Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:20:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525154.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_SRR10525154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:20:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,610,705
Mapped reads	905,375 / 34.68%
Unmapped reads	1,705,330 / 65.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,863 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	22,592 / 0.87%
Duplication rate	1.86%
Clipped reads	904,891 / 34.66%

2.2. ACGT Content

Number/percentage of A's	13,761,124 / 25.83%
Number/percentage of C's	9,241,131 / 17.34%
Number/percentage of T's	16,788,169 / 31.51%
Number/percentage of G's	13,491,665 / 25.32%
Number/percentage of N's	1,271 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1814

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

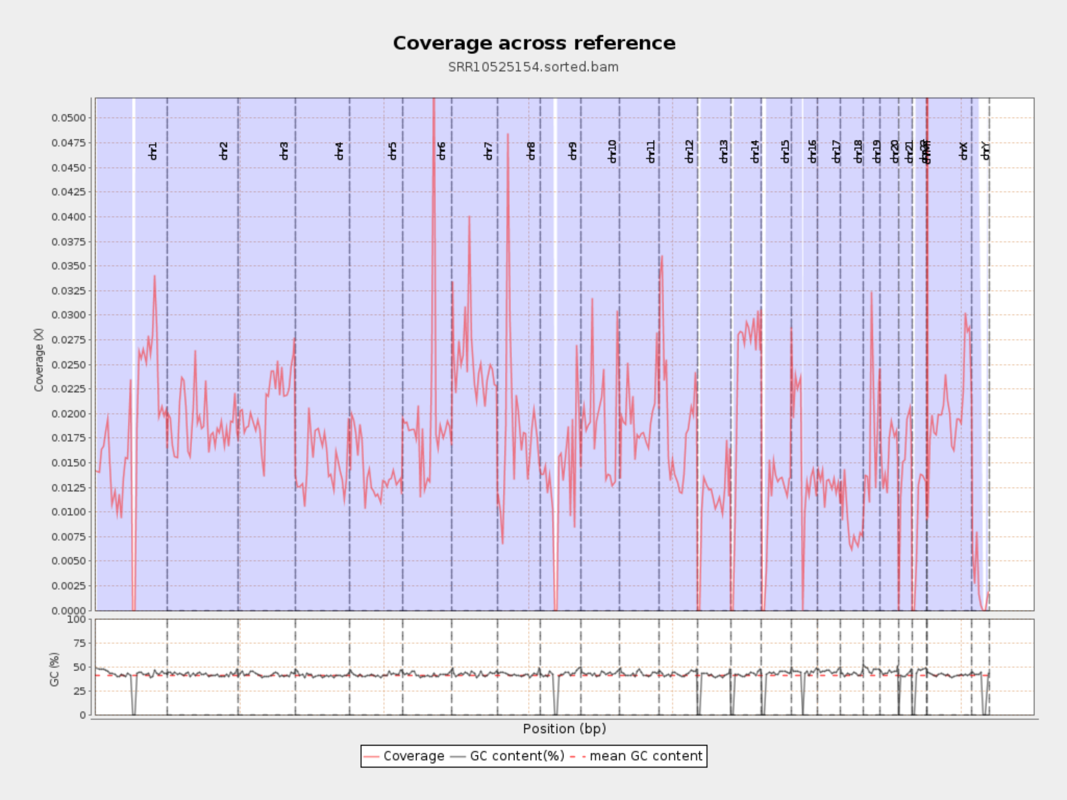
General error rate	0.51%
Mismatches	267,236
Insertions	3,931
Mapped reads with at least one insertion	0.43%
Deletions	10,400
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.06%

2.6. Chromosome stats

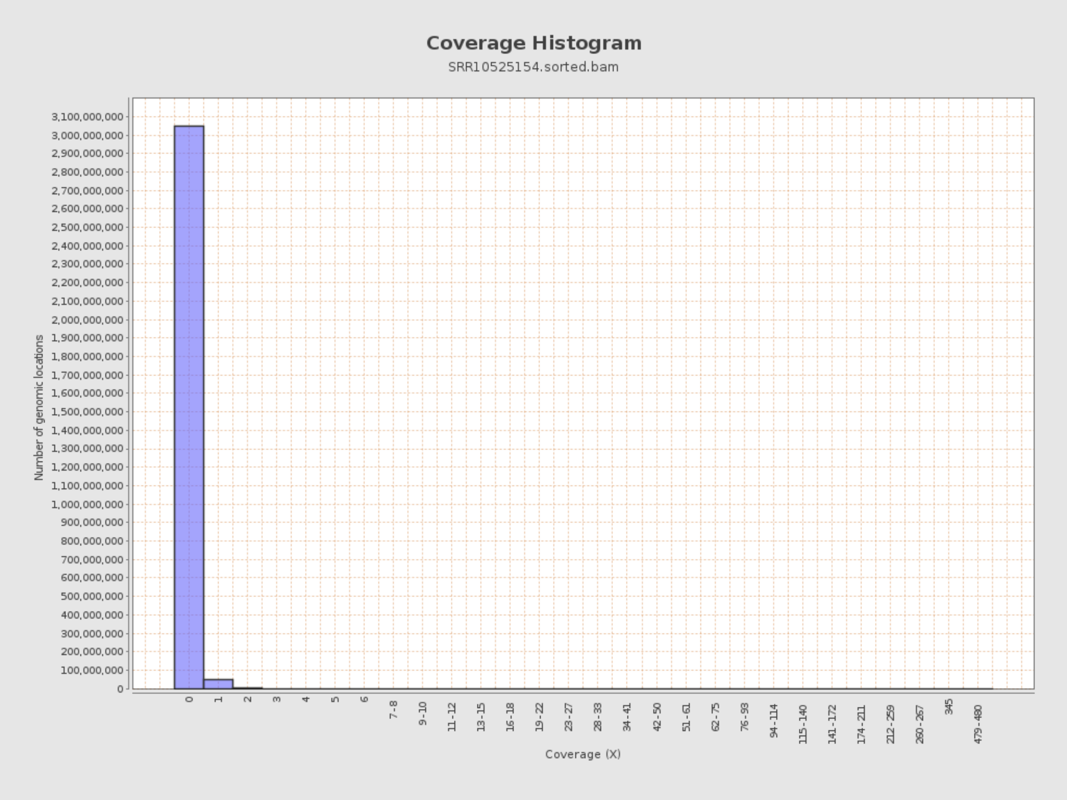
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4541750	0.0182	0.261
chr2	243199373	4637100	0.0191	0.2419
chr3	198022430	4157351	0.021	0.1528
chr4	191154276	2894235	0.0151	0.1341
chr5	180915260	2557330	0.0141	0.1249
chr6	171115067	3341274	0.0195	0.1576
chr7	159138663	4057754	0.0255	0.3108

chr8	146364022	2727426	0.0186	0.1628
chr9	141213431	1905392	0.0135	0.1405
chr10	135534747	2621026	0.0193	0.1847
chr11	135006516	2623760	0.0194	0.1645
chr12	133851895	2587068	0.0193	0.1467
chr13	115169878	1240586	0.0108	0.1096
chr14	107349540	2498566	0.0233	0.1638
chr15	102531392	1102864	0.0108	0.1108
chr16	90354753	1414905	0.0157	0.1407
chr17	81195210	1041571	0.0128	0.1237
chr18	78077248	662254	0.0085	0.2239
chr19	59128983	1072196	0.0181	0.2084
chr20	63025520	1000231	0.0159	0.1338
chr21	48129895	722151	0.015	0.1337
chr22	51304566	469059	0.0091	0.1009
chrMT	16571	80914	4.8829	3.2371
chrX	155270560	3199401	0.0206	0.1565
chrY	59373566	143664	0.0024	0.0739

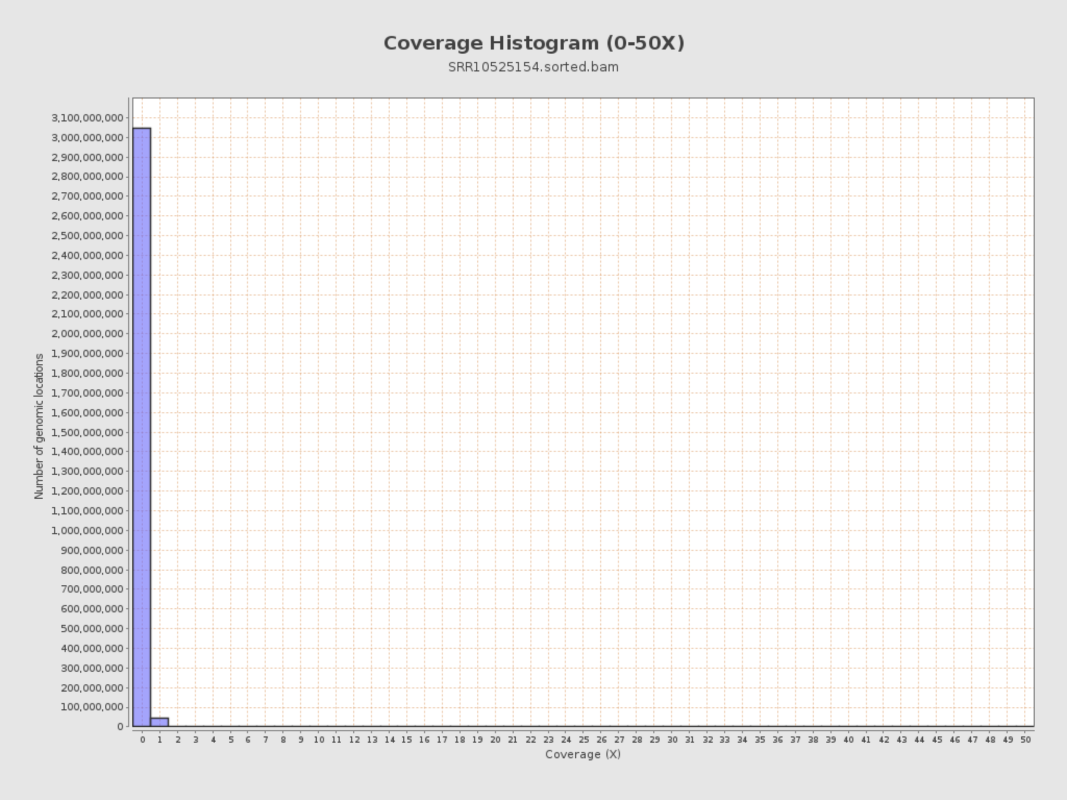
3. Results : Coverage across reference



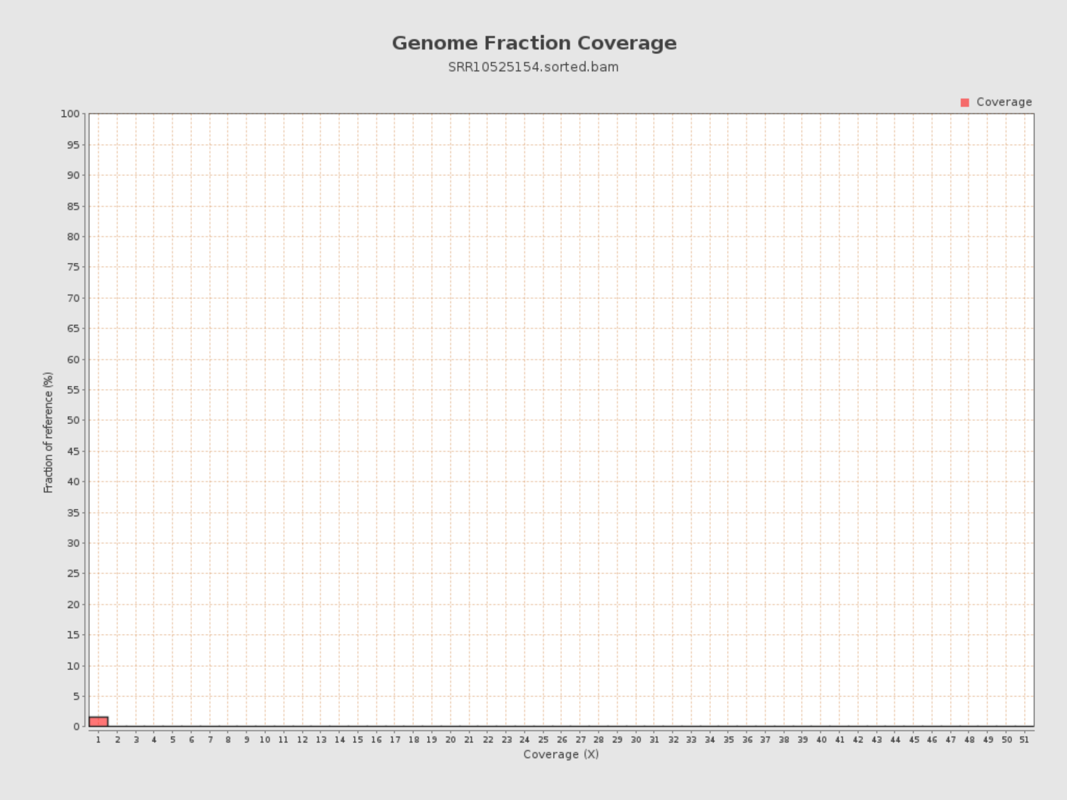
4. Results : Coverage Histogram



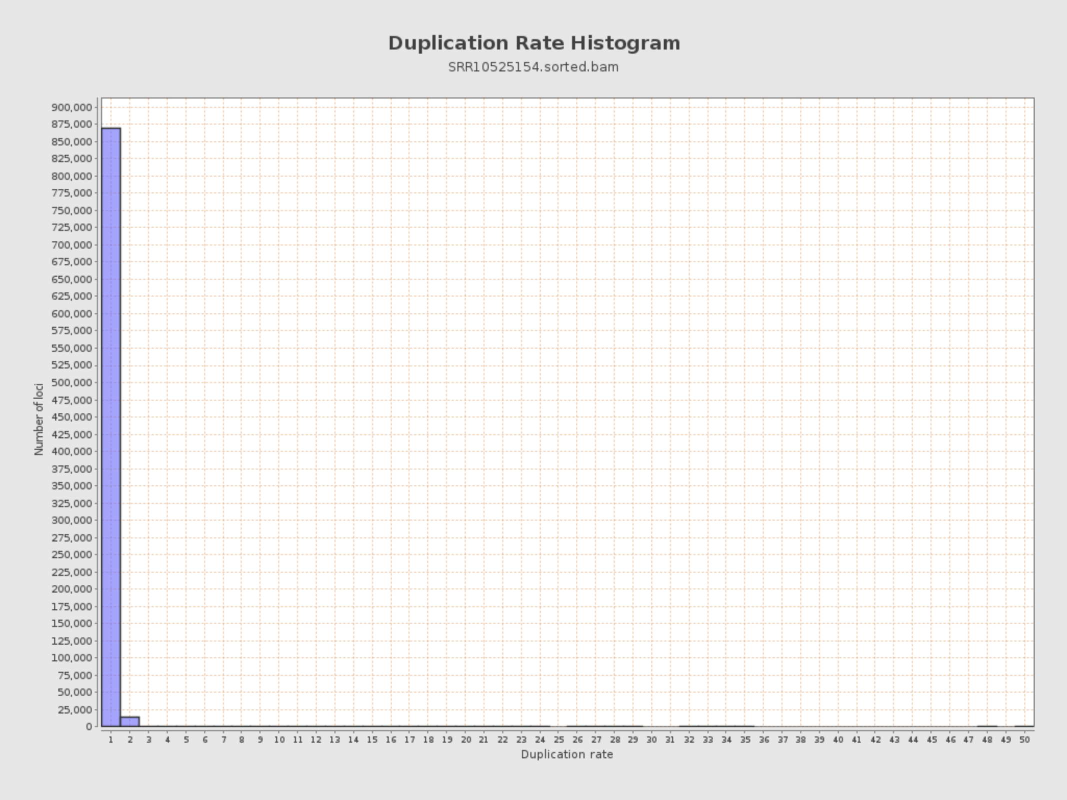
5. Results : Coverage Histogram (0-50X)



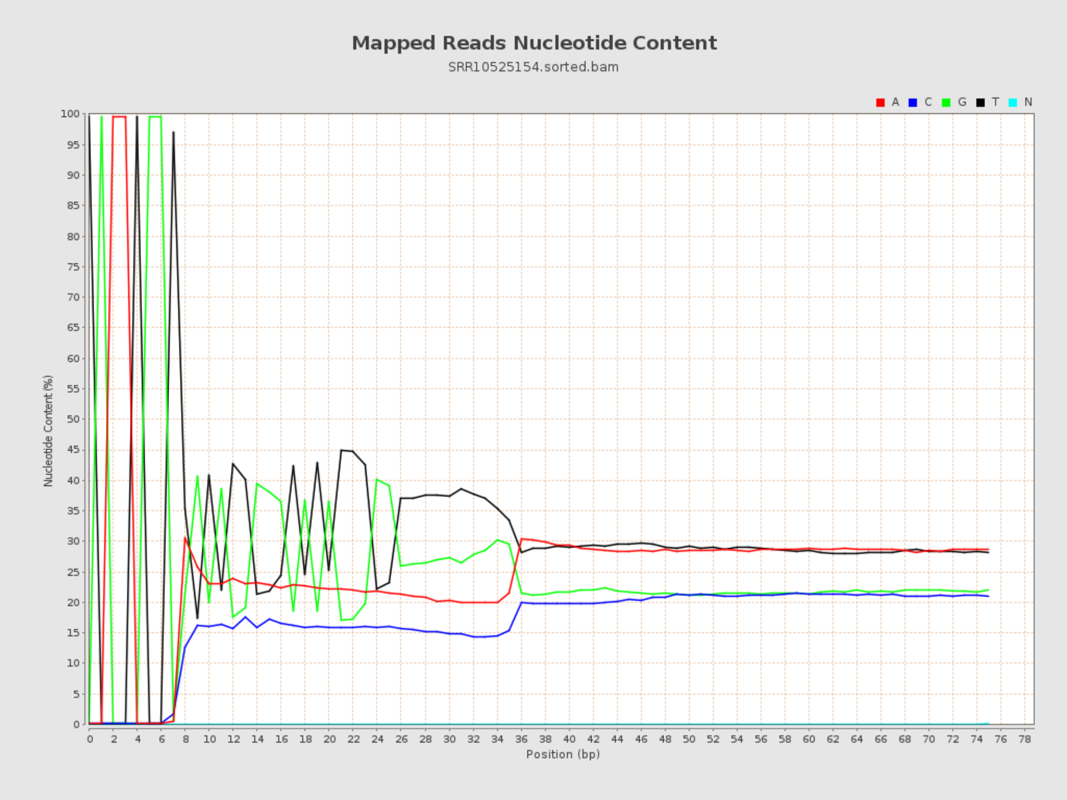
6. Results : Genome Fraction Coverage



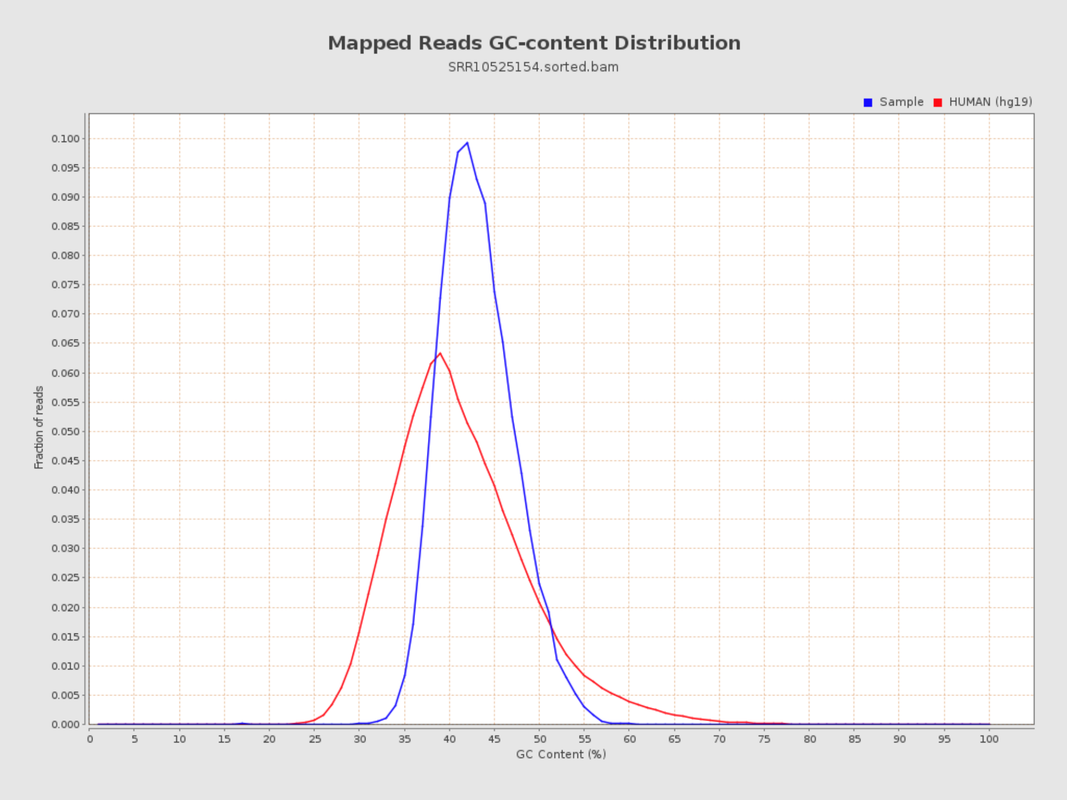
7. Results : Duplication Rate Histogram



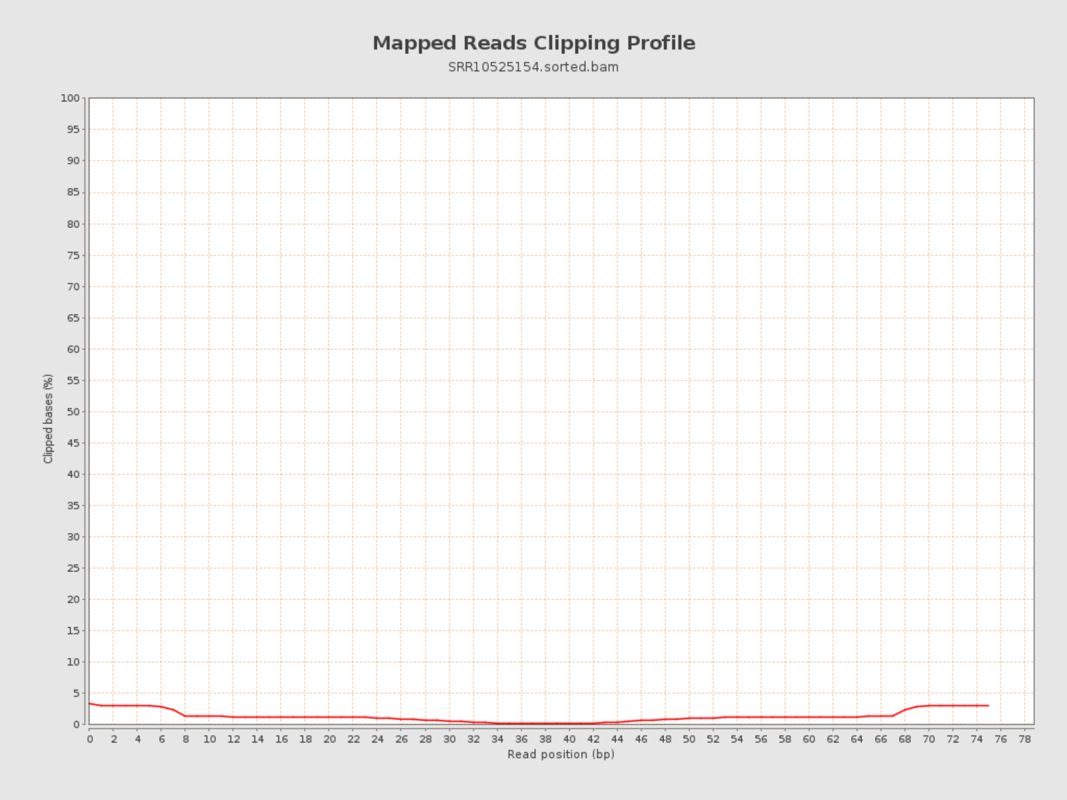
8. Results : Mapped Reads Nucleotide Content



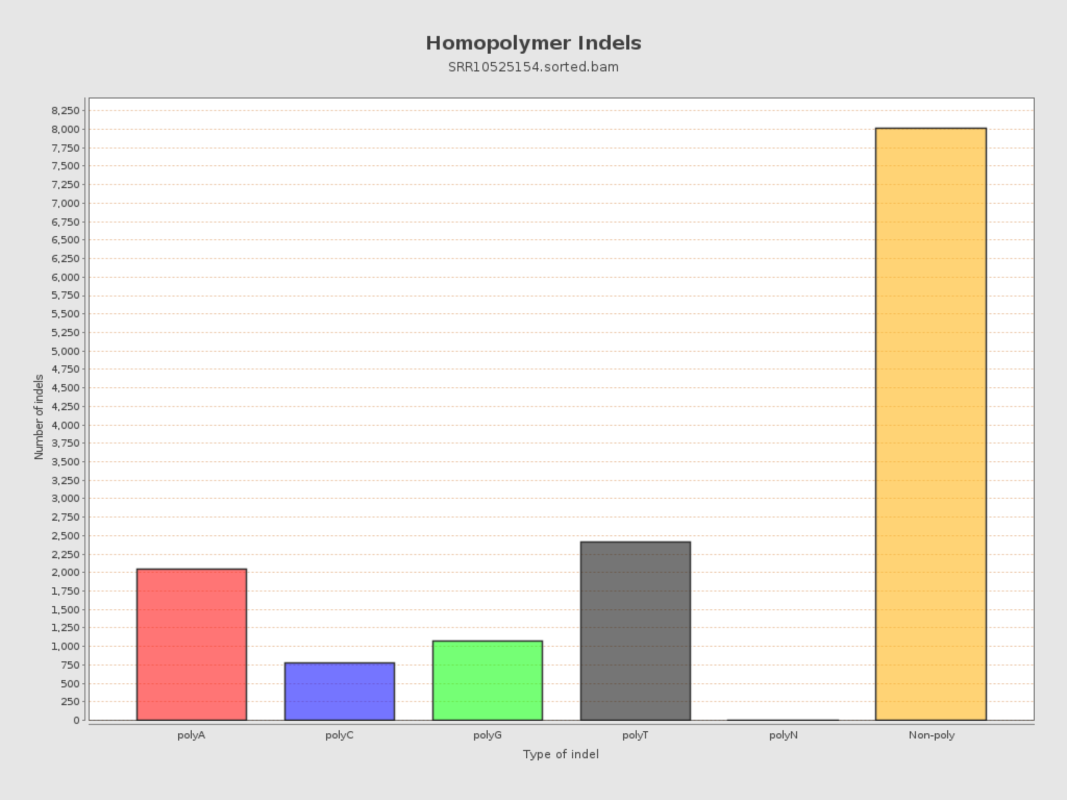
9. Results : Mapped Reads GC-content Distribution



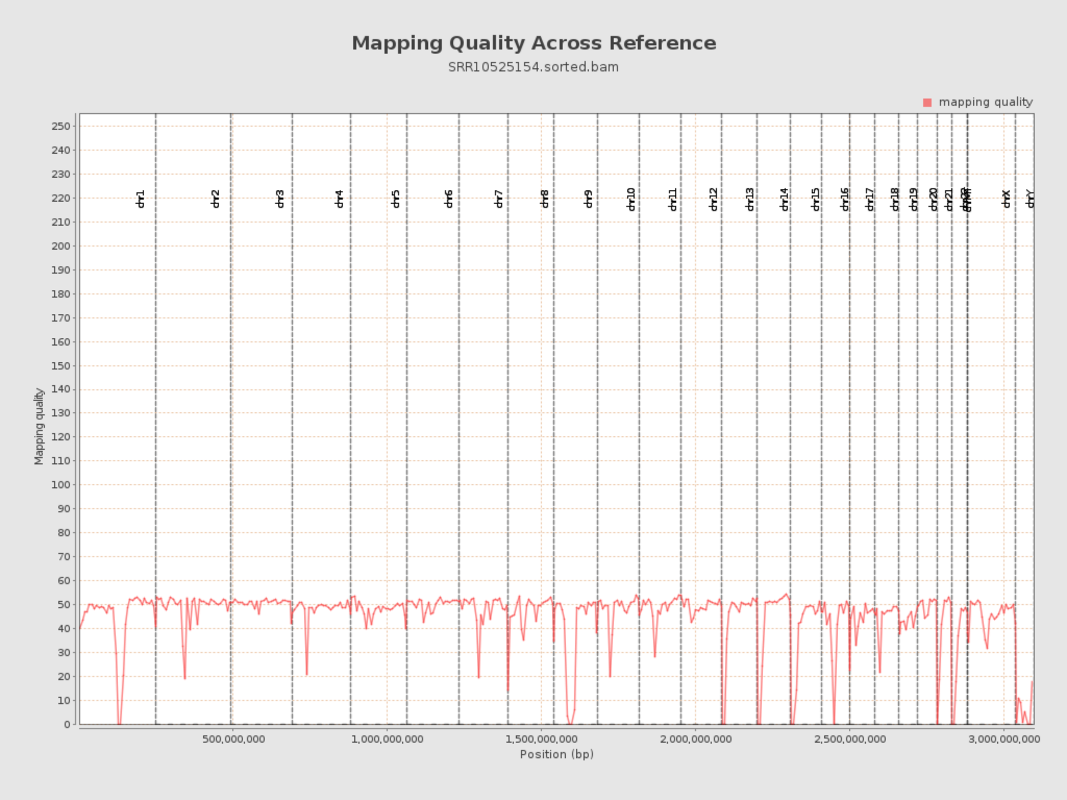
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram