

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:45:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240021.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_SRR6240021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:45:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,203,882
Mapped reads	1,464,122 / 66.43%
Unmapped reads	739,760 / 33.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,729 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	121,340 / 5.51%
Duplication rate	6.77%
Clipped reads	1,023,474 / 46.44%

2.2. ACGT Content

Number/percentage of A's	23,548,380 / 26.48%
Number/percentage of C's	15,038,003 / 16.91%
Number/percentage of T's	29,106,982 / 32.73%
Number/percentage of G's	21,177,313 / 23.81%
Number/percentage of N's	56,296 / 0.06%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2845
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.9
----------------------	------

2.5. Mismatches and indels

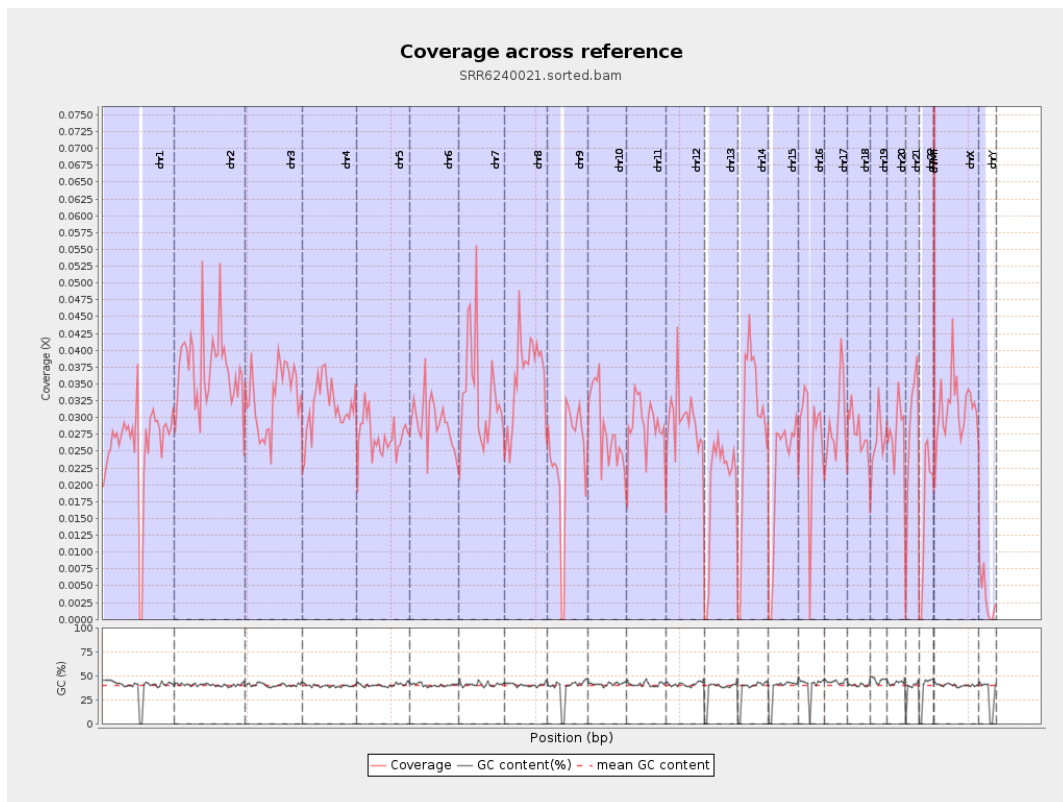
General error rate	1.04%
Mismatches	916,989
Insertions	6,426
Mapped reads with at least one insertion	0.44%
Deletions	31,211
Mapped reads with at least one deletion	2.1%
Homopolymer indels	49.5%

2.6. Chromosome stats

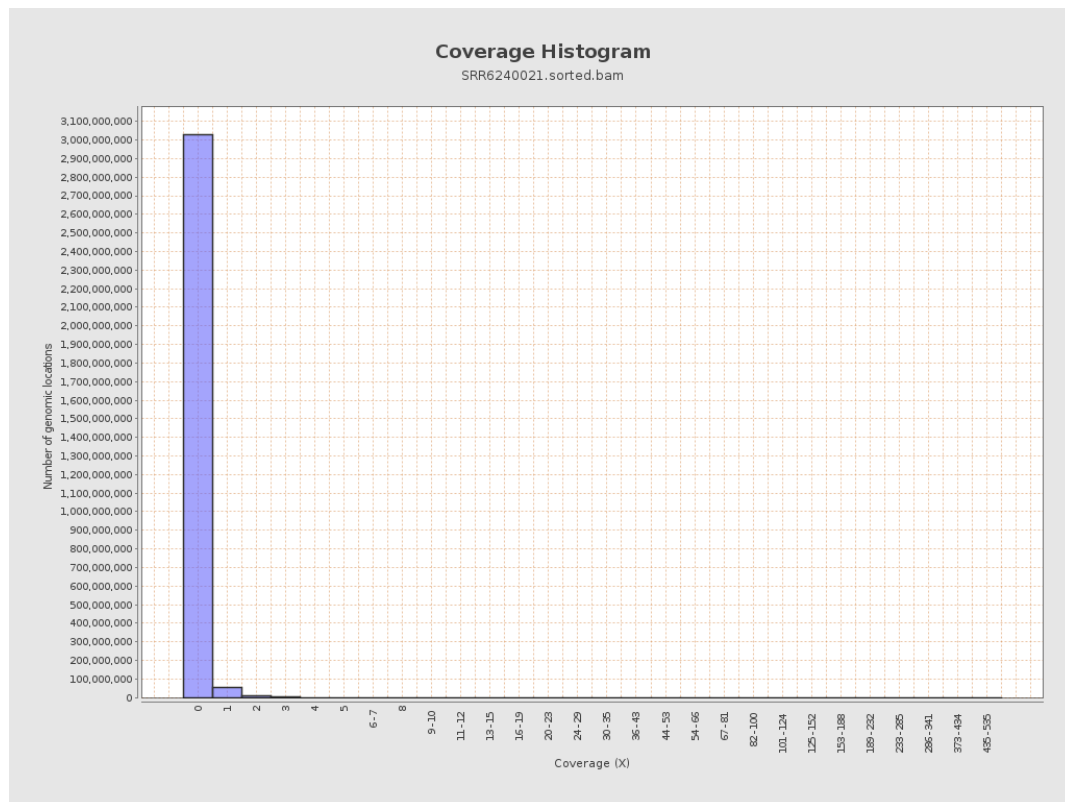
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6444695	0.0259	0.3716
chr2	243199373	9069312	0.0373	0.3421
chr3	198022430	6521440	0.0329	0.2293
chr4	191154276	6022215	0.0315	0.2296
chr5	180915260	4941338	0.0273	0.21
chr6	171115067	4996440	0.0292	0.2474
chr7	159138663	5315956	0.0334	0.5119

chr8	146364022	5288005	0.0361	0.3651
chr9	141213431	3370036	0.0239	0.2686
chr10	135534747	3828546	0.0282	0.2447
chr11	135006516	3940981	0.0292	0.2588
chr12	133851895	3960834	0.0296	0.217
chr13	115169878	2282105	0.0198	0.1766
chr14	107349540	3130045	0.0292	0.2221
chr15	102531392	2259680	0.022	0.1967
chr16	90354753	2393916	0.0265	0.2095
chr17	81195210	2359514	0.0291	0.2291
chr18	78077248	2170235	0.0278	0.3725
chr19	59128983	1583114	0.0268	0.3023
chr20	63025520	1749114	0.0278	0.2145
chr21	48129895	1359551	0.0282	0.2148
chr22	51304566	854086	0.0166	0.1576
chrMT	16571	55730	3.3631	4.1195
chrX	155270560	4893426	0.0315	0.2441
chrY	59373566	189961	0.0032	0.0761

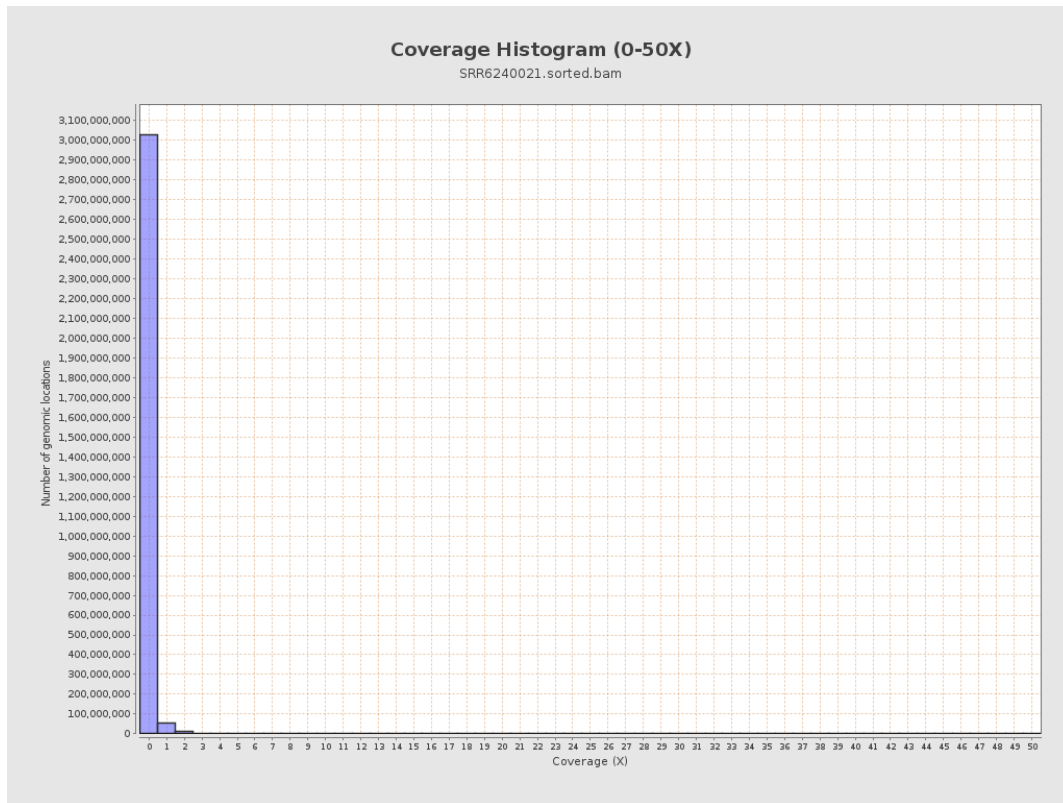
3. Results : Coverage across reference



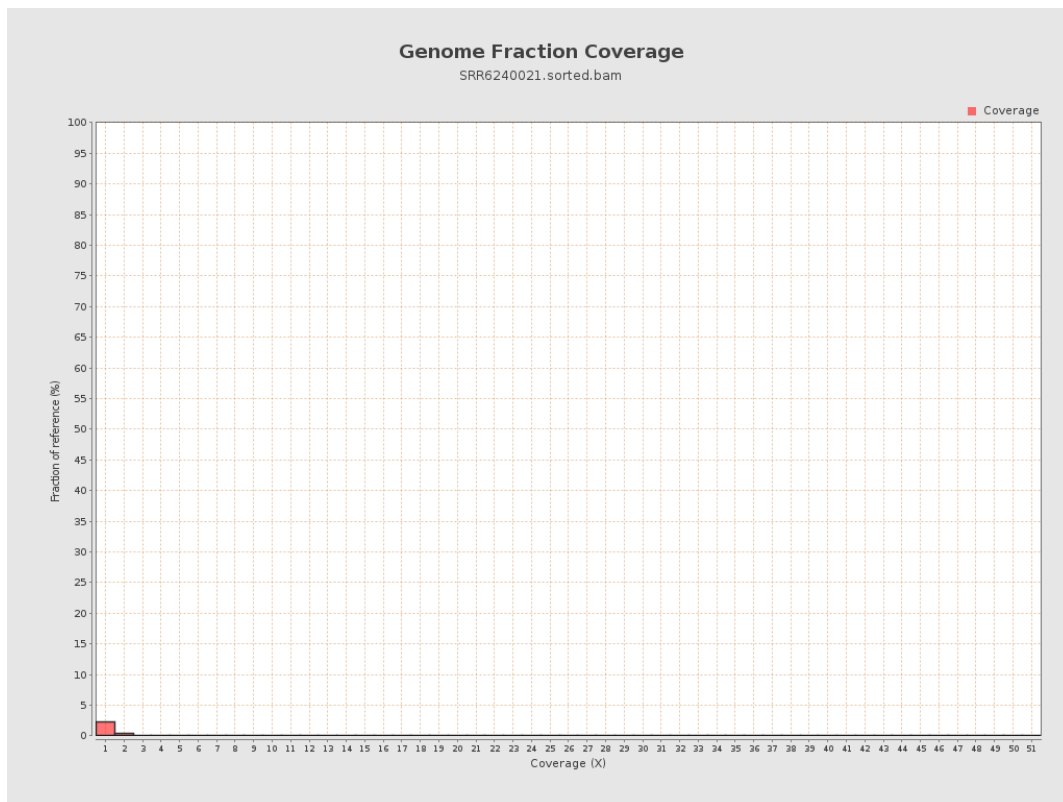
4. Results : Coverage Histogram



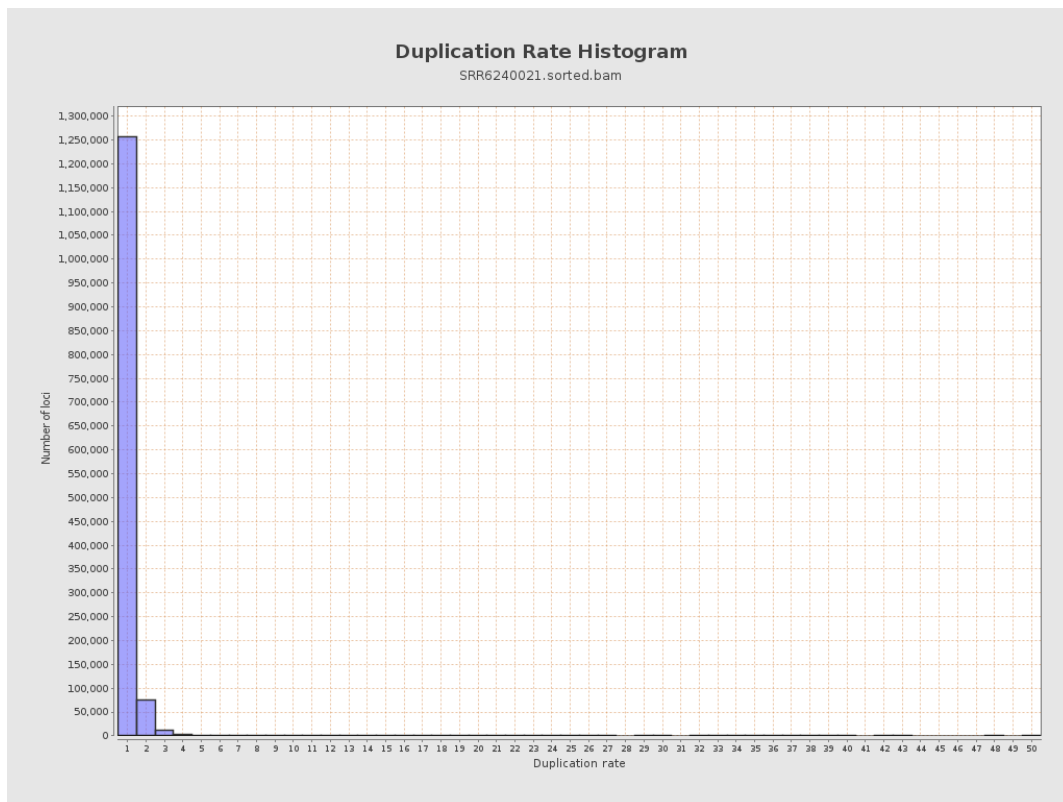
5. Results : Coverage Histogram (0-50X)



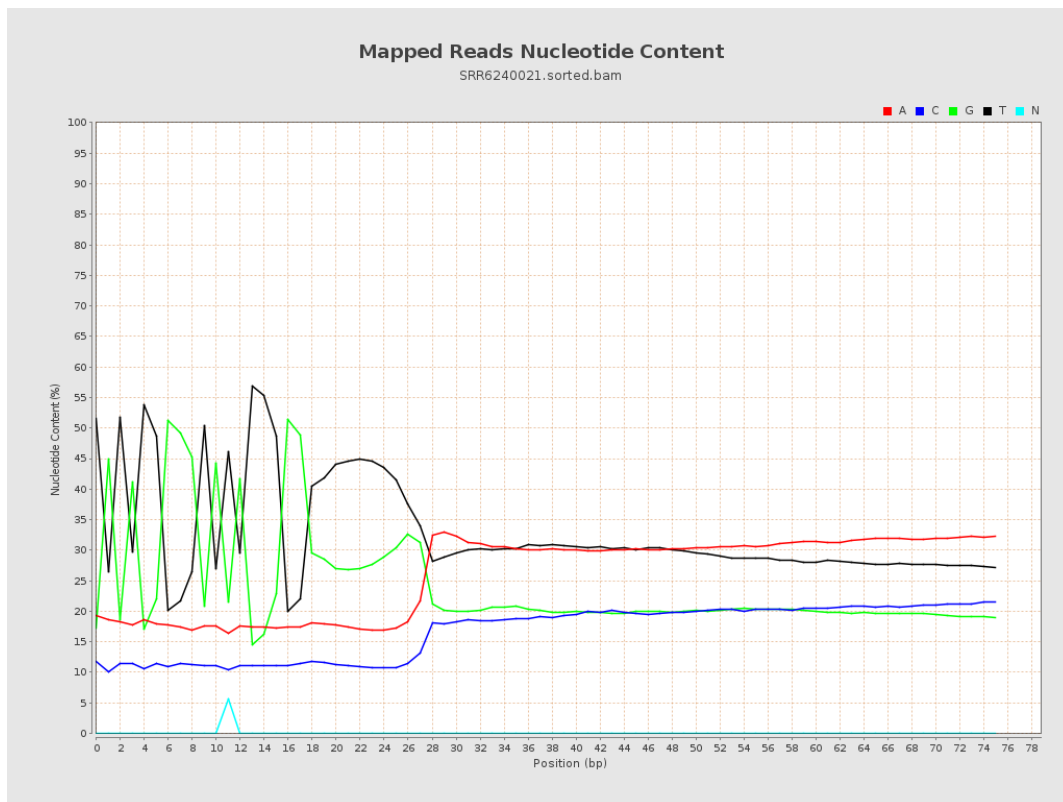
6. Results : Genome Fraction Coverage



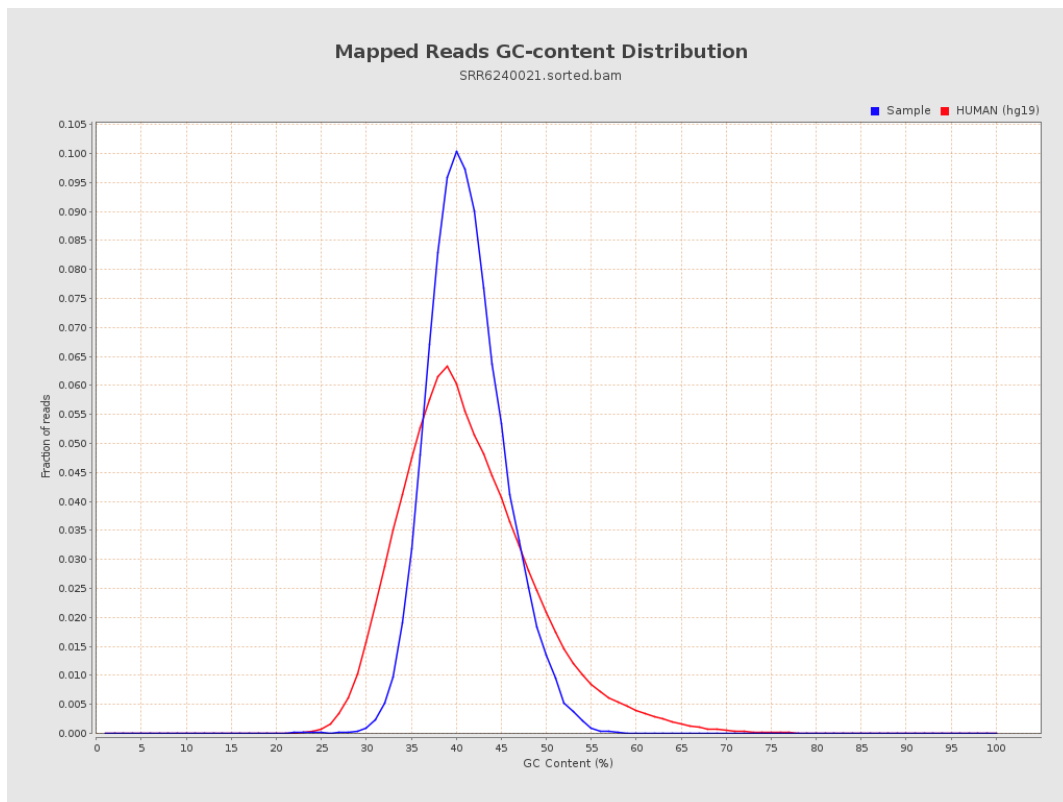
7. Results : Duplication Rate Histogram



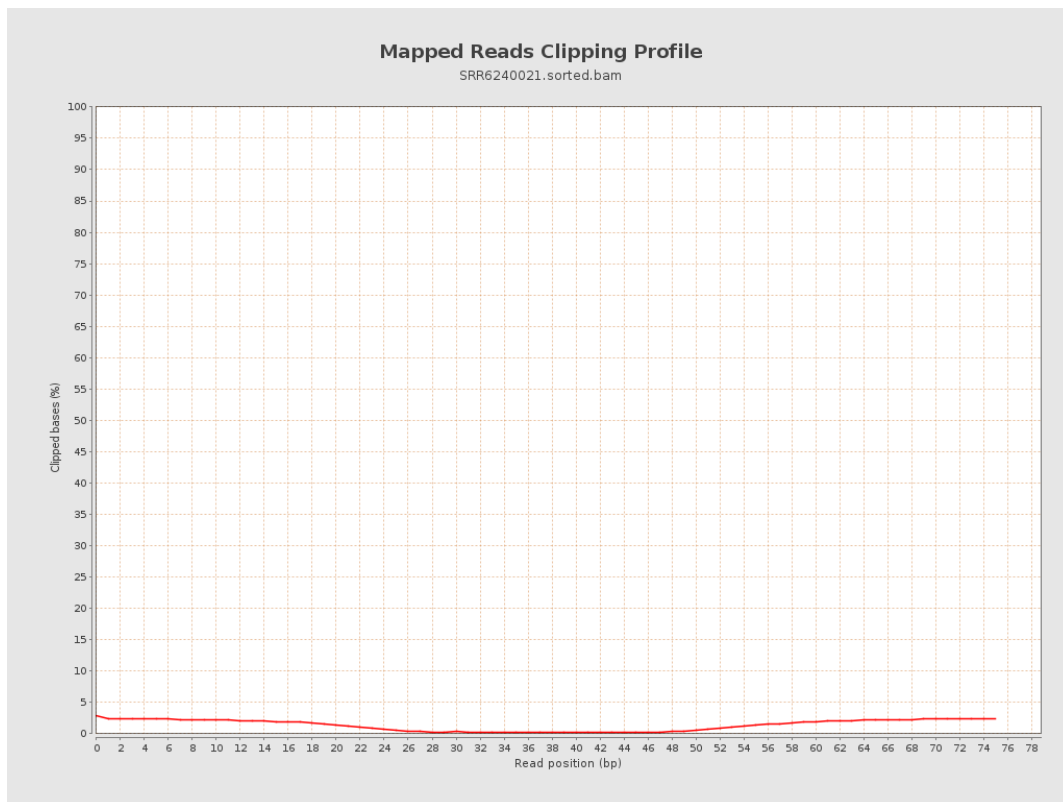
8. Results : Mapped Reads Nucleotide Content



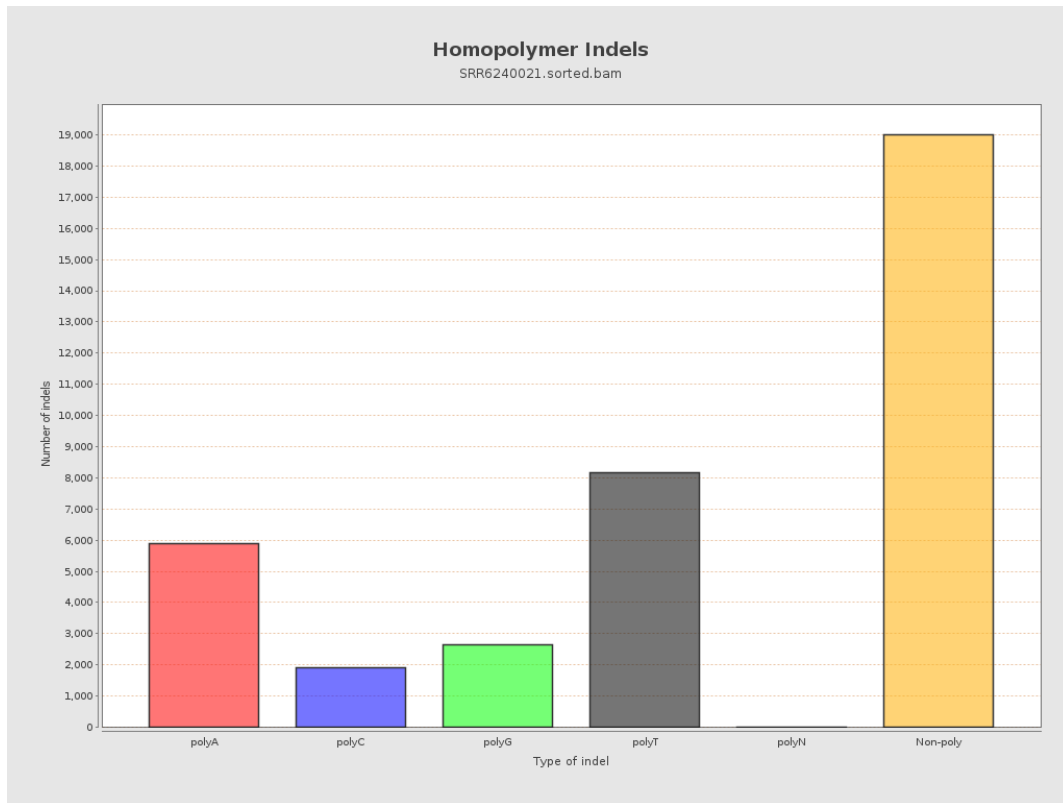
9. Results : Mapped Reads GC-content Distribution



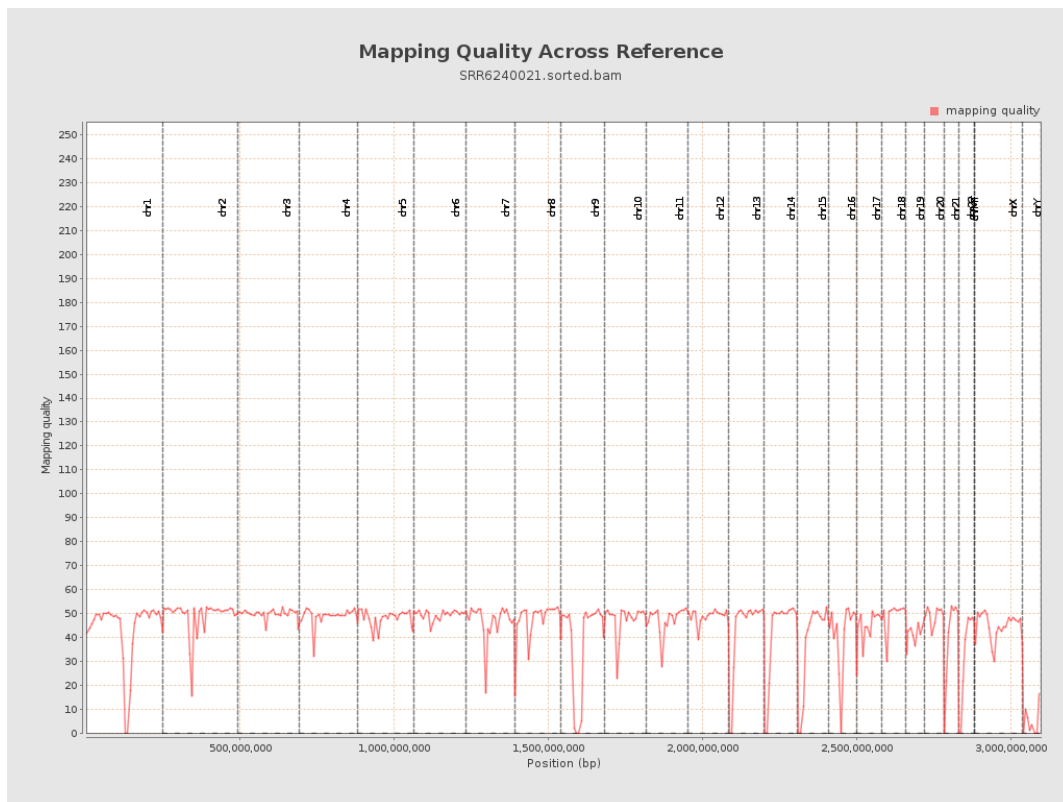
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

