Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:27:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524496.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_SRR10524496 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524496.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:27:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,066,607
Mapped reads	6,545,756 / 92.63%
Unmapped reads	520,851 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,763 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	634,463 / 8.98%
Duplication rate	6.94%
Clipped reads	6,543,129 / 92.59%

2.2. ACGT Content

Number/percentage of A's	92,049,307 / 24.04%
Number/percentage of C's	68,221,335 / 17.82%
Number/percentage of T's	125,127,245 / 32.68%
Number/percentage of G's	97,452,123 / 25.45%
Number/percentage of N's	7,703 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.1237

Standard Deviation	0.9214

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

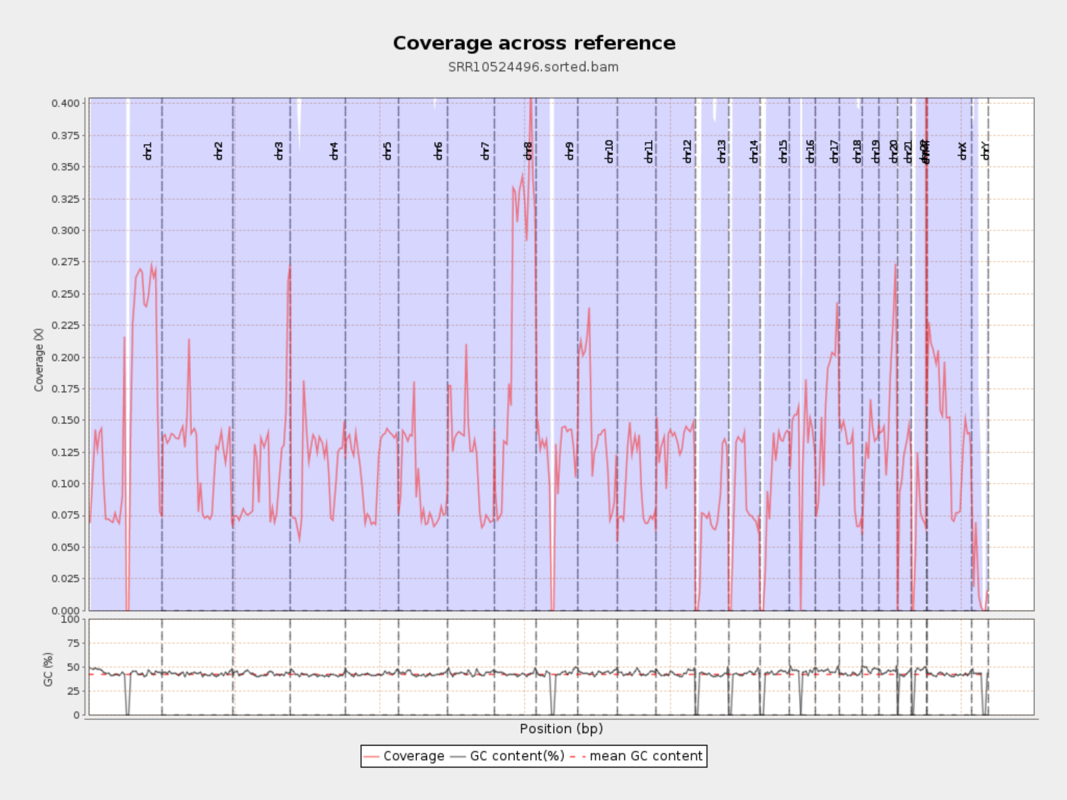
General error rate	0.47%
Mismatches	1,770,739
Insertions	24,364
Mapped reads with at least one insertion	0.37%
Deletions	71,570
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.13%

2.6. Chromosome stats

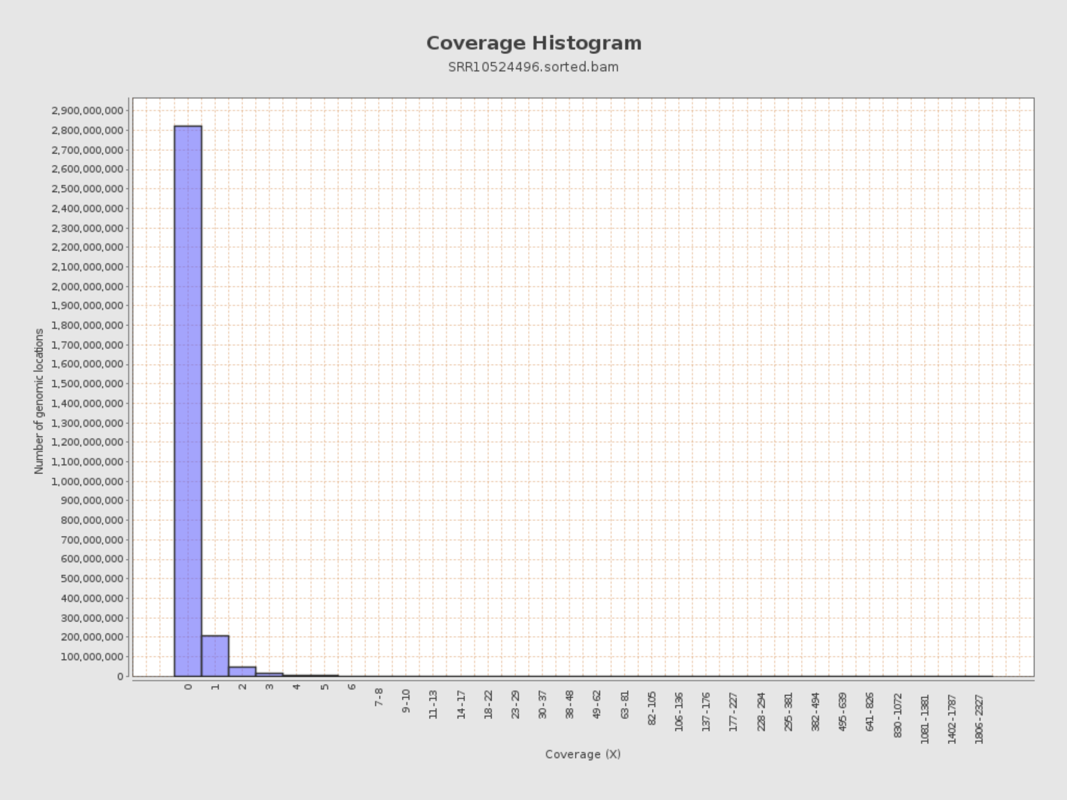
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37654333	0.1511	1.8095
chr2	243199373	30067023	0.1236	1.0736
chr3	198022430	21074465	0.1064	0.4514
chr4	191154276	21368976	0.1118	0.6079
chr5	180915260	21002630	0.1161	0.4647
chr6	171115067	16531415	0.0966	0.6944
chr7	159138663	19096249	0.12	1.3323

chr8	146364022	35305703	0.2412	0.8931
chr9	141213431	16292328	0.1154	0.7561
chr10	135534747	20084016	0.1482	0.9962
chr11	135006516	13014089	0.0964	0.9113
chr12	133851895	18013682	0.1346	0.5013
chr13	115169878	8511227	0.0739	0.371
chr14	107349540	9128547	0.085	0.4197
chr15	102531392	10133140	0.0988	0.4777
chr16	90354753	11985434	0.1326	0.5841
chr17	81195210	13348199	0.1644	0.6258
chr18	78077248	9008671	0.1154	1.5533
chr19	59128983	7756799	0.1312	1.2687
chr20	63025520	10884455	0.1727	0.5949
chr21	48129895	5250009	0.1091	0.5394
chr22	51304566	3113630	0.0607	0.3294
chrMT	16571	245116	14.7919	9.1731
chrX	155270560	22879808	0.1474	0.6681
chrY	59373566	1230948	0.0207	0.4873

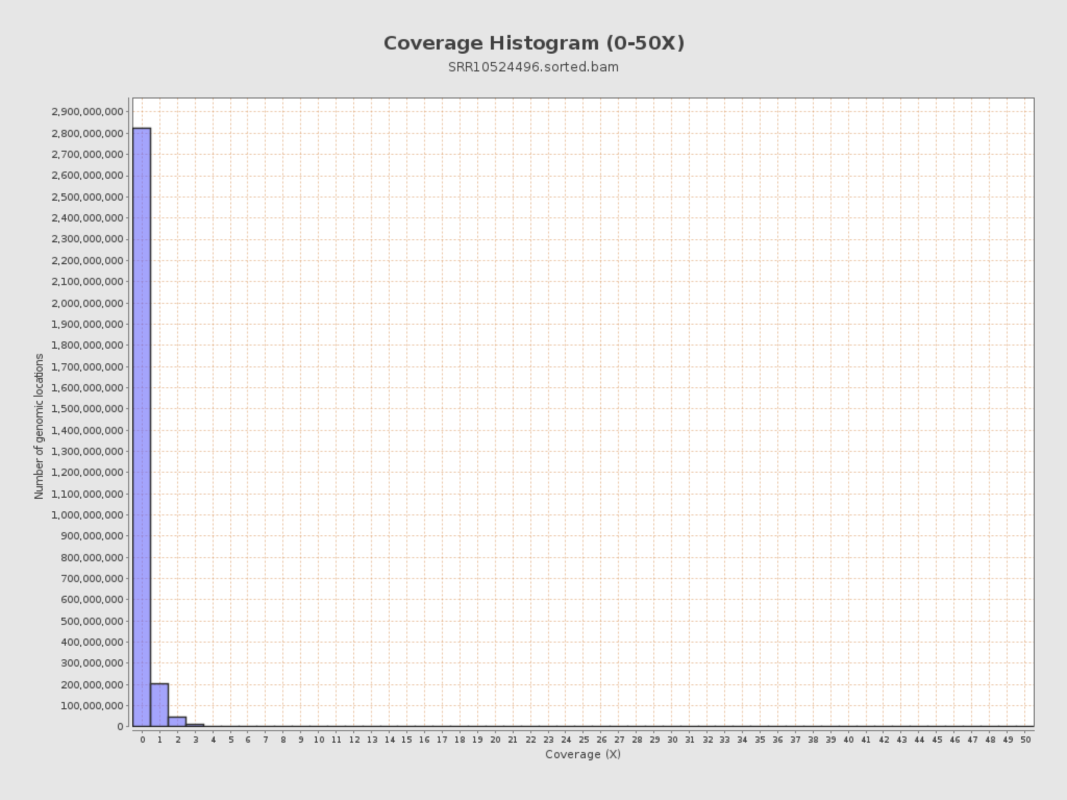
3. Results : Coverage across reference



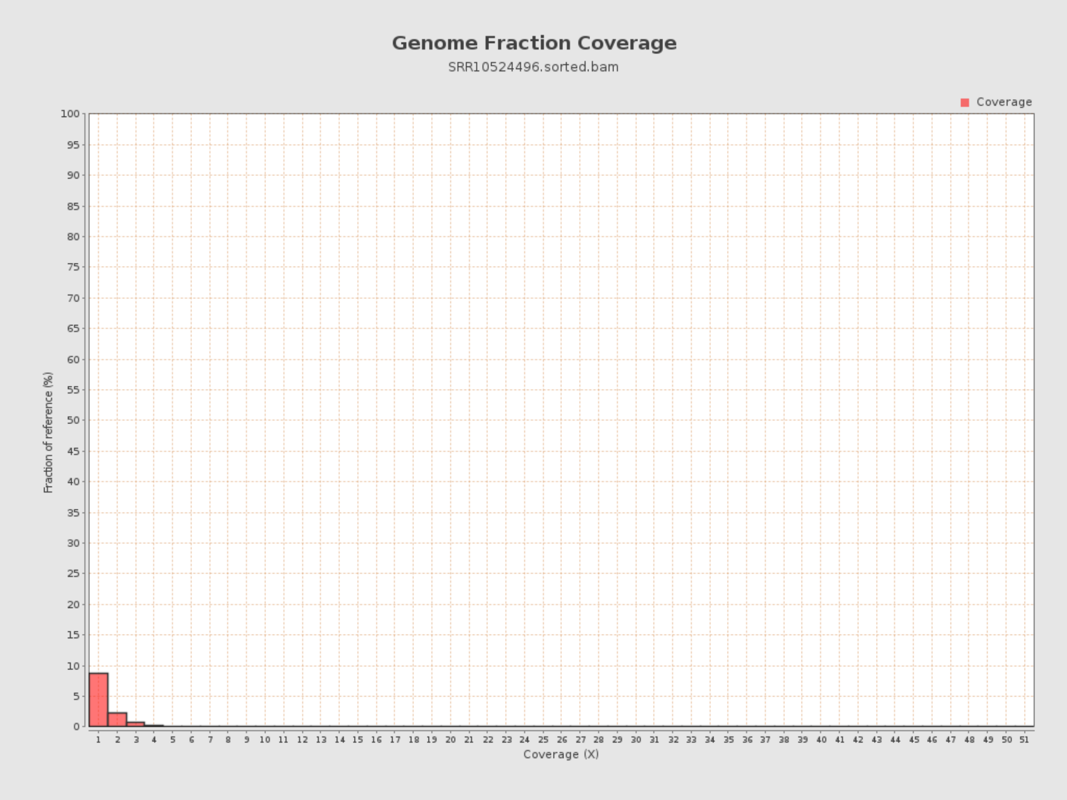
4. Results : Coverage Histogram



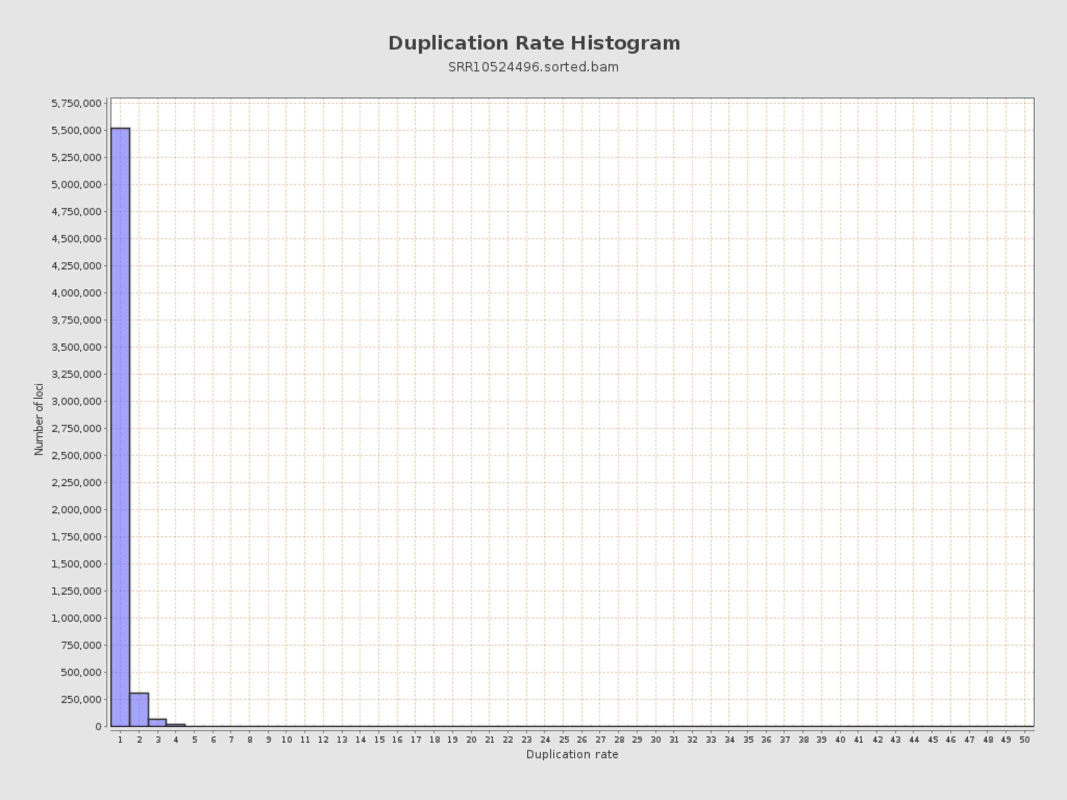
5. Results : Coverage Histogram (0-50X)



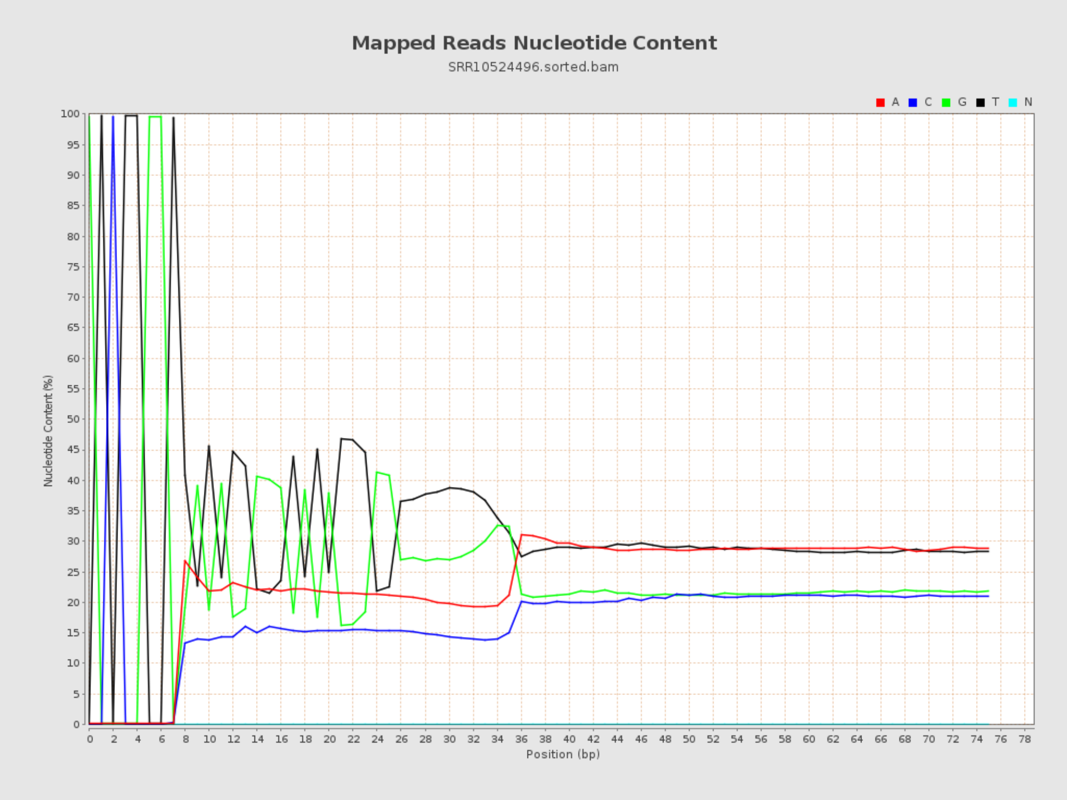
6. Results : Genome Fraction Coverage



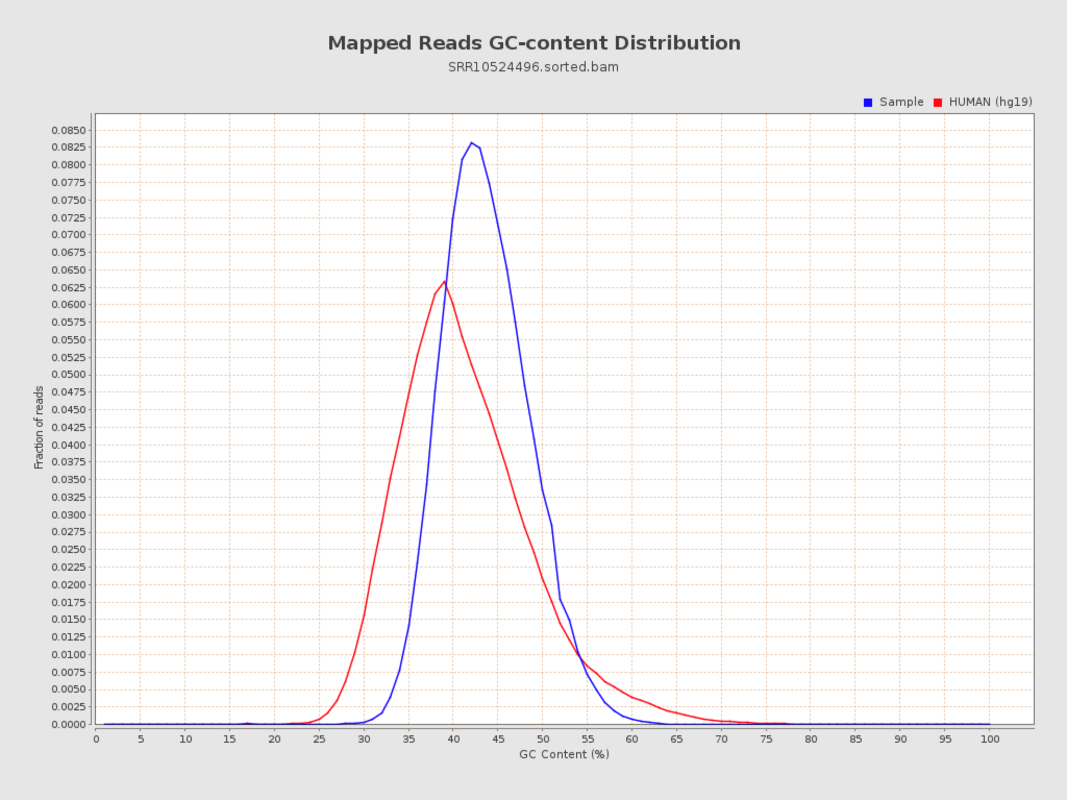
7. Results : Duplication Rate Histogram



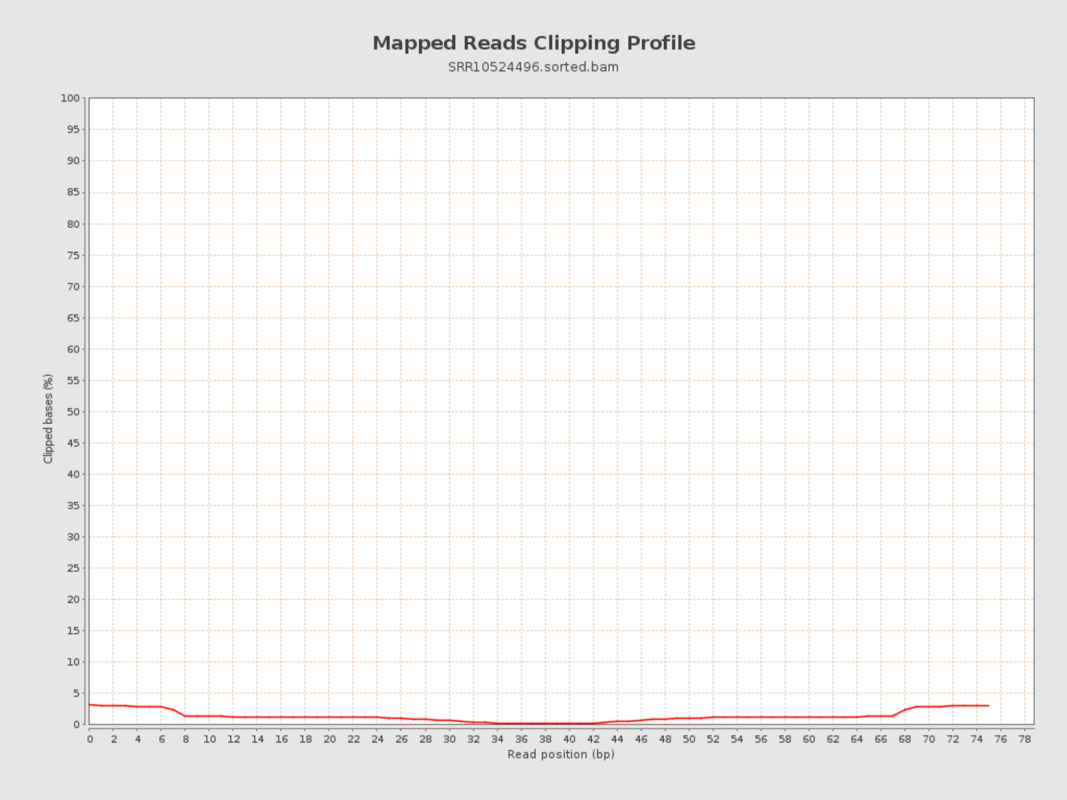
8. Results : Mapped Reads Nucleotide Content



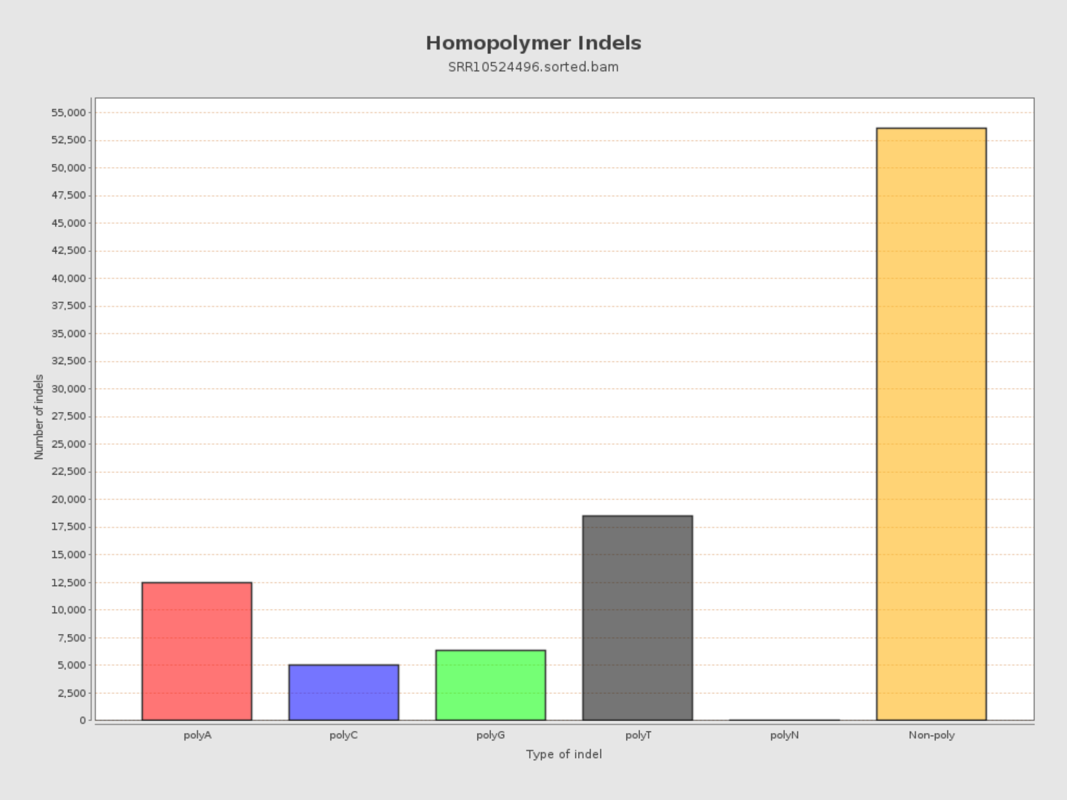
9. Results : Mapped Reads GC-content Distribution



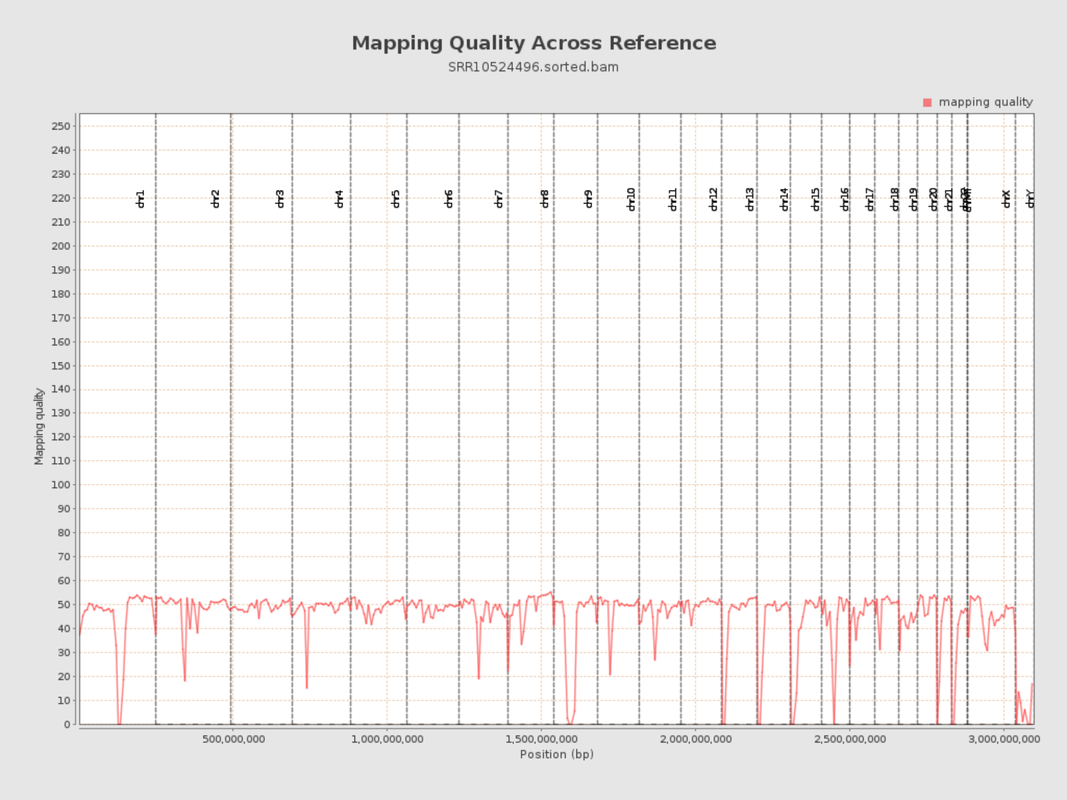
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram