

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:01:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236088.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_SRR6236088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:01:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,403,578
Mapped reads	2,930,416 / 86.1%
Unmapped reads	473,162 / 13.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,555 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	285,426 / 8.39%
Duplication rate	7.47%
Clipped reads	1,358,016 / 39.9%

2.2. ACGT Content

Number/percentage of A's	53,843,600 / 27.82%
Number/percentage of C's	34,261,777 / 17.7%
Number/percentage of T's	62,949,435 / 32.52%
Number/percentage of G's	42,443,058 / 21.93%
Number/percentage of N's	75,433 / 0.04%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0626

Standard Deviation	0.7672
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2.4. Mapping Quality

Mean Mapping Quality	44.18
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2.5. Mismatches and indels

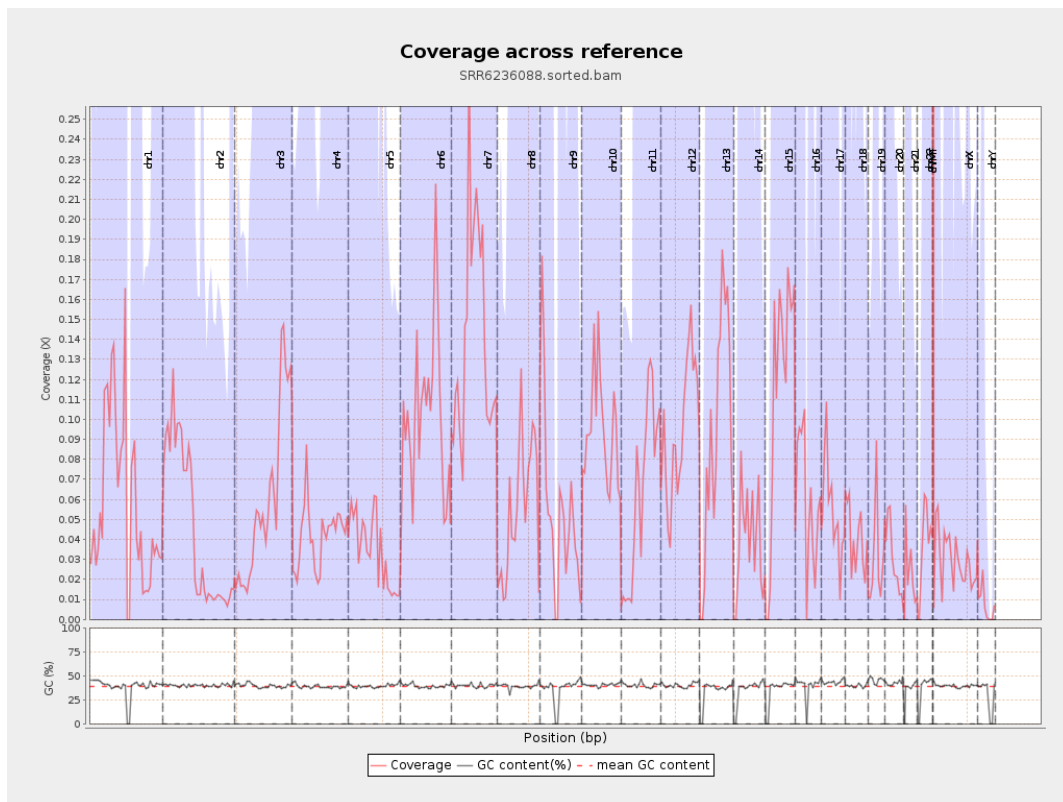
General error rate	0.84%
Mismatches	1,598,806
Insertions	13,408
Mapped reads with at least one insertion	0.45%
Deletions	58,431
Mapped reads with at least one deletion	1.97%
Homopolymer indels	46.49%

2.6. Chromosome stats

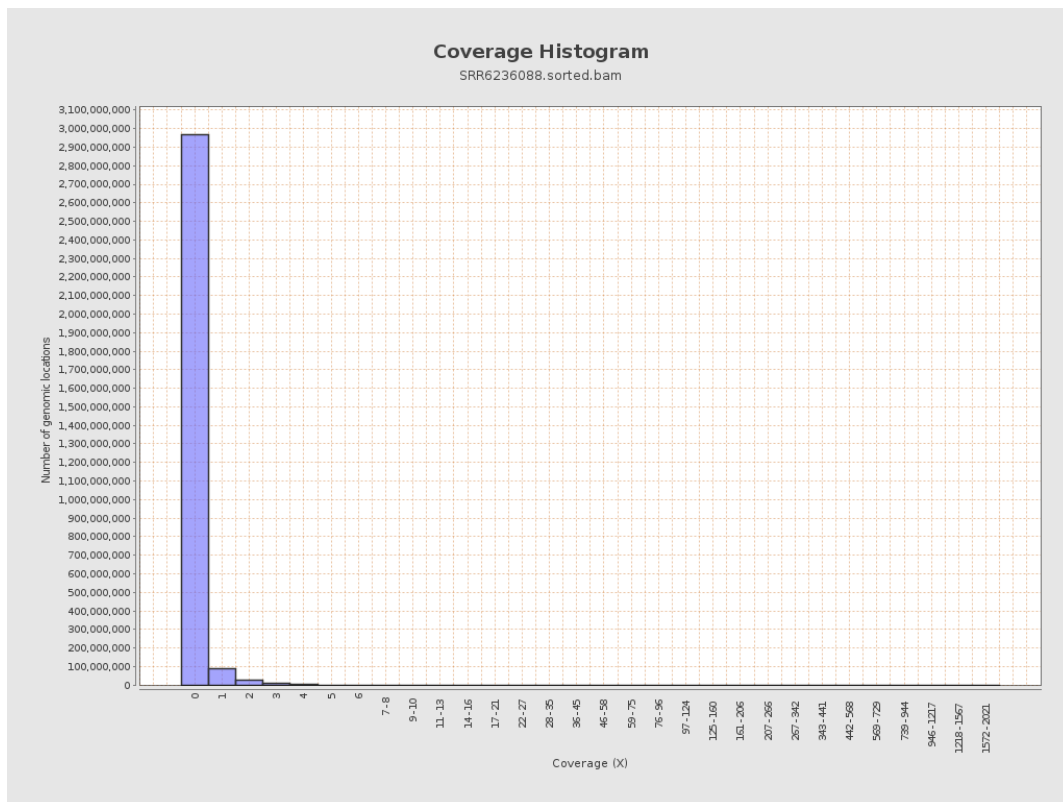
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14356500	0.0576	1.5269
chr2	243199373	11107302	0.0457	0.4978
chr3	198022430	11935502	0.0603	0.3466
chr4	191154276	8095362	0.0423	0.2935
chr5	180915260	6262329	0.0346	0.2656
chr6	171115067	17402603	0.1017	0.6266
chr7	159138663	22753915	0.143	1.6562

chr8	146364022	8315721	0.0568	1.2993
chr9	141213431	7613603	0.0539	0.44
chr10	135534747	12826291	0.0946	0.6295
chr11	135006516	8672326	0.0642	0.5326
chr12	133851895	12822103	0.0958	0.4365
chr13	115169878	10712358	0.093	0.4315
chr14	107349540	4233796	0.0394	0.2862
chr15	102531392	11422757	0.1114	0.4741
chr16	90354753	5328281	0.059	0.3559
chr17	81195210	4390917	0.0541	0.529
chr18	78077248	3144230	0.0403	0.7615
chr19	59128983	1900182	0.0321	0.9306
chr20	63025520	1889630	0.03	0.2479
chr21	48129895	1091728	0.0227	0.2297
chr22	51304566	1872083	0.0365	0.2584
chrMT	16571	512792	30.9451	18.384
chrX	155270560	4568058	0.0294	0.2795
chrY	59373566	444257	0.0075	0.1818

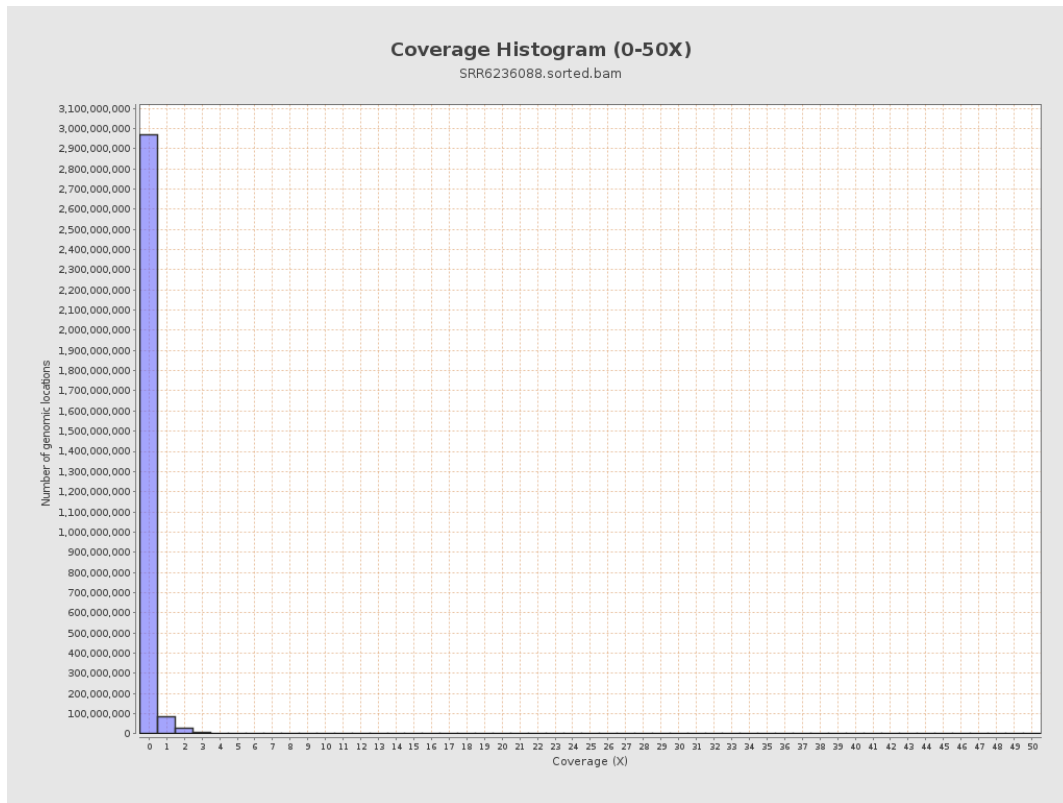
3. Results : Coverage across reference



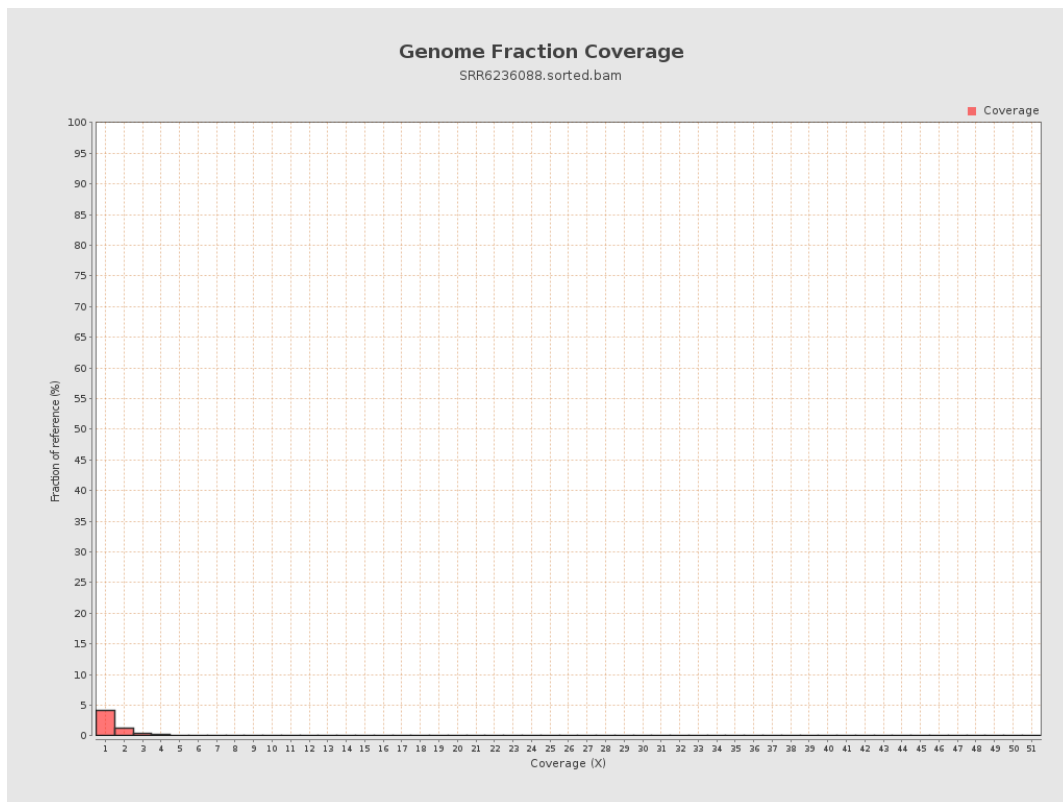
4. Results : Coverage Histogram



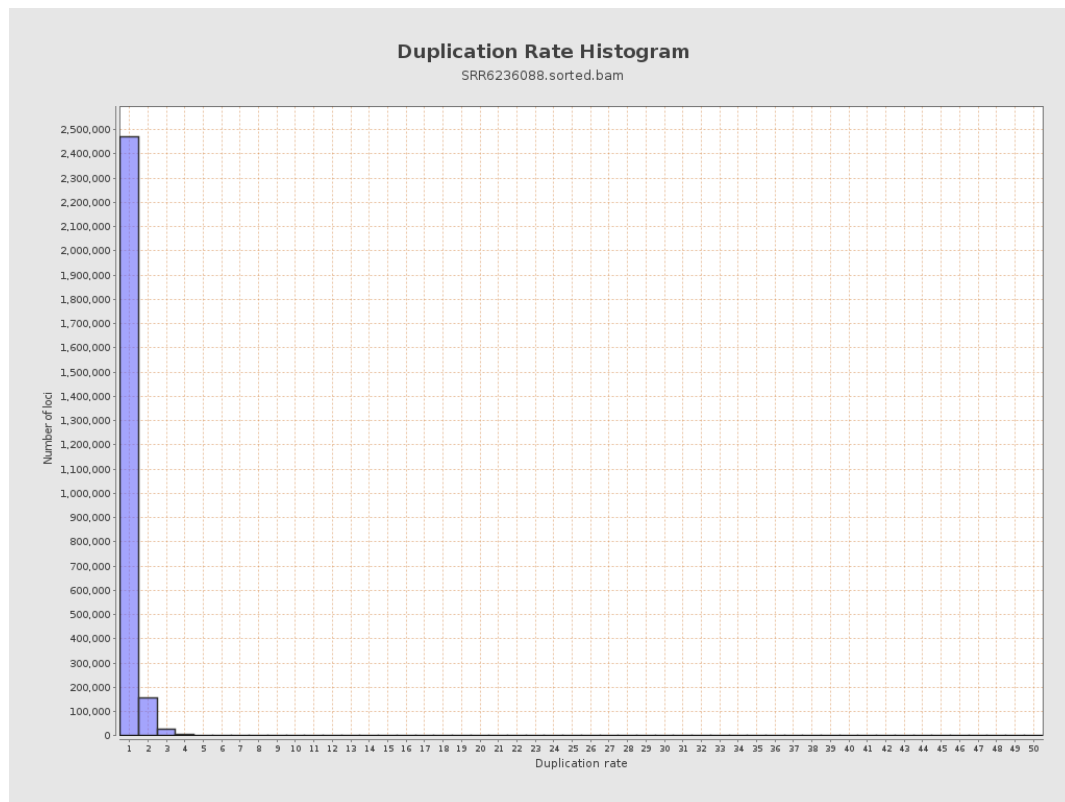
5. Results : Coverage Histogram (0-50X)



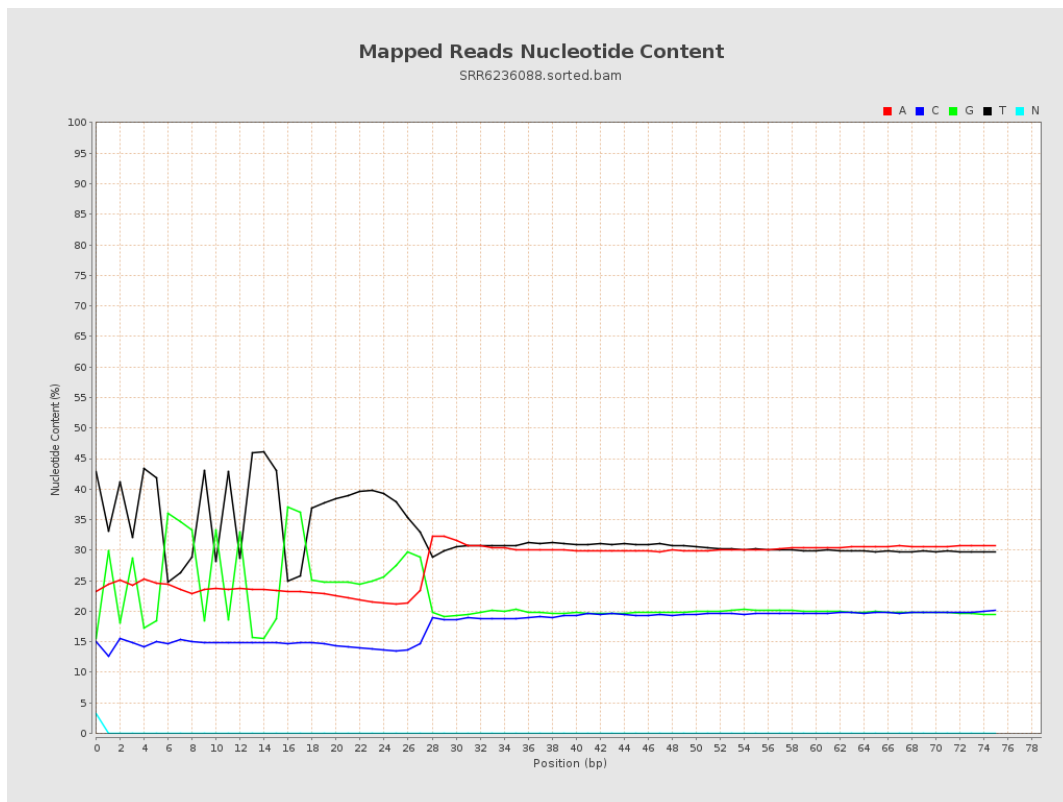
6. Results : Genome Fraction Coverage



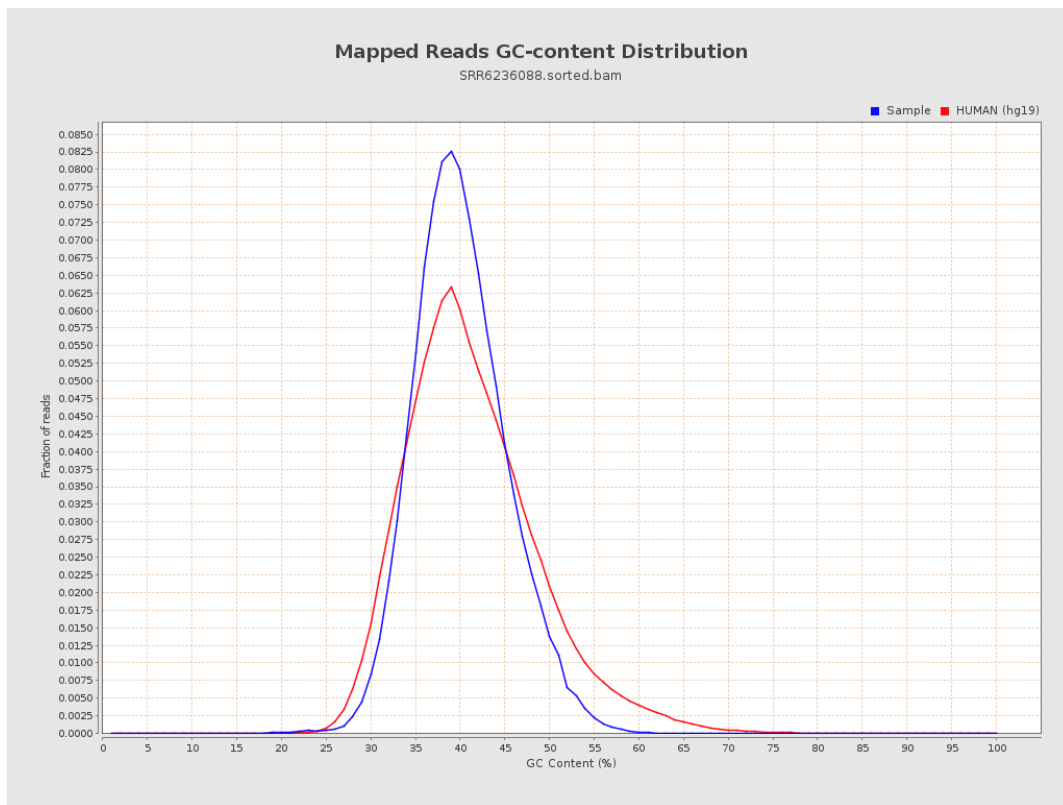
7. Results : Duplication Rate Histogram



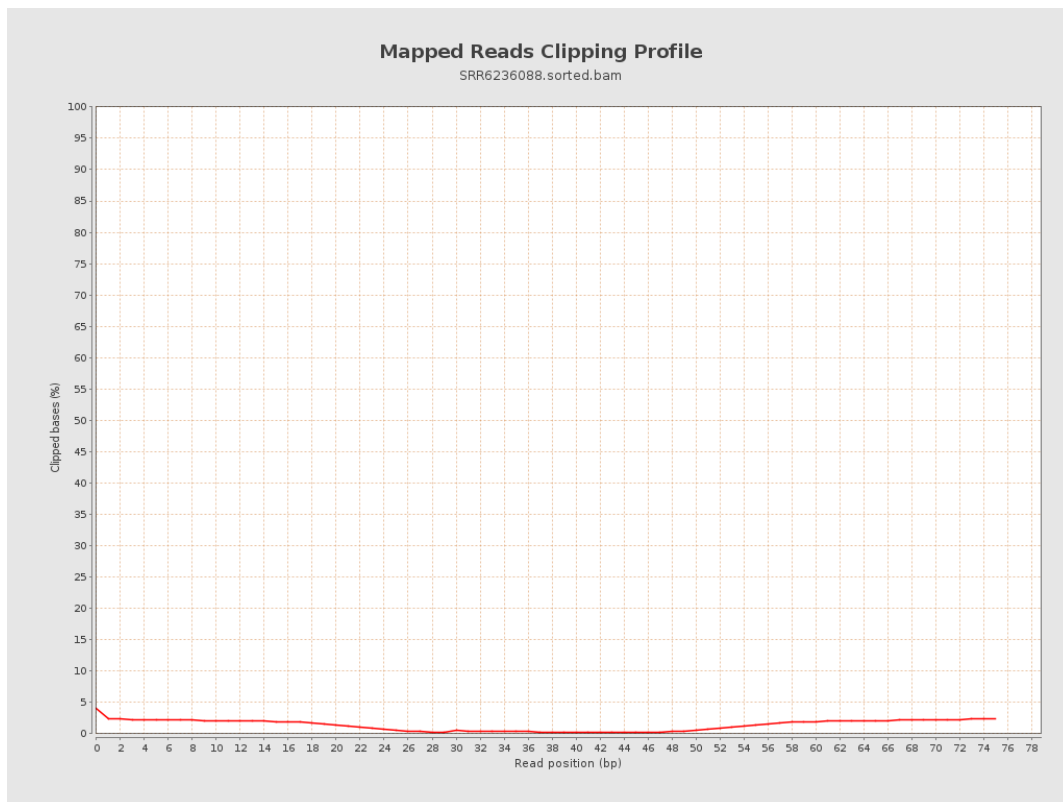
8. Results : Mapped Reads Nucleotide Content



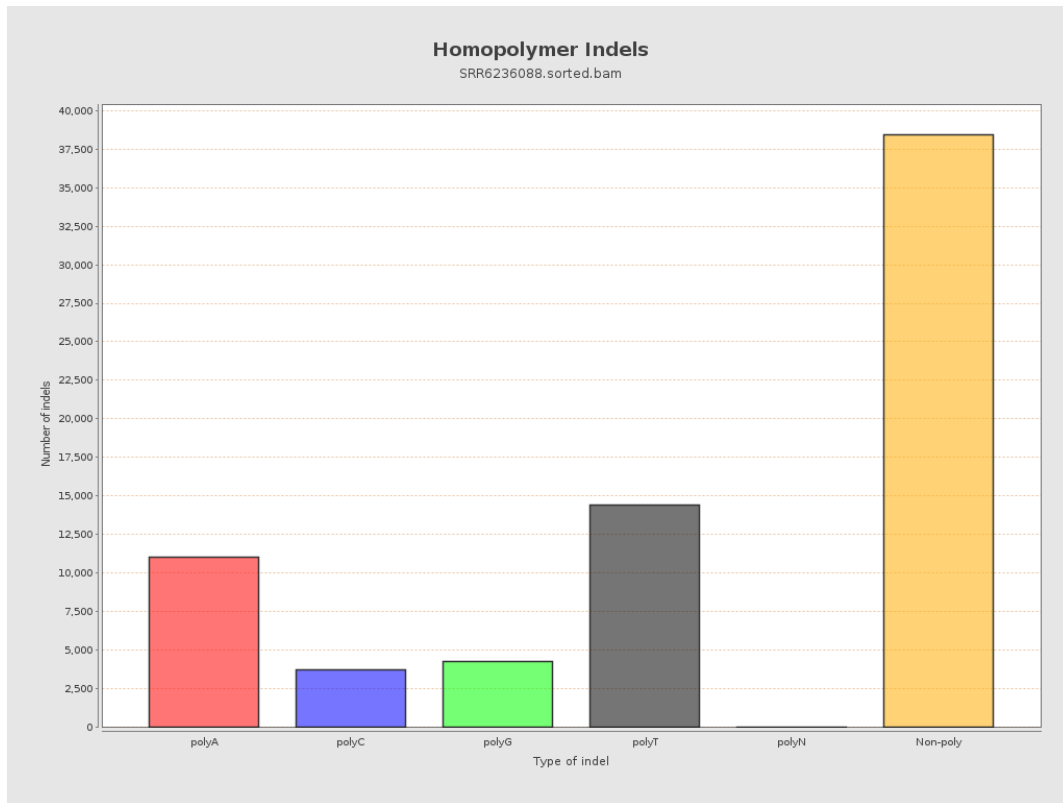
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

