

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:29:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238598.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_SRR6238598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:29:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,632,413
Mapped reads	3,029,402 / 83.4%
Unmapped reads	603,011 / 16.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,806 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,378,740 / 37.96%
Duplication rate	22.89%
Clipped reads	2,078,437 / 57.22%

2.2. ACGT Content

Number/percentage of A's	44,414,807 / 24.31%
Number/percentage of C's	31,244,734 / 17.1%
Number/percentage of T's	62,885,315 / 34.42%
Number/percentage of G's	44,132,413 / 24.16%
Number/percentage of N's	3,832 / 0%
GC Percentage	41.26%

2.3. Coverage

Mean	0.059

Standard Deviation	1.4562
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2.4. Mapping Quality

Mean Mapping Quality	39.17
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2.5. Mismatches and indels

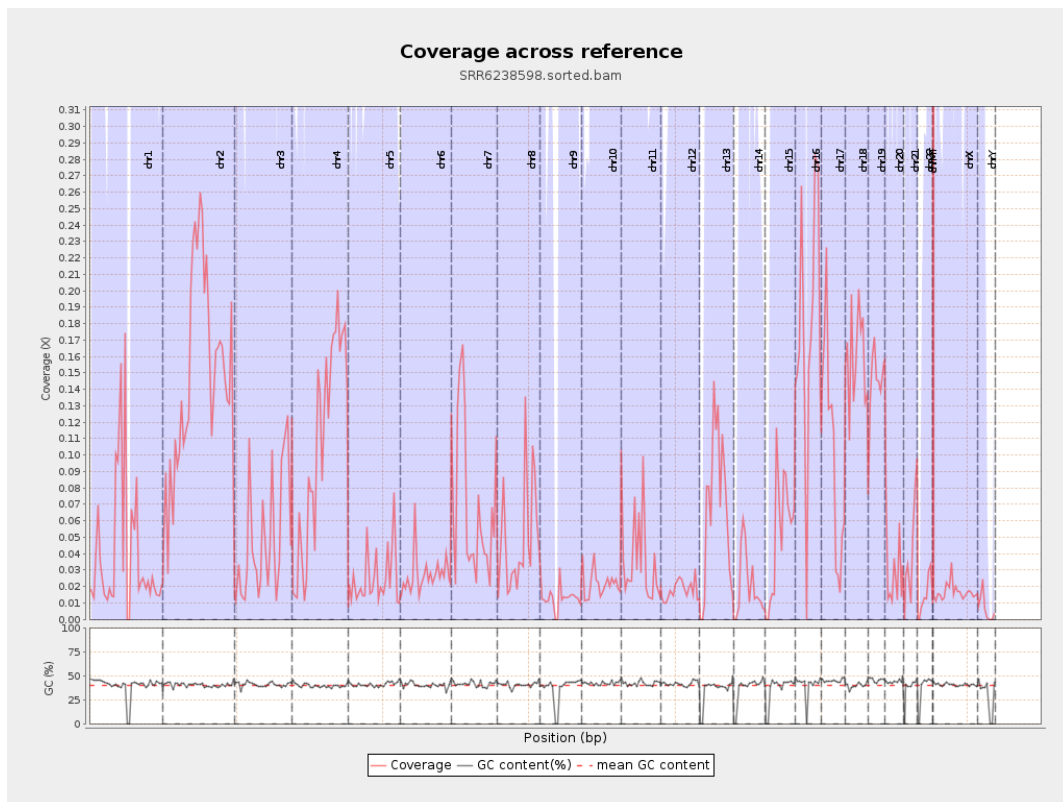
General error rate	0.66%
Mismatches	1,186,678
Insertions	12,411
Mapped reads with at least one insertion	0.41%
Deletions	70,420
Mapped reads with at least one deletion	2.3%
Homopolymer indels	39.62%

2.6. Chromosome stats

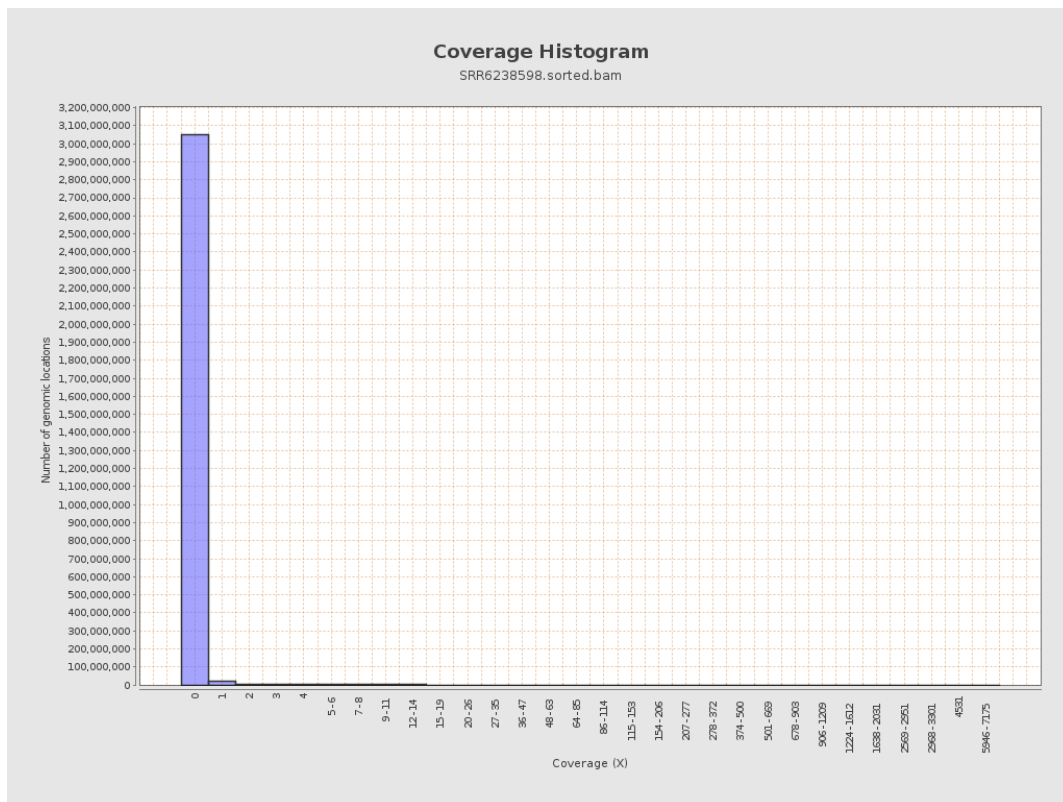
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9793081	0.0393	1.5518
chr2	243199373	36134907	0.1486	3.3674
chr3	198022430	9740616	0.0492	0.7199
chr4	191154276	20218294	0.1058	1.3349
chr5	180915260	4479134	0.0248	0.5017
chr6	171115067	4690230	0.0274	1.077
chr7	159138663	10928764	0.0687	0.9766

chr8	146364022	7149722	0.0488	0.8656
chr9	141213431	1833379	0.013	0.3698
chr10	135534747	2907103	0.0214	0.4714
chr11	135006516	4614413	0.0342	0.5728
chr12	133851895	2406115	0.018	0.4204
chr13	115169878	7682553	0.0667	1.0764
chr14	107349540	2309680	0.0215	0.4529
chr15	102531392	5119497	0.0499	0.9243
chr16	90354753	15665631	0.1734	1.3808
chr17	81195210	8248309	0.1016	1.0617
chr18	78077248	12442897	0.1594	4.2572
chr19	59128983	8680429	0.1468	1.4637
chr20	63025520	1842599	0.0292	0.5248
chr21	48129895	2066427	0.0429	0.6666
chr22	51304566	765760	0.0149	0.349
chrMT	16571	68372	4.126	6.7836
chrX	155270560	2591370	0.0167	0.3711
chrY	59373566	420386	0.0071	0.5396

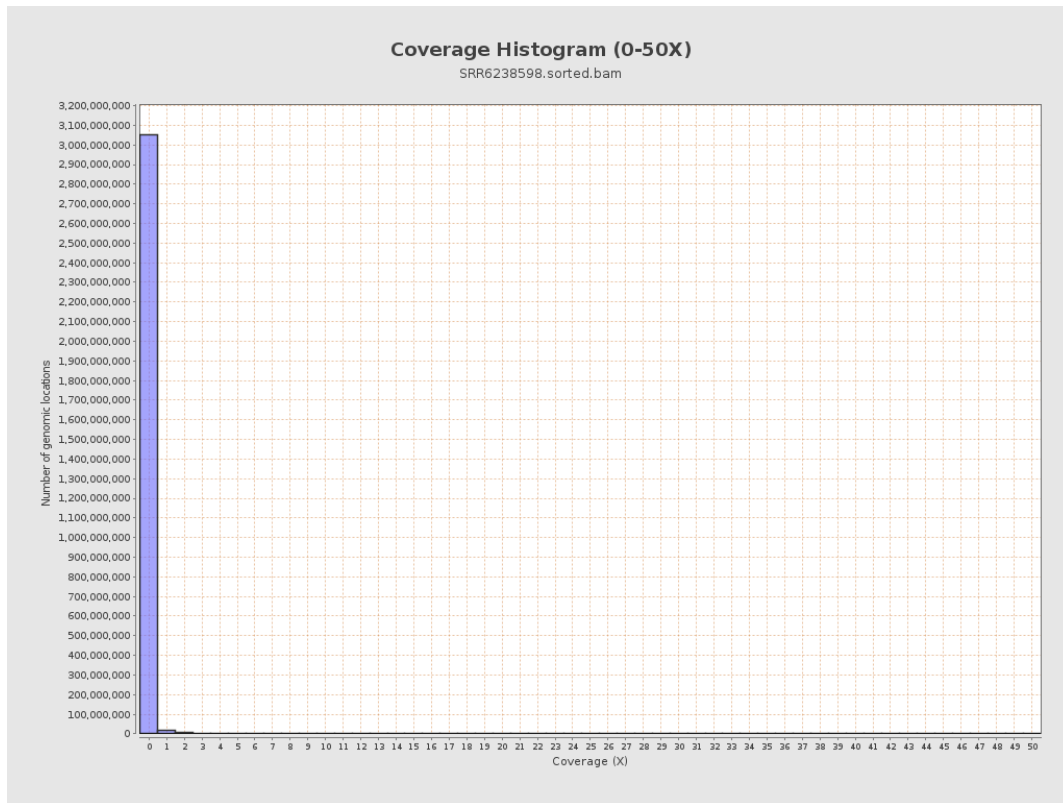
3. Results : Coverage across reference



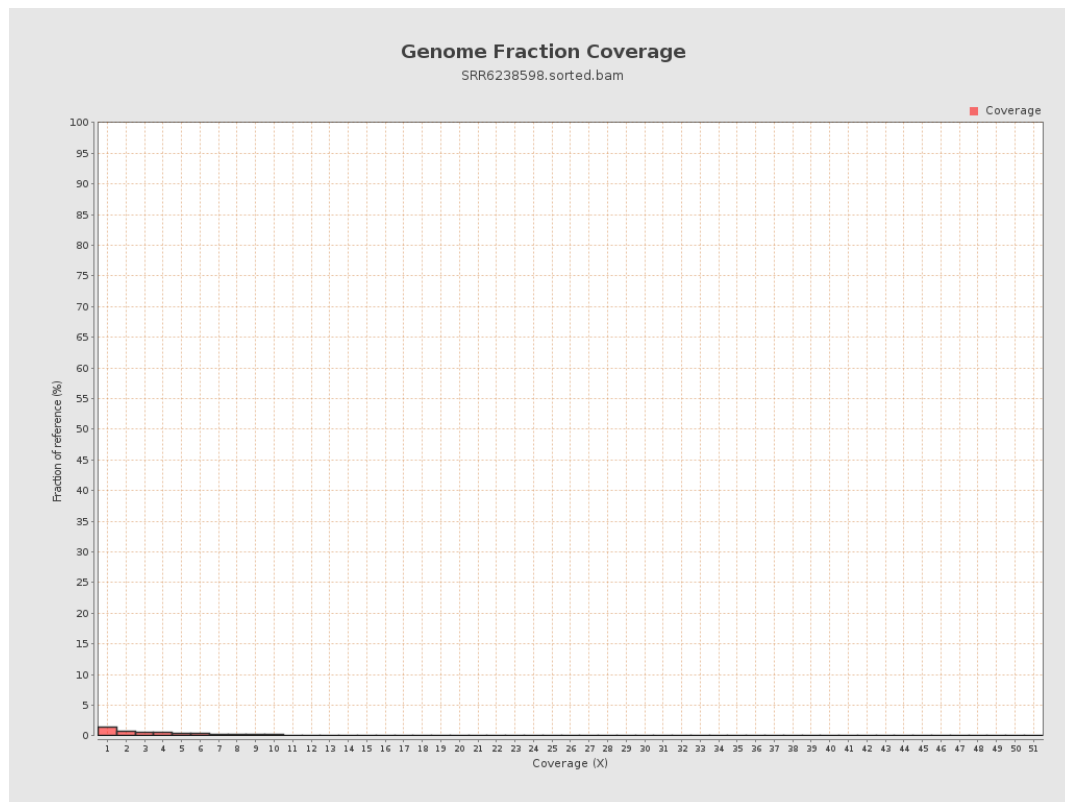
4. Results : Coverage Histogram



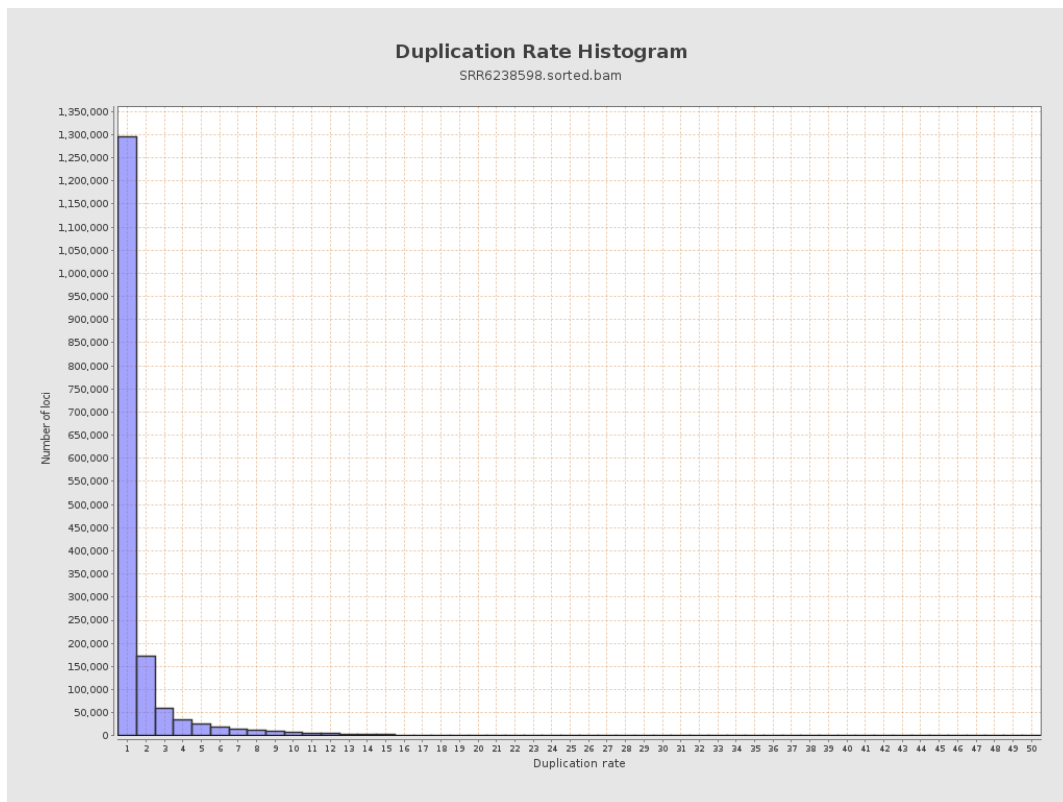
5. Results : Coverage Histogram (0-50X)



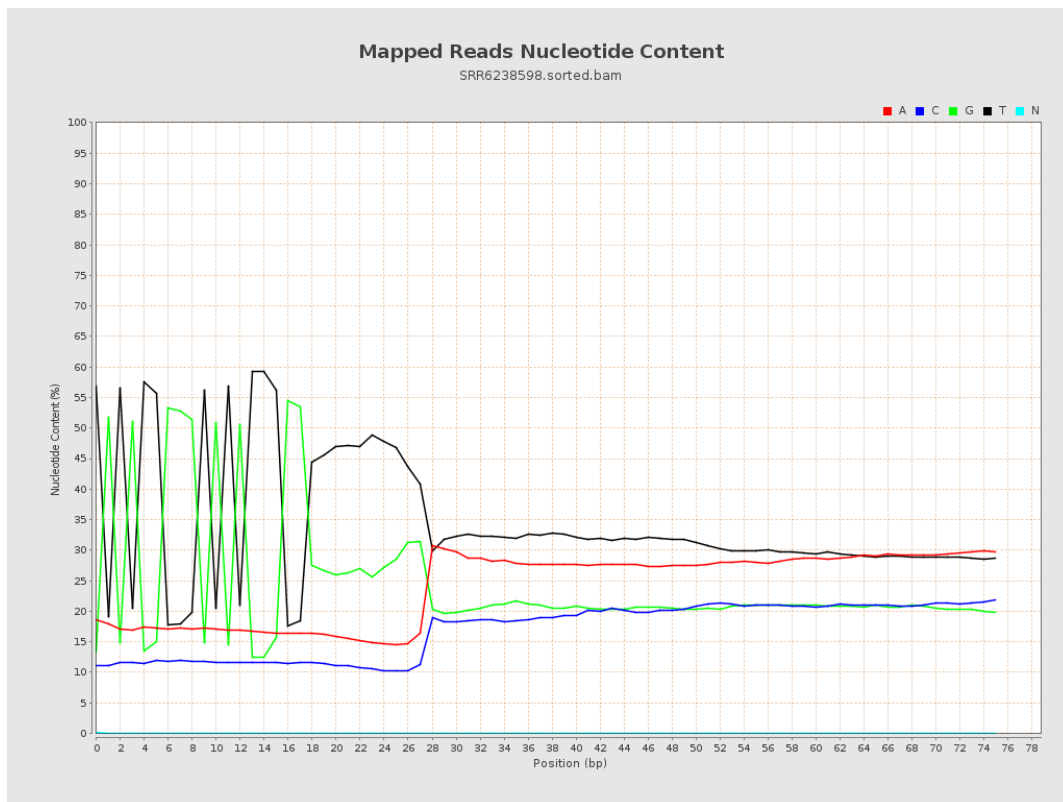
6. Results : Genome Fraction Coverage



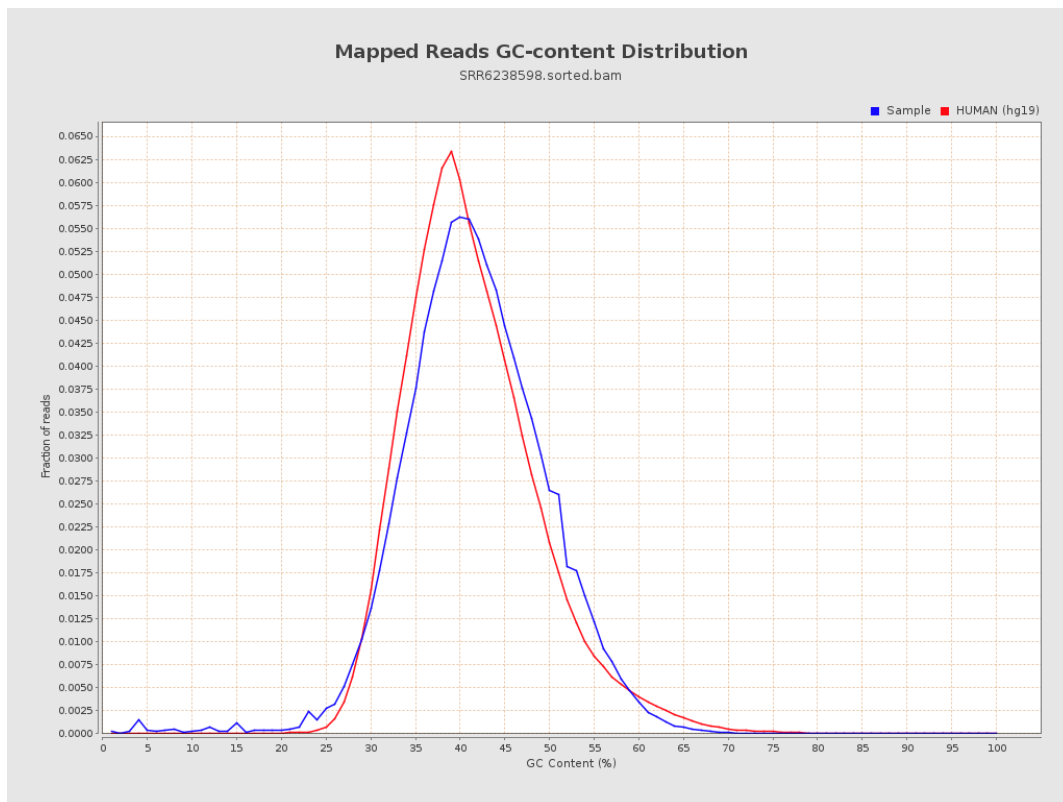
7. Results : Duplication Rate Histogram



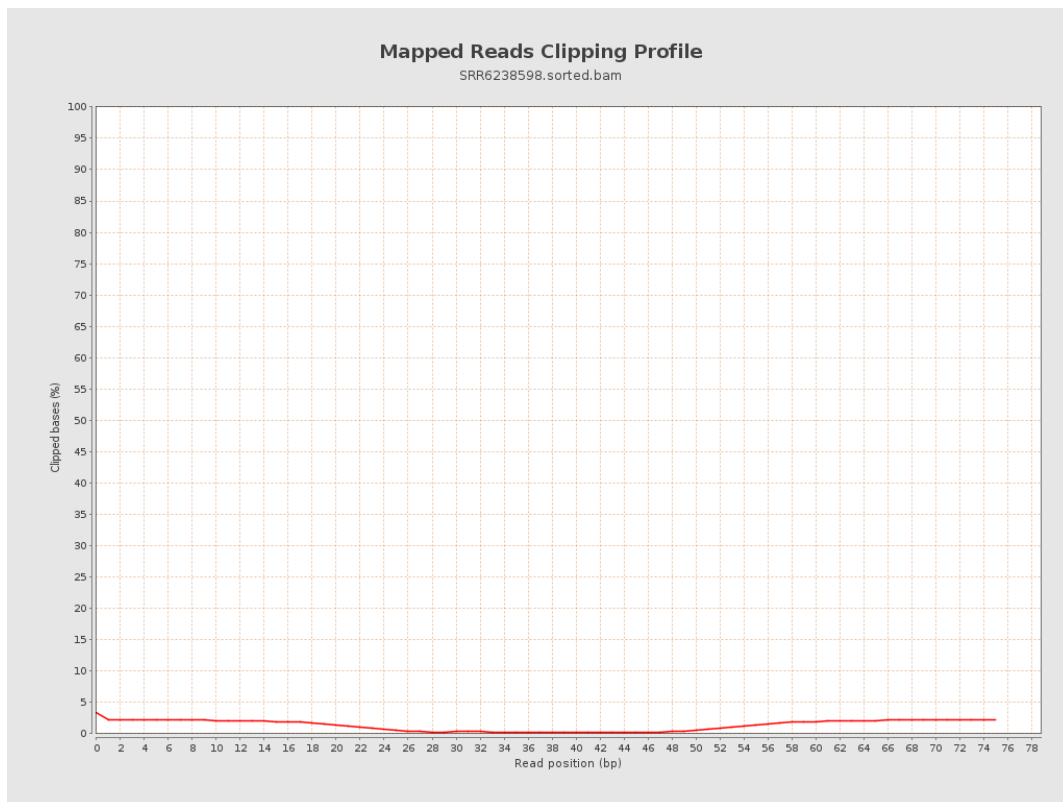
8. Results : Mapped Reads Nucleotide Content



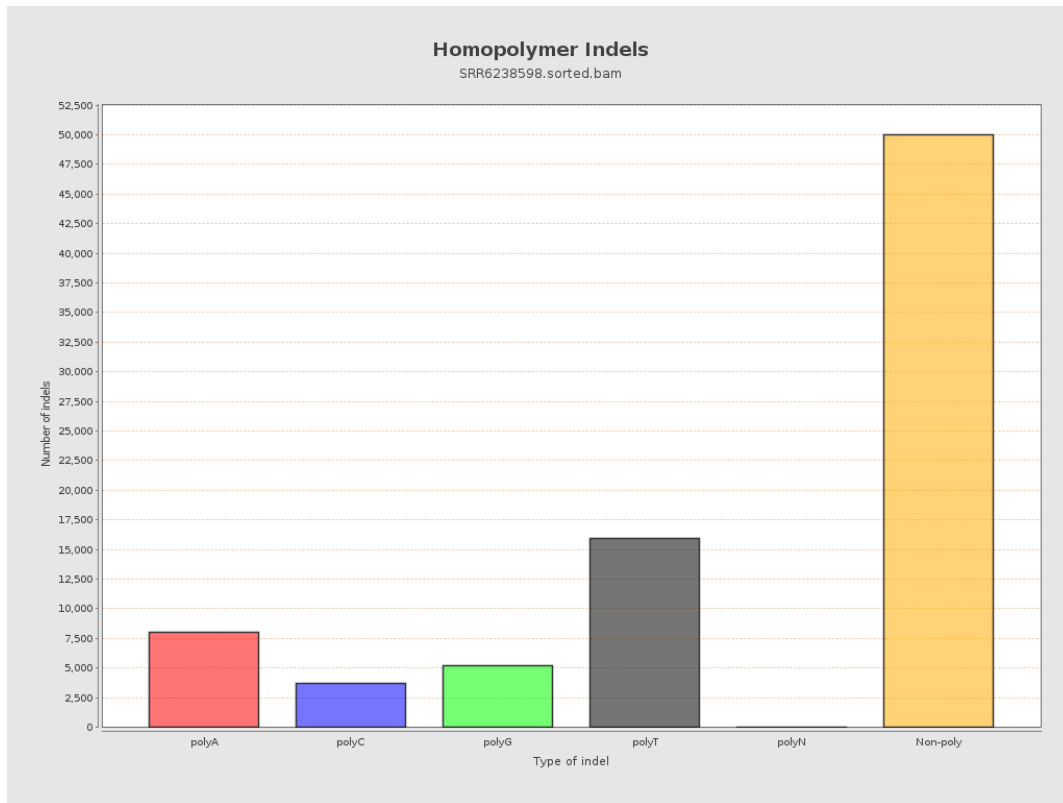
9. Results : Mapped Reads GC-content Distribution



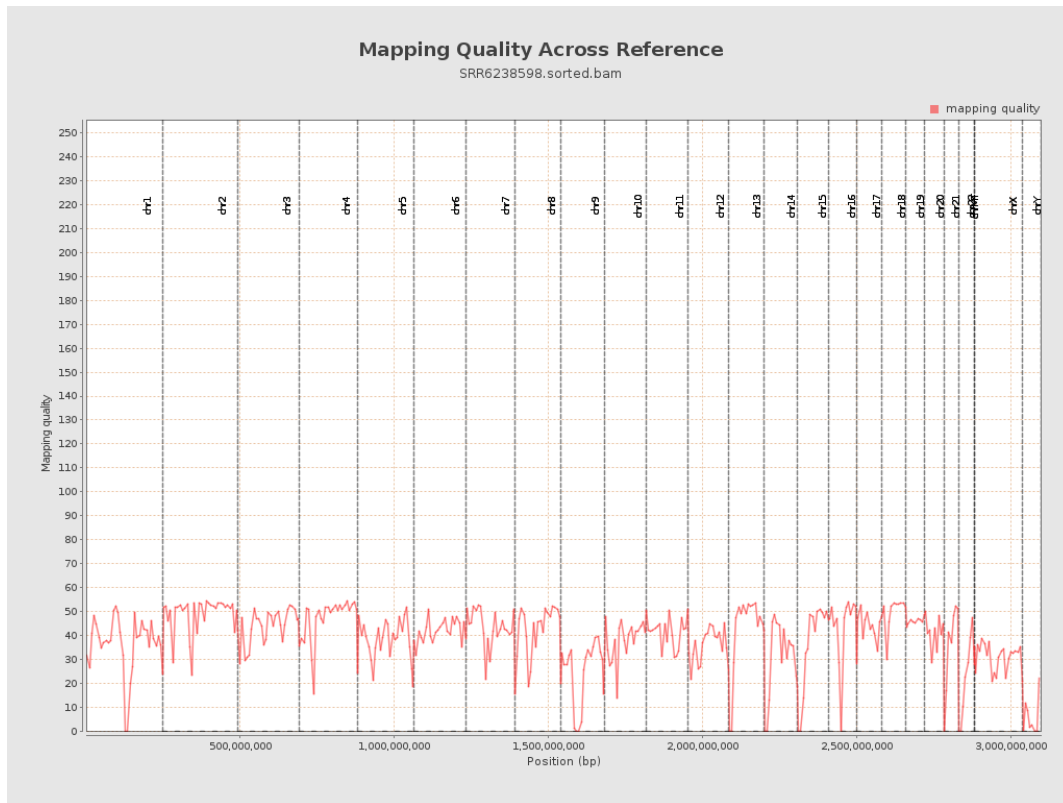
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

