Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:03:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238076.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_SRR6238076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:03:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,490,029
Mapped reads	1,251,584 / 84%
Unmapped reads	238,445 / 16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,198 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	141,472 / 9.49%
Duplication rate	8.25%
Clipped reads	824,304 / 55.32%

2.2. ACGT Content

Number/percentage of A's	19,636,400 / 25.71%
Number/percentage of C's	12,575,544 / 16.46%
Number/percentage of T's	25,585,578 / 33.5%
Number/percentage of G's	18,583,802 / 24.33%
Number/percentage of N's	3,489 / 0%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2691

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

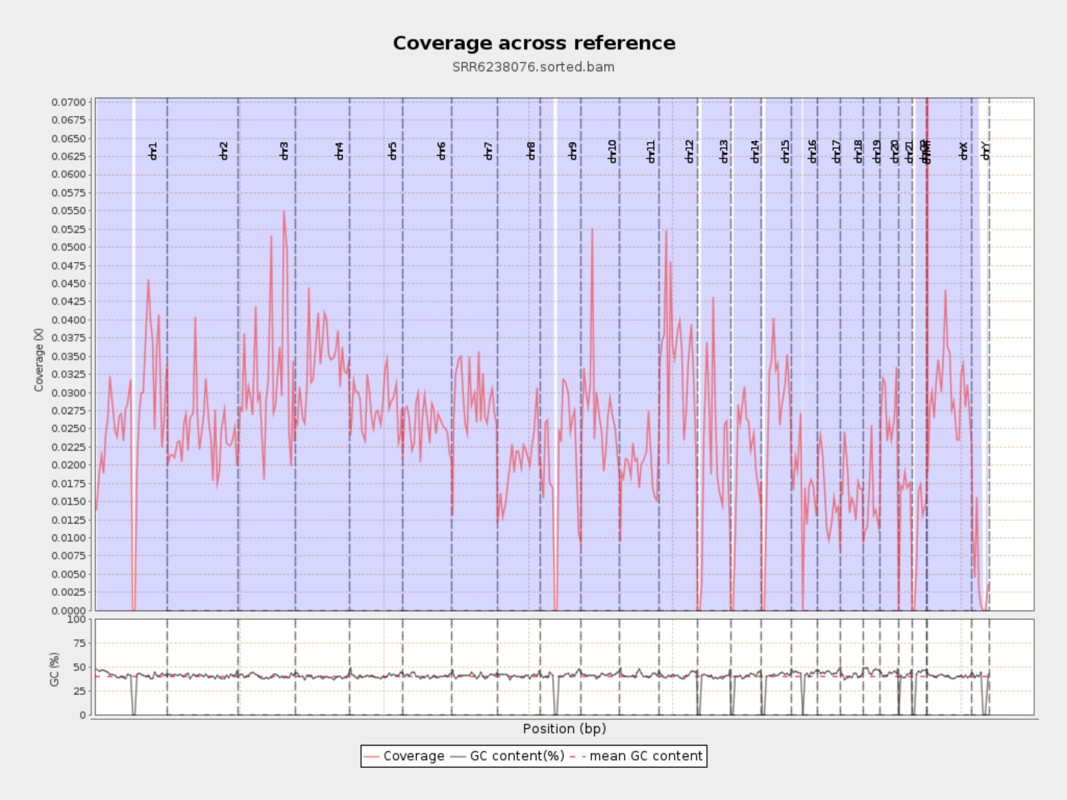
General error rate	0.84%
Mismatches	625,614
Insertions	6,933
Mapped reads with at least one insertion	0.55%
Deletions	30,453
Mapped reads with at least one deletion	2.4%
Homopolymer indels	47.28%

2.6. Chromosome stats

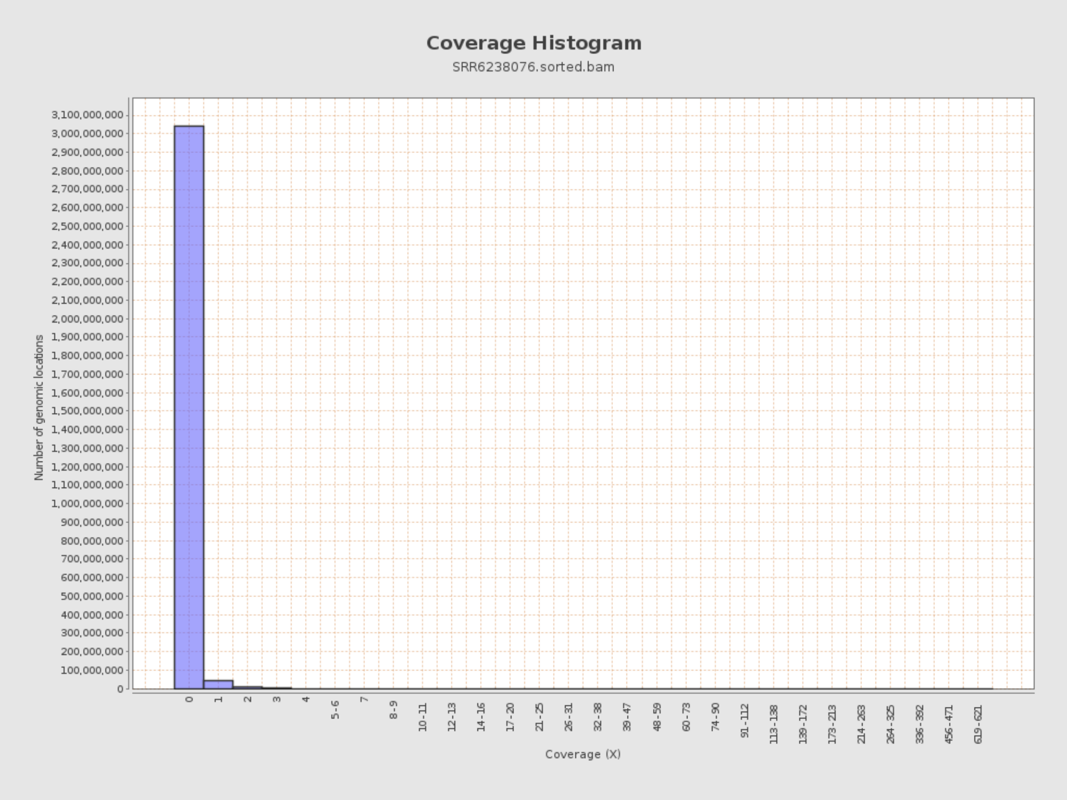
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6630841	0.0266	0.3415
chr2	243199373	5901015	0.0243	0.3666
chr3	198022430	6289873	0.0318	0.2577
chr4	191154276	6492091	0.034	0.2536
chr5	180915260	5112073	0.0283	0.2179
chr6	171115067	4376384	0.0256	0.2476
chr7	159138663	4599778	0.0289	0.2946

chr8	146364022	2955323	0.0202	0.2979
chr9	141213431	2895014	0.0205	0.2317
chr10	135534747	3750016	0.0277	0.2959
chr11	135006516	2663687	0.0197	0.2075
chr12	133851895	4648950	0.0347	0.2731
chr13	115169878	2337542	0.0203	0.2164
chr14	107349540	2134431	0.0199	0.1957
chr15	102531392	2698095	0.0263	0.2196
chr16	90354753	1484079	0.0164	0.188
chr17	81195210	1270717	0.0157	0.1839
chr18	78077248	1311217	0.0168	0.4551
chr19	59128983	859222	0.0145	0.2371
chr20	63025520	1727546	0.0274	0.2257
chr21	48129895	731624	0.0152	0.1778
chr22	51304566	555064	0.0108	0.1577
chrMT	16571	24908	1.5031	1.7313
chrX	155270560	4719793	0.0304	0.2326
chrY	59373566	265995	0.0045	0.1532

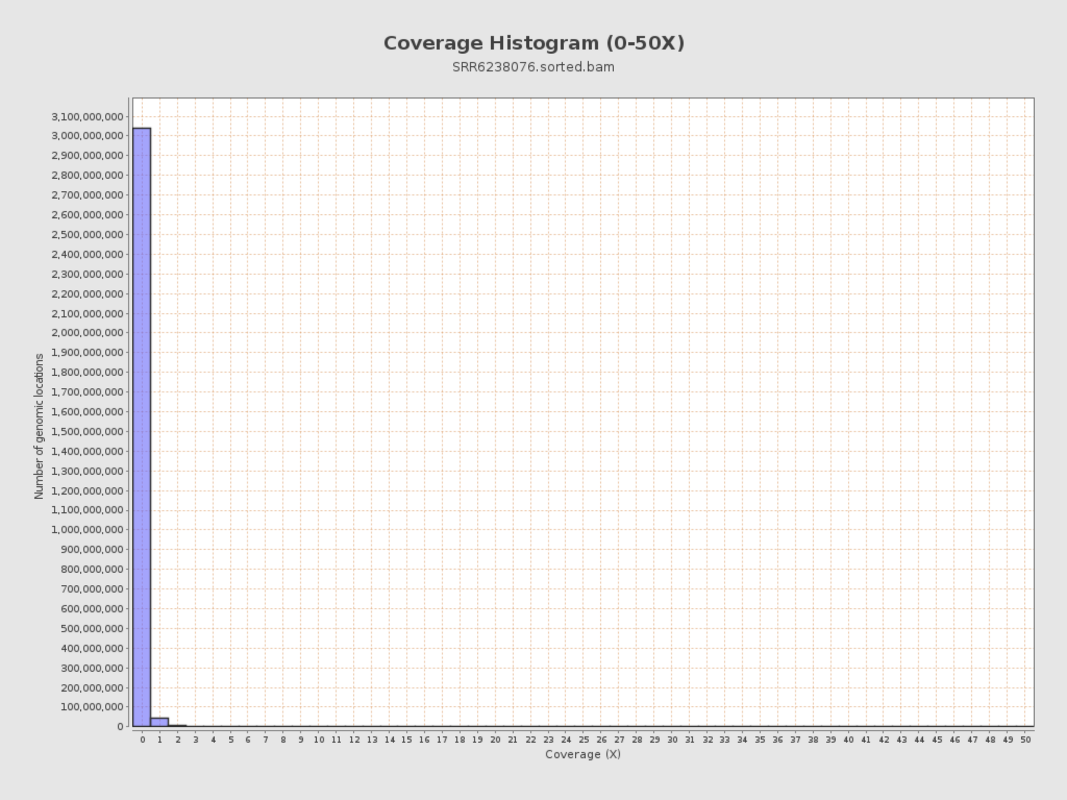
3. Results : Coverage across reference



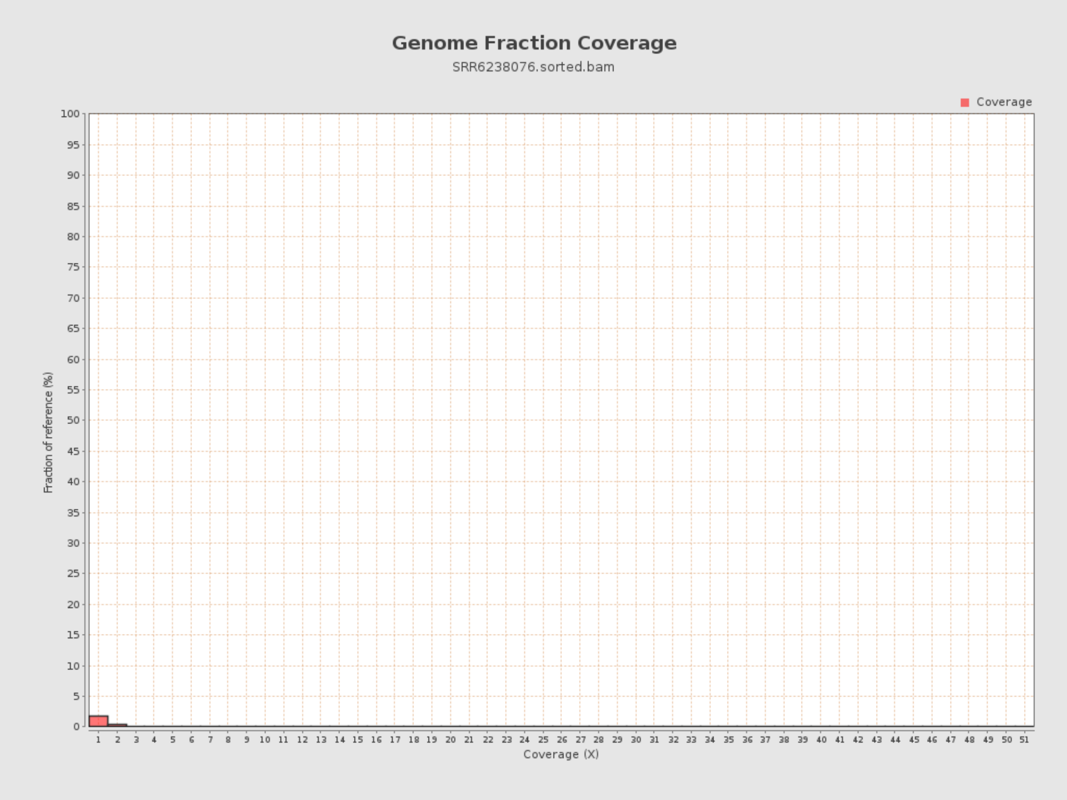
4. Results : Coverage Histogram



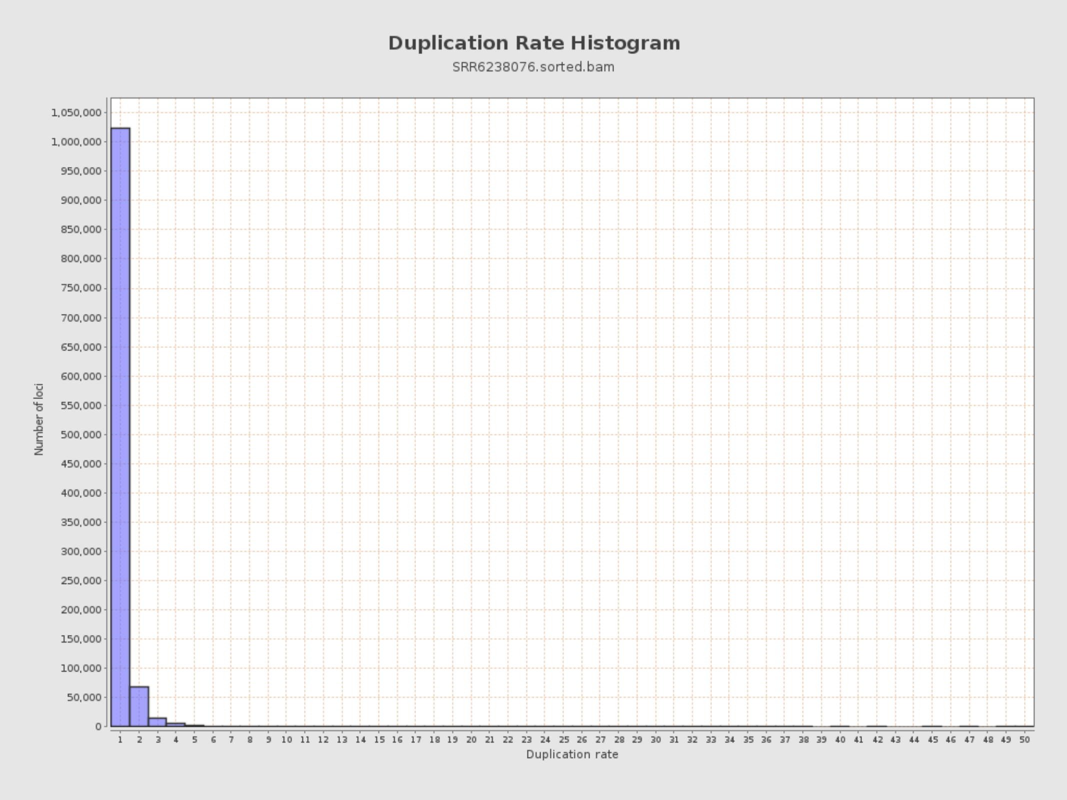
5. Results : Coverage Histogram (0-50X)



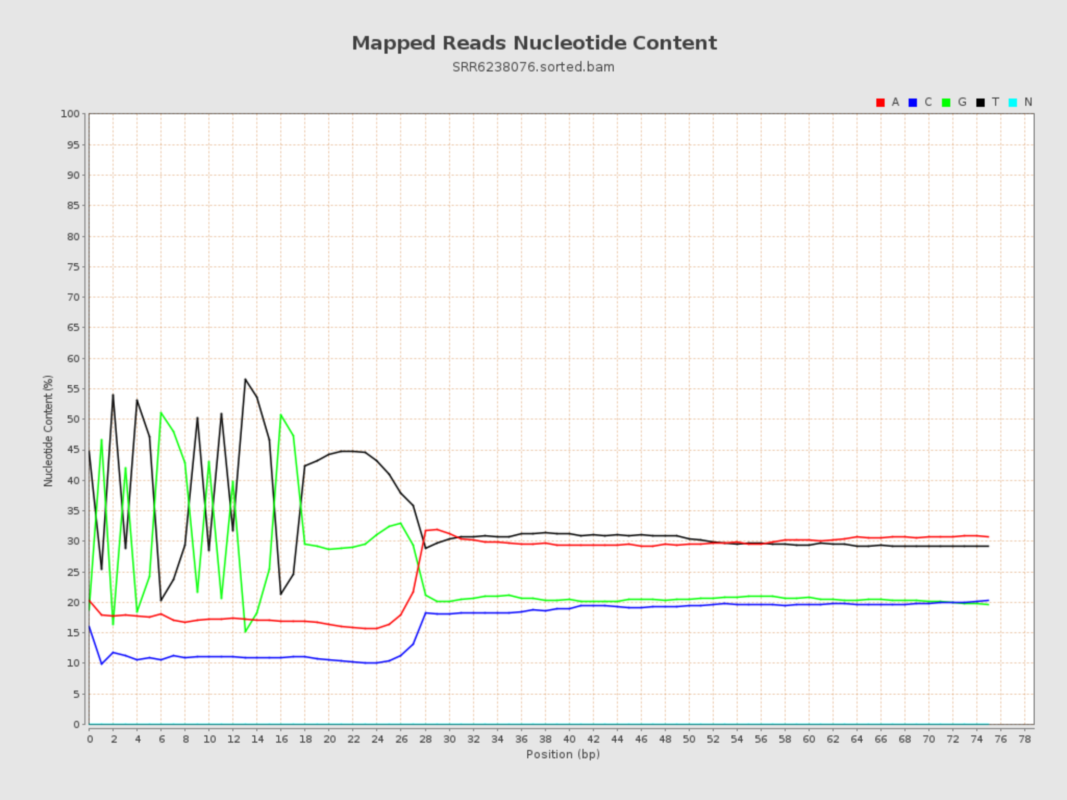
6. Results : Genome Fraction Coverage



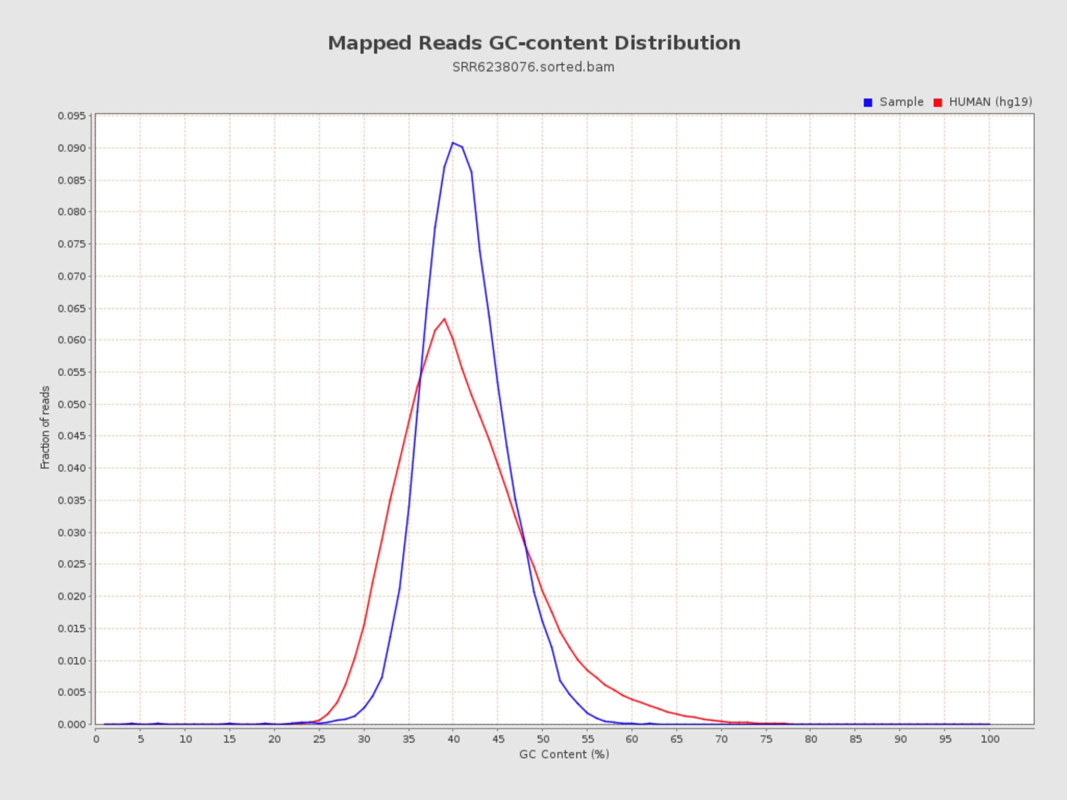
7. Results : Duplication Rate Histogram



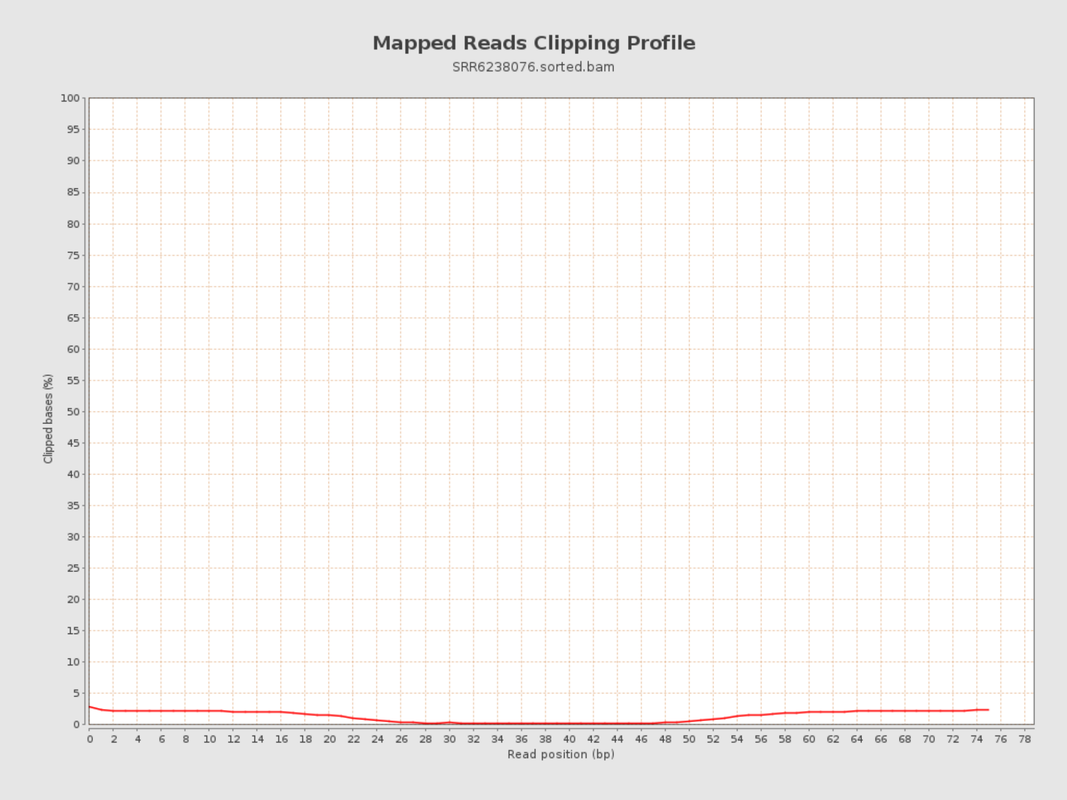
8. Results : Mapped Reads Nucleotide Content



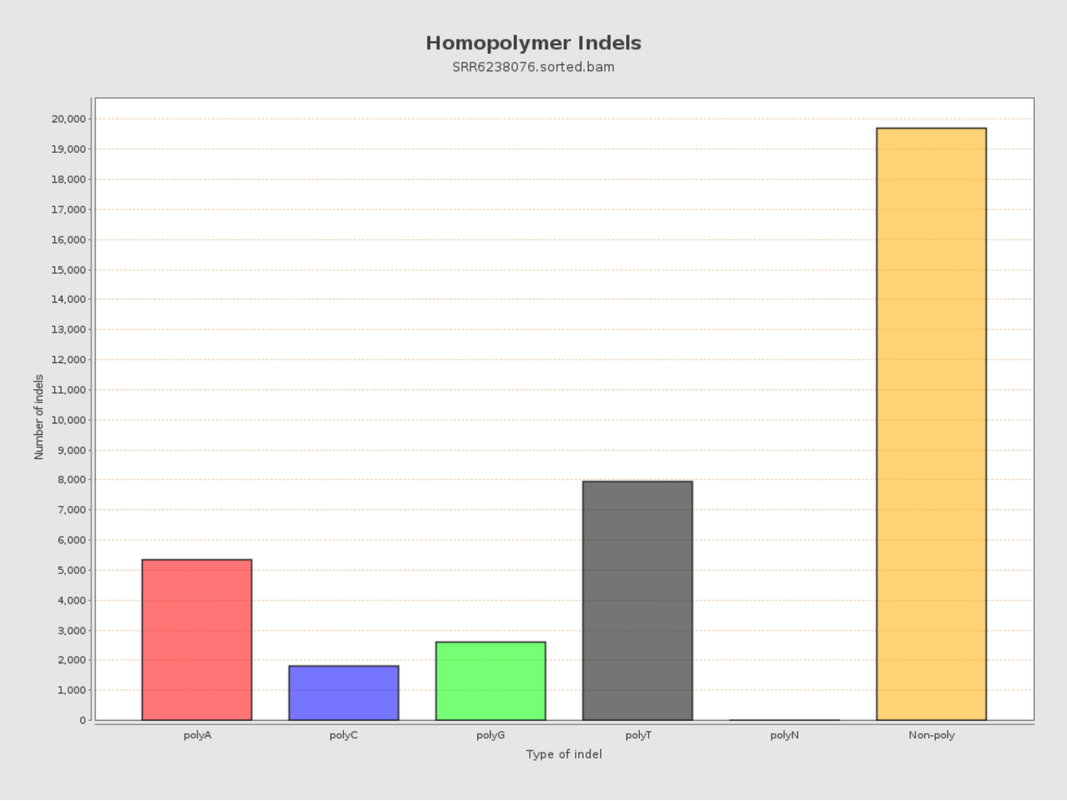
9. Results : Mapped Reads GC-content Distribution



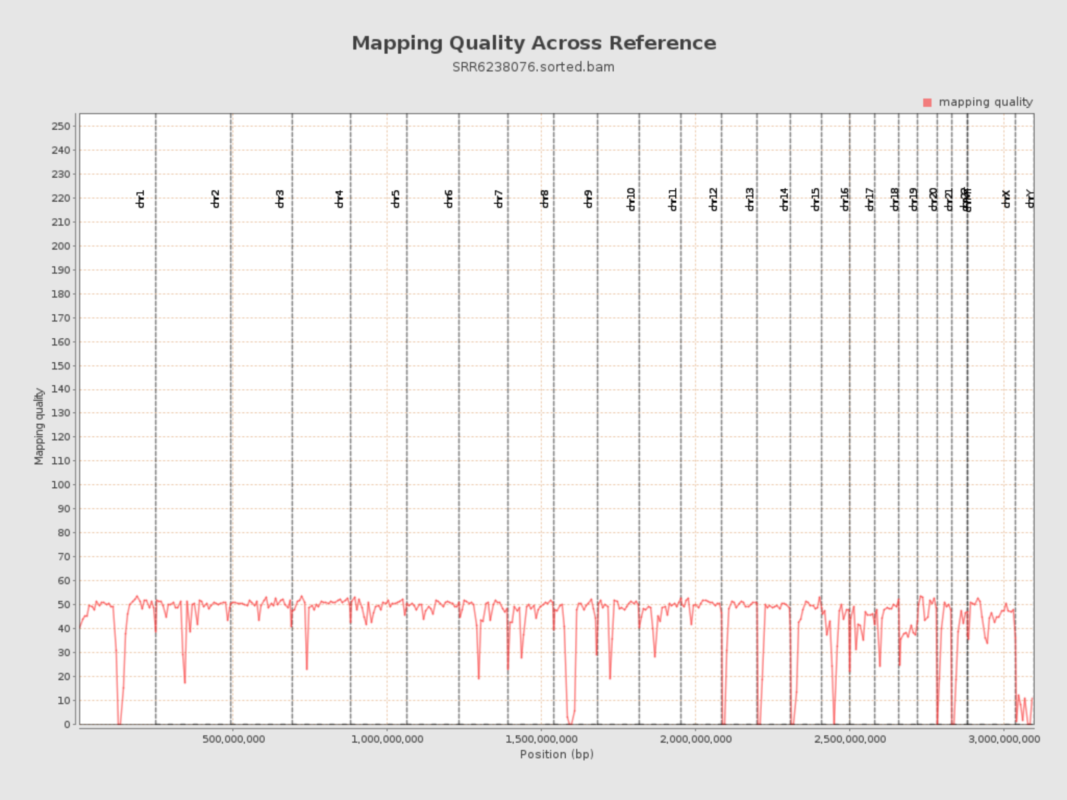
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram