Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:35:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237805.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_SRR6237805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:35:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,702,219
Mapped reads	1,461,487 / 54.08%
Unmapped reads	1,240,732 / 45.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,057 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	101,296 / 3.75%
Duplication rate	5.64%
Clipped reads	899,853 / 33.3%

2.2. ACGT Content

Number/percentage of A's	24,505,572 / 27.13%
Number/percentage of C's	17,861,074 / 19.78%
Number/percentage of T's	27,210,391 / 30.13%
Number/percentage of G's	20,656,383 / 22.87%
Number/percentage of N's	77,348 / 0.09%
GC Percentage	42.65%

2.3. Coverage

Mean	0.0292

Standard Deviation	0.2996

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

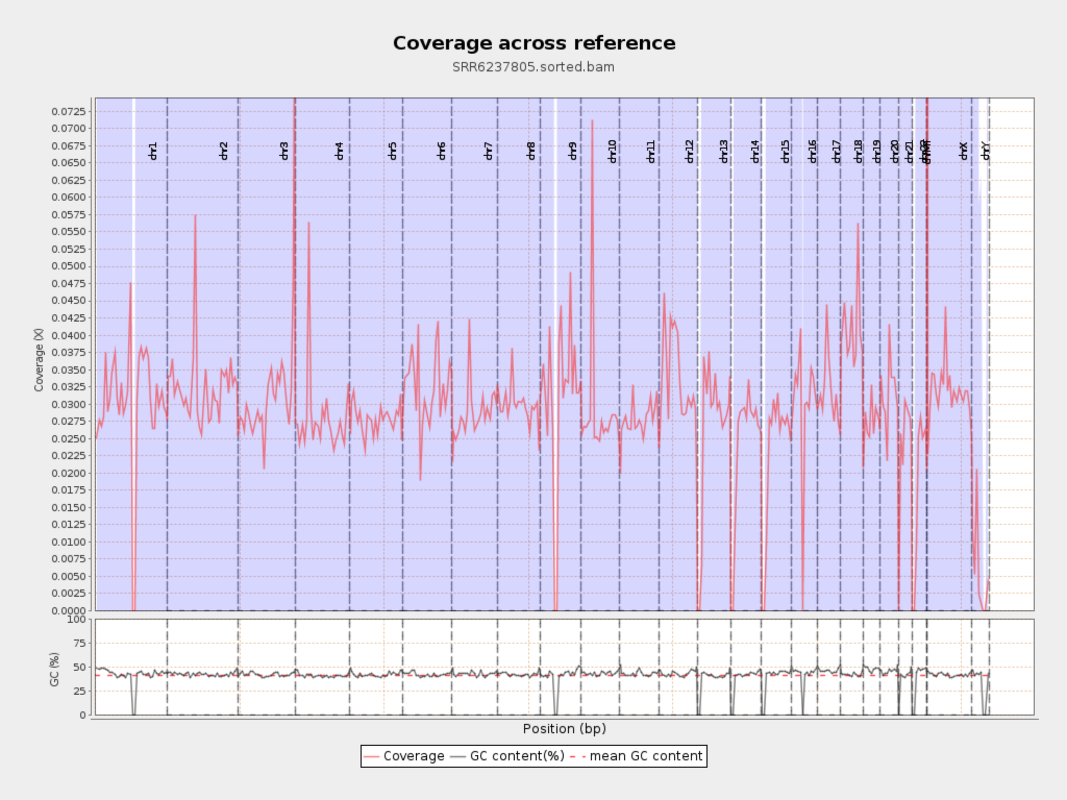
General error rate	0.81%
Mismatches	719,443
Insertions	7,004
Mapped reads with at least one insertion	0.48%
Deletions	19,940
Mapped reads with at least one deletion	1.35%
Homopolymer indels	46.14%

2.6. Chromosome stats

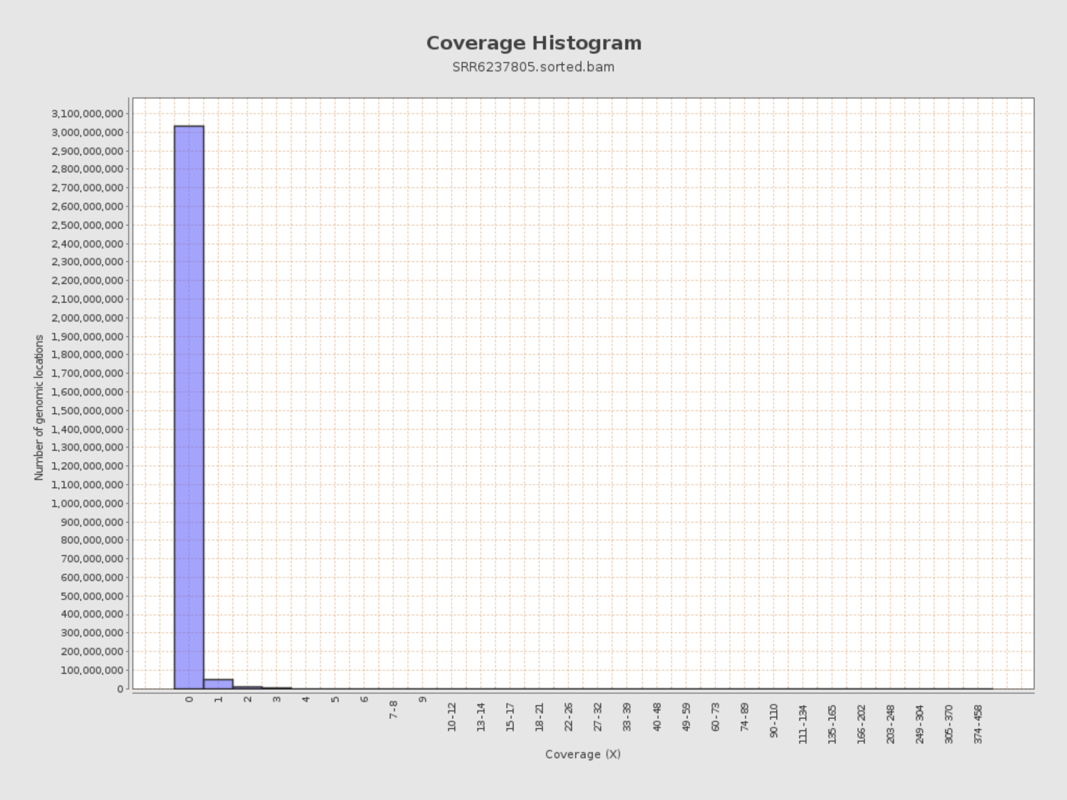
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7474326	0.03	0.3969
chr2	243199373	7882230	0.0324	0.3954
chr3	198022430	6092421	0.0308	0.2381
chr4	191154276	5366878	0.0281	0.2559
chr5	180915260	5062657	0.028	0.2236
chr6	171115067	5521778	0.0323	0.282
chr7	159138663	4569576	0.0287	0.3001

chr8	146364022	4361411	0.0298	0.3052
chr9	141213431	4359860	0.0309	0.3158
chr10	135534747	3945785	0.0291	0.3969
chr11	135006516	3768762	0.0279	0.263
chr12	133851895	4527052	0.0338	0.2512
chr13	115169878	2998318	0.026	0.2165
chr14	107349540	2566936	0.0239	0.2261
chr15	102531392	2323737	0.0227	0.1986
chr16	90354753	2673650	0.0296	0.2578
chr17	81195210	2585733	0.0318	0.251
chr18	78077248	3223229	0.0413	0.4885
chr19	59128983	1629409	0.0276	0.3364
chr20	63025520	1995322	0.0317	0.256
chr21	48129895	1169494	0.0243	0.2383
chr22	51304566	925490	0.018	0.1792
chrMT	16571	35384	2.1353	2.0829
chrX	155270560	4960897	0.032	0.2661
chrY	59373566	323480	0.0054	0.177

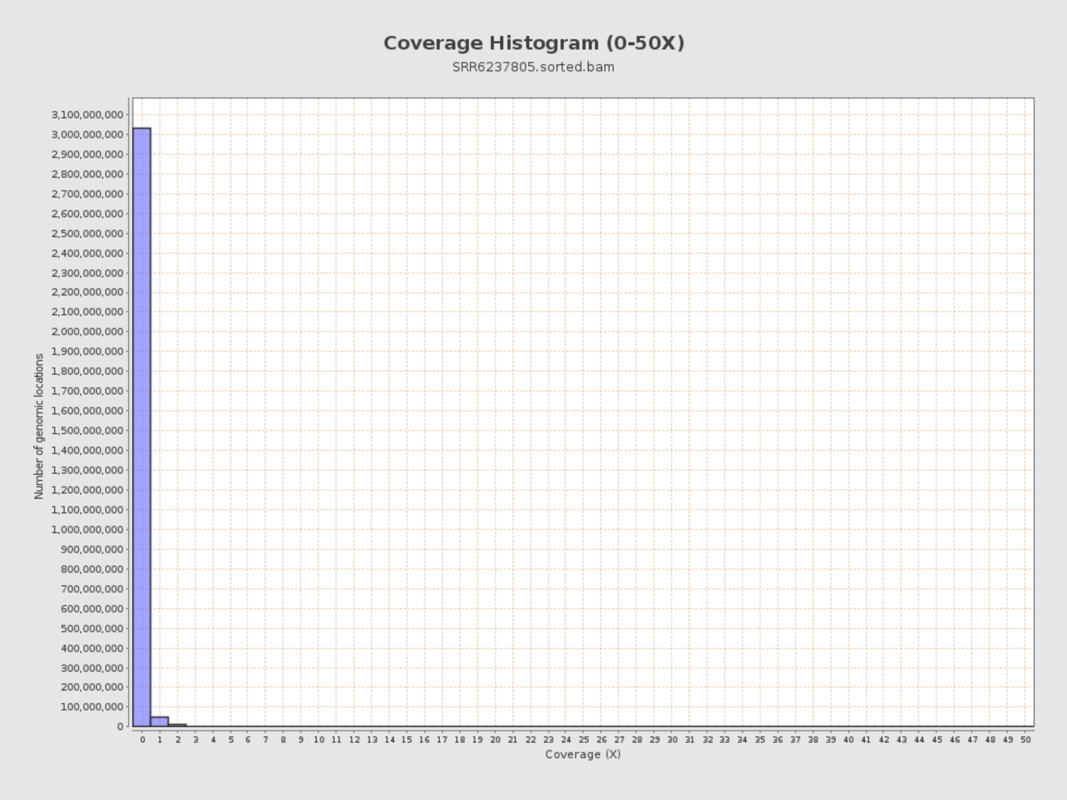
3. Results : Coverage across reference



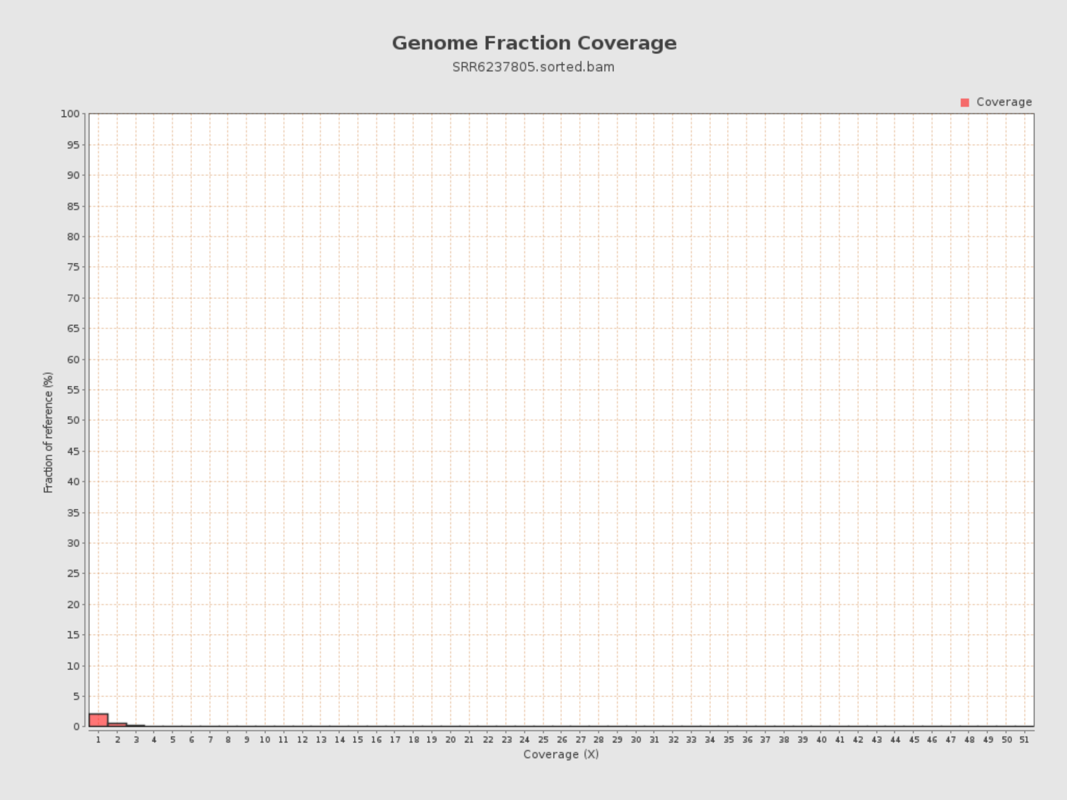
4. Results : Coverage Histogram



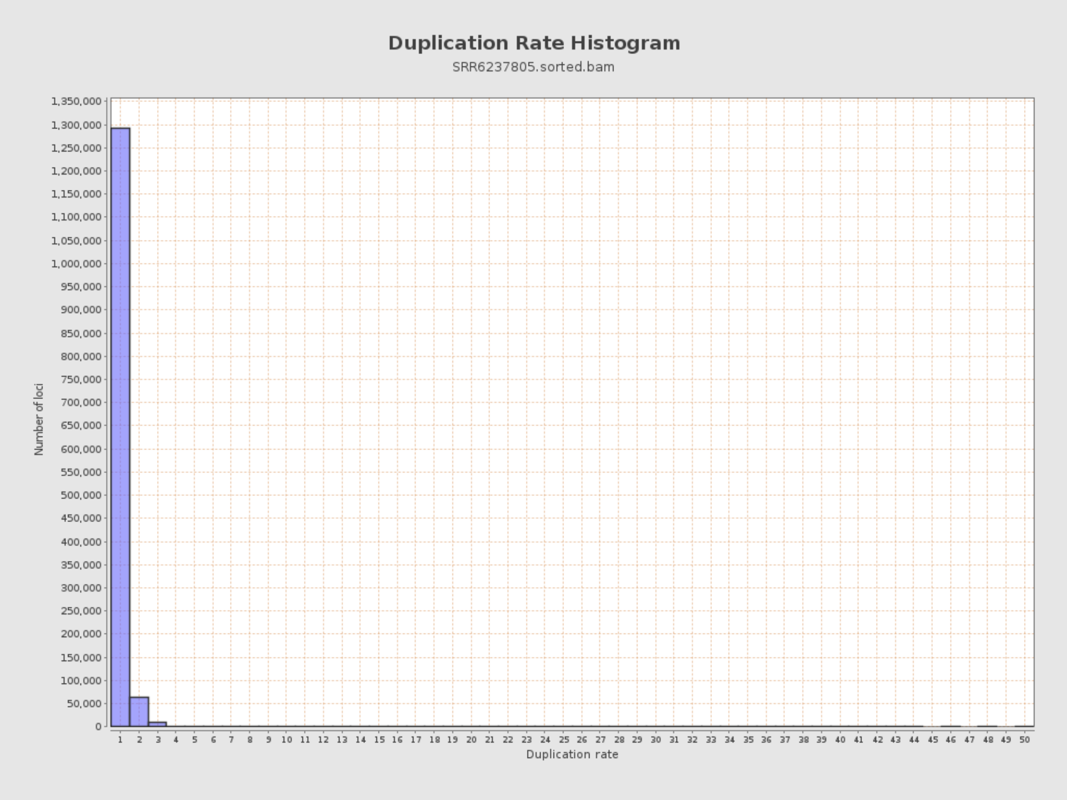
5. Results : Coverage Histogram (0-50X)



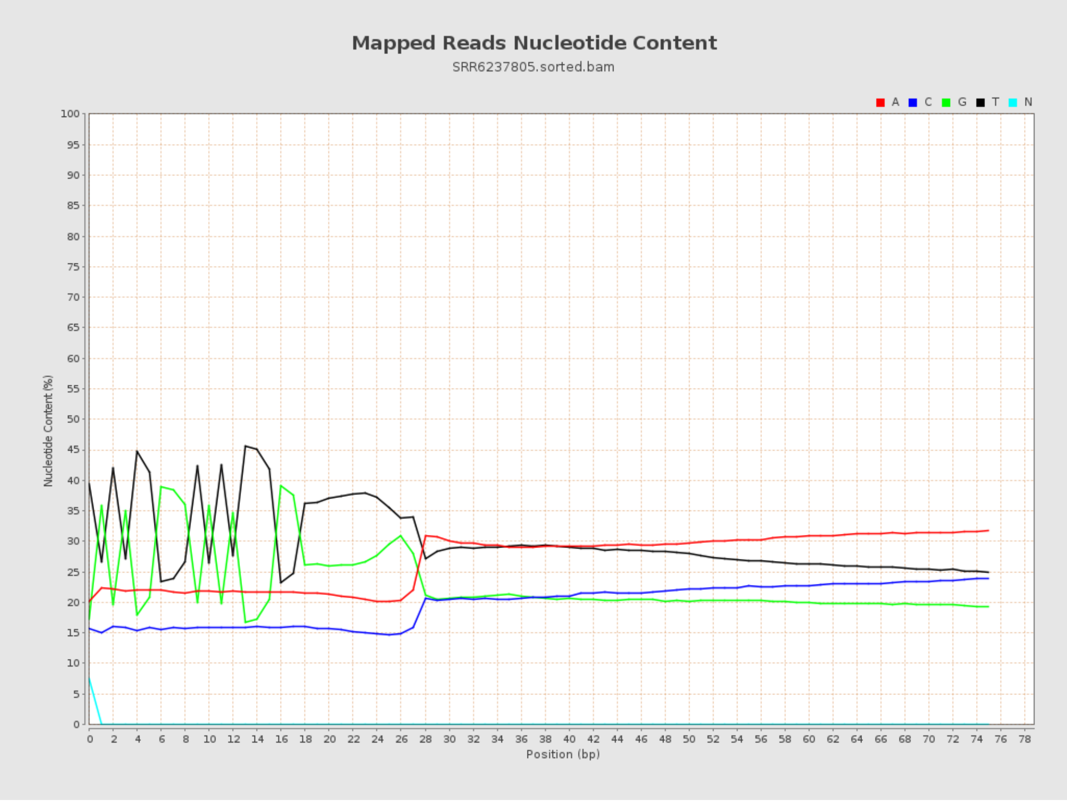
6. Results : Genome Fraction Coverage



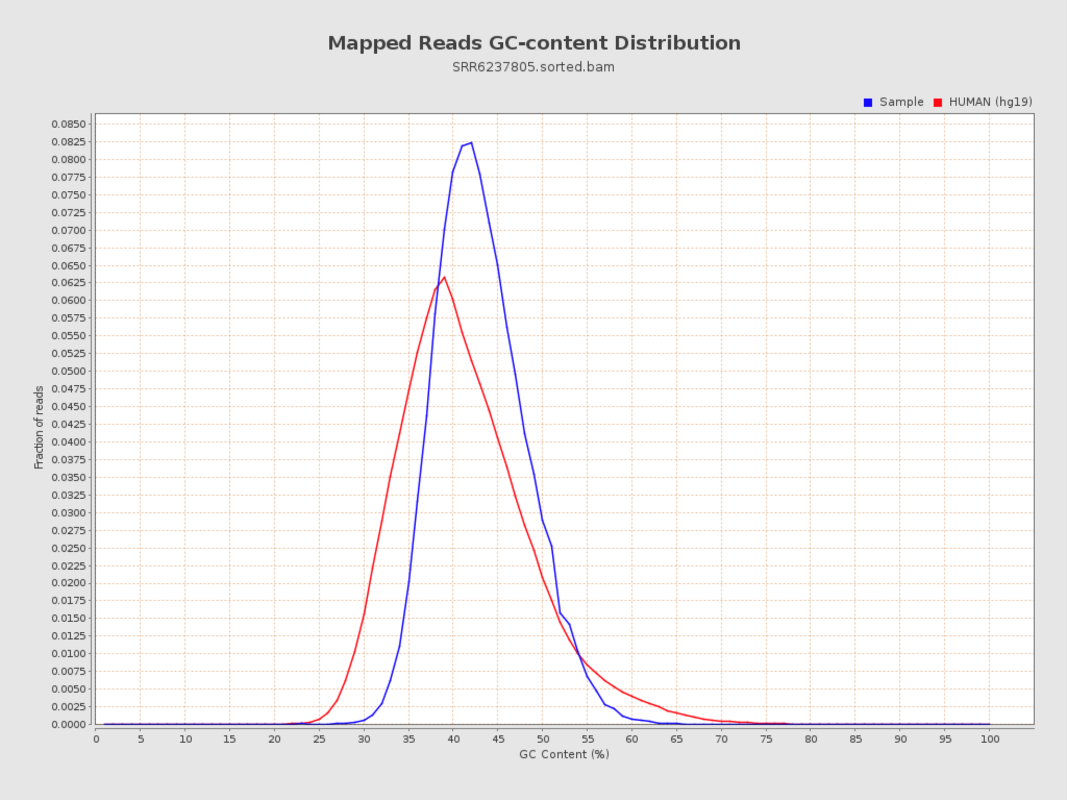
7. Results : Duplication Rate Histogram



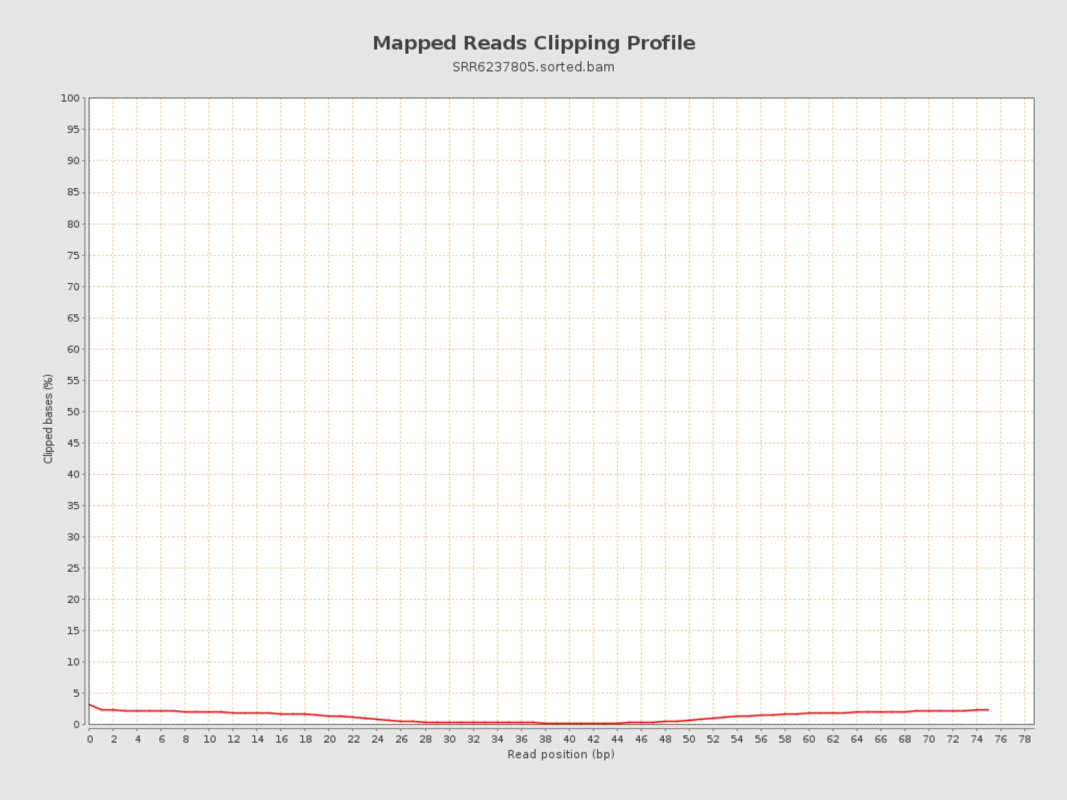
8. Results : Mapped Reads Nucleotide Content



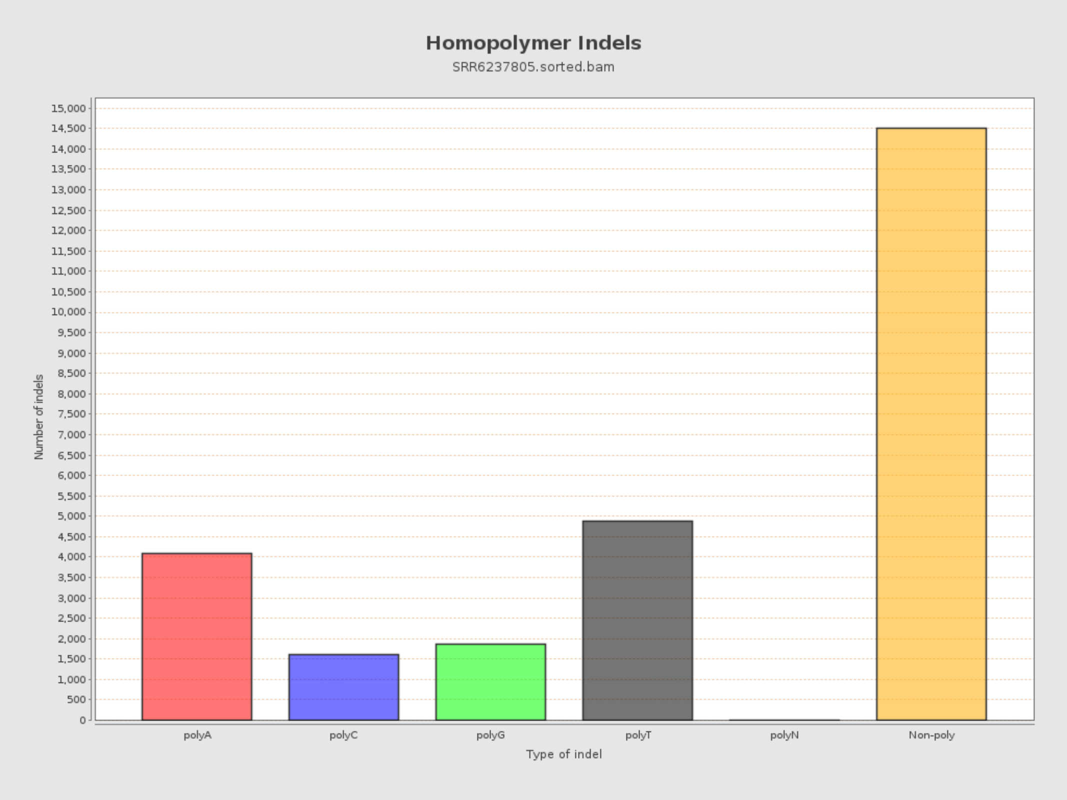
9. Results : Mapped Reads GC-content Distribution



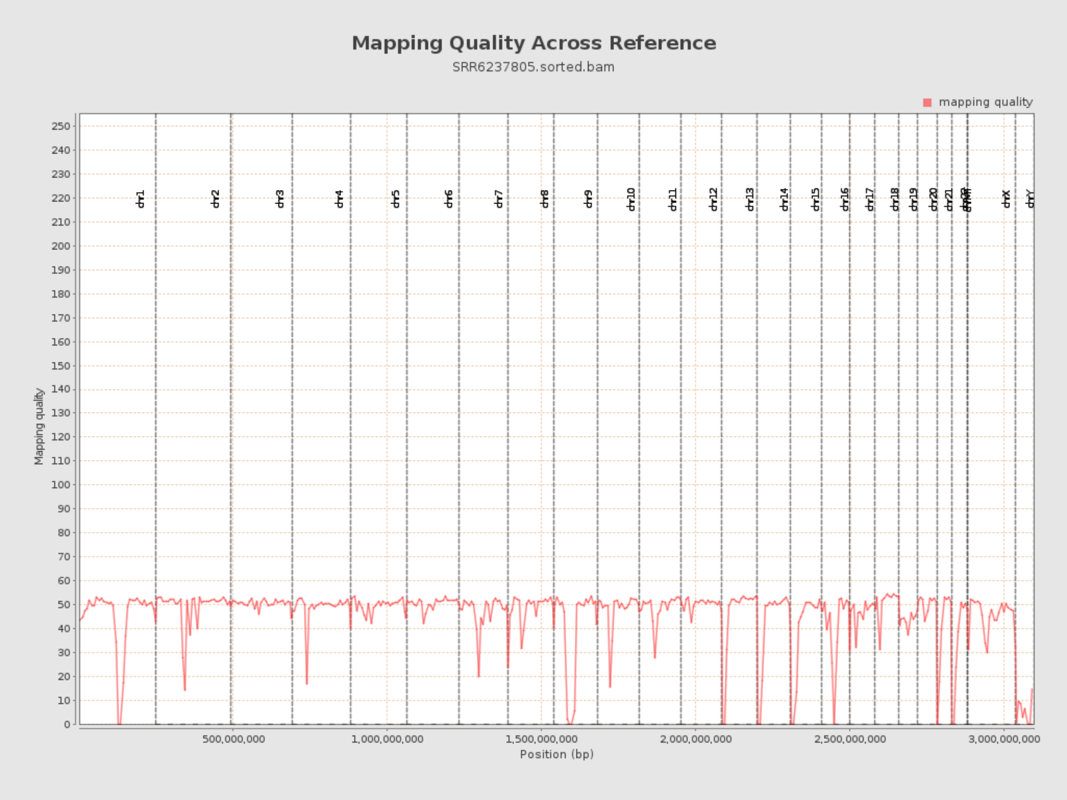
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram