Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:54:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240046.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_SRR6240046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:54:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,238,559
Mapped reads	1,014,379 / 81.9%
Unmapped reads	224,180 / 18.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,378 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,884 / 3.38%
Duplication rate	3.39%
Clipped reads	610,199 / 49.27%

2.2. ACGT Content

Number/percentage of A's	17,443,437 / 27.4%
Number/percentage of C's	10,998,291 / 17.28%
Number/percentage of T's	20,558,744 / 32.3%
Number/percentage of G's	14,615,601 / 22.96%
Number/percentage of N's	41,290 / 0.06%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0206

Standard Deviation	0.2143

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

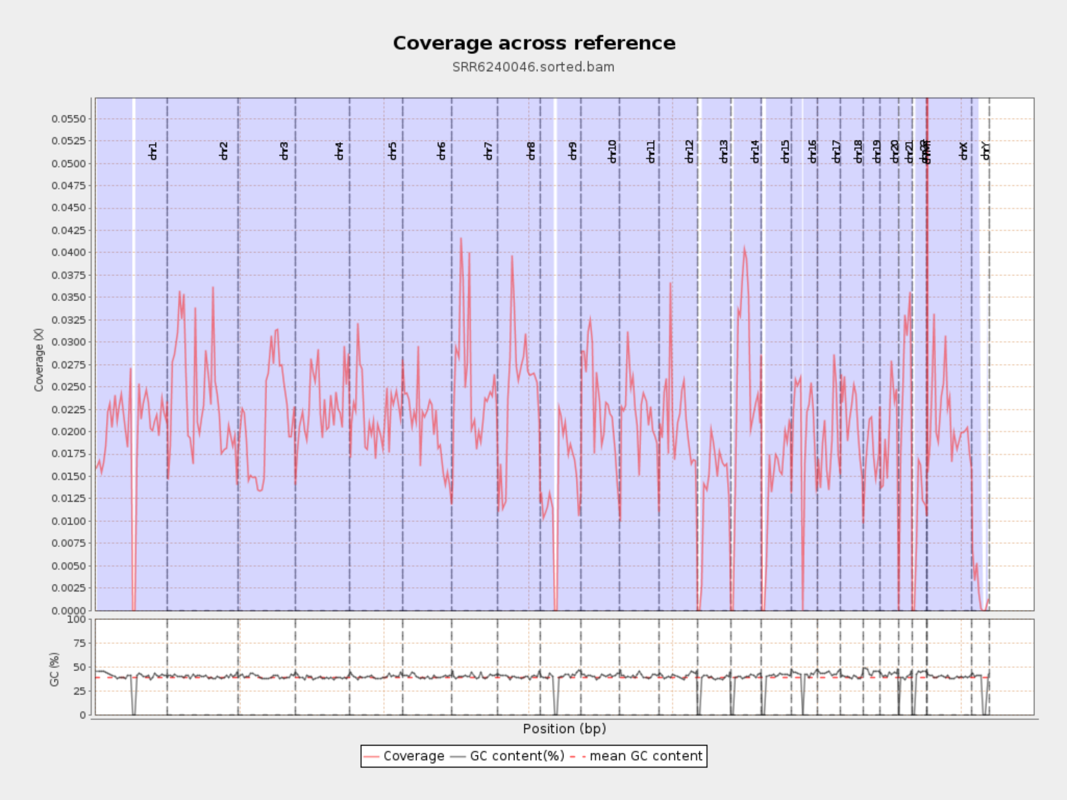
General error rate	0.98%
Mismatches	614,181
Insertions	4,553
Mapped reads with at least one insertion	0.44%
Deletions	20,343
Mapped reads with at least one deletion	1.98%
Homopolymer indels	48.81%

2.6. Chromosome stats

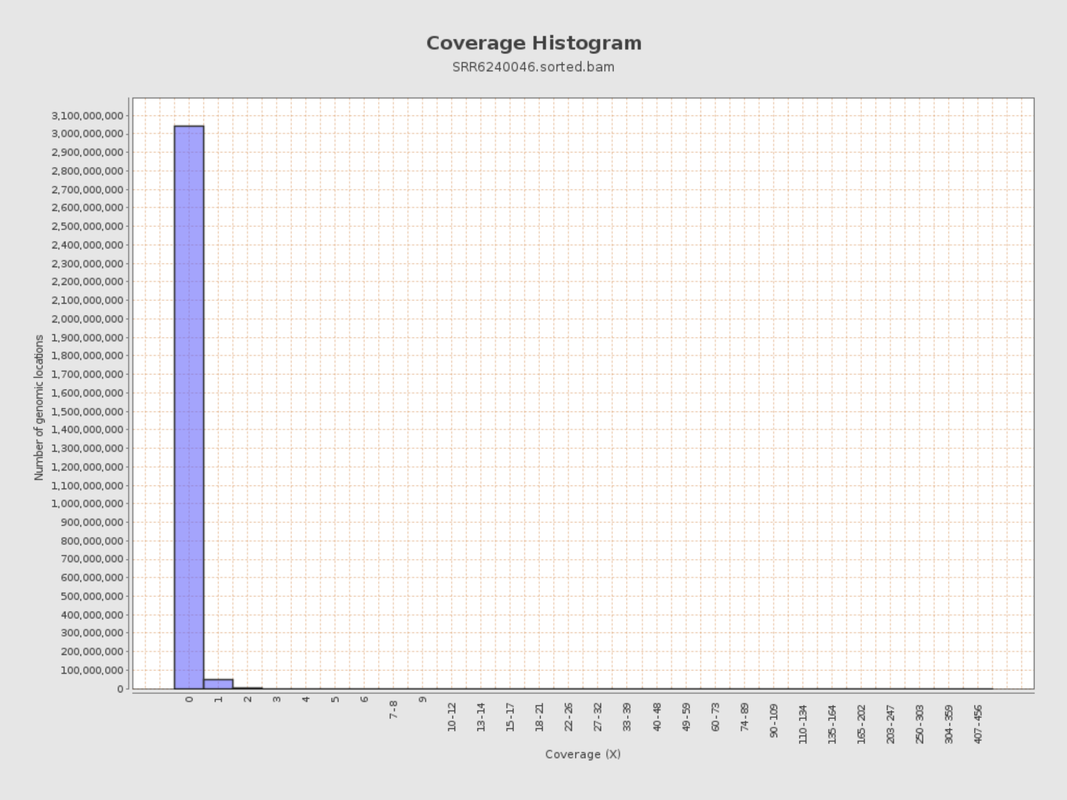
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4942162	0.0198	0.29
chr2	243199373	5795420	0.0238	0.2555
chr3	198022430	4234765	0.0214	0.1638
chr4	191154276	4361957	0.0228	0.1739
chr5	180915260	3986564	0.022	0.1662
chr6	171115067	3538116	0.0207	0.187
chr7	159138663	4050578	0.0255	0.3267

chr8	146364022	3620649	0.0247	0.3218
chr9	141213431	1975221	0.014	0.1837
chr10	135534747	3167216	0.0234	0.1937
chr11	135006516	2989800	0.0221	0.2103
chr12	133851895	2856806	0.0213	0.1652
chr13	115169878	1538111	0.0134	0.1279
chr14	107349540	2670935	0.0249	0.1808
chr15	102531392	1424381	0.0139	0.1397
chr16	90354753	1793097	0.0198	0.1632
chr17	81195210	1529641	0.0188	0.1608
chr18	78077248	1707562	0.0219	0.3179
chr19	59128983	1060068	0.0179	0.2172
chr20	63025520	1237197	0.0196	0.1619
chr21	48129895	1216615	0.0253	0.1835
chr22	51304566	518954	0.0101	0.1096
chrMT	16571	20747	1.252	1.5407
chrX	155270560	3326302	0.0214	0.1774
chrY	59373566	129092	0.0022	0.0562

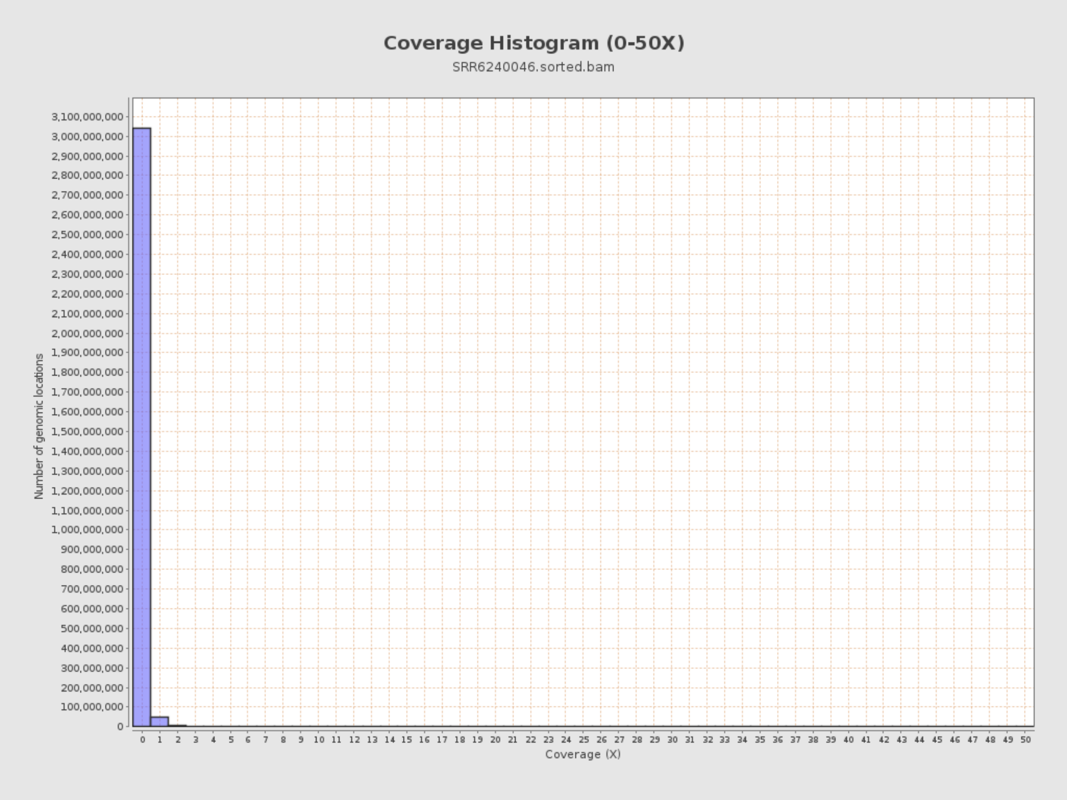
3. Results : Coverage across reference



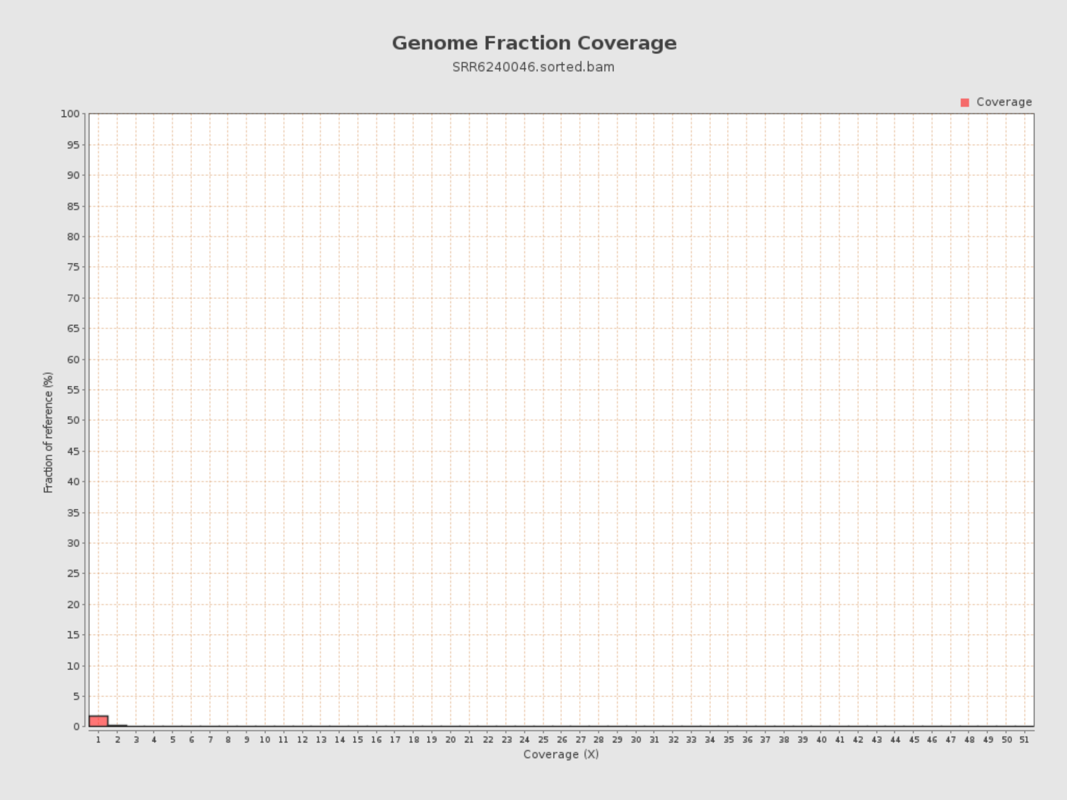
4. Results : Coverage Histogram



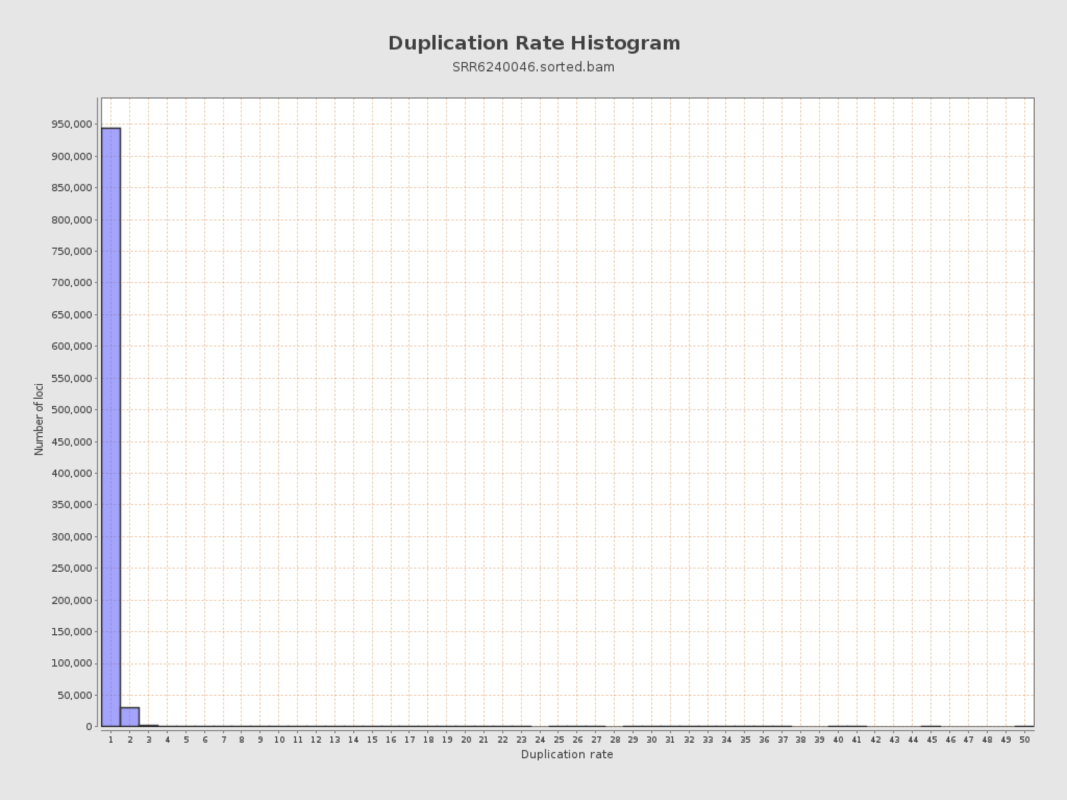
5. Results : Coverage Histogram (0-50X)



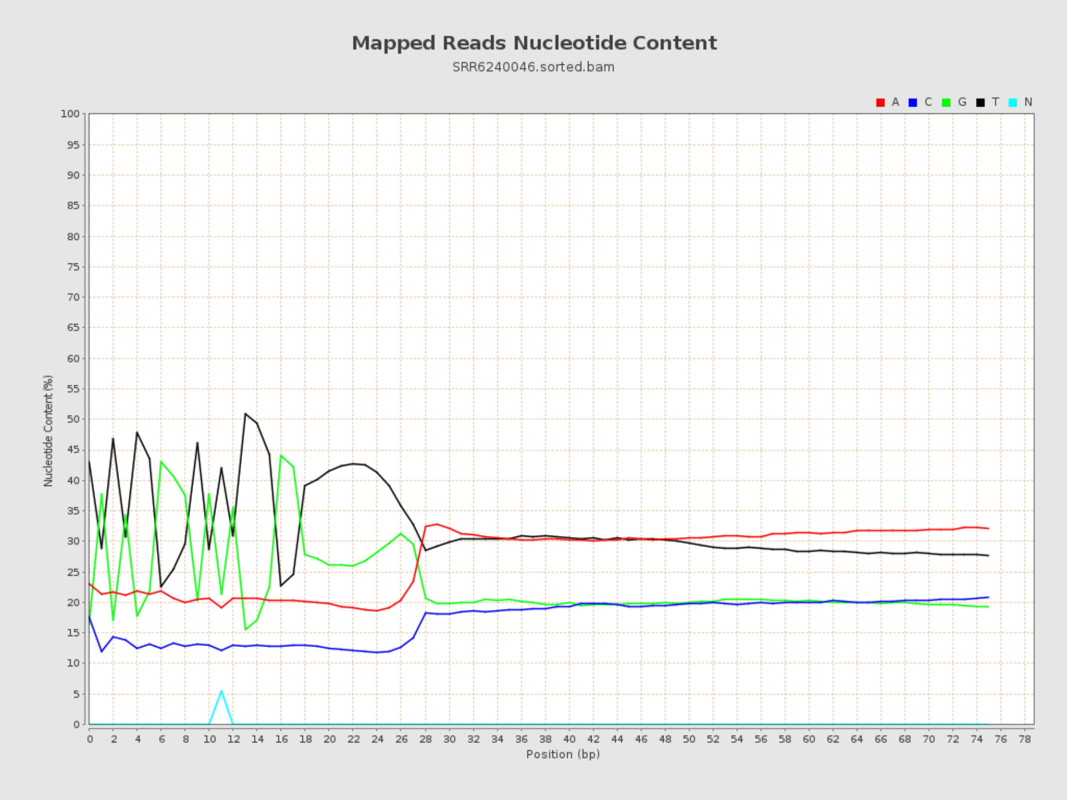
6. Results : Genome Fraction Coverage



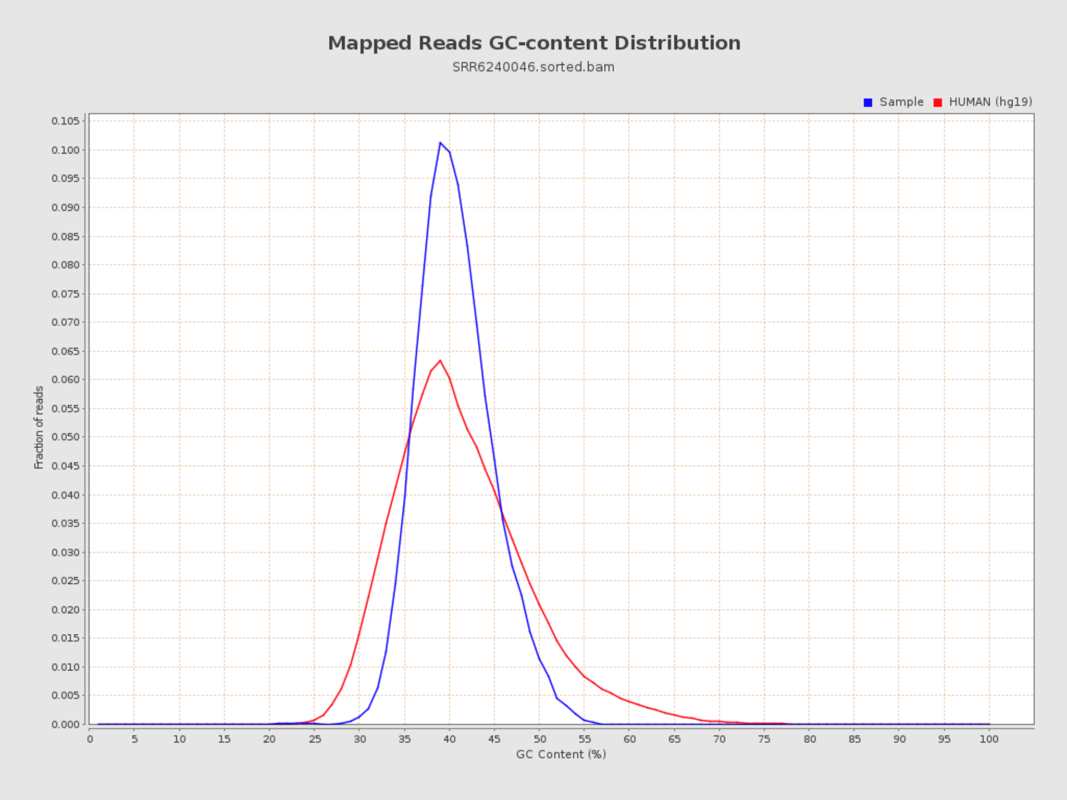
7. Results : Duplication Rate Histogram



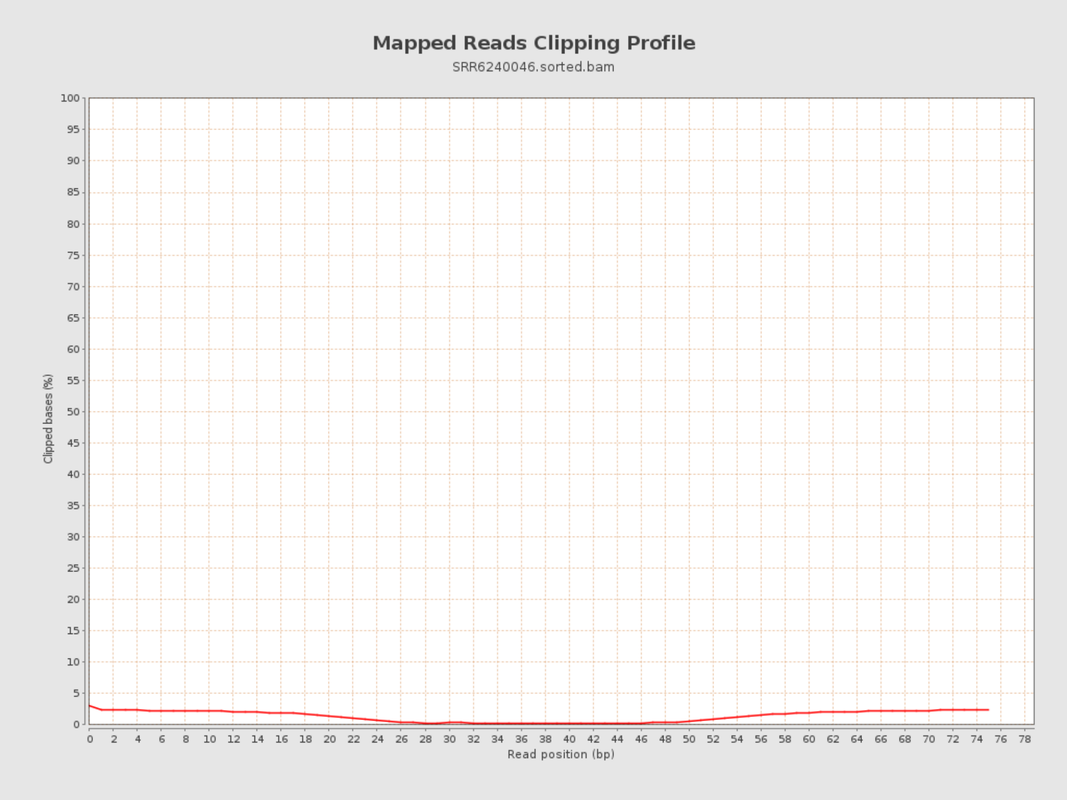
8. Results : Mapped Reads Nucleotide Content



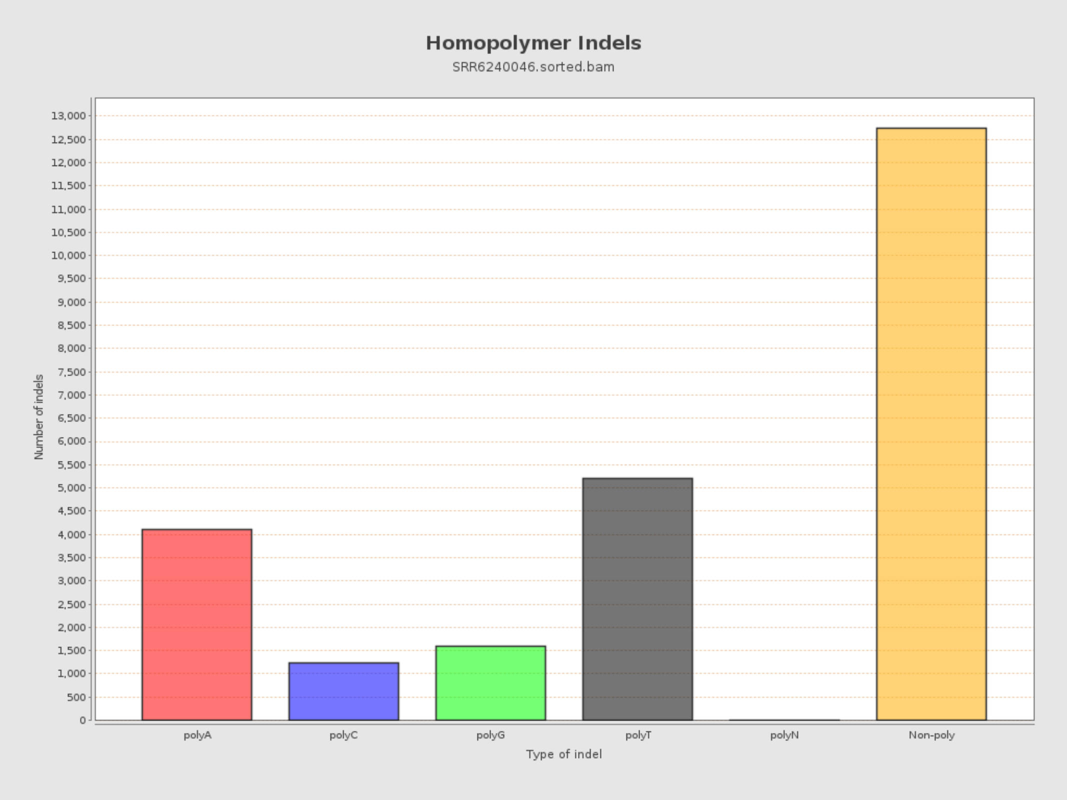
9. Results : Mapped Reads GC-content Distribution



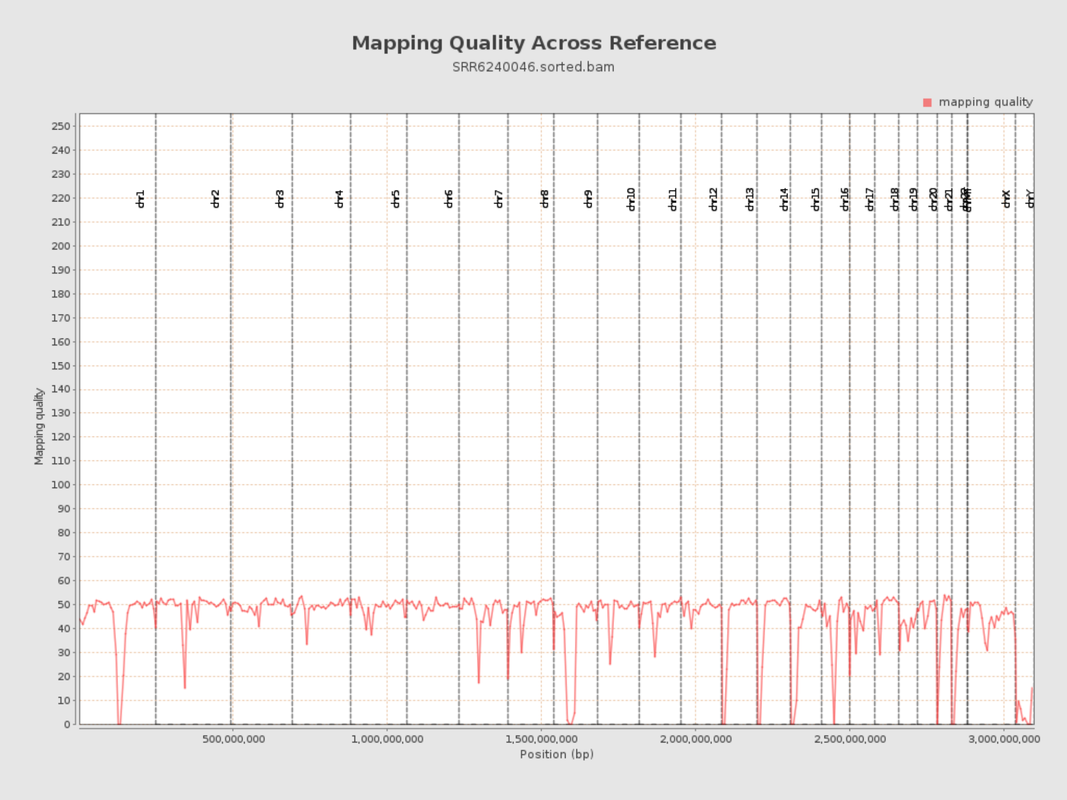
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram