Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:12:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524485.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_SRR10524485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524485.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:12:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,051,999
Mapped reads	2,824,332 / 92.54%
Unmapped reads	227,667 / 7.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,038 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	160,749 / 5.27%
Duplication rate	4.24%
Clipped reads	2,820,195 / 92.4%

2.2. ACGT Content

Number/percentage of A's	40,282,877 / 24.3%
Number/percentage of C's	32,252,332 / 19.46%
Number/percentage of T's	54,335,840 / 32.78%
Number/percentage of G's	38,882,093 / 23.46%
Number/percentage of N's	3,292 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.4481

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

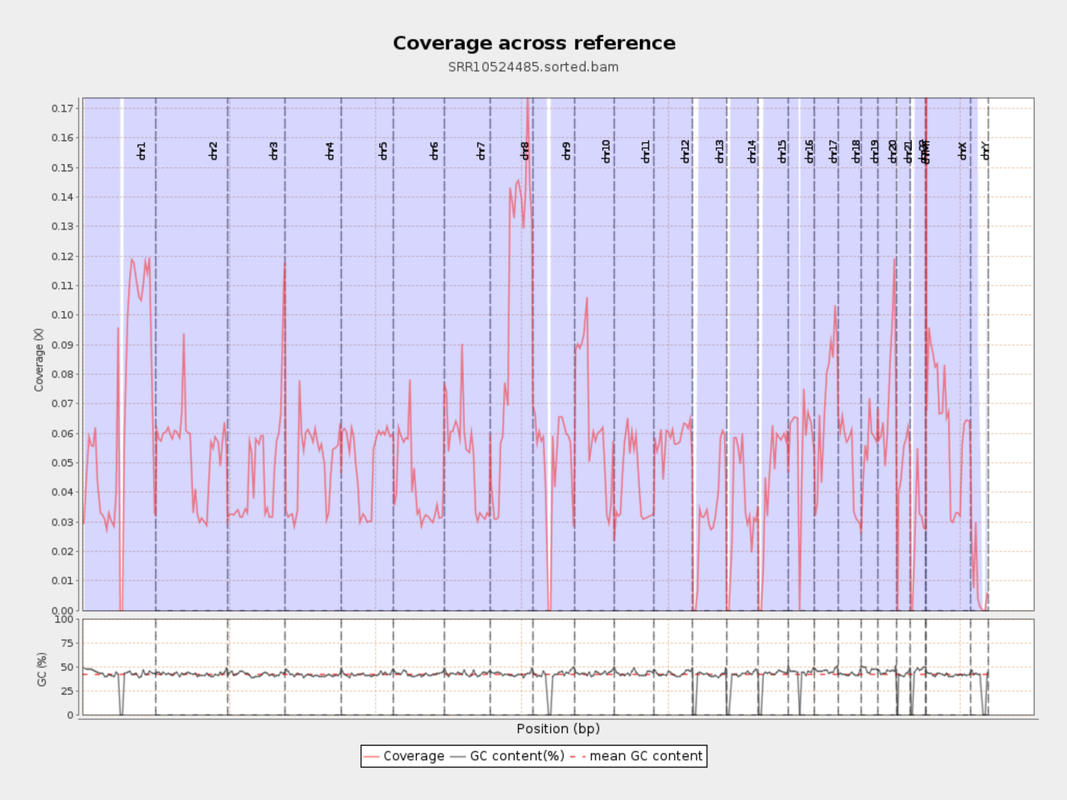
General error rate	0.47%
Mismatches	764,970
Insertions	11,398
Mapped reads with at least one insertion	0.4%
Deletions	32,017
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.23%

2.6. Chromosome stats

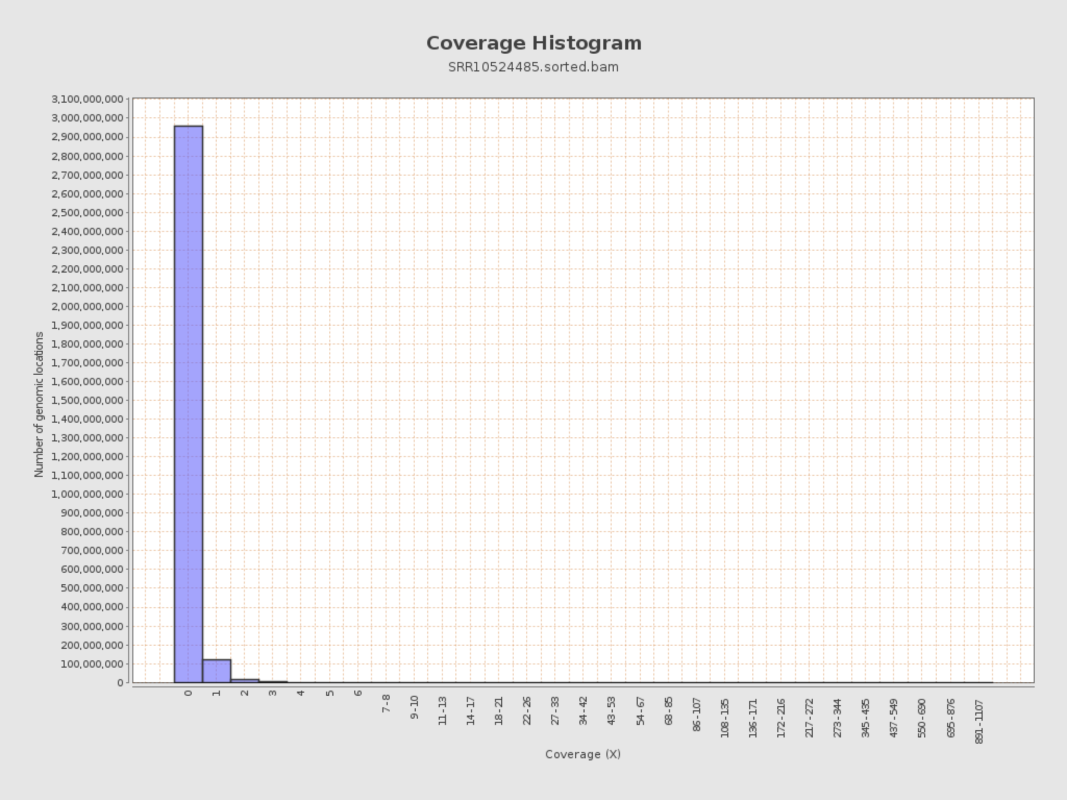
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16295460	0.0654	0.8848
chr2	243199373	13067781	0.0537	0.4905
chr3	198022430	9202614	0.0465	0.2573
chr4	191154276	9506372	0.0497	0.3153
chr5	180915260	9212901	0.0509	0.2652
chr6	171115067	7149300	0.0418	0.3321
chr7	159138663	8318445	0.0523	0.5887

chr8	146364022	15111007	0.1032	0.4611
chr9	141213431	7051193	0.0499	0.3848
chr10	135534747	8787781	0.0648	0.4875
chr11	135006516	5708271	0.0423	0.4028
chr12	133851895	7838412	0.0586	0.2842
chr13	115169878	3758565	0.0326	0.2109
chr14	107349540	3750719	0.0349	0.2317
chr15	102531392	4364071	0.0426	0.2536
chr16	90354753	5081210	0.0562	0.3093
chr17	81195210	5716155	0.0704	0.3362
chr18	78077248	3920275	0.0502	0.7044
chr19	59128983	3312389	0.056	0.633
chr20	63025520	4735356	0.0751	0.3297
chr21	48129895	2276652	0.0473	0.2876
chr22	51304566	1333333	0.026	0.1886
chrMT	16571	31708	1.9135	1.9862
chrX	155270560	9769163	0.0629	0.3418
chrY	59373566	511862	0.0086	0.2164

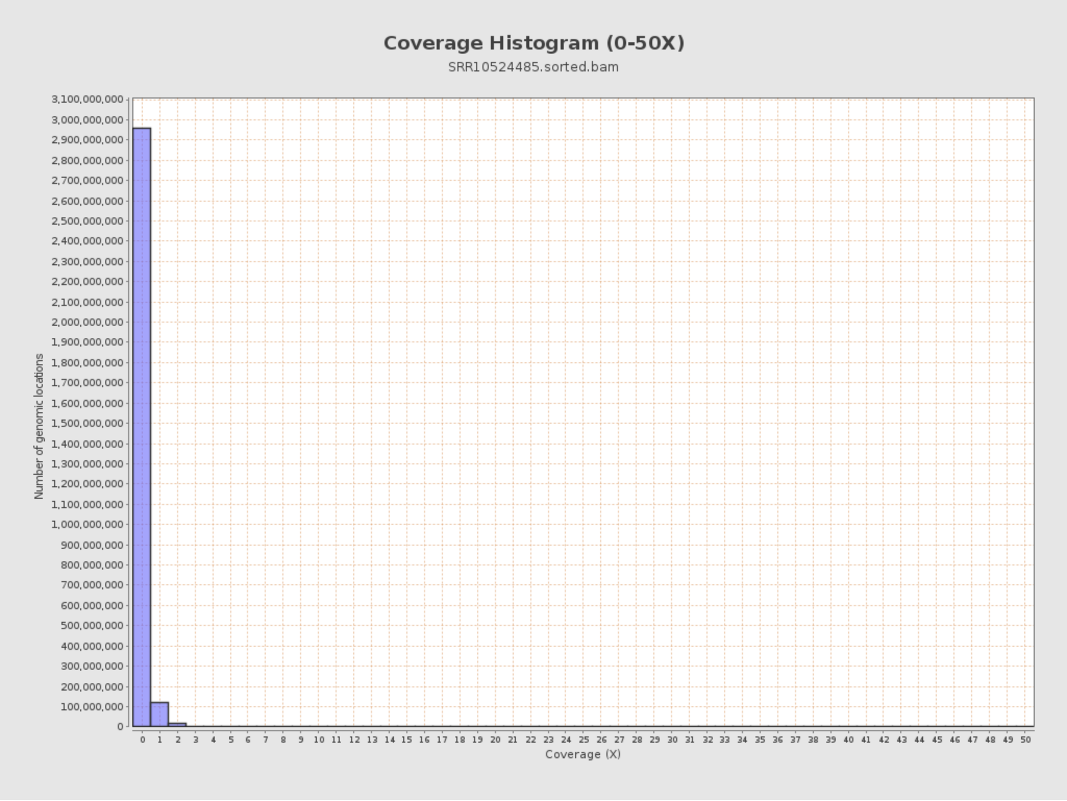
3. Results : Coverage across reference



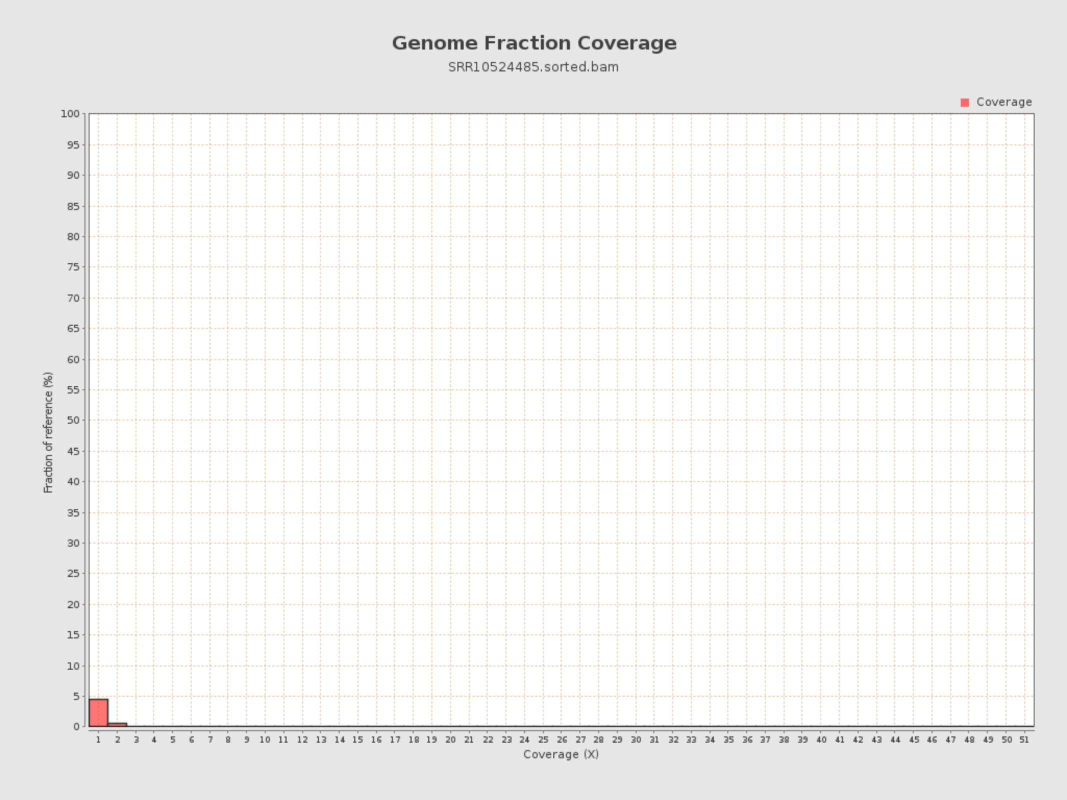
4. Results : Coverage Histogram



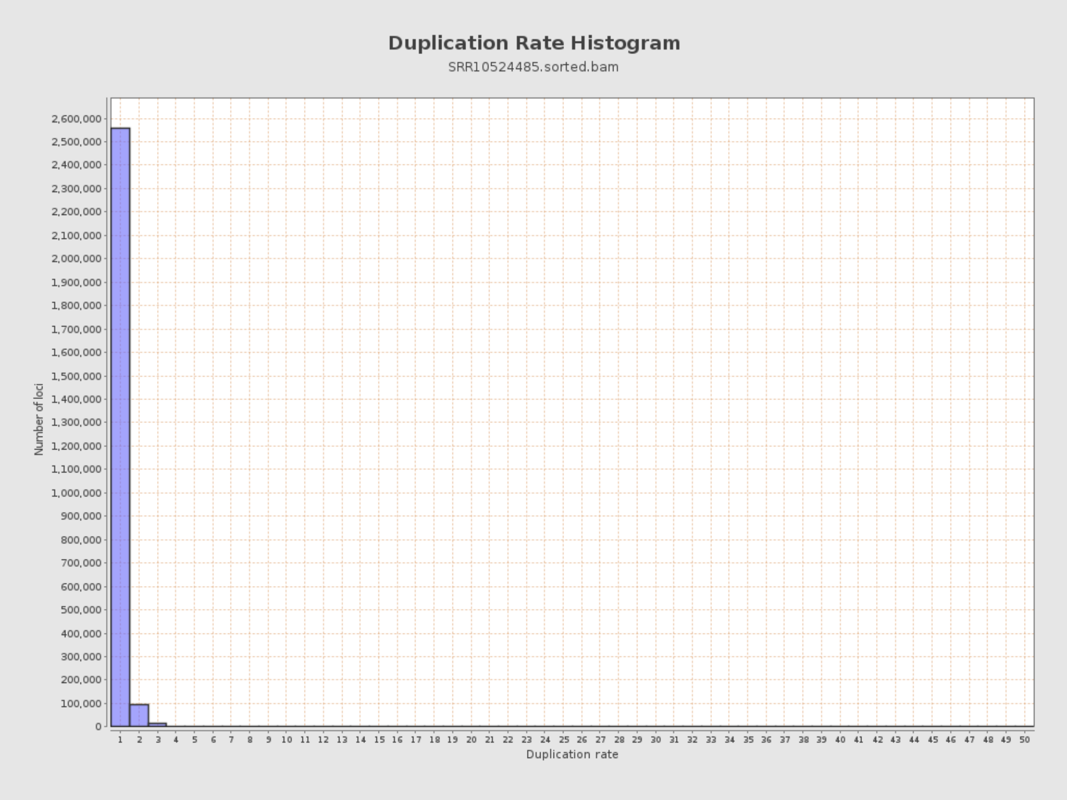
5. Results : Coverage Histogram (0-50X)



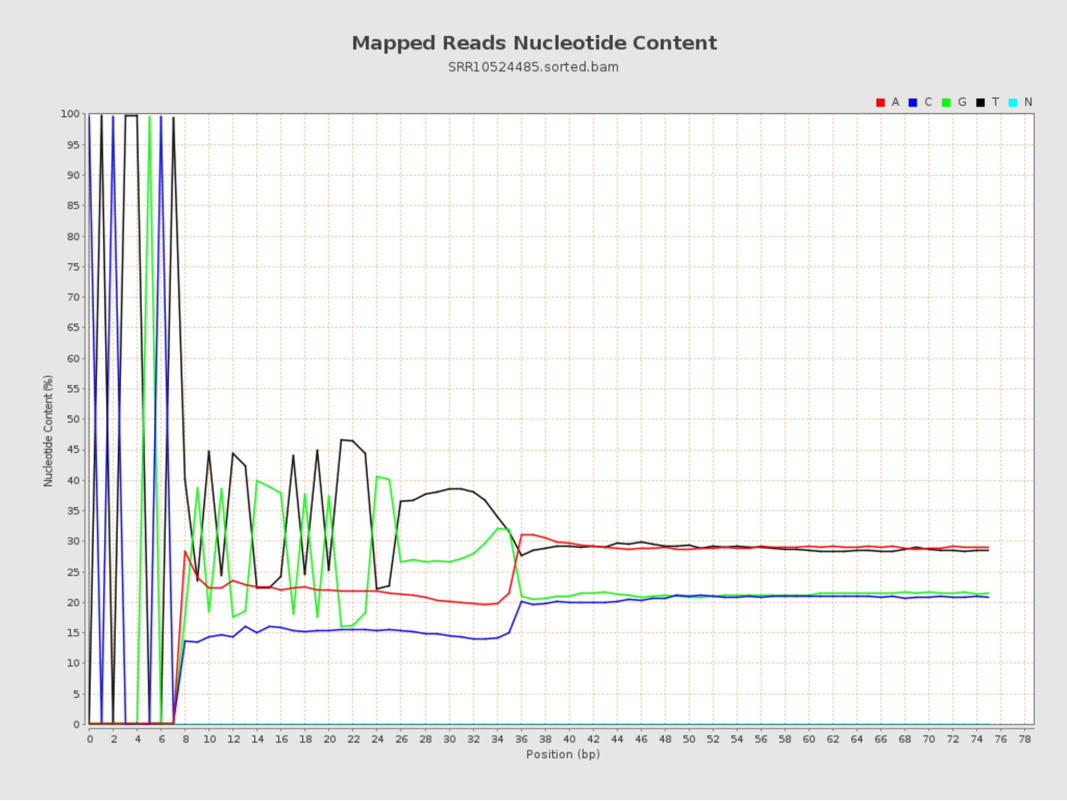
6. Results : Genome Fraction Coverage



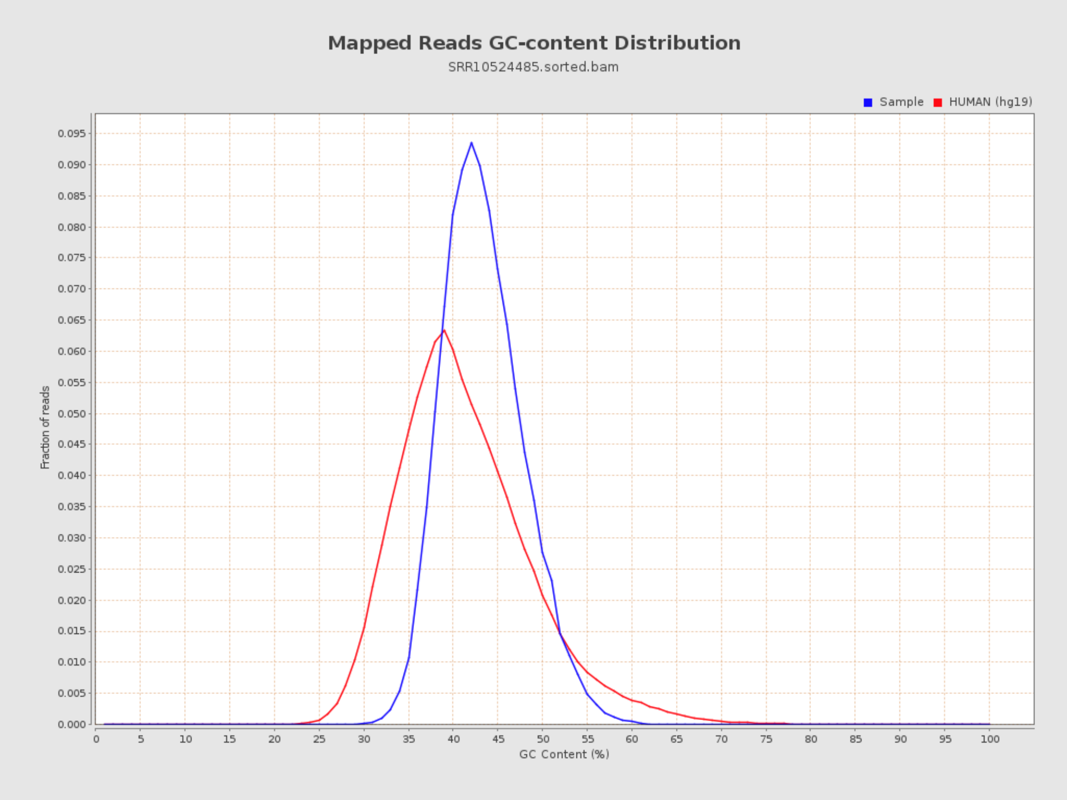
7. Results : Duplication Rate Histogram



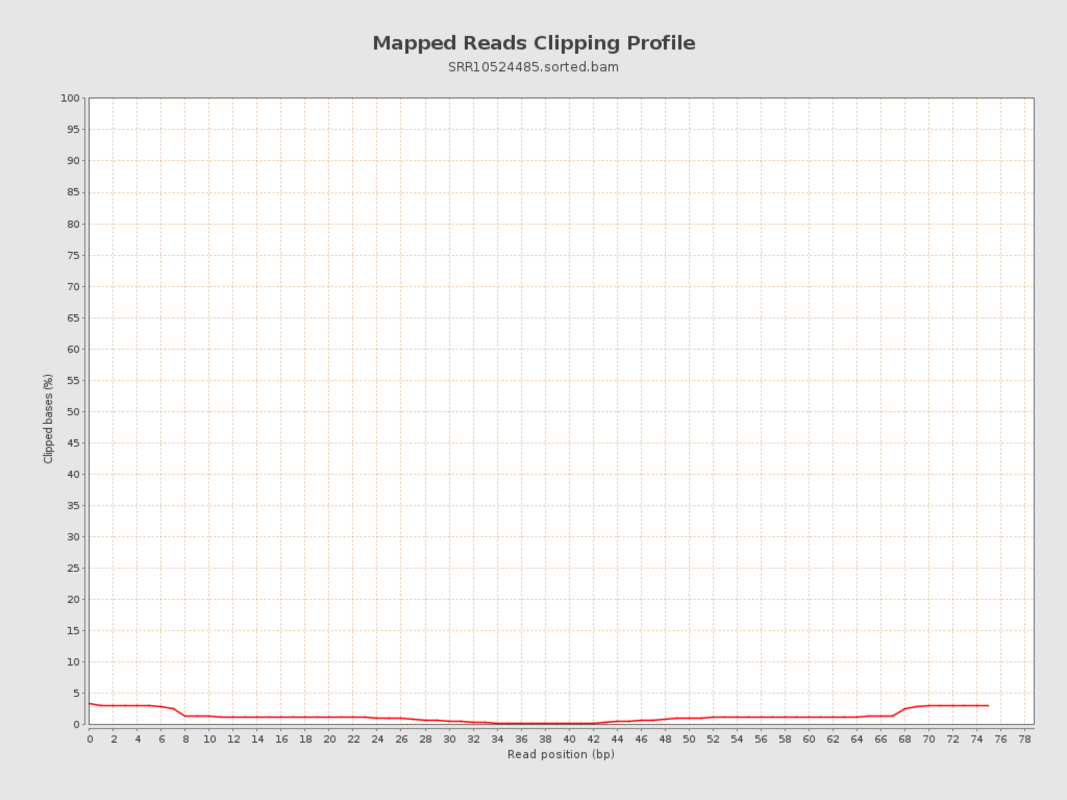
8. Results : Mapped Reads Nucleotide Content



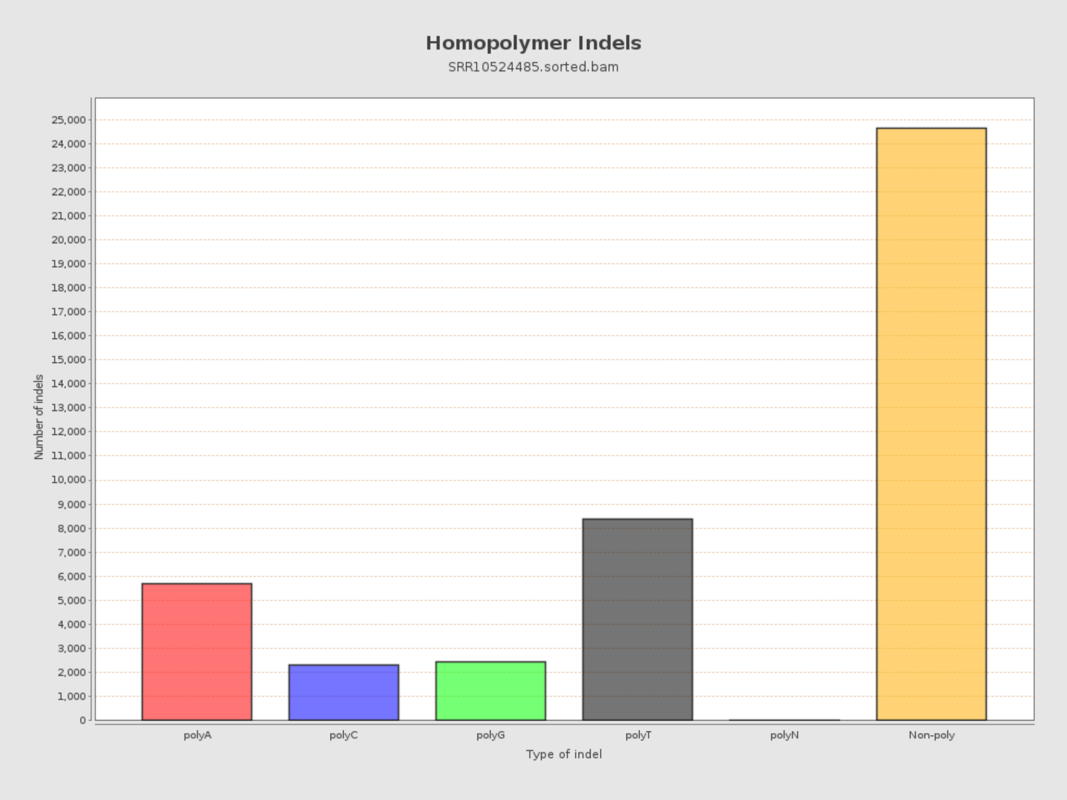
9. Results : Mapped Reads GC-content Distribution



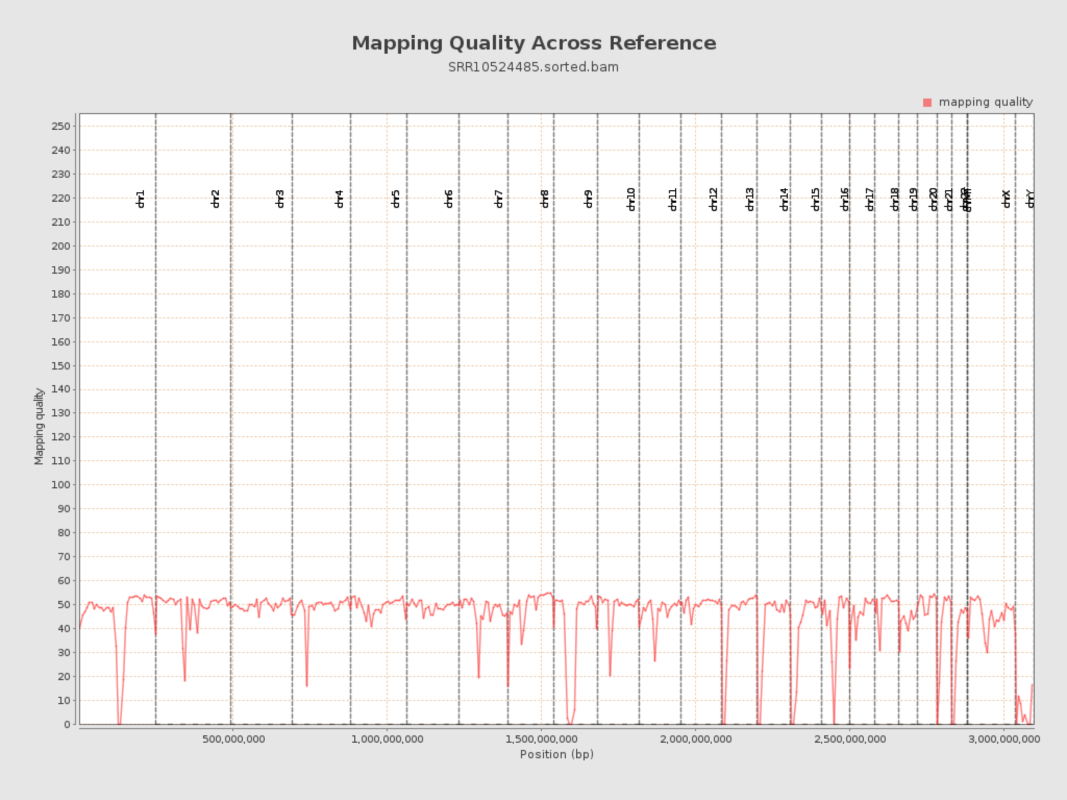
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram