

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:58:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549104.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_SRR1549104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:58:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,770,868
Mapped reads	10,193,919 / 86.6%
Unmapped reads	1,576,949 / 13.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	440,659 / 3.74%
Duplication rate	3.12%
Clipped reads	526,593 / 4.47%

2.2. ACGT Content

Number/percentage of A's	122,519,103 / 30.29%
Number/percentage of C's	79,507,194 / 19.66%
Number/percentage of T's	123,253,507 / 30.47%
Number/percentage of G's	79,212,047 / 19.58%
Number/percentage of N's	1,691 / 0%
GC Percentage	39.24%

2.3. Coverage

Mean	0.1307
Standard Deviation	0.8654

2.4. Mapping Quality

Mean Mapping Quality	44.32
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2.5. Mismatches and indels

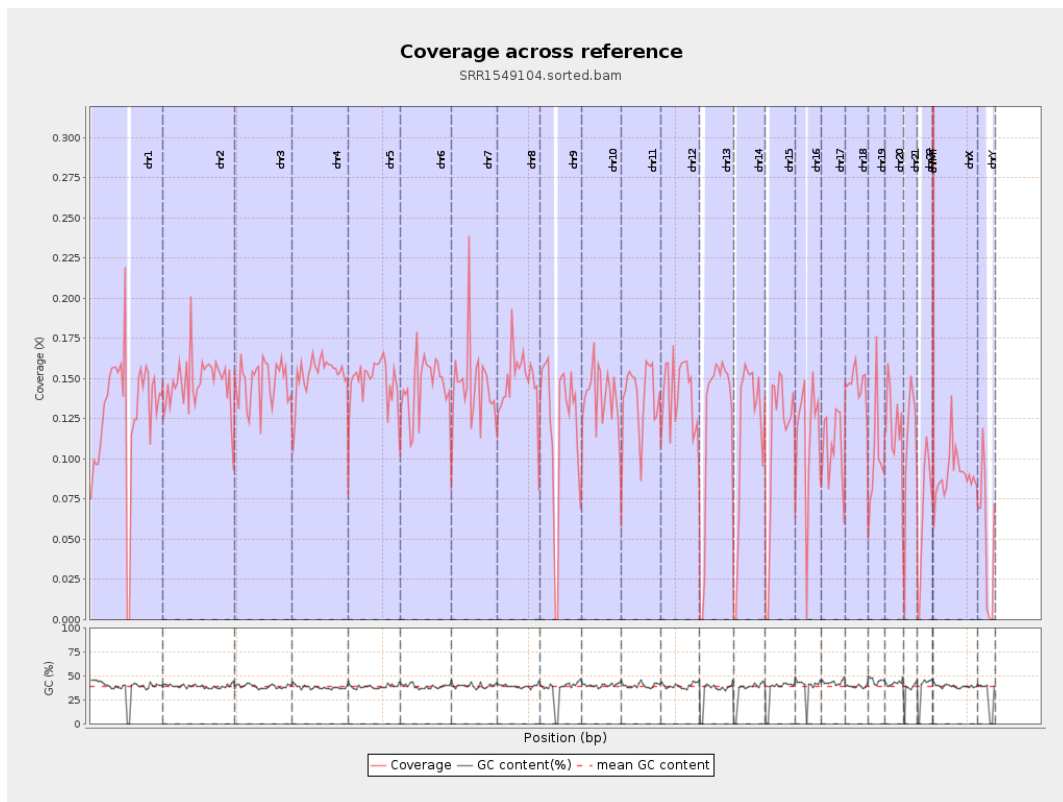
General error rate	0.3%
Mismatches	1,208,586
Insertions	10,507
Mapped reads with at least one insertion	0.1%
Deletions	31,066
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.49%

2.6. Chromosome stats

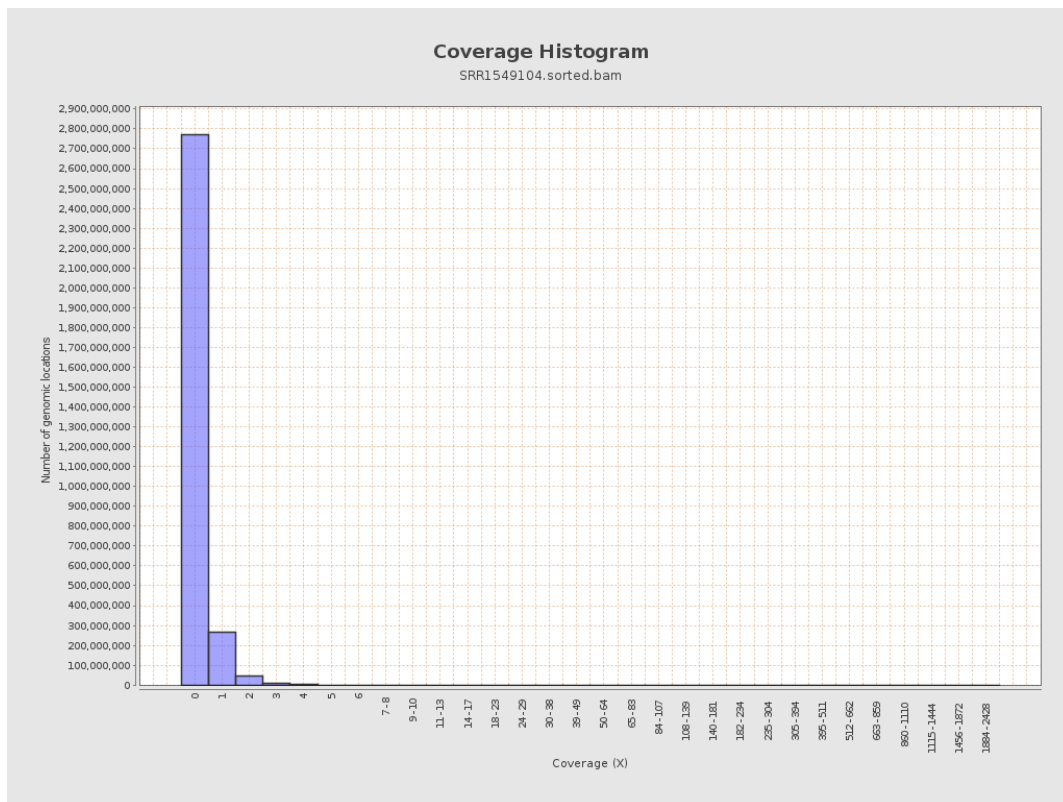
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31977441	0.1283	1.8143
chr2	243199373	35852289	0.1474	0.7872
chr3	198022430	29215359	0.1475	0.4649
chr4	191154276	29167563	0.1526	0.4753
chr5	180915260	26677004	0.1475	0.4781
chr6	171115067	24930212	0.1457	0.5549
chr7	159138663	23058661	0.1449	1.3216
chr8	146364022	21648000	0.1479	0.6947

chr9	141213431	17149790	0.1214	0.7469
chr10	135534747	18849650	0.1391	0.7114
chr11	135006516	18748427	0.1389	0.7725
chr12	133851895	18776545	0.1403	0.4907
chr13	115169878	14276770	0.124	0.4106
chr14	107349540	12621291	0.1176	0.5961
chr15	102531392	11346130	0.1107	0.3933
chr16	90354753	10090907	0.1117	0.4863
chr17	81195210	8850802	0.109	0.4593
chr18	78077248	11484393	0.1471	1.7333
chr19	59128983	6025896	0.1019	1.4501
chr20	63025520	7713903	0.1224	0.4745
chr21	48129895	5331316	0.1108	0.4931
chr22	51304566	3537277	0.0689	0.3401
chrMT	16571	53008	3.1988	4.2894
chrX	155270560	14006708	0.0902	0.5333
chrY	59373566	3142682	0.0529	0.4014

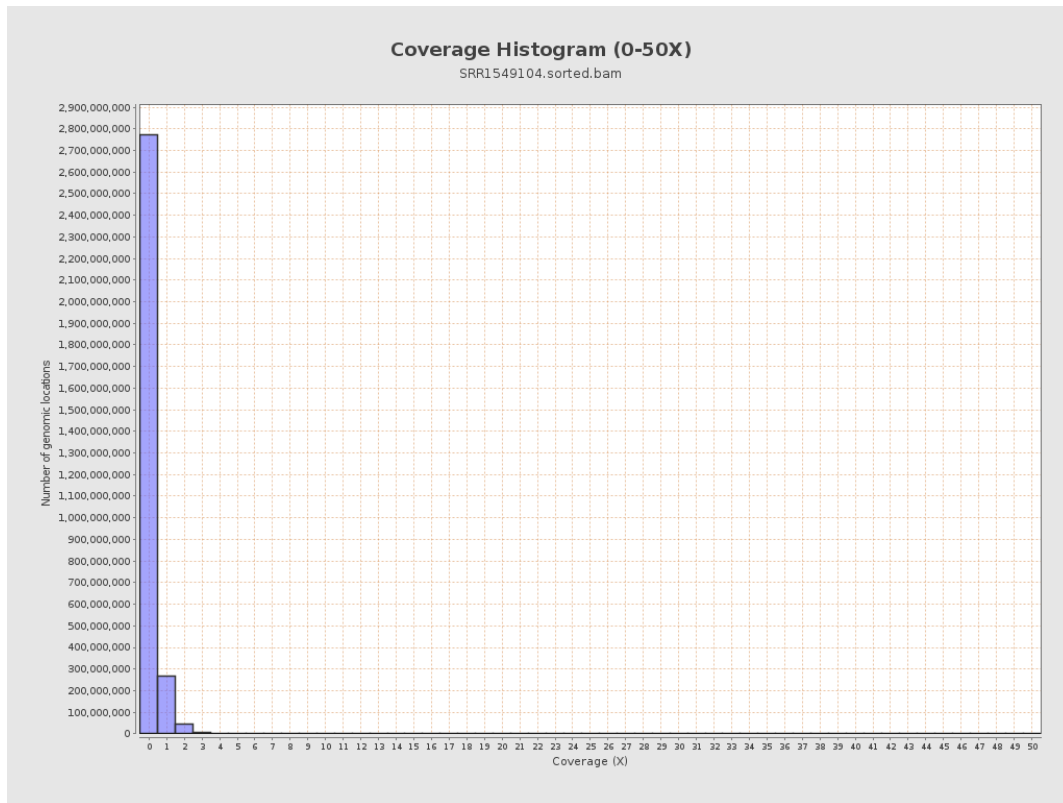
3. Results : Coverage across reference



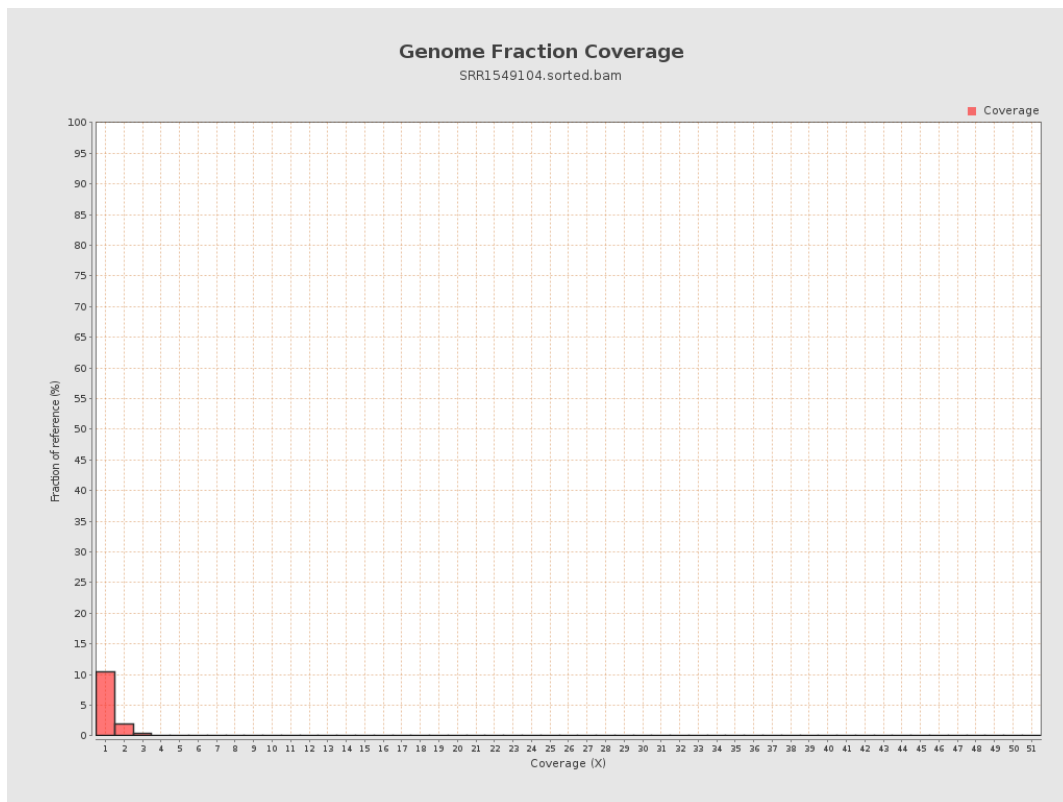
4. Results : Coverage Histogram



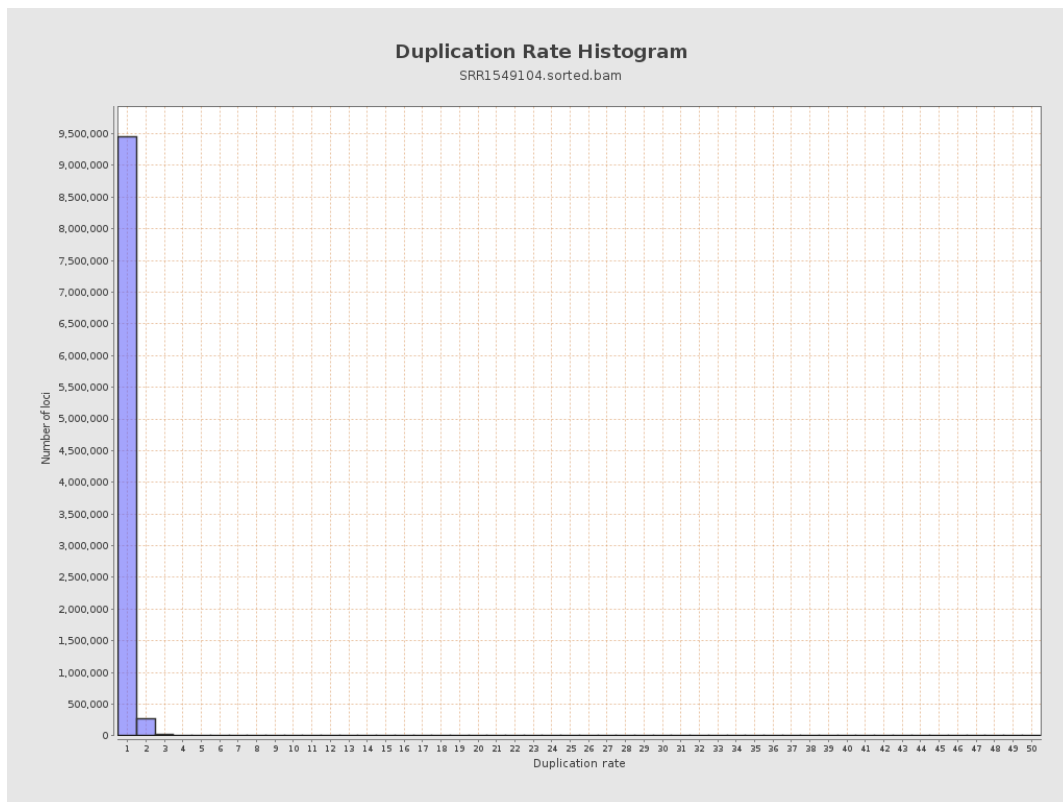
5. Results : Coverage Histogram (0-50X)



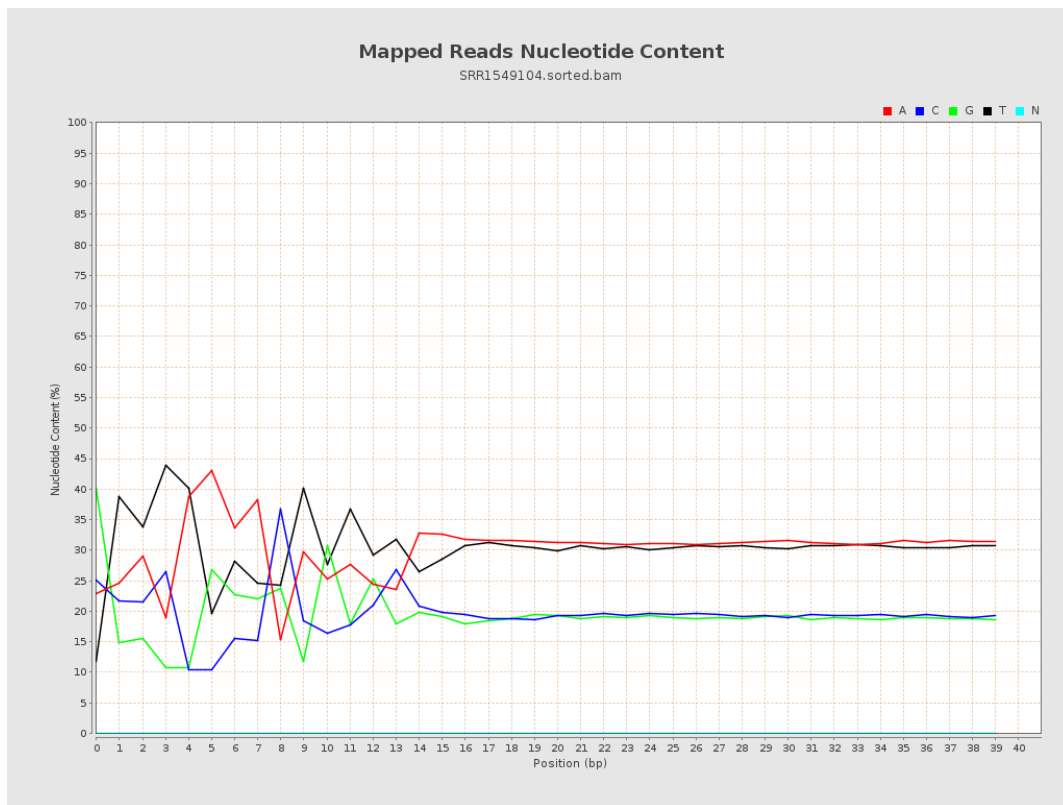
6. Results : Genome Fraction Coverage



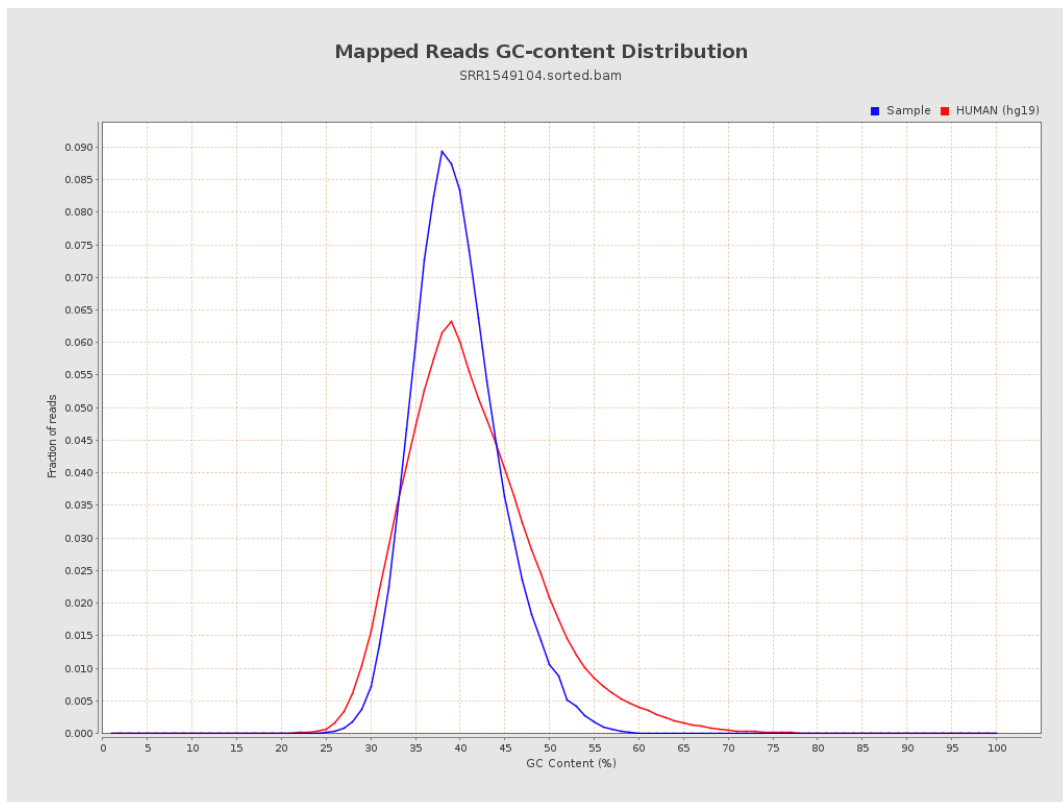
7. Results : Duplication Rate Histogram



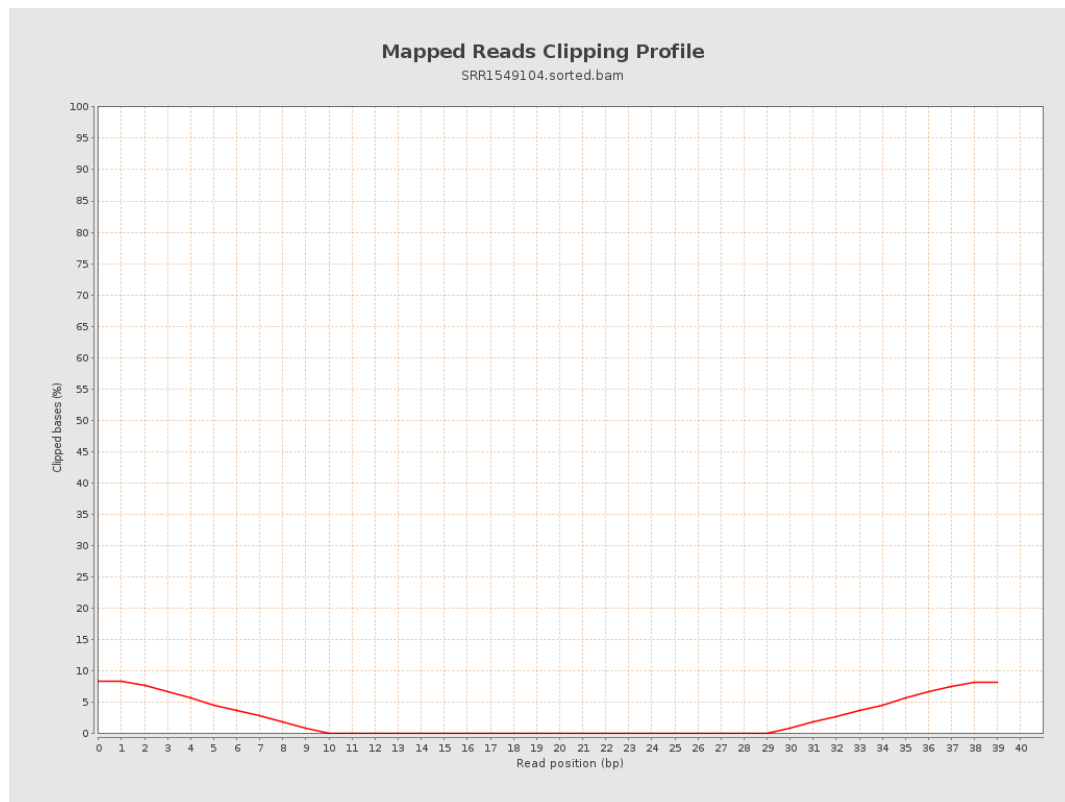
8. Results : Mapped Reads Nucleotide Content



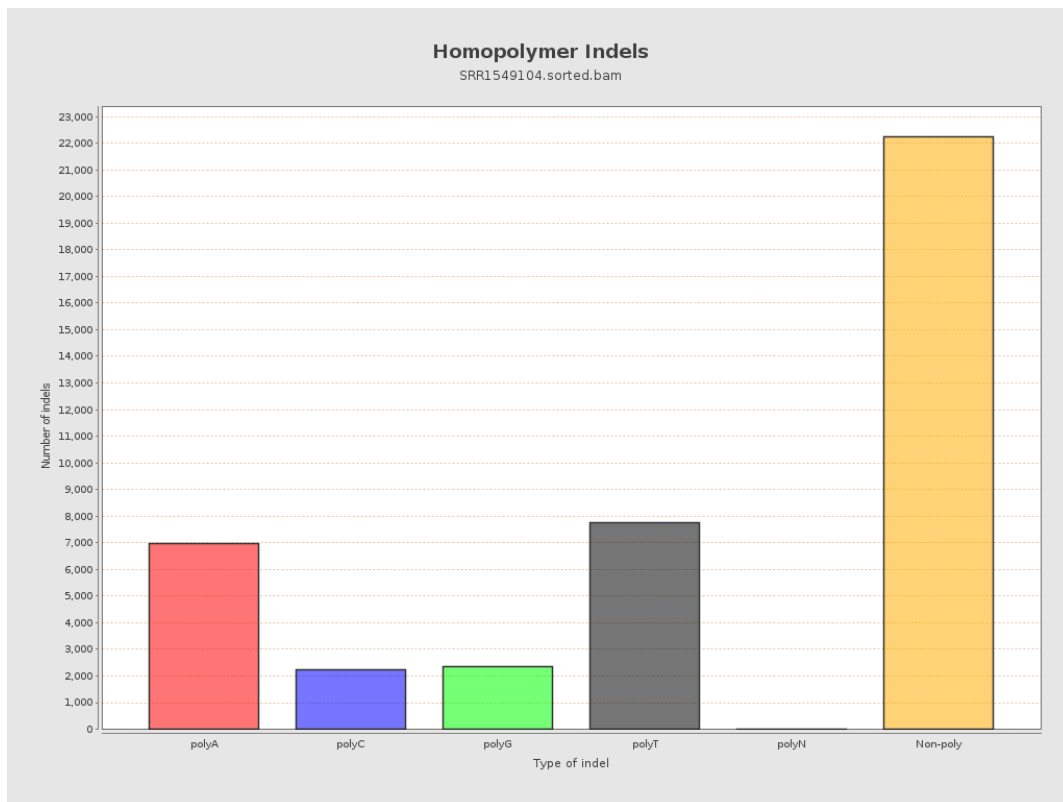
9. Results : Mapped Reads GC-content Distribution



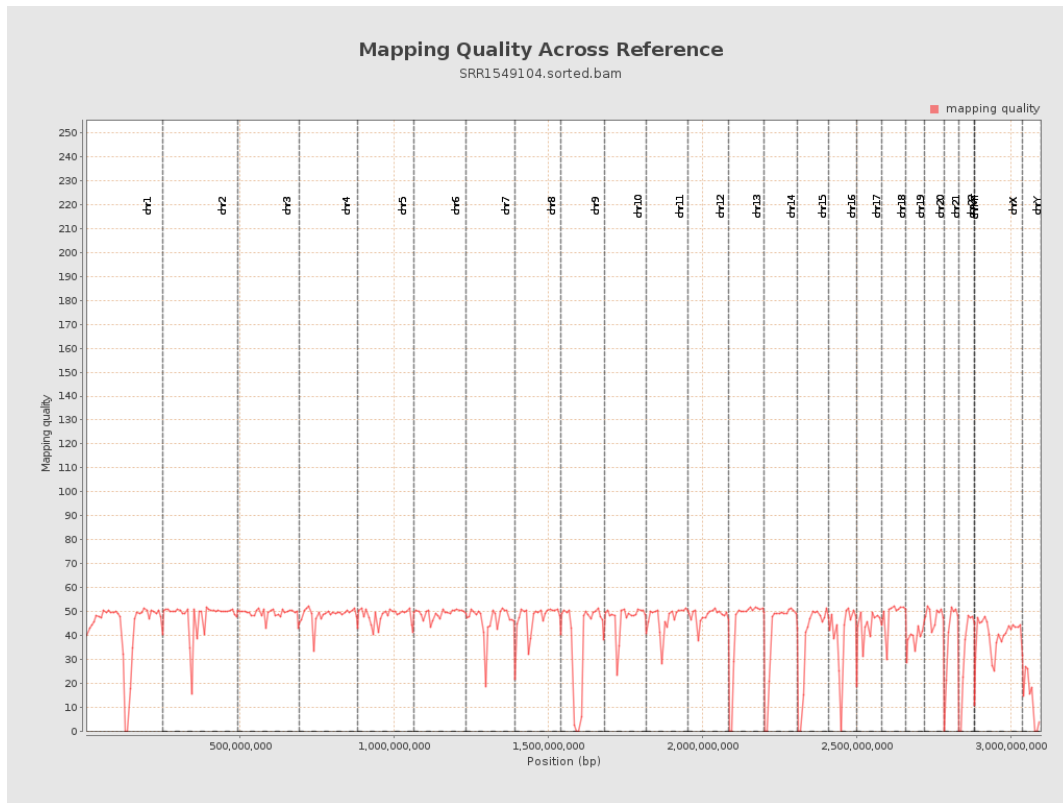
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

