Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:10:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080716.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_SRR3080716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080716.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:10:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,232,367
Mapped reads	2,022,455 / 90.6%
Unmapped reads	209,912 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,749 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	105,306 / 4.72%
Duplication rate	4.44%
Clipped reads	834,979 / 37.4%

2.2. ACGT Content

Number/percentage of A's	38,273,921 / 28.07%
Number/percentage of C's	25,056,365 / 18.38%
Number/percentage of T's	43,558,830 / 31.95%
Number/percentage of G's	29,449,617 / 21.6%
Number/percentage of N's	1,841 / 0%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.3589

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

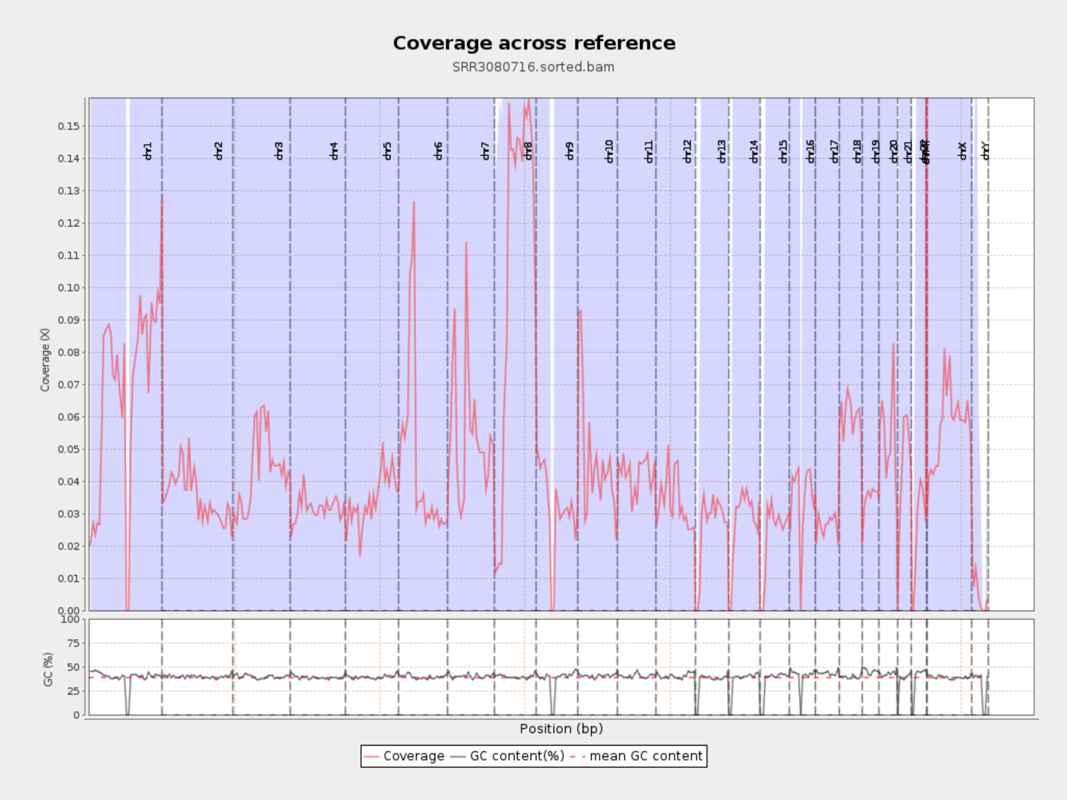
General error rate	0.83%
Mismatches	1,114,805
Insertions	9,592
Mapped reads with at least one insertion	0.47%
Deletions	28,993
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.94%

2.6. Chromosome stats

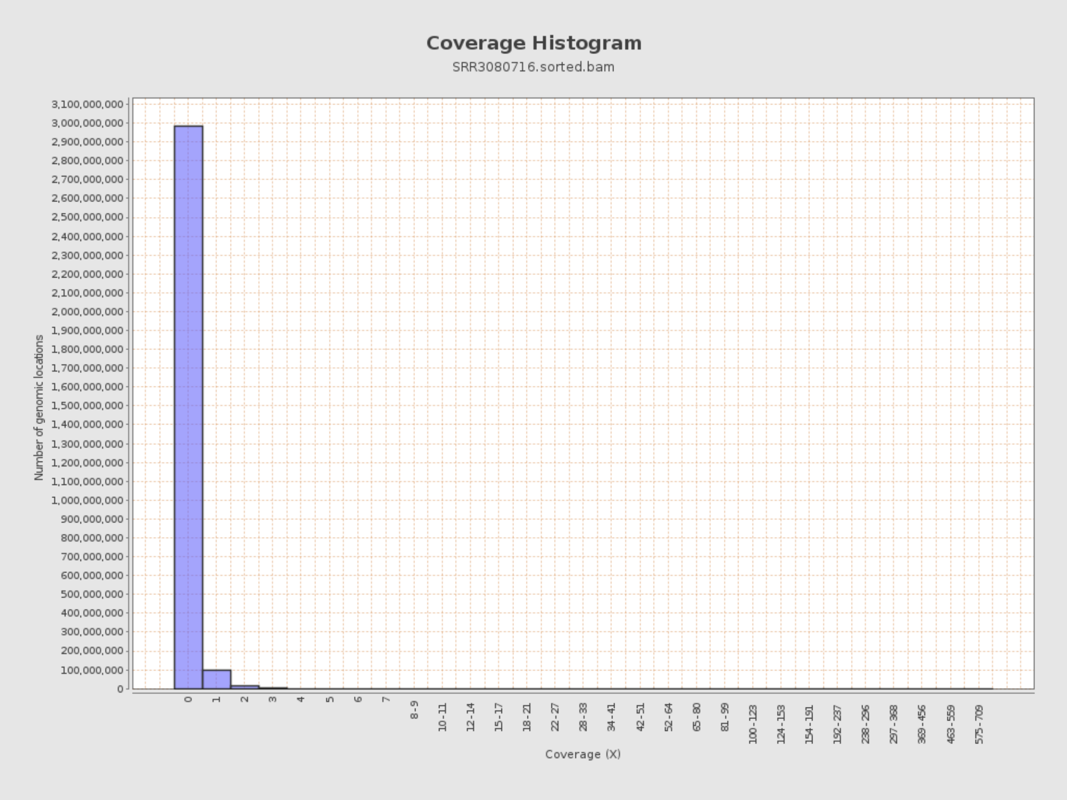
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16849750	0.0676	0.4596
chr2	243199373	8625419	0.0355	0.342
chr3	198022430	8609753	0.0435	0.24
chr4	191154276	6040338	0.0316	0.2091
chr5	180915260	6278750	0.0347	0.2121
chr6	171115067	7916622	0.0463	0.3573
chr7	159138663	8866551	0.0557	0.9043

chr8	146364022	15951564	0.109	0.512
chr9	141213431	4429266	0.0314	0.2498
chr10	135534747	6397361	0.0472	0.3228
chr11	135006516	5700347	0.0422	0.253
chr12	133851895	4467353	0.0334	0.2112
chr13	115169878	2965301	0.0257	0.1848
chr14	107349540	2890369	0.0269	0.1937
chr15	102531392	2396517	0.0234	0.1762
chr16	90354753	3160503	0.035	0.2291
chr17	81195210	2116781	0.0261	0.1899
chr18	78077248	4726407	0.0605	0.4166
chr19	59128983	2079050	0.0352	0.3046
chr20	63025520	3405604	0.054	0.2718
chr21	48129895	2100657	0.0436	0.2451
chr22	51304566	1249650	0.0244	0.1773
chrMT	16571	21496	1.2972	1.373
chrX	155270560	8852240	0.057	0.2891
chrY	59373566	294229	0.005	0.103

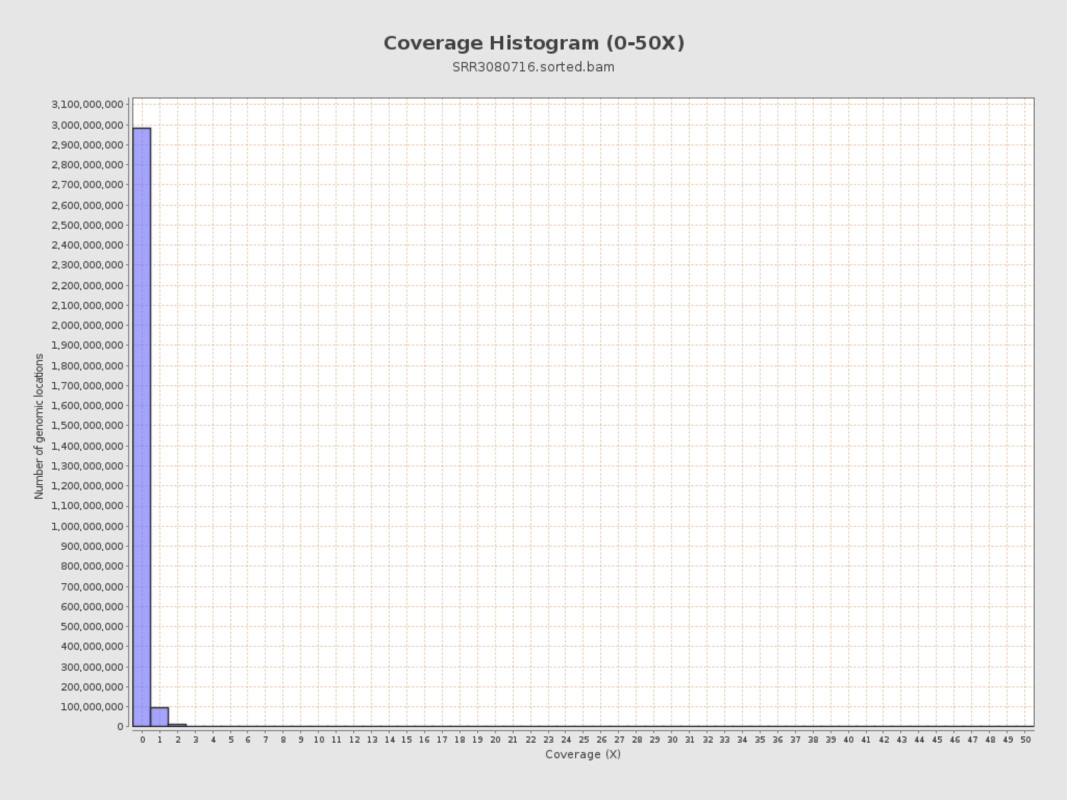
3. Results : Coverage across reference



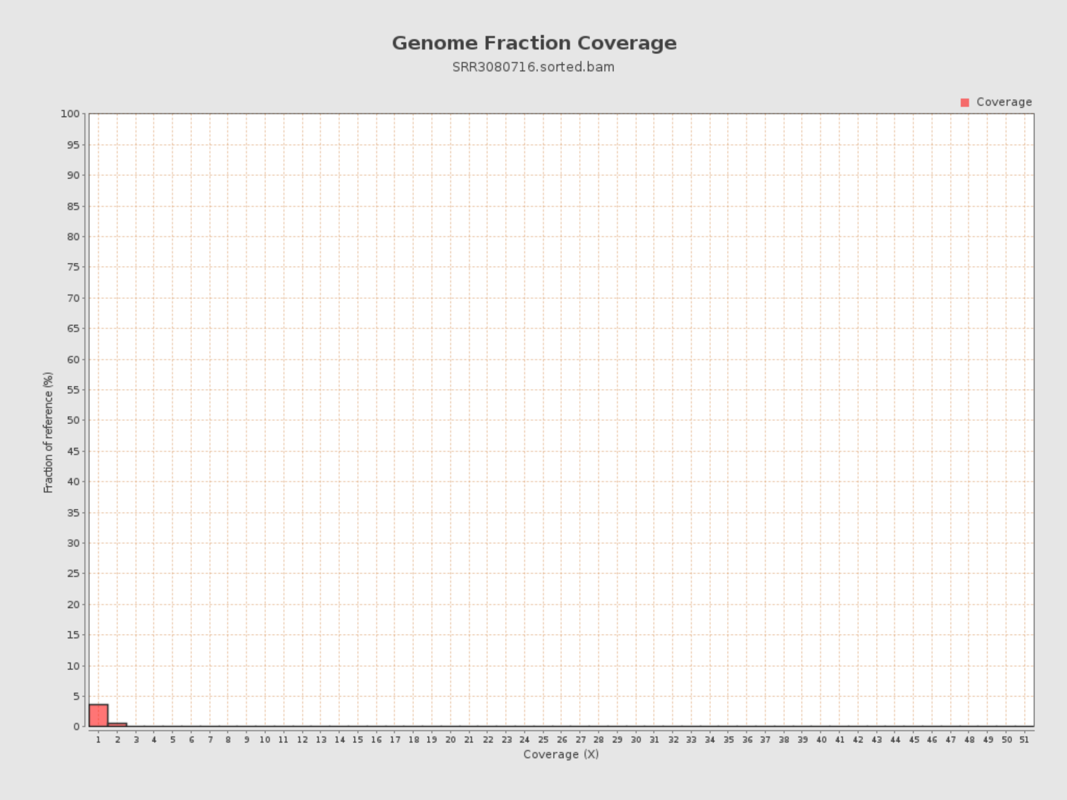
4. Results : Coverage Histogram



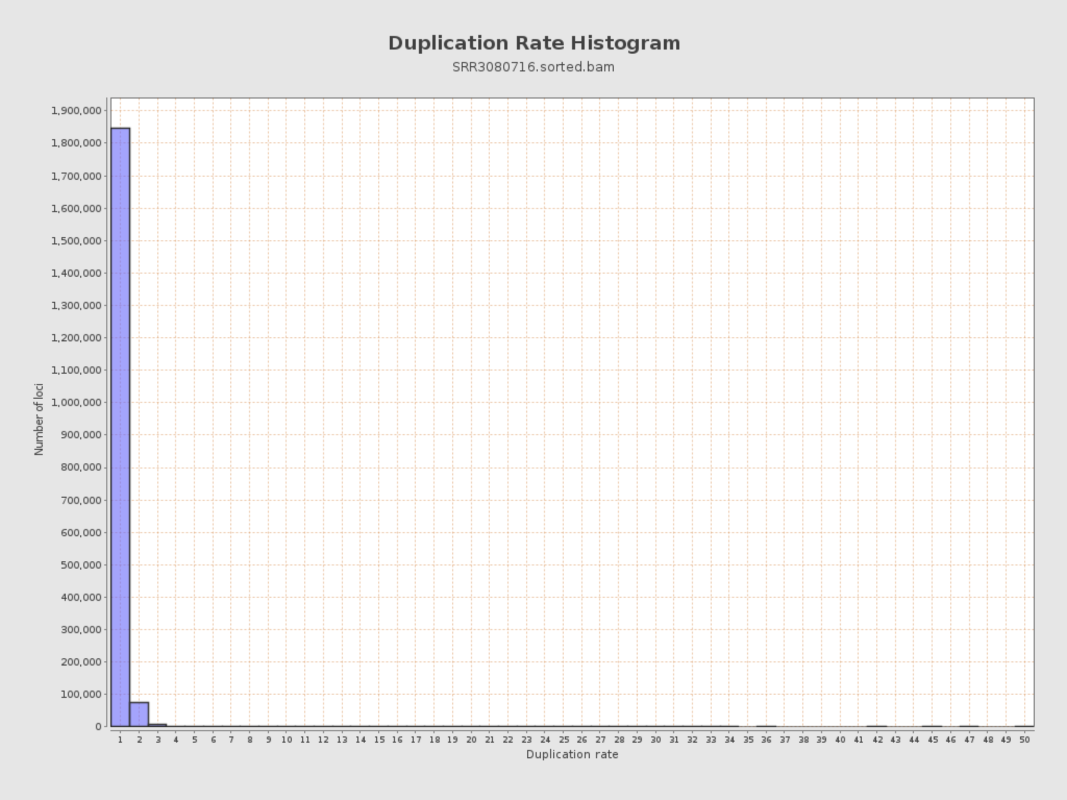
5. Results : Coverage Histogram (0-50X)



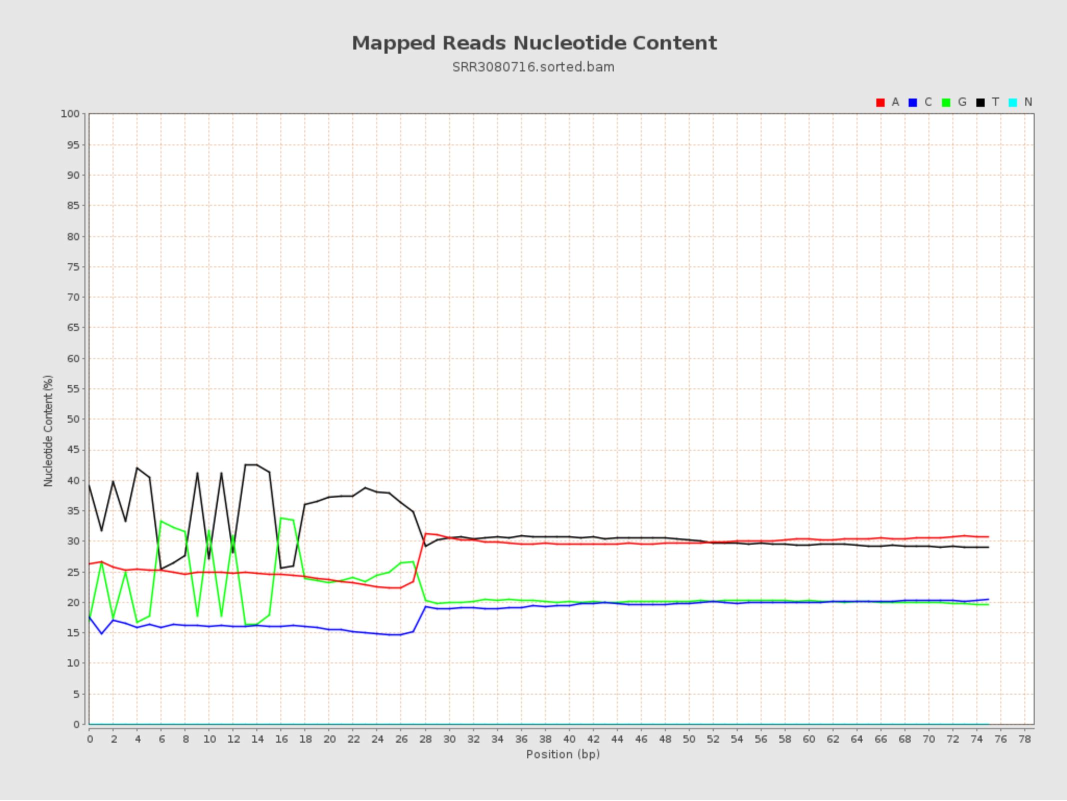
6. Results : Genome Fraction Coverage



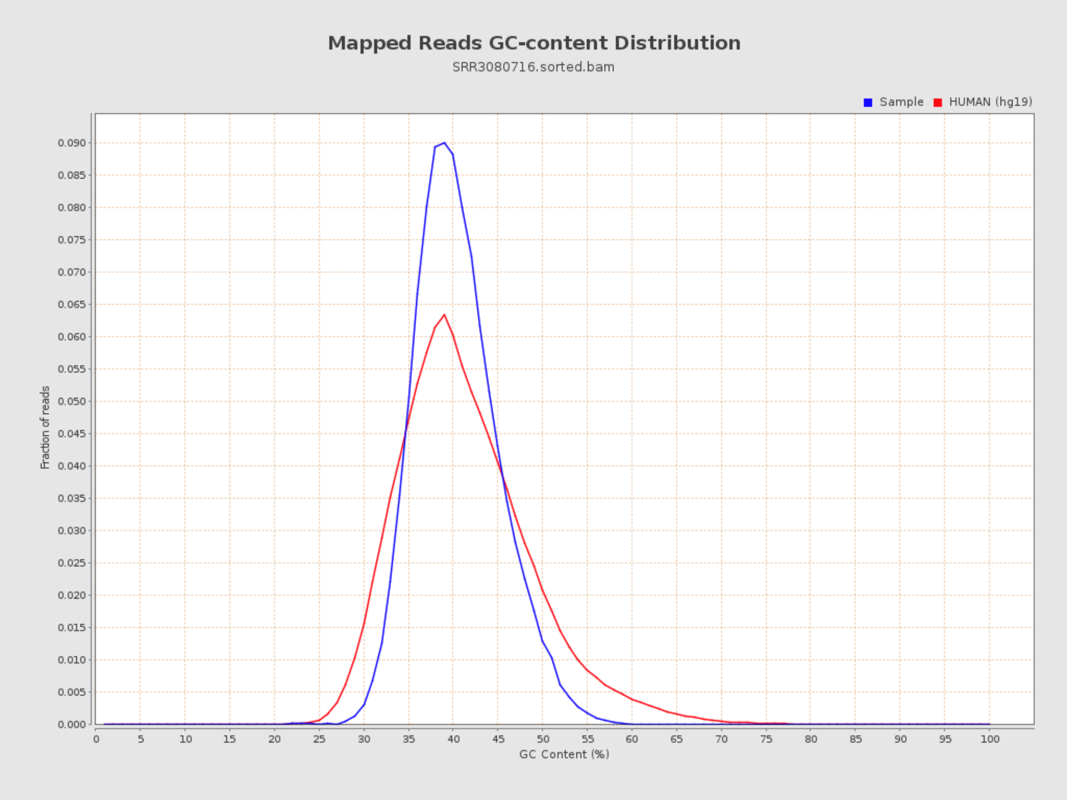
7. Results : Duplication Rate Histogram



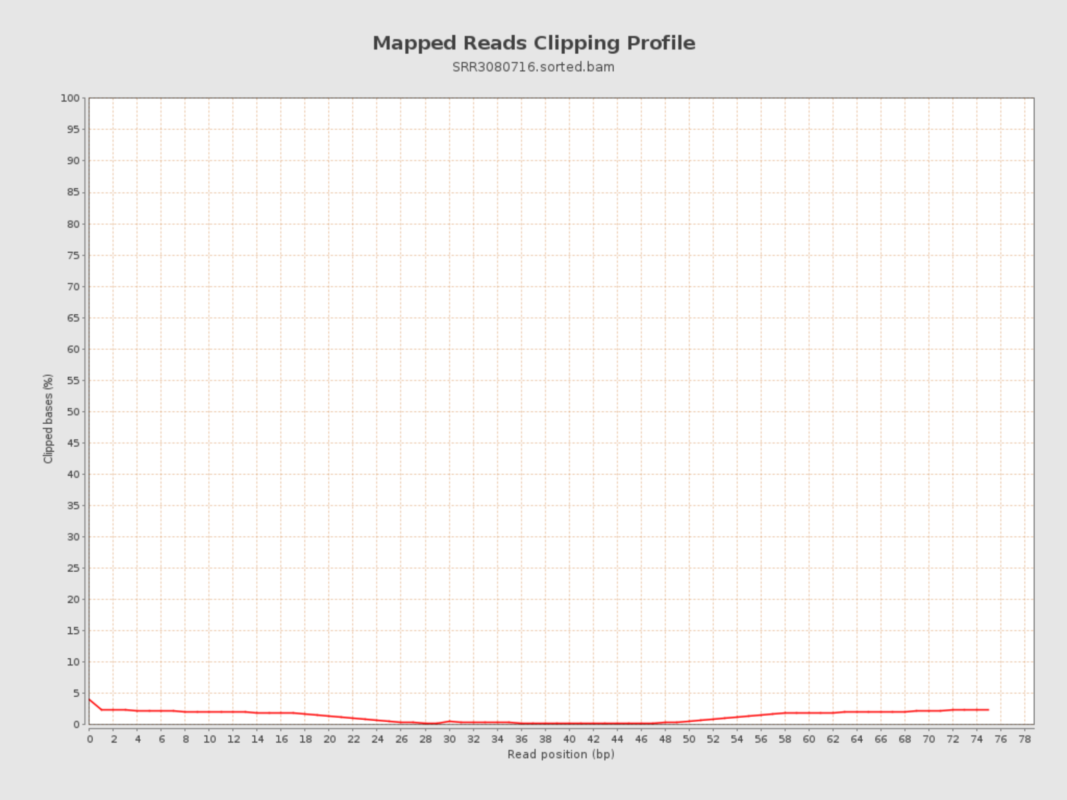
8. Results : Mapped Reads Nucleotide Content



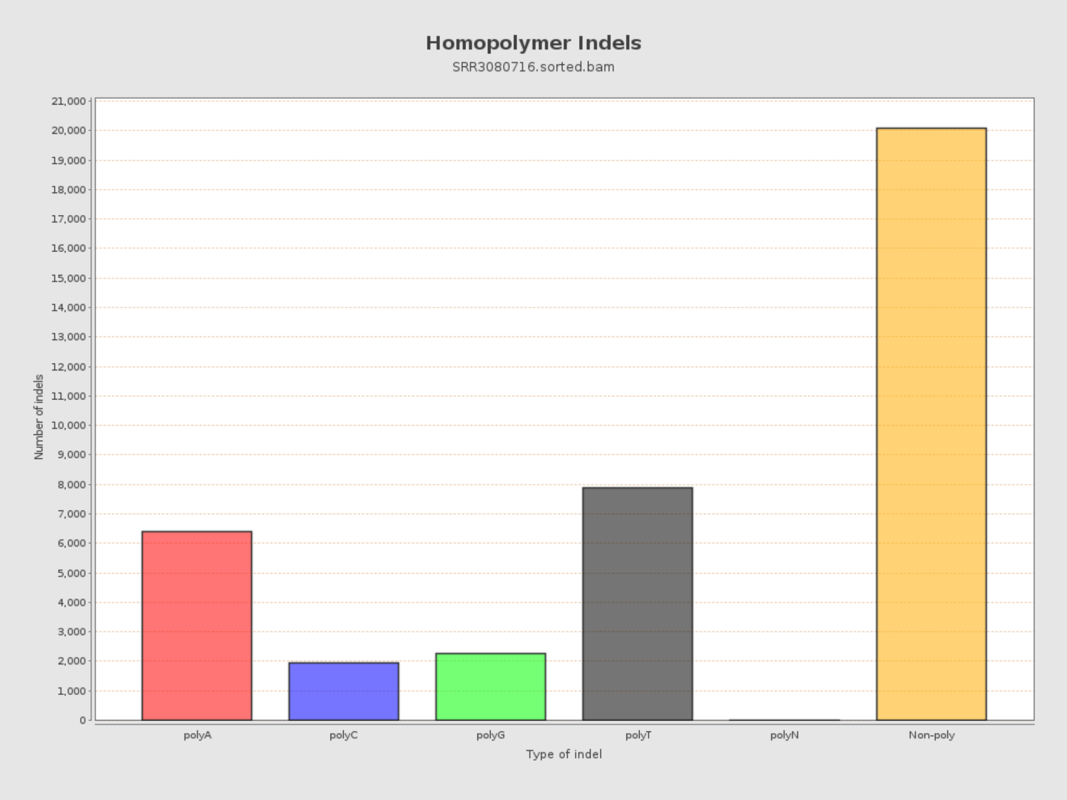
9. Results : Mapped Reads GC-content Distribution



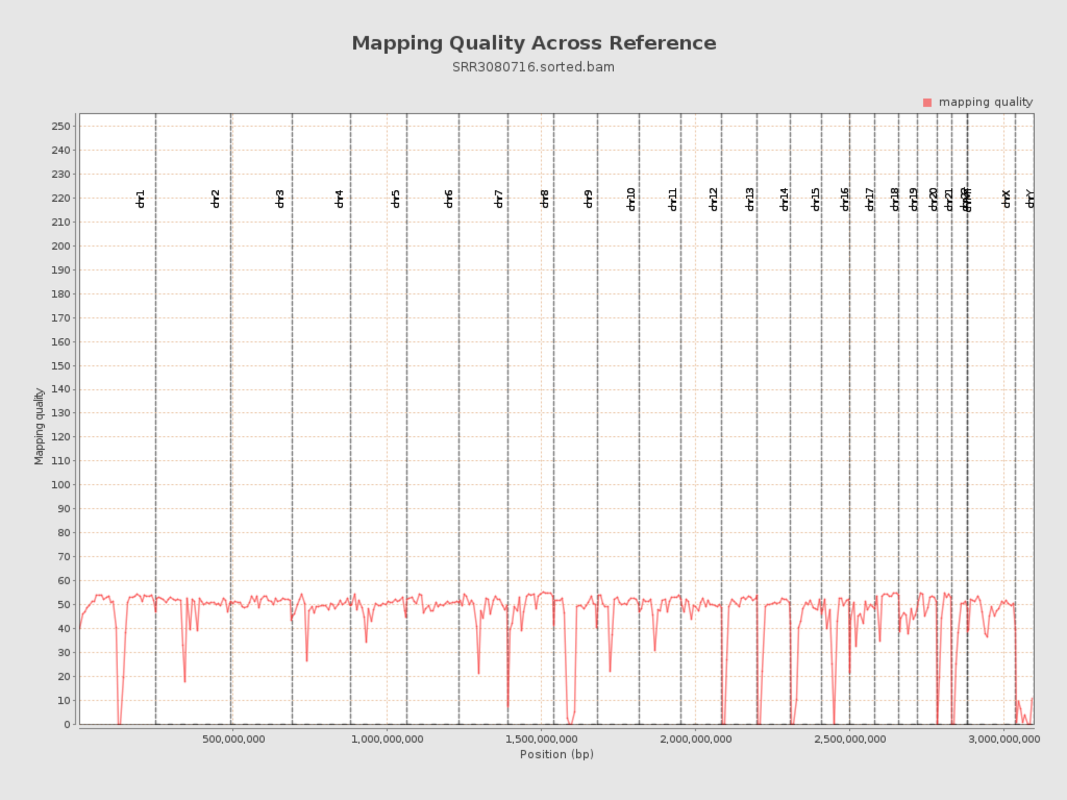
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram