Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:00:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084792.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_SRR3084792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:00:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,941
Mapped reads	1,437,042 / 89.26%
Unmapped reads	172,899 / 10.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,118 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	50,609 / 3.14%
Duplication rate	2.79%
Clipped reads	630,653 / 39.17%

2.2. ACGT Content

Number/percentage of A's	26,950,813 / 28%
Number/percentage of C's	18,099,584 / 18.8%
Number/percentage of T's	29,956,805 / 31.12%
Number/percentage of G's	21,217,560 / 22.04%
Number/percentage of N's	31,690 / 0.03%
GC Percentage	40.85%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.2715

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

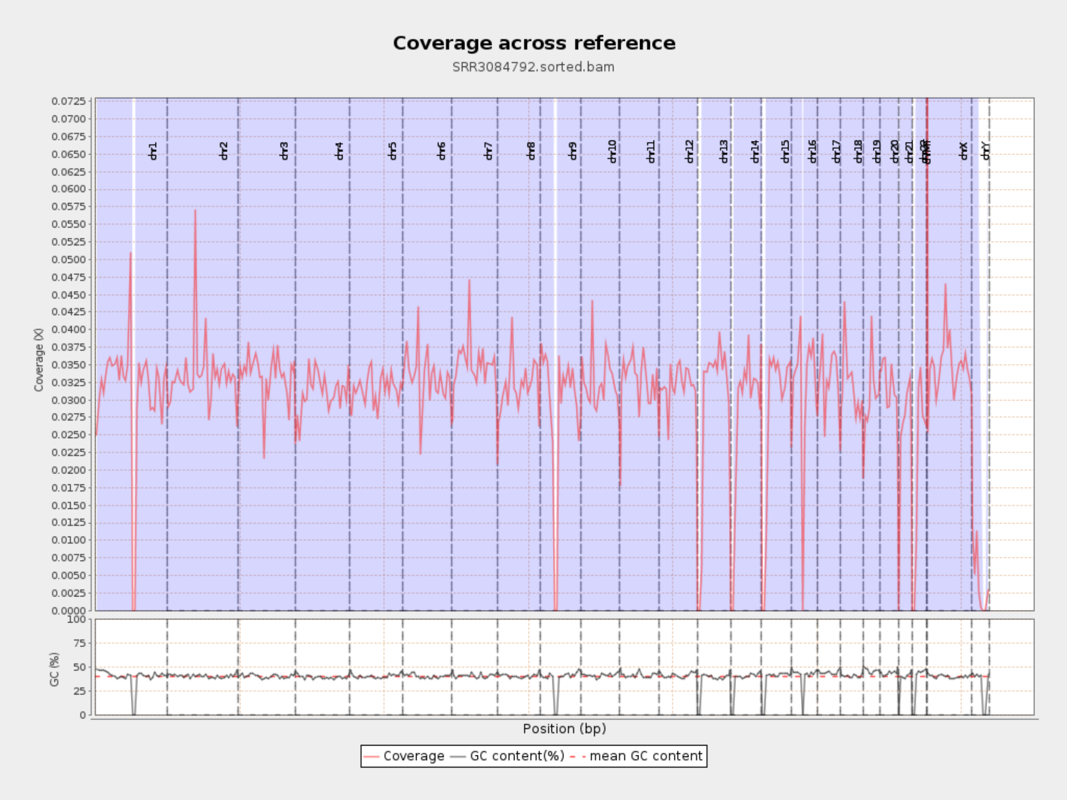
General error rate	0.86%
Mismatches	818,061
Insertions	7,534
Mapped reads with at least one insertion	0.52%
Deletions	23,766
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.81%

2.6. Chromosome stats

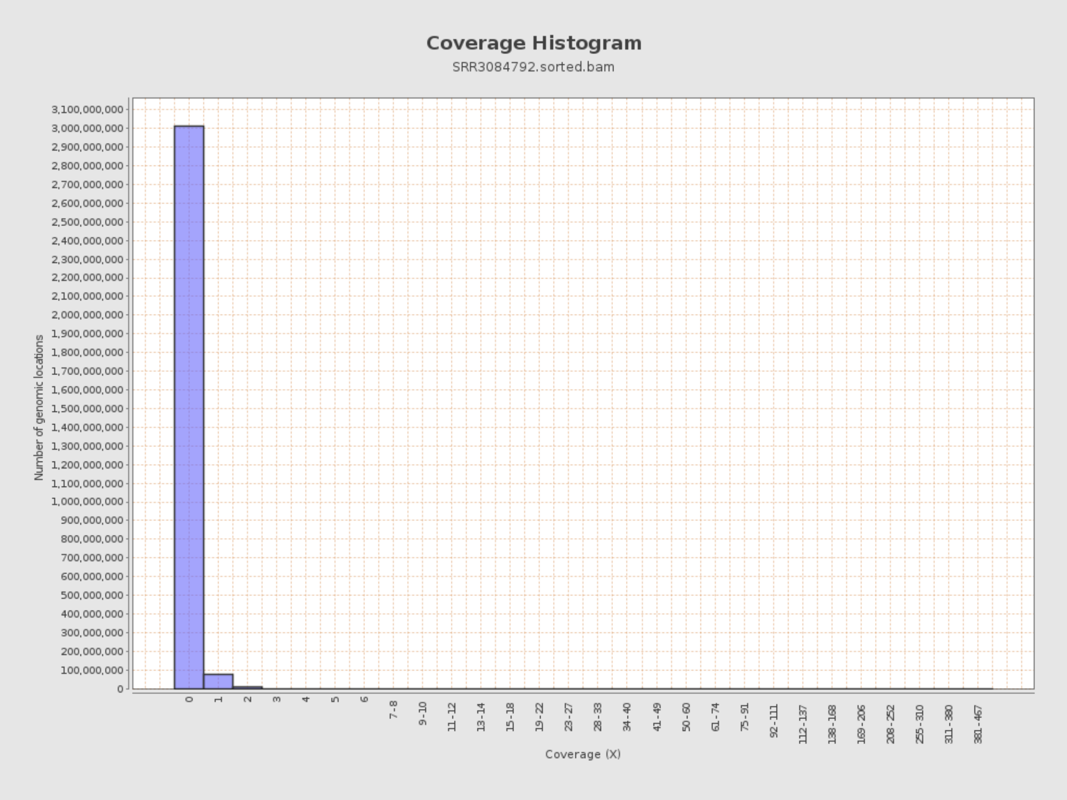
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7783504	0.0312	0.4365
chr2	243199373	8199719	0.0337	0.3271
chr3	198022430	6632109	0.0335	0.1991
chr4	191154276	5931686	0.031	0.1989
chr5	180915260	5723219	0.0316	0.1957
chr6	171115067	5661524	0.0331	0.2318
chr7	159138663	5597143	0.0352	0.307

chr8	146364022	4682379	0.032	0.2934
chr9	141213431	4063355	0.0288	0.2657
chr10	135534747	4435971	0.0327	0.2453
chr11	135006516	4447986	0.0329	0.2611
chr12	133851895	4287991	0.032	0.1975
chr13	115169878	3303560	0.0287	0.1863
chr14	107349540	2920157	0.0272	0.1963
chr15	102531392	2832715	0.0276	0.185
chr16	90354753	2814817	0.0312	0.2103
chr17	81195210	2683007	0.033	0.2264
chr18	78077248	2500095	0.032	0.5306
chr19	59128983	1822402	0.0308	0.3495
chr20	63025520	2016842	0.032	0.2044
chr21	48129895	1232192	0.0256	0.1834
chr22	51304566	1065125	0.0208	0.1566
chrMT	16571	4977	0.3003	0.6384
chrX	155270560	5419170	0.0349	0.2272
chrY	59373566	233356	0.0039	0.0881

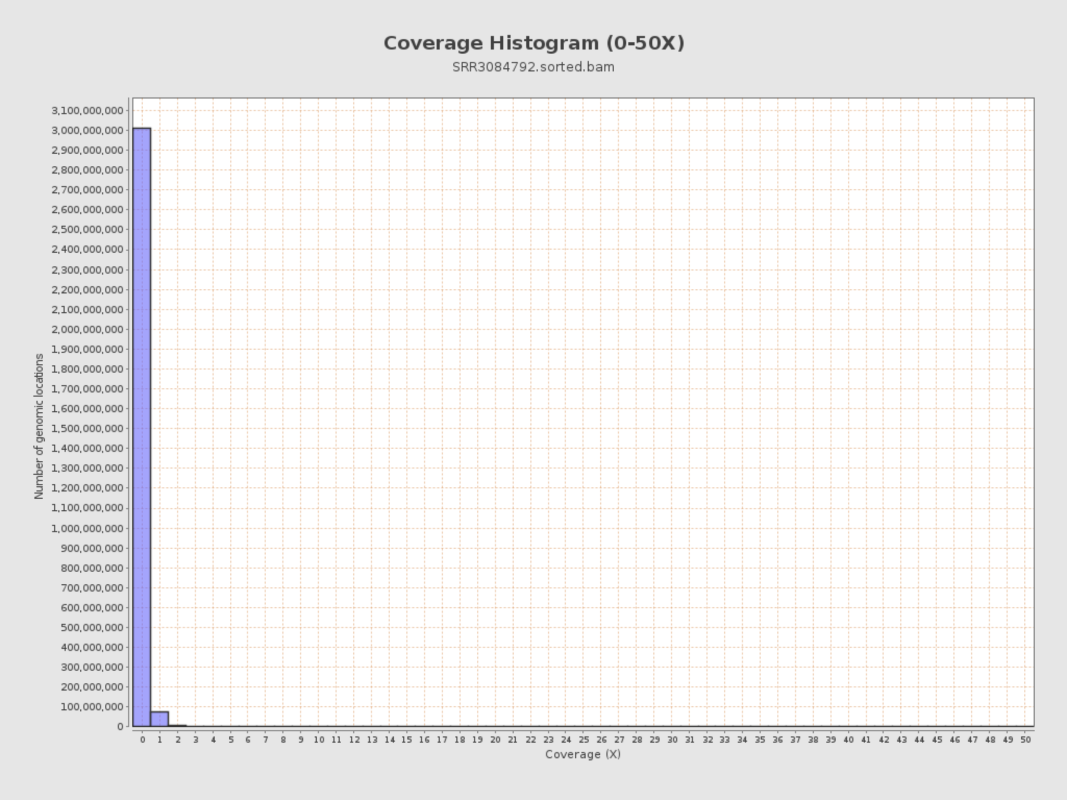
3. Results : Coverage across reference



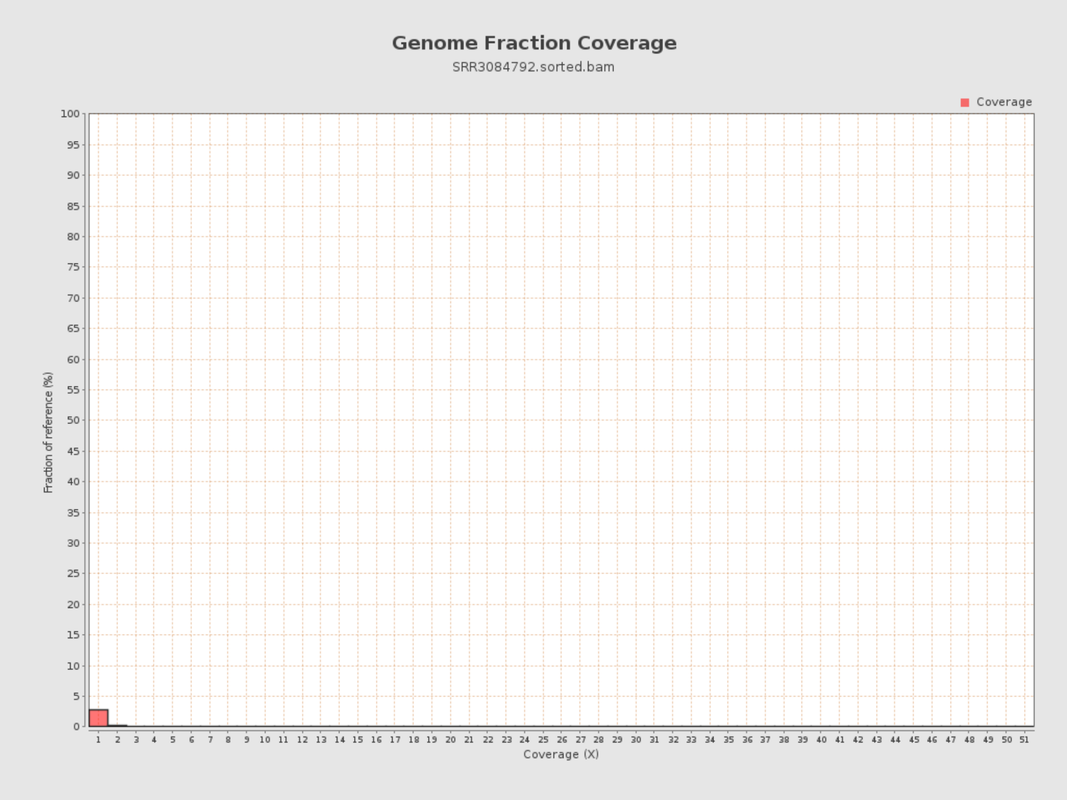
4. Results : Coverage Histogram



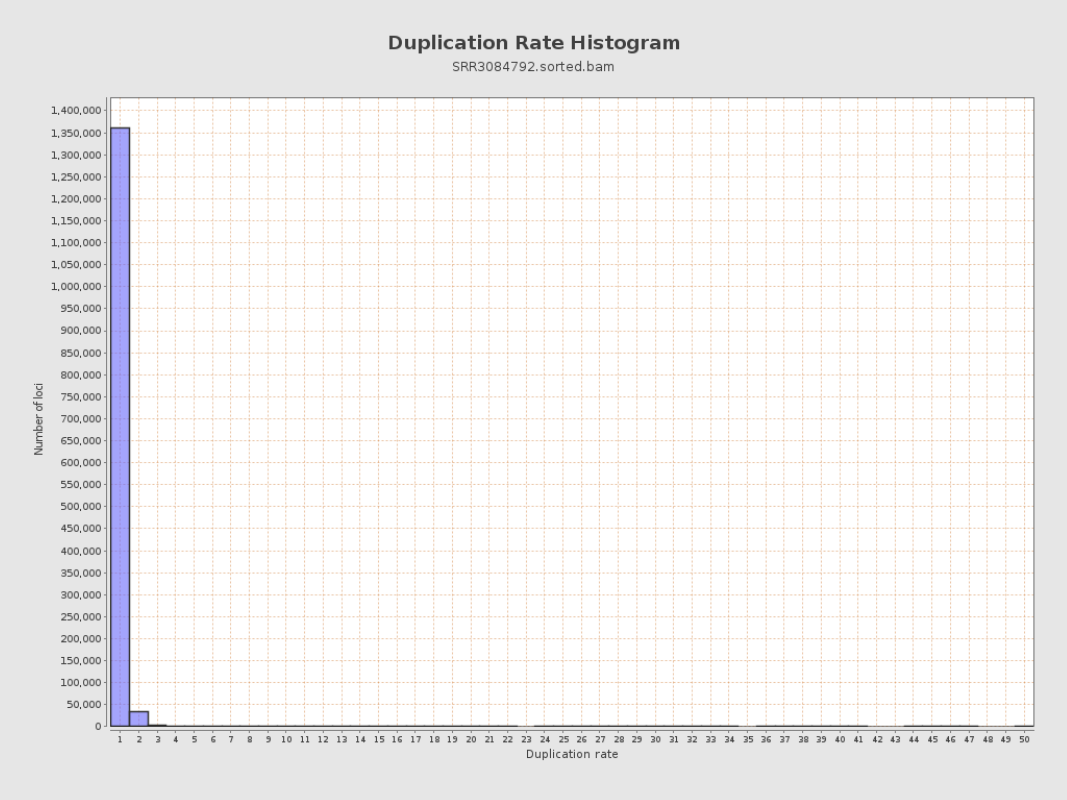
5. Results : Coverage Histogram (0-50X)



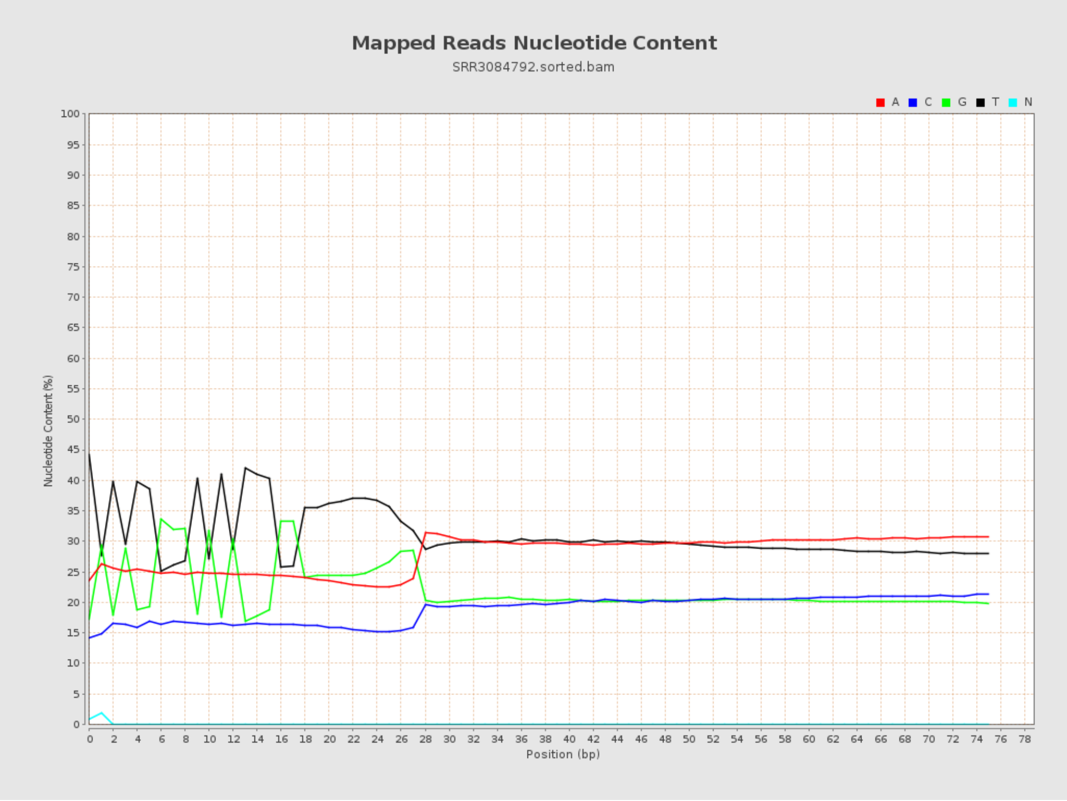
6. Results : Genome Fraction Coverage



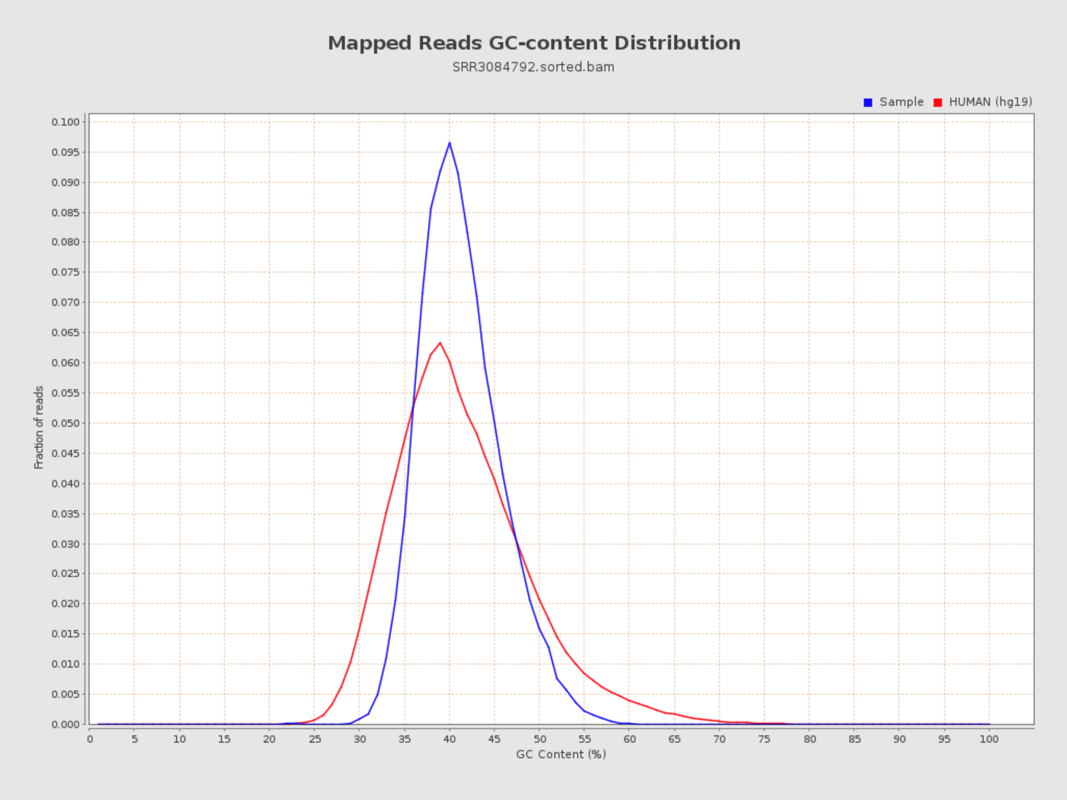
7. Results : Duplication Rate Histogram



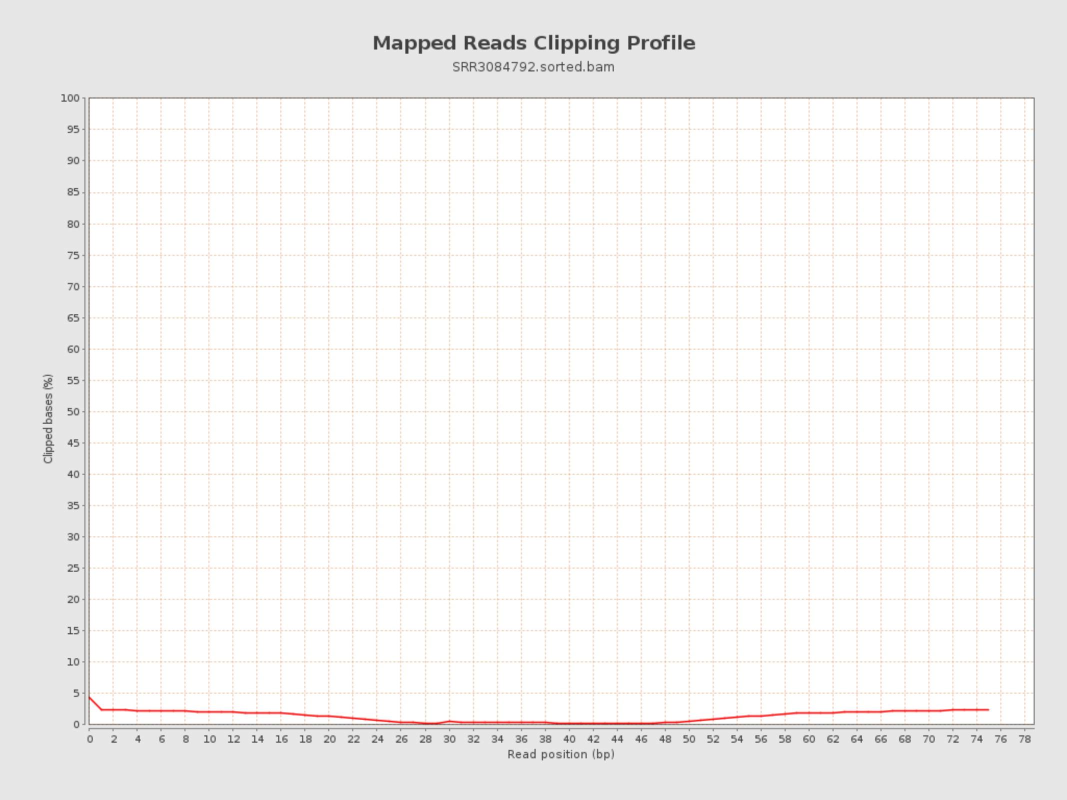
8. Results : Mapped Reads Nucleotide Content



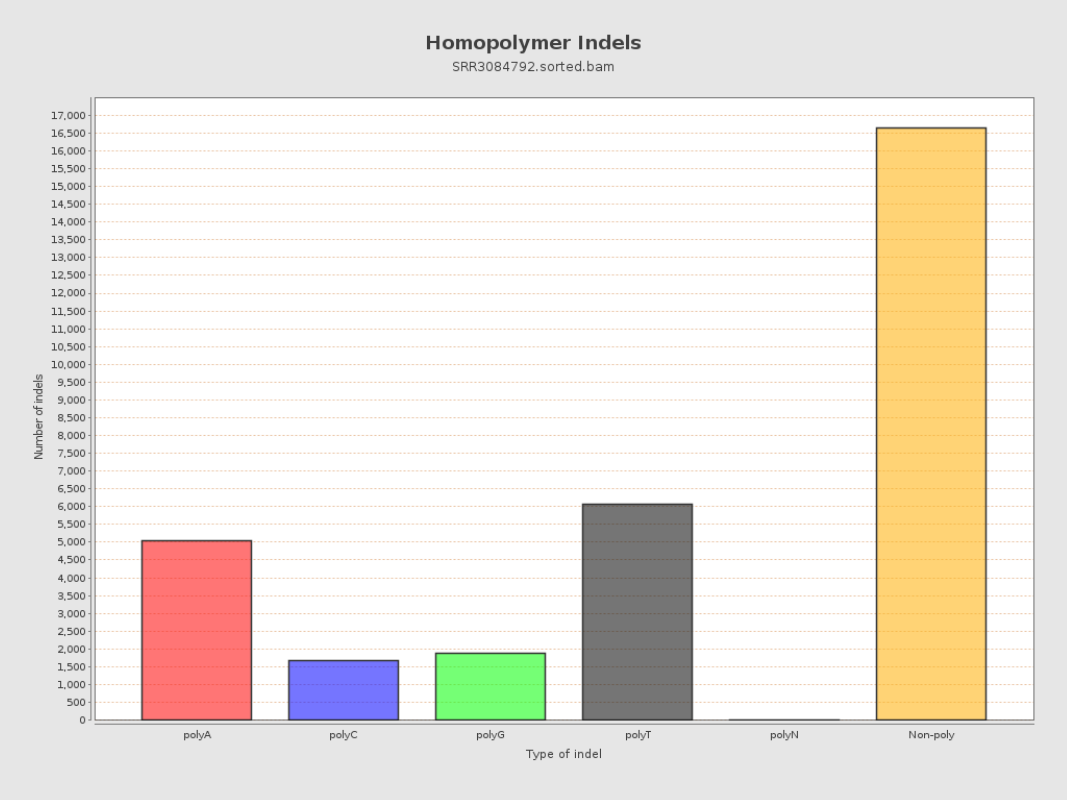
9. Results : Mapped Reads GC-content Distribution



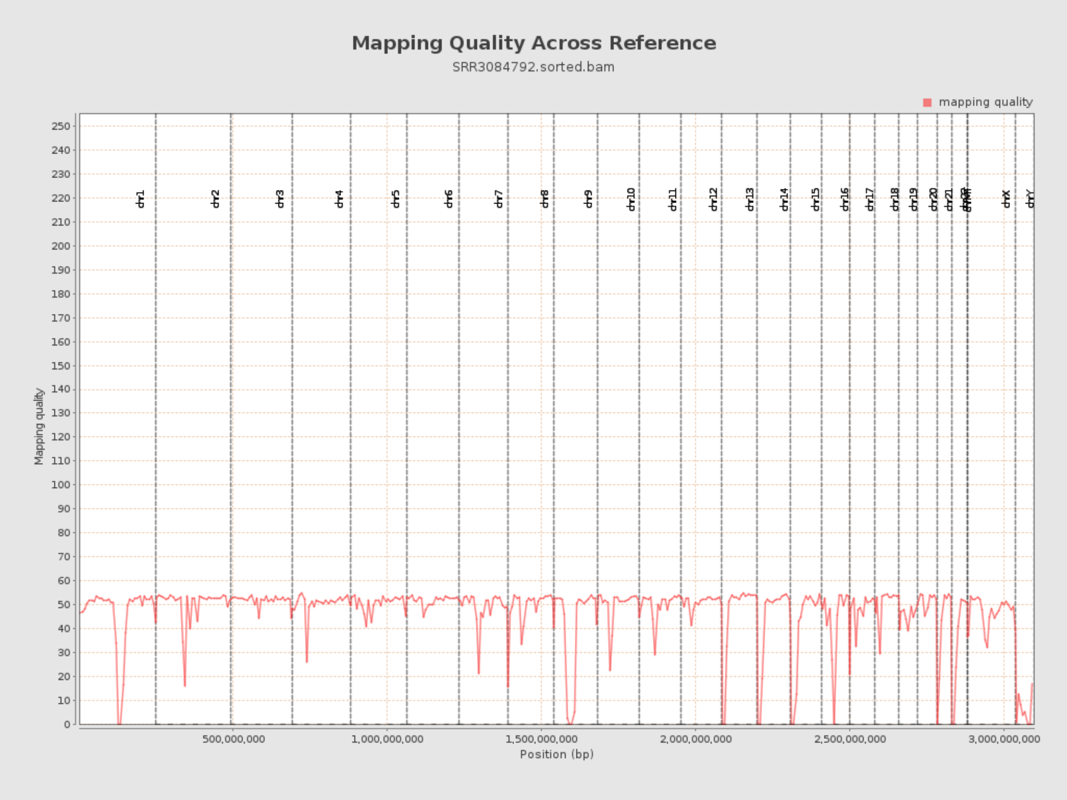
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram