Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:49:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238493.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_SRR6238493 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238493.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:49:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238493.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,026,485
Mapped reads	3,269,545 / 81.2%
Unmapped reads	756,940 / 18.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,775 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,774,506 / 44.07%
Duplication rate	23.64%
Clipped reads	2,357,020 / 58.54%

2.2. ACGT Content

Number/percentage of A's	46,851,632 / 24.06%
Number/percentage of C's	32,437,096 / 16.66%
Number/percentage of T's	67,665,047 / 34.75%
Number/percentage of G's	47,760,522 / 24.53%
Number/percentage of N's	11,936 / 0.01%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0629

Standard Deviation	1.3501

2.4. Mapping Quality

Mean Mapping Quality	38.29

2.5. Mismatches and indels

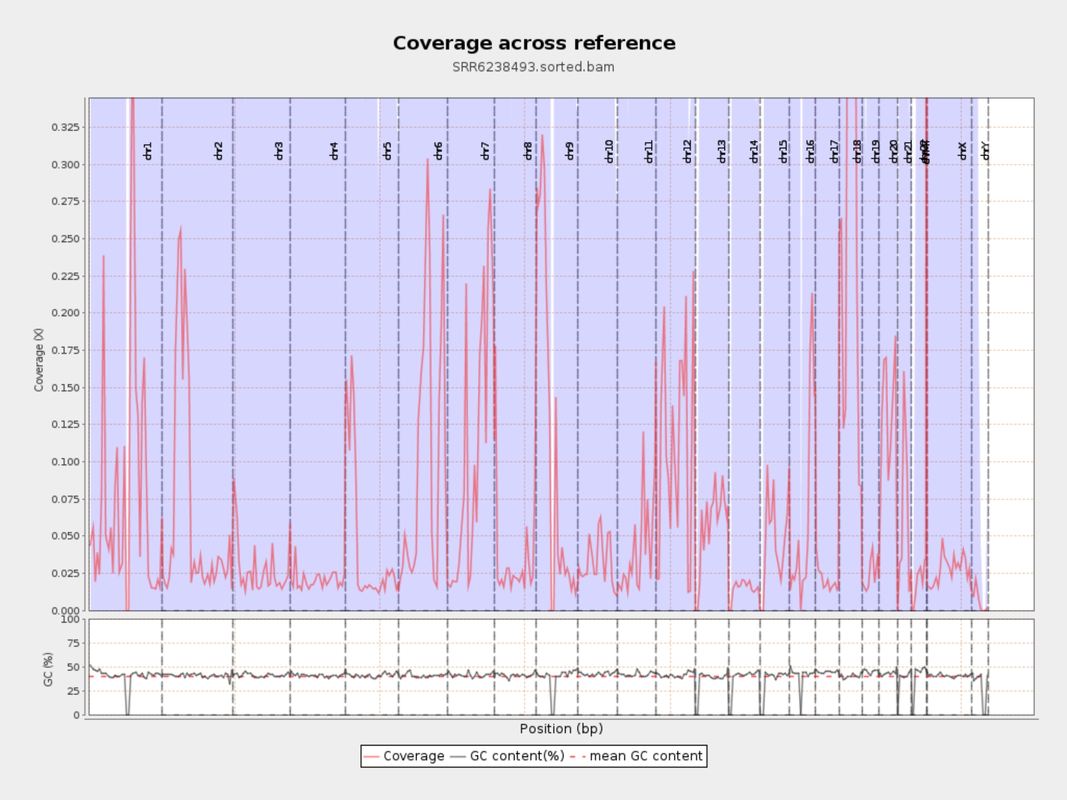
General error rate	0.66%
Mismatches	1,269,649
Insertions	12,386
Mapped reads with at least one insertion	0.38%
Deletions	64,260
Mapped reads with at least one deletion	1.95%
Homopolymer indels	40.87%

2.6. Chromosome stats

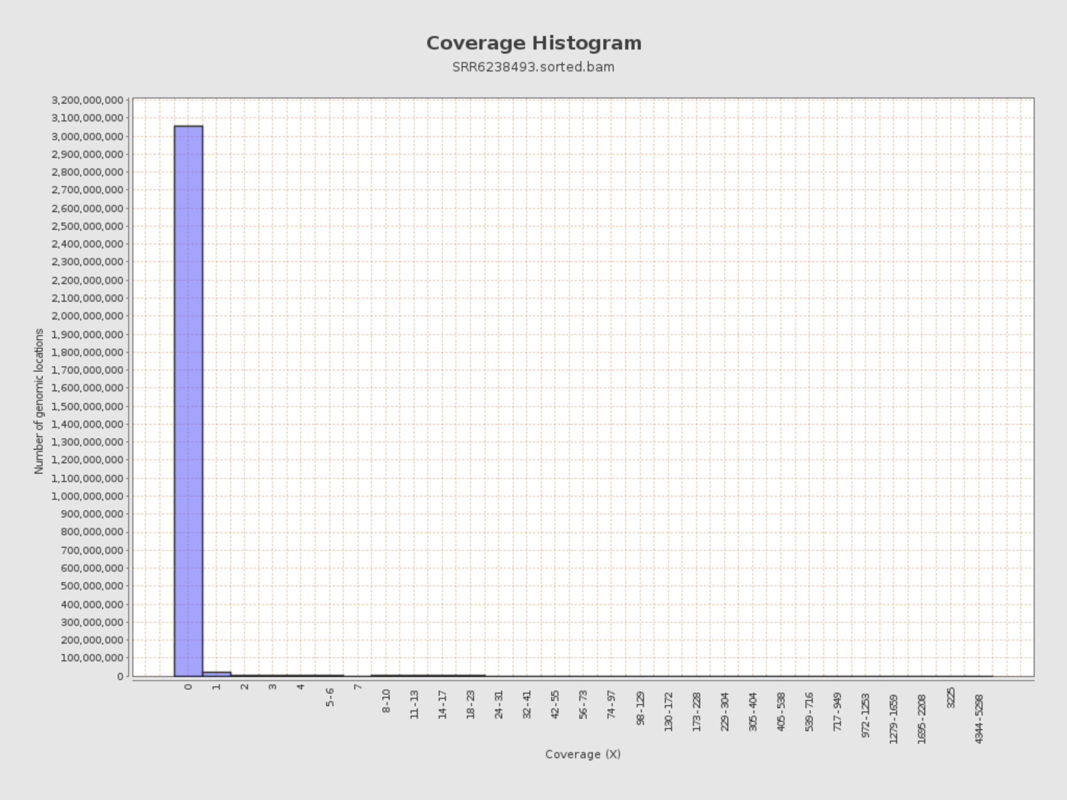
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19563929	0.0785	1.2291
chr2	243199373	16078051	0.0661	2.5523
chr3	198022430	5438046	0.0275	0.6208
chr4	191154276	3890515	0.0204	0.5037
chr5	180915260	7831885	0.0433	0.7895
chr6	171115067	17899183	0.1046	1.4925
chr7	159138663	16811595	0.1056	2.0105

chr8	146364022	5160300	0.0353	0.8169
chr9	141213431	14917864	0.1056	1.4667
chr10	135534747	4493610	0.0332	0.7638
chr11	135006516	5581402	0.0413	0.8083
chr12	133851895	14880982	0.1112	1.3768
chr13	115169878	6609593	0.0574	1.0428
chr14	107349540	1555810	0.0145	0.6505
chr15	102531392	4803848	0.0469	0.9477
chr16	90354753	5903940	0.0653	1.1266
chr17	81195210	1658109	0.0204	0.5139
chr18	78077248	23590188	0.3021	3.3585
chr19	59128983	1479587	0.025	0.7528
chr20	63025520	8297689	0.1317	1.5191
chr21	48129895	2749741	0.0571	0.9626
chr22	51304566	962852	0.0188	0.5205
chrMT	16571	25981	1.5679	4.0654
chrX	155270560	4281883	0.0276	0.6391
chrY	59373566	366201	0.0062	0.3868

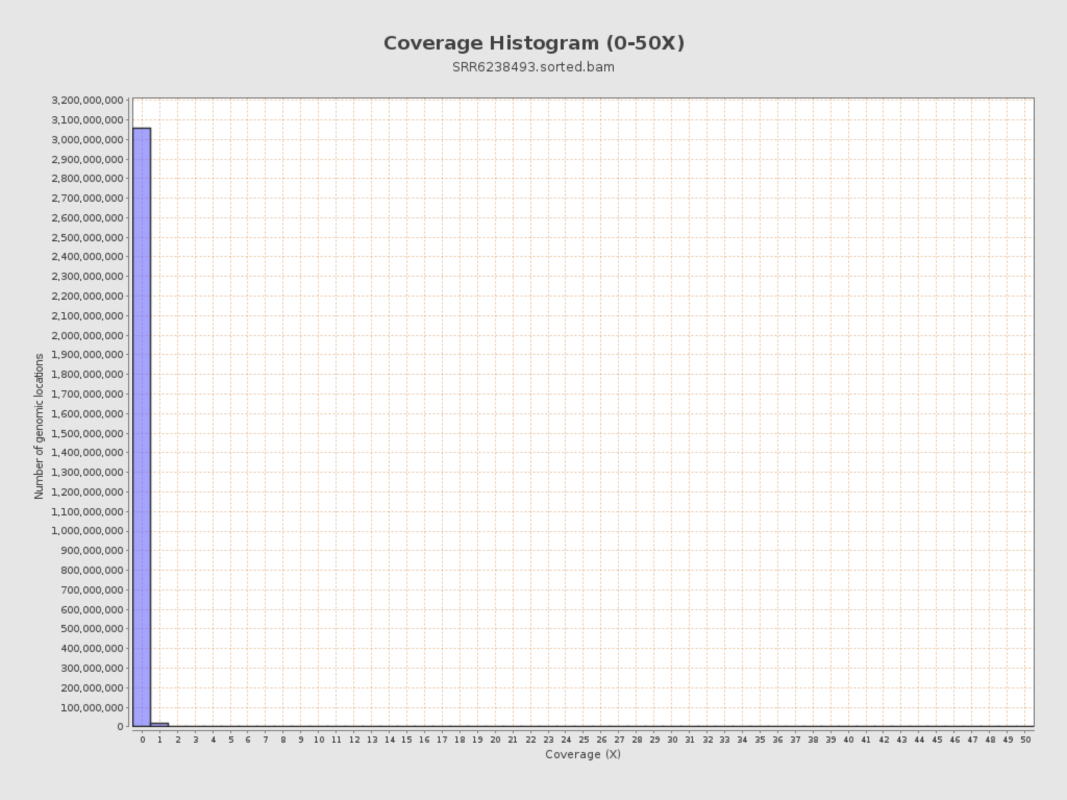
3. Results : Coverage across reference



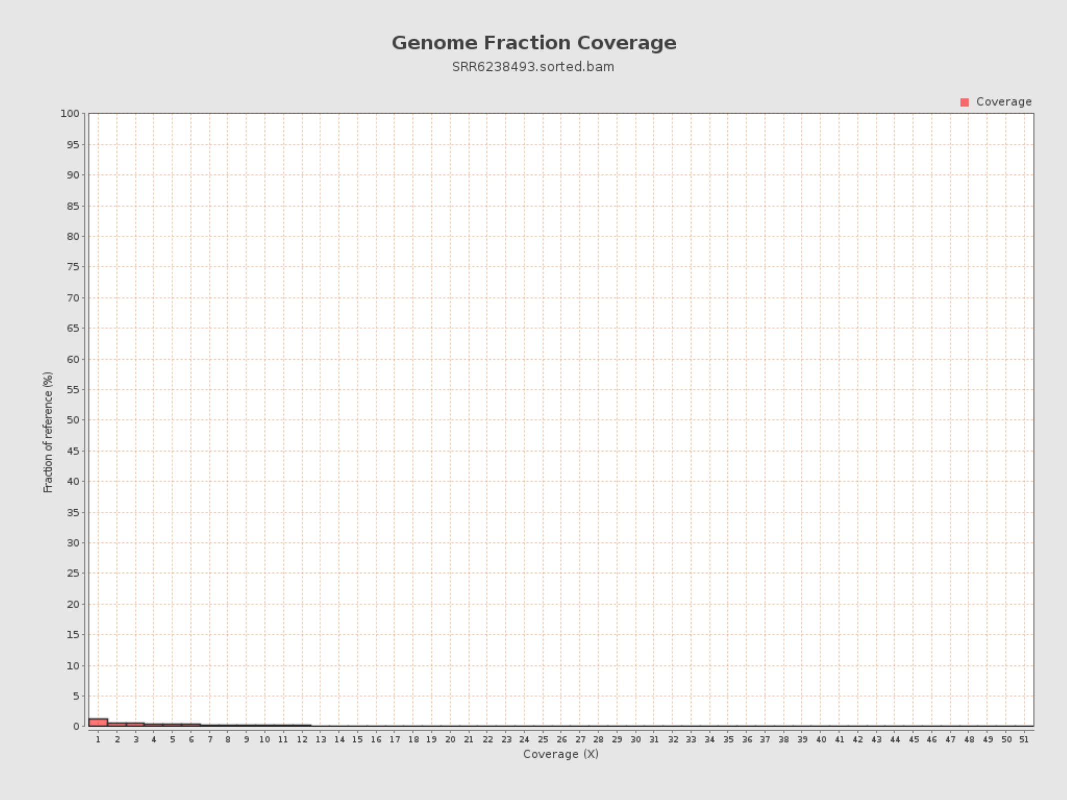
4. Results : Coverage Histogram



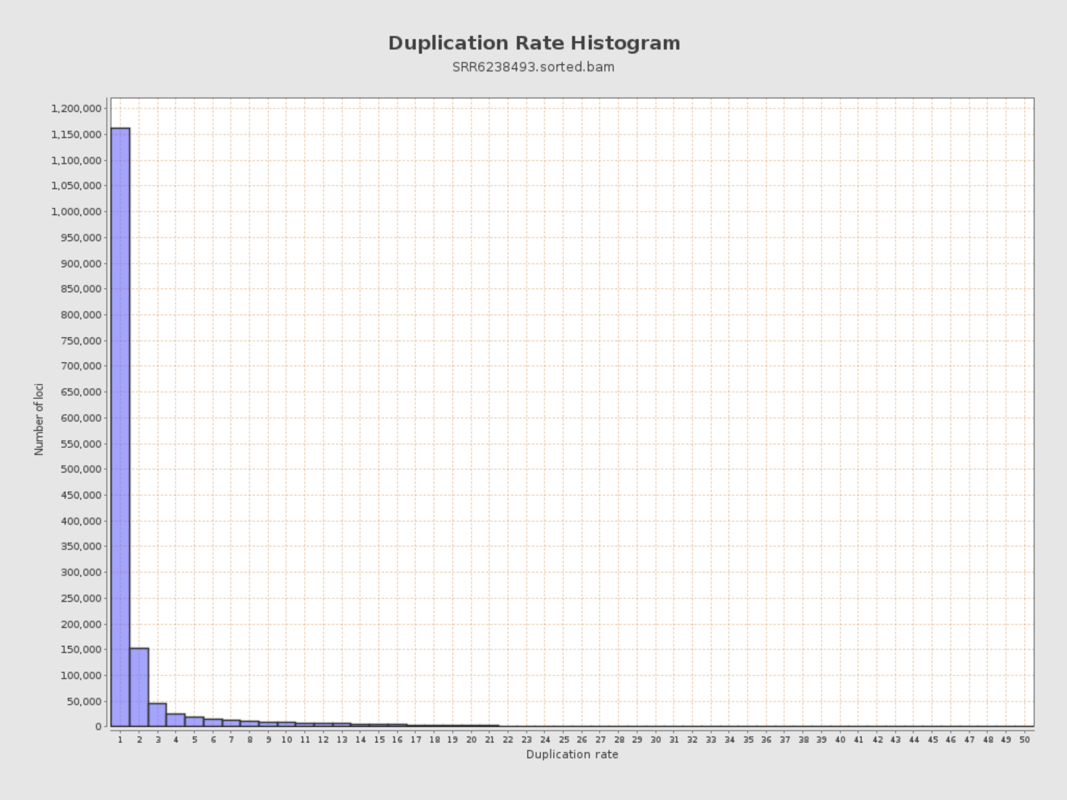
5. Results : Coverage Histogram (0-50X)



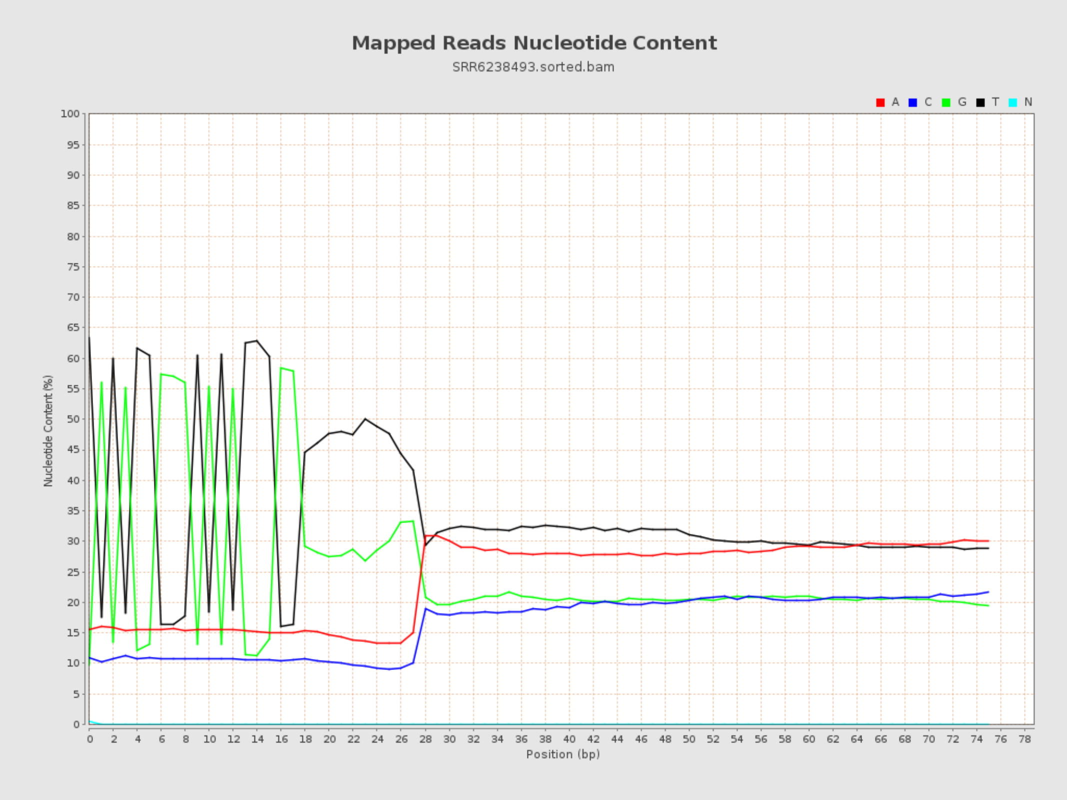
6. Results : Genome Fraction Coverage



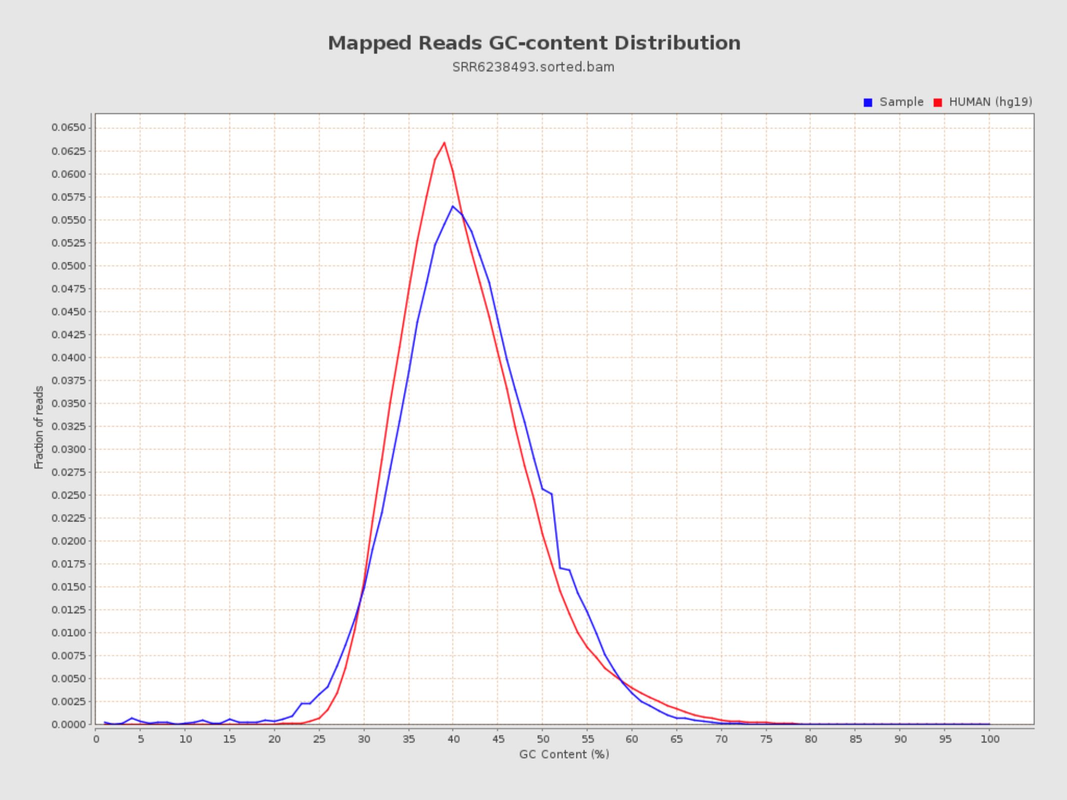
7. Results : Duplication Rate Histogram



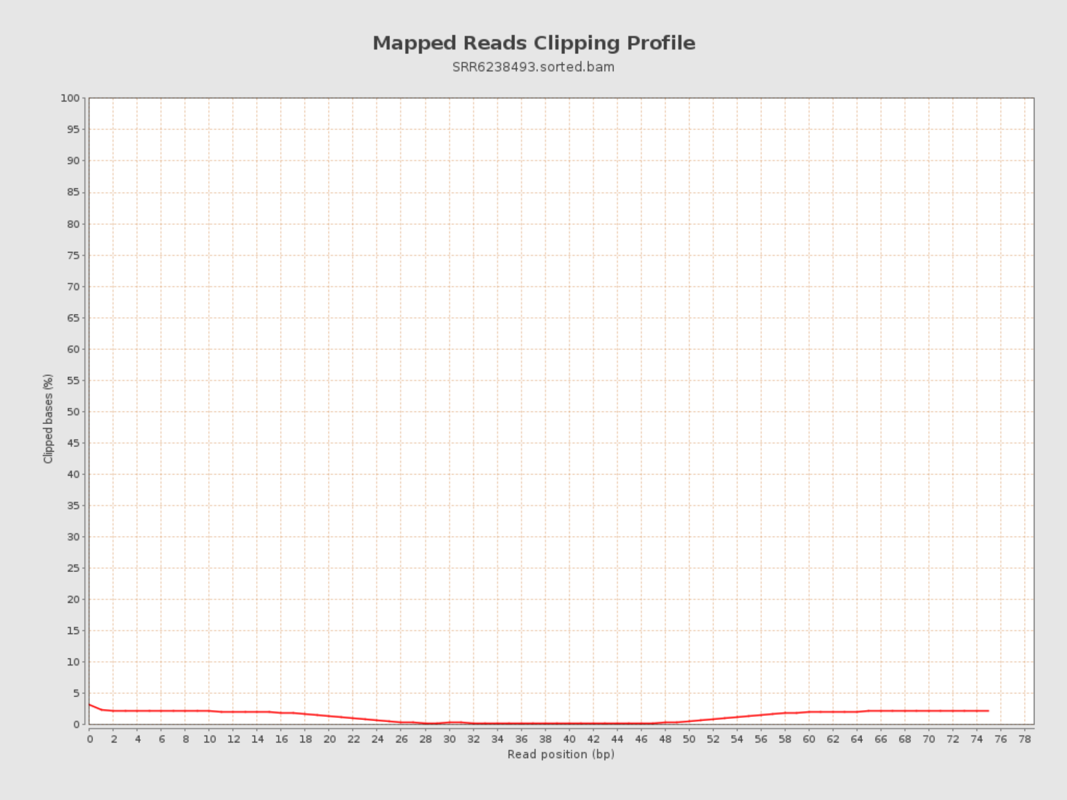
8. Results : Mapped Reads Nucleotide Content



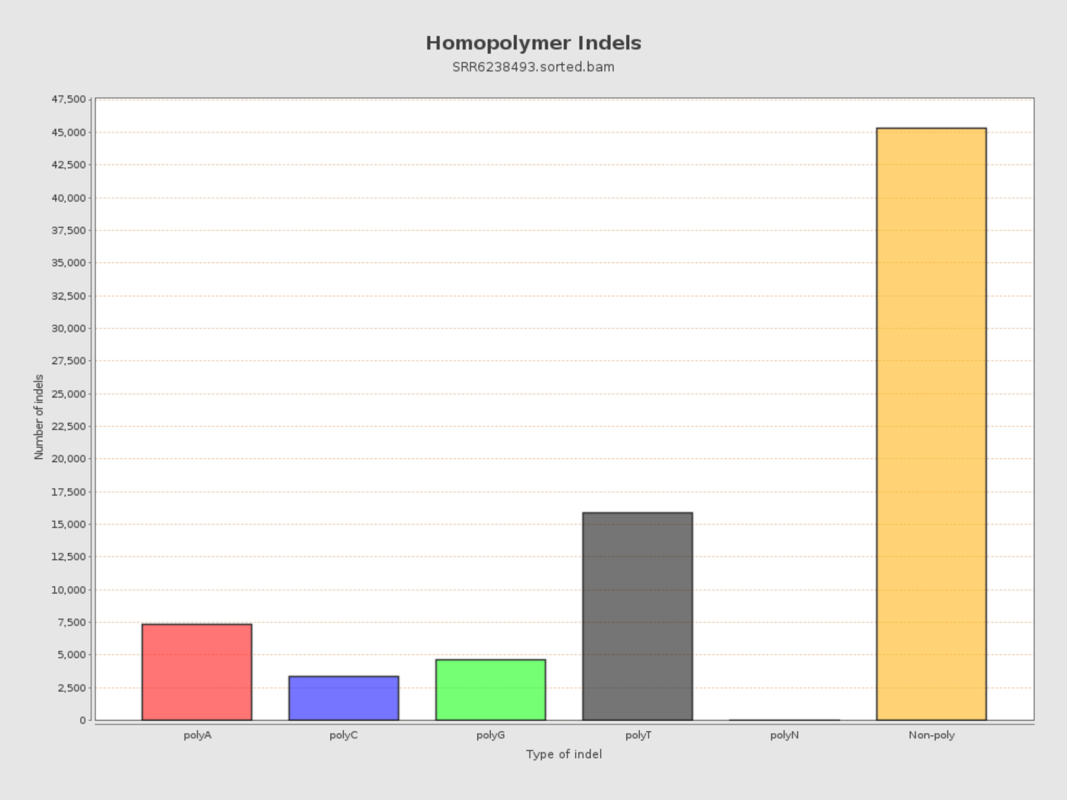
9. Results : Mapped Reads GC-content Distribution



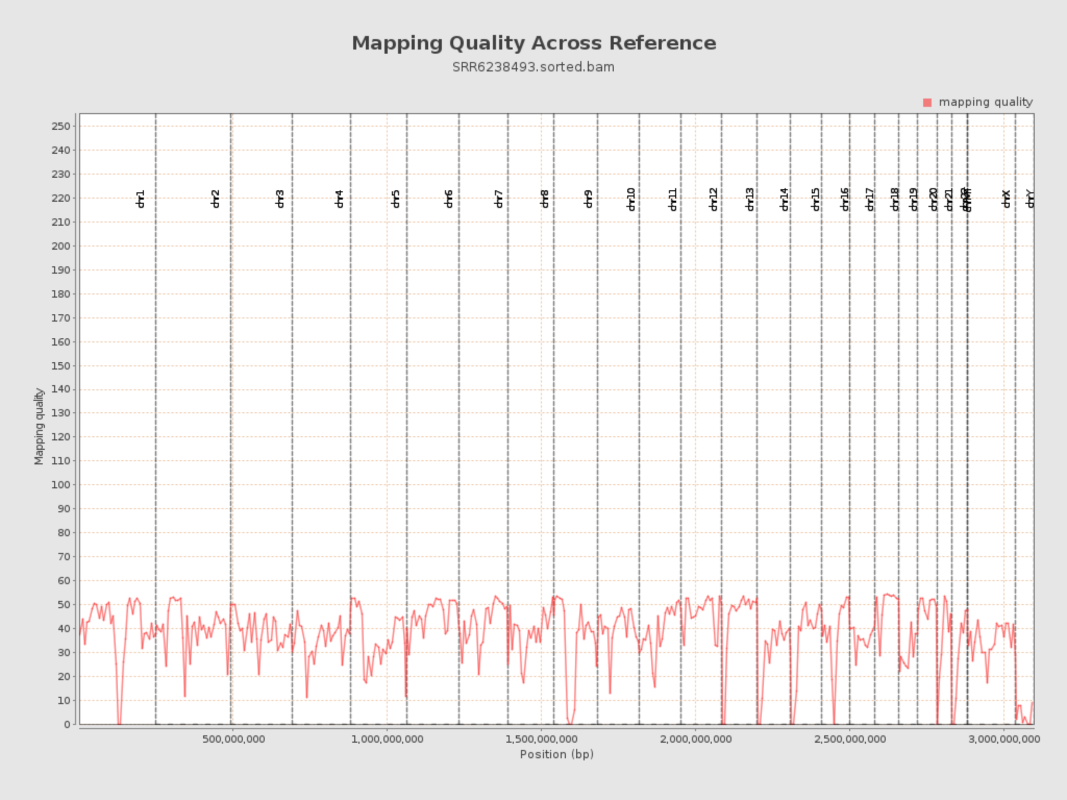
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram