

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:20:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238061.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_SRR6238061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:20:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,949,865
Mapped reads	1,798,710 / 92.25%
Unmapped reads	151,155 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,286 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	54,553 / 2.8%
Duplication rate	1.96%
Clipped reads	775,991 / 39.8%

2.2. ACGT Content

Number/percentage of A's	32,294,643 / 26.91%
Number/percentage of C's	23,100,124 / 19.25%
Number/percentage of T's	36,744,822 / 30.62%
Number/percentage of G's	27,870,059 / 23.22%
Number/percentage of N's	6,543 / 0.01%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3806
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2.4. Mapping Quality

Mean Mapping Quality	44.11
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2.5. Mismatches and indels

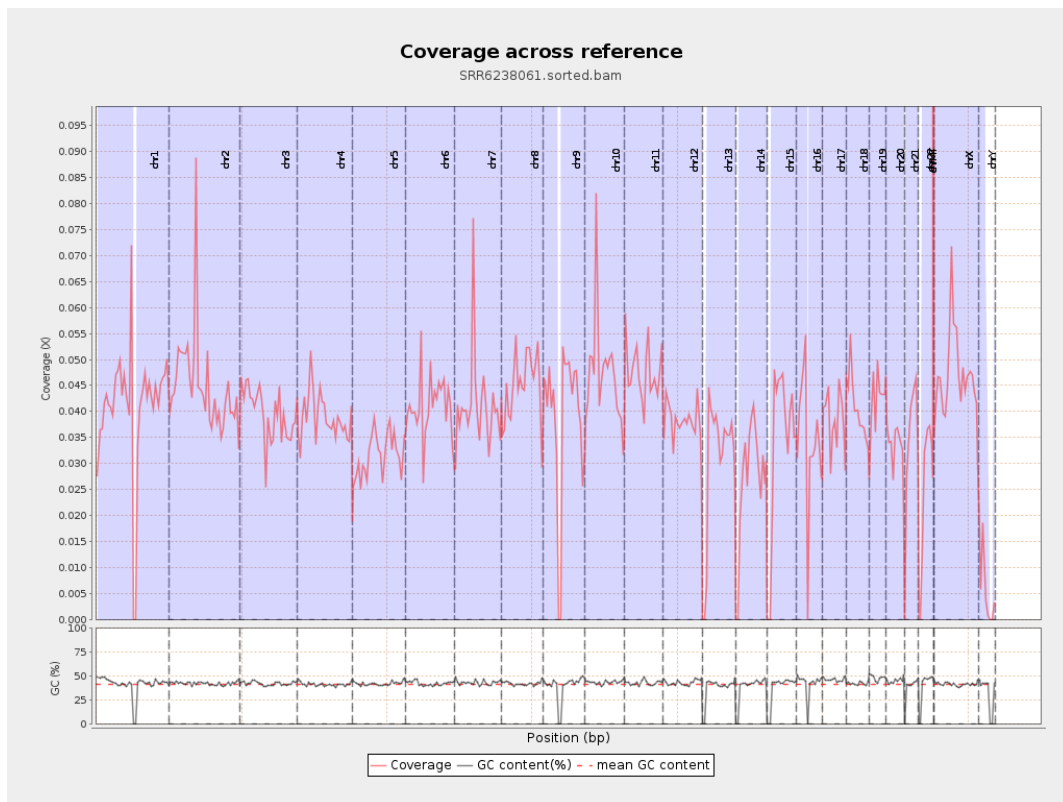
General error rate	0.76%
Mismatches	889,486
Insertions	8,658
Mapped reads with at least one insertion	0.48%
Deletions	31,809
Mapped reads with at least one deletion	1.75%
Homopolymer indels	45.56%

2.6. Chromosome stats

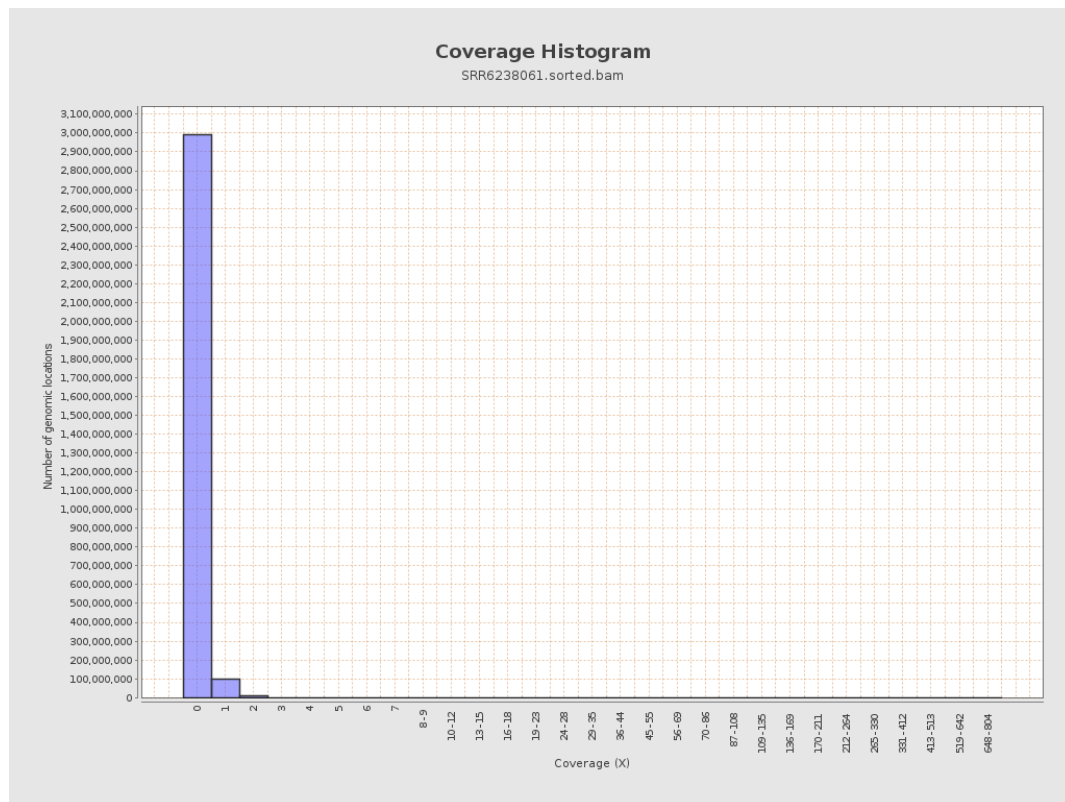
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10204266	0.0409	0.702
chr2	243199373	10924899	0.0449	0.455
chr3	198022430	7832733	0.0396	0.2204
chr4	191154276	7438319	0.0389	0.239
chr5	180915260	5732207	0.0317	0.1986
chr6	171115067	6983186	0.0408	0.2916
chr7	159138663	6543244	0.0411	0.5471

chr8	146364022	6579337	0.045	0.4104
chr9	141213431	5458501	0.0387	0.3884
chr10	135534747	6398759	0.0472	0.394
chr11	135006516	6418354	0.0475	0.3466
chr12	133851895	5081587	0.038	0.2199
chr13	115169878	3501821	0.0304	0.1892
chr14	107349540	2885026	0.0269	0.2437
chr15	102531392	3508869	0.0342	0.205
chr16	90354753	3136594	0.0347	0.2437
chr17	81195210	3090432	0.0381	0.254
chr18	78077248	3198579	0.041	0.6783
chr19	59128983	2522104	0.0427	0.4634
chr20	63025520	2103360	0.0334	0.2122
chr21	48129895	1651494	0.0343	0.2457
chr22	51304566	1240402	0.0242	0.1681
chrMT	16571	25866	1.5609	1.5524
chrX	155270560	7278246	0.0469	0.285
chrY	59373566	334085	0.0056	0.1666

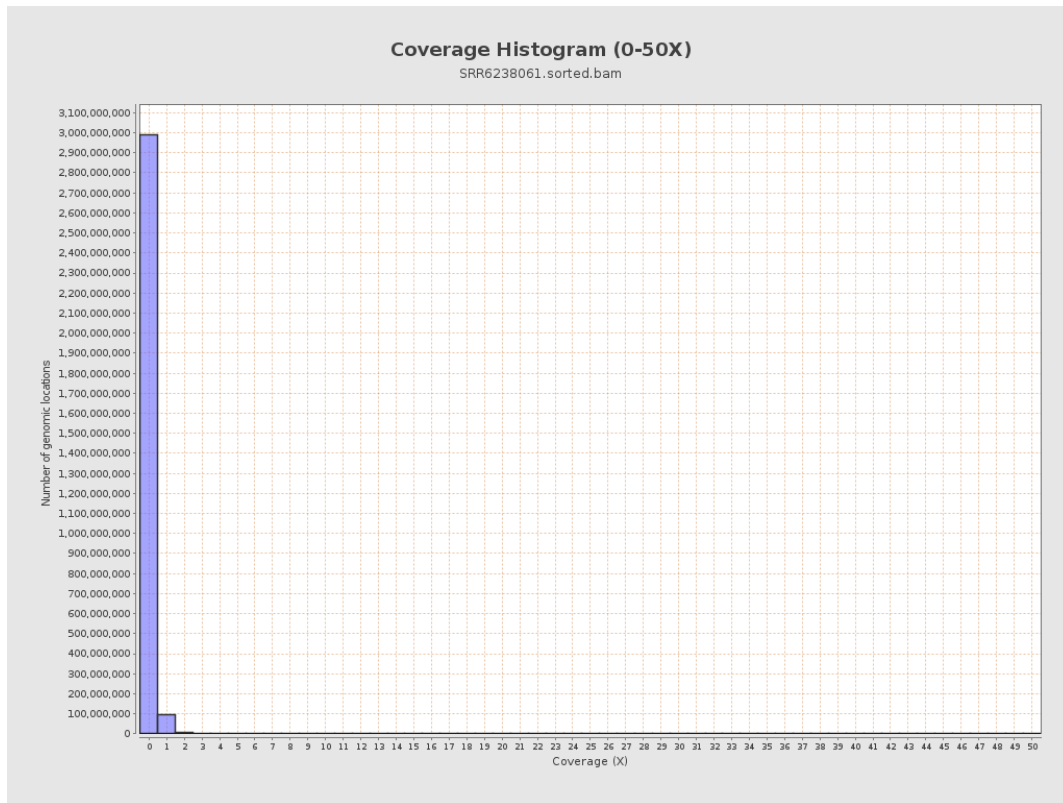
3. Results : Coverage across reference



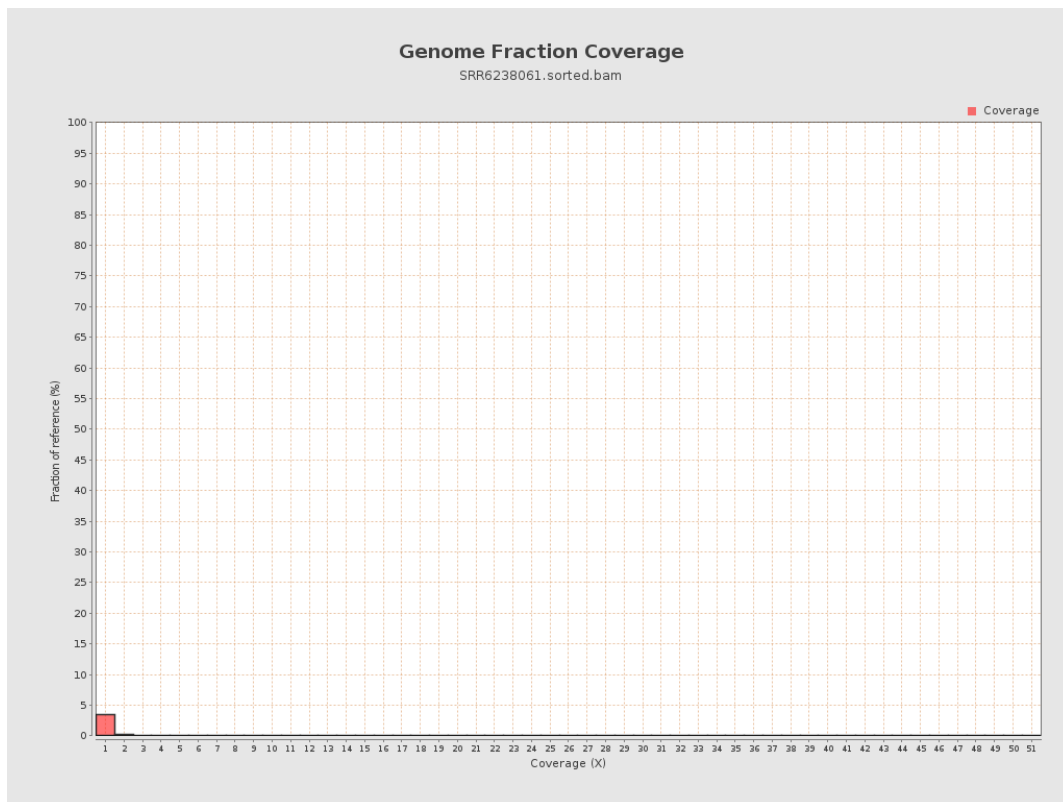
4. Results : Coverage Histogram



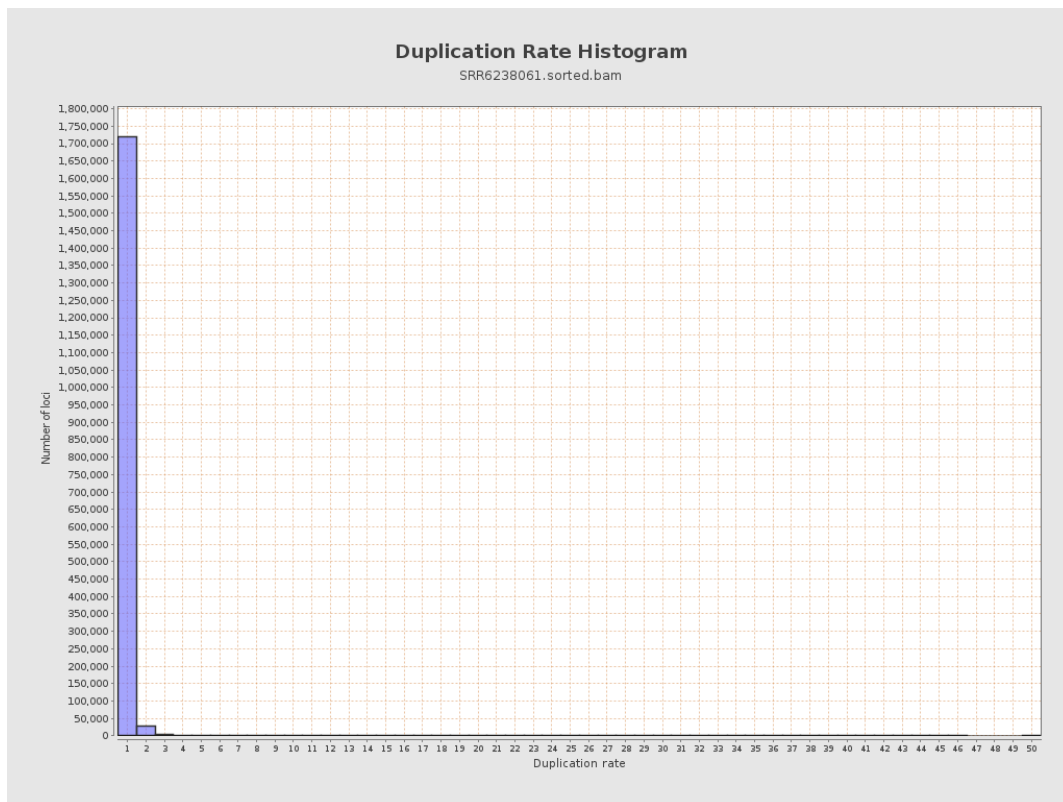
5. Results : Coverage Histogram (0-50X)



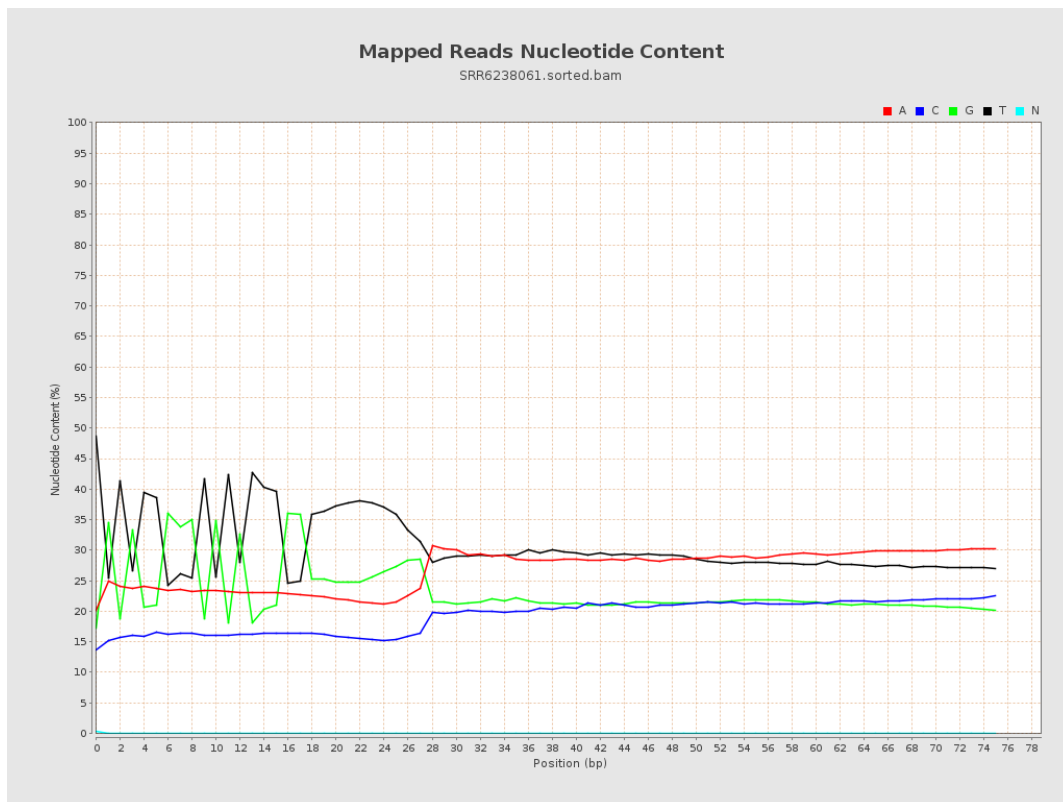
6. Results : Genome Fraction Coverage



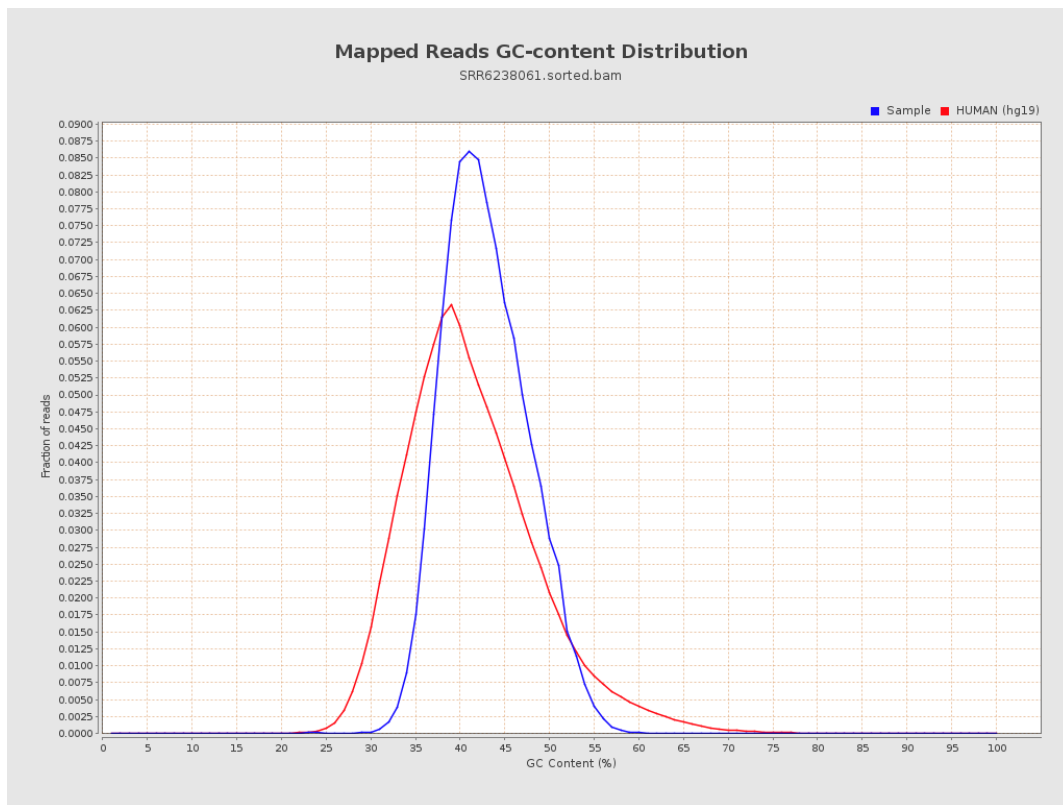
7. Results : Duplication Rate Histogram



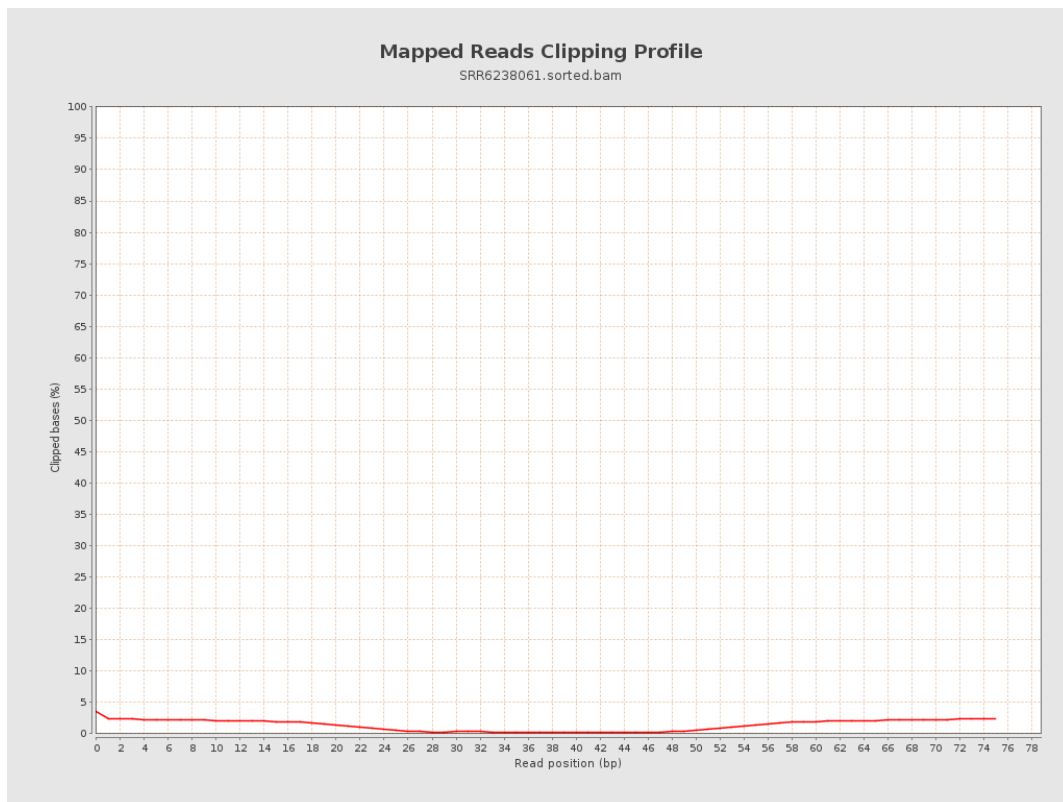
8. Results : Mapped Reads Nucleotide Content



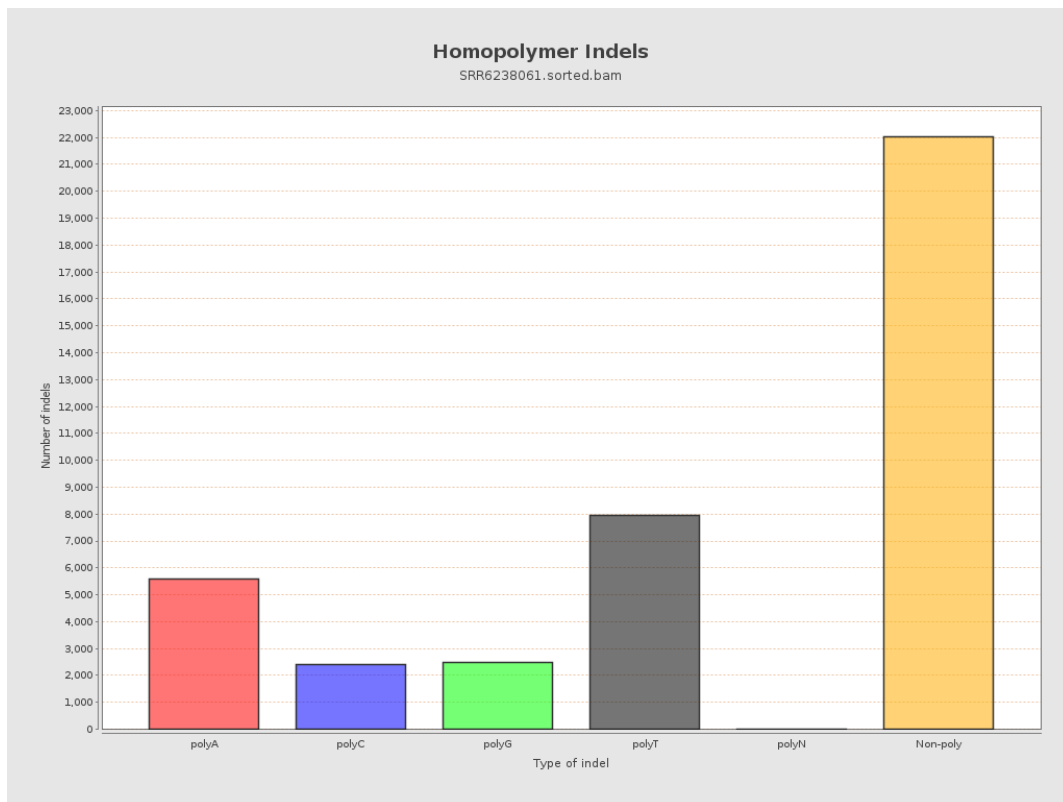
9. Results : Mapped Reads GC-content Distribution



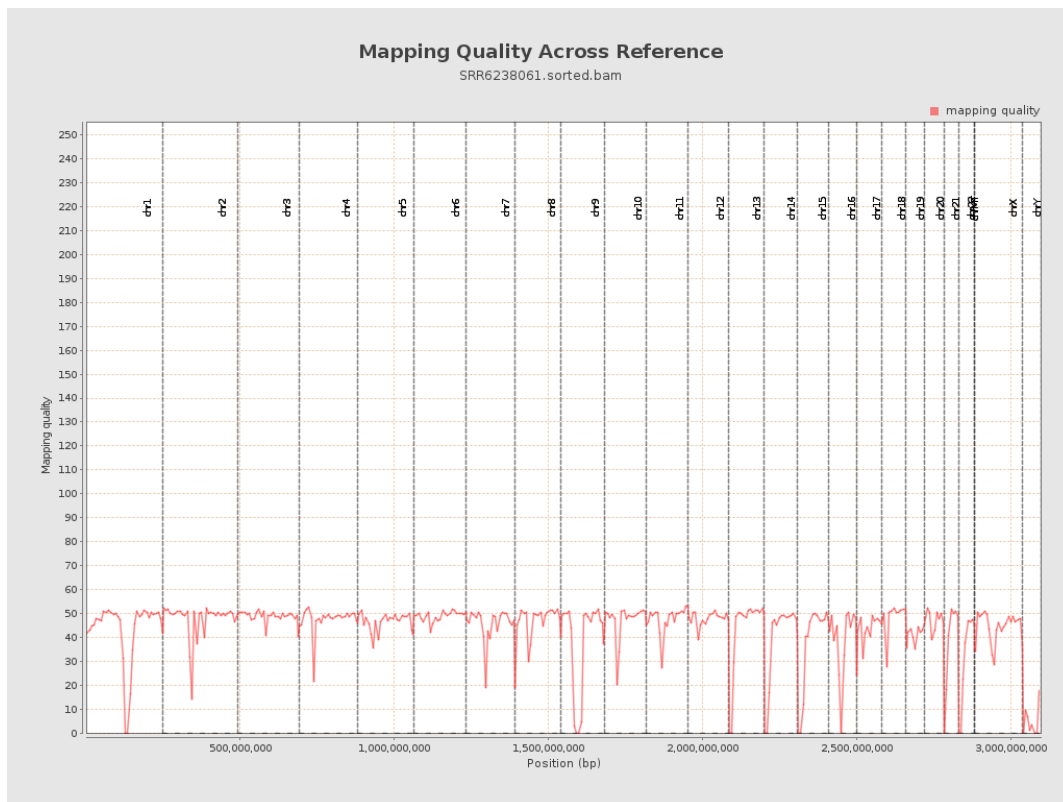
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

