

## Biomek Normalization

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Input: Cleaned-up PCR product plate and quantitation data

Output: Normalized plate, 1 picomole in 50 ul water

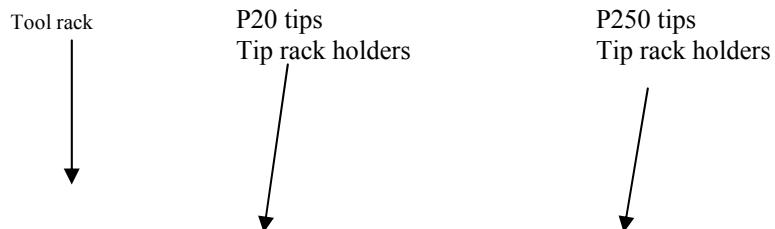
Next method: T4 polymerase reaction

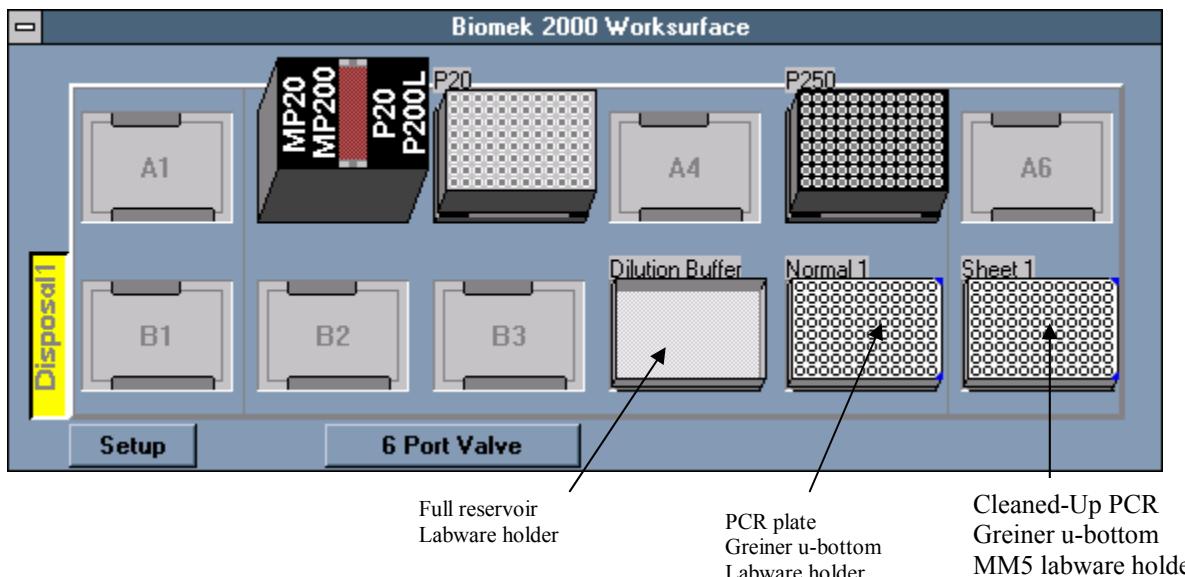
Materials/Reagents/Equipment	Vendor
<b>Disposables</b>	
PCR plate & mat	E&K (Cat#: 489096 & 402096)
<b>Reagents</b>	
Cleaned-up PCR product	Freezer
Water, sterile, for dilution reservoir	
<b>Equipment</b>	
Biomek 2000	Beckmann Coulter
Floppy disk w/ quantitation Excel table	

### I. Importing Normalization Data

- \_\_\_ 1. Double click on Biomek Lab Book Manager icon on the desktop.
- \_\_\_ 2. Select the **Normalization** folder and click on **Set as Current Lab Book**. Click **Close**.
- \_\_\_ 3. Insert floppy disk with Normalization Excel file (see Picogreen Quantitation Protocol). Open My Computer on Desktop, double-click on Floppy (A:) drive.
- \_\_\_ 4. Open Normalization-date file, click File → Save as → Save in: Desktop → Normalization Test folder.

### II. Setting up the Biomek worksurface





- \_\_\_ 1. Fill reservoir with autoclaved water.
- \_\_\_ 2. Place Cleaned-Up PCR Product plate on support Greiner u-bottom plate at B6.
- \_\_\_ 3. Place empty PCR plate on support Greiner u-bottom plate at B5.

### III. Generating Normalization Method

- \_\_\_ 1. Click Start → Bioworks → Normalization Wizard → Next → Import plates.
- \_\_\_ 2. Look in: Desktop/Normalization Test folder.
- \_\_\_ 3. Select Normalization-date file and click Open: file becomes Sheet1 in Wizard.
- \_\_\_ 4. Click Next for the “Configure Options” window.  
Change **Final Concentration** to **1.0**.  
Change **Final Well Volume** to **50**.
- \_\_\_ 5. Click Next for “Configure Transfer” window, then Next for “View Plates”
- \_\_\_ 6. Click **Exclude Errors** to remove empty wells highlighted in red.
- \_\_\_ 7. Click Next for “Generate Method” window, OK to No Lids warning.
- \_\_\_ 8. Click **Generate Method**. The method is saved in Normalization Lab Book as Norm-date-hour.

### IV. Editing and Running Method

- \_\_\_ 1. Click **View Method**.
- \_\_\_ 2. Click on Sheet1 at B6 to highlight plate in green. Press Delete key to remove.
- \_\_\_ 3. Click on **Devices** on Function Palette, scroll down and select **Norm MM5-B6**.
- \_\_\_ 4. Click on B6 to place Norm MM5-B6 (shaker labware holder).
- \_\_\_ 5. Click on **Plates** on Function Palette, select **96-well u-bottom**, place on B6 holder.
- \_\_\_ 6. Click on tip boxes at A4 and A6 to highlight and press Delete.
- \_\_\_ 7. Click on the running man button to start the method. (Note: Save all the settings and click **Accept All** to confirm the configuration.)
- \_\_\_ 8. After the run, cover and label normalized plate (1 picomole in 50 ul), store in Freezer 318 until T4 polymerase digestion (see protocol).
- \_\_\_ 9. Cover and store Cleaned-Up PCR plate in Freezer 318.

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