Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:20:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238630.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_SRR6238630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238630.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:20:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,670,290
Mapped reads	2,091,951 / 78.34%
Unmapped reads	578,339 / 21.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,201 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	707,921 / 26.51%
Duplication rate	23.21%
Clipped reads	1,425,276 / 53.38%

2.2. ACGT Content

Number/percentage of A's	31,517,217 / 24.97%
Number/percentage of C's	21,596,204 / 17.11%
Number/percentage of T's	42,911,003 / 34%
Number/percentage of G's	30,165,583 / 23.9%
Number/percentage of N's	6,132 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.7327

2.4. Mapping Quality

Mean Mapping Quality	41.39

2.5. Mismatches and indels

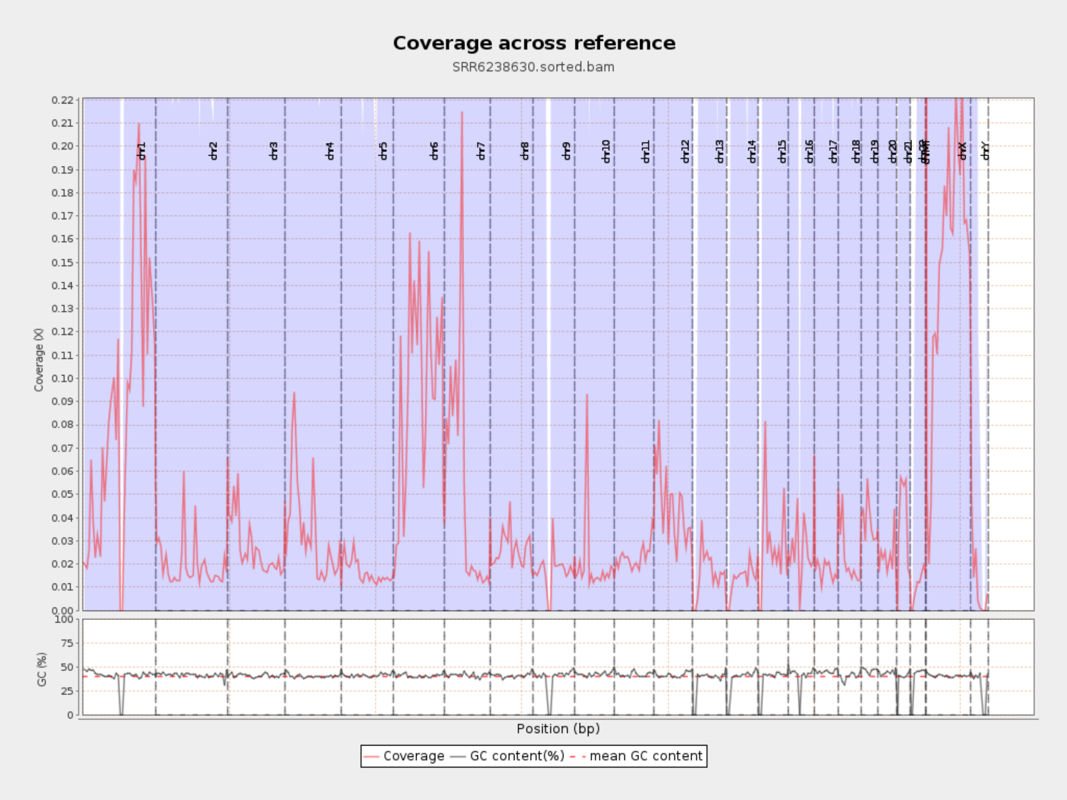
General error rate	0.63%
Mismatches	782,235
Insertions	7,586
Mapped reads with at least one insertion	0.36%
Deletions	36,422
Mapped reads with at least one deletion	1.72%
Homopolymer indels	41.74%

2.6. Chromosome stats

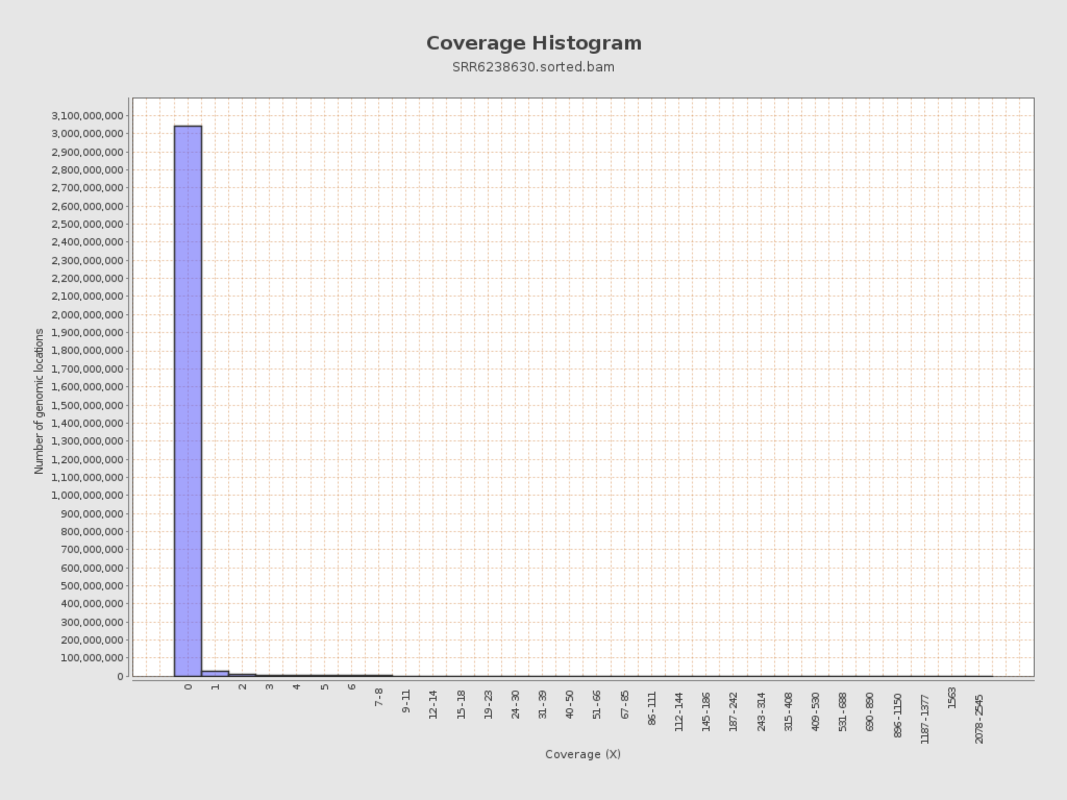
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21511422	0.0863	0.882
chr2	243199373	4741022	0.0195	1.1739
chr3	198022430	5466157	0.0276	0.3513
chr4	191154276	6468253	0.0338	0.3836
chr5	180915260	3032240	0.0168	0.2689
chr6	171115067	16510286	0.0965	0.9764
chr7	159138663	8610114	0.0541	1.5359

chr8	146364022	3874513	0.0265	0.512
chr9	141213431	2417603	0.0171	0.3518
chr10	135534747	2672067	0.0197	0.6585
chr11	135006516	3137659	0.0232	0.3194
chr12	133851895	6034958	0.0451	0.4603
chr13	115169878	1851940	0.0161	0.3714
chr14	107349540	1451313	0.0135	0.2664
chr15	102531392	2877249	0.0281	0.4233
chr16	90354753	2286763	0.0253	0.3511
chr17	81195210	1394897	0.0172	0.2665
chr18	78077248	1778746	0.0228	1.4196
chr19	59128983	2286241	0.0387	0.5855
chr20	63025520	1522100	0.0242	0.3313
chr21	48129895	1771160	0.0368	0.3938
chr22	51304566	546034	0.0106	0.2014
chrMT	16571	28648	1.7288	2.7666
chrX	155270560	23314880	0.1502	0.8395
chrY	59373566	671375	0.0113	0.3149

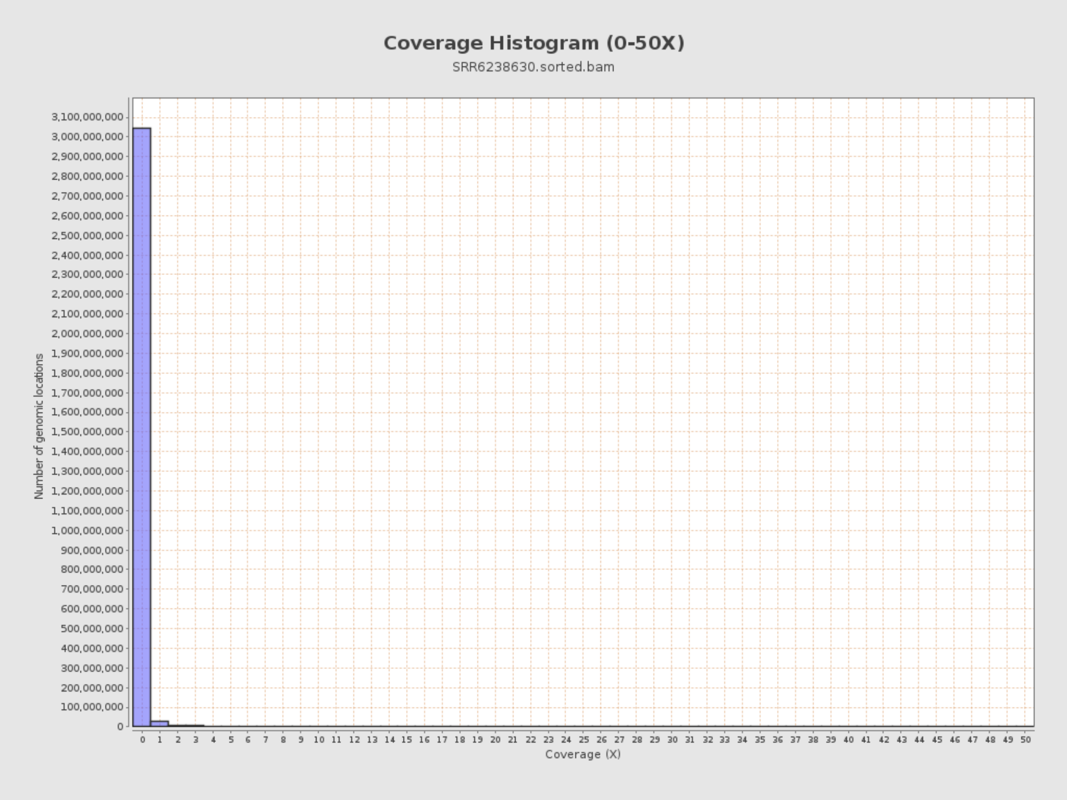
3. Results : Coverage across reference



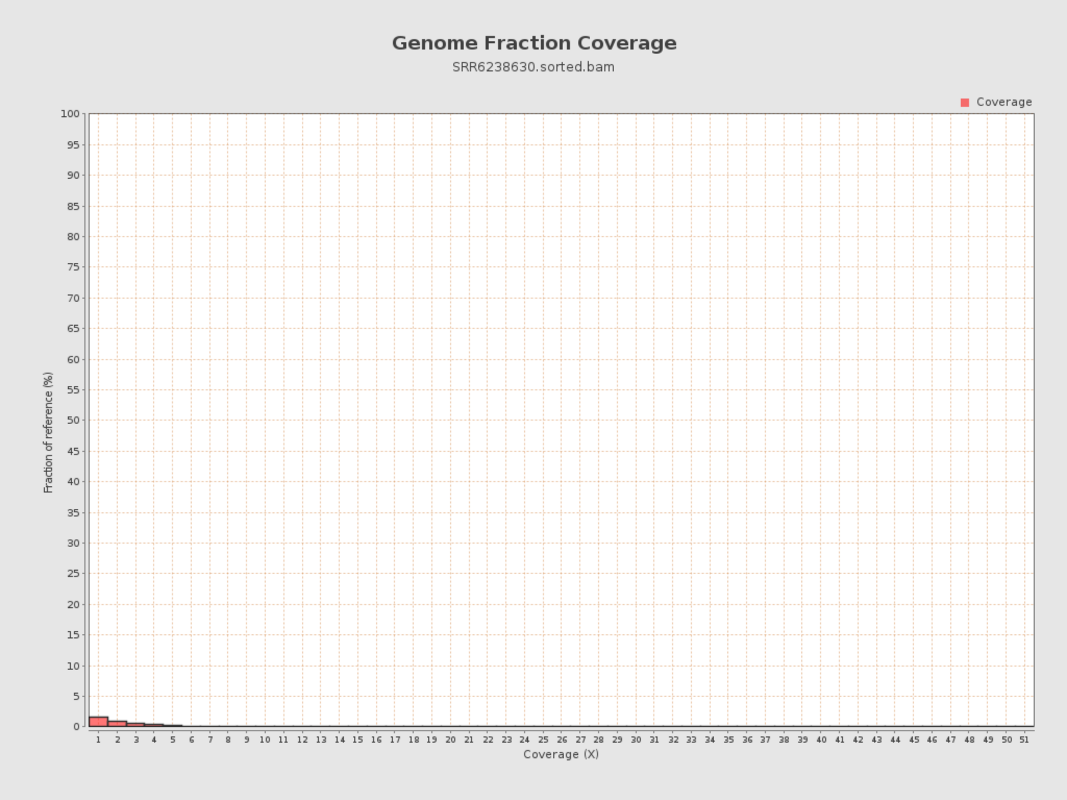
4. Results : Coverage Histogram



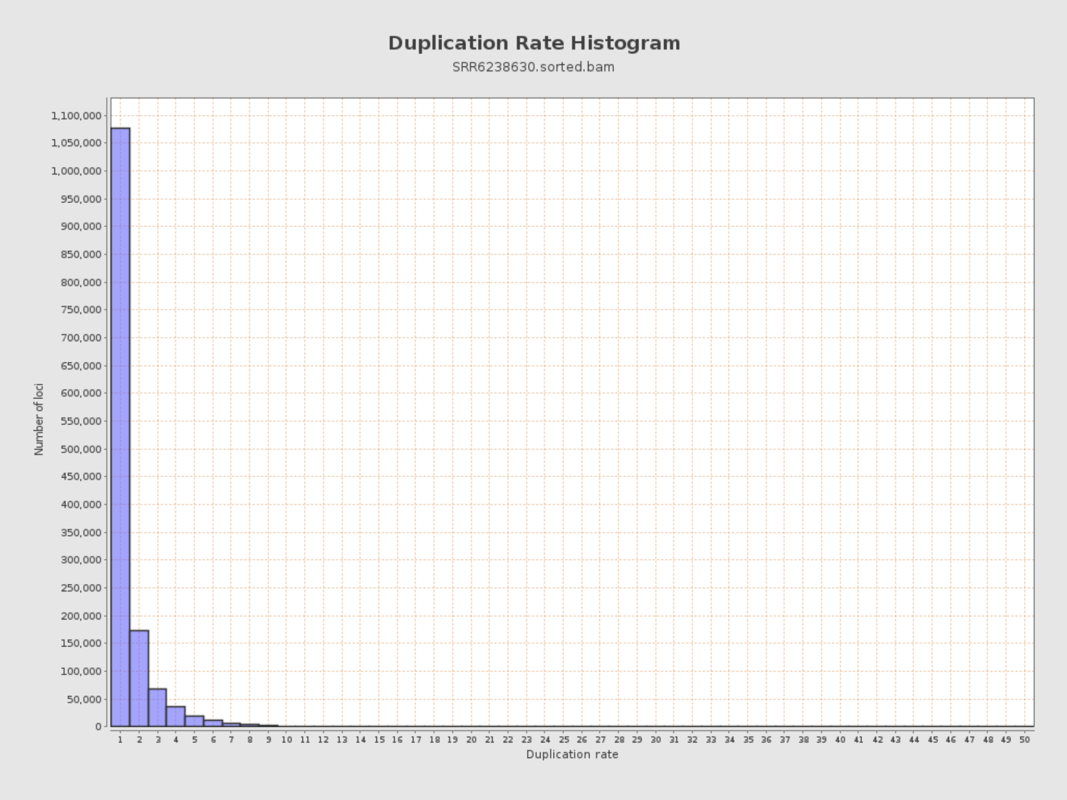
5. Results : Coverage Histogram (0-50X)



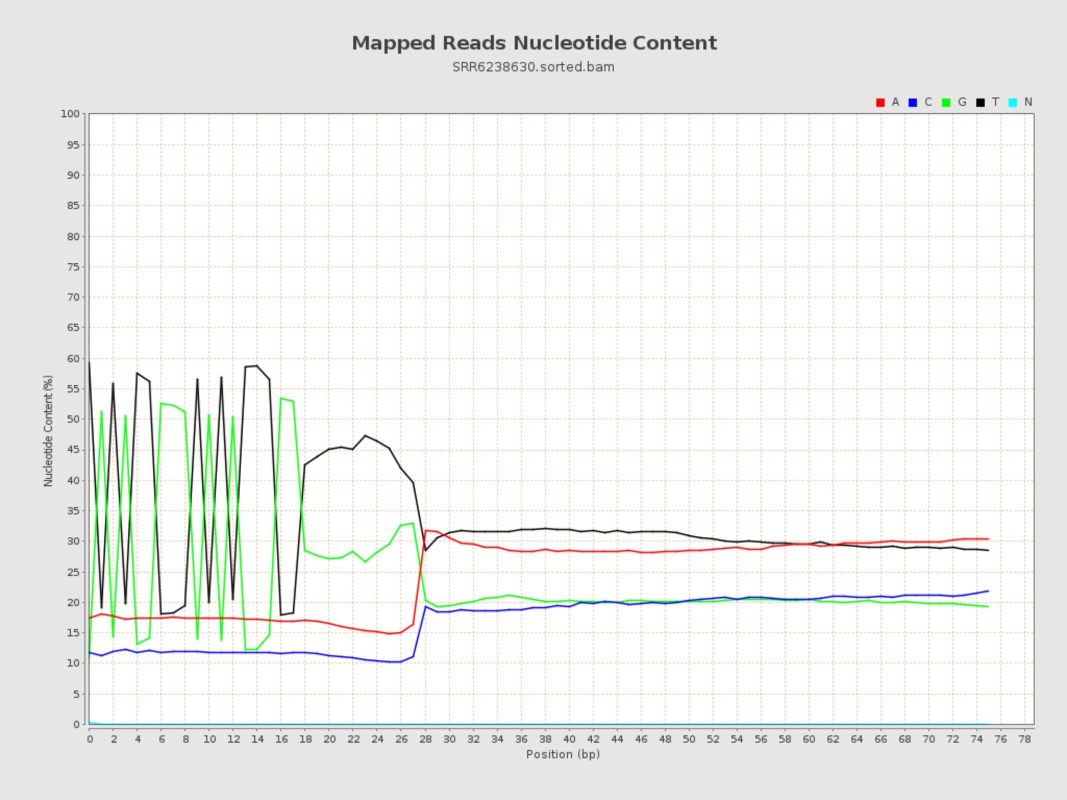
6. Results : Genome Fraction Coverage



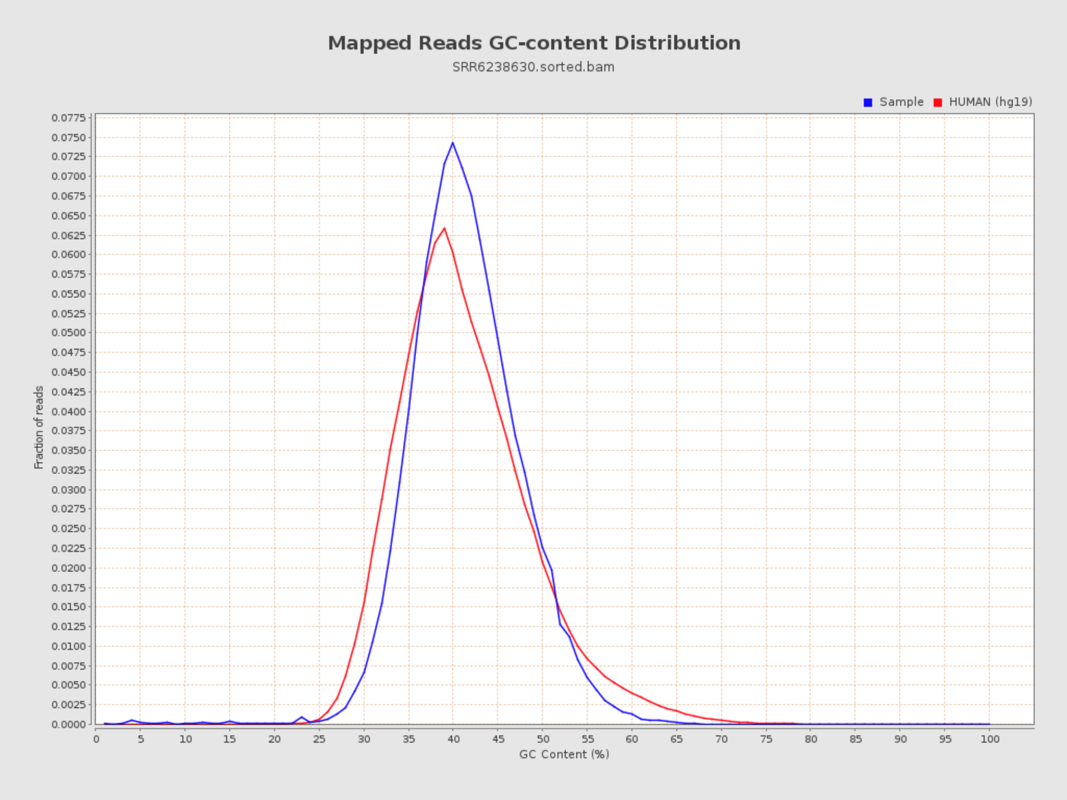
7. Results : Duplication Rate Histogram



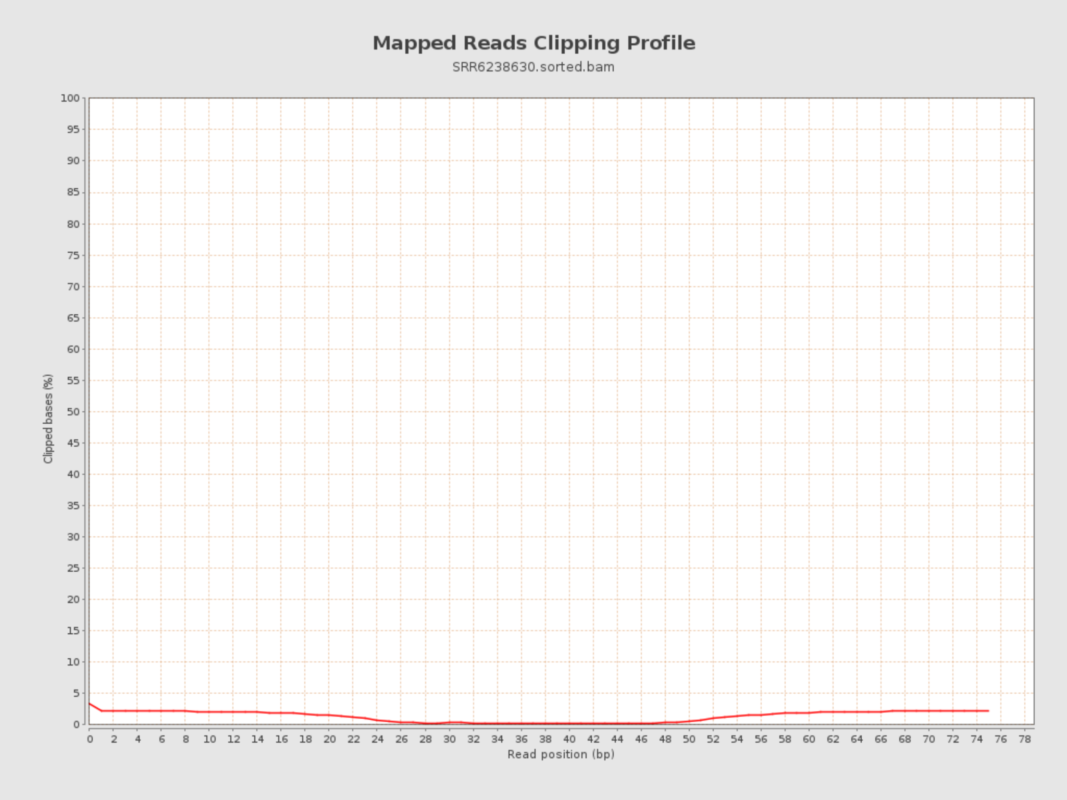
8. Results : Mapped Reads Nucleotide Content



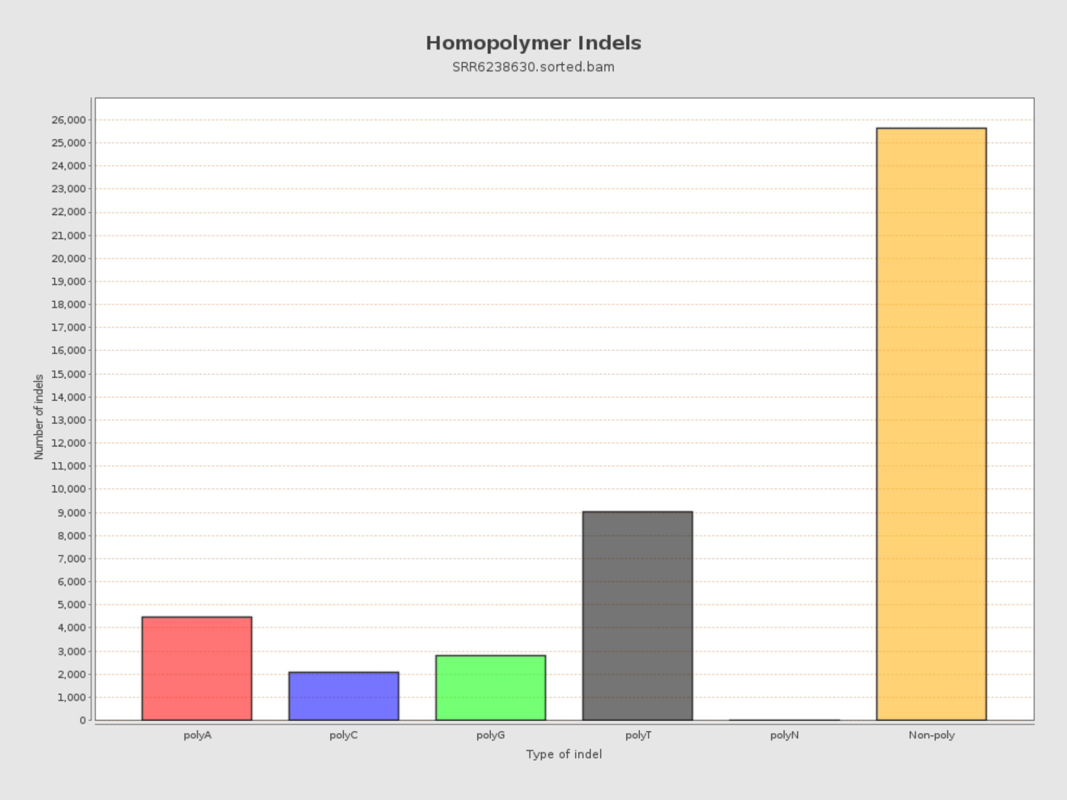
9. Results : Mapped Reads GC-content Distribution



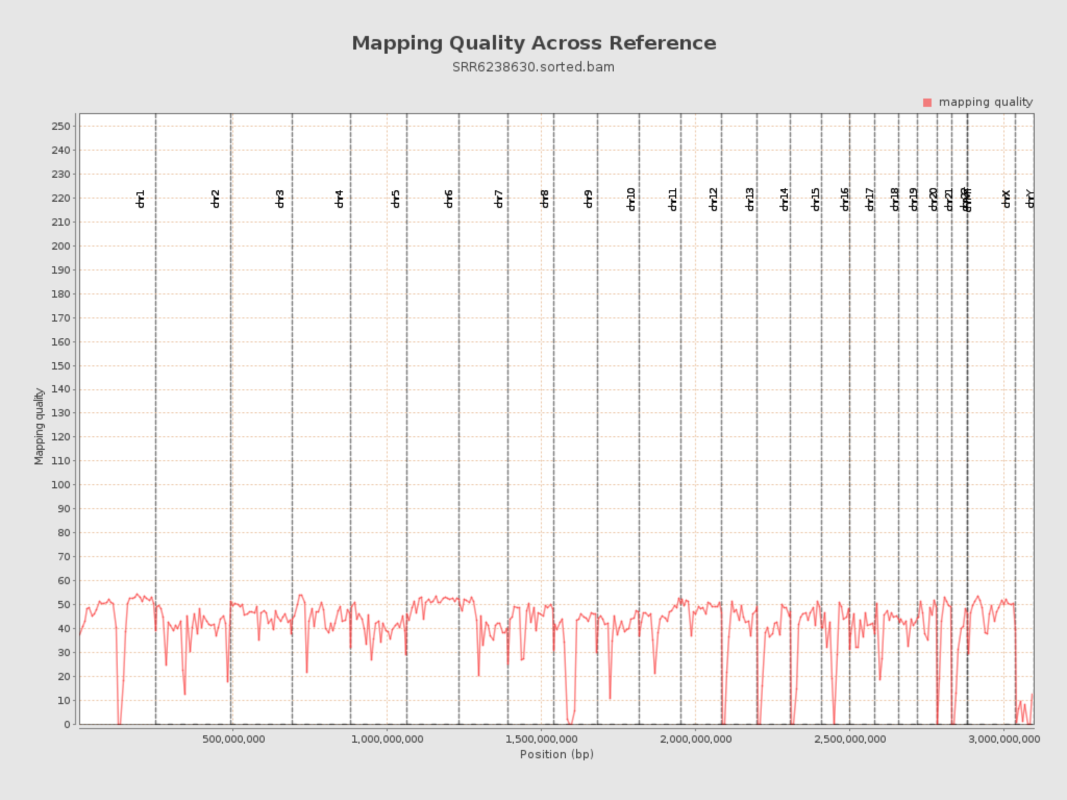
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram