



C4-NT-SEV1\_S11\_R1\_001.fastq.gz

## Mapping Results

File	Reads processed	Unmapped	One hit / one genome	Multiple hits / one genome	One hit / multiple genomes	Multiple hits / multiple genomes
Human	99,859	99,030	301	84	44	400
Mouse	99,859	99,533	1	0	69	256
Rat	99,859	99,430	1	0	52	376
Drosophila	99,859	99,819	0	0	2	38
Worm	99,859	99,823	0	0	12	24
Yeast	99,859	99,824	0	5	1	29
Arabidopsis	99,859	99,814	1	2	1	41
Ecoli	99,859	99,832	6	21	0	0
rRNA	99,859	99,668	0	0	32	159
MT	99,859	99,841	0	0	14	4
PhiX	99,859	99,859	0	0	0	0
Lambda	99,859	99,859	0	0	0	0
Vectors	99,859	99,809	0	0	35	15
Adapters	99,859	99,351	459	13	0	36





Analysis produced by **FastQ Screen** (0.15.1) - a tool for screening FASTQ files of sequences against multiple reference genomes

Date generated: 12-16-49 23-08-2022

Mapping parameters: bowtie2

Subset data size: 100000

