# ChIP-Seq Coverage

The workflow sample, described below, prepare ChIP-Seq processed data (with BedTools and bedGraphToBigWig) for visualization in a genome browser. For input BED-file produces BigWig file.
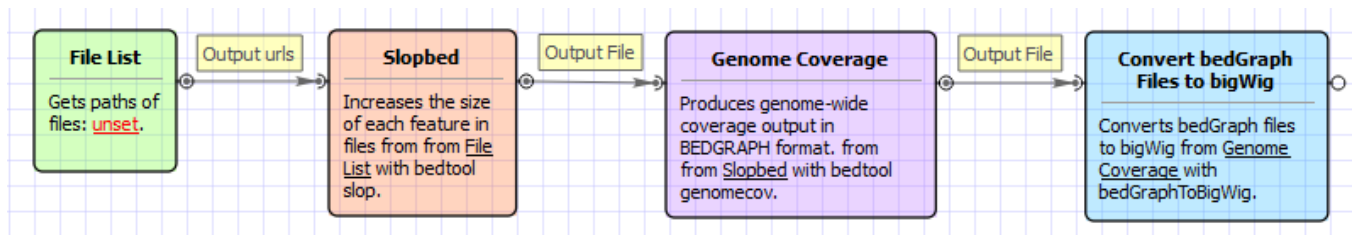
> ⊘ **How to Use This Sample**
>
> If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

## Workflow Sample Location

The workflow sample "ChIP-Seq Coverage" can be found in the "NGS" section of the Workflow Designer samples.
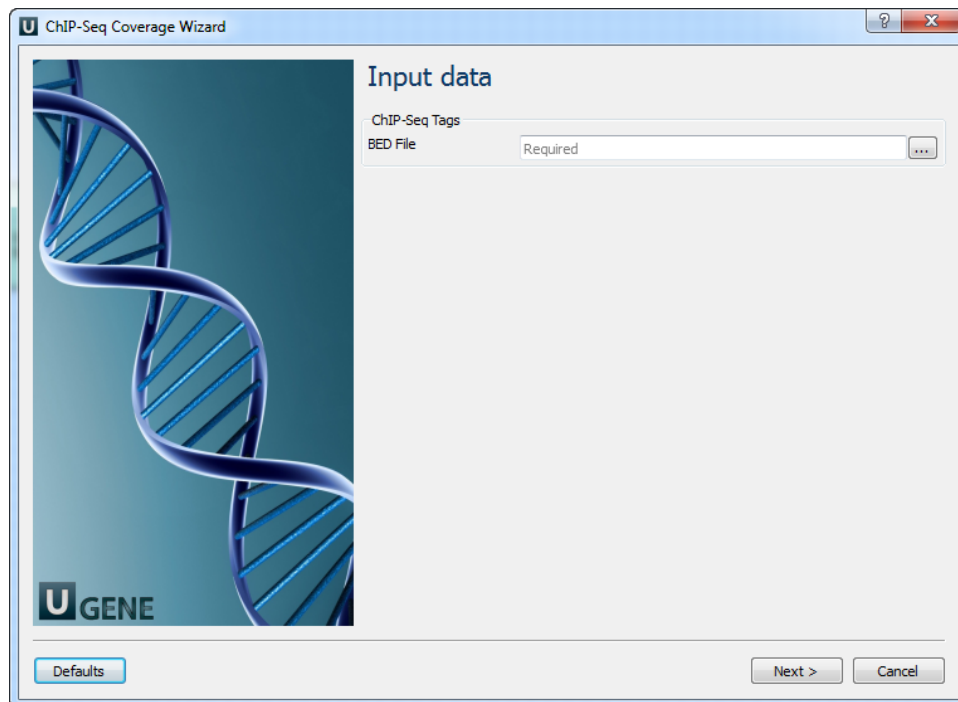
## Workflow Image

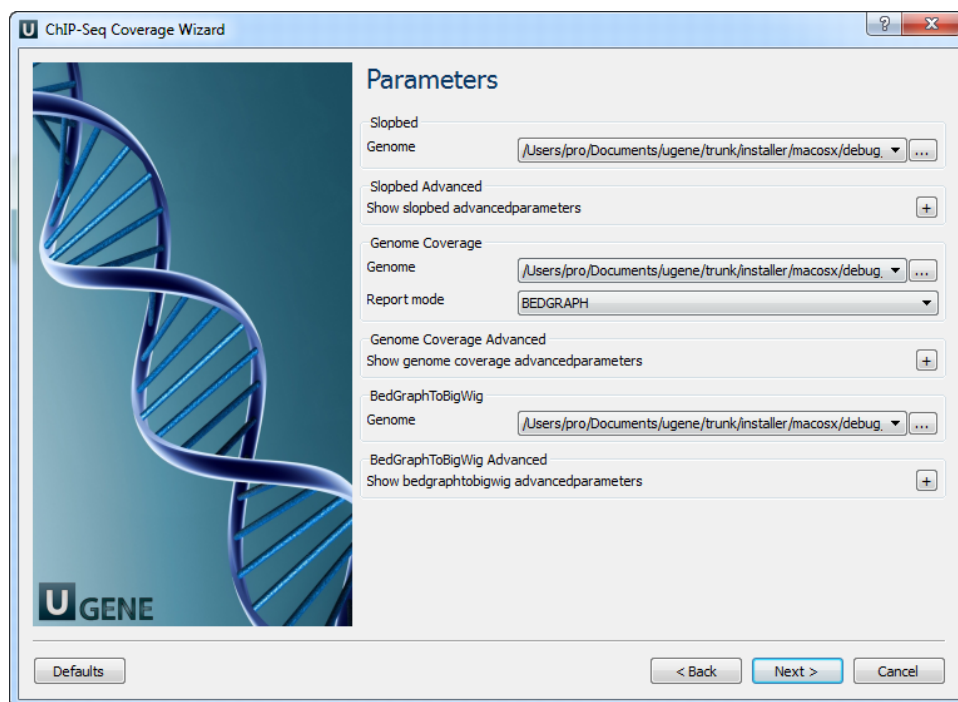The opened workflow looks as follows:



## Workflow Wizard

The wizard has 3 pages.

1. Input data Page: On this page you must input BED file with ChIP-Seq tags.



2. Parameters Page: Here you can optionally modify parameters that should be used for the Slopbed, Genome Coverage and BedGraphToBigWig elements.

3. Output Files Page: On this page you can select an output directory: