

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:34:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549065.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1549065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:34:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,421,460
Mapped reads	8,083,725 / 85.8%
Unmapped reads	1,337,735 / 14.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	348,438 / 3.7%
Duplication rate	3.17%
Clipped reads	349,711 / 3.71%

2.2. ACGT Content

Number/percentage of A's	94,546,061 / 29.43%
Number/percentage of C's	66,012,776 / 20.55%
Number/percentage of T's	94,562,904 / 29.44%
Number/percentage of G's	66,123,089 / 20.58%
Number/percentage of N's	6,023 / 0%
GC Percentage	41.13%

2.3. Coverage

Mean	0.1038
Standard Deviation	1.1274

2.4. Mapping Quality

Mean Mapping Quality	44.46
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2.5. Mismatches and indels

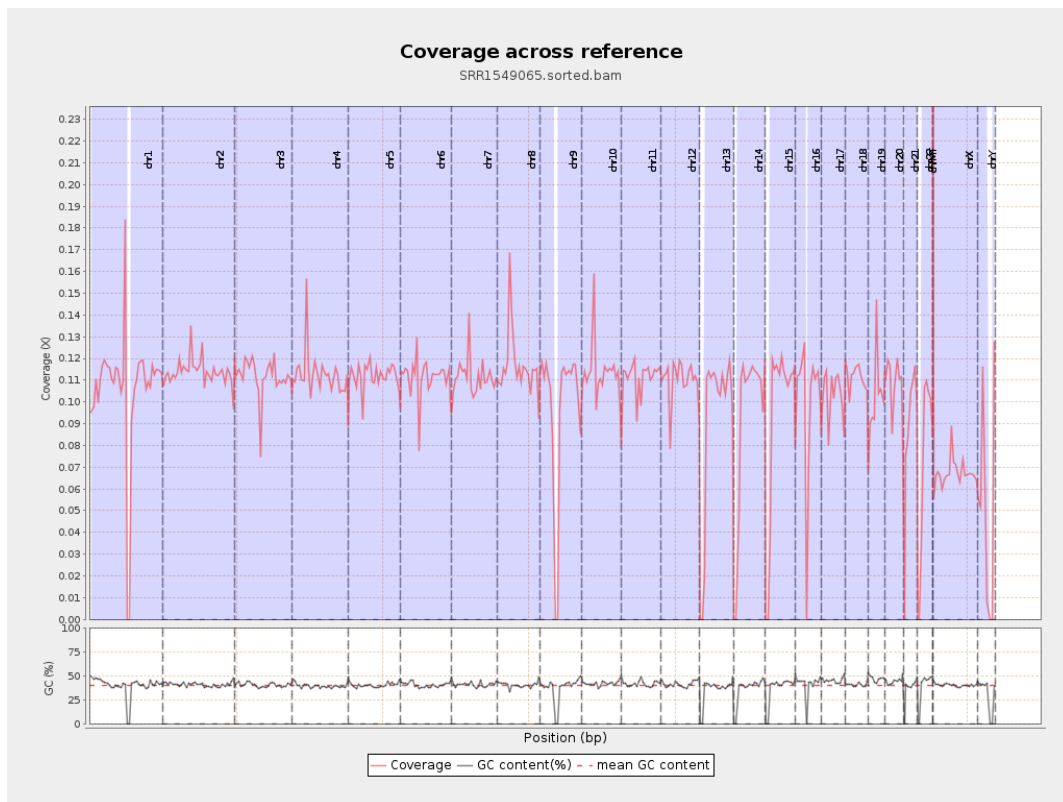
General error rate	0.31%
Mismatches	989,415
Insertions	7,687
Mapped reads with at least one insertion	0.1%
Deletions	26,223
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.34%

2.6. Chromosome stats

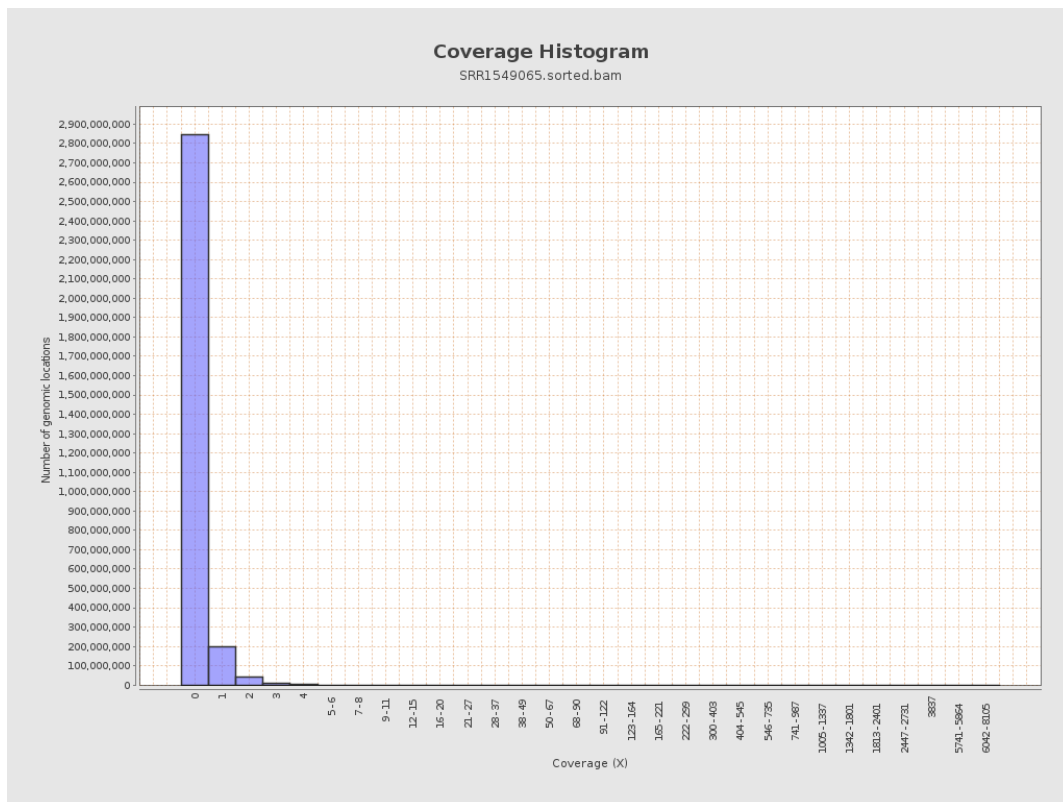
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26393631	0.1059	1.8621
chr2	243199373	27710041	0.1139	0.568
chr3	198022430	22120339	0.1117	0.4102
chr4	191154276	21581662	0.1129	0.4738
chr5	180915260	20195910	0.1116	0.4137
chr6	171115067	19087329	0.1115	0.4553
chr7	159138663	17731371	0.1114	0.709
chr8	146364022	17081714	0.1167	3.9564

chr9	141213431	13683764	0.0969	0.5056
chr10	135534747	15414110	0.1137	0.6514
chr11	135006516	15003931	0.1111	0.5384
chr12	133851895	14791702	0.1105	0.4183
chr13	115169878	10556612	0.0917	0.3644
chr14	107349540	9936192	0.0926	0.406
chr15	102531392	9488918	0.0925	0.3663
chr16	90354753	8880931	0.0983	0.4271
chr17	81195210	8418577	0.1037	0.4222
chr18	78077248	8685381	0.1112	0.9456
chr19	59128983	6094809	0.1031	1.3046
chr20	63025520	6857251	0.1088	0.4218
chr21	48129895	4262980	0.0886	0.4448
chr22	51304566	3705438	0.0722	0.3566
chrMT	16571	8284	0.4999	0.8794
chrX	155270560	10451452	0.0673	0.3789
chrY	59373566	3142223	0.0529	0.6362

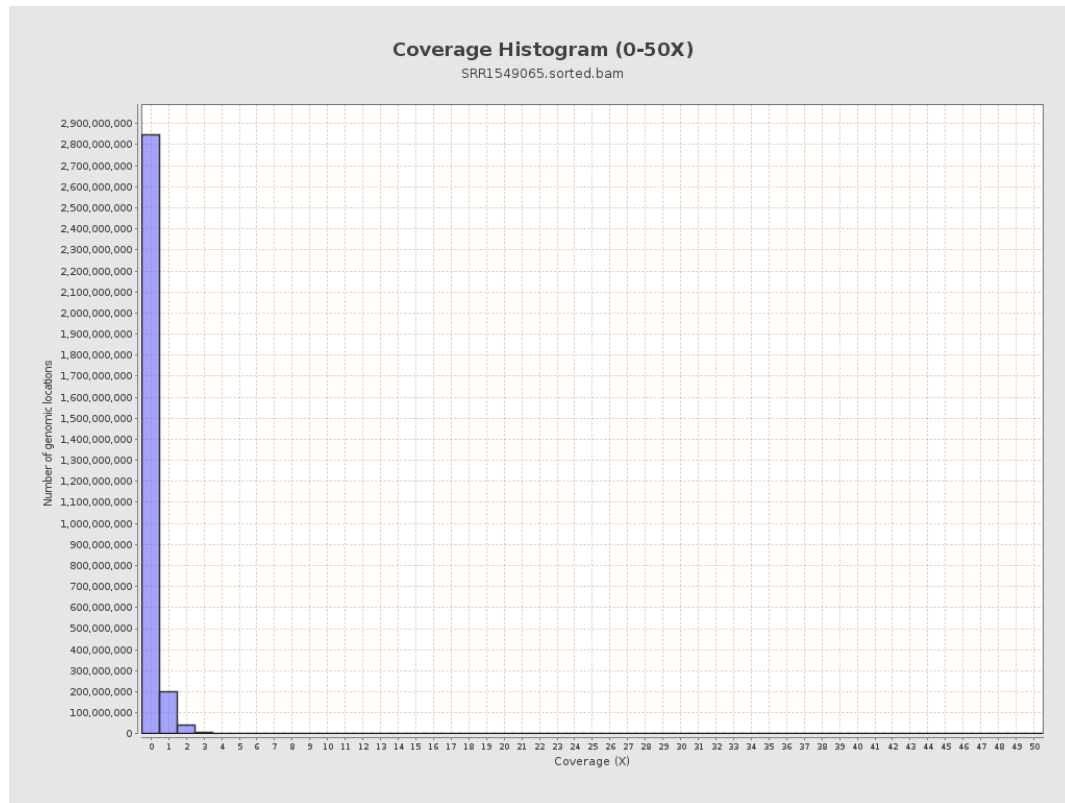
3. Results : Coverage across reference



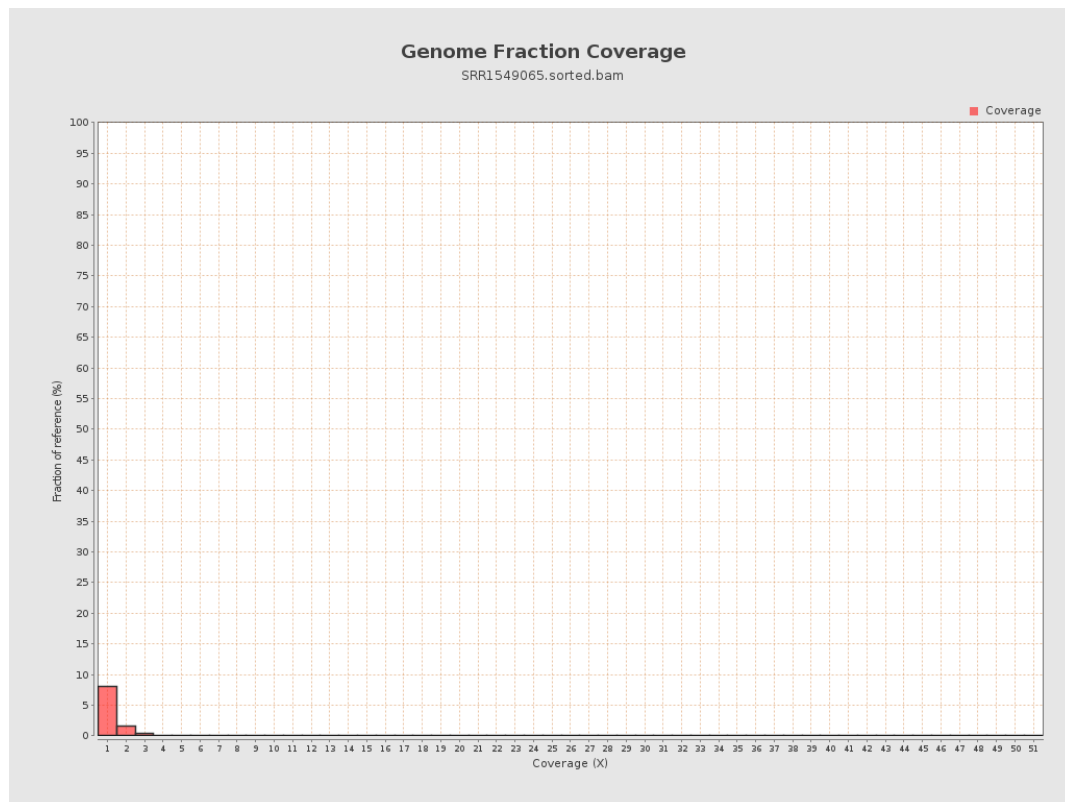
4. Results : Coverage Histogram



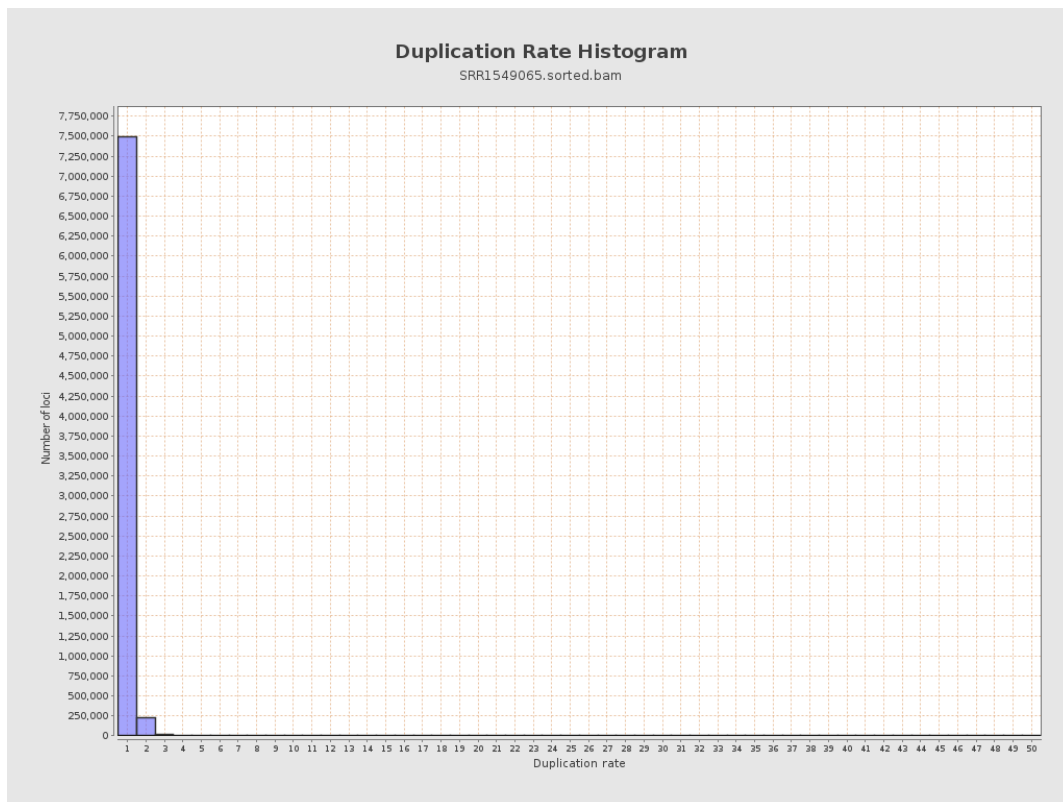
5. Results : Coverage Histogram (0-50X)



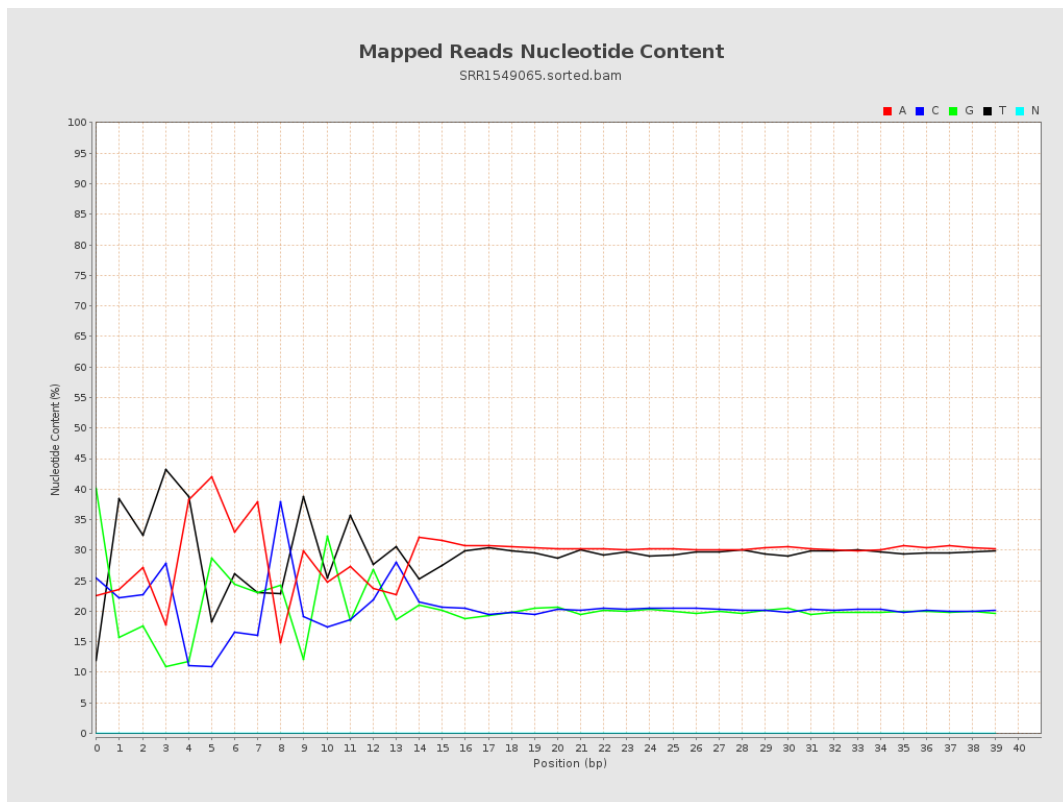
6. Results : Genome Fraction Coverage



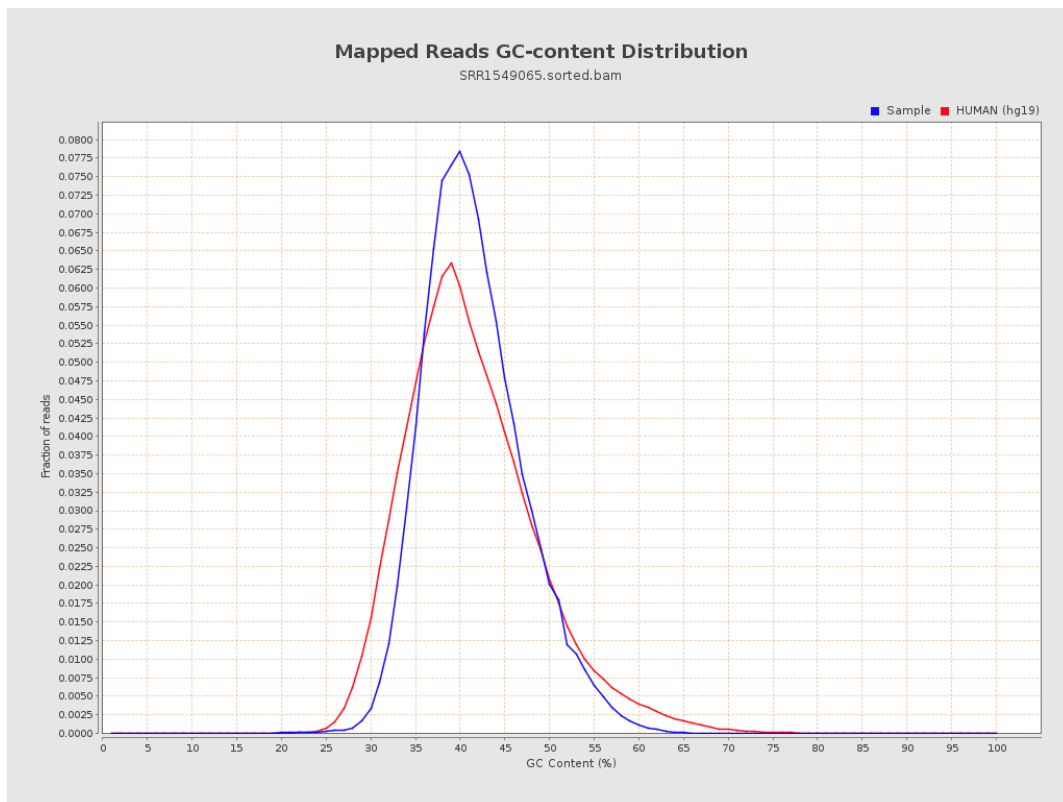
7. Results : Duplication Rate Histogram



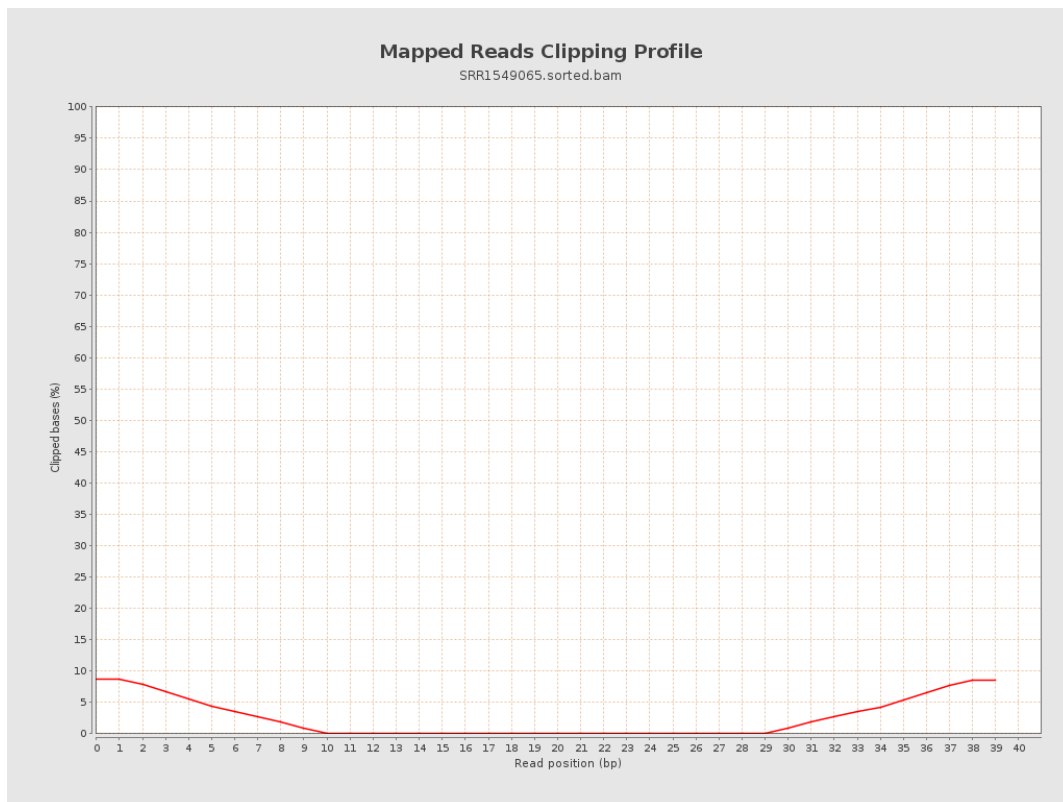
8. Results : Mapped Reads Nucleotide Content



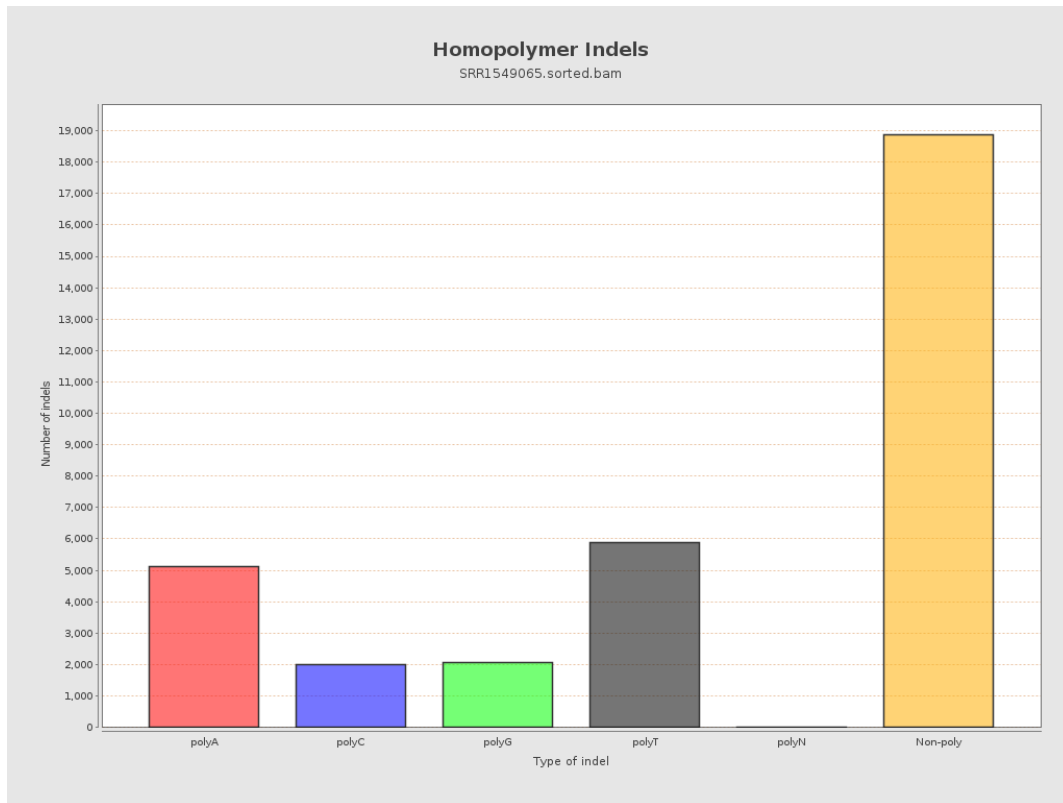
9. Results : Mapped Reads GC-content Distribution



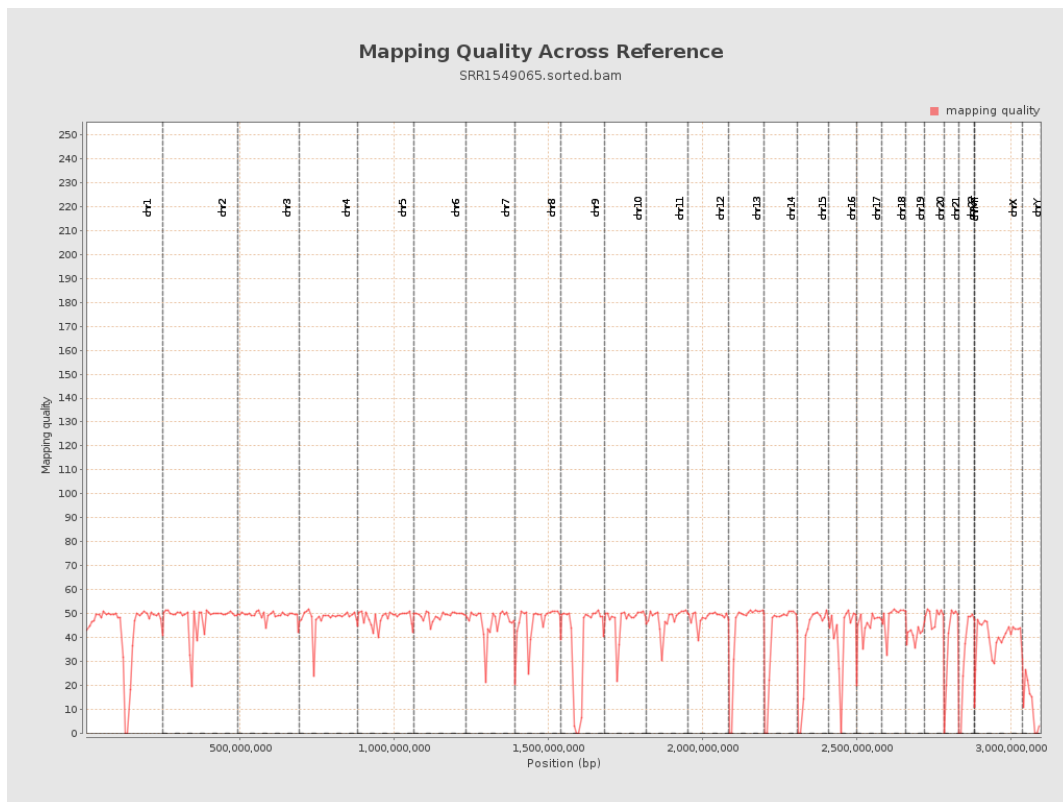
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

