

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:10:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238498.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_SRR6238498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238498.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:10:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,757,350
Mapped reads	5,051,220 / 87.74%
Unmapped reads	706,130 / 12.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,162 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	1,685,802 / 29.28%
Duplication rate	20.88%
Clipped reads	3,263,012 / 56.68%

2.2. ACGT Content

Number/percentage of A's	76,063,780 / 24.61%
Number/percentage of C's	54,040,414 / 17.48%
Number/percentage of T's	104,283,162 / 33.74%
Number/percentage of G's	74,672,537 / 24.16%
Number/percentage of N's	20,222 / 0.01%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0999

Standard Deviation	1.5517
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	41.95
----------------------	-------

2.5. Mismatches and indels

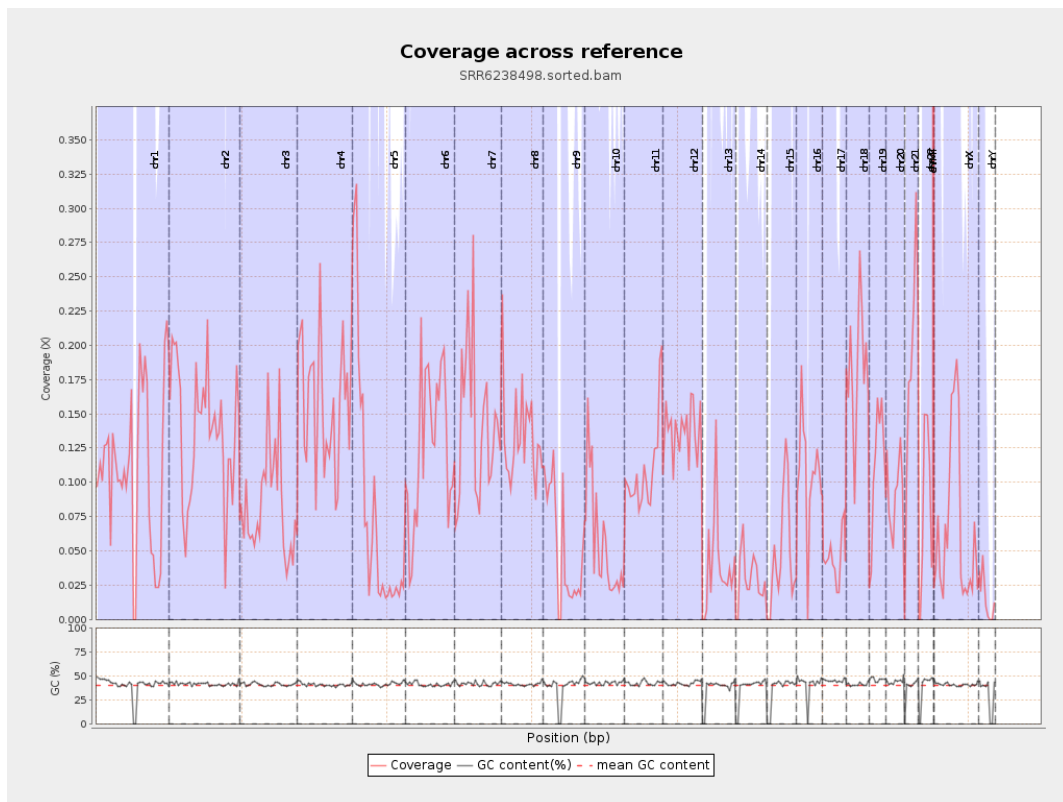
General error rate	0.65%
Mismatches	1,982,823
Insertions	20,737
Mapped reads with at least one insertion	0.41%
Deletions	98,556
Mapped reads with at least one deletion	1.93%
Homopolymer indels	41.49%

2.6. Chromosome stats

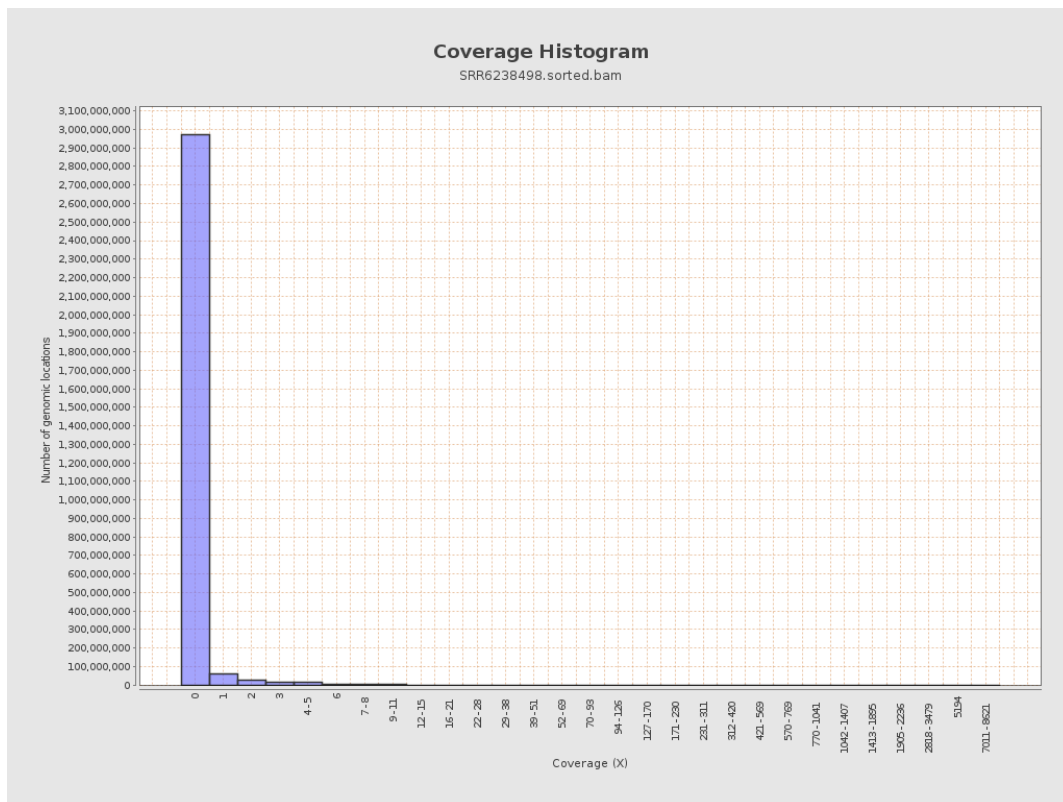
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27111593	0.1088	1.7292
chr2	243199373	33591797	0.1381	3.8581
chr3	198022430	16582100	0.0837	0.6409
chr4	191154276	30229747	0.1581	0.8557
chr5	180915260	13855102	0.0766	0.6199
chr6	171115067	21442837	0.1253	1.5
chr7	159138663	22341918	0.1404	1.939

chr8	146364022	19586938	0.1338	1.1273
chr9	141213431	7092959	0.0502	0.9341
chr10	135534747	7614126	0.0562	0.8245
chr11	135006516	14723754	0.1091	0.8653
chr12	133851895	18416440	0.1376	0.8443
chr13	115169878	4488068	0.039	0.7582
chr14	107349540	3053232	0.0284	0.5487
chr15	102531392	4775985	0.0466	0.7625
chr16	90354753	9716040	0.1075	0.8768
chr17	81195210	3656802	0.045	0.4603
chr18	78077248	14548236	0.1863	2.8942
chr19	59128983	6698087	0.1133	1.4011
chr20	63025520	5615151	0.0891	0.759
chr21	48129895	8807825	0.183	0.9661
chr22	51304566	3949226	0.077	0.597
chrMT	16571	100422	6.0601	5.8224
chrX	155270560	10376969	0.0668	0.7207
chrY	59373566	871086	0.0147	0.4986

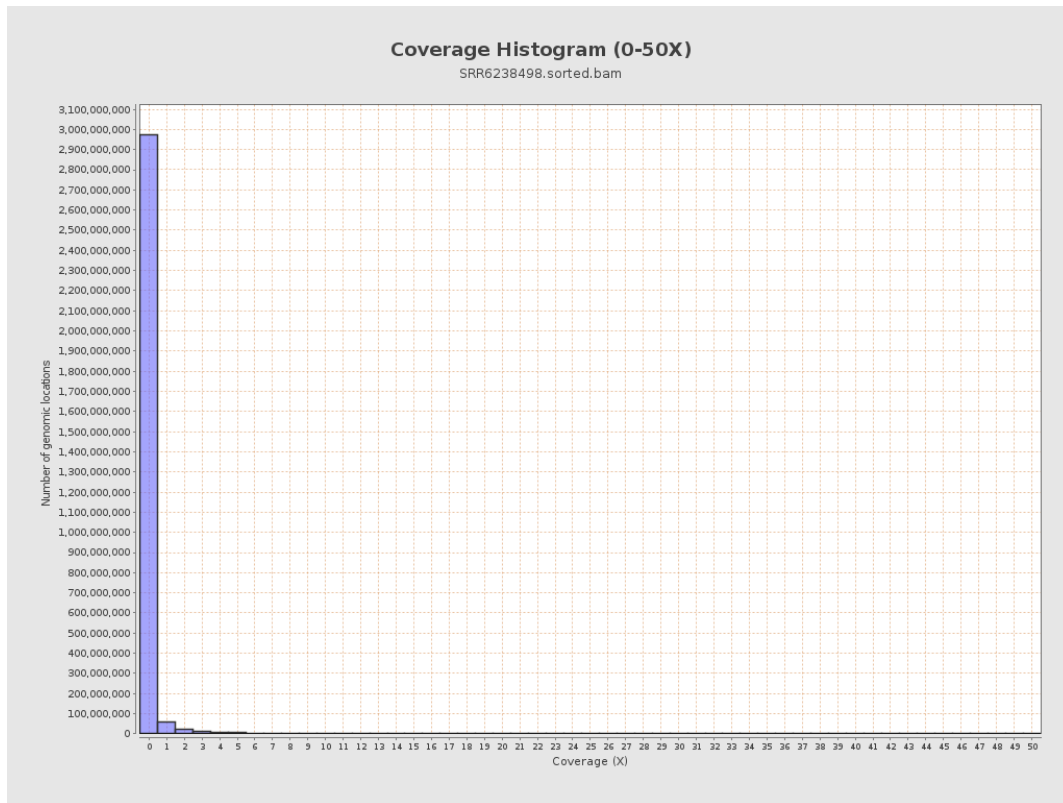
3. Results : Coverage across reference



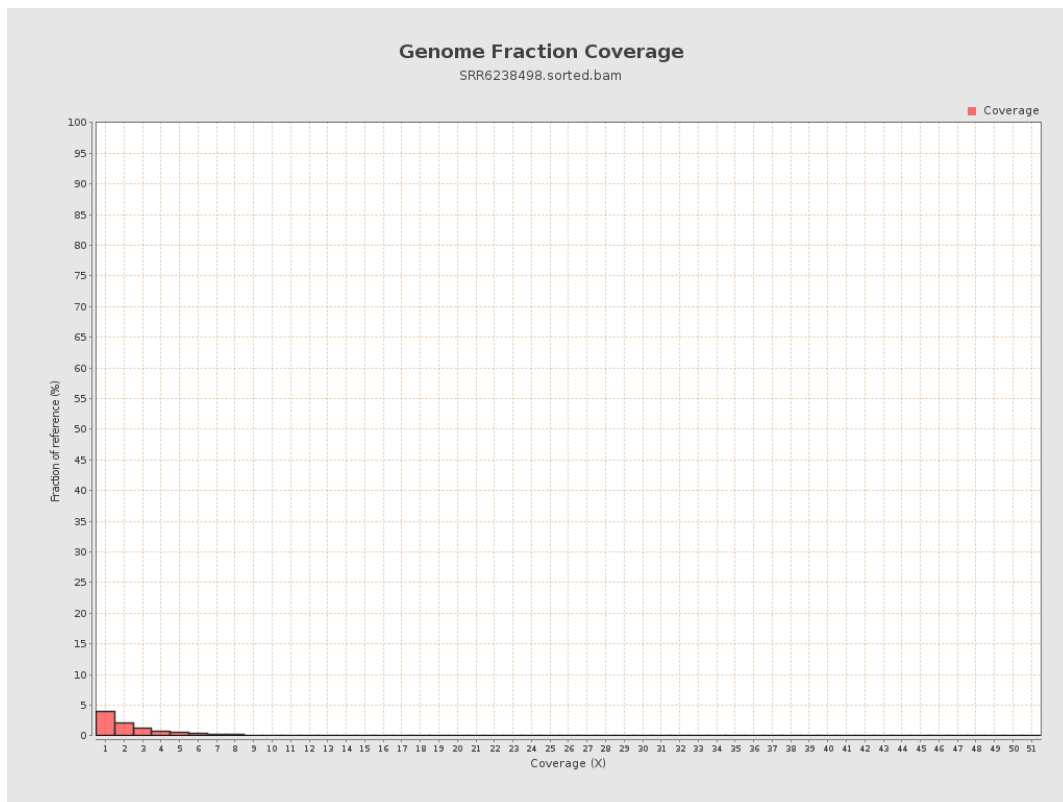
4. Results : Coverage Histogram



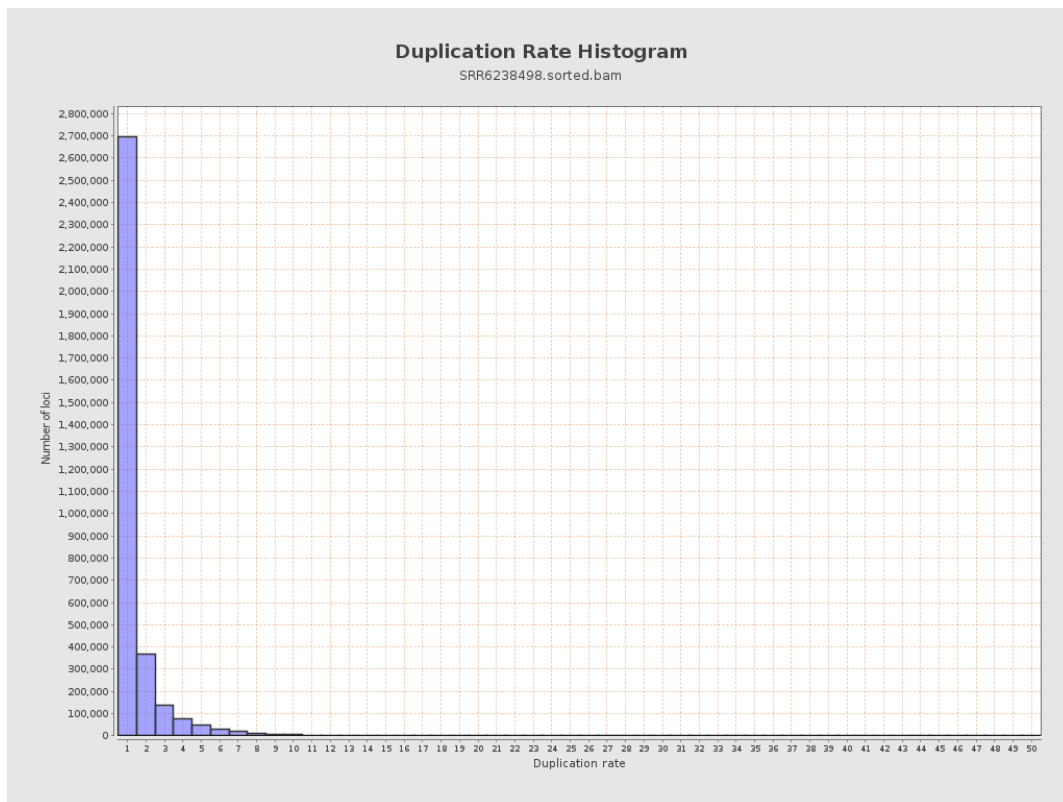
5. Results : Coverage Histogram (0-50X)



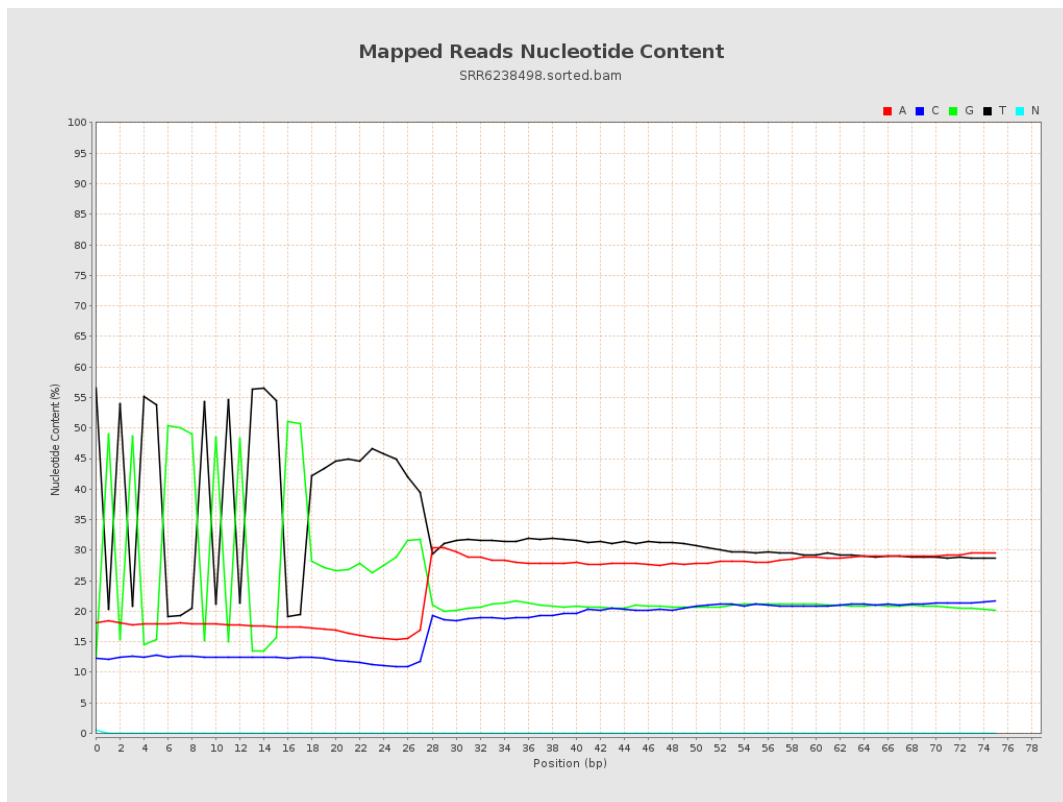
6. Results : Genome Fraction Coverage



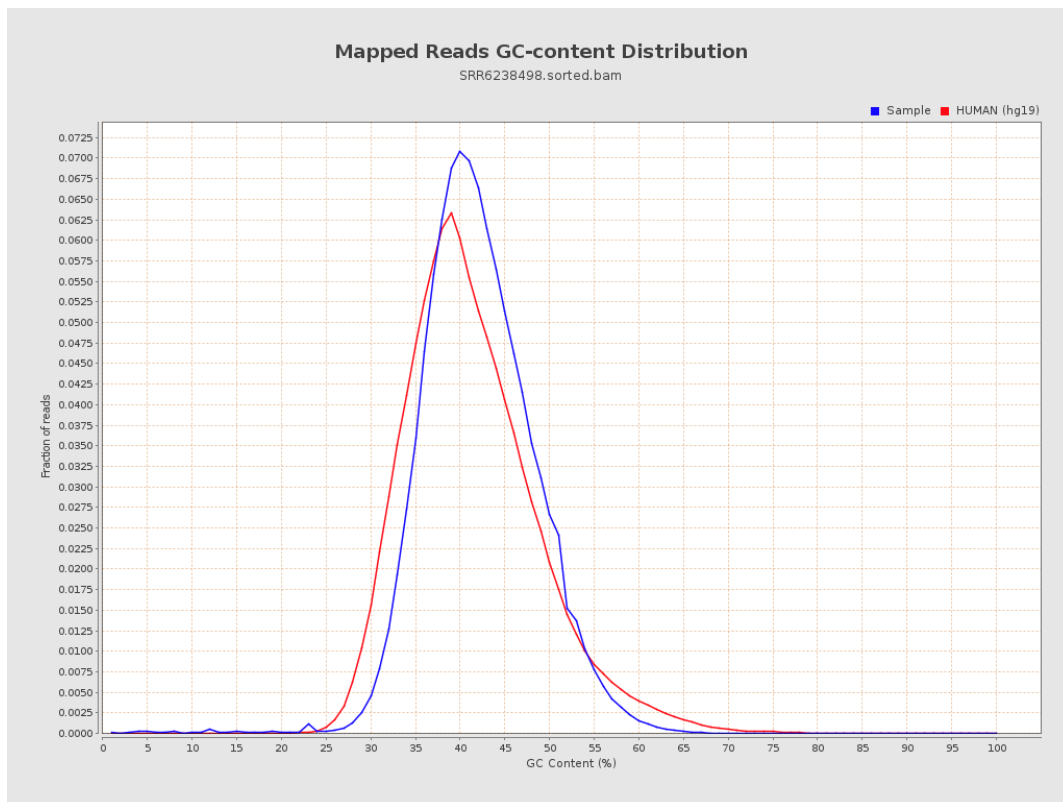
7. Results : Duplication Rate Histogram



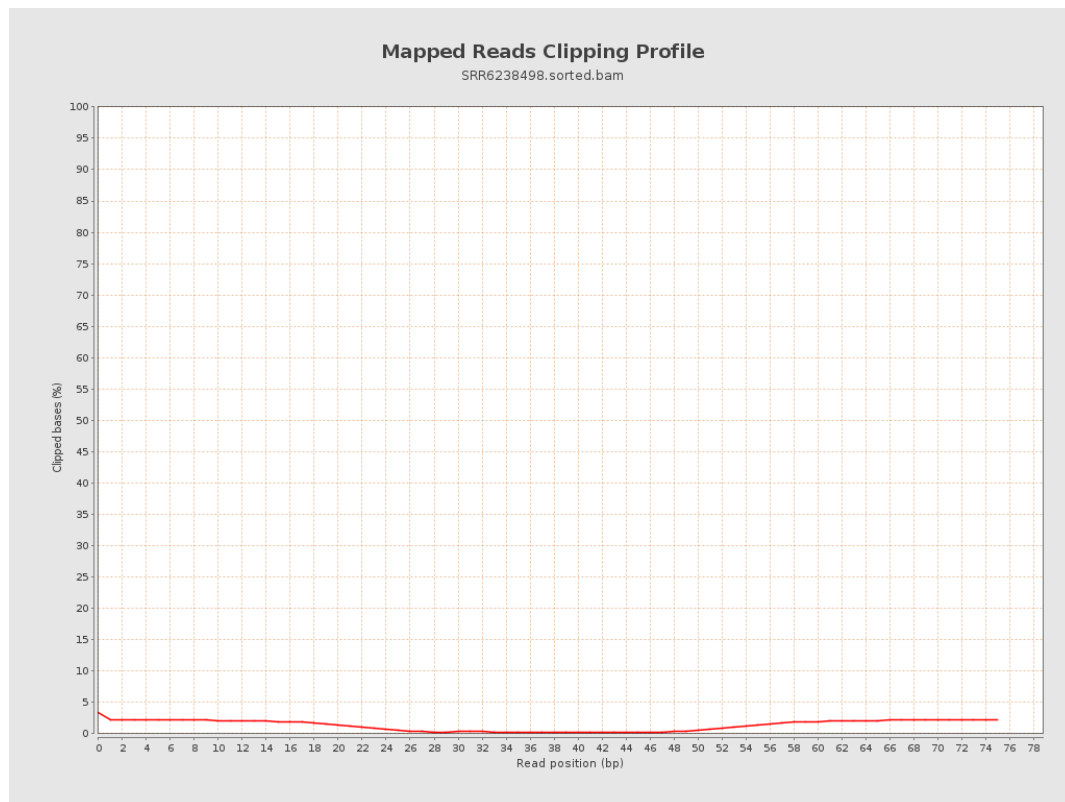
8. Results : Mapped Reads Nucleotide Content



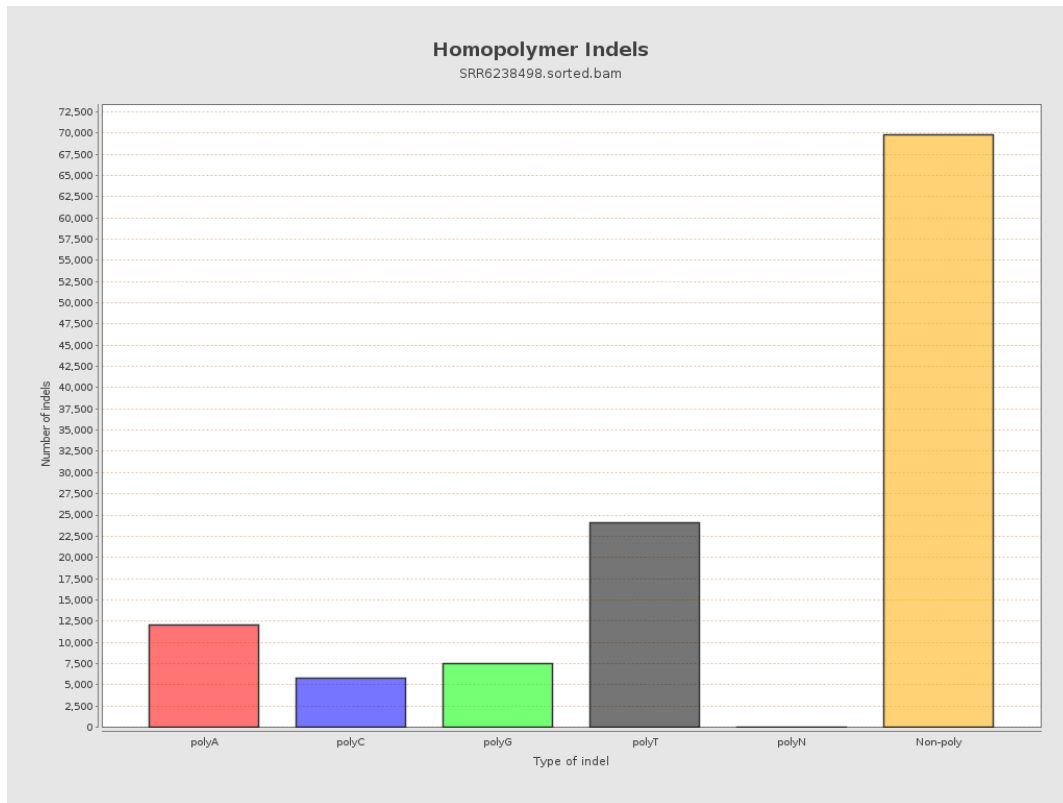
9. Results : Mapped Reads GC-content Distribution



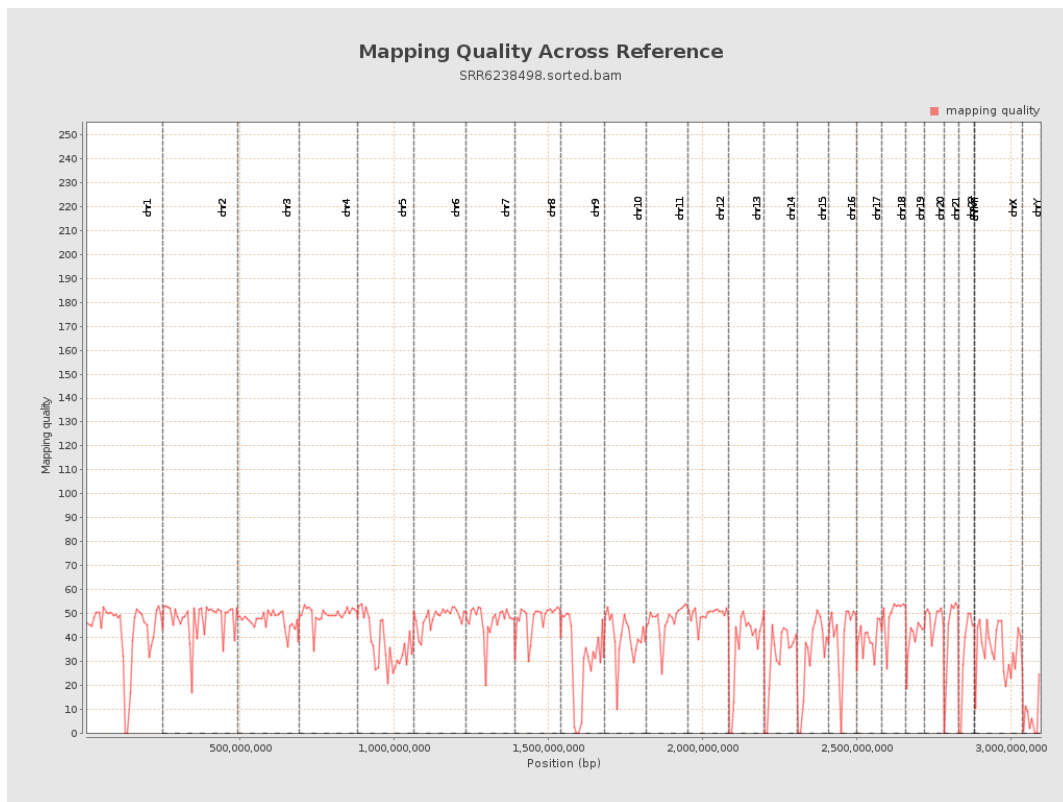
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

