

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:23:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237250.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_SRR6237250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:23:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,845,576
Mapped reads	1,635,213 / 57.47%
Unmapped reads	1,210,363 / 42.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,842 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	439,241 / 15.44%
Duplication rate	16.6%
Clipped reads	995,733 / 34.99%

2.2. ACGT Content

Number/percentage of A's	28,021,544 / 27.5%
Number/percentage of C's	18,117,402 / 17.78%
Number/percentage of T's	33,184,424 / 32.56%
Number/percentage of G's	22,543,317 / 22.12%
Number/percentage of N's	35,921 / 0.04%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.4885
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2.4. Mapping Quality

Mean Mapping Quality	44.25
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2.5. Mismatches and indels

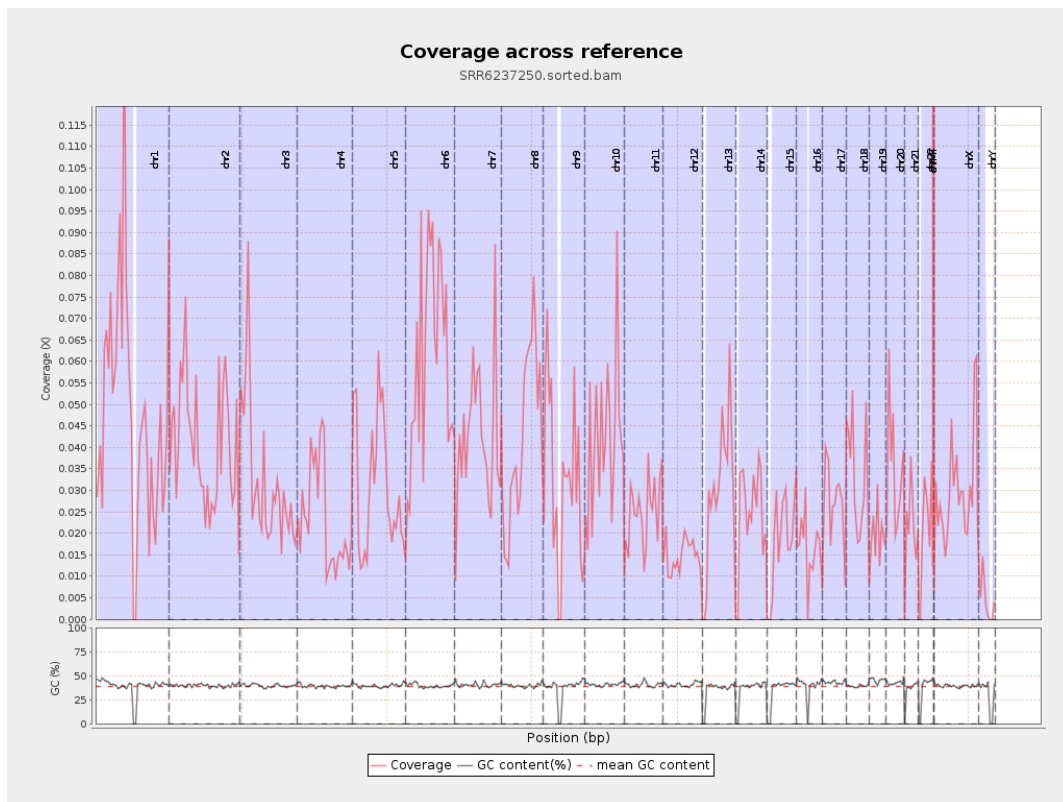
General error rate	0.89%
Mismatches	893,089
Insertions	8,097
Mapped reads with at least one insertion	0.49%
Deletions	32,177
Mapped reads with at least one deletion	1.94%
Homopolymer indels	44.65%

2.6. Chromosome stats

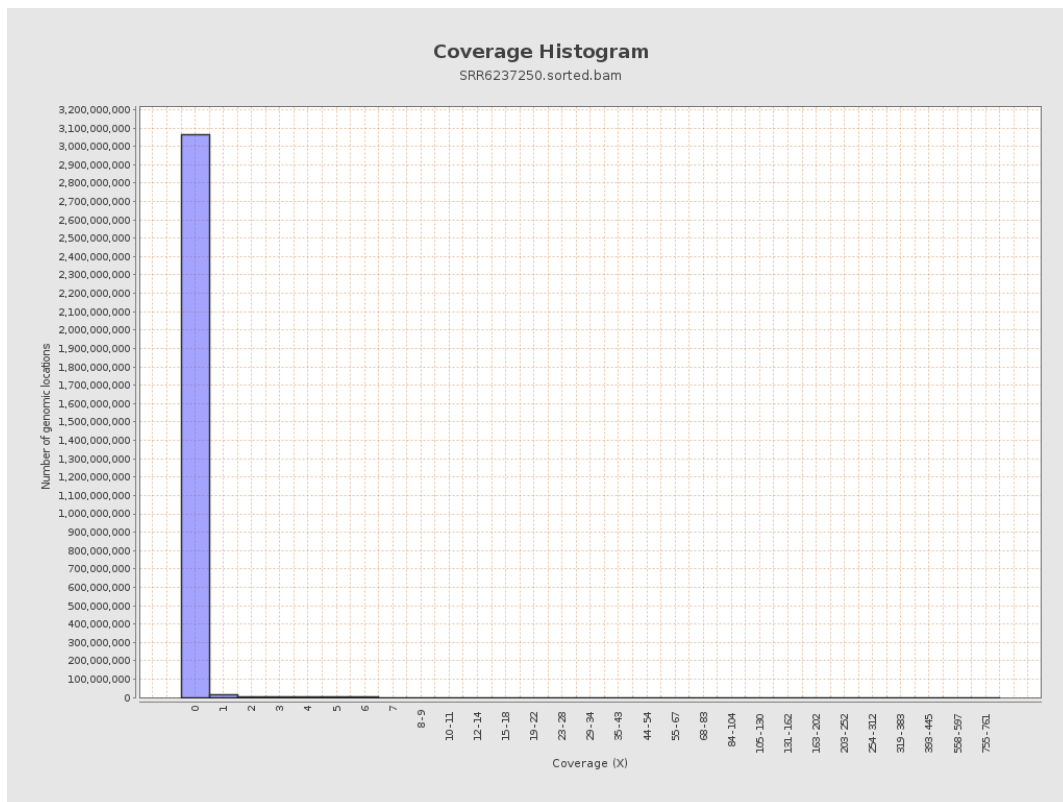
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11877804	0.0477	0.6145
chr2	243199373	9856593	0.0405	0.6265
chr3	198022430	6430195	0.0325	0.4296
chr4	191154276	4475943	0.0234	0.4016
chr5	180915260	5493595	0.0304	0.4082
chr6	171115067	10252227	0.0599	0.7483
chr7	159138663	6835046	0.043	0.5206

chr8	146364022	6183761	0.0422	0.5105
chr9	141213431	4646875	0.0329	0.464
chr10	135534747	5742945	0.0424	0.5488
chr11	135006516	3390022	0.0251	0.3749
chr12	133851895	2000583	0.0149	0.2799
chr13	115169878	3441935	0.0299	0.4355
chr14	107349540	2605691	0.0243	0.4251
chr15	102531392	1826385	0.0178	0.394
chr16	90354753	1497570	0.0166	0.2963
chr17	81195210	2134941	0.0263	0.3691
chr18	78077248	2607417	0.0334	0.5593
chr19	59128983	1149373	0.0194	0.3607
chr20	63025520	2211835	0.0351	0.433
chr21	48129895	1006093	0.0209	0.3365
chr22	51304566	1045587	0.0204	0.3435
chrMT	16571	376458	22.7179	16.4832
chrX	155270560	4613054	0.0297	0.4179
chrY	59373566	255144	0.0043	0.1633

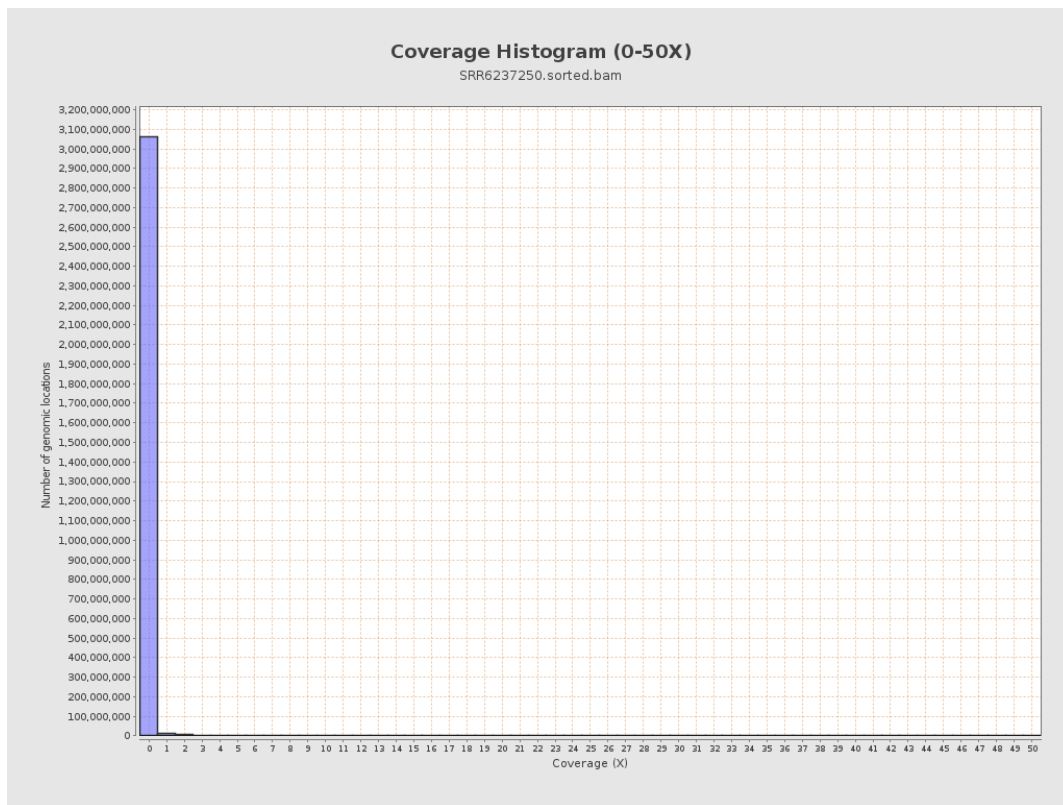
3. Results : Coverage across reference



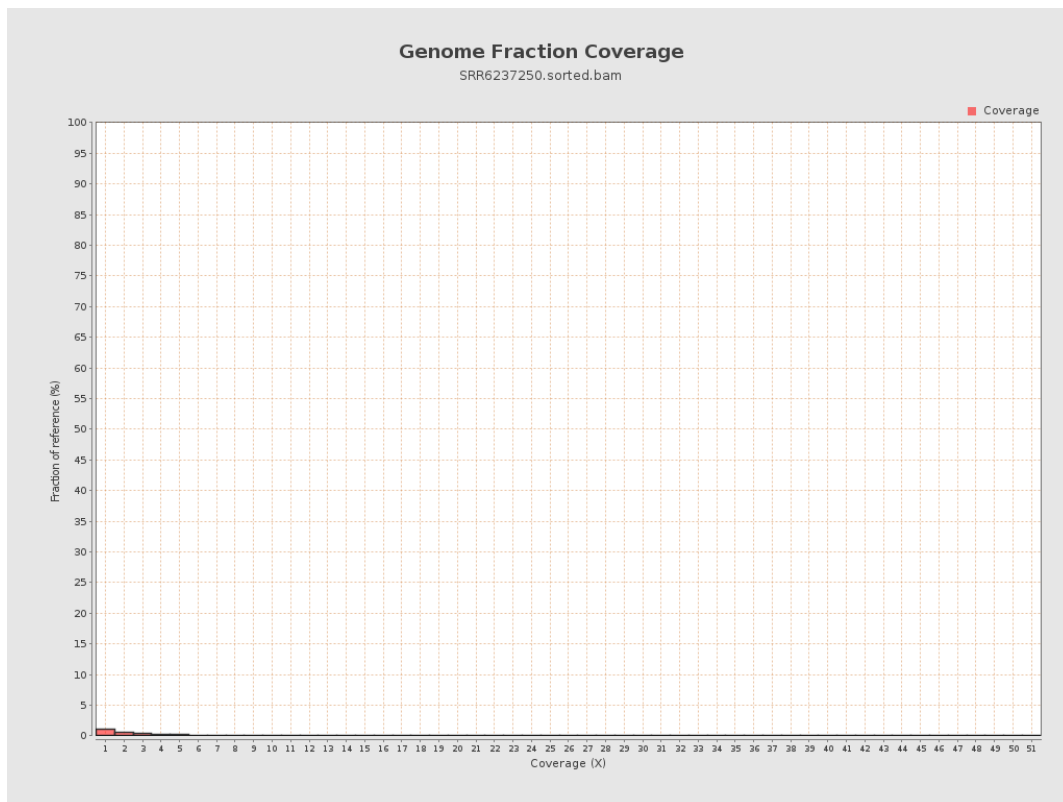
4. Results : Coverage Histogram



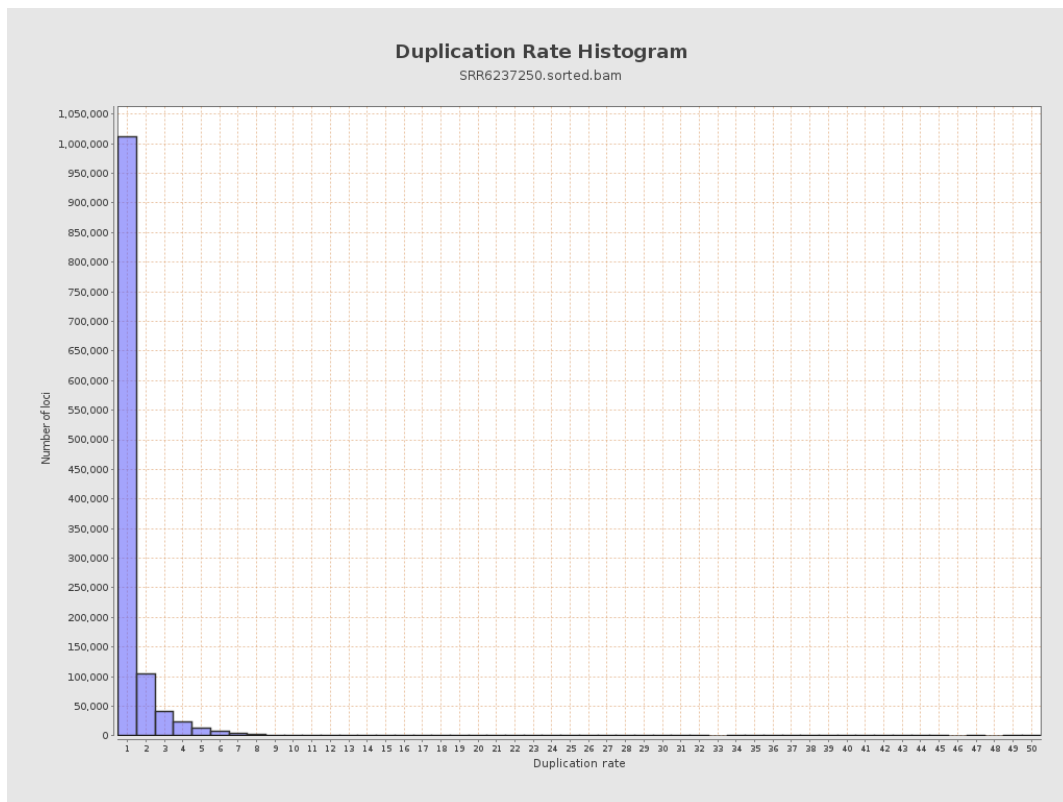
5. Results : Coverage Histogram (0-50X)



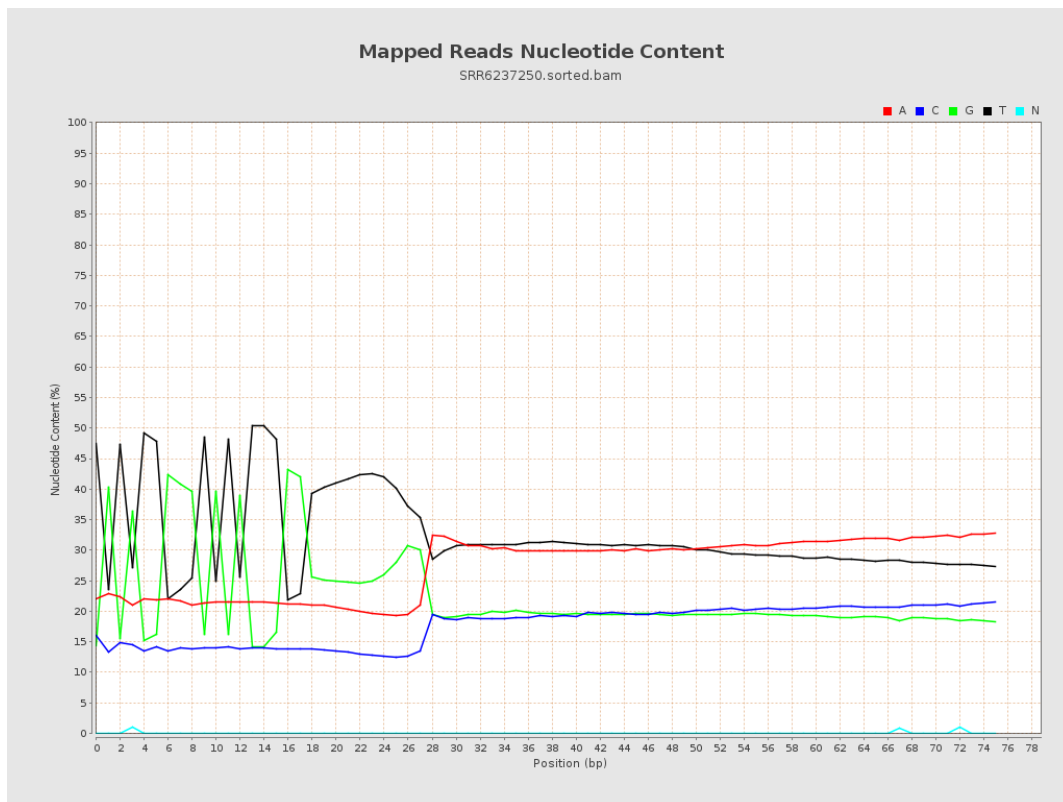
6. Results : Genome Fraction Coverage



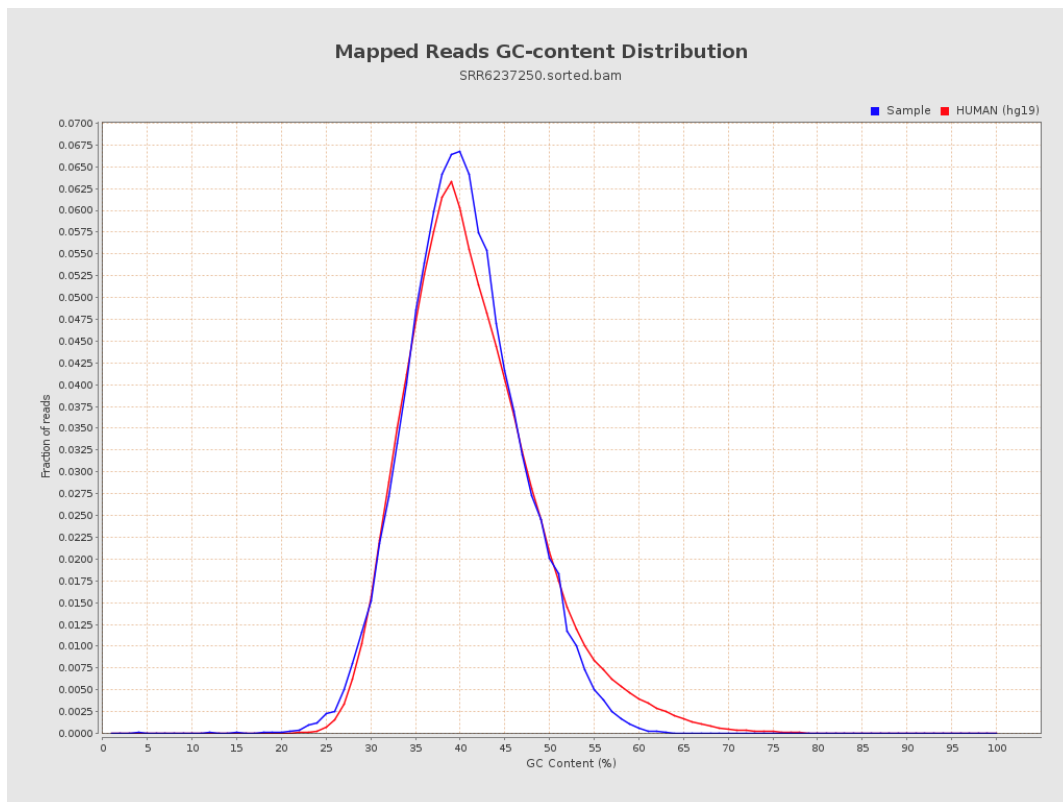
7. Results : Duplication Rate Histogram



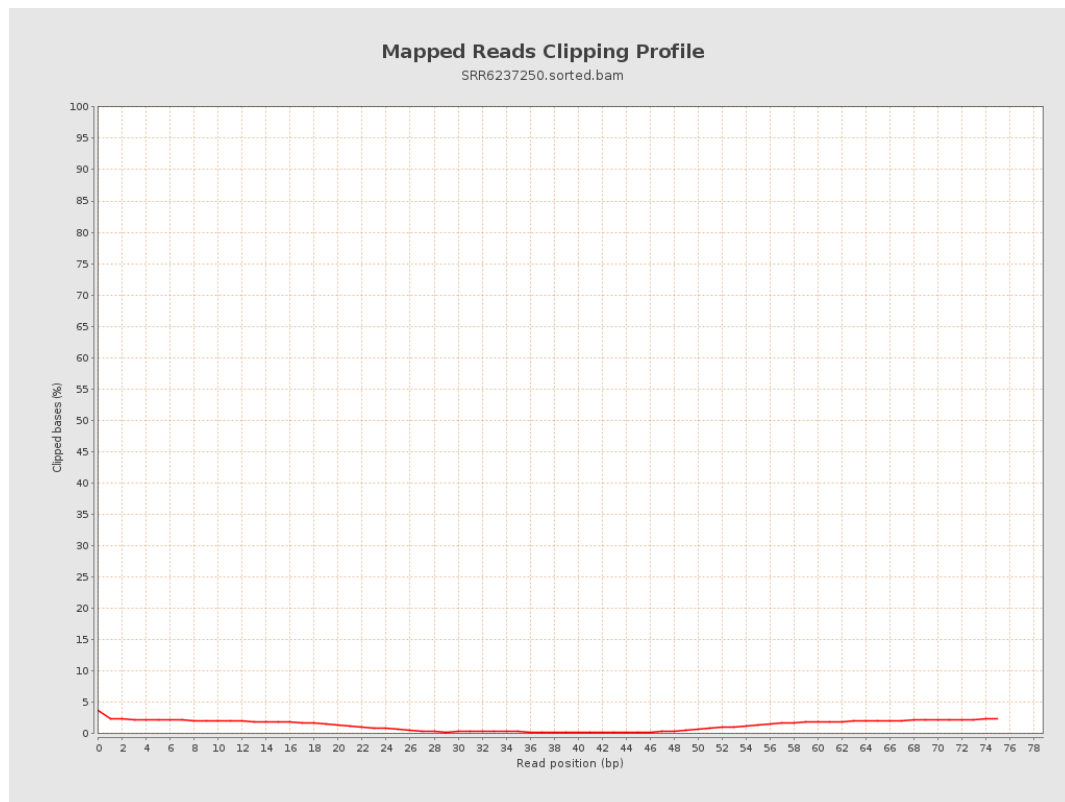
8. Results : Mapped Reads Nucleotide Content



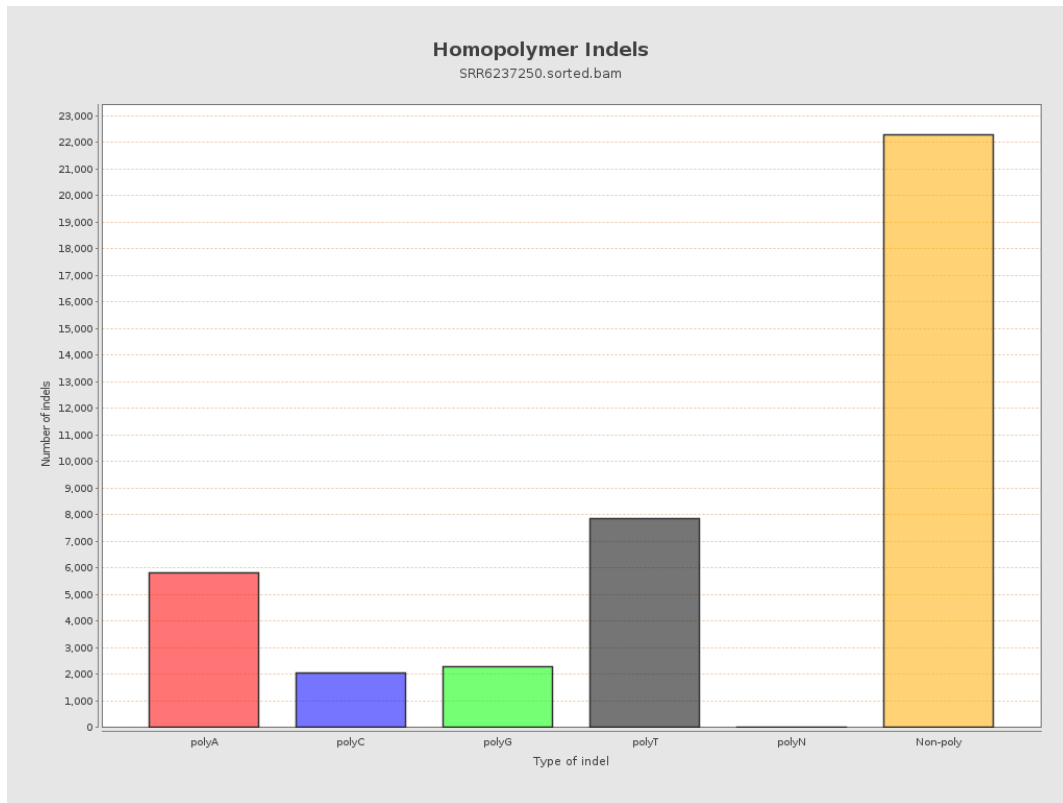
9. Results : Mapped Reads GC-content Distribution



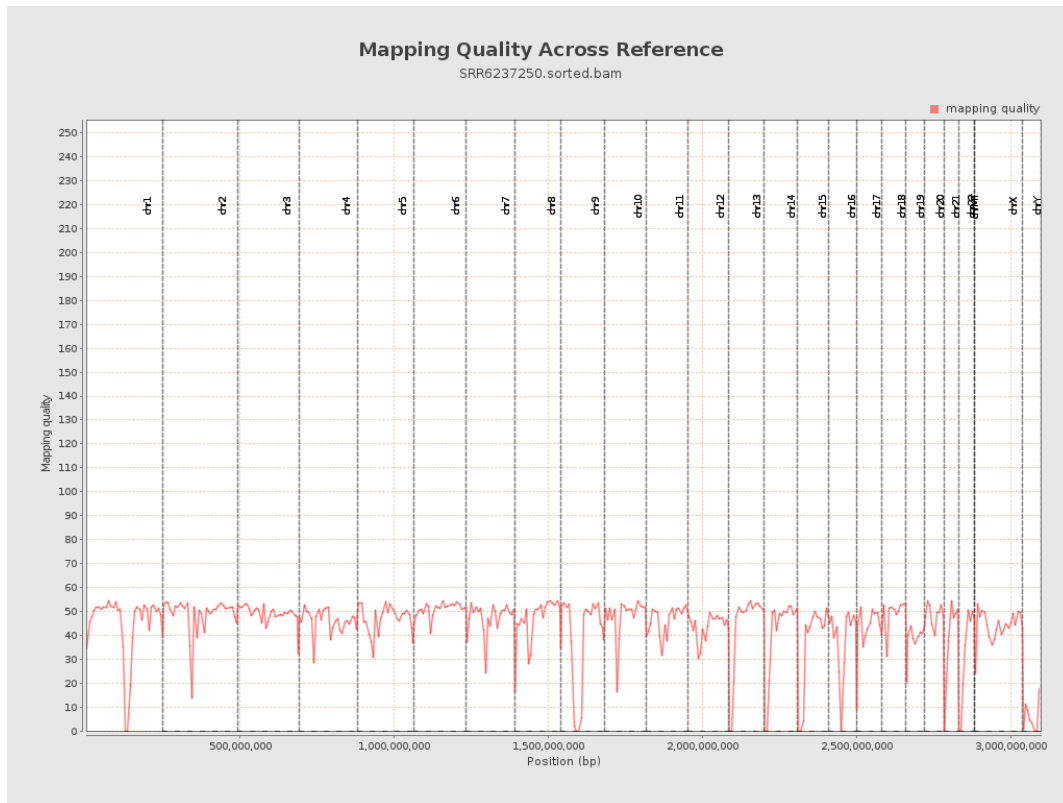
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

