Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524482.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_SRR10524482 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524482.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:54:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524482.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	643,557
Mapped reads	597,631 / 92.86%
Unmapped reads	45,926 / 7.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,370 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	14,501 / 2.25%
Duplication rate	1.89%
Clipped reads	597,528 / 92.85%

2.2. ACGT Content

Number/percentage of A's	8,658,902 / 24.81%
Number/percentage of C's	6,821,274 / 19.54%
Number/percentage of T's	10,835,041 / 31.04%
Number/percentage of G's	8,591,010 / 24.61%
Number/percentage of N's	728 / 0%
GC Percentage	44.15%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1333

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

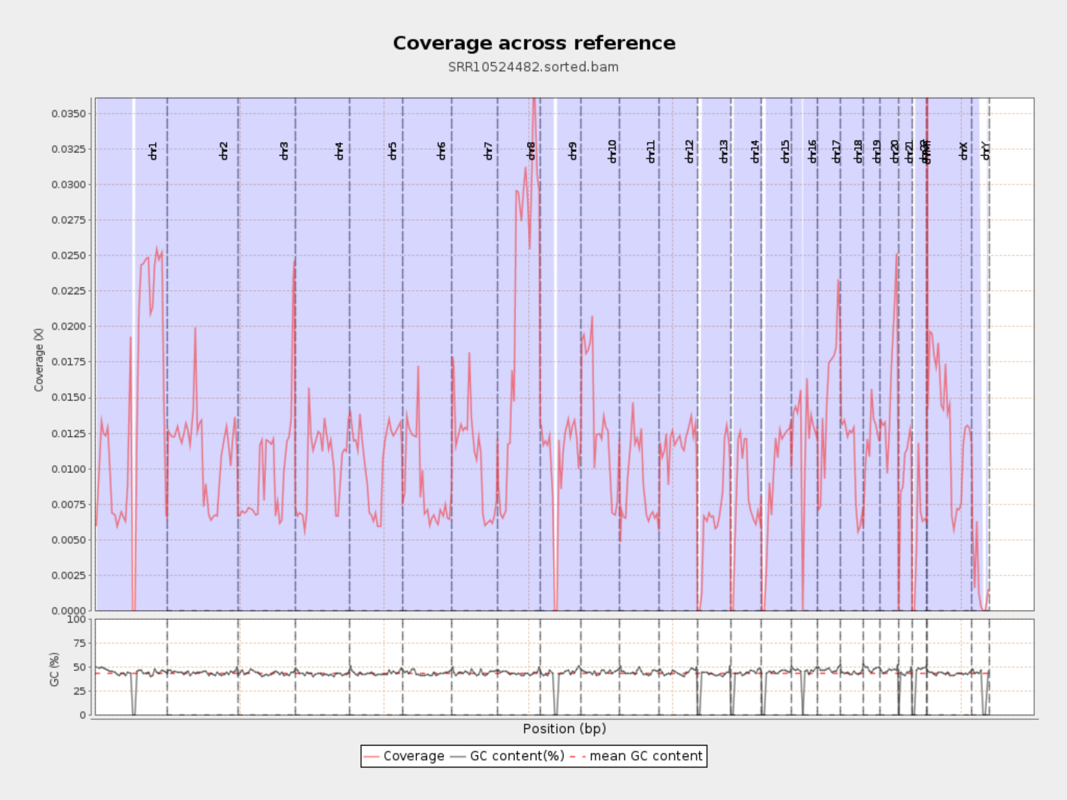
General error rate	0.48%
Mismatches	162,935
Insertions	2,194
Mapped reads with at least one insertion	0.37%
Deletions	6,491
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.08%

2.6. Chromosome stats

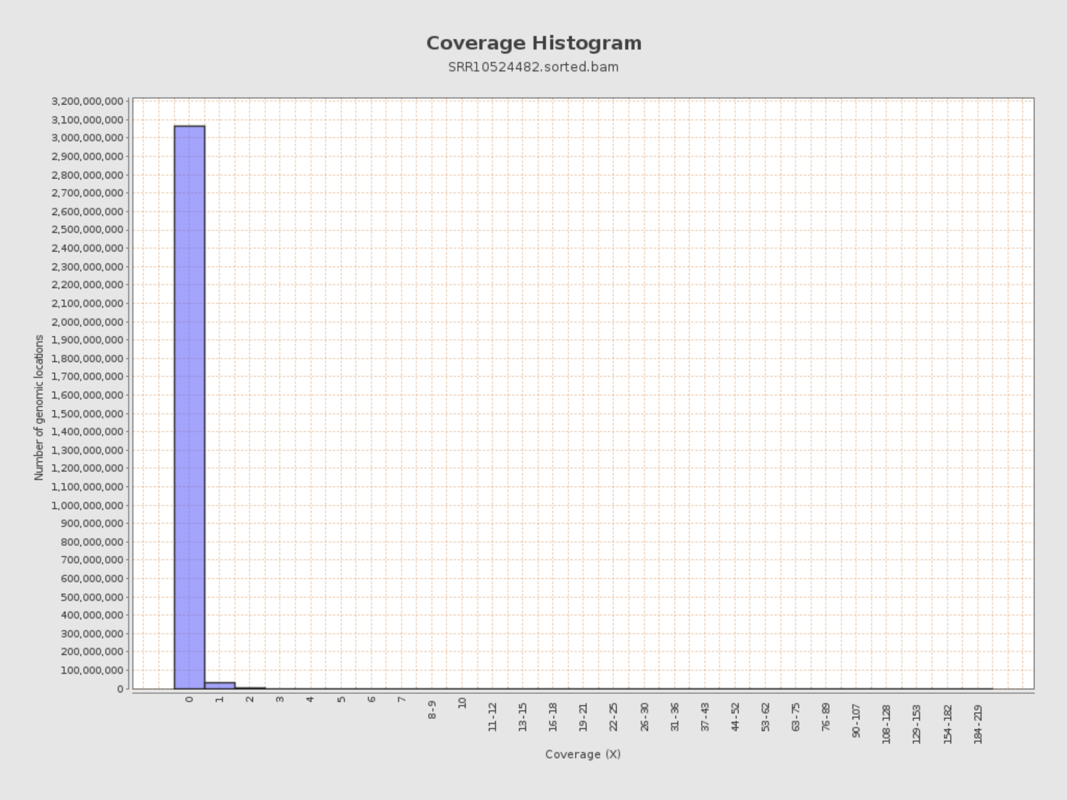
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3469715	0.0139	0.2076
chr2	243199373	2759940	0.0113	0.146
chr3	198022430	1916362	0.0097	0.1031
chr4	191154276	1963623	0.0103	0.1122
chr5	180915260	1931225	0.0107	0.1084
chr6	171115067	1513021	0.0088	0.1121
chr7	159138663	1748487	0.011	0.1539

chr8	146364022	3191451	0.0218	0.1644
chr9	141213431	1475596	0.0104	0.122
chr10	135534747	1838270	0.0136	0.1412
chr11	135006516	1204666	0.0089	0.1255
chr12	133851895	1596710	0.0119	0.1145
chr13	115169878	780120	0.0068	0.0869
chr14	107349540	822340	0.0077	0.0931
chr15	102531392	921224	0.009	0.1013
chr16	90354753	1099114	0.0122	0.1185
chr17	81195210	1215649	0.015	0.1309
chr18	78077248	821533	0.0105	0.1652
chr19	59128983	718647	0.0122	0.1599
chr20	63025520	1002952	0.0159	0.1329
chr21	48129895	463208	0.0096	0.1057
chr22	51304566	287579	0.0056	0.0788
chrMT	16571	1470	0.0887	0.3037
chrX	155270560	2062392	0.0133	0.1261
chrY	59373566	113039	0.0019	0.0609

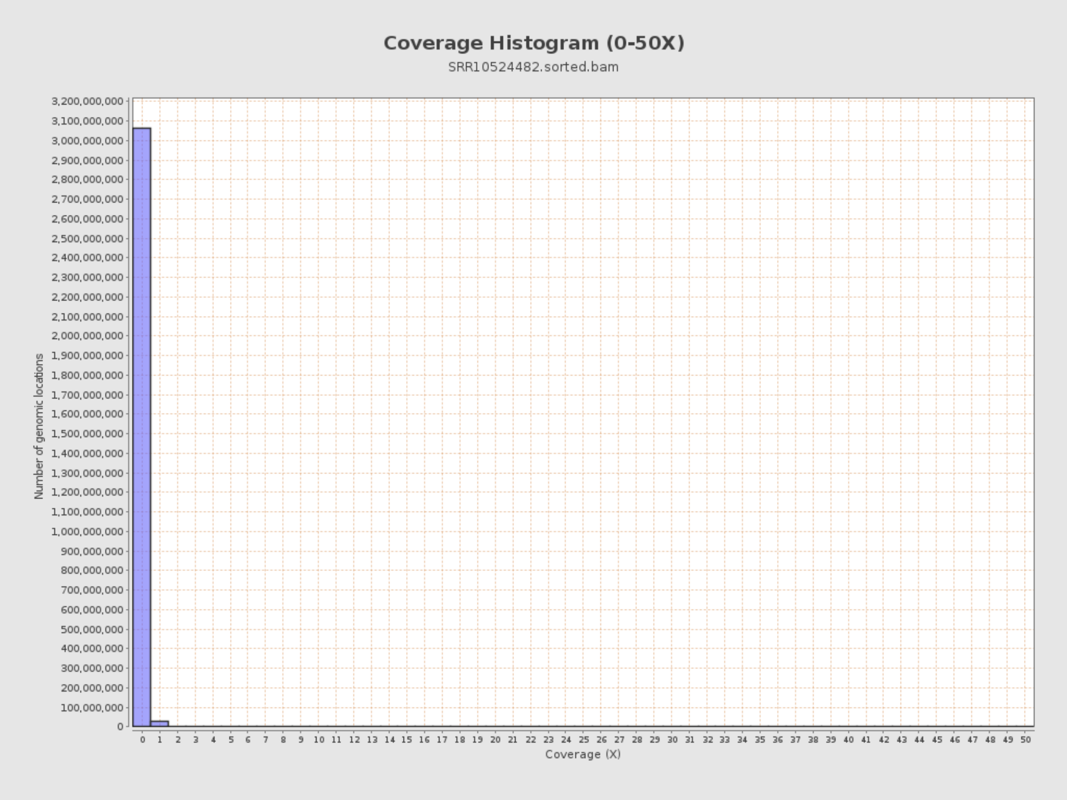
3. Results : Coverage across reference



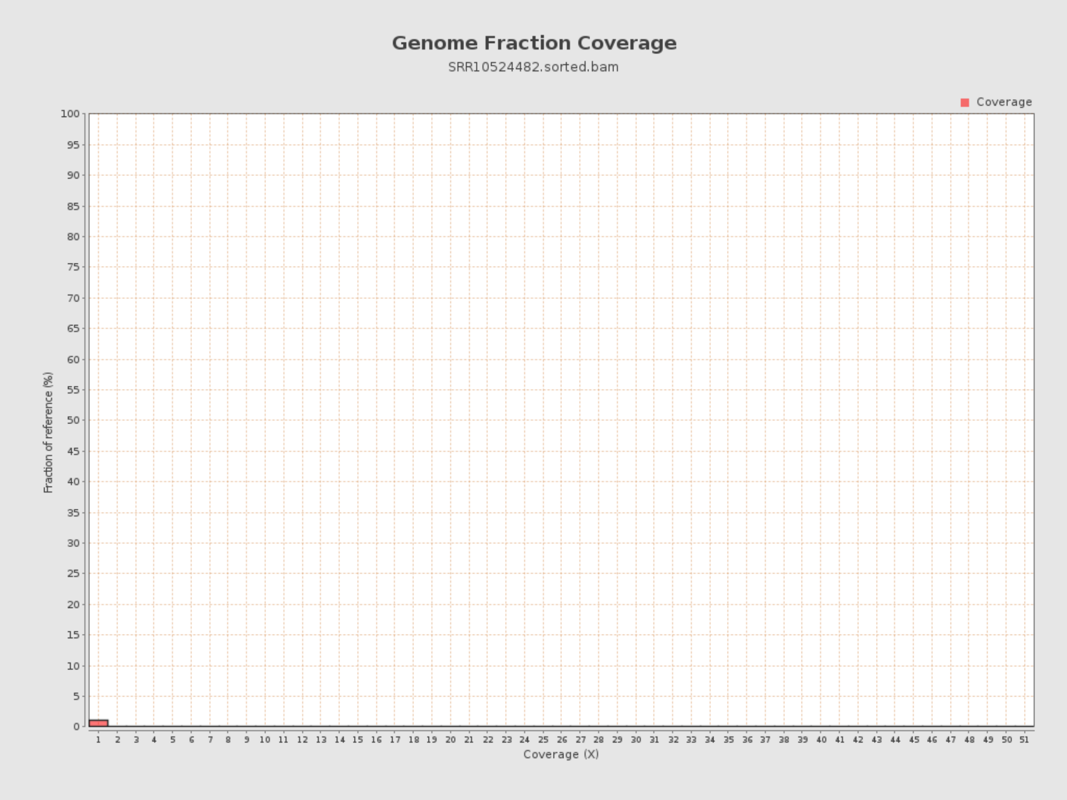
4. Results : Coverage Histogram



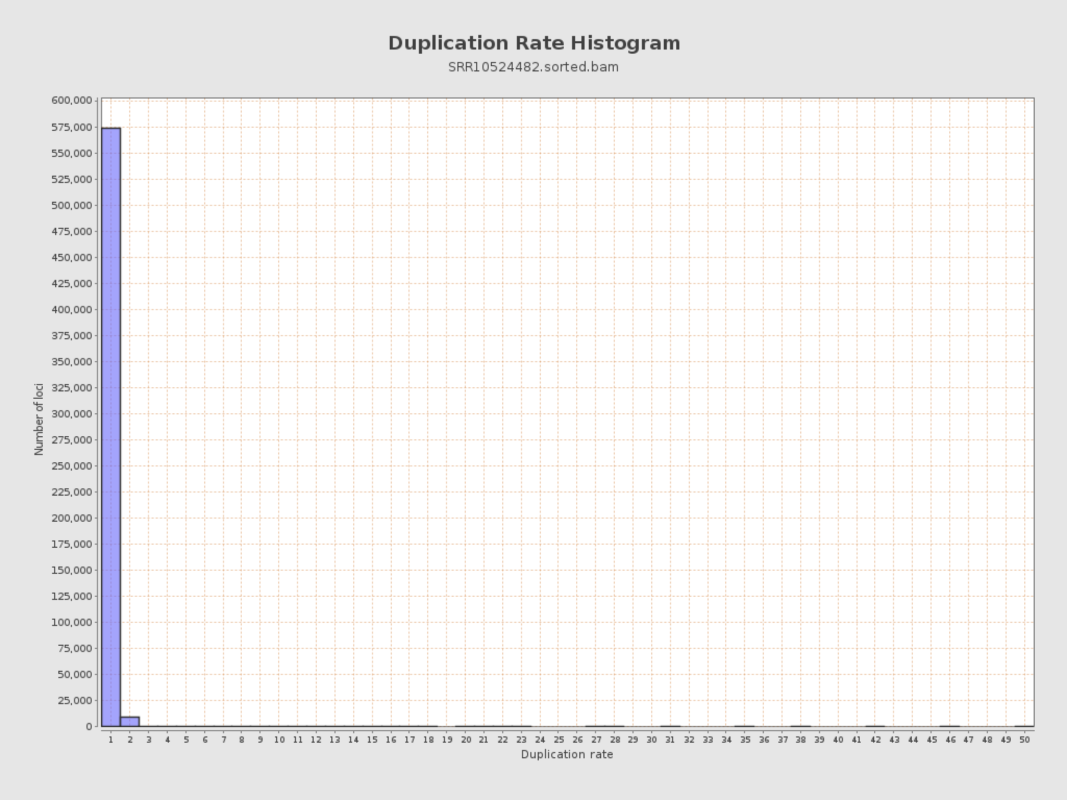
5. Results : Coverage Histogram (0-50X)



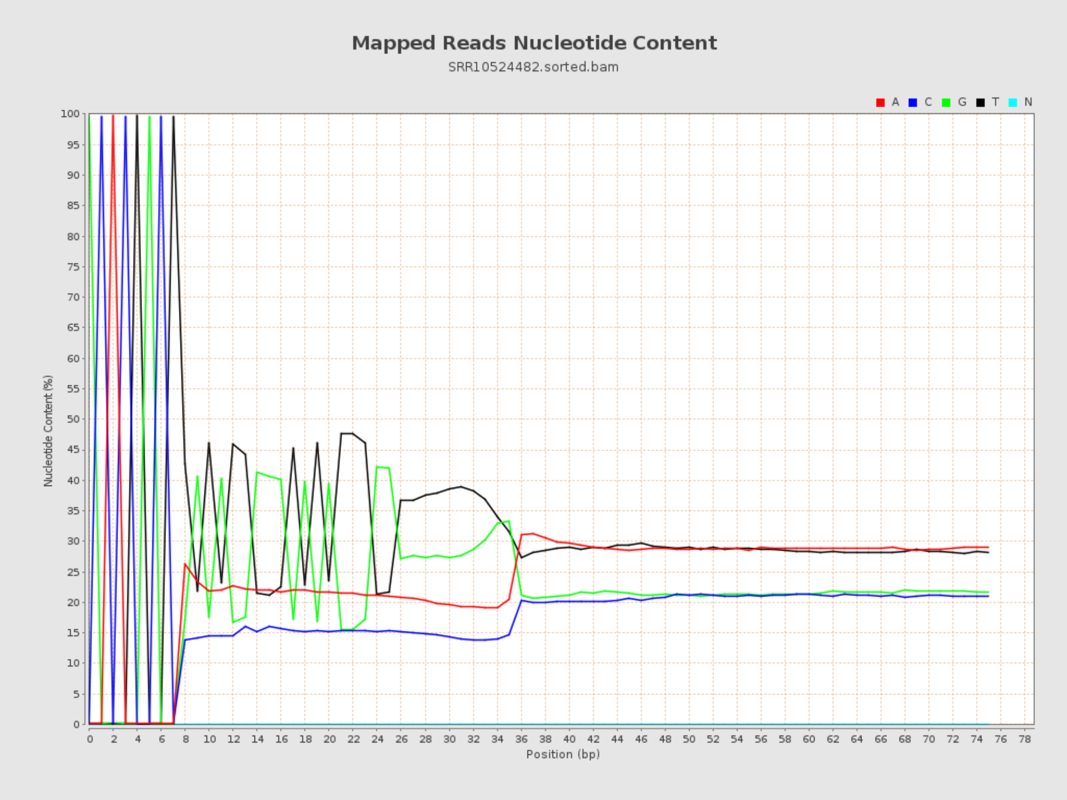
6. Results : Genome Fraction Coverage



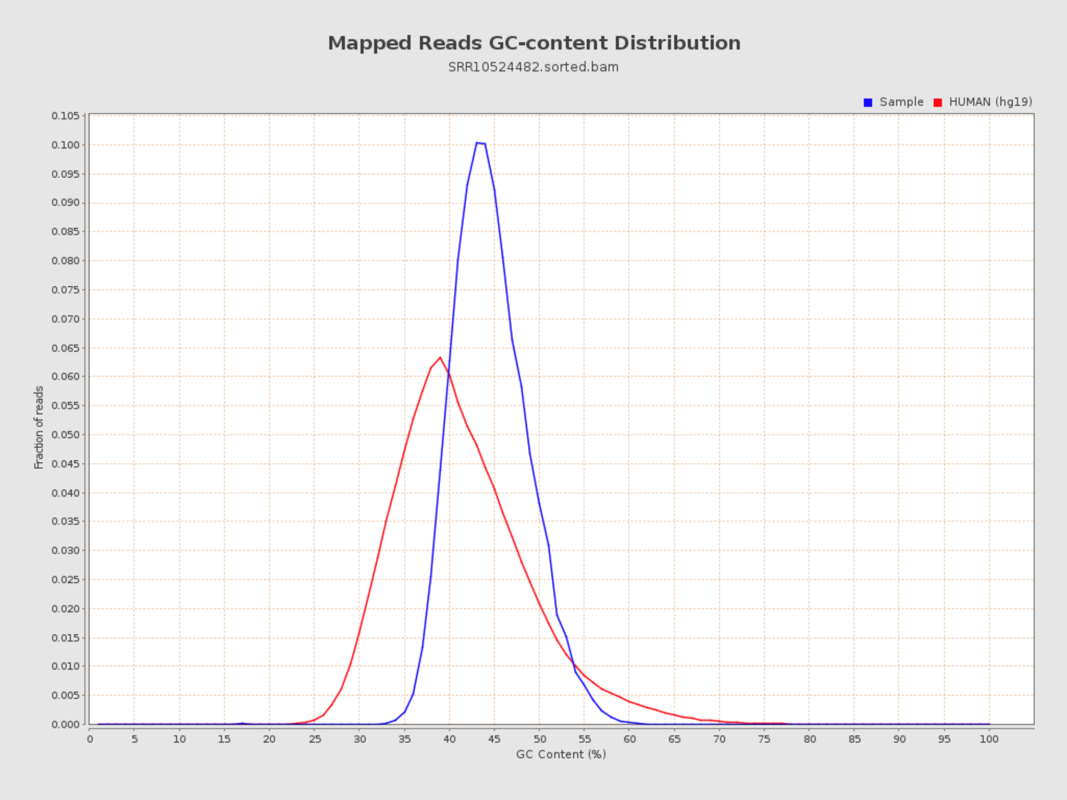
7. Results : Duplication Rate Histogram



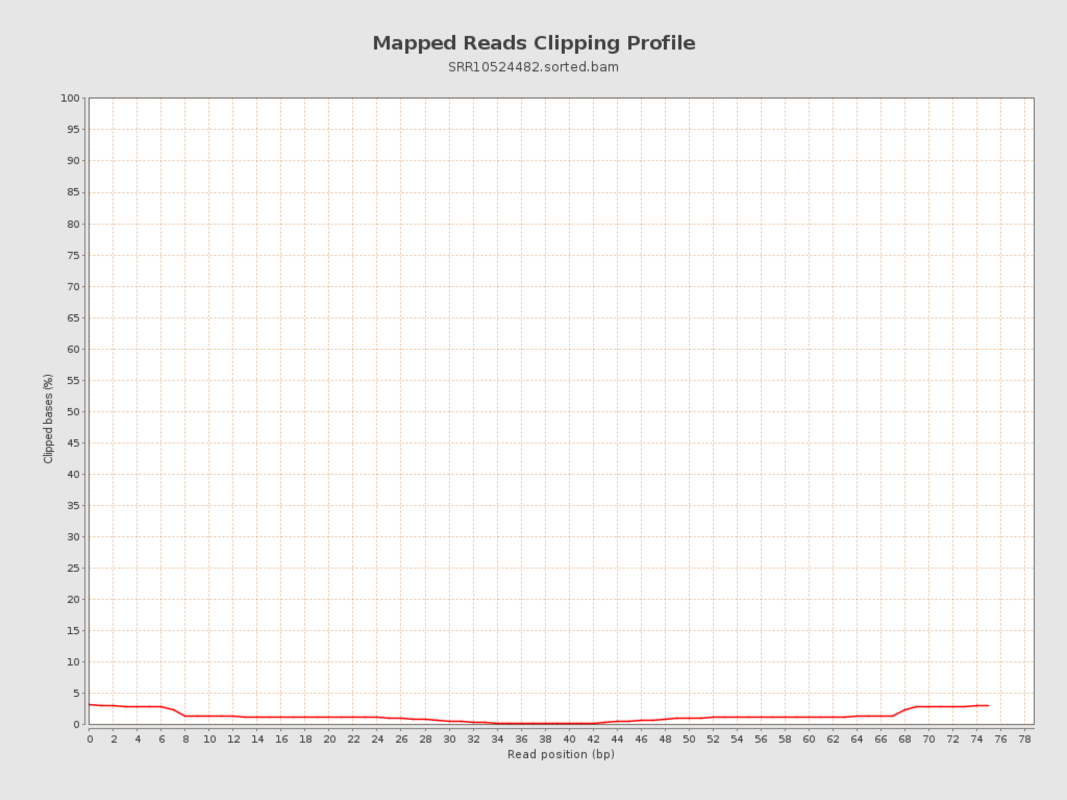
8. Results : Mapped Reads Nucleotide Content



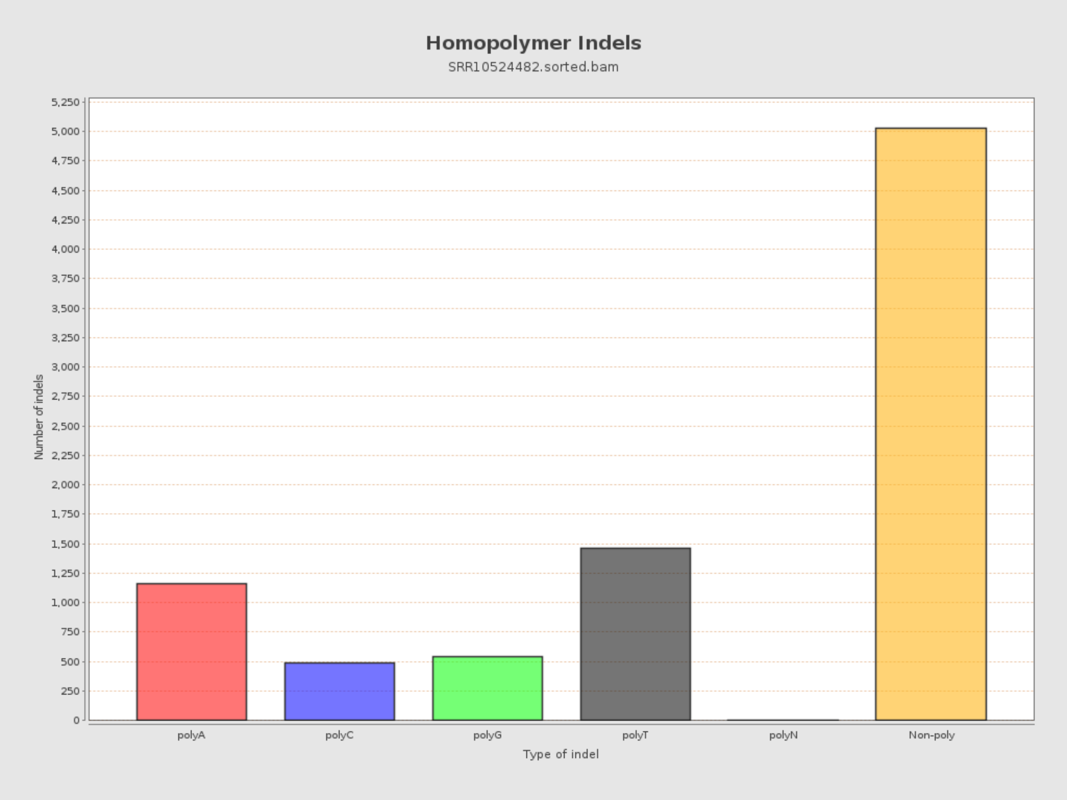
9. Results : Mapped Reads GC-content Distribution



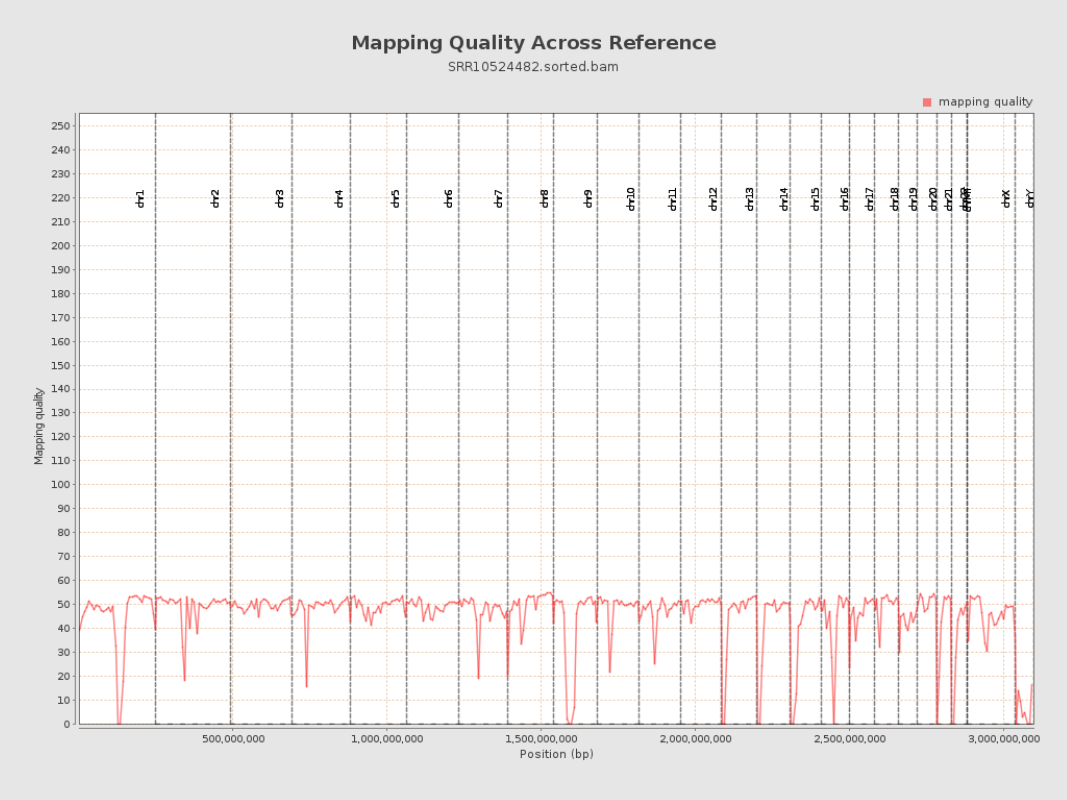
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram