

# BlueFuse Workflow Manager v1.3 for VeriSeq PGS

## User Guide

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## Introduction

The Illumina® BlueFuse Workflow Manager (BWM) lets you create and edit well-formed sample sheets for Illumina workflows. These sample sheets define the indexing and other sequencer parameters to be used for each sample.

BWM performs dilution calculations and detects and warns you when an index combination specified is suboptimal. By creating the sample sheet before library preparation, you can try a different index combination without risking your samples.

There are two steps to creating a sample sheet with the BWM for Illumina sequencing systems:

- ▶ First, you create a **worklist**. The worklist contains information about the samples in each well of a 96-well (or fewer) plate, including the type of library prep, the plate name, and sample indexes.
- ▶ Second, you create a **sample sheet** based on the information defined in the worklist. The sample sheet passes run and sample information in the correct file format (\*.csv) to the instrument control and analysis software.

## Getting Started

### Downloading the Software

You can download BWM from the Illumina website at [https://support.illumina.com/sequencing/sequencing\\_software/bluefuse-workflow-manager.html](https://support.illumina.com/sequencing/sequencing_software/bluefuse-workflow-manager.html). From the BlueFuse Workflow Manager Support page, select **Downloads**. A MyIllumina account is required.

### Installing the Software

BWM can be run on Windows 7 and 8.1. To start the installation, double-click the downloaded install file. The installation wizard opens. Select **Next** to accept all default settings.

### Starting the Software

To start the software, go to **Start | All Programs | Illumina | BlueFuse Workflow Manager**.

### Settings

You can specify where your worklists and sample sheets are saved by selecting **Folder Settings** on the main screen of BWM. Select **Browse** to navigate to the desired folders for each type of file, and then select **OK**.



#### TIP

To make sure that the files are accessible from the sequencing instrument in your lab, save the files in a shared network folder. Alternatively, sample sheets can be copied to a USB drive.

### Concepts

- ▶ **Worklist** — A temporary file that holds the run data used to create the sample sheet. BlueFuse Workflow Manager uses worklist files to let users prepare a run in advance, and then add the final parameters (eg Flow Cell ID and Reagent Cartridge ID) at the time of the run to create the sample sheet. Worklists can be edited and reused.

- ▶ **Sample Sheet** — A comma-separated text file with the extension CSV. It is created by BlueFuse Workflow Manager from the worklist data and is then fed to the sequencer or the secondary analysis program.
- ▶ **Plate Graphic** — A visual depiction of the data required to prepare a library, organized in the same way as the wells on a standard plate. The plate graphic can be printed and used as an aid in library preparation.

## For VeriSeq PGS

### Prepare MiSeq Worklist

- 1 From the BWM main screen, select **Create Worklist**.
- 2 Select **VeriSeq PGS** from the Category section, then select the **VeriSeq PGS** workflow, and click **Next**.
- 3 On the Run Parameters screen, do the following:
  - ▶ **Worklist Name**—Enter a name for the worklist.
  - ▶ **Number of Samples**—Select the number of samples: up to 12 (Single Index) or up to 24 (Dual Index).
  - ▶ **Default Cell Type**—Select the default cell type of the samples.
  - ▶ **Experiment Name**—Enter a name for the experiment.
  - ▶ **Investigator Name**—[Optional] Enter the name of the investigator.
  - ▶ **Run Date**—Select the date of the run from the calendar drop-down.
  - ▶ **Description**—[Optional] To record more detailed information about the samples, enter a sample description.
- 4 Click **Next**.

To edit an existing worklist, click **Edit Worklist** on the main screen and navigate to the worklist that you want to edit.

### Enter MiSeq Sample Information

Take the following into consideration when entering sample information:

- ▶ Text fields cannot contain spaces or special characters:
    - ? () [] / \ = + < > : ; " , \* ^ | &
  - ▶ Exception: The Description field can contain spaces.
  - ▶ The Cycle ID and Embryo ID fields must not contain a double hyphen or have leading or trailing hyphens. This can cause the BAM file to not be recognized by BlueFuse Multi.
- 1 From the Table tab or the Plate tab, enter the following information for each well containing a sample:
    - ▶ **Cycle ID**—Enter a cycle ID.
    - ▶ **Embryo ID** —Enter an embryo ID. For each sample, the combination of the Cycle ID and Embryo ID must be unique.
    - ▶ **Cell Type**—[Pre-populated] Specify the type of cell in the sample.
    - ▶ Calculate the dilution:
      - ▶ Enter the DNA concentration of the 1/10 diluted SurePlex reaction obtained from dsDNA quantification.
      - ▶ Enter the volume of the 1/10 dilution that will be transferred to the clean plate for library preparation.
      - ▶ BWM calculates the volume of MBG water required to prepare dsDNA at 0.2 ng/μl.

- ▶ **Index 1 (i7)**—[Pre-populated] Optimal Index 1 layout has been selected. Use the drop-down menu to adjust the index.
- ▶ **Index 2 (i5)**—[Pre-populated] Optimal Index 2 layout has been selected. Use the drop-down menu to adjust the index.
- ▶ **Description**—[Optional] To record more detailed information about the samples, enter a sample description.



#### TIP

Use the BWM Fill feature to populate your sample sheet quickly. The Fill feature can copy data as-is from cell to cell, or can automatically increase numerical data by 1 to create sequential data. The BWM determines which method is appropriate based on what type of data are in the cell or cells being copied.

- ▶ To copy data, populate 1 cell, then highlight, right-click, and fill the other cells you want to populate with the same information.
  - ▶ To generate sequential data, enter sequential data in 2 adjacent wells, then highlight the other cells you want to populate. Select the highlighted area and select **Fill Down** or **Fill Right**. The highlighted cells are numbered in sequential order.
  - ▶ **Content can be pasted directly from a spreadsheet table.**
- 2 Click the **Plate Graphic** tab to visualize the Plate Graphic:
    - ▶ Wells corresponding to filled samples contain their Cycle ID and Embryo ID and the correspondent Index 1 (i7) and Index 2 (i5).
    - ▶ Invalid wells, where either Embryo ID or Cycle ID is missing, are shown with a red background and red border.
    - ▶ Use the **Copy to Clipboard** or **Print** option to capture an image of the sample plate.
  - 3 Click **Save Worklist**. The default worklist file name is vs-ms\_[current date]\_[worklist name].wls.

## Create Sample Sheet

Create the sample sheet when the libraries are completed, using a unique Flow Cell ID selected for the run.

- 1 From the BWM main screen, select **Create Sample Sheet**. The Enter Run Settings screen opens.
- 2 Select a worklist from the **Select Worklist** drop-down or click **Browse** and select an existing worklist.
- 3 Enter the **Flow Cell ID** and the **Cartridge Number**. Typical cartridge number format:
  - ▶ MiSeq—MSXXXXXXXX-PGS or MSXXXXXXXX-00PGS
- 4 Click **Save Sample Sheet** and save the sample sheet file in the designated folder. By default, the file is saved as [worklist file name].csv.
 

*Do not open or modify any files within the run folder while the sequencing run is in progress. Do not modify sample sheet files using any program other than BWM. Files modified outside of BWM are rendered invalid for use.*
- 5 Copy the sample sheet to the MiSeq sample sheet folder before executing a sequencing run.

## Technical Assistance

For technical assistance, contact Illumina Technical Support.

Website: [www.illumina.com](http://www.illumina.com)  
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**Safety data sheets (SDSs)**—Available on the Illumina website at [support.illumina.com/sds.html](http://support.illumina.com/sds.html).

**Product documentation**—Available for download in PDF from the Illumina website. Go to [support.illumina.com](http://support.illumina.com), select a product, then select **Documentation & Literature**.



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