Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238632.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_SRR6238632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:27:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,756,079
Mapped reads	1,511,140 / 86.05%
Unmapped reads	244,939 / 13.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,857 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	417,286 / 23.76%
Duplication rate	19.9%
Clipped reads	960,941 / 54.72%

2.2. ACGT Content

Number/percentage of A's	23,498,822 / 25.21%
Number/percentage of C's	16,261,849 / 17.45%
Number/percentage of T's	31,325,045 / 33.61%
Number/percentage of G's	22,120,699 / 23.73%
Number/percentage of N's	4,506 / 0%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.4931

2.4. Mapping Quality

Mean Mapping Quality	41.42

2.5. Mismatches and indels

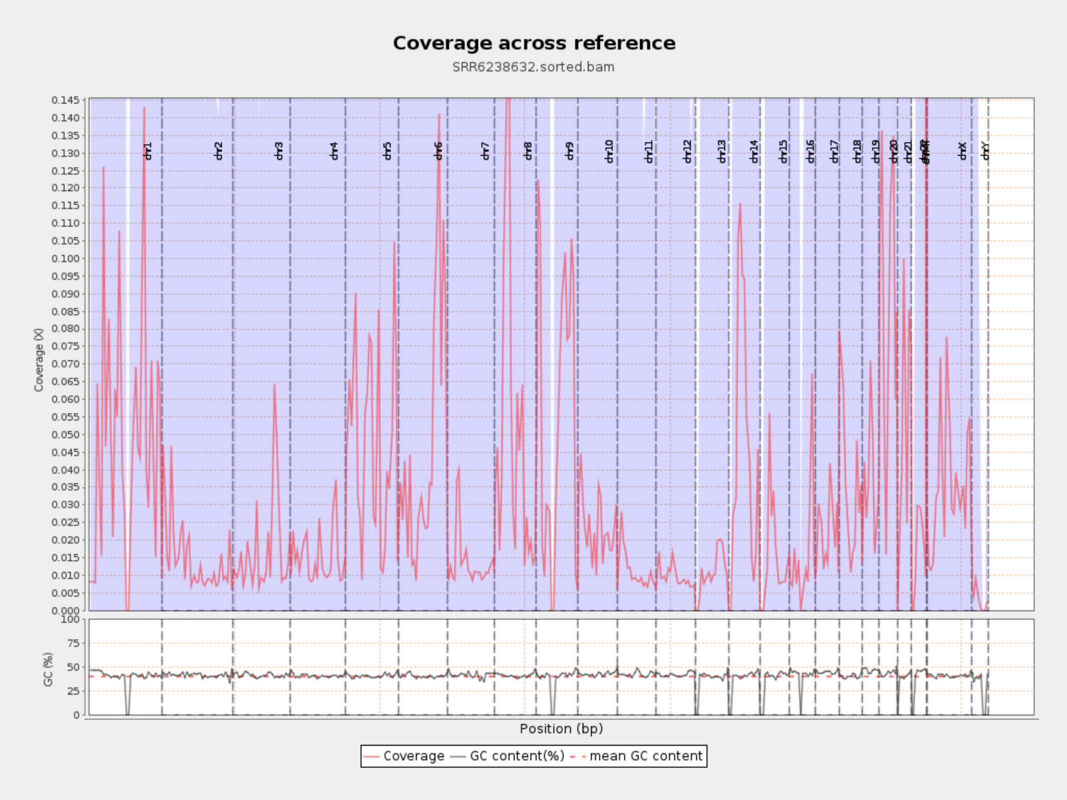
General error rate	0.6%
Mismatches	545,696
Insertions	6,016
Mapped reads with at least one insertion	0.39%
Deletions	29,462
Mapped reads with at least one deletion	1.93%
Homopolymer indels	41.02%

2.6. Chromosome stats

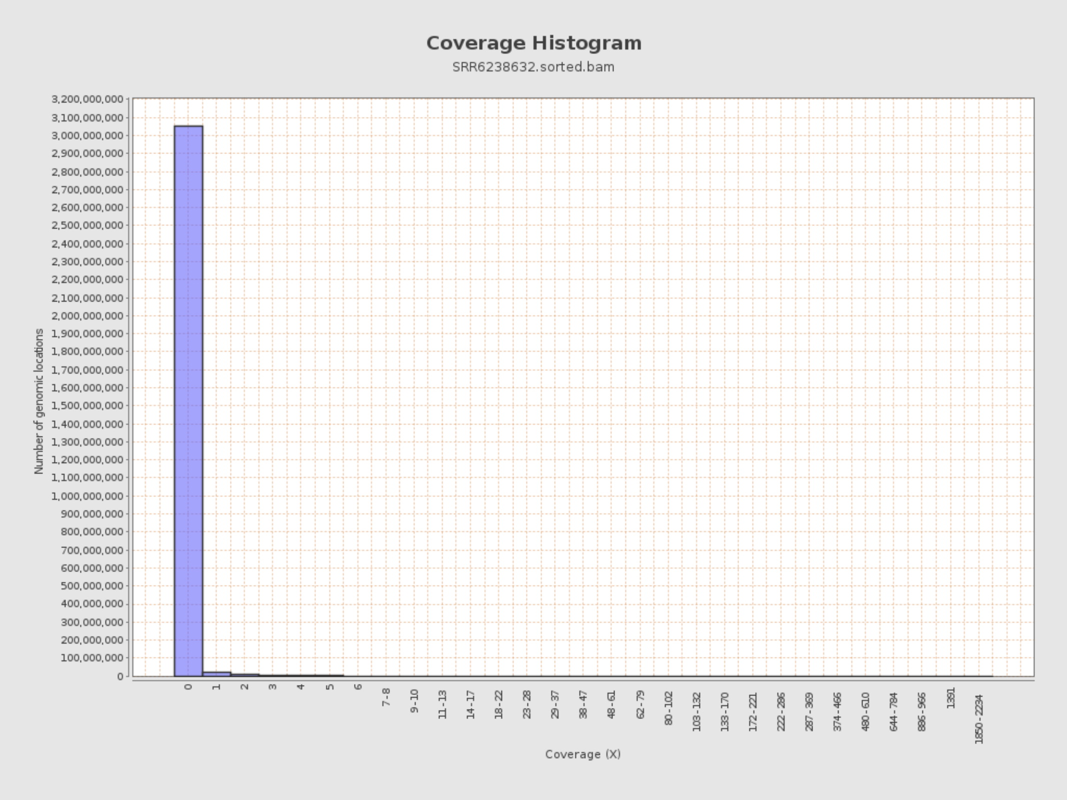
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12098713	0.0485	0.5733
chr2	243199373	3645472	0.015	0.9983
chr3	198022430	3373817	0.017	0.2456
chr4	191154276	2844010	0.0149	0.2279
chr5	180915260	8859210	0.049	0.423
chr6	171115067	7920287	0.0463	0.535
chr7	159138663	2227259	0.014	0.3046

chr8	146364022	7268218	0.0497	0.5846
chr9	141213431	8023596	0.0568	0.4752
chr10	135534747	3240553	0.0239	0.3036
chr11	135006516	1516866	0.0112	0.1974
chr12	133851895	1315424	0.0098	0.1888
chr13	115169878	1214563	0.0105	0.2931
chr14	107349540	5073571	0.0473	0.4249
chr15	102531392	1575050	0.0154	0.3097
chr16	90354753	1502069	0.0166	0.2557
chr17	81195210	1839780	0.0227	0.2843
chr18	78077248	2926173	0.0375	1.0447
chr19	59128983	2211299	0.0374	0.4298
chr20	63025520	5445494	0.0864	0.5874
chr21	48129895	2463182	0.0512	0.4348
chr22	51304566	847879	0.0165	0.233
chrMT	16571	58250	3.5152	4.1176
chrX	155270560	5594640	0.036	0.3721
chrY	59373566	176122	0.003	0.1682

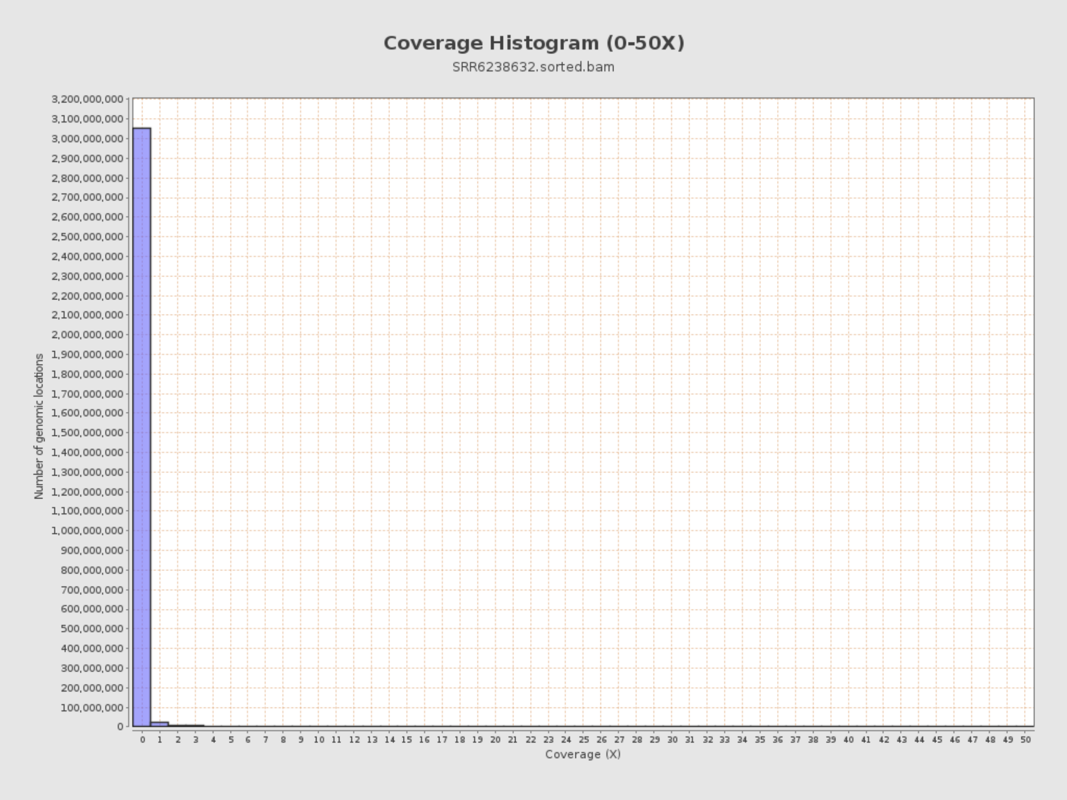
3. Results : Coverage across reference



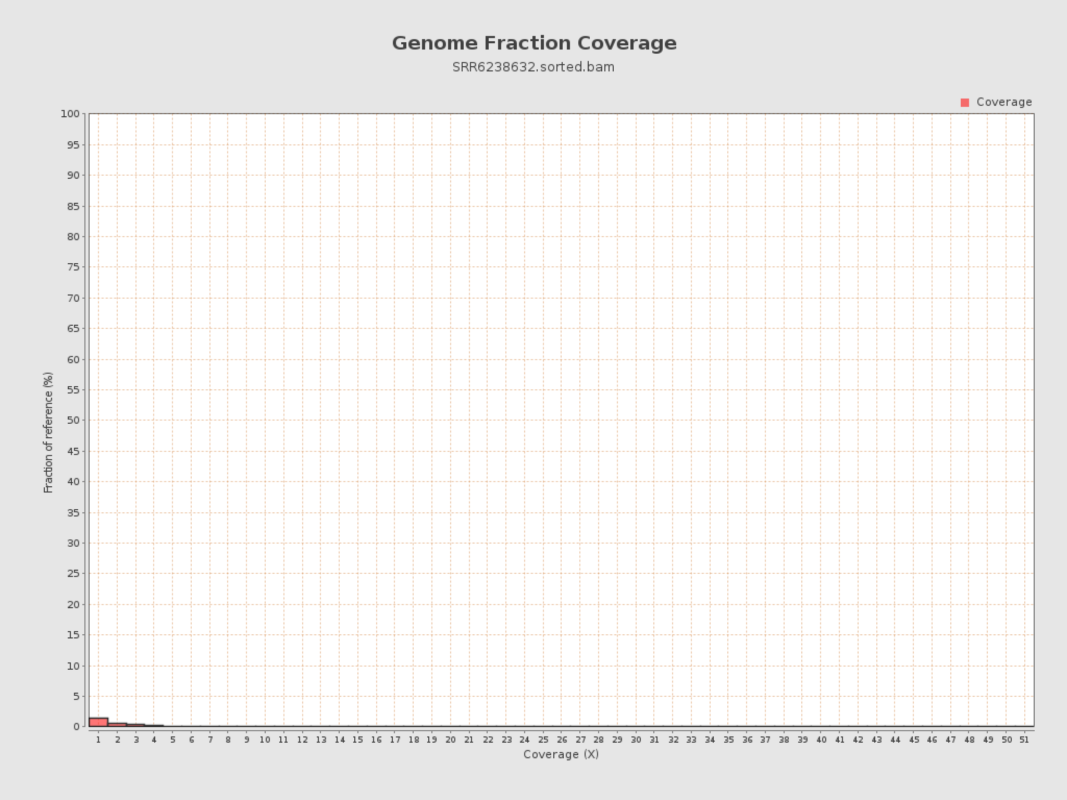
4. Results : Coverage Histogram



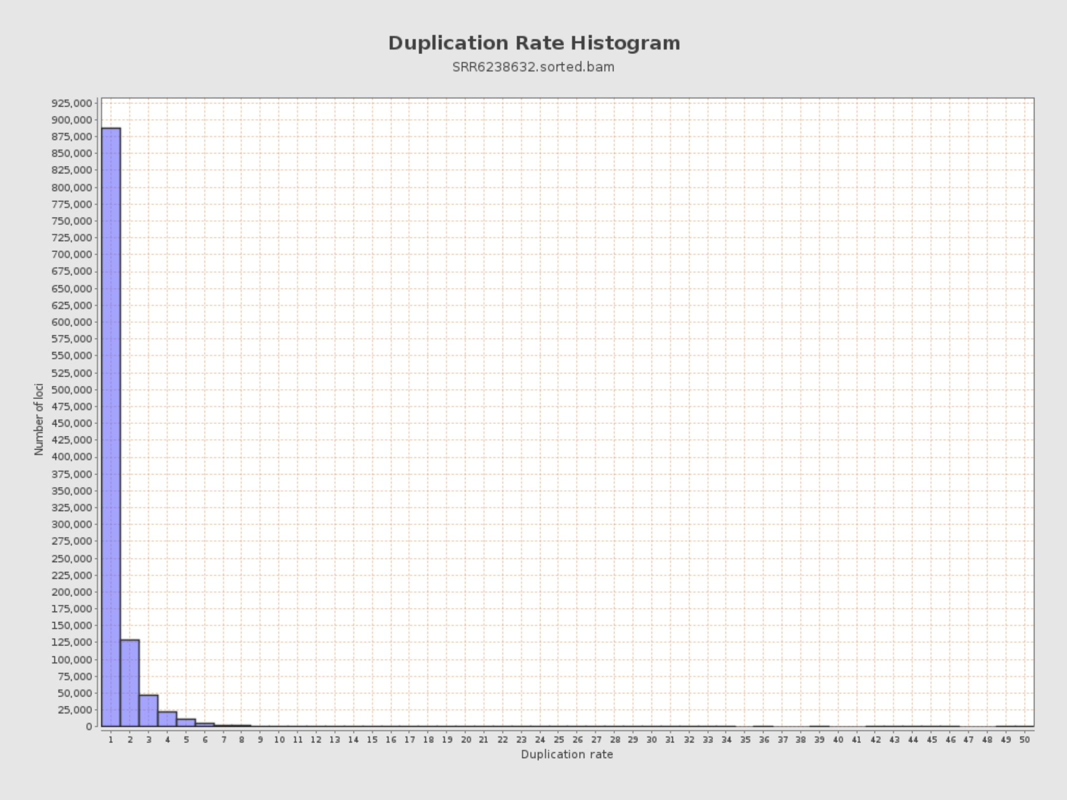
5. Results : Coverage Histogram (0-50X)



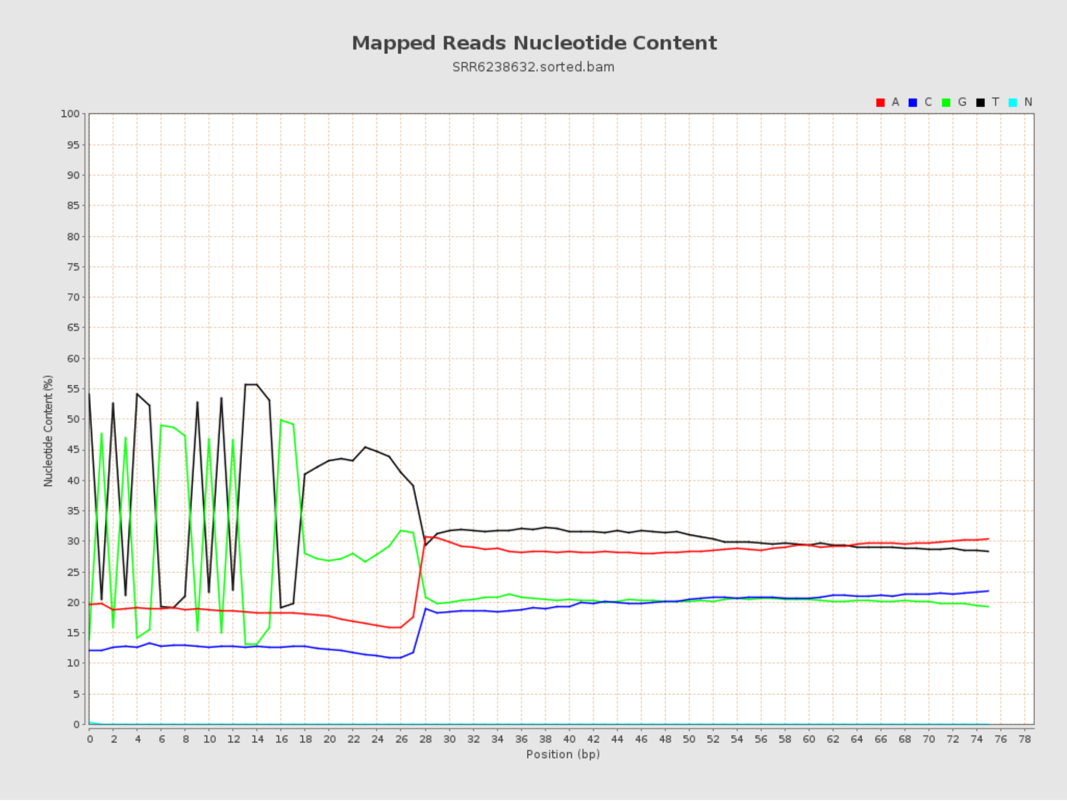
6. Results : Genome Fraction Coverage



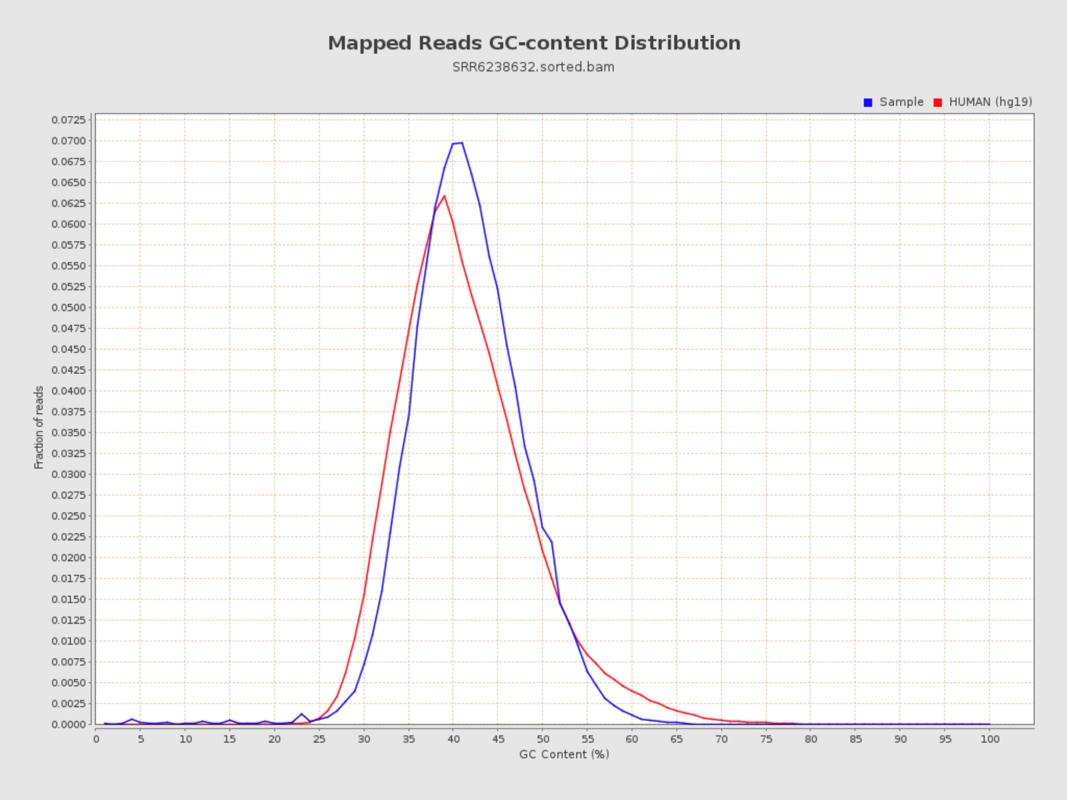
7. Results : Duplication Rate Histogram



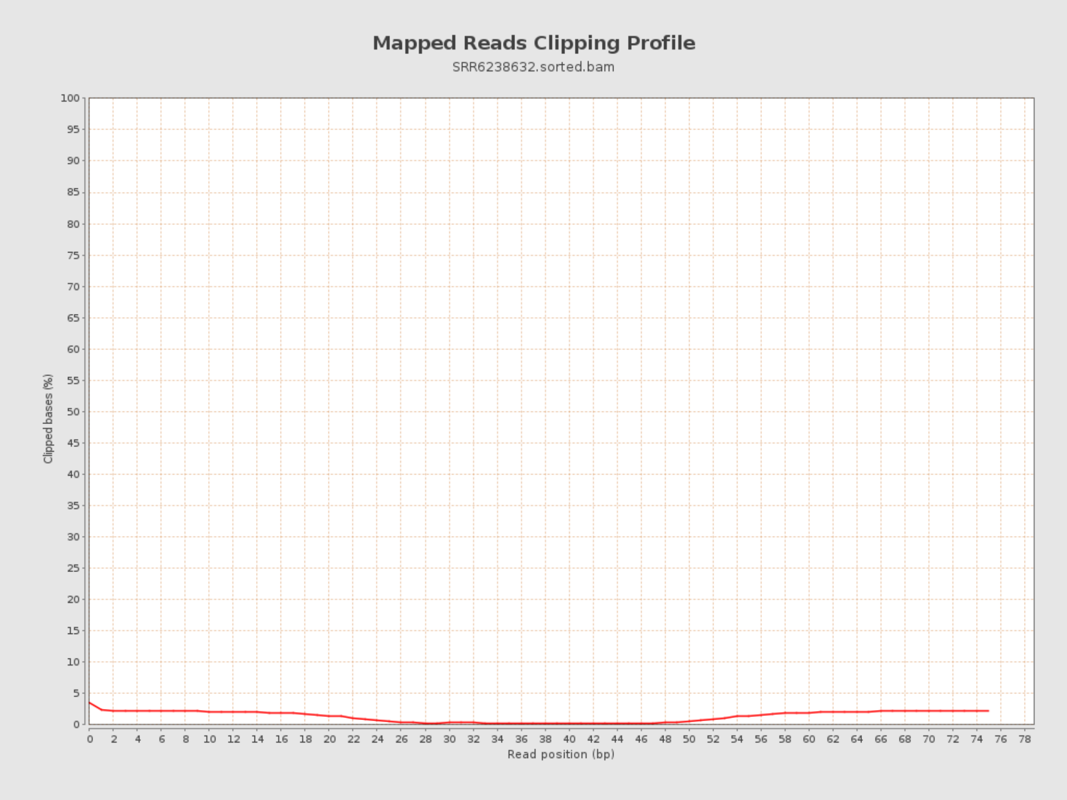
8. Results : Mapped Reads Nucleotide Content



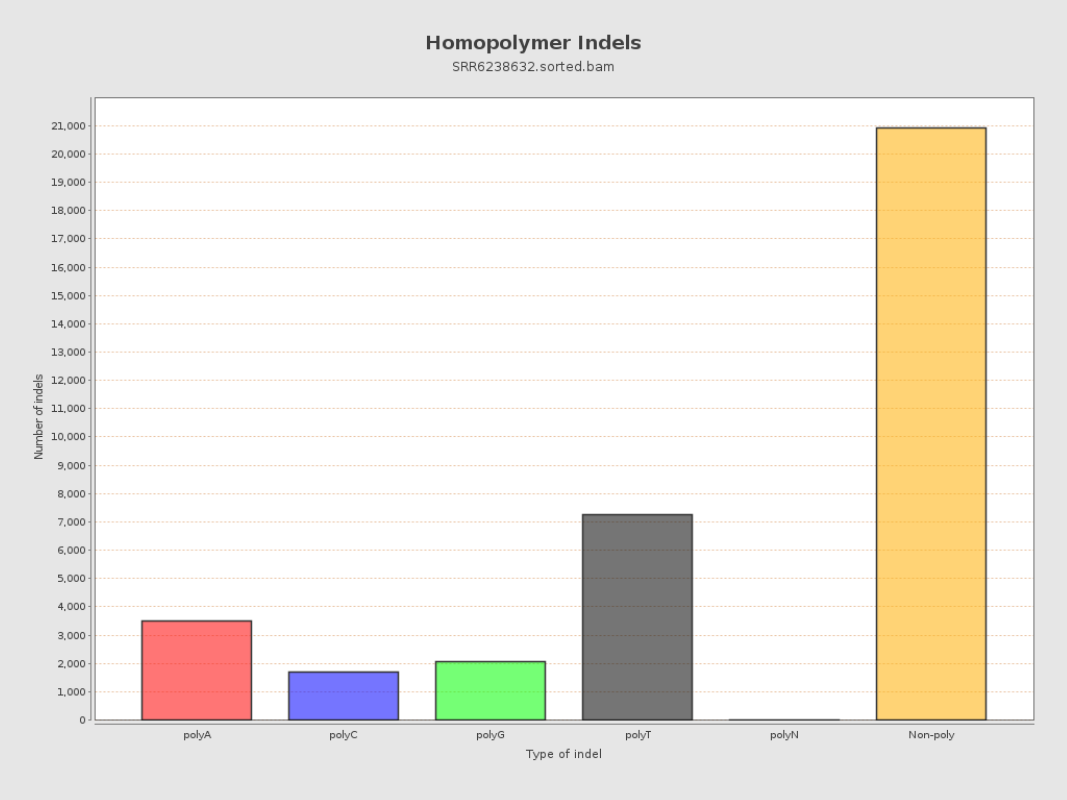
9. Results : Mapped Reads GC-content Distribution



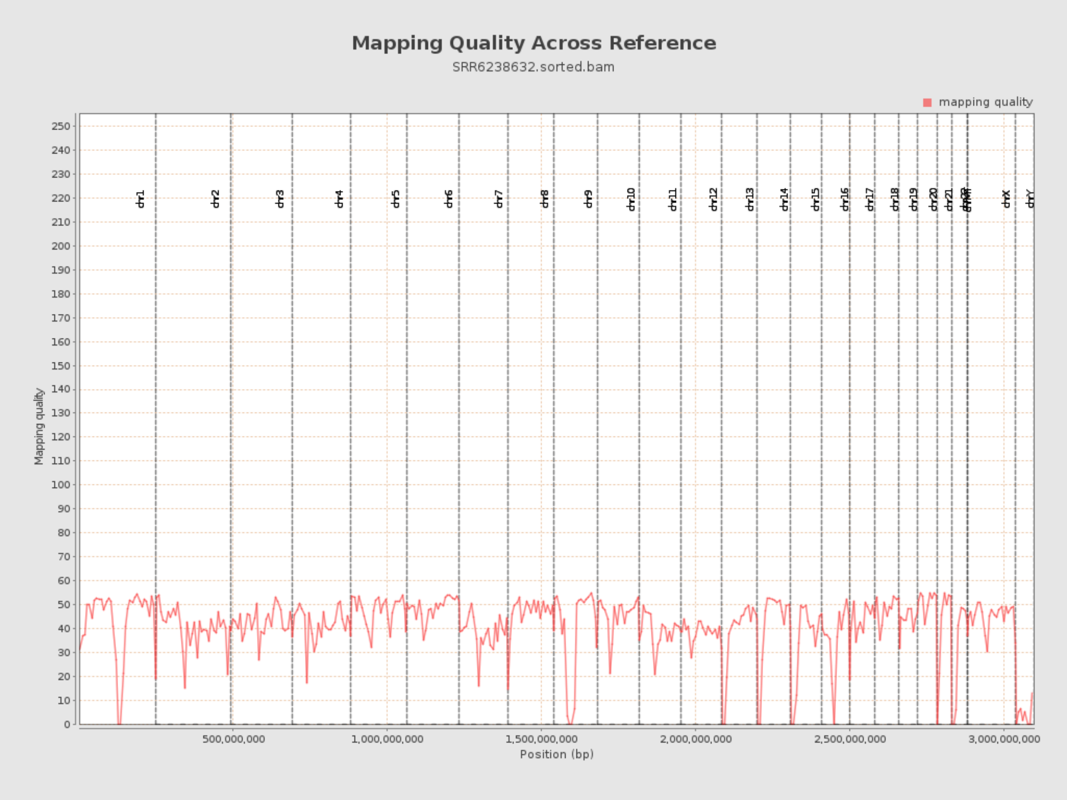
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram