Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:52:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080692.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_SRR3080692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080692.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:52:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080692.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,800,294
Mapped reads	2,489,469 / 88.9%
Unmapped reads	310,825 / 11.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,510 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	139,299 / 4.97%
Duplication rate	4.39%
Clipped reads	740,579 / 26.45%

2.2. ACGT Content

Number/percentage of A's	53,327,433 / 30.35%
Number/percentage of C's	32,481,615 / 18.49%
Number/percentage of T's	54,768,362 / 31.17%
Number/percentage of G's	35,124,914 / 19.99%
Number/percentage of N's	2,774 / 0%
GC Percentage	38.48%

2.3. Coverage

Mean	0.0568

Standard Deviation	0.6191

2.4. Mapping Quality

Mean Mapping Quality	48.19

2.5. Mismatches and indels

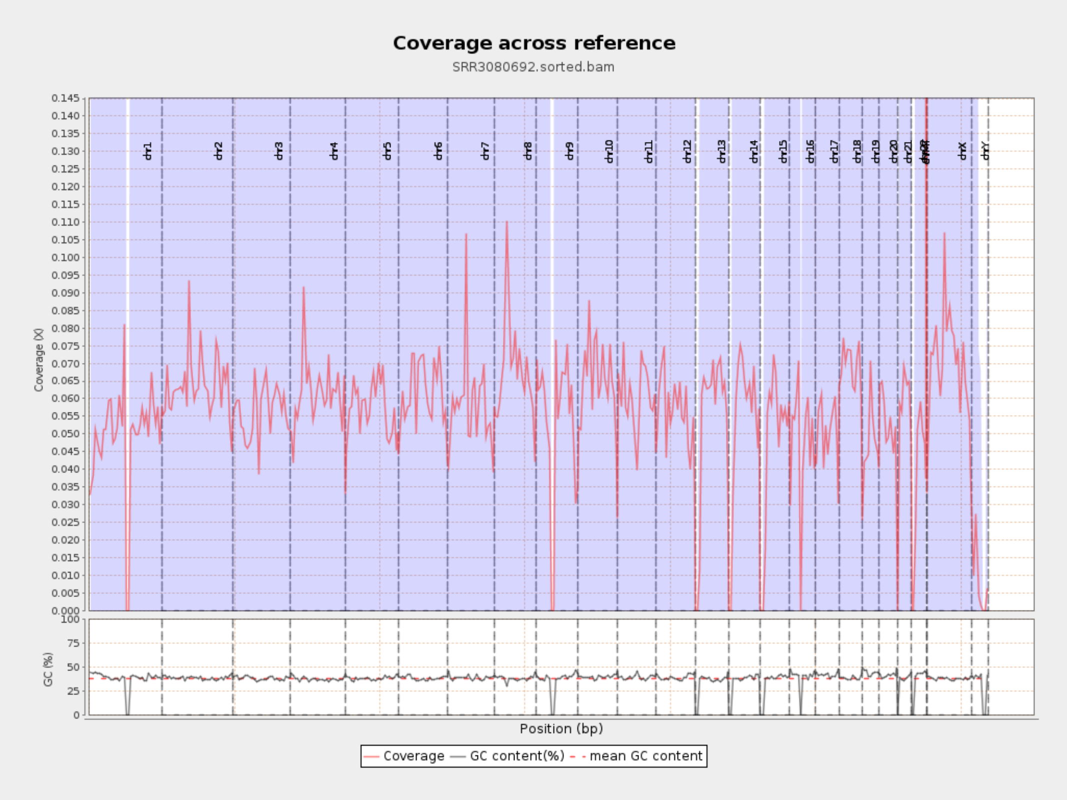
General error rate	0.83%
Mismatches	1,420,218
Insertions	14,617
Mapped reads with at least one insertion	0.58%
Deletions	38,335
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.17%

2.6. Chromosome stats

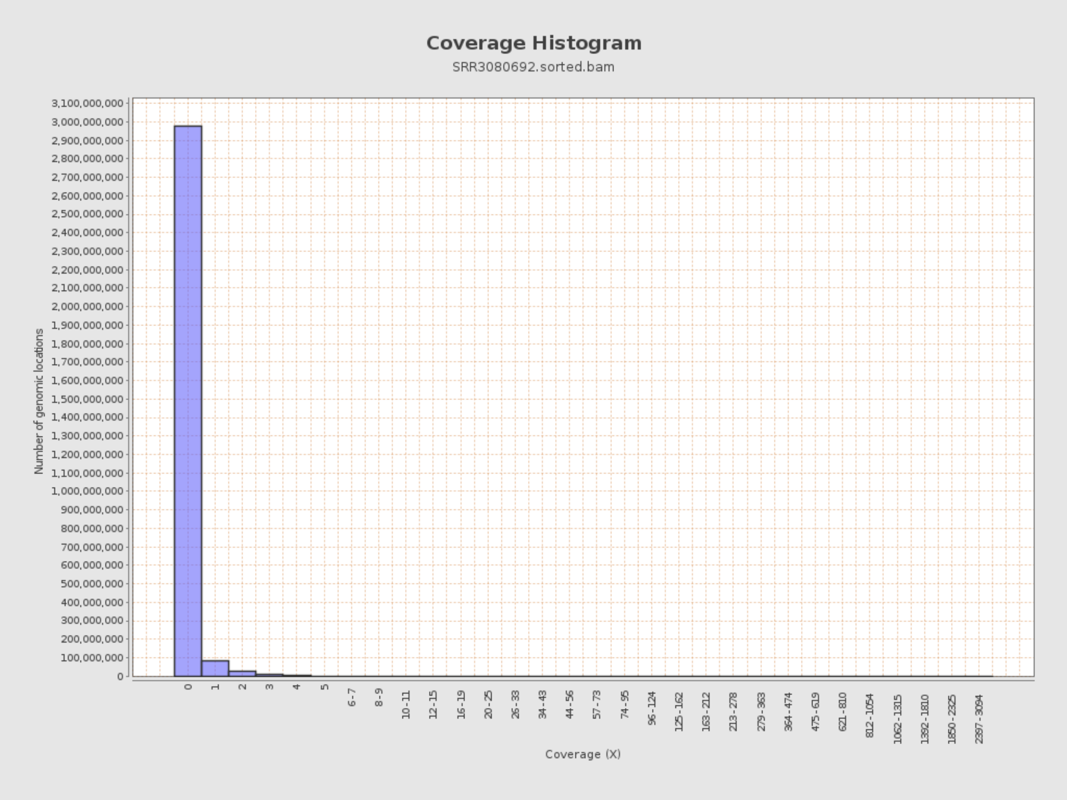
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12293806	0.0493	0.7057
chr2	243199373	15573256	0.064	0.4958
chr3	198022430	11155330	0.0563	0.3277
chr4	191154276	11722385	0.0613	0.3781
chr5	180915260	10433071	0.0577	0.3331
chr6	171115067	10566772	0.0618	0.3569
chr7	159138663	9318661	0.0586	0.8136

chr8	146364022	9951339	0.068	1.9366
chr9	141213431	7483078	0.053	0.4583
chr10	135534747	8960340	0.0661	0.4589
chr11	135006516	8118016	0.0601	0.4075
chr12	133851895	7557447	0.0565	0.3332
chr13	115169878	6113036	0.0531	0.3206
chr14	107349540	5686872	0.053	0.3411
chr15	102531392	4832950	0.0471	0.2972
chr16	90354753	4280785	0.0474	0.327
chr17	81195210	4055949	0.05	0.3453
chr18	78077248	5437219	0.0696	0.7769
chr19	59128983	2849521	0.0482	0.4736
chr20	63025520	3330323	0.0528	0.3236
chr21	48129895	2654060	0.0551	0.3585
chr22	51304566	1844150	0.0359	0.2502
chrMT	16571	254630	15.366	9.0766
chrX	155270560	10828685	0.0697	0.4
chrY	59373566	473164	0.008	0.2241

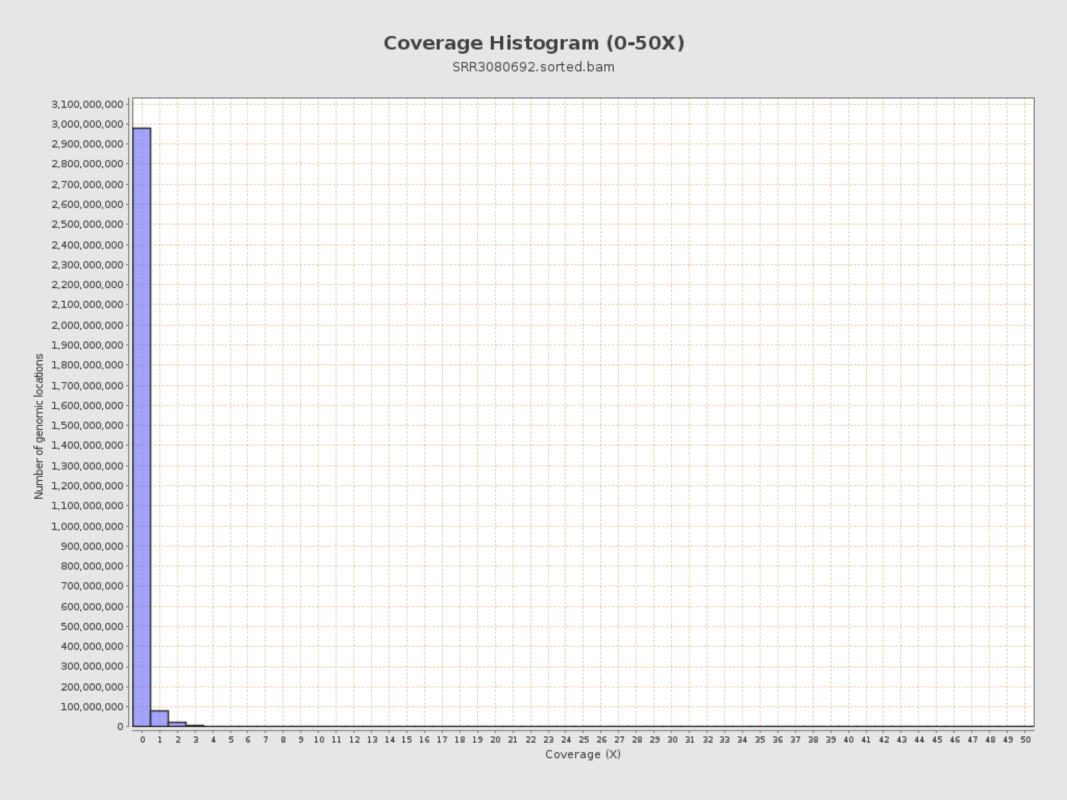
3. Results : Coverage across reference



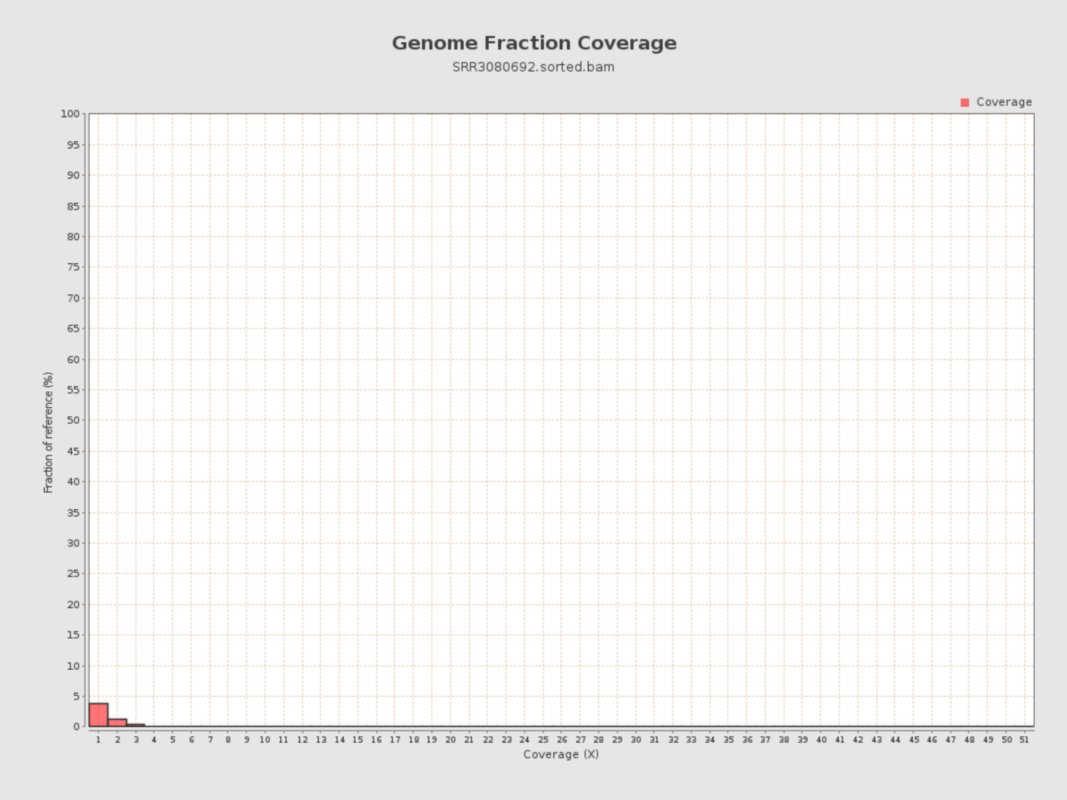
4. Results : Coverage Histogram



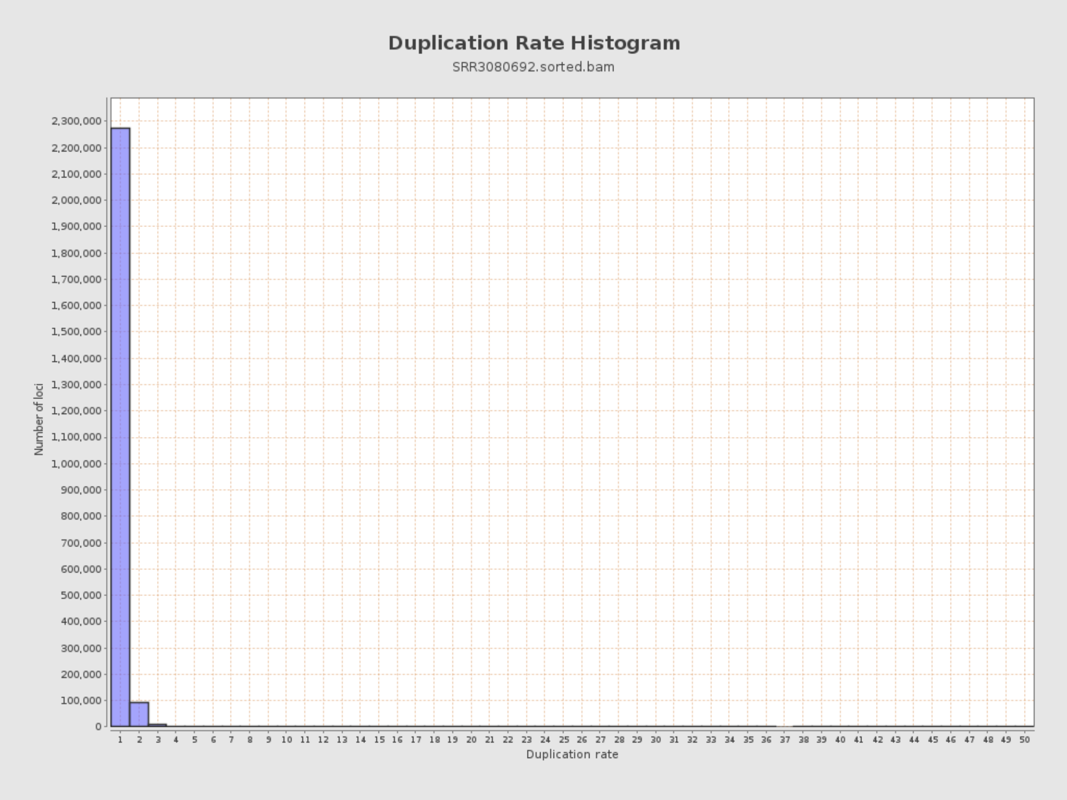
5. Results : Coverage Histogram (0-50X)



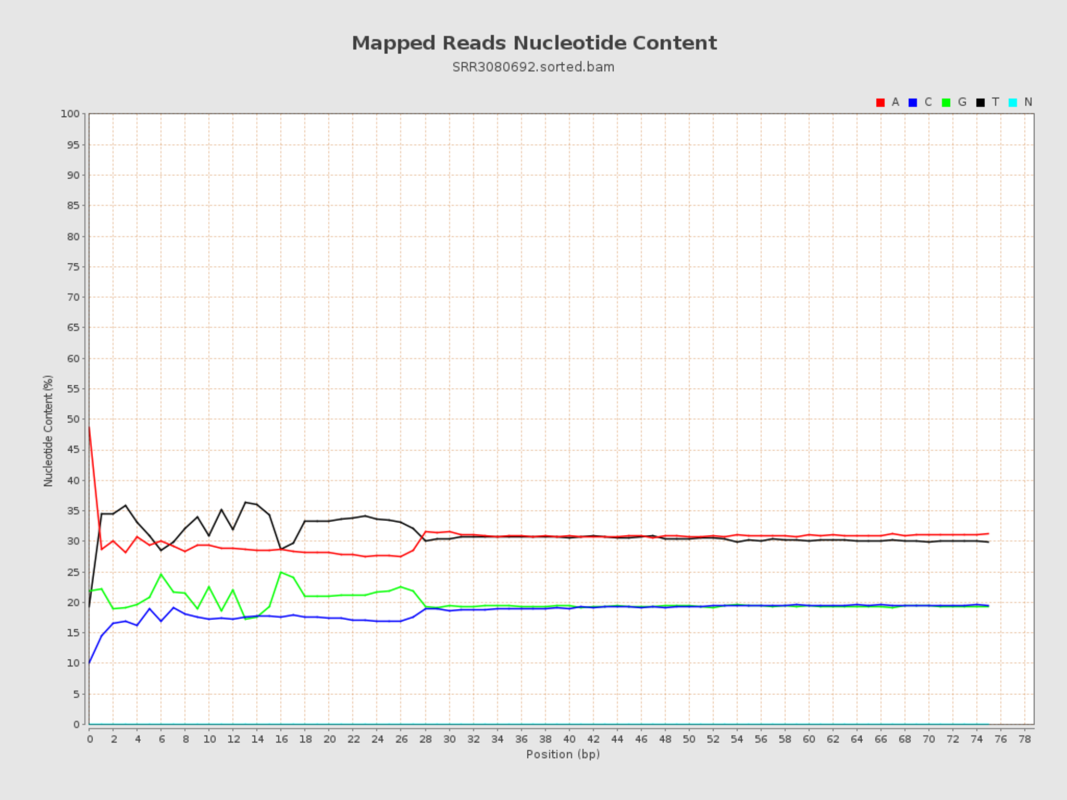
6. Results : Genome Fraction Coverage



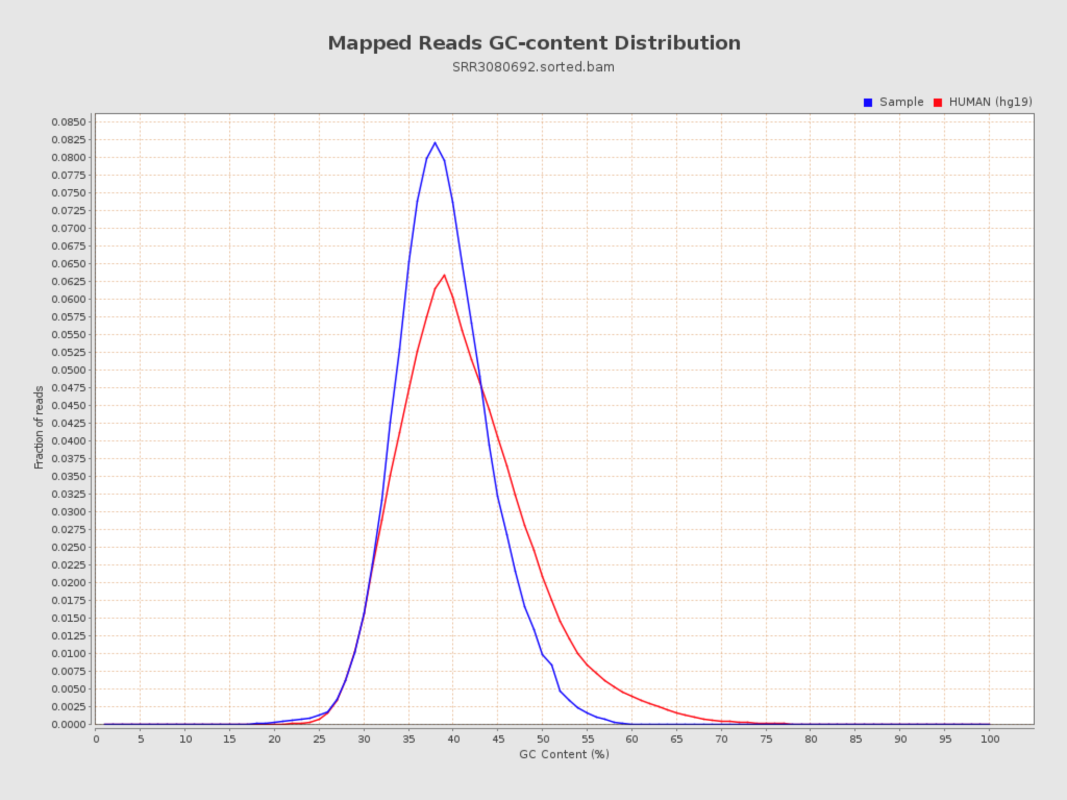
7. Results : Duplication Rate Histogram



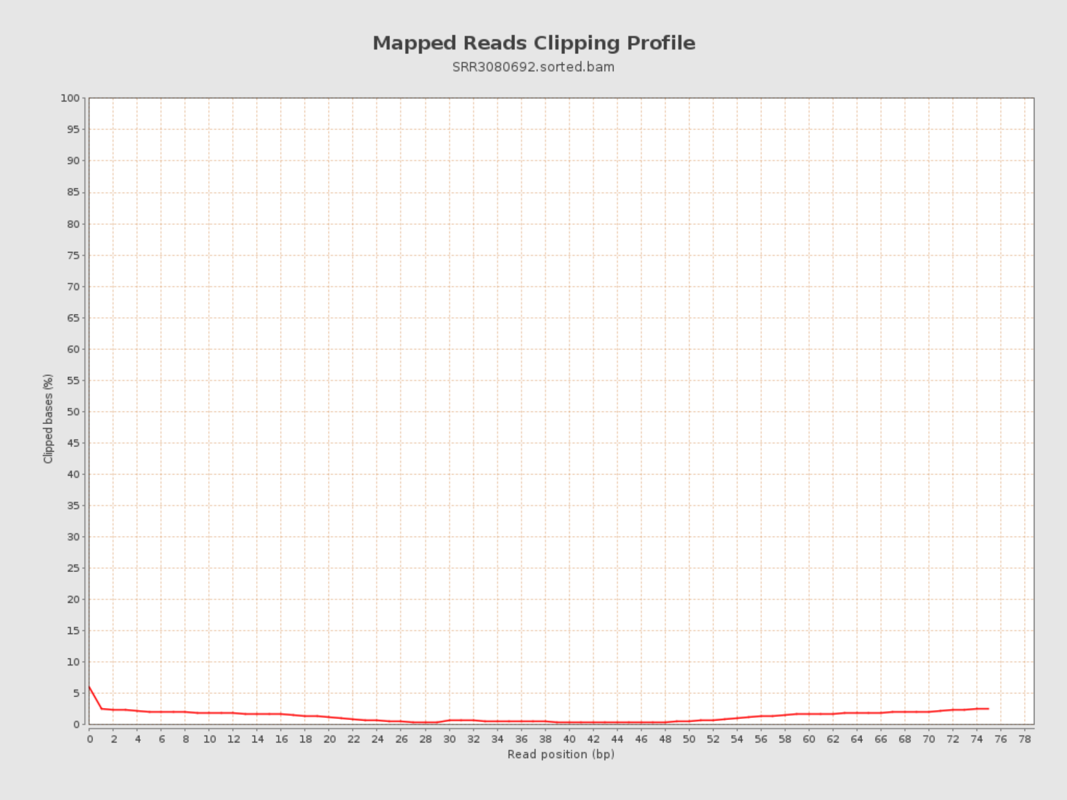
8. Results : Mapped Reads Nucleotide Content



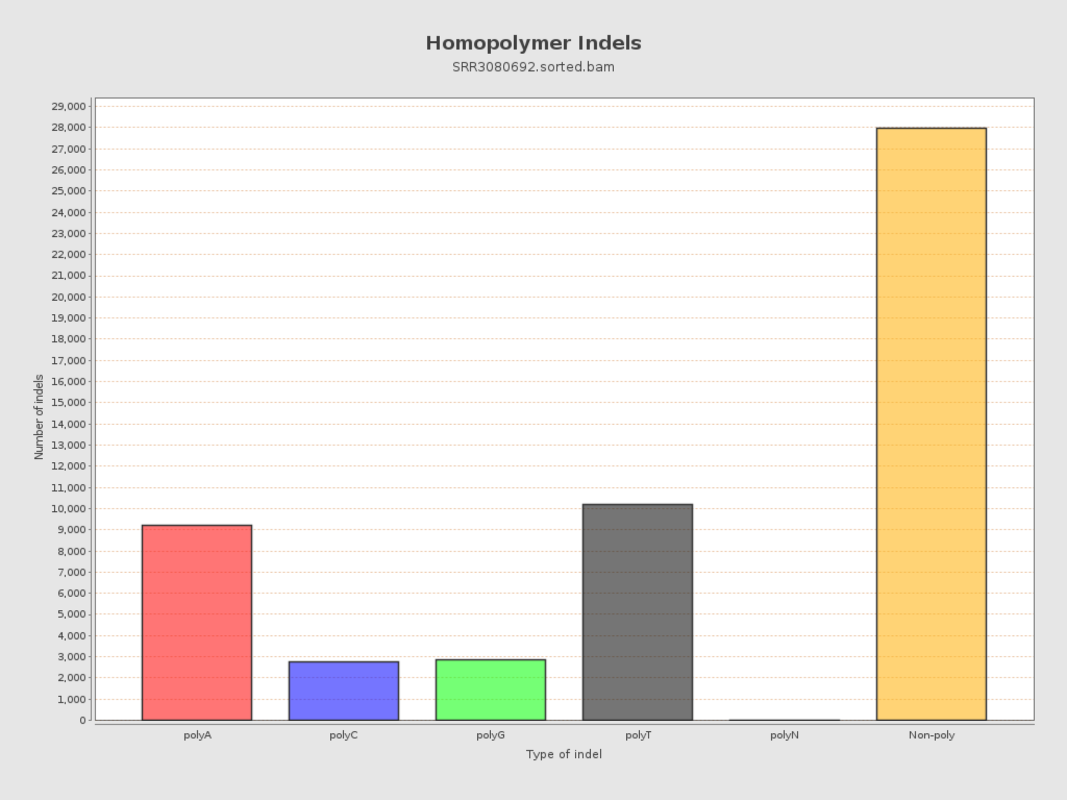
9. Results : Mapped Reads GC-content Distribution



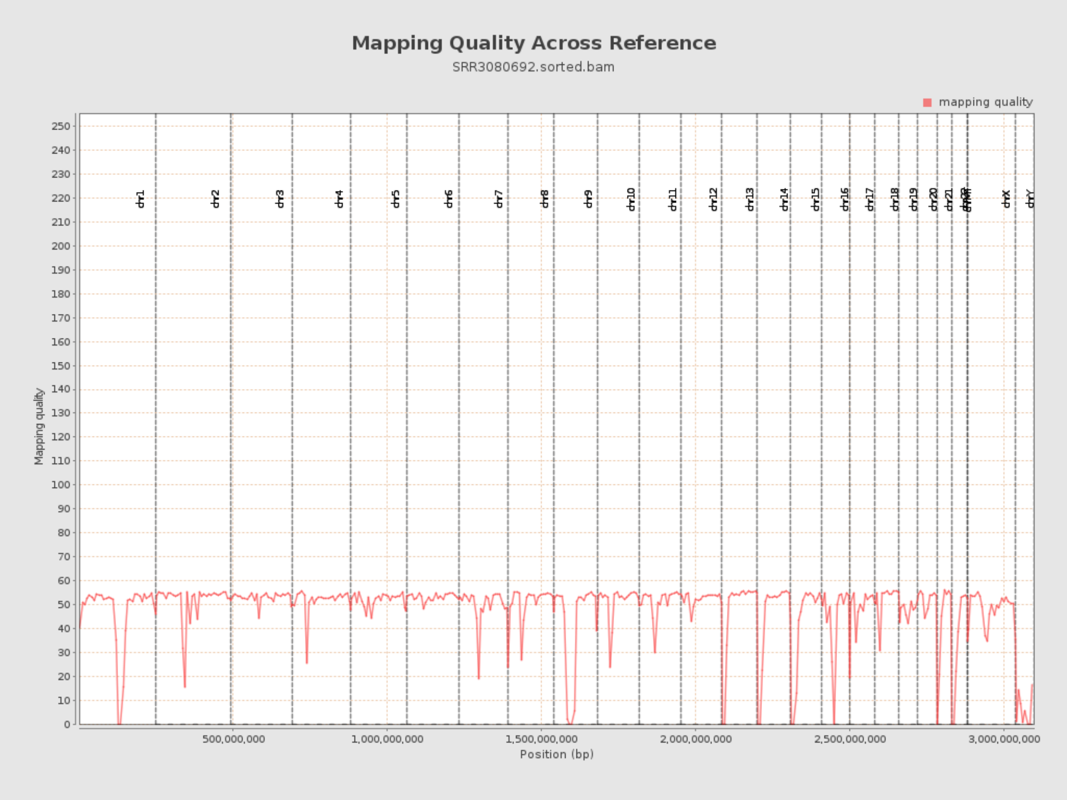
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram