

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:30:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238647.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_SRR6238647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238647.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:30:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238647.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,940,198
Mapped reads	3,044,310 / 77.26%
Unmapped reads	895,888 / 22.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,610 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,481,318 / 37.6%
Duplication rate	22.61%
Clipped reads	2,014,043 / 51.12%

2.2. ACGT Content

Number/percentage of A's	46,304,821 / 25%
Number/percentage of C's	32,387,369 / 17.48%
Number/percentage of T's	62,462,350 / 33.72%
Number/percentage of G's	44,076,127 / 23.79%
Number/percentage of N's	4,168 / 0%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0599

Standard Deviation	1.9401
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2.4. Mapping Quality

Mean Mapping Quality	38.62
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2.5. Mismatches and indels

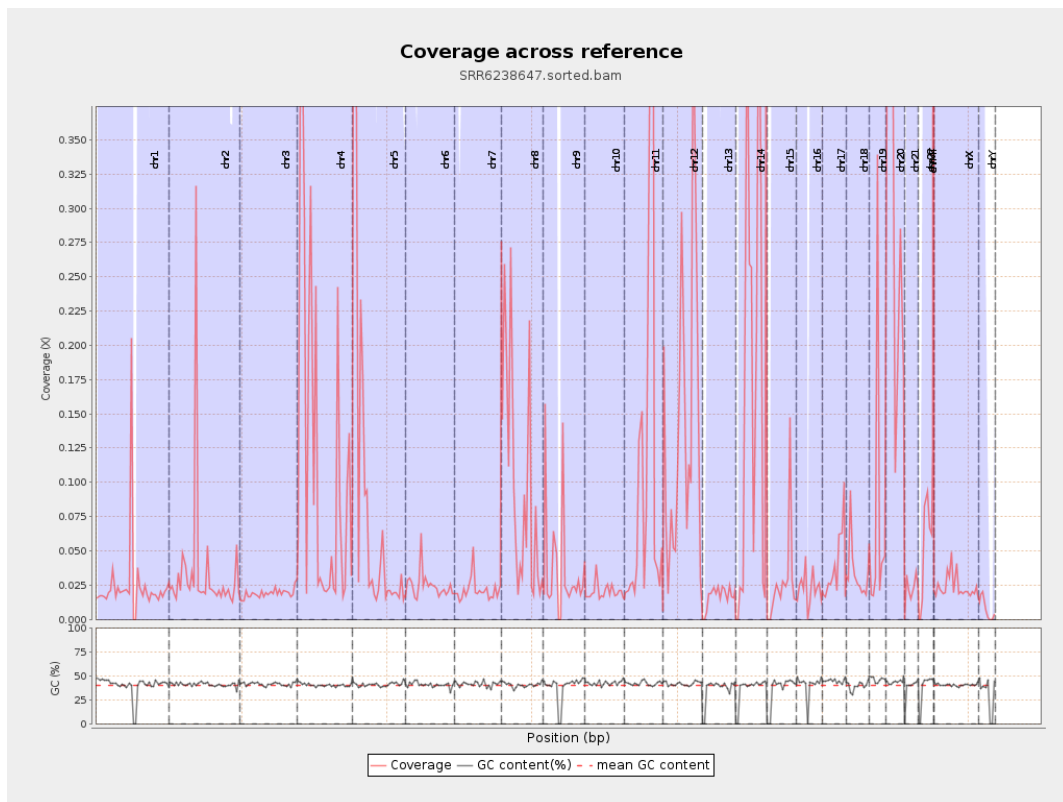
General error rate	0.7%
Mismatches	1,278,582
Insertions	13,570
Mapped reads with at least one insertion	0.44%
Deletions	52,703
Mapped reads with at least one deletion	1.71%
Homopolymer indels	41.26%

2.6. Chromosome stats

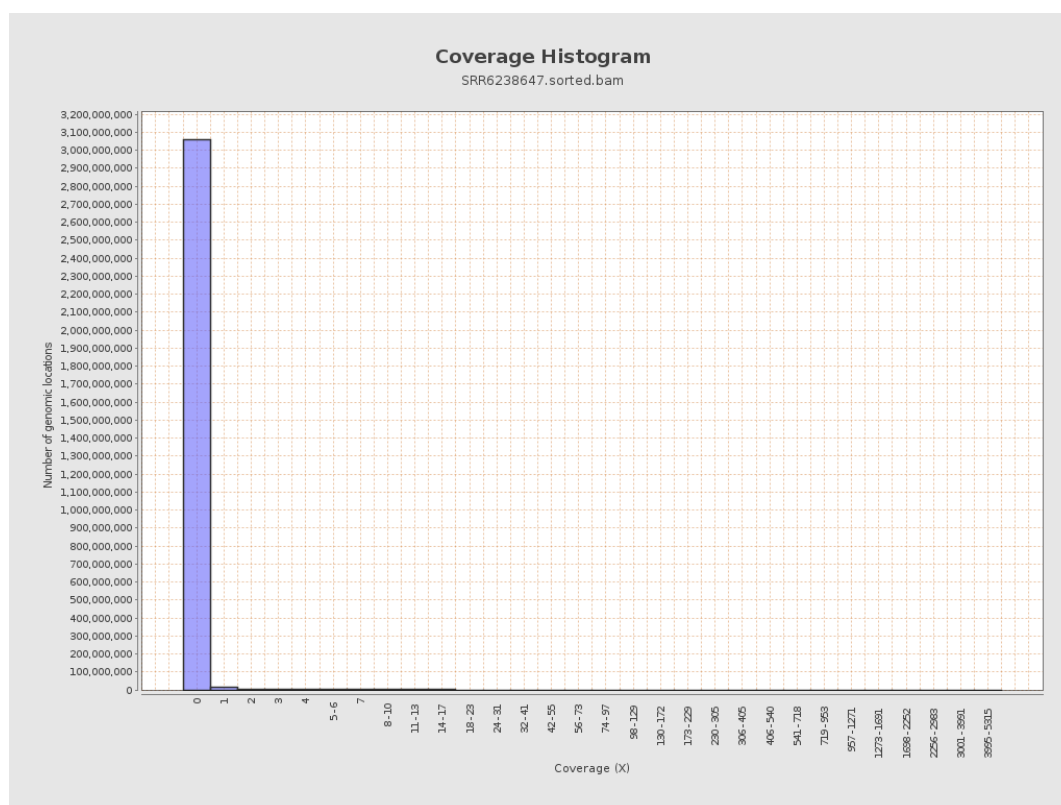
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6162354	0.0247	4.2529
chr2	243199373	8313445	0.0342	3.1744
chr3	198022430	3762784	0.019	0.5091
chr4	191154276	22309546	0.1167	1.2711
chr5	180915260	14577572	0.0806	1.1007
chr6	171115067	4198317	0.0245	0.9298
chr7	159138663	3394724	0.0213	0.743

chr8	146364022	13821309	0.0944	2.3157
chr9	141213431	5209971	0.0369	1.6194
chr10	135534747	2741925	0.0202	0.559
chr11	135006516	16645525	0.1233	1.4113
chr12	133851895	19549924	0.1461	1.4963
chr13	115169878	1900092	0.0165	0.7589
chr14	107349540	18950271	0.1765	1.6728
chr15	102531392	2840095	0.0277	0.711
chr16	90354753	2047121	0.0227	0.6336
chr17	81195210	3190499	0.0393	0.7637
chr18	78077248	2670788	0.0342	3.4062
chr19	59128983	4590768	0.0776	2.0377
chr20	63025520	20390653	0.3235	2.2269
chr21	48129895	1095280	0.0228	0.5627
chr22	51304566	2731534	0.0532	0.8732
chrMT	16571	34185	2.0629	4.8869
chrX	155270560	3741638	0.0241	0.6706
chrY	59373566	451950	0.0076	0.4126

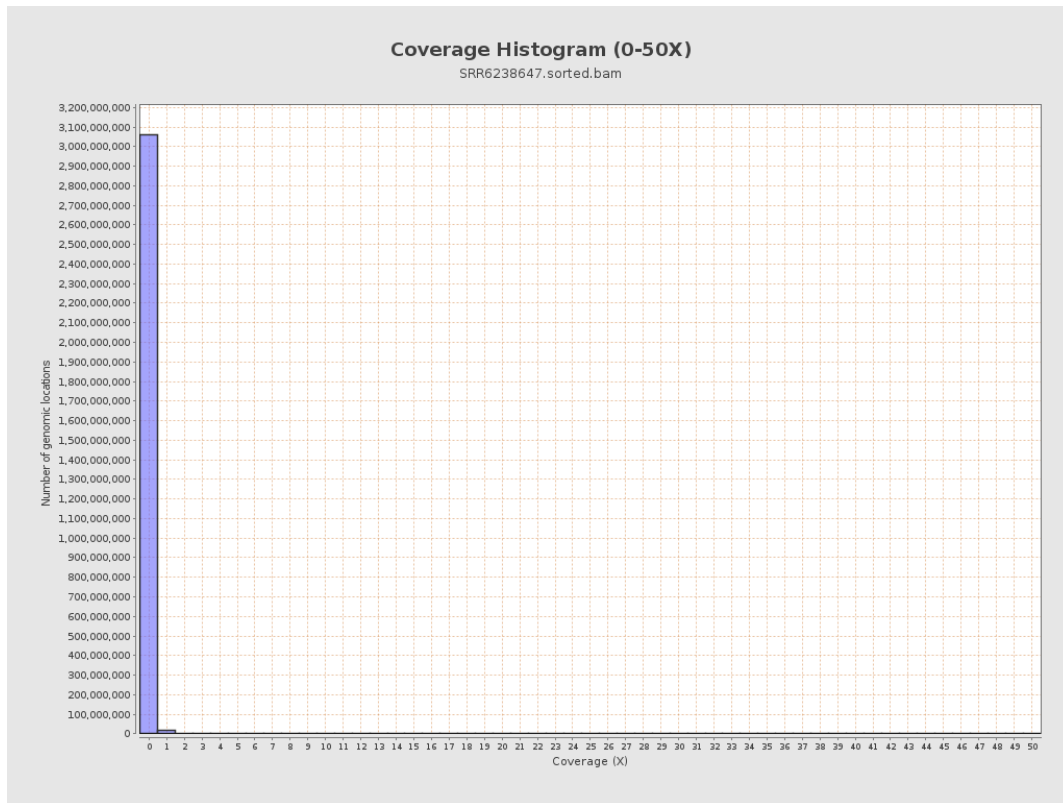
3. Results : Coverage across reference



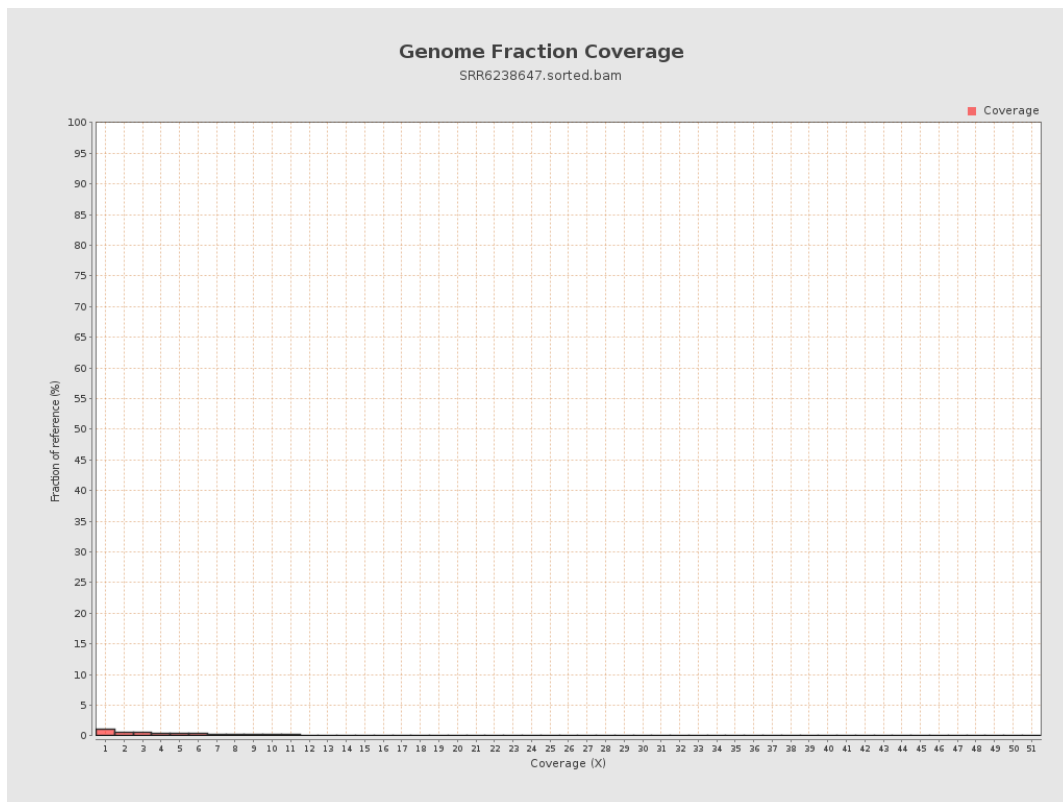
4. Results : Coverage Histogram



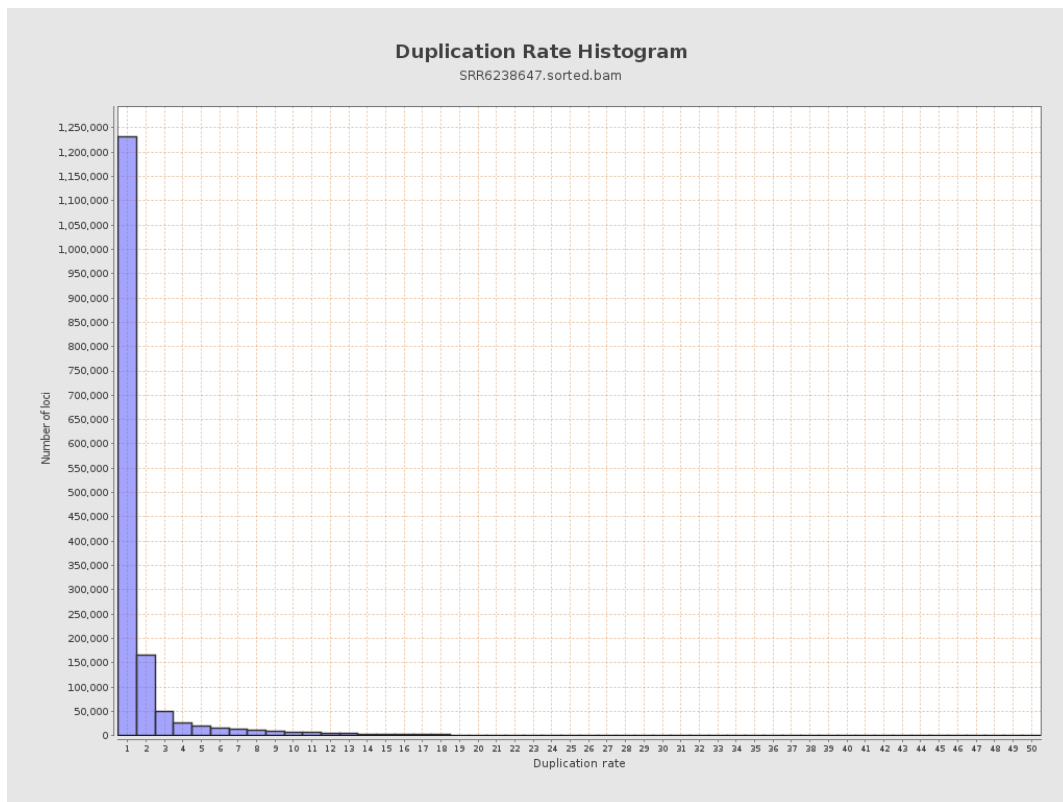
5. Results : Coverage Histogram (0-50X)



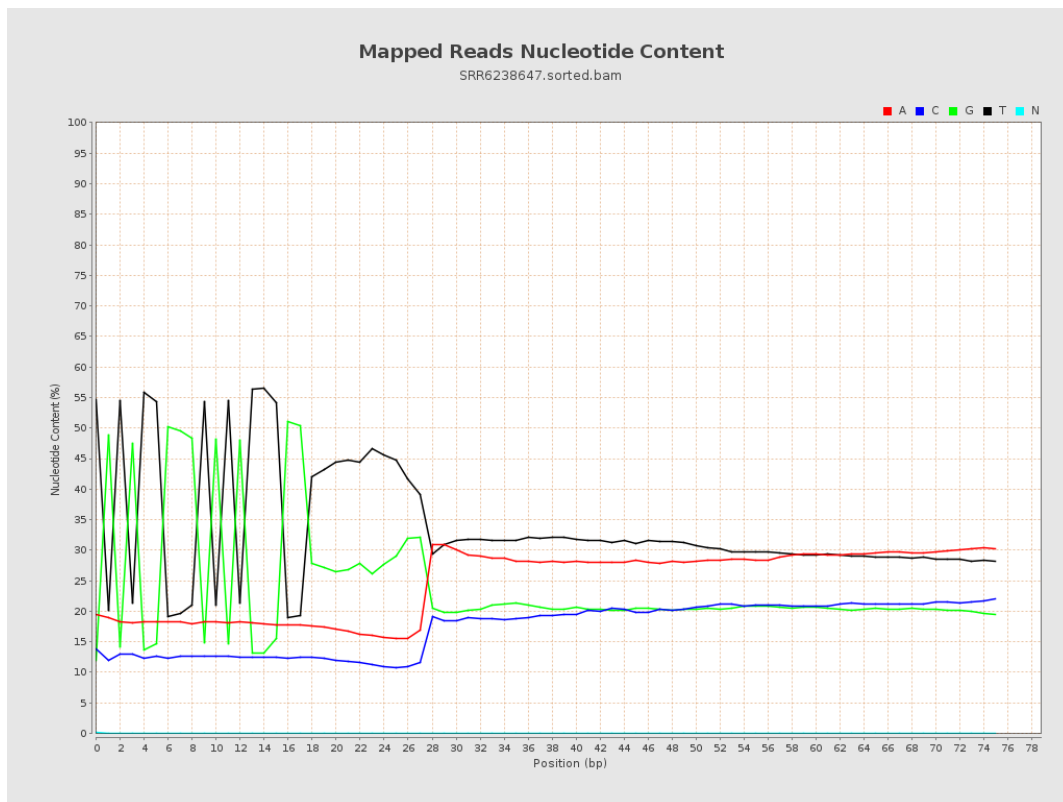
6. Results : Genome Fraction Coverage



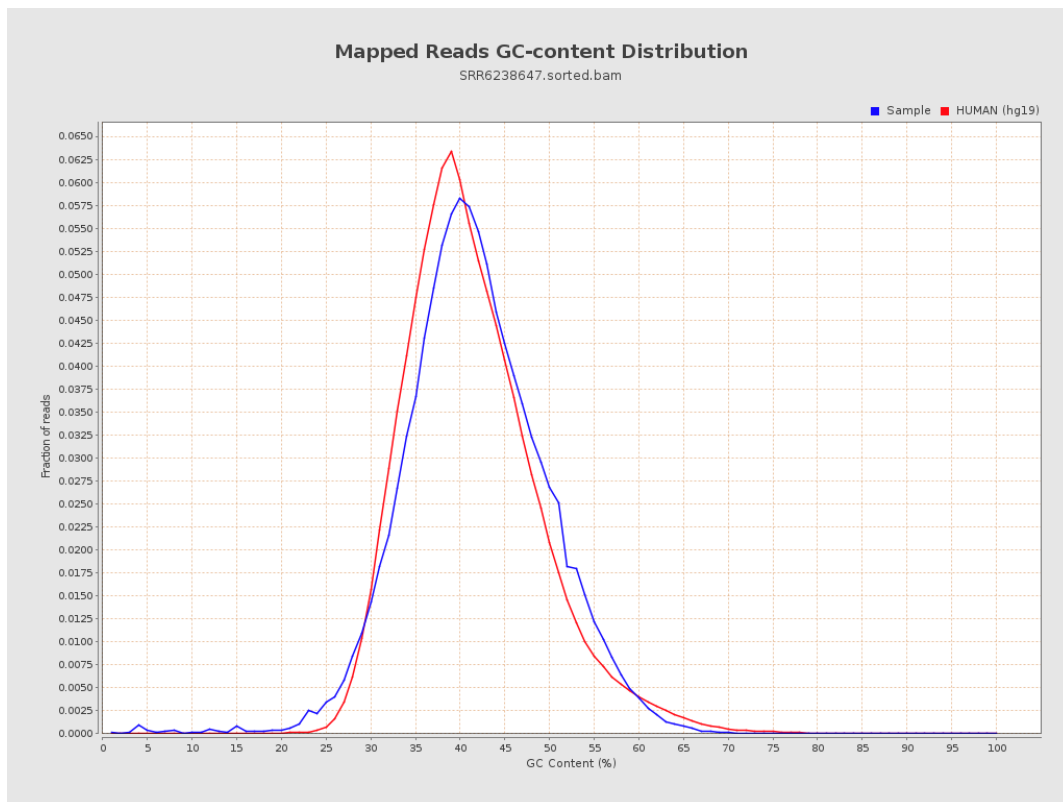
7. Results : Duplication Rate Histogram



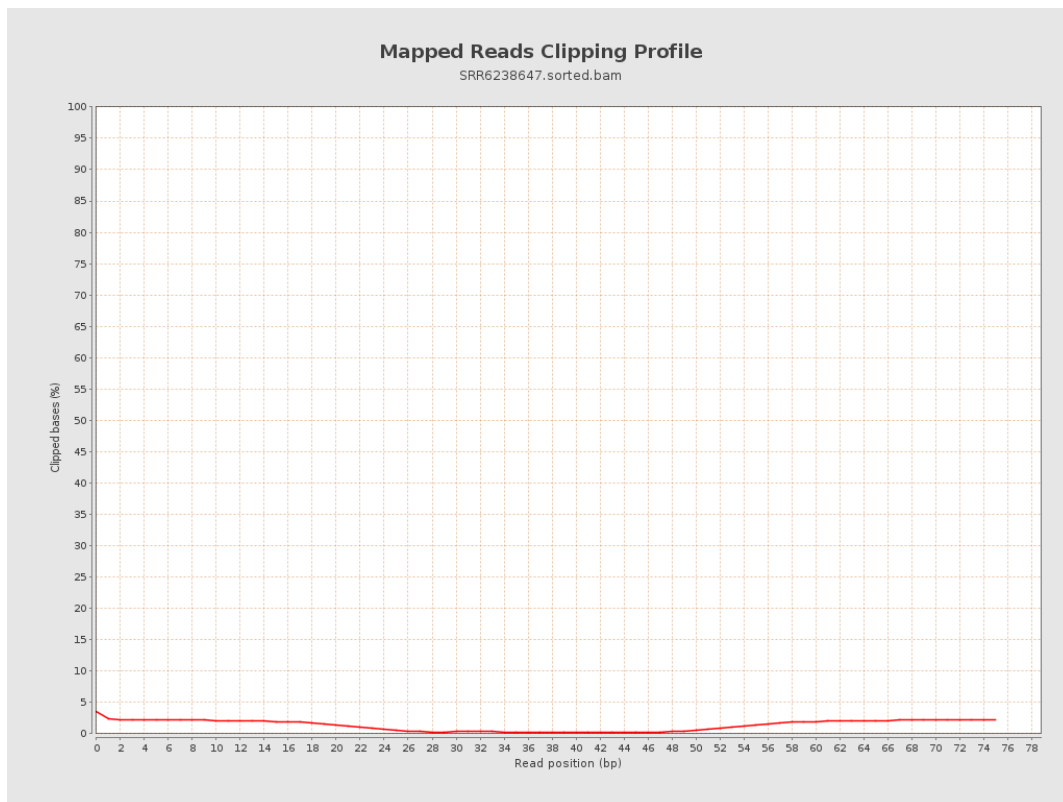
8. Results : Mapped Reads Nucleotide Content



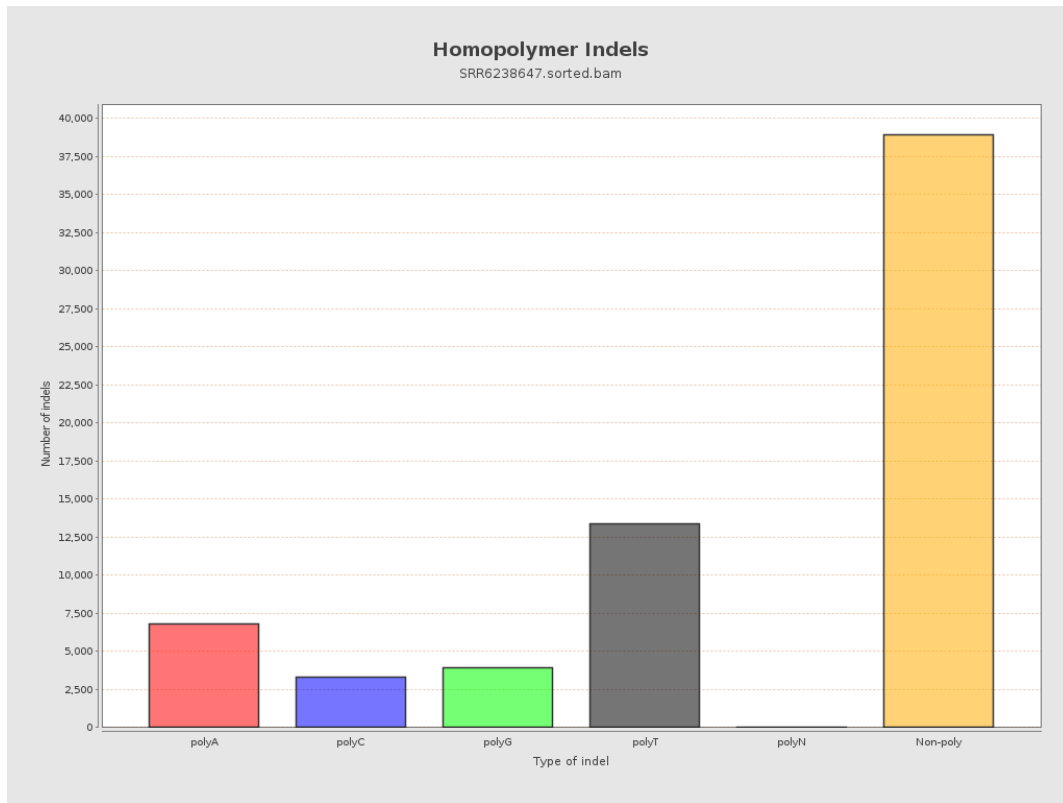
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

