

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:37:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237308.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_SRR6237308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:37:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,386,182
Mapped reads	3,329,647 / 75.91%
Unmapped reads	1,056,535 / 24.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,035 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	1,526,440 / 34.8%
Duplication rate	22.58%
Clipped reads	2,382,422 / 54.32%

2.2. ACGT Content

Number/percentage of A's	48,821,044 / 24.47%
Number/percentage of C's	34,922,953 / 17.5%
Number/percentage of T's	66,109,359 / 33.13%
Number/percentage of G's	49,669,705 / 24.89%
Number/percentage of N's	19,526 / 0.01%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0645

Standard Deviation	1.1224
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2.4. Mapping Quality

Mean Mapping Quality	41.31
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2.5. Mismatches and indels

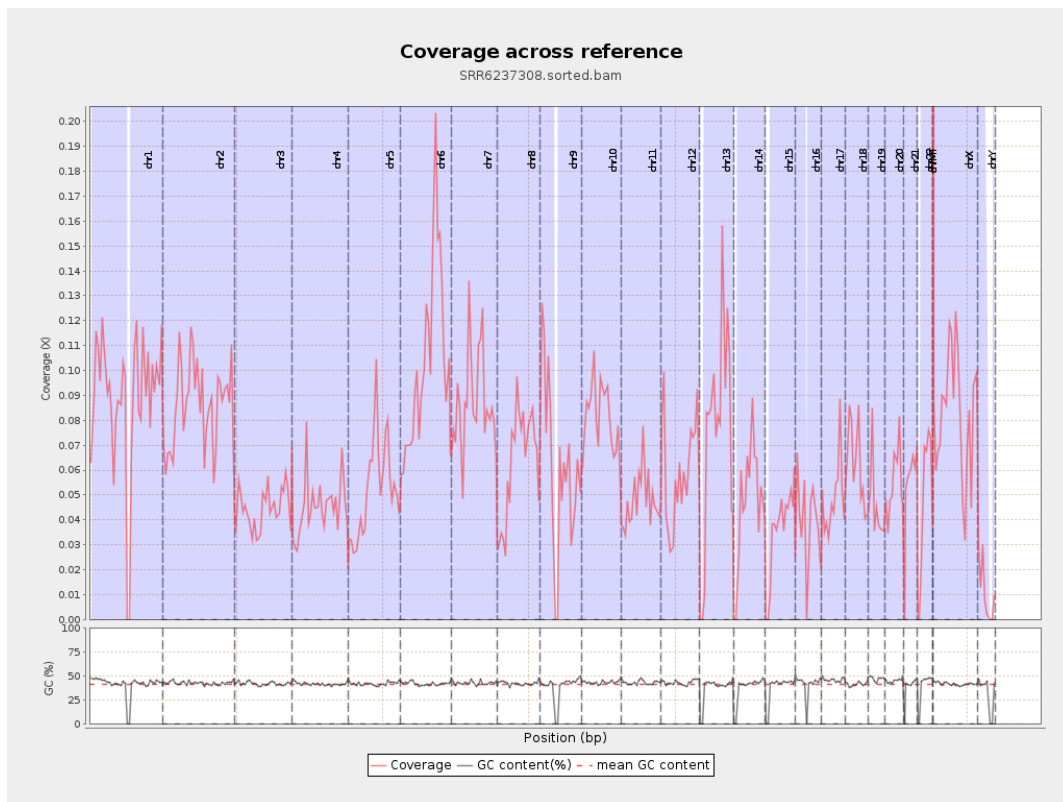
General error rate	0.73%
Mismatches	1,429,408
Insertions	14,145
Mapped reads with at least one insertion	0.42%
Deletions	66,126
Mapped reads with at least one deletion	1.96%
Homopolymer indels	46.48%

2.6. Chromosome stats

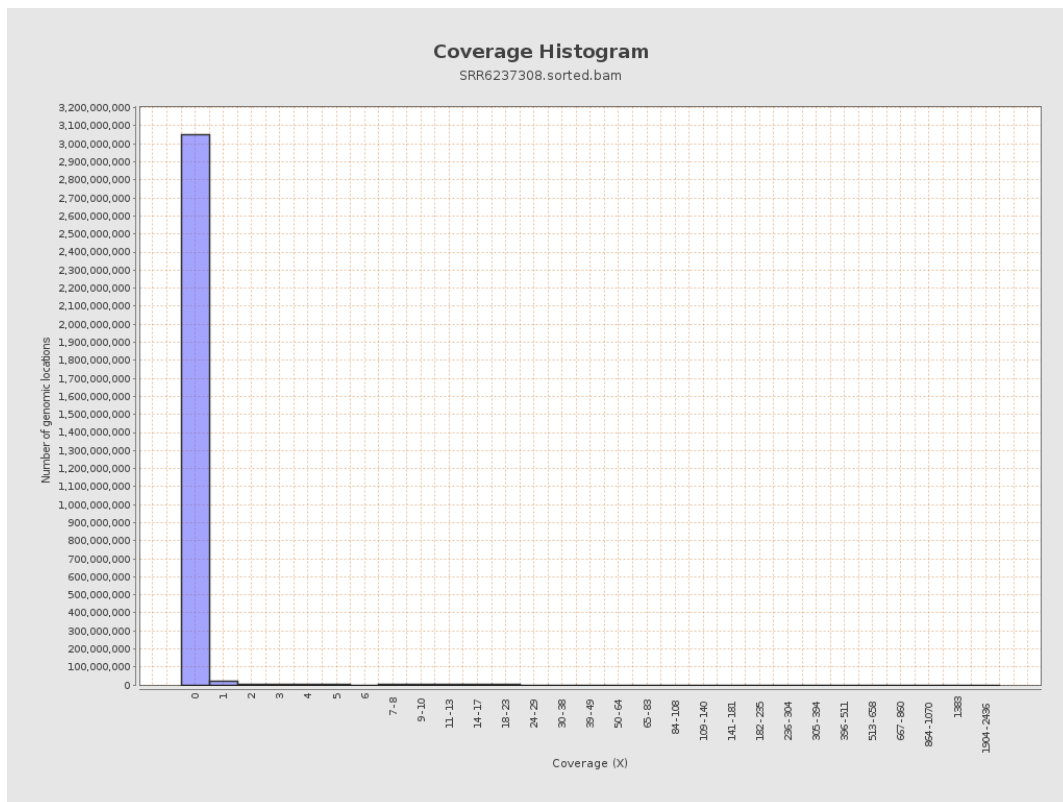
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22109884	0.0887	1.2984
chr2	243199373	20941188	0.0861	1.6792
chr3	198022430	8841153	0.0446	0.7828
chr4	191154276	8620646	0.0451	0.8203
chr5	180915260	9506946	0.0525	0.8764
chr6	171115067	17781212	0.1039	1.3075
chr7	159138663	13974102	0.0878	1.46

chr8	146364022	9330005	0.0637	1.0168
chr9	141213431	8558012	0.0606	1.0307
chr10	135534747	11005723	0.0812	1.2517
chr11	135006516	6446076	0.0477	0.9164
chr12	133851895	7978389	0.0596	1.0016
chr13	115169878	8739472	0.0759	1.1102
chr14	107349540	5095258	0.0475	0.8345
chr15	102531392	3559159	0.0347	0.6842
chr16	90354753	3448743	0.0382	0.7191
chr17	81195210	4020890	0.0495	0.8579
chr18	78077248	4868905	0.0624	1.6998
chr19	59128983	2735181	0.0463	0.8409
chr20	63025520	3462310	0.0549	0.9397
chr21	48129895	2637626	0.0548	0.9277
chr22	51304566	2459427	0.0479	0.8817
chrMT	16571	40095	2.4196	5.5509
chrX	155270560	12864367	0.0829	1.2084
chrY	59373566	635781	0.0107	0.3541

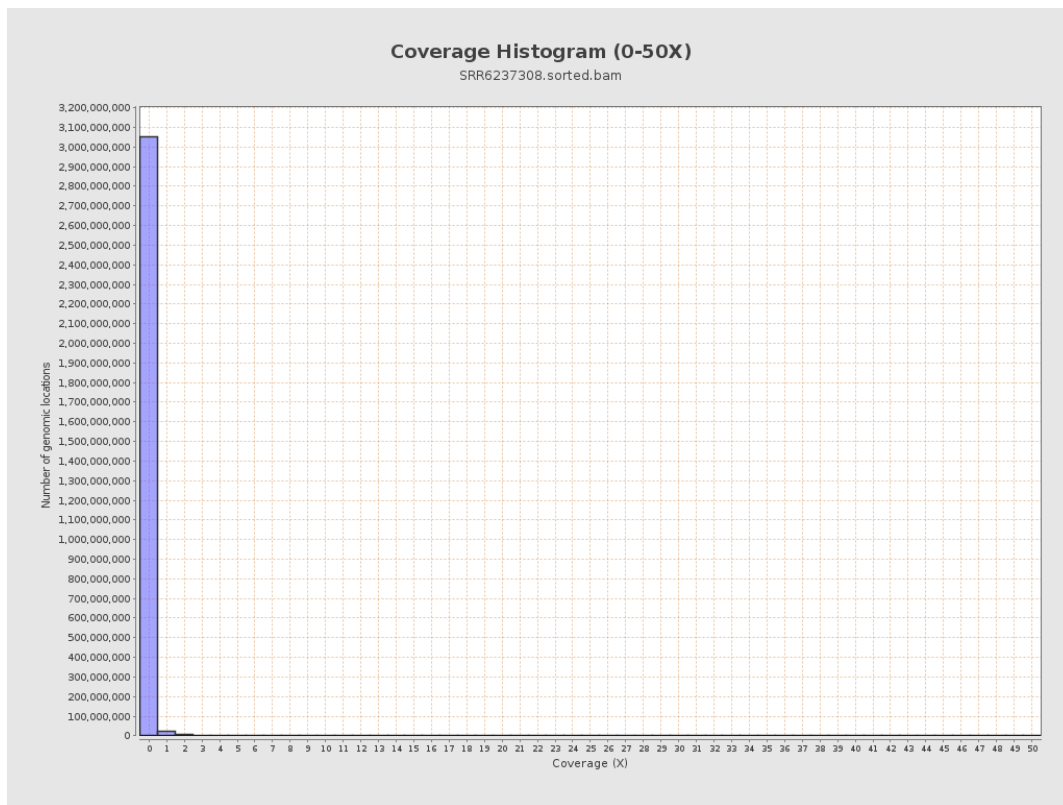
3. Results : Coverage across reference



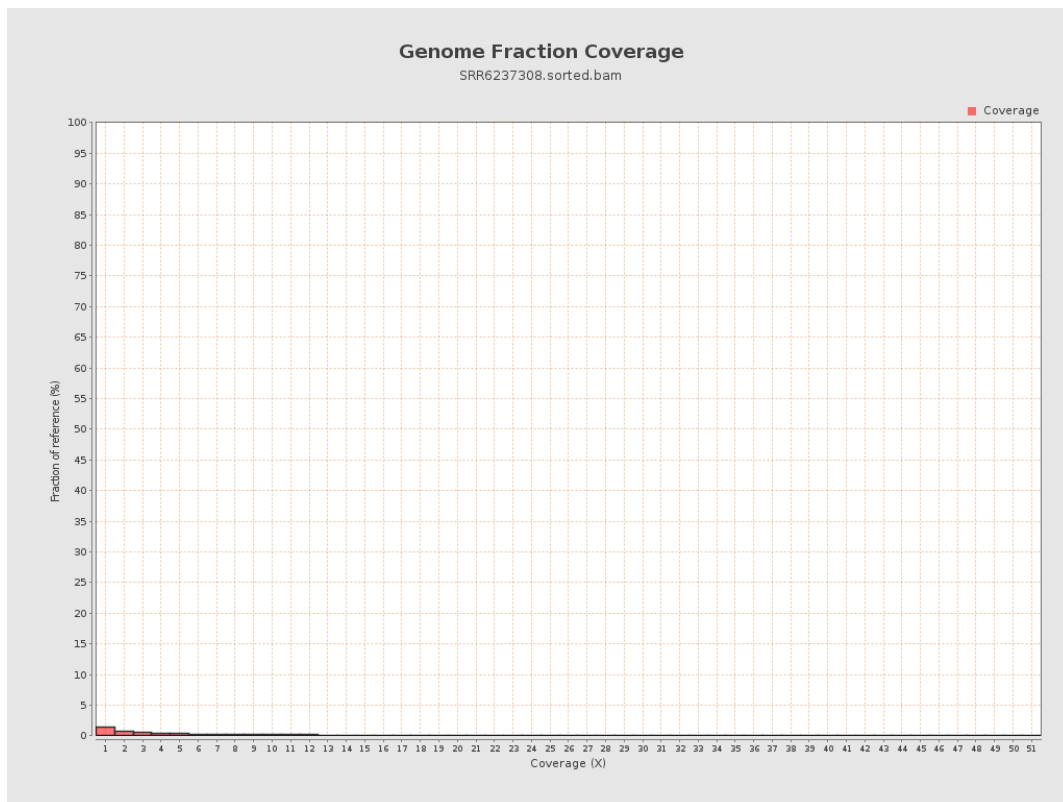
4. Results : Coverage Histogram



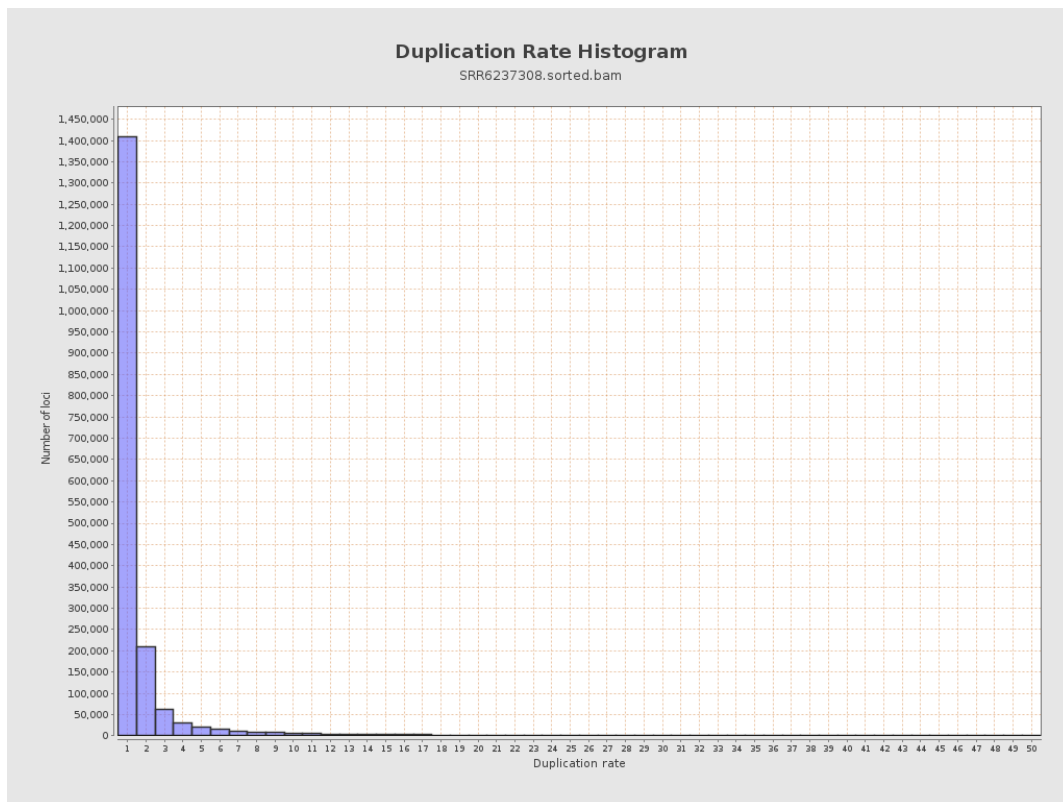
5. Results : Coverage Histogram (0-50X)



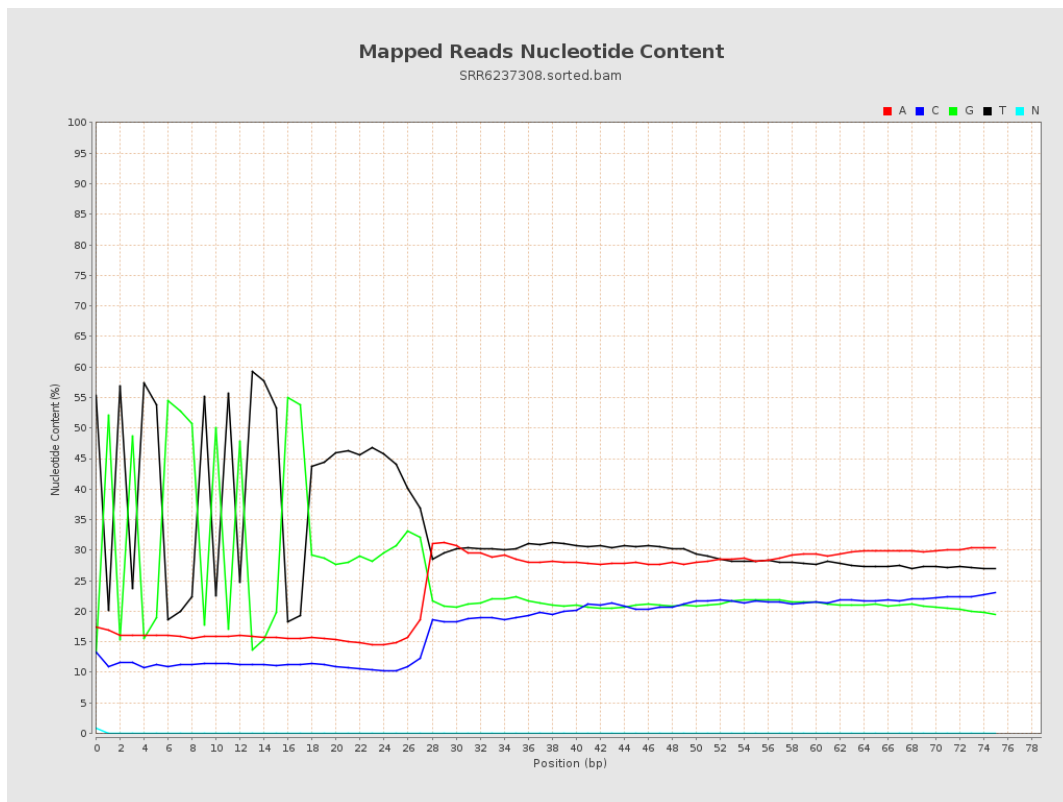
6. Results : Genome Fraction Coverage



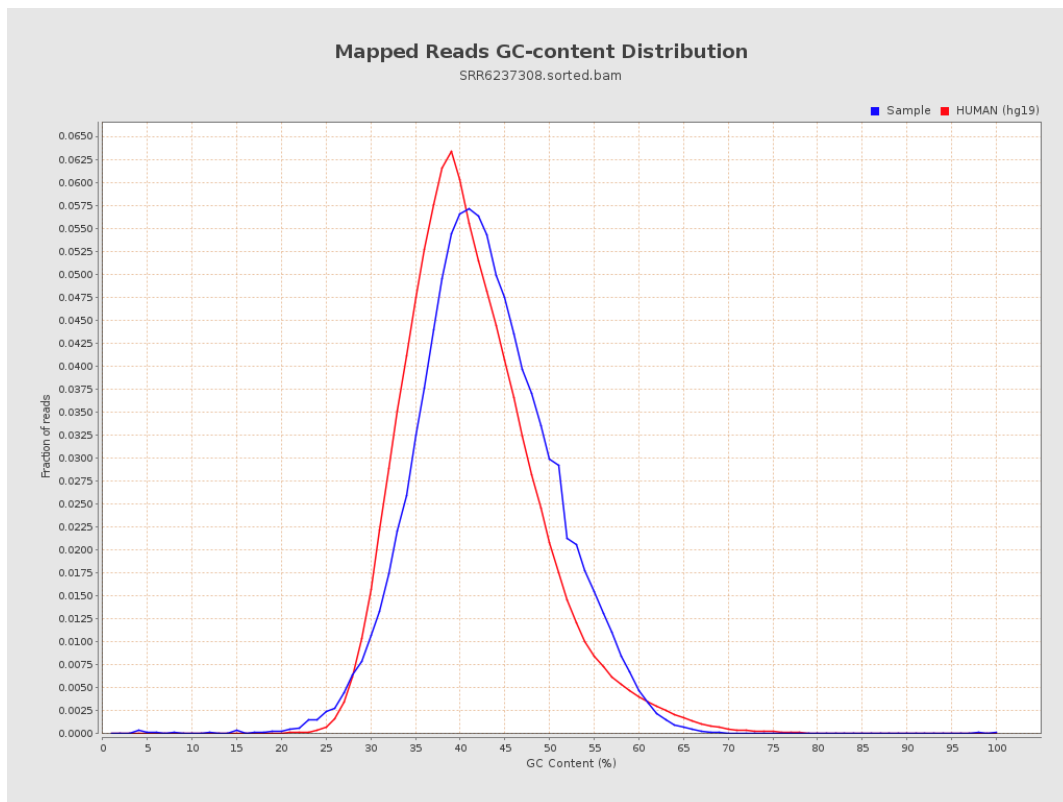
7. Results : Duplication Rate Histogram



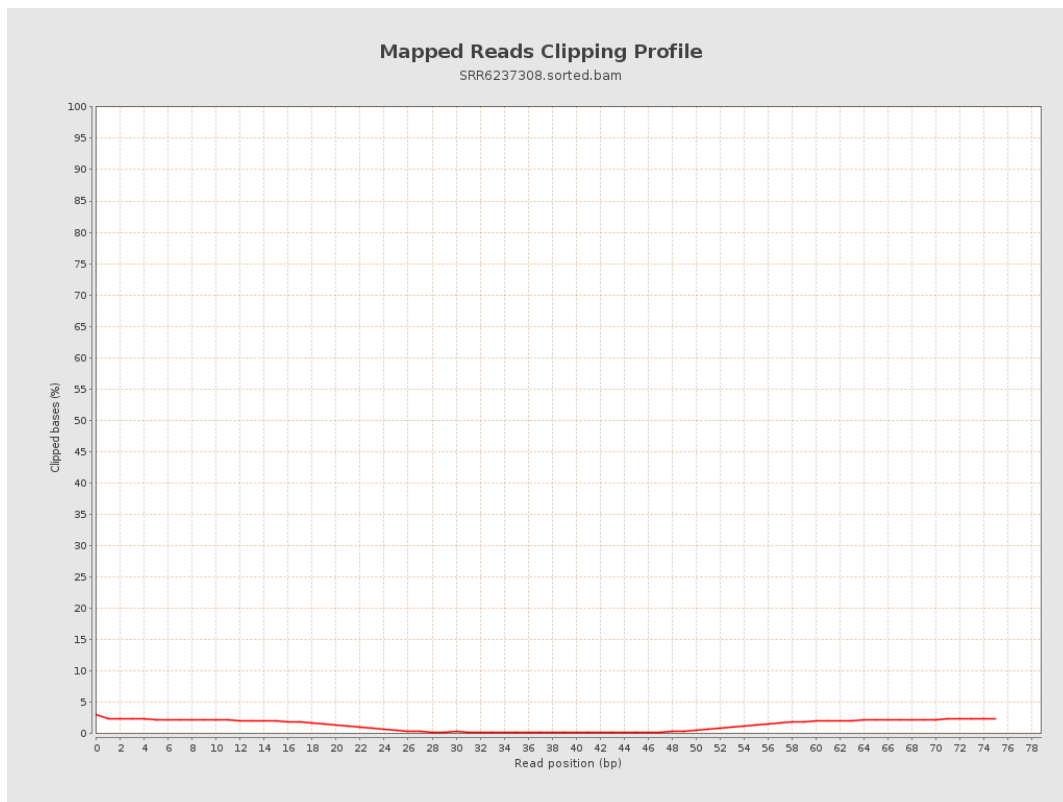
8. Results : Mapped Reads Nucleotide Content



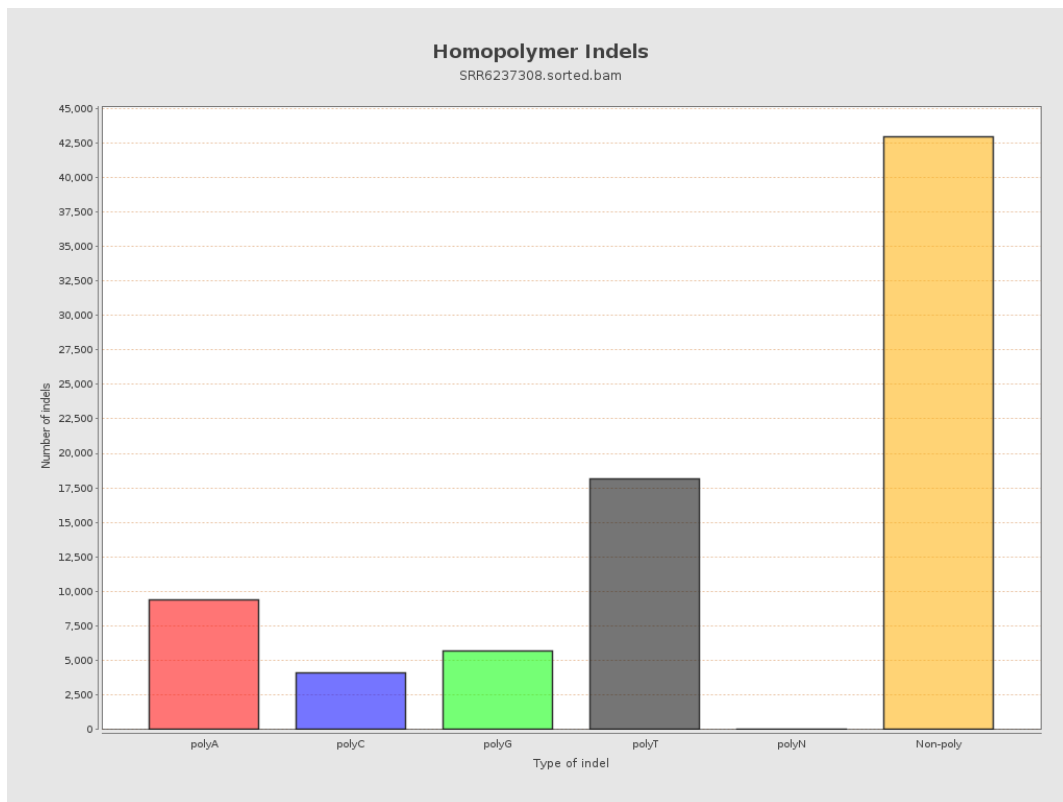
9. Results : Mapped Reads GC-content Distribution



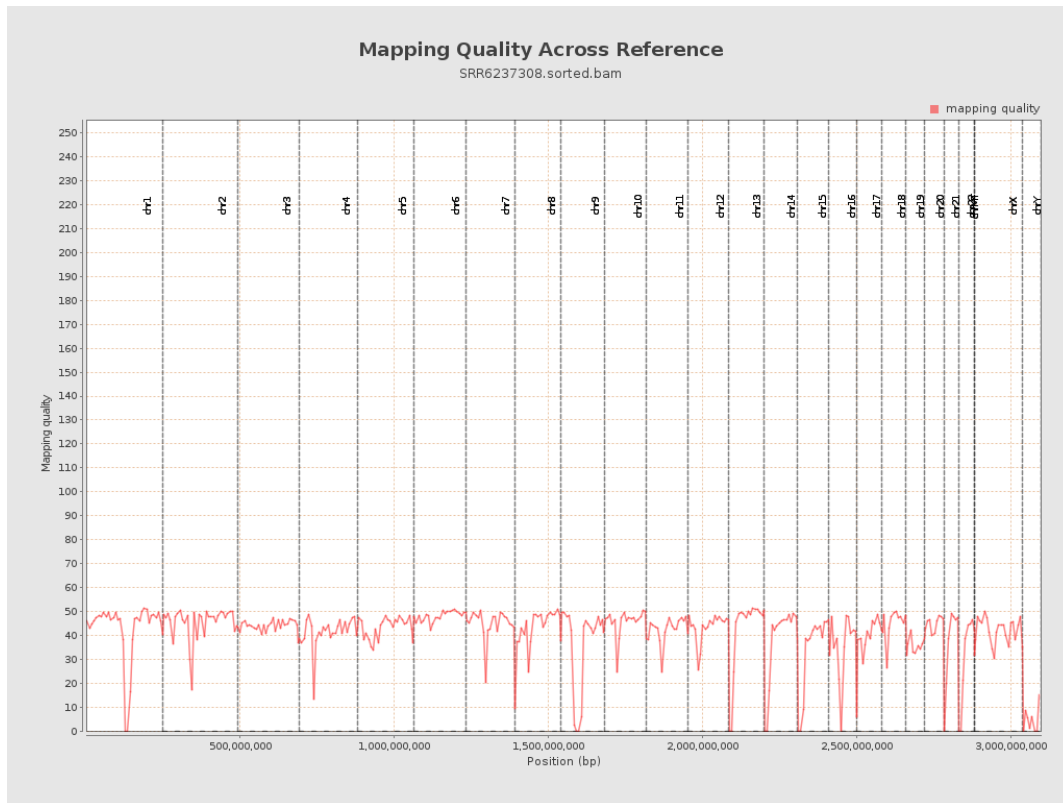
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

