Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:10:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008802.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_SRR6008802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:10:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,262,778
Mapped reads	1,154,571 / 91.43%
Unmapped reads	108,207 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,837 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	49,674 / 3.93%
Duplication rate	3.61%
Clipped reads	492,742 / 39.02%

2.2. ACGT Content

Number/percentage of A's	21,220,443 / 27.3%
Number/percentage of C's	15,250,463 / 19.62%
Number/percentage of T's	23,683,619 / 30.46%
Number/percentage of G's	17,477,990 / 22.48%
Number/percentage of N's	108,068 / 0.14%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2349

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

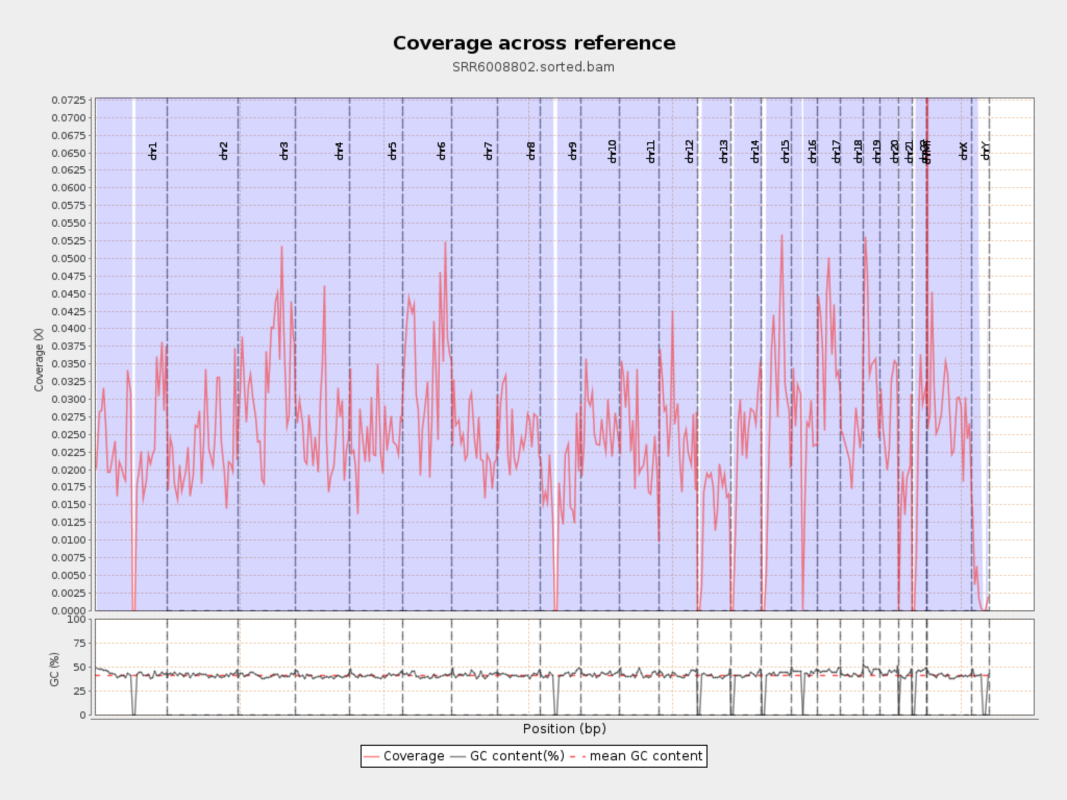
General error rate	0.82%
Mismatches	630,642
Insertions	5,464
Mapped reads with at least one insertion	0.47%
Deletions	21,124
Mapped reads with at least one deletion	1.81%
Homopolymer indels	46.29%

2.6. Chromosome stats

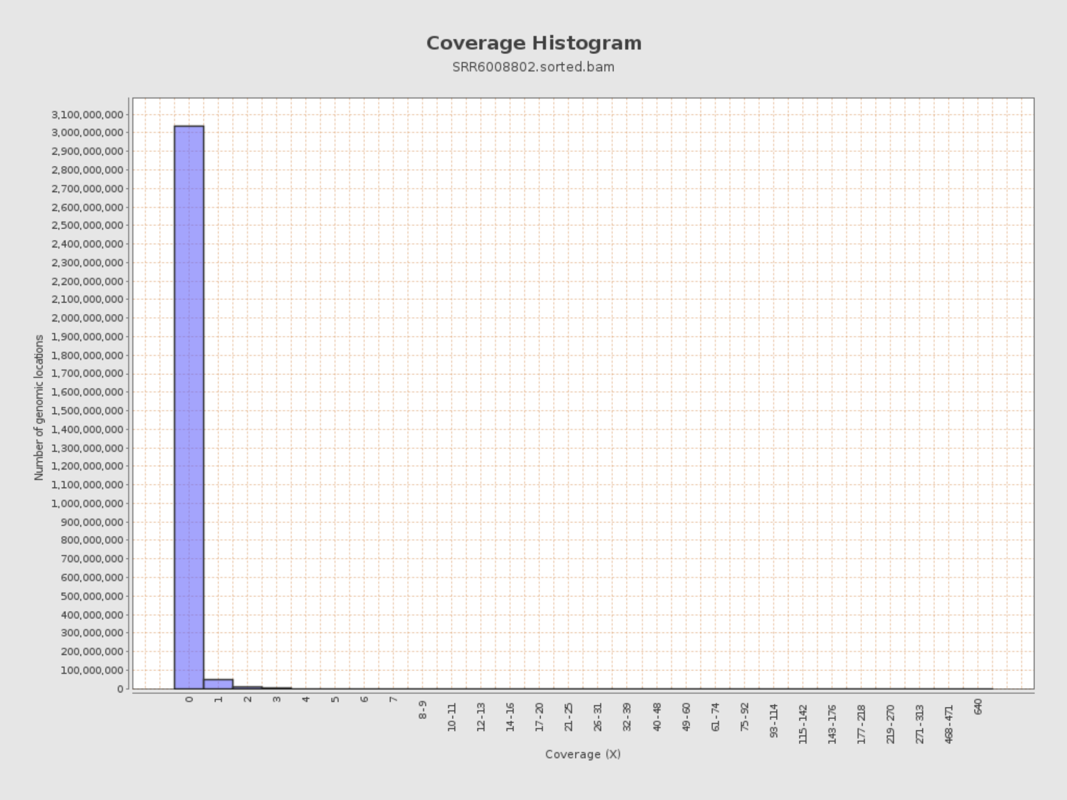
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5719842	0.0229	0.326
chr2	243199373	5523992	0.0227	0.3222
chr3	198022430	6620542	0.0334	0.2251
chr4	191154276	4913946	0.0257	0.1988
chr5	180915260	4371998	0.0242	0.1898
chr6	171115067	5910641	0.0345	0.246
chr7	159138663	3772936	0.0237	0.2501

chr8	146364022	3693287	0.0252	0.2346
chr9	141213431	2239226	0.0159	0.1691
chr10	135534747	3549605	0.0262	0.258
chr11	135006516	3283744	0.0243	0.2059
chr12	133851895	3552783	0.0265	0.2005
chr13	115169878	1661091	0.0144	0.1476
chr14	107349540	2457096	0.0229	0.1892
chr15	102531392	2829964	0.0276	0.205
chr16	90354753	2188703	0.0242	0.1942
chr17	81195210	3145026	0.0387	0.2461
chr18	78077248	1851956	0.0237	0.2508
chr19	59128983	2210526	0.0374	0.3104
chr20	63025520	1776760	0.0282	0.208
chr21	48129895	819225	0.017	0.1616
chr22	51304566	1074299	0.0209	0.1775
chrMT	16571	7874	0.4752	0.8956
chrX	155270560	4419503	0.0285	0.2095
chrY	59373566	183039	0.0031	0.0682

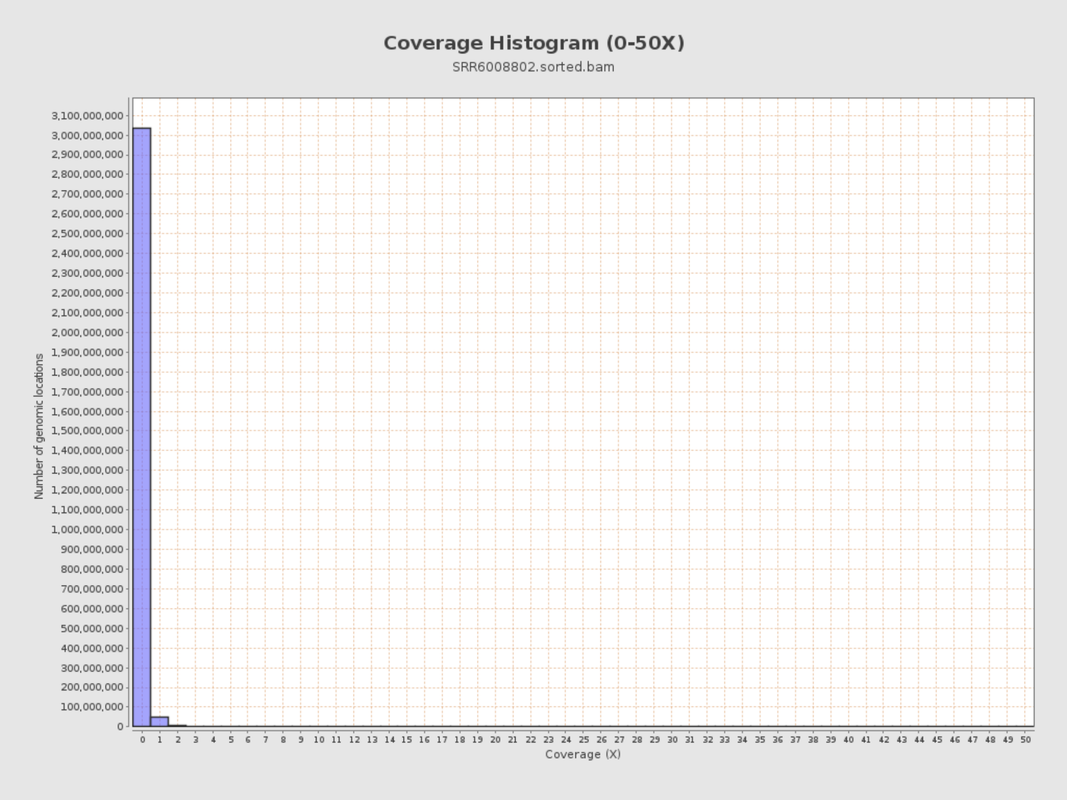
3. Results : Coverage across reference



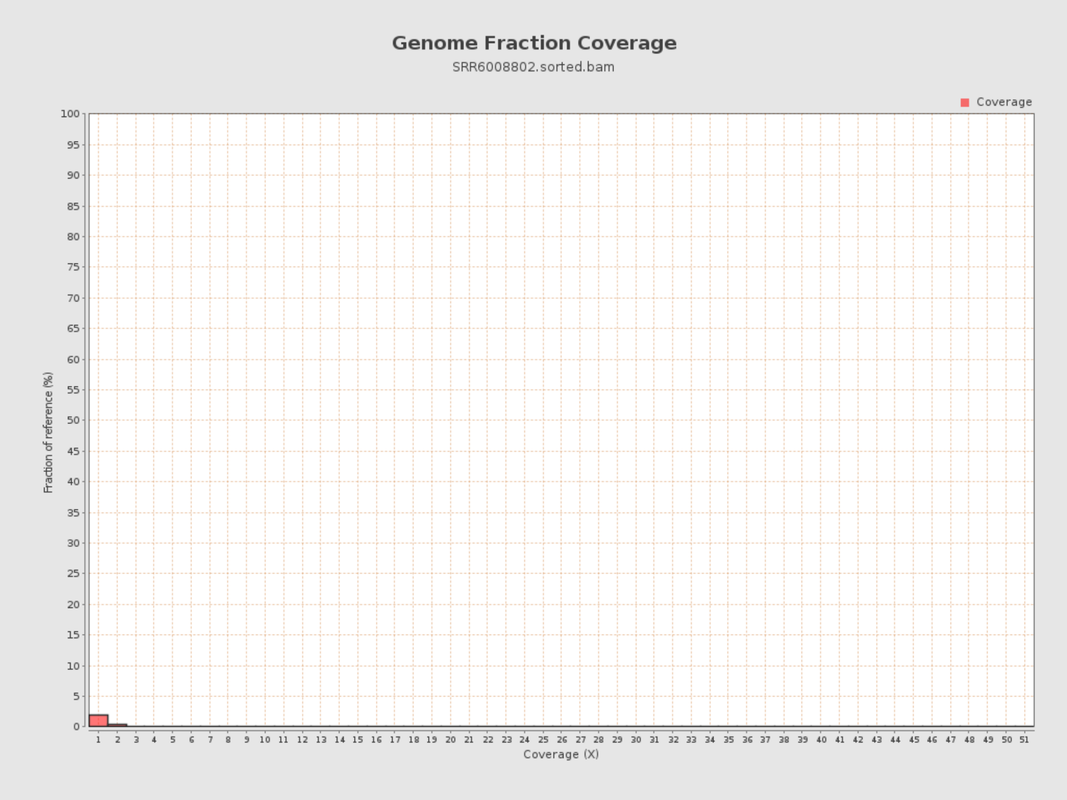
4. Results : Coverage Histogram



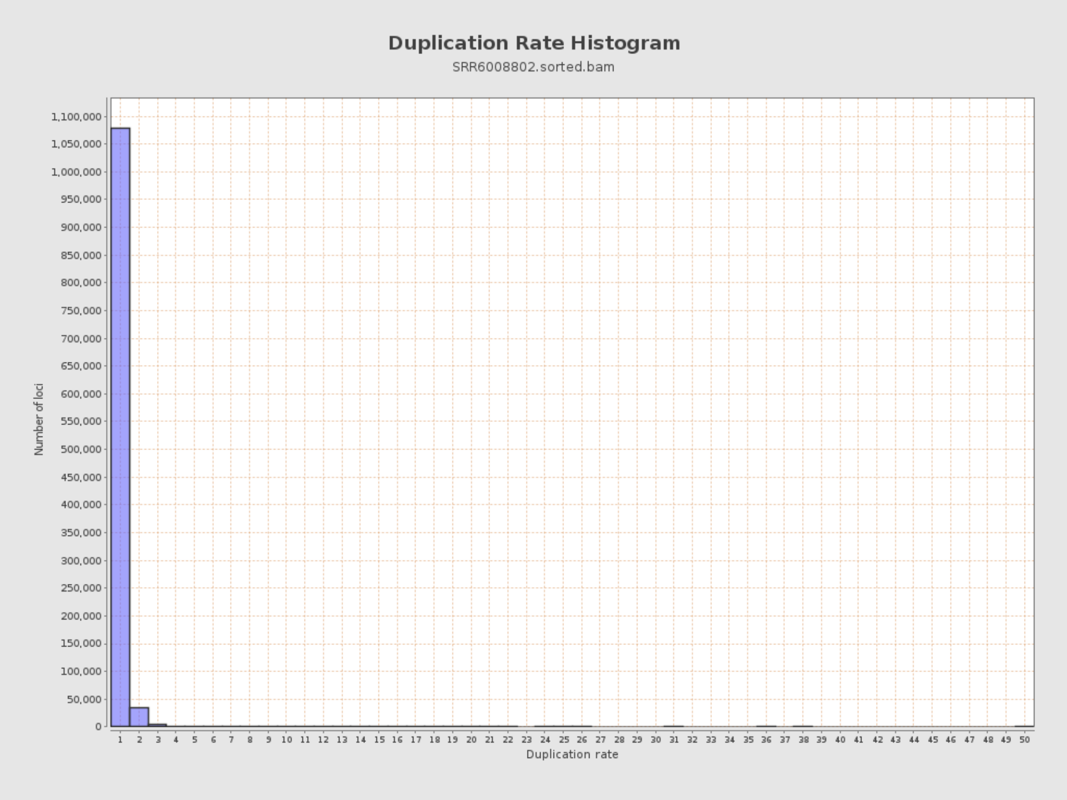
5. Results : Coverage Histogram (0-50X)



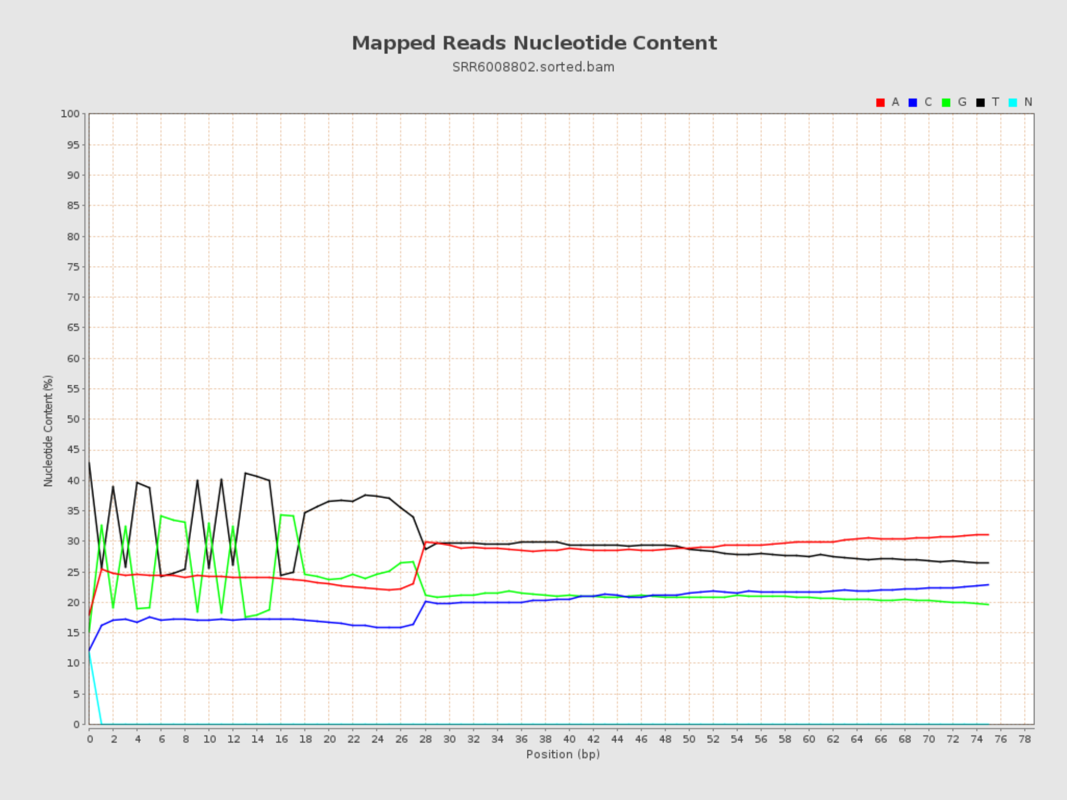
6. Results : Genome Fraction Coverage



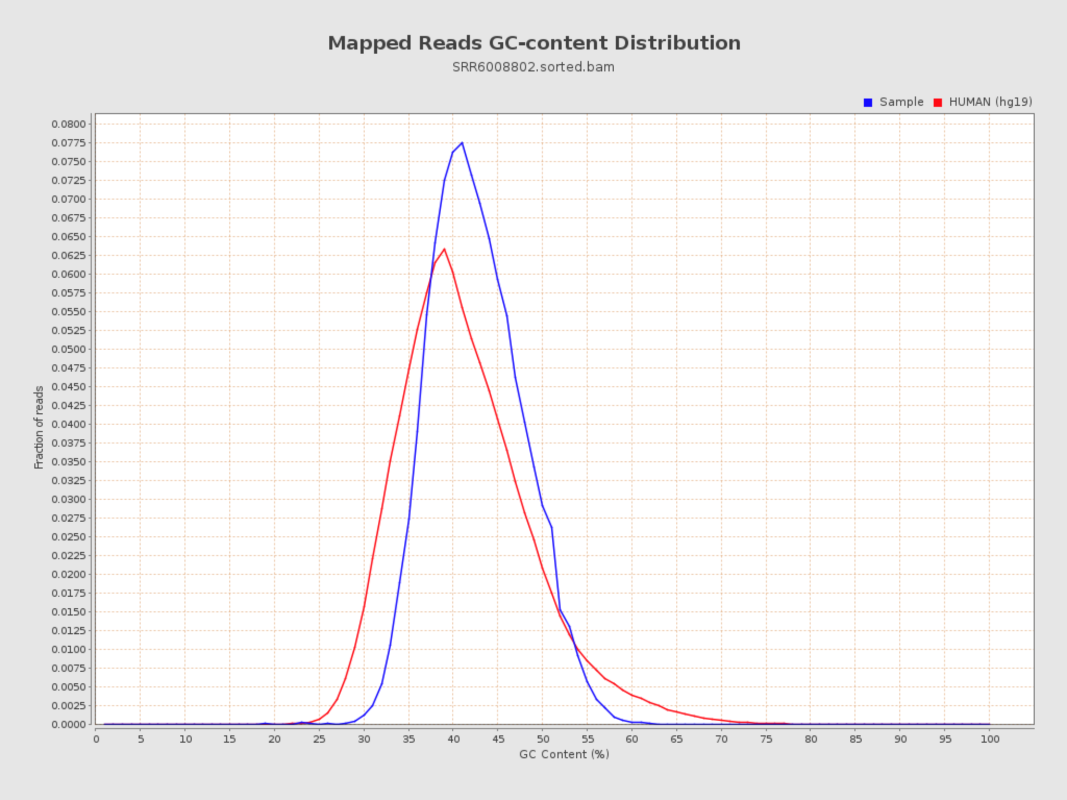
7. Results : Duplication Rate Histogram



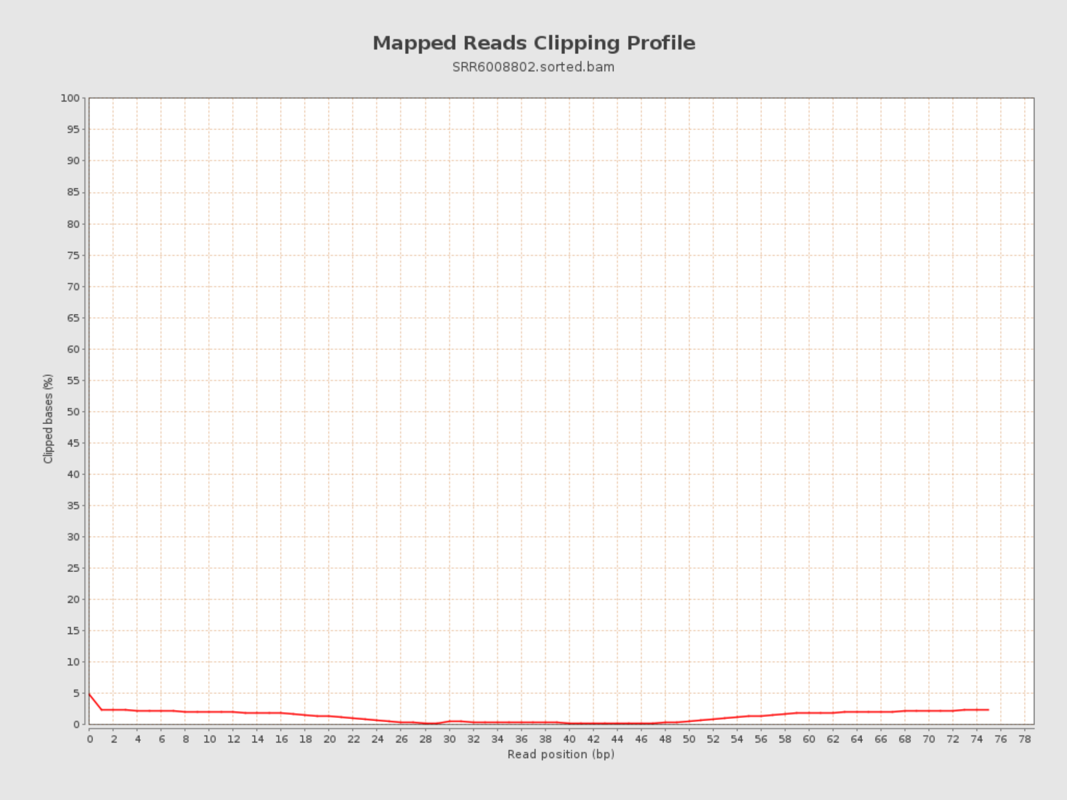
8. Results : Mapped Reads Nucleotide Content



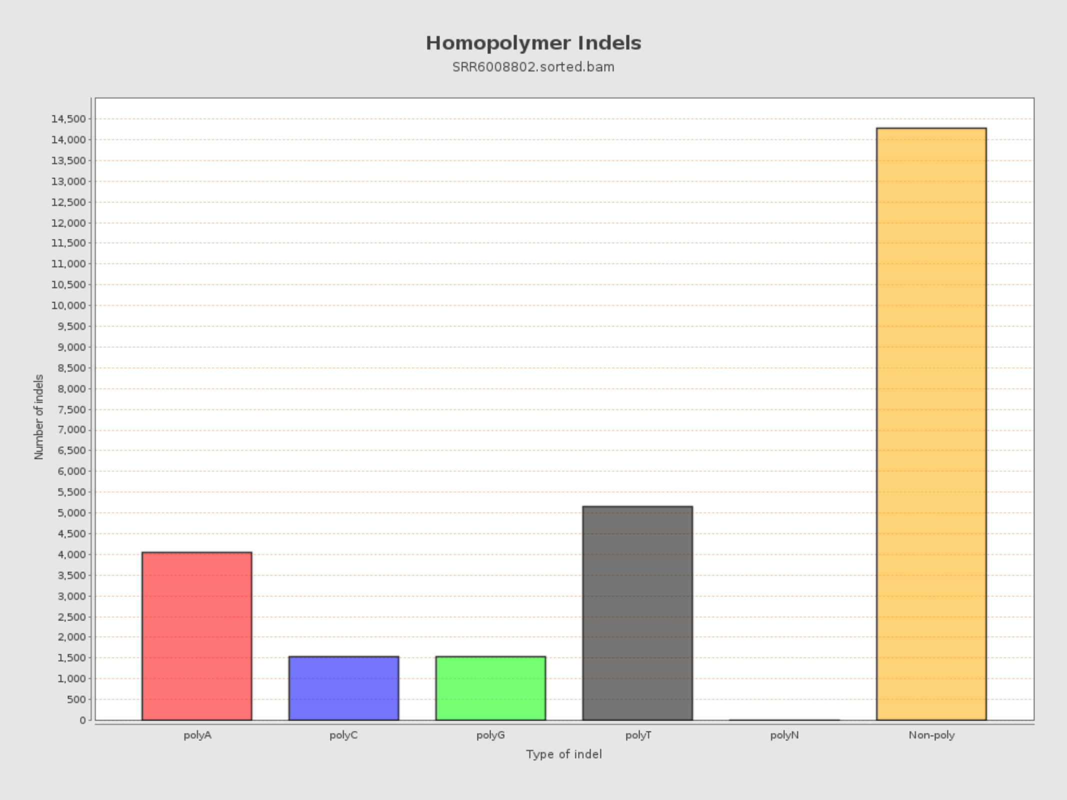
9. Results : Mapped Reads GC-content Distribution



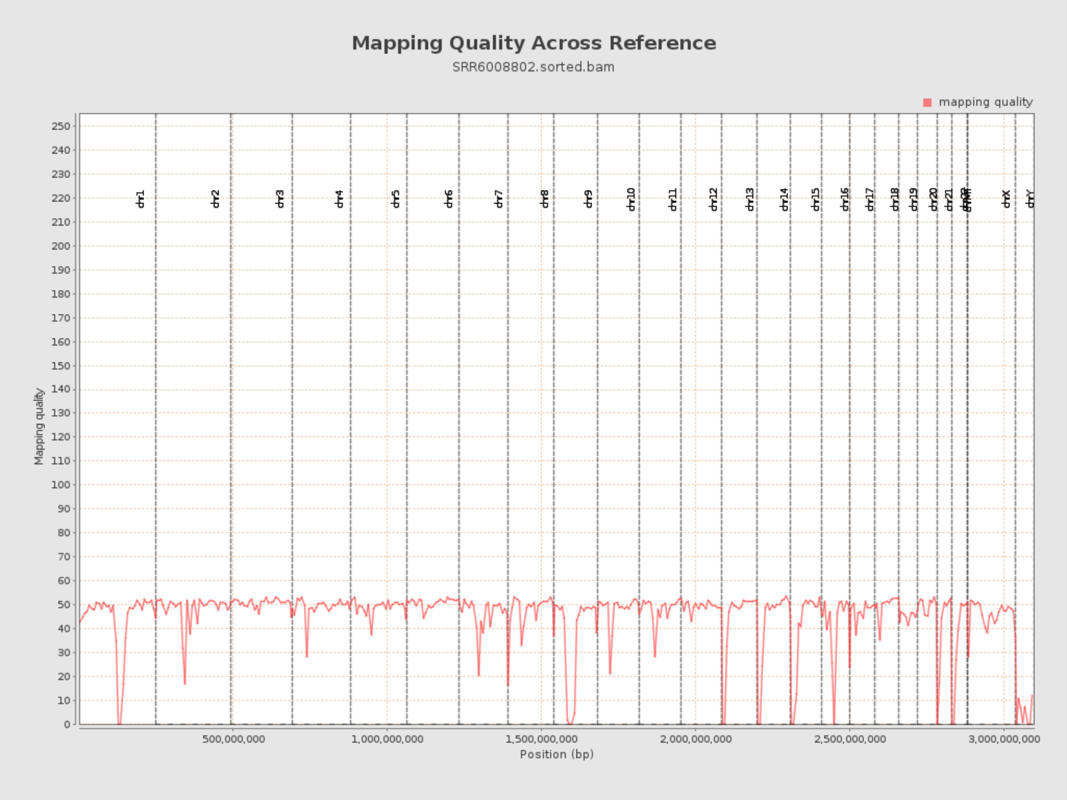
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram