Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:00:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524543.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_SRR10524543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524543.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:00:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,215,471
Mapped reads	1,123,292 / 92.42%
Unmapped reads	92,179 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,700 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	39,204 / 3.23%
Duplication rate	2.7%
Clipped reads	1,127,181 / 92.74%

2.2. ACGT Content

Number/percentage of A's	17,061,475 / 25.76%
Number/percentage of C's	12,022,130 / 18.15%
Number/percentage of T's	20,511,574 / 30.97%
Number/percentage of G's	16,631,711 / 25.11%
Number/percentage of N's	1,080 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.209

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

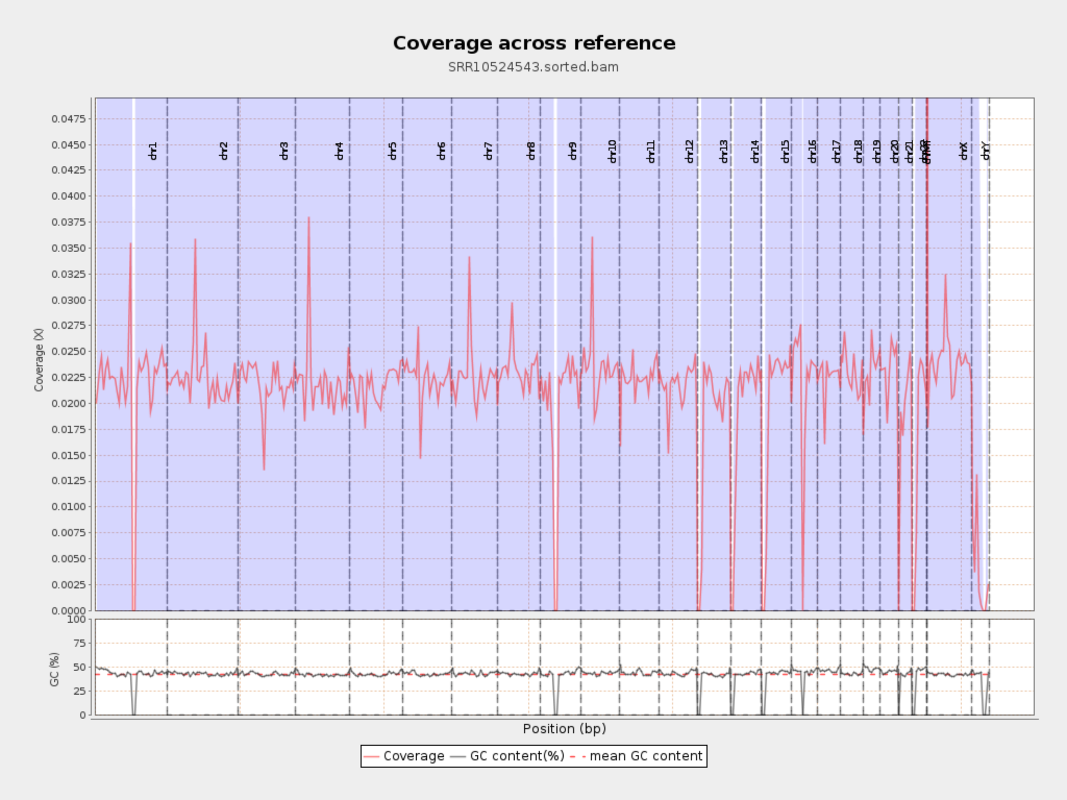
General error rate	0.5%
Mismatches	323,861
Insertions	3,726
Mapped reads with at least one insertion	0.33%
Deletions	12,114
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.46%

2.6. Chromosome stats

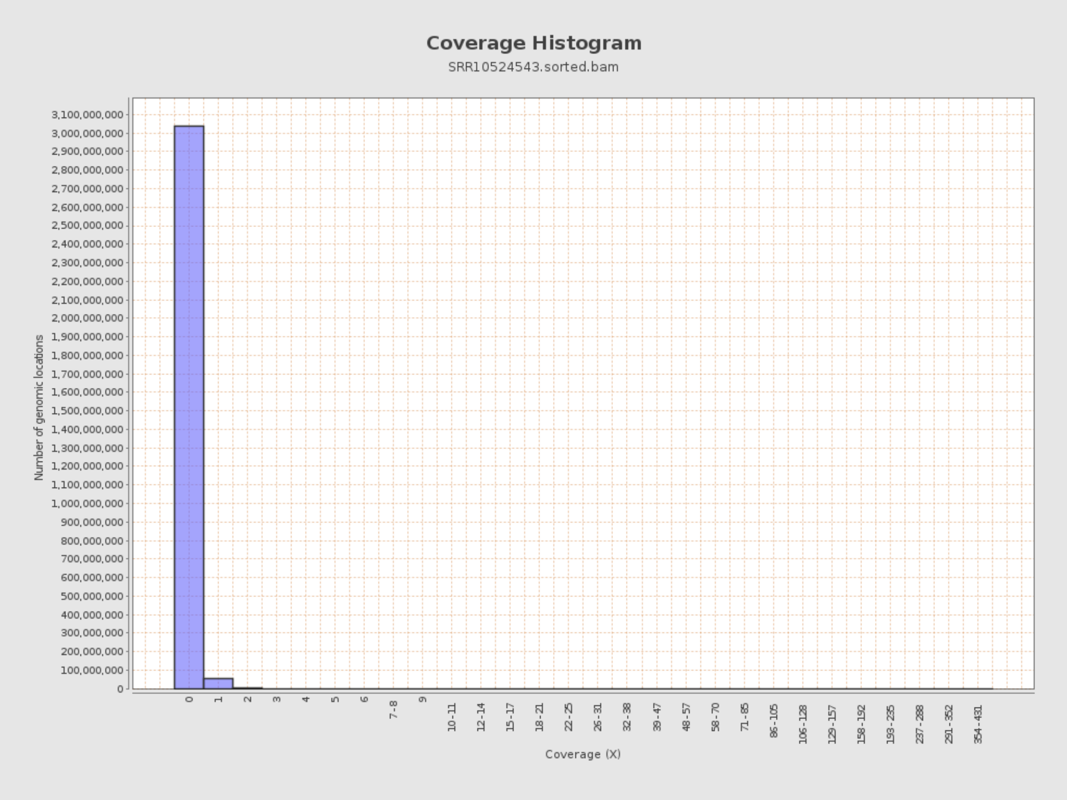
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5379497	0.0216	0.3552
chr2	243199373	5484822	0.0226	0.2321
chr3	198022430	4326820	0.0219	0.1591
chr4	191154276	4240241	0.0222	0.1774
chr5	180915260	3946370	0.0218	0.1593
chr6	171115067	3827676	0.0224	0.1788
chr7	159138663	3611340	0.0227	0.2473

chr8	146364022	3408799	0.0233	0.2216
chr9	141213431	2745675	0.0194	0.1792
chr10	135534747	3210665	0.0237	0.2053
chr11	135006516	3039859	0.0225	0.199
chr12	133851895	2911162	0.0217	0.1598
chr13	115169878	2062564	0.0179	0.1438
chr14	107349540	2014637	0.0188	0.1493
chr15	102531392	1951184	0.019	0.149
chr16	90354753	1953491	0.0216	0.1658
chr17	81195210	1823258	0.0225	0.171
chr18	78077248	1795226	0.023	0.3278
chr19	59128983	1371033	0.0232	0.2465
chr20	63025520	1462655	0.0232	0.1659
chr21	48129895	911106	0.0189	0.1669
chr22	51304566	809419	0.0158	0.1349
chrMT	16571	7883	0.4757	0.7639
chrX	155270560	3740284	0.0241	0.179
chrY	59373566	212641	0.0036	0.1163

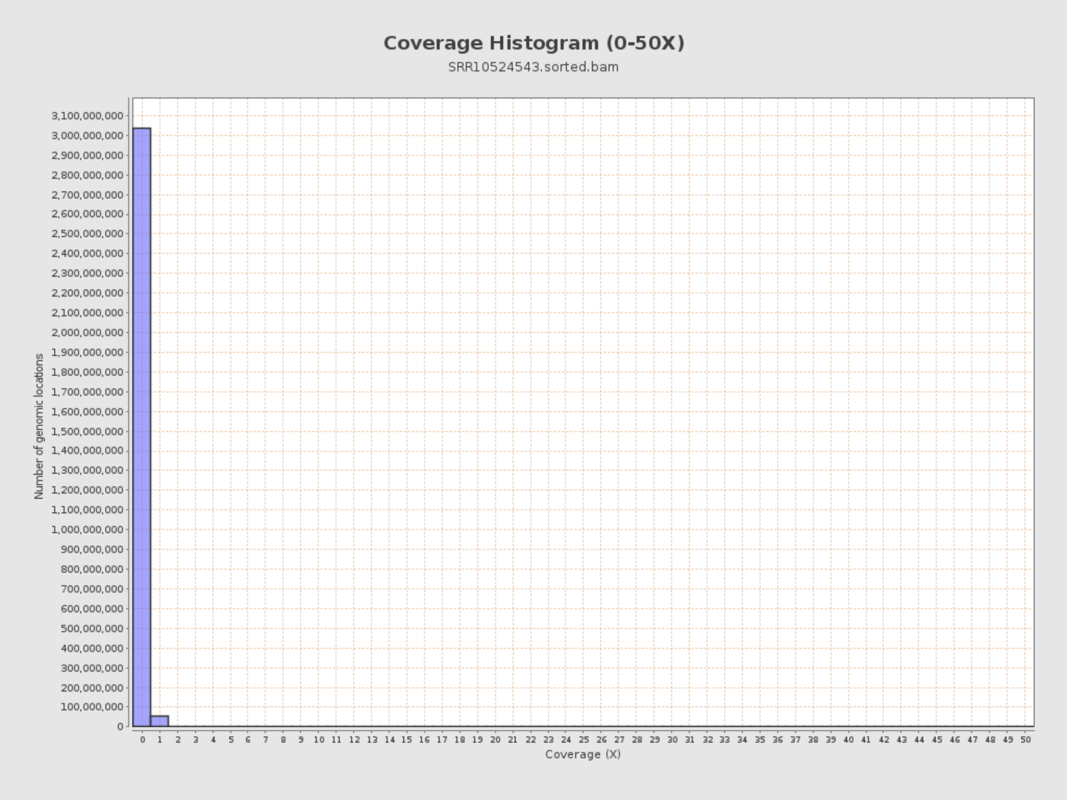
3. Results : Coverage across reference



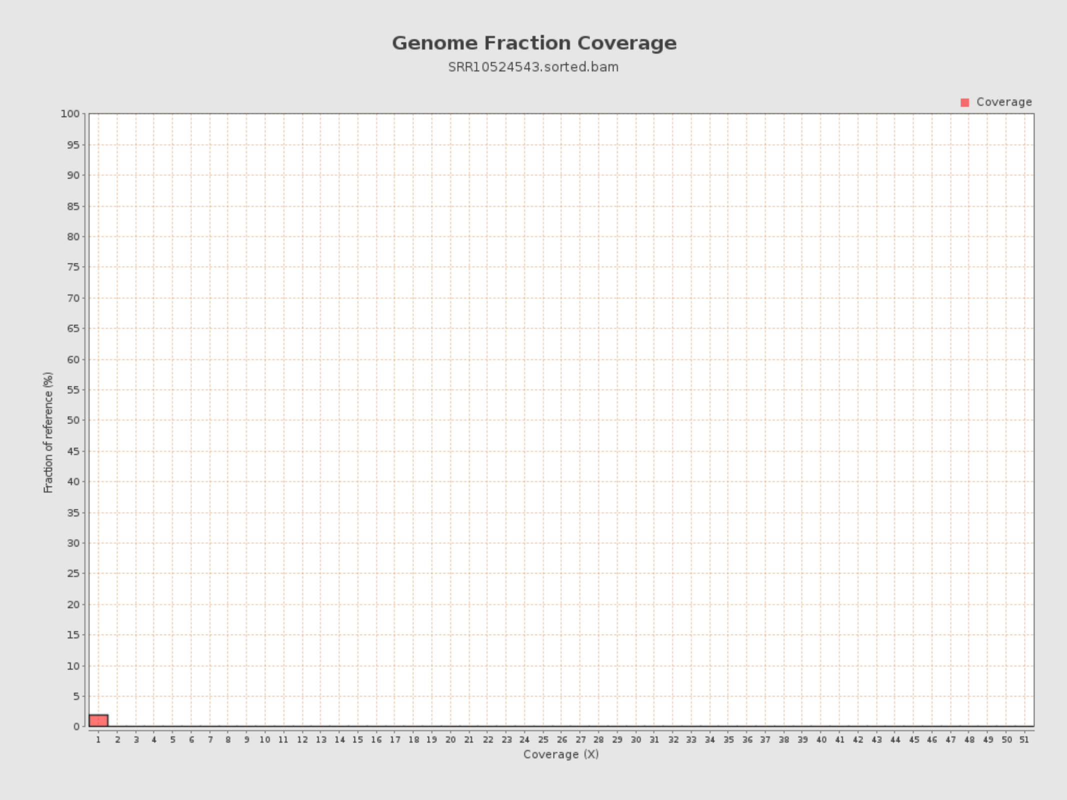
4. Results : Coverage Histogram



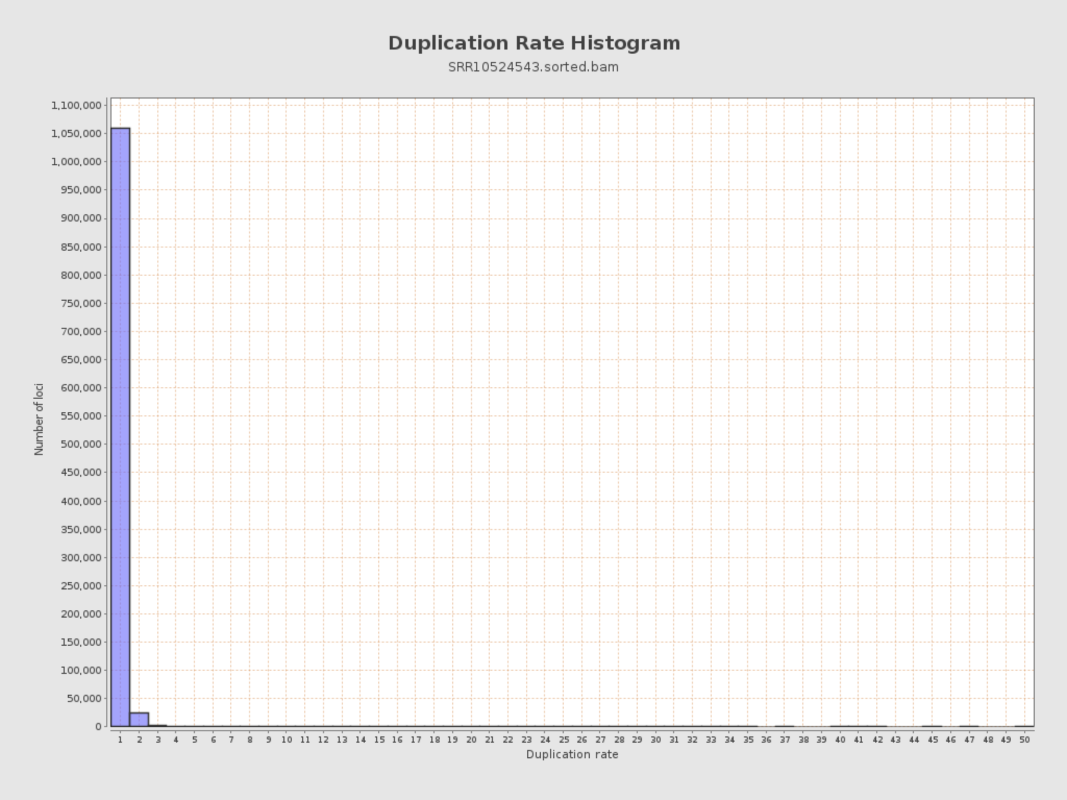
5. Results : Coverage Histogram (0-50X)



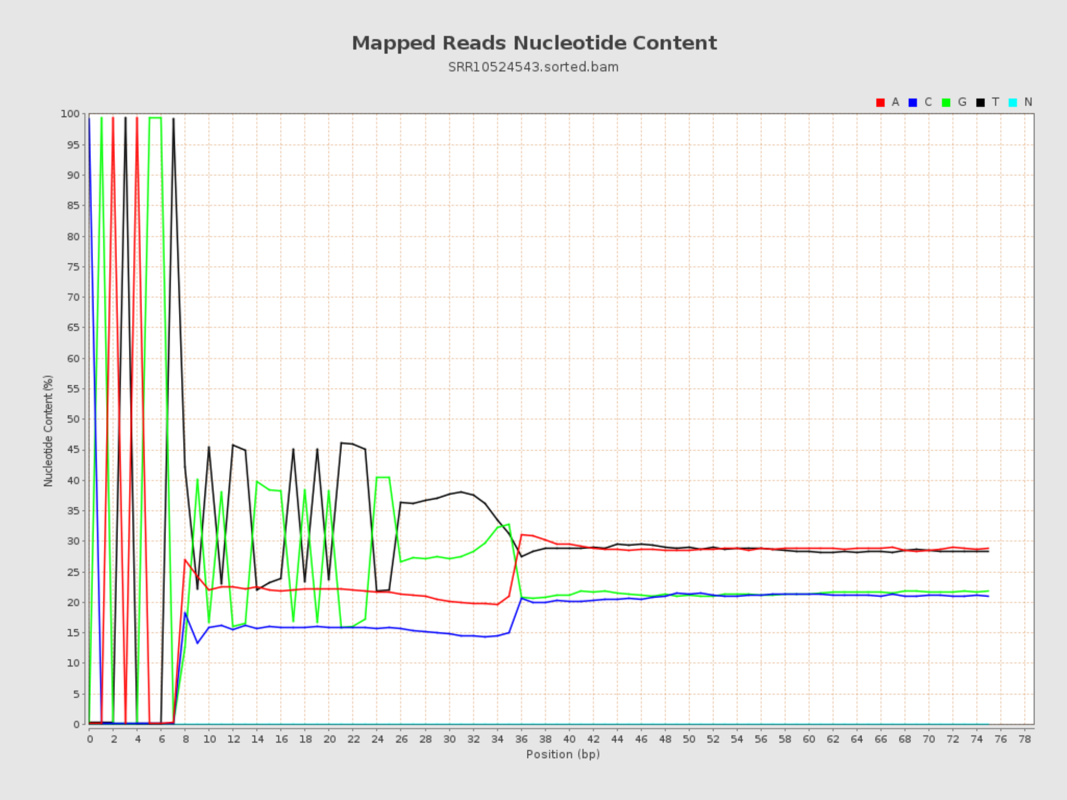
6. Results : Genome Fraction Coverage



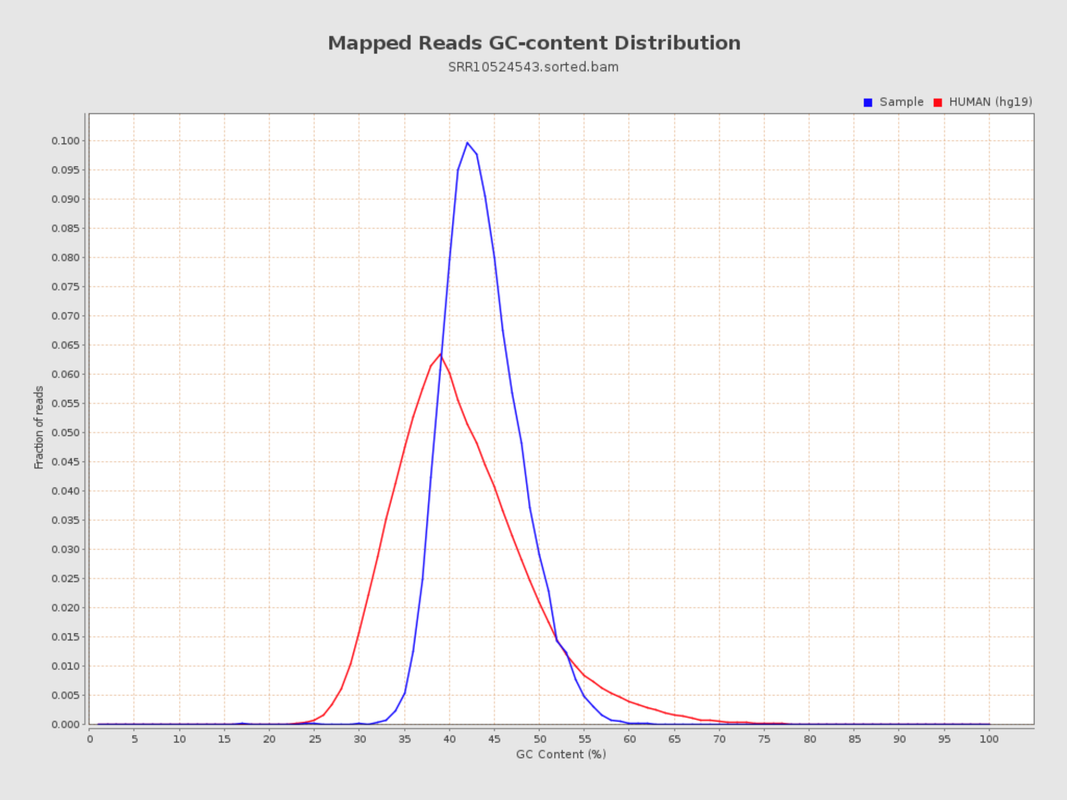
7. Results : Duplication Rate Histogram



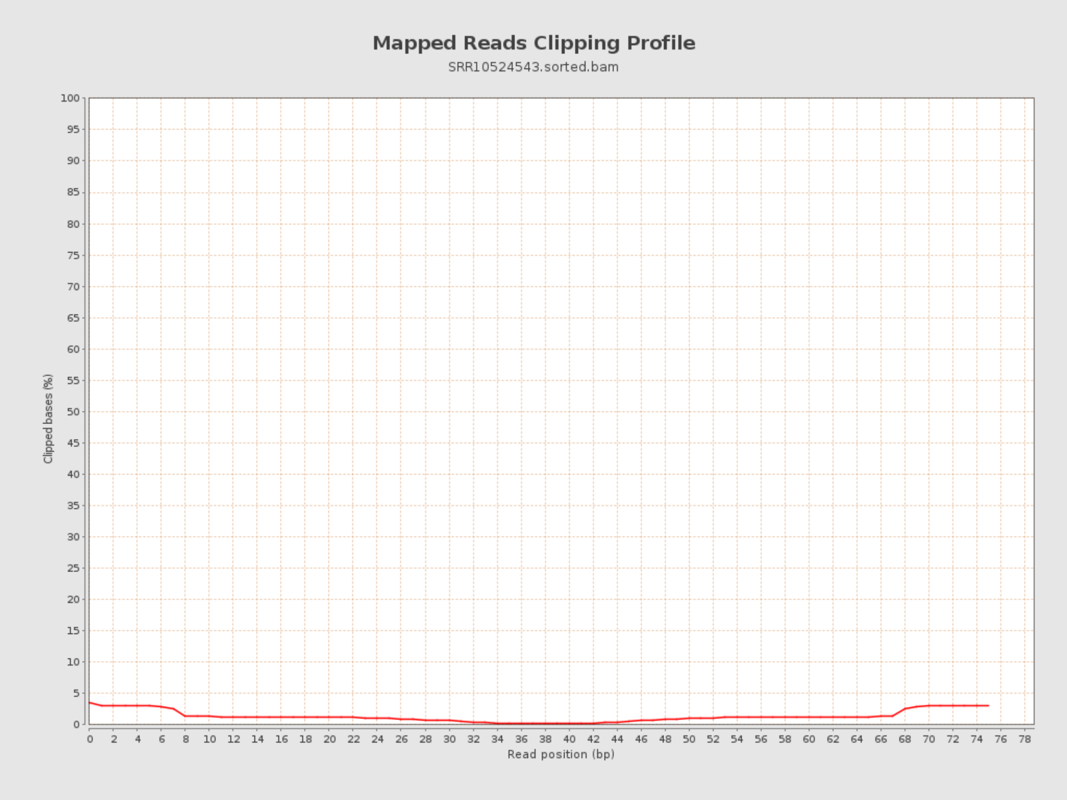
8. Results : Mapped Reads Nucleotide Content



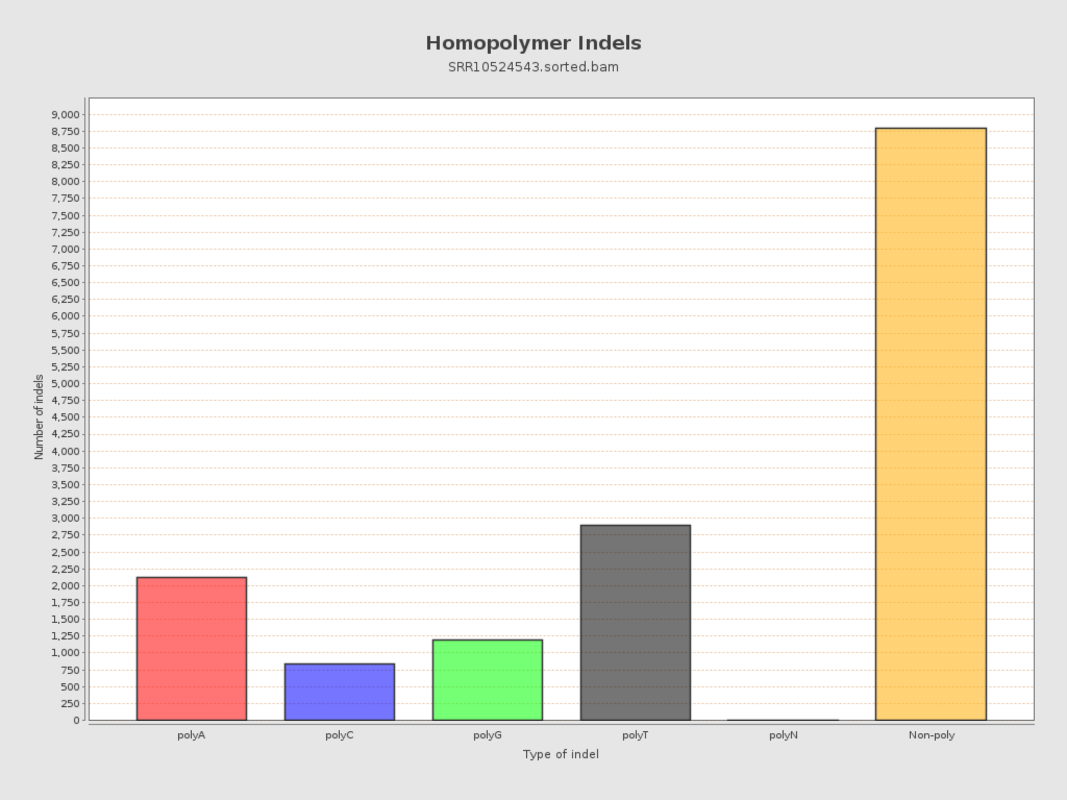
9. Results : Mapped Reads GC-content Distribution



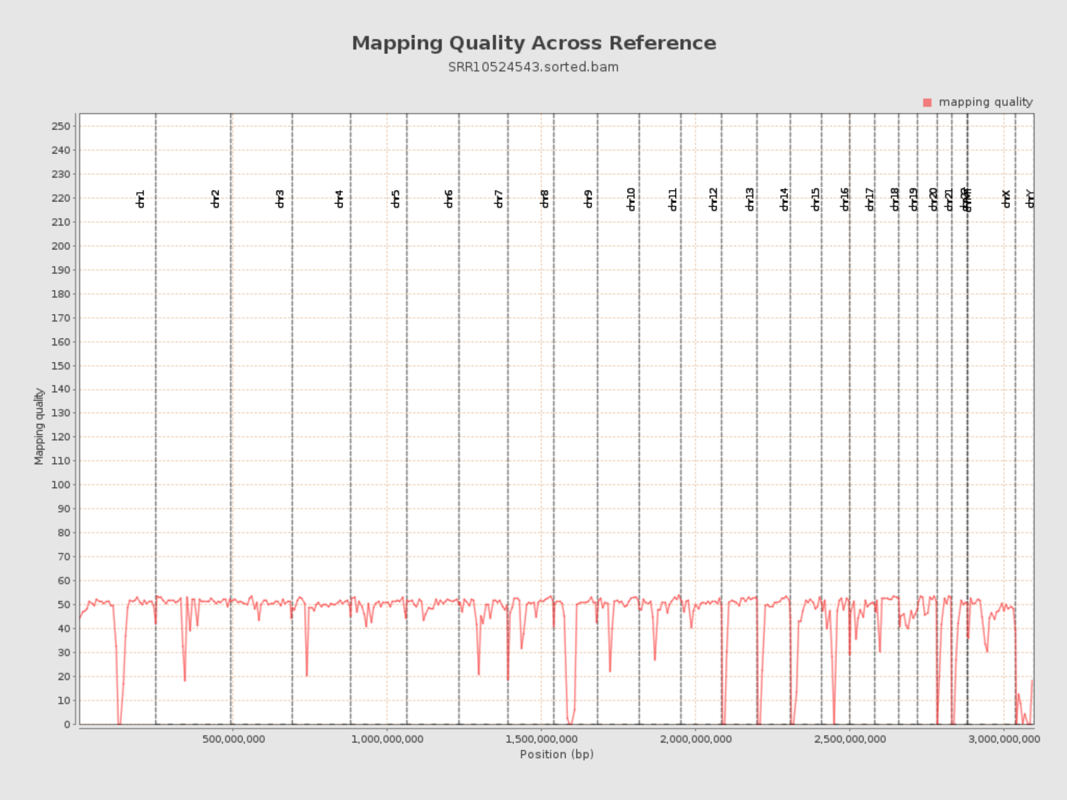
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram