ProductInformation

GenomePlex® Whole Genome Amplification: Importing Method Files for the Biomek® FX (Beckman Coulter)

I. Introduction

The Biomek® FX files provided along with this document were designed to run Sigma's GenomePlex Whole Genome Amplification (WGA) Kits for the amplification of genomic DNA from trace samples. The following describes the hardware requirements necessary to utilize this method, along with instructions on how to import the files. Before running the automated method, please review the Automation Protocol for GenomePlex WGA on the Biomek FX located at www.sigma-aldrich.com/automation

II. Hardware Requirements

The method provided for the GenomePlex WGA Kits was developed for the Biomek FX with a dual pod configuration. Modifications will need to be made to the methods if using with an instrument with a single pod configuration.

Part Description	Qty	Ordering Information
Span-8 Pod	1	Contact Beckman Coulter
Span-8 Tip Trash	1	Contact Beckman Coulter
Span-8 Tip Wash	1	Contact Beckman Coulter
Standard Passive ALPs (One by Three)	3	Contact Beckman Coulter
Standard Passive ALPs (One by One)	1	Contact Beckman Coulter
Span-8 P250 Barrier Tips, Sterile	1	BK379503 (Beckman Coulter)
Span-8 P20 Barrier Tips, Sterile	3	BK379506 (Beckman Coulter)

III. Software Requirements

The GenomePlex WGA method was developed using Biomek software version 3.1. If using another version of this software, confirm the method's compatibility prior to use.

IV. Method Download Instruction

1. Download the self-extracting archive (GenomePlex WGA_BiomekFX.zip) containing method and import files necessary to run the GenomePlex WGA method on the Biomek FX. Files included in this archive are as follows:
    WGA.imp
    WGA.bmf
2. Click on files to select for extraction.
3. Copy files to a directory on the computer for the Biomek FX.

V. Importing Method Files into the Biomek Software

1. Open the Biomek software program.
2. To create a new project, go to the **Project** menu and select **New Project**. Enter **GenomePlex WGA** as the new name.
3. To import information such as labware definitions, liquid type, and pipetting templates, go to the **Project** menu and select **Import Project**.
4. Navigate to the directory where the extracted files are saved.
5. Select **WGA.imp** and click **Open**.
6. To import the method, go to the **File** menu and choose **Import**.
7. Navigate to the directory where the extracted files are saved.
8. Select **WGA.bmf** and click **Open**.
9. Choose **Yes** when asked if you wish to import the methods into the current project.

VI. Configuring the Deck for GenomePlex WGA Method

Instrument configurations, deck definitions, or numbering of deck positions may vary from those used at Sigma-Aldrich in development of these methods. To run these methods, some labware rearrangement may be required. The deck layout for the GenomePlex WGA method is provided below as a guide.
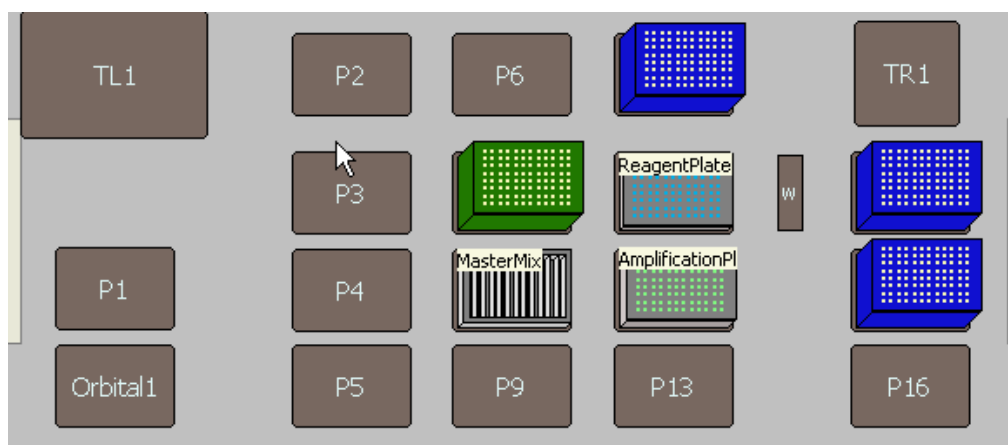
Deck Position	Equipment
P7	Span-8 P250 Barrier Tips
P8	12 column reservoir for amplification master mix
P10	Span-8 P20 Barrier Tips
P11	96-well PCR plate with full skirt containing reagents
P12	96-well PCR plate with genomic DNA samples to be amplified (seated into a plate holder)
P14	Span-8 P20 Barrier Tips
P15	Span-8 P20 Barrier Tips

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GenomePlex is a registered trademark of Rubicon Genomics, Inc.

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