

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:41:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231848.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_SRR6231848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231848.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:41:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,167,022
Mapped reads	5,678,421 / 69.53%
Unmapped reads	2,488,601 / 30.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,325 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	378,681 / 4.64%
Duplication rate	3.31%
Clipped reads	3,203,908 / 39.23%

2.2. ACGT Content

Number/percentage of A's	104,525,541 / 28.64%
Number/percentage of C's	74,903,943 / 20.53%
Number/percentage of T's	100,236,718 / 27.47%
Number/percentage of G's	85,213,974 / 23.35%
Number/percentage of N's	27,826 / 0.01%
GC Percentage	43.88%

2.3. Coverage

Mean	0.1179

Standard Deviation	13.8224
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2.4. Mapping Quality

Mean Mapping Quality	42.13
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2.5. Mismatches and indels

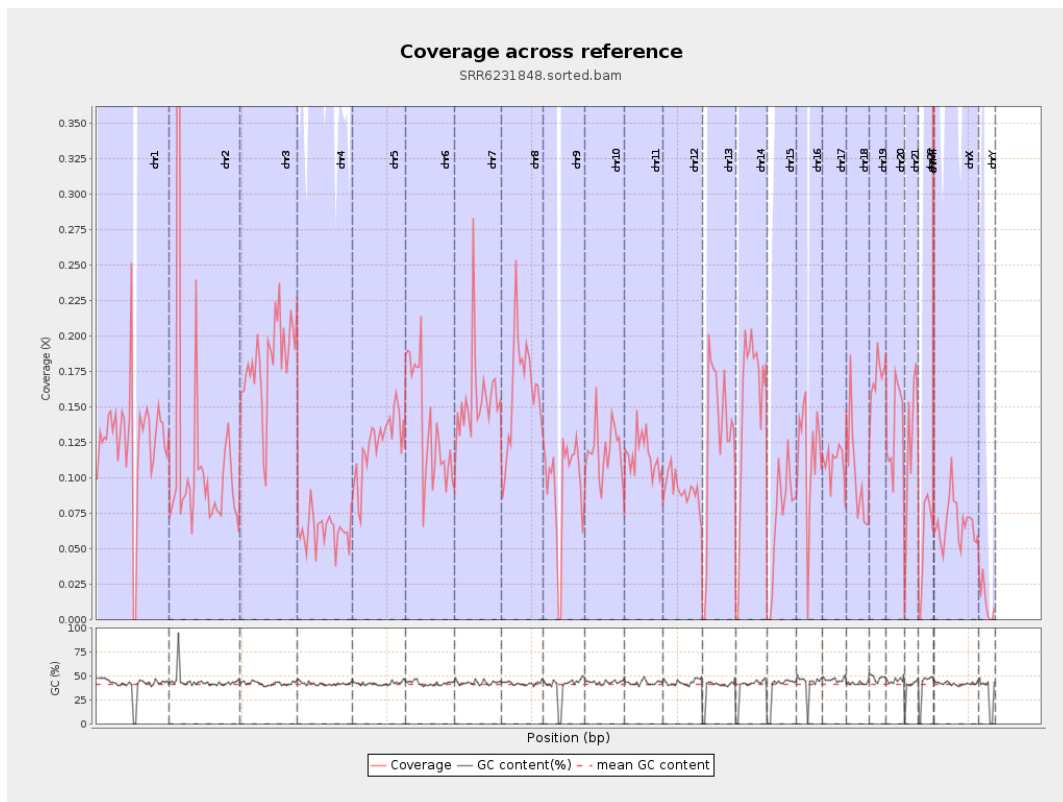
General error rate	0.65%
Mismatches	2,313,650
Insertions	26,893
Mapped reads with at least one insertion	0.47%
Deletions	83,904
Mapped reads with at least one deletion	1.46%
Homopolymer indels	43.19%

2.6. Chromosome stats

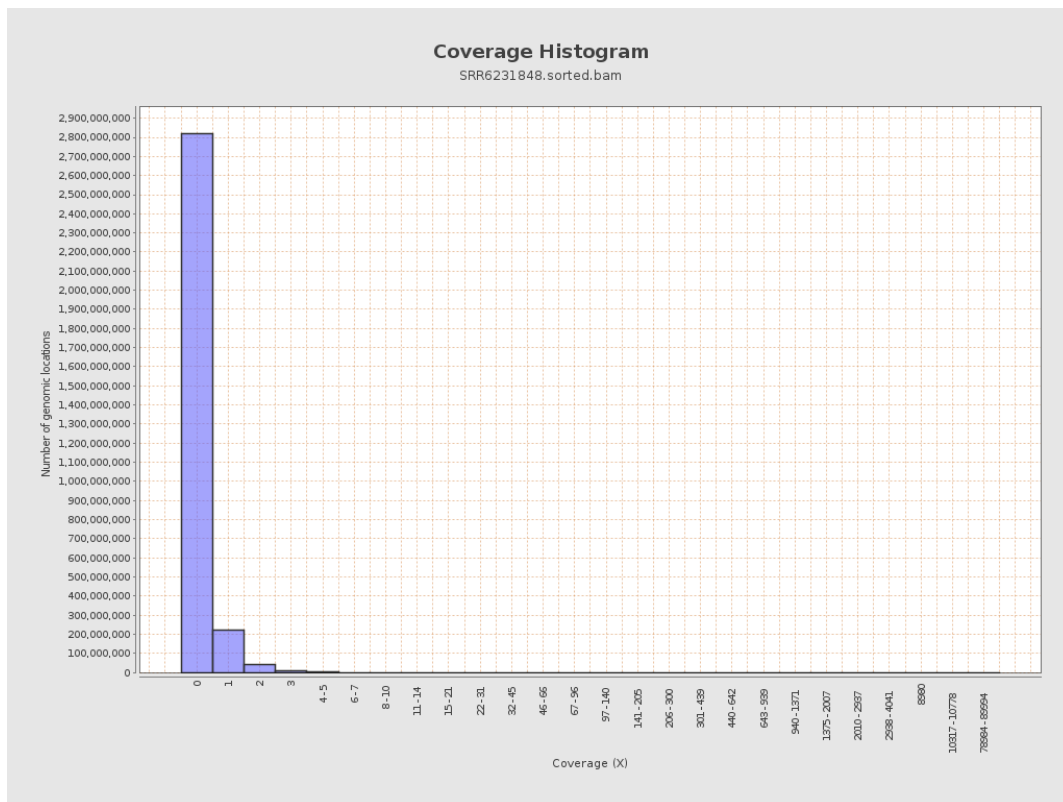
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31443609	0.1262	2.7139
chr2	243199373	30080358	0.1237	49.1507
chr3	198022430	35823858	0.1809	0.524
chr4	191154276	11953491	0.0625	0.3675
chr5	180915260	22368364	0.1236	0.4556
chr6	171115067	23296015	0.1361	0.752
chr7	159138663	24933162	0.1567	1.888

chr8	146364022	23475468	0.1604	1.0688
chr9	141213431	13298834	0.0942	0.8984
chr10	135534747	16123415	0.119	0.9071
chr11	135006516	15533422	0.1151	0.9881
chr12	133851895	12246936	0.0915	0.4074
chr13	115169878	14732781	0.1279	0.4416
chr14	107349540	16064611	0.1496	0.7024
chr15	102531392	7357443	0.0718	0.353
chr16	90354753	10532296	0.1166	0.6041
chr17	81195210	8912621	0.1098	0.5385
chr18	78077248	7971094	0.1021	2.2872
chr19	59128983	10120722	0.1712	1.5367
chr20	63025520	8476507	0.1345	0.52
chr21	48129895	5924668	0.1231	0.4715
chr22	51304566	2878545	0.0561	0.2814
chrMT	16571	209865	12.6646	8.018
chrX	155270560	10576864	0.0681	0.521
chrY	59373566	712566	0.012	0.2131

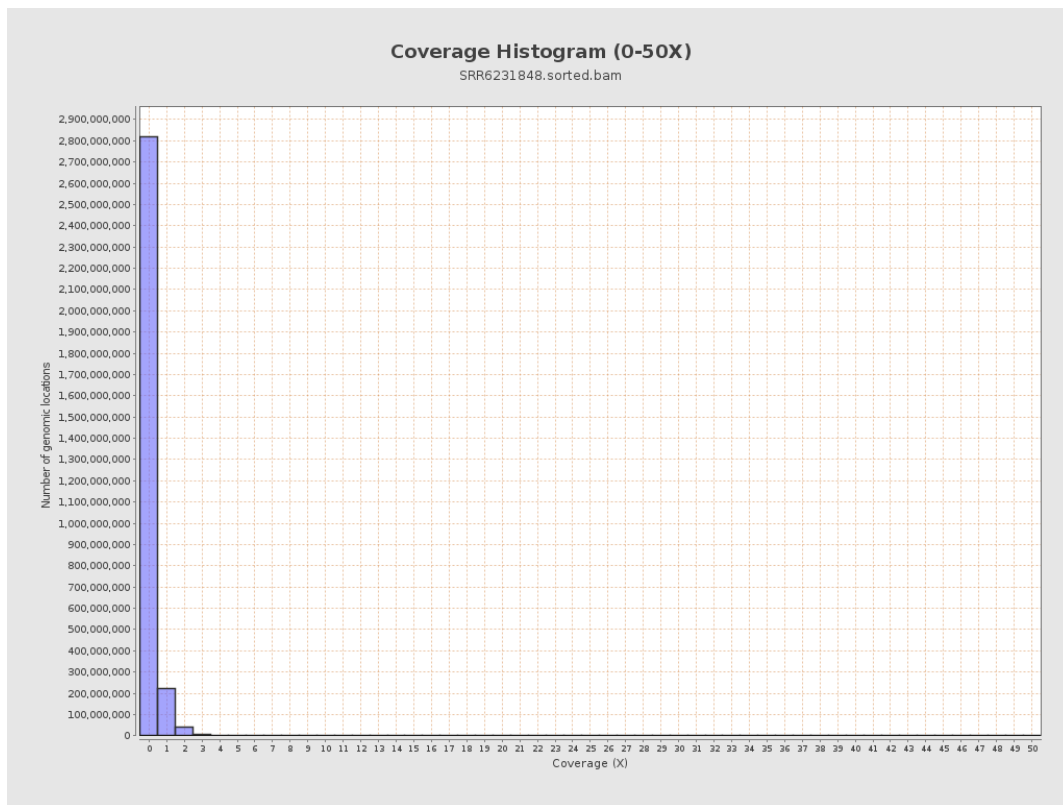
3. Results : Coverage across reference



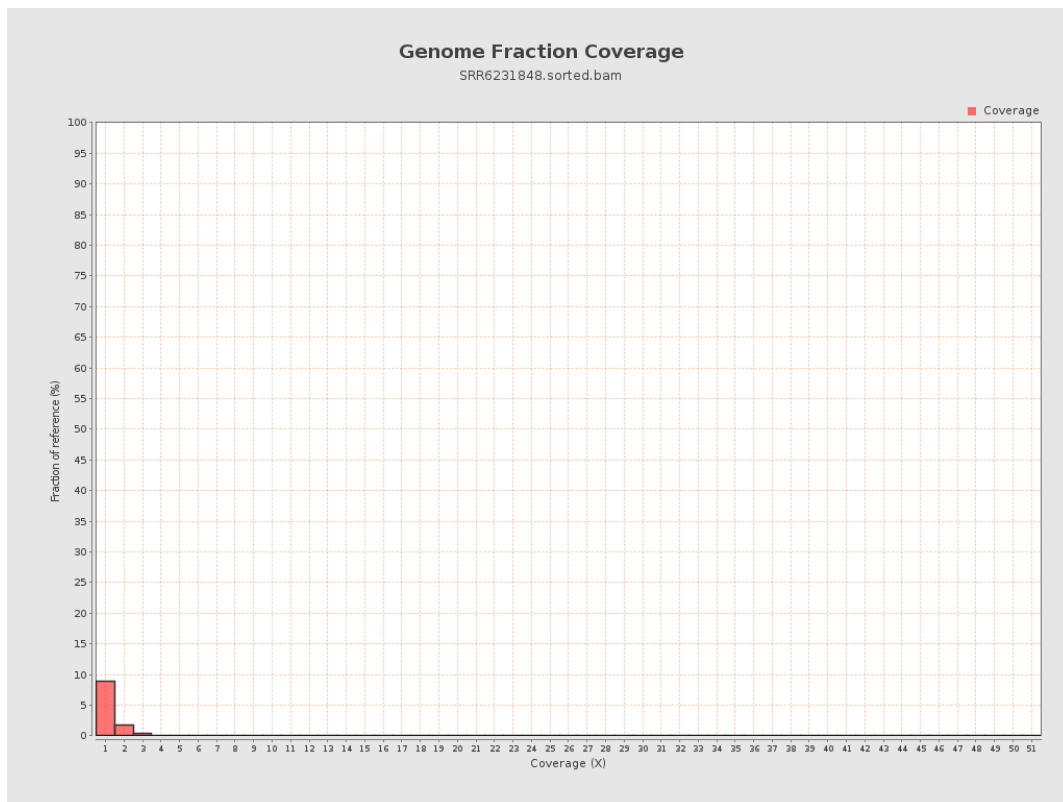
4. Results : Coverage Histogram



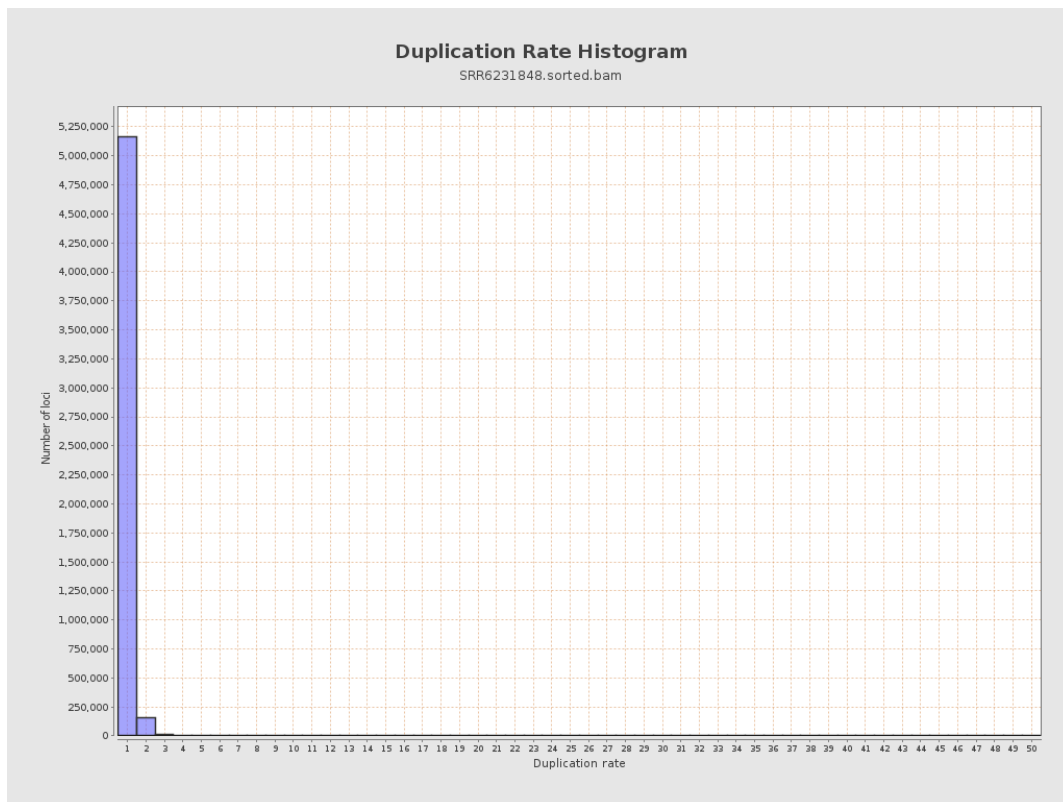
5. Results : Coverage Histogram (0-50X)



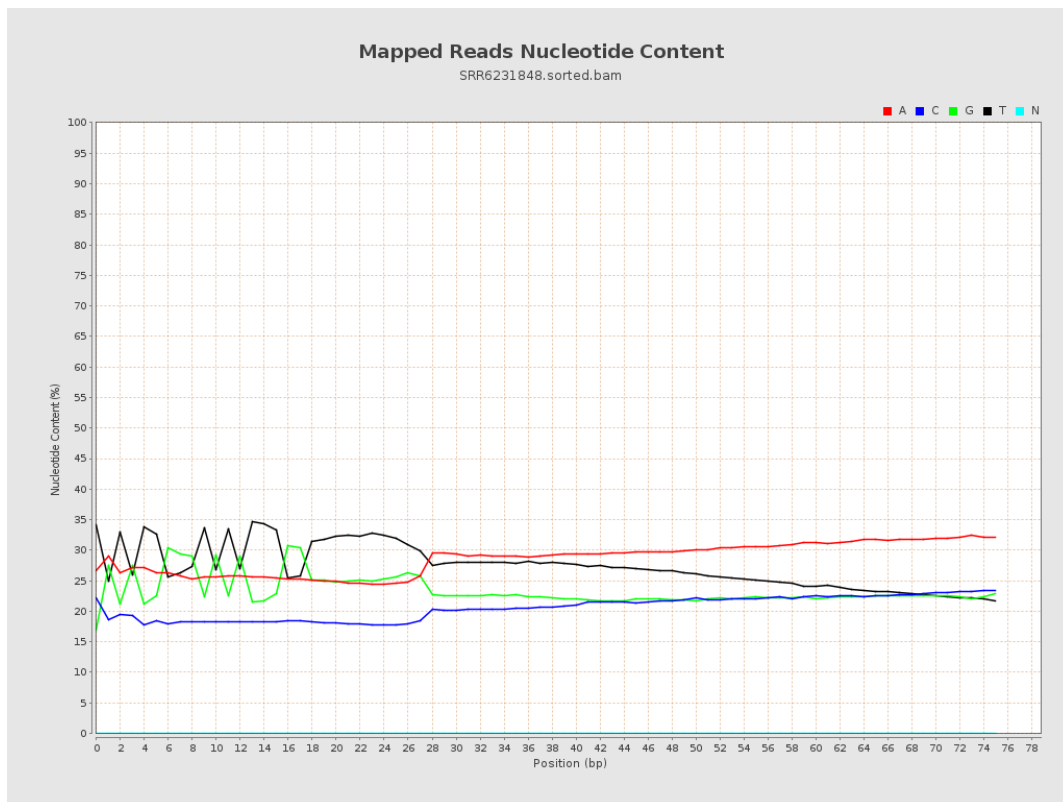
6. Results : Genome Fraction Coverage



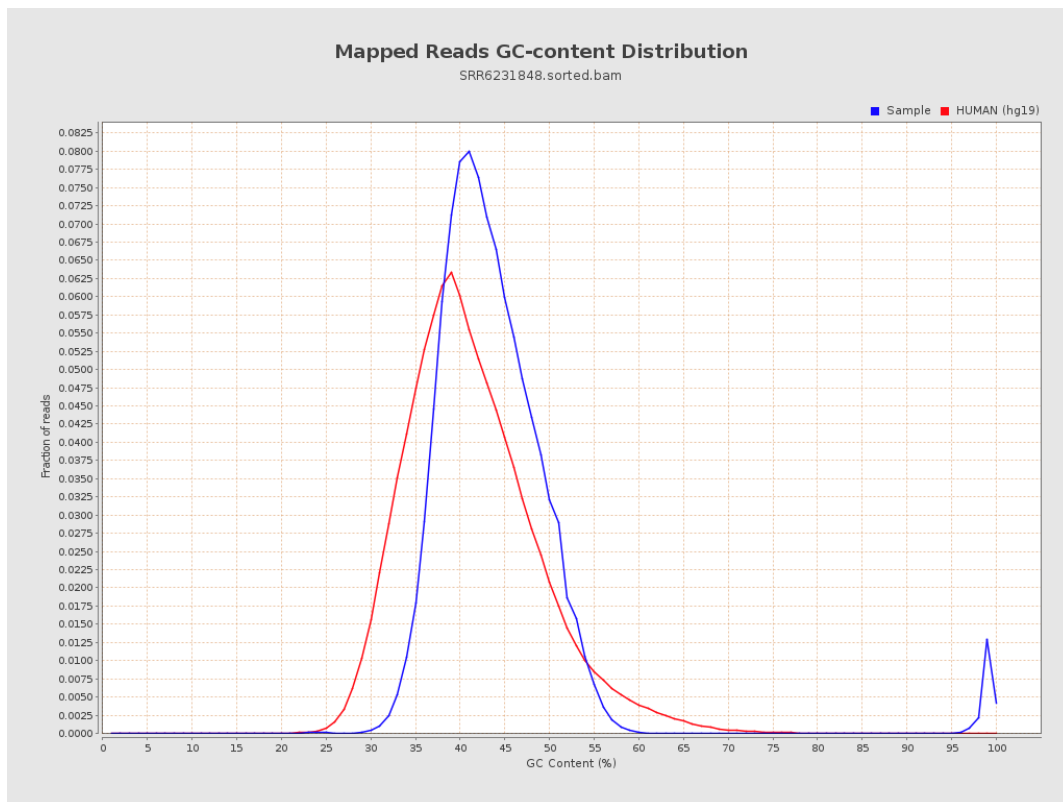
7. Results : Duplication Rate Histogram



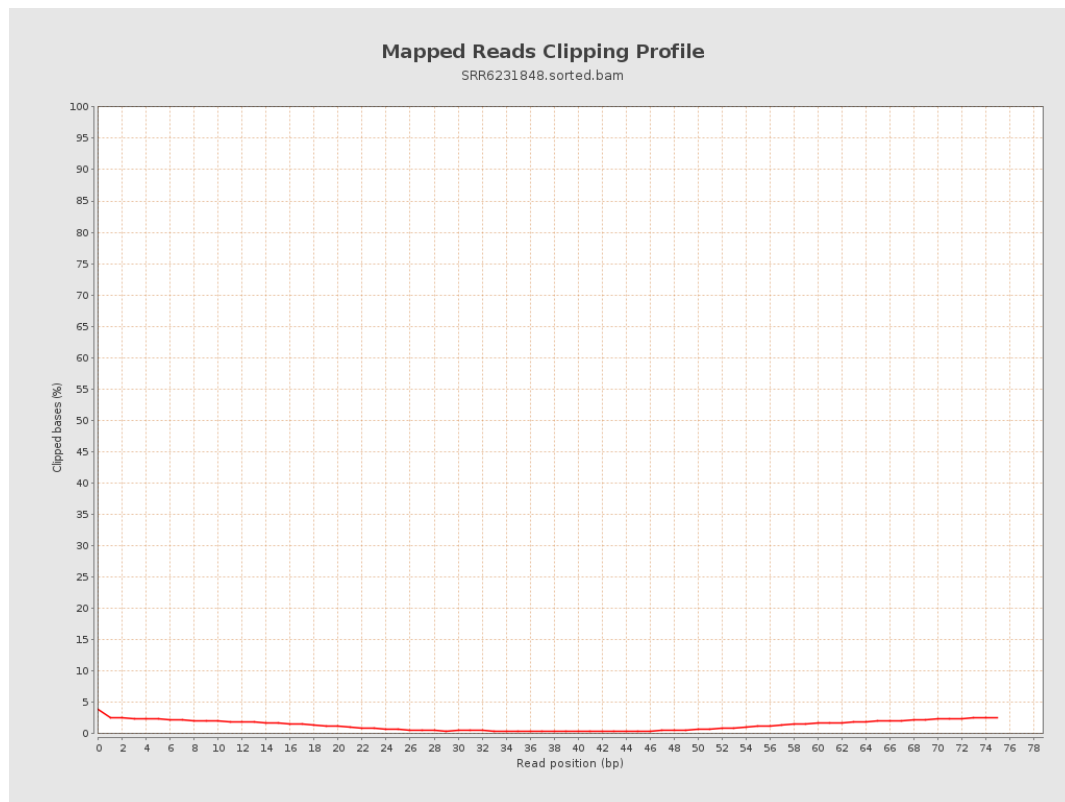
8. Results : Mapped Reads Nucleotide Content



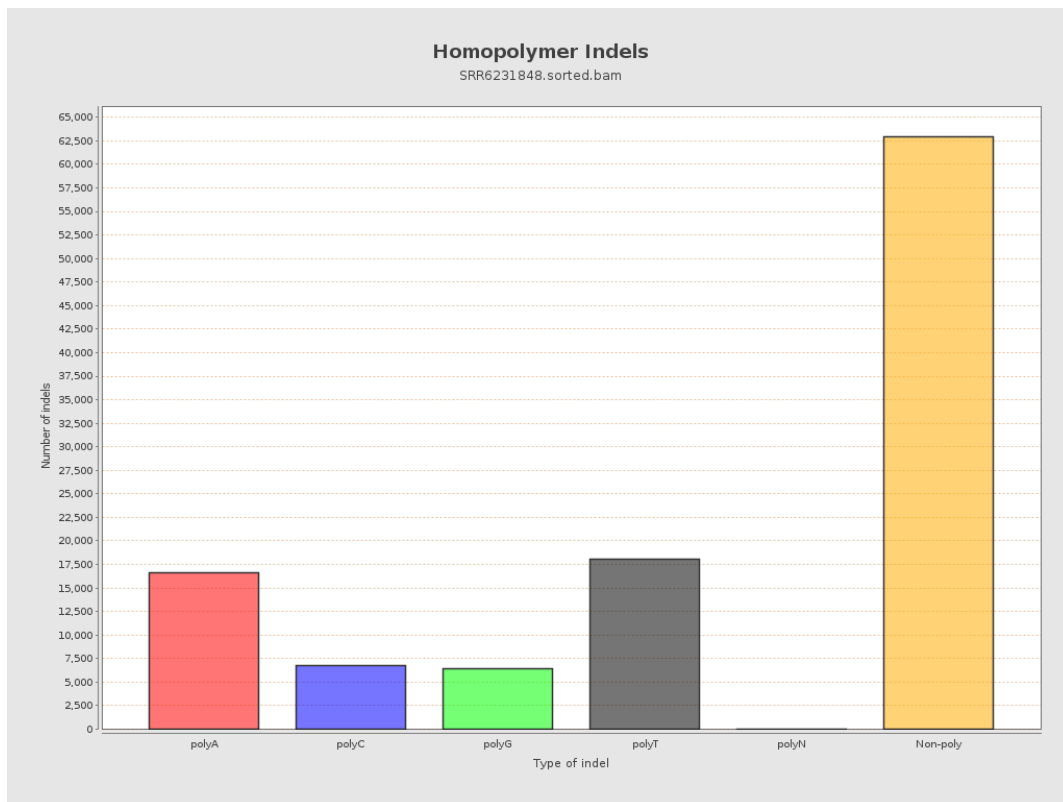
9. Results : Mapped Reads GC-content Distribution



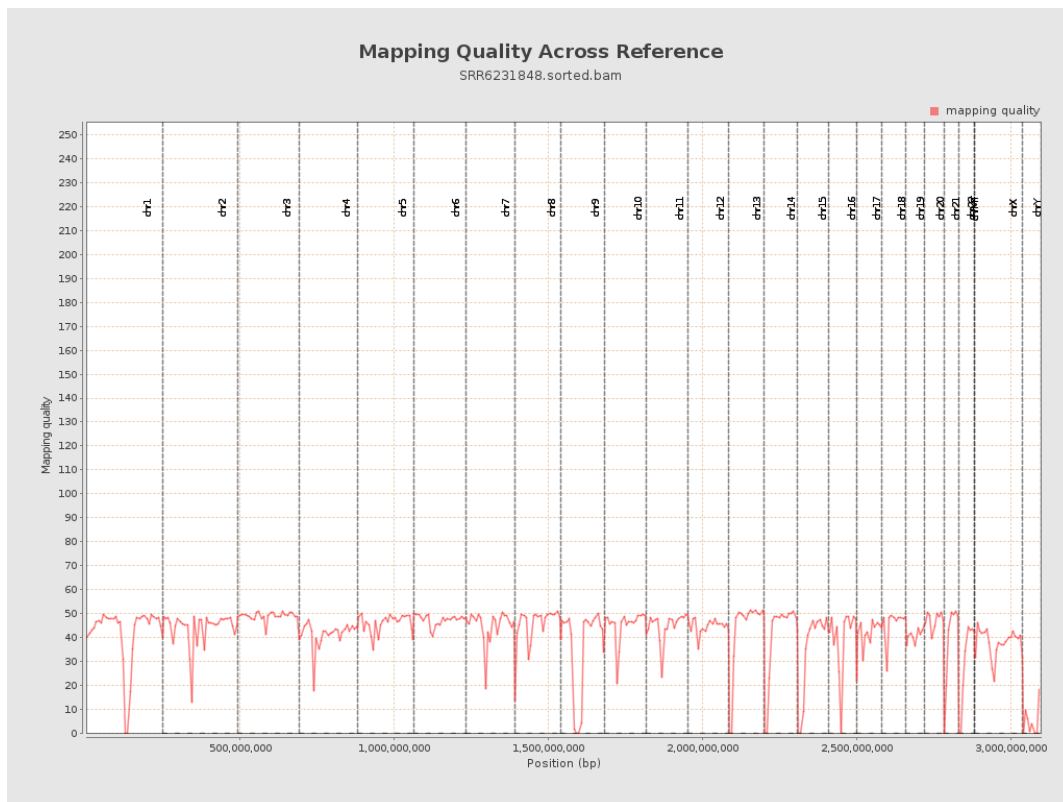
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

