Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:53:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238604.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_SRR6238604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:53:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,172,059
Mapped reads	2,789,837 / 87.95%
Unmapped reads	382,222 / 12.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,298 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,284,985 / 40.51%
Duplication rate	23.15%
Clipped reads	1,869,835 / 58.95%

2.2. ACGT Content

Number/percentage of A's	42,269,715 / 24.93%
Number/percentage of C's	28,791,267 / 16.98%
Number/percentage of T's	58,283,018 / 34.37%
Number/percentage of G's	40,202,914 / 23.71%
Number/percentage of N's	3,909 / 0%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0548

Standard Deviation	1.1299

2.4. Mapping Quality

Mean Mapping Quality	40.28

2.5. Mismatches and indels

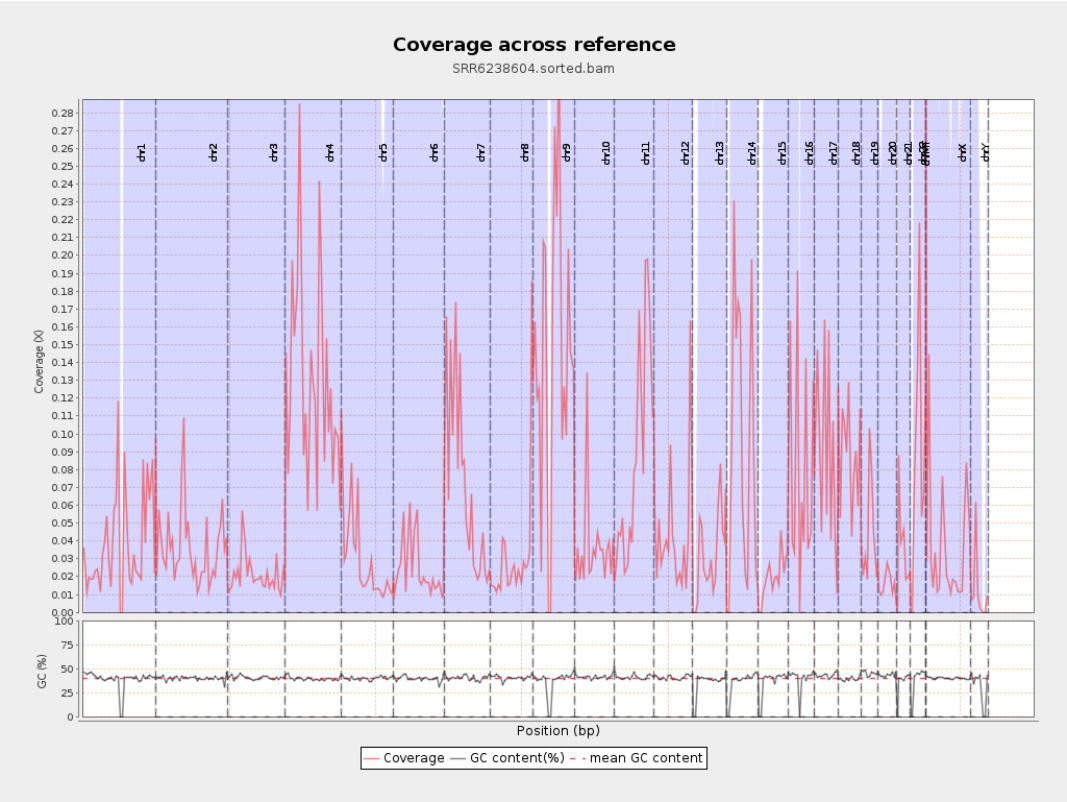
General error rate	0.68%
Mismatches	1,105,959
Insertions	16,015
Mapped reads with at least one insertion	0.57%
Deletions	52,872
Mapped reads with at least one deletion	1.87%
Homopolymer indels	42.21%

2.6. Chromosome stats

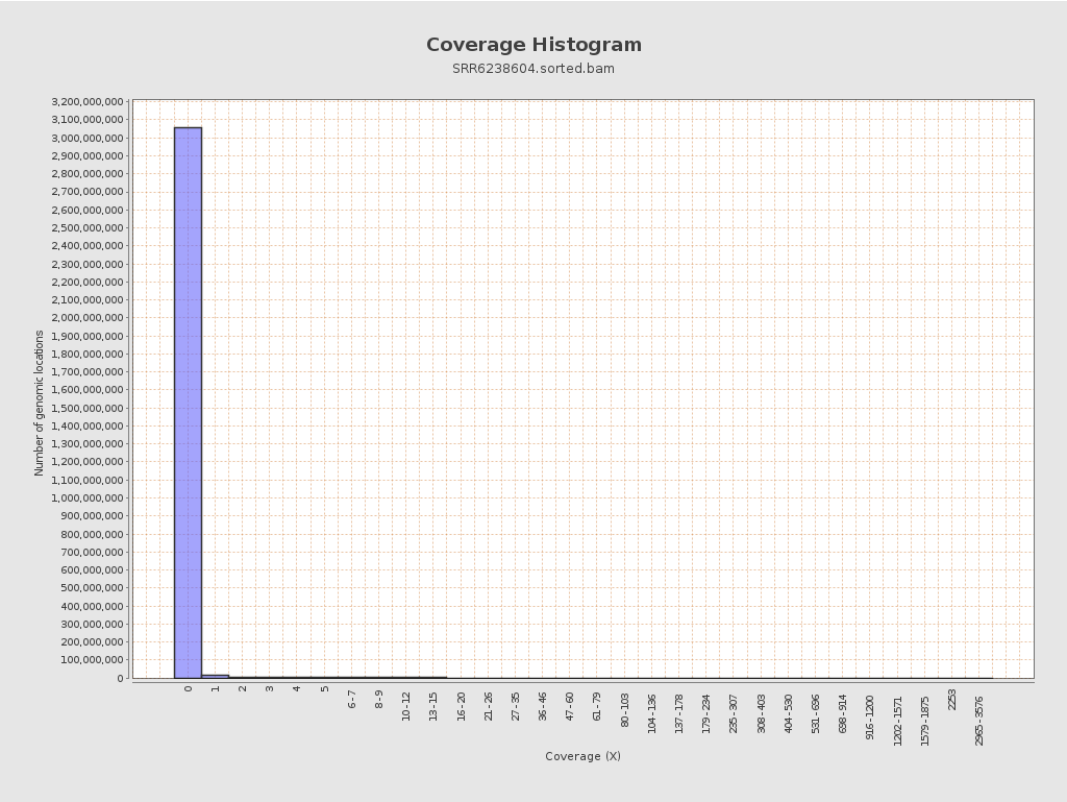
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9531002	0.0382	1.6075
chr2	243199373	8977581	0.0369	1.942
chr3	198022430	4198412	0.0212	0.4561
chr4	191154276	25094630	0.1313	1.3421
chr5	180915260	5332357	0.0295	0.5339
chr6	171115067	4177898	0.0244	0.7079
chr7	159138663	11192103	0.0703	0.9498

chr8	146364022	4373884	0.0299	1.0104
chr9	141213431	20694854	0.1466	1.2589
chr10	135534747	4835087	0.0357	1.2639
chr11	135006516	11792544	0.0873	1.0013
chr12	133851895	5834025	0.0436	0.6639
chr13	115169878	3716581	0.0323	0.6948
chr14	107349540	10371653	0.0966	1.0273
chr15	102531392	1972396	0.0192	0.5414
chr16	90354753	7191012	0.0796	0.9372
chr17	81195210	7411593	0.0913	1.0672
chr18	78077248	6894861	0.0883	2.0456
chr19	59128983	2647888	0.0448	0.999
chr20	63025520	1007344	0.016	0.4561
chr21	48129895	1760241	0.0366	0.7954
chr22	51304566	4455547	0.0868	0.9435
chrMT	16571	5822	0.3513	1.4527
chrX	155270560	5425751	0.0349	0.6122
chrY	59373566	748810	0.0126	0.7339

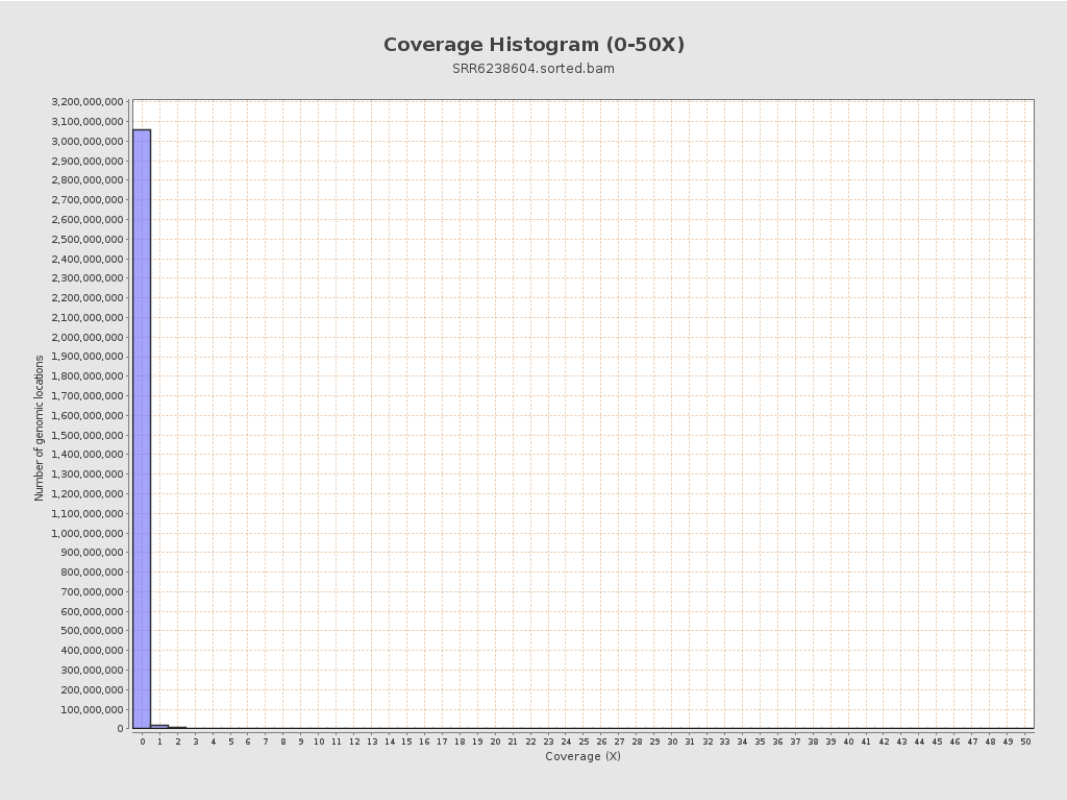
3. Results : Coverage across reference



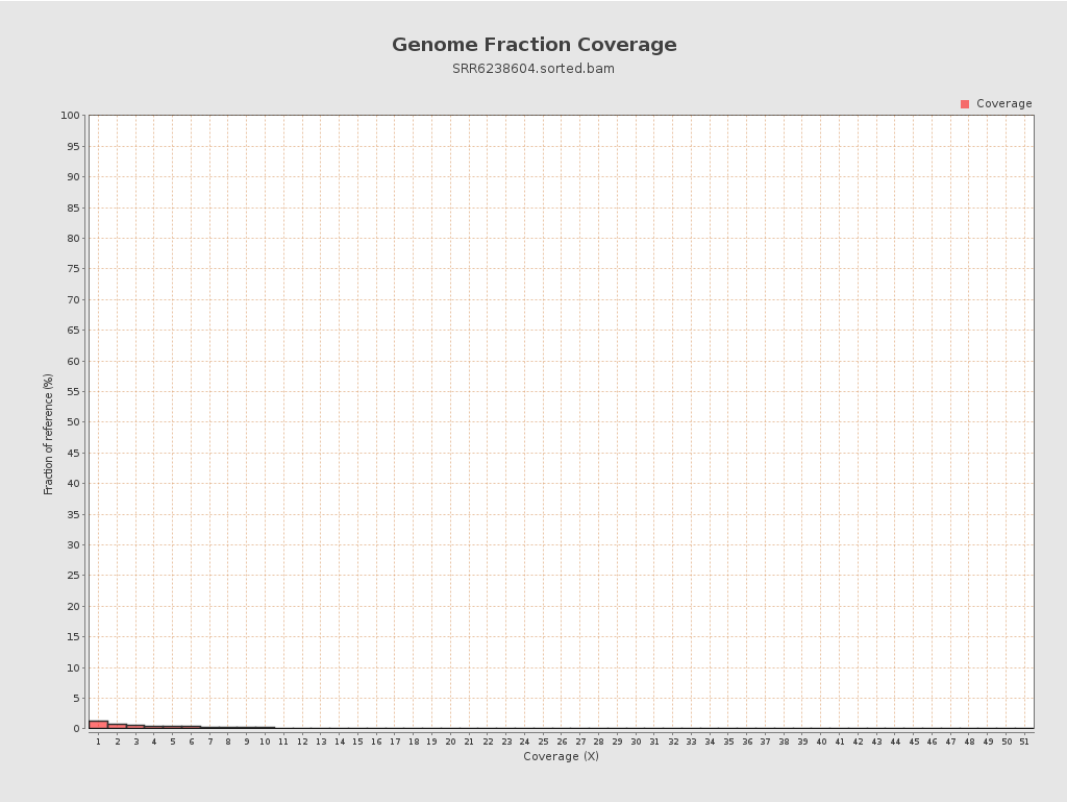
4. Results : Coverage Histogram



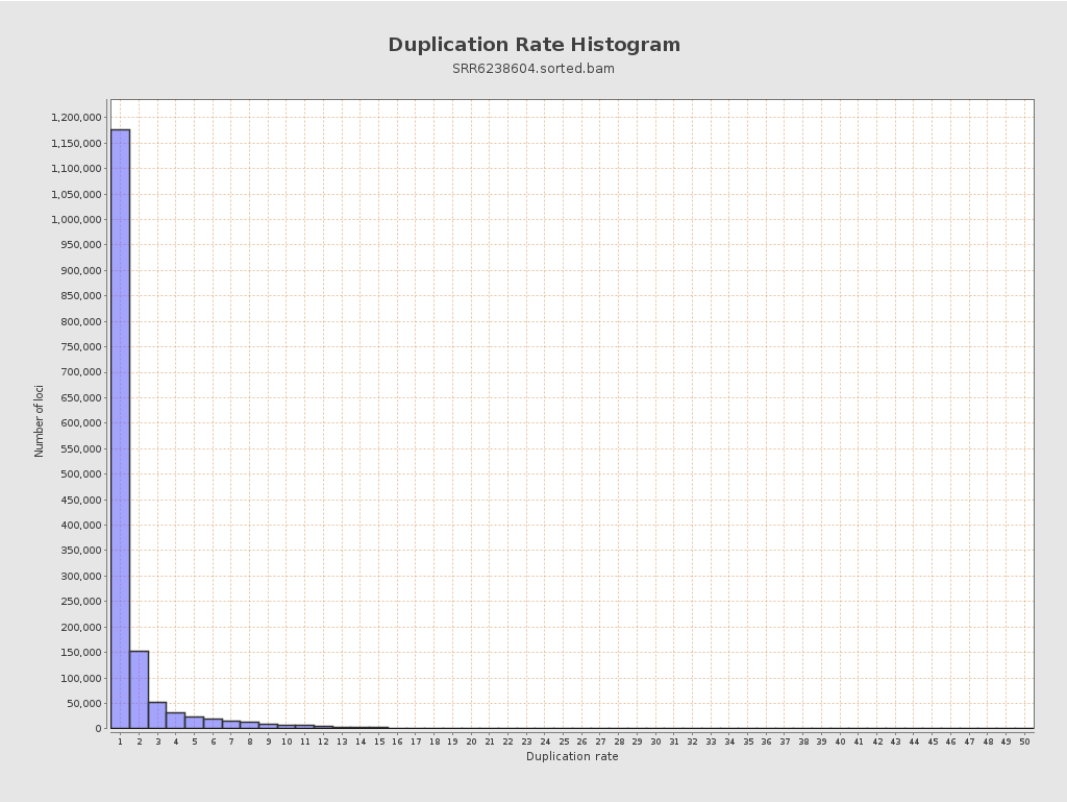
5. Results : Coverage Histogram (0-50X)



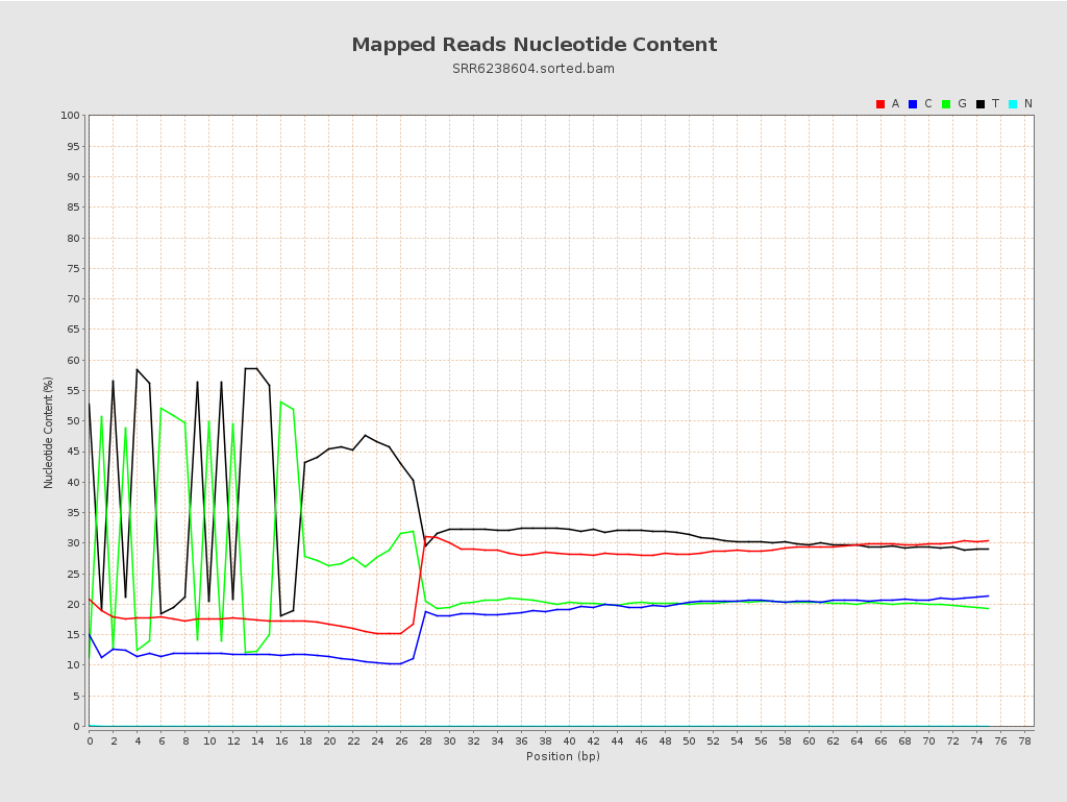
6. Results : Genome Fraction Coverage



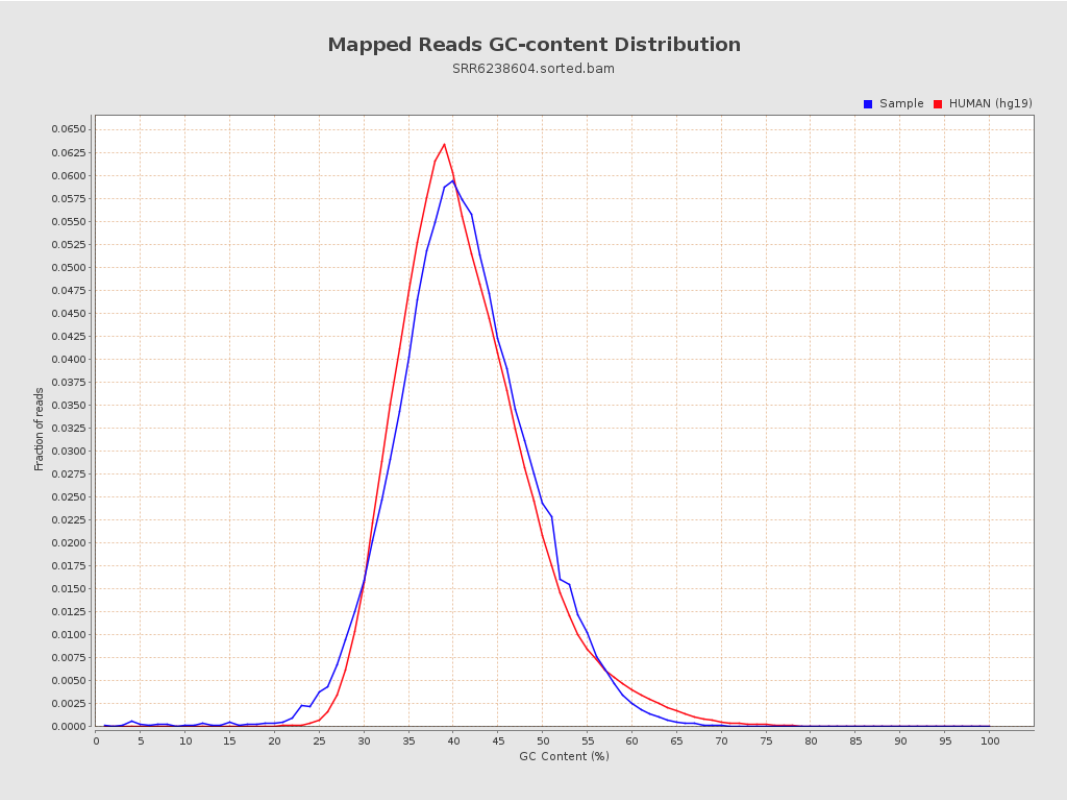
7. Results : Duplication Rate Histogram



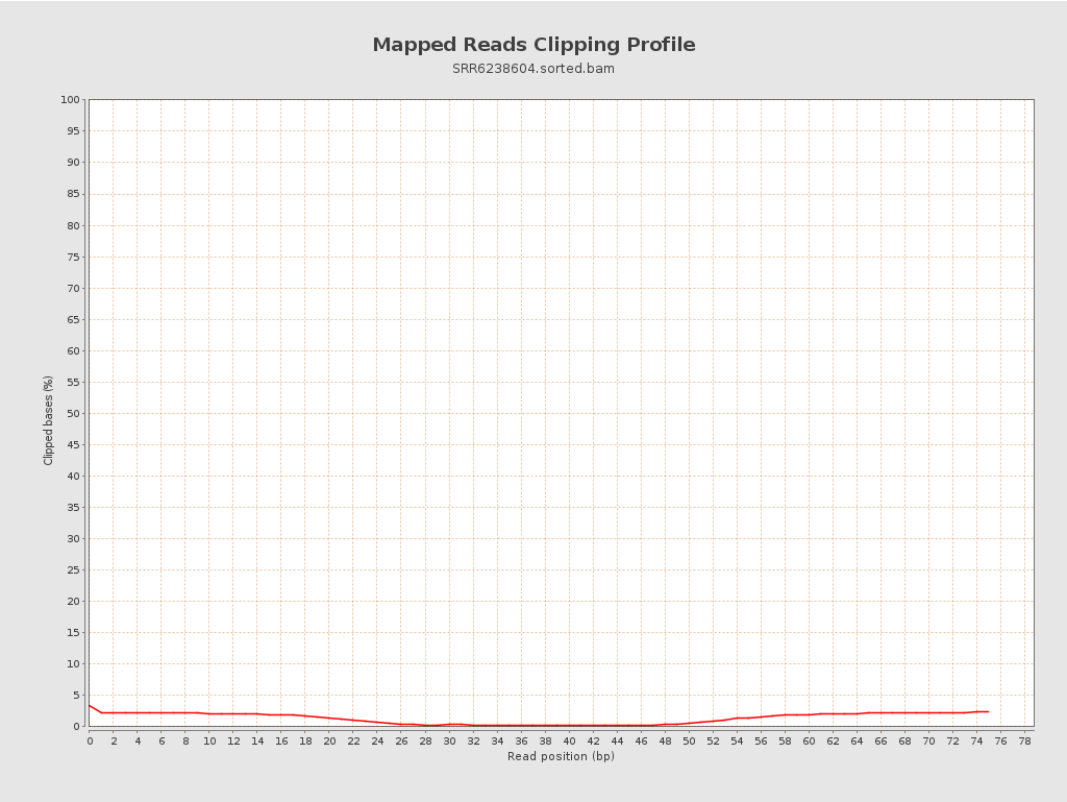
8. Results : Mapped Reads Nucleotide Content



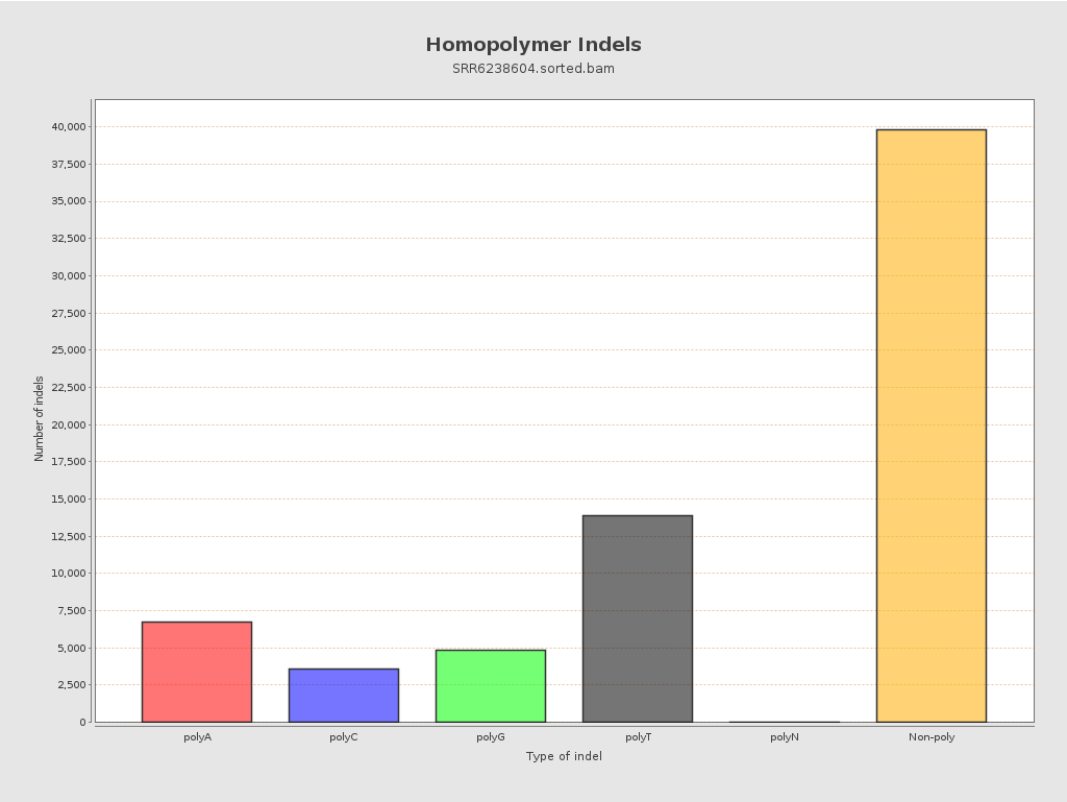
9. Results : Mapped Reads GC-content Distribution



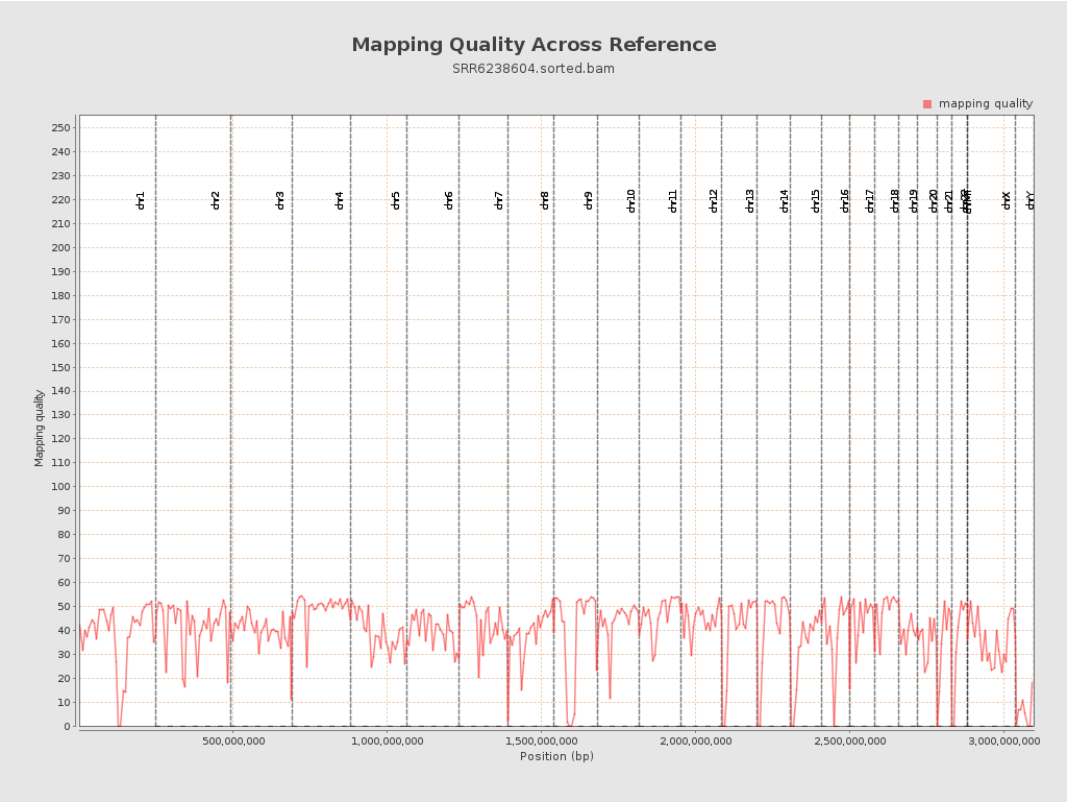
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram