Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:21:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238516.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_SRR6238516 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238516.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:21:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238516.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,664,592
Mapped reads	2,086,414 / 78.3%
Unmapped reads	578,178 / 21.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,974 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	958,156 / 35.96%
Duplication rate	22.74%
Clipped reads	1,433,282 / 53.79%

2.2. ACGT Content

Number/percentage of A's	31,355,915 / 25%
Number/percentage of C's	21,163,627 / 16.87%
Number/percentage of T's	43,332,239 / 34.55%
Number/percentage of G's	29,569,297 / 23.58%
Number/percentage of N's	2,624 / 0%
GC Percentage	40.45%

2.3. Coverage

Mean	0.0405

Standard Deviation	1.0658

2.4. Mapping Quality

Mean Mapping Quality	43.38

2.5. Mismatches and indels

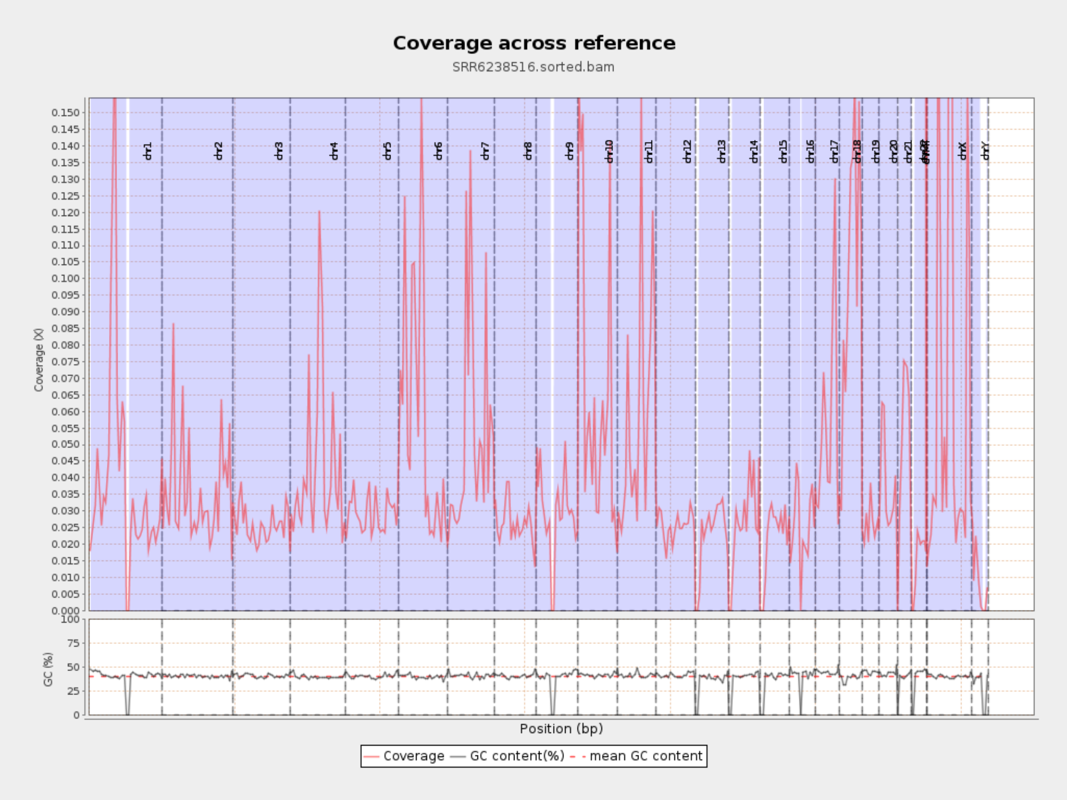
General error rate	0.61%
Mismatches	748,147
Insertions	7,791
Mapped reads with at least one insertion	0.37%
Deletions	34,347
Mapped reads with at least one deletion	1.63%
Homopolymer indels	40.19%

2.6. Chromosome stats

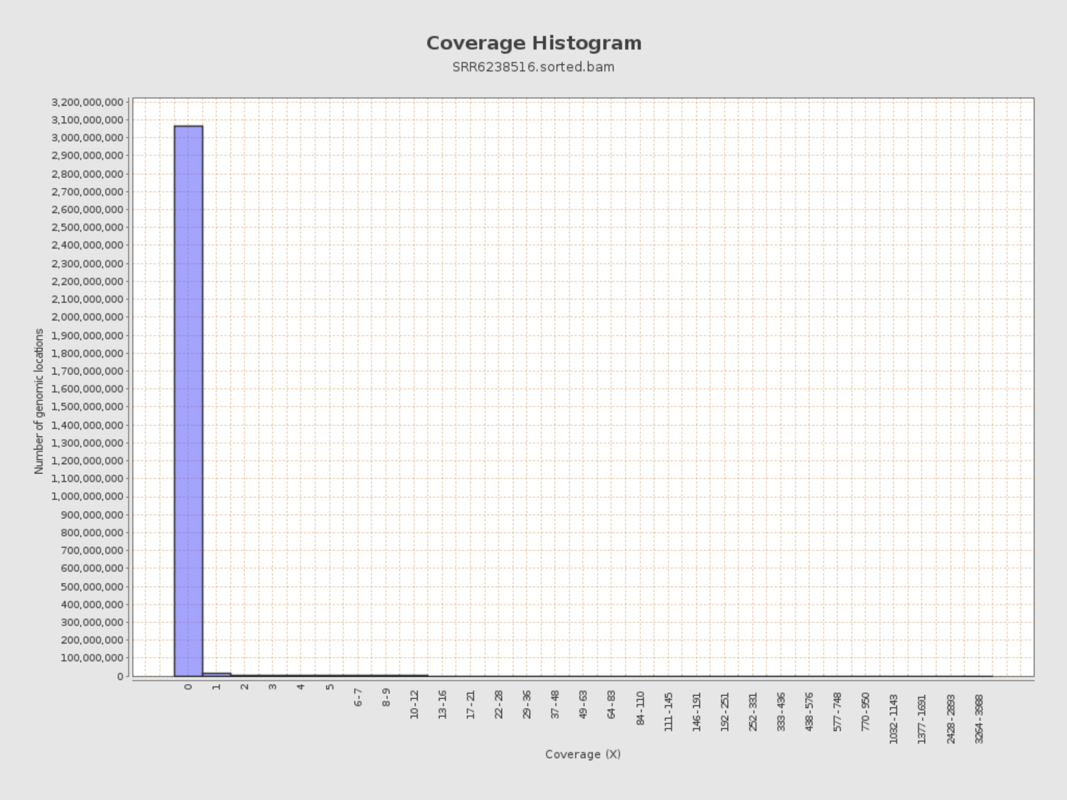
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10070378	0.0404	0.9291
chr2	243199373	8809254	0.0362	1.8355
chr3	198022430	5188541	0.0262	0.5392
chr4	191154276	8078812	0.0423	0.6717
chr5	180915260	5292161	0.0293	0.5549
chr6	171115067	9908139	0.0579	1.0791
chr7	159138663	8699315	0.0547	1.1331

chr8	146364022	3825741	0.0261	0.6878
chr9	141213431	4042807	0.0286	0.5587
chr10	135534747	9101675	0.0672	0.8901
chr11	135006516	7993334	0.0592	0.808
chr12	133851895	3401305	0.0254	0.5169
chr13	115169878	2618842	0.0227	0.7692
chr14	107349540	2766207	0.0258	0.5463
chr15	102531392	2242895	0.0219	0.5776
chr16	90354753	2288952	0.0253	0.5343
chr17	81195210	4524318	0.0557	0.8038
chr18	78077248	7977250	0.1022	3.7558
chr19	59128983	1559468	0.0264	0.675
chr20	63025520	2421825	0.0384	0.6378
chr21	48129895	2371987	0.0493	0.7268
chr22	51304566	762619	0.0149	0.3723
chrMT	16571	33770	2.0379	4.9031
chrX	155270560	10995230	0.0708	0.8864
chrY	59373566	508041	0.0086	0.4368

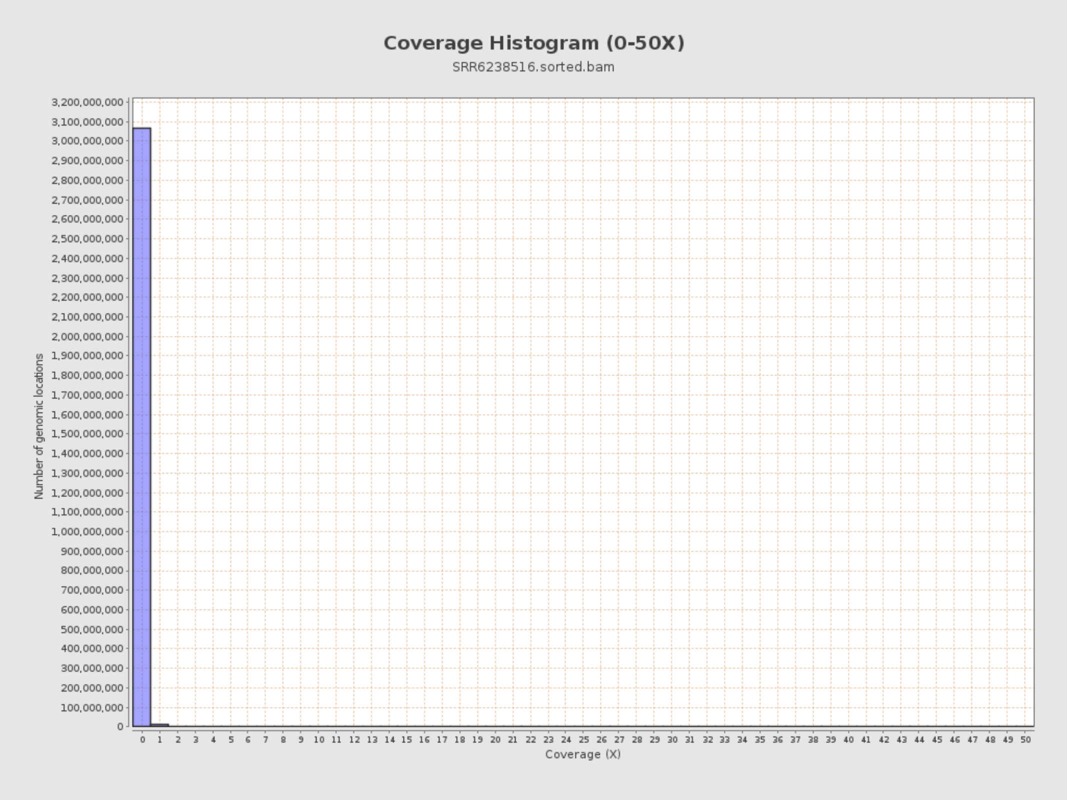
3. Results : Coverage across reference



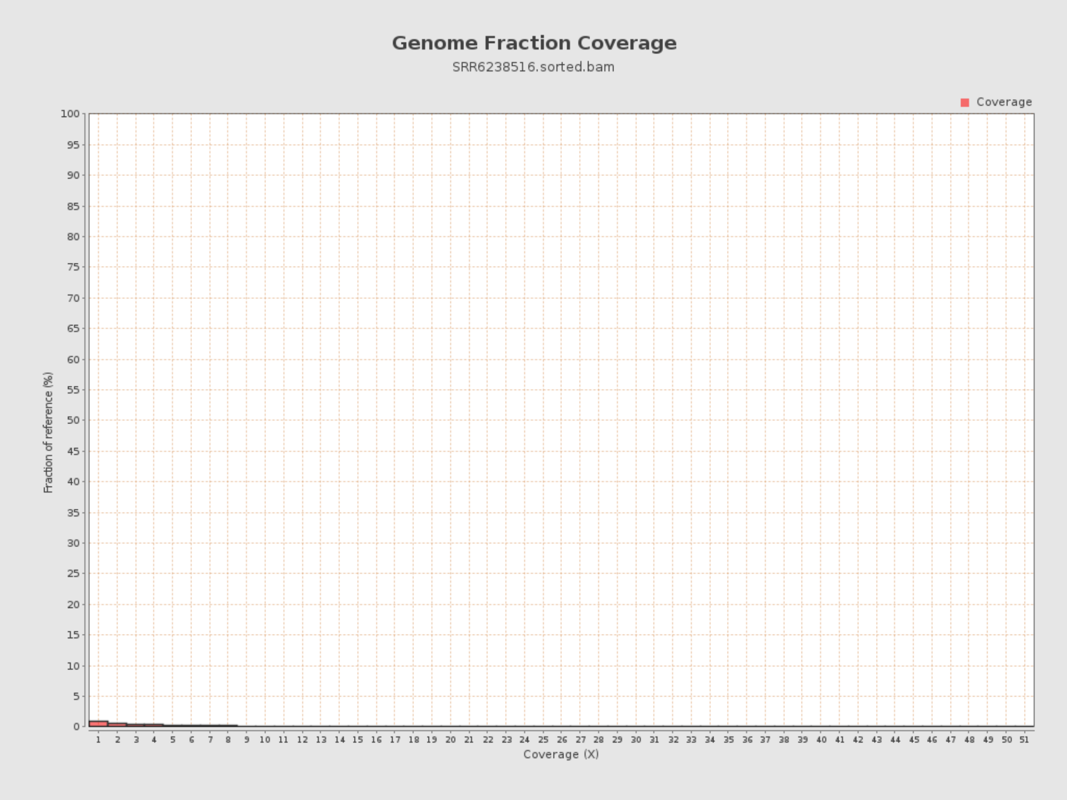
4. Results : Coverage Histogram



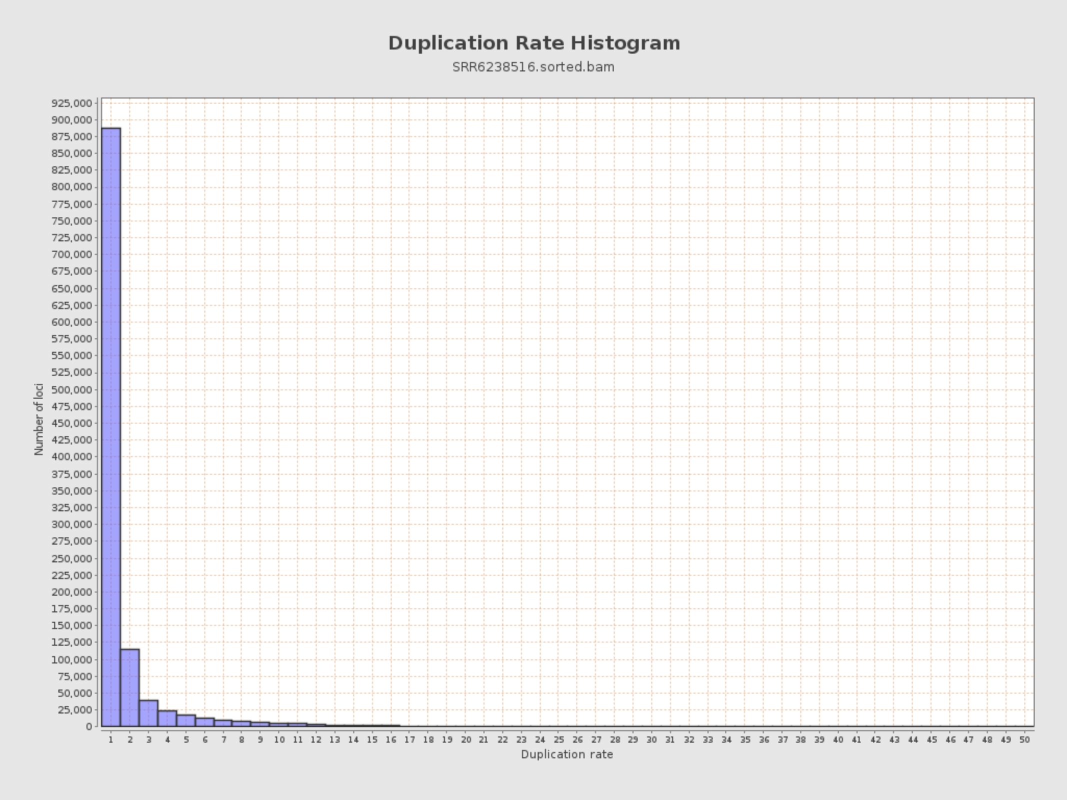
5. Results : Coverage Histogram (0-50X)



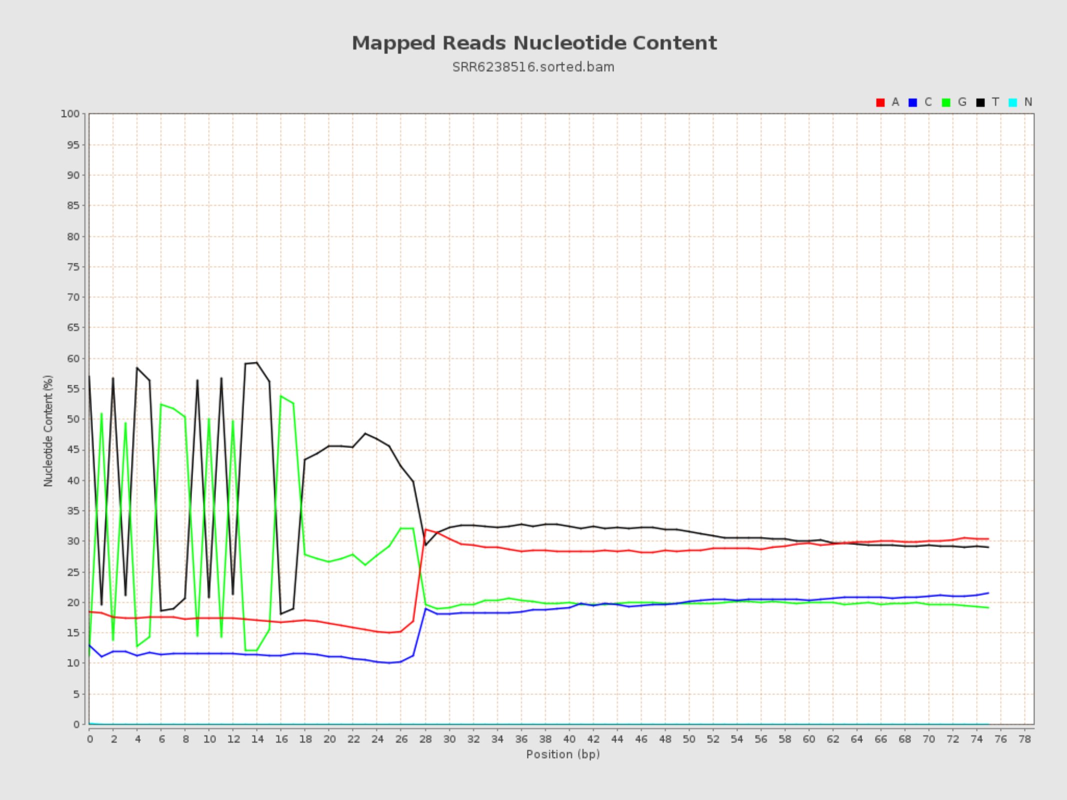
6. Results : Genome Fraction Coverage



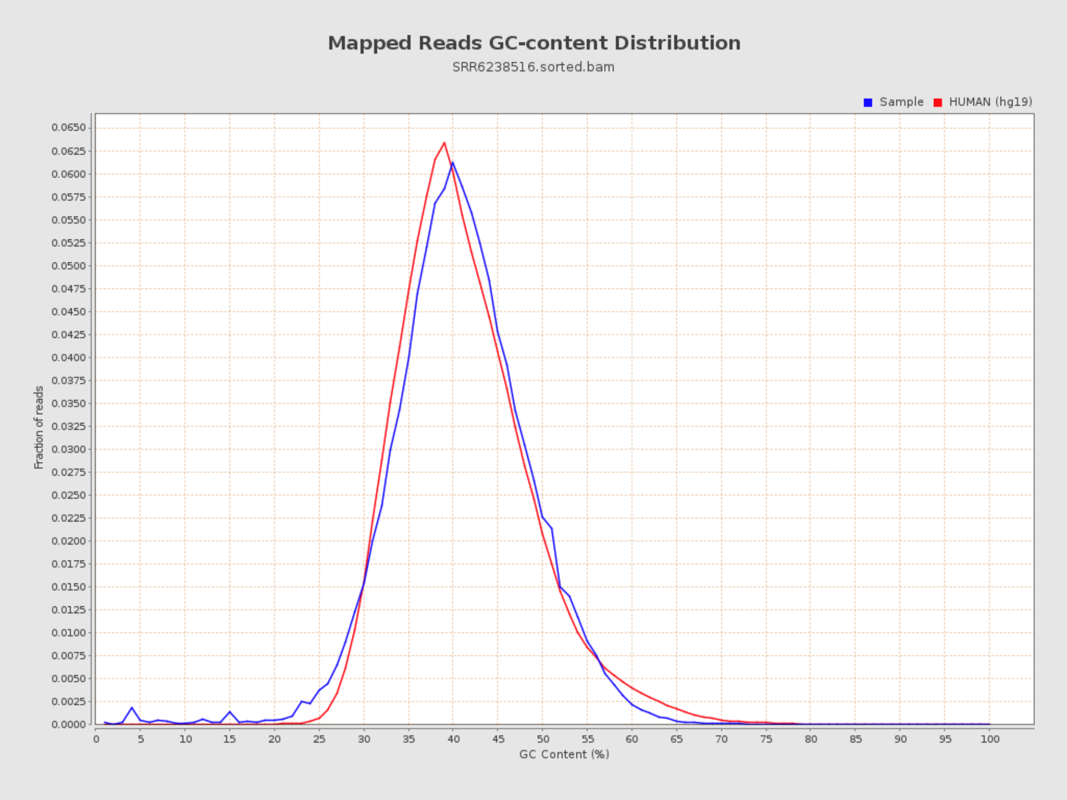
7. Results : Duplication Rate Histogram



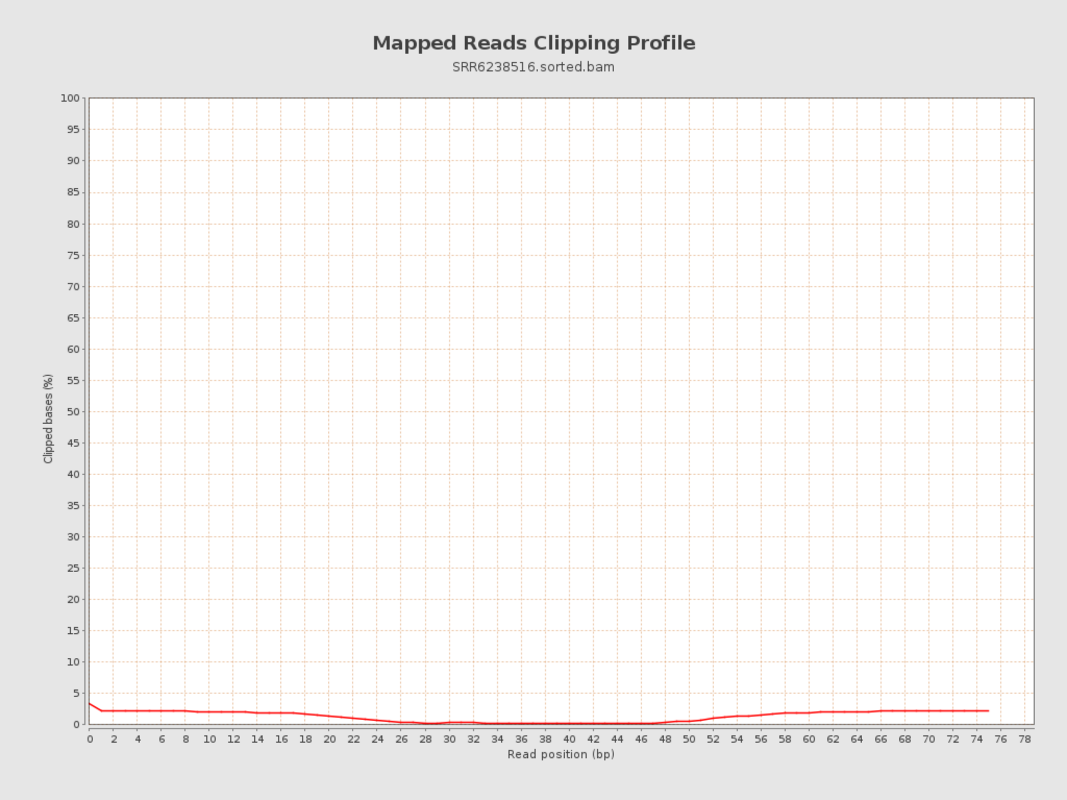
8. Results : Mapped Reads Nucleotide Content



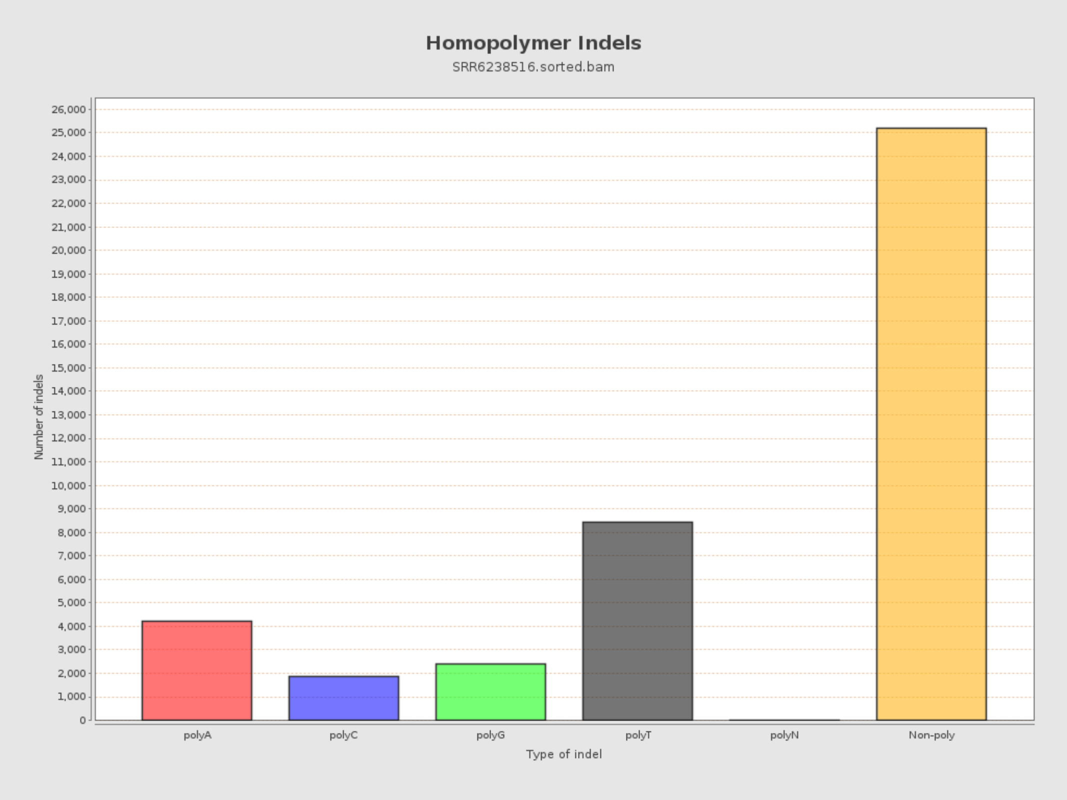
9. Results : Mapped Reads GC-content Distribution



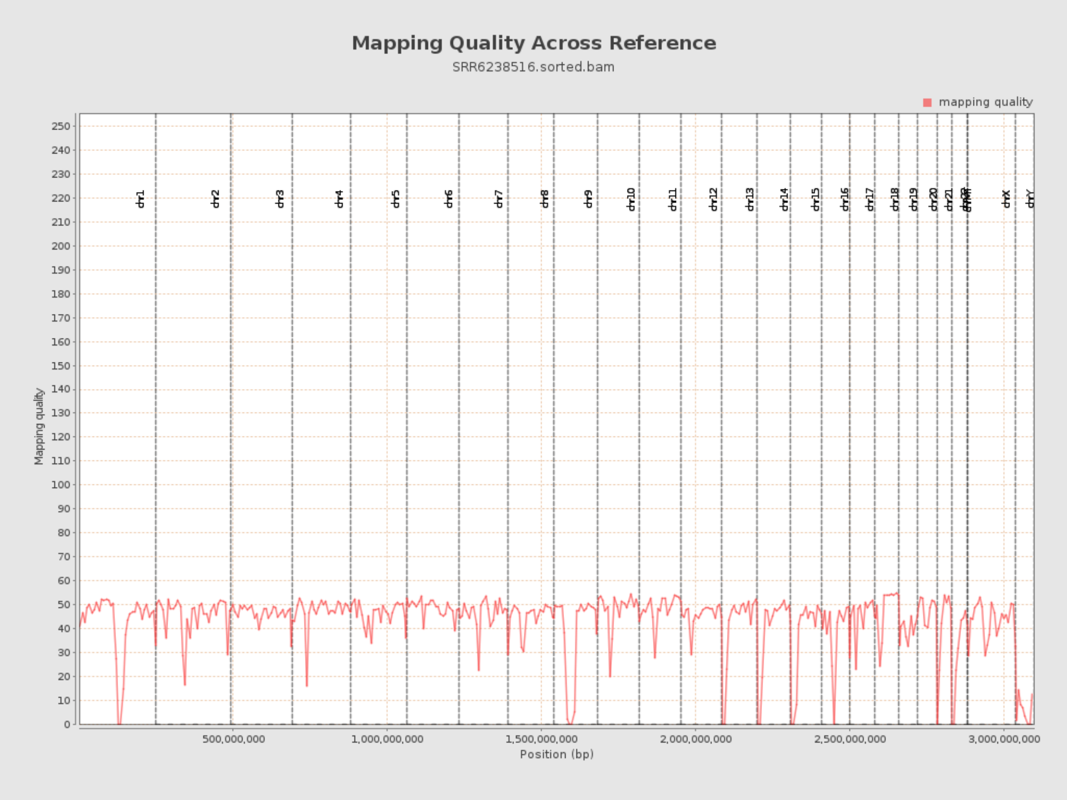
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram