Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:25:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238261.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_SRR6238261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238261.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:25:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,562,948
Mapped reads	1,393,418 / 89.15%
Unmapped reads	169,530 / 10.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,201 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	39,970 / 2.56%
Duplication rate	1.92%
Clipped reads	740,542 / 47.38%

2.2. ACGT Content

Number/percentage of A's	25,214,010 / 27.86%
Number/percentage of C's	17,371,512 / 19.2%
Number/percentage of T's	27,092,008 / 29.94%
Number/percentage of G's	20,795,522 / 22.98%
Number/percentage of N's	18,481 / 0.02%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0292

Standard Deviation	0.3072

2.4. Mapping Quality

Mean Mapping Quality	42.82

2.5. Mismatches and indels

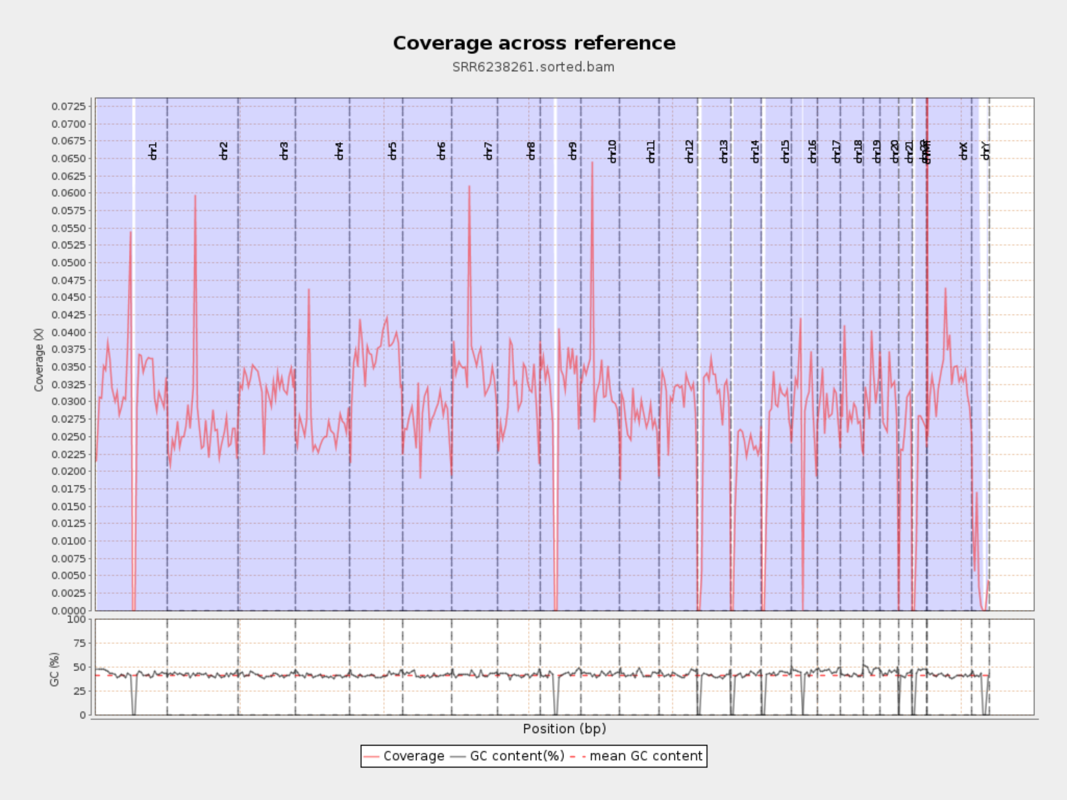
General error rate	0.9%
Mismatches	797,925
Insertions	7,926
Mapped reads with at least one insertion	0.56%
Deletions	25,893
Mapped reads with at least one deletion	1.84%
Homopolymer indels	44.18%

2.6. Chromosome stats

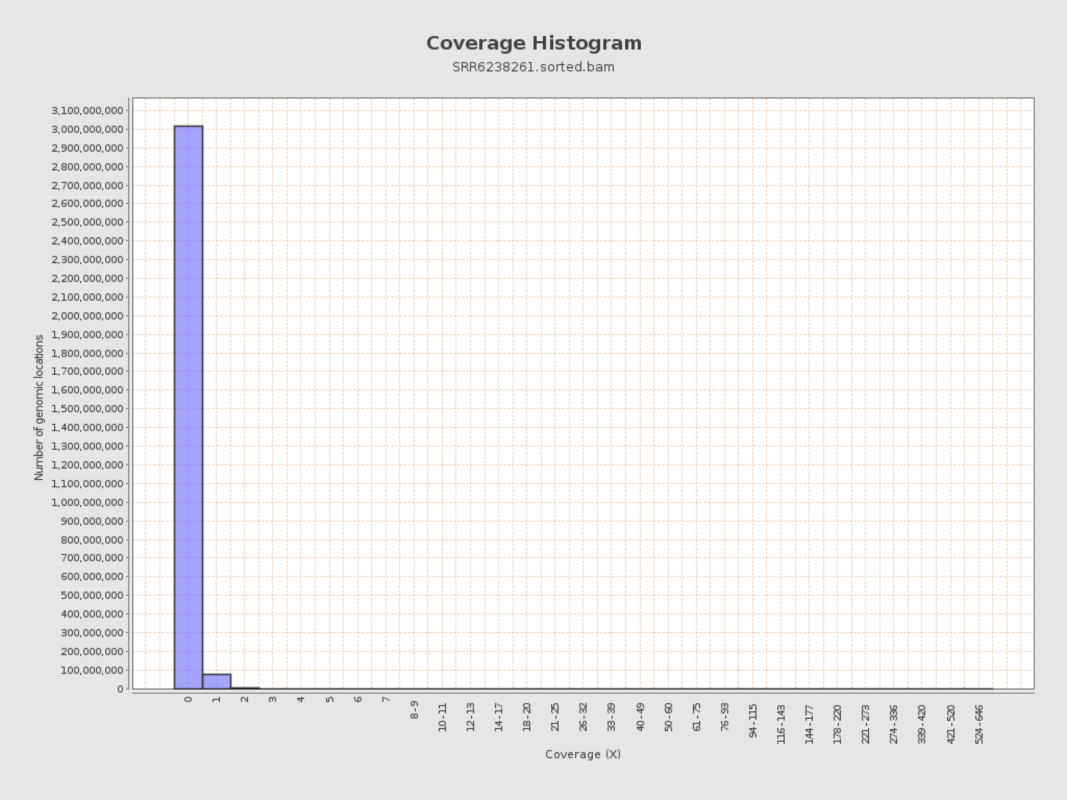
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7759094	0.0311	0.5296
chr2	243199373	6443048	0.0265	0.3456
chr3	198022430	6395402	0.0323	0.1932
chr4	191154276	5069141	0.0265	0.2017
chr5	180915260	6721109	0.0372	0.2094
chr6	171115067	4710802	0.0275	0.2043
chr7	159138663	5693415	0.0358	0.4401

chr8	146364022	4496040	0.0307	0.4318
chr9	141213431	4301463	0.0305	0.2926
chr10	135534747	4601032	0.0339	0.3433
chr11	135006516	3747260	0.0278	0.2282
chr12	133851895	4132933	0.0309	0.1924
chr13	115169878	3105853	0.027	0.1752
chr14	107349540	2196135	0.0205	0.1957
chr15	102531392	2534248	0.0247	0.1701
chr16	90354753	2540598	0.0281	0.2145
chr17	81195210	2386095	0.0294	0.2026
chr18	78077248	2260586	0.029	0.5301
chr19	59128983	1902681	0.0322	0.4187
chr20	63025520	1876463	0.0298	0.1954
chr21	48129895	1166798	0.0242	0.1935
chr22	51304566	971706	0.0189	0.1473
chrMT	16571	4387	0.2647	0.5526
chrX	155270560	5212468	0.0336	0.2197
chrY	59373566	306205	0.0052	0.1521

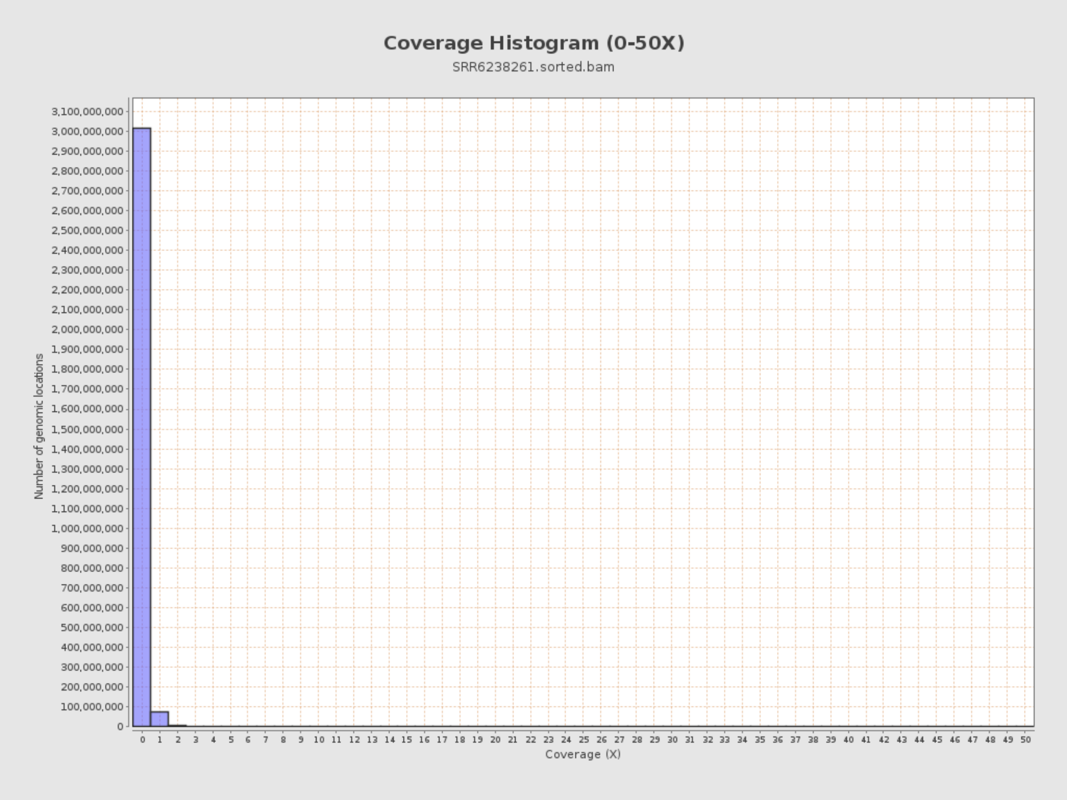
3. Results : Coverage across reference



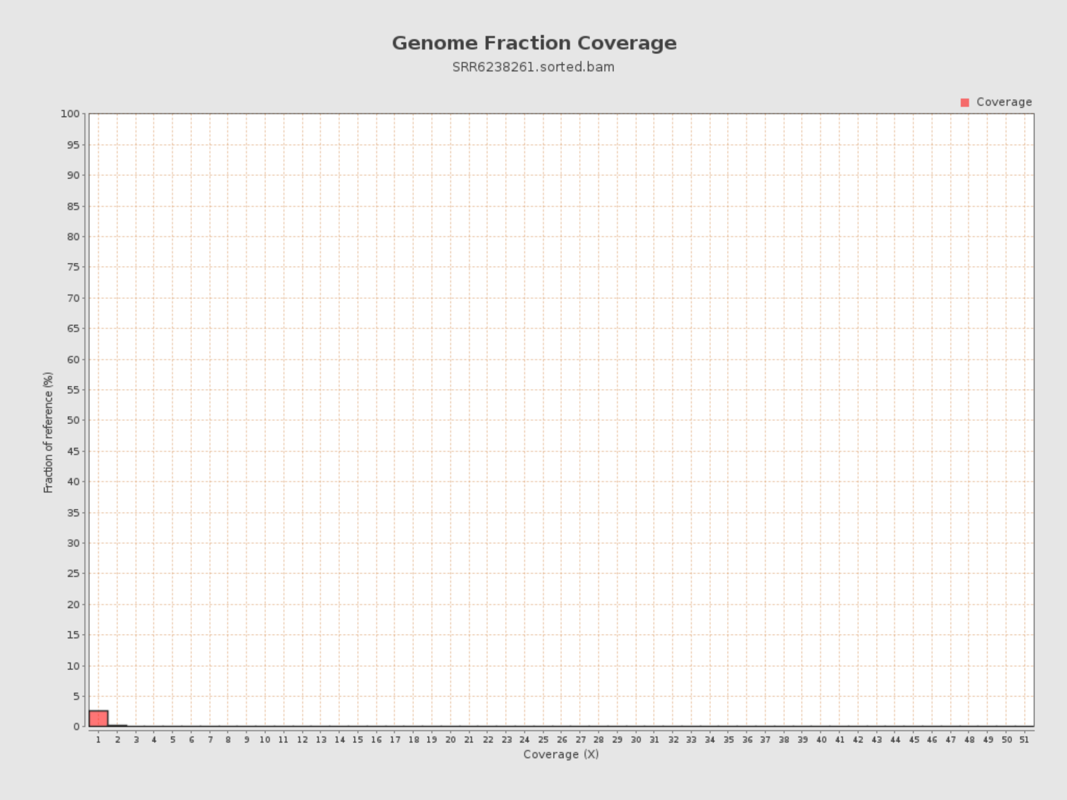
4. Results : Coverage Histogram



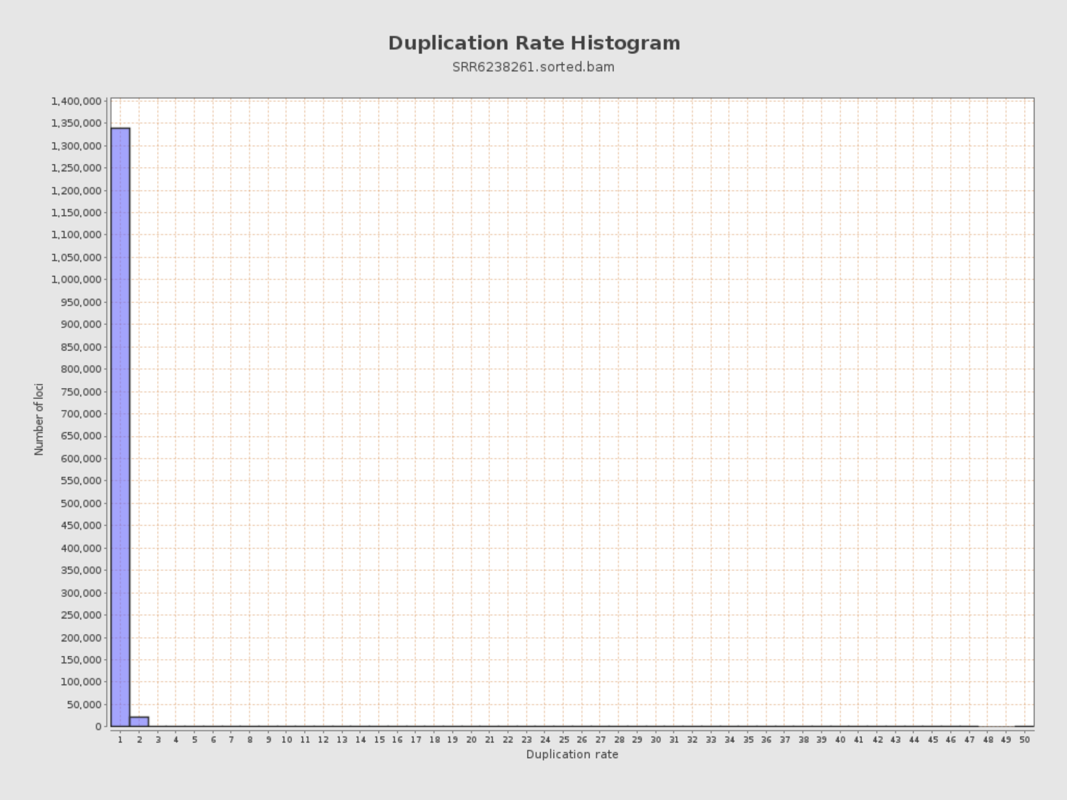
5. Results : Coverage Histogram (0-50X)



