Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:10:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524610.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_SRR10524610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:10:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,190,699
Mapped reads	2,040,472 / 93.14%
Unmapped reads	150,227 / 6.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,447 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	114,152 / 5.21%
Duplication rate	4.36%
Clipped reads	2,039,431 / 93.09%

2.2. ACGT Content

Number/percentage of A's	30,483,042 / 25.59%
Number/percentage of C's	23,004,984 / 19.31%
Number/percentage of T's	37,471,793 / 31.45%
Number/percentage of G's	28,169,761 / 23.65%
Number/percentage of N's	779 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3243

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

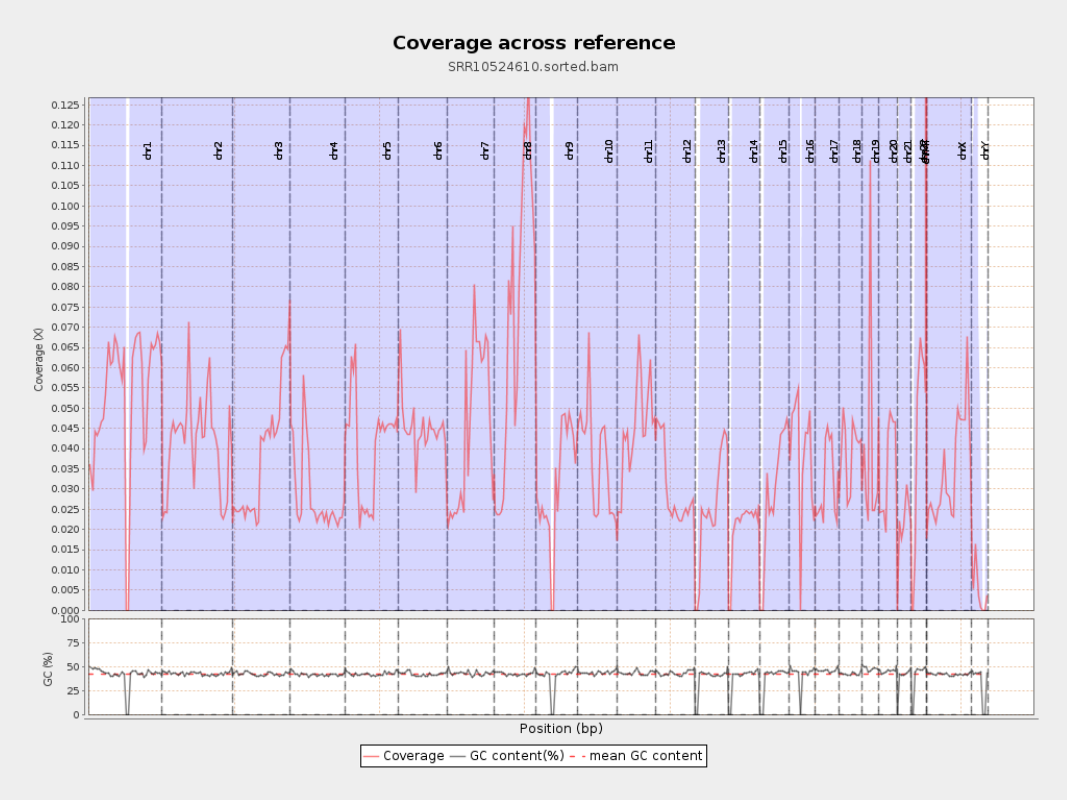
General error rate	0.48%
Mismatches	559,958
Insertions	7,186
Mapped reads with at least one insertion	0.35%
Deletions	21,963
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.86%

2.6. Chromosome stats

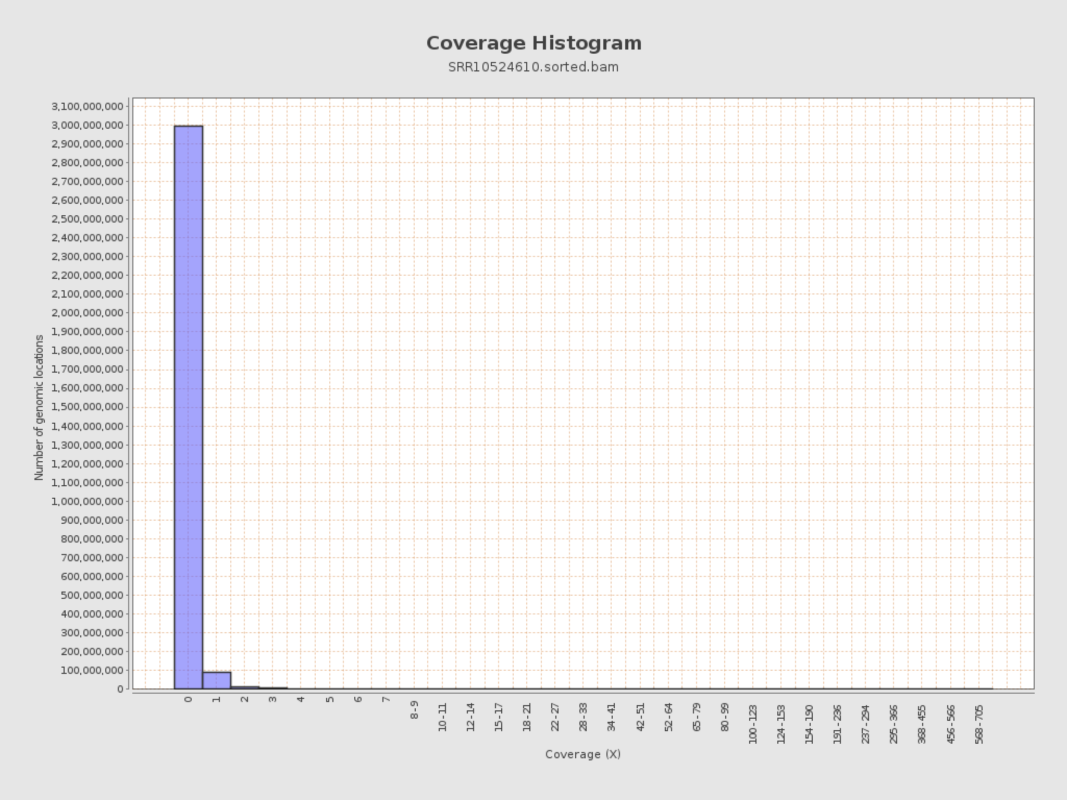
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13140871	0.0527	0.5644
chr2	243199373	10128980	0.0416	0.3788
chr3	198022430	7520061	0.038	0.224
chr4	191154276	5407757	0.0283	0.2303
chr5	180915260	7340378	0.0406	0.232
chr6	171115067	7723706	0.0451	0.2658
chr7	159138663	7256943	0.0456	0.4437

chr8	146364022	10586633	0.0723	0.4237
chr9	141213431	4337042	0.0307	0.2921
chr10	135534747	5045657	0.0372	0.3225
chr11	135006516	6064720	0.0449	0.3186
chr12	133851895	3956353	0.0296	0.2042
chr13	115169878	2893487	0.0251	0.1823
chr14	107349540	2165844	0.0202	0.1737
chr15	102531392	3012355	0.0294	0.2079
chr16	90354753	3491488	0.0386	0.2381
chr17	81195210	2578547	0.0318	0.2138
chr18	78077248	3105977	0.0398	0.4764
chr19	59128983	2357169	0.0399	0.3945
chr20	63025520	2206420	0.035	0.2211
chr21	48129895	1020219	0.0212	0.1889
chr22	51304566	2101367	0.041	0.2313
chrMT	16571	47809	2.8851	2.5627
chrX	155270560	5403292	0.0348	0.252
chrY	59373566	274361	0.0046	0.125

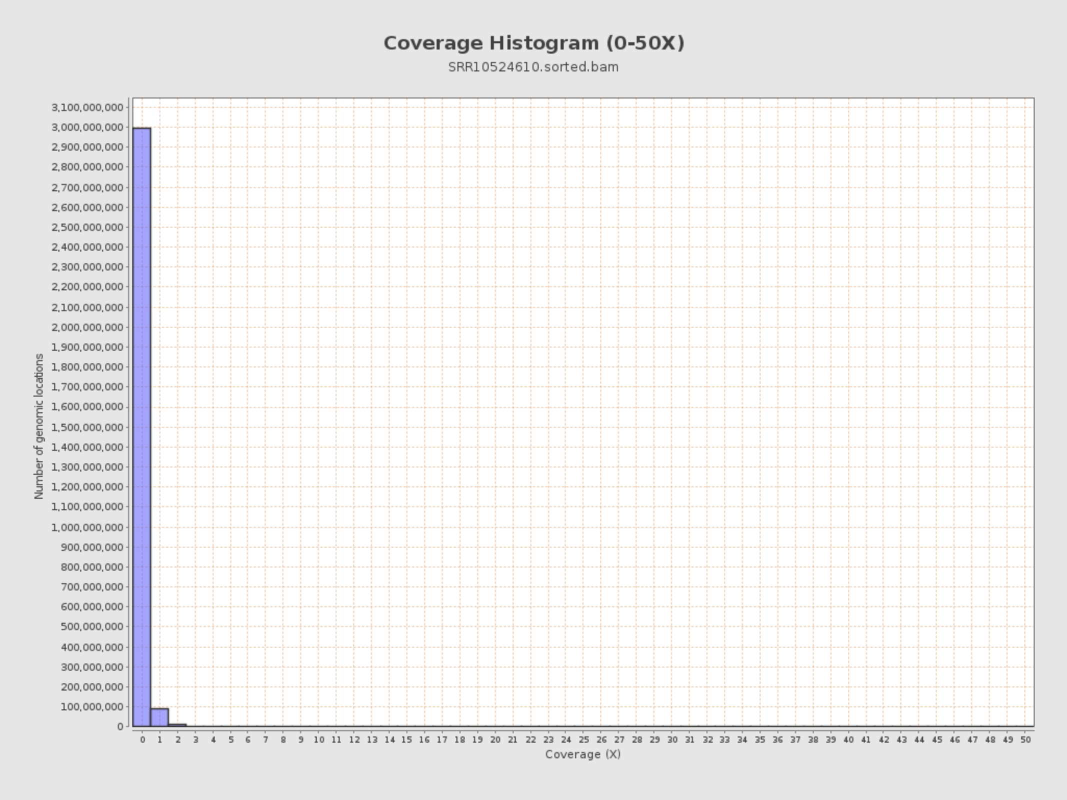
3. Results : Coverage across reference



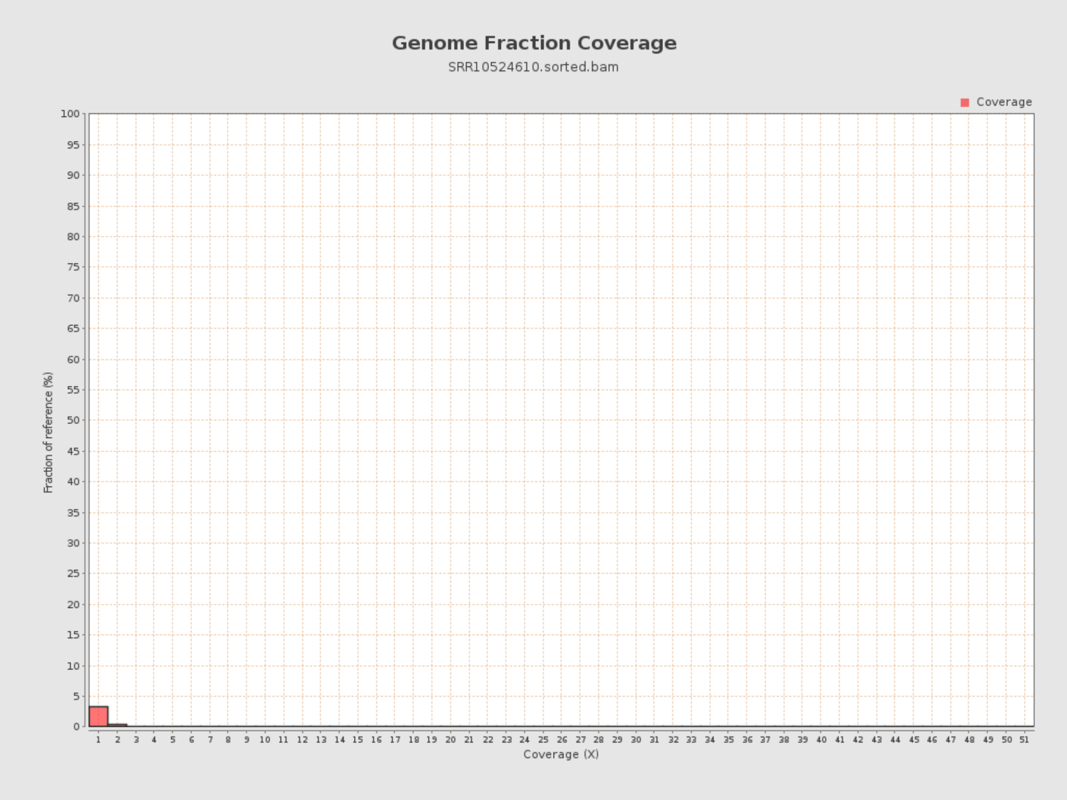
4. Results : Coverage Histogram



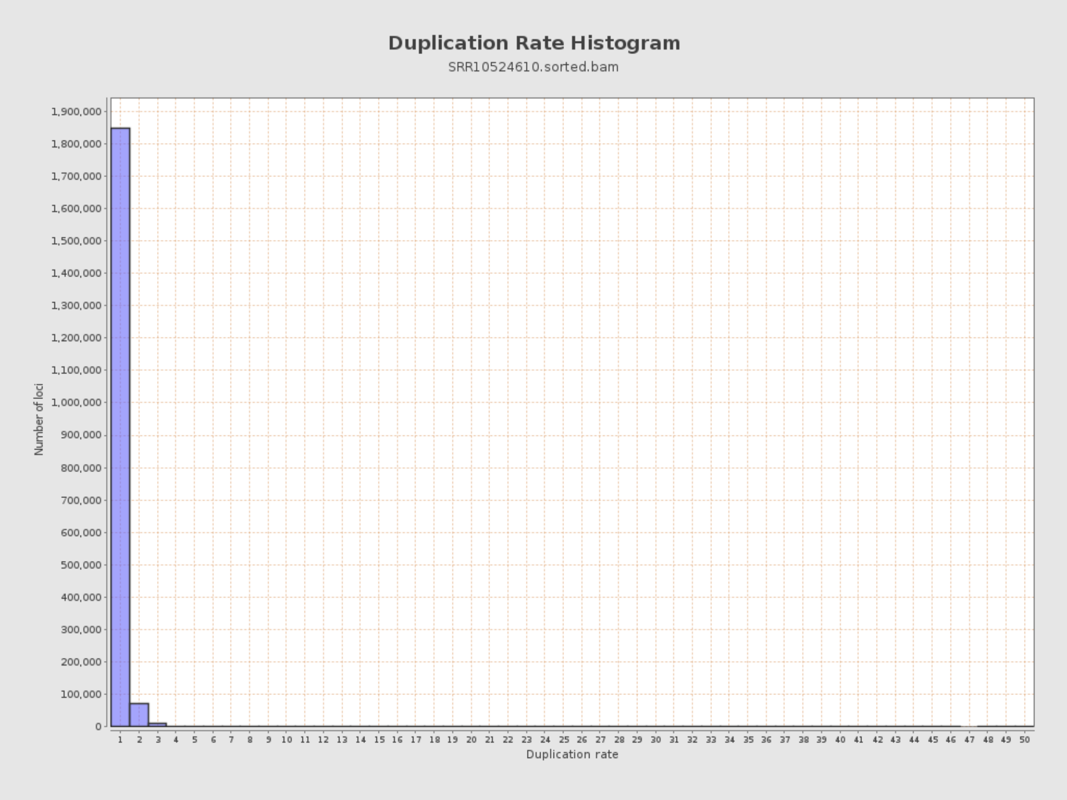
5. Results : Coverage Histogram (0-50X)



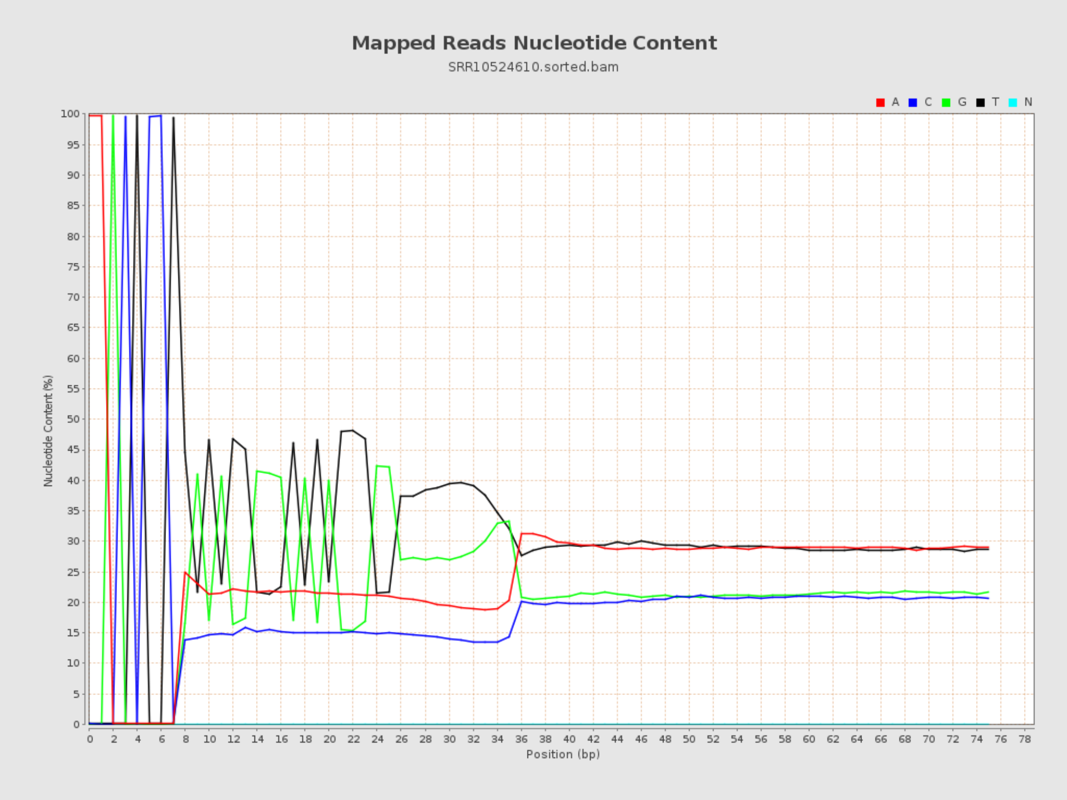
6. Results : Genome Fraction Coverage



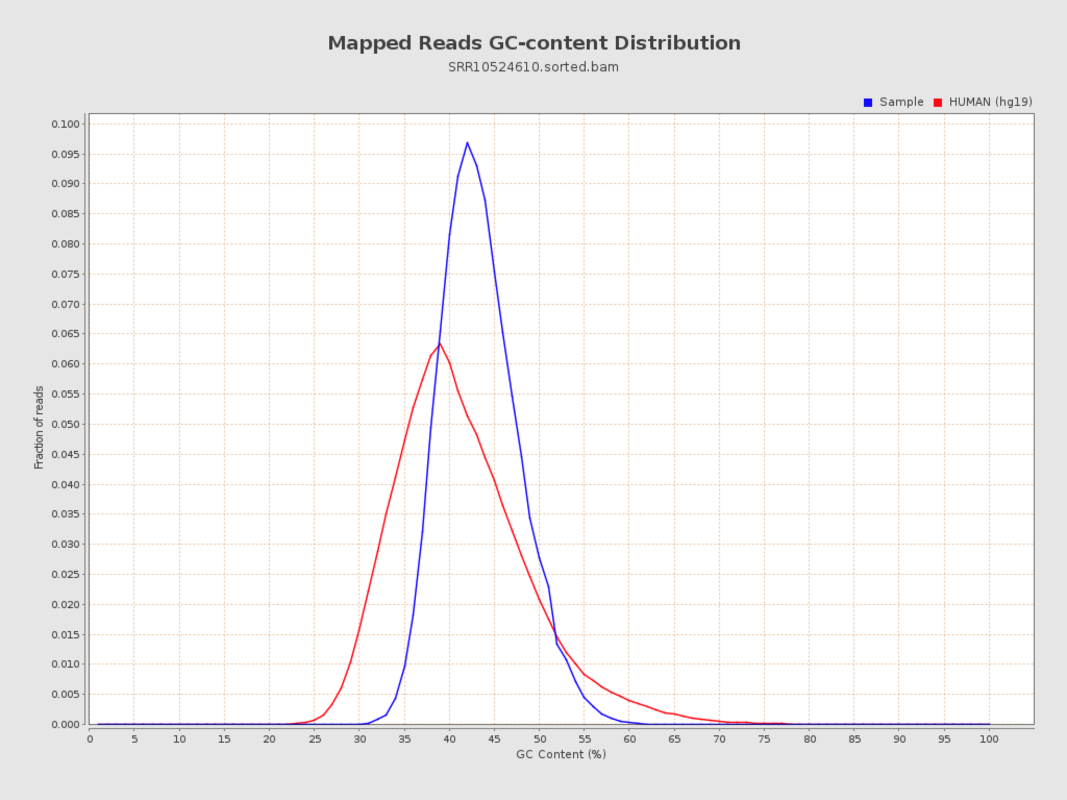
7. Results : Duplication Rate Histogram



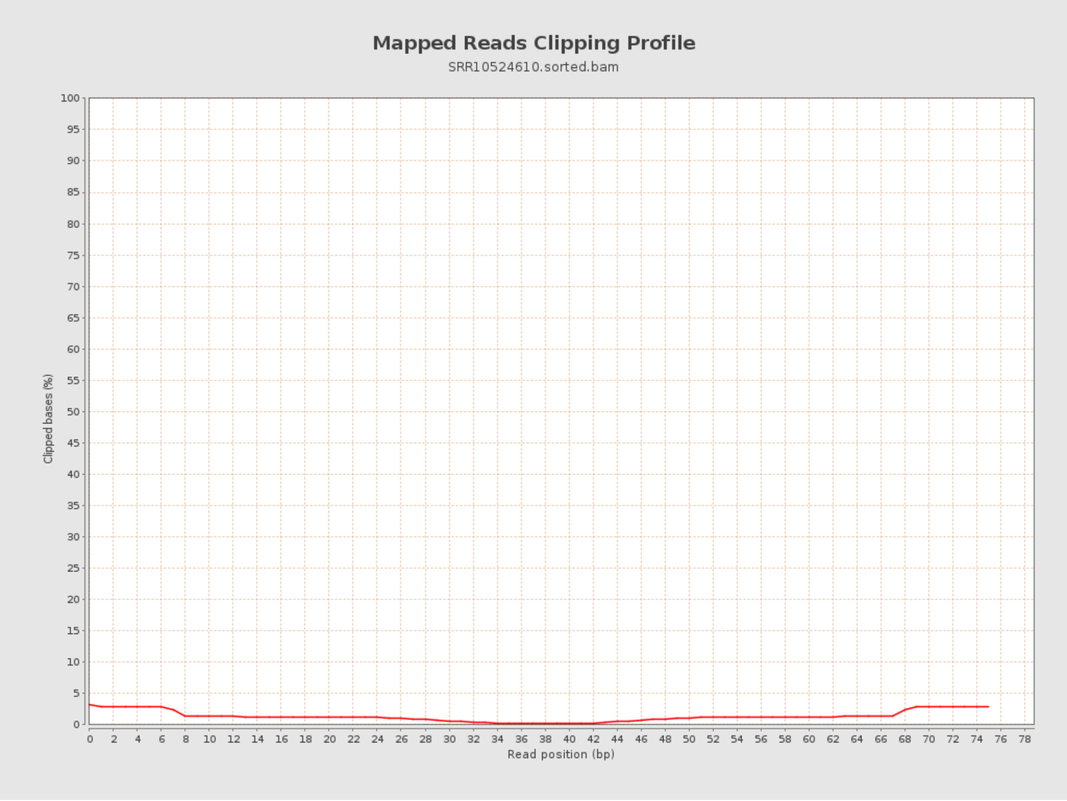
8. Results : Mapped Reads Nucleotide Content



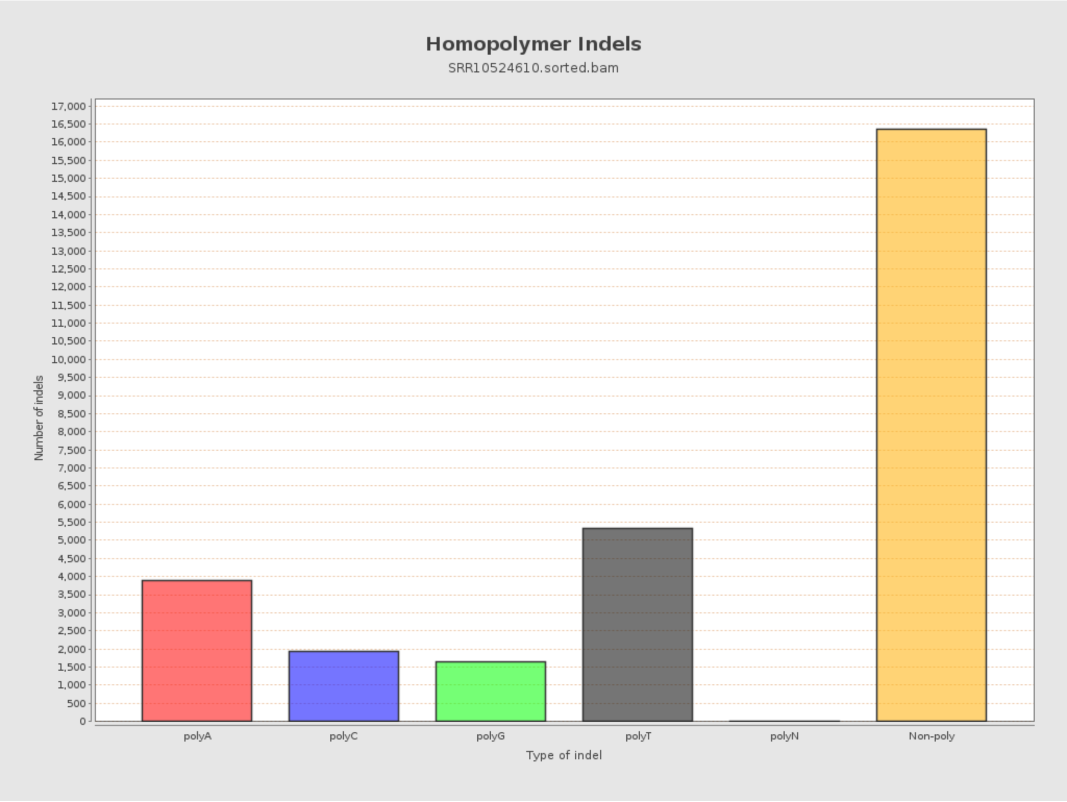
9. Results : Mapped Reads GC-content Distribution



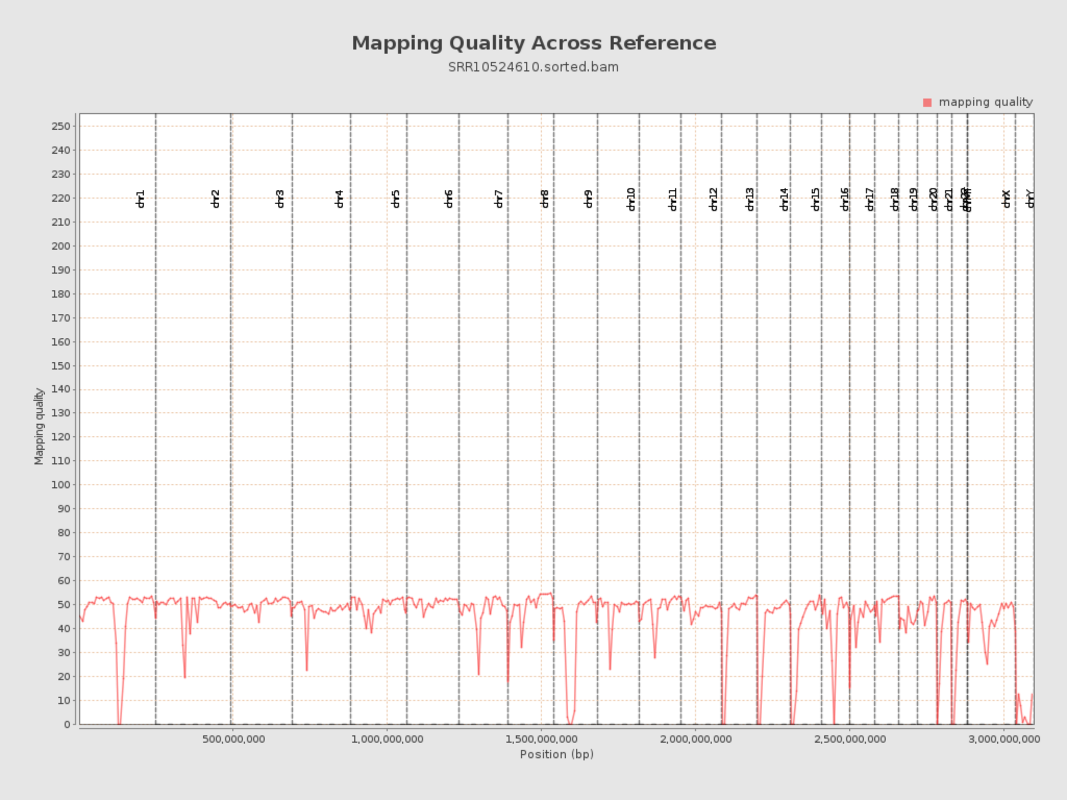
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram