Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238528.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_SRR6238528 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238528.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:07:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238528.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,348,761
Mapped reads	2,927,361 / 87.42%
Unmapped reads	421,400 / 12.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,643 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	896,120 / 26.76%
Duplication rate	19.95%
Clipped reads	1,885,601 / 56.31%

2.2. ACGT Content

Number/percentage of A's	43,962,722 / 24.46%
Number/percentage of C's	31,258,801 / 17.39%
Number/percentage of T's	60,982,218 / 33.93%
Number/percentage of G's	43,492,322 / 24.2%
Number/percentage of N's	11,994 / 0.01%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0581

Standard Deviation	0.9722

2.4. Mapping Quality

Mean Mapping Quality	38.97

2.5. Mismatches and indels

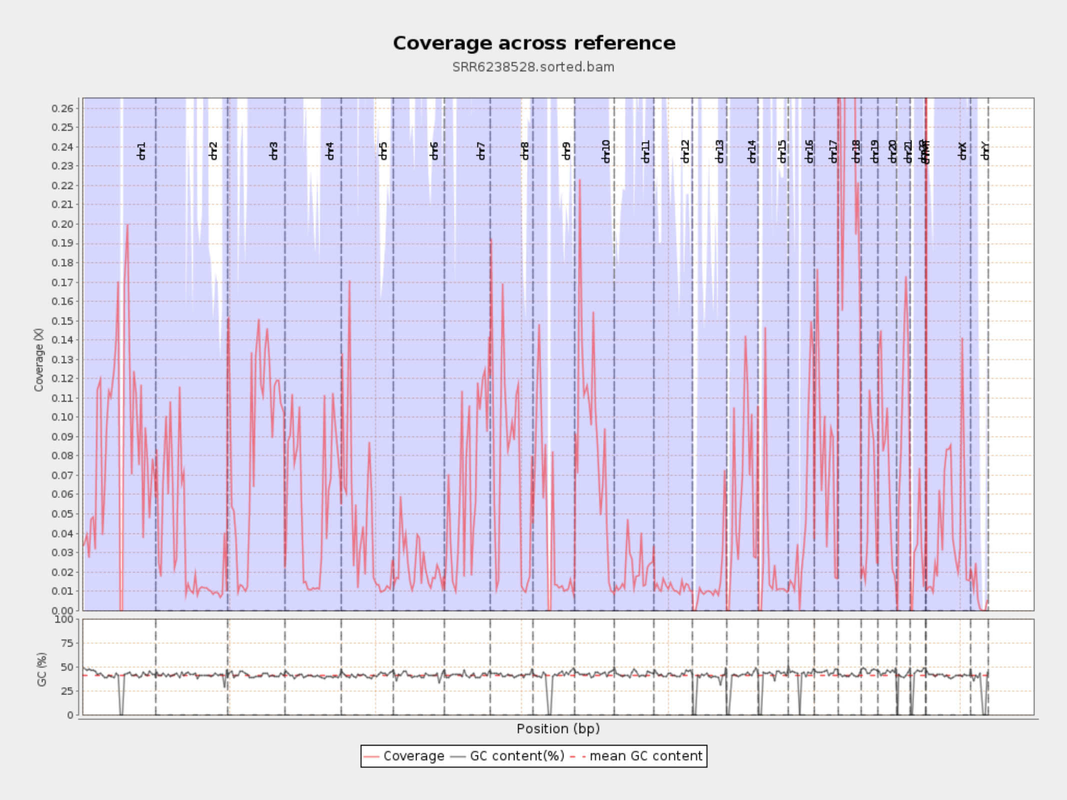
General error rate	0.64%
Mismatches	1,129,548
Insertions	11,729
Mapped reads with at least one insertion	0.4%
Deletions	52,653
Mapped reads with at least one deletion	1.78%
Homopolymer indels	40.58%

2.6. Chromosome stats

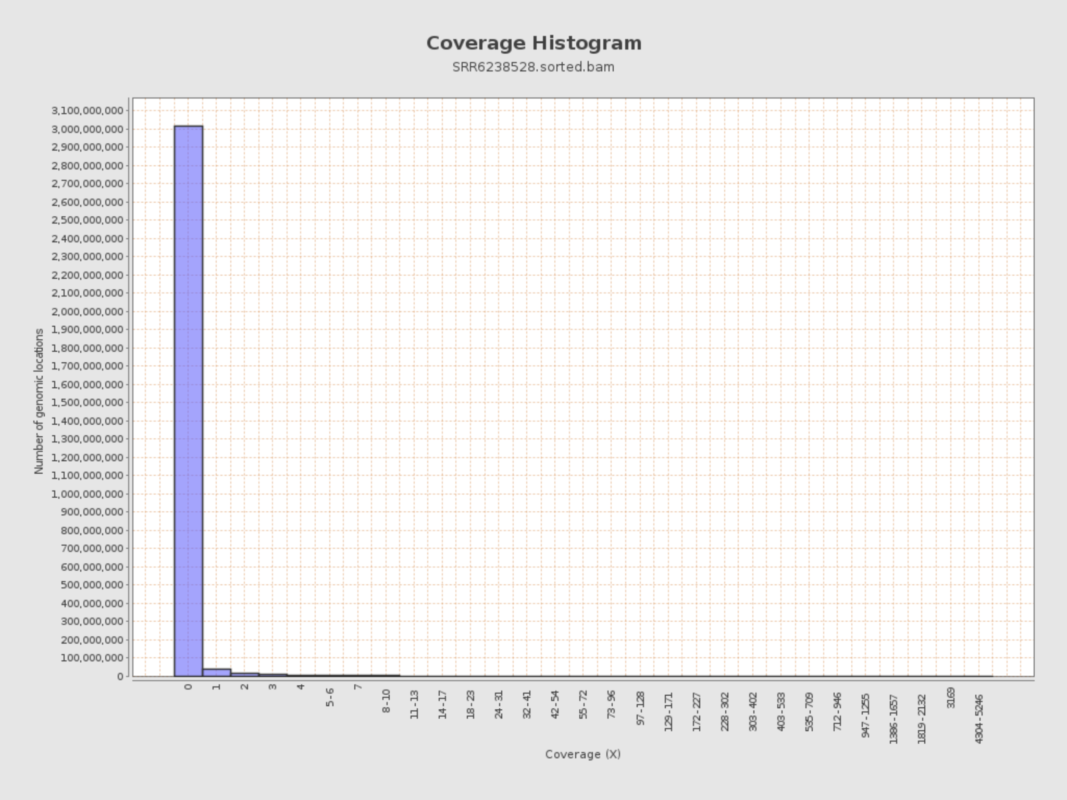
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21171196	0.0849	1.0298
chr2	243199373	8092669	0.0333	2.2803
chr3	198022430	17286498	0.0873	0.6054
chr4	191154276	10770776	0.0563	0.4754
chr5	180915260	7905980	0.0437	0.4233
chr6	171115067	3908482	0.0228	0.7033
chr7	159138663	10722196	0.0674	1.2513

chr8	146364022	10691615	0.073	1.1243
chr9	141213431	6064440	0.0429	0.6069
chr10	135534747	12153040	0.0897	0.6705
chr11	135006516	2752712	0.0204	0.3695
chr12	133851895	1612702	0.012	0.2454
chr13	115169878	1726962	0.015	0.4428
chr14	107349540	6379323	0.0594	0.5171
chr15	102531392	2526424	0.0246	0.4834
chr16	90354753	4350646	0.0482	0.5095
chr17	81195210	6647486	0.0819	0.6136
chr18	78077248	23468104	0.3006	2.076
chr19	59128983	3190037	0.054	0.7322
chr20	63025520	4741411	0.0752	0.5768
chr21	48129895	4816986	0.1001	0.6561
chr22	51304566	1494125	0.0291	0.3464
chrMT	16571	111206	6.7109	6.3649
chrX	155270560	6744383	0.0434	0.4472
chrY	59373566	467154	0.0079	0.3153

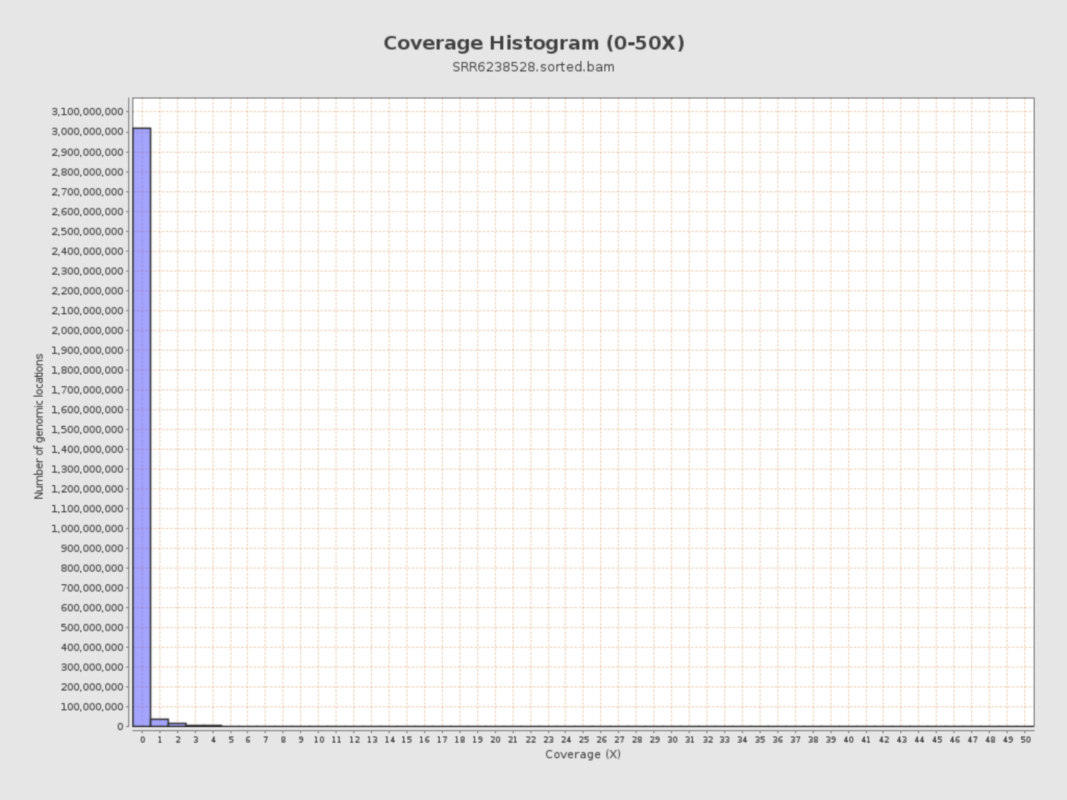
3. Results : Coverage across reference



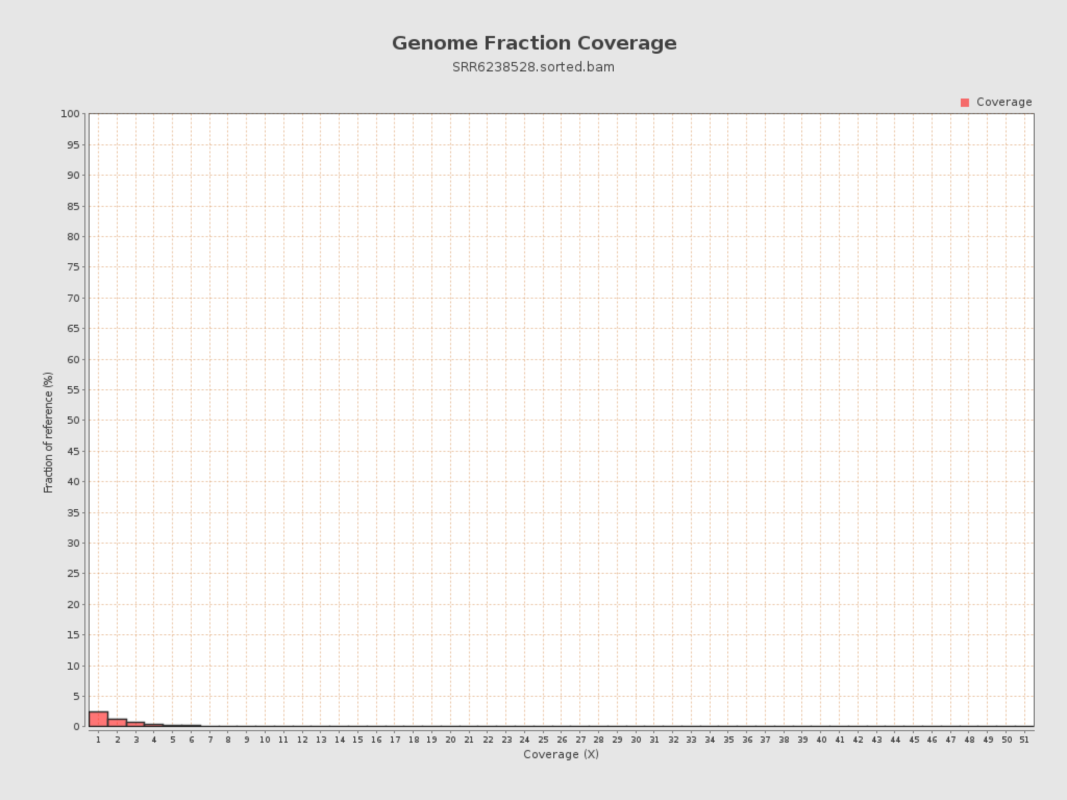
4. Results : Coverage Histogram



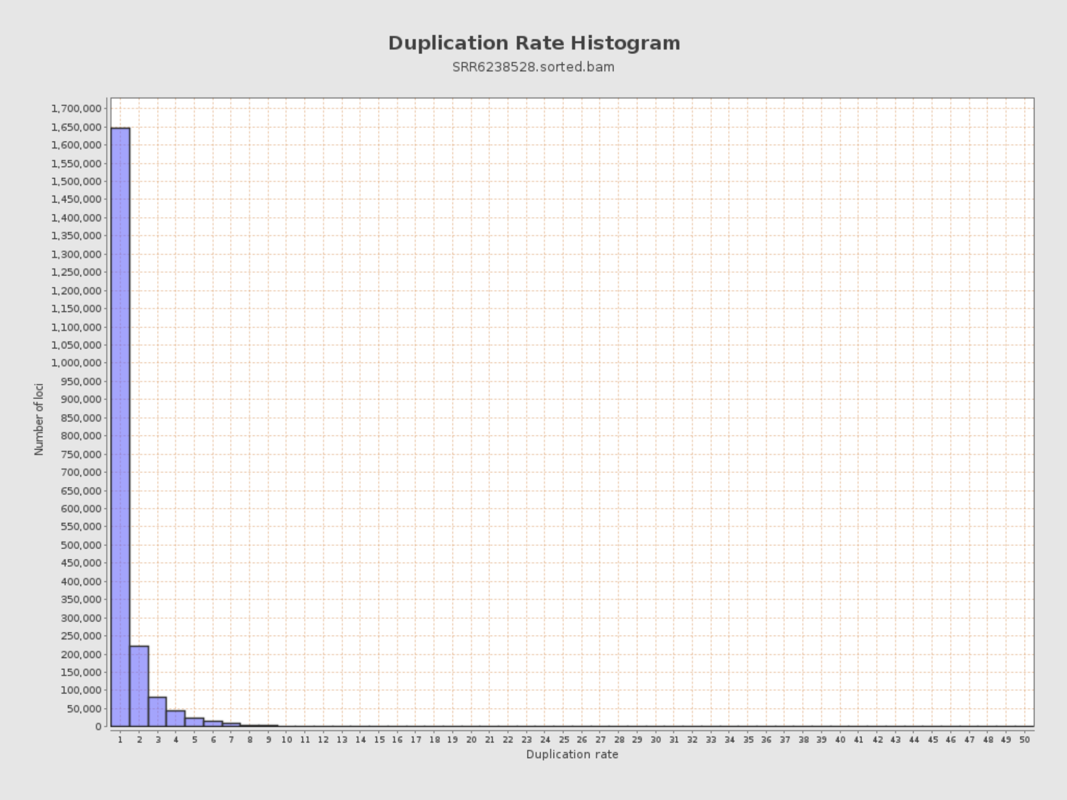
5. Results : Coverage Histogram (0-50X)



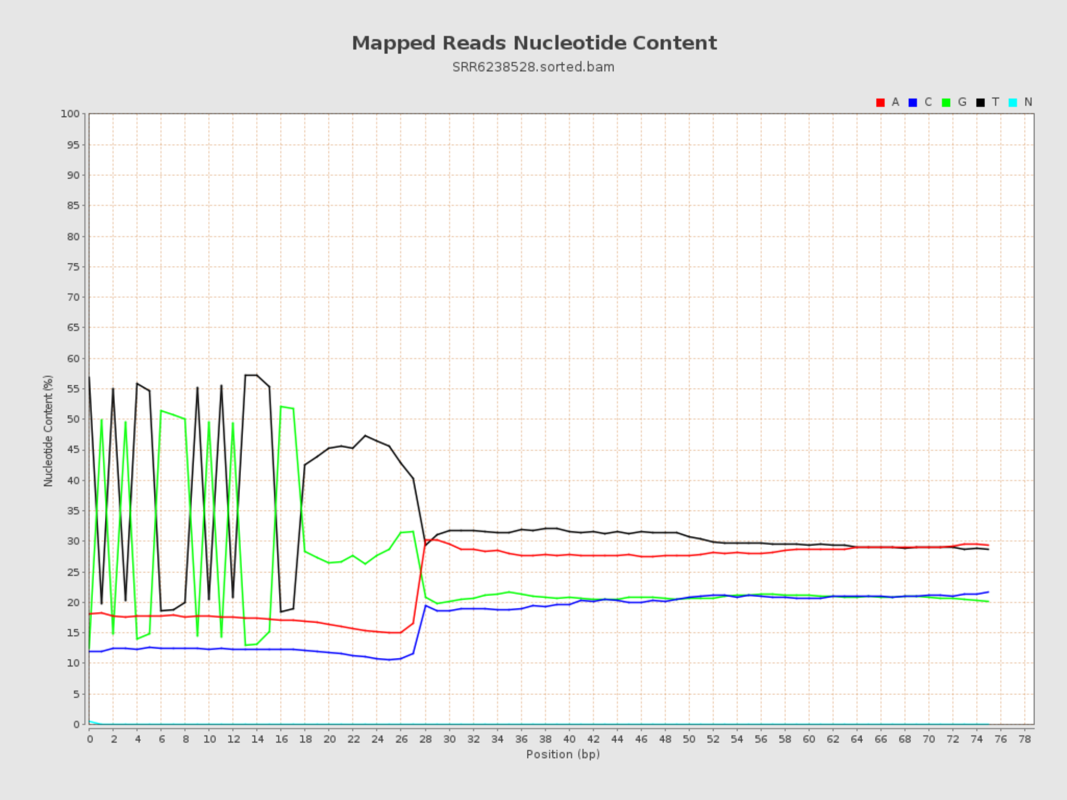
6. Results : Genome Fraction Coverage



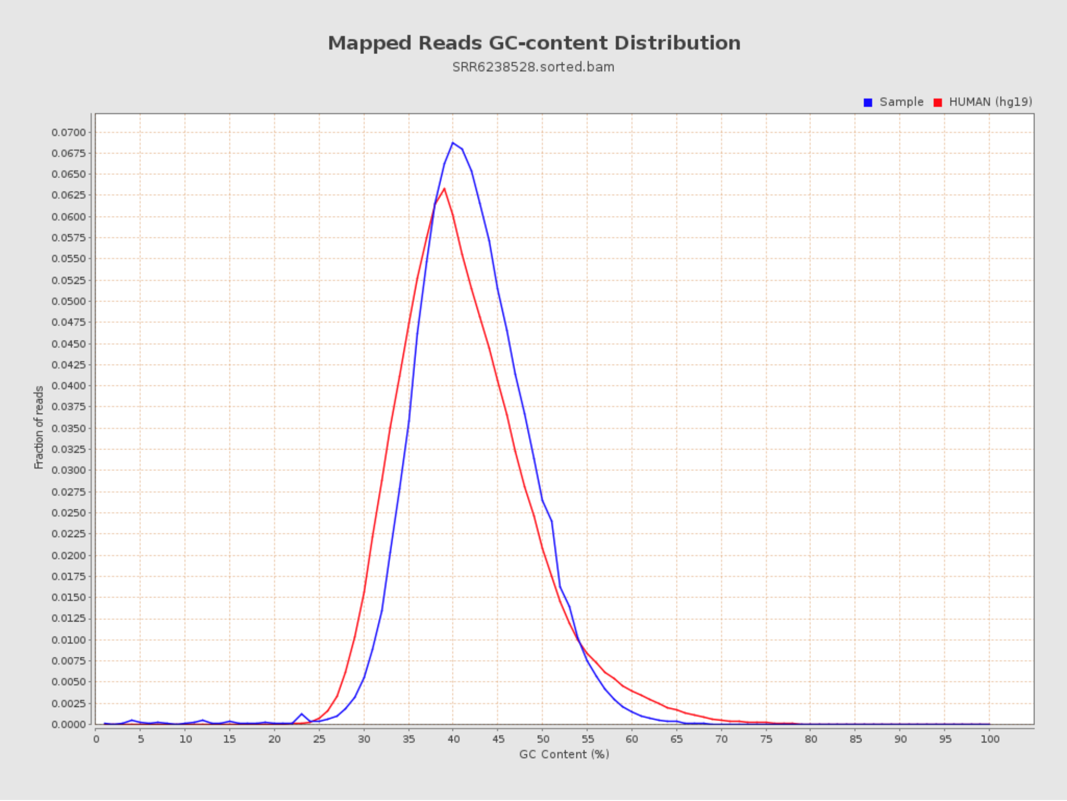
7. Results : Duplication Rate Histogram



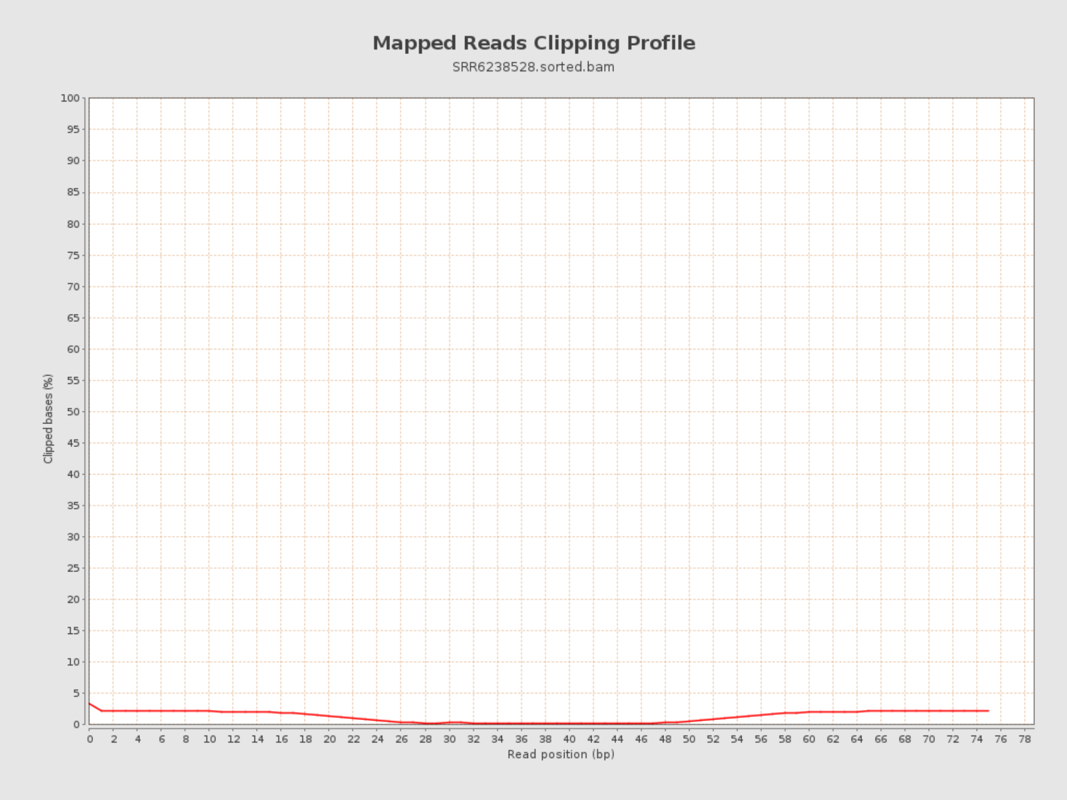
8. Results : Mapped Reads Nucleotide Content



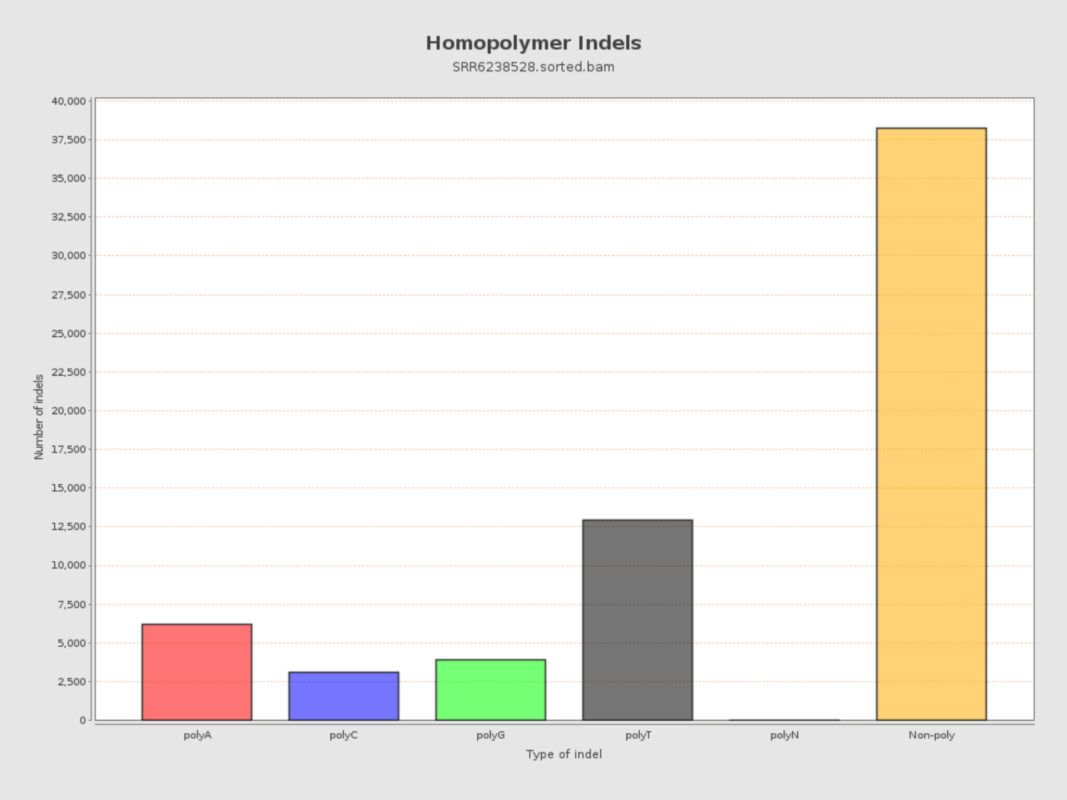
9. Results : Mapped Reads GC-content Distribution



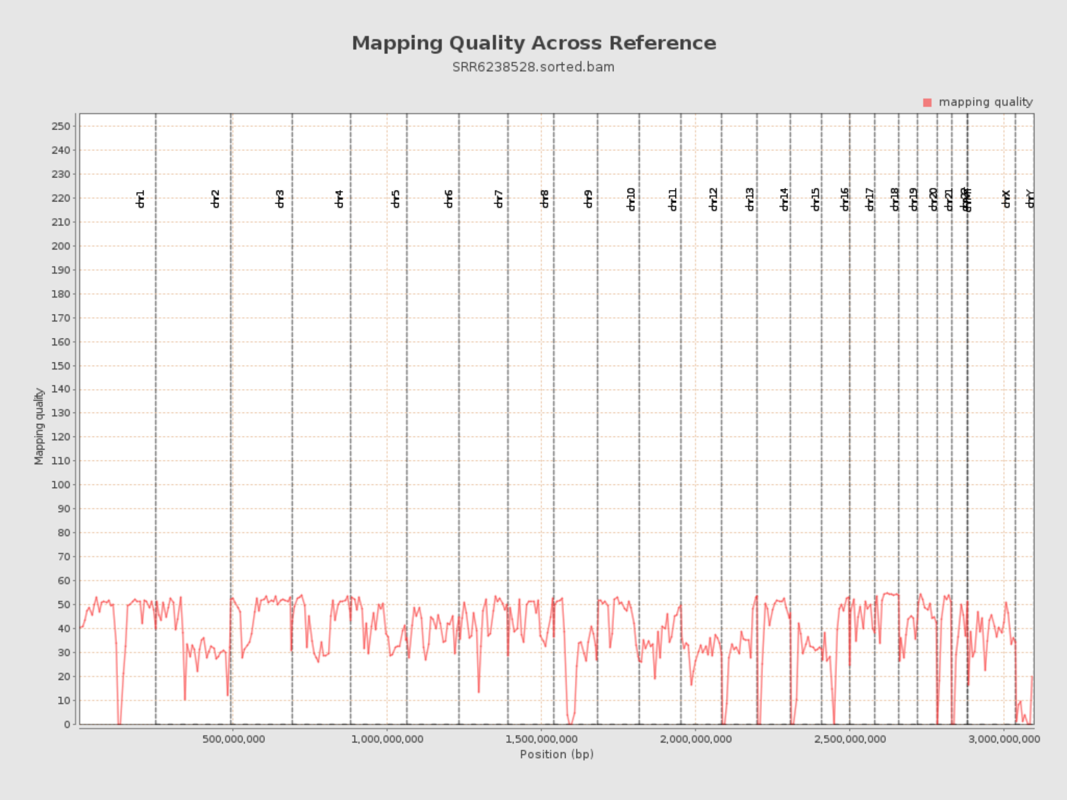
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram