Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:39:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238649.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_SRR6238649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238649.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:39:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,956,425
Mapped reads	2,540,861 / 85.94%
Unmapped reads	415,564 / 14.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,098 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,025,440 / 34.69%
Duplication rate	21.59%
Clipped reads	1,711,232 / 57.88%

2.2. ACGT Content

Number/percentage of A's	36,946,999 / 23.99%
Number/percentage of C's	27,088,483 / 17.59%
Number/percentage of T's	52,316,251 / 33.97%
Number/percentage of G's	37,639,044 / 24.44%
Number/percentage of N's	3,310 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0498

Standard Deviation	1.1339

2.4. Mapping Quality

Mean Mapping Quality	37.46

2.5. Mismatches and indels

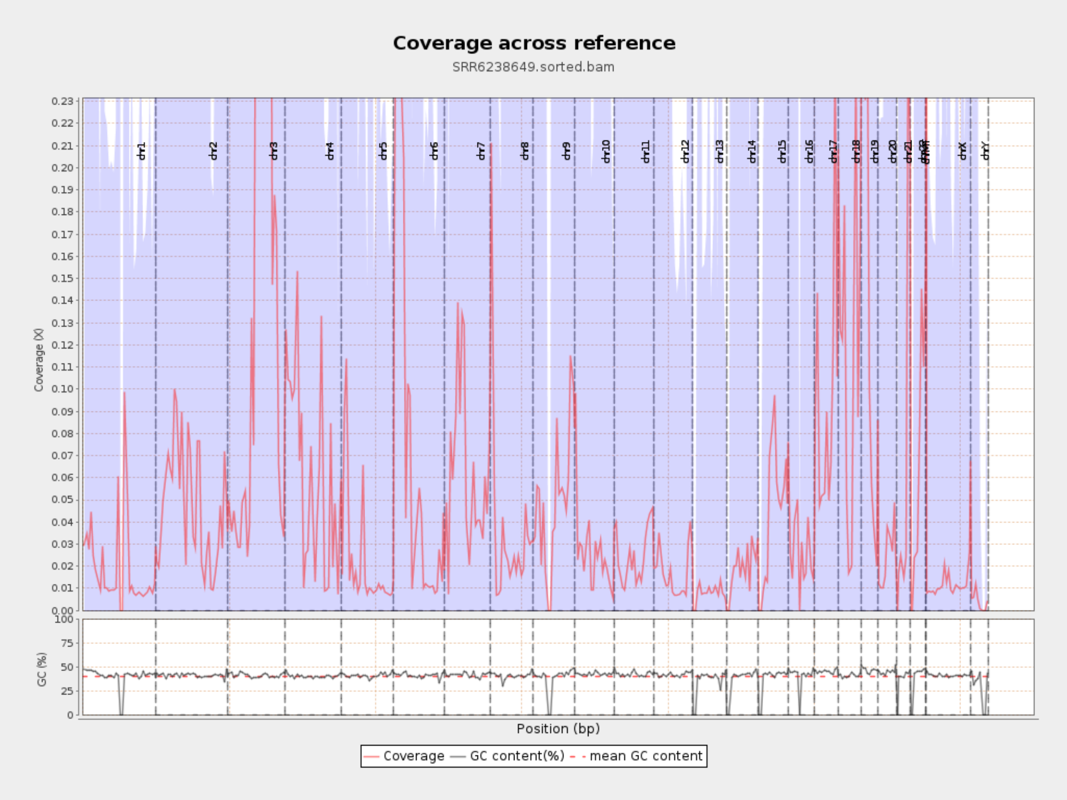
General error rate	0.61%
Mismatches	915,785
Insertions	10,268
Mapped reads with at least one insertion	0.4%
Deletions	44,705
Mapped reads with at least one deletion	1.75%
Homopolymer indels	40.35%

2.6. Chromosome stats

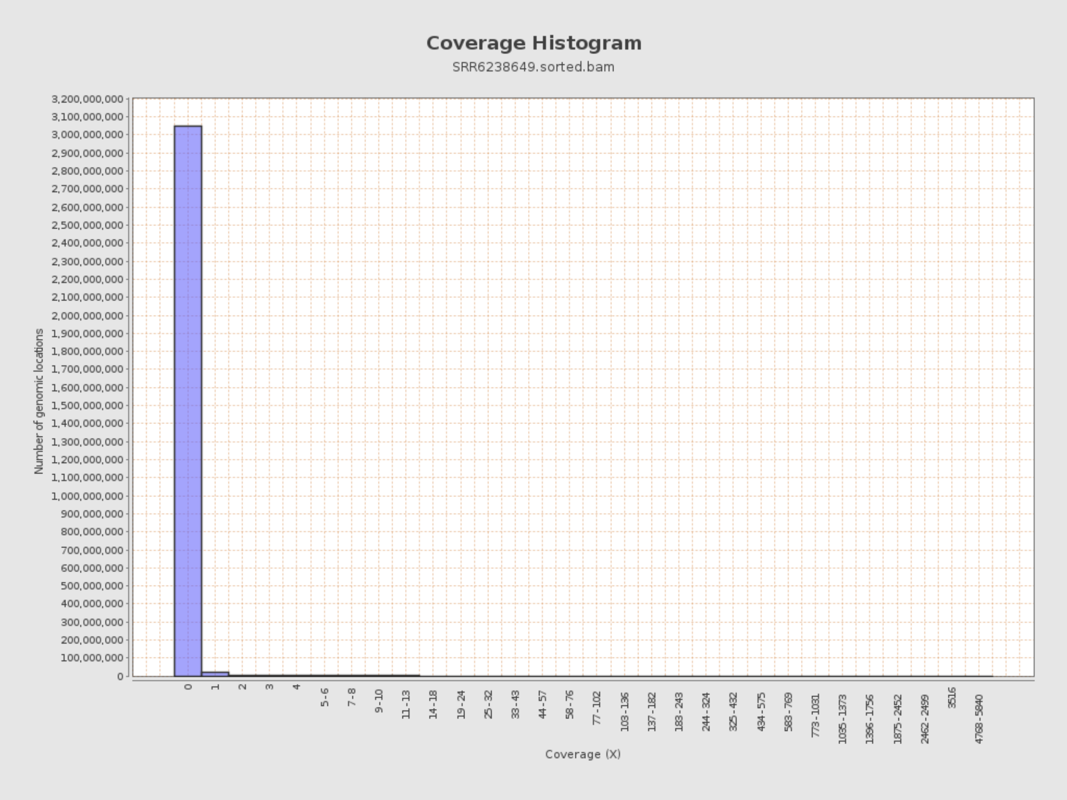
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4718279	0.0189	1.0567
chr2	243199373	11616750	0.0478	2.601
chr3	198022430	31976106	0.1615	1.1504
chr4	191154276	11429896	0.0598	0.6574
chr5	180915260	3891064	0.0215	0.3927
chr6	171115067	13426870	0.0785	1.1296
chr7	159138663	9929118	0.0624	1.2667

chr8	146364022	5112913	0.0349	1.4638
chr9	141213431	6865978	0.0486	0.6723
chr10	135534747	3504395	0.0259	0.4418
chr11	135006516	3340584	0.0247	0.4403
chr12	133851895	2257187	0.0169	0.3602
chr13	115169878	917629	0.008	0.5733
chr14	107349540	2034557	0.019	0.4134
chr15	102531392	4524716	0.0441	0.7555
chr16	90354753	2449941	0.0271	0.4643
chr17	81195210	7841588	0.0966	0.8971
chr18	78077248	9250603	0.1185	2.2223
chr19	59128983	8279066	0.14	1.1958
chr20	63025520	1567265	0.0249	0.4307
chr21	48129895	3608841	0.075	0.7827
chr22	51304566	3306735	0.0645	0.7131
chrMT	16571	36714	2.2156	3.9618
chrX	155270560	1935569	0.0125	0.2997
chrY	59373566	246466	0.0042	0.3365

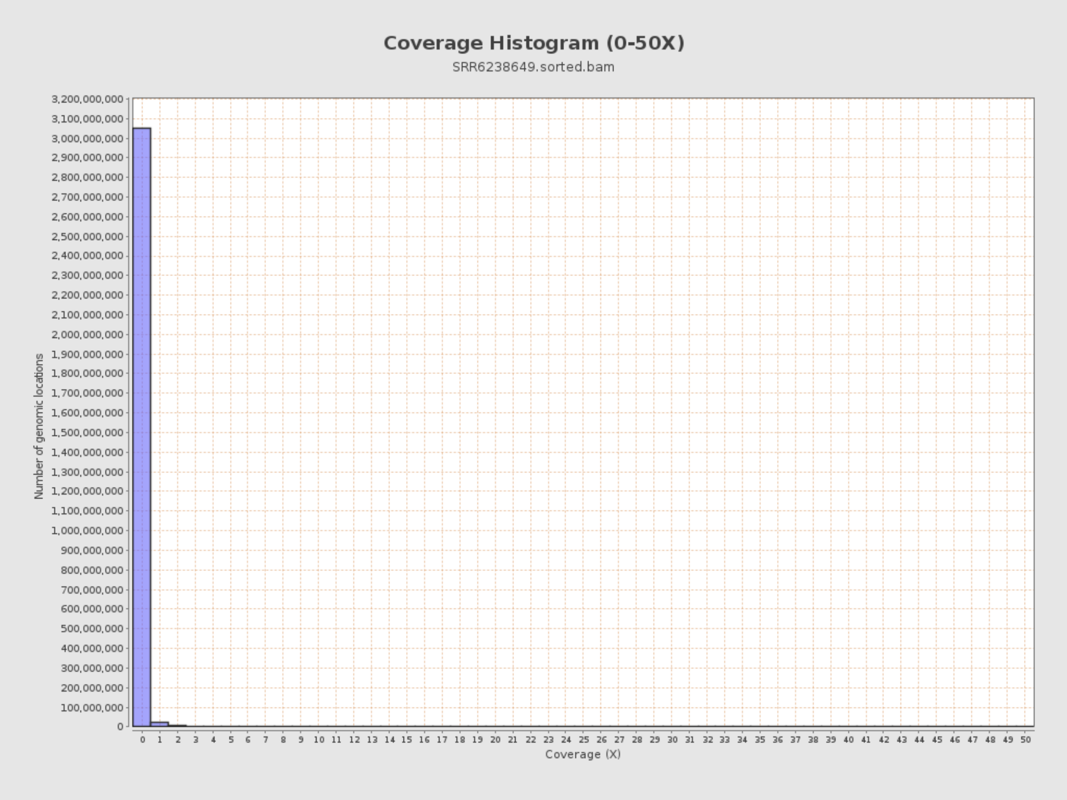
3. Results : Coverage across reference



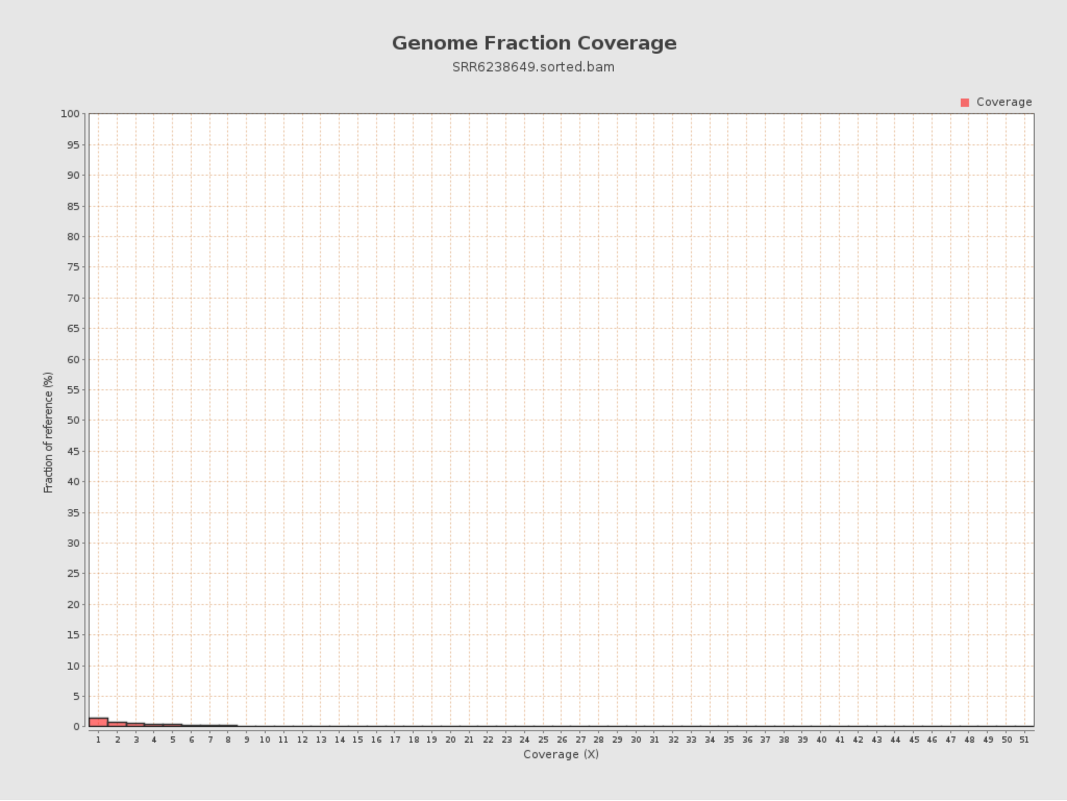
4. Results : Coverage Histogram



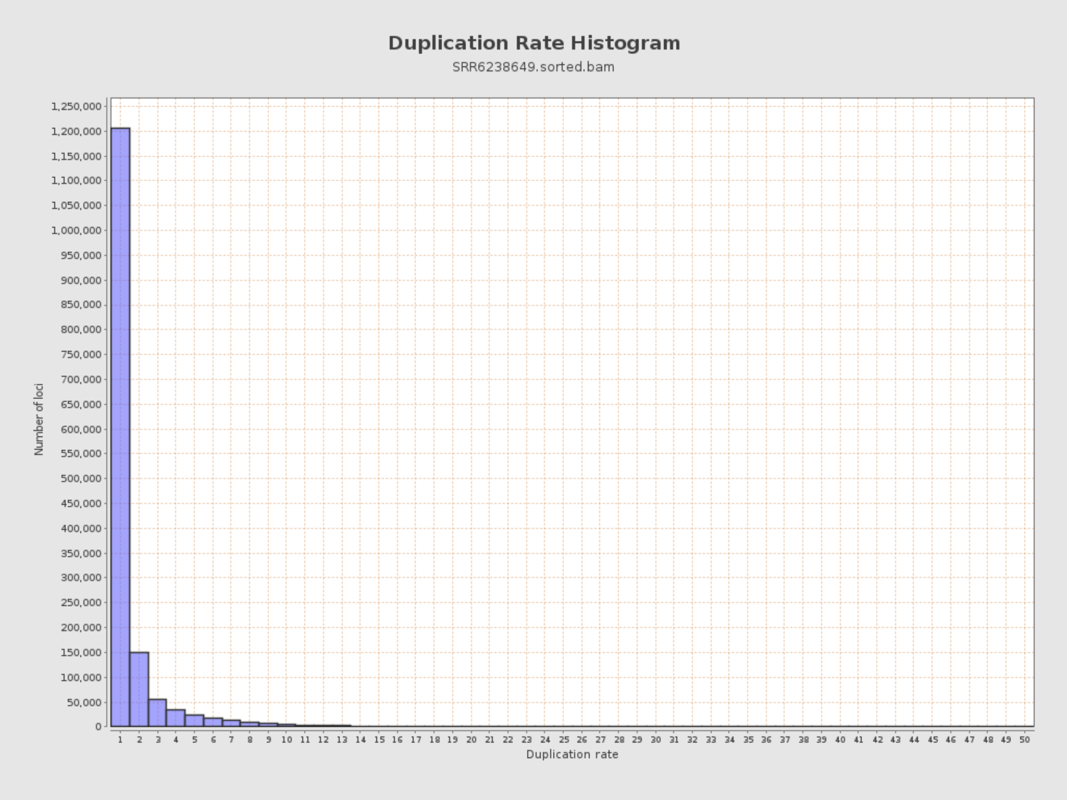
5. Results : Coverage Histogram (0-50X)



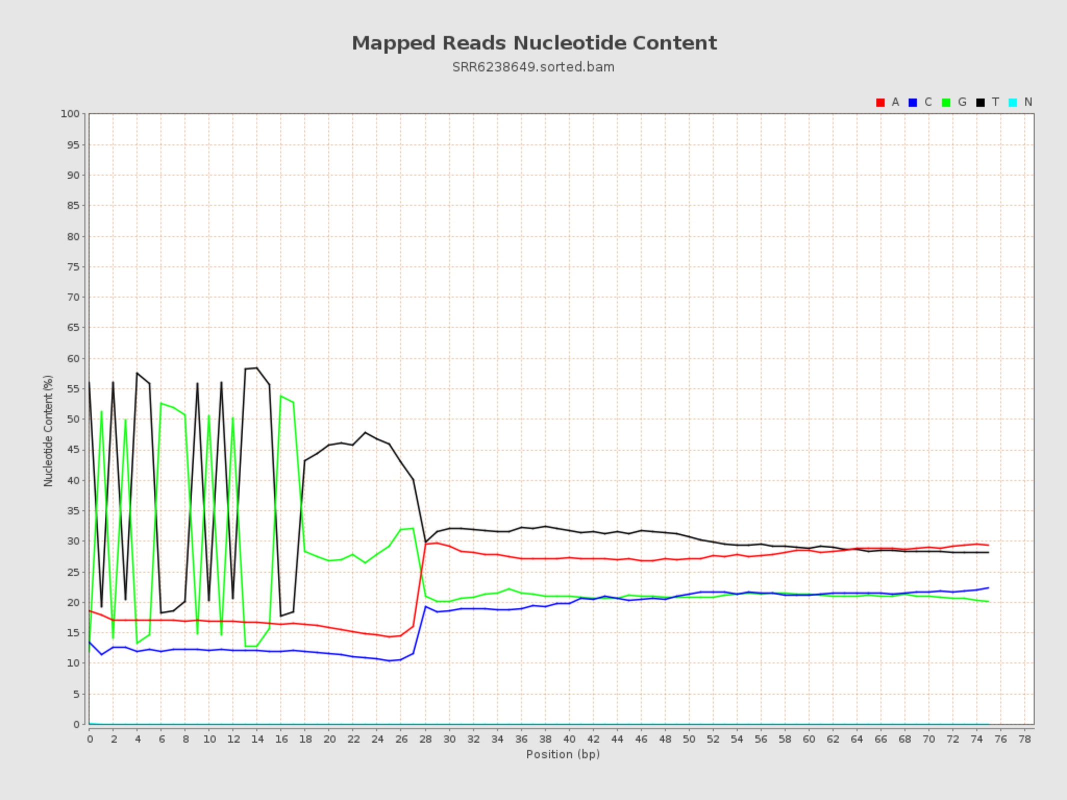
6. Results : Genome Fraction Coverage



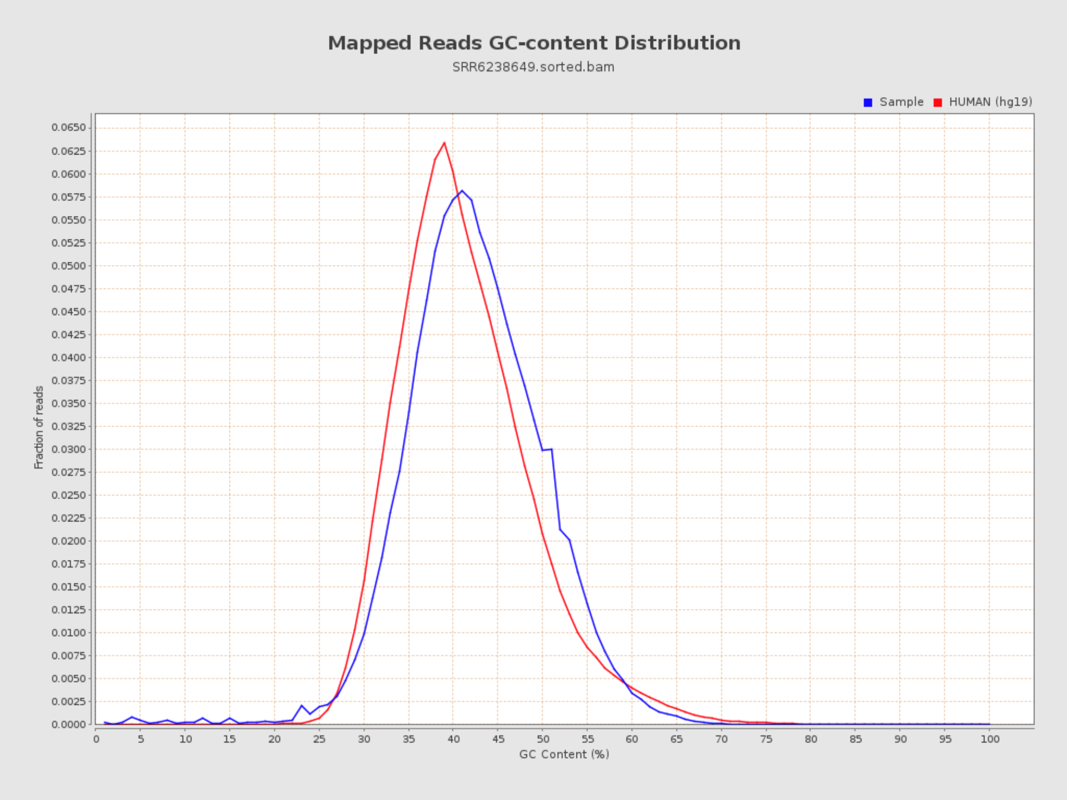
7. Results : Duplication Rate Histogram



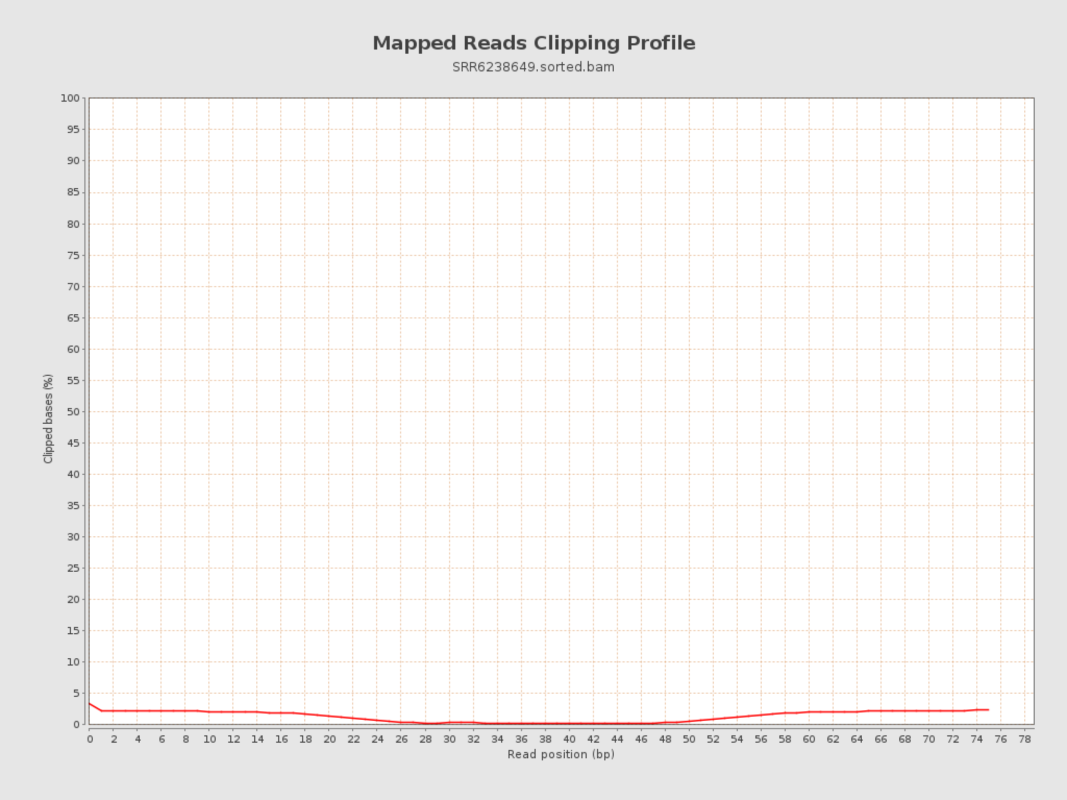
8. Results : Mapped Reads Nucleotide Content



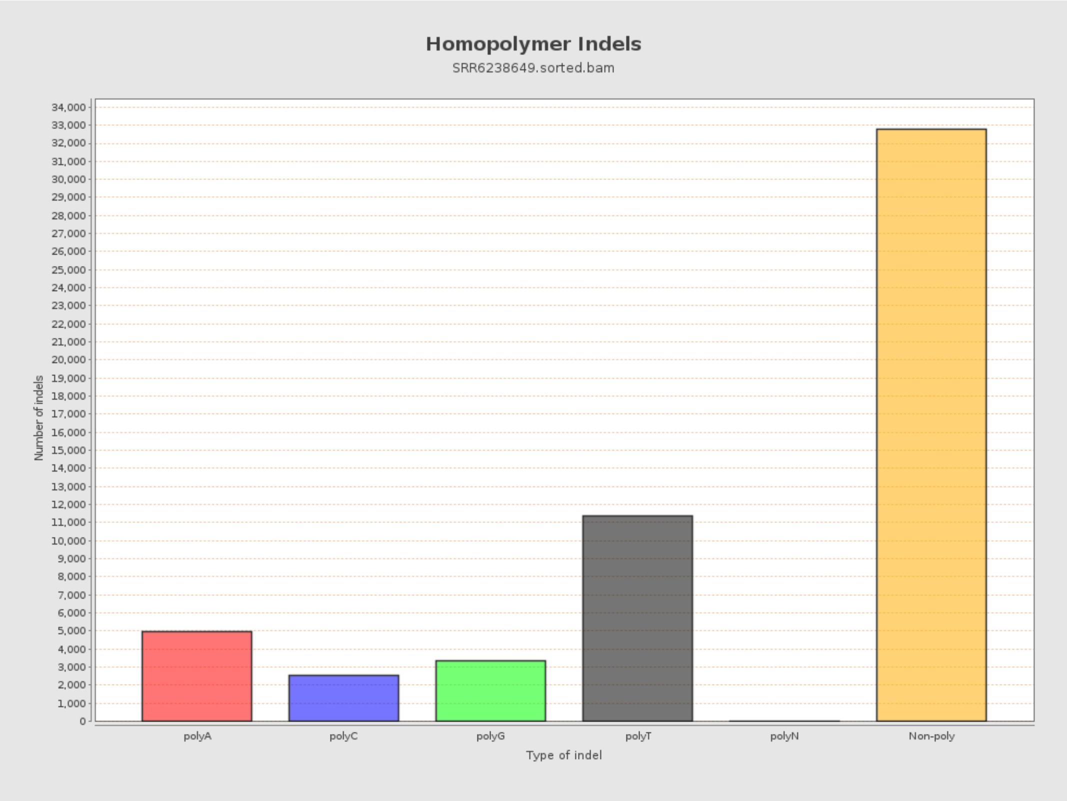
9. Results : Mapped Reads GC-content Distribution



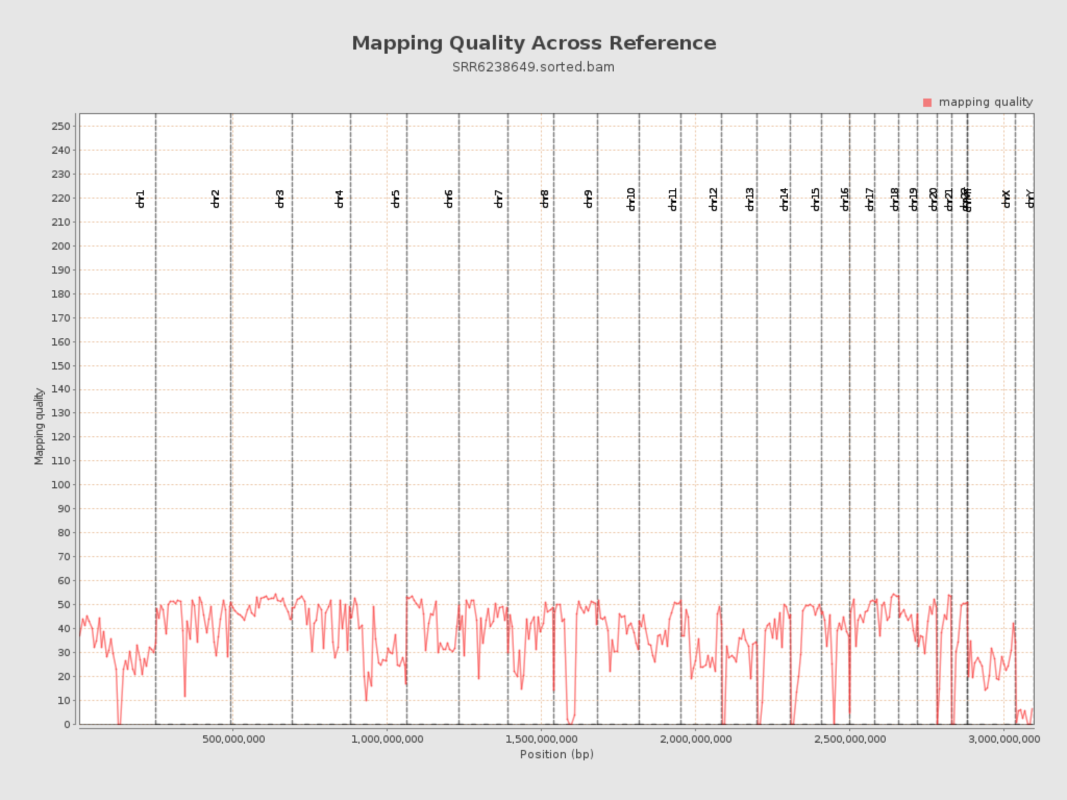
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram