Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008752.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_SRR6008752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:50:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,590,550
Mapped reads	1,170,177 / 73.57%
Unmapped reads	420,373 / 26.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,360 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	37,265 / 2.34%
Duplication rate	2.59%
Clipped reads	547,538 / 34.42%

2.2. ACGT Content

Number/percentage of A's	24,586,401 / 31.66%
Number/percentage of C's	13,220,603 / 17.02%
Number/percentage of T's	22,836,910 / 29.4%
Number/percentage of G's	17,006,762 / 21.9%
Number/percentage of N's	14,733 / 0.02%
GC Percentage	38.92%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2128

2.4. Mapping Quality

Mean Mapping Quality	48.6

2.5. Mismatches and indels

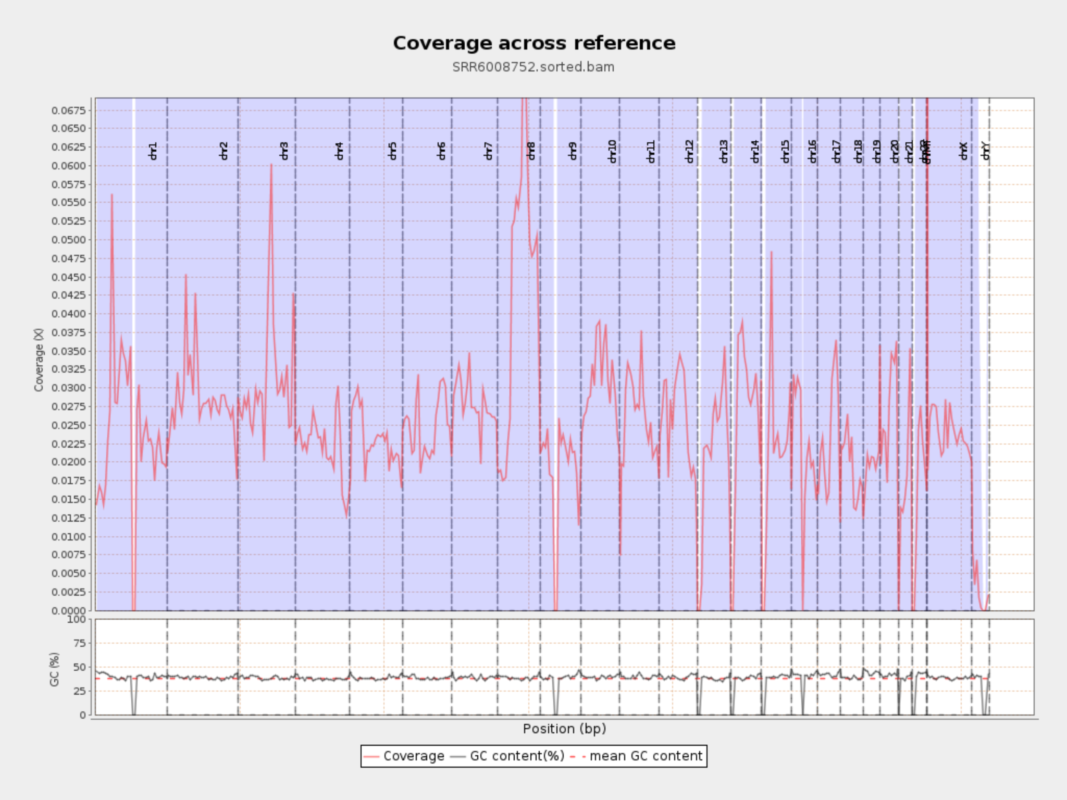
General error rate	1.17%
Mismatches	896,428
Insertions	6,204
Mapped reads with at least one insertion	0.53%
Deletions	31,414
Mapped reads with at least one deletion	2.65%
Homopolymer indels	49.83%

2.6. Chromosome stats

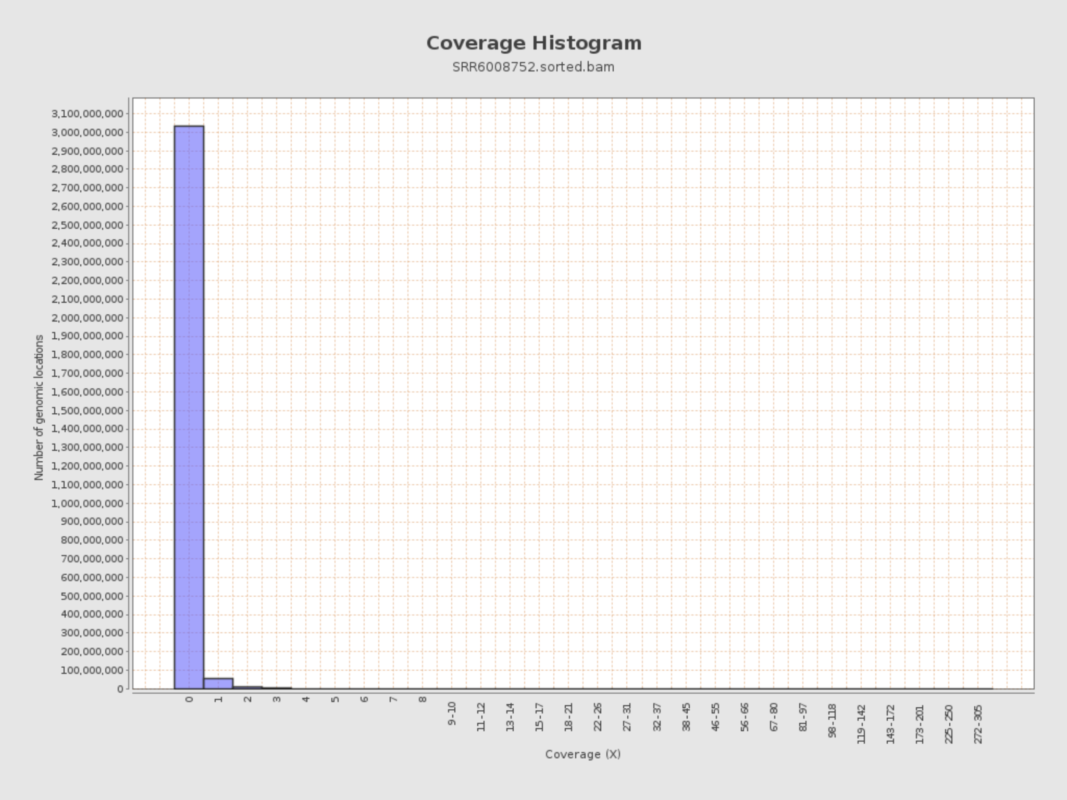
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5920677	0.0238	0.238
chr2	243199373	6991696	0.0287	0.249
chr3	198022430	6162669	0.0311	0.2084
chr4	191154276	4212635	0.022	0.1755
chr5	180915260	4203037	0.0232	0.1788
chr6	171115067	4250846	0.0248	0.1986
chr7	159138663	4449811	0.028	0.2612

chr8	146364022	6453408	0.0441	0.3193
chr9	141213431	2651990	0.0188	0.1882
chr10	135534747	4154424	0.0307	0.2256
chr11	135006516	3517834	0.0261	0.2149
chr12	133851895	3506267	0.0262	0.1912
chr13	115169878	2422484	0.021	0.1708
chr14	107349540	2813992	0.0262	0.1933
chr15	102531392	2169796	0.0212	0.1724
chr16	90354753	1908100	0.0211	0.1749
chr17	81195210	1904415	0.0235	0.1985
chr18	78077248	1512125	0.0194	0.2806
chr19	59128983	1187447	0.0201	0.1783
chr20	63025520	1702905	0.027	0.192
chr21	48129895	855960	0.0178	0.1613
chr22	51304566	829789	0.0162	0.1489
chrMT	16571	25330	1.5286	2.0215
chrX	155270560	3749894	0.0242	0.1884
chrY	59373566	155261	0.0026	0.0652

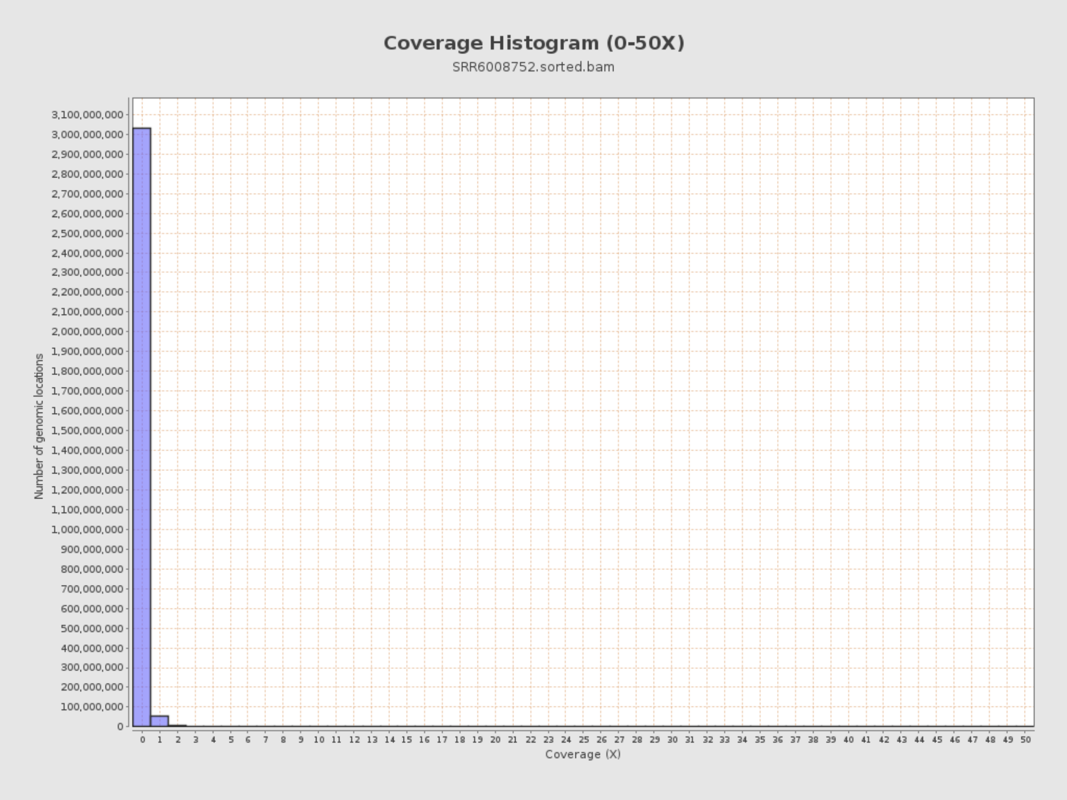
3. Results : Coverage across reference



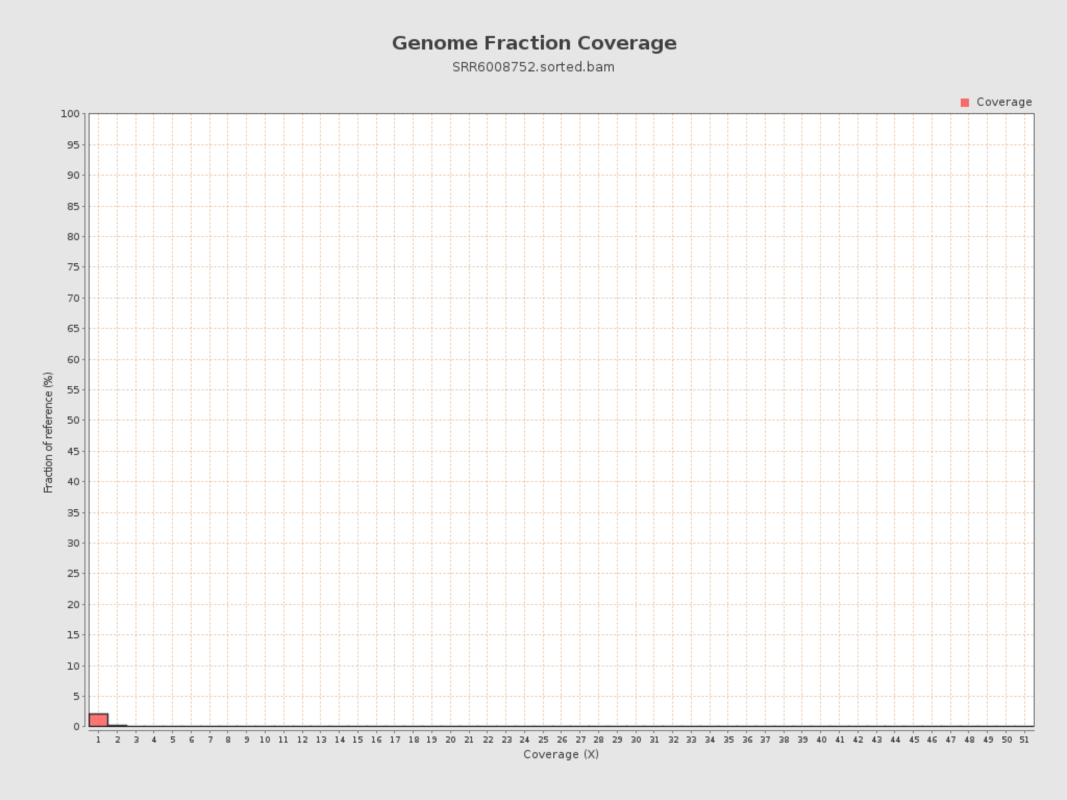
4. Results : Coverage Histogram



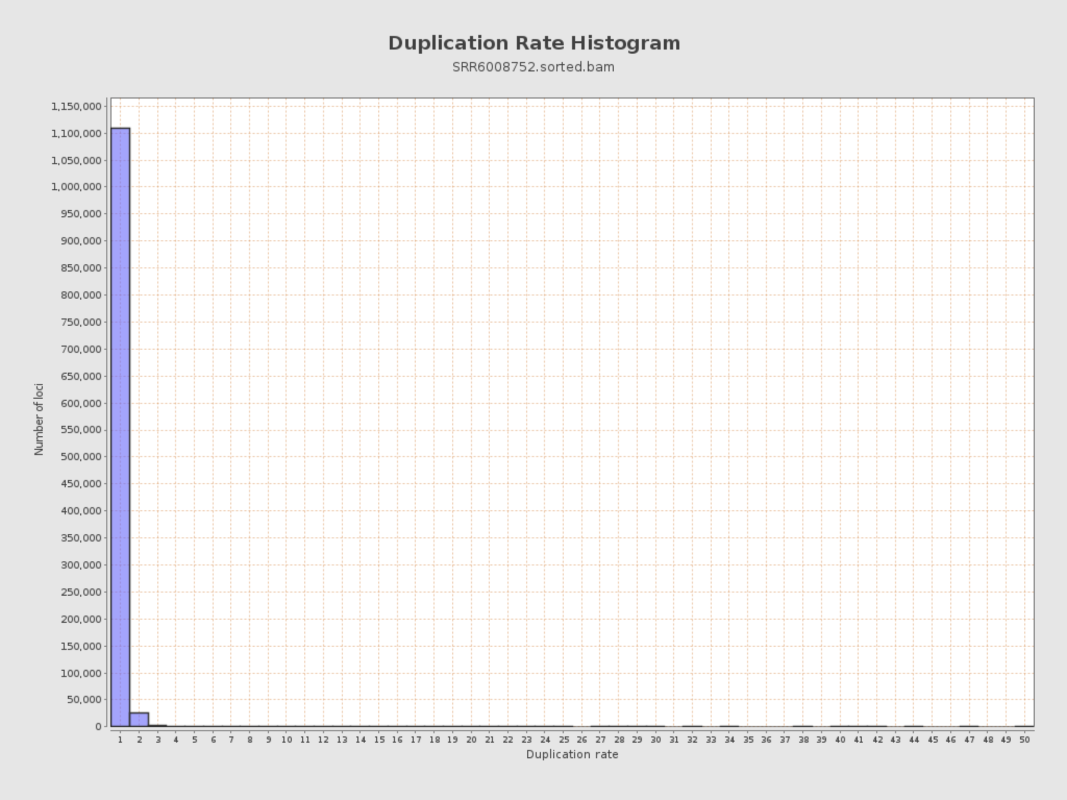
5. Results : Coverage Histogram (0-50X)



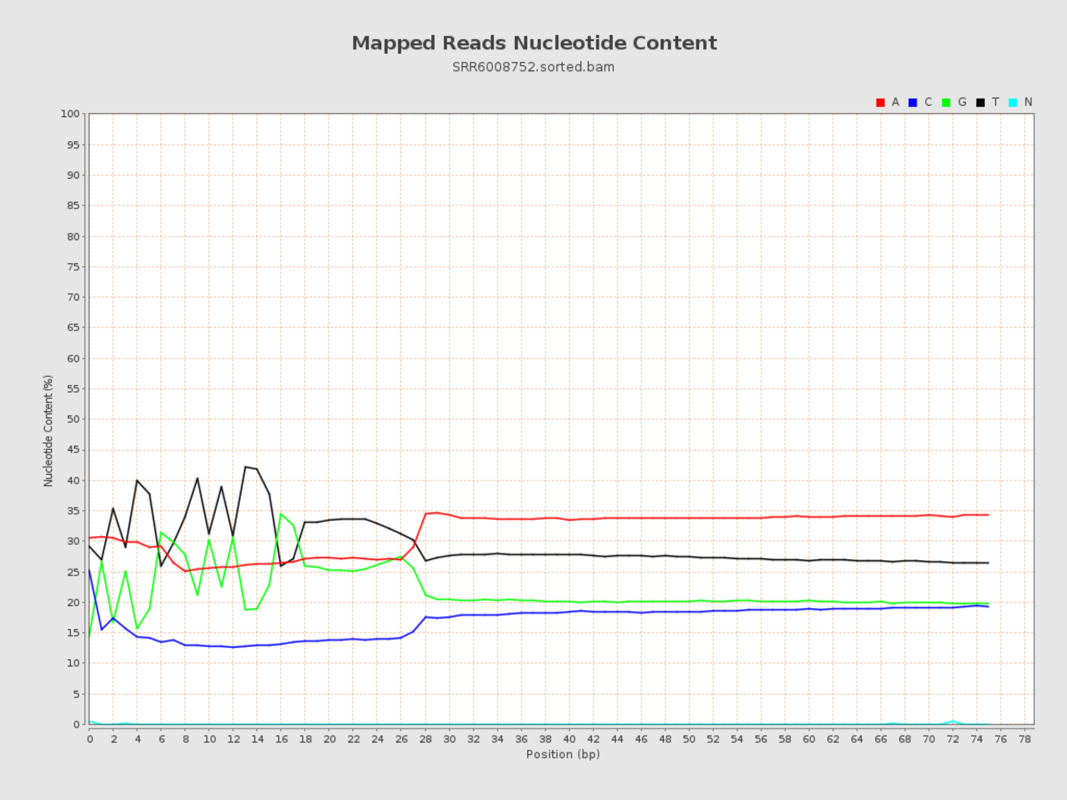
6. Results : Genome Fraction Coverage



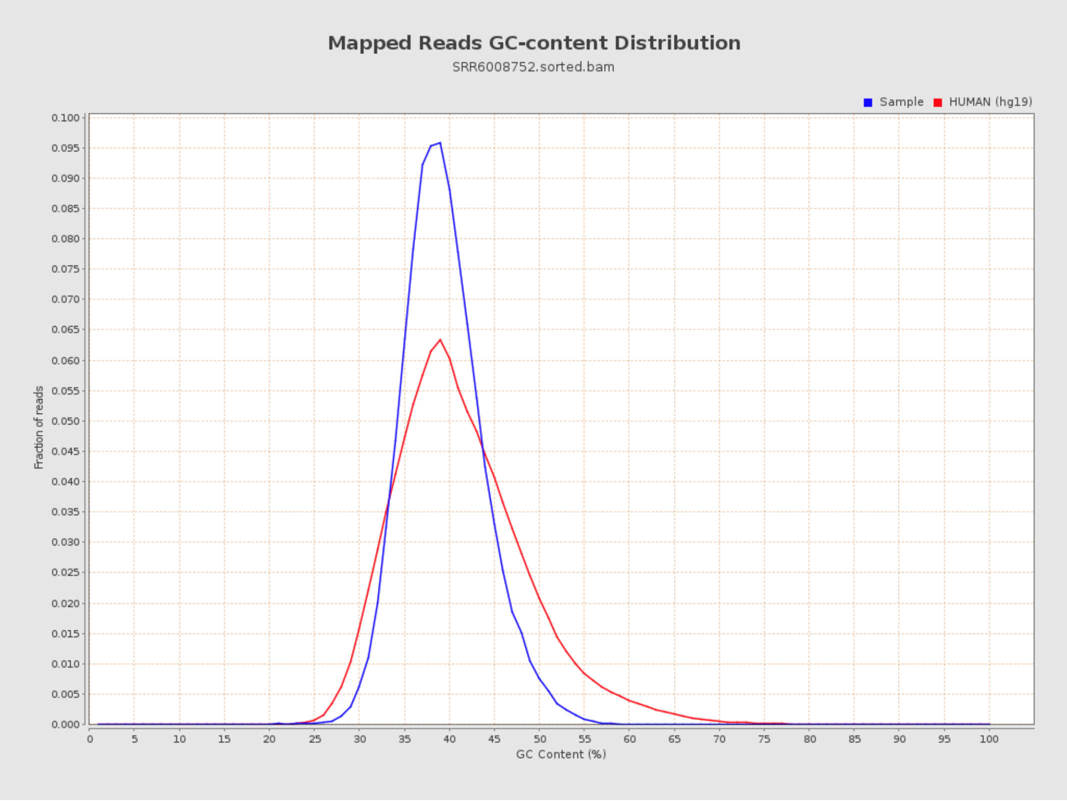
7. Results : Duplication Rate Histogram



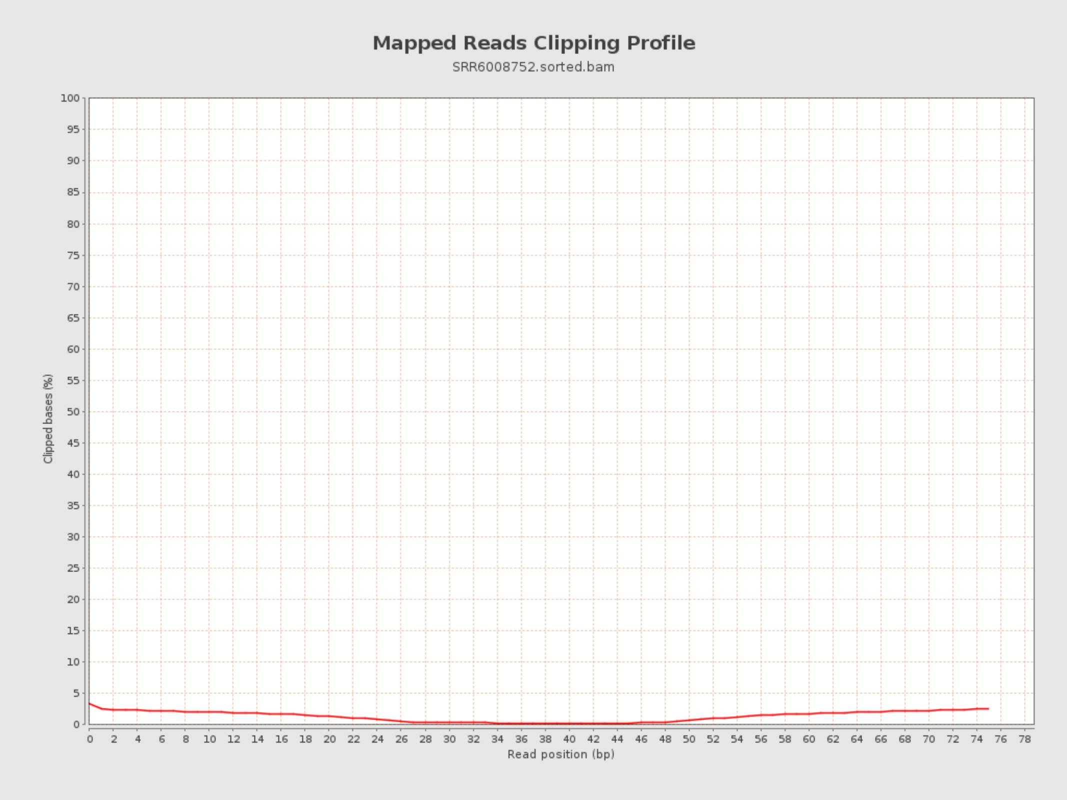
8. Results : Mapped Reads Nucleotide Content



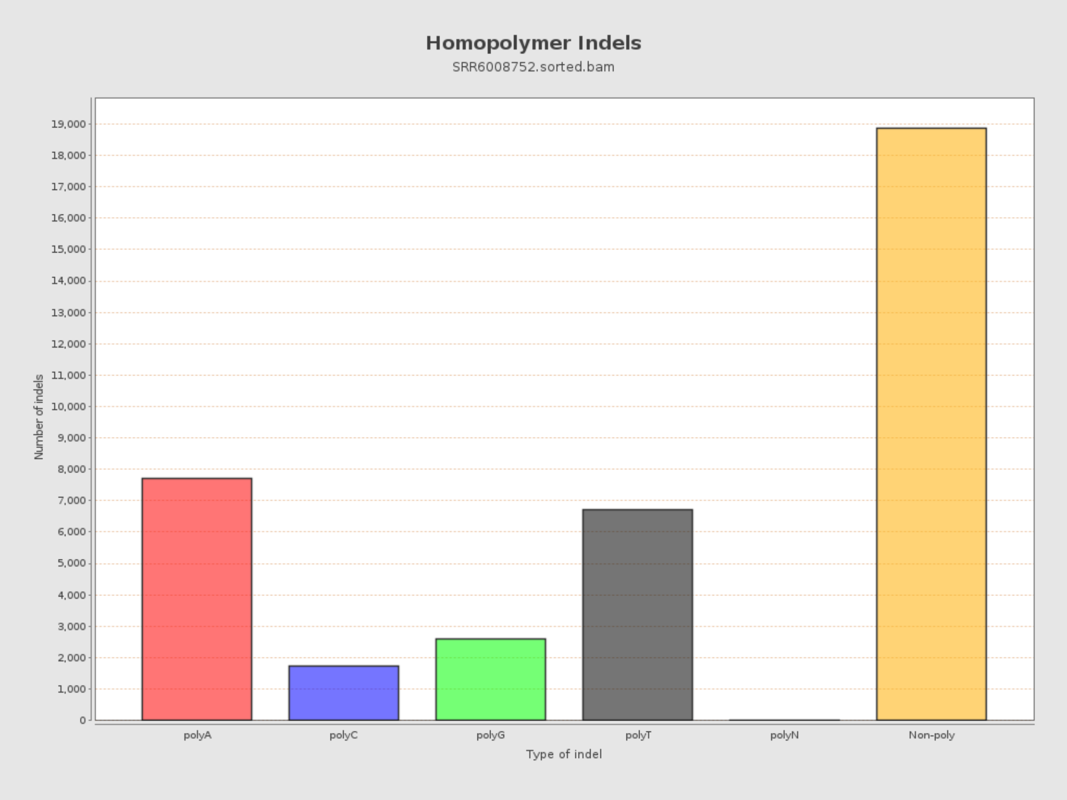
9. Results : Mapped Reads GC-content Distribution



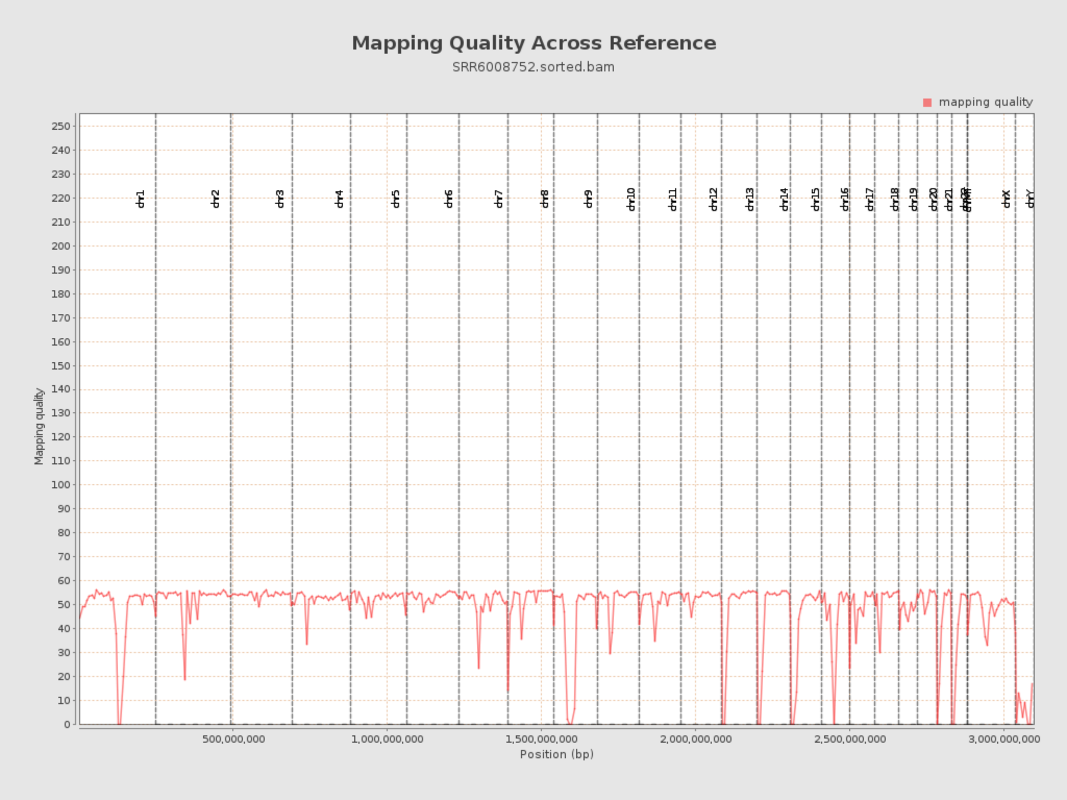
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram