

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:36:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085089.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_SRR3085089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:36:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,666,392
Mapped reads	2,200,413 / 82.52%
Unmapped reads	465,979 / 17.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,060 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	81,713 / 3.06%
Duplication rate	2.98%
Clipped reads	1,503,558 / 56.39%

2.2. ACGT Content

Number/percentage of A's	38,302,115 / 28.99%
Number/percentage of C's	25,790,024 / 19.52%
Number/percentage of T's	39,163,628 / 29.64%
Number/percentage of G's	28,856,260 / 21.84%
Number/percentage of N's	3,053 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.0427

Standard Deviation	0.3382
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2.4. Mapping Quality

Mean Mapping Quality	44.58
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2.5. Mismatches and indels

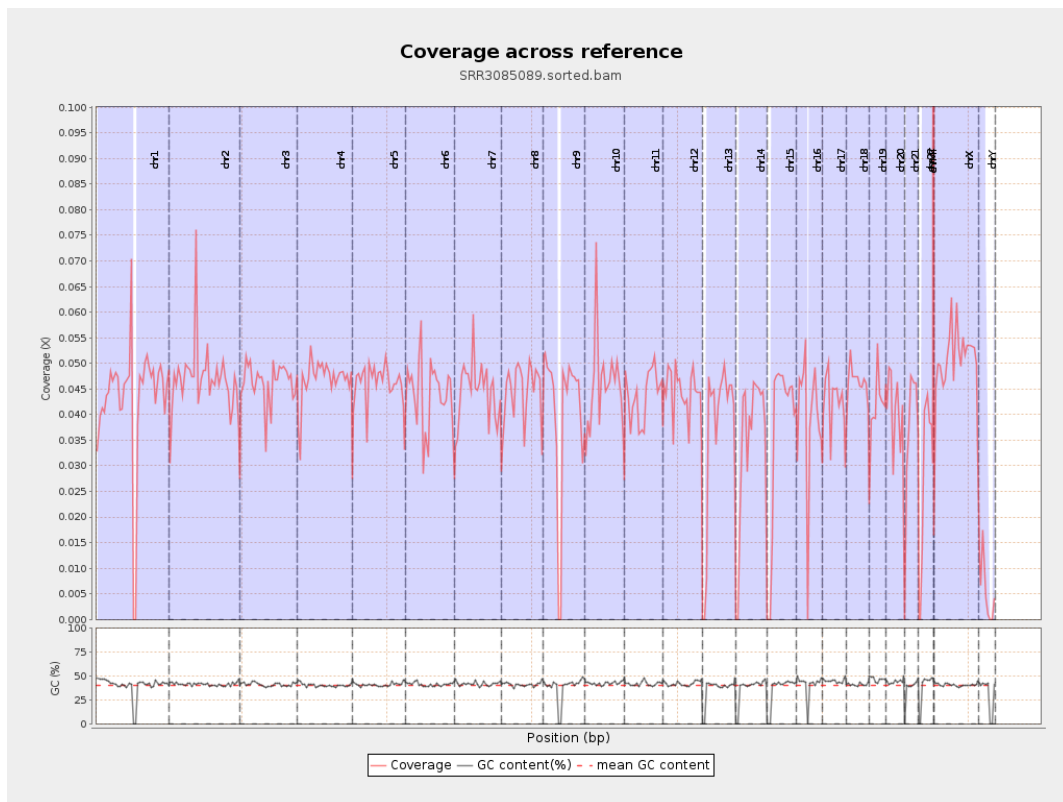
General error rate	0.86%
Mismatches	1,114,556
Insertions	9,920
Mapped reads with at least one insertion	0.45%
Deletions	27,889
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.71%

2.6. Chromosome stats

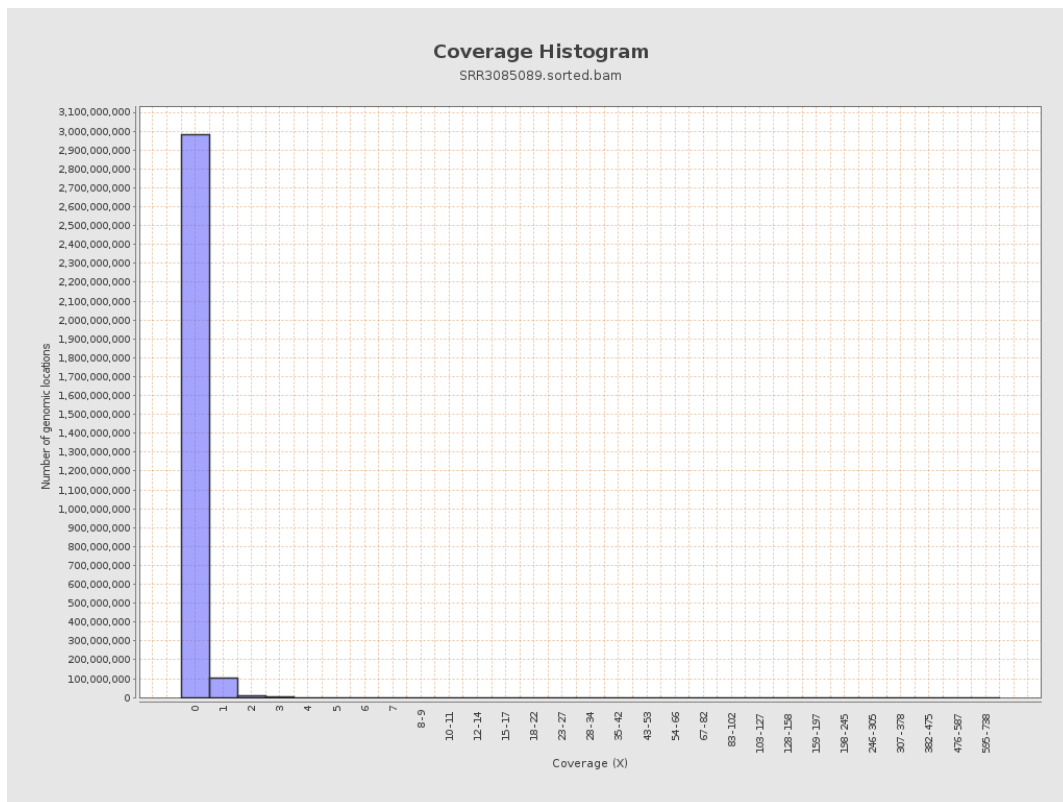
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10748362	0.0431	0.6065
chr2	243199373	11423028	0.047	0.3698
chr3	198022430	9140576	0.0462	0.2386
chr4	191154276	8960792	0.0469	0.2487
chr5	180915260	8350086	0.0462	0.2375
chr6	171115067	7513058	0.0439	0.2892
chr7	159138663	7127014	0.0448	0.328

chr8	146364022	6509643	0.0445	0.4707
chr9	141213431	5695367	0.0403	0.3042
chr10	135534747	6184877	0.0456	0.3574
chr11	135006516	5883178	0.0436	0.2927
chr12	133851895	5944335	0.0444	0.2358
chr13	115169878	4224454	0.0367	0.21
chr14	107349540	3713499	0.0346	0.2212
chr15	102531392	3771185	0.0368	0.212
chr16	90354753	3565964	0.0395	0.2383
chr17	81195210	3429754	0.0422	0.2531
chr18	78077248	3628923	0.0465	0.5627
chr19	59128983	2484067	0.042	0.4582
chr20	63025520	2524362	0.0401	0.2302
chr21	48129895	1771044	0.0368	0.2195
chr22	51304566	1422789	0.0277	0.1819
chrMT	16571	9002	0.5432	0.8354
chrX	155270560	7818210	0.0504	0.2768
chrY	59373566	316233	0.0053	0.1143

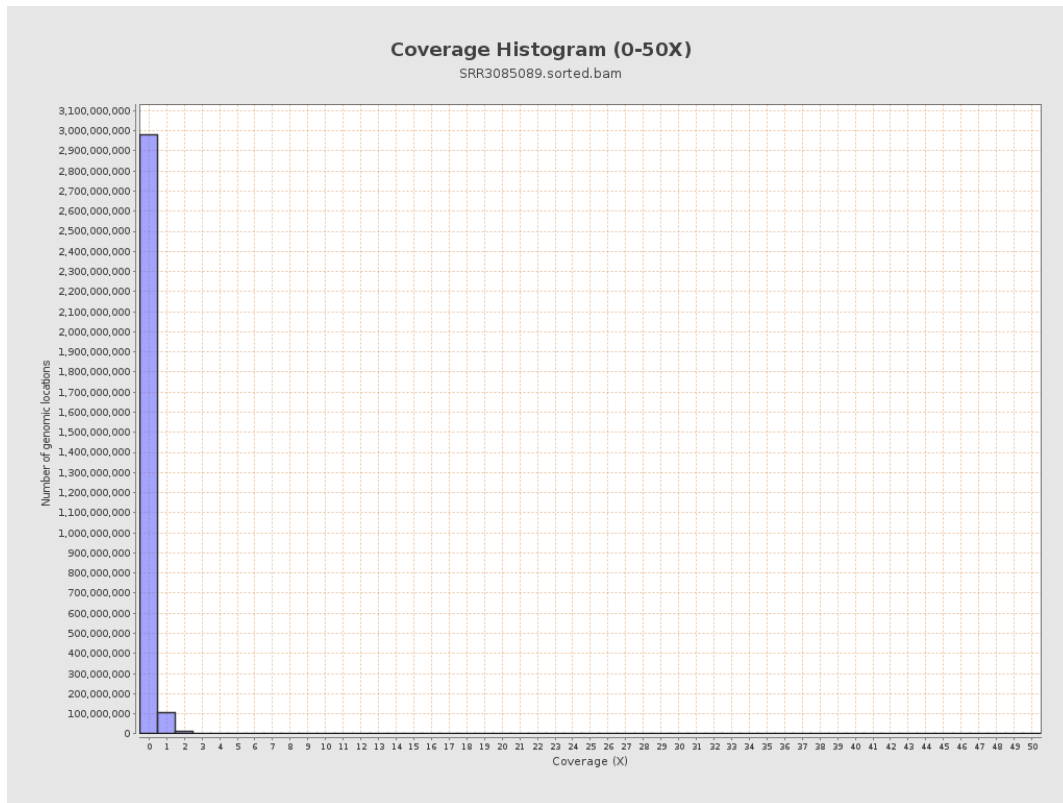
3. Results : Coverage across reference



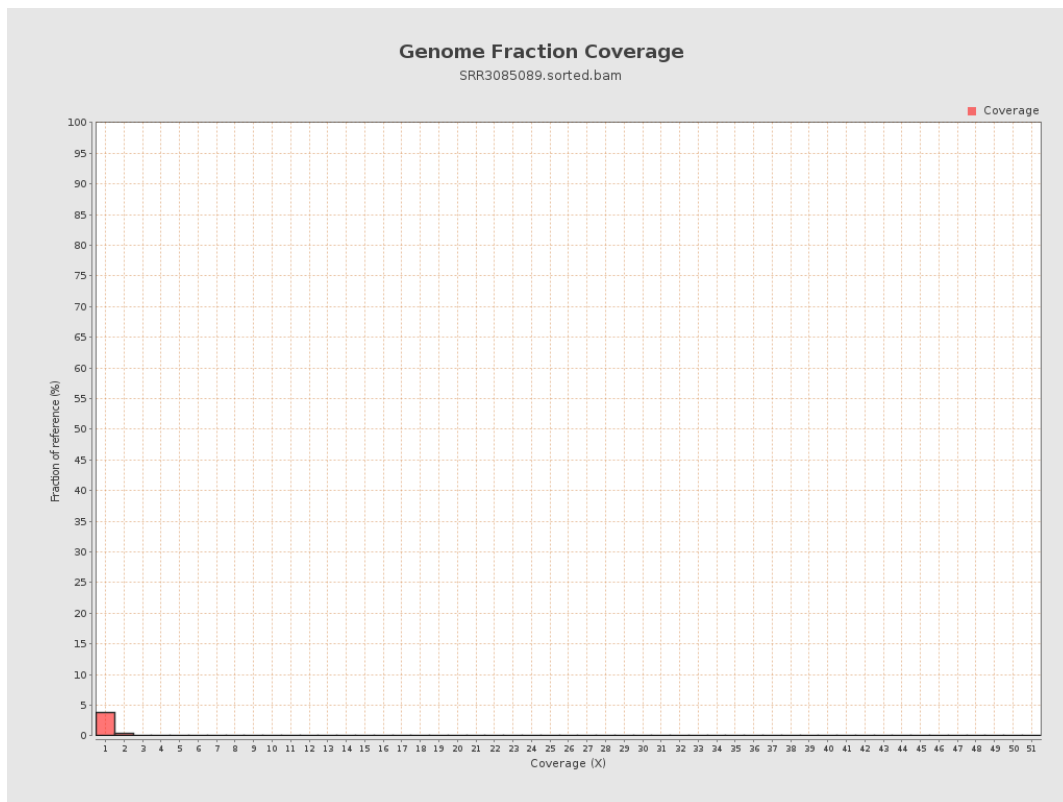
4. Results : Coverage Histogram



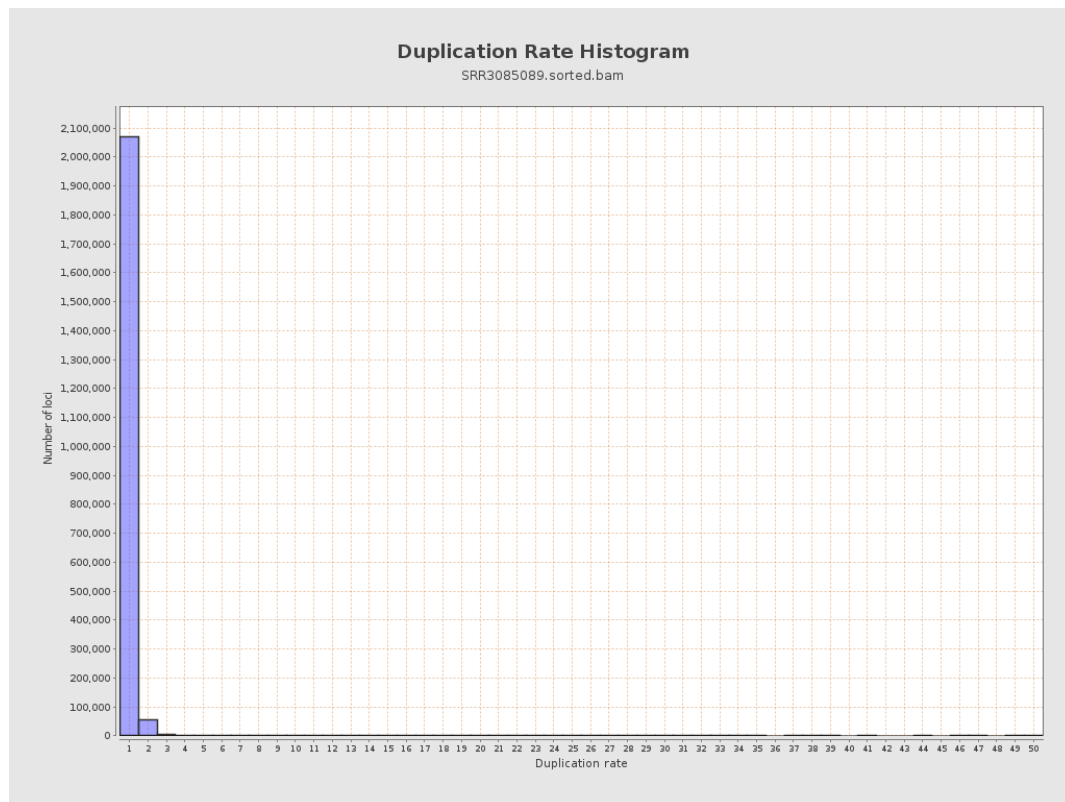
5. Results : Coverage Histogram (0-50X)



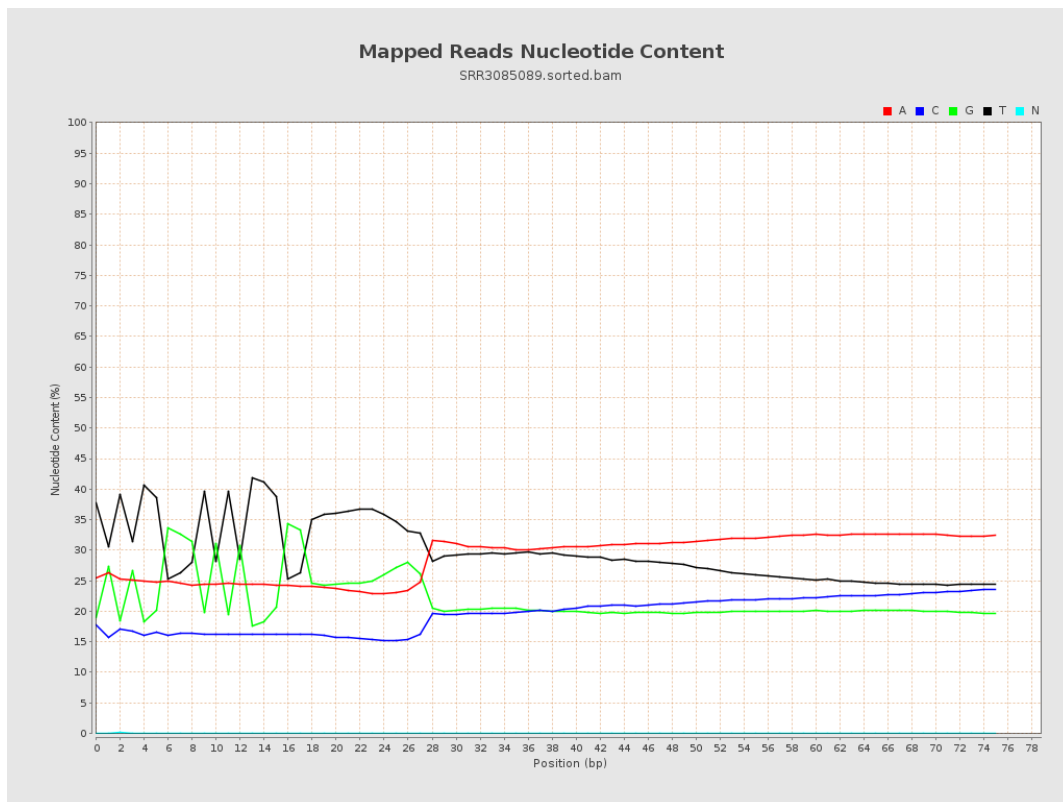
6. Results : Genome Fraction Coverage



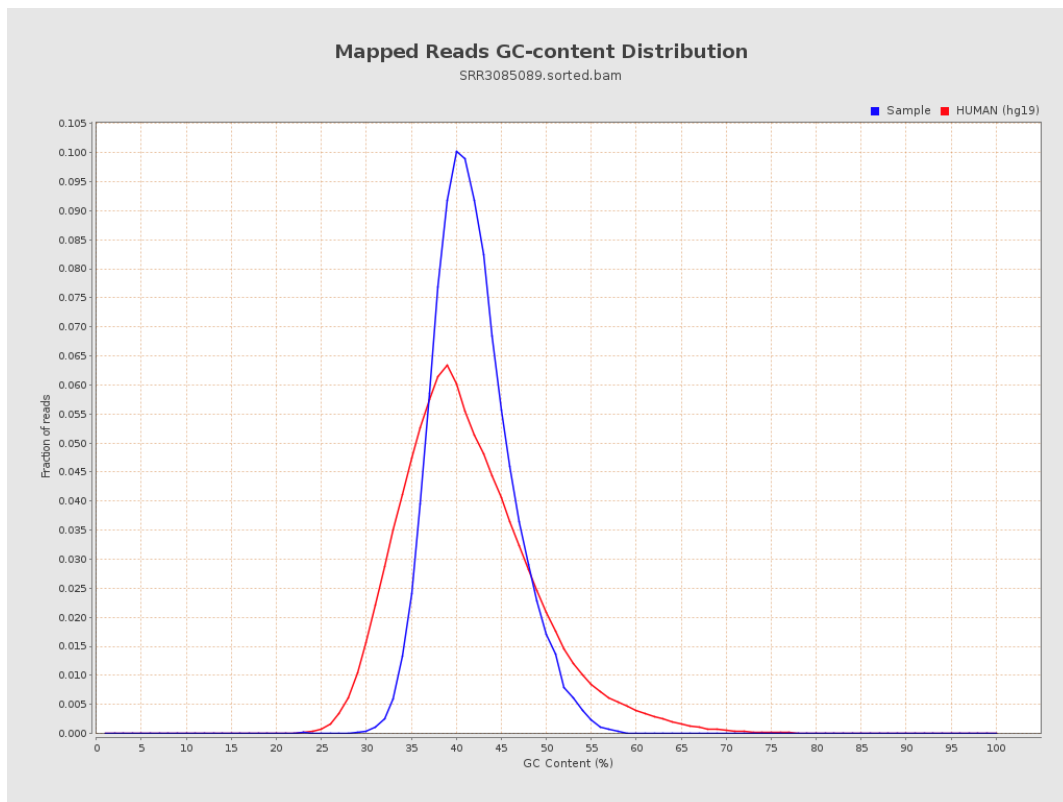
7. Results : Duplication Rate Histogram



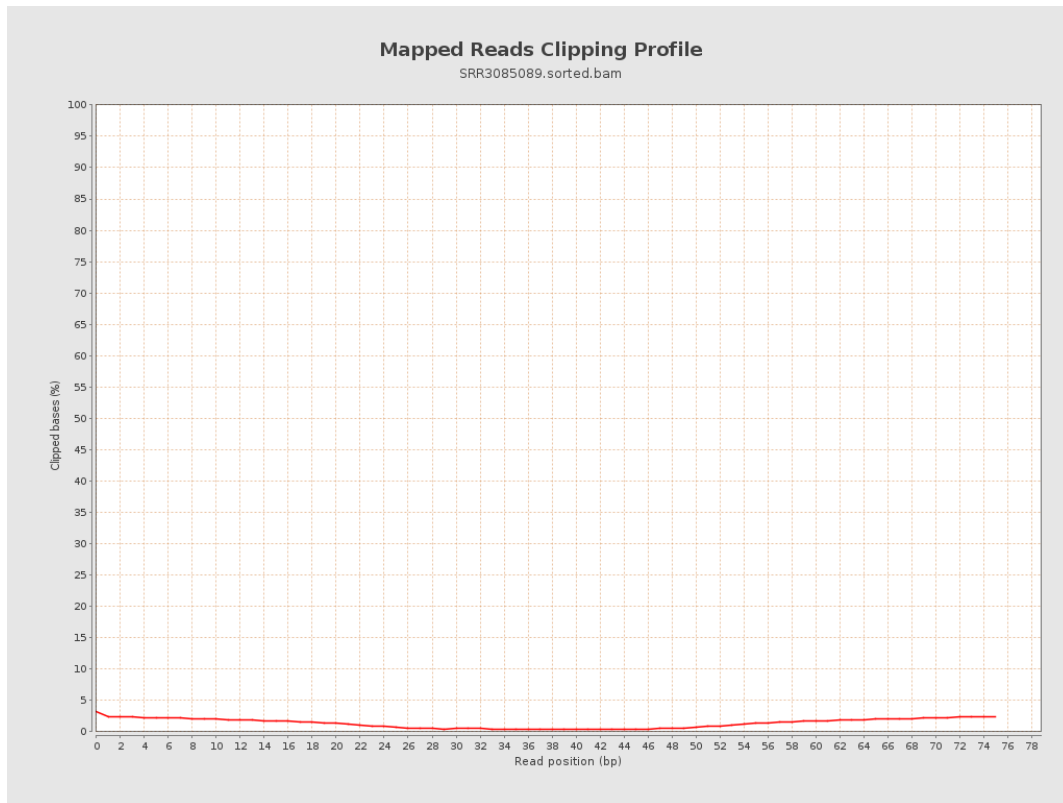
8. Results : Mapped Reads Nucleotide Content



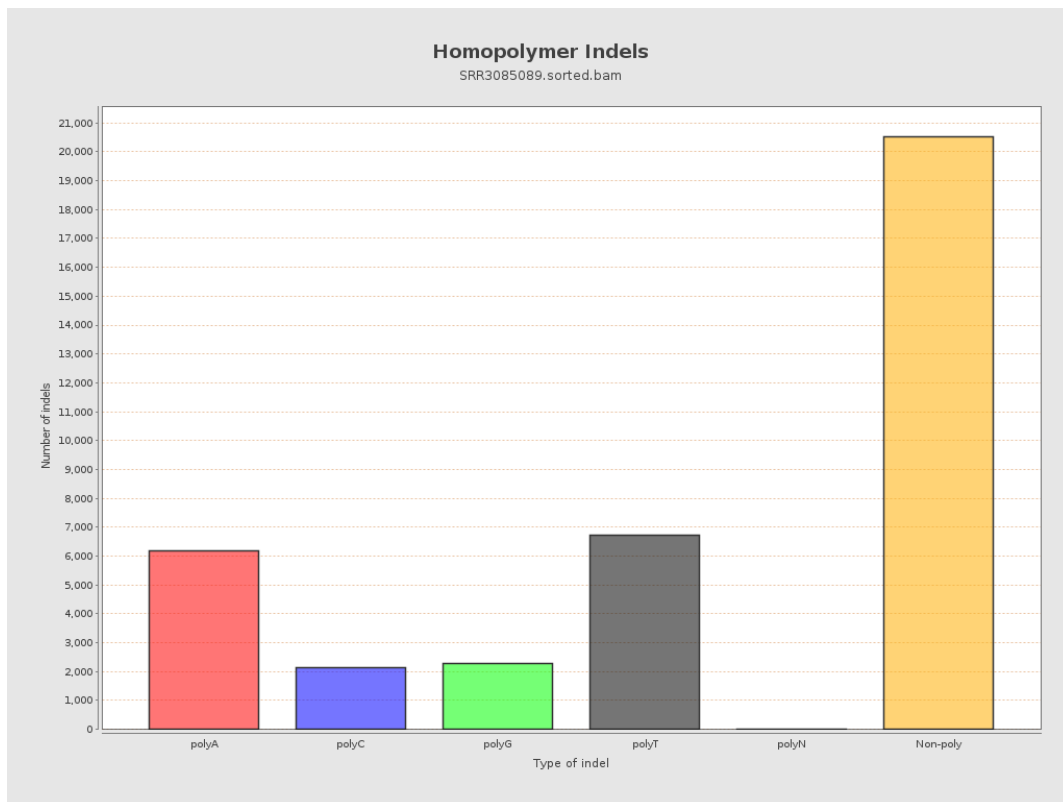
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