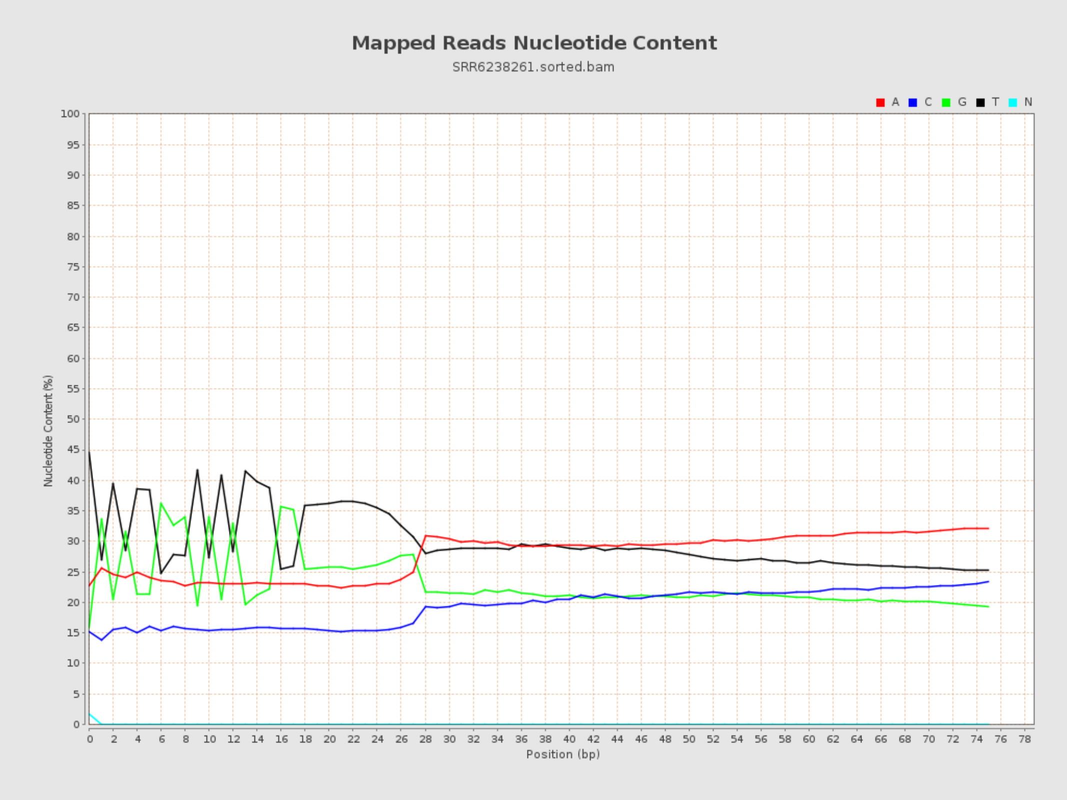
6. Results : Genome Fraction Coverage



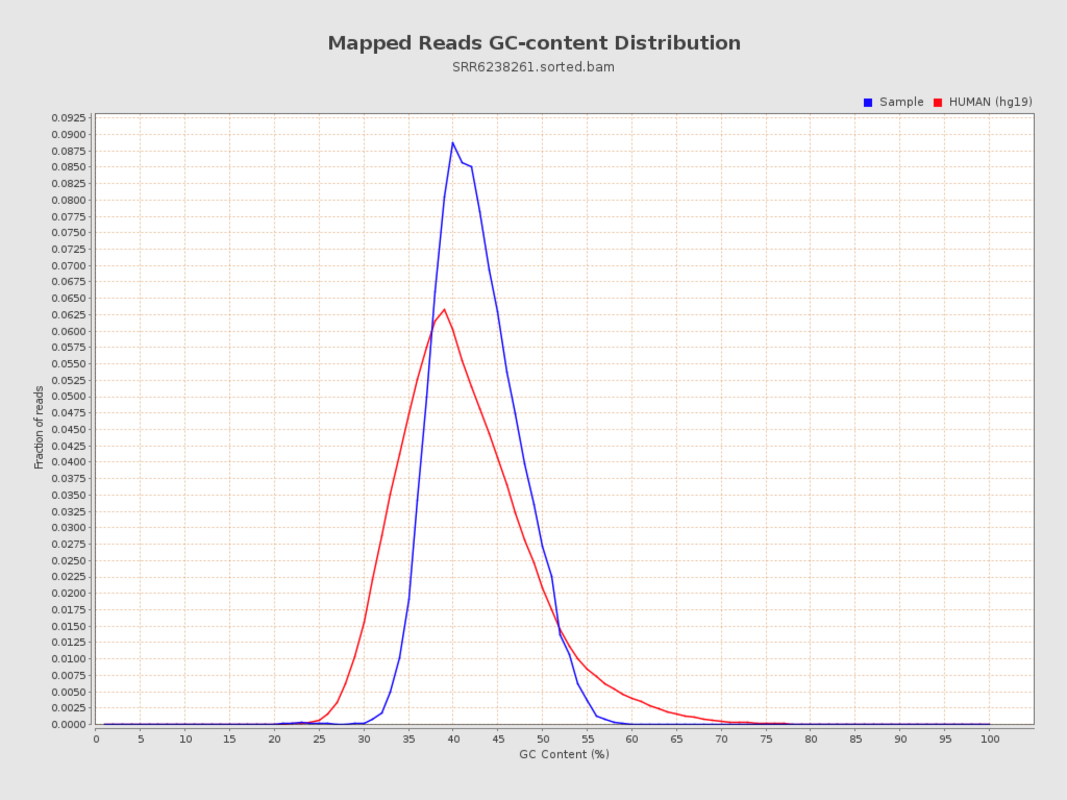
7. Results : Duplication Rate Histogram



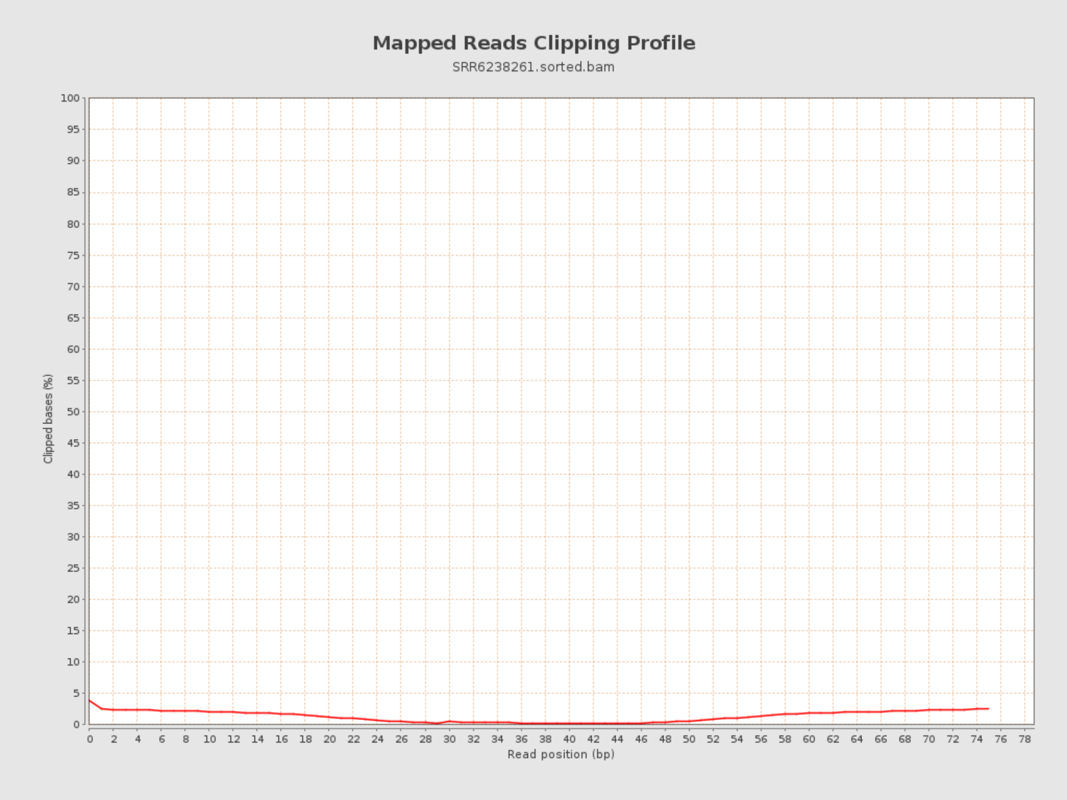
8. Results : Mapped Reads Nucleotide Content



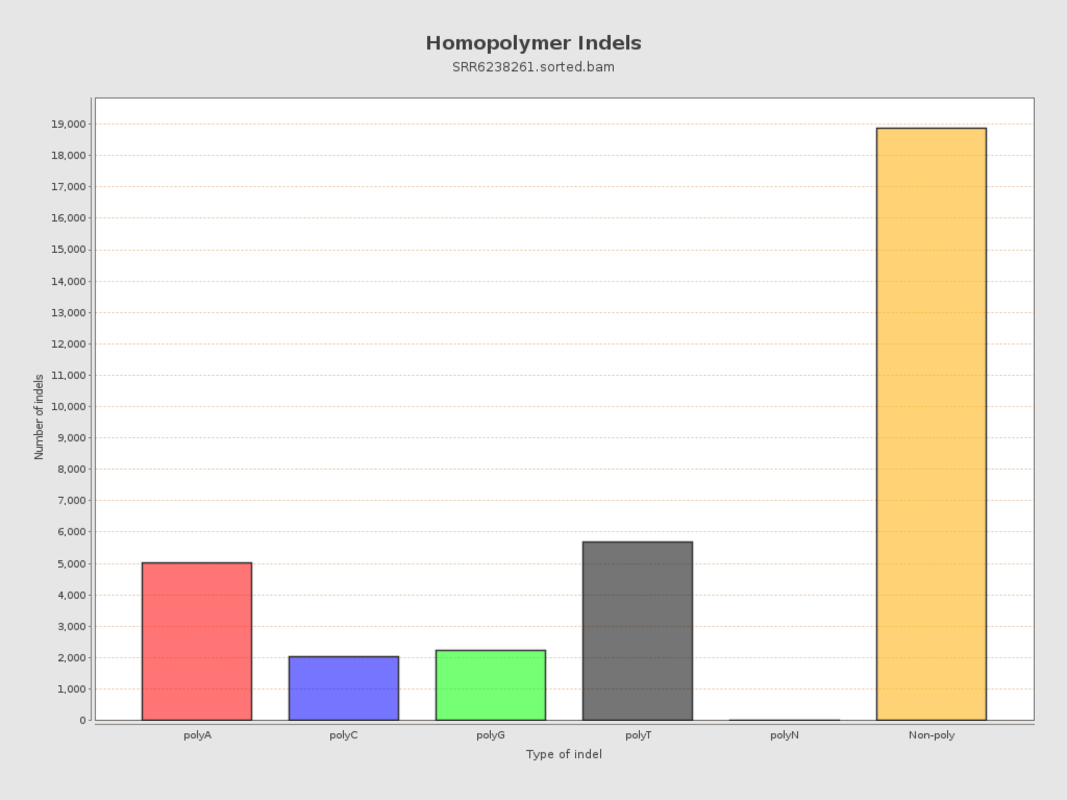
9. Results : Mapped Reads GC-content Distribution



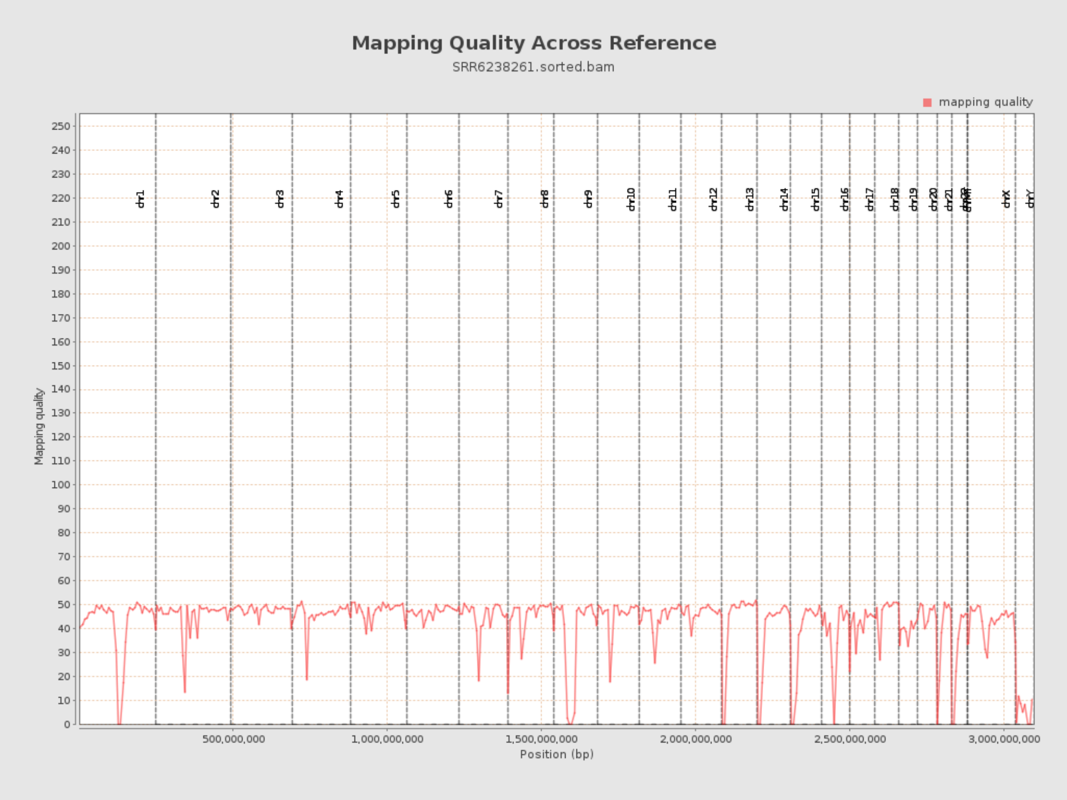
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram