

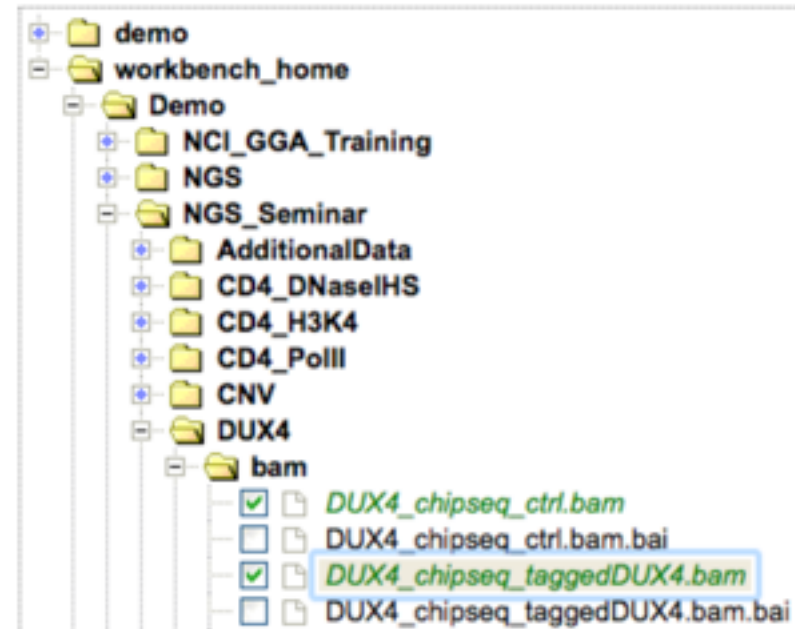
# BTEP ChIP-Seq Workshop

**Screenshots from Genomatix**

## — Loading input files

Browse the file tree below and select your files of interest.

Base directory: /mounts/



## — Loading input files

Input file(s) with read positions (Sample or Treatment)  
Note: multiple files are treated as replicates

Available files	Listing files for Homo sapiens / GRCh38: Select <input type="radio"/> BED files or <input checked="" type="radio"/> BAM files	
	DUX4_chipseq_ctrl.bam (7012583 regions) DUX4_chipseq_taggedDUX4.bam (6559864 regions)	<a href="#">Add BAM files</a>
		<a href="#">Upload more files to your project</a>

Hint: To get more statistics on your BAM files or to filter them: [BAM Toolbox](#)

### BAM File Upload

Current Project: "ChIP-seq\_demo"

Upload alignments

Upload file(s) with genomic regions in <a href="#">BAM file format</a> ?	Import BAM file(s) from <input type="radio"/> your local computer <input checked="" type="radio"/> the GGA
	Assuming input is for Homo sapiens / GRCh38 Multiple files can be uploaded: <a href="#">Browse GGA...</a>
	Optional name/prefix for y on the server: <input type="text" value="Browse GGA directories for input files"/>

# EXACT PARAMETER SETTINGS

## Analysis Parameters

Input files:	"DUX4_chipseq_taggedDUX4.bam", 6559864 regions, Homo sapiens, GRCh38
Control files:	"DUX4_chipseq_ctrl.bam", 7012583 regions, Homo sapiens, GRCh38
Database version:	EIDorado 12-2016
Result name:	DUX4-result_chipseq
Read Classification:	on
Peak Finding:	on (mandatory)
Peak finding algorithm:	NGSAnalyzer
NGSAnalyzer parameters:	window size for peak finding: 250 reads not strand specific min. reads per peak: determined from input data
Differential analysis method:	Audic-Claverie
Differential analysis thresholds:	$\log_2(\text{fold-change}) \geq 1$ for enrichment $\log_2(\text{fold-change}) \leq -1$ for depletion adjusted p_value_threshold = 0.05
Peak Classification:	on
Sequence Extraction:	on
TFBS Overrepresentation:	on
Definition of new TFBS:	off