Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:55:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524651.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_SRR10524651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524651.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:55:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,970,624
Mapped reads	2,743,624 / 92.36%
Unmapped reads	227,000 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,845 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	336,543 / 11.33%
Duplication rate	8.7%
Clipped reads	2,751,878 / 92.64%

2.2. ACGT Content

Number/percentage of A's	39,563,260 / 24.64%
Number/percentage of C's	31,704,965 / 19.74%
Number/percentage of T's	49,969,929 / 31.12%
Number/percentage of G's	39,348,557 / 24.5%
Number/percentage of N's	1,216 / 0%
GC Percentage	44.25%

2.3. Coverage

Mean	0.0519

Standard Deviation	0.4695

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

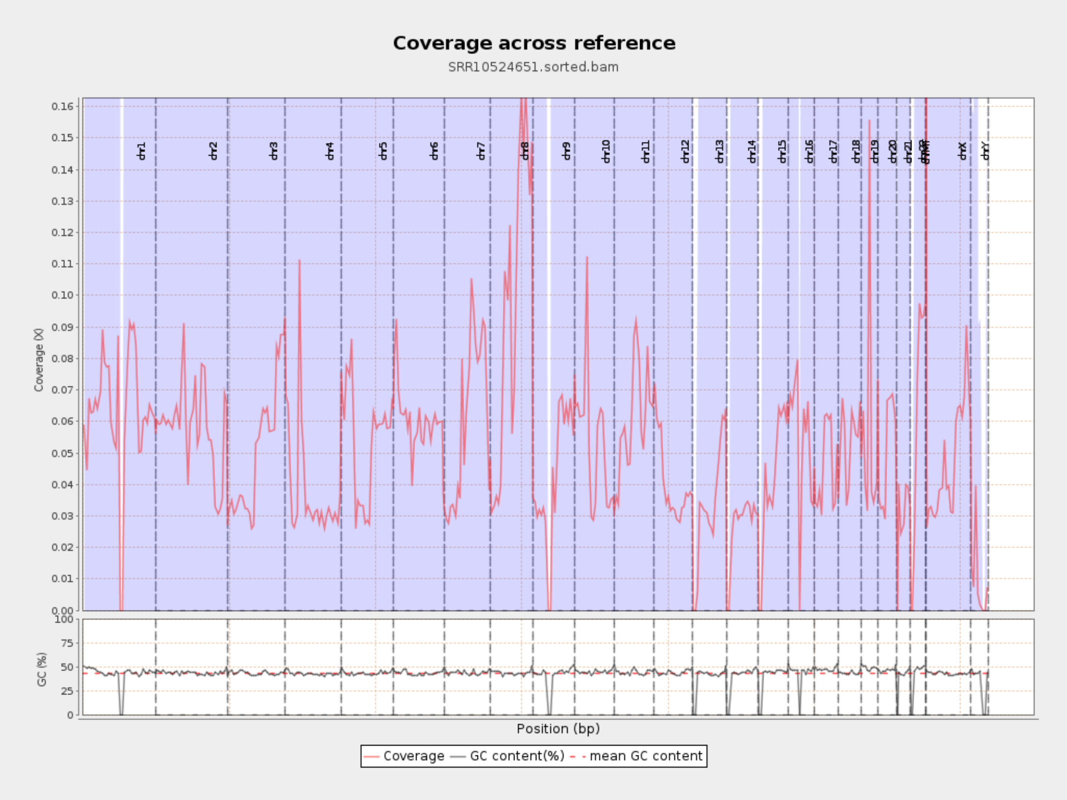
General error rate	0.52%
Mismatches	813,933
Insertions	9,342
Mapped reads with at least one insertion	0.34%
Deletions	29,341
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.74%

2.6. Chromosome stats

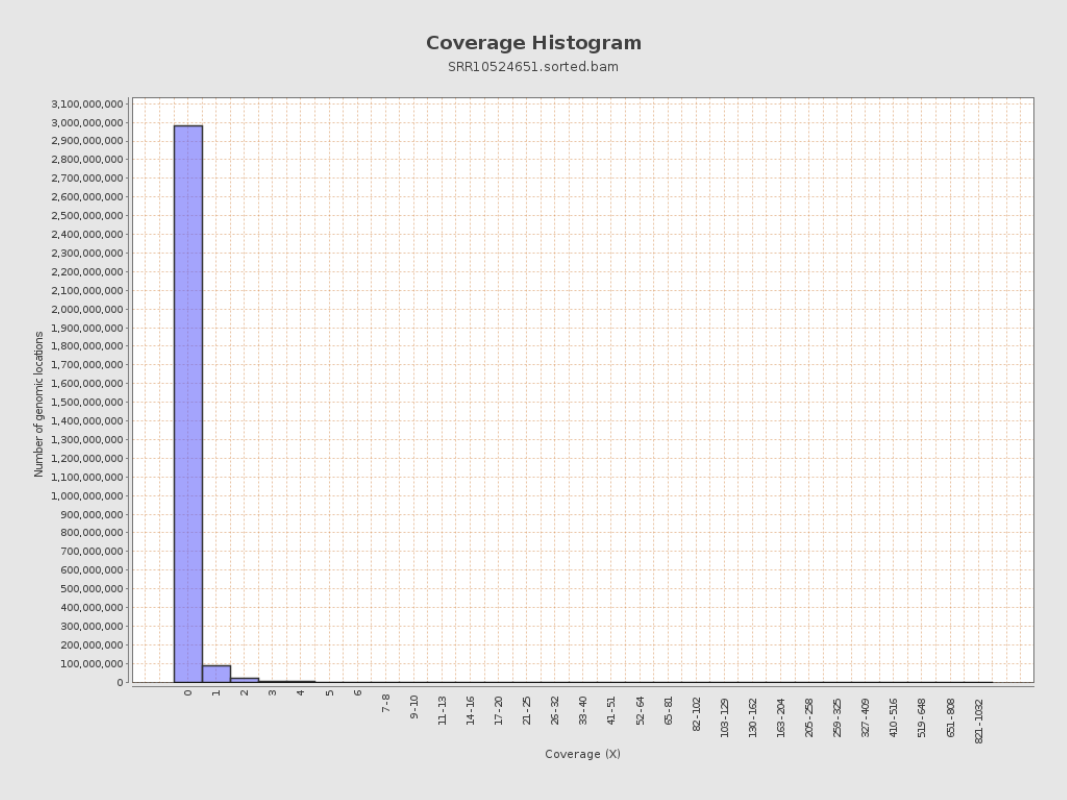
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15817845	0.0635	0.8138
chr2	243199373	14225869	0.0585	0.6118
chr3	198022430	9949536	0.0502	0.2972
chr4	191154276	7391233	0.0387	0.4014
chr5	180915260	9734828	0.0538	0.3102
chr6	171115067	10377198	0.0606	0.3474
chr7	159138663	9619288	0.0604	0.5344

chr8	146364022	14179665	0.0969	0.6684
chr9	141213431	5935228	0.042	0.3673
chr10	135534747	7107829	0.0524	0.5876
chr11	135006516	8191905	0.0607	0.403
chr12	133851895	5415658	0.0405	0.2775
chr13	115169878	3796717	0.033	0.2432
chr14	107349540	2899861	0.027	0.2268
chr15	102531392	4208616	0.041	0.2699
chr16	90354753	4814505	0.0533	0.332
chr17	81195210	3686498	0.0454	0.3026
chr18	78077248	4205485	0.0539	0.6248
chr19	59128983	3406229	0.0576	0.5824
chr20	63025520	3182985	0.0505	0.3207
chr21	48129895	1484537	0.0308	0.3365
chr22	51304566	3145049	0.0613	0.3389
chrMT	16571	13147	0.7934	1.1992
chrX	155270560	7300285	0.047	0.3215
chrY	59373566	547455	0.0092	0.3804

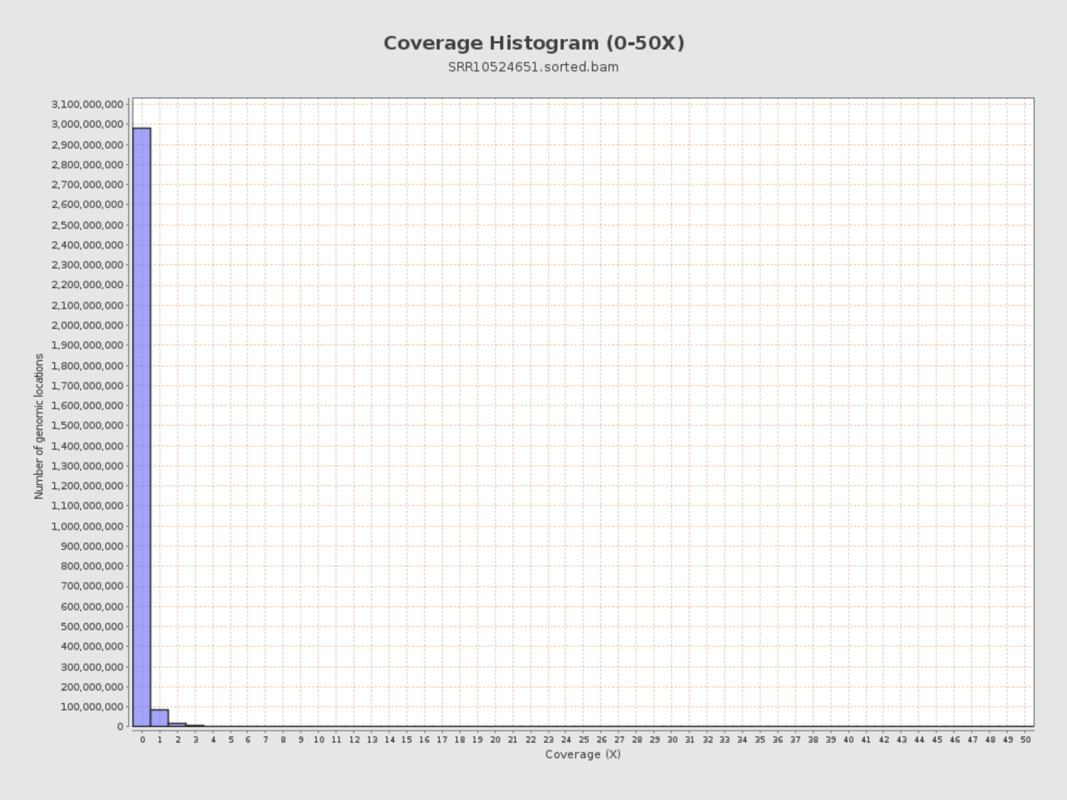
3. Results : Coverage across reference



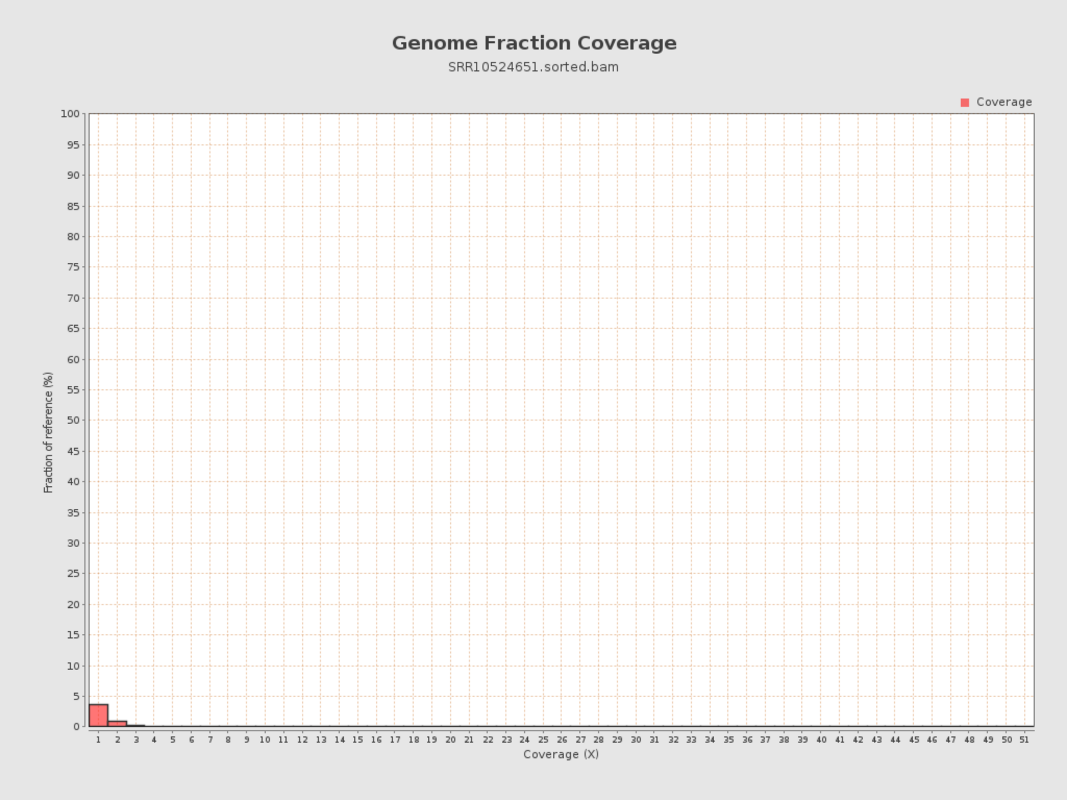
4. Results : Coverage Histogram



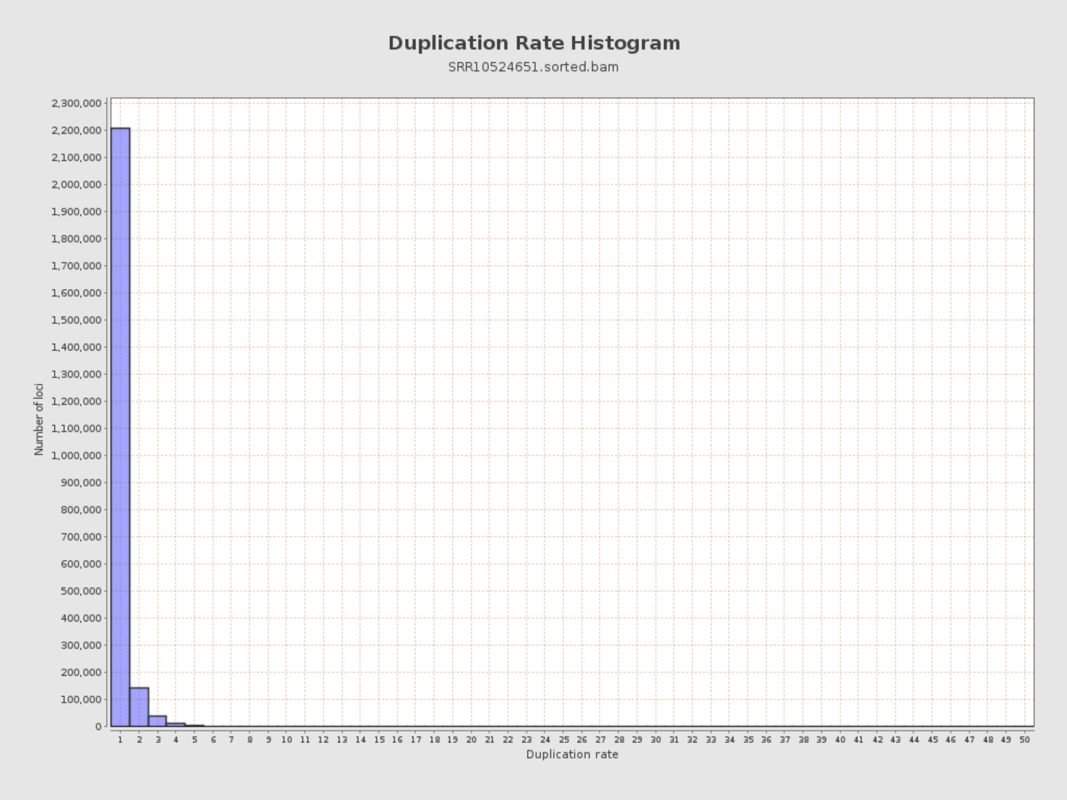
5. Results : Coverage Histogram (0-50X)



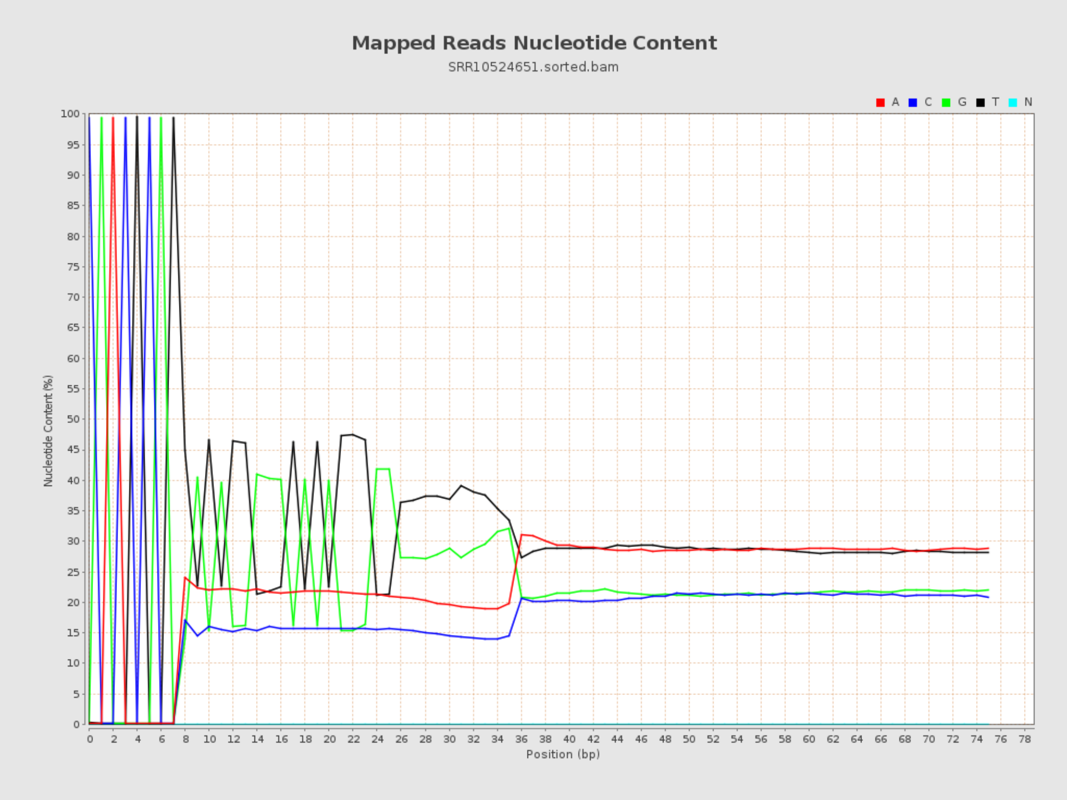
6. Results : Genome Fraction Coverage



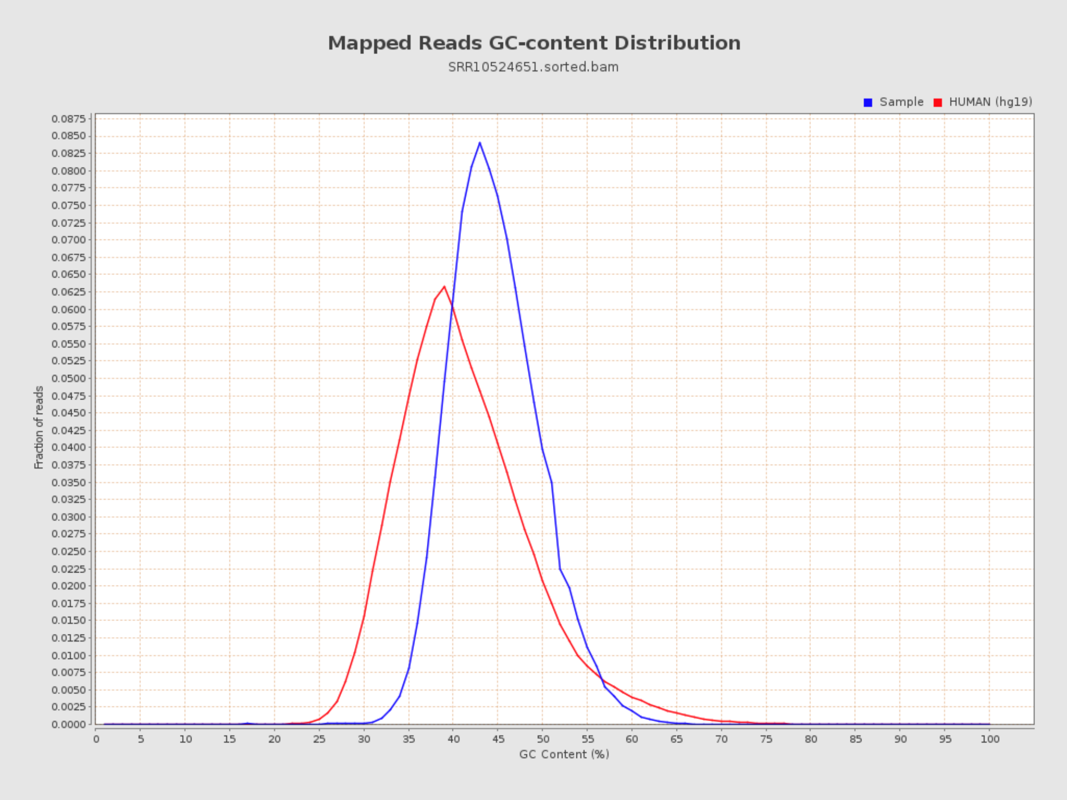
7. Results : Duplication Rate Histogram



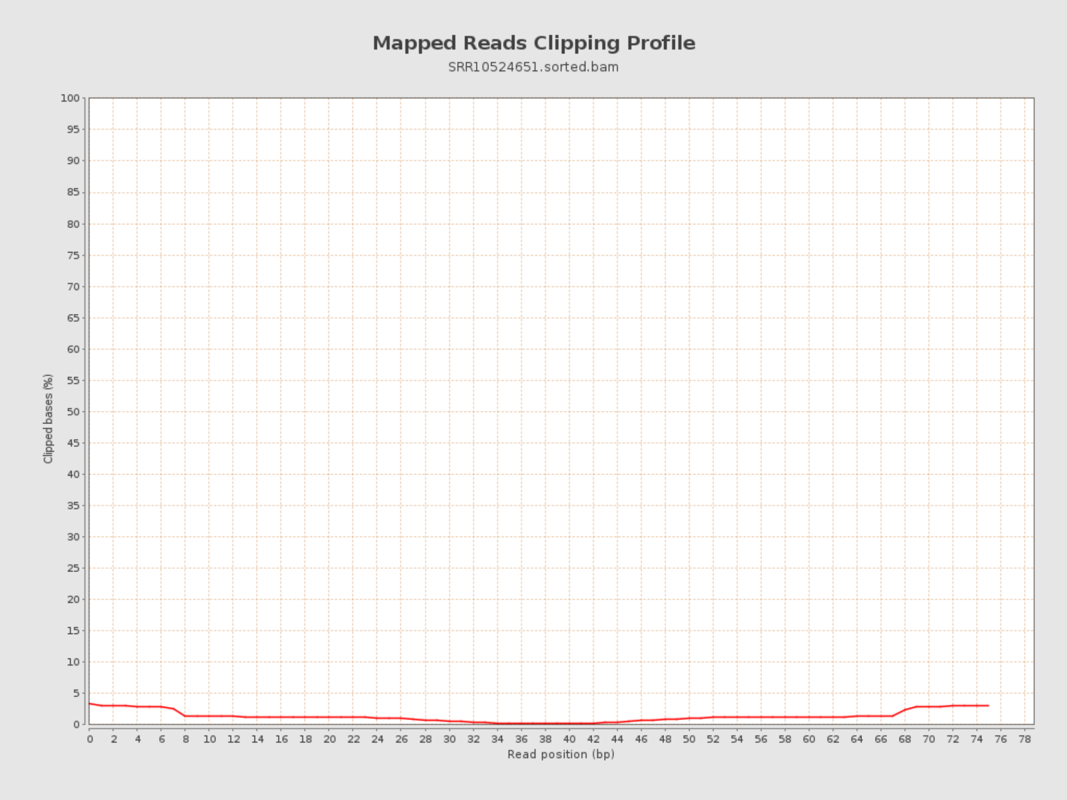
8. Results : Mapped Reads Nucleotide Content



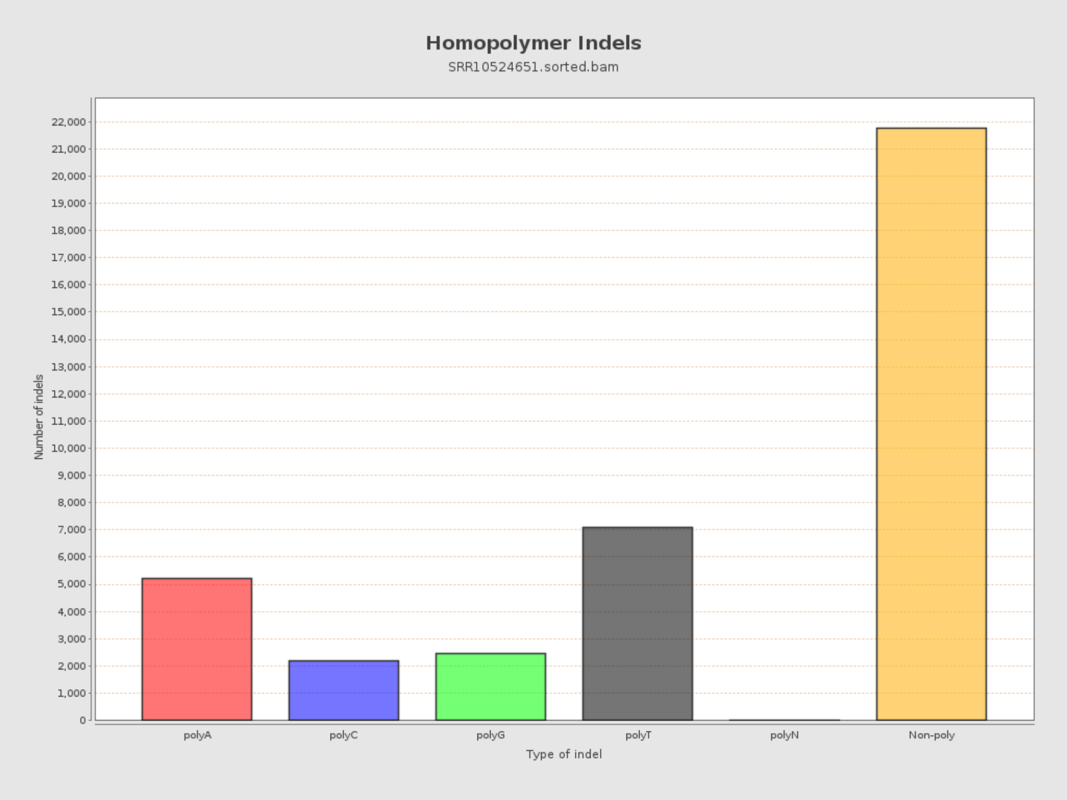
9. Results : Mapped Reads GC-content Distribution



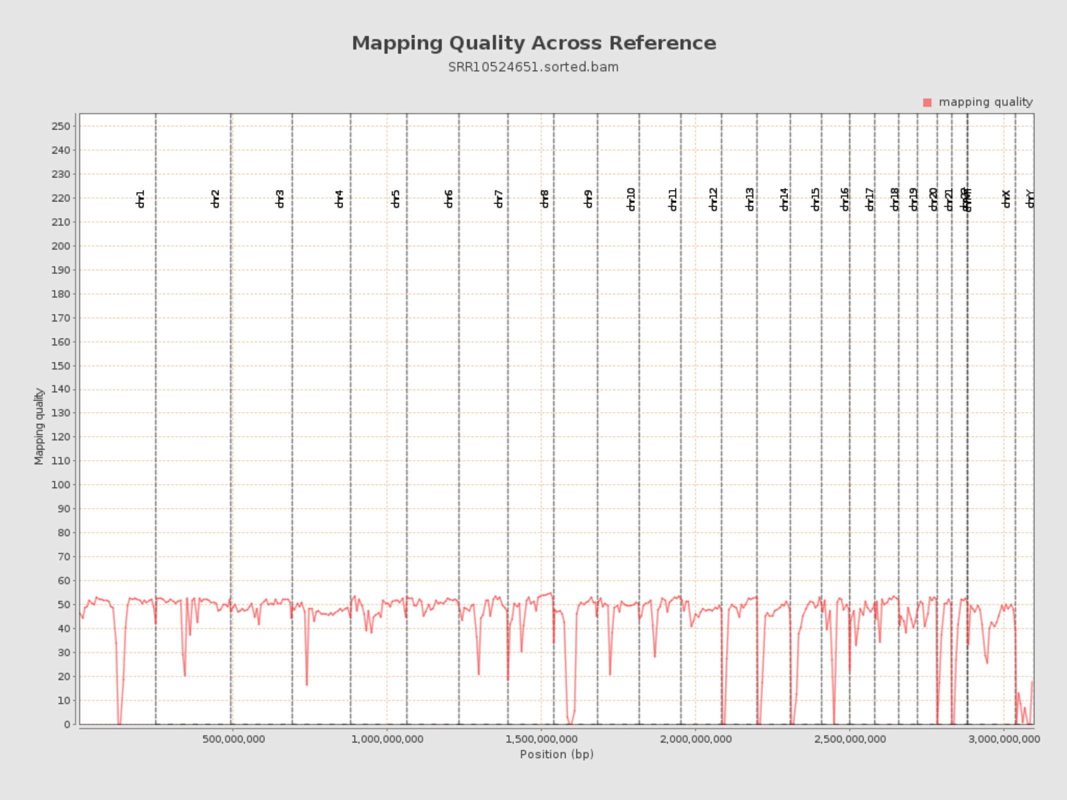
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram