Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:18:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238659.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_SRR6238659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:18:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,913,485
Mapped reads	3,383,205 / 86.45%
Unmapped reads	530,280 / 13.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,968 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,491,908 / 38.12%
Duplication rate	22.09%
Clipped reads	2,236,013 / 57.14%

2.2. ACGT Content

Number/percentage of A's	52,371,217 / 25.25%
Number/percentage of C's	36,027,516 / 17.37%
Number/percentage of T's	69,393,735 / 33.46%
Number/percentage of G's	49,574,613 / 23.91%
Number/percentage of N's	4,823 / 0%
GC Percentage	41.28%

2.3. Coverage

Mean	0.067

Standard Deviation	1.0446

2.4. Mapping Quality

Mean Mapping Quality	42.32

2.5. Mismatches and indels

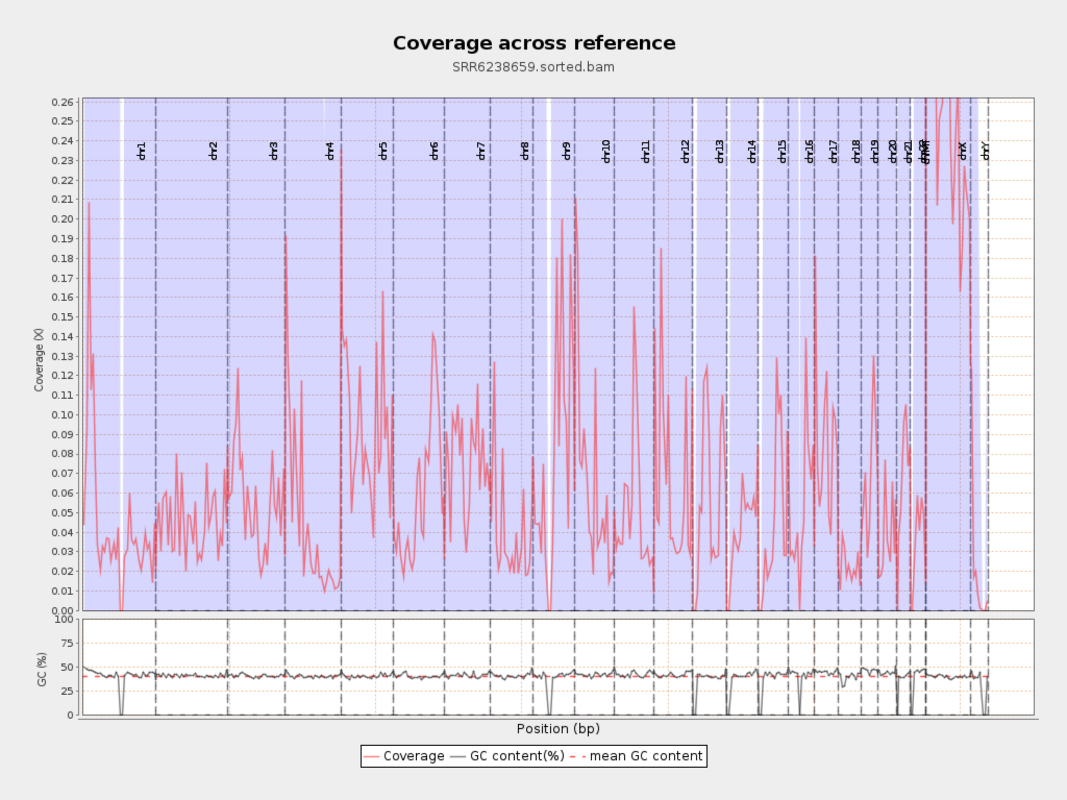
General error rate	0.54%
Mismatches	1,101,135
Insertions	14,013
Mapped reads with at least one insertion	0.41%
Deletions	56,388
Mapped reads with at least one deletion	1.65%
Homopolymer indels	42.33%

2.6. Chromosome stats

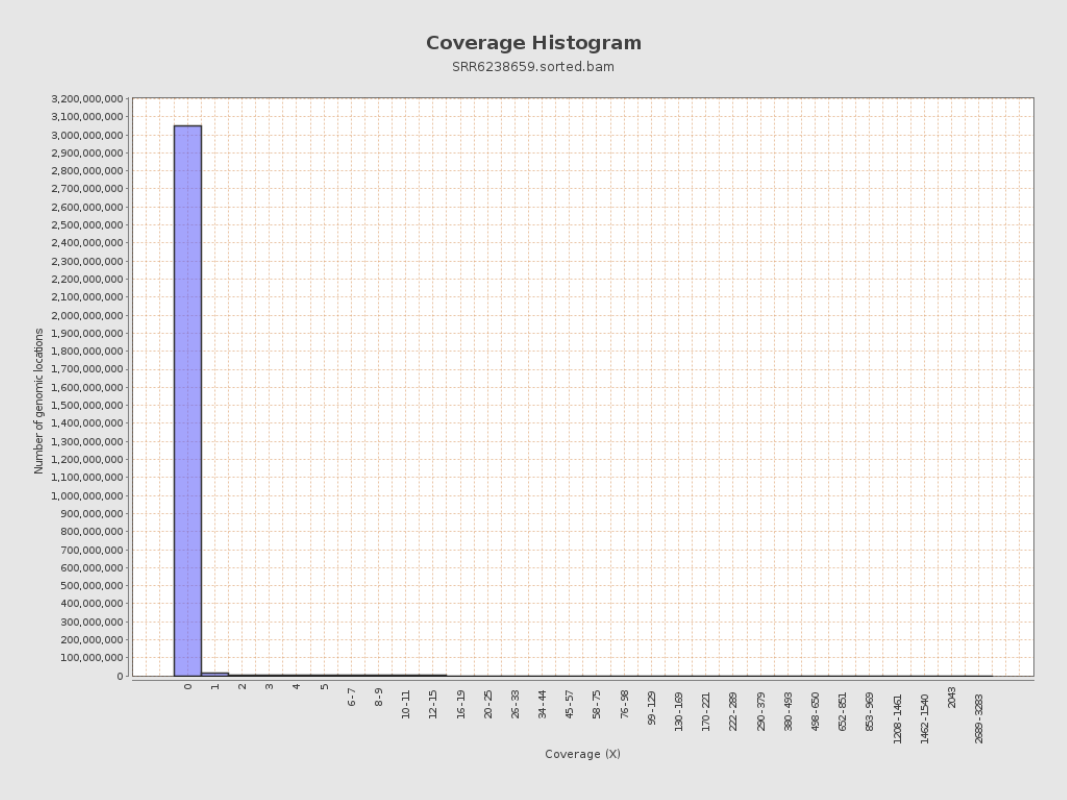
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11221394	0.045	0.823
chr2	243199373	11033060	0.0454	1.5972
chr3	198022430	11124119	0.0562	0.7702
chr4	191154276	8293405	0.0434	0.6661
chr5	180915260	16717411	0.0924	0.9859
chr6	171115067	10444509	0.061	0.9679
chr7	159138663	12048779	0.0757	1.2877

chr8	146364022	5580996	0.0381	0.8692
chr9	141213431	11090761	0.0785	0.9236
chr10	135534747	8957270	0.0661	0.959
chr11	135006516	6928045	0.0513	0.7206
chr12	133851895	8997881	0.0672	0.8448
chr13	115169878	6649819	0.0577	0.8931
chr14	107349540	4354330	0.0406	0.7334
chr15	102531392	4533400	0.0442	0.7718
chr16	90354753	4906417	0.0543	0.7816
chr17	81195210	7148971	0.088	0.9603
chr18	78077248	1734893	0.0222	1.957
chr19	59128983	4068458	0.0688	0.917
chr20	63025520	2394567	0.038	0.6261
chr21	48129895	3233604	0.0672	0.8412
chr22	51304566	1822786	0.0355	0.573
chrMT	16571	25300	1.5268	4.0891
chrX	155270560	43119807	0.2777	1.7586
chrY	59373566	1038007	0.0175	0.4316

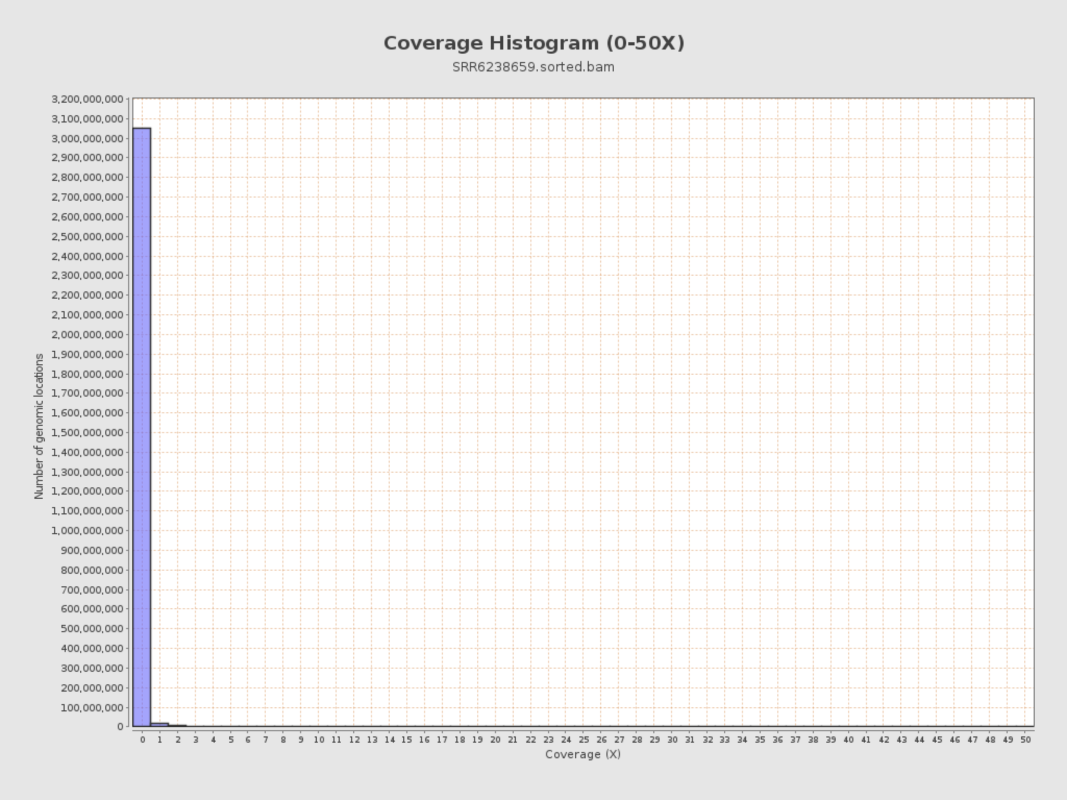
3. Results : Coverage across reference



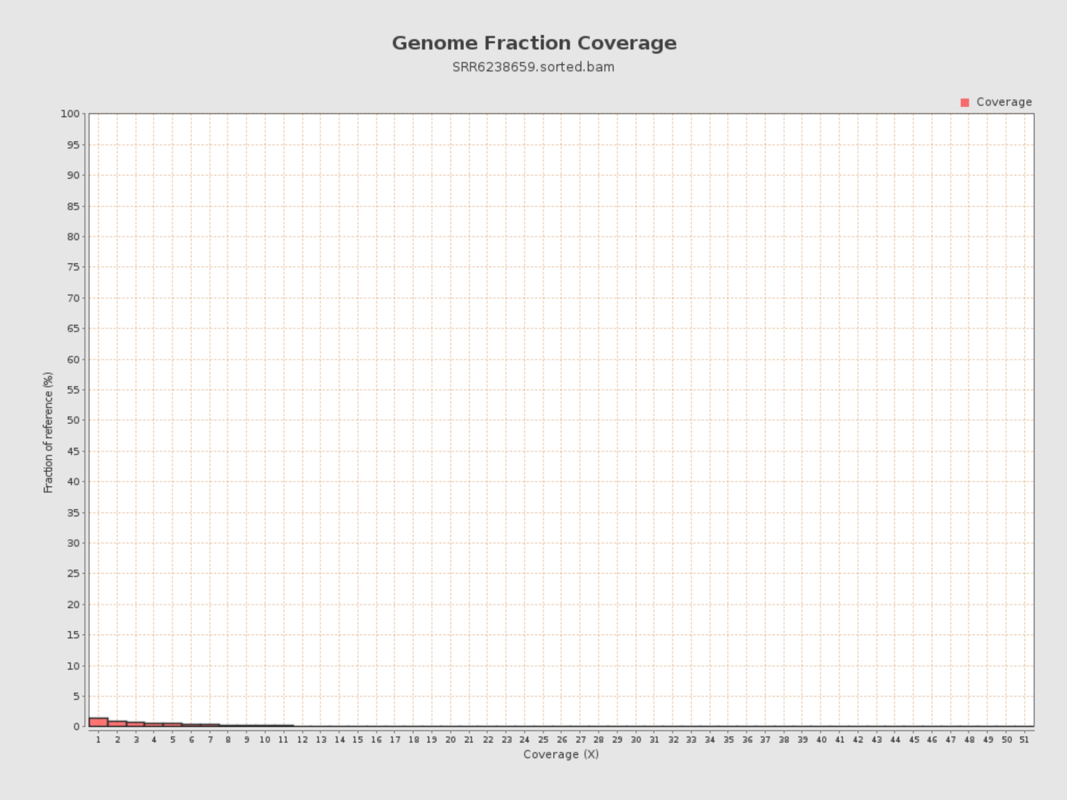
4. Results : Coverage Histogram



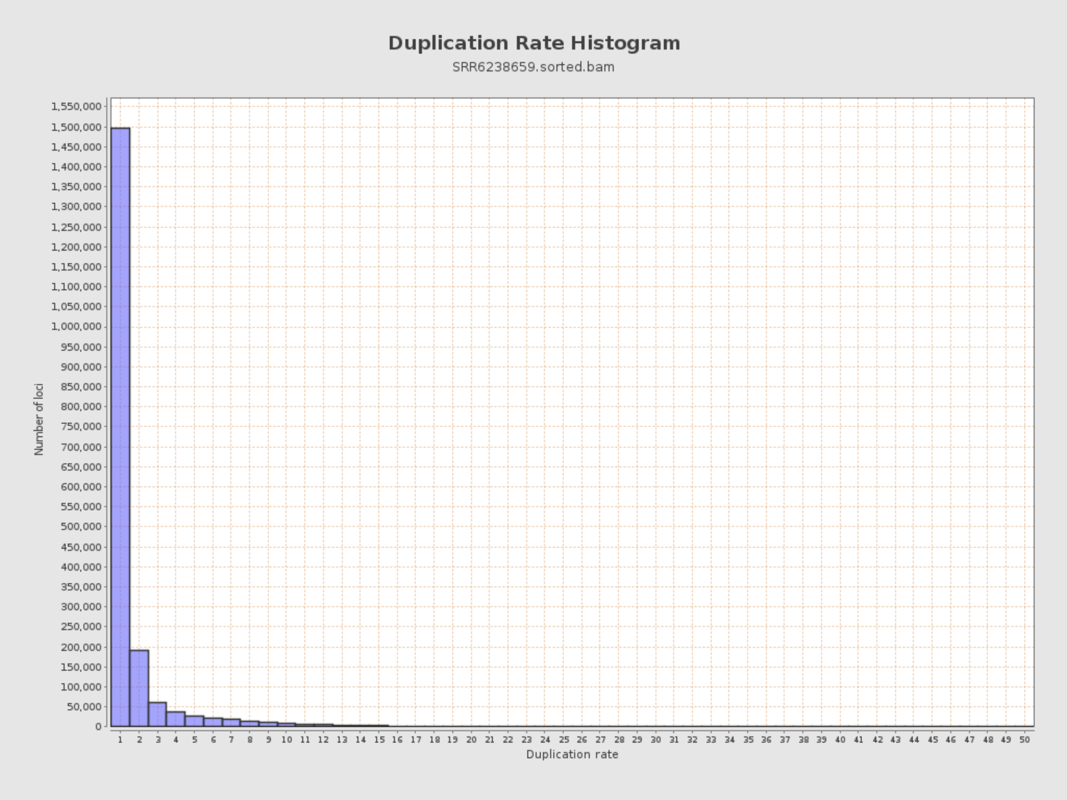
5. Results : Coverage Histogram (0-50X)



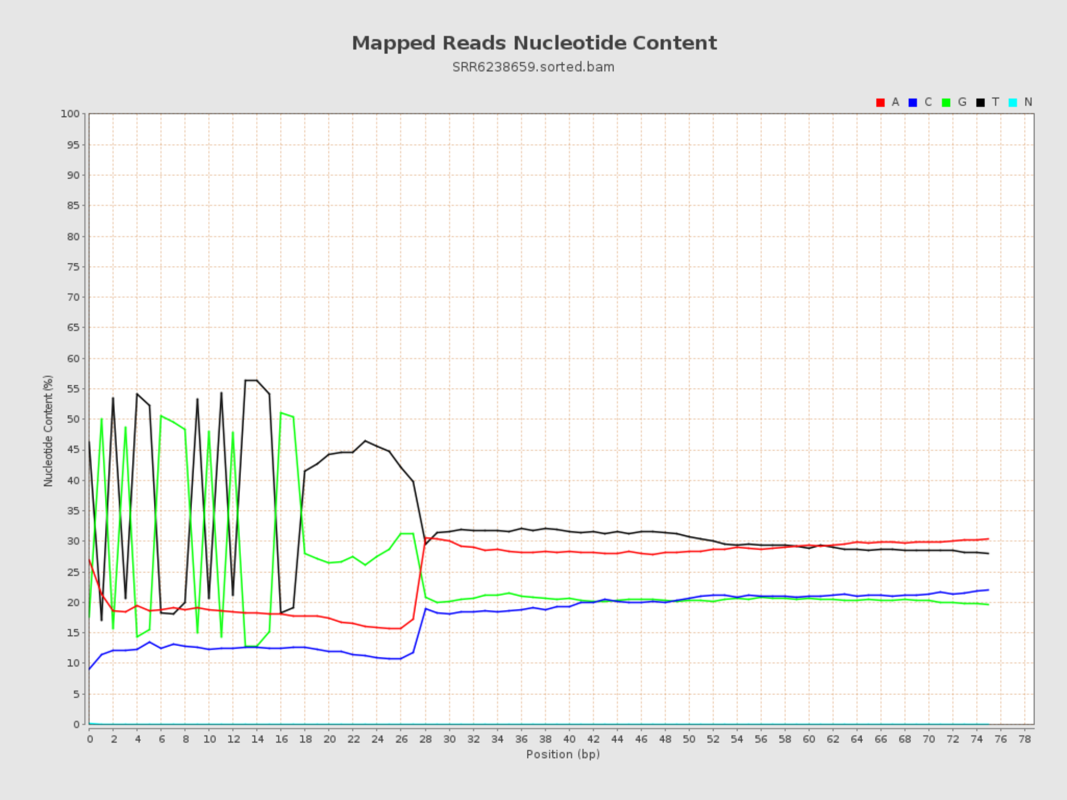
6. Results : Genome Fraction Coverage



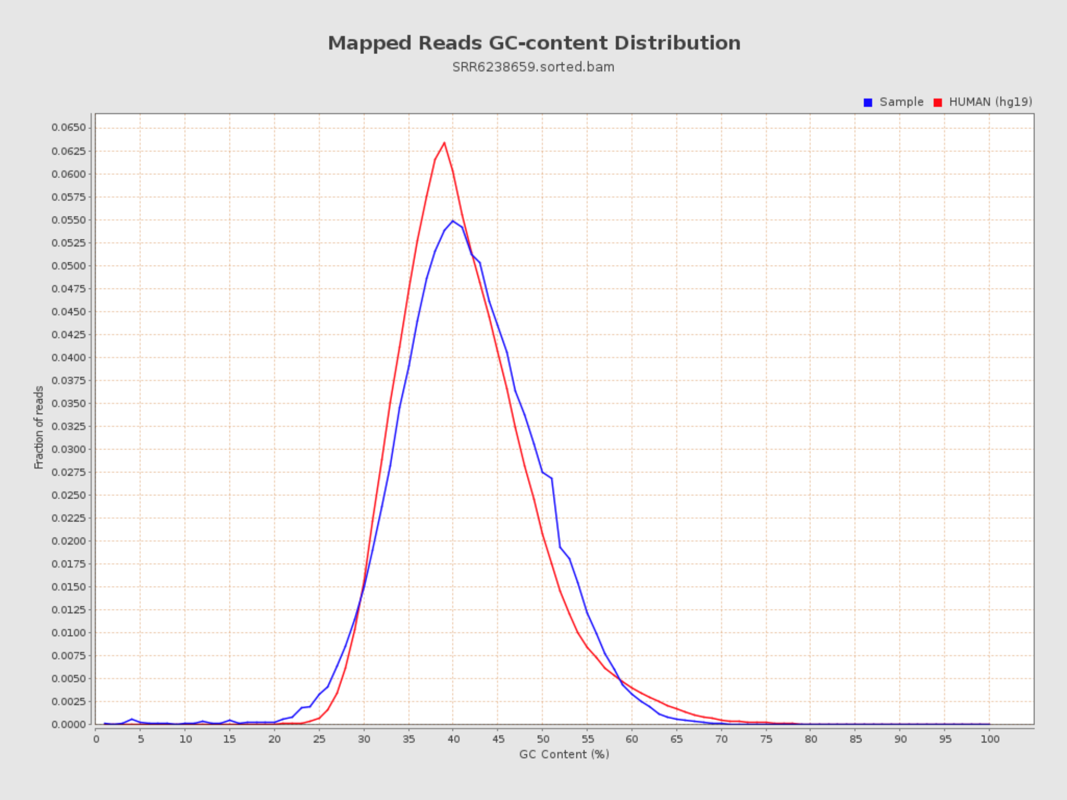
7. Results : Duplication Rate Histogram



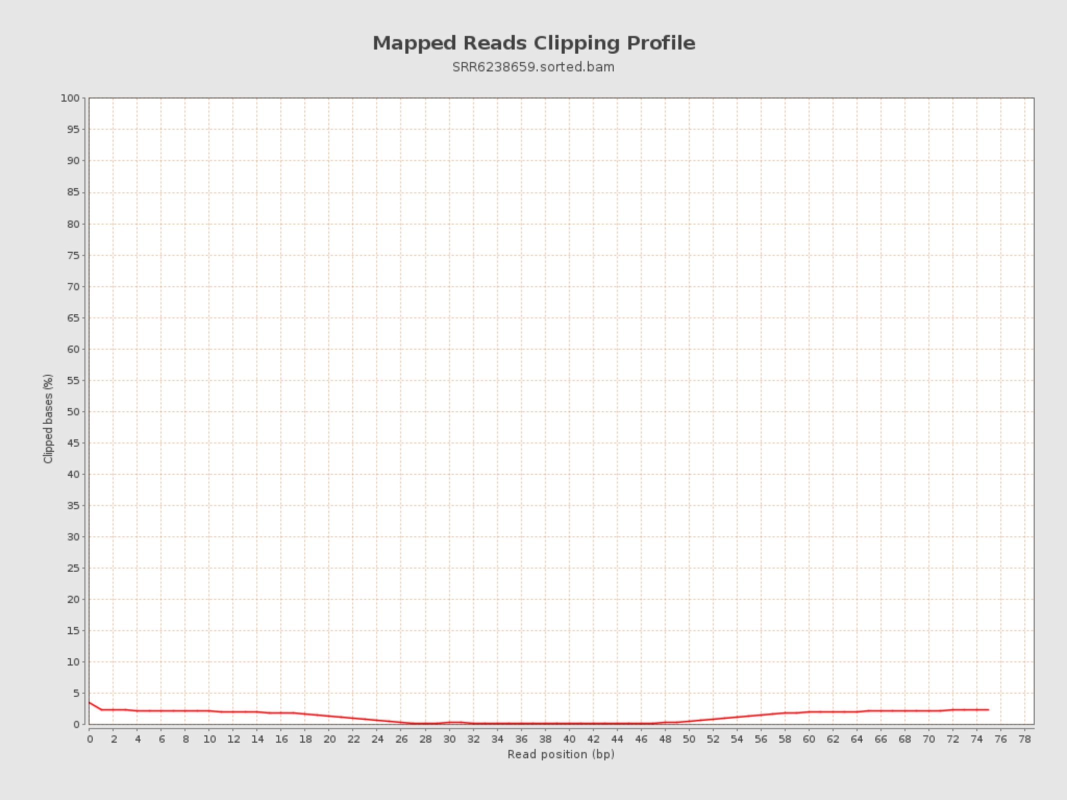
8. Results : Mapped Reads Nucleotide Content



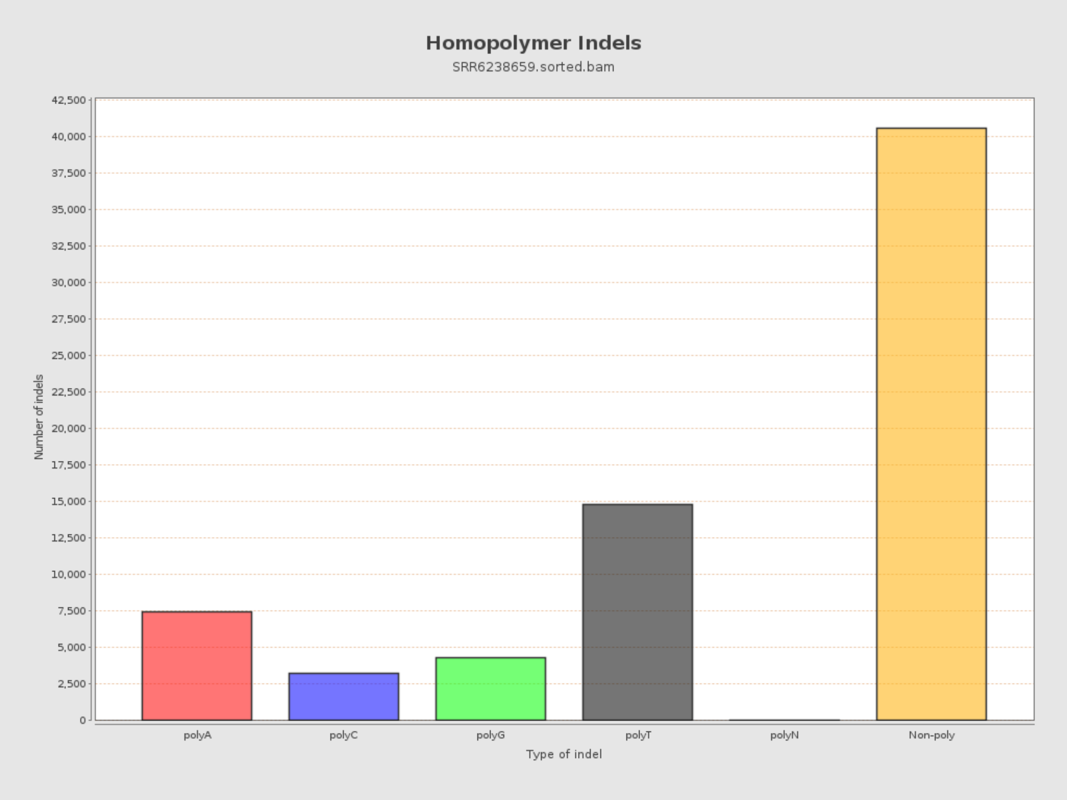
9. Results : Mapped Reads GC-content Distribution



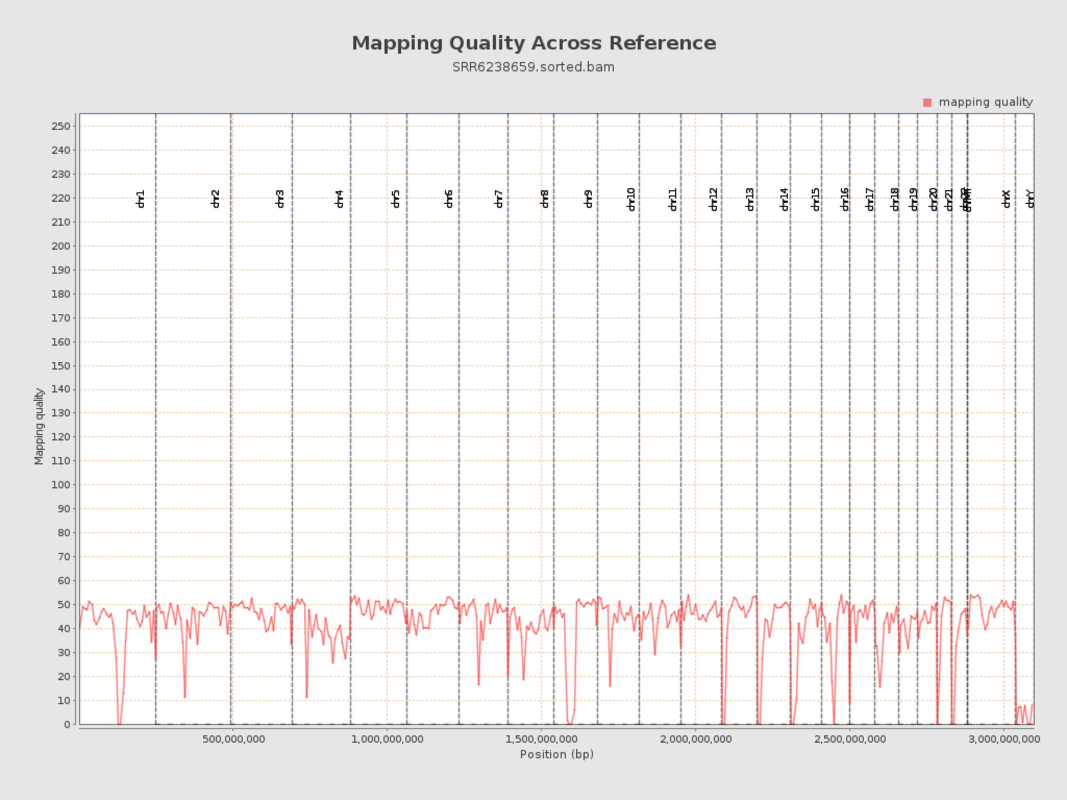
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram