

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:41:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085045.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_SRR3085045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:41:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,139,364
Mapped reads	2,893,368 / 92.16%
Unmapped reads	245,996 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,065 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	97,670 / 3.11%
Duplication rate	2.5%
Clipped reads	1,196,635 / 38.12%

2.2. ACGT Content

Number/percentage of A's	56,342,665 / 28.76%
Number/percentage of C's	37,649,124 / 19.22%
Number/percentage of T's	59,955,545 / 30.6%
Number/percentage of G's	41,964,533 / 21.42%
Number/percentage of N's	22,052 / 0.01%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0633

Standard Deviation	0.4803
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2.4. Mapping Quality

Mean Mapping Quality	46.11
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2.5. Mismatches and indels

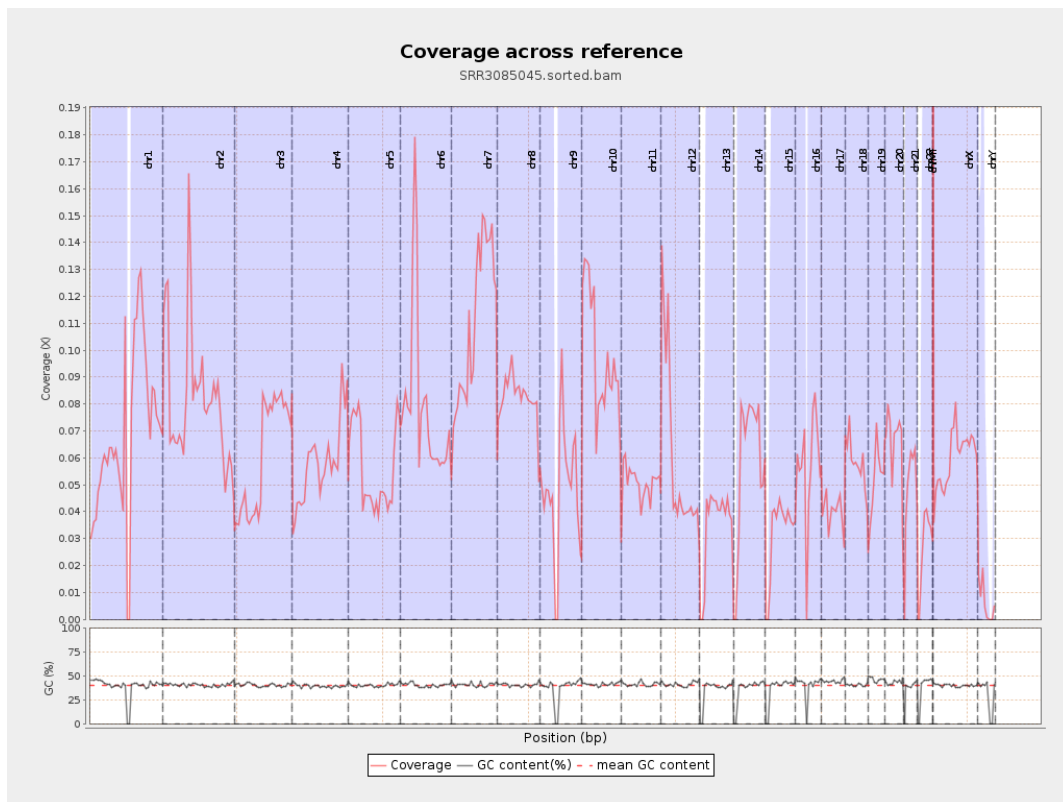
General error rate	0.93%
Mismatches	1,793,792
Insertions	13,708
Mapped reads with at least one insertion	0.47%
Deletions	43,883
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.86%

2.6. Chromosome stats

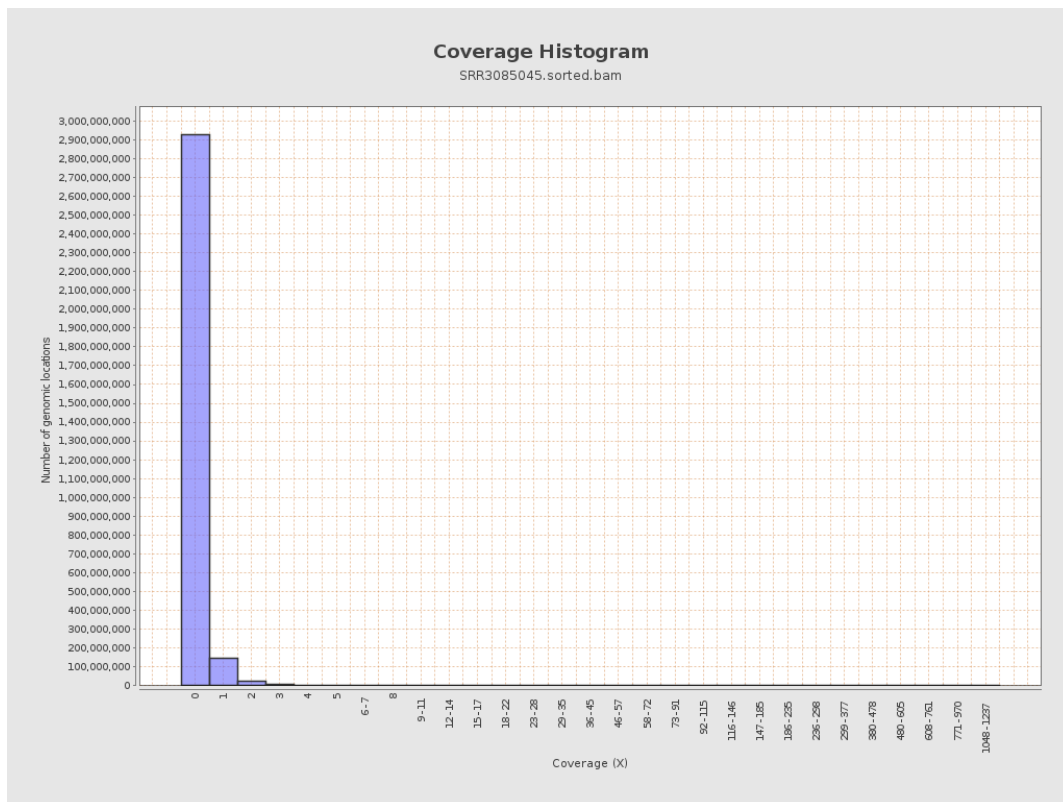
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17074208	0.0685	0.7407
chr2	243199373	20077850	0.0826	0.5808
chr3	198022430	11962662	0.0604	0.2887
chr4	191154276	11095209	0.058	0.2861
chr5	180915260	10118387	0.0559	0.2697
chr6	171115067	13695763	0.08	0.4846
chr7	159138663	17514680	0.1101	0.6542

chr8	146364022	12075183	0.0825	0.8124
chr9	141213431	6863846	0.0486	0.4459
chr10	135534747	13315877	0.0982	0.5816
chr11	135006516	6866210	0.0509	0.4158
chr12	133851895	8084104	0.0604	0.2899
chr13	115169878	4003097	0.0348	0.2082
chr14	107349540	6400640	0.0596	0.3052
chr15	102531392	3234261	0.0315	0.2067
chr16	90354753	5034441	0.0557	0.2949
chr17	81195210	3270898	0.0403	0.2747
chr18	78077248	4585544	0.0587	0.8605
chr19	59128983	3111175	0.0526	0.5103
chr20	63025520	4252170	0.0675	0.3039
chr21	48129895	2307243	0.0479	0.2757
chr22	51304566	1366059	0.0266	0.1821
chrMT	16571	8188	0.4941	0.7721
chrX	155270560	9311197	0.06	0.3253
chrY	59373566	381682	0.0064	0.1295

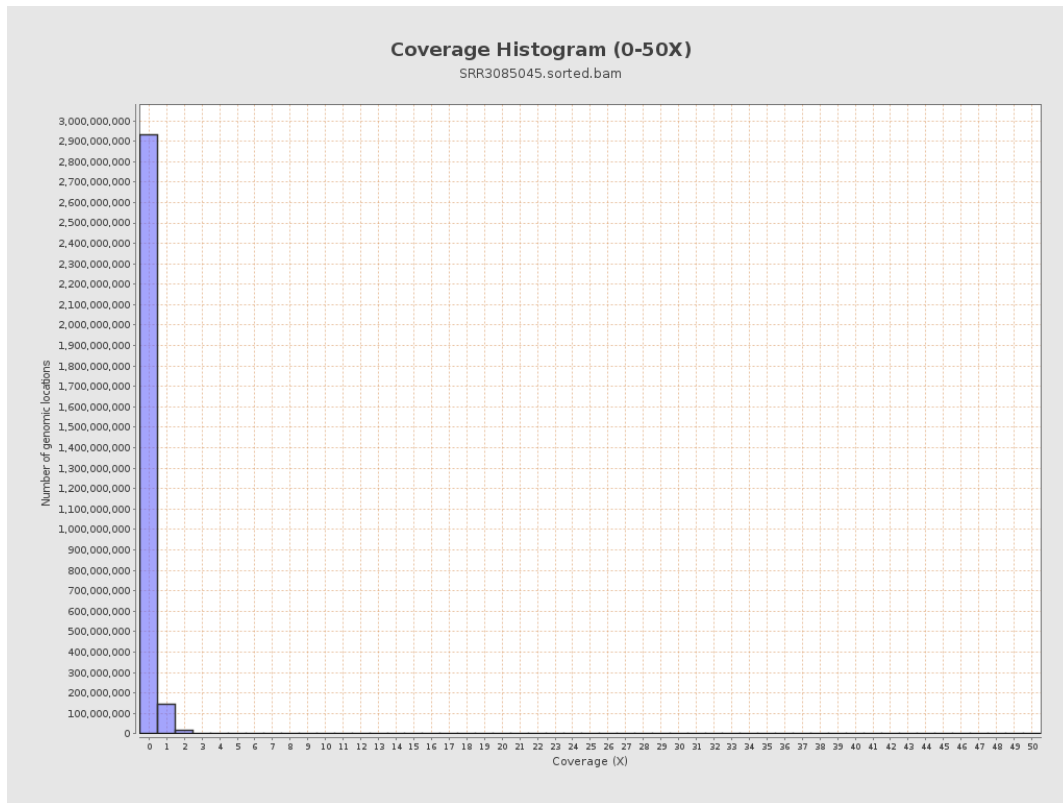
3. Results : Coverage across reference



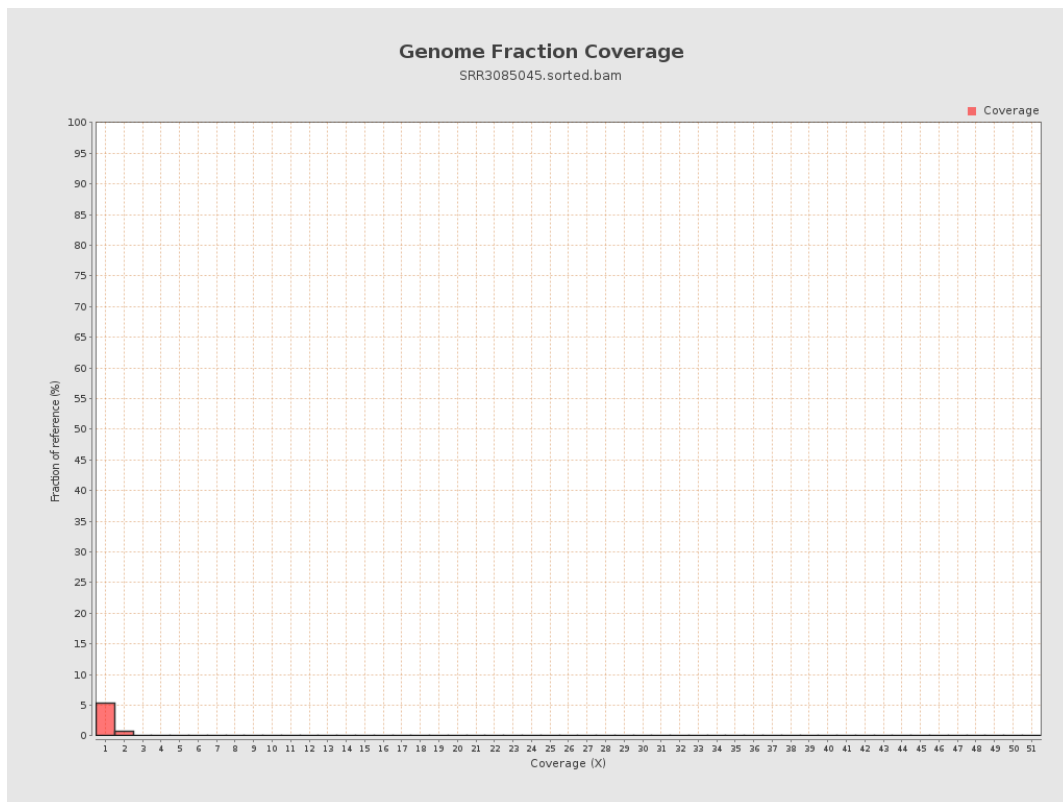
4. Results : Coverage Histogram



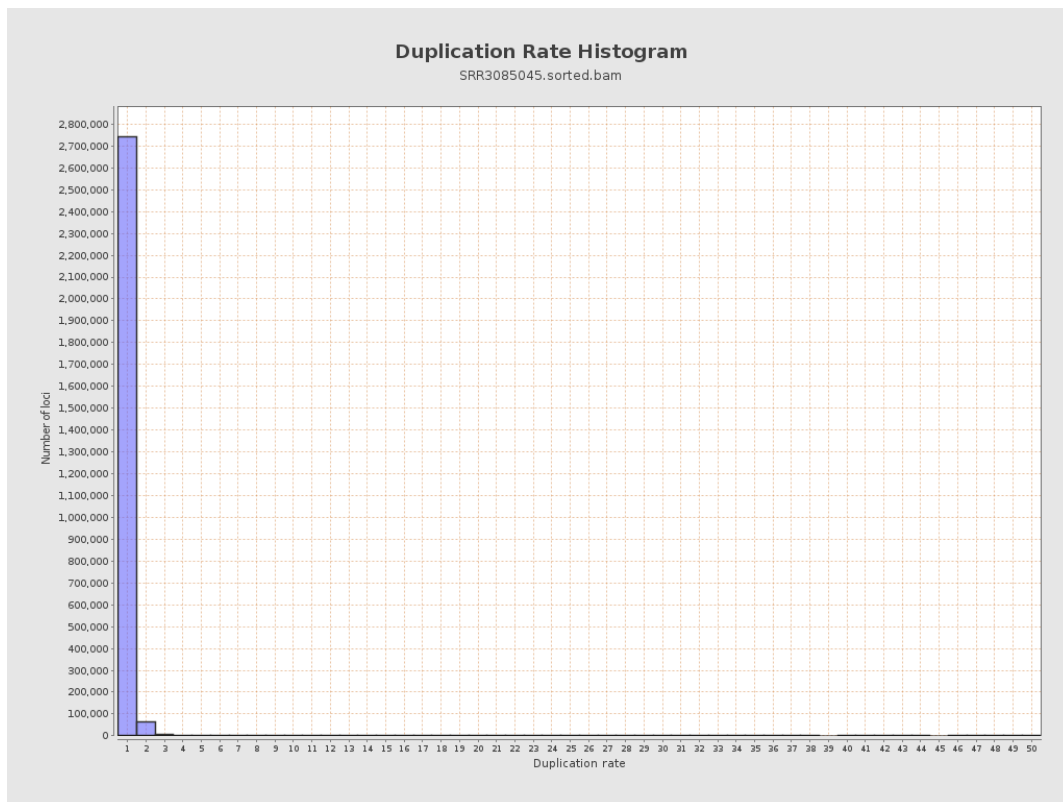
5. Results : Coverage Histogram (0-50X)



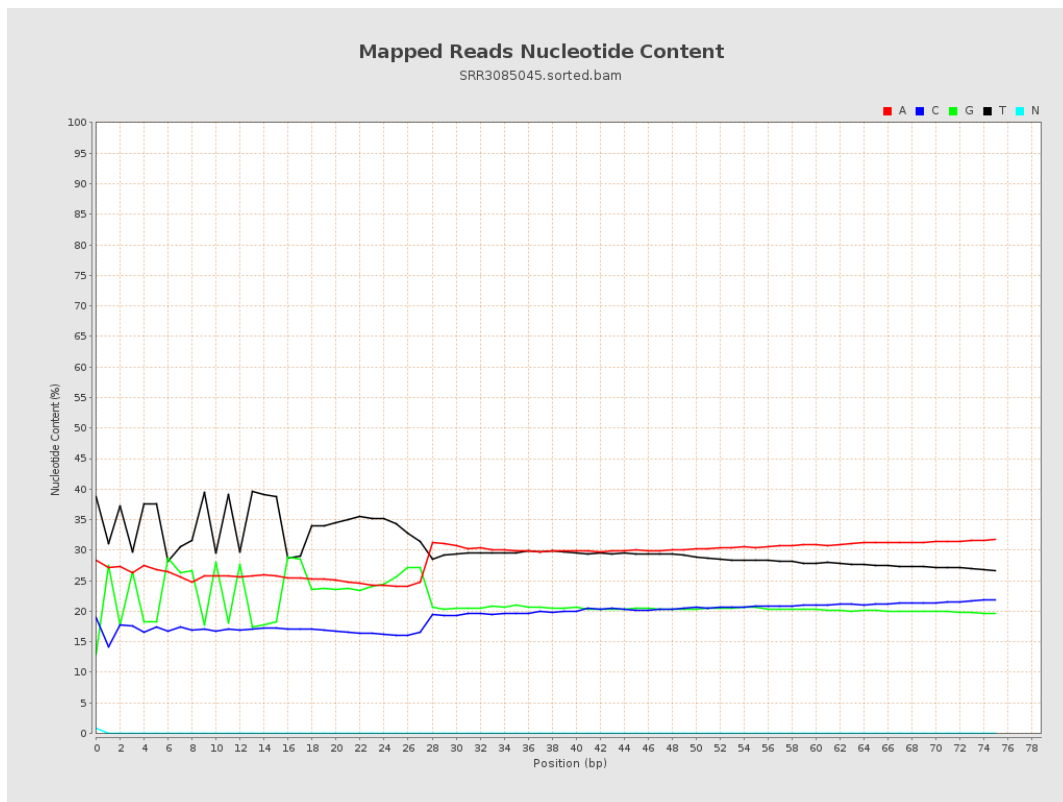
6. Results : Genome Fraction Coverage



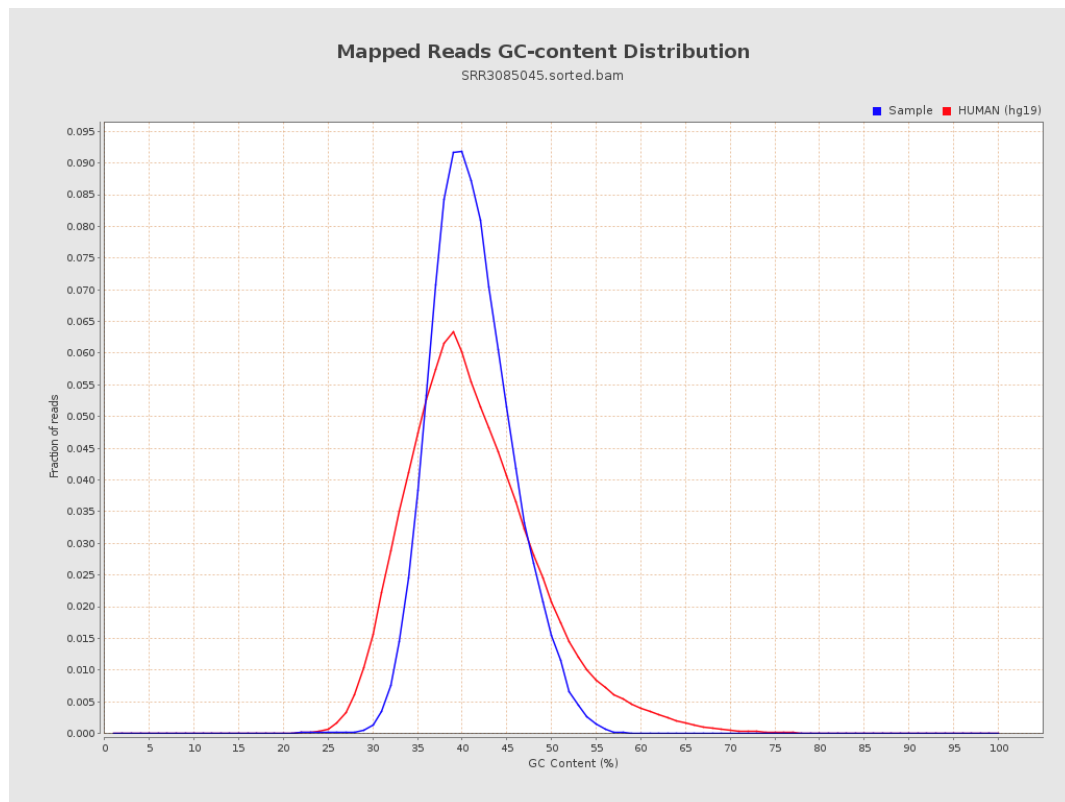
7. Results : Duplication Rate Histogram



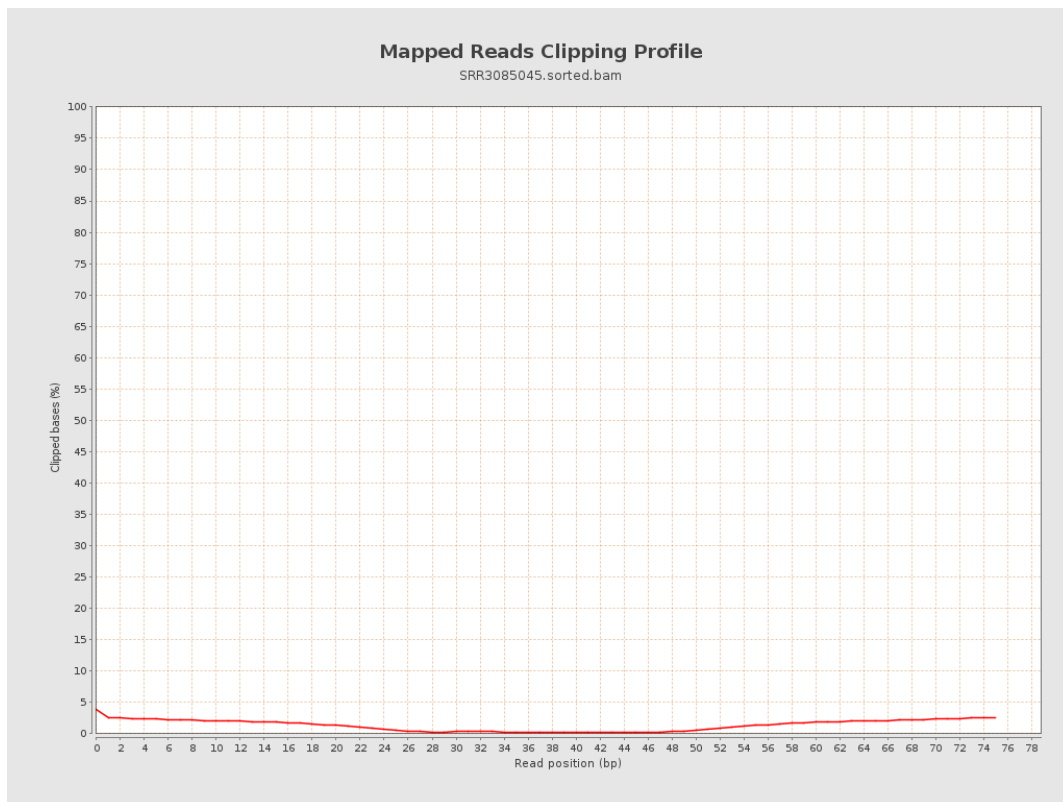
8. Results : Mapped Reads Nucleotide Content



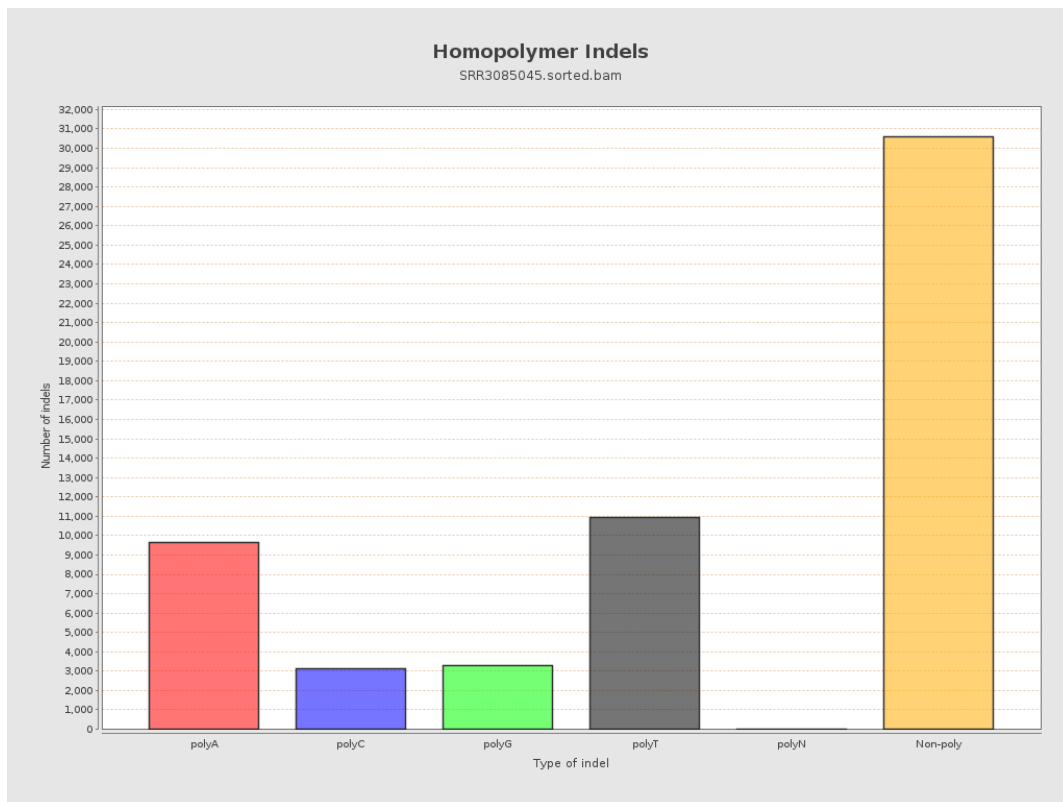
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

