Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:32:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085011.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_SRR3085011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085011.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:32:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,444,583
Mapped reads	2,210,637 / 90.43%
Unmapped reads	233,946 / 9.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,848 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	70,262 / 2.87%
Duplication rate	2.3%
Clipped reads	1,056,618 / 43.22%

2.2. ACGT Content

Number/percentage of A's	40,583,181 / 27.69%
Number/percentage of C's	28,871,368 / 19.7%
Number/percentage of T's	43,668,330 / 29.8%
Number/percentage of G's	33,423,690 / 22.81%
Number/percentage of N's	5,746 / 0%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.3932

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

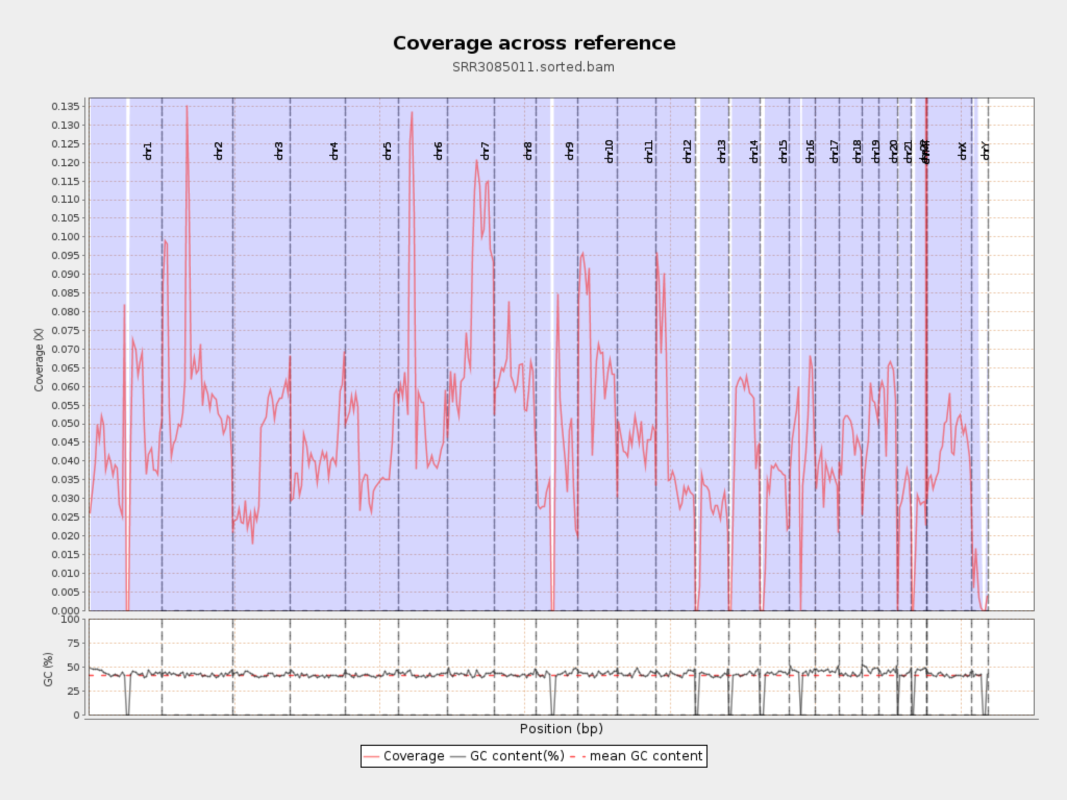
General error rate	0.89%
Mismatches	1,281,526
Insertions	10,967
Mapped reads with at least one insertion	0.49%
Deletions	31,745
Mapped reads with at least one deletion	1.42%
Homopolymer indels	45.98%

2.6. Chromosome stats

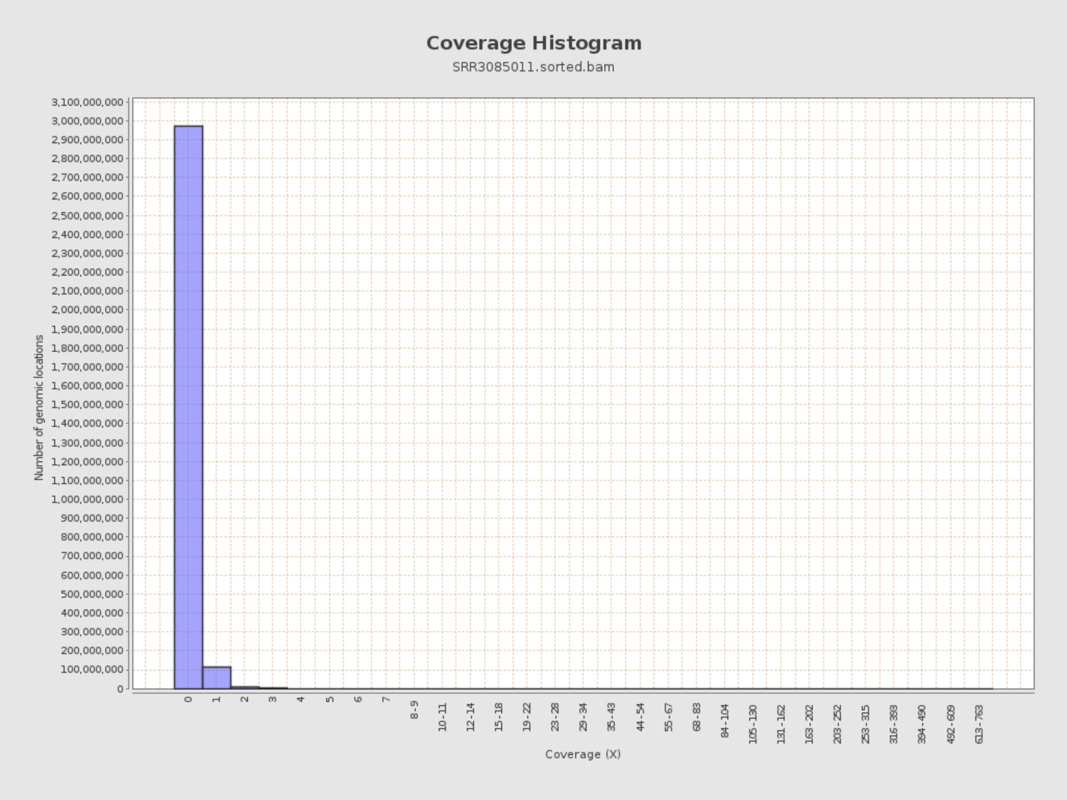
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10778887	0.0432	0.6374
chr2	243199373	15237780	0.0627	0.521
chr3	198022430	8066773	0.0407	0.2312
chr4	191154276	7958198	0.0416	0.2402
chr5	180915260	7540373	0.0417	0.2279
chr6	171115067	10030139	0.0586	0.3951
chr7	159138663	13256932	0.0833	0.4639

chr8	146364022	9099664	0.0622	0.5564
chr9	141213431	5113730	0.0362	0.3745
chr10	135534747	9632375	0.0711	0.4819
chr11	135006516	6159035	0.0456	0.3797
chr12	133851895	6213219	0.0464	0.2482
chr13	115169878	2841468	0.0247	0.1727
chr14	107349540	5040243	0.047	0.2673
chr15	102531392	2873568	0.028	0.1986
chr16	90354753	4197386	0.0465	0.2637
chr17	81195210	2863706	0.0353	0.2376
chr18	78077248	3626539	0.0464	0.6659
chr19	59128983	2870895	0.0486	0.4629
chr20	63025520	3638471	0.0577	0.275
chr21	48129895	1383420	0.0287	0.2077
chr22	51304566	1061933	0.0207	0.158
chrMT	16571	15102	0.9114	1.193
chrX	155270560	6790622	0.0437	0.278
chrY	59373566	317260	0.0053	0.119

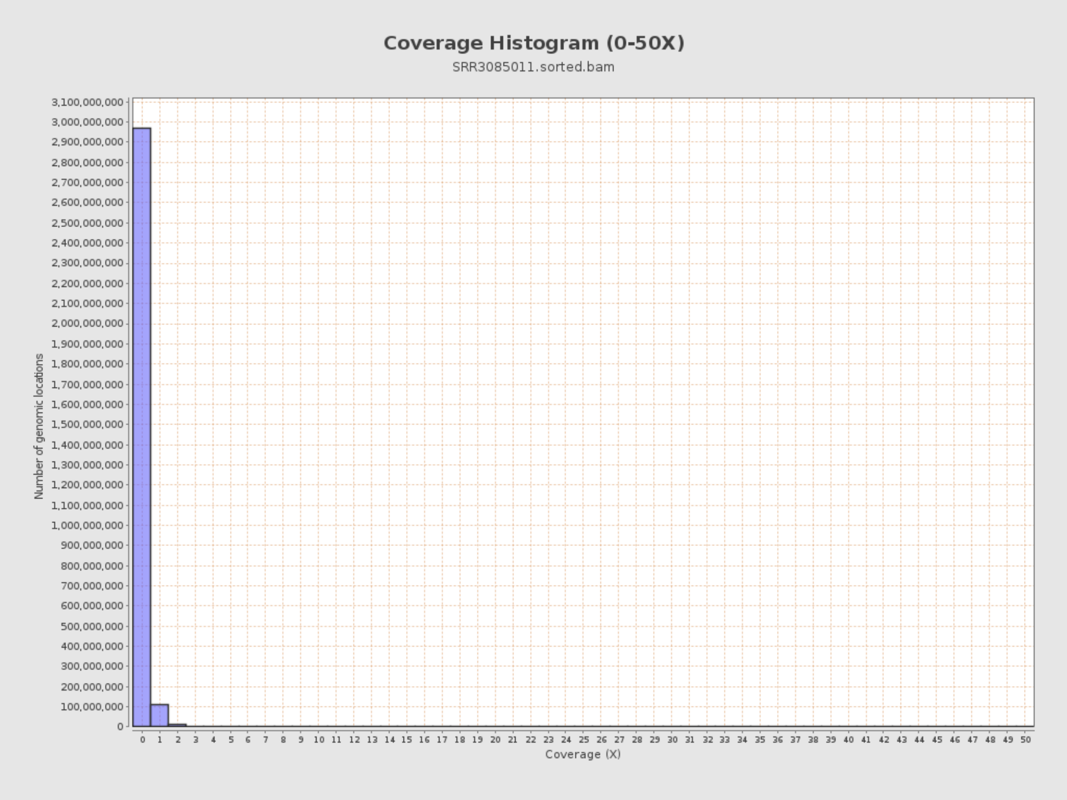
3. Results : Coverage across reference



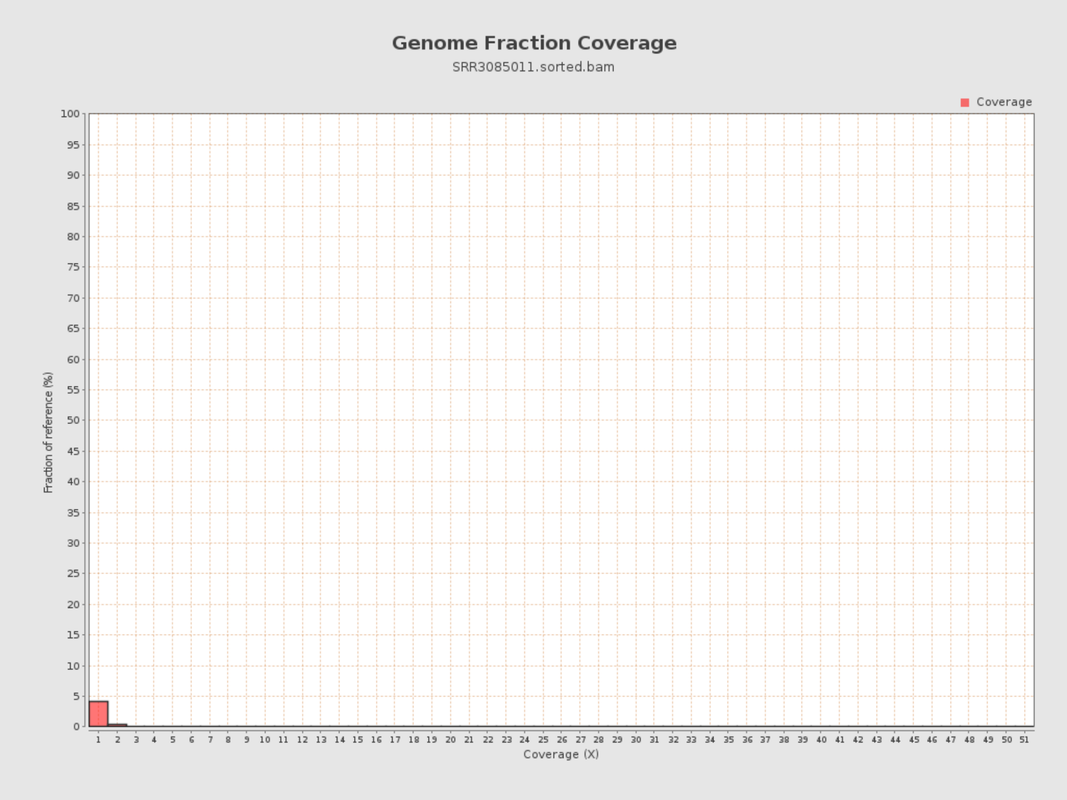
4. Results : Coverage Histogram



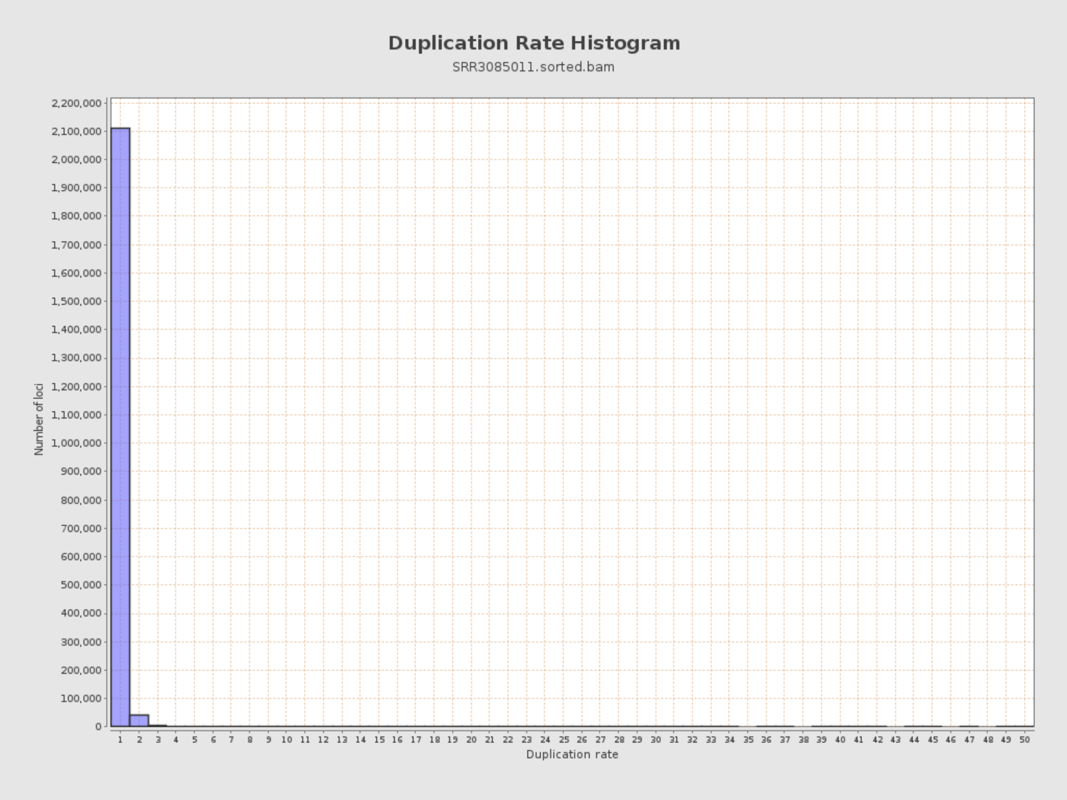
5. Results : Coverage Histogram (0-50X)



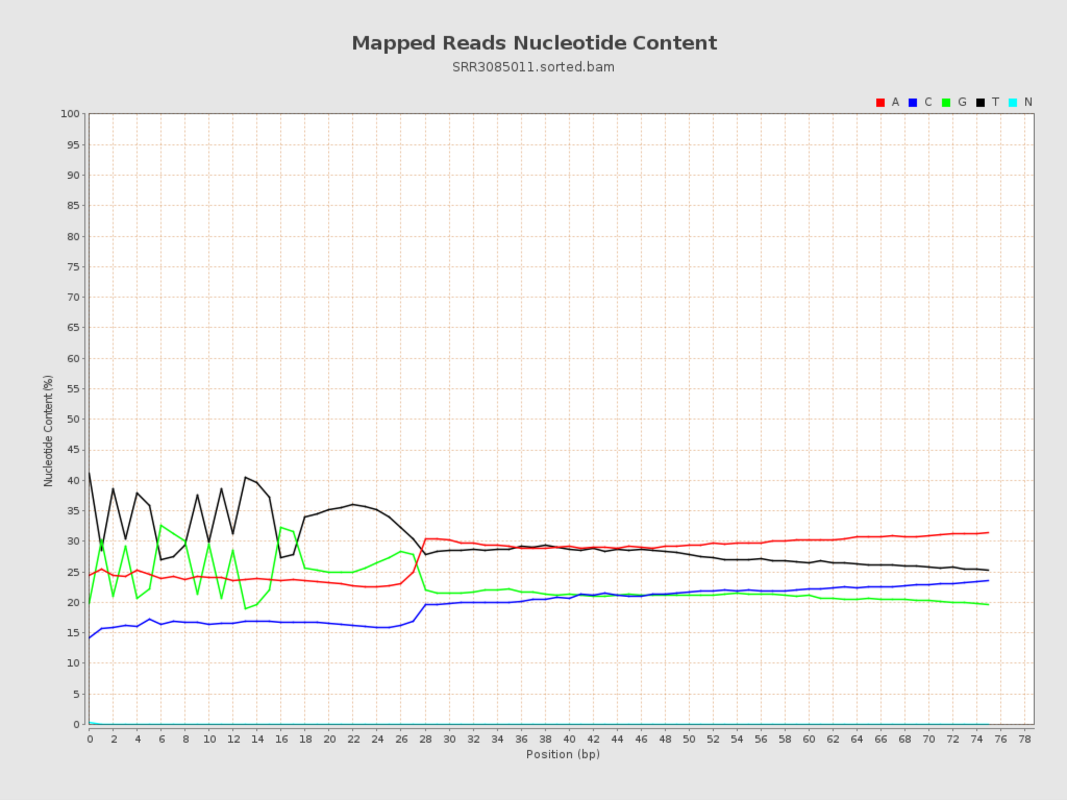
6. Results : Genome Fraction Coverage



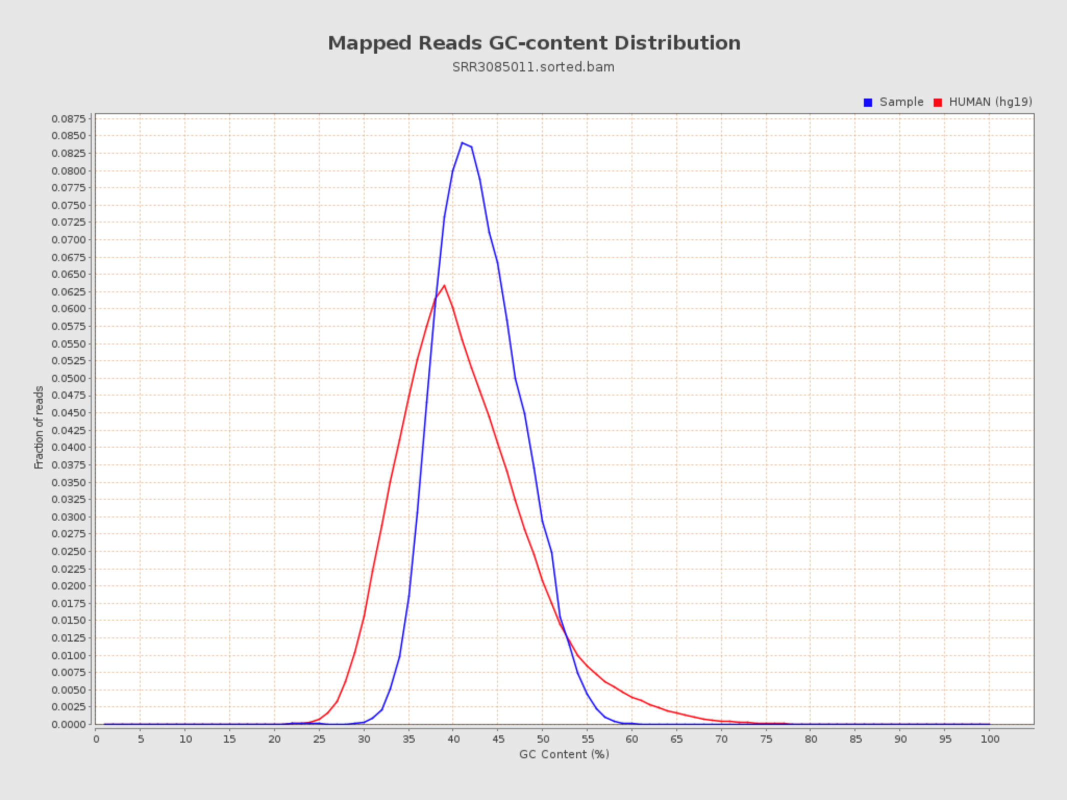
7. Results : Duplication Rate Histogram



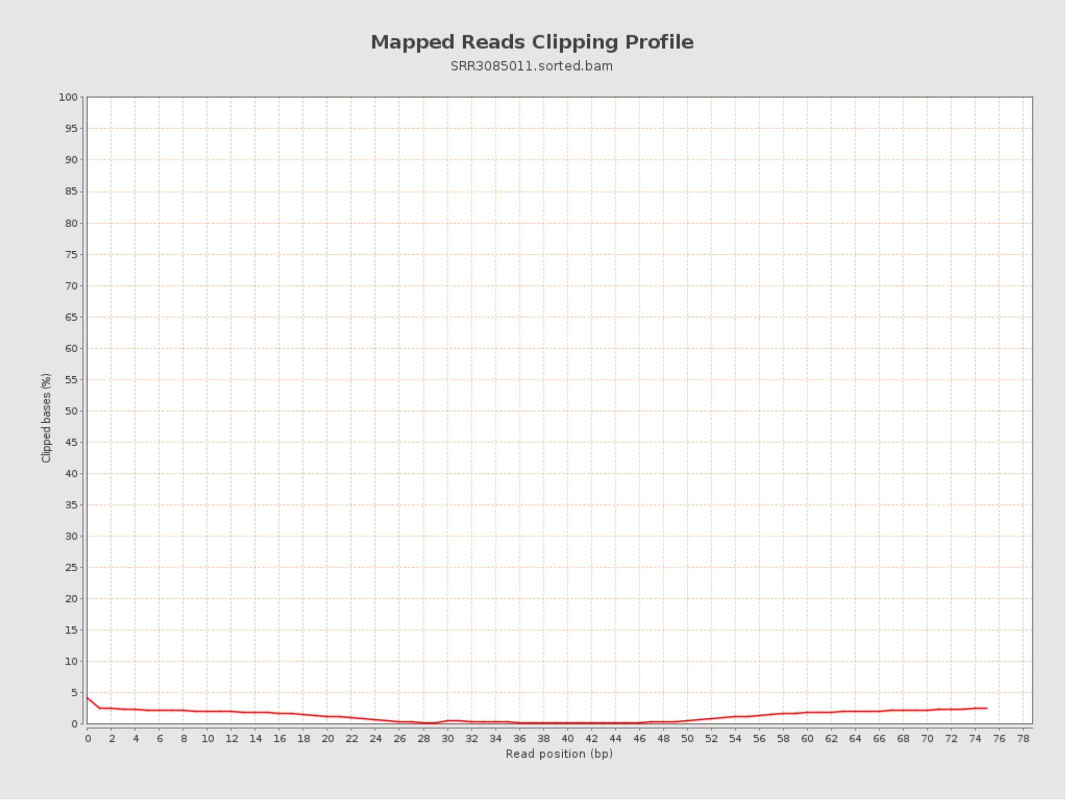
8. Results : Mapped Reads Nucleotide Content



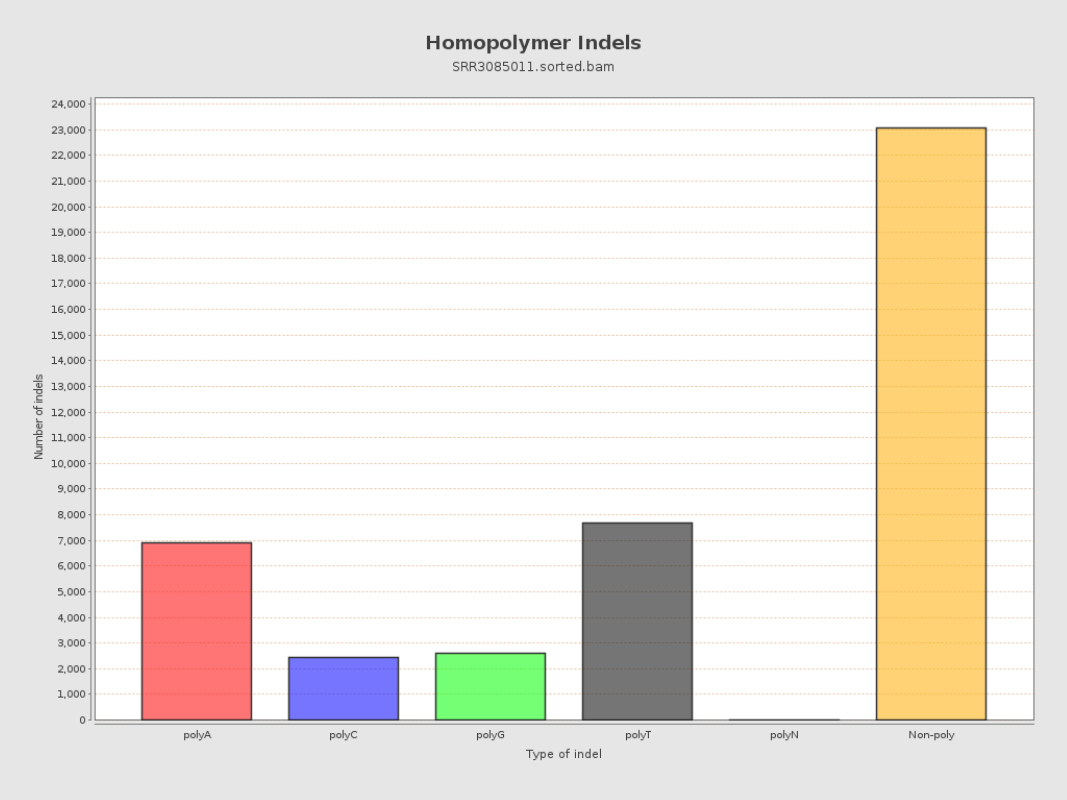
9. Results : Mapped Reads GC-content Distribution



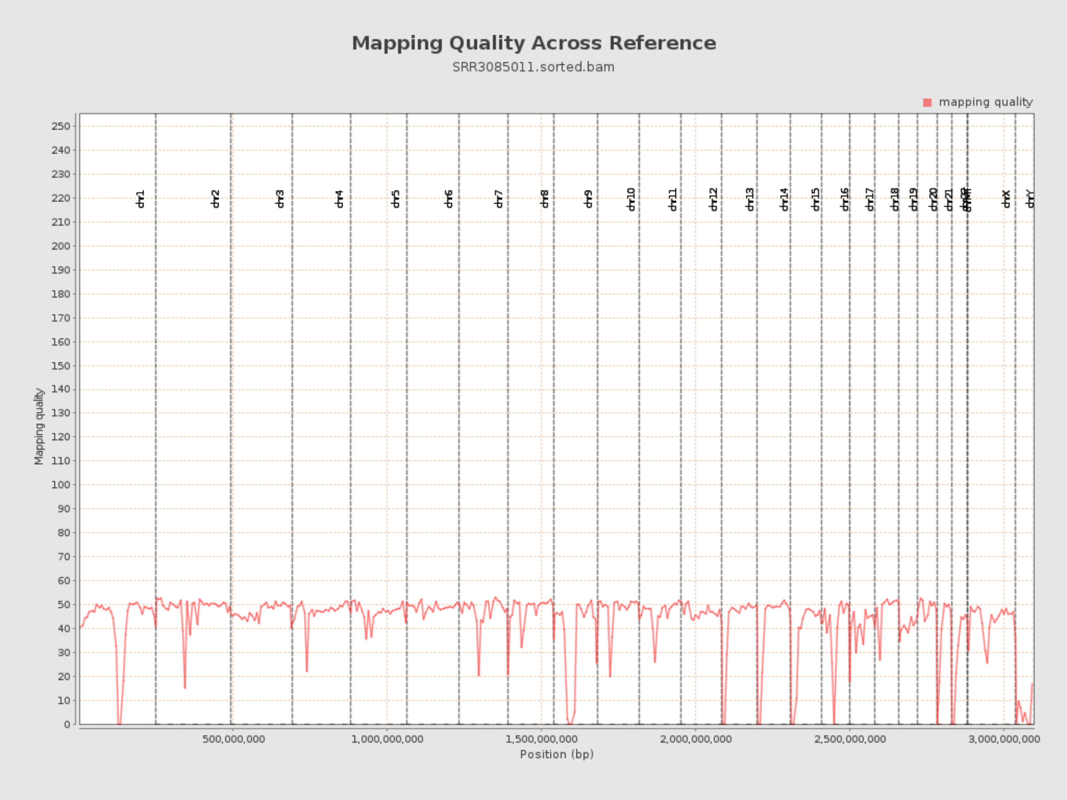
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram