Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:23:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524634.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_SRR10524634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:23:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,148,658
Mapped reads	1,074,502 / 93.54%
Unmapped reads	74,156 / 6.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,398 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	34,028 / 2.96%
Duplication rate	2.49%
Clipped reads	1,073,648 / 93.47%

2.2. ACGT Content

Number/percentage of A's	16,152,973 / 25.67%
Number/percentage of C's	11,725,865 / 18.64%
Number/percentage of T's	19,137,946 / 30.42%
Number/percentage of G's	15,898,727 / 25.27%
Number/percentage of N's	332 / 0%
GC Percentage	43.91%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.1918

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

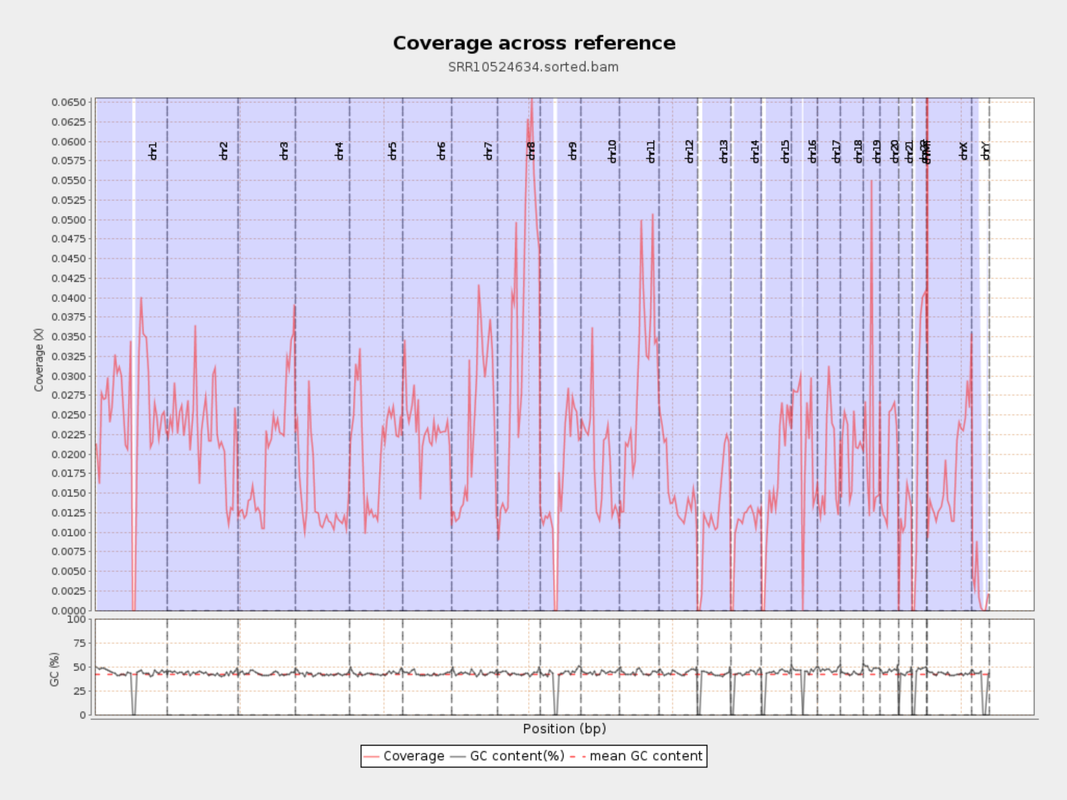
General error rate	0.47%
Mismatches	285,442
Insertions	4,337
Mapped reads with at least one insertion	0.4%
Deletions	11,714
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.75%

2.6. Chromosome stats

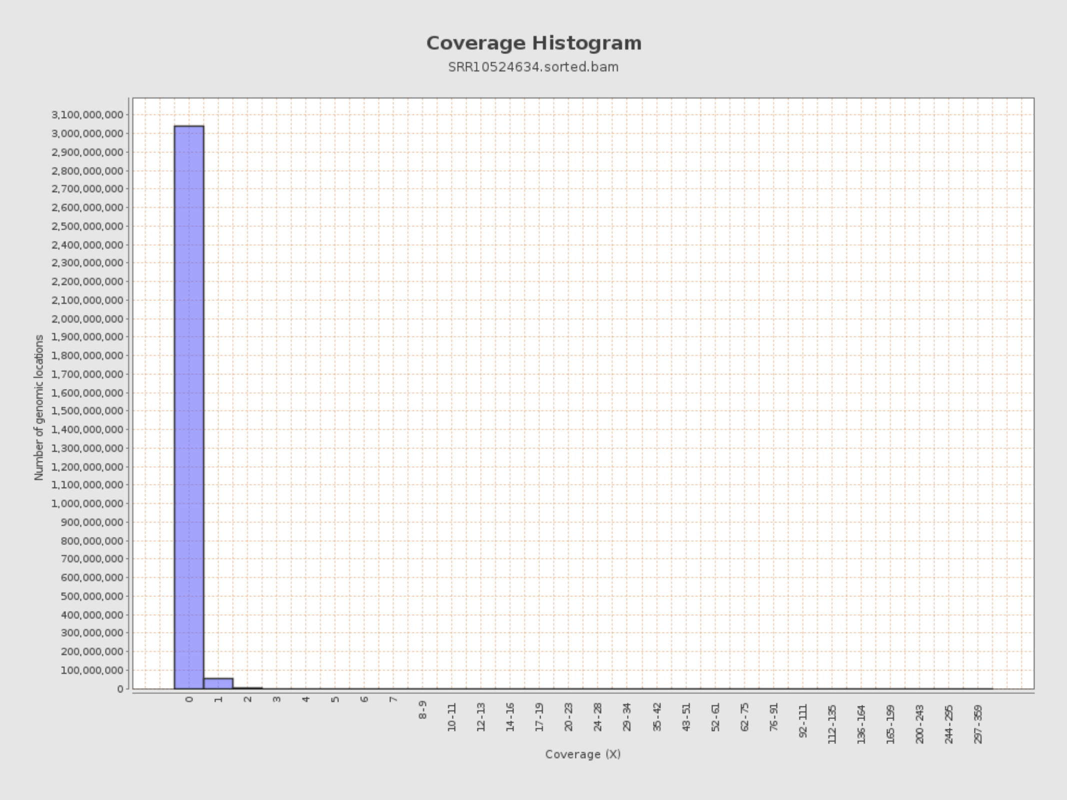
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6290140	0.0252	0.2993
chr2	243199373	5575084	0.0229	0.2208
chr3	198022430	3917525	0.0198	0.1515
chr4	191154276	2733662	0.0143	0.1425
chr5	180915260	3823842	0.0211	0.1561
chr6	171115067	4033527	0.0236	0.1717
chr7	159138663	3748134	0.0236	0.2466

chr8	146364022	5356869	0.0366	0.2565
chr9	141213431	2300465	0.0163	0.1739
chr10	135534747	2630484	0.0194	0.1927
chr11	135006516	3945311	0.0292	0.2055
chr12	133851895	2071958	0.0155	0.1363
chr13	115169878	1413393	0.0123	0.1191
chr14	107349540	1130252	0.0105	0.1148
chr15	102531392	1640818	0.016	0.1393
chr16	90354753	1963170	0.0217	0.1638
chr17	81195210	1499507	0.0185	0.1488
chr18	78077248	1616361	0.0207	0.249
chr19	59128983	1299639	0.022	0.2193
chr20	63025520	1196082	0.019	0.1501
chr21	48129895	553669	0.0115	0.1248
chr22	51304566	1274897	0.0248	0.1697
chrMT	16571	51770	3.1241	2.51
chrX	155270560	2722816	0.0175	0.1544
chrY	59373566	146589	0.0025	0.0806

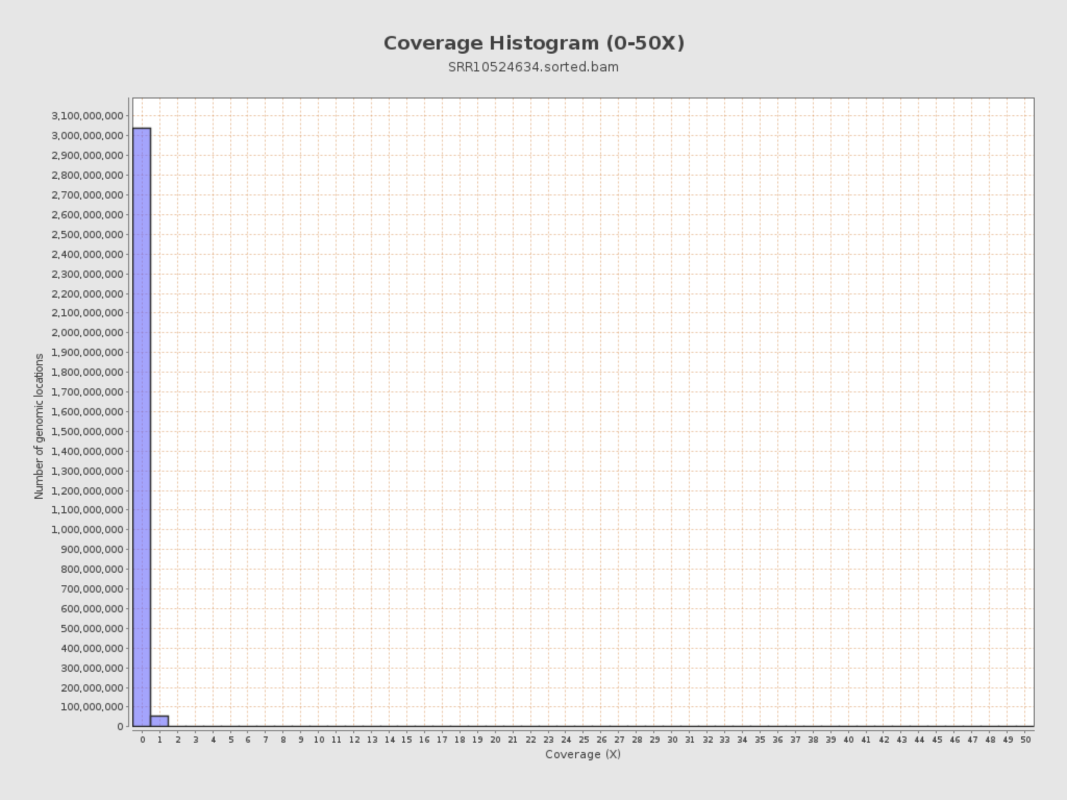
3. Results : Coverage across reference



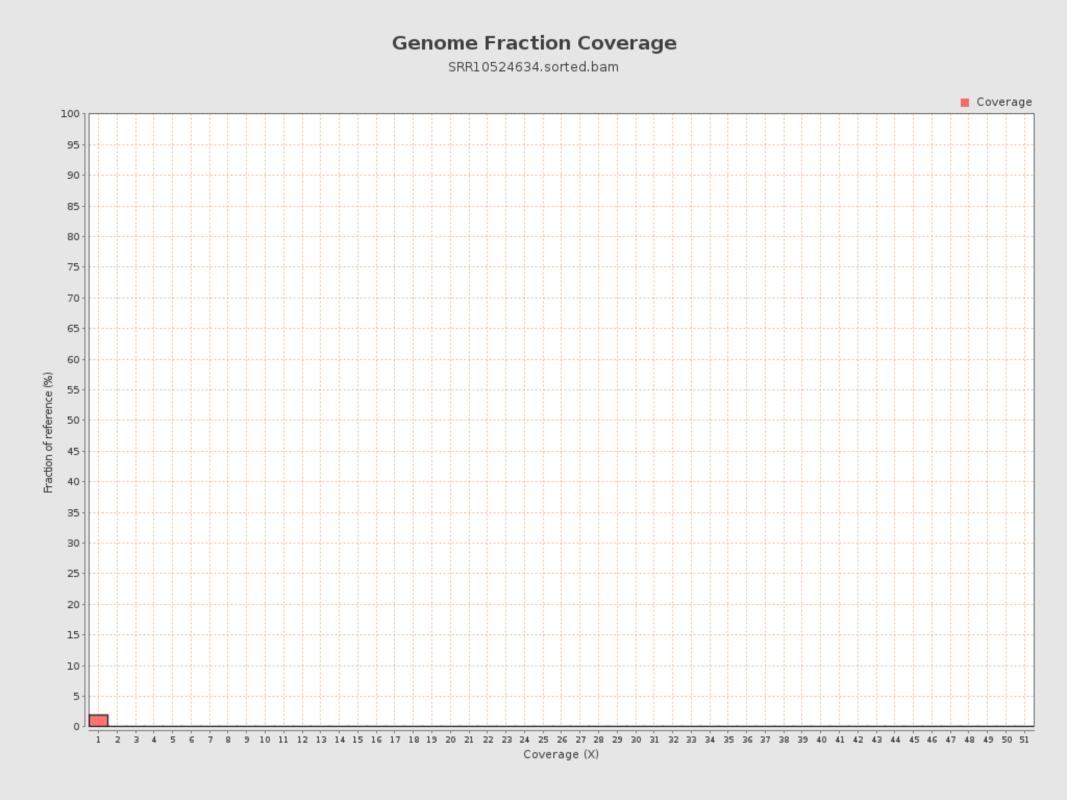
4. Results : Coverage Histogram



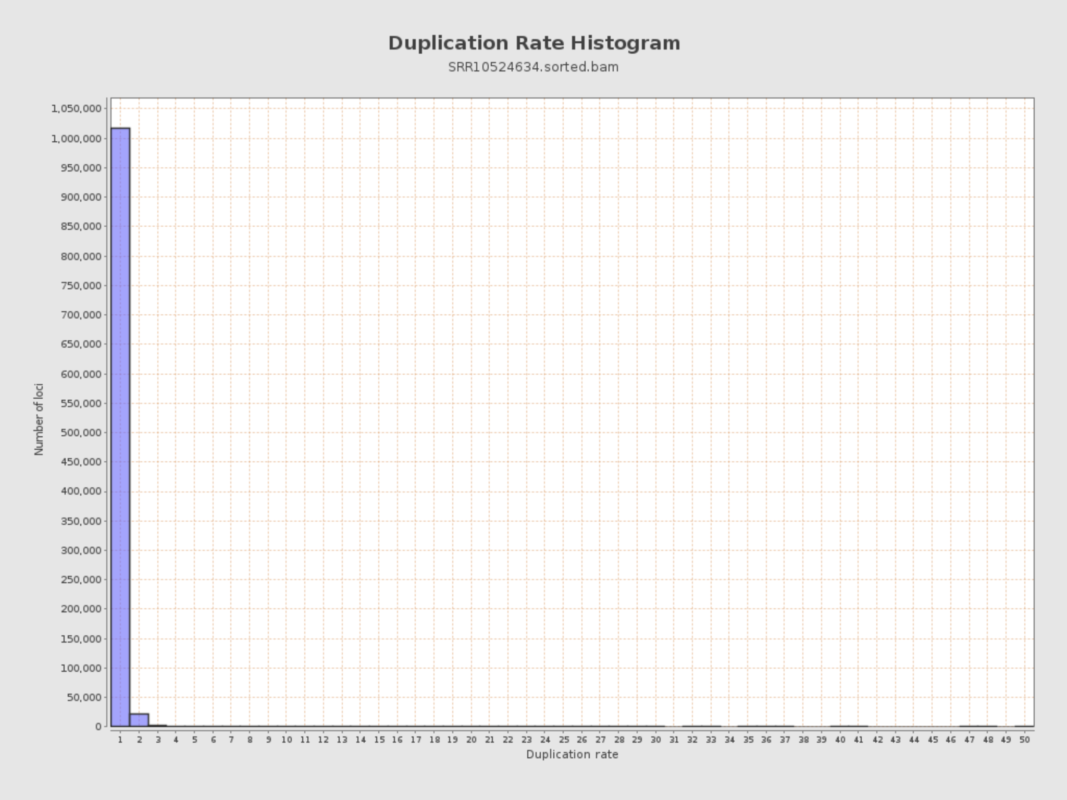
5. Results : Coverage Histogram (0-50X)



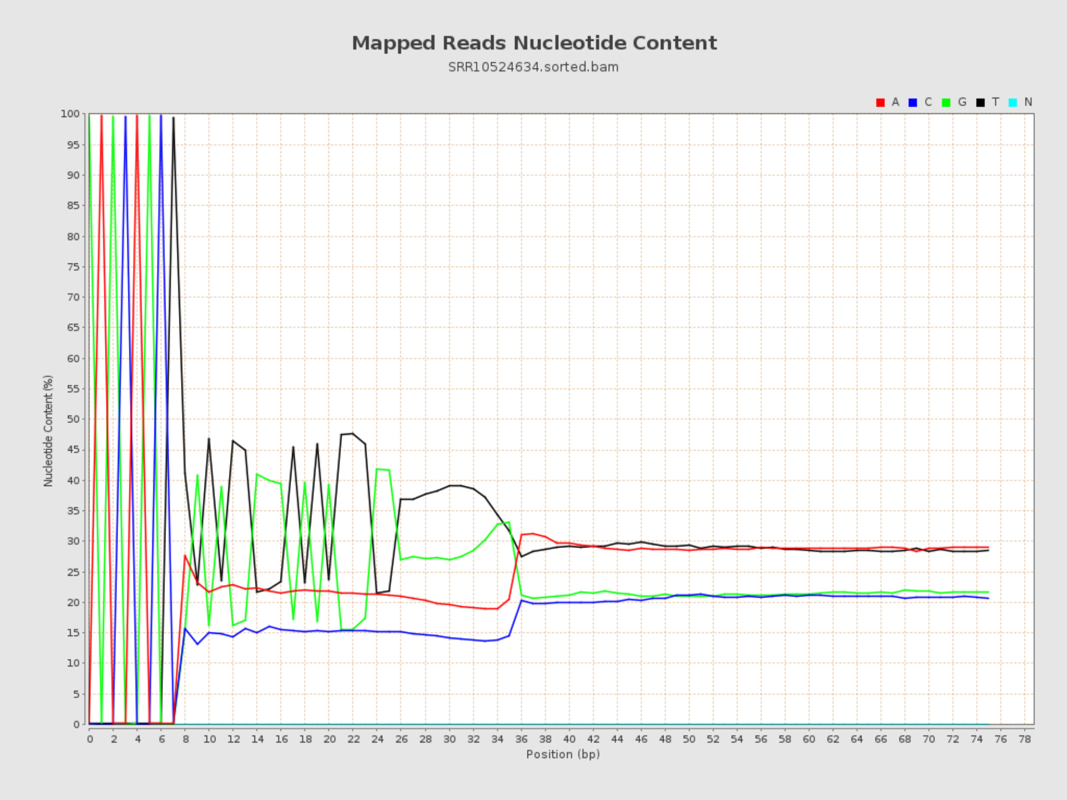
6. Results : Genome Fraction Coverage



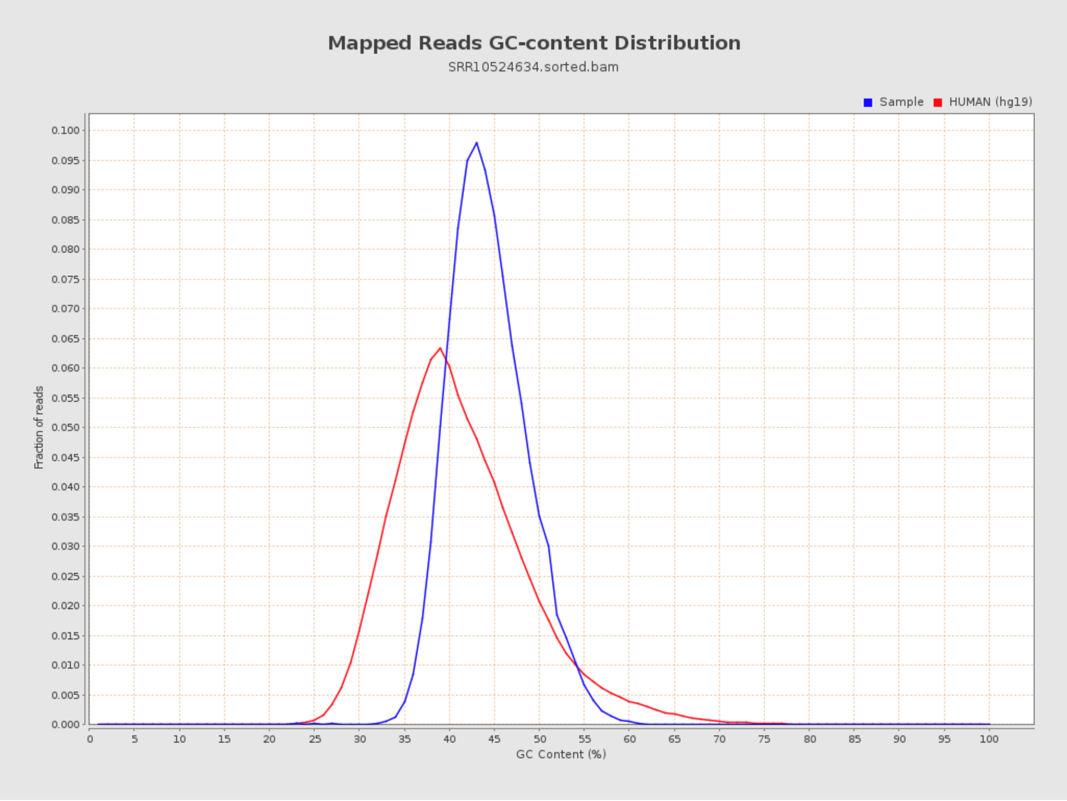
7. Results : Duplication Rate Histogram



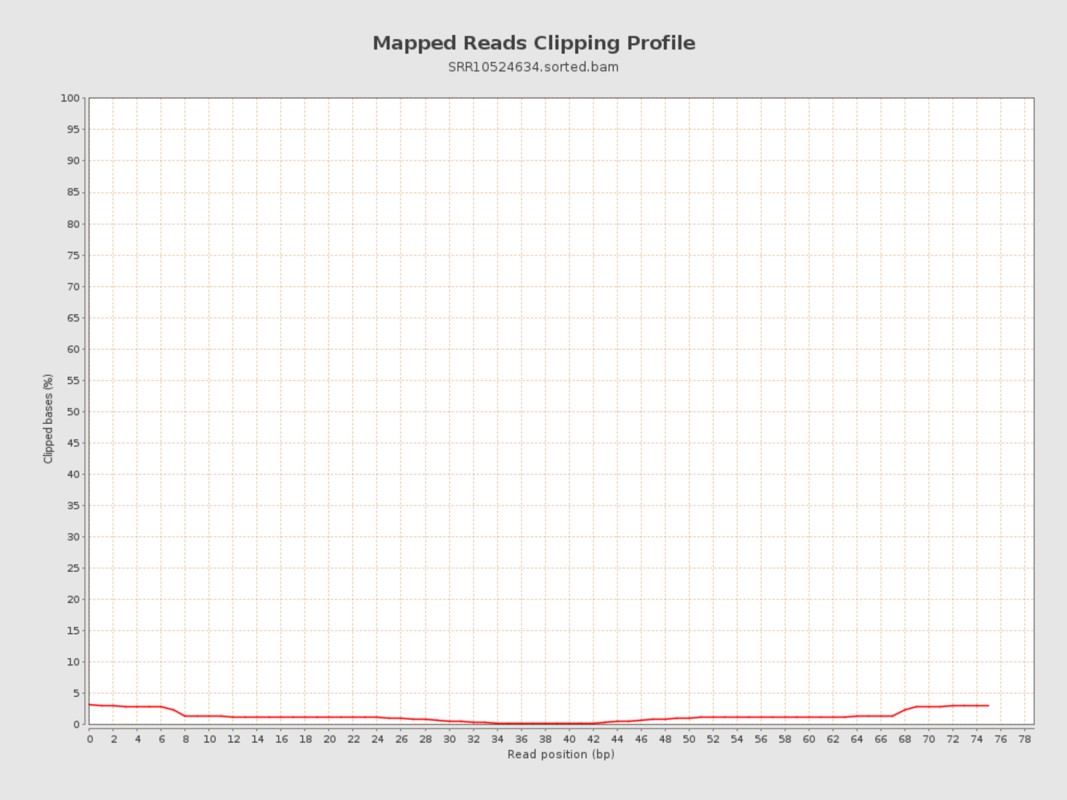
8. Results : Mapped Reads Nucleotide Content



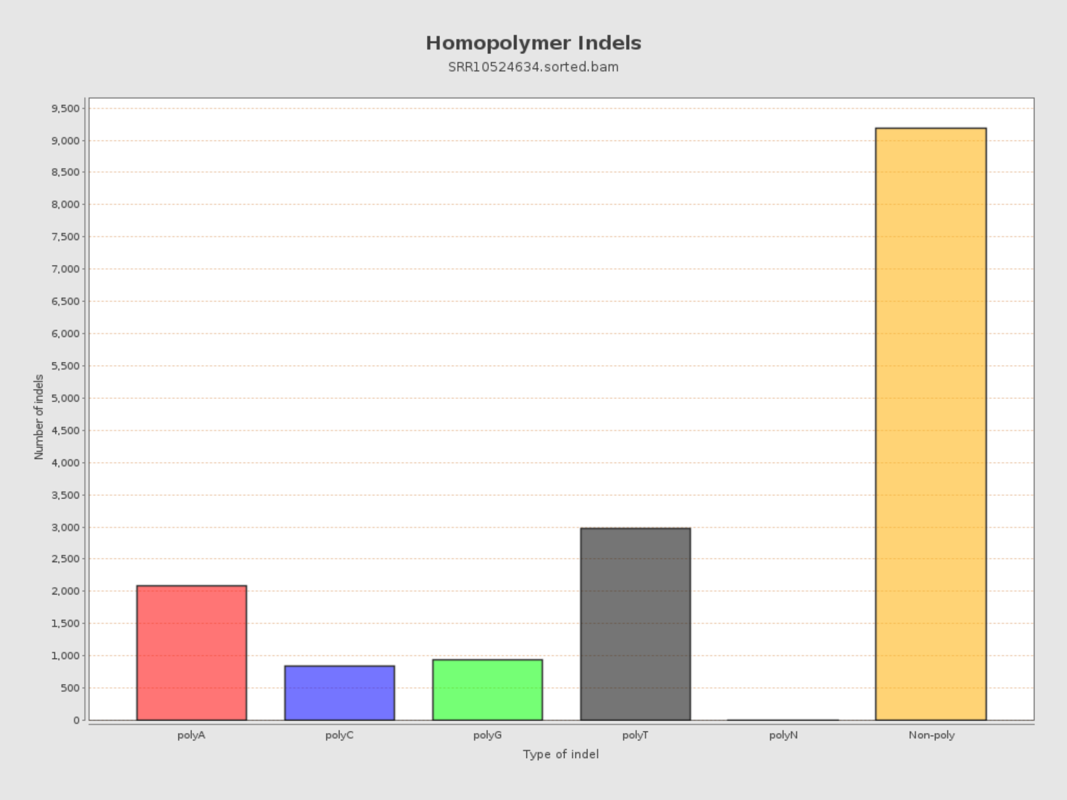
9. Results : Mapped Reads GC-content Distribution



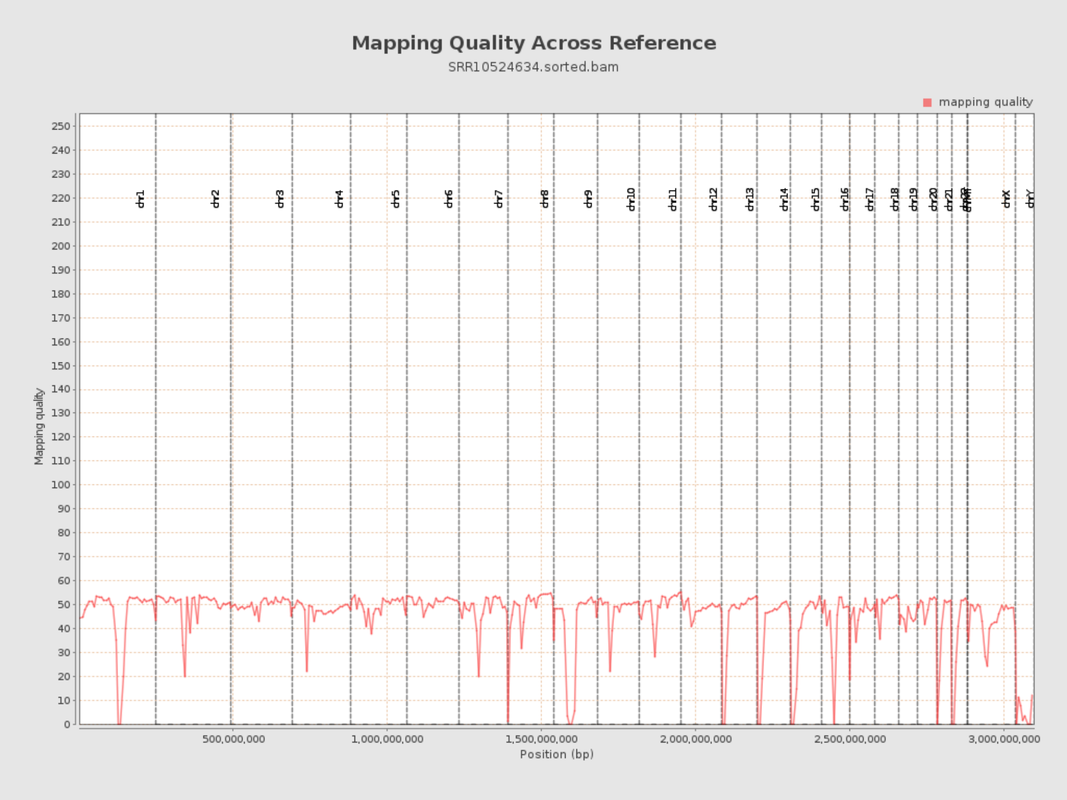
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram