Using Illumina Genotyping Data with dChip

This document describes Illumina's data compatibility with dChip. Data sharing between BeadStudio and dChip occurs via a DLL plug-in. This plug-in allows you to use BeadStudio's Genotyping Module to create a dChip-compatible report.

For information about the dChip algorithm, visit http://biosun1.harvard.edu/complab/dchip/.

NOTE: Because dChip is not an Illumina product, Illumina Technical Support cannot provide support for the dChip algorithm.

Illumina Data Compatibility with dChip

Perform the following steps to import data from a dChip-compatible BeadStudio report into dChip.

1. Open dChip.

2. Get External Data.

   a. Select **Analysis | Get External Data**.

   b. Enter a group name.

   c. Click **Data File** and choose the intensity and call file
      (e.g., projectname_dChip_raw_intensity_and_call_data.txt).

   d. Check all three checkboxes.

   e. Select the **Other Information** tab.

   f. Select **External SNP data from Array Type** from the dropdown menu.

   g. [OPTIONAL] Adjust the ploidy column in the sample info file.
      Use ploidy = 2 for normal samples, blank for tumor samples.

   h. In the information files area, click in the **Sample** field and choose the sample information file (e.g. projectname_dChip_sample_info.txt).

3. Observe LOH and copy number data in dChip.

   a. Select **Analysis | Chromosome**.

   b. Click the **Genome Information File** field and choose the genome information file (e.g. projectname_dChip_genome_info.txt).

   c. Select **Copy number & LOH** from the dropdown menu.

   d. Click **Options** and adjust the settings as desired.

   e. Click **OK** and observe LOH and copy number data in dChip.

4. [OPTIONAL] Export copy number data from dChip.

   a. Select **Chromosome | Export SNP Data**.

   b. Specify the output file and click **OK**.