Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:18:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238318.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_SRR6238318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:18:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,601,166
Mapped reads	2,350,347 / 90.36%
Unmapped reads	250,819 / 9.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,763 / 1.34%
Read min/max/mean length	30 / 76 / 76.47
Duplicated reads (estimated)	212,369 / 8.16%
Duplication rate	7.02%
Clipped reads	1,089,939 / 41.9%

2.2. ACGT Content

Number/percentage of A's	45,323,165 / 28.76%
Number/percentage of C's	29,614,486 / 18.79%
Number/percentage of T's	49,556,666 / 31.45%
Number/percentage of G's	33,042,639 / 20.97%
Number/percentage of N's	50,472 / 0.03%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.5584

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

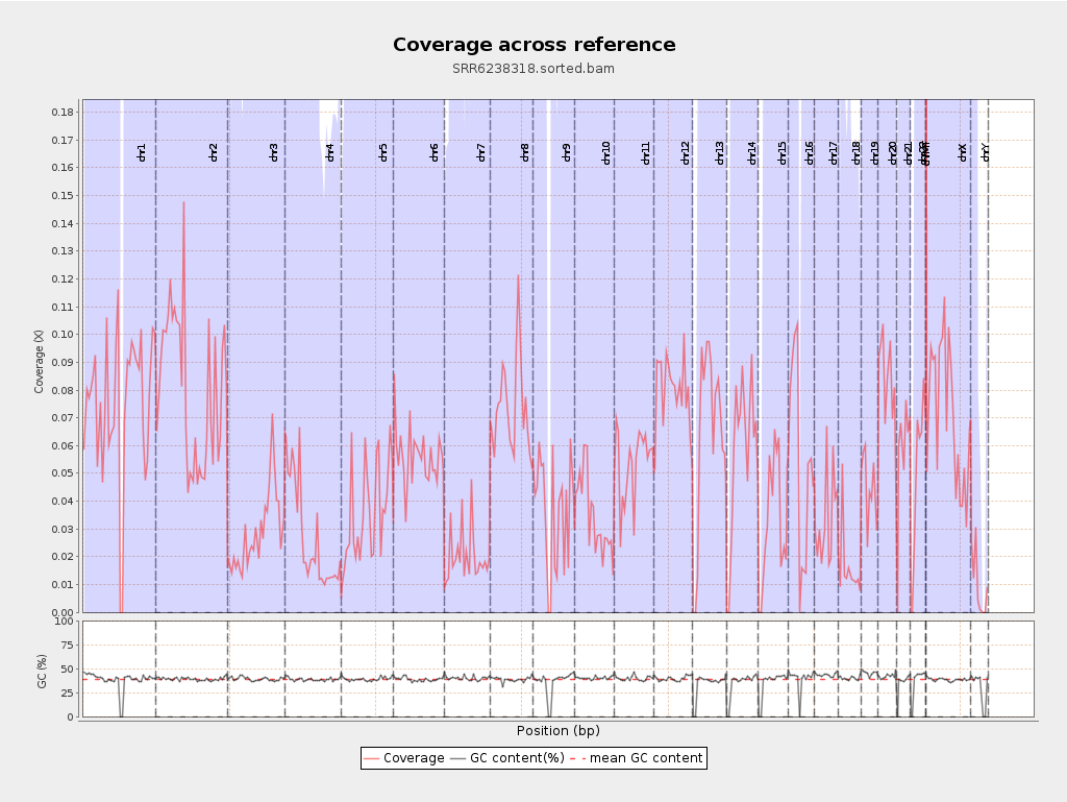
General error rate	0.9%
Mismatches	1,401,468
Insertions	12,553
Mapped reads with at least one insertion	0.53%
Deletions	47,410
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.68%

2.6. Chromosome stats

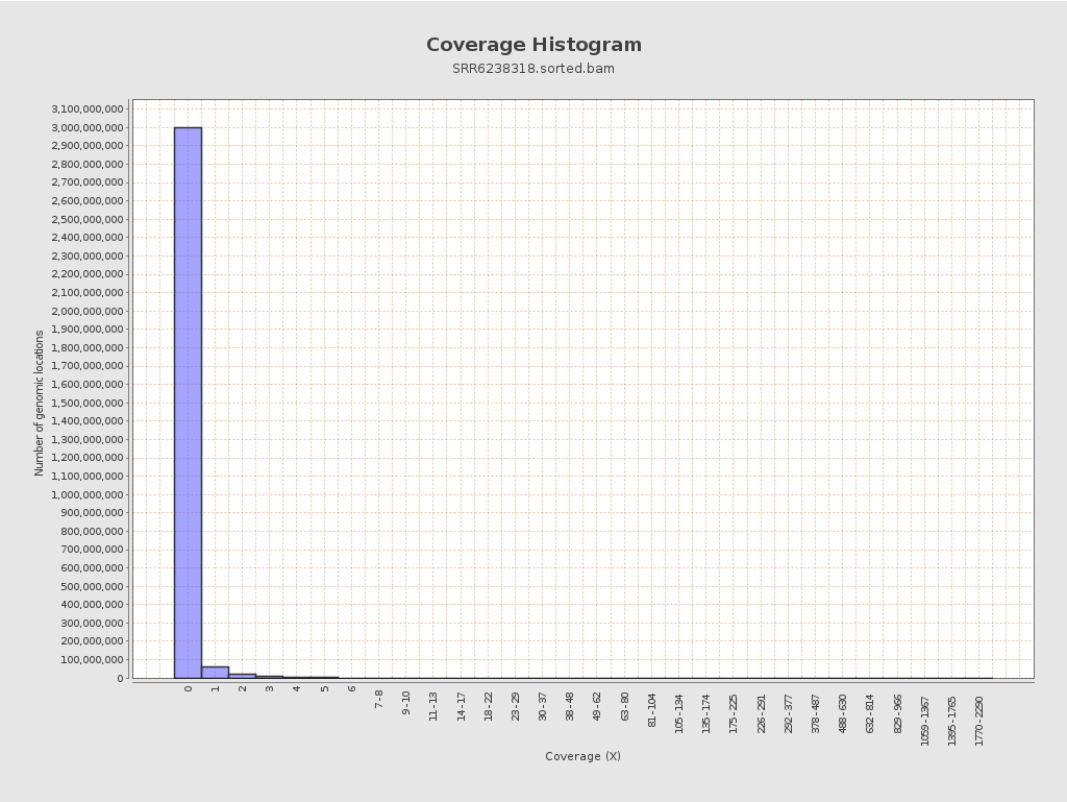
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18746687	0.0752	0.7642
chr2	243199373	19519265	0.0803	0.6429
chr3	198022430	5765779	0.0291	0.2553
chr4	191154276	5139748	0.0269	0.2685
chr5	180915260	6507801	0.036	0.2862
chr6	171115067	9553389	0.0558	0.4209
chr7	159138663	3241399	0.0204	0.2874

chr8	146364022	10734498	0.0733	1.4575
chr9	141213431	5038229	0.0357	0.441
chr10	135534747	4673988	0.0345	0.4018
chr11	135006516	7223291	0.0535	0.5083
chr12	133851895	10721768	0.0801	0.4274
chr13	115169878	7443588	0.0646	0.3849
chr14	107349540	6333889	0.059	0.378
chr15	102531392	3328554	0.0325	0.2677
chr16	90354753	4744779	0.0525	0.3753
chr17	81195210	2732239	0.0337	0.2954
chr18	78077248	1277043	0.0164	0.9806
chr19	59128983	2614230	0.0442	0.5609
chr20	63025520	5343348	0.0848	0.4511
chr21	48129895	2822009	0.0586	0.3746
chr22	51304566	2504626	0.0488	0.3192
chrMT	16571	13261	0.8003	1.3956
chrX	155270560	11074528	0.0713	0.4526
chrY	59373566	571472	0.0096	0.235

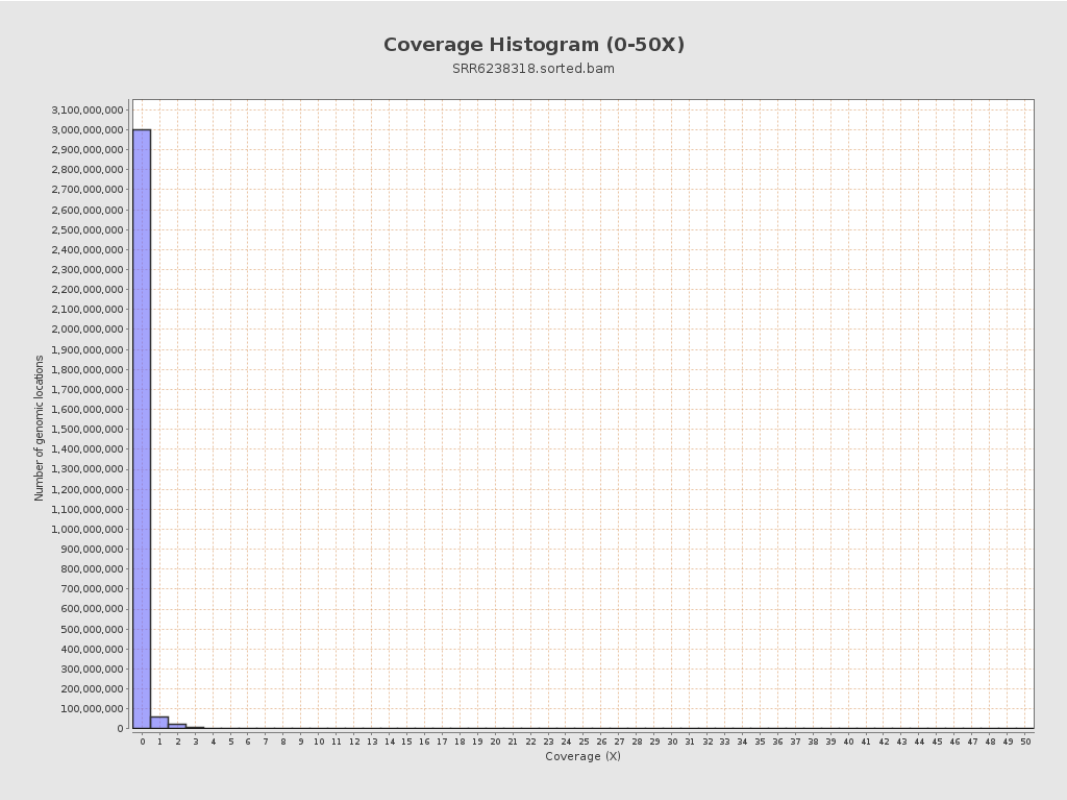
3. Results : Coverage across reference



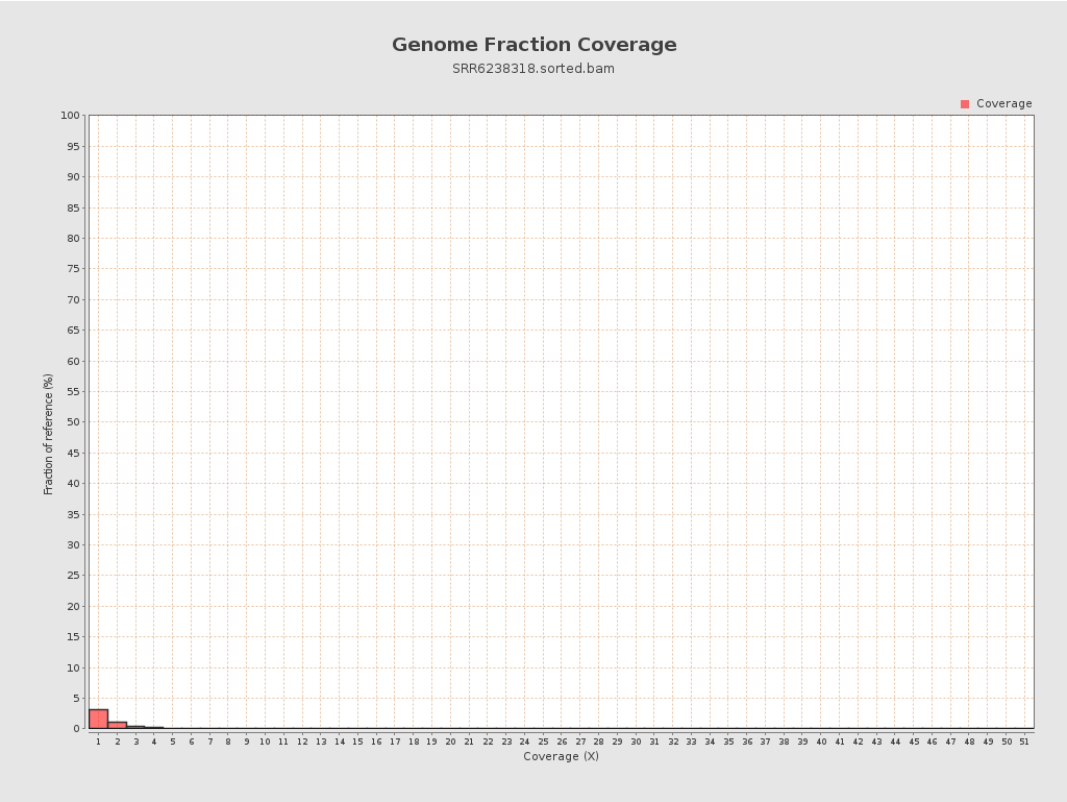
4. Results : Coverage Histogram



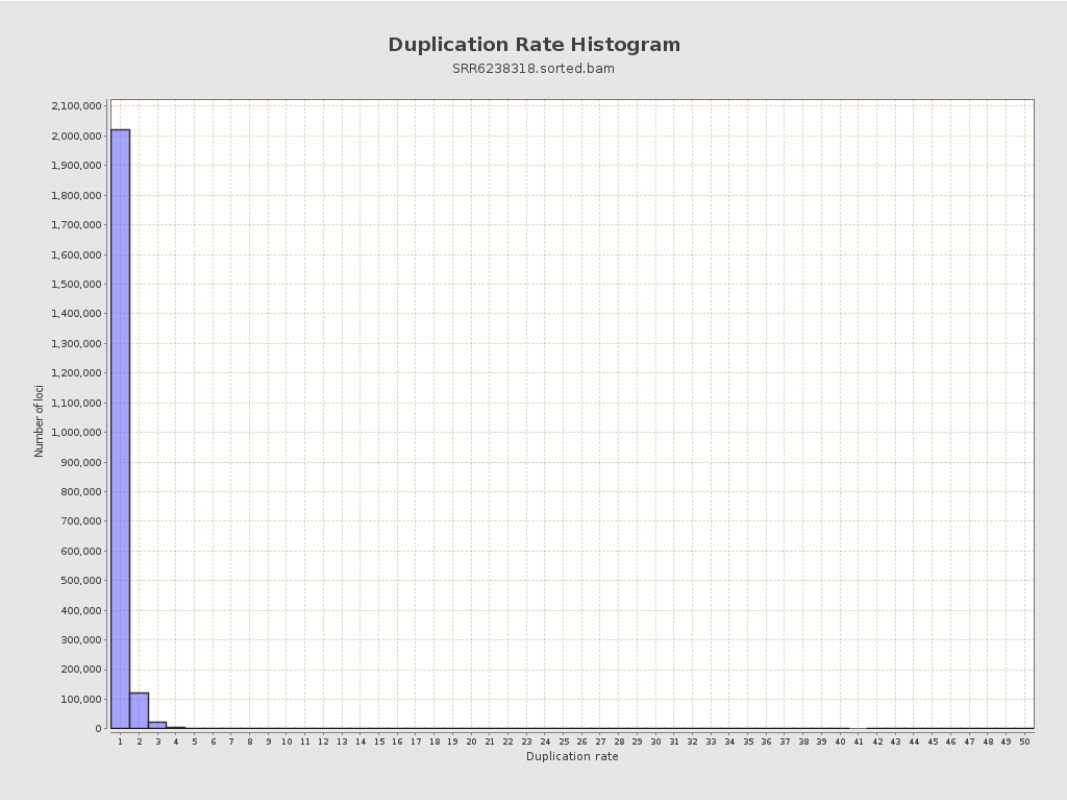
5. Results : Coverage Histogram (0-50X)



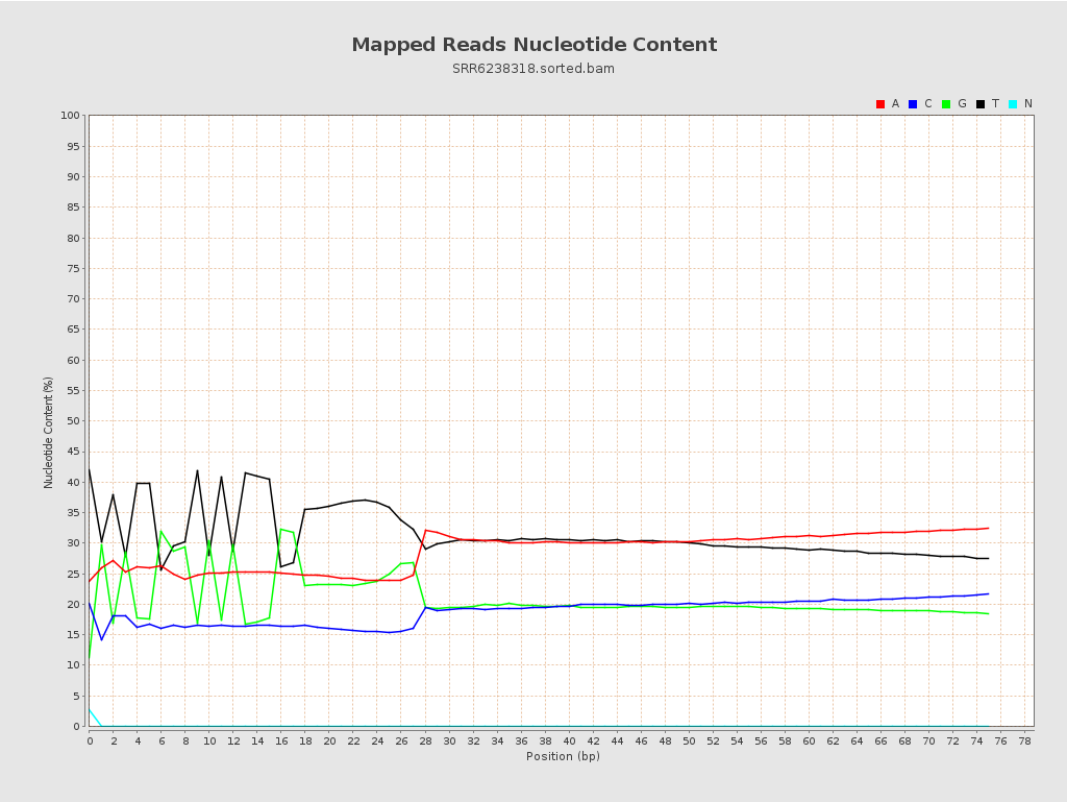
6. Results : Genome Fraction Coverage



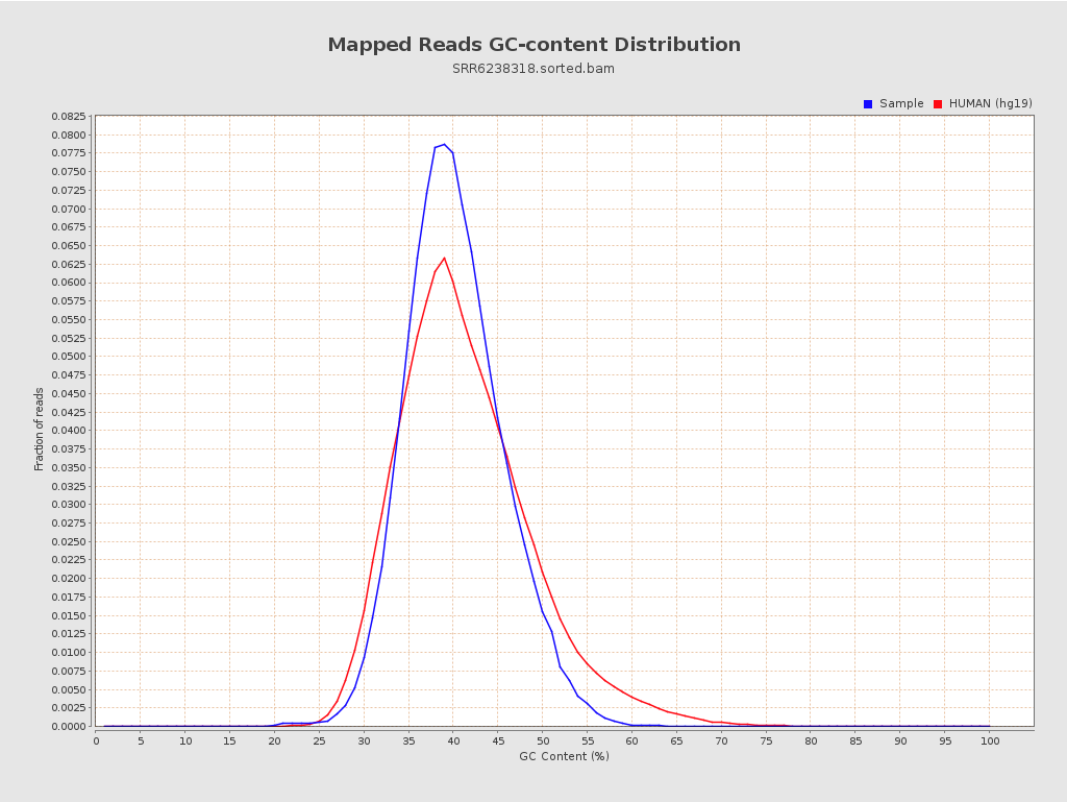
7. Results : Duplication Rate Histogram



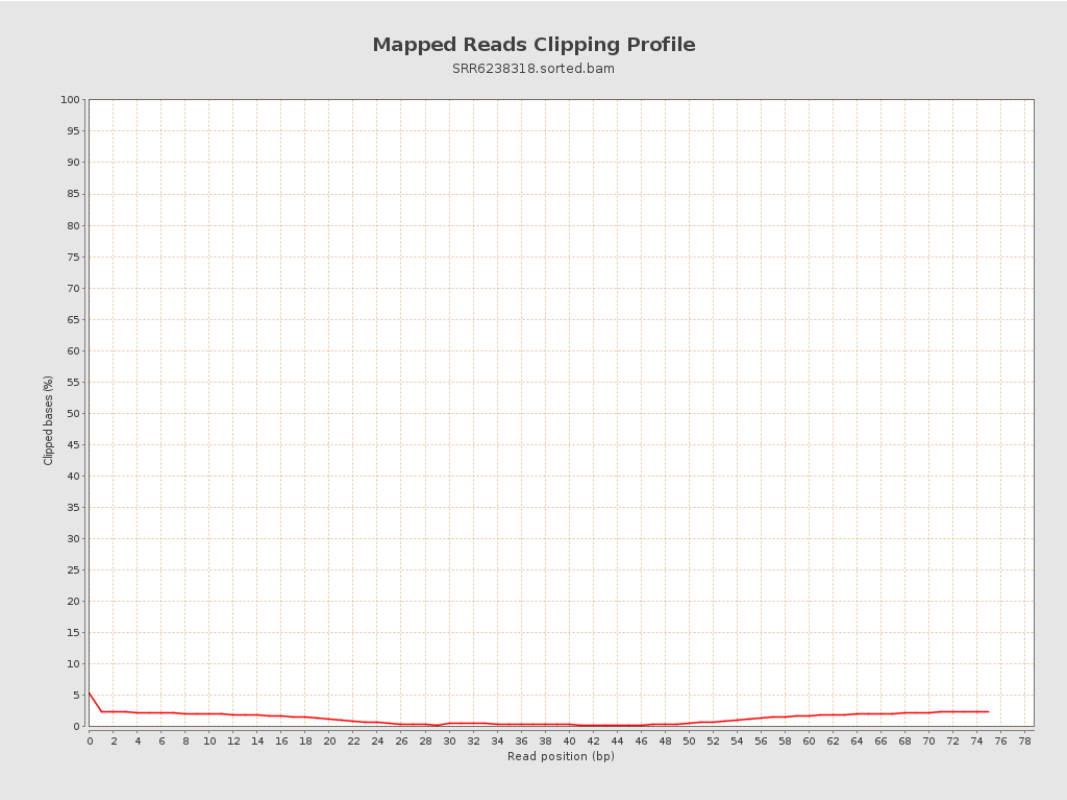
8. Results : Mapped Reads Nucleotide Content



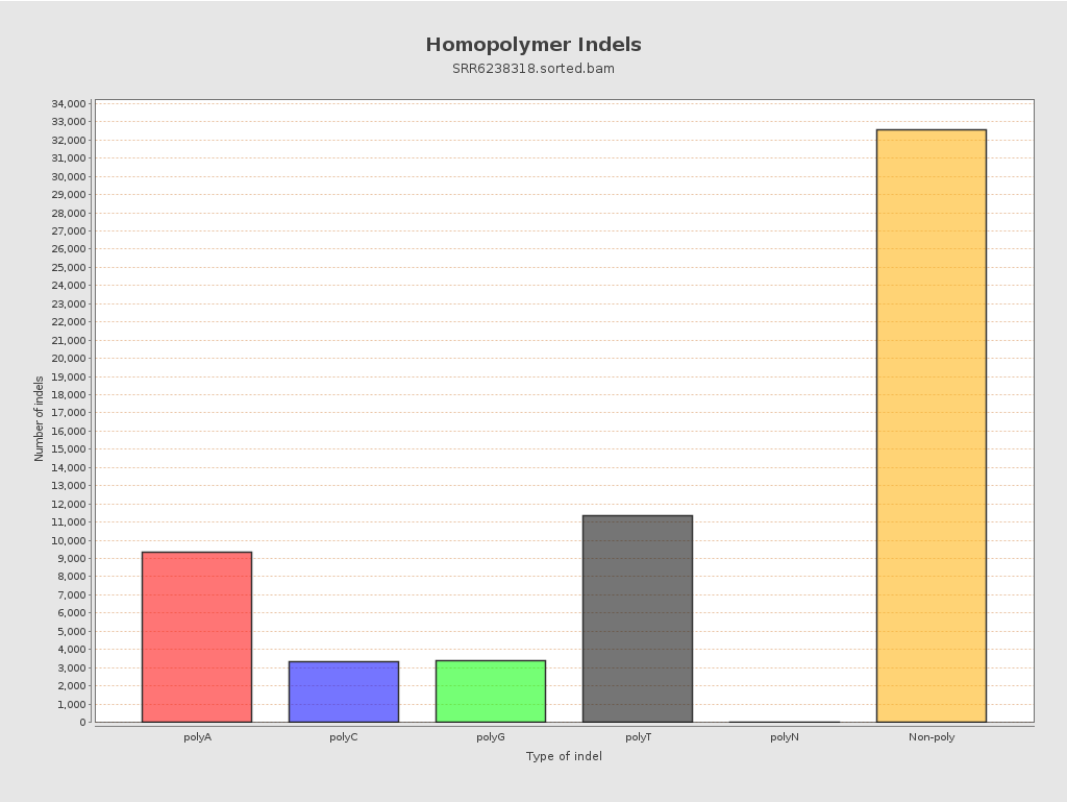
9. Results : Mapped Reads GC-content Distribution



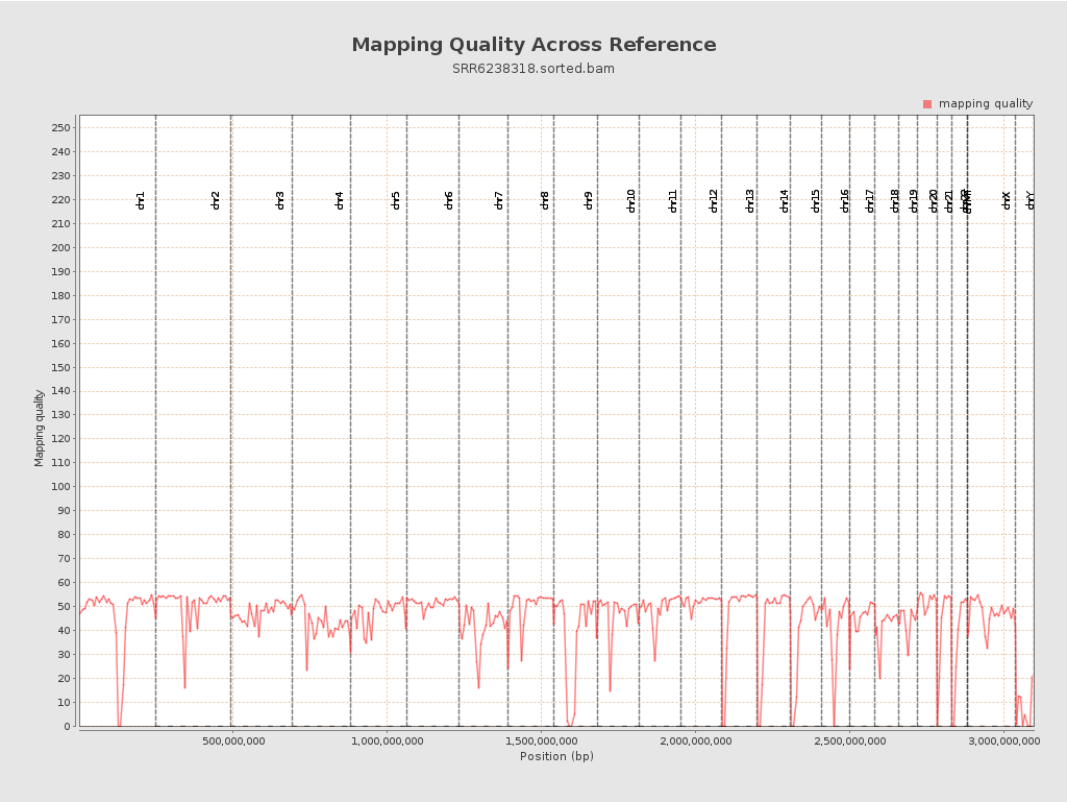
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram