Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:42:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008791.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_SRR6008791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:42:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,256,701
Mapped reads	1,018,393 / 81.04%
Unmapped reads	238,308 / 18.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,404 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	44,204 / 3.52%
Duplication rate	3.46%
Clipped reads	555,359 / 44.19%

2.2. ACGT Content

Number/percentage of A's	17,526,909 / 26.91%
Number/percentage of C's	11,741,560 / 18.03%
Number/percentage of T's	20,946,102 / 32.16%
Number/percentage of G's	14,895,511 / 22.87%
Number/percentage of N's	25,062 / 0.04%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.2412

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

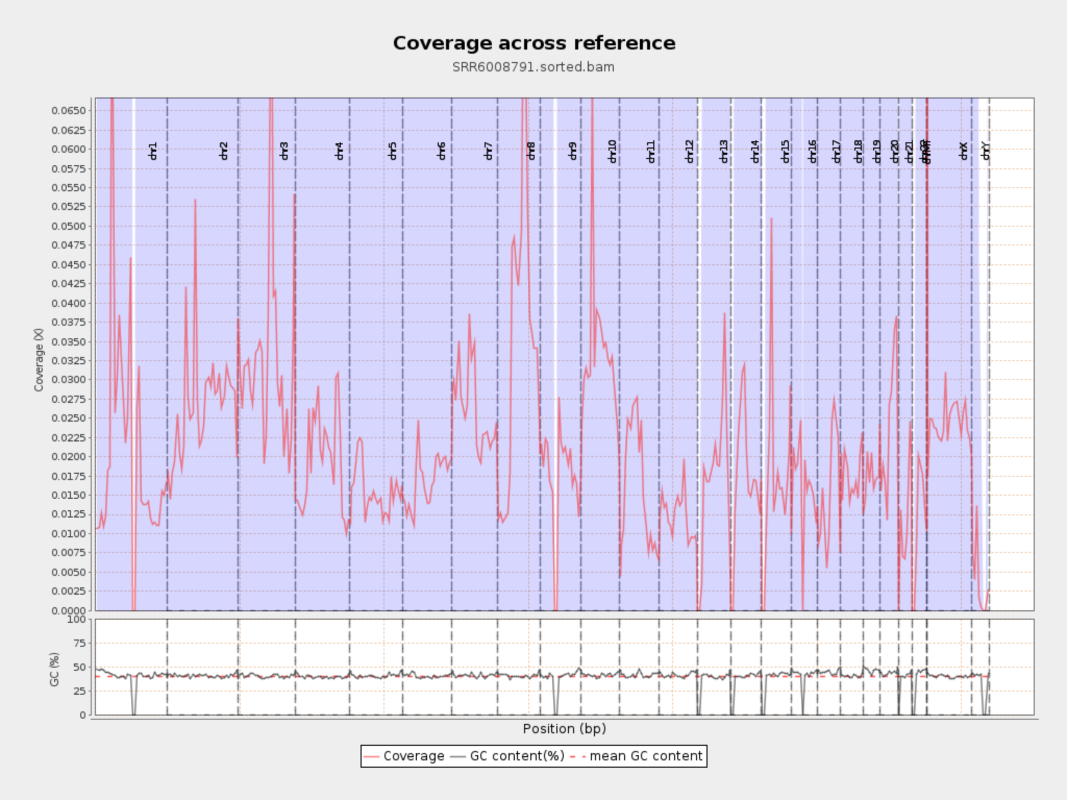
General error rate	0.88%
Mismatches	563,419
Insertions	4,320
Mapped reads with at least one insertion	0.42%
Deletions	21,245
Mapped reads with at least one deletion	2.06%
Homopolymer indels	43.55%

2.6. Chromosome stats

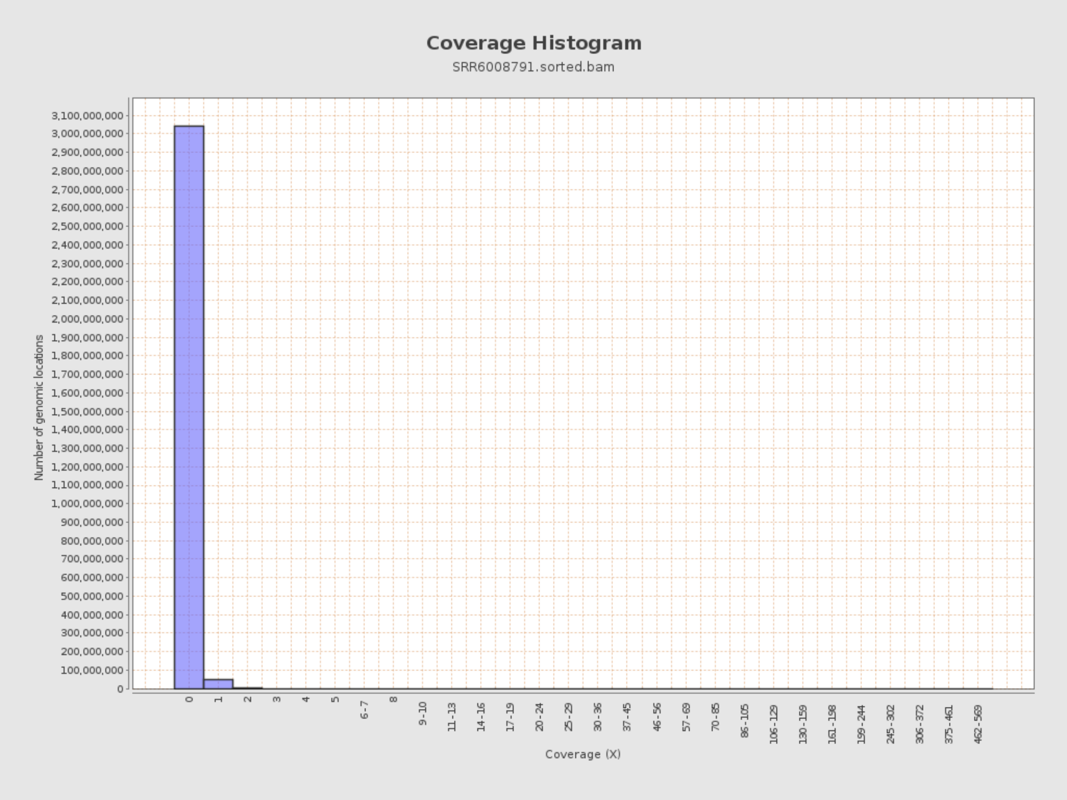
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5023666	0.0202	0.456
chr2	243199373	6543894	0.0269	0.2742
chr3	198022430	6434527	0.0325	0.2094
chr4	191154276	3712138	0.0194	0.1644
chr5	180915260	2813662	0.0156	0.14
chr6	171115067	2906002	0.017	0.1619
chr7	159138663	4183806	0.0263	0.2582

chr8	146364022	5285997	0.0361	0.2746
chr9	141213431	2440340	0.0173	0.2076
chr10	135534747	4562300	0.0337	0.3662
chr11	135006516	2193726	0.0162	0.1822
chr12	133851895	1667393	0.0125	0.1275
chr13	115169878	1992393	0.0173	0.1467
chr14	107349540	1855685	0.0173	0.1521
chr15	102531392	1730858	0.0169	0.1454
chr16	90354753	1433116	0.0159	0.1656
chr17	81195210	1265013	0.0156	0.1496
chr18	78077248	1353098	0.0173	0.3185
chr19	59128983	1034518	0.0175	0.3176
chr20	63025520	1534936	0.0244	0.1781
chr21	48129895	578190	0.012	0.1319
chr22	51304566	609038	0.0119	0.1206
chrMT	16571	5163	0.3116	0.5985
chrX	155270560	3799331	0.0245	0.187
chrY	59373566	212631	0.0036	0.1296

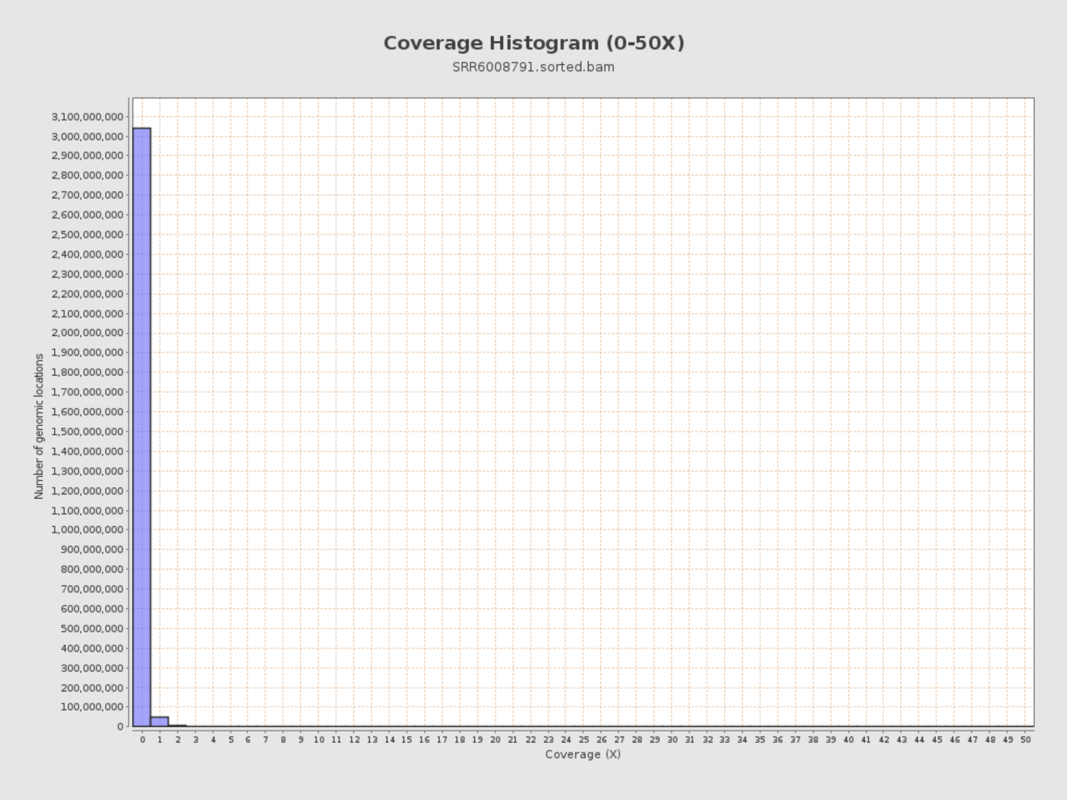
3. Results : Coverage across reference



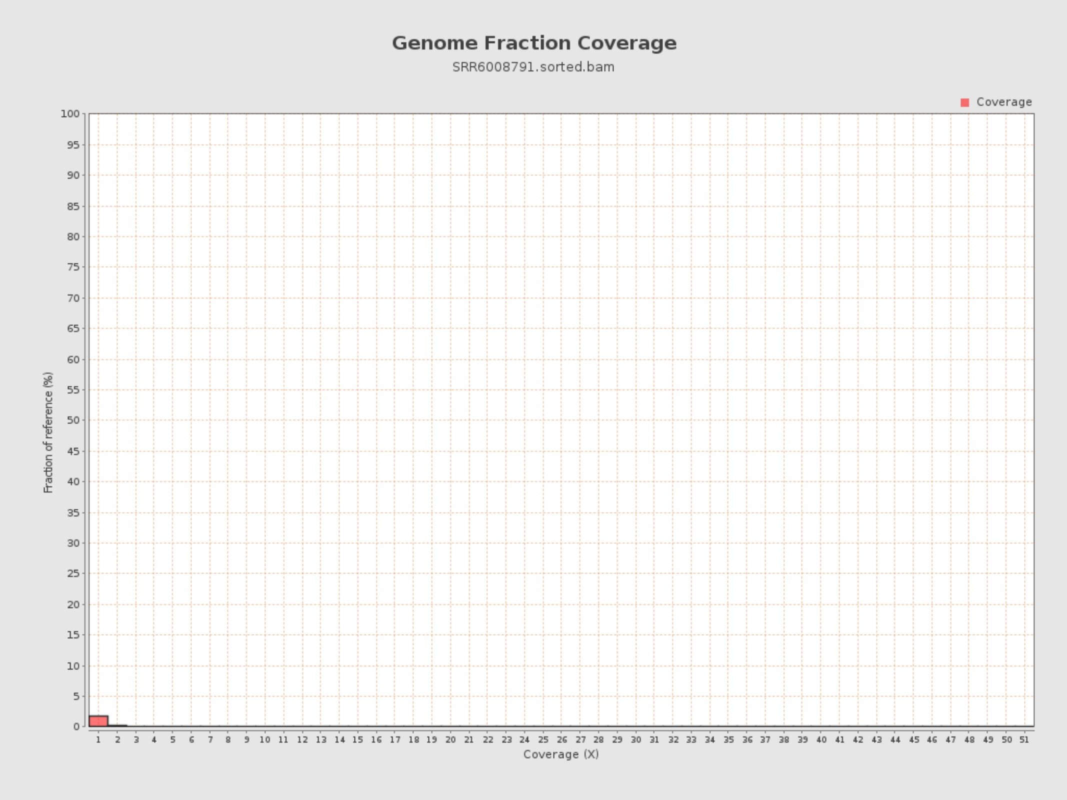
4. Results : Coverage Histogram



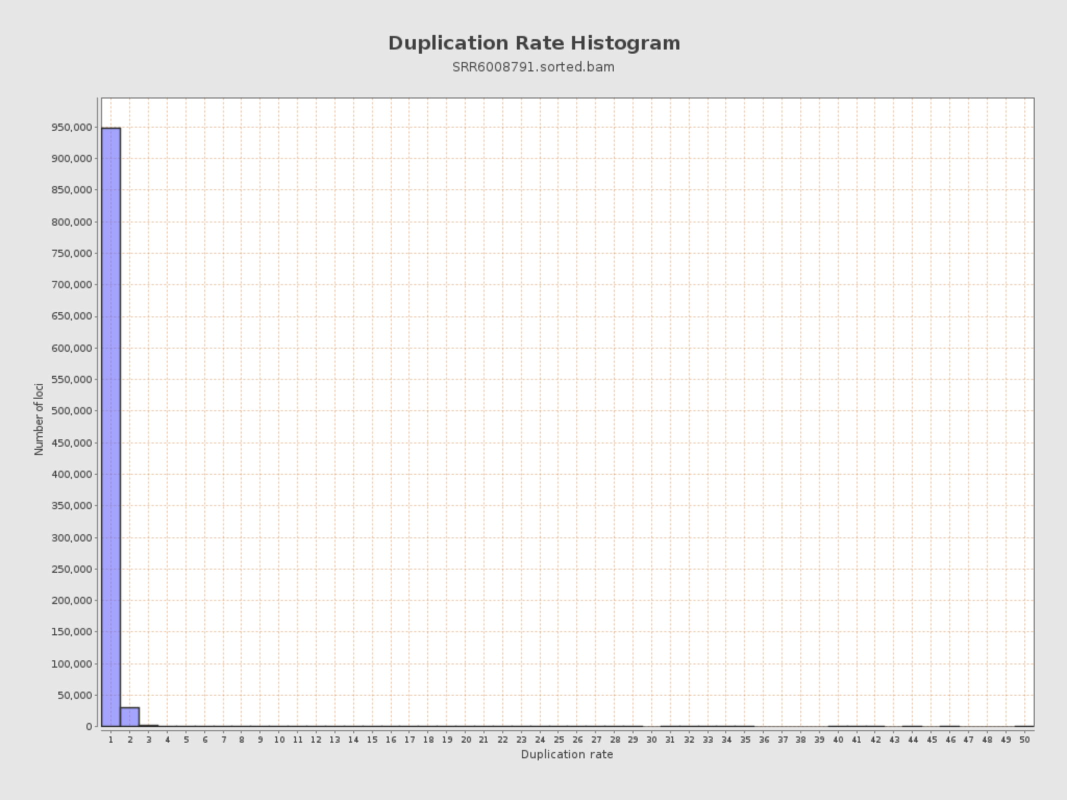
5. Results : Coverage Histogram (0-50X)



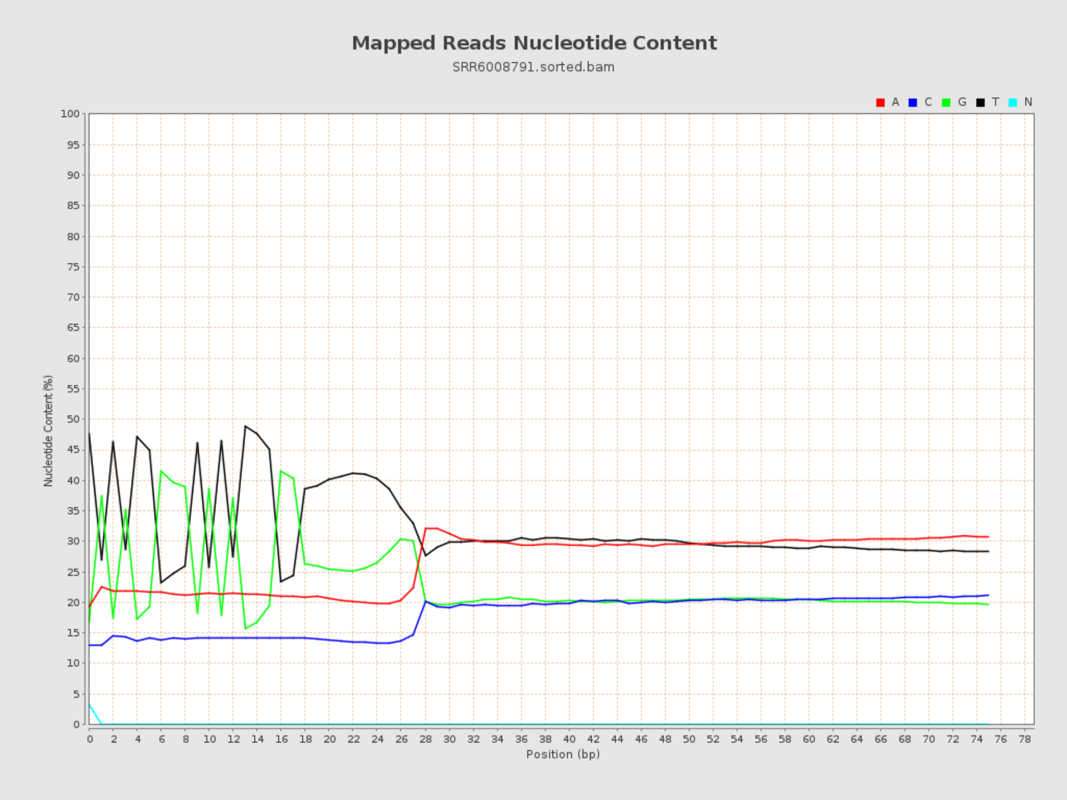
6. Results : Genome Fraction Coverage



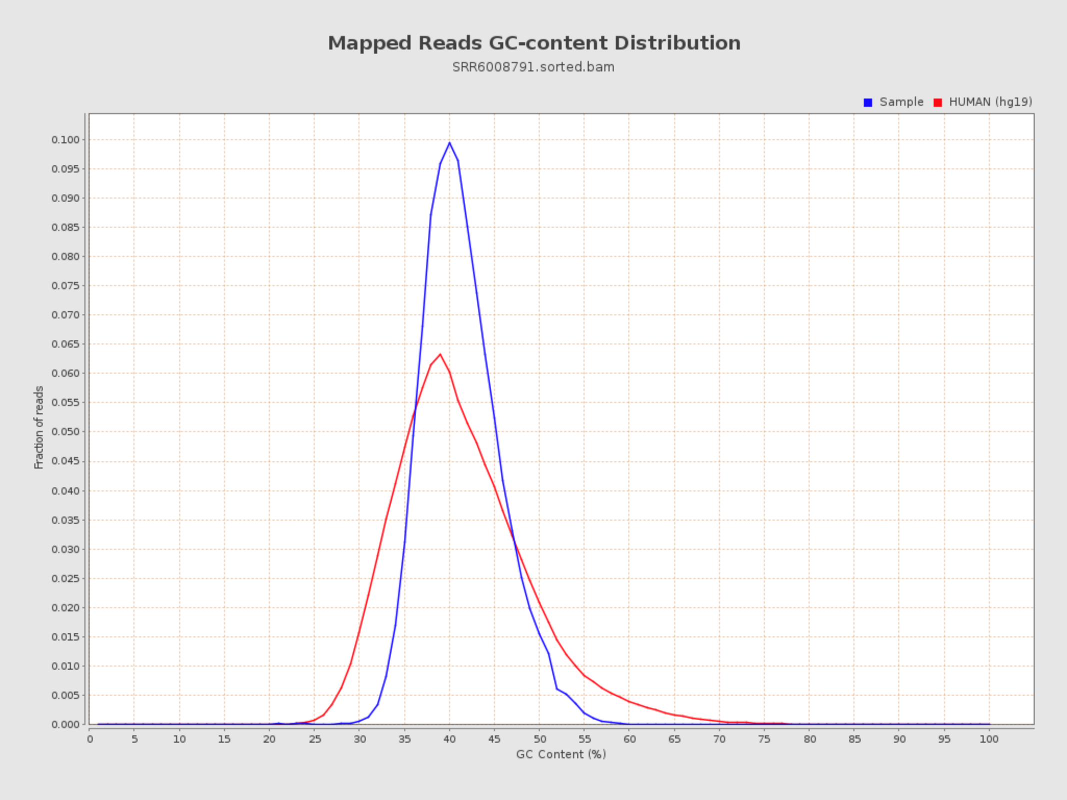
7. Results : Duplication Rate Histogram



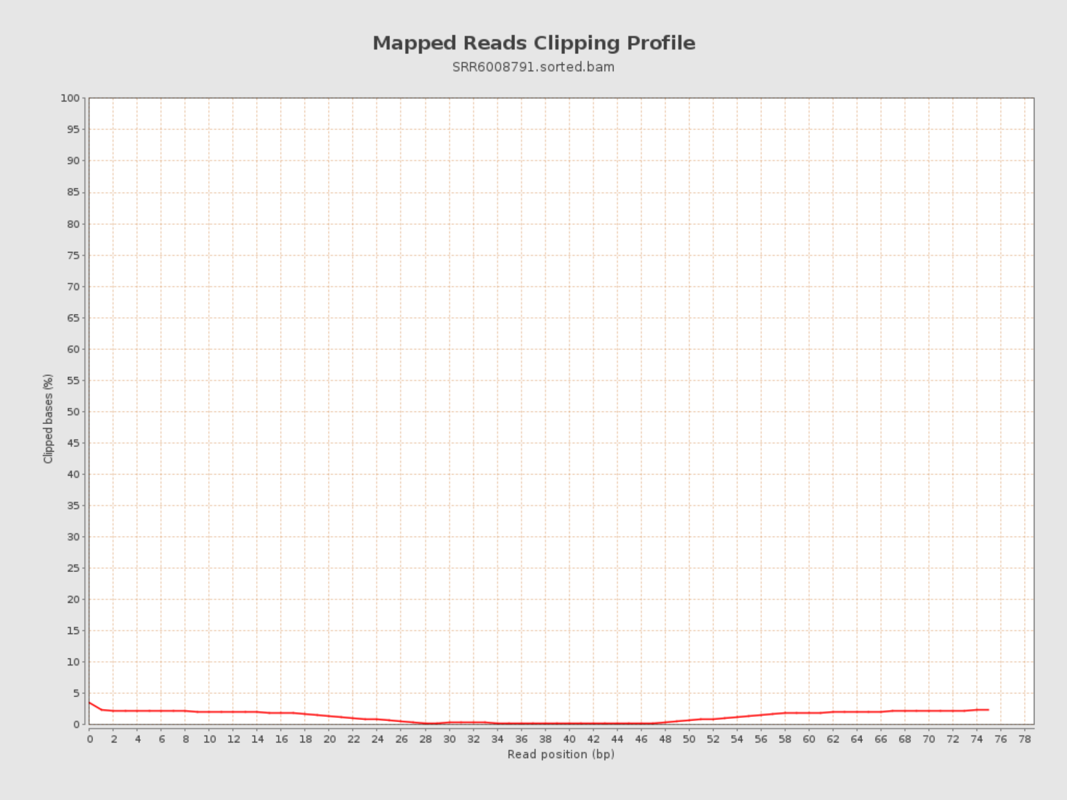
8. Results : Mapped Reads Nucleotide Content



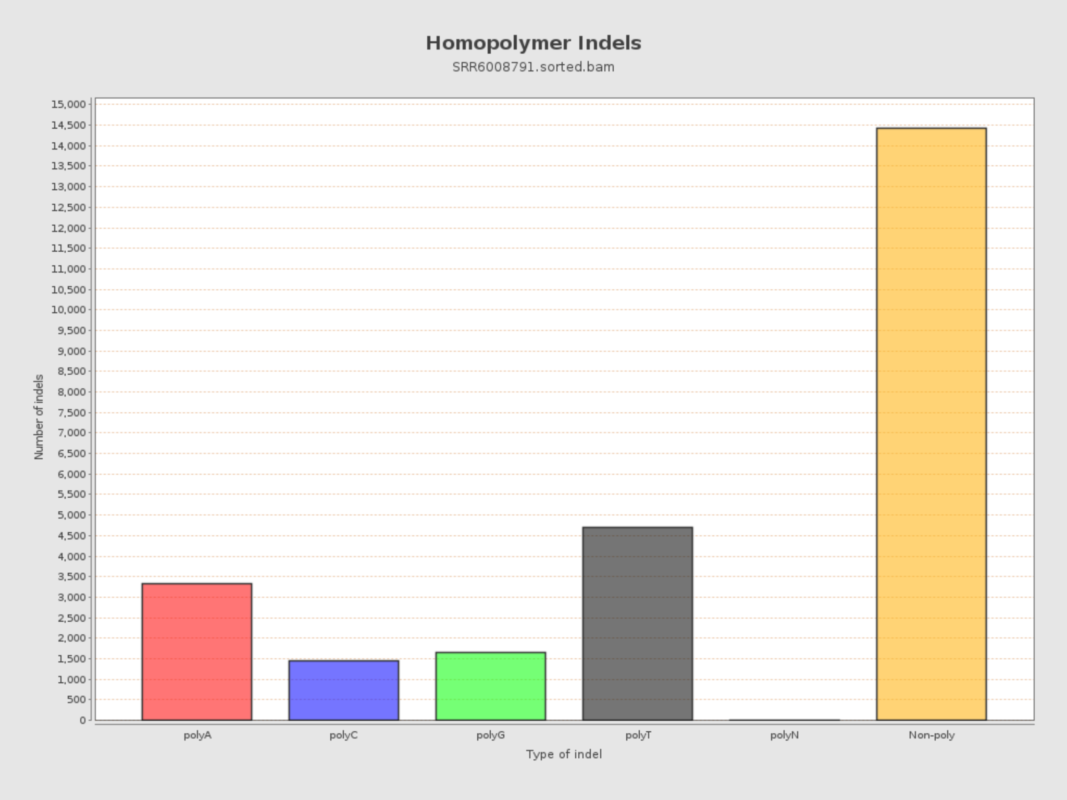
9. Results : Mapped Reads GC-content Distribution



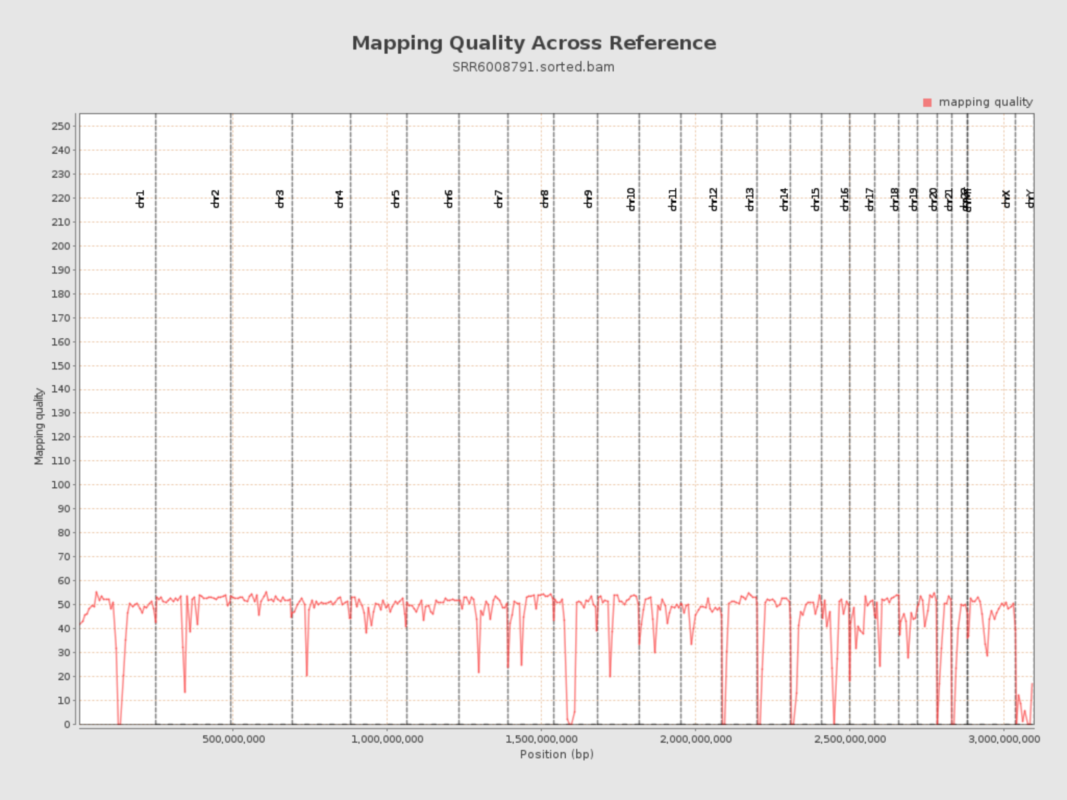
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram