Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:33:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238242.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_SRR6238242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238242.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:33:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,437,016
Mapped reads	1,104,816 / 76.88%
Unmapped reads	332,200 / 23.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,687 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	116,330 / 8.1%
Duplication rate	8.05%
Clipped reads	660,804 / 45.98%

2.2. ACGT Content

Number/percentage of A's	19,501,326 / 27.92%
Number/percentage of C's	13,773,342 / 19.72%
Number/percentage of T's	21,122,369 / 30.24%
Number/percentage of G's	15,442,048 / 22.1%
Number/percentage of N's	20,504 / 0.03%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.3021

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

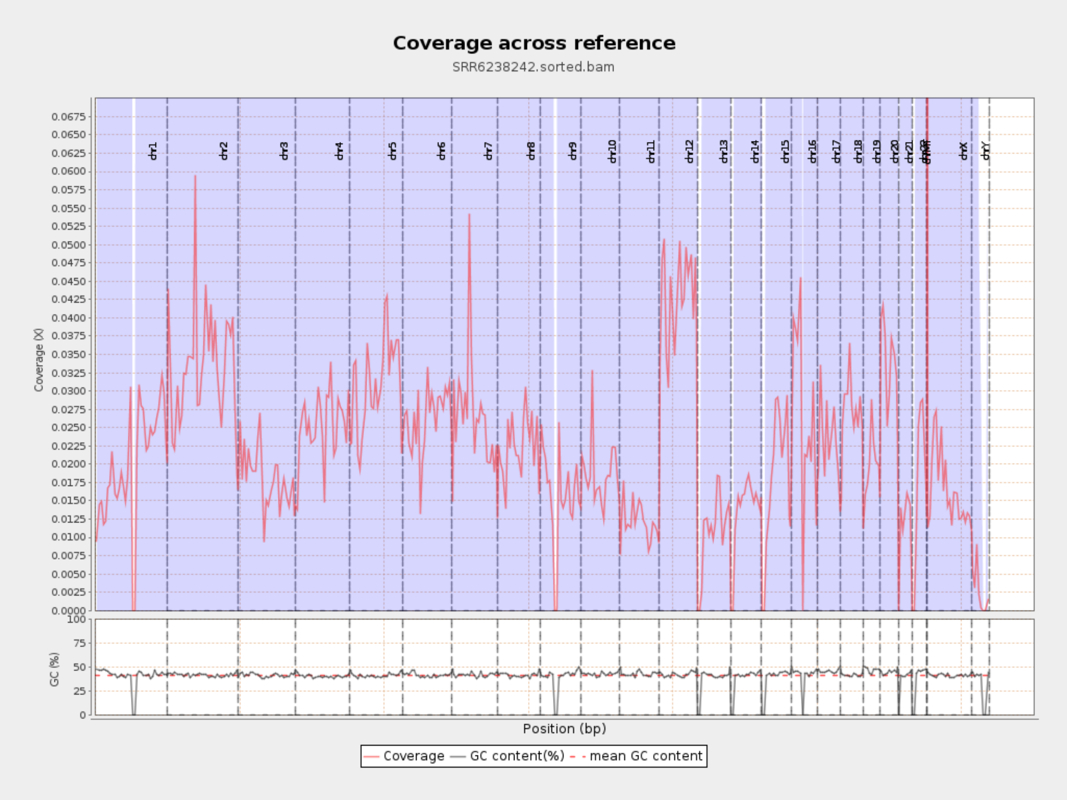
General error rate	0.92%
Mismatches	629,909
Insertions	5,420
Mapped reads with at least one insertion	0.49%
Deletions	19,237
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.43%

2.6. Chromosome stats

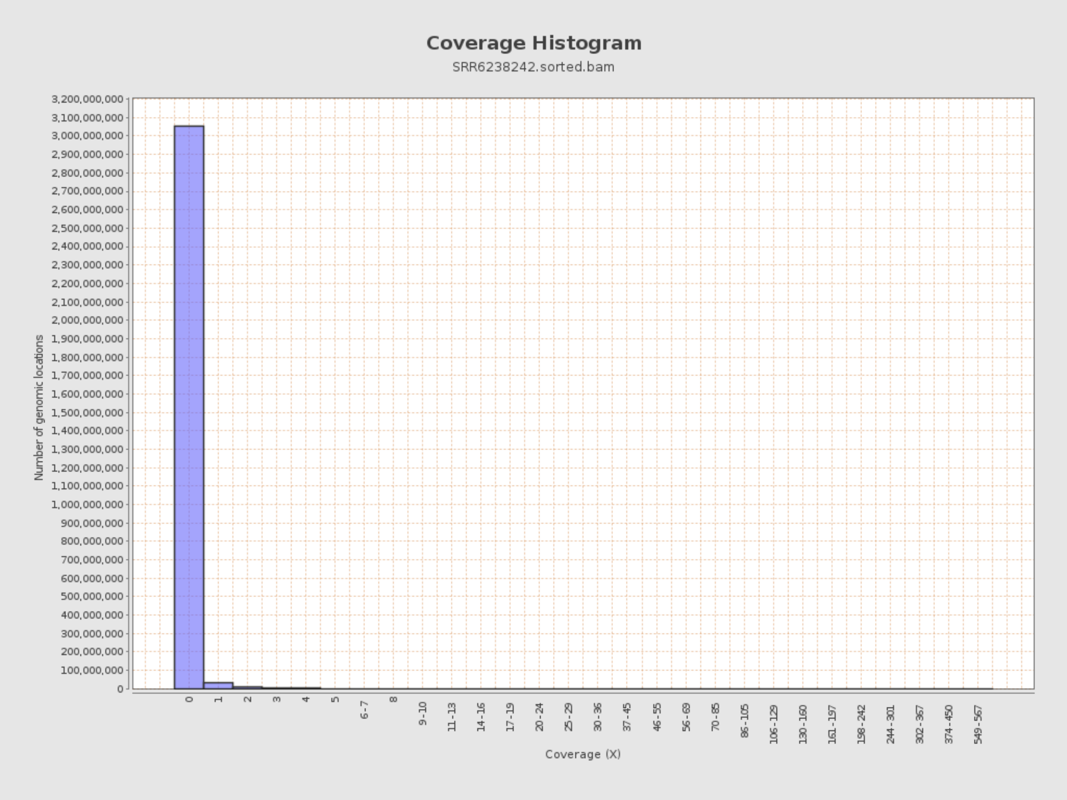
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4918605	0.0197	0.3969
chr2	243199373	8196820	0.0337	0.4444
chr3	198022430	3618466	0.0183	0.2037
chr4	191154276	4781437	0.025	0.2472
chr5	180915260	5656847	0.0313	0.2708
chr6	171115067	4493975	0.0263	0.2765
chr7	159138663	4291199	0.027	0.3967

chr8	146364022	3315480	0.0227	0.3268
chr9	141213431	2223358	0.0157	0.2549
chr10	135534747	2528512	0.0187	0.2609
chr11	135006516	1658903	0.0123	0.1836
chr12	133851895	5749259	0.043	0.3238
chr13	115169878	1240747	0.0108	0.1874
chr14	107349540	1448540	0.0135	0.3058
chr15	102531392	1855349	0.0181	0.3836
chr16	90354753	2343685	0.0259	0.2422
chr17	81195210	1898736	0.0234	0.2419
chr18	78077248	2158411	0.0276	0.3481
chr19	59128983	1187527	0.0201	0.3139
chr20	63025520	2142857	0.034	0.2782
chr21	48129895	572507	0.0119	0.1613
chr22	51304566	890510	0.0174	0.1985
chrMT	16571	15941	0.962	1.459
chrX	155270560	2548880	0.0164	0.2276
chrY	59373566	154183	0.0026	0.0853

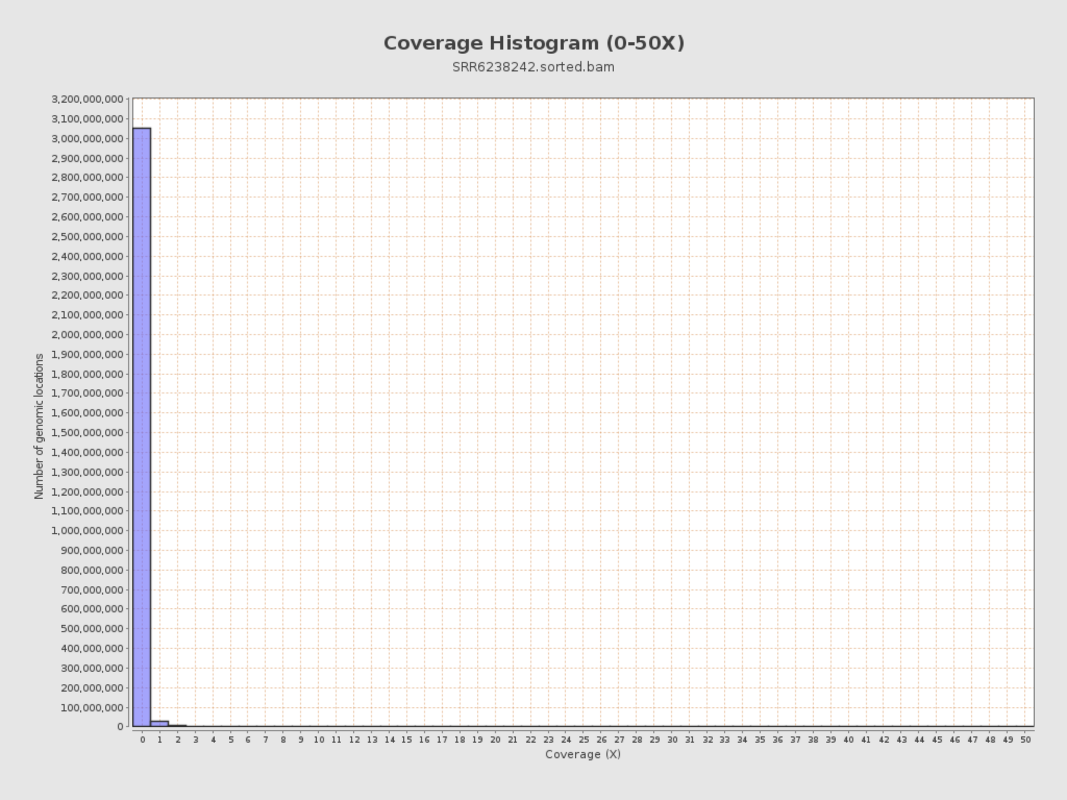
3. Results : Coverage across reference



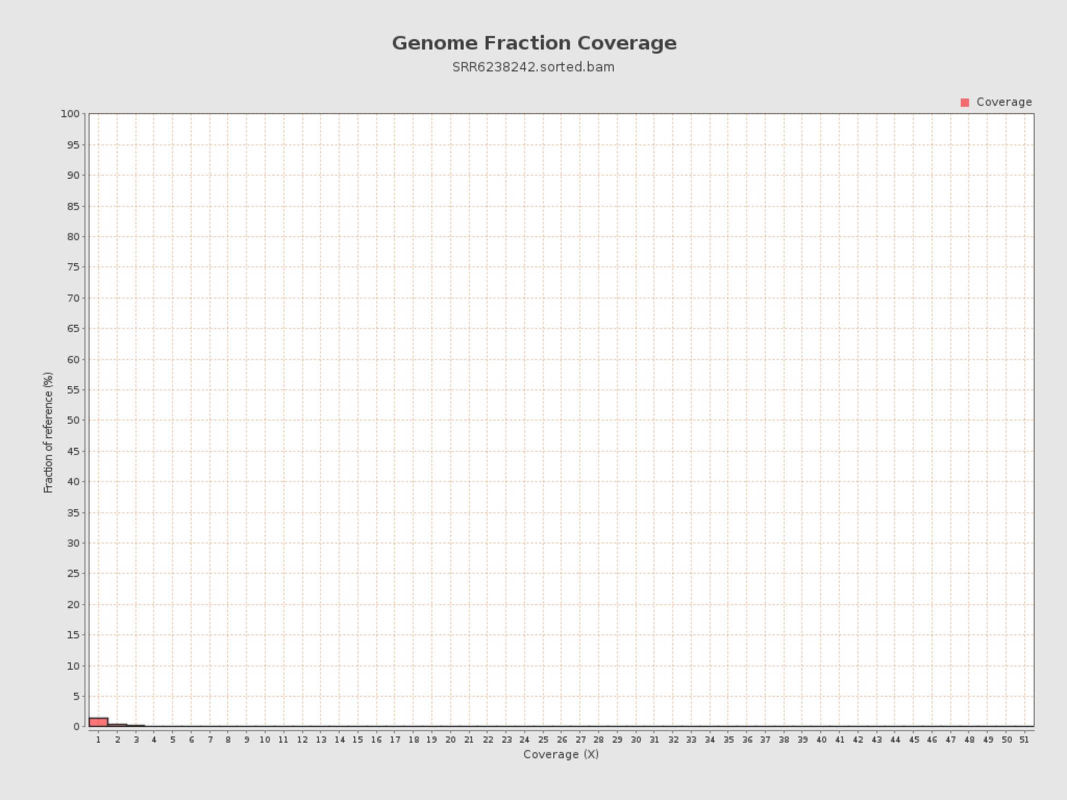
4. Results : Coverage Histogram



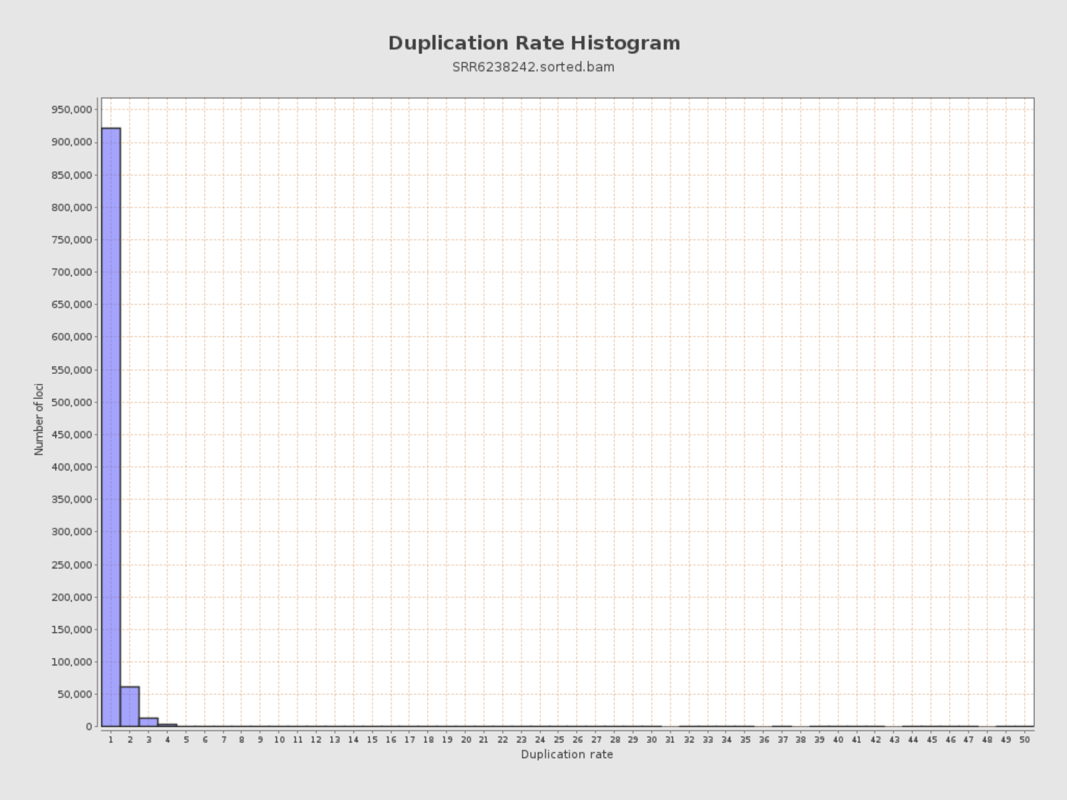
5. Results : Coverage Histogram (0-50X)



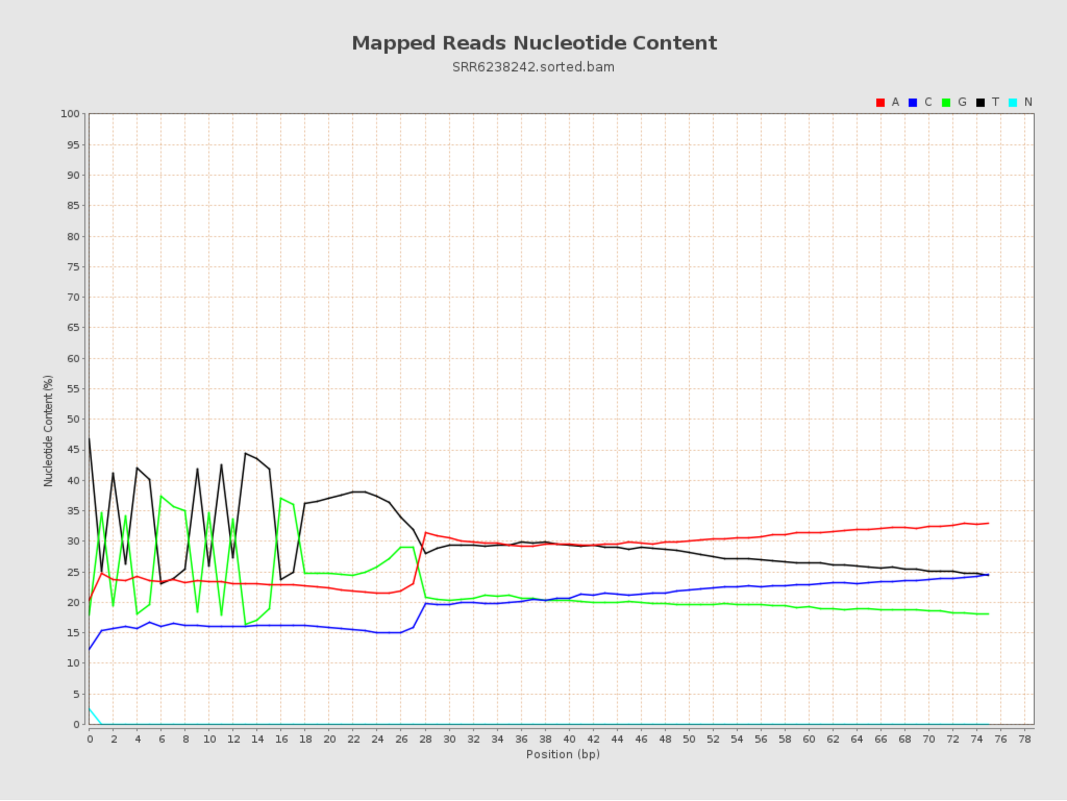
6. Results : Genome Fraction Coverage



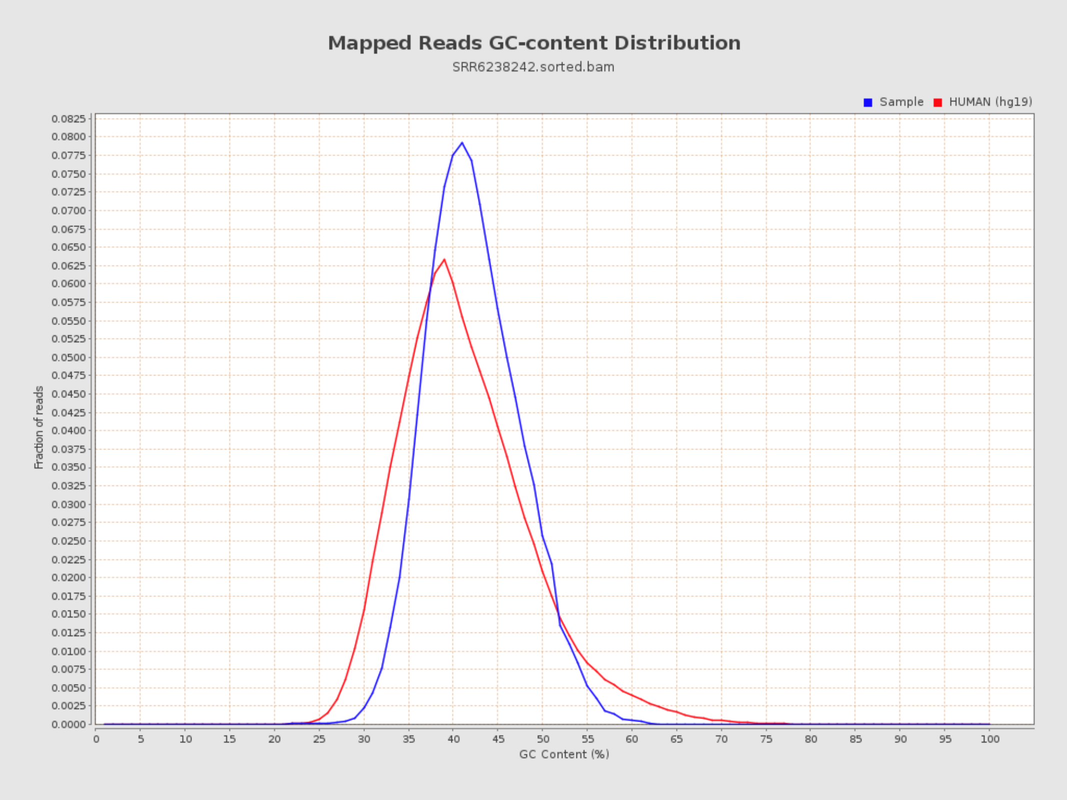
7. Results : Duplication Rate Histogram



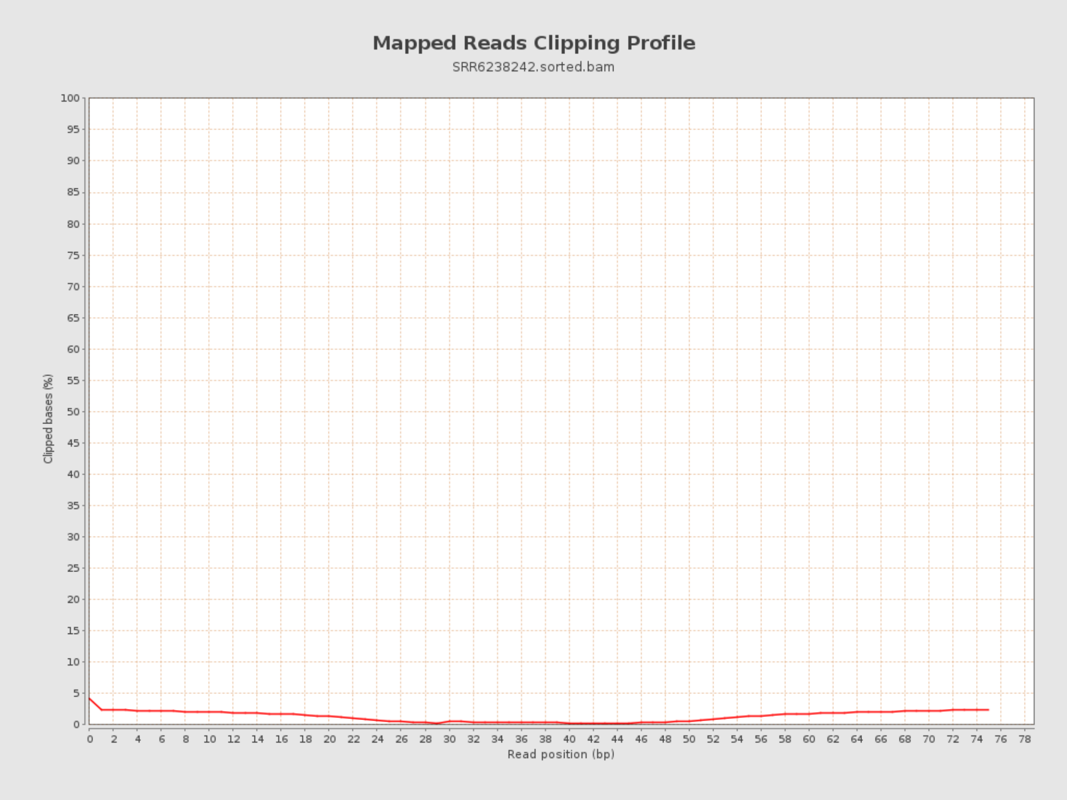
8. Results : Mapped Reads Nucleotide Content



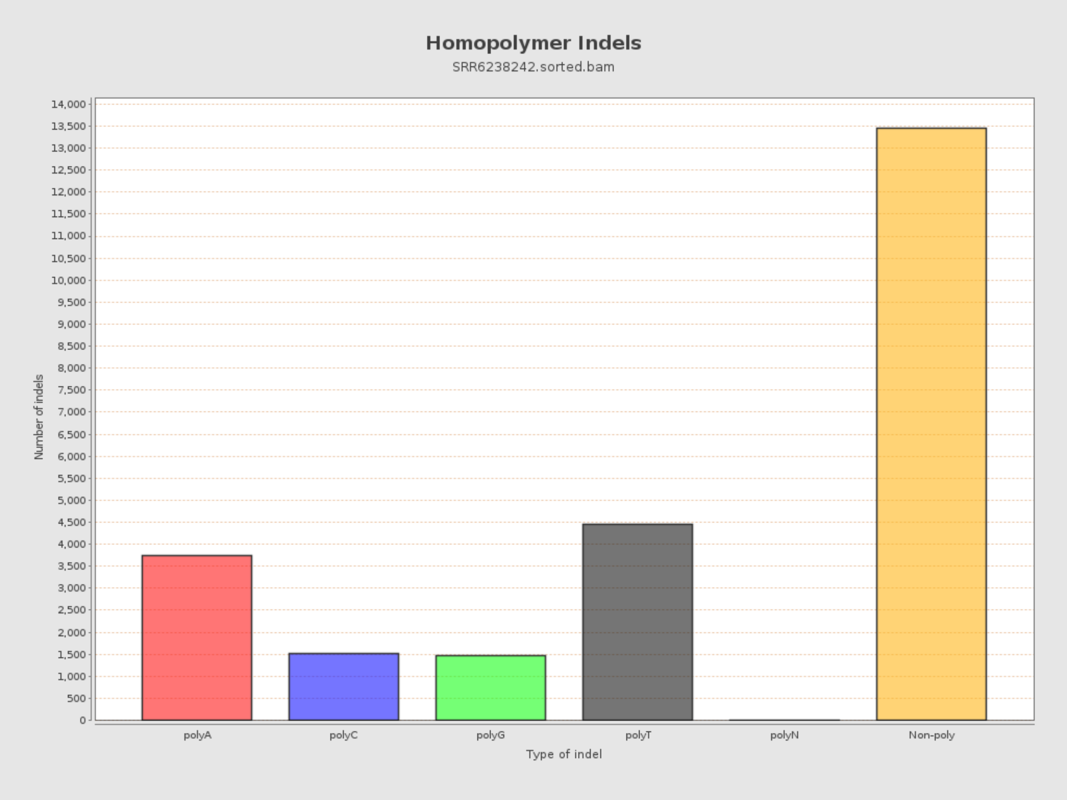
9. Results : Mapped Reads GC-content Distribution



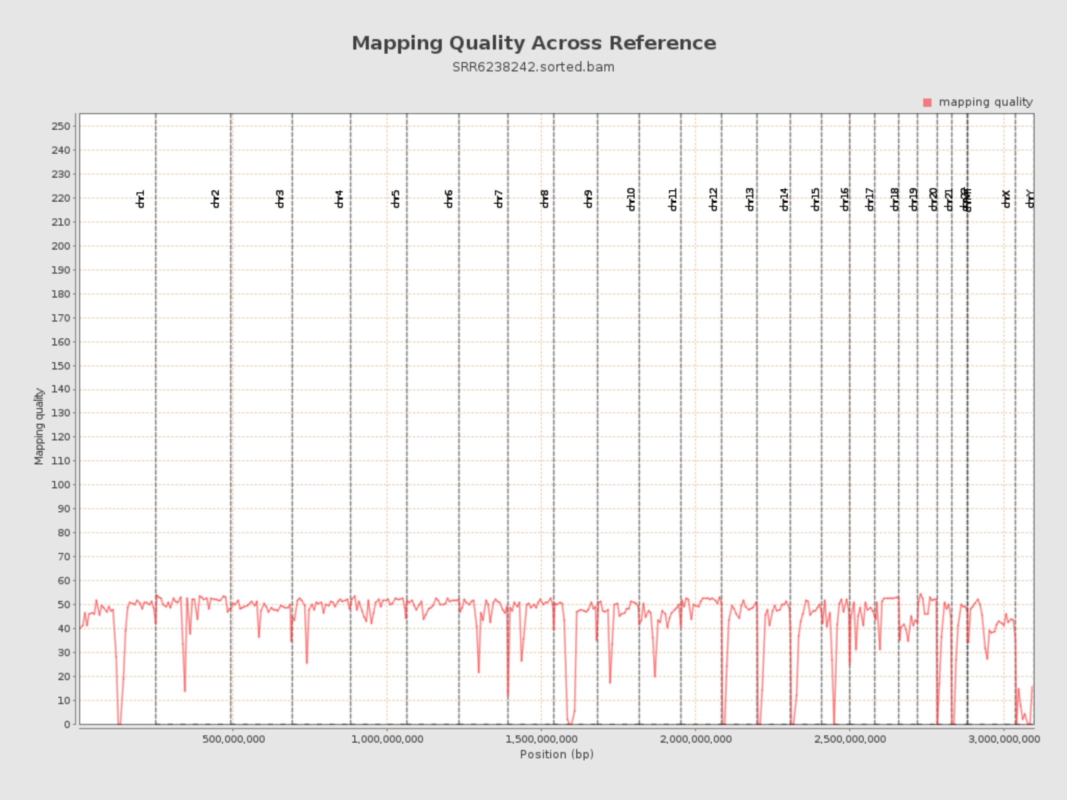
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram