Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:35:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524712.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_SRR10524712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:35:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	264,971
Mapped reads	246,508 / 93.03%
Unmapped reads	18,463 / 6.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	899 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	2,818 / 1.06%
Duplication rate	0.85%
Clipped reads	246,667 / 93.09%

2.2. ACGT Content

Number/percentage of A's	4,023,663 / 27.02%
Number/percentage of C's	2,952,130 / 19.82%
Number/percentage of T's	4,588,526 / 30.81%
Number/percentage of G's	3,324,688 / 22.33%
Number/percentage of N's	2,194 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0048

Standard Deviation	0.0786

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

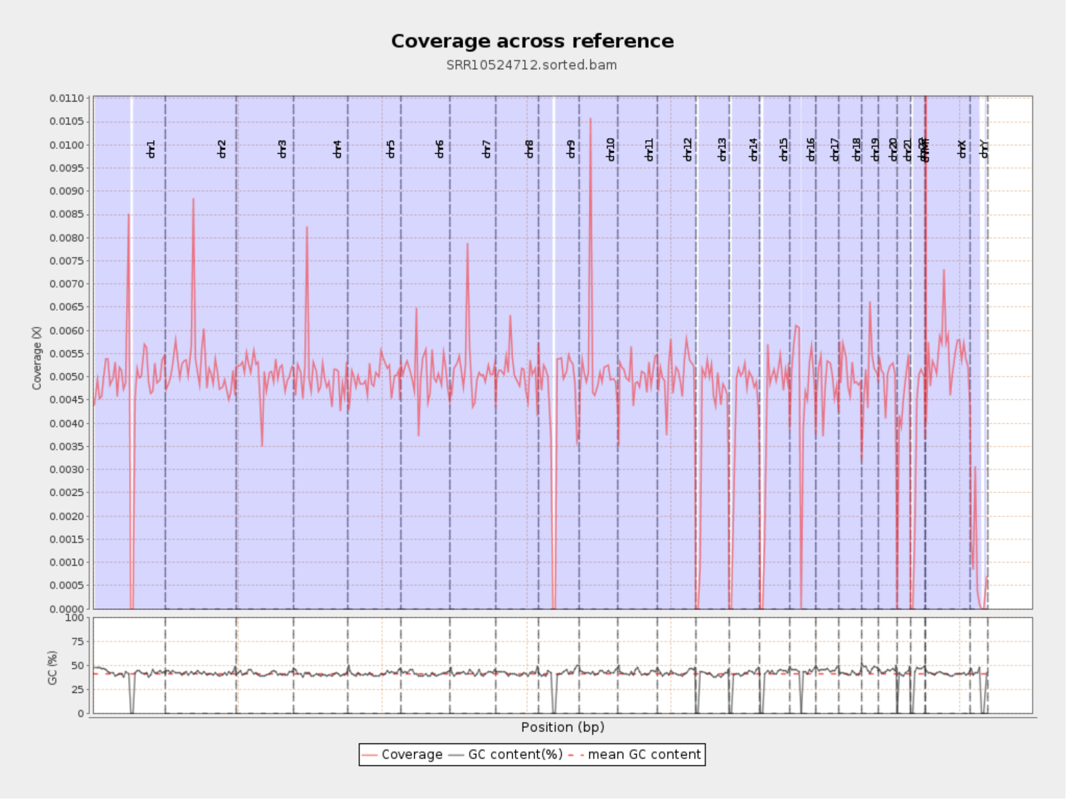
General error rate	0.5%
Mismatches	72,148
Insertions	1,238
Mapped reads with at least one insertion	0.5%
Deletions	2,832
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.54%

2.6. Chromosome stats

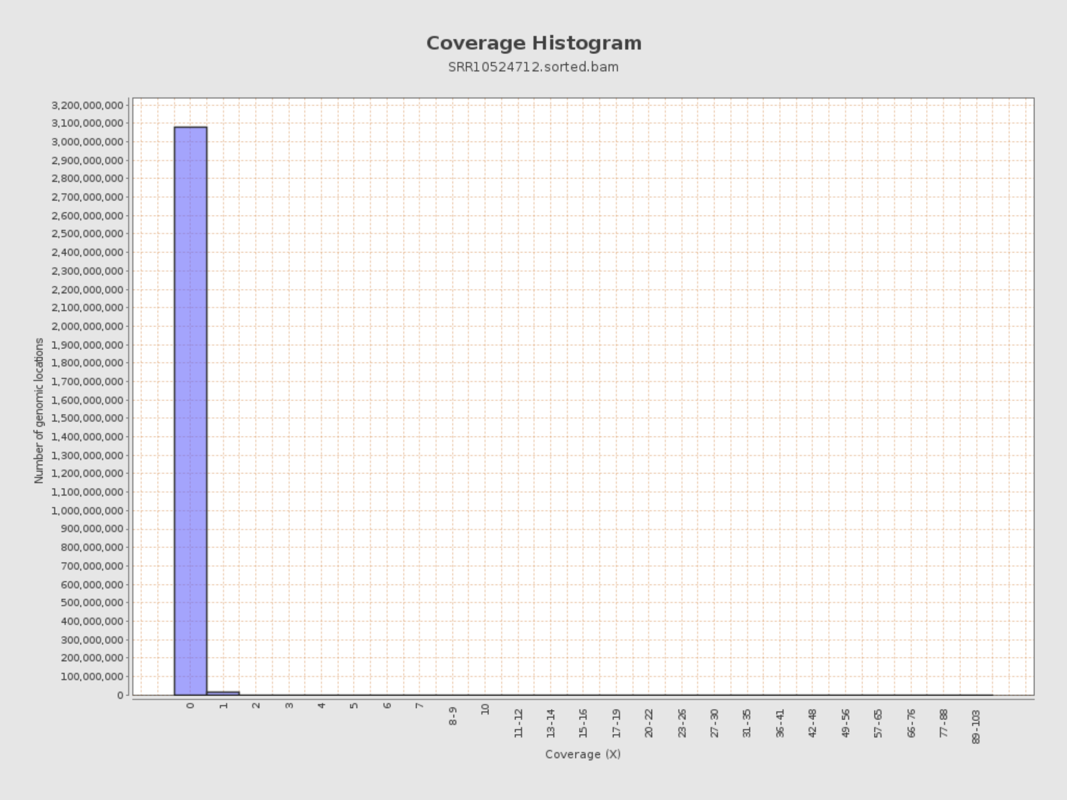
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1196644	0.0048	0.109
chr2	243199373	1270826	0.0052	0.0858
chr3	198022430	1002066	0.0051	0.0722
chr4	191154276	966837	0.0051	0.0737
chr5	180915260	903948	0.005	0.0717
chr6	171115067	866721	0.0051	0.0744
chr7	159138663	823604	0.0052	0.0856

chr8	146364022	744451	0.0051	0.0822
chr9	141213431	627493	0.0044	0.0721
chr10	135534747	715708	0.0053	0.0847
chr11	135006516	676679	0.005	0.0753
chr12	133851895	675894	0.005	0.073
chr13	115169878	466298	0.004	0.0648
chr14	107349540	440226	0.0041	0.0652
chr15	102531392	421820	0.0041	0.0652
chr16	90354753	421415	0.0047	0.0717
chr17	81195210	394484	0.0049	0.0713
chr18	78077248	394805	0.0051	0.0924
chr19	59128983	300455	0.0051	0.0889
chr20	63025520	312075	0.005	0.0716
chr21	48129895	200733	0.0042	0.0674
chr22	51304566	172491	0.0034	0.0587
chrMT	16571	4813	0.2904	0.6054
chrX	155270560	848288	0.0055	0.0759
chrY	59373566	46964	0.0008	0.0386

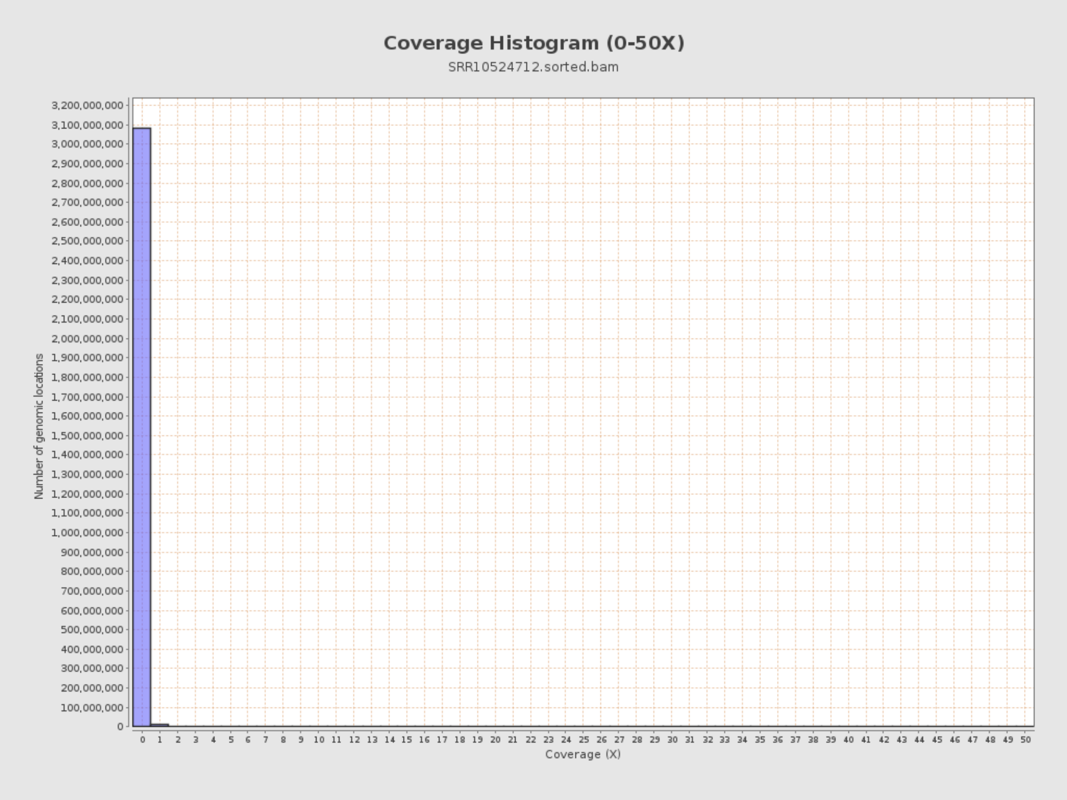
3. Results : Coverage across reference



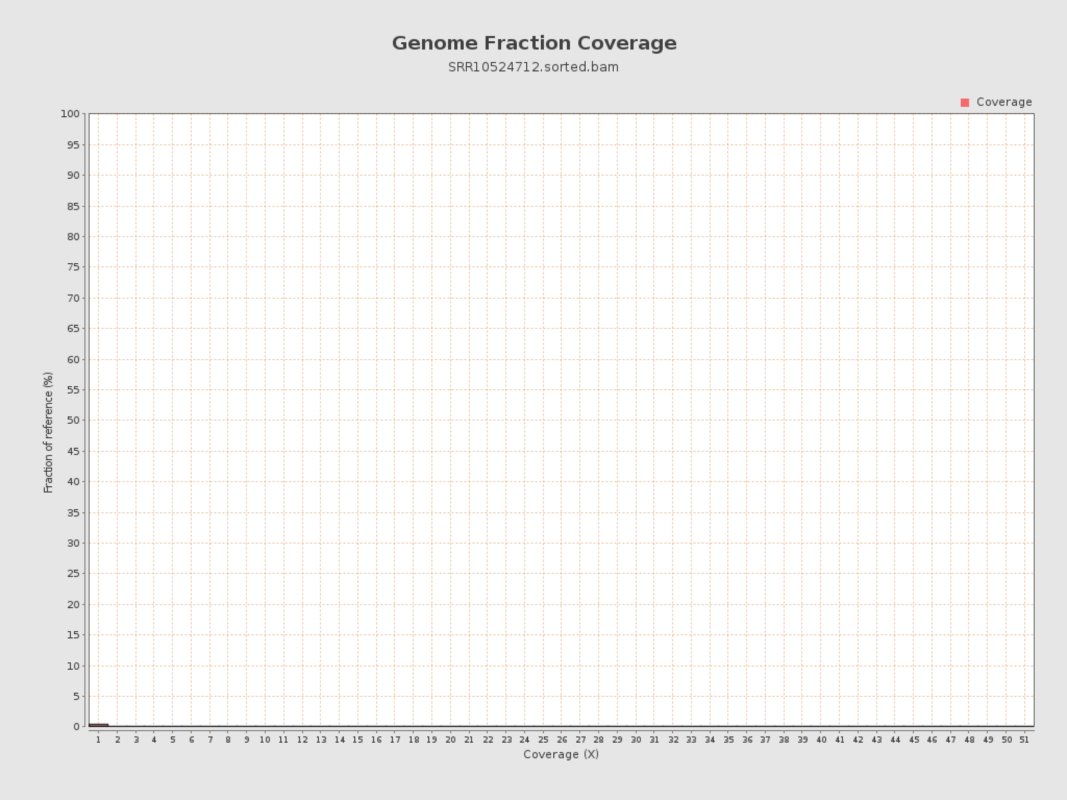
4. Results : Coverage Histogram



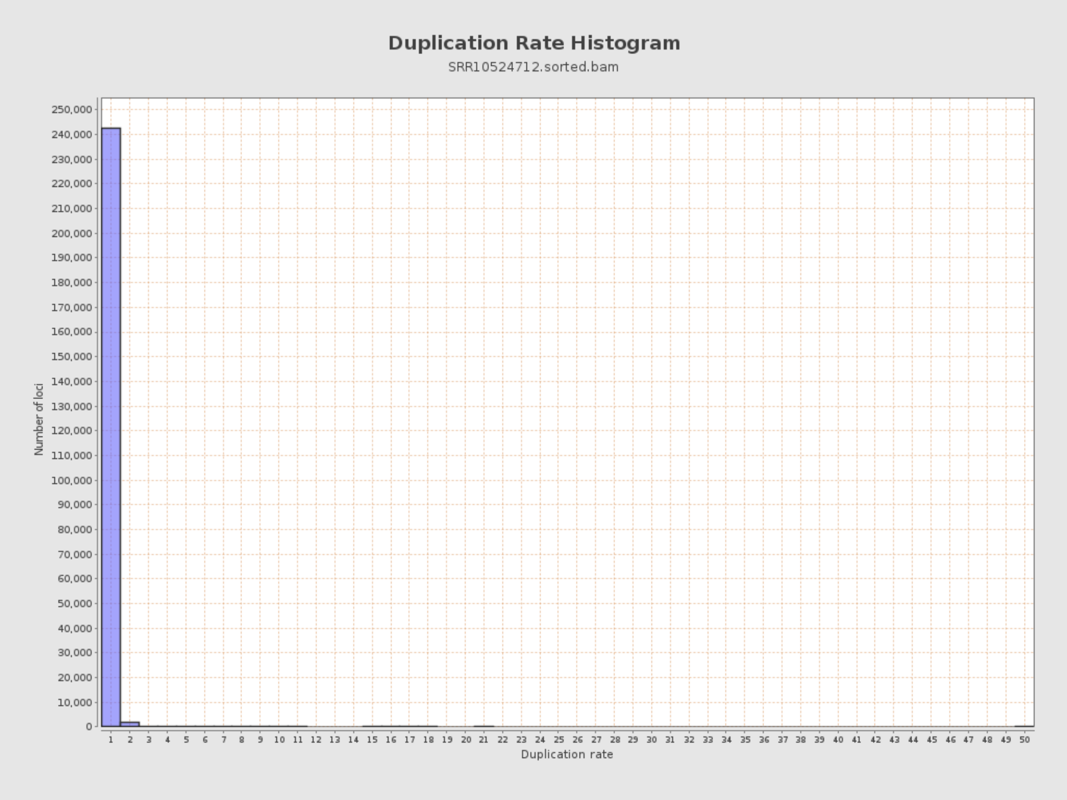
5. Results : Coverage Histogram (0-50X)



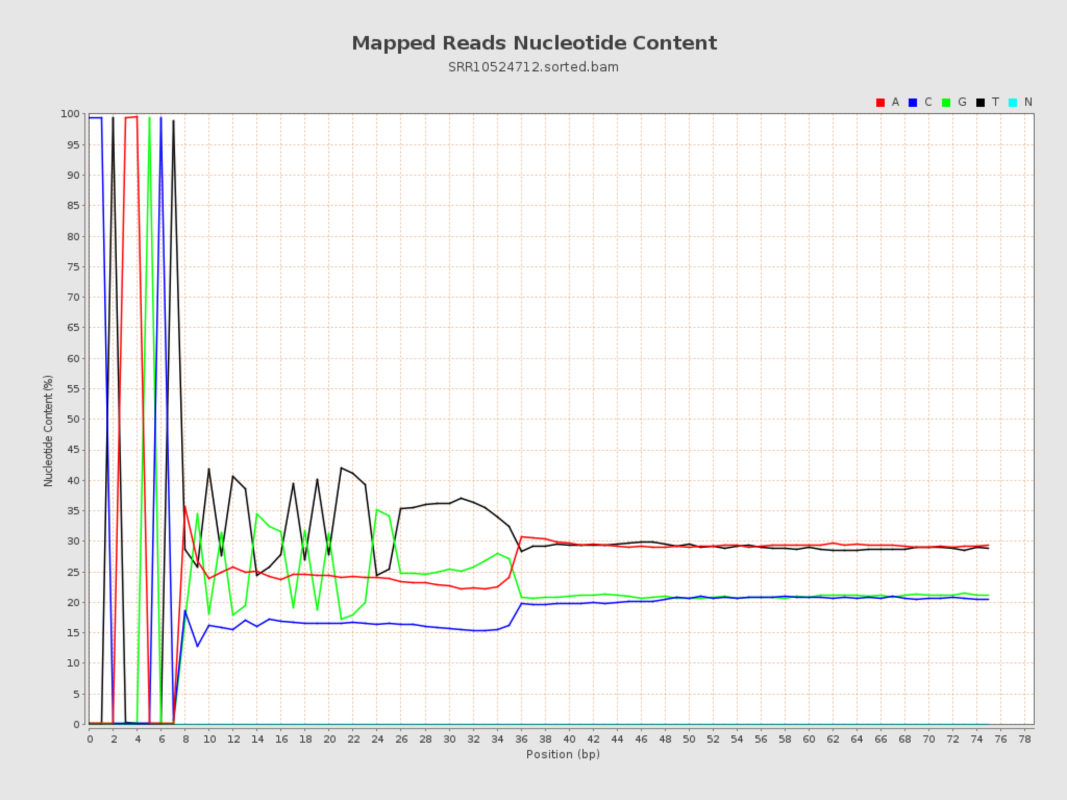
6. Results : Genome Fraction Coverage



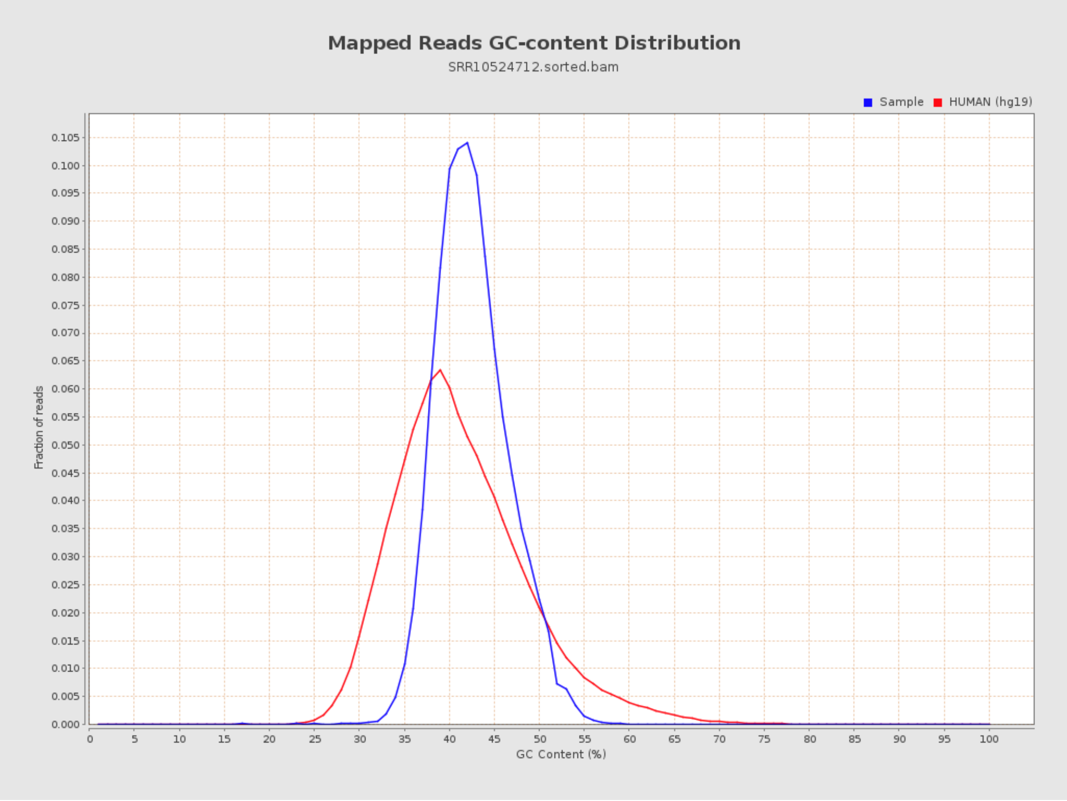
7. Results : Duplication Rate Histogram



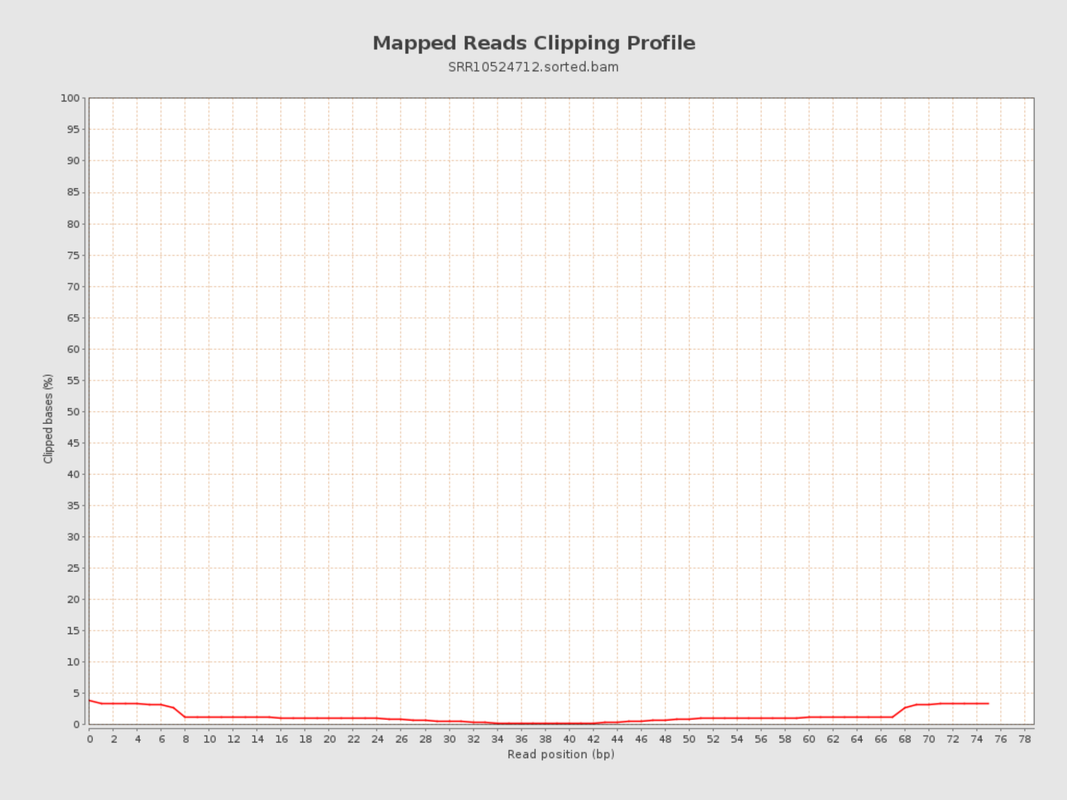
8. Results : Mapped Reads Nucleotide Content



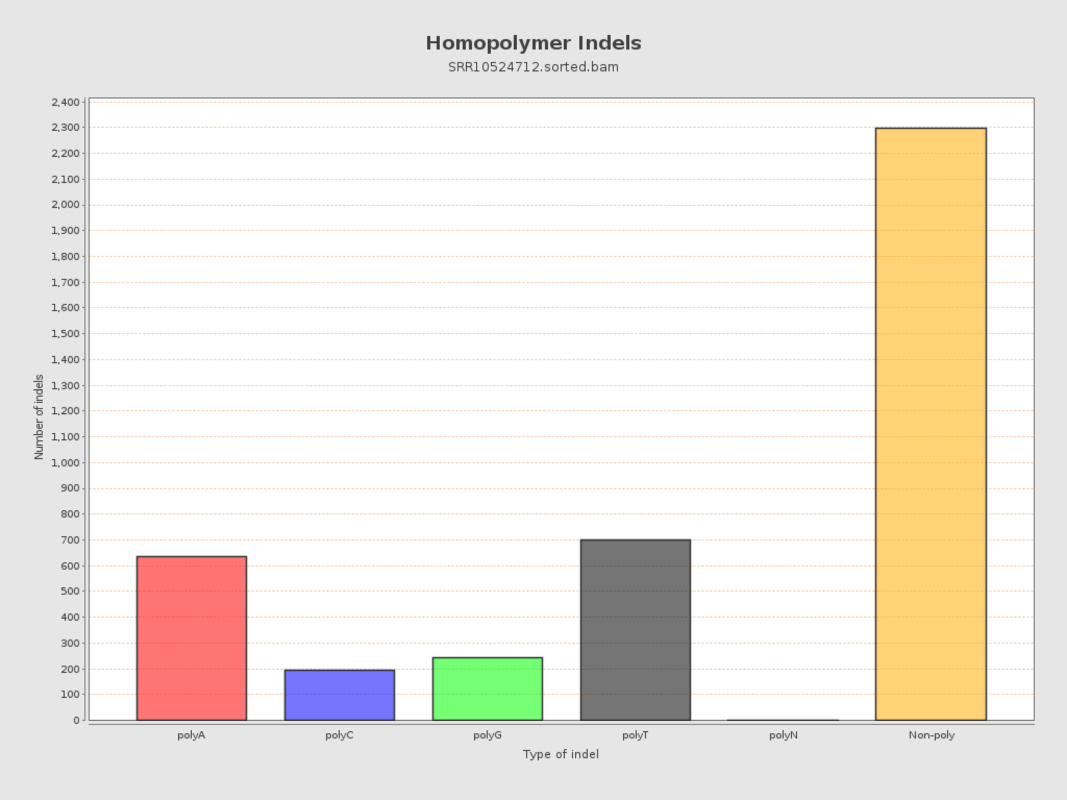
9. Results : Mapped Reads GC-content Distribution



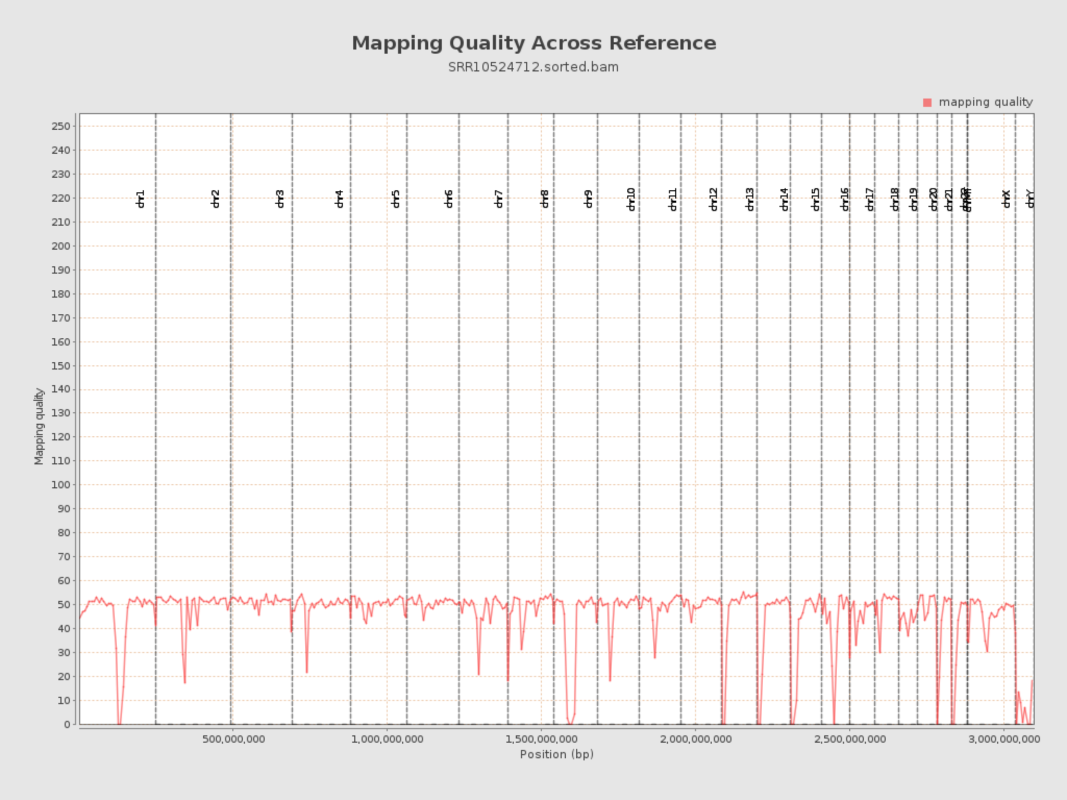
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram