Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:38:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234108.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_SRR6234108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:38:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,178,341
Mapped reads	4,885,807 / 94.35%
Unmapped reads	292,534 / 5.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,498 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	768,290 / 14.84%
Duplication rate	13.26%
Clipped reads	2,456,273 / 47.43%

2.2. ACGT Content

Number/percentage of A's	83,274,781 / 26.19%
Number/percentage of C's	57,282,339 / 18.02%
Number/percentage of T's	103,386,040 / 32.52%
Number/percentage of G's	73,976,700 / 23.27%
Number/percentage of N's	31,362 / 0.01%
GC Percentage	41.28%

2.3. Coverage

Mean	0.1027

Standard Deviation	1.0295

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

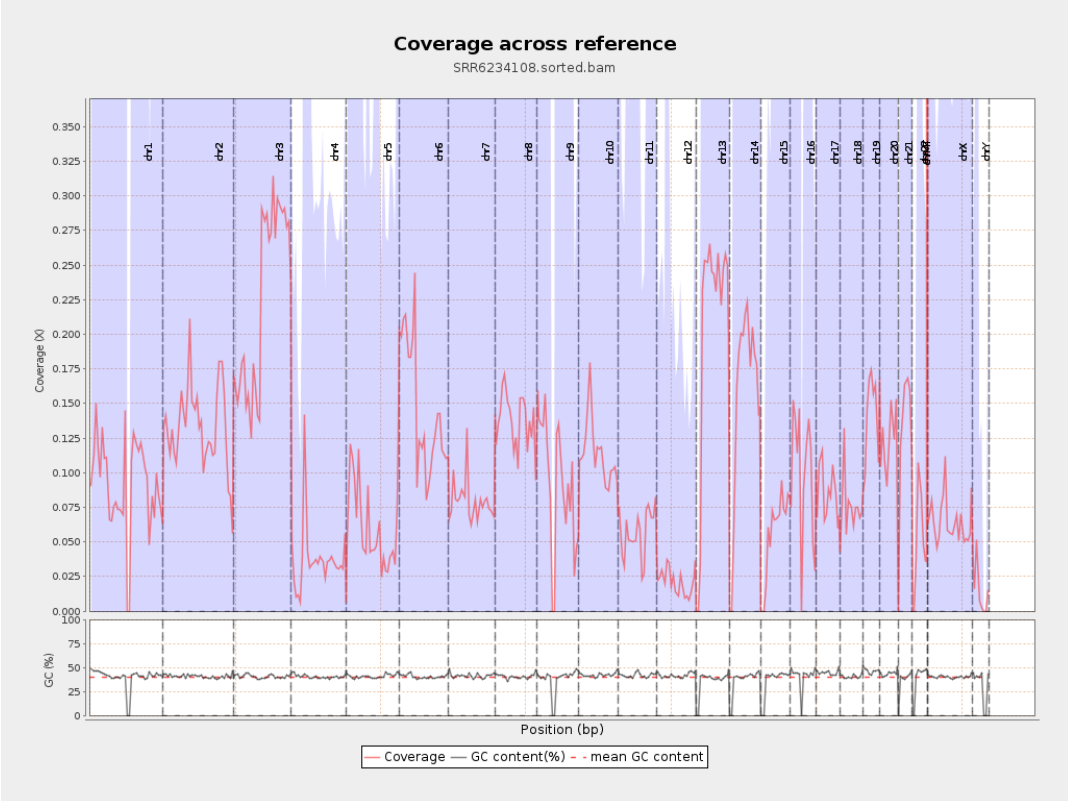
General error rate	0.56%
Mismatches	1,722,903
Insertions	22,449
Mapped reads with at least one insertion	0.45%
Deletions	69,565
Mapped reads with at least one deletion	1.41%
Homopolymer indels	45.03%

2.6. Chromosome stats

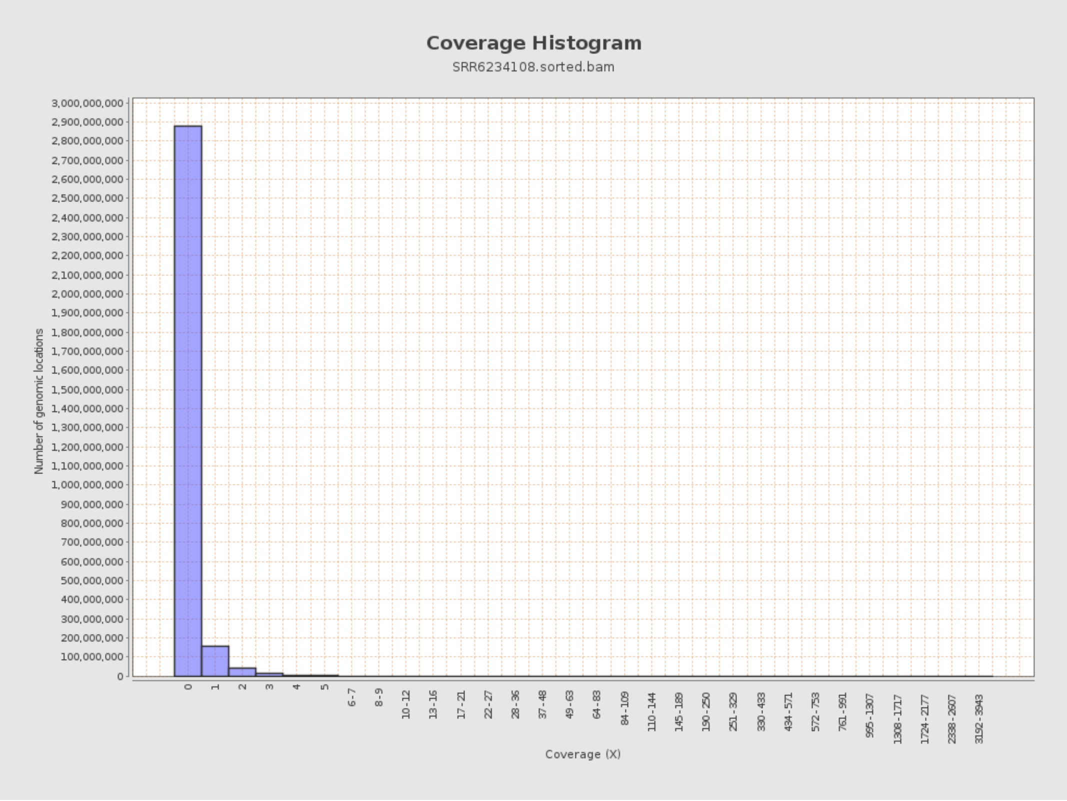
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22853957	0.0917	1.7184
chr2	243199373	32438301	0.1334	1.9027
chr3	198022430	44284283	0.2236	0.6539
chr4	191154276	7049146	0.0369	0.4269
chr5	180915260	10940303	0.0605	0.3611
chr6	171115067	24867800	0.1453	0.8216
chr7	159138663	12694293	0.0798	0.8244

chr8	146364022	19957937	0.1364	1.6301
chr9	141213431	12876752	0.0912	0.7807
chr10	135534747	15535024	0.1146	0.7753
chr11	135006516	7700593	0.057	0.5501
chr12	133851895	2819240	0.0211	0.283
chr13	115169878	23554905	0.2045	0.6774
chr14	107349540	16656903	0.1552	0.6374
chr15	102531392	5836817	0.0569	0.3643
chr16	90354753	8898943	0.0985	0.6191
chr17	81195210	6838167	0.0842	0.4335
chr18	78077248	5911031	0.0757	2.112
chr19	59128983	8446970	0.1429	1.0128
chr20	63025520	7612129	0.1208	0.5875
chr21	48129895	6349585	0.1319	0.5598
chr22	51304566	2505817	0.0488	0.2898
chrMT	16571	570517	34.4286	20.9207
chrX	155270560	10007757	0.0645	0.4793
chrY	59373566	865960	0.0146	0.3722

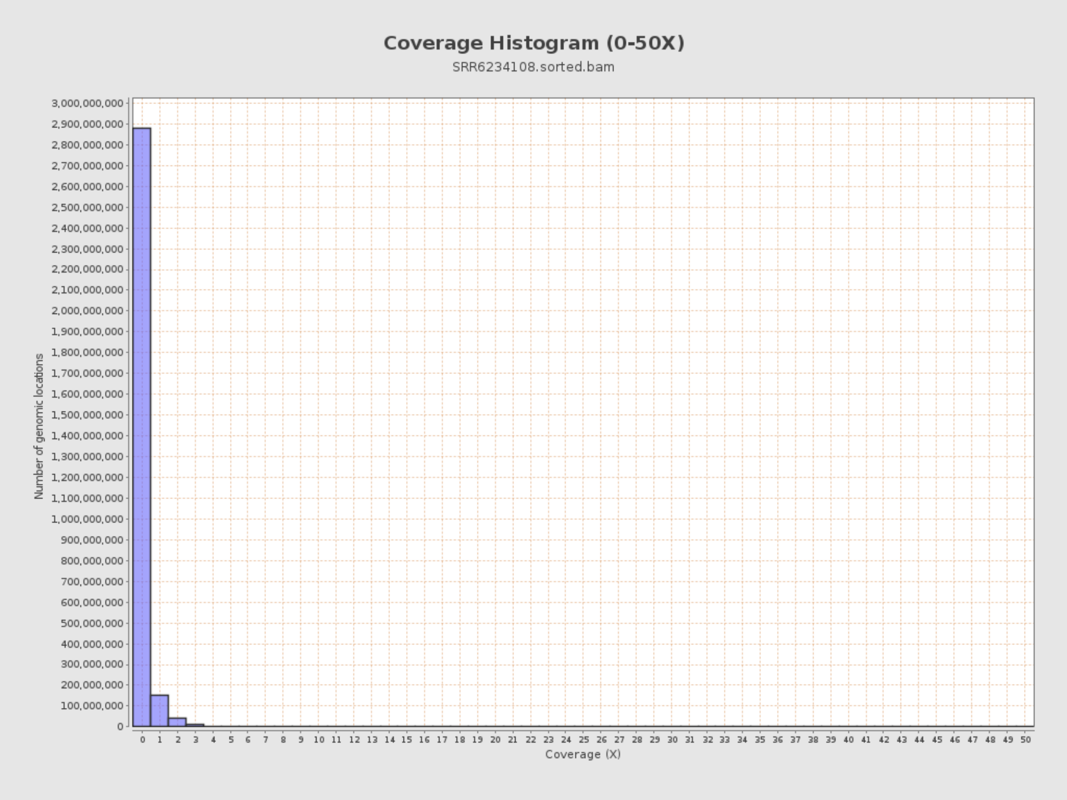
3. Results : Coverage across reference



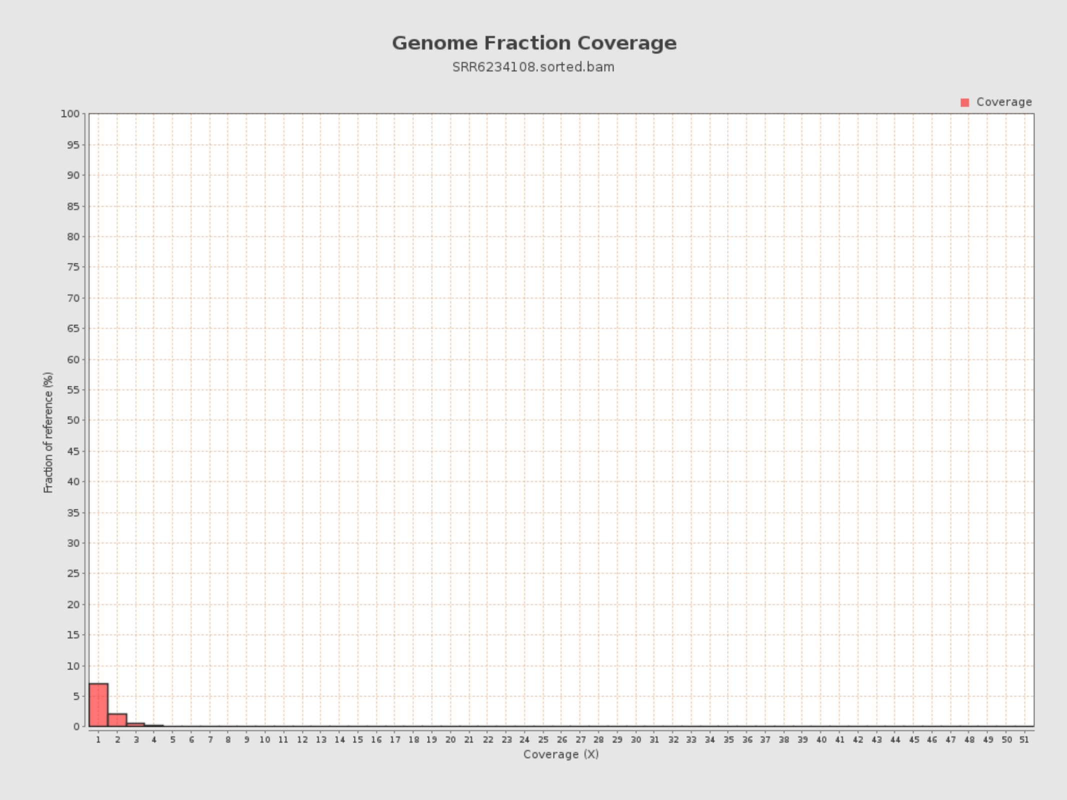
4. Results : Coverage Histogram



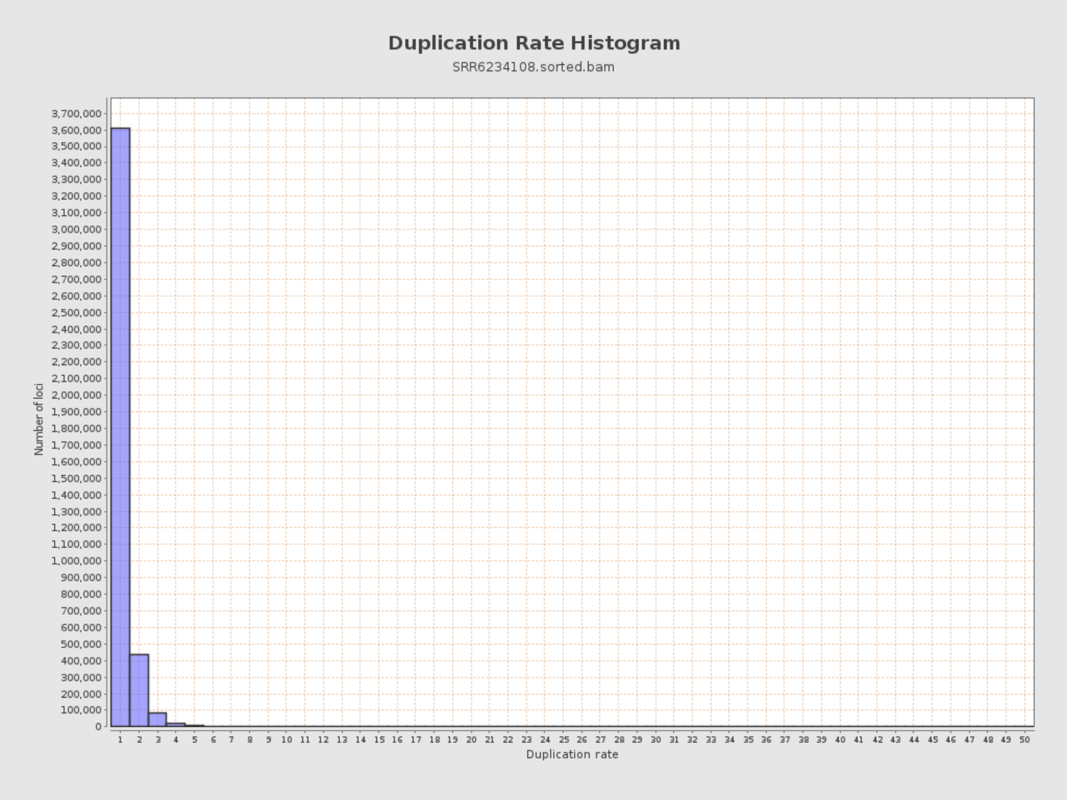
5. Results : Coverage Histogram (0-50X)



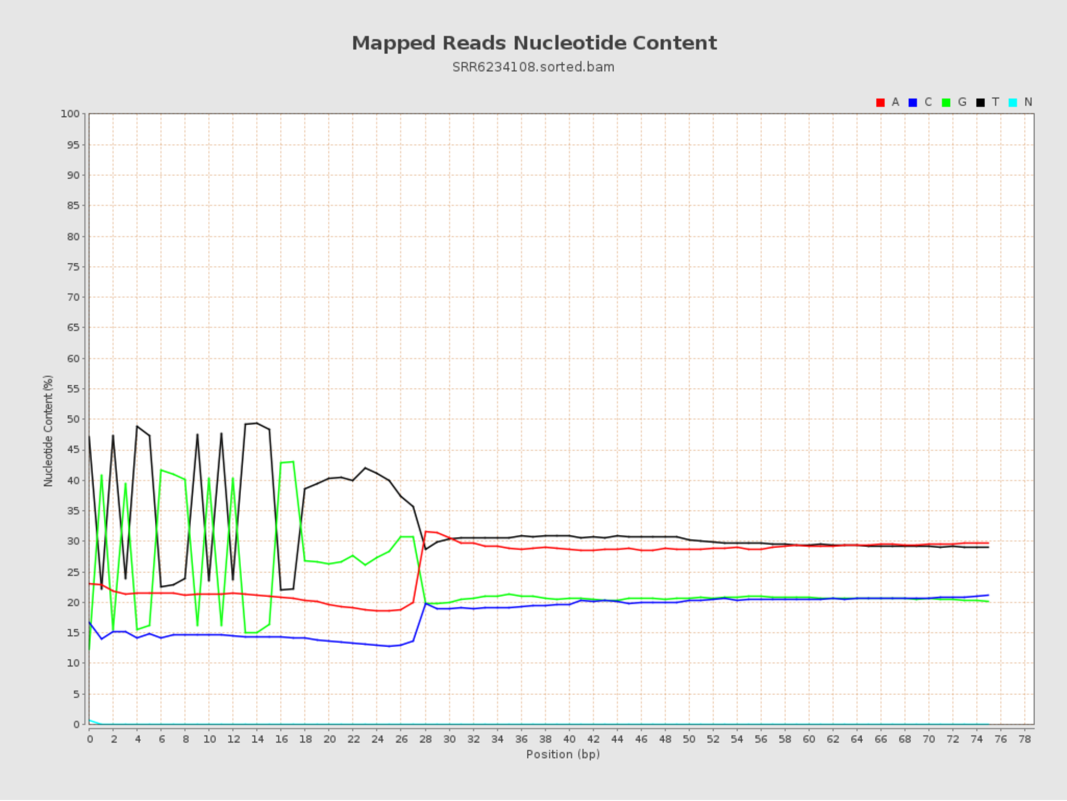
6. Results : Genome Fraction Coverage



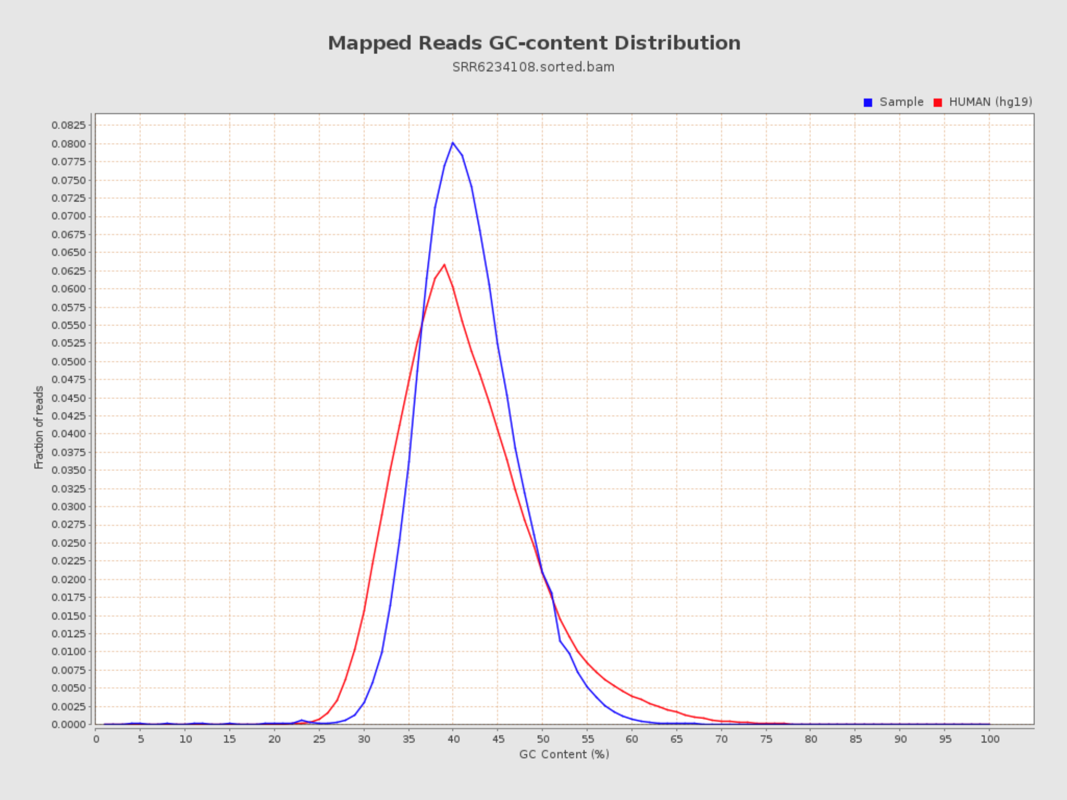
7. Results : Duplication Rate Histogram



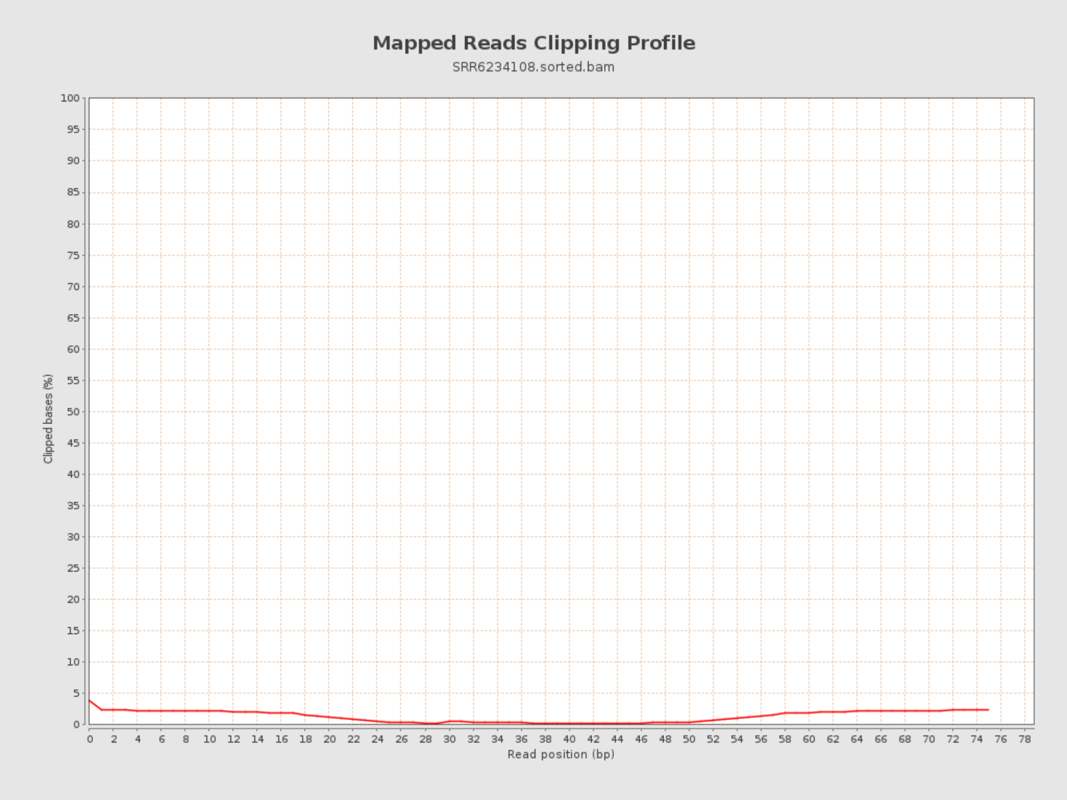
8. Results : Mapped Reads Nucleotide Content



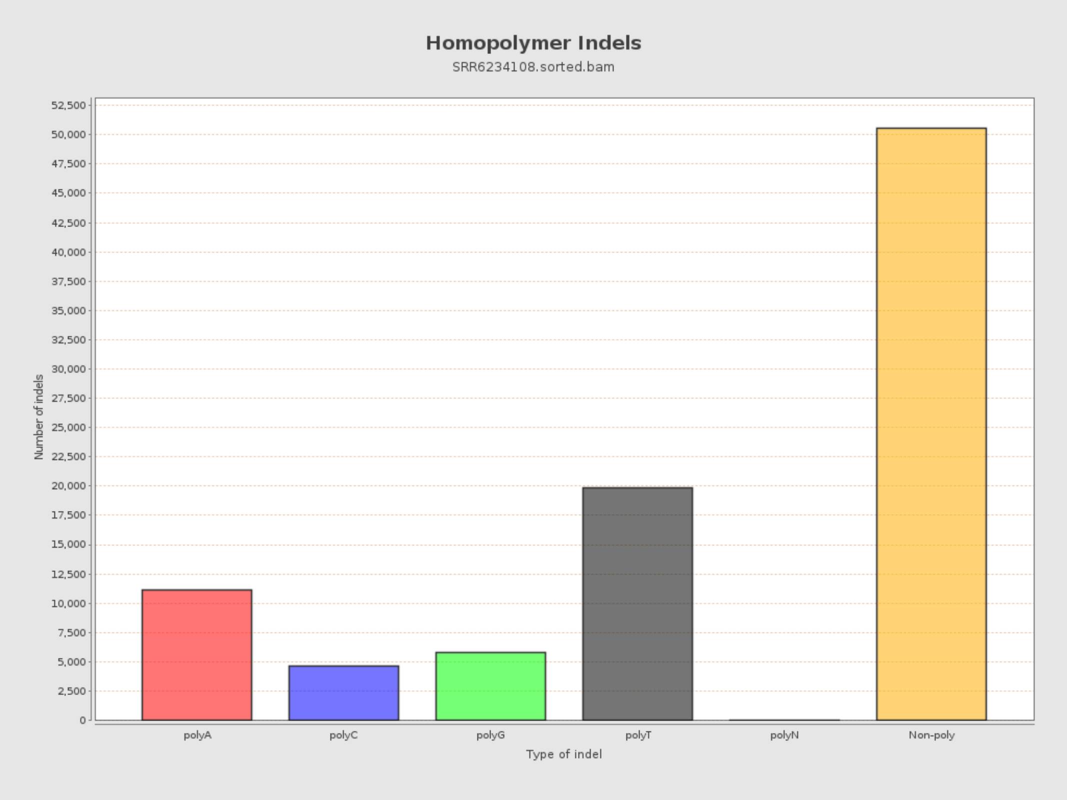
9. Results : Mapped Reads GC-content Distribution



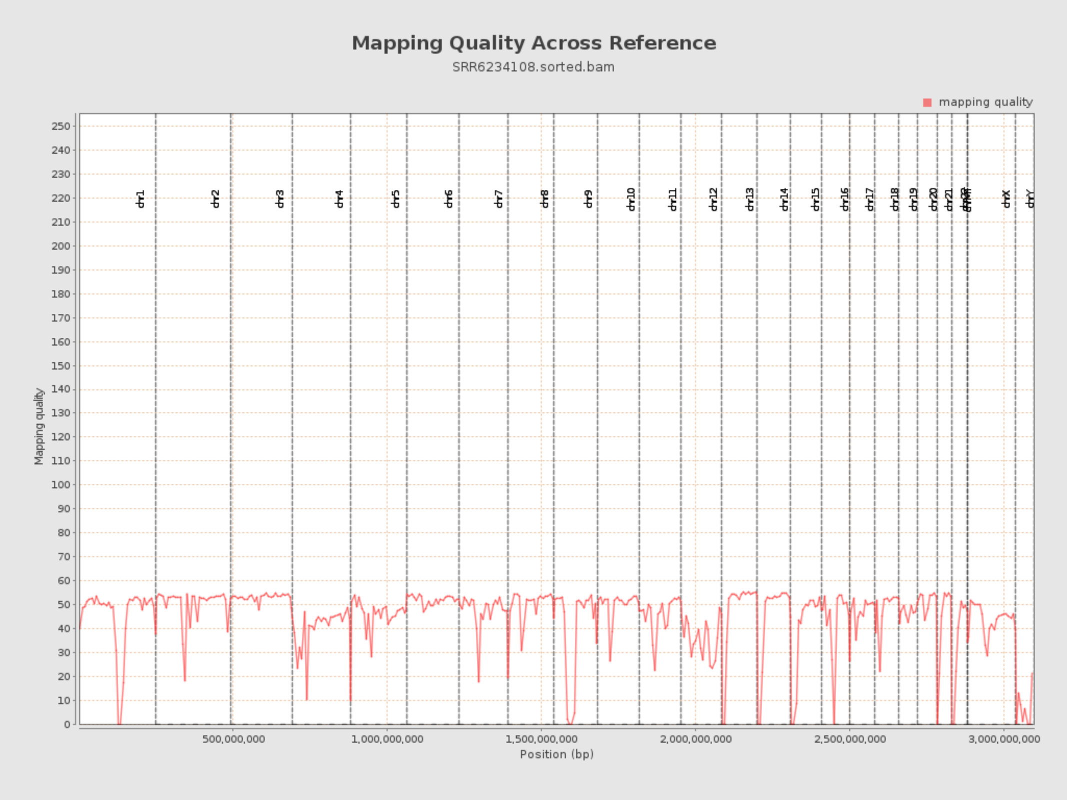
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram