BTEP ChIP-Seq Workshop

Screenshots from Genomatix

Loading the BAM files - 1

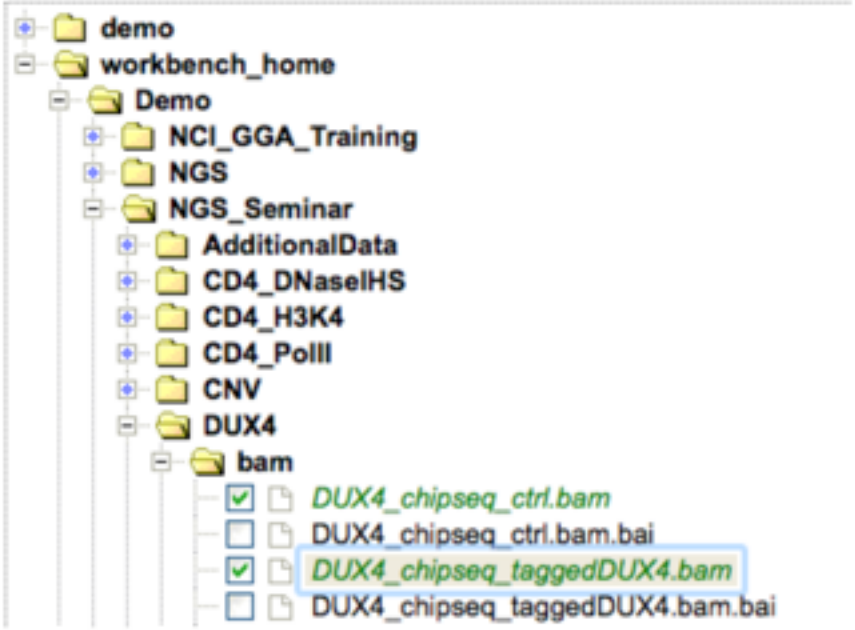
genomatix

Thomas Werner
Scientific & Business Consulting

Loading input files

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

Base directory: /mounts/



Loading the BAM files - 2

genomatix

Thomas Werner
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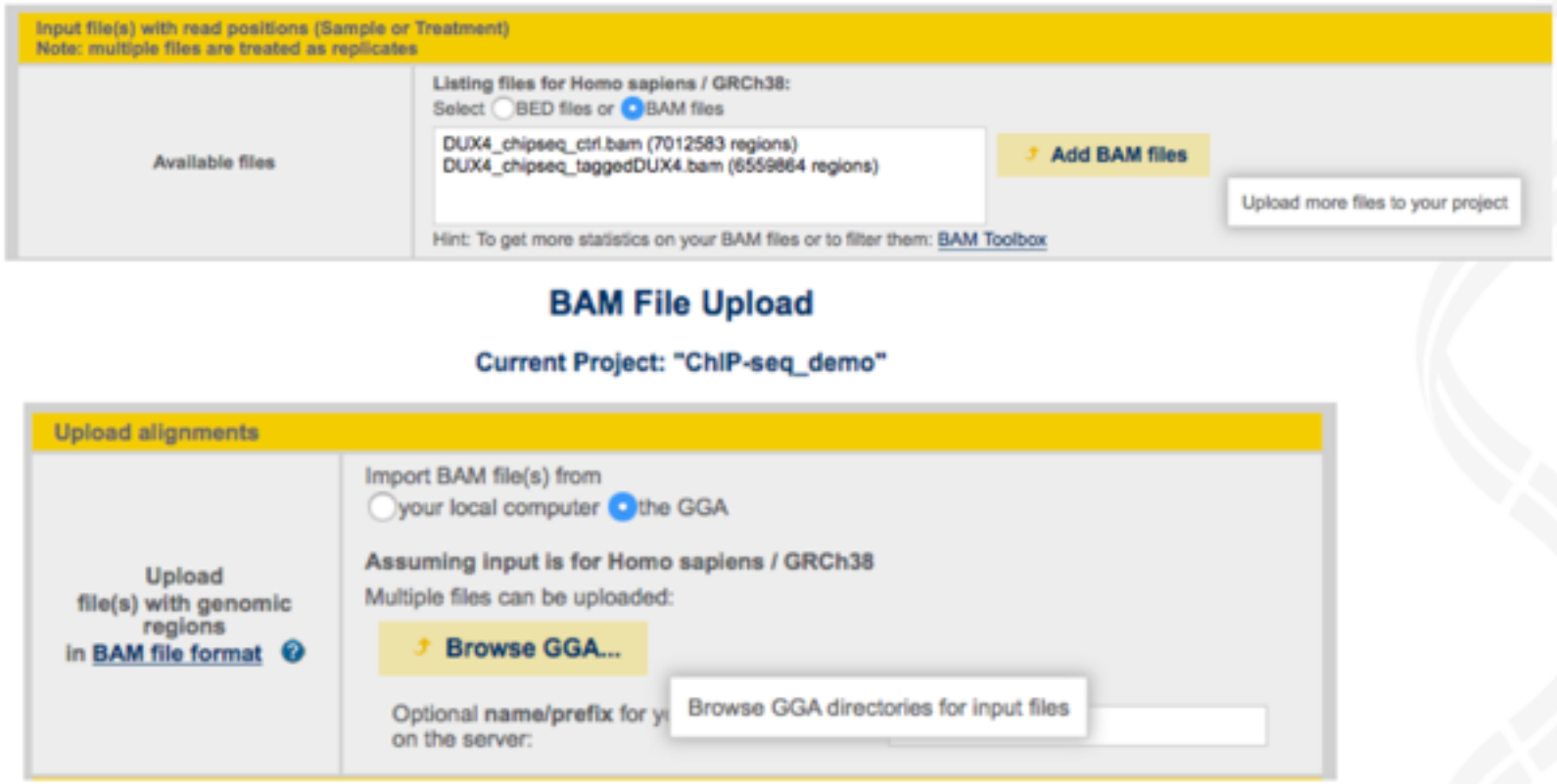
Loading input files



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:	ElDorado 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:	log2(fold-change) ≥ 1 for enrichment log2(fold-change) ≤ -1 for depletion adjusted p_value_threshold = 0.05
Peak Classification:	on
Sequence Extraction:	on
TFBS Overrepresentation:	on
Definition of new TFBS:	off