Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:37:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008701.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_SRR6008701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008701.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:37:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,837,552
Mapped reads	1,460,454 / 79.48%
Unmapped reads	377,098 / 20.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,059 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	100,937 / 5.49%
Duplication rate	5.74%
Clipped reads	830,417 / 45.19%

2.2. ACGT Content

Number/percentage of A's	27,591,731 / 29.41%
Number/percentage of C's	17,945,762 / 19.13%
Number/percentage of T's	28,470,207 / 30.35%
Number/percentage of G's	19,790,924 / 21.09%
Number/percentage of N's	19,836 / 0.02%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.3269

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

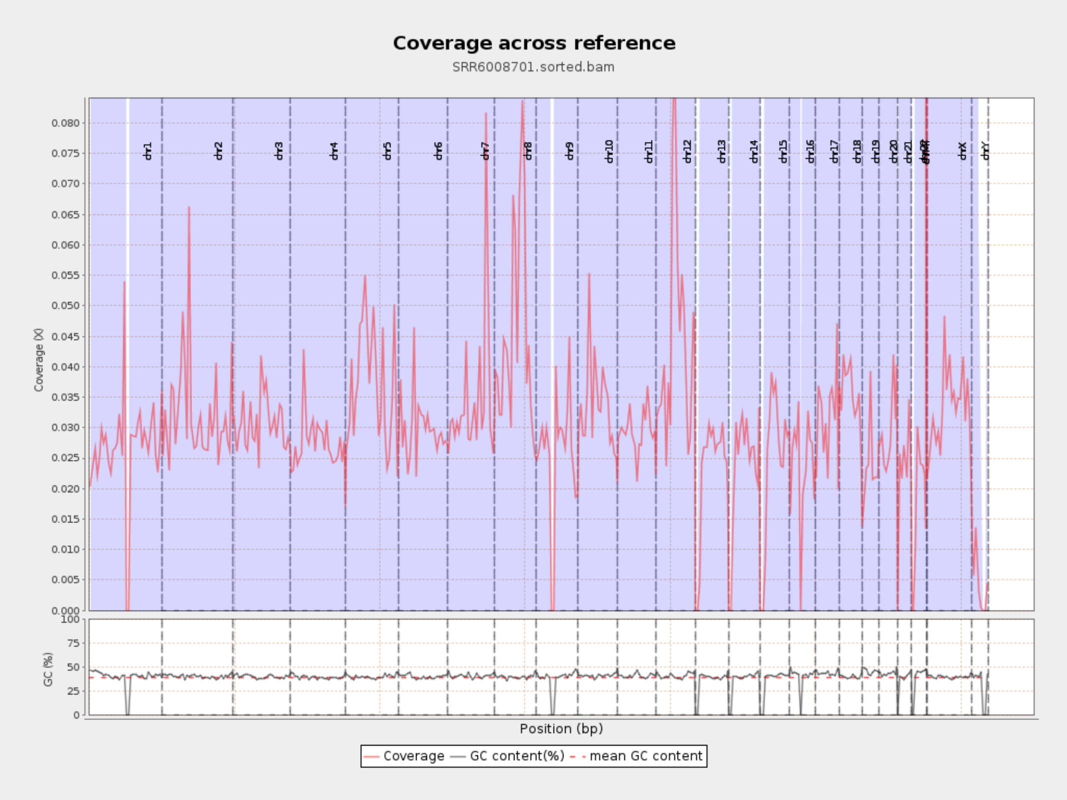
General error rate	0.85%
Mismatches	781,362
Insertions	8,116
Mapped reads with at least one insertion	0.55%
Deletions	28,090
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.72%

2.6. Chromosome stats

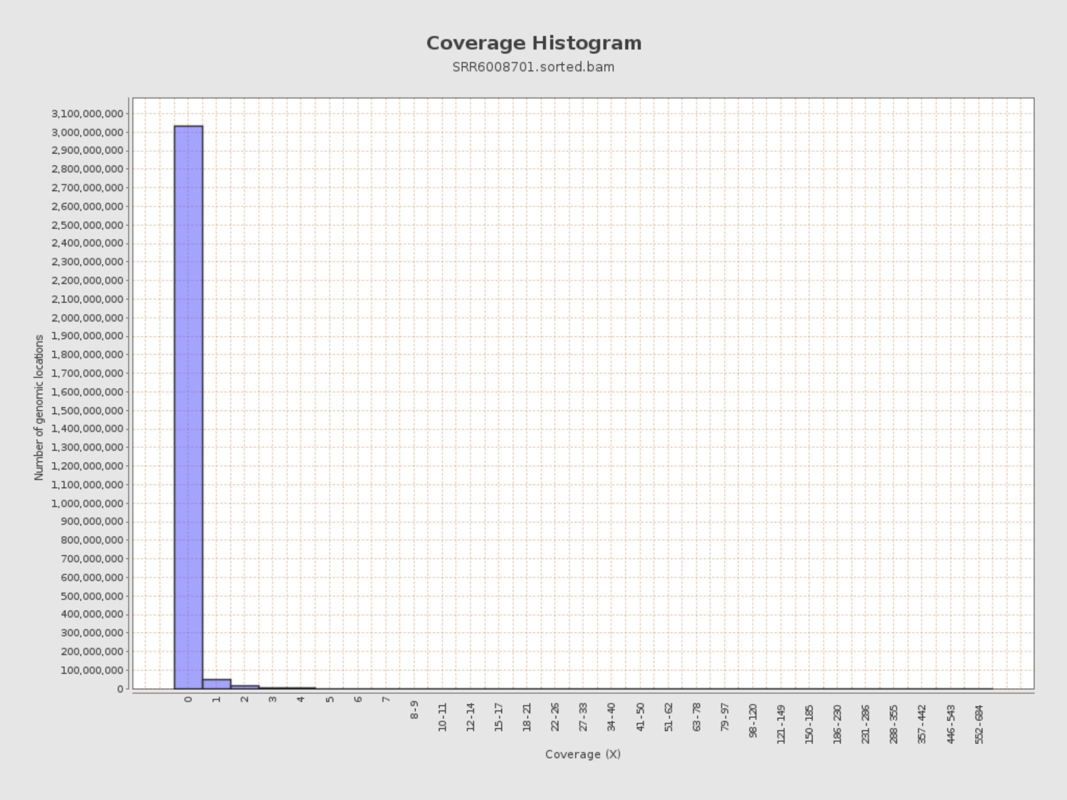
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6590793	0.0264	0.5499
chr2	243199373	7890768	0.0324	0.364
chr3	198022430	6092737	0.0308	0.2366
chr4	191154276	5265903	0.0275	0.231
chr5	180915260	6781919	0.0375	0.261
chr6	171115067	5117478	0.0299	0.2661
chr7	159138663	5564699	0.035	0.3416

chr8	146364022	6639626	0.0454	0.5201
chr9	141213431	3647588	0.0258	0.3053
chr10	135534747	4600647	0.0339	0.3093
chr11	135006516	3958313	0.0293	0.2807
chr12	133851895	5917411	0.0442	0.2885
chr13	115169878	2615817	0.0227	0.2032
chr14	107349540	2458931	0.0229	0.2144
chr15	102531392	2505271	0.0244	0.2099
chr16	90354753	2147572	0.0238	0.2193
chr17	81195210	2564817	0.0316	0.2486
chr18	78077248	2798399	0.0358	0.5014
chr19	59128983	1415793	0.0239	0.4003
chr20	63025520	1835813	0.0291	0.2306
chr21	48129895	1123676	0.0233	0.218
chr22	51304566	884295	0.0172	0.1721
chrMT	16571	43036	2.5971	2.2078
chrX	155270560	5142888	0.0331	0.2617
chrY	59373566	259157	0.0044	0.1045

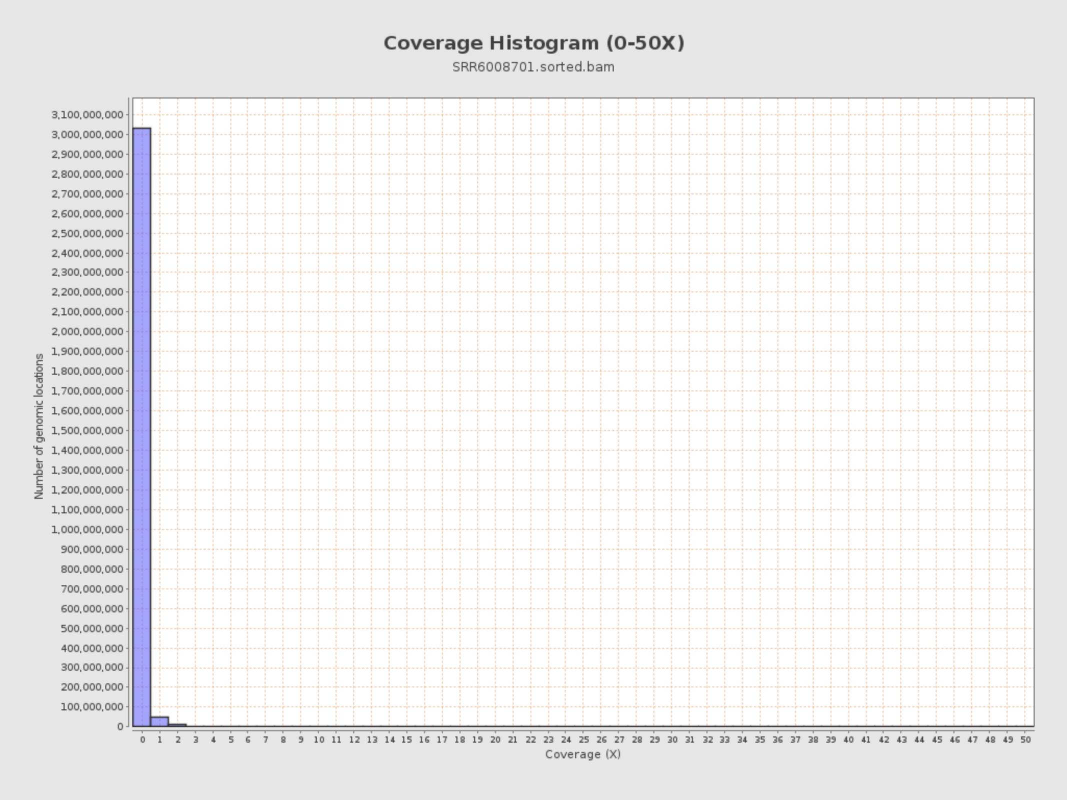
3. Results : Coverage across reference



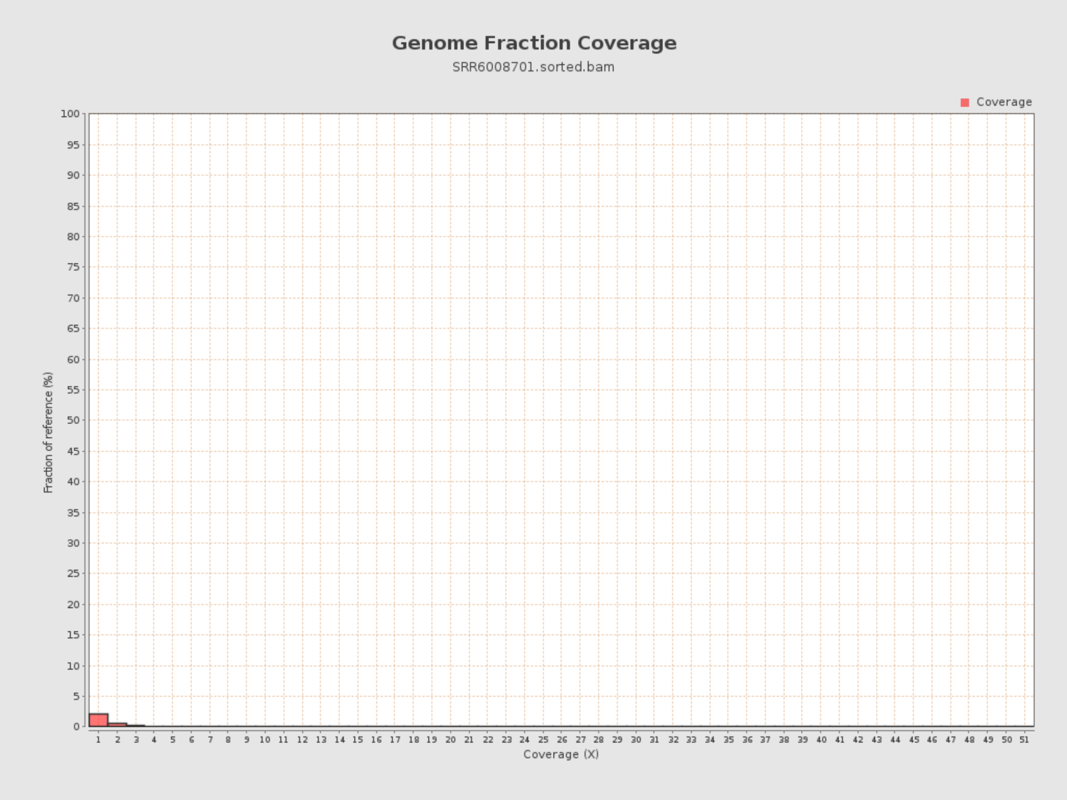
4. Results : Coverage Histogram



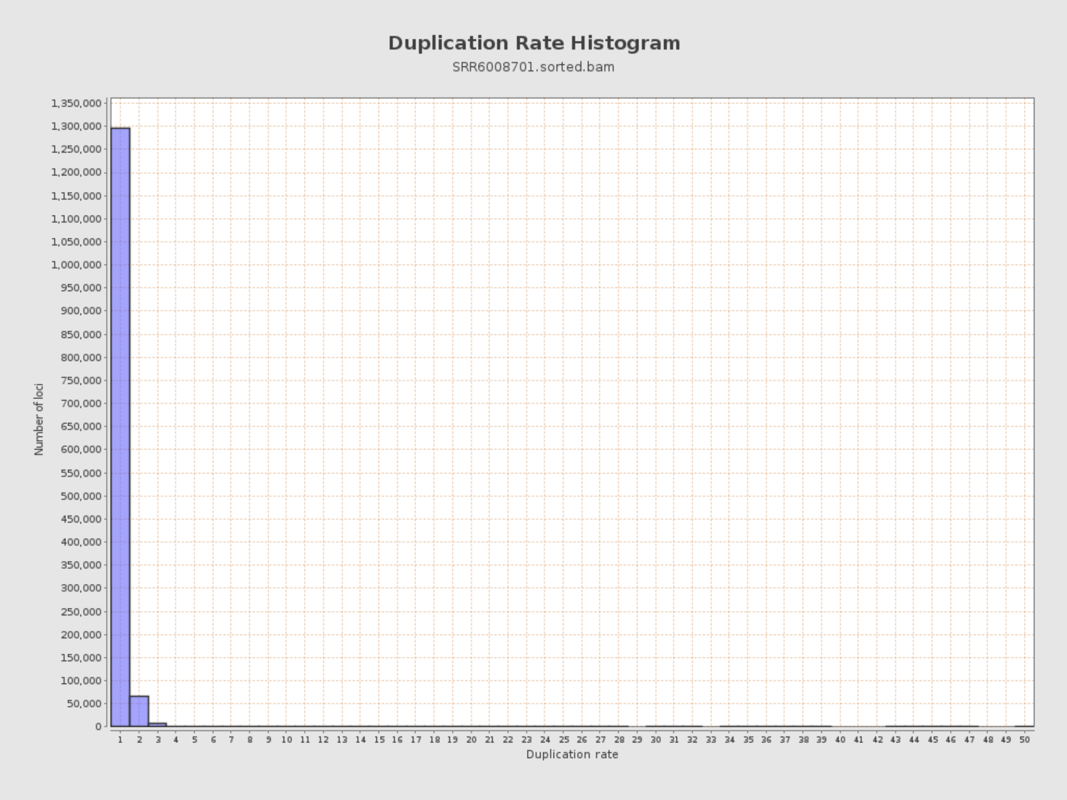
5. Results : Coverage Histogram (0-50X)



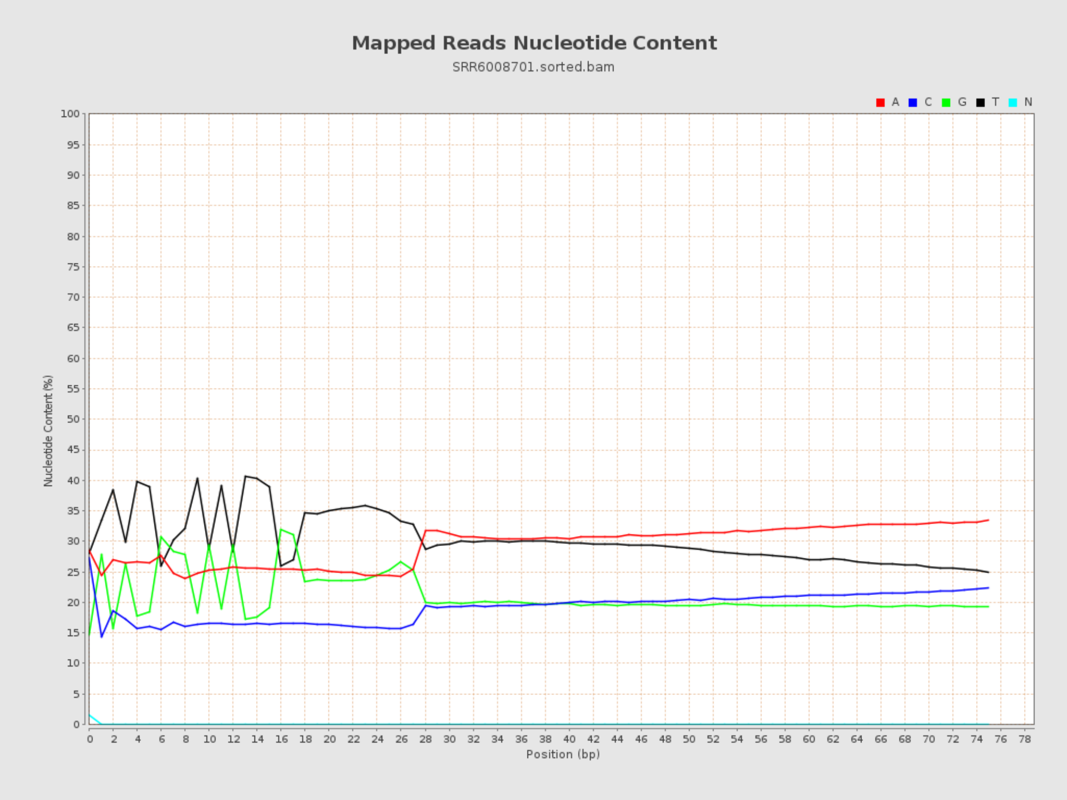
6. Results : Genome Fraction Coverage



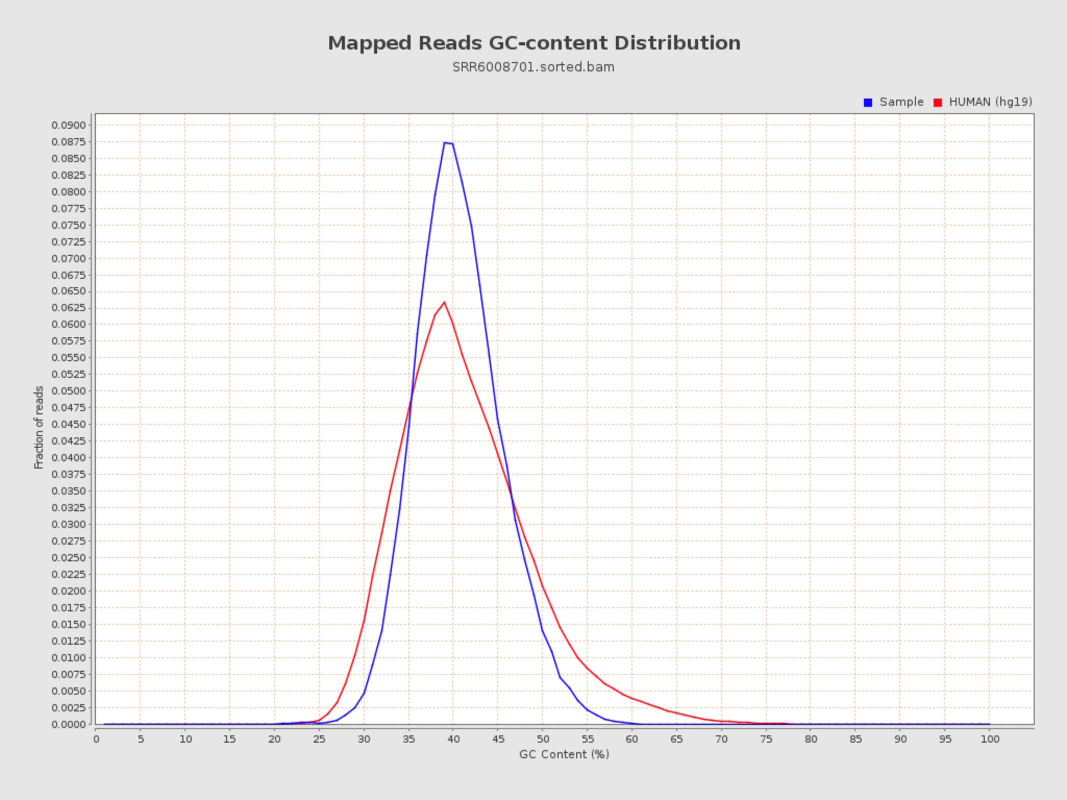
7. Results : Duplication Rate Histogram



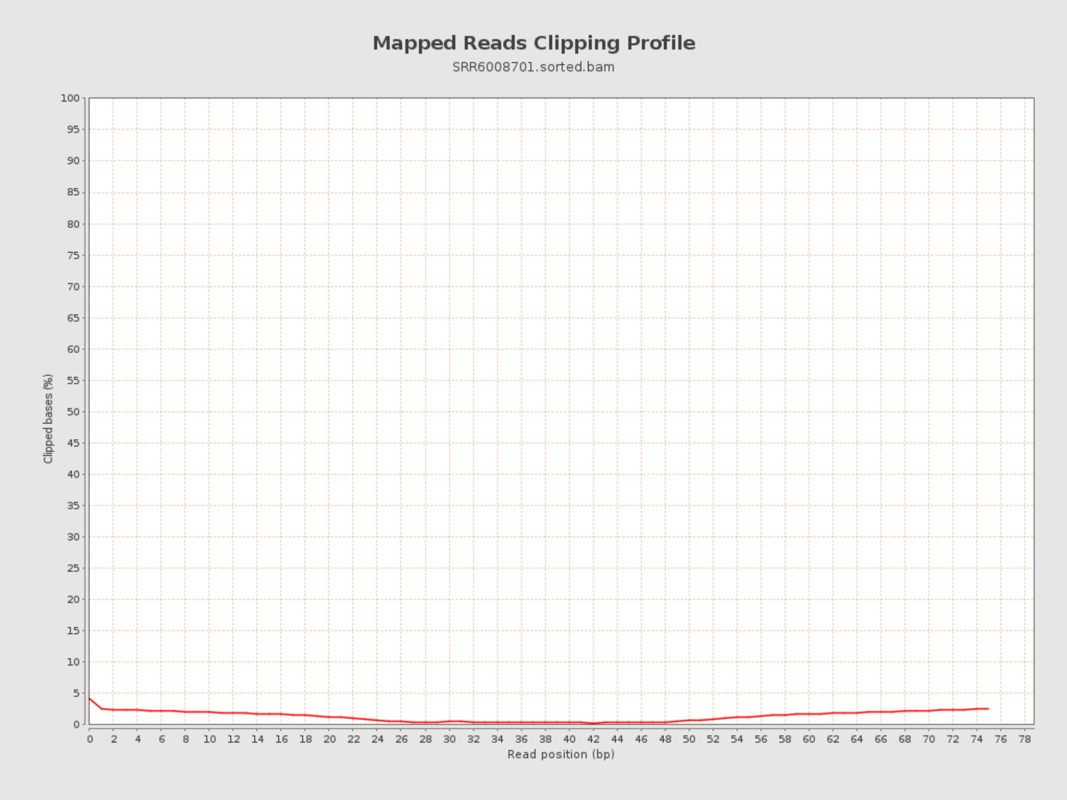
8. Results : Mapped Reads Nucleotide Content



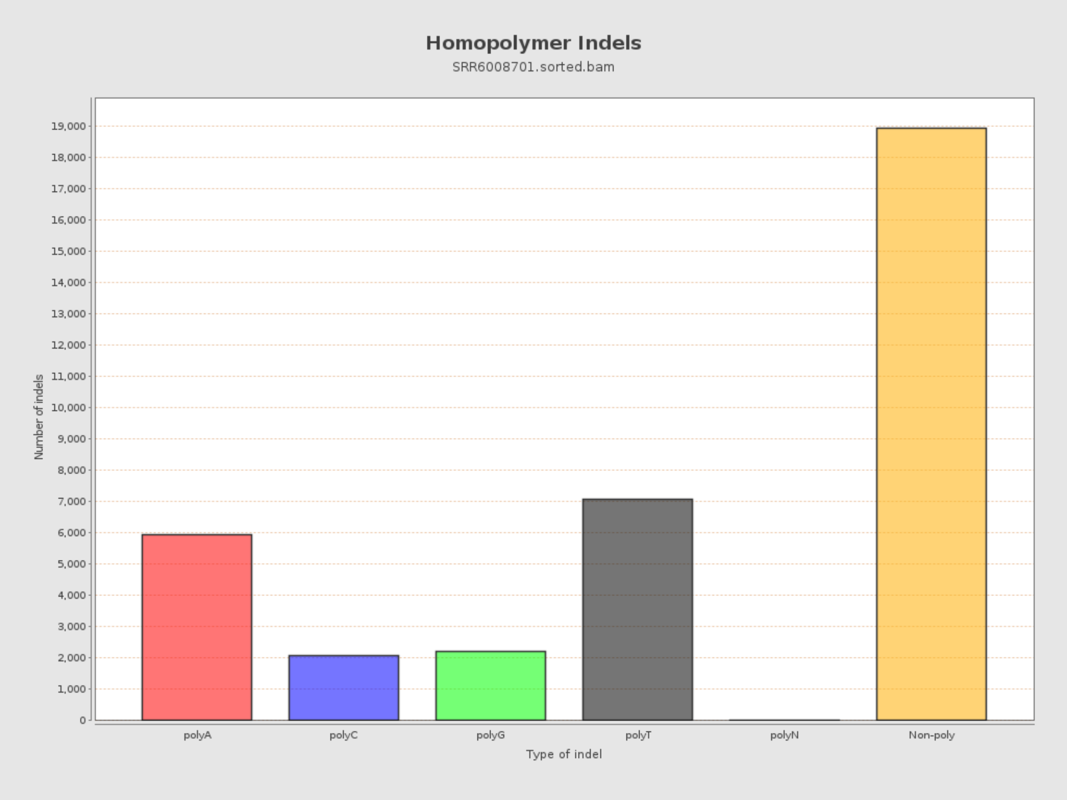
9. Results : Mapped Reads GC-content Distribution



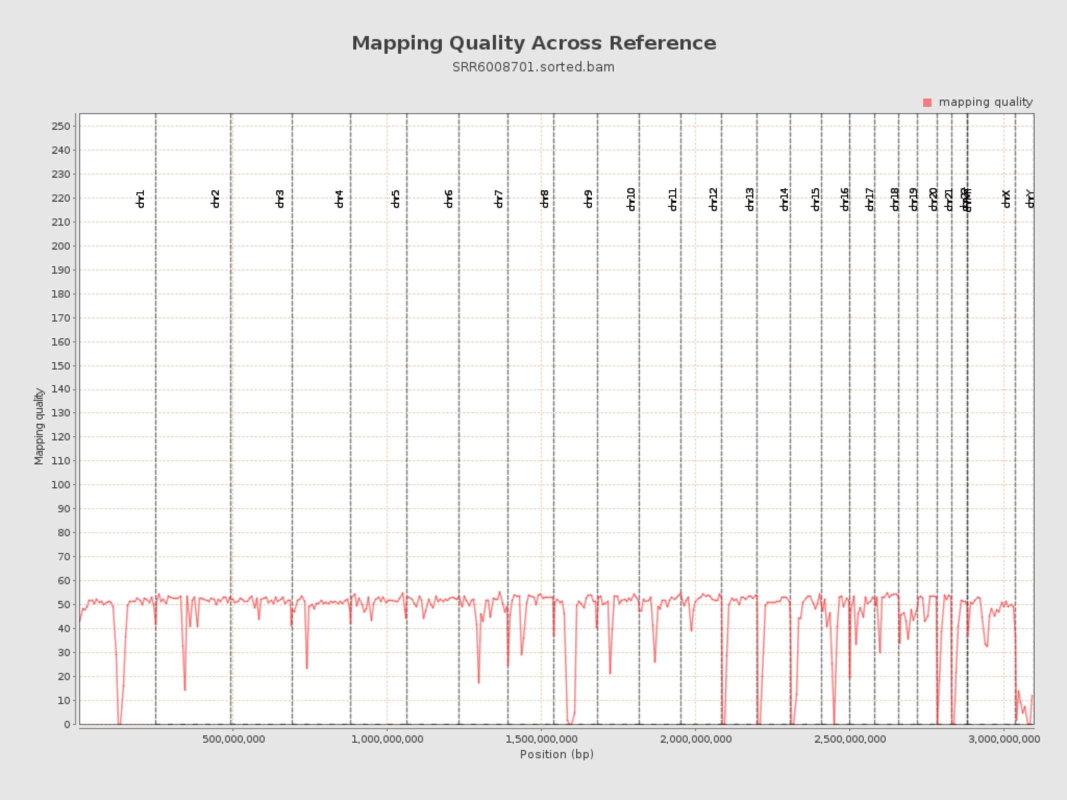
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram