Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238063.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_SRR6238063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:27:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,550,477
Mapped reads	2,319,704 / 90.95%
Unmapped reads	230,773 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,535 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	81,353 / 3.19%
Duplication rate	2.69%
Clipped reads	947,193 / 37.14%

2.2. ACGT Content

Number/percentage of A's	42,172,865 / 27.08%
Number/percentage of C's	29,682,960 / 19.06%
Number/percentage of T's	48,331,950 / 31.04%
Number/percentage of G's	35,522,748 / 22.81%
Number/percentage of N's	21,370 / 0.01%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0503

Standard Deviation	0.407

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

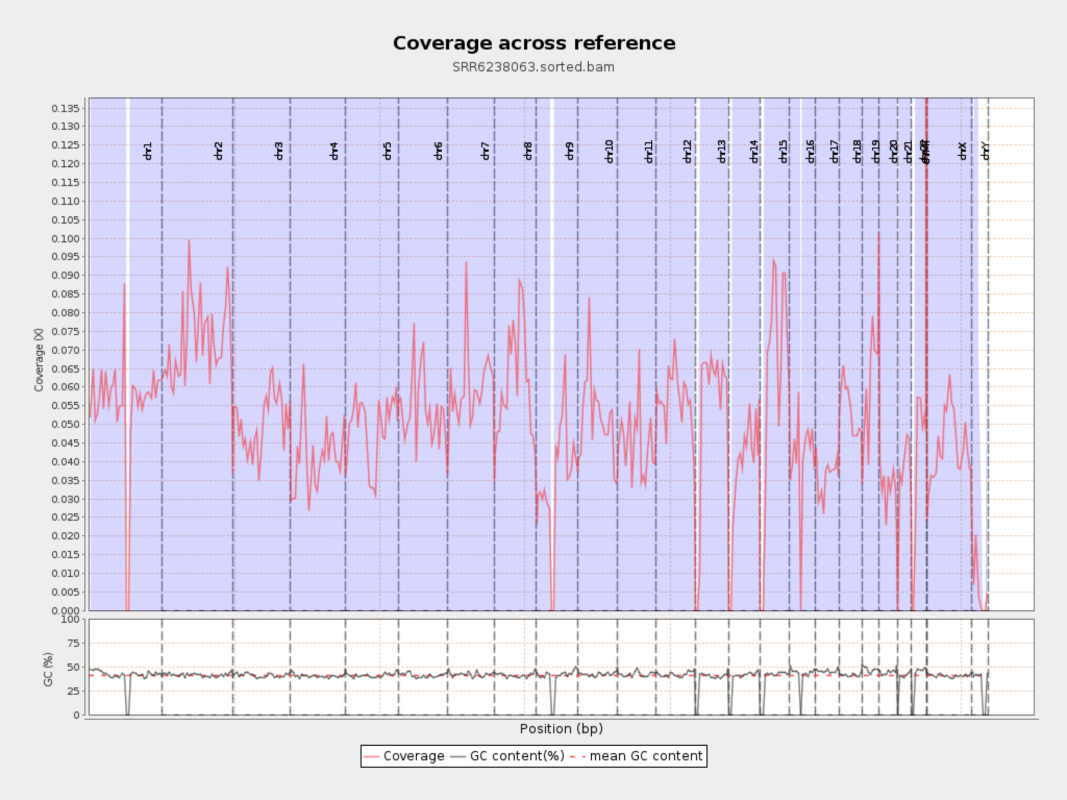
General error rate	0.74%
Mismatches	1,138,045
Insertions	10,213
Mapped reads with at least one insertion	0.44%
Deletions	41,755
Mapped reads with at least one deletion	1.78%
Homopolymer indels	46.11%

2.6. Chromosome stats

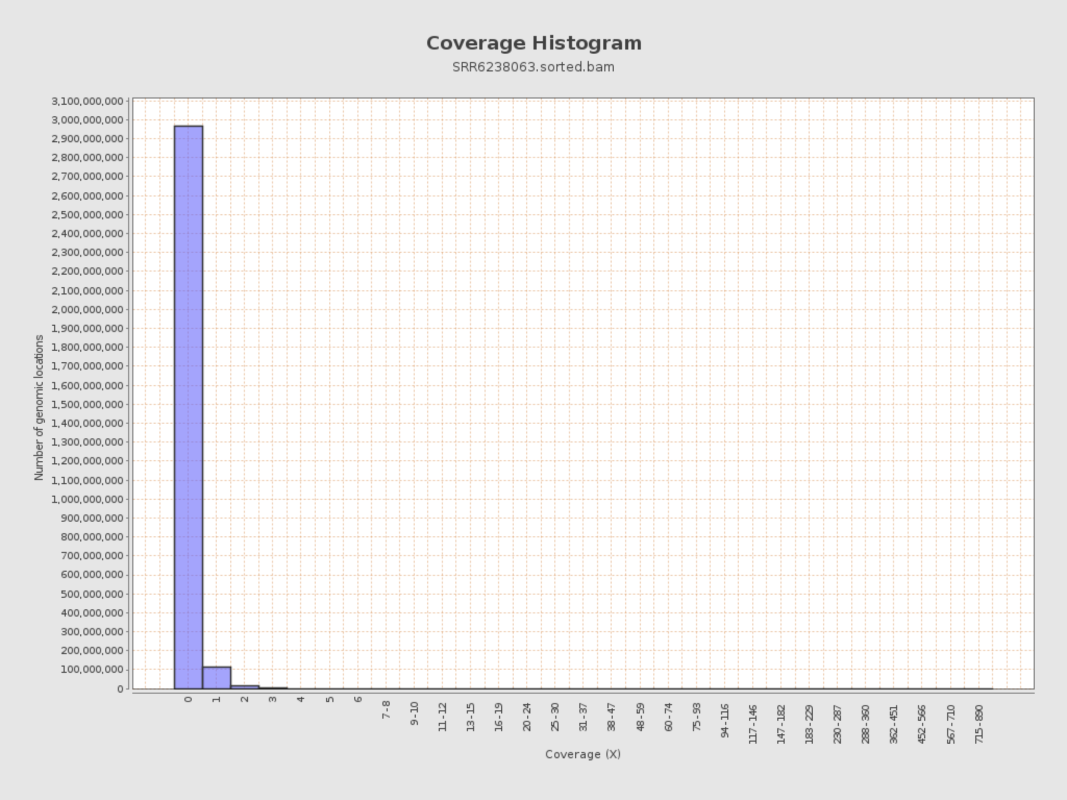
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13733970	0.0551	0.8075
chr2	243199373	17704645	0.0728	0.4486
chr3	198022430	10007078	0.0505	0.2579
chr4	191154276	7875598	0.0412	0.2465
chr5	180915260	8868421	0.049	0.2547
chr6	171115067	9263300	0.0541	0.3285
chr7	159138663	9615518	0.0604	0.6305

chr8	146364022	9061602	0.0619	0.4481
chr9	141213431	4961497	0.0351	0.3078
chr10	135534747	7107042	0.0524	0.4222
chr11	135006516	6066678	0.0449	0.2829
chr12	133851895	7624950	0.057	0.2742
chr13	115169878	6114142	0.0531	0.2625
chr14	107349540	3971837	0.037	0.2338
chr15	102531392	6392609	0.0623	0.2892
chr16	90354753	3669305	0.0406	0.2524
chr17	81195210	2929921	0.0361	0.2331
chr18	78077248	4216919	0.054	0.5719
chr19	59128983	3659956	0.0619	0.5236
chr20	63025520	2078117	0.033	0.2105
chr21	48129895	1735653	0.0361	0.2351
chr22	51304566	1923361	0.0375	0.2212
chrMT	16571	52257	3.1535	2.7642
chrX	155270560	6814709	0.0439	0.2607
chrY	59373566	356727	0.006	0.1667

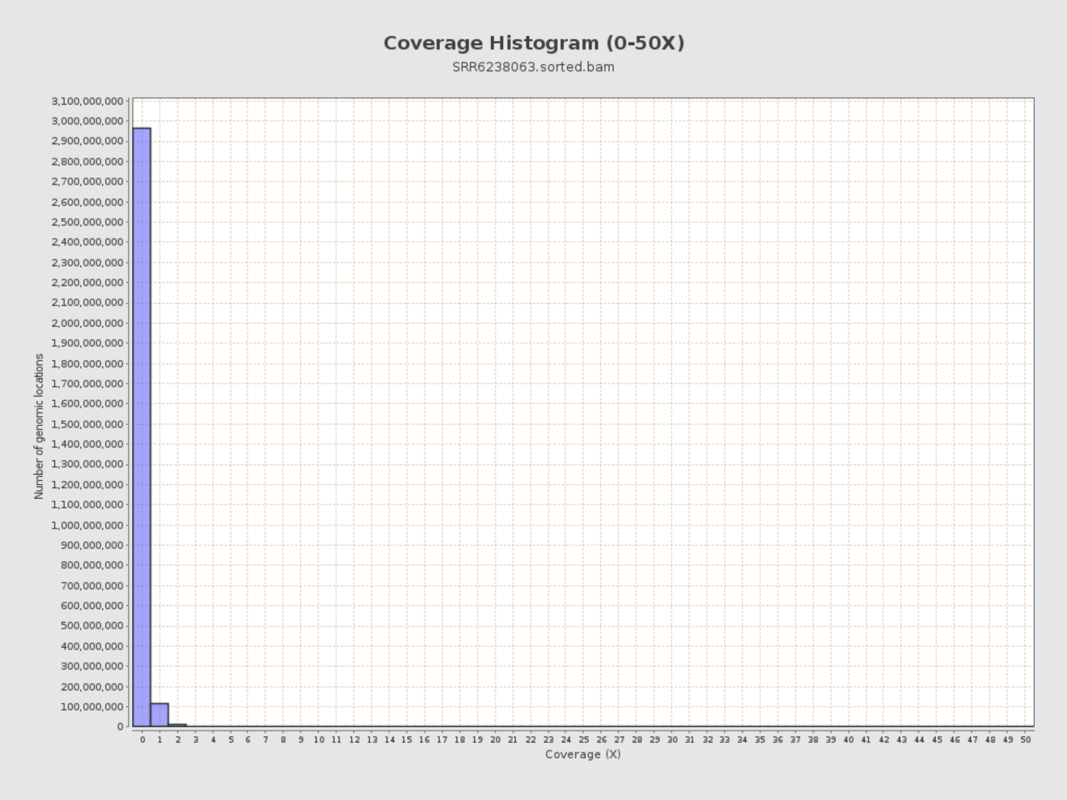
3. Results : Coverage across reference



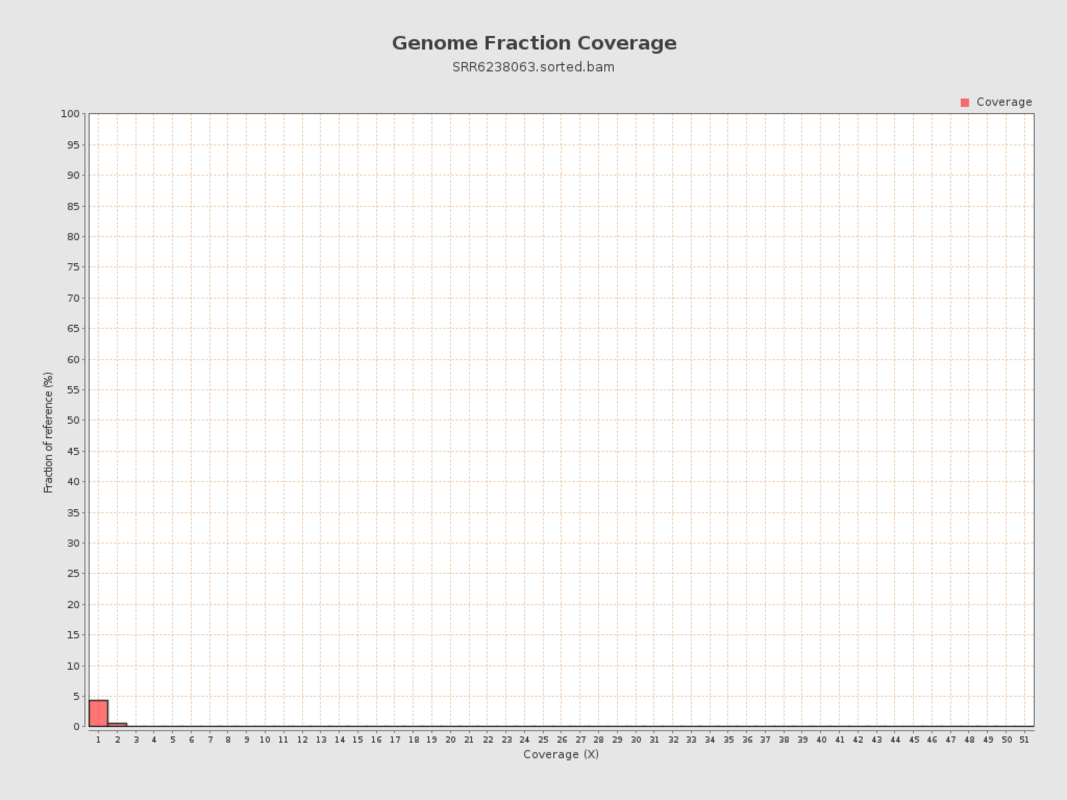
4. Results : Coverage Histogram



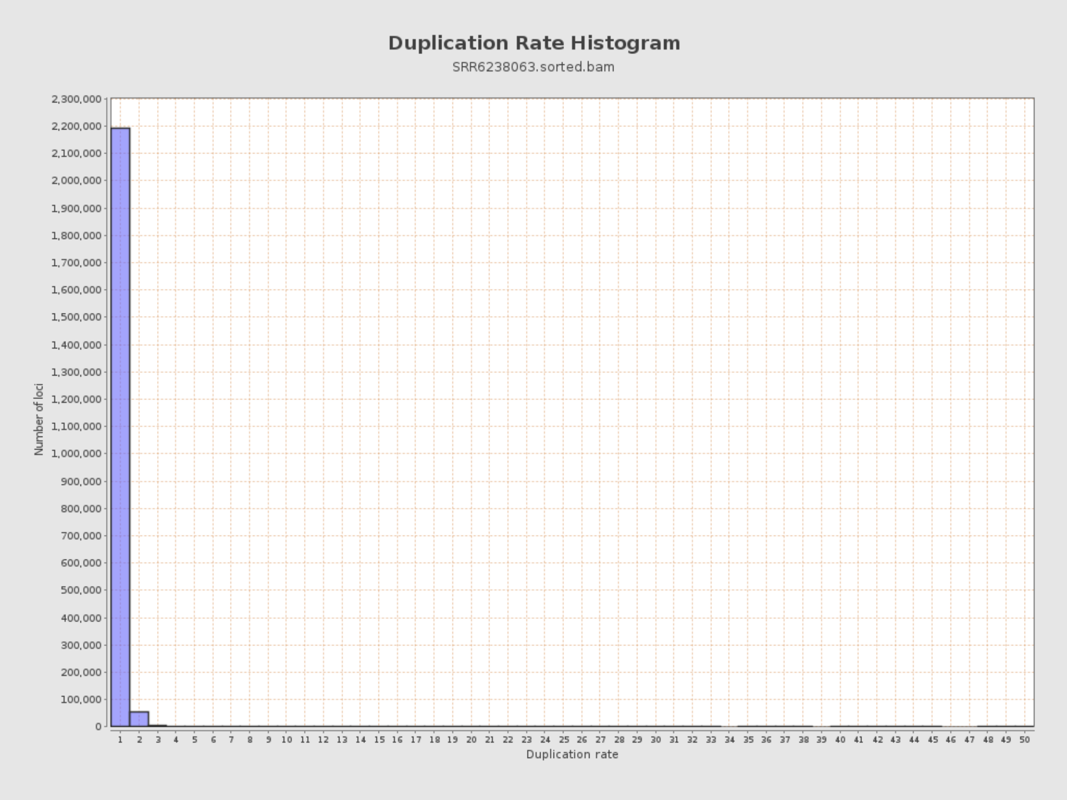
5. Results : Coverage Histogram (0-50X)



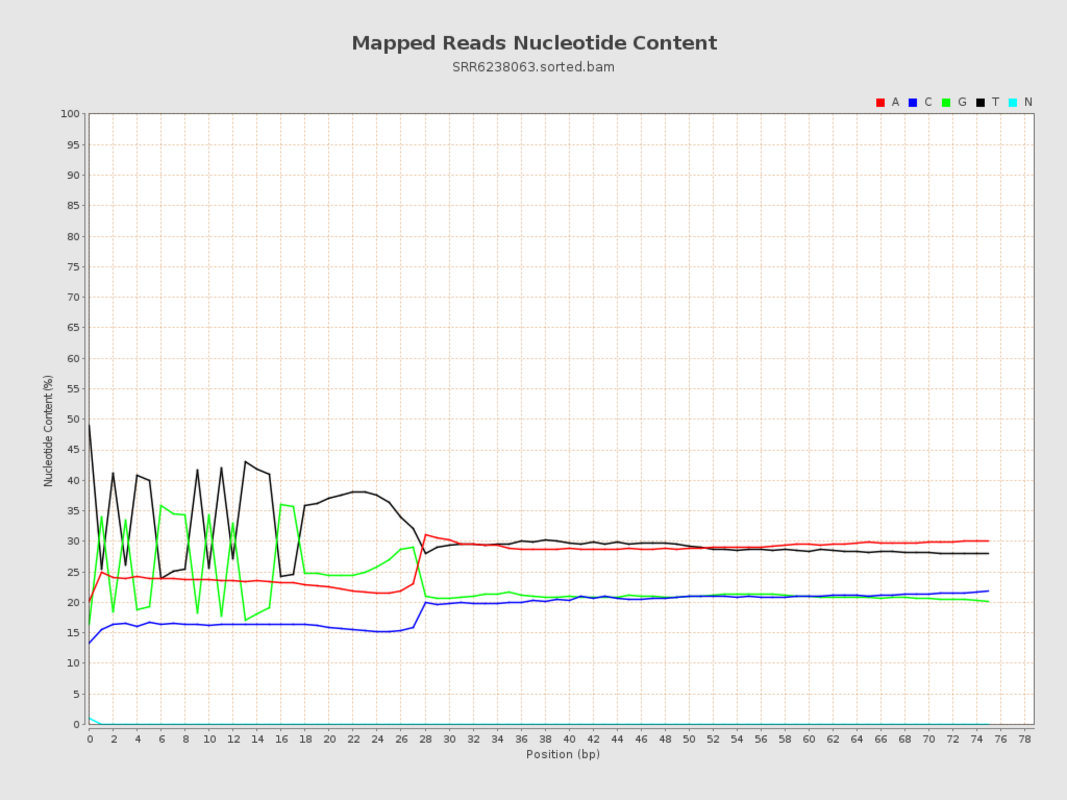
6. Results : Genome Fraction Coverage



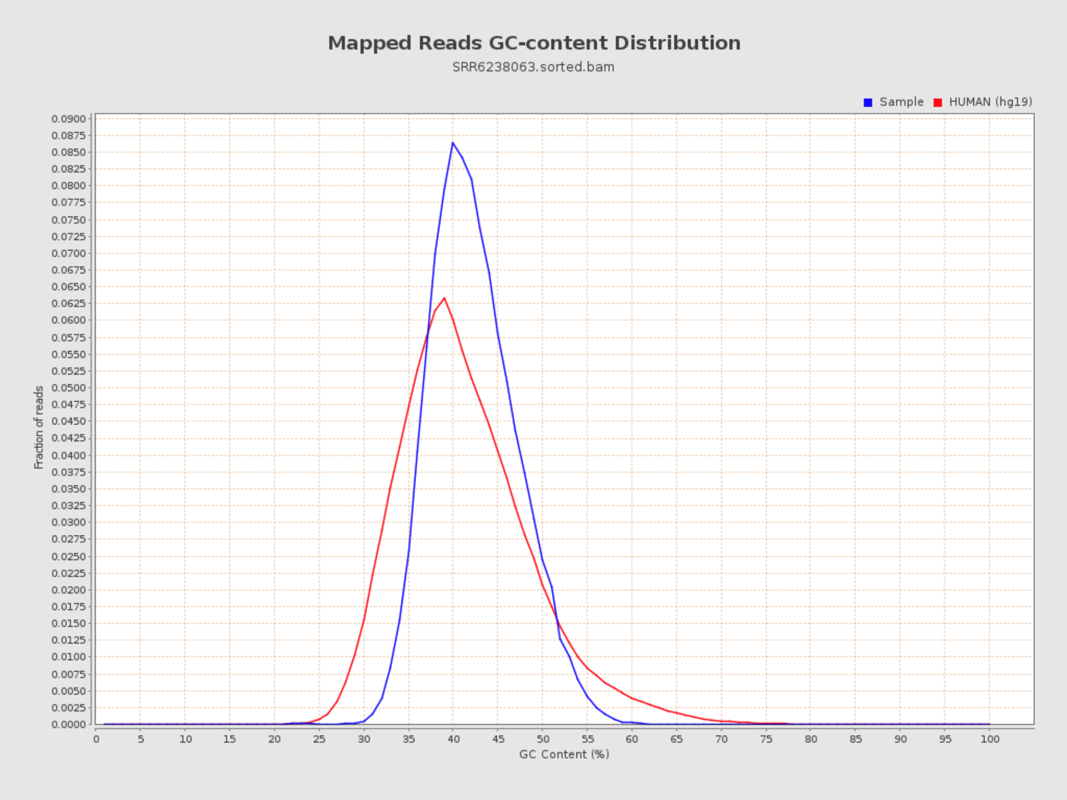
7. Results : Duplication Rate Histogram



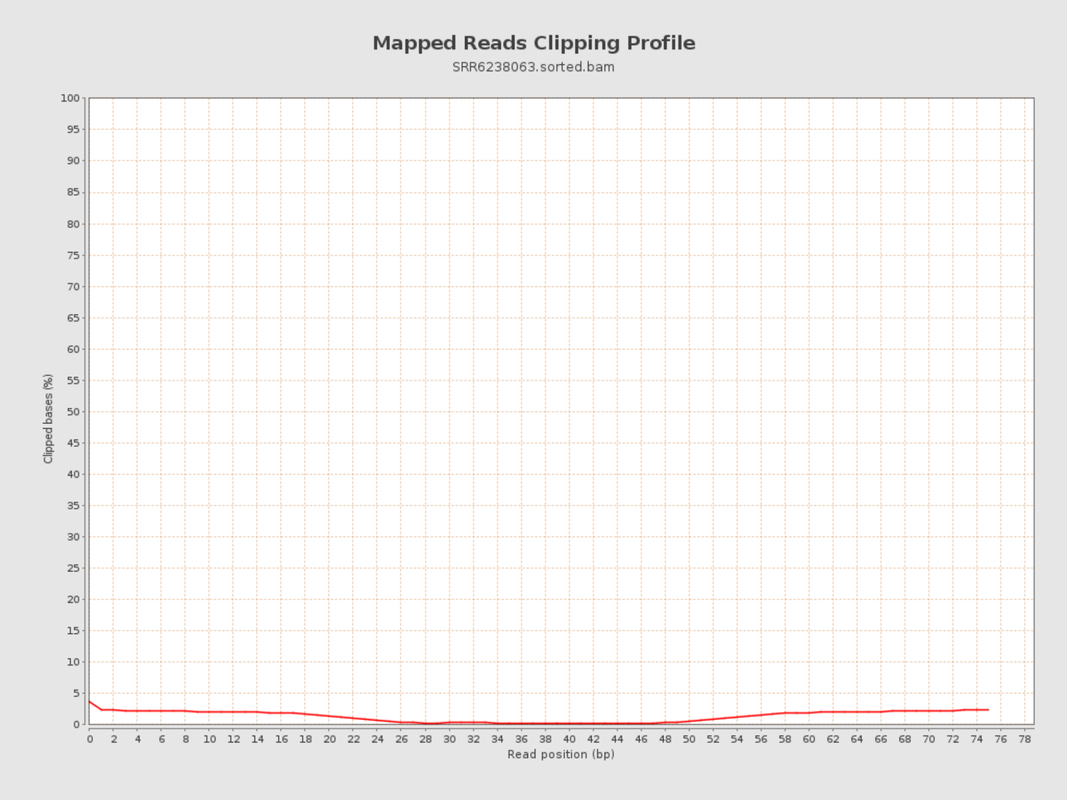
8. Results : Mapped Reads Nucleotide Content



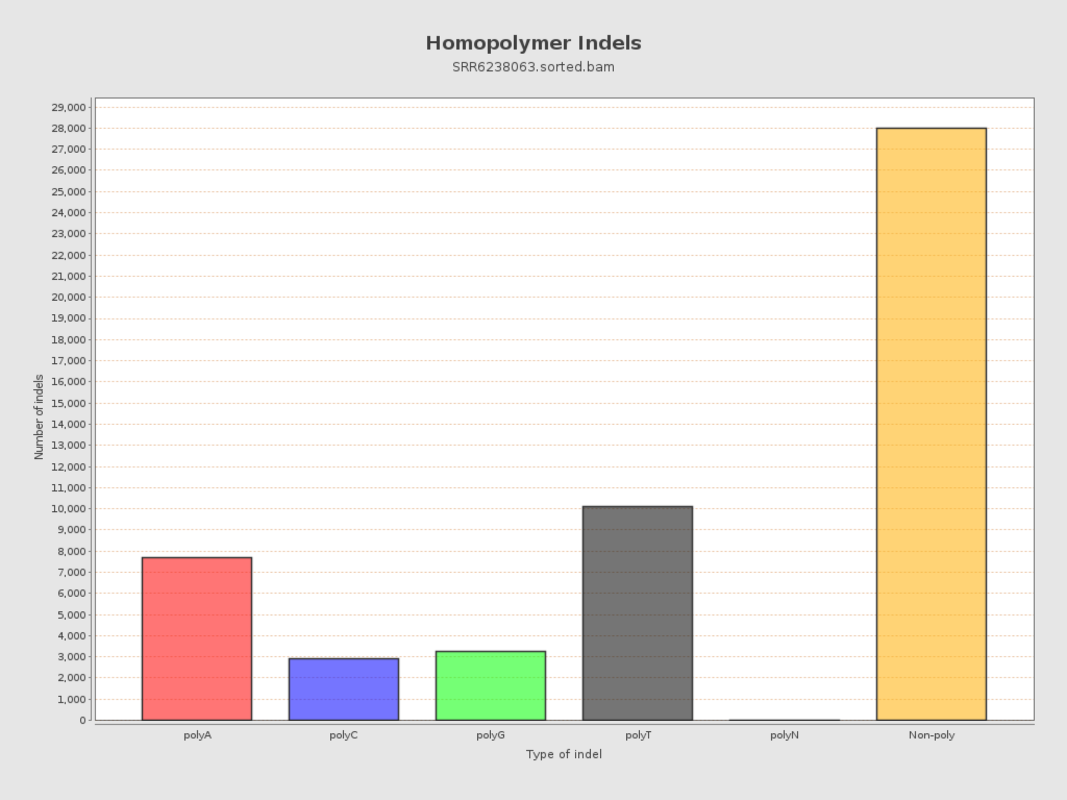
9. Results : Mapped Reads GC-content Distribution



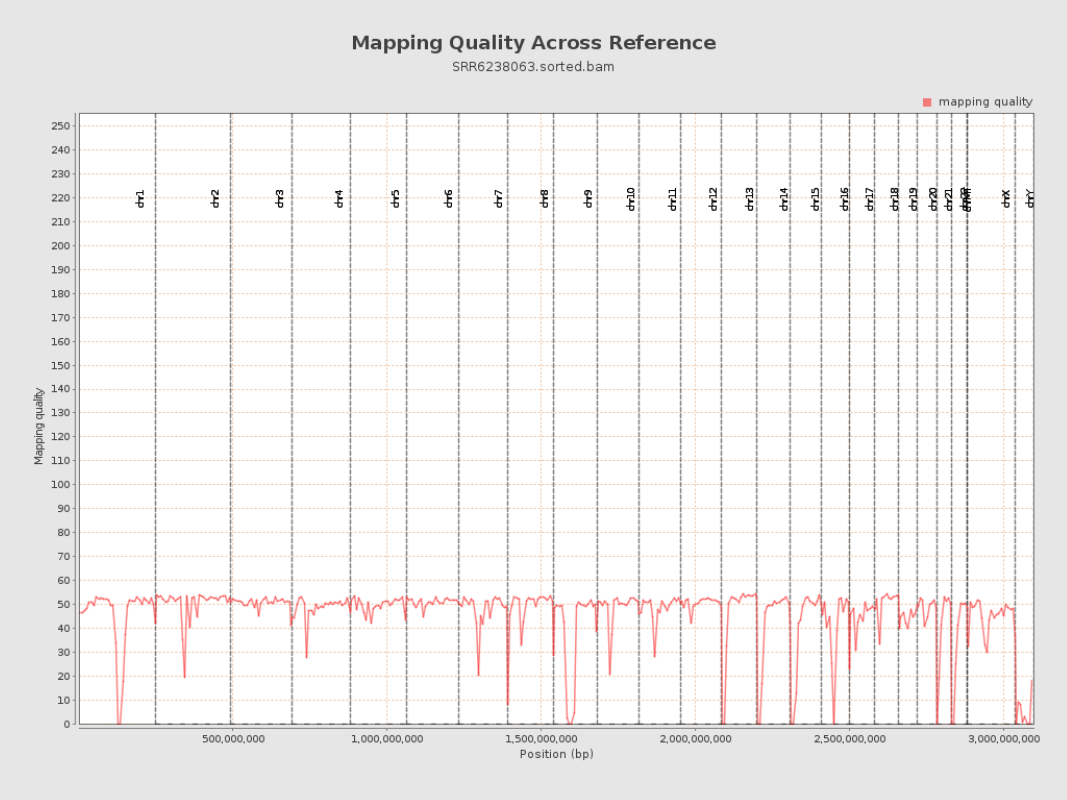
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram