Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:30:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080983.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_SRR3080983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:30:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,917,180
Mapped reads	3,228,494 / 82.42%
Unmapped reads	688,686 / 17.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,592 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	242,851 / 6.2%
Duplication rate	6.17%
Clipped reads	1,282,307 / 32.74%

2.2. ACGT Content

Number/percentage of A's	61,808,927 / 28.35%
Number/percentage of C's	38,193,667 / 17.52%
Number/percentage of T's	71,501,623 / 32.79%
Number/percentage of G's	46,098,453 / 21.14%
Number/percentage of N's	438,116 / 0.2%
GC Percentage	38.66%

2.3. Coverage

Mean	0.0705

Standard Deviation	0.5038

2.4. Mapping Quality

Mean Mapping Quality	47.44

2.5. Mismatches and indels

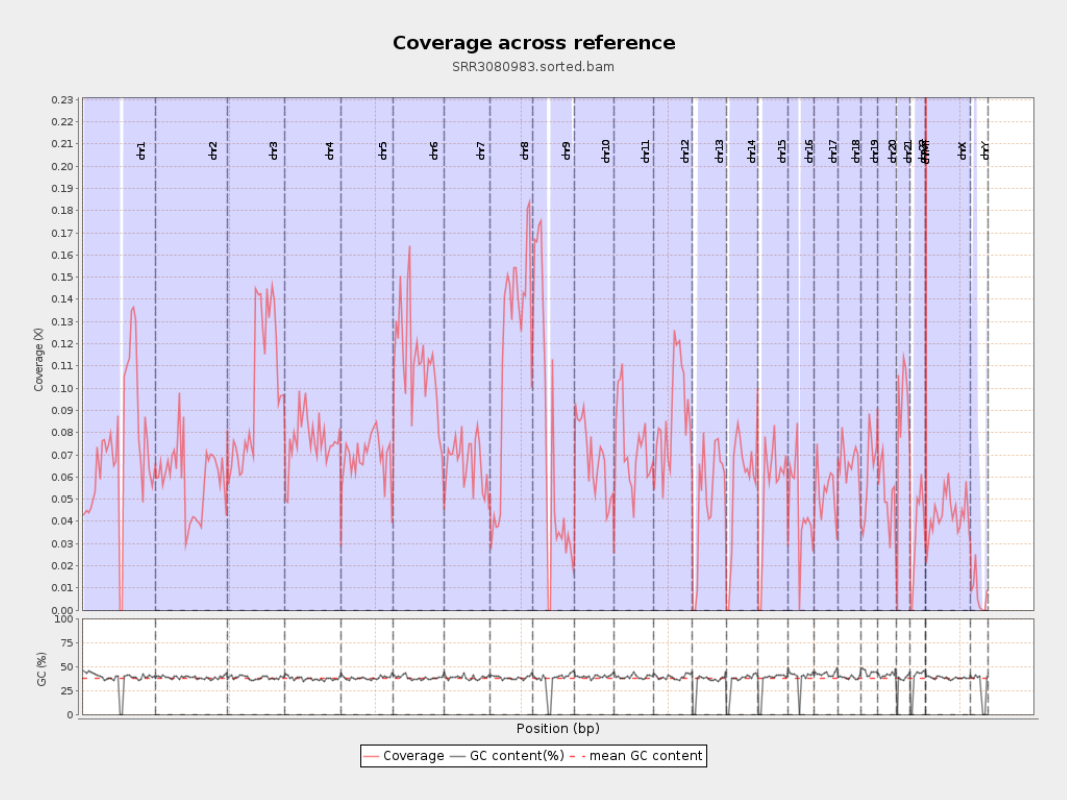
General error rate	0.98%
Mismatches	2,102,859
Insertions	16,245
Mapped reads with at least one insertion	0.5%
Deletions	43,758
Mapped reads with at least one deletion	1.34%
Homopolymer indels	49.32%

2.6. Chromosome stats

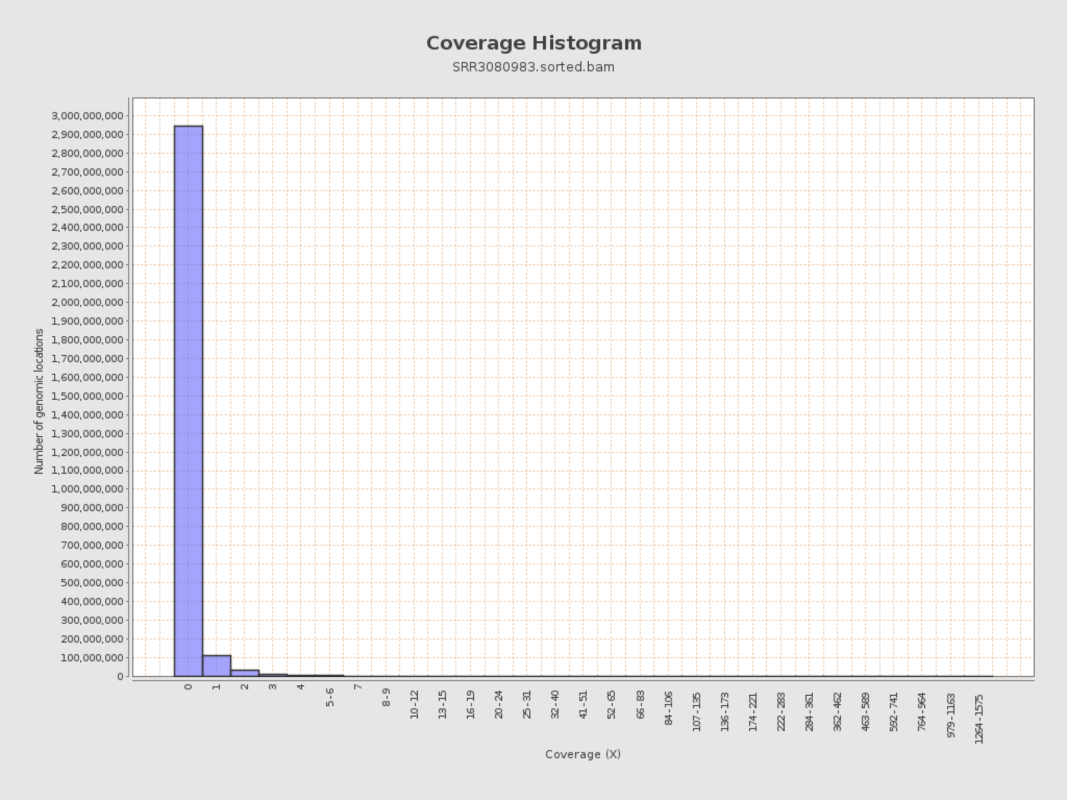
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17771662	0.0713	0.6799
chr2	243199373	14318697	0.0589	0.4389
chr3	198022430	19546585	0.0987	0.4285
chr4	191154276	14690936	0.0769	0.3875
chr5	180915260	12449154	0.0688	0.3551
chr6	171115067	19105772	0.1117	0.5668
chr7	159138663	10524511	0.0661	0.4559

chr8	146364022	16902697	0.1155	1.0515
chr9	141213431	10416112	0.0738	0.5757
chr10	135534747	9290125	0.0685	0.4155
chr11	135006516	9891357	0.0733	0.4149
chr12	133851895	11737711	0.0877	0.4115
chr13	115169878	5874302	0.051	0.3042
chr14	107349540	6140944	0.0572	0.3762
chr15	102531392	5631196	0.0549	0.3161
chr16	90354753	3967053	0.0439	0.3223
chr17	81195210	4398112	0.0542	0.3159
chr18	78077248	5270858	0.0675	0.9036
chr19	59128983	3678628	0.0622	0.5124
chr20	63025520	3326281	0.0528	0.3224
chr21	48129895	4236388	0.088	0.453
chr22	51304566	1795801	0.035	0.249
chrMT	16571	13350	0.8056	1.1492
chrX	155270560	6694069	0.0431	0.3063
chrY	59373566	444794	0.0075	0.1563

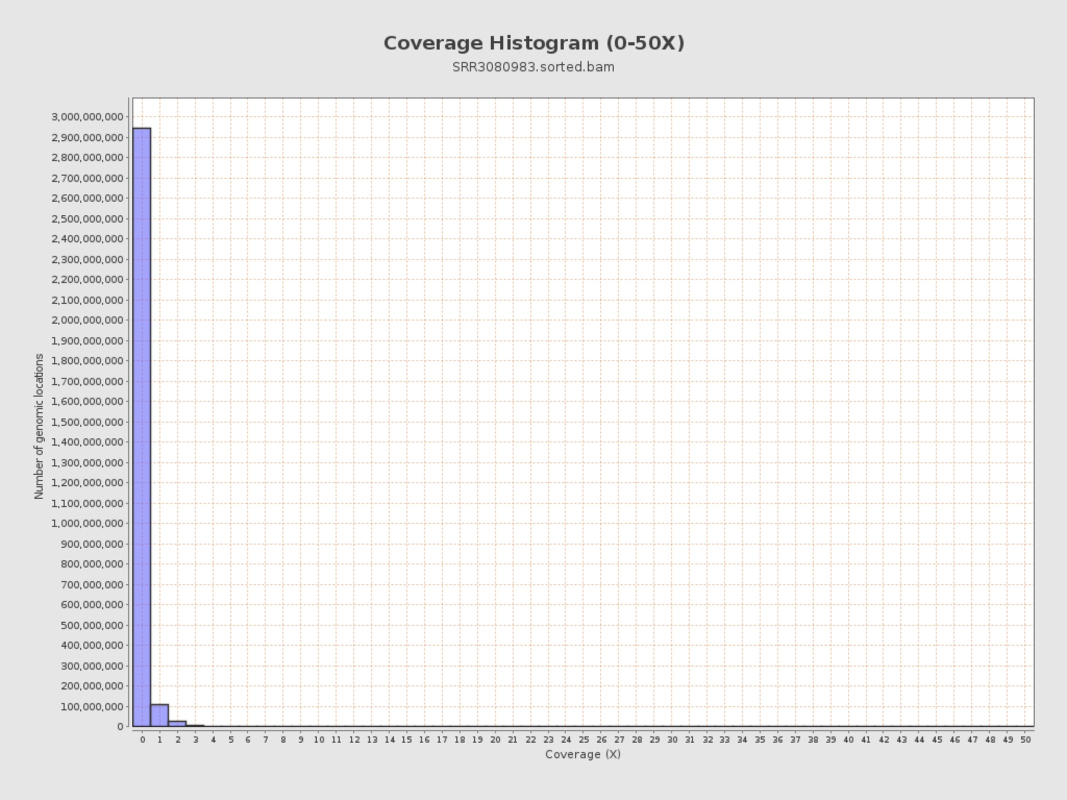
3. Results : Coverage across reference



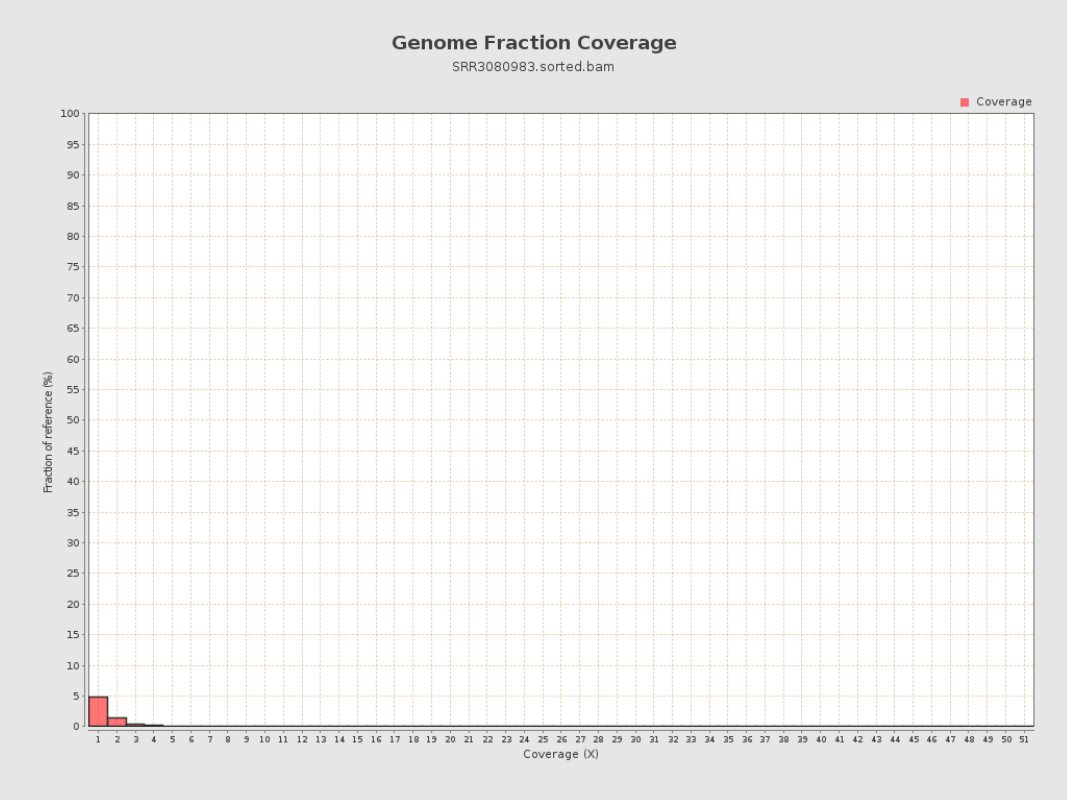
4. Results : Coverage Histogram



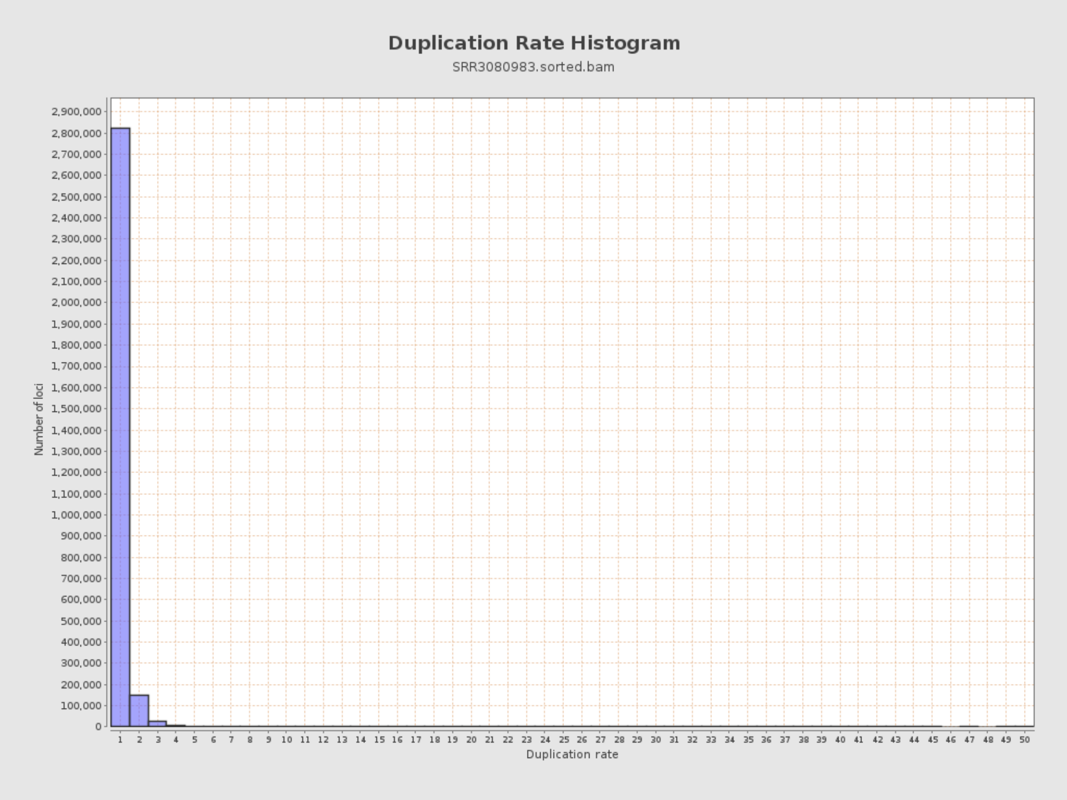
5. Results : Coverage Histogram (0-50X)



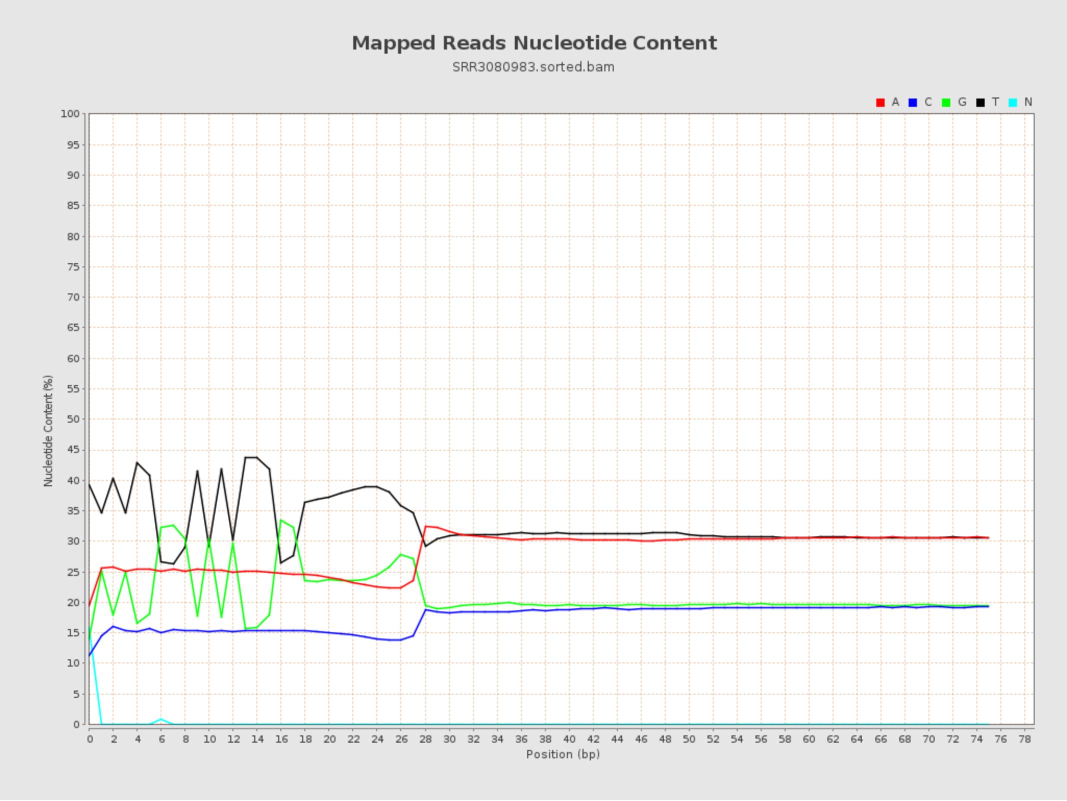
6. Results : Genome Fraction Coverage



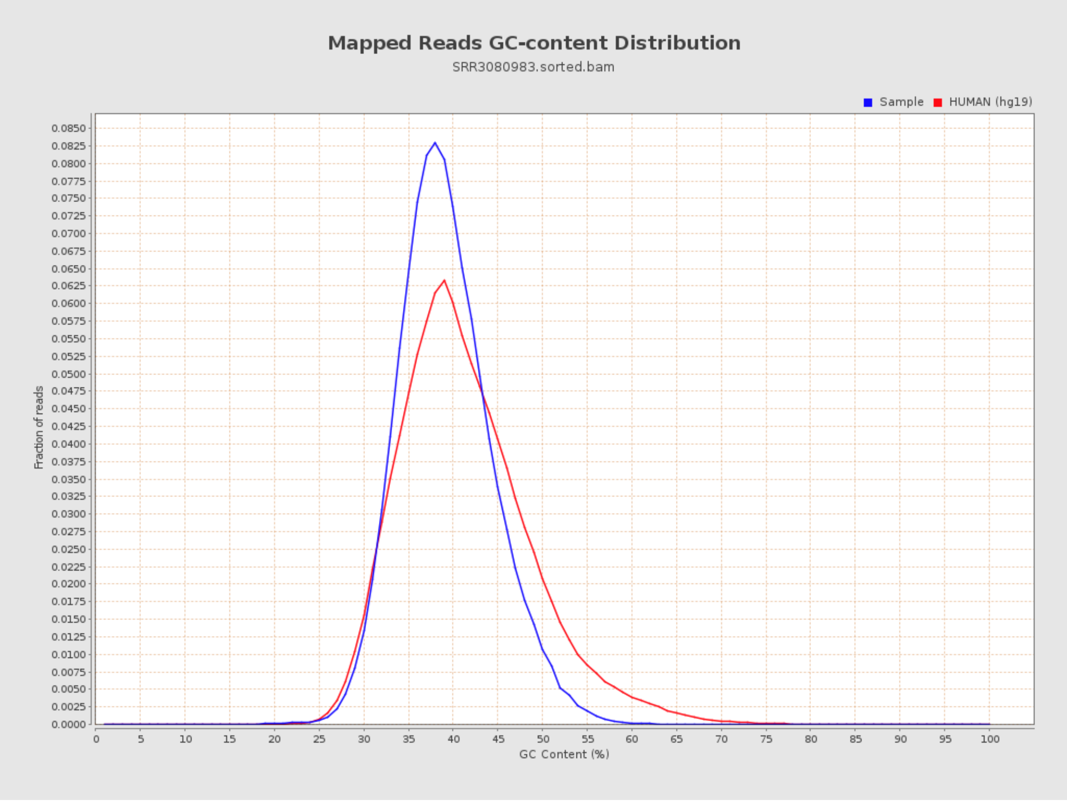
7. Results : Duplication Rate Histogram



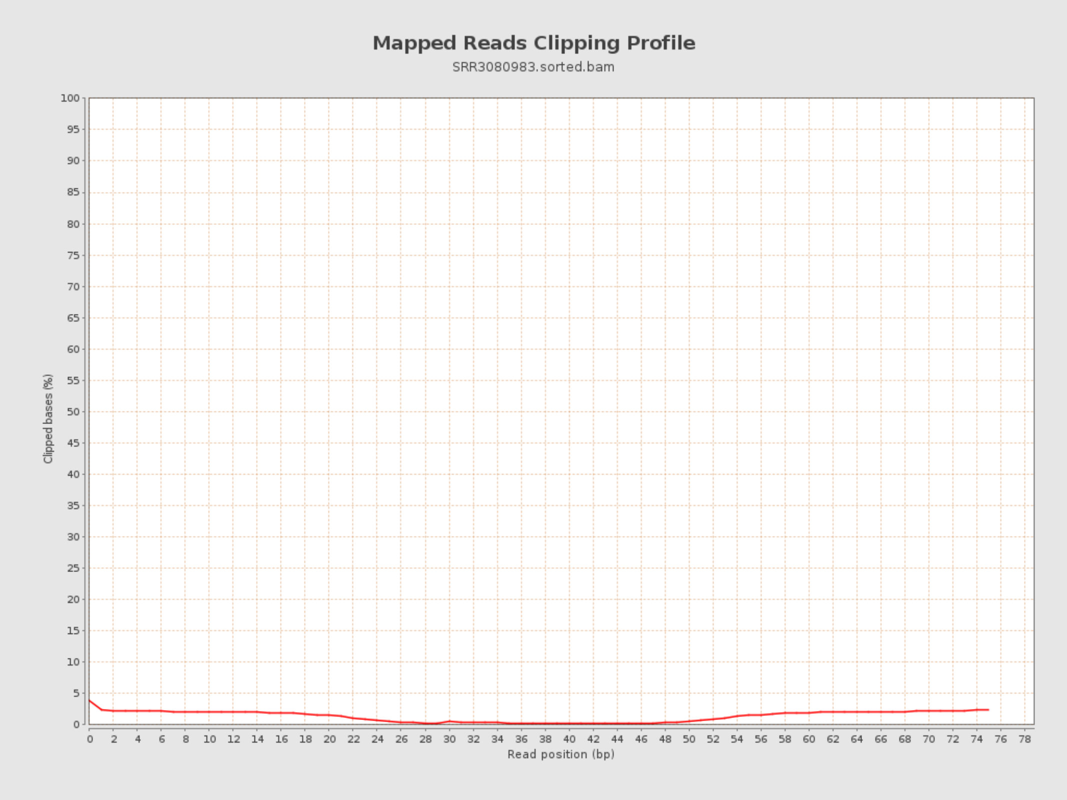
8. Results : Mapped Reads Nucleotide Content



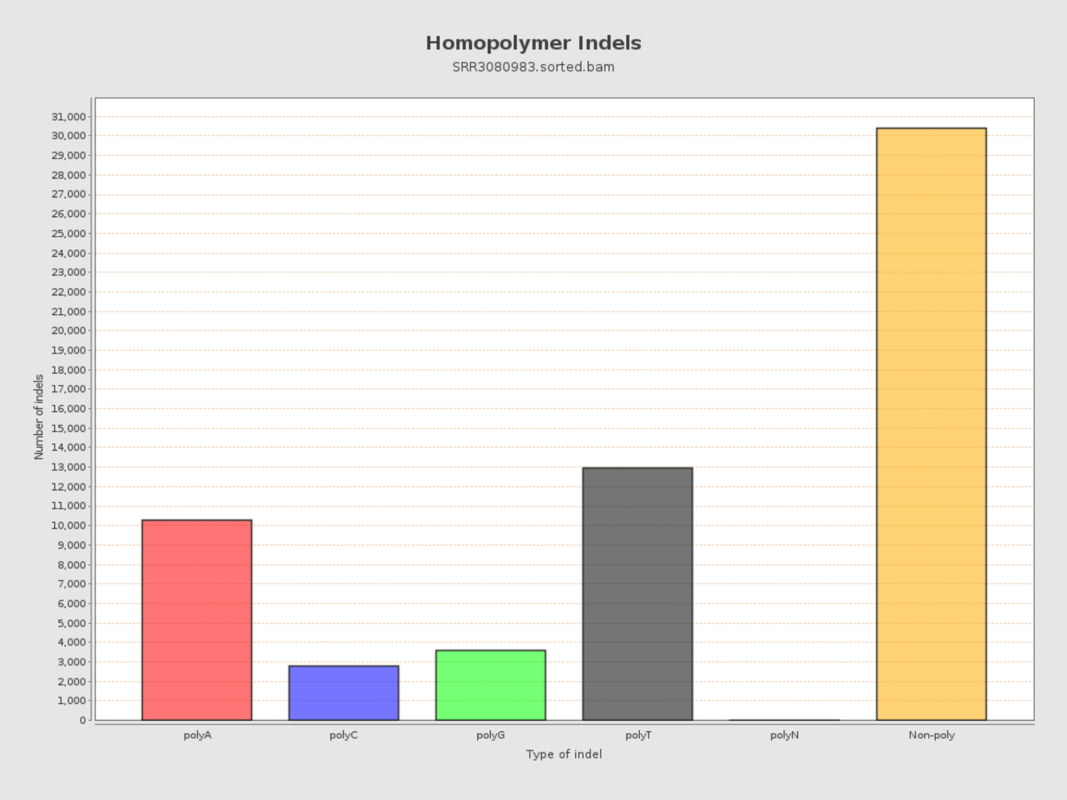
9. Results : Mapped Reads GC-content Distribution



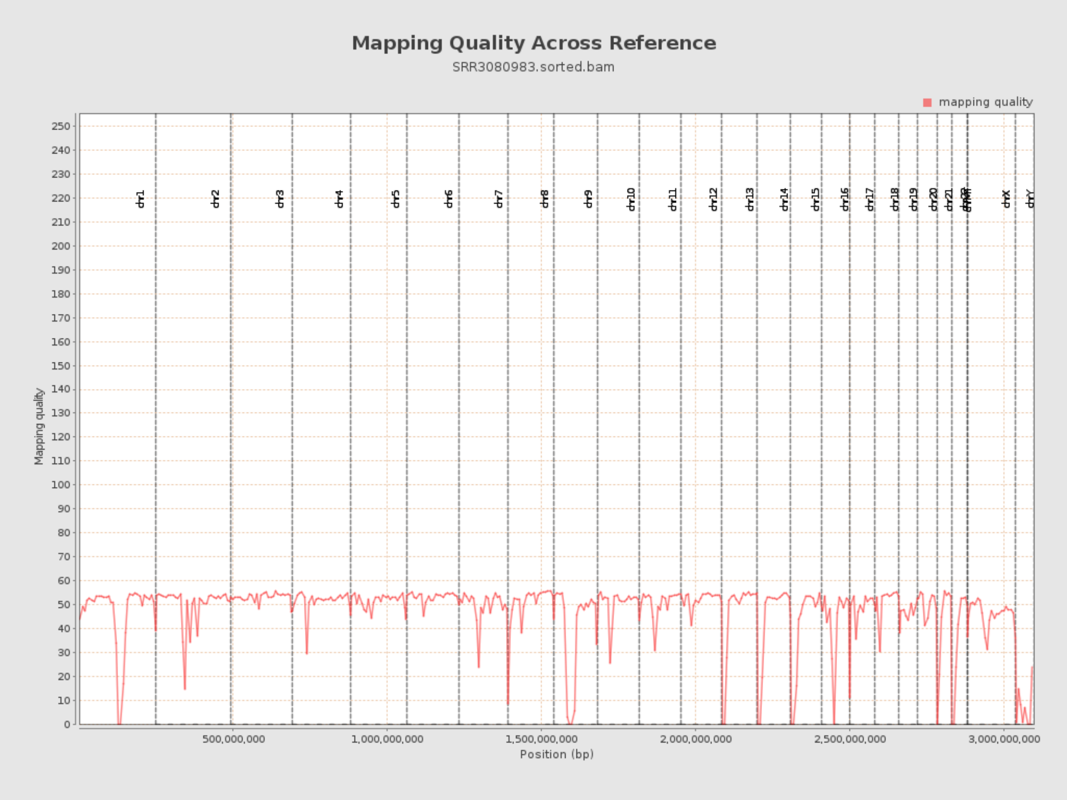
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram