Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:07:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549152.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_SRR1549152 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549152.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:07:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549152.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,547,033
Mapped reads	11,899,771 / 87.84%
Unmapped reads	1,647,262 / 12.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	714,532 / 5.27%
Duplication rate	4.76%
Clipped reads	677,715 / 5%

2.2. ACGT Content

Number/percentage of A's	133,058,648 / 28.2%
Number/percentage of C's	101,673,772 / 21.55%
Number/percentage of T's	135,014,009 / 28.61%
Number/percentage of G's	102,069,288 / 21.63%
Number/percentage of N's	96,269 / 0.02%
GC Percentage	43.17%

2.3. Coverage

Mean	0.1525
Standard Deviation	0.8892

2.4. Mapping Quality

Mean Mapping Quality	42.37

2.5. Mismatches and indels

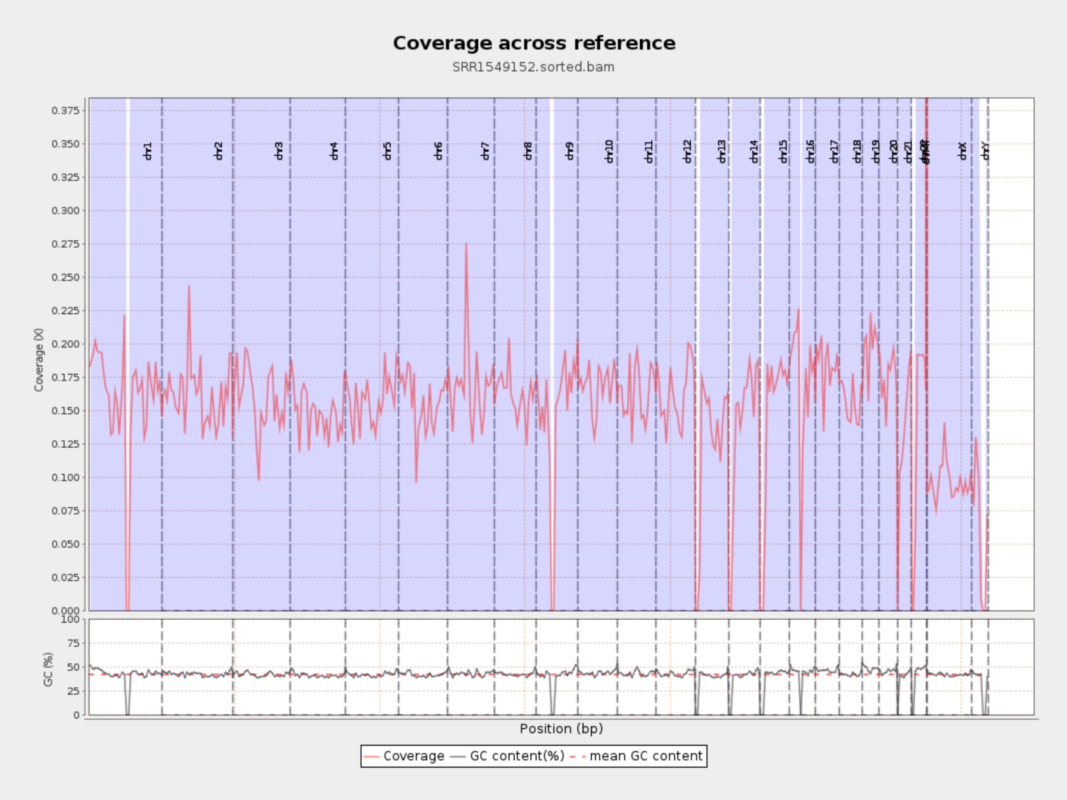
General error rate	0.32%
Mismatches	1,502,384
Insertions	12,896
Mapped reads with at least one insertion	0.11%
Deletions	37,853
Mapped reads with at least one deletion	0.32%
Homopolymer indels	46.09%

2.6. Chromosome stats

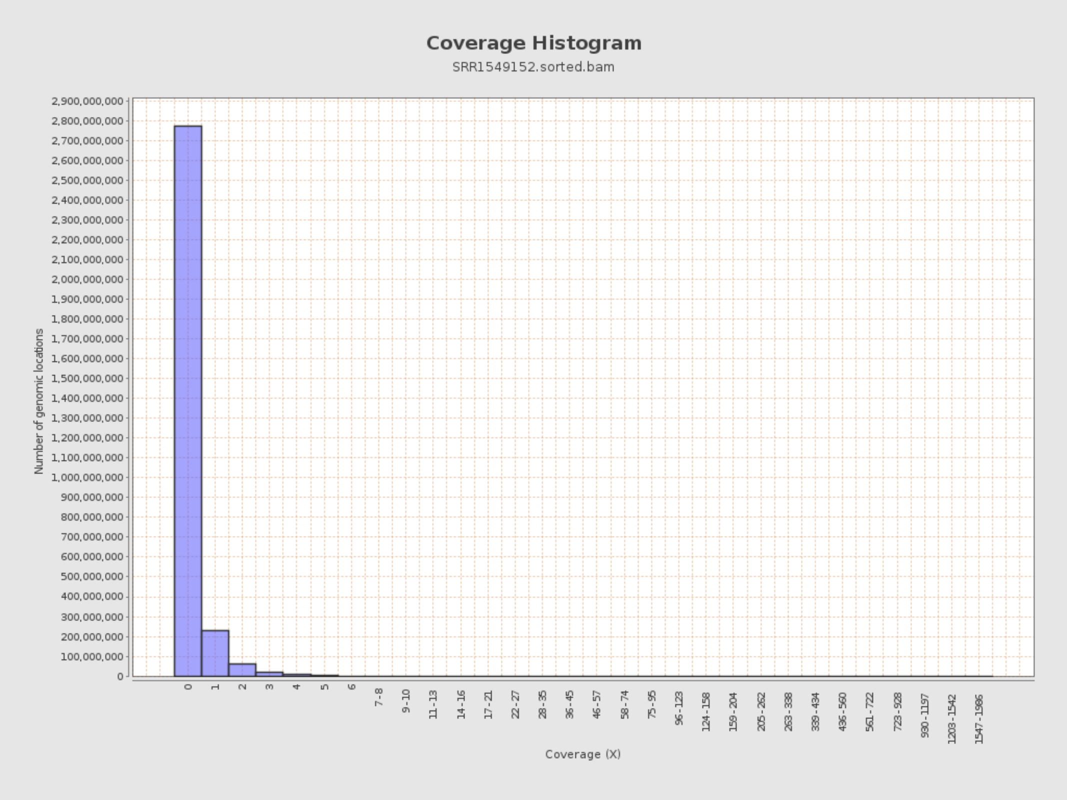
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39480283	0.1584	1.5433
chr2	243199373	39577673	0.1627	0.8622
chr3	198022430	31493052	0.159	0.5512
chr4	191154276	28337378	0.1482	0.5592
chr5	180915260	28501813	0.1575	0.5666
chr6	171115067	26859247	0.157	0.6376
chr7	159138663	26915226	0.1691	1.4626
chr8	146364022	23732648	0.1621	0.845

chr9	141213431	20317277	0.1439	0.8499
chr10	135534747	22741918	0.1678	0.8088
chr11	135006516	22000150	0.163	0.7769
chr12	133851895	21810457	0.1629	0.5945
chr13	115169878	14094522	0.1224	0.4751
chr14	107349540	14662813	0.1366	0.7218
chr15	102531392	14670537	0.1431	0.5161
chr16	90354753	15345130	0.1698	0.6337
chr17	81195210	14925432	0.1838	0.6532
chr18	78077248	12204868	0.1563	1.7394
chr19	59128983	11680479	0.1975	1.4235
chr20	63025520	11007302	0.1746	0.6242
chr21	48129895	6304776	0.131	0.6063
chr22	51304566	6671248	0.13	0.5424
chrMT	16571	167018	10.0789	13.6676
chrX	155270560	14991029	0.0965	0.5679
chrY	59373566	3467610	0.0584	0.4393

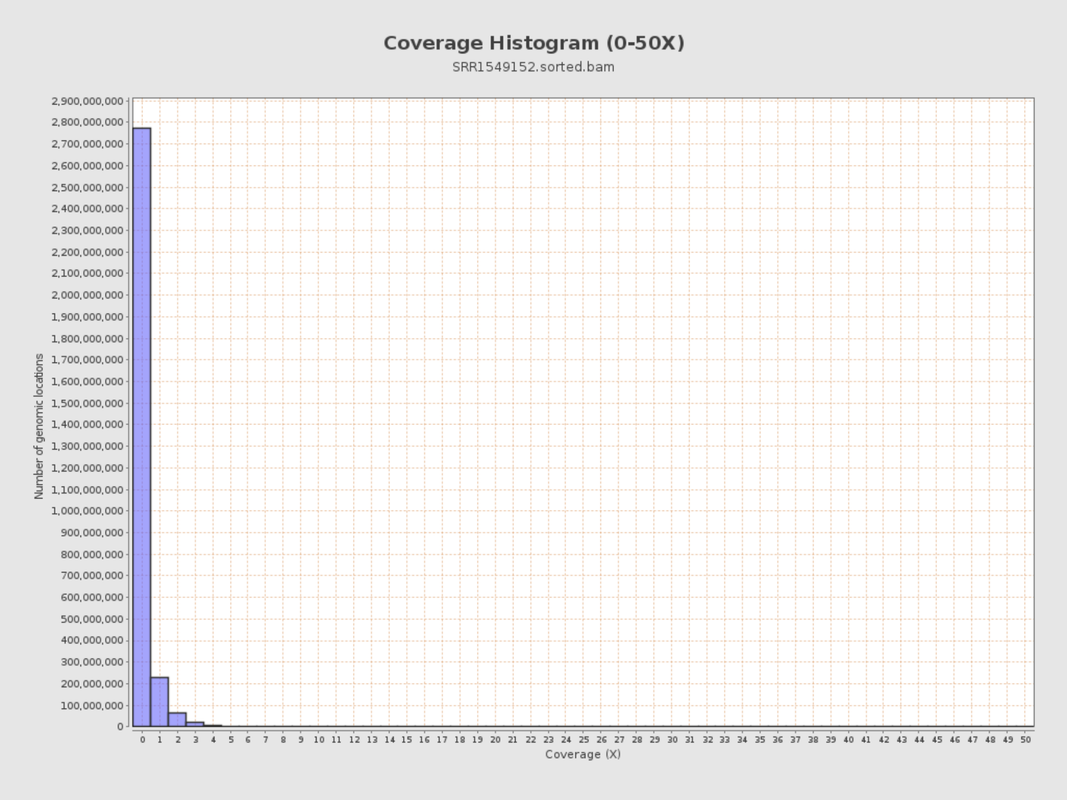
3. Results : Coverage across reference



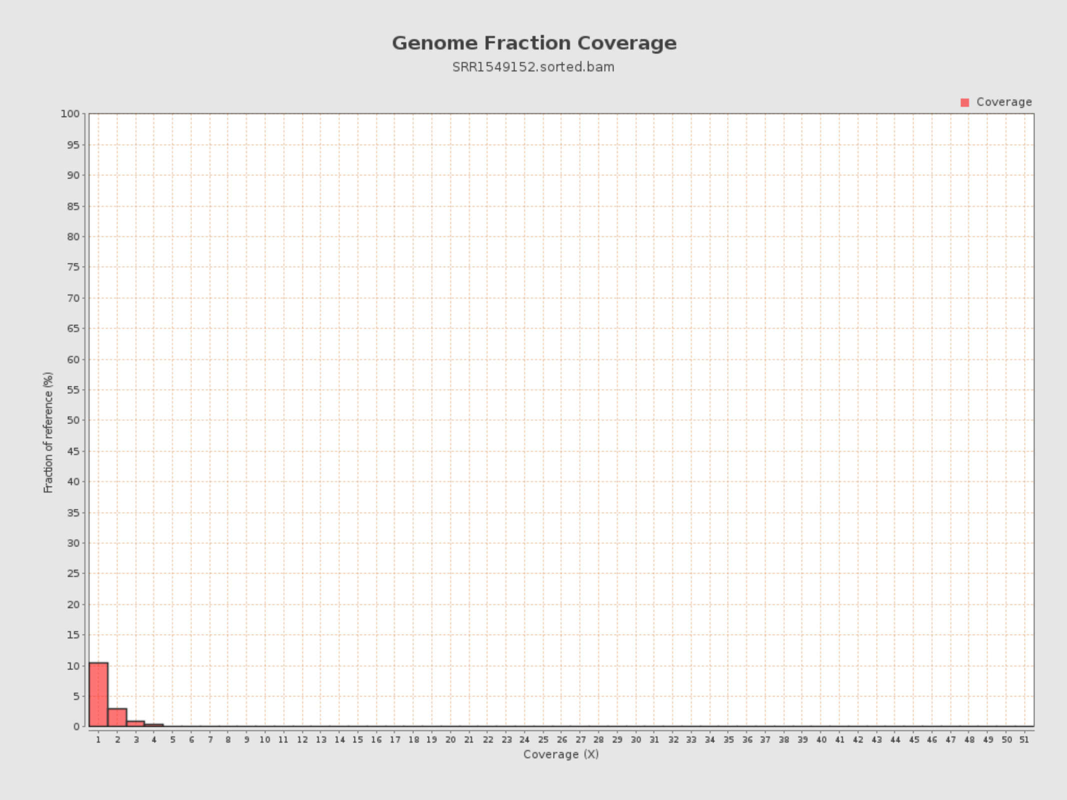
4. Results : Coverage Histogram



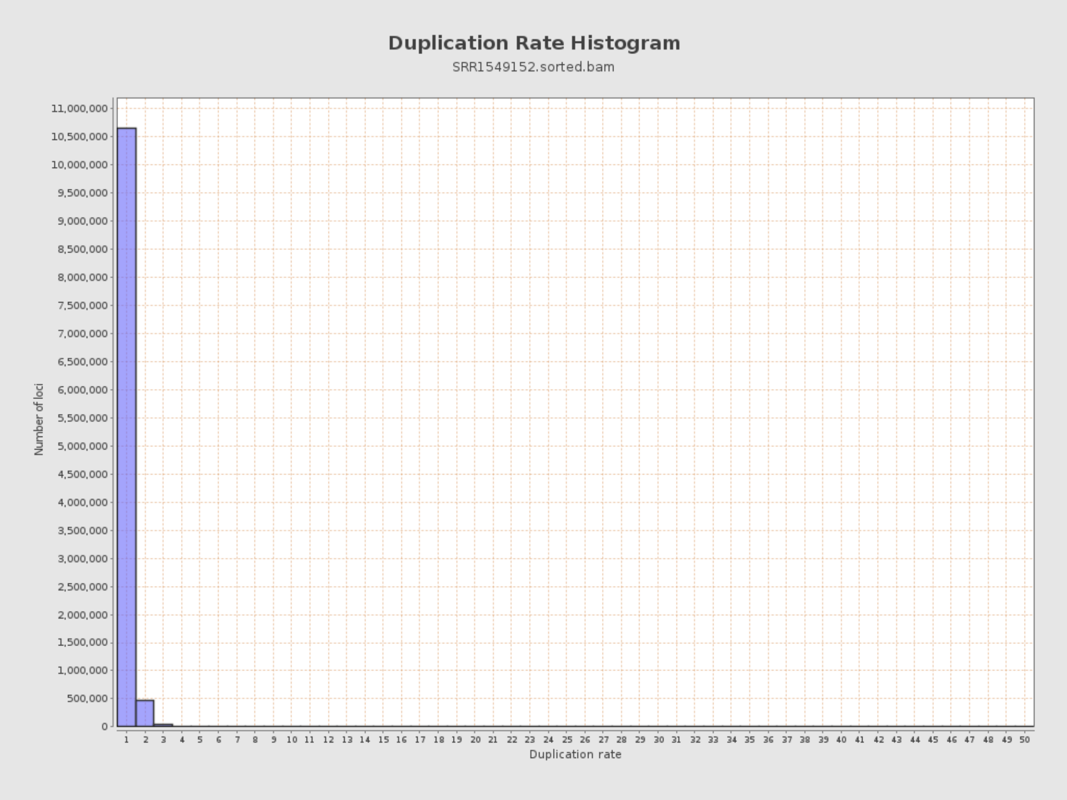
5. Results : Coverage Histogram (0-50X)



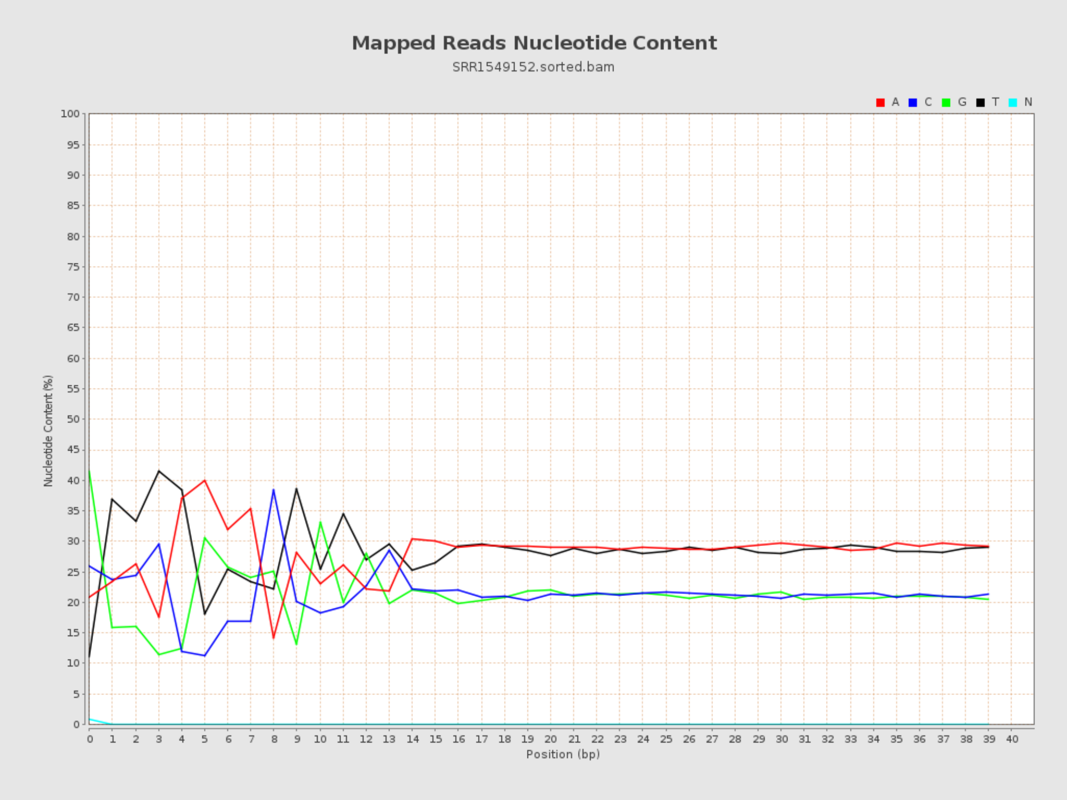
6. Results : Genome Fraction Coverage



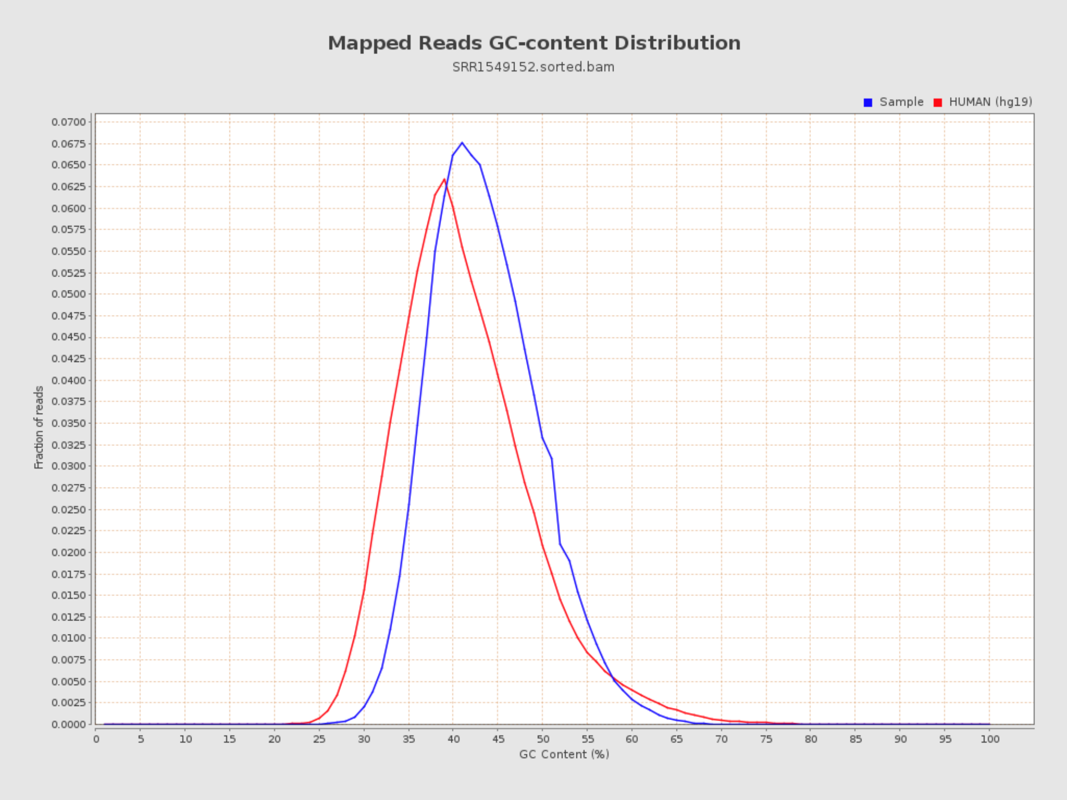
7. Results : Duplication Rate Histogram



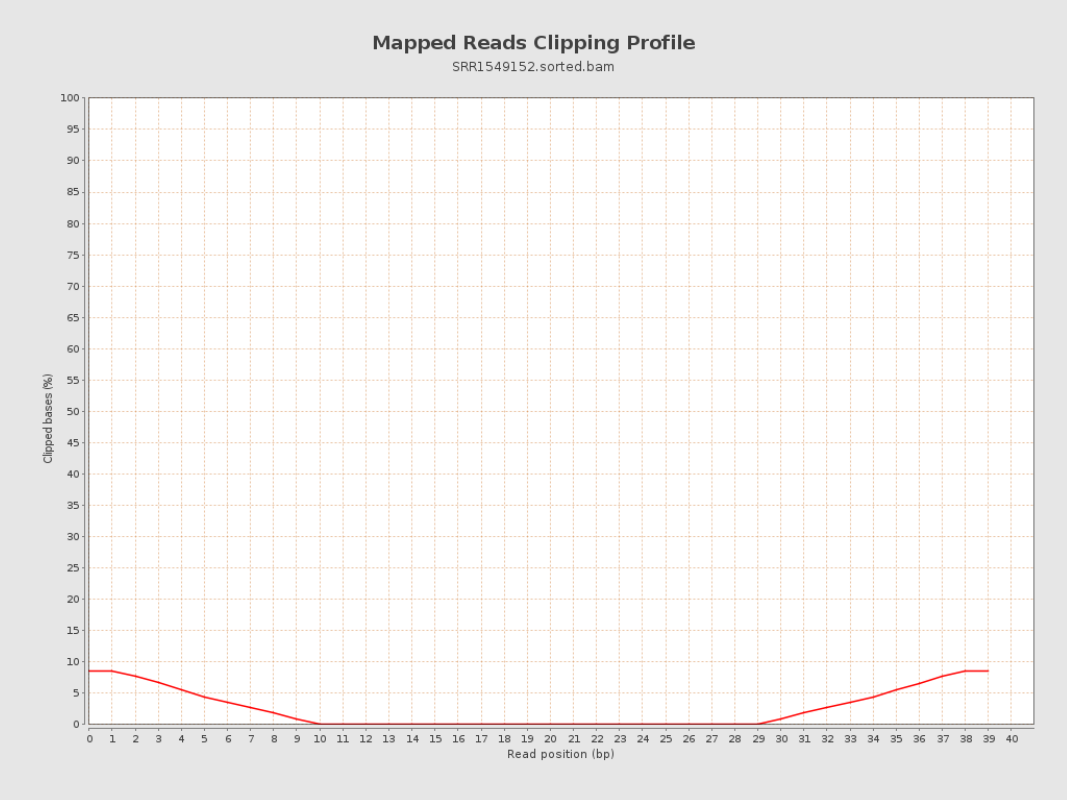
8. Results : Mapped Reads Nucleotide Content



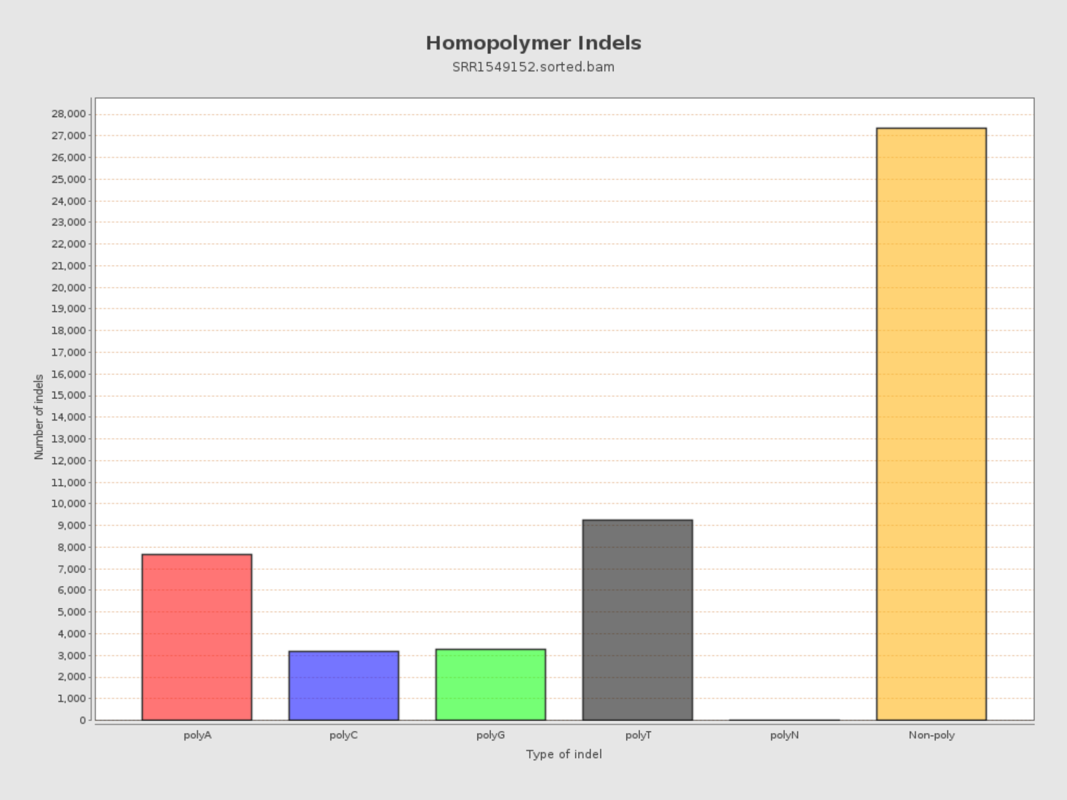
9. Results : Mapped Reads GC-content Distribution



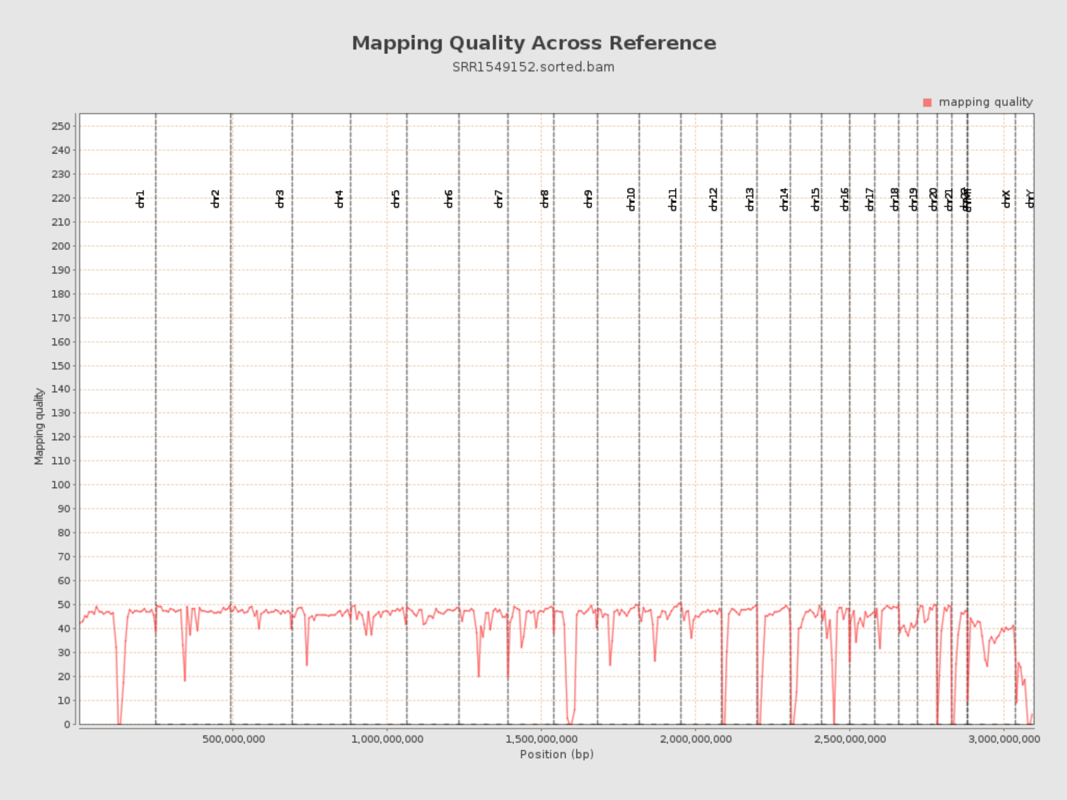
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram