Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:40:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524450.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_SRR10524450 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524450.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:40:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524450.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,419,907
Mapped reads	4,969,242 / 91.69%
Unmapped reads	450,665 / 8.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,126 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	510,241 / 9.41%
Duplication rate	7.54%
Clipped reads	4,964,253 / 91.59%

2.2. ACGT Content

Number/percentage of A's	75,576,066 / 26.29%
Number/percentage of C's	50,345,874 / 17.51%
Number/percentage of T's	90,322,066 / 31.42%
Number/percentage of G's	71,254,717 / 24.78%
Number/percentage of N's	6,168 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0929

Standard Deviation	0.7227

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

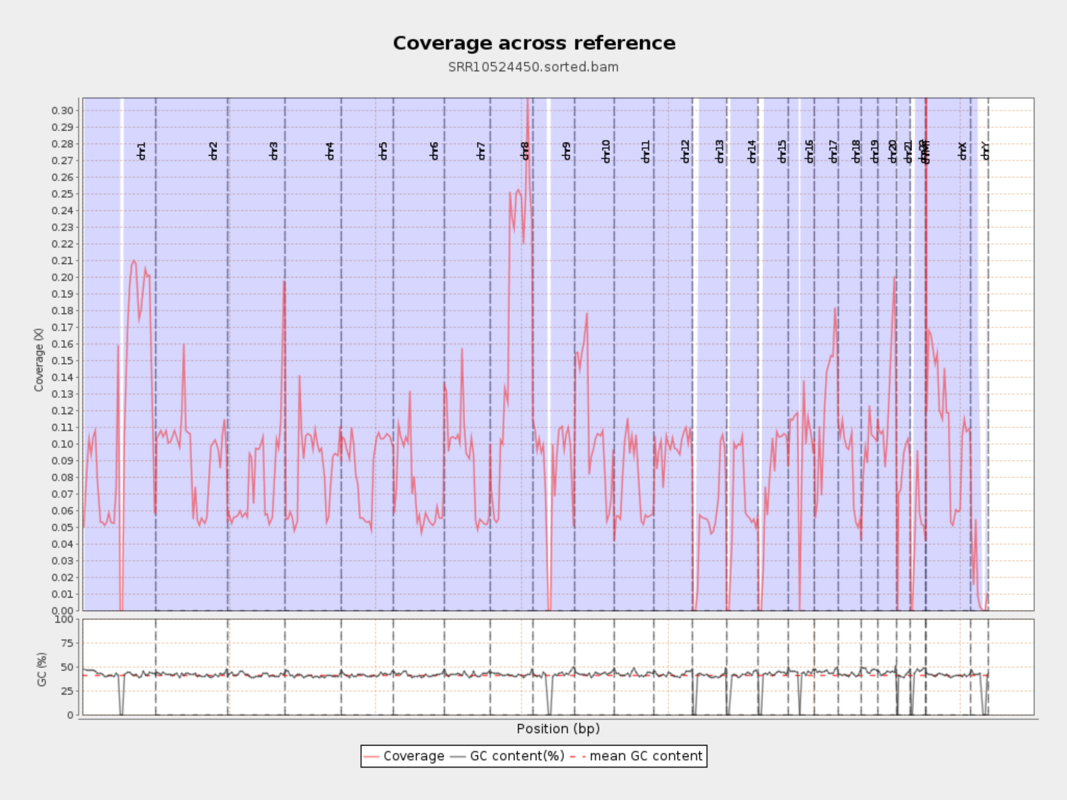
General error rate	0.48%
Mismatches	1,347,853
Insertions	20,241
Mapped reads with at least one insertion	0.41%
Deletions	53,081
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.71%

2.6. Chromosome stats

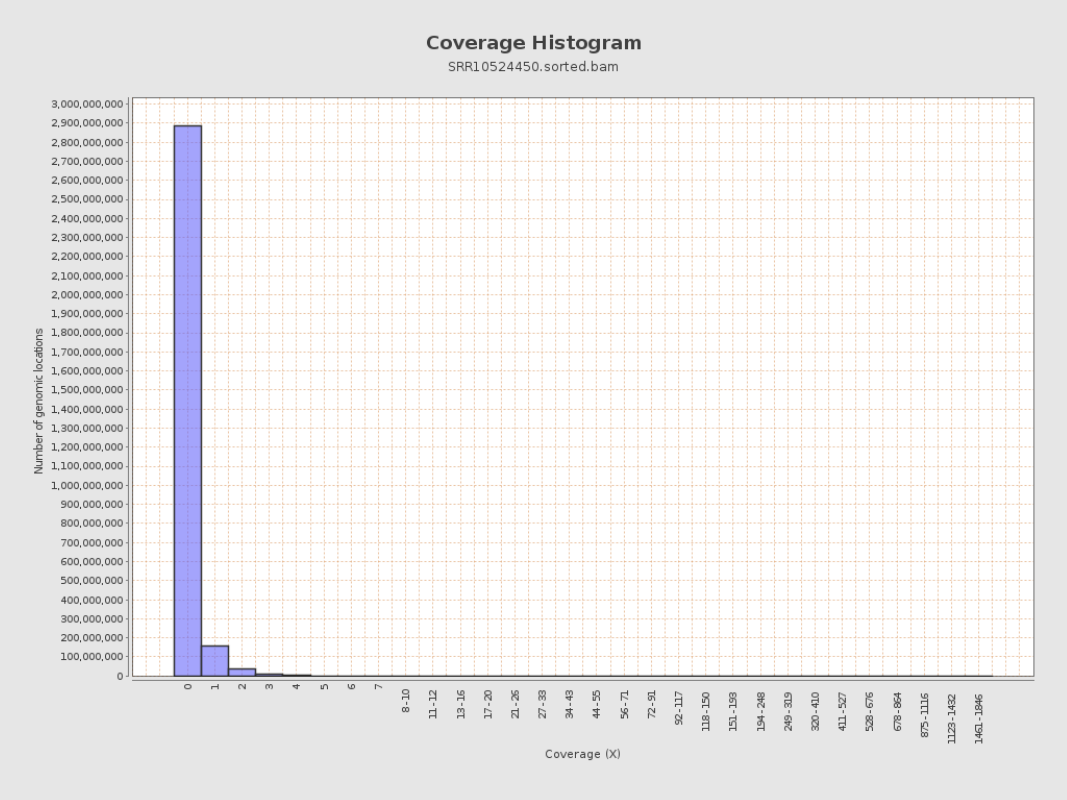
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28393371	0.1139	1.3904
chr2	243199373	22912969	0.0942	0.8758
chr3	198022430	15759077	0.0796	0.3761
chr4	191154276	16370517	0.0856	0.5123
chr5	180915260	15789774	0.0873	0.395
chr6	171115067	12365726	0.0723	0.5307
chr7	159138663	14279005	0.0897	1.0515

chr8	146364022	26343644	0.18	0.7179
chr9	141213431	11942449	0.0846	0.6016
chr10	135534747	15052691	0.1111	0.7424
chr11	135006516	9987057	0.074	0.6933
chr12	133851895	13239615	0.0989	0.4193
chr13	115169878	6391633	0.0555	0.3194
chr14	107349540	6802121	0.0634	0.3511
chr15	102531392	7631943	0.0744	0.4022
chr16	90354753	8965996	0.0992	0.4726
chr17	81195210	9948435	0.1225	0.5106
chr18	78077248	6769940	0.0867	1.1394
chr19	59128983	5801340	0.0981	0.9599
chr20	63025520	8281895	0.1314	0.5016
chr21	48129895	3858022	0.0802	0.4382
chr22	51304566	2325918	0.0453	0.2787
chrMT	16571	22843	1.3785	1.6586
chrX	155270560	17413003	0.1121	0.5608
chrY	59373566	946489	0.0159	0.386

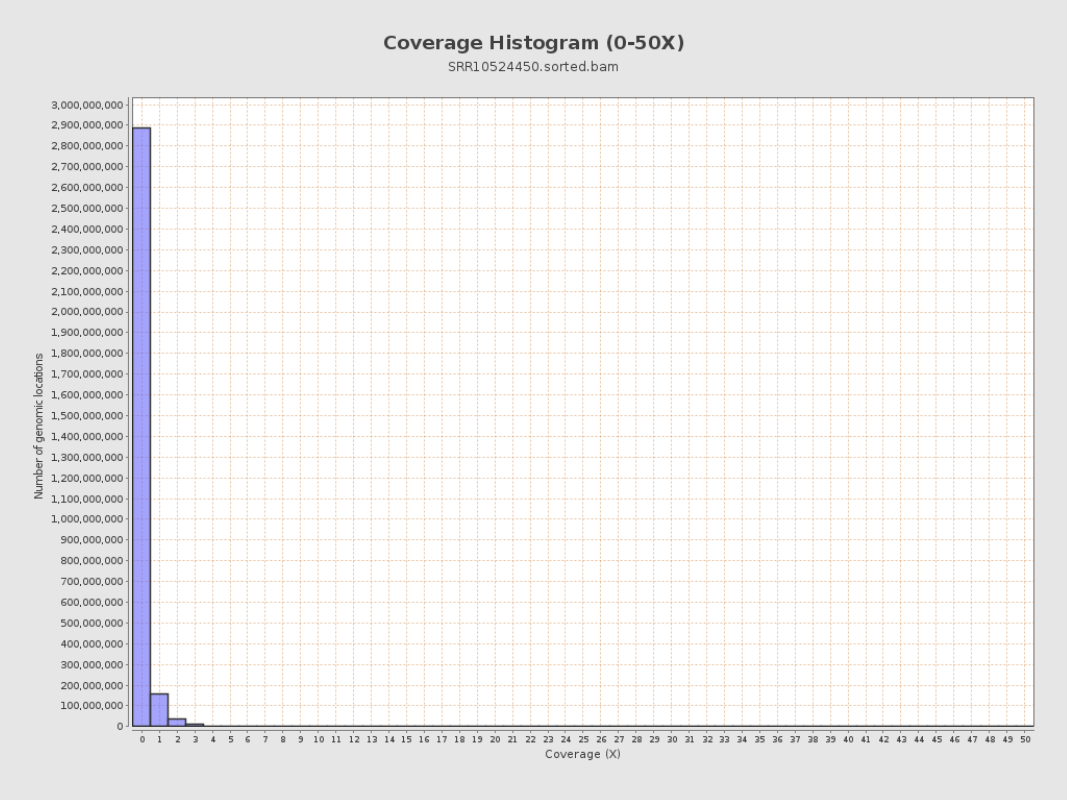
3. Results : Coverage across reference



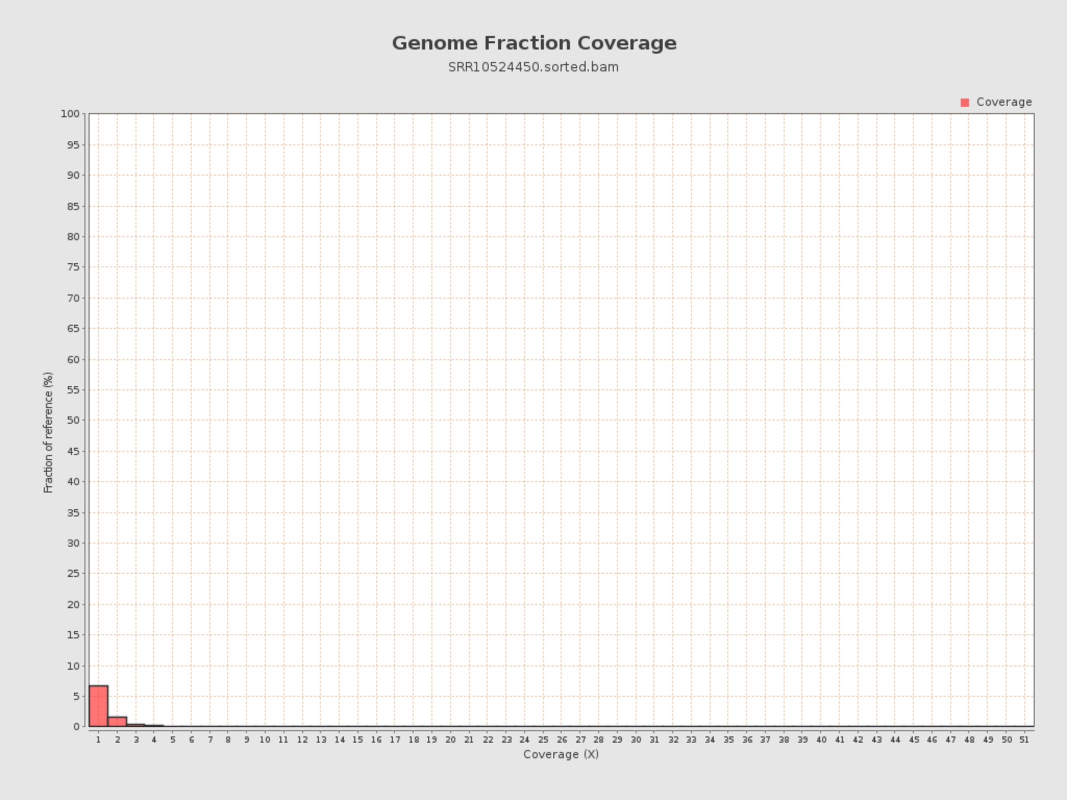
4. Results : Coverage Histogram



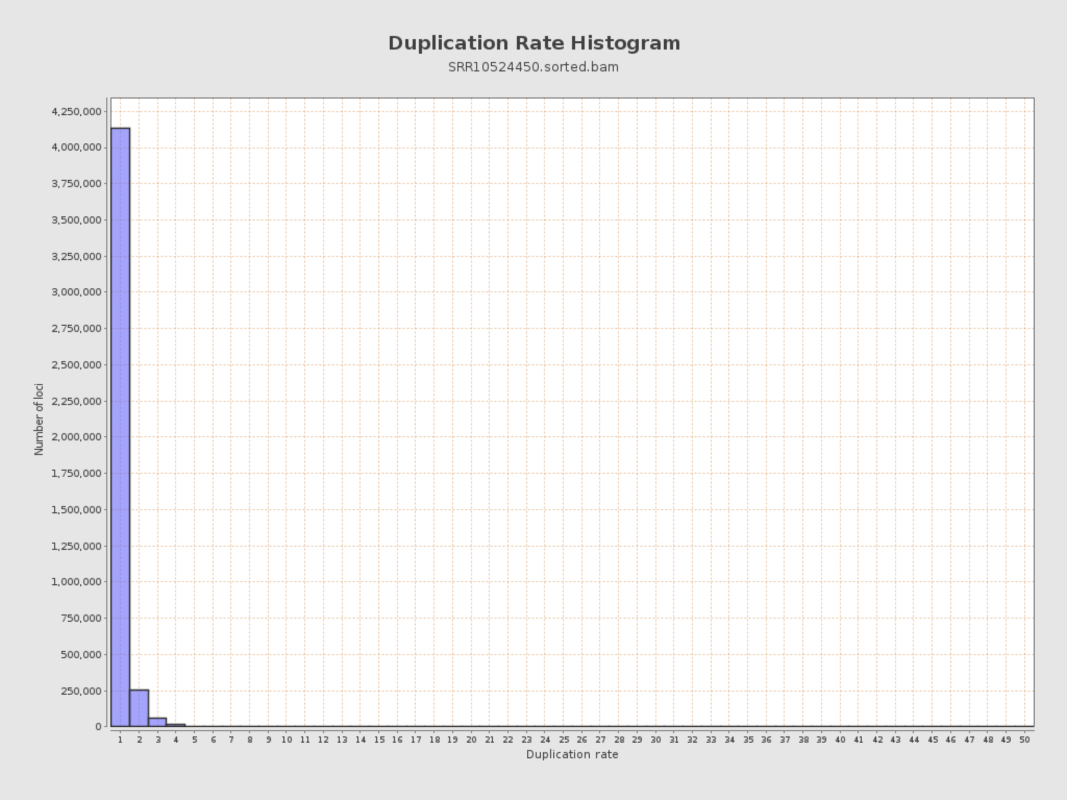
5. Results : Coverage Histogram (0-50X)



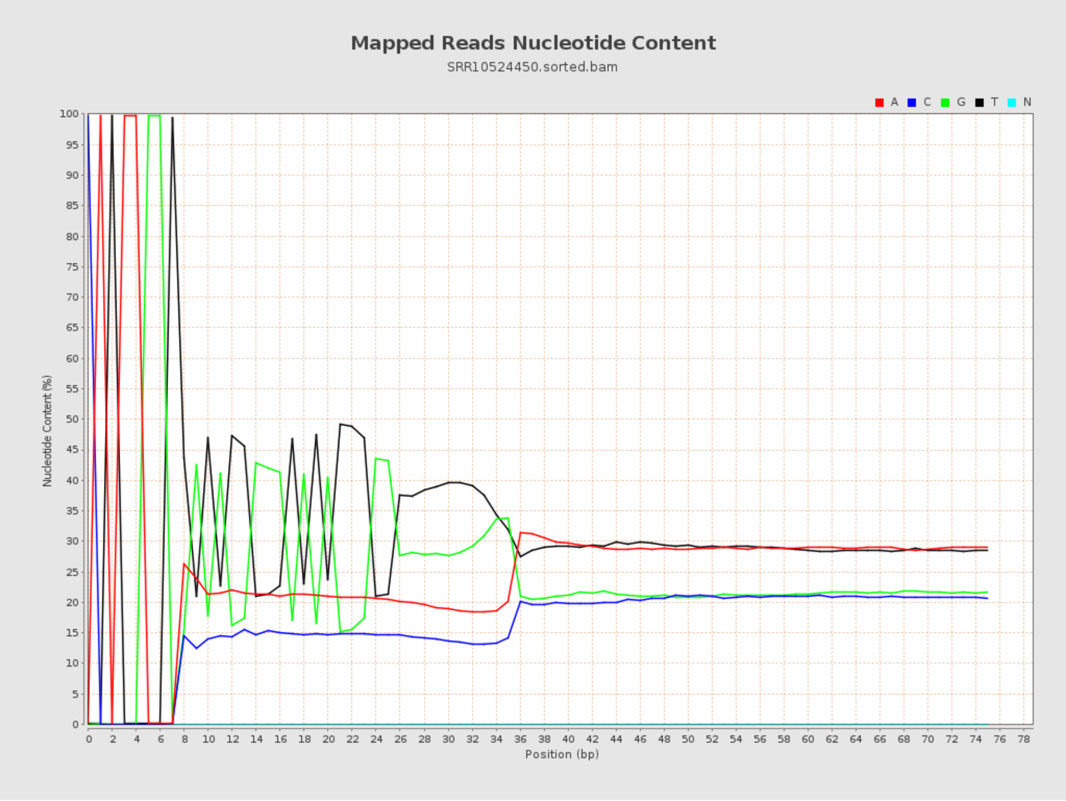
6. Results : Genome Fraction Coverage



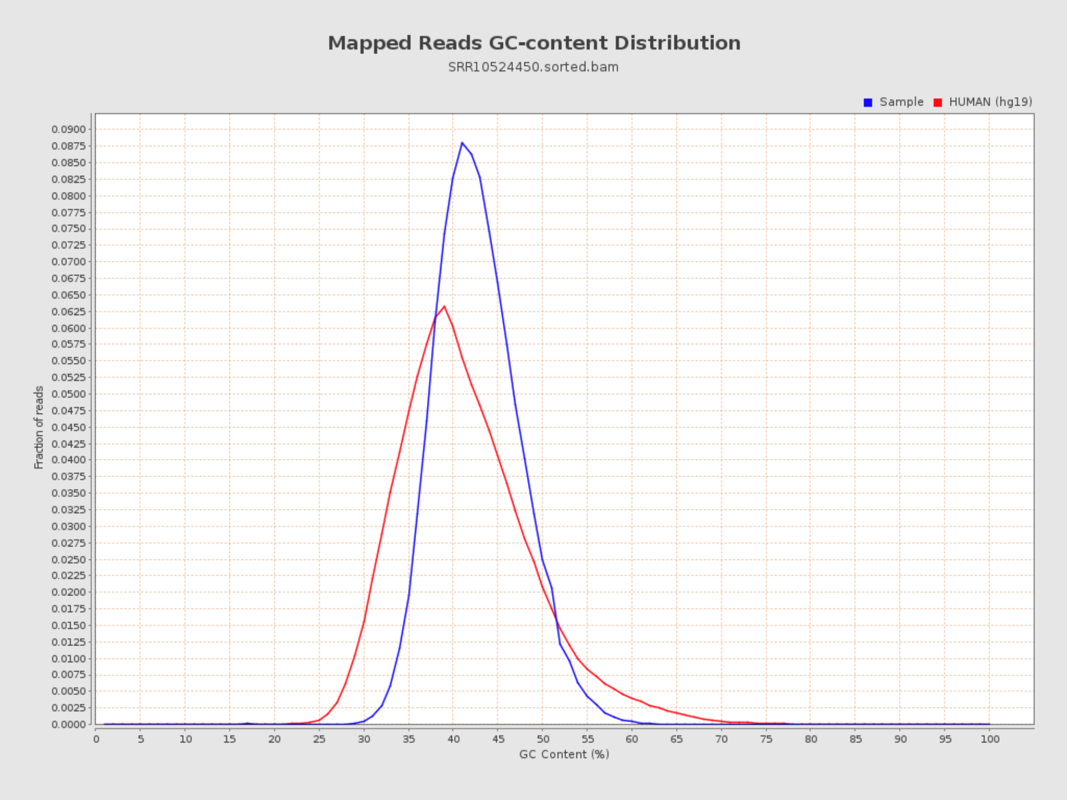
7. Results : Duplication Rate Histogram



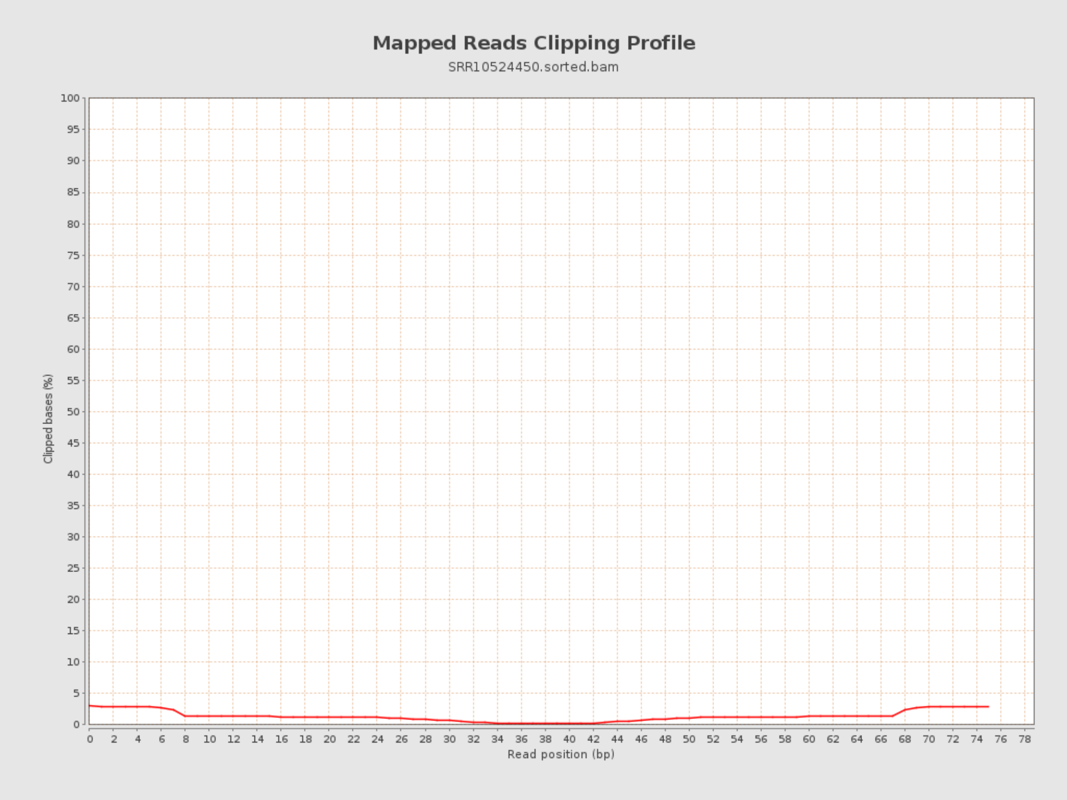
8. Results : Mapped Reads Nucleotide Content



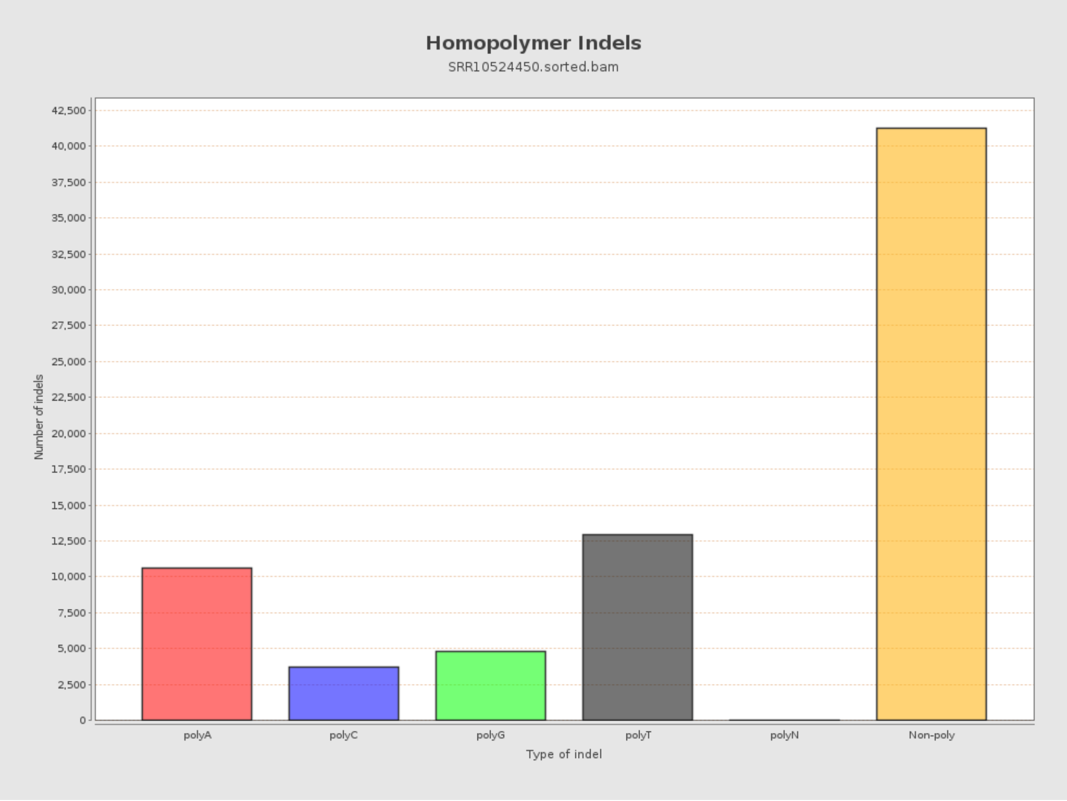
9. Results : Mapped Reads GC-content Distribution



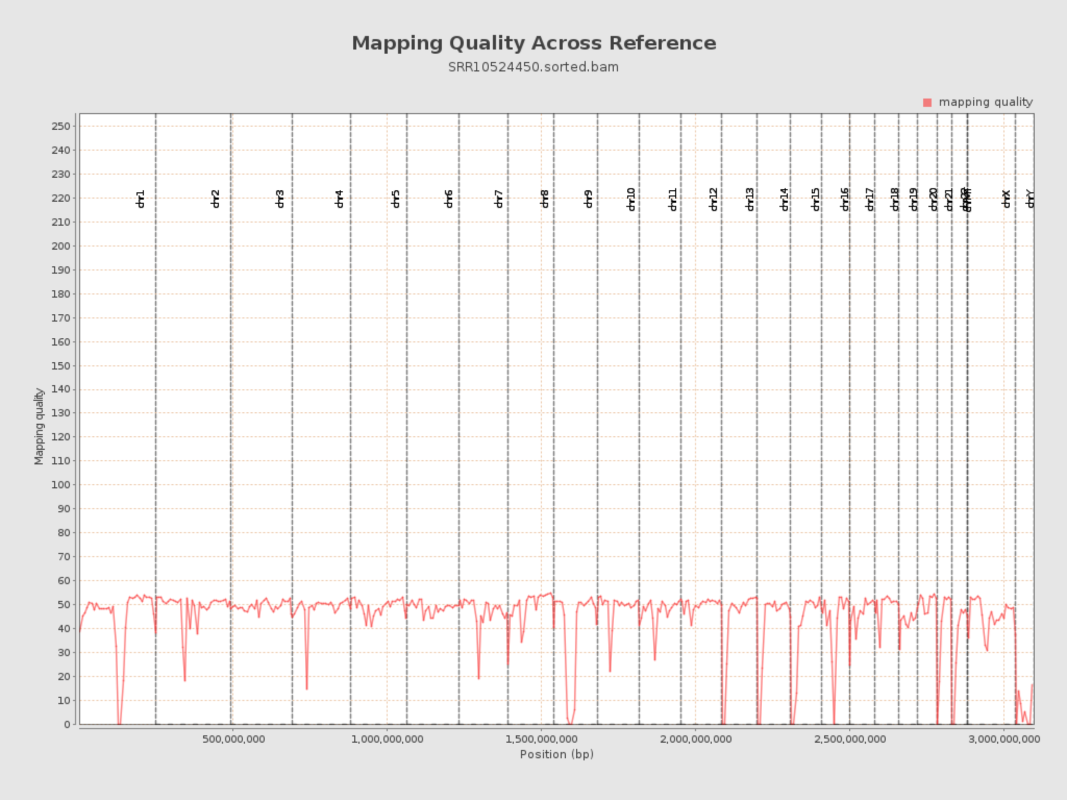
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram