

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:31:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238241.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_SRR6238241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:31:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,243,082
Mapped reads	795,215 / 63.97%
Unmapped reads	447,867 / 36.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,639 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	92,769 / 7.46%
Duplication rate	8.36%
Clipped reads	490,226 / 39.44%

2.2. ACGT Content

Number/percentage of A's	13,928,757 / 28.04%
Number/percentage of C's	9,978,746 / 20.09%
Number/percentage of T's	14,797,165 / 29.79%
Number/percentage of G's	10,960,263 / 22.06%
Number/percentage of N's	11,045 / 0.02%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.303
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2.4. Mapping Quality

Mean Mapping Quality	44.15
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2.5. Mismatches and indels

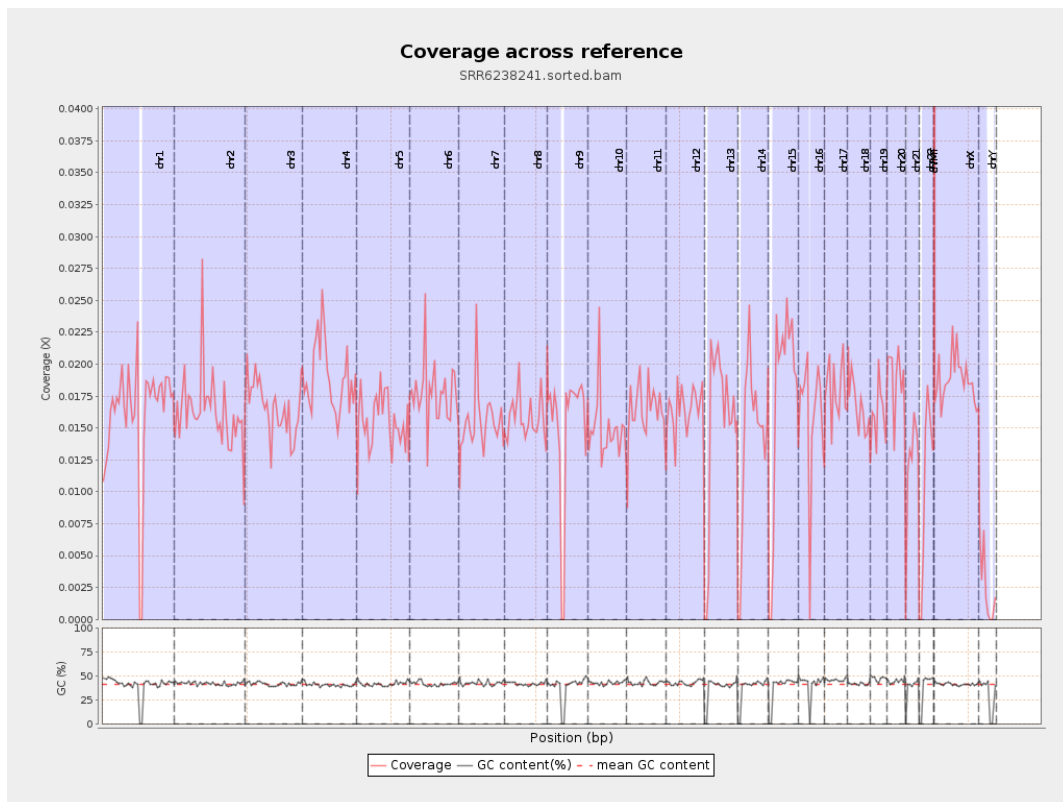
General error rate	0.88%
Mismatches	432,031
Insertions	4,122
Mapped reads with at least one insertion	0.51%
Deletions	11,895
Mapped reads with at least one deletion	1.48%
Homopolymer indels	45.45%

2.6. Chromosome stats

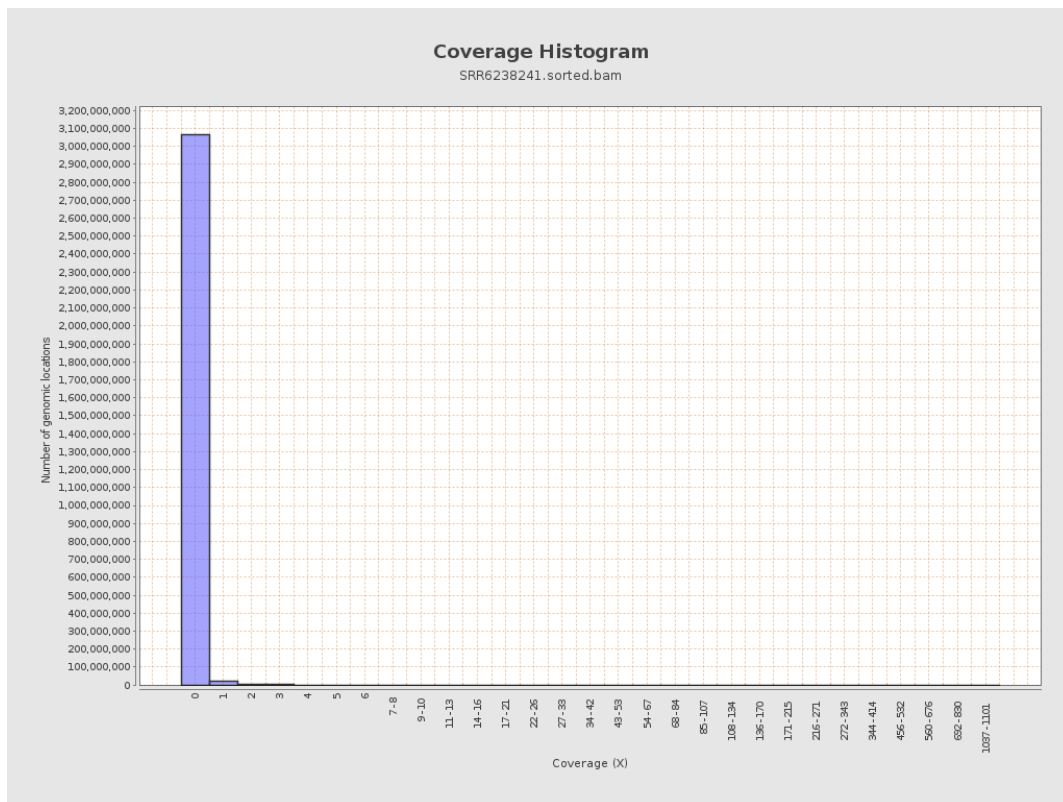
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3997997	0.016	0.3528
chr2	243199373	3968413	0.0163	0.4184
chr3	198022430	3279718	0.0166	0.2198
chr4	191154276	3621470	0.0189	0.2562
chr5	180915260	2831013	0.0156	0.2186
chr6	171115067	3033719	0.0177	0.2979
chr7	159138663	2461580	0.0155	0.2495

chr8	146364022	2305214	0.0157	0.2436
chr9	141213431	2124505	0.015	0.2145
chr10	135534747	2020653	0.0149	0.222
chr11	135006516	2231836	0.0165	0.2215
chr12	133851895	2203352	0.0165	0.2297
chr13	115169878	1753438	0.0152	0.2648
chr14	107349540	1529693	0.0142	0.5071
chr15	102531392	1776217	0.0173	0.6663
chr16	90354753	1420772	0.0157	0.205
chr17	81195210	1470645	0.0181	0.2351
chr18	78077248	1303163	0.0167	0.266
chr19	59128983	954998	0.0162	0.2555
chr20	63025520	1188505	0.0189	0.2196
chr21	48129895	589788	0.0123	0.1767
chr22	51304566	556854	0.0109	0.1644
chrMT	16571	6265	0.3781	1.1989
chrX	155270560	2919012	0.0188	0.3009
chrY	59373566	146293	0.0025	0.0775

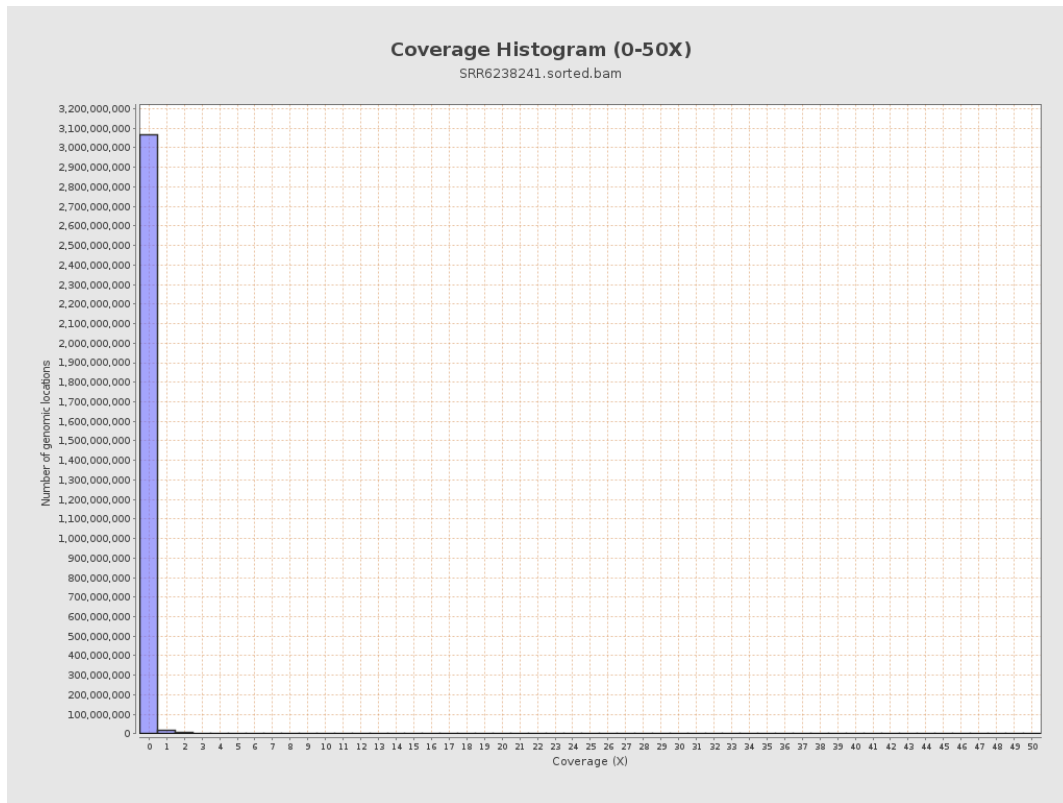
3. Results : Coverage across reference



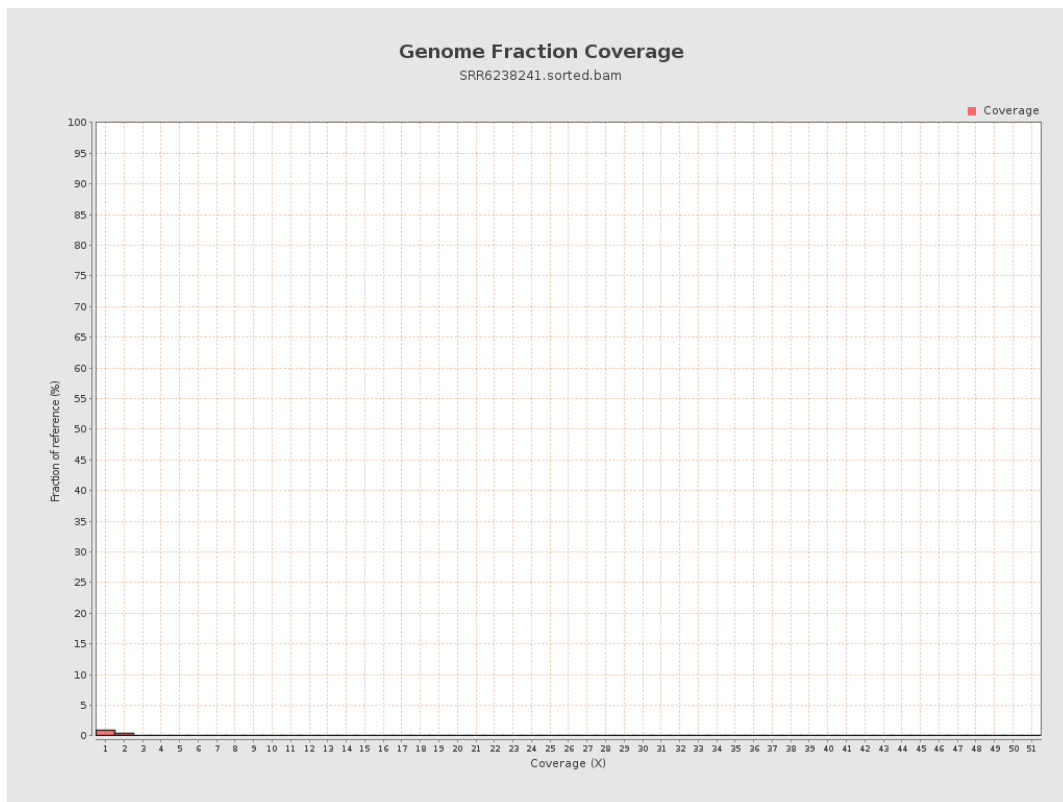
4. Results : Coverage Histogram



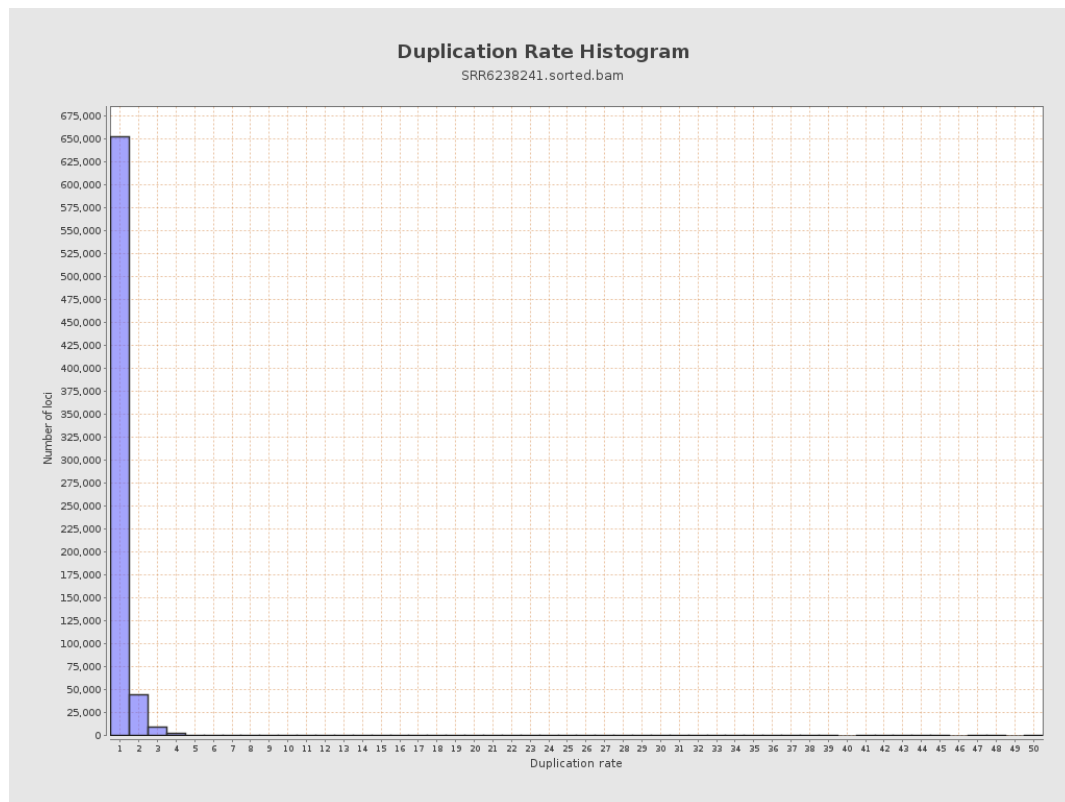
5. Results : Coverage Histogram (0-50X)



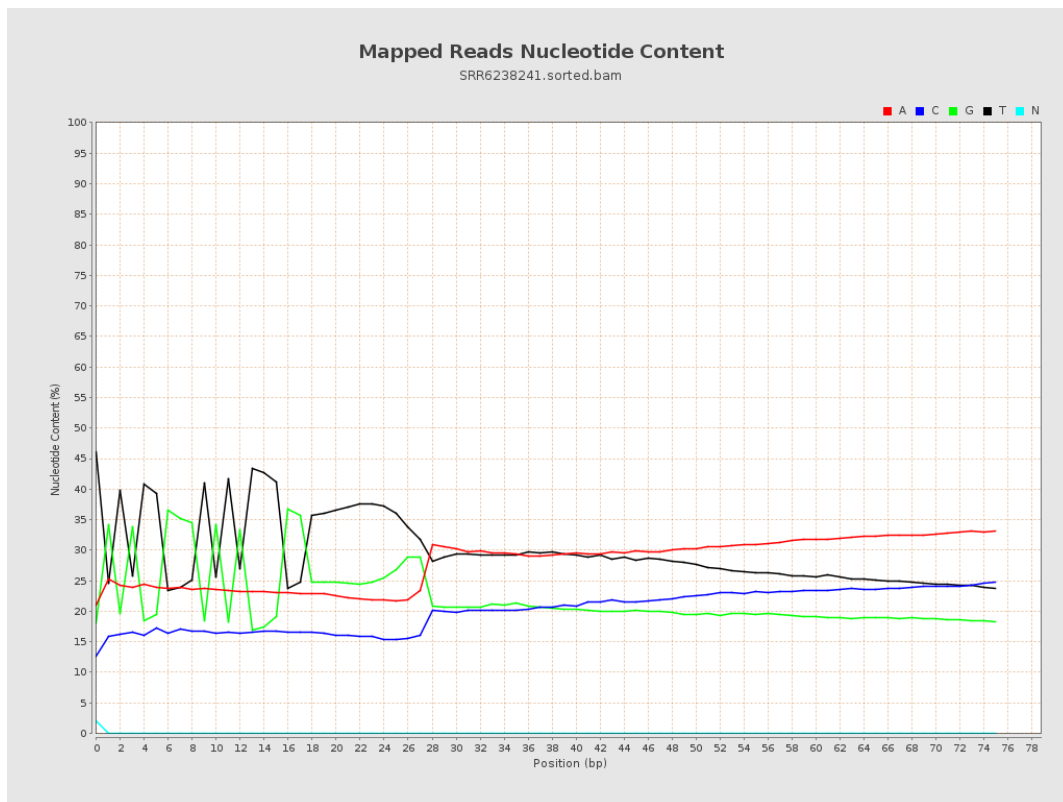
6. Results : Genome Fraction Coverage



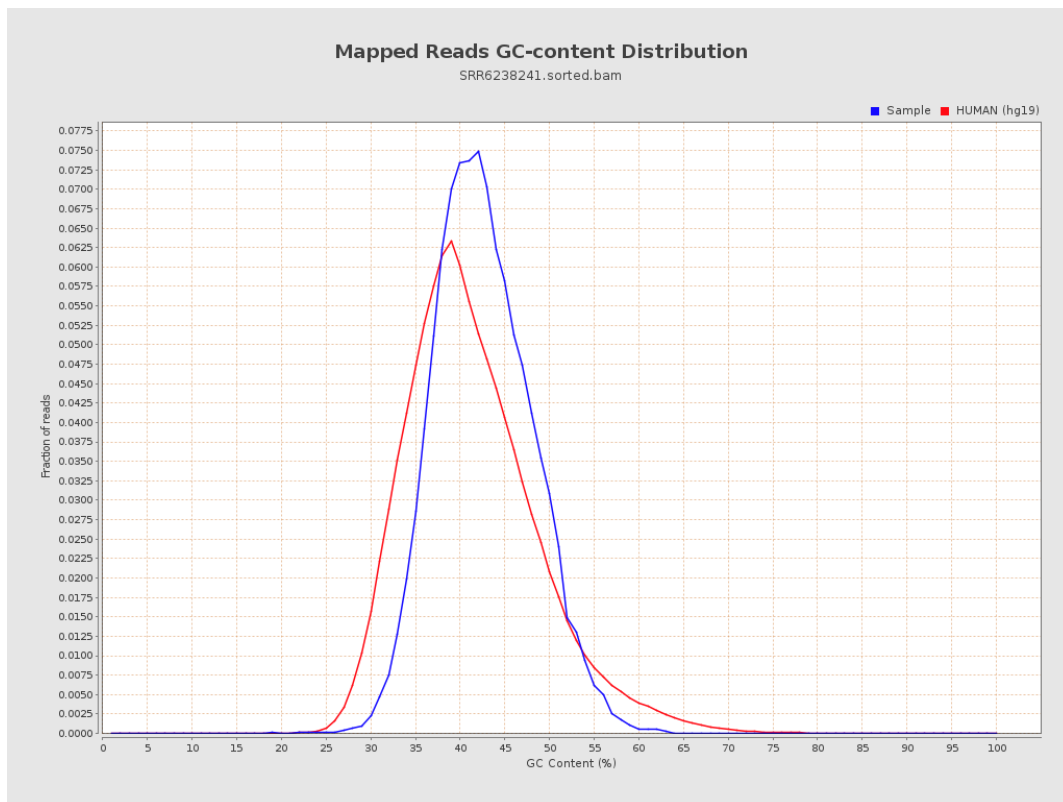
7. Results : Duplication Rate Histogram



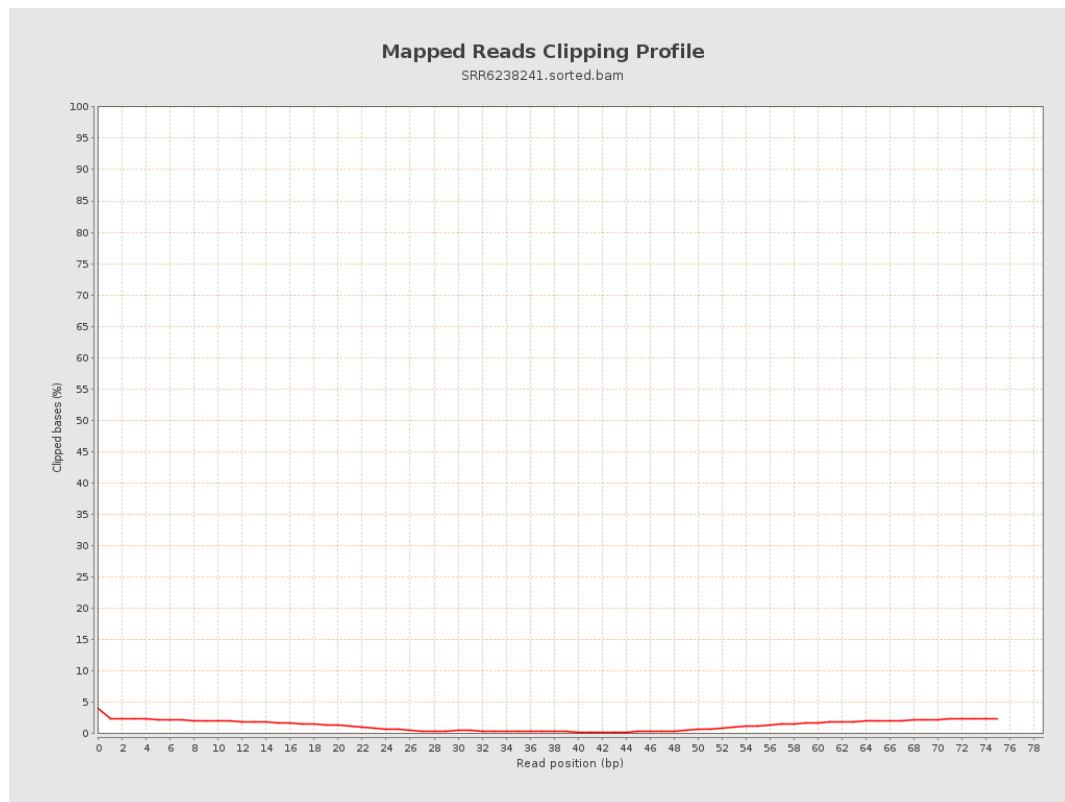
8. Results : Mapped Reads Nucleotide Content



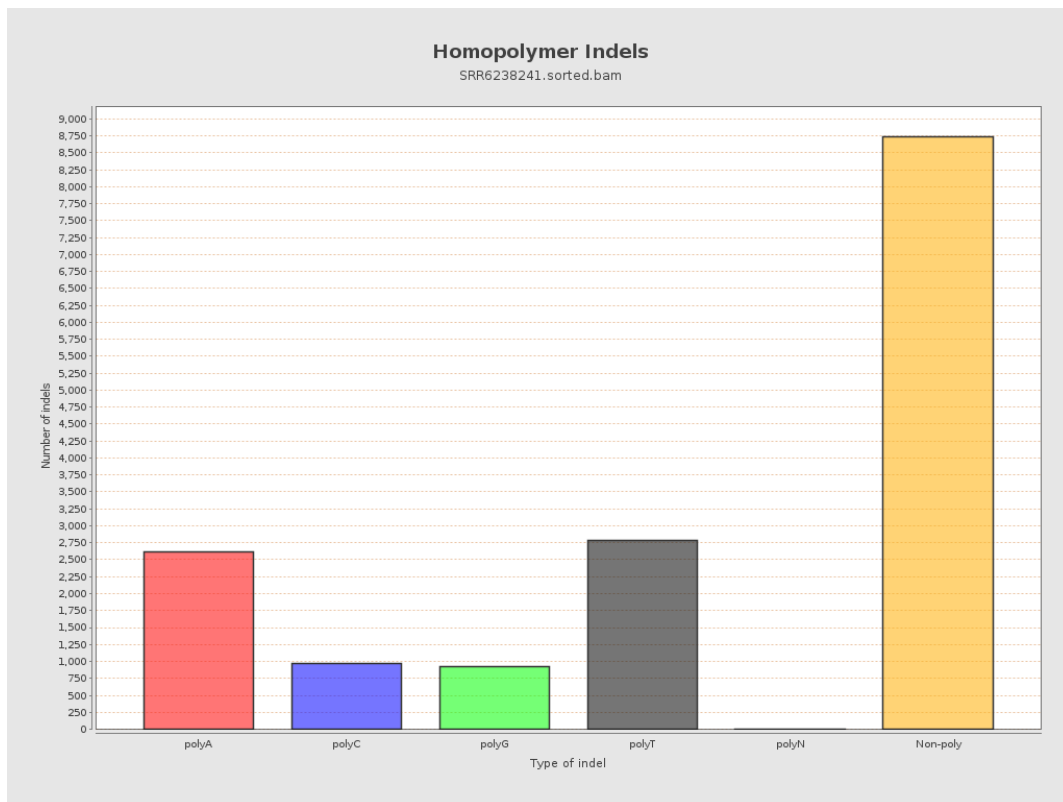
9. Results : Mapped Reads GC-content Distribution



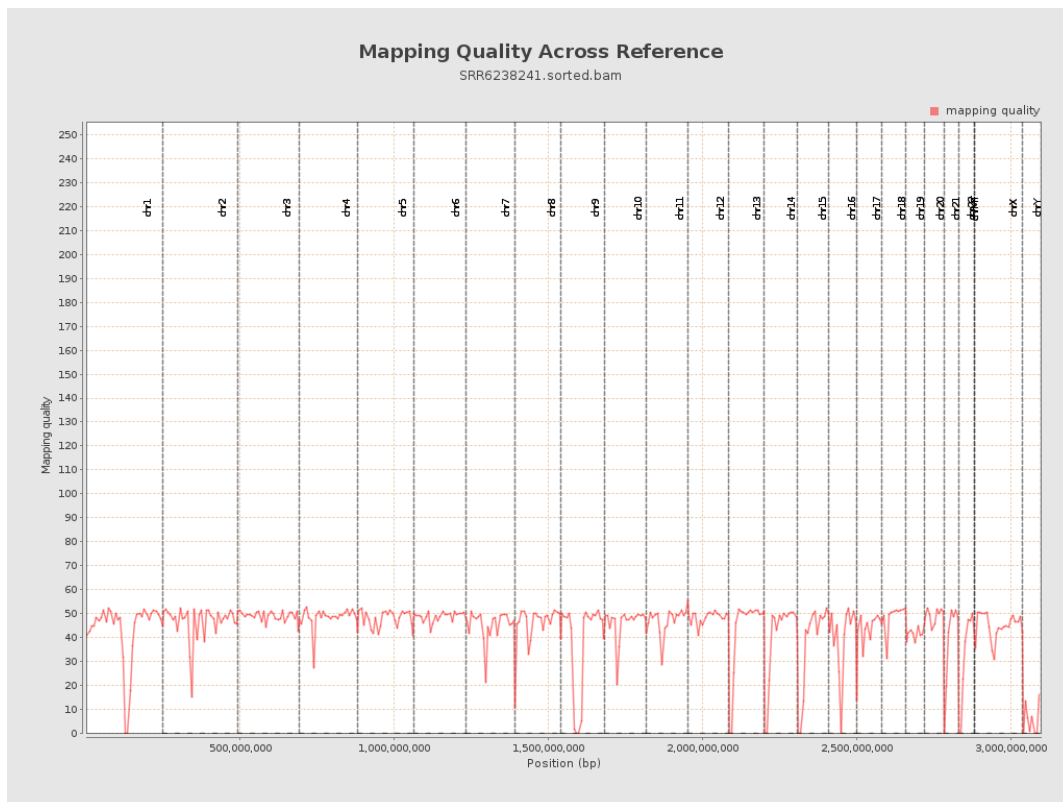
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

