Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:13:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240074.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_SRR6240074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:13:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,886,261
Mapped reads	494,484 / 26.22%
Unmapped reads	1,391,777 / 73.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,138 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	75,994 / 4.03%
Duplication rate	11.13%
Clipped reads	260,641 / 13.82%

2.2. ACGT Content

Number/percentage of A's	8,890,933 / 27.86%
Number/percentage of C's	5,599,519 / 17.54%
Number/percentage of T's	10,583,796 / 33.16%
Number/percentage of G's	6,840,773 / 21.43%
Number/percentage of N's	2,831 / 0.01%
GC Percentage	38.98%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.2164

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

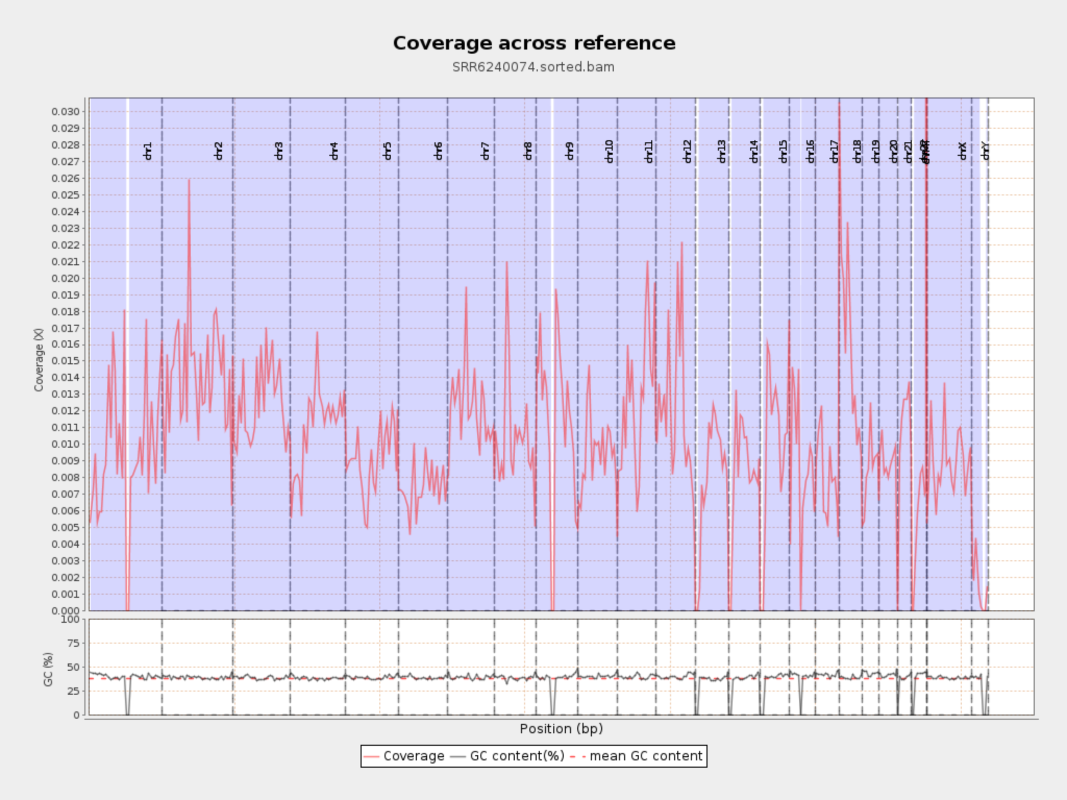
General error rate	0.93%
Mismatches	291,031
Insertions	2,489
Mapped reads with at least one insertion	0.5%
Deletions	9,015
Mapped reads with at least one deletion	1.8%
Homopolymer indels	47.35%

2.6. Chromosome stats

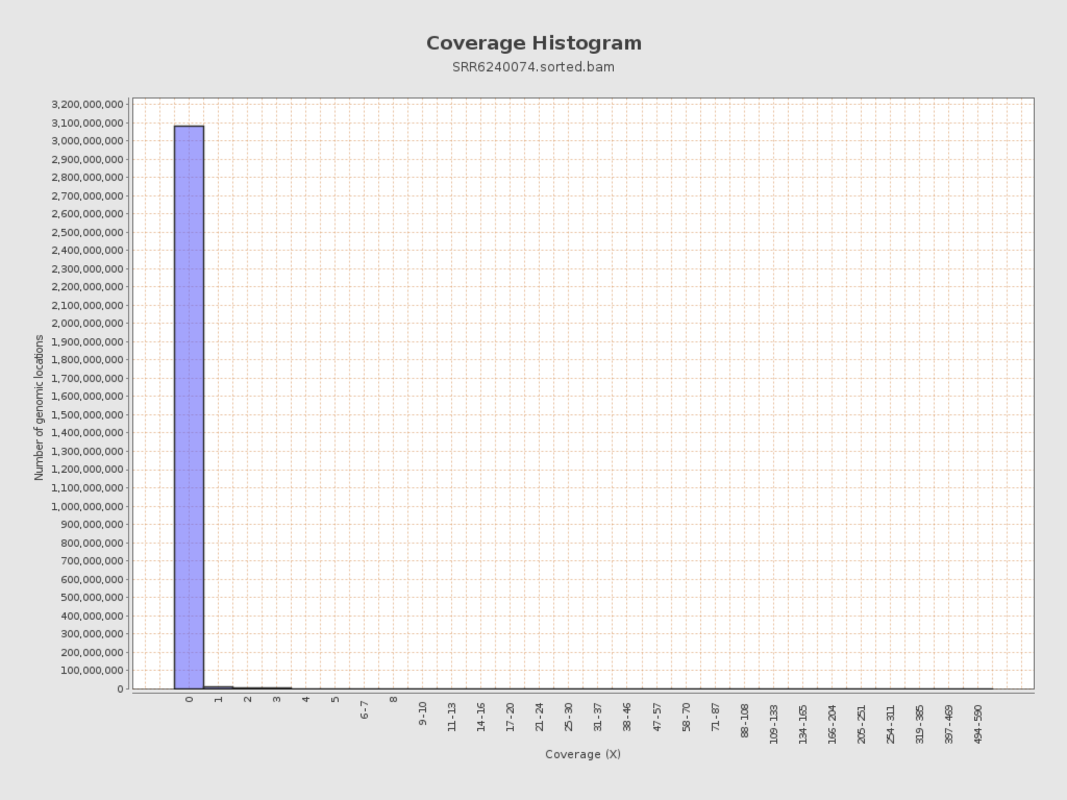
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2370442	0.0095	0.2529
chr2	243199373	3444482	0.0142	0.2919
chr3	198022430	2494542	0.0126	0.1999
chr4	191154276	2116957	0.0111	0.1812
chr5	180915260	1651106	0.0091	0.1626
chr6	171115067	1268064	0.0074	0.159
chr7	159138663	1977179	0.0124	0.2181

chr8	146364022	1523022	0.0104	0.3953
chr9	141213431	1643579	0.0116	0.2101
chr10	135534747	1296171	0.0096	0.1739
chr11	135006516	1712782	0.0127	0.2064
chr12	133851895	1630258	0.0122	0.2033
chr13	115169878	910802	0.0079	0.1537
chr14	107349540	867435	0.0081	0.1554
chr15	102531392	1006708	0.0098	0.1732
chr16	90354753	795081	0.0088	0.1702
chr17	81195210	640621	0.0079	0.1552
chr18	78077248	1257494	0.0161	0.3158
chr19	59128983	505824	0.0086	0.1854
chr20	63025520	562717	0.0089	0.1664
chr21	48129895	513204	0.0107	0.2288
chr22	51304566	268553	0.0052	0.1149
chrMT	16571	13655	0.824	1.6518
chrX	155270560	1380400	0.0089	0.1776
chrY	59373566	82336	0.0014	0.0648

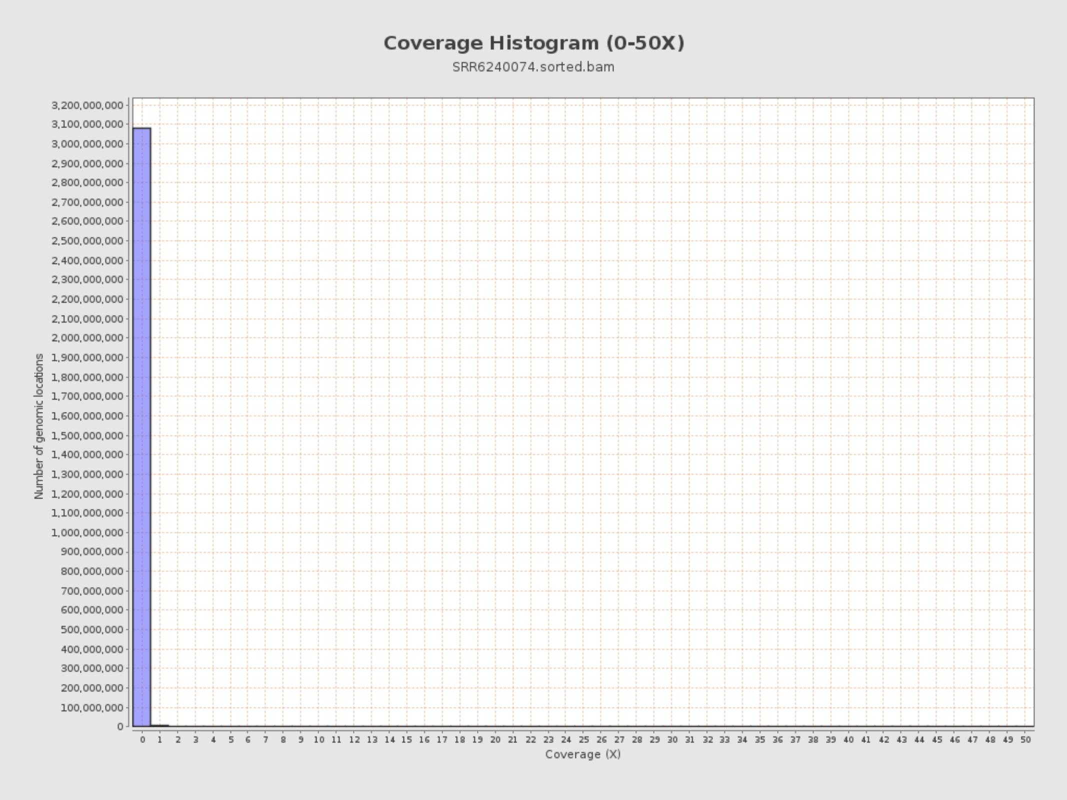
3. Results : Coverage across reference



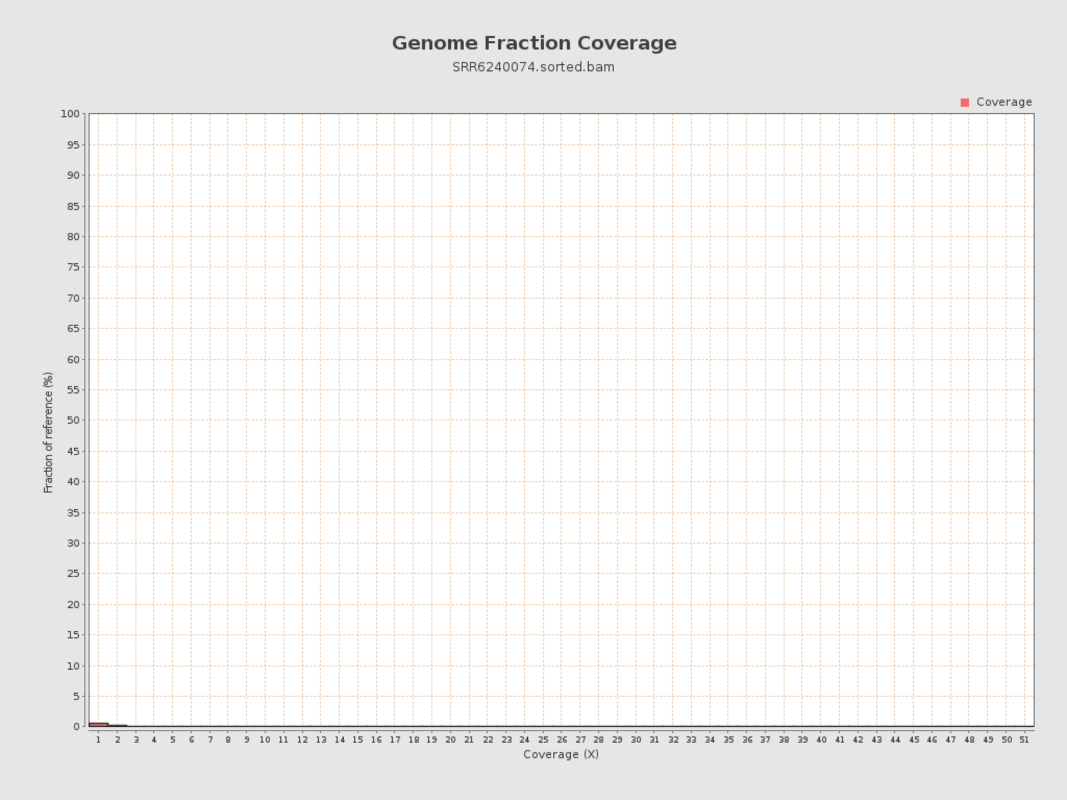
4. Results : Coverage Histogram



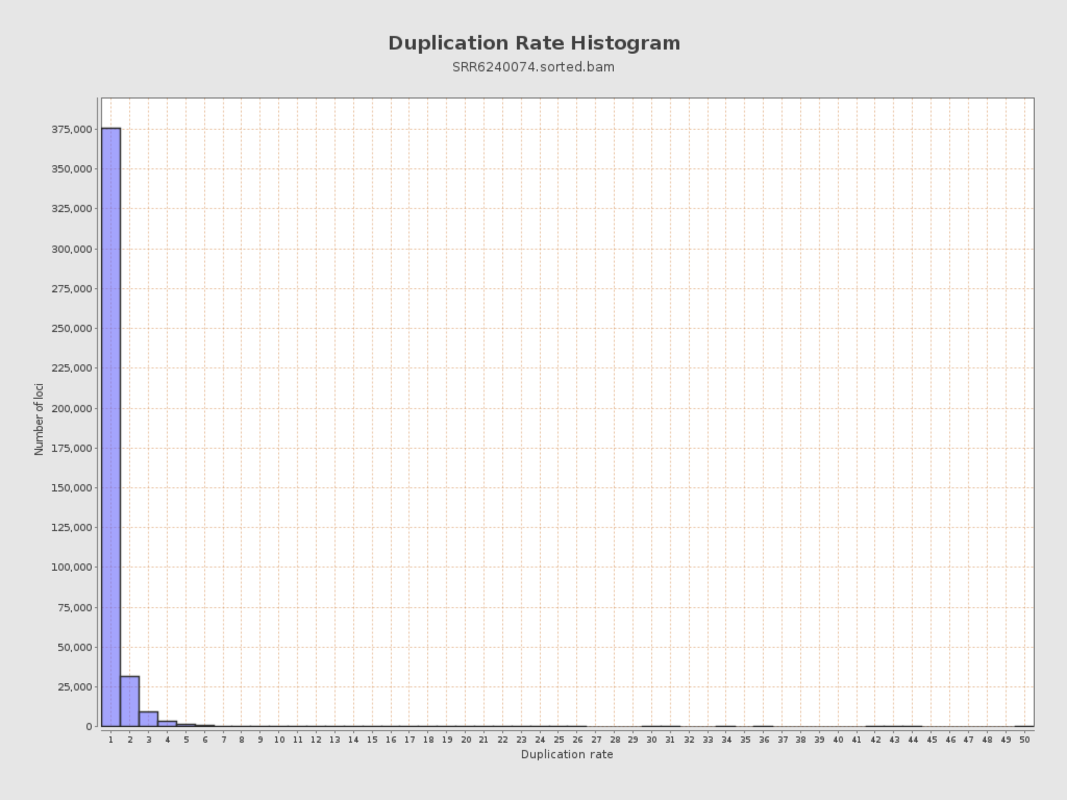
5. Results : Coverage Histogram (0-50X)



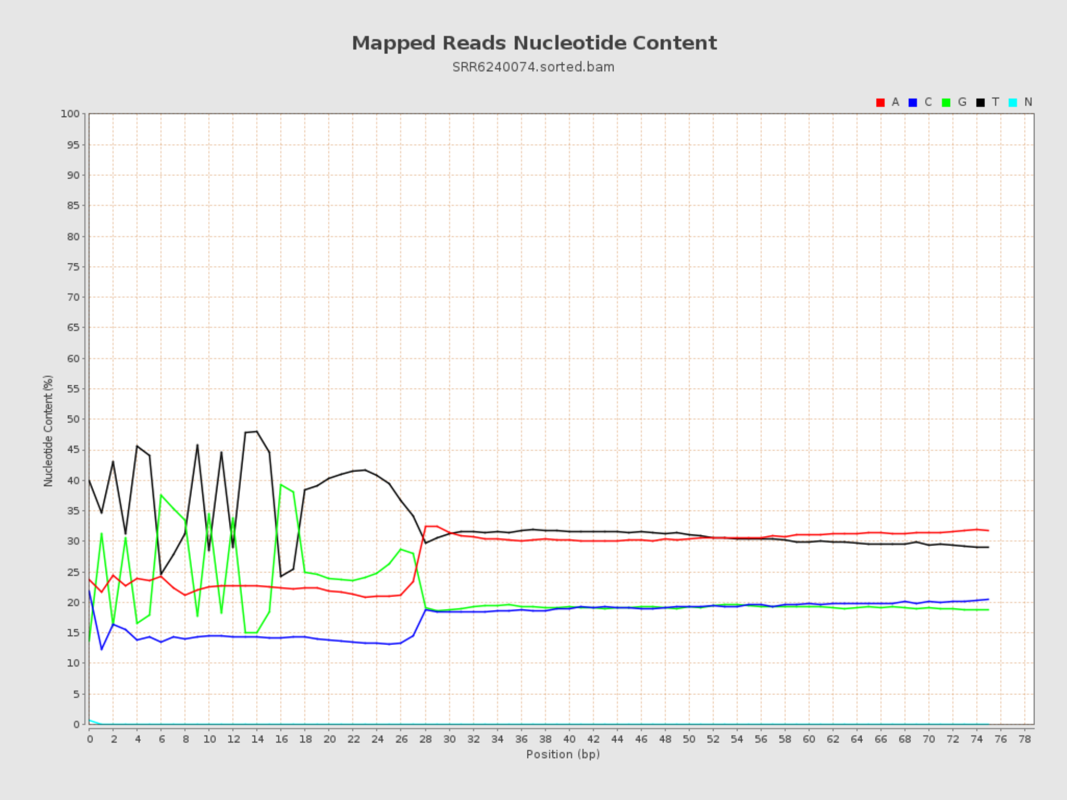
6. Results : Genome Fraction Coverage



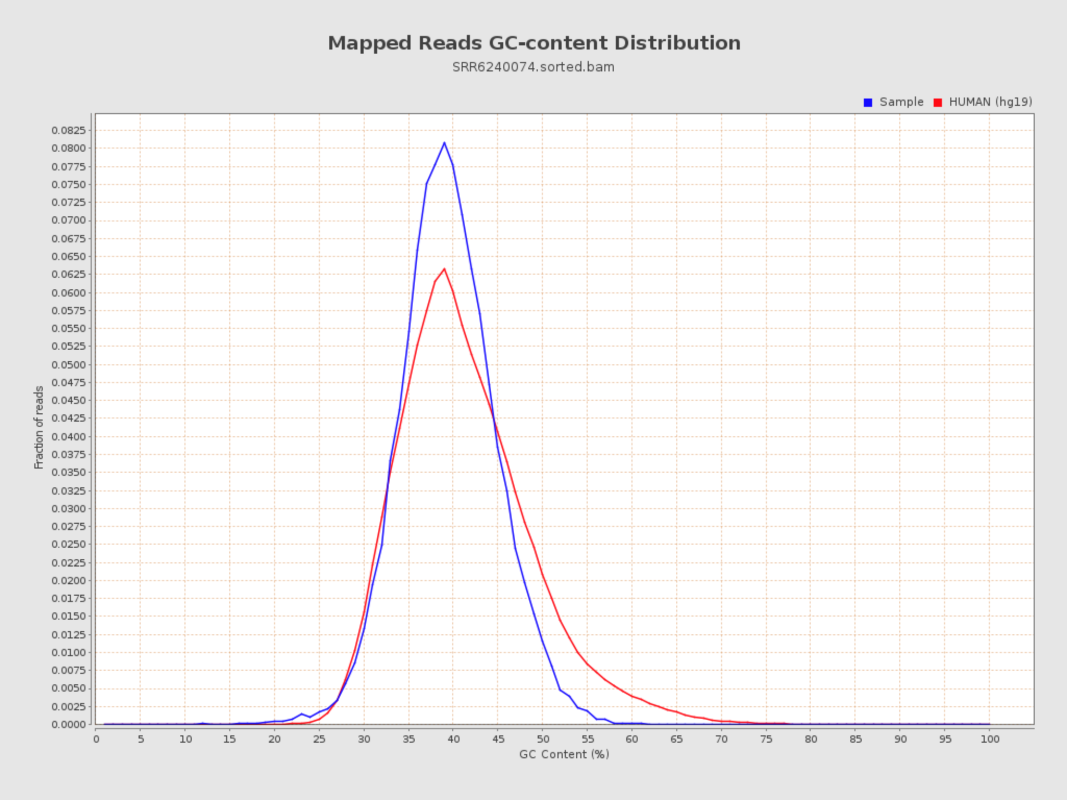
7. Results : Duplication Rate Histogram



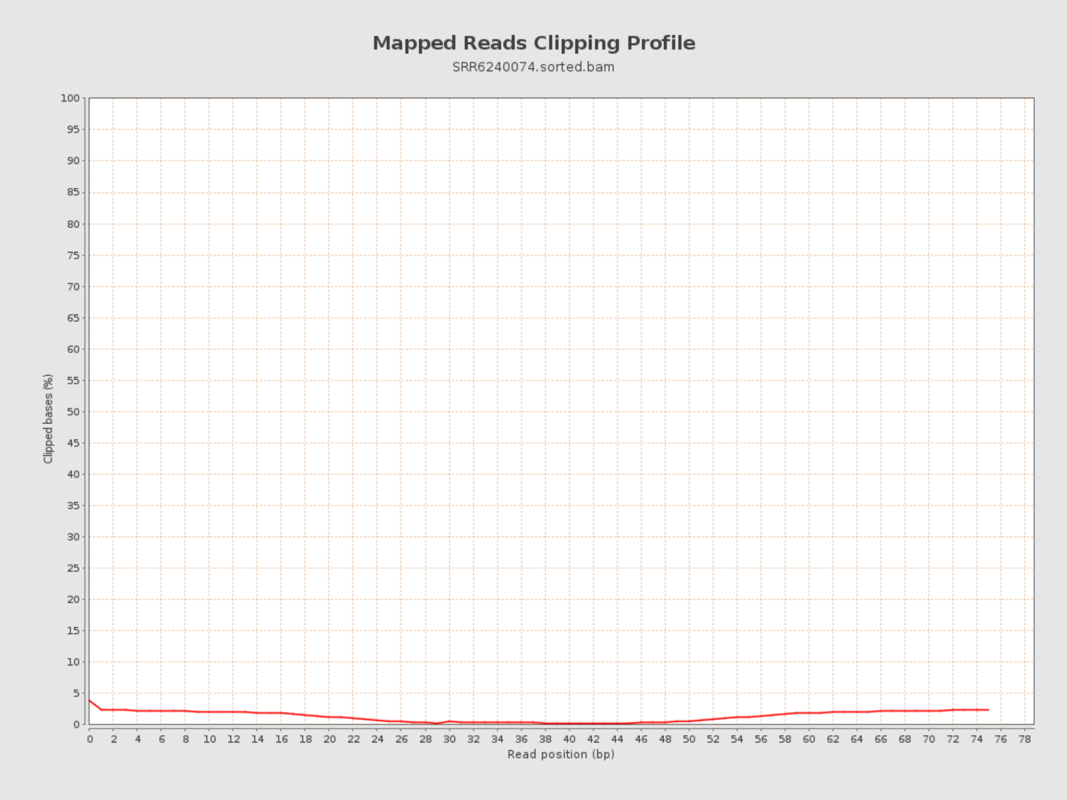
8. Results : Mapped Reads Nucleotide Content



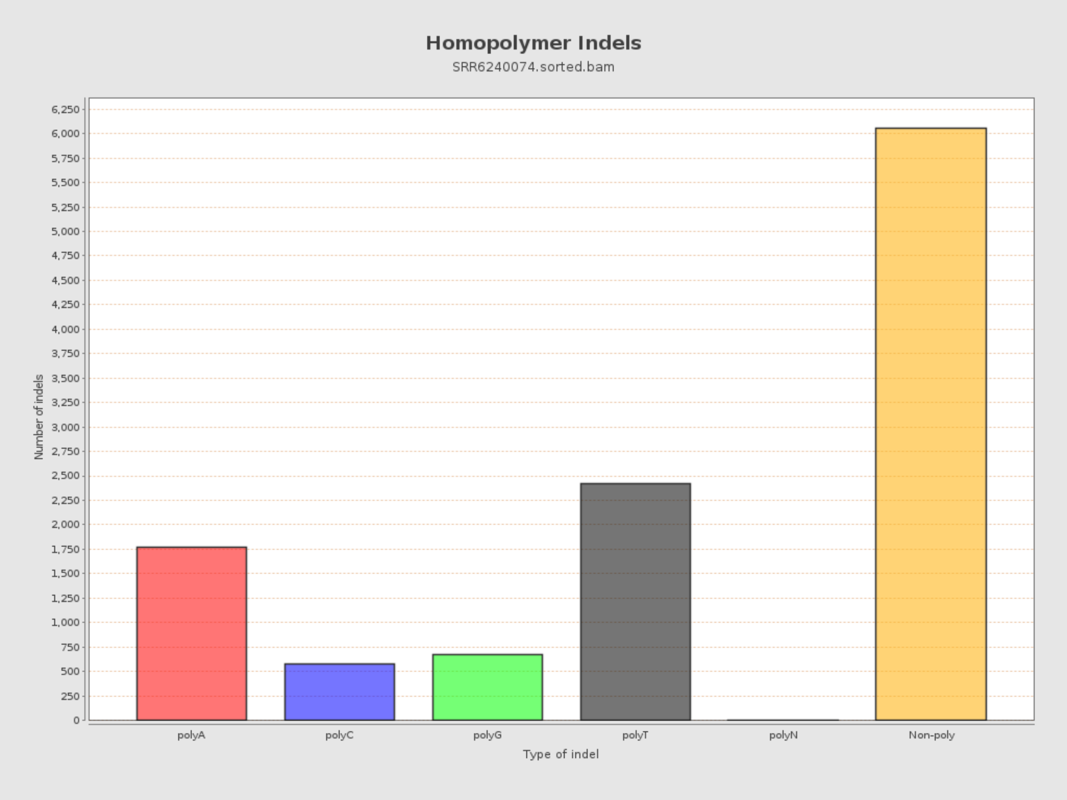
9. Results : Mapped Reads GC-content Distribution



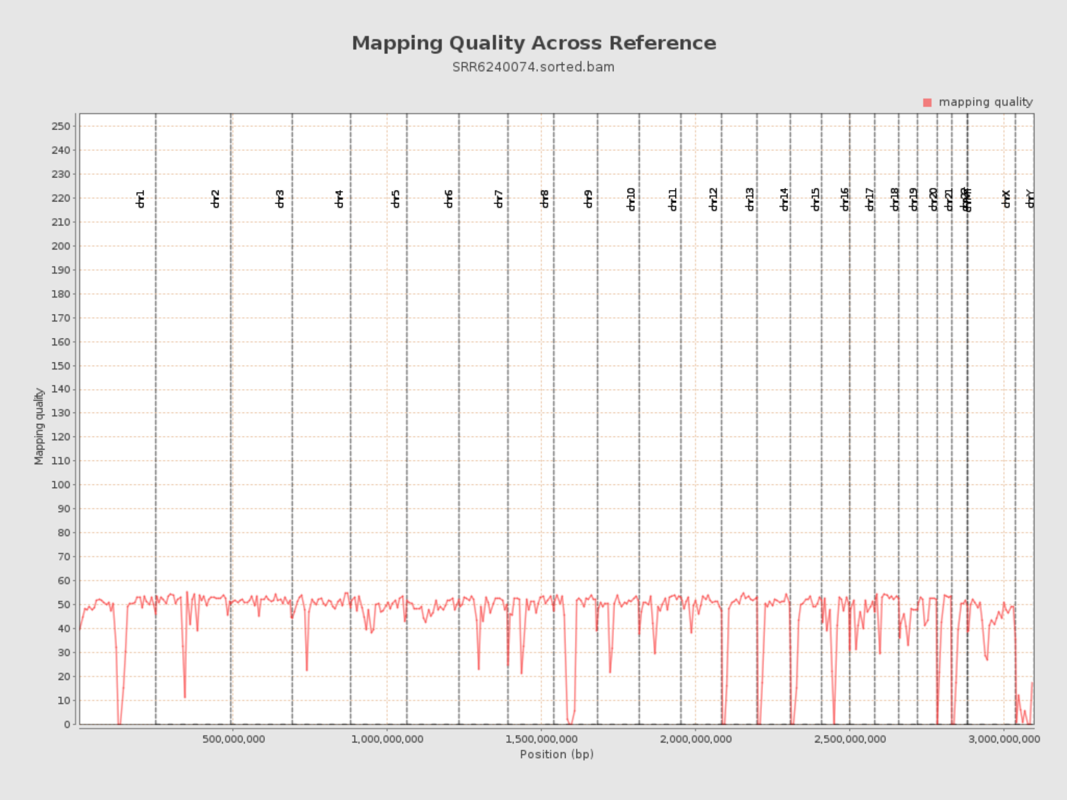
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram