Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:56:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008664.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_SRR6008664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:56:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,928,342
Mapped reads	1,625,745 / 84.31%
Unmapped reads	302,597 / 15.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,464 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	107,583 / 5.58%
Duplication rate	5.52%
Clipped reads	923,551 / 47.89%

2.2. ACGT Content

Number/percentage of A's	26,938,785 / 26.07%
Number/percentage of C's	19,115,435 / 18.5%
Number/percentage of T's	32,495,542 / 31.45%
Number/percentage of G's	24,701,997 / 23.91%
Number/percentage of N's	82,253 / 0.08%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3209

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

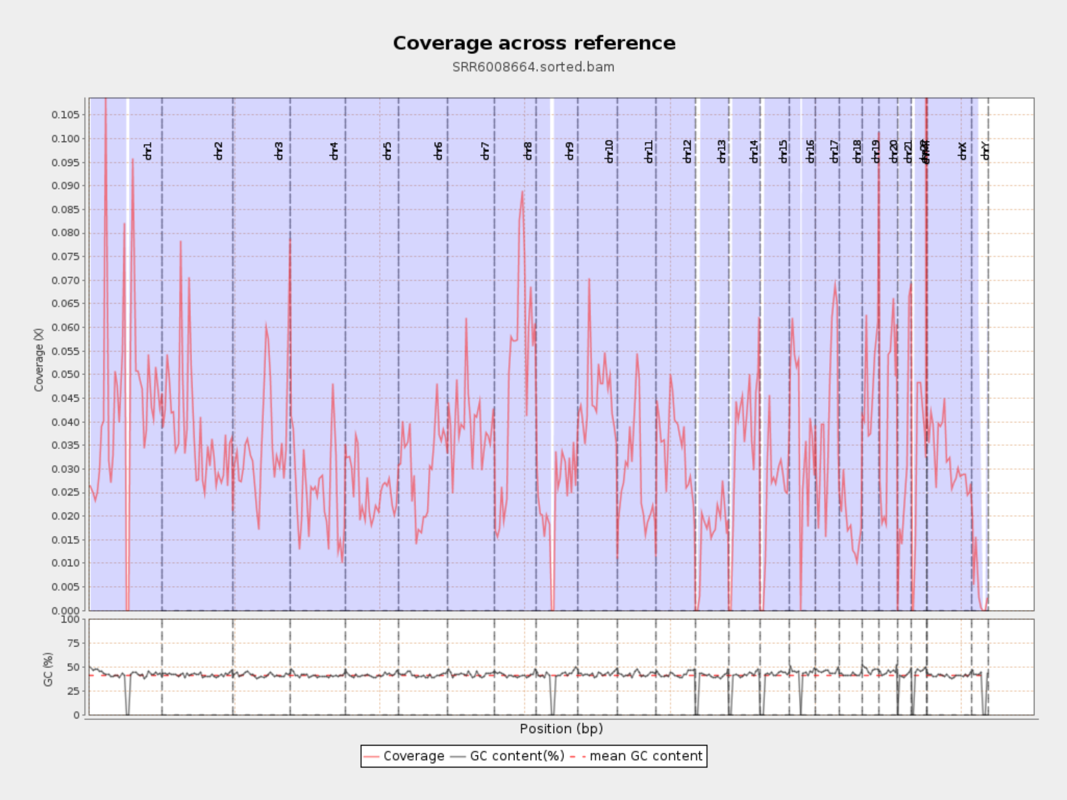
General error rate	0.85%
Mismatches	869,992
Insertions	6,993
Mapped reads with at least one insertion	0.43%
Deletions	29,219
Mapped reads with at least one deletion	1.78%
Homopolymer indels	44.57%

2.6. Chromosome stats

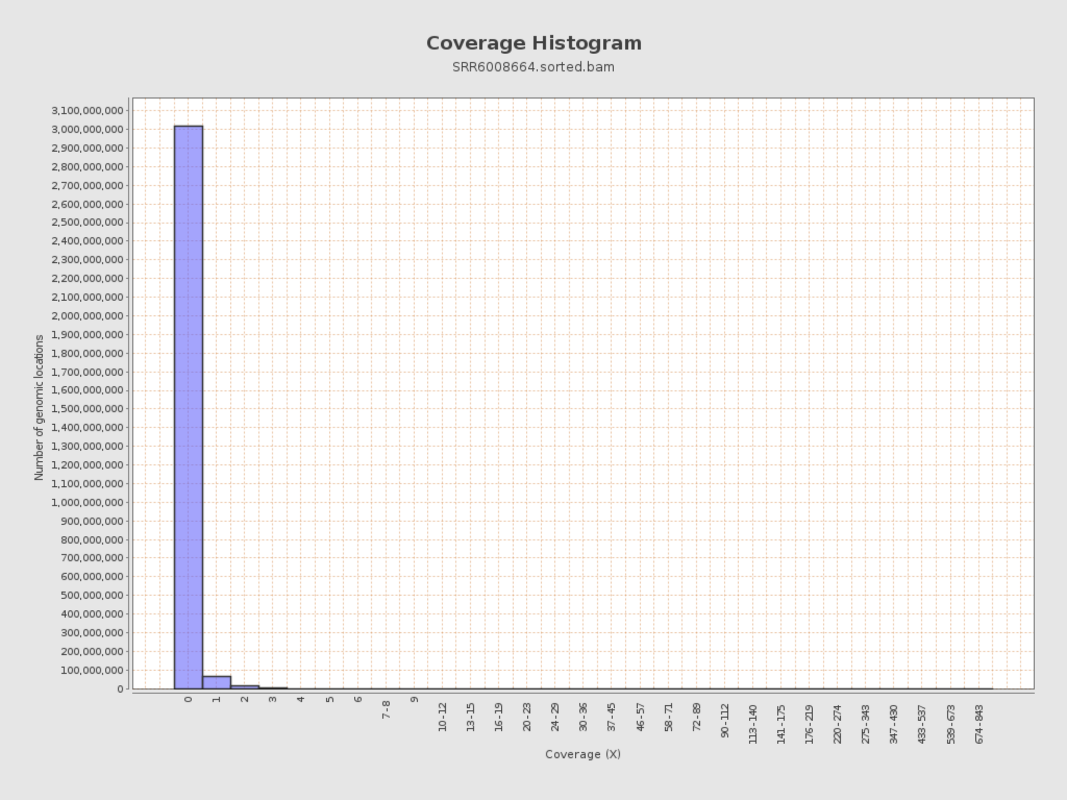
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10838026	0.0435	0.6536
chr2	243199373	9312269	0.0383	0.3142
chr3	198022430	6975046	0.0352	0.2318
chr4	191154276	4697758	0.0246	0.2054
chr5	180915260	4575843	0.0253	0.1955
chr6	171115067	5177590	0.0303	0.2329
chr7	159138663	6287690	0.0395	0.4054

chr8	146364022	7173236	0.049	0.3208
chr9	141213431	3283845	0.0233	0.2487
chr10	135534747	6181722	0.0456	0.3328
chr11	135006516	3846591	0.0285	0.2999
chr12	133851895	4749577	0.0355	0.2327
chr13	115169878	1873505	0.0163	0.1535
chr14	107349540	3772724	0.0351	0.2336
chr15	102531392	2522424	0.0246	0.2035
chr16	90354753	3415688	0.0378	0.2672
chr17	81195210	3349044	0.0412	0.2934
chr18	78077248	1390241	0.0178	0.3854
chr19	59128983	2948105	0.0499	0.4399
chr20	63025520	2525491	0.0401	0.2507
chr21	48129895	1498451	0.0311	0.227
chr22	51304566	1541622	0.03	0.2105
chrMT	16571	52274	3.1545	2.5826
chrX	155270560	5087575	0.0328	0.2439
chrY	59373566	309266	0.0052	0.1421

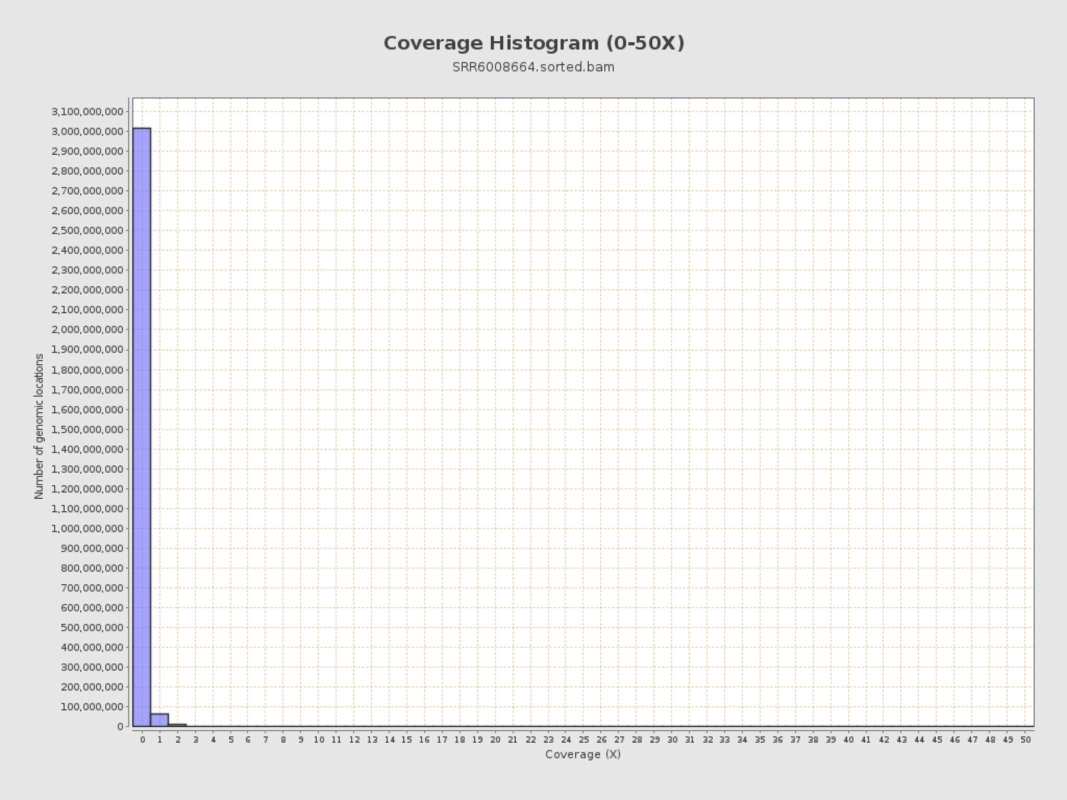
3. Results : Coverage across reference



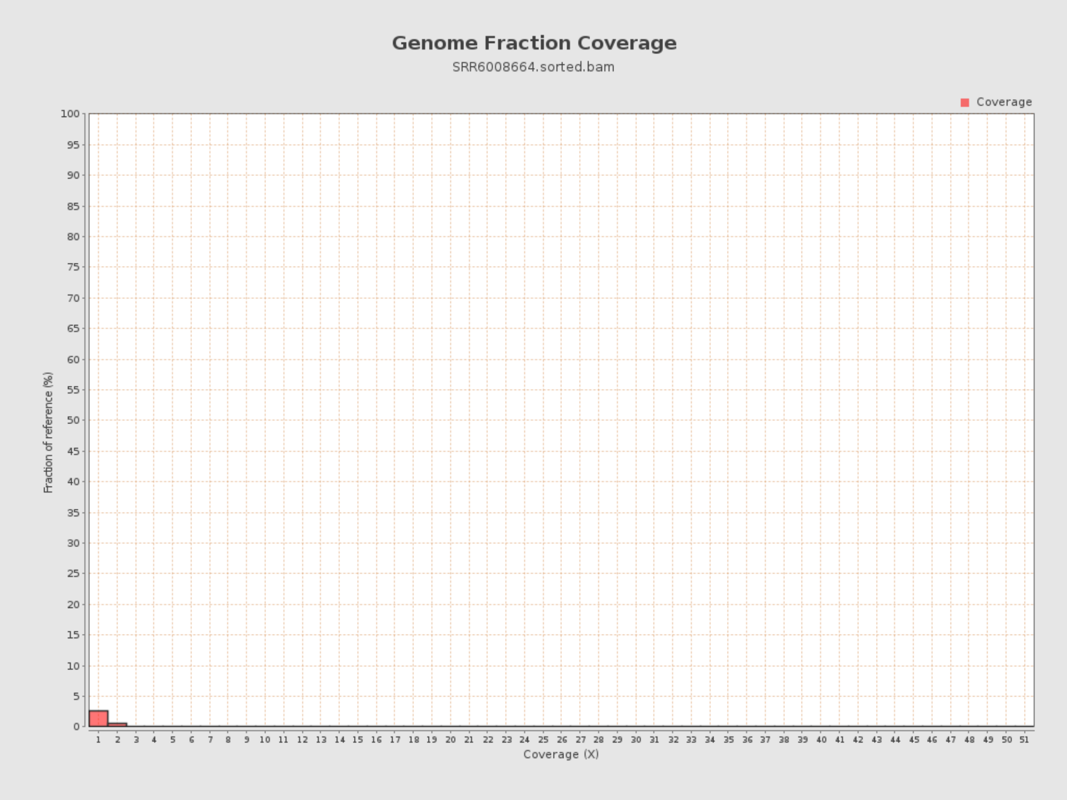
4. Results : Coverage Histogram



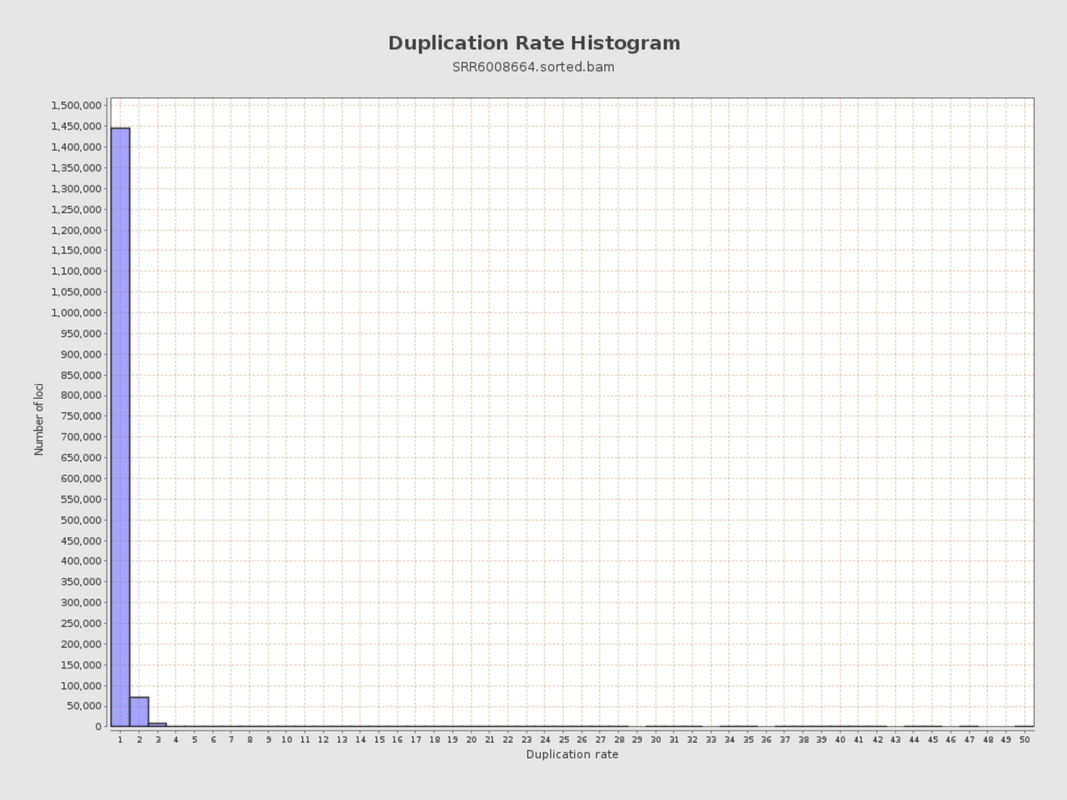
5. Results : Coverage Histogram (0-50X)



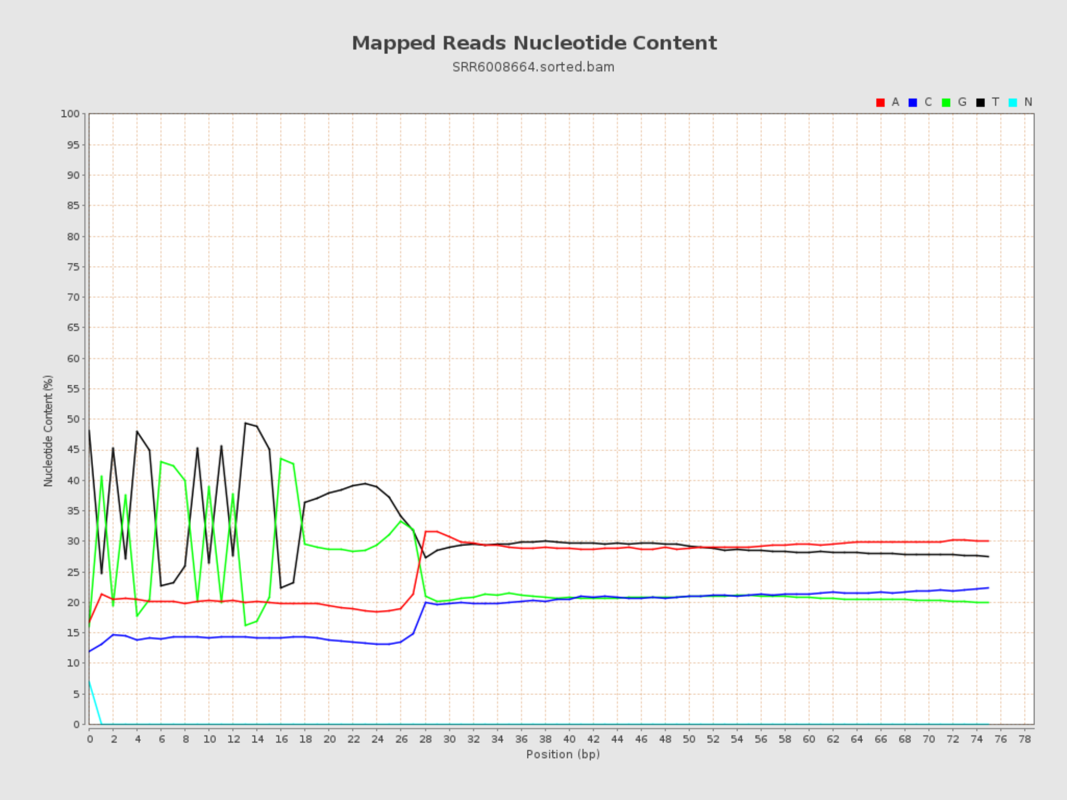
6. Results : Genome Fraction Coverage



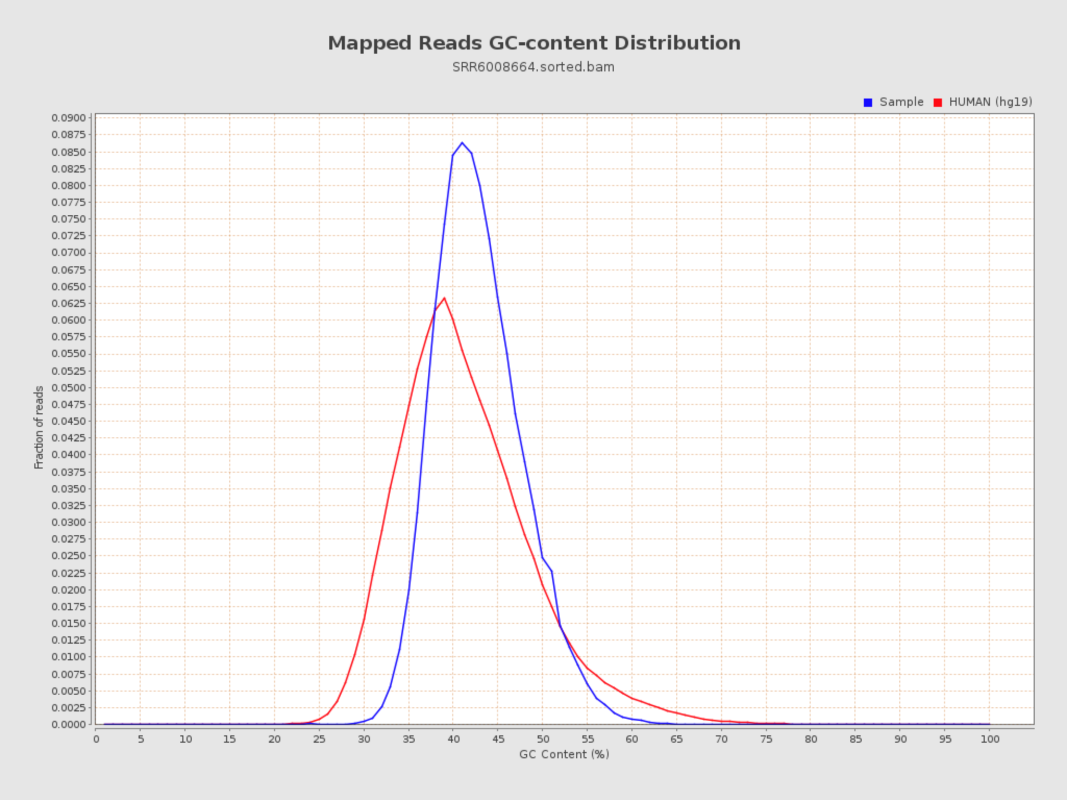
7. Results : Duplication Rate Histogram



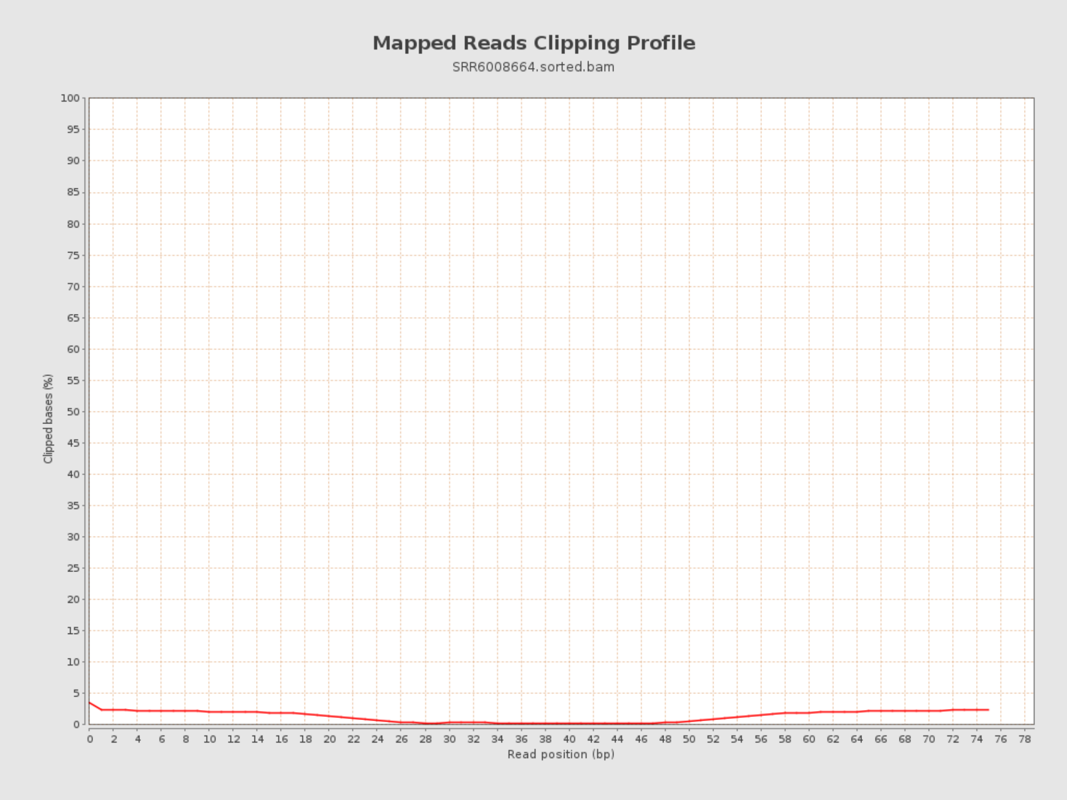
8. Results : Mapped Reads Nucleotide Content



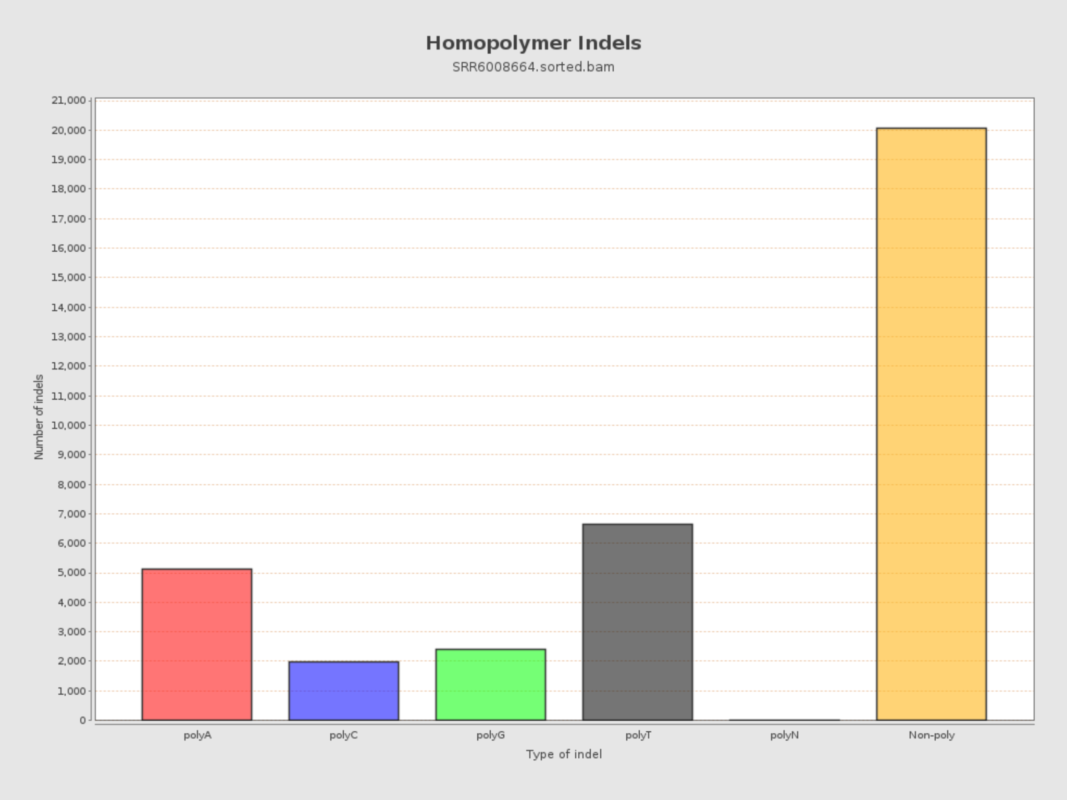
9. Results : Mapped Reads GC-content Distribution



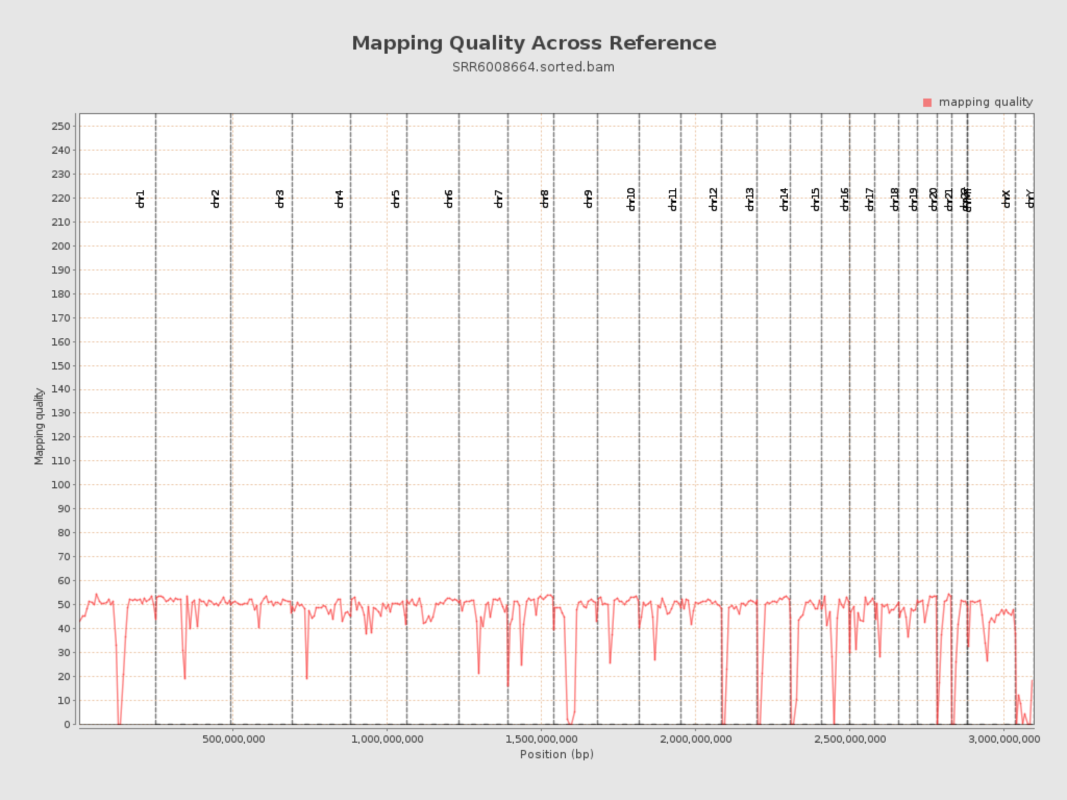
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram