Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:30:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068124.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_SRR6068124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:30:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,910,782
Mapped reads	4,686,598 / 95.43%
Unmapped reads	224,184 / 4.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,988 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	466,025 / 9.49%
Duplication rate	7.97%
Clipped reads	2,229,978 / 45.41%

2.2. ACGT Content

Number/percentage of A's	83,268,078 / 27.05%
Number/percentage of C's	56,278,182 / 18.28%
Number/percentage of T's	98,926,008 / 32.13%
Number/percentage of G's	69,370,643 / 22.53%
Number/percentage of N's	36,705 / 0.01%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0995

Standard Deviation	1.0091

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

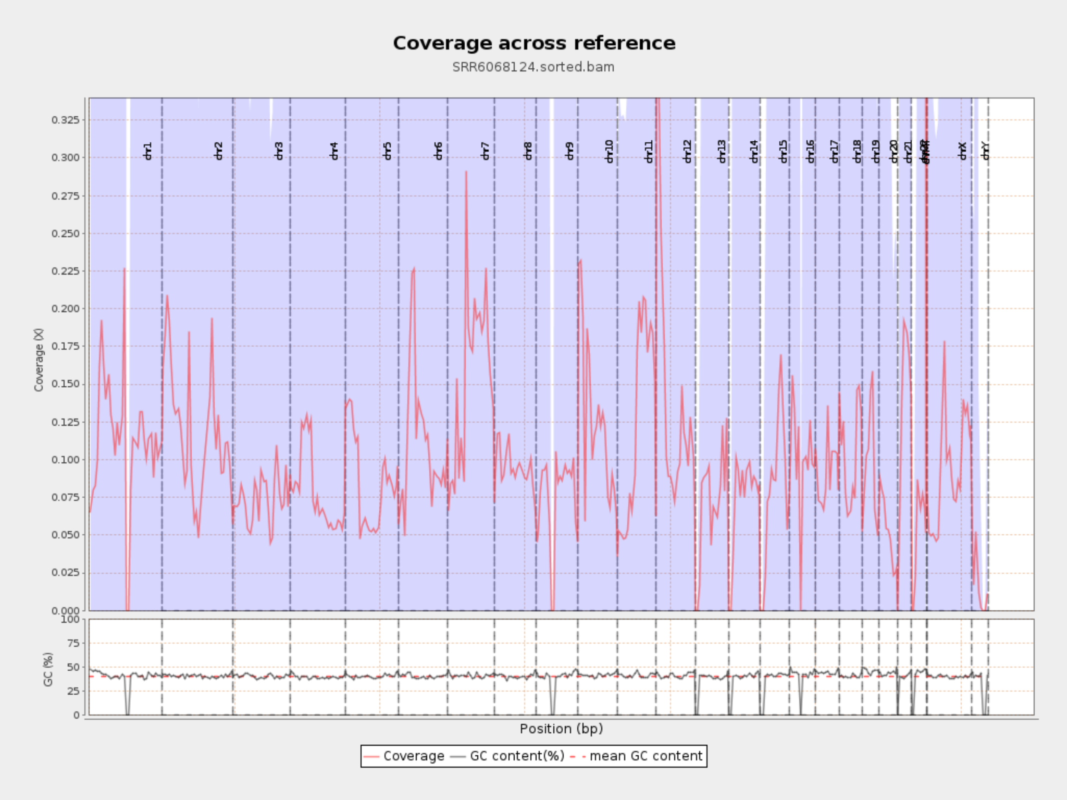
General error rate	0.57%
Mismatches	1,701,222
Insertions	20,403
Mapped reads with at least one insertion	0.43%
Deletions	76,033
Mapped reads with at least one deletion	1.6%
Homopolymer indels	45.68%

2.6. Chromosome stats

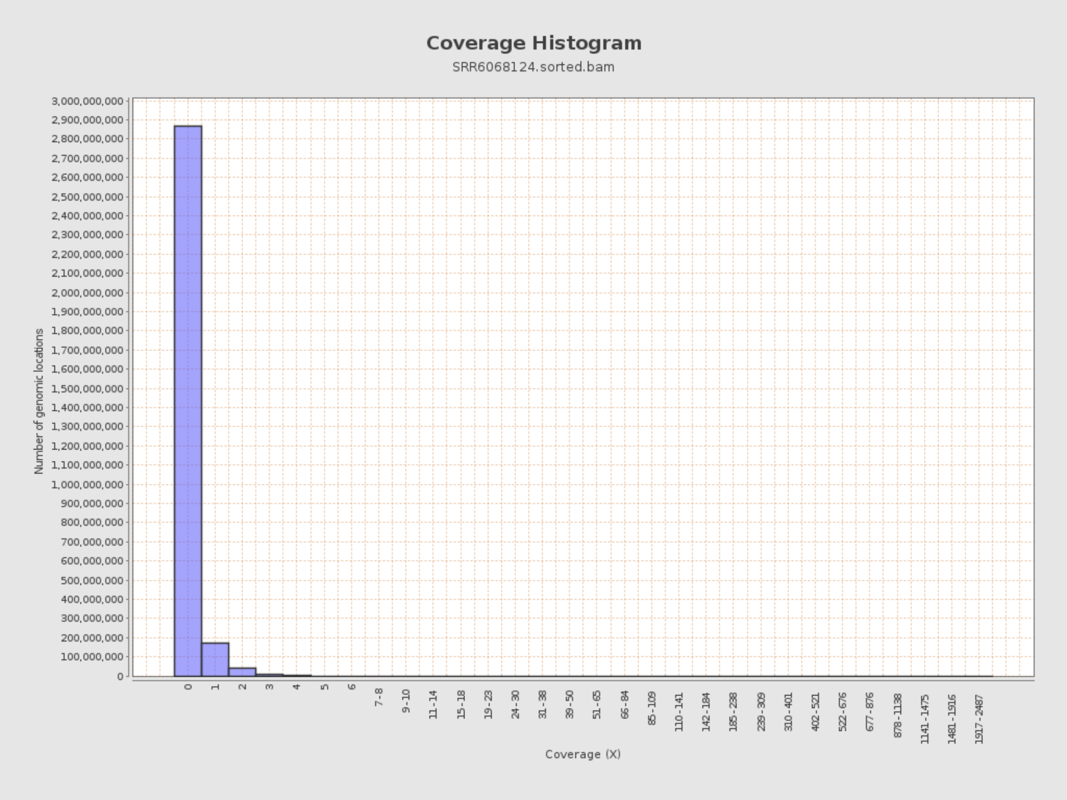
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28200719	0.1131	2.1339
chr2	243199373	29104010	0.1197	1.0322
chr3	198022430	14503285	0.0732	0.3478
chr4	191154276	14940551	0.0782	0.3986
chr5	180915260	15232395	0.0842	0.3767
chr6	171115067	19190298	0.1121	0.6064
chr7	159138663	24921040	0.1566	2.0389

chr8	146364022	13923963	0.0951	1.3139
chr9	141213431	10649774	0.0754	0.7296
chr10	135534747	17405663	0.1284	0.7793
chr11	135006516	16837055	0.1247	0.5603
chr12	133851895	20121218	0.1503	0.5555
chr13	115169878	8094236	0.0703	0.3553
chr14	107349540	7822609	0.0729	0.4343
chr15	102531392	8293228	0.0809	0.3895
chr16	90354753	9123787	0.101	0.4741
chr17	81195210	7432772	0.0915	0.4081
chr18	78077248	8071870	0.1034	1.3928
chr19	59128983	5774461	0.0977	1.484
chr20	63025520	3365995	0.0534	0.3441
chr21	48129895	6487132	0.1348	0.5068
chr22	51304566	2582446	0.0503	0.2779
chrMT	16571	430255	25.9643	14.3143
chrX	155270560	14577464	0.0939	0.4861
chrY	59373566	929058	0.0156	0.5257

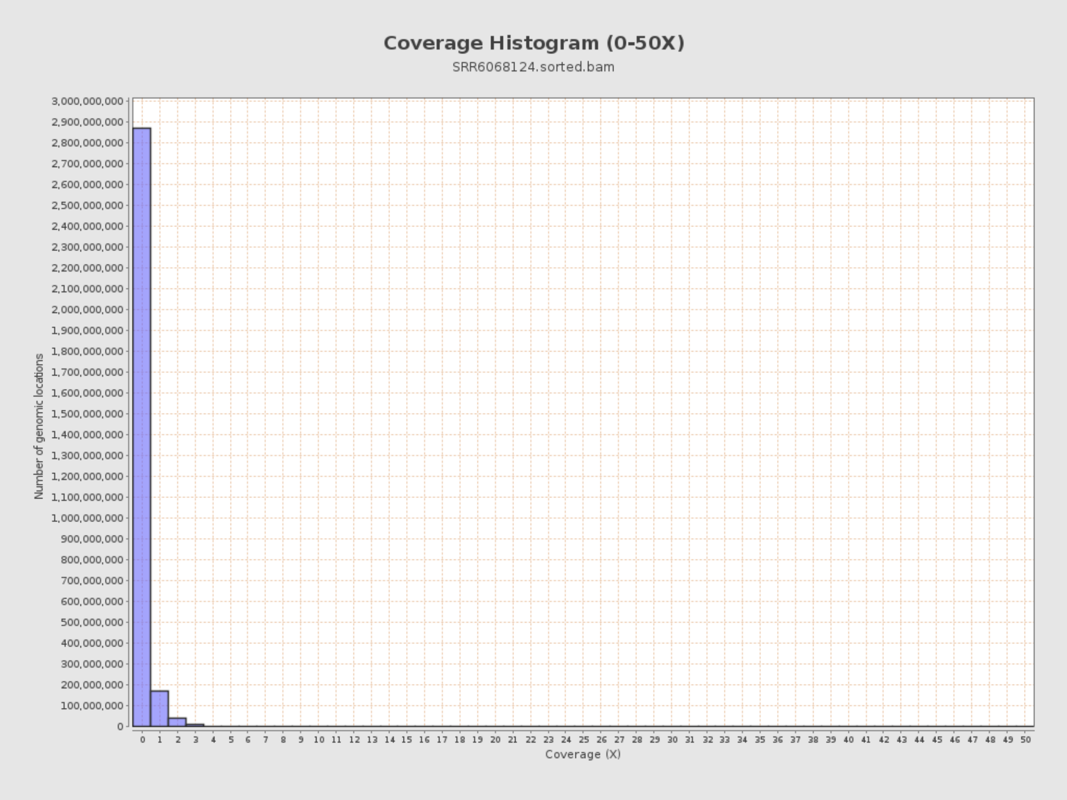
3. Results : Coverage across reference



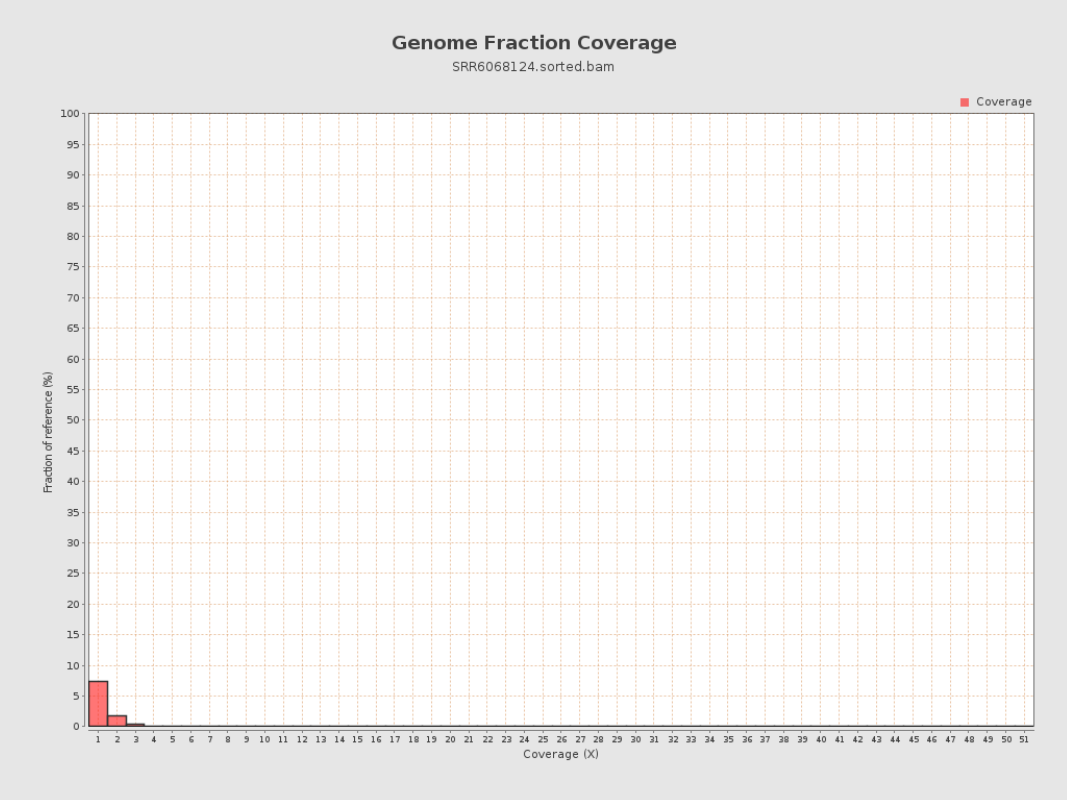
4. Results : Coverage Histogram



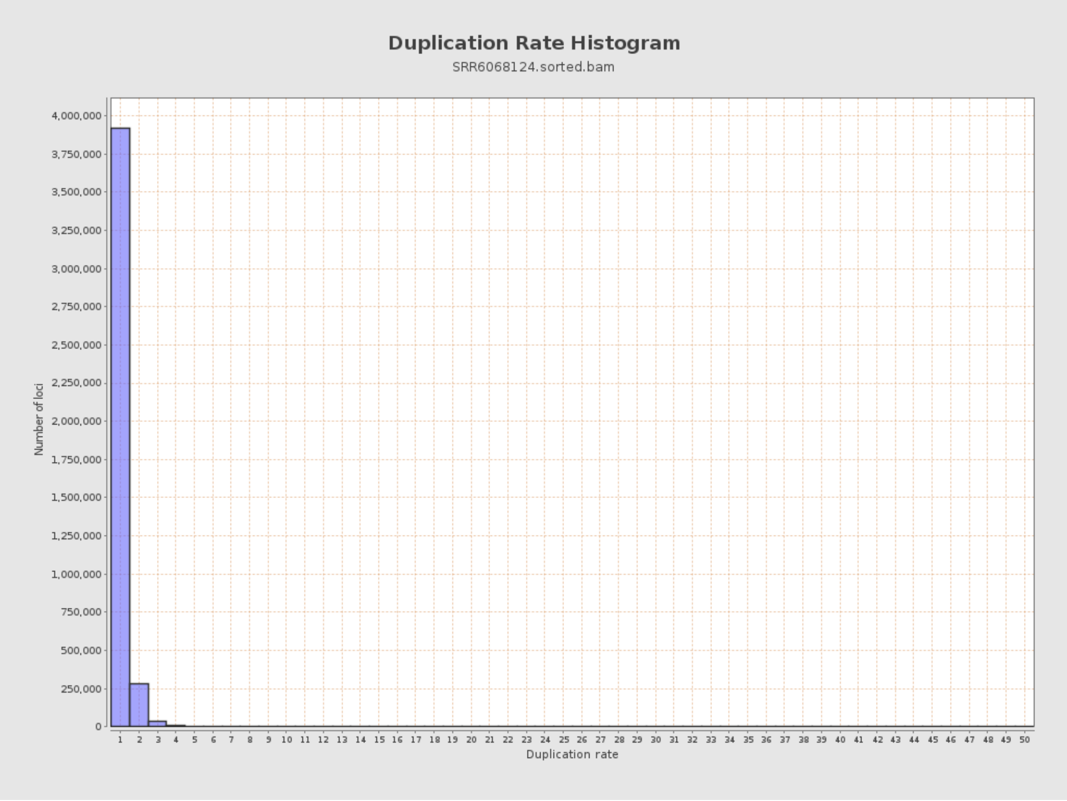
5. Results : Coverage Histogram (0-50X)



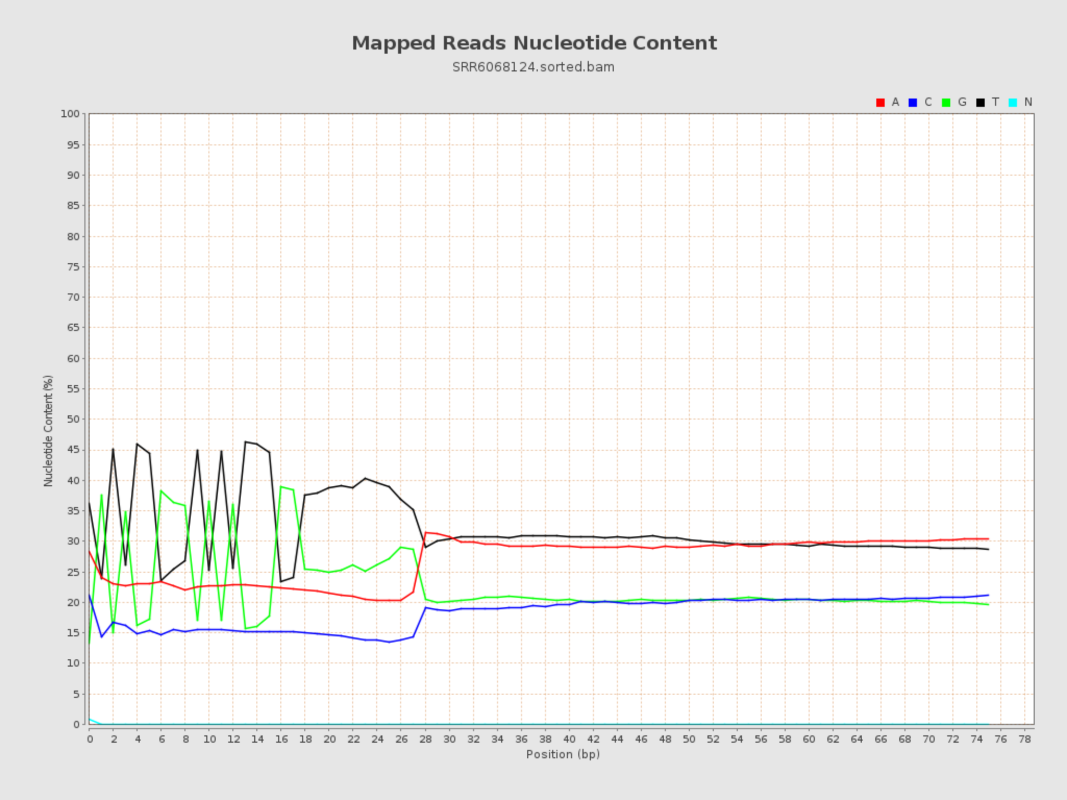
6. Results : Genome Fraction Coverage



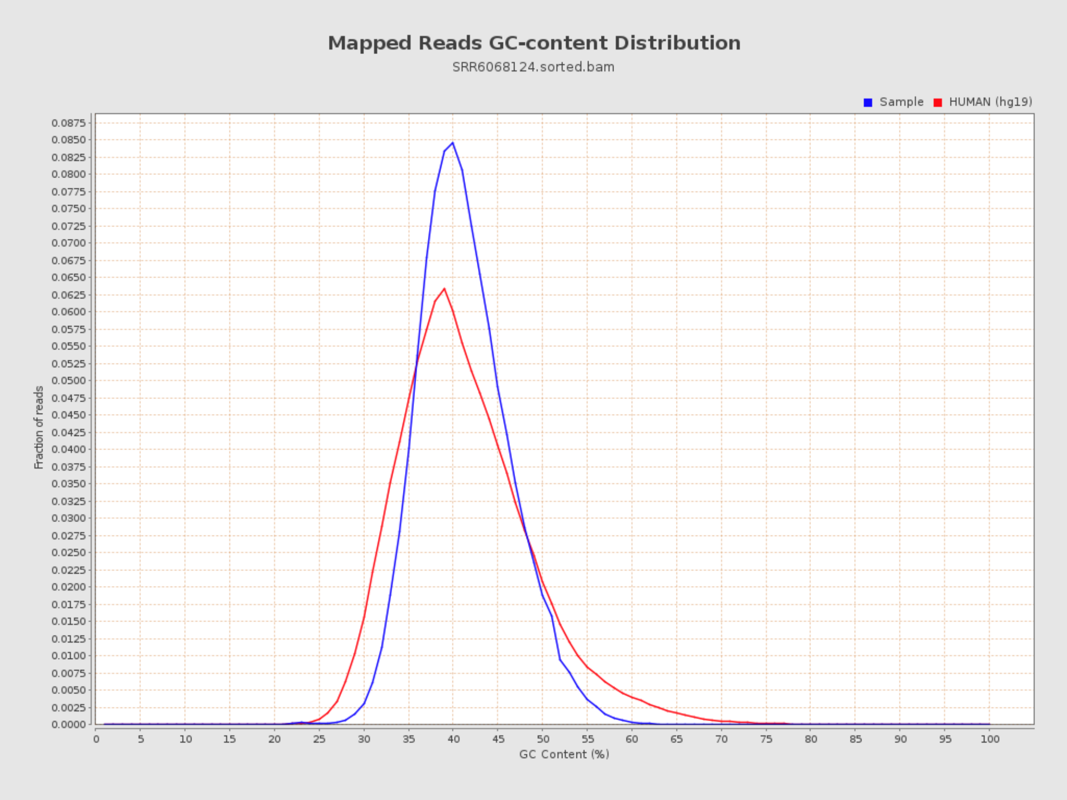
7. Results : Duplication Rate Histogram



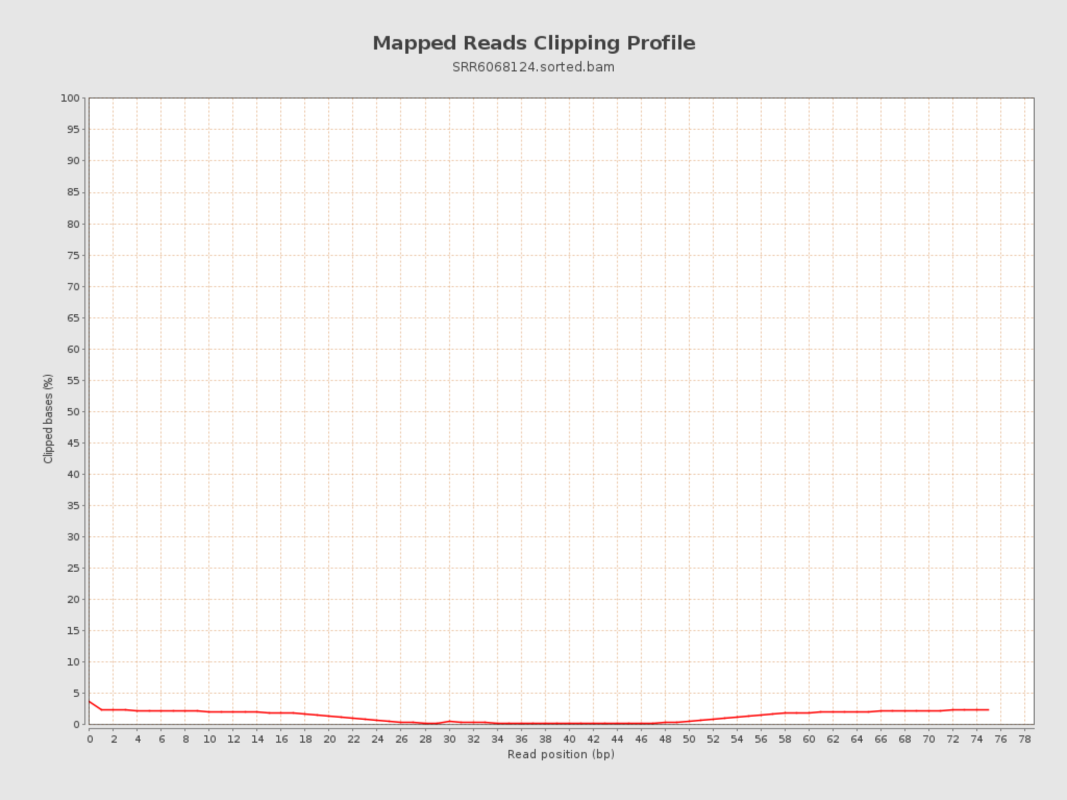
8. Results : Mapped Reads Nucleotide Content



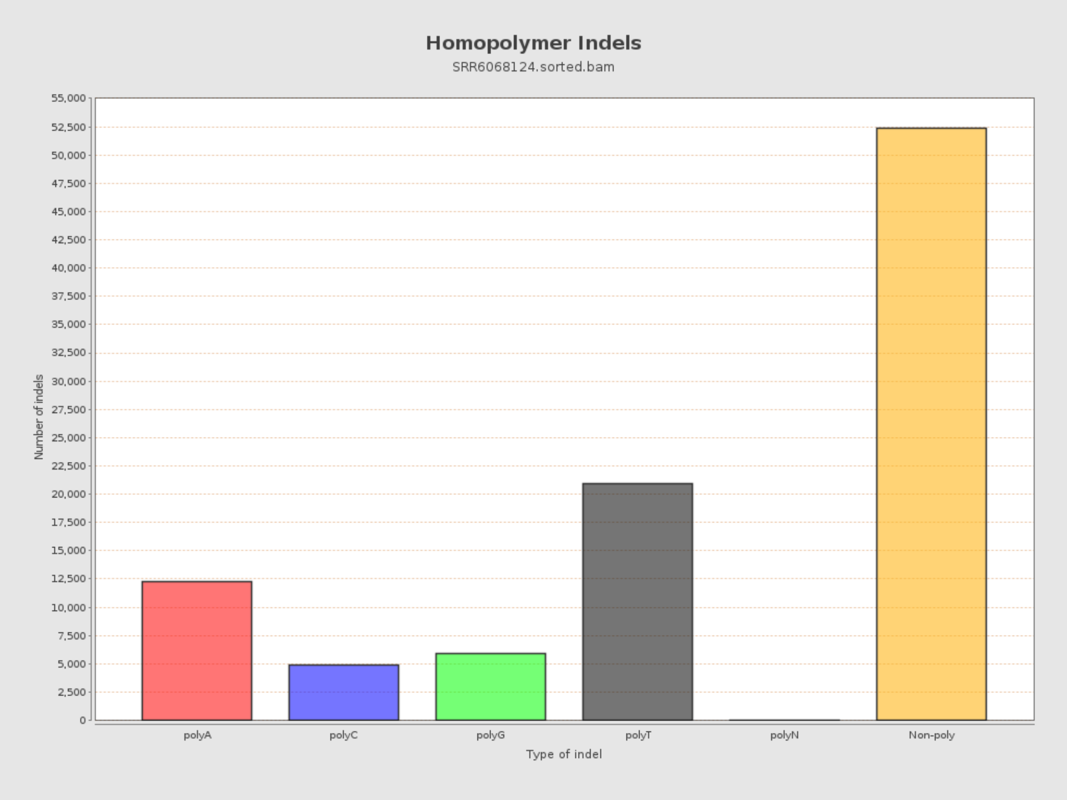
9. Results : Mapped Reads GC-content Distribution



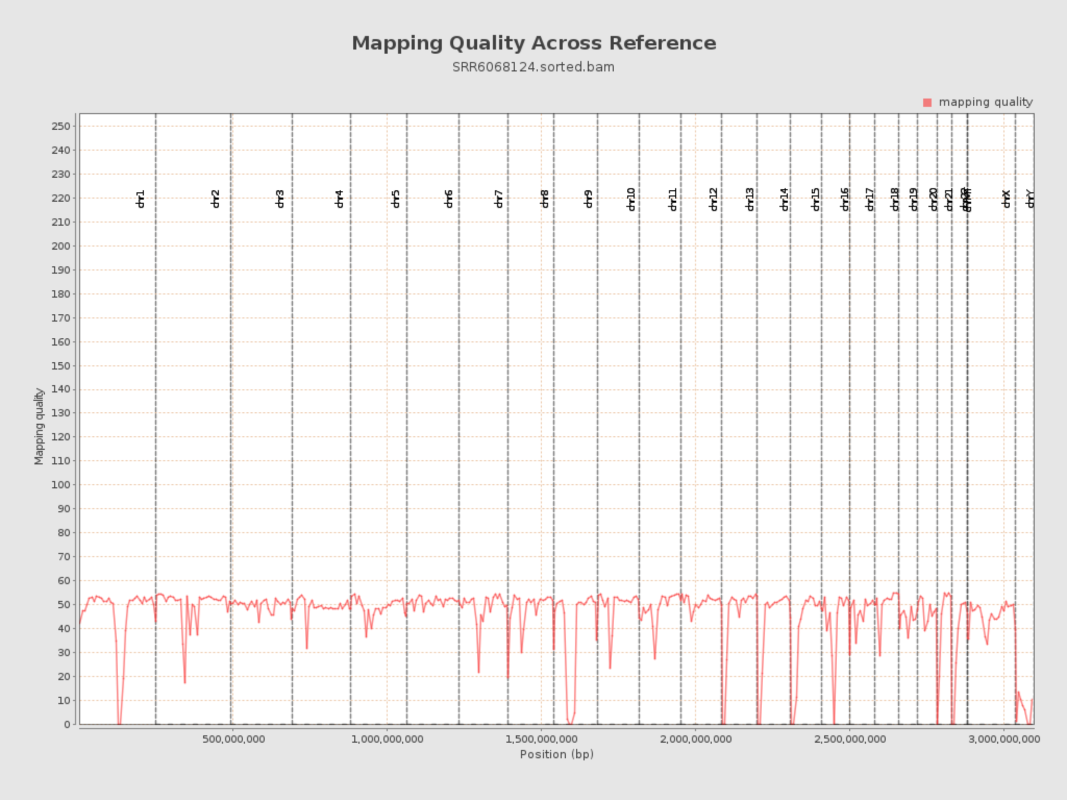
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram