Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:22:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238660.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_SRR6238660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:22:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,065,938
Mapped reads	2,693,817 / 87.86%
Unmapped reads	372,121 / 12.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,718 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,253,776 / 40.89%
Duplication rate	24.07%
Clipped reads	1,947,336 / 63.52%

2.2. ACGT Content

Number/percentage of A's	39,131,844 / 24.41%
Number/percentage of C's	26,485,250 / 16.52%
Number/percentage of T's	56,060,240 / 34.96%
Number/percentage of G's	38,656,355 / 24.11%
Number/percentage of N's	3,566 / 0%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.9914

2.4. Mapping Quality

Mean Mapping Quality	41.04

2.5. Mismatches and indels

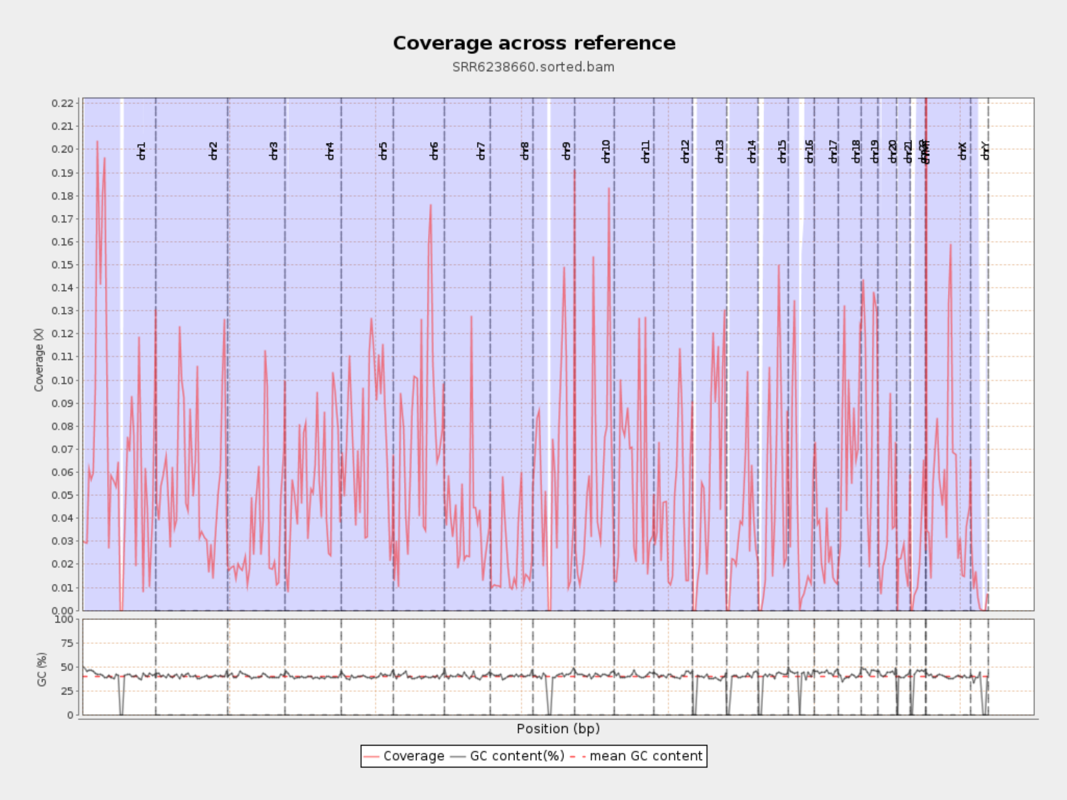
General error rate	0.6%
Mismatches	948,357
Insertions	10,082
Mapped reads with at least one insertion	0.37%
Deletions	42,752
Mapped reads with at least one deletion	1.57%
Homopolymer indels	42.09%

2.6. Chromosome stats

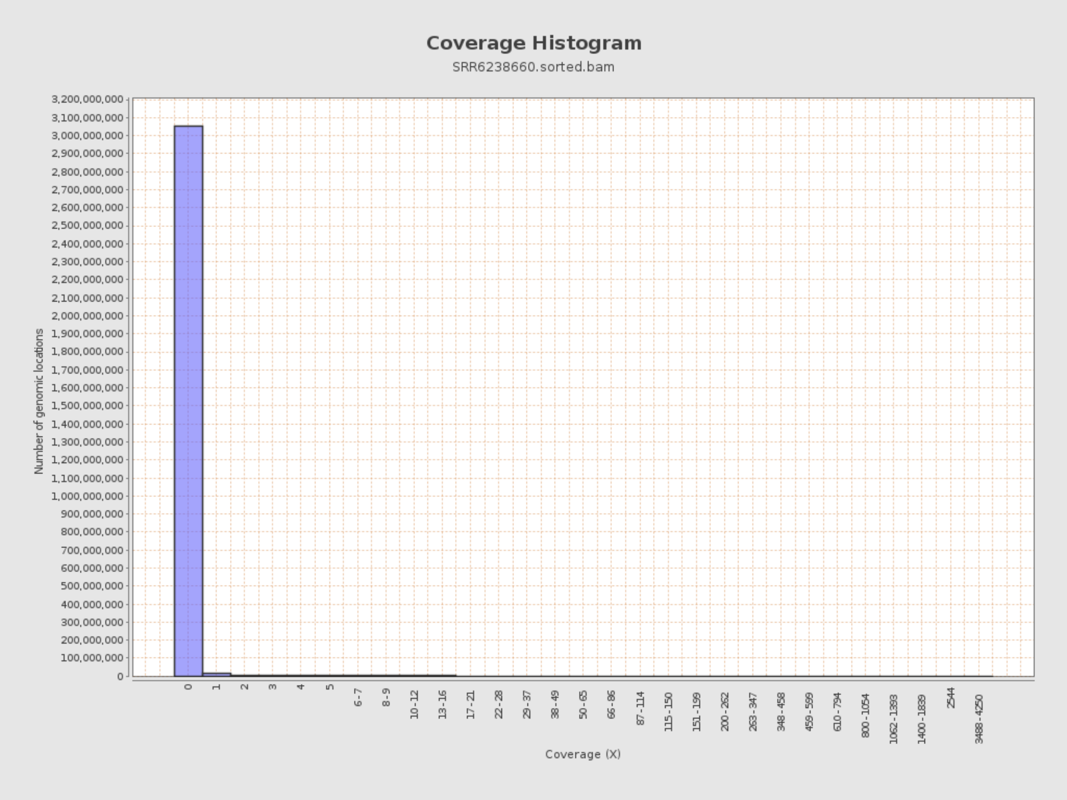
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17531773	0.0703	0.8426
chr2	243199373	13649630	0.0561	1.9874
chr3	198022430	6666361	0.0337	0.5419
chr4	191154276	10515243	0.055	0.6845
chr5	180915260	13587510	0.0751	0.8125
chr6	171115067	12735760	0.0744	1.0427
chr7	159138663	6259350	0.0393	0.7111

chr8	146364022	3009525	0.0206	0.8478
chr9	141213431	8297511	0.0588	0.9382
chr10	135534747	8029566	0.0592	0.7664
chr11	135006516	7633735	0.0565	0.7735
chr12	133851895	5939002	0.0444	0.6675
chr13	115169878	6944656	0.0603	0.8578
chr14	107349540	3869153	0.036	0.6617
chr15	102531392	5030240	0.0491	0.7512
chr16	90354753	3509925	0.0388	0.6583
chr17	81195210	2347450	0.0289	0.4762
chr18	78077248	5851639	0.0749	2.5192
chr19	59128983	5577800	0.0943	0.9418
chr20	63025520	2239111	0.0355	0.6022
chr21	48129895	1073435	0.0223	0.4588
chr22	51304566	1164828	0.0227	0.4321
chrMT	16571	21735	1.3116	3.4239
chrX	155270560	8464461	0.0545	0.6995
chrY	59373566	457727	0.0077	0.3395

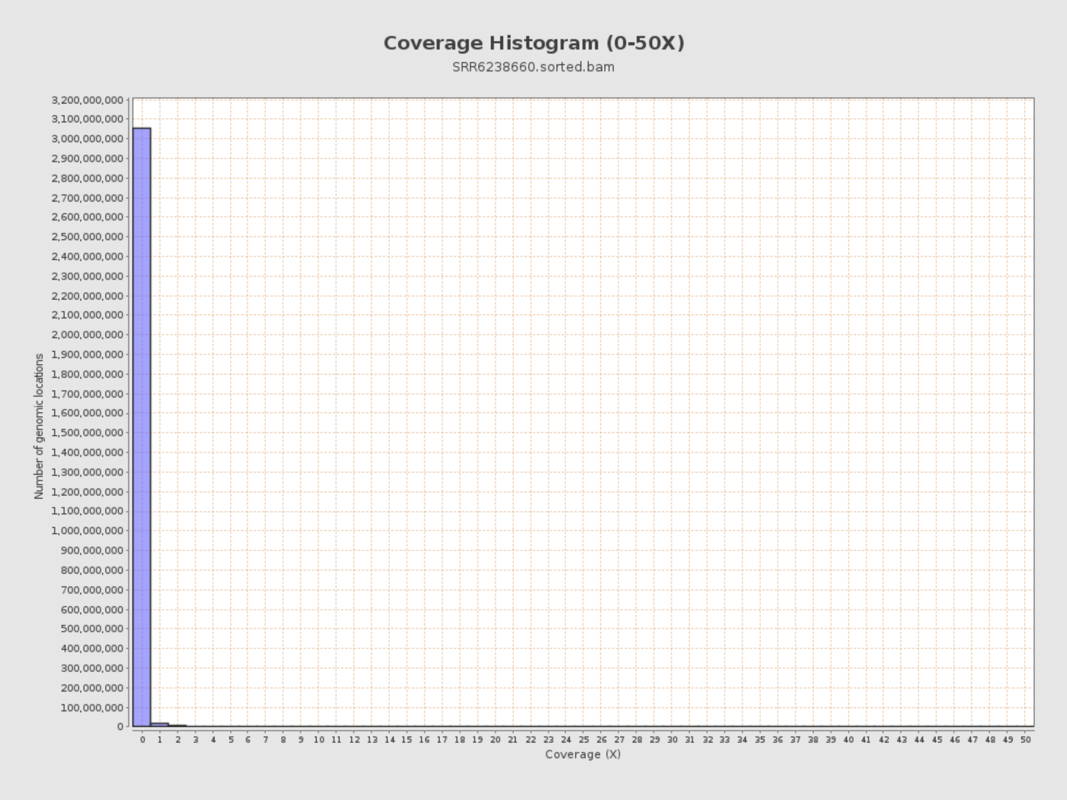
3. Results : Coverage across reference



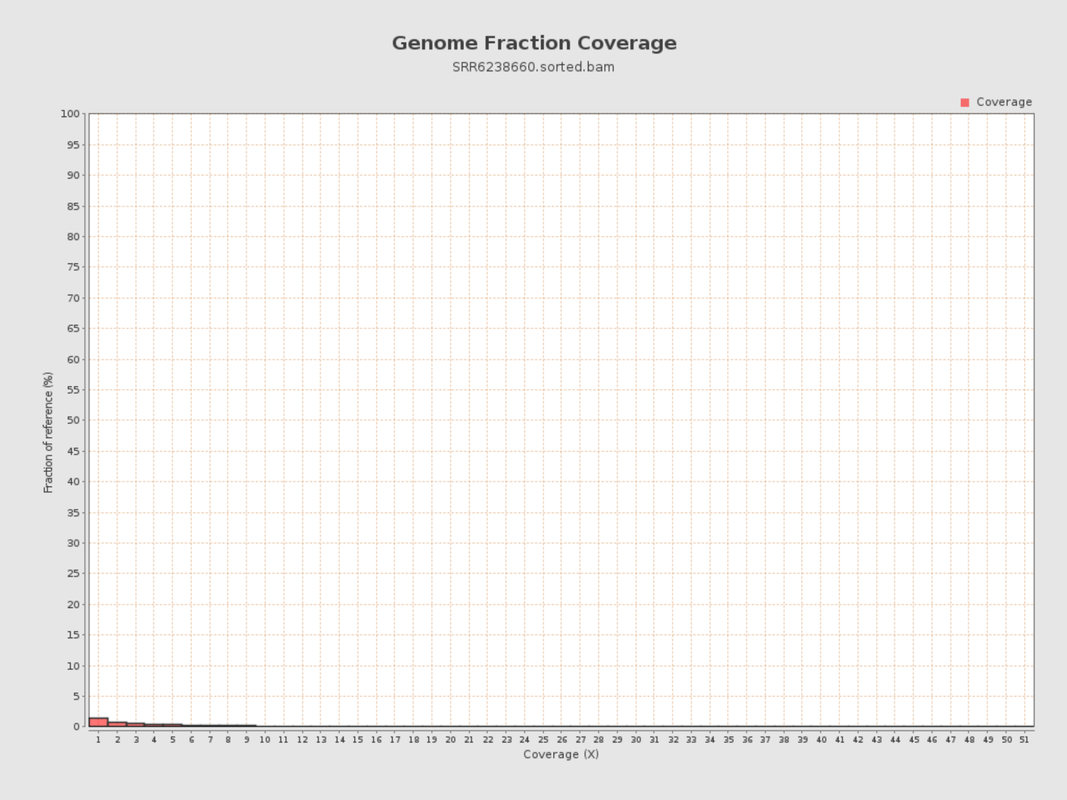
4. Results : Coverage Histogram



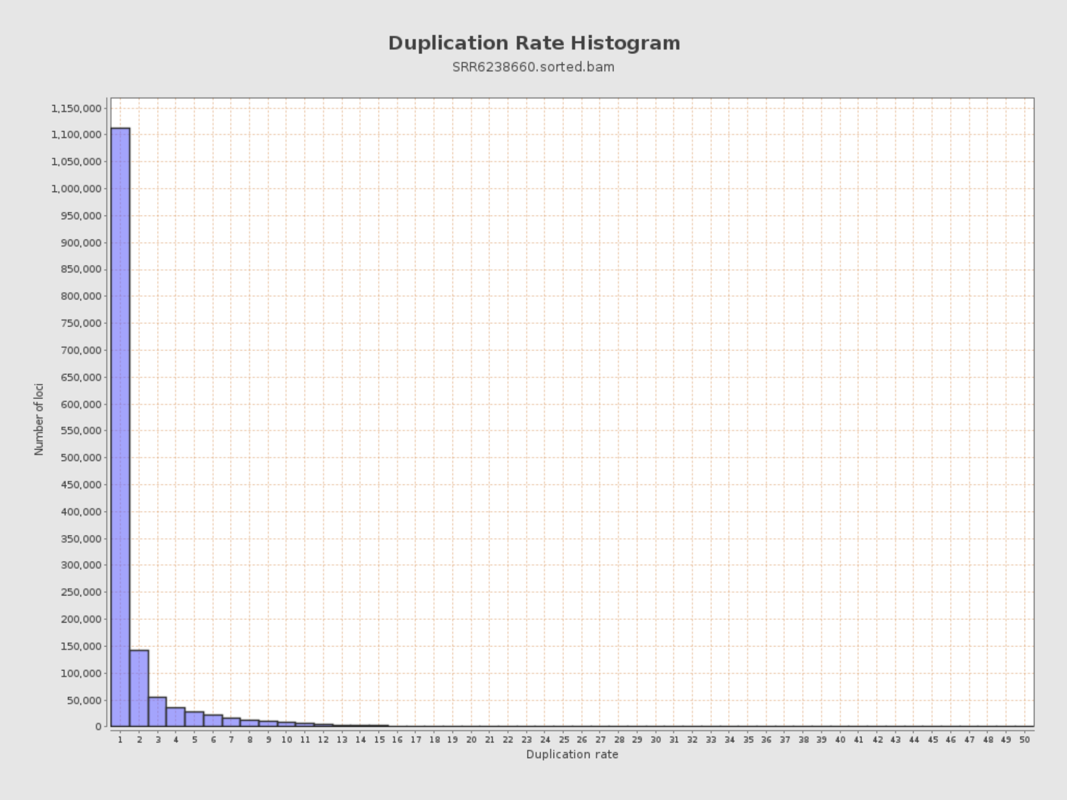
5. Results : Coverage Histogram (0-50X)



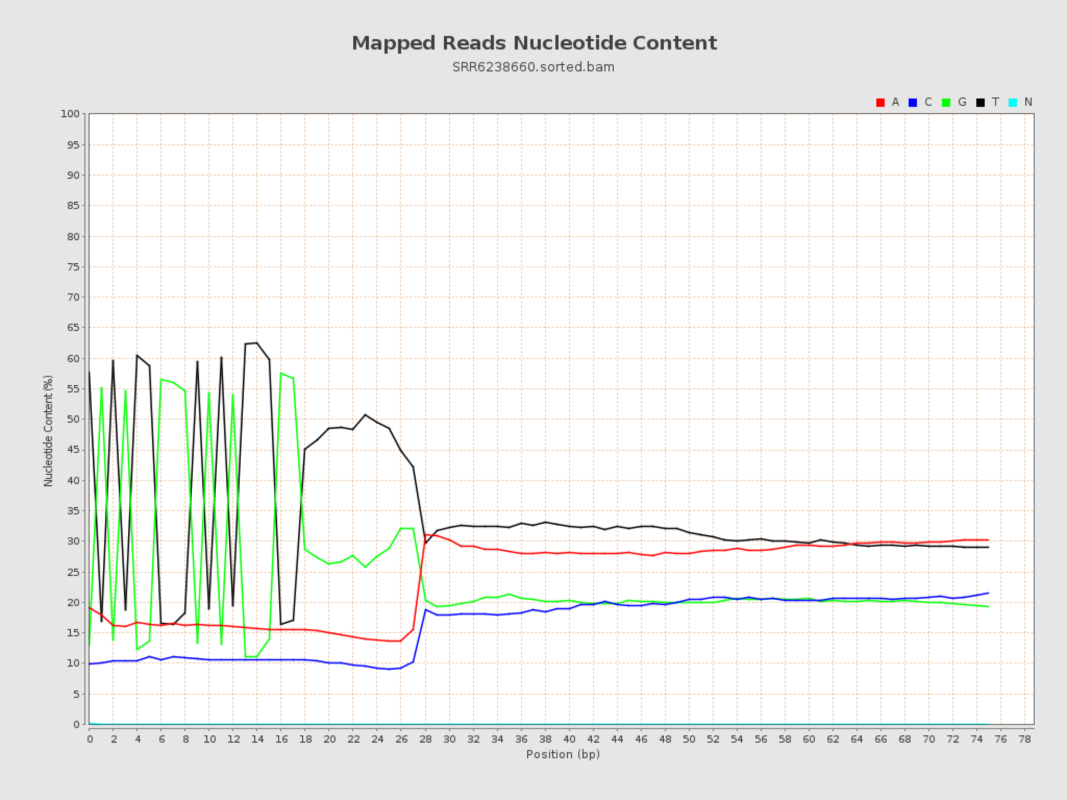
6. Results : Genome Fraction Coverage



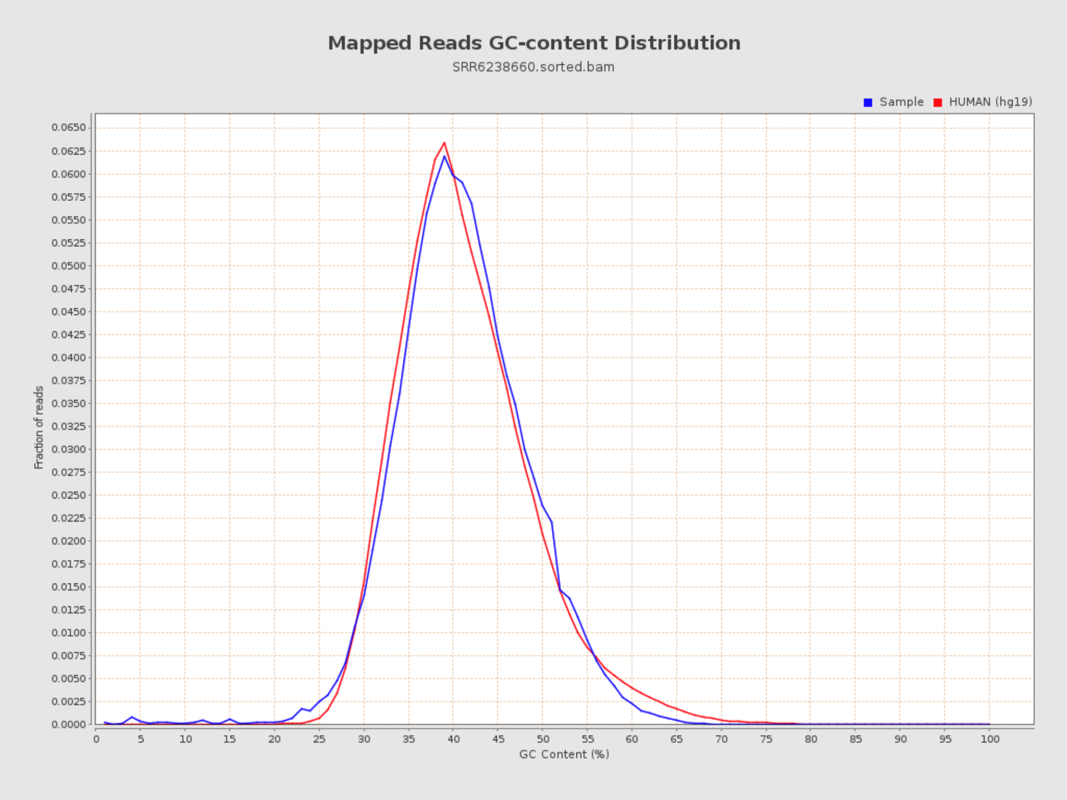
7. Results : Duplication Rate Histogram



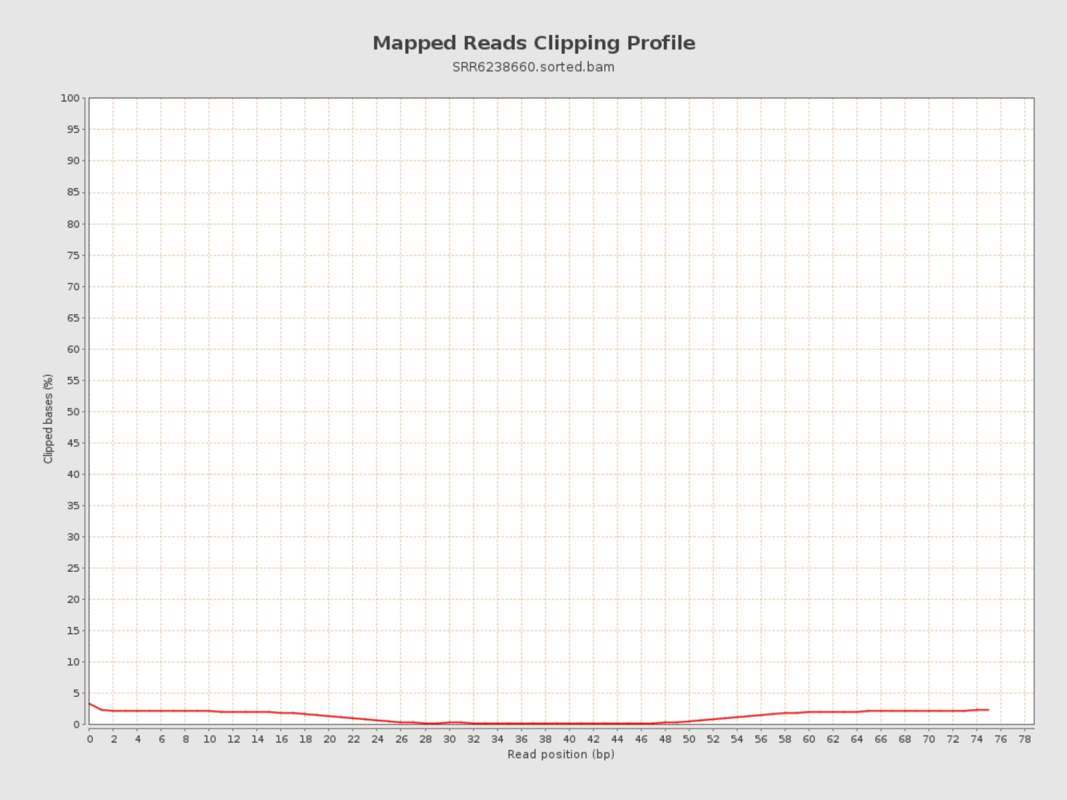
8. Results : Mapped Reads Nucleotide Content



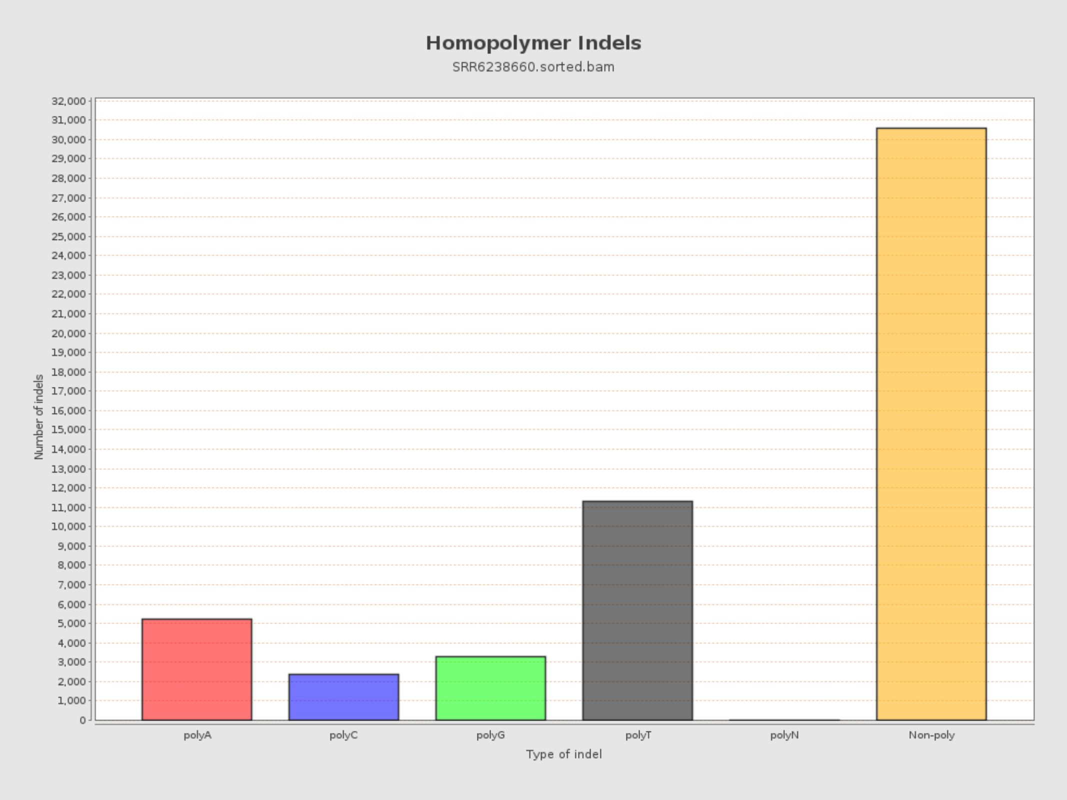
9. Results : Mapped Reads GC-content Distribution



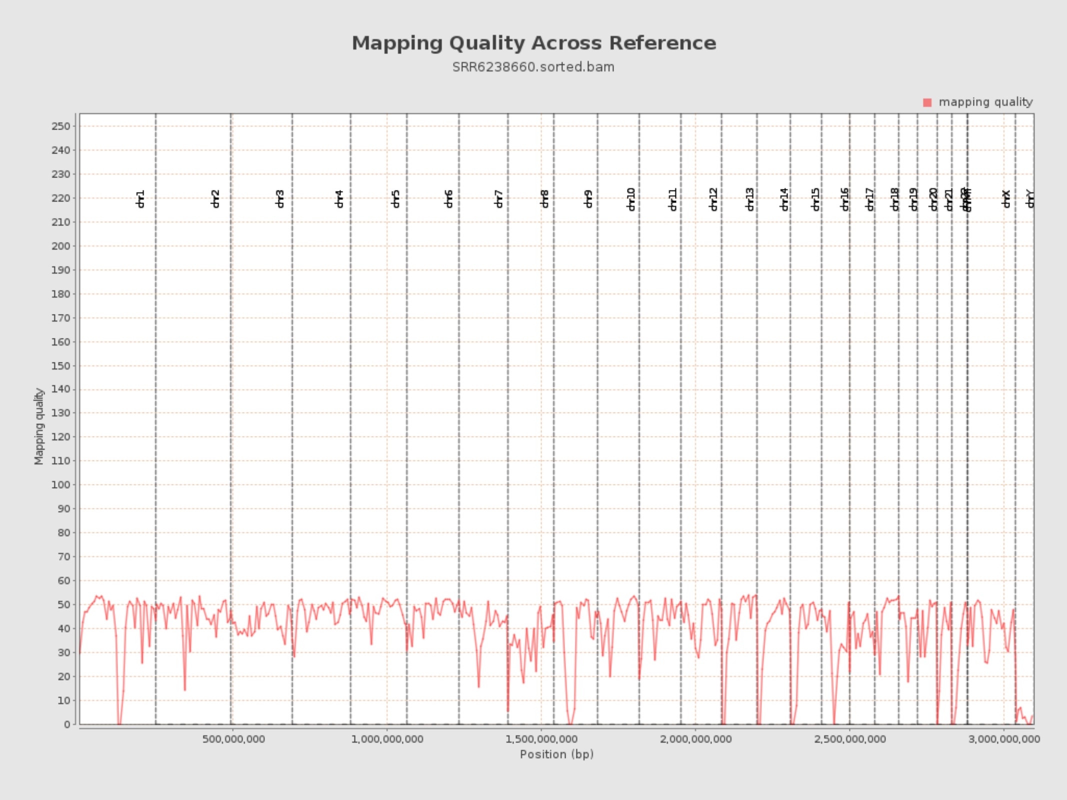
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram