

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:39:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081202.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_SRR3081202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:39:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,098,886
Mapped reads	6,661,661 / 73.21%
Unmapped reads	2,437,225 / 26.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	75,683 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	786,653 / 8.65%
Duplication rate	8.42%
Clipped reads	3,034,102 / 33.35%

2.2. ACGT Content

Number/percentage of A's	122,614,008 / 27.57%
Number/percentage of C's	85,473,665 / 19.22%
Number/percentage of T's	138,061,185 / 31.05%
Number/percentage of G's	98,302,741 / 22.11%
Number/percentage of N's	255,508 / 0.06%
GC Percentage	41.33%

2.3. Coverage

Mean	0.1437

Standard Deviation	1.4531
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2.4. Mapping Quality

Mean Mapping Quality	46.54
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2.5. Mismatches and indels

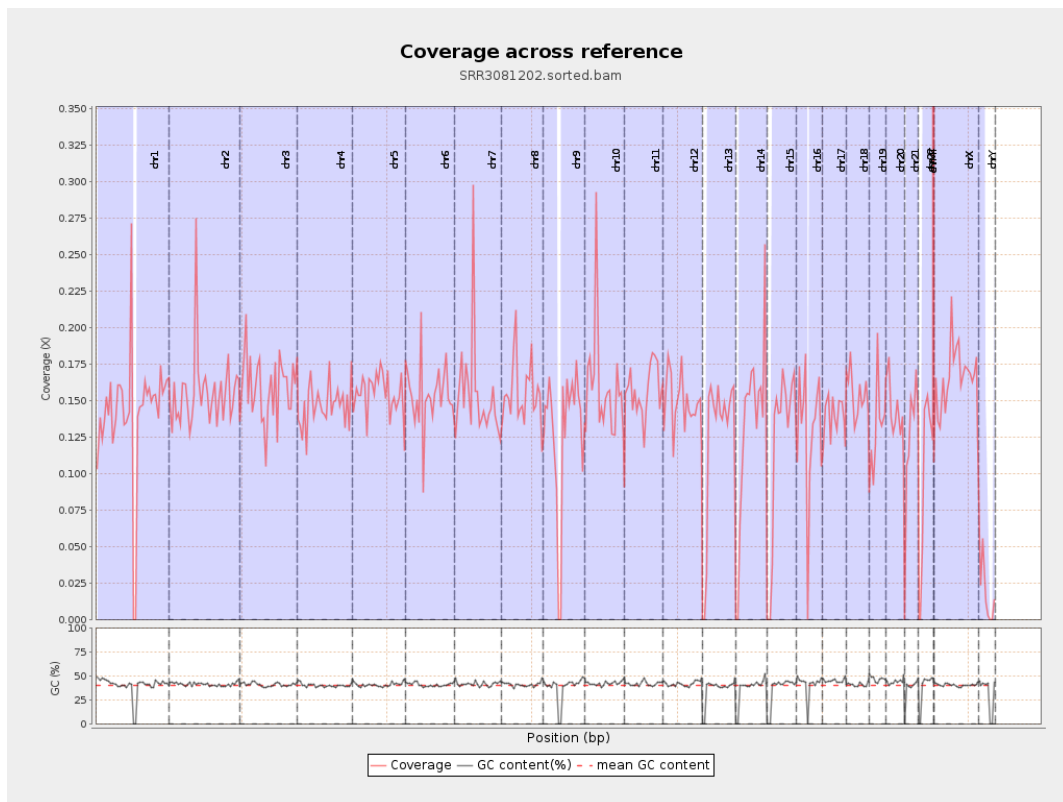
General error rate	1.05%
Mismatches	4,598,322
Insertions	32,595
Mapped reads with at least one insertion	0.49%
Deletions	93,189
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.06%

2.6. Chromosome stats

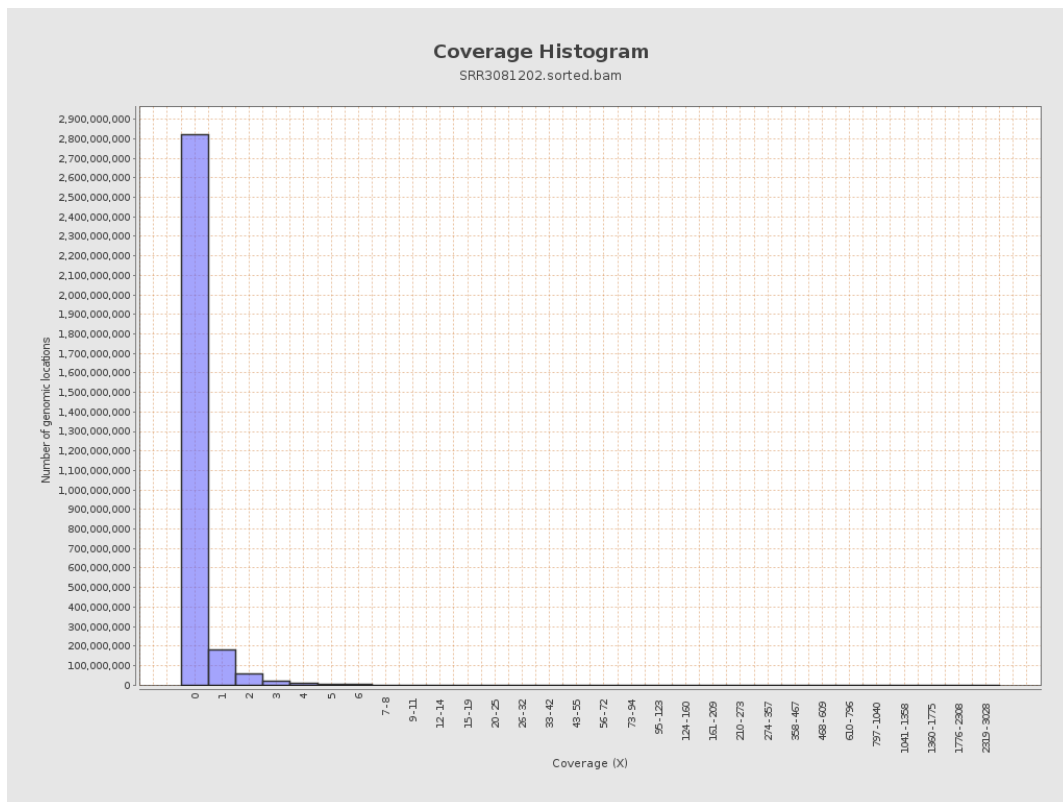
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	35320808	0.1417	2.579
chr2	243199373	37593691	0.1546	1.0465
chr3	198022430	31306231	0.1581	0.6009
chr4	191154276	27977729	0.1464	0.5914
chr5	180915260	28080945	0.1552	0.5903
chr6	171115067	26330960	0.1539	0.8258
chr7	159138663	24567311	0.1544	2.219

chr8	146364022	22678455	0.1549	1.859
chr9	141213431	18062218	0.1279	0.9645
chr10	135534747	21540880	0.1589	1.4233
chr11	135006516	21020948	0.1557	1.0837
chr12	133851895	19813327	0.148	0.6003
chr13	115169878	14213787	0.1234	0.5163
chr14	107349540	14297874	0.1332	3.9047
chr15	102531392	12350634	0.1205	0.509
chr16	90354753	11701073	0.1295	0.6409
chr17	81195210	11239837	0.1384	0.7494
chr18	78077248	12104225	0.155	1.8829
chr19	59128983	7841457	0.1326	1.8413
chr20	63025520	8993347	0.1427	0.6577
chr21	48129895	5957870	0.1238	0.5796
chr22	51304566	5003825	0.0975	0.4637
chrMT	16571	97745	5.8986	4.8316
chrX	155270560	25649532	0.1652	0.6936
chrY	59373566	1106875	0.0186	0.3273

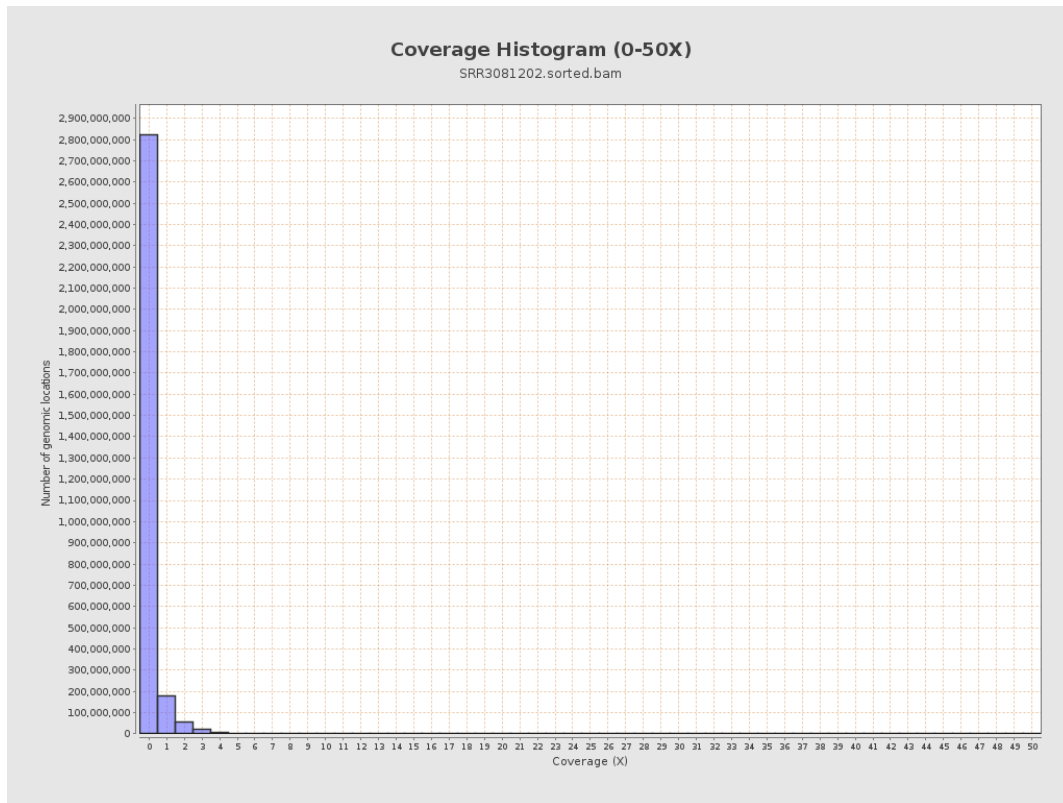
3. Results : Coverage across reference



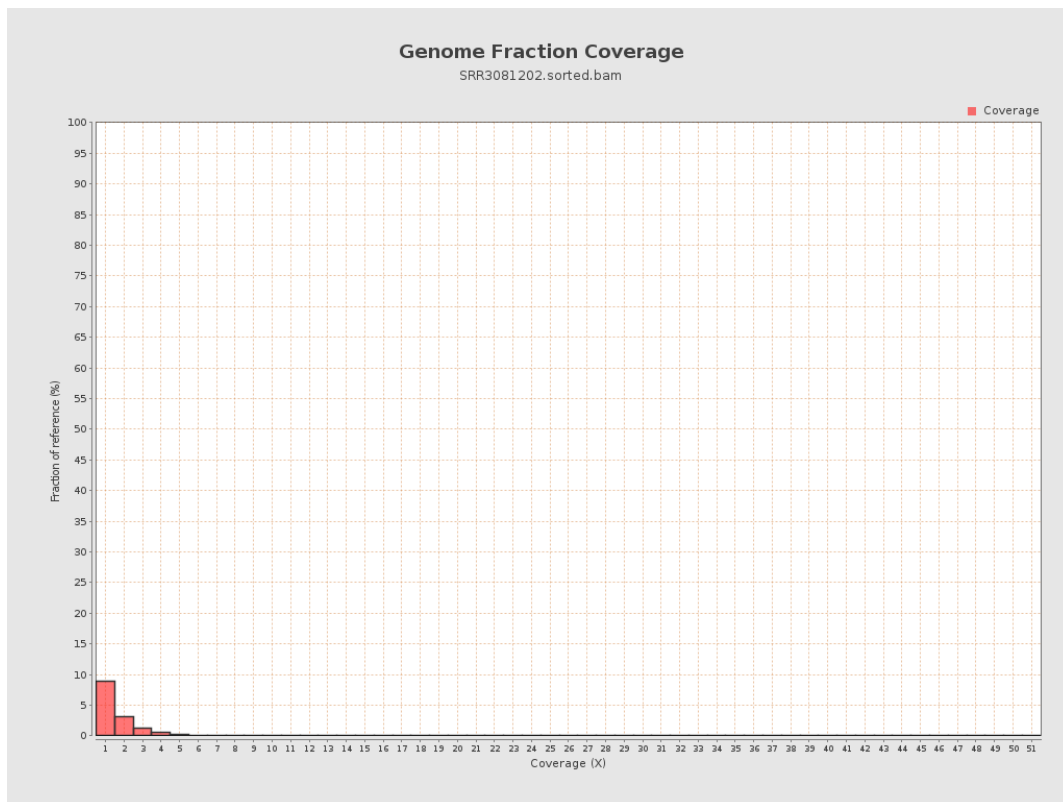
4. Results : Coverage Histogram



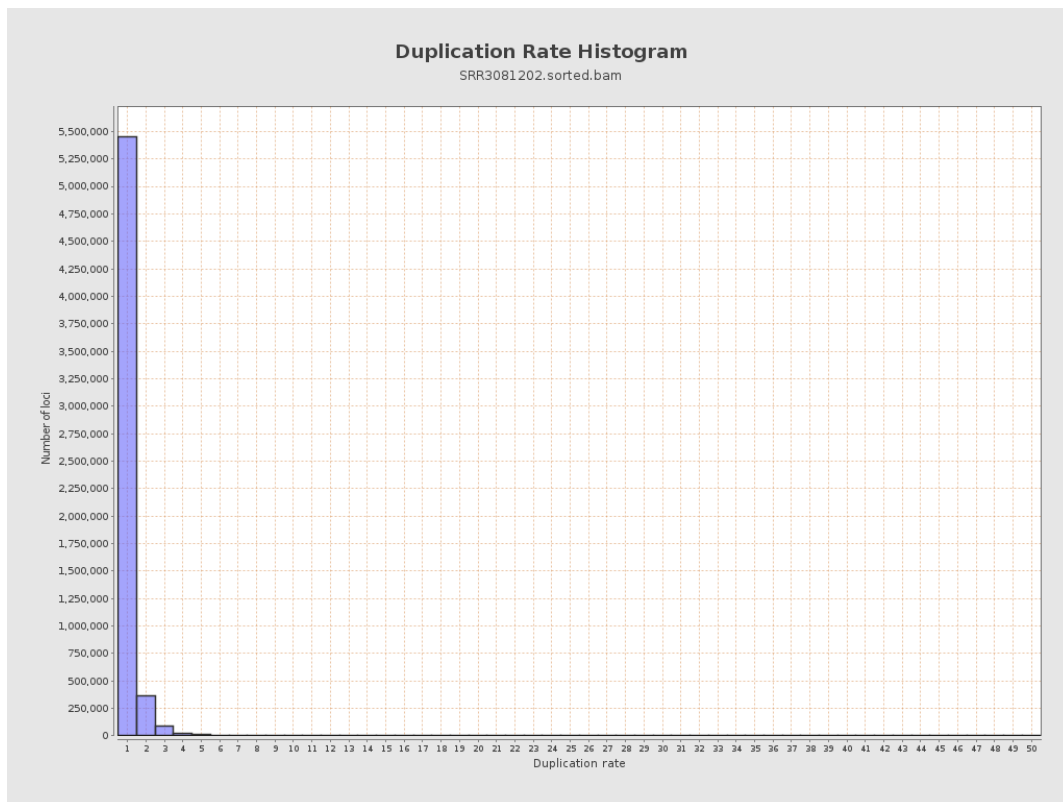
5. Results : Coverage Histogram (0-50X)



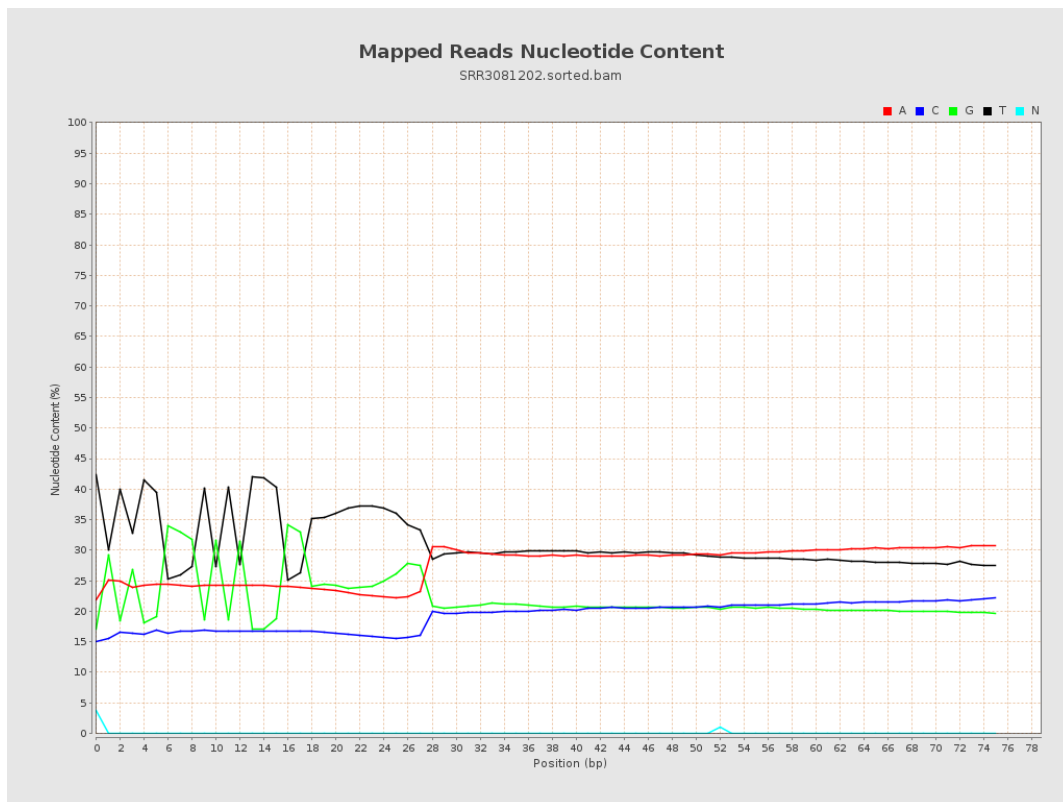
6. Results : Genome Fraction Coverage



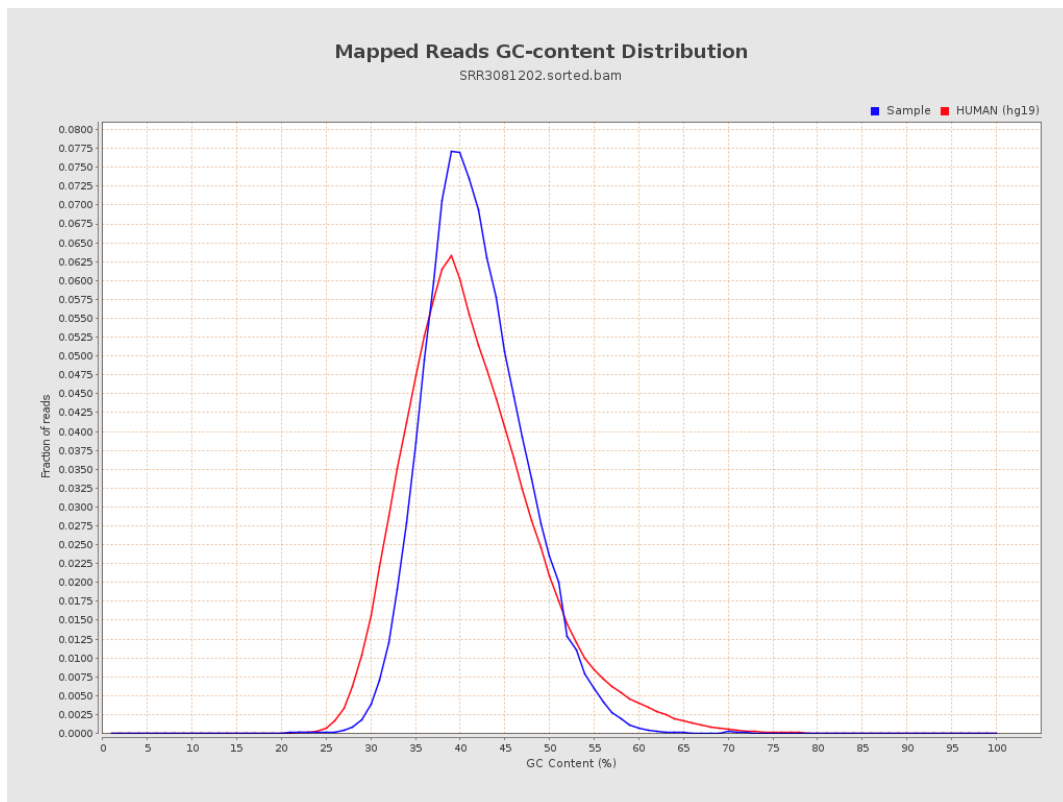
7. Results : Duplication Rate Histogram



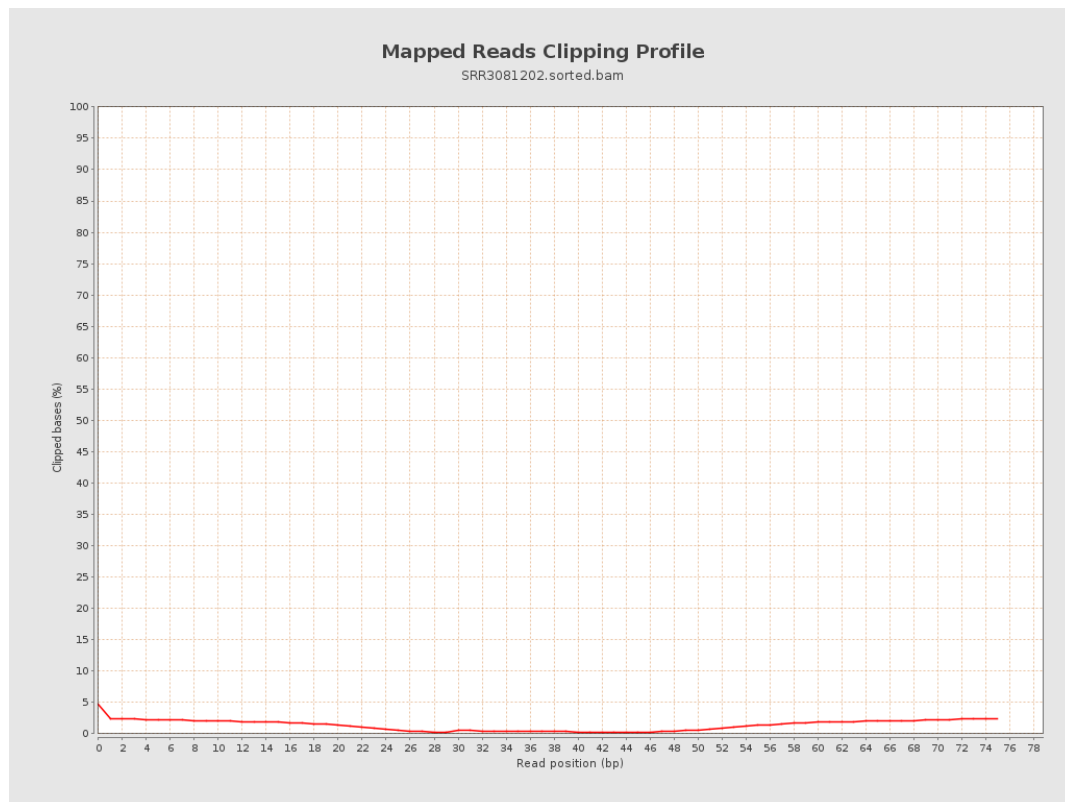
8. Results : Mapped Reads Nucleotide Content



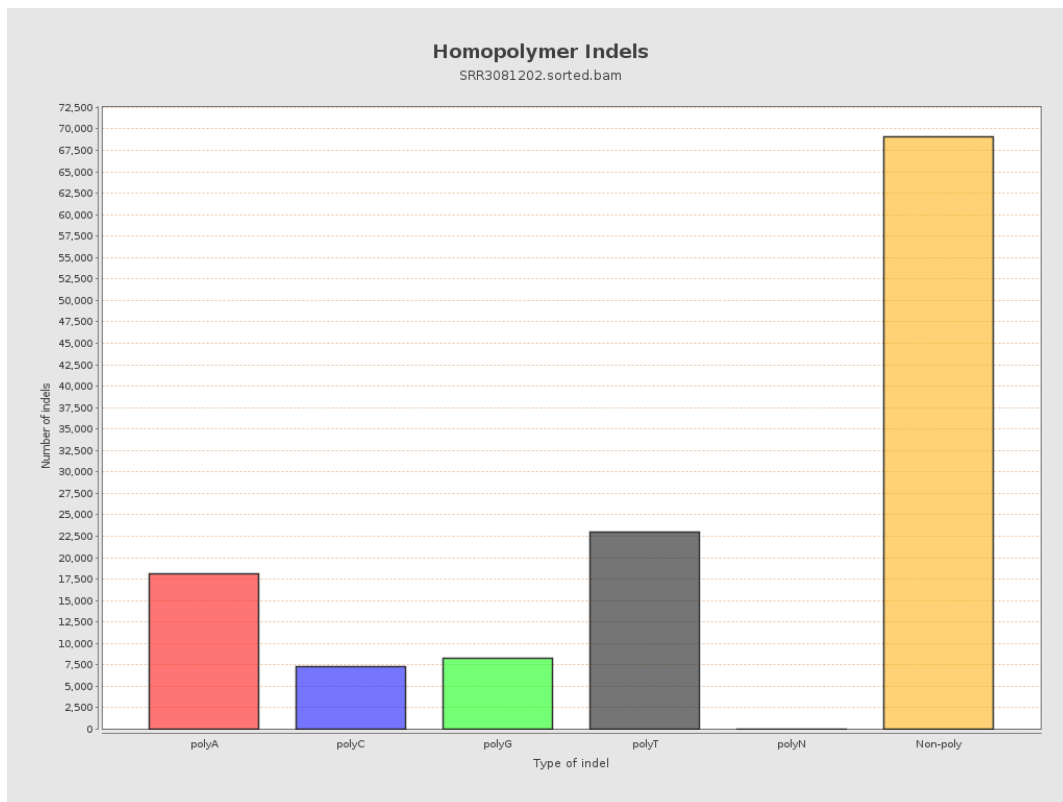
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

