Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:38:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238324.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_SRR6238324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:38:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,469,056
Mapped reads	2,253,316 / 91.26%
Unmapped reads	215,740 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,843 / 1.13%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	99,298 / 4.02%
Duplication rate	3.28%
Clipped reads	1,089,605 / 44.13%

2.2. ACGT Content

Number/percentage of A's	42,985,089 / 28.79%
Number/percentage of C's	27,720,186 / 18.57%
Number/percentage of T's	47,032,392 / 31.5%
Number/percentage of G's	31,504,986 / 21.1%
Number/percentage of N's	45,632 / 0.03%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.4584

2.4. Mapping Quality

Mean Mapping Quality	46.5

2.5. Mismatches and indels

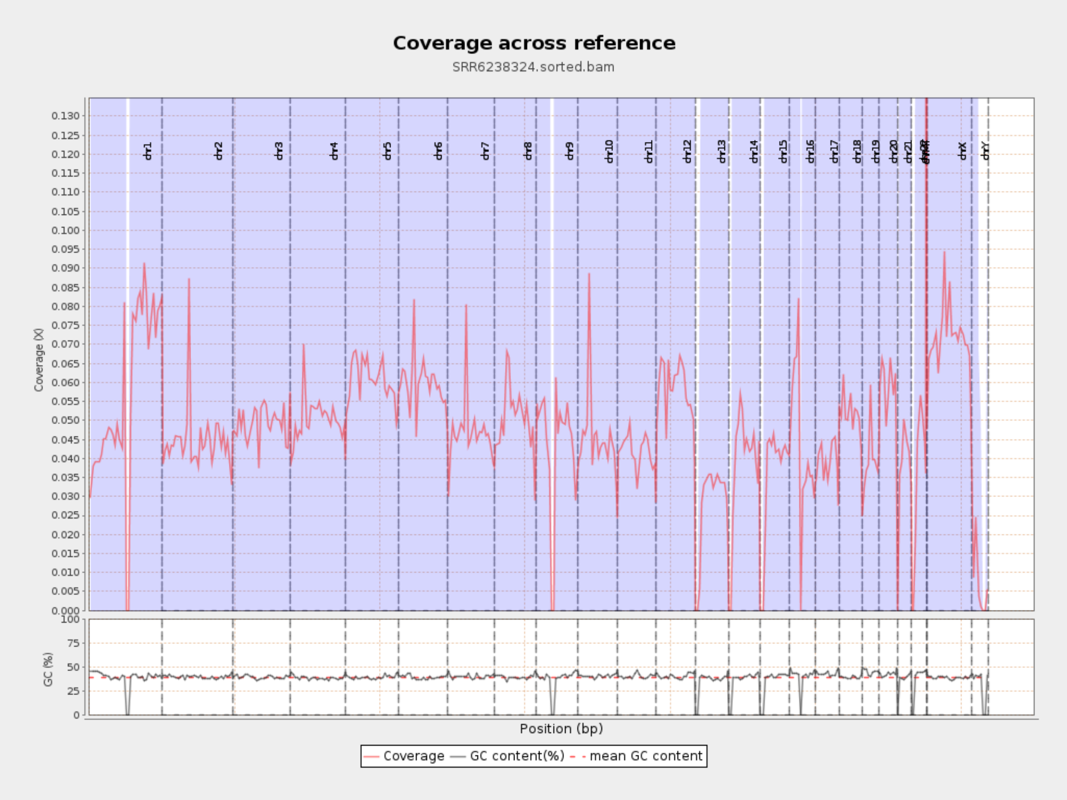
General error rate	0.89%
Mismatches	1,309,775
Insertions	11,602
Mapped reads with at least one insertion	0.51%
Deletions	45,415
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.17%

2.6. Chromosome stats

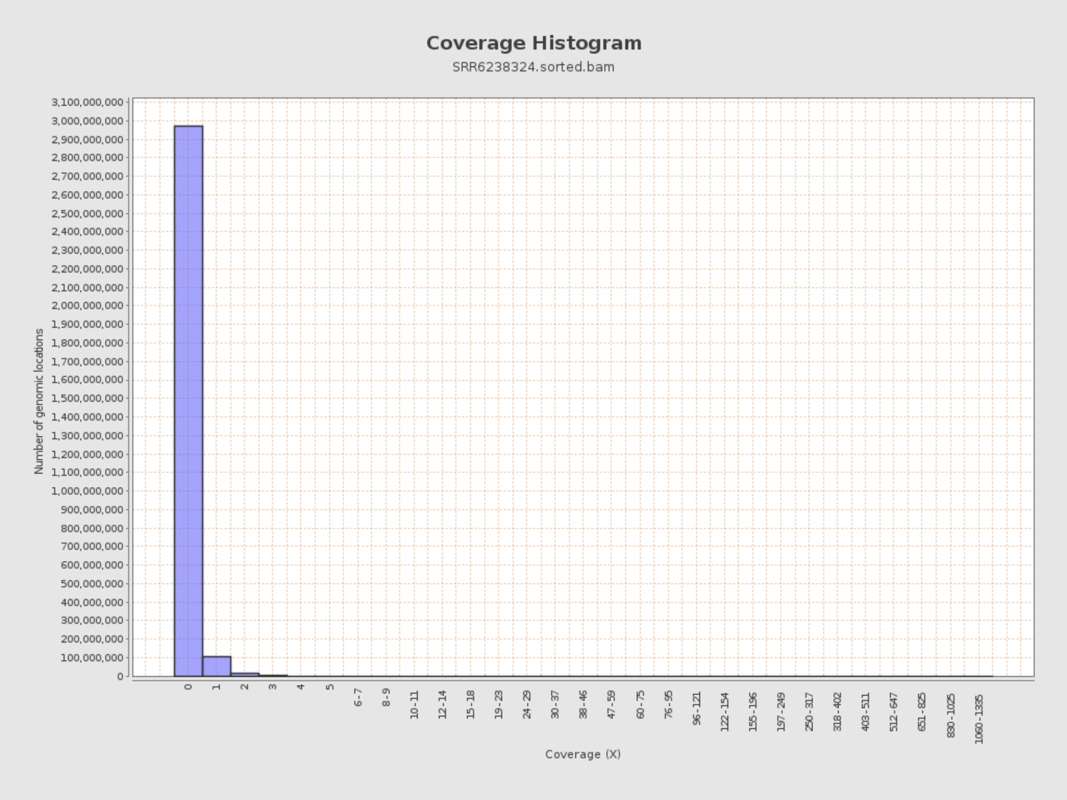
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14104026	0.0566	0.8505
chr2	243199373	10866401	0.0447	0.4669
chr3	198022430	9723012	0.0491	0.2571
chr4	191154276	9606175	0.0503	0.2923
chr5	180915260	10990242	0.0607	0.288
chr6	171115067	10217234	0.0597	0.3712
chr7	159138663	7519184	0.0472	0.5406

chr8	146364022	7382766	0.0504	0.847
chr9	141213431	6078962	0.043	0.4074
chr10	135534747	6226369	0.0459	0.4369
chr11	135006516	5618035	0.0416	0.321
chr12	133851895	7835339	0.0585	0.2886
chr13	115169878	3180609	0.0276	0.1914
chr14	107349540	4080930	0.038	0.258
chr15	102531392	3603000	0.0351	0.2212
chr16	90354753	3948158	0.0437	0.2804
chr17	81195210	3155619	0.0389	0.2591
chr18	78077248	4070118	0.0521	0.7275
chr19	59128983	2346150	0.0397	0.5909
chr20	63025520	3695296	0.0586	0.2882
chr21	48129895	1799286	0.0374	0.2608
chr22	51304566	1731671	0.0338	0.2103
chrMT	16571	17923	1.0816	1.4091
chrX	155270560	11116436	0.0716	0.3492
chrY	59373566	454445	0.0077	0.1981

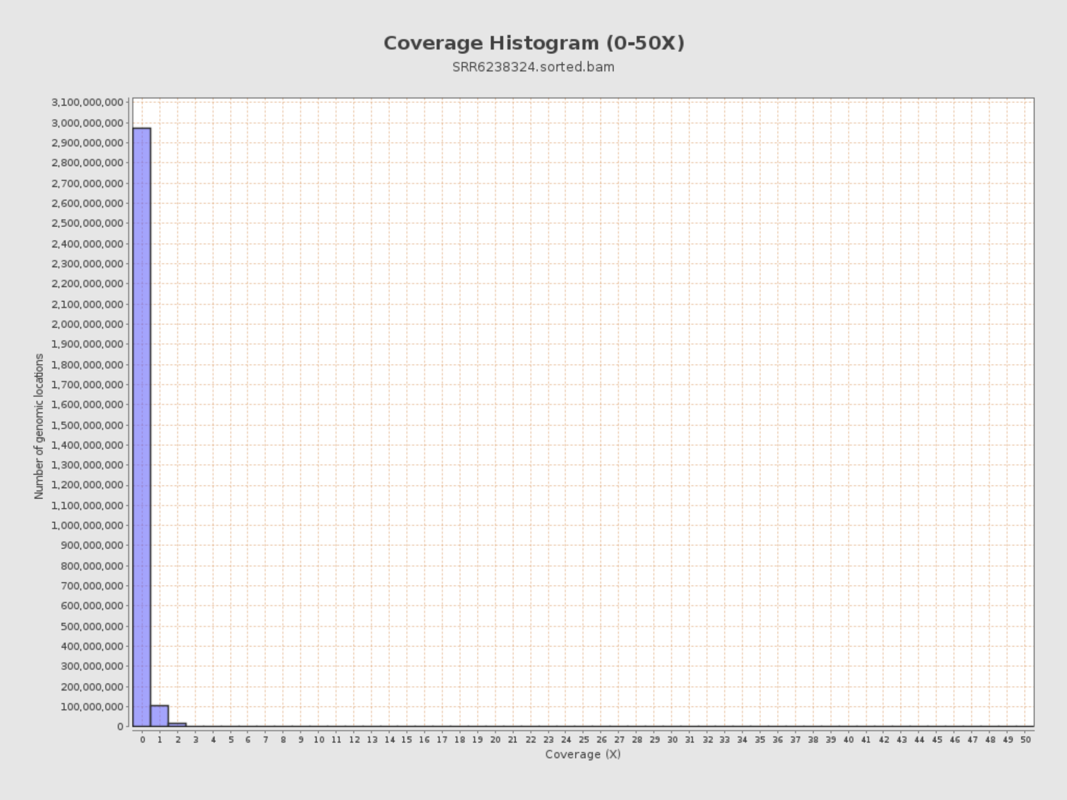
3. Results : Coverage across reference



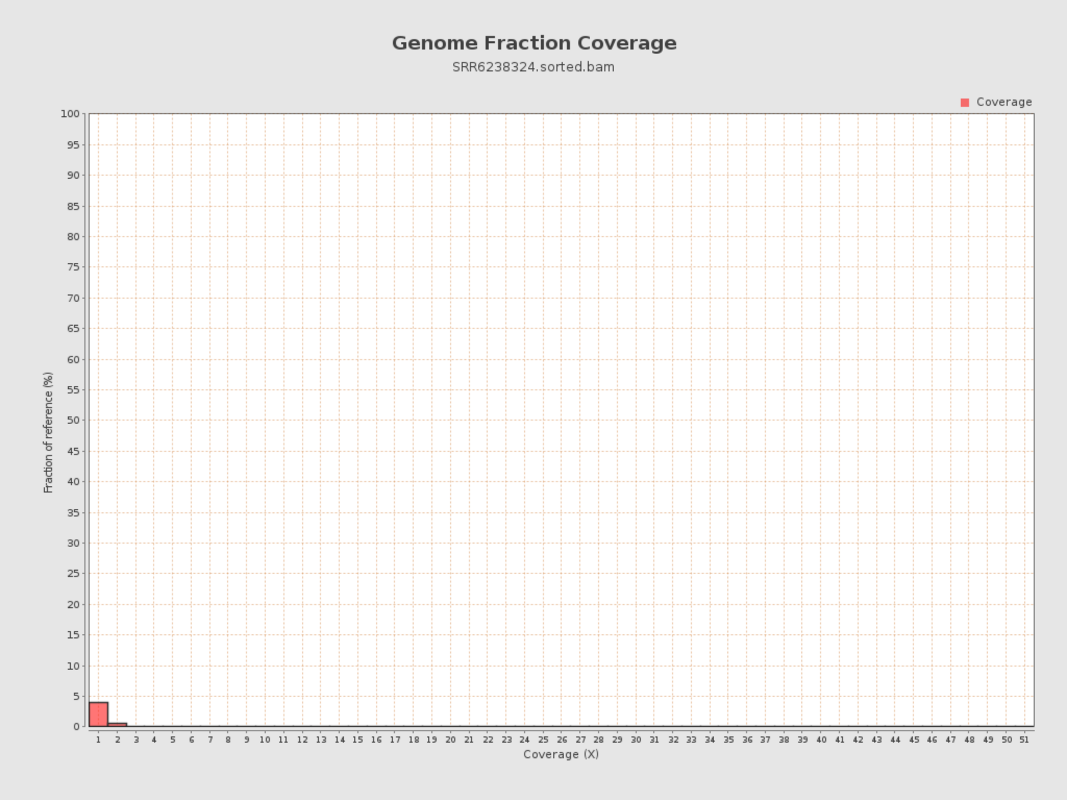
4. Results : Coverage Histogram



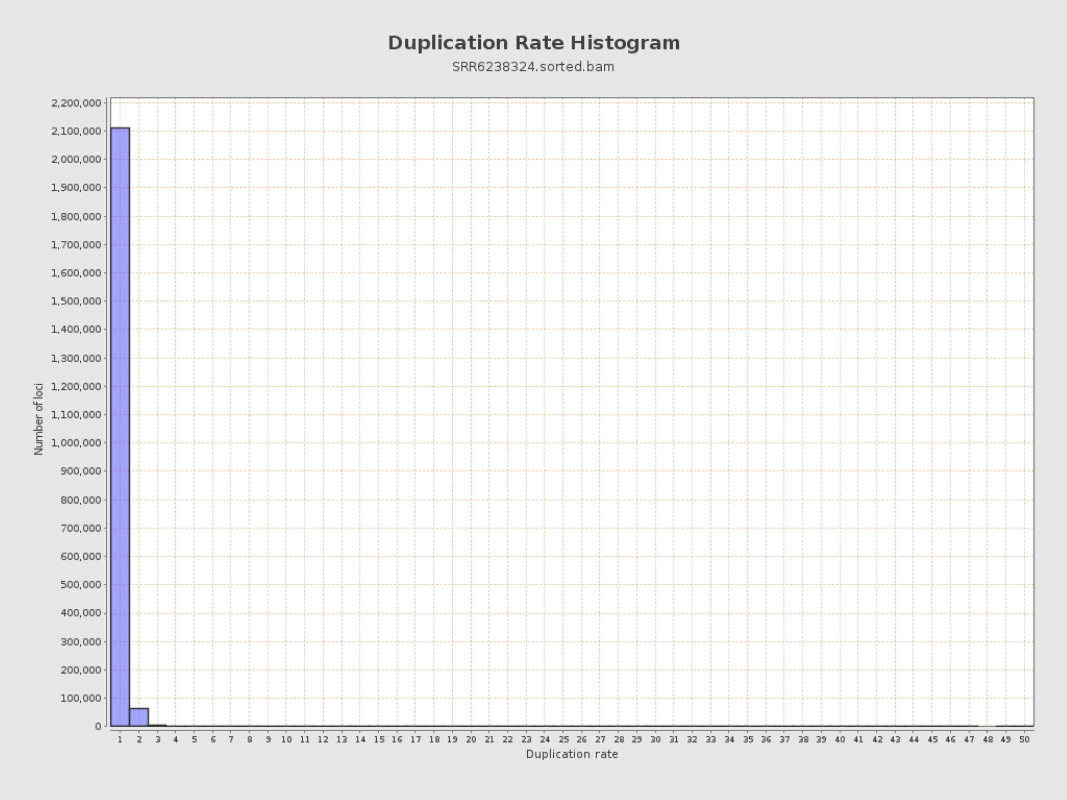
5. Results : Coverage Histogram (0-50X)



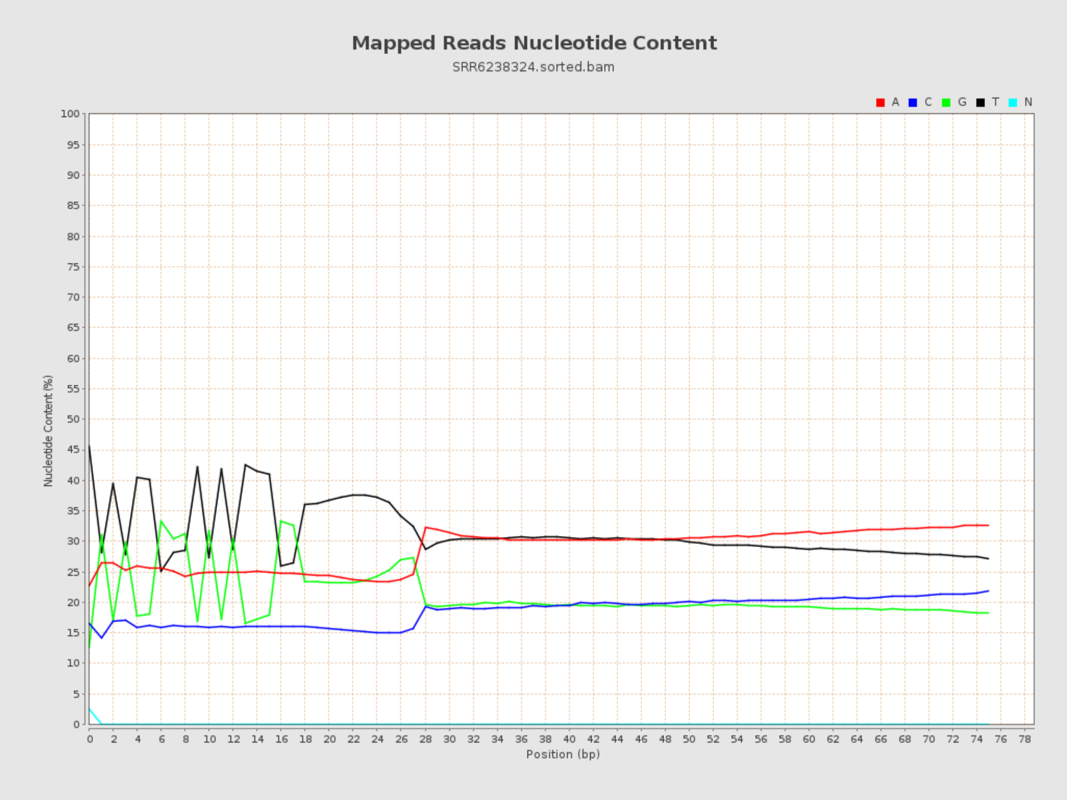
6. Results : Genome Fraction Coverage



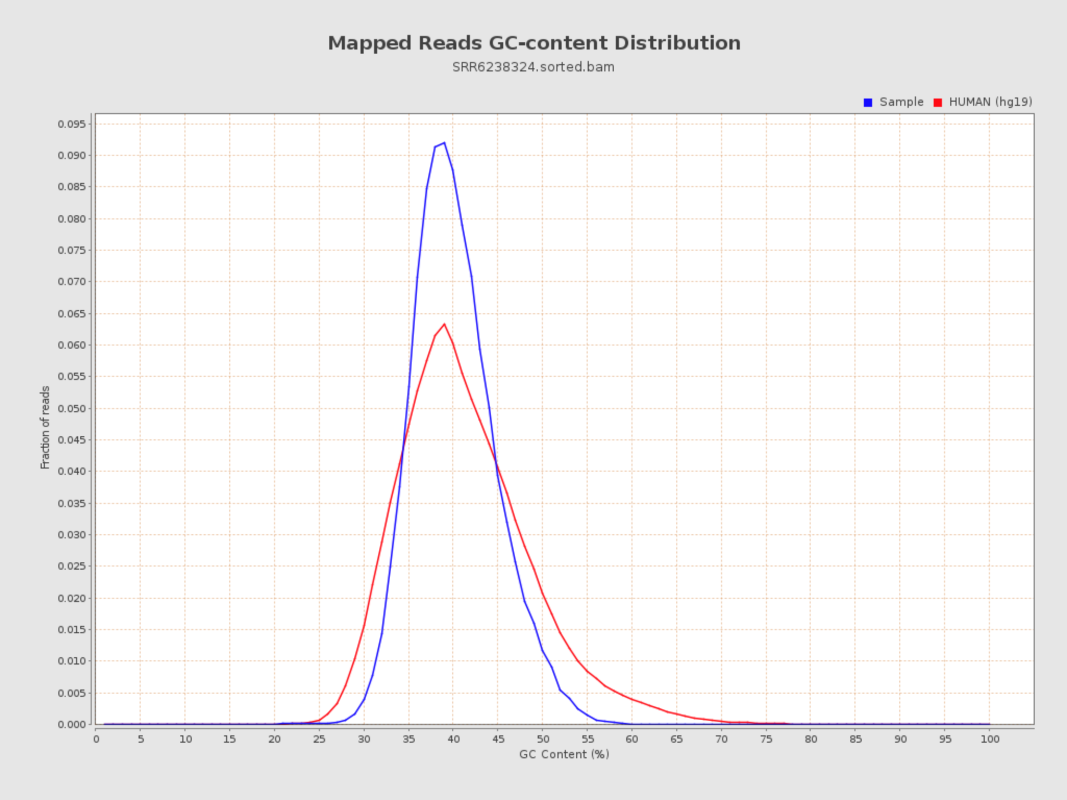
7. Results : Duplication Rate Histogram



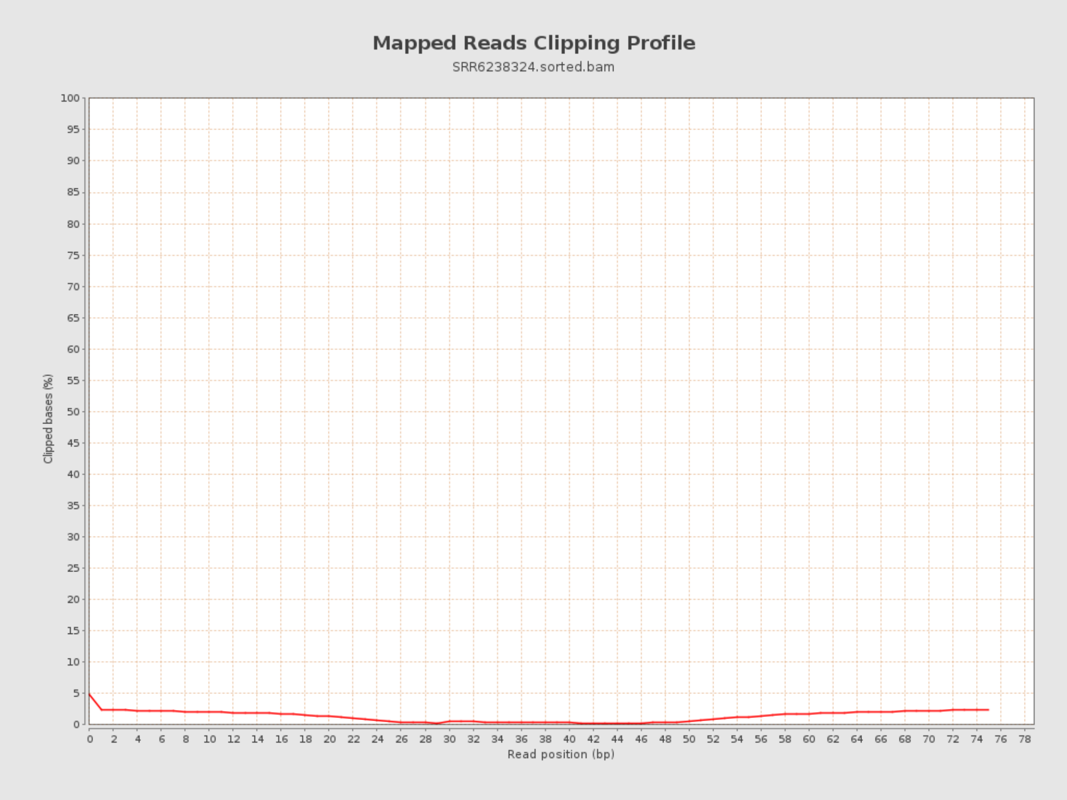
8. Results : Mapped Reads Nucleotide Content



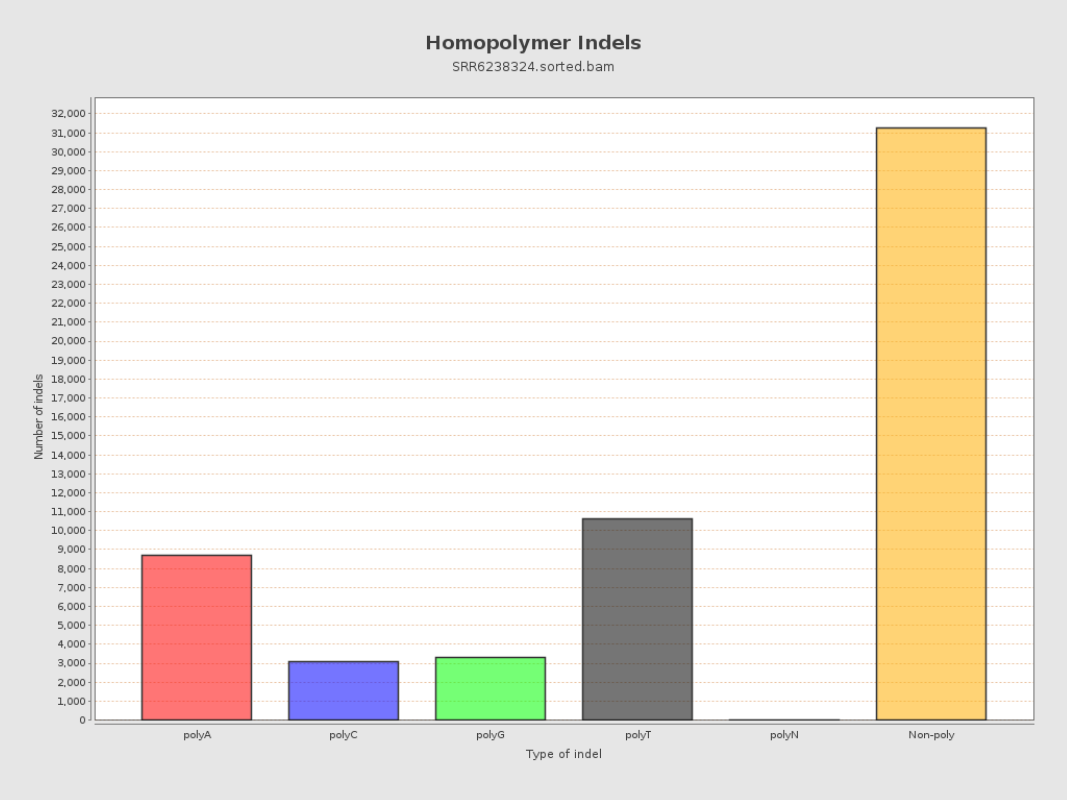
9. Results : Mapped Reads GC-content Distribution



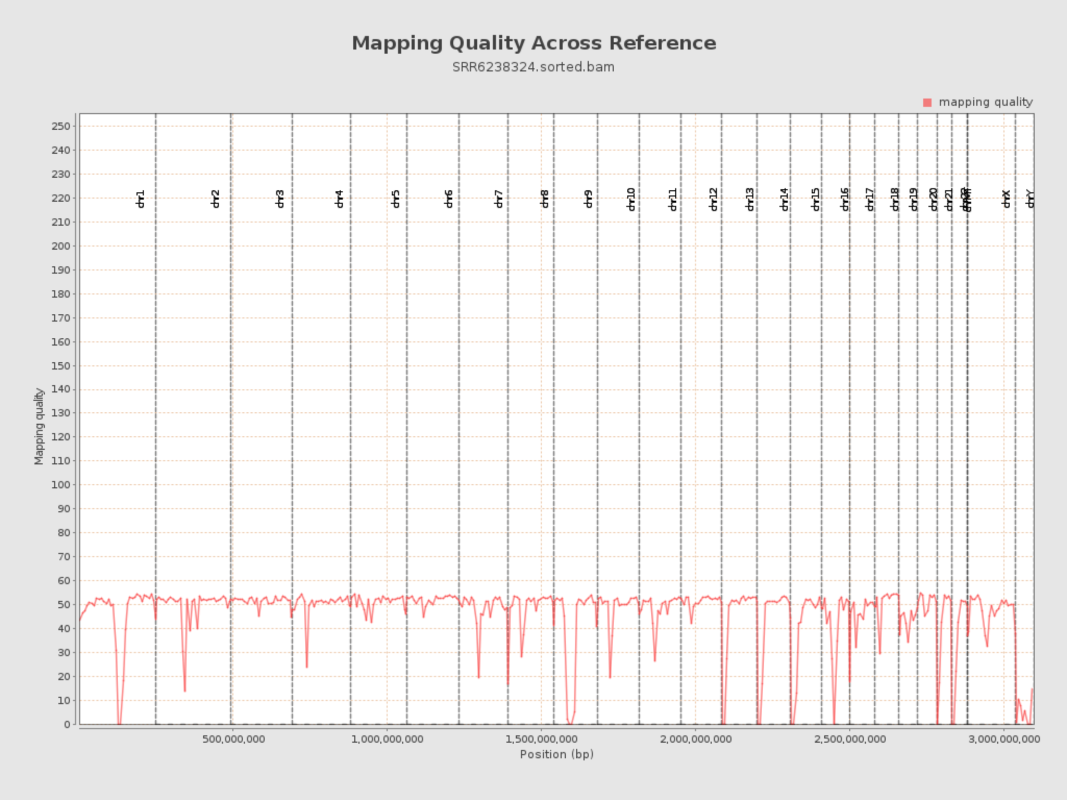
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram