Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:46:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238602.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_SRR6238602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:46:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,361,462
Mapped reads	1,660,810 / 70.33%
Unmapped reads	700,652 / 29.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,870 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,073,663 / 45.47%
Duplication rate	28.74%
Clipped reads	1,122,377 / 47.53%

2.2. ACGT Content

Number/percentage of A's	24,367,381 / 24.25%
Number/percentage of C's	16,443,411 / 16.37%
Number/percentage of T's	36,407,112 / 36.24%
Number/percentage of G's	23,244,639 / 23.14%
Number/percentage of N's	2,178 / 0%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0325

Standard Deviation	2.7739

2.4. Mapping Quality

Mean Mapping Quality	41.77

2.5. Mismatches and indels

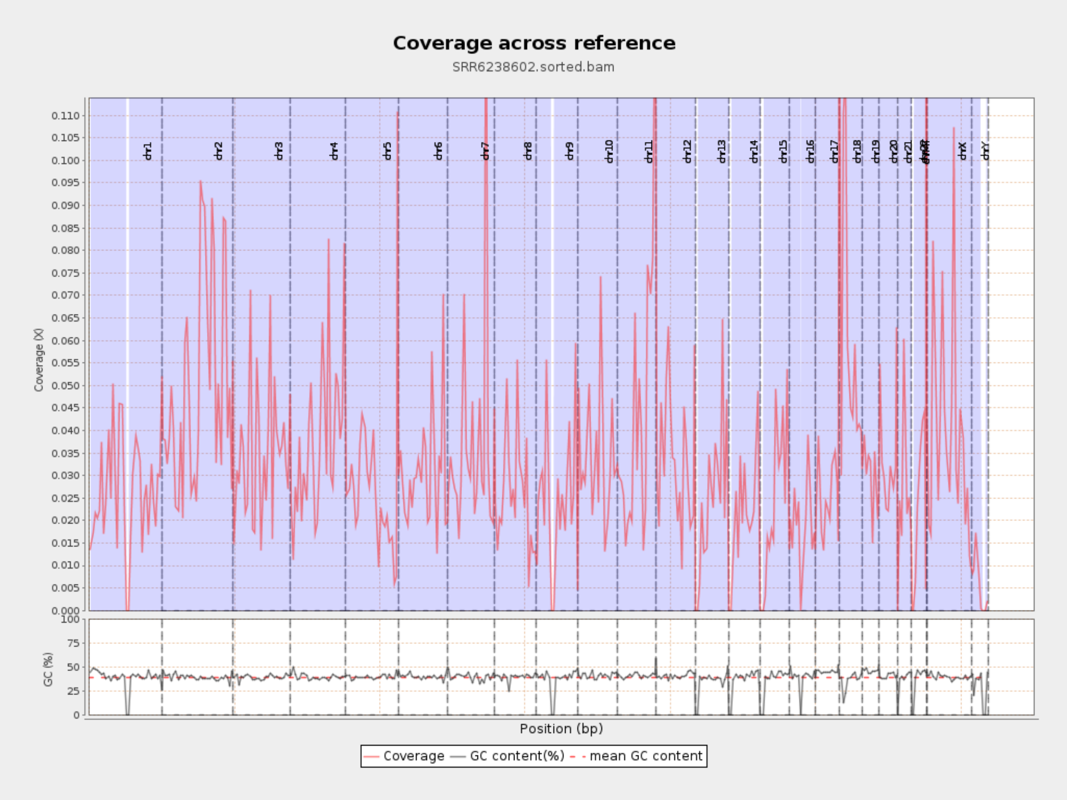
General error rate	0.65%
Mismatches	638,061
Insertions	7,450
Mapped reads with at least one insertion	0.45%
Deletions	33,054
Mapped reads with at least one deletion	1.97%
Homopolymer indels	39.6%

2.6. Chromosome stats

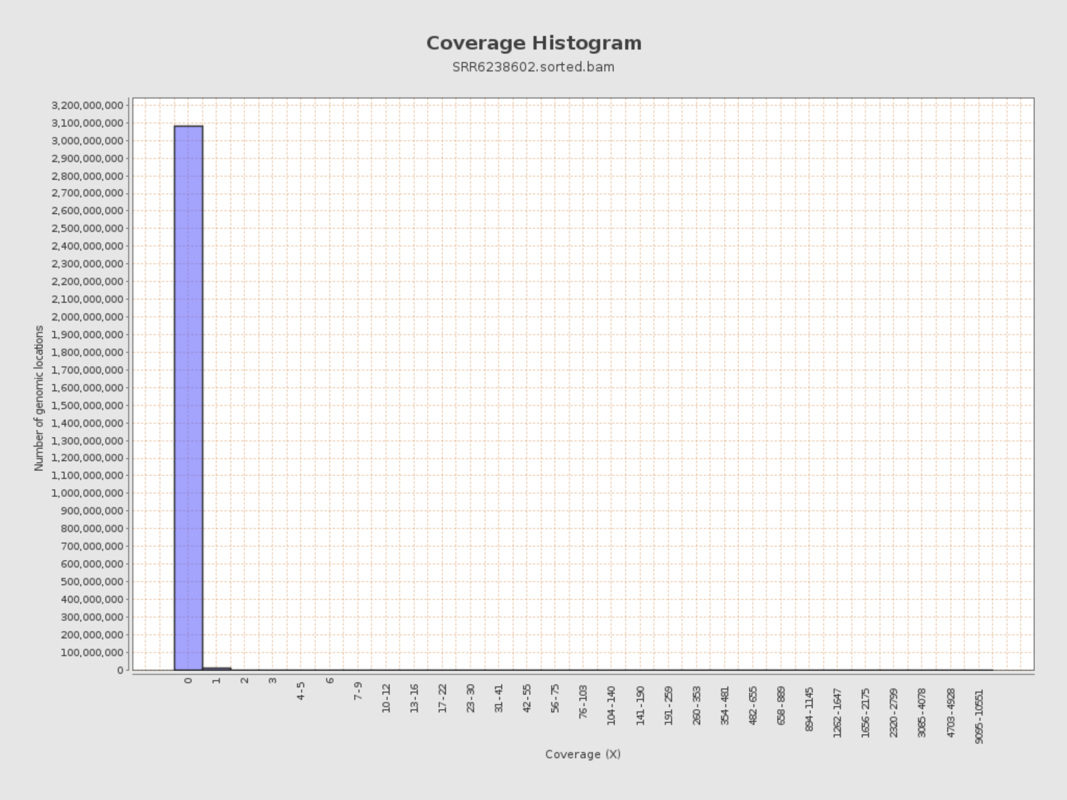
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6434495	0.0258	1.4115
chr2	243199373	12267688	0.0504	3.0675
chr3	198022430	6948887	0.0351	1.7302
chr4	191154276	7196746	0.0376	1.7339
chr5	180915260	4681124	0.0259	1.3799
chr6	171115067	5335698	0.0312	2.1143
chr7	159138663	5947328	0.0374	2.0144

chr8	146364022	3776384	0.0258	1.9167
chr9	141213431	3583844	0.0254	1.4711
chr10	135534747	4751409	0.0351	1.6428
chr11	135006516	5946429	0.044	1.8653
chr12	133851895	4468456	0.0334	1.6839
chr13	115169878	2902211	0.0252	2.2613
chr14	107349540	2357557	0.022	1.7392
chr15	102531392	2411375	0.0235	1.765
chr16	90354753	1741519	0.0193	1.1854
chr17	81195210	2038111	0.0251	1.306
chr18	78077248	4949618	0.0634	13.1457
chr19	59128983	1753259	0.0297	1.5417
chr20	63025520	2044032	0.0324	1.5482
chr21	48129895	1231242	0.0256	1.3923
chr22	51304566	1189515	0.0232	1.715
chrMT	16571	11297	0.6817	3.878
chrX	155270560	6222748	0.0401	1.7615
chrY	59373566	327791	0.0055	0.8646

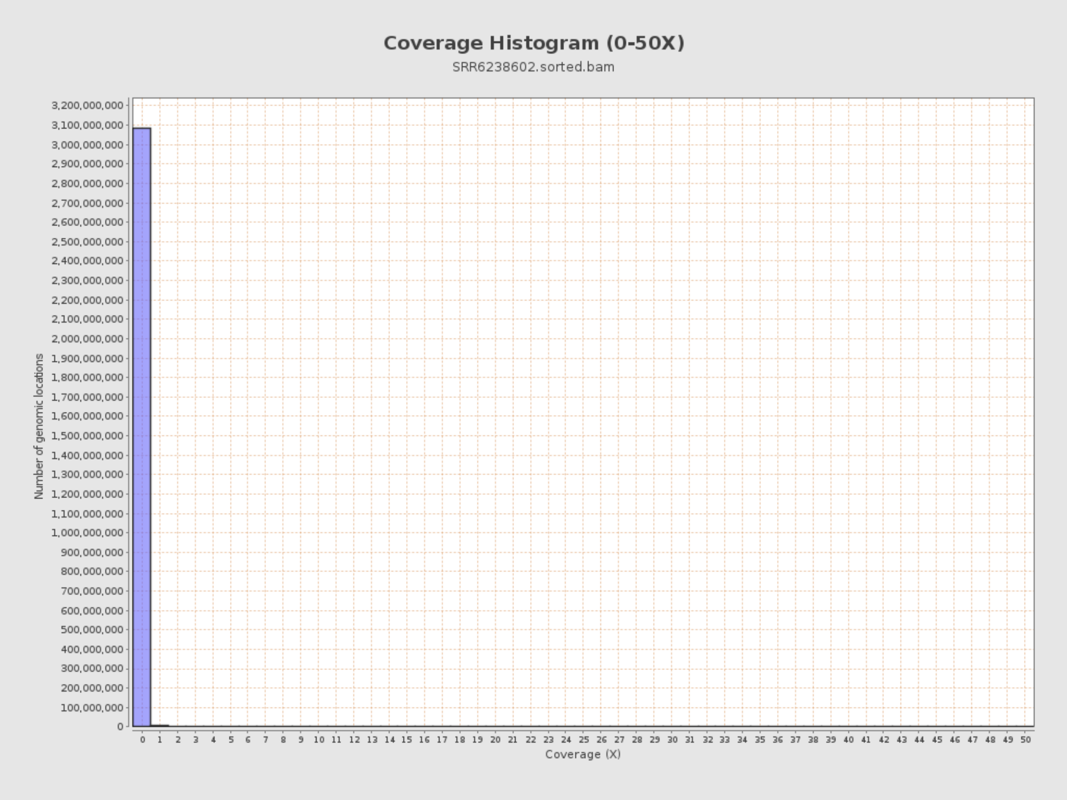
3. Results : Coverage across reference



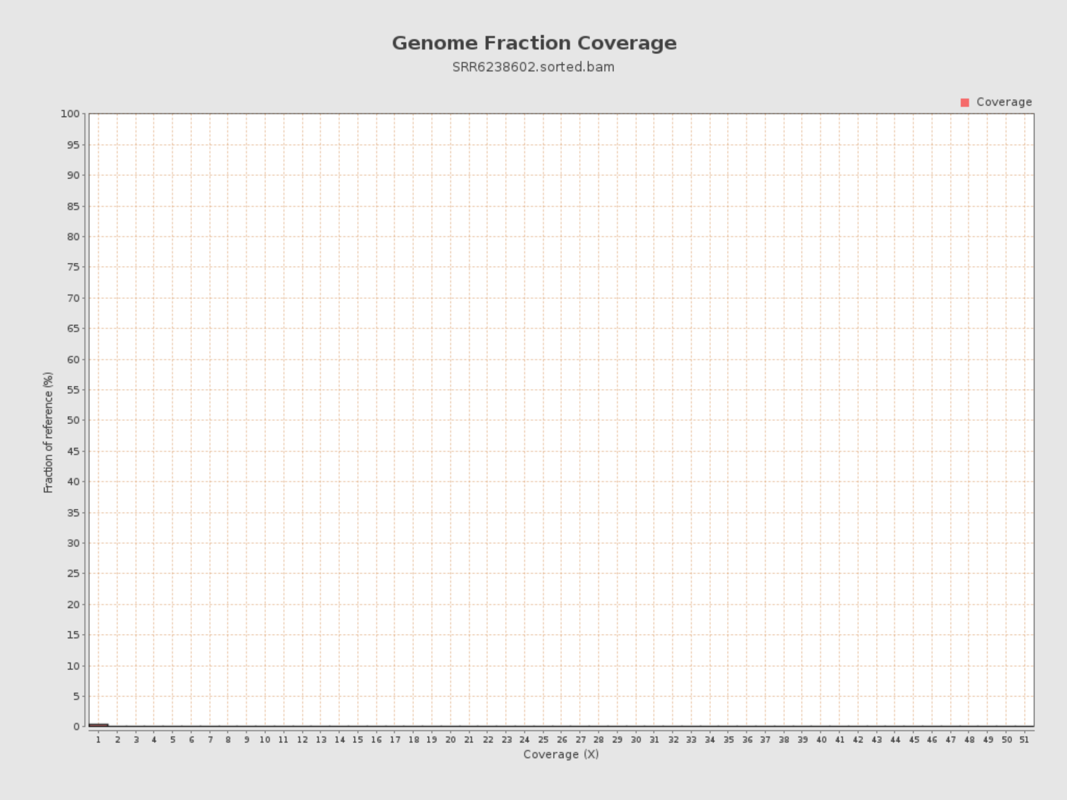
4. Results : Coverage Histogram



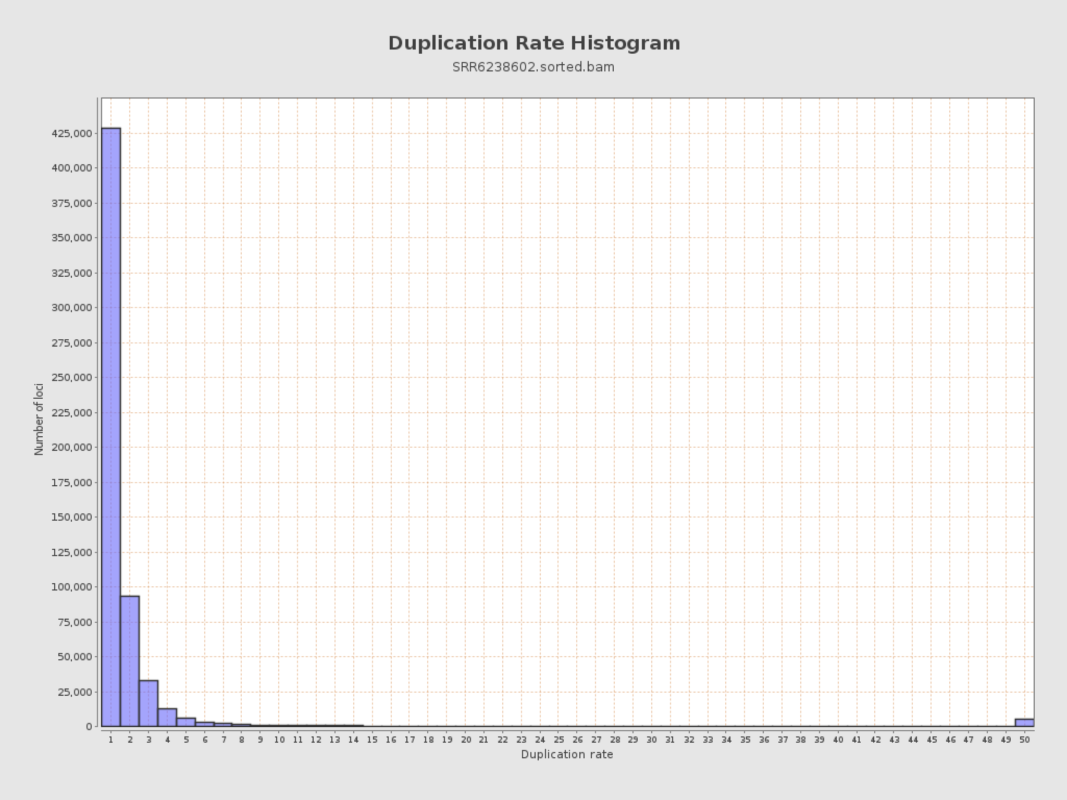
5. Results : Coverage Histogram (0-50X)



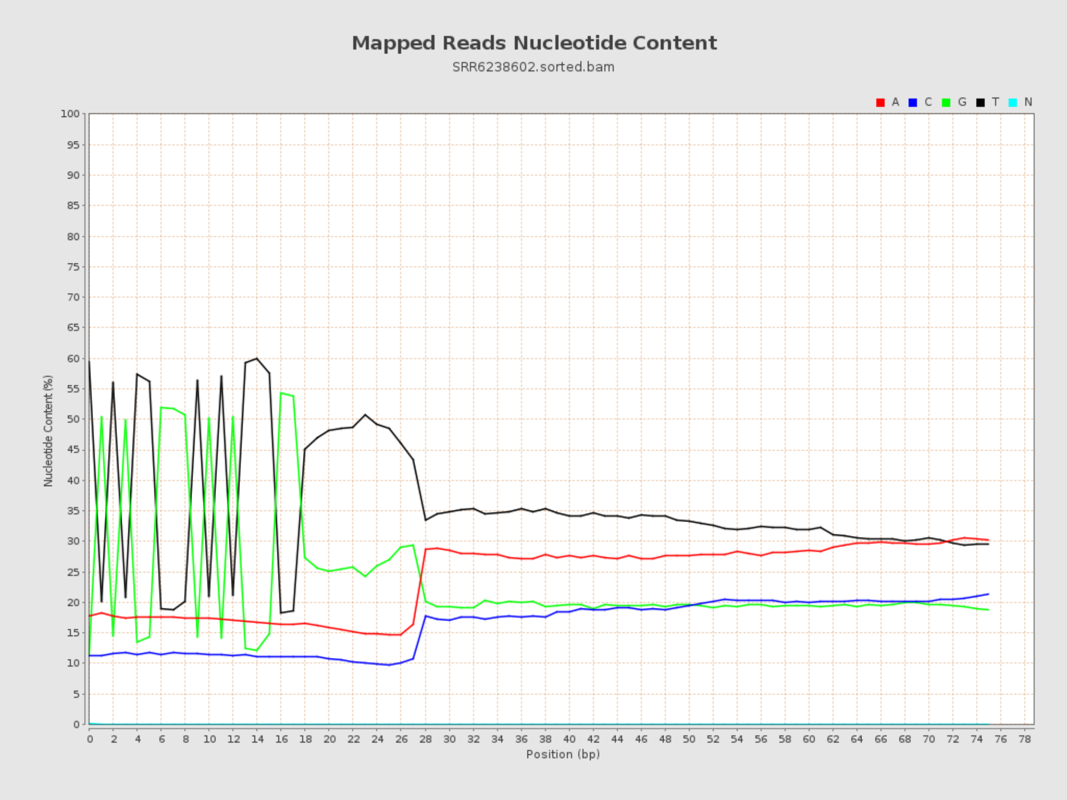
6. Results : Genome Fraction Coverage



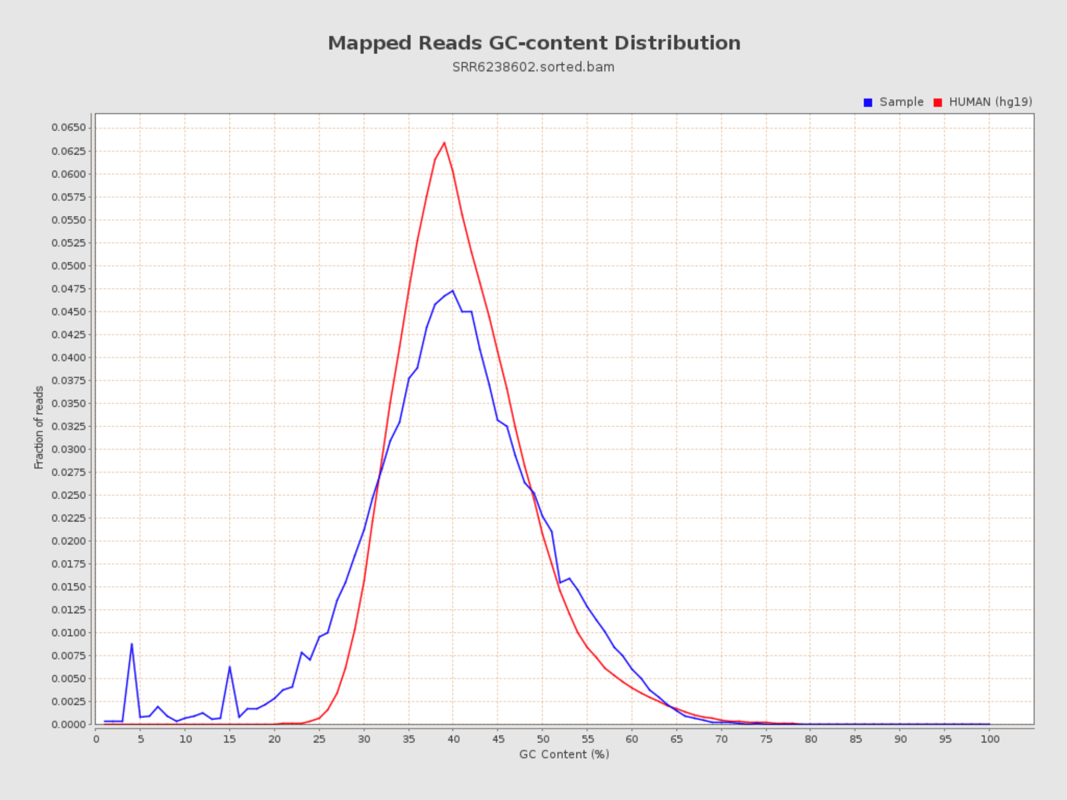
7. Results : Duplication Rate Histogram



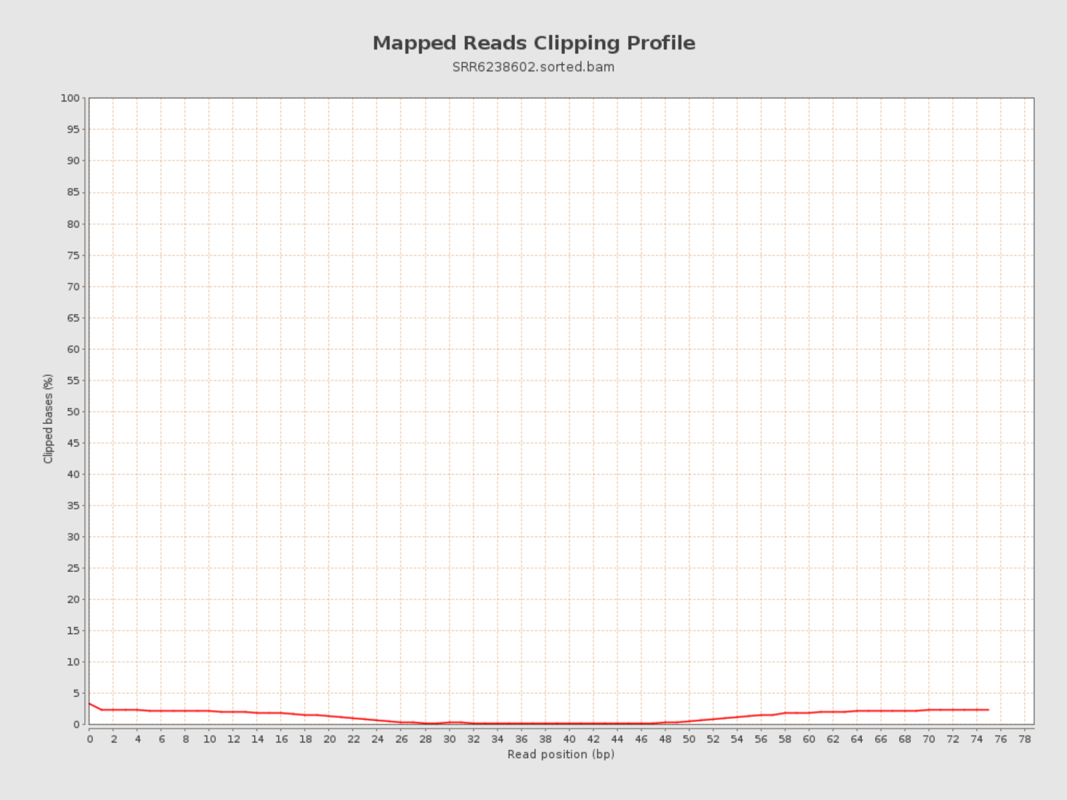
8. Results : Mapped Reads Nucleotide Content



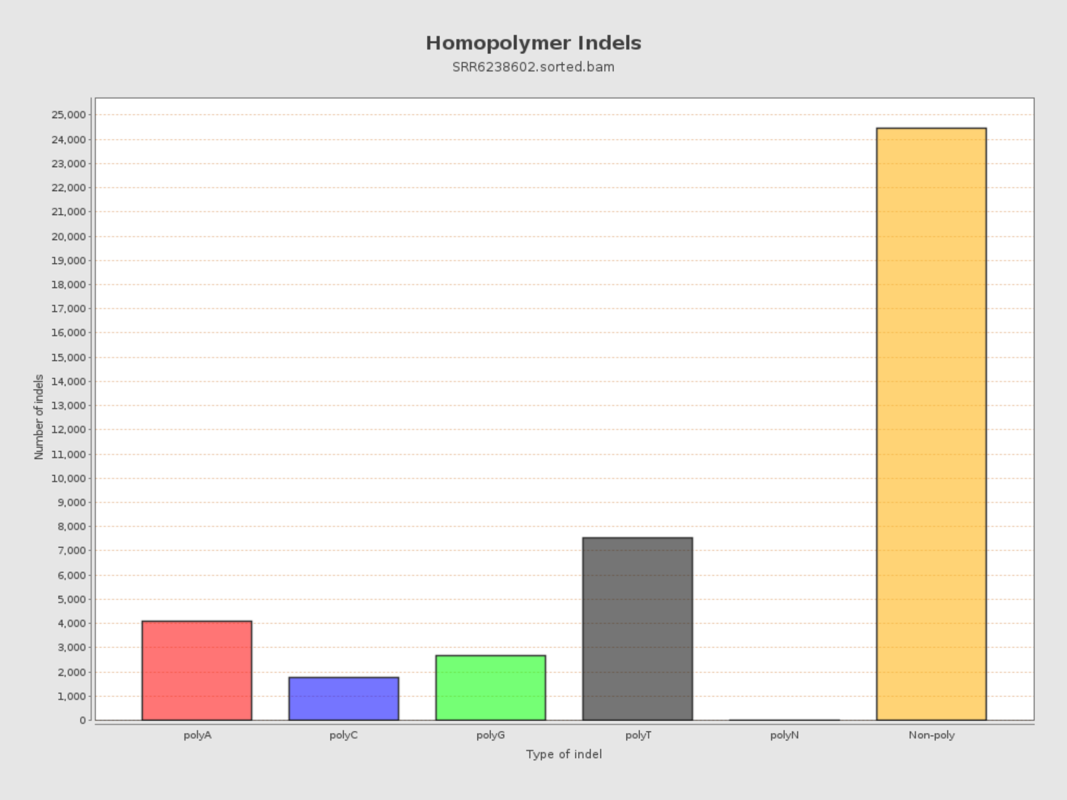
9. Results : Mapped Reads GC-content Distribution



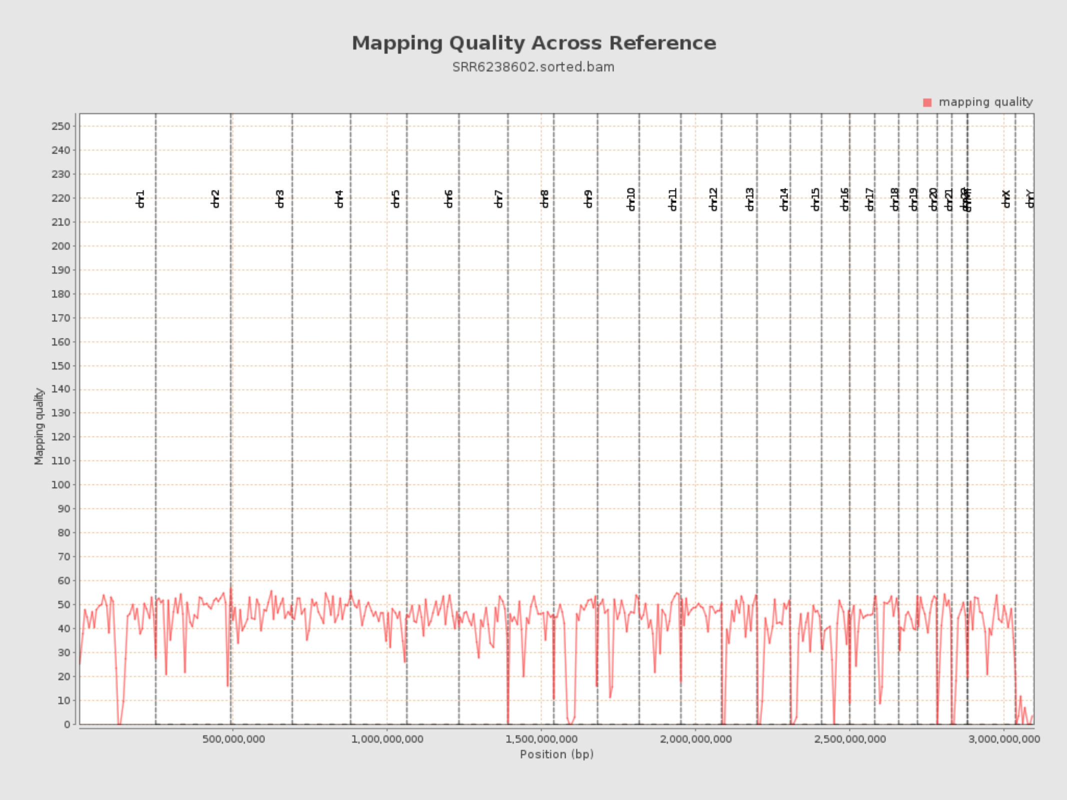
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram