Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:15:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524901.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_SRR10524901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524901.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,407,153
Mapped reads	3,144,871 / 92.3%
Unmapped reads	262,282 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,853 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	258,864 / 7.6%
Duplication rate	6.13%
Clipped reads	3,146,963 / 92.36%

2.2. ACGT Content

Number/percentage of A's	46,197,860 / 25.37%
Number/percentage of C's	32,282,619 / 17.73%
Number/percentage of T's	57,502,498 / 31.58%
Number/percentage of G's	46,098,939 / 25.32%
Number/percentage of N's	1,607 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0588

Standard Deviation	0.5024

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

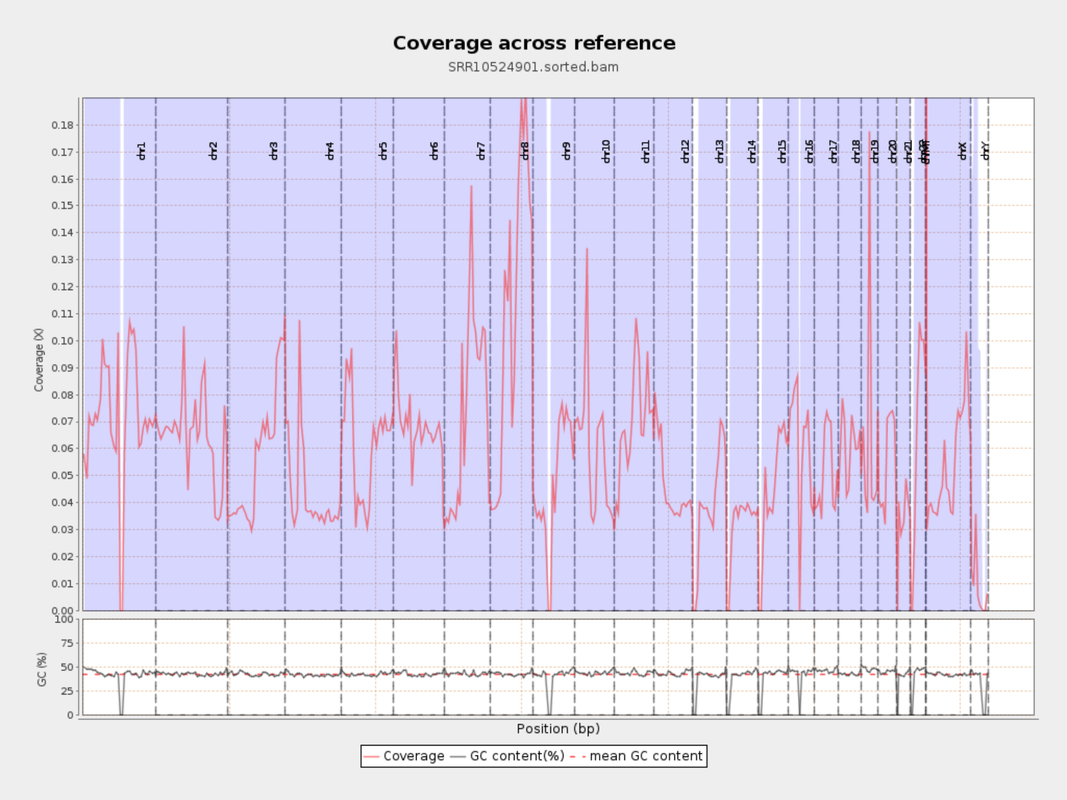
General error rate	0.51%
Mismatches	906,425
Insertions	12,357
Mapped reads with at least one insertion	0.39%
Deletions	35,636
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.01%

2.6. Chromosome stats

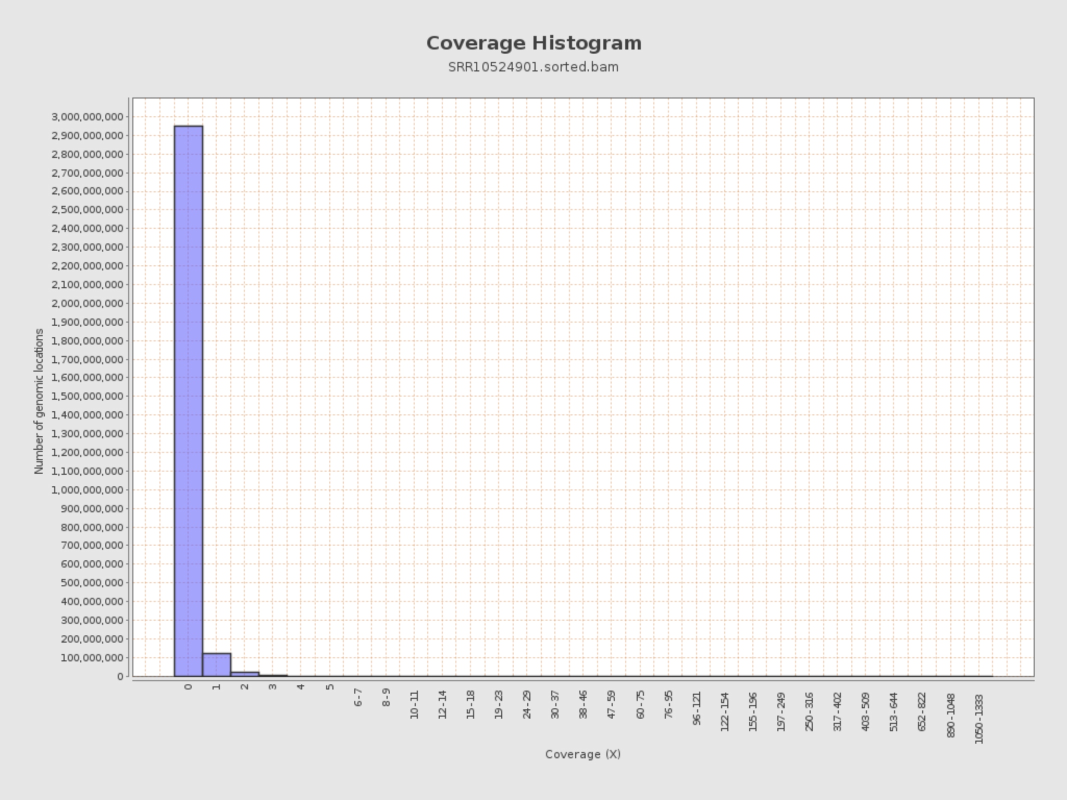
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17930038	0.0719	0.9722
chr2	243199373	15800489	0.065	0.6054
chr3	198022430	11148862	0.0563	0.2997
chr4	191154276	8355997	0.0437	0.3559
chr5	180915260	11032054	0.061	0.3007
chr6	171115067	11742517	0.0686	0.3547
chr7	159138663	11645336	0.0732	0.6581

chr8	146364022	16290640	0.1113	0.6462
chr9	141213431	6613577	0.0468	0.3839
chr10	135534747	8021265	0.0592	0.5886
chr11	135006516	9393156	0.0696	0.4218
chr12	133851895	6204326	0.0464	0.2841
chr13	115169878	4499224	0.0391	0.2418
chr14	107349540	3429180	0.0319	0.2307
chr15	102531392	4504399	0.0439	0.2648
chr16	90354753	5401979	0.0598	0.3426
chr17	81195210	4172023	0.0514	0.2917
chr18	78077248	4772333	0.0611	0.6807
chr19	59128983	3793463	0.0642	0.7133
chr20	63025520	3498973	0.0555	0.3003
chr21	48129895	1655421	0.0344	0.3273
chr22	51304566	3356518	0.0654	0.3163
chrMT	16571	19751	1.1919	1.4231
chrX	155270560	8332352	0.0537	0.34
chrY	59373566	529351	0.0089	0.3098

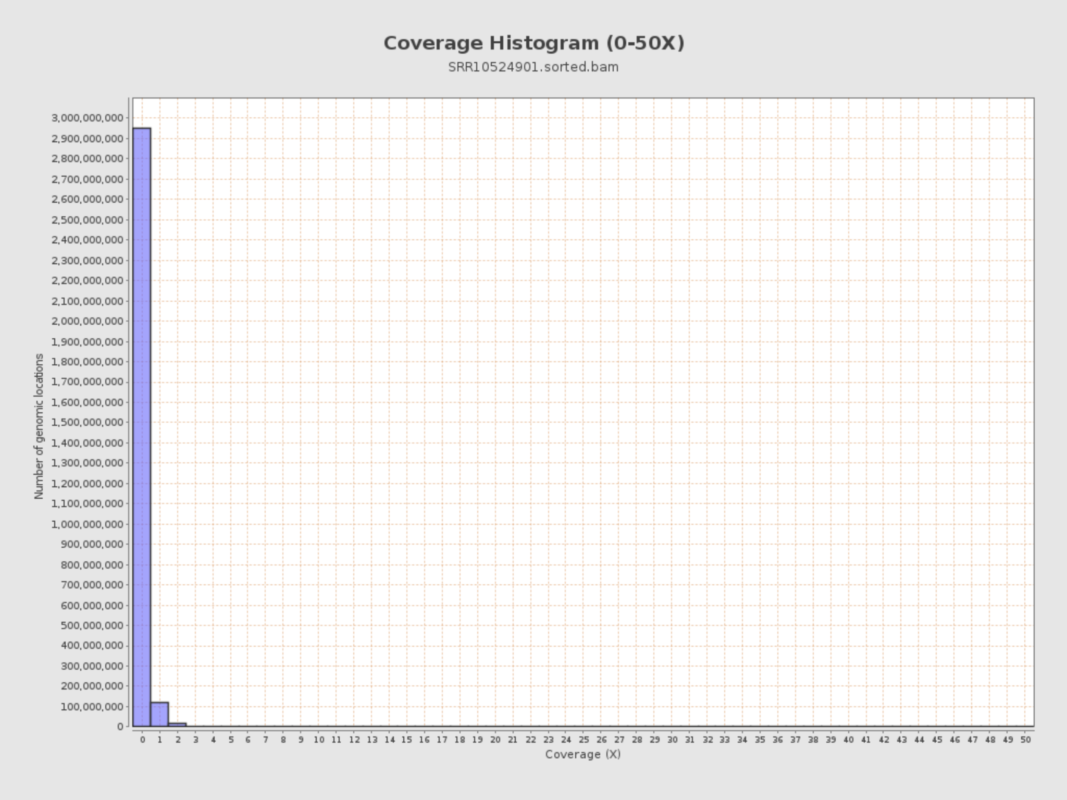
3. Results : Coverage across reference



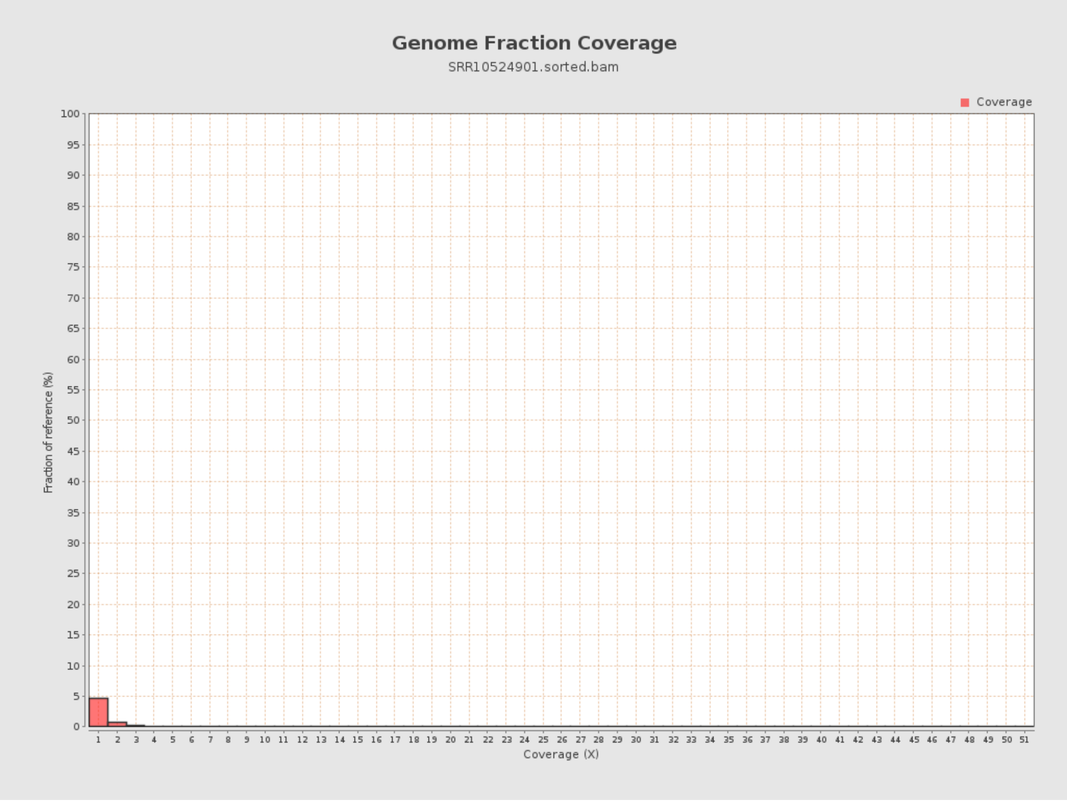
4. Results : Coverage Histogram



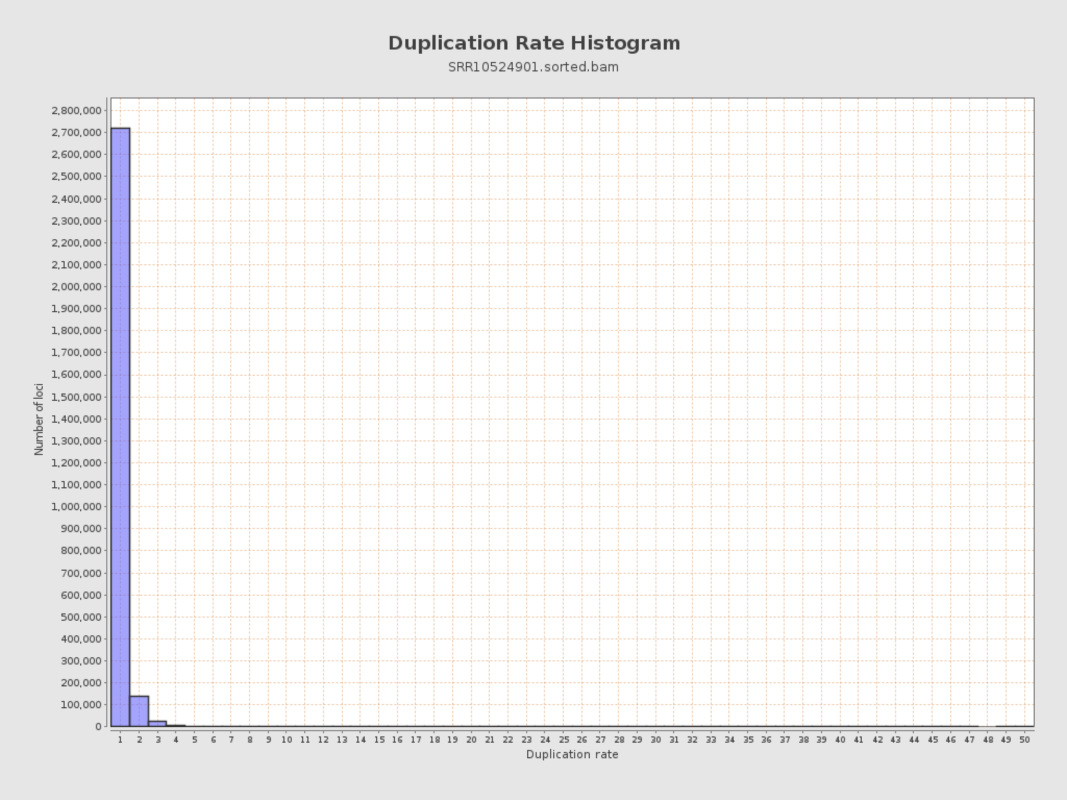
5. Results : Coverage Histogram (0-50X)



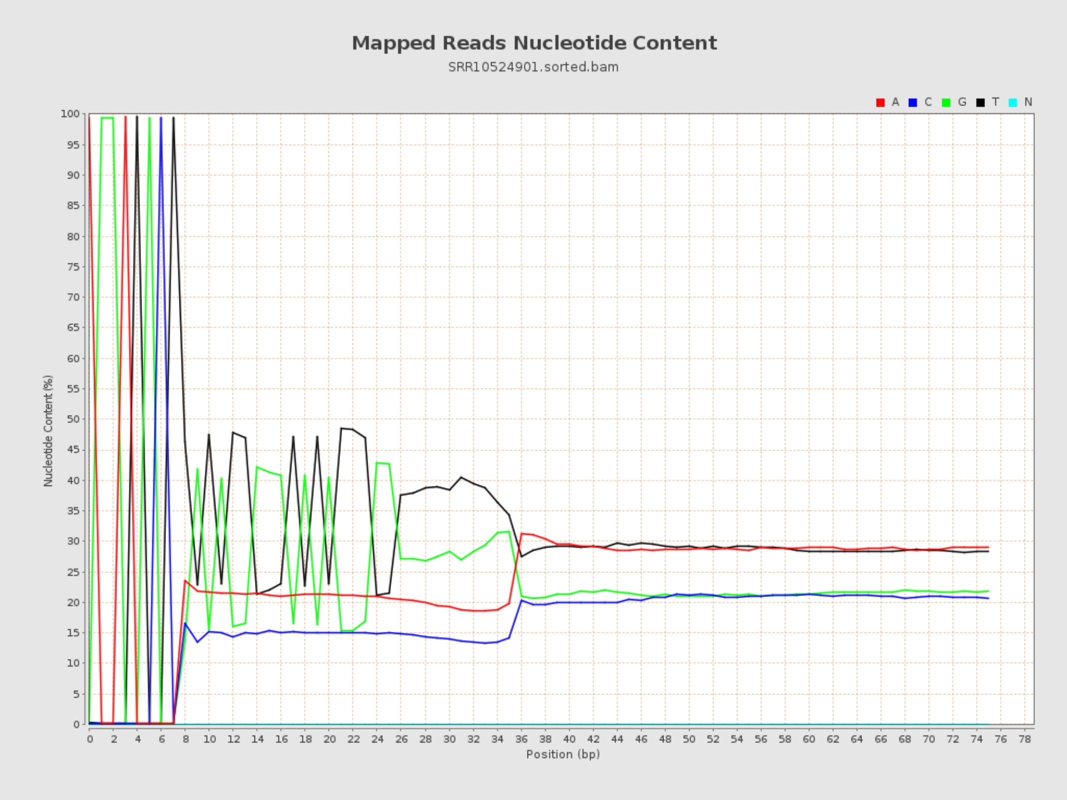
6. Results : Genome Fraction Coverage



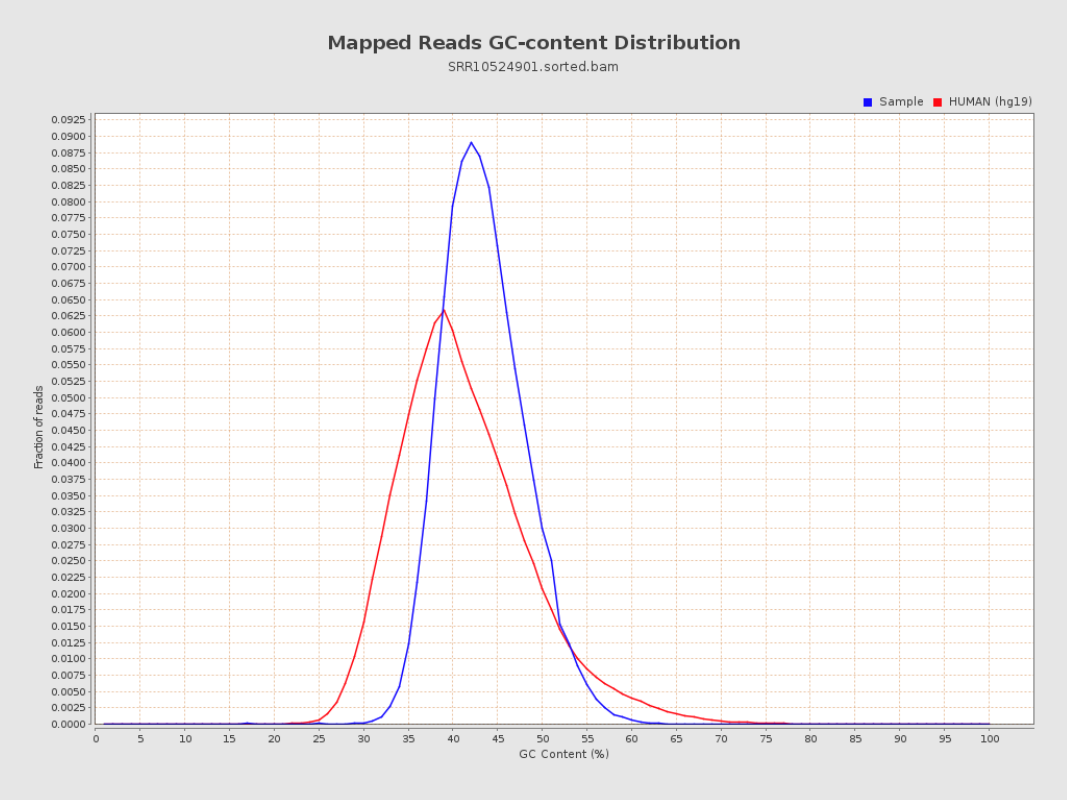
7. Results : Duplication Rate Histogram



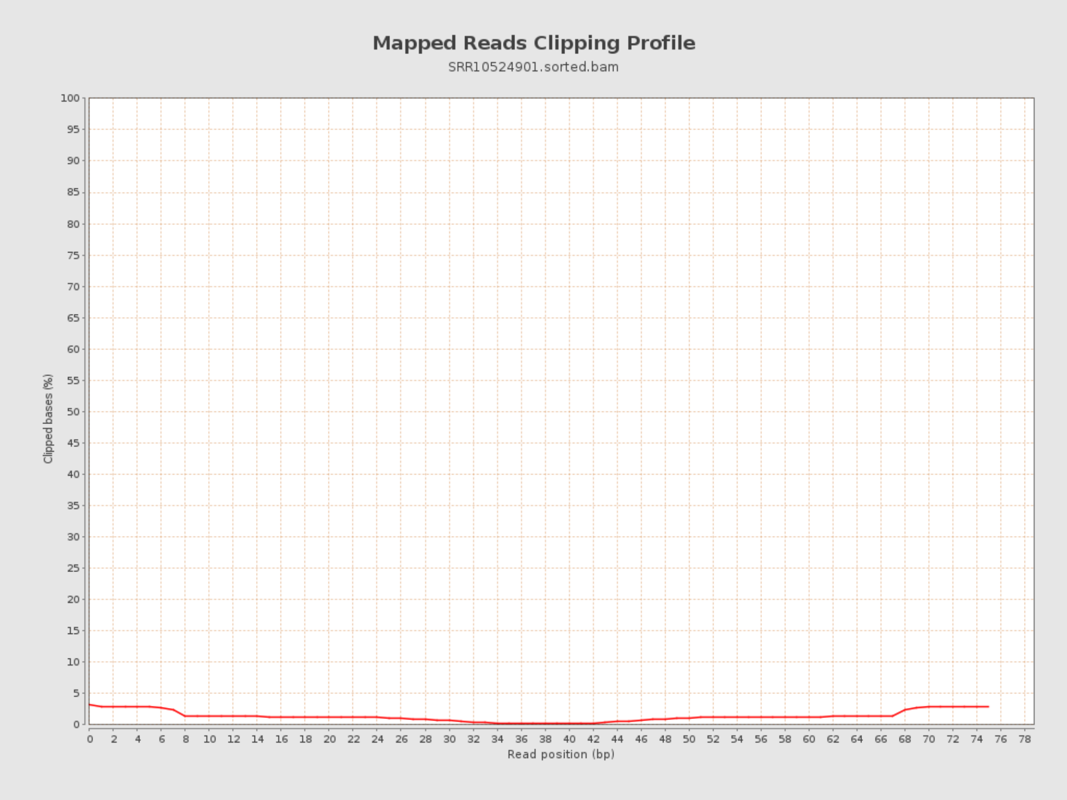
8. Results : Mapped Reads Nucleotide Content



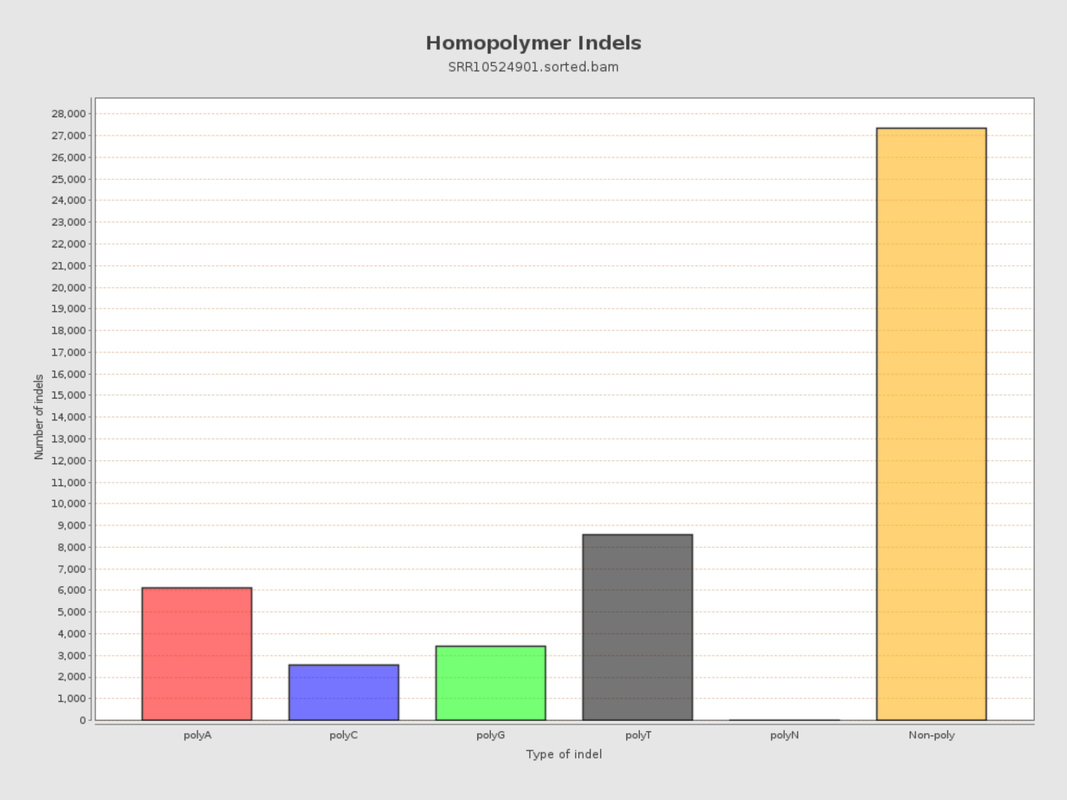
9. Results : Mapped Reads GC-content Distribution



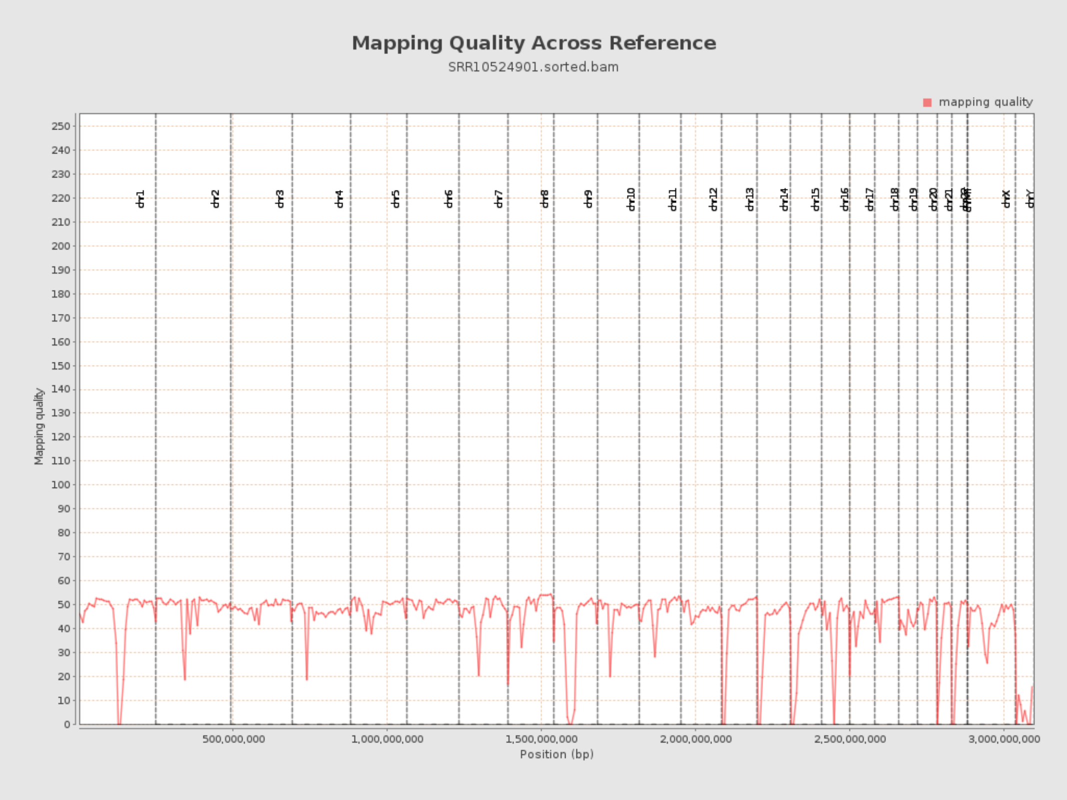
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram