Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:42:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238068.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_SRR6238068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:42:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,883,985
Mapped reads	1,650,883 / 87.63%
Unmapped reads	233,102 / 12.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,872 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	71,036 / 3.77%
Duplication rate	3.35%
Clipped reads	705,074 / 37.42%

2.2. ACGT Content

Number/percentage of A's	30,269,574 / 27.4%
Number/percentage of C's	21,101,660 / 19.1%
Number/percentage of T's	34,367,424 / 31.1%
Number/percentage of G's	24,737,031 / 22.39%
Number/percentage of N's	14,164 / 0.01%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3405

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

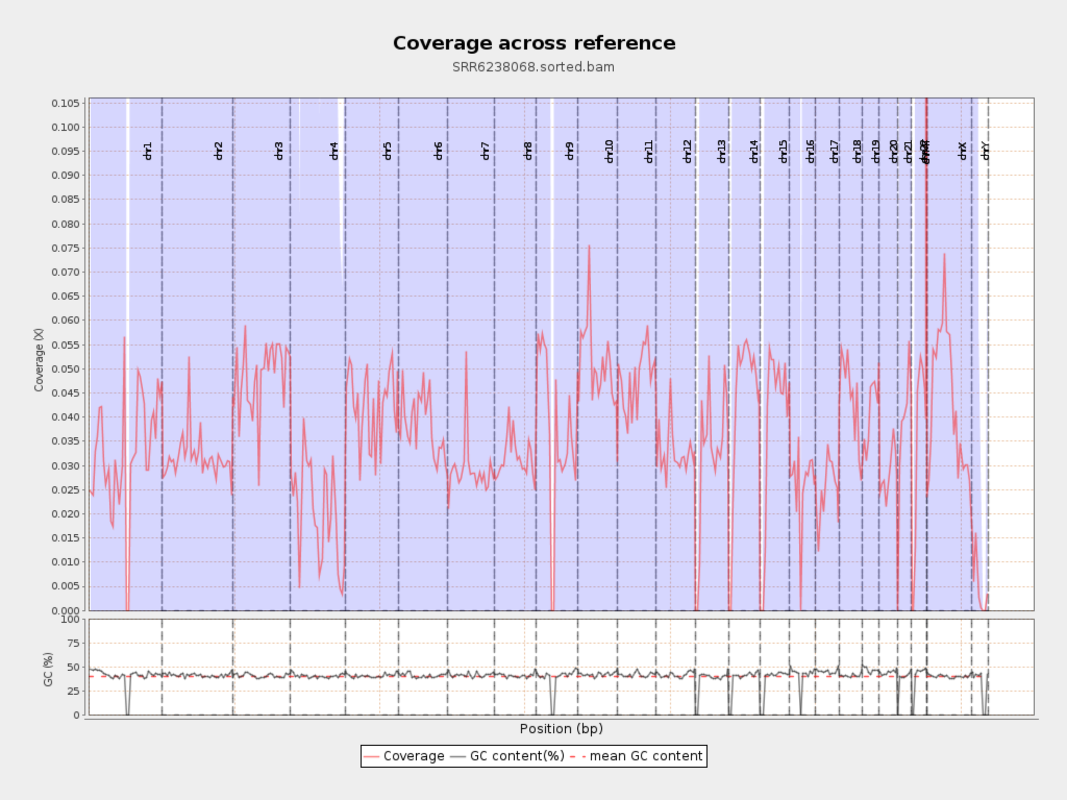
General error rate	0.77%
Mismatches	833,523
Insertions	7,823
Mapped reads with at least one insertion	0.47%
Deletions	29,487
Mapped reads with at least one deletion	1.76%
Homopolymer indels	46.01%

2.6. Chromosome stats

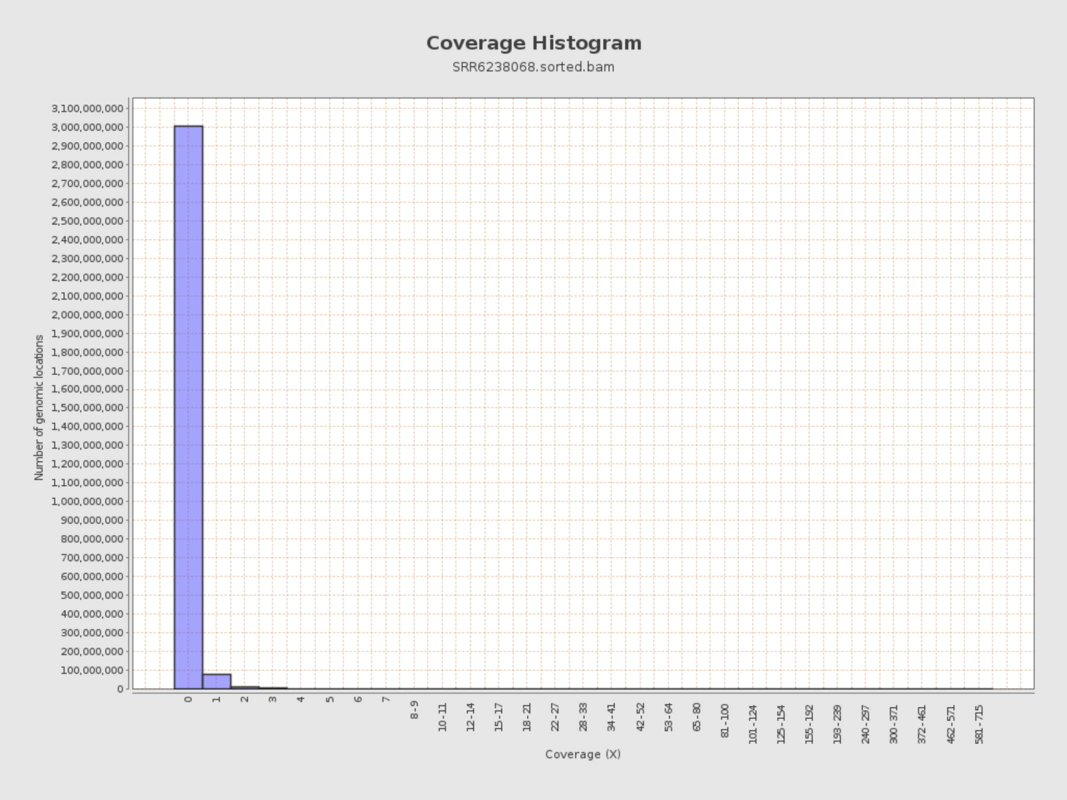
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8107411	0.0325	0.6445
chr2	243199373	7730422	0.0318	0.3402
chr3	198022430	9605447	0.0485	0.2582
chr4	191154276	3830725	0.02	0.1843
chr5	180915260	7625082	0.0421	0.2427
chr6	171115067	6588355	0.0385	0.2655
chr7	159138663	4650159	0.0292	0.3962

chr8	146364022	4631064	0.0316	0.3667
chr9	141213431	5160757	0.0365	0.32
chr10	135534747	6968067	0.0514	0.3795
chr11	135006516	6432380	0.0476	0.3217
chr12	133851895	4402693	0.0329	0.2193
chr13	115169878	3693516	0.0321	0.2081
chr14	107349540	4586777	0.0427	0.2647
chr15	102531392	3938608	0.0384	0.2287
chr16	90354753	2344041	0.0259	0.2172
chr17	81195210	2034567	0.0251	0.196
chr18	78077248	3464473	0.0444	0.5992
chr19	59128983	2403000	0.0406	0.4242
chr20	63025520	1787069	0.0284	0.2074
chr21	48129895	1823931	0.0379	0.2516
chr22	51304566	1682258	0.0328	0.212
chrMT	16571	80943	4.8846	3.7301
chrX	155270560	6672683	0.043	0.2747
chrY	59373566	297858	0.005	0.136

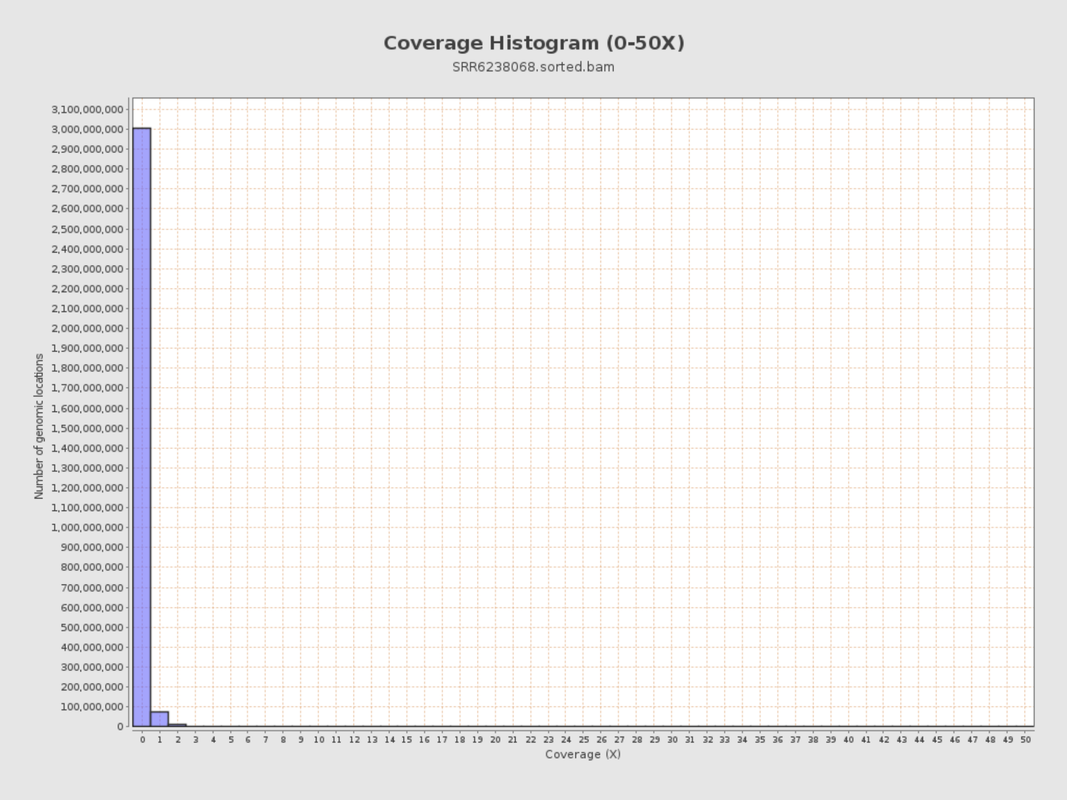
3. Results : Coverage across reference



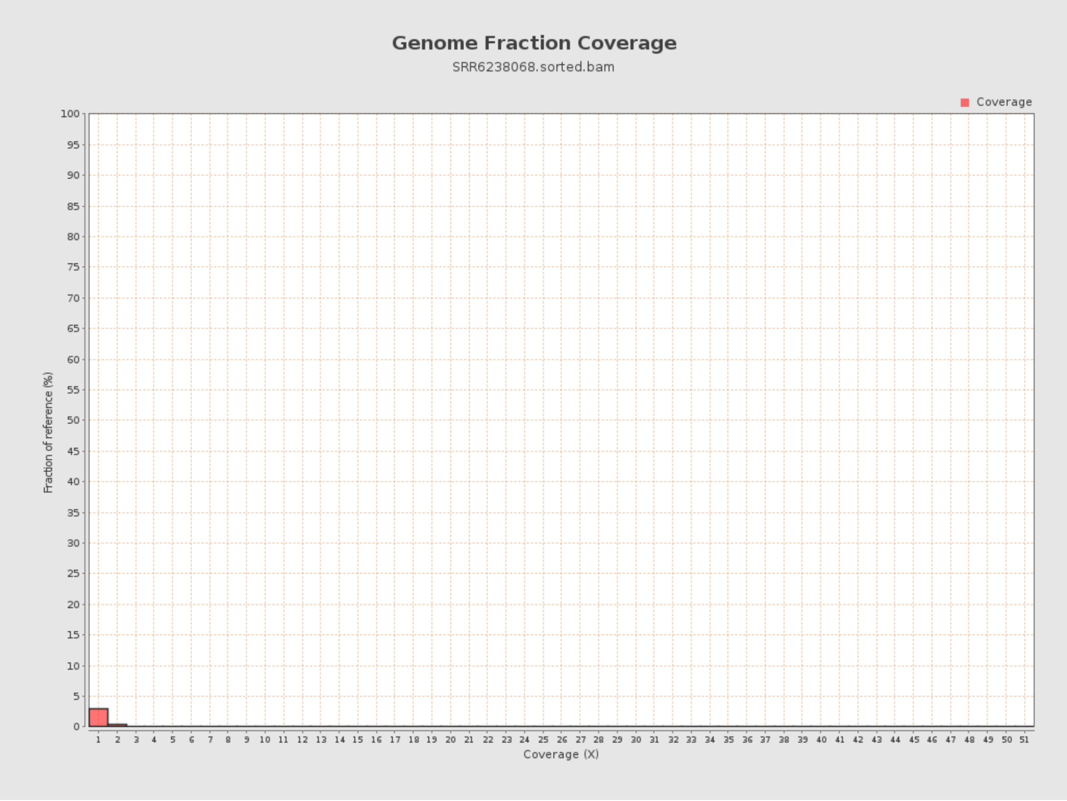
4. Results : Coverage Histogram



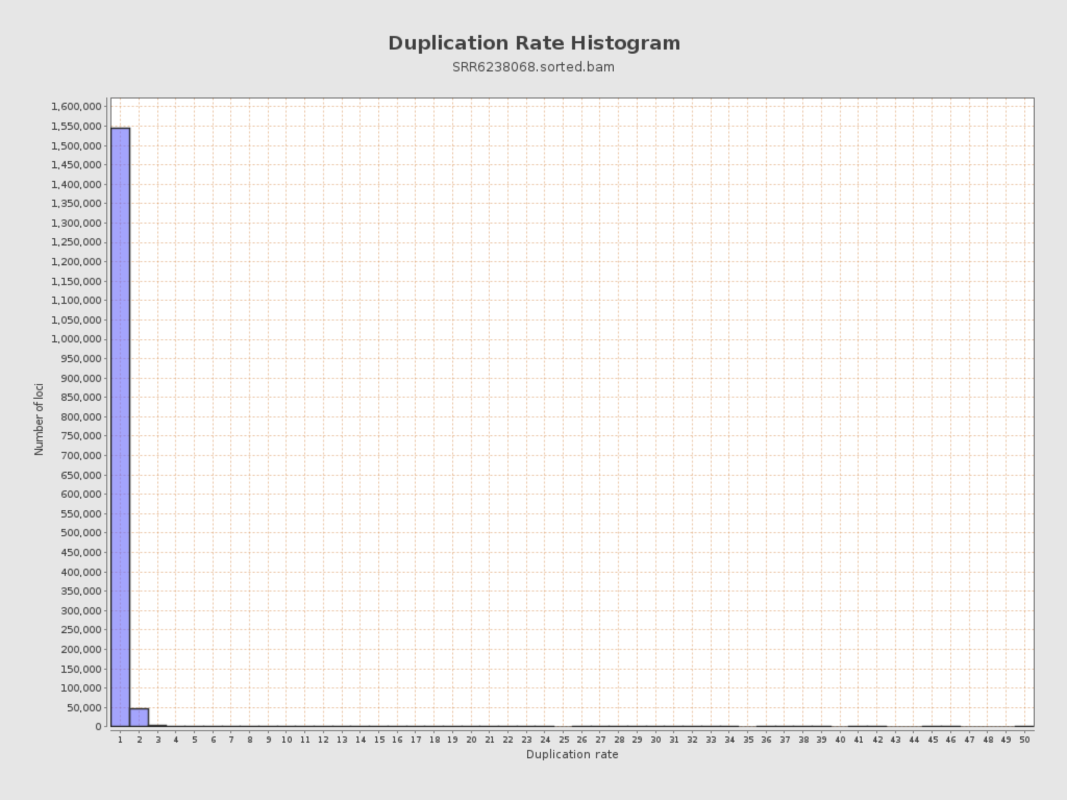
5. Results : Coverage Histogram (0-50X)



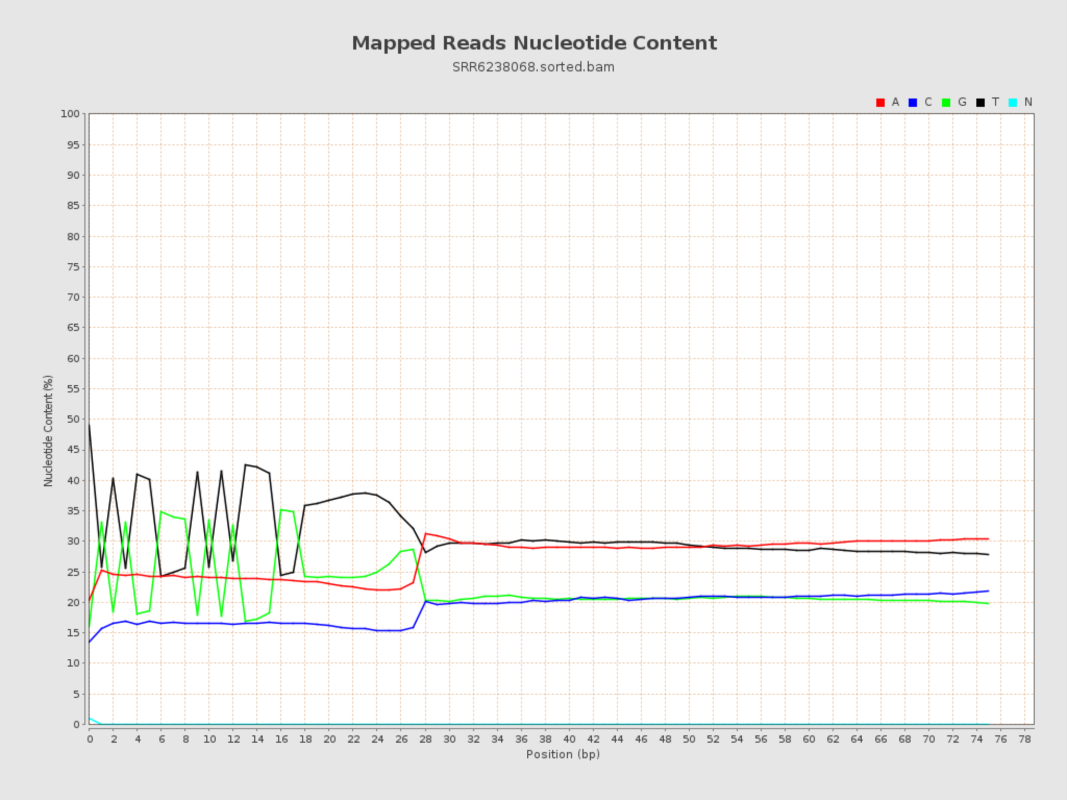
6. Results : Genome Fraction Coverage



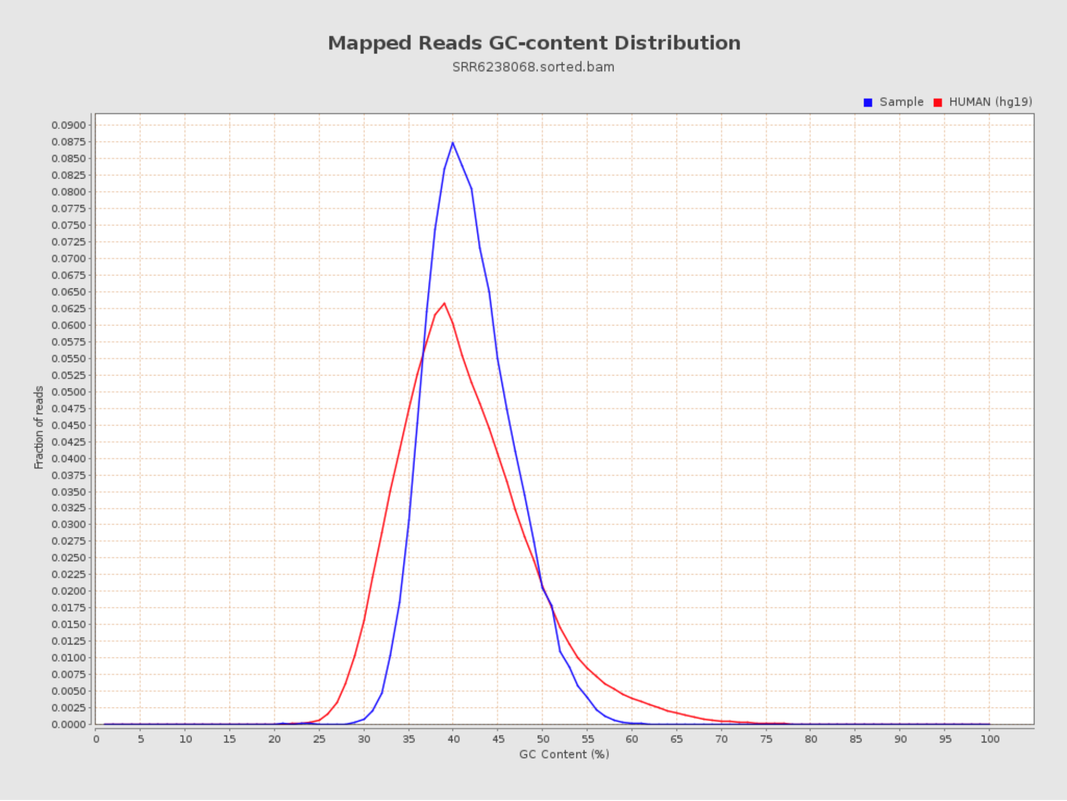
7. Results : Duplication Rate Histogram



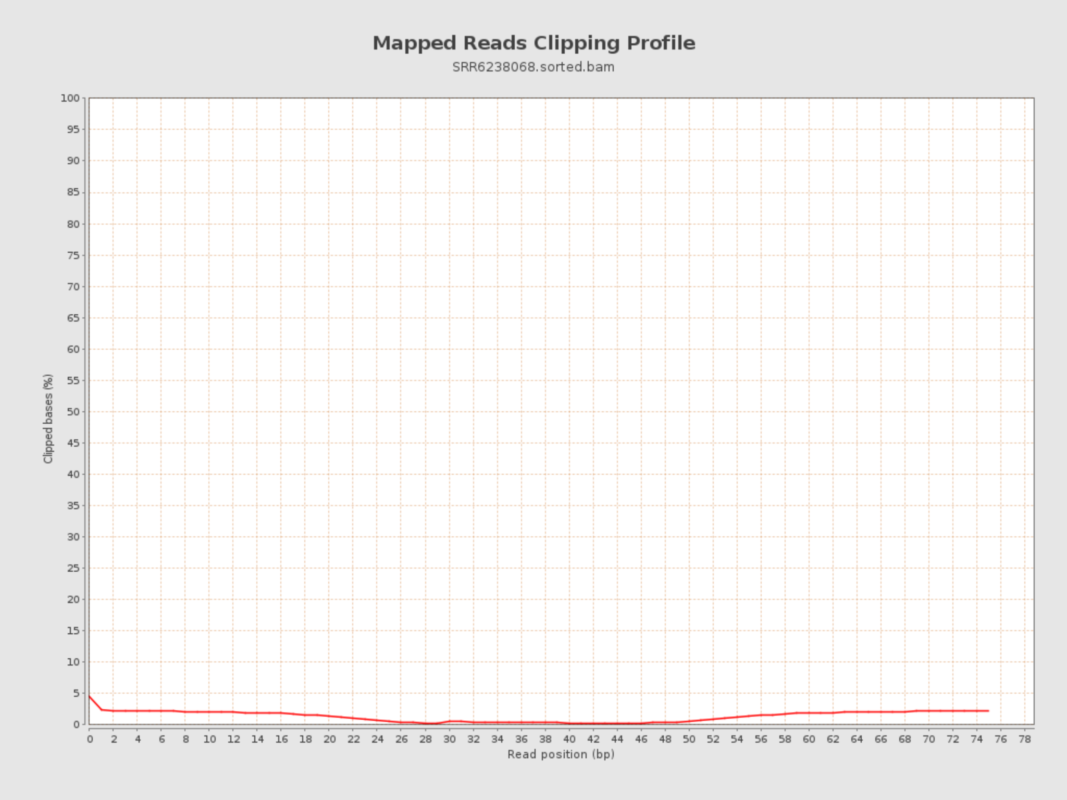
8. Results : Mapped Reads Nucleotide Content



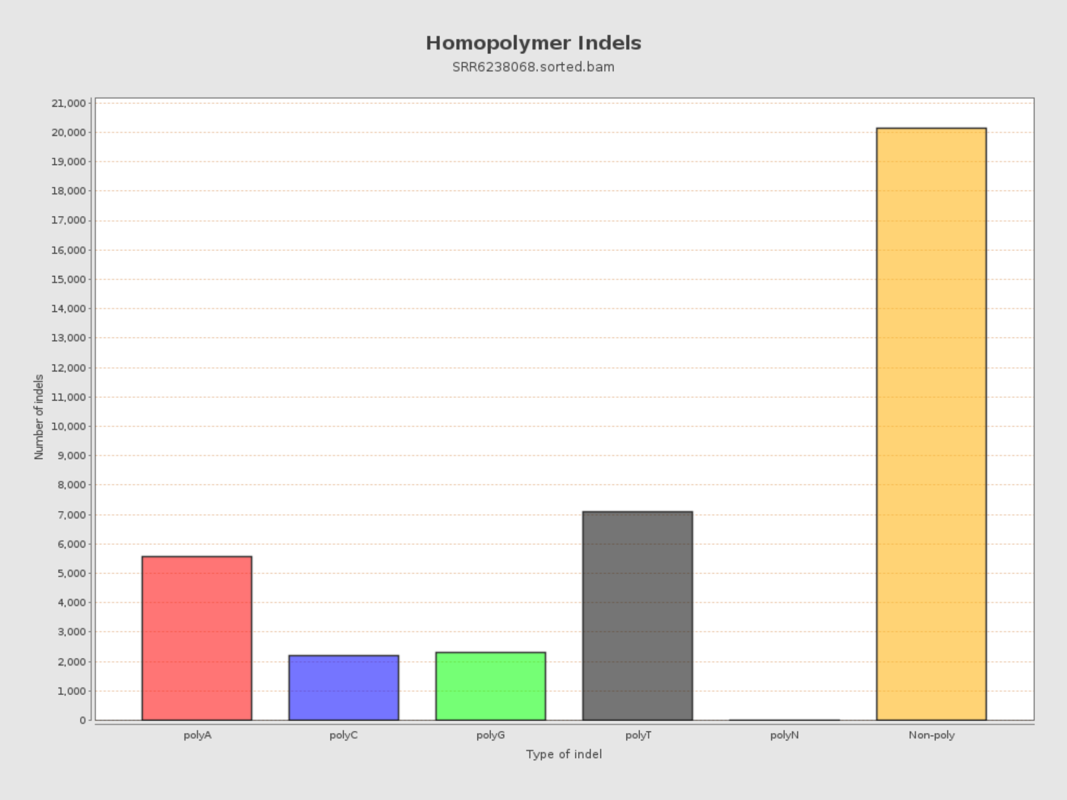
9. Results : Mapped Reads GC-content Distribution



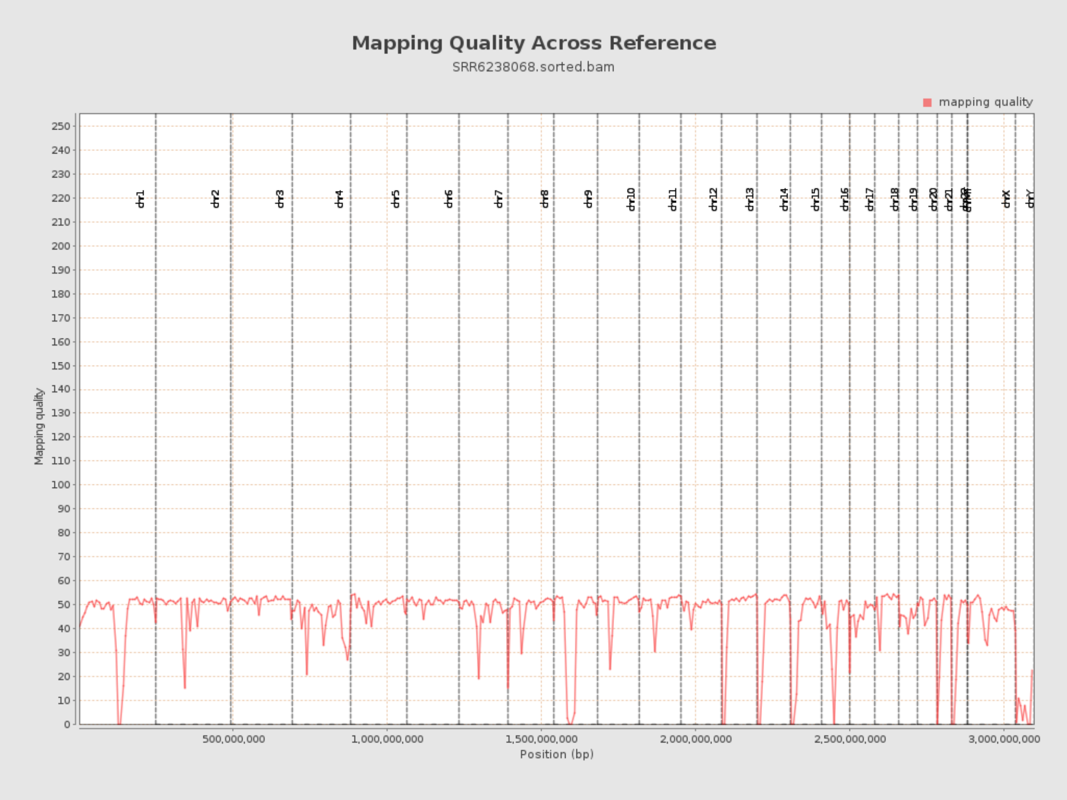
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram