Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:16:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238081.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_SRR6238081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:16:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,913,795
Mapped reads	1,220,055 / 63.75%
Unmapped reads	693,740 / 36.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,110 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	181,185 / 9.47%
Duplication rate	12.01%
Clipped reads	817,931 / 42.74%

2.2. ACGT Content

Number/percentage of A's	19,598,816 / 26.49%
Number/percentage of C's	12,763,497 / 17.25%
Number/percentage of T's	24,207,177 / 32.72%
Number/percentage of G's	17,406,128 / 23.53%
Number/percentage of N's	3,465 / 0%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.3112

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

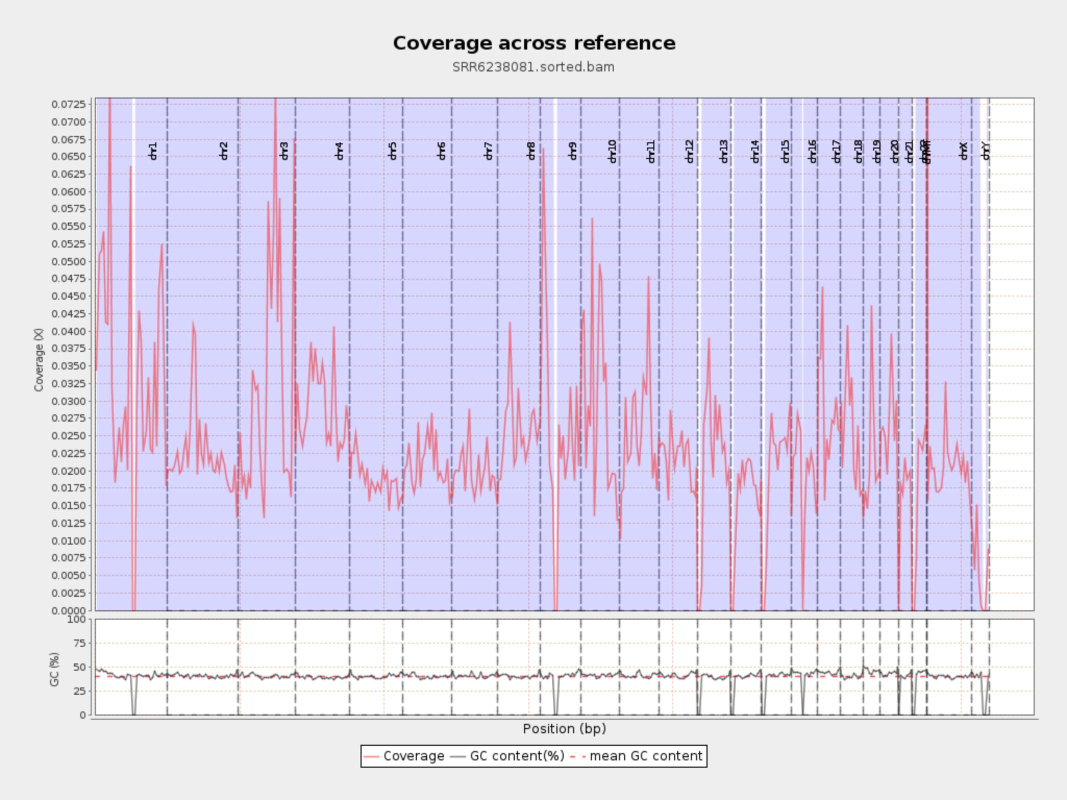
General error rate	0.77%
Mismatches	561,100
Insertions	5,687
Mapped reads with at least one insertion	0.46%
Deletions	22,705
Mapped reads with at least one deletion	1.84%
Homopolymer indels	45.88%

2.6. Chromosome stats

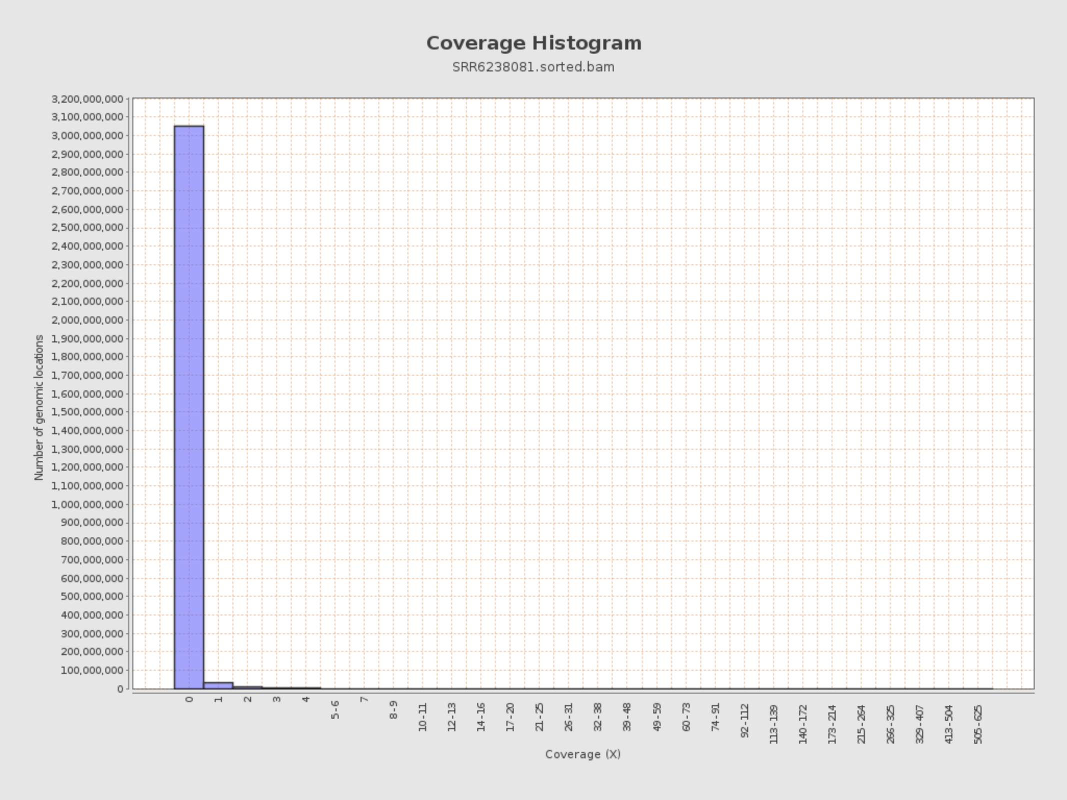
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8281430	0.0332	0.5431
chr2	243199373	5414338	0.0223	0.3747
chr3	198022430	6289283	0.0318	0.2748
chr4	191154276	5548823	0.029	0.2592
chr5	180915260	3424351	0.0189	0.2018
chr6	171115067	3581945	0.0209	0.25
chr7	159138663	3187919	0.02	0.2585

chr8	146364022	3775164	0.0258	0.4045
chr9	141213431	3706067	0.0262	0.2755
chr10	135534747	3948014	0.0291	0.3227
chr11	135006516	3455714	0.0256	0.2843
chr12	133851895	2943012	0.022	0.2339
chr13	115169878	2456379	0.0213	0.2276
chr14	107349540	1675055	0.0156	0.1921
chr15	102531392	2013218	0.0196	0.2099
chr16	90354753	1710942	0.0189	0.2089
chr17	81195210	2345856	0.0289	0.263
chr18	78077248	1985748	0.0254	0.5114
chr19	59128983	1327673	0.0225	0.358
chr20	63025520	1688674	0.0268	0.2432
chr21	48129895	806488	0.0168	0.1942
chr22	51304566	866742	0.0169	0.1908
chrMT	16571	55138	3.3274	3.1249
chrX	155270560	3198027	0.0206	0.2259
chrY	59373566	329104	0.0055	0.1215

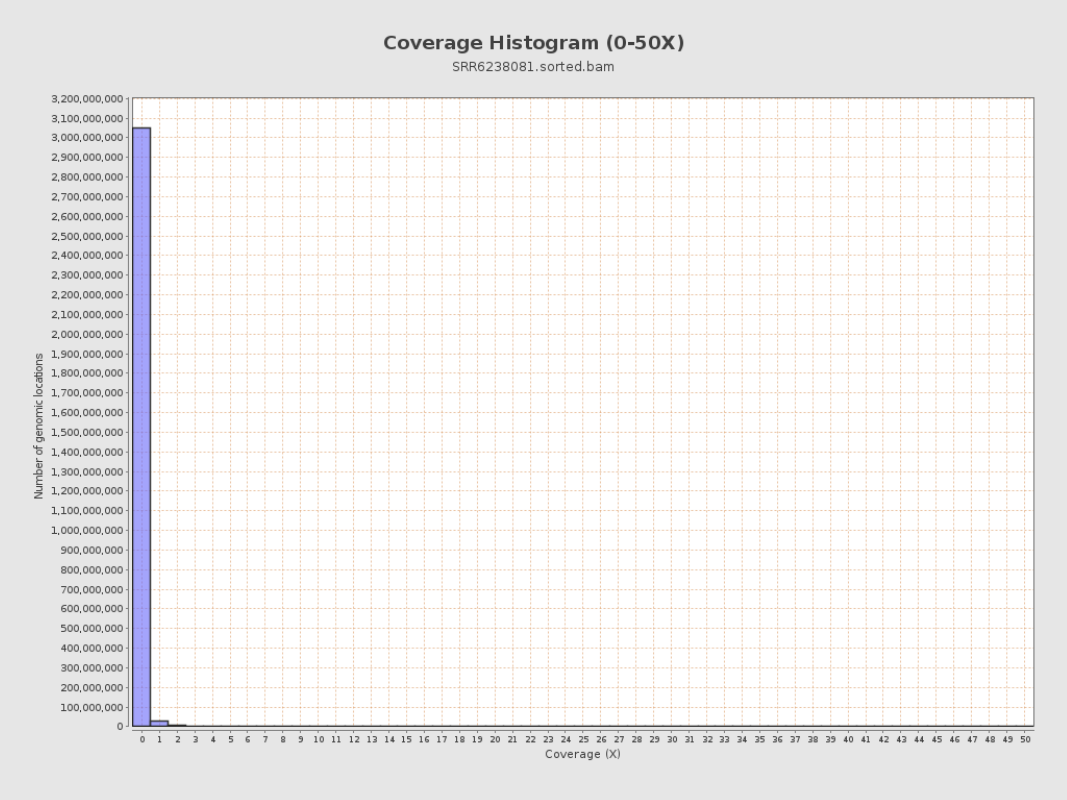
3. Results : Coverage across reference



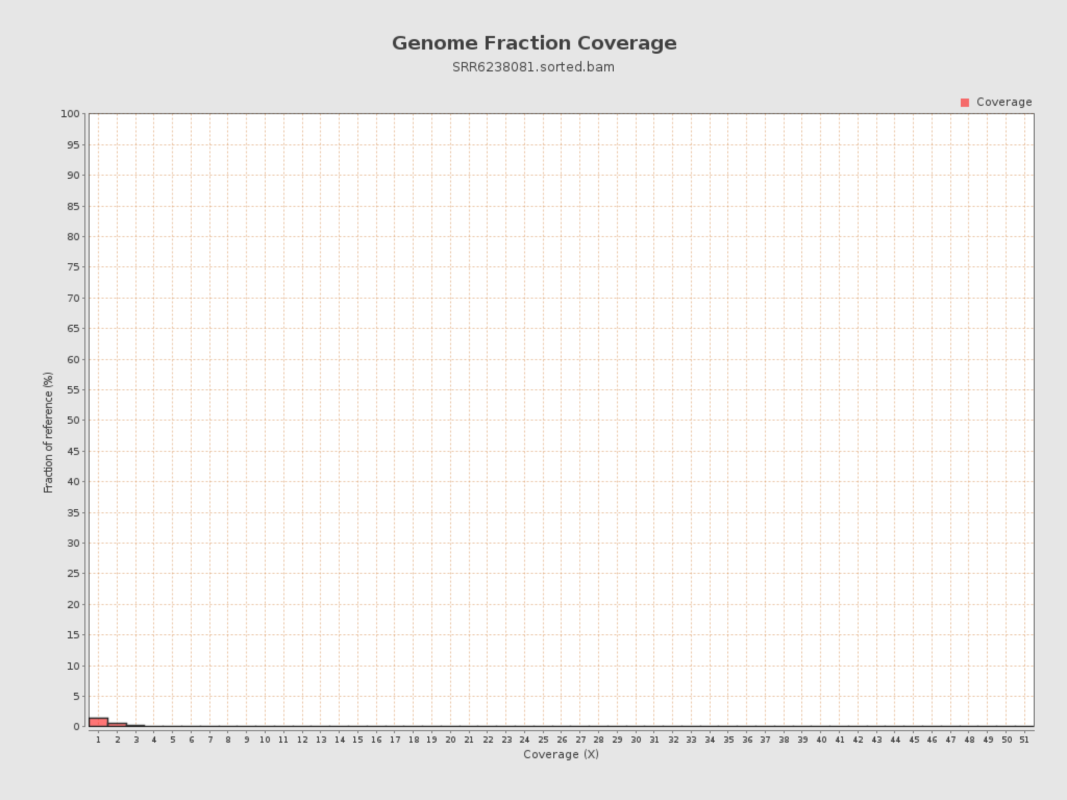
4. Results : Coverage Histogram



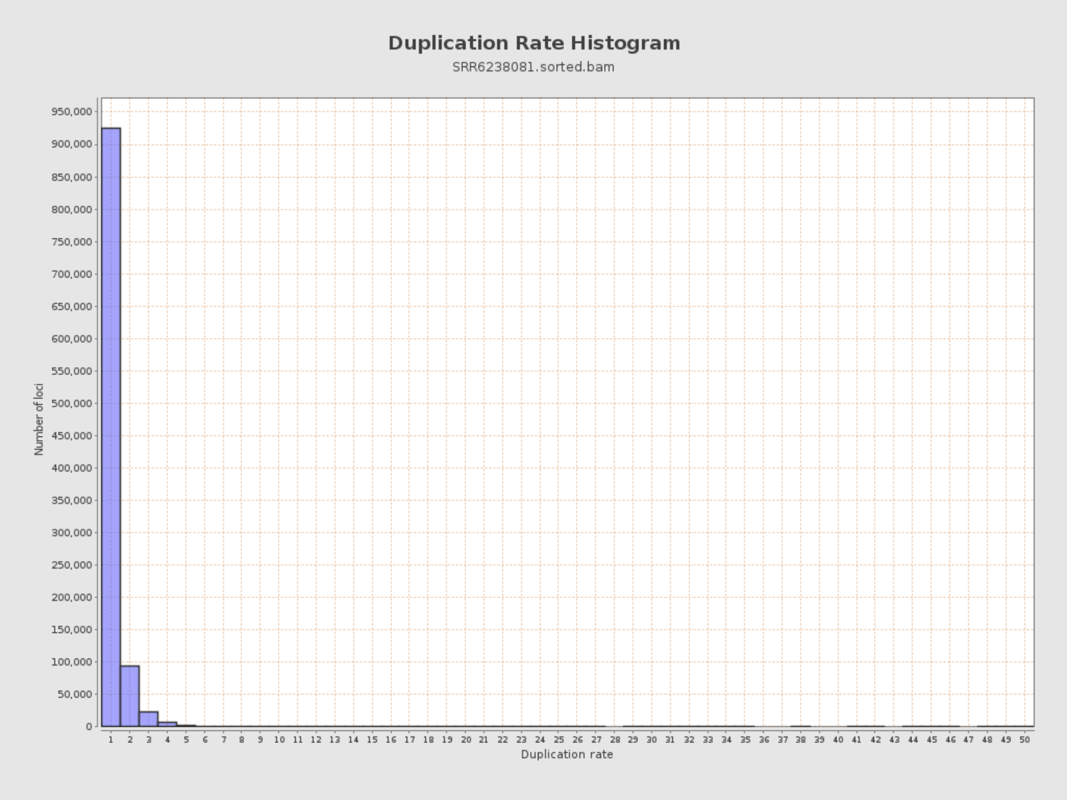
5. Results : Coverage Histogram (0-50X)



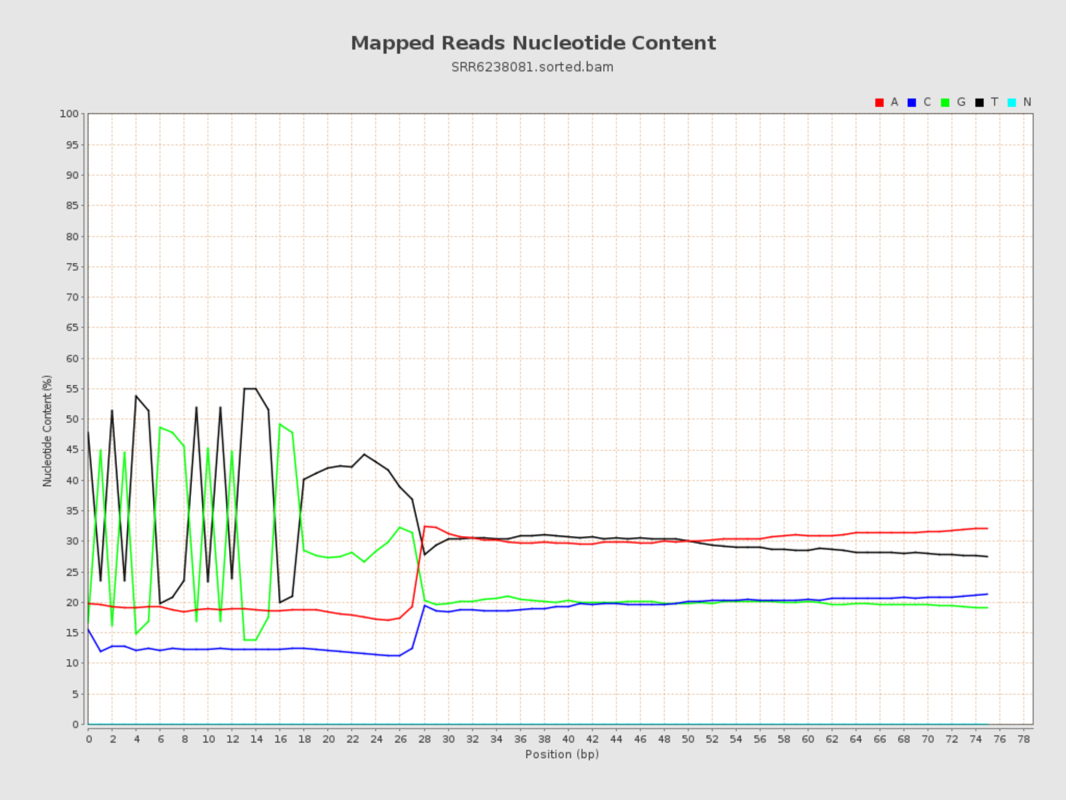
6. Results : Genome Fraction Coverage



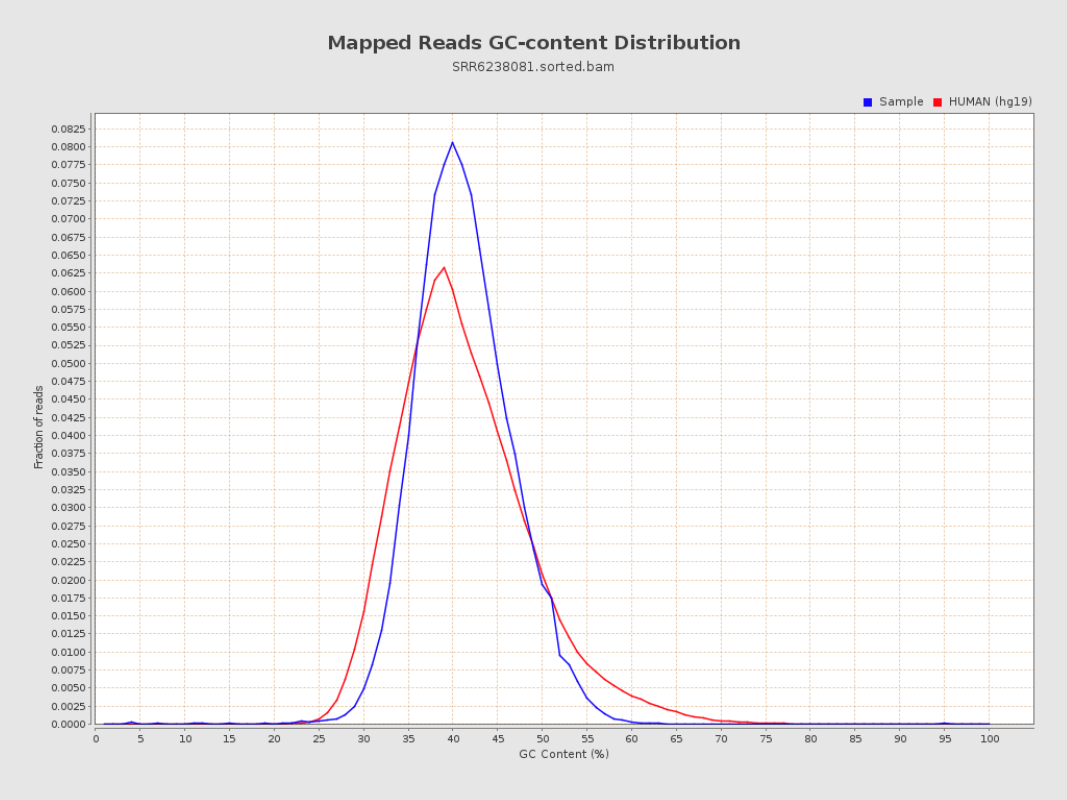
7. Results : Duplication Rate Histogram



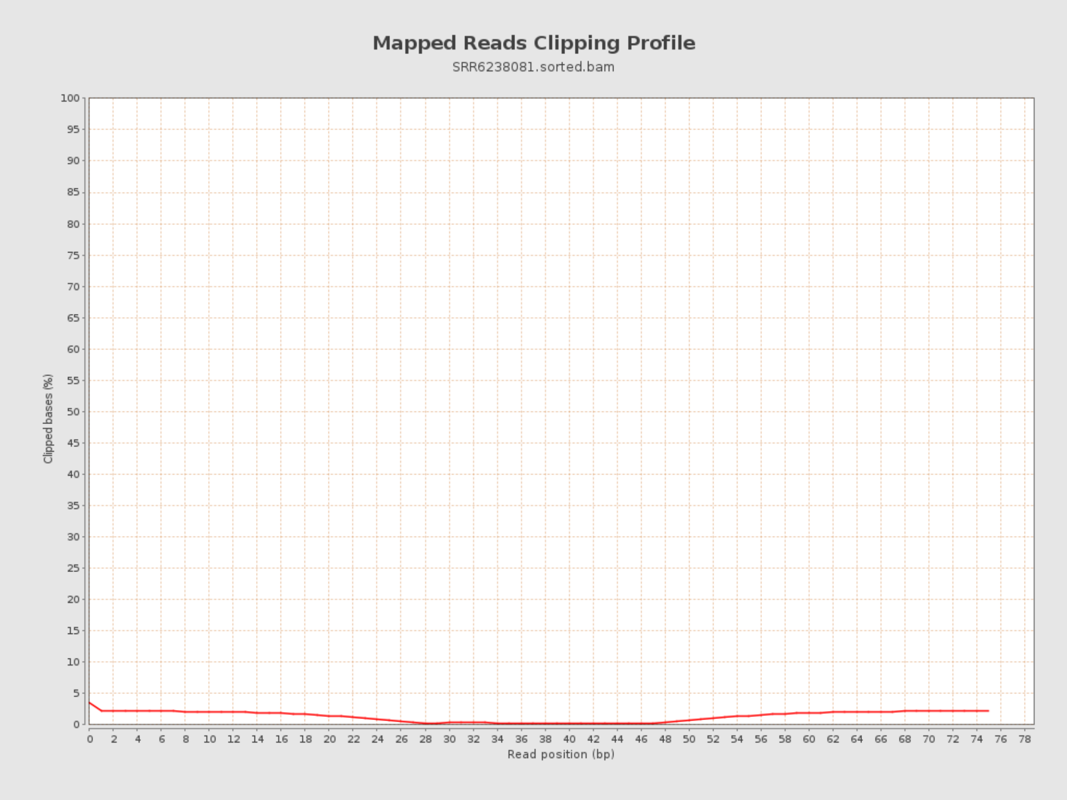
8. Results : Mapped Reads Nucleotide Content



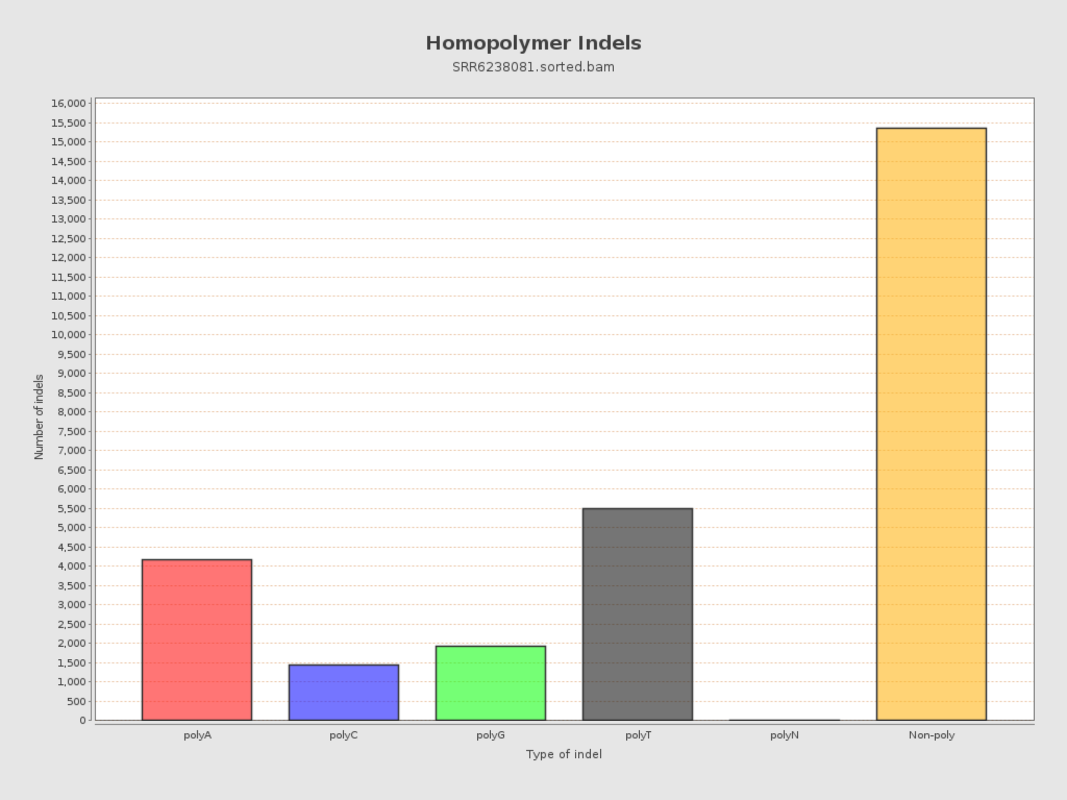
9. Results : Mapped Reads GC-content Distribution



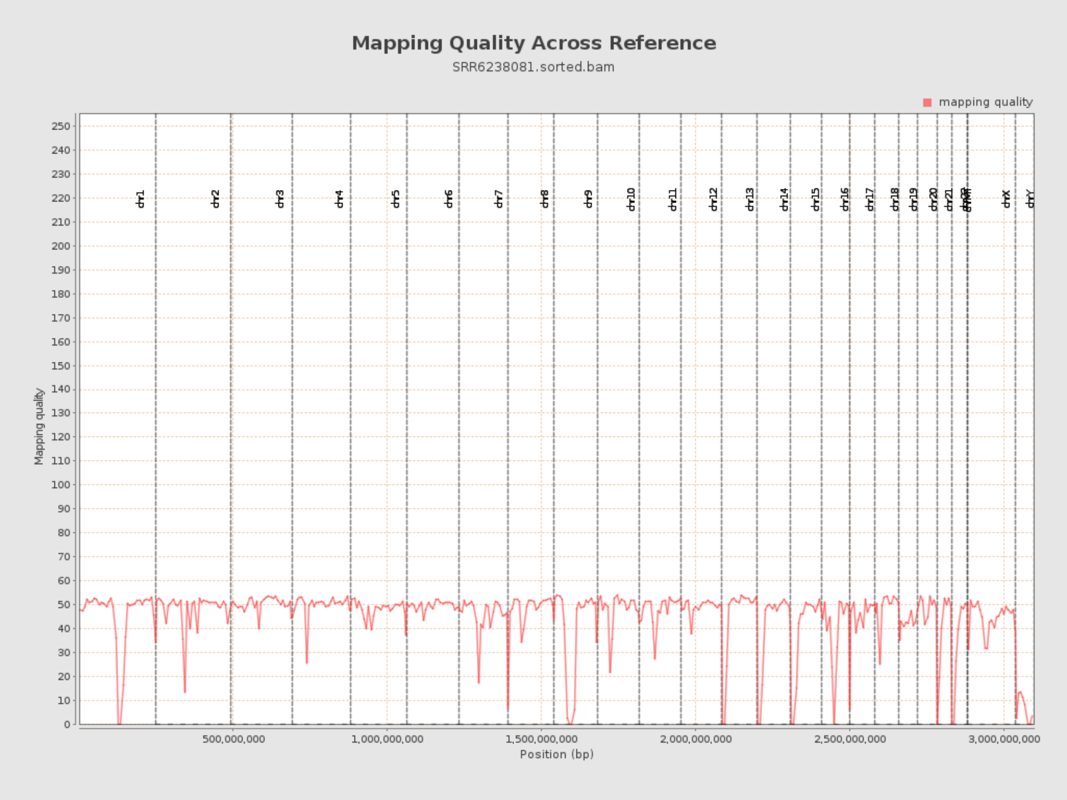
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram