Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:31:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082692.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_SRR3082692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082692.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:31:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082692.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,574,281
Mapped reads	3,286,643 / 91.95%
Unmapped reads	287,638 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,954 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	147,413 / 4.12%
Duplication rate	3.35%
Clipped reads	1,589,793 / 44.48%

2.2. ACGT Content

Number/percentage of A's	59,447,447 / 27.41%
Number/percentage of C's	37,069,051 / 17.09%
Number/percentage of T's	72,487,054 / 33.42%
Number/percentage of G's	47,859,780 / 22.06%
Number/percentage of N's	56,382 / 0.03%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0701

Standard Deviation	0.5532

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

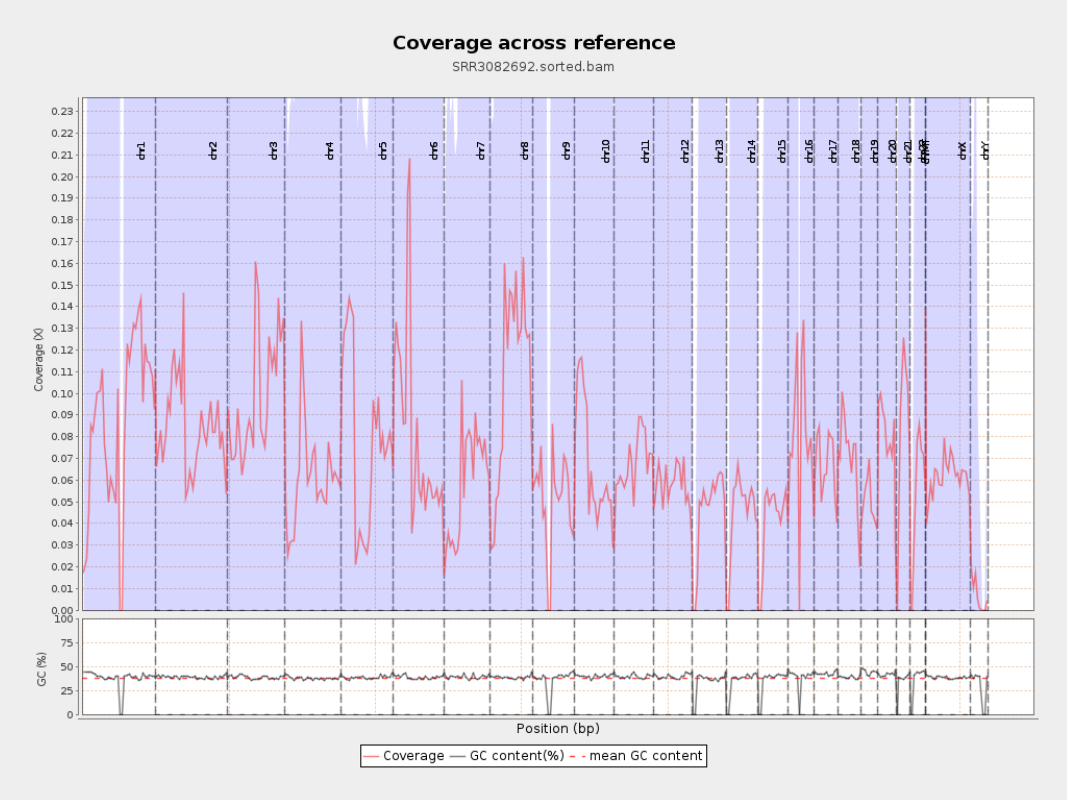
General error rate	0.93%
Mismatches	1,976,087
Insertions	19,815
Mapped reads with at least one insertion	0.6%
Deletions	51,933
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.1%

2.6. Chromosome stats

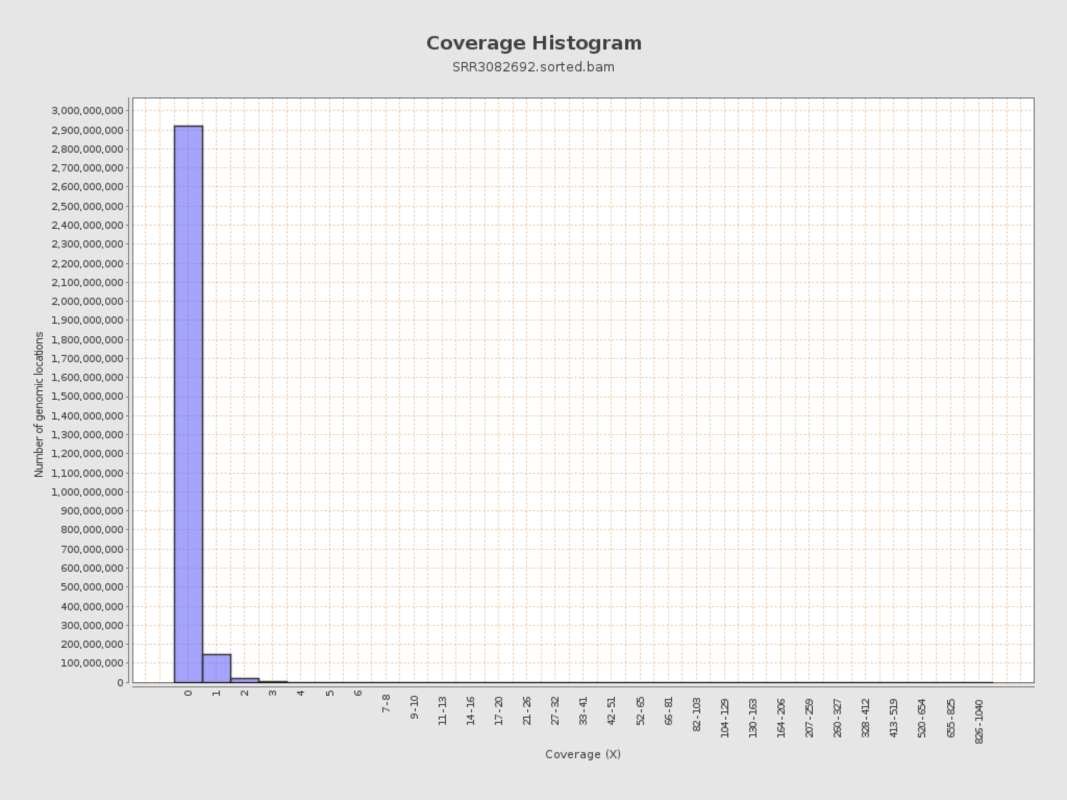
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21440470	0.086	0.8761
chr2	243199373	20433469	0.084	0.7685
chr3	198022430	19287531	0.0974	0.3716
chr4	191154276	11793098	0.0617	0.3036
chr5	180915260	14020367	0.0775	0.3333
chr6	171115067	14000121	0.0818	0.5203
chr7	159138663	9352006	0.0588	0.8237

chr8	146364022	15796272	0.1079	0.5497
chr9	141213431	7252924	0.0514	0.6099
chr10	135534747	9264724	0.0684	0.4793
chr11	135006516	9184900	0.068	0.4916
chr12	133851895	7720308	0.0577	0.2888
chr13	115169878	5238160	0.0455	0.2468
chr14	107349540	4912326	0.0458	0.2981
chr15	102531392	4156019	0.0405	0.2337
chr16	90354753	7193426	0.0796	0.3828
chr17	81195210	5563070	0.0685	0.4409
chr18	78077248	5597622	0.0717	1.1457
chr19	59128983	2992854	0.0506	0.662
chr20	63025520	5175756	0.0821	0.3602
chr21	48129895	3962477	0.0823	0.3552
chr22	51304566	2756285	0.0537	0.2713
chrMT	16571	2311	0.1395	0.3838
chrX	155270560	9517763	0.0613	0.374
chrY	59373566	388309	0.0065	0.1357

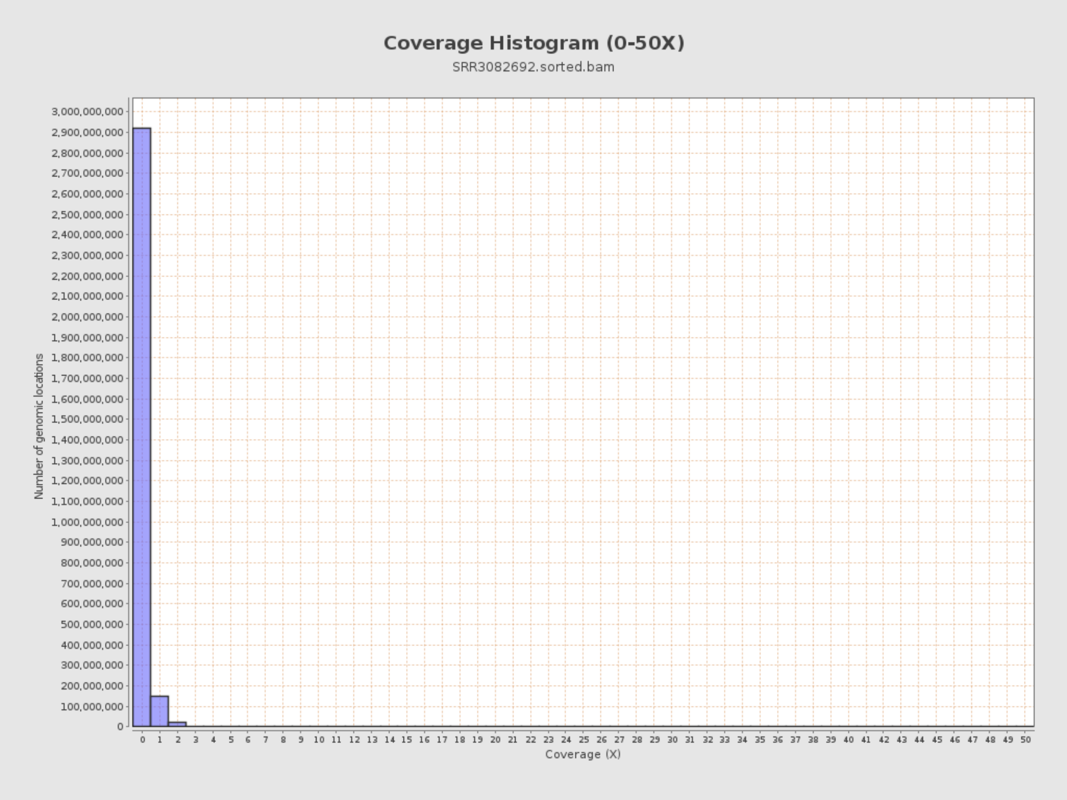
3. Results : Coverage across reference



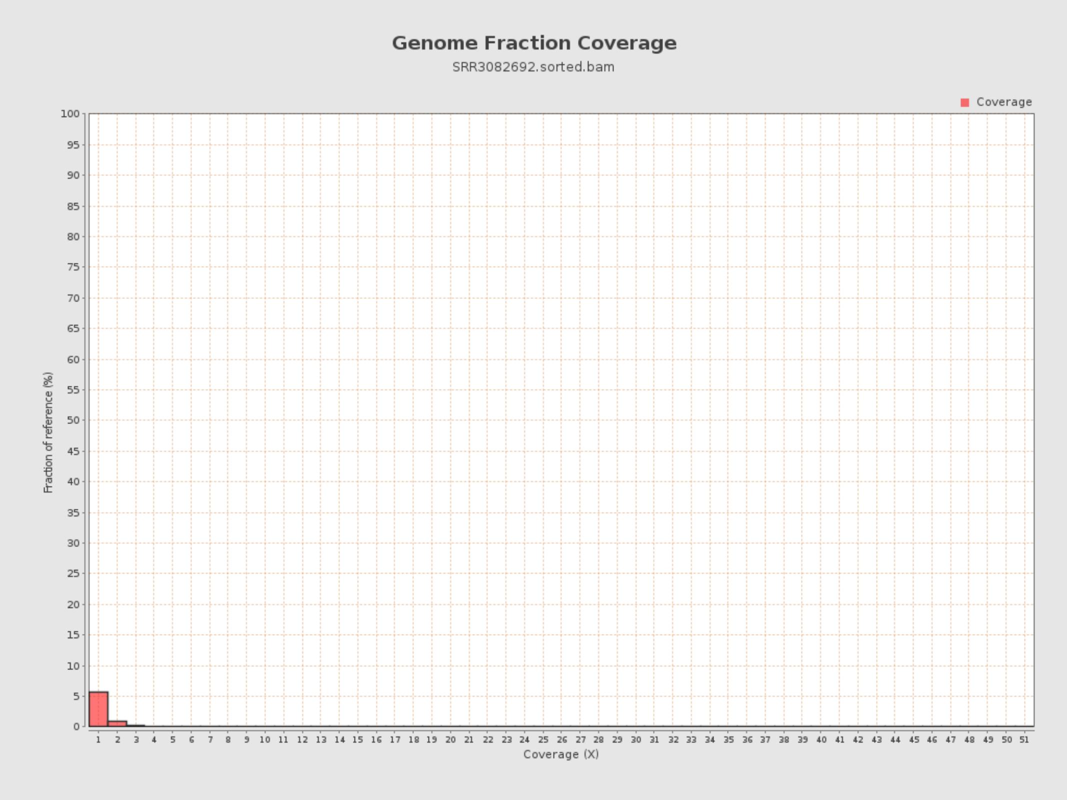
4. Results : Coverage Histogram



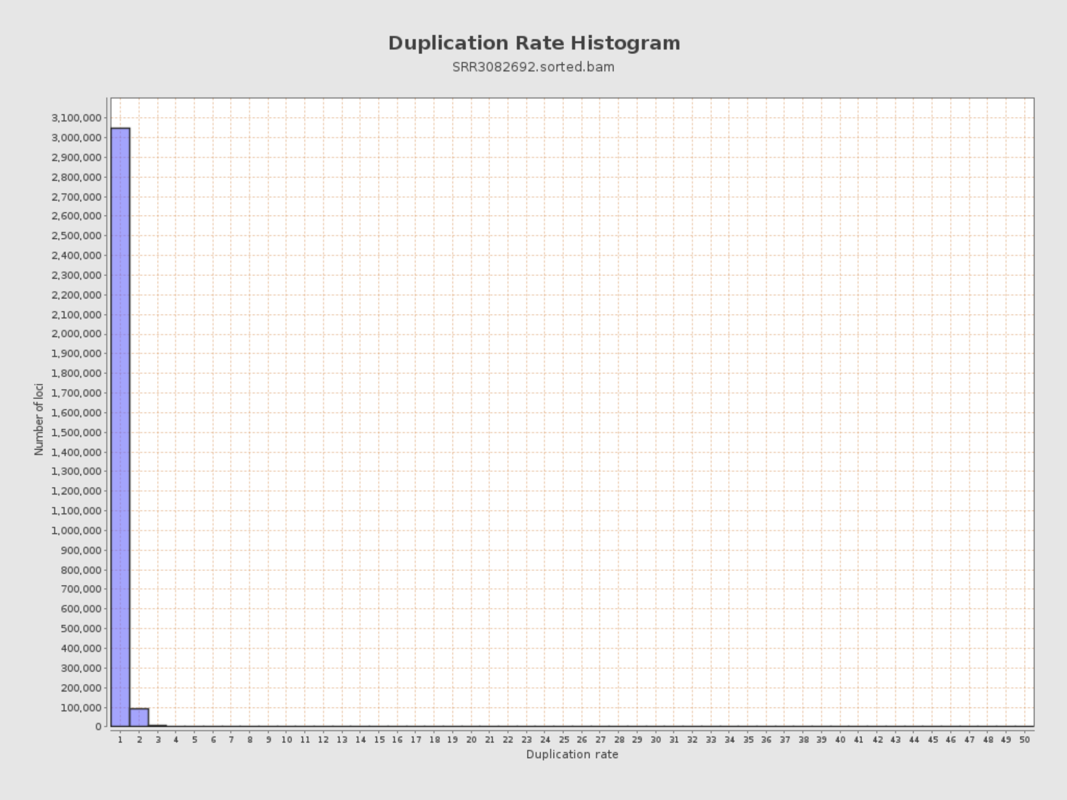
5. Results : Coverage Histogram (0-50X)



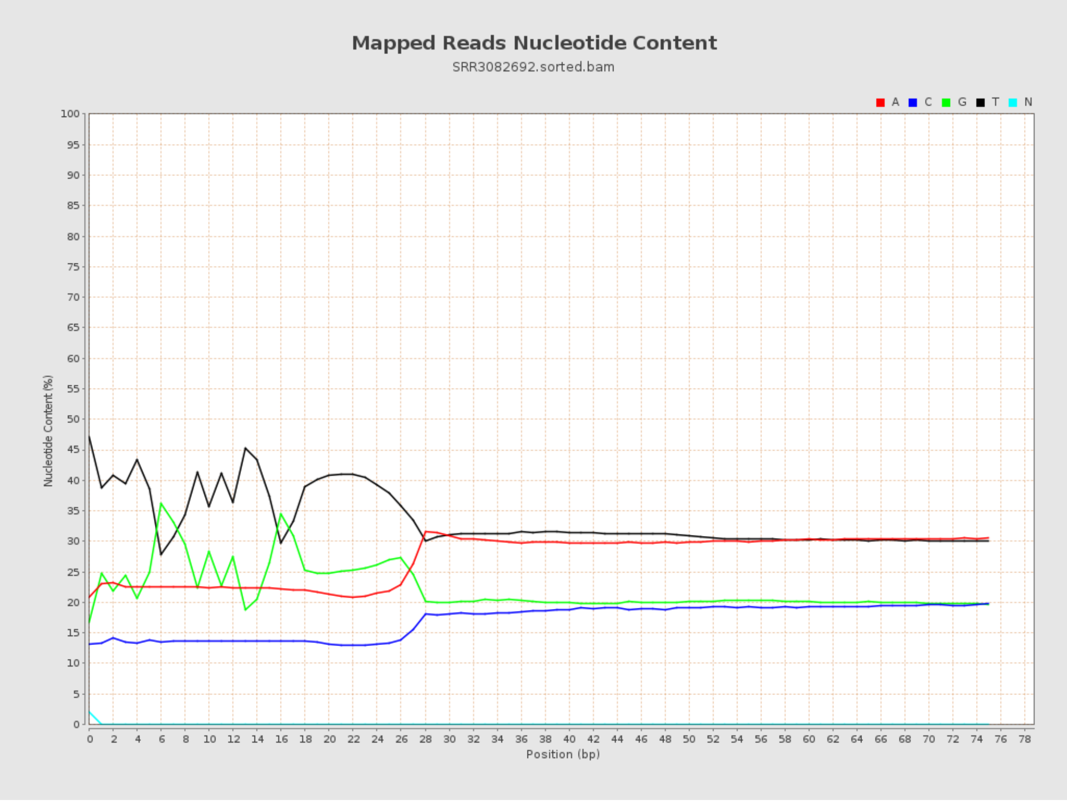
6. Results : Genome Fraction Coverage



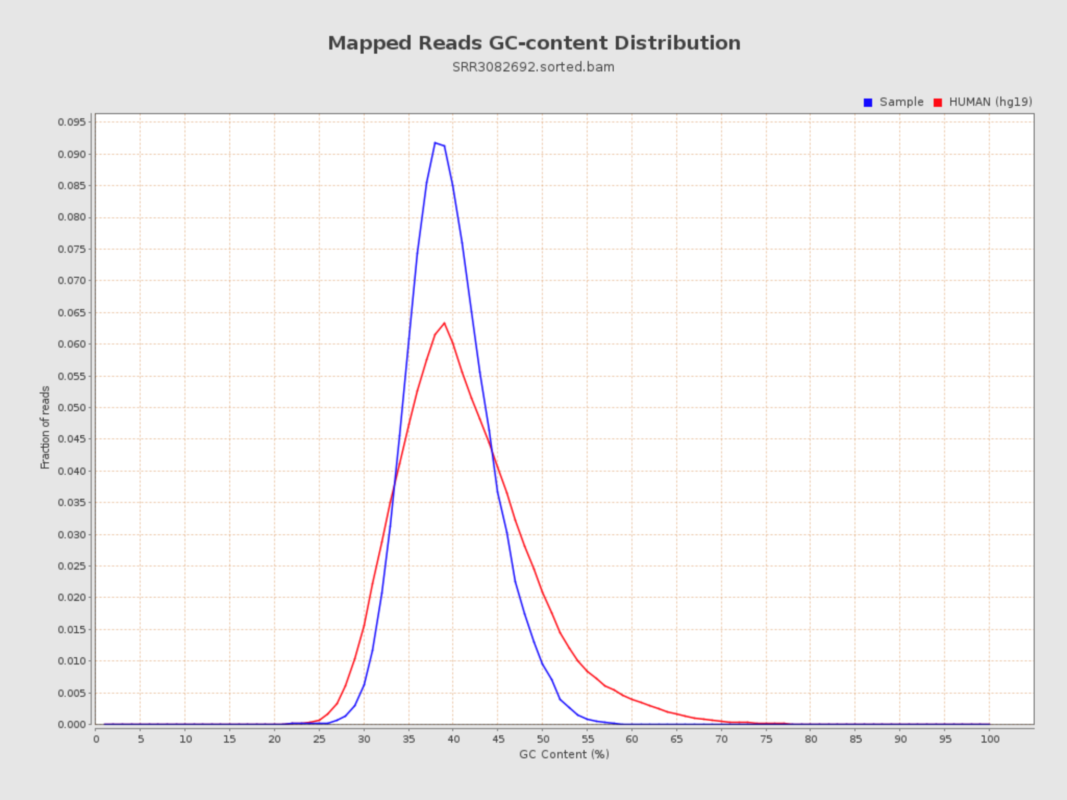
7. Results : Duplication Rate Histogram



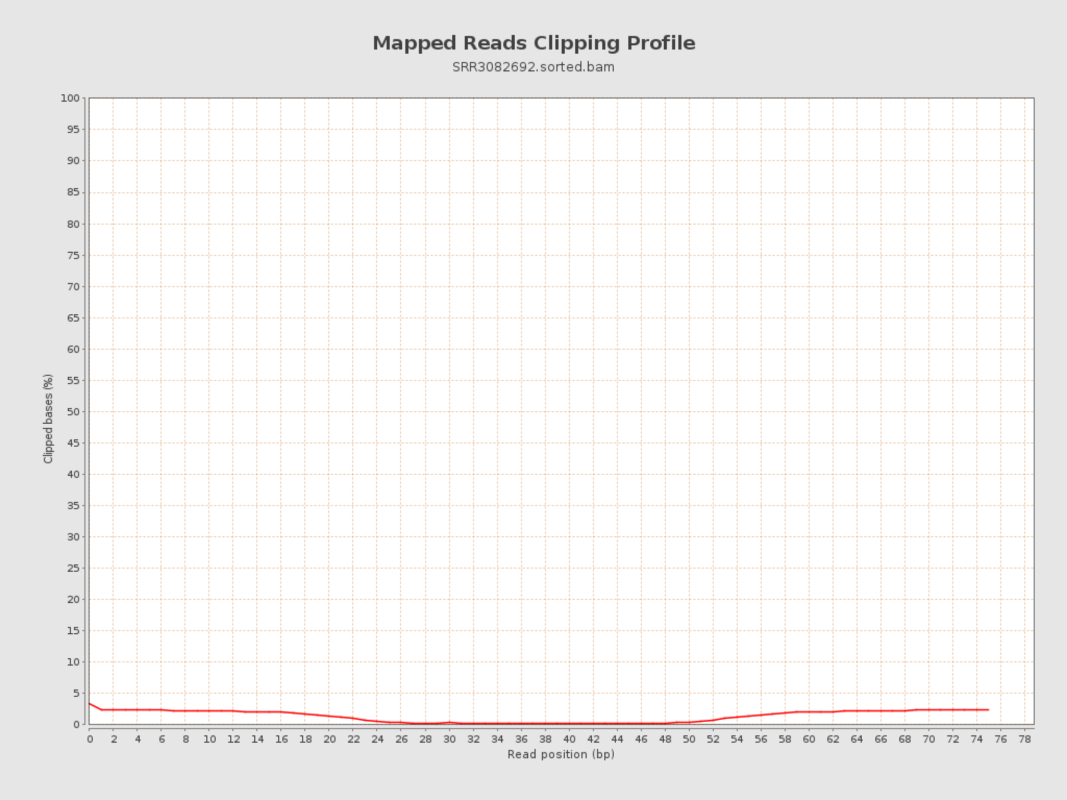
8. Results : Mapped Reads Nucleotide Content



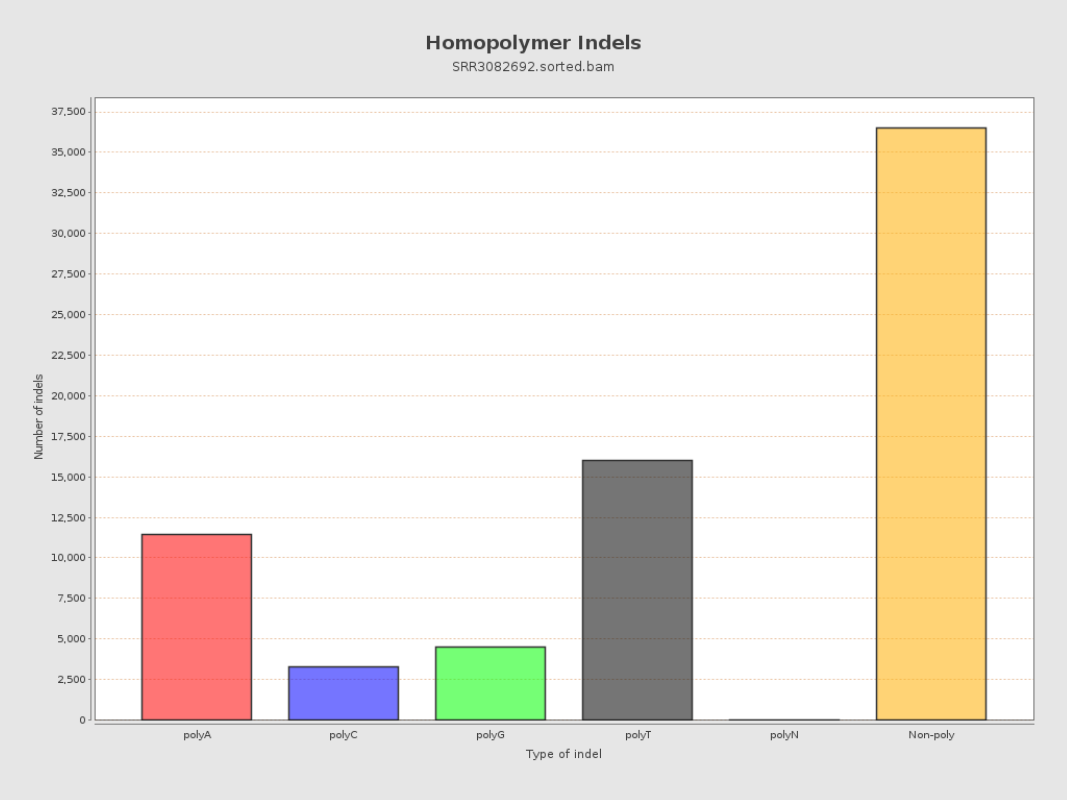
9. Results : Mapped Reads GC-content Distribution



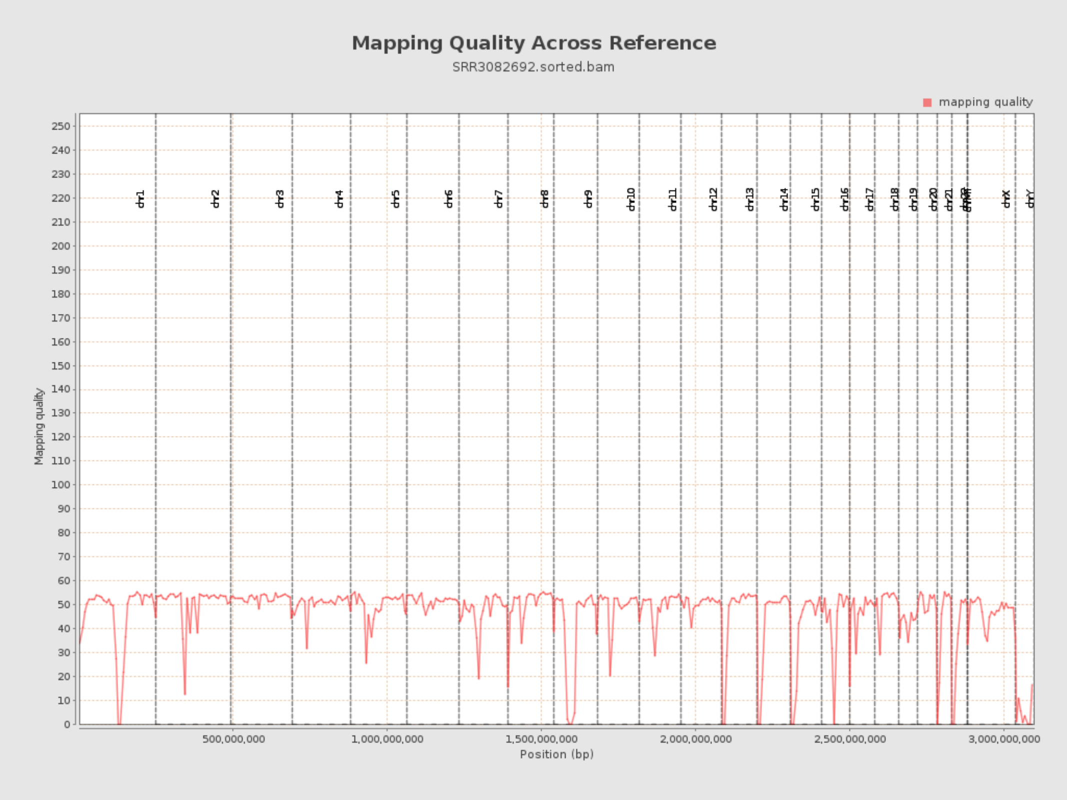
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram