Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:12:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524465.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_SRR10524465 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524465.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:12:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524465.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	812,293
Mapped reads	738,880 / 90.96%
Unmapped reads	73,413 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,549 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	25,537 / 3.14%
Duplication rate	2.72%
Clipped reads	738,877 / 90.96%

2.2. ACGT Content

Number/percentage of A's	10,732,308 / 25.23%
Number/percentage of C's	7,802,820 / 18.35%
Number/percentage of T's	13,782,366 / 32.4%
Number/percentage of G's	10,213,640 / 24.01%
Number/percentage of N's	848 / 0%
GC Percentage	42.36%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.1578

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

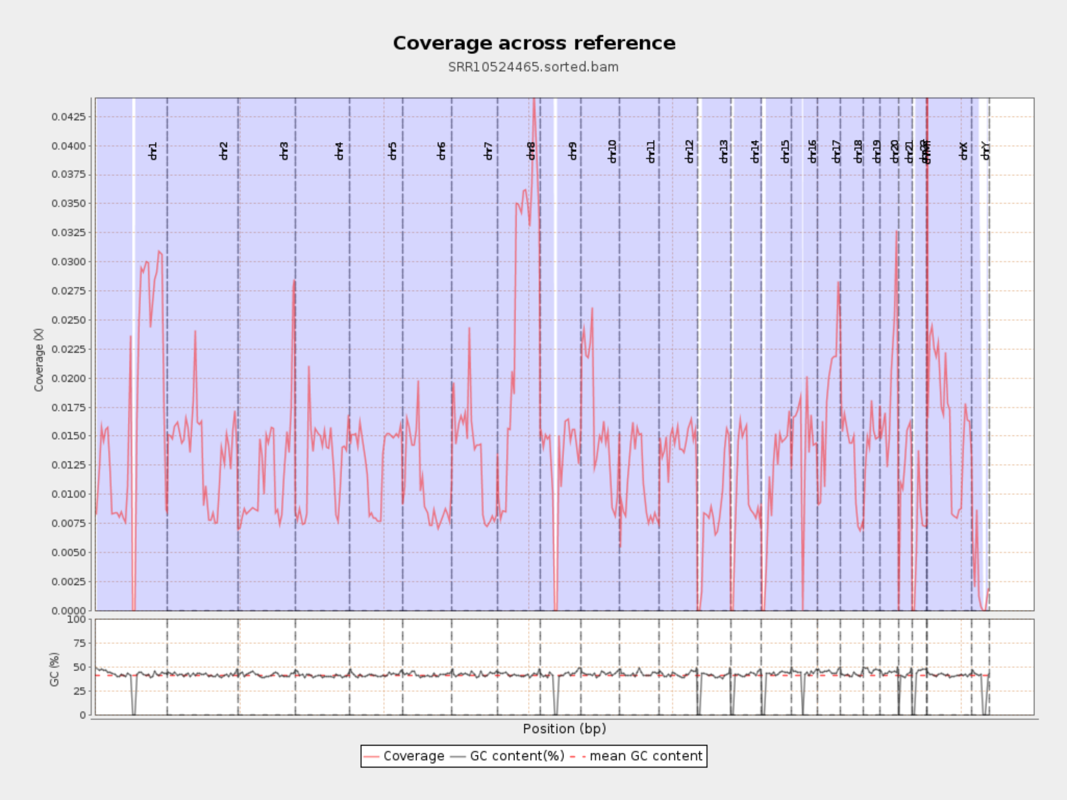
General error rate	0.49%
Mismatches	201,839
Insertions	2,546
Mapped reads with at least one insertion	0.34%
Deletions	7,774
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.69%

2.6. Chromosome stats

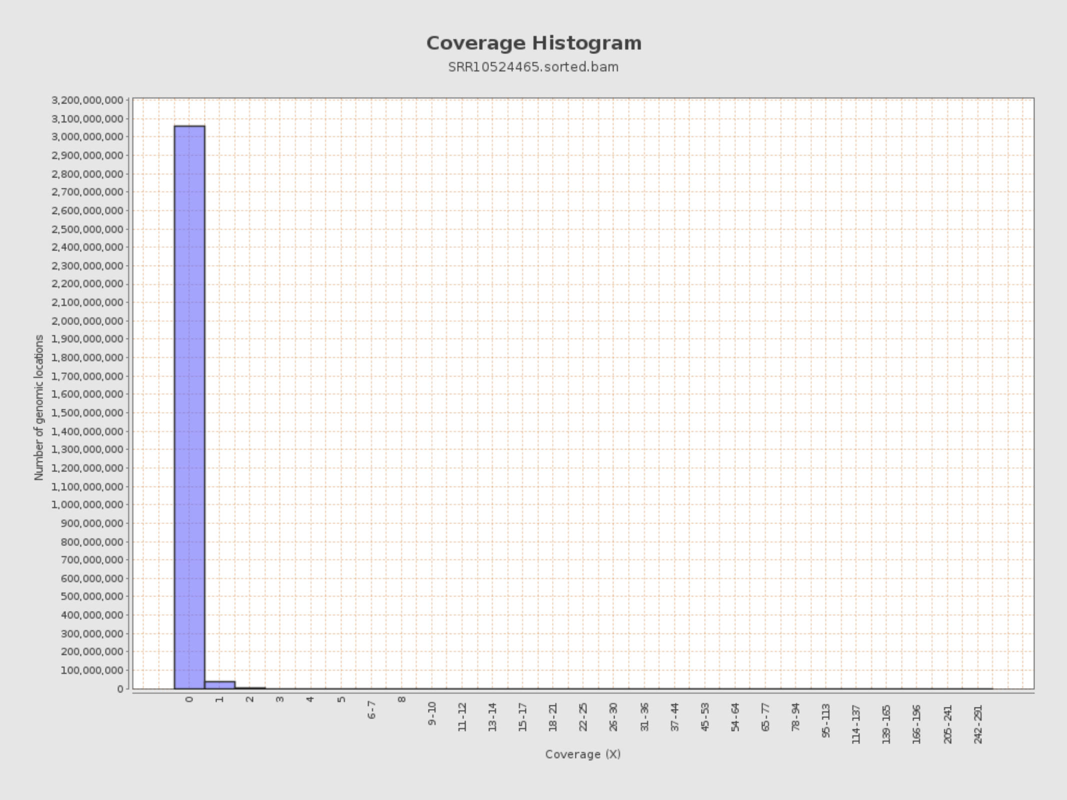
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4209454	0.0169	0.2482
chr2	243199373	3359741	0.0138	0.1857
chr3	198022430	2336196	0.0118	0.116
chr4	191154276	2412832	0.0126	0.1295
chr5	180915260	2353189	0.013	0.1218
chr6	171115067	1823712	0.0107	0.1285
chr7	159138663	2148865	0.0135	0.2022

chr8	146364022	3866047	0.0264	0.1884
chr9	141213431	1803123	0.0128	0.1407
chr10	135534747	2218590	0.0164	0.1603
chr11	135006516	1465641	0.0109	0.1474
chr12	133851895	1934948	0.0145	0.1287
chr13	115169878	949558	0.0082	0.0979
chr14	107349540	1049679	0.0098	0.1067
chr15	102531392	1135243	0.0111	0.1145
chr16	90354753	1302502	0.0144	0.1341
chr17	81195210	1471024	0.0181	0.1475
chr18	78077248	989119	0.0127	0.2089
chr19	59128983	865806	0.0146	0.1868
chr20	63025520	1227371	0.0195	0.1507
chr21	48129895	580723	0.0121	0.1244
chr22	51304566	341331	0.0067	0.0868
chrMT	16571	3237	0.1953	0.4497
chrX	155270560	2556263	0.0165	0.146
chrY	59373566	141066	0.0024	0.0769

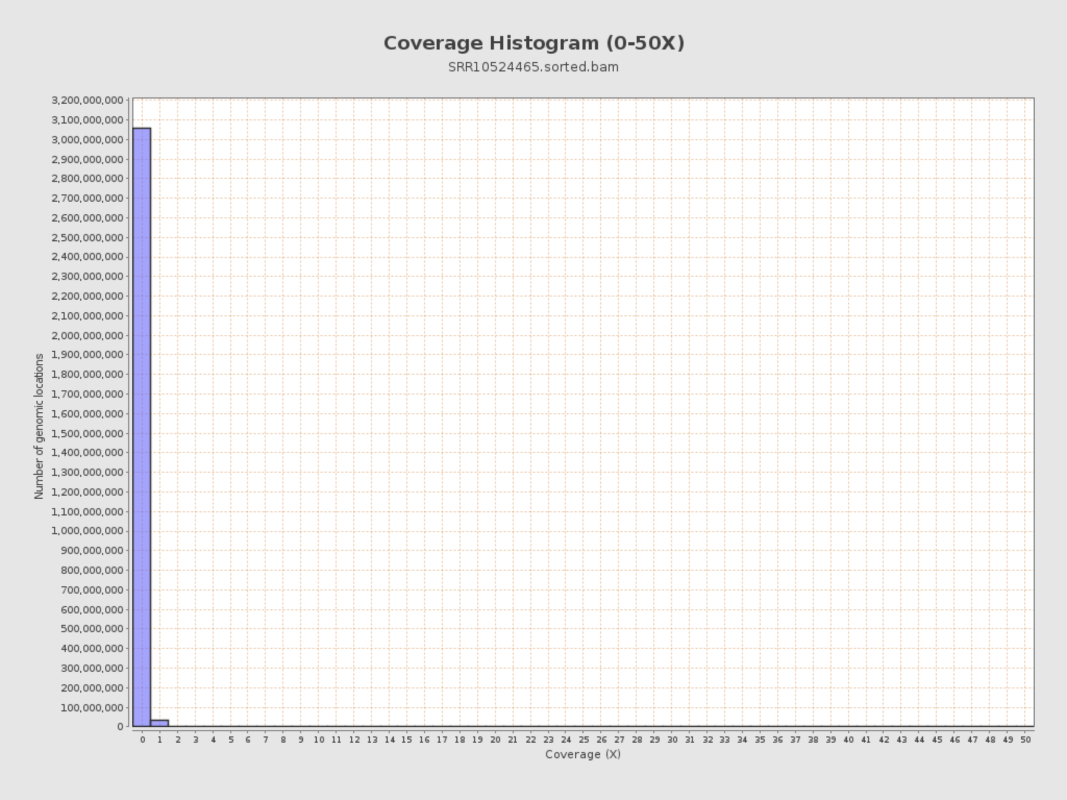
3. Results : Coverage across reference



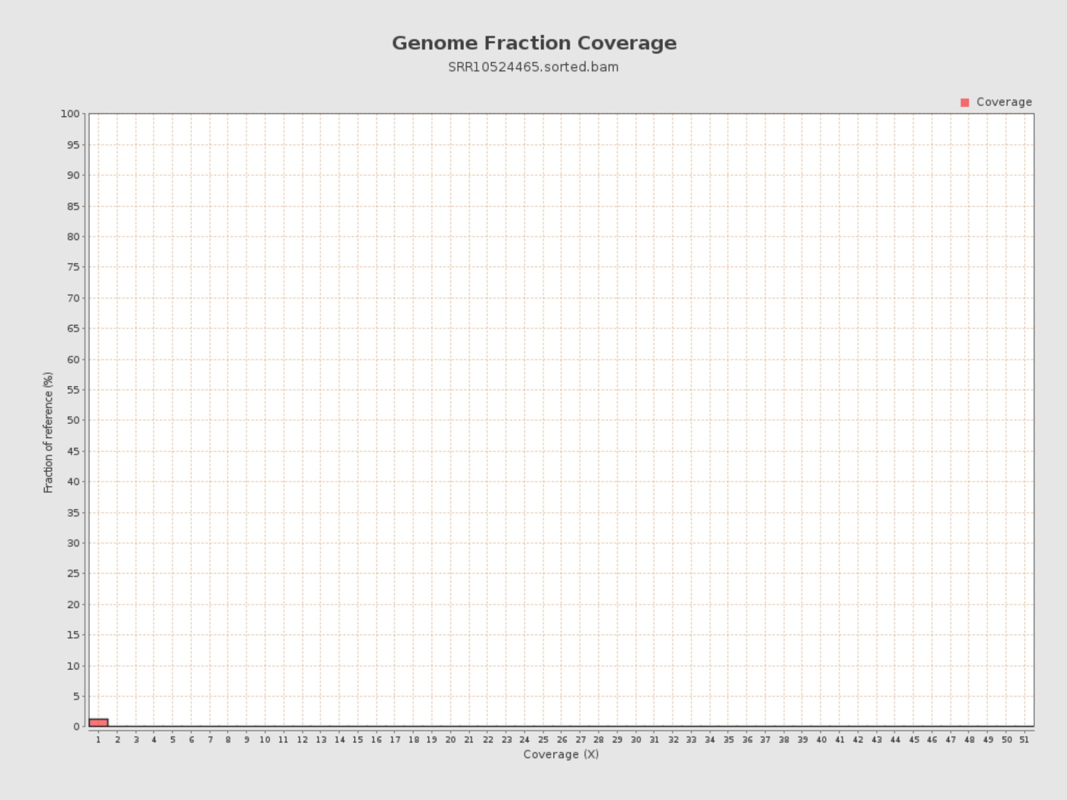
4. Results : Coverage Histogram



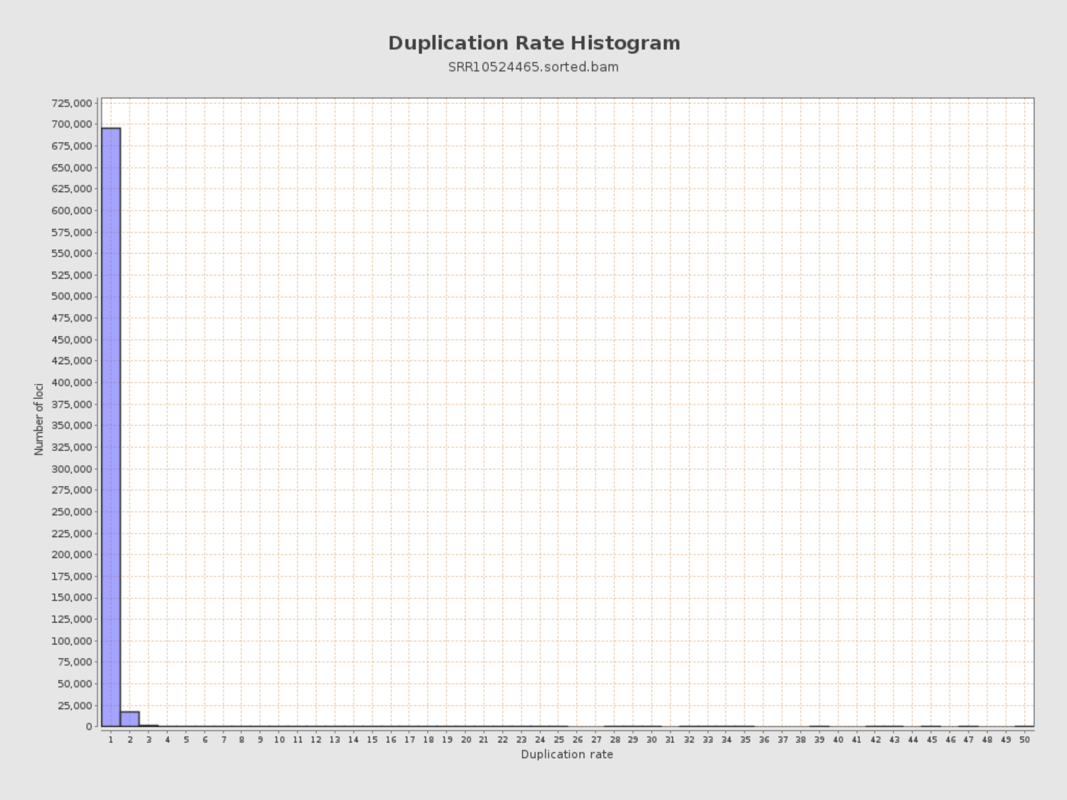
5. Results : Coverage Histogram (0-50X)



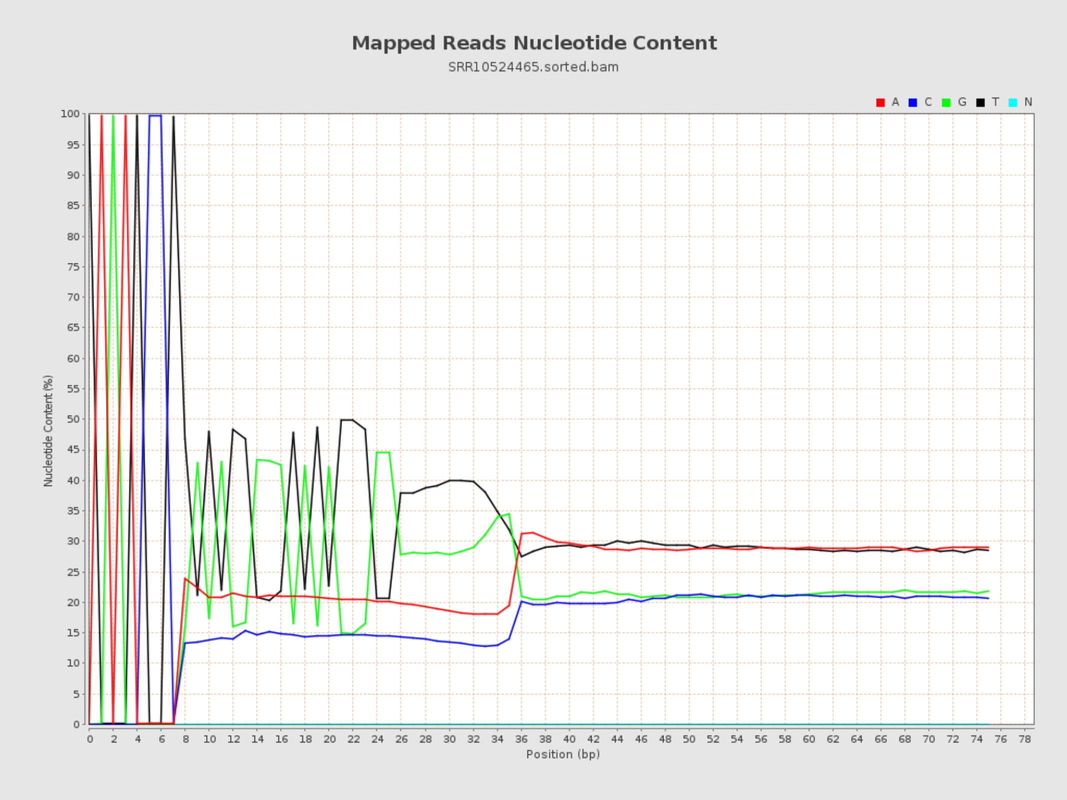
6. Results : Genome Fraction Coverage



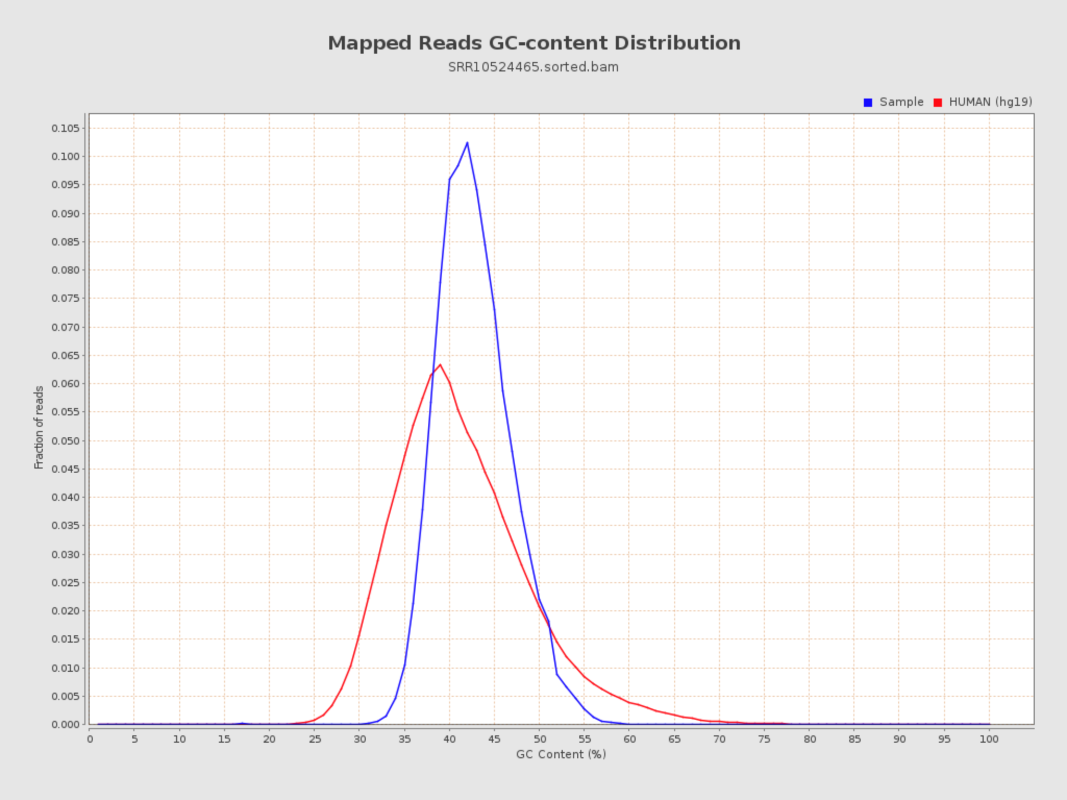
7. Results : Duplication Rate Histogram



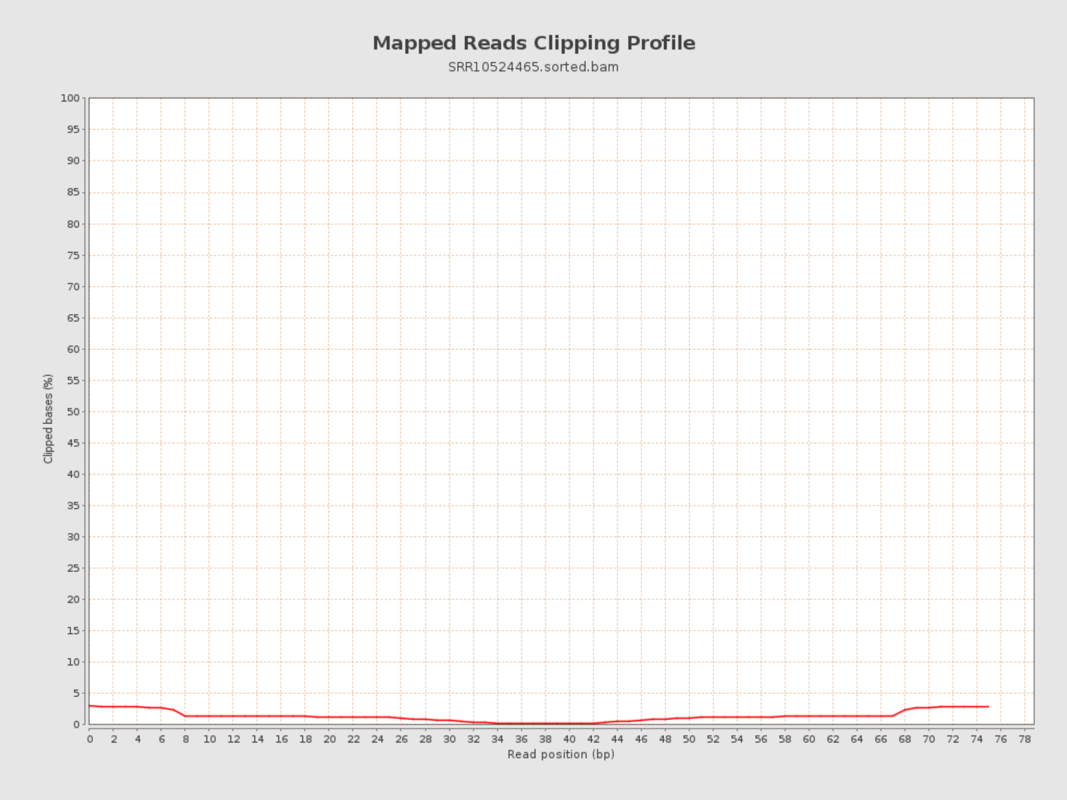
8. Results : Mapped Reads Nucleotide Content



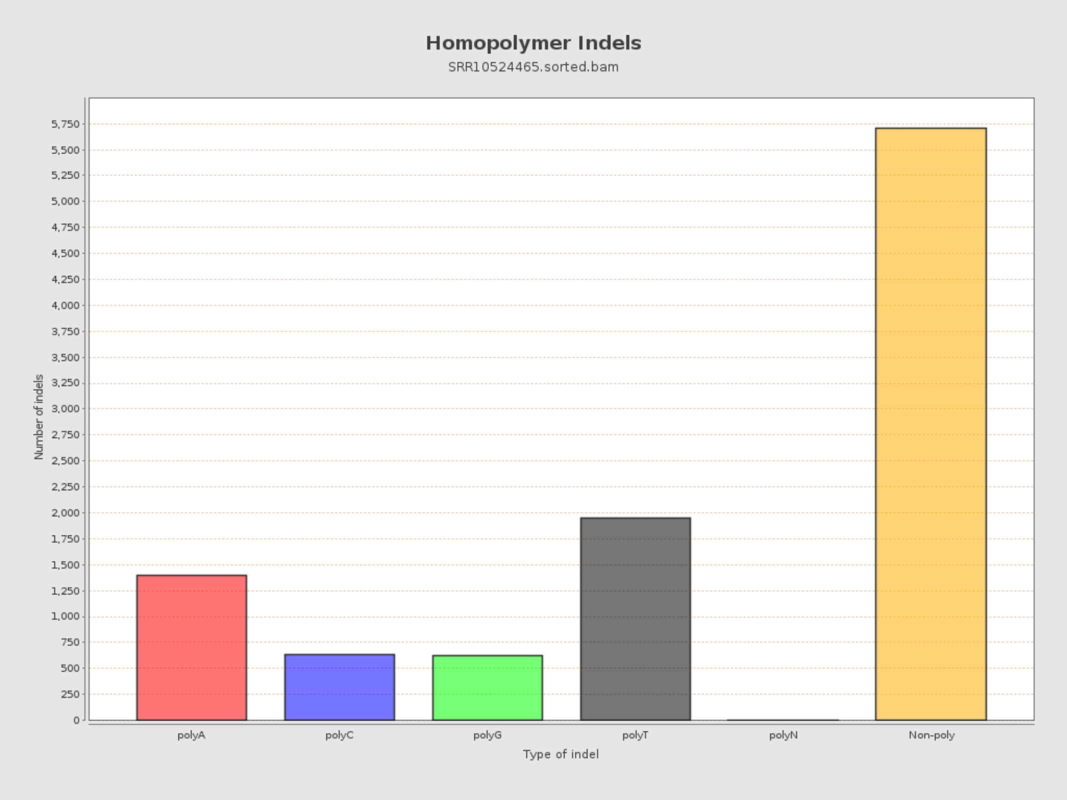
9. Results : Mapped Reads GC-content Distribution



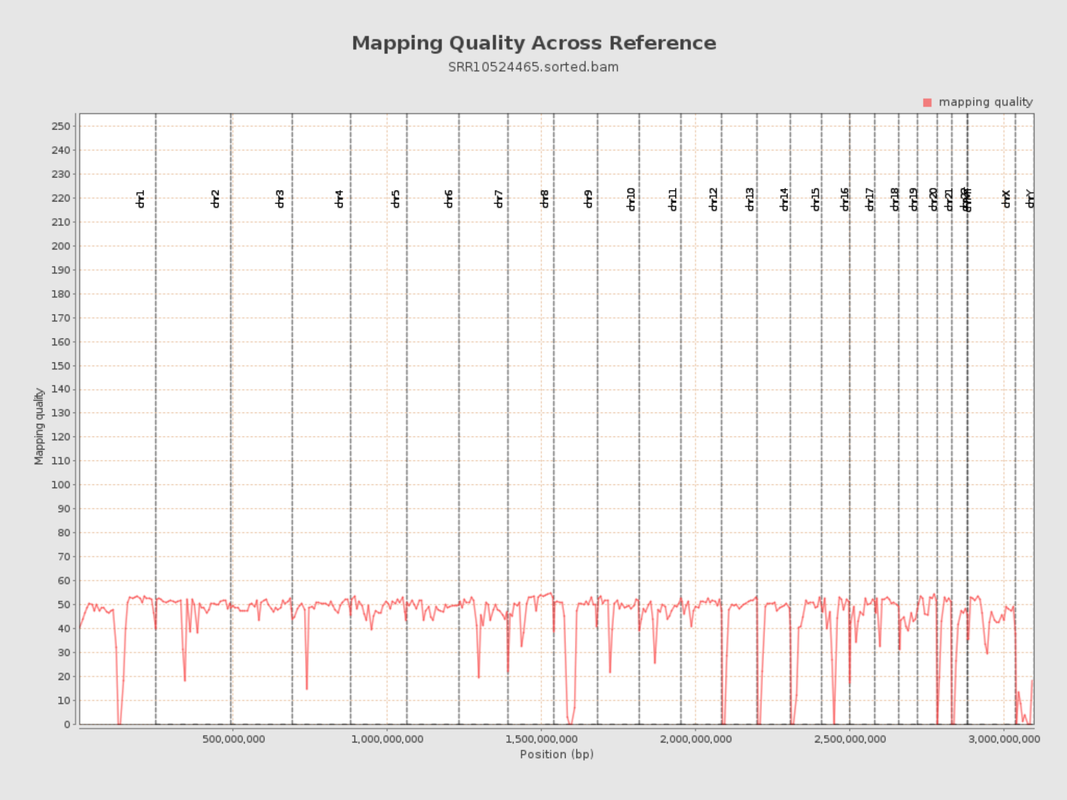
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram