Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:45:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085099.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_SRR3085099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:45:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,425,781
Mapped reads	1,112,649 / 78.04%
Unmapped reads	313,132 / 21.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,553 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	22,132 / 1.55%
Duplication rate	1.59%
Clipped reads	605,025 / 42.43%

2.2. ACGT Content

Number/percentage of A's	21,585,991 / 30.11%
Number/percentage of C's	13,416,608 / 18.72%
Number/percentage of T's	20,861,474 / 29.1%
Number/percentage of G's	15,816,773 / 22.07%
Number/percentage of N's	1,555 / 0%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2066

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

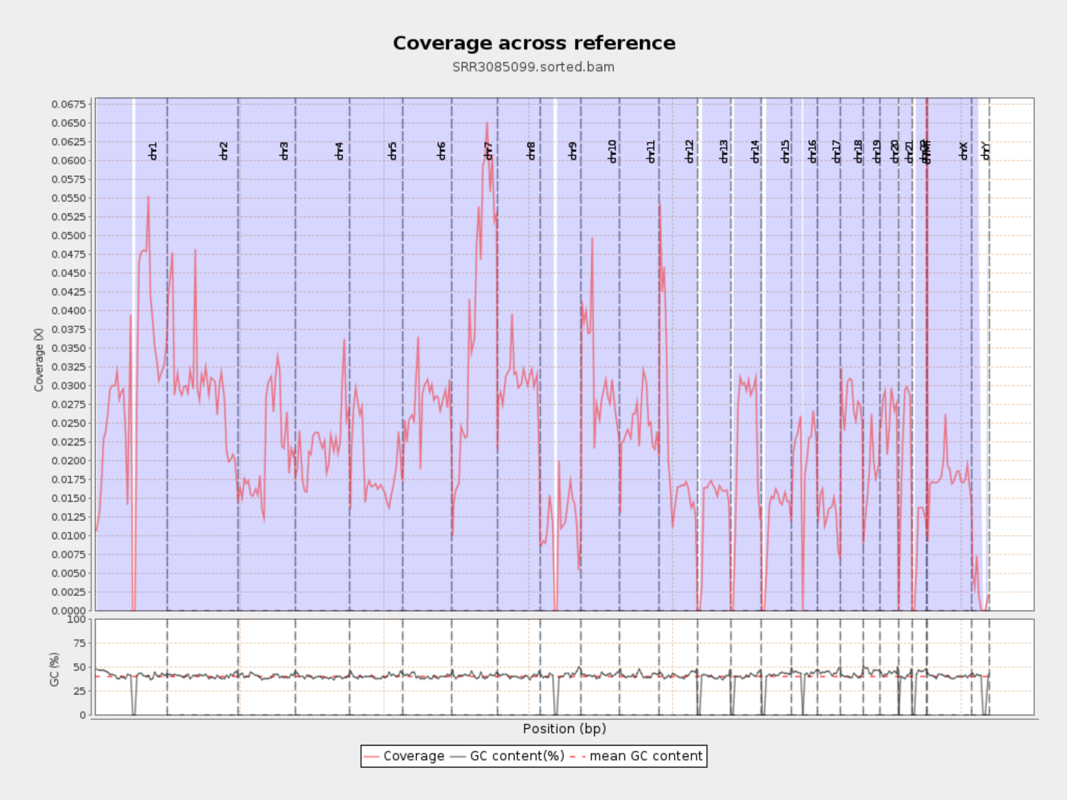
General error rate	0.93%
Mismatches	656,544
Insertions	5,598
Mapped reads with at least one insertion	0.5%
Deletions	15,905
Mapped reads with at least one deletion	1.41%
Homopolymer indels	45.87%

2.6. Chromosome stats

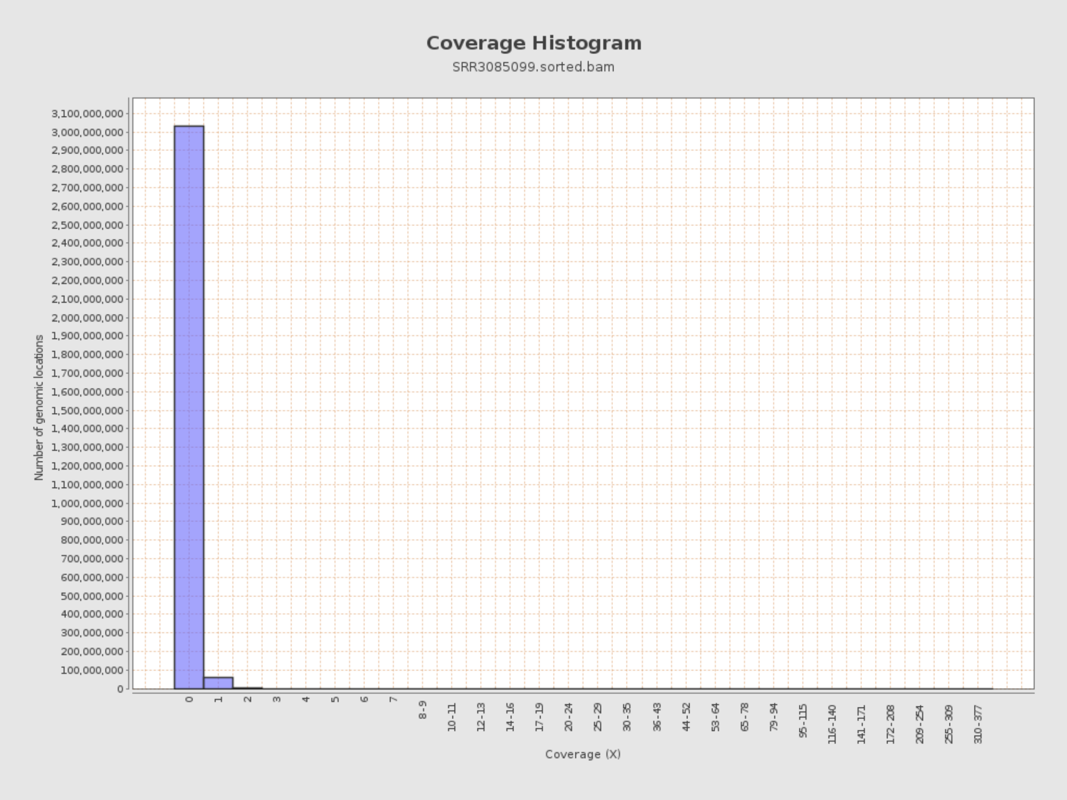
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7442329	0.0299	0.3242
chr2	243199373	7313201	0.0301	0.239
chr3	198022430	4210006	0.0213	0.1547
chr4	191154276	4264913	0.0223	0.1589
chr5	180915260	3508507	0.0194	0.1457
chr6	171115067	4712696	0.0275	0.1933
chr7	159138663	6301059	0.0396	0.2562

chr8	146364022	4486822	0.0307	0.2934
chr9	141213431	1546917	0.011	0.153
chr10	135534747	4283870	0.0316	0.2789
chr11	135006516	3341647	0.0248	0.2121
chr12	133851895	2936022	0.0219	0.1569
chr13	115169878	1547233	0.0134	0.1204
chr14	107349540	2385586	0.0222	0.1597
chr15	102531392	1233879	0.012	0.1142
chr16	90354753	1822975	0.0202	0.1581
chr17	81195210	1038103	0.0128	0.1289
chr18	78077248	2177933	0.0279	0.2848
chr19	59128983	1079192	0.0183	0.2182
chr20	63025520	1629708	0.0259	0.1716
chr21	48129895	1055996	0.0219	0.1592
chr22	51304566	475069	0.0093	0.1001
chrMT	16571	2598	0.1568	0.3917
chrX	155270560	2772378	0.0179	0.1511
chrY	59373566	139502	0.0023	0.0601

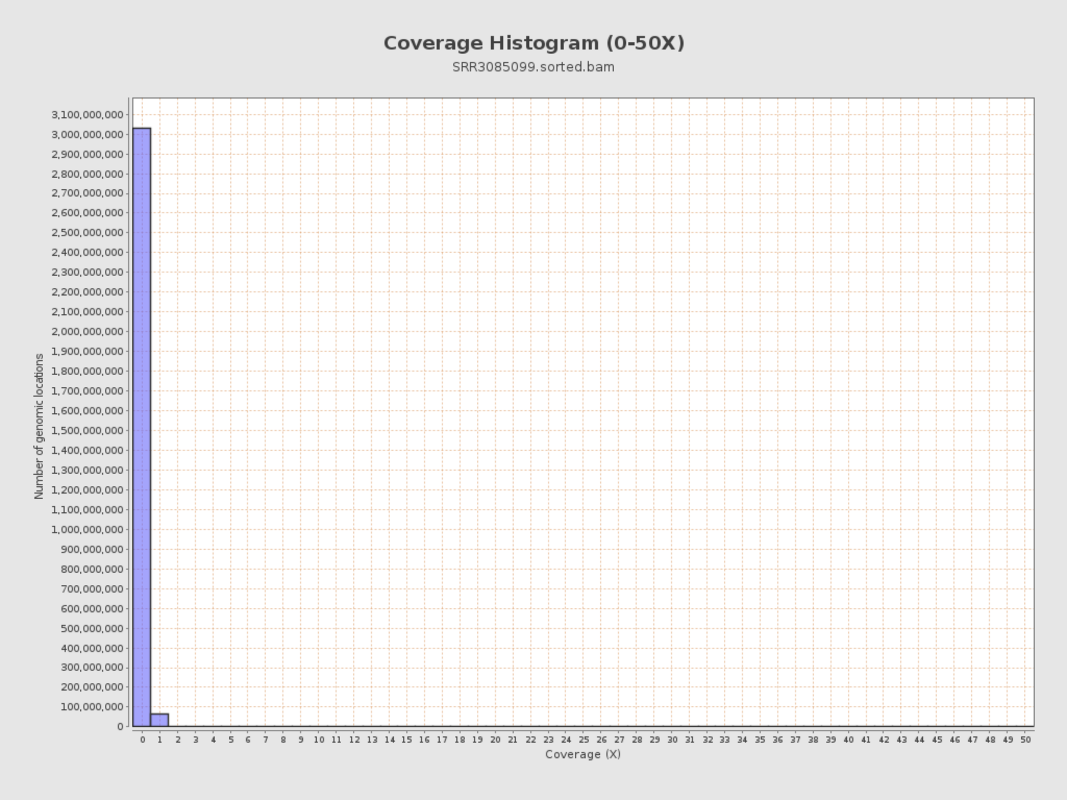
3. Results : Coverage across reference



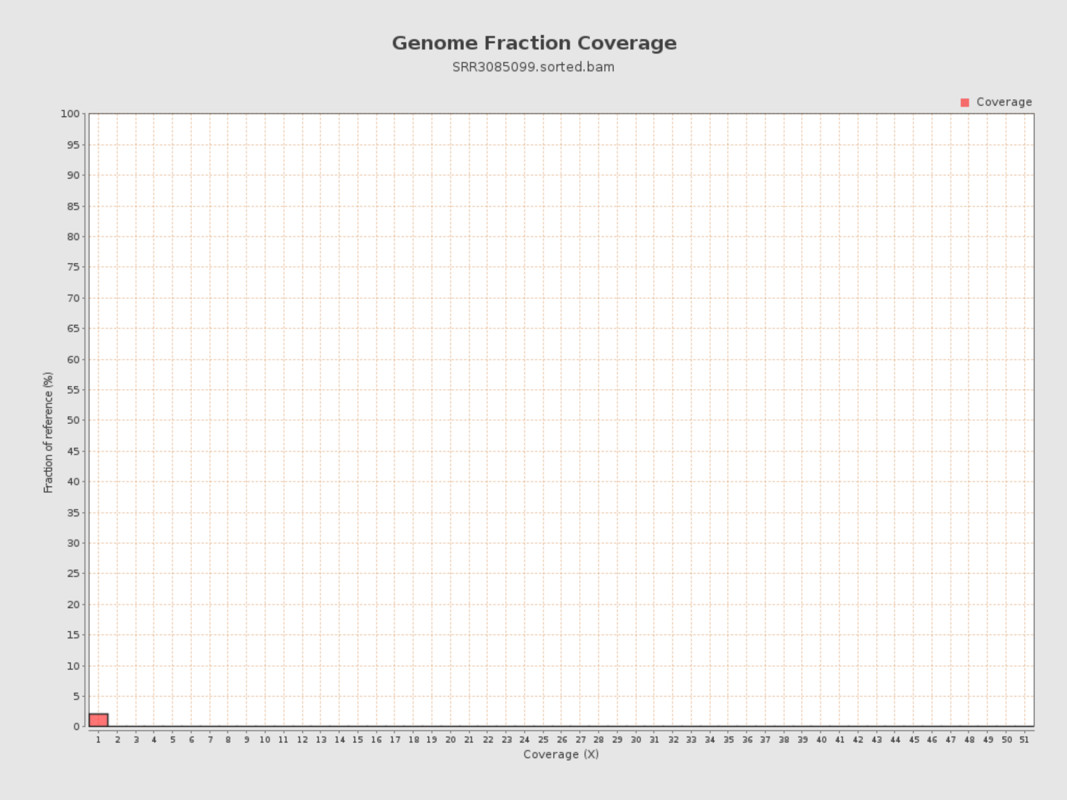
4. Results : Coverage Histogram



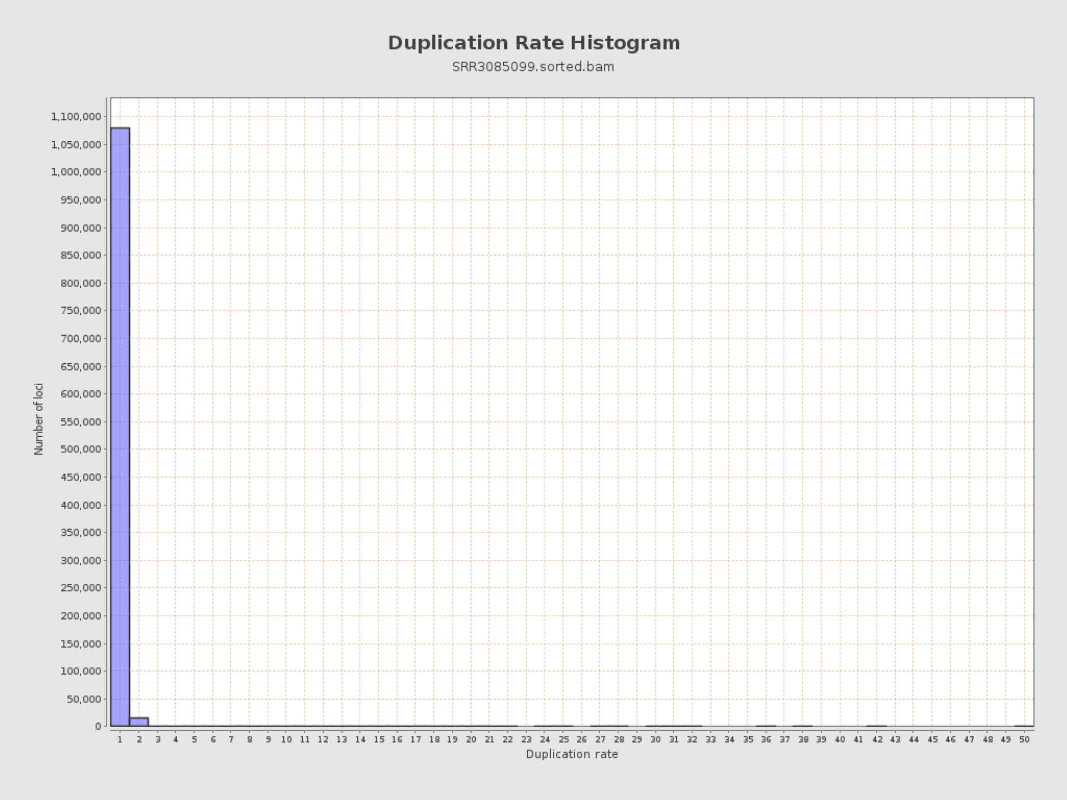
5. Results : Coverage Histogram (0-50X)



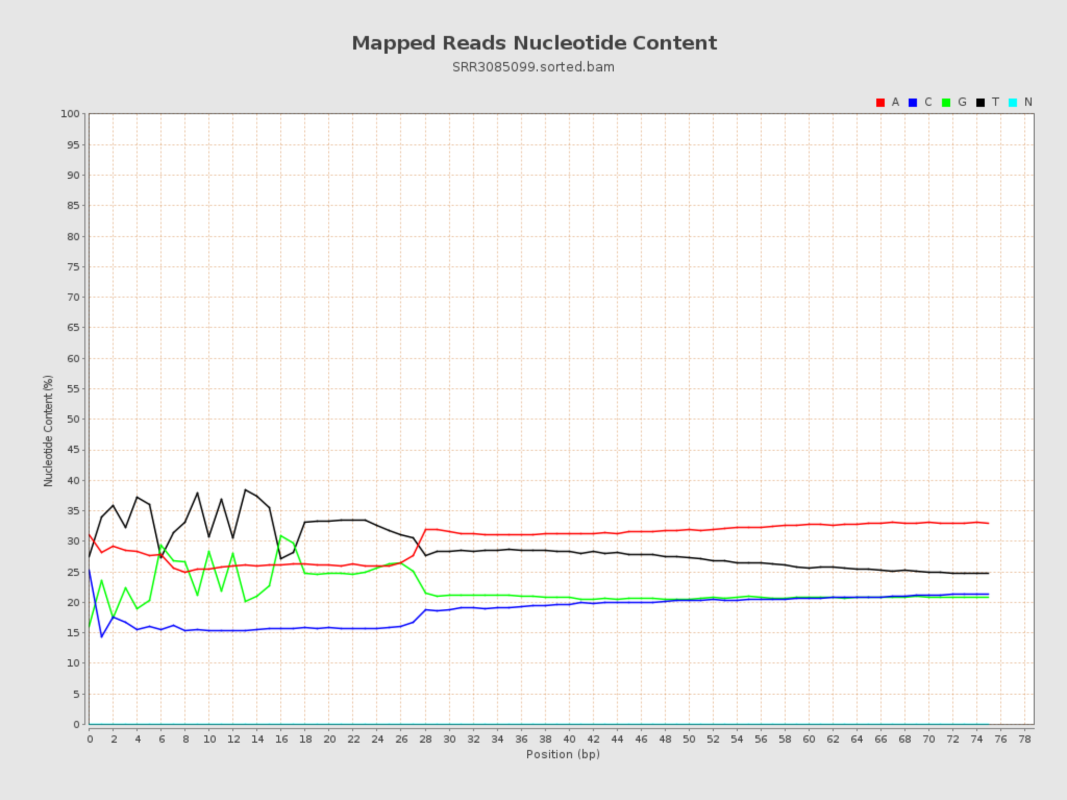
6. Results : Genome Fraction Coverage



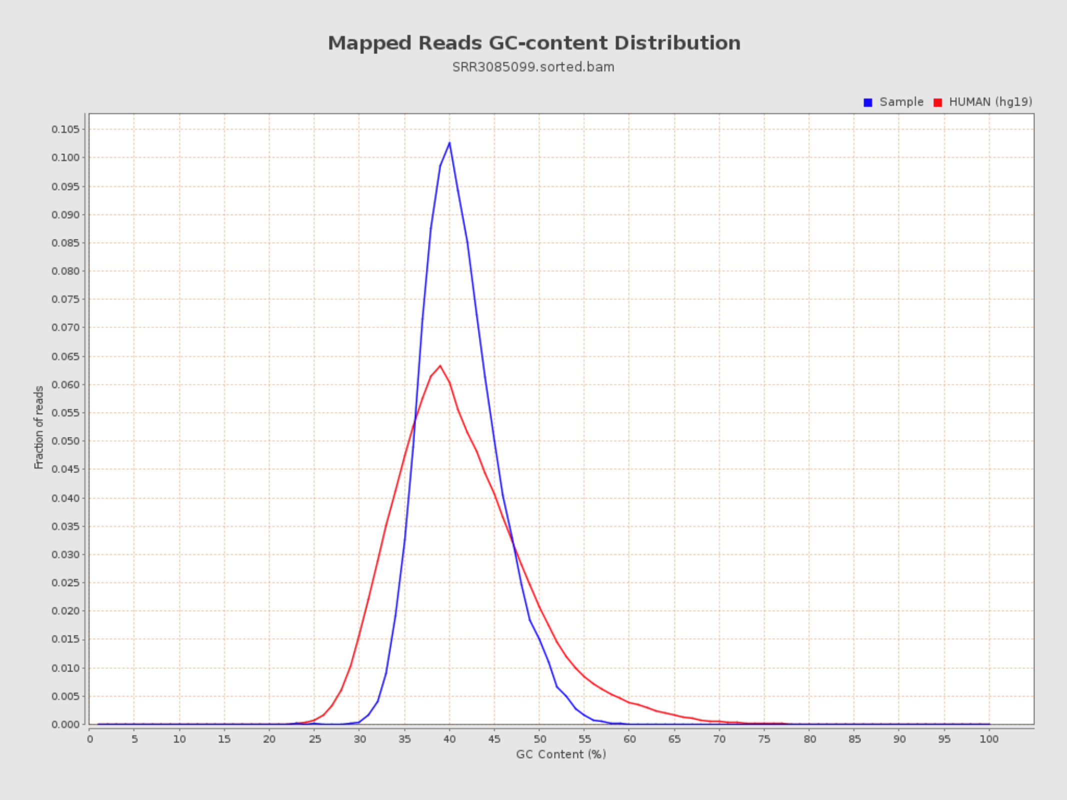
7. Results : Duplication Rate Histogram



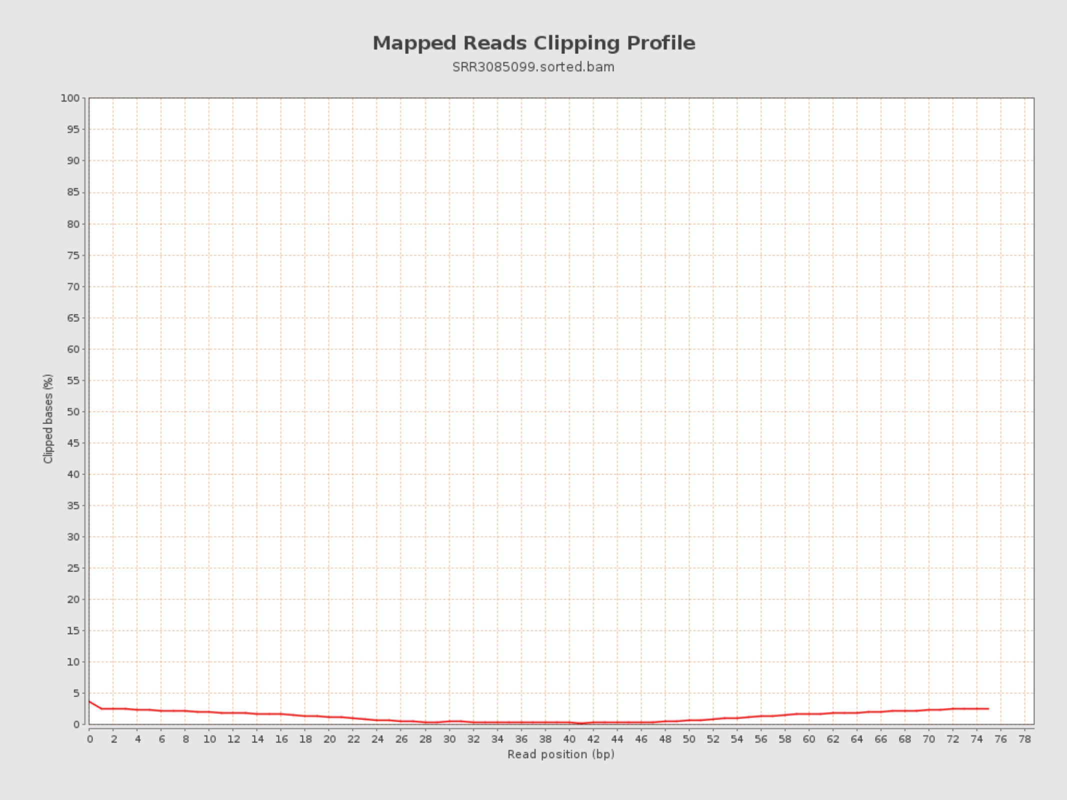
8. Results : Mapped Reads Nucleotide Content



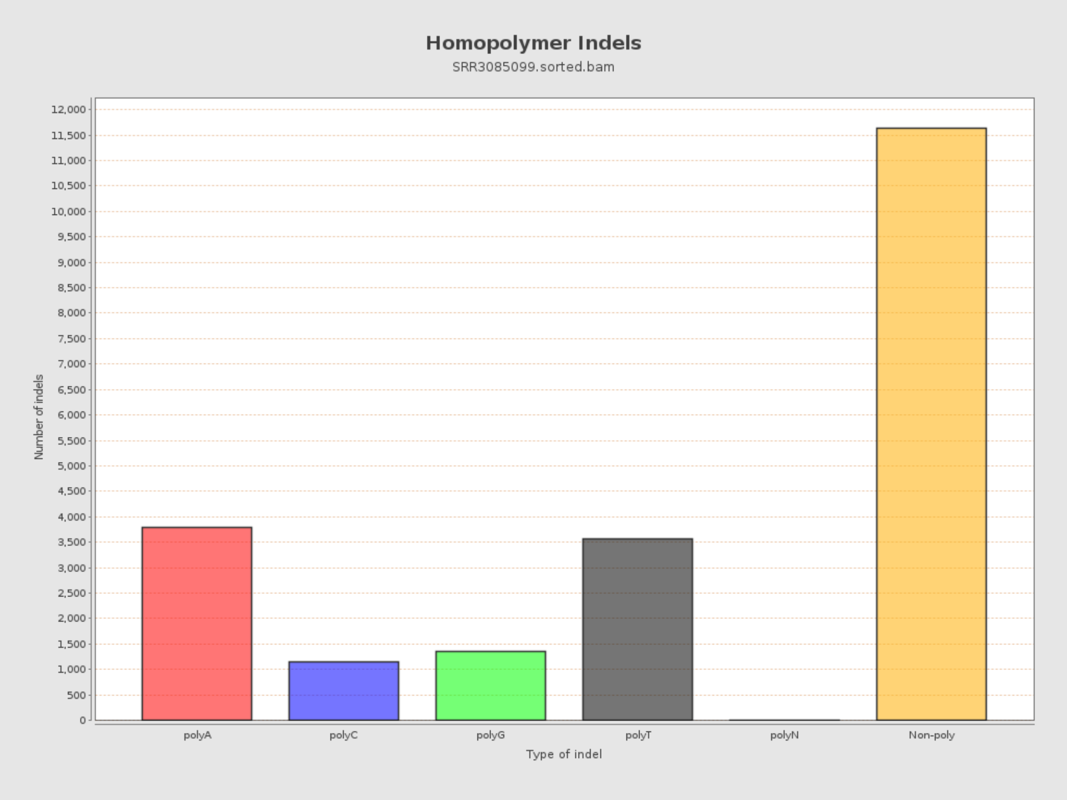
9. Results : Mapped Reads GC-content Distribution



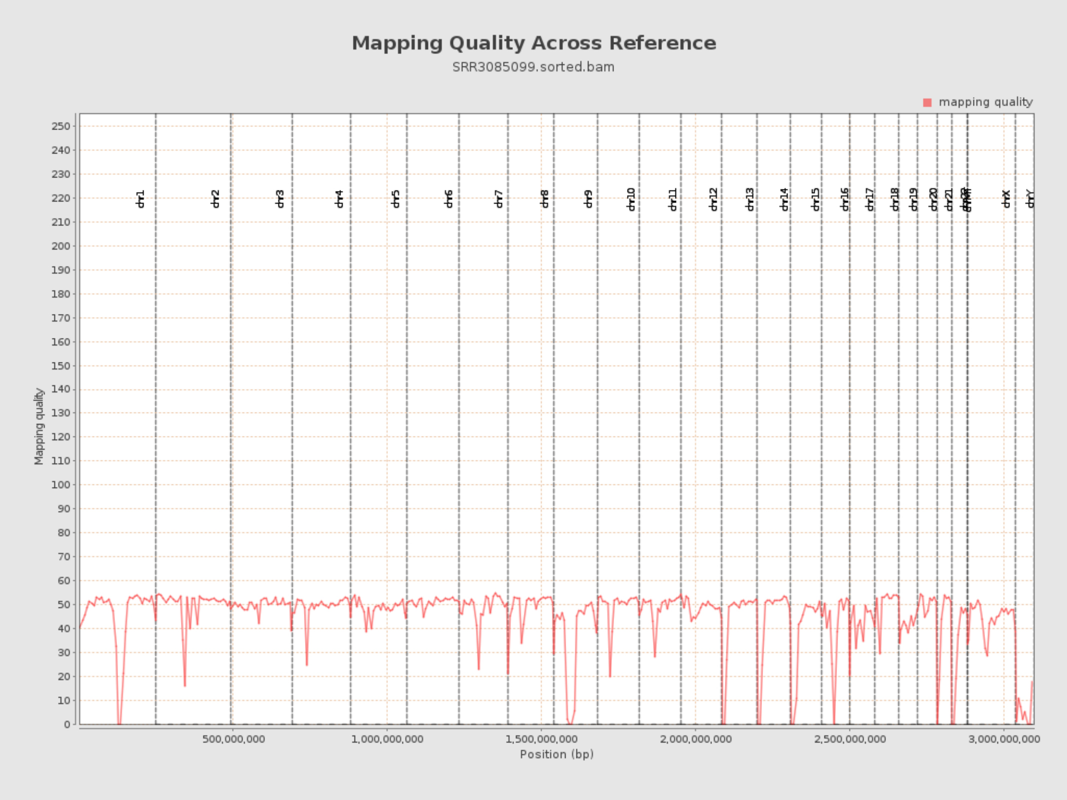
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram