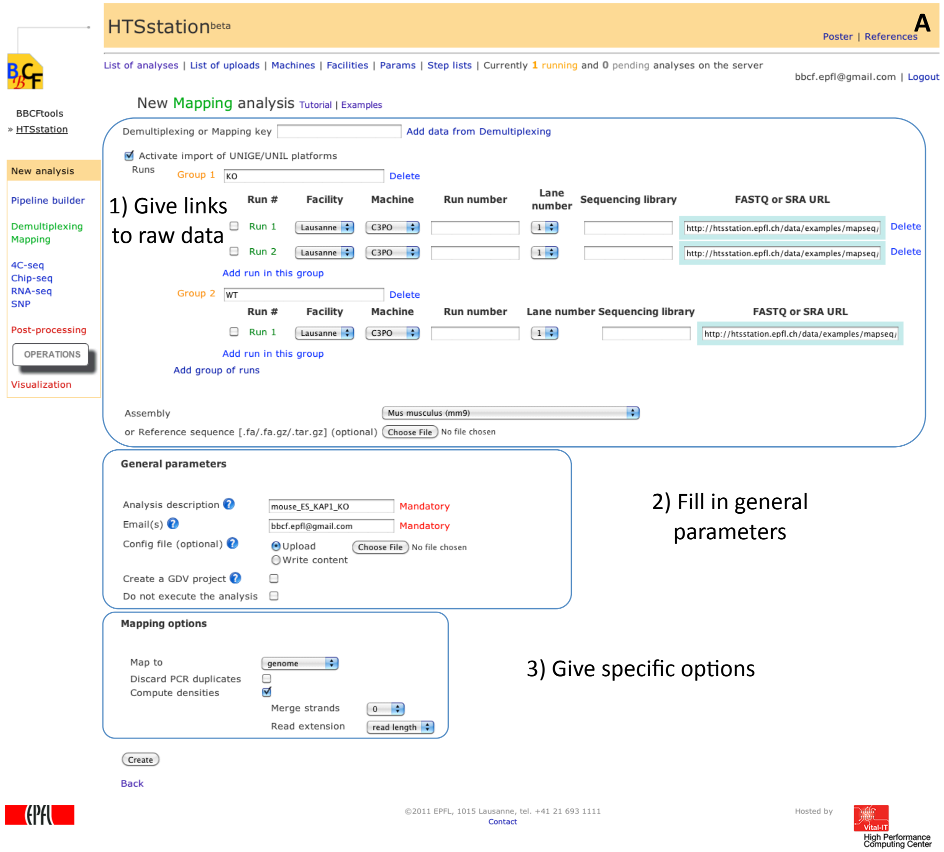

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New Mapping analysis

Demultiplexing or Mapping key

☑ Activate import of UNIGE/UNIL platforms

Runs

Group 1: KO

1) Give links to raw data

	Run #	Facility	Machine	Run number	Lane number	Sequencing library	FASTQ or SRA URL	
☐	Run 1	Lausanne	C3PO		1		http://htsstation.epfl.ch/data/examples/mapseq/	Delete
☐	Run 2	Lausanne	C3PO		1		http://htsstation.epfl.ch/data/examples/mapseq/	Delete

Group 2: WT

	Run #	Facility	Machine	Run number	Lane number	Sequencing library	FASTQ or SRA URL
☐	Run 1	Lausanne	C3PO		1		http://htsstation.epfl.ch/data/examples/mapseq/

Assembly: Mus musculus (mm9)

or Reference sequence [.fa/.fa.gz/.tar.gz] (optional): No file chosen

General parameters

2) Fill in general parameters

Analysis description: mouse_ES_KAP1_KO Mandatory

Email(s): bbcf.epfl@gmail.com Mandatory

Config file (optional): ● Upload ○ Write content — No file chosen

Create a GDV project ☐

Do not execute the analysis ☐

Mapping options

3) Give specific options

Map to: genome

Discard PCR duplicates ☐

Compute densities ☑

Merge strands: 0

Read extension: read length

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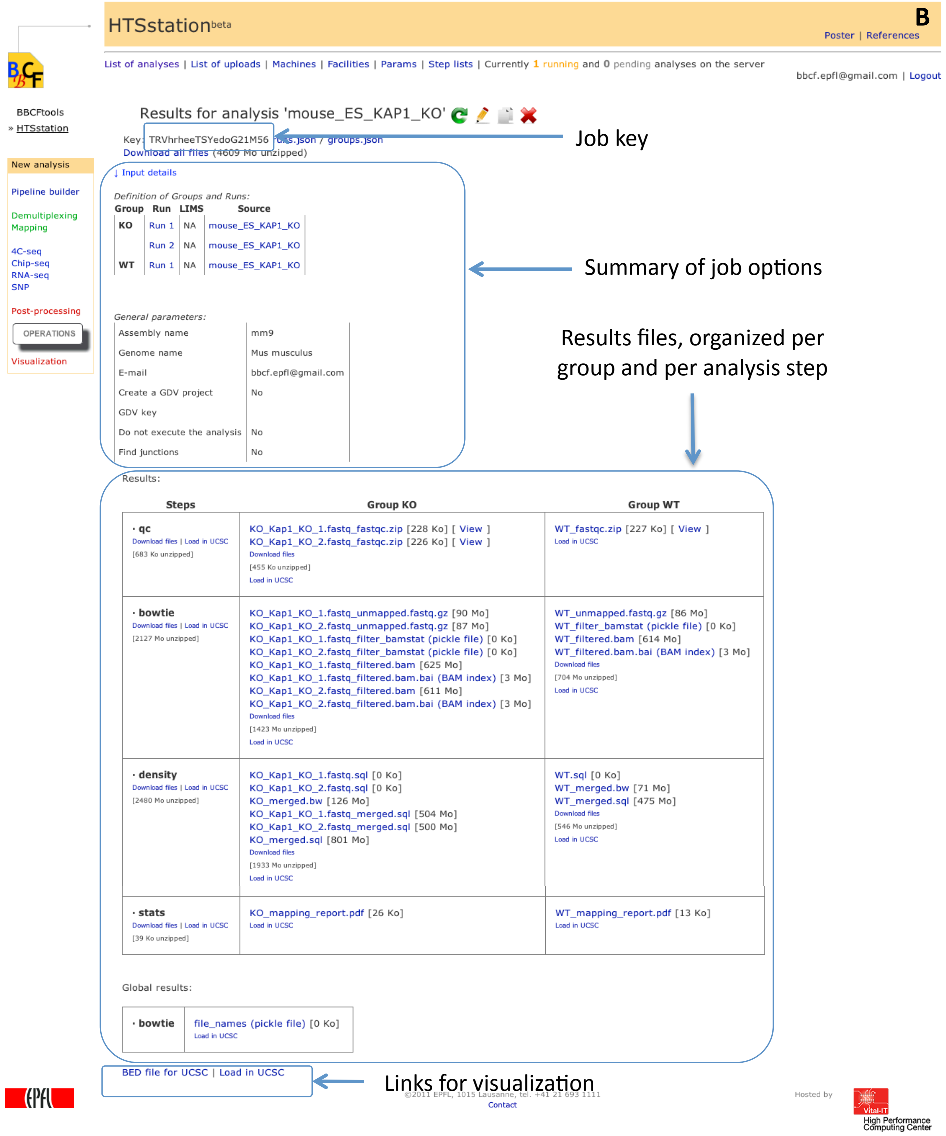

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Results for analysis 'mouse_ES_KAP1_KO'

Key: TRVhrheeTSYedoG21M56 runs.json / groups.json

Download all files (4609 Mo unzipped)

Job key

↓ Input details

Definition of Groups and Runs:

Group	Run	LIMS	Source
KO	Run 1	NA	mouse_ES_KAP1_KO
	Run 2	NA	mouse_ES_KAP1_KO
WT	Run 1	NA	mouse_ES_KAP1_KO

Summary of job options

General parameters:

Assembly name	mm9
Genome name	Mus musculus
E-mail	bbcf.epfl@gmail.com
Create a GDV project	No
GDV key	
Do not execute the analysis	No
Find junctions	No

Results files, organized per group and per analysis step

Results:

Steps	Group KO	Group WT
· qc Download files | Load in UCSC [683 Ko unzipped]	KO_Kap1_KO_1.fastq_fastqc.zip [228 Ko] [View] KO_Kap1_KO_2.fastq_fastqc.zip [226 Ko] [View] Download files [455 Ko unzipped] Load in UCSC	WT_fastqc.zip [227 Ko] [View] Load in UCSC
· bowtie Download files | Load in UCSC [2127 Mo unzipped]	KO_Kap1_KO_1.fastq_unmapped.fastq.gz [90 Mo] KO_Kap1_KO_2.fastq_unmapped.fastq.gz [87 Mo] KO_Kap1_KO_1.fastq_filter_bamstat (pickle file) [0 Ko] KO_Kap1_KO_2.fastq_filter_bamstat (pickle file) [0 Ko] KO_Kap1_KO_1.fastq_filtered.bam [625 Mo] KO_Kap1_KO_1.fastq_filtered.bam.bai (BAM index) [3 Mo] KO_Kap1_KO_2.fastq_filtered.bam [611 Mo] KO_Kap1_KO_2.fastq_filtered.bam.bai (BAM index) [3 Mo] Download files [1423 Mo unzipped] Load in UCSC	WT_unmapped.fastq.gz [86 Mo] WT_filter_bamstat (pickle file) [0 Ko] WT_filtered.bam [614 Mo] WT_filtered.bam.bai (BAM index) [3 Mo] Download files [704 Mo unzipped] Load in UCSC
· density Download files | Load in UCSC [2480 Mo unzipped]	KO_Kap1_KO_1.fastq.sql [0 Ko] KO_Kap1_KO_2.fastq.sql [0 Ko] KO_merged.bw [126 Mo] KO_Kap1_KO_1.fastq_merged.sql [504 Mo] KO_Kap1_KO_2.fastq_merged.sql [500 Mo] KO_merged.sql [801 Mo] Download files [1933 Mo unzipped] Load in UCSC	WT.sql [0 Ko] WT_merged.bw [71 Mo] WT_merged.sql [475 Mo] Download files [546 Mo unzipped] Load in UCSC
· stats Download files | Load in UCSC [39 Ko unzipped]	KO_mapping_report.pdf [26 Ko] Load in UCSC	WT_mapping_report.pdf [13 Ko] Load in UCSC

Global results:

· bowtie	file_names (pickle file) [0 Ko] Load in UCSC

BED file for UCSC | Load in UCSC

Links for visualization

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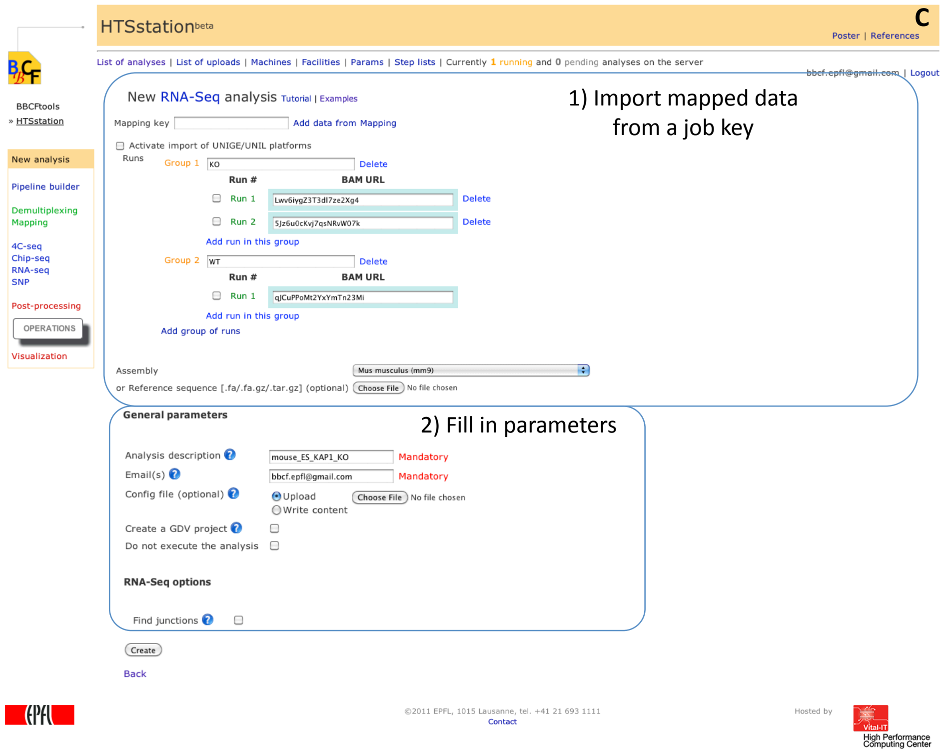

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New RNA-Seq analysis Tutorial | Examples

1) Import mapped data from a job key

Mapping key ____ Add data from Mapping

☐ Activate import of UNIGE/UNIL platforms

Runs

Group 1: KO — Delete

	Run #	BAM URL	
☐	Run 1	Lwv6iygZ3T3dl7ze2Xg4	Delete
☐	Run 2	5Jz6u0cKvj7qsNRvW07k	Delete

Add run in this group

Group 2: WT — Delete

	Run #	BAM URL
☐	Run 1	qJCuPPoMt2YxYmTn23Mi

Add run in this group

Add group of runs

Assembly: Mus musculus (mm9)

or Reference sequence [.fa/.fa.gz/.tar.gz] (optional) Choose File No file chosen

General parameters

2) Fill in parameters

Analysis description: mouse_ES_KAP1_KO — Mandatory

Email(s): bbcf.epfl@gmail.com — Mandatory

Config file (optional): ● Upload Choose File No file chosen / ○ Write content

Create a GDV project ☐

Do not execute the analysis ☐

RNA-Seq options

Find junctions ☐

Create

Back

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Contact

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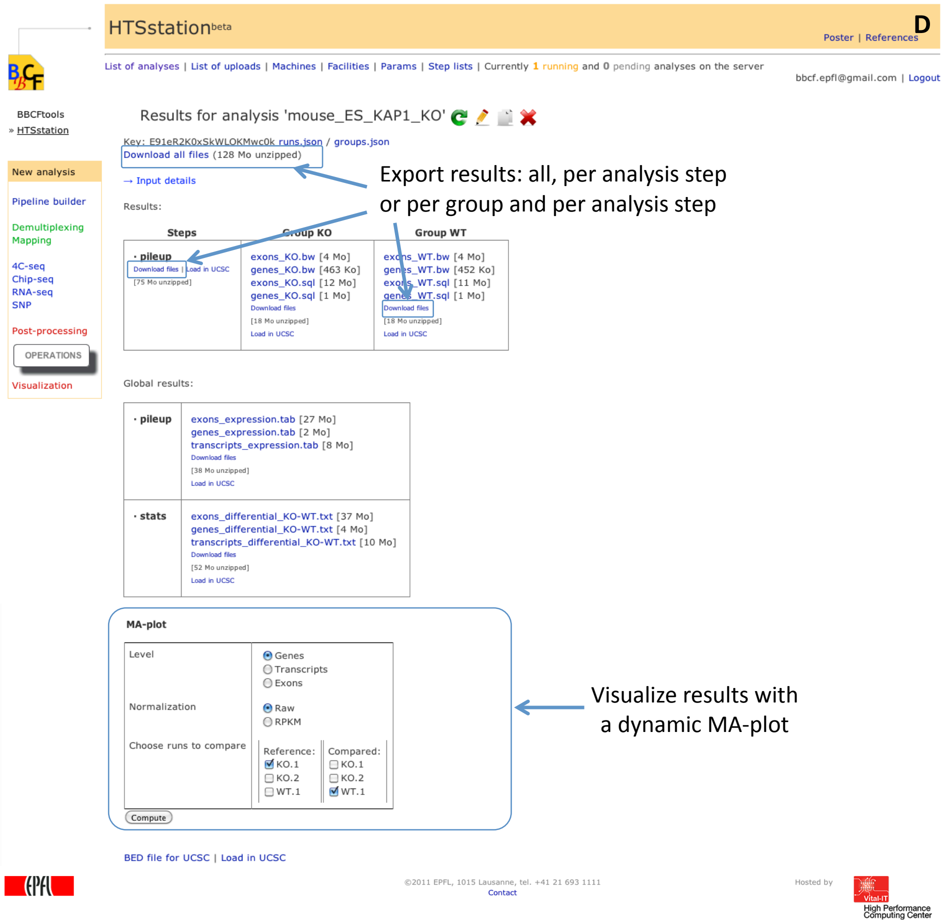

Currently 1 running and 0 pending analyses on the server

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Results for analysis 'mouse_ES_KAP1_KO'

Key: E91eR2K0xSkWLOKMwc0k runs.json / groups.json

Download all files (128 Mo unzipped)

→ Input details

Export results: all, per analysis step or per group and per analysis step

Results:

Steps	Group KO	Group WT
· pileup Download files | Load in UCSC [75 Mo unzipped]	exons_KO.bw [4 Mo] genes_KO.bw [463 Ko] exons_KO.sql [12 Mo] genes_KO.sql [1 Mo] Download files [18 Mo unzipped] Load in UCSC	exons_WT.bw [4 Mo] genes_WT.bw [452 Ko] exons_WT.sql [11 Mo] genes_WT.sql [1 Mo] Download files [18 Mo unzipped] Load in UCSC

Global results:

· pileup	exons_expression.tab [27 Mo] genes_expression.tab [2 Mo] transcripts_expression.tab [8 Mo] Download files [38 Mo unzipped] Load in UCSC
· stats	exons_differential_KO-WT.txt [37 Mo] genes_differential_KO-WT.txt [4 Mo] transcripts_differential_KO-WT.txt [10 Mo] Download files [52 Mo unzipped] Load in UCSC

MA-plot

Level	● Genes ○ Transcripts ○ Exons
Normalization	● Raw ○ RPKM
Choose runs to compare	Reference: ☑ KO.1 ☐ KO.2 ☐ WT.1 Compared: ☐ KO.1 ☐ KO.2 ☑ WT.1

Compute

Visualize results with a dynamic MA-plot

BED file for UCSC | Load in UCSC

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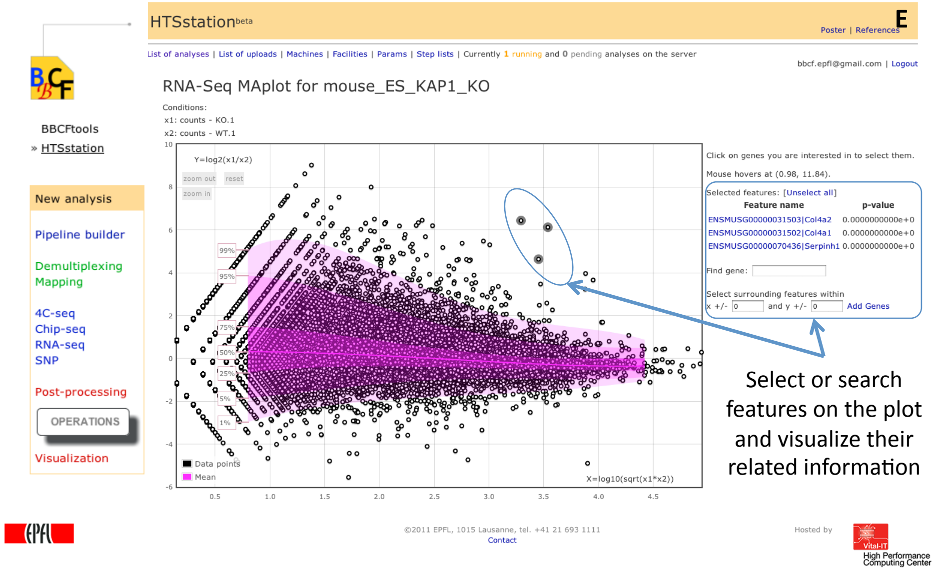

Currently 1 running and 0 pending analyses on the server

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RNA-Seq MAplot for mouse_ES_KAP1_KO

Conditions:
x1: counts - KO.1
x2: counts - WT.1

Click on genes you are interested in to select them.

Mouse hovers at (0.98, 11.84).

Selected features: [Unselect all]

Feature name	p-value
ENSMUSG00000031503|Col4a2	0.0000000000e+0
ENSMUSG00000031502|Col4a1	0.0000000000e+0
ENSMUSG00000070436|Serpinh1	0.0000000000e+0

Find gene:

Select surrounding features within
x +/- 0 and y +/- 0 Add Genes

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Select or search features on the plot and visualize their related information