Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:45:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524345.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_SRR10524345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524345.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:45:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	472,227
Mapped reads	435,940 / 92.32%
Unmapped reads	36,287 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,014 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	7,079 / 1.5%
Duplication rate	1.18%
Clipped reads	437,492 / 92.64%

2.2. ACGT Content

Number/percentage of A's	6,474,987 / 25.35%
Number/percentage of C's	4,884,074 / 19.12%
Number/percentage of T's	7,684,451 / 30.09%
Number/percentage of G's	6,494,017 / 25.43%
Number/percentage of N's	3,220 / 0.01%
GC Percentage	44.55%

2.3. Coverage

Mean	0.0083

Standard Deviation	0.1107

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

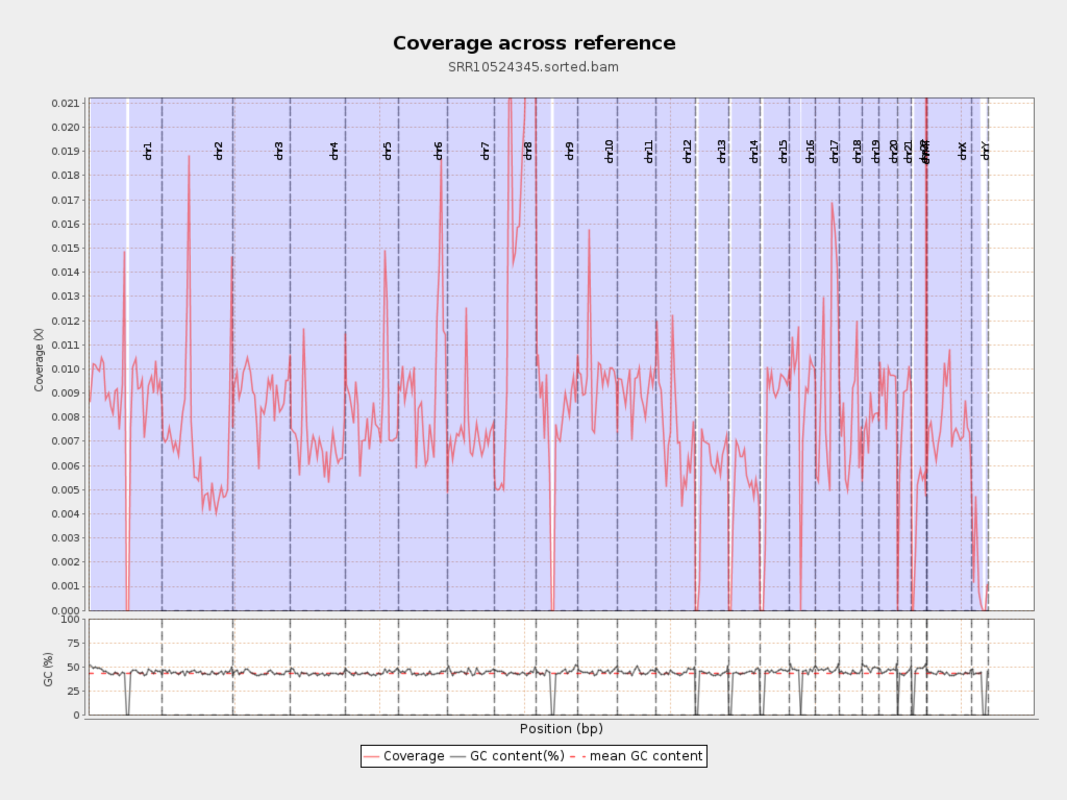
General error rate	0.52%
Mismatches	129,195
Insertions	1,447
Mapped reads with at least one insertion	0.33%
Deletions	4,362
Mapped reads with at least one deletion	0.99%
Homopolymer indels	42.73%

2.6. Chromosome stats

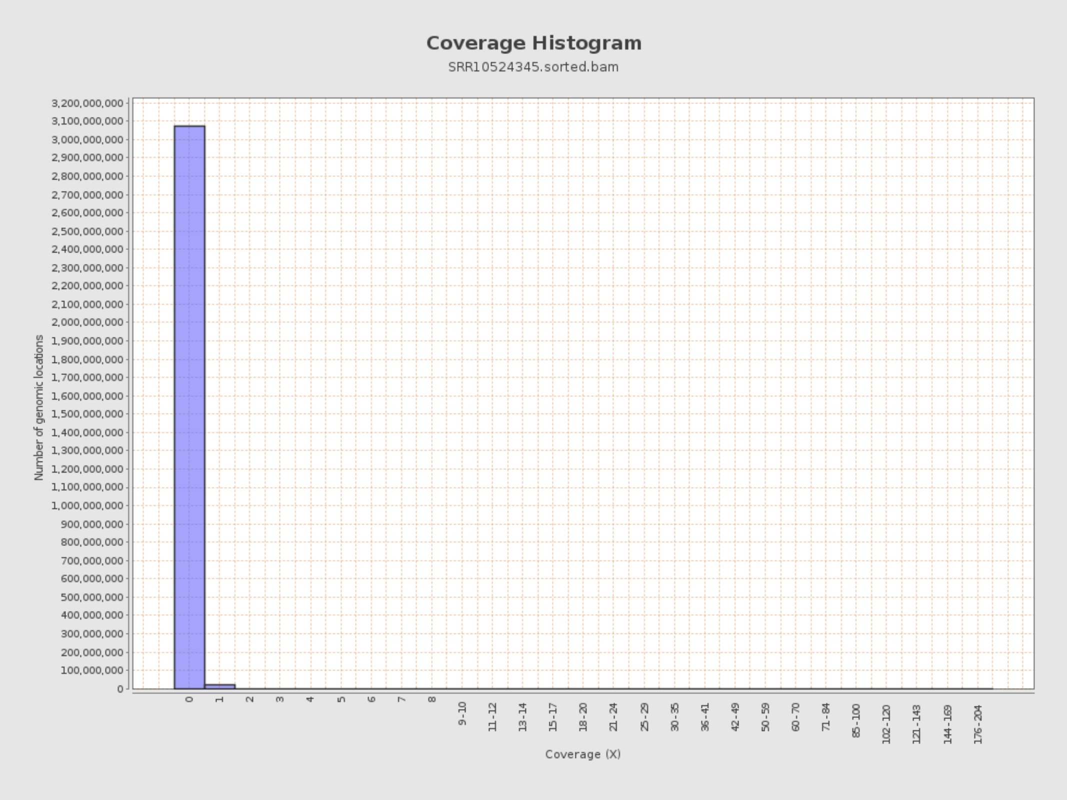
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2198880	0.0088	0.174
chr2	243199373	1662106	0.0068	0.1214
chr3	198022430	1773168	0.009	0.0972
chr4	191154276	1318892	0.0069	0.0901
chr5	180915260	1494883	0.0083	0.0931
chr6	171115067	1596977	0.0093	0.1019
chr7	159138663	1166066	0.0073	0.118

chr8	146364022	2658701	0.0182	0.1522
chr9	141213431	1057380	0.0075	0.0961
chr10	135534747	1317608	0.0097	0.113
chr11	135006516	1232209	0.0091	0.1043
chr12	133851895	997992	0.0075	0.0889
chr13	115169878	629899	0.0055	0.0754
chr14	107349540	528854	0.0049	0.0731
chr15	102531392	782457	0.0076	0.0891
chr16	90354753	817384	0.009	0.0996
chr17	81195210	814620	0.01	0.1062
chr18	78077248	606367	0.0078	0.1362
chr19	59128983	457899	0.0077	0.1143
chr20	63025520	592525	0.0094	0.1004
chr21	48129895	364986	0.0076	0.0931
chr22	51304566	198690	0.0039	0.0637
chrMT	16571	2515	0.1518	0.4531
chrX	155270560	1198209	0.0077	0.093
chrY	59373566	78496	0.0013	0.051

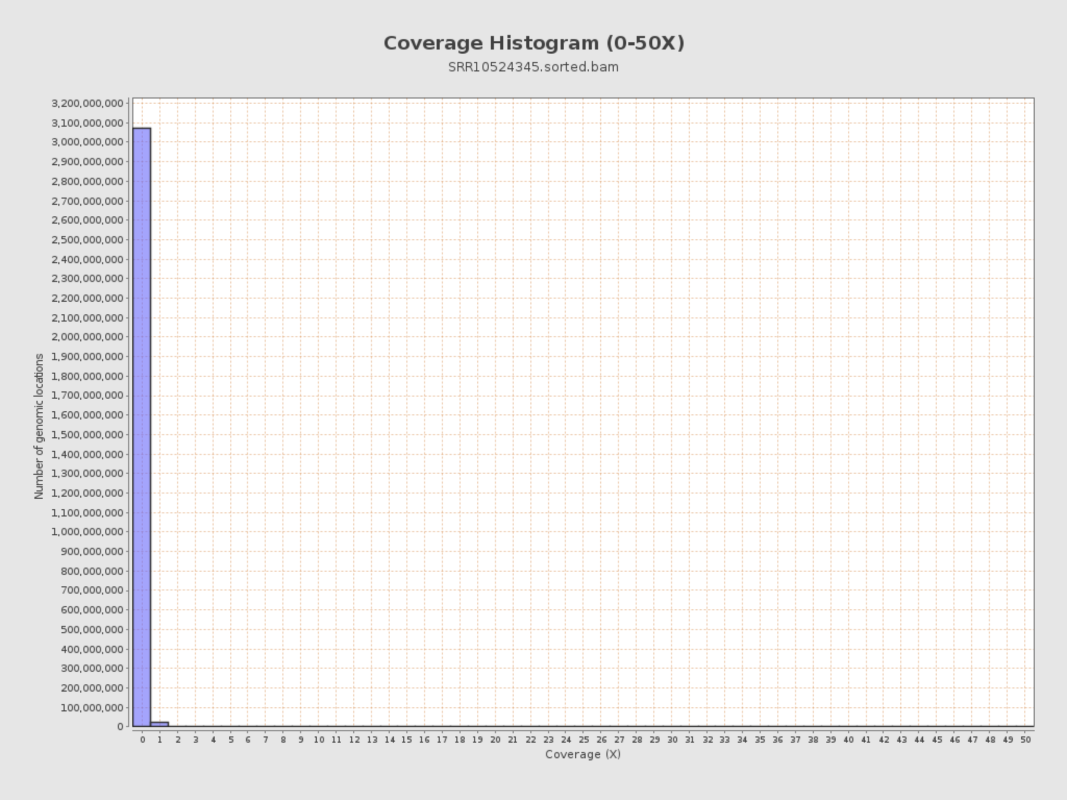
3. Results : Coverage across reference



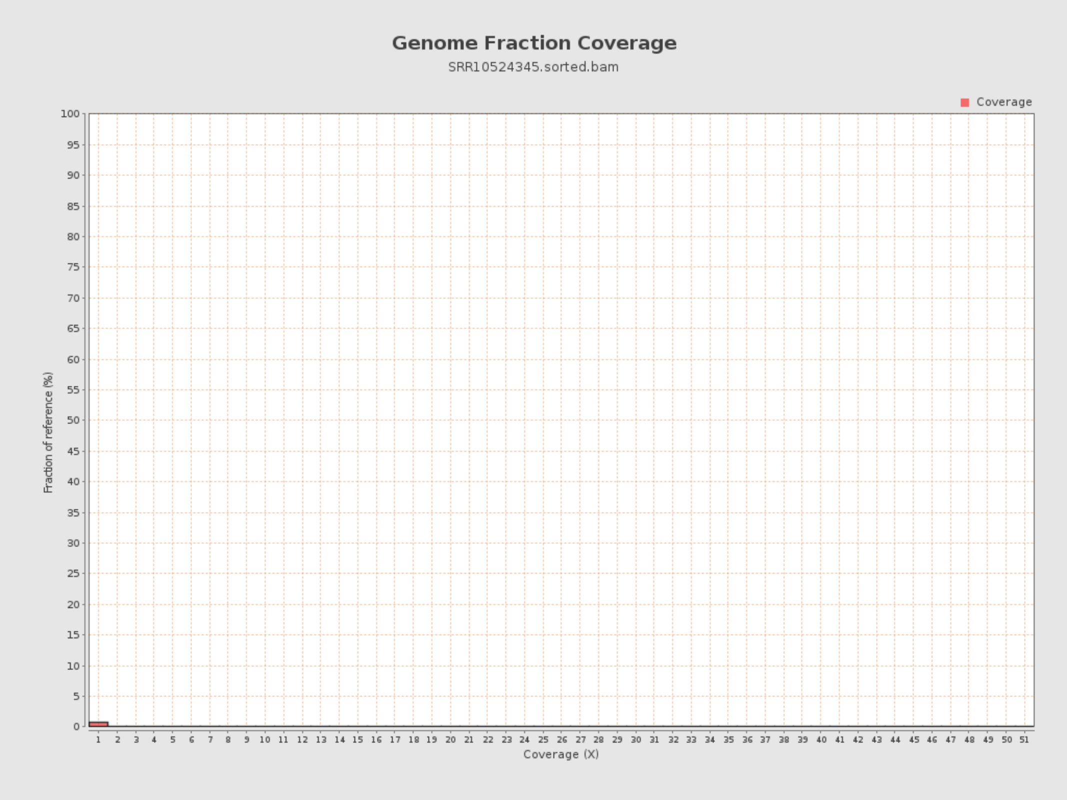
4. Results : Coverage Histogram



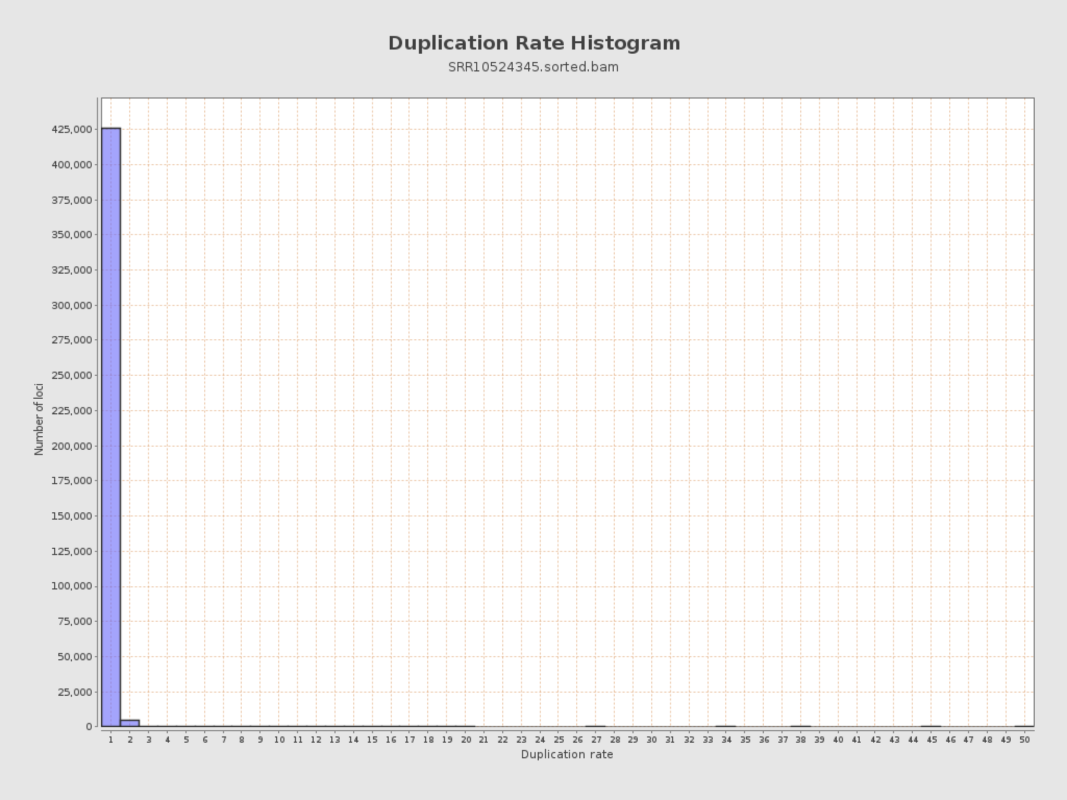
5. Results : Coverage Histogram (0-50X)



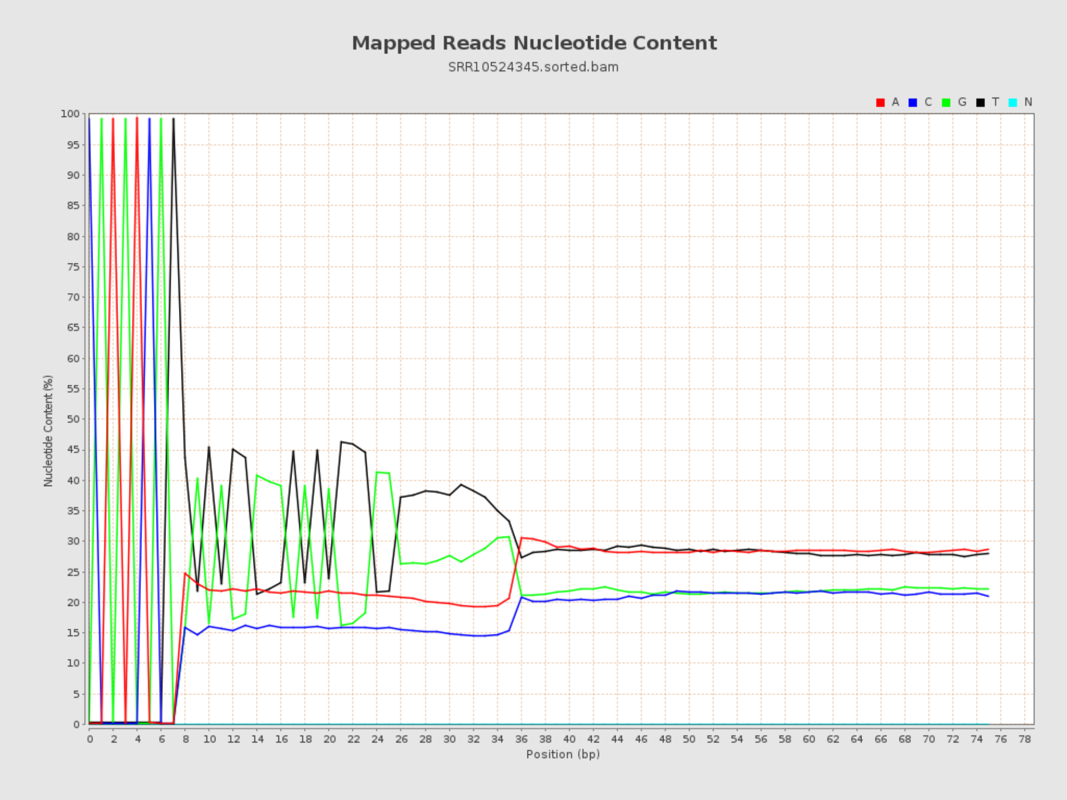
6. Results : Genome Fraction Coverage



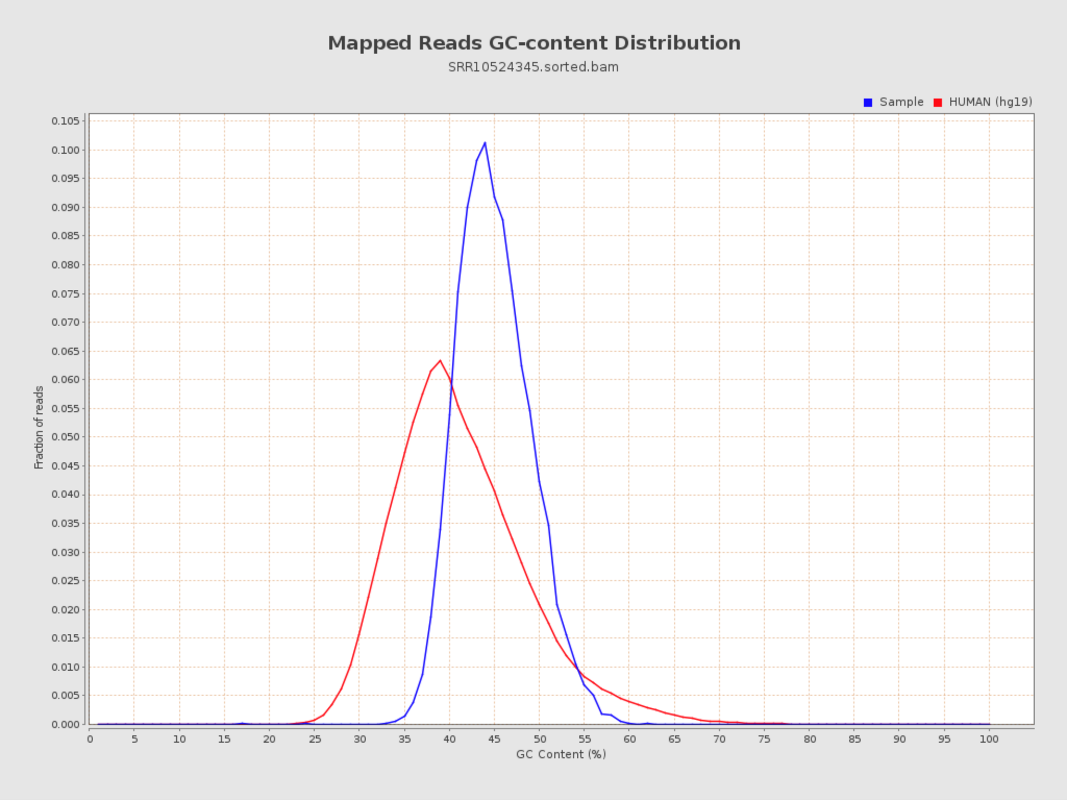
7. Results : Duplication Rate Histogram



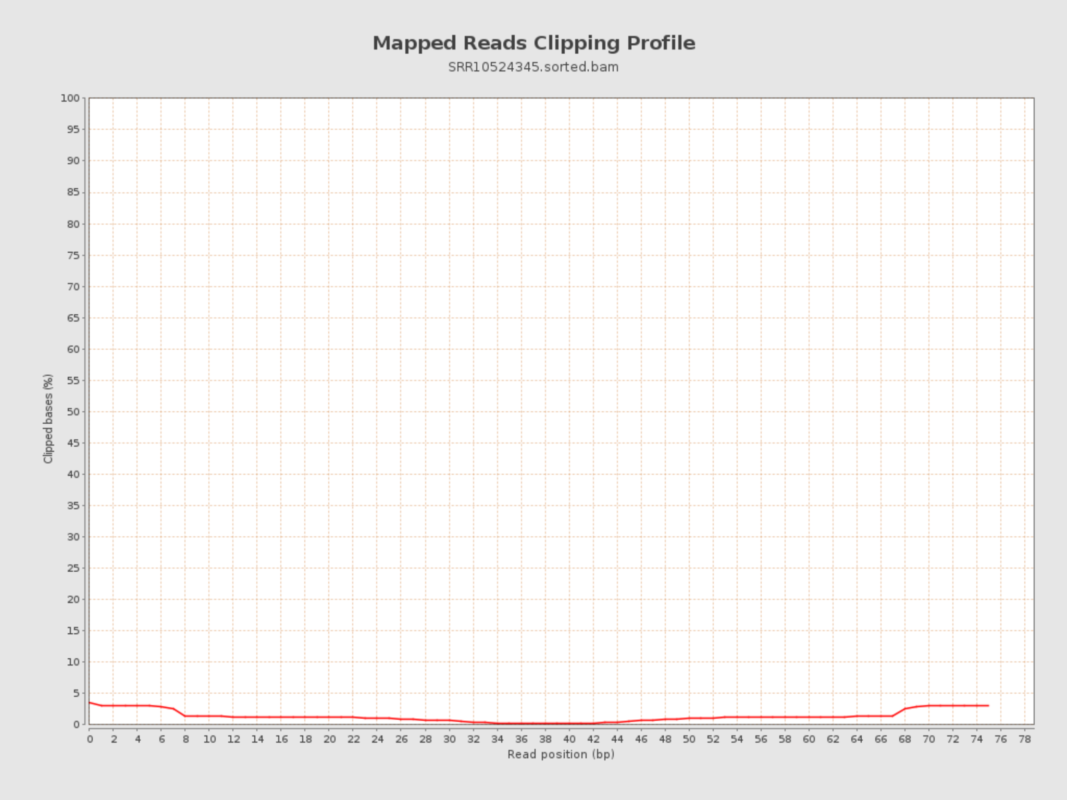
8. Results : Mapped Reads Nucleotide Content



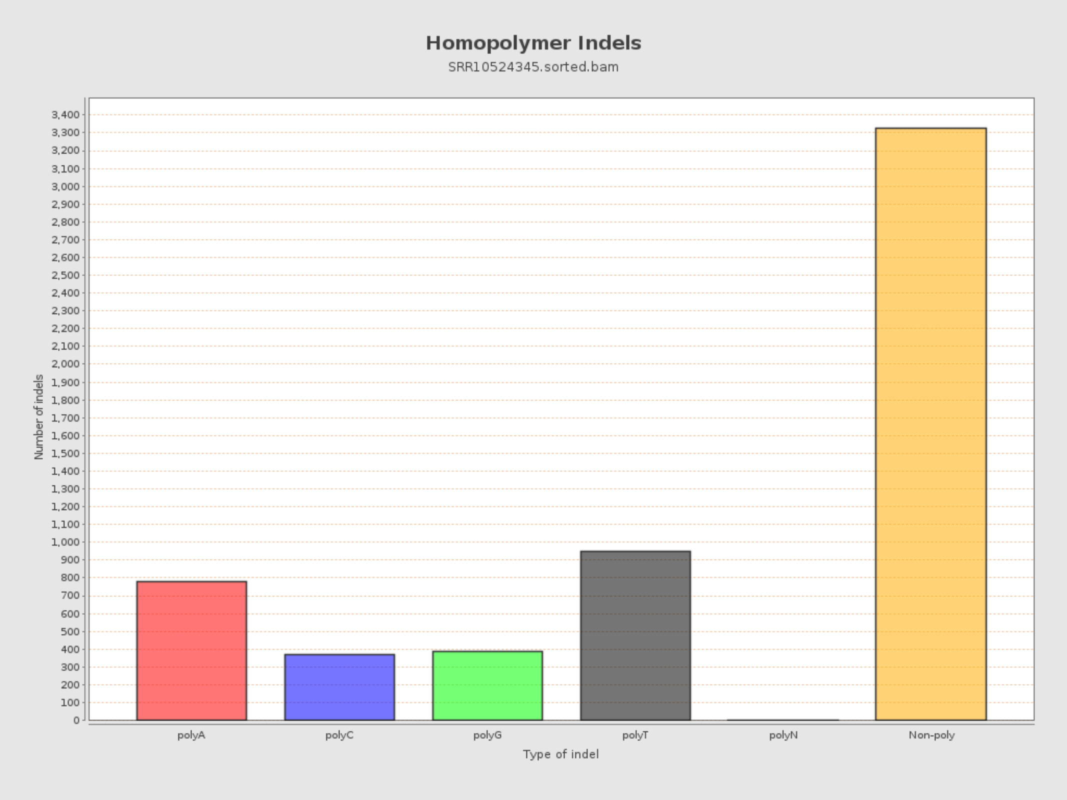
9. Results : Mapped Reads GC-content Distribution



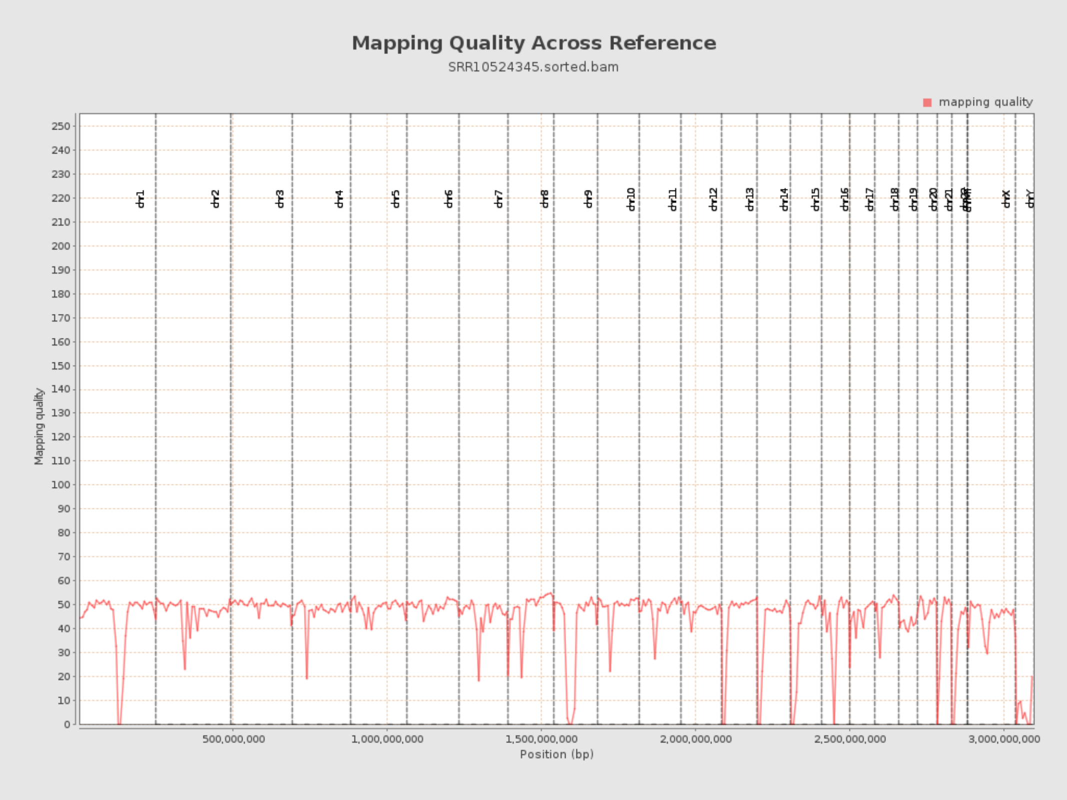
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram