Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:33:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238599.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_SRR6238599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238599.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:33:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,806,221
Mapped reads	3,367,760 / 88.48%
Unmapped reads	438,461 / 11.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,861 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	870,947 / 22.88%
Duplication rate	18.24%
Clipped reads	2,178,629 / 57.24%

2.2. ACGT Content

Number/percentage of A's	51,298,743 / 24.87%
Number/percentage of C's	37,428,646 / 18.15%
Number/percentage of T's	67,644,777 / 32.8%
Number/percentage of G's	49,850,035 / 24.17%
Number/percentage of N's	10,496 / 0.01%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0667

Standard Deviation	0.973

2.4. Mapping Quality

Mean Mapping Quality	42.63

2.5. Mismatches and indels

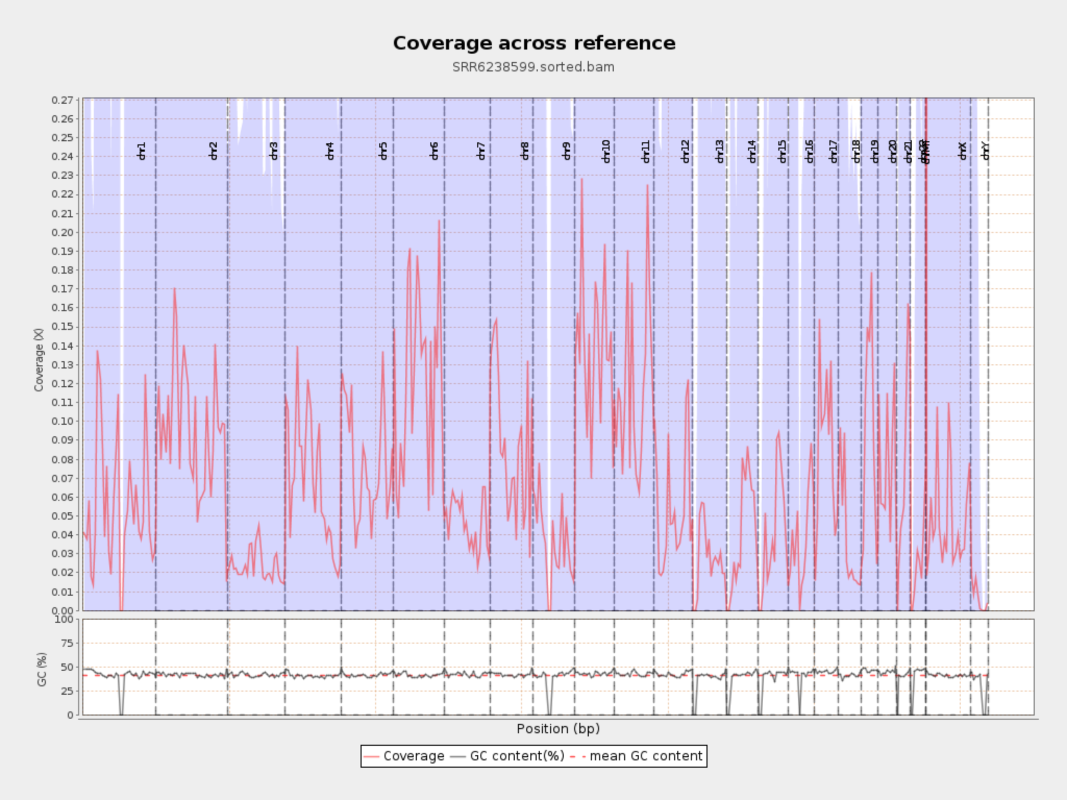
General error rate	0.59%
Mismatches	1,190,810
Insertions	11,656
Mapped reads with at least one insertion	0.34%
Deletions	60,945
Mapped reads with at least one deletion	1.79%
Homopolymer indels	40.6%

2.6. Chromosome stats

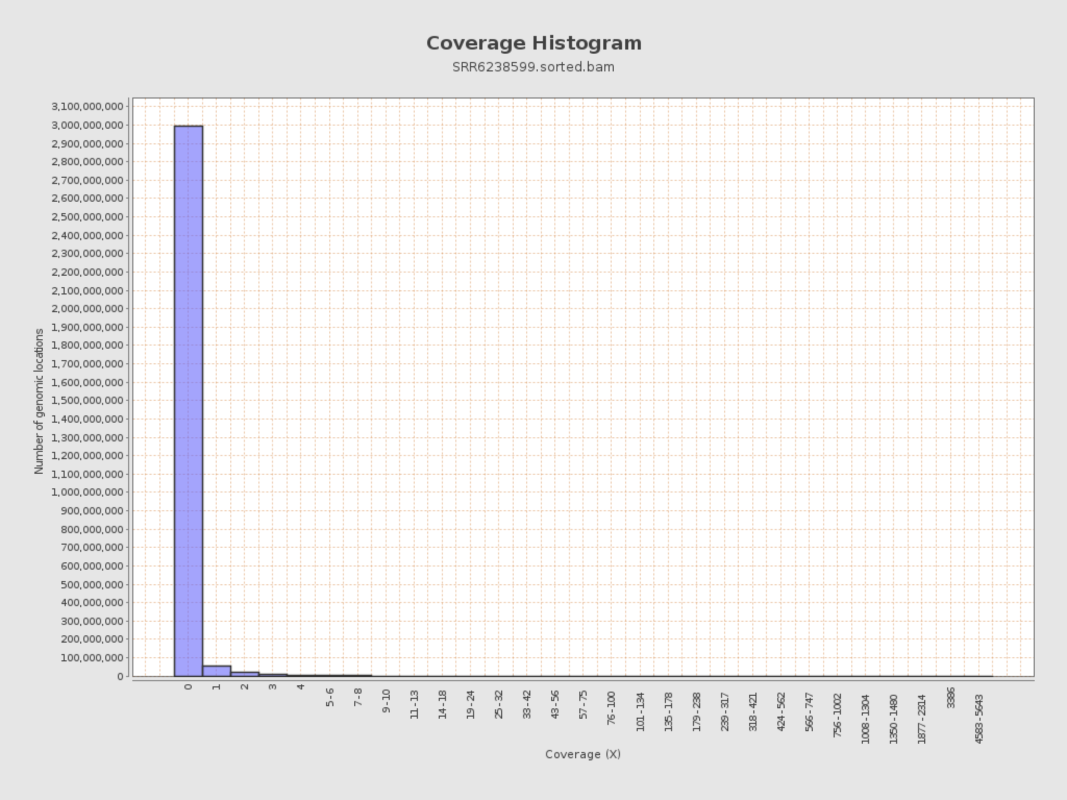
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13729167	0.0551	1.1959
chr2	243199373	23615395	0.0971	2.5124
chr3	198022430	4680263	0.0236	0.297
chr4	191154276	12965471	0.0678	0.4781
chr5	180915260	14203446	0.0785	0.5152
chr6	171115067	21004778	0.1228	1.114
chr7	159138663	7298177	0.0459	0.5041

chr8	146364022	12738960	0.087	0.8025
chr9	141213431	5063101	0.0359	0.4602
chr10	135534747	18988902	0.1401	0.7111
chr11	135006516	15945211	0.1181	0.7129
chr12	133851895	7309949	0.0546	0.4489
chr13	115169878	3141518	0.0273	0.5086
chr14	107349540	4494046	0.0419	0.4126
chr15	102531392	4105385	0.04	0.6956
chr16	90354753	3351077	0.0371	0.4028
chr17	81195210	6976382	0.0859	0.5637
chr18	78077248	3073873	0.0394	1.3426
chr19	59128983	5755902	0.0973	0.8347
chr20	63025520	5066999	0.0804	0.5371
chr21	48129895	3719742	0.0773	0.5273
chr22	51304566	1165944	0.0227	0.27
chrMT	16571	53919	3.2538	3.2112
chrX	155270560	7486653	0.0482	0.4094
chrY	59373566	402597	0.0068	0.2504

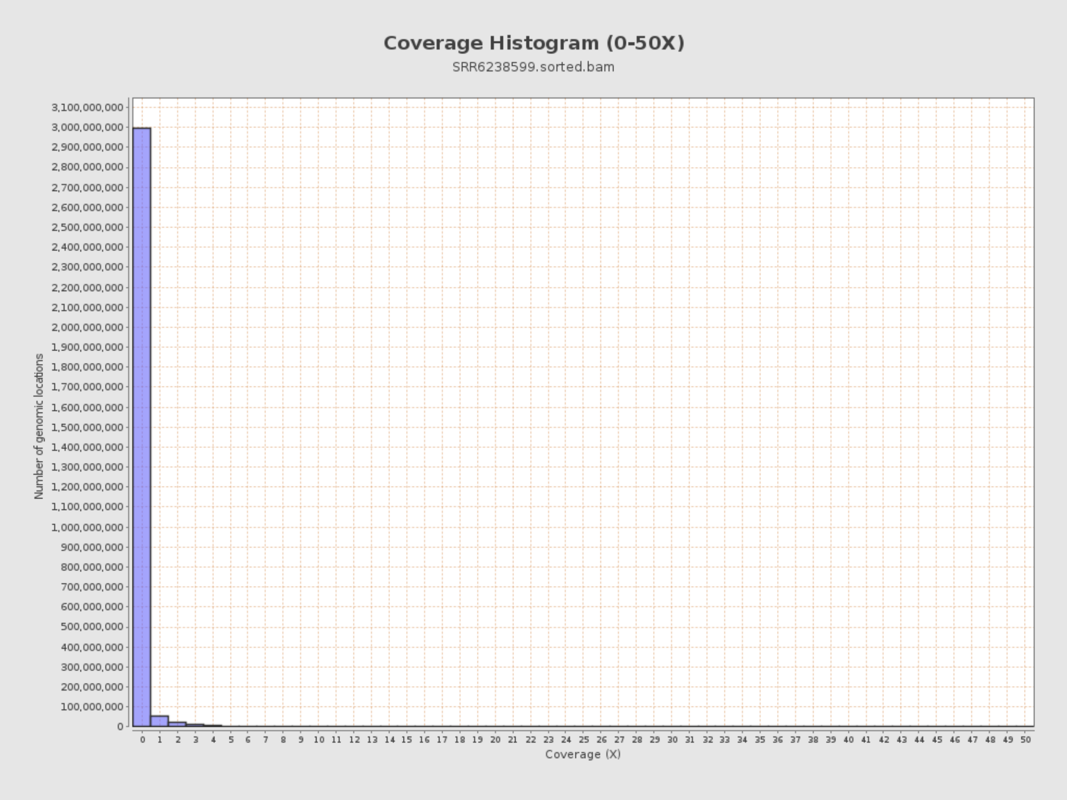
3. Results : Coverage across reference



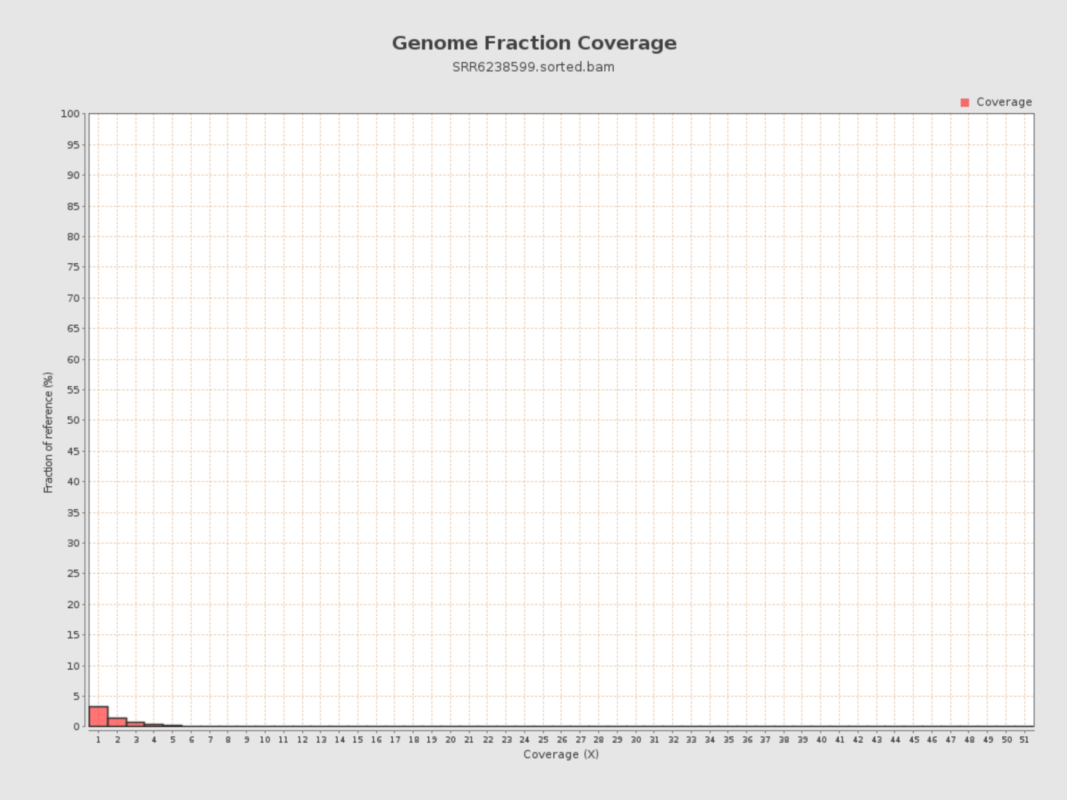
4. Results : Coverage Histogram



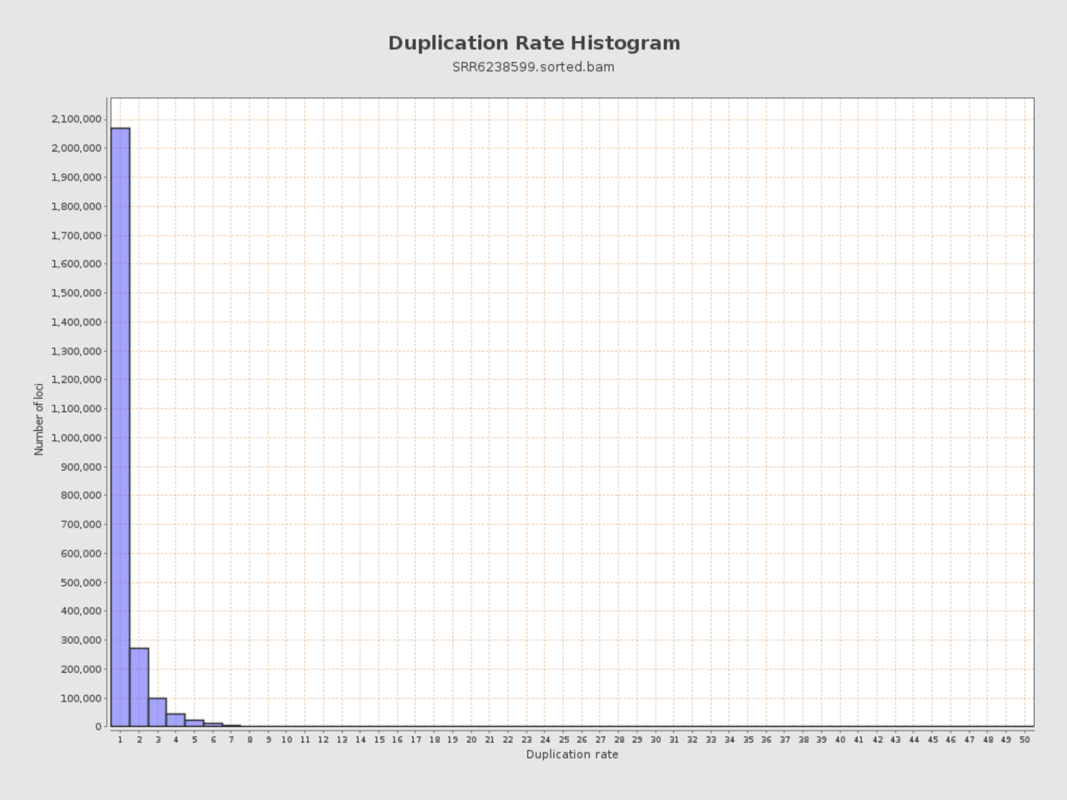
5. Results : Coverage Histogram (0-50X)



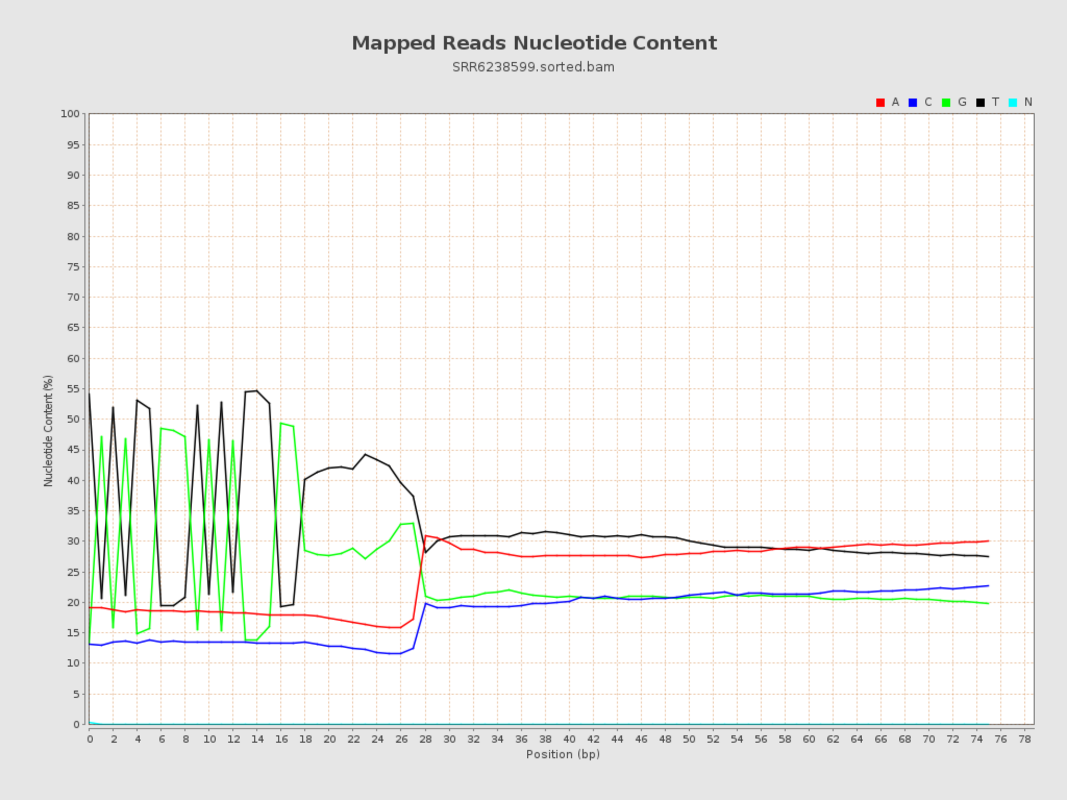
6. Results : Genome Fraction Coverage



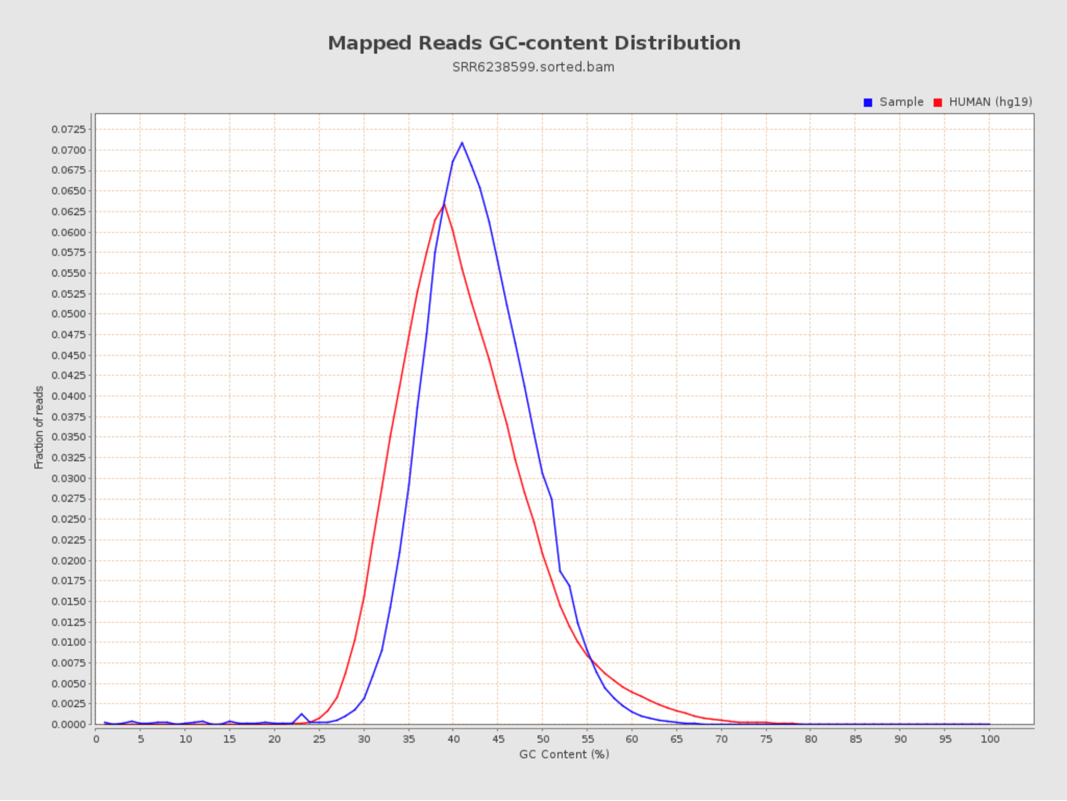
7. Results : Duplication Rate Histogram



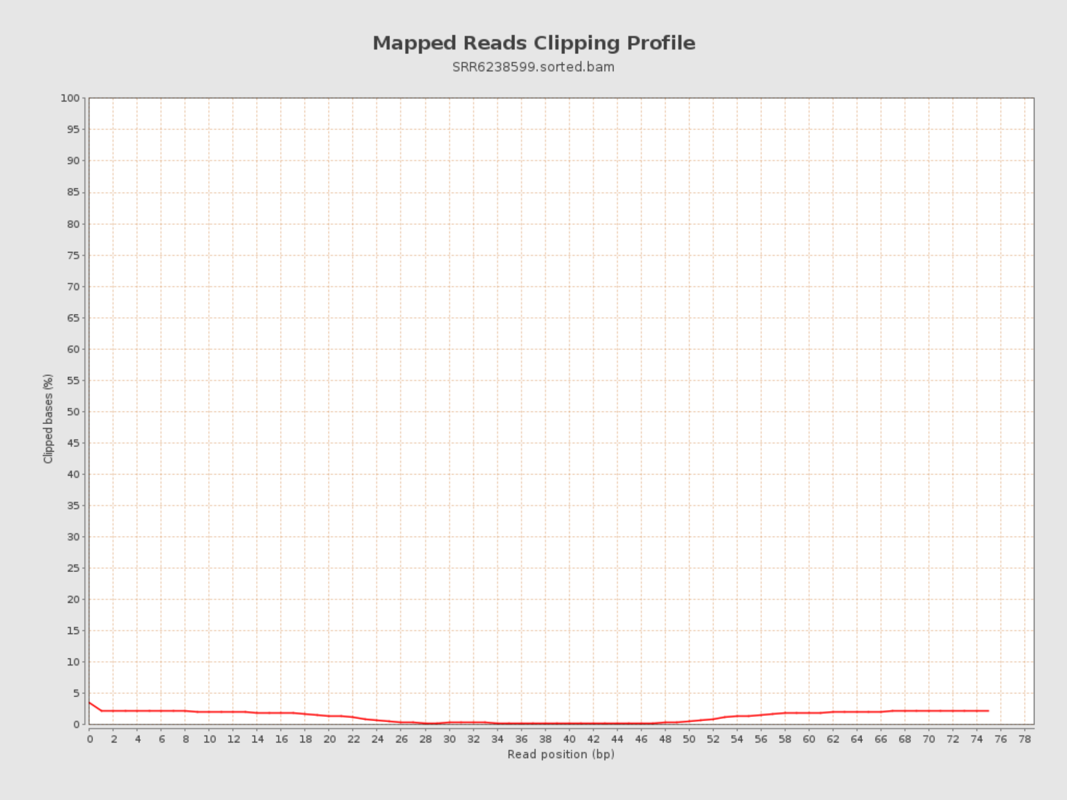
8. Results : Mapped Reads Nucleotide Content



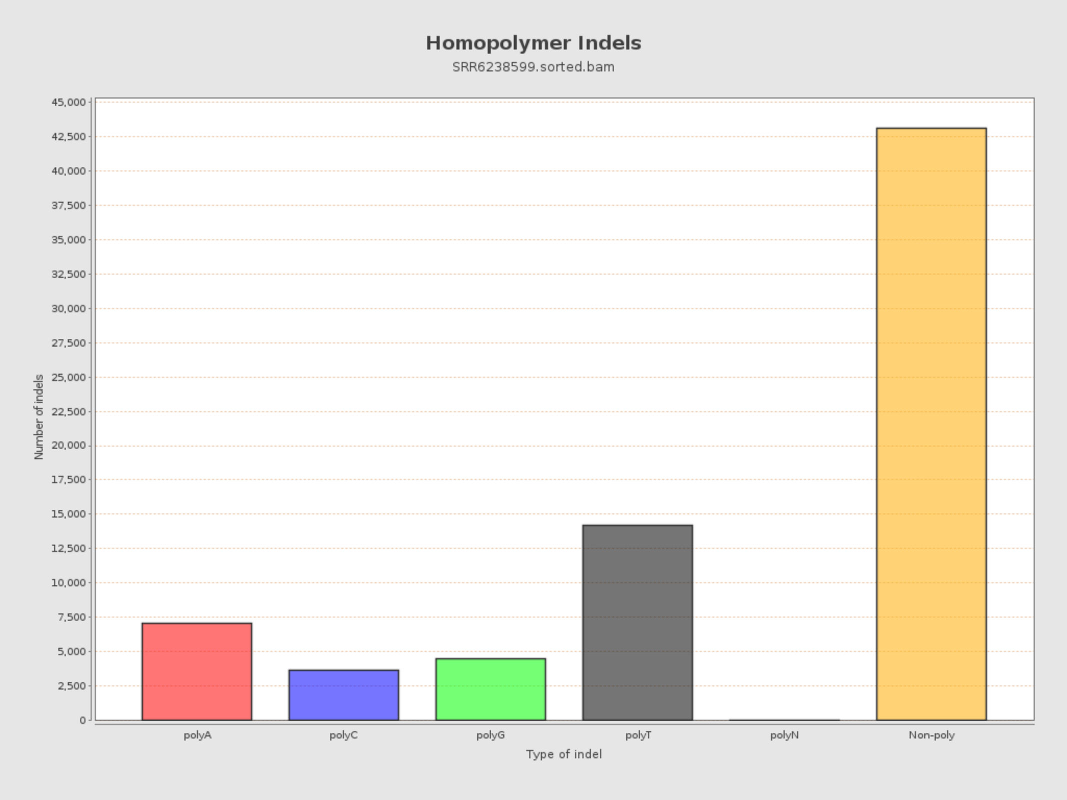
9. Results : Mapped Reads GC-content Distribution



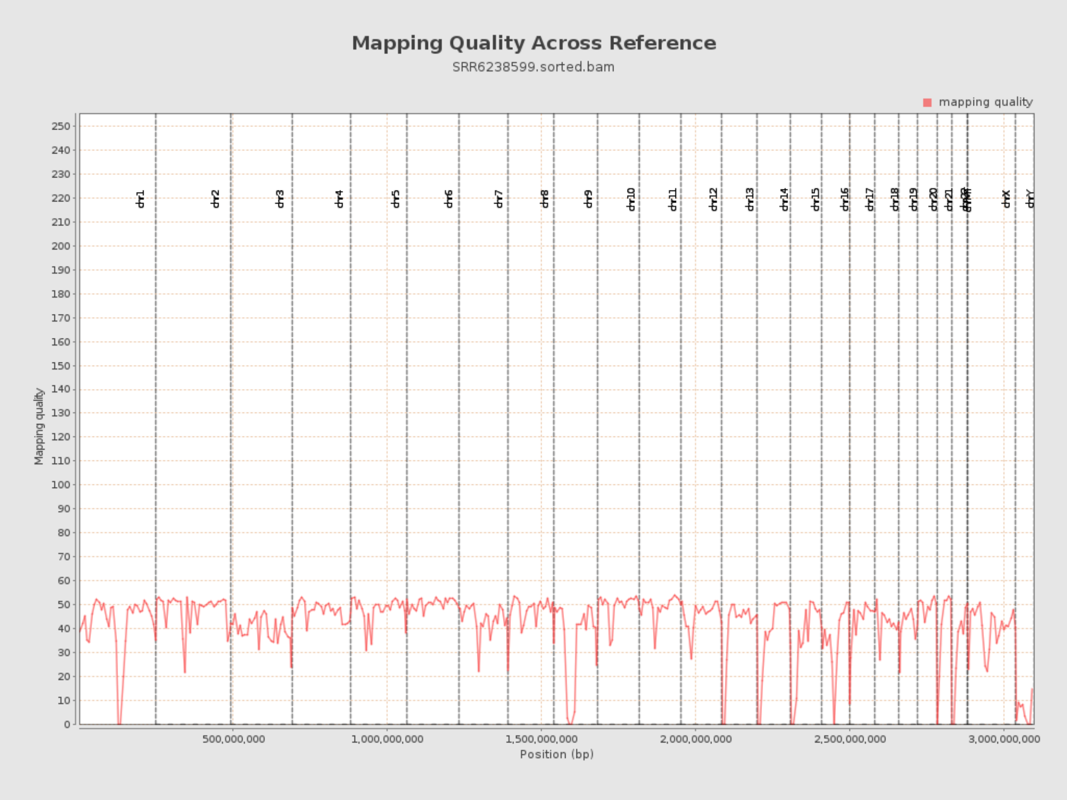
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram