

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237811.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_SRR6237811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,455,026
Mapped reads	1,341,361 / 38.82%
Unmapped reads	2,113,665 / 61.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,125 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	56,557 / 1.64%
Duplication rate	2.9%
Clipped reads	1,040,777 / 30.12%

2.2. ACGT Content

Number/percentage of A's	20,056,993 / 25.85%
Number/percentage of C's	14,517,038 / 18.71%
Number/percentage of T's	23,529,809 / 30.33%
Number/percentage of G's	19,418,199 / 25.03%
Number/percentage of N's	61,425 / 0.08%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2474
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2.4. Mapping Quality

Mean Mapping Quality	40.16
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2.5. Mismatches and indels

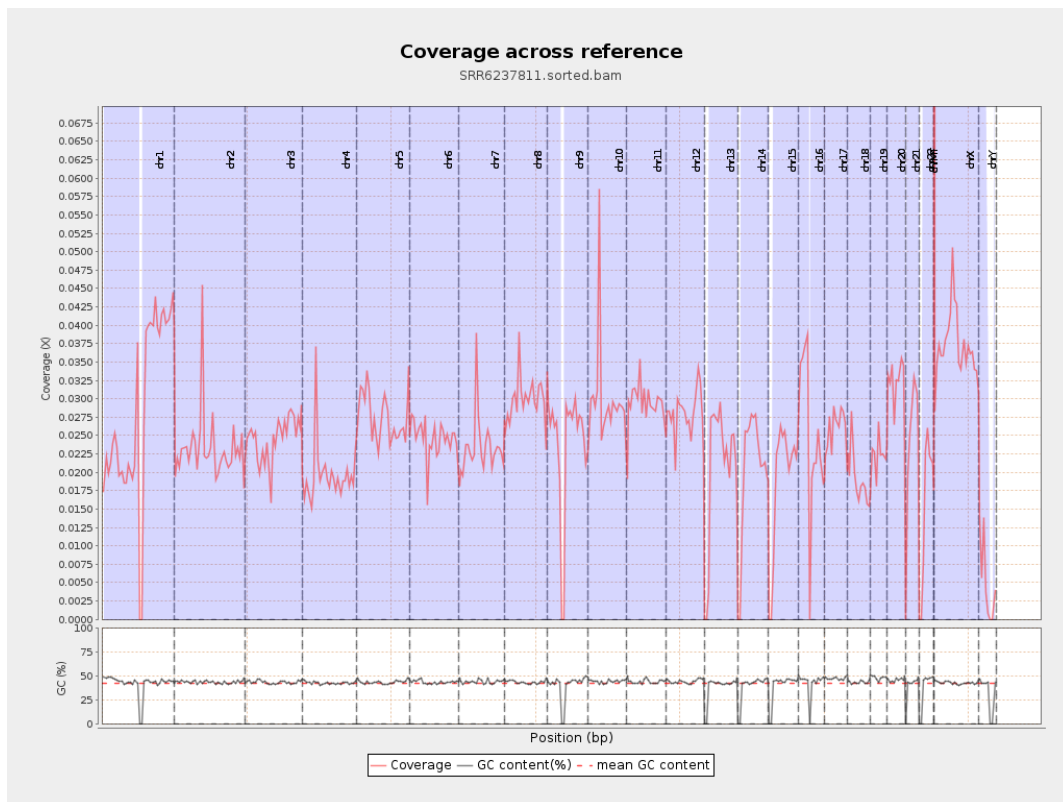
General error rate	0.91%
Mismatches	695,354
Insertions	6,622
Mapped reads with at least one insertion	0.49%
Deletions	22,770
Mapped reads with at least one deletion	1.68%
Homopolymer indels	44.85%

2.6. Chromosome stats

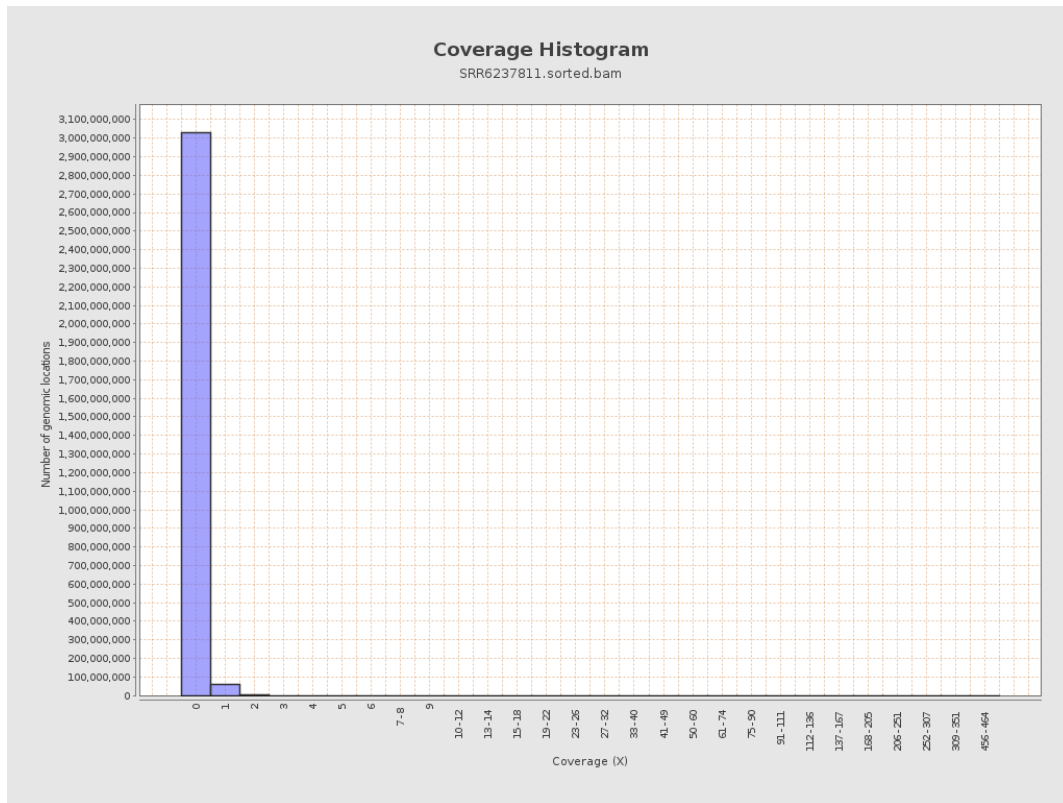
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7099897	0.0285	0.3314
chr2	243199373	5660612	0.0233	0.3314
chr3	198022430	4860211	0.0245	0.1861
chr4	191154276	3755152	0.0196	0.1786
chr5	180915260	4962528	0.0274	0.1867
chr6	171115067	4207027	0.0246	0.2085
chr7	159138663	3723346	0.0234	0.2953

chr8	146364022	4365278	0.0298	0.2389
chr9	141213431	3355654	0.0238	0.2533
chr10	135534747	4043128	0.0298	0.3324
chr11	135006516	4006690	0.0297	0.256
chr12	133851895	3748838	0.028	0.197
chr13	115169878	2384064	0.0207	0.1688
chr14	107349540	2185201	0.0204	0.1834
chr15	102531392	1938364	0.0189	0.1642
chr16	90354753	2258970	0.025	0.211
chr17	81195210	2107041	0.026	0.2089
chr18	78077248	1484213	0.019	0.3754
chr19	59128983	1317455	0.0223	0.2616
chr20	63025520	2029462	0.0322	0.2131
chr21	48129895	1184409	0.0246	0.1957
chr22	51304566	812667	0.0158	0.144
chrMT	16571	35326	2.1318	2.3985
chrX	155270560	5808008	0.0374	0.2452
chrY	59373566	286967	0.0048	0.1116

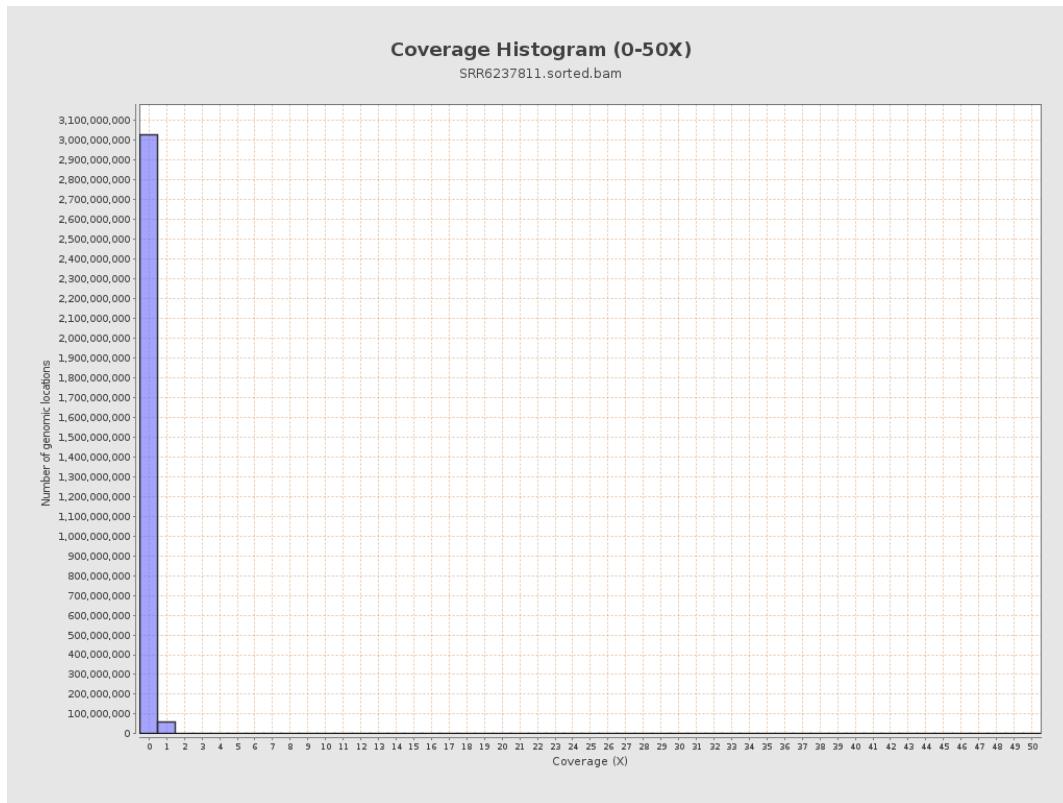
3. Results : Coverage across reference



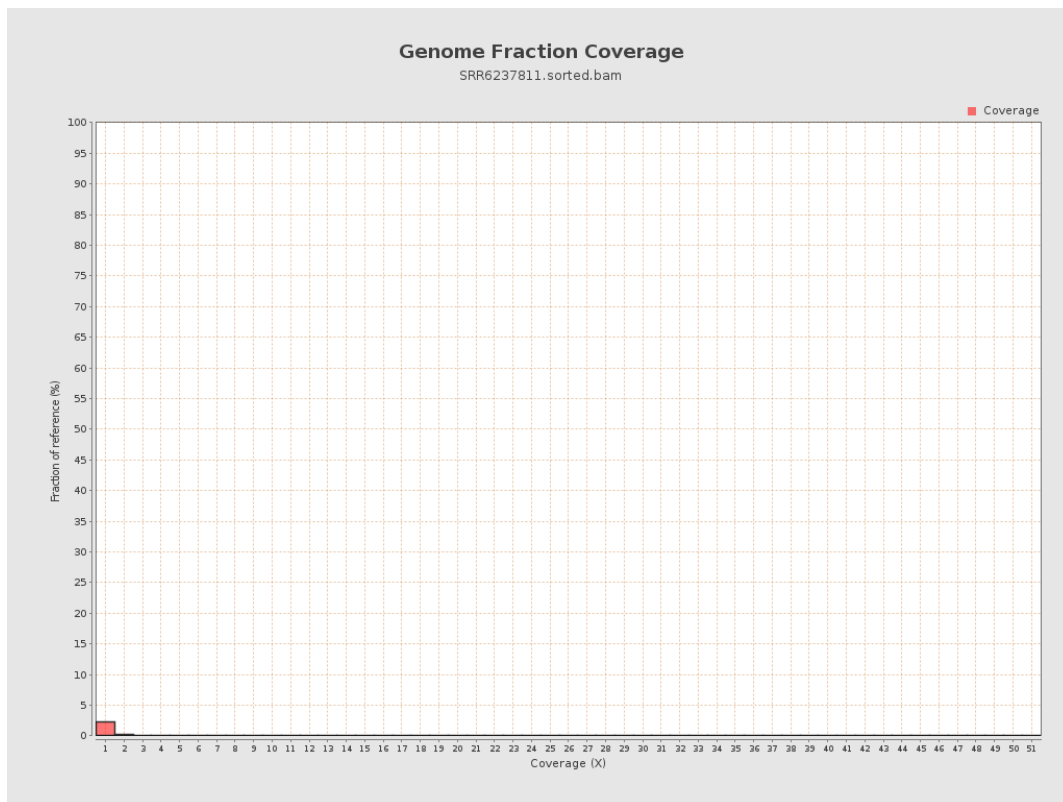
4. Results : Coverage Histogram



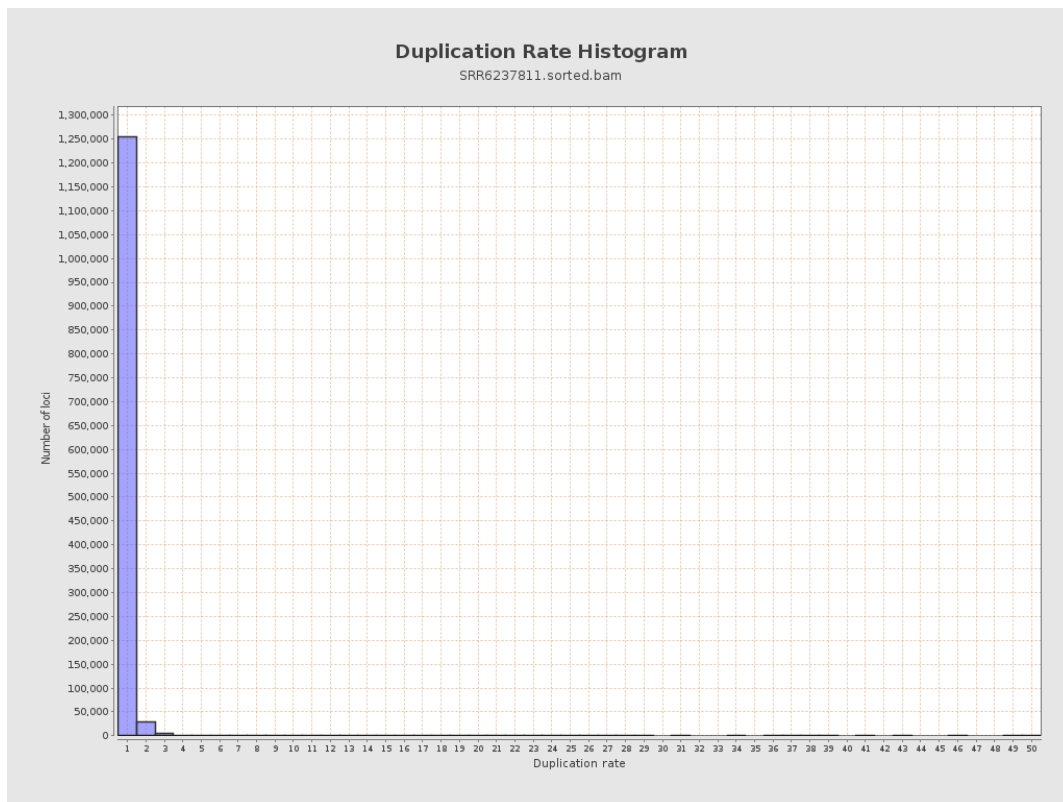
5. Results : Coverage Histogram (0-50X)



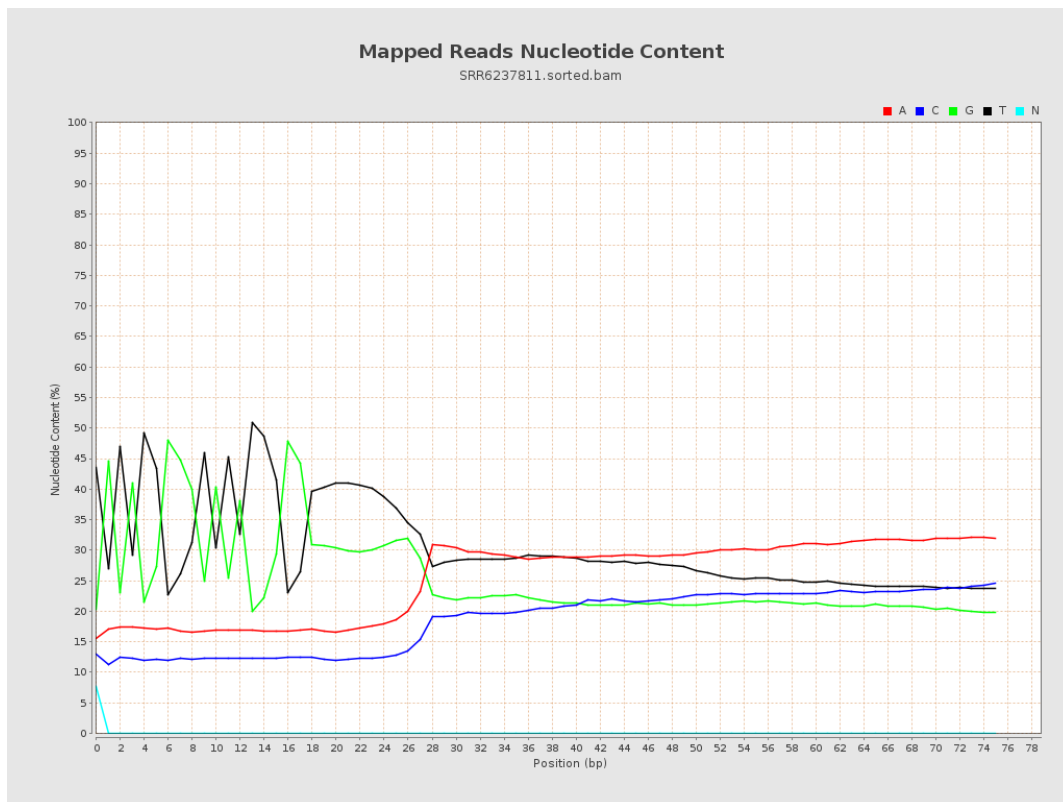
6. Results : Genome Fraction Coverage



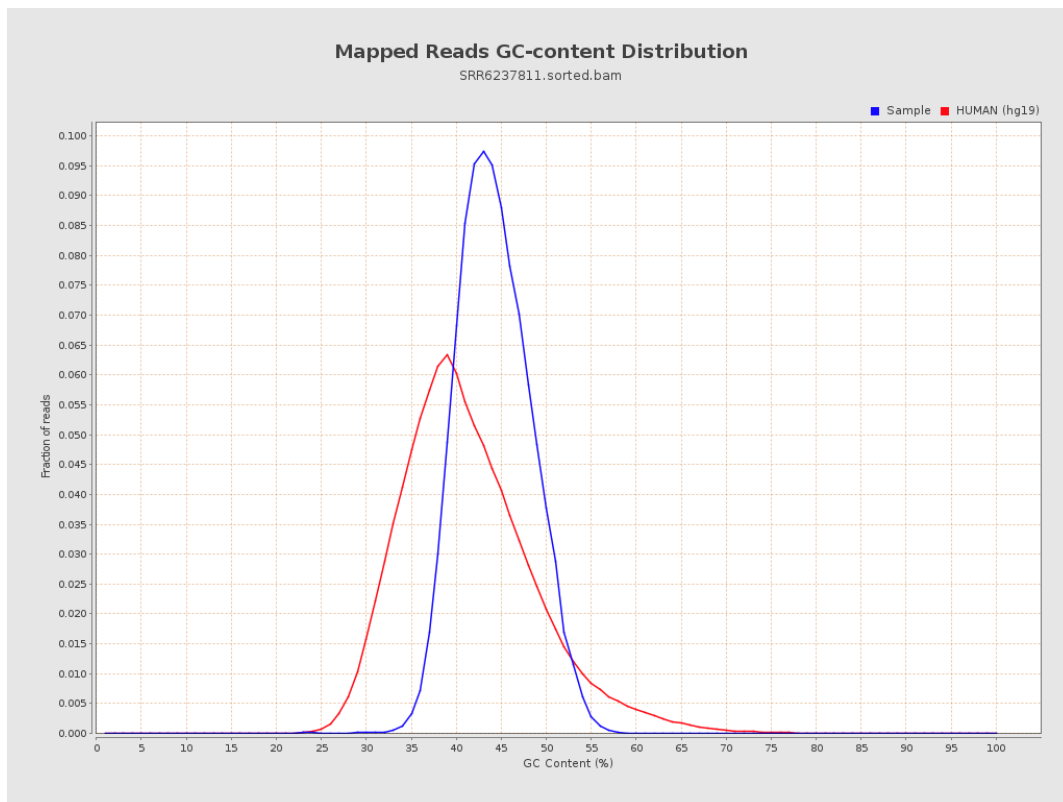
7. Results : Duplication Rate Histogram



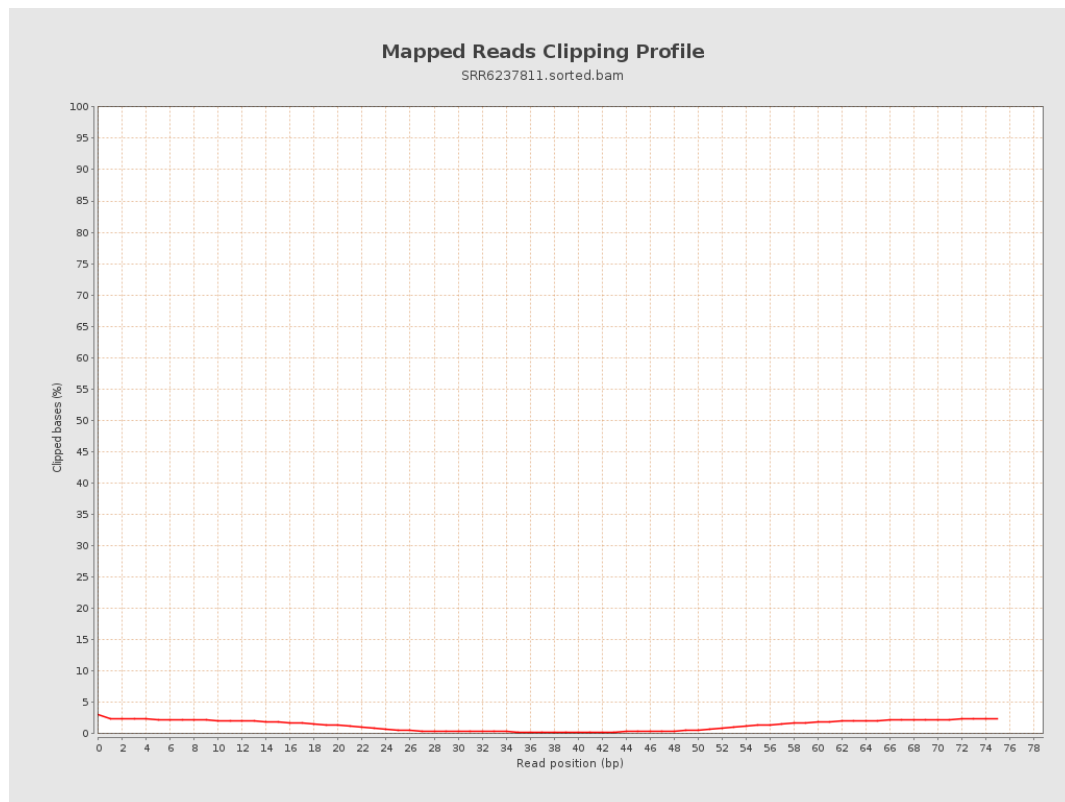
8. Results : Mapped Reads Nucleotide Content



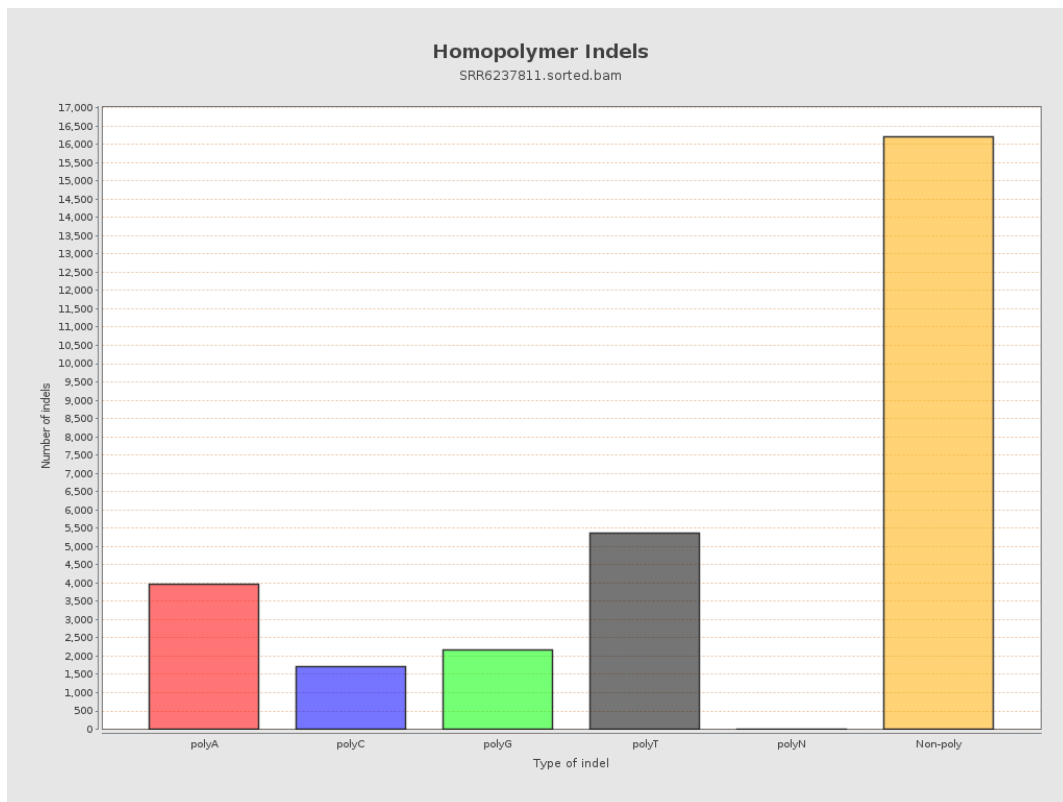
9. Results : Mapped Reads GC-content Distribution



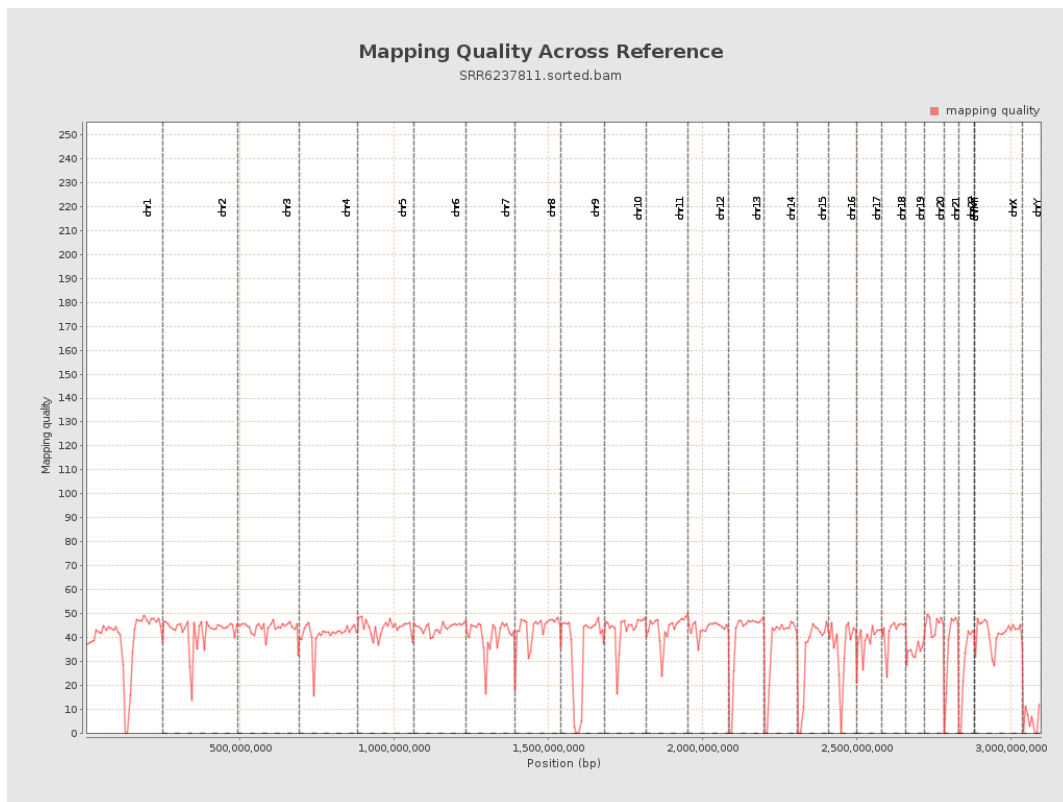
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

