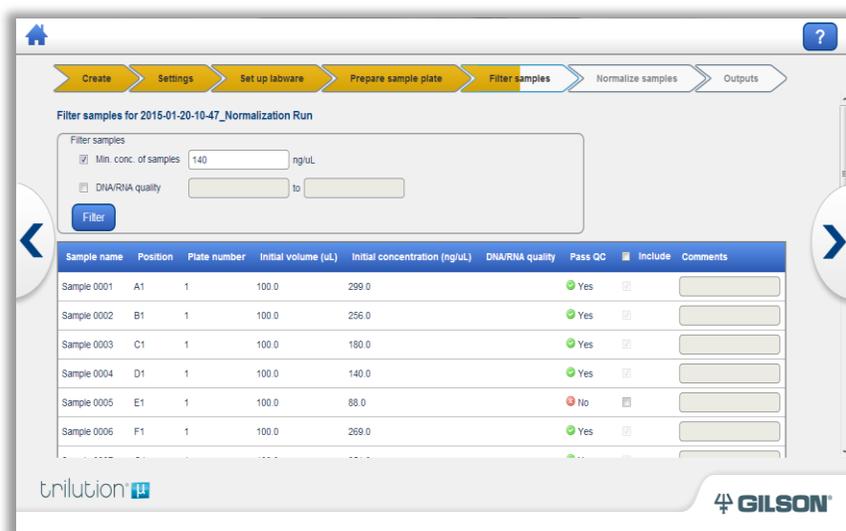
SETTING UP METHODS

Can I import my list of samples to Normalization Assistant?
Yes, PIPETMAX Normalization Assistant allows you to import .CSV files with sample information. You can import a sample name, location, initial volume, initial concentration, DNA or RNA quality, extraction code and comments.

Can I use a .CSV file with a header?
Yes, the .CSV file must have a header. The columns for sample name, location, initial volume, initial concentration, DNA or RNA quality, extraction code and comments can be in any order or and have heading. Normalization Assistant allows you to link the column names in the sample table with the column names in your import file.

Can I use one .CSV file in one run for all the sample information?
Yes, all the information required for importing samples for one run is in one file.

ISO 9001 CERTIFIED

Do I need to have the sample location information from file for .CSV file to be imported successfully?

You have the option to either import the sample locations from the import file or to fill the sample position automatically in columns or in rows.

LABWARE

Is my labware supported? Can I add my own labware?

A generic list of microplates, reservoirs and tube racks is included with the qPCR Assistant installation. Gilson recommends having labware files made for your exact labware for best performance. Labware Creator can be used to define your labware.

Can I use a passive cooling block?

PIPETMAX freezer blocks can be used to mitigate evaporation. When using cooling blocks, the labware positions must be designated as heavy bed elements.

Can I create an experiment on more than one plate?

Yes, samples in one or multiple 96-well plates can be normalized in one run.

Can I perform dilutions in tubes?

Normalization Assistant is capable of performing normalization methods in tubes, however mixing performance is better in microplates. For this reason, Gilson recommends using microplates with Normalization Assistant.

Can I use 384-well plates for highly concentrated samples?

384-well plates are supported for normalized samples with Normalization Assistant.
It is recommended to avoid the use of 384-well plates for normalization of samples with concentration above 2,000 ng/µL because the DNA at those concentrations is very viscous and this can impact pipetting performance

SAMPLE CONCENTRATIONS

What are the DNA concentrations usually used for samples in the lab?

Mostly researchers work with concentrations of DNA up to a few hundred ng/µL. Very rarely the concentrations exceed 1,000 ng/µl.
Most column based preps will result in concentrations of DNA/RNA at max to a few hundred ng/µl