Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:59:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238526.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_SRR6238526 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238526.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:59:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238526.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,788,625
Mapped reads	2,428,902 / 87.1%
Unmapped reads	359,723 / 12.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,843 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	557,102 / 19.98%
Duplication rate	17.51%
Clipped reads	1,550,292 / 55.59%

2.2. ACGT Content

Number/percentage of A's	36,732,975 / 24.56%
Number/percentage of C's	26,681,315 / 17.84%
Number/percentage of T's	49,768,257 / 33.27%
Number/percentage of G's	36,385,921 / 24.33%
Number/percentage of N's	9,982 / 0.01%
GC Percentage	42.16%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.6361

2.4. Mapping Quality

Mean Mapping Quality	42.35

2.5. Mismatches and indels

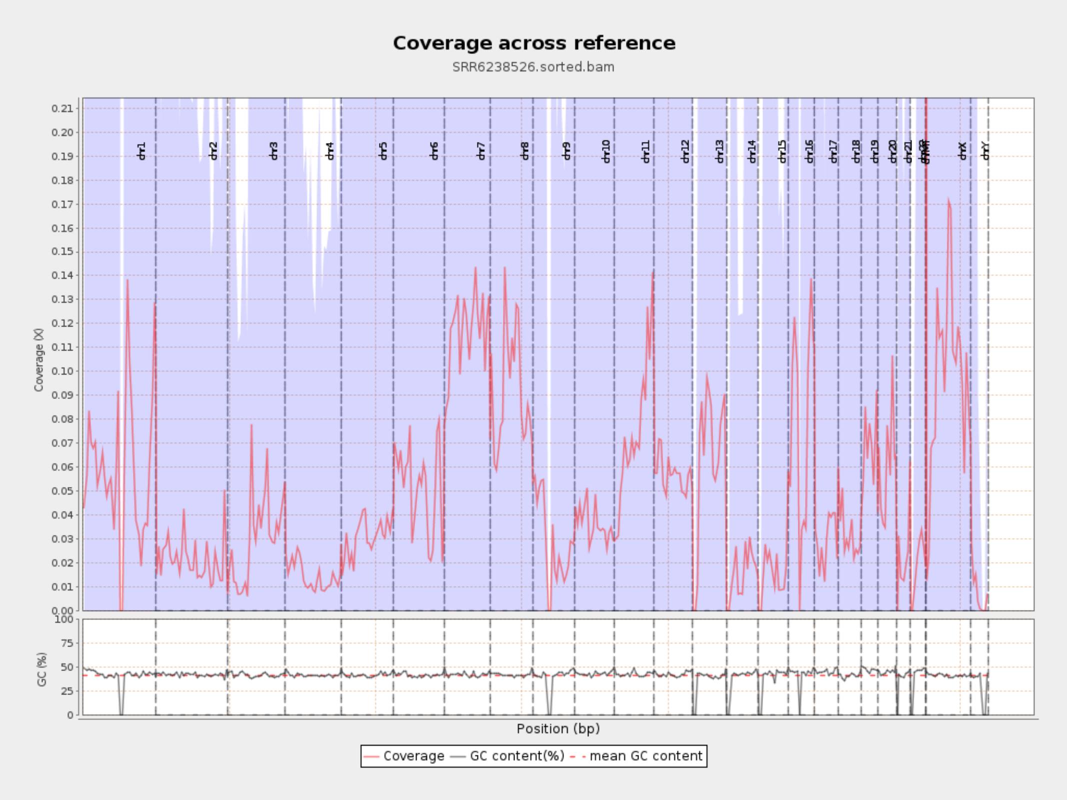
General error rate	0.59%
Mismatches	870,350
Insertions	8,924
Mapped reads with at least one insertion	0.36%
Deletions	42,264
Mapped reads with at least one deletion	1.72%
Homopolymer indels	41.23%

2.6. Chromosome stats

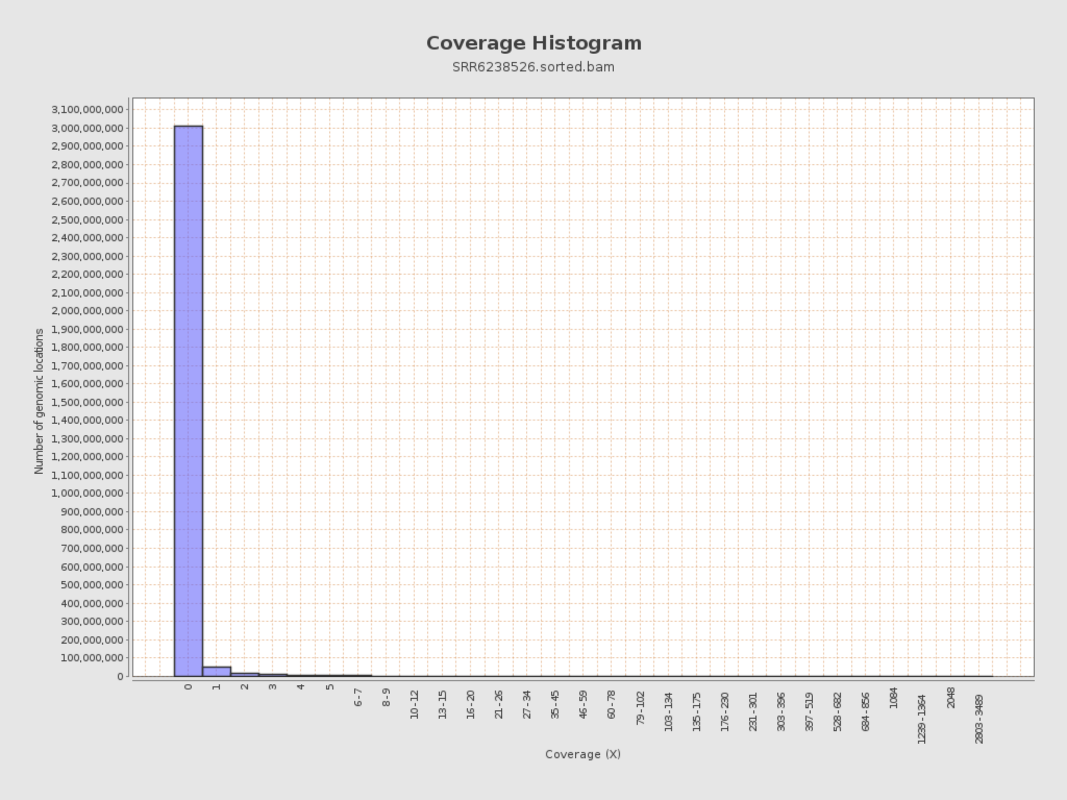
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14784975	0.0593	0.6977
chr2	243199373	5222648	0.0215	1.5151
chr3	198022430	6003916	0.0303	0.2899
chr4	191154276	2741705	0.0143	0.1871
chr5	180915260	5553848	0.0307	0.2873
chr6	171115067	8800259	0.0514	0.5775
chr7	159138663	18578161	0.1167	0.7928

chr8	146364022	13413261	0.0916	0.5903
chr9	141213431	3968090	0.0281	0.344
chr10	135534747	4917760	0.0363	0.3792
chr11	135006516	10104493	0.0748	0.5428
chr12	133851895	7638061	0.0571	0.398
chr13	115169878	7363062	0.0639	0.4772
chr14	107349540	1701975	0.0159	0.2243
chr15	102531392	1514289	0.0148	0.3156
chr16	90354753	6794831	0.0752	0.4965
chr17	81195210	2446204	0.0301	0.3093
chr18	78077248	2500439	0.032	0.9602
chr19	59128983	4035197	0.0682	0.552
chr20	63025520	3834326	0.0608	0.4184
chr21	48129895	1088686	0.0226	0.2592
chr22	51304566	978834	0.0191	0.221
chrMT	16571	51171	3.088	3.1336
chrX	155270560	15170609	0.0977	0.5383
chrY	59373566	443417	0.0075	0.2168

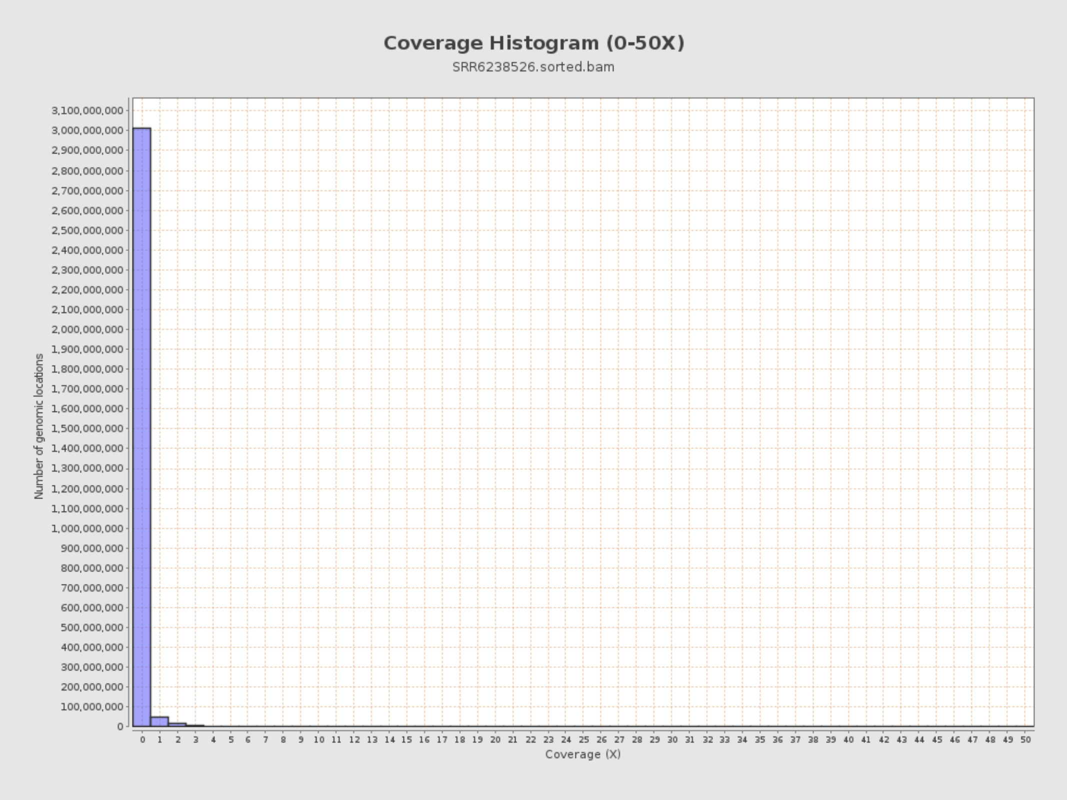
3. Results : Coverage across reference



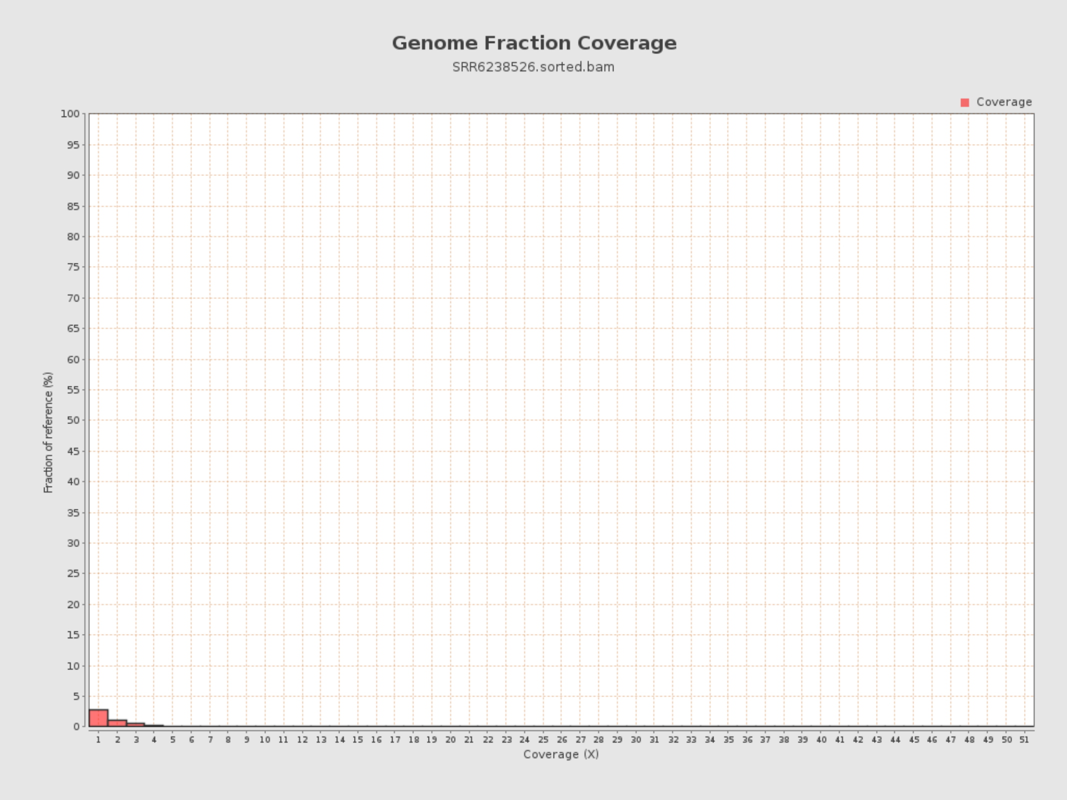
