Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:39:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238505.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_SRR6238505 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238505.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:39:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238505.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,004,667
Mapped reads	2,719,813 / 90.52%
Unmapped reads	284,854 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,695 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	376,736 / 12.54%
Duplication rate	11.9%
Clipped reads	1,693,097 / 56.35%

2.2. ACGT Content

Number/percentage of A's	41,446,165 / 24.67%
Number/percentage of C's	29,668,290 / 17.66%
Number/percentage of T's	55,716,081 / 33.17%
Number/percentage of G's	41,128,480 / 24.49%
Number/percentage of N's	11,445 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.5768

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

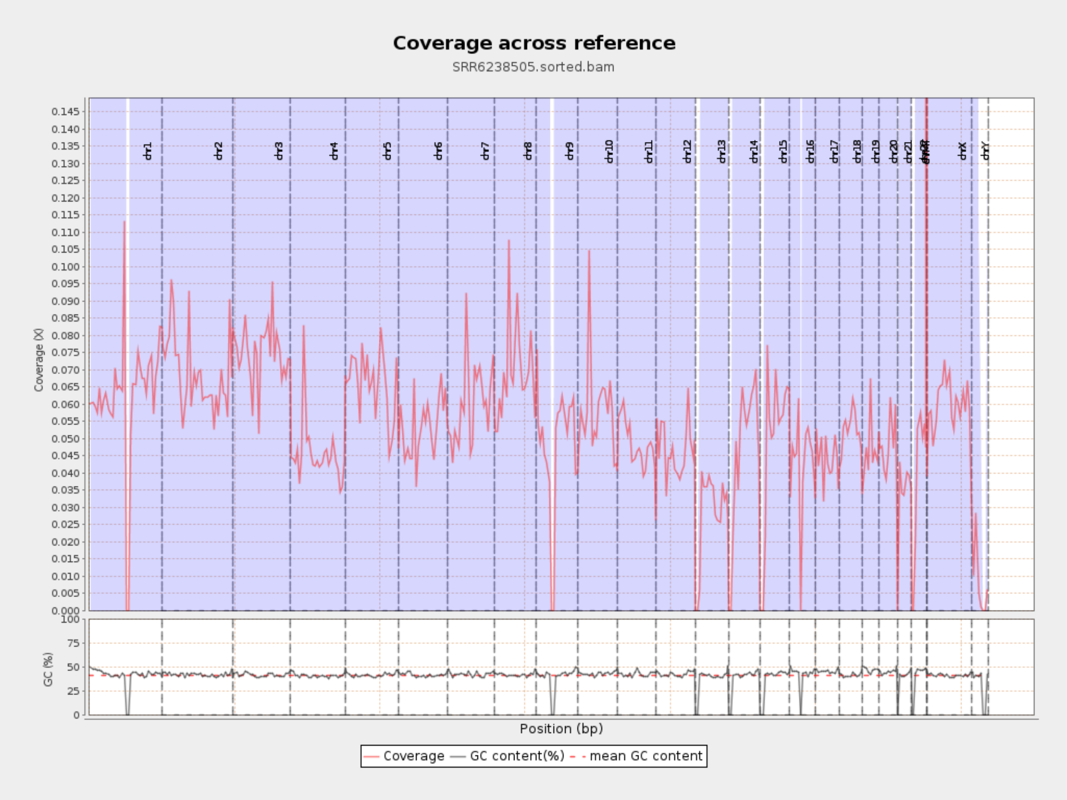
General error rate	0.56%
Mismatches	910,826
Insertions	10,816
Mapped reads with at least one insertion	0.39%
Deletions	40,968
Mapped reads with at least one deletion	1.49%
Homopolymer indels	43.14%

2.6. Chromosome stats

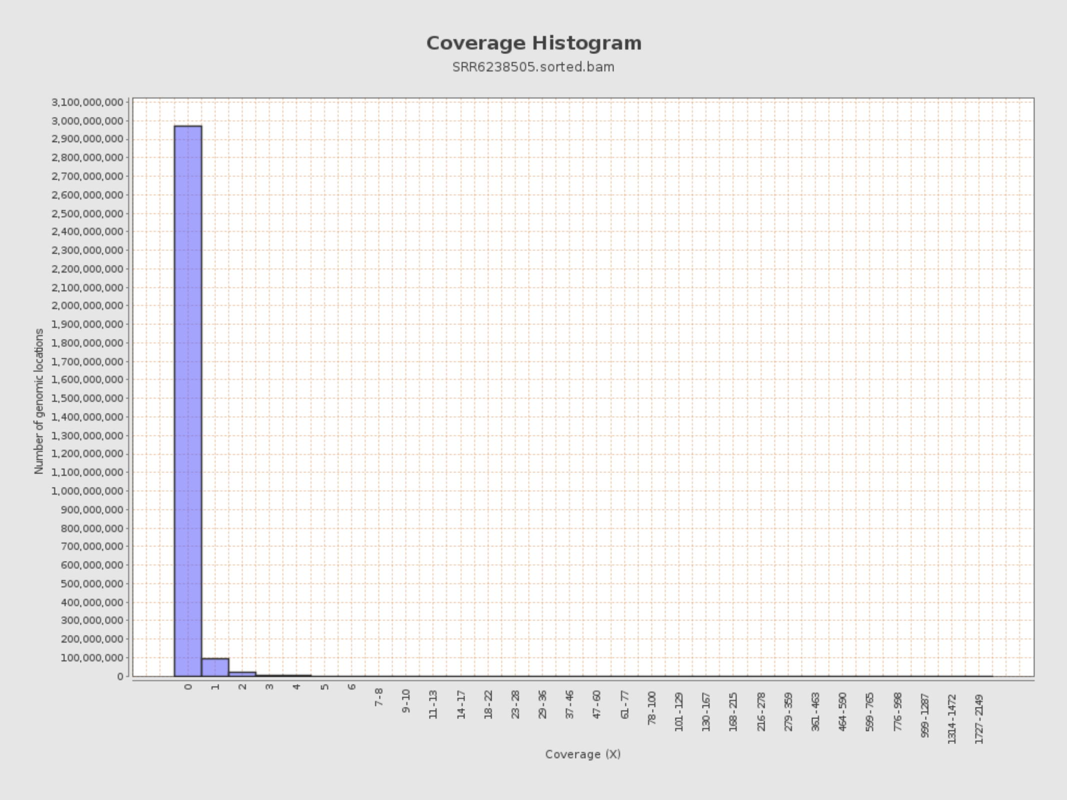
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15512091	0.0622	1.127
chr2	243199373	16727756	0.0688	1.0294
chr3	198022430	14861254	0.075	0.3575
chr4	191154276	8642946	0.0452	0.3187
chr5	180915260	12052558	0.0666	0.3386
chr6	171115067	9164444	0.0536	0.4565
chr7	159138663	9562694	0.0601	0.6753

chr8	146364022	10153062	0.0694	0.4725
chr9	141213431	6624970	0.0469	0.3697
chr10	135534747	7926139	0.0585	0.5101
chr11	135006516	6536691	0.0484	0.3587
chr12	133851895	6234463	0.0466	0.2881
chr13	115169878	3250400	0.0282	0.2768
chr14	107349540	5045326	0.047	0.2907
chr15	102531392	4993458	0.0487	0.3401
chr16	90354753	3852285	0.0426	0.32
chr17	81195210	3590008	0.0442	0.2886
chr18	78077248	4119357	0.0528	0.8497
chr19	59128983	2755544	0.0466	0.7029
chr20	63025520	3028210	0.048	0.2981
chr21	48129895	1650008	0.0343	0.2775
chr22	51304566	1912629	0.0373	0.248
chrMT	16571	66640	4.0215	3.1559
chrX	155270560	9287045	0.0598	0.3403
chrY	59373566	491831	0.0083	0.2348

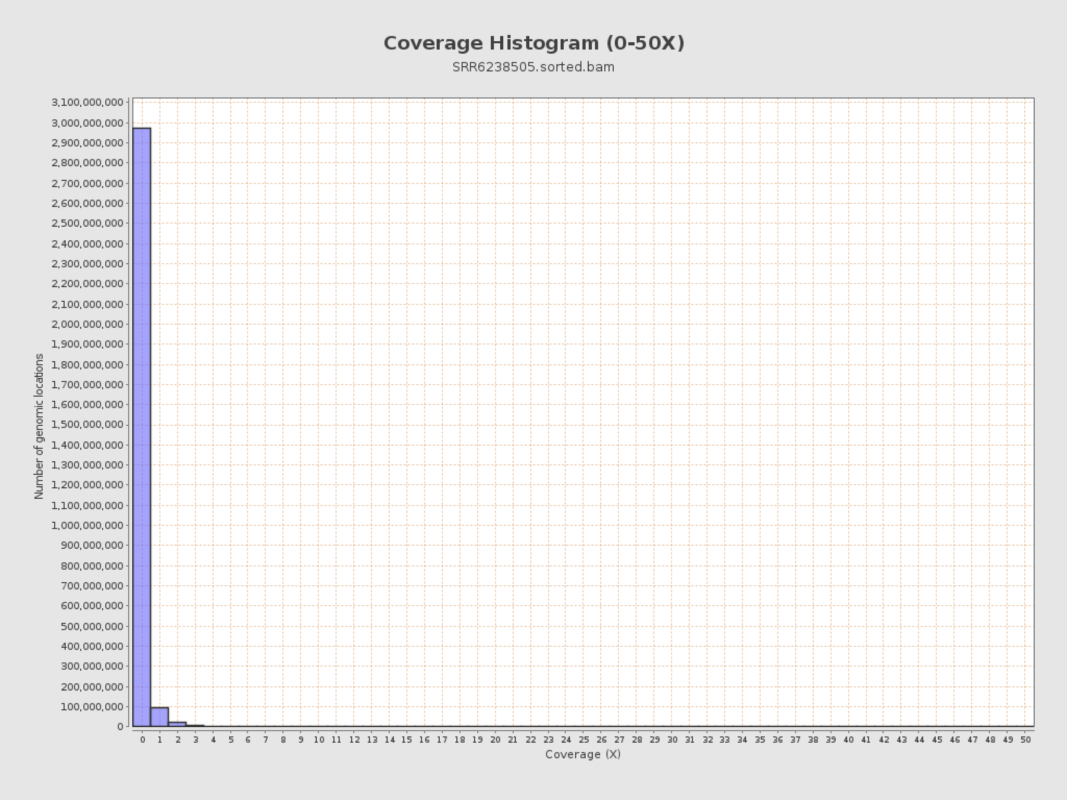
3. Results : Coverage across reference



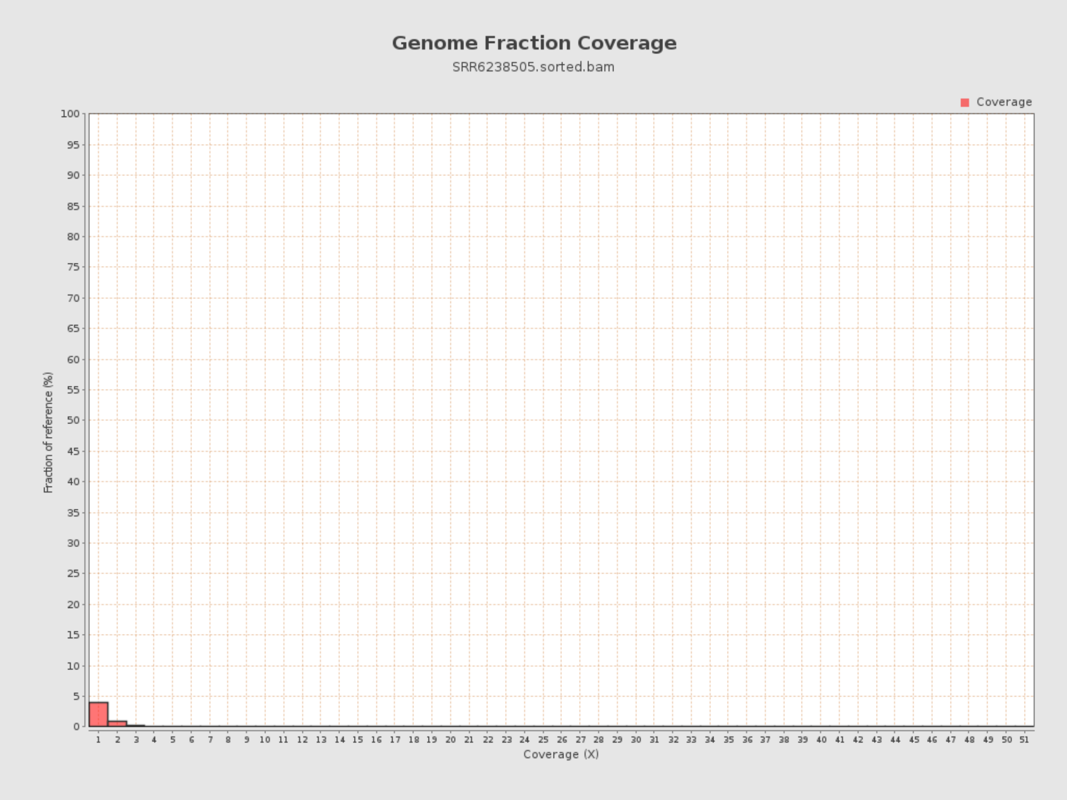
4. Results : Coverage Histogram



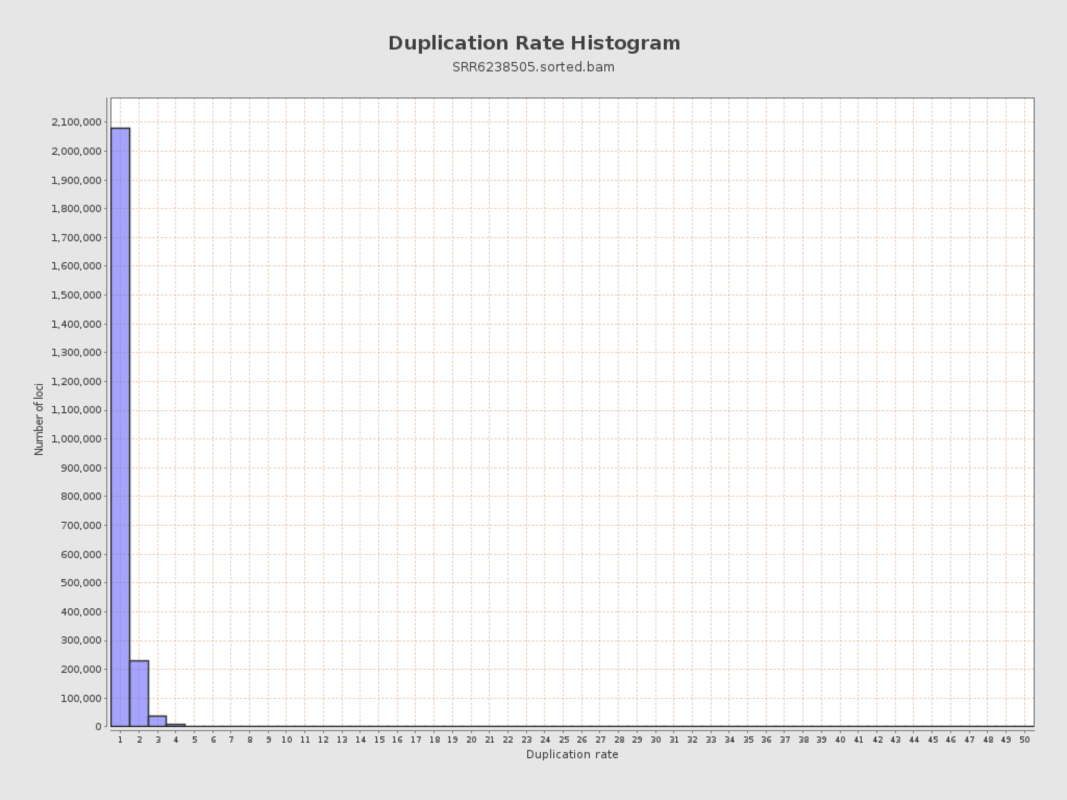
5. Results : Coverage Histogram (0-50X)



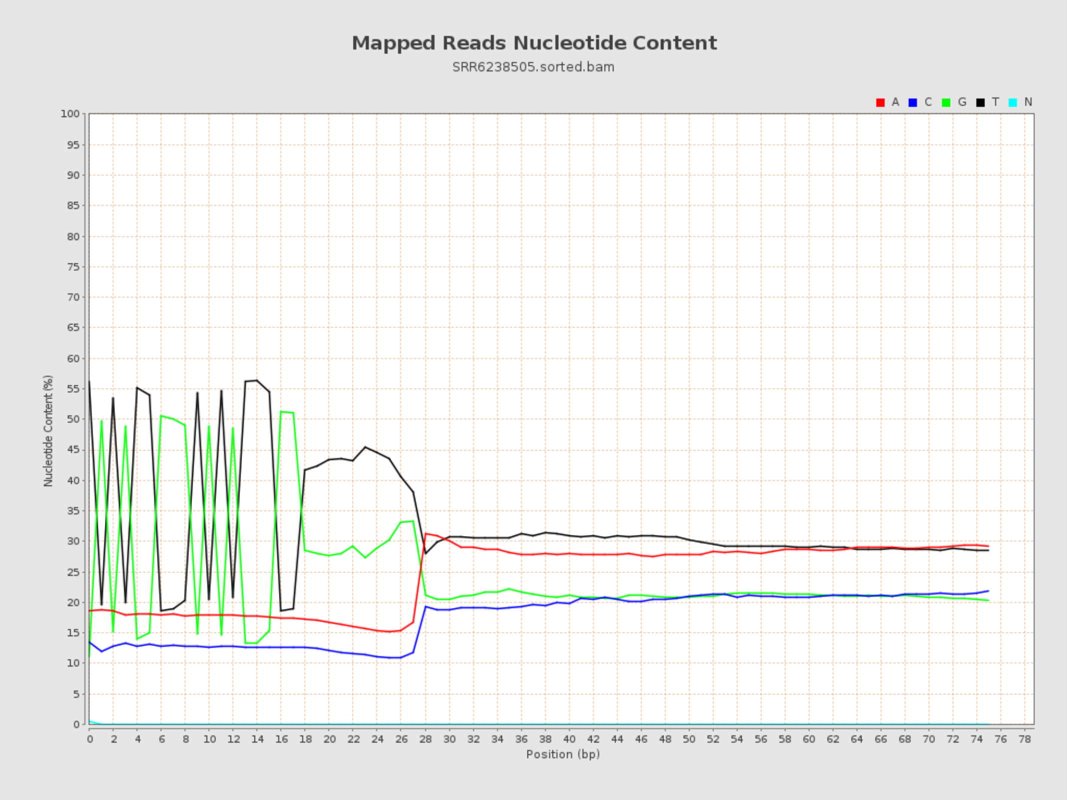
6. Results : Genome Fraction Coverage



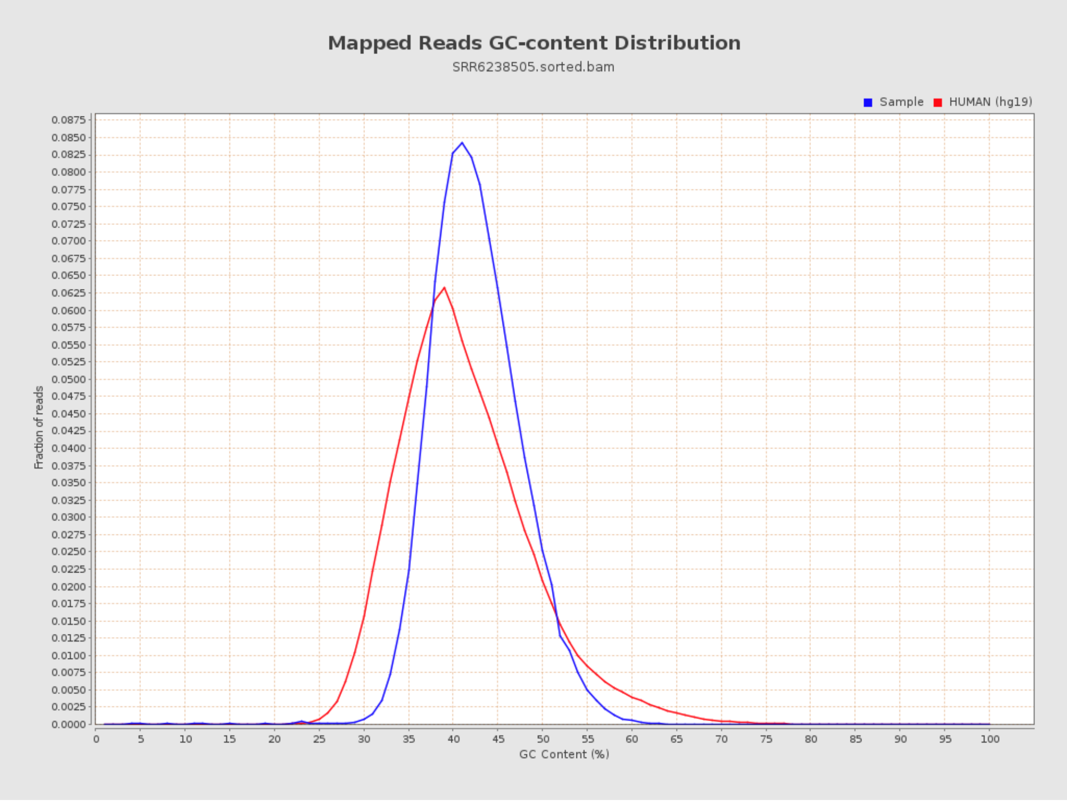
7. Results : Duplication Rate Histogram



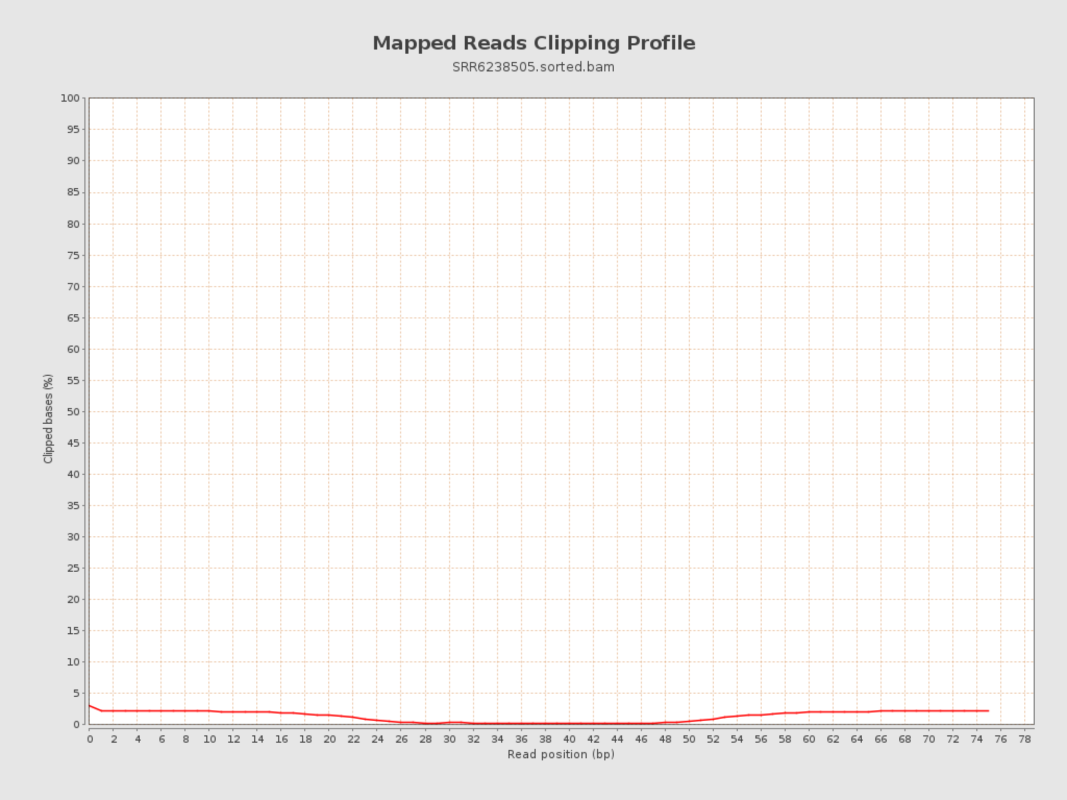
8. Results : Mapped Reads Nucleotide Content



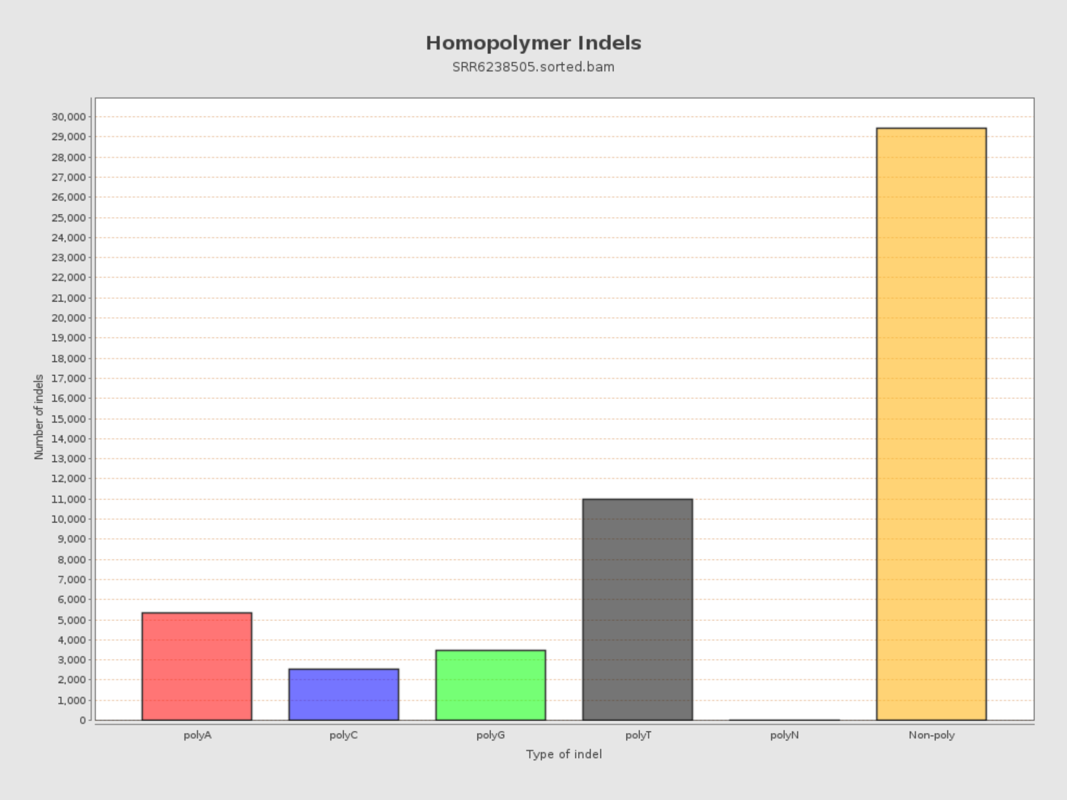
9. Results : Mapped Reads GC-content Distribution



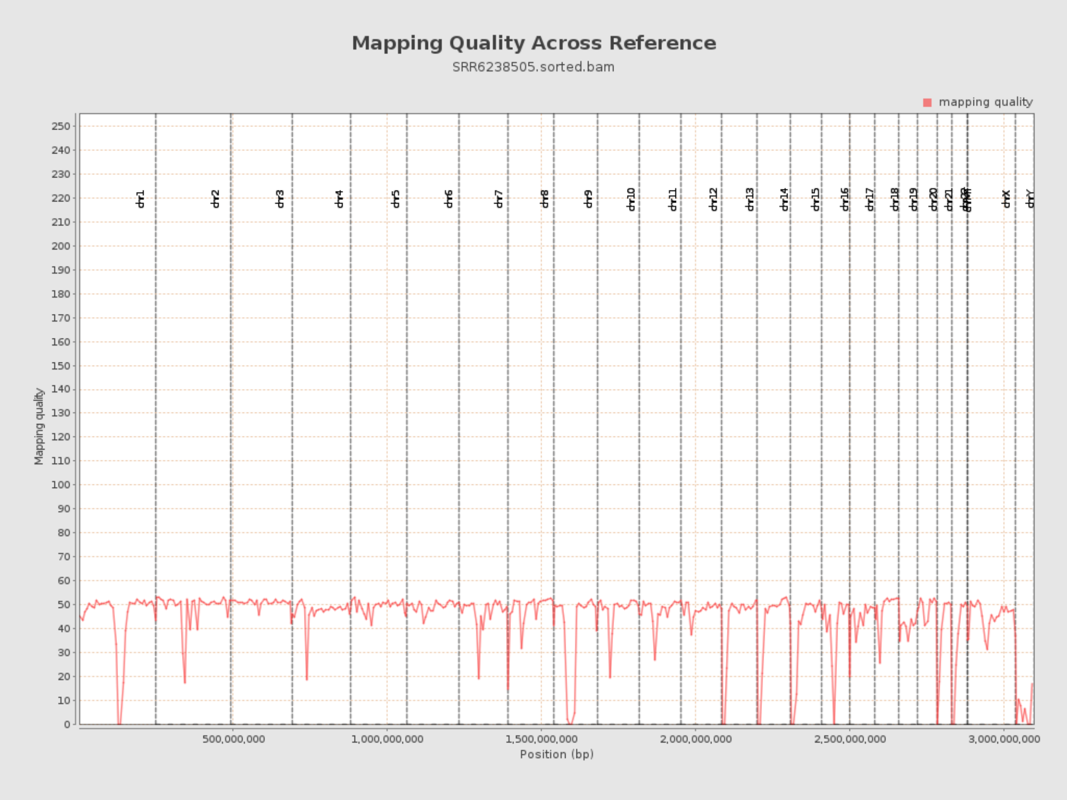
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram