

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:48:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238523.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_SRR6238523 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238523.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:48:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238523.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,919,547
Mapped reads	3,441,599 / 87.81%
Unmapped reads	477,948 / 12.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,833 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,468,229 / 37.46%
Duplication rate	24.87%
Clipped reads	2,434,598 / 62.11%

2.2. ACGT Content

Number/percentage of A's	50,002,908 / 24.27%
Number/percentage of C's	34,445,134 / 16.72%
Number/percentage of T's	71,278,699 / 34.6%
Number/percentage of G's	50,281,619 / 24.41%
Number/percentage of N's	12,921 / 0.01%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0666

Standard Deviation	1.017
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	39.4
----------------------	------

2.5. Mismatches and indels

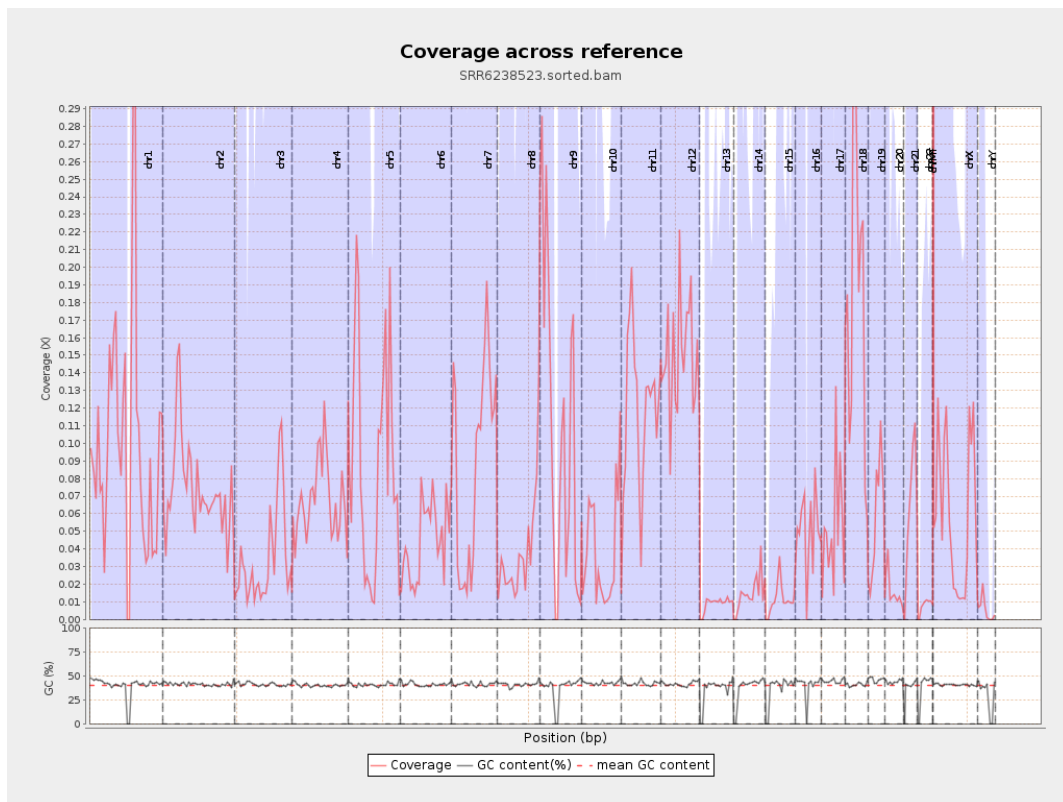
General error rate	0.67%
Mismatches	1,347,757
Insertions	12,935
Mapped reads with at least one insertion	0.37%
Deletions	83,125
Mapped reads with at least one deletion	2.39%
Homopolymer indels	41.09%

2.6. Chromosome stats

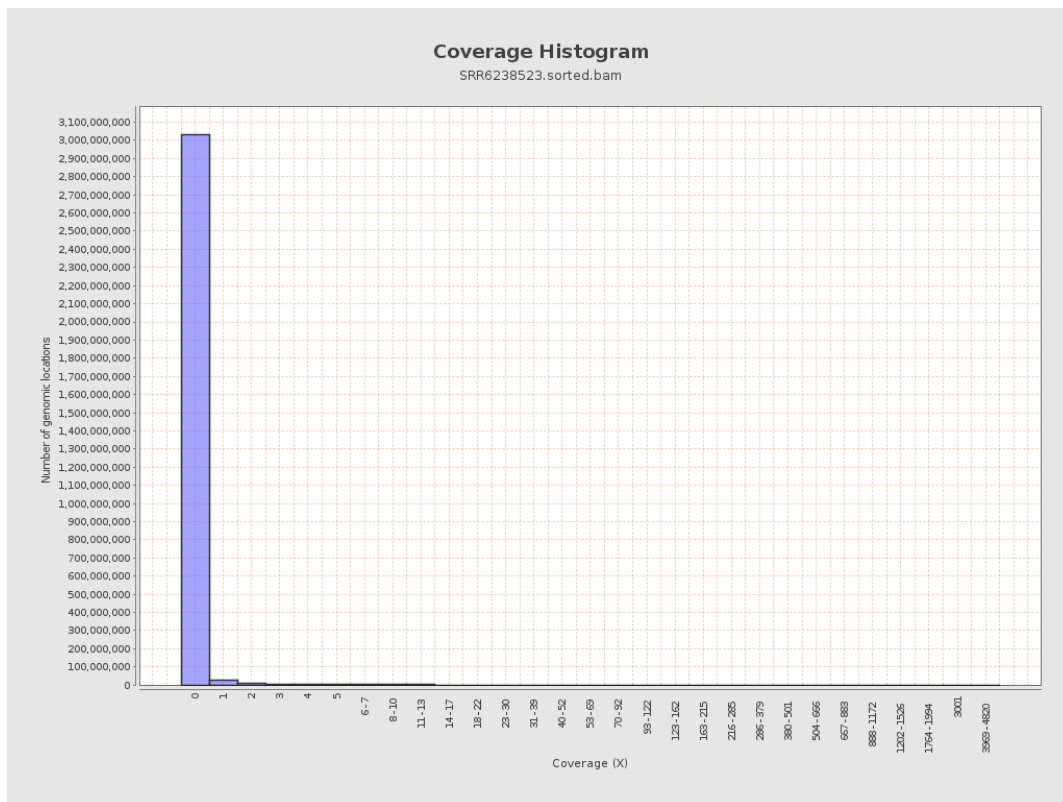
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24633862	0.0988	1.1811
chr2	243199373	18126894	0.0745	2.1903
chr3	198022430	6830816	0.0345	0.742
chr4	191154276	12930353	0.0676	0.654
chr5	180915260	15590168	0.0862	0.7615
chr6	171115067	7575053	0.0443	0.8465
chr7	159138663	14151572	0.0889	0.8654

chr8	146364022	5631838	0.0385	0.6637
chr9	141213431	14952614	0.1059	0.8903
chr10	135534747	4978300	0.0367	0.6598
chr11	135006516	16116796	0.1194	1.0173
chr12	133851895	20083867	0.15	1.1137
chr13	115169878	1045609	0.0091	0.4757
chr14	107349540	1581661	0.0147	0.3316
chr15	102531392	1122916	0.011	0.4978
chr16	90354753	4407029	0.0488	0.6097
chr17	81195210	4228402	0.0521	0.6177
chr18	78077248	14734848	0.1887	2.0562
chr19	59128983	3318874	0.0561	0.8011
chr20	63025520	1023291	0.0162	0.2877
chr21	48129895	3004846	0.0624	0.6635
chr22	51304566	391214	0.0076	0.1784
chrMT	16571	288270	17.3961	16.4046
chrX	155270560	9065144	0.0584	0.6413
chrY	59373566	347320	0.0058	0.3269

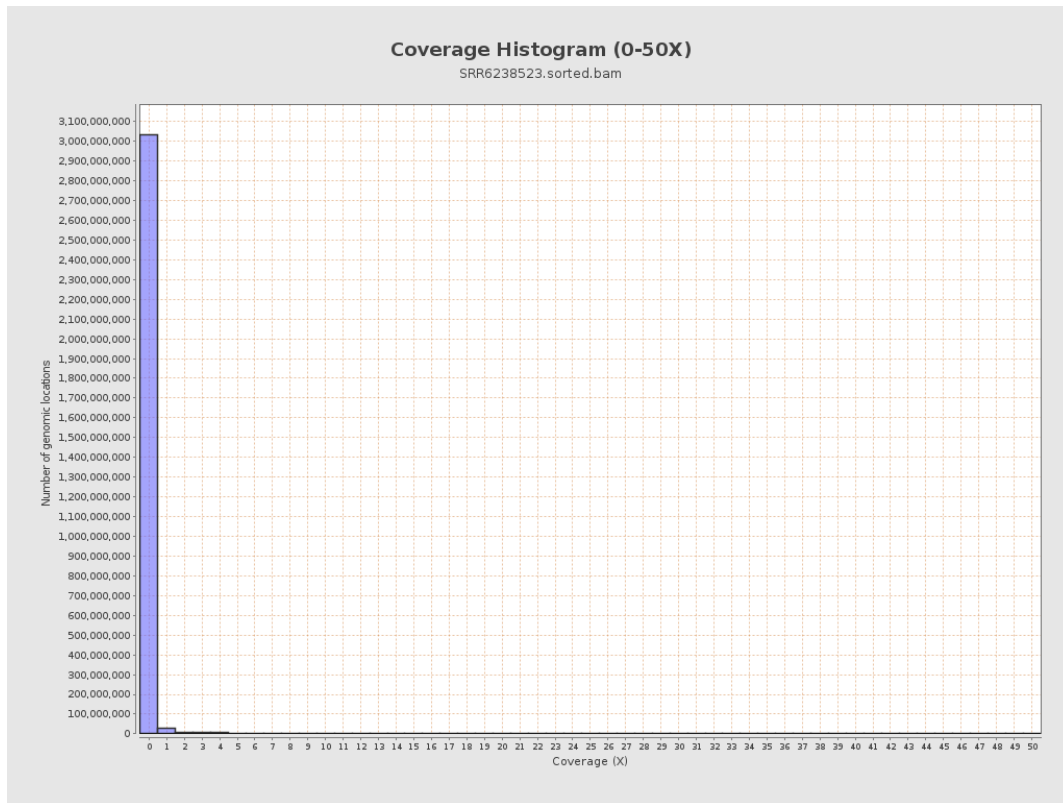
3. Results : Coverage across reference



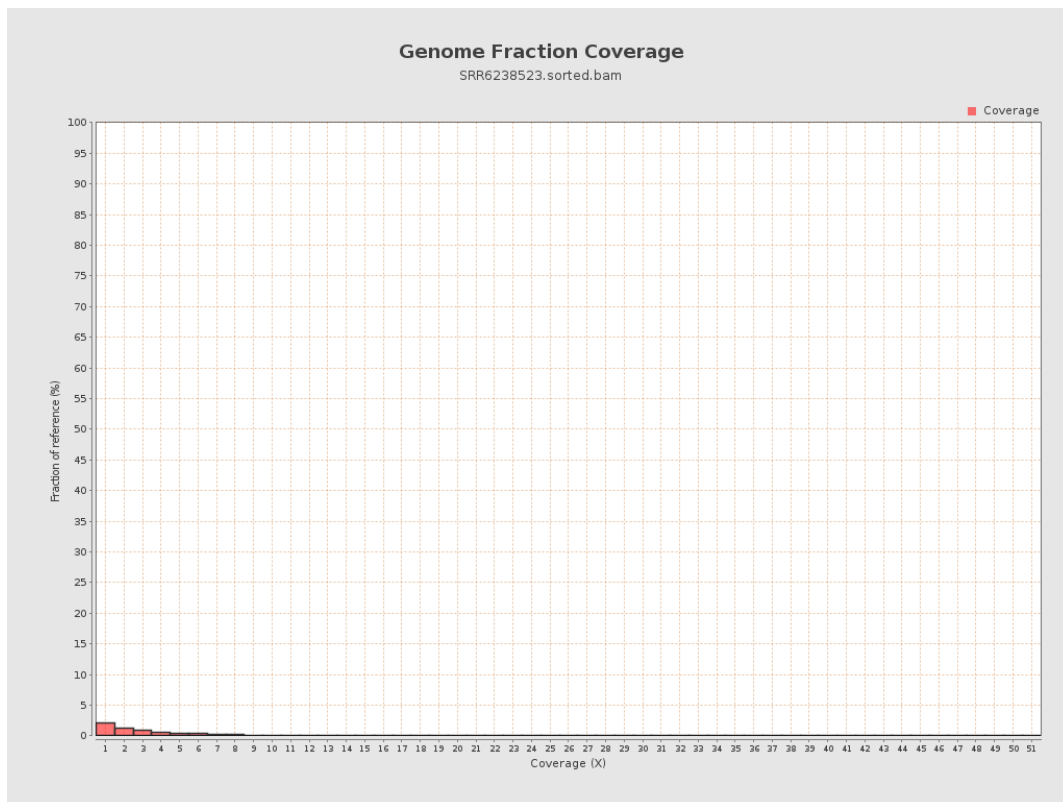
4. Results : Coverage Histogram



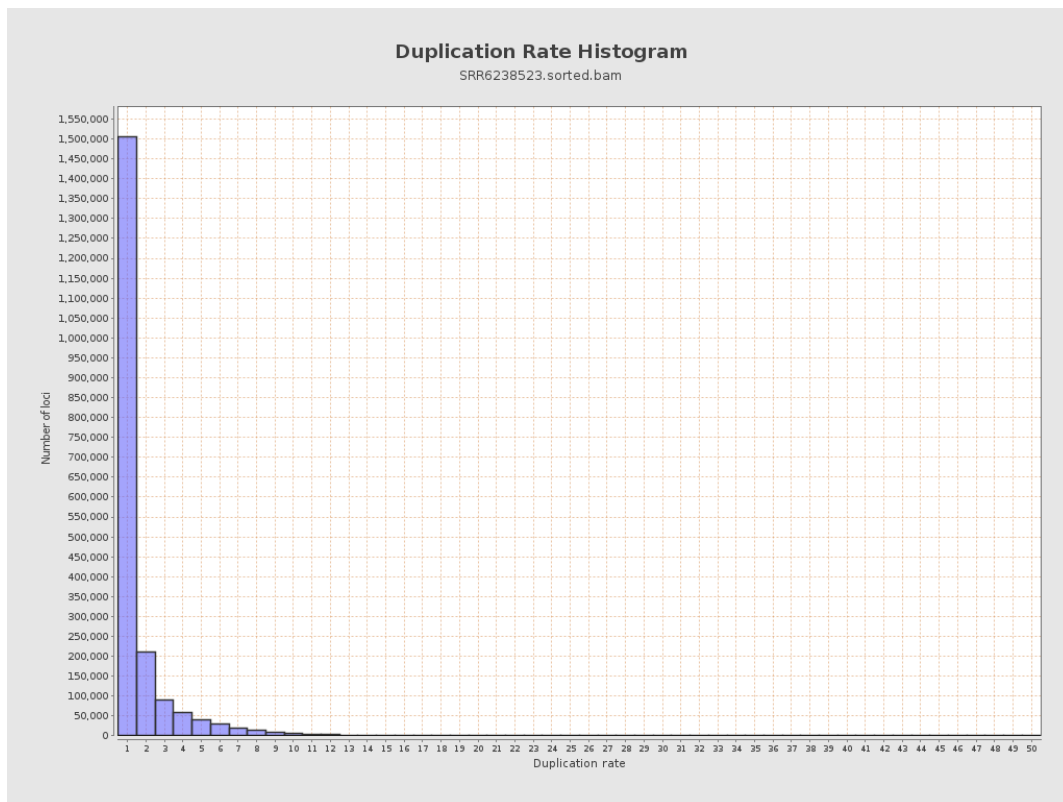
5. Results : Coverage Histogram (0-50X)



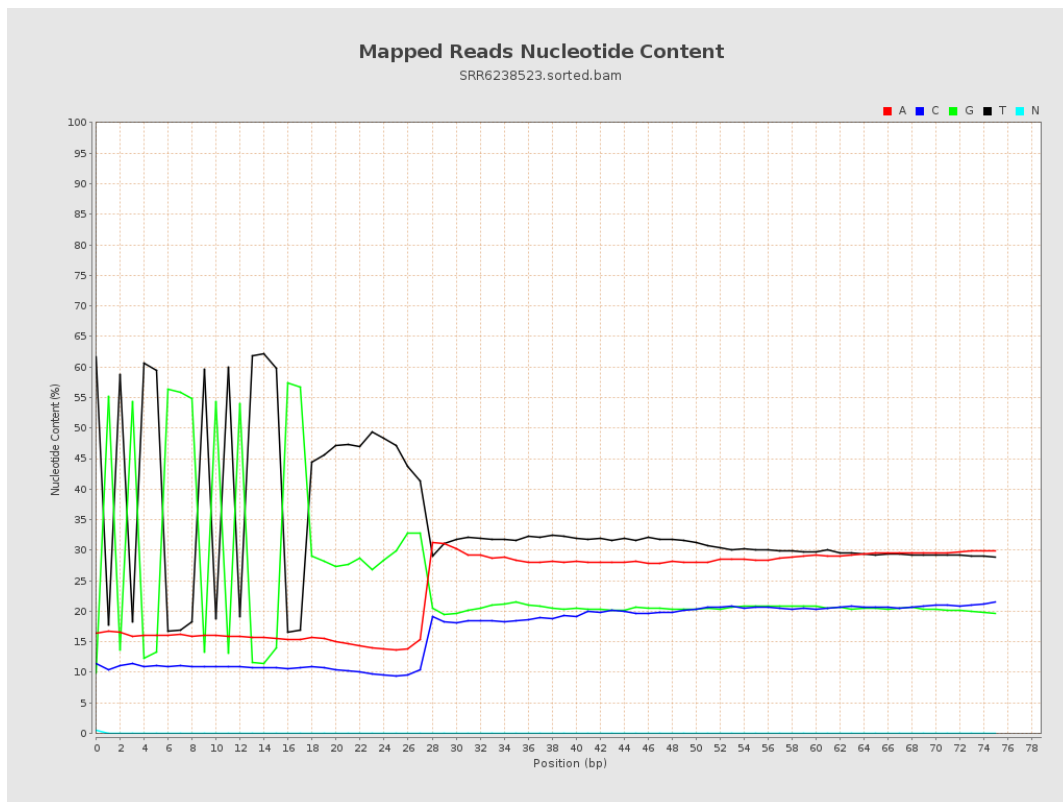
6. Results : Genome Fraction Coverage



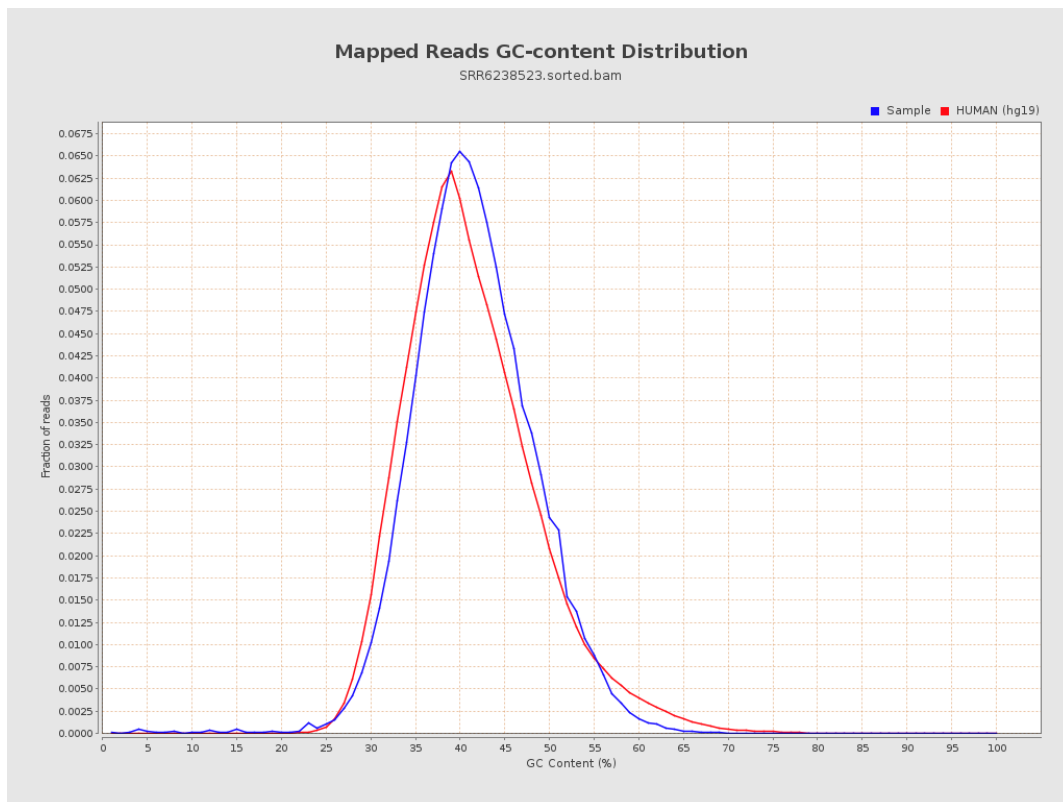
7. Results : Duplication Rate Histogram



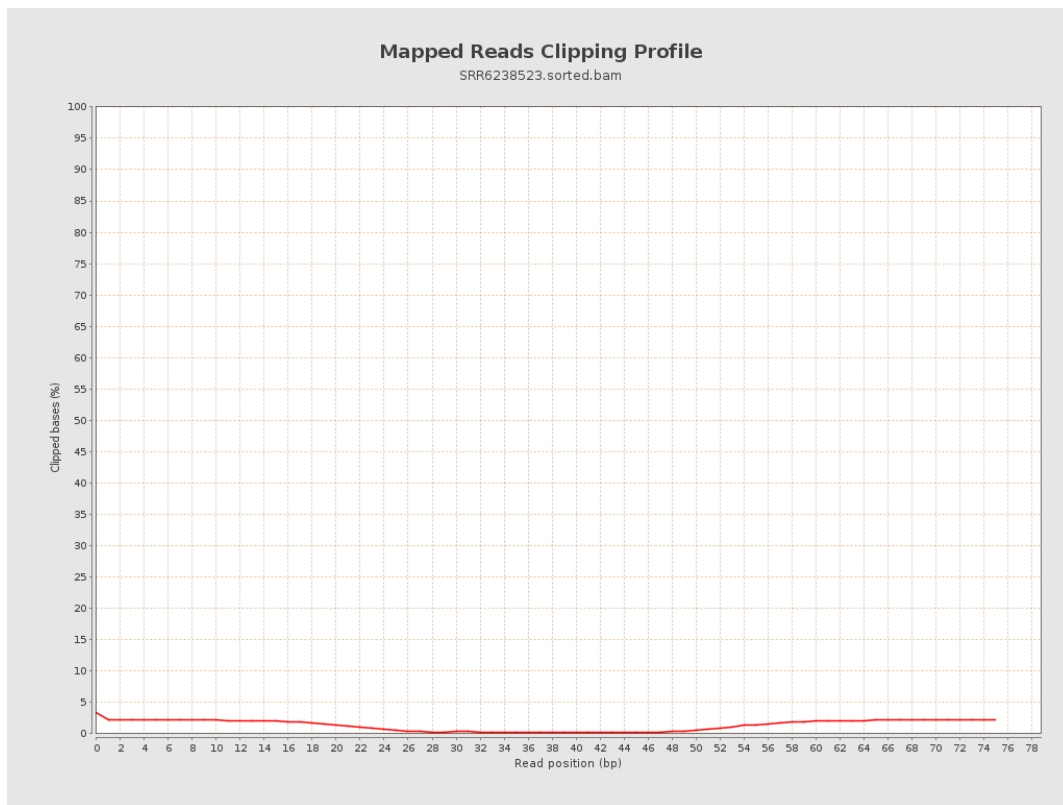
8. Results : Mapped Reads Nucleotide Content



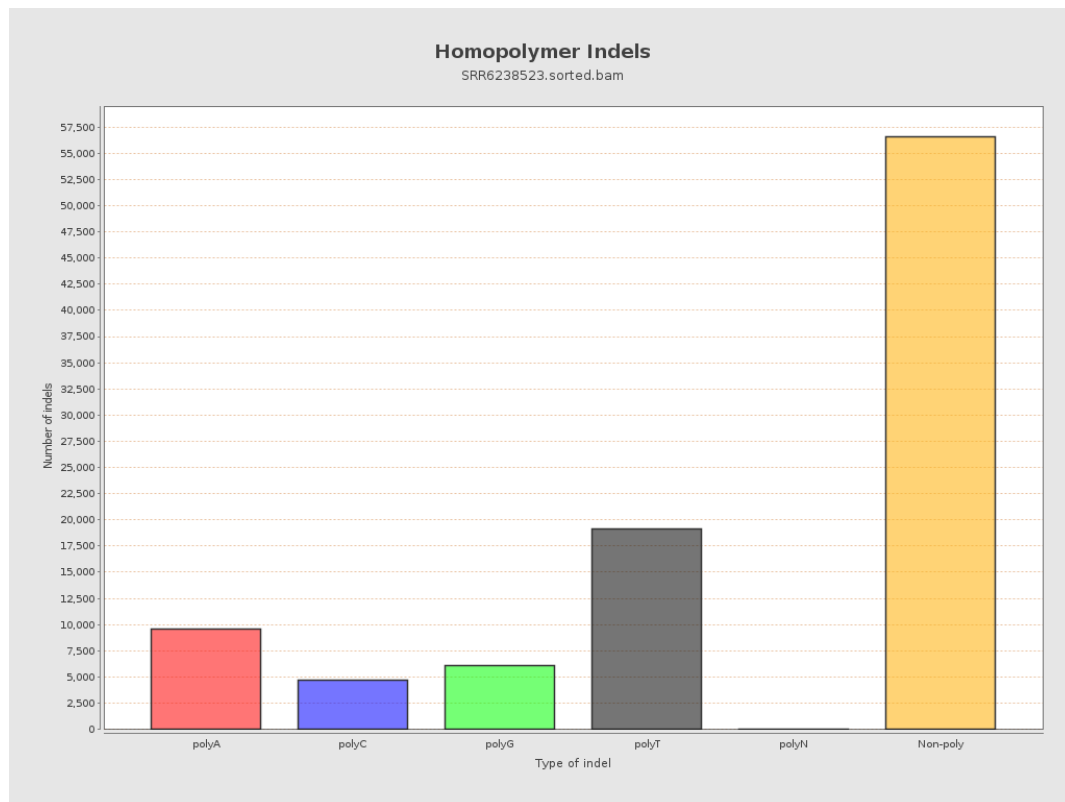
9. Results : Mapped Reads GC-content Distribution



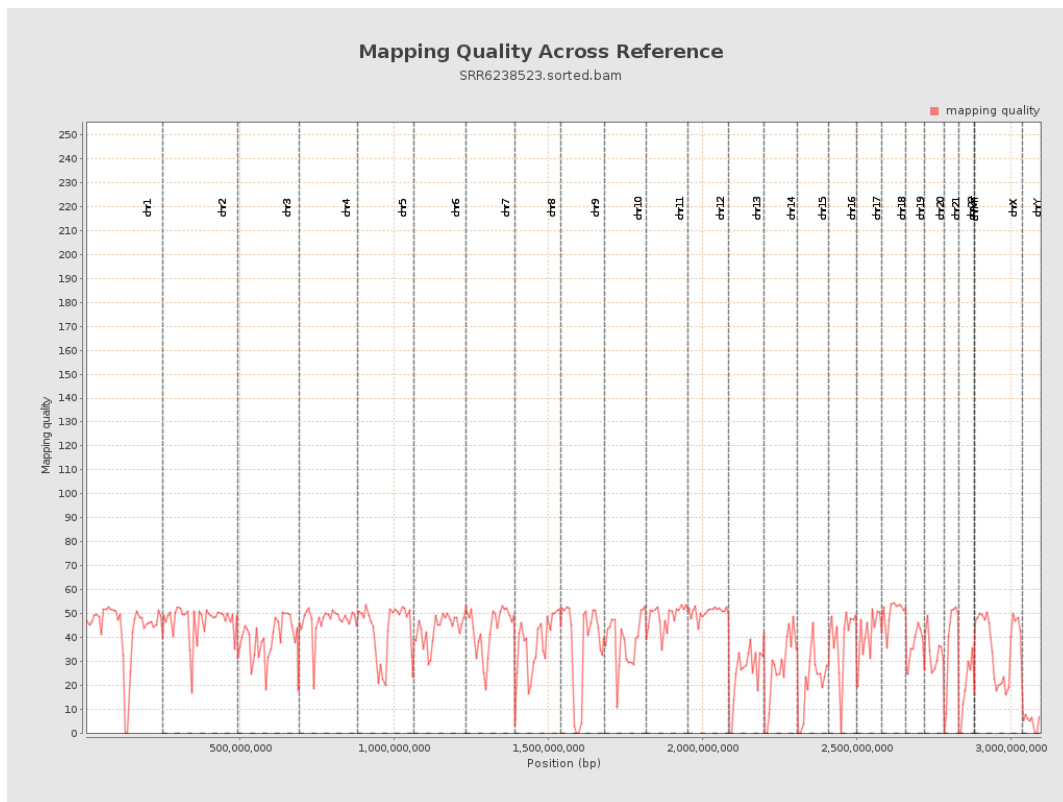
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

