Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:49:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238638.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_SRR6238638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:49:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,929,050
Mapped reads	2,560,329 / 87.41%
Unmapped reads	368,721 / 12.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,384 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,169,673 / 39.93%
Duplication rate	22.69%
Clipped reads	1,614,145 / 55.11%

2.2. ACGT Content

Number/percentage of A's	39,311,138 / 24.86%
Number/percentage of C's	27,169,042 / 17.18%
Number/percentage of T's	54,038,012 / 34.17%
Number/percentage of G's	37,638,415 / 23.8%
Number/percentage of N's	3,746 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0511

Standard Deviation	0.9468

2.4. Mapping Quality

Mean Mapping Quality	41.62

2.5. Mismatches and indels

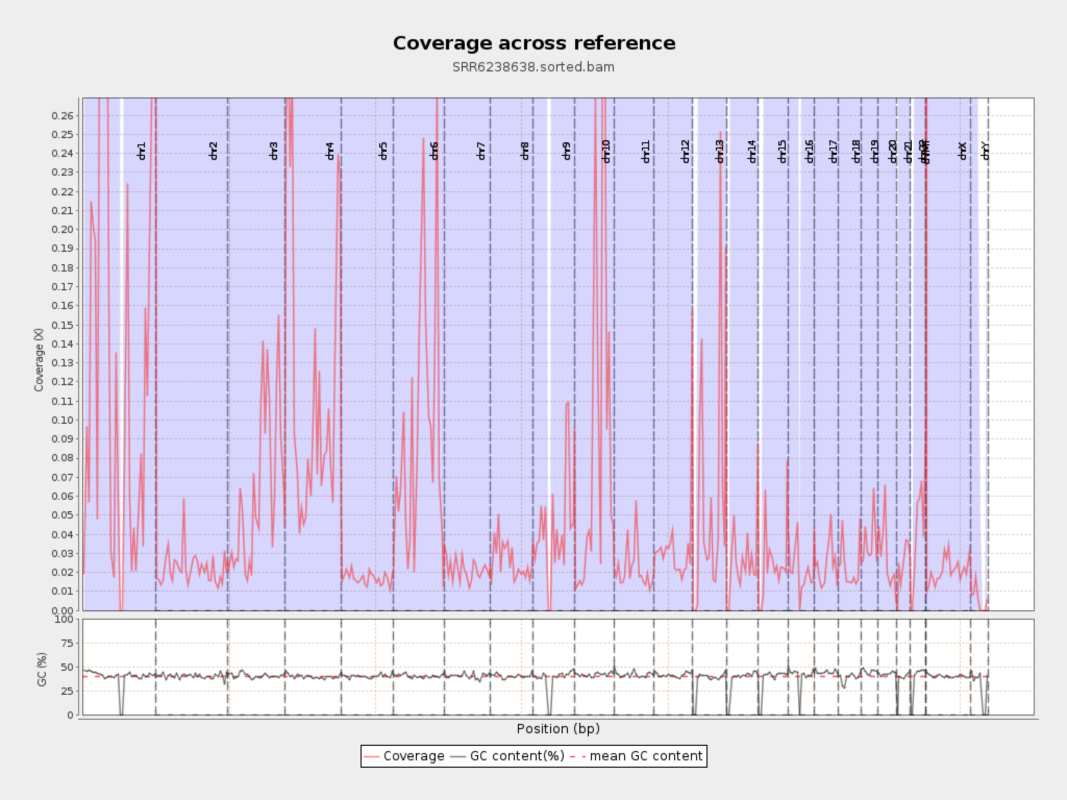
General error rate	0.55%
Mismatches	847,357
Insertions	10,483
Mapped reads with at least one insertion	0.41%
Deletions	43,638
Mapped reads with at least one deletion	1.69%
Homopolymer indels	42.09%

2.6. Chromosome stats

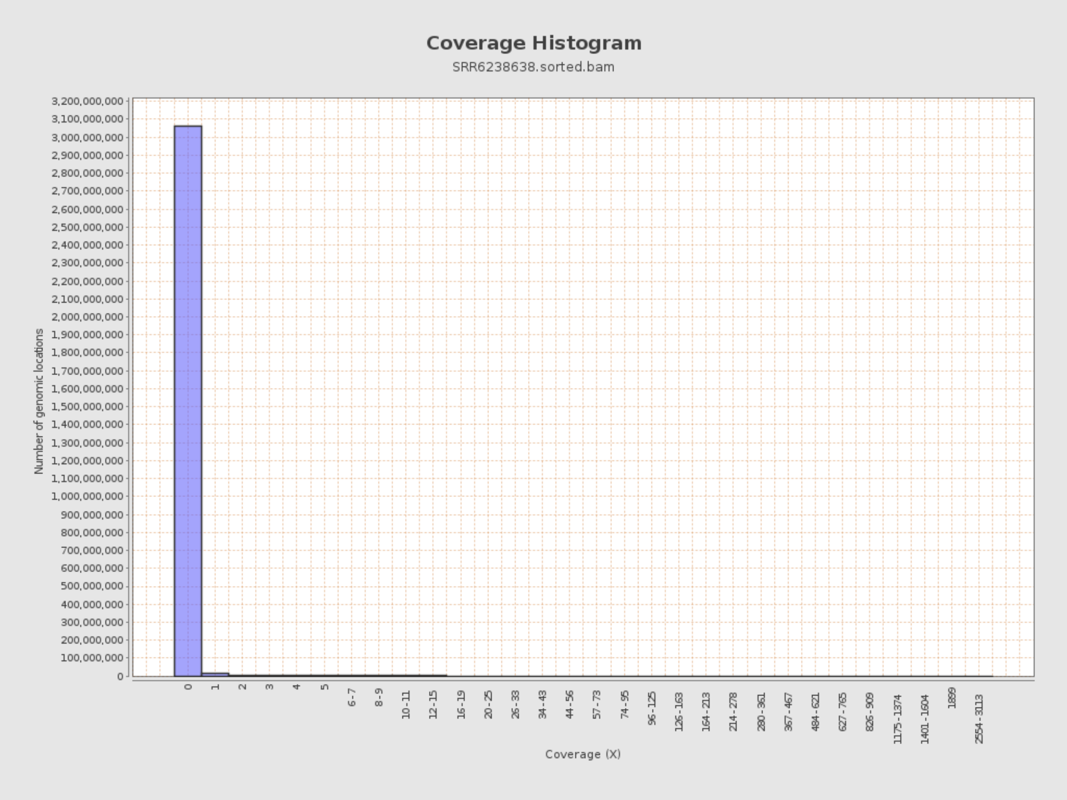
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34984691	0.1404	1.3213
chr2	243199373	5388992	0.0222	1.4582
chr3	198022430	12563287	0.0634	0.9054
chr4	191154276	23297167	0.1219	1.2075
chr5	180915260	3085692	0.0171	0.4178
chr6	171115067	17016573	0.0994	1.203
chr7	159138663	3452825	0.0217	0.5867

chr8	146364022	3765297	0.0257	0.7153
chr9	141213431	6099843	0.0432	0.7145
chr10	135534747	13346102	0.0985	1.086
chr11	135006516	2928884	0.0217	0.4827
chr12	133851895	4171164	0.0312	0.5951
chr13	115169878	6694672	0.0581	0.8935
chr14	107349540	2519400	0.0235	0.5482
chr15	102531392	2348405	0.0229	0.5769
chr16	90354753	1862726	0.0206	0.4961
chr17	81195210	2037265	0.0251	0.5094
chr18	78077248	1794699	0.023	2.0542
chr19	59128983	2088529	0.0353	0.6568
chr20	63025520	1856623	0.0295	0.5935
chr21	48129895	1220554	0.0254	0.5315
chr22	51304566	2066856	0.0403	0.6565
chrMT	16571	43422	2.6204	5.283
chrX	155270560	3250889	0.0209	0.4676
chrY	59373566	349817	0.0059	0.3603

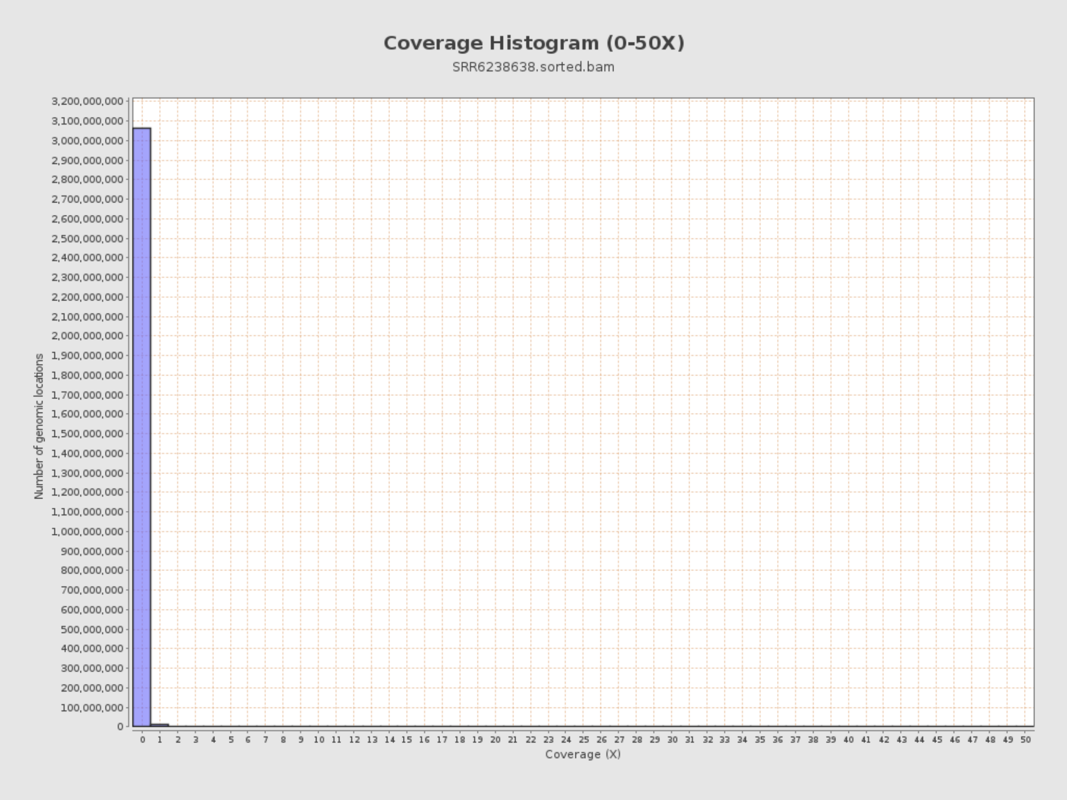
3. Results : Coverage across reference



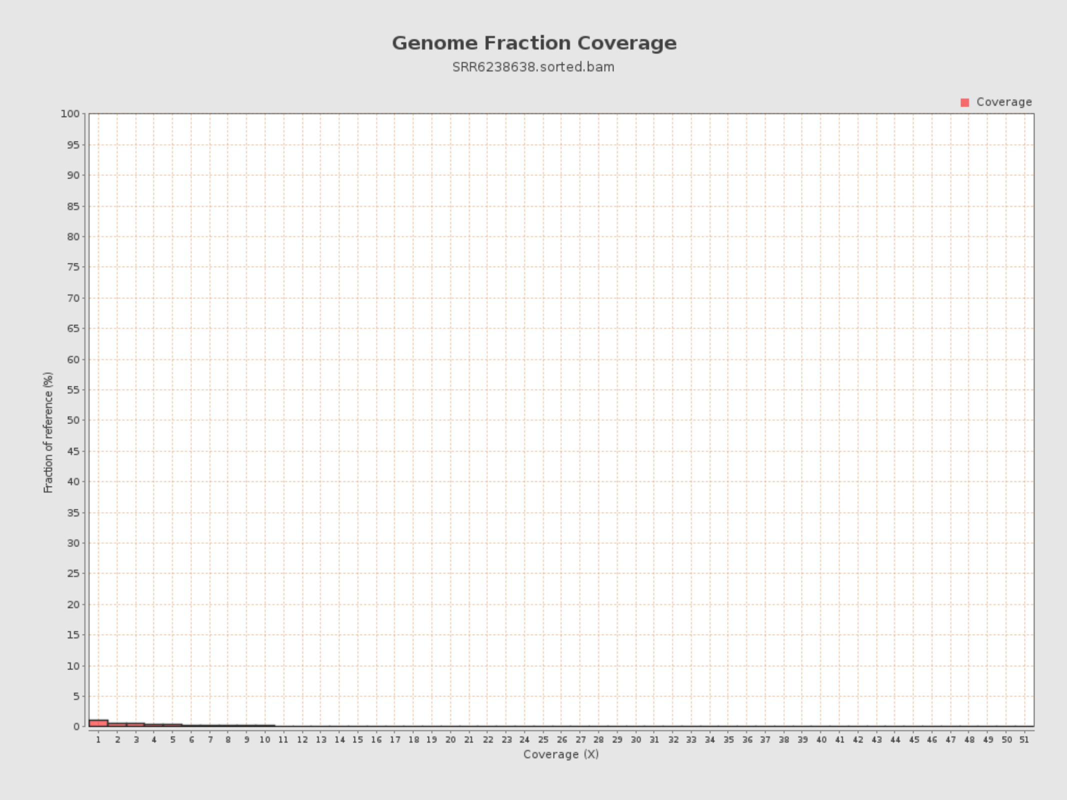
4. Results : Coverage Histogram



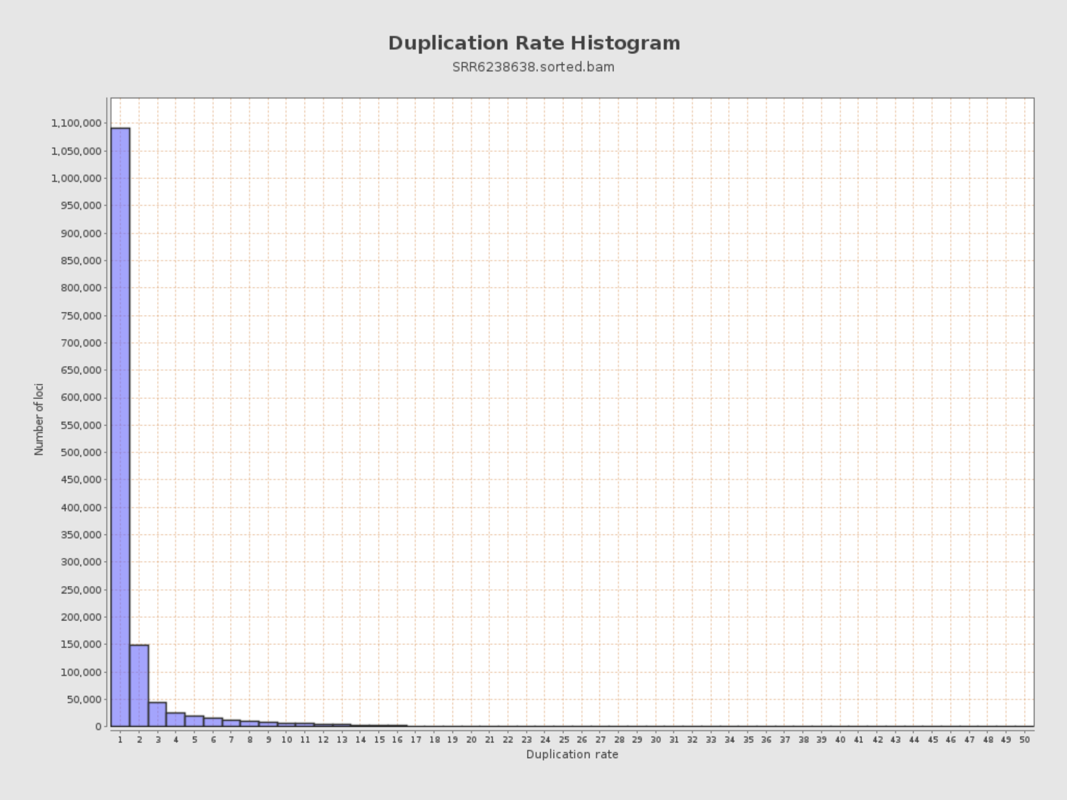
5. Results : Coverage Histogram (0-50X)



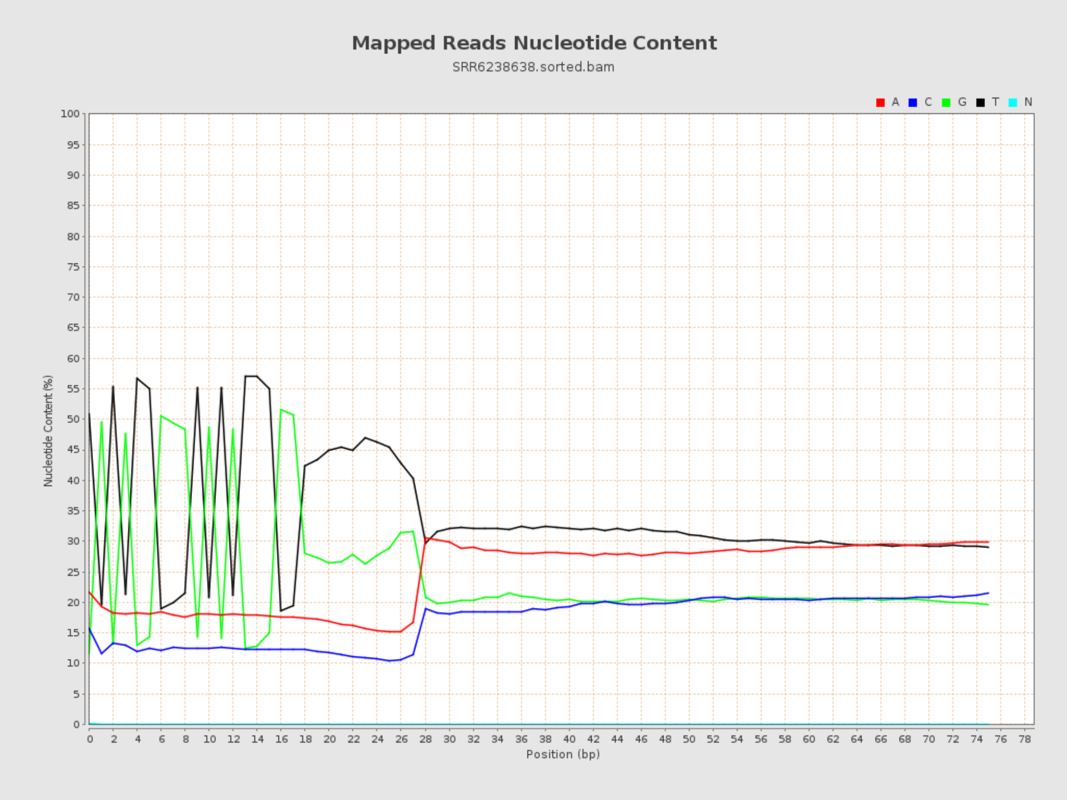
6. Results : Genome Fraction Coverage



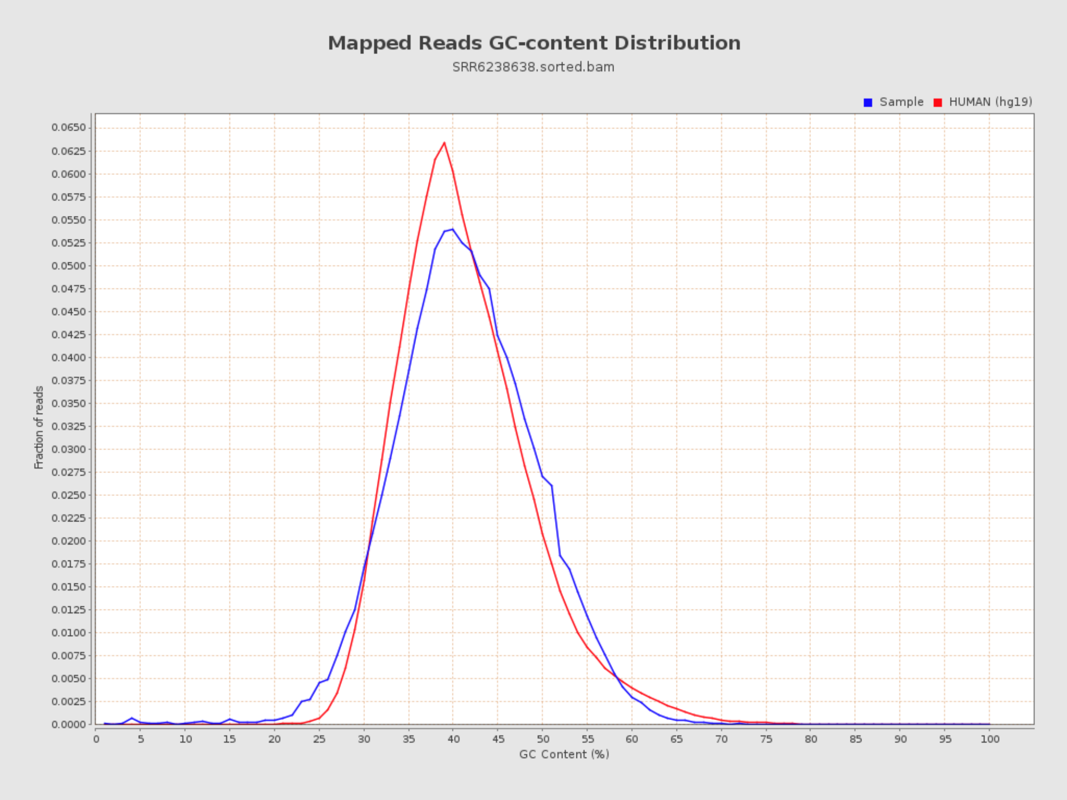
7. Results : Duplication Rate Histogram



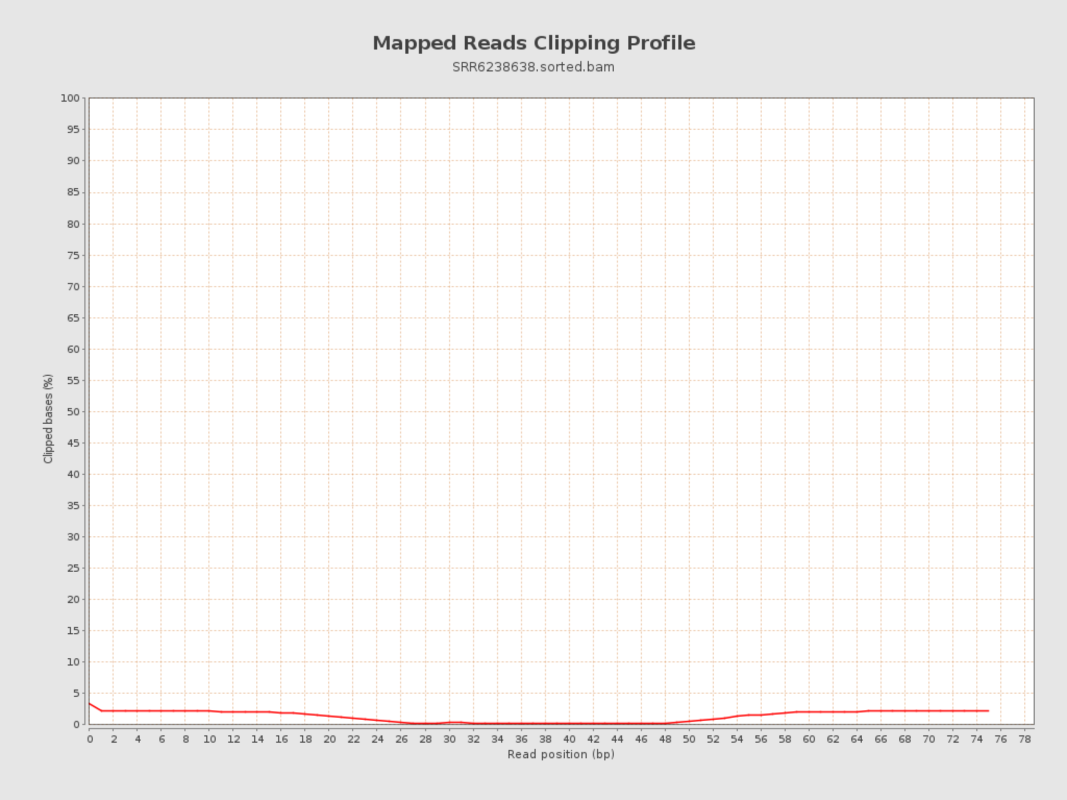
8. Results : Mapped Reads Nucleotide Content



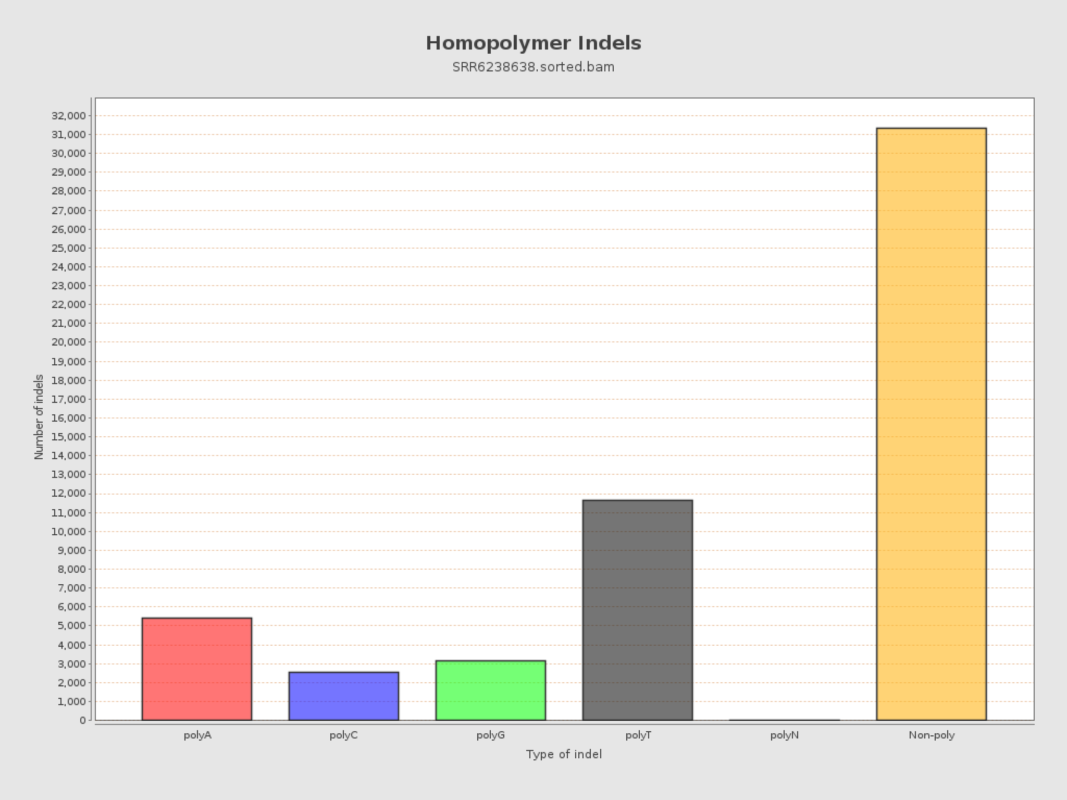
9. Results : Mapped Reads GC-content Distribution



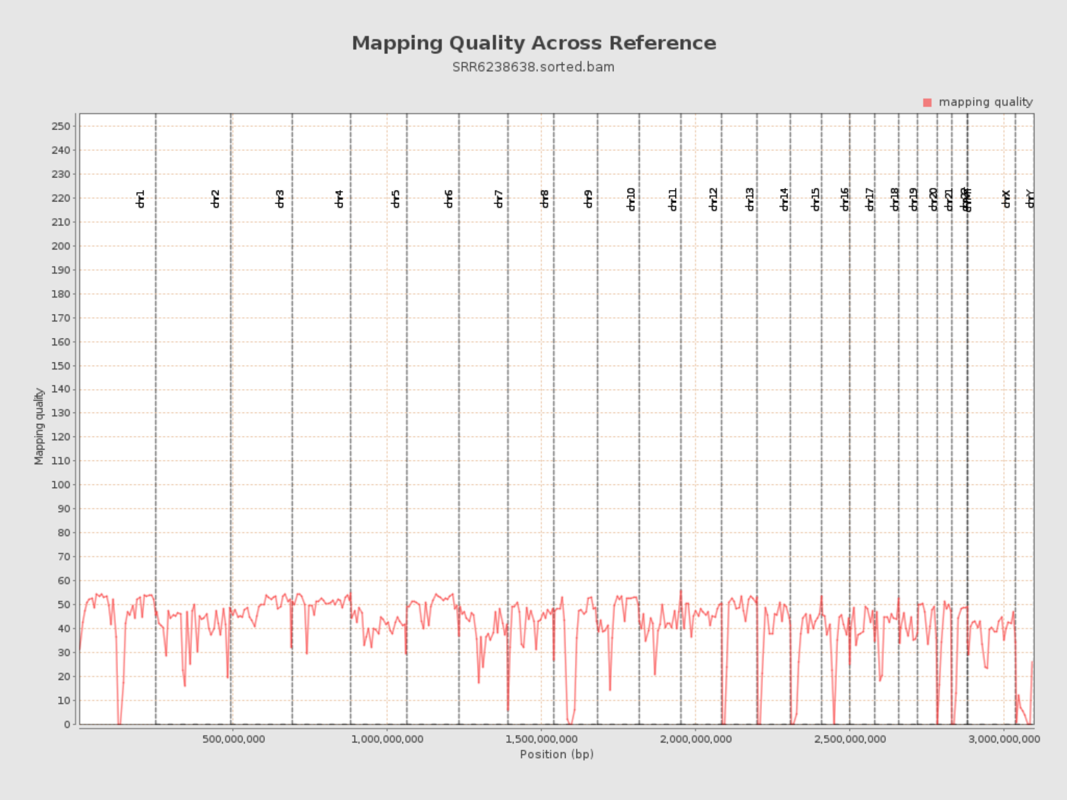
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram