Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:34:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237862.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_SRR6237862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:34:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,265,640
Mapped reads	1,085,494 / 85.77%
Unmapped reads	180,146 / 14.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,108 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	65,683 / 5.19%
Duplication rate	5.22%
Clipped reads	565,616 / 44.69%

2.2. ACGT Content

Number/percentage of A's	18,988,036 / 27.15%
Number/percentage of C's	12,605,972 / 18.02%
Number/percentage of T's	22,519,235 / 32.2%
Number/percentage of G's	15,764,695 / 22.54%
Number/percentage of N's	63,622 / 0.09%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2406

2.4. Mapping Quality

Mean Mapping Quality	47.09

2.5. Mismatches and indels

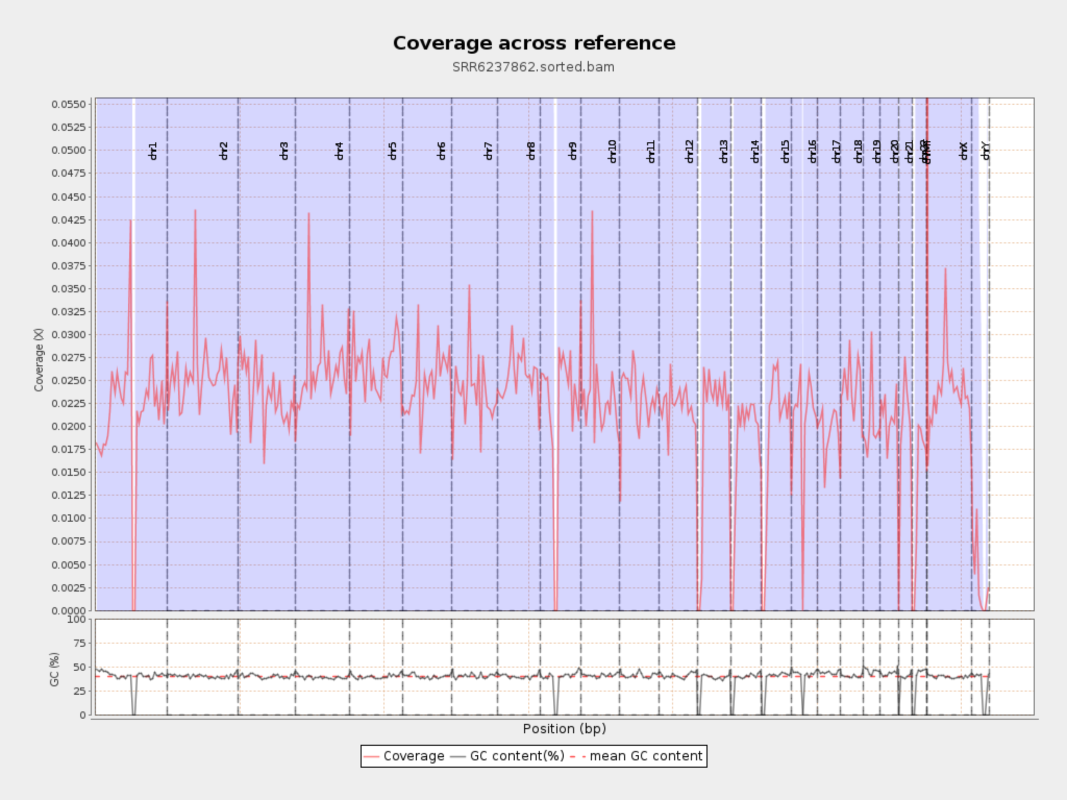
General error rate	0.78%
Mismatches	534,930
Insertions	5,384
Mapped reads with at least one insertion	0.49%
Deletions	15,397
Mapped reads with at least one deletion	1.4%
Homopolymer indels	48.84%

2.6. Chromosome stats

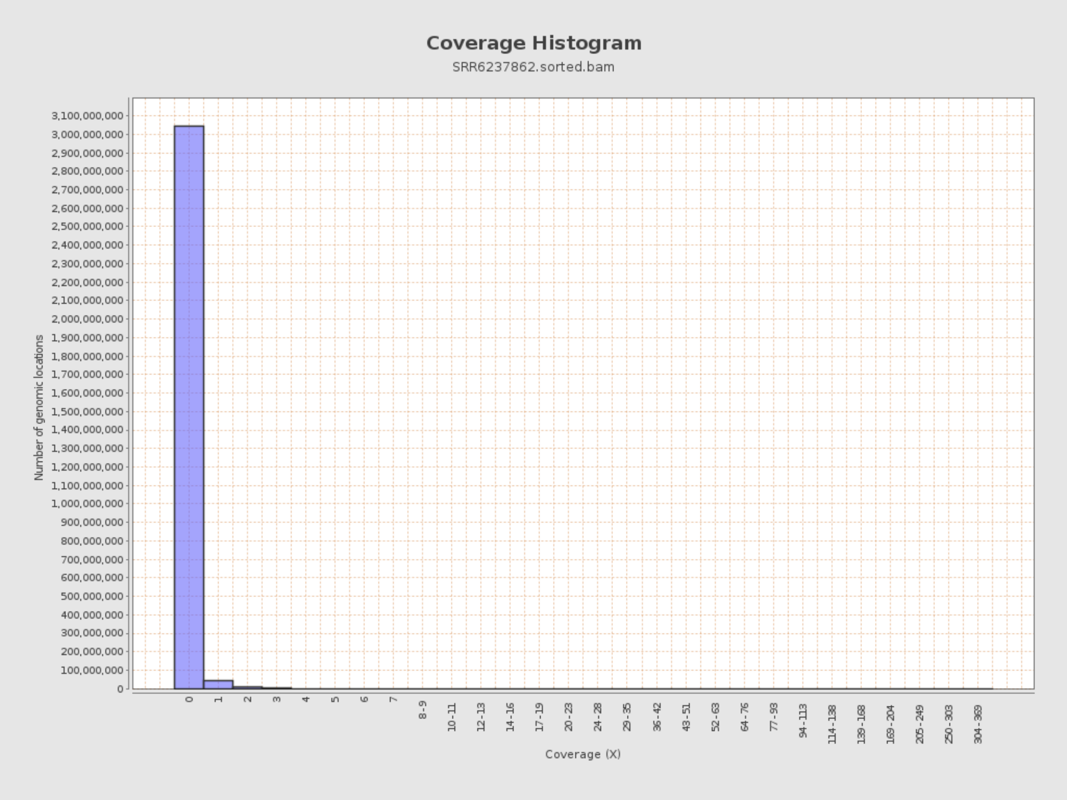
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5418608	0.0217	0.3665
chr2	243199373	6158716	0.0253	0.2589
chr3	198022430	4701074	0.0237	0.194
chr4	191154276	5048838	0.0264	0.2155
chr5	180915260	4842949	0.0268	0.2065
chr6	171115067	4235783	0.0248	0.2175
chr7	159138663	3773350	0.0237	0.2713

chr8	146364022	3741603	0.0256	0.2697
chr9	141213431	3083898	0.0218	0.2311
chr10	135534747	3154216	0.0233	0.2567
chr11	135006516	3150933	0.0233	0.2197
chr12	133851895	2973049	0.0222	0.188
chr13	115169878	2276878	0.0198	0.1765
chr14	107349540	1869065	0.0174	0.1718
chr15	102531392	1943716	0.019	0.1723
chr16	90354753	1839530	0.0204	0.1915
chr17	81195210	1569891	0.0193	0.1892
chr18	78077248	1909073	0.0245	0.3442
chr19	59128983	1198830	0.0203	0.3058
chr20	63025520	1319886	0.0209	0.186
chr21	48129895	932933	0.0194	0.1839
chr22	51304566	675267	0.0132	0.1397
chrMT	16571	231808	13.9888	7.8011
chrX	155270560	3725324	0.024	0.2088
chrY	59373566	192293	0.0032	0.0928

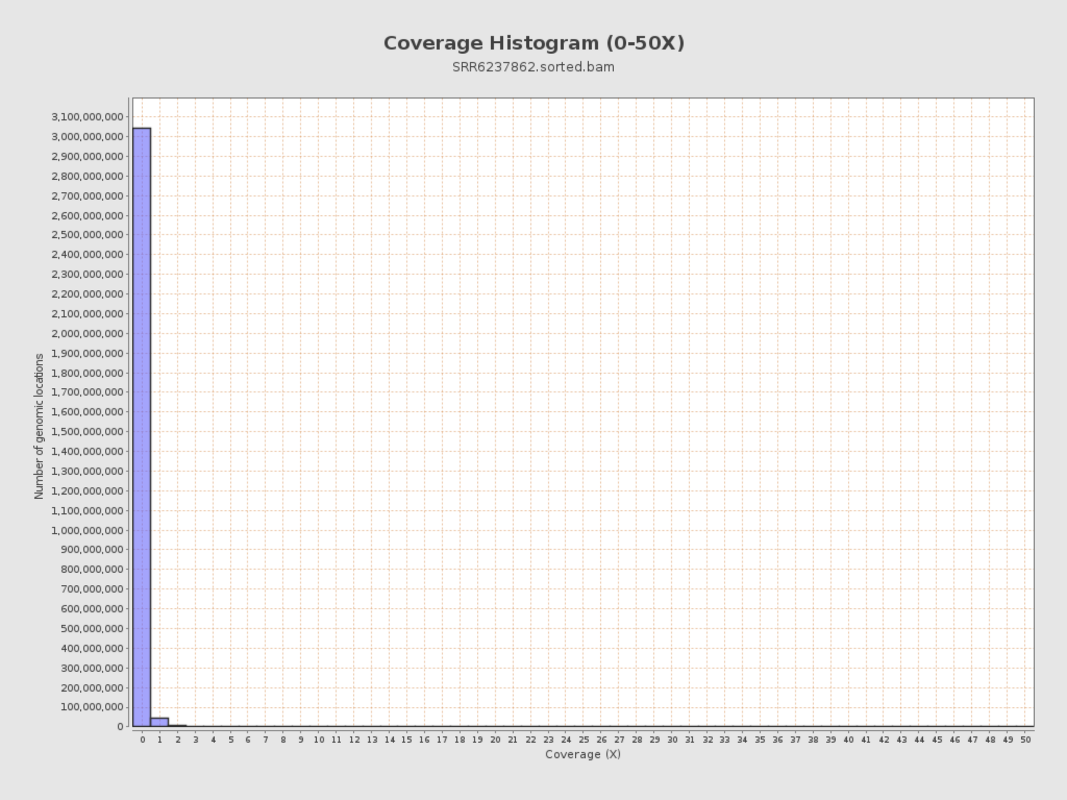
3. Results : Coverage across reference



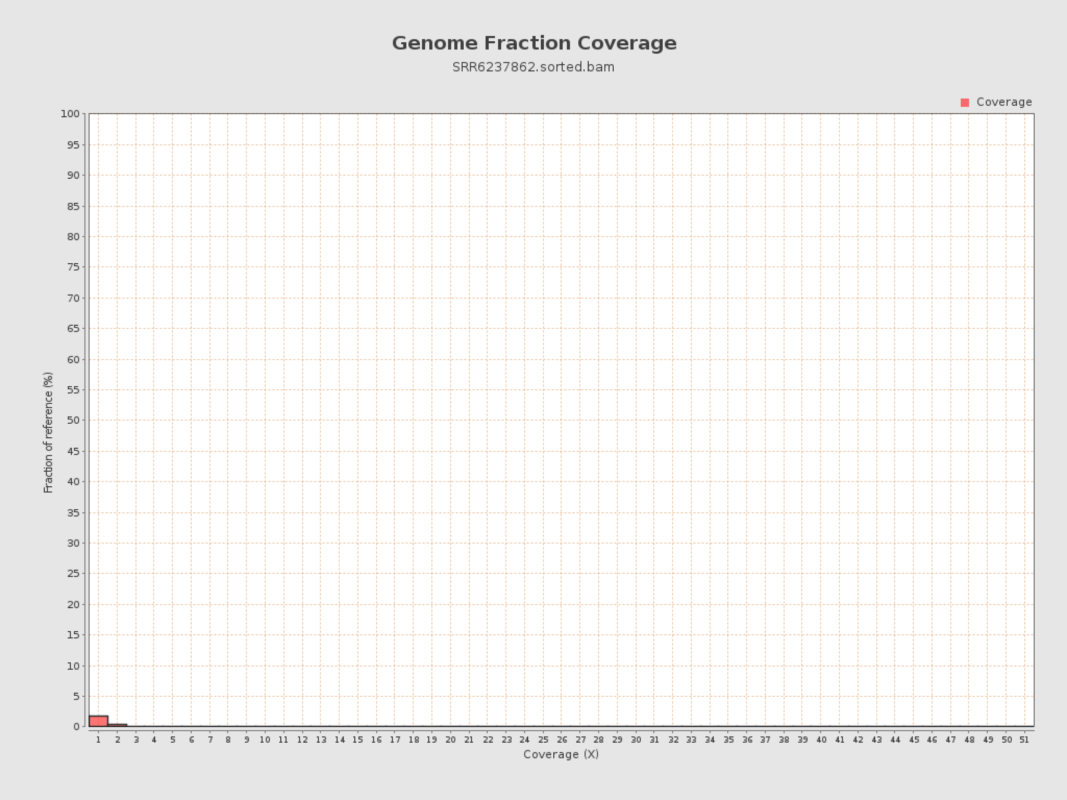
4. Results : Coverage Histogram



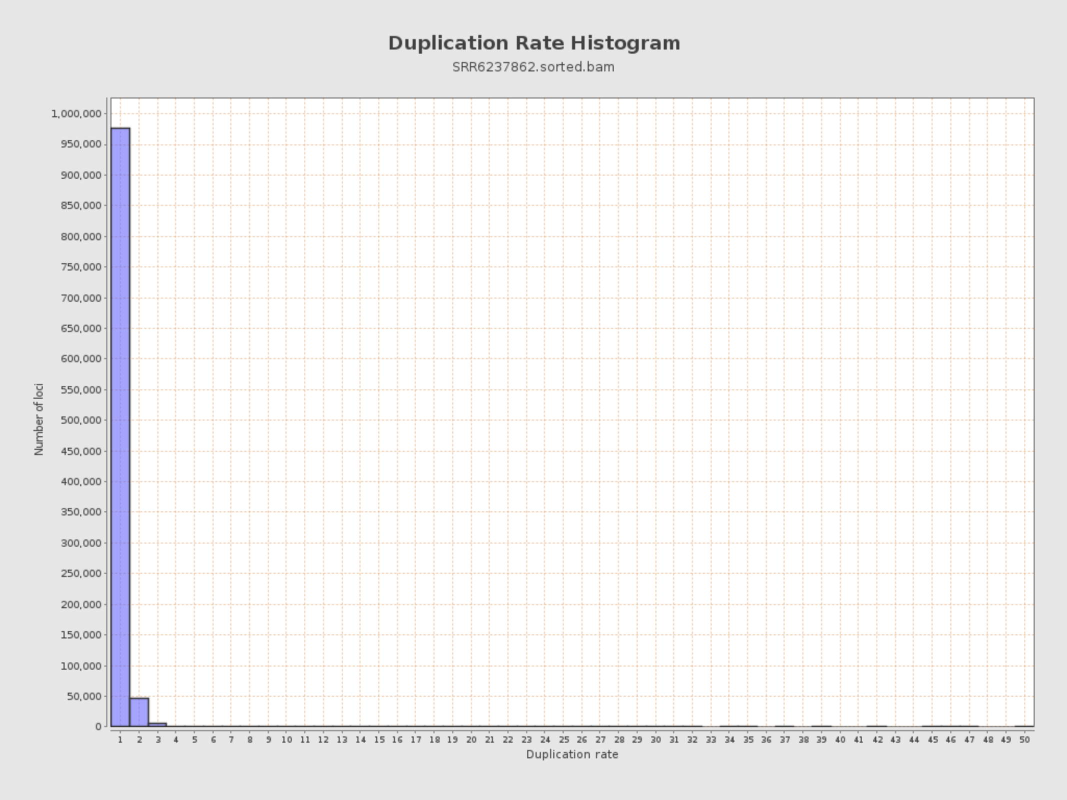
5. Results : Coverage Histogram (0-50X)



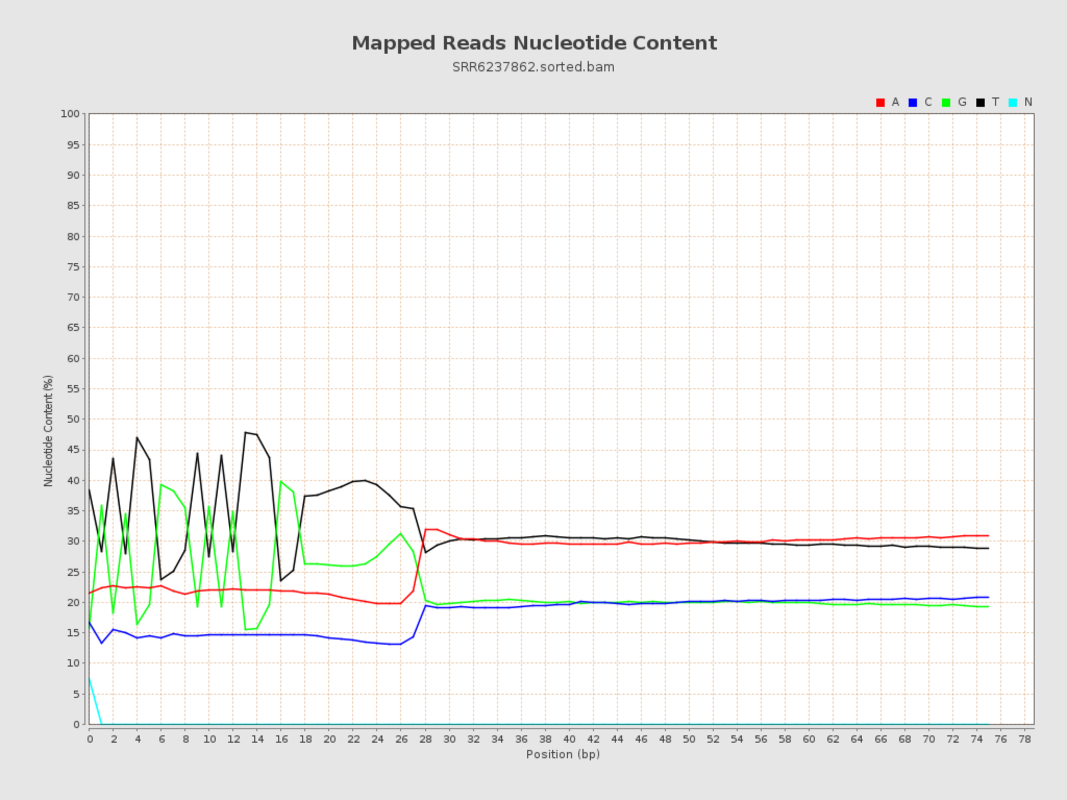
6. Results : Genome Fraction Coverage



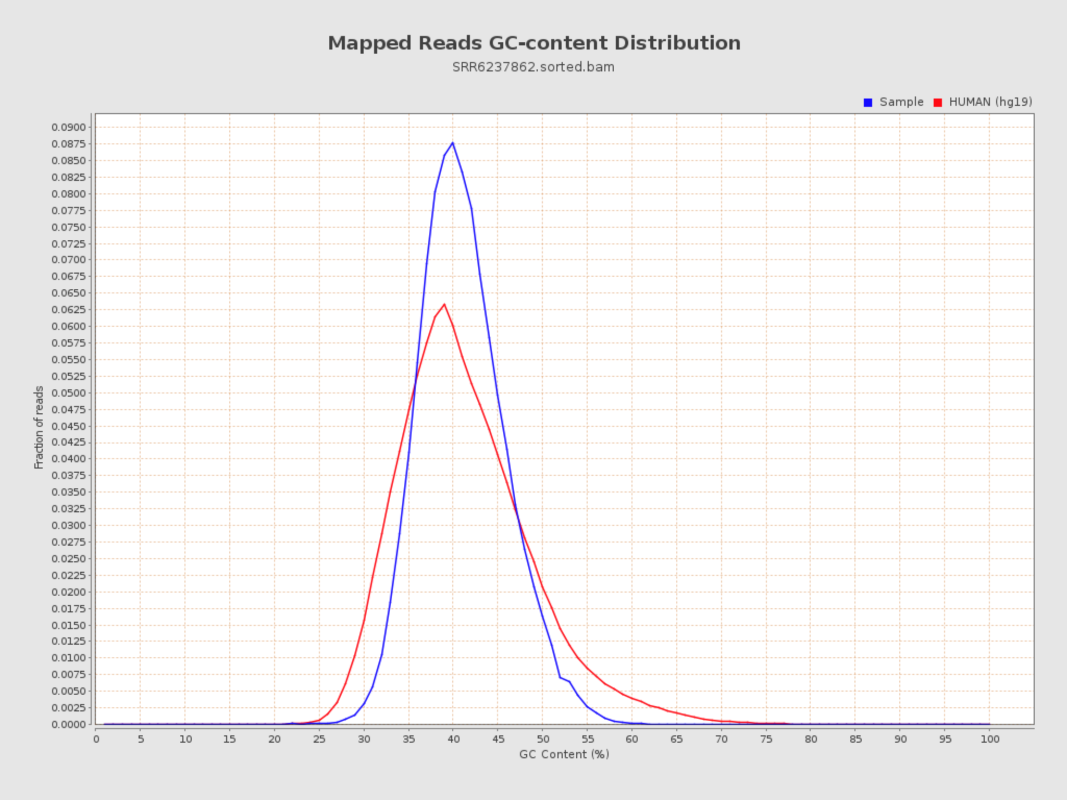
7. Results : Duplication Rate Histogram



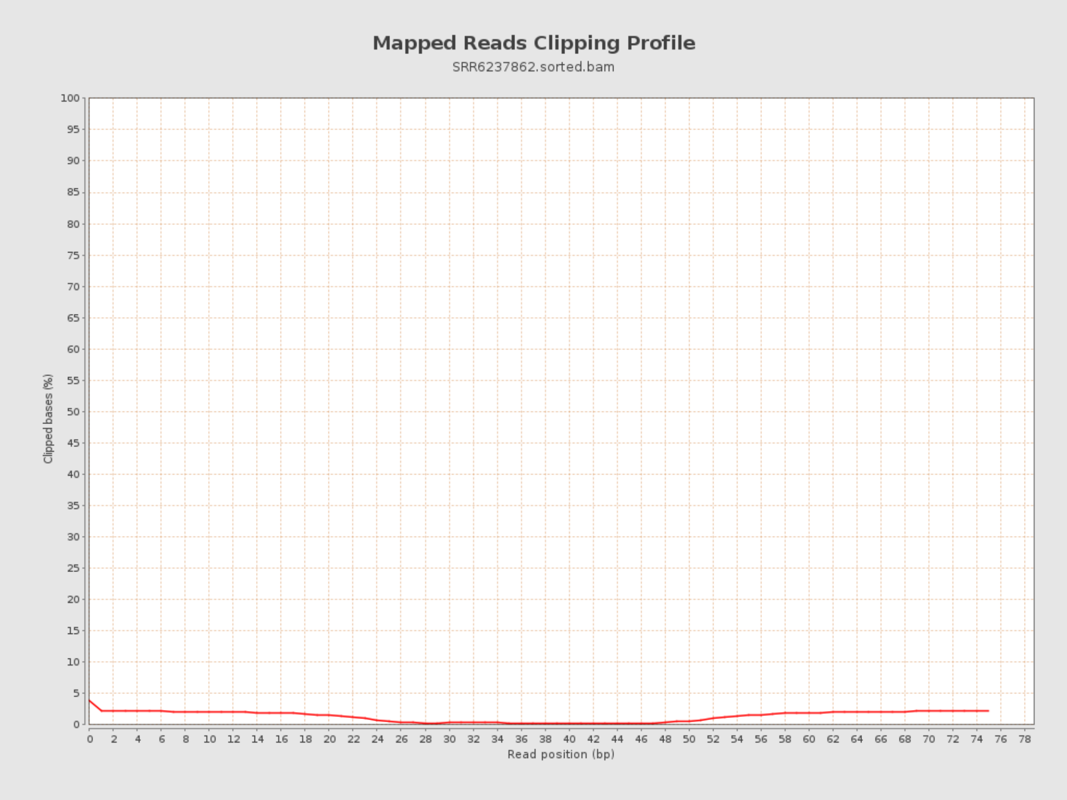
8. Results : Mapped Reads Nucleotide Content



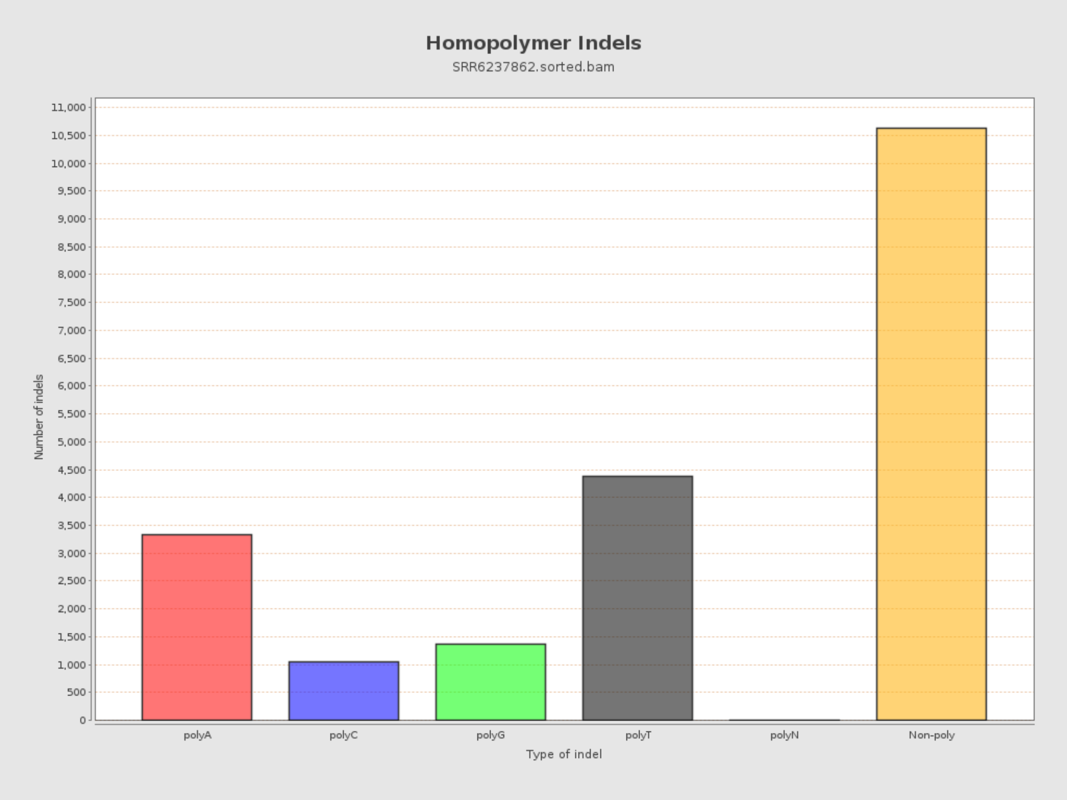
9. Results : Mapped Reads GC-content Distribution



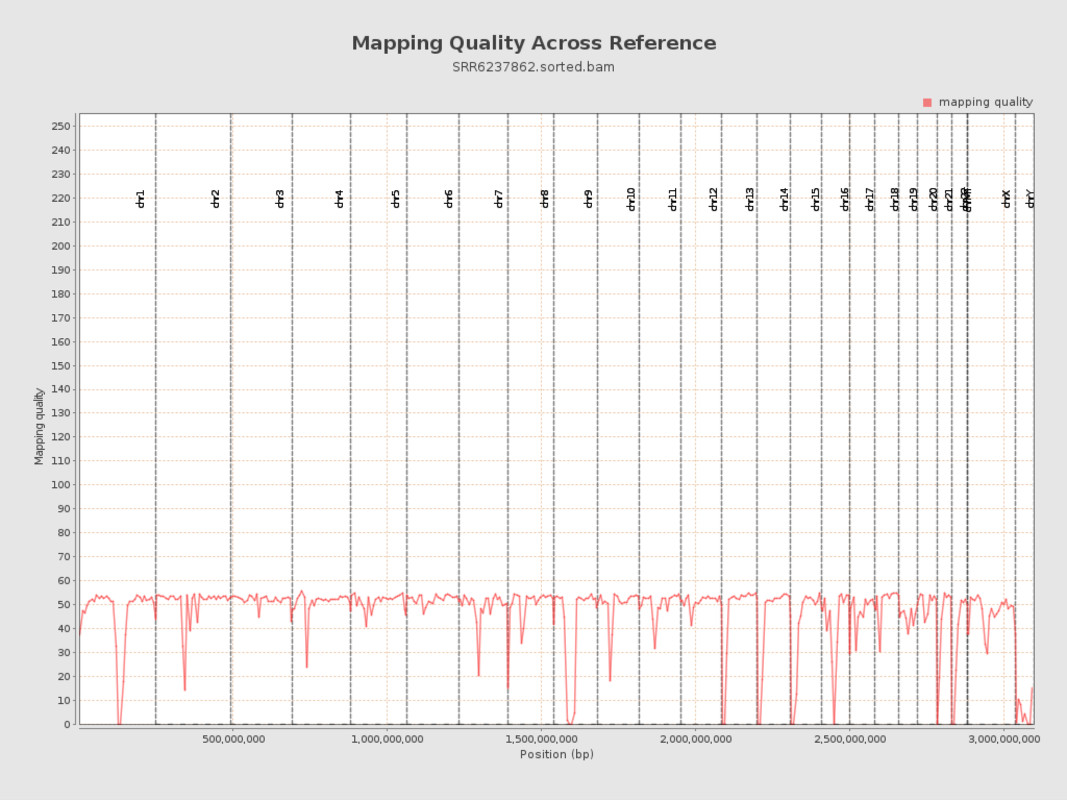
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram