

General Stats	
FactOC	

Adapter Content

Status Checks

FastQC
Sequence Counts
Sequence Quality Histograms
Per Sequence Quality Scores
Per Base Sequence Content
Per Sequence GC Content
Per Base N Content
Sequence Length Distribution
Sequence Duplication Levels
Overrepresented sequences

# MultiQC

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report. Report generated on 2023-06-14, 09:48 UTC based on data in: /mnt/volume\_sgp1\_01/tung/fastqc

<b>B Welcomel</b> Not sure where to start?	Watch a tutorial video	(6.06)
Weicome: Not sure where to start?	watch a tutorial video	(6:06)

# **General Statistics 9** SI

Showing 502 samples.										
Hover over a data point for	more information									
FastQC % Dups	٩		25	*	50 ·			<<<		* 100
FastQC % GC	0		25 ·		50 50		75			100
FastQC Average Read Length	0		100	ata (1777) ata	an (a ser as age	<b>K. 14 (</b> 1442)	00		~~~	300
FastQC Median Read Length	0		• • 100		• •	• • 2	00 •	( ) (		300
FastQC % Failed	0		25 •		50		75			100
FastQC M Seqs	Stan C.	C + + +	1 •		• 2			3		• •

## FastQC

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

### **Sequence Counts**

Sequence counts for each sample. Duplicate read counts are an estimate only.

Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

Percentages Number of reads

	FastQC: Sequence Counts								
IPM5572_S1_L001_R1_001									
IPM5574_S3_L001_R1_001 IPM5576_S5_L001_R1_001									
IPM5578_S7_L001_R1_001 IPM5580_S9_L001_R1_001									
IPM5582_S11_L001_R1_001 IPM5584_S13_L001_R1_001									
IPM5586_S15_L001_R1_001 IPM5588_S17_L001_R1_001	Ē.								
IPM5590_S19_L001_R1_001									
IPM5592_521_L001_R1_001 IPM5594_S23_L001_R1_001									
IPM5596_S25_L001_R1_001 IPM5598_S27_L001_R1_001									
IPM5600_S29_L001_R1_001 IPM5602_S31_L001_R1_001									
IPM5604_S33_L001_R1_001 IPM5606 S35 L001 R1 001									
IPM5608_S37_L001_R1_001 IPM5610_S39_L001_R1_001									
IPM5615_S44_L001_R1_001									
IPM5619_548_L001_R1_001	<u> </u>								
IPM5632_S61_L001_R1_001 IPM5632_S61_L001_R1_001									
IPM5634_S63_L001_R1_001 IPM5636_S65_L001_R1_001									
IPM5638_S67_L001_R1_001 IPM5640_S69_L001_R1_001									
IPM5642_S71_L001_R1_001 IPM5644 S73 L001 R1 001									
IPM5646_S75_L001_R1_001									
IPM5650_S79_L001_R1_001									
IPM5652_581_L001_R1_001 IPM5654_S83_L001_R1_001									
IPM5656_S85_L001_R1_001 IPM5658_S87_L001_R1_001									
IPM5660_S89_L001_R1_001 IPM5662_S91_L001_R1_001									
IPM5664_S93_L001_R1_001 IPM5666_S95_L001_R1_001									
IPM5851_S1_L001_R1_001 IPM5853_S3_L001_R1_001									
IPM5855_S5_L001_R1_001									
IPM5859_S9_L001_R1_001									
IPM5861_S11_L001_R1_001 IPM5863_S13_L001_R1_001									
IPM5865_S15_L001_R1_001 IPM5867_S17_L001_R1_001									
IPM5869_S19_L001_R1_001 IPM5871_S21_L001_R1_001									
IPM5873_S23_L001_R1_001 IPM5875 S25 L001 R1 001									
IPM5877_S27_L001_R1_001 IPM5879_S29_L001_R1_001									
IPM5881_S31_L001_R1_001									
IPM5885_S35_L001_R1_001									
IPM5887_537_L001_R1_001 IPM5889_S39_L001_R1_001	E								
IPM5891_S41_L001_R1_001 IPM5893_S43_L001_R1_001									
IPM5895_S45_L001_R1_001 IPM5897_S47_L001_R1_001									
IPM5901_S51_L001_R1_001 IPM5903_S53_L001_R1_001									
IPM5905_S55_L001_R1_001 IPM5907 S57 L001 R1 001									
IPM5909_S59_L001_R1_001									
IPM5913_S63_L001_R1_001									
IPM5915_565_L001_R1_001									
IPM5919_569_L001_R1_001 IPM5921_S71_L001_R1_001									
IPM5923_S73_L001_R1_001 IPM5925_S75_L001_R1_001									
IPM5927_S77_L001_R1_001 IPM5929_S79_L001_R1_001									
IPM5931_S81_L001_R1_001 IPM5933_S83_L001_R1_001									
IPM5935_S85_L001_R1_001 IPM5937_S87_L001_R1_001									
IPM5939_S89_L001_R1_001									
IPM5941_591_L001_R1_001									
IPM5945_595_L001_R1_001 IPM6417_S1_L001_R1_001									
IPM6419_S3_L001_R1_001 IPM6421_S5_L001_R1_001									
IPM6423_S7_L001_R1_001 IPM6425_S9_L001_R1_001									
IPM6427_S11_L001_R1_001 IPM6429_S13_L001_R1_001									
IPM6431_S15_L001_R1_001									
IPM6435_S19_L001_R1_001									
IPM6439_S23_L001_R1_001									
IPM6444_S28_L001_R1_001									

don't show again 🗙

Help





Help

Help

497

#### Per Sequence Quality Scores

The number of reads with average quality scores. Shows if a subset of reads has poor quality. Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).



#### Per Base Sequence Content 502

The proportion of each base position for which each of the four normal DNA bases has been called.

Click a sample row to see a line plot for that dataset.







#### Adapter Content 441

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position. Flat image plot. Toolbox functions such as highlighting / hiding samples will not work (see the docs).

![](_page_0_Figure_29.jpeg)

## **Status Checks**

Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red).

![](_page_0_Figure_32.jpeg)

Help

Help