Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:58:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524486.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_SRR10524486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524486.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:58:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	867,401
Mapped reads	794,684 / 91.62%
Unmapped reads	72,717 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,837 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	24,360 / 2.81%
Duplication rate	2.39%
Clipped reads	794,204 / 91.56%

2.2. ACGT Content

Number/percentage of A's	11,894,019 / 25.67%
Number/percentage of C's	8,201,712 / 17.7%
Number/percentage of T's	14,494,895 / 31.28%
Number/percentage of G's	11,742,475 / 25.34%
Number/percentage of N's	907 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1657

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

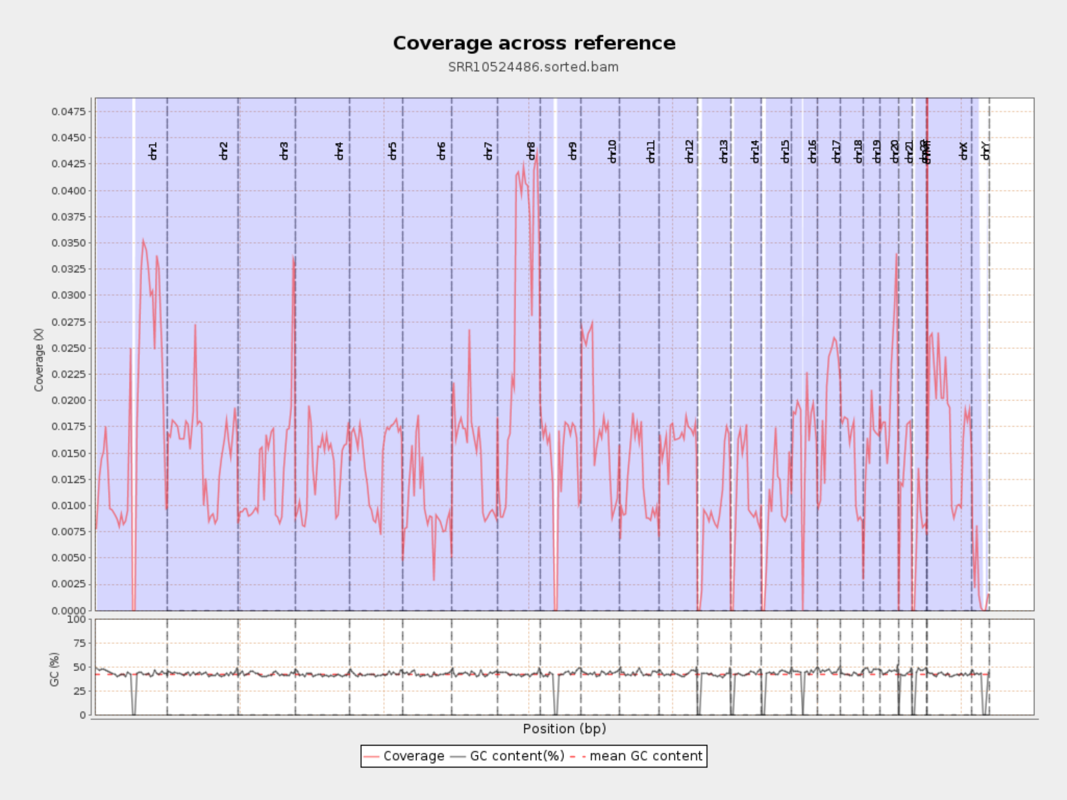
General error rate	0.48%
Mismatches	216,902
Insertions	2,898
Mapped reads with at least one insertion	0.36%
Deletions	8,717
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.04%

2.6. Chromosome stats

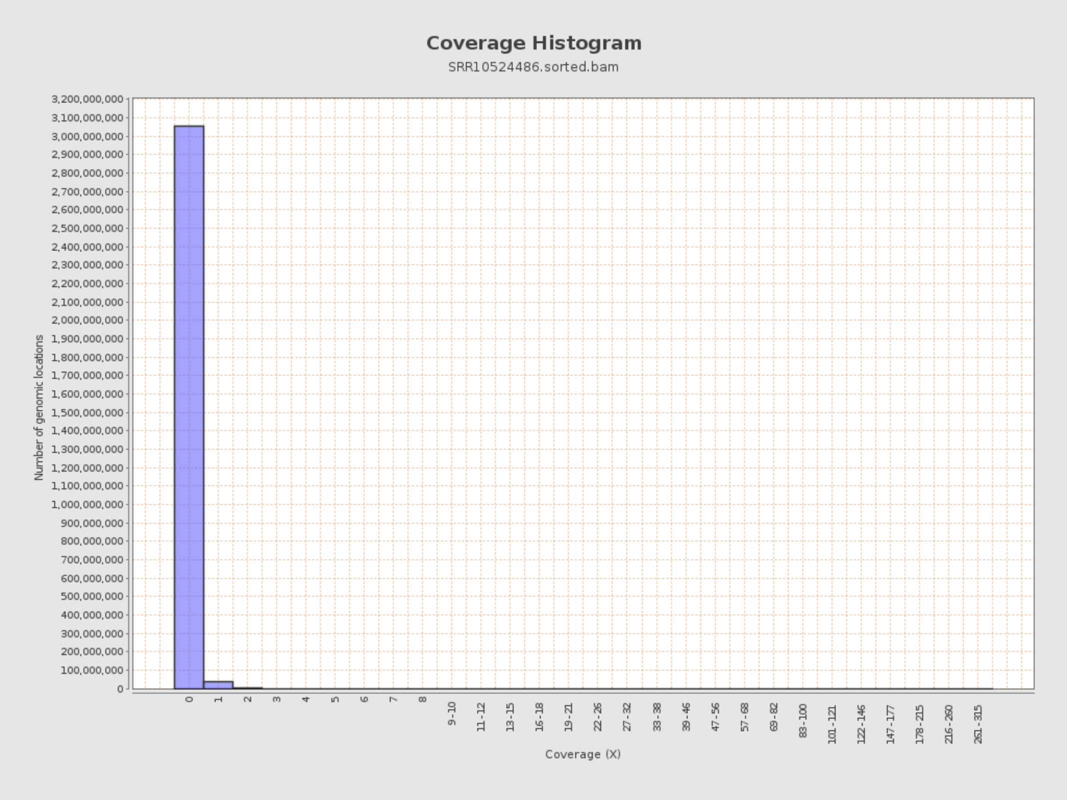
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4402256	0.0177	0.2721
chr2	243199373	3782767	0.0156	0.1839
chr3	198022430	2624133	0.0133	0.1231
chr4	191154276	2574460	0.0135	0.1324
chr5	180915260	2631537	0.0145	0.1285
chr6	171115067	1700360	0.0099	0.1253
chr7	159138663	2391969	0.015	0.201

chr8	146364022	4214991	0.0288	0.1965
chr9	141213431	2005437	0.0142	0.1487
chr10	135534747	2505834	0.0185	0.1701
chr11	135006516	1652100	0.0122	0.1666
chr12	133851895	2206642	0.0165	0.1365
chr13	115169878	1068730	0.0093	0.1037
chr14	107349540	1112727	0.0104	0.1092
chr15	102531392	992188	0.0097	0.1099
chr16	90354753	1475266	0.0163	0.1414
chr17	81195210	1611328	0.0198	0.1545
chr18	78077248	1135600	0.0145	0.226
chr19	59128983	935029	0.0158	0.2115
chr20	63025520	1355528	0.0215	0.1566
chr21	48129895	653637	0.0136	0.1285
chr22	51304566	364406	0.0071	0.0898
chrMT	16571	2959	0.1786	0.4298
chrX	155270560	2807152	0.0181	0.1525
chrY	59373566	141631	0.0024	0.0722

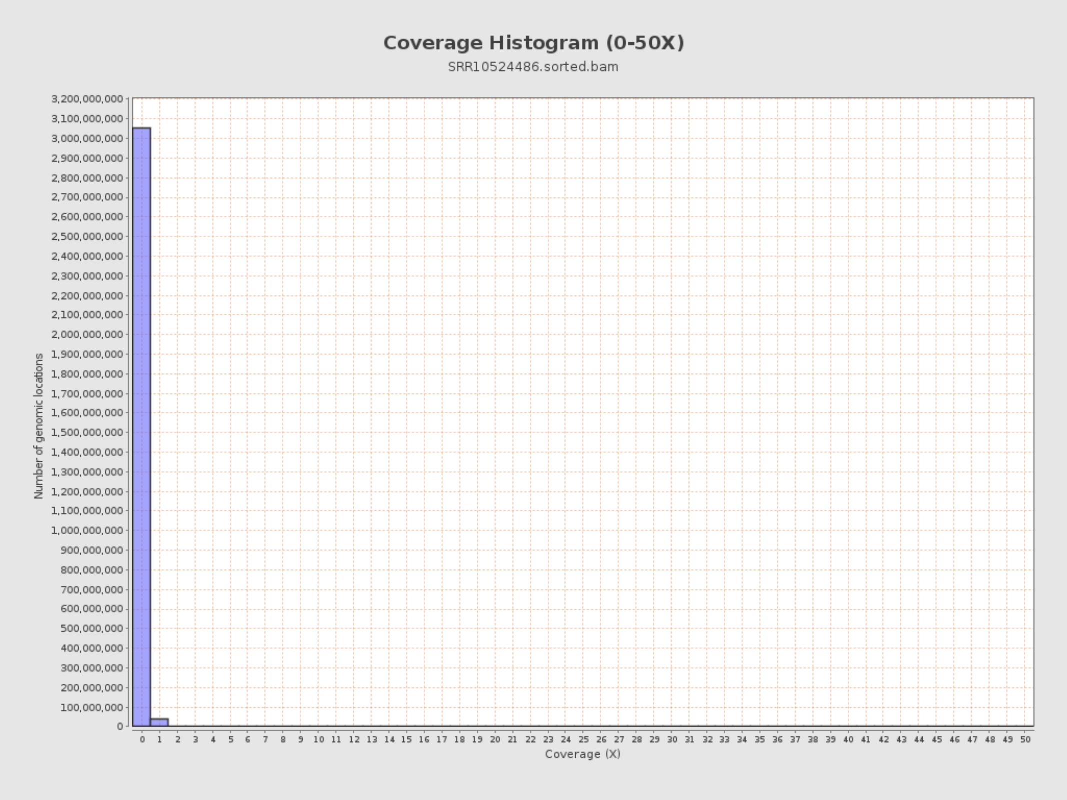
3. Results : Coverage across reference



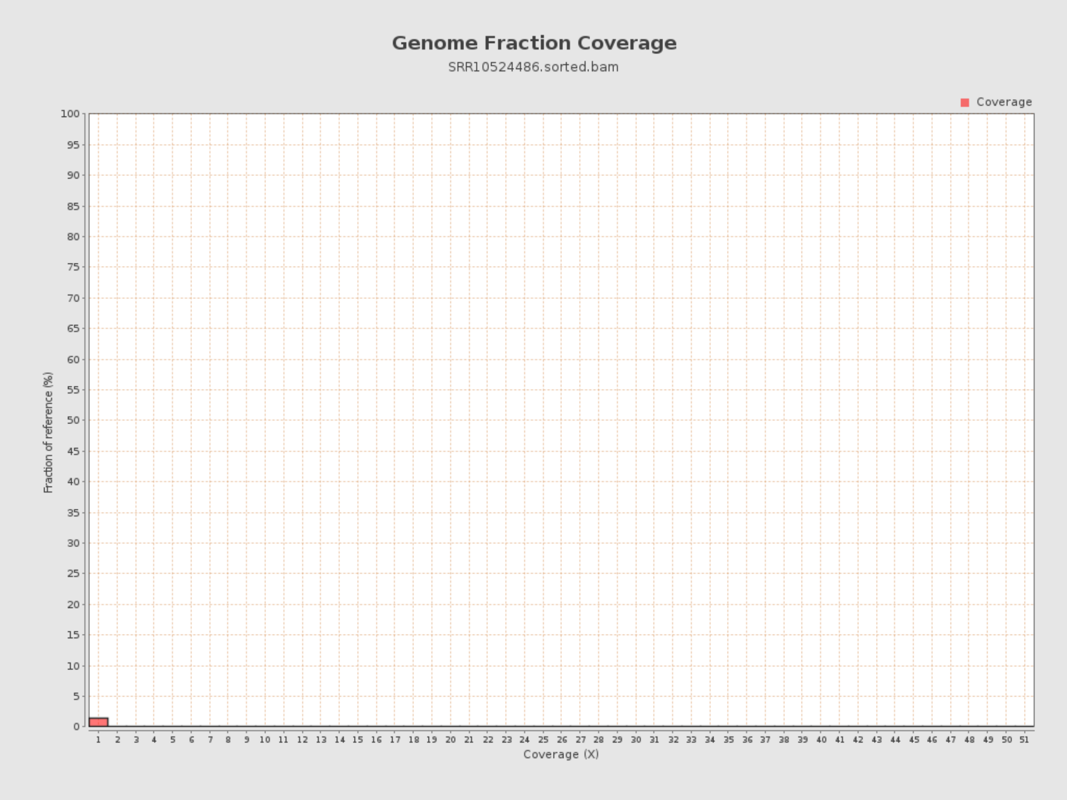
4. Results : Coverage Histogram



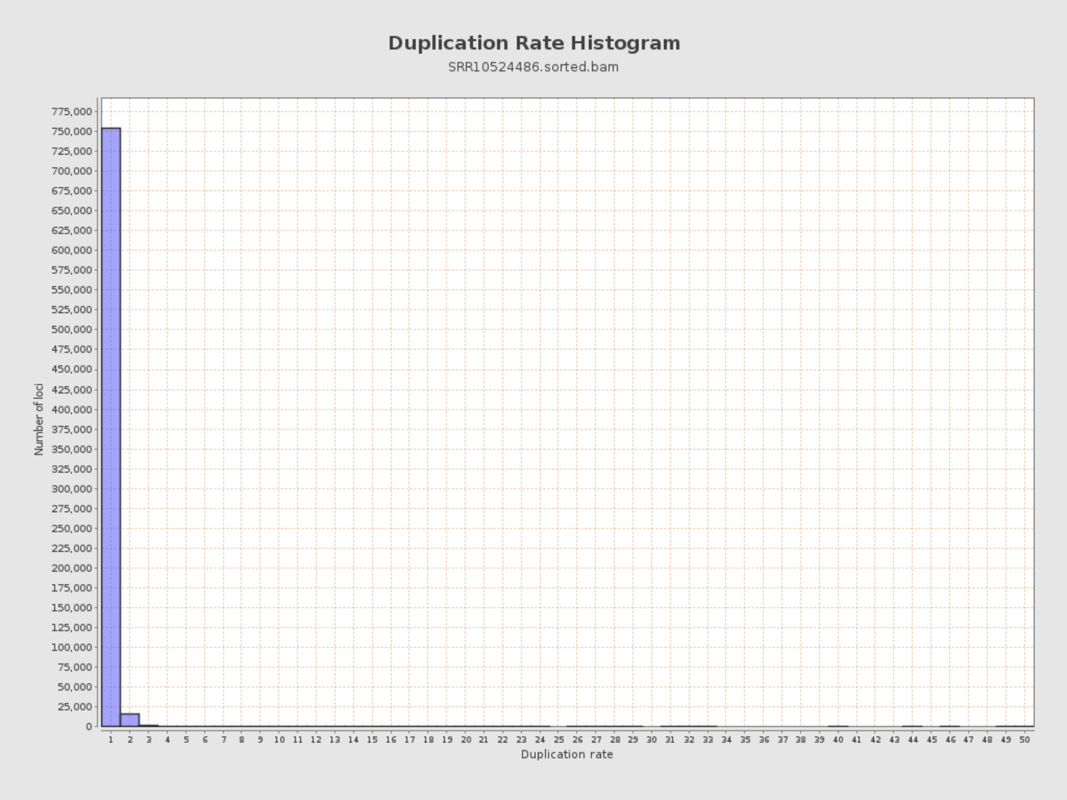
5. Results : Coverage Histogram (0-50X)



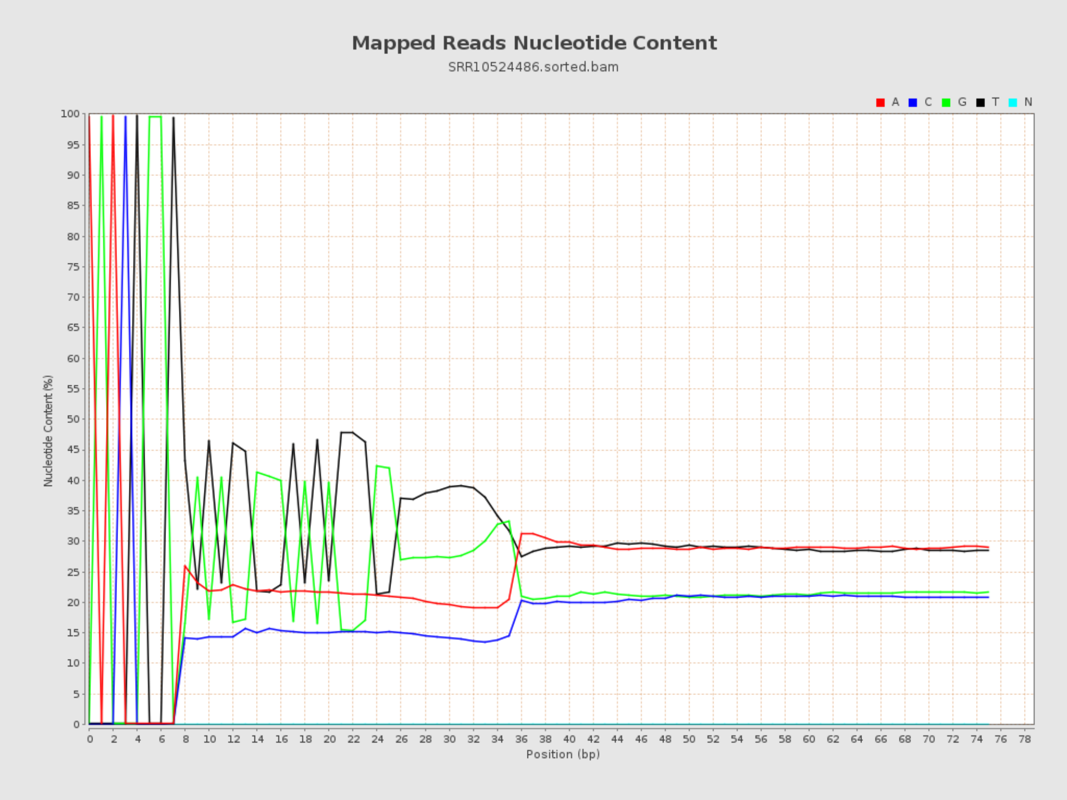
6. Results : Genome Fraction Coverage



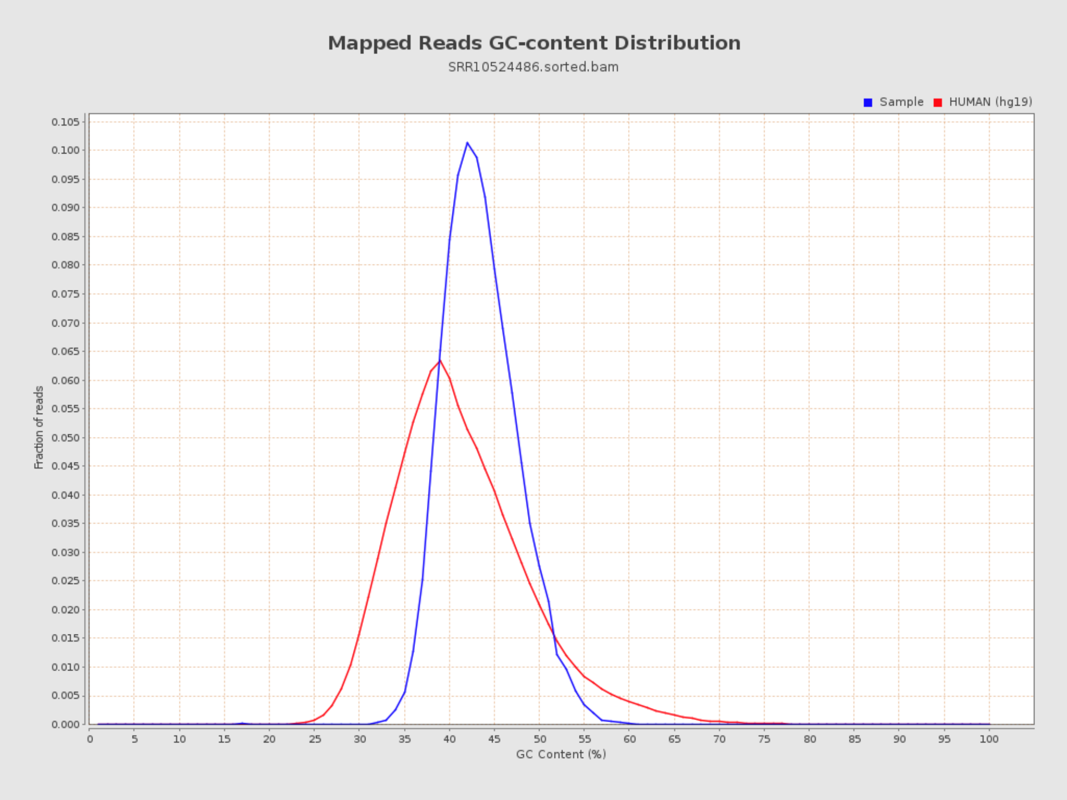
7. Results : Duplication Rate Histogram



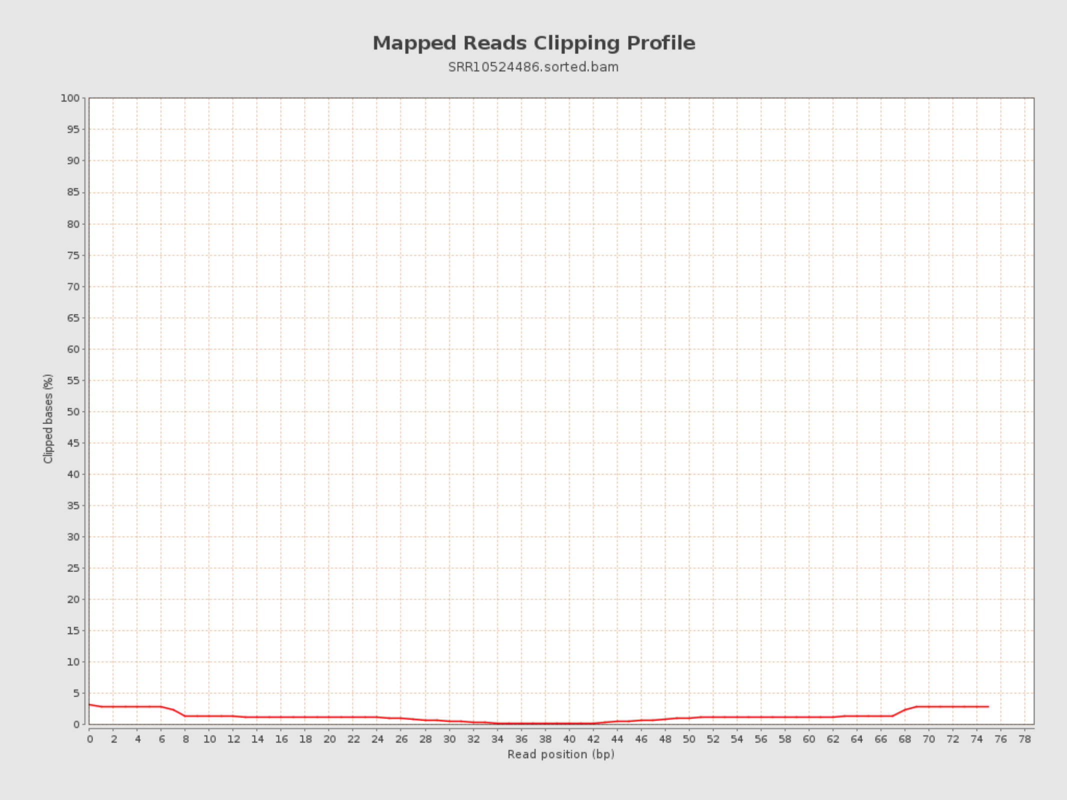
8. Results : Mapped Reads Nucleotide Content



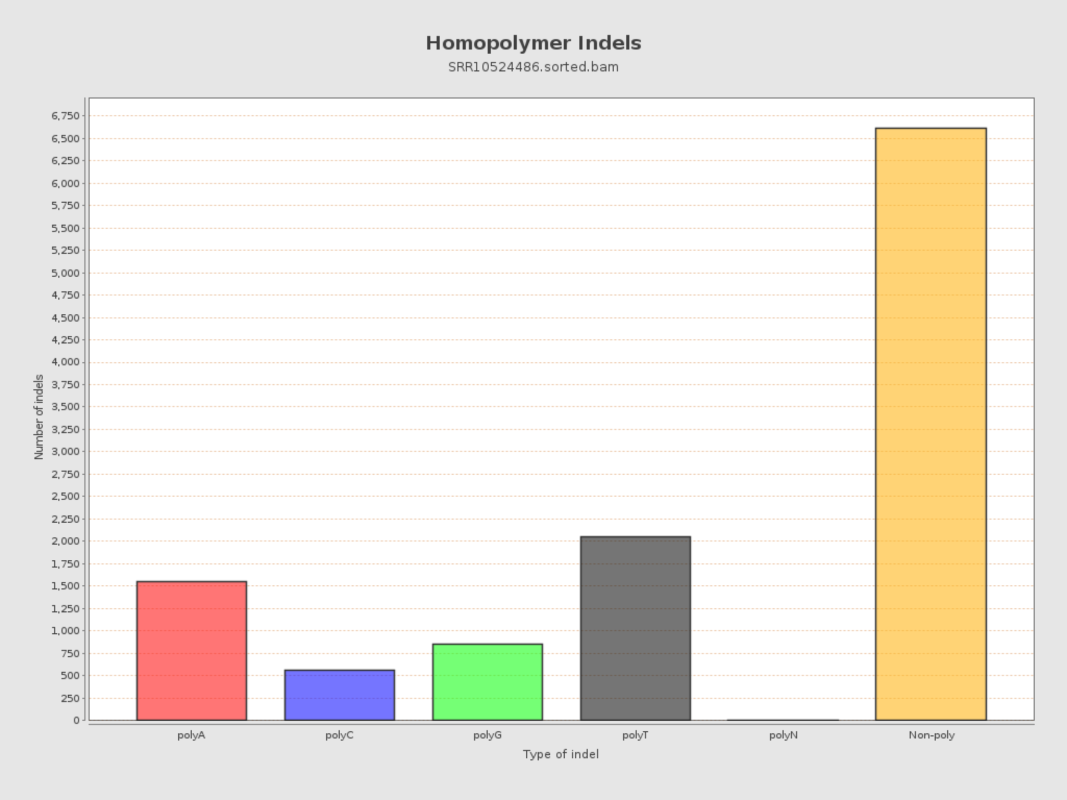
9. Results : Mapped Reads GC-content Distribution



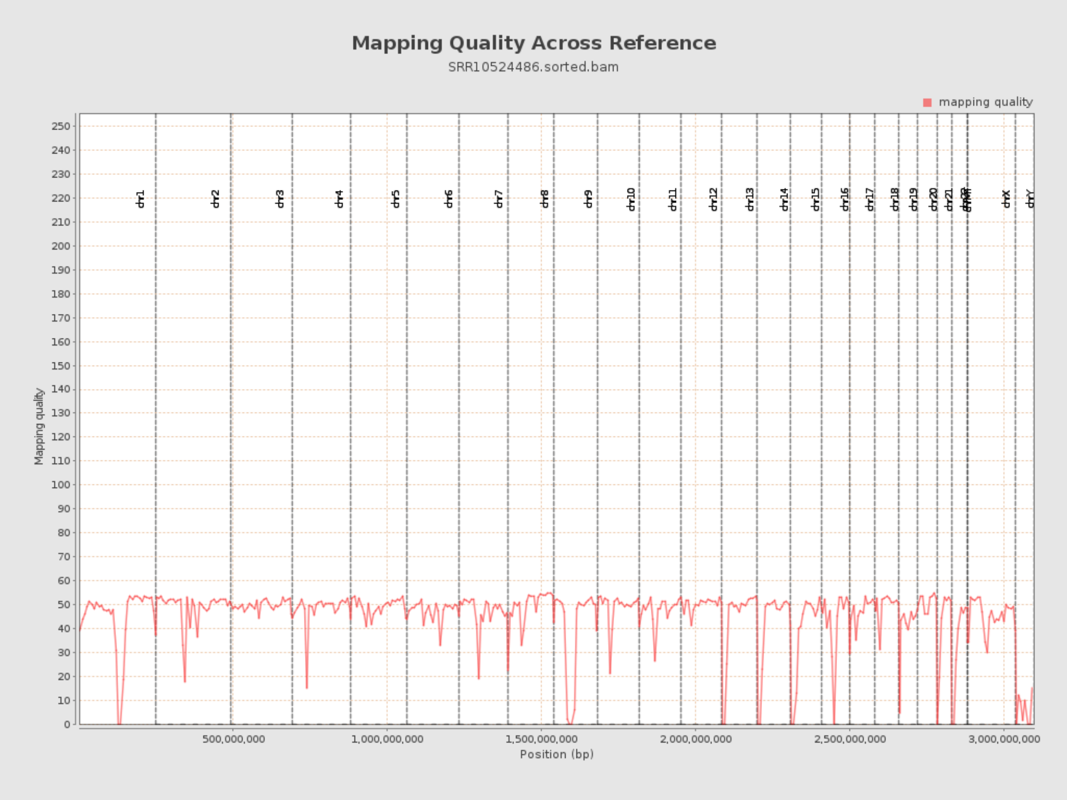
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram