Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:14:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238499.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_SRR6238499 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238499.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:14:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238499.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,880,970
Mapped reads	2,510,218 / 87.13%
Unmapped reads	370,752 / 12.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,492 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	790,438 / 27.44%
Duplication rate	20.77%
Clipped reads	1,710,612 / 59.38%

2.2. ACGT Content

Number/percentage of A's	37,219,475 / 24.52%
Number/percentage of C's	26,406,647 / 17.4%
Number/percentage of T's	51,484,854 / 33.92%
Number/percentage of G's	36,645,834 / 24.15%
Number/percentage of N's	9,621 / 0.01%
GC Percentage	41.55%

2.3. Coverage

Mean	0.049

Standard Deviation	0.8497

2.4. Mapping Quality

Mean Mapping Quality	43.05

2.5. Mismatches and indels

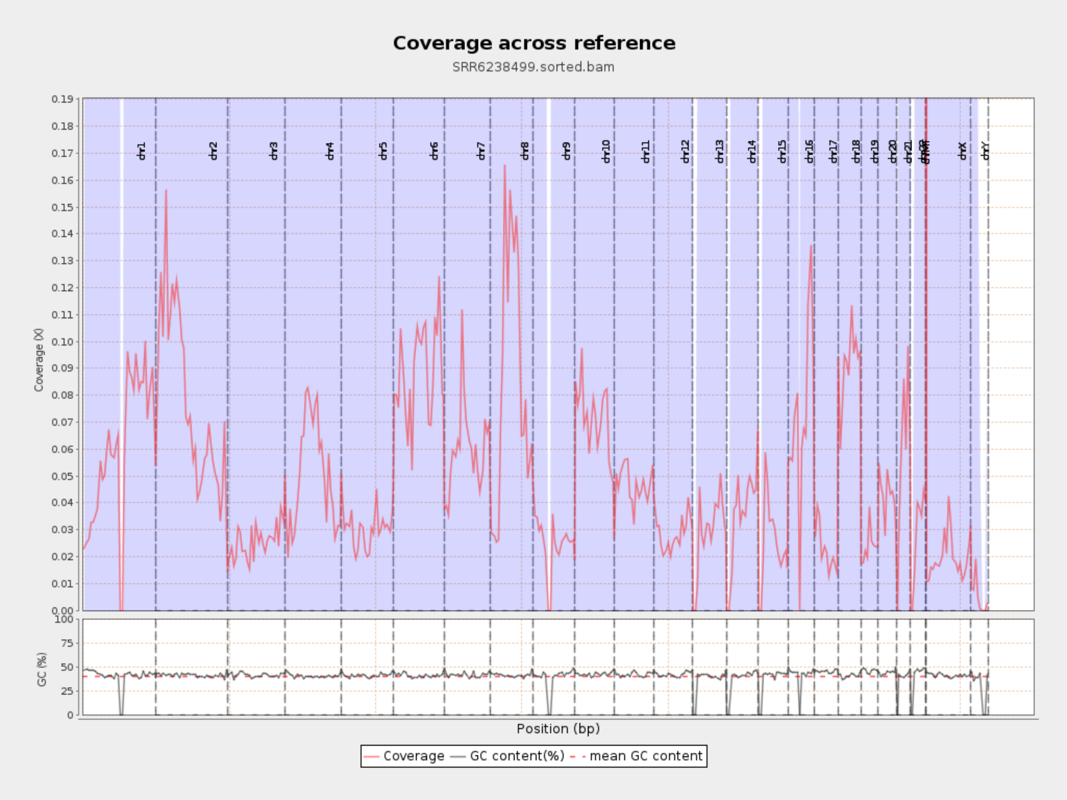
General error rate	0.6%
Mismatches	892,423
Insertions	9,803
Mapped reads with at least one insertion	0.39%
Deletions	43,783
Mapped reads with at least one deletion	1.73%
Homopolymer indels	40.65%

2.6. Chromosome stats

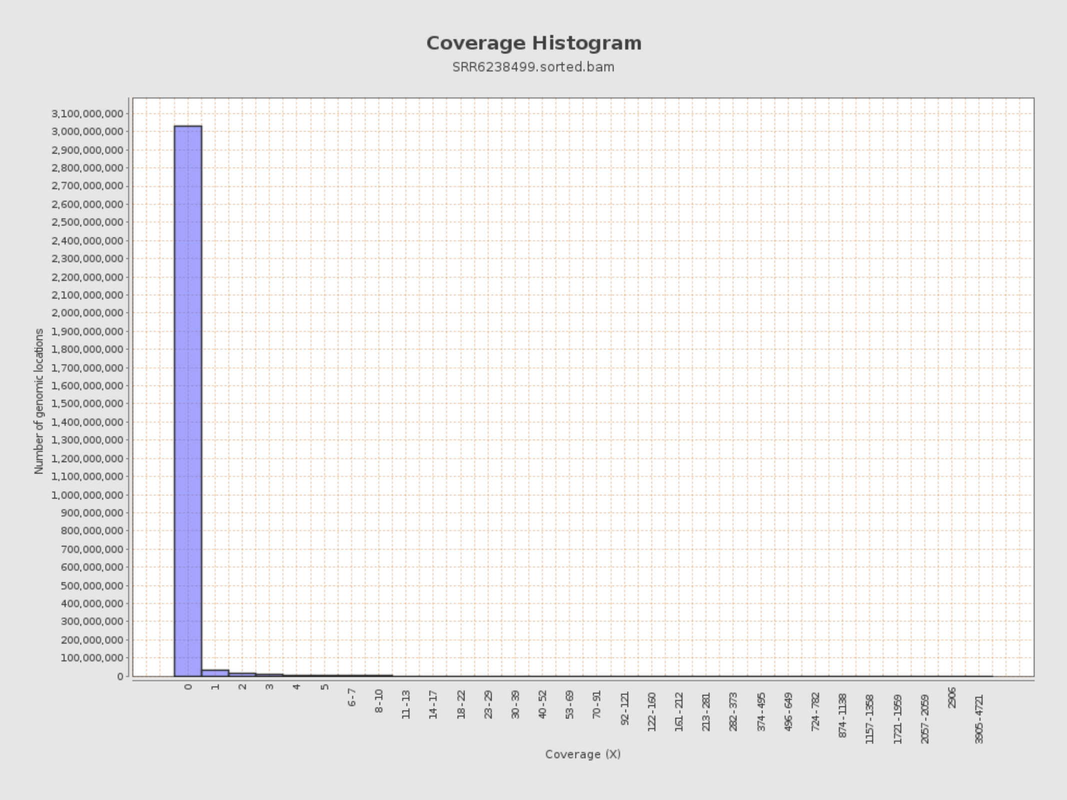
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14829208	0.0595	0.6935
chr2	243199373	18981908	0.0781	2.1434
chr3	198022430	5048512	0.0255	0.3513
chr4	191154276	9712999	0.0508	0.4615
chr5	180915260	5488099	0.0303	0.3606
chr6	171115067	15111442	0.0883	0.9167
chr7	159138663	9613169	0.0604	0.8895

chr8	146364022	12652230	0.0864	0.7311
chr9	141213431	3493590	0.0247	0.3857
chr10	135534747	9742456	0.0719	0.5943
chr11	135006516	6276820	0.0465	0.4595
chr12	133851895	3859339	0.0288	0.3616
chr13	115169878	3386377	0.0294	0.5799
chr14	107349540	3758890	0.035	0.3956
chr15	102531392	2592054	0.0253	0.499
chr16	90354753	6493082	0.0719	0.5913
chr17	81195210	1851846	0.0228	0.3107
chr18	78077248	7112091	0.0911	1.8212
chr19	59128983	1435257	0.0243	0.5052
chr20	63025520	2718523	0.0431	0.4313
chr21	48129895	2812750	0.0584	0.5203
chr22	51304566	1403375	0.0274	0.3504
chrMT	16571	81200	4.9001	4.9897
chrX	155270560	3067701	0.0198	0.2846
chrY	59373566	316154	0.0053	0.3134

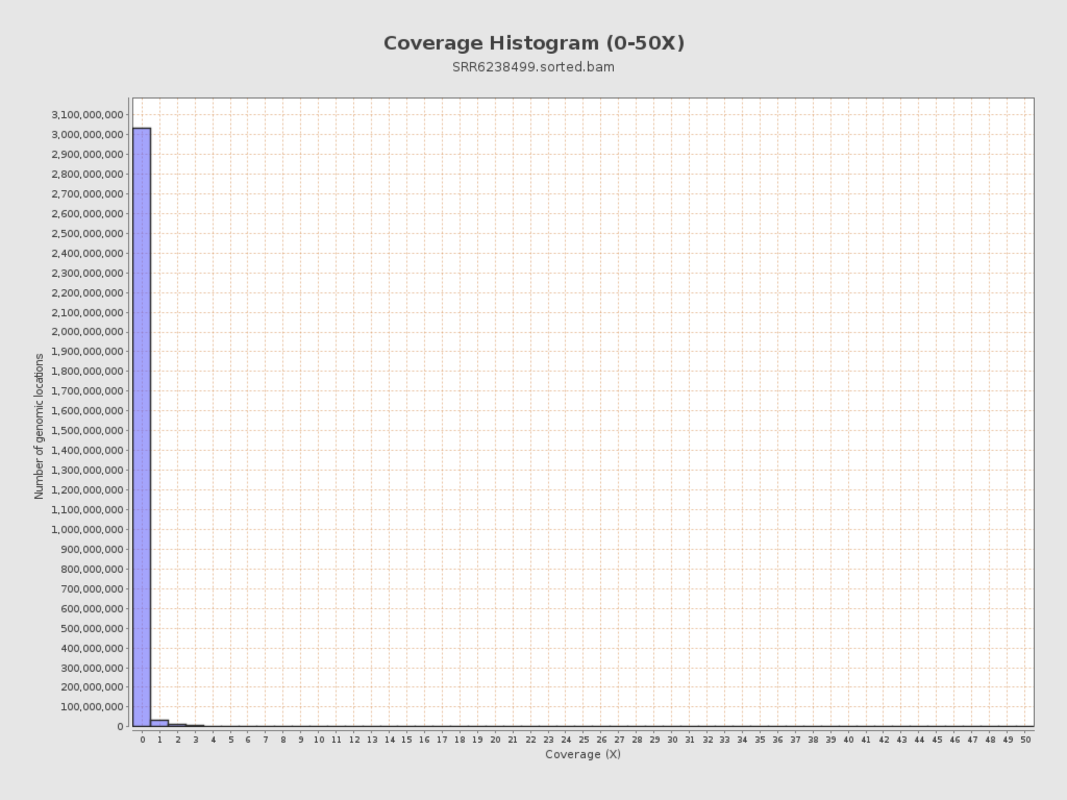
3. Results : Coverage across reference



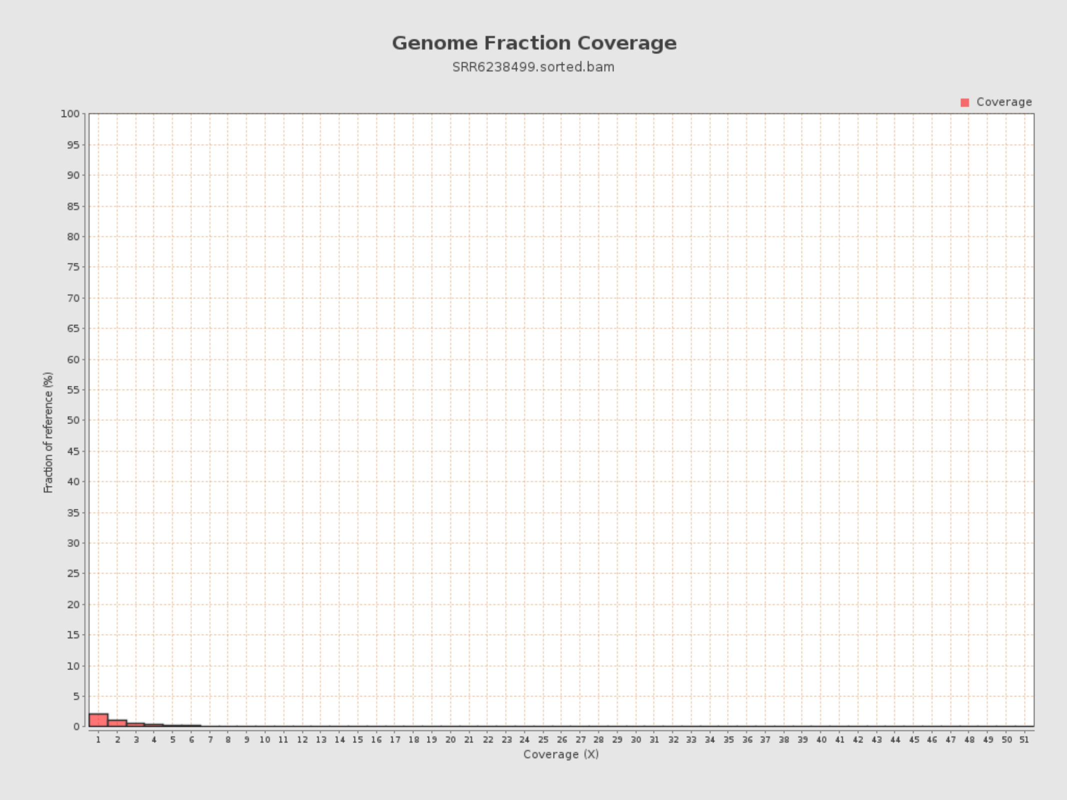
4. Results : Coverage Histogram



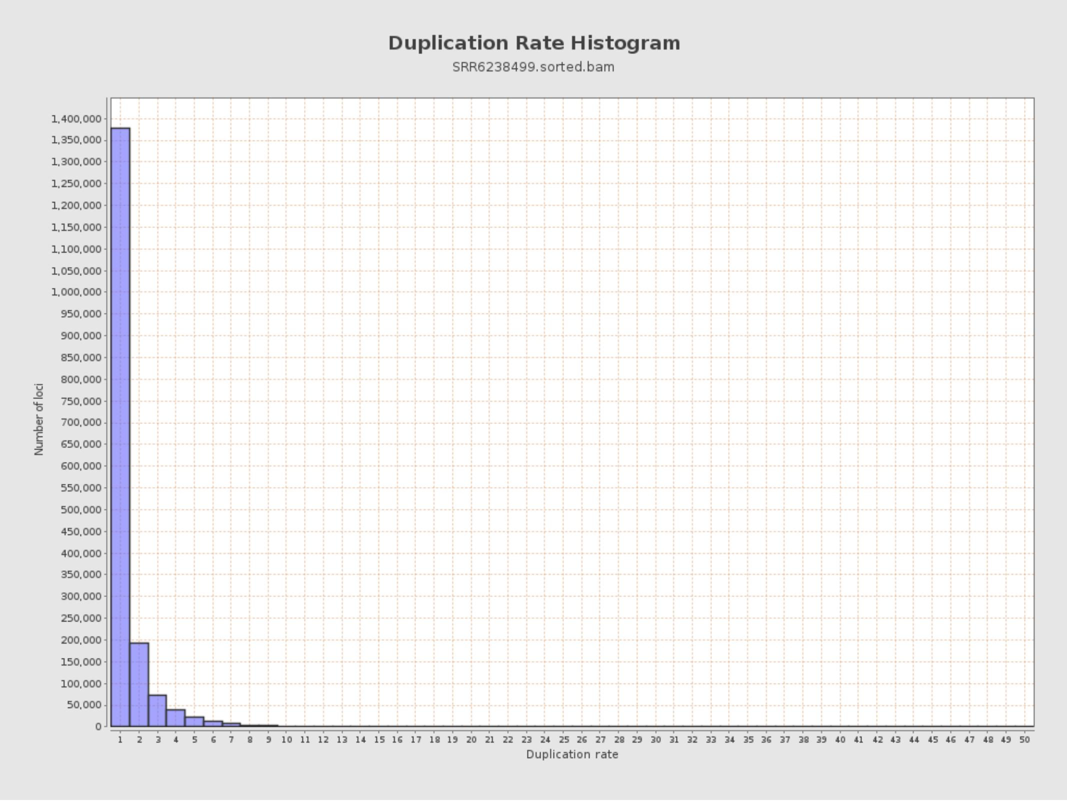
5. Results : Coverage Histogram (0-50X)



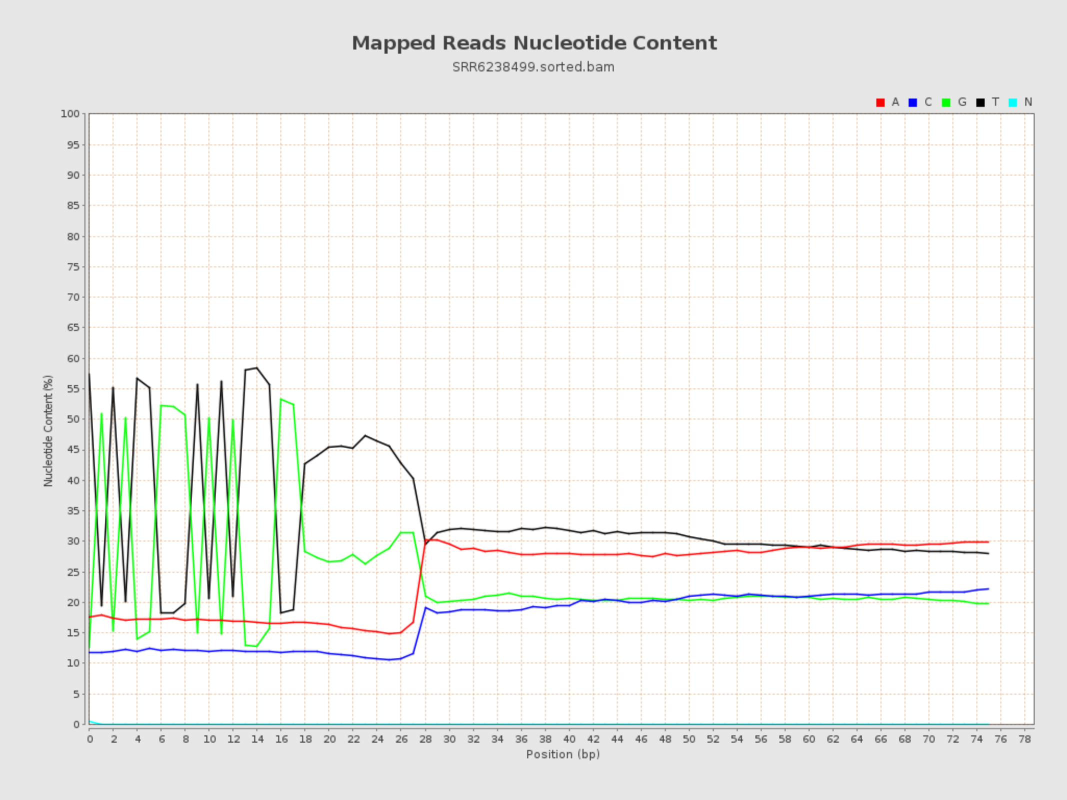
6. Results : Genome Fraction Coverage



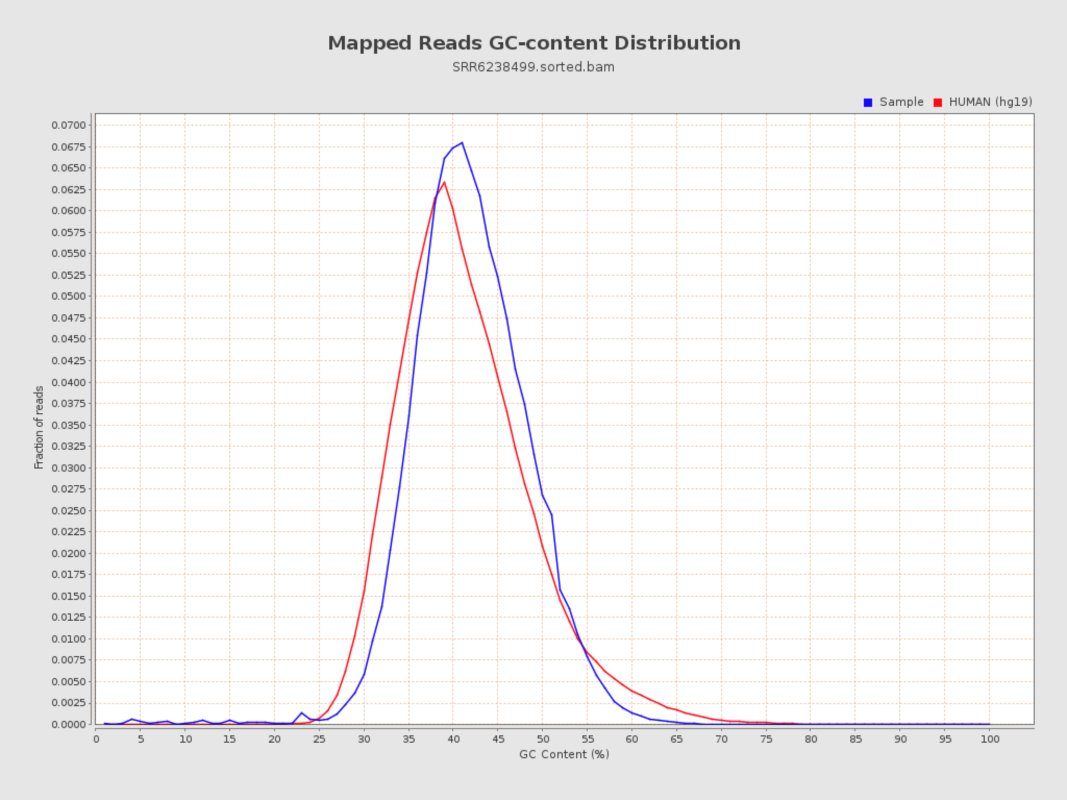
7. Results : Duplication Rate Histogram



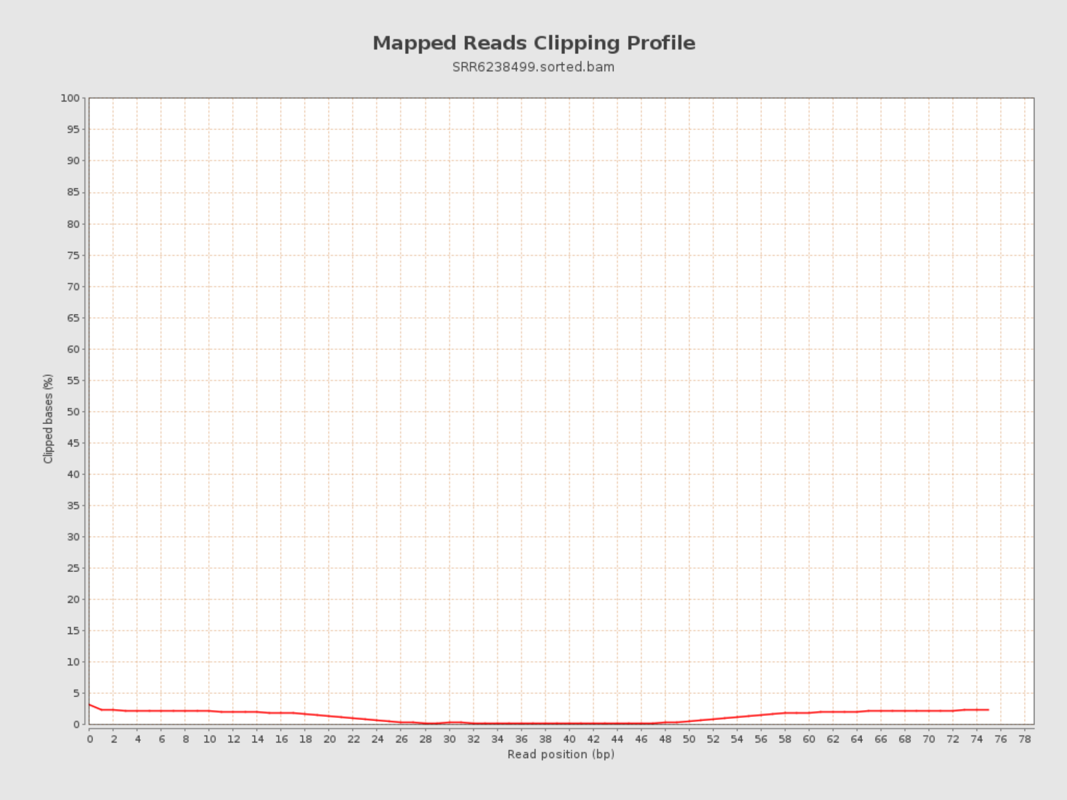
8. Results : Mapped Reads Nucleotide Content



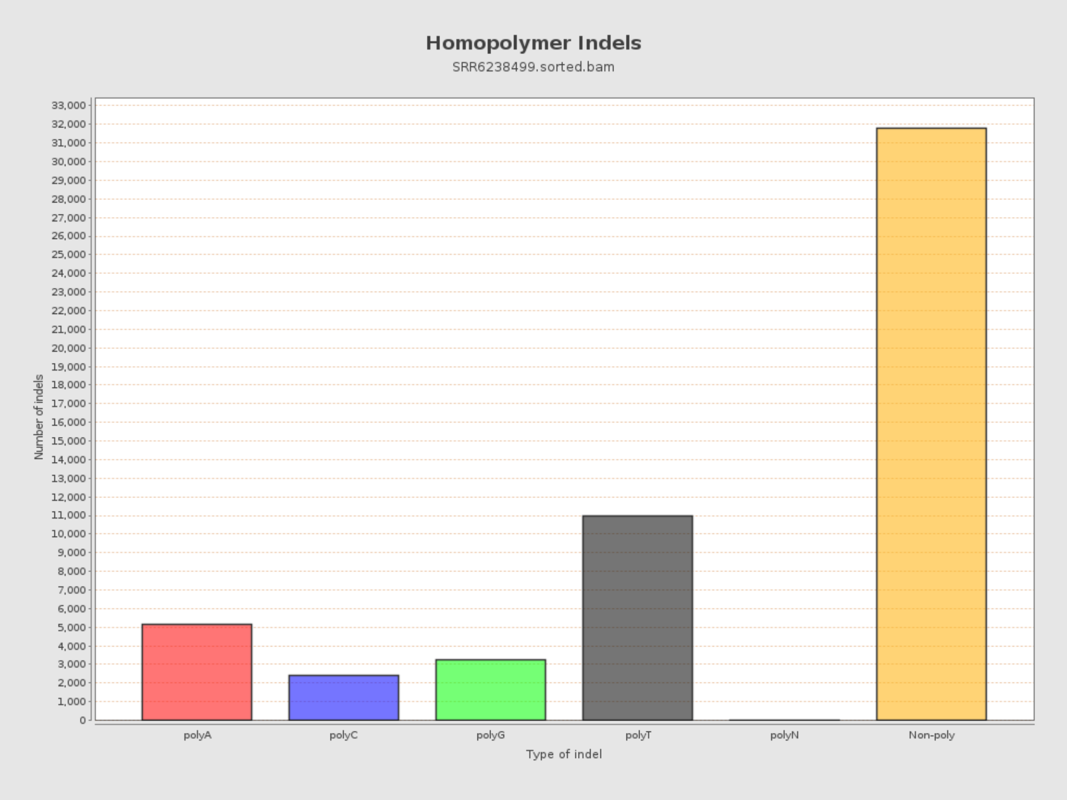
9. Results : Mapped Reads GC-content Distribution



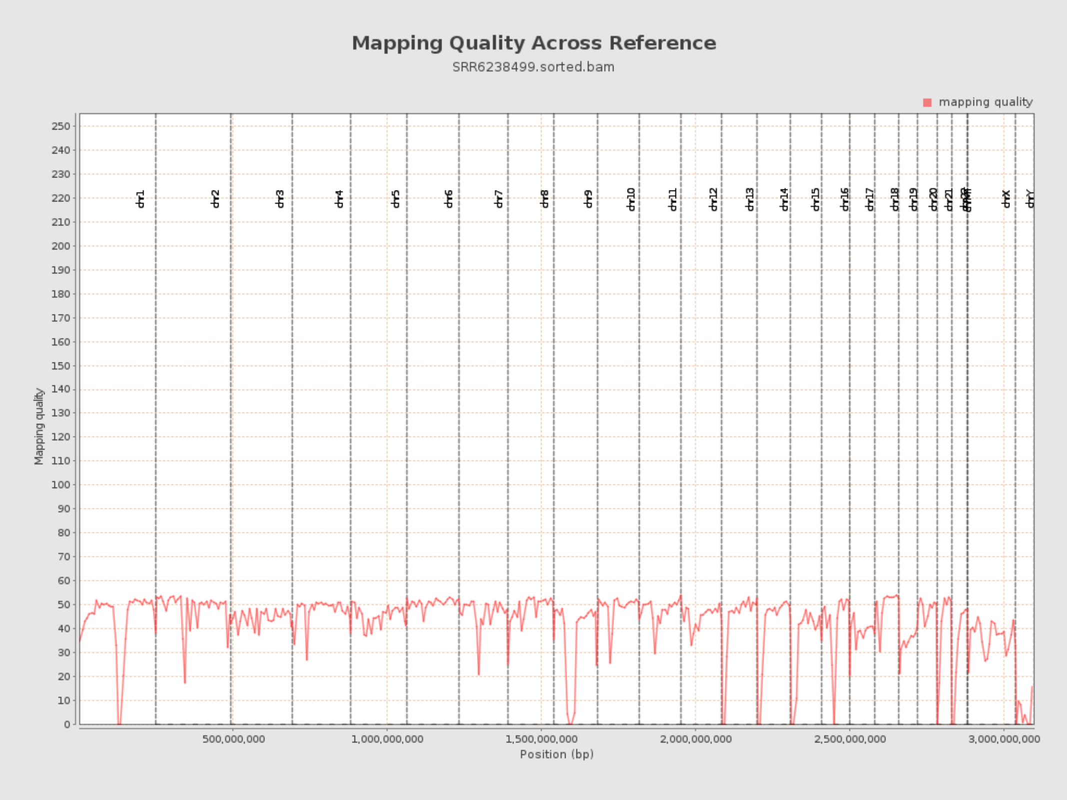
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram