Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:47:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080908.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_SRR3080908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:47:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,852,271
Mapped reads	4,435,169 / 91.4%
Unmapped reads	417,102 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	69,243 / 1.43%
Read min/max/mean length	30 / 76 / 76.5
Duplicated reads (estimated)	228,454 / 4.71%
Duplication rate	4.16%
Clipped reads	1,622,647 / 33.44%

2.2. ACGT Content

Number/percentage of A's	89,985,693 / 29.34%
Number/percentage of C's	55,830,516 / 18.21%
Number/percentage of T's	96,328,988 / 31.41%
Number/percentage of G's	63,019,744 / 20.55%
Number/percentage of N's	1,505,216 / 0.49%
GC Percentage	38.76%

2.3. Coverage

Mean	0.0991

Standard Deviation	0.5868

2.4. Mapping Quality

Mean Mapping Quality	47.89

2.5. Mismatches and indels

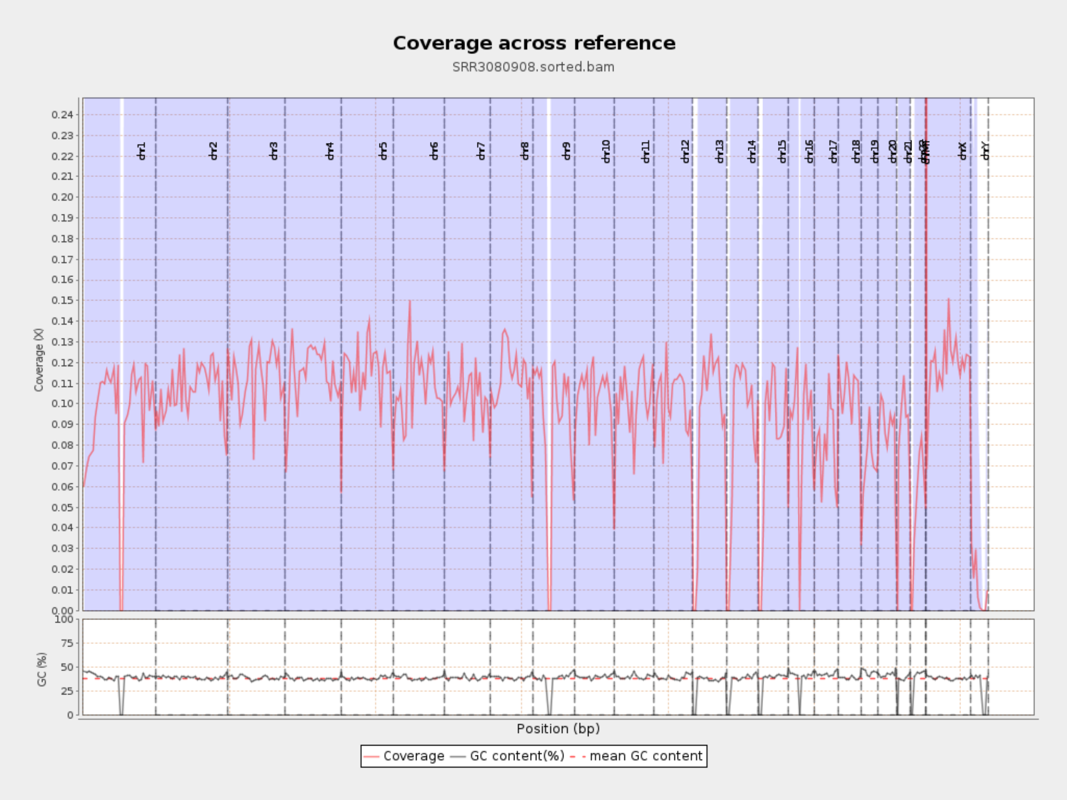
General error rate	1.16%
Mismatches	3,524,110
Insertions	22,594
Mapped reads with at least one insertion	0.51%
Deletions	68,333
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.21%

2.6. Chromosome stats

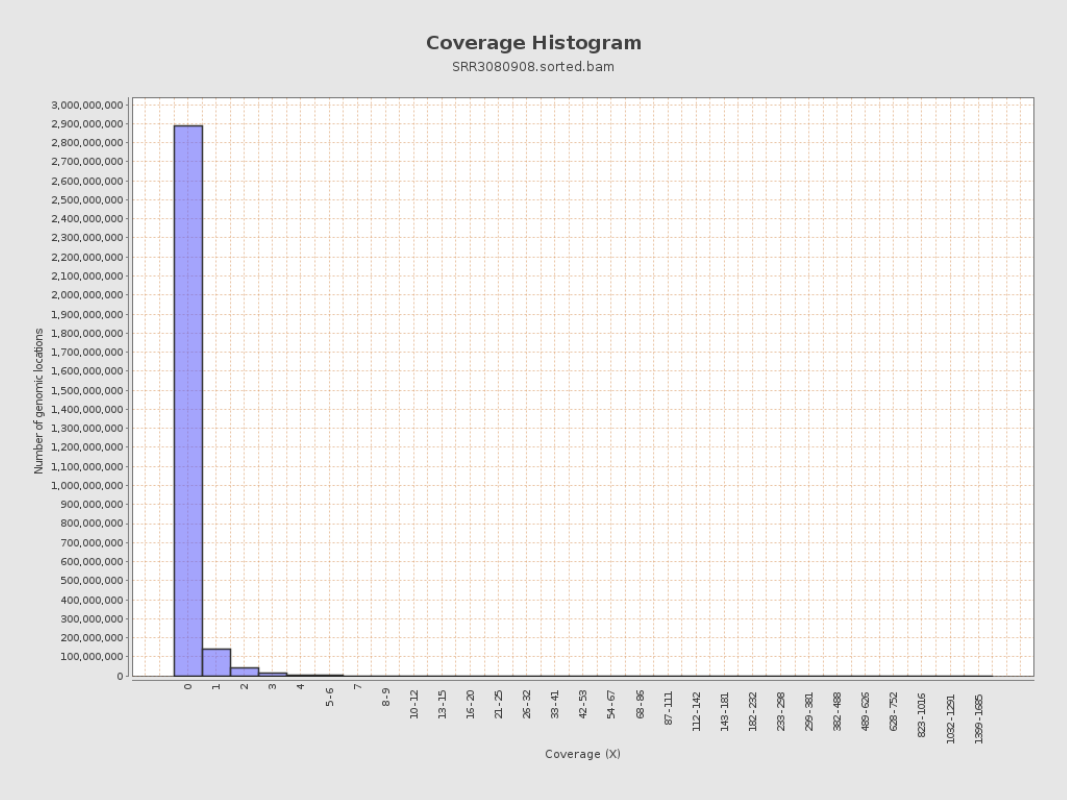
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23492210	0.0943	0.7283
chr2	243199373	25914451	0.1066	0.6026
chr3	198022430	22377923	0.113	0.466
chr4	191154276	21899154	0.1146	0.4784
chr5	180915260	20645960	0.1141	0.4699
chr6	171115067	18774665	0.1097	0.5445
chr7	159138663	16503775	0.1037	0.7363

chr8	146364022	16371414	0.1119	1.1209
chr9	141213431	12770631	0.0904	0.5451
chr10	135534747	14130458	0.1043	0.537
chr11	135006516	13757489	0.1019	0.5511
chr12	133851895	13540609	0.1012	0.4433
chr13	115169878	10557170	0.0917	0.4221
chr14	107349540	9497511	0.0885	0.4722
chr15	102531392	8292305	0.0809	0.3963
chr16	90354753	7792619	0.0862	0.4337
chr17	81195210	6544690	0.0806	0.4286
chr18	78077248	8345770	0.1069	0.9071
chr19	59128983	4240495	0.0717	0.6267
chr20	63025520	5667677	0.0899	0.4311
chr21	48129895	3937932	0.0818	0.4142
chr22	51304566	2610104	0.0509	0.3053
chrMT	16571	78285	4.7242	3.8877
chrX	155270560	18389088	0.1184	0.515
chrY	59373566	649091	0.0109	0.182

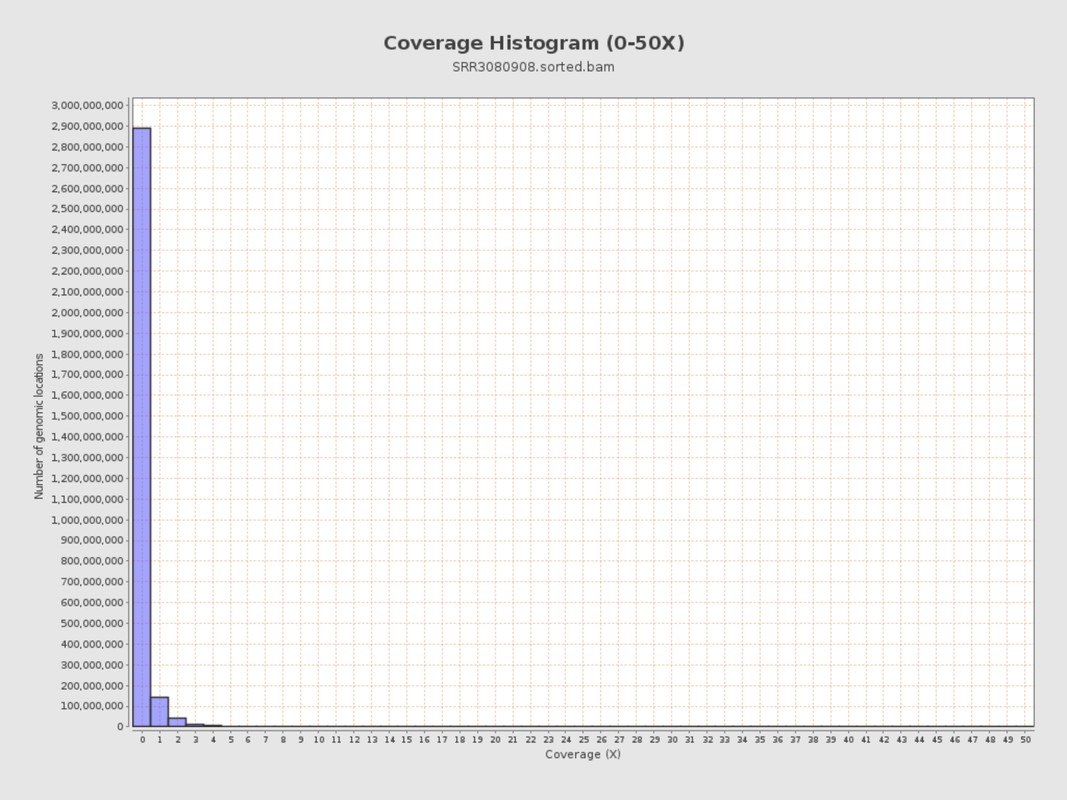
3. Results : Coverage across reference



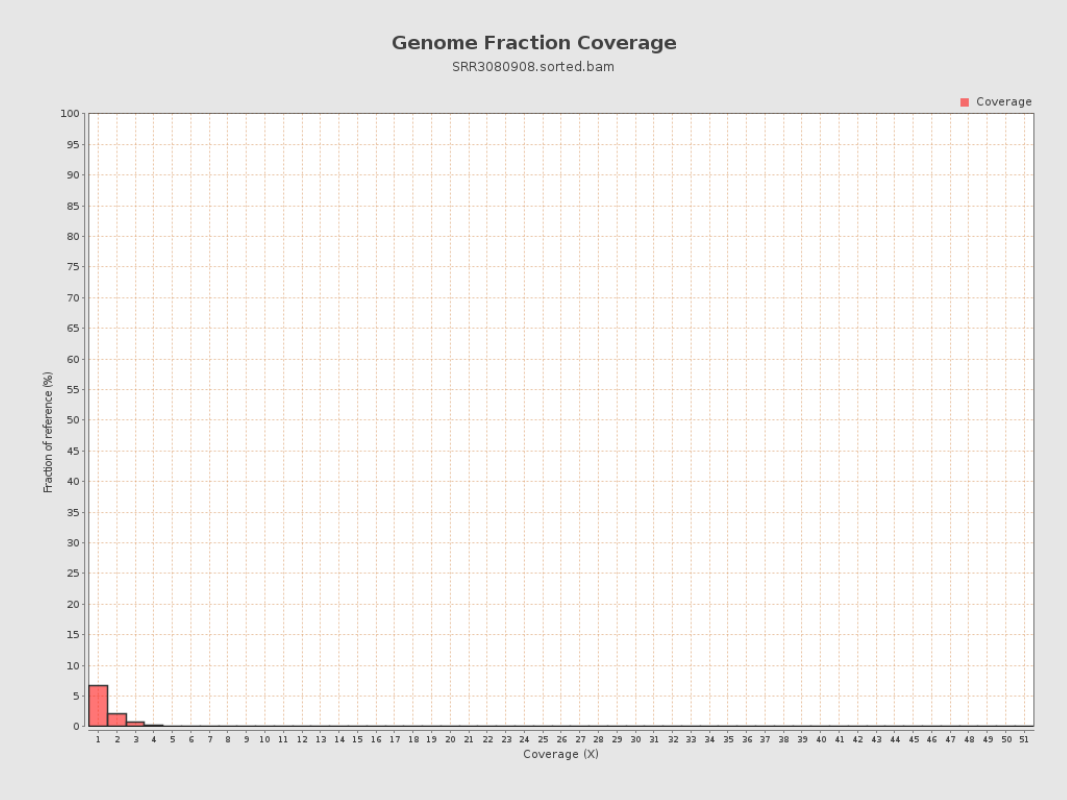
4. Results : Coverage Histogram



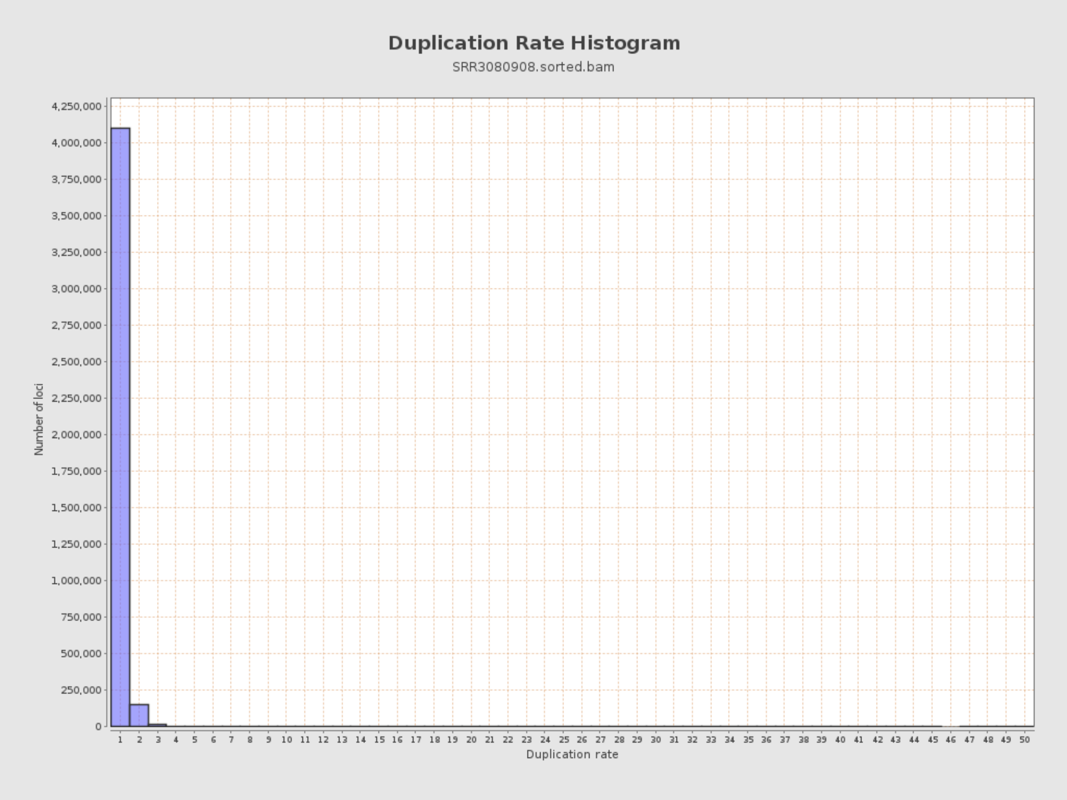
5. Results : Coverage Histogram (0-50X)



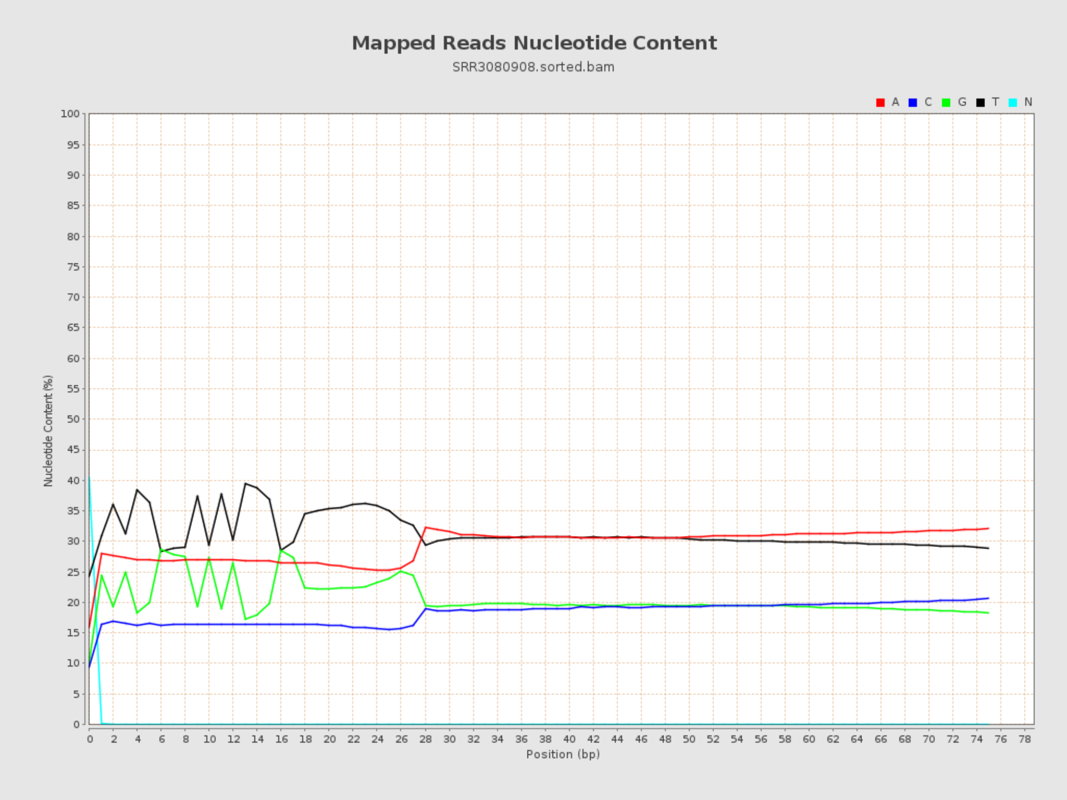
6. Results : Genome Fraction Coverage



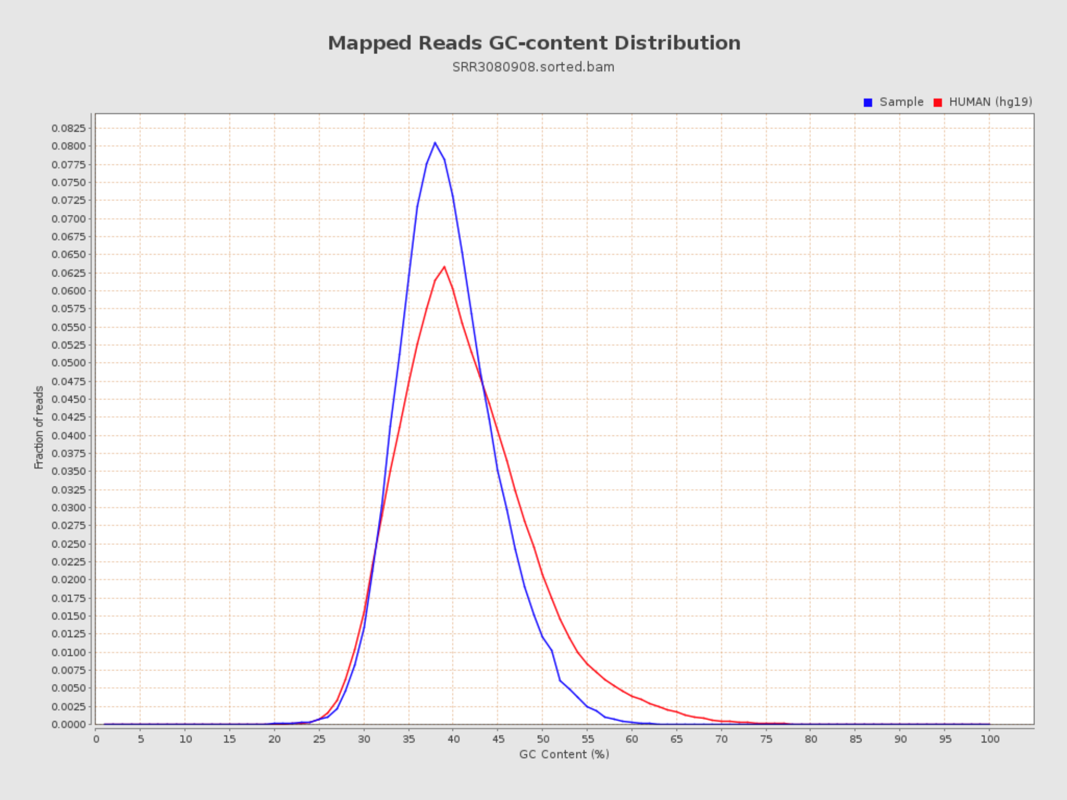
7. Results : Duplication Rate Histogram



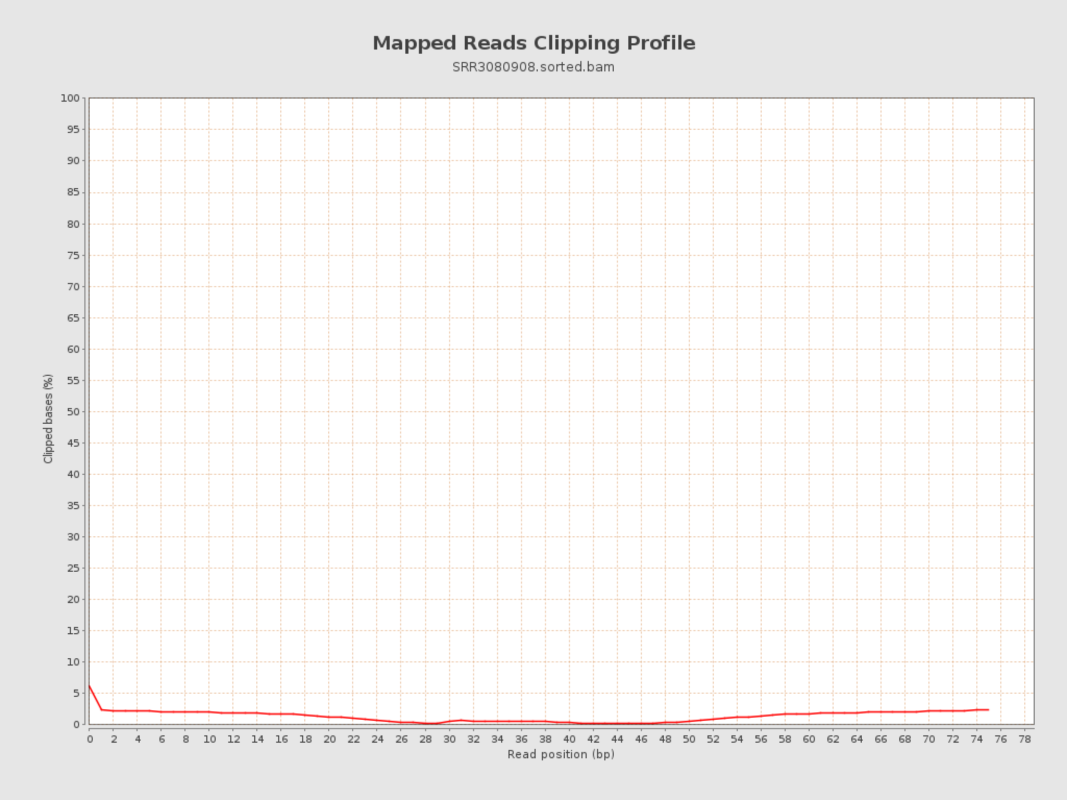
8. Results : Mapped Reads Nucleotide Content



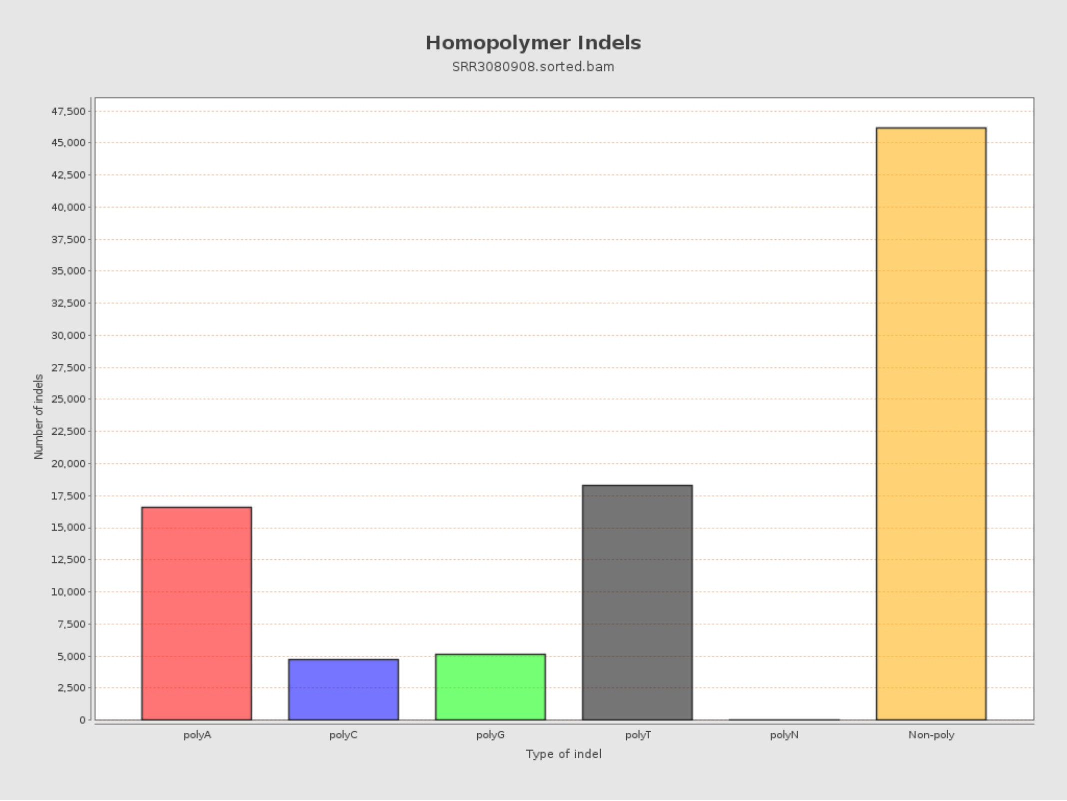
9. Results : Mapped Reads GC-content Distribution



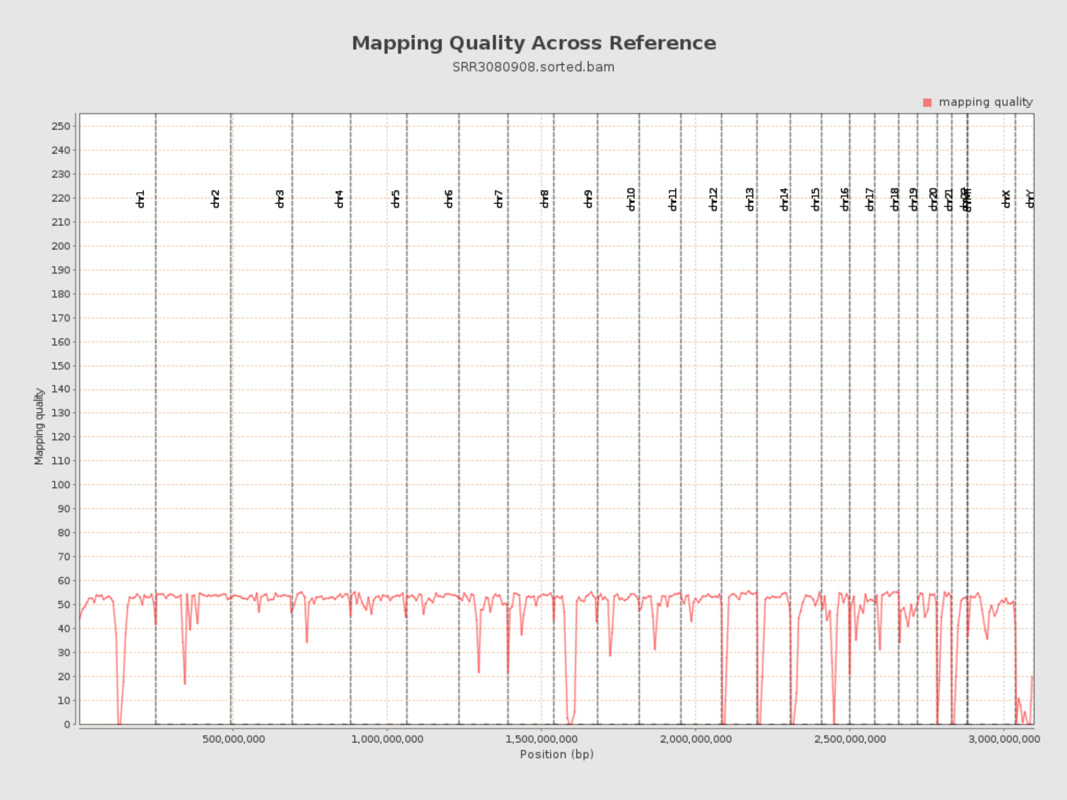
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram