Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:11:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238256.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_SRR6238256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:11:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,107,107
Mapped reads	600,603 / 54.25%
Unmapped reads	506,504 / 45.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,408 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	57,685 / 5.21%
Duplication rate	7.35%
Clipped reads	383,740 / 34.66%

2.2. ACGT Content

Number/percentage of A's	10,501,717 / 28.19%
Number/percentage of C's	7,259,809 / 19.49%
Number/percentage of T's	11,355,747 / 30.49%
Number/percentage of G's	8,121,768 / 21.8%
Number/percentage of N's	8,707 / 0.02%
GC Percentage	41.3%

2.3. Coverage

Mean	0.012

Standard Deviation	0.2007

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

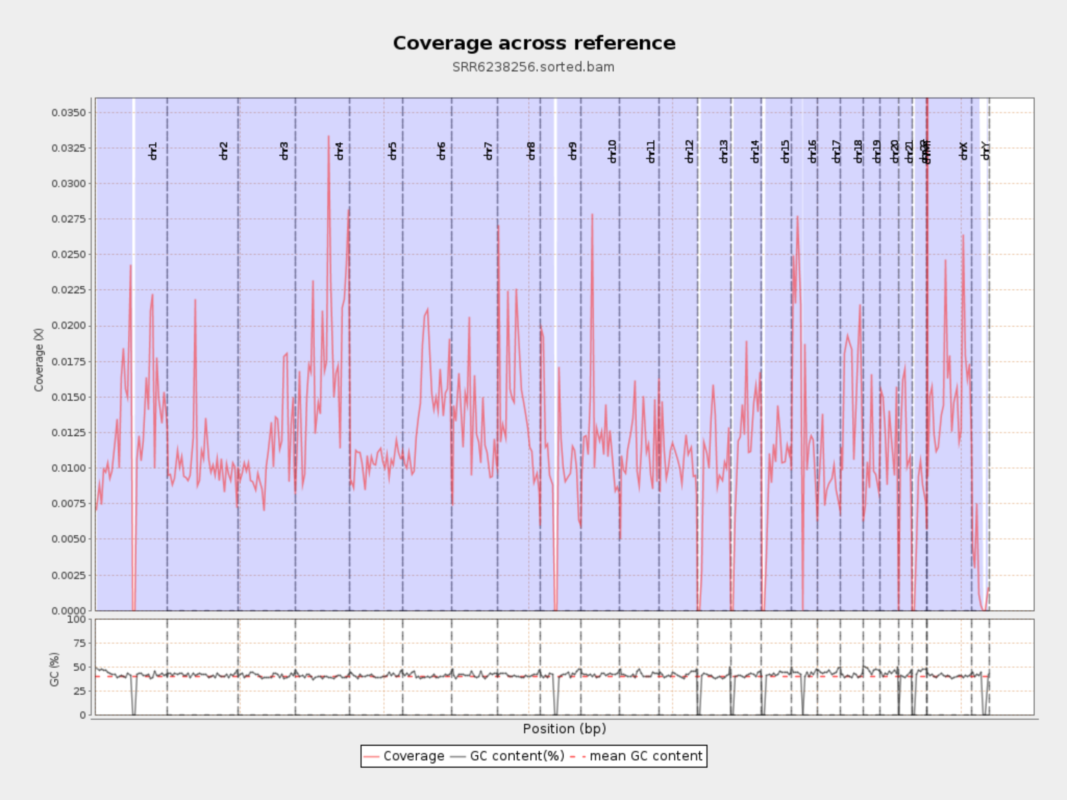
General error rate	0.99%
Mismatches	362,779
Insertions	3,066
Mapped reads with at least one insertion	0.5%
Deletions	10,028
Mapped reads with at least one deletion	1.65%
Homopolymer indels	45.17%

2.6. Chromosome stats

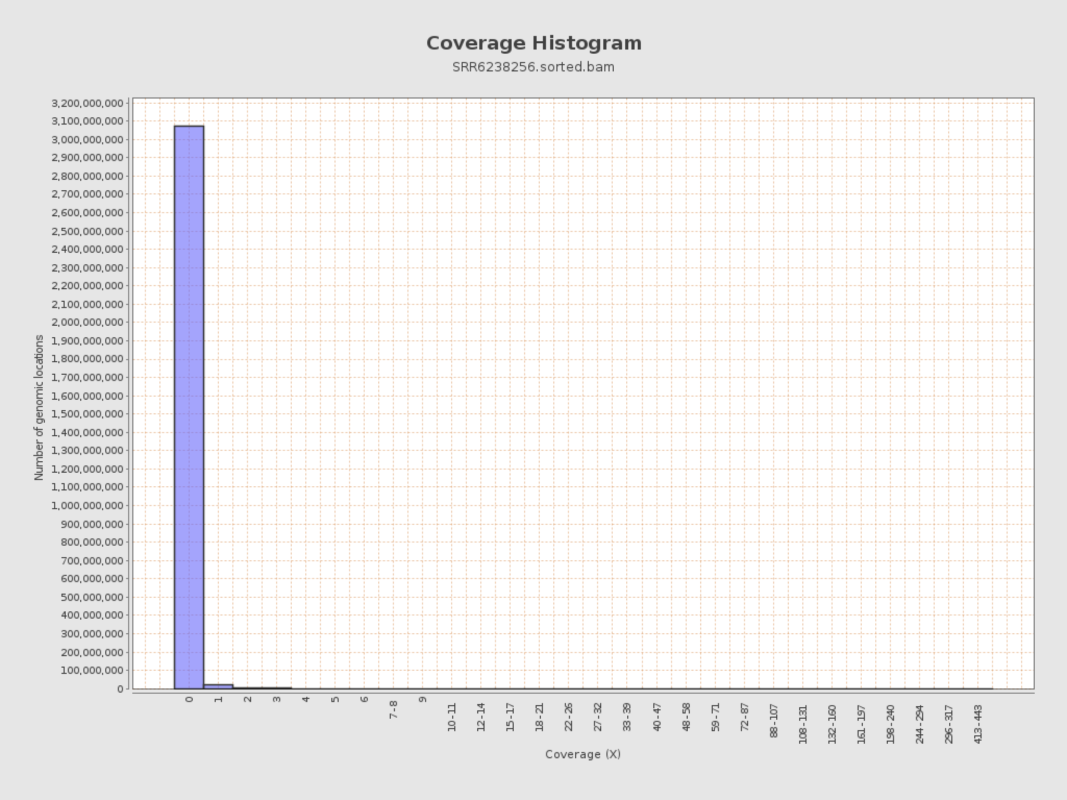
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3127323	0.0125	0.268
chr2	243199373	2516724	0.0103	0.2058
chr3	198022430	2196914	0.0111	0.1517
chr4	191154276	3342926	0.0175	0.2677
chr5	180915260	1884786	0.0104	0.1516
chr6	171115067	2476817	0.0145	0.1913
chr7	159138663	2041739	0.0128	0.2013

chr8	146364022	2164298	0.0148	0.2034
chr9	141213431	1458572	0.0103	0.1746
chr10	135534747	1671727	0.0123	0.2063
chr11	135006516	1522614	0.0113	0.1628
chr12	133851895	1427445	0.0107	0.148
chr13	115169878	1088630	0.0095	0.1499
chr14	107349540	1252047	0.0117	0.2334
chr15	102531392	933486	0.0091	0.2498
chr16	90354753	1352464	0.015	0.1838
chr17	81195210	749969	0.0092	0.1457
chr18	78077248	1254708	0.0161	0.2886
chr19	59128983	588431	0.01	0.218
chr20	63025520	792828	0.0126	0.1601
chr21	48129895	552095	0.0115	0.1553
chr22	51304566	326850	0.0064	0.1076
chrMT	16571	22552	1.3609	2.0671
chrX	155270560	2389556	0.0154	0.1924
chrY	59373566	128940	0.0022	0.0982

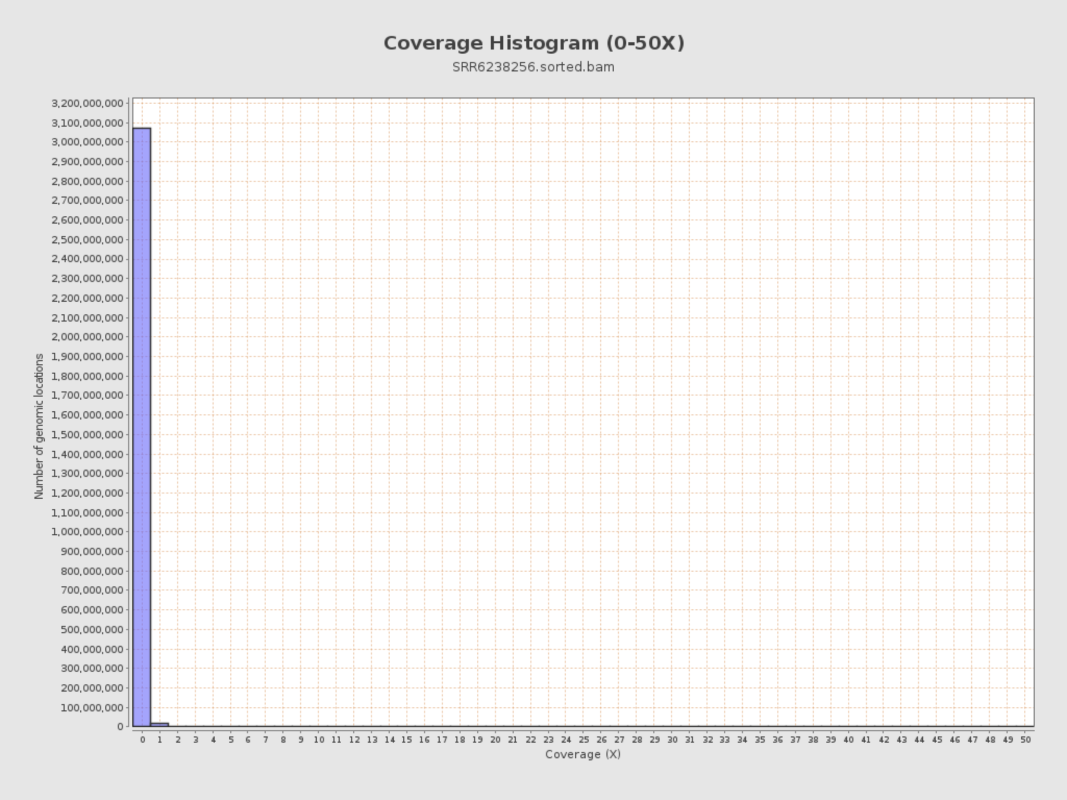
3. Results : Coverage across reference



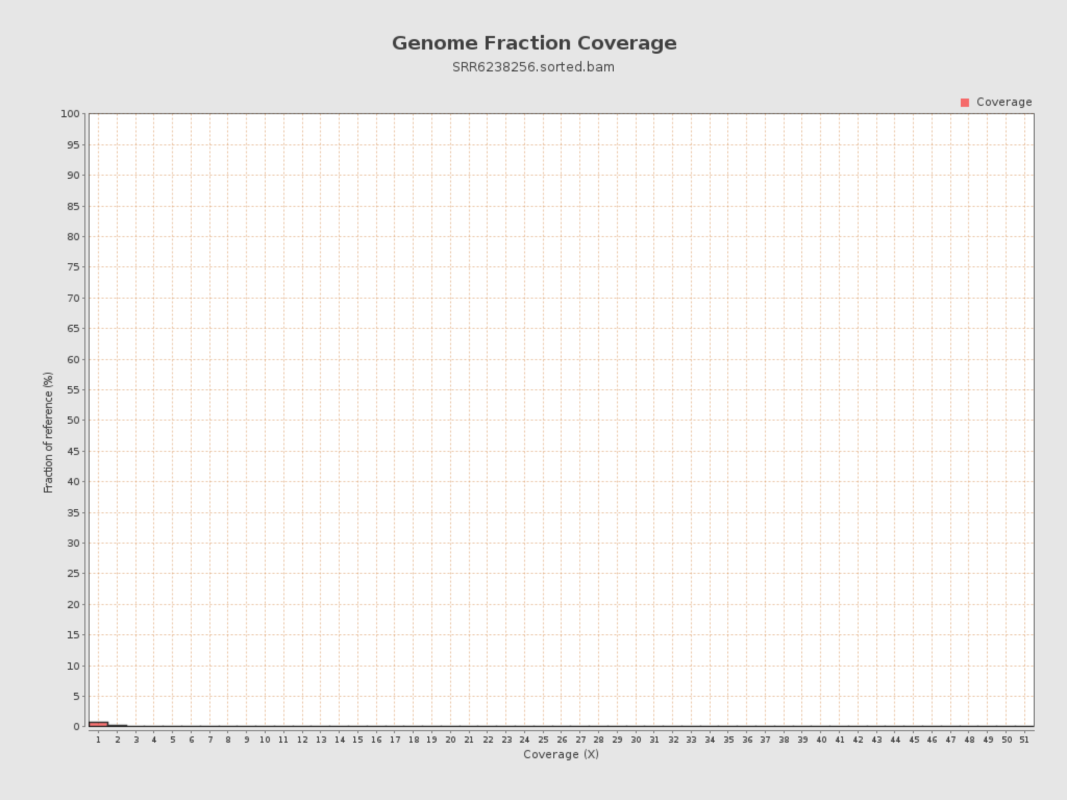
4. Results : Coverage Histogram



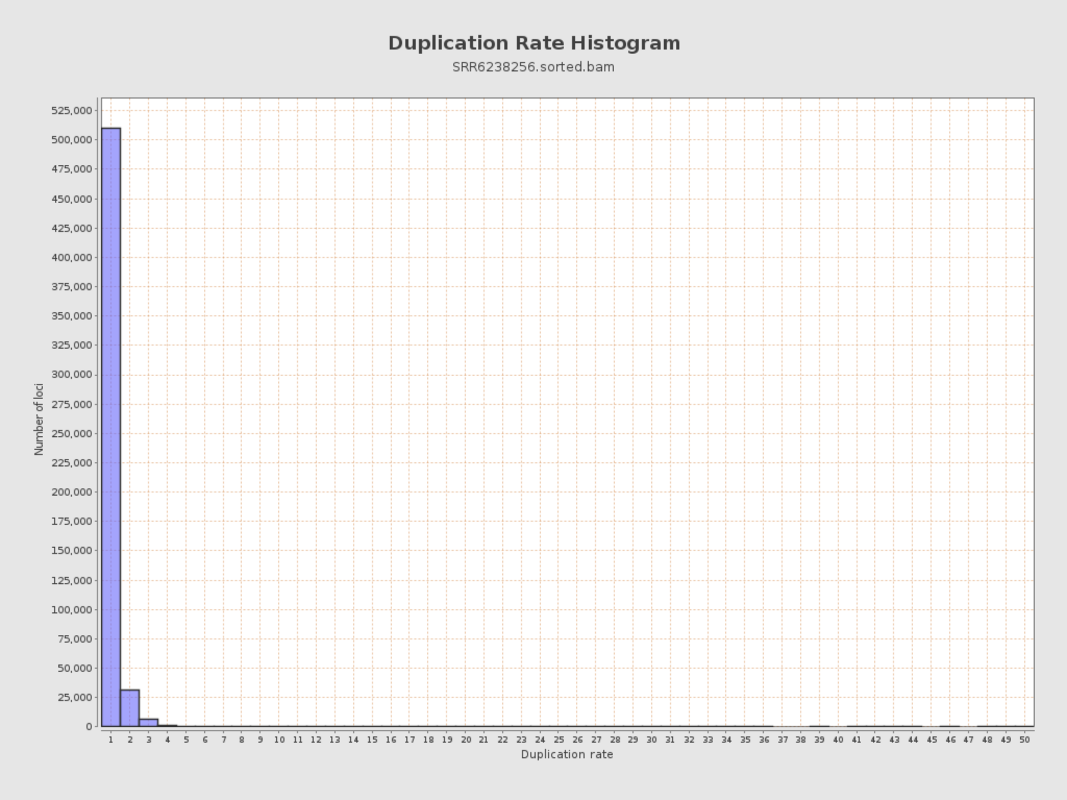
5. Results : Coverage Histogram (0-50X)



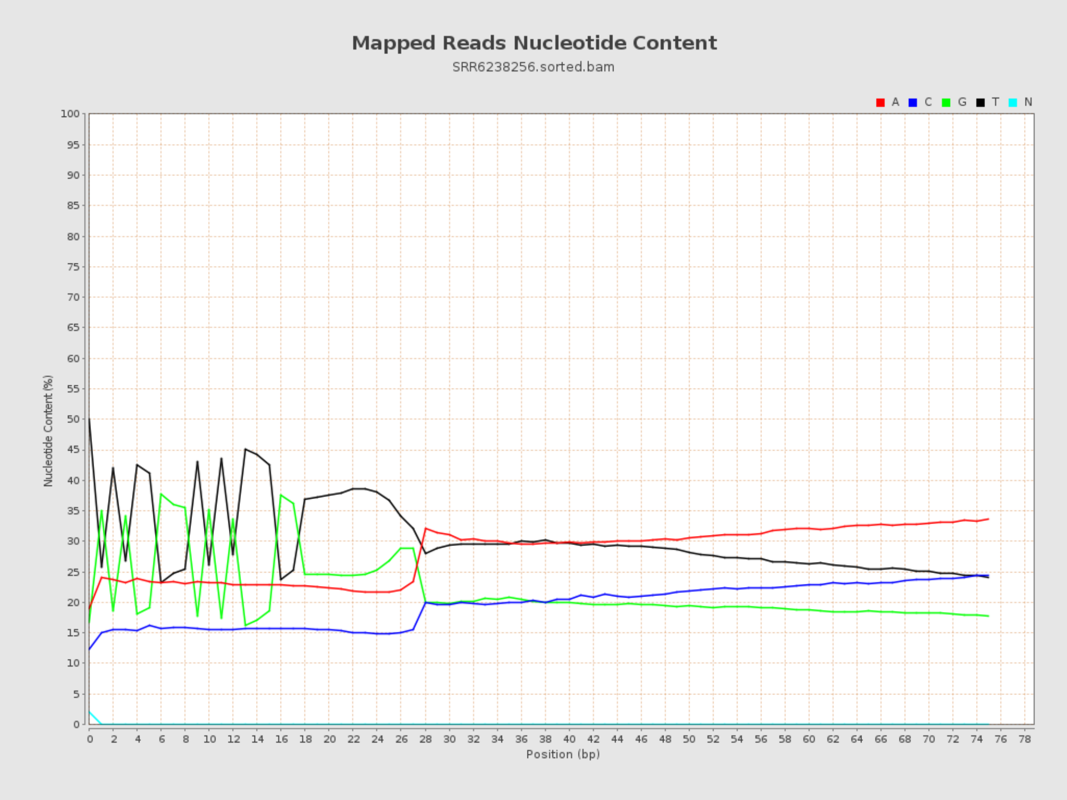
6. Results : Genome Fraction Coverage



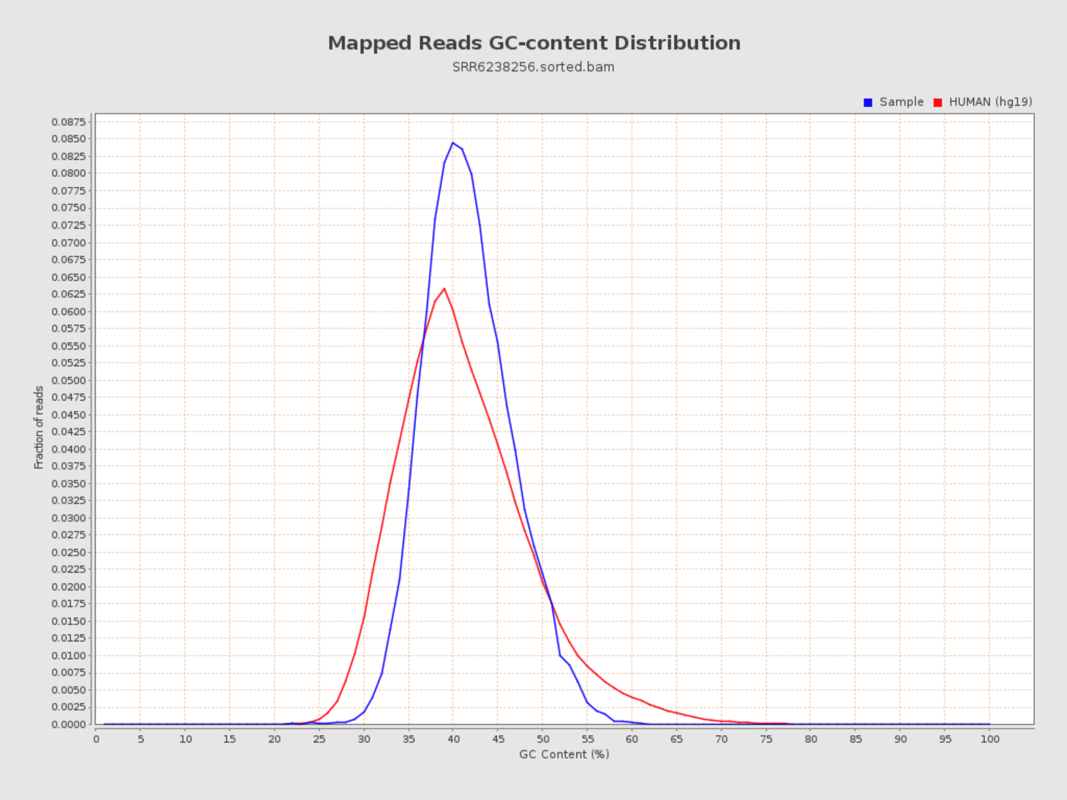
7. Results : Duplication Rate Histogram



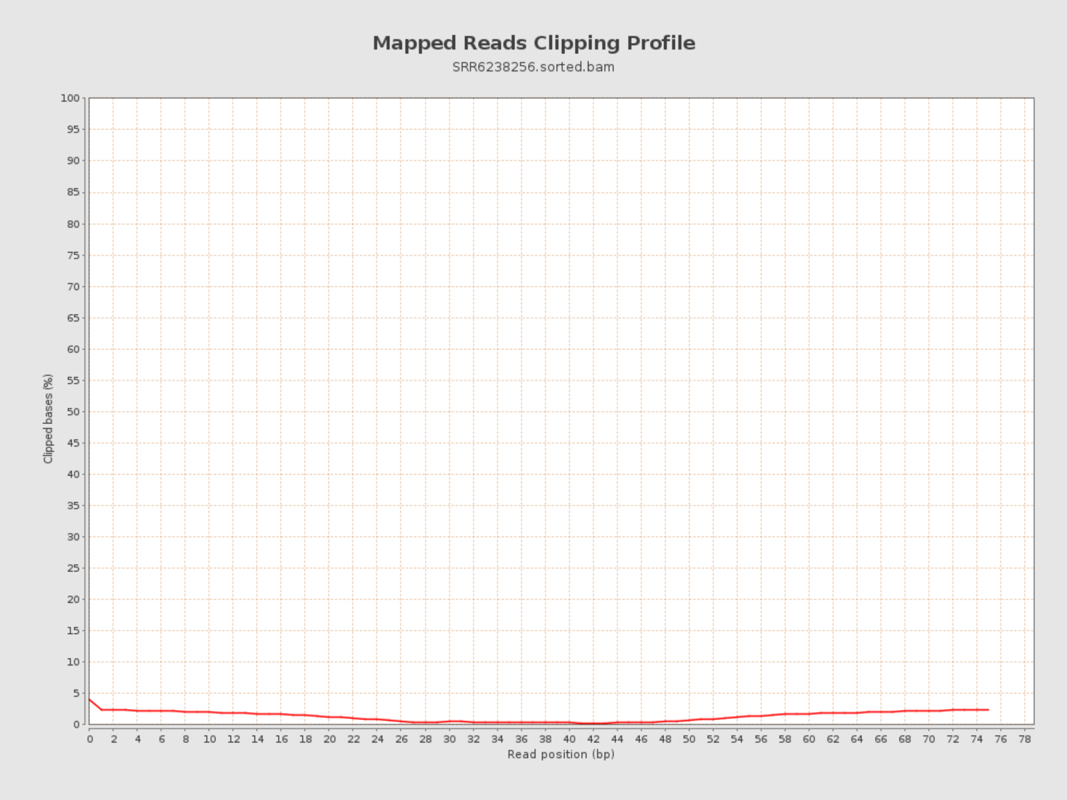
8. Results : Mapped Reads Nucleotide Content



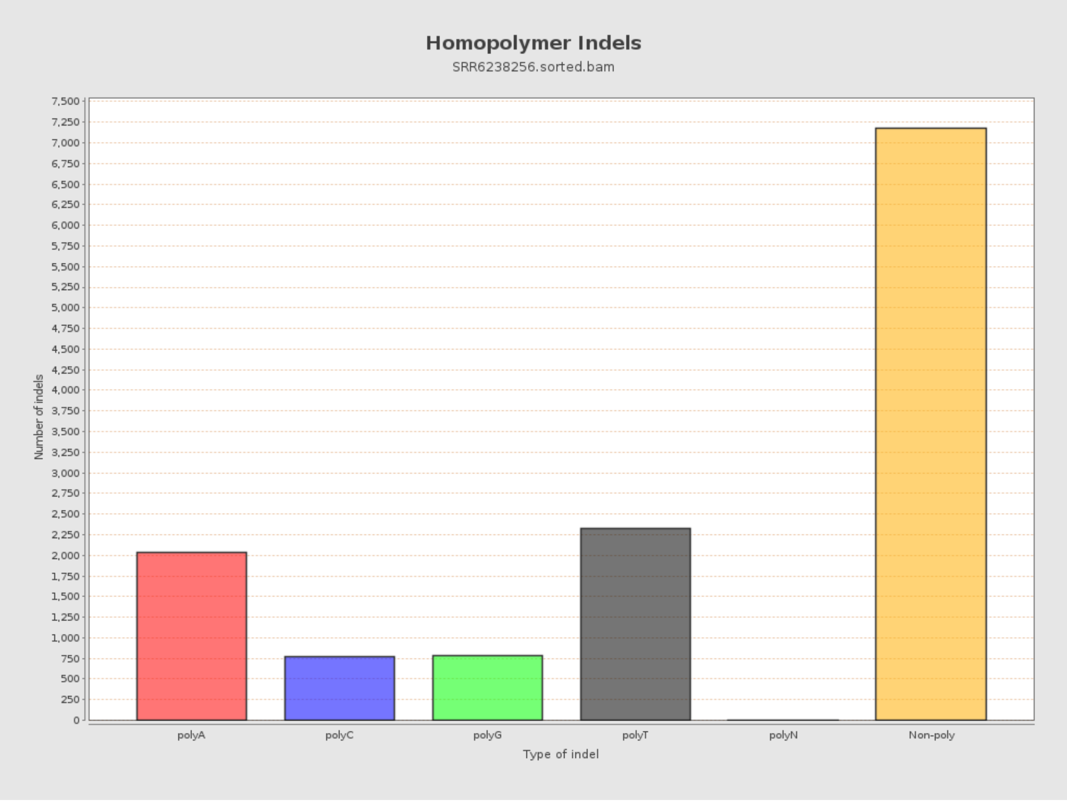
9. Results : Mapped Reads GC-content Distribution



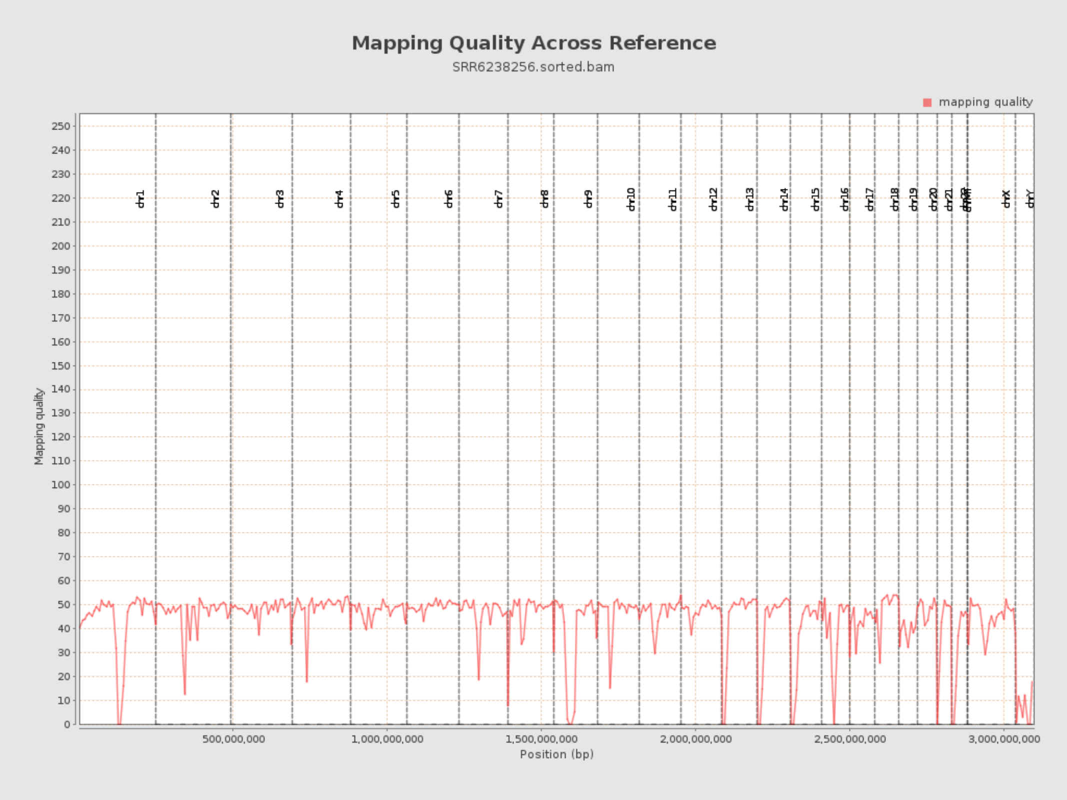
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram