

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:13:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238530.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_SRR6238530 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238530.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238530.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,363,841
Mapped reads	1,181,422 / 86.62%
Unmapped reads	182,419 / 13.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,737 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	166,767 / 12.23%
Duplication rate	12.13%
Clipped reads	771,455 / 56.56%

2.2. ACGT Content

Number/percentage of A's	17,953,297 / 24.98%
Number/percentage of C's	11,779,765 / 16.39%
Number/percentage of T's	25,436,030 / 35.39%
Number/percentage of G's	16,706,398 / 23.24%
Number/percentage of N's	4,368 / 0.01%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.39
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2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Mismatches and indels

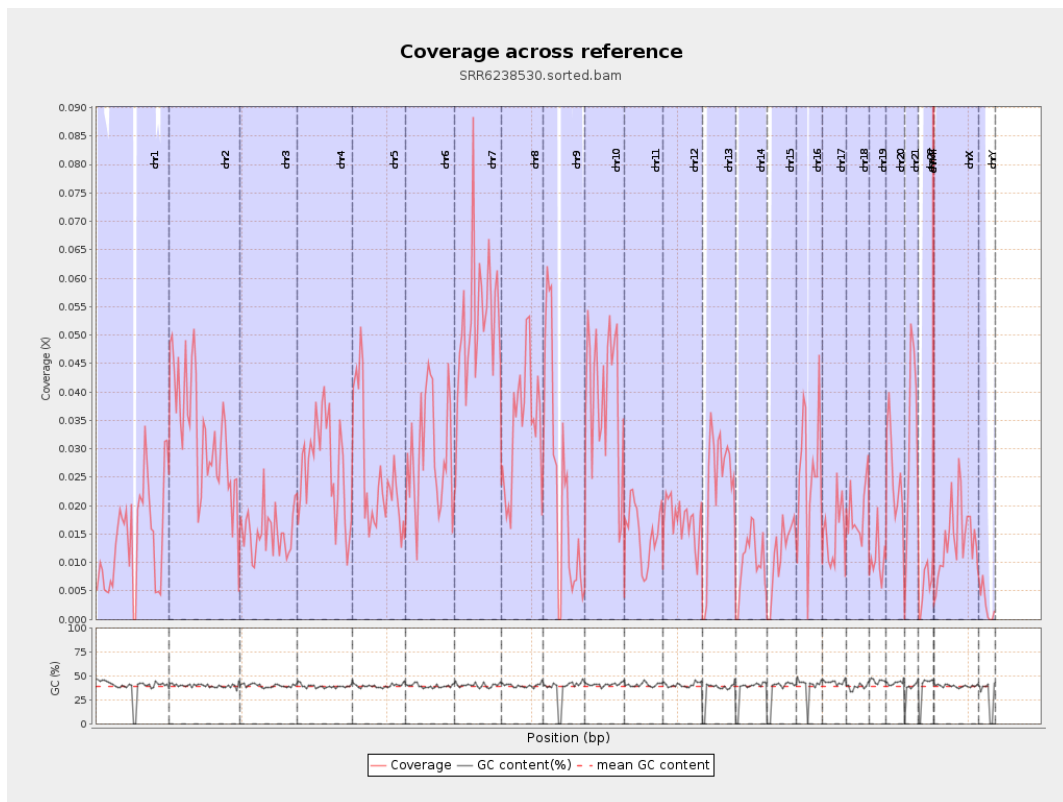
General error rate	0.64%
Mismatches	454,390
Insertions	4,789
Mapped reads with at least one insertion	0.4%
Deletions	20,531
Mapped reads with at least one deletion	1.72%
Homopolymer indels	42.07%

2.6. Chromosome stats

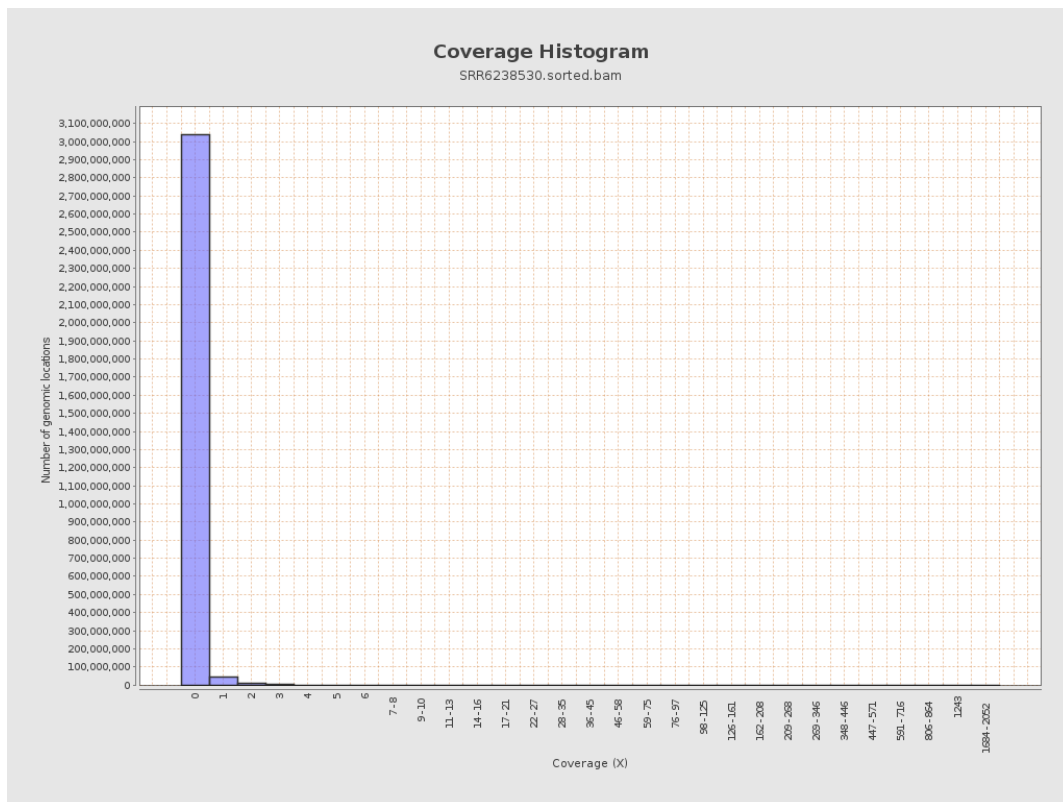
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3551125	0.0142	0.2471
chr2	243199373	7956294	0.0327	0.9194
chr3	198022430	3050262	0.0154	0.1613
chr4	191154276	5072475	0.0265	0.2032
chr5	180915260	4604564	0.0255	0.2012
chr6	171115067	4953557	0.0289	0.3715
chr7	159138663	8360394	0.0525	0.6631

chr8	146364022	4948822	0.0338	0.4241
chr9	141213431	3300759	0.0234	0.2662
chr10	135534747	5360879	0.0396	0.2878
chr11	135006516	2053151	0.0152	0.1628
chr12	133851895	2360149	0.0176	0.1846
chr13	115169878	2677970	0.0233	0.2629
chr14	107349540	1092250	0.0102	0.1529
chr15	102531392	1172711	0.0114	0.2142
chr16	90354753	2349914	0.026	0.2265
chr17	81195210	1214298	0.015	0.1521
chr18	78077248	1470823	0.0188	0.7614
chr19	59128983	640726	0.0108	0.2094
chr20	63025520	1601670	0.0254	0.2071
chr21	48129895	1480366	0.0308	0.2268
chr22	51304566	290006	0.0057	0.0891
chrMT	16571	8457	0.5103	0.851
chrX	155270560	2185382	0.0141	0.1599
chrY	59373566	156760	0.0026	0.1316

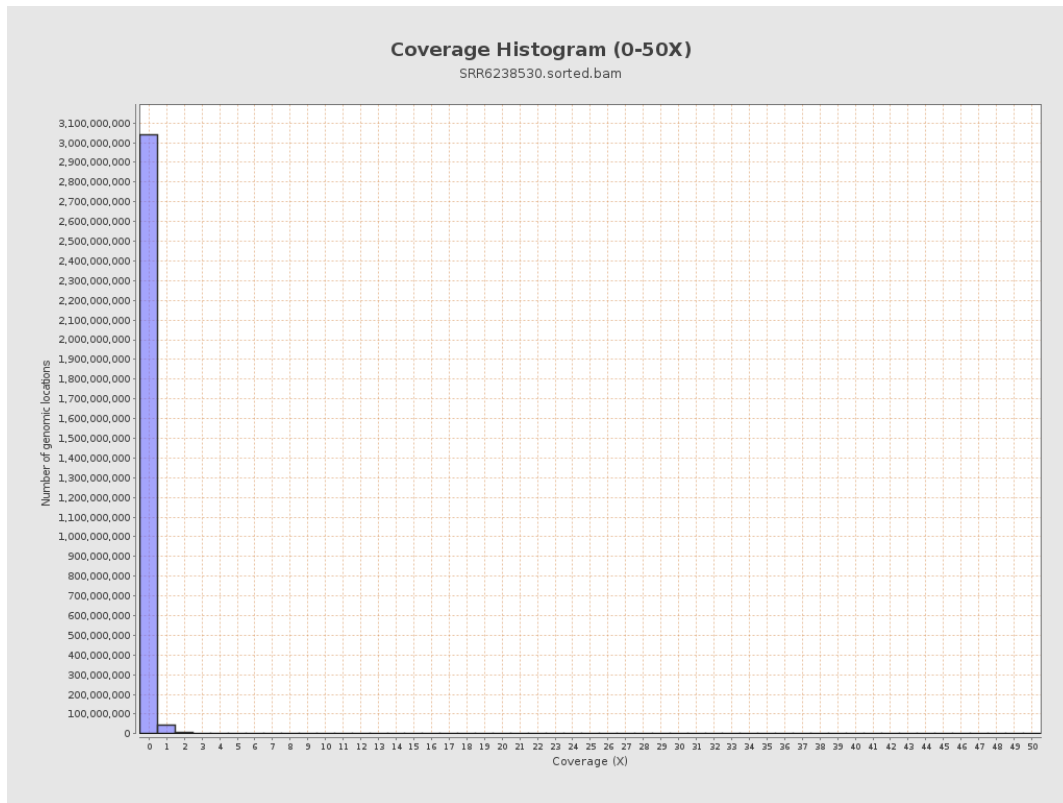
3. Results : Coverage across reference



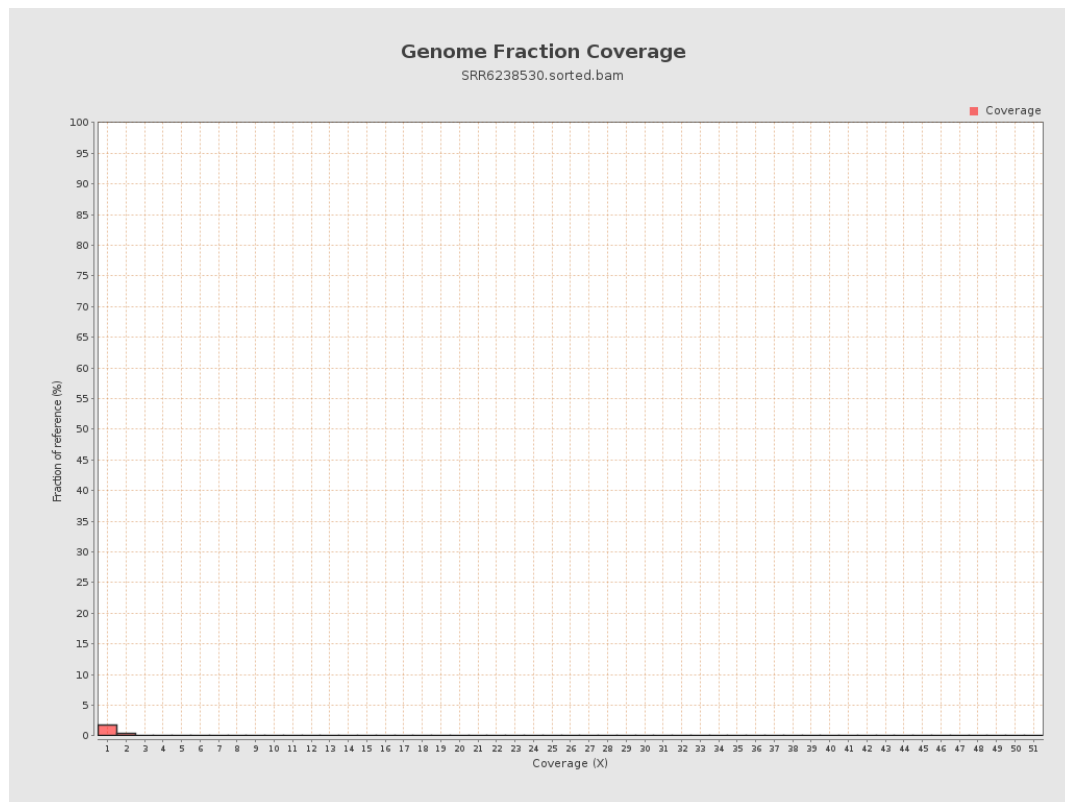
4. Results : Coverage Histogram



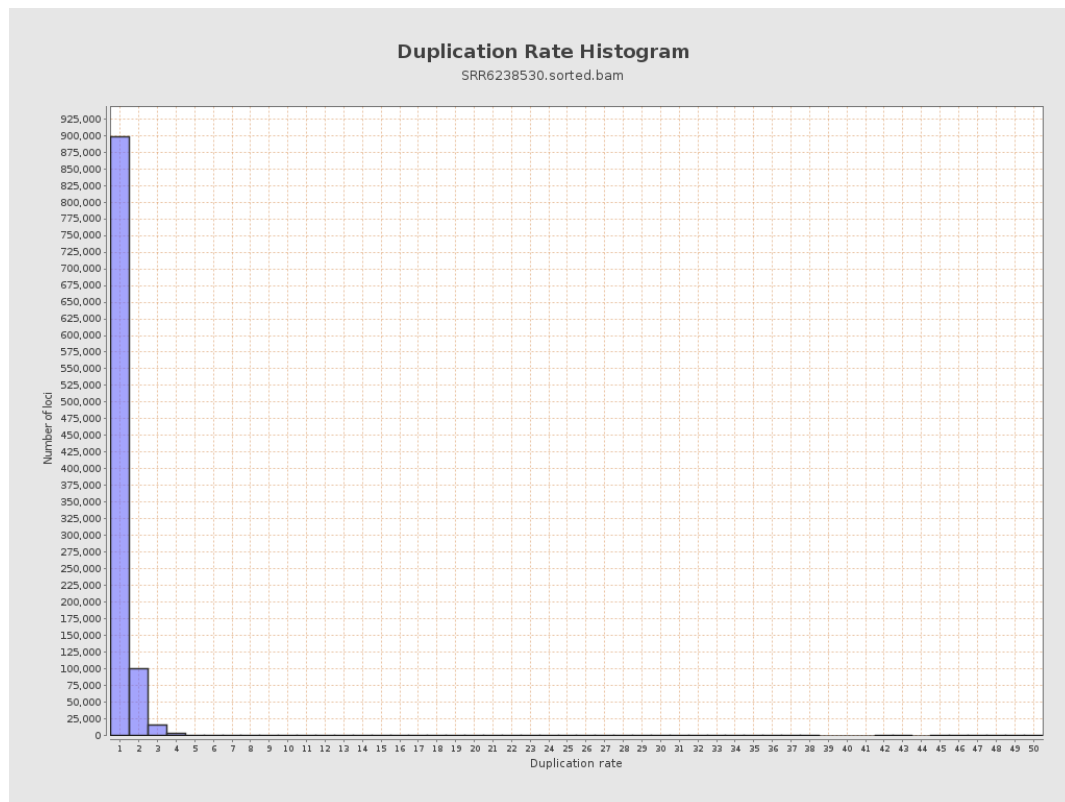
5. Results : Coverage Histogram (0-50X)



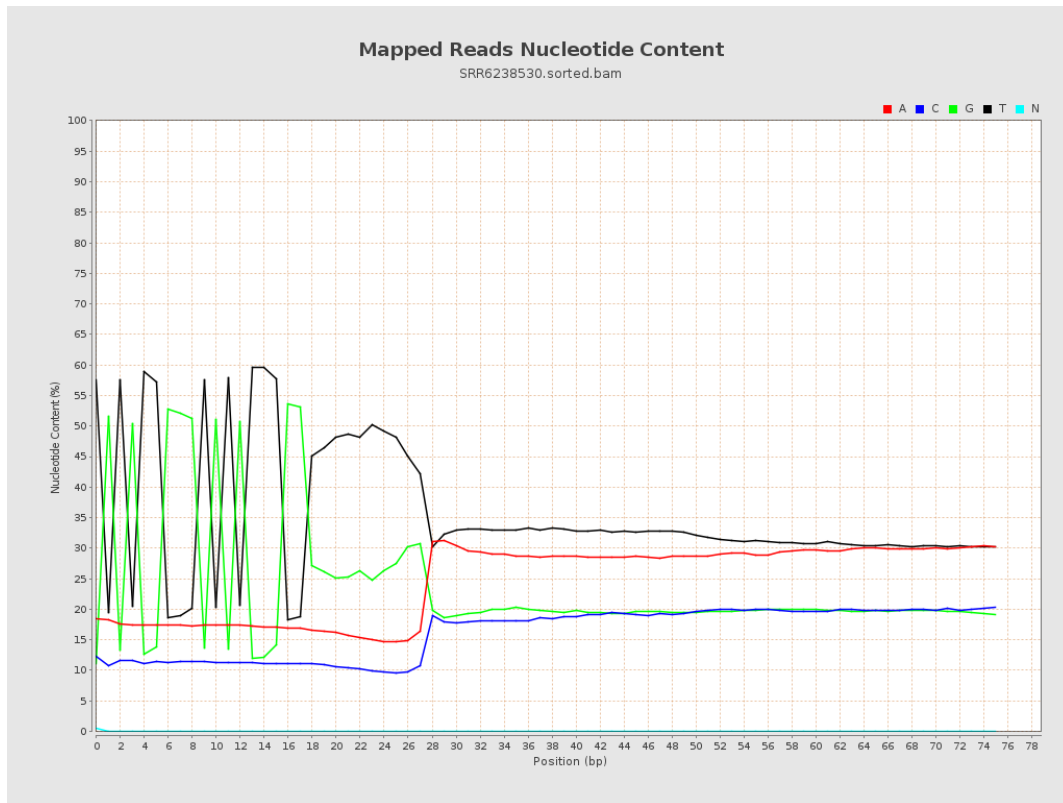
6. Results : Genome Fraction Coverage



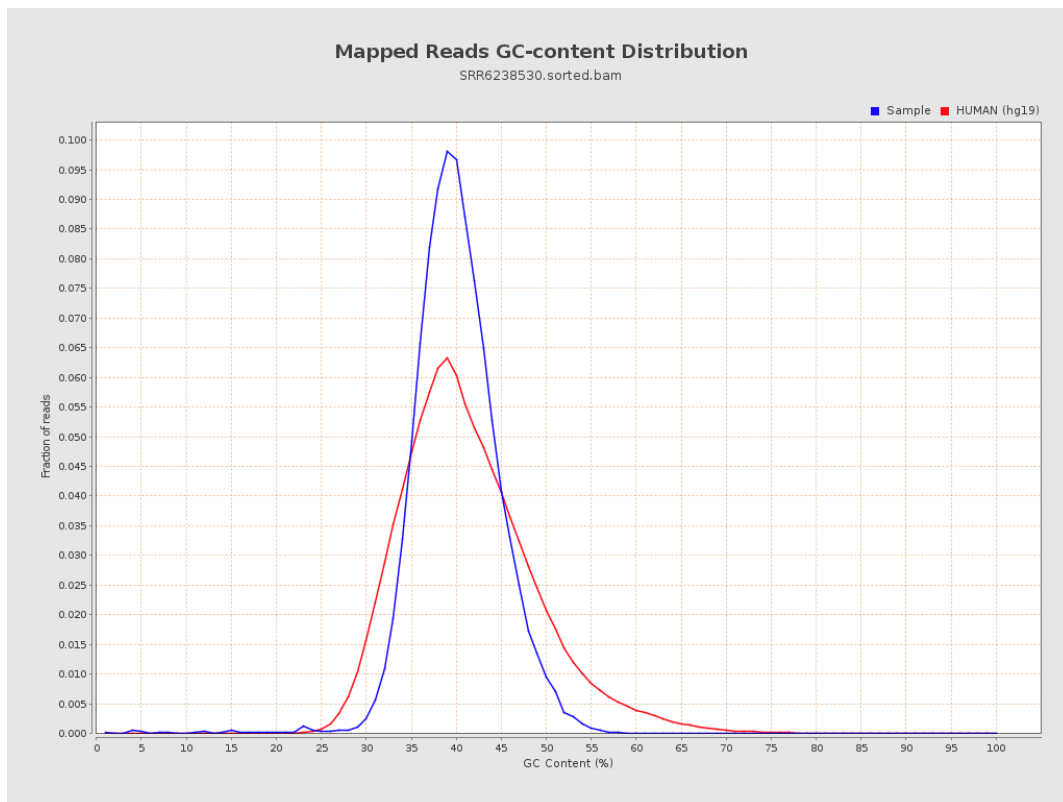
7. Results : Duplication Rate Histogram



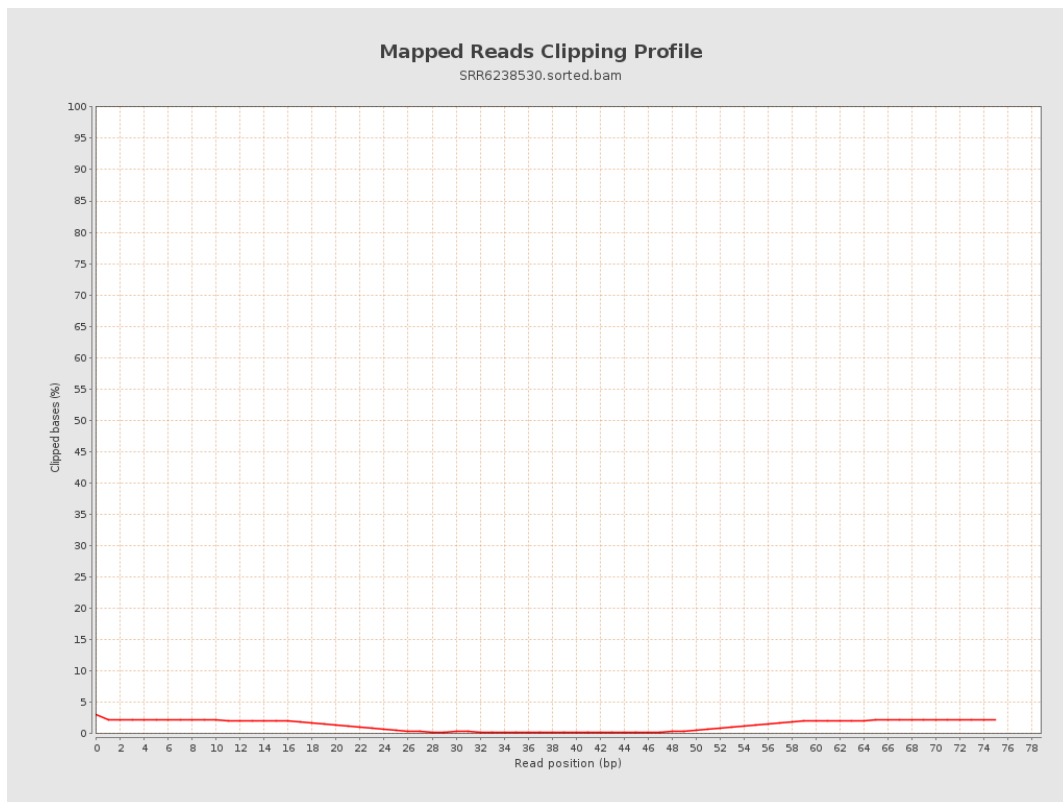
8. Results : Mapped Reads Nucleotide Content



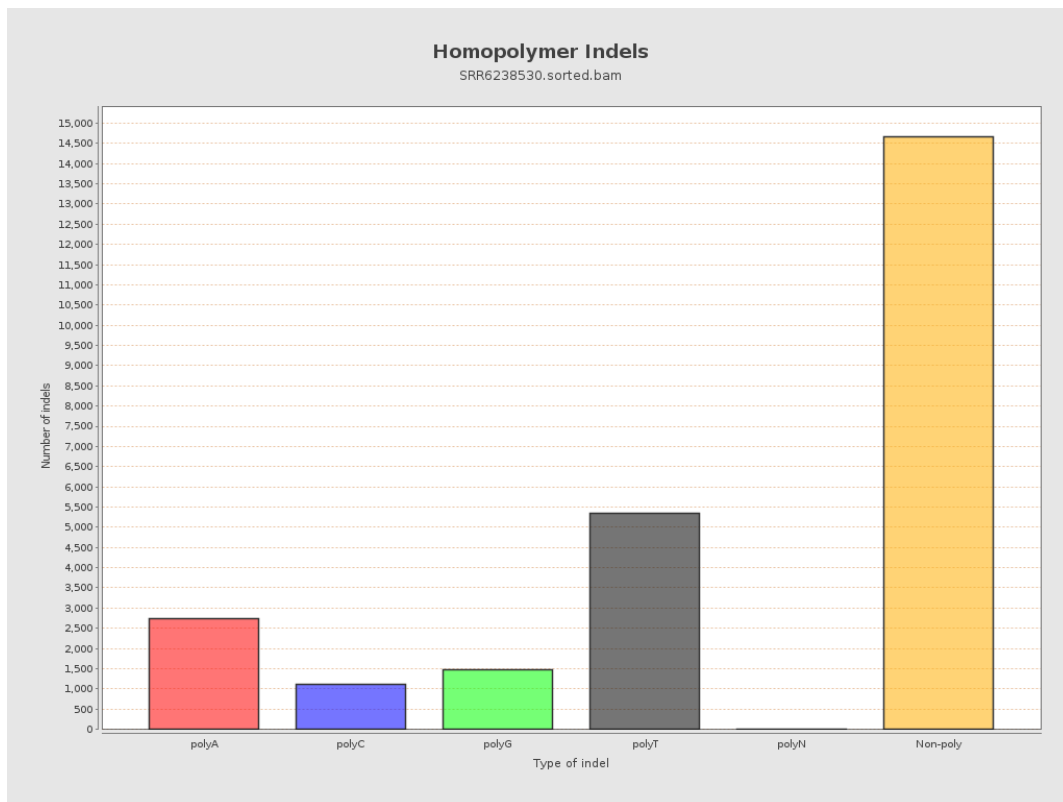
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

