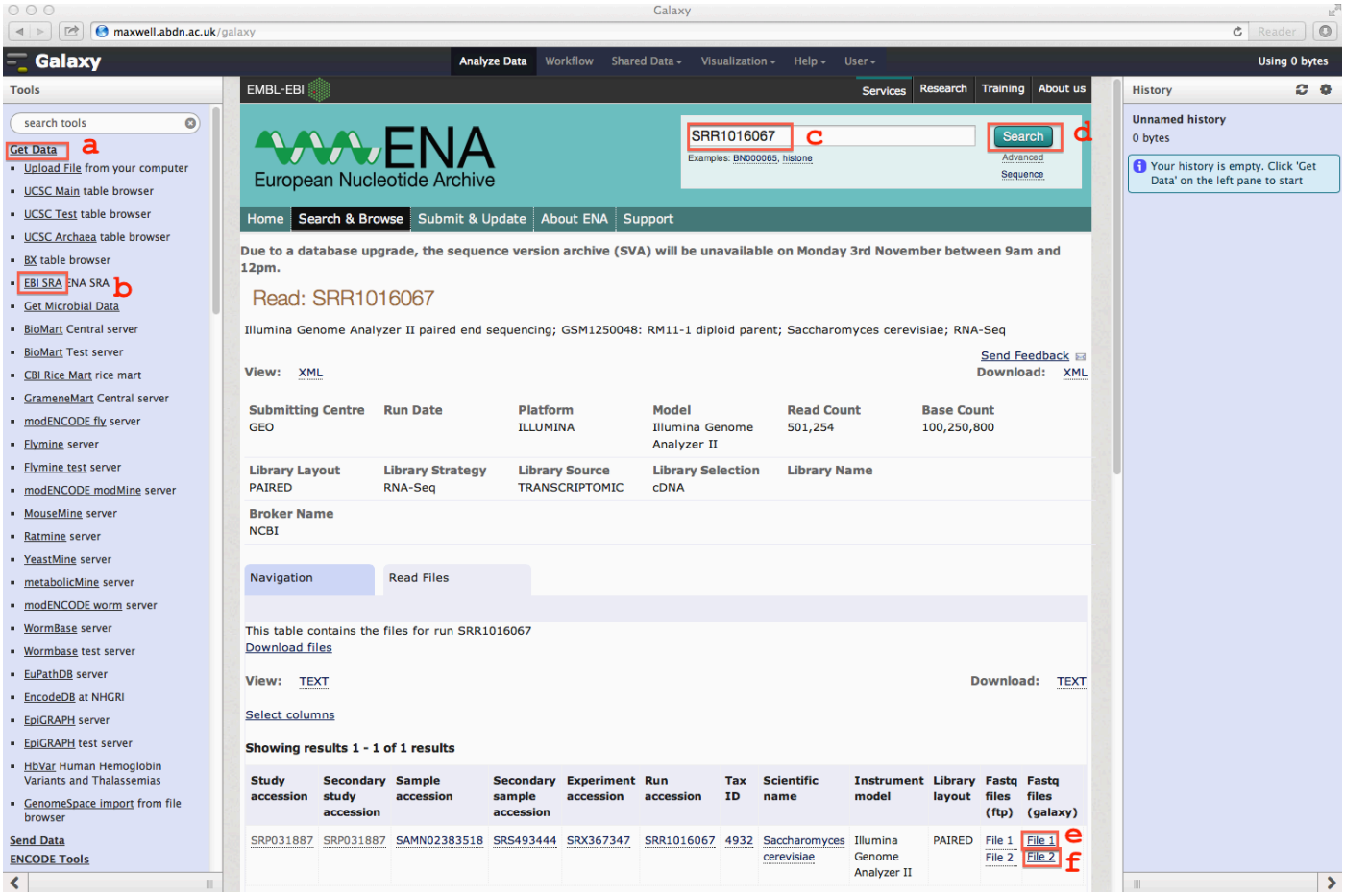
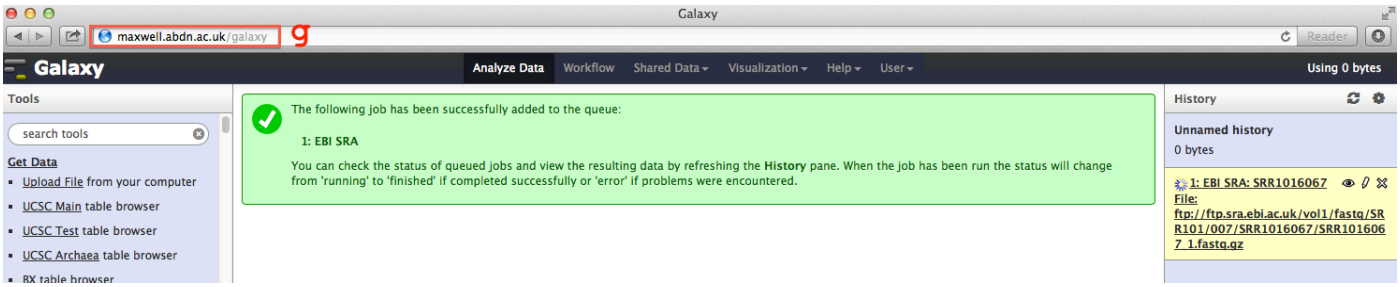
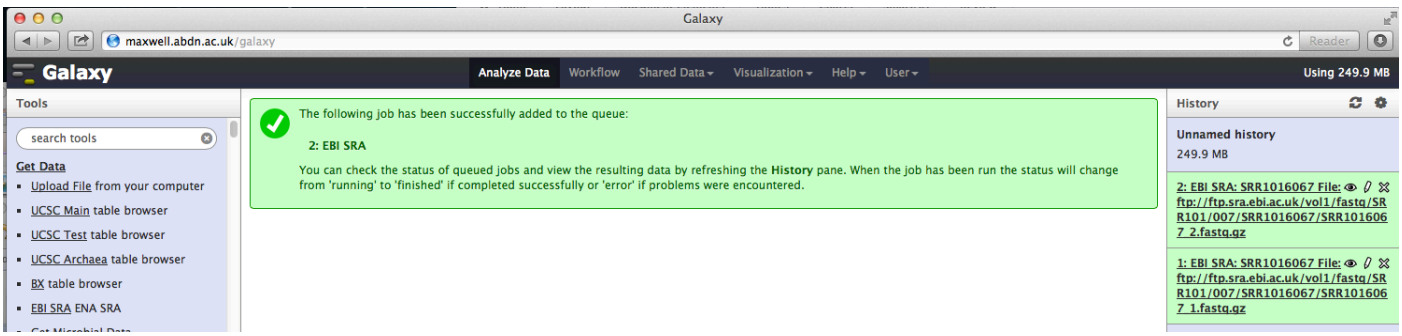
Exercise Instructions for Galaxy Tutorial

1. Get data from EBI SRA exercise
   a. Click on Get data on the left side panel
   b. Click on EBI SRA
   c. Enter SRR1016067 on the search box and
   d. Click search
   e. Click on Fastq files (galaxy)  File1
   f. repeat steps a-d and select c click on Fastq files (galaxy)  File2

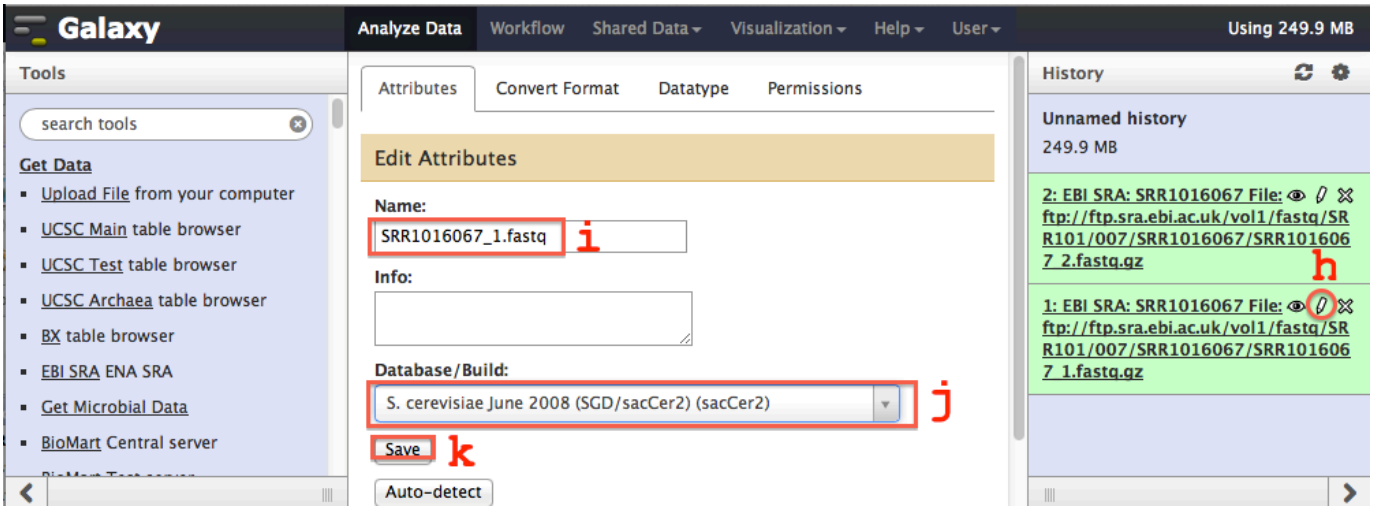



g. check if you were redirected back to maxwell.abdn.ac.uk/galaxy and not usegalaxy.org, or try again

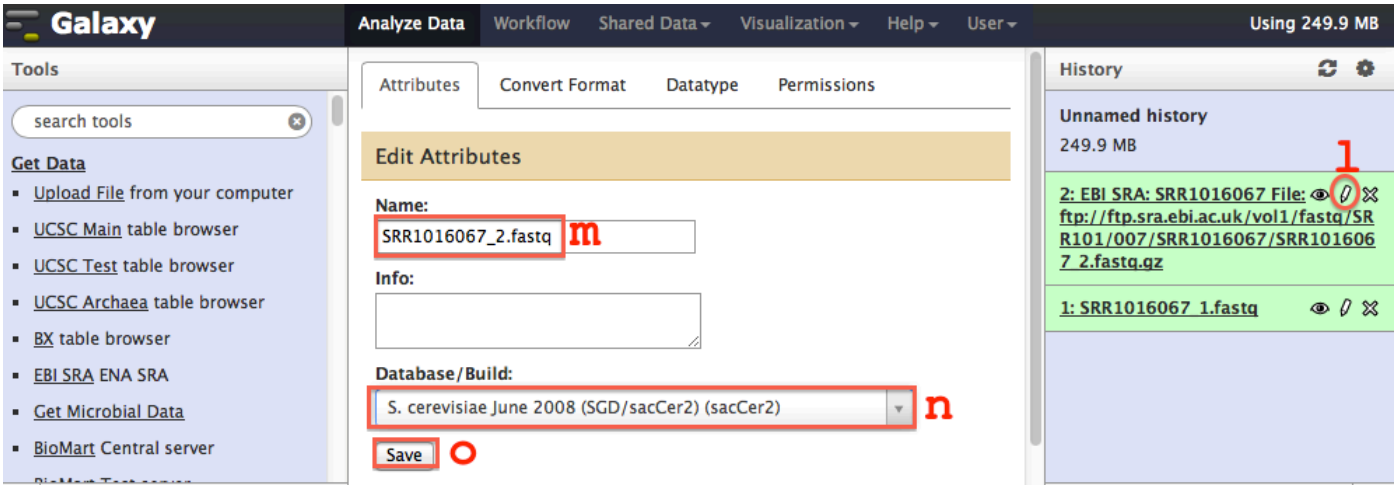


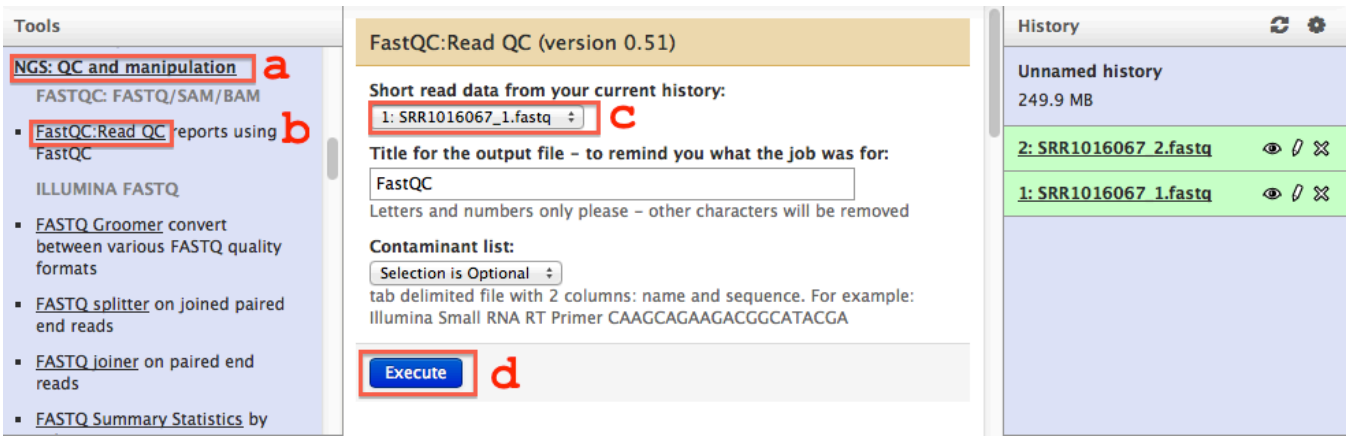
h. click on the pencil icon for result 1 in history
i. change the name to SRR1016067_1.fastq (or any name without gz extension)
j. select “SacCer2” in  the Database/Build” dropdown and save
k. click Save



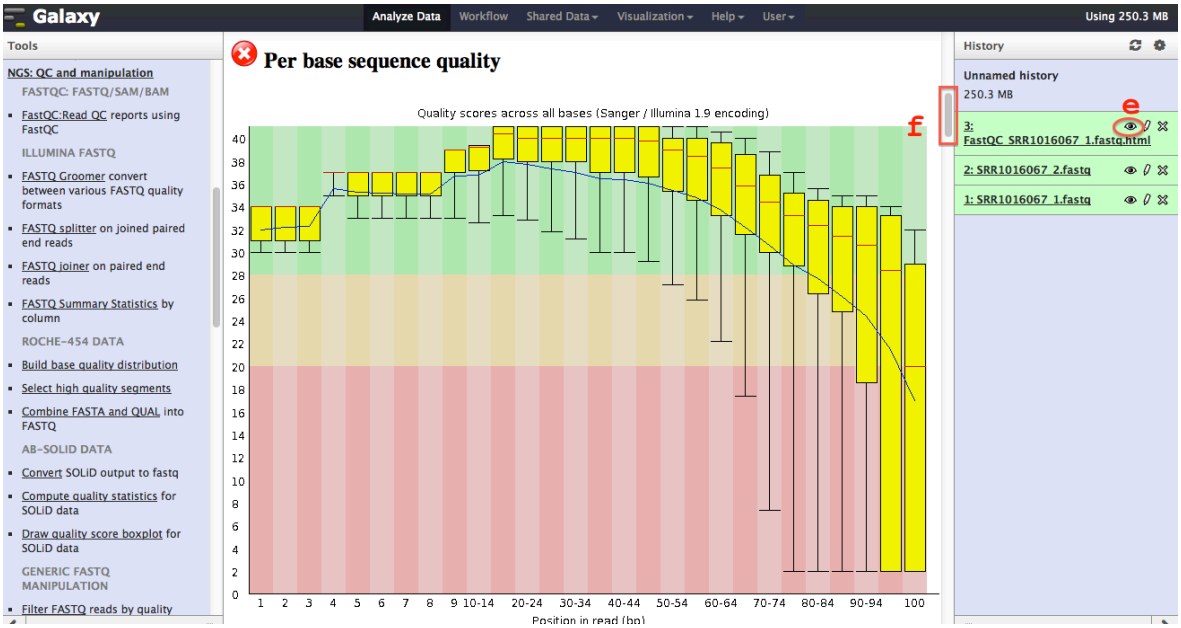

l. click on the pencil icon for result 2 in history
m. change the name to SRR1016067_2.fastq (or any name without gz extension)
n. select “SacCer2” in  the Database/Build” dropdown and save
o. click Save



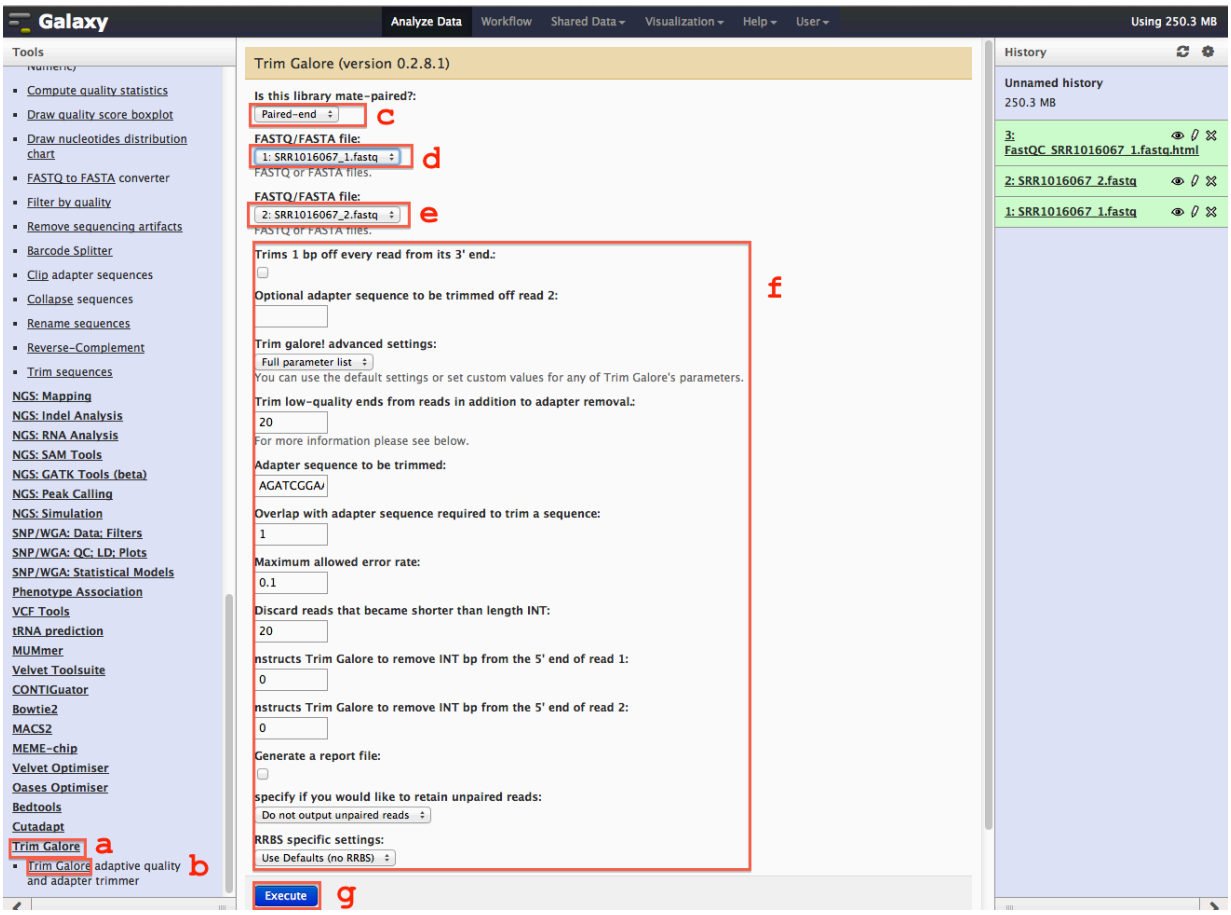

2. QA using FastQC exercise
a. click on NGS:QC and manipulation
b. click on FASTQC : Reads QC
c: Select result 1
d. Click execute



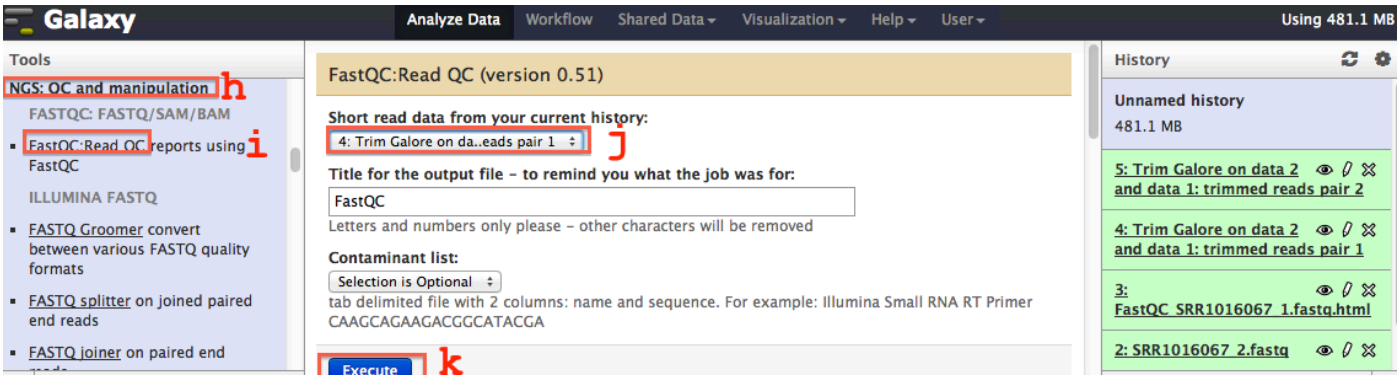
e. click on the eye icon to visualize the results
f. scroll down to per base sequence



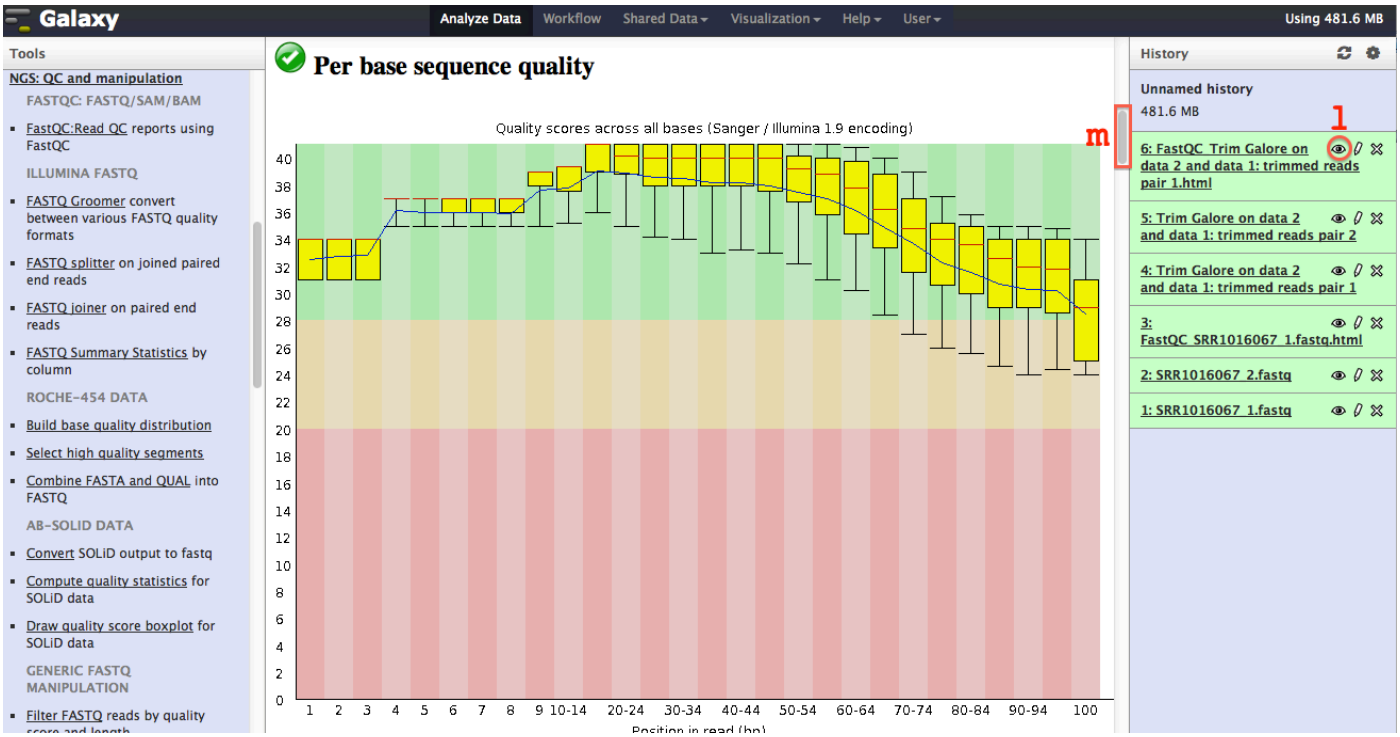

3. Filtering using trimgalore! exercise
a. click on Trim Galore in the tools panel
b click on trimgalore sub menu
c. select paired-end
d. select result 1
e. select result 2
f. check that all parameters are adequate
g. click on execute



h. click on NGS: Qc and manipulation
i. click on FASTQC : Reads QC
j: Select result 4
k. Click execute

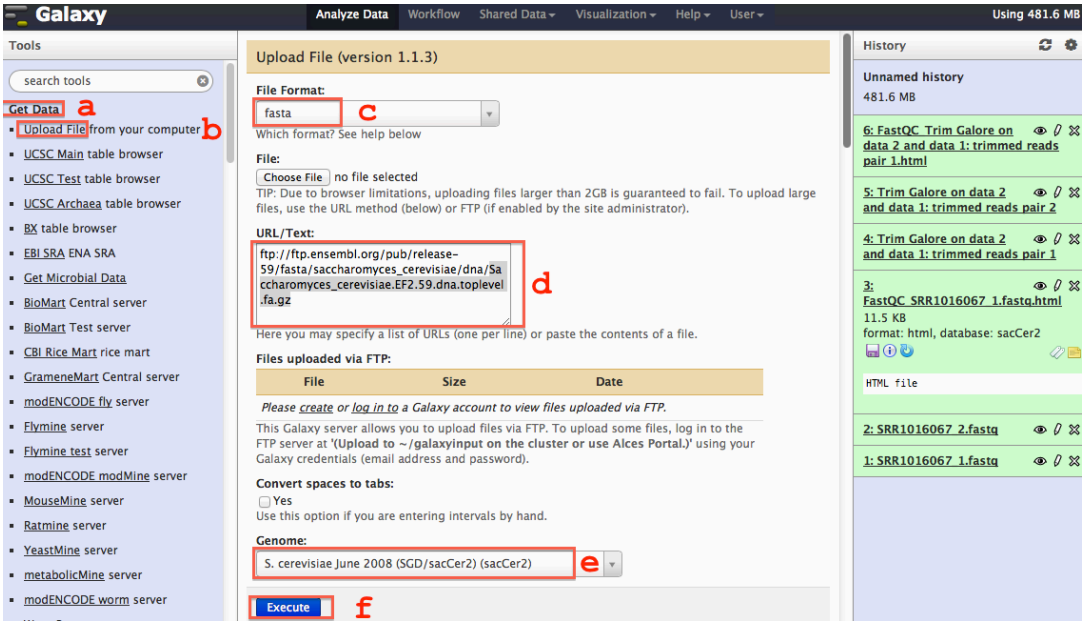



l. click on the eye icon to visualize the results
m. scroll down to per base sequence



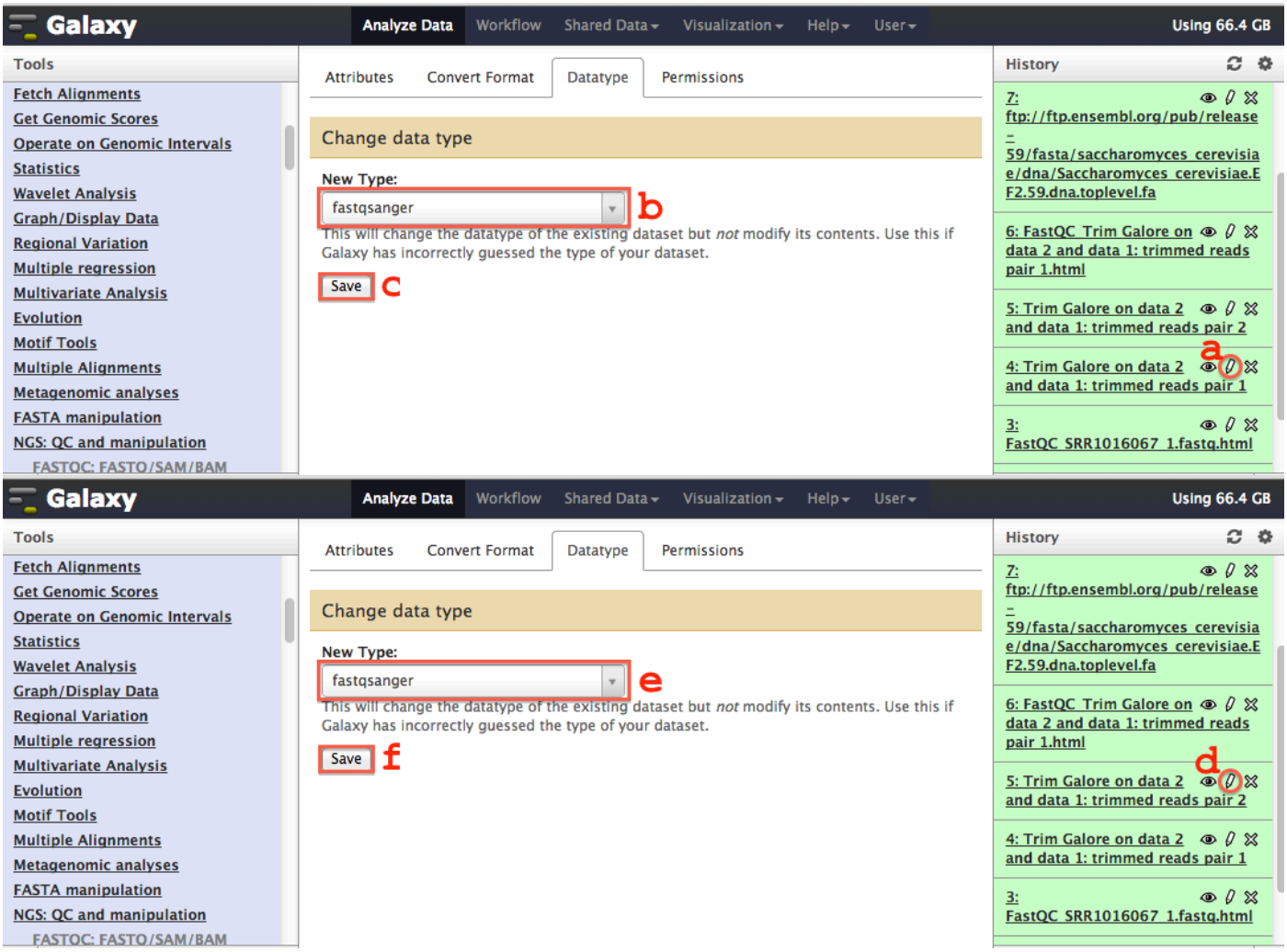
4a. Upload data using ftp exercise

a. click on Get Data
b. click on Upload file
c. select File Format fasta
d. paste into URL/File ftp://ftp.ensembl.org/pub/release-59/fasta/saccharomyces_cerevisiae/dna/Saccharomyces_cerevisiae.EF2.59.dna.toplevel.fa.gz
e. select Genome SacCer2
f. click Execute



4b. Modify datatype

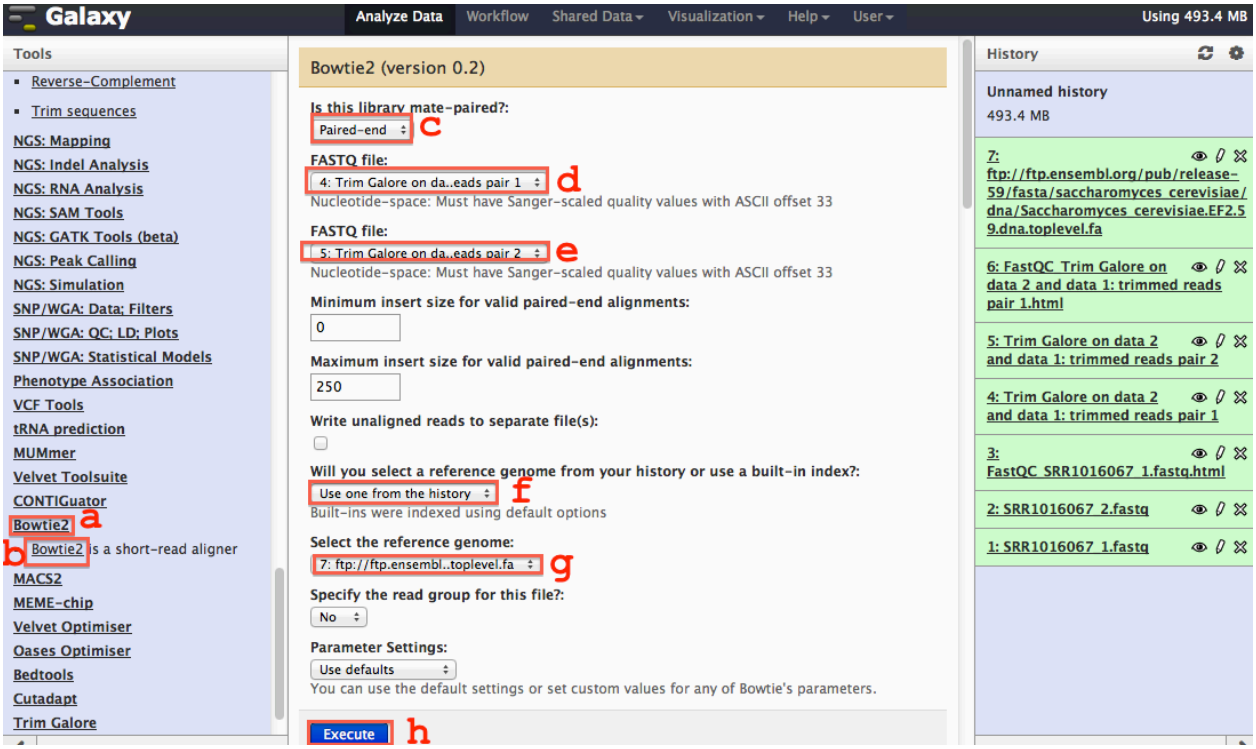
a. click on the pencil icon for Trim Galore trimmed reads pair 1
b. select New Type: fastqsanger
c. Click Save
d. click on the pencil icon for Trim Galore trimmed reads pair 2
e. select New Type: fastqsanger
f. Click Save




4c. Bowtie alignment

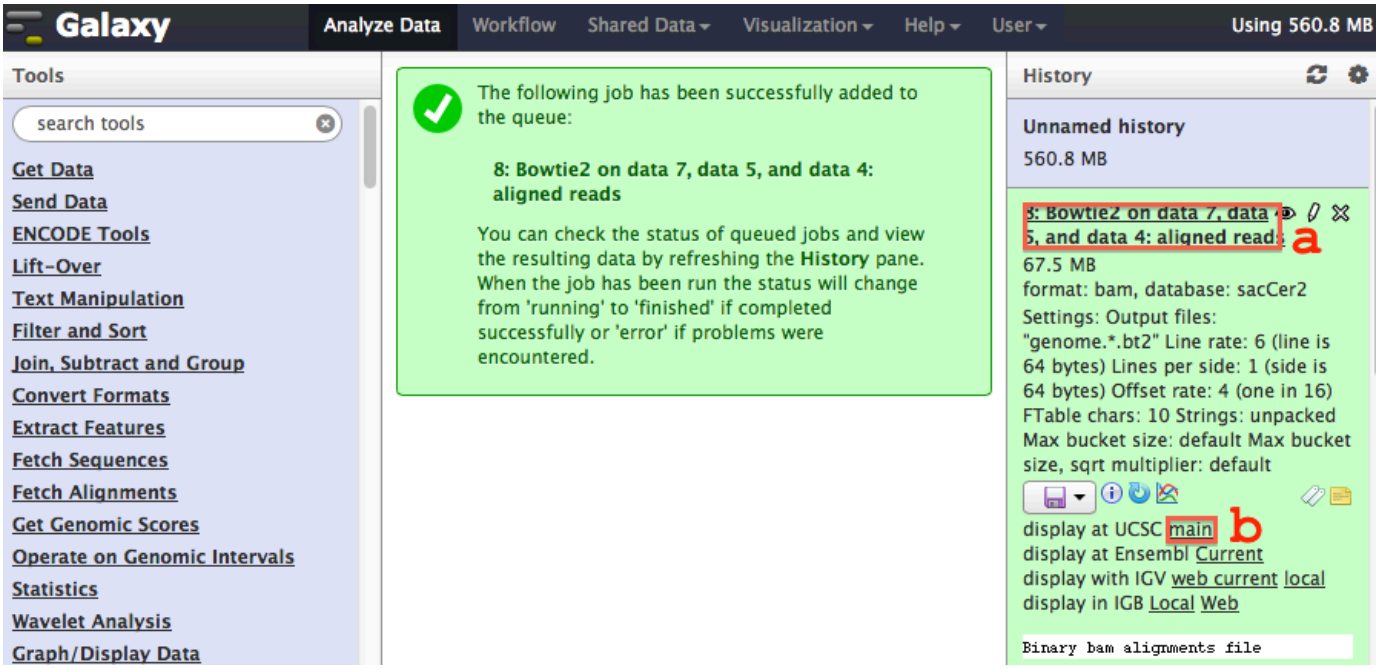
a. Click on Bowtie2 category
b. Click on Bowtie2
c. Select paired-end
d. Select Trim Galore trimmed reads pair 1
e. Select Trim Galore trimmed reads pair 2
f. Select “use one form history”
g. Select result 7 (ftp://ftp.ensembl.org/pub/release-59/fasta/saccharomyces_cerevisiae/dna/Saccharomyces_cerevisiae.EF2.59.dna.toplevel.fa)

h. Click Execute

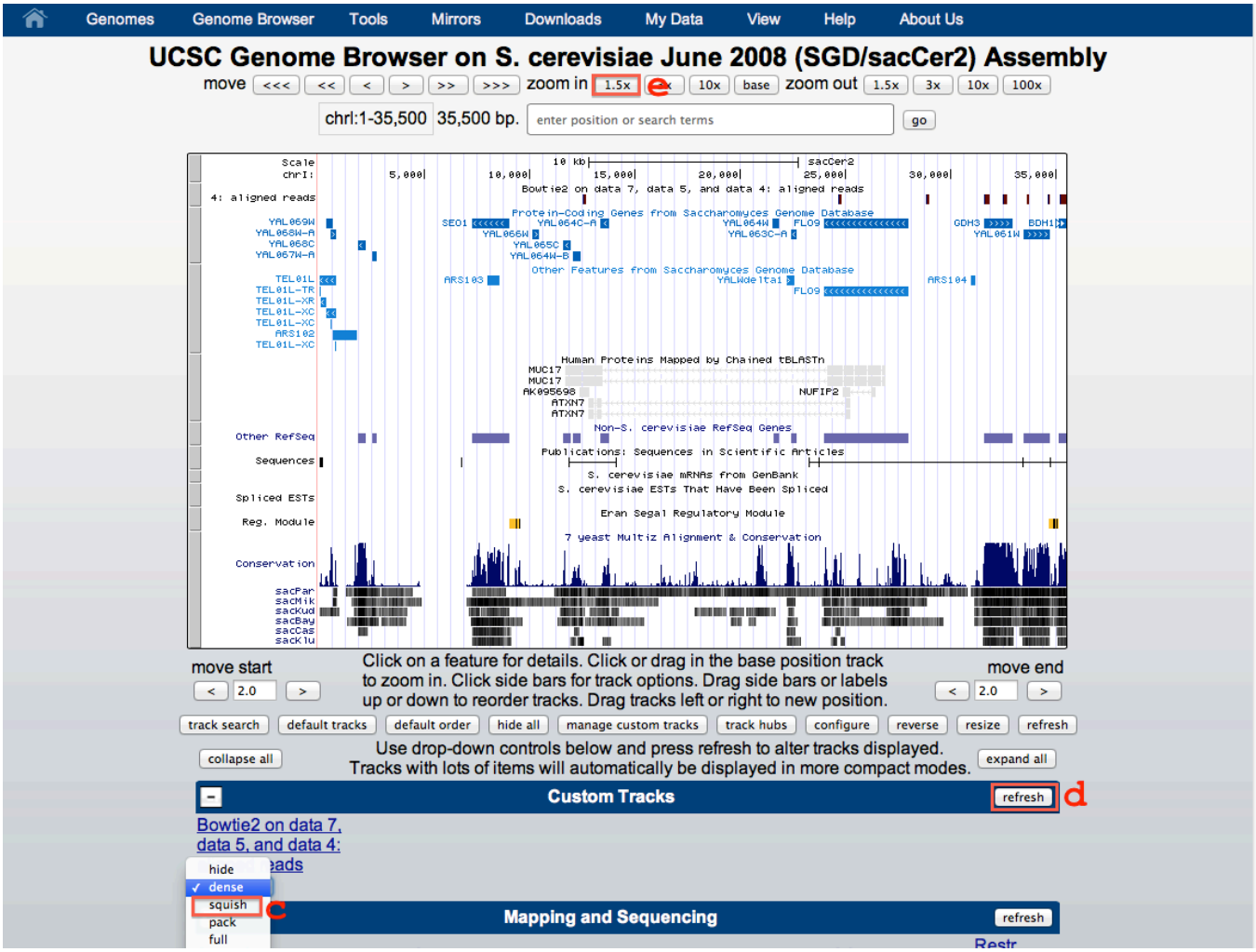



4d. Visualizing results in UCSC

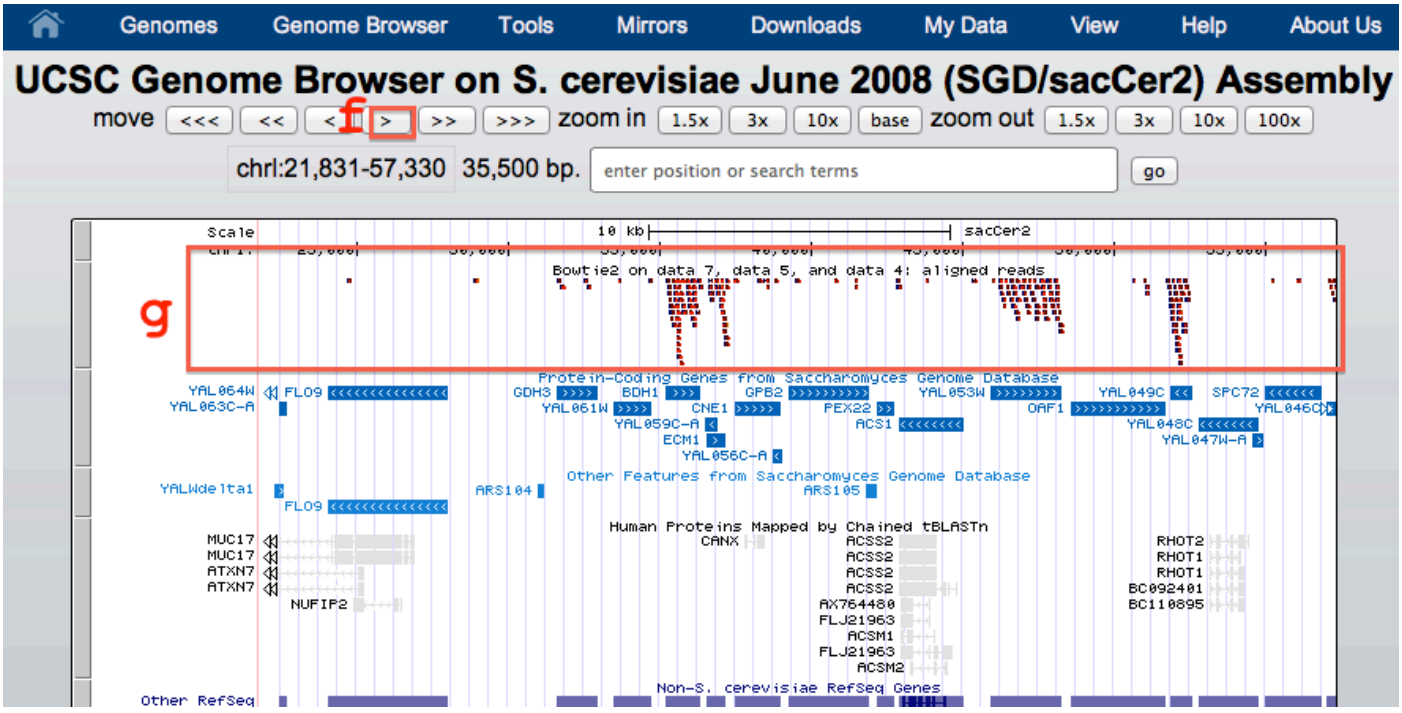
a. Click on result 8 link (on the underlined result name “Bowtie 2 on data…”)
b. Click on display at UCSC Main




c. Select “squished”
d. Click “refresh”
e. Click Zoom 1.5x

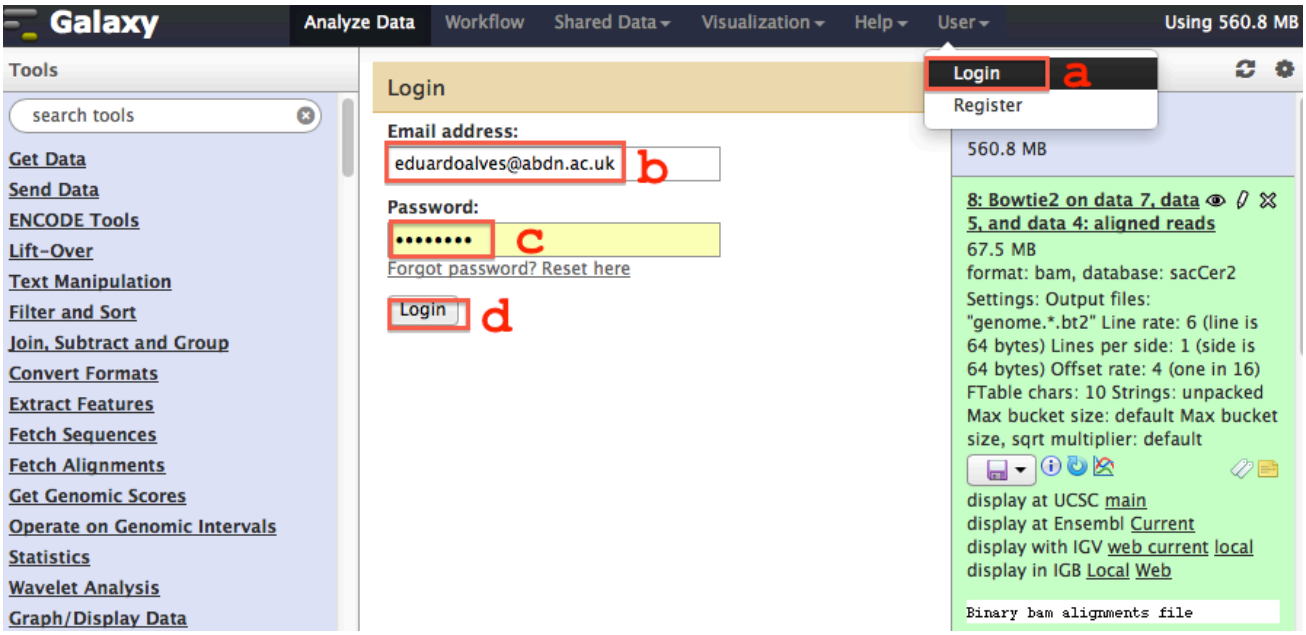



f. use the buttons to navigate
g. or right click on the browser to navigate

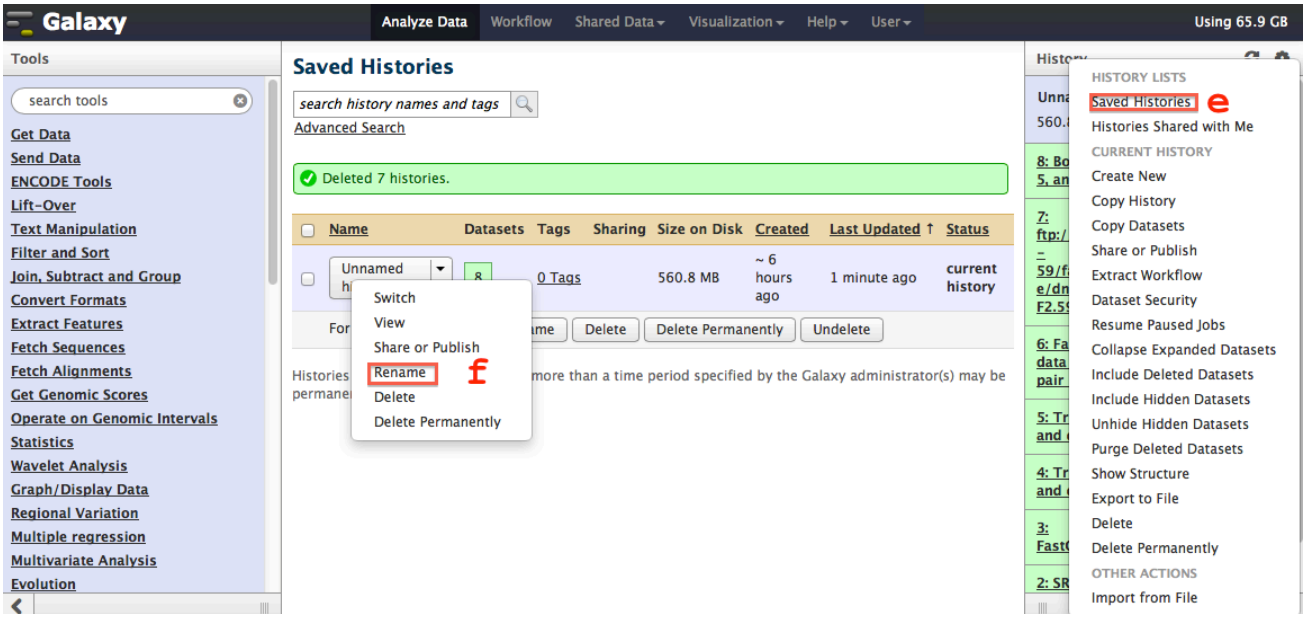


5a. Sharing history and creating workflow exercises (requires Galaxy Account)

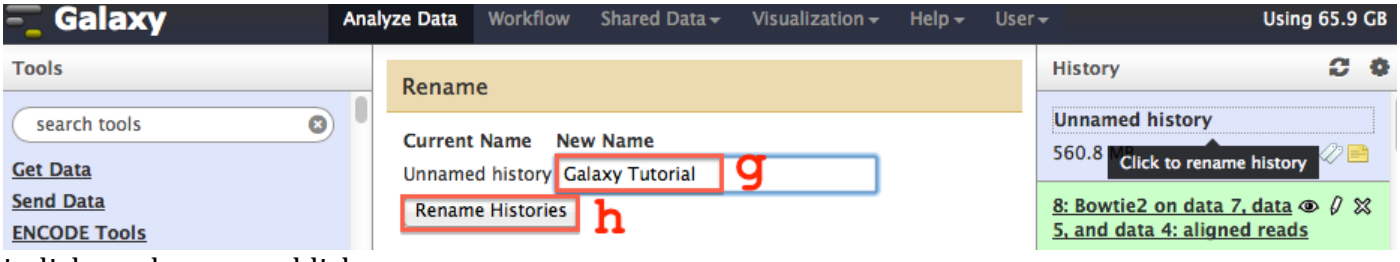
a. click on User -> Login
b. Enter your meail address
c. enter your password
d. Click “Login”




e. Click on saved histories
f. Click on rename

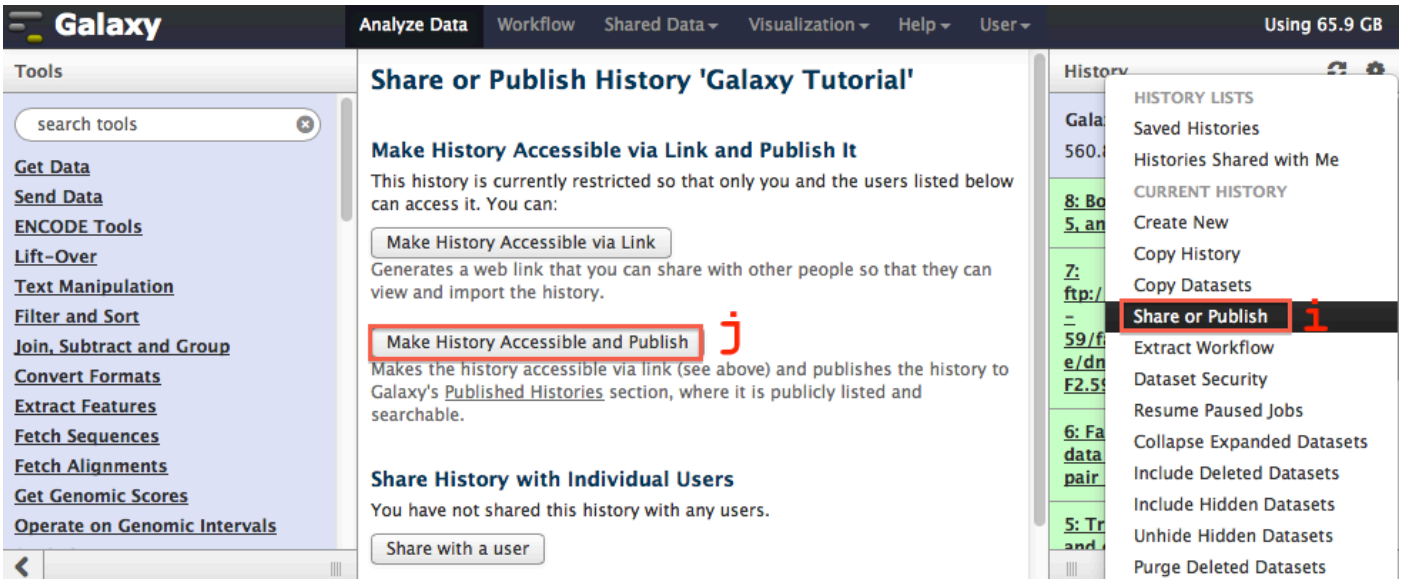



g. Enter a name for the History
h. Click rename history



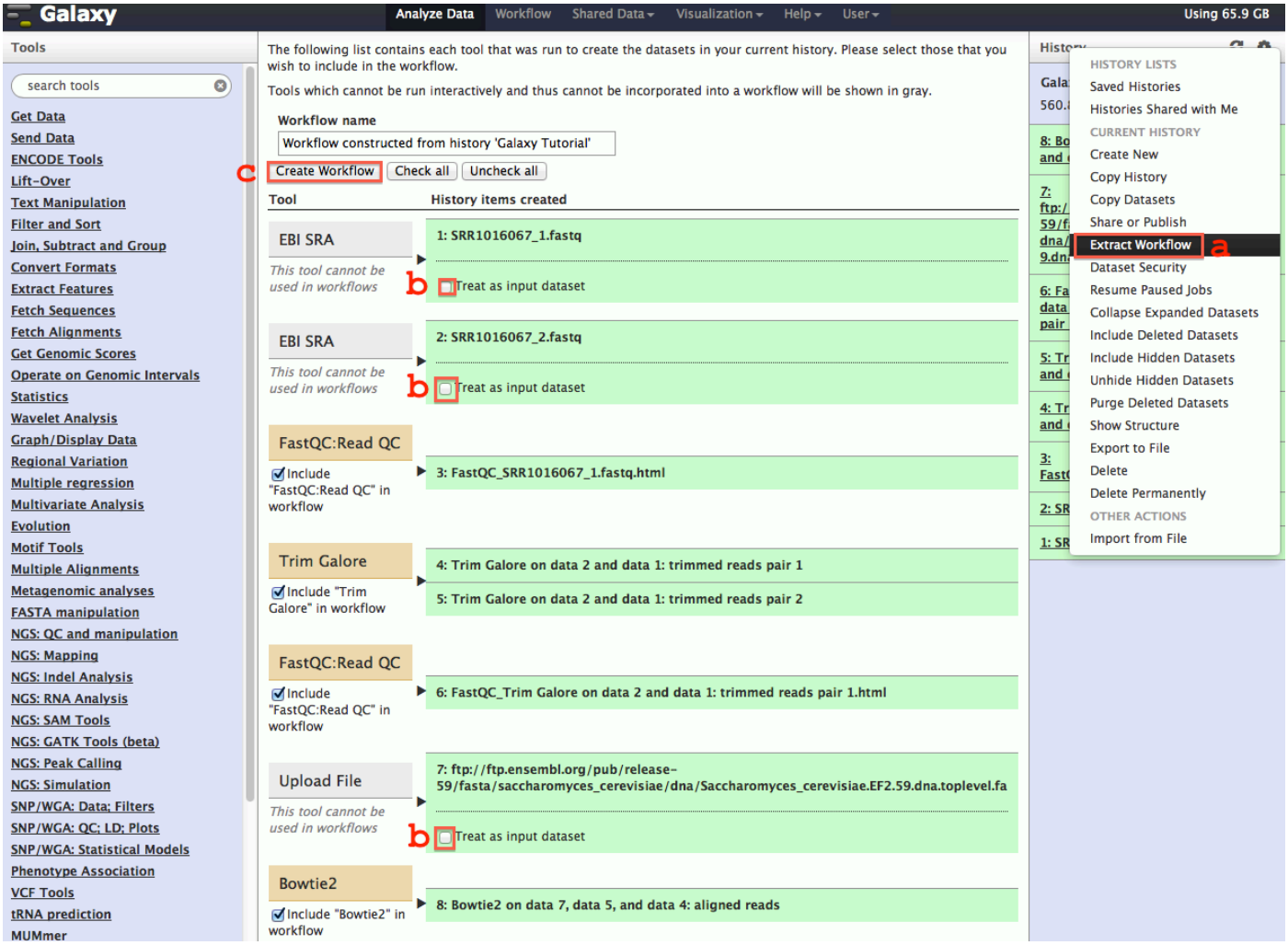

i. click on share or publish

j. click Make accessible and publish



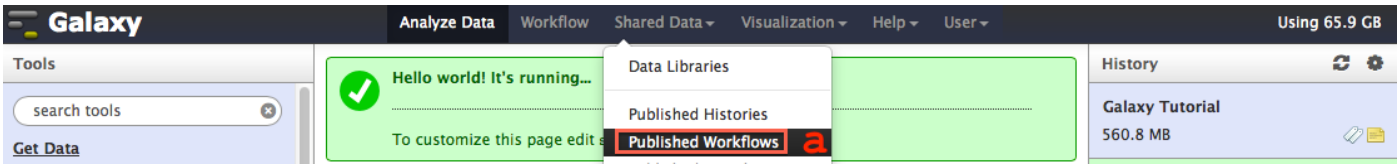

5b. Create workflow exercise (requires Galaxy Account)

a. Select Extract Workflow
b. Uncheck "treat as input dataset" 3x
c. Click on "Create Workflow"

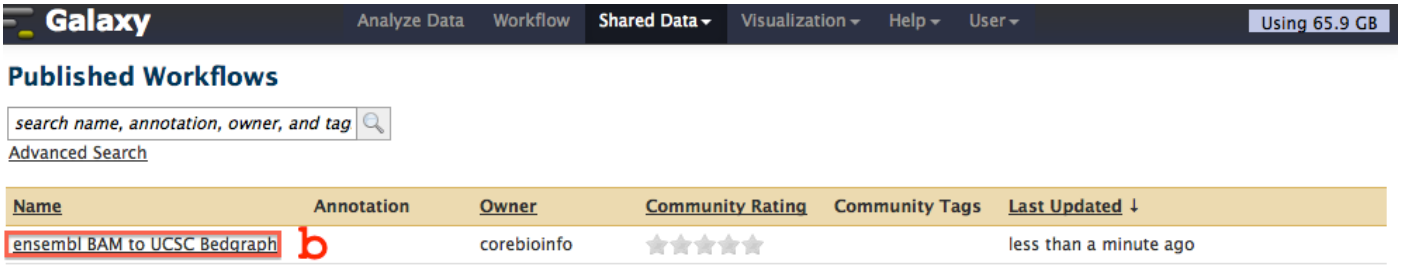


6. Converting BAM to UCSC bedGraph using a public workflow

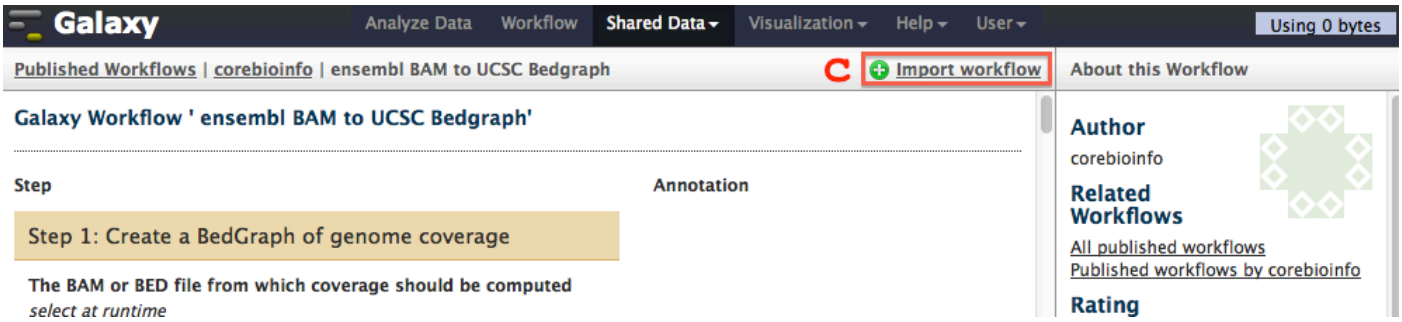
a. click on Shared Data -> Published Workflows




b. Click on Ensembl BAM to UCSC bedGraph



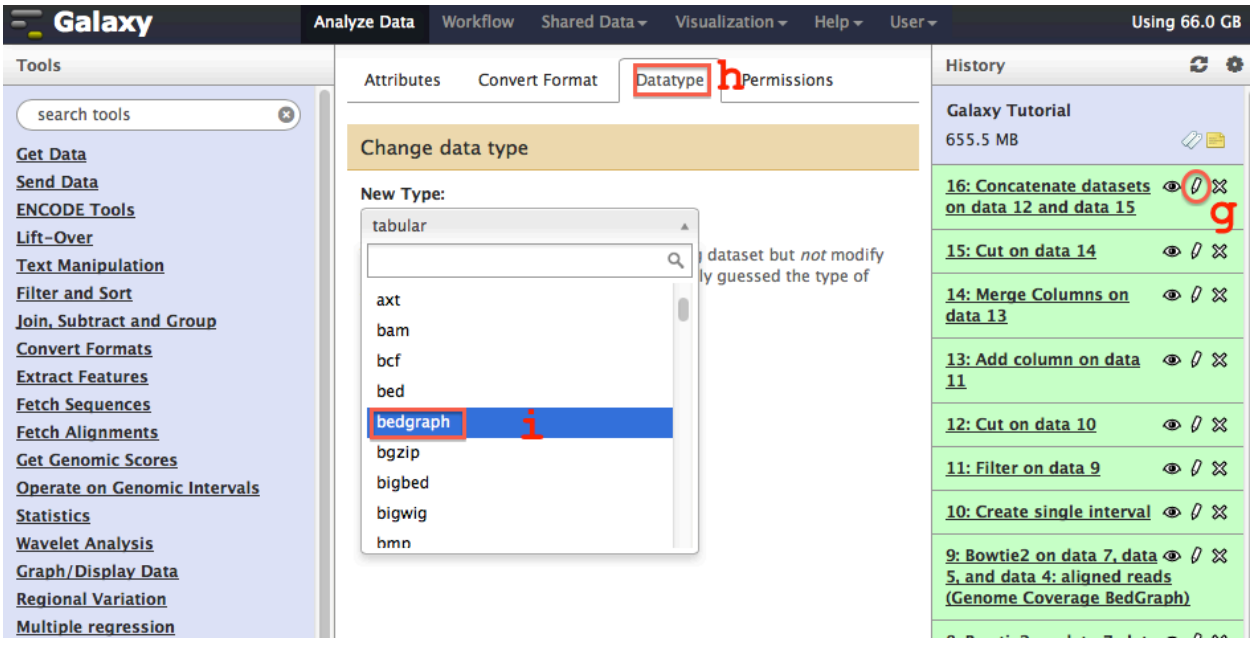

c. Click on Import Workflow



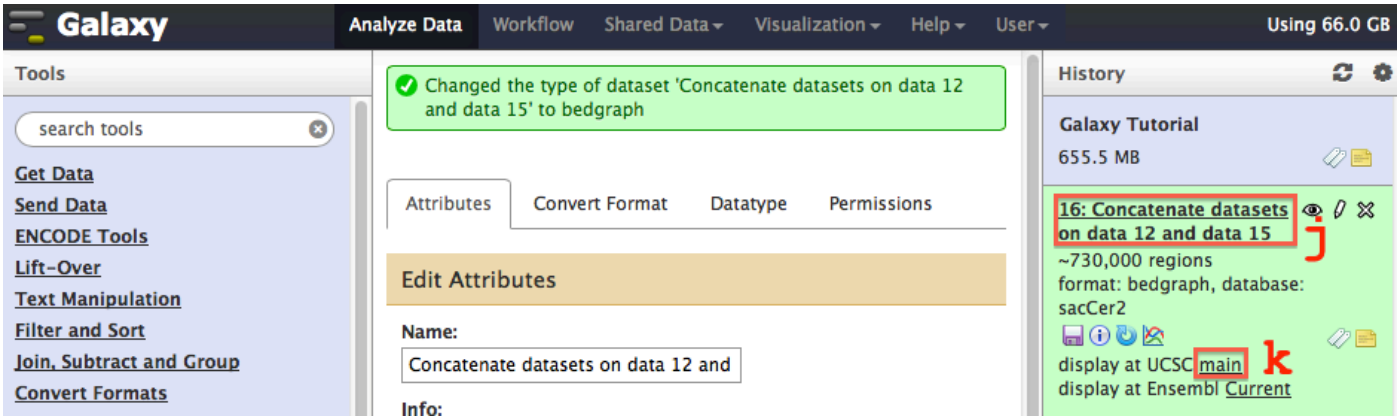

d. Click on imported: ensembl BAM to UCSC bedGraph

e. Select result 8 (Bowtie 2 on data…")
f. Click on run Workflow

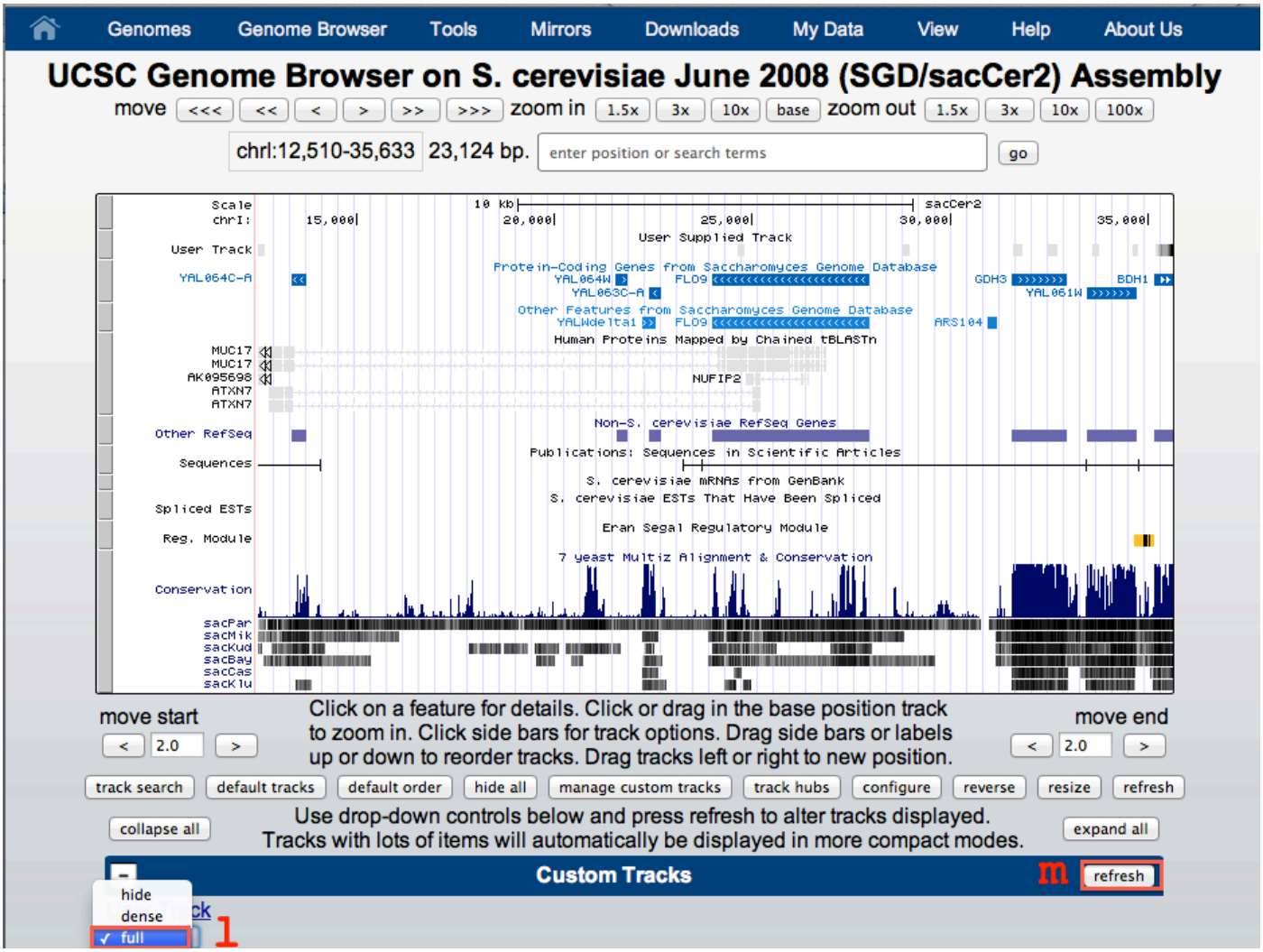

g. click on the pencil icon
h. Select Datatype tab
i. Select New Type: bedGraph and press Save



j. Click on the result link
k. Click on display at UCSC Main




l. click on full
m. click refresh



n. click on the bowser area to scroll along the genome