

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:28:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234077.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_SRR6234077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:28:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,263,786
Mapped reads	4,965,413 / 94.33%
Unmapped reads	298,373 / 5.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,151 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	521,028 / 9.9%
Duplication rate	8.5%
Clipped reads	2,618,016 / 49.74%

2.2. ACGT Content

Number/percentage of A's	82,794,269 / 25.88%
Number/percentage of C's	58,398,358 / 18.25%
Number/percentage of T's	103,465,299 / 32.34%
Number/percentage of G's	75,244,186 / 23.52%
Number/percentage of N's	31,235 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.1034

Standard Deviation	1.1839
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.86
----------------------	-------

2.5. Mismatches and indels

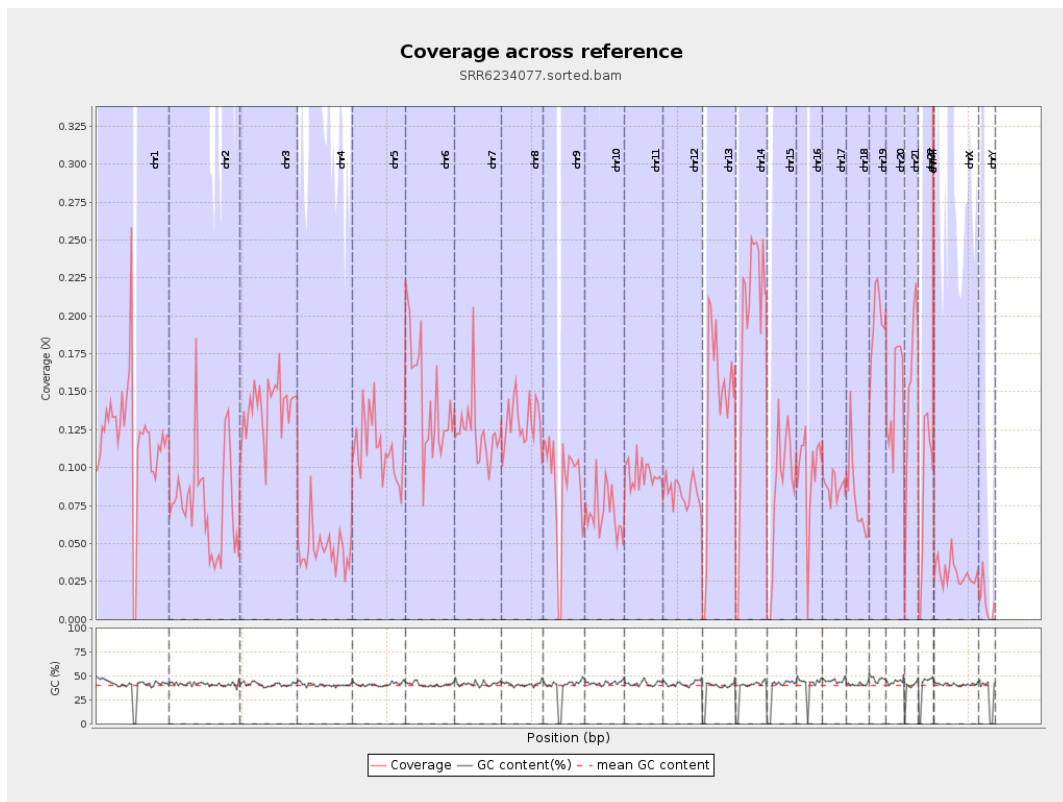
General error rate	0.57%
Mismatches	1,777,016
Insertions	20,392
Mapped reads with at least one insertion	0.41%
Deletions	68,622
Mapped reads with at least one deletion	1.37%
Homopolymer indels	43.89%

2.6. Chromosome stats

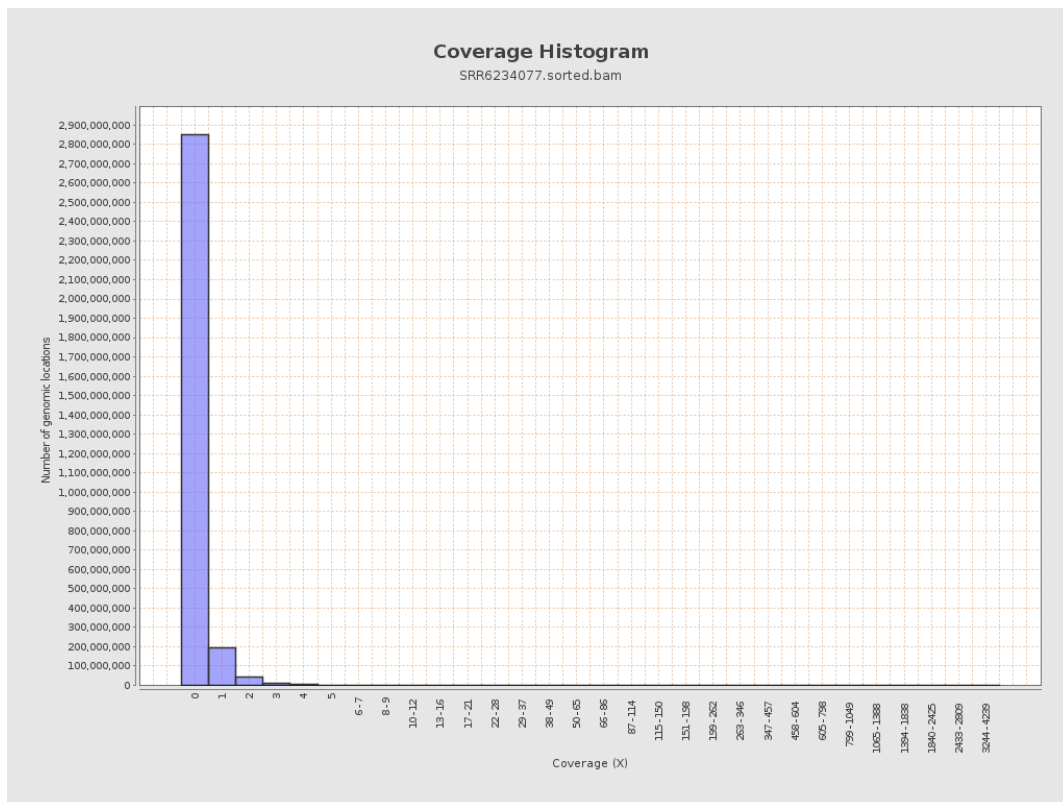
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29819313	0.1196	2.7118
chr2	243199373	18626615	0.0766	1.9762
chr3	198022430	27597235	0.1394	0.4666
chr4	191154276	8749474	0.0458	0.3433
chr5	180915260	20451024	0.113	0.4453
chr6	171115067	24923607	0.1457	0.7714
chr7	159138663	19557358	0.1229	1.3039

chr8	146364022	18936702	0.1294	1.2278
chr9	141213431	12425045	0.088	0.7455
chr10	135534747	9581406	0.0707	0.6258
chr11	135006516	12837032	0.0951	0.7624
chr12	133851895	11272982	0.0842	0.3879
chr13	115169878	15995561	0.1389	0.5329
chr14	107349540	20076205	0.187	0.623
chr15	102531392	8697973	0.0848	0.437
chr16	90354753	8748696	0.0968	0.5366
chr17	81195210	7115307	0.0876	0.4162
chr18	78077248	6282989	0.0805	1.9977
chr19	59128983	11720236	0.1982	1.3501
chr20	63025520	9268192	0.1471	0.5526
chr21	48129895	7422442	0.1542	0.5304
chr22	51304566	4378331	0.0853	0.3575
chrMT	16571	210286	12.69	8.0738
chrX	155270560	4716297	0.0304	0.4179
chrY	59373566	641311	0.0108	0.2263

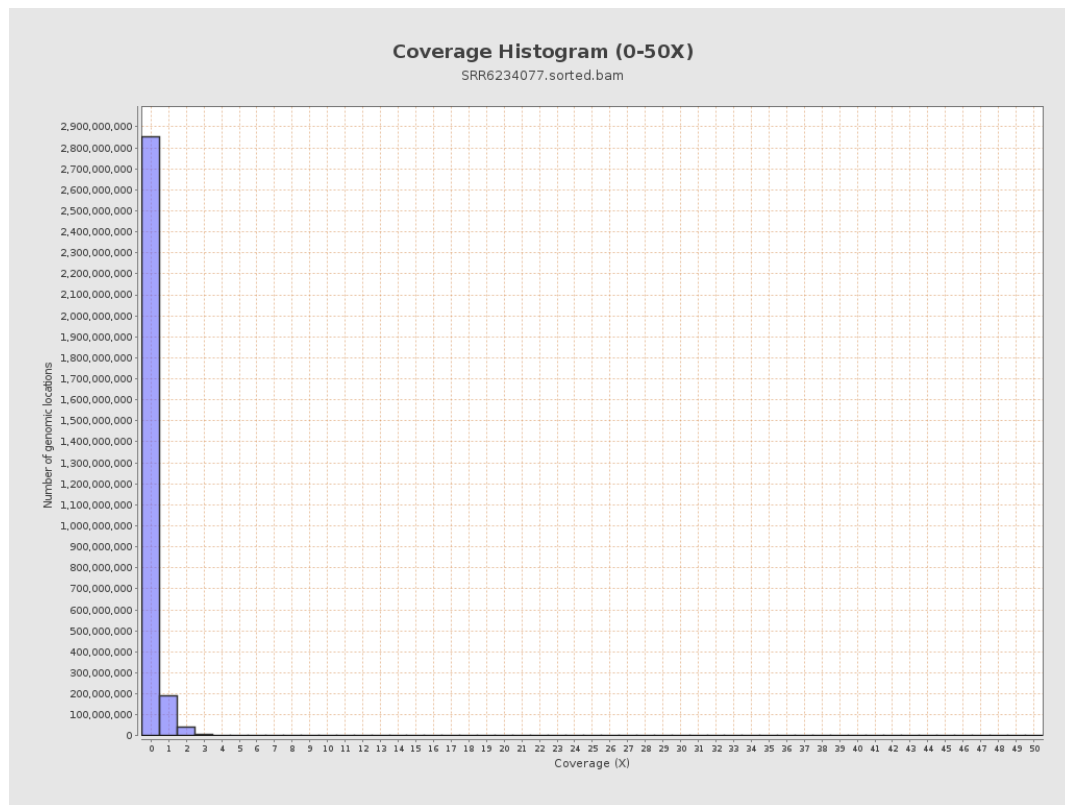
3. Results : Coverage across reference



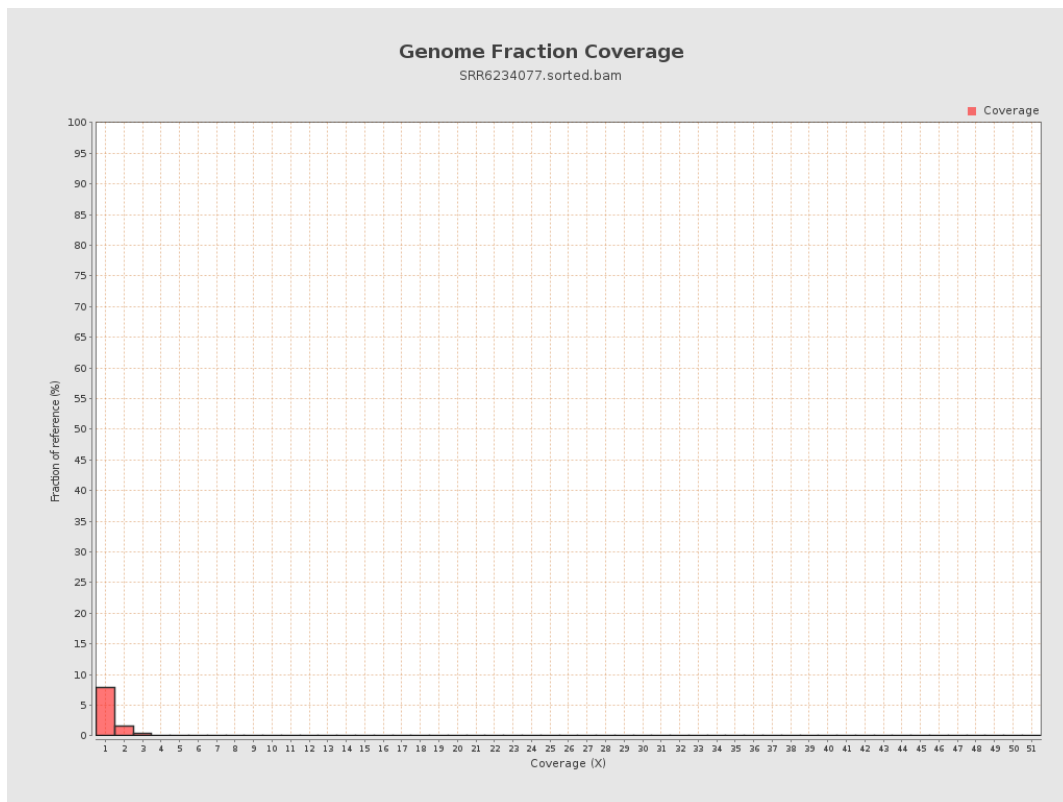
4. Results : Coverage Histogram



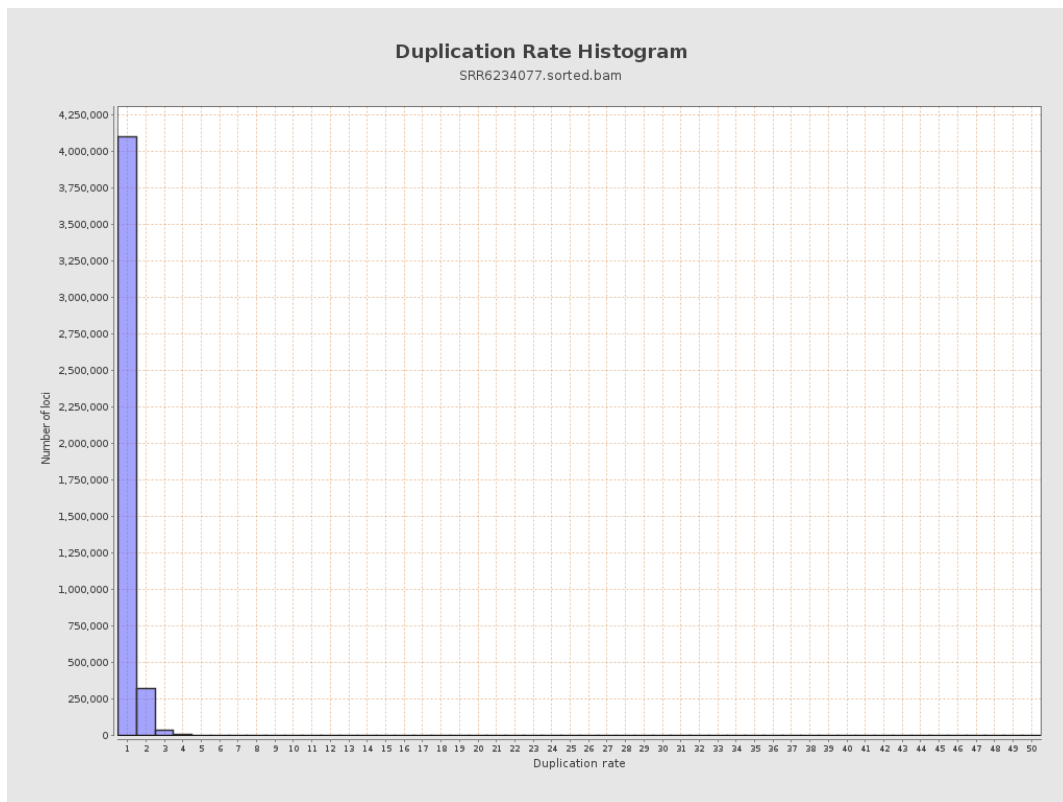
5. Results : Coverage Histogram (0-50X)



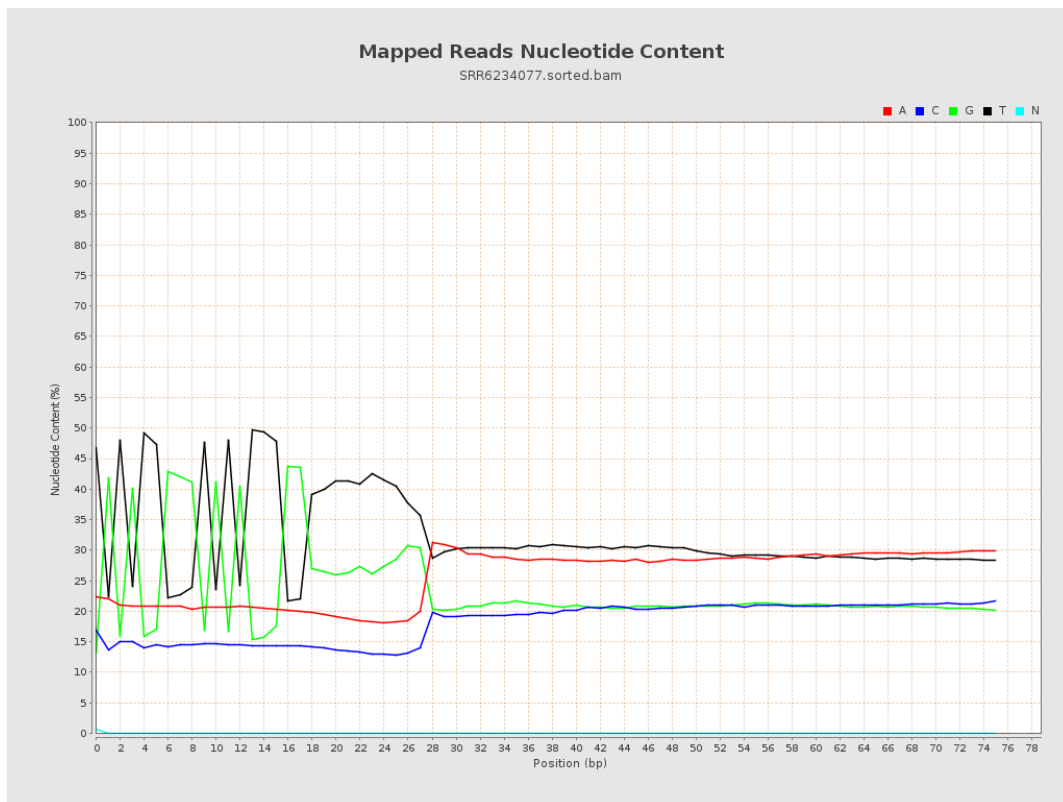
6. Results : Genome Fraction Coverage



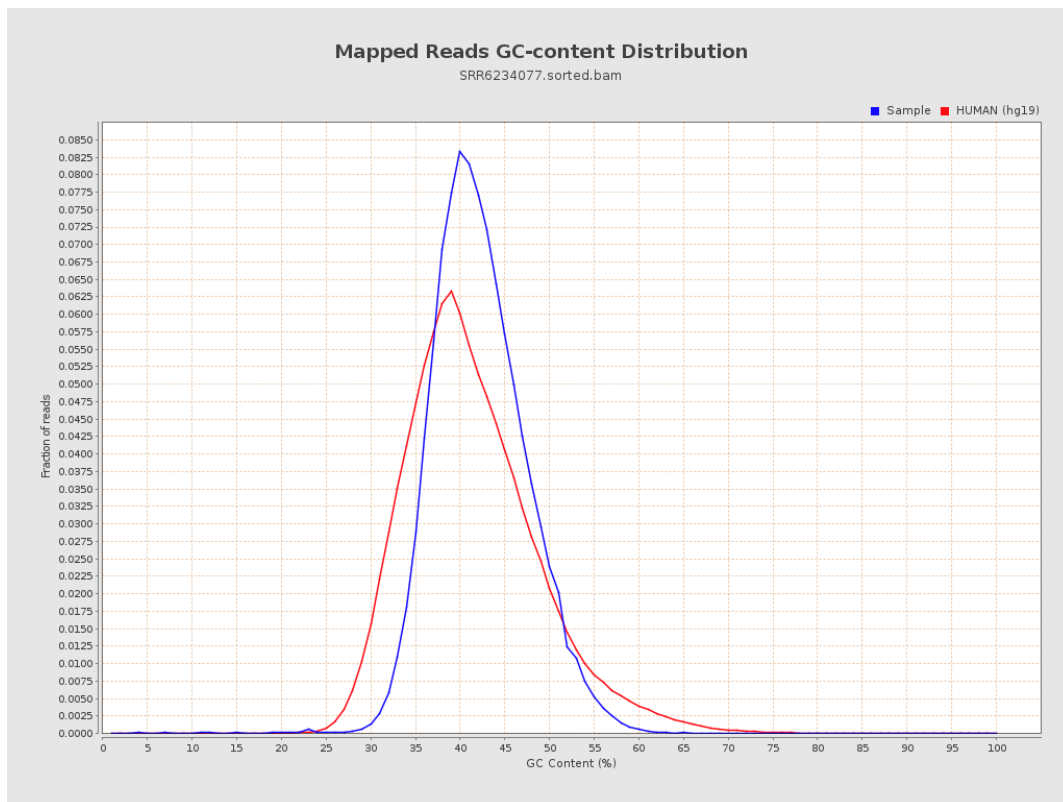
7. Results : Duplication Rate Histogram



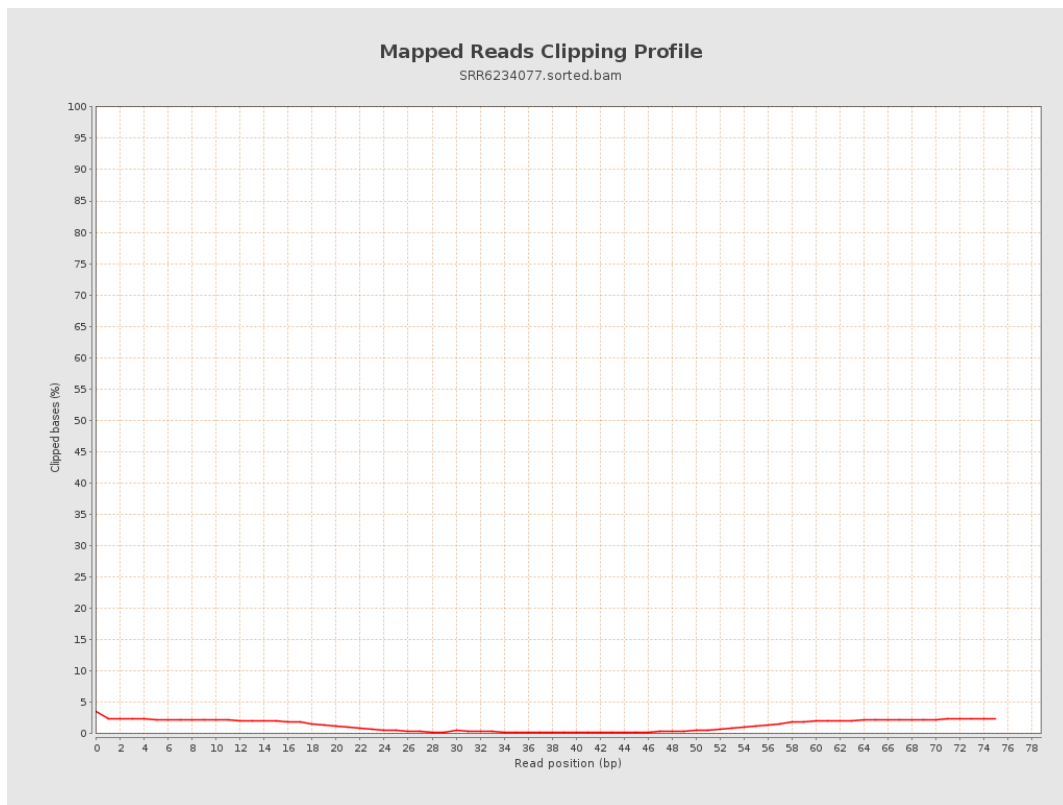
8. Results : Mapped Reads Nucleotide Content



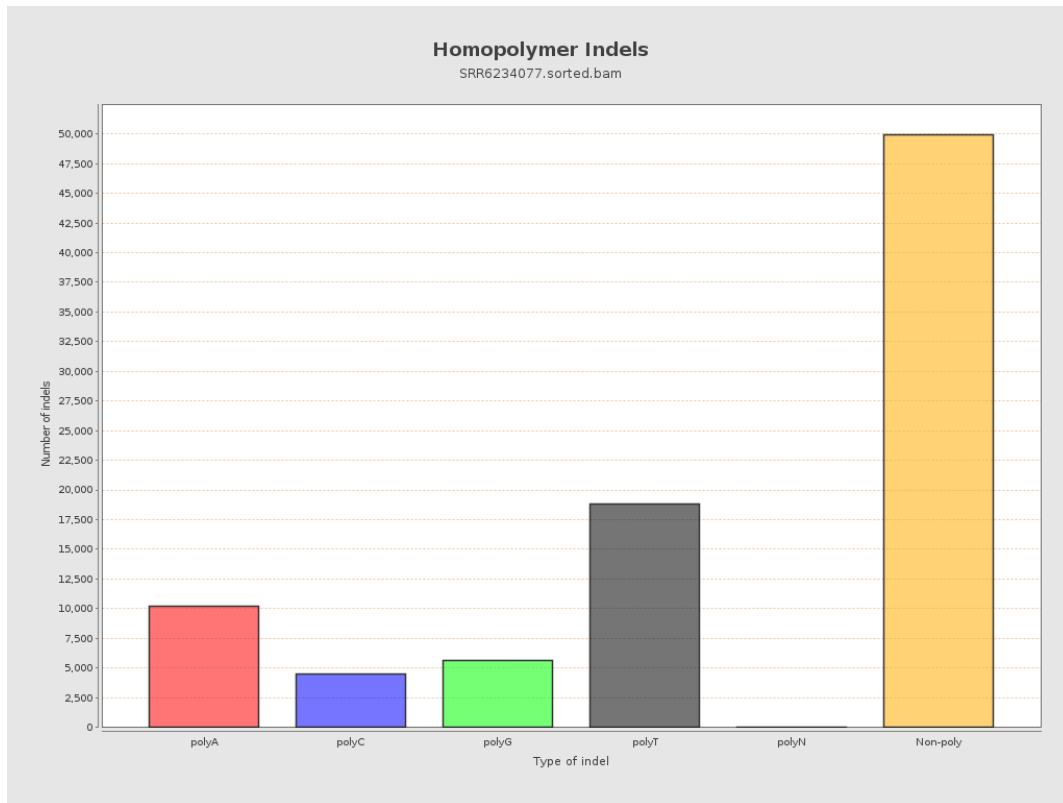
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

