Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:46:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525264.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_SRR10525264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:46:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,649,686
Mapped reads	1,520,216 / 92.15%
Unmapped reads	129,470 / 7.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,502 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	56,340 / 3.42%
Duplication rate	2.73%
Clipped reads	1,525,273 / 92.46%

2.2. ACGT Content

Number/percentage of A's	22,849,442 / 25.82%
Number/percentage of C's	17,644,655 / 19.94%
Number/percentage of T's	27,433,086 / 31%
Number/percentage of G's	20,554,404 / 23.23%
Number/percentage of N's	1,745 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2792

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

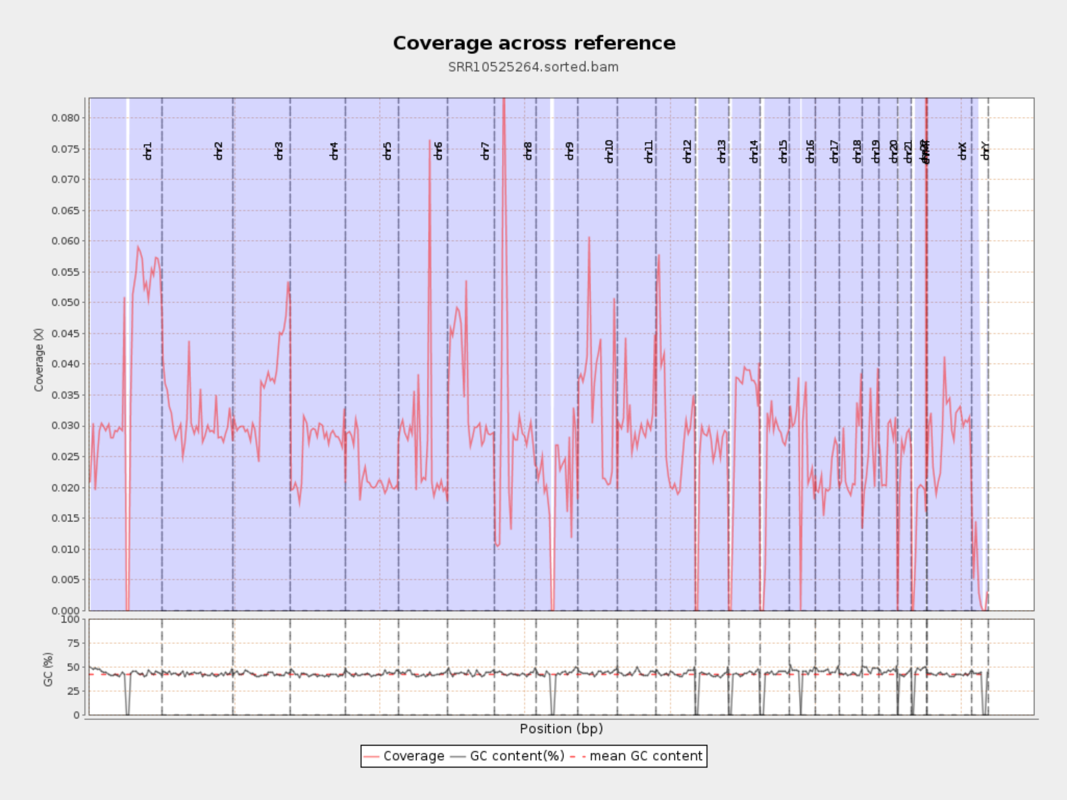
General error rate	0.5%
Mismatches	435,780
Insertions	5,471
Mapped reads with at least one insertion	0.36%
Deletions	18,681
Mapped reads with at least one deletion	1.22%
Homopolymer indels	45.11%

2.6. Chromosome stats

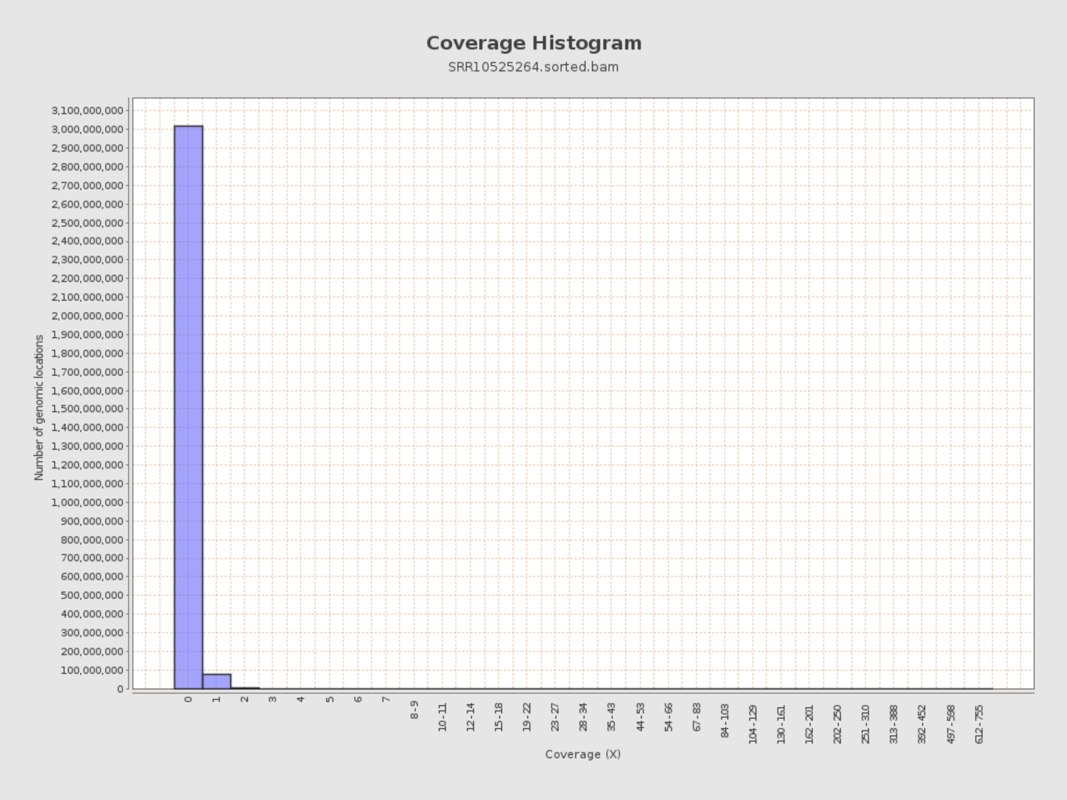
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9521892	0.0382	0.5133
chr2	243199373	7508797	0.0309	0.3663
chr3	198022430	7006420	0.0354	0.2052
chr4	191154276	5129378	0.0268	0.1863
chr5	180915260	4082546	0.0226	0.163
chr6	171115067	4685535	0.0274	0.2046
chr7	159138663	5703579	0.0358	0.41

chr8	146364022	4311275	0.0295	0.2672
chr9	141213431	2885407	0.0204	0.2031
chr10	135534747	4805421	0.0355	0.2977
chr11	135006516	4191352	0.031	0.2329
chr12	133851895	4029865	0.0301	0.1926
chr13	115169878	2830262	0.0246	0.1717
chr14	107349540	3339287	0.0311	0.196
chr15	102531392	2441262	0.0238	0.1702
chr16	90354753	2353418	0.026	0.1951
chr17	81195210	1744317	0.0215	0.1645
chr18	78077248	1921905	0.0246	0.3848
chr19	59128983	1557722	0.0263	0.3479
chr20	63025520	1618432	0.0257	0.1757
chr21	48129895	1147323	0.0238	0.1743
chr22	51304566	709777	0.0138	0.1266
chrMT	16571	172304	10.3979	6.1025
chrX	155270560	4553771	0.0293	0.2008
chrY	59373566	261487	0.0044	0.1203

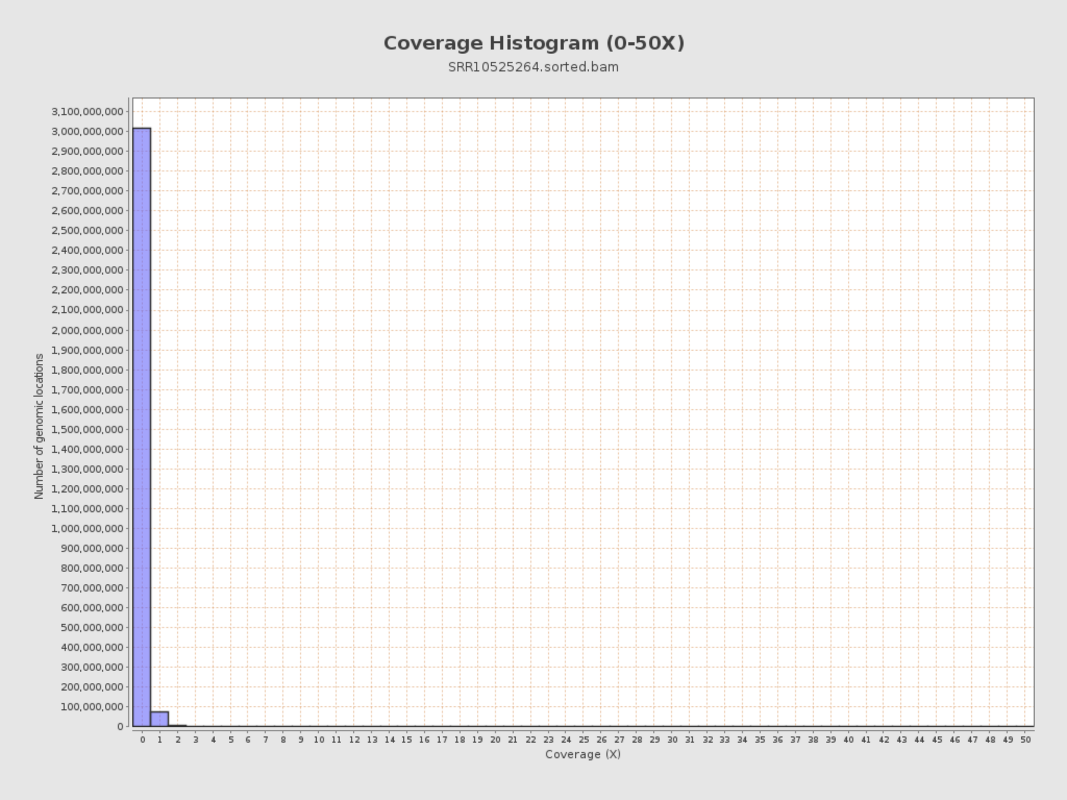
3. Results : Coverage across reference



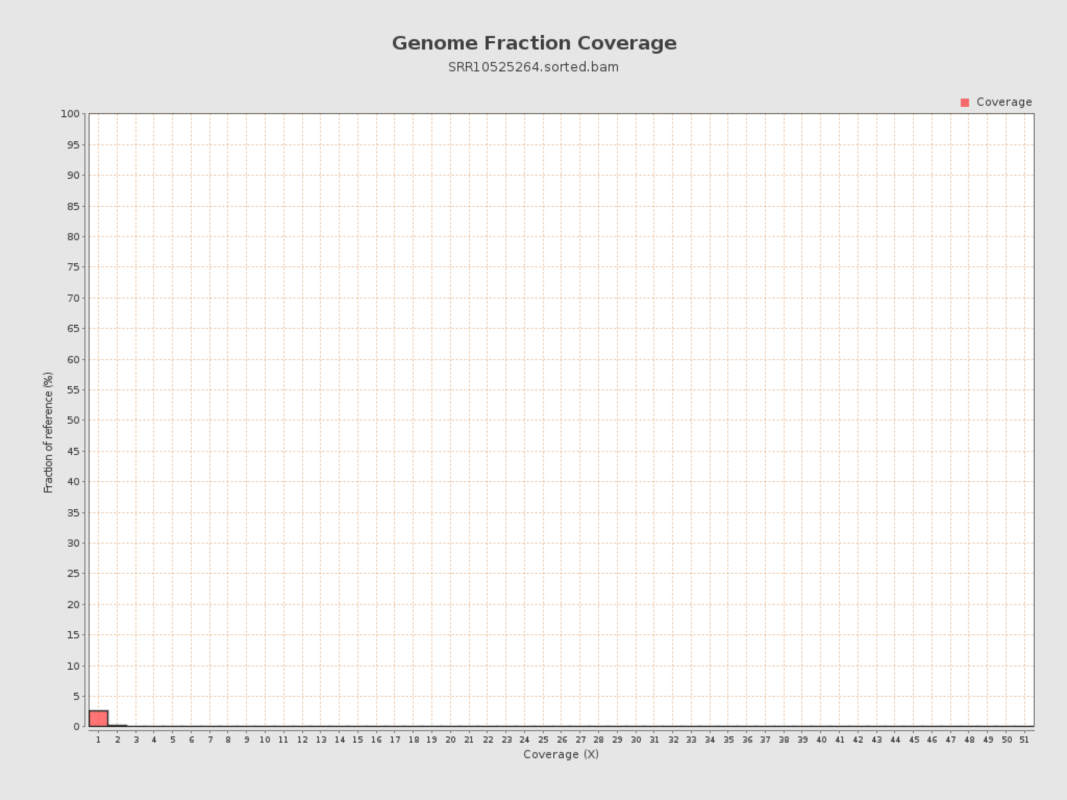
4. Results : Coverage Histogram



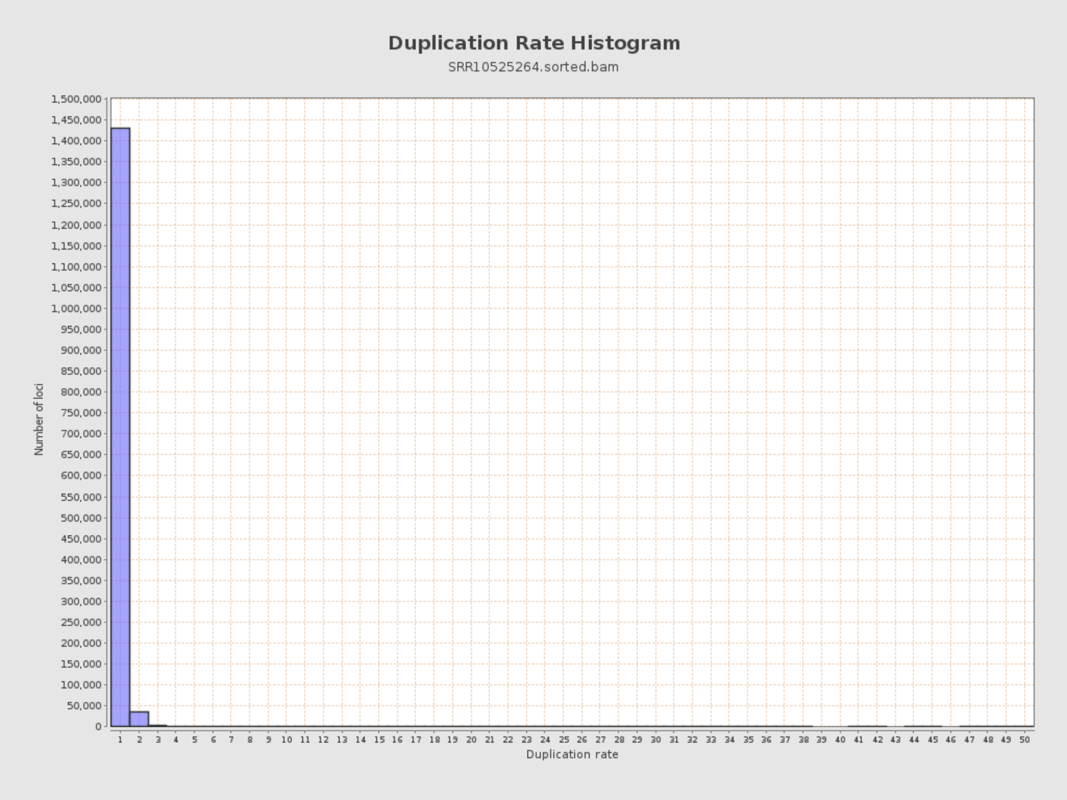
5. Results : Coverage Histogram (0-50X)



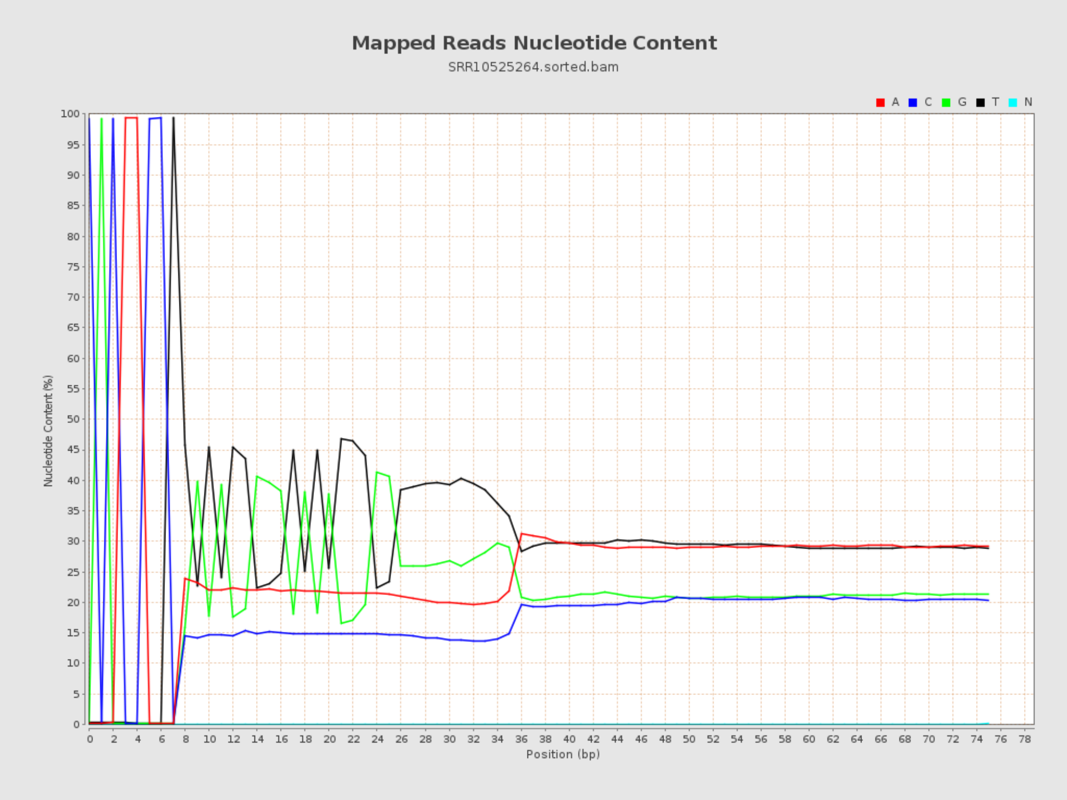
6. Results : Genome Fraction Coverage



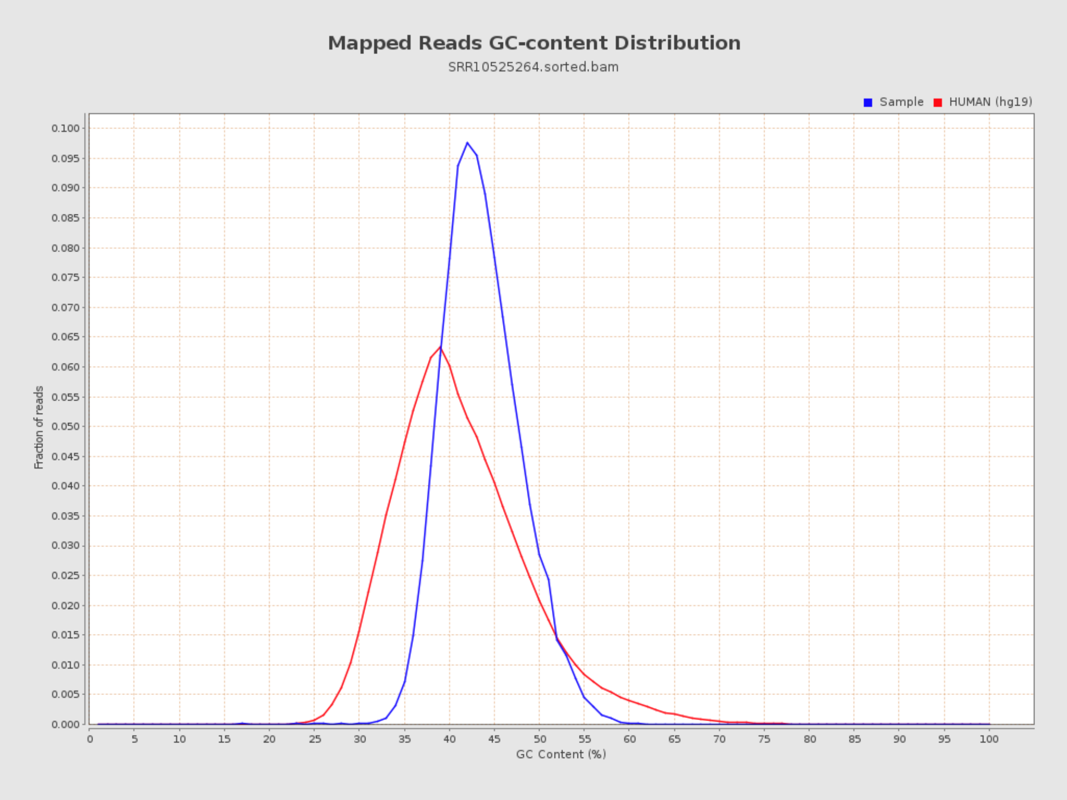
7. Results : Duplication Rate Histogram



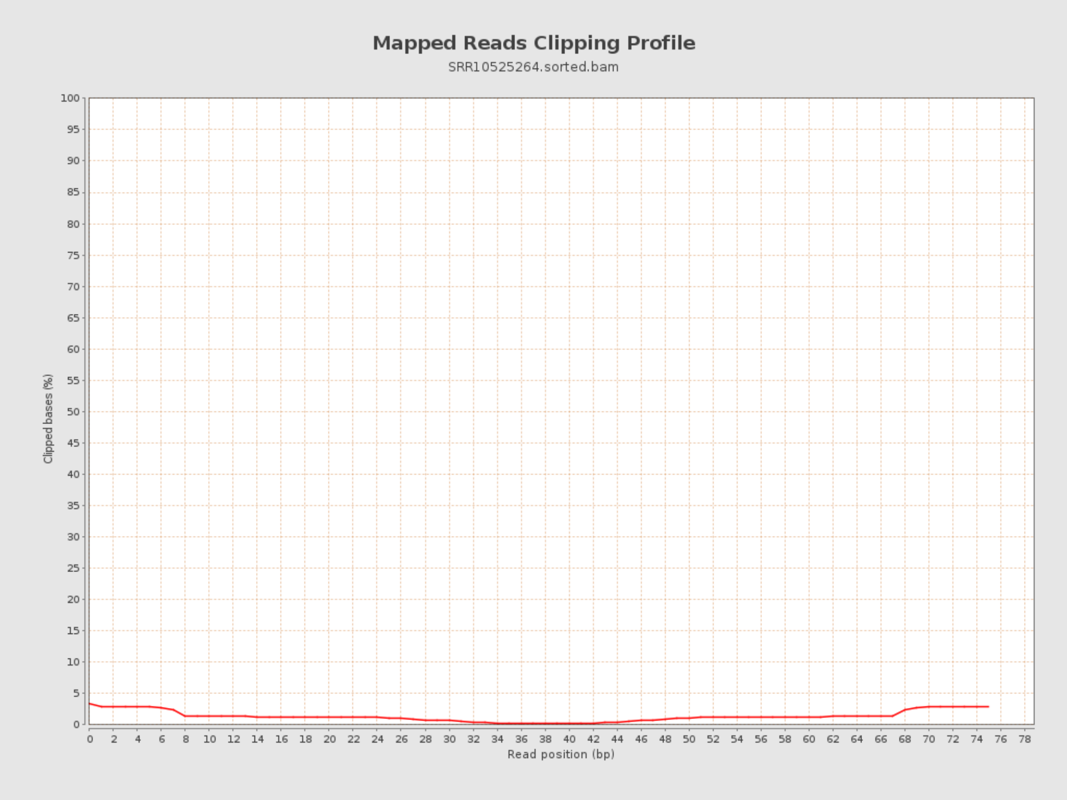
8. Results : Mapped Reads Nucleotide Content



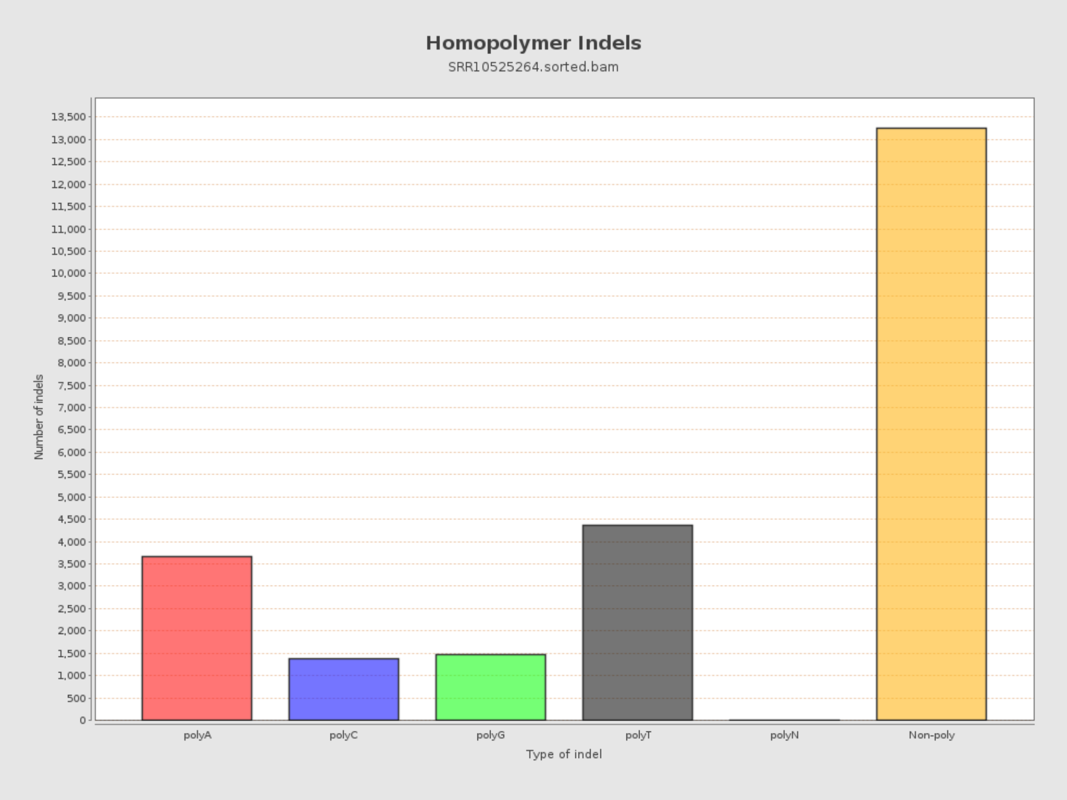
9. Results : Mapped Reads GC-content Distribution



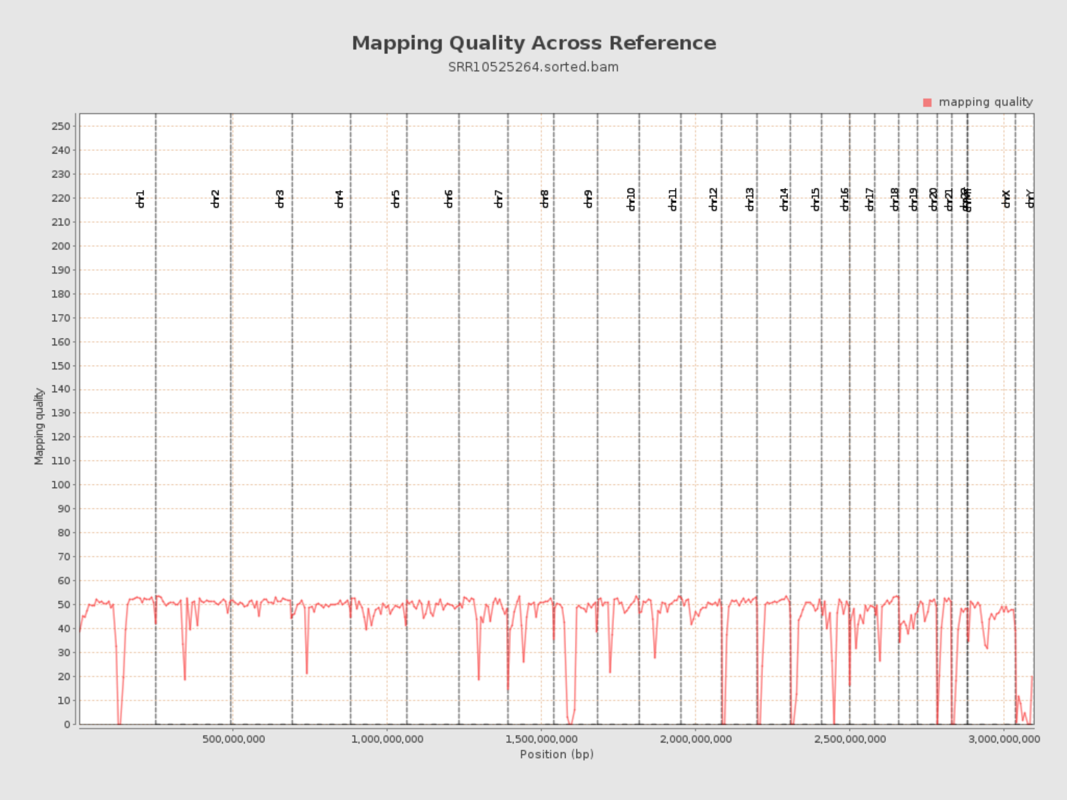
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram