

# NGS Project

BioProject: [PRJNA781995](#)

- By using this bioproject, download the paper for this project and analyze it by clarifying the tools used. Your Samples are **SAMN23311524** and **SAMN23311529**

- Search on NCBI, and transfer your data to Galaxy, and make Quality control, Mapping, and Quantification using tools.

- Note: Each sample has 4 runs. Thus, Total samples = 8**

(Select 8 samples to make these steps)

Get data

Selected

02.23 Gb5.24 G

MetadataAccession ListJWT Cart

Deliver Data

Galaxy

Found 8 items

<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Run	BioSample	Bases	Bytes	Experiment	genotype	GEO_Accession	create_date	Sample Name
<input checked="" type="checkbox"/>	1	SRR16989402	SAMN23311524	1.10 G	477.13 Mb	SRX13179918	tub-Gal80ts; dMef2-GAL4 x w[1118]	GSM5696269	2021-11-19 08:37:00Z	GSM5696269
<input checked="" type="checkbox"/>	2	SRR16989403	SAMN23311524	659.81 M	286.46 Mb	SRX13179918	tub-Gal80ts; dMef2-GAL4 x w[1118]	GSM5696269	2021-11-19 08:38:00Z	GSM5696269
<input checked="" type="checkbox"/>	3	SRR16989404	SAMN23311524	728.70 M	320.52 Mb	SRX13179918	tub-Gal80ts; dMef2-GAL4 x w[1118]	GSM5696269	2021-11-19 08:39:00Z	GSM5696269
<input checked="" type="checkbox"/>	4	SRR16989405	SAMN23311524	75.05 M	32.43 Mb	SRX13179918	tub-Gal80ts; dMef2-GAL4 x w[1118]	GSM5696269	2021-11-19 08:37:00Z	GSM5696269
<input checked="" type="checkbox"/>	5	SRR16989422	SAMN23311529	1.15 G	501.85 Mb	SRX13179923	tub-Gal80ts; dMef2-GAL4 x UAS-REPTOR[ACT]	GSM5696274	2021-11-19 08:39:00Z	GSM5696274
<input checked="" type="checkbox"/>	6	SRR16989423	SAMN23311529	683.98 M	297.77 Mb	SRX13179923	tub-Gal80ts; dMef2-GAL4 x UAS-REPTOR[ACT]	GSM5696274	2021-11-19 08:38:00Z	GSM5696274
<input checked="" type="checkbox"/>	7	SRR16989424	SAMN23311529	764.71 M	337.21 Mb	SRX13179923	tub-Gal80ts; dMef2-GAL4 x UAS-REPTOR[ACT]	GSM5696274	2021-11-19 08:39:00Z	GSM5696274
<input checked="" type="checkbox"/>	8	SRR16989425	SAMN23311529	78.09 M	33.87 Mb	SRX13179923	tub-Gal80ts; dMef2-GAL4 x UAS-REPTOR[ACT]	GSM5696274	2021-11-19 08:37:00Z	GSM5696274

Upload to galaxy

1: SRA

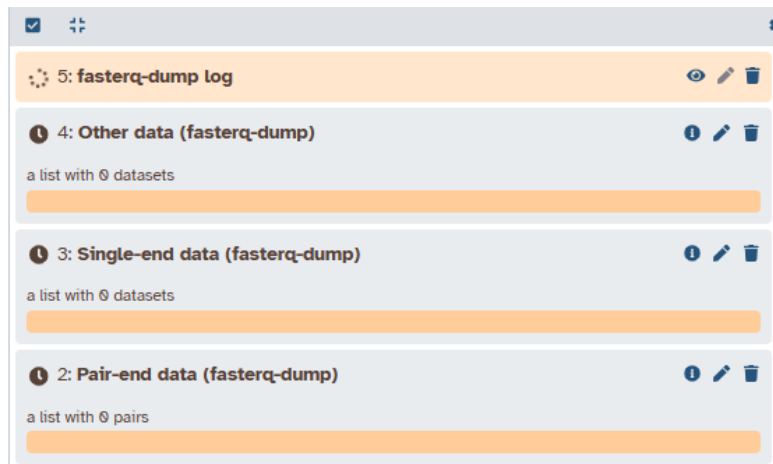
9 lines 28 columns, 1 comments

format **sra\_manifest.tabular**, database ?

1.Run	2.Assay	Type	3.AvgSpotLen	4.Bases	5.BioProject	6.BioSample	7.Bytes	8.Center
SRR16989402	RNA-Seq	75	1096722375	PRJNA781995	SAMN23311524	500308384	GEO	
SRR16989403	RNA-Seq	75	659811975	PRJNA781995	SAMN23311524	300374173	GEO	
SRR16989404	RNA-Seq	75	728703975	PRJNA781995	SAMN23311524	336087885	GEO	
SRR16989405	RNA-Seq	75	75050700	PRJNA781995	SAMN23311524	34008349	GEO	

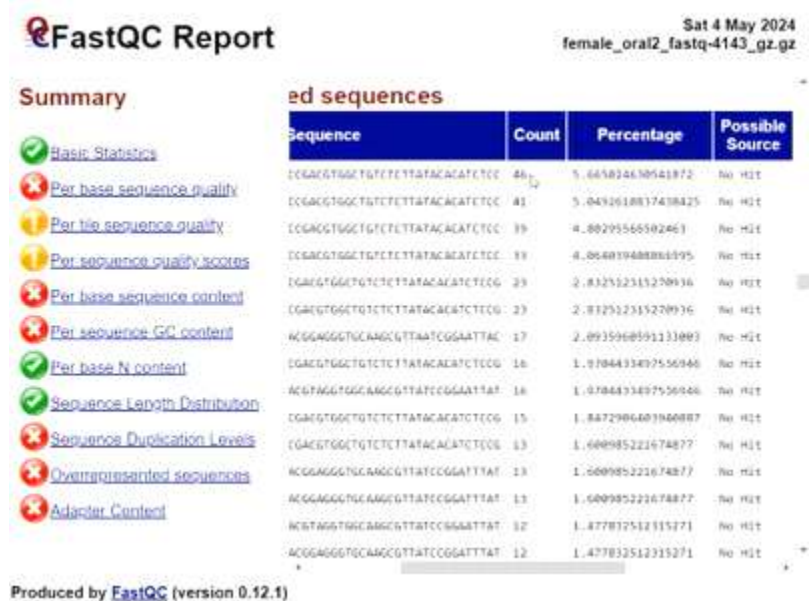
# NGS Project

## Faster Download and Extract Reads in FASTQ tool



solution

### 1) Quality control (**FASTQC**)



### 2) Mapping (**HISAT2** or **Bowtie2** tool)

# NGS Project

## 3) Quantification (feature count)

Tools

feature

Upload Data

Show Sections

**featureCounts** Measure gene expression in RNA-Seq experiments from SAM or BAM files

**Feature coverage**

**FeatureLinkerLabeled** Groups corresponding isotope-labeled features in a feature map.

**FeatureFinderMetabo** Assembles metabolite features from centroided (LC-)MS data using the mass trace approach.

**FeatureFinderMultiplex** Determination of peak ratios in LC-MS data

**FeatureLinkerUnlabeledKD** Groups corresponding features from multiple maps.

**FeatureFinderIdentification** Detects features in MS1 data based on peptide identifications.

**FeatureLinkerUnlabeledQT** Groups

Column 1	Column 2	Column 3	Column 4	Column 5	Column 6	Column 7	Column 8	Column 9	Column 10	Column 11	Column 12
# This file was produced by samtools stats (1.15.1+htslib-1.15.1) and can be plotted using plot-bamstats											
# This file contains statistics for all reads.											
# The command line was: stats --ref-seq /data/db/reference_genomes/mm10/seq/mm10.fa -@ 8 infile											
# CHK,	[2]Read	[3]Sequences	[4]Qualities								
Checksum	Names										
# CHK, CRC32 of reads which passed filtering followed by addition (32bit overflow)											
CHK	195ef5c8	83b341d3	1829c979								
# Summary Numbers. Use 'grep ^SN   cut -f 2-' to extract this part.											
SN	raw total	199999	# excluding								
	sequences:		supplementary								
			and secondary								
			reads								
SN	filtered	0									
	sequences:										
SN	sequences:	199999									
SN	is sorted:	0									
SN	1st fragments:	50000									
SN	last fragments:	50000									
SN	reads	98118									