Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:56:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238251.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_SRR6238251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:56:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,202,158
Mapped reads	810,179 / 67.39%
Unmapped reads	391,979 / 32.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,359 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	84,372 / 7.02%
Duplication rate	7.92%
Clipped reads	489,882 / 40.75%

2.2. ACGT Content

Number/percentage of A's	14,321,719 / 28.1%
Number/percentage of C's	9,984,168 / 19.59%
Number/percentage of T's	15,455,893 / 30.33%
Number/percentage of G's	11,187,347 / 21.95%
Number/percentage of N's	10,569 / 0.02%
GC Percentage	41.55%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.2458

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Mismatches and indels

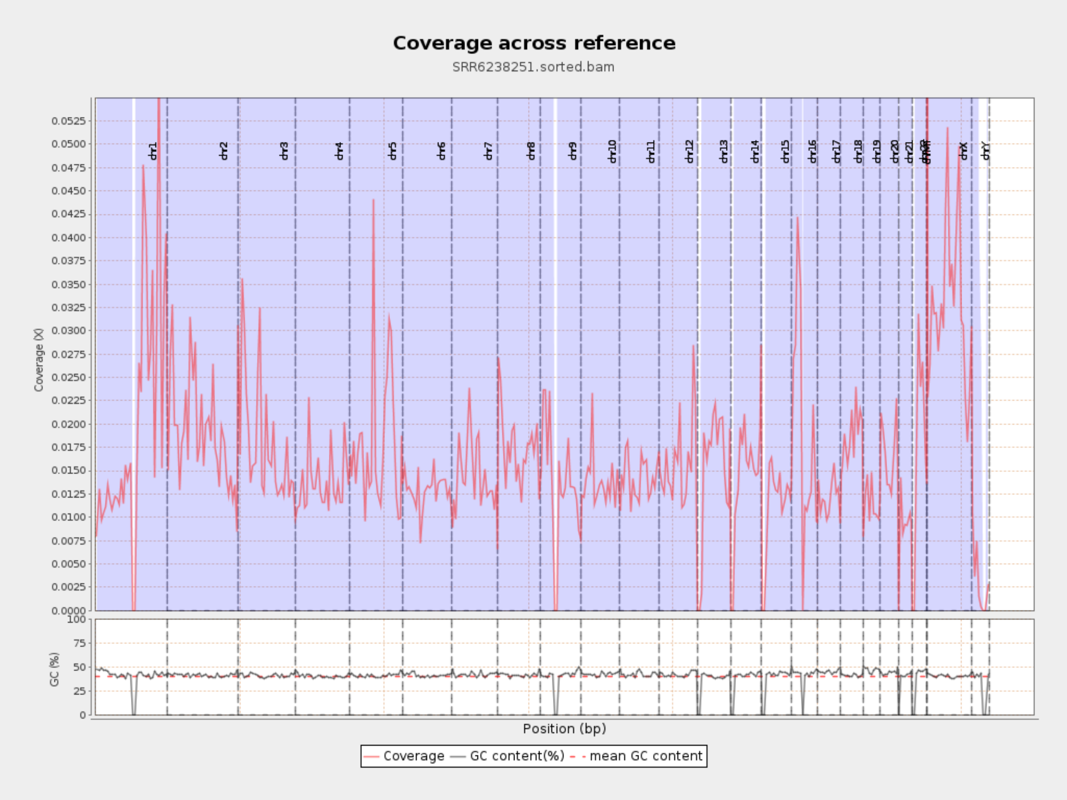
General error rate	0.93%
Mismatches	464,647
Insertions	4,149
Mapped reads with at least one insertion	0.51%
Deletions	14,123
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.36%

2.6. Chromosome stats

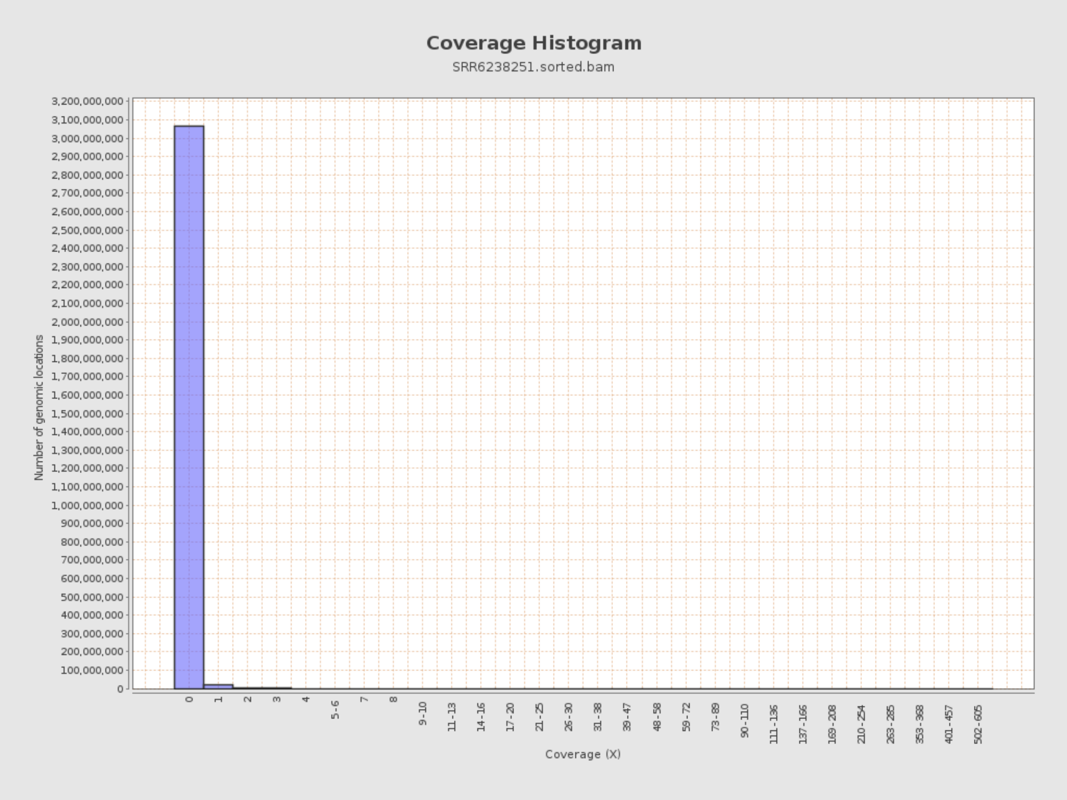
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4938241	0.0198	0.2776
chr2	243199373	4654011	0.0191	0.3253
chr3	198022430	3619896	0.0183	0.2088
chr4	191154276	2615663	0.0137	0.1998
chr5	180915260	3279206	0.0181	0.2126
chr6	171115067	2209320	0.0129	0.2166
chr7	159138663	2331100	0.0146	0.2345

chr8	146364022	2578896	0.0176	0.247
chr9	141213431	1916786	0.0136	0.1928
chr10	135534747	1871156	0.0138	0.1992
chr11	135006516	1904101	0.0141	0.2056
chr12	133851895	2113948	0.0158	0.2046
chr13	115169878	1685385	0.0146	0.2161
chr14	107349540	1535223	0.0143	0.3543
chr15	102531392	1127425	0.011	0.3812
chr16	90354753	1697831	0.0188	0.2116
chr17	81195210	990741	0.0122	0.18
chr18	78077248	1468518	0.0188	0.2558
chr19	59128983	681424	0.0115	0.188
chr20	63025520	1073564	0.017	0.2037
chr21	48129895	443801	0.0092	0.1444
chr22	51304566	917314	0.0179	0.1996
chrMT	16571	40158	2.4234	2.718
chrX	155270560	5112778	0.0329	0.3204
chrY	59373566	176278	0.003	0.084

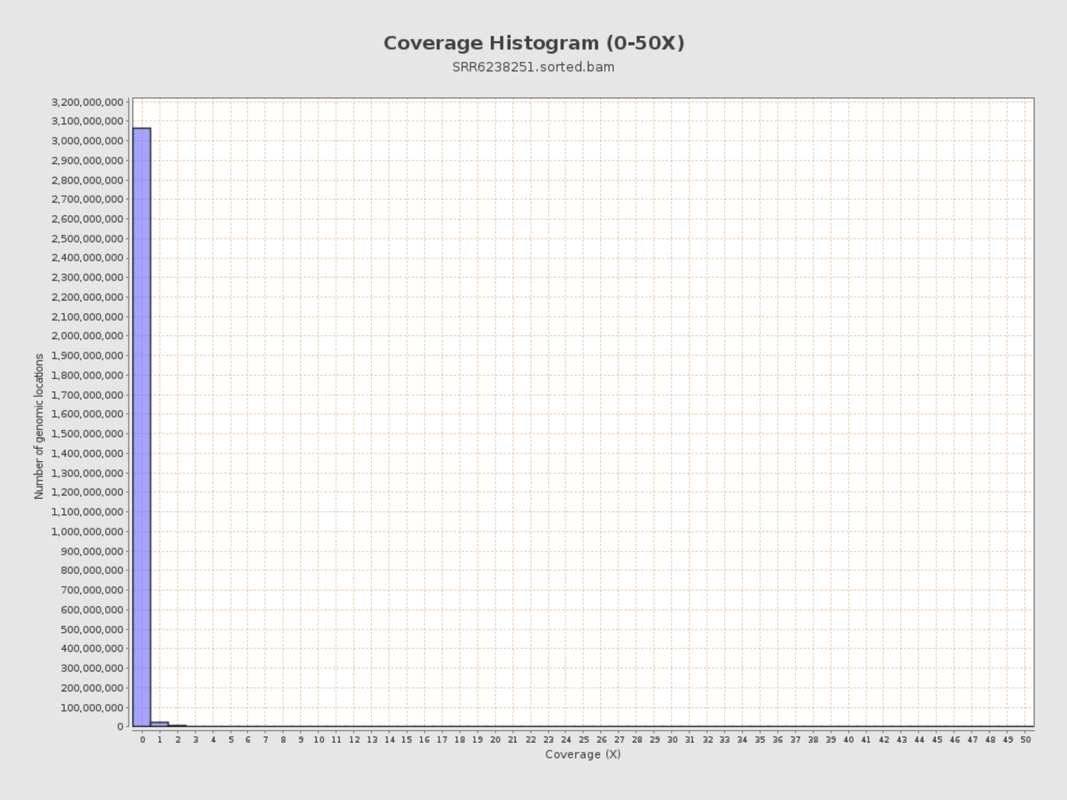
3. Results : Coverage across reference



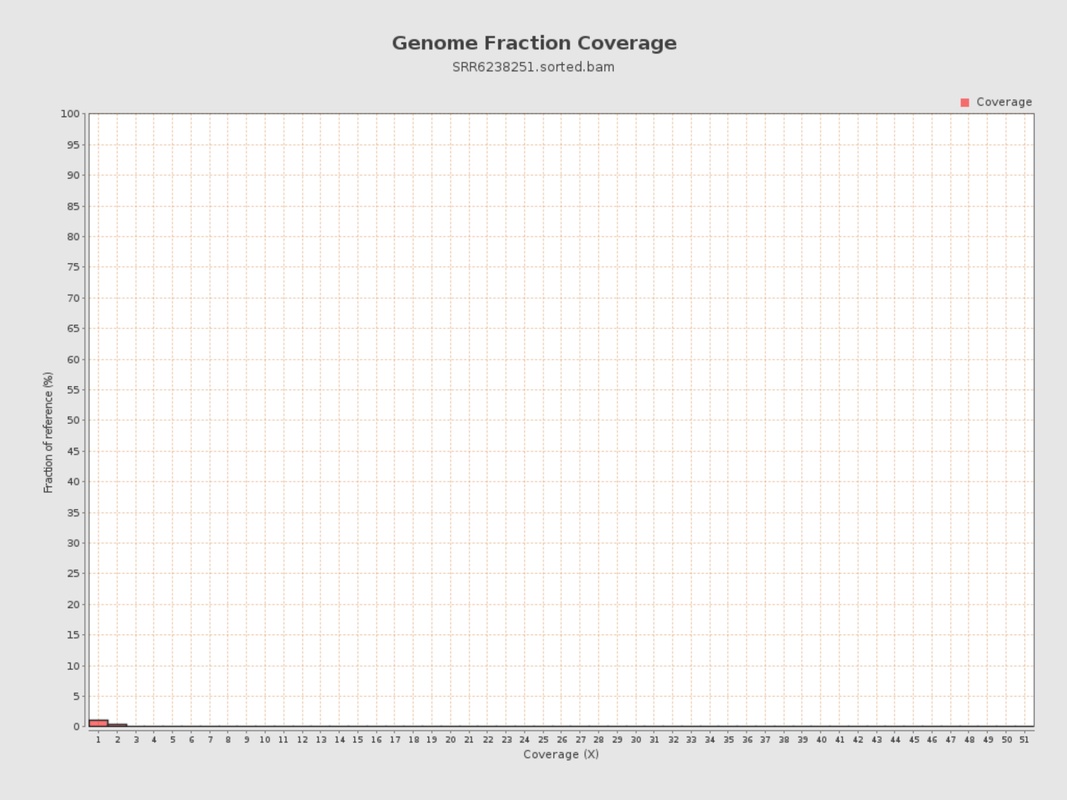
4. Results : Coverage Histogram



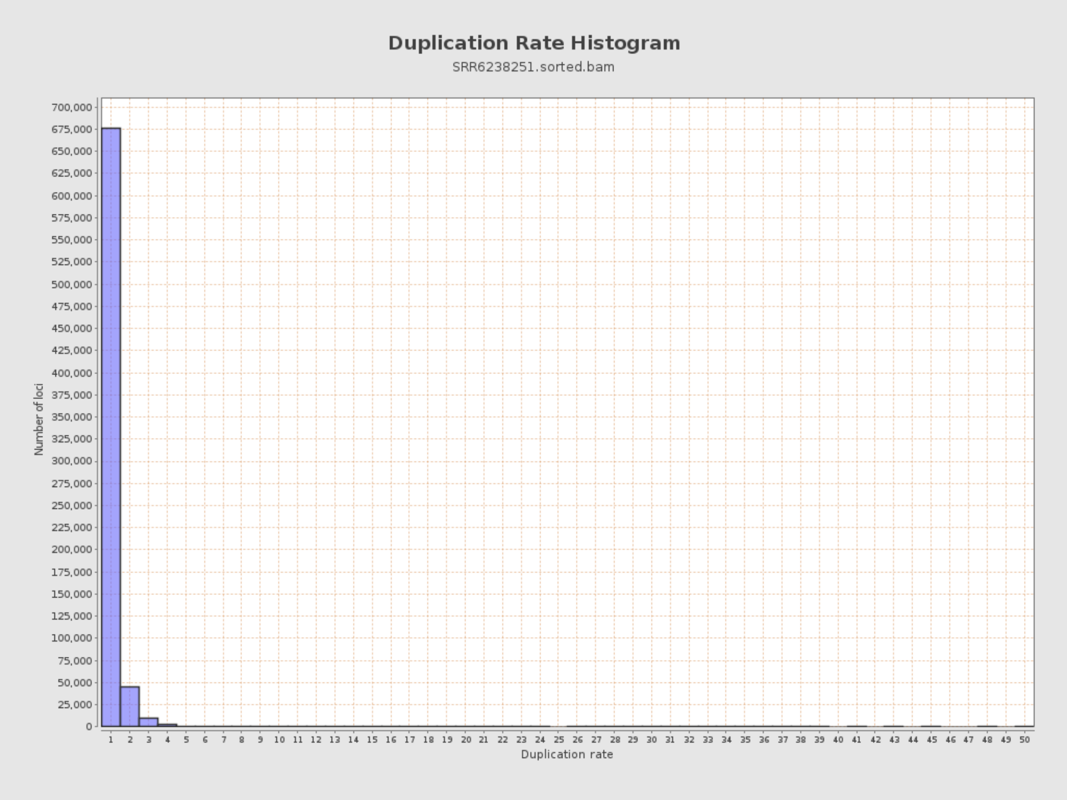
5. Results : Coverage Histogram (0-50X)



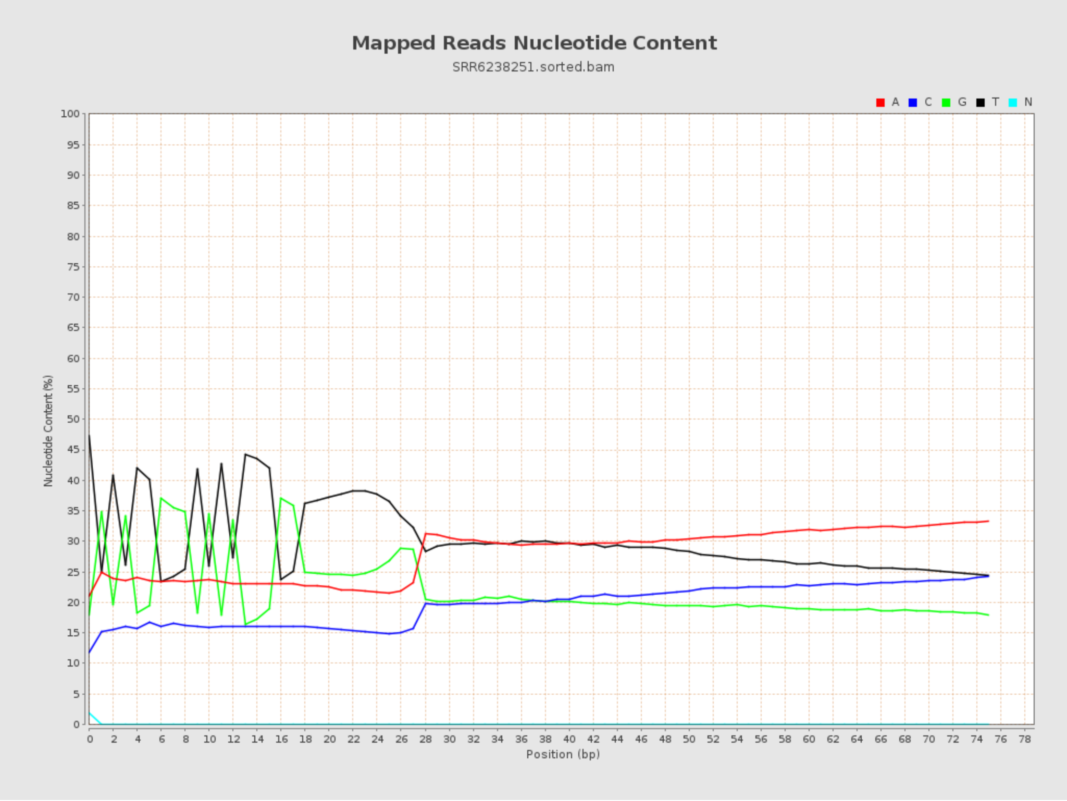
6. Results : Genome Fraction Coverage



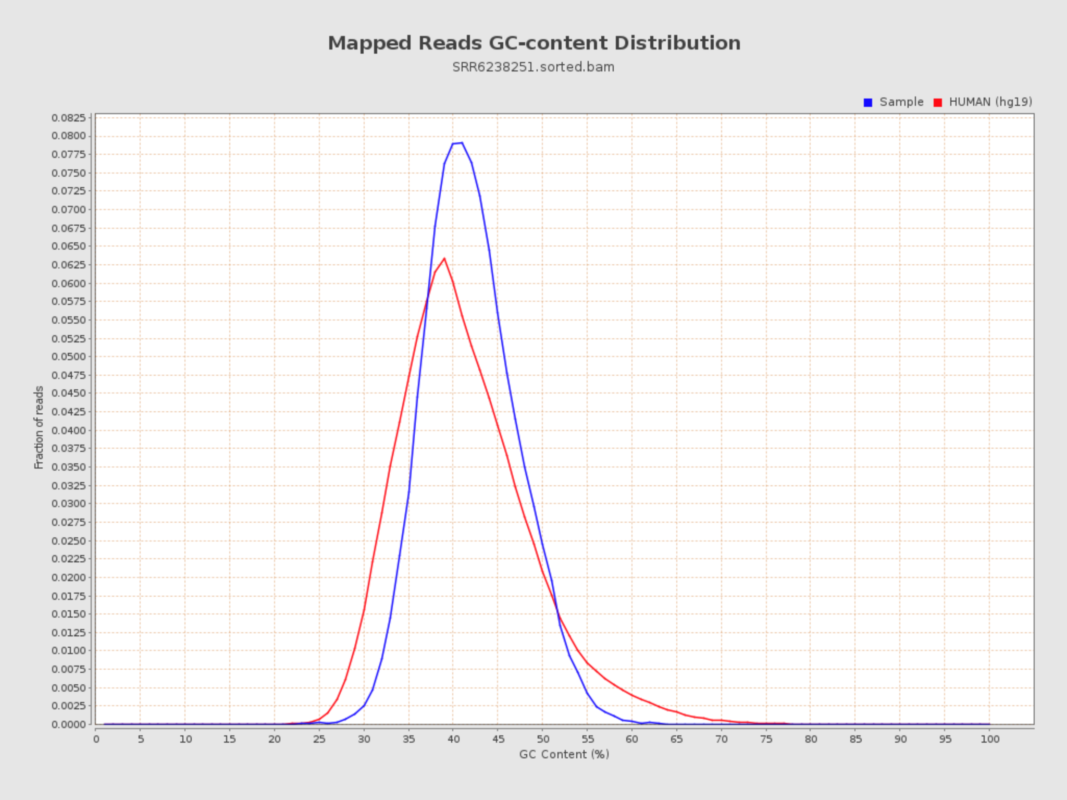
7. Results : Duplication Rate Histogram



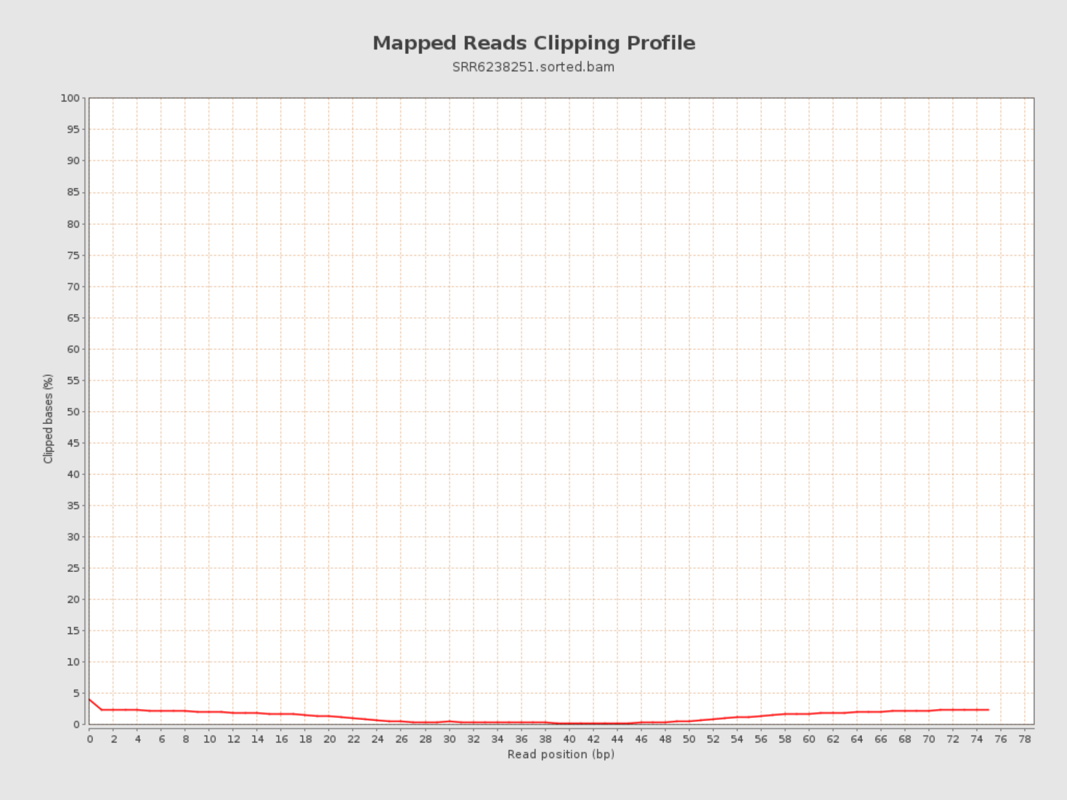
8. Results : Mapped Reads Nucleotide Content



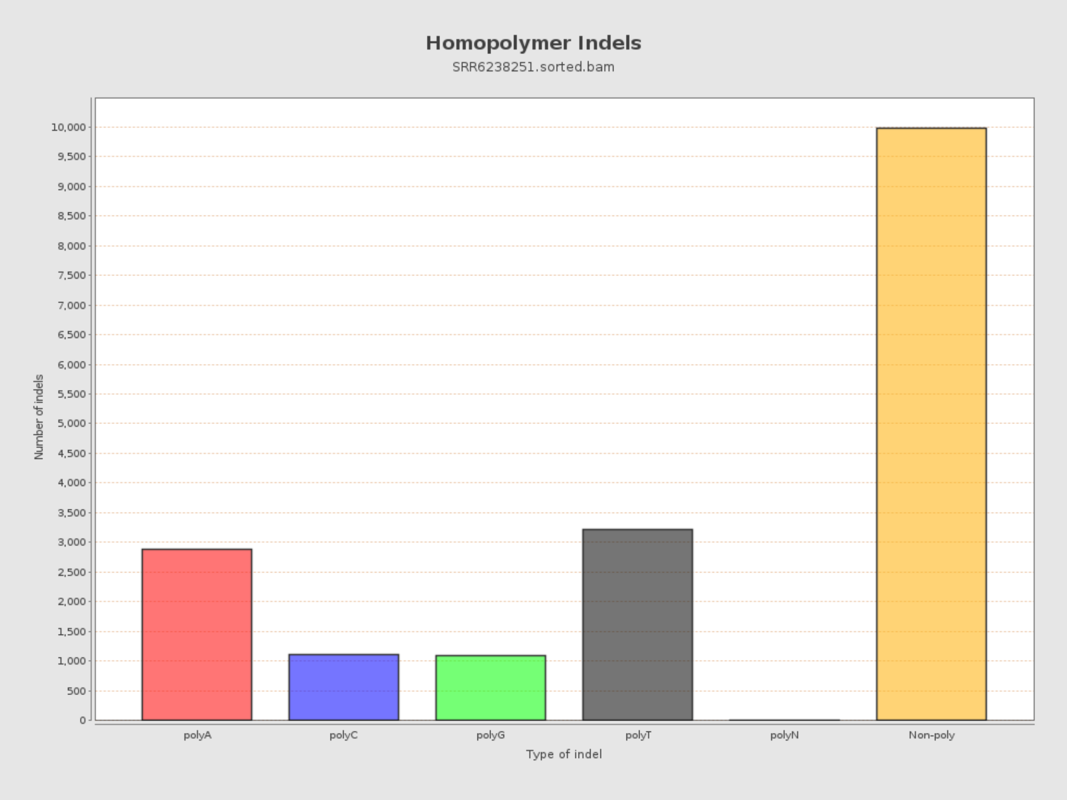
9. Results : Mapped Reads GC-content Distribution



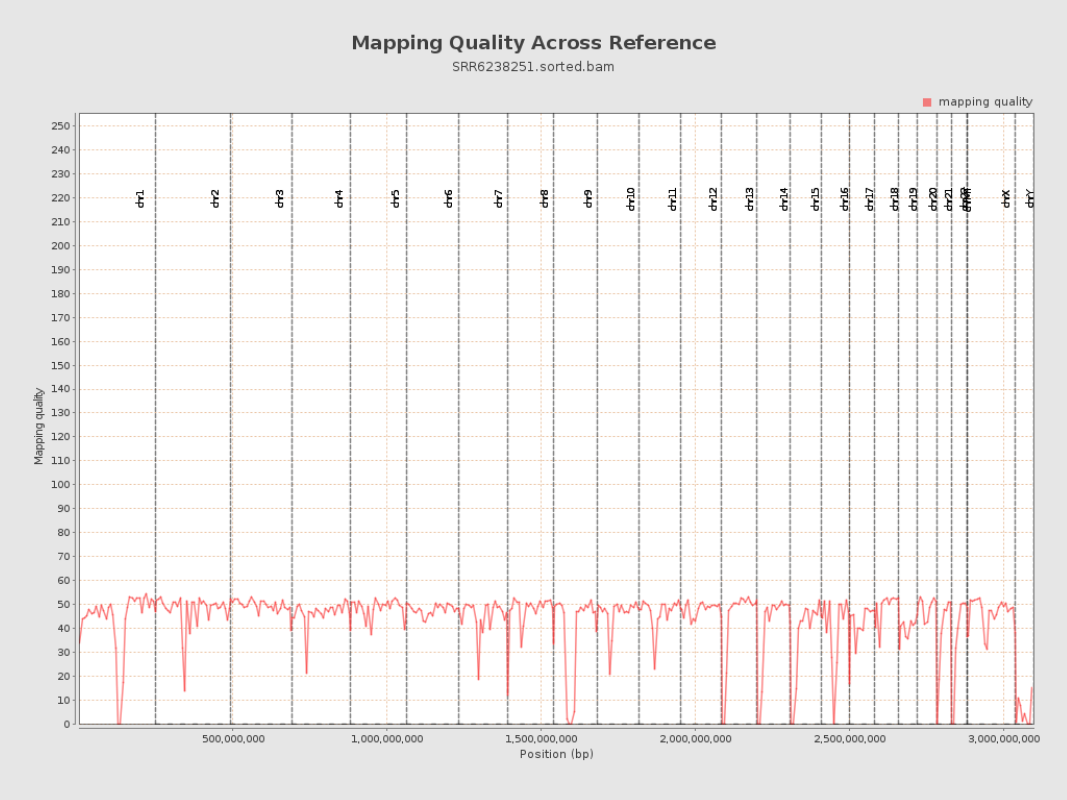
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram