Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:37:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524392.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_SRR10524392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524392.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:37:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,219
Mapped reads	499,688 / 91.15%
Unmapped reads	48,531 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,862 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,164 / 1.67%
Duplication rate	1.39%
Clipped reads	500,175 / 91.24%

2.2. ACGT Content

Number/percentage of A's	7,540,503 / 25.75%
Number/percentage of C's	5,479,991 / 18.72%
Number/percentage of T's	9,358,800 / 31.96%
Number/percentage of G's	6,897,467 / 23.56%
Number/percentage of N's	3,934 / 0.01%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1229

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

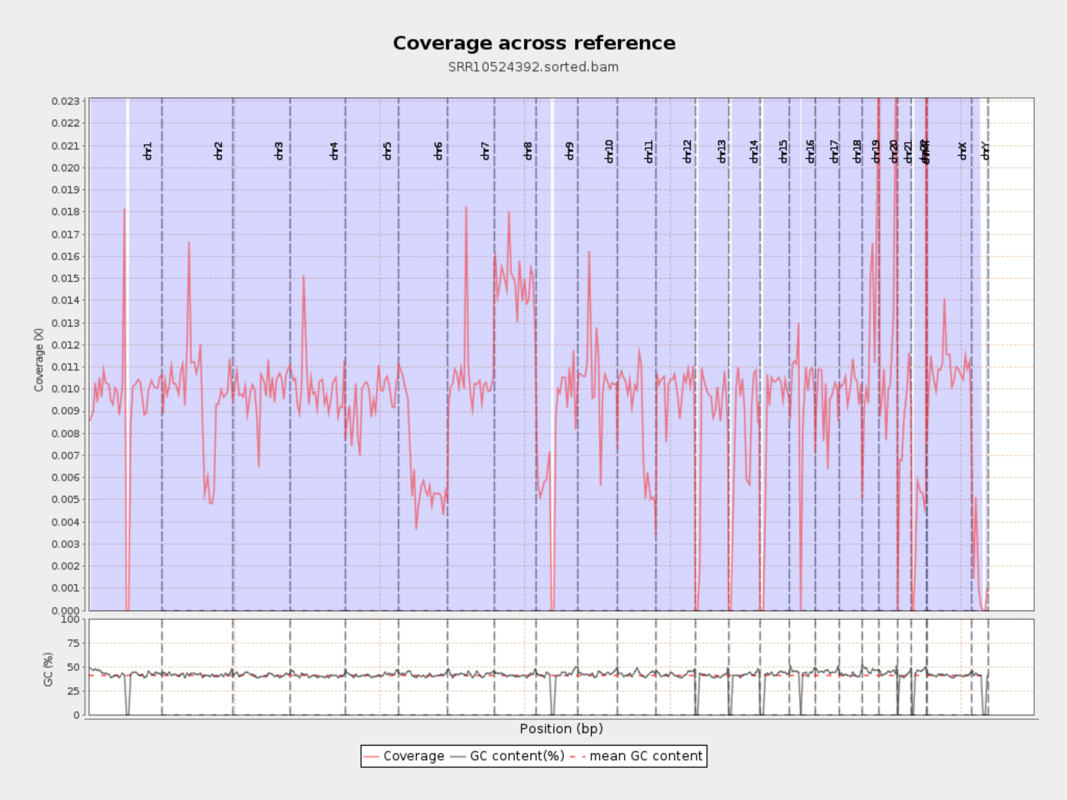
General error rate	0.5%
Mismatches	142,562
Insertions	2,054
Mapped reads with at least one insertion	0.41%
Deletions	5,227
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.93%

2.6. Chromosome stats

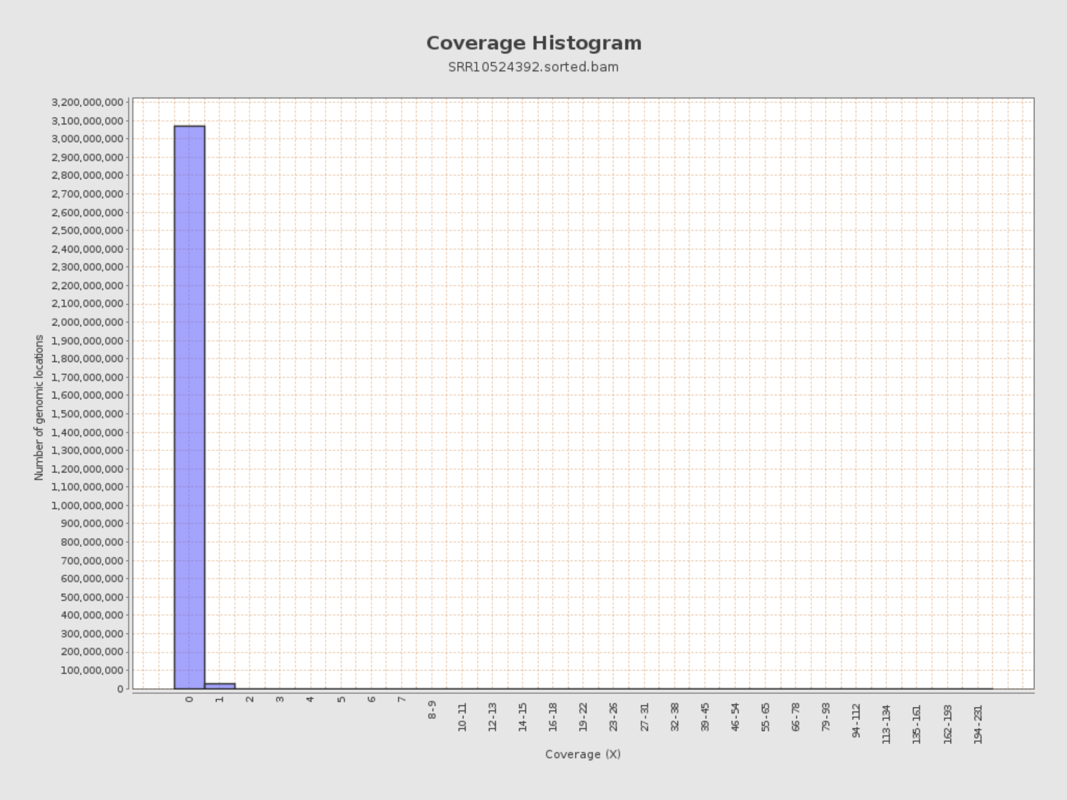
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2361406	0.0095	0.2103
chr2	243199373	2360592	0.0097	0.1306
chr3	198022430	1968582	0.0099	0.1027
chr4	191154276	1925510	0.0101	0.1076
chr5	180915260	1712355	0.0095	0.1002
chr6	171115067	1096614	0.0064	0.0846
chr7	159138663	1683495	0.0106	0.1558

chr8	146364022	2177033	0.0149	0.1393
chr9	141213431	1057502	0.0075	0.0977
chr10	135534747	1436448	0.0106	0.1195
chr11	135006516	1164650	0.0086	0.1045
chr12	133851895	1353230	0.0101	0.1049
chr13	115169878	935850	0.0081	0.0926
chr14	107349540	826991	0.0077	0.0919
chr15	102531392	850147	0.0083	0.0938
chr16	90354753	876120	0.0097	0.1037
chr17	81195210	765245	0.0094	0.1035
chr18	78077248	797954	0.0102	0.1347
chr19	59128983	799630	0.0135	0.1646
chr20	63025520	777985	0.0123	0.1154
chr21	48129895	386090	0.008	0.0965
chr22	51304566	191175	0.0037	0.063
chrMT	16571	5054	0.305	0.6054
chrX	155270560	1690666	0.0109	0.1119
chrY	59373566	88723	0.0015	0.0517

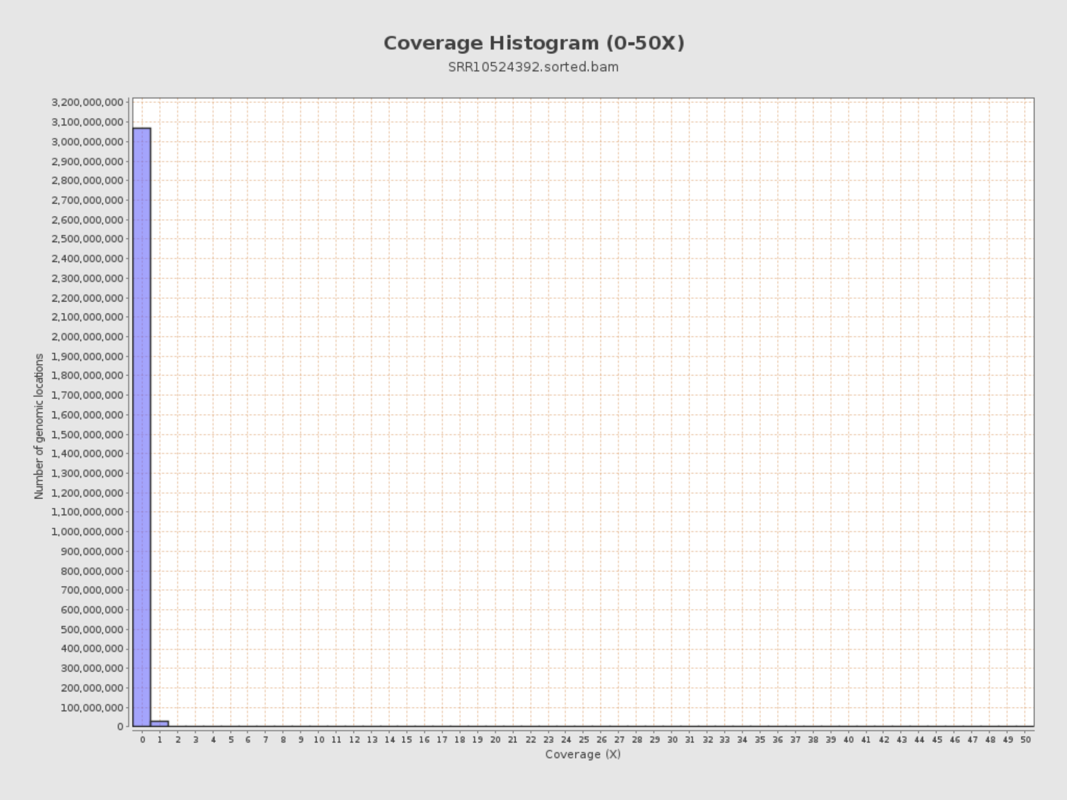
3. Results : Coverage across reference



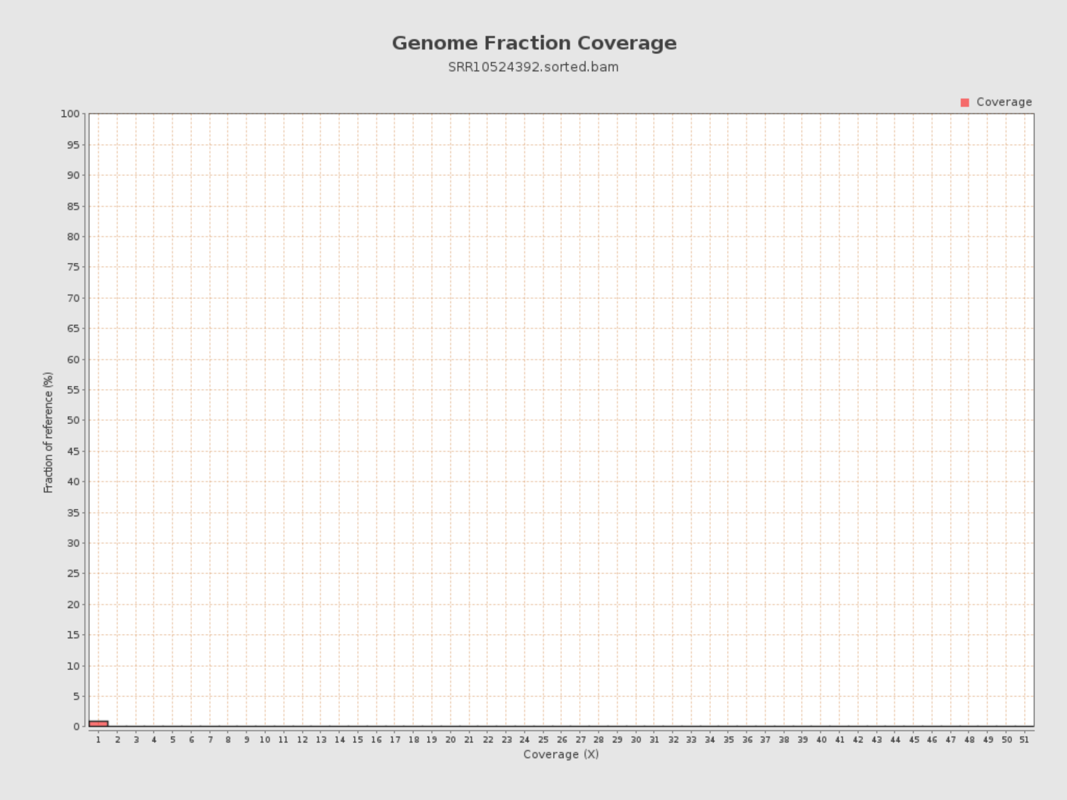
4. Results : Coverage Histogram



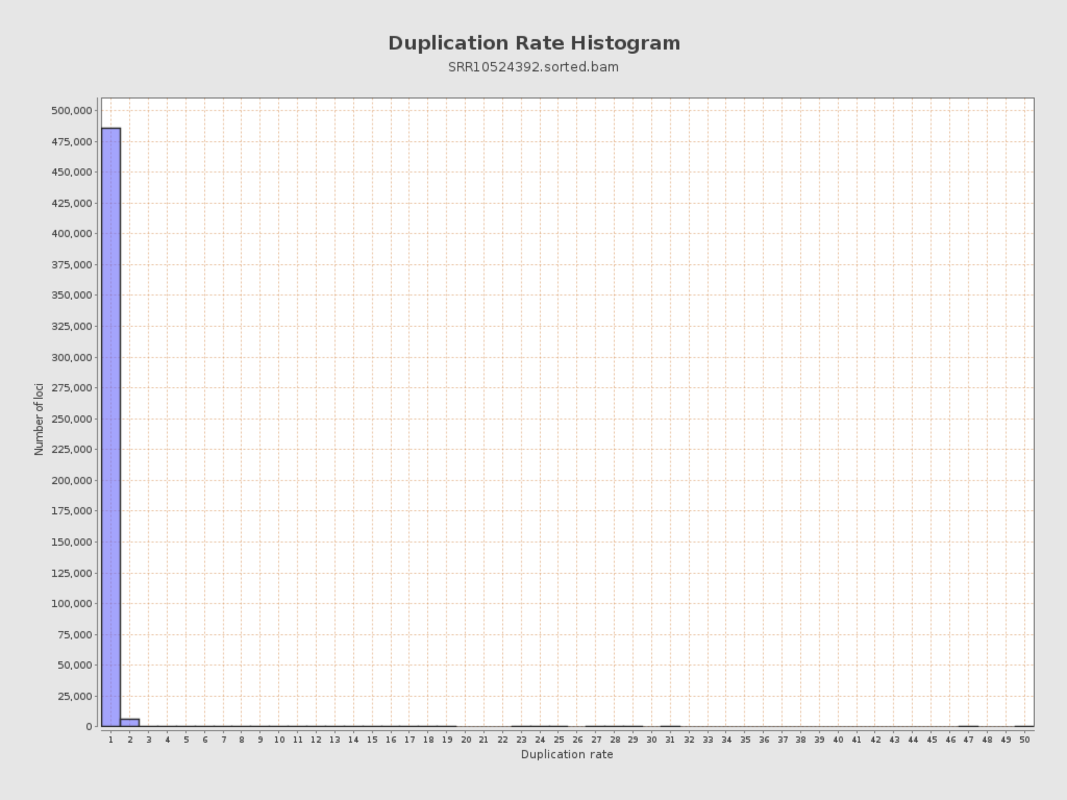
5. Results : Coverage Histogram (0-50X)



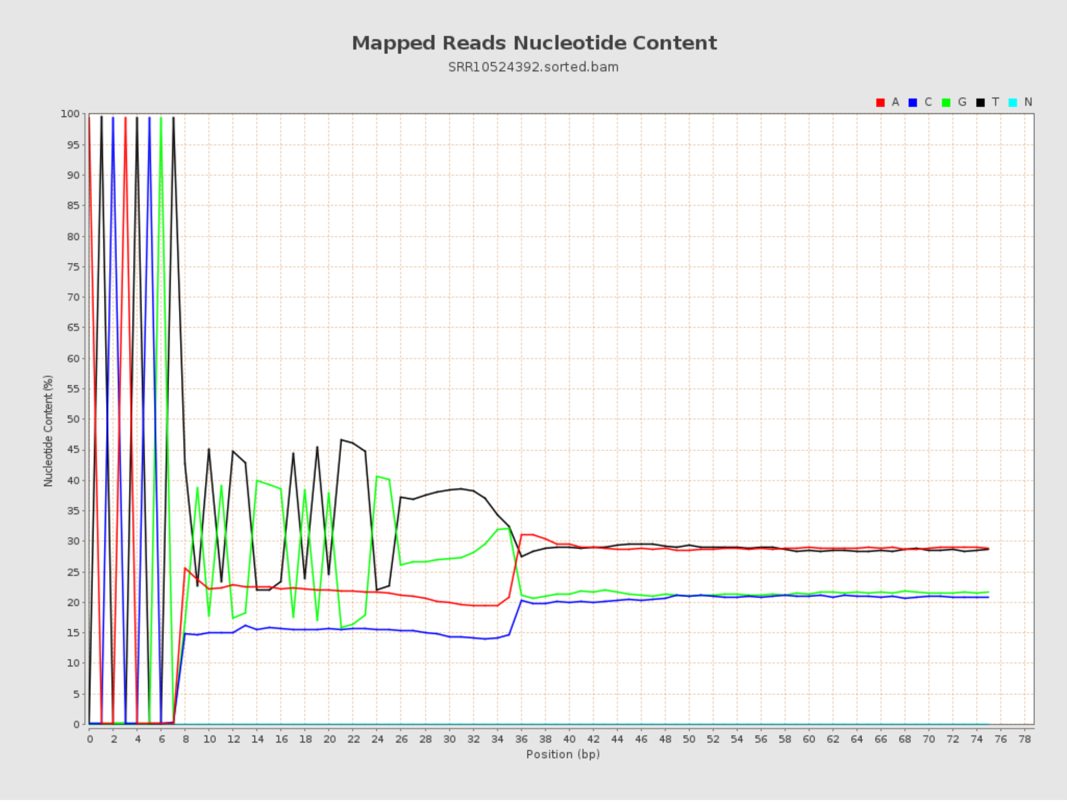
6. Results : Genome Fraction Coverage



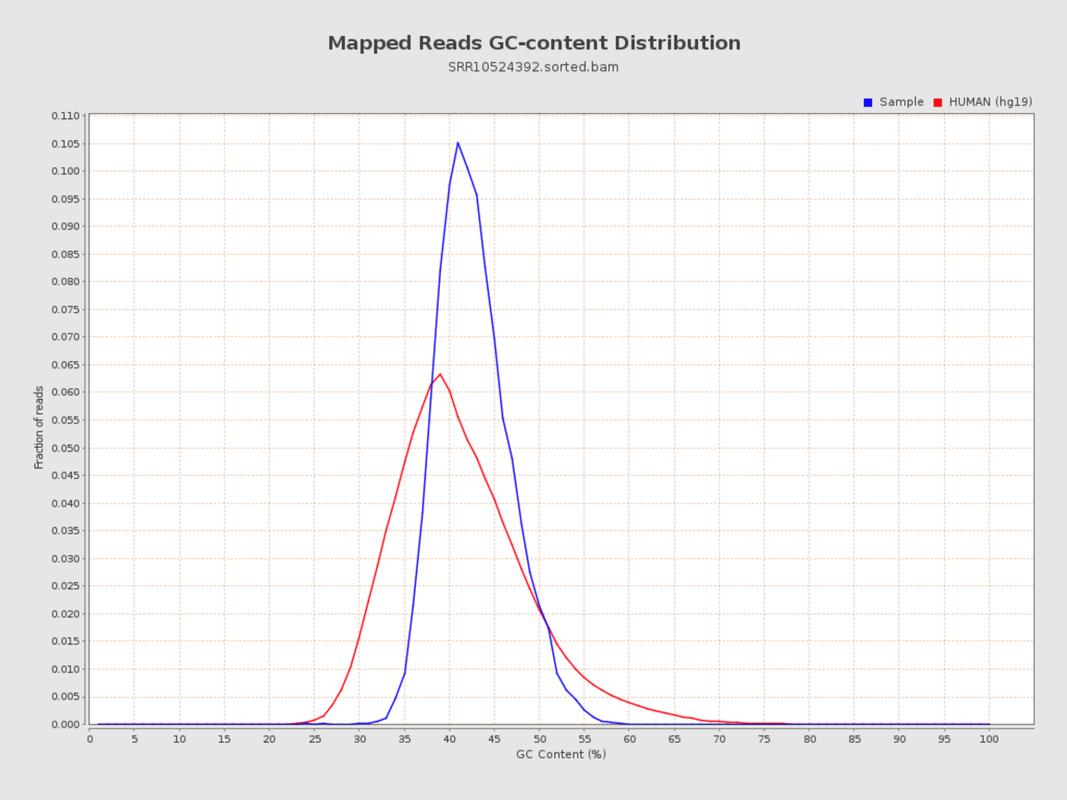
7. Results : Duplication Rate Histogram



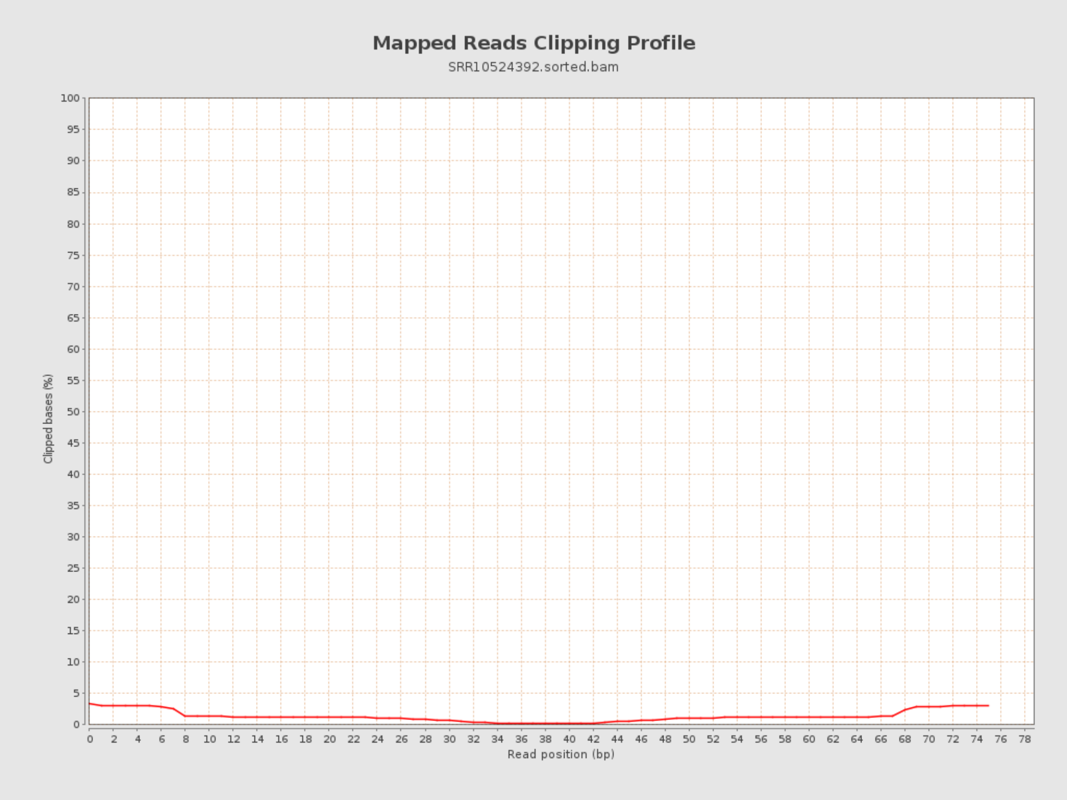
8. Results : Mapped Reads Nucleotide Content



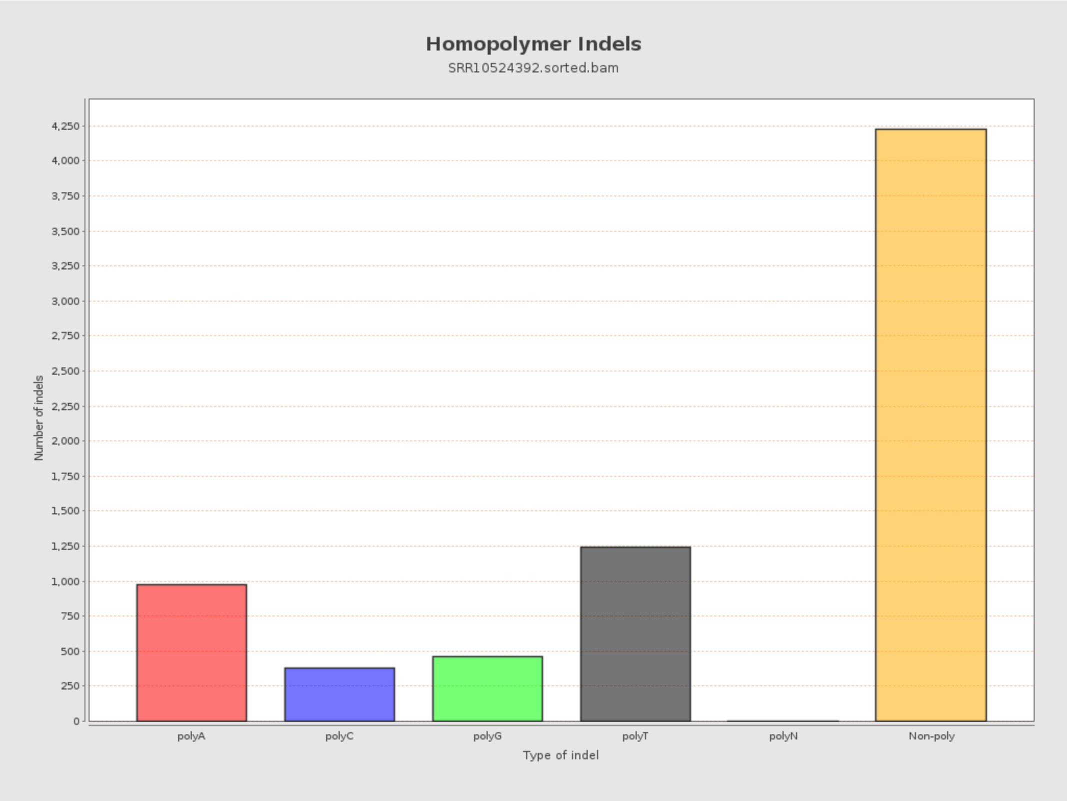
9. Results : Mapped Reads GC-content Distribution



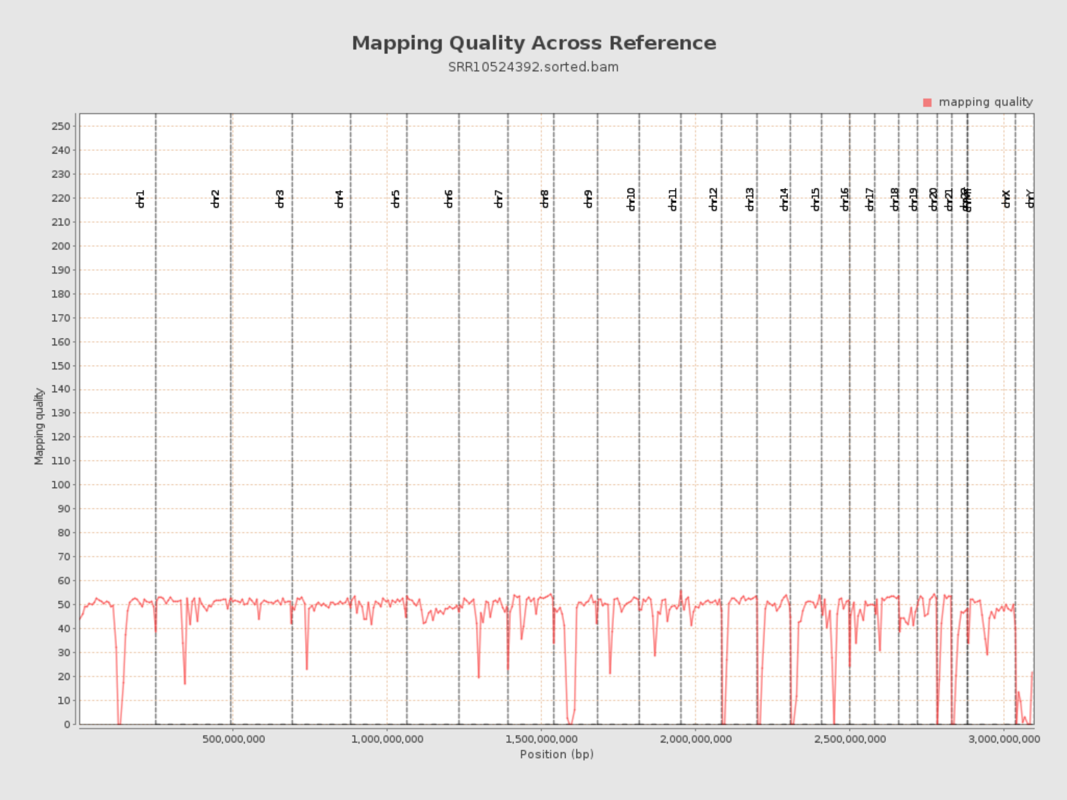
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram