

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:07:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238671.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_SRR6238671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238671.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:07:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,989,002
Mapped reads	2,010,750 / 67.27%
Unmapped reads	978,252 / 32.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,042 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,079,779 / 36.13%
Duplication rate	21.01%
Clipped reads	1,432,316 / 47.92%

2.2. ACGT Content

Number/percentage of A's	29,584,648 / 24.75%
Number/percentage of C's	20,422,438 / 17.08%
Number/percentage of T's	41,053,382 / 34.34%
Number/percentage of G's	28,481,024 / 23.82%
Number/percentage of N's	5,311 / 0%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0386

Standard Deviation	1.1886
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2.4. Mapping Quality

Mean Mapping Quality	42.51
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2.5. Mismatches and indels

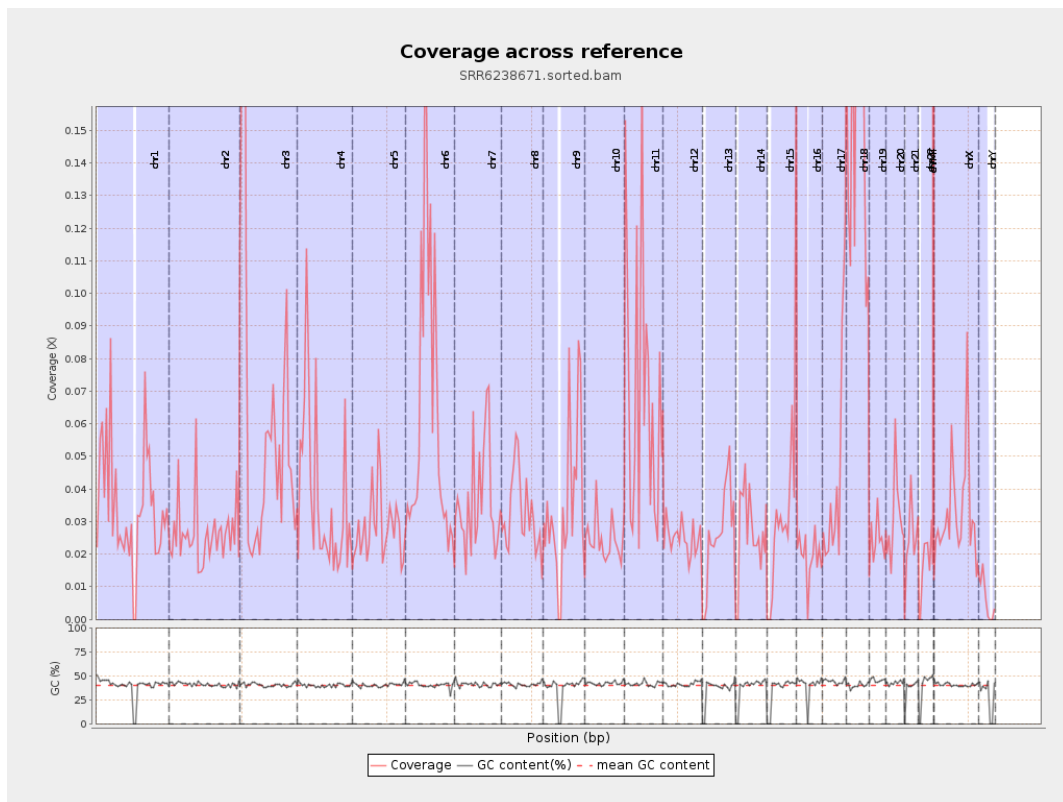
General error rate	0.64%
Mismatches	747,976
Insertions	7,353
Mapped reads with at least one insertion	0.36%
Deletions	31,483
Mapped reads with at least one deletion	1.55%
Homopolymer indels	40.63%

2.6. Chromosome stats

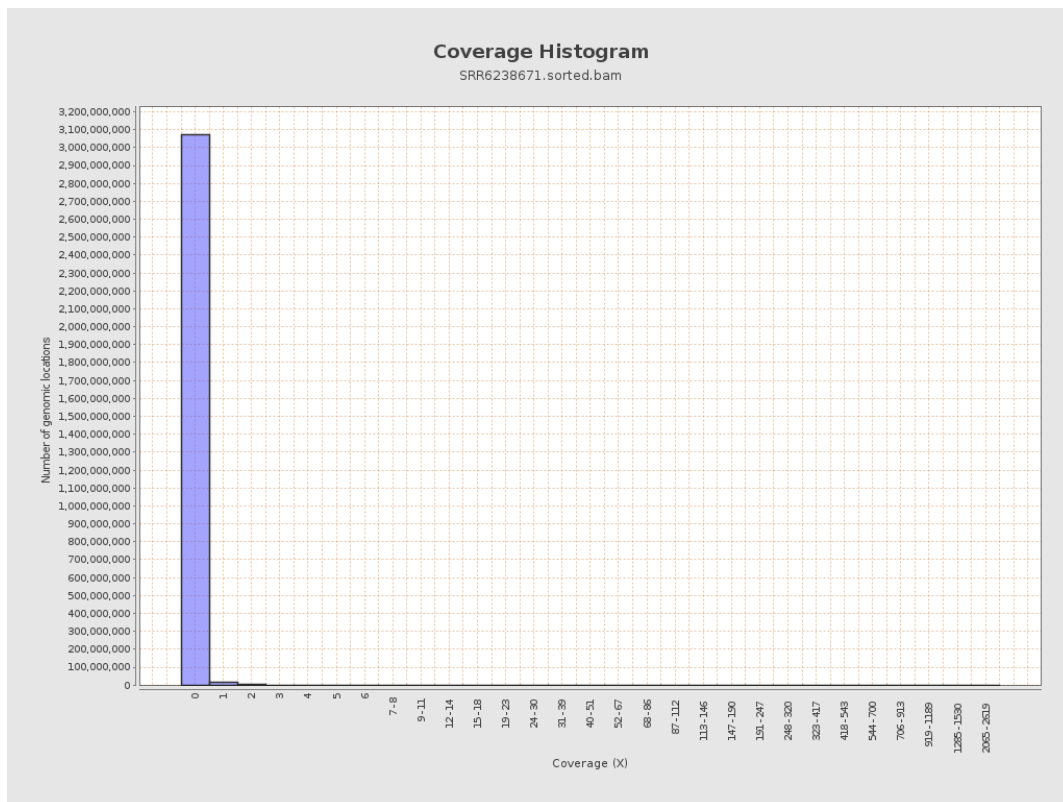
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8638779	0.0347	0.8881
chr2	243199373	6385454	0.0263	1.5503
chr3	198022430	12156605	0.0614	1.1749
chr4	191154276	7230209	0.0378	0.8869
chr5	180915260	5107866	0.0282	0.7823
chr6	171115067	10451901	0.0611	1.5676
chr7	159138663	5763964	0.0362	1.1253

chr8	146364022	4720501	0.0323	1.059
chr9	141213431	4928697	0.0349	0.8592
chr10	135534747	3250997	0.024	0.8206
chr11	135006516	9210698	0.0682	1.2039
chr12	133851895	3322306	0.0248	0.7278
chr13	115169878	2997296	0.026	1.0506
chr14	107349540	2776666	0.0259	1.0394
chr15	102531392	3251376	0.0317	0.9845
chr16	90354753	1739279	0.0192	0.6059
chr17	81195210	3727066	0.0459	0.9626
chr18	78077248	13000316	0.1665	3.7751
chr19	59128983	1450084	0.0245	0.7697
chr20	63025520	1967934	0.0312	0.793
chr21	48129895	1170634	0.0243	0.6799
chr22	51304566	859536	0.0168	0.5406
chrMT	16571	96637	5.8317	12.4703
chrX	155270560	5035690	0.0324	0.8671
chrY	59373566	359217	0.0061	0.4553

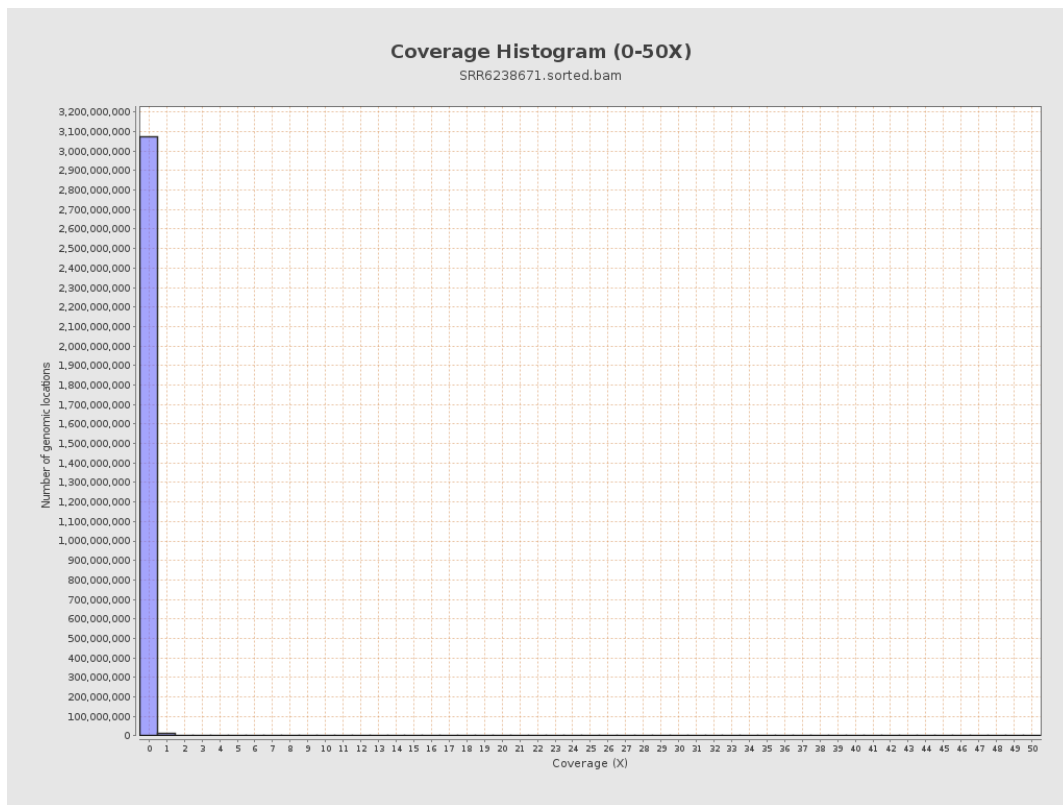
3. Results : Coverage across reference



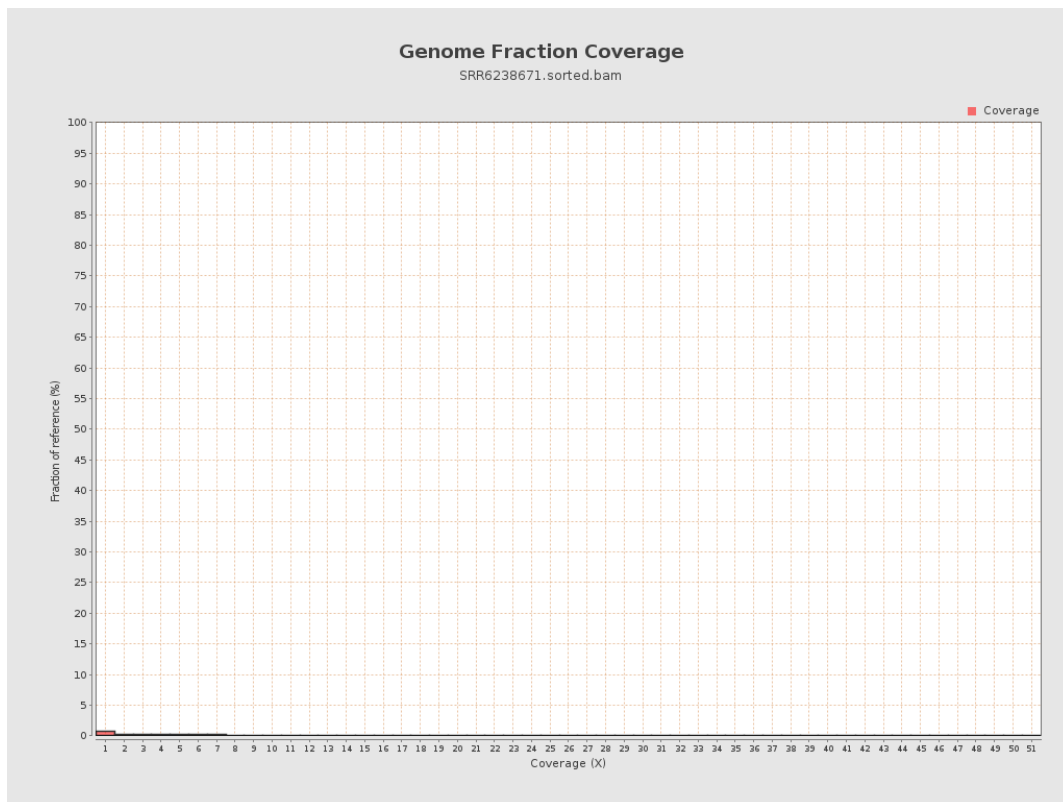
4. Results : Coverage Histogram



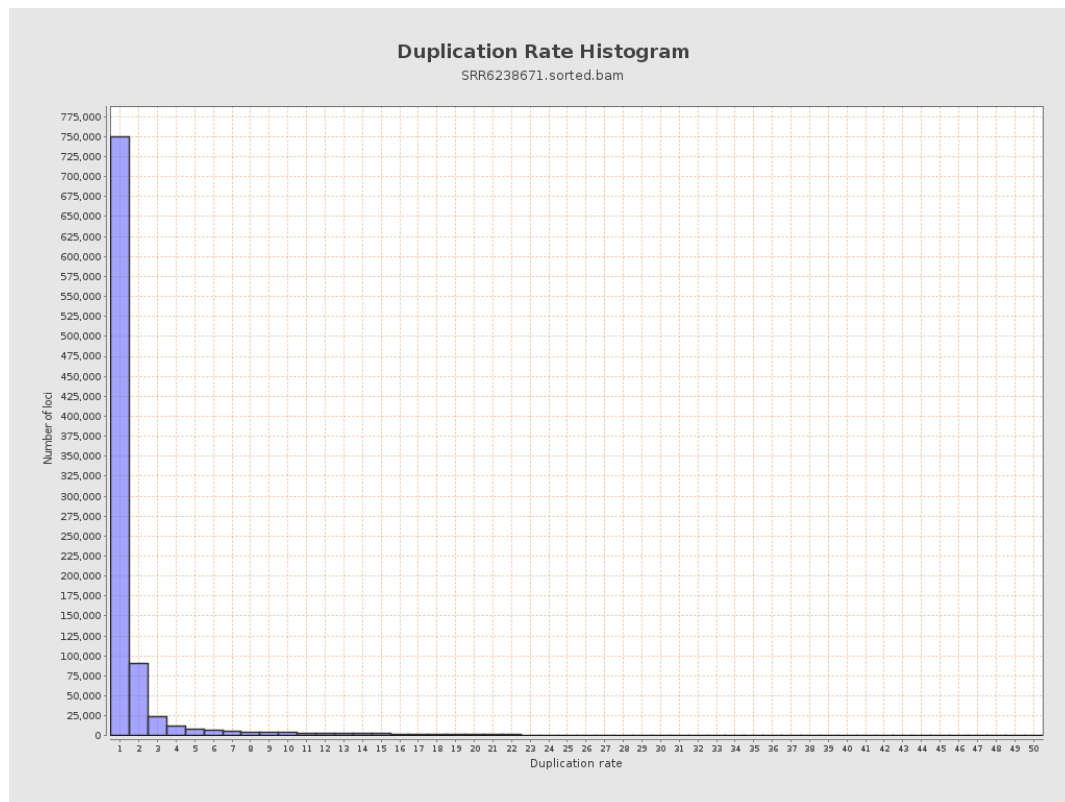
5. Results : Coverage Histogram (0-50X)



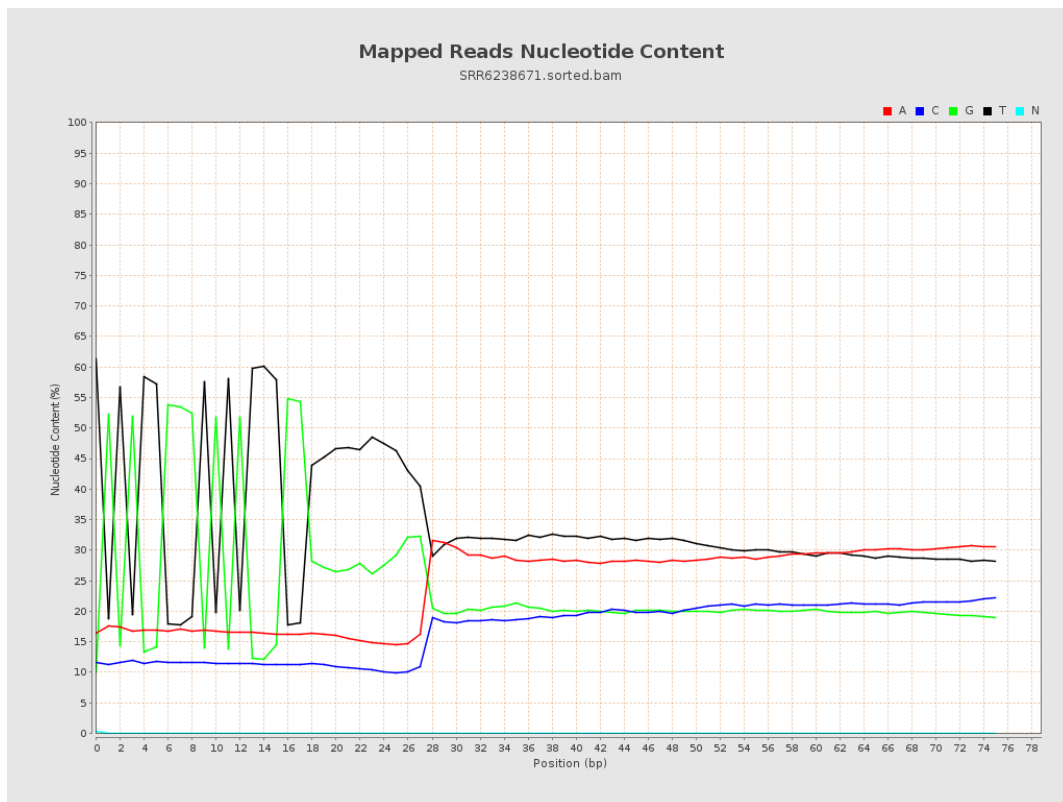
6. Results : Genome Fraction Coverage



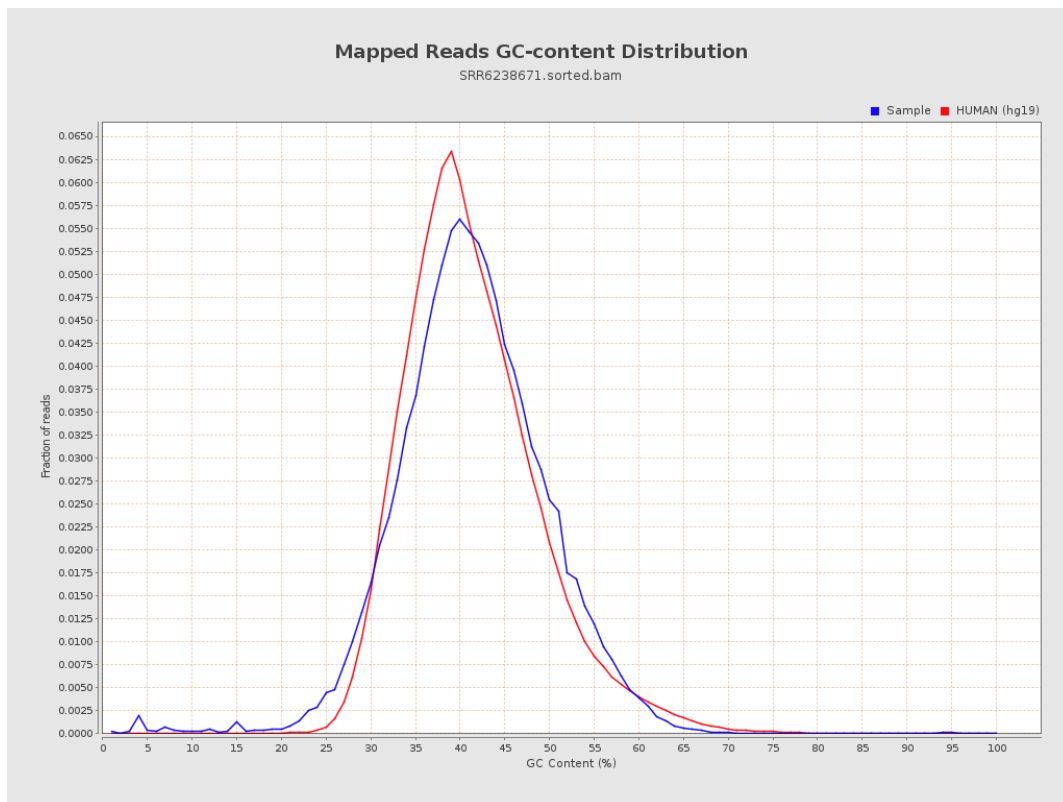
7. Results : Duplication Rate Histogram



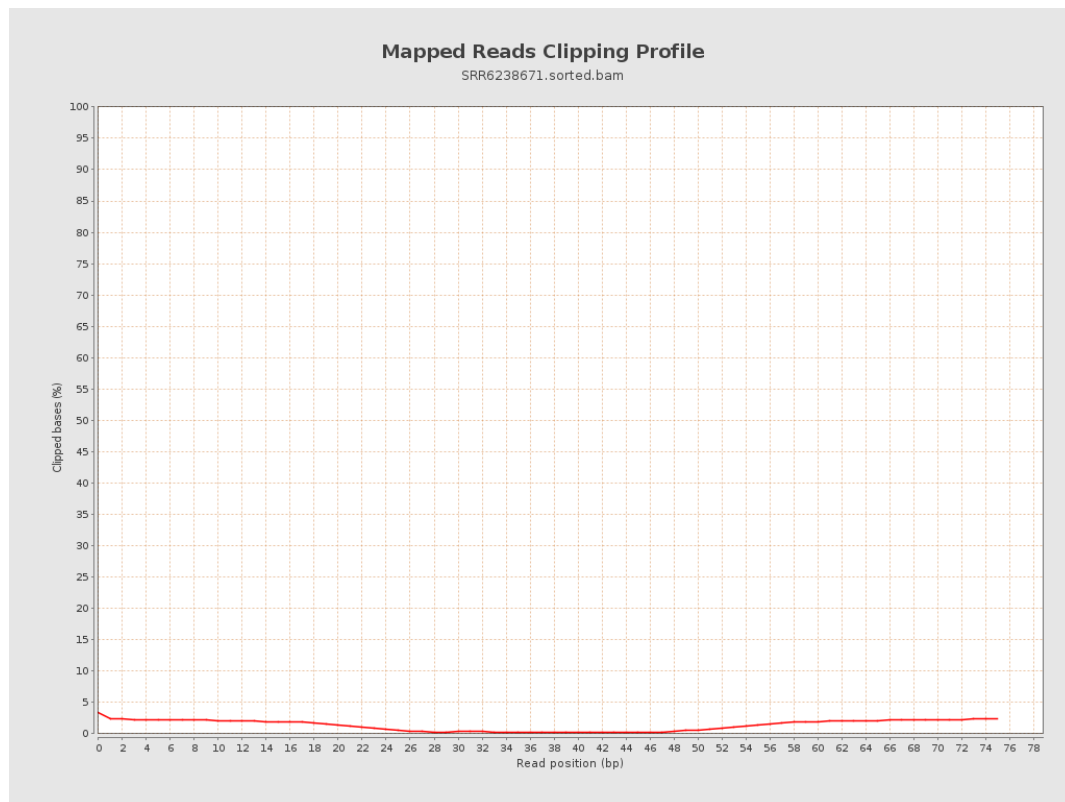
8. Results : Mapped Reads Nucleotide Content



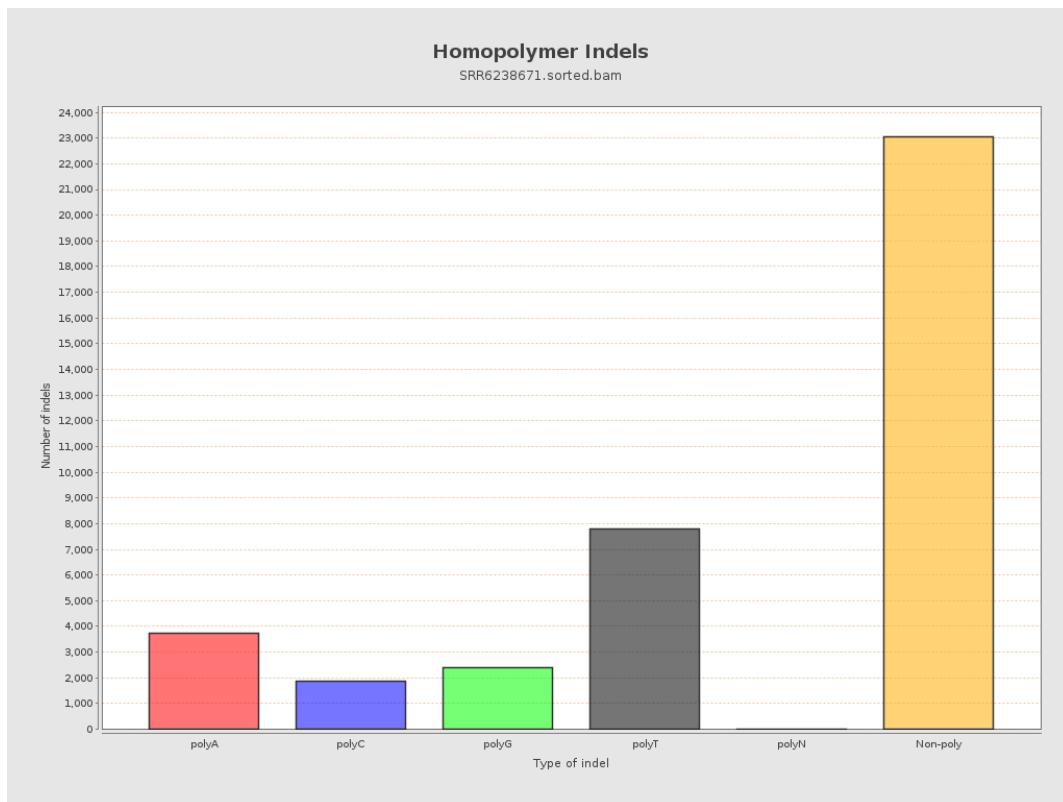
9. Results : Mapped Reads GC-content Distribution



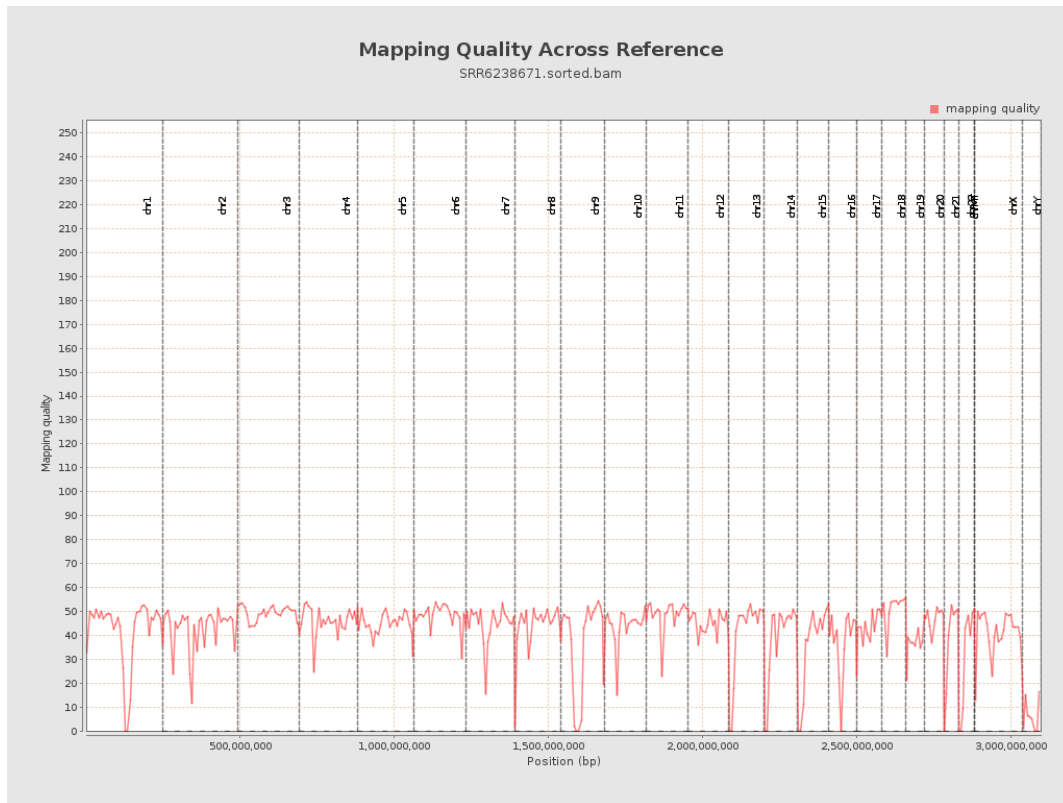
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