4. Results : Coverage Histogram



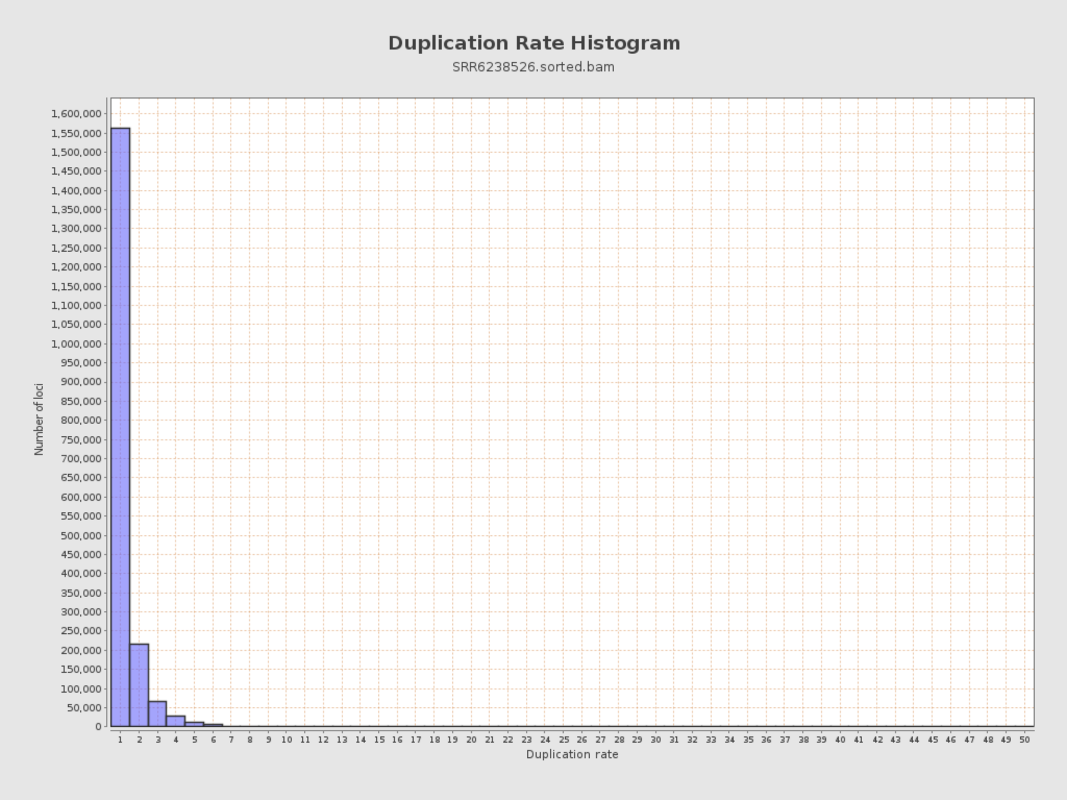
5. Results : Coverage Histogram (0-50X)



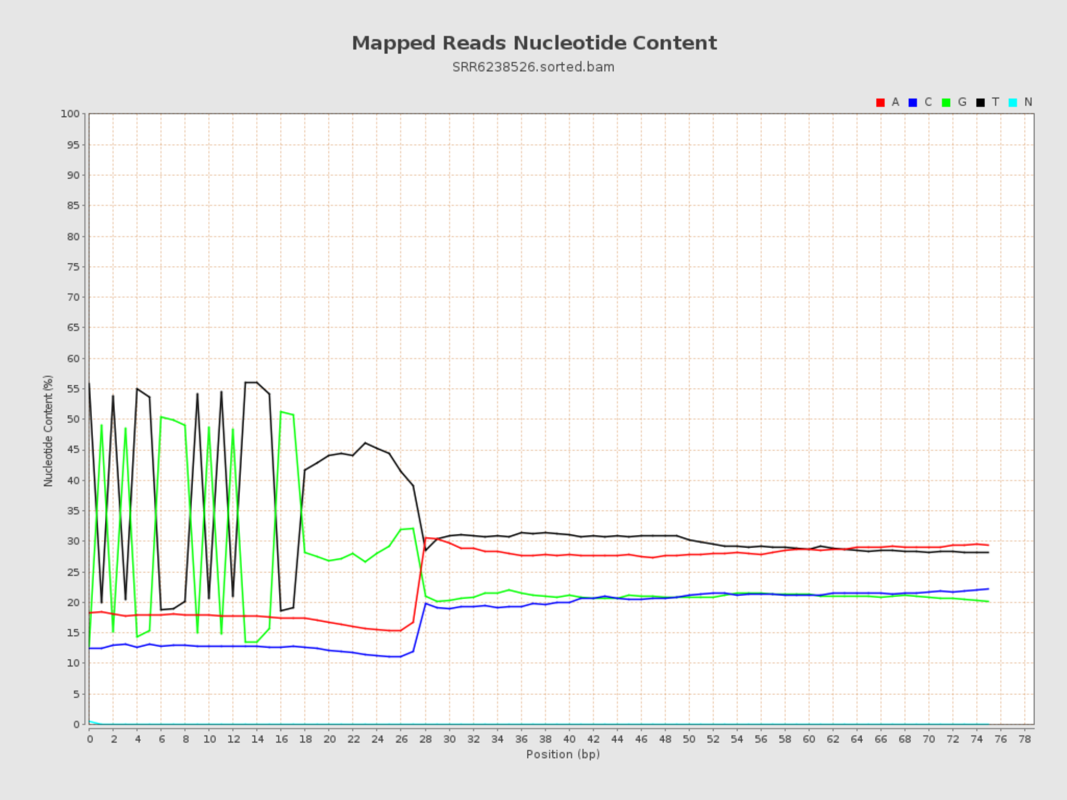
6. Results : Genome Fraction Coverage



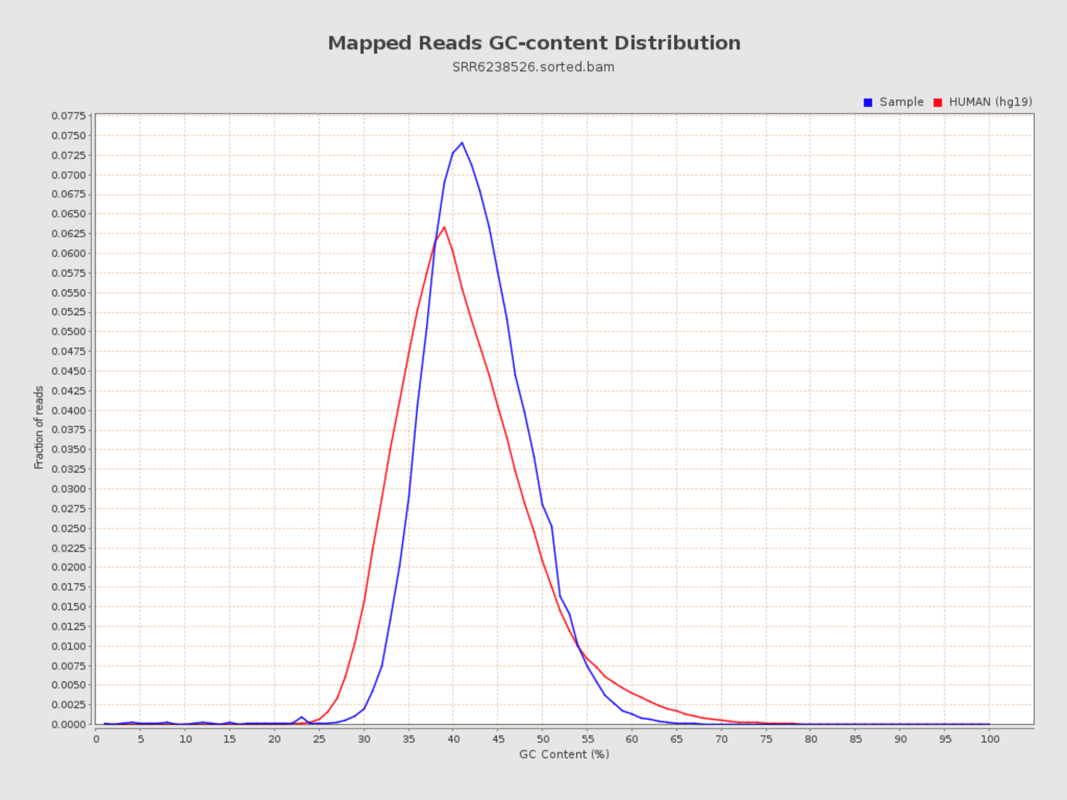
7. Results : Duplication Rate Histogram



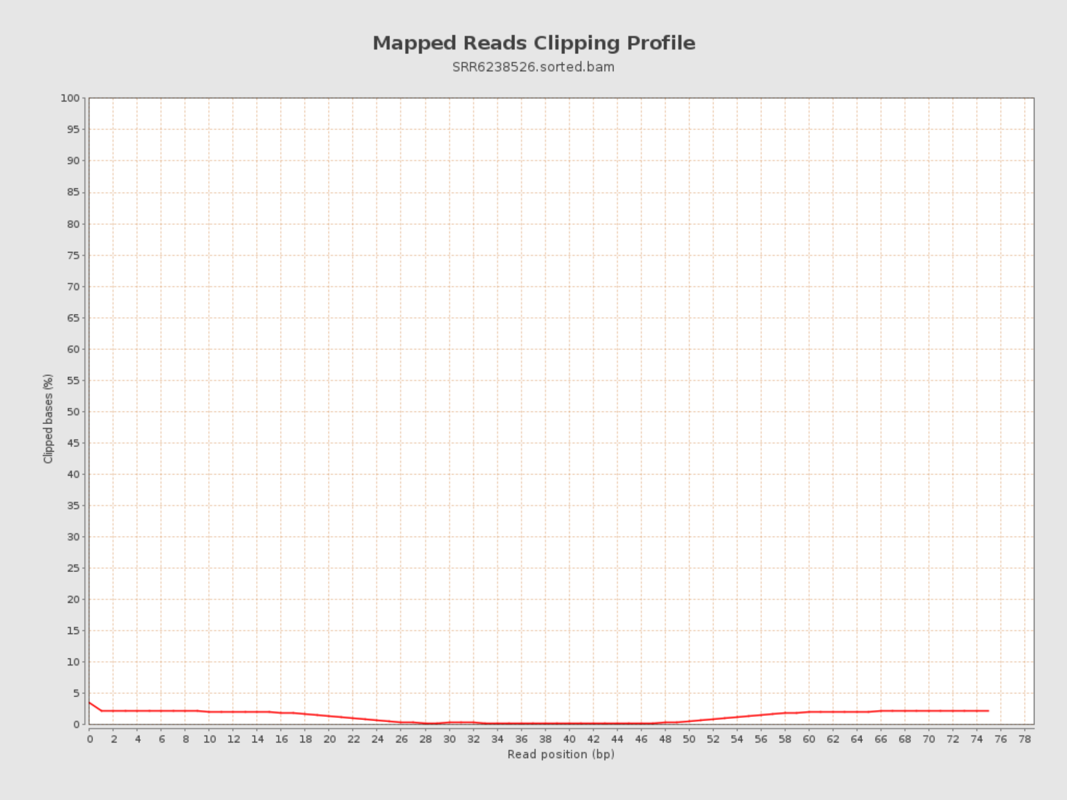
8. Results : Mapped Reads Nucleotide Content



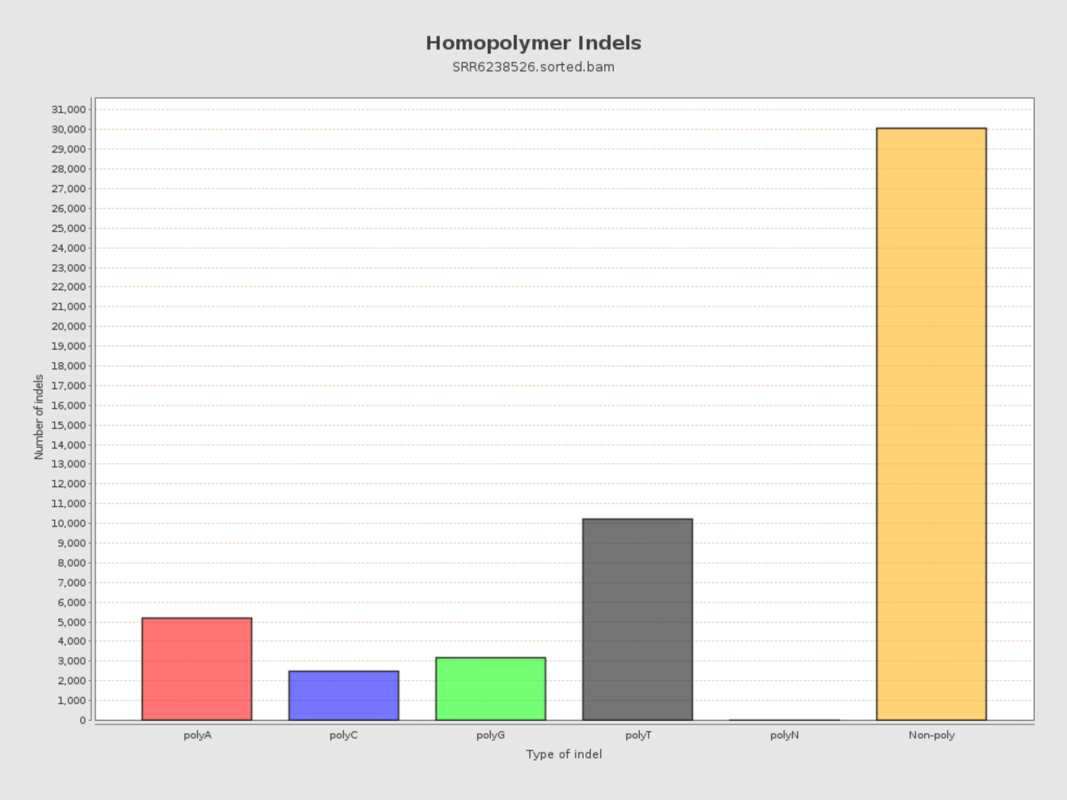
9. Results : Mapped Reads GC-content Distribution



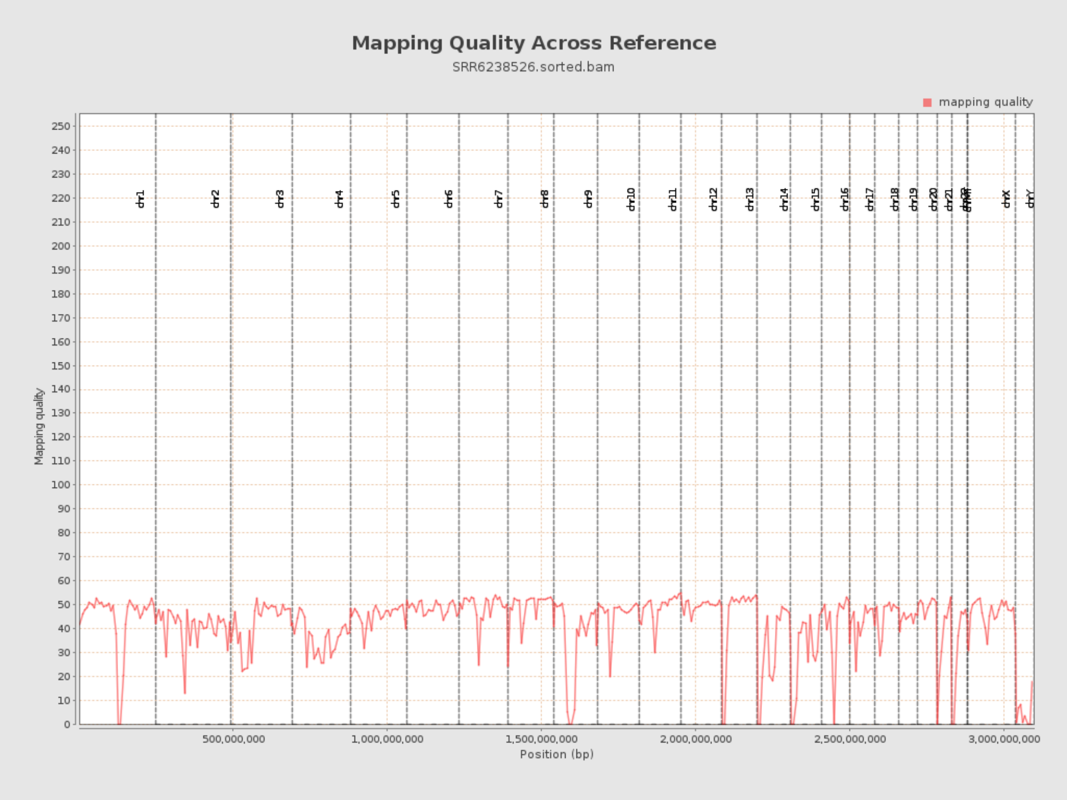
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram