Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:31:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054605.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_SRR054605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:31:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,399,173
Mapped reads	3,733,948 / 84.88%
Unmapped reads	665,225 / 15.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	108 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	952,680 / 21.66%
Duplication rate	17.32%
Clipped reads	426,492 / 9.69%

2.2. ACGT Content

Number/percentage of A's	53,440,460 / 30.46%
Number/percentage of C's	35,501,551 / 20.23%
Number/percentage of T's	50,508,735 / 28.79%
Number/percentage of G's	35,981,724 / 20.51%
Number/percentage of N's	17,545 / 0.01%
GC Percentage	40.74%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.602

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

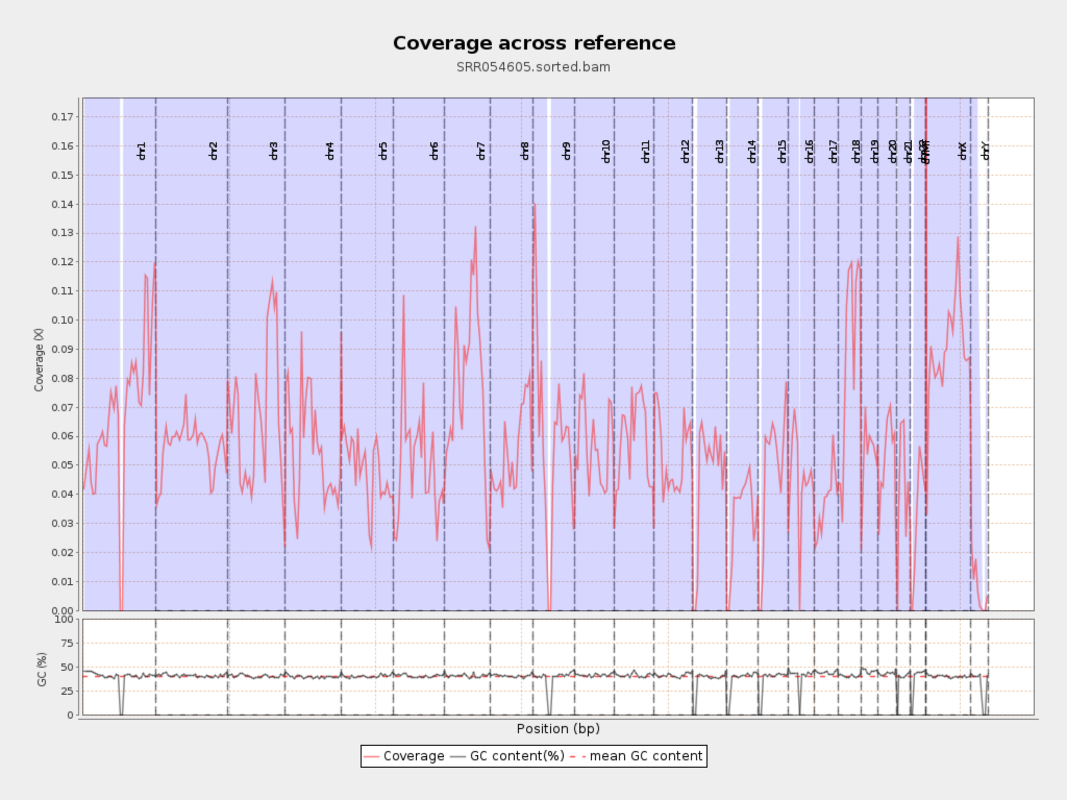
General error rate	0.51%
Mismatches	885,354
Insertions	6,887
Mapped reads with at least one insertion	0.18%
Deletions	21,535
Mapped reads with at least one deletion	0.58%
Homopolymer indels	43.35%

2.6. Chromosome stats

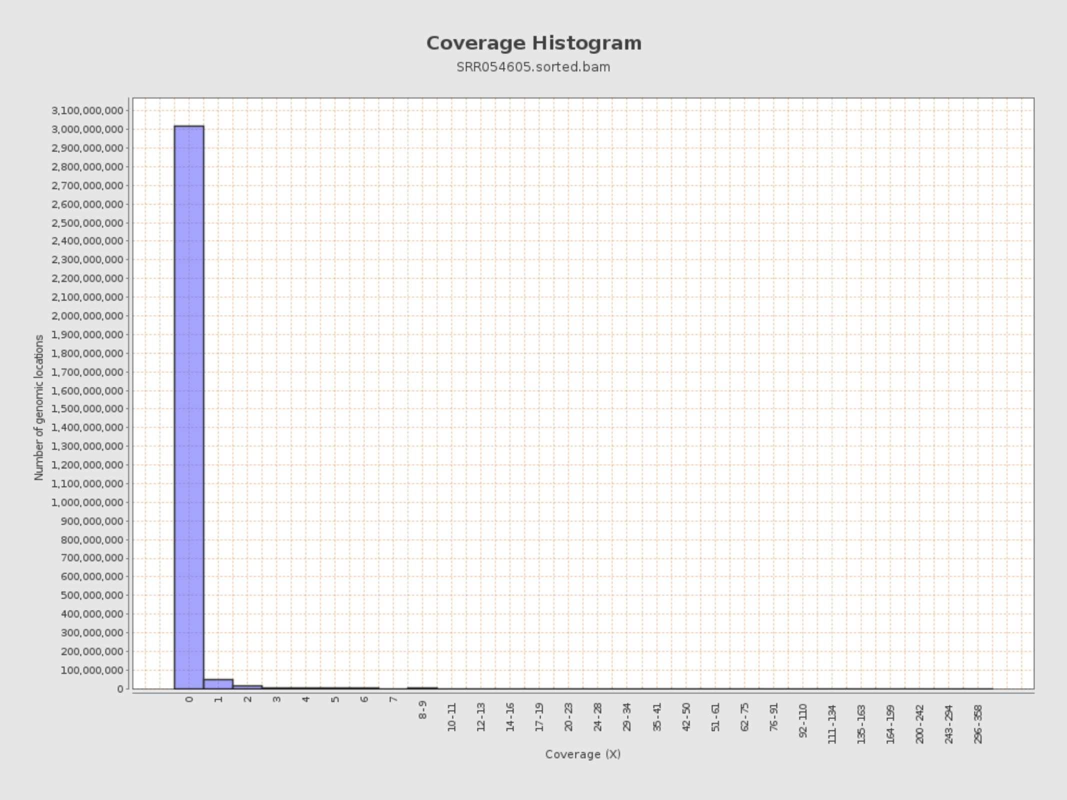
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16826104	0.0675	0.7028
chr2	243199373	13651972	0.0561	0.6039
chr3	198022430	13183988	0.0666	0.637
chr4	191154276	10661147	0.0558	0.5762
chr5	180915260	8735734	0.0483	0.507
chr6	171115067	8667790	0.0507	0.5746
chr7	159138663	12309023	0.0773	0.7688

chr8	146364022	7965858	0.0544	0.5696
chr9	141213431	8278617	0.0586	0.61
chr10	135534747	7723862	0.057	0.596
chr11	135006516	7932938	0.0588	0.6005
chr12	133851895	7222157	0.054	0.5501
chr13	115169878	5335767	0.0463	0.5241
chr14	107349540	3484820	0.0325	0.4311
chr15	102531392	4898485	0.0478	0.5321
chr16	90354753	3992814	0.0442	0.5237
chr17	81195210	3057423	0.0377	0.4327
chr18	78077248	6868087	0.088	0.7795
chr19	59128983	3254453	0.055	0.603
chr20	63025520	3330117	0.0528	0.5433
chr21	48129895	1957578	0.0407	0.5362
chr22	51304566	1676700	0.0327	0.4046
chrMT	16571	14300	0.863	2.0888
chrX	155270560	14015708	0.0903	0.7977
chrY	59373566	437116	0.0074	0.1828

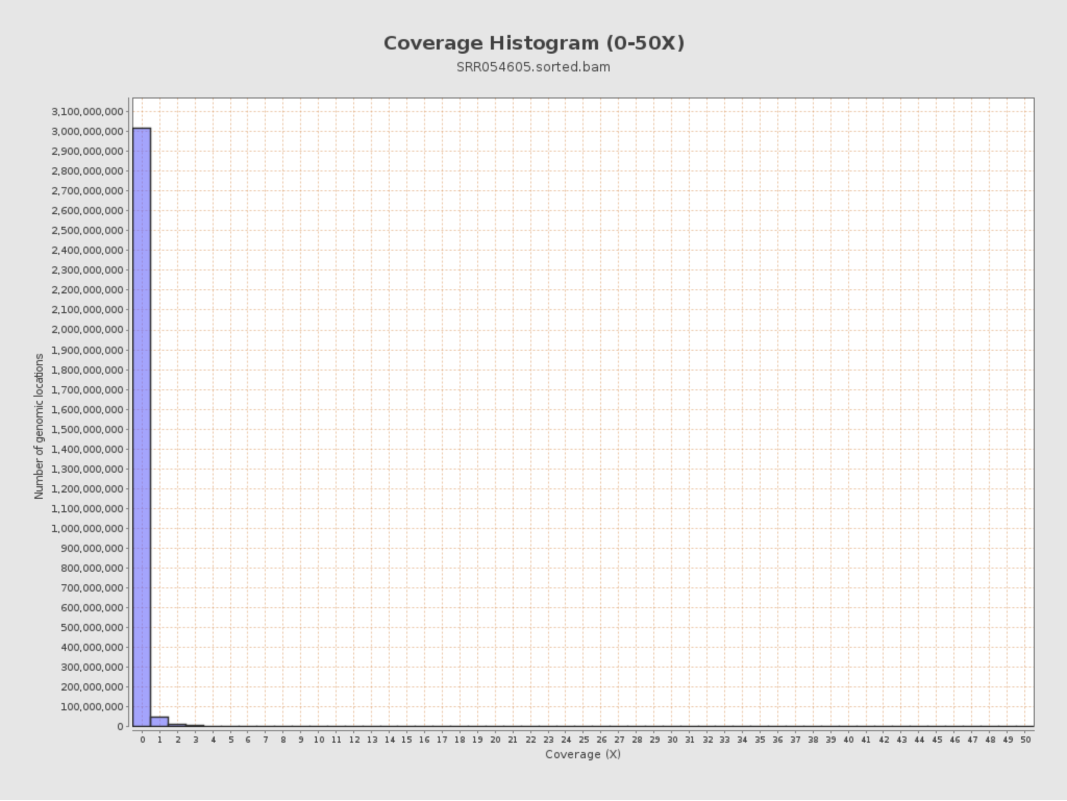
3. Results : Coverage across reference



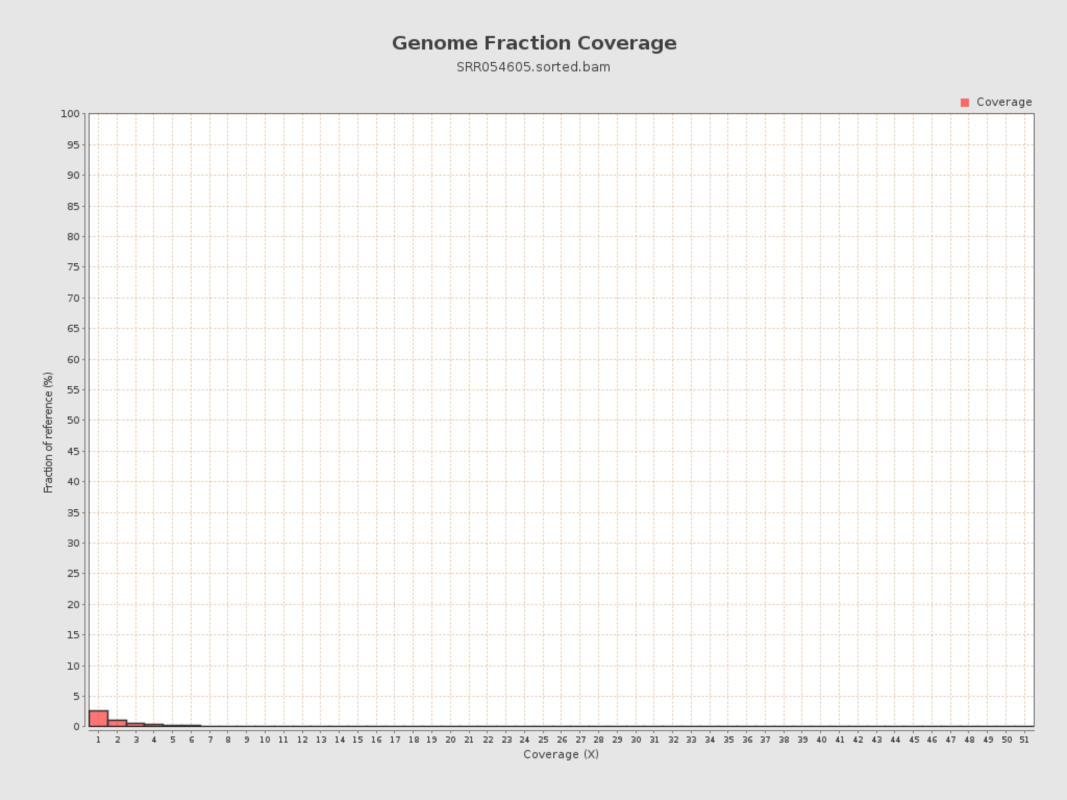
4. Results : Coverage Histogram



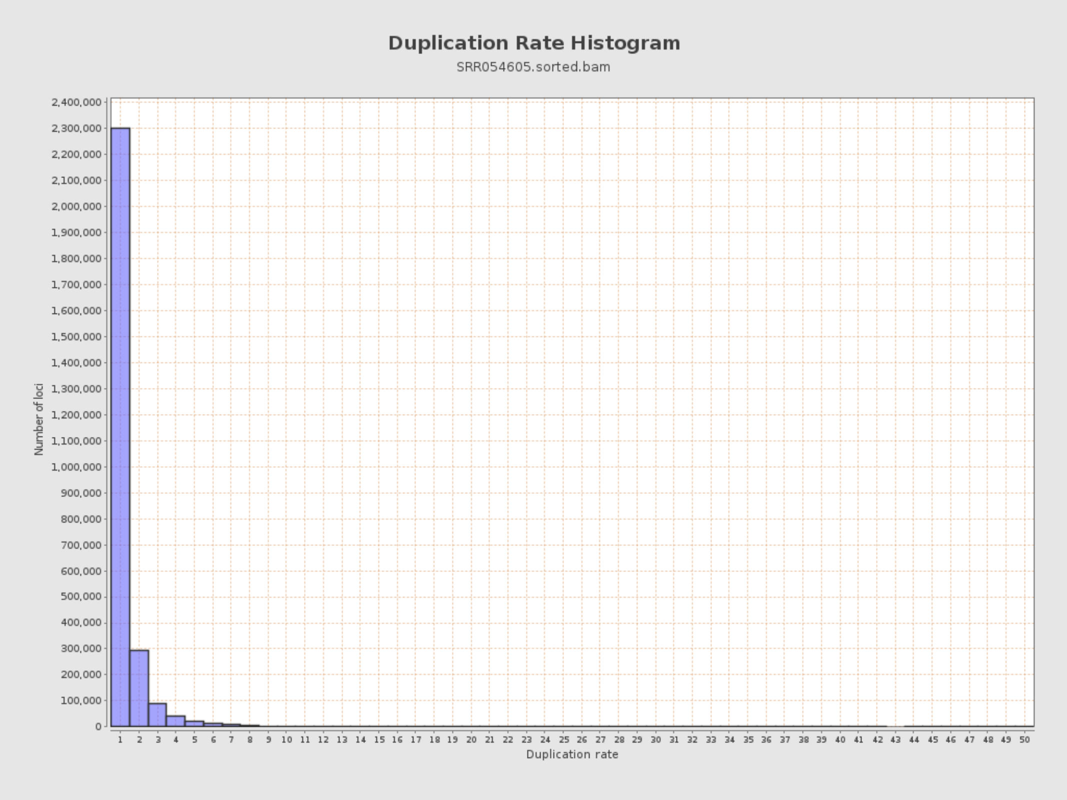
5. Results : Coverage Histogram (0-50X)



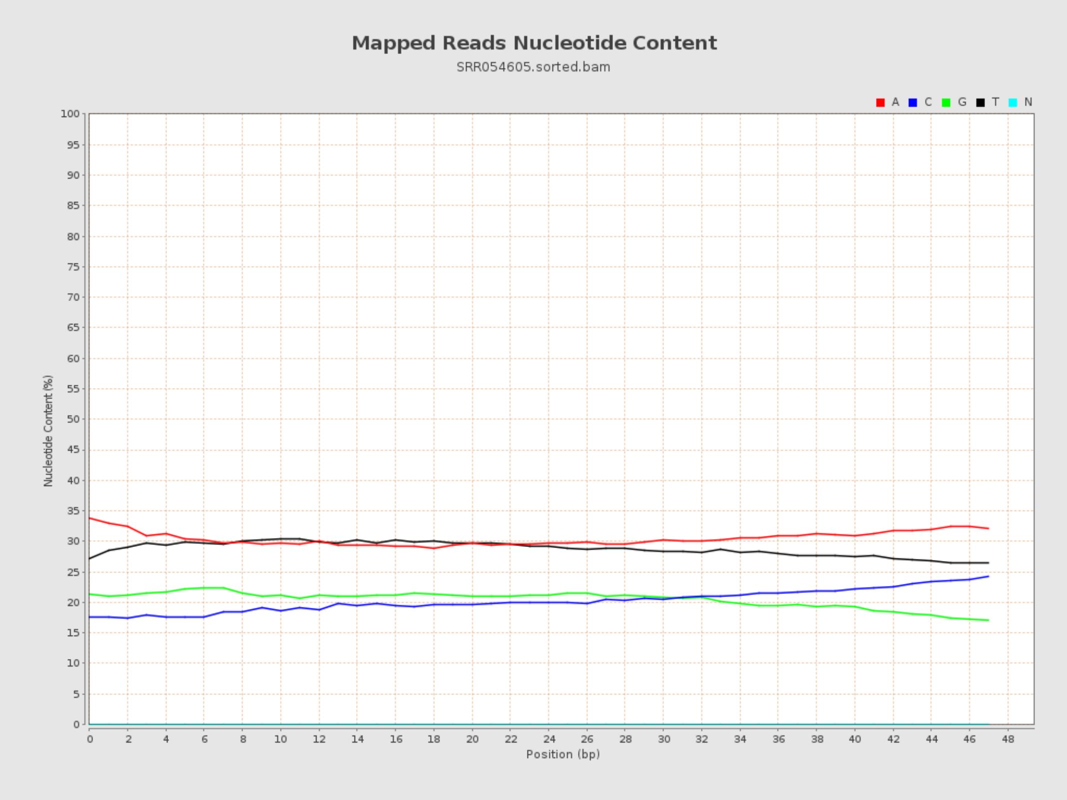
6. Results : Genome Fraction Coverage



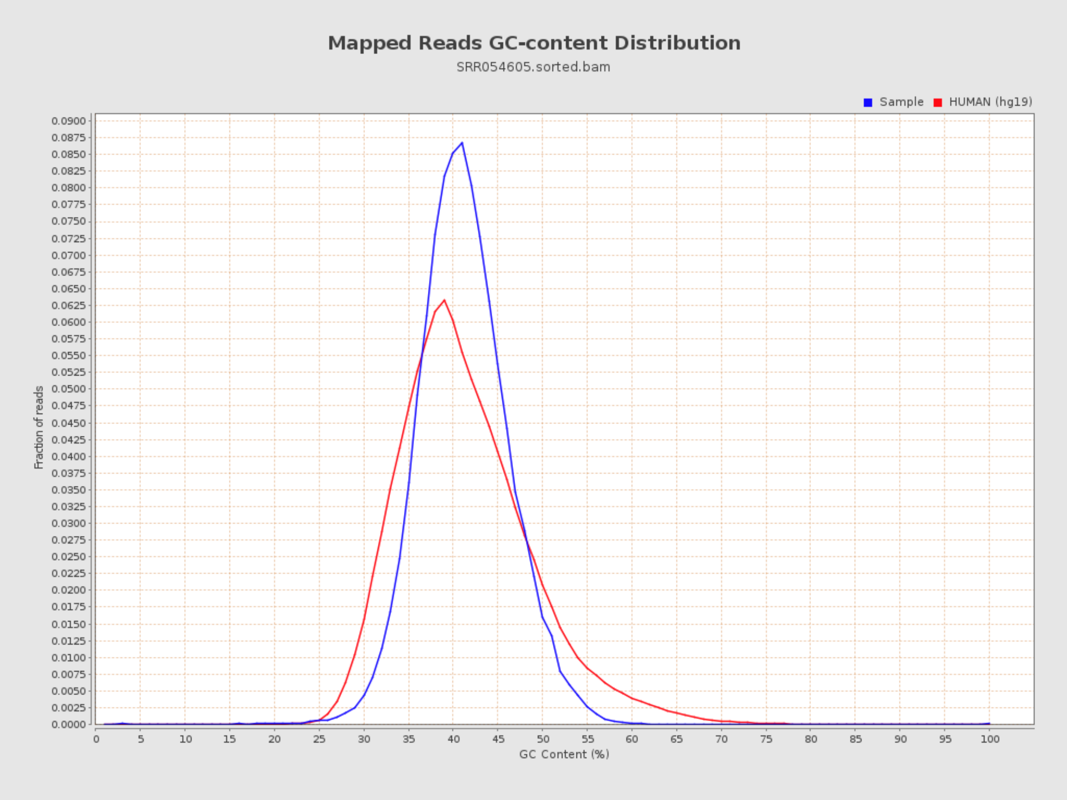
7. Results : Duplication Rate Histogram



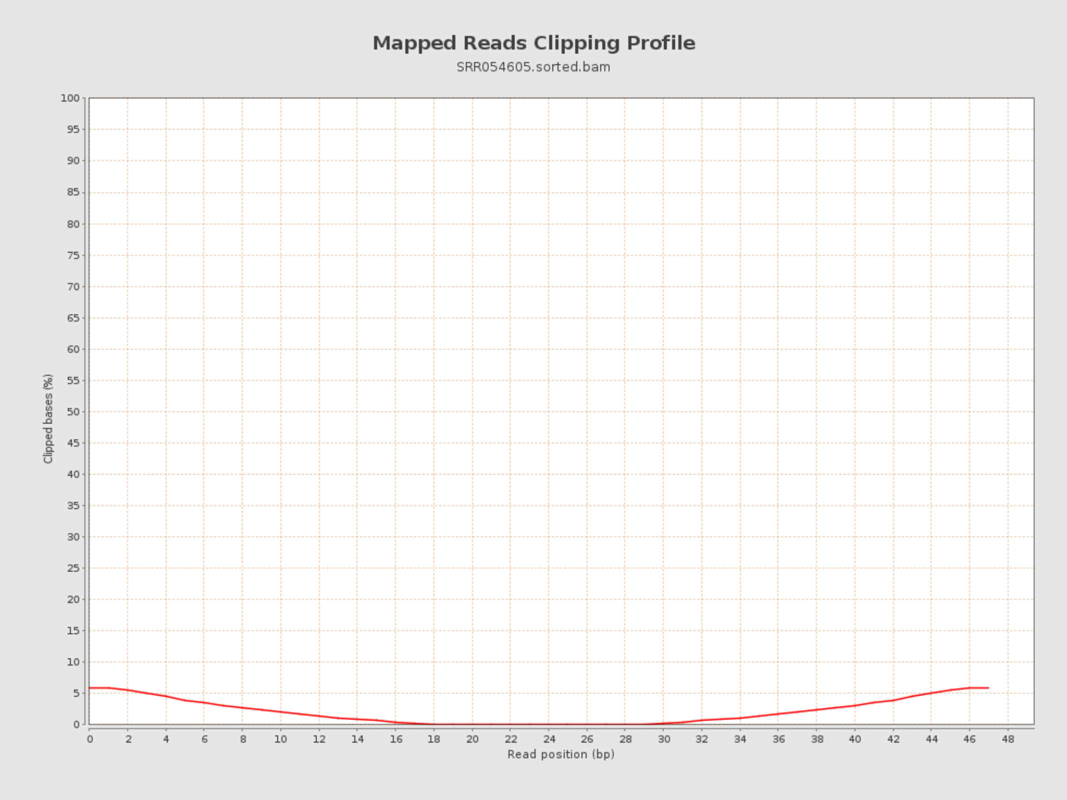
8. Results : Mapped Reads Nucleotide Content



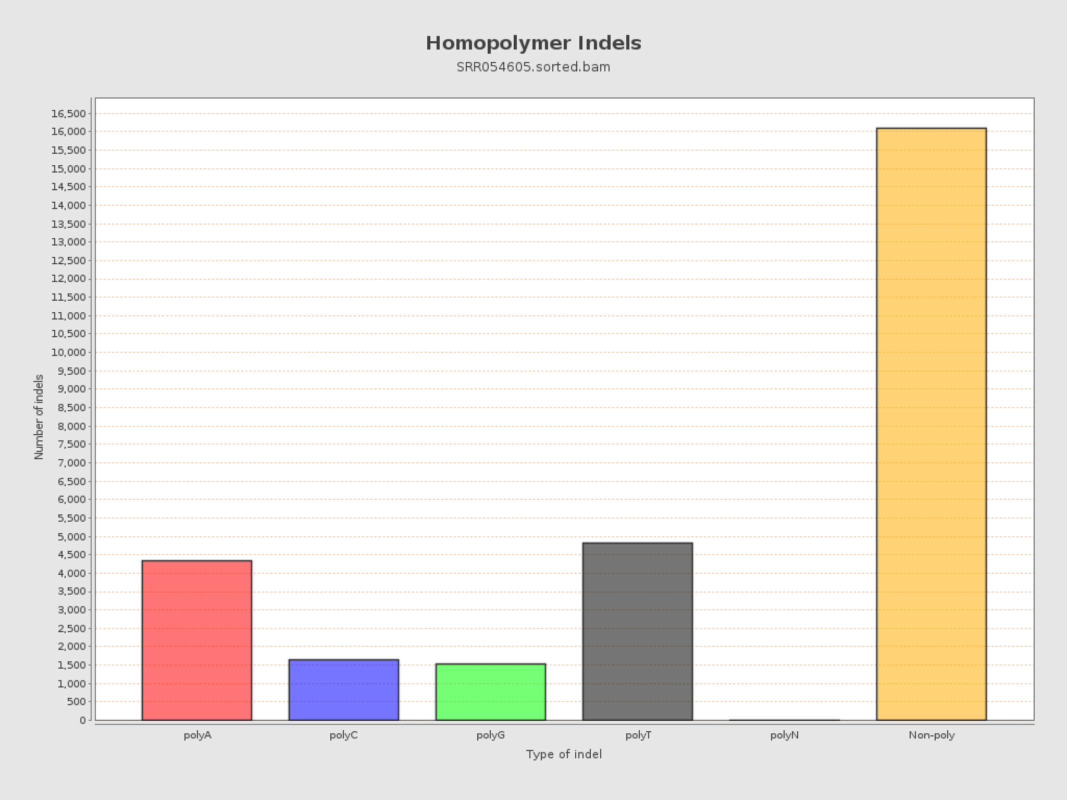
9. Results : Mapped Reads GC-content Distribution



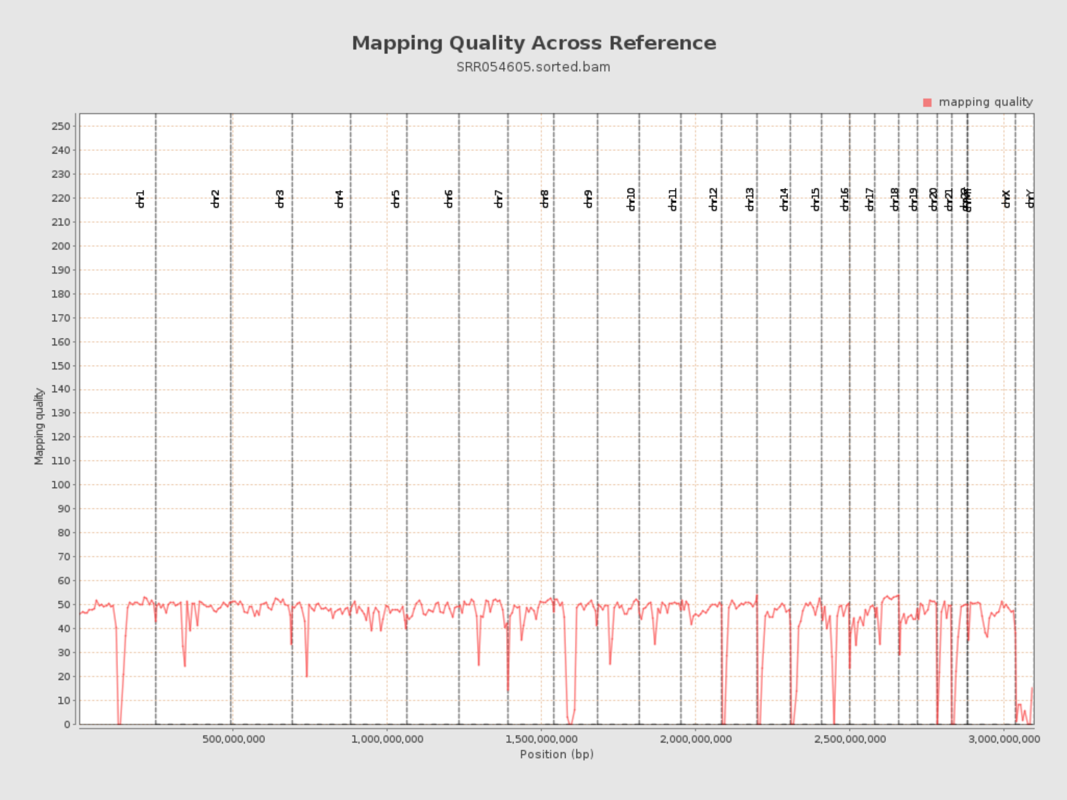
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram