Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:41:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524393.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_SRR10524393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524393.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:41:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,567,832
Mapped reads	6,069,104 / 92.41%
Unmapped reads	498,728 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,649 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	588,124 / 8.95%
Duplication rate	7%
Clipped reads	6,074,789 / 92.49%

2.2. ACGT Content

Number/percentage of A's	88,431,263 / 24.9%
Number/percentage of C's	63,384,076 / 17.85%
Number/percentage of T's	116,503,988 / 32.8%
Number/percentage of G's	86,799,138 / 24.44%
Number/percentage of N's	44,564 / 0.01%
GC Percentage	42.29%

2.3. Coverage

Mean	0.1148

Standard Deviation	0.9911

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

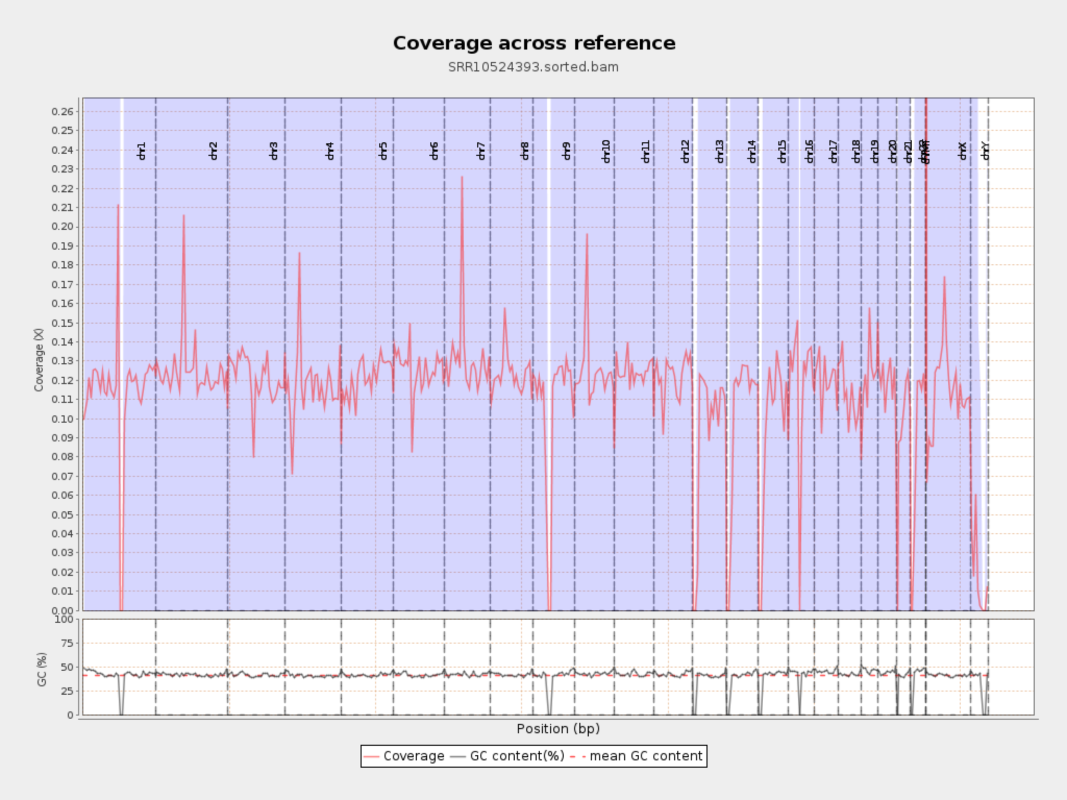
General error rate	0.5%
Mismatches	1,725,262
Insertions	27,638
Mapped reads with at least one insertion	0.45%
Deletions	61,724
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.2%

2.6. Chromosome stats

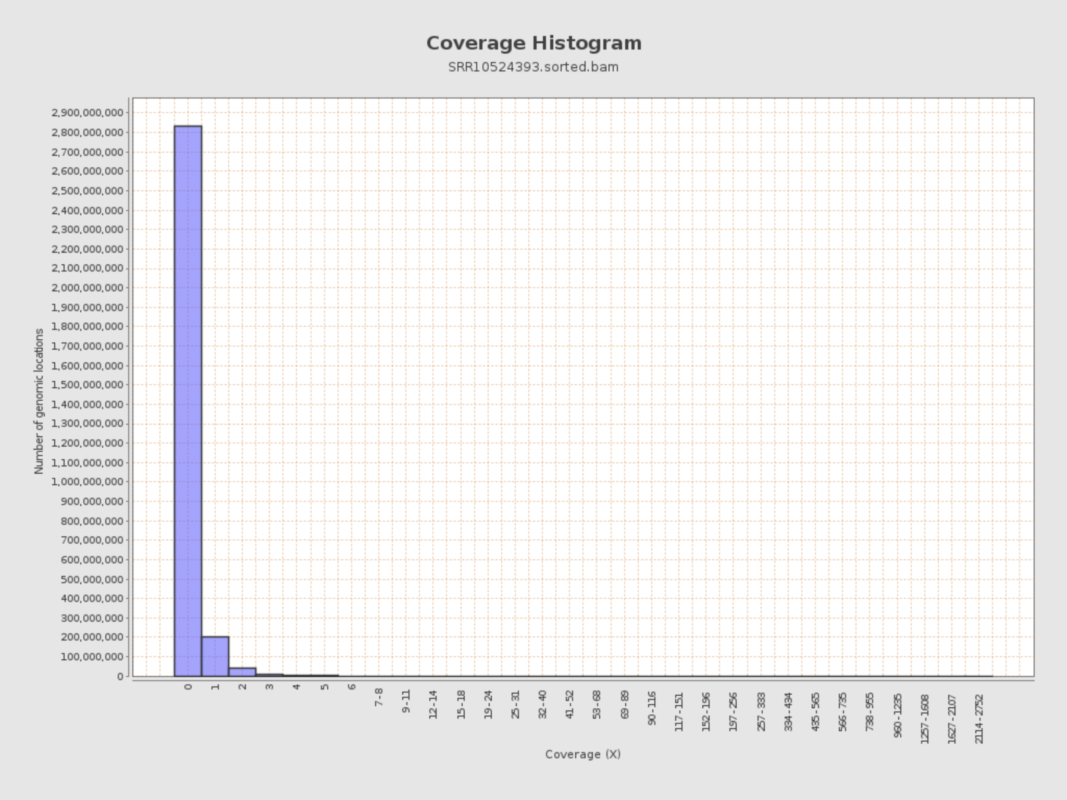
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28291544	0.1135	2.1839
chr2	243199373	30569173	0.1257	1.149
chr3	198022430	24021159	0.1213	0.4527
chr4	191154276	22468725	0.1175	0.5926
chr5	180915260	21997532	0.1216	0.455
chr6	171115067	21481885	0.1255	0.6081
chr7	159138663	20939673	0.1316	1.5738

chr8	146364022	18030100	0.1232	0.8079
chr9	141213431	14789503	0.1047	0.746
chr10	135534747	16910173	0.1248	0.8468
chr11	135006516	16740128	0.124	0.8741
chr12	133851895	16428050	0.1227	0.5004
chr13	115169878	10662596	0.0926	0.3952
chr14	107349540	10845596	0.101	0.4628
chr15	102531392	9526176	0.0929	0.4044
chr16	90354753	10425602	0.1154	0.5086
chr17	81195210	9823137	0.121	0.5676
chr18	78077248	8830028	0.1131	1.5977
chr19	59128983	7295490	0.1234	1.3827
chr20	63025520	7534240	0.1195	0.4814
chr21	48129895	4584143	0.0952	0.5224
chr22	51304566	4230597	0.0825	0.3723
chrMT	16571	117447	7.0875	5.1309
chrX	155270560	17695362	0.114	0.5877
chrY	59373566	1023546	0.0172	0.4083

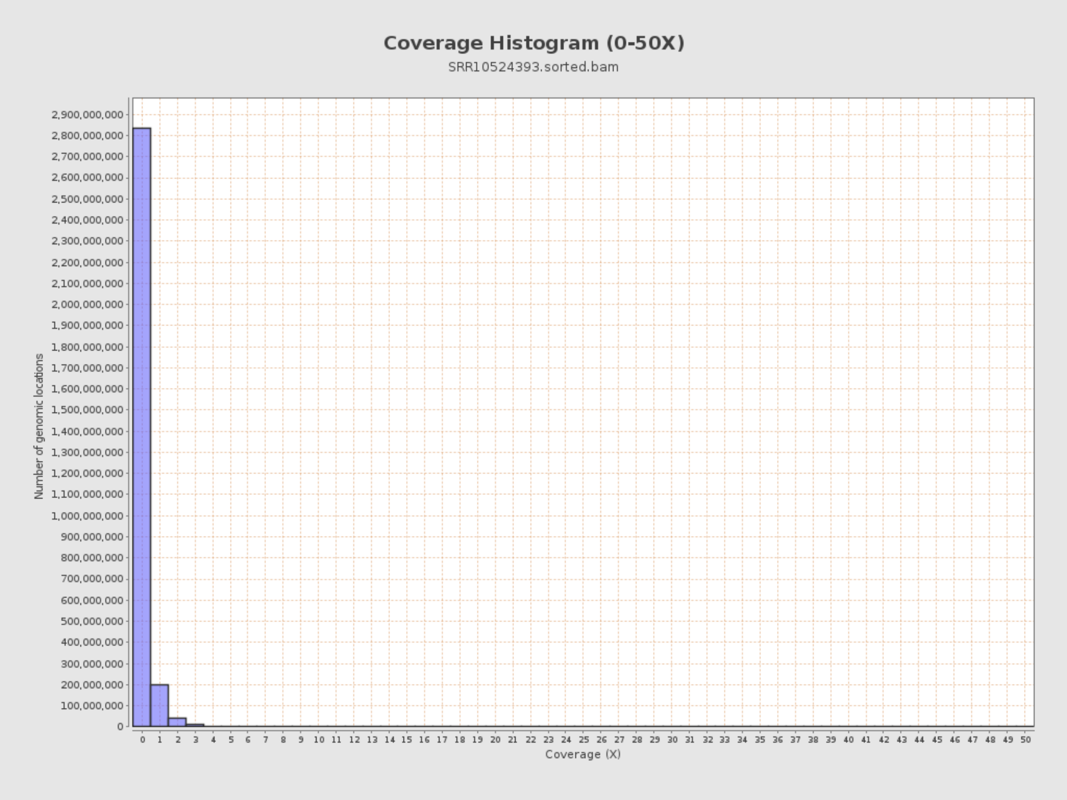
3. Results : Coverage across reference



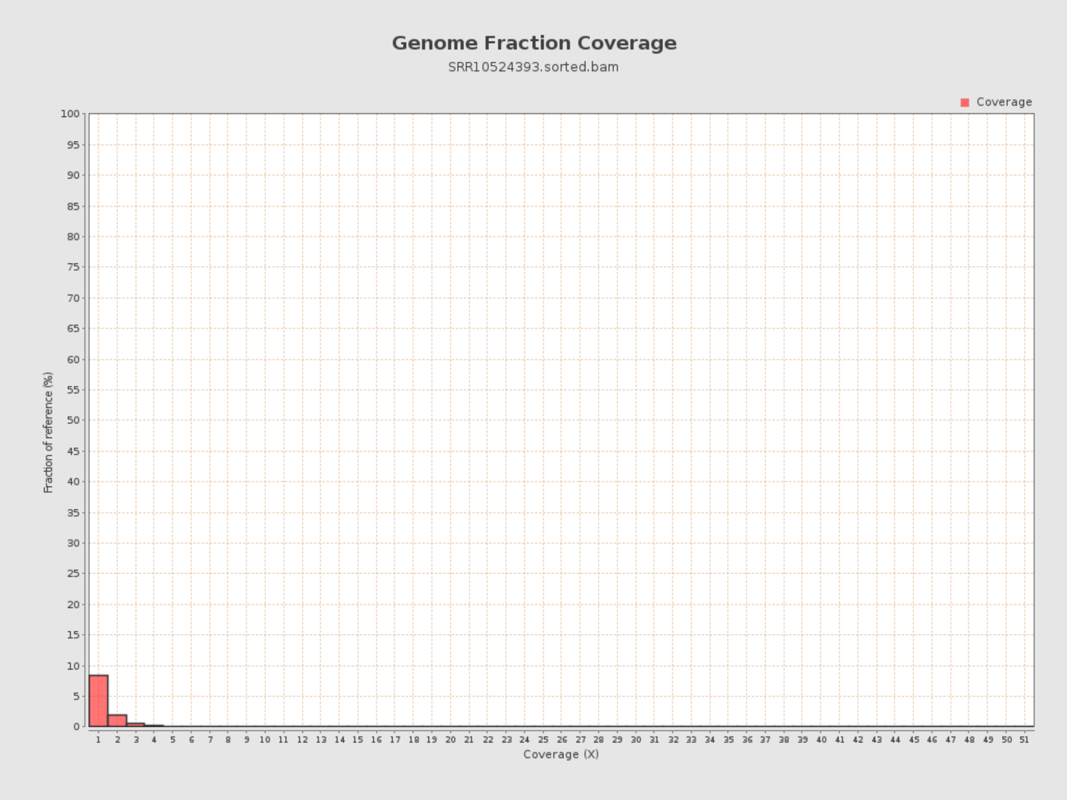
4. Results : Coverage Histogram



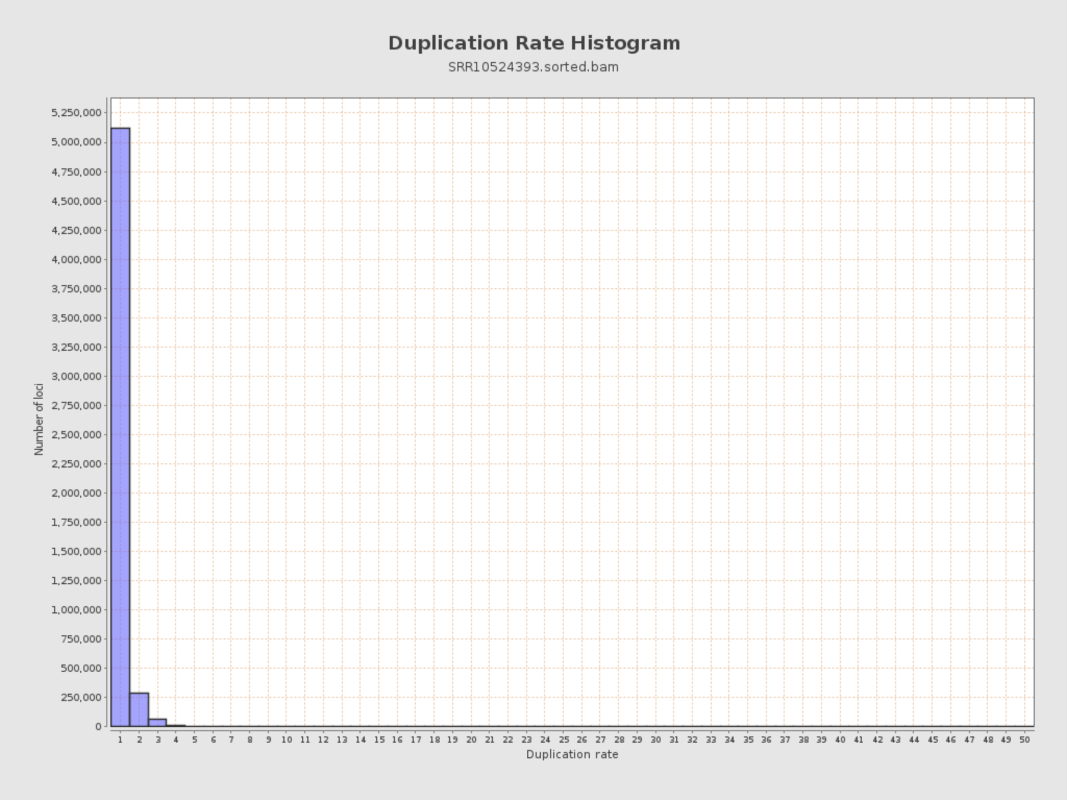
5. Results : Coverage Histogram (0-50X)



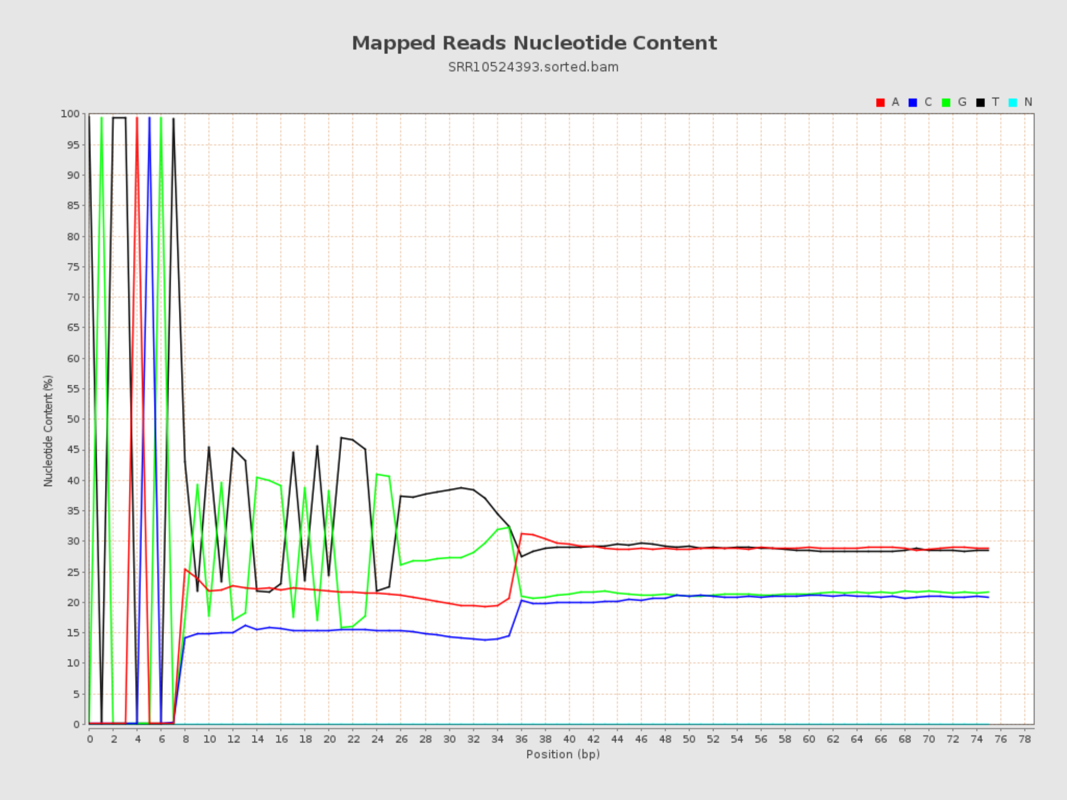
6. Results : Genome Fraction Coverage



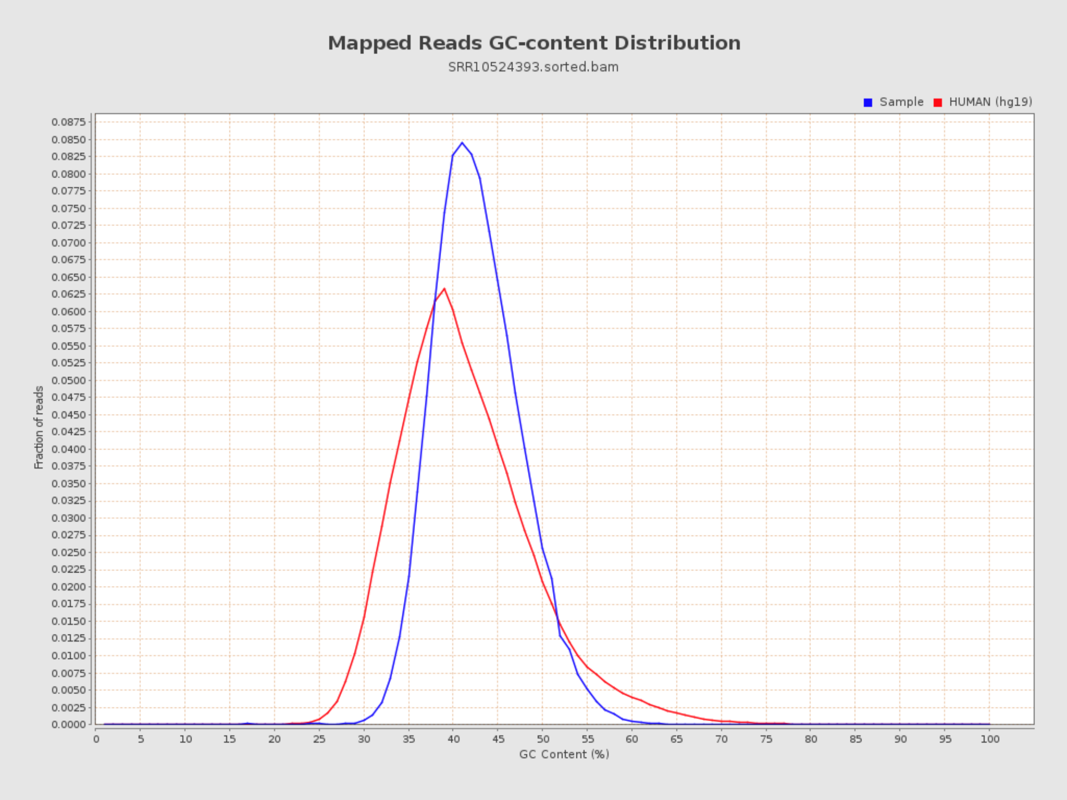
7. Results : Duplication Rate Histogram



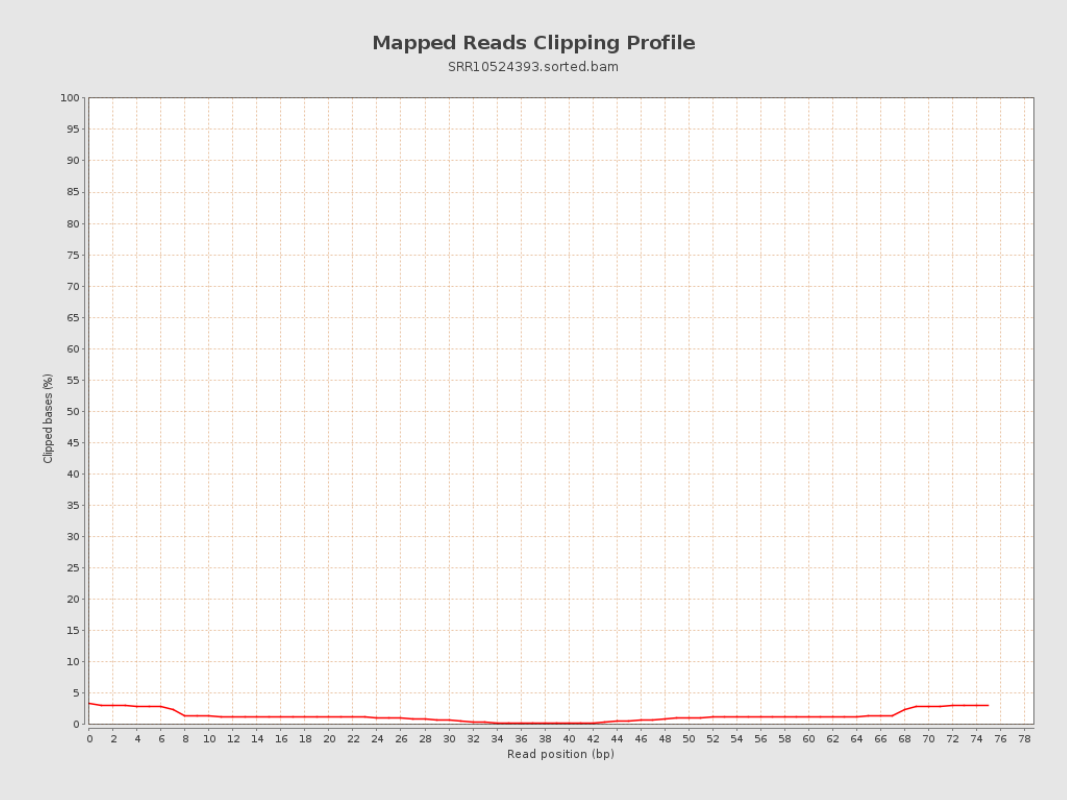
8. Results : Mapped Reads Nucleotide Content



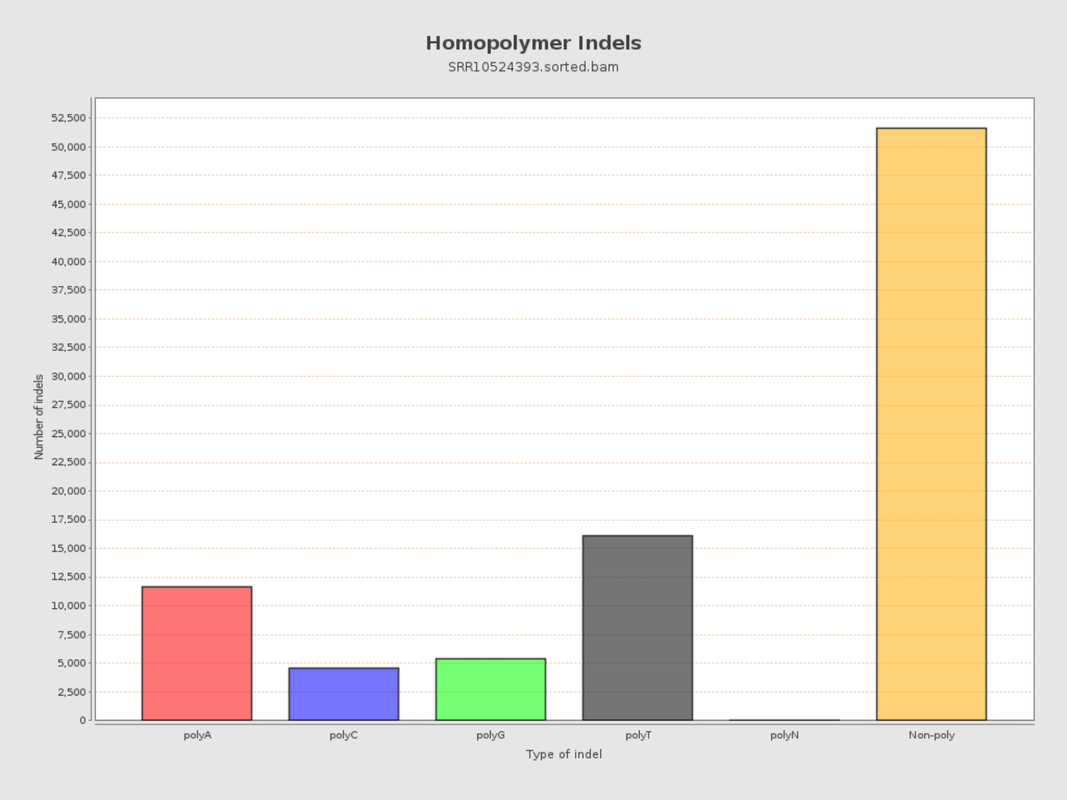
9. Results : Mapped Reads GC-content Distribution



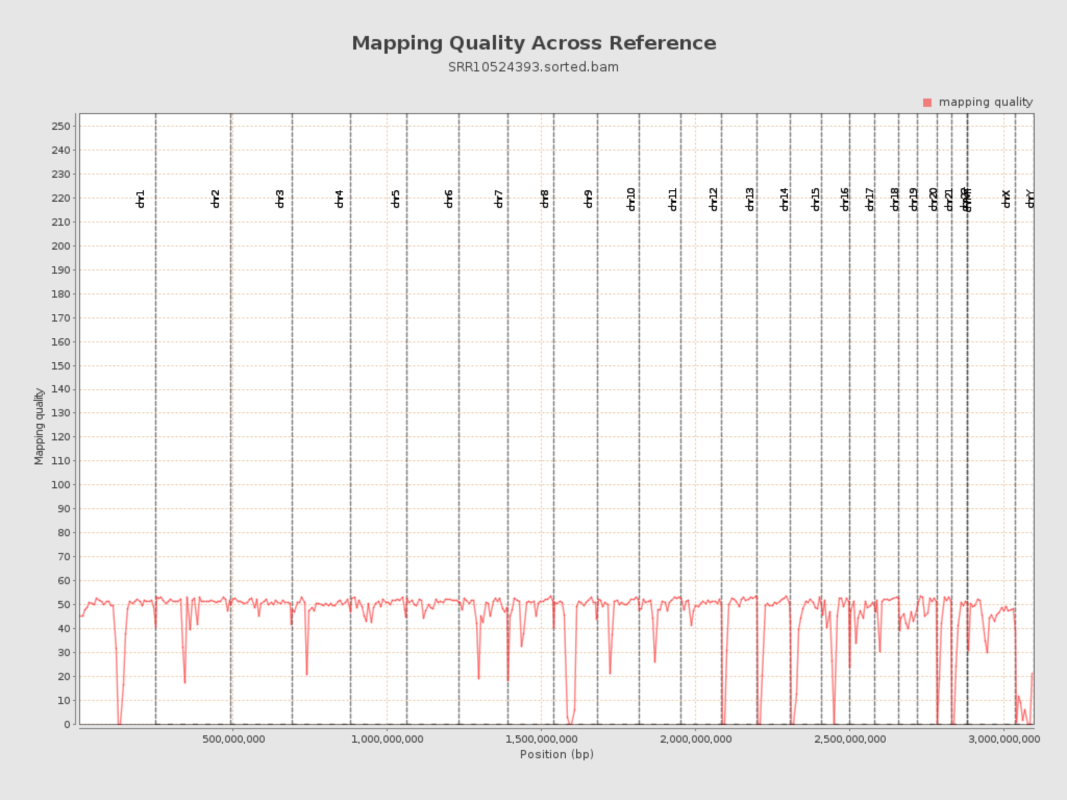
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram