

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:43:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238308.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_SRR6238308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:43:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,741,633
Mapped reads	2,481,835 / 90.52%
Unmapped reads	259,798 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,468 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	95,839 / 3.5%
Duplication rate	2.79%
Clipped reads	1,380,084 / 50.34%

2.2. ACGT Content

Number/percentage of A's	43,320,434 / 27.06%
Number/percentage of C's	30,706,673 / 19.18%
Number/percentage of T's	48,709,925 / 30.43%
Number/percentage of G's	37,292,927 / 23.3%
Number/percentage of N's	39,401 / 0.02%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0517

Standard Deviation	0.4348
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2.4. Mapping Quality

Mean Mapping Quality	44.12
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2.5. Mismatches and indels

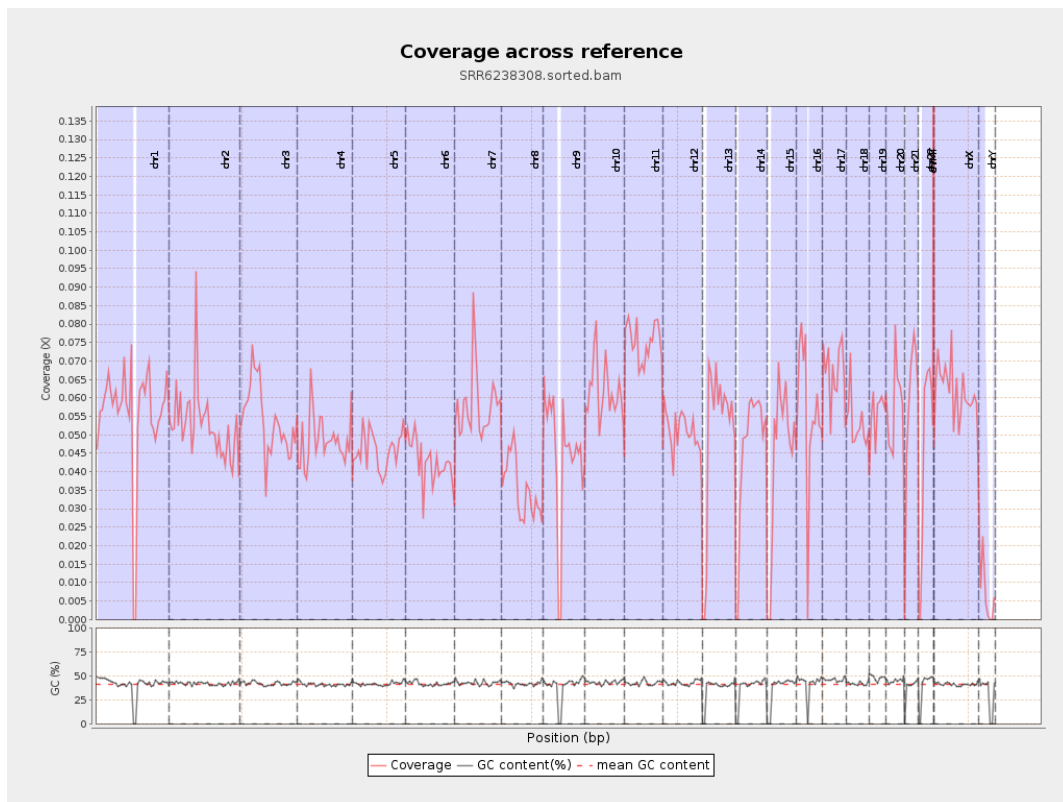
General error rate	0.89%
Mismatches	1,401,245
Insertions	12,863
Mapped reads with at least one insertion	0.51%
Deletions	49,413
Mapped reads with at least one deletion	1.97%
Homopolymer indels	44.36%

2.6. Chromosome stats

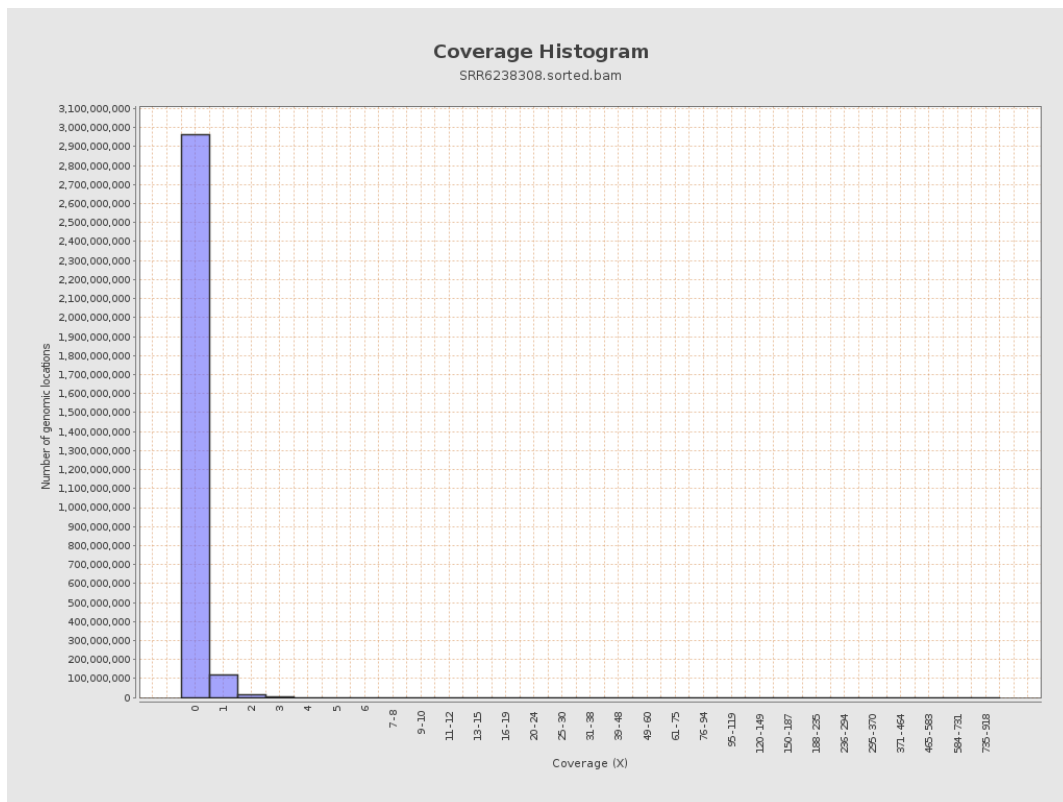
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13911499	0.0558	0.6713
chr2	243199373	12819491	0.0527	0.5709
chr3	198022430	10680293	0.0539	0.2651
chr4	191154276	9254723	0.0484	0.2744
chr5	180915260	8313955	0.046	0.2472
chr6	171115067	7285428	0.0426	0.2829
chr7	159138663	9327530	0.0586	0.5925

chr8	146364022	5125574	0.035	0.5561
chr9	141213431	6228972	0.0441	0.4166
chr10	135534747	8414957	0.0621	0.3849
chr11	135006516	10037795	0.0744	0.5258
chr12	133851895	6816381	0.0509	0.2721
chr13	115169878	5794956	0.0503	0.2573
chr14	107349540	4959599	0.0462	0.3047
chr15	102531392	4569884	0.0446	0.2533
chr16	90354753	5094584	0.0564	0.3129
chr17	81195210	5405364	0.0666	0.4272
chr18	78077248	4154993	0.0532	0.8228
chr19	59128983	3306158	0.0559	0.5039
chr20	63025520	3580590	0.0568	0.2883
chr21	48129895	2783300	0.0578	0.3071
chr22	51304566	2291269	0.0447	0.2451
chrMT	16571	3950	0.2384	0.5025
chrX	155270560	9562047	0.0616	0.3307
chrY	59373566	428216	0.0072	0.1634

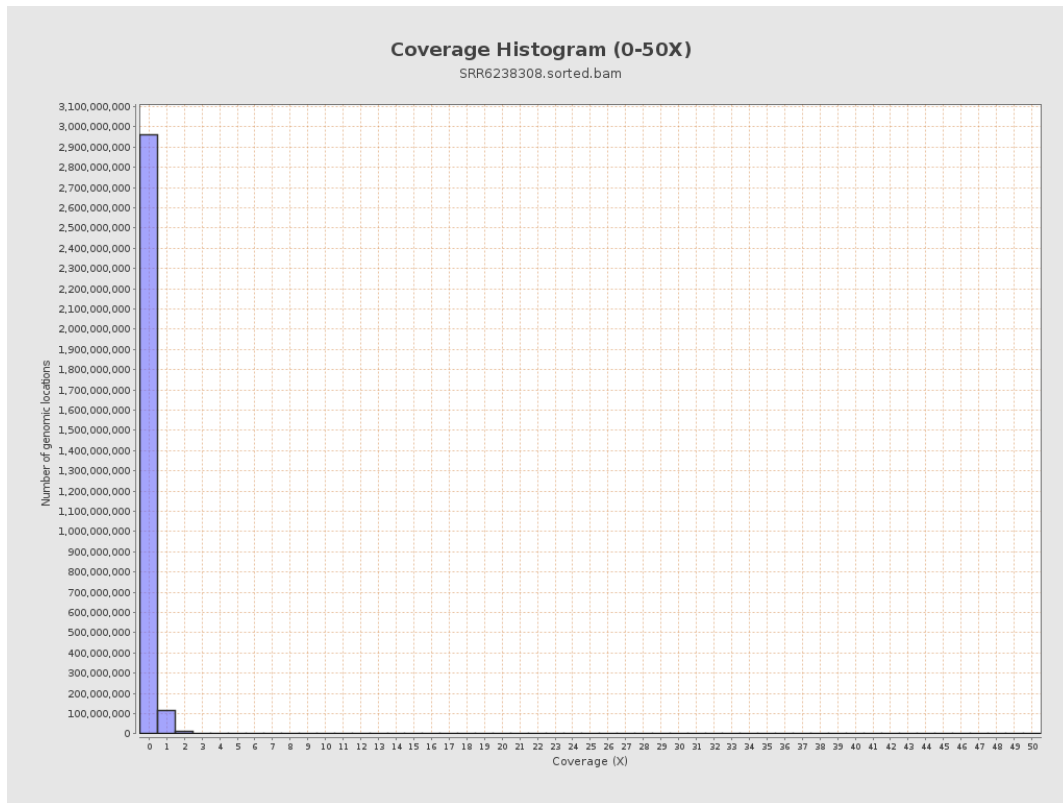
3. Results : Coverage across reference



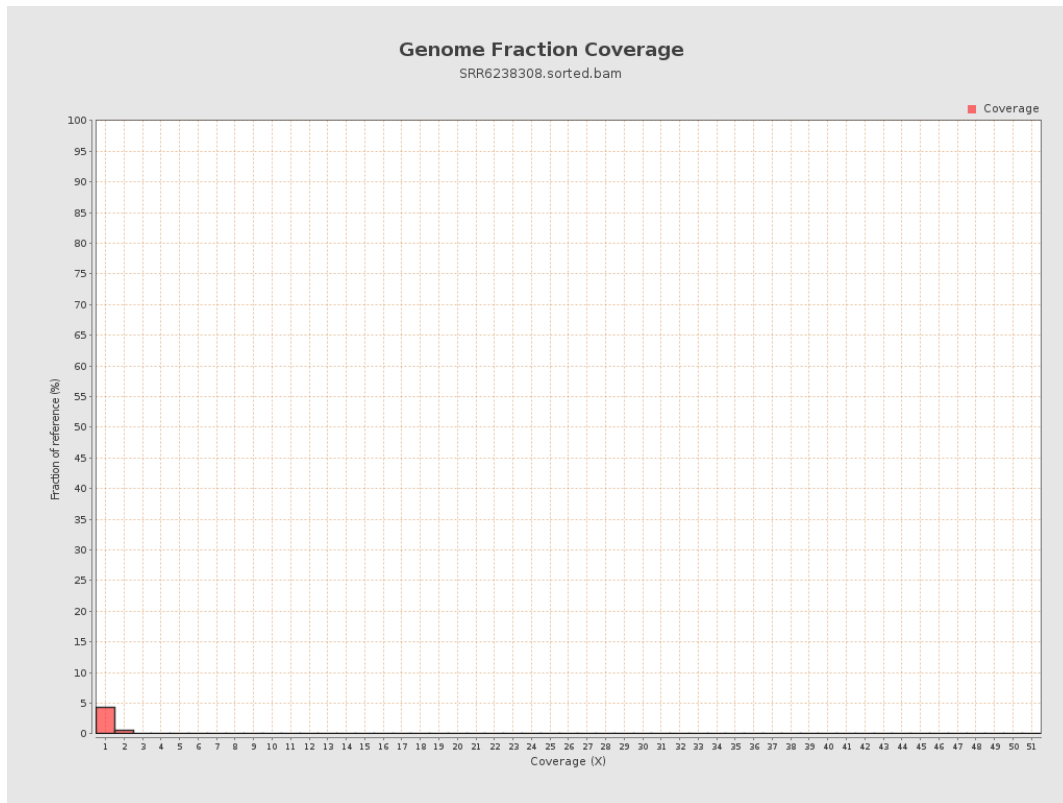
4. Results : Coverage Histogram



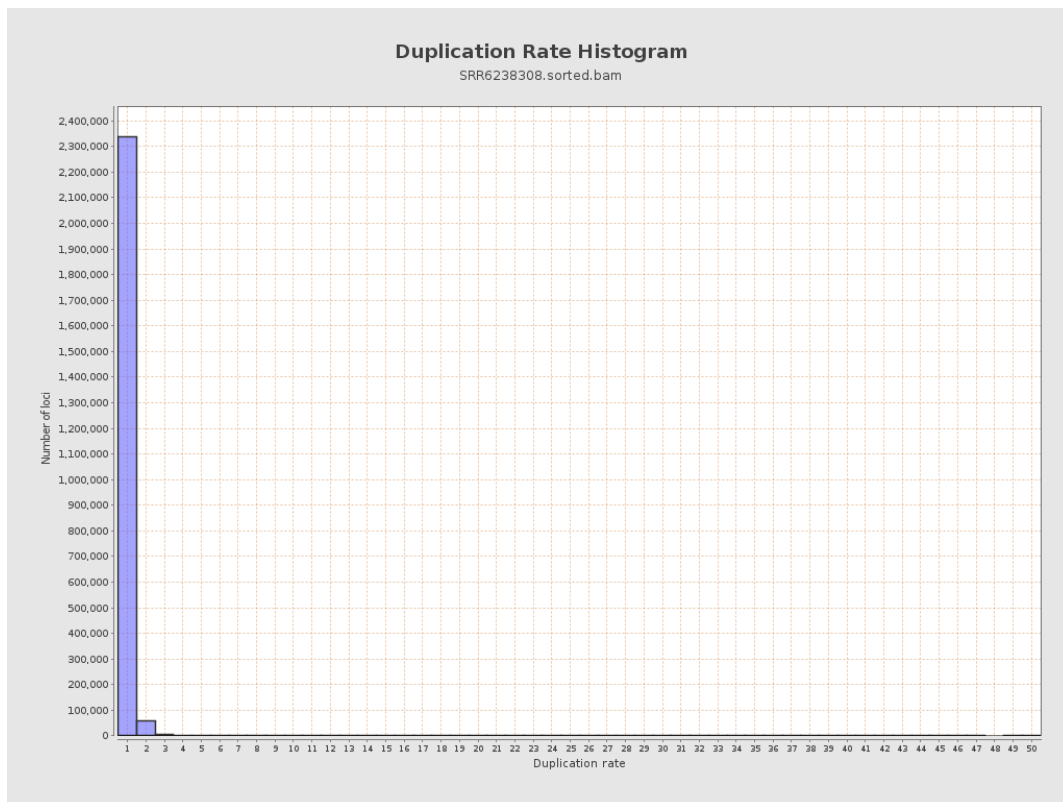
5. Results : Coverage Histogram (0-50X)



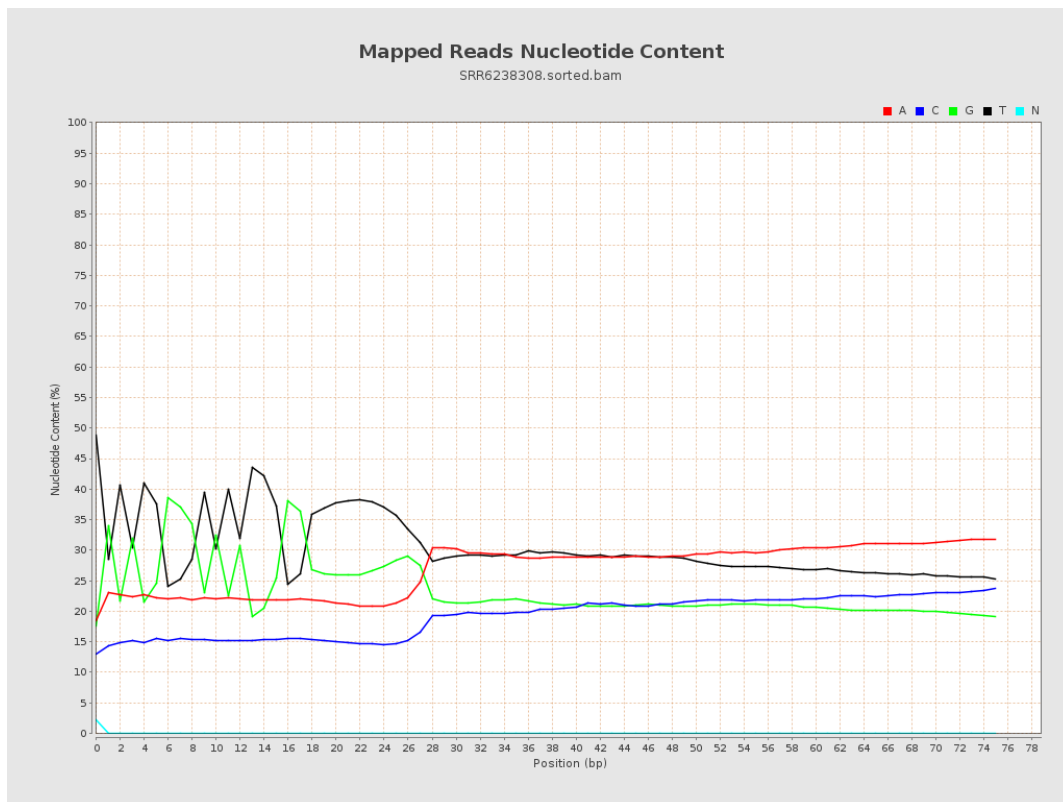
6. Results : Genome Fraction Coverage



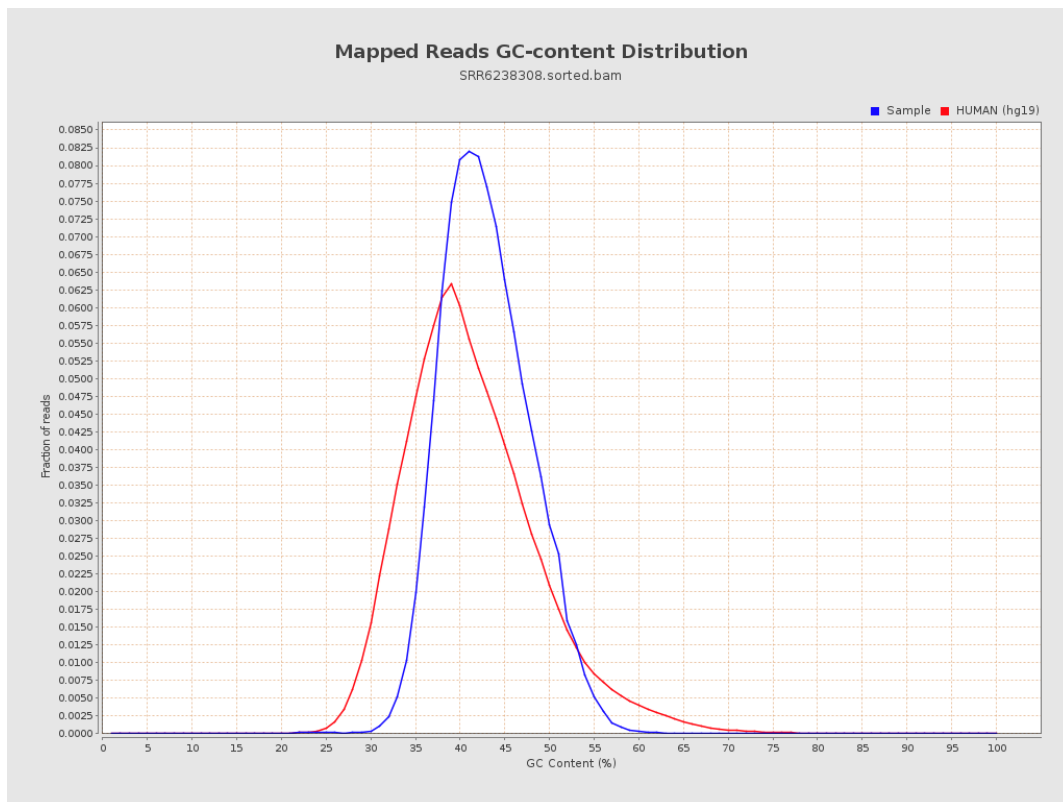
7. Results : Duplication Rate Histogram



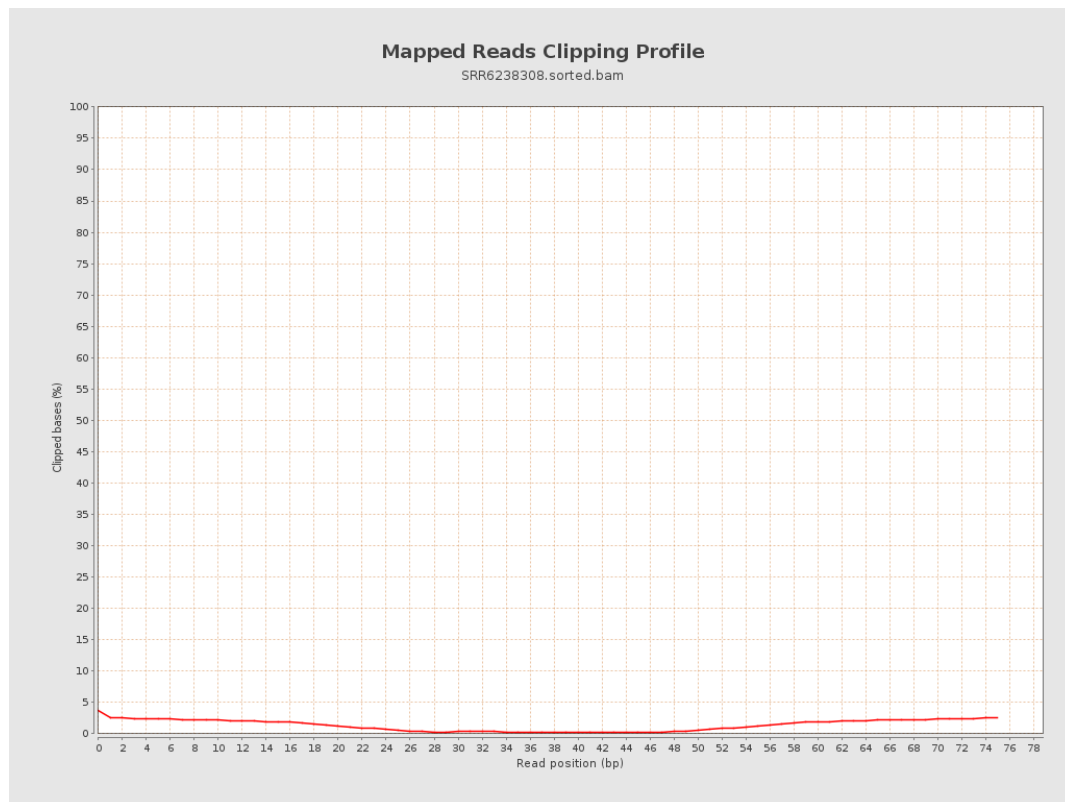
8. Results : Mapped Reads Nucleotide Content



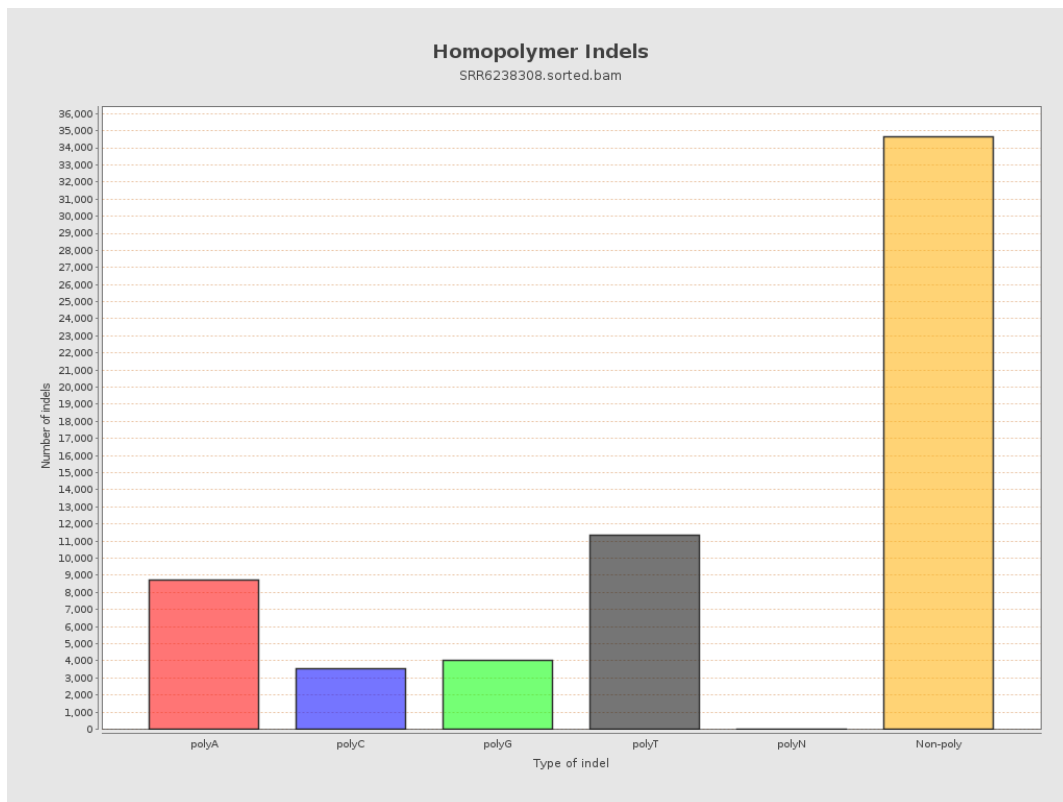
9. Results : Mapped Reads GC-content Distribution



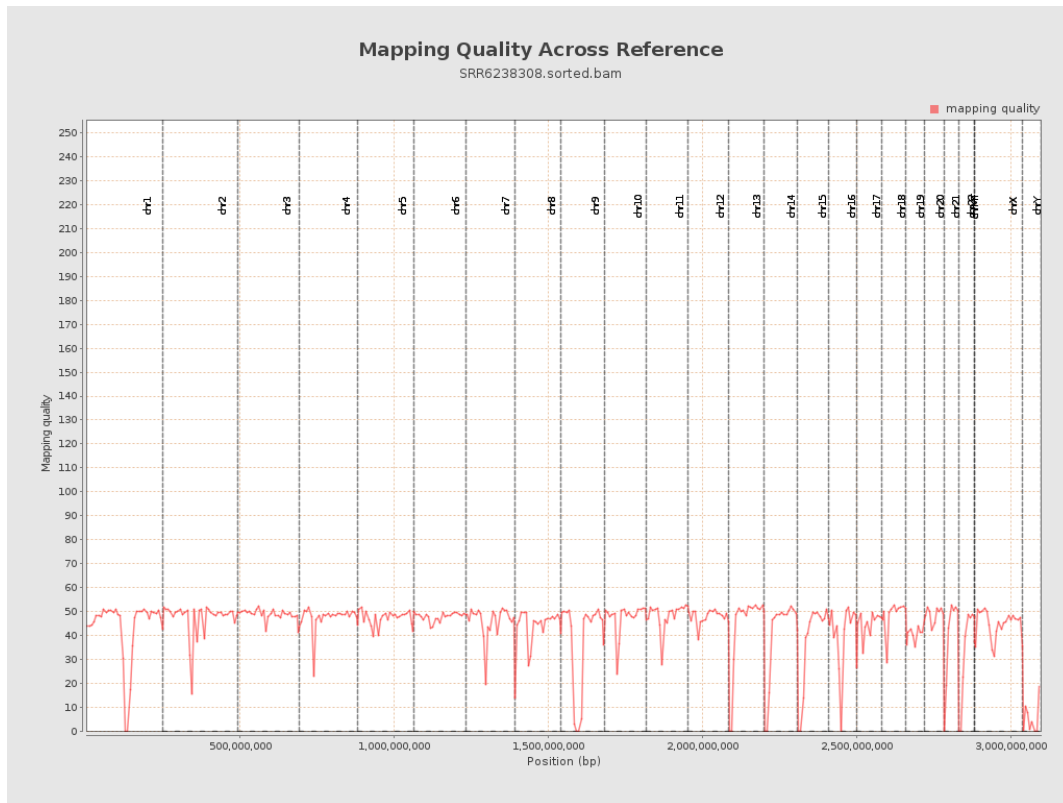
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

