

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:15:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231833.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_SRR6231833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,682,739
Mapped reads	4,342,405 / 92.73%
Unmapped reads	340,334 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,216 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	385,298 / 8.23%
Duplication rate	6.84%
Clipped reads	2,429,858 / 51.89%

2.2. ACGT Content

Number/percentage of A's	69,819,293 / 25.35%
Number/percentage of C's	49,330,654 / 17.91%
Number/percentage of T's	89,361,143 / 32.45%
Number/percentage of G's	66,790,426 / 24.25%
Number/percentage of N's	102,628 / 0.04%
GC Percentage	42.16%

2.3. Coverage

Mean	0.089

Standard Deviation	0.9777
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2.4. Mapping Quality

Mean Mapping Quality	43.83
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2.5. Mismatches and indels

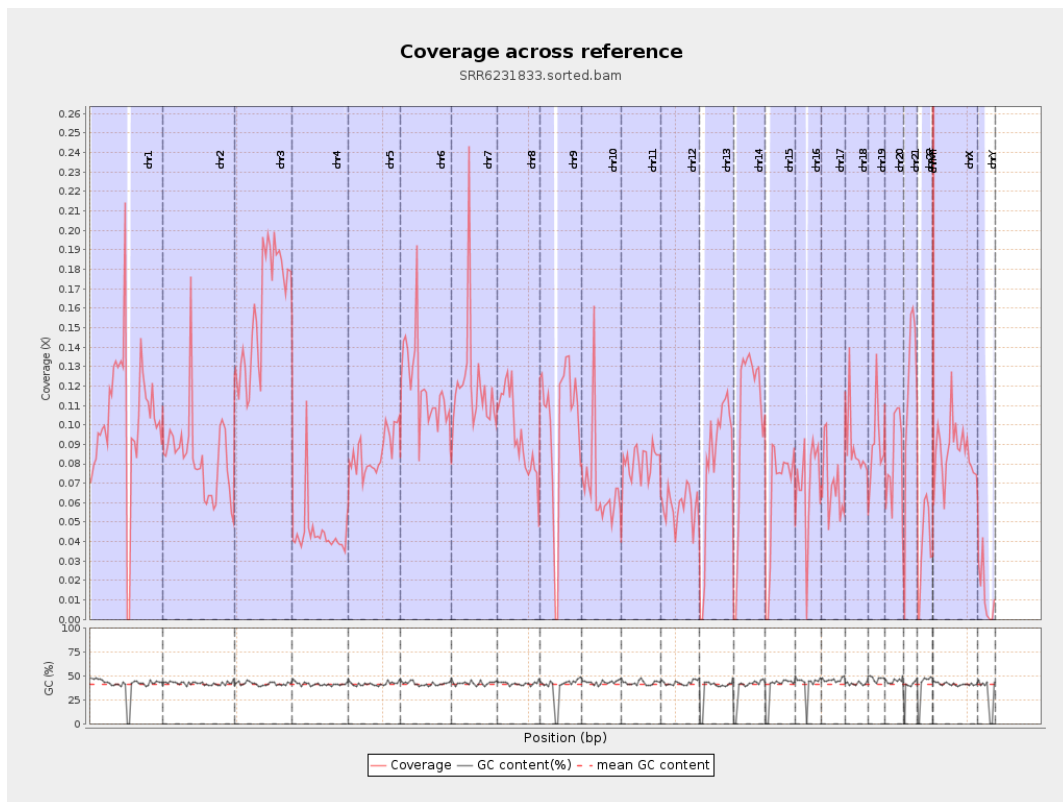
General error rate	0.63%
Mismatches	1,706,450
Insertions	18,291
Mapped reads with at least one insertion	0.42%
Deletions	57,876
Mapped reads with at least one deletion	1.32%
Homopolymer indels	44.82%

2.6. Chromosome stats

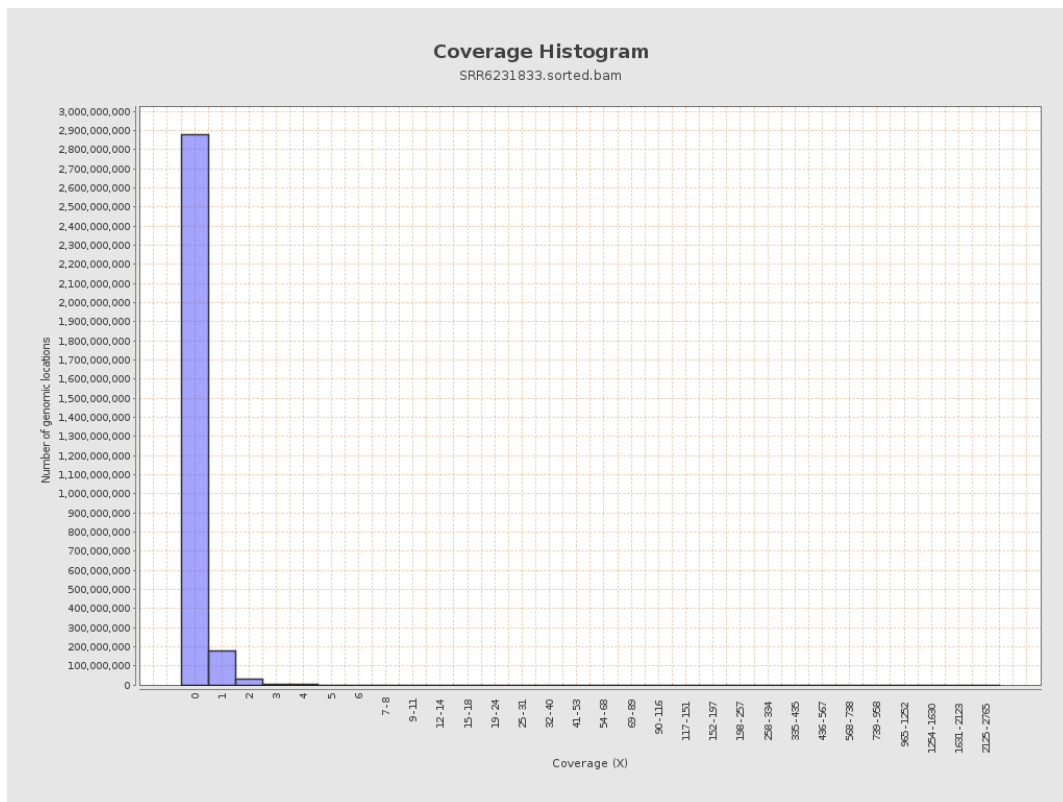
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25719523	0.1032	2.1107
chr2	243199373	20119801	0.0827	1.0395
chr3	198022430	31475051	0.1589	0.4963
chr4	191154276	8561473	0.0448	0.3515
chr5	180915260	15518592	0.0858	0.3694
chr6	171115067	20410466	0.1193	0.751
chr7	159138663	19096876	0.12	1.8157

chr8	146364022	13900286	0.095	0.7582
chr9	141213431	14205428	0.1006	0.7794
chr10	135534747	9133642	0.0674	0.8134
chr11	135006516	10886805	0.0806	0.7288
chr12	133851895	7743861	0.0579	0.3457
chr13	115169878	9351626	0.0812	0.3561
chr14	107349540	11224311	0.1046	0.4805
chr15	102531392	6655643	0.0649	0.3659
chr16	90354753	6184756	0.0684	0.4429
chr17	81195210	5631831	0.0694	0.4284
chr18	78077248	6967914	0.0892	1.8475
chr19	59128983	5430309	0.0918	1.2266
chr20	63025520	5249753	0.0833	0.4353
chr21	48129895	5717569	0.1188	0.4811
chr22	51304566	1972144	0.0384	0.2314
chrMT	16571	207451	12.5189	7.6594
chrX	155270560	13381446	0.0862	0.5221
chrY	59373566	762073	0.0128	0.2823

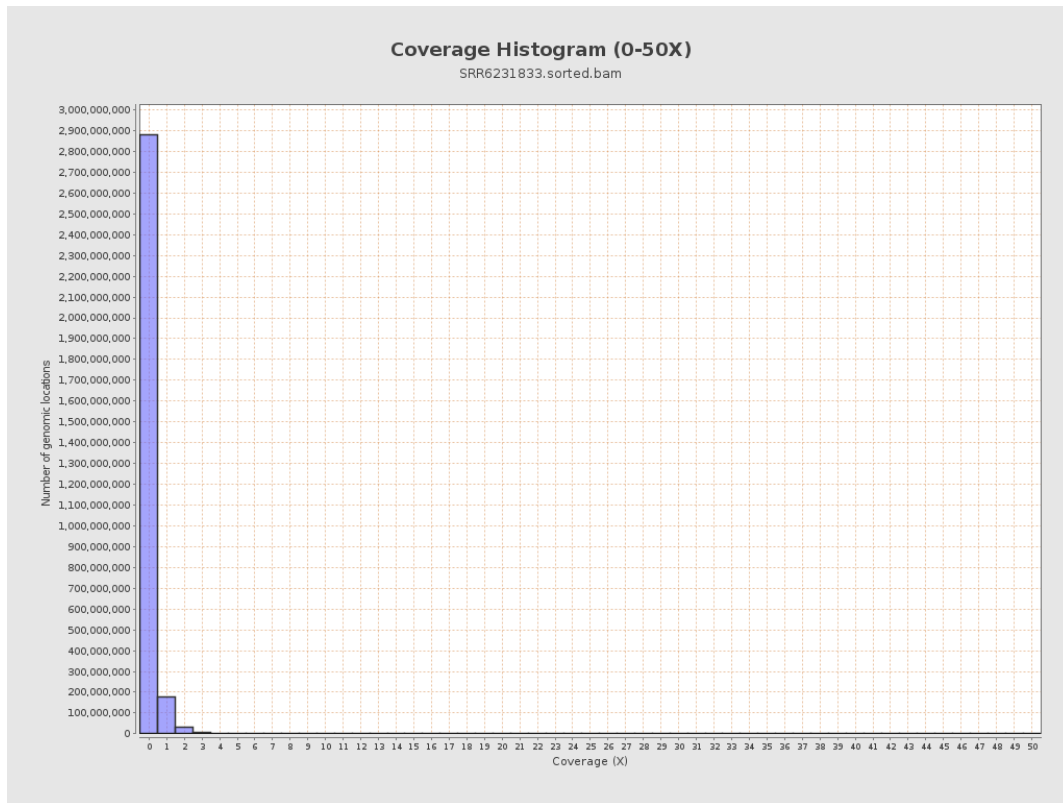
3. Results : Coverage across reference



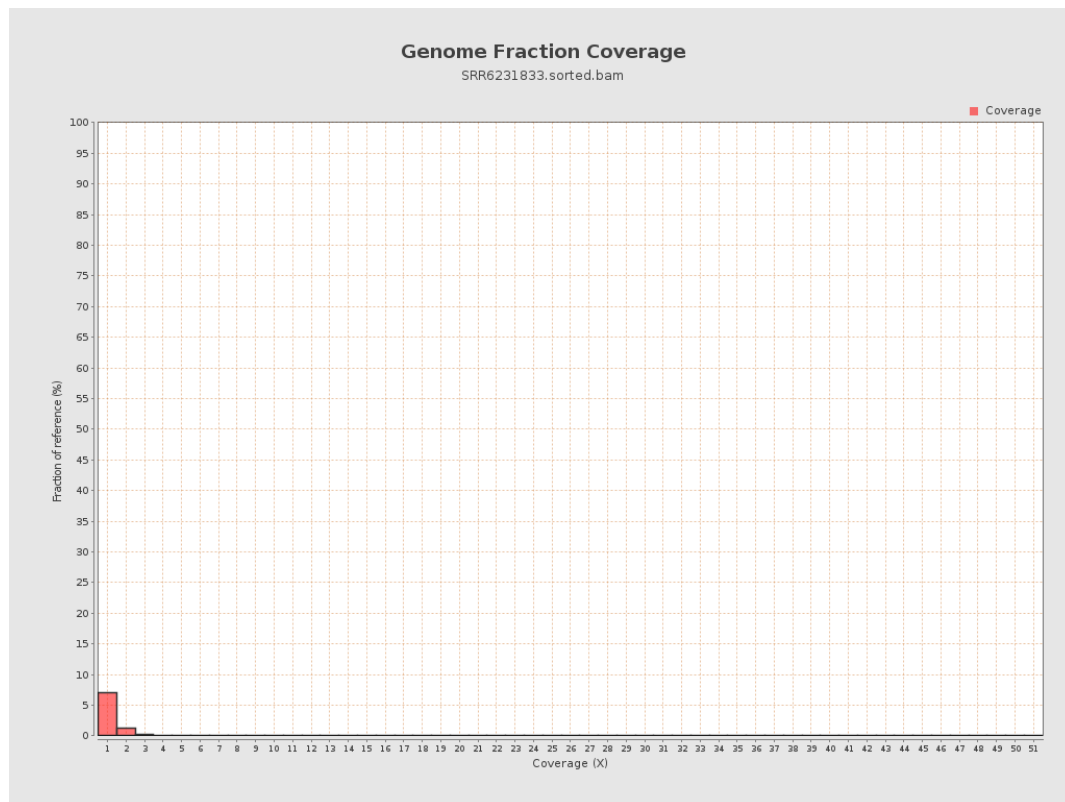
4. Results : Coverage Histogram



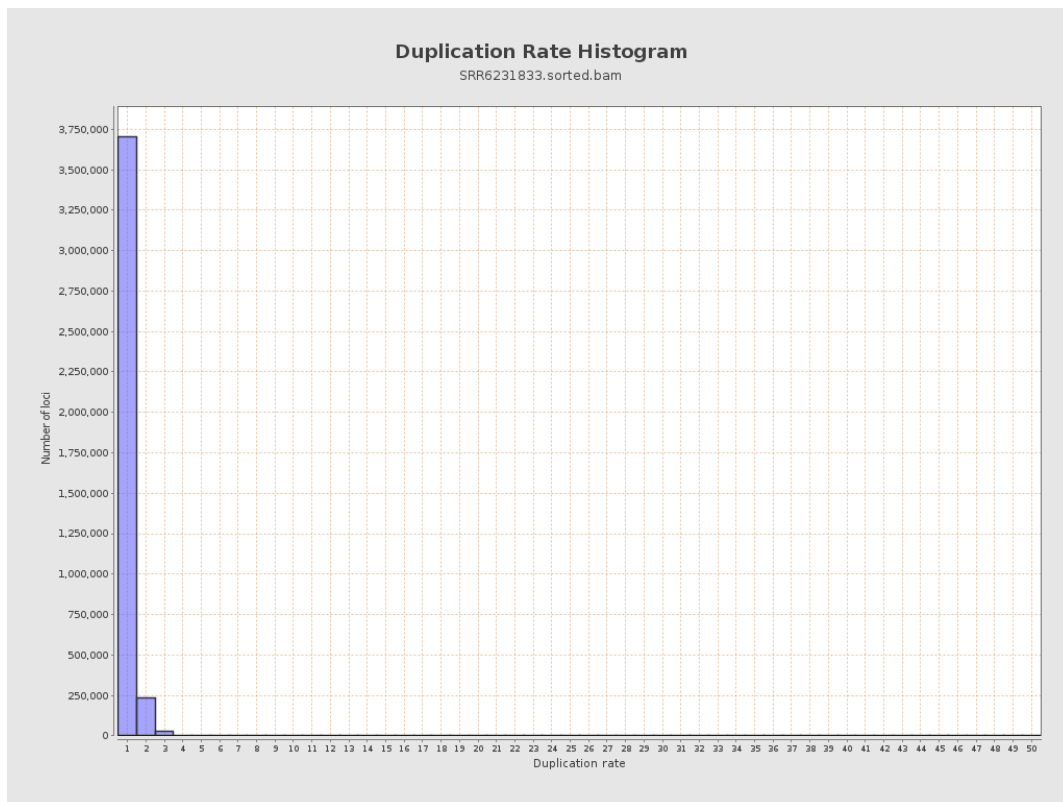
5. Results : Coverage Histogram (0-50X)



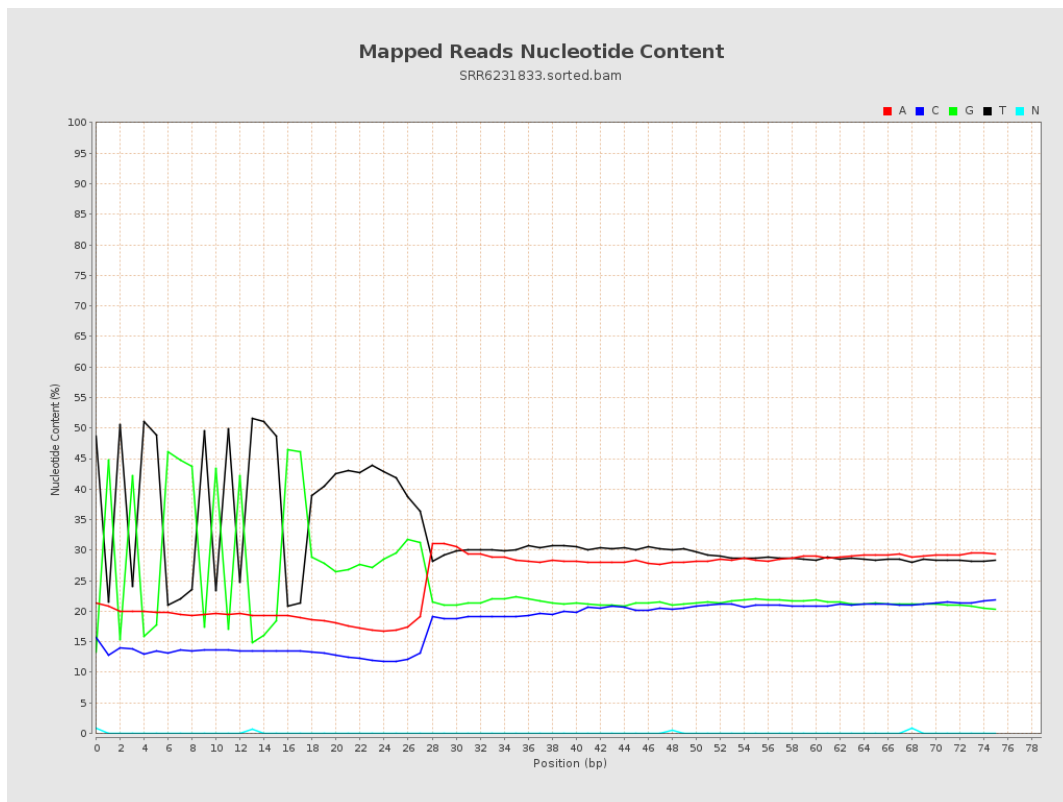
6. Results : Genome Fraction Coverage



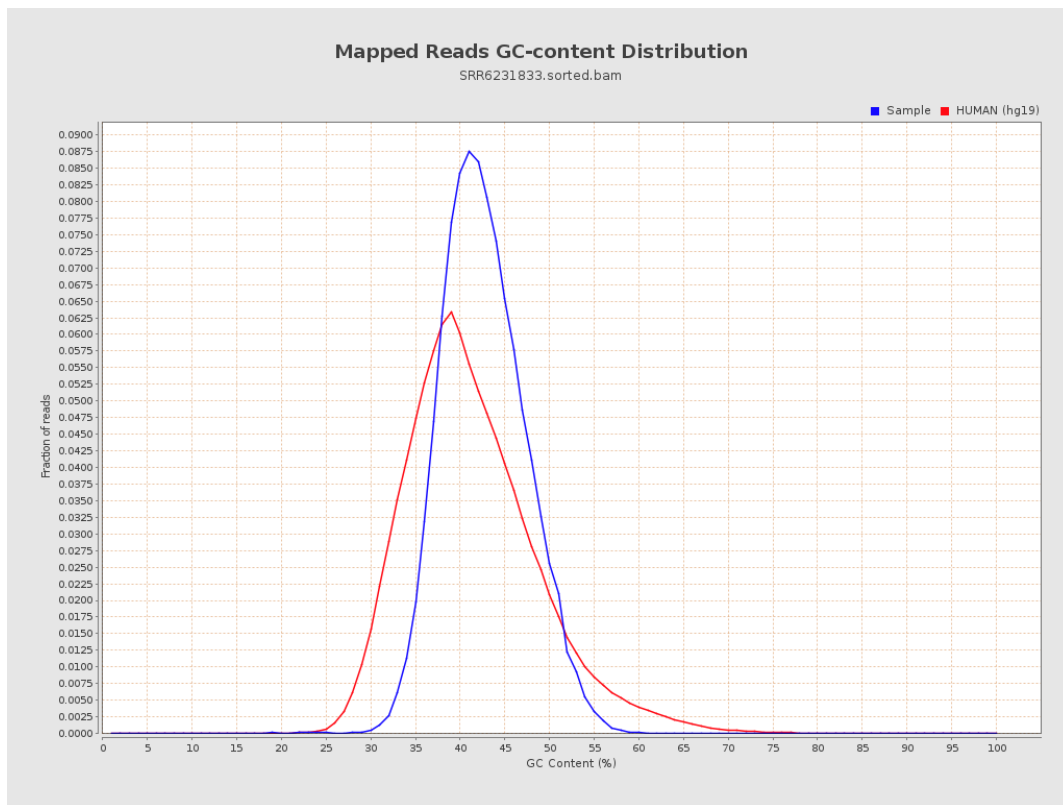
7. Results : Duplication Rate Histogram



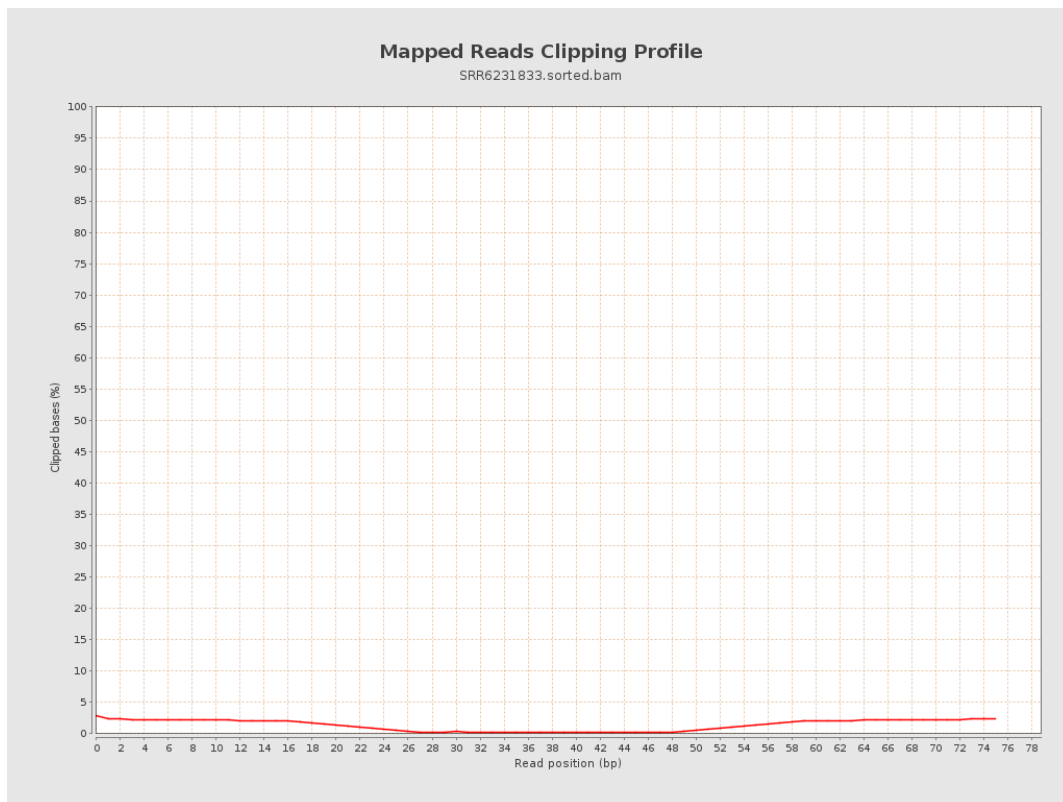
8. Results : Mapped Reads Nucleotide Content



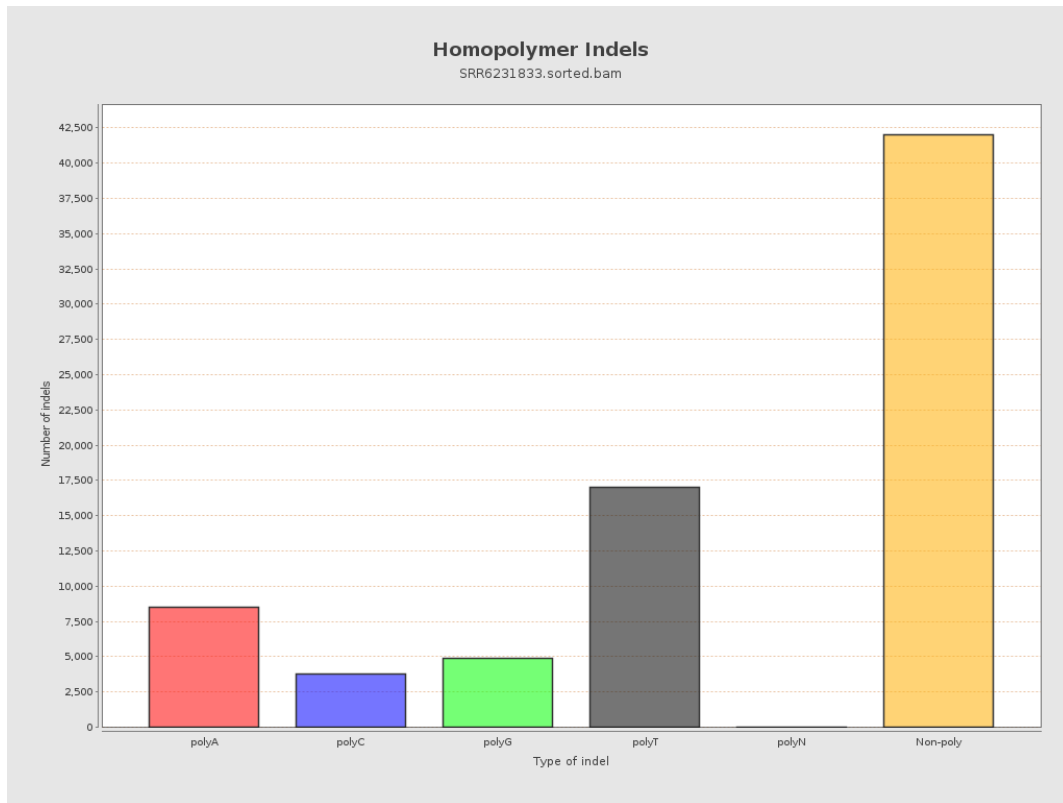
9. Results : Mapped Reads GC-content Distribution



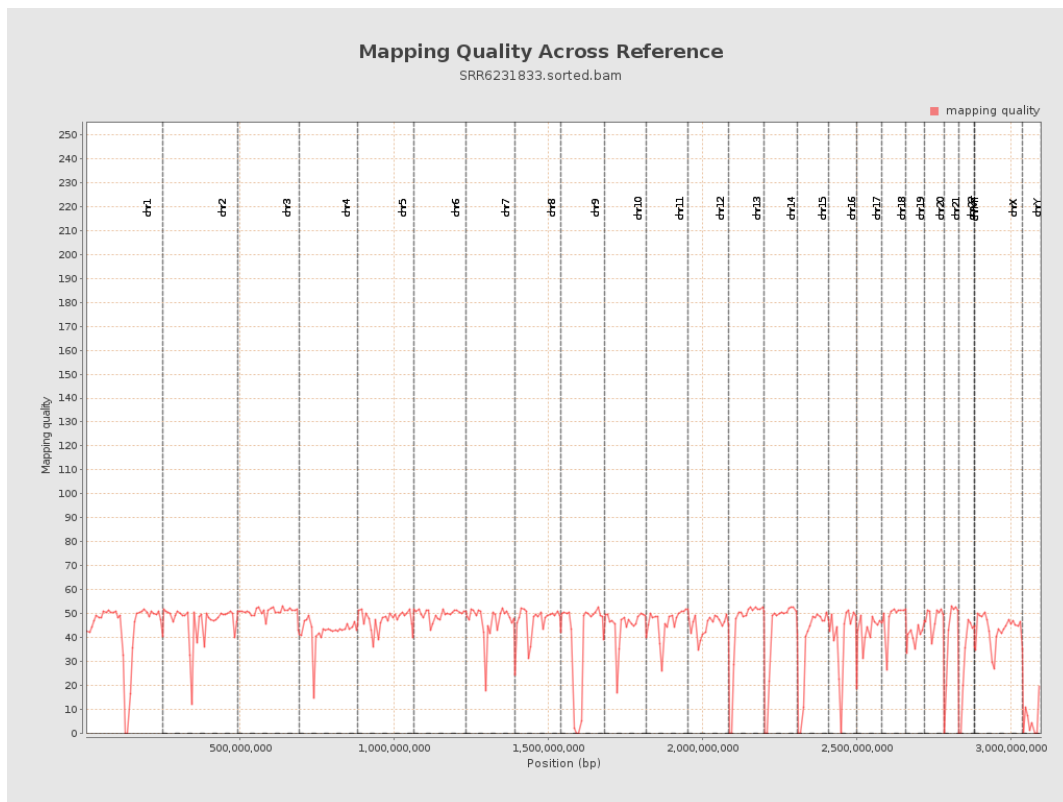
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

