Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:10:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524802.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_SRR10524802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:10:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,518,812
Mapped reads	1,383,966 / 91.12%
Unmapped reads	134,846 / 8.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,385 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	60,148 / 3.96%
Duplication rate	3.39%
Clipped reads	1,385,745 / 91.24%

2.2. ACGT Content

Number/percentage of A's	18,917,047 / 23.98%
Number/percentage of C's	13,831,744 / 17.53%
Number/percentage of T's	26,372,191 / 33.43%
Number/percentage of G's	19,765,342 / 25.05%
Number/percentage of N's	8,686 / 0.01%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2332

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

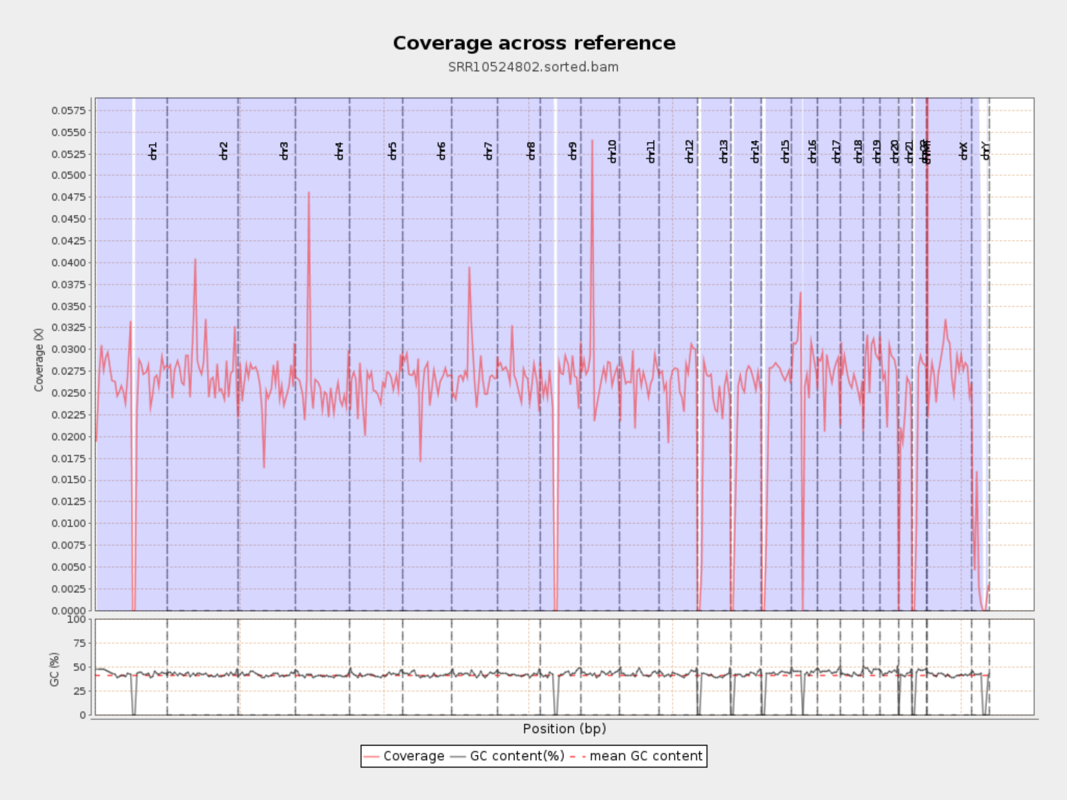
General error rate	0.52%
Mismatches	397,730
Insertions	6,024
Mapped reads with at least one insertion	0.43%
Deletions	14,947
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.85%

2.6. Chromosome stats

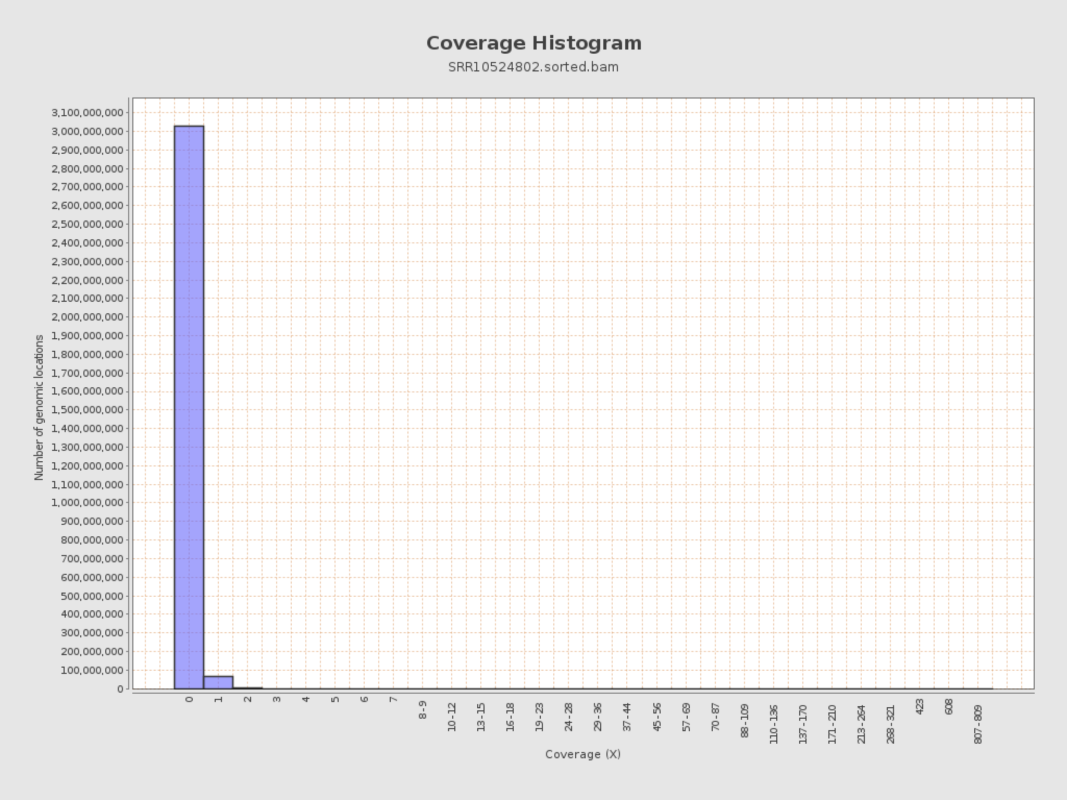
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6278527	0.0252	0.2937
chr2	243199373	6777023	0.0279	0.3859
chr3	198022430	5123455	0.0259	0.1811
chr4	191154276	4964988	0.026	0.204
chr5	180915260	4699875	0.026	0.1789
chr6	171115067	4549913	0.0266	0.2
chr7	159138663	4325047	0.0272	0.2727

chr8	146364022	3933740	0.0269	0.2139
chr9	141213431	3354465	0.0238	0.2023
chr10	135534747	3846875	0.0284	0.2765
chr11	135006516	3598241	0.0267	0.2077
chr12	133851895	3576254	0.0267	0.1837
chr13	115169878	2455306	0.0213	0.1618
chr14	107349540	2369464	0.0221	0.1675
chr15	102531392	2278804	0.0222	0.1667
chr16	90354753	2416644	0.0267	0.2007
chr17	81195210	2220229	0.0273	0.1901
chr18	78077248	2080210	0.0266	0.3013
chr19	59128983	1719834	0.0291	0.2467
chr20	63025520	1714336	0.0272	0.1918
chr21	48129895	1011133	0.021	0.1789
chr22	51304566	1000106	0.0195	0.1577
chrMT	16571	22333	1.3477	1.4769
chrX	155270560	4335016	0.0279	0.1995
chrY	59373566	267563	0.0045	0.1256

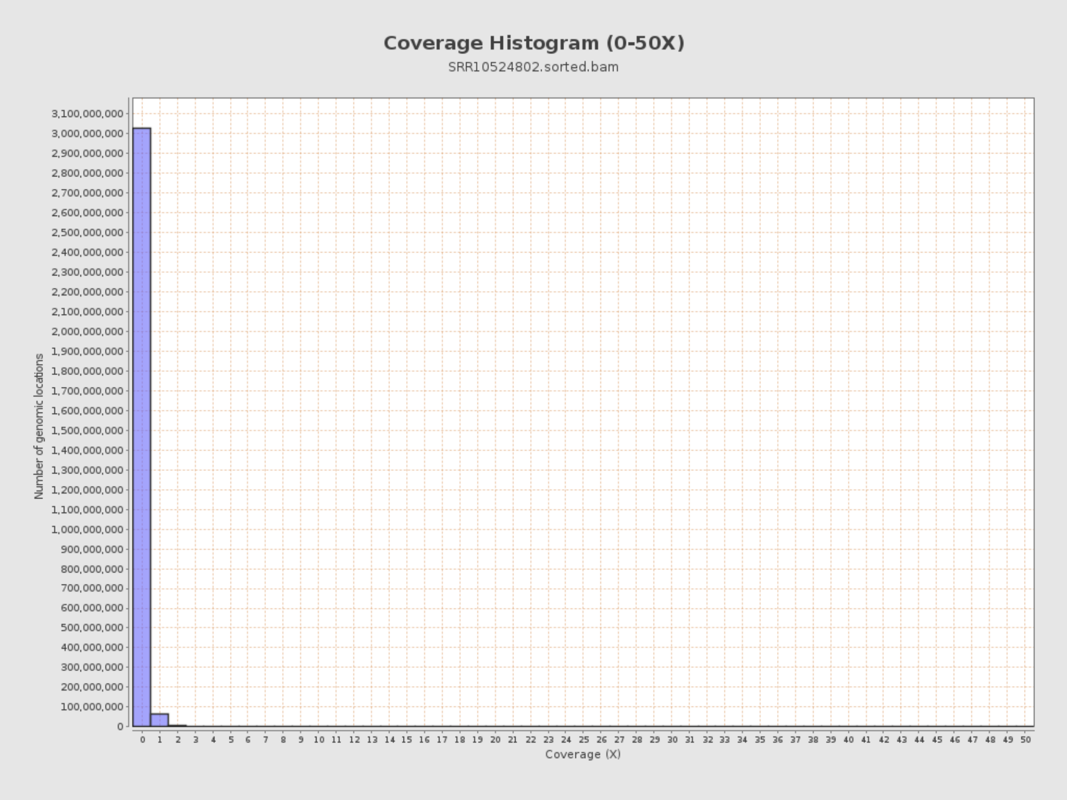
3. Results : Coverage across reference



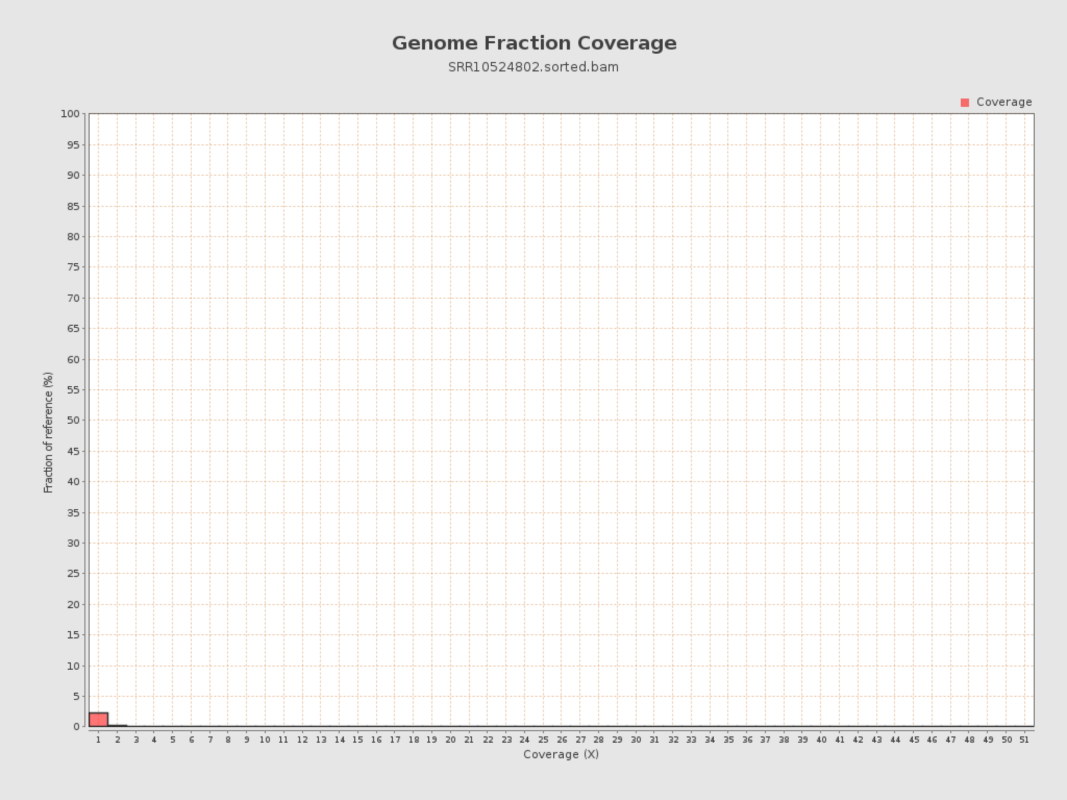
4. Results : Coverage Histogram



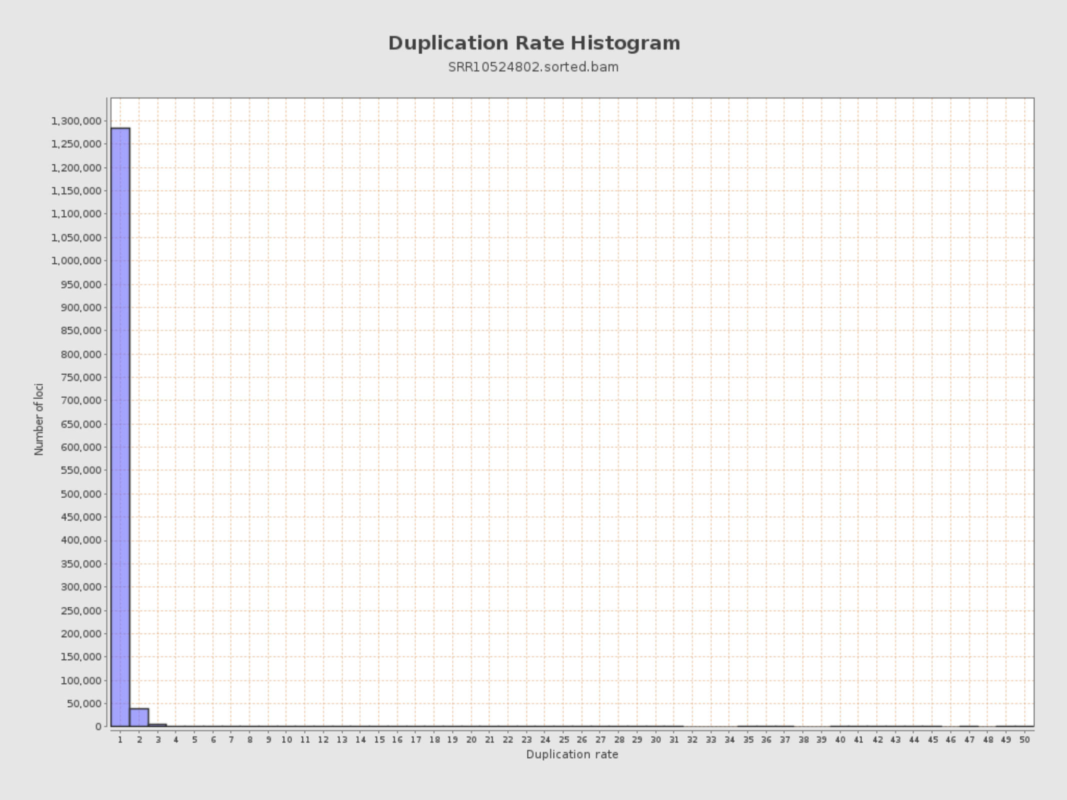
5. Results : Coverage Histogram (0-50X)



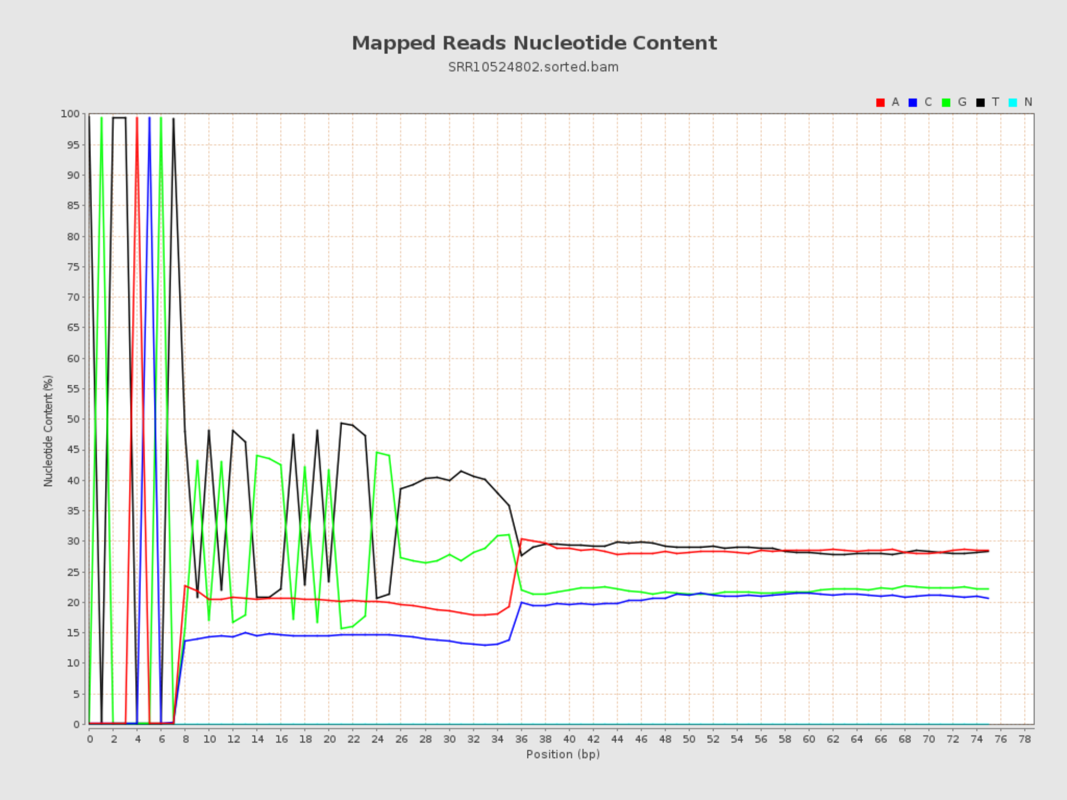
6. Results : Genome Fraction Coverage



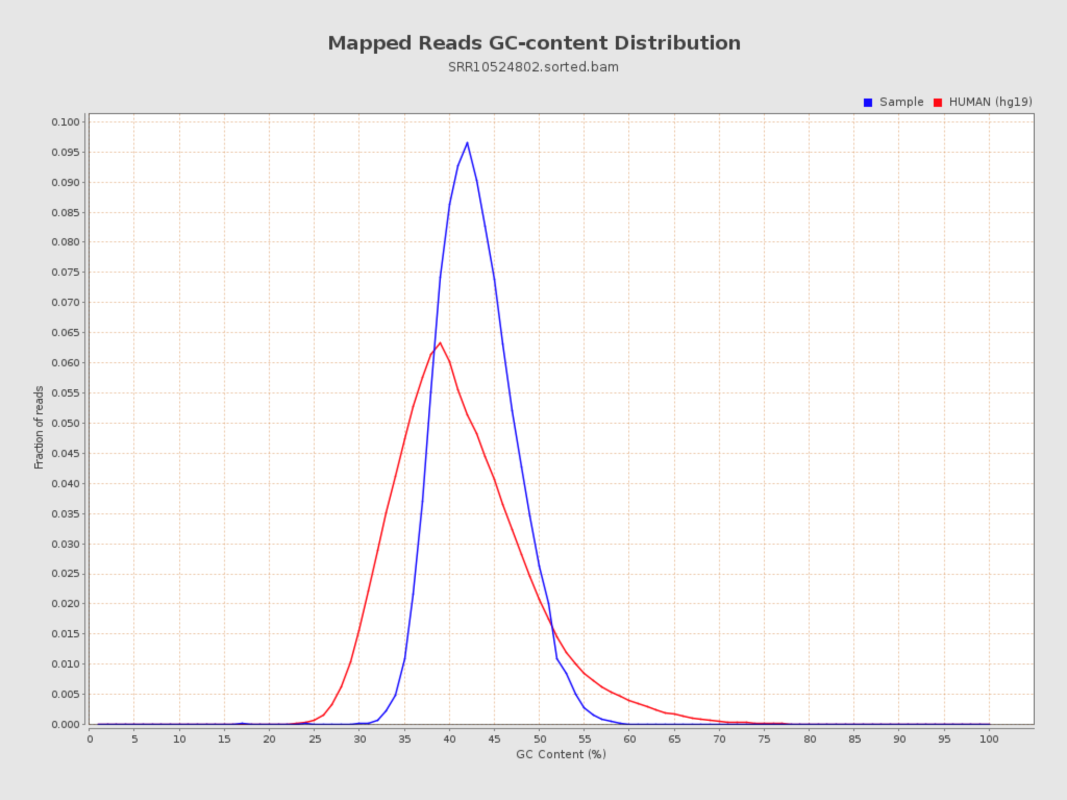
7. Results : Duplication Rate Histogram



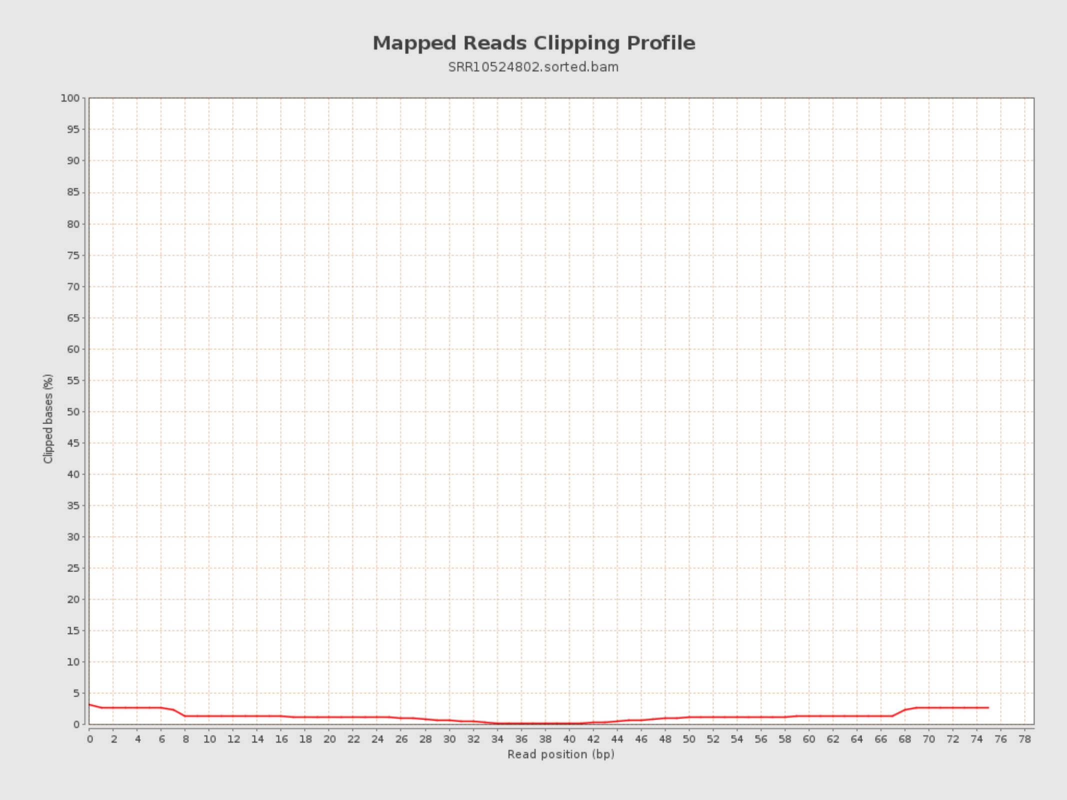
8. Results : Mapped Reads Nucleotide Content



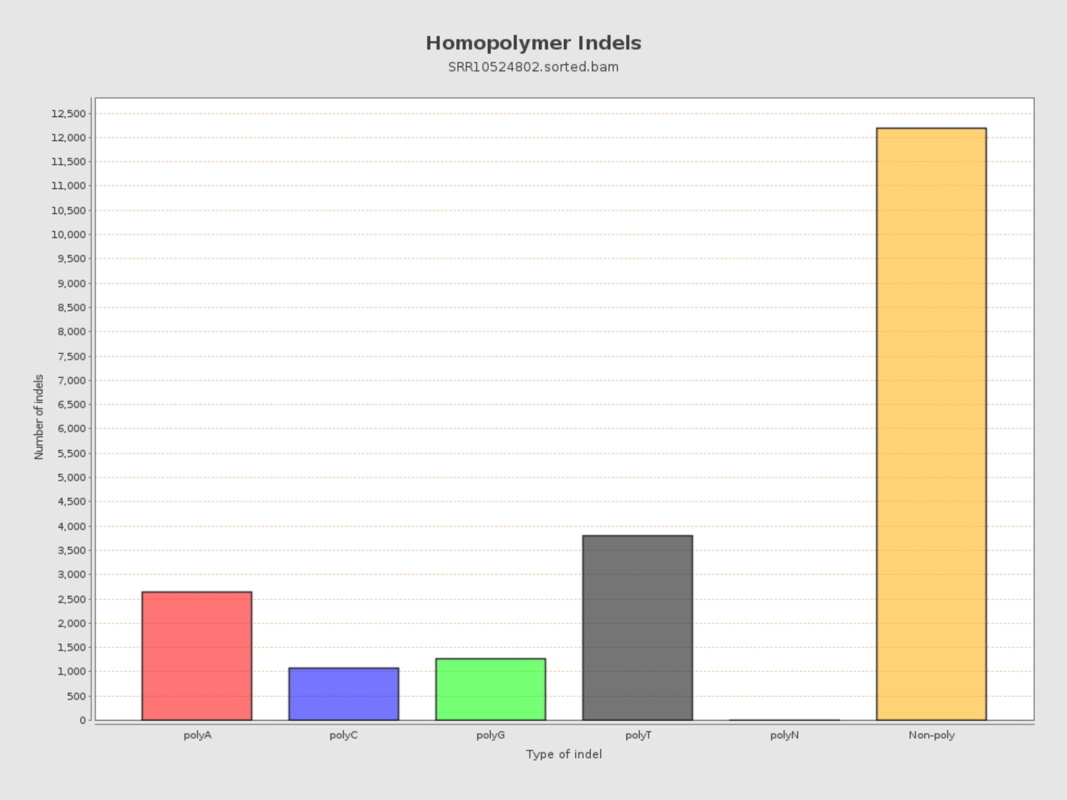
9. Results : Mapped Reads GC-content Distribution



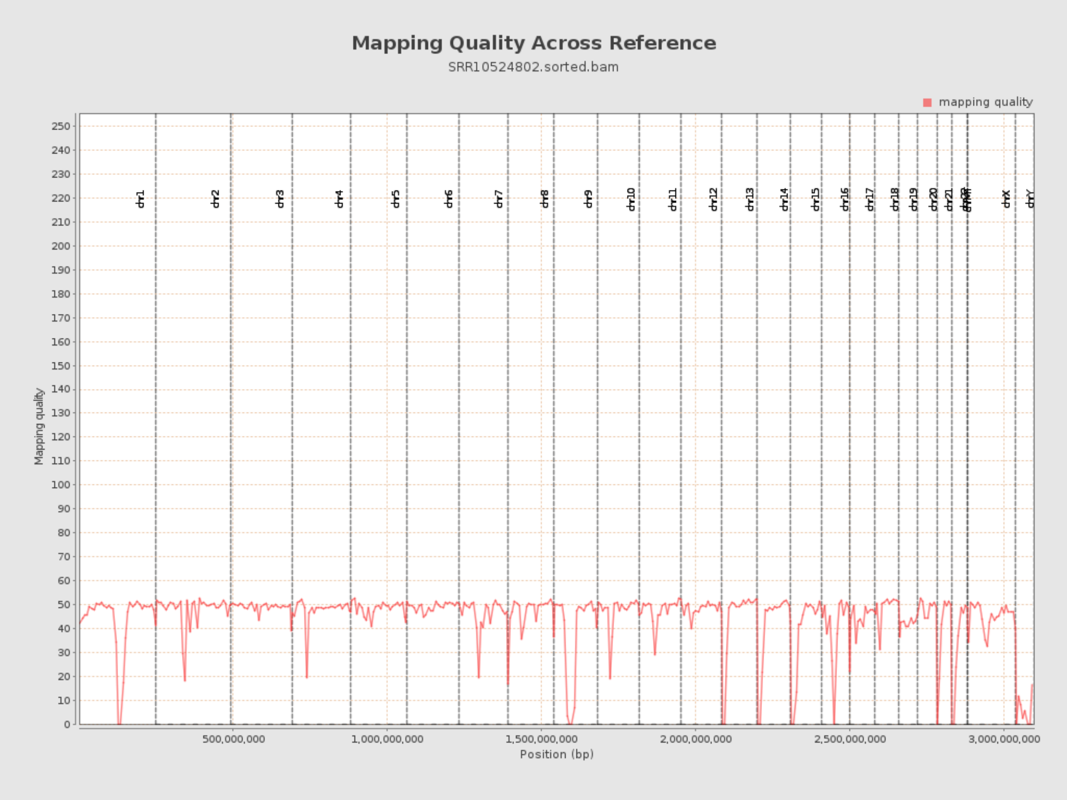
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram