Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:23:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238040.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_SRR6238040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:23:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,888,765
Mapped reads	1,565,766 / 82.9%
Unmapped reads	322,999 / 17.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,641 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	237,976 / 12.6%
Duplication rate	11.48%
Clipped reads	847,526 / 44.87%

2.2. ACGT Content

Number/percentage of A's	27,899,885 / 27.66%
Number/percentage of C's	18,368,283 / 18.21%
Number/percentage of T's	32,051,137 / 31.77%
Number/percentage of G's	22,373,354 / 22.18%
Number/percentage of N's	186,580 / 0.18%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.3877

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

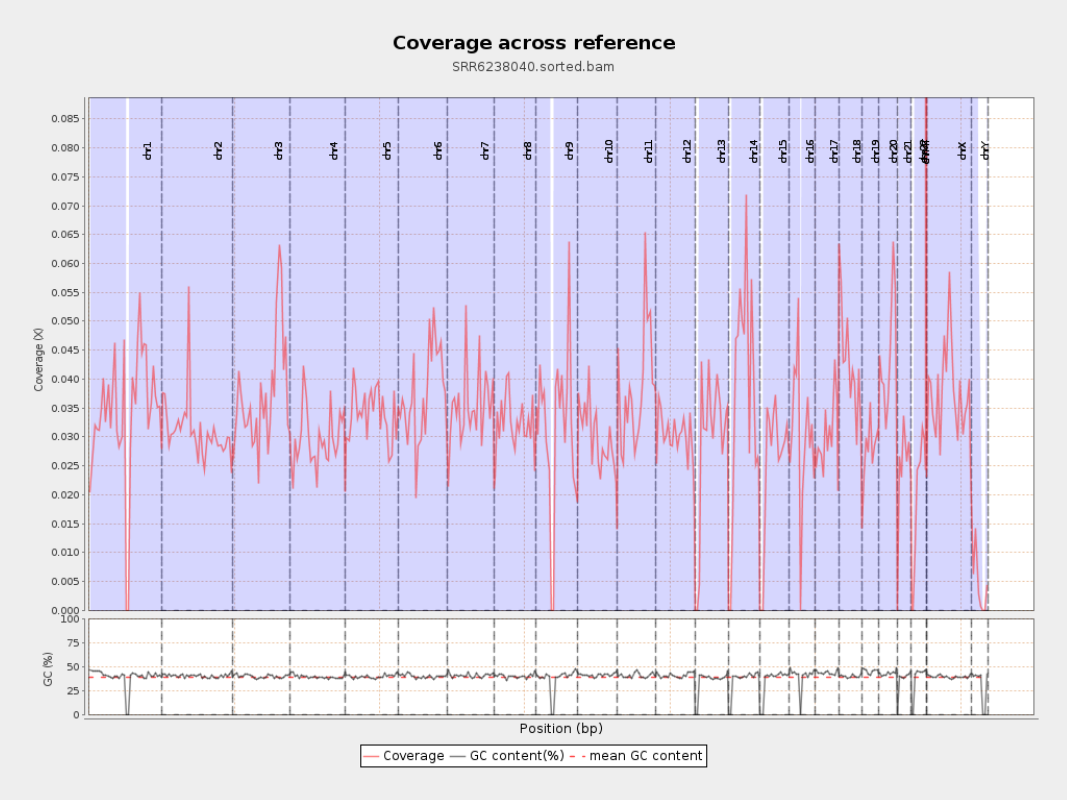
General error rate	0.95%
Mismatches	948,277
Insertions	8,499
Mapped reads with at least one insertion	0.54%
Deletions	31,971
Mapped reads with at least one deletion	2.02%
Homopolymer indels	47.84%

2.6. Chromosome stats

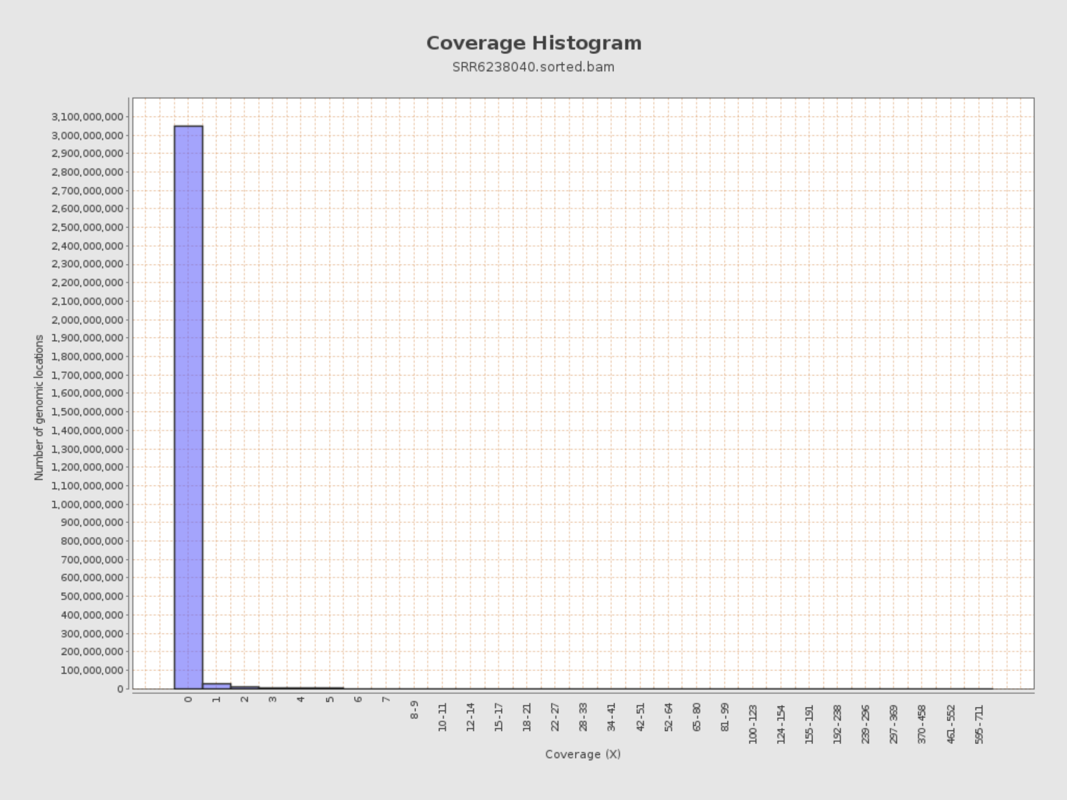
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8570870	0.0344	0.5031
chr2	243199373	7588507	0.0312	0.4509
chr3	198022430	7337237	0.0371	0.3444
chr4	191154276	5644322	0.0295	0.3121
chr5	180915260	6140632	0.0339	0.3253
chr6	171115067	6397851	0.0374	0.3685
chr7	159138663	5650780	0.0355	0.4492

chr8	146364022	4706687	0.0322	0.5258
chr9	141213431	4418270	0.0313	0.3719
chr10	135534747	4096770	0.0302	0.3385
chr11	135006516	5111257	0.0379	0.3979
chr12	133851895	4030075	0.0301	0.3093
chr13	115169878	3331269	0.0289	0.3065
chr14	107349540	4008604	0.0373	0.3543
chr15	102531392	2602518	0.0254	0.2815
chr16	90354753	2758416	0.0305	0.3073
chr17	81195210	2441254	0.0301	0.3102
chr18	78077248	3332557	0.0427	0.6185
chr19	59128983	1661328	0.0281	0.4432
chr20	63025520	2771003	0.044	0.3698
chr21	48129895	1182027	0.0246	0.2834
chr22	51304566	990090	0.0193	0.2317
chrMT	16571	57380	3.4627	3.749
chrX	155270560	5820009	0.0375	0.3541
chrY	59373566	280856	0.0047	0.1307

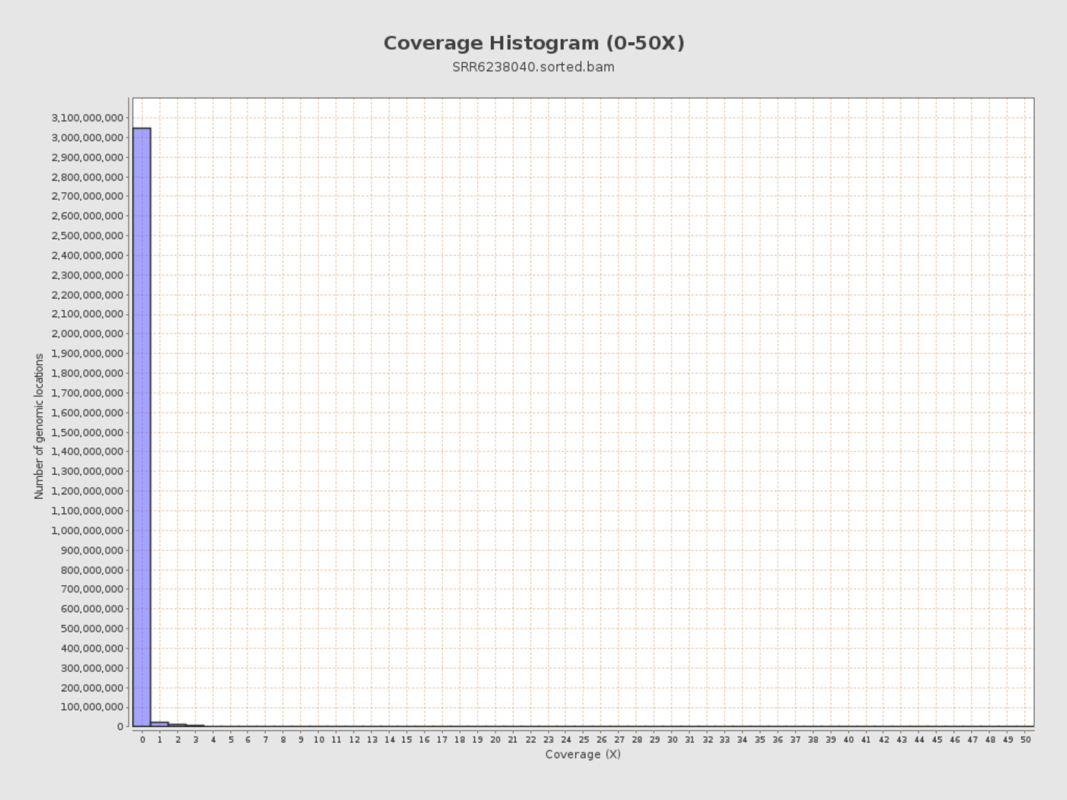
3. Results : Coverage across reference



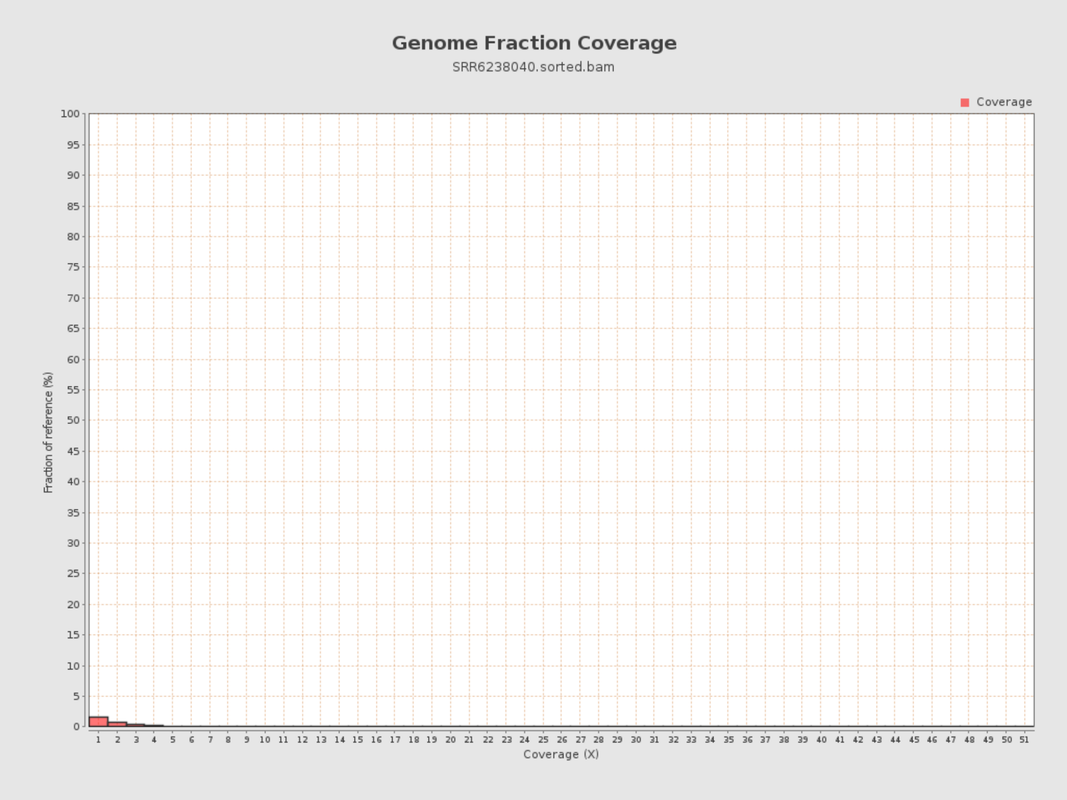
4. Results : Coverage Histogram



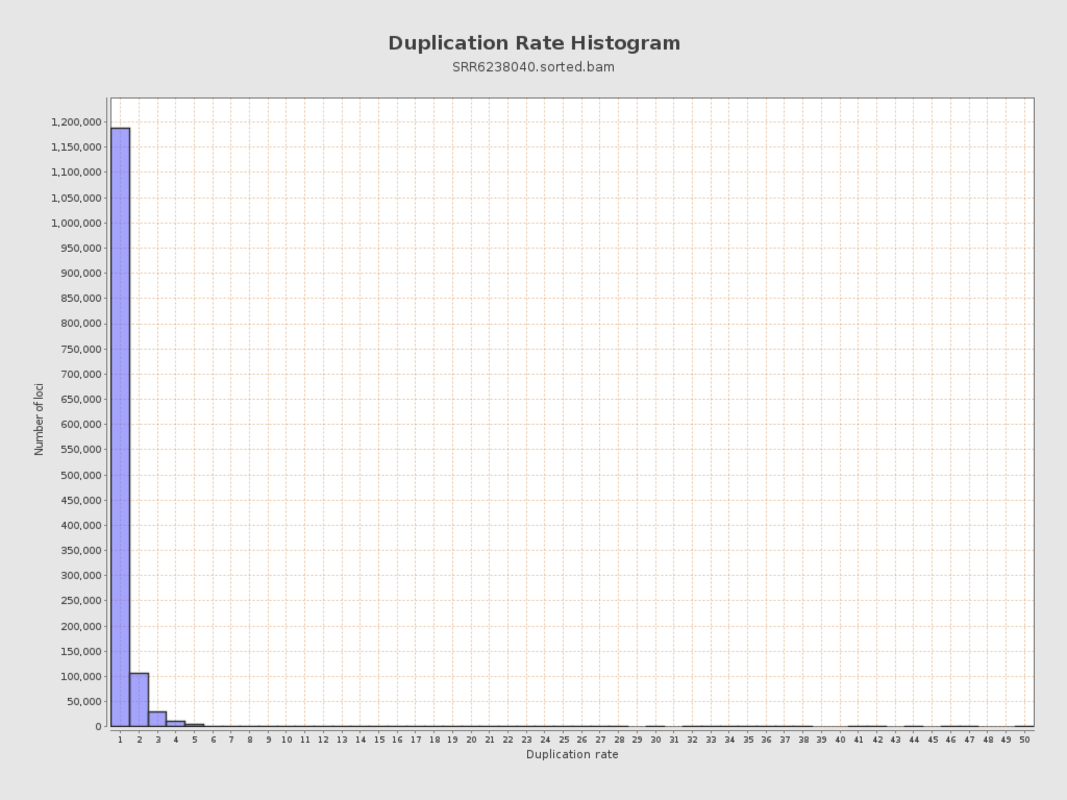
5. Results : Coverage Histogram (0-50X)



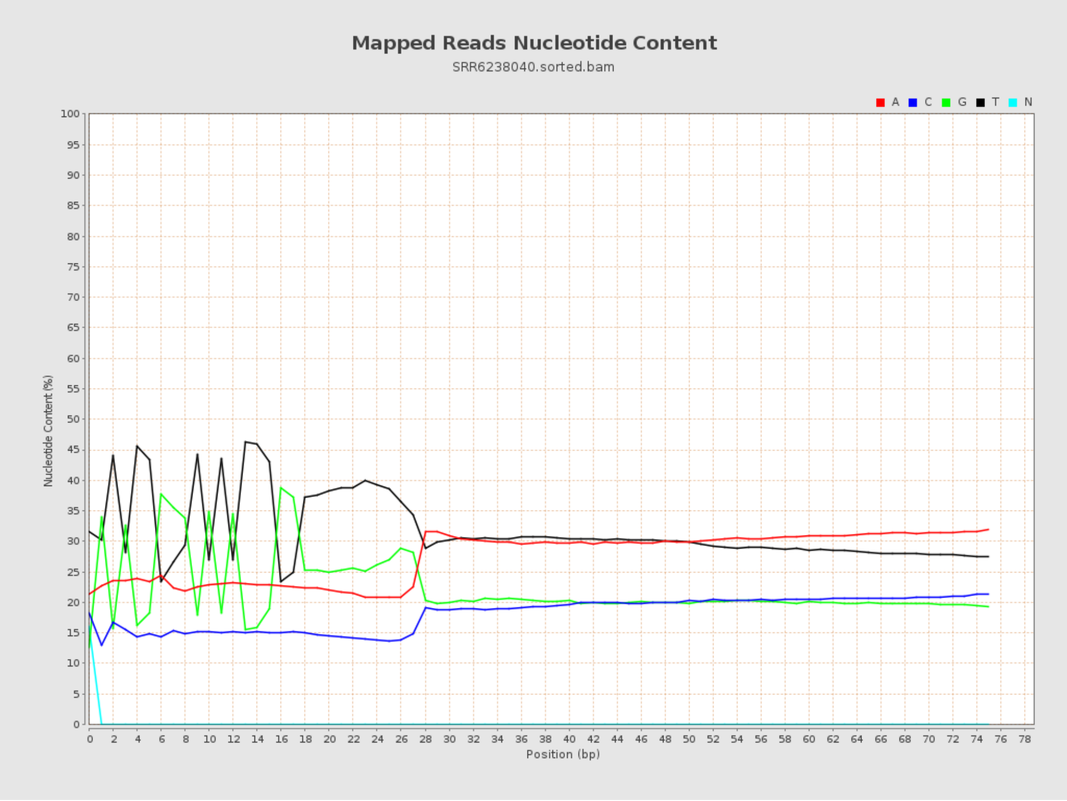
6. Results : Genome Fraction Coverage



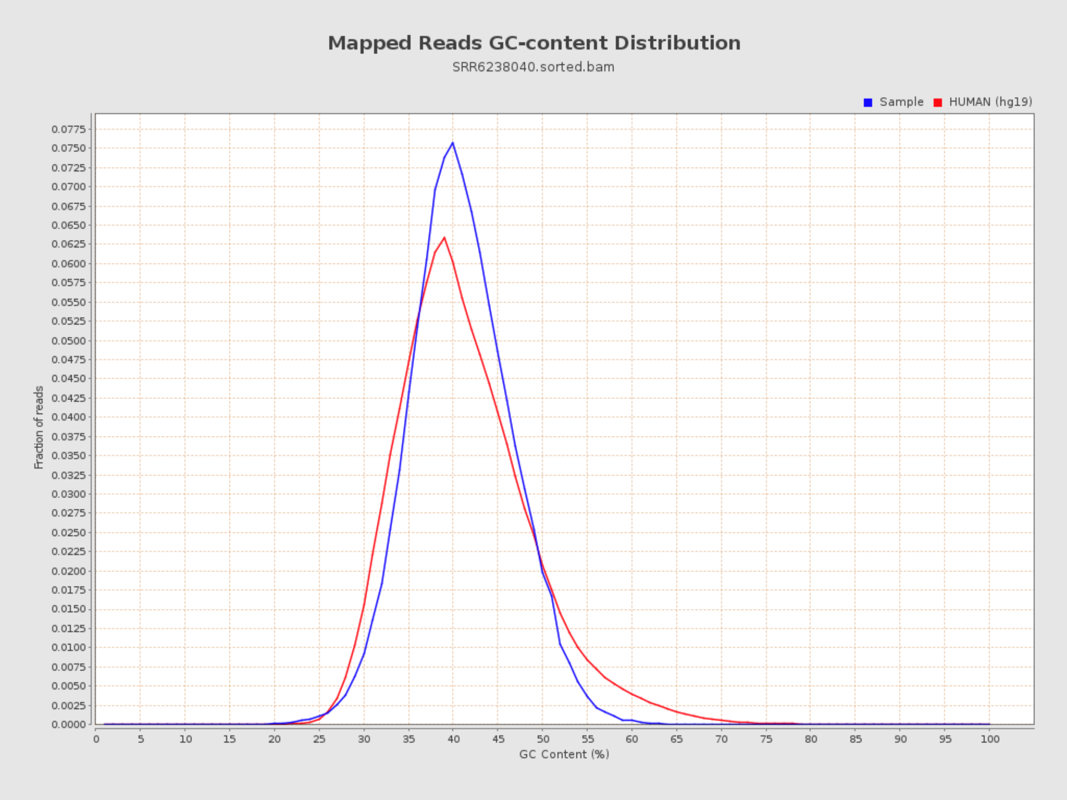
7. Results : Duplication Rate Histogram



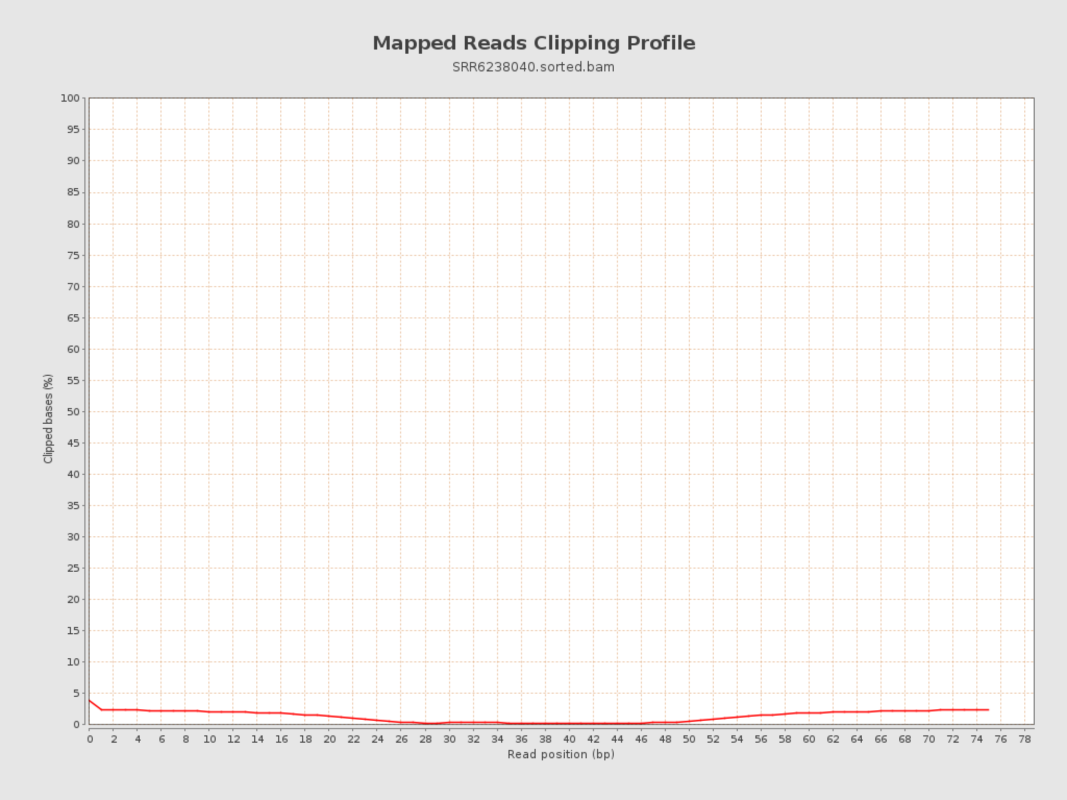
8. Results : Mapped Reads Nucleotide Content



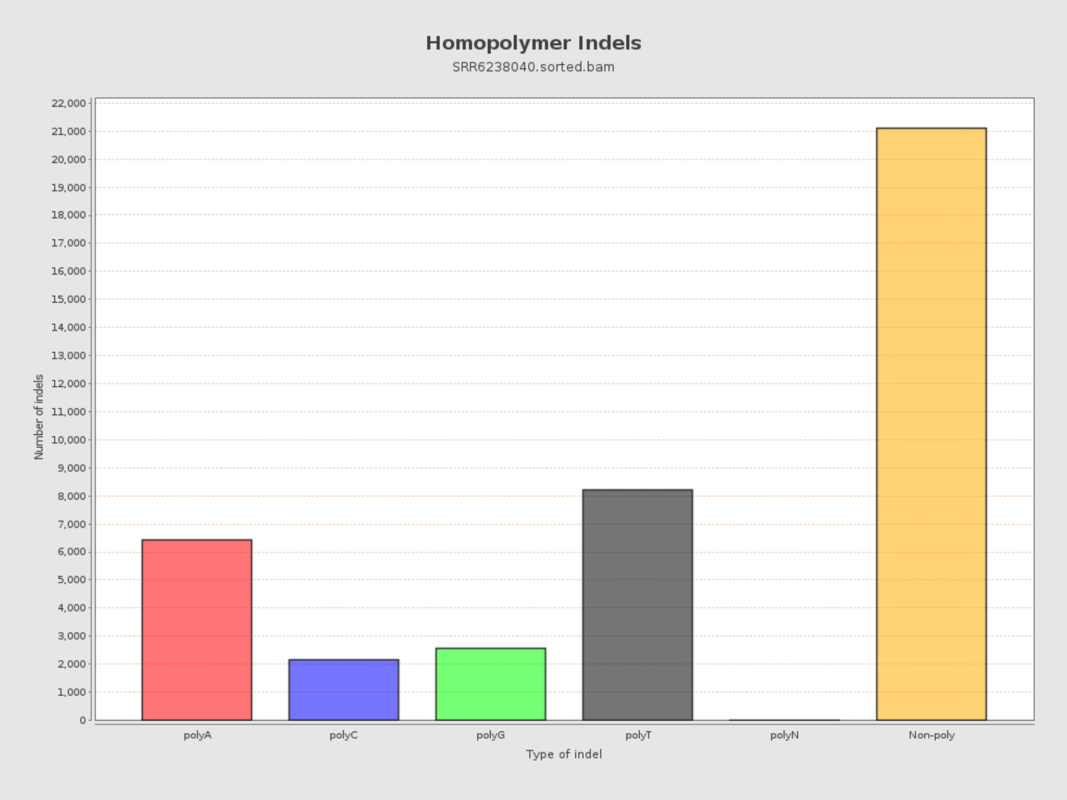
9. Results : Mapped Reads GC-content Distribution



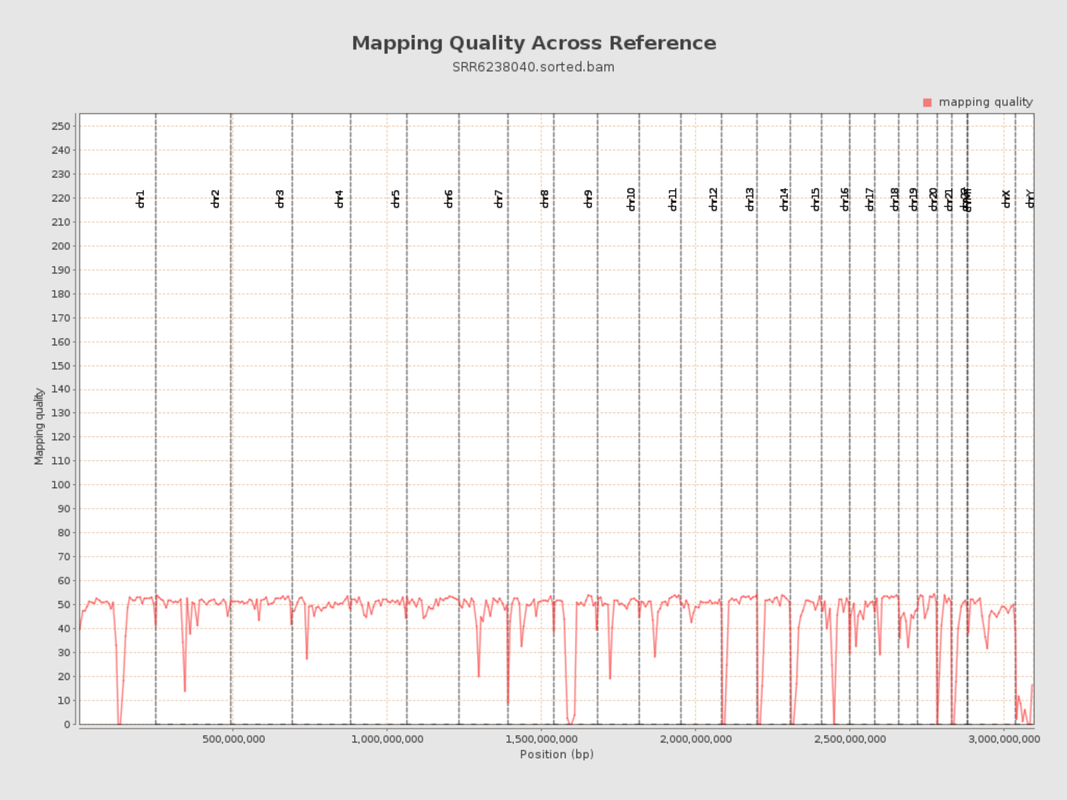
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram