Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:30:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524410.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_SRR10524410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524410.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:30:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,315,167
Mapped reads	1,222,606 / 92.96%
Unmapped reads	92,561 / 7.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,637 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	45,719 / 3.48%
Duplication rate	2.81%
Clipped reads	1,225,660 / 93.19%

2.2. ACGT Content

Number/percentage of A's	17,798,417 / 24.85%
Number/percentage of C's	14,031,786 / 19.59%
Number/percentage of T's	22,290,517 / 31.13%
Number/percentage of G's	17,486,294 / 24.42%
Number/percentage of N's	8,582 / 0.01%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2459

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

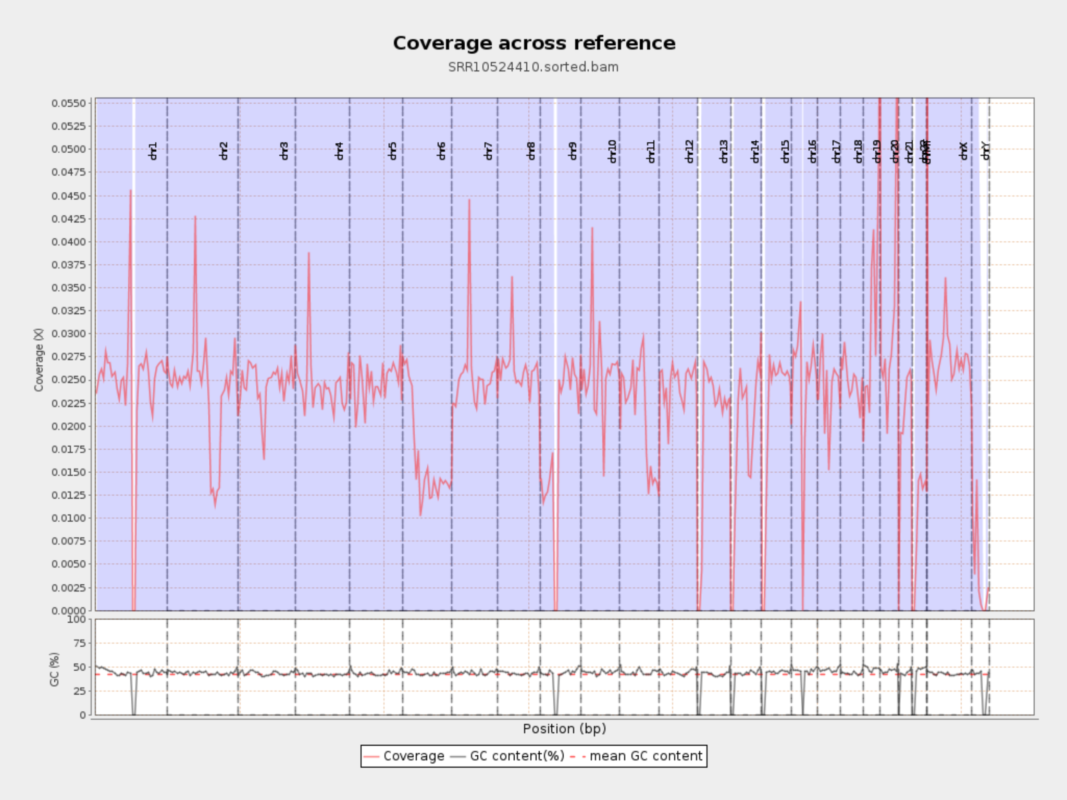
General error rate	0.49%
Mismatches	344,777
Insertions	4,345
Mapped reads with at least one insertion	0.35%
Deletions	12,618
Mapped reads with at least one deletion	1.03%
Homopolymer indels	43.39%

2.6. Chromosome stats

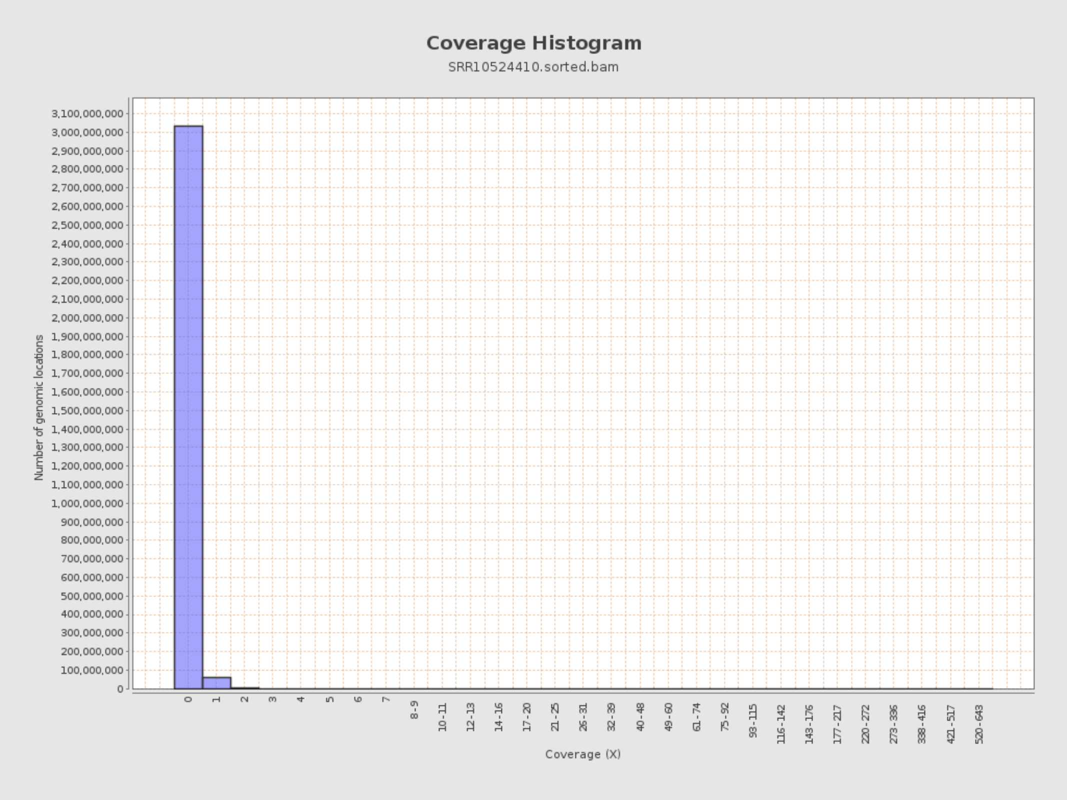
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6094207	0.0245	0.5003
chr2	243199373	5825862	0.024	0.2651
chr3	198022430	4853069	0.0245	0.1682
chr4	191154276	4720241	0.0247	0.1856
chr5	180915260	4514027	0.025	0.1703
chr6	171115067	2818176	0.0165	0.1481
chr7	159138663	4082798	0.0257	0.3428

chr8	146364022	3845157	0.0263	0.2336
chr9	141213431	2620249	0.0186	0.1877
chr10	135534747	3495869	0.0258	0.2264
chr11	135006516	2900559	0.0215	0.1926
chr12	133851895	3291380	0.0246	0.1728
chr13	115169878	2292653	0.0199	0.1508
chr14	107349540	2026395	0.0189	0.1517
chr15	102531392	2181709	0.0213	0.1565
chr16	90354753	2193350	0.0243	0.1736
chr17	81195210	1965791	0.0242	0.1809
chr18	78077248	1942073	0.0249	0.3133
chr19	59128983	1986827	0.0336	0.349
chr20	63025520	2010572	0.0319	0.1968
chr21	48129895	992451	0.0206	0.1706
chr22	51304566	509706	0.0099	0.1071
chrMT	16571	3306	0.1995	0.49
chrX	155270560	4233504	0.0273	0.1934
chrY	59373566	235795	0.004	0.1166

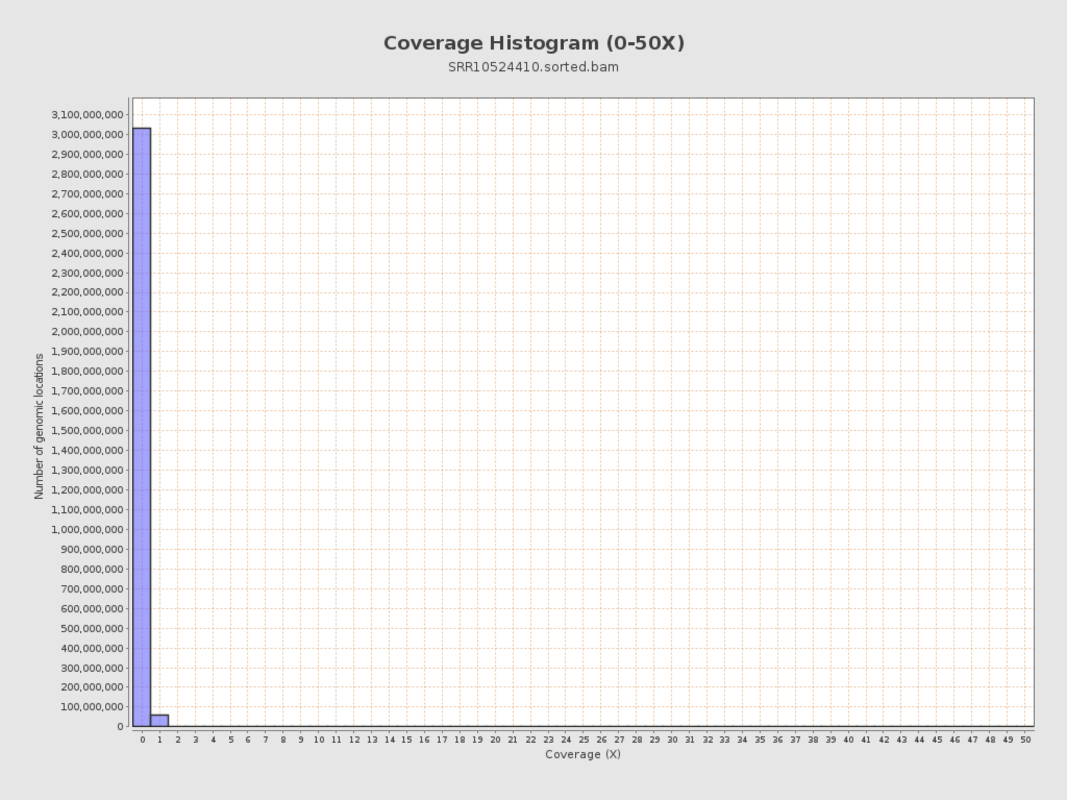
3. Results : Coverage across reference



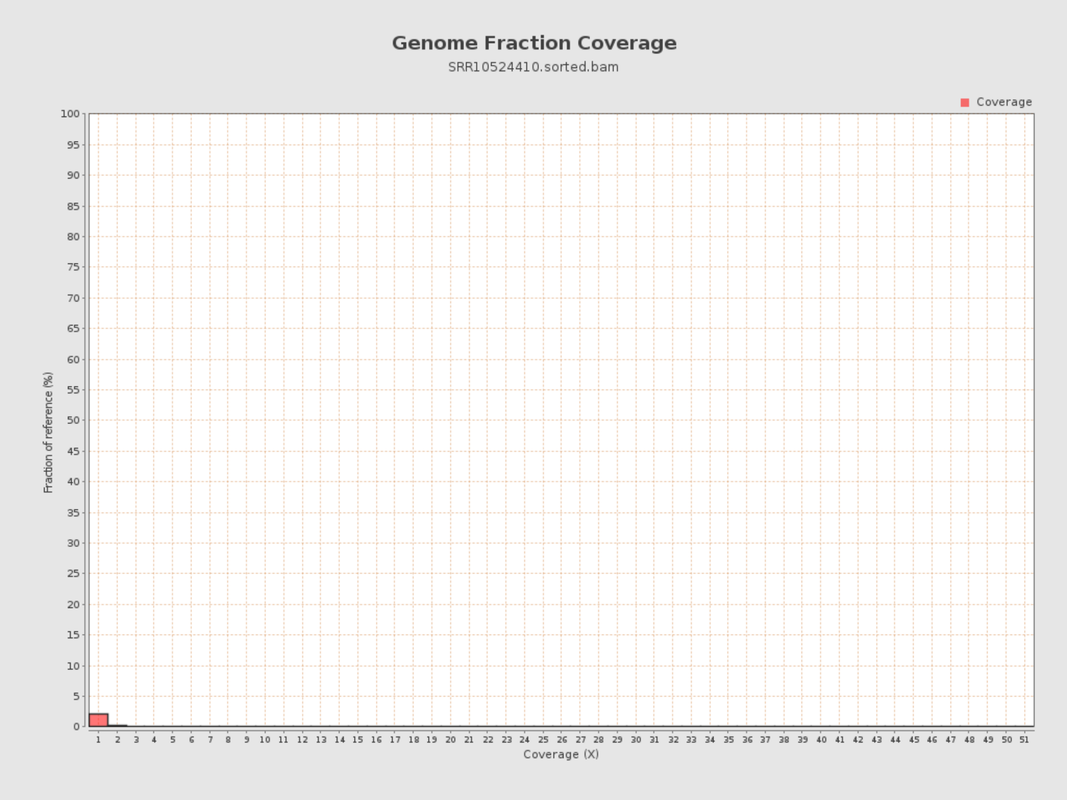
4. Results : Coverage Histogram



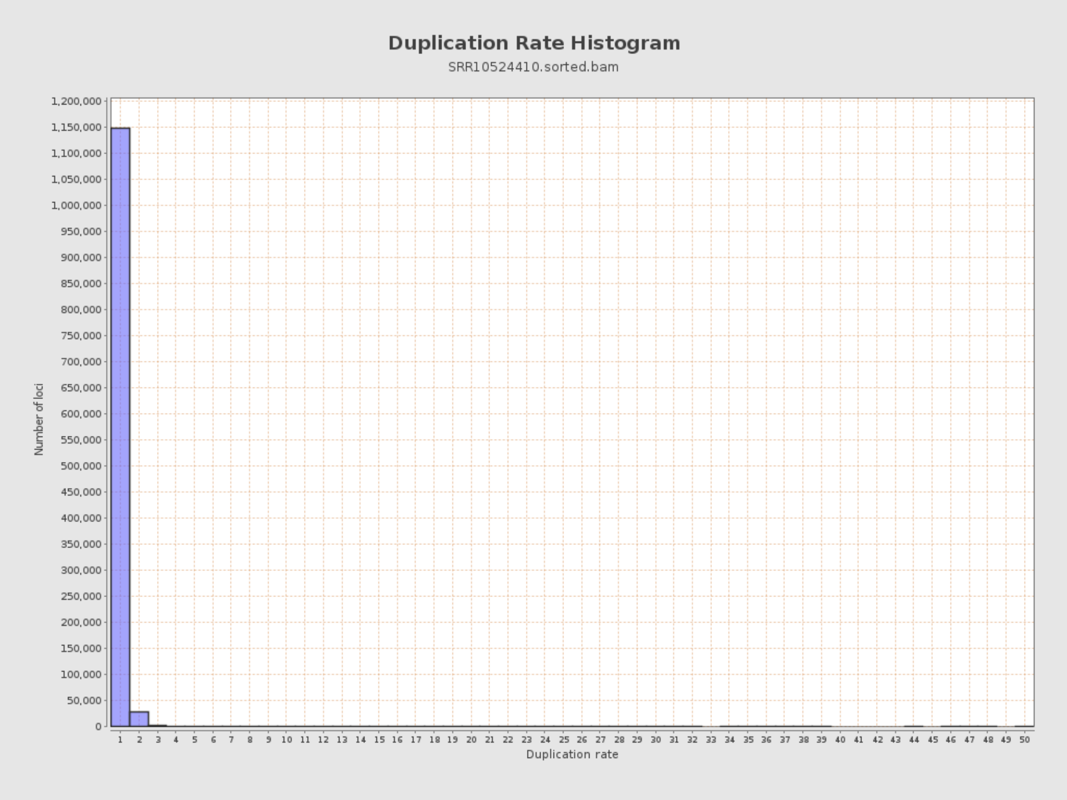
5. Results : Coverage Histogram (0-50X)



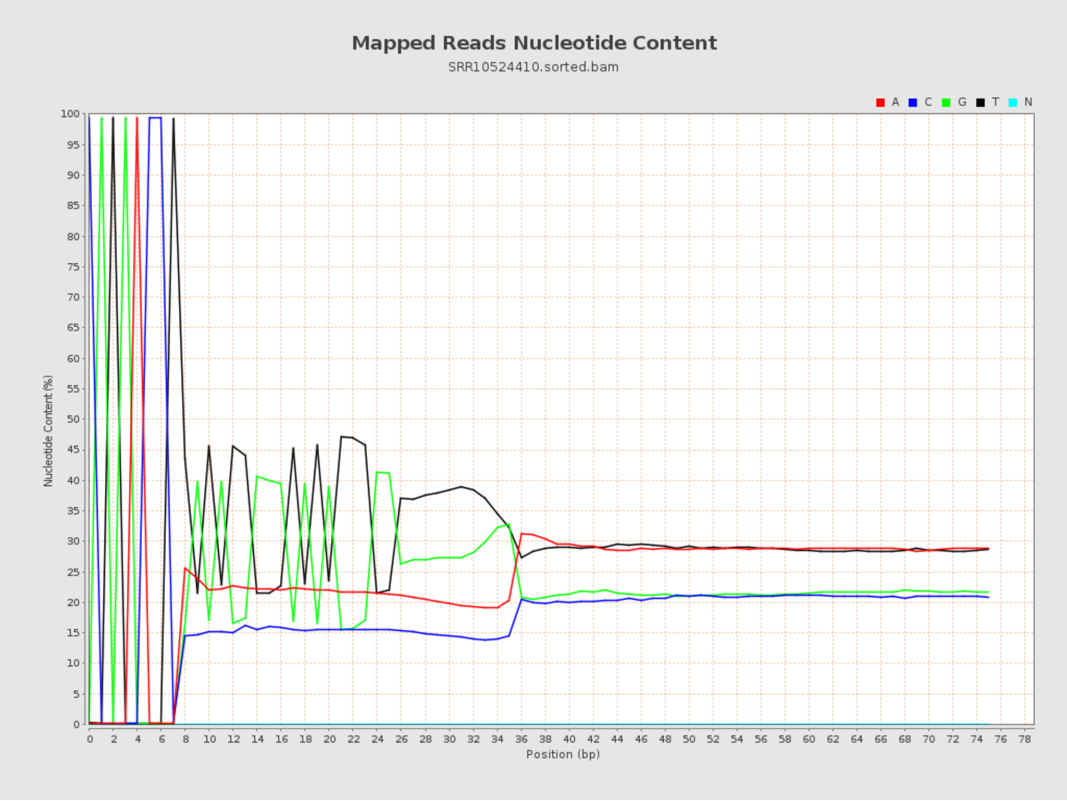
6. Results : Genome Fraction Coverage



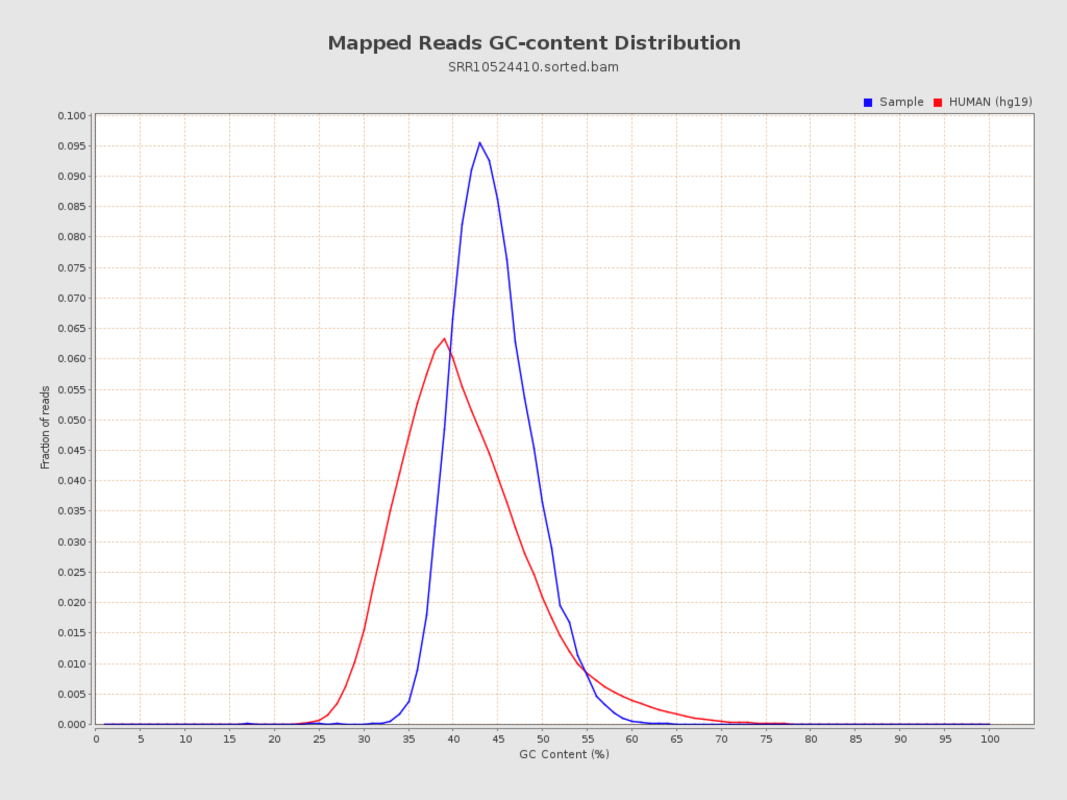
7. Results : Duplication Rate Histogram



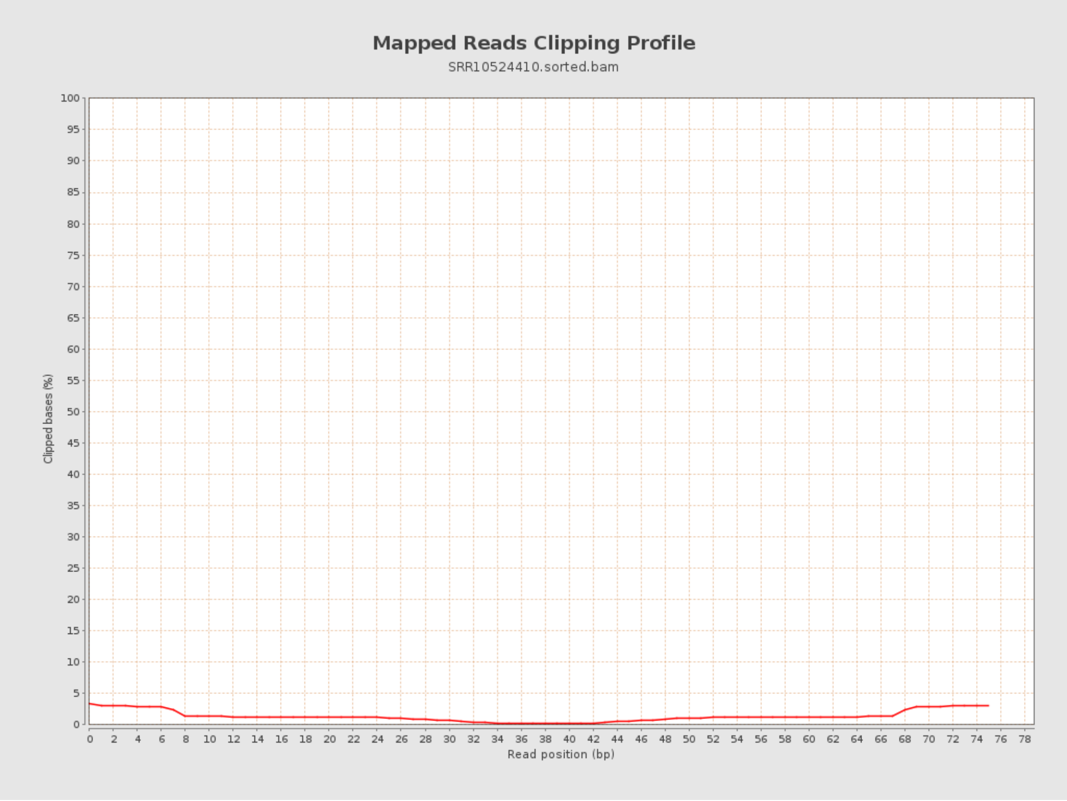
8. Results : Mapped Reads Nucleotide Content



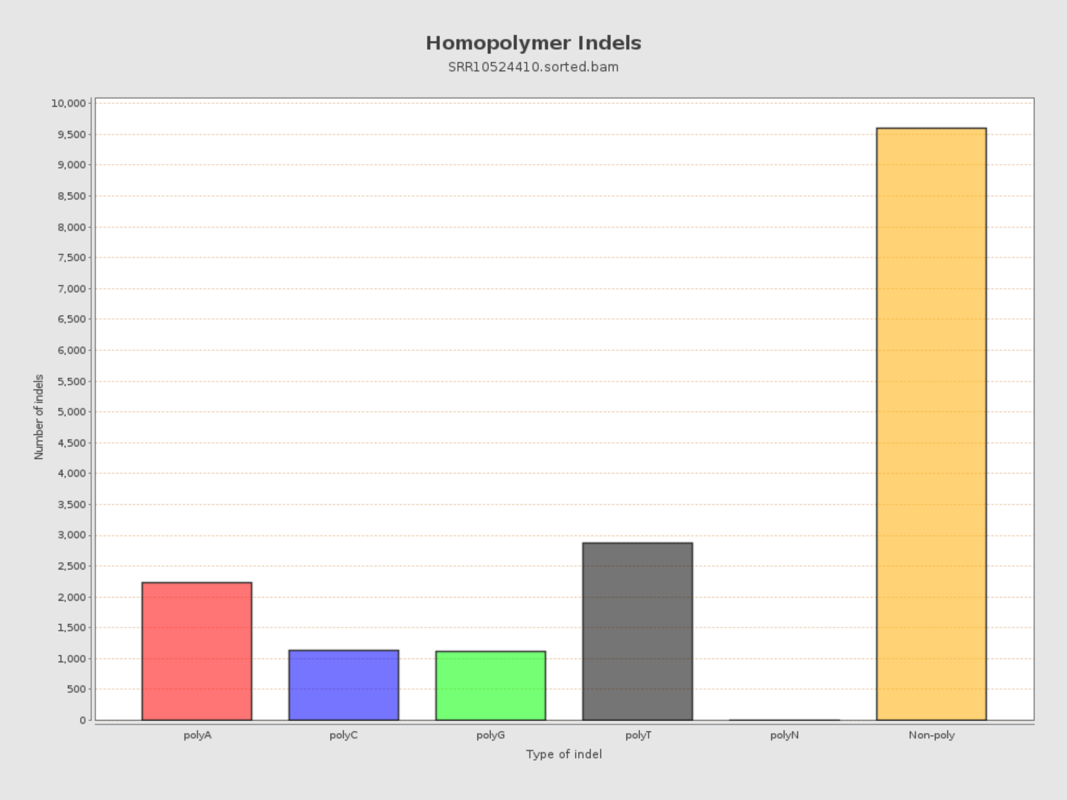
9. Results : Mapped Reads GC-content Distribution



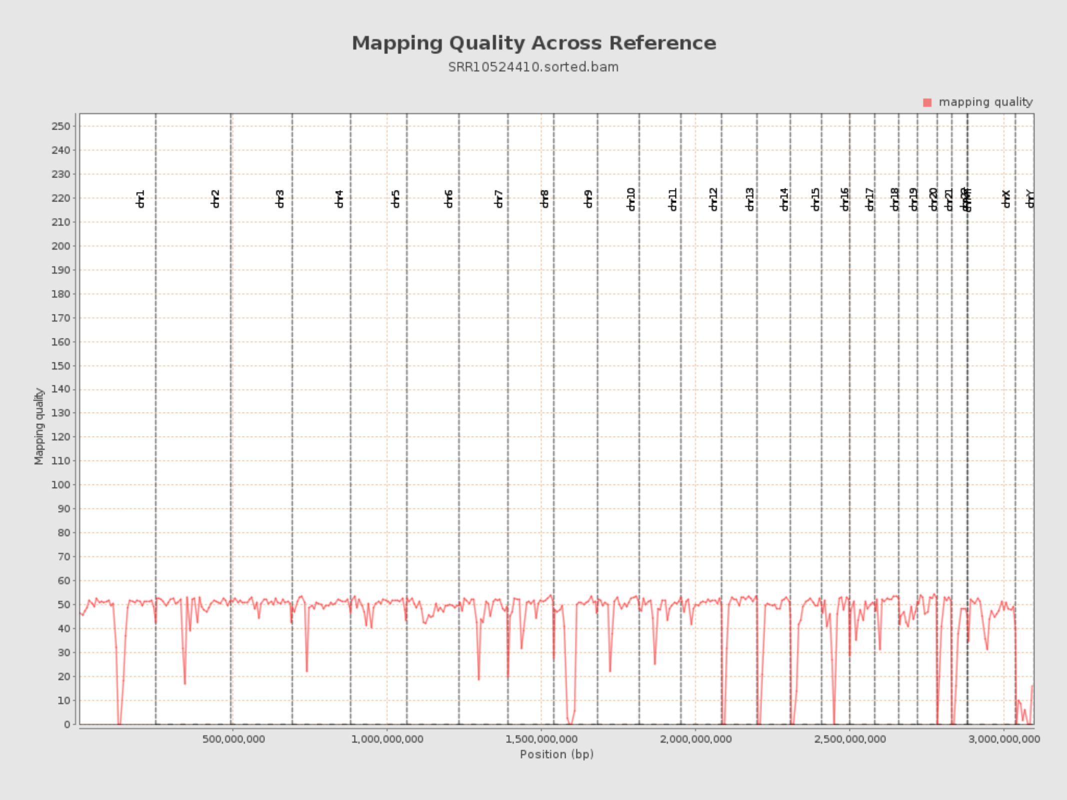
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram