Guidelines to Prepare a Sample Sheet for Demultiplexing NEBNext Direct GS Libraries using bcl2fastq

NEBNEXT DIRECT[®] GENOTYPING SOLUTION PANELS (NEB #E9500/#E9530)

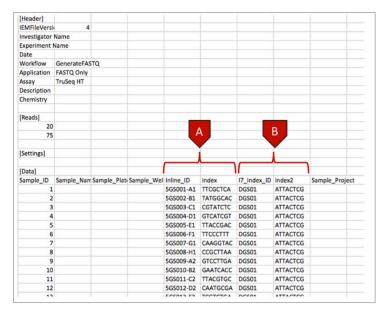
1. Download an NEBNext Direct GS sample sheet for use with *bcl2fastq* from the product page for the NEBNext Direct GS Target Enrichment Kit (NEB #E9530).

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- 2. Update the (Data) fields with the barcodes used in your experiment. The *bcl2fastq* software uses the sample barcodes to demultiplex in the order in which they are read by the sequencer. Therefore, the "index" column is required to contain the sample barcodes from the Read1 site, while the "index2" column is required to contain the sample barcodes from the i7 site.
- 3. Save the sample sheet as a csv file (.csv) for use with the *bcl2fastq* software. Do not use this sample sheet to run NEBNext Direct GS libraries on an Illumina sequencer.

Example bcl2fastq Sample Sheet:

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- A. The Inline_ID/index columns should contain the inline sample IDs/indexes that were sequenced in Read1.
- B. The I7_Index_ID/index2 columns should contain the pool IDs/indexes that were sequenced from the i7 site (Index1).

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