Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:28:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240208.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_SRR6240208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:28:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,965,064
Mapped reads	1,484,271 / 75.53%
Unmapped reads	480,793 / 24.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,197 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	165,052 / 8.4%
Duplication rate	9.37%
Clipped reads	1,052,331 / 53.55%

2.2. ACGT Content

Number/percentage of A's	23,330,437 / 26.12%
Number/percentage of C's	15,074,530 / 16.88%
Number/percentage of T's	29,820,715 / 33.39%
Number/percentage of G's	21,067,241 / 23.59%
Number/percentage of N's	21,656 / 0.02%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2809

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

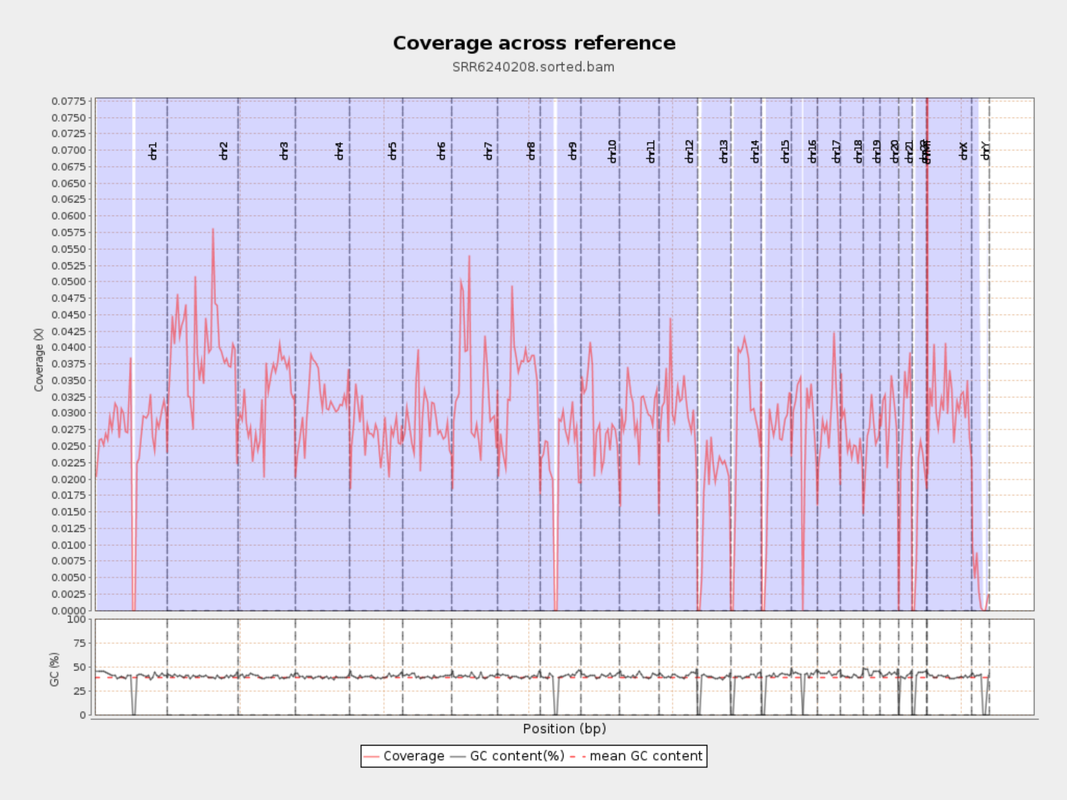
General error rate	0.95%
Mismatches	842,267
Insertions	6,031
Mapped reads with at least one insertion	0.4%
Deletions	27,409
Mapped reads with at least one deletion	1.83%
Homopolymer indels	49.99%

