Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:22:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238644.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_SRR6238644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238644.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:22:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,971,356
Mapped reads	2,494,822 / 83.96%
Unmapped reads	476,534 / 16.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,510 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	626,597 / 21.09%
Duplication rate	18.6%
Clipped reads	1,698,308 / 57.16%

2.2. ACGT Content

Number/percentage of A's	37,826,914 / 25.06%
Number/percentage of C's	26,607,921 / 17.63%
Number/percentage of T's	50,181,147 / 33.24%
Number/percentage of G's	36,330,092 / 24.07%
Number/percentage of N's	6,989 / 0%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.6236

2.4. Mapping Quality

Mean Mapping Quality	40

2.5. Mismatches and indels

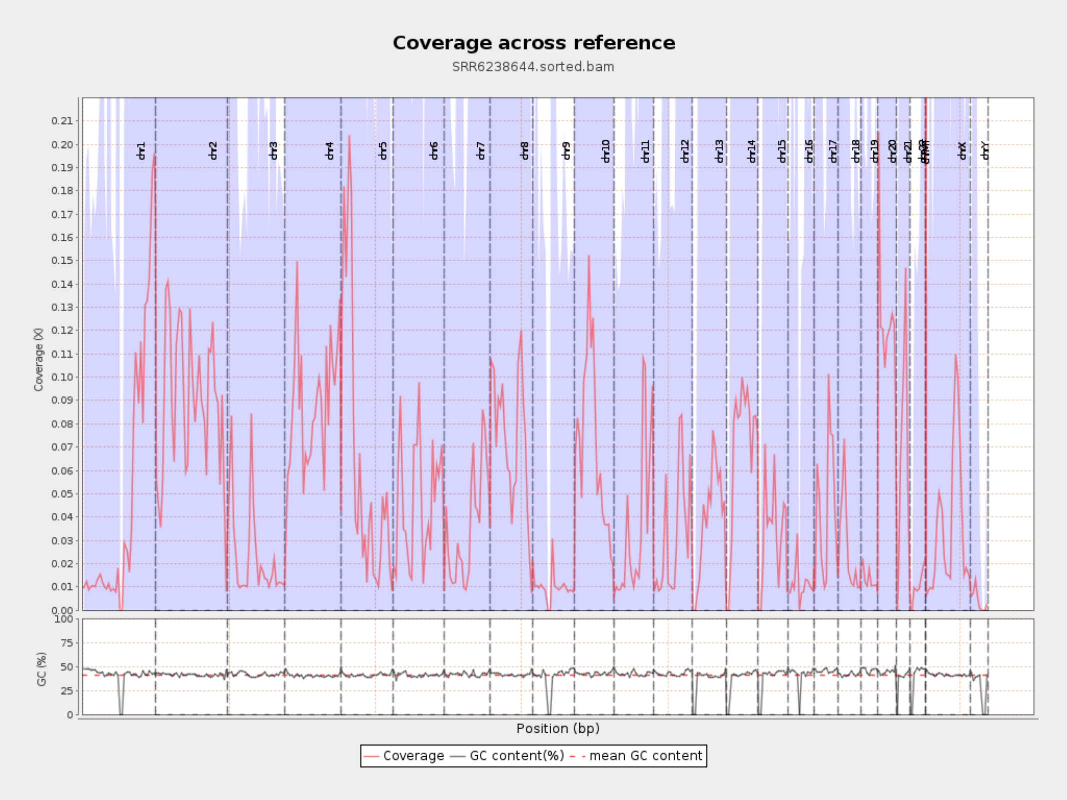
General error rate	0.69%
Mismatches	1,024,758
Insertions	8,815
Mapped reads with at least one insertion	0.35%
Deletions	59,179
Mapped reads with at least one deletion	2.34%
Homopolymer indels	41.07%

2.6. Chromosome stats

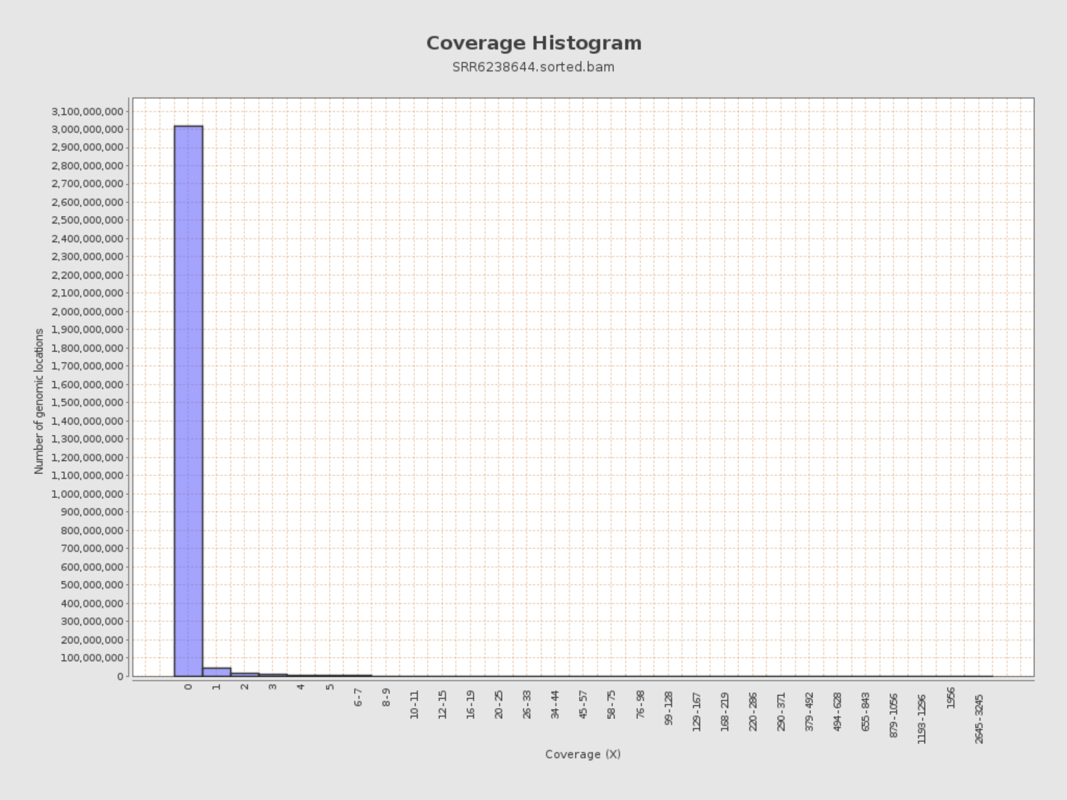
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12271845	0.0492	0.4311
chr2	243199373	21610420	0.0889	1.5486
chr3	198022430	4757634	0.024	0.2792
chr4	191154276	16791769	0.0878	0.5415
chr5	180915260	11171638	0.0618	0.4503
chr6	171115067	7974729	0.0466	0.6104
chr7	159138663	5816721	0.0366	0.3909

chr8	146364022	10554827	0.0721	0.7926
chr9	141213431	1391502	0.0099	0.2767
chr10	135534747	9659359	0.0713	0.4897
chr11	135006516	4780376	0.0354	0.3378
chr12	133851895	4132065	0.0309	0.3285
chr13	115169878	4496496	0.039	0.4387
chr14	107349540	7527583	0.0701	0.5502
chr15	102531392	3356121	0.0327	0.562
chr16	90354753	986924	0.0109	0.2039
chr17	81195210	3680118	0.0453	0.413
chr18	78077248	2172722	0.0278	0.7446
chr19	59128983	796885	0.0135	0.2426
chr20	63025520	7925451	0.1257	0.6481
chr21	48129895	3015914	0.0627	0.4539
chr22	51304566	518901	0.0101	0.1664
chrMT	16571	30696	1.8524	2.4397
chrX	155270560	5372803	0.0346	0.3506
chrY	59373566	259615	0.0044	0.2001

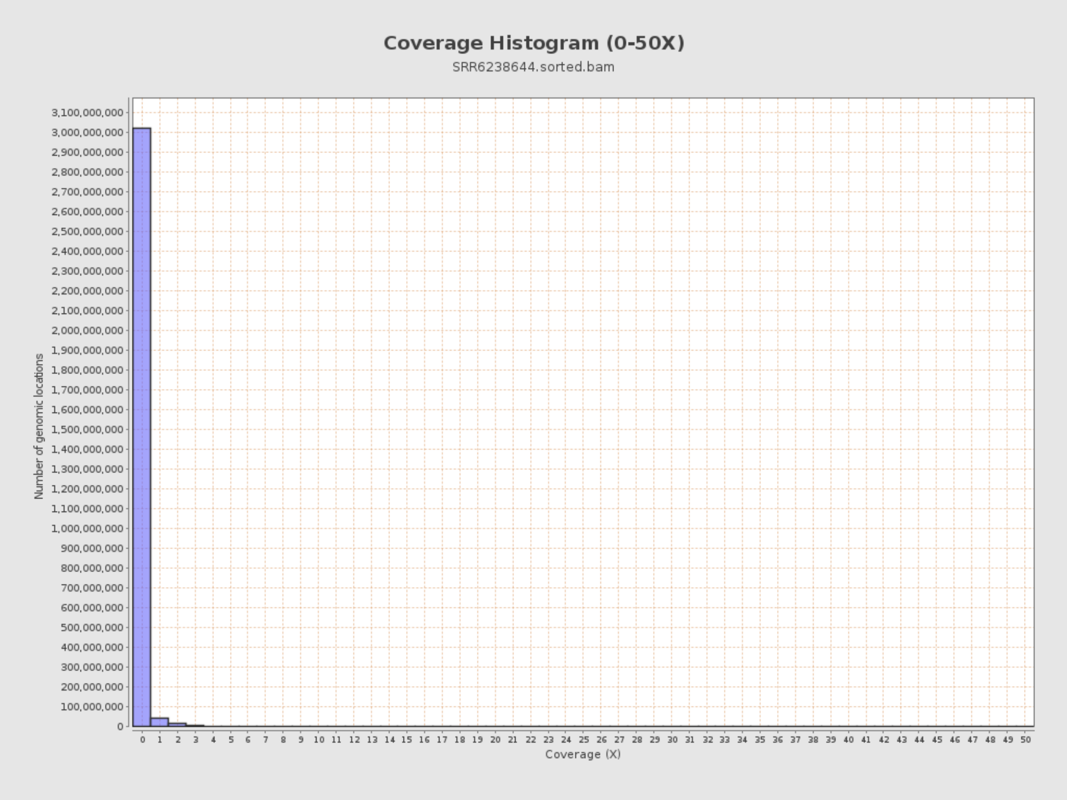
3. Results : Coverage across reference



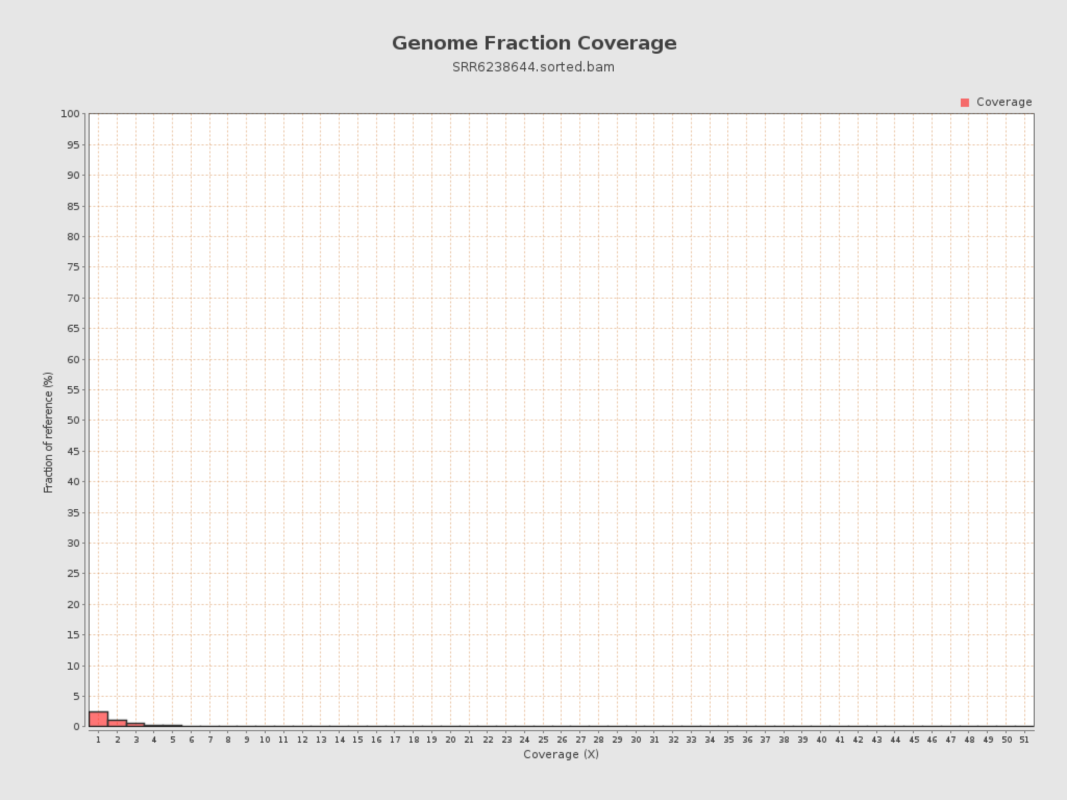
4. Results : Coverage Histogram



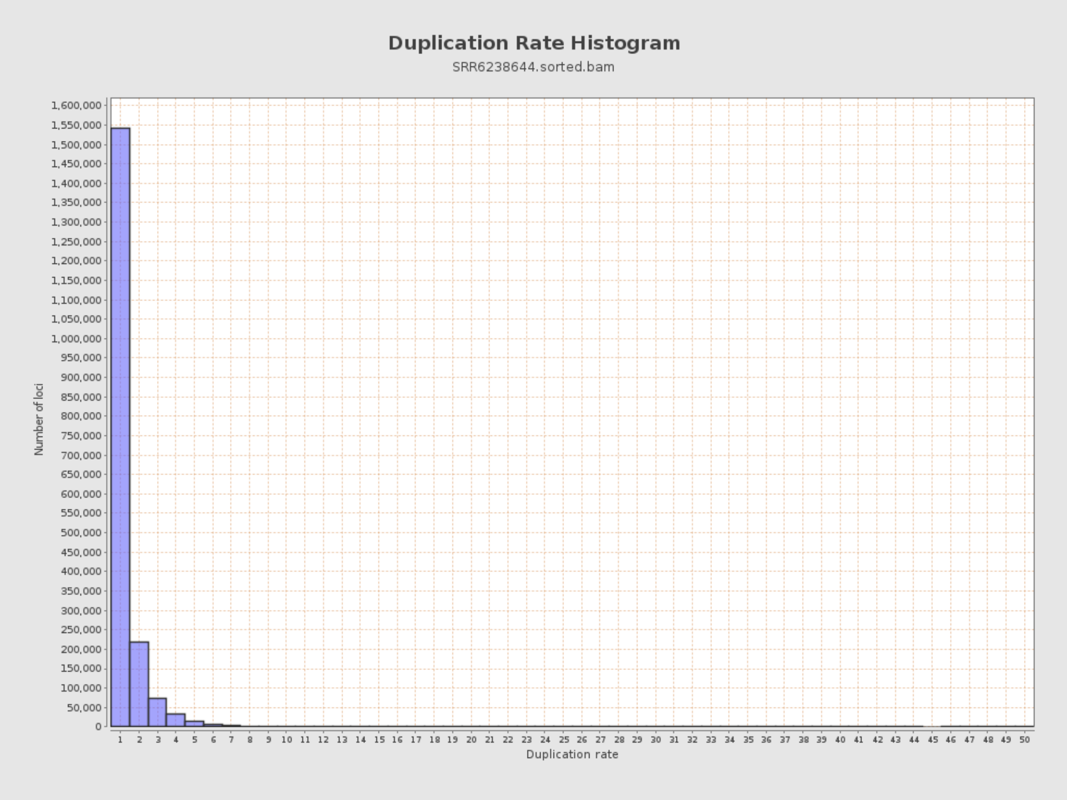
5. Results : Coverage Histogram (0-50X)



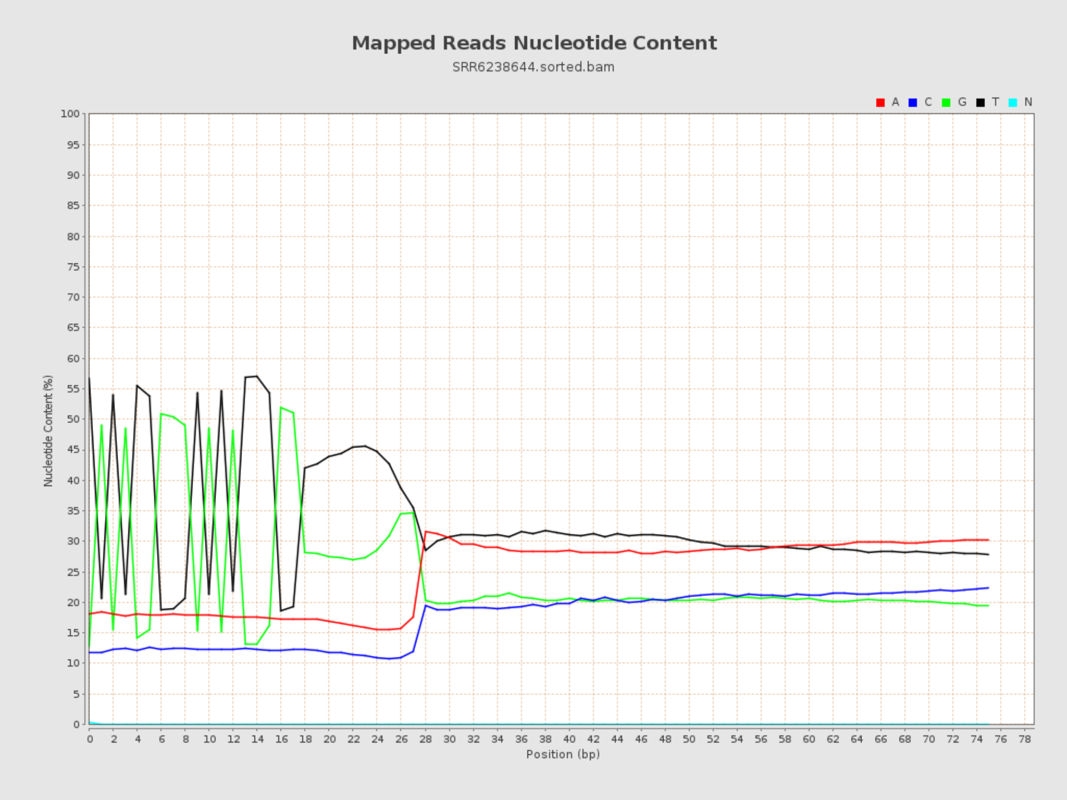
6. Results : Genome Fraction Coverage



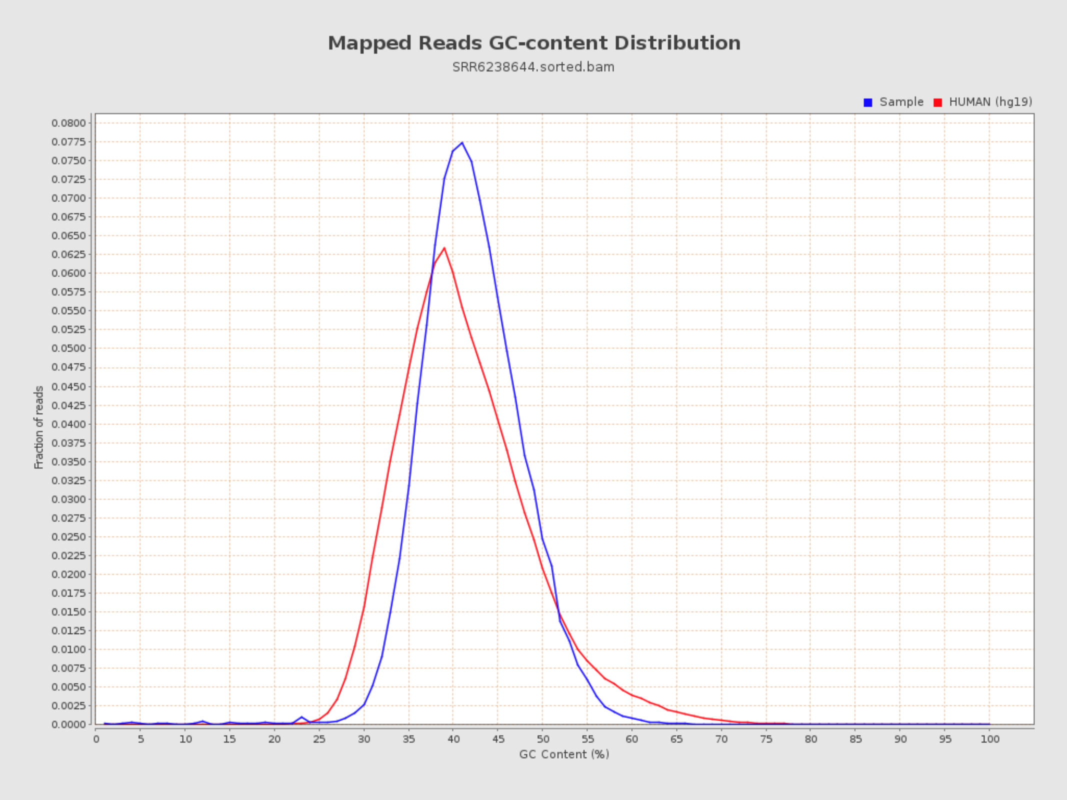
7. Results : Duplication Rate Histogram



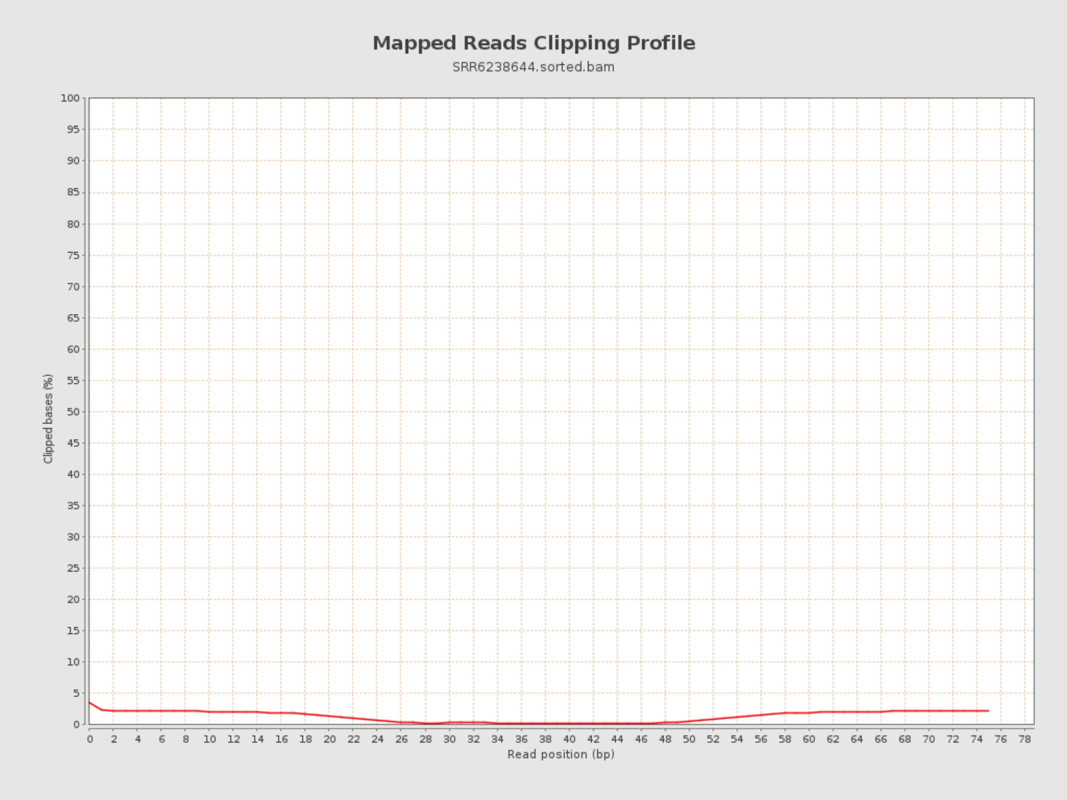
8. Results : Mapped Reads Nucleotide Content



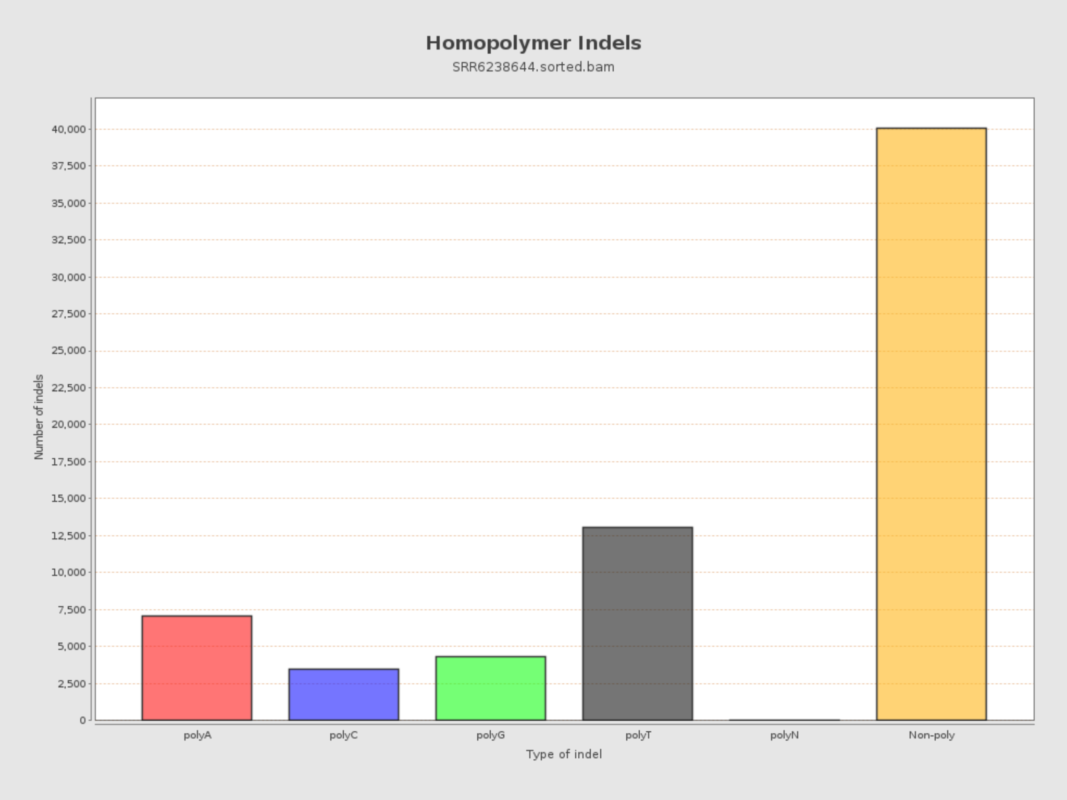
9. Results : Mapped Reads GC-content Distribution



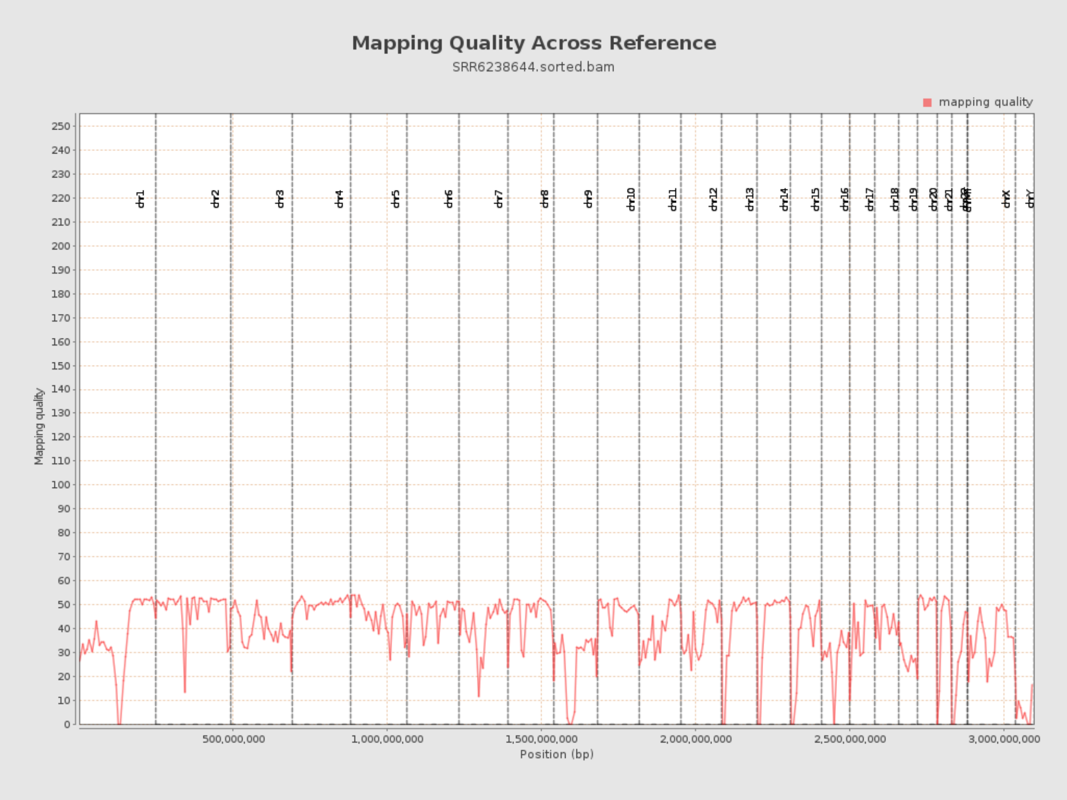
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram