

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:08:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238609.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_SRR6238609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:08:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,829,772
Mapped reads	3,359,903 / 87.73%
Unmapped reads	469,869 / 12.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,814 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	1,185,564 / 30.96%
Duplication rate	20.57%
Clipped reads	2,195,030 / 57.31%

2.2. ACGT Content

Number/percentage of A's	51,088,488 / 24.84%
Number/percentage of C's	36,261,176 / 17.63%
Number/percentage of T's	69,003,935 / 33.55%
Number/percentage of G's	49,327,444 / 23.98%
Number/percentage of N's	10,187 / 0%
GC Percentage	41.61%

2.3. Coverage

Mean	0.0665

Standard Deviation	1.0798
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2.4. Mapping Quality

Mean Mapping Quality	37.52
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2.5. Mismatches and indels

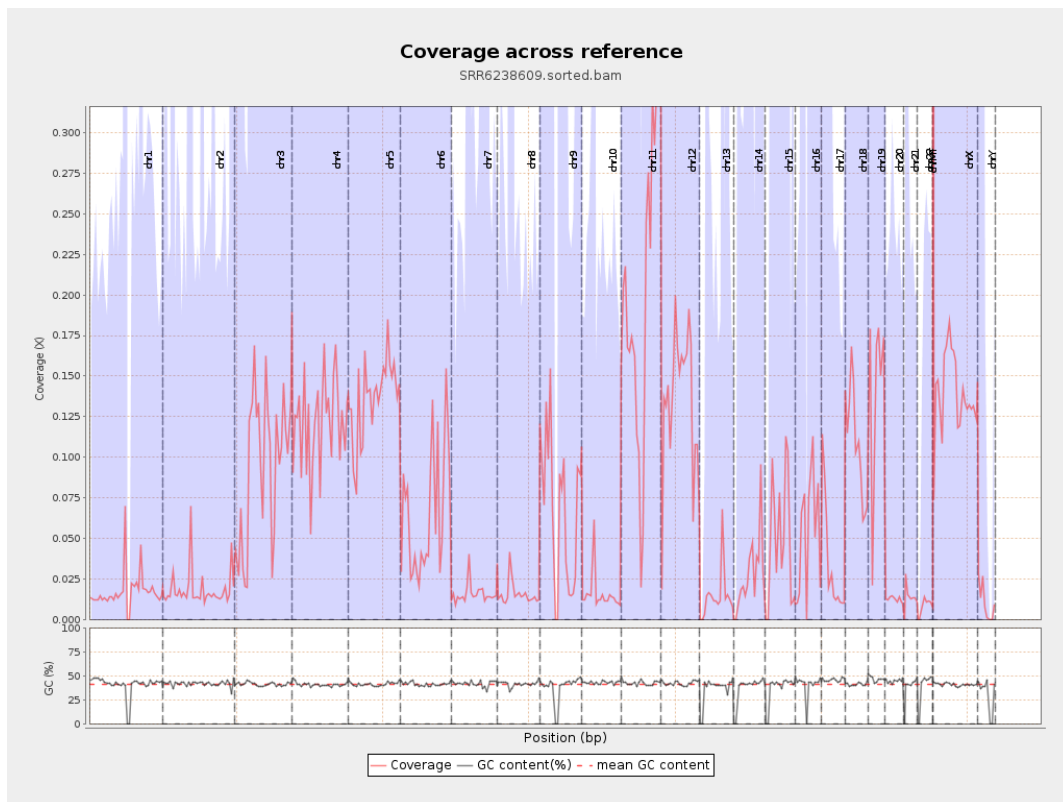
General error rate	0.65%
Mismatches	1,307,420
Insertions	12,947
Mapped reads with at least one insertion	0.38%
Deletions	68,171
Mapped reads with at least one deletion	2.01%
Homopolymer indels	40.34%

2.6. Chromosome stats

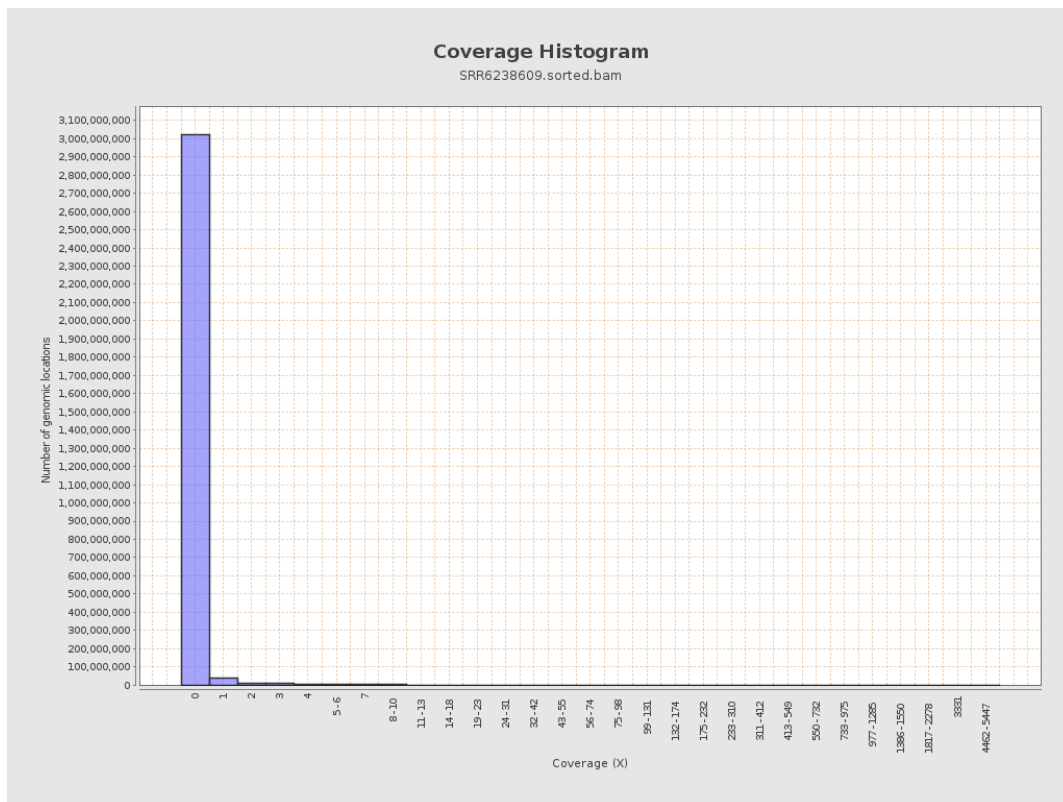
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4310493	0.0173	1.085
chr2	243199373	4467206	0.0184	2.4538
chr3	198022430	18619738	0.094	0.7345
chr4	191154276	23208978	0.1214	0.8412
chr5	180915260	24706841	0.1366	0.8987
chr6	171115067	10947330	0.064	0.8968
chr7	159138663	2525347	0.0159	0.5386

chr8	146364022	2300720	0.0157	0.9518
chr9	141213431	9372510	0.0664	0.7807
chr10	135534747	2086202	0.0154	0.5183
chr11	135006516	27028813	0.2002	1.3017
chr12	133851895	18213795	0.1361	0.9158
chr13	115169878	1639981	0.0142	0.5182
chr14	107349540	2996156	0.0279	0.4548
chr15	102531392	4960241	0.0484	0.6646
chr16	90354753	4743326	0.0525	0.6332
chr17	81195210	2933511	0.0361	0.5483
chr18	78077248	8532738	0.1093	1.8329
chr19	59128983	8001902	0.1353	1.2371
chr20	63025520	785555	0.0125	0.2263
chr21	48129895	690118	0.0143	0.2781
chr22	51304566	422921	0.0082	0.1906
chrMT	16571	44779	2.7023	3.7109
chrX	155270560	21676305	0.1396	0.9663
chrY	59373566	590196	0.0099	0.3771

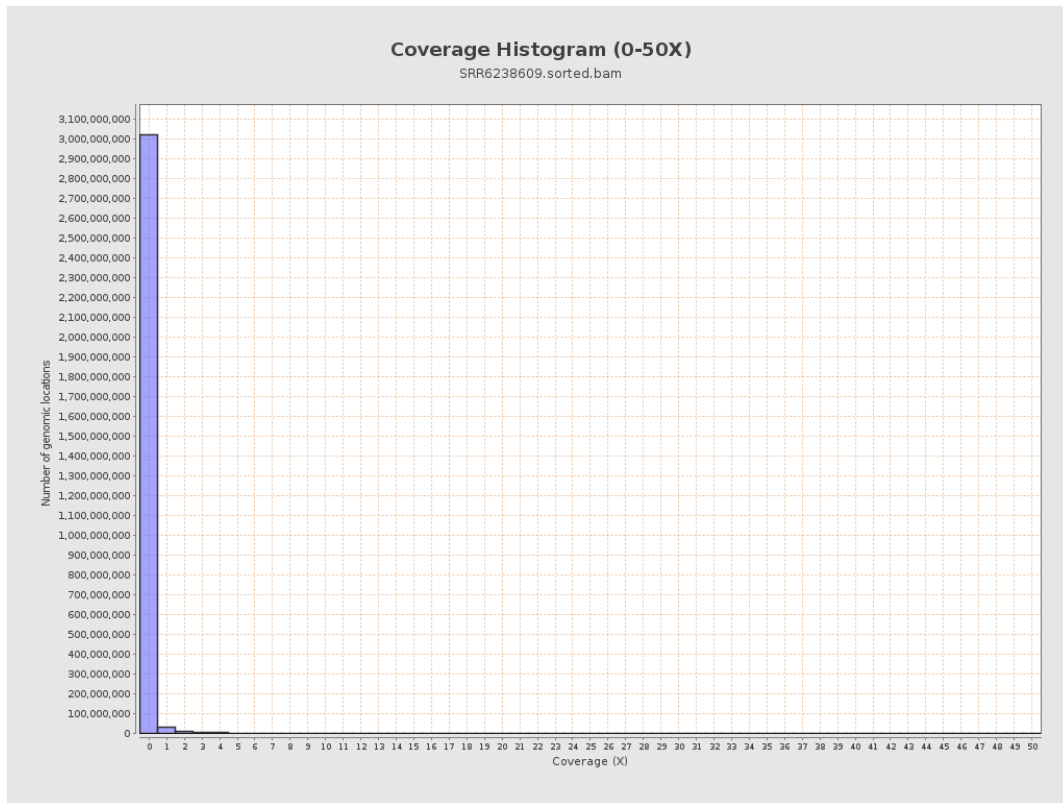
3. Results : Coverage across reference



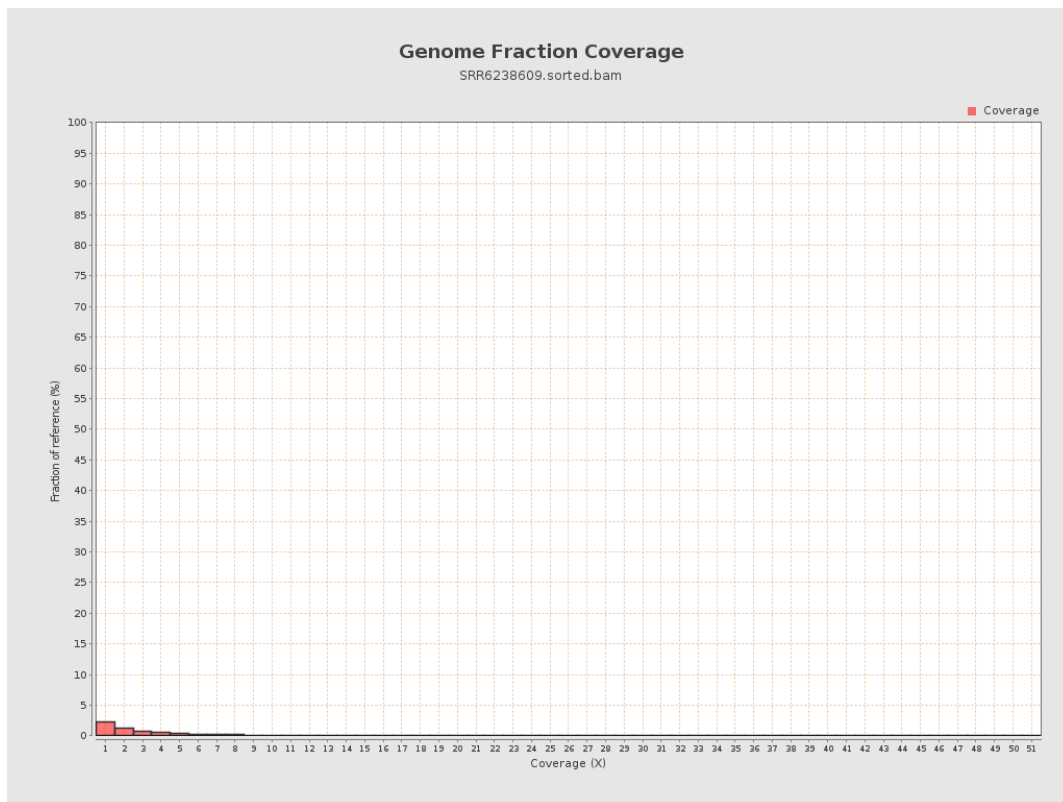
4. Results : Coverage Histogram



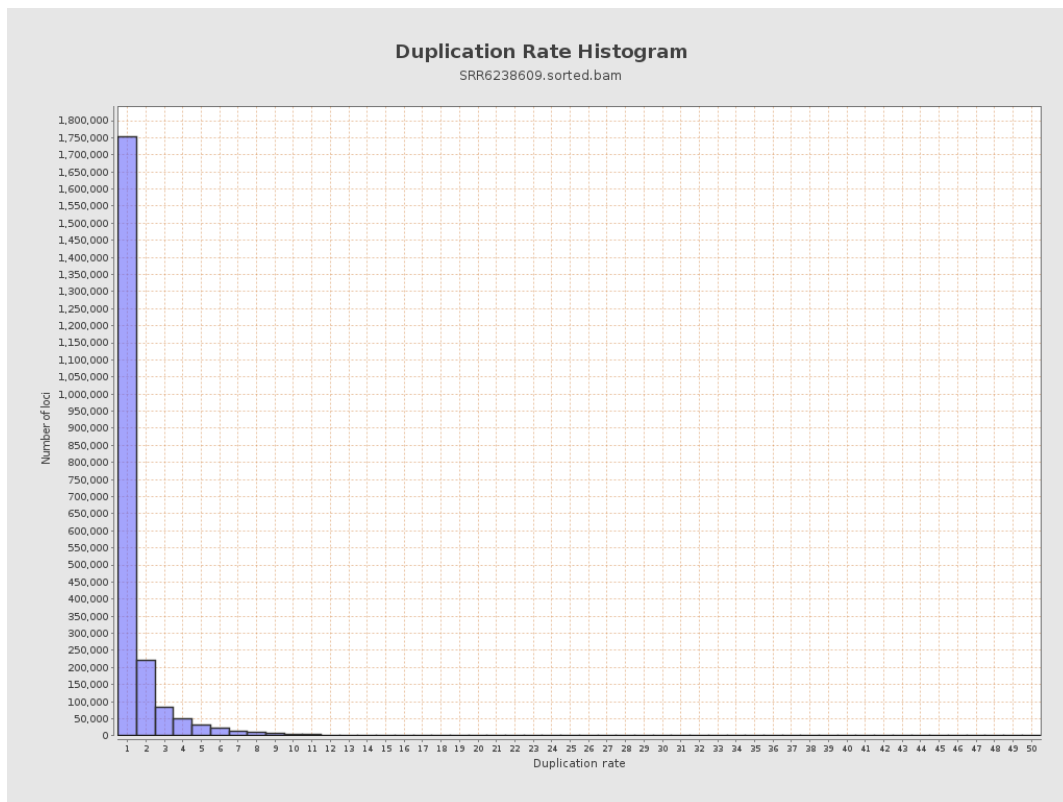
5. Results : Coverage Histogram (0-50X)



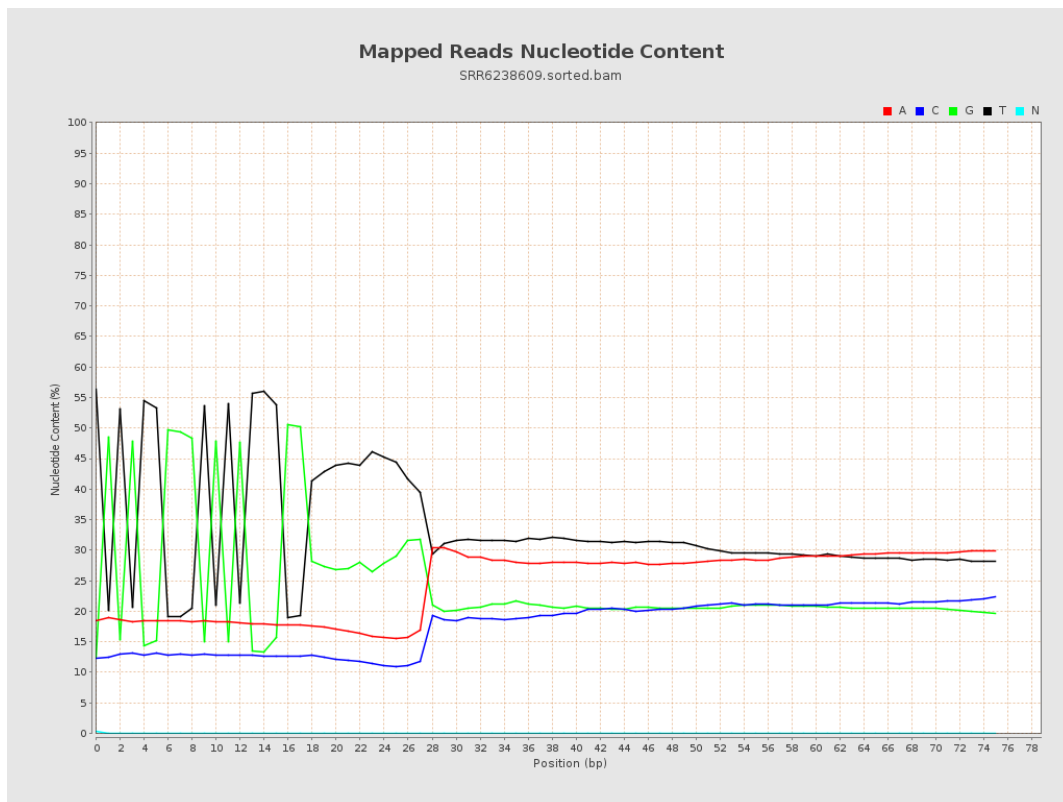
6. Results : Genome Fraction Coverage



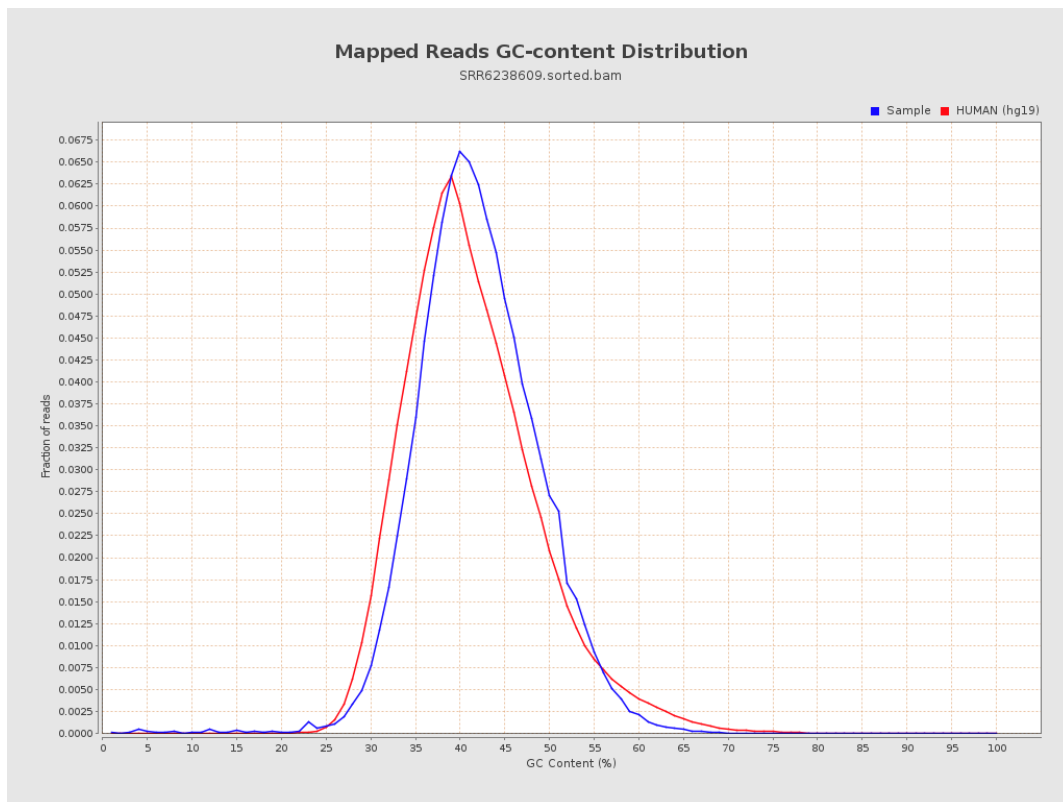
7. Results : Duplication Rate Histogram



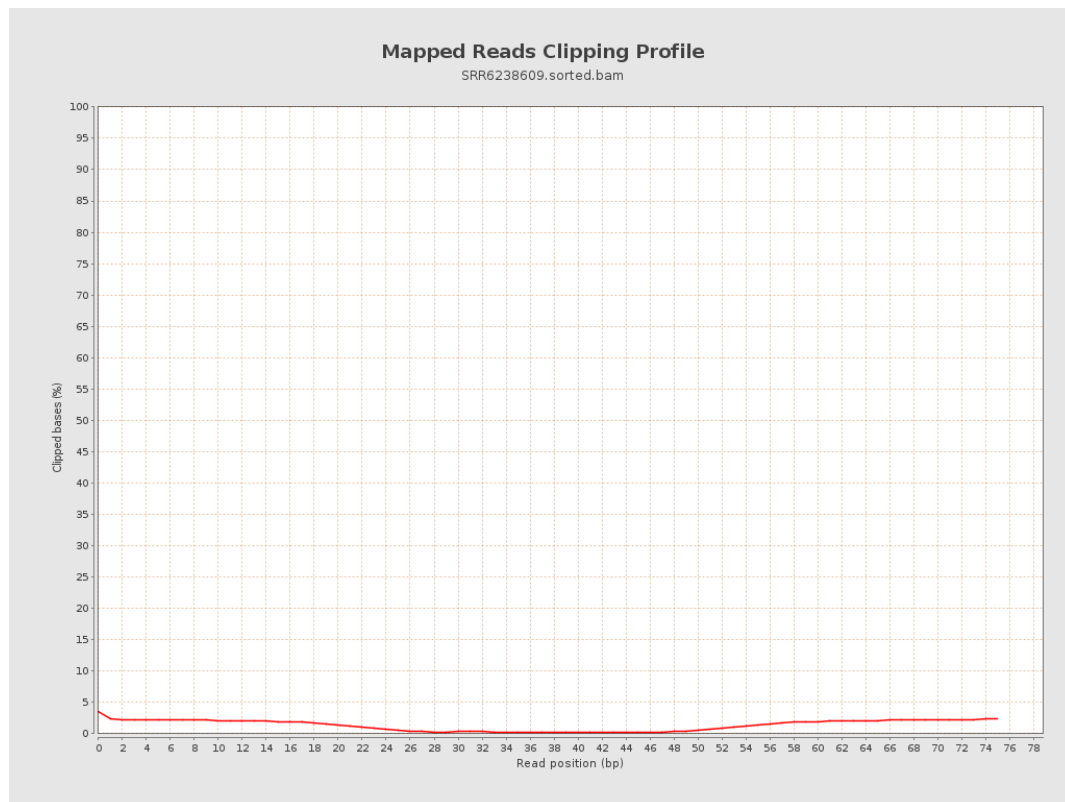
8. Results : Mapped Reads Nucleotide Content



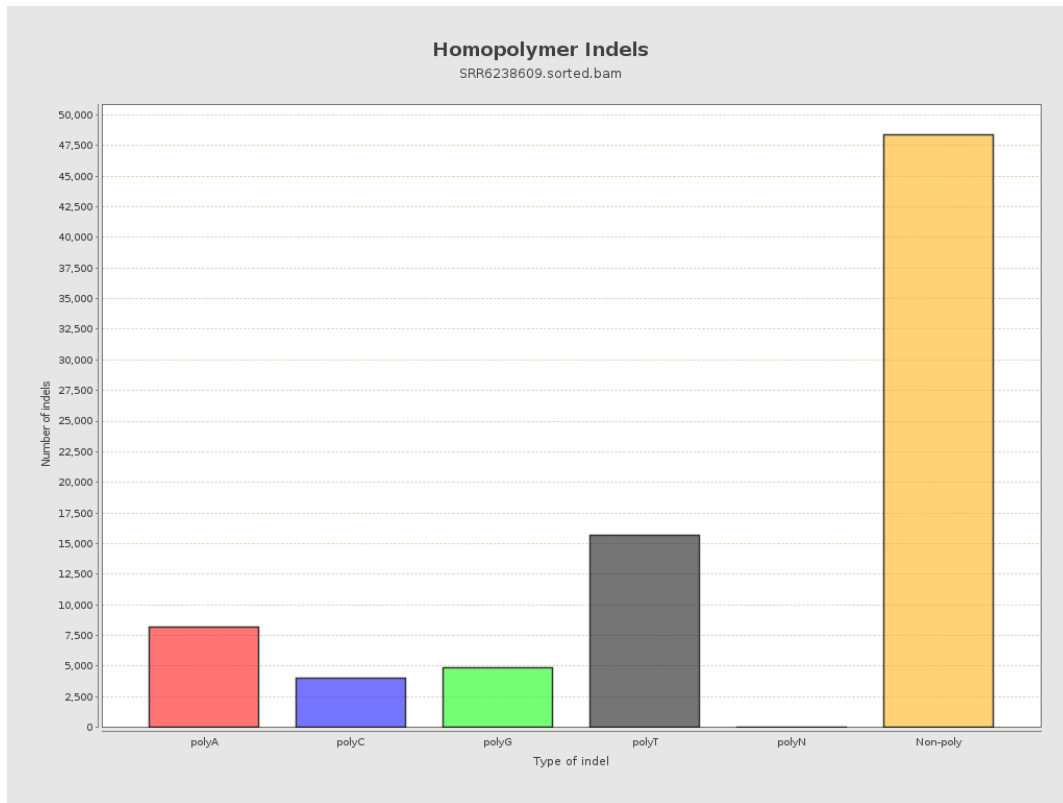
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

