Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:43:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238047.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_SRR6238047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:43:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,997,996
Mapped reads	1,714,118 / 85.79%
Unmapped reads	283,878 / 14.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,086 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	126,259 / 6.32%
Duplication rate	5.68%
Clipped reads	768,025 / 38.44%

2.2. ACGT Content

Number/percentage of A's	30,967,178 / 27.18%
Number/percentage of C's	21,748,622 / 19.09%
Number/percentage of T's	35,450,542 / 31.11%
Number/percentage of G's	25,771,629 / 22.62%
Number/percentage of N's	6,534 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3845

2.4. Mapping Quality

Mean Mapping Quality	40.94

2.5. Mismatches and indels

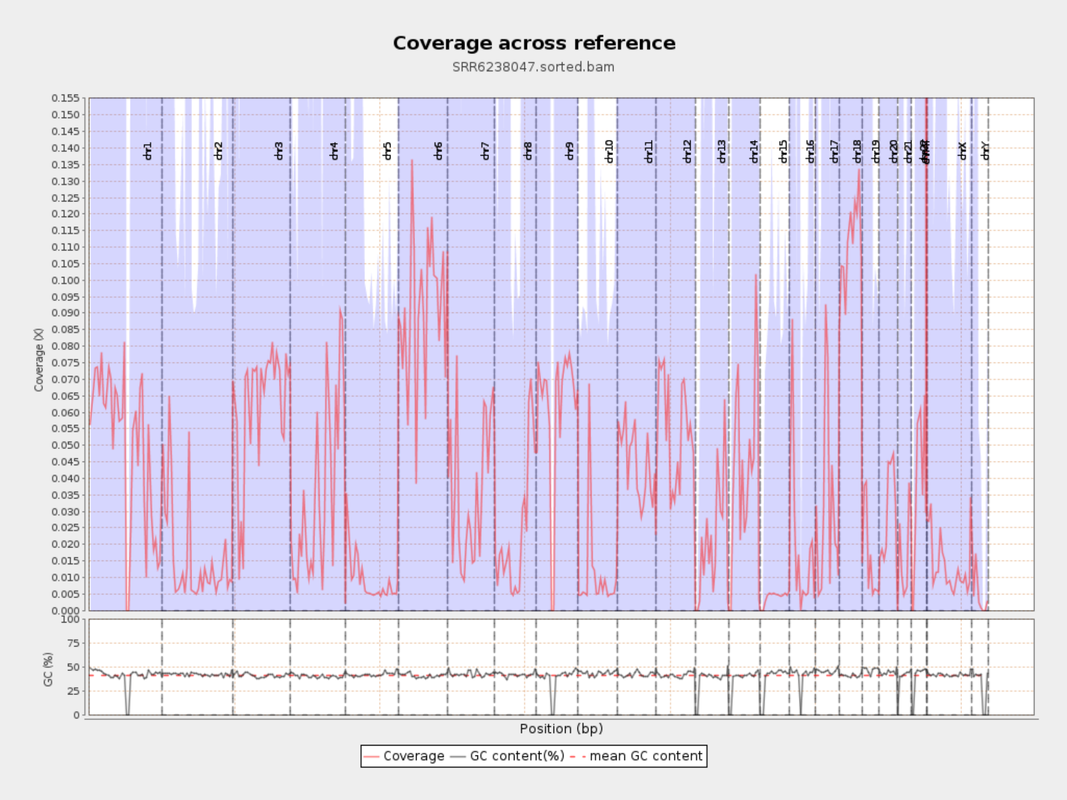
General error rate	0.77%
Mismatches	866,299
Insertions	8,100
Mapped reads with at least one insertion	0.47%
Deletions	28,848
Mapped reads with at least one deletion	1.66%
Homopolymer indels	45.72%

2.6. Chromosome stats

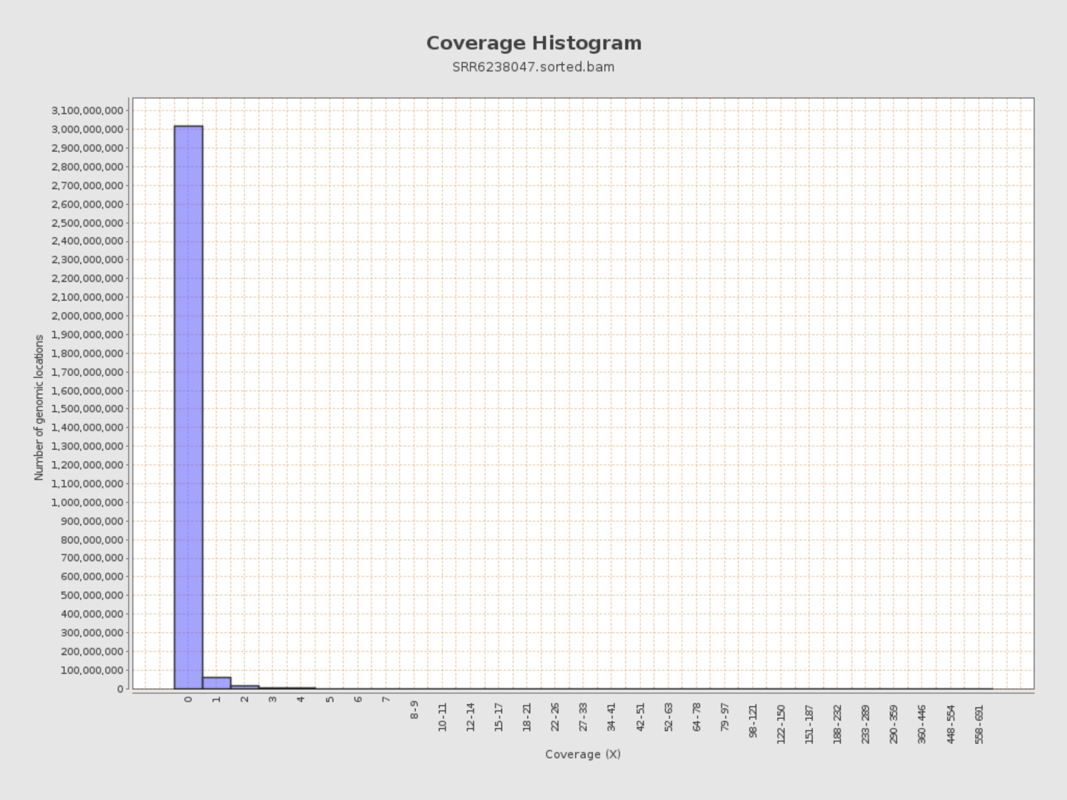
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12264693	0.0492	0.5303
chr2	243199373	3893236	0.016	0.4806
chr3	198022430	12326366	0.0622	0.3408
chr4	191154276	6896070	0.0361	0.283
chr5	180915260	1686957	0.0093	0.1301
chr6	171115067	15640615	0.0914	0.4318
chr7	159138663	5732544	0.036	0.3308

chr8	146364022	3562570	0.0243	0.3502
chr9	141213431	8645553	0.0612	0.502
chr10	135534747	1389866	0.0103	0.4401
chr11	135006516	5907152	0.0438	0.4437
chr12	133851895	7243189	0.0541	0.3215
chr13	115169878	2538226	0.022	0.1997
chr14	107349540	4723600	0.044	0.3271
chr15	102531392	414170	0.004	0.0879
chr16	90354753	1775435	0.0196	0.2384
chr17	81195210	2613997	0.0322	0.2684
chr18	78077248	8715774	0.1116	0.8918
chr19	59128983	963958	0.0163	0.4026
chr20	63025520	1855071	0.0294	0.2385
chr21	48129895	823059	0.0171	0.2337
chr22	51304566	1935673	0.0377	0.2622
chrMT	16571	40805	2.4624	2.5702
chrX	155270560	2105326	0.0136	0.2196
chrY	59373566	301893	0.0051	0.1595

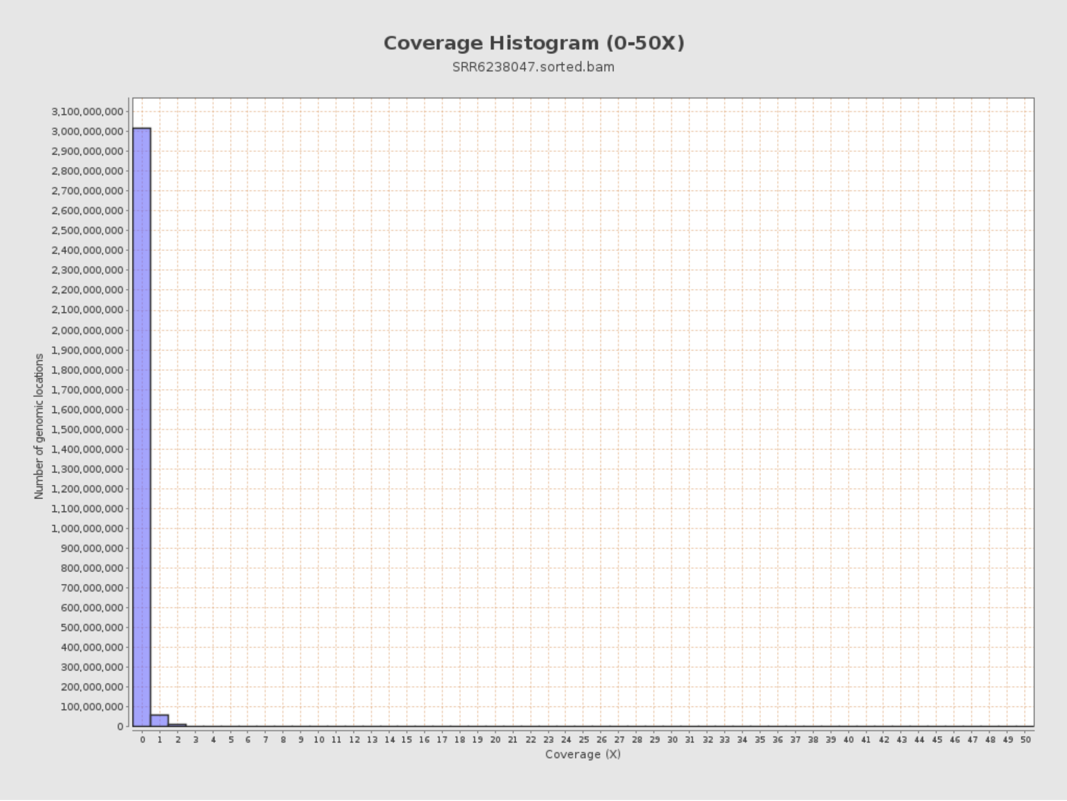
3. Results : Coverage across reference



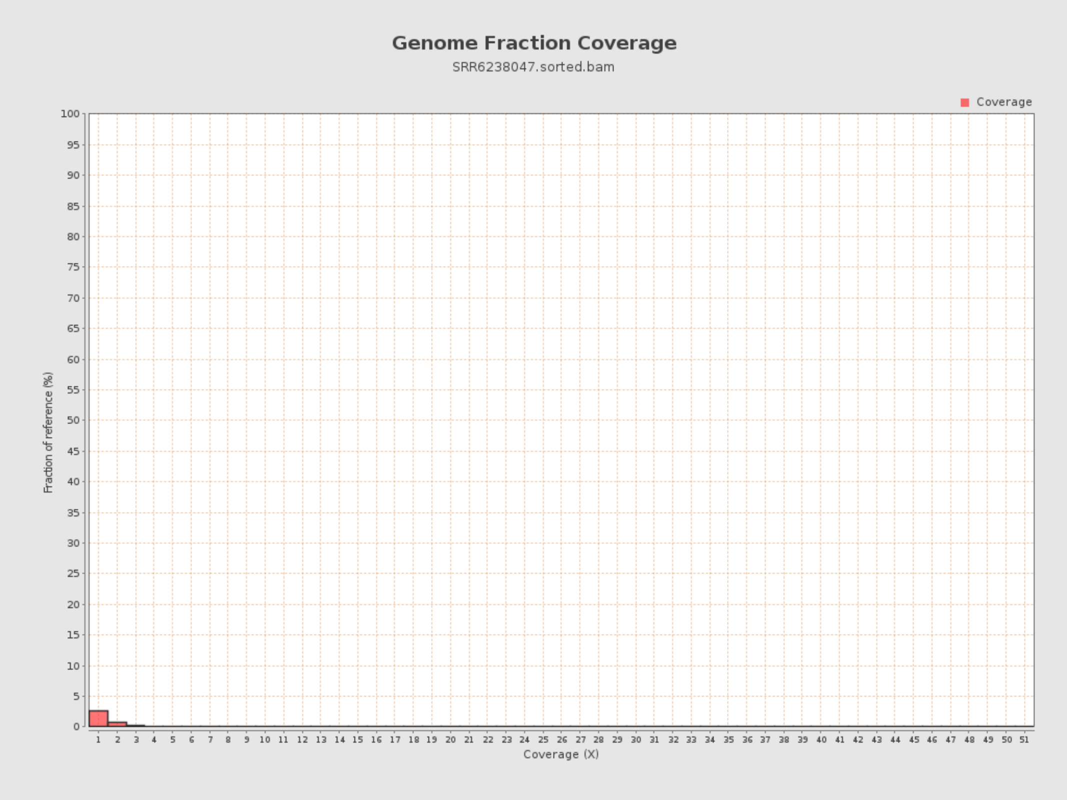
4. Results : Coverage Histogram



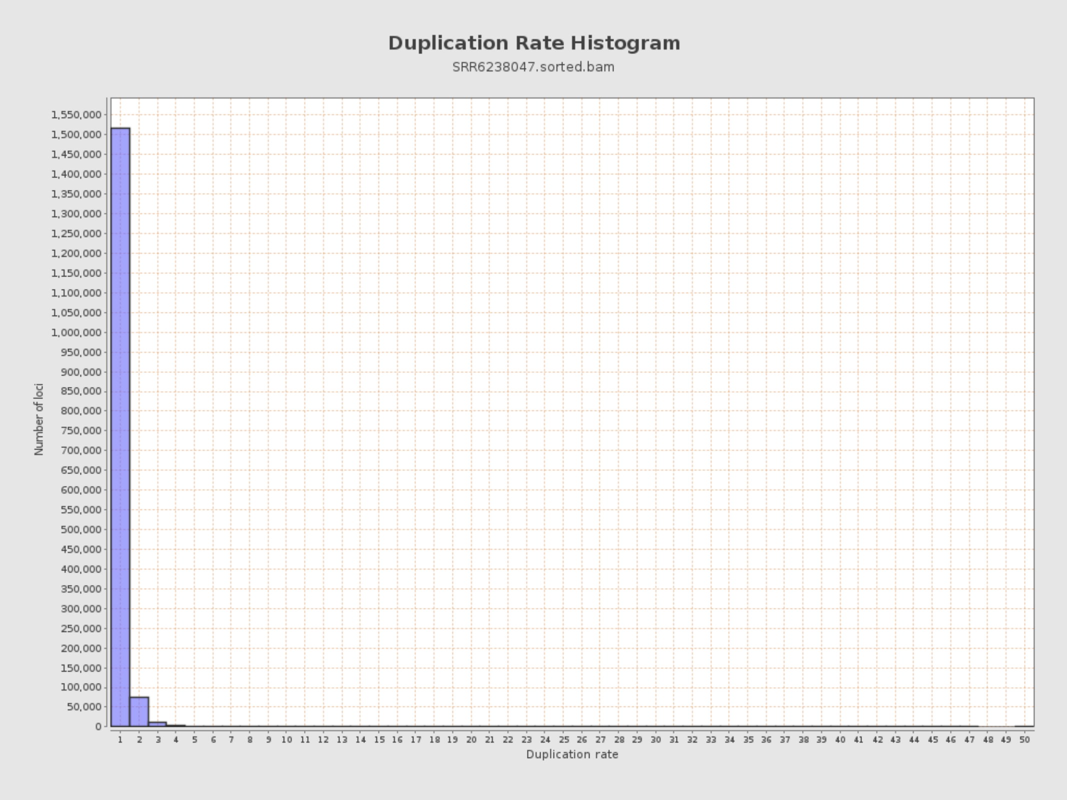
5. Results : Coverage Histogram (0-50X)



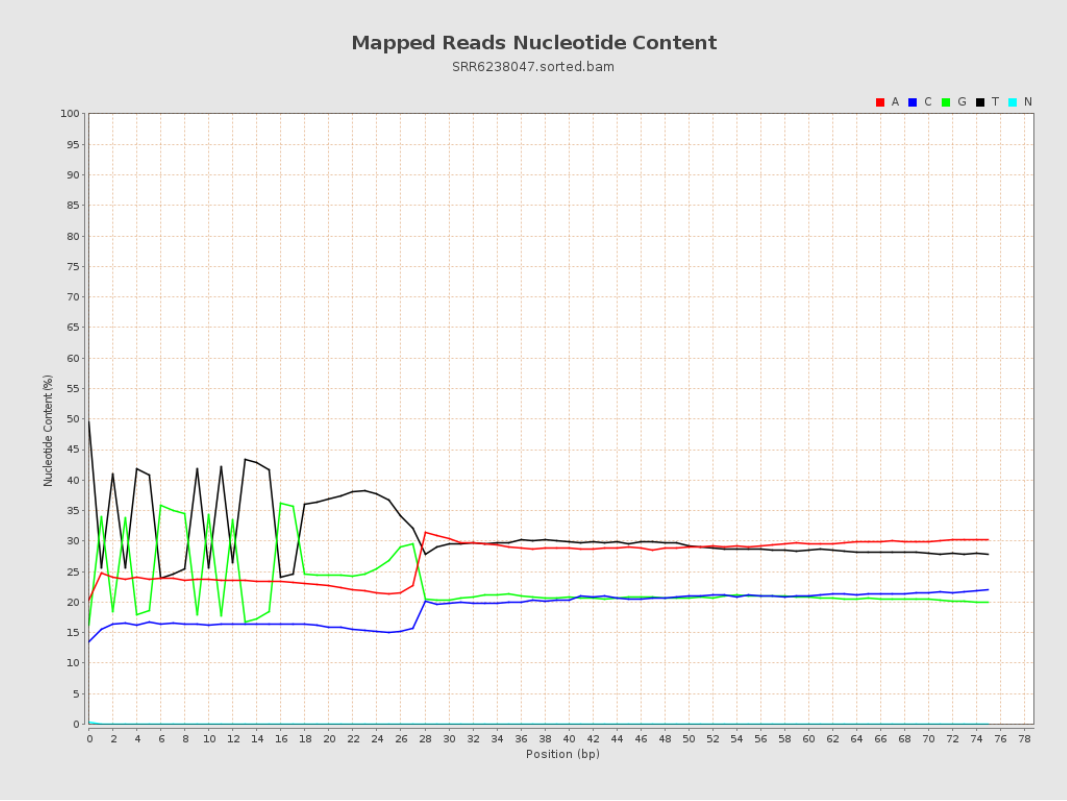
6. Results : Genome Fraction Coverage



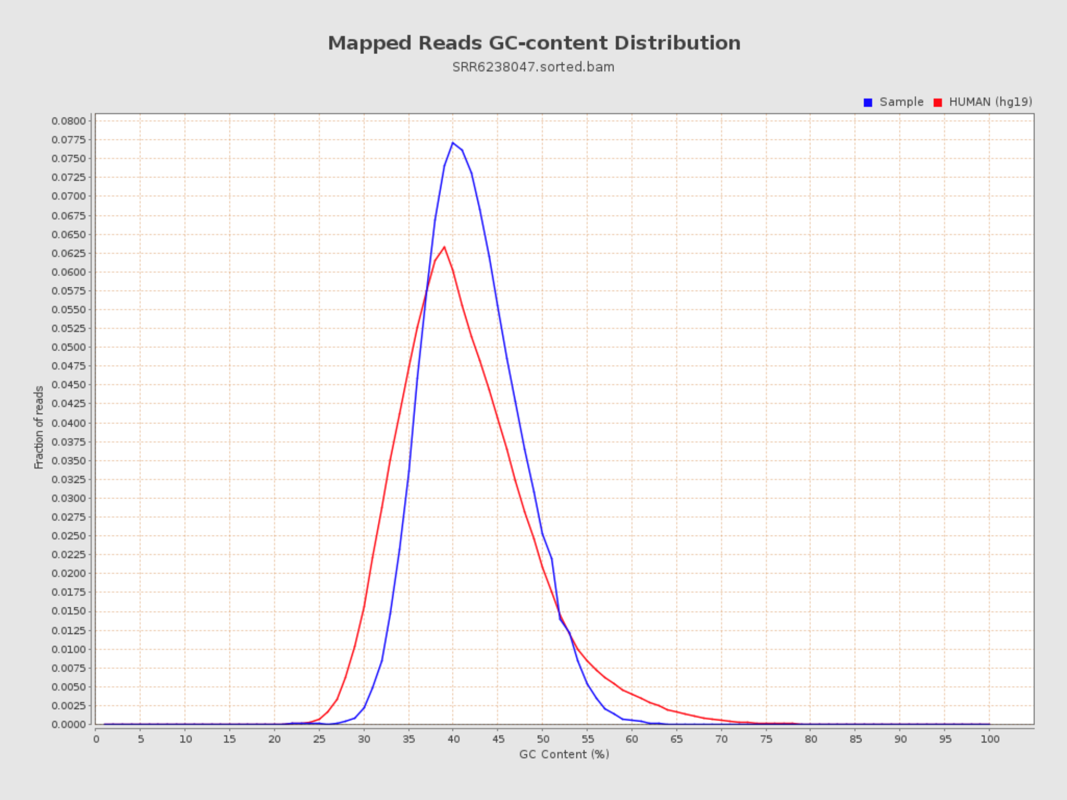
7. Results : Duplication Rate Histogram



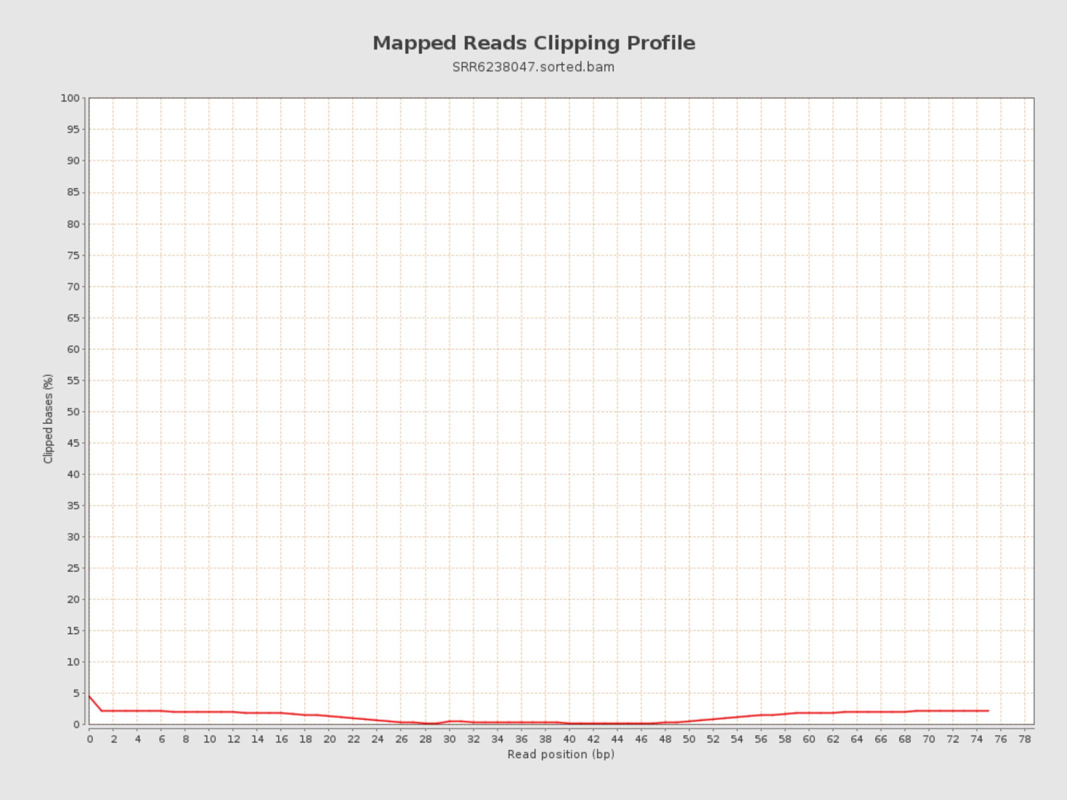
8. Results : Mapped Reads Nucleotide Content



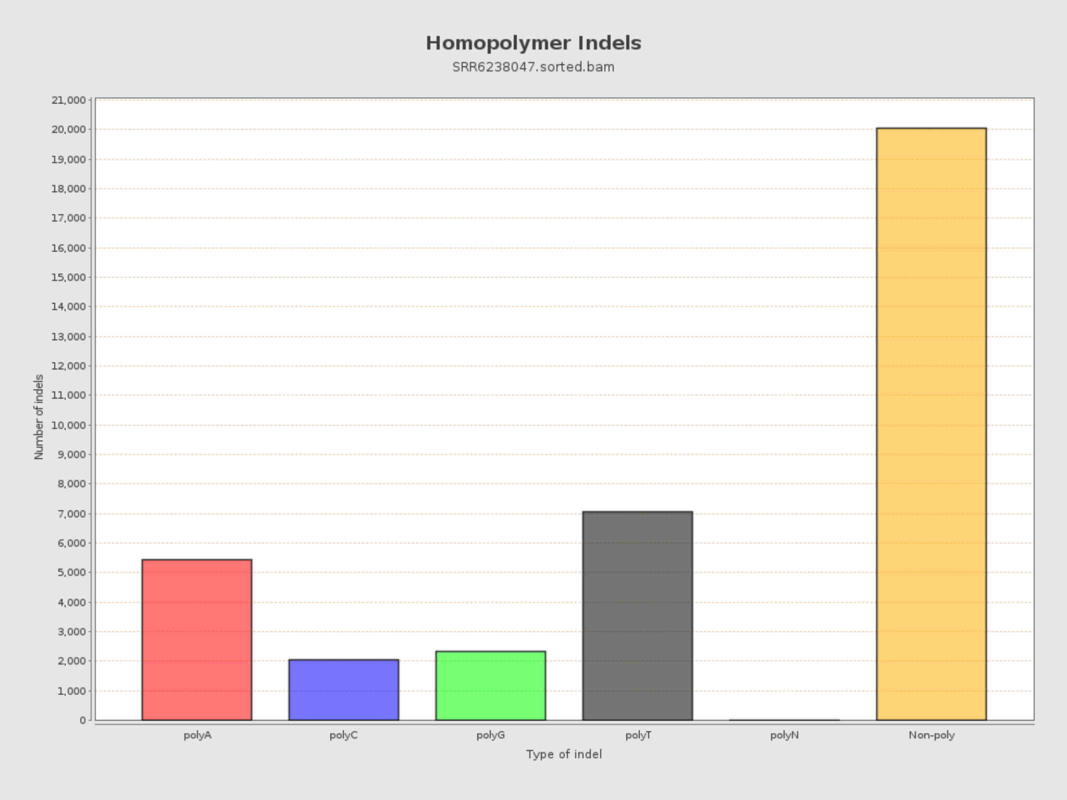
9. Results : Mapped Reads GC-content Distribution



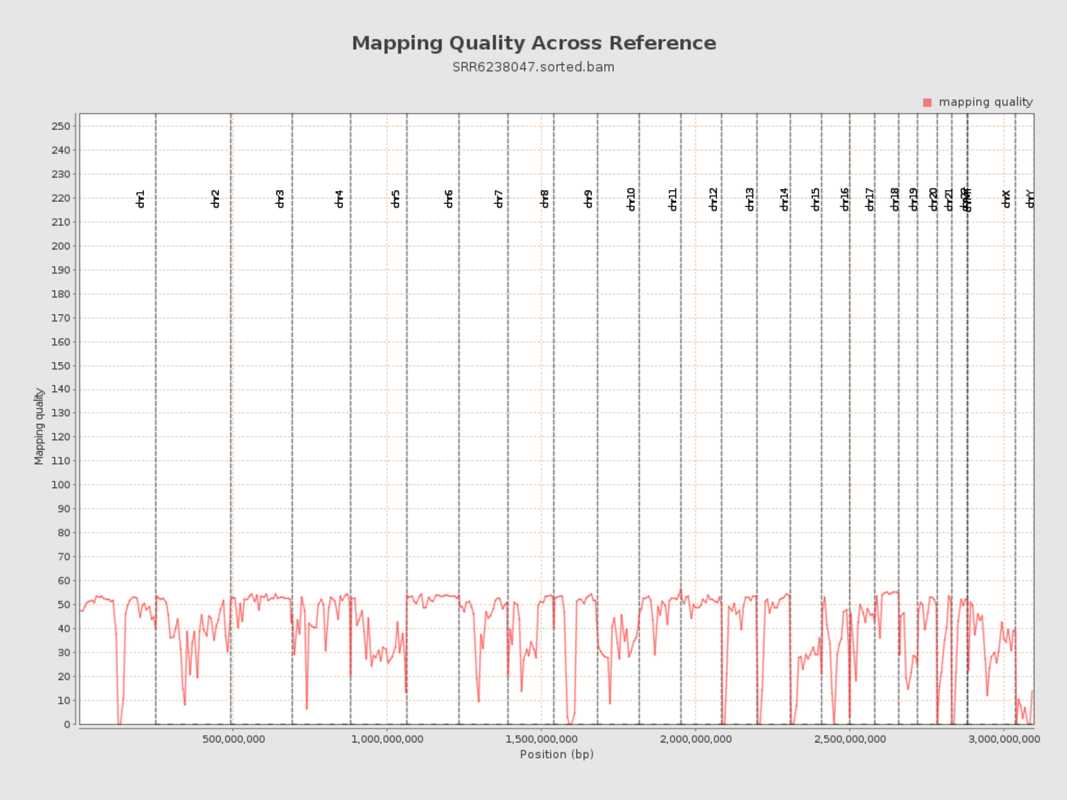
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram