

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:16:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251075.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_SRR10251075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:16:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,227,322
Mapped reads	3,076,122 / 95.32%
Unmapped reads	151,200 / 4.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,838 / 0.8%
Read min/max/mean length	30 / 80 / 80.29
Duplicated reads (estimated)	685,591 / 21.24%
Duplication rate	19.58%
Clipped reads	386,001 / 11.96%

2.2. ACGT Content

Number/percentage of A's	69,830,714 / 29.17%
Number/percentage of C's	47,595,583 / 19.88%
Number/percentage of T's	71,016,343 / 29.66%
Number/percentage of G's	50,965,072 / 21.29%
Number/percentage of N's	18,878 / 0.01%
GC Percentage	41.17%

2.3. Coverage

Mean	0.0774

Standard Deviation	0.927
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2.4. Mapping Quality

Mean Mapping Quality	48.12
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2.5. Mismatches and indels

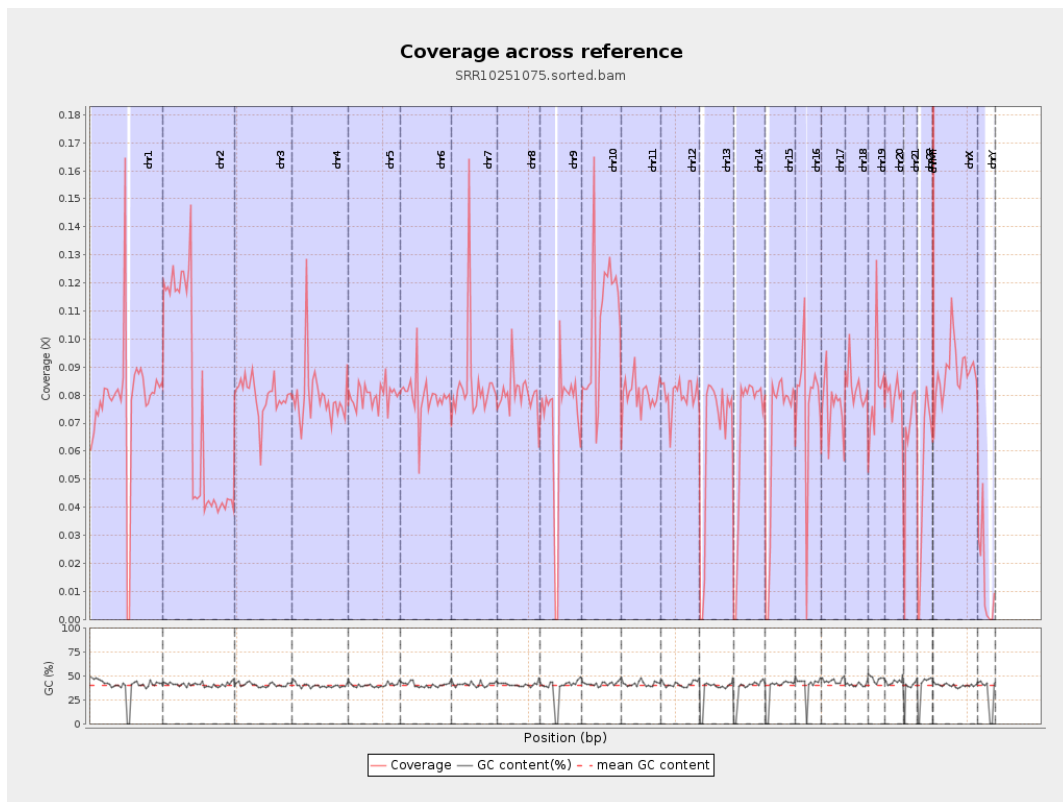
General error rate	0.61%
Mismatches	1,406,796
Insertions	29,241
Mapped reads with at least one insertion	0.93%
Deletions	76,338
Mapped reads with at least one deletion	2.44%
Homopolymer indels	45.4%

2.6. Chromosome stats

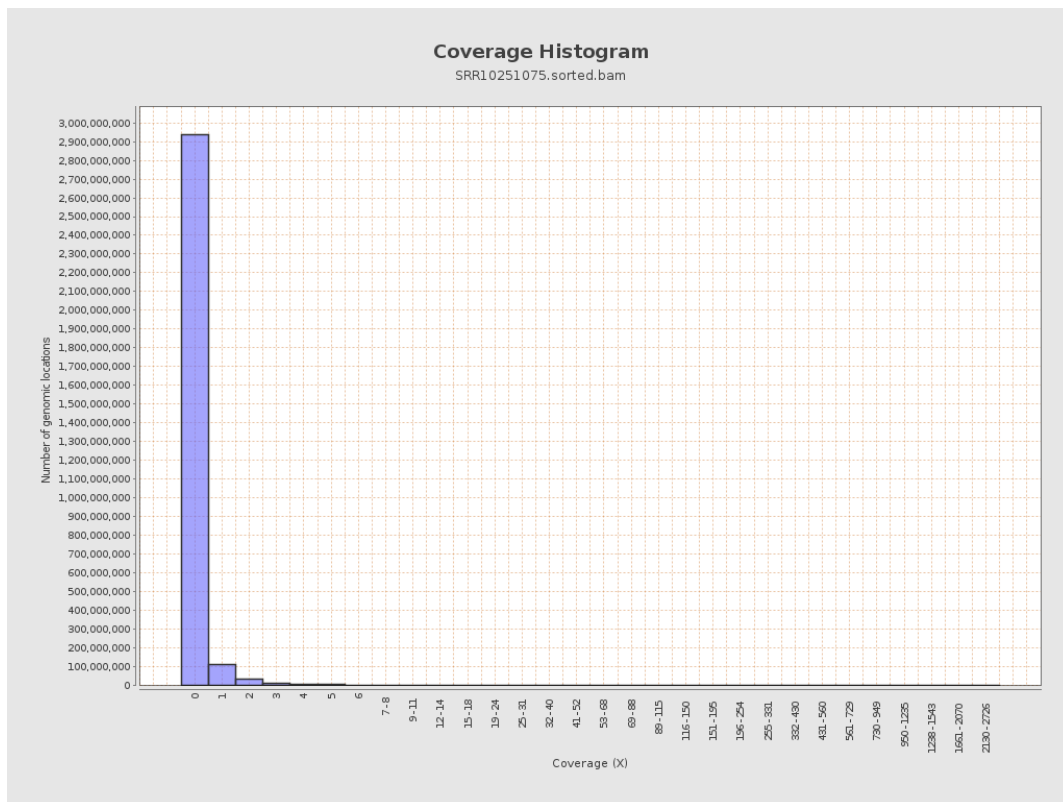
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19369938	0.0777	1.9409
chr2	243199373	18454504	0.0759	1.0168
chr3	198022430	15780230	0.0797	0.4007
chr4	191154276	15250098	0.0798	0.4913
chr5	180915260	14457482	0.0799	0.413
chr6	171115067	13598470	0.0795	0.5196
chr7	159138663	13396577	0.0842	1.4211

chr8	146364022	11760774	0.0804	0.6165
chr9	141213431	10032866	0.071	1.1916
chr10	135534747	14303106	0.1055	0.9833
chr11	135006516	10840830	0.0803	0.5497
chr12	133851895	10736352	0.0802	0.4116
chr13	115169878	7415802	0.0644	0.3528
chr14	107349540	7295677	0.068	0.6297
chr15	102531392	6689039	0.0652	0.3556
chr16	90354753	6940266	0.0768	0.6416
chr17	81195210	6250853	0.077	0.5334
chr18	78077248	6468495	0.0828	1.15
chr19	59128983	4884847	0.0826	1.8509
chr20	63025520	5014924	0.0796	0.4608
chr21	48129895	3163862	0.0657	0.4406
chr22	51304566	2675892	0.0522	0.3318
chrMT	16571	243489	14.6937	8.9626
chrX	155270560	13720816	0.0884	0.5037
chrY	59373566	818363	0.0138	0.7561

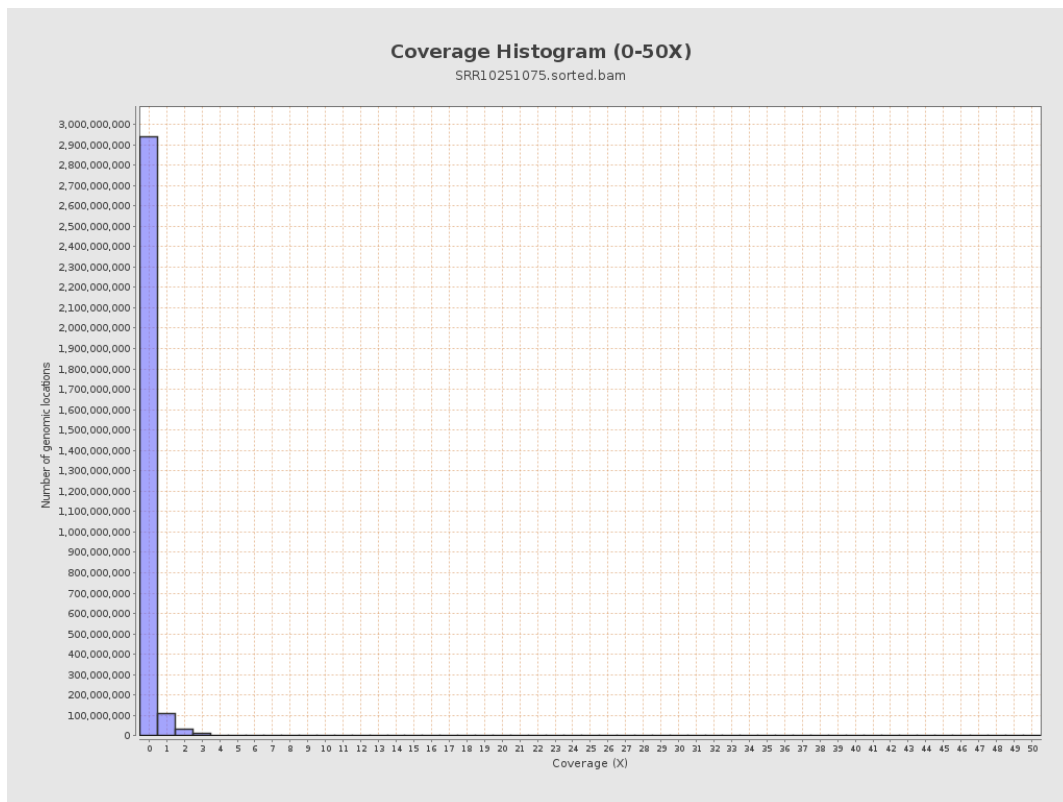
3. Results : Coverage across reference



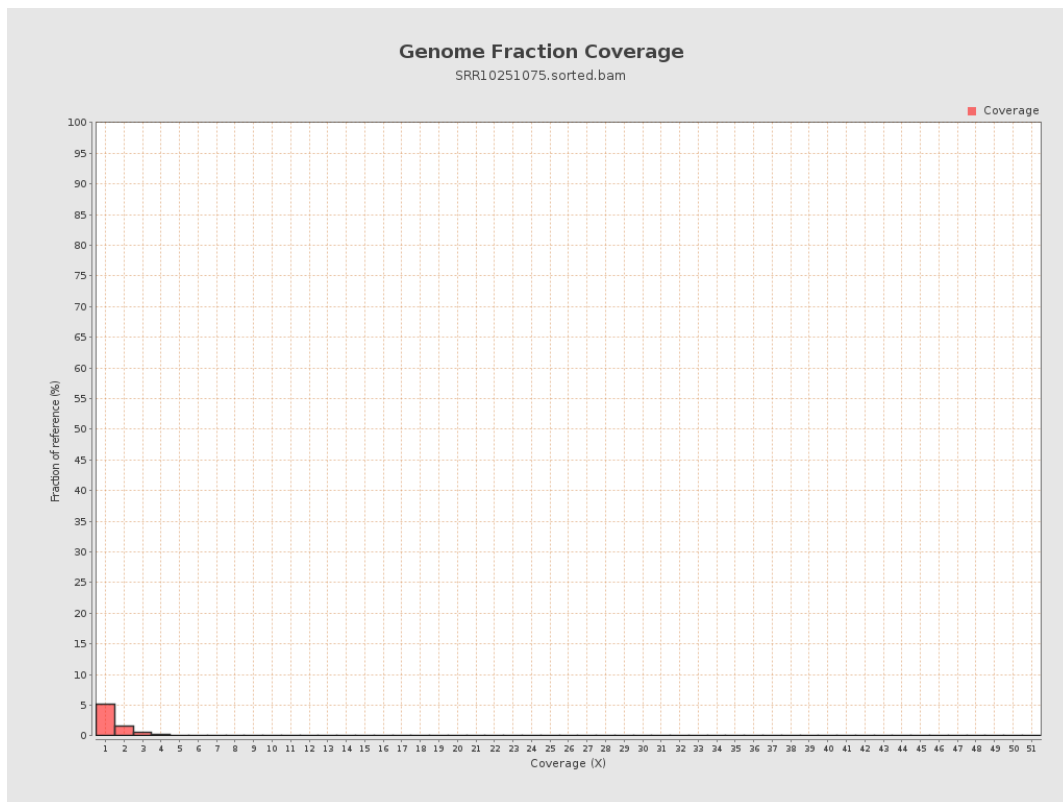
4. Results : Coverage Histogram



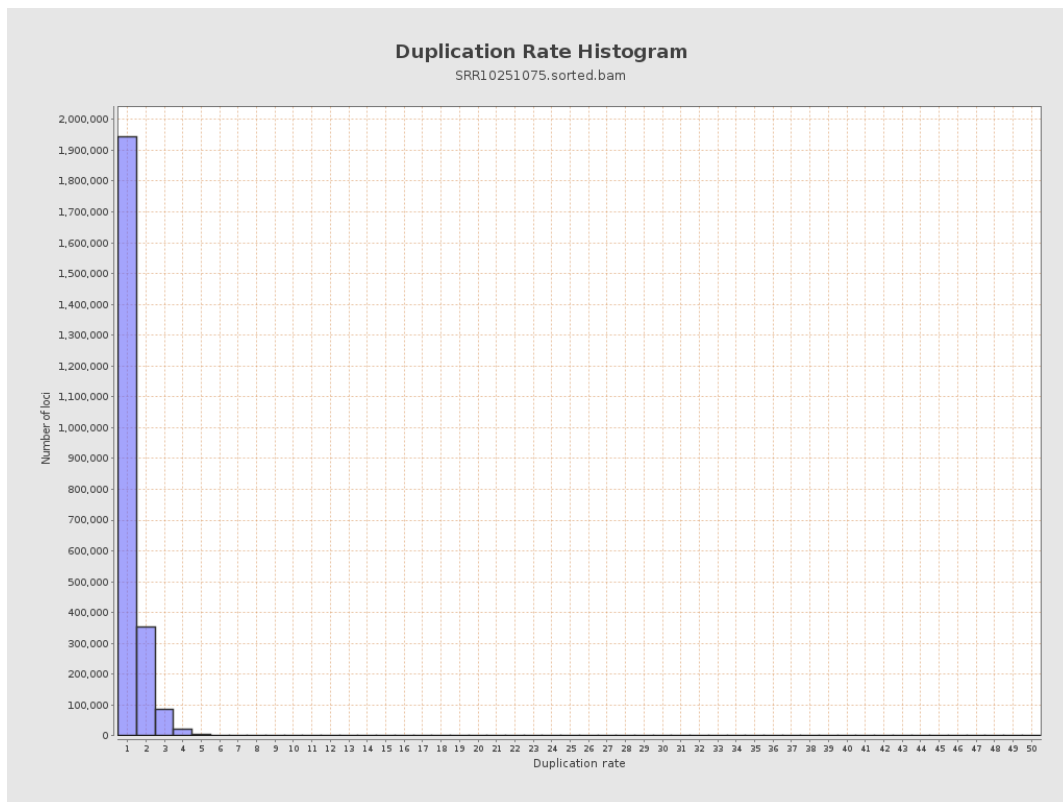
5. Results : Coverage Histogram (0-50X)



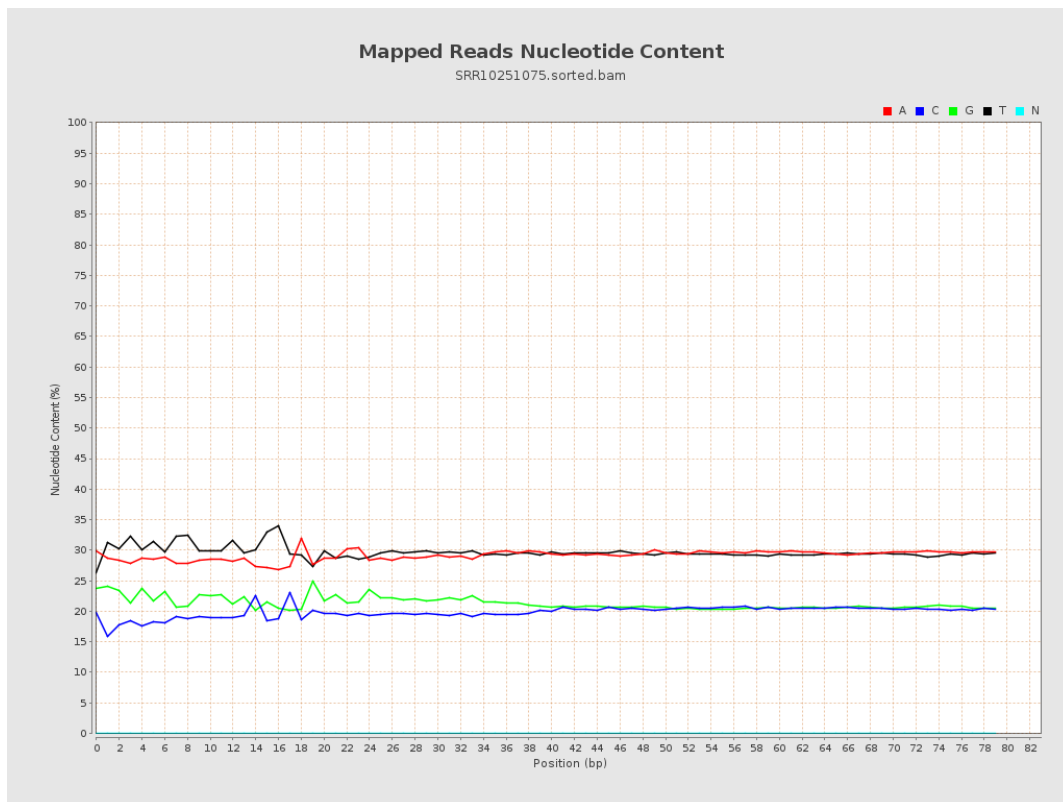
6. Results : Genome Fraction Coverage



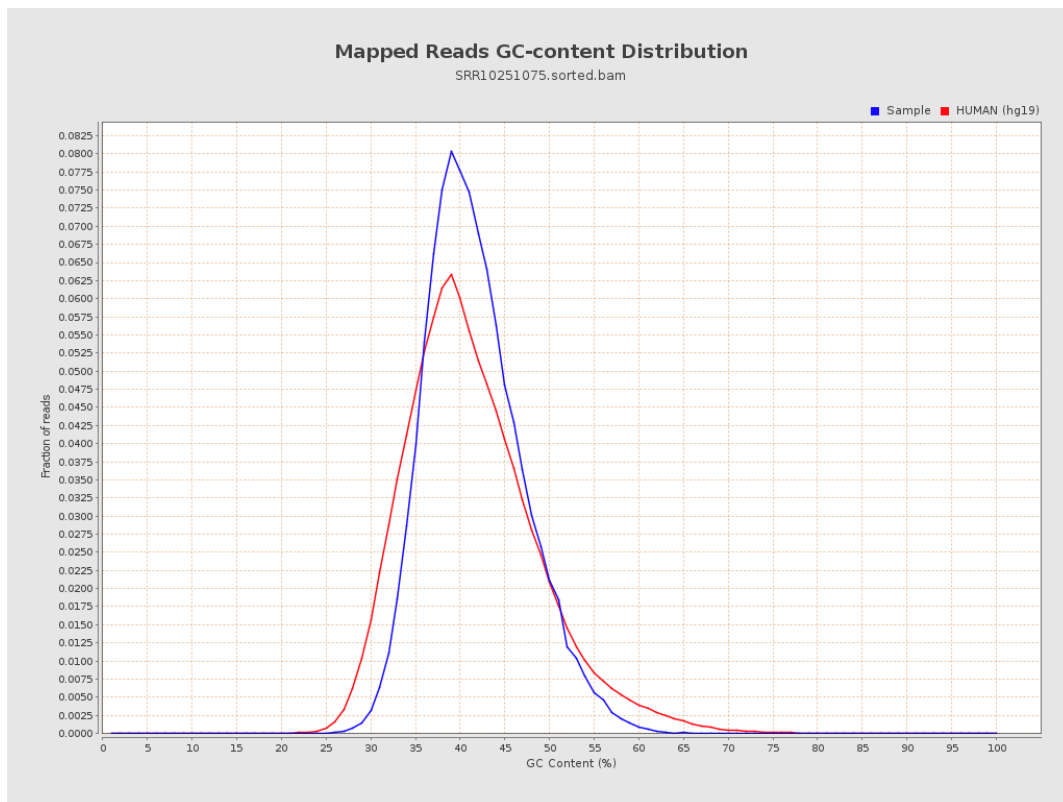
7. Results : Duplication Rate Histogram



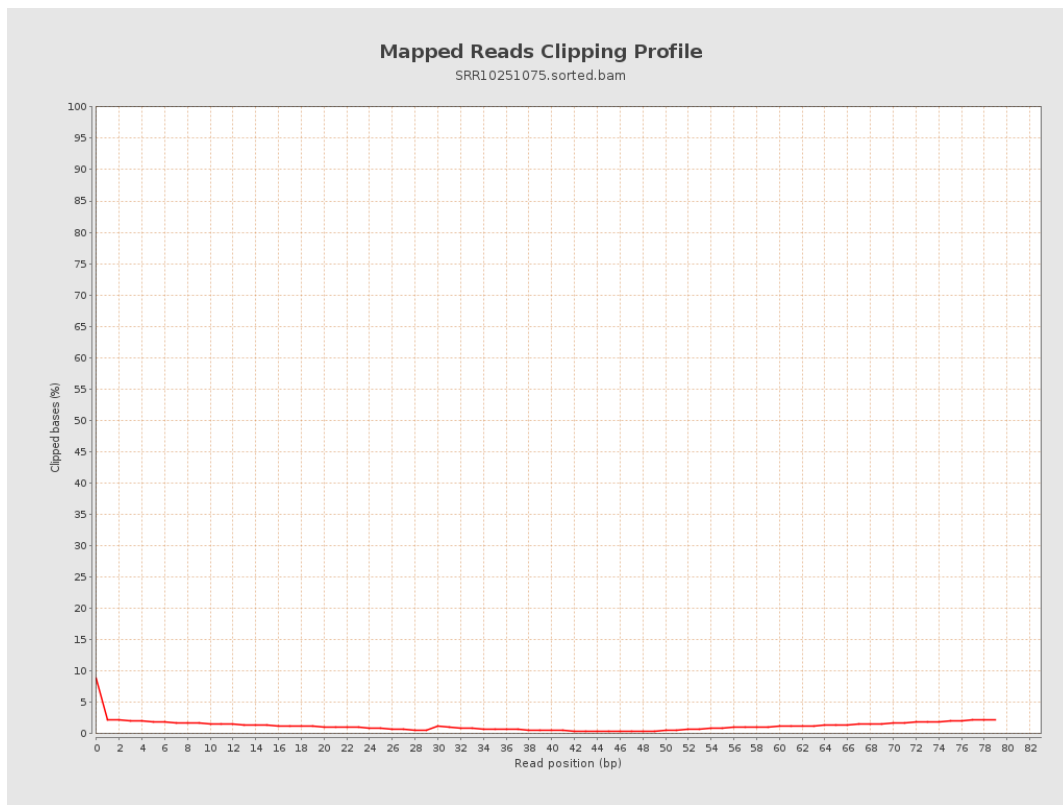
8. Results : Mapped Reads Nucleotide Content



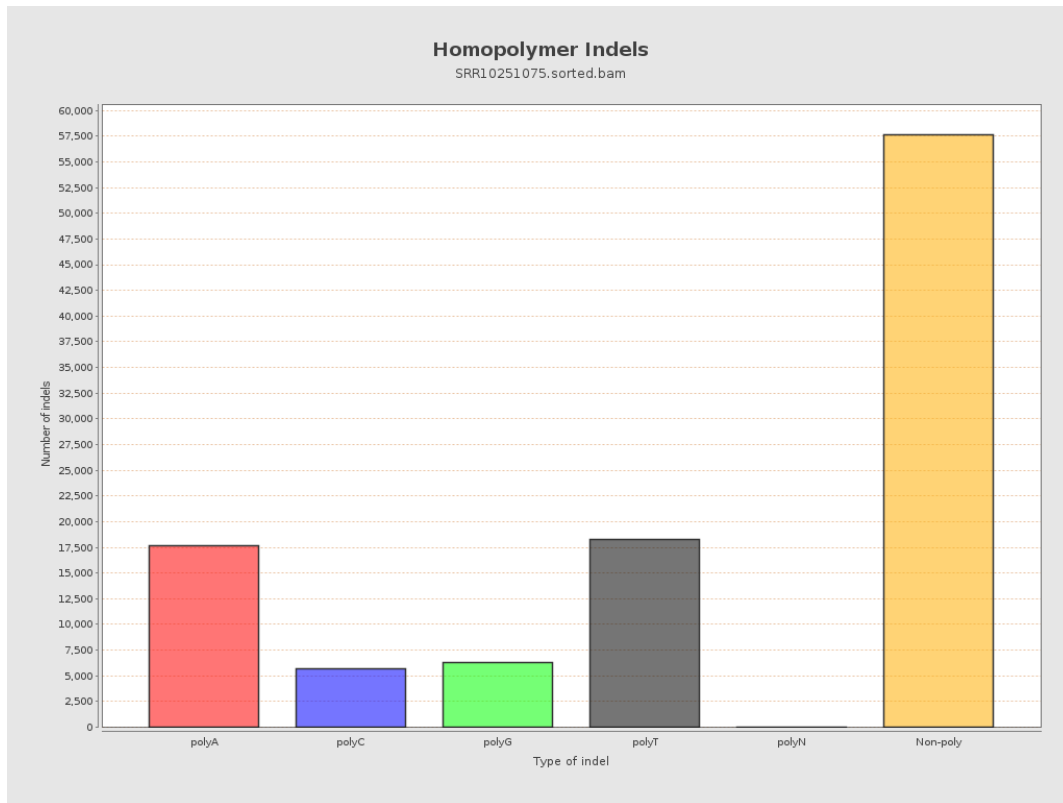
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

