Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:35:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238648.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_SRR6238648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:35:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,606,269
Mapped reads	3,099,461 / 85.95%
Unmapped reads	506,808 / 14.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,048 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	1,117,996 / 31%
Duplication rate	21.22%
Clipped reads	1,965,446 / 54.5%

2.2. ACGT Content

Number/percentage of A's	46,307,752 / 24.2%
Number/percentage of C's	33,811,267 / 17.67%
Number/percentage of T's	64,823,140 / 33.87%
Number/percentage of G's	46,432,713 / 24.26%
Number/percentage of N's	4,492 / 0%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0618

Standard Deviation	1.156

2.4. Mapping Quality

Mean Mapping Quality	38.31

2.5. Mismatches and indels

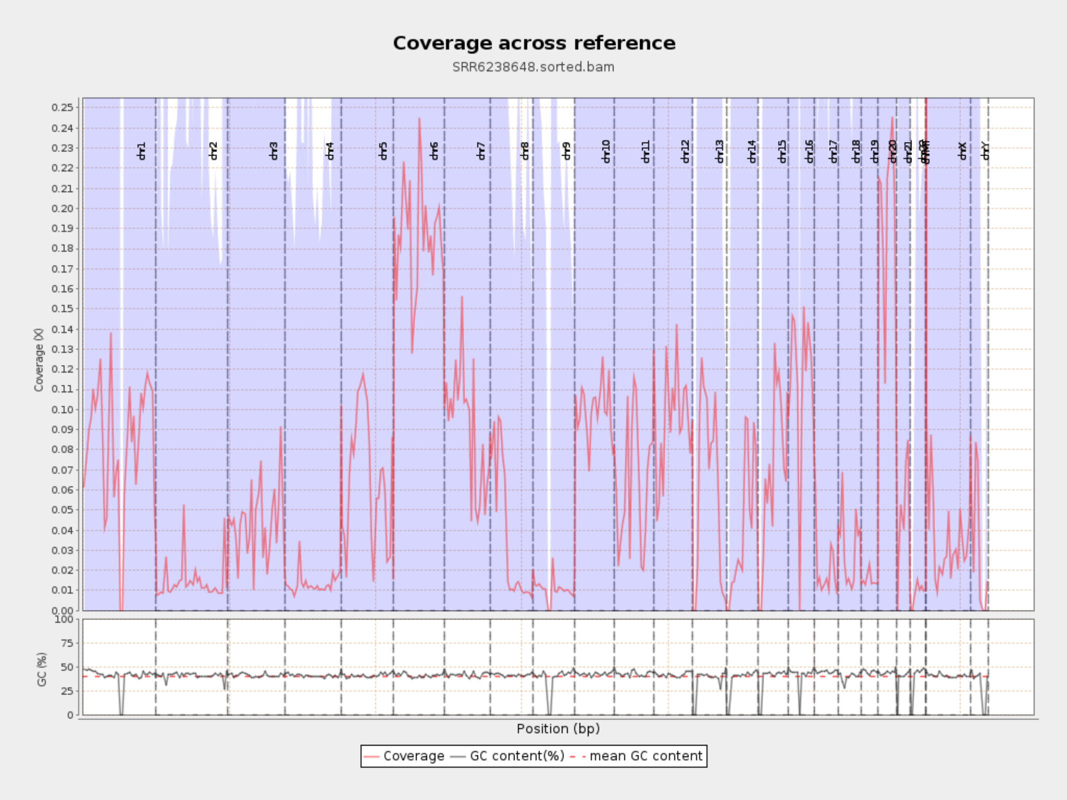
General error rate	0.56%
Mismatches	1,052,506
Insertions	12,580
Mapped reads with at least one insertion	0.4%
Deletions	51,841
Mapped reads with at least one deletion	1.66%
Homopolymer indels	41.87%

2.6. Chromosome stats

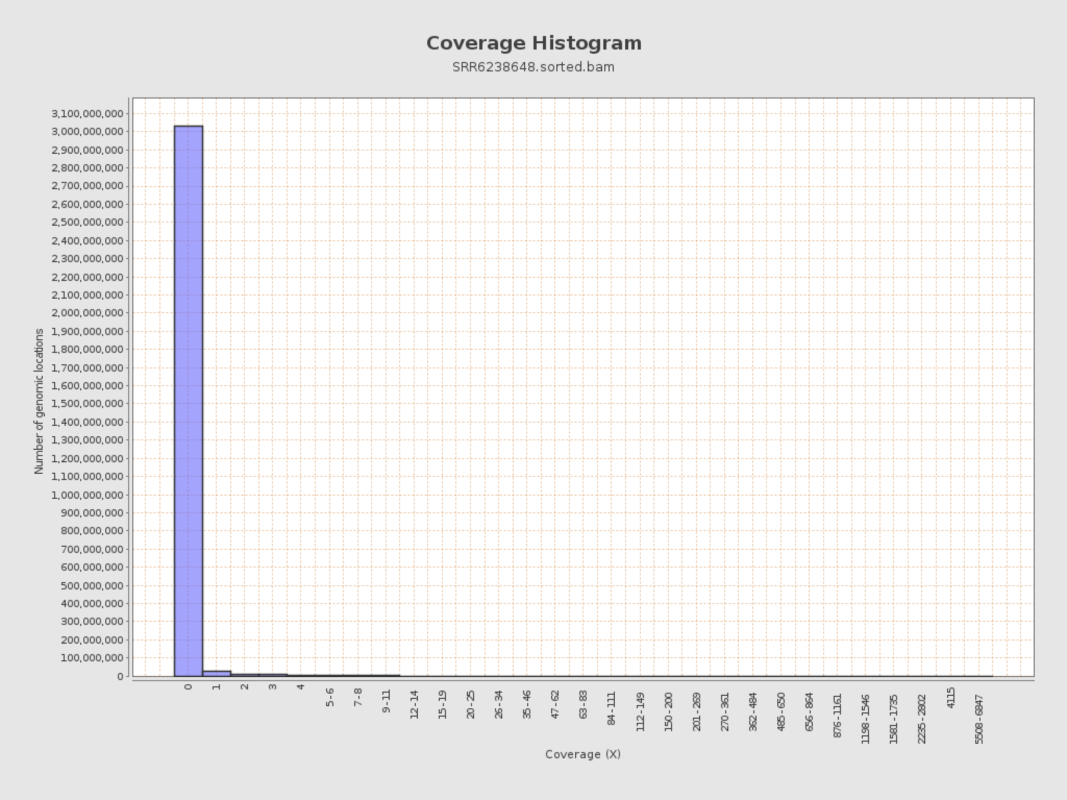
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20747114	0.0832	0.8082
chr2	243199373	3508277	0.0144	2.9459
chr3	198022430	8516709	0.043	0.5249
chr4	191154276	2564679	0.0134	0.2489
chr5	180915260	12146263	0.0671	0.6322
chr6	171115067	32026118	0.1872	1.5287
chr7	159138663	14384616	0.0904	1.3071

chr8	146364022	5272568	0.036	0.5899
chr9	141213431	1470552	0.0104	0.3137
chr10	135534747	13564242	0.1001	0.8328
chr11	135006516	8340301	0.0618	0.6501
chr12	133851895	12601809	0.0941	0.7495
chr13	115169878	6948407	0.0603	0.7976
chr14	107349540	4464645	0.0416	0.5066
chr15	102531392	6977951	0.0681	0.8176
chr16	90354753	10178061	0.1126	0.8515
chr17	81195210	1703459	0.021	0.3428
chr18	78077248	2463359	0.0316	2.1352
chr19	59128983	915683	0.0155	0.4166
chr20	63025520	12569277	0.1994	1.1354
chr21	48129895	2199477	0.0457	0.5188
chr22	51304566	437789	0.0085	0.1854
chrMT	16571	17865	1.0781	2.2279
chrX	155270560	5636190	0.0363	0.4522
chrY	59373566	1810840	0.0305	0.5278

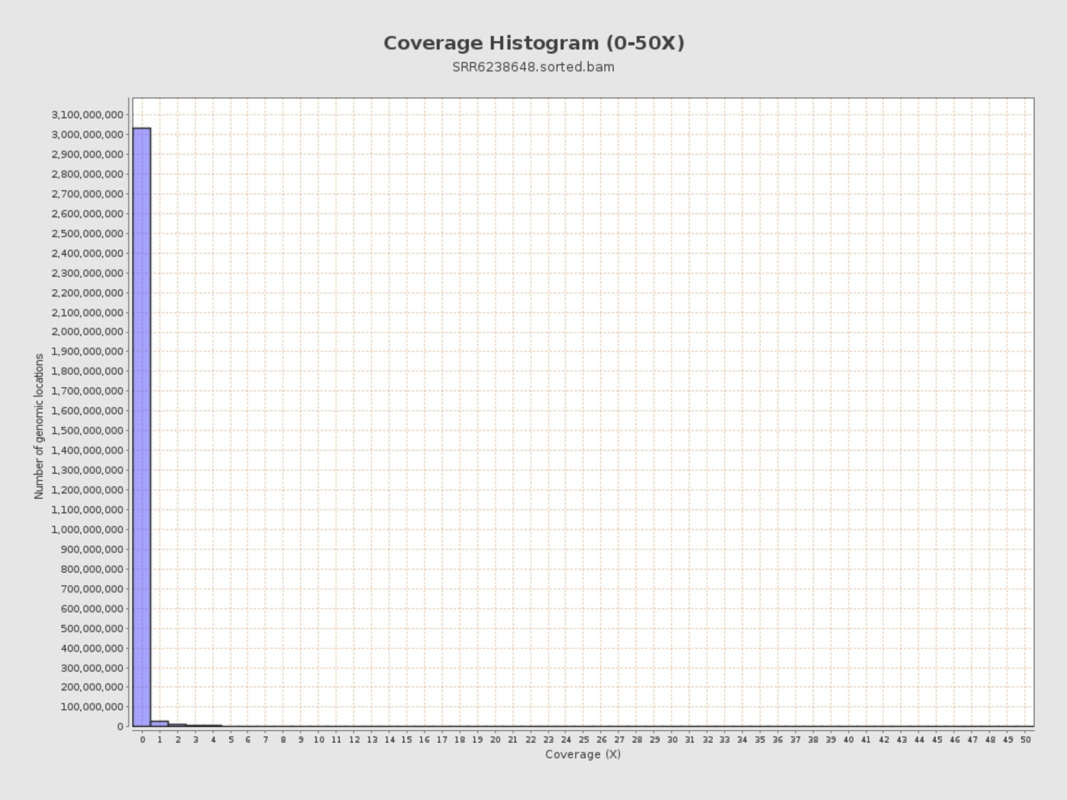
3. Results : Coverage across reference



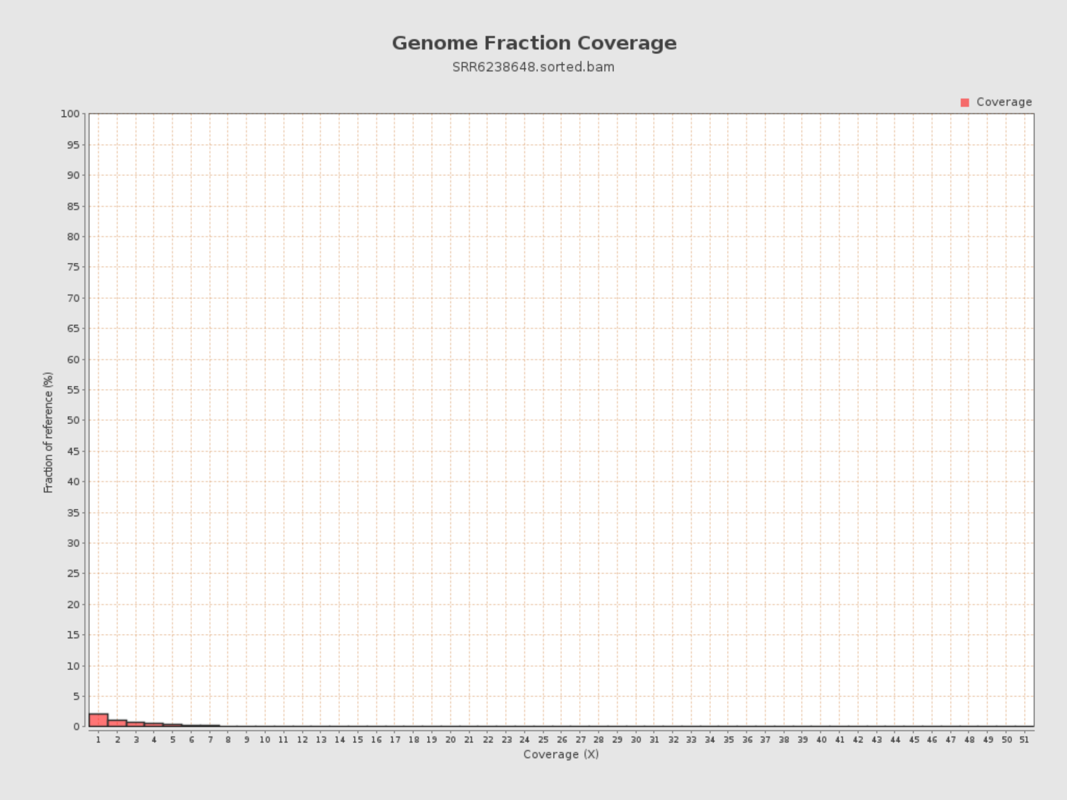
4. Results : Coverage Histogram



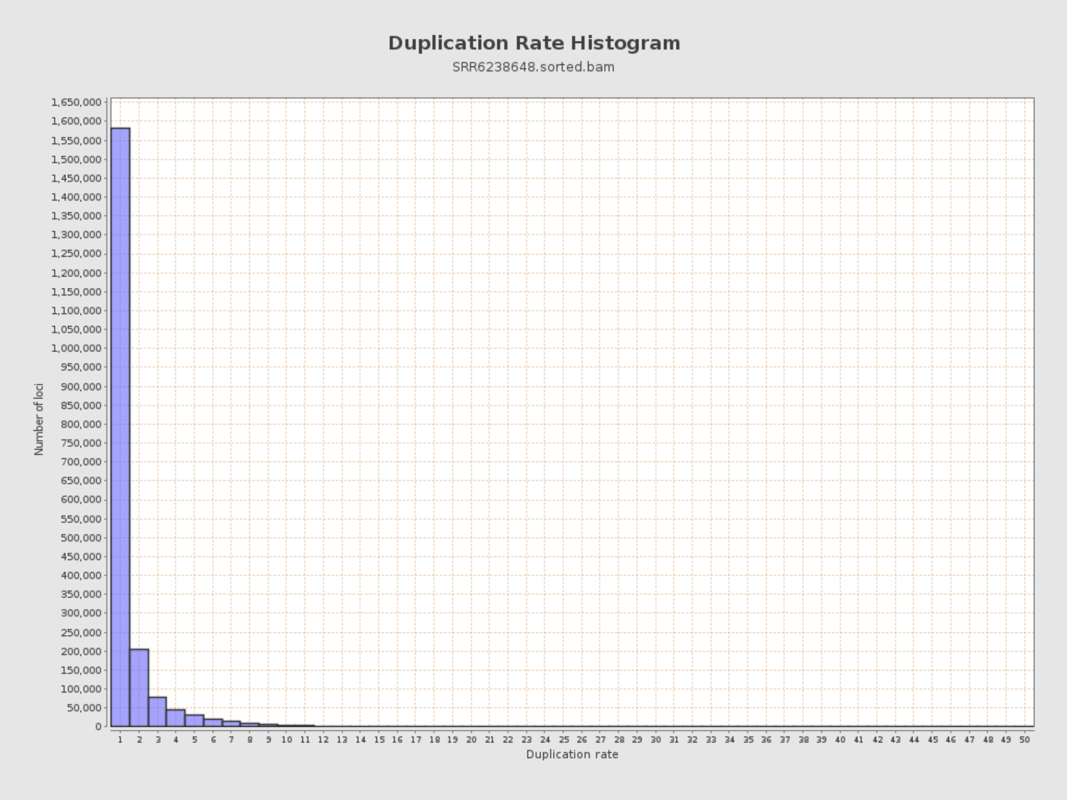
5. Results : Coverage Histogram (0-50X)



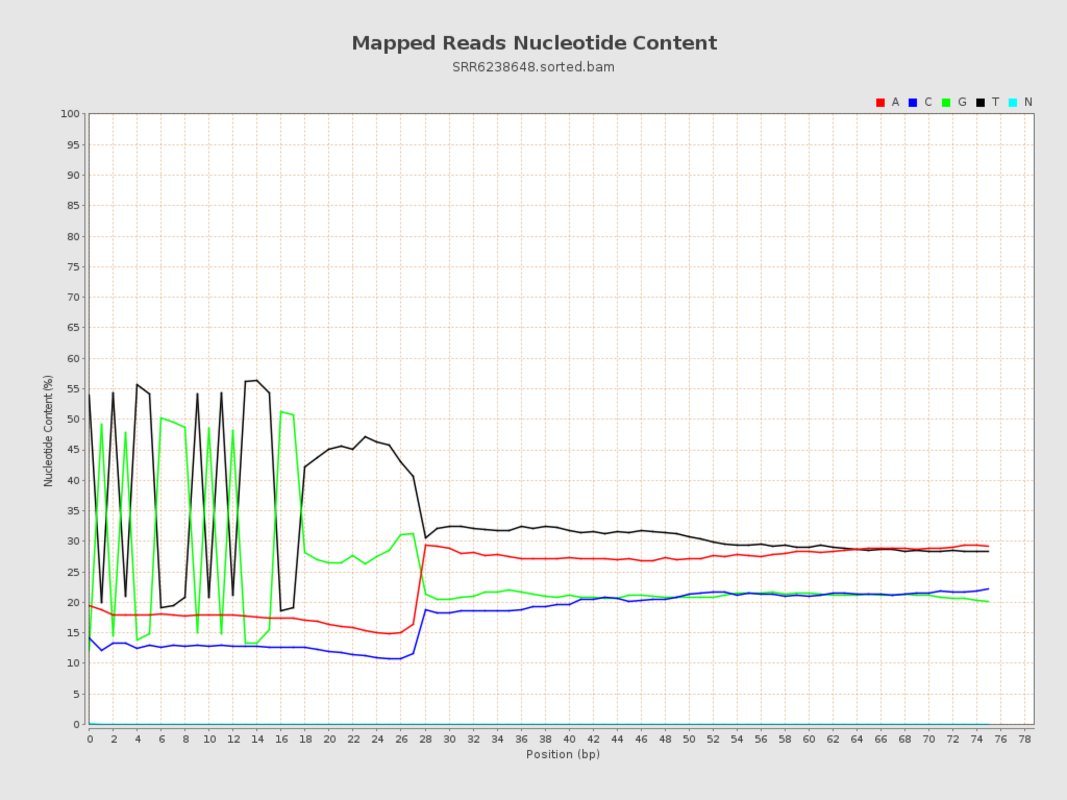
6. Results : Genome Fraction Coverage



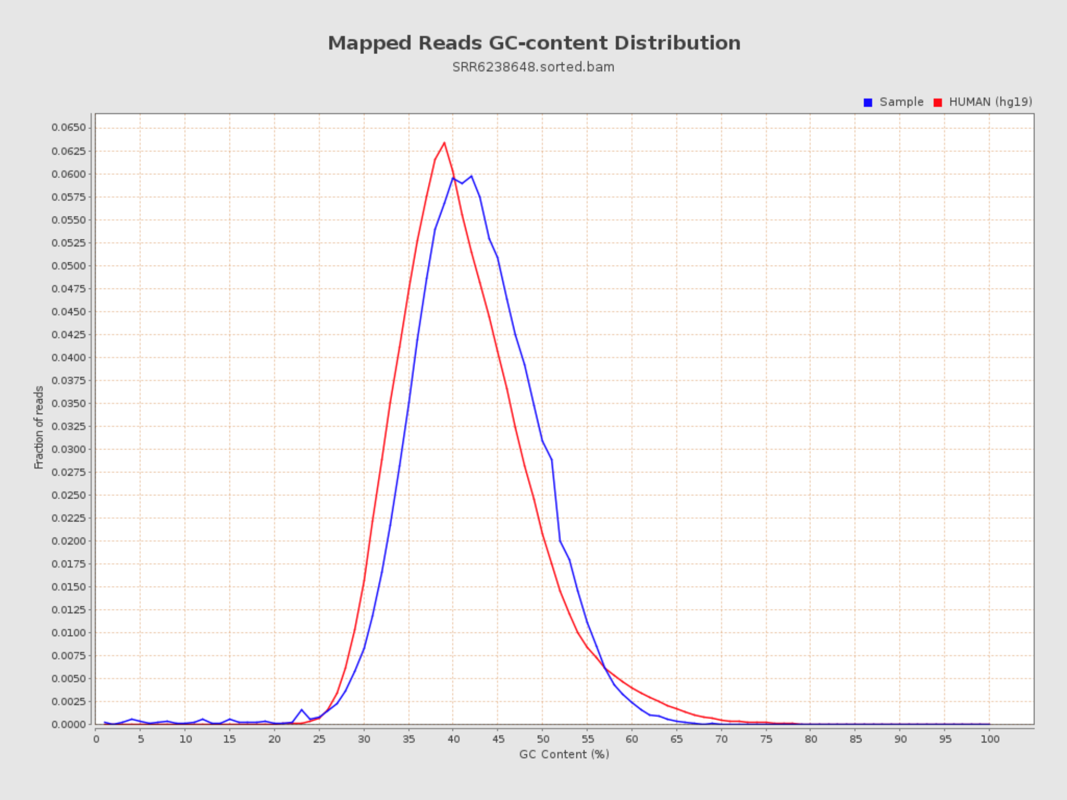
7. Results : Duplication Rate Histogram



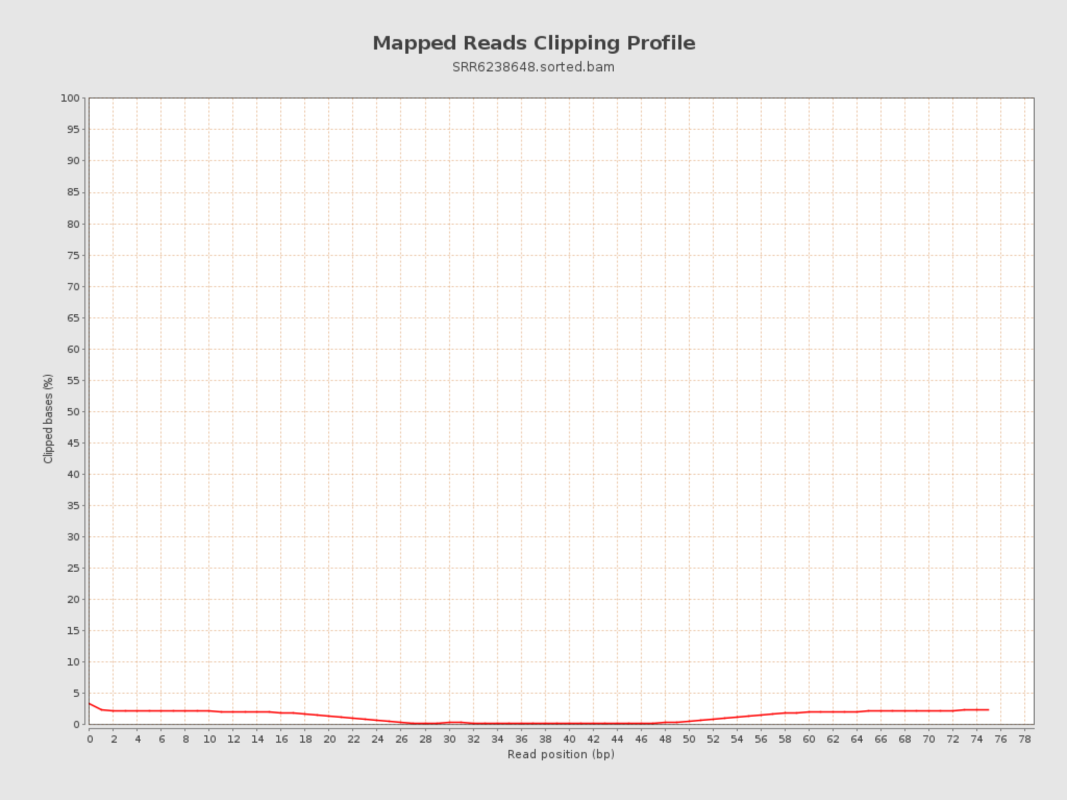
8. Results : Mapped Reads Nucleotide Content



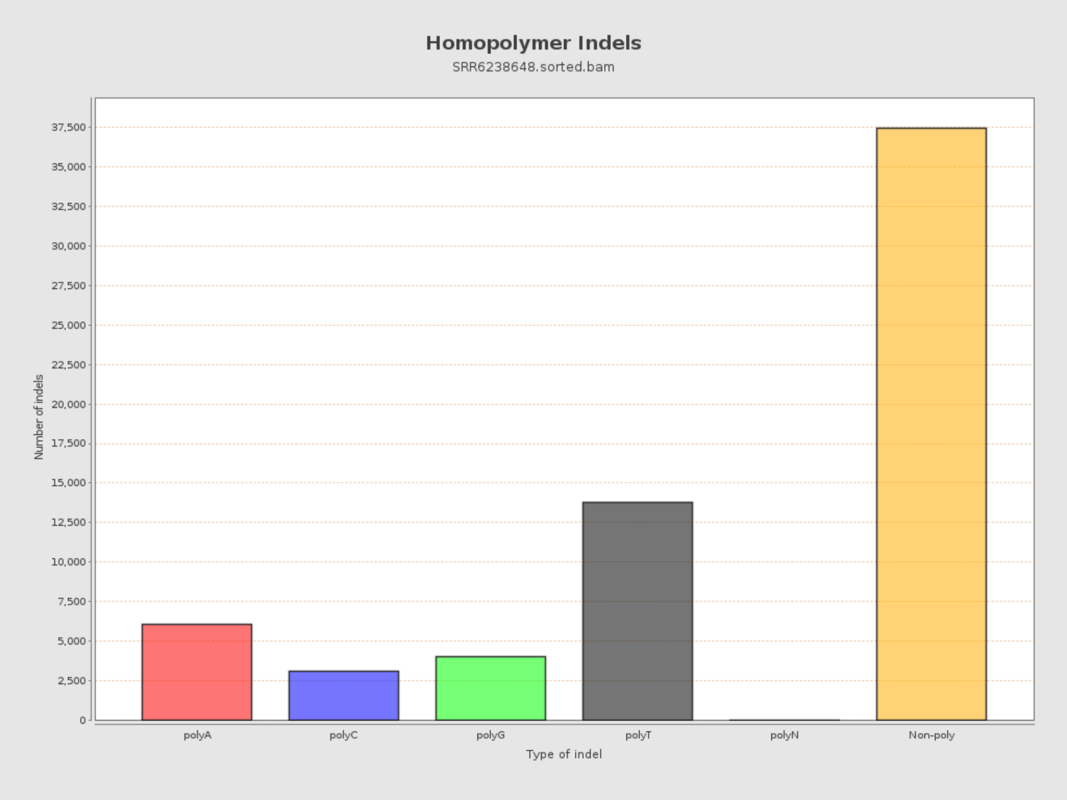
9. Results : Mapped Reads GC-content Distribution



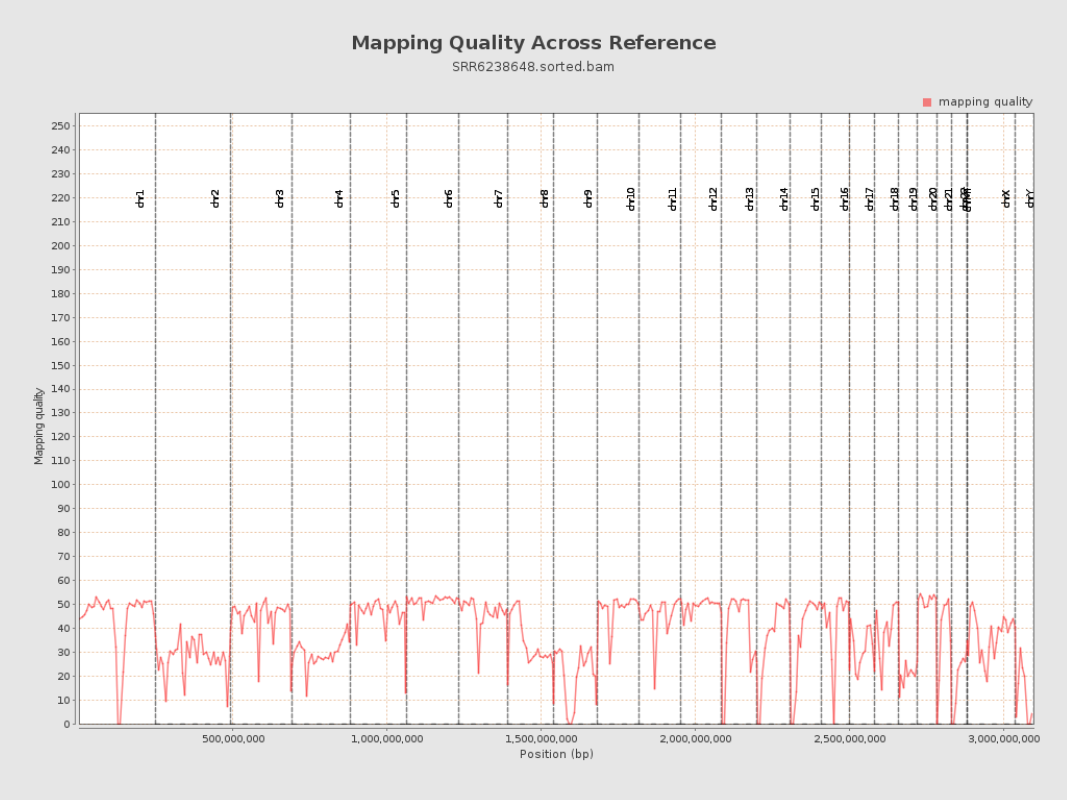
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram