Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:50:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240023.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_SRR6240023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:50:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,435,313
Mapped reads	1,148,331 / 80.01%
Unmapped reads	286,982 / 19.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,976 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	67,303 / 4.69%
Duplication rate	4.96%
Clipped reads	743,607 / 51.81%

2.2. ACGT Content

Number/percentage of A's	18,927,727 / 26.69%
Number/percentage of C's	12,030,339 / 16.97%
Number/percentage of T's	23,335,625 / 32.91%
Number/percentage of G's	16,569,613 / 23.37%
Number/percentage of N's	46,245 / 0.07%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.2288

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

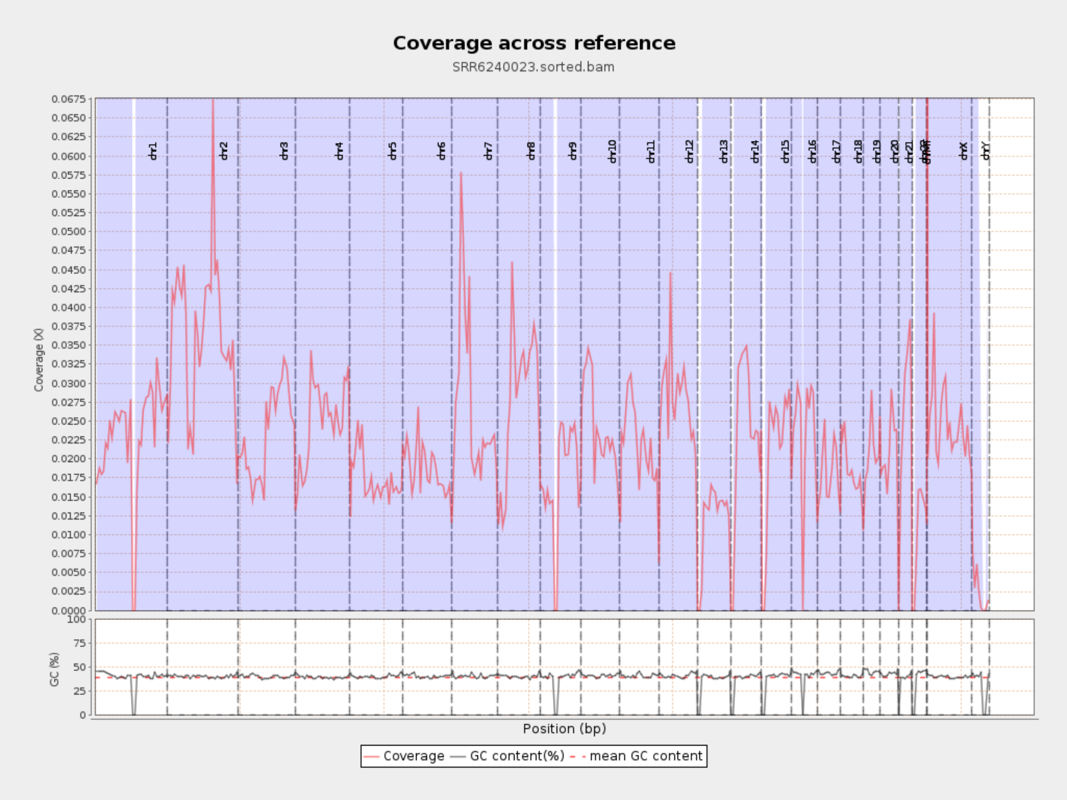
General error rate	0.98%
Mismatches	685,819
Insertions	4,911
Mapped reads with at least one insertion	0.43%
Deletions	22,438
Mapped reads with at least one deletion	1.93%
Homopolymer indels	49.86%

2.6. Chromosome stats

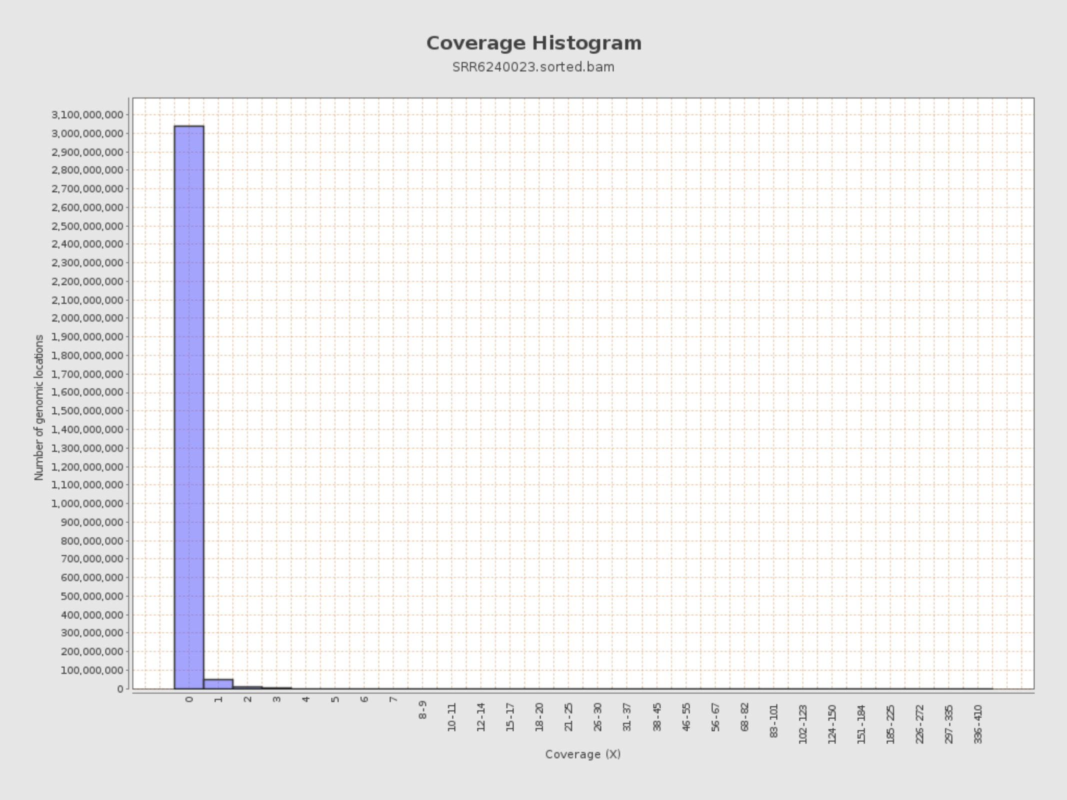
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5736261	0.023	0.3002
chr2	243199373	8983648	0.0369	0.2968
chr3	198022430	4644520	0.0235	0.1796
chr4	191154276	4772199	0.025	0.1908
chr5	180915260	3162103	0.0175	0.1554
chr6	171115067	3213772	0.0188	0.1802
chr7	159138663	4326771	0.0272	0.4074

chr8	146364022	4154697	0.0284	0.2775
chr9	141213431	2441930	0.0173	0.197
chr10	135534747	3313829	0.0245	0.2077
chr11	135006516	3015024	0.0223	0.2232
chr12	133851895	3776449	0.0282	0.1988
chr13	115169878	1368086	0.0119	0.1277
chr14	107349540	2523637	0.0235	0.1835
chr15	102531392	2128314	0.0208	0.1815
chr16	90354753	2079745	0.023	0.1798
chr17	81195210	1488185	0.0183	0.1697
chr18	78077248	1461424	0.0187	0.2805
chr19	59128983	1234110	0.0209	0.2271
chr20	63025520	1313305	0.0208	0.1702
chr21	48129895	1269218	0.0264	0.1943
chr22	51304566	544786	0.0106	0.1179
chrMT	16571	17179	1.0367	1.4559
chrX	155270560	3836841	0.0247	0.1939
chrY	59373566	142786	0.0024	0.0594

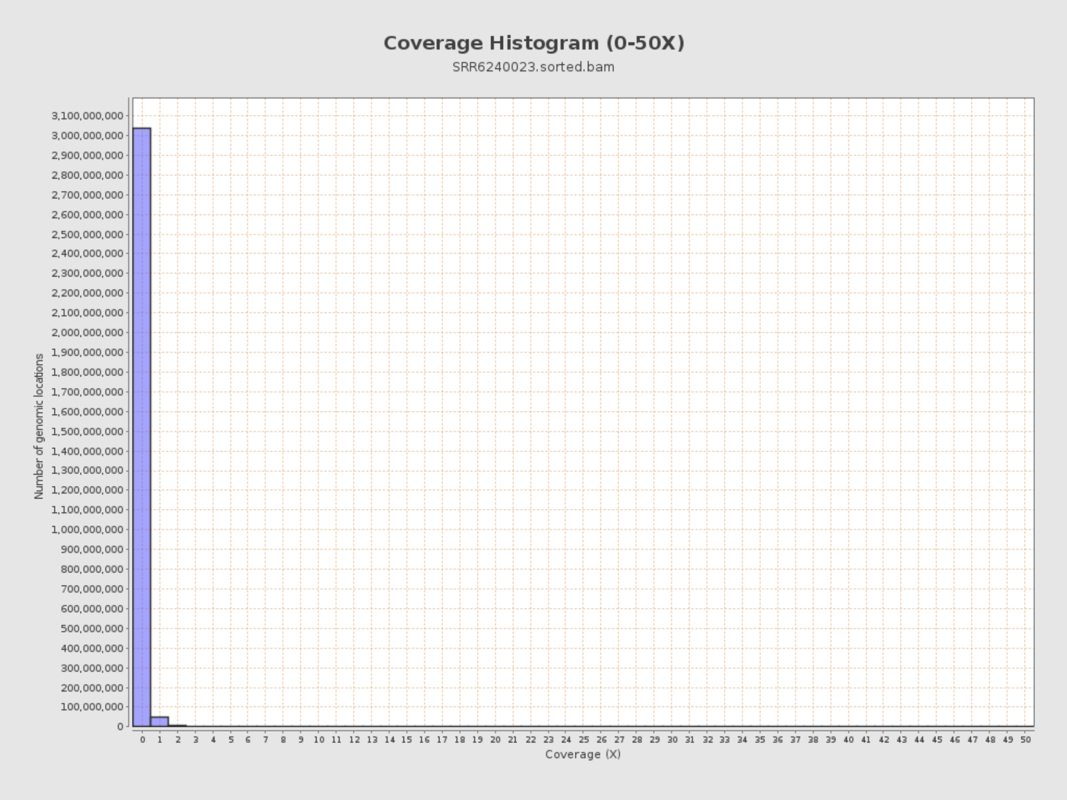
3. Results : Coverage across reference



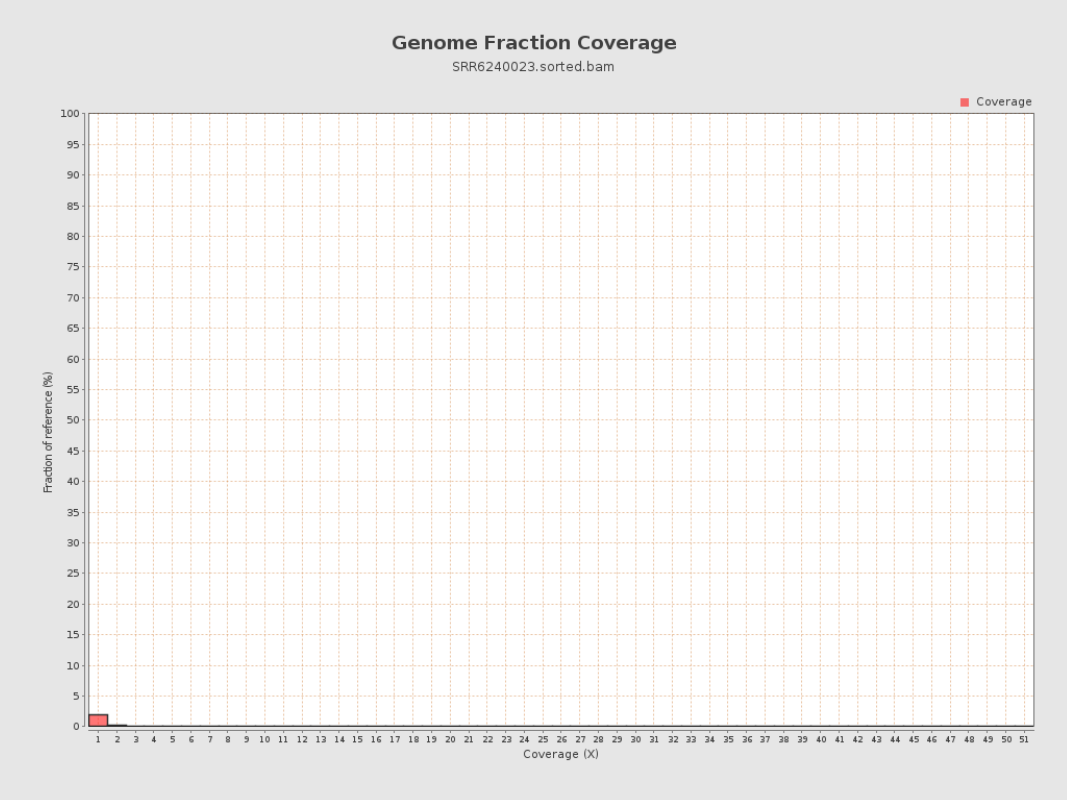
4. Results : Coverage Histogram



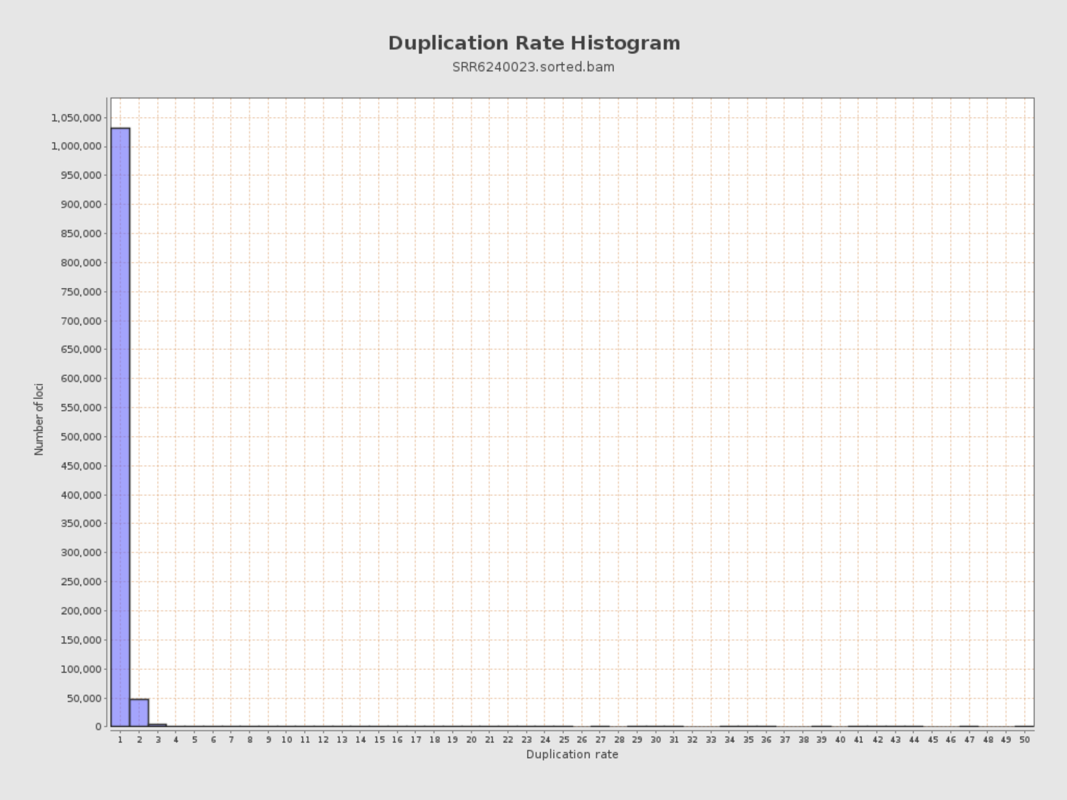
5. Results : Coverage Histogram (0-50X)



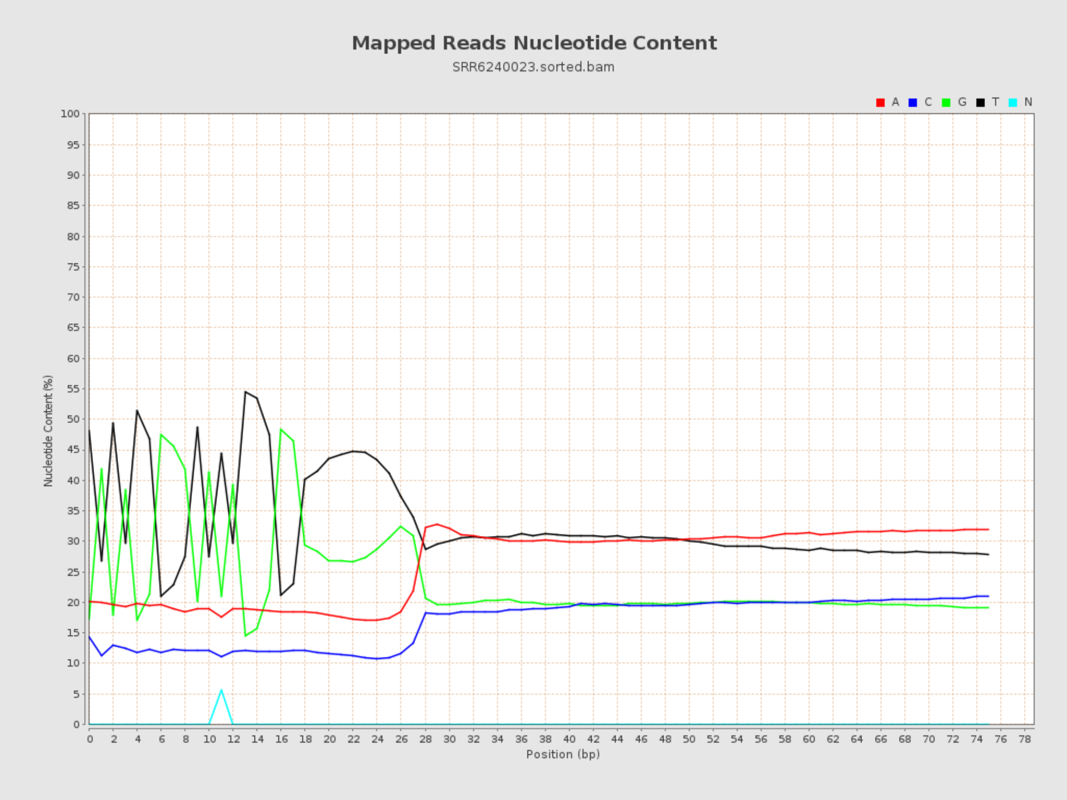
6. Results : Genome Fraction Coverage



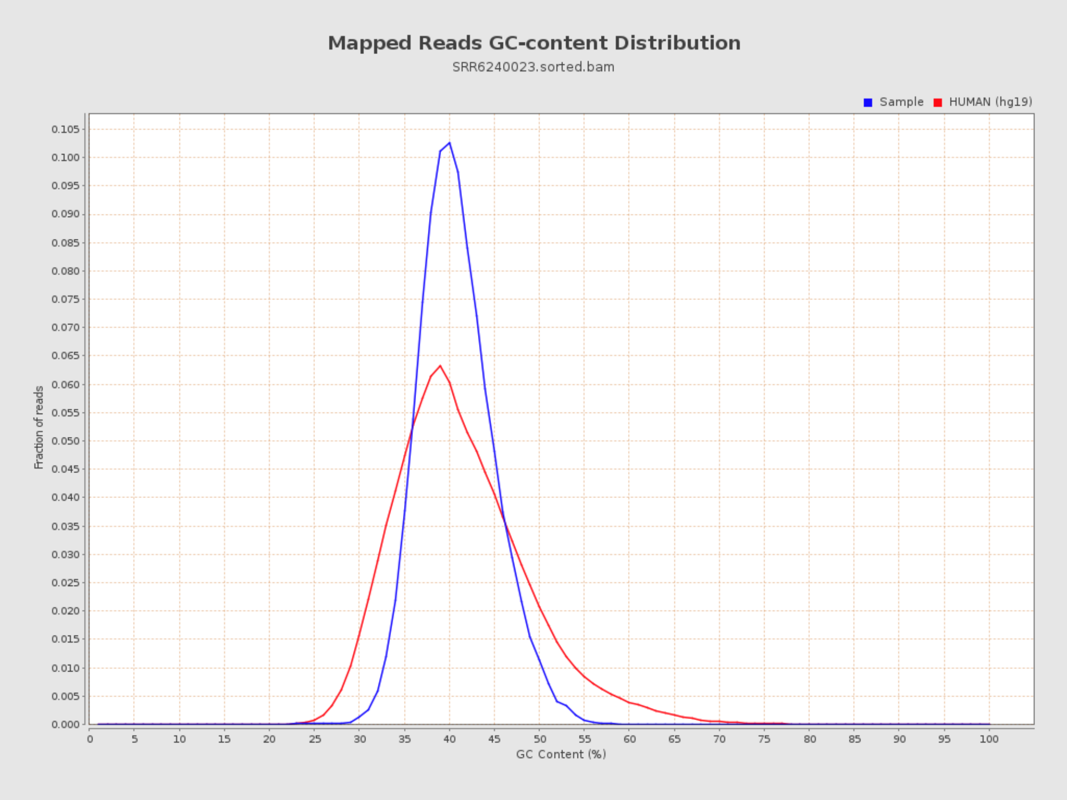
7. Results : Duplication Rate Histogram



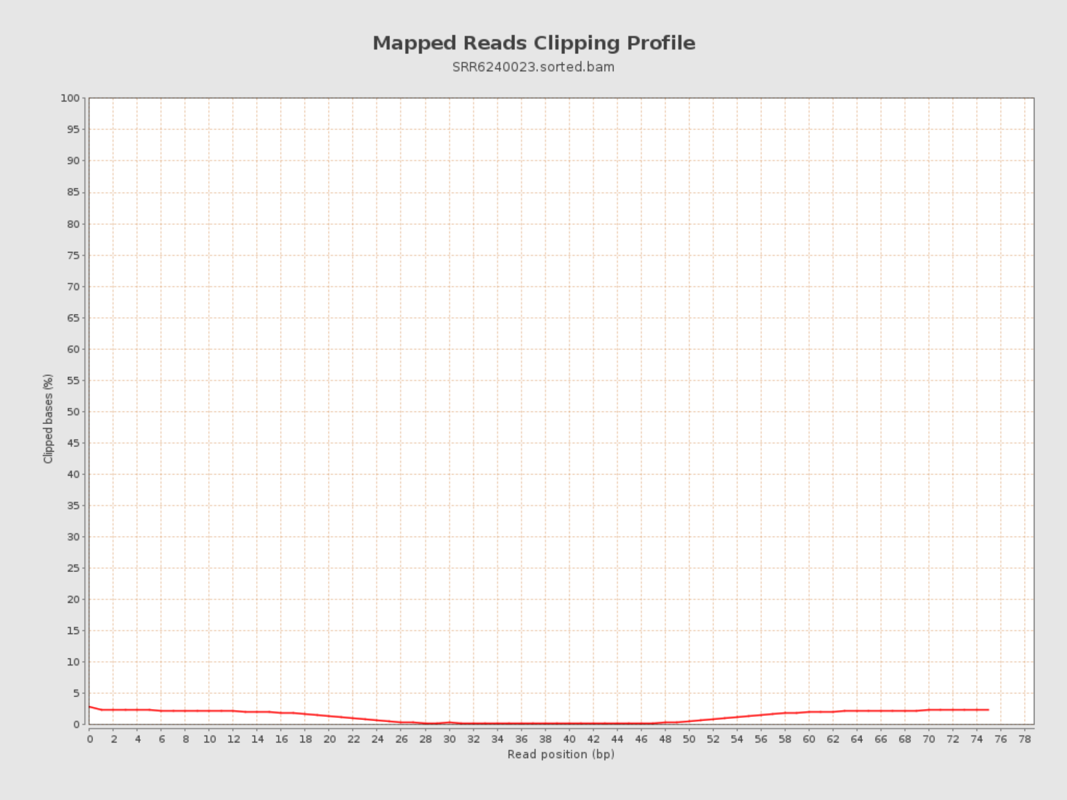
8. Results : Mapped Reads Nucleotide Content



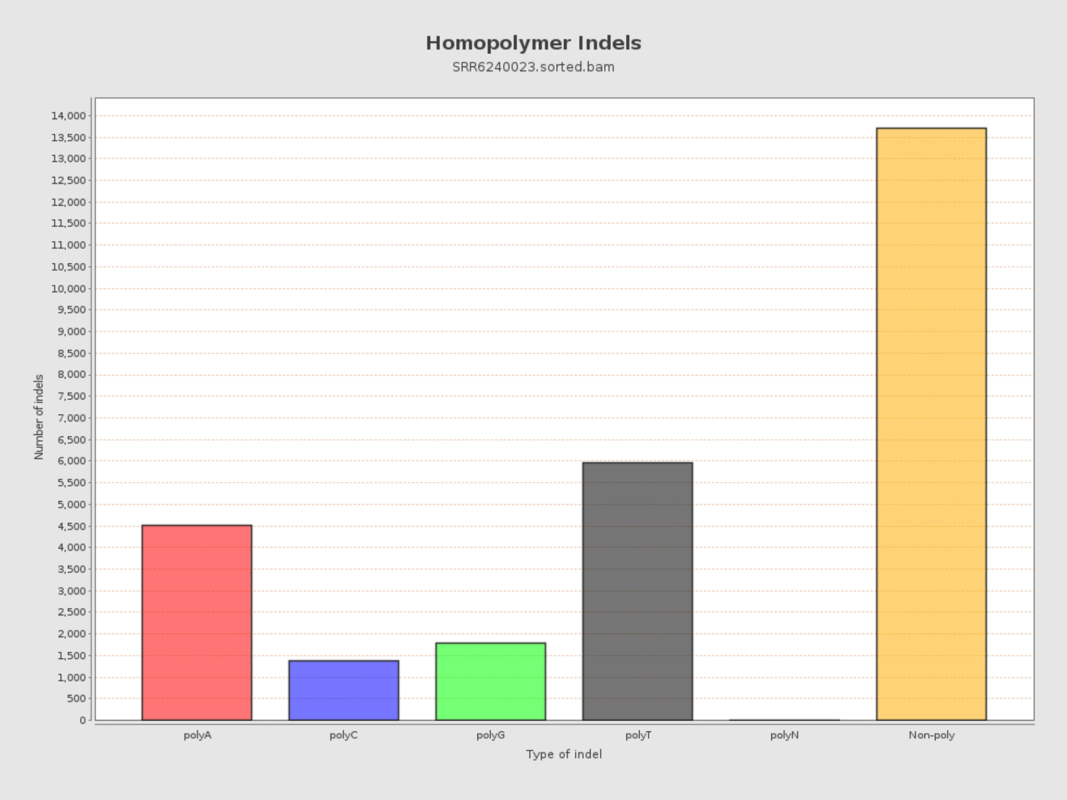
9. Results : Mapped Reads GC-content Distribution



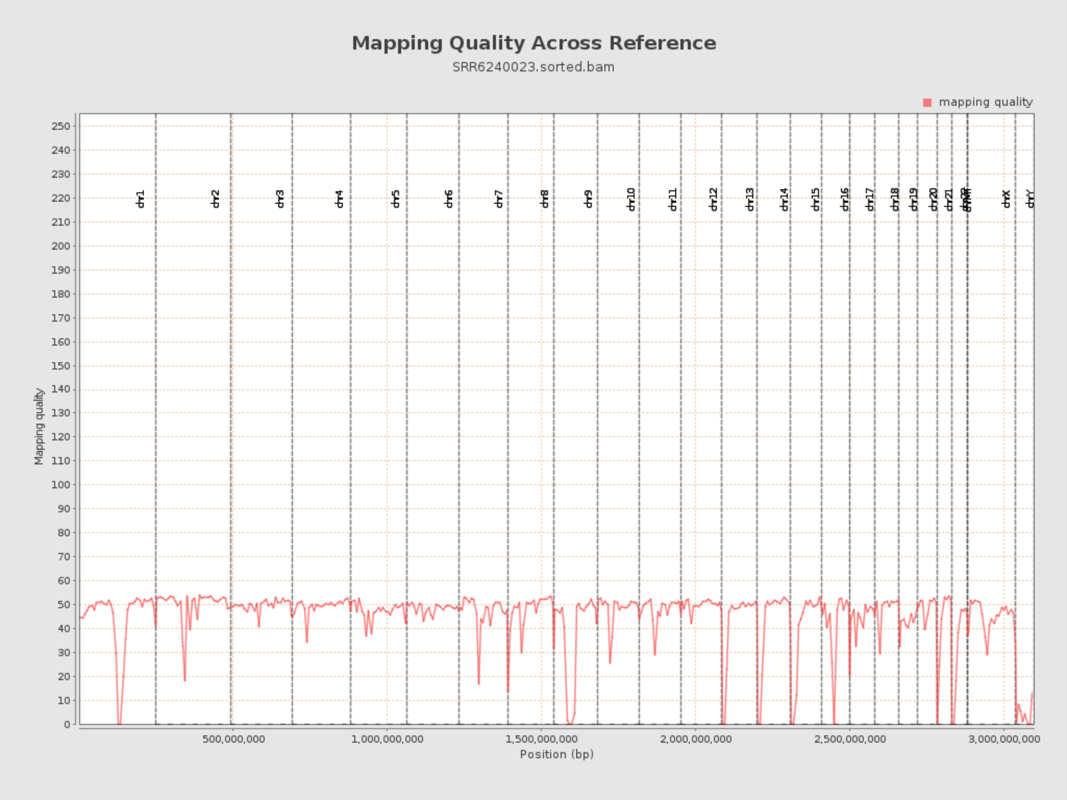
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram