Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:08:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081985.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_SRR3081985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:08:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,493,990
Mapped reads	2,338,470 / 93.76%
Unmapped reads	155,520 / 6.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,499 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	91,201 / 3.66%
Duplication rate	3.2%
Clipped reads	795,805 / 31.91%

2.2. ACGT Content

Number/percentage of A's	46,763,435 / 28.91%
Number/percentage of C's	30,068,225 / 18.59%
Number/percentage of T's	51,055,977 / 31.56%
Number/percentage of G's	33,857,483 / 20.93%
Number/percentage of N's	21,160 / 0.01%
GC Percentage	39.52%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.3748

2.4. Mapping Quality

Mean Mapping Quality	47.16

2.5. Mismatches and indels

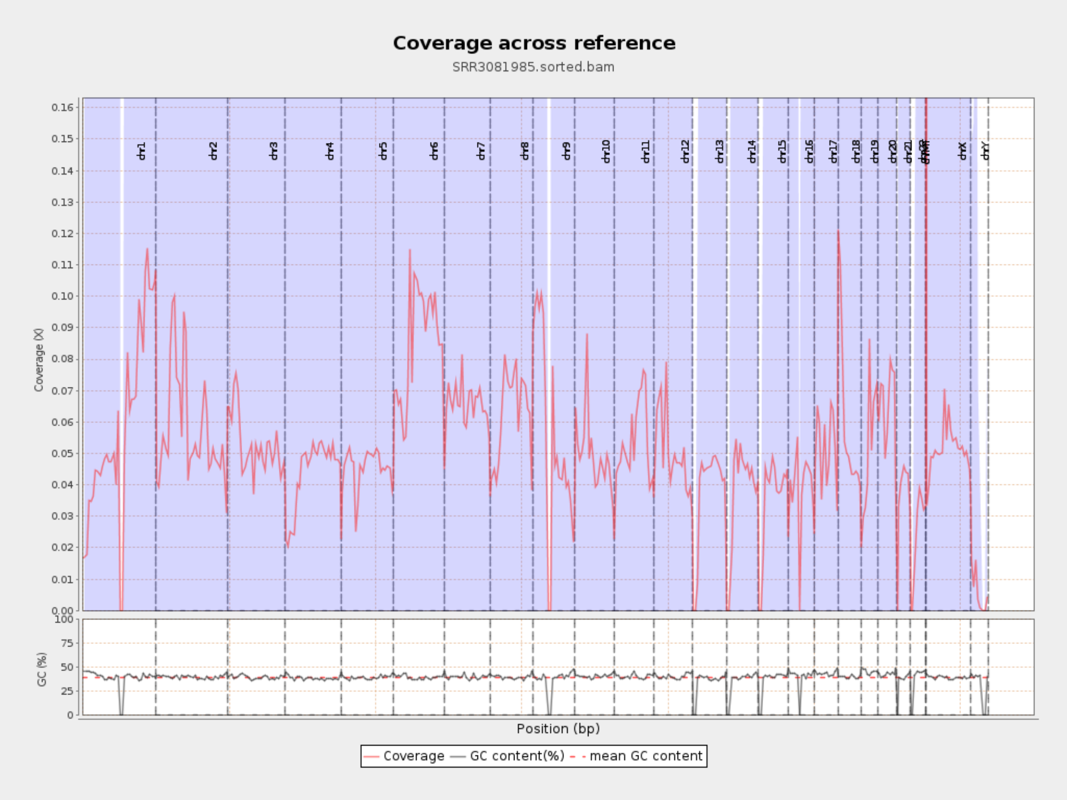
General error rate	0.74%
Mismatches	1,177,049
Insertions	11,274
Mapped reads with at least one insertion	0.48%
Deletions	32,955
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.62%

2.6. Chromosome stats

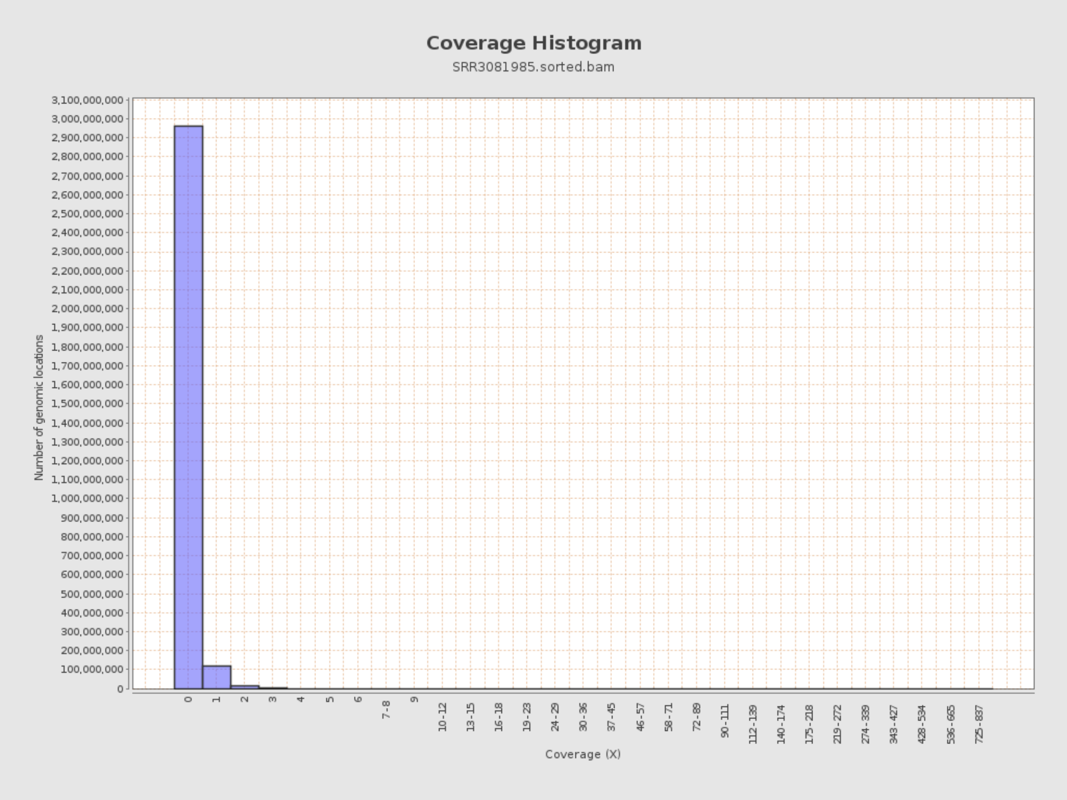
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14637694	0.0587	0.5655
chr2	243199373	14162559	0.0582	0.4656
chr3	198022430	10508323	0.0531	0.2634
chr4	191154276	8424653	0.0441	0.2508
chr5	180915260	8163173	0.0451	0.2425
chr6	171115067	14725551	0.0861	0.4044
chr7	159138663	10425514	0.0655	0.4525

chr8	146364022	9198717	0.0628	0.5971
chr9	141213431	7857153	0.0556	0.3891
chr10	135534747	6759400	0.0499	0.3853
chr11	135006516	7270677	0.0539	0.315
chr12	133851895	6749380	0.0504	0.2624
chr13	115169878	4329902	0.0376	0.2209
chr14	107349540	4101485	0.0382	0.2376
chr15	102531392	3528443	0.0344	0.212
chr16	90354753	3406392	0.0377	0.2472
chr17	81195210	4252847	0.0524	0.2761
chr18	78077248	4641372	0.0594	0.5725
chr19	59128983	3120778	0.0528	0.4381
chr20	63025520	4189338	0.0665	0.2993
chr21	48129895	1763392	0.0366	0.2376
chr22	51304566	1240458	0.0242	0.1737
chrMT	16571	44752	2.7006	2.3183
chrX	155270560	7992531	0.0515	0.2843
chrY	59373566	330540	0.0056	0.1315

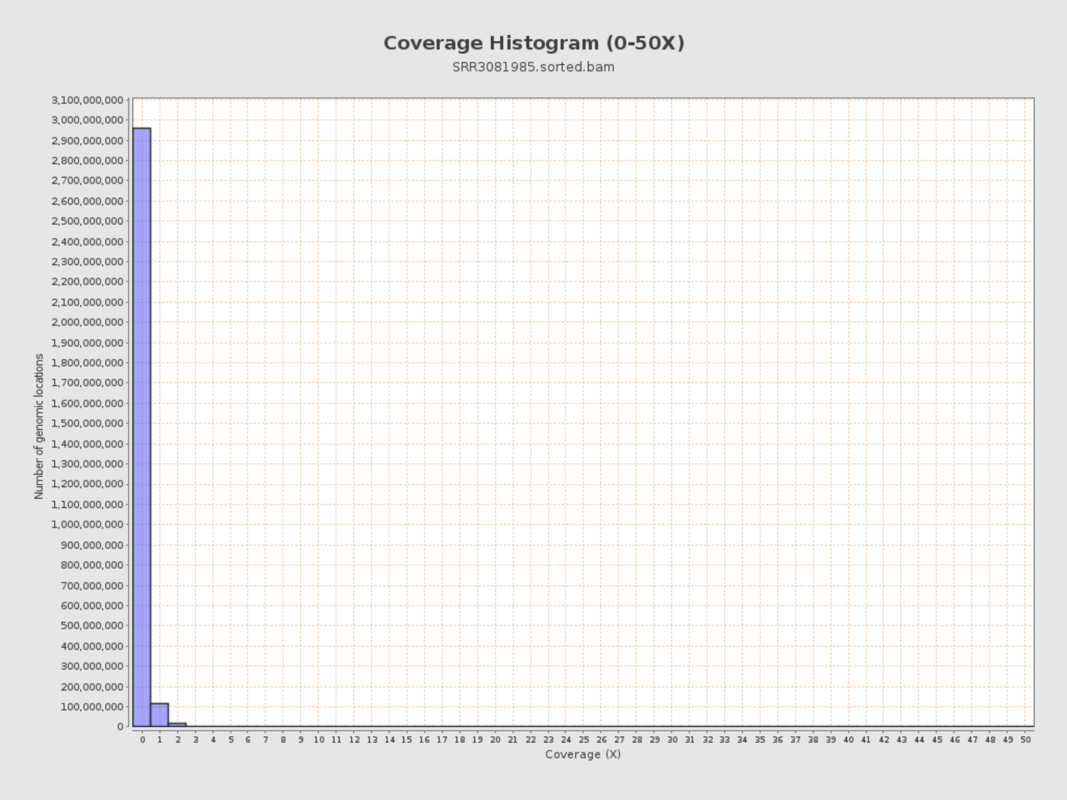
3. Results : Coverage across reference



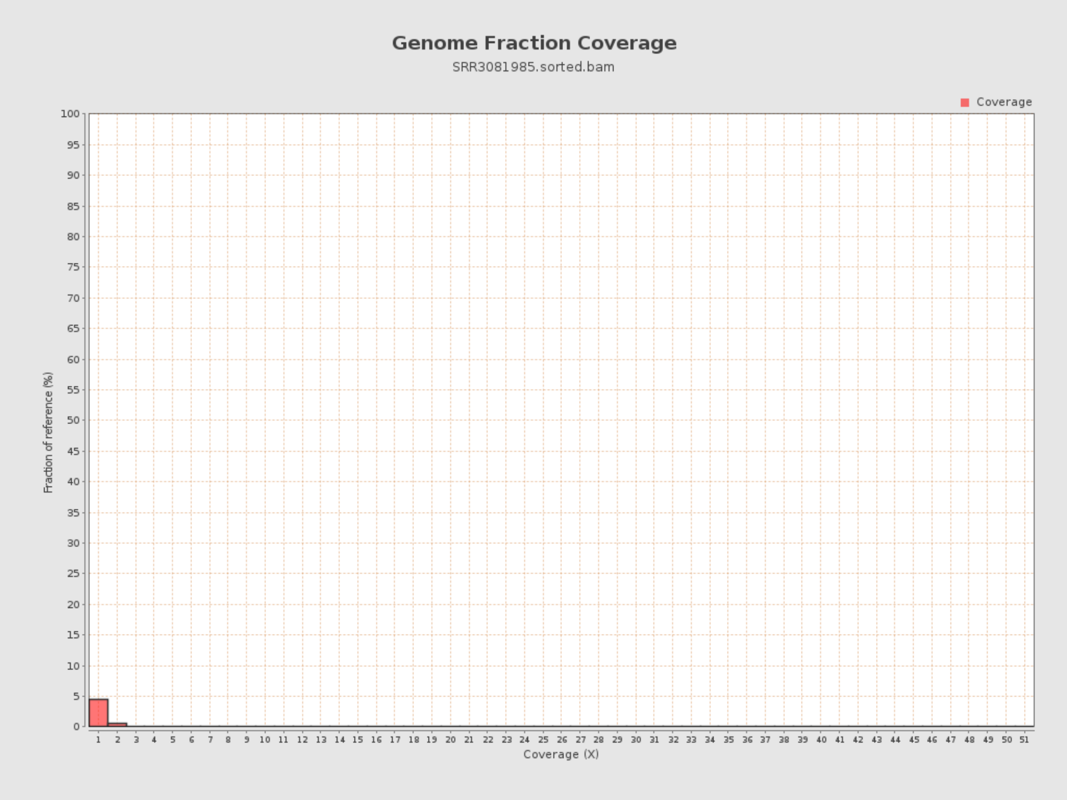
4. Results : Coverage Histogram



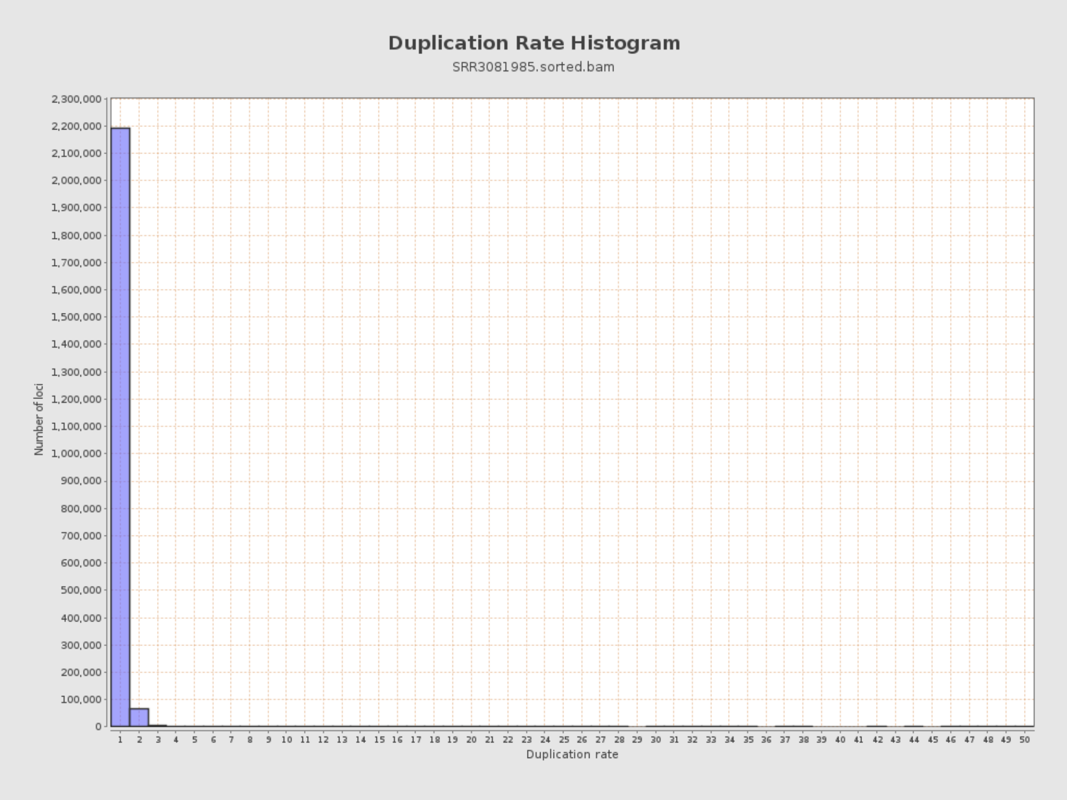
5. Results : Coverage Histogram (0-50X)



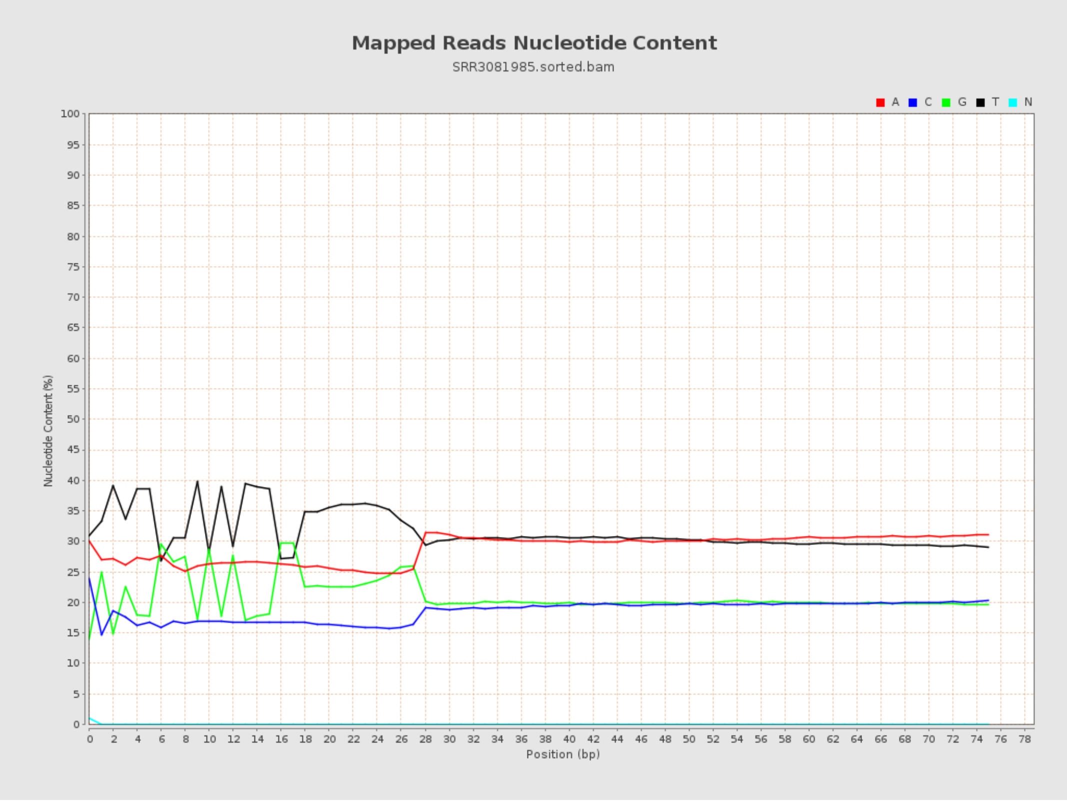
6. Results : Genome Fraction Coverage



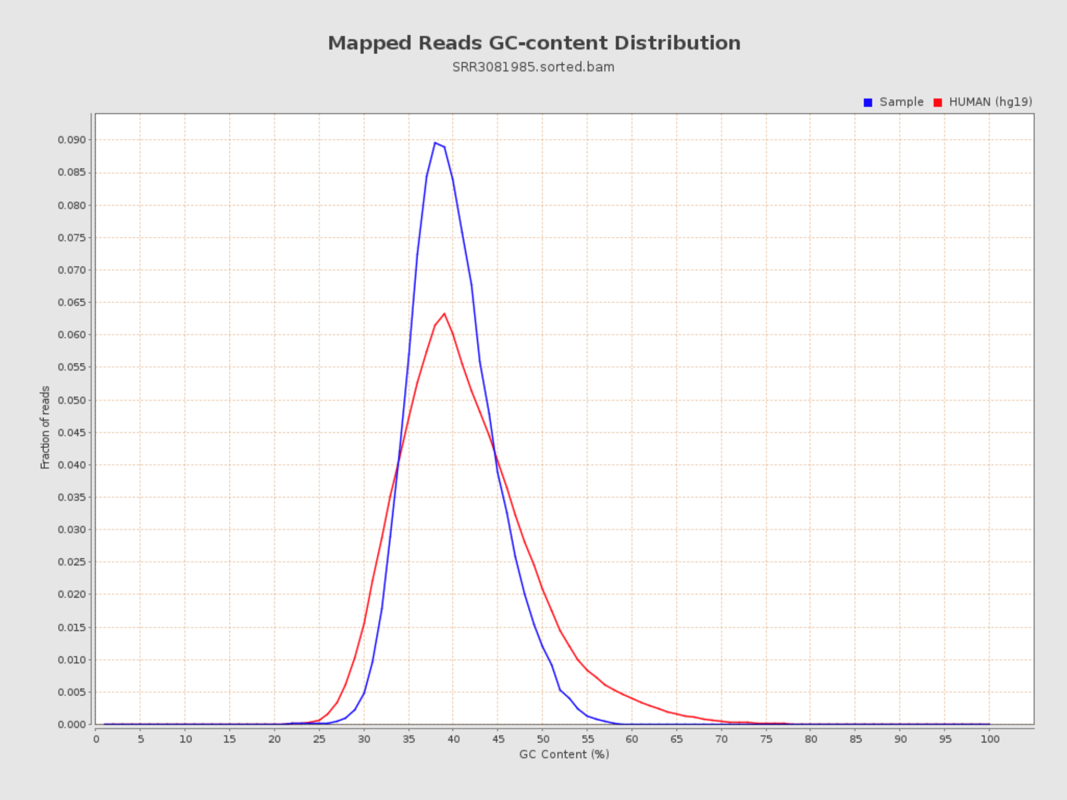
7. Results : Duplication Rate Histogram



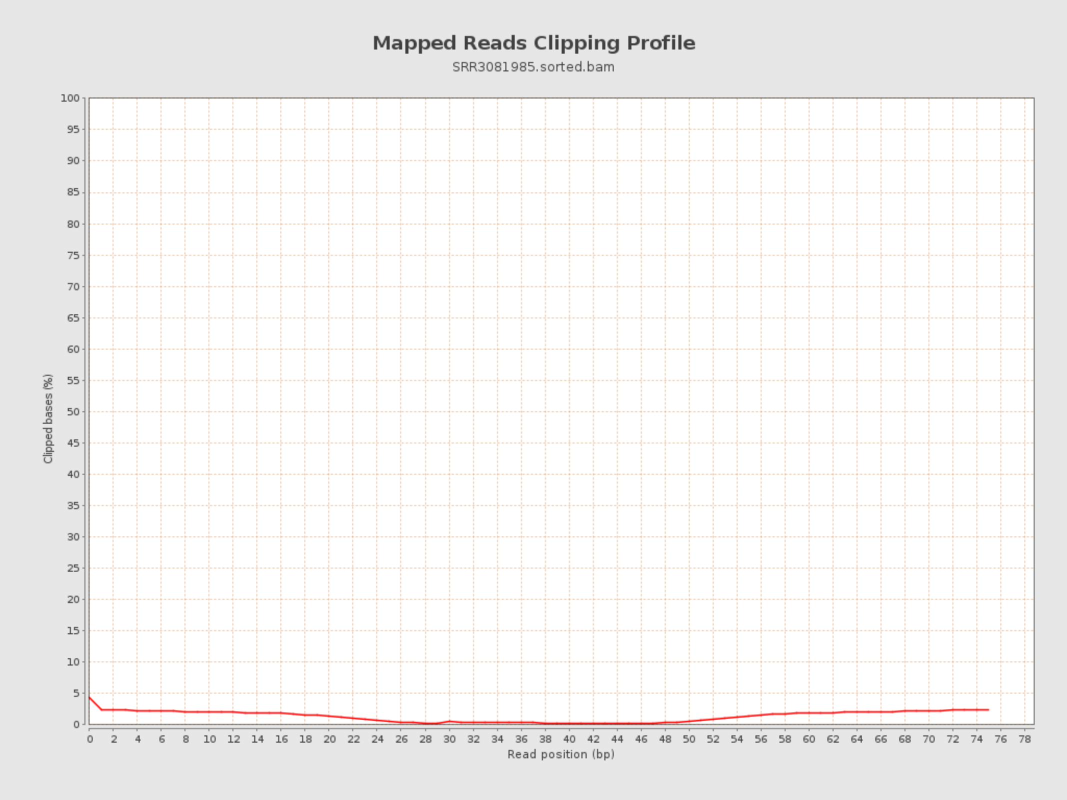
8. Results : Mapped Reads Nucleotide Content



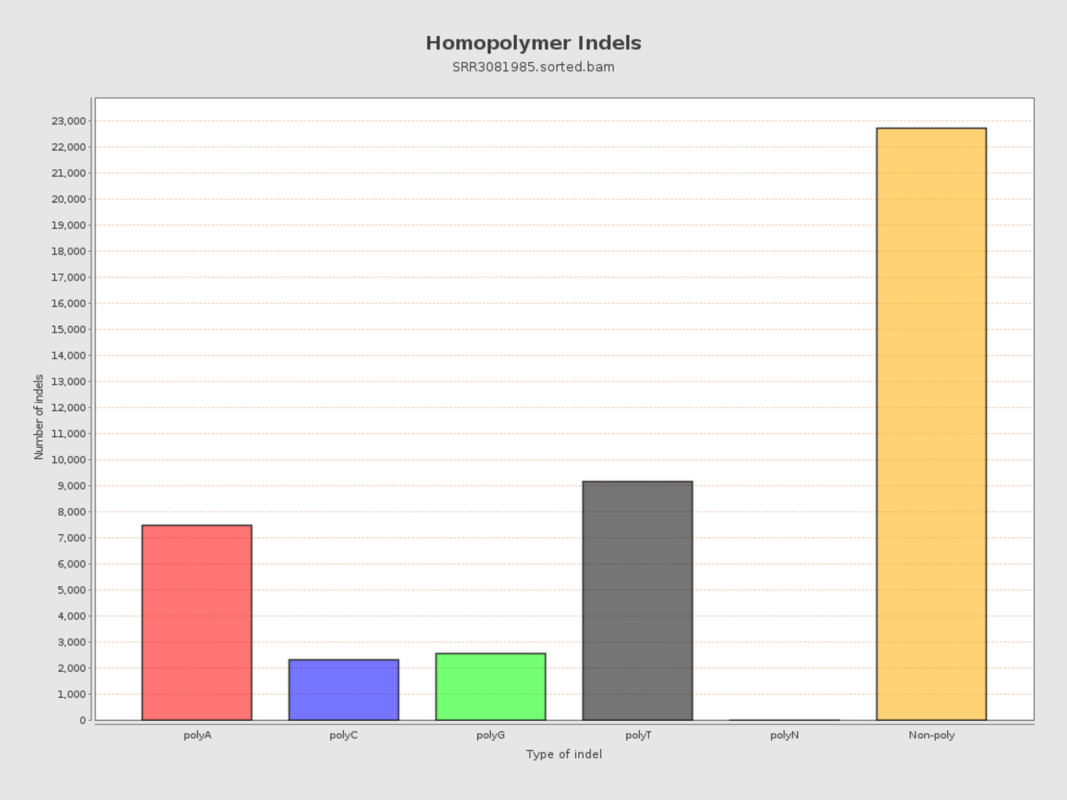
9. Results : Mapped Reads GC-content Distribution



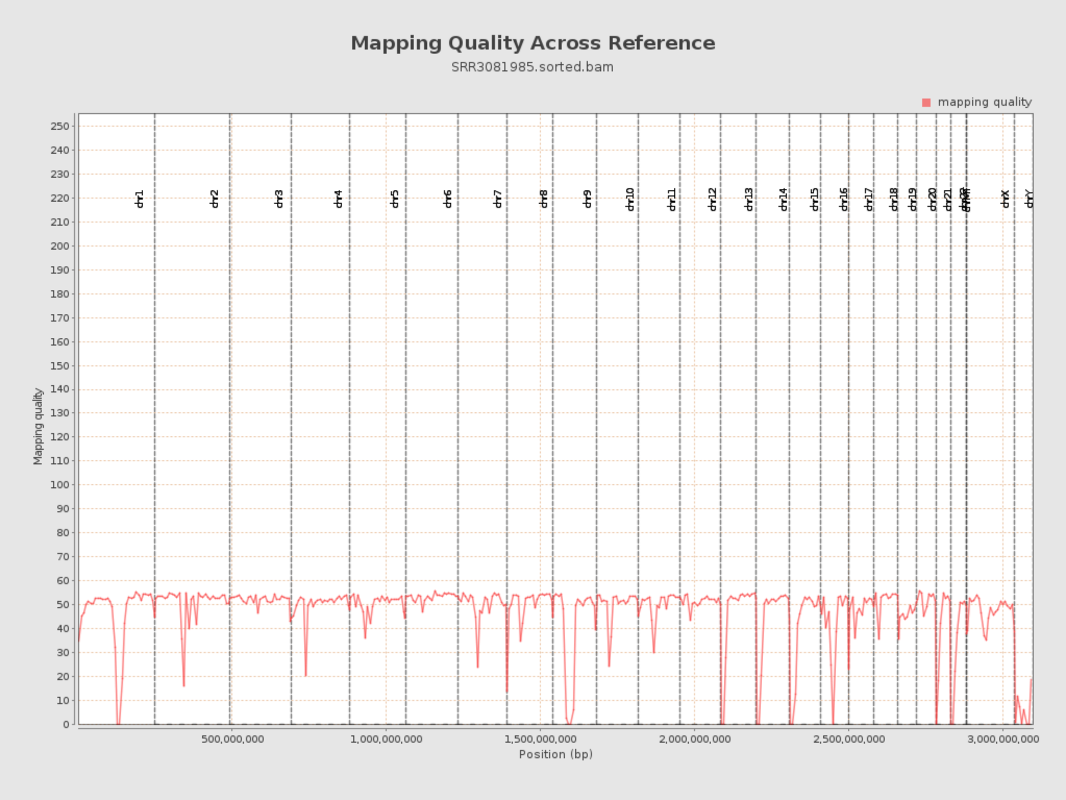
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram