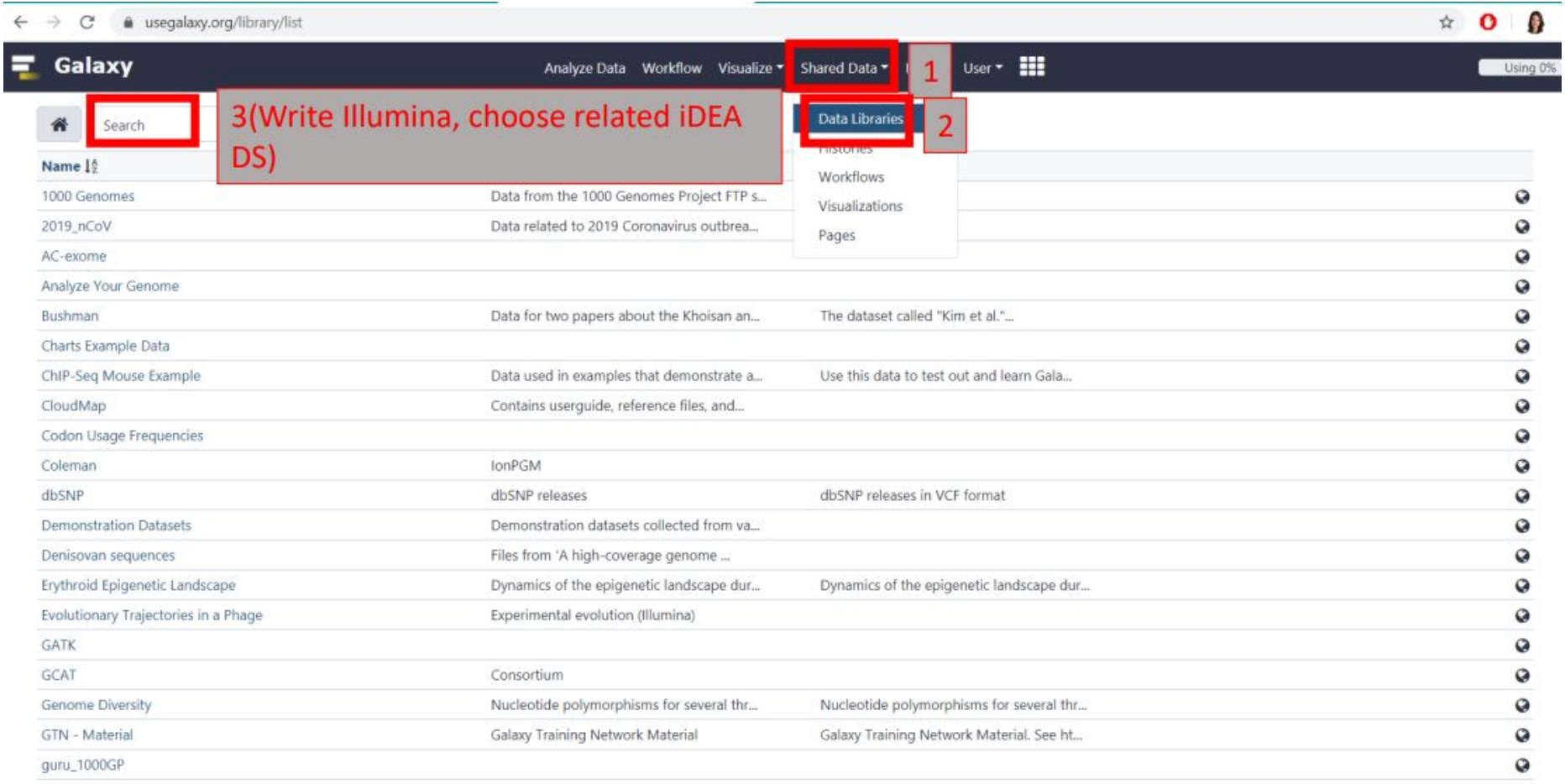
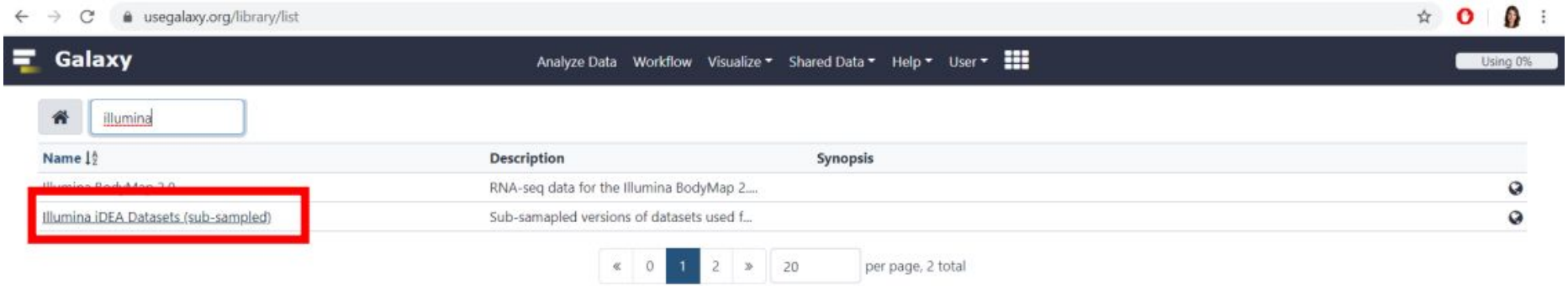
Getting the data


usegalaxy.org/library/list
Galaxy
Analyze Data
Workflow
Visualize
Shared Data
1
User
Using 0%
Search
3(Write Illumina, choose related iDEA DS)
Data Libraries
2
Histories
Workflows
Visualizations
Pages
Name
1000 Genomes
Data from the 1000 Genomes Project FTP s...
2019_nCoV
Data related to 2019 Coronavirus outbrea...
AC-exome
Analyze Your Genome
Bushman
Data for two papers about the Khoisan an...
The dataset called "Kim et al."...
Charts Example Data
ChIP-Seq Mouse Example
Data used in examples that demonstrate a...
Use this data to test out and learn Gala...
CloudMap
Contains userguide, reference files, and...
Codon Usage Frequencies
Coleman
IonPGM
dbSNP
dbSNP releases
dbSNP releases in VCF format
Demonstration Datasets
Demonstration datasets collected from va...
Denisovan sequences
Files from 'A high-coverage genome ...
Erythroid Epigenetic Landscape
Dynamics of the epigenetic landscape dur...
Dynamics of the epigenetic landscape dur...
Evolutionary Trajectories in a Phage
Experimental evolution (Illumina)
GATK
GCAT
Consortium
Genome Diversity
Nucleotide polymorphisms for several thr...
Nucleotide polymorphisms for several thr...
GTN - Material
Galaxy Training Network Material
Galaxy Training Network Material. See ht...
guru_1000GP


usegalaxy.org/library/list
Galaxy
Analyze Data
Workflow
Visualize
Shared Data
Help
User
Using 0%
illumina
Name
Description
Synopsis
RNA-seq data for the Illumina BodyMap 2....
Illumina iDEA Datasets (sub-sampled)
Sub-samapled versions of datasets used f...
«
0
1
2
»
20
per page, 2 total

usegalaxy.org/library/list#folders/F77ce11b6d3c0d73a

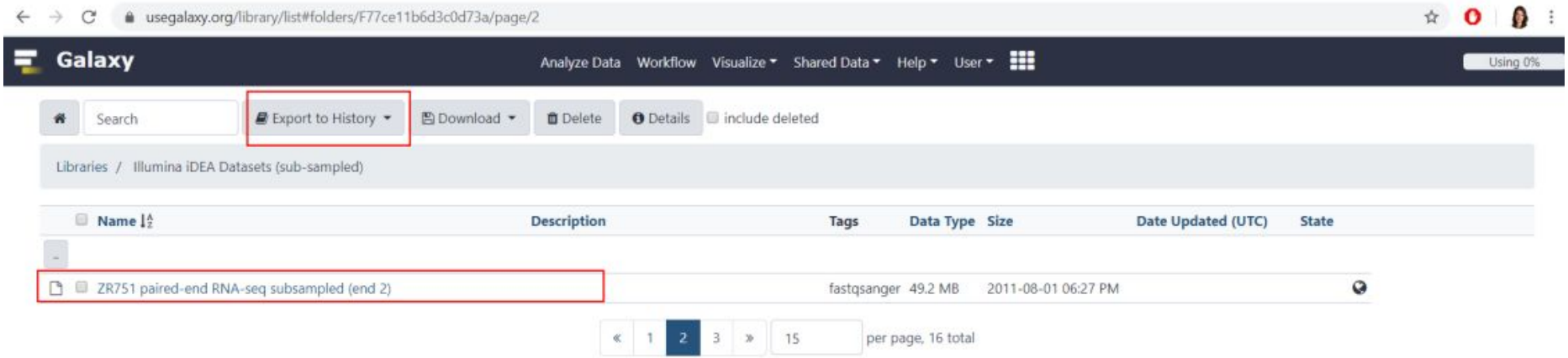
Galaxy | Analyze Data | Workflow | Visualize | Shared Data | Help | User | Using 0%

Search | Export to History | Download | Delete | Details | include deleted

Libraries / Illumina iDEA Datasets (sub-sampled)

Name	Description	Tags	Data Type	Size	Date Updated (UTC)	State
BT20 paired-end RNA-seq subsampled (end 1)			fastqsanger	60.8 MB	2011-08-01 06:26 PM	
BT20 paired-end RNA-seq subsampled (end 2)			fastqsanger	60.8 MB	2011-08-01 06:26 PM	
BT474 paired-end RNA-seq subsampled (end 1)			fastqsanger	58.5 MB	2011-08-01 06:26 PM	
BT474 paired-end RNA-seq subsampled (end 2)			fastqsanger	58.5 MB	2011-08-01 06:26 PM	
MB231 paired-end RNA-seq subsampled (end 1)			fastqsanger	57.7 MB	2011-08-01 06:26 PM	
MB231 paired-end RNA-seq subsampled (end 2)			fastqsanger	57.7 MB	2011-08-01 06:26 PM	
MB468 paired-end RNA-seq subsampled (end 1)			fastqsanger	30.9 MB	2011-08-01 06:26 PM	
MB468 paired-end RNA-seq subsampled (end 2)			fastqsanger	30.9 MB	2011-08-01 06:27 PM	
MCF10 paired-end RNA-seq subsampled (end 1)			fastqsanger	53.2 MB	2011-08-01 06:27 PM	
MCF10 paired-end RNA-seq subsampled (end 2)			fastqsanger	53.2 MB	2011-08-01 06:27 PM	
MCF7 paired-end RNA-seq subsampled (end 1)			fastqsanger	24.3 MB	2011-08-01 06:27 PM	
MCF7 paired-end RNA-seq subsampled (end 2)			fastqsanger	24.3 MB	2011-08-01 06:27 PM	
T47D paired-end RNA-seq subsampled (end 1)			fastqsanger	60.4 MB	2011-08-01 06:27 PM	
T47D paired-end RNA-seq subsampled (end 2)			fastqsanger	60.4 MB	2011-08-01 06:27 PM	
ZR751 paired-end RNA-seq subsampled (end 1)			fastqsanger	49.2 MB	2011-08-01 06:27 PM	

« 0 1 2 » 15 per page, 16 total


usegalaxy.org/library/list#folders/F77ce11b6d3c0d73a/page/2
Galaxy
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Workflow
Visualize
Shared Data
Help
User
Using 0%
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Download
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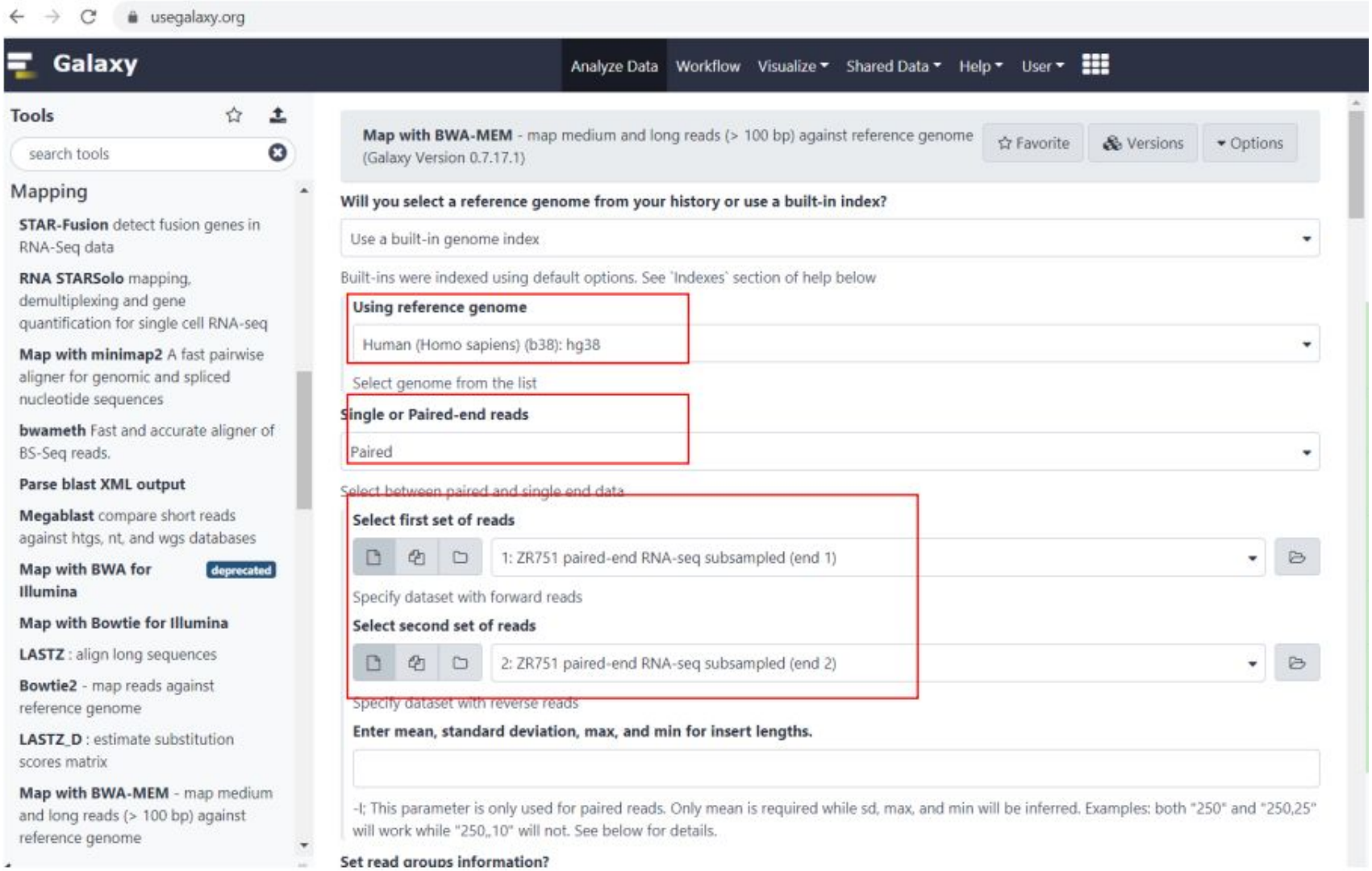
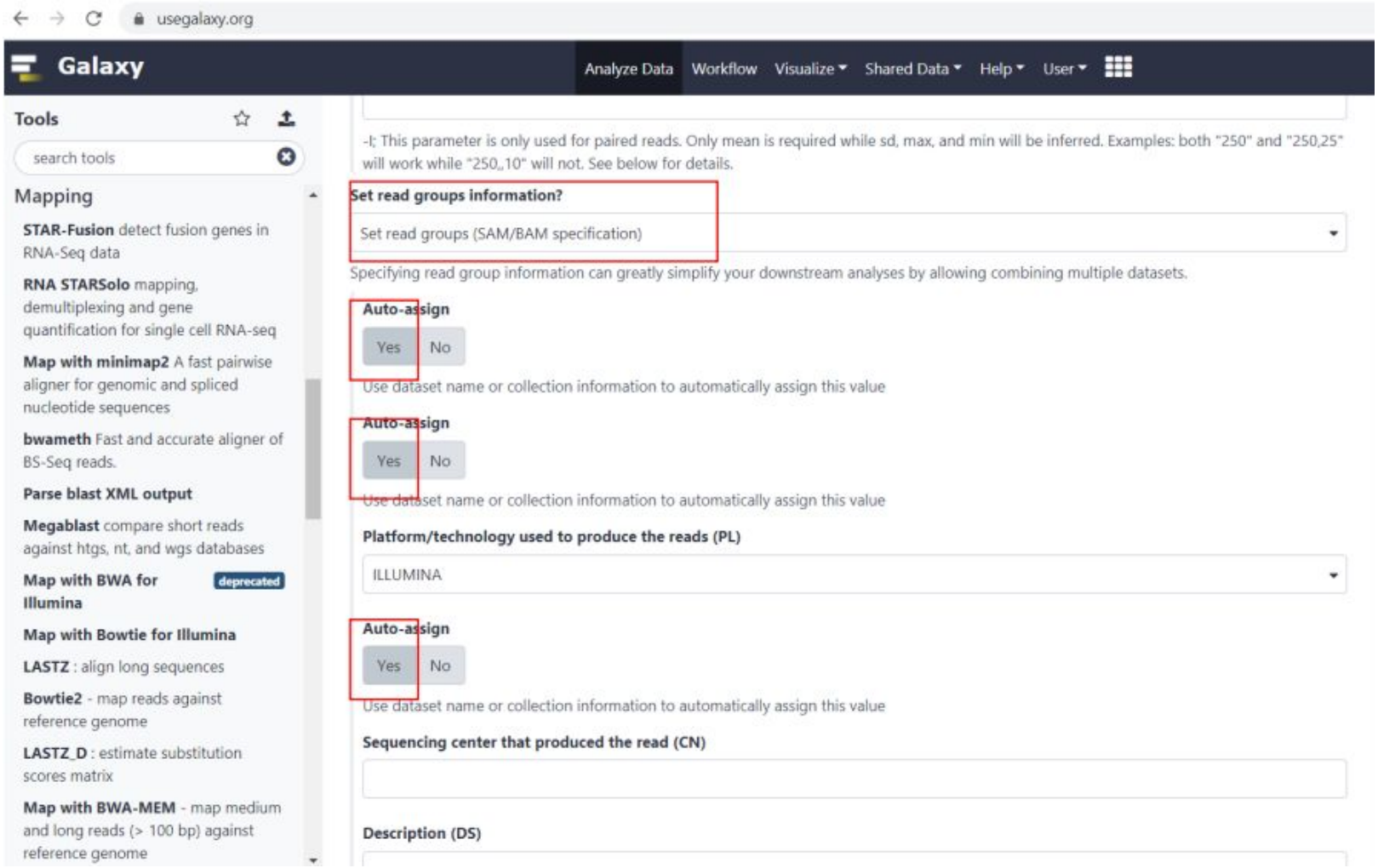
Details
include deleted
Libraries / Illumina iDEA Datasets (sub-sampled)
Name
Description
Tags
Data Type
Size
Date Updated (UTC)
State
ZR751 paired-end RNA-seq subsampled (end 2)
fastqsanger
49.2 MB
2011-08-01 06:27 PM
1
2
3
15
per page, 16 total

Map with BWA-MEM parameters


usegalaxy.org
Galaxy
Analyze Data
Workflow
Visualize
Shared Data
Help
User
Tools
search tools
Mapping
STAR-Fusion detect fusion genes in RNA-Seq data
RNA STARSolo mapping, demultiplexing and gene quantification for single cell RNA-seq
Map with minimap2 A fast pairwise aligner for genomic and spliced nucleotide sequences
bwameth Fast and accurate aligner of BS-Seq reads.
Parse blast XML output
Megablast compare short reads against htgs, nt, and wgs databases
Map with BWA for Illumina
deprecated
Map with Bowtie for Illumina
LASTZ : align long sequences
Bowtie2 - map reads against reference genome
LASTZ_D : estimate substitution scores matrix
Map with BWA-MEM - map medium and long reads (> 100 bp) against reference genome
Map with BWA-MEM - map medium and long reads (> 100 bp) against reference genome (Galaxy Version 0.7.17.1)
Favorite
Versions
Options
Will you select a reference genome from your history or use a built-in index?
Use a built-in genome index
Built-ins were indexed using default options. See `Indexes` section of help below
Using reference genome
Human (Homo sapiens) (b38): hg38
Select genome from the list
Single or Paired-end reads
Paired
Select between paired and single end data
Select first set of reads
1: ZR751 paired-end RNA-seq subsampled (end 1)
Specify dataset with forward reads
Select second set of reads
2: ZR751 paired-end RNA-seq subsampled (end 2)
Specify dataset with reverse reads
Enter mean, standard deviation, max, and min for insert lengths.
-I; This parameter is only used for paired reads. Only mean is required while sd, max, and min will be inferred. Examples: both "250" and "250,25" will work while "250,,10" will not. See below for details.
Set read groups information?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Help
User
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Mapping
STAR-Fusion detect fusion genes in RNA-Seq data
RNA STARSolo mapping, demultiplexing and gene quantification for single cell RNA-seq
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LASTZ_D : estimate substitution scores matrix
Map with BWA-MEM - map medium and long reads (> 100 bp) against reference genome
-l; This parameter is only used for paired reads. Only mean is required while sd, max, and min will be inferred. Examples: both "250" and "250,25" will work while "250,,10" will not. See below for details.
Set read groups information?
Set read groups (SAM/BAM specification)
Specifying read group information can greatly simplify your downstream analyses by allowing combining multiple datasets.
Auto-assign
Yes
No
Use dataset name or collection information to automatically assign this value
Auto-assign
Yes
No
Use dataset name or collection information to automatically assign this value
Platform/technology used to produce the reads (PL)
ILLUMINA
Auto-assign
Yes
No
Use dataset name or collection information to automatically assign this value
Sequencing center that produced the read (CN)
Description (DS)