Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:36:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524475.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_SRR10524475 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524475.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:36:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524475.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	821,960
Mapped reads	761,984 / 92.7%
Unmapped reads	59,976 / 7.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,686 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	21,661 / 2.64%
Duplication rate	2.19%
Clipped reads	761,559 / 92.65%

2.2. ACGT Content

Number/percentage of A's	11,008,413 / 24.79%
Number/percentage of C's	8,254,364 / 18.59%
Number/percentage of T's	14,259,350 / 32.12%
Number/percentage of G's	10,875,928 / 24.5%
Number/percentage of N's	939 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.1603

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

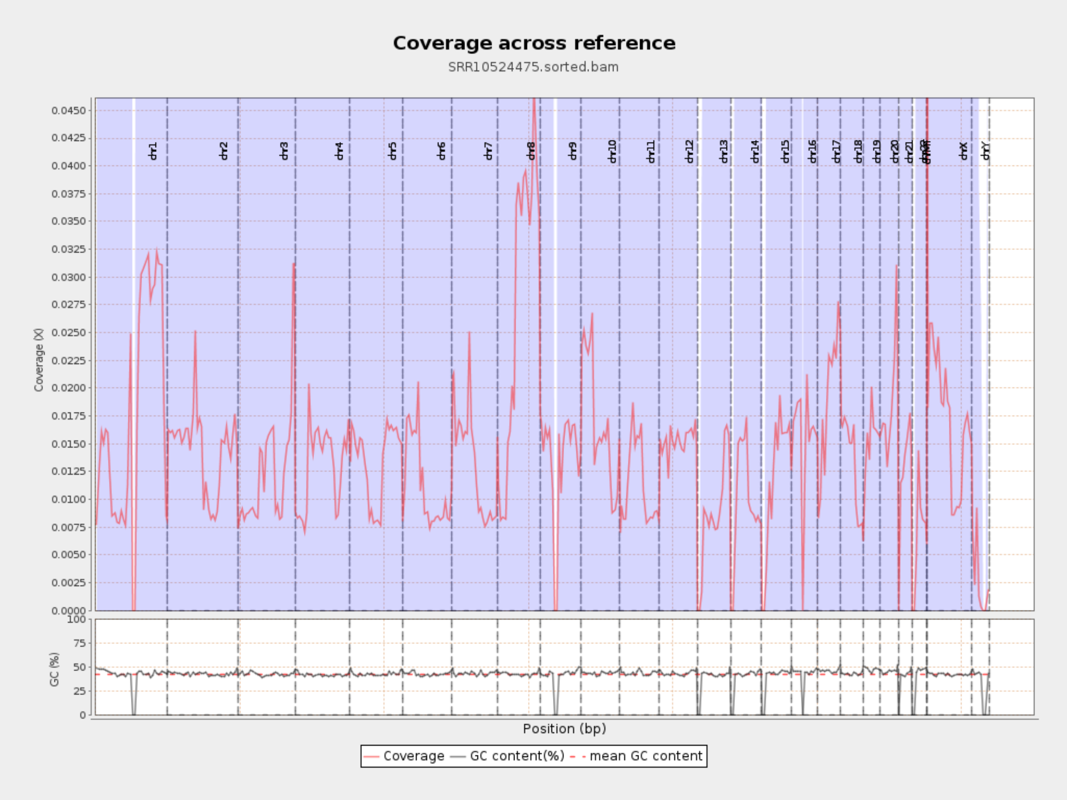
General error rate	0.48%
Mismatches	208,208
Insertions	2,916
Mapped reads with at least one insertion	0.38%
Deletions	8,500
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.67%

2.6. Chromosome stats

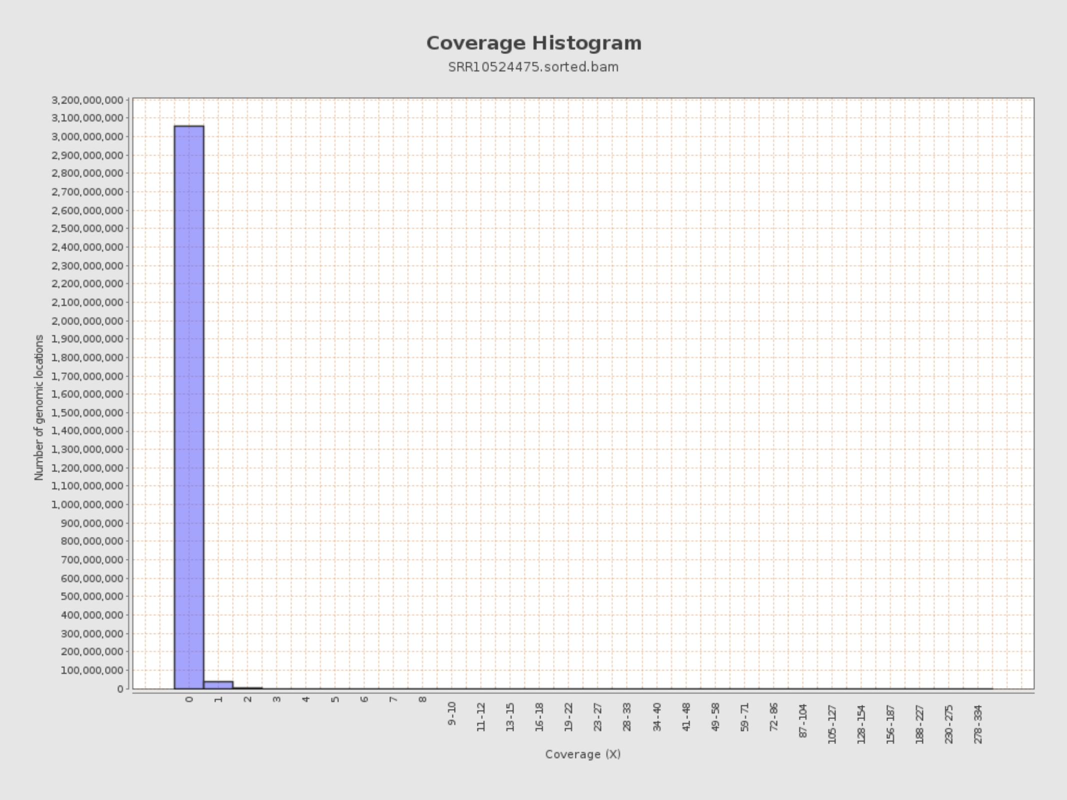
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4384591	0.0176	0.2644
chr2	243199373	3539242	0.0146	0.1694
chr3	198022430	2459731	0.0124	0.1183
chr4	191154276	2500520	0.0131	0.1299
chr5	180915260	2440337	0.0135	0.1229
chr6	171115067	1927242	0.0113	0.1292
chr7	159138663	2109220	0.0133	0.1976

chr8	146364022	4043867	0.0276	0.1918
chr9	141213431	1898542	0.0134	0.1475
chr10	135534747	2336688	0.0172	0.1699
chr11	135006516	1540757	0.0114	0.1521
chr12	133851895	2045494	0.0153	0.1308
chr13	115169878	1003024	0.0087	0.0987
chr14	107349540	1064745	0.0099	0.1064
chr15	102531392	1221346	0.0119	0.1186
chr16	90354753	1381852	0.0153	0.1359
chr17	81195210	1537624	0.0189	0.1498
chr18	78077248	1043470	0.0134	0.2154
chr19	59128983	908392	0.0154	0.2005
chr20	63025520	1194276	0.0189	0.1465
chr21	48129895	618741	0.0129	0.1248
chr22	51304566	356654	0.007	0.0883
chrMT	16571	5590	0.3373	0.6443
chrX	155270560	2698486	0.0174	0.1476
chrY	59373566	153202	0.0026	0.0802

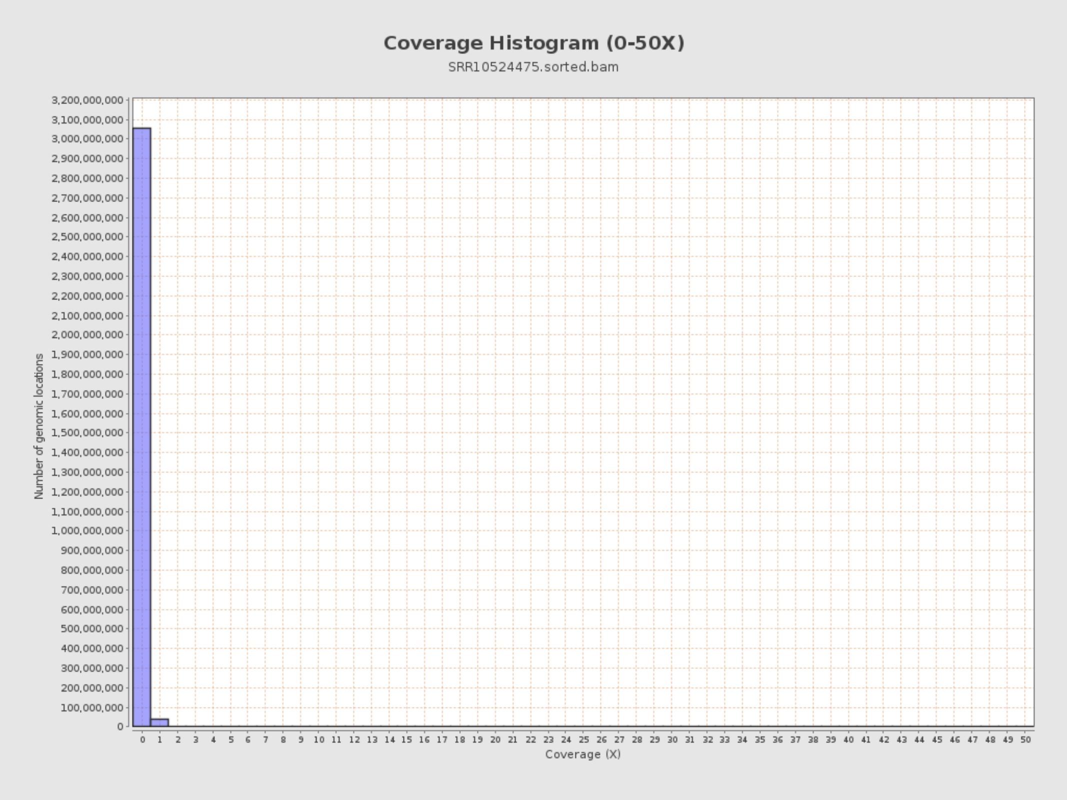
3. Results : Coverage across reference



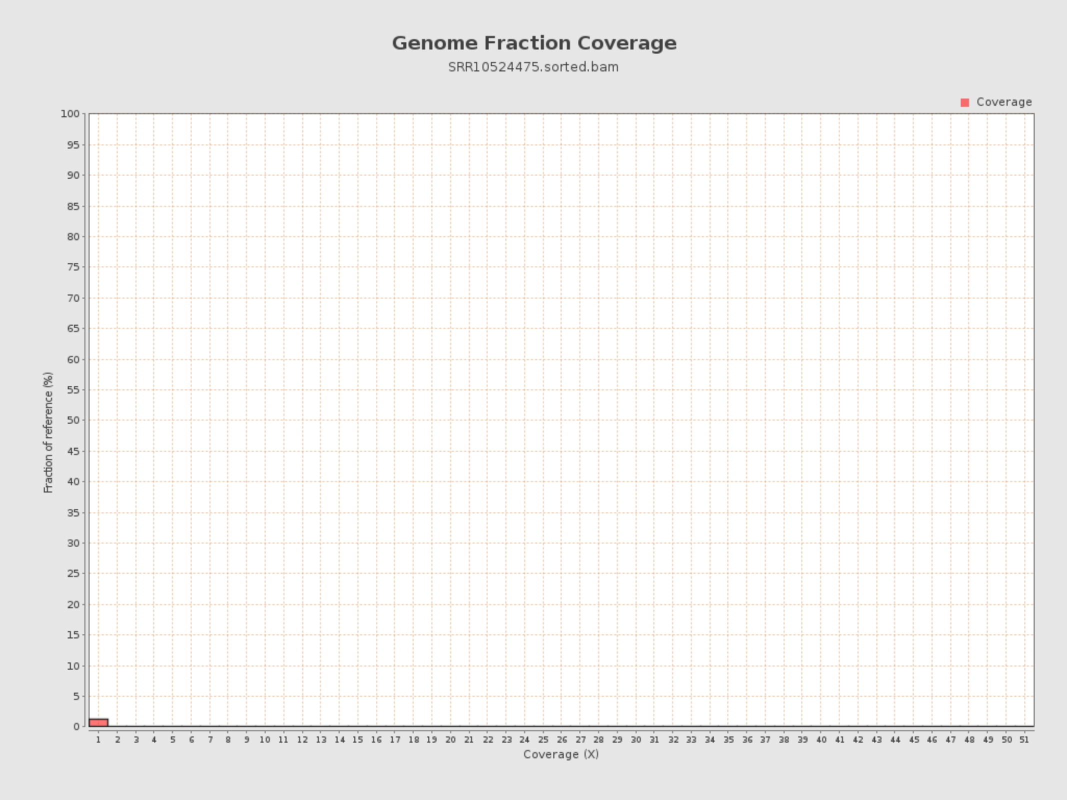
4. Results : Coverage Histogram



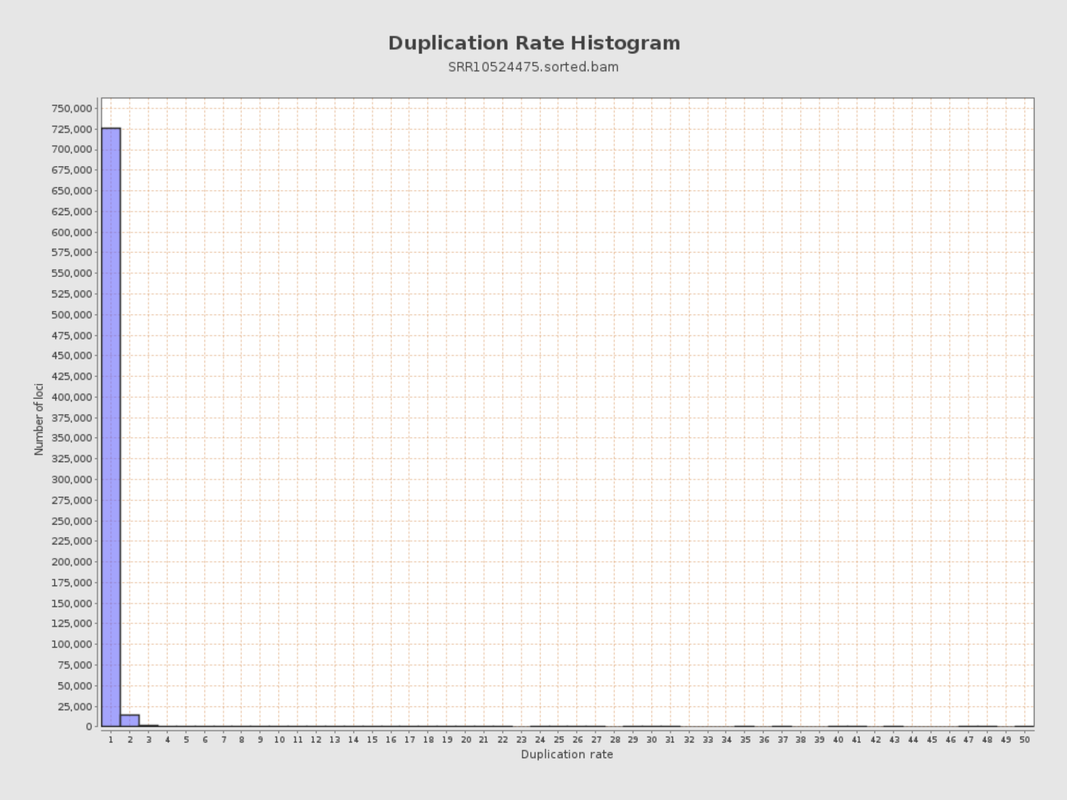
5. Results : Coverage Histogram (0-50X)



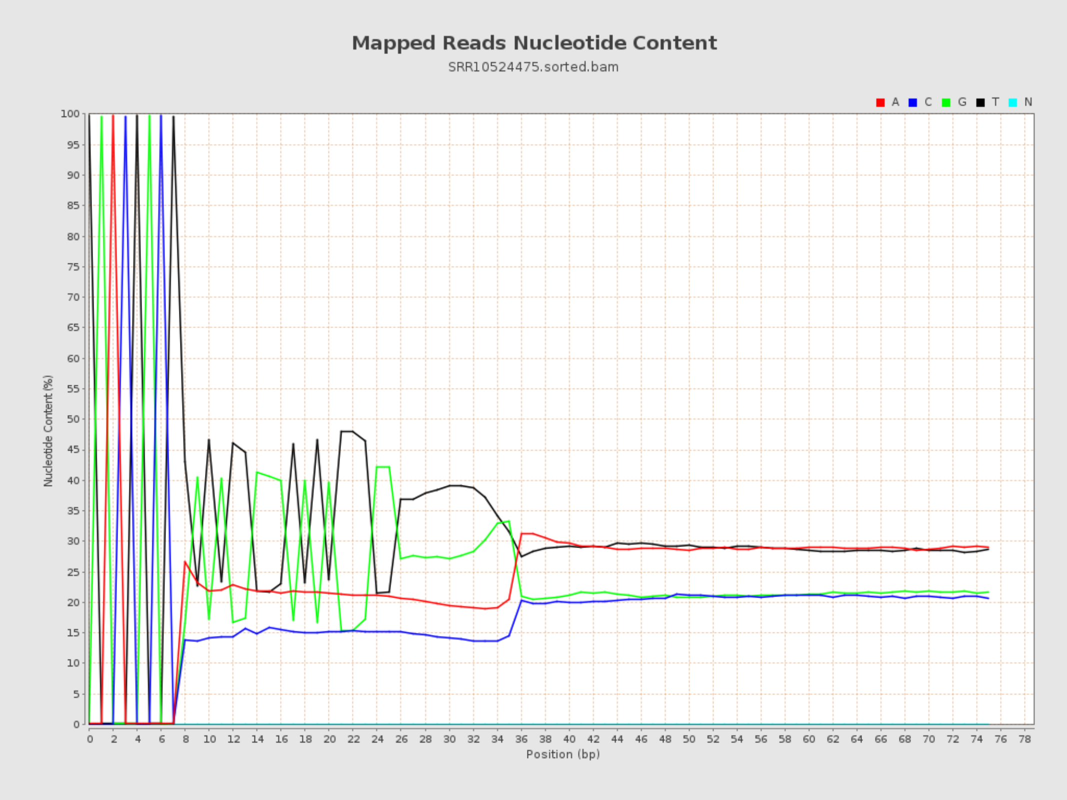
6. Results : Genome Fraction Coverage



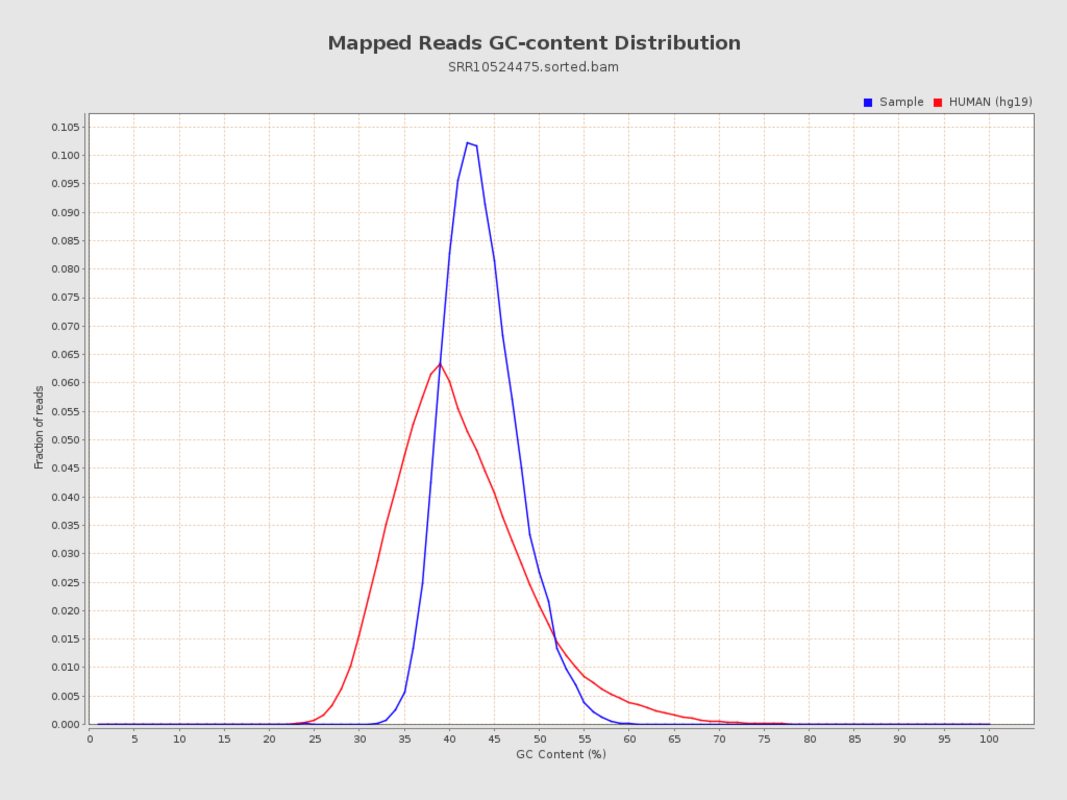
7. Results : Duplication Rate Histogram



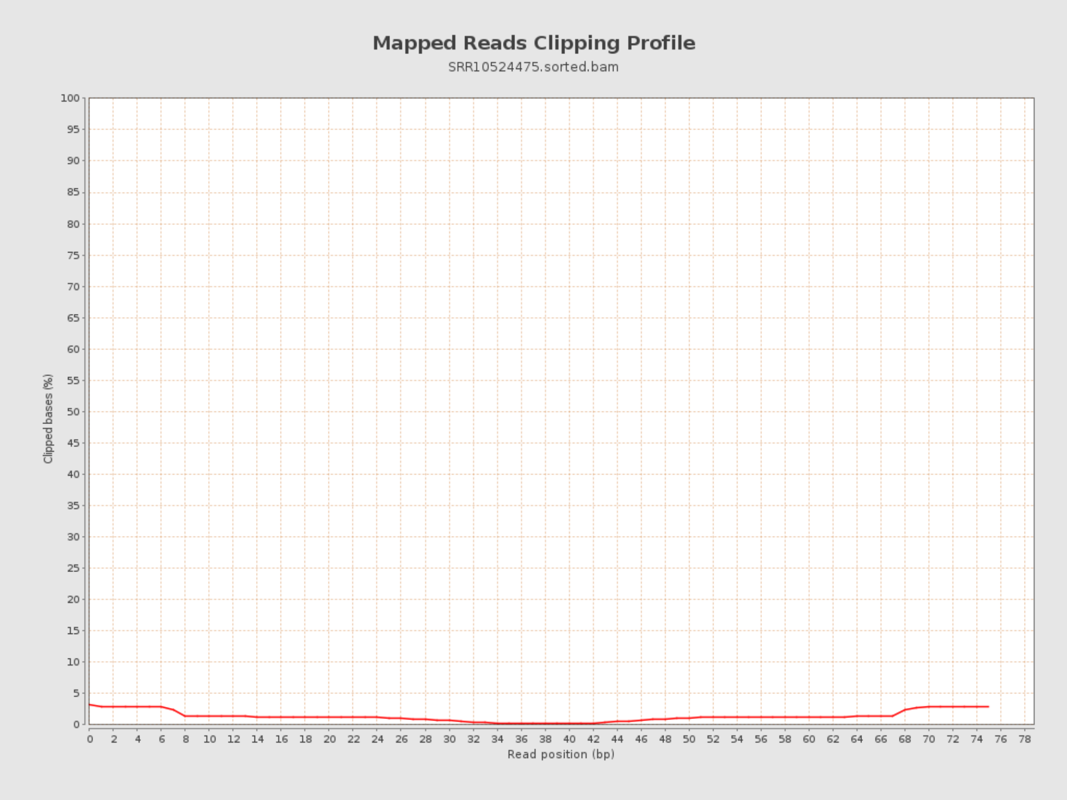
8. Results : Mapped Reads Nucleotide Content



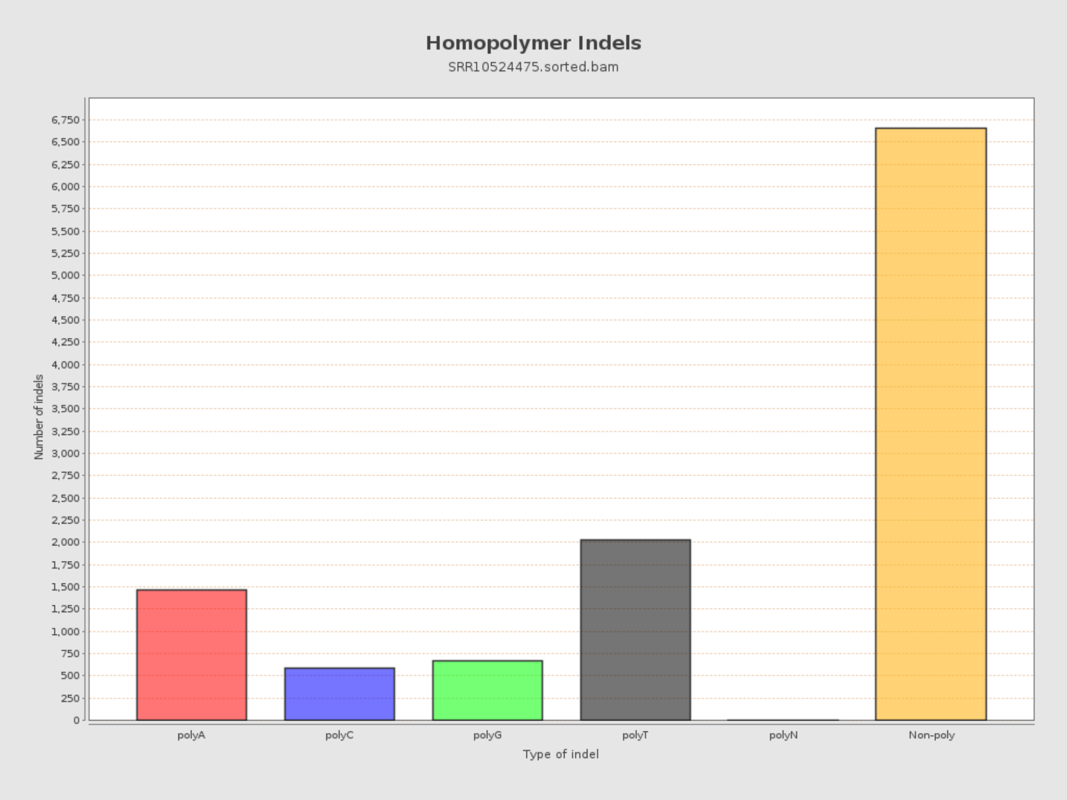
9. Results : Mapped Reads GC-content Distribution



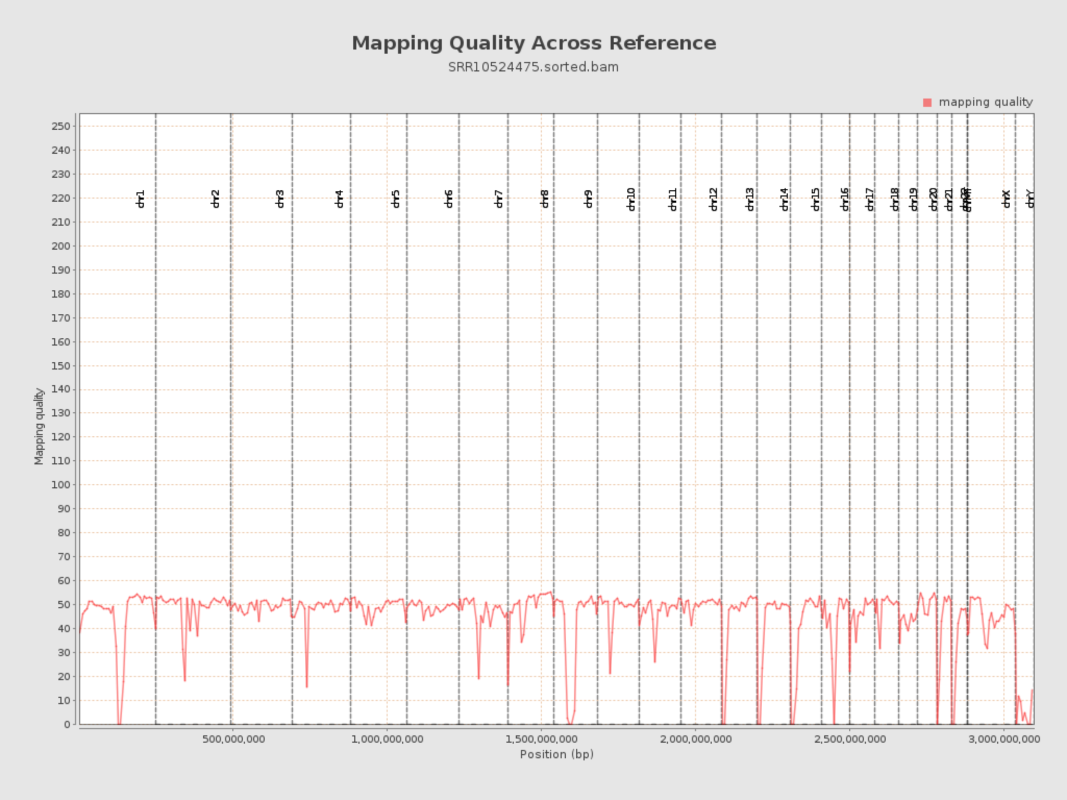
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram