Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:28:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085010.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_SRR3085010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:28:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,204,722
Mapped reads	1,852,133 / 84.01%
Unmapped reads	352,589 / 15.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,133 / 1.82%
Read min/max/mean length	30 / 76 / 76.64
Duplicated reads (estimated)	62,028 / 2.81%
Duplication rate	2.04%
Clipped reads	980,775 / 44.49%

2.2. ACGT Content

Number/percentage of A's	37,190,885 / 30.55%
Number/percentage of C's	22,637,078 / 18.59%
Number/percentage of T's	36,287,100 / 29.8%
Number/percentage of G's	25,622,589 / 21.04%
Number/percentage of N's	15,677 / 0.01%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.4599

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

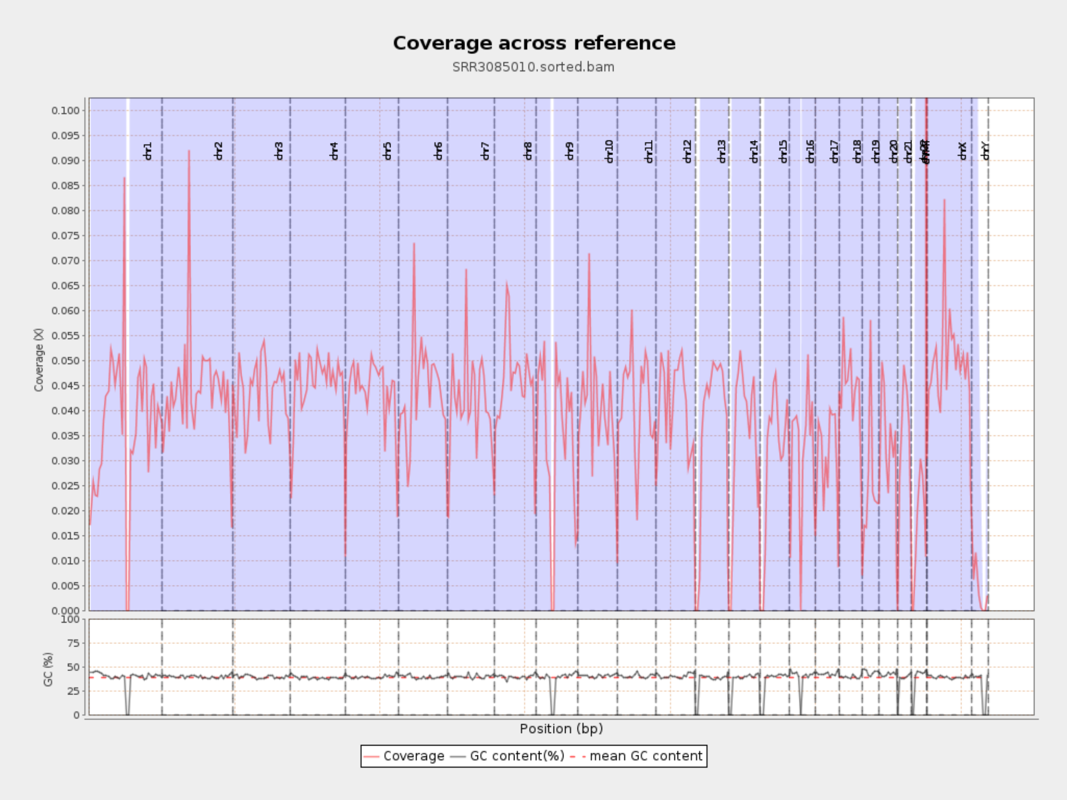
General error rate	0.89%
Mismatches	1,070,511
Insertions	10,188
Mapped reads with at least one insertion	0.55%
Deletions	21,667
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.33%

2.6. Chromosome stats

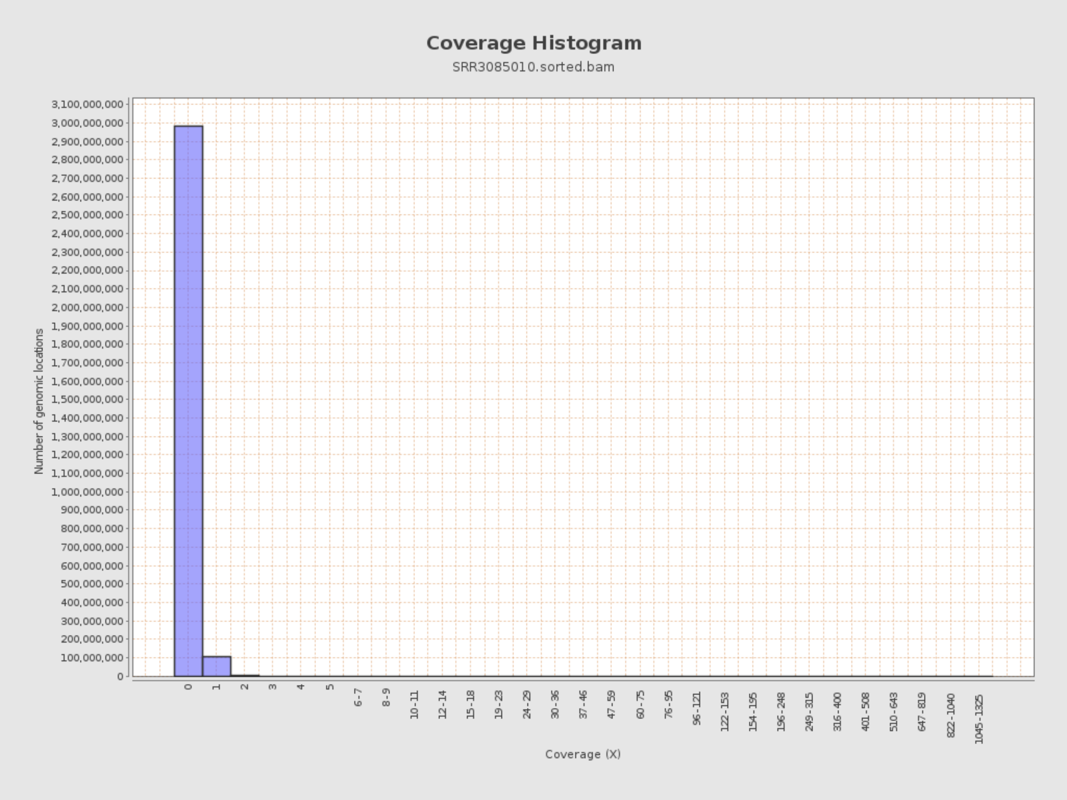
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9352664	0.0375	0.908
chr2	243199373	10779757	0.0443	0.4634
chr3	198022430	8637369	0.0436	0.2209
chr4	191154276	8704244	0.0455	0.2297
chr5	180915260	7929482	0.0438	0.2253
chr6	171115067	7484182	0.0437	0.3681
chr7	159138663	6750699	0.0424	0.4308

chr8	146364022	6669724	0.0456	0.8281
chr9	141213431	4998384	0.0354	0.4141
chr10	135534747	5548707	0.0409	0.4193
chr11	135006516	5558314	0.0412	0.4717
chr12	133851895	5466873	0.0408	0.2267
chr13	115169878	4214876	0.0366	0.1994
chr14	107349540	3679868	0.0343	0.2473
chr15	102531392	3101219	0.0302	0.1864
chr16	90354753	2896964	0.0321	0.2652
chr17	81195210	2442712	0.0301	0.2597
chr18	78077248	3506163	0.0449	0.8509
chr19	59128983	1508034	0.0255	0.6418
chr20	63025520	2150339	0.0341	0.207
chr21	48129895	1568051	0.0326	0.2177
chr22	51304566	843069	0.0164	0.1327
chrMT	16571	36717	2.2157	1.9331
chrX	155270560	7707441	0.0496	0.3207
chrY	59373566	251956	0.0042	0.0933

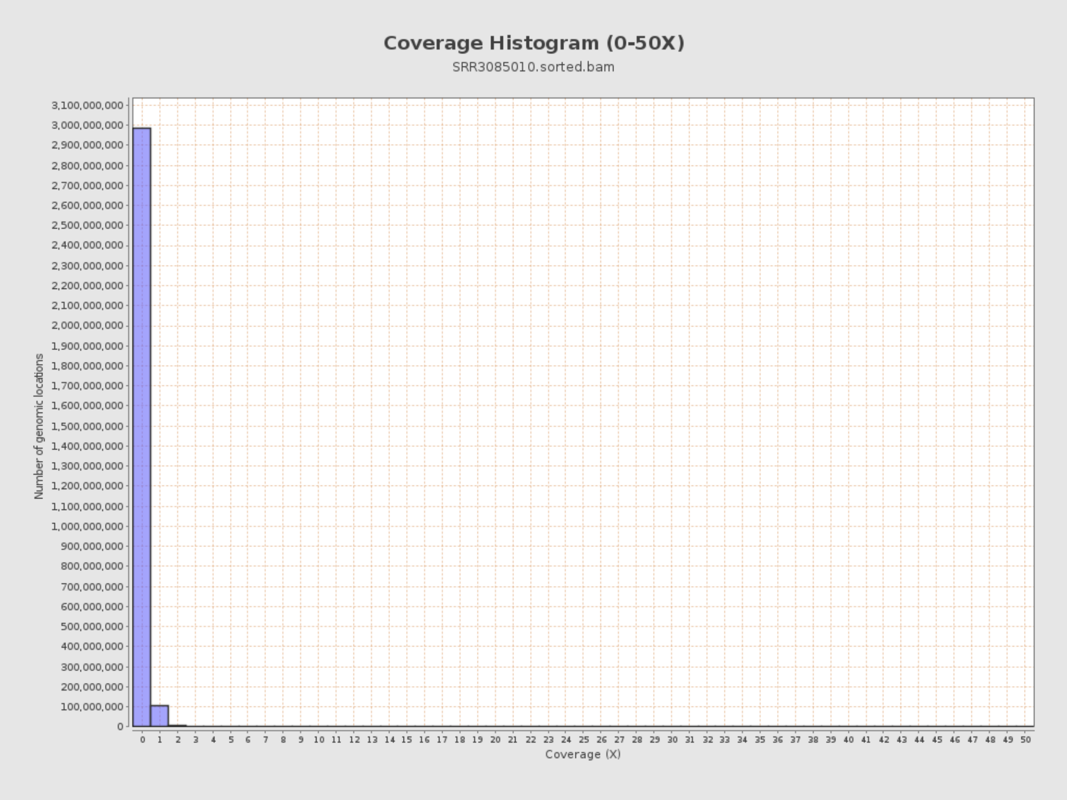
3. Results : Coverage across reference



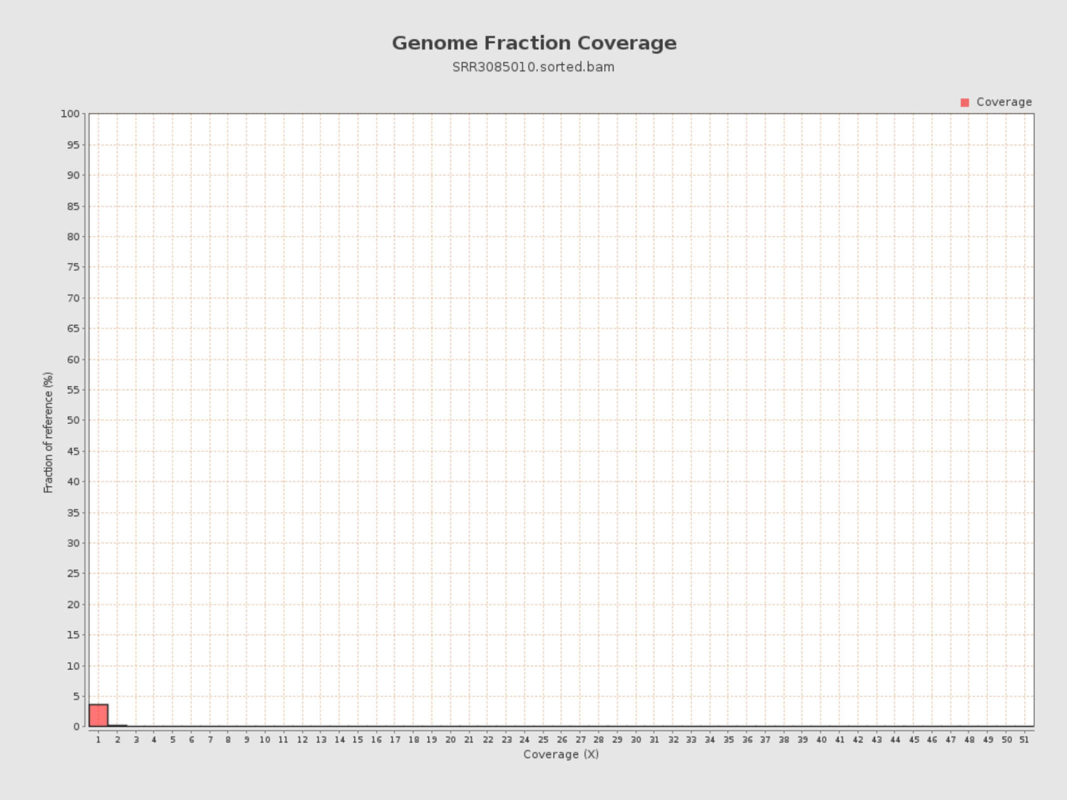
4. Results : Coverage Histogram



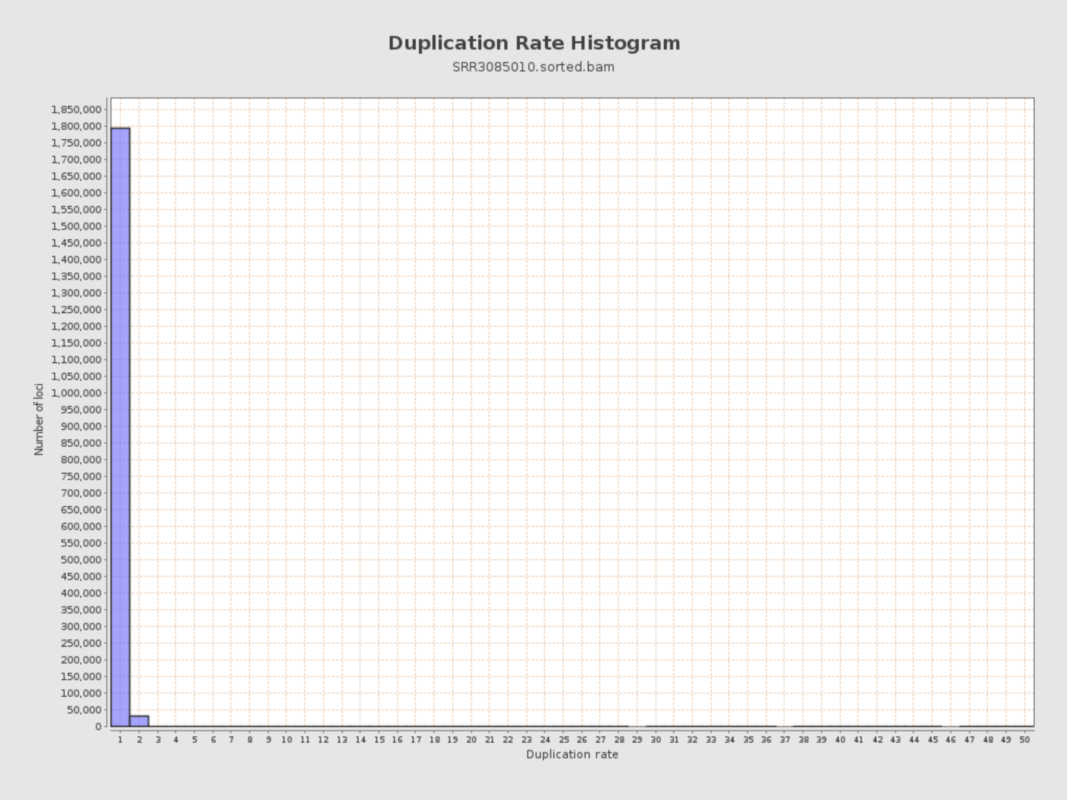
5. Results : Coverage Histogram (0-50X)



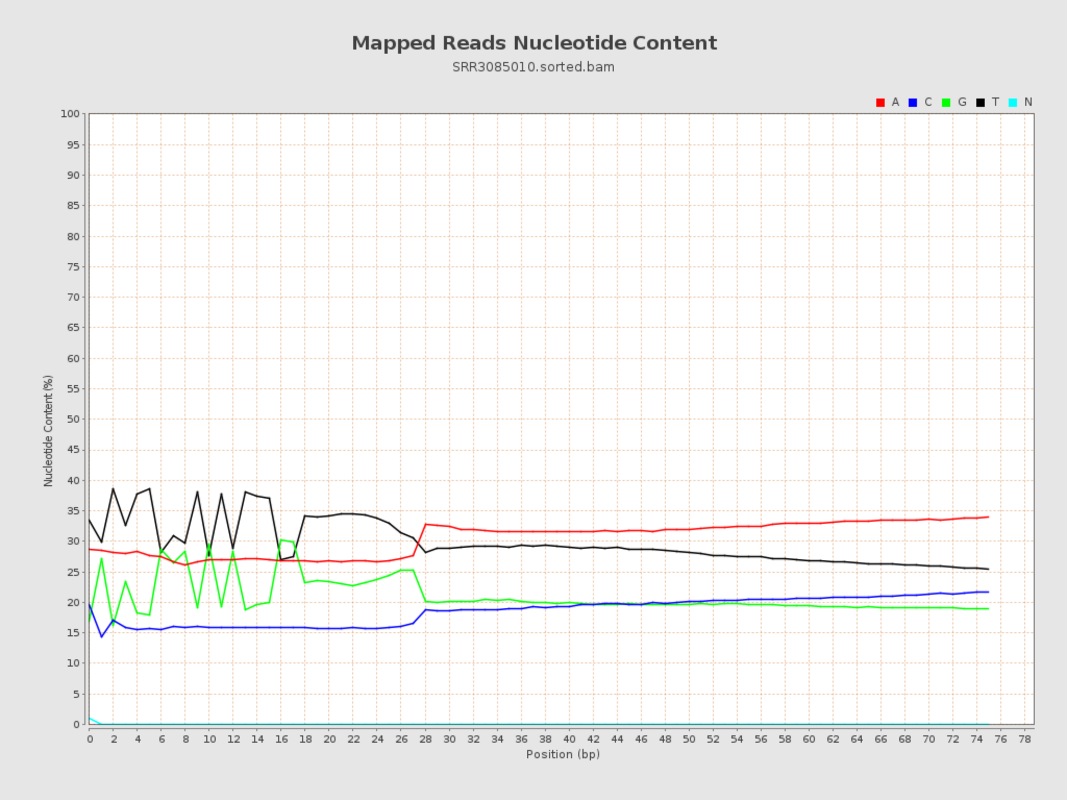
6. Results : Genome Fraction Coverage



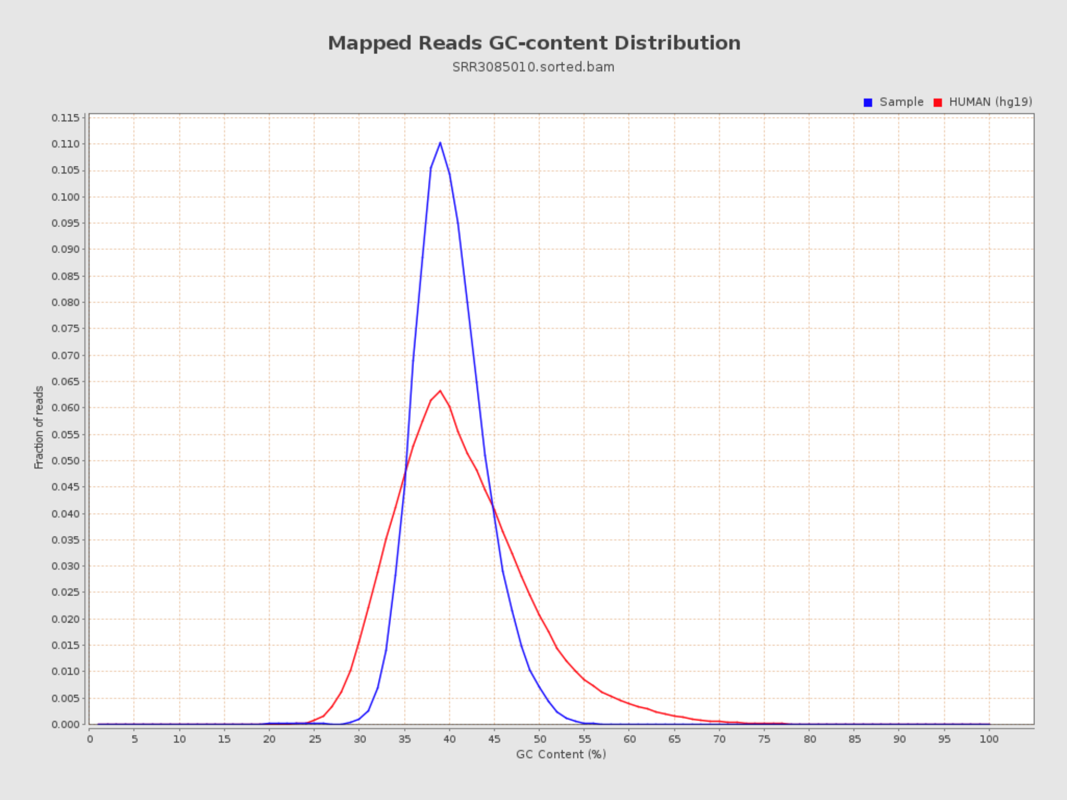
7. Results : Duplication Rate Histogram



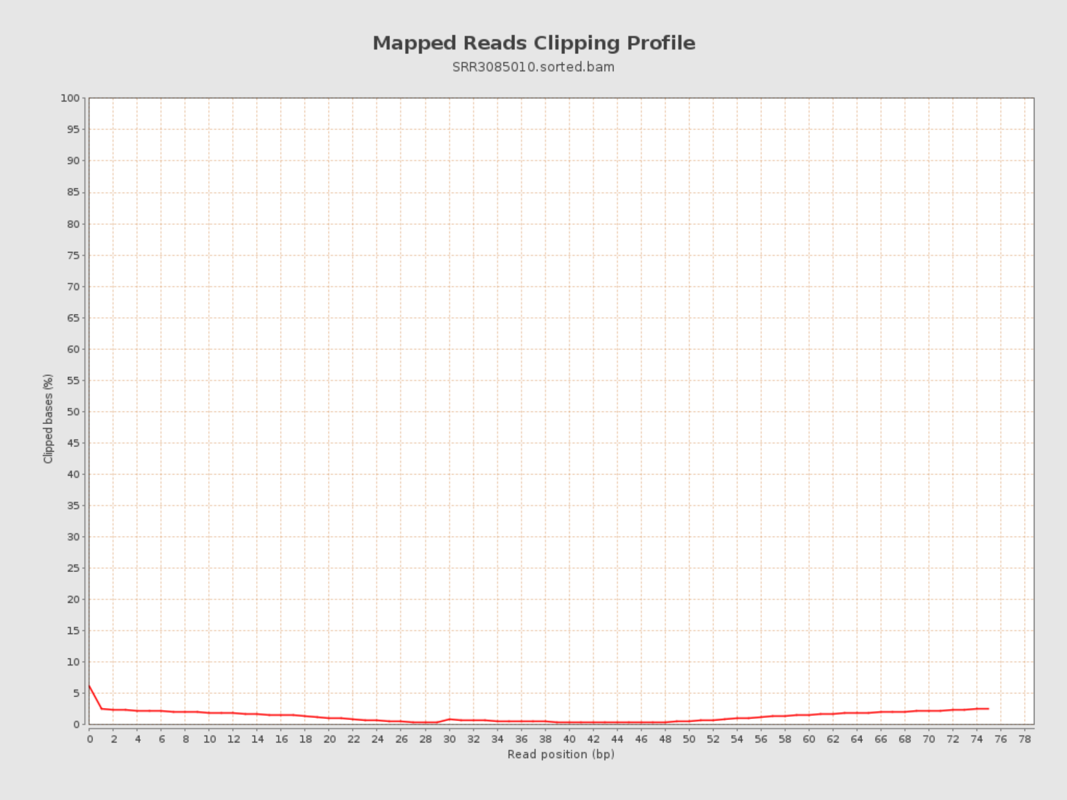
8. Results : Mapped Reads Nucleotide Content



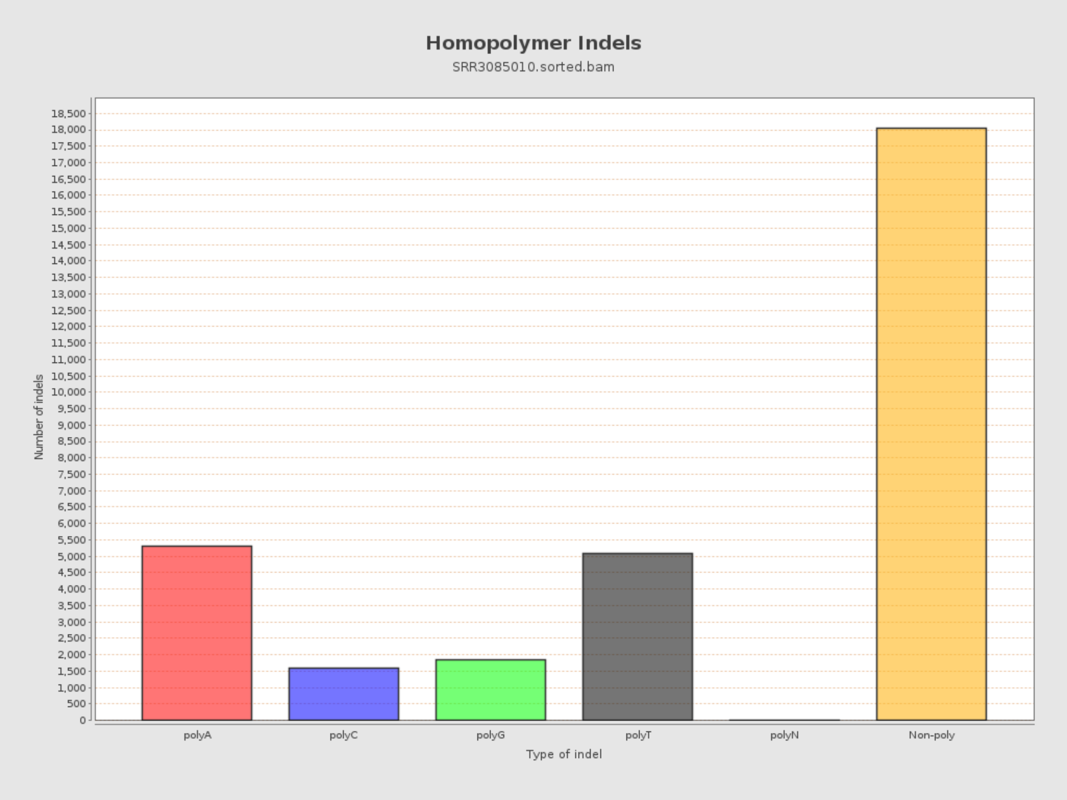
9. Results : Mapped Reads GC-content Distribution



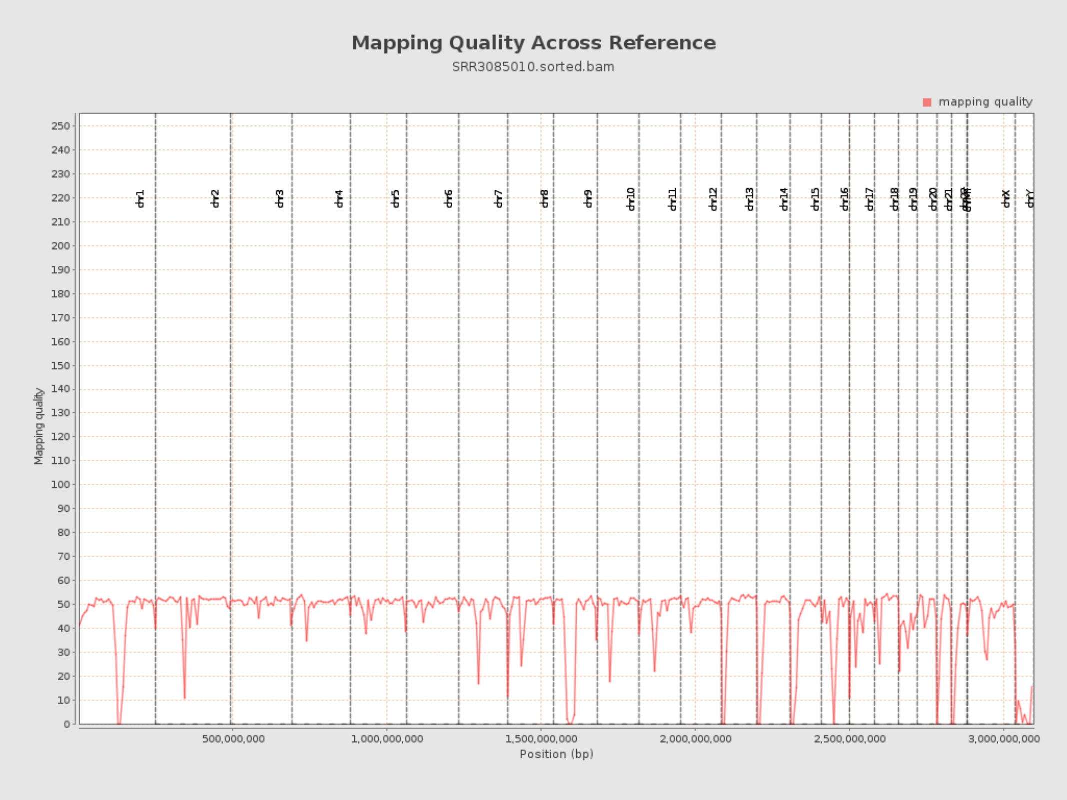
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram