Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:02:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524966.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_SRR10524966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524966.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:02:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,308,756
Mapped reads	1,211,933 / 92.6%
Unmapped reads	96,823 / 7.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,826 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	36,461 / 2.79%
Duplication rate	2.16%
Clipped reads	1,211,227 / 92.55%

2.2. ACGT Content

Number/percentage of A's	17,933,624 / 25.53%
Number/percentage of C's	13,503,257 / 19.22%
Number/percentage of T's	22,050,776 / 31.39%
Number/percentage of G's	16,768,857 / 23.87%
Number/percentage of N's	846 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.2264

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Mismatches and indels

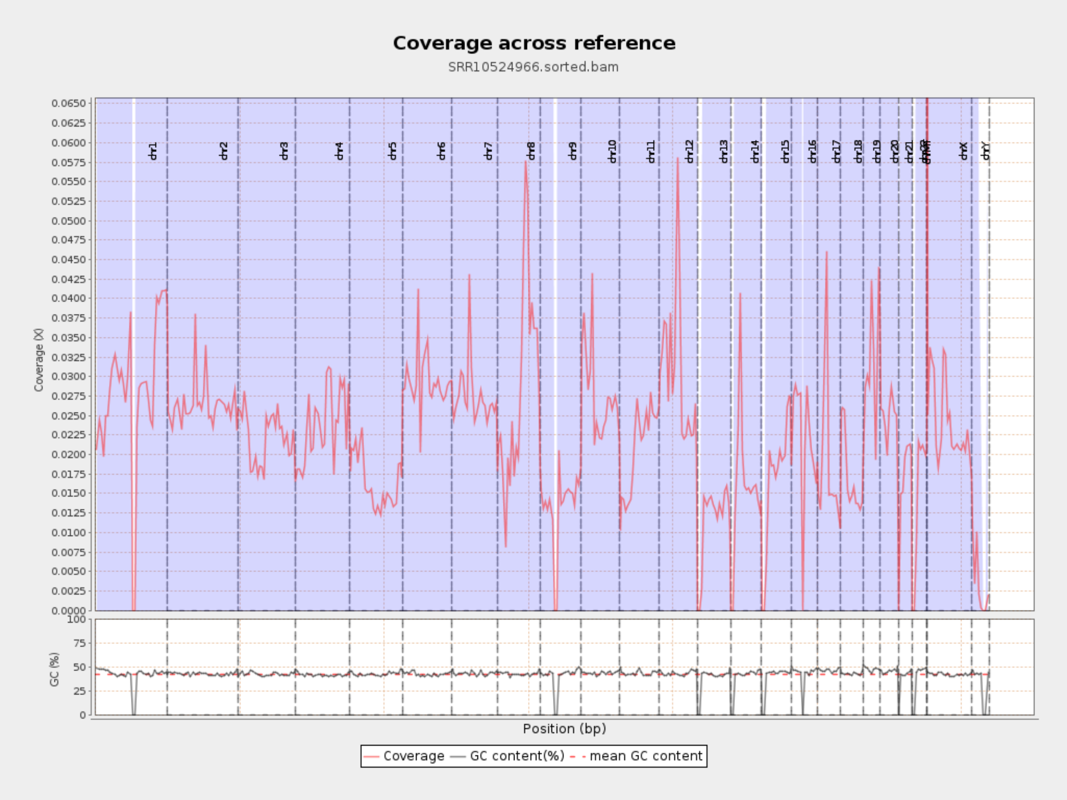
General error rate	0.49%
Mismatches	336,292
Insertions	5,059
Mapped reads with at least one insertion	0.42%
Deletions	12,226
Mapped reads with at least one deletion	1%
Homopolymer indels	42%

2.6. Chromosome stats

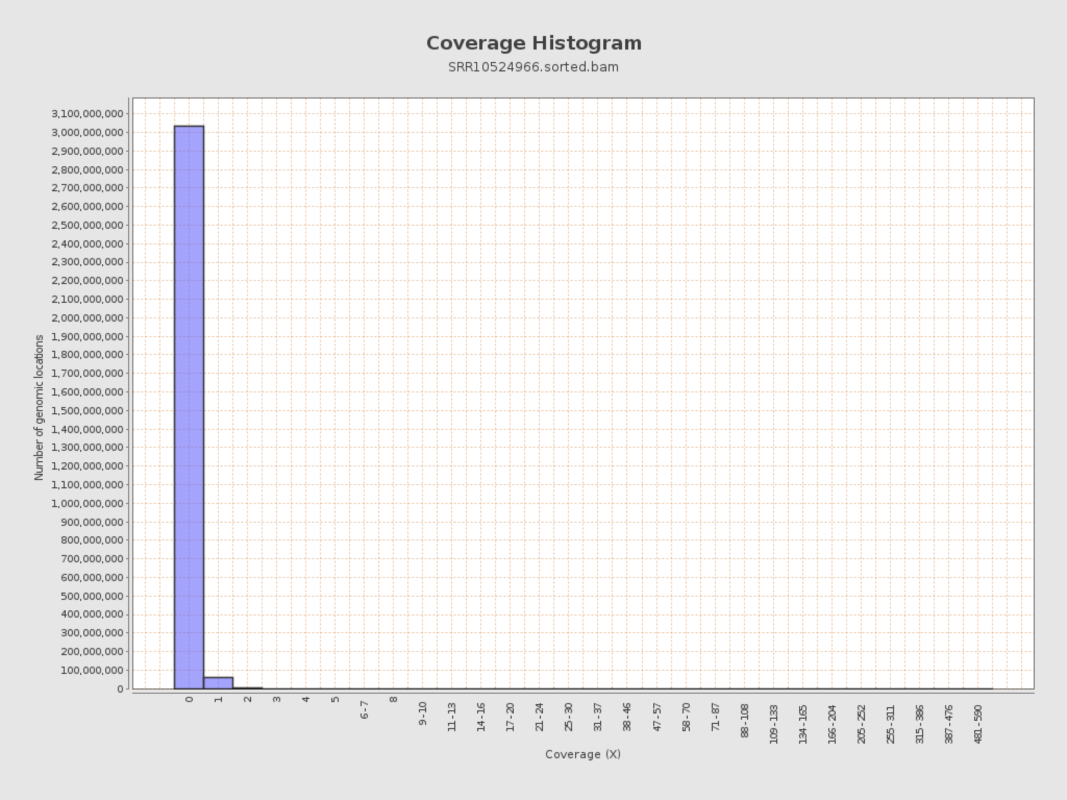
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7007003	0.0281	0.4227
chr2	243199373	6422684	0.0264	0.2488
chr3	198022430	4416610	0.0223	0.1618
chr4	191154276	4551247	0.0238	0.1742
chr5	180915260	2969964	0.0164	0.1411
chr6	171115067	5027872	0.0294	0.2323
chr7	159138663	4386506	0.0276	0.31

chr8	146364022	4250584	0.029	0.224
chr9	141213431	1867148	0.0132	0.1713
chr10	135534747	3786827	0.0279	0.227
chr11	135006516	2817310	0.0209	0.2051
chr12	133851895	4106839	0.0307	0.1905
chr13	115169878	1325934	0.0115	0.1199
chr14	107349540	1702367	0.0159	0.1402
chr15	102531392	1723917	0.0168	0.1509
chr16	90354753	1969463	0.0218	0.1655
chr17	81195210	1592538	0.0196	0.1866
chr18	78077248	1334806	0.0171	0.2658
chr19	59128983	1893127	0.032	0.2721
chr20	63025520	1552344	0.0246	0.1708
chr21	48129895	815699	0.0169	0.1463
chr22	51304566	752328	0.0147	0.1292
chrMT	16571	28612	1.7266	1.6782
chrX	155270560	3782015	0.0244	0.1867
chrY	59373566	194401	0.0033	0.0785

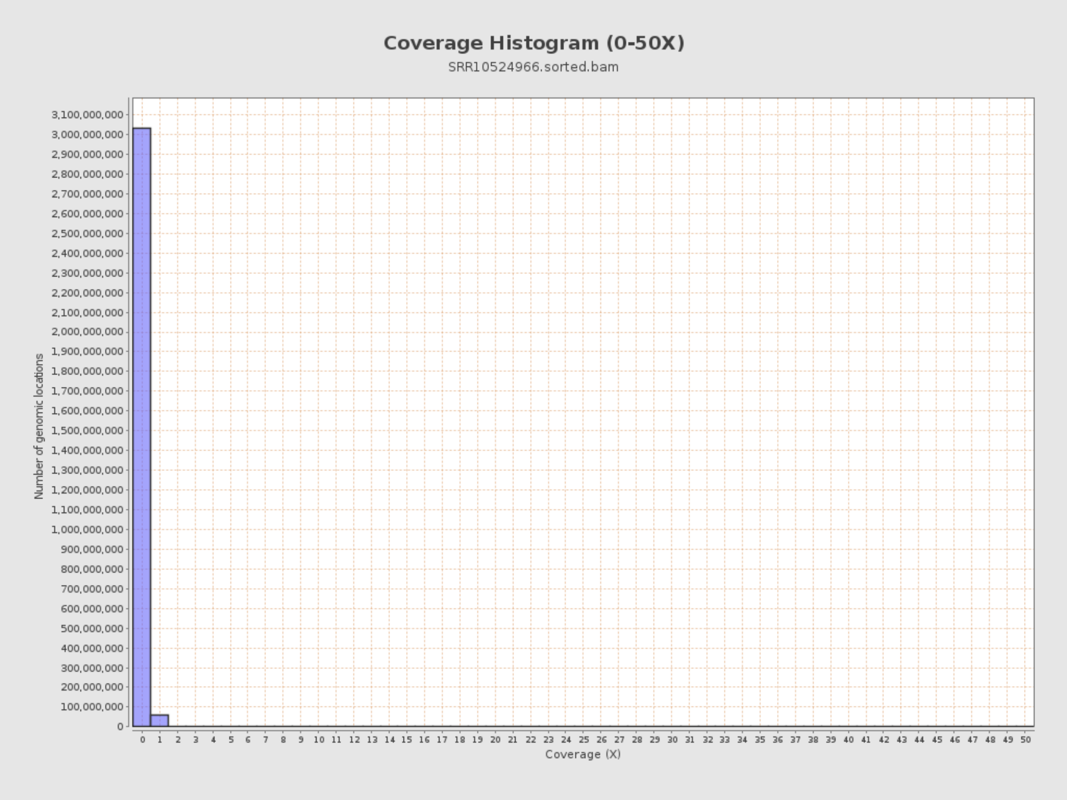
3. Results : Coverage across reference



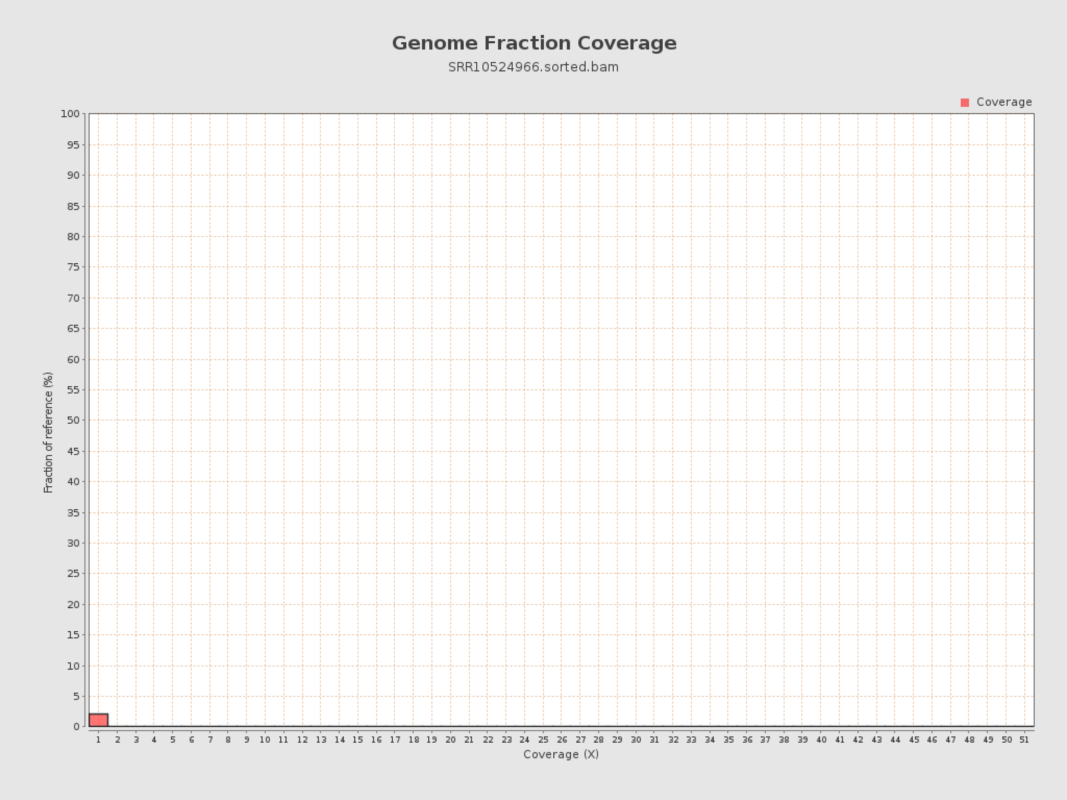
4. Results : Coverage Histogram



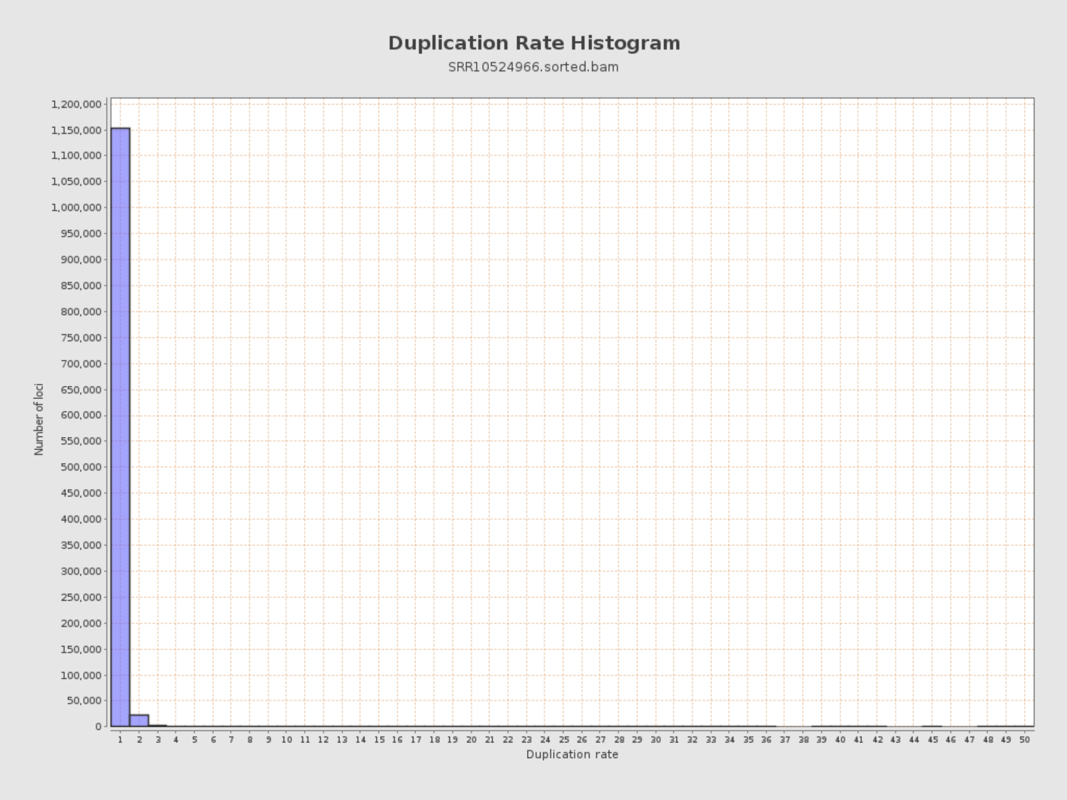
5. Results : Coverage Histogram (0-50X)



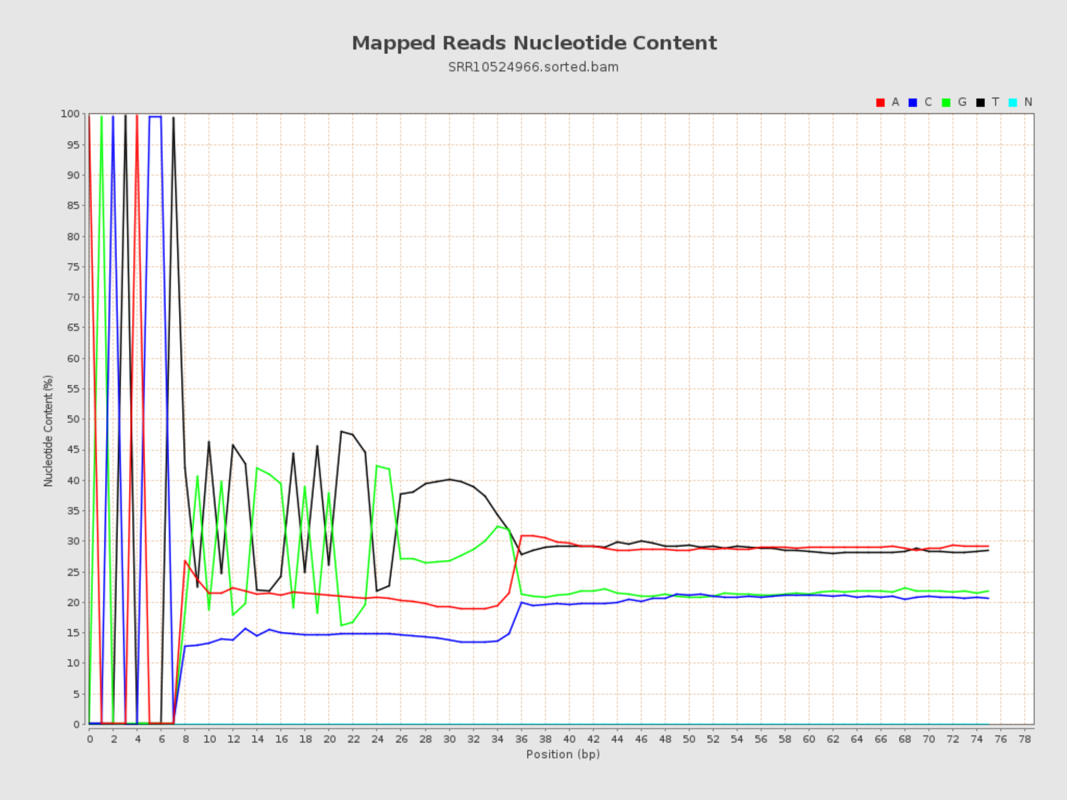
6. Results : Genome Fraction Coverage



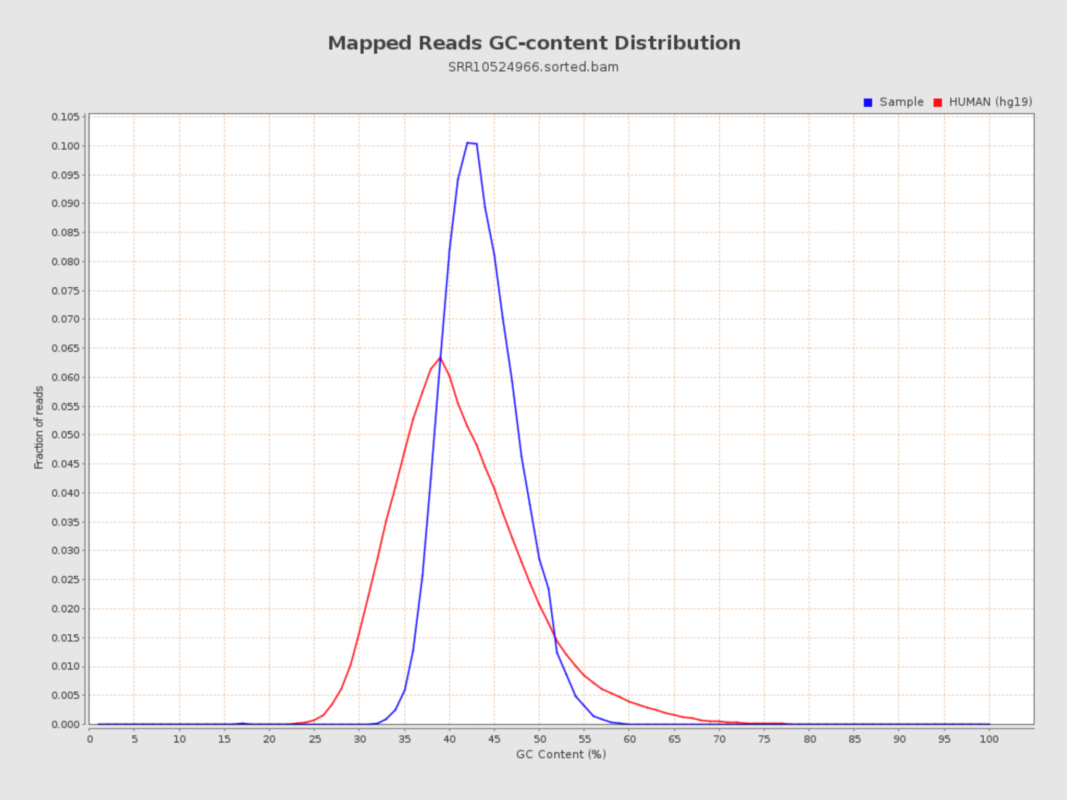
7. Results : Duplication Rate Histogram



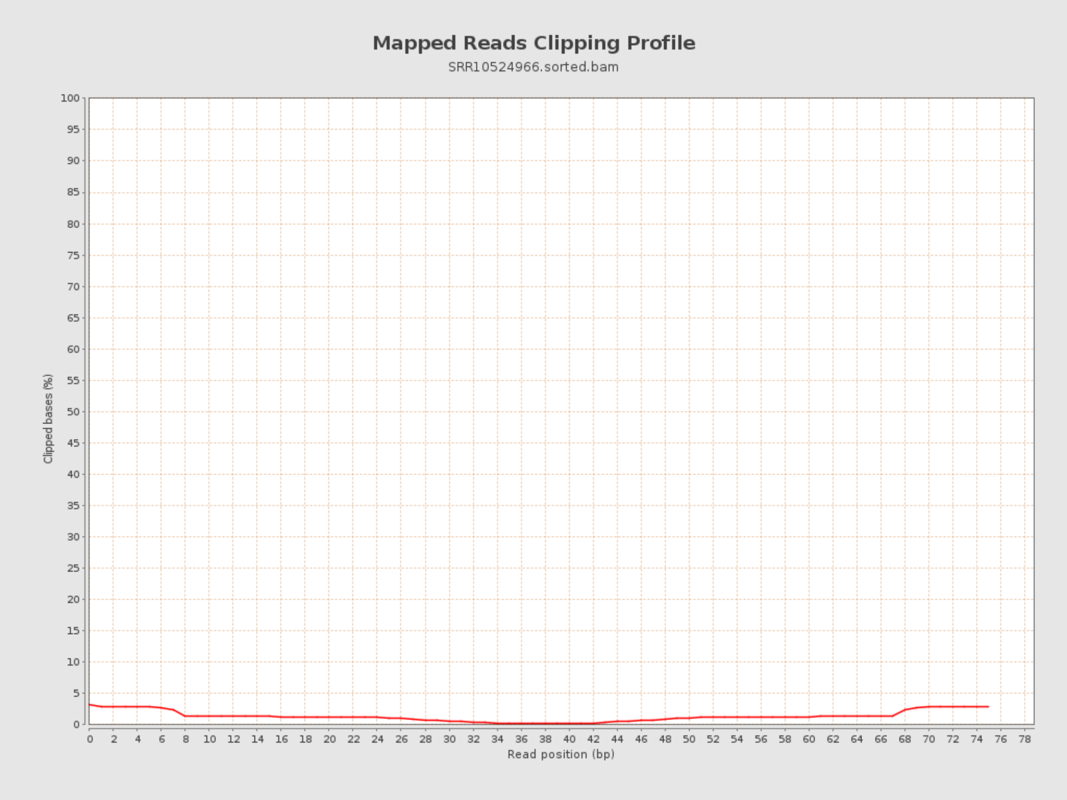
8. Results : Mapped Reads Nucleotide Content



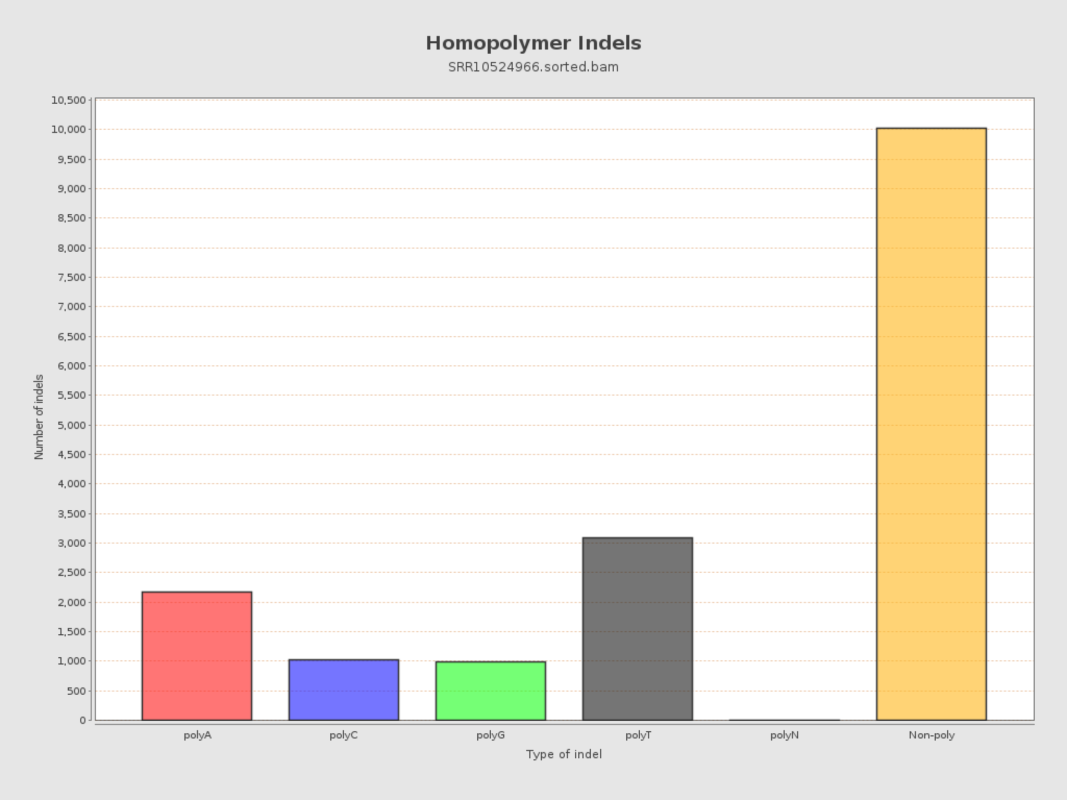
9. Results : Mapped Reads GC-content Distribution



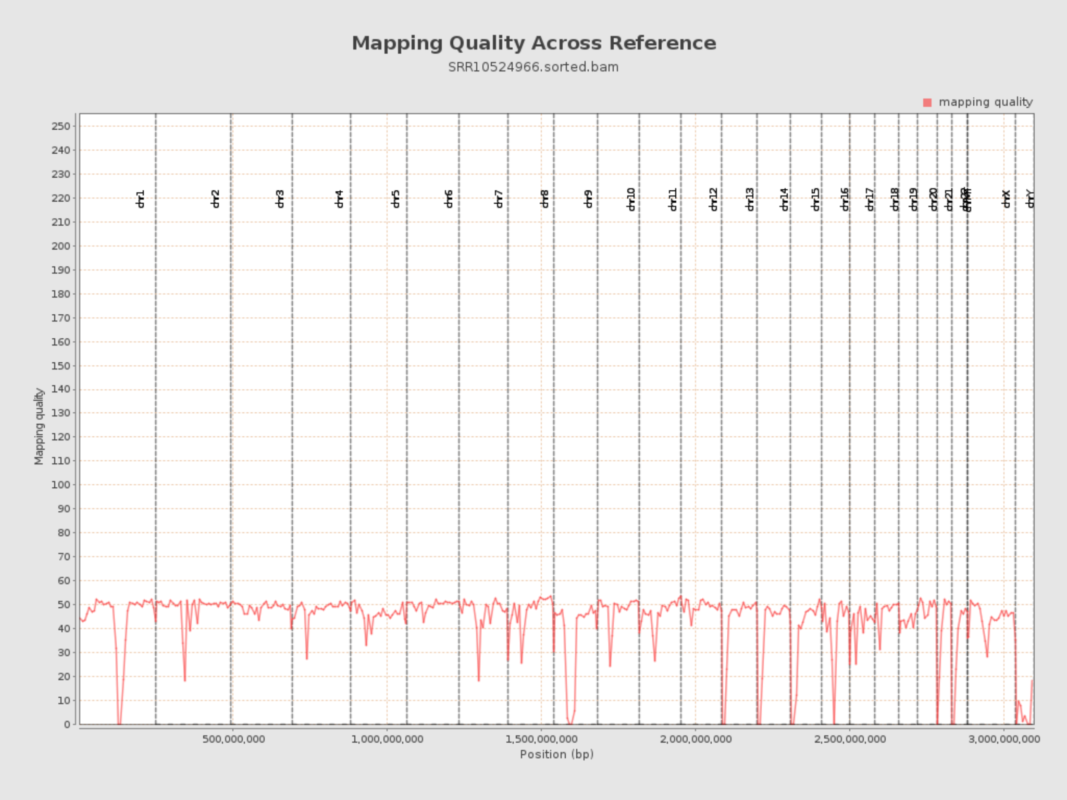
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram