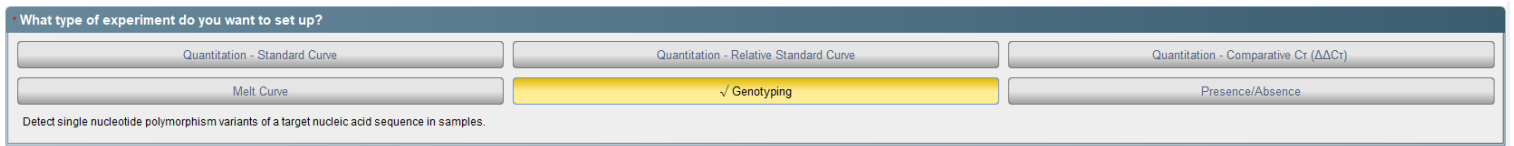
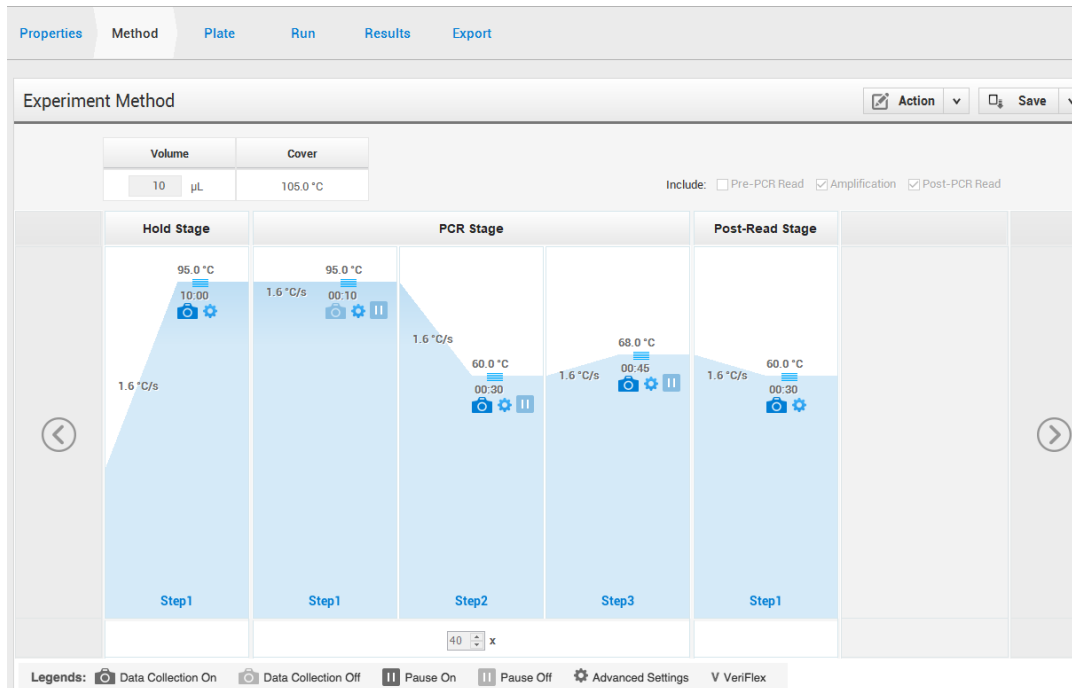


EpiGe QuantStudio6 Flex Real time Configuration Protocol

1. Select the Genotyping experiment type:



2. Method



3. Edit the SNP Assays:

- a. Assign to the SNP Assays the following names: cg18849583, cg01268345, cg10333416, cg12925355, cg25542041, cg02227036.
- 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.

4. 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 'Assign SNP Assays and Samples' window. On the left, there is a table with columns for Name, NCBI ID, Cont., Allele, Rep., Que., Allele, Rep., Que., and Task. The 'Task' column is highlighted with a red box. On the right, there is a grid of wells (A-E rows, 1-12 columns). A red arrow points from the 'Task' column in the table to a 'Task' dropdown menu on the far right. The dropdown menu shows options: 'U', 'N', '1', '2', '2'.

5. Assign names to the samples

Samples		+	Action
	Sample Name	Comments	
<input checked="" type="checkbox"/>	cg01268345_Unmethylated	gBlock	✕
<input type="checkbox"/>	cg02227036_Methylated	gBlock	✕
<input checked="" type="checkbox"/>	cg02227036_Unmethylated	gBlock	✕
<input type="checkbox"/>	cg10333416_Methylated	gBlock	✕
<input checked="" type="checkbox"/>	cg10333416_Unmethylated	gBlock	✕

6. Exportation of Results
 - a. File Type (*.txt)
 - b. Select all contents
 - i. Sample Setup
 - ii. Raw Data
 - iii. Amplification Data
 - iv. Multicomponent Data
 - v. Results
 - vi. Reagent Information

