

# MAGeCK Count Report

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## 1 Summary

The statistics of comparisons are listed in Table 1 and Table 2. The corresponding fastq files in each row are listed in Table 3.

	Label	Reads	Mapped	Percentage
1	test1_fastq.gz	2500	1453	0.58

Table 1: Summary of comparisons

	Label	TotalsgRNA	ZeroCounts	GiniIndex
1	test1_fastq.gz	2550	1276	0.53

Table 2: Summary of comparisons

	File	Label
1	input_0.gz	test1_fastq.gz

Table 3: Summary of samples

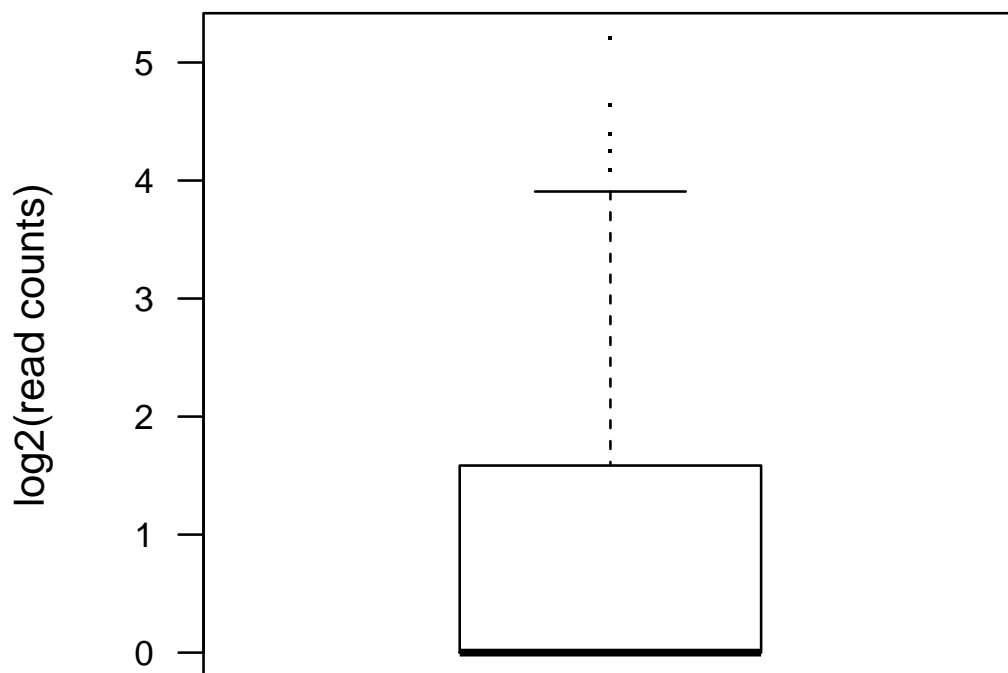
The meanings of the columns are as follows.

- **Row:** The row number in the table;
- **File:** The filename of fastq file;
- **Label:** Assigned label;
- **Reads:** The total read count in the fastq file;
- **Mapped:** Reads that can be mapped to gRNA library;
- **Percentage:** The percentage of mapped reads;
- **TotalsgRNAs:** The number of sgRNAs in the library;

- **ZeroCounts:** The number of sgRNA with 0 read counts;
- **GiniIndex:** The Gini Index of the read count distribution. Gini index can be used to measure the evenness of the read counts, and a smaller value means a more even distribution of the read counts.

## 2 Normalized read count distribution of all samples

The following figure shows the distribution of median-normalized read counts in all samples.



The following figure shows the histogram of median-normalized read counts in all samples.

## Distribution of read counts