2.6. Chromosome stats

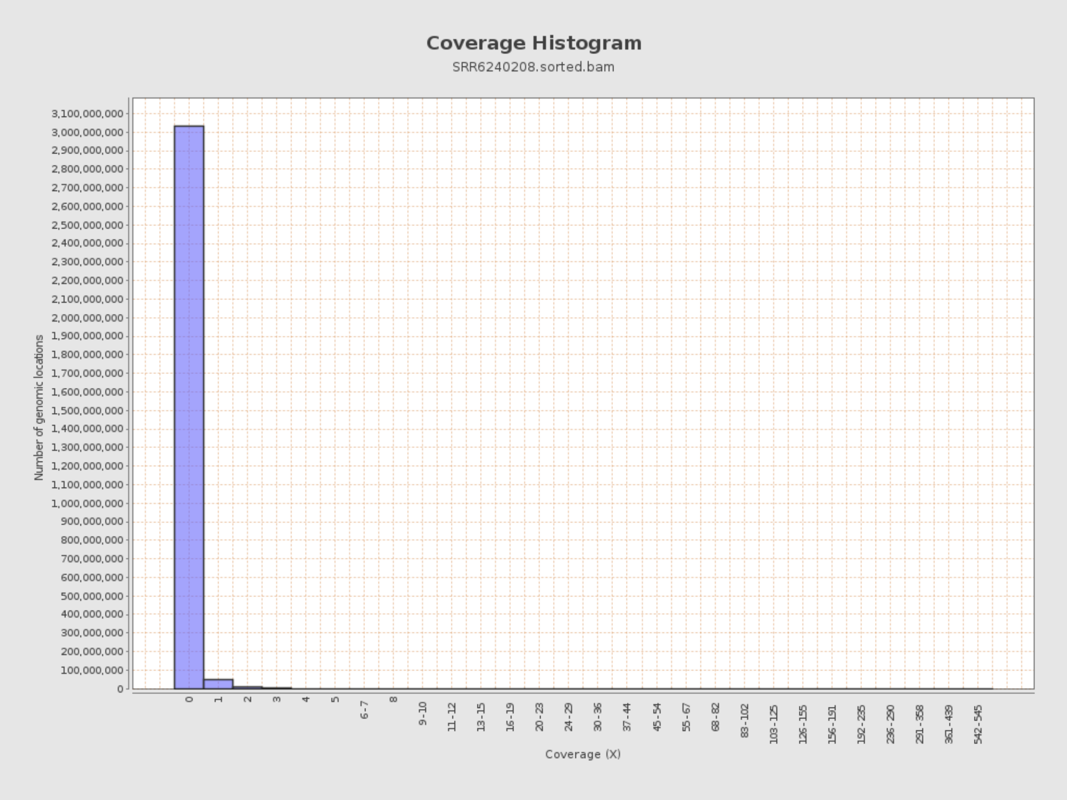
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6562798	0.0263	0.3663
chr2	243199373	9752062	0.0401	0.3803
chr3	198022430	6355442	0.0321	0.2368
chr4	191154276	6004961	0.0314	0.2391
chr5	180915260	4903469	0.0271	0.2179
chr6	171115067	4896745	0.0286	0.2515
chr7	159138663	5341187	0.0336	0.4497

chr8	146364022	5019783	0.0343	0.3288
chr9	141213431	3248500	0.023	0.2525
chr10	135534747	3903950	0.0288	0.2501
chr11	135006516	4043894	0.03	0.2493
chr12	133851895	4168666	0.0311	0.2337
chr13	115169878	2106181	0.0183	0.1776
chr14	107349540	3090126	0.0288	0.2271
chr15	102531392	2404408	0.0235	0.2165
chr16	90354753	2474998	0.0274	0.2203
chr17	81195210	2331453	0.0287	0.2274
chr18	78077248	2029169	0.026	0.3248
chr19	59128983	1566226	0.0265	0.2907
chr20	63025520	1839305	0.0292	0.2268
chr21	48129895	1348099	0.028	0.2249
chr22	51304566	814418	0.0159	0.1608
chrMT	16571	48067	2.9007	3.8148
chrX	155270560	4906713	0.0316	0.2457
chrY	59373566	199908	0.0034	0.076

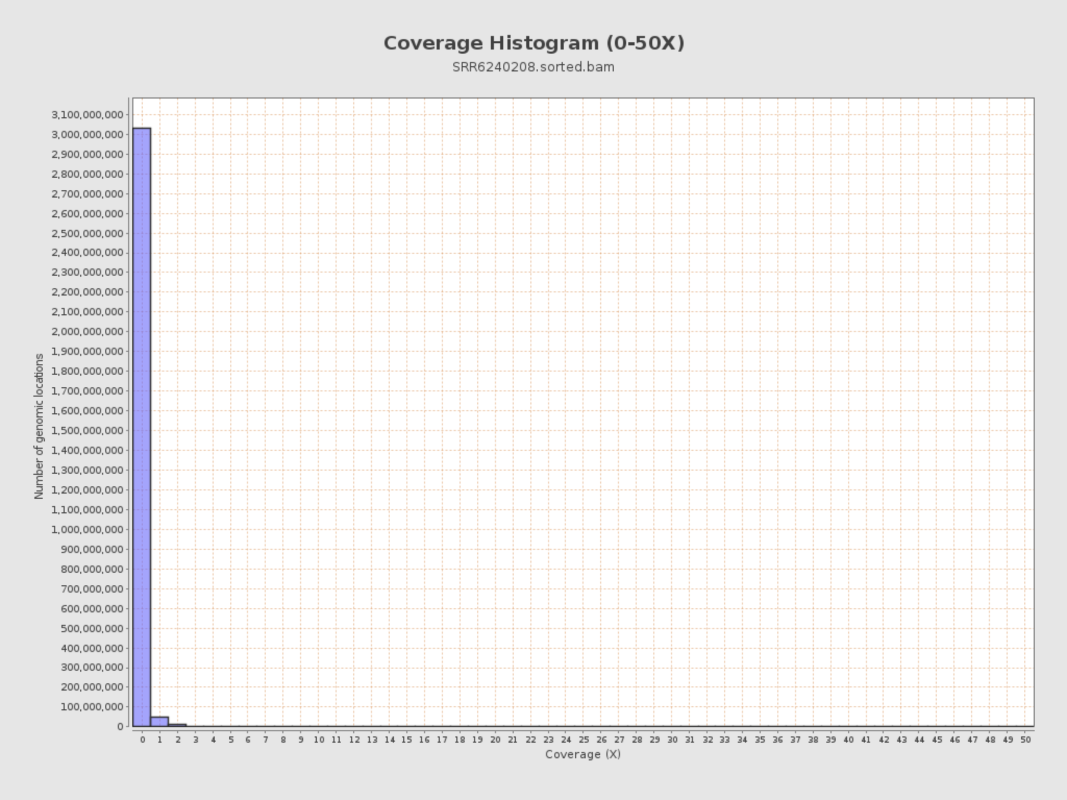
3. Results : Coverage across reference



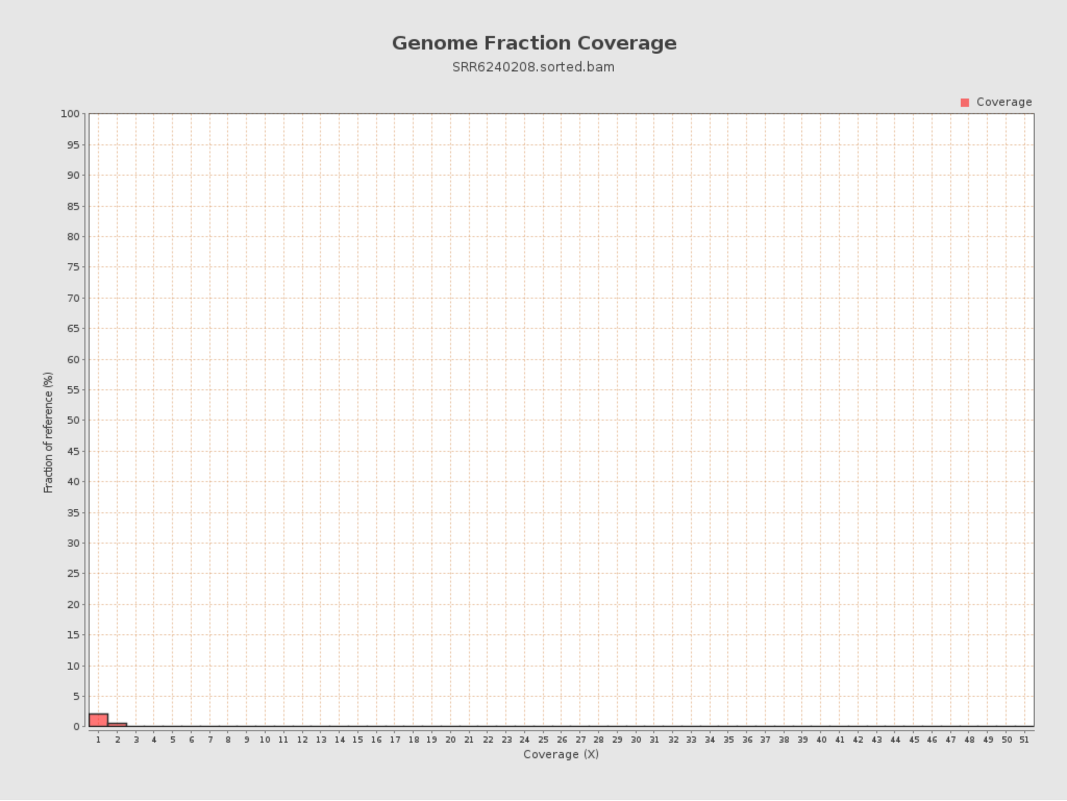
4. Results : Coverage Histogram



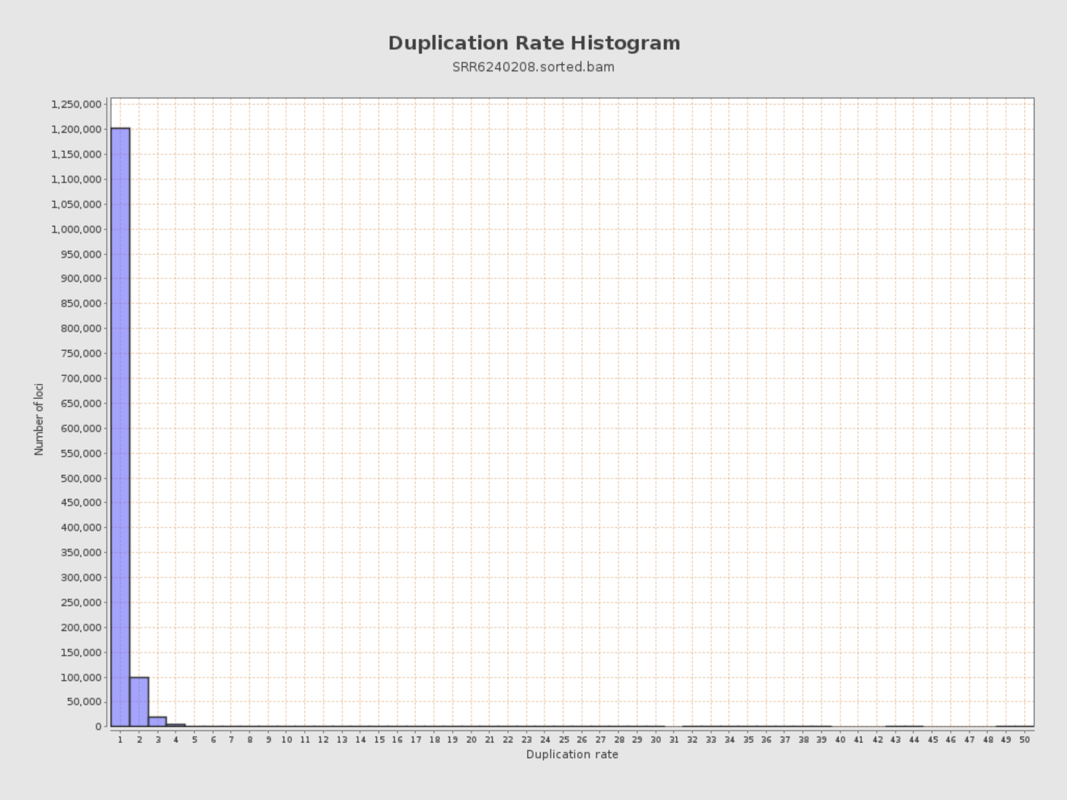
5. Results : Coverage Histogram (0-50X)



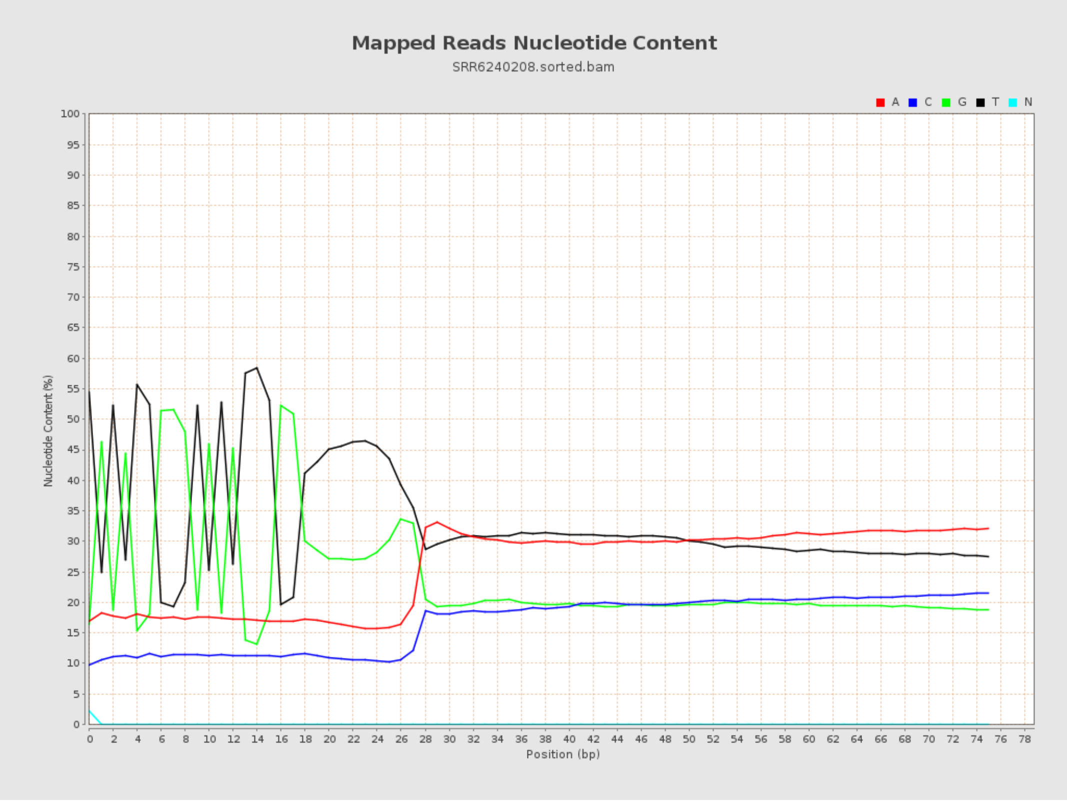
6. Results : Genome Fraction Coverage



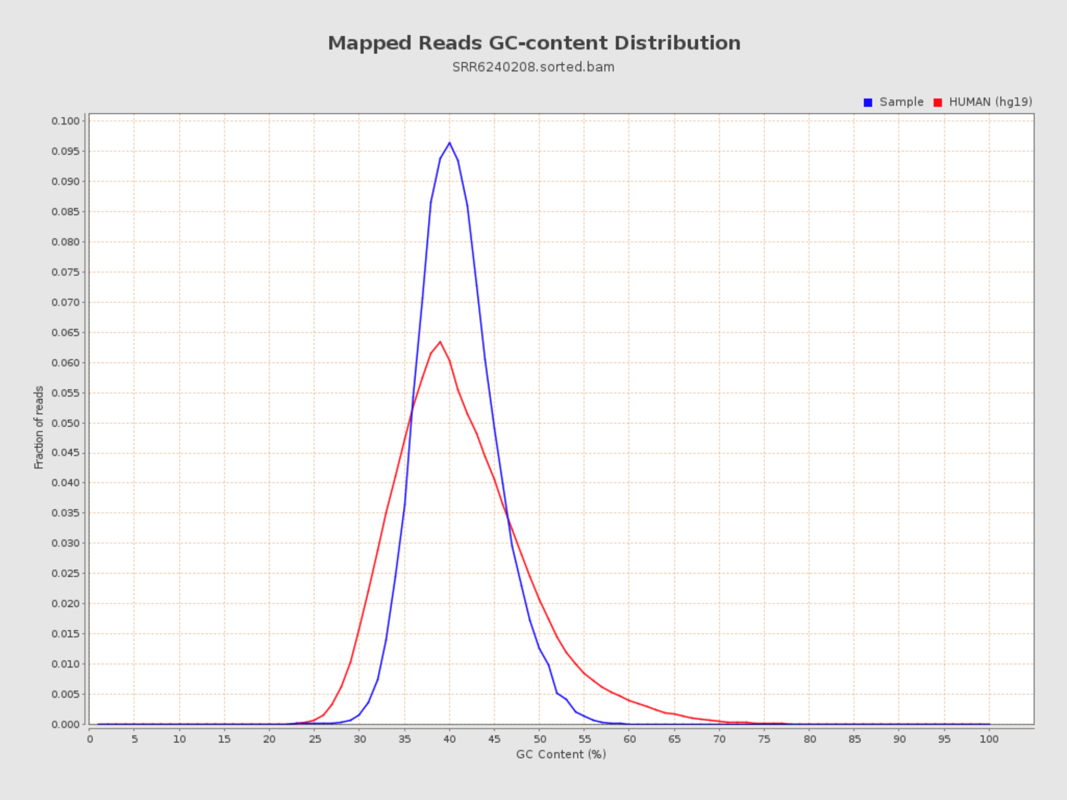
7. Results : Duplication Rate Histogram



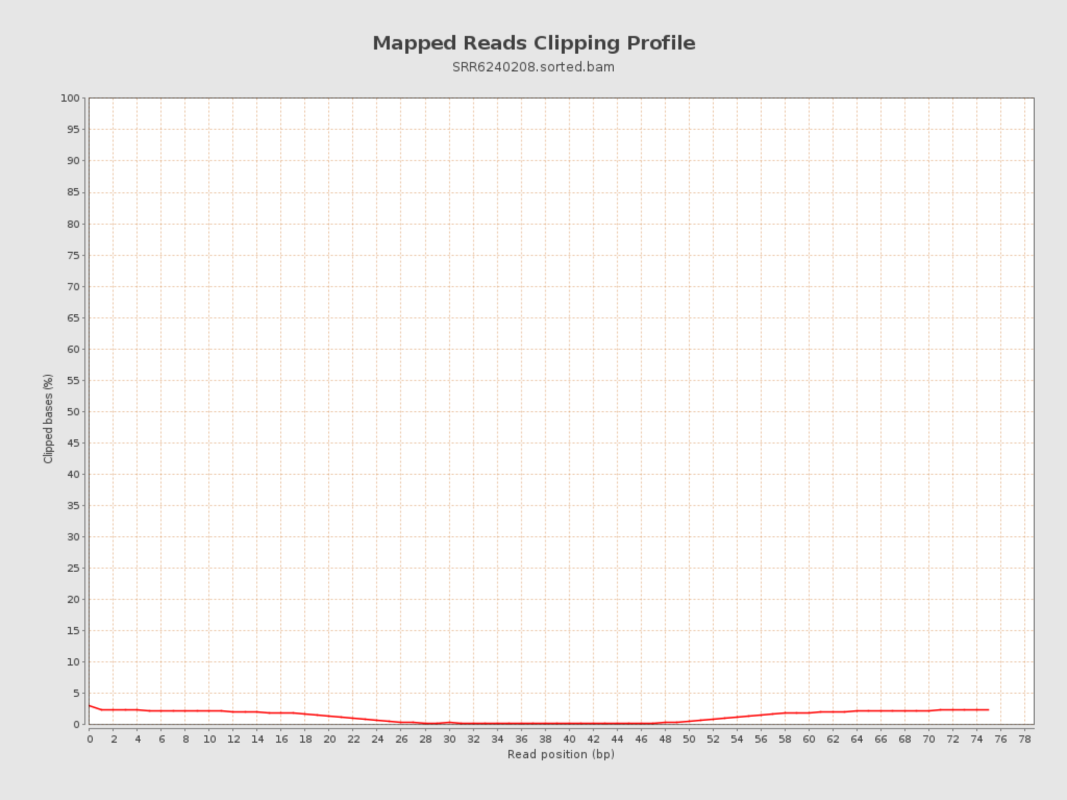
8. Results : Mapped Reads Nucleotide Content



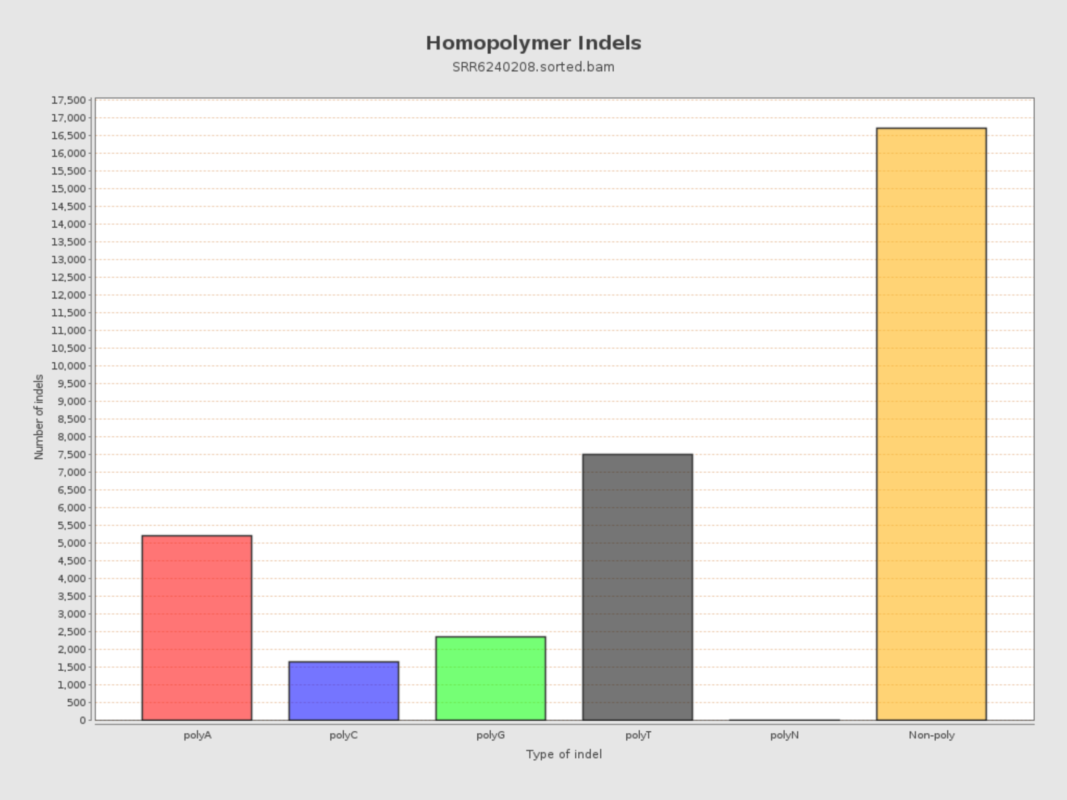
9. Results : Mapped Reads GC-content Distribution



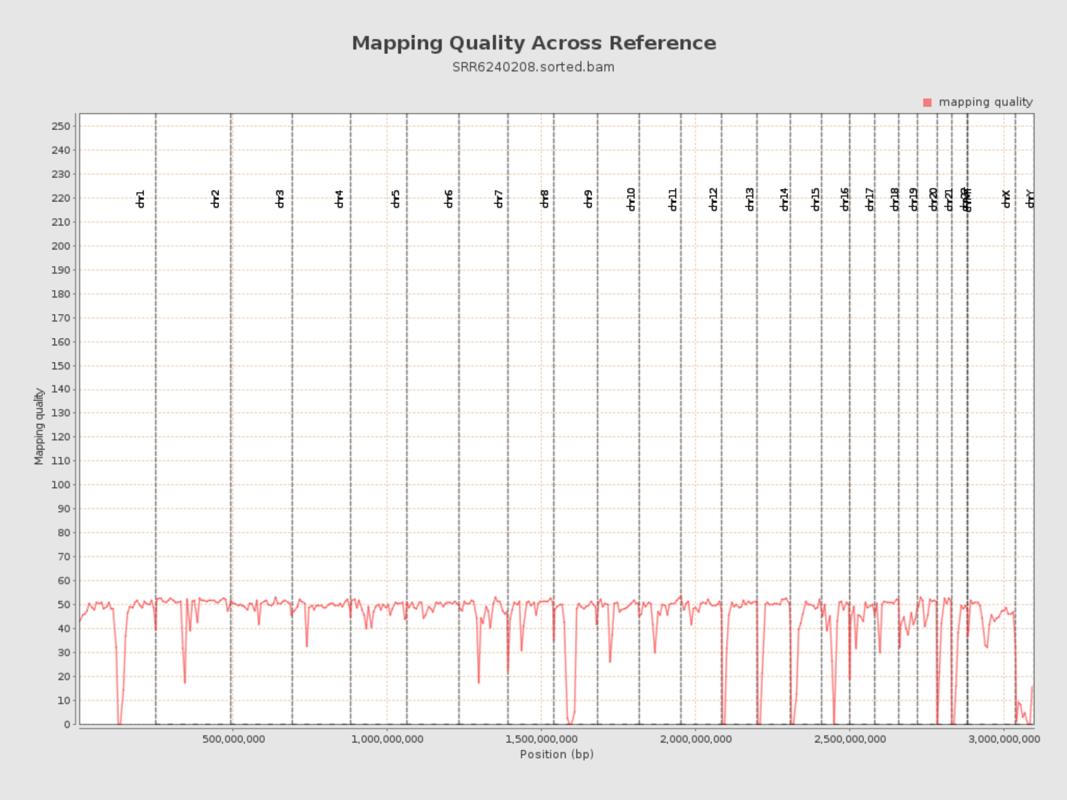
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram