Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:50:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238310.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_SRR6238310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:50:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,557,575
Mapped reads	2,184,399 / 85.41%
Unmapped reads	373,176 / 14.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,335 / 1.19%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	154,627 / 6.05%
Duplication rate	5.74%
Clipped reads	1,294,792 / 50.63%

2.2. ACGT Content

Number/percentage of A's	38,856,428 / 27.91%
Number/percentage of C's	26,683,752 / 19.17%
Number/percentage of T's	42,811,812 / 30.75%
Number/percentage of G's	30,827,316 / 22.14%
Number/percentage of N's	36,529 / 0.03%
GC Percentage	41.31%

2.3. Coverage

Mean	0.045

Standard Deviation	0.392

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

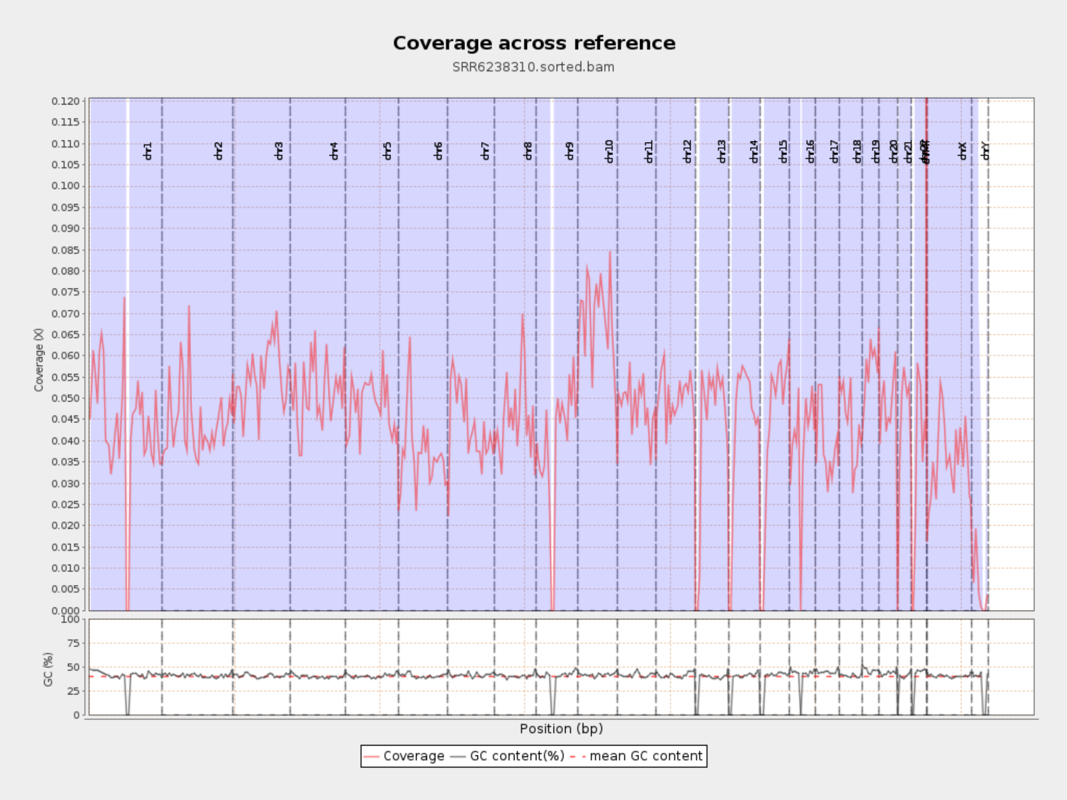
General error rate	0.95%
Mismatches	1,300,770
Insertions	10,951
Mapped reads with at least one insertion	0.5%
Deletions	51,172
Mapped reads with at least one deletion	2.31%
Homopolymer indels	44.25%

2.6. Chromosome stats

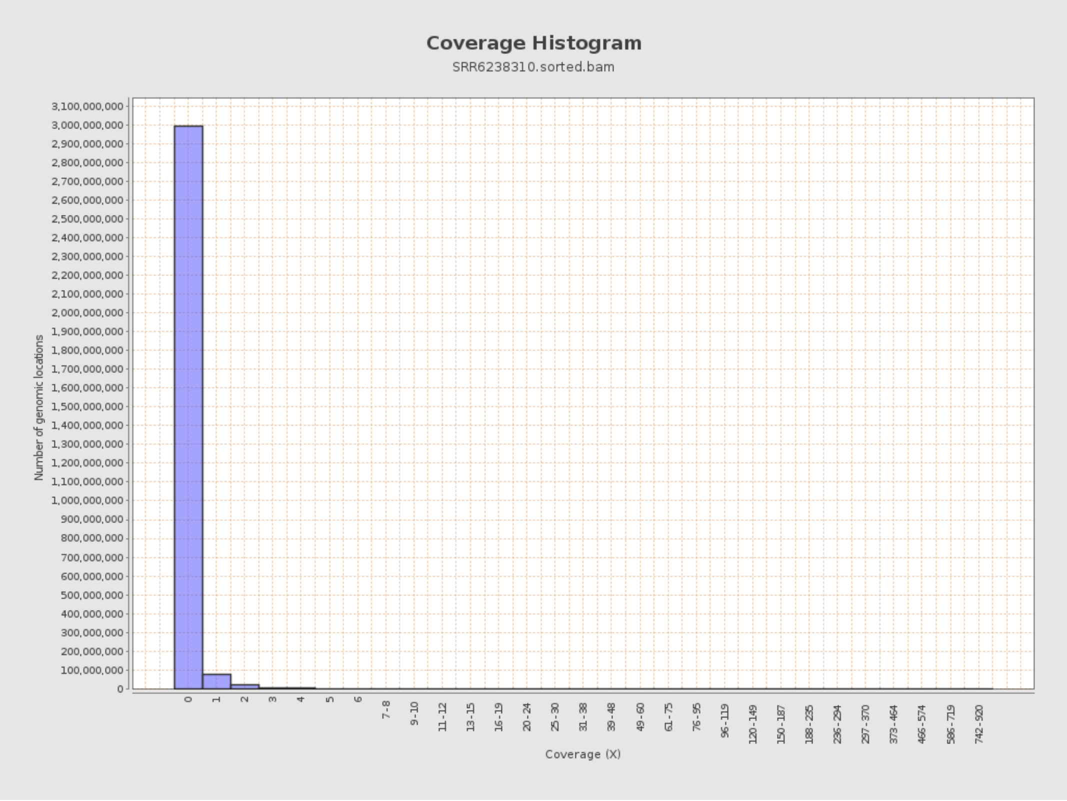
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10895575	0.0437	0.6446
chr2	243199373	10767465	0.0443	0.4796
chr3	198022430	10888419	0.055	0.303
chr4	191154276	9812311	0.0513	0.3059
chr5	180915260	8777947	0.0485	0.2856
chr6	171115067	6335501	0.037	0.2714
chr7	159138663	7022273	0.0441	0.3727

chr8	146364022	6624004	0.0453	0.6101
chr9	141213431	5425222	0.0384	0.3478
chr10	135534747	9397187	0.0693	0.4285
chr11	135006516	6510562	0.0482	0.3482
chr12	133851895	6748303	0.0504	0.2961
chr13	115169878	4928922	0.0428	0.2703
chr14	107349540	4639056	0.0432	0.3052
chr15	102531392	4343877	0.0424	0.2956
chr16	90354753	3593008	0.0398	0.2793
chr17	81195210	3118132	0.0384	0.2773
chr18	78077248	3407244	0.0436	0.5644
chr19	59128983	3378969	0.0571	0.5121
chr20	63025520	3051511	0.0484	0.2946
chr21	48129895	2081426	0.0432	0.2828
chr22	51304566	1712806	0.0334	0.2344
chrMT	16571	6790	0.4098	0.8093
chrX	155270560	5523601	0.0356	0.27
chrY	59373566	311075	0.0052	0.1513

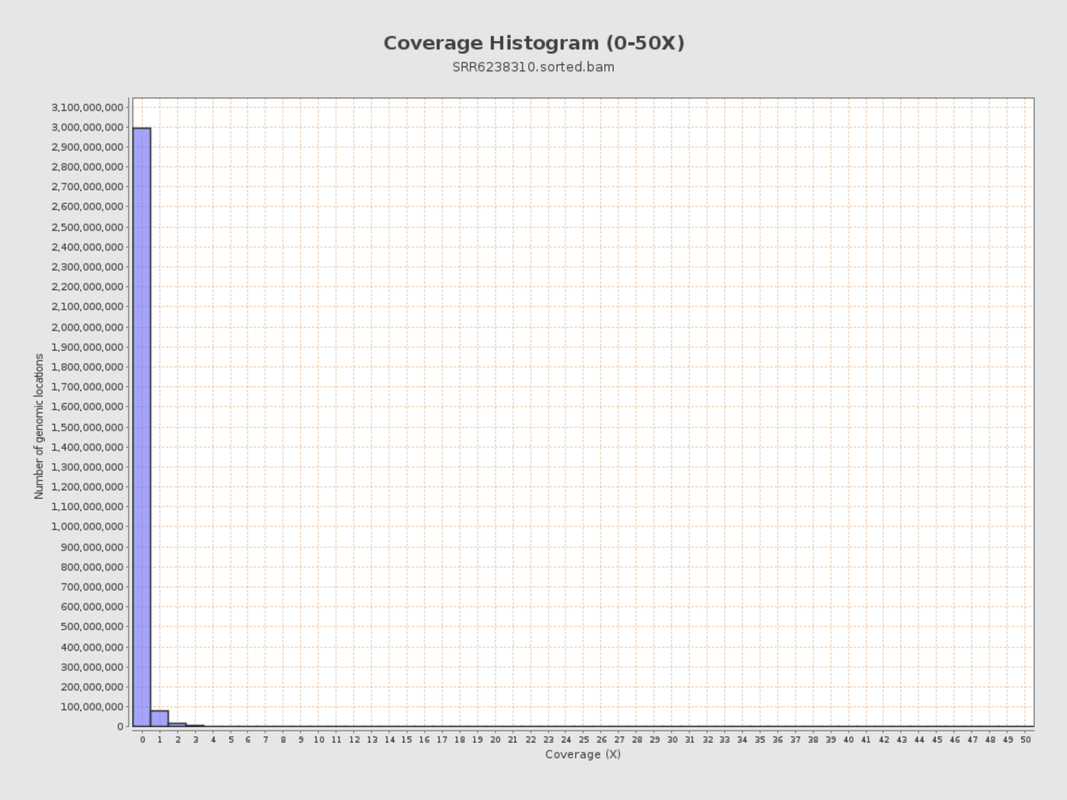
3. Results : Coverage across reference



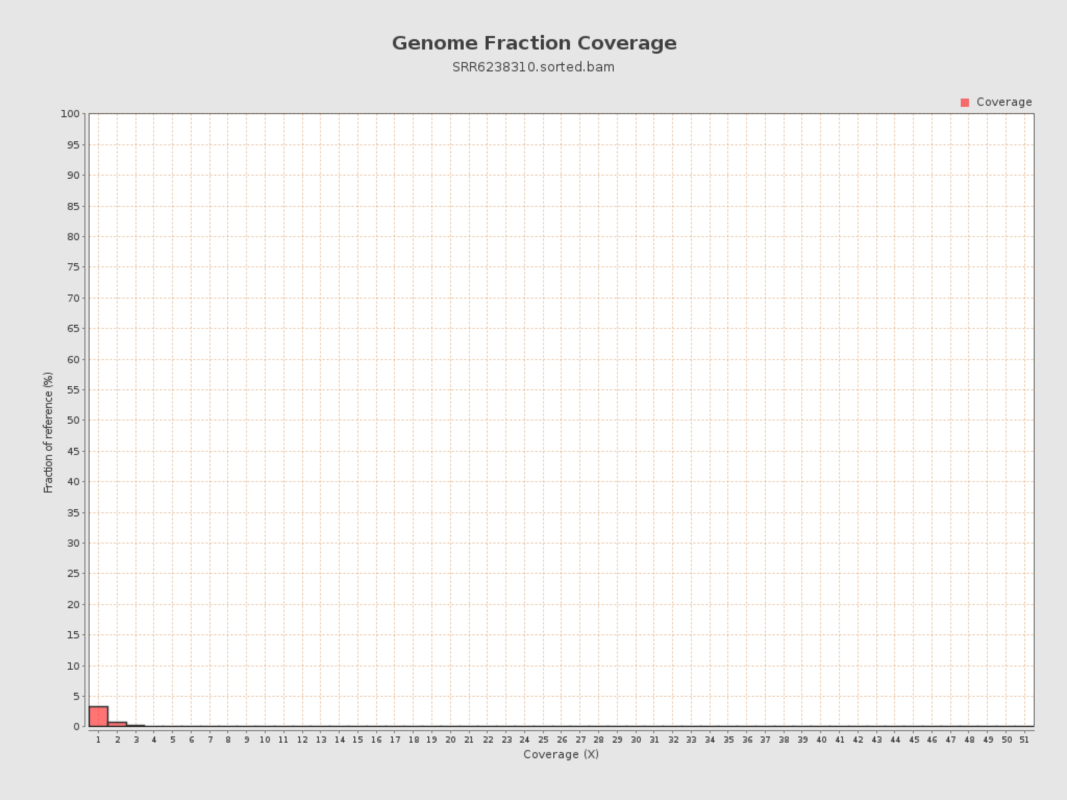
4. Results : Coverage Histogram



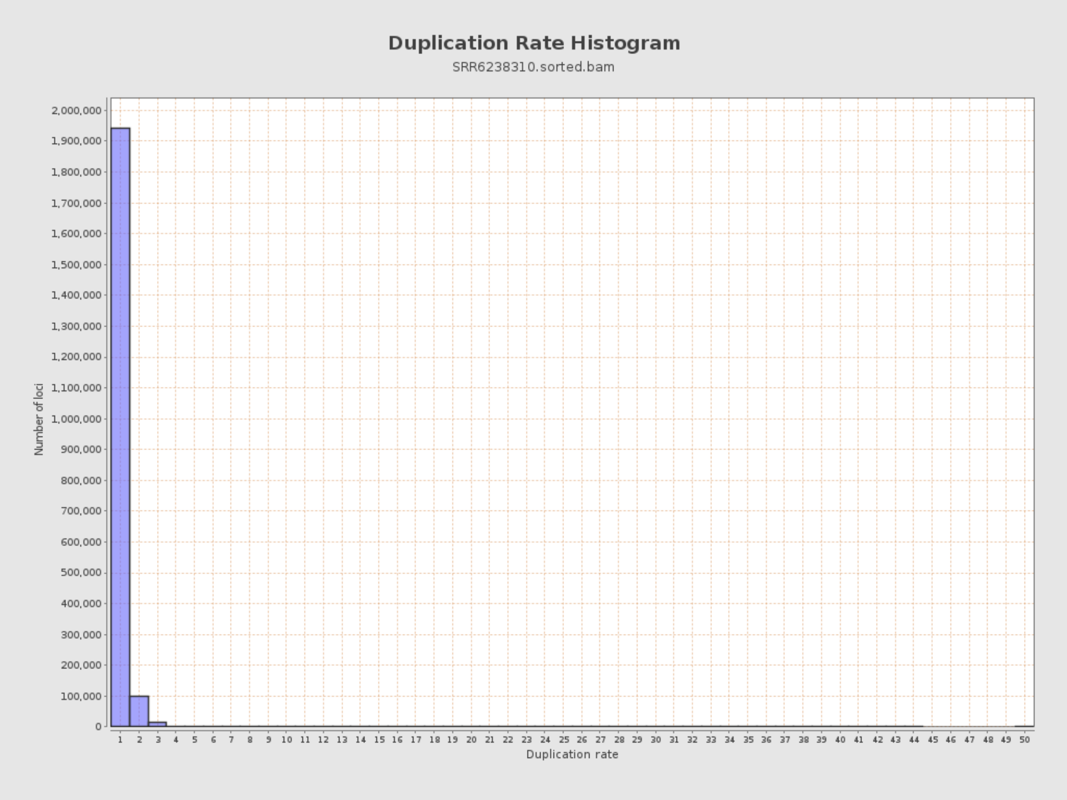
5. Results : Coverage Histogram (0-50X)



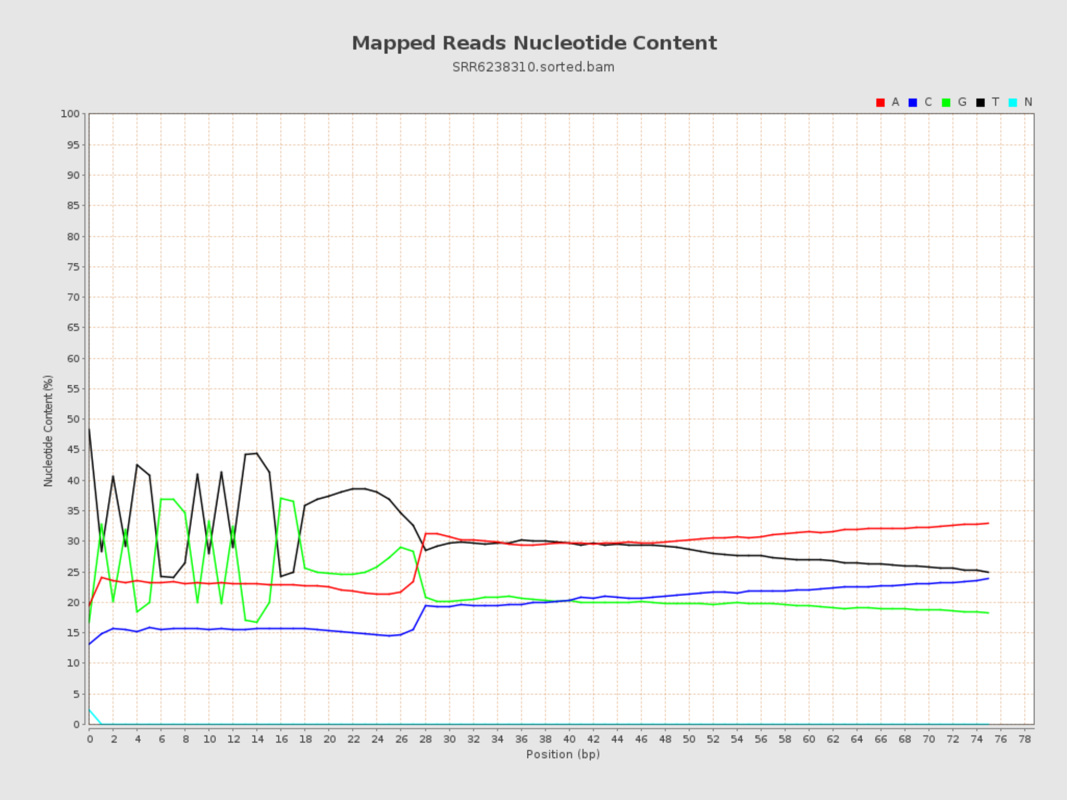
6. Results : Genome Fraction Coverage



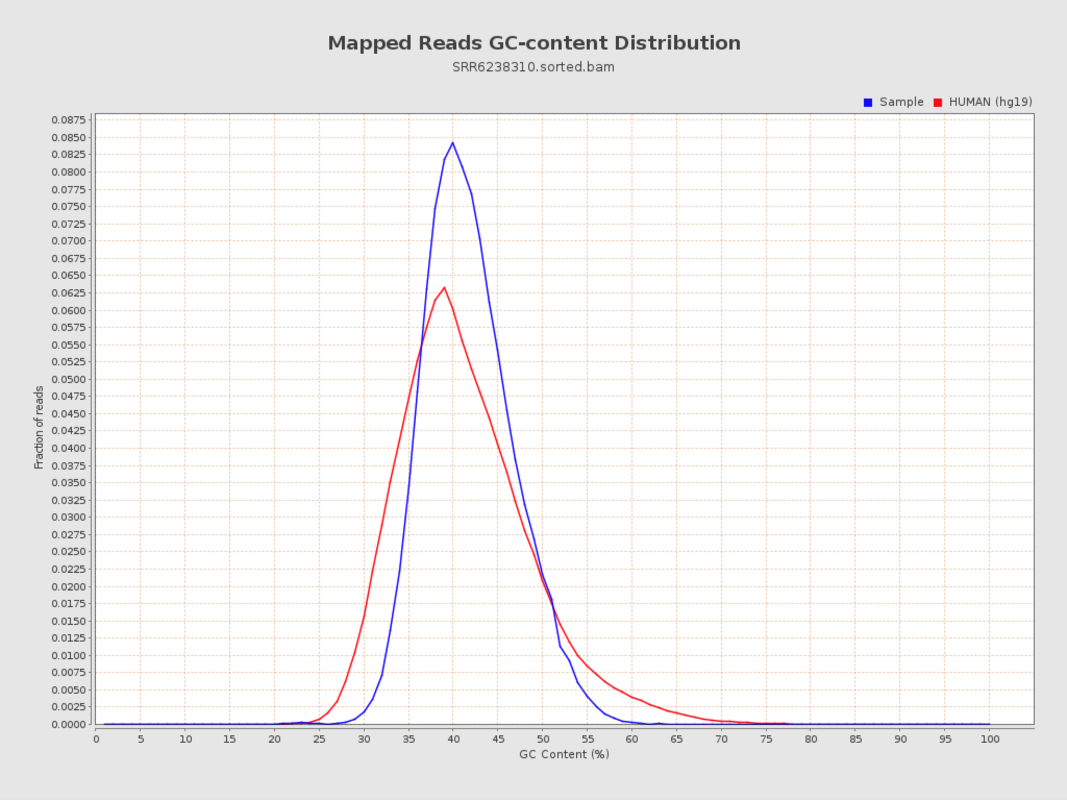
7. Results : Duplication Rate Histogram



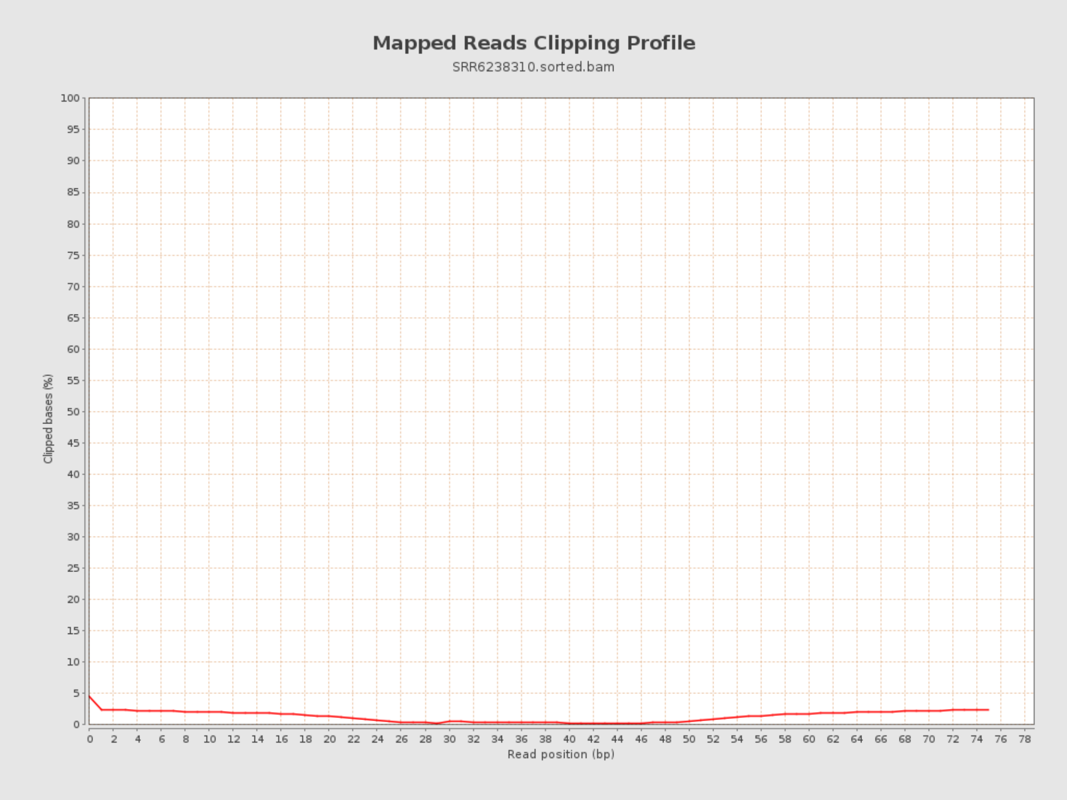
8. Results : Mapped Reads Nucleotide Content



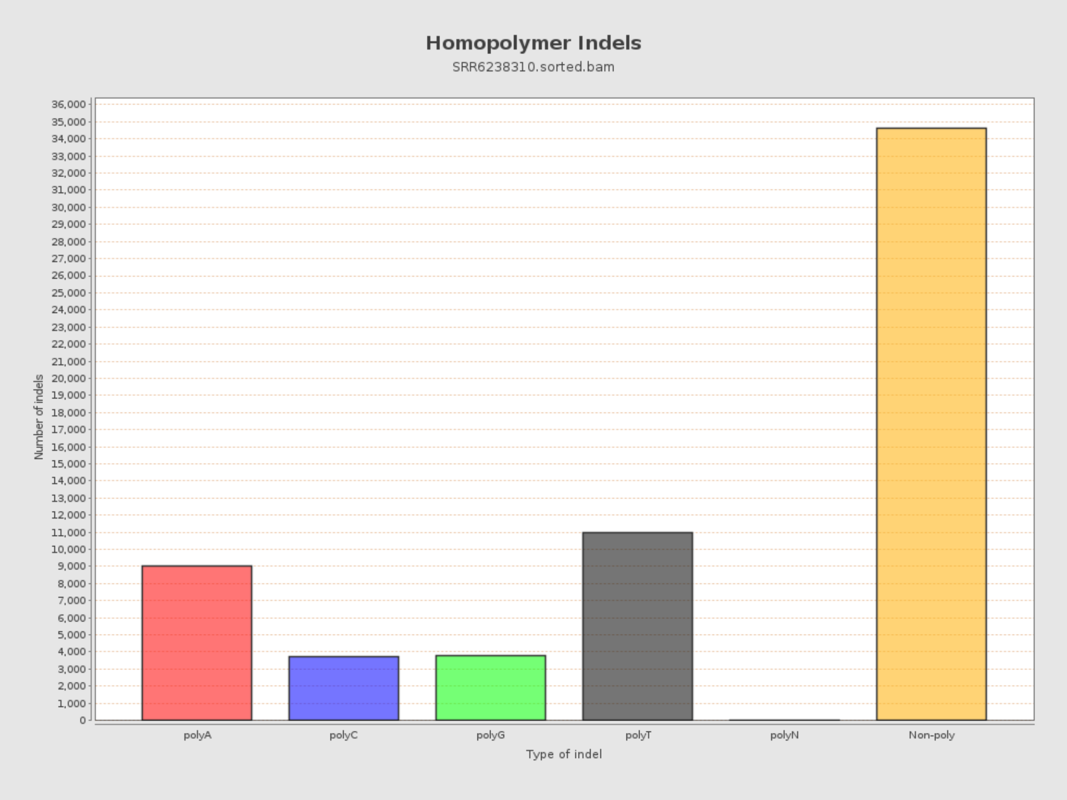
9. Results : Mapped Reads GC-content Distribution



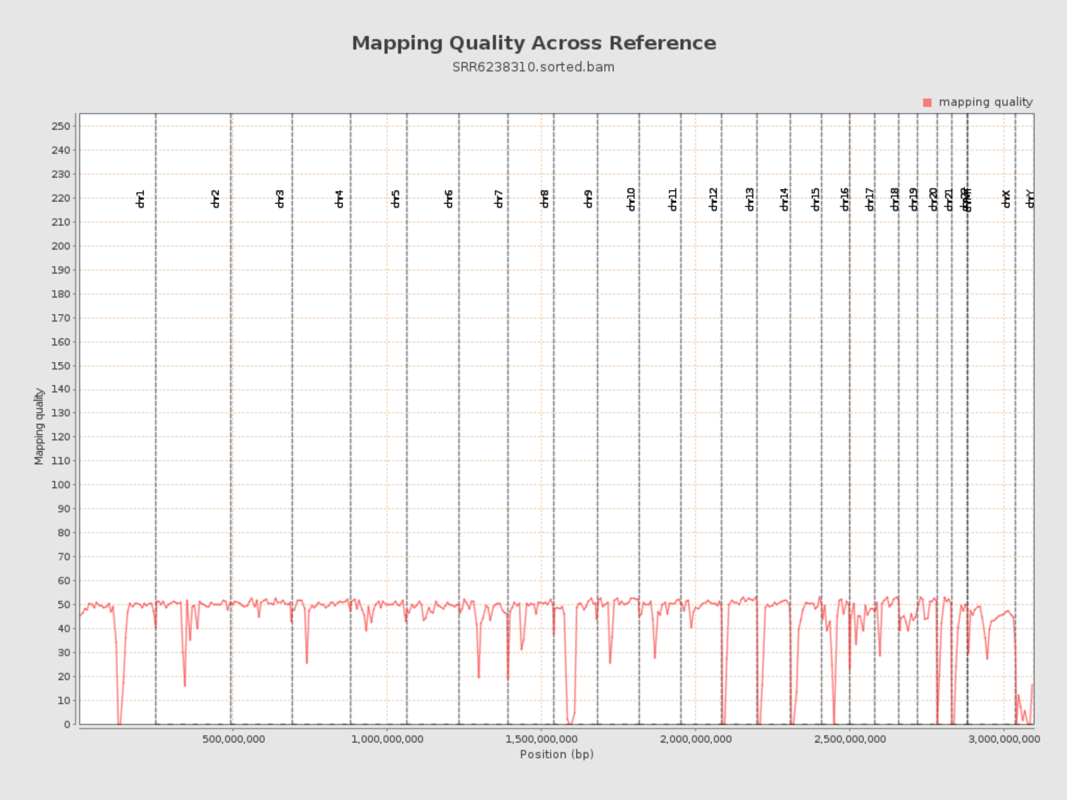
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram