Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:55:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238330.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_SRR6238330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:55:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,493,975
Mapped reads	2,244,765 / 90.01%
Unmapped reads	249,210 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,121 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	150,911 / 6.05%
Duplication rate	5.17%
Clipped reads	1,054,323 / 42.27%

2.2. ACGT Content

Number/percentage of A's	41,999,820 / 28.07%
Number/percentage of C's	28,898,267 / 19.31%
Number/percentage of T's	45,887,325 / 30.67%
Number/percentage of G's	32,808,703 / 21.93%
Number/percentage of N's	44,773 / 0.03%
GC Percentage	41.24%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.4797

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

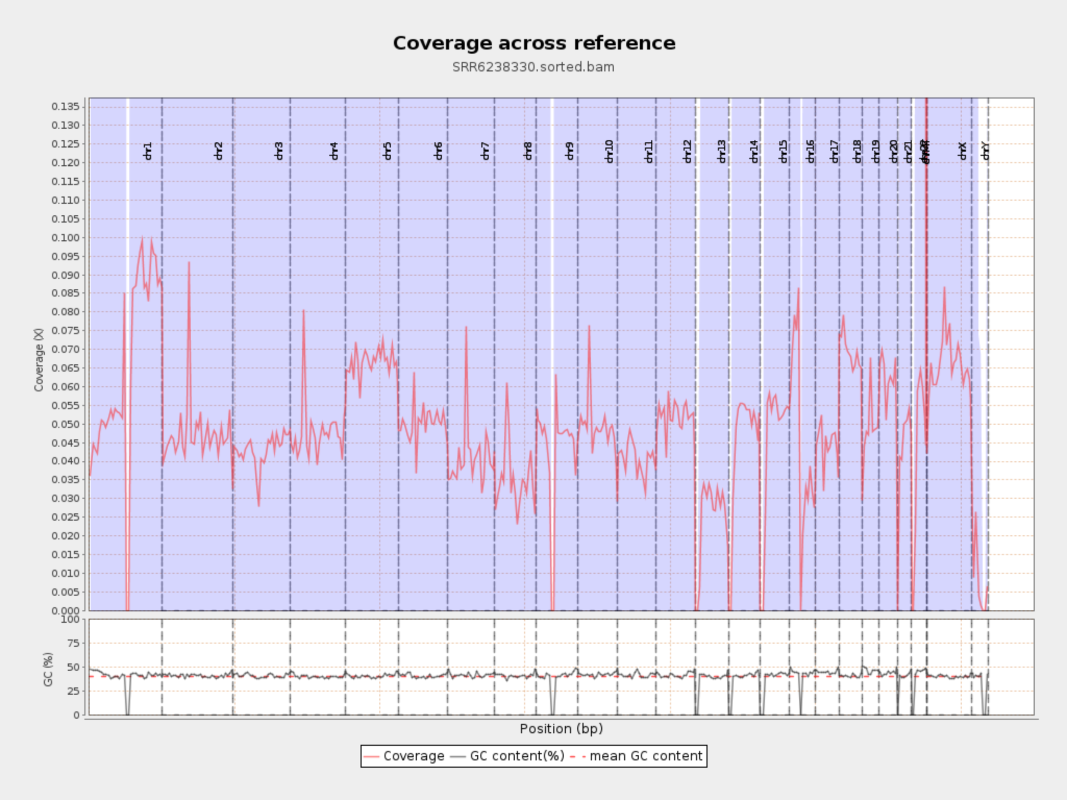
General error rate	0.85%
Mismatches	1,253,889
Insertions	12,004
Mapped reads with at least one insertion	0.53%
Deletions	37,478
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.09%

2.6. Chromosome stats

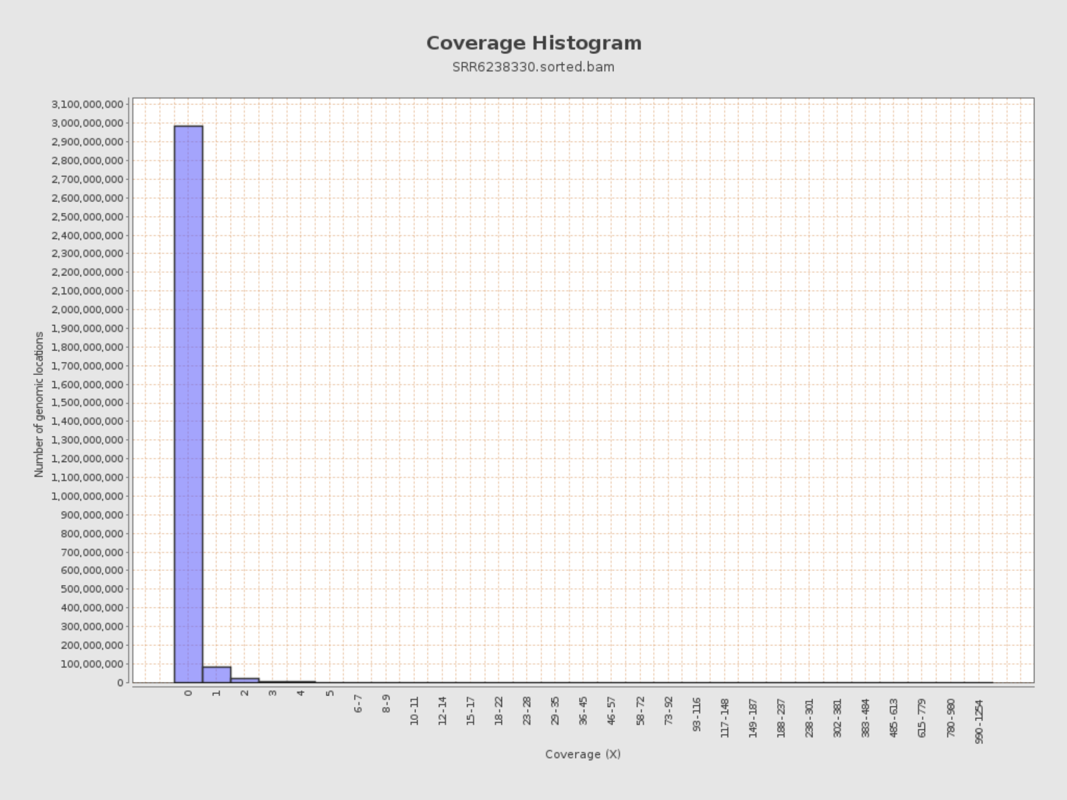
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16108701	0.0646	0.798
chr2	243199373	11588789	0.0477	0.6033
chr3	198022430	8466204	0.0428	0.2631
chr4	191154276	9076607	0.0475	0.3506
chr5	180915260	12073393	0.0667	0.333
chr6	171115067	8605722	0.0503	0.3432
chr7	159138663	6560670	0.0412	0.546

chr8	146364022	5132558	0.0351	0.7785
chr9	141213431	5976969	0.0423	0.4713
chr10	135534747	6736795	0.0497	0.4221
chr11	135006516	5452240	0.0404	0.4262
chr12	133851895	6966320	0.052	0.3017
chr13	115169878	2839641	0.0247	0.2003
chr14	107349540	4745030	0.0442	0.3072
chr15	102531392	4567433	0.0445	0.2733
chr16	90354753	4105295	0.0454	0.3016
chr17	81195210	3586938	0.0442	0.309
chr18	78077248	5429395	0.0695	0.8924
chr19	59128983	2928412	0.0495	0.5608
chr20	63025520	3911689	0.0621	0.3321
chr21	48129895	2067647	0.043	0.3027
chr22	51304566	2070819	0.0404	0.2545
chrMT	16571	20214	1.2198	1.664
chrX	155270560	10216865	0.0658	0.3771
chrY	59373566	469460	0.0079	0.2237

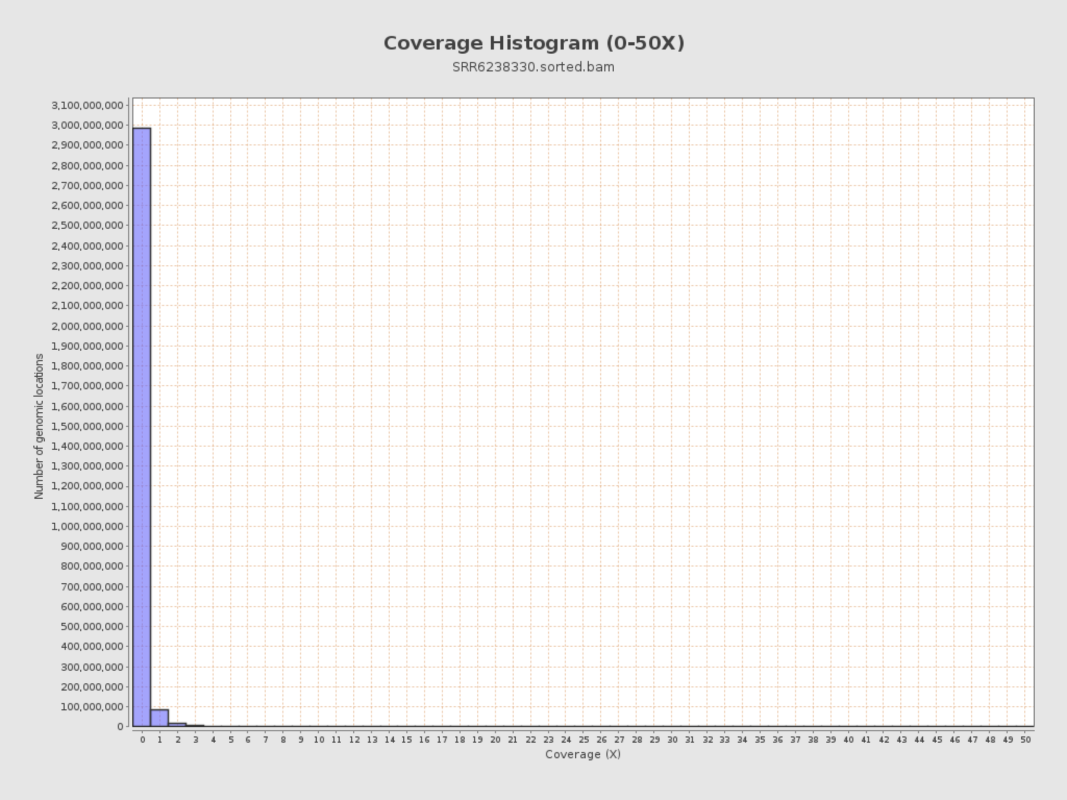
3. Results : Coverage across reference



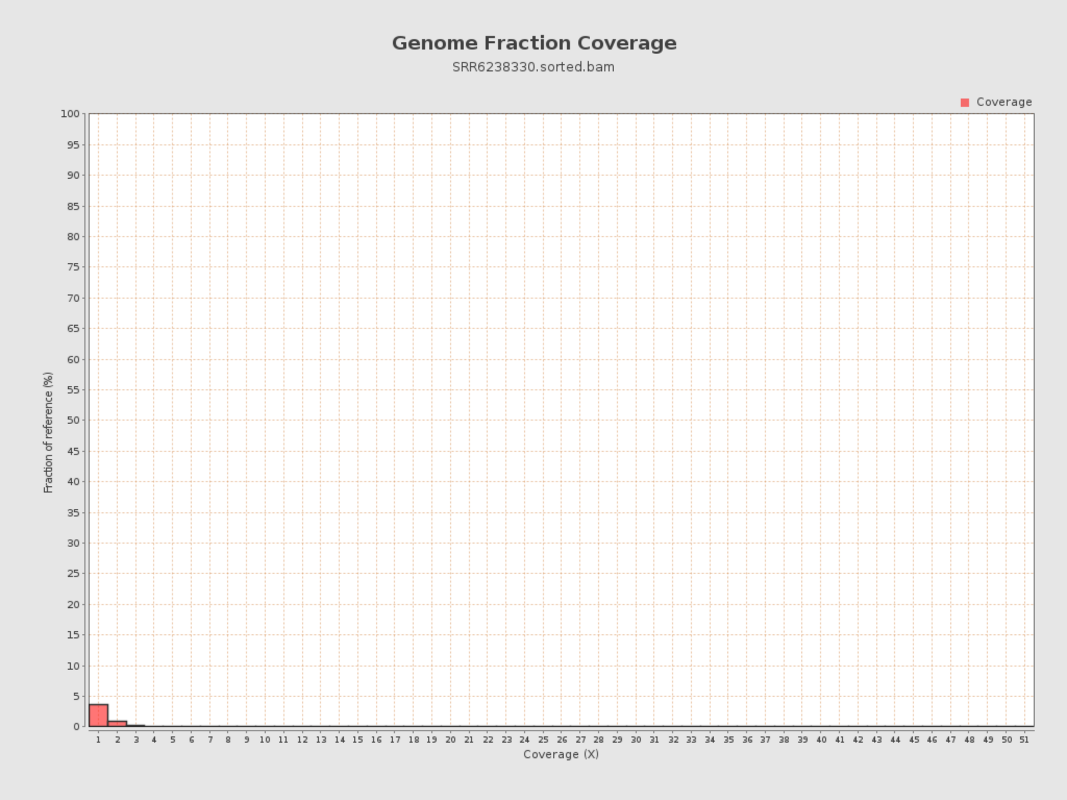
4. Results : Coverage Histogram



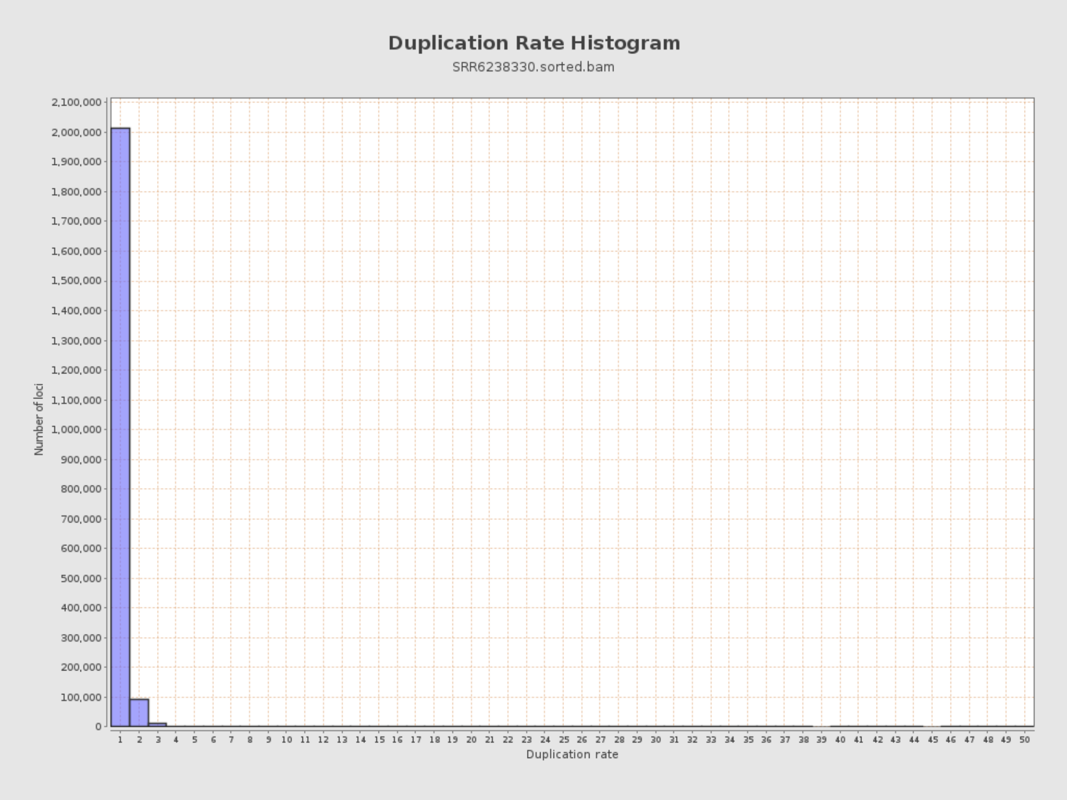
5. Results : Coverage Histogram (0-50X)



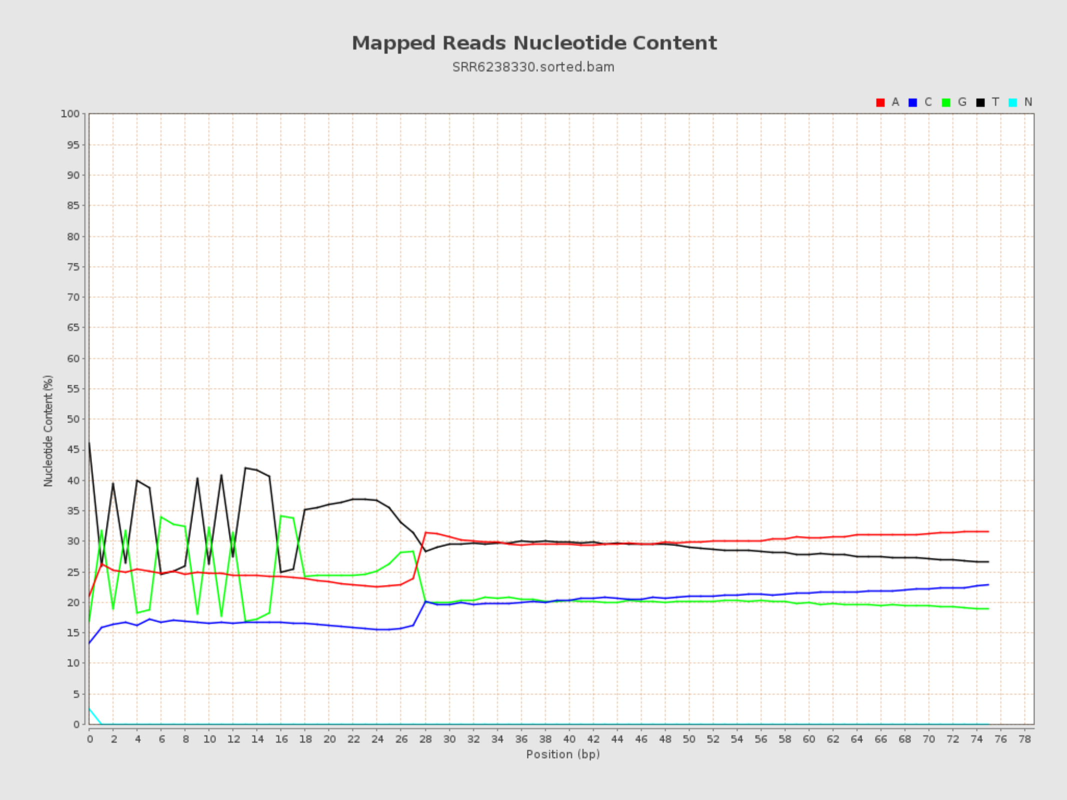
6. Results : Genome Fraction Coverage



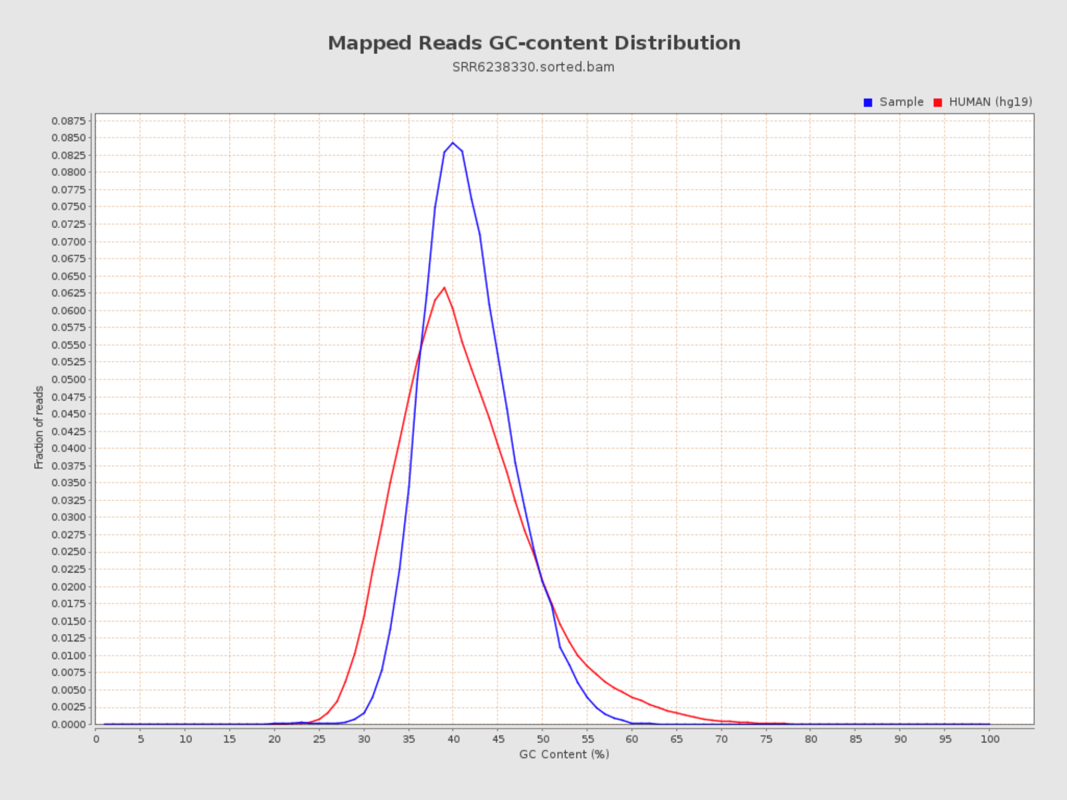
7. Results : Duplication Rate Histogram



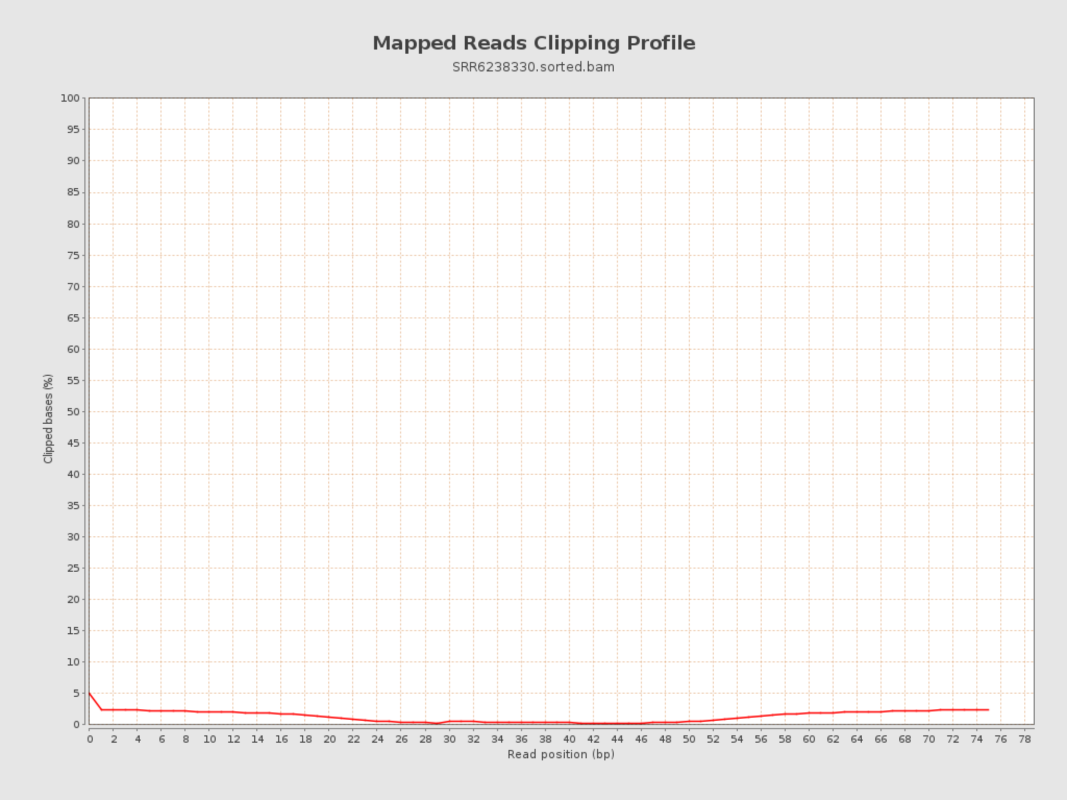
8. Results : Mapped Reads Nucleotide Content



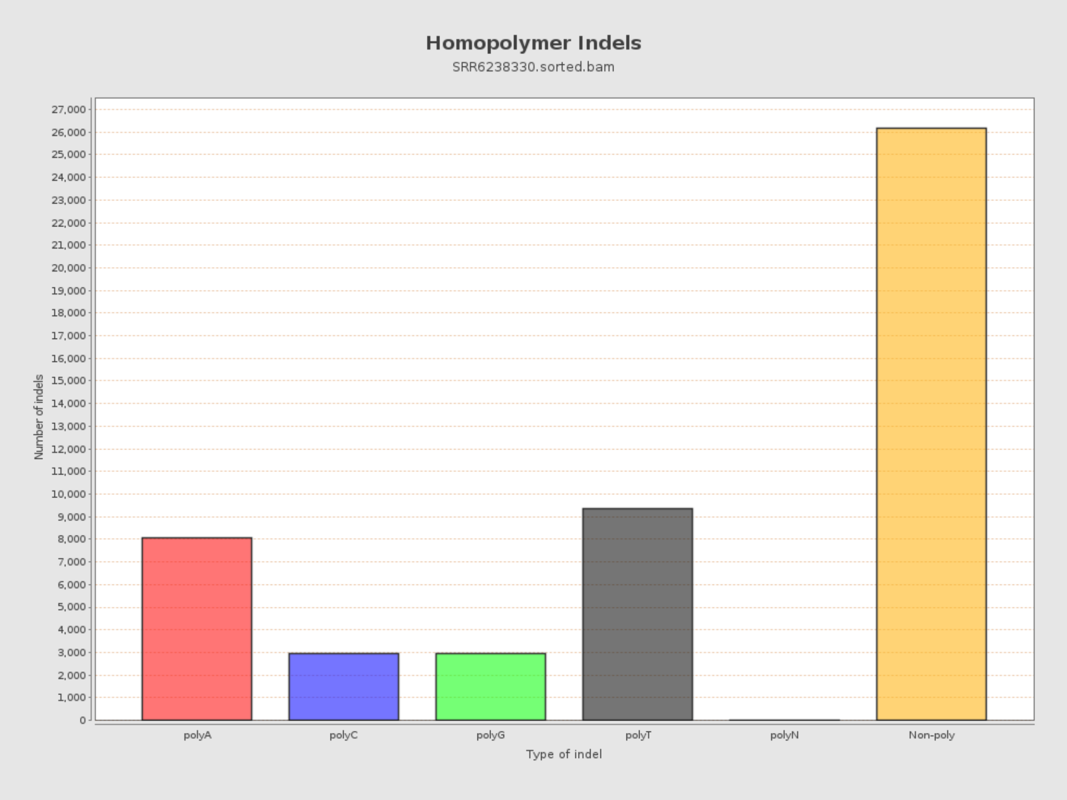
9. Results : Mapped Reads GC-content Distribution



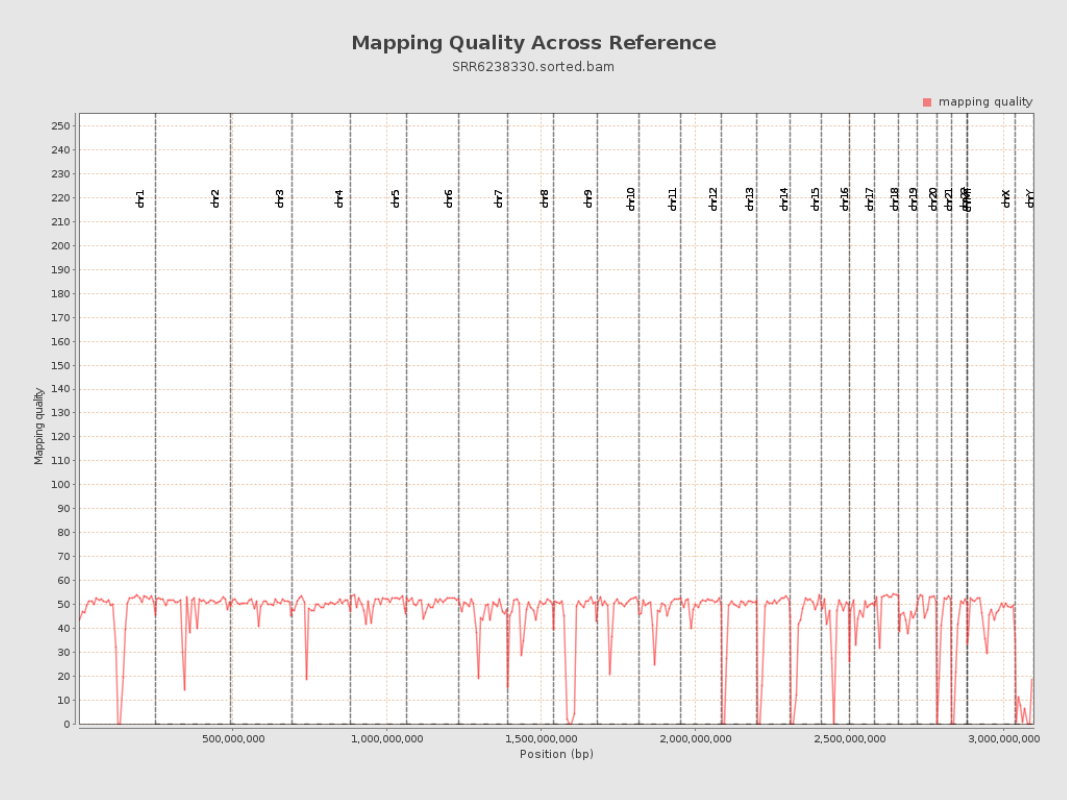
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram