Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:22:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238501.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_SRR6238501 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238501.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:22:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,915,929
Mapped reads	4,250,671 / 86.47%
Unmapped reads	665,258 / 13.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,907 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,089,025 / 22.15%
Duplication rate	18.77%
Clipped reads	2,829,860 / 57.57%

2.2. ACGT Content

Number/percentage of A's	64,227,022 / 24.81%
Number/percentage of C's	45,317,264 / 17.5%
Number/percentage of T's	87,245,680 / 33.7%
Number/percentage of G's	62,083,141 / 23.98%
Number/percentage of N's	17,078 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0837

Standard Deviation	1.1578

2.4. Mapping Quality

Mean Mapping Quality	42.26

2.5. Mismatches and indels

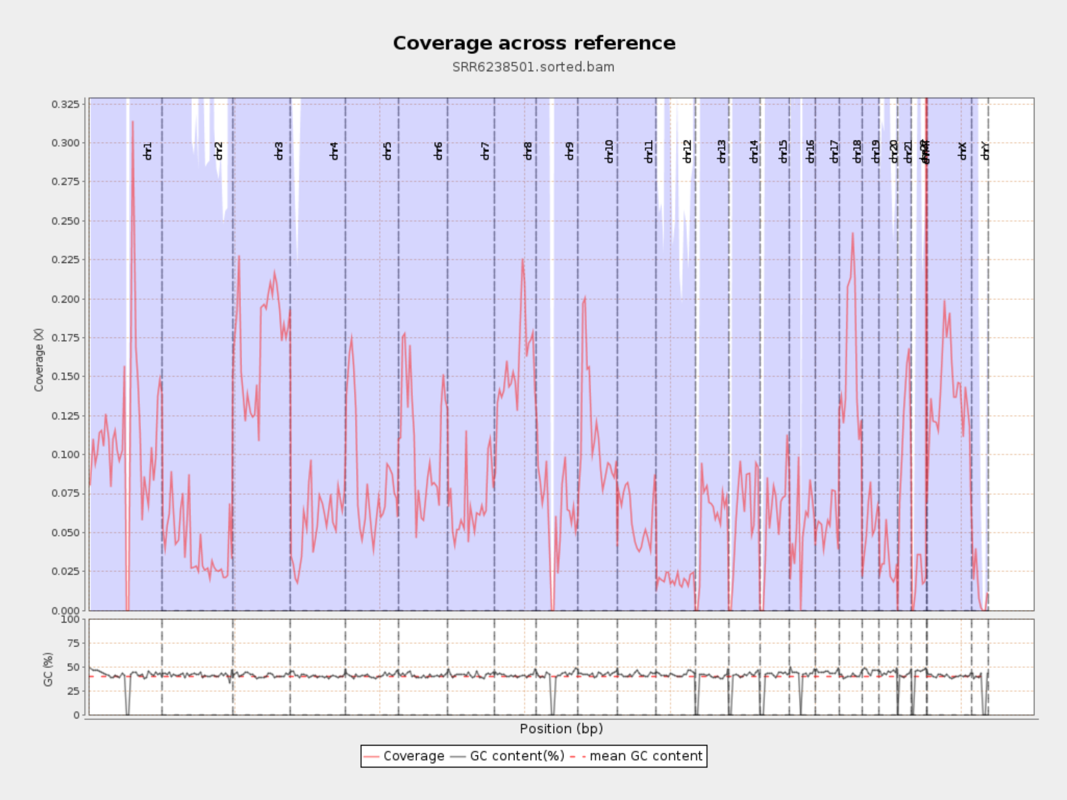
General error rate	0.69%
Mismatches	1,743,368
Insertions	17,533
Mapped reads with at least one insertion	0.41%
Deletions	106,396
Mapped reads with at least one deletion	2.47%
Homopolymer indels	40.78%

2.6. Chromosome stats

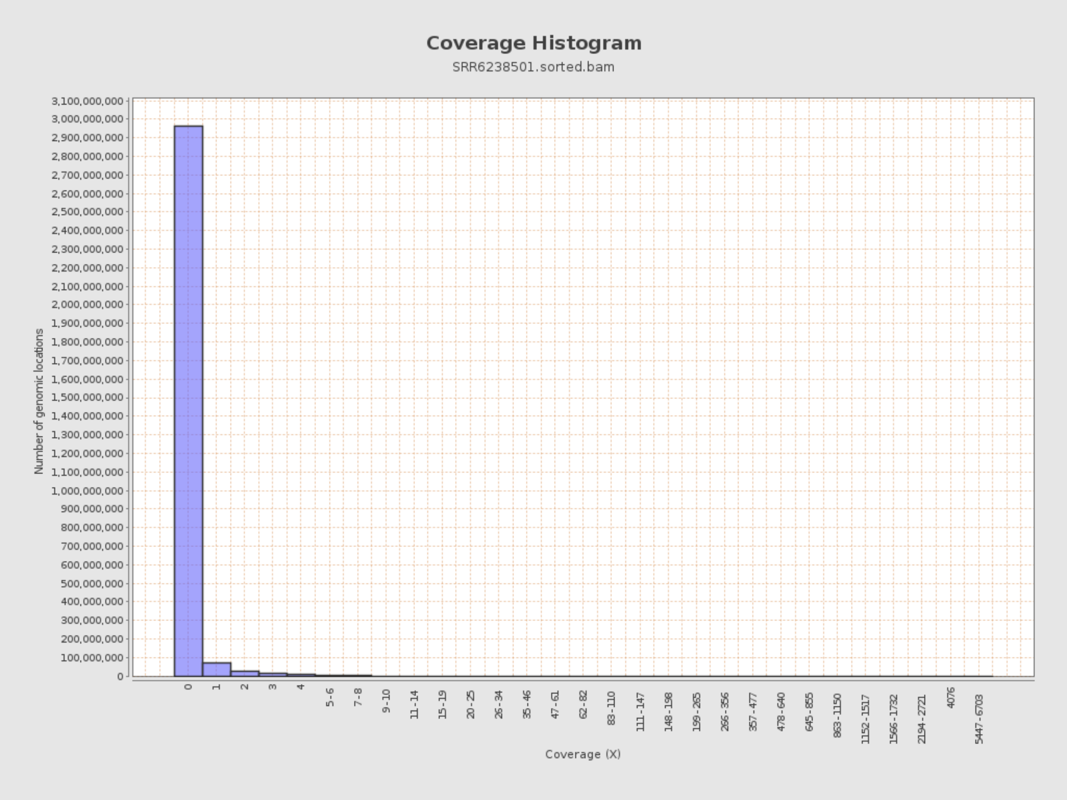
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27106351	0.1088	1.4301
chr2	243199373	10135717	0.0417	2.9241
chr3	198022430	34067919	0.172	0.7555
chr4	191154276	10659679	0.0558	0.4317
chr5	180915260	15388149	0.0851	0.5263
chr6	171115067	18278882	0.1068	1.0341
chr7	159138663	10571858	0.0664	0.9227

chr8	146364022	22713163	0.1552	1.0008
chr9	141213431	8418750	0.0596	0.5602
chr10	135534747	15368696	0.1134	0.8552
chr11	135006516	8019913	0.0594	0.483
chr12	133851895	2643222	0.0197	0.2854
chr13	115169878	6777612	0.0588	0.7194
chr14	107349540	6704020	0.0625	0.468
chr15	102531392	6197084	0.0604	0.673
chr16	90354753	4842409	0.0536	0.5729
chr17	81195210	4540437	0.0559	0.4283
chr18	78077248	12780547	0.1637	2.1479
chr19	59128983	3325629	0.0562	0.9437
chr20	63025520	1938219	0.0308	0.3461
chr21	48129895	5278599	0.1097	0.6112
chr22	51304566	972151	0.0189	0.2284
chrMT	16571	47335	2.8565	3.3216
chrX	155270560	21466909	0.1383	0.7087
chrY	59373566	827215	0.0139	0.4391

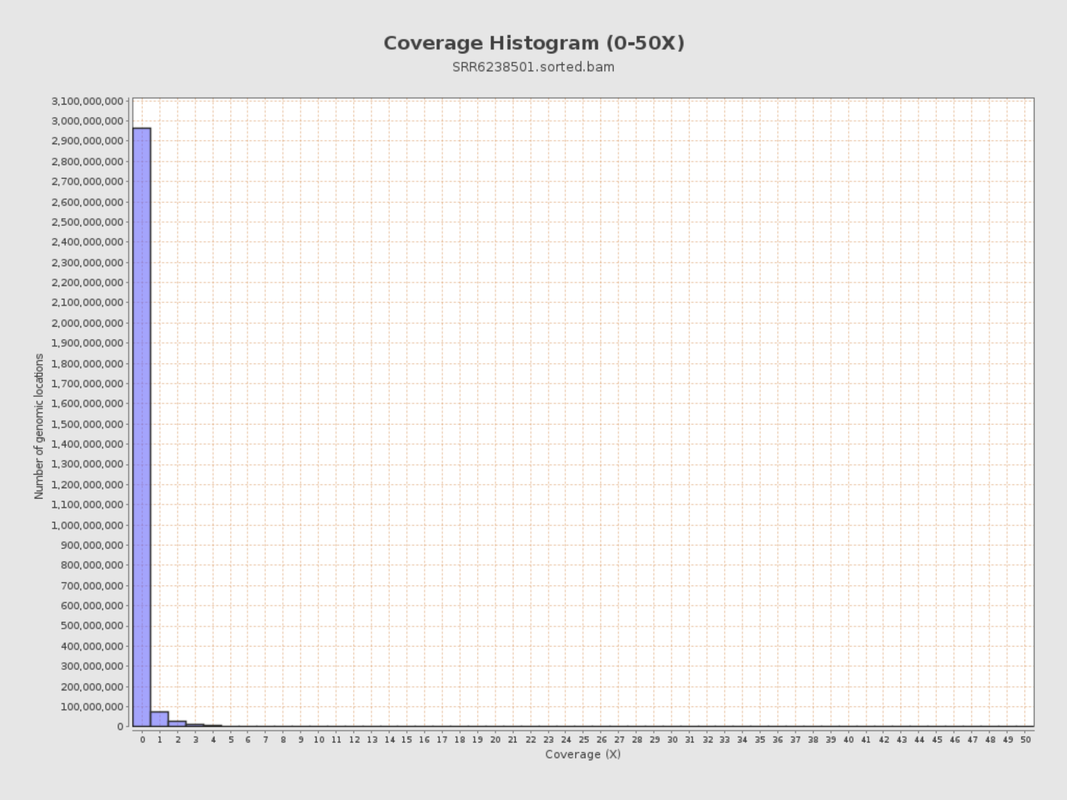
3. Results : Coverage across reference



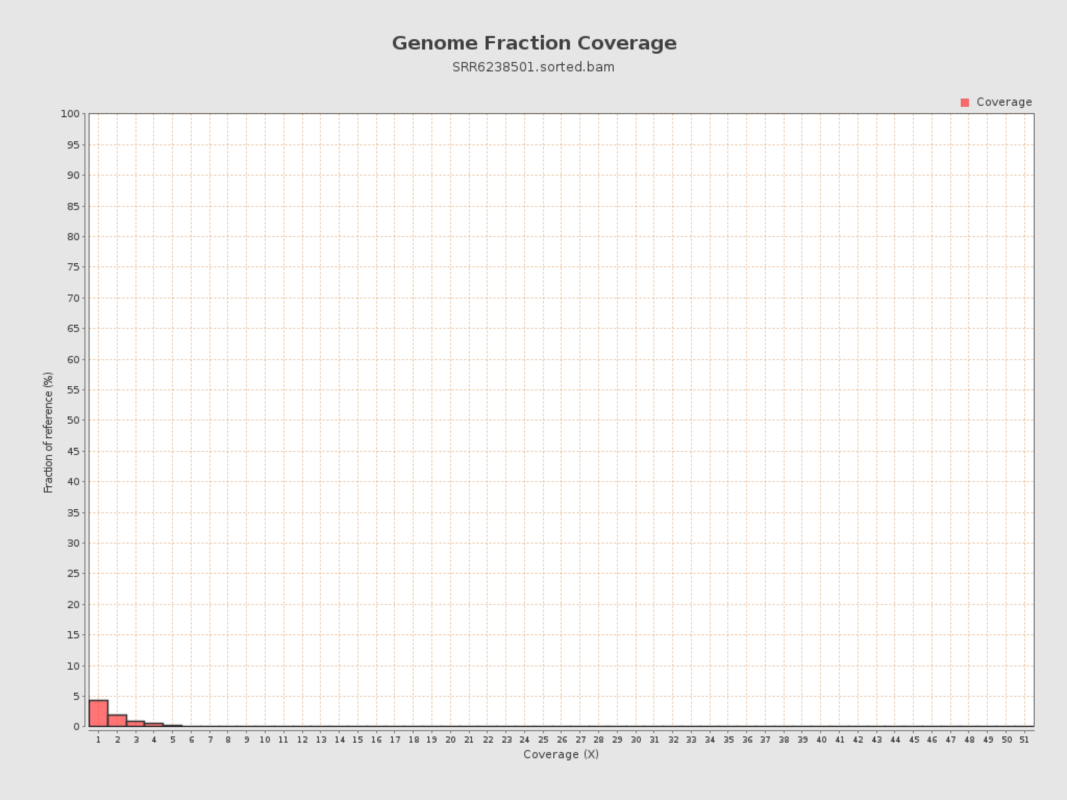
4. Results : Coverage Histogram



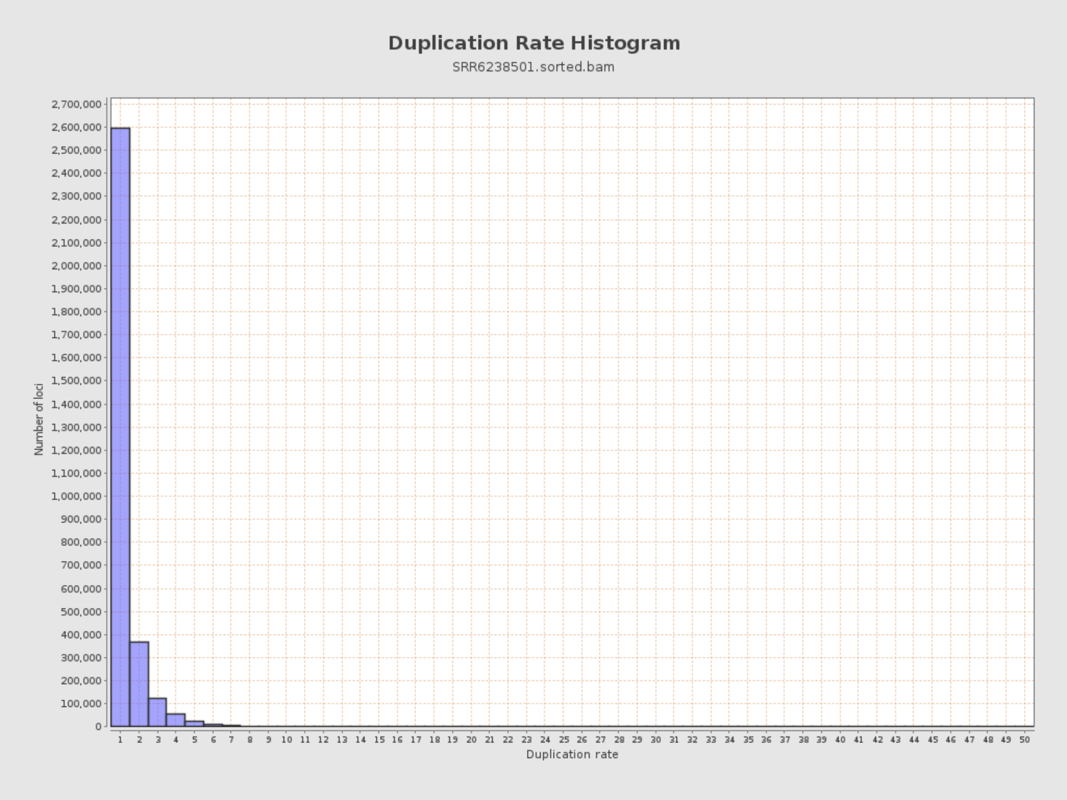
5. Results : Coverage Histogram (0-50X)



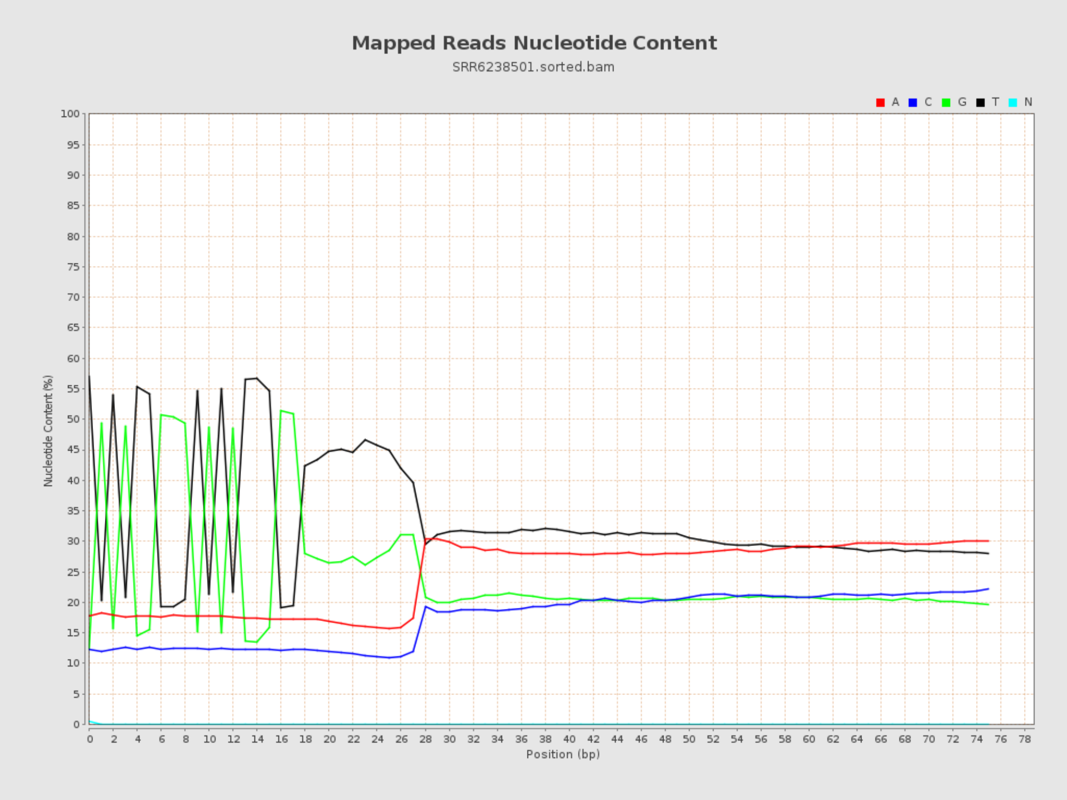
6. Results : Genome Fraction Coverage



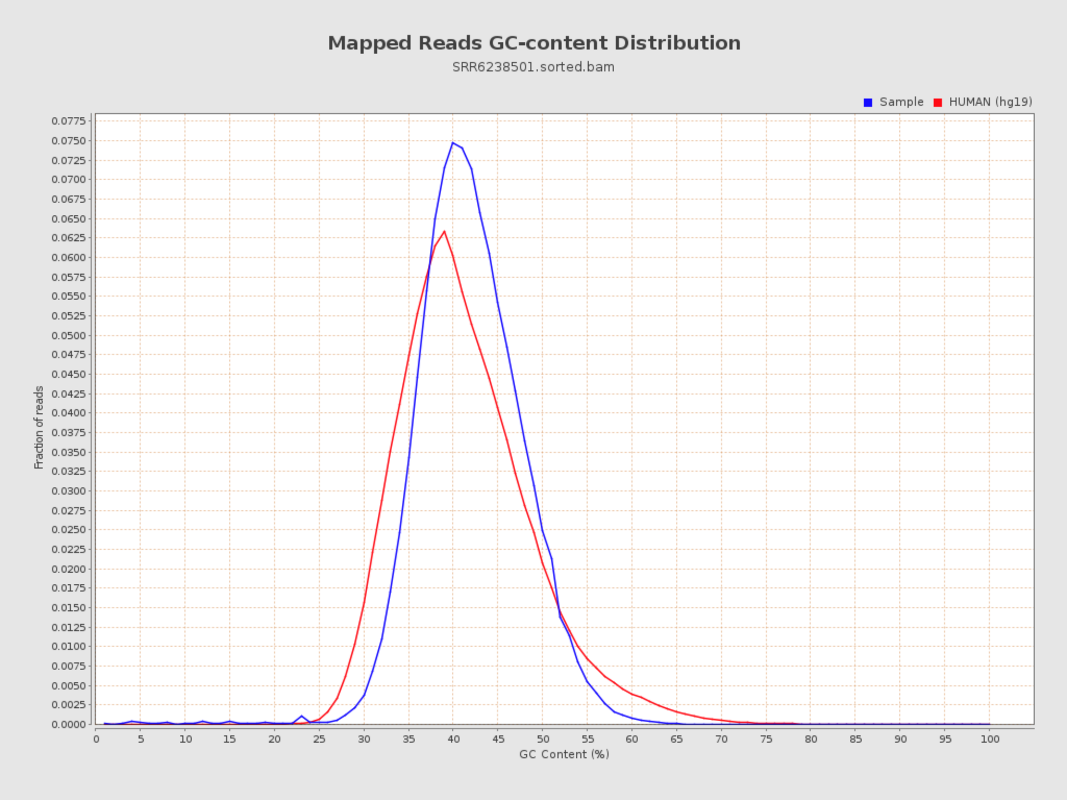
7. Results : Duplication Rate Histogram



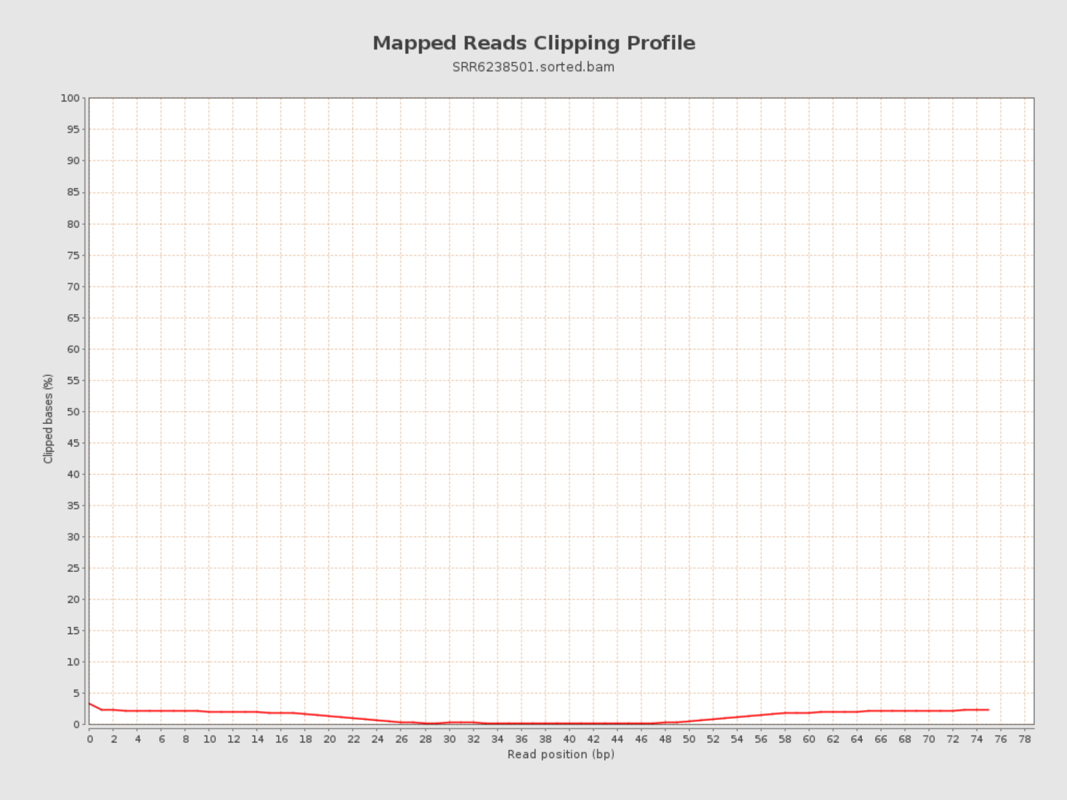
8. Results : Mapped Reads Nucleotide Content



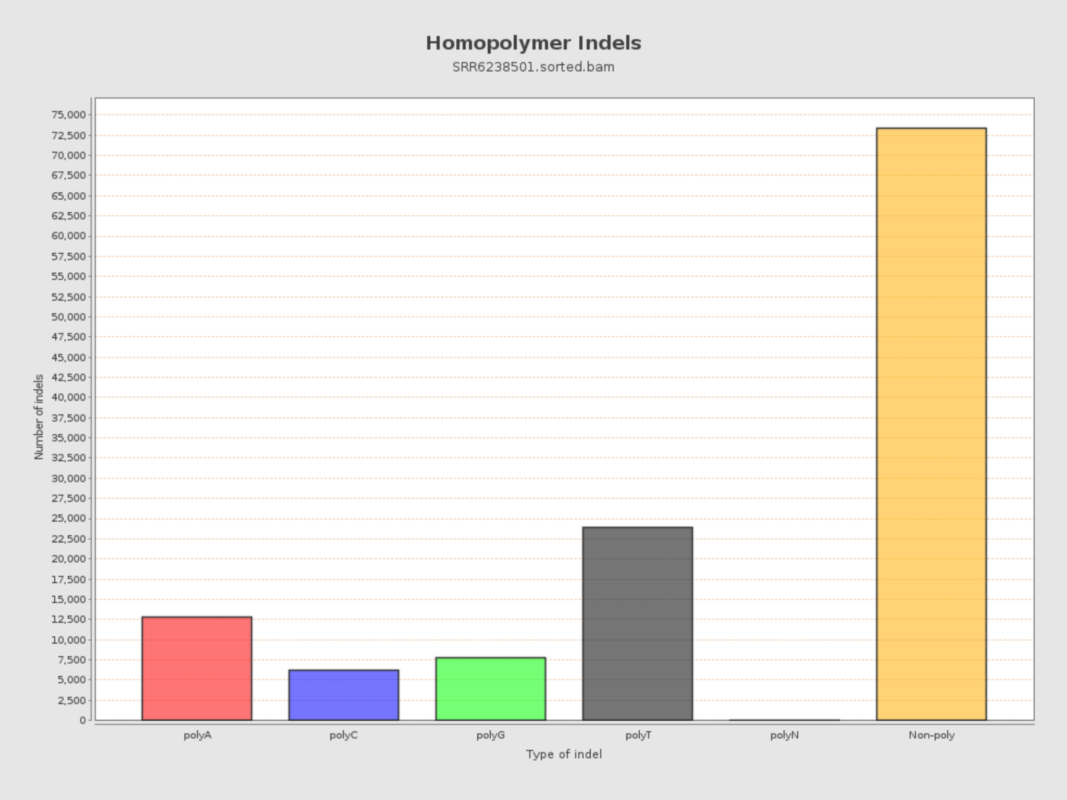
9. Results : Mapped Reads GC-content Distribution



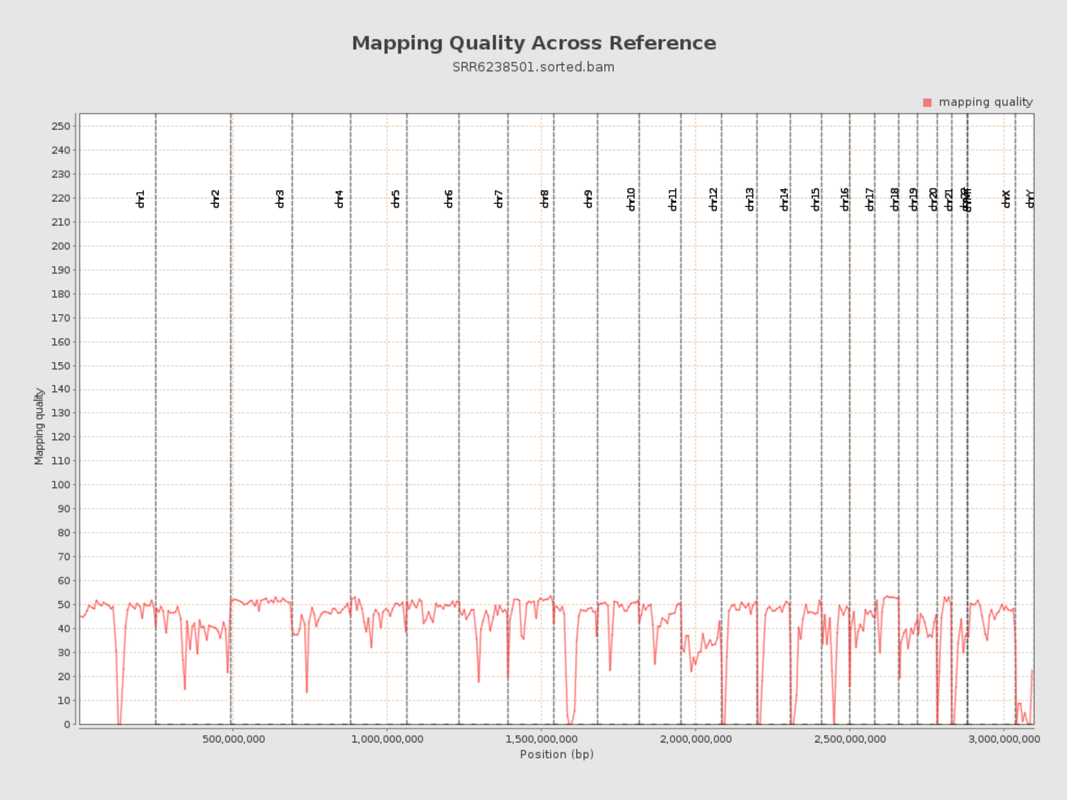
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram