

EpiGe QuantStudio6 Flex Real time Configuration Protocol

1. Select the Genotyping experiment type:

What type of experiment do you want to set up?

Quantitation - Standard Curve	Quantitation - Relative Standard Curve
Melt Curve	✓ Genotyping

Detected single nucleotide polymorphism variants of a target nucleic acid sequence in samples.

2. Edit the SNP Assays:
 - a. Assign to the SNP Assays the following names: W1_2554, W3_0222, S1_1033, S3_1292, G1_1884, and G3_0126.
 - b. Assign FAM reporter for the Methylated allele (Allele 1), and assign VIC reporter for the alternate Unmethylated allele (Allele 2). Both allele use the NFQ Quencher.

Edit SNP Assay

SNP Assay Name: <input type="text" value="S1_1033"/> Gene Symbol: <input type="text"/> NCBI SNP Reference: <input type="text"/> Allele 1 Name or Base(s): <input type="text" value="Allele 1_M"/> Allele 2 Name or Base(s): <input type="text" value="Allele 2_U"/> Comments: <input type="text"/>	Color: ■ ▼ Assay ID: <input type="text" value="CD.GT.SPDR8897.10"/> Gene Name: <input type="text"/> Context Sequence: <input type="text"/> Color: ■ ▼ Reporter: <input type="text" value="FAM"/> ▼ Quencher: <input type="text" value="NFQ-M..."/> ▼ Color: ■ ▼ Reporter: <input type="text" value="VIC"/> ▼ Quencher: <input type="text" value="NFQ-M..."/> ▼
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3. Assign the following task to the samples:
 - a. Allele 1 Homozygous (1/1): Methylated synthetic control.
 - b. Allele 2 Homozygous (2/2): Unmethylated synthetic control.
 - c. NTC (N): To the wells without sample.
 - d. Unknown (U): To the samples of interest.

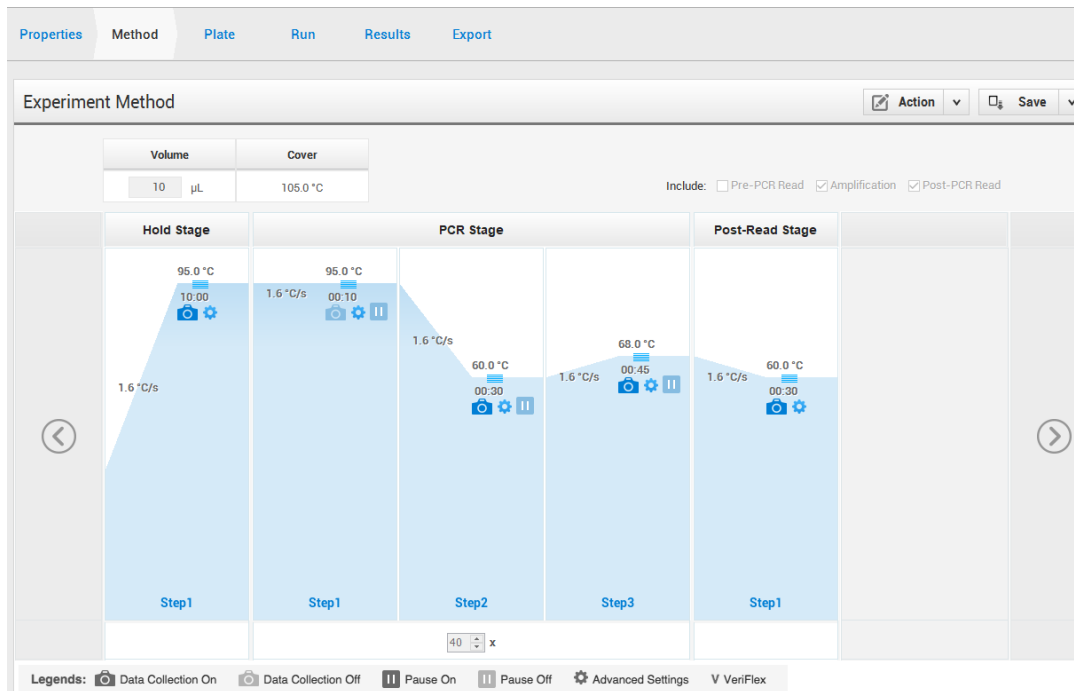
The screenshot shows the 'Genetic Data' application interface. On the left, there are two tables: 'SNPs' and 'Samples'. The 'SNPs' table has columns: Name, NCBI SNP ID, Context, Allele 1, Reporter, Quescher, Allele 2, Reporter, Quescher, and Task. The 'Samples' table has columns: Sample Name and Comments. A red box highlights the 'Task' column in the 'SNPs' table, and a red arrow points from it to the 'Task' column in the 'Genetic Data' table on the right.

SNPs	Name	NCBI SNP ID	Context	Allele 1	Reporter	Quescher	Allele 2	Reporter	Quescher	Task
<input checked="" type="checkbox"/>	S1_1033			Allele 1_M	FAM	NFG-MDB	Allele 2_U	VIC	NFG-MDB	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	S3_1292			Allele 1_M	FAM	NFG-MDB	Allele 2_U	VIC	NFG-MDB	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	W1_2554			Allele 1_M	FAM	NFG-MDB	Allele 2_U	VIC	NFG-MDB	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	W3_8222			Allele 1_M	FAM	NFG-MDB	Allele 2_U	VIC	NFG-MDB	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	G1_1884			Allele 1_M	FAM	NFG-MDB	Allele 2_U	VIC	NFG-MDB	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	G3_0126			Allele 1_M	FAM	NFG-MDB	Allele 2_U	VIC	NFG-MDB	<input checked="" type="checkbox"/>

Samples	Sample Name	Comments
<input checked="" type="checkbox"/>	G1_1884_M	gliblock
<input checked="" type="checkbox"/>	G1_1884_U	gliblock
<input checked="" type="checkbox"/>	G3_0126_M	gliblock
<input checked="" type="checkbox"/>	G3_0126_U	gliblock
<input checked="" type="checkbox"/>	NTC	
<input checked="" type="checkbox"/>	G1_1033_M	ntfivk

The 'Genetic Data' table on the right shows a grid of data for various samples (A, B, C, D, E, F, G, H) across different SNPs (S1_1033, S3_1292, W1_2554, W3_8222, G1_1884, G3_0126). The 'Task' column is highlighted in red, and a red arrow points from the 'Task' column in the 'SNPs' table to it.

4. Method



5. Exportation of Results

- File Type (*.txt)
- Select all contents
 - Sample Setup
 - Raw Data
 - Amplification Data
 - Multicomponent Data
 - Results
 - Reagent Information

