Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:27:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524930.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_SRR10524930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524930.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:27:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,404
Mapped reads	507,639 / 92.57%
Unmapped reads	40,765 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,130 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	13,146 / 2.4%
Duplication rate	2.08%
Clipped reads	508,281 / 92.68%

2.2. ACGT Content

Number/percentage of A's	7,628,767 / 25.69%
Number/percentage of C's	5,609,233 / 18.89%
Number/percentage of T's	9,041,854 / 30.45%
Number/percentage of G's	7,418,018 / 24.98%
Number/percentage of N's	243 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1214

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

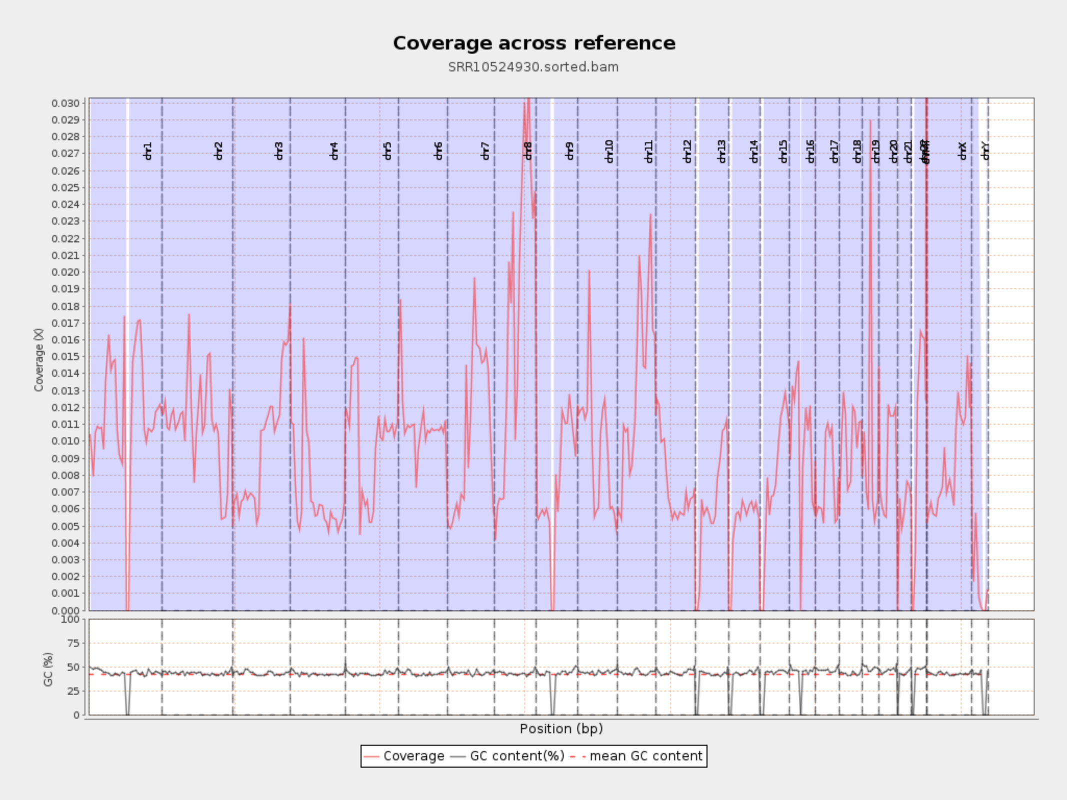
General error rate	0.5%
Mismatches	145,376
Insertions	2,153
Mapped reads with at least one insertion	0.42%
Deletions	5,264
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.15%

2.6. Chromosome stats

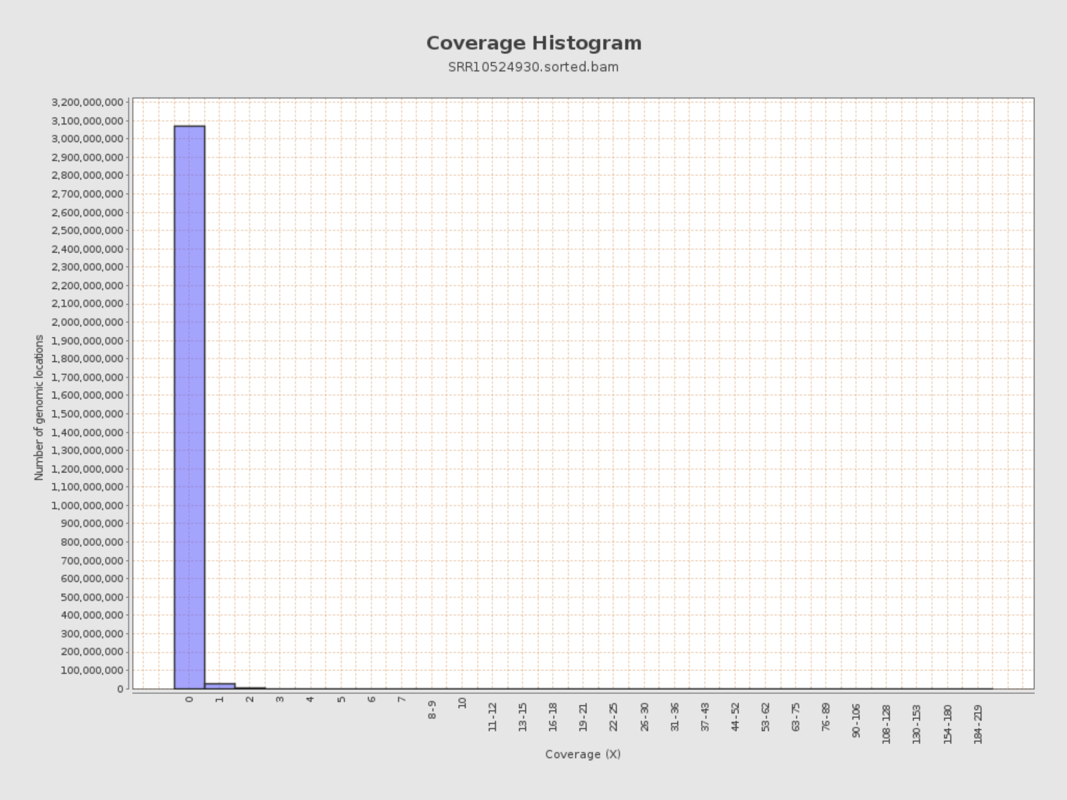
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2868707	0.0115	0.1913
chr2	243199373	2691505	0.0111	0.1406
chr3	198022430	1905038	0.0096	0.1028
chr4	191154276	1309396	0.0068	0.0956
chr5	180915260	1798931	0.0099	0.1043
chr6	171115067	1885768	0.011	0.1114
chr7	159138663	1704568	0.0107	0.1334

chr8	146364022	2594312	0.0177	0.1602
chr9	141213431	1052294	0.0075	0.0994
chr10	135534747	1310239	0.0097	0.1251
chr11	135006516	1806239	0.0134	0.1265
chr12	133851895	988532	0.0074	0.0906
chr13	115169878	720792	0.0063	0.0829
chr14	107349540	548813	0.0051	0.0755
chr15	102531392	781595	0.0076	0.0911
chr16	90354753	899346	0.01	0.1076
chr17	81195210	621876	0.0077	0.0932
chr18	78077248	798709	0.0102	0.144
chr19	59128983	601413	0.0102	0.1485
chr20	63025520	566977	0.009	0.1002
chr21	48129895	281632	0.0059	0.0866
chr22	51304566	524855	0.0102	0.1063
chrMT	16571	1428	0.0862	0.3027
chrX	155270560	1355222	0.0087	0.1011
chrY	59373566	88723	0.0015	0.0662

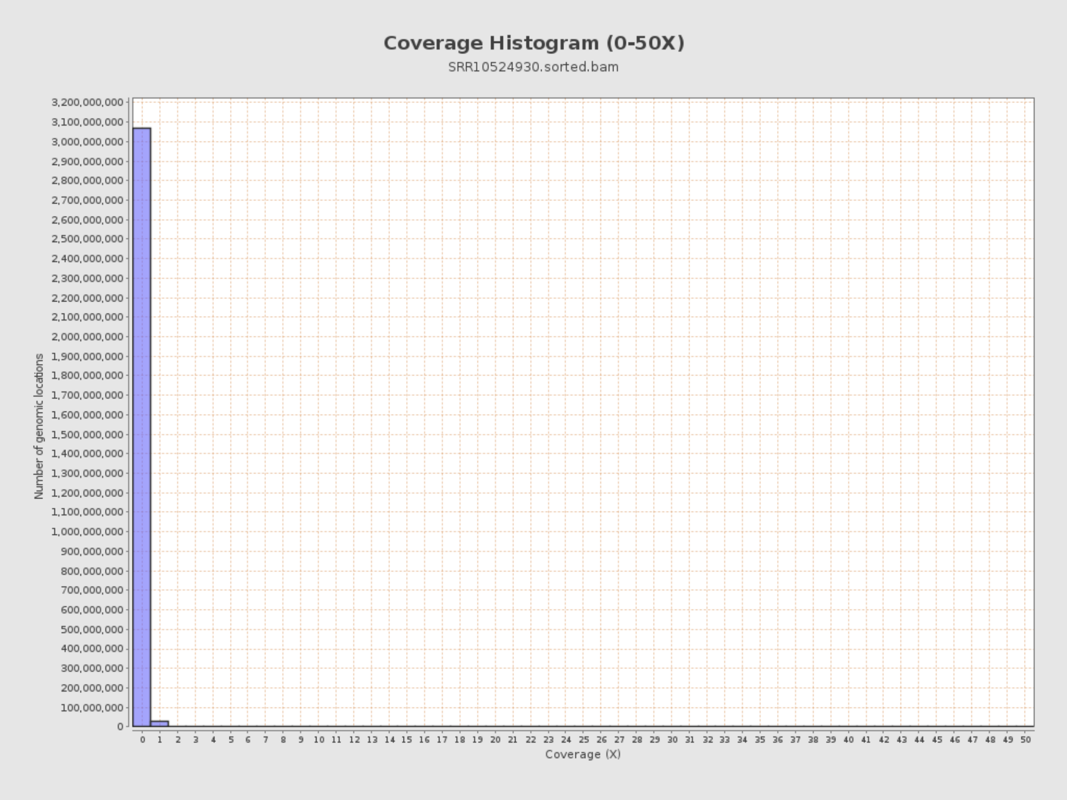
3. Results : Coverage across reference



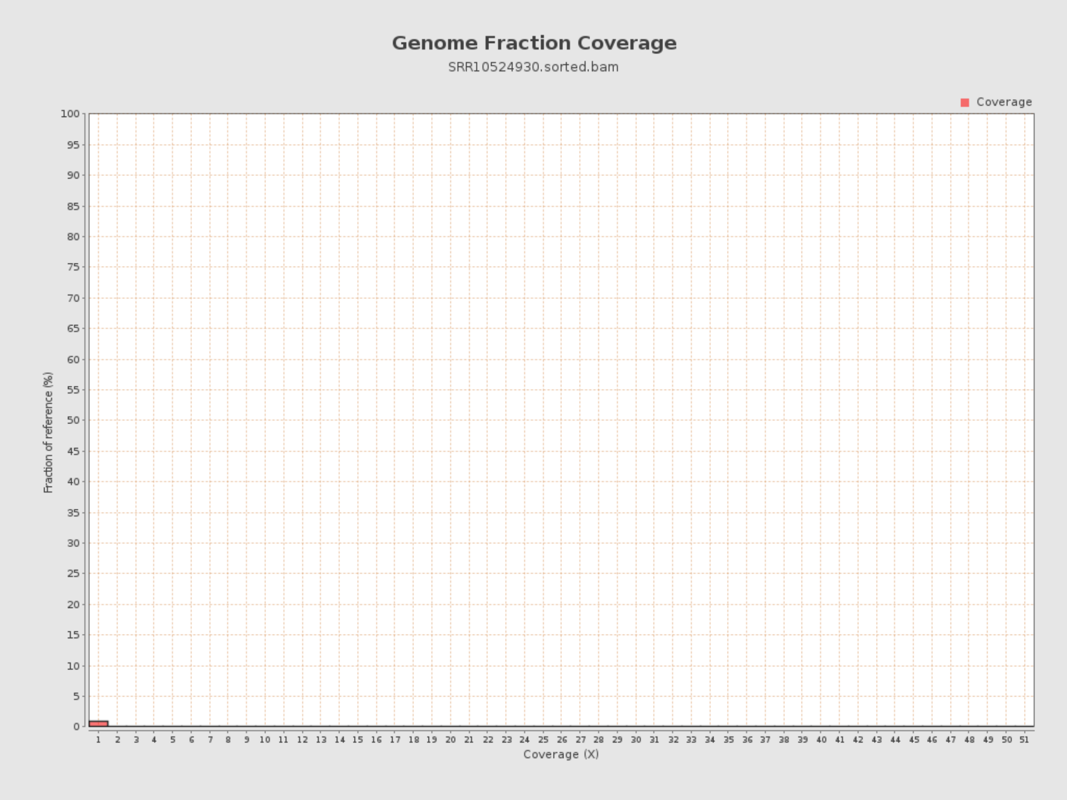
4. Results : Coverage Histogram



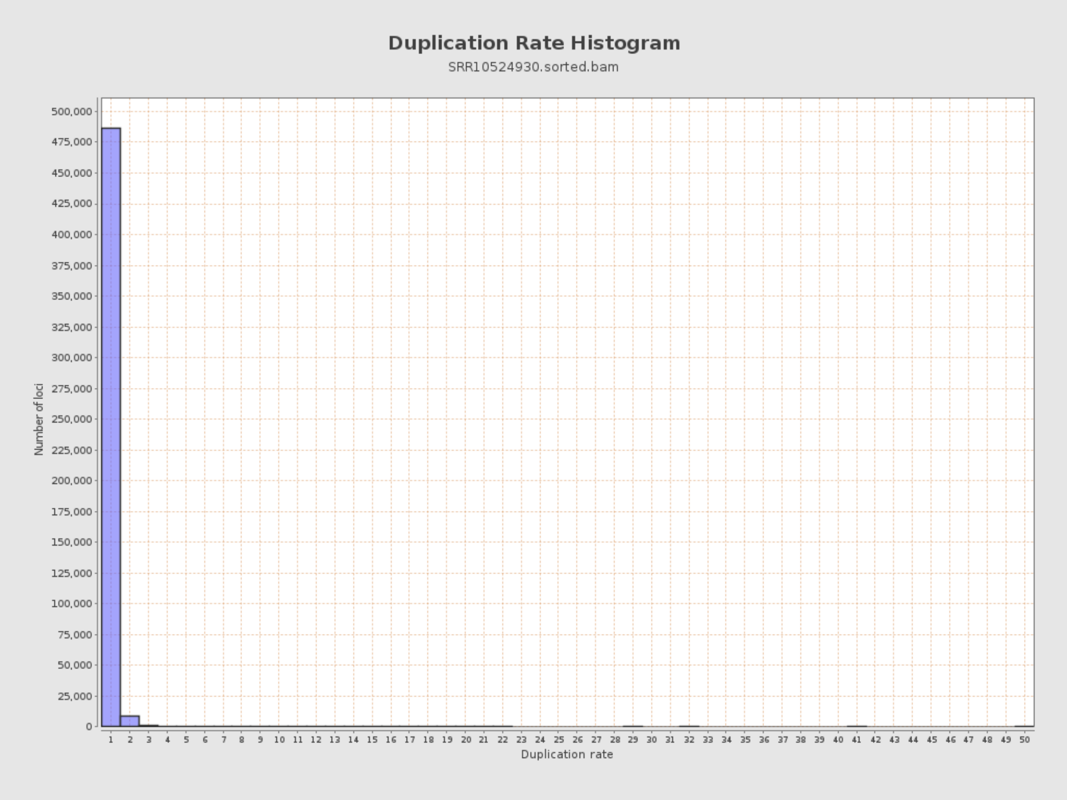
5. Results : Coverage Histogram (0-50X)



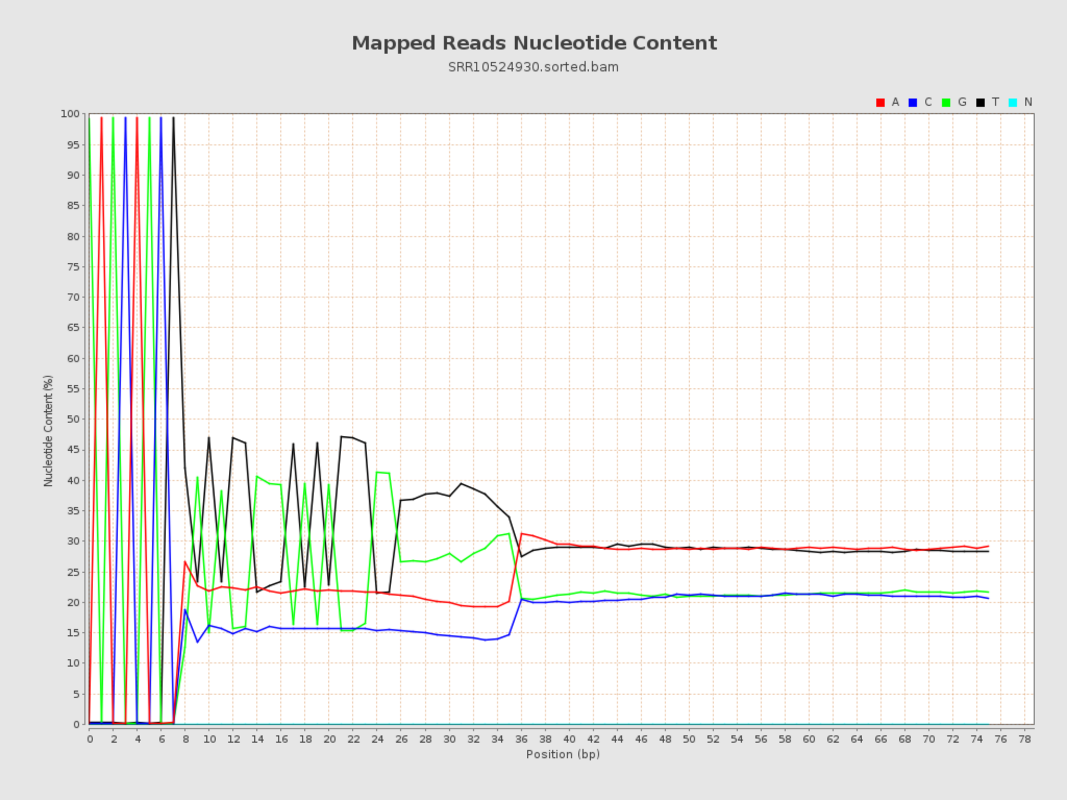
6. Results : Genome Fraction Coverage



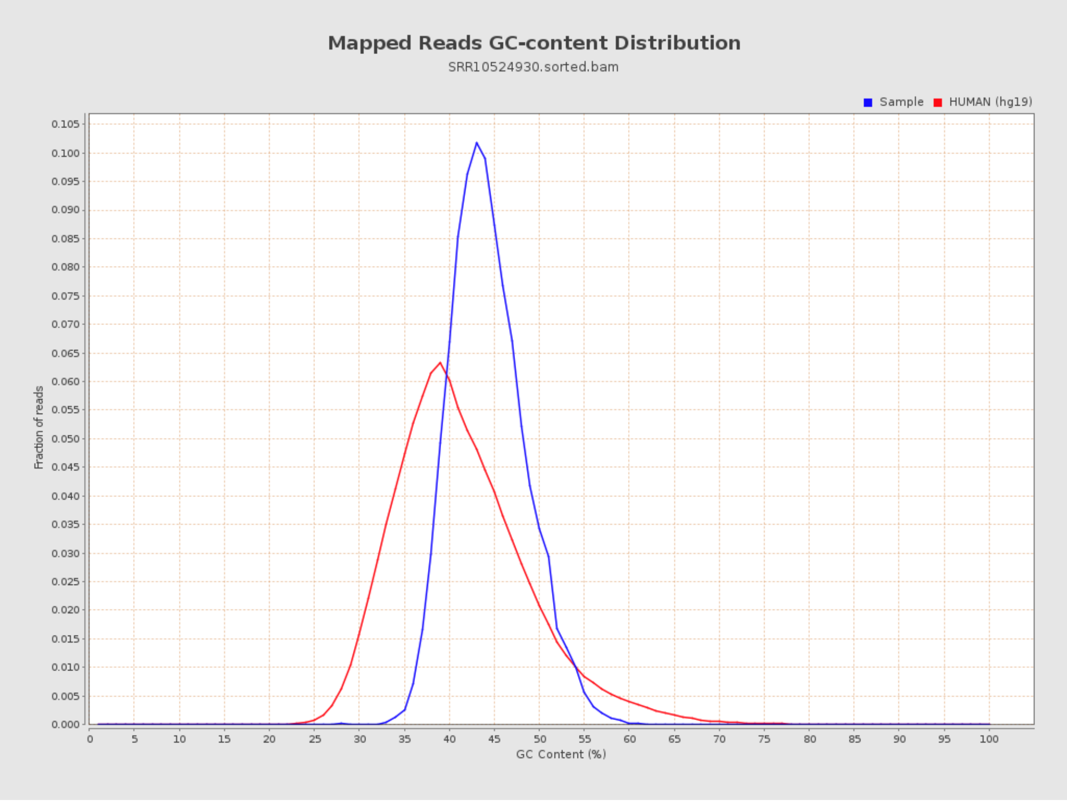
7. Results : Duplication Rate Histogram



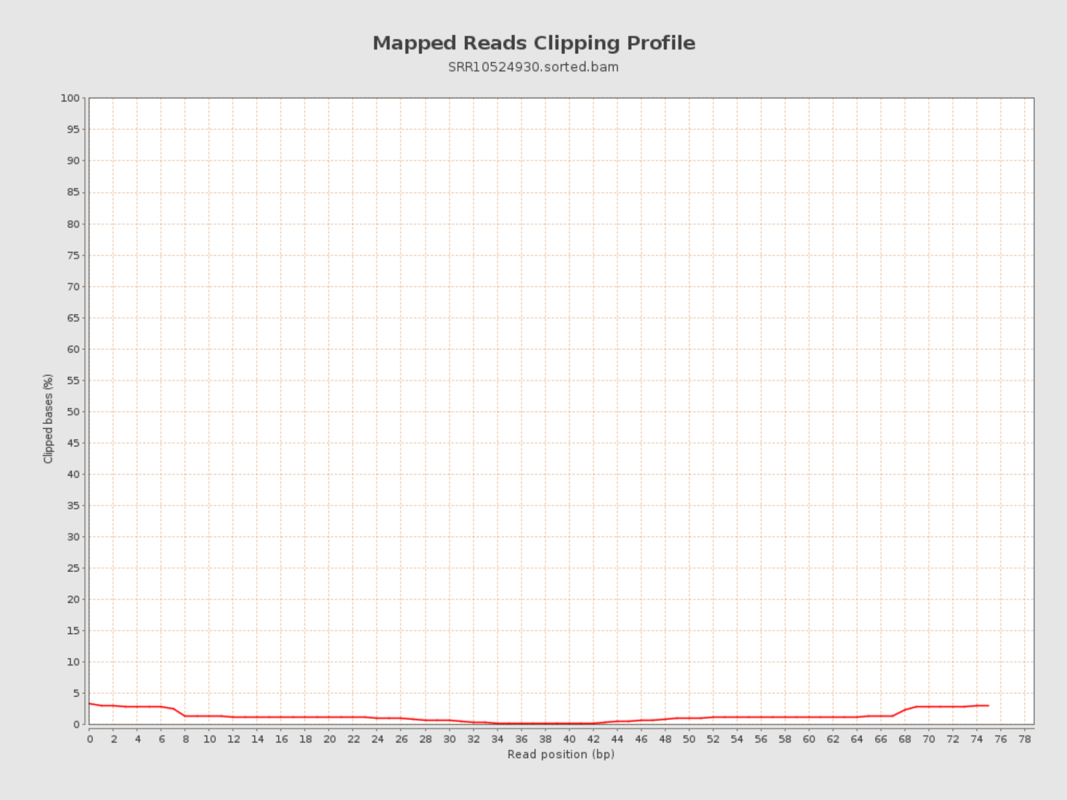
8. Results : Mapped Reads Nucleotide Content



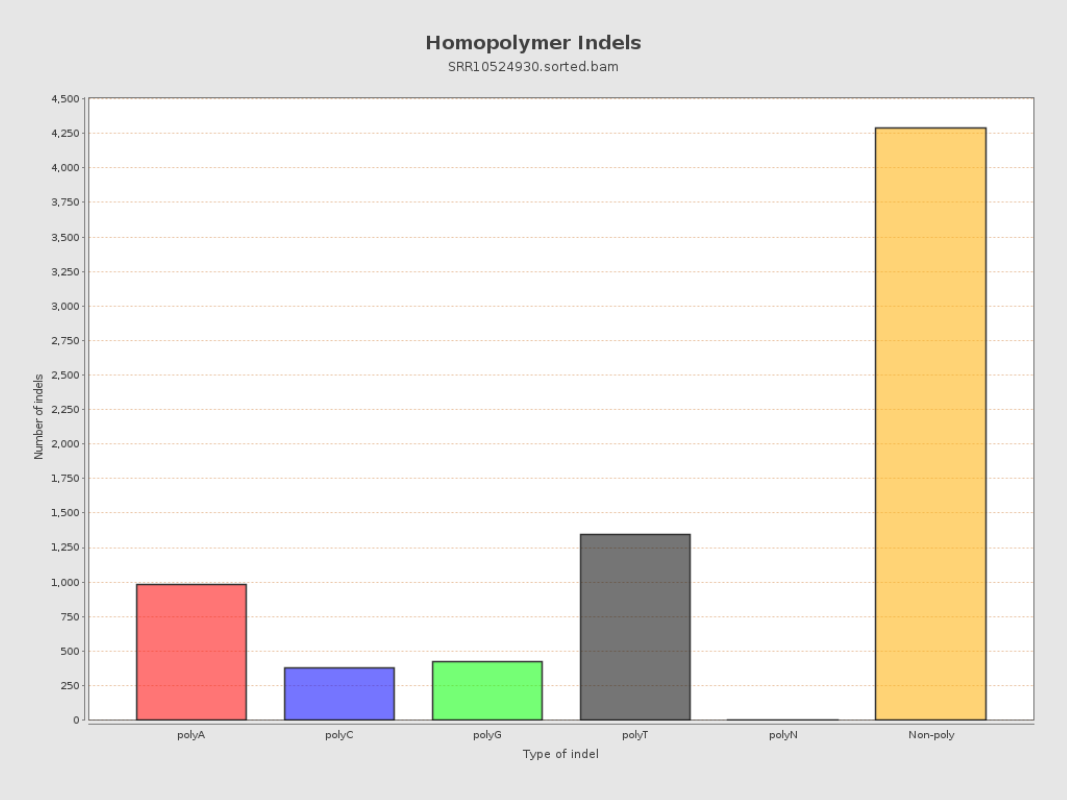
9. Results : Mapped Reads GC-content Distribution



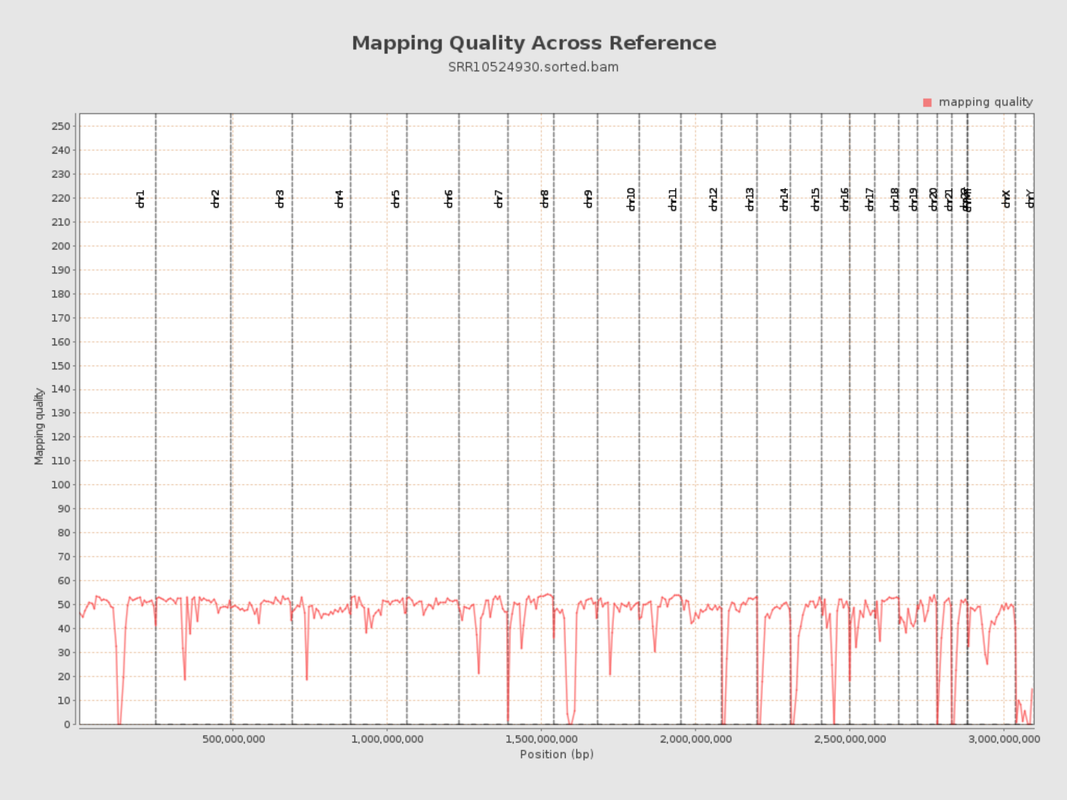
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram