

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:35:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971305.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_SRR2971305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971305.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:35:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,668,941
Mapped reads	8,187,534 / 84.68%
Unmapped reads	1,481,407 / 15.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	465,816 / 4.82%
Duplication rate	4.44%
Clipped reads	780,108 / 8.07%

2.2. ACGT Content

Number/percentage of A's	94,193,175 / 29.17%
Number/percentage of C's	65,589,196 / 20.31%
Number/percentage of T's	96,051,943 / 29.75%
Number/percentage of G's	67,032,443 / 20.76%
Number/percentage of N's	15,288 / 0%
GC Percentage	41.07%

2.3. Coverage

Mean	0.1043
Standard Deviation	0.837

2.4. Mapping Quality

Mean Mapping Quality	40.39
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2.5. Mismatches and indels

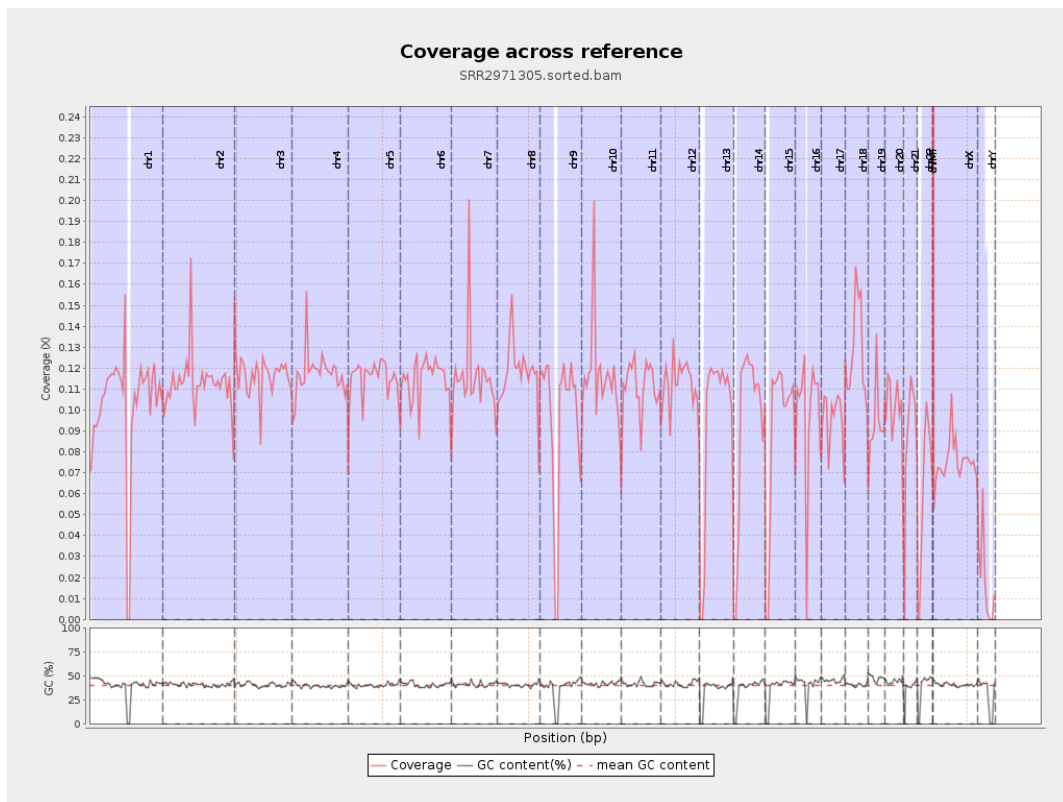
General error rate	0.3%
Mismatches	957,452
Insertions	11,493
Mapped reads with at least one insertion	0.14%
Deletions	26,696
Mapped reads with at least one deletion	0.33%
Homopolymer indels	40.37%

2.6. Chromosome stats

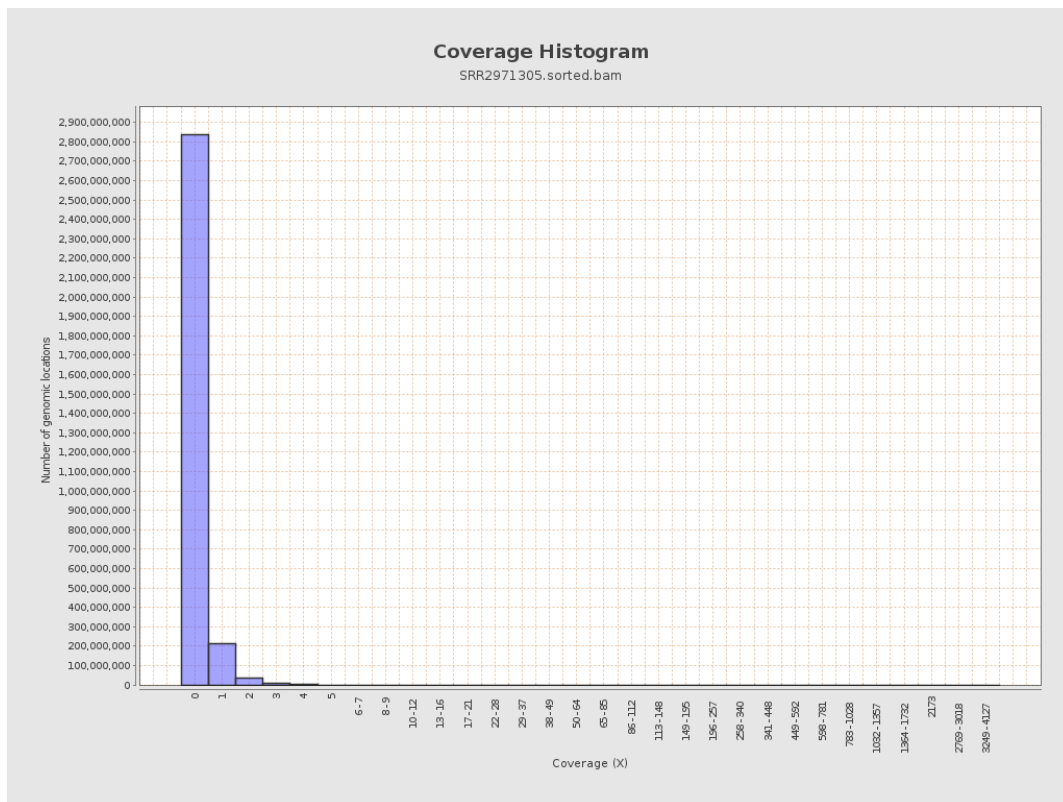
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25565688	0.1026	1.3707
chr2	243199373	27384296	0.1126	0.6987
chr3	198022430	23109794	0.1167	0.4108
chr4	191154276	22442822	0.1174	0.4803
chr5	180915260	20800504	0.115	0.4145
chr6	171115067	19723187	0.1153	0.4332
chr7	159138663	18308920	0.1151	1.2036
chr8	146364022	17233532	0.1177	2.0448

chr9	141213431	13579171	0.0962	0.6695
chr10	135534747	15738748	0.1161	0.8187
chr11	135006516	15024543	0.1113	0.6439
chr12	133851895	15057764	0.1125	0.4198
chr13	115169878	10895516	0.0946	0.3603
chr14	107349540	10164903	0.0947	0.4621
chr15	102531392	9190496	0.0896	0.3525
chr16	90354753	8664169	0.0959	0.4518
chr17	81195210	7858819	0.0968	0.429
chr18	78077248	9998784	0.1281	1.2532
chr19	59128983	5612684	0.0949	1.2908
chr20	63025520	6383063	0.1013	0.4069
chr21	48129895	4184121	0.0869	0.4478
chr22	51304566	3205996	0.0625	0.2996
chrMT	16571	26784	1.6163	1.8357
chrX	155270560	11677674	0.0752	0.4186
chrY	59373566	1083437	0.0182	0.342

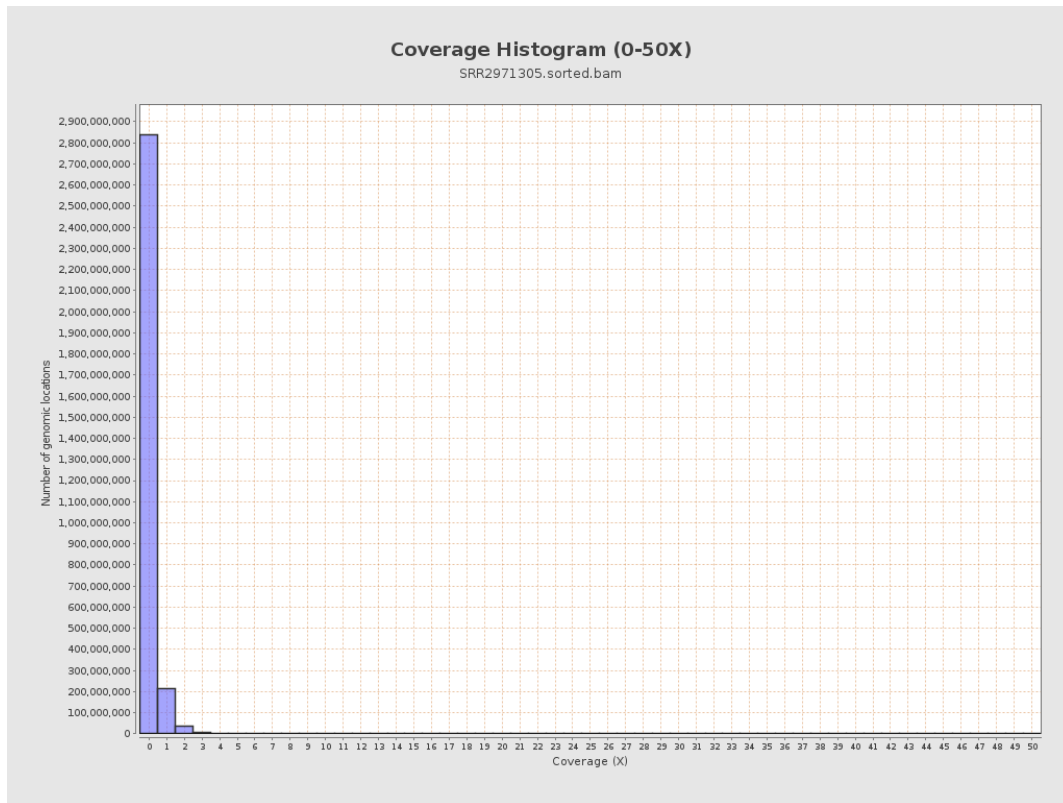
3. Results : Coverage across reference



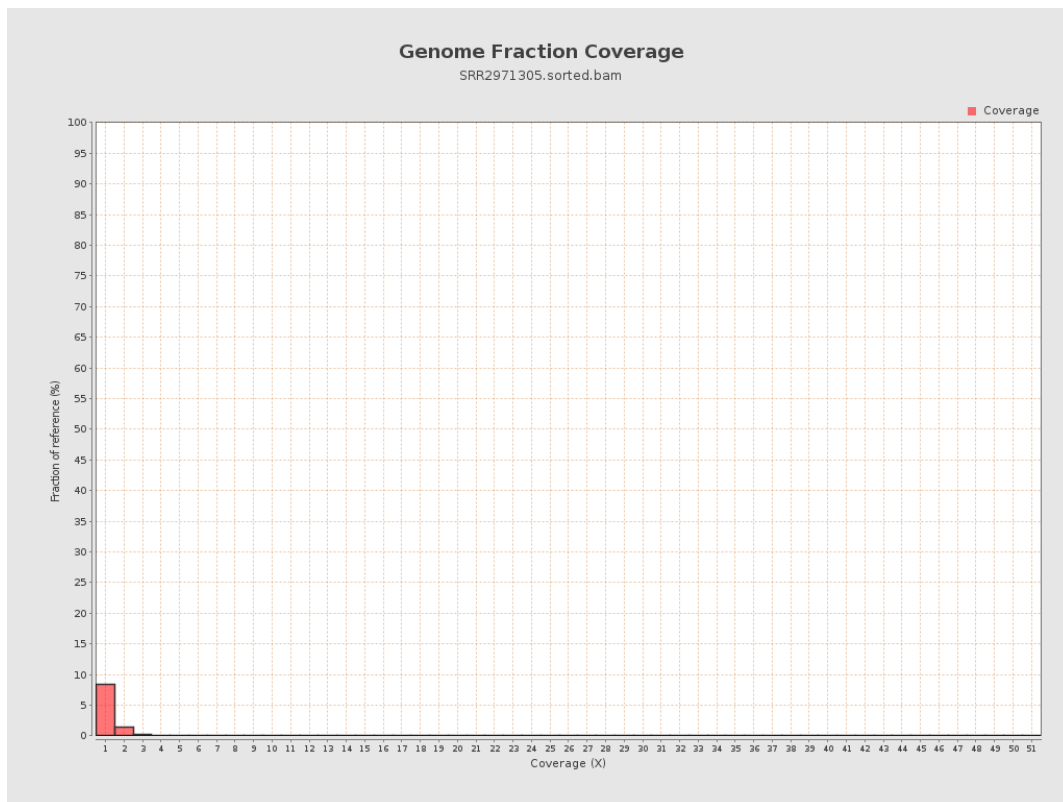
4. Results : Coverage Histogram



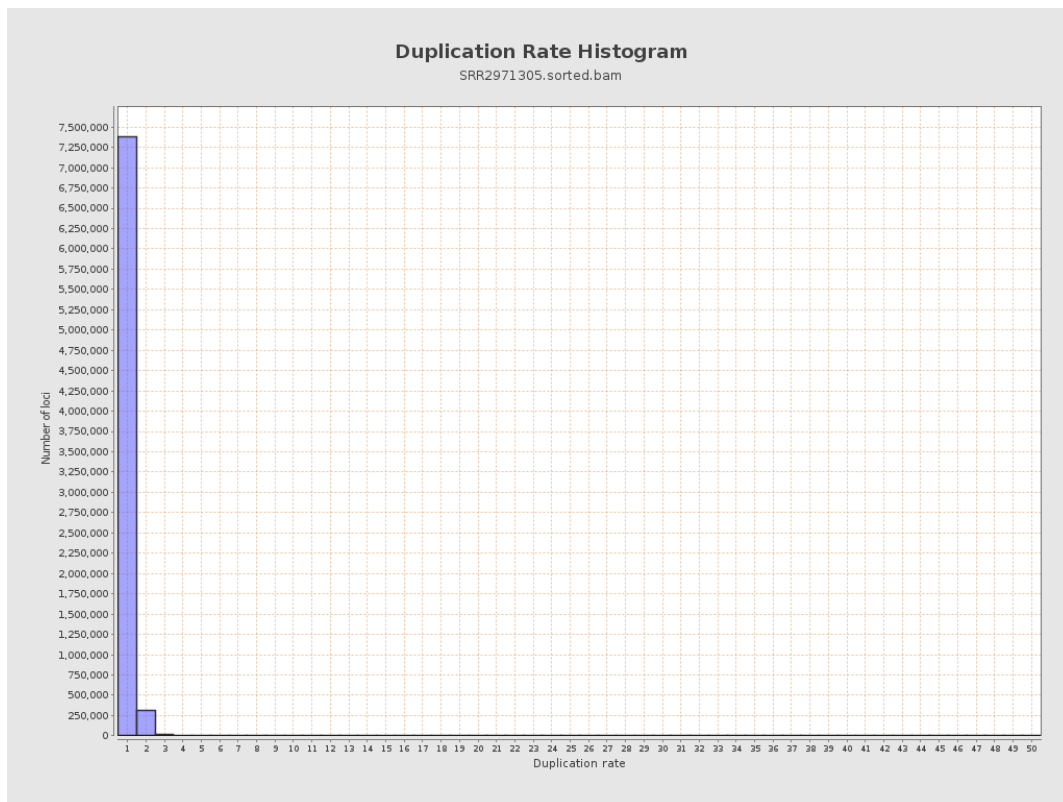
5. Results : Coverage Histogram (0-50X)



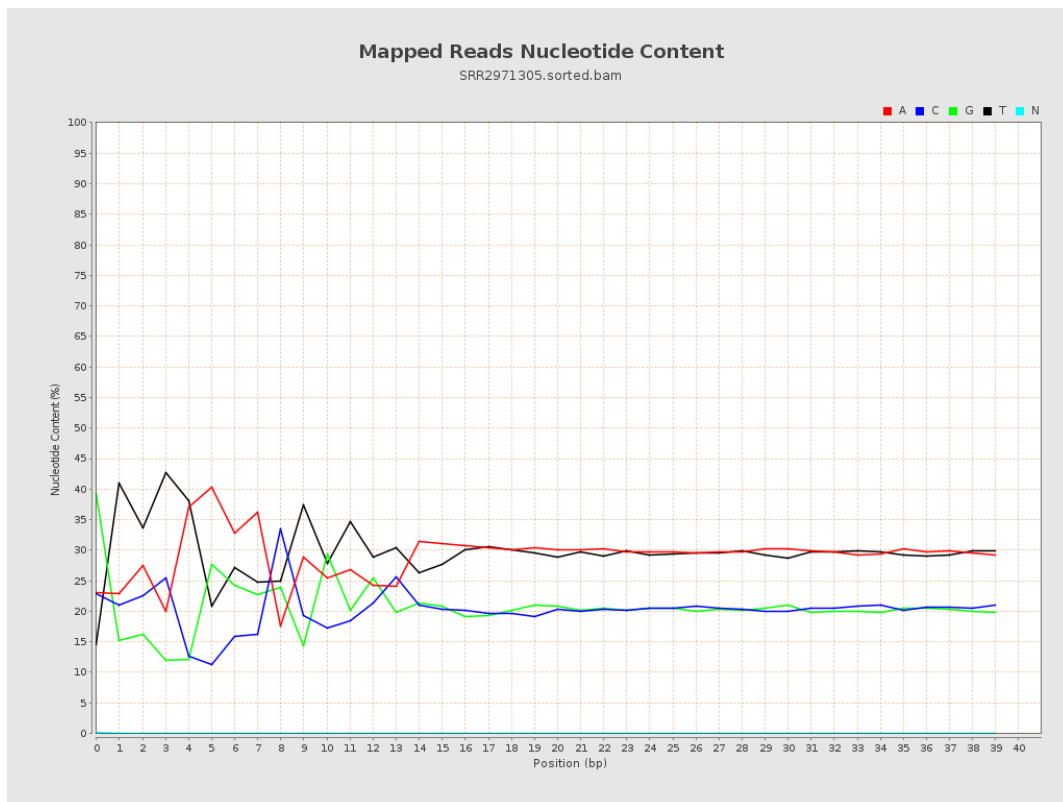
6. Results : Genome Fraction Coverage



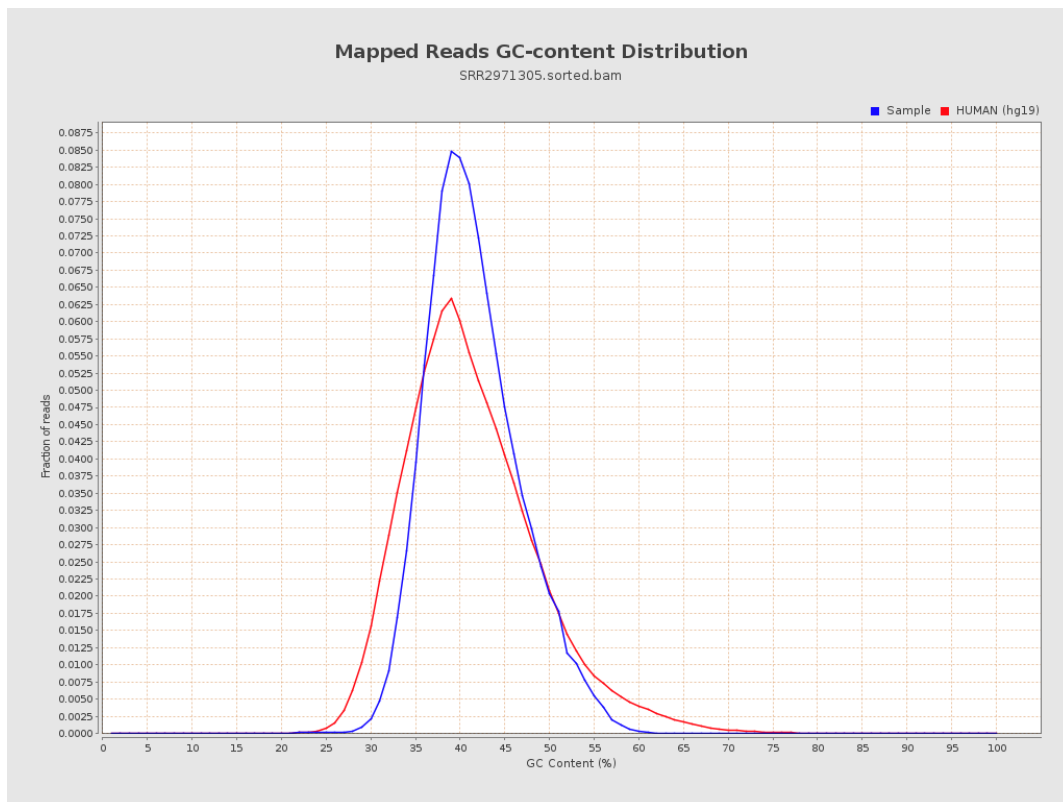
7. Results : Duplication Rate Histogram



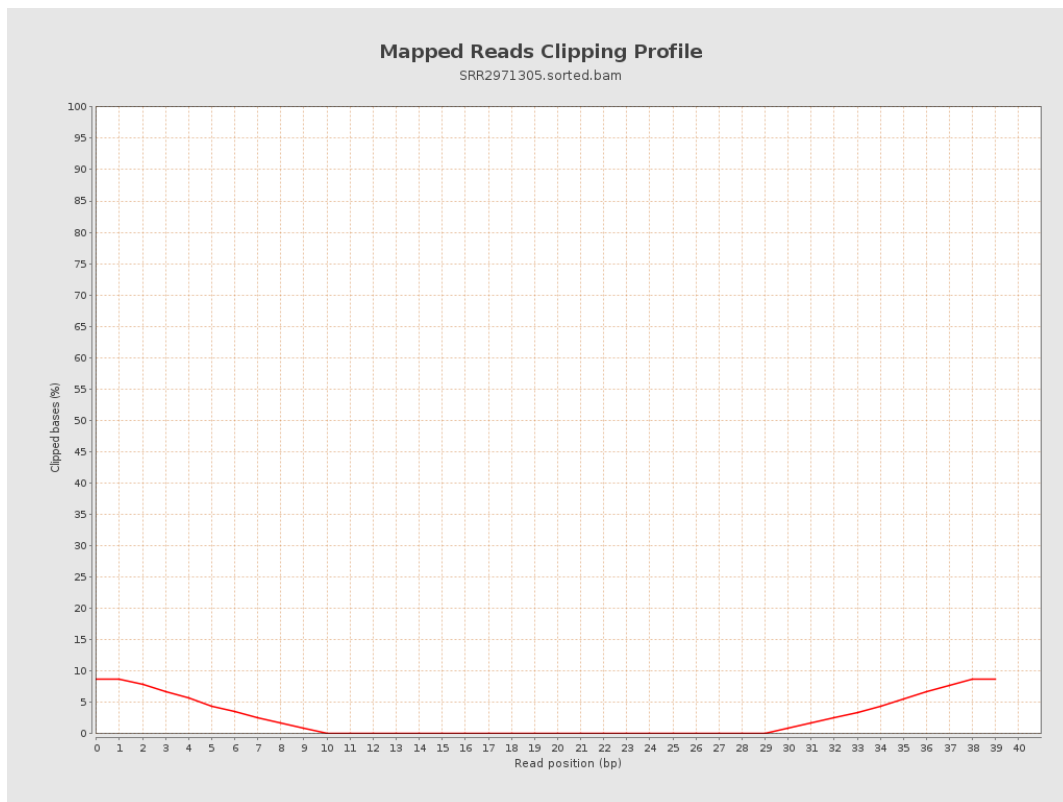
8. Results : Mapped Reads Nucleotide Content



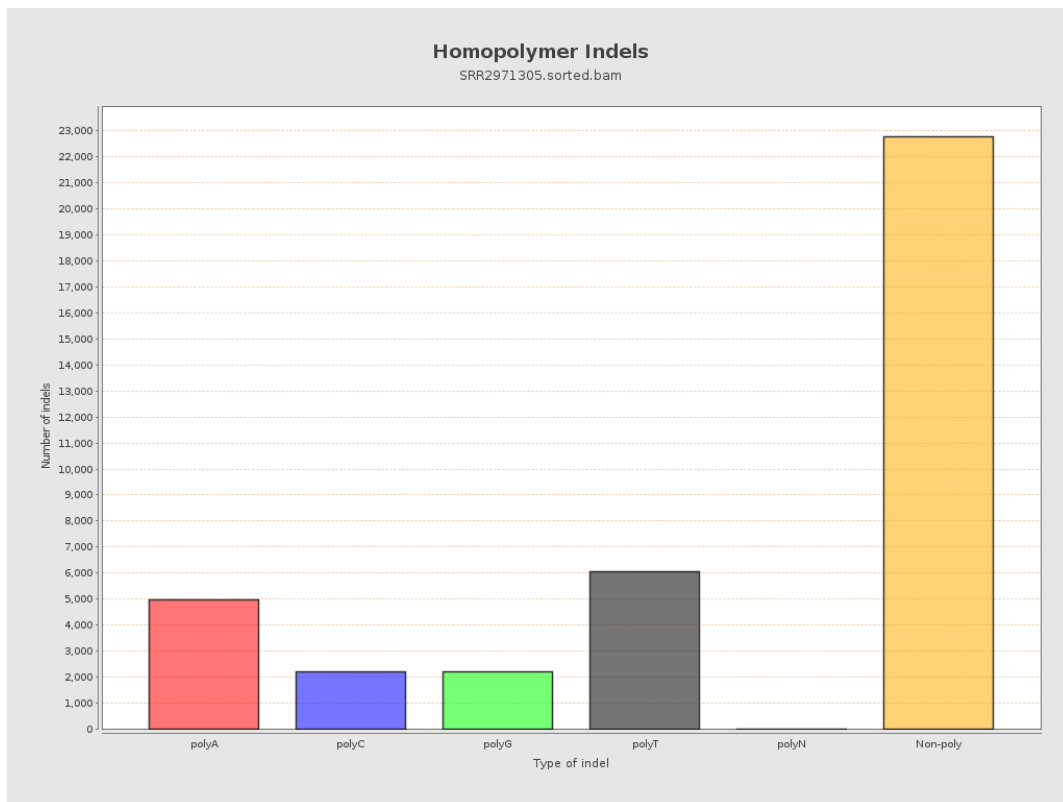
9. Results : Mapped Reads GC-content Distribution



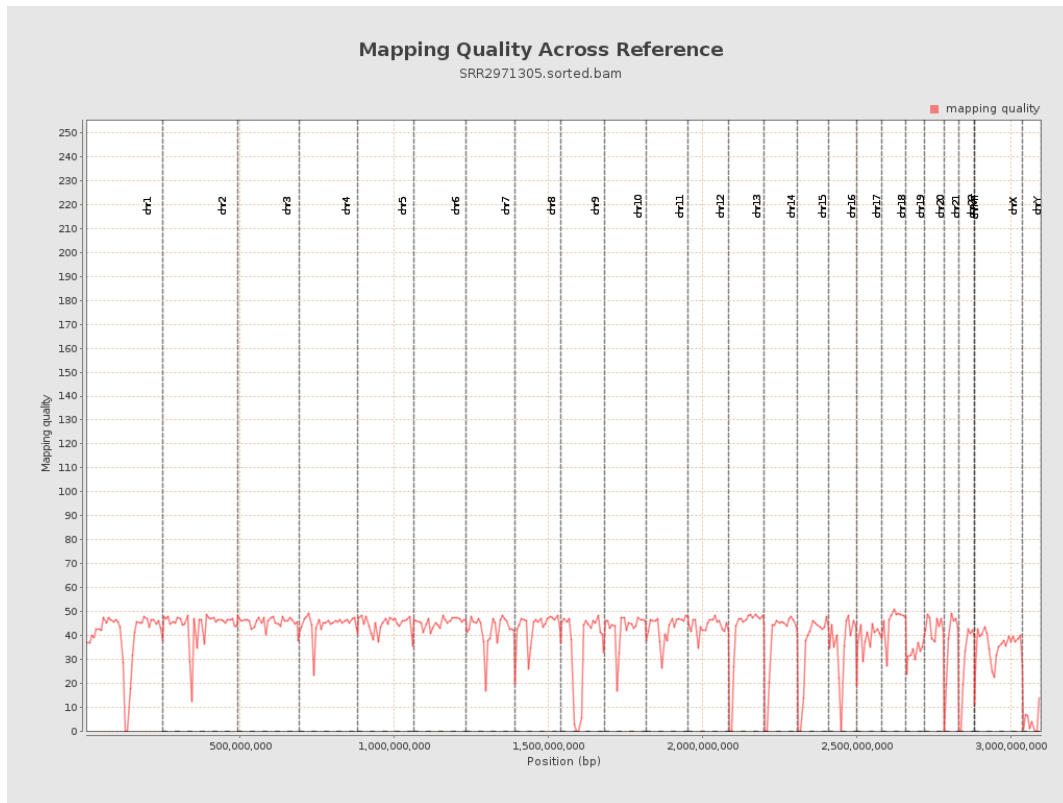
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

