

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:06:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525072.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_SRR10525072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:06:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,389,913
Mapped reads	16,148,646 / 92.86%
Unmapped reads	1,241,267 / 7.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	67,464 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	2,942,571 / 16.92%
Duplication rate	11.42%
Clipped reads	16,185,776 / 93.08%

2.2. ACGT Content

Number/percentage of A's	240,243,518 / 25.19%
Number/percentage of C's	178,861,467 / 18.76%
Number/percentage of T's	304,499,641 / 31.93%
Number/percentage of G's	229,945,797 / 24.11%
Number/percentage of N's	102,088 / 0.01%
GC Percentage	42.87%

2.3. Coverage

Mean	0.3081

Standard Deviation	1.9728
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2.4. Mapping Quality

Mean Mapping Quality	46.08
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2.5. Mismatches and indels

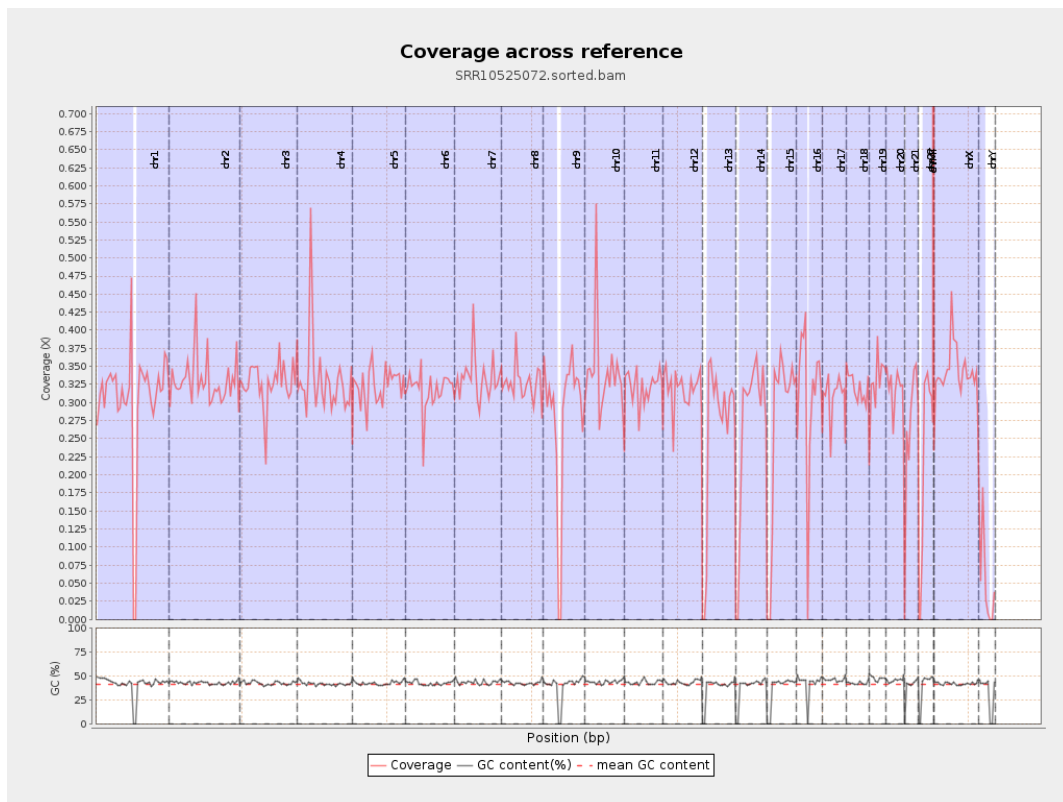
General error rate	0.46%
Mismatches	4,236,513
Insertions	59,809
Mapped reads with at least one insertion	0.37%
Deletions	166,687
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.55%

2.6. Chromosome stats

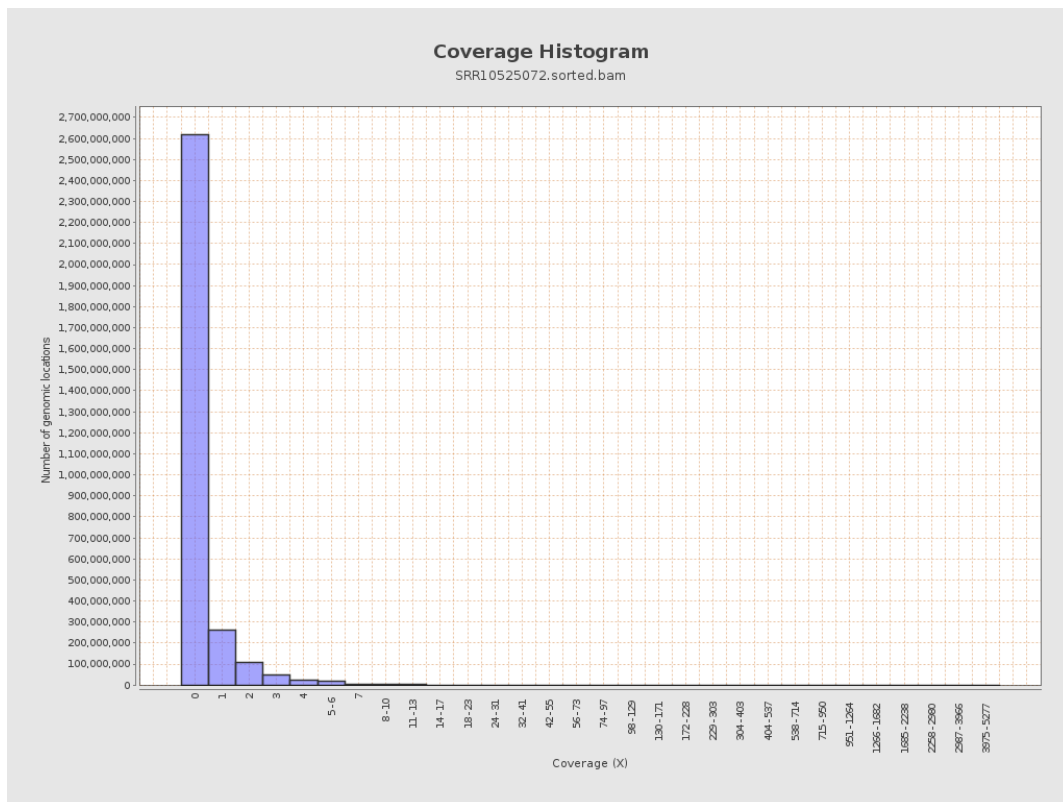
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	75742568	0.3039	3.9675
chr2	243199373	80335459	0.3303	2.6156
chr3	198022430	64664341	0.3266	1.035
chr4	191154276	62884738	0.329	1.4467
chr5	180915260	58418863	0.3229	1.02
chr6	171115067	54333530	0.3175	1.2177
chr7	159138663	53219595	0.3344	2.3618

chr8	146364022	47644621	0.3255	2.2243
chr9	141213431	39427932	0.2792	1.4749
chr10	135534747	46134189	0.3404	2.31
chr11	135006516	43317083	0.3209	1.5015
chr12	133851895	42733688	0.3193	1.0619
chr13	115169878	29825803	0.259	0.913
chr14	107349540	28851048	0.2688	0.9972
chr15	102531392	27924341	0.2723	0.9437
chr16	90354753	28185184	0.3119	1.2313
chr17	81195210	24913459	0.3068	1.1376
chr18	78077248	25056868	0.3209	3.0773
chr19	59128983	19578746	0.3311	2.6857
chr20	63025520	19907648	0.3159	1.1097
chr21	48129895	12823272	0.2664	1.2693
chr22	51304566	11340350	0.221	0.8532
chrMT	16571	444727	26.8377	14.5106
chrX	155270560	53175234	0.3425	1.3372
chrY	59373566	3039769	0.0512	1.3962

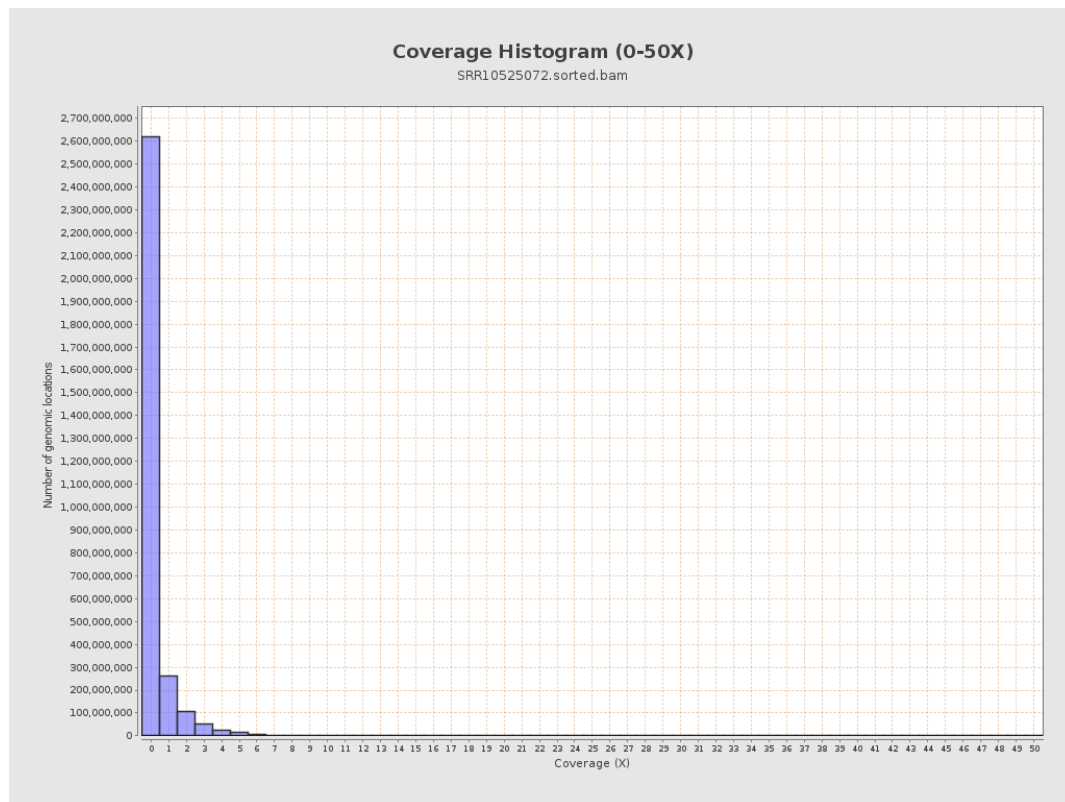
3. Results : Coverage across reference



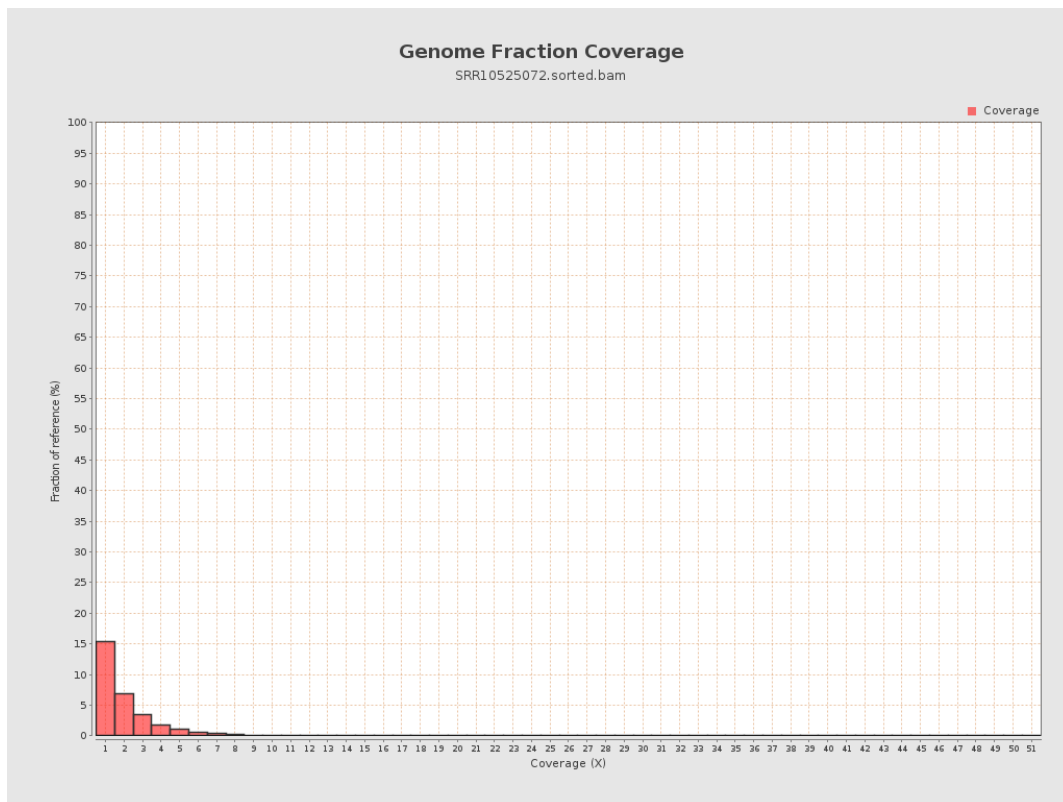
4. Results : Coverage Histogram



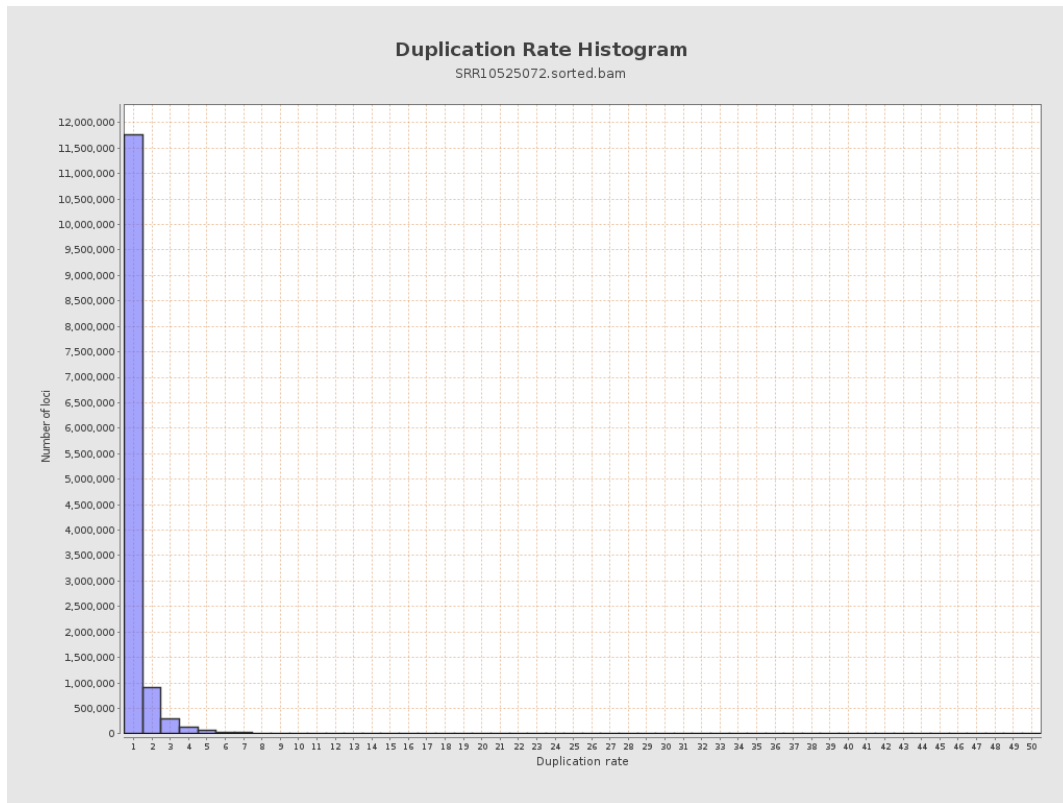
5. Results : Coverage Histogram (0-50X)



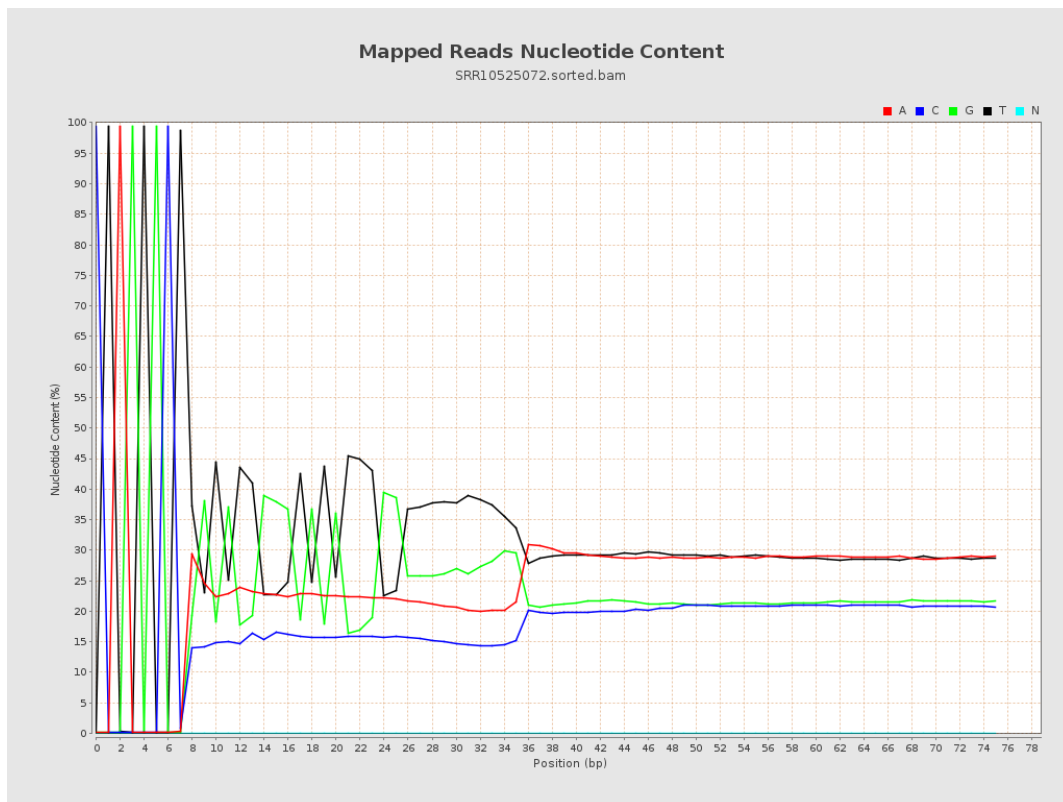
6. Results : Genome Fraction Coverage



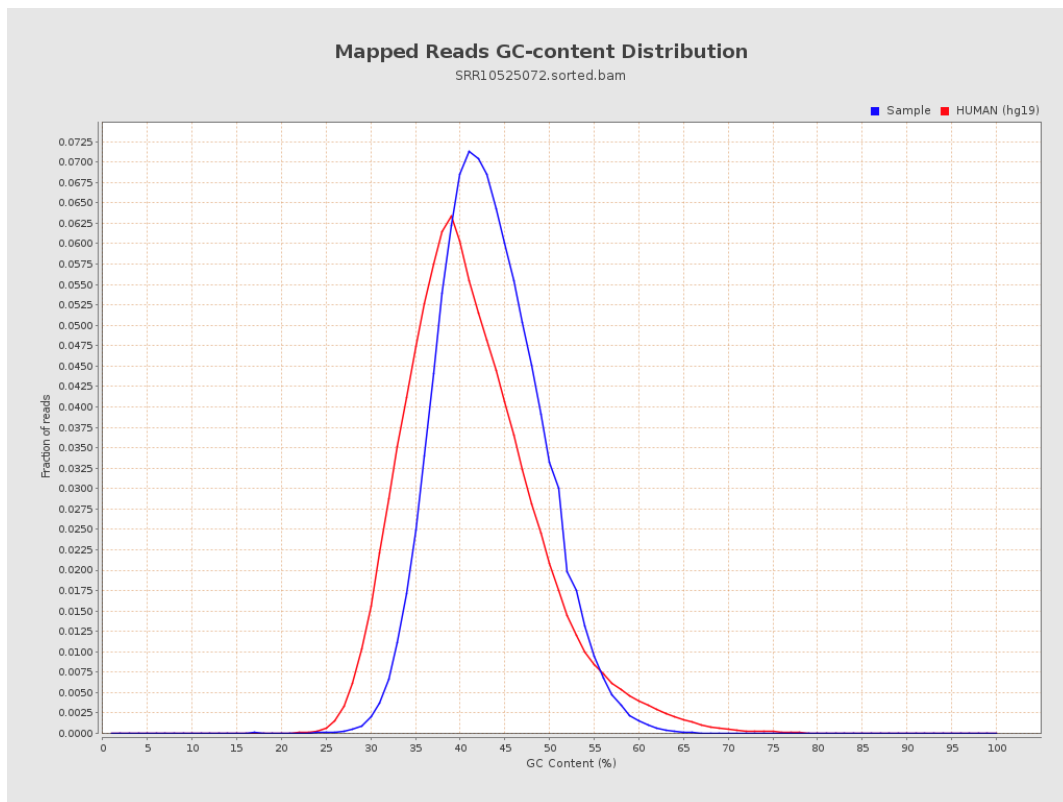
7. Results : Duplication Rate Histogram



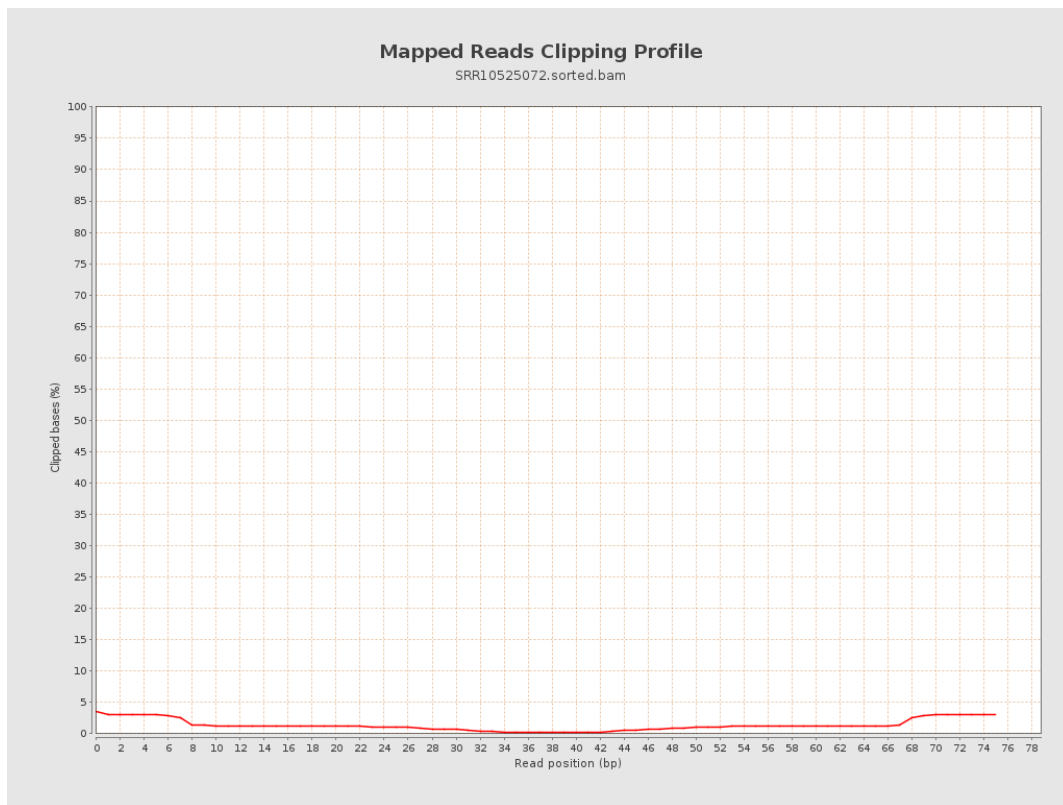
8. Results : Mapped Reads Nucleotide Content



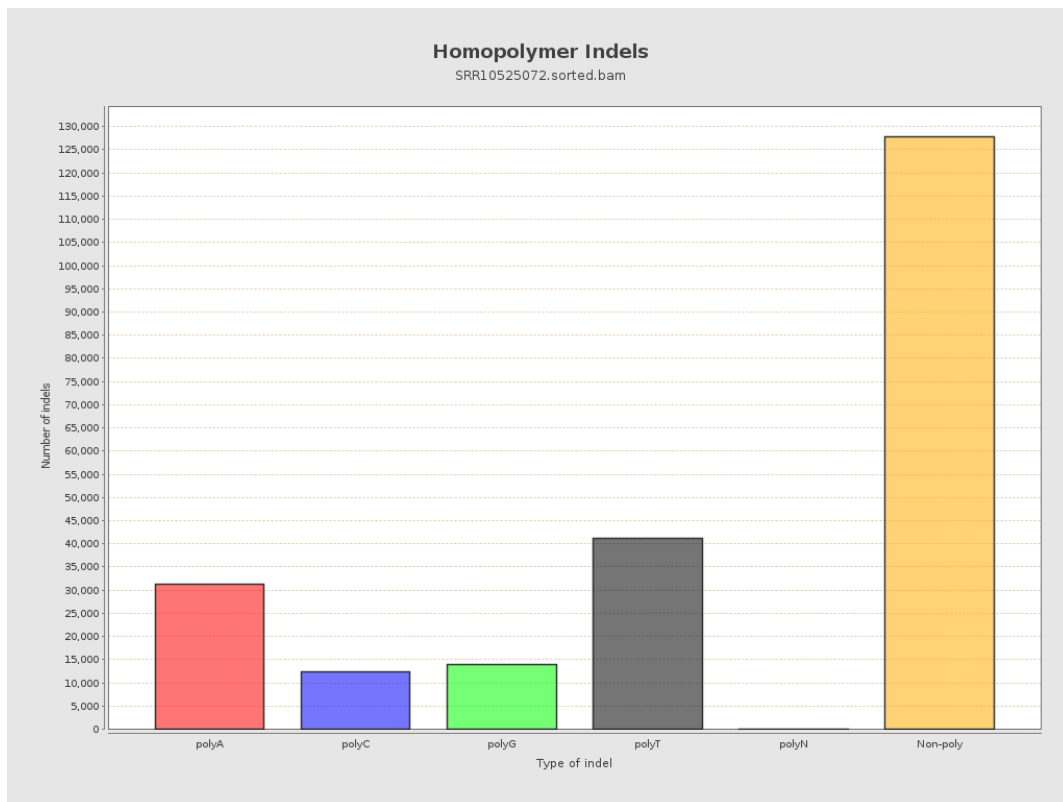
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

