Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:45:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085014.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_SRR3085014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:45:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,234,303
Mapped reads	1,989,544 / 89.05%
Unmapped reads	244,759 / 10.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,018 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	57,220 / 2.56%
Duplication rate	2.35%
Clipped reads	938,428 / 42%

2.2. ACGT Content

Number/percentage of A's	35,920,782 / 27.24%
Number/percentage of C's	26,421,502 / 20.04%
Number/percentage of T's	39,331,026 / 29.83%
Number/percentage of G's	30,170,654 / 22.88%
Number/percentage of N's	6,544 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.2952

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

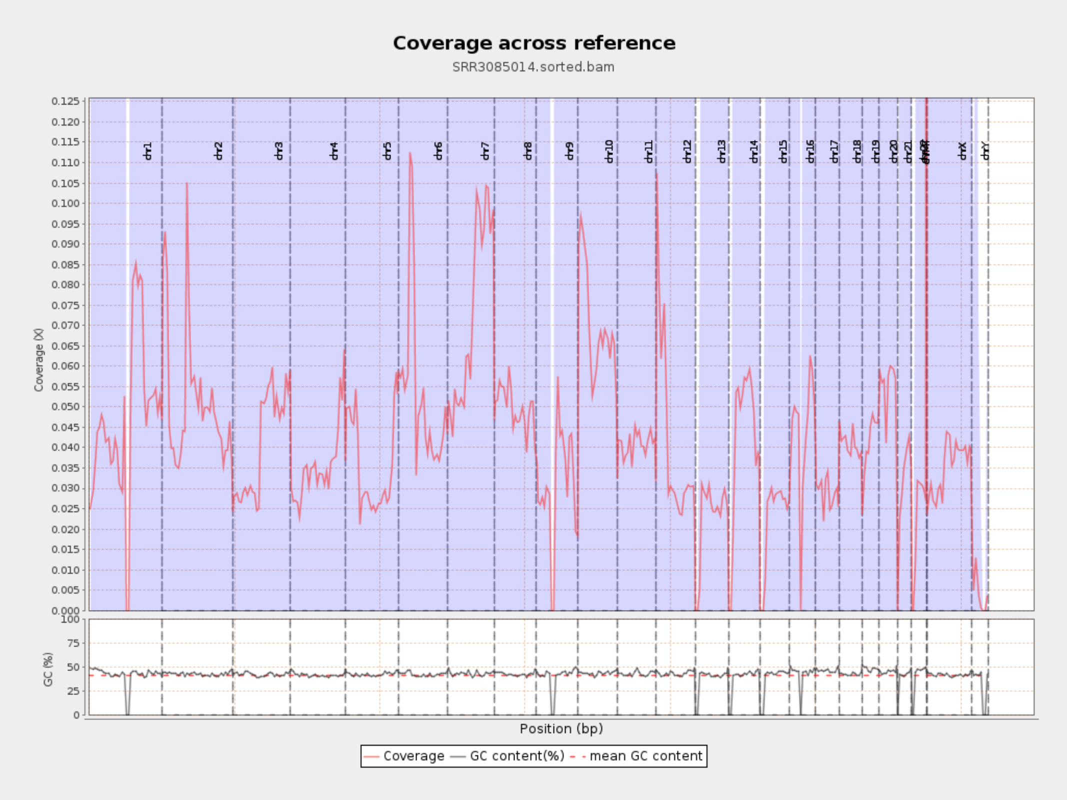
General error rate	0.99%
Mismatches	1,291,057
Insertions	9,142
Mapped reads with at least one insertion	0.46%
Deletions	31,817
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.34%

2.6. Chromosome stats

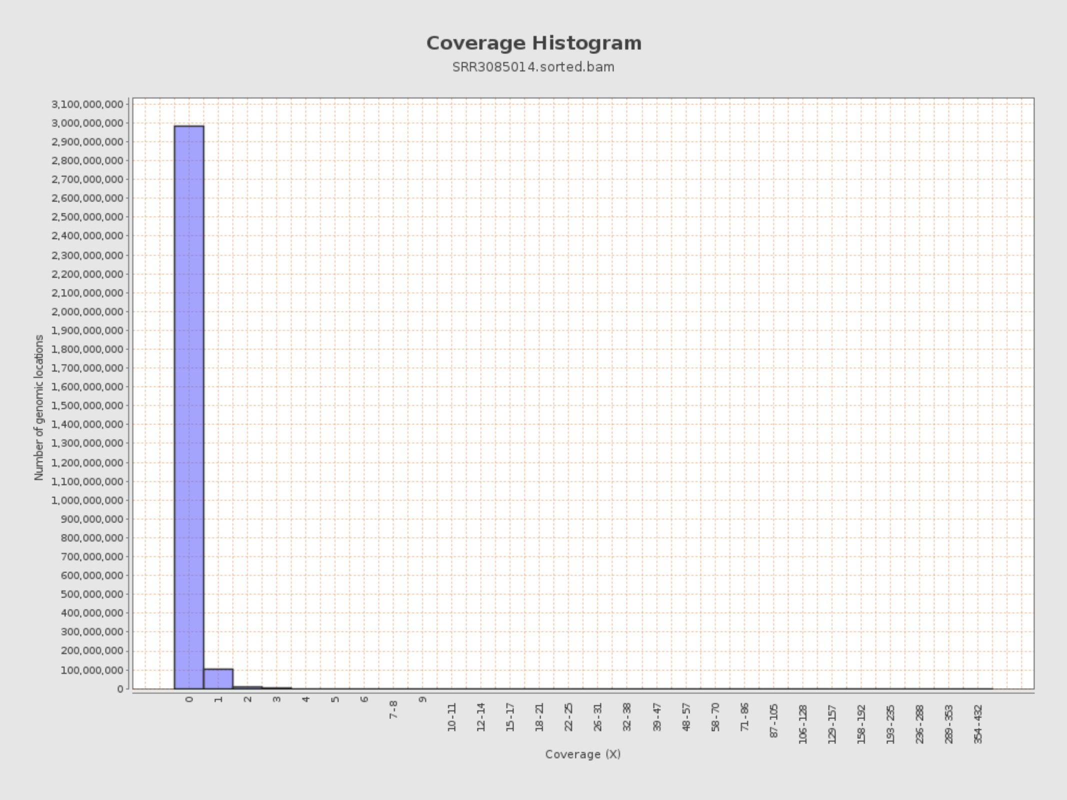
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11669063	0.0468	0.3445
chr2	243199373	12652810	0.052	0.3887
chr3	198022430	8052291	0.0407	0.2244
chr4	191154276	6805758	0.0356	0.2164
chr5	180915260	6418070	0.0355	0.2094
chr6	171115067	9215188	0.0539	0.3366
chr7	159138663	11614515	0.073	0.4115

chr8	146364022	7288966	0.0498	0.3692
chr9	141213431	4327876	0.0306	0.2575
chr10	135534747	9628852	0.071	0.3469
chr11	135006516	5499212	0.0407	0.3676
chr12	133851895	5576256	0.0417	0.2319
chr13	115169878	2618259	0.0227	0.1653
chr14	107349540	4523254	0.0421	0.2351
chr15	102531392	2297120	0.0224	0.1741
chr16	90354753	3975301	0.044	0.2396
chr17	81195210	2348607	0.0289	0.2276
chr18	78077248	3198221	0.041	0.4477
chr19	59128983	2468696	0.0418	0.2997
chr20	63025520	3447173	0.0547	0.2626
chr21	48129895	1479698	0.0307	0.2071
chr22	51304566	1093324	0.0213	0.1606
chrMT	16571	13510	0.8153	1.112
chrX	155270560	5440026	0.035	0.2241
chrY	59373566	255975	0.0043	0.0981

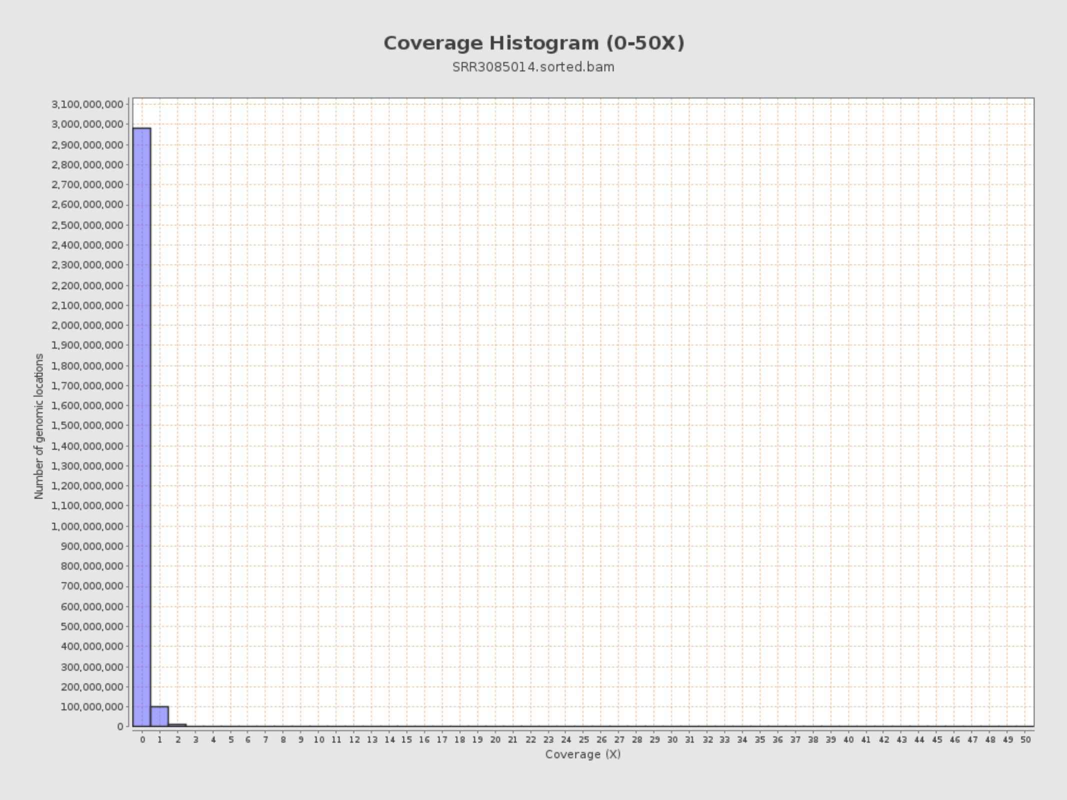
3. Results : Coverage across reference



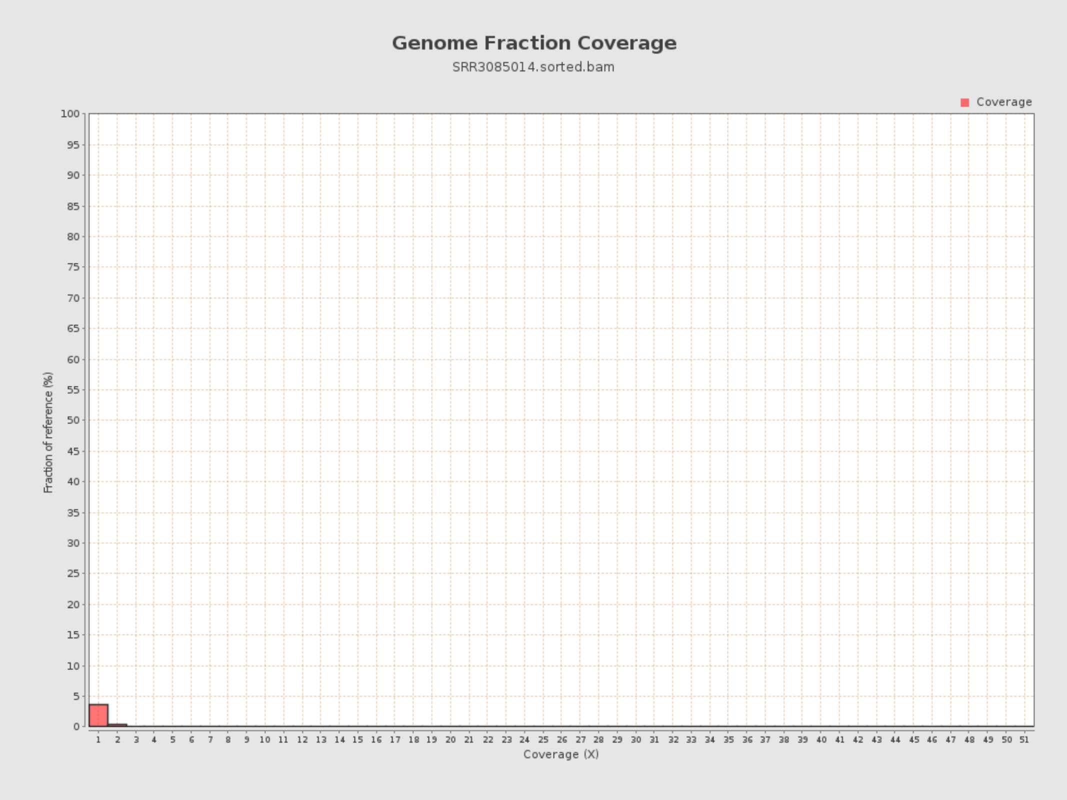
4. Results : Coverage Histogram



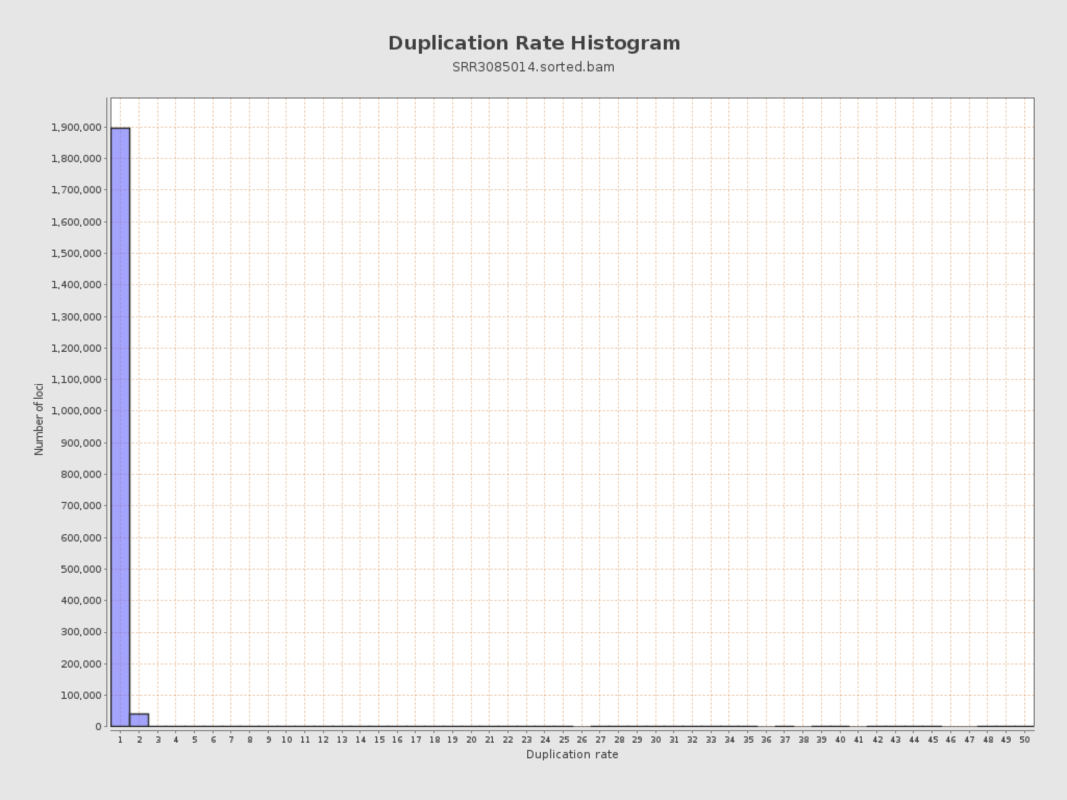
5. Results : Coverage Histogram (0-50X)



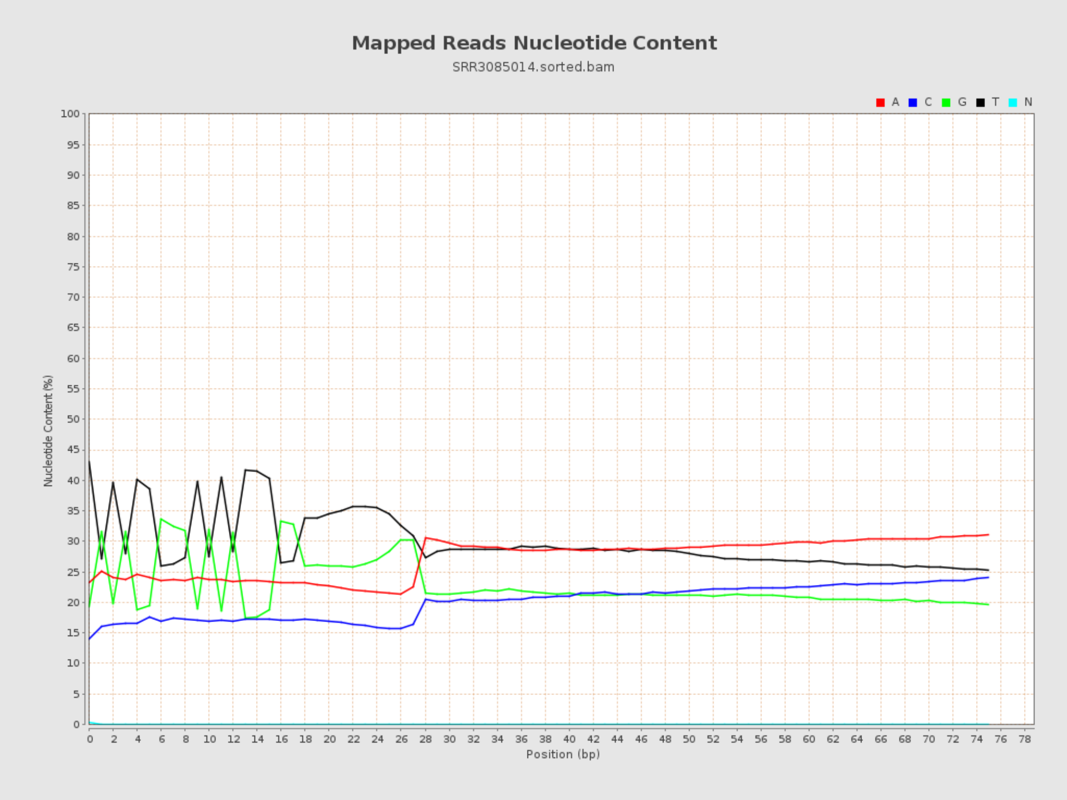
6. Results : Genome Fraction Coverage



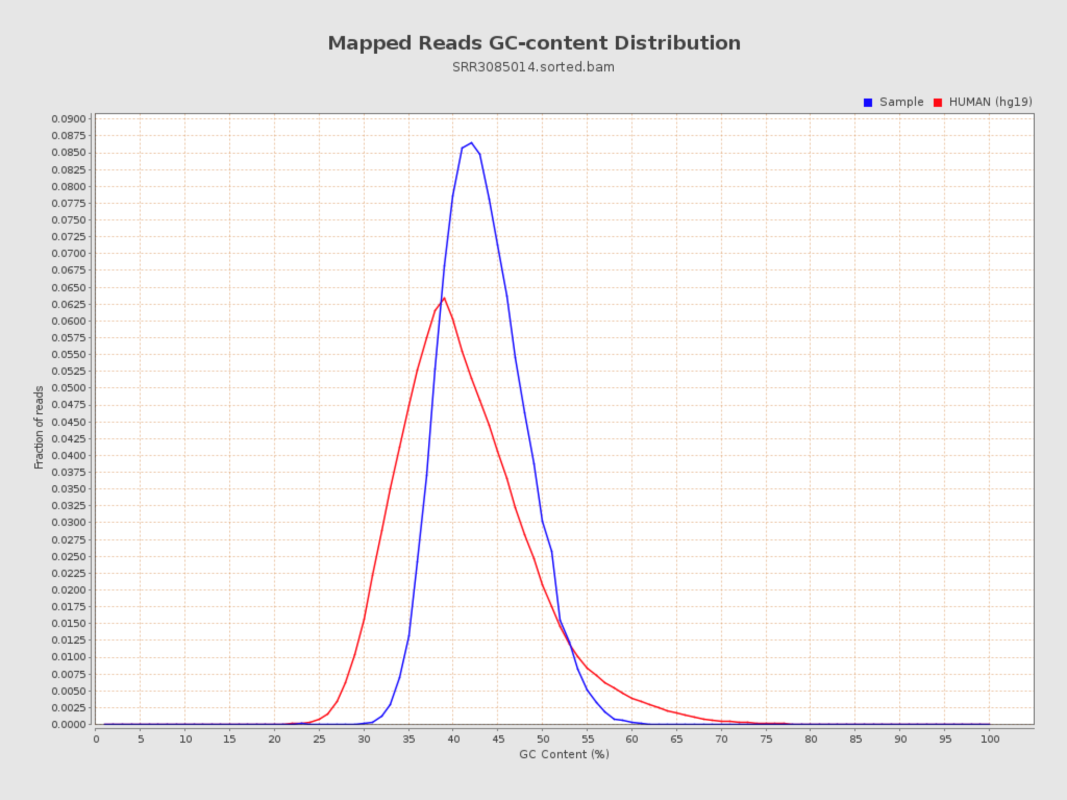
7. Results : Duplication Rate Histogram



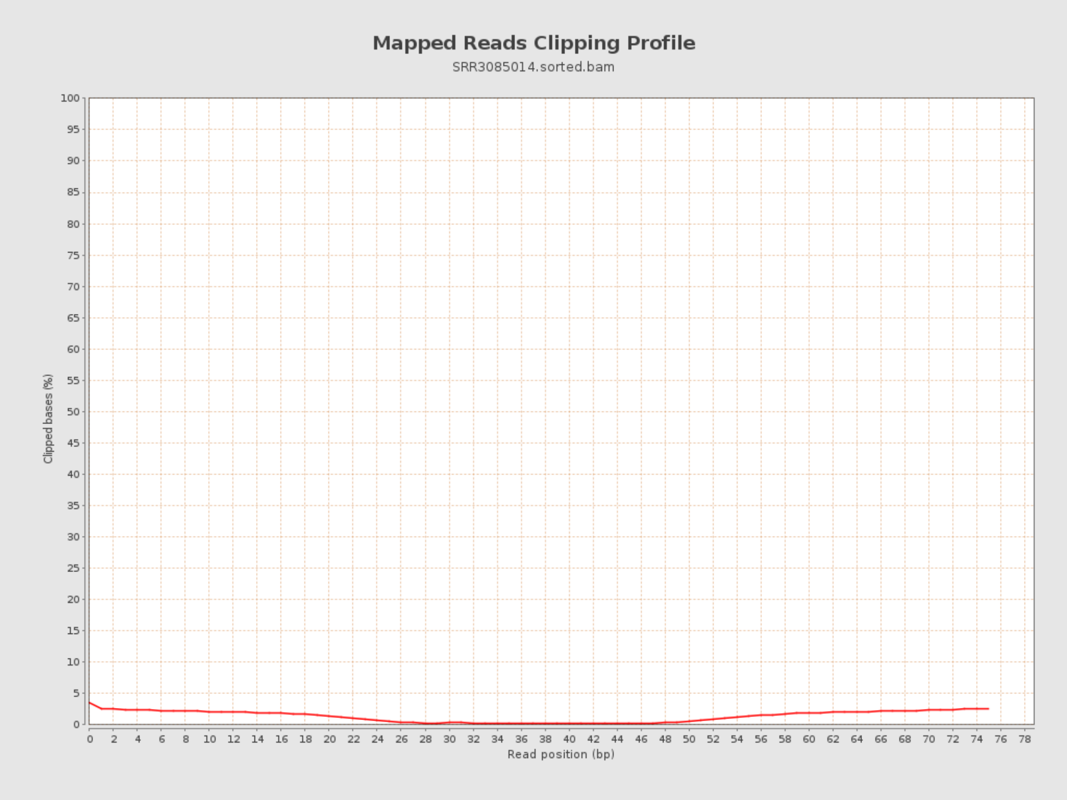
8. Results : Mapped Reads Nucleotide Content



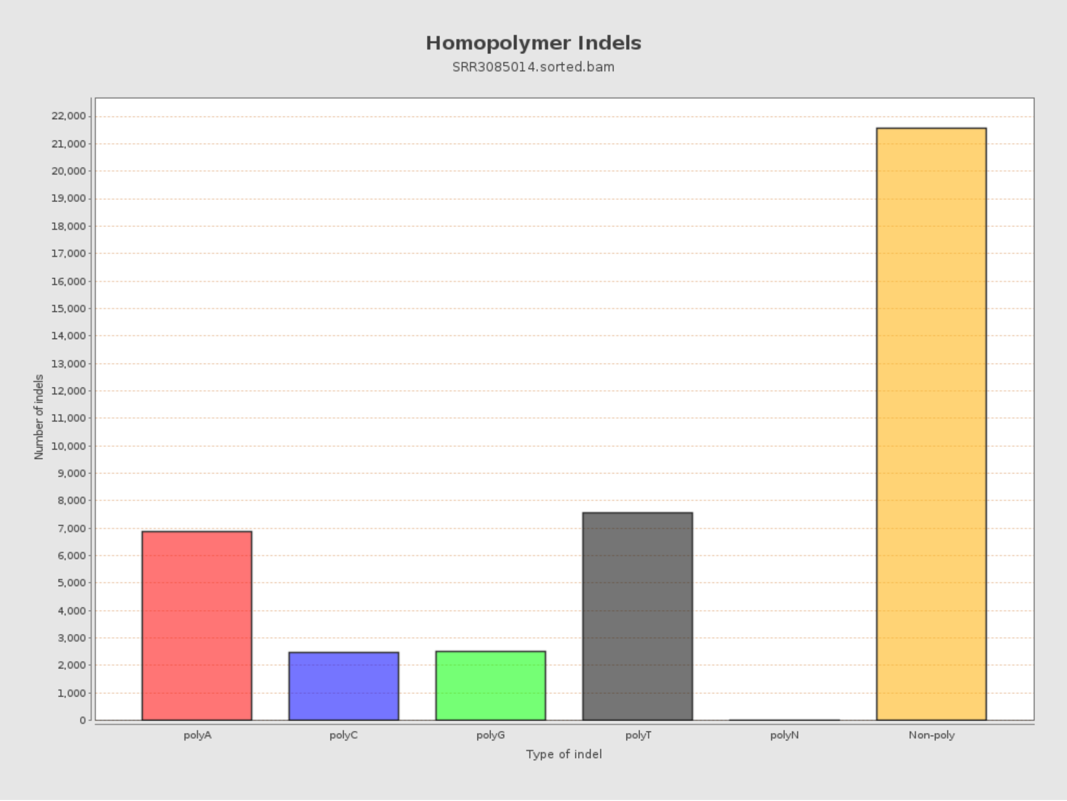
9. Results : Mapped Reads GC-content Distribution



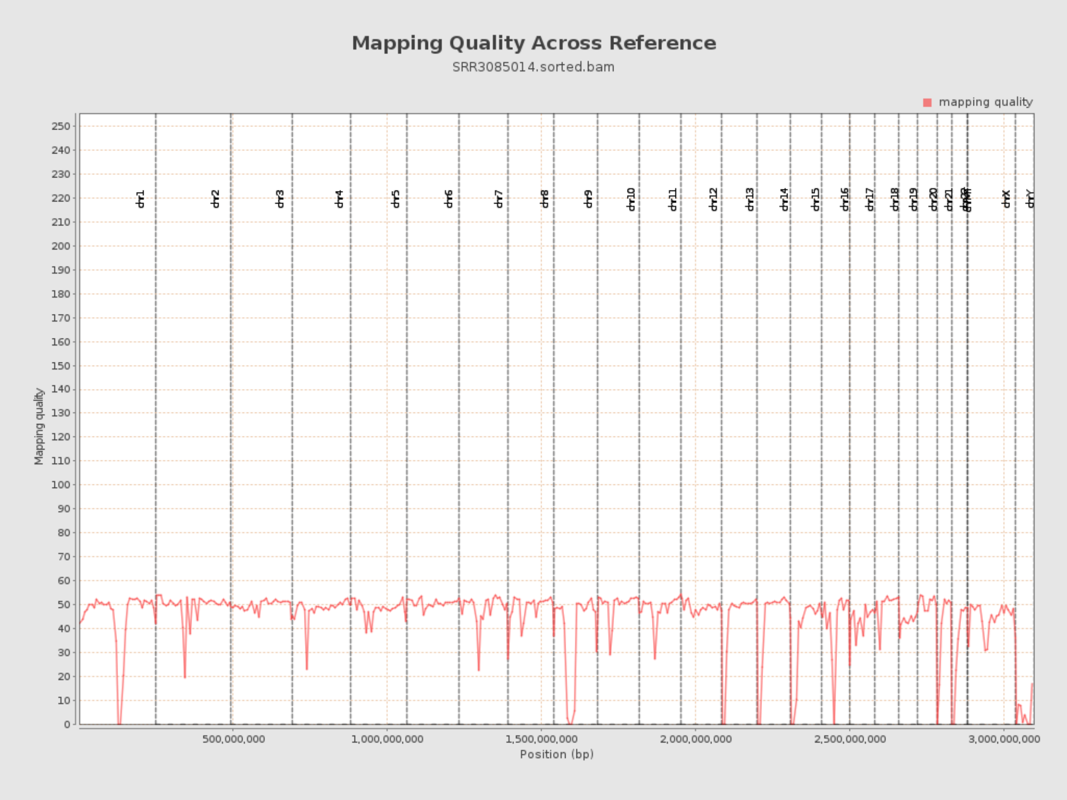
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram