Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:22:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238300.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_SRR6238300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238300.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:22:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,861,842
Mapped reads	61,244 / 3.29%
Unmapped reads	1,800,598 / 96.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	650 / 0.03%
Read min/max/mean length	30 / 76 / 76.01
Duplicated reads (estimated)	4,501 / 0.24%
Duplication rate	3.08%
Clipped reads	42,024 / 2.26%

2.2. ACGT Content

Number/percentage of A's	986,671 / 28.25%
Number/percentage of C's	601,800 / 17.23%
Number/percentage of T's	1,167,795 / 33.44%
Number/percentage of G's	735,442 / 21.06%
Number/percentage of N's	536 / 0.02%
GC Percentage	38.29%

2.3. Coverage

Mean	0.0011

Standard Deviation	0.0924

2.4. Mapping Quality

Mean Mapping Quality	36.9

2.5. Mismatches and indels

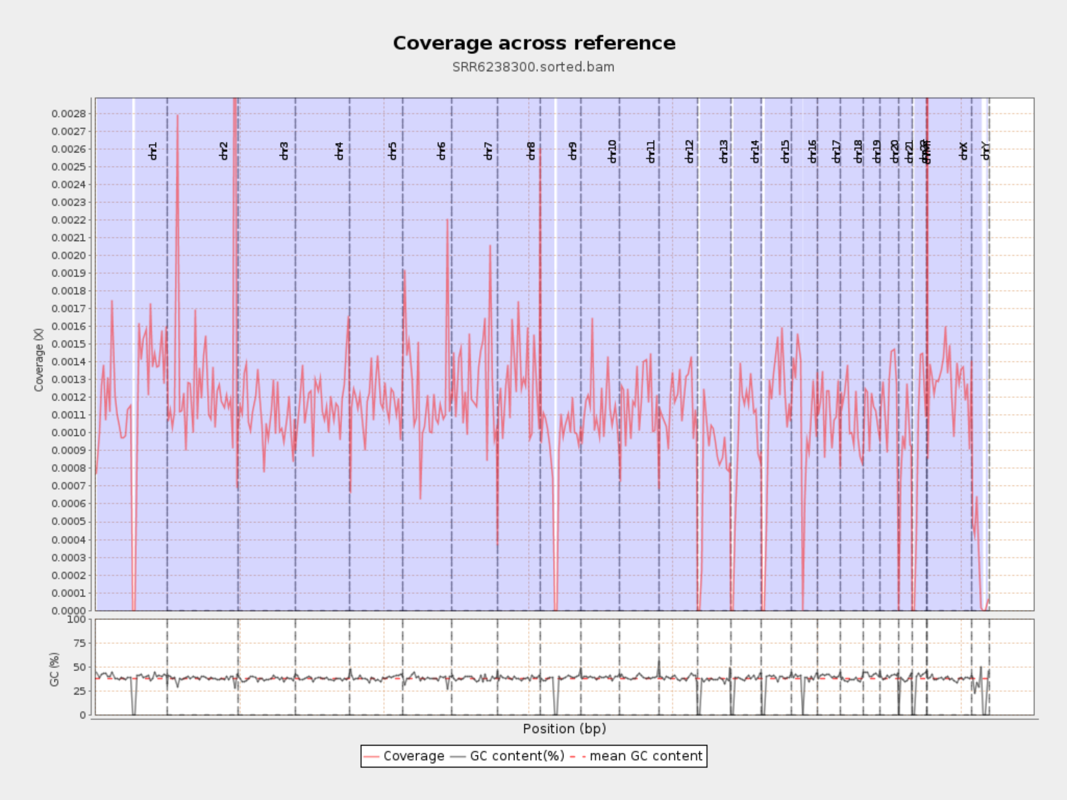
General error rate	1.39%
Mismatches	47,703
Insertions	455
Mapped reads with at least one insertion	0.72%
Deletions	1,384
Mapped reads with at least one deletion	2.23%
Homopolymer indels	31.48%

2.6. Chromosome stats

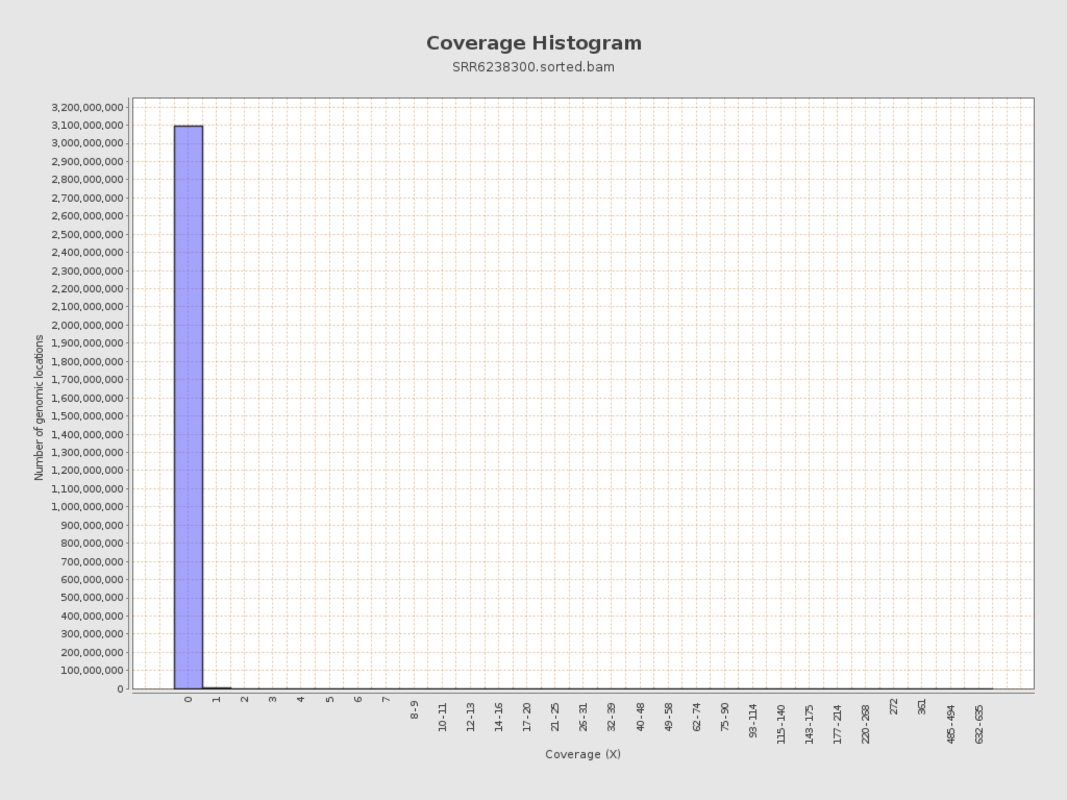
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	297793	0.0012	0.0826
chr2	243199373	324443	0.0013	0.2676
chr3	198022430	218354	0.0011	0.0422
chr4	191154276	224738	0.0012	0.0409
chr5	180915260	212486	0.0012	0.0488
chr6	171115067	210444	0.0012	0.1072
chr7	159138663	206369	0.0013	0.0878

chr8	146364022	187397	0.0013	0.0502
chr9	141213431	128414	0.0009	0.0375
chr10	135534747	154241	0.0011	0.0402
chr11	135006516	159009	0.0012	0.0396
chr12	133851895	156963	0.0012	0.0431
chr13	115169878	91296	0.0008	0.0452
chr14	107349540	100845	0.0009	0.0344
chr15	102531392	107422	0.001	0.0518
chr16	90354753	95504	0.0011	0.0384
chr17	81195210	90557	0.0011	0.0389
chr18	78077248	83973	0.0011	0.0504
chr19	59128983	65498	0.0011	0.0381
chr20	63025520	76792	0.0012	0.0388
chr21	48129895	42030	0.0009	0.0333
chr22	51304566	45334	0.0009	0.0333
chrMT	16571	1112	0.0671	0.25
chrX	155270560	199417	0.0013	0.0448
chrY	59373566	13836	0.0002	0.0274

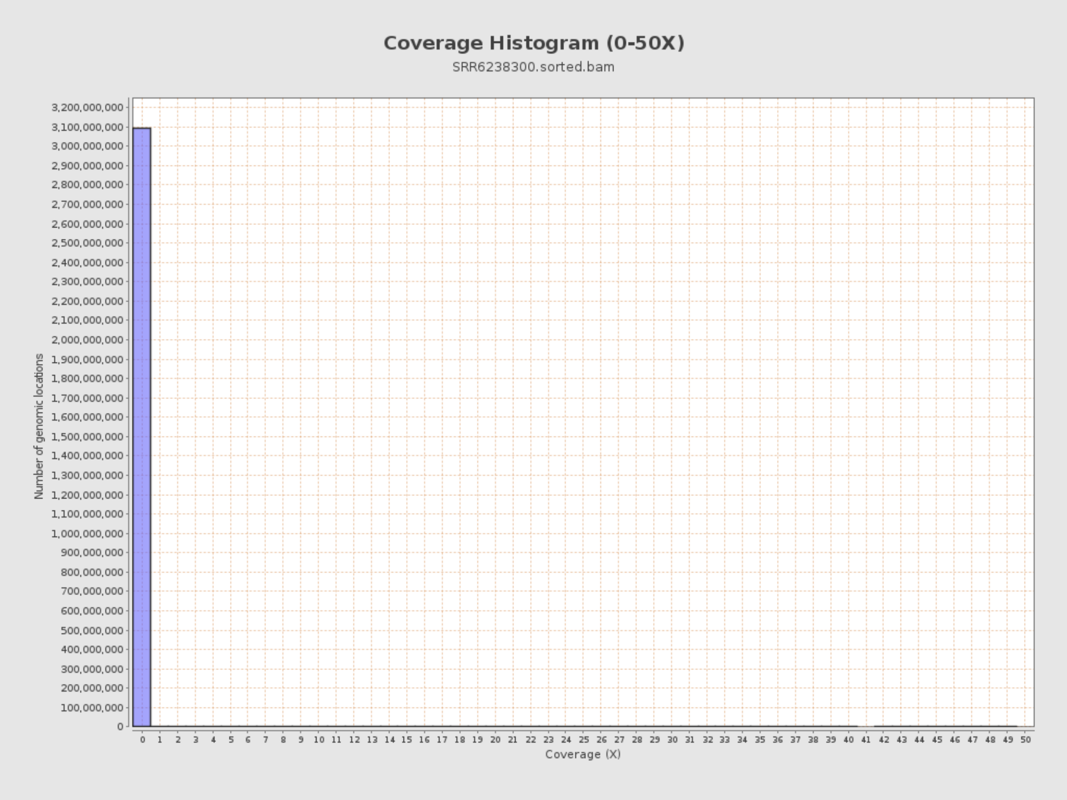
3. Results : Coverage across reference



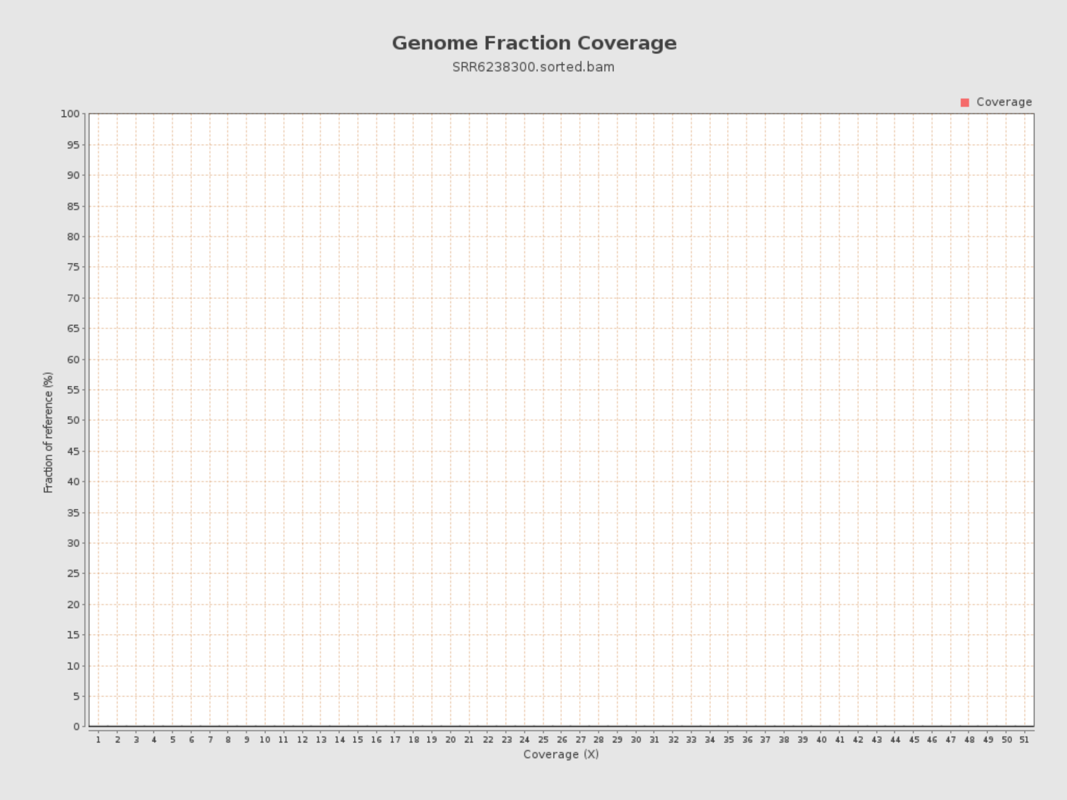
4. Results : Coverage Histogram



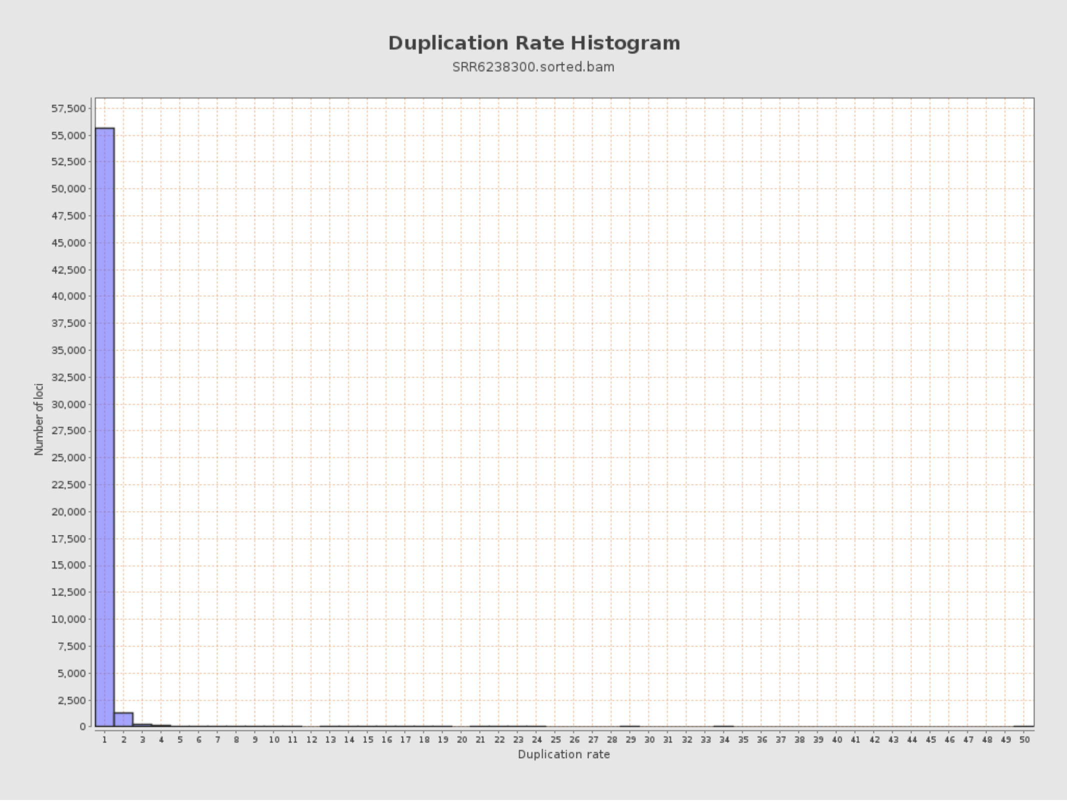
5. Results : Coverage Histogram (0-50X)



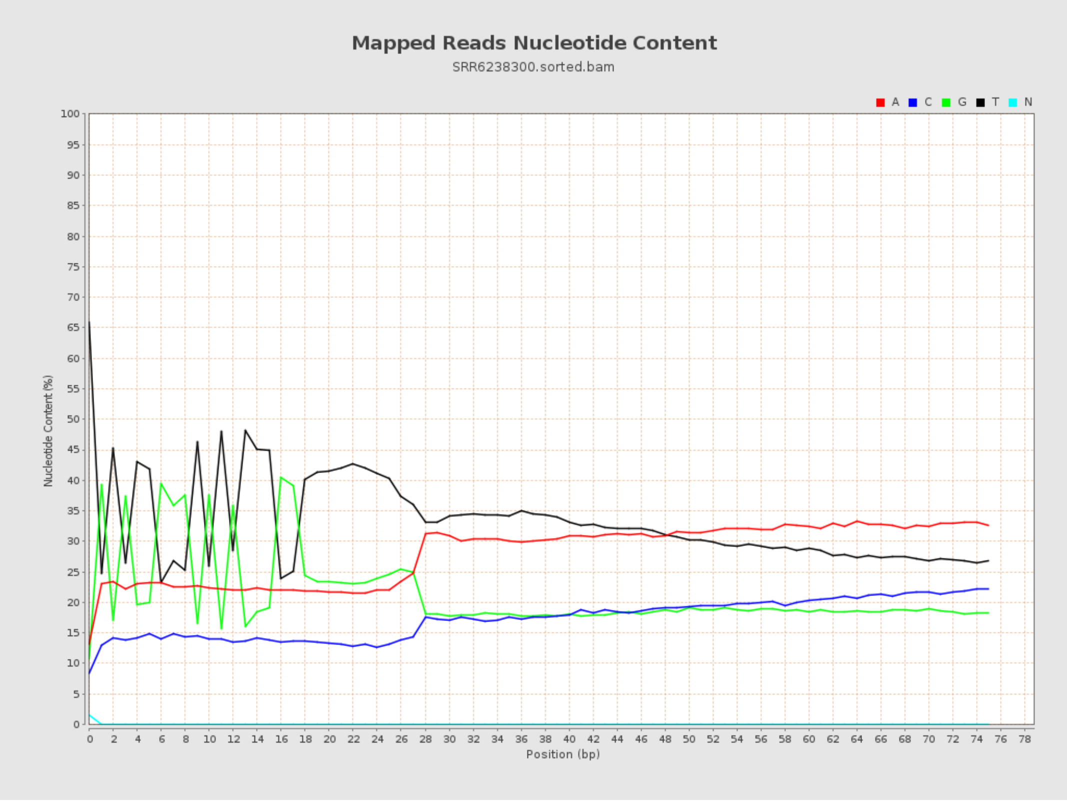
6. Results : Genome Fraction Coverage



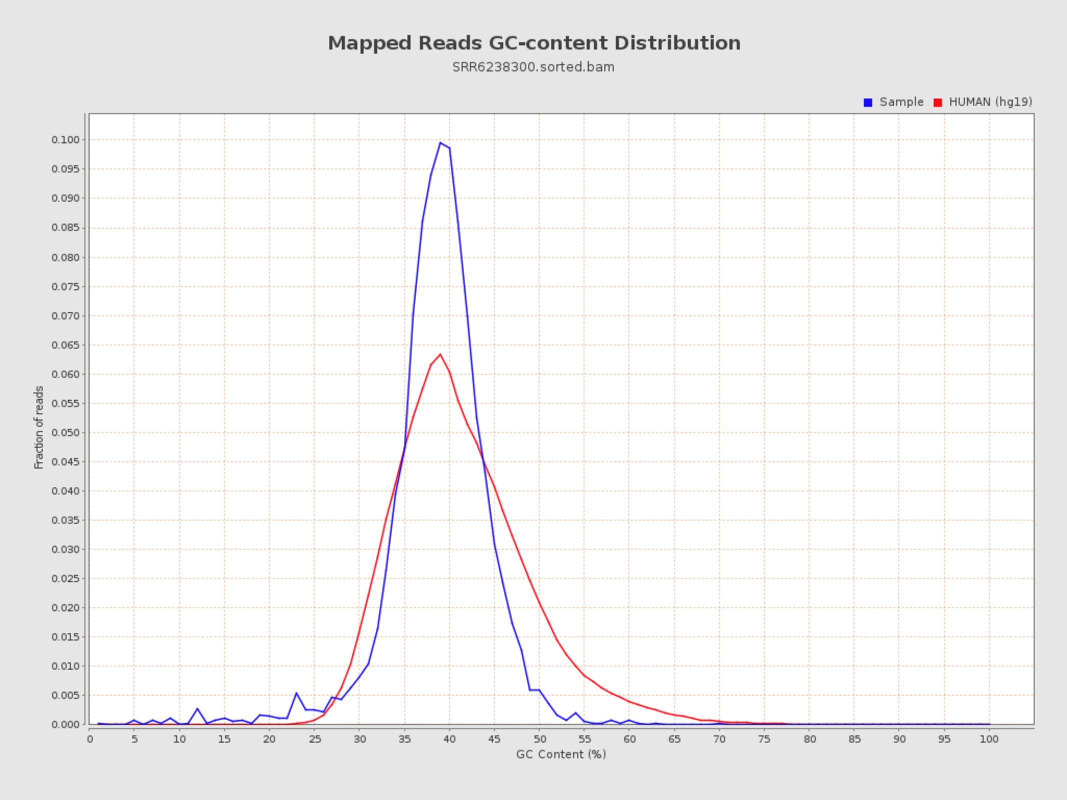
7. Results : Duplication Rate Histogram



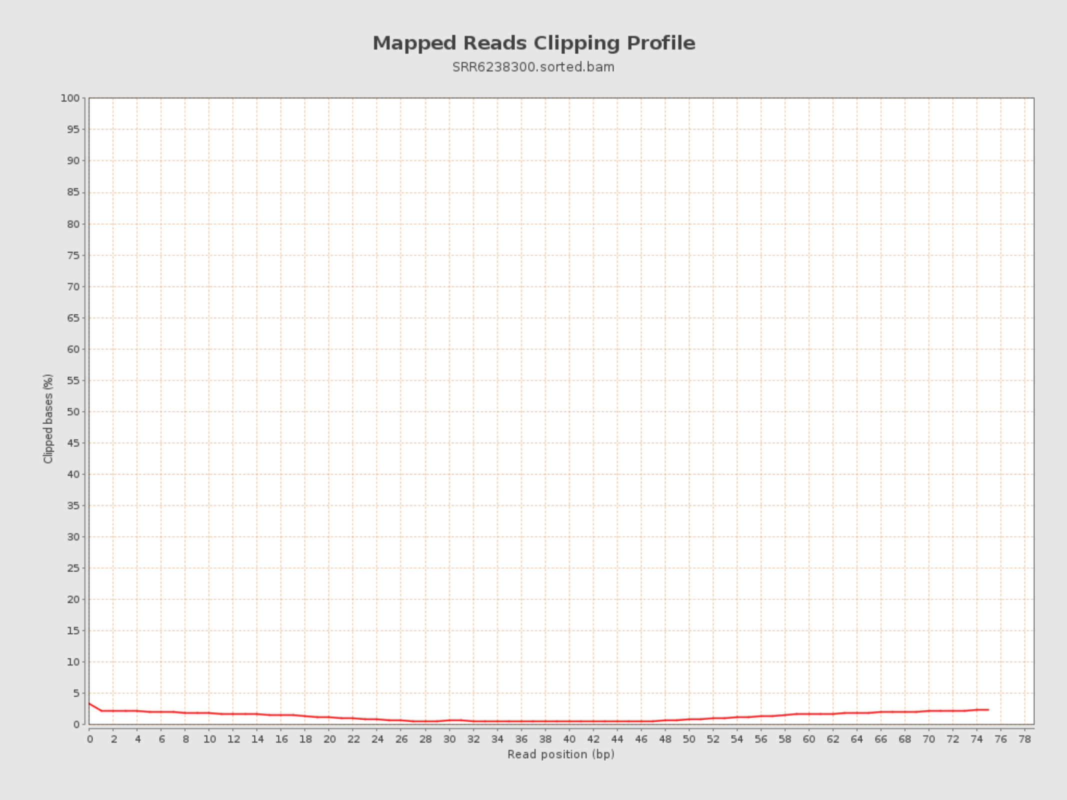
8. Results : Mapped Reads Nucleotide Content



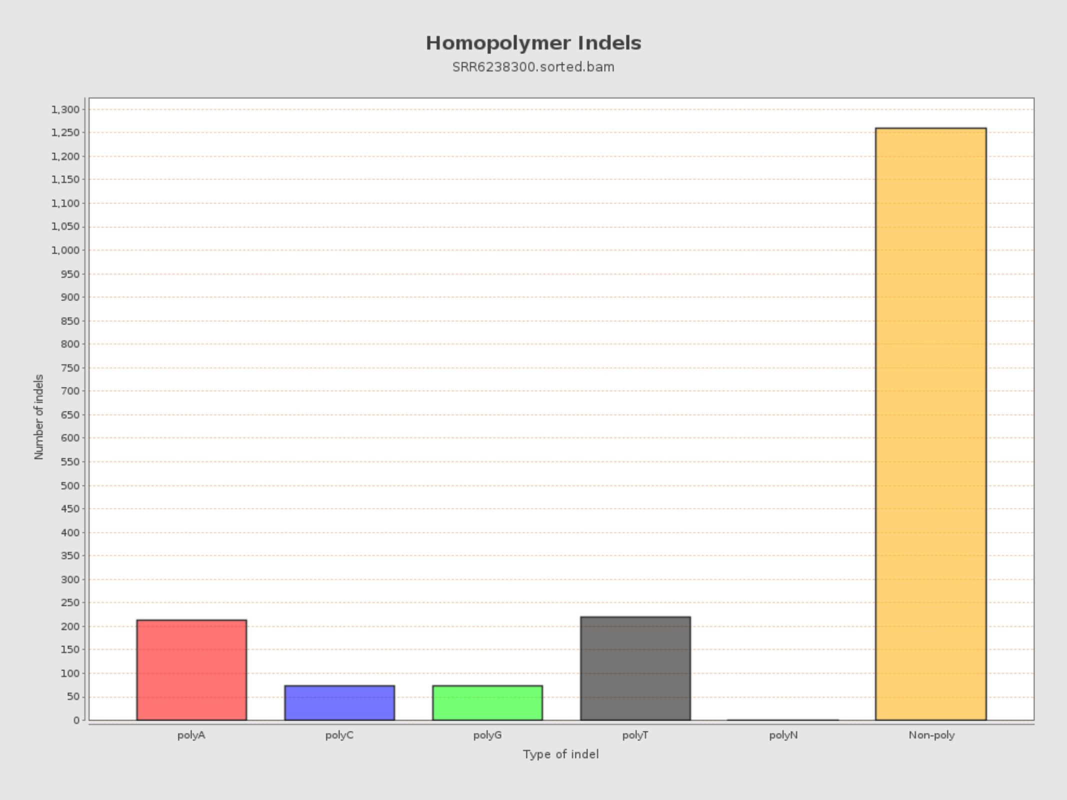
9. Results : Mapped Reads GC-content Distribution



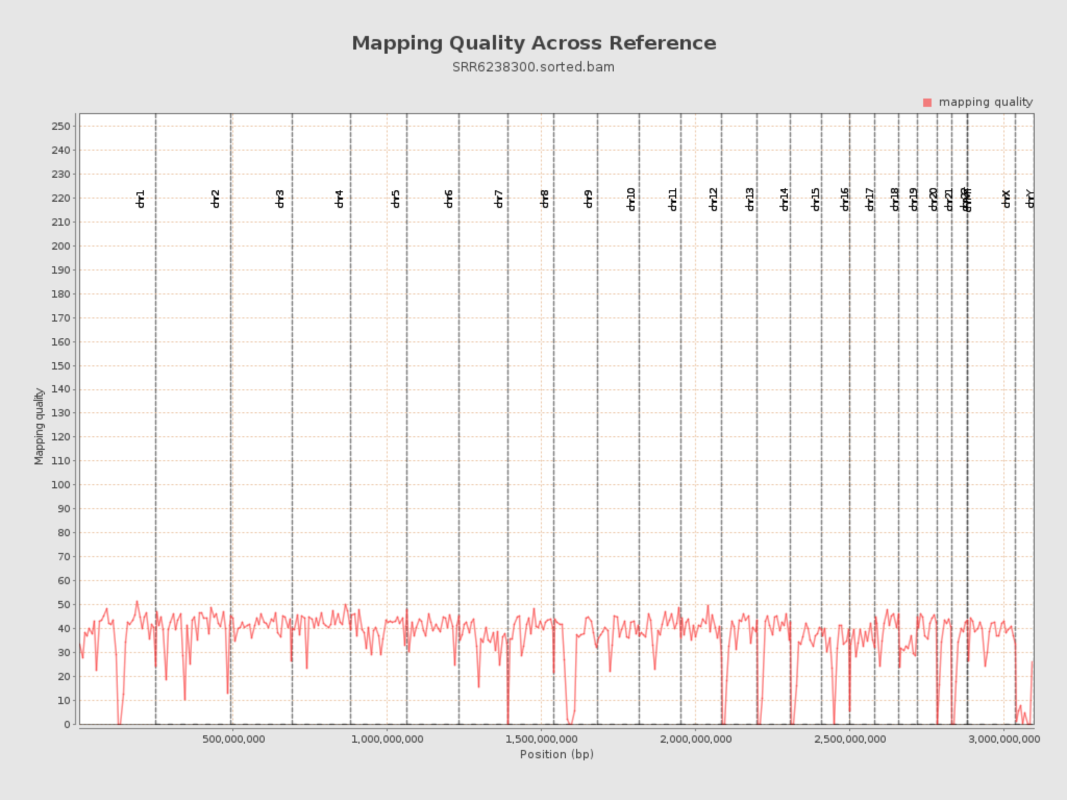
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram