Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:08:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524460.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_SRR10524460 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524460.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:08:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524460.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	575,215
Mapped reads	533,651 / 92.77%
Unmapped reads	41,564 / 7.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,283 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	12,468 / 2.17%
Duplication rate	1.87%
Clipped reads	533,478 / 92.74%

2.2. ACGT Content

Number/percentage of A's	7,444,182 / 23.89%
Number/percentage of C's	5,561,262 / 17.85%
Number/percentage of T's	10,239,042 / 32.86%
Number/percentage of G's	7,911,975 / 25.39%
Number/percentage of N's	698 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0101

Standard Deviation	0.1239

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

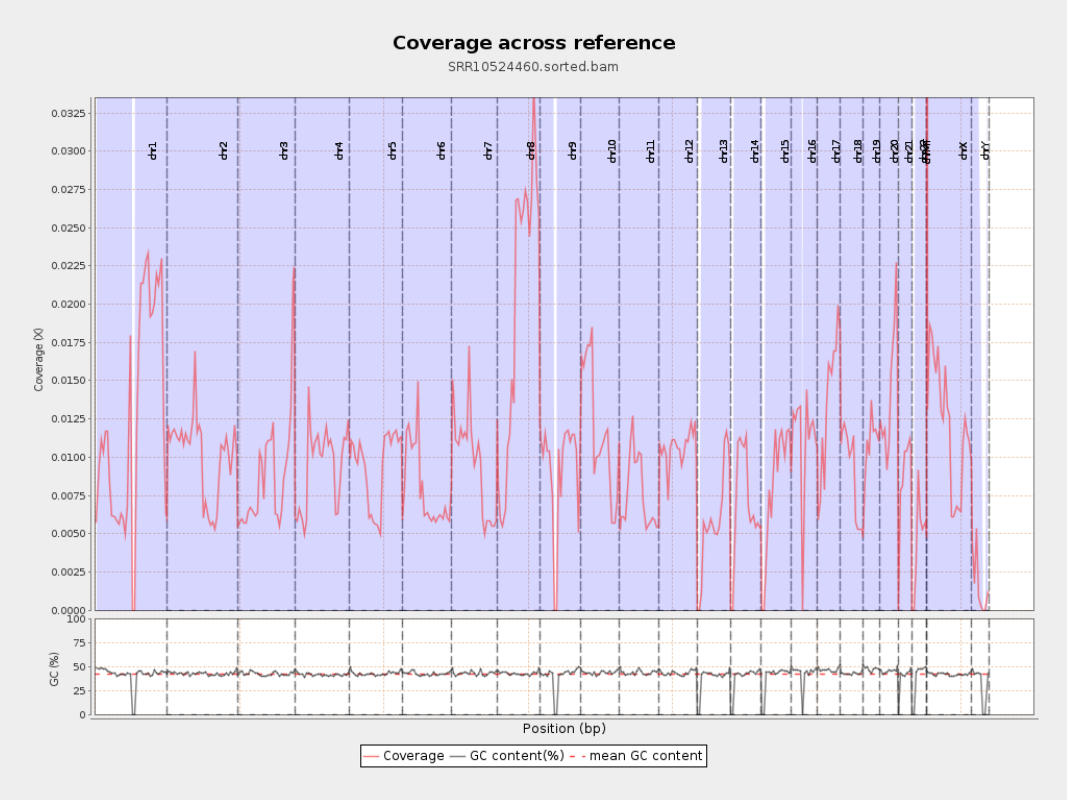
General error rate	0.47%
Mismatches	142,965
Insertions	2,039
Mapped reads with at least one insertion	0.38%
Deletions	5,442
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.01%

2.6. Chromosome stats

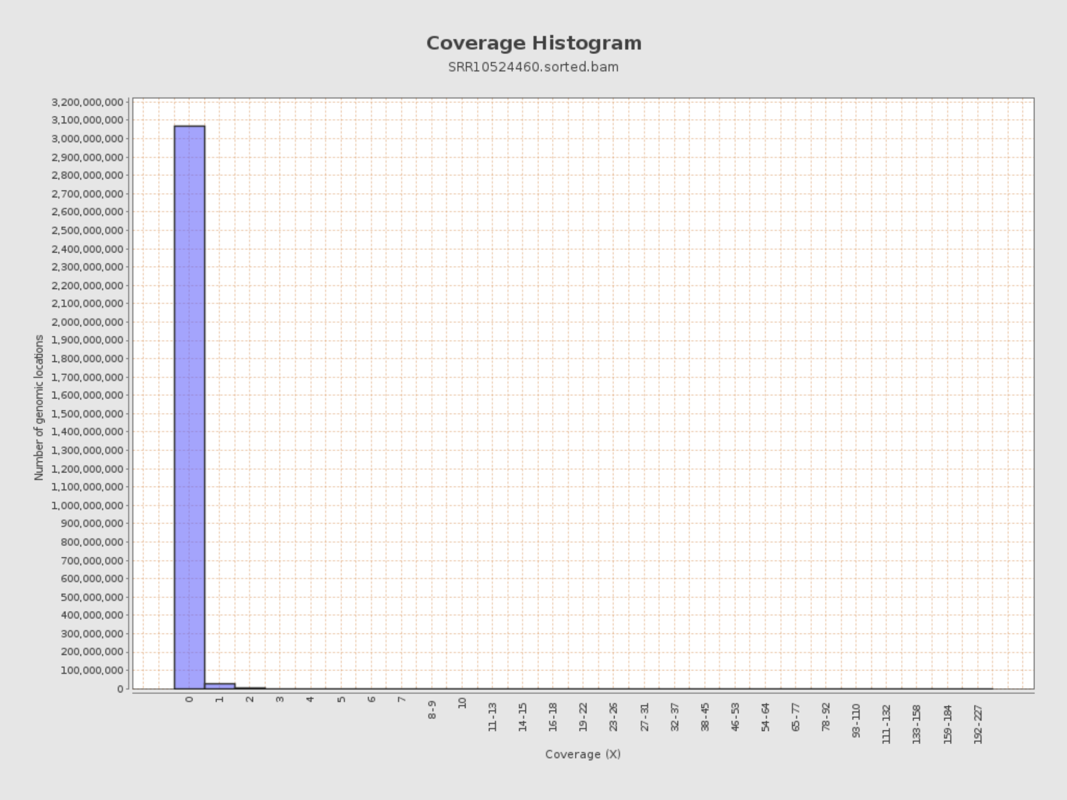
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3069313	0.0123	0.1928
chr2	243199373	2467412	0.0101	0.1287
chr3	198022430	1731018	0.0087	0.0977
chr4	191154276	1803926	0.0094	0.1061
chr5	180915260	1700319	0.0094	0.1015
chr6	171115067	1360522	0.008	0.1019
chr7	159138663	1548460	0.0097	0.1517

chr8	146364022	2888221	0.0197	0.1545
chr9	141213431	1280349	0.0091	0.1121
chr10	135534747	1614857	0.0119	0.1301
chr11	135006516	1030272	0.0076	0.1121
chr12	133851895	1423586	0.0106	0.1075
chr13	115169878	678002	0.0059	0.0799
chr14	107349540	740399	0.0069	0.0874
chr15	102531392	833589	0.0081	0.0948
chr16	90354753	985557	0.0109	0.1112
chr17	81195210	1087781	0.0134	0.1229
chr18	78077248	711207	0.0091	0.1494
chr19	59128983	643695	0.0109	0.1467
chr20	63025520	900669	0.0143	0.1256
chr21	48129895	423451	0.0088	0.1003
chr22	51304566	237191	0.0046	0.0709
chrMT	16571	17454	1.0533	1.2145
chrX	155270560	1893955	0.0122	0.1204
chrY	59373566	95212	0.0016	0.0519

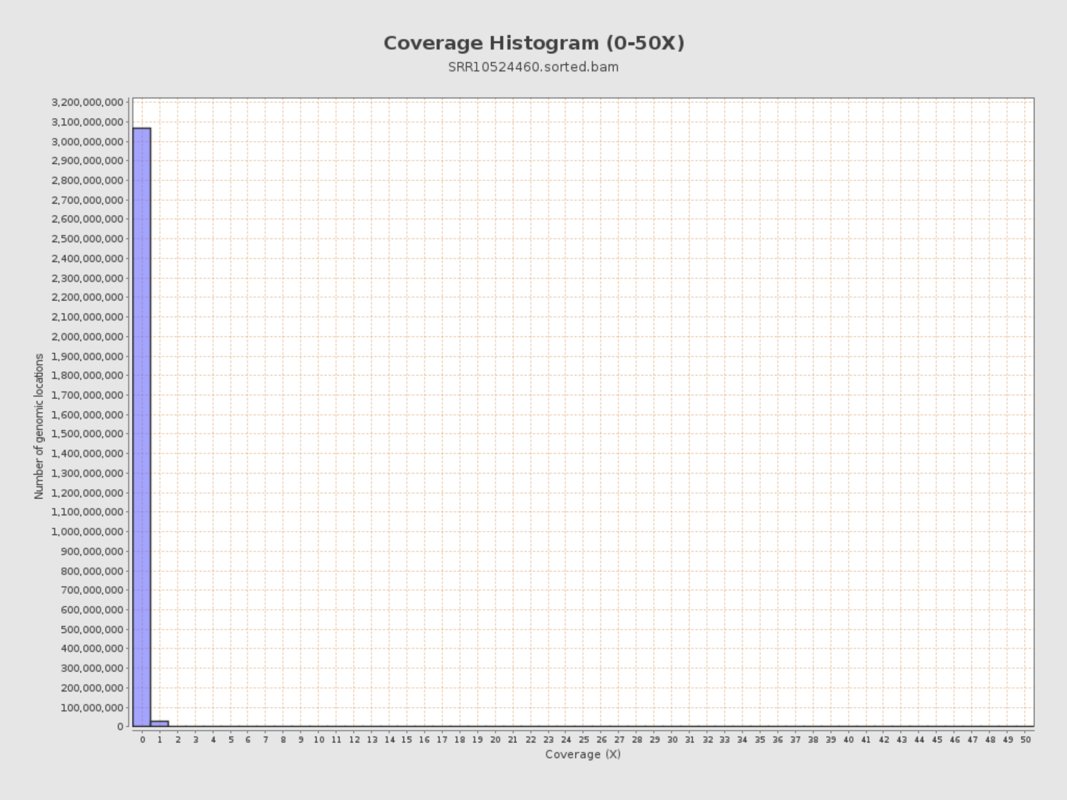
3. Results : Coverage across reference



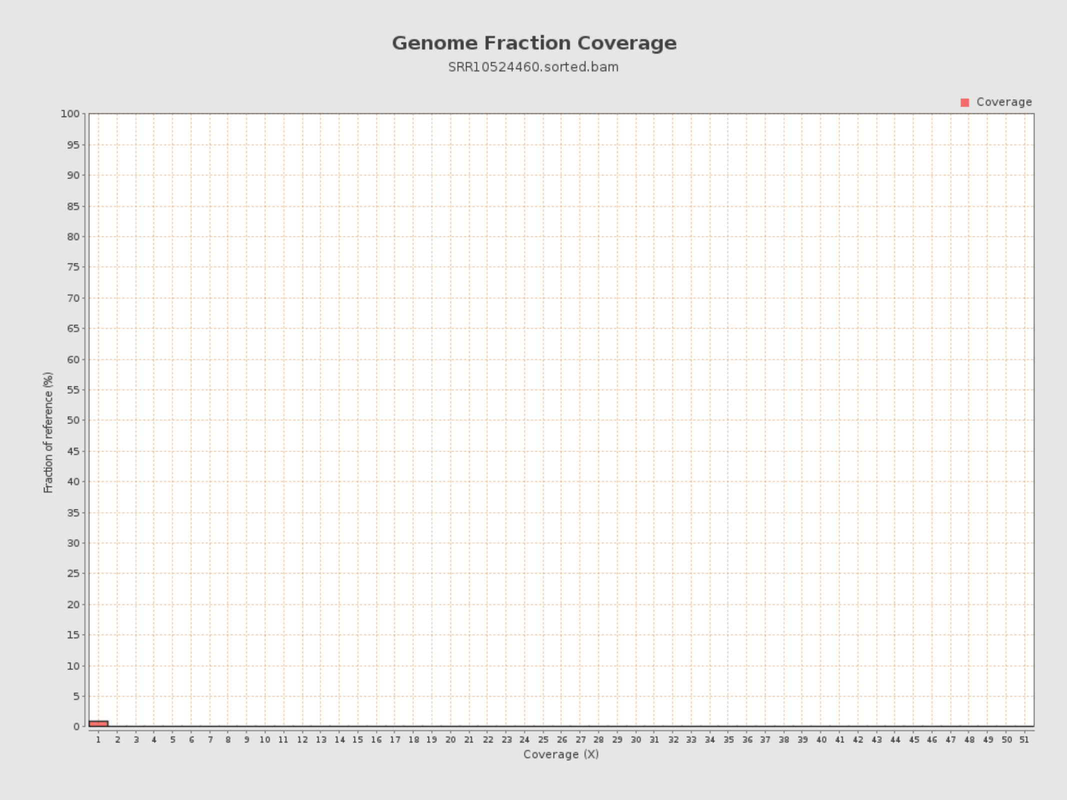
4. Results : Coverage Histogram



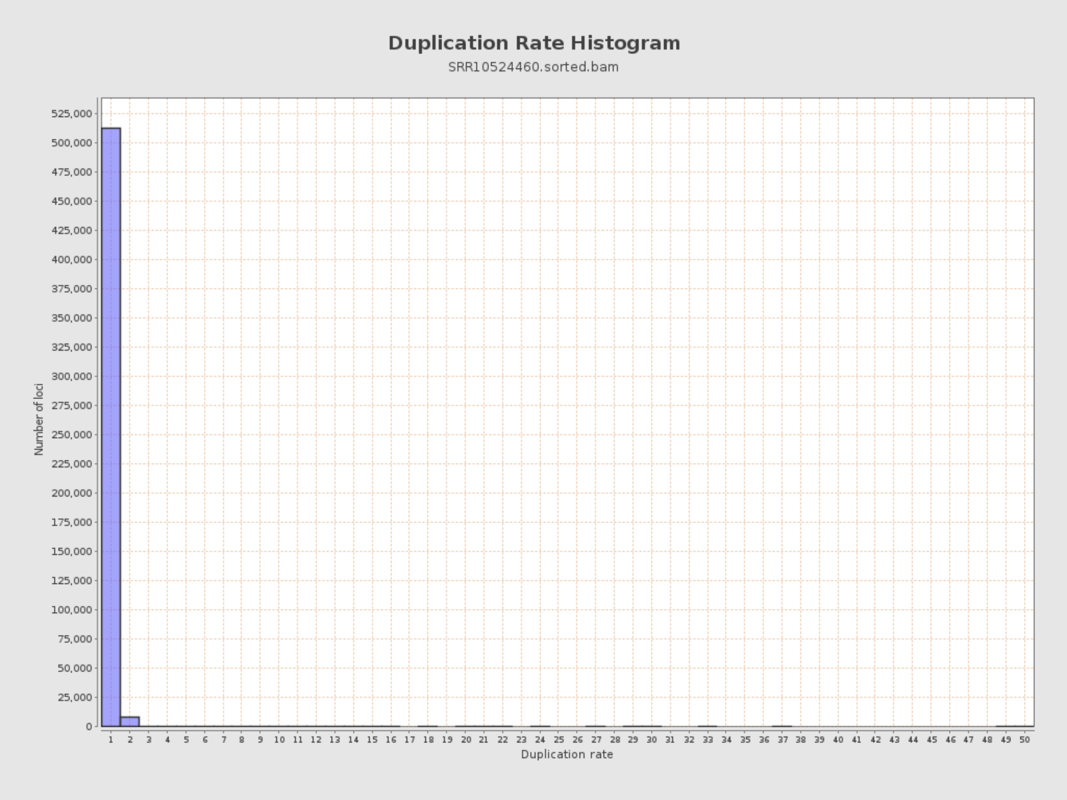
5. Results : Coverage Histogram (0-50X)



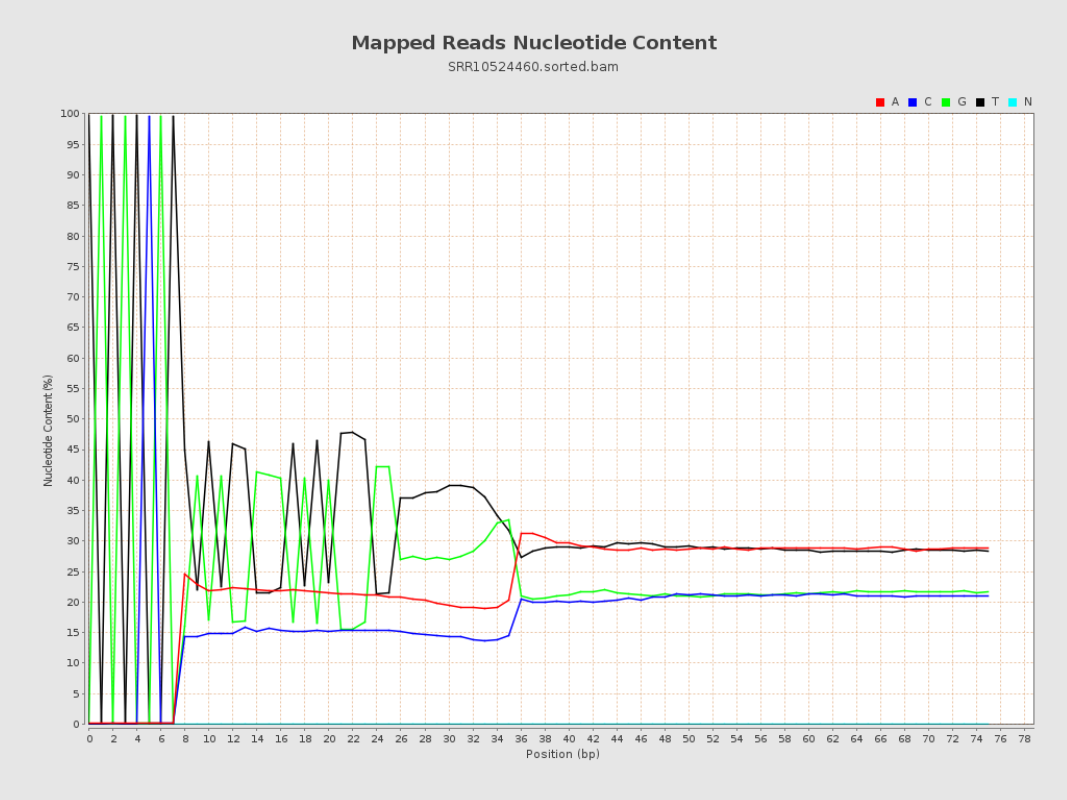
6. Results : Genome Fraction Coverage



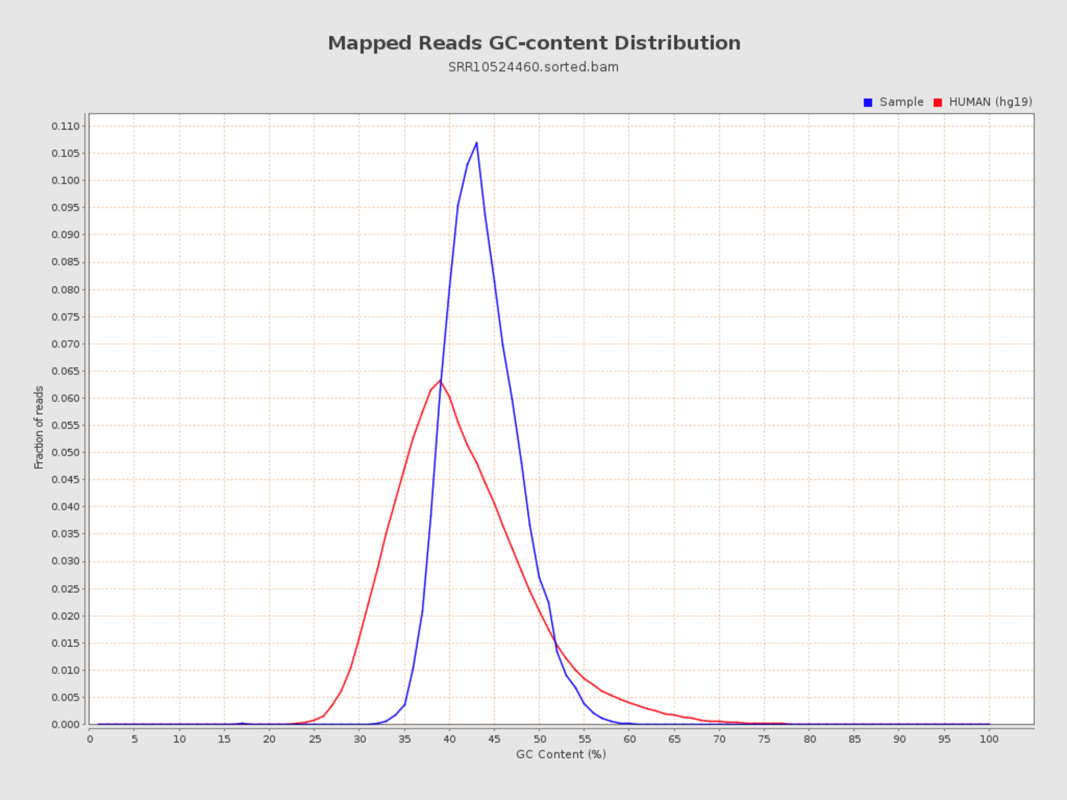
7. Results : Duplication Rate Histogram



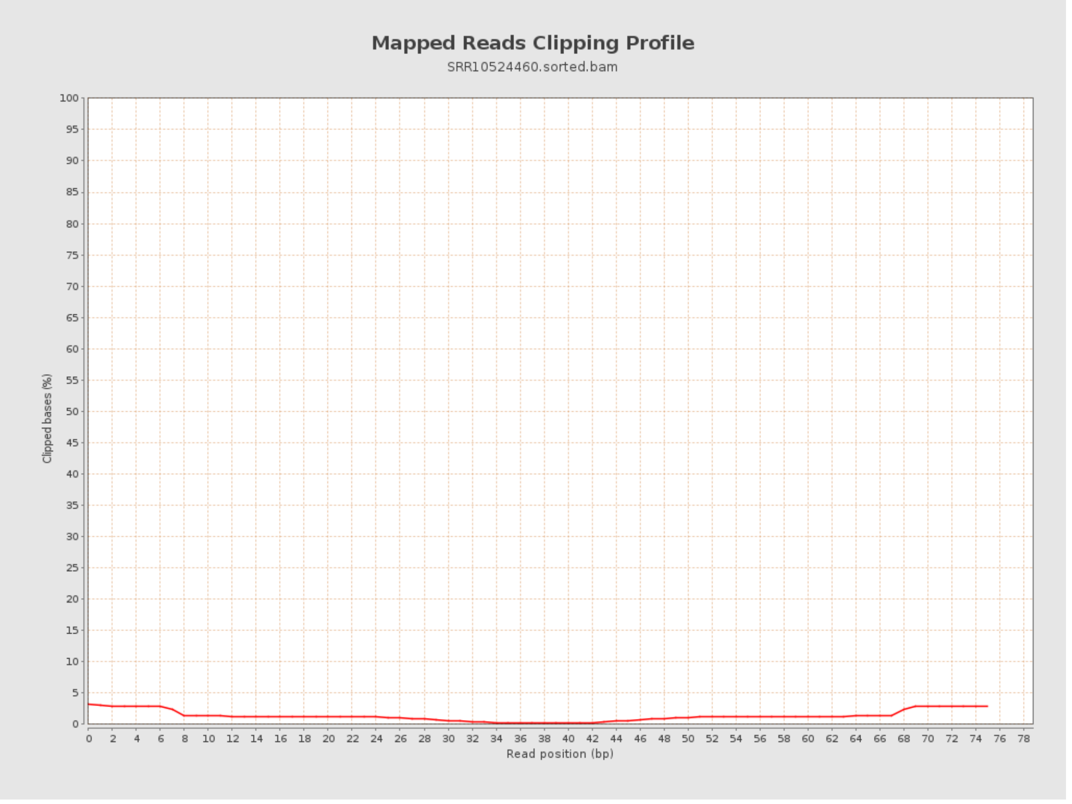
8. Results : Mapped Reads Nucleotide Content



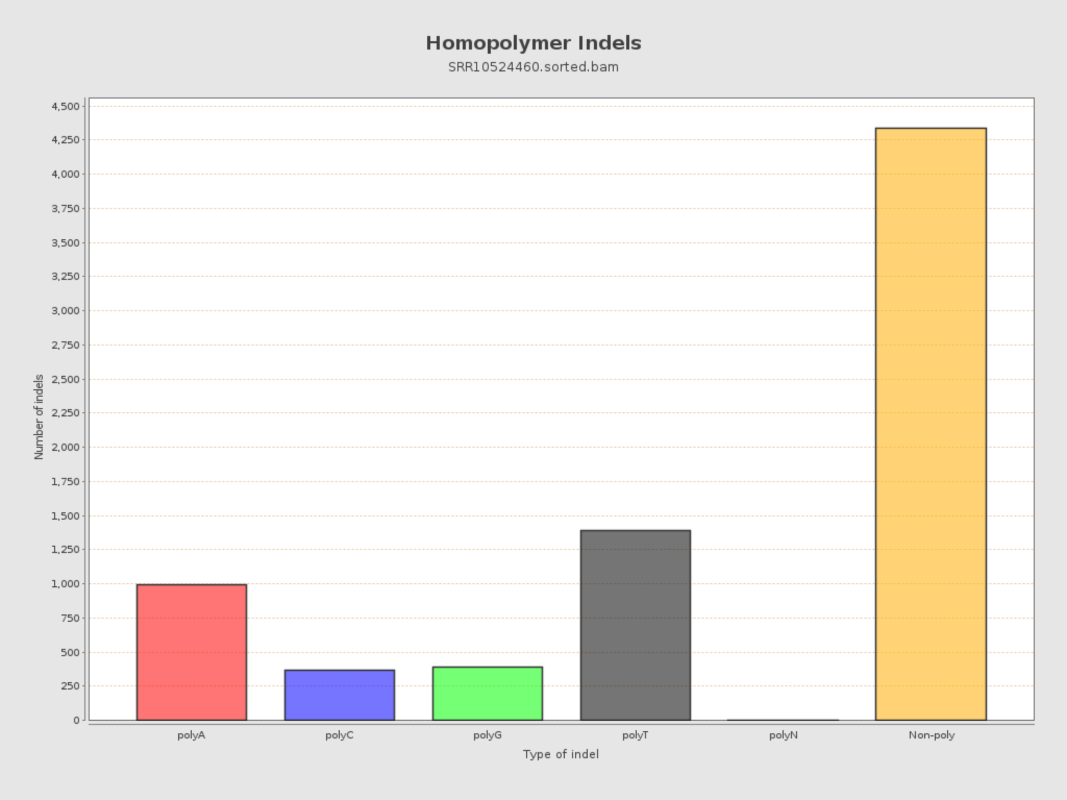
9. Results : Mapped Reads GC-content Distribution



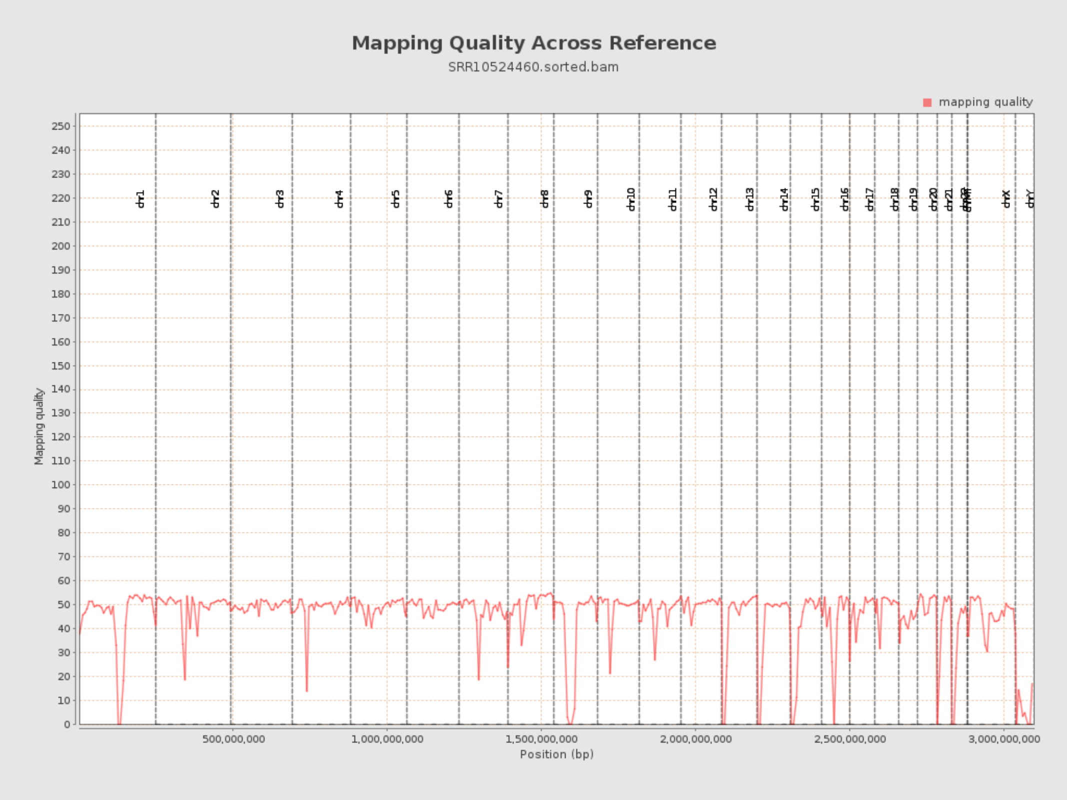
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram