Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:08:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237263.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_SRR6237263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:08:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,599
Mapped reads	1,179 / 45.36%
Unmapped reads	1,420 / 54.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	8 / 0.31%
Duplication rate	0.68%
Clipped reads	589 / 22.66%

2.2. ACGT Content

Number/percentage of A's	21,048 / 27.24%
Number/percentage of C's	14,965 / 19.37%
Number/percentage of T's	23,589 / 30.53%
Number/percentage of G's	17,654 / 22.85%
Number/percentage of N's	8 / 0.01%
GC Percentage	42.22%

2.3. Coverage

Mean	0

Standard Deviation	0.005

2.4. Mapping Quality

Mean Mapping Quality	42.16

2.5. Mismatches and indels

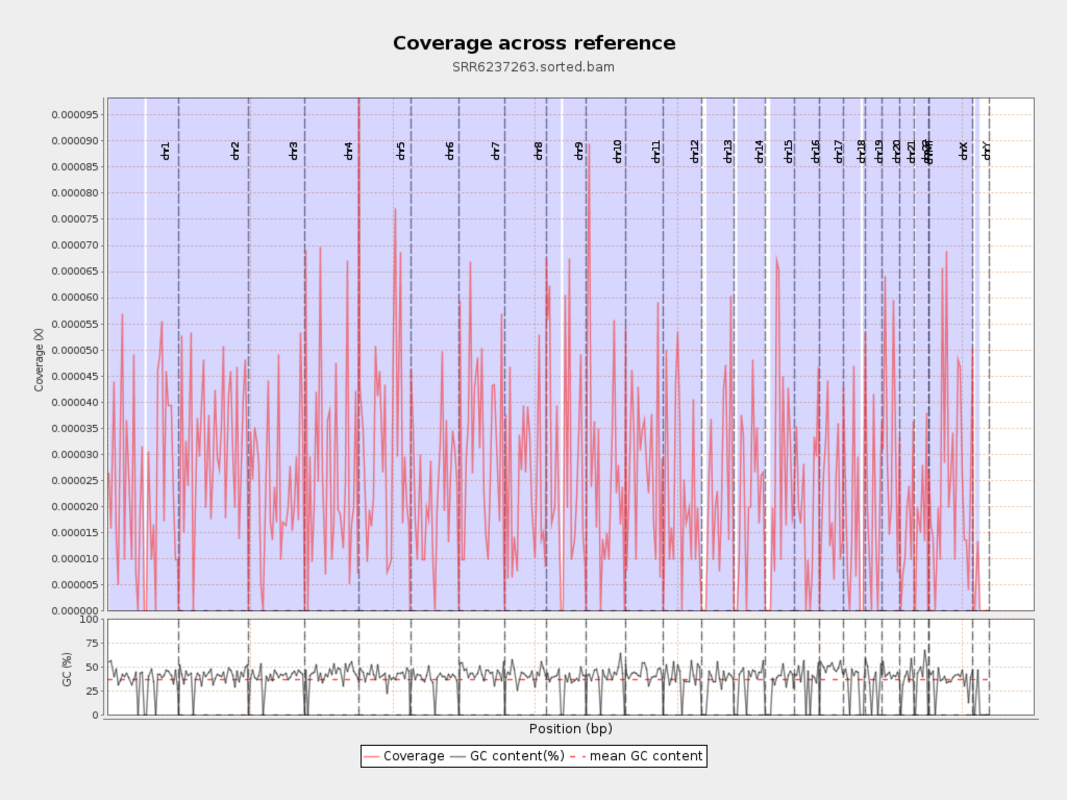
General error rate	0.78%
Mismatches	590
Insertions	8
Mapped reads with at least one insertion	0.59%
Deletions	22
Mapped reads with at least one deletion	1.87%
Homopolymer indels	36.67%

2.6. Chromosome stats

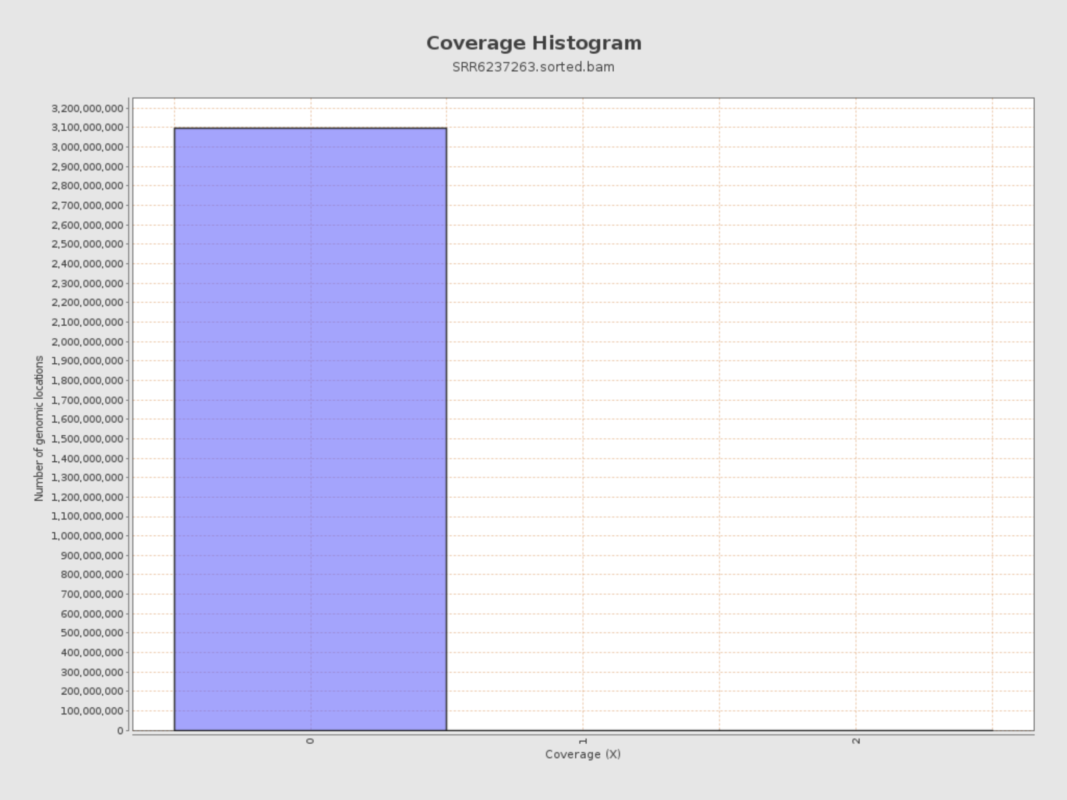
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6023	0	0.0049
chr2	243199373	7701	0	0.0057
chr3	198022430	4743	0	0.005
chr4	191154276	5124	0	0.0052
chr5	180915260	5555	0	0.0055
chr6	171115067	3920	0	0.0048
chr7	159138663	5064	0	0.0056

chr8	146364022	3587	0	0.005
chr9	141213431	4011	0	0.0053
chr10	135534747	3646	0	0.0053
chr11	135006516	3802	0	0.0055
chr12	133851895	2925	0	0.0048
chr13	115169878	2482	0	0.0046
chr14	107349540	2322	0	0.0047
chr15	102531392	2559	0	0.005
chr16	90354753	1874	0	0.0045
chr17	81195210	1748	0	0.0046
chr18	78077248	1279	0	0.004
chr19	59128983	1130	0	0.0044
chr20	63025520	2047	0	0.0057
chr21	48129895	721	0	0.0039
chr22	51304566	880	0	0.0041
chrMT	16571	0	0	0
chrX	155270560	4055	0	0.0051
chrY	59373566	103	0	0.0013

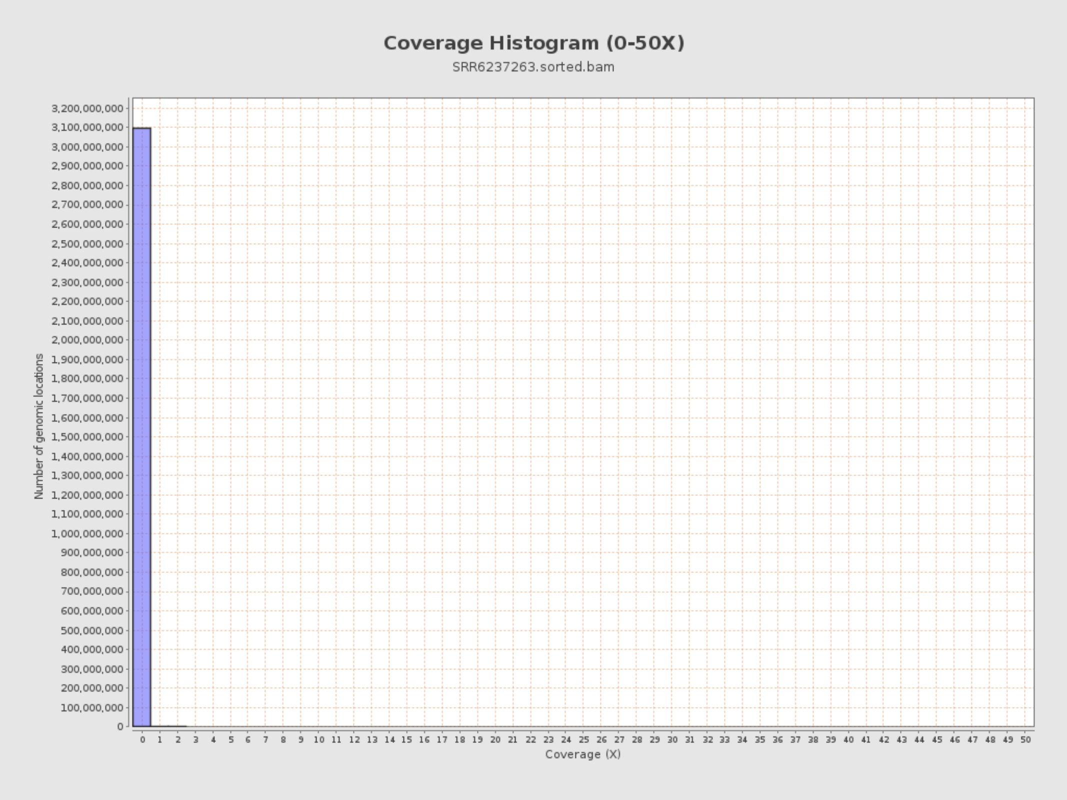
3. Results : Coverage across reference



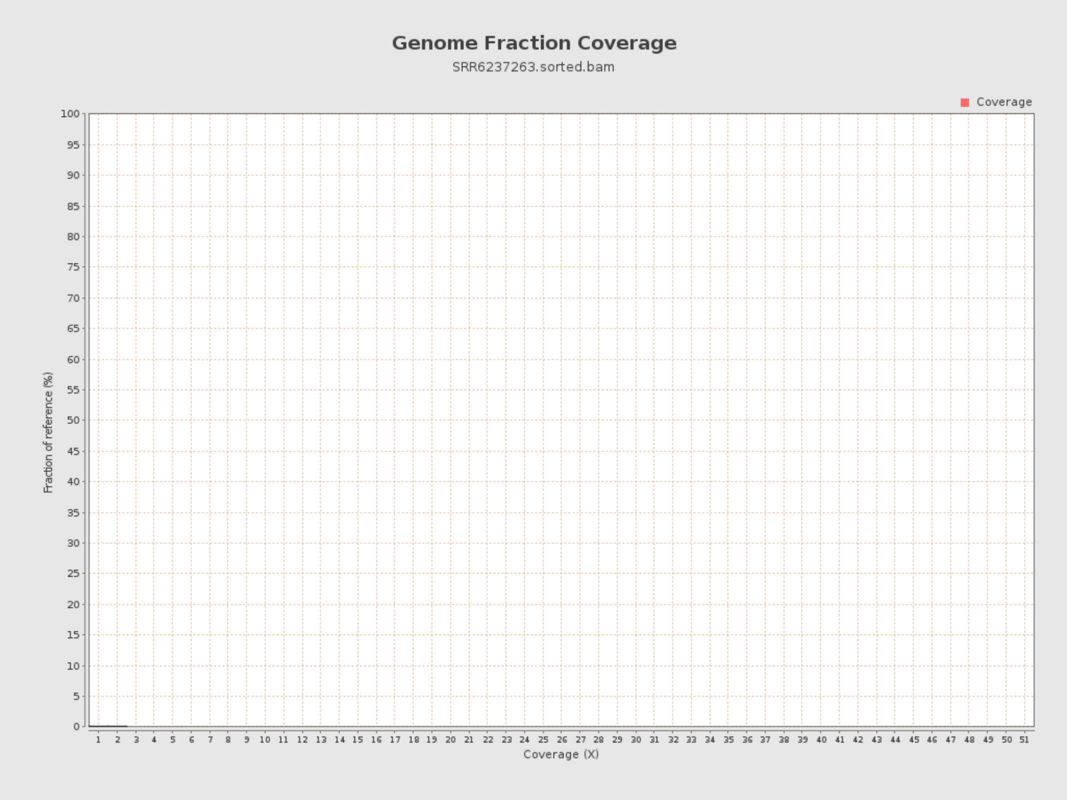
4. Results : Coverage Histogram



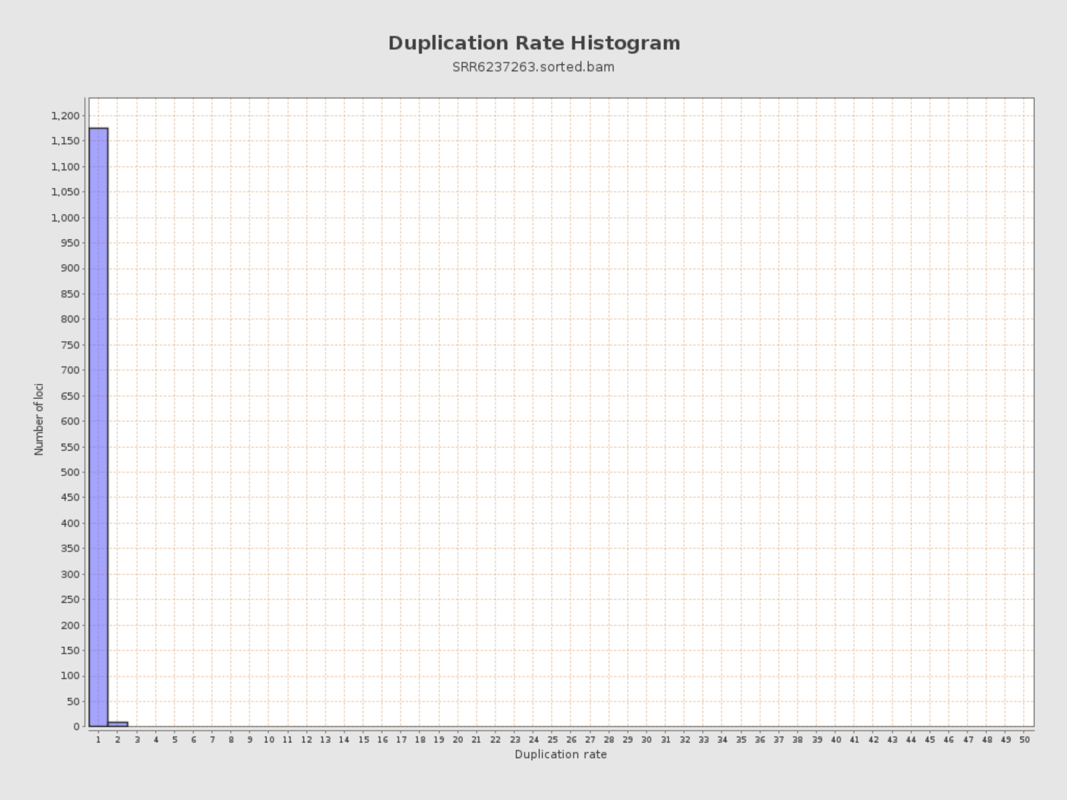
5. Results : Coverage Histogram (0-50X)



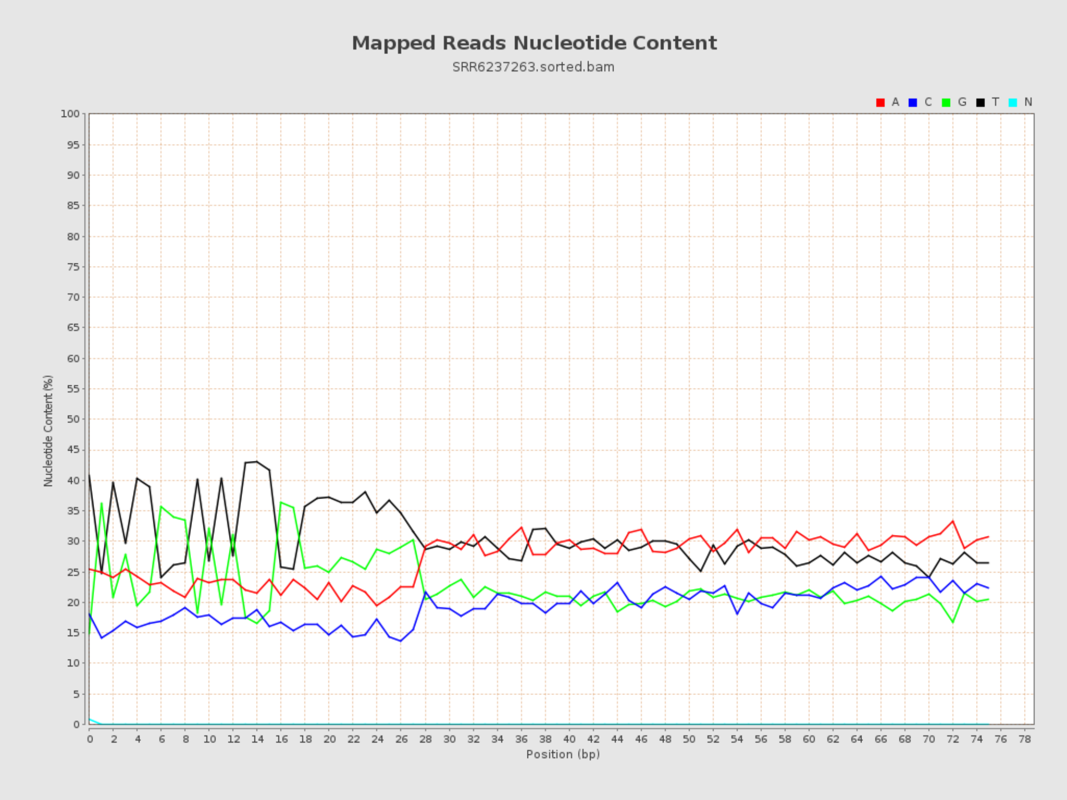
6. Results : Genome Fraction Coverage



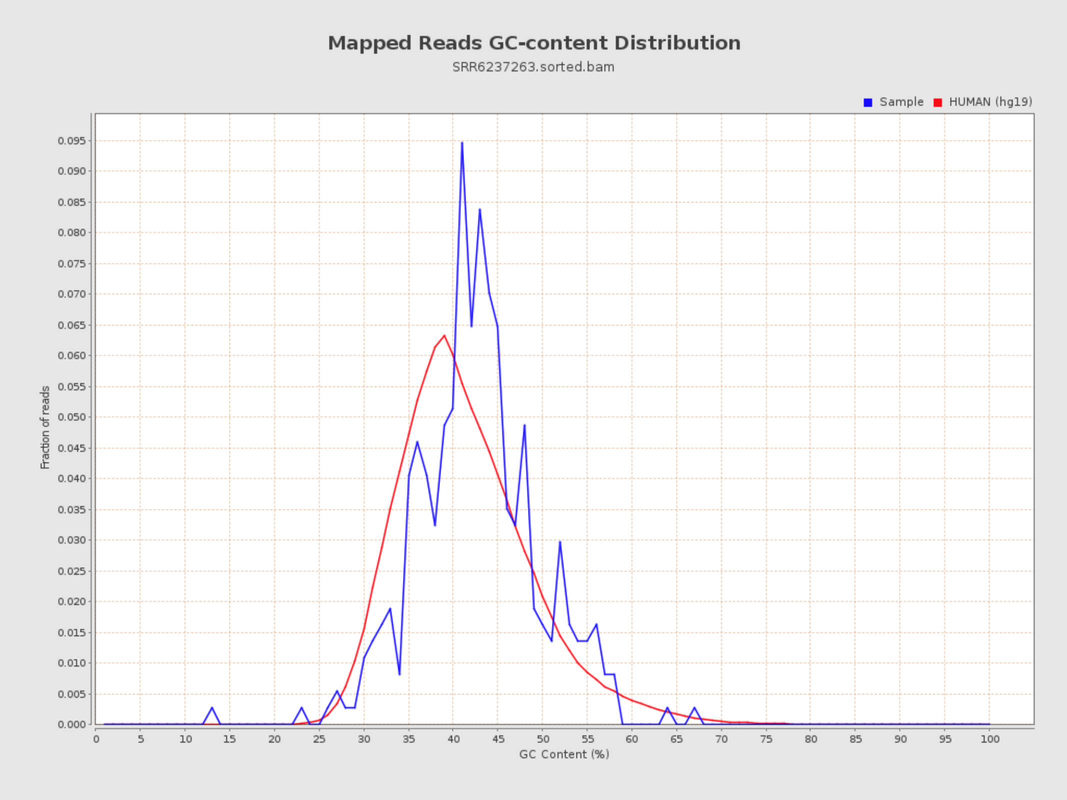
7. Results : Duplication Rate Histogram



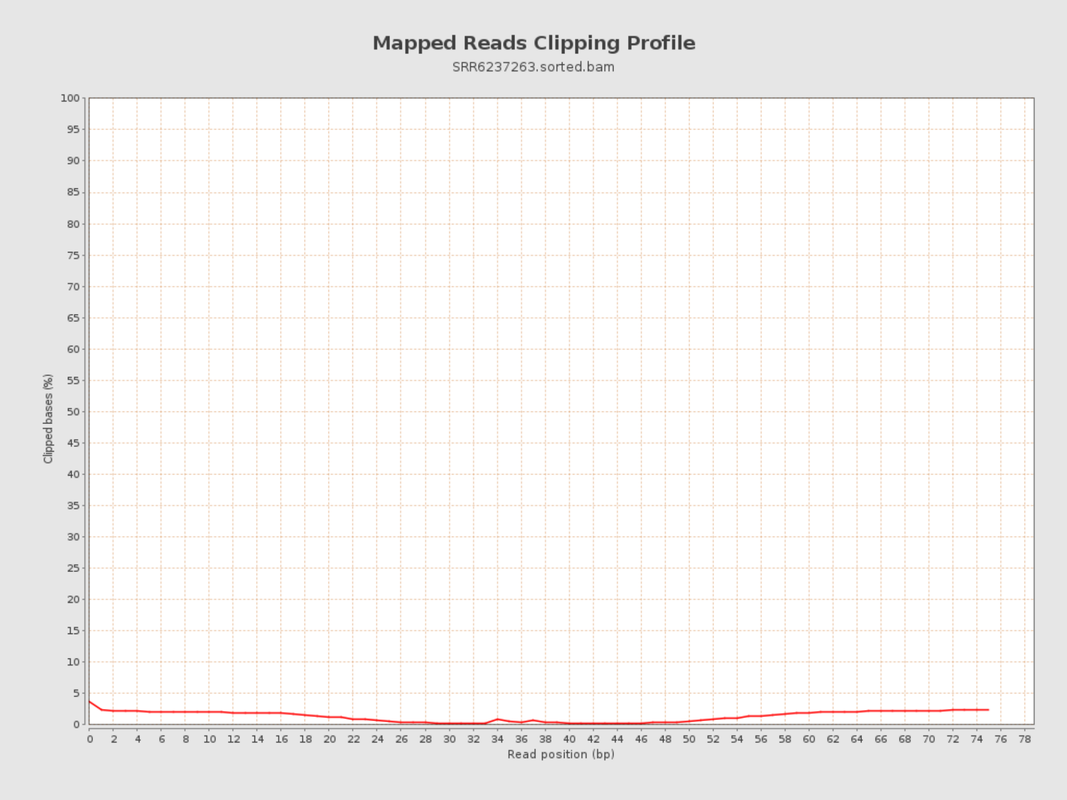
8. Results : Mapped Reads Nucleotide Content



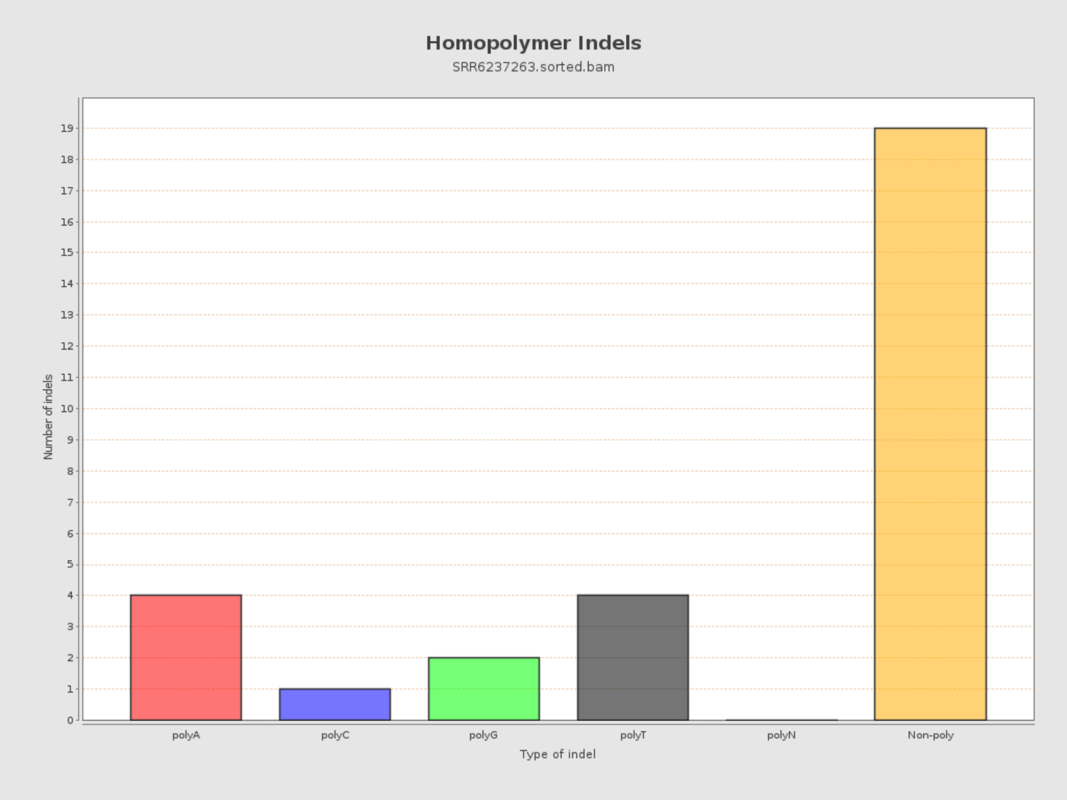
9. Results : Mapped Reads GC-content Distribution



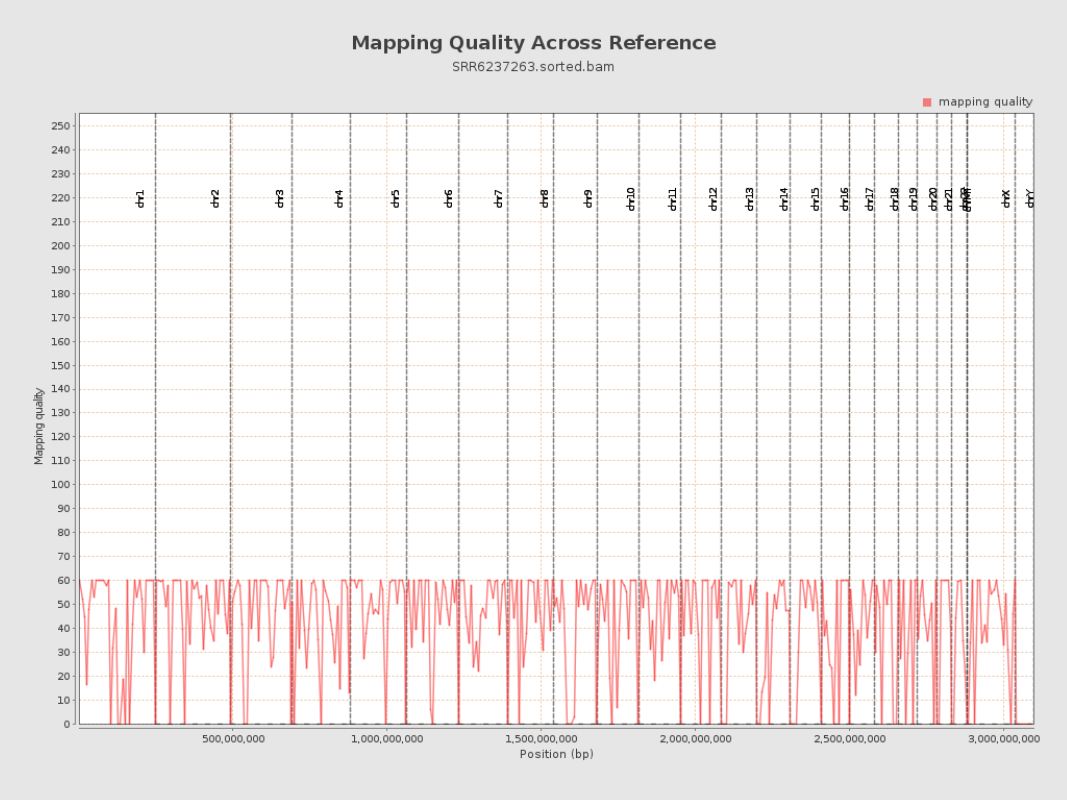
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram