Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238328.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_SRR6238328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:50:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,151,665
Mapped reads	1,066,286 / 92.59%
Unmapped reads	85,379 / 7.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,248 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	33,585 / 2.92%
Duplication rate	2.19%
Clipped reads	410,396 / 35.64%

2.2. ACGT Content

Number/percentage of A's	20,311,283 / 28.14%
Number/percentage of C's	13,194,175 / 18.28%
Number/percentage of T's	23,050,504 / 31.93%
Number/percentage of G's	15,587,495 / 21.6%
Number/percentage of N's	36,090 / 0.05%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2746

2.4. Mapping Quality

Mean Mapping Quality	46.81

2.5. Mismatches and indels

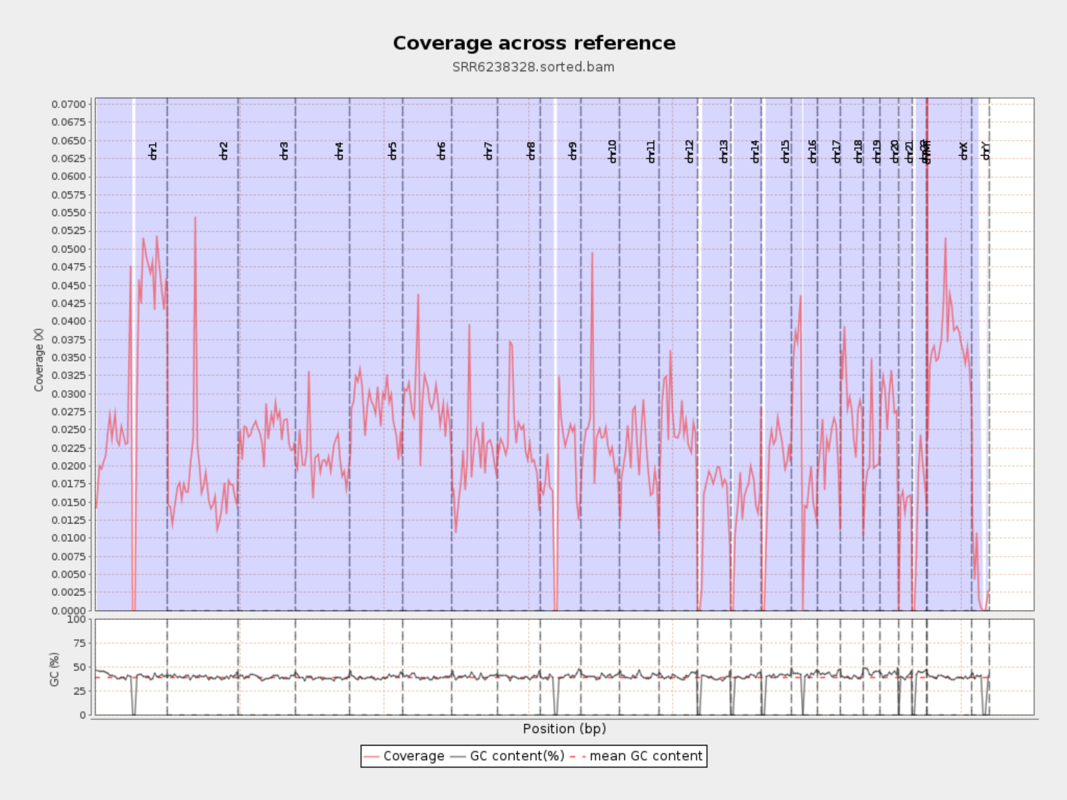
General error rate	0.82%
Mismatches	581,137
Insertions	5,263
Mapped reads with at least one insertion	0.49%
Deletions	21,104
Mapped reads with at least one deletion	1.96%
Homopolymer indels	46.52%

2.6. Chromosome stats

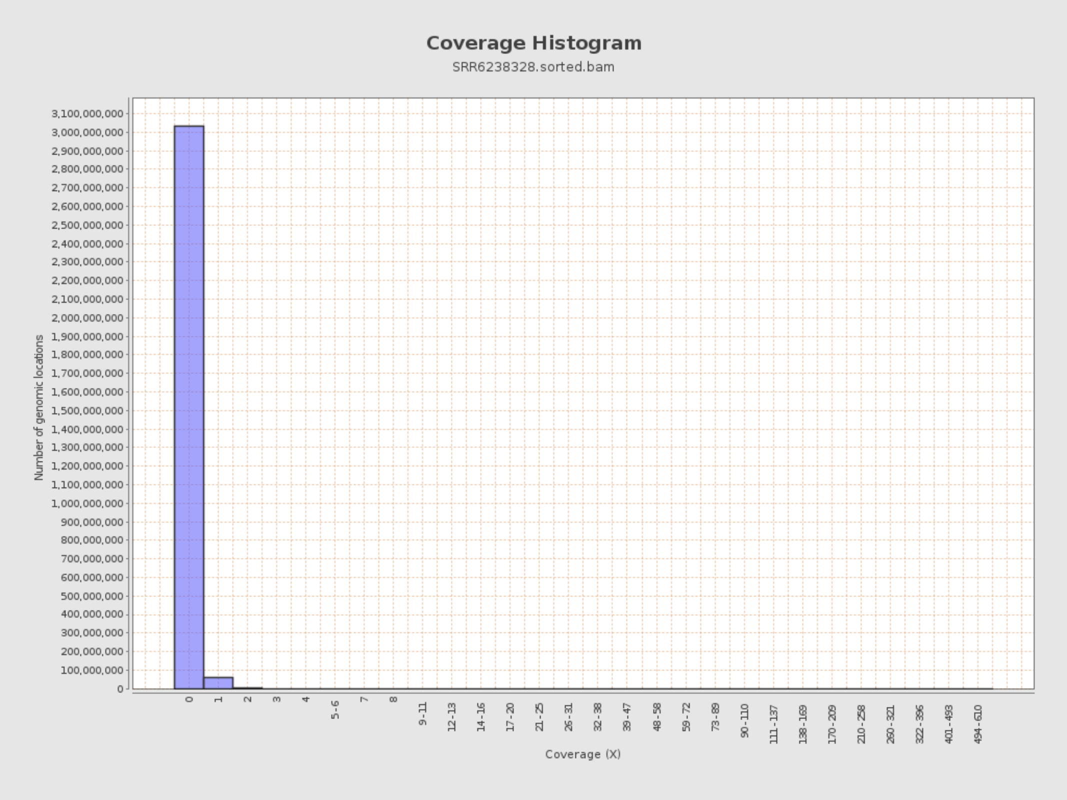
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7989294	0.0321	0.5462
chr2	243199373	4272746	0.0176	0.2743
chr3	198022430	4908848	0.0248	0.1707
chr4	191154276	4035591	0.0211	0.17
chr5	180915260	5138318	0.0284	0.1827
chr6	171115067	4980929	0.0291	0.2271
chr7	159138663	3347120	0.021	0.2907

chr8	146364022	3505382	0.0239	0.3938
chr9	141213431	2673285	0.0189	0.2449
chr10	135534747	3264208	0.0241	0.2727
chr11	135006516	2887393	0.0214	0.2125
chr12	133851895	3513569	0.0262	0.1797
chr13	115169878	1680970	0.0146	0.1292
chr14	107349540	1501750	0.014	0.1451
chr15	102531392	1939609	0.0189	0.1473
chr16	90354753	2036965	0.0225	0.1822
chr17	81195210	1814020	0.0223	0.1822
chr18	78077248	2259480	0.0289	0.4425
chr19	59128983	1247443	0.0211	0.3856
chr20	63025520	1815400	0.0288	0.186
chr21	48129895	671644	0.014	0.1558
chr22	51304566	706150	0.0138	0.1247
chrMT	16571	3934	0.2374	0.5145
chrX	155270560	5809875	0.0374	0.2323
chrY	59373566	212441	0.0036	0.1025

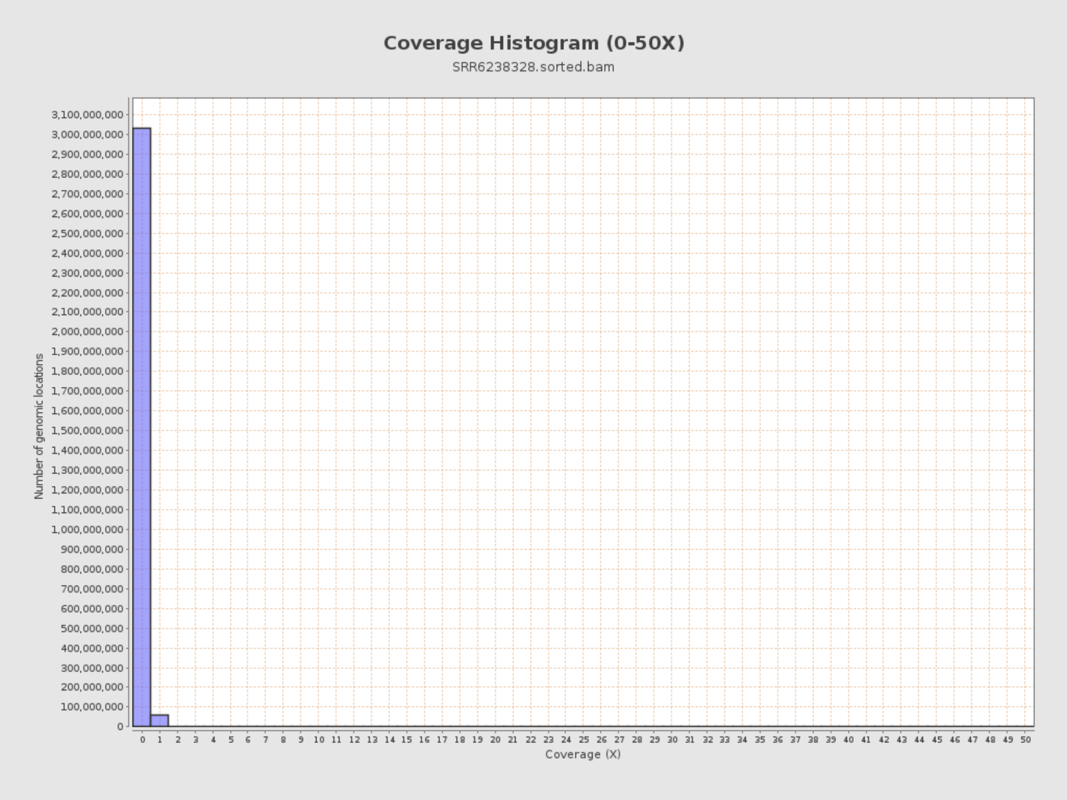
3. Results : Coverage across reference



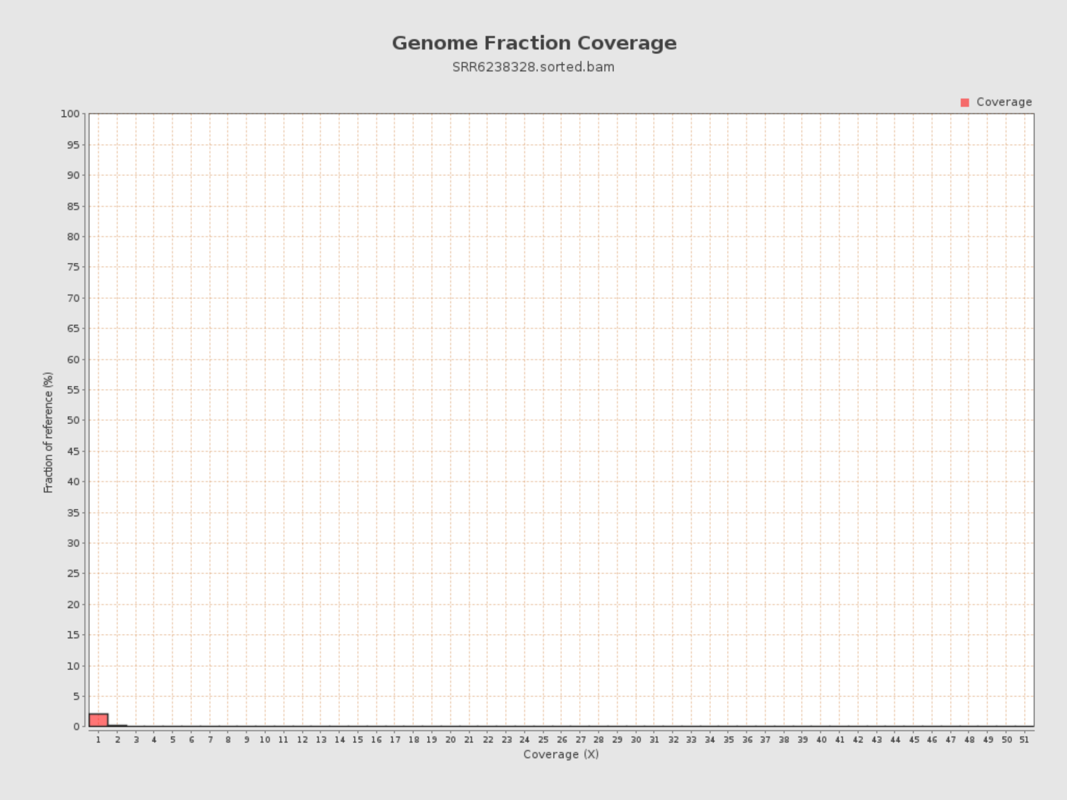
4. Results : Coverage Histogram



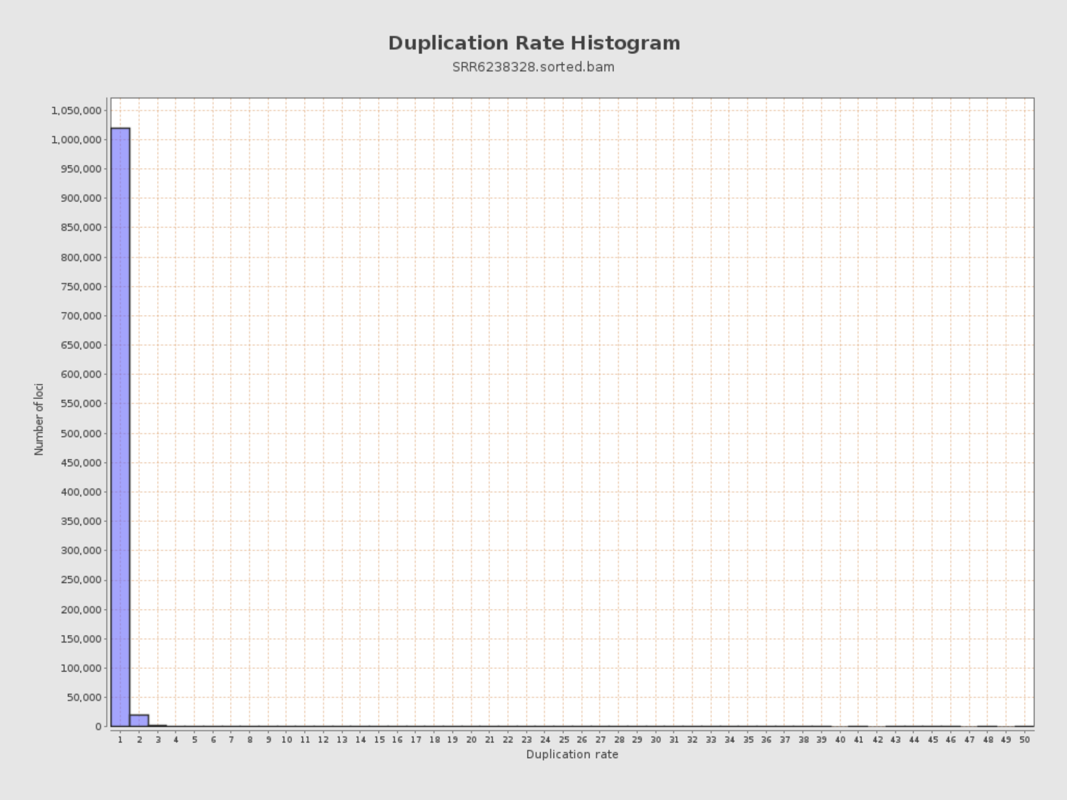
5. Results : Coverage Histogram (0-50X)



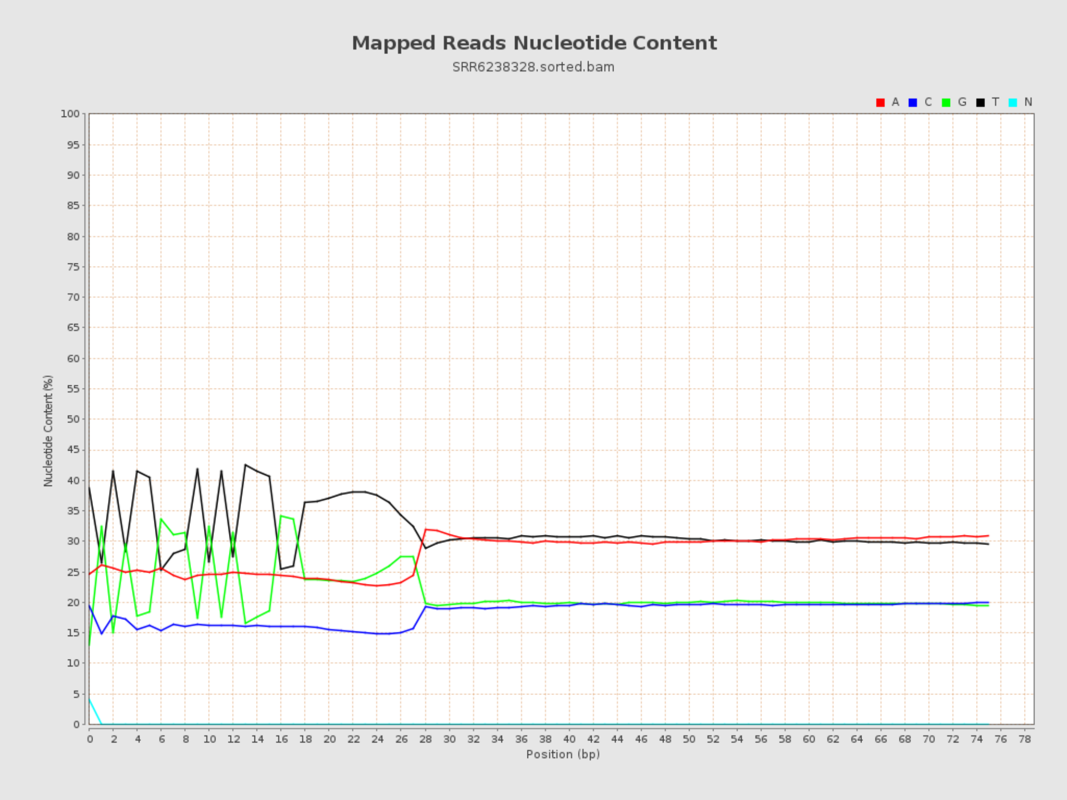
6. Results : Genome Fraction Coverage



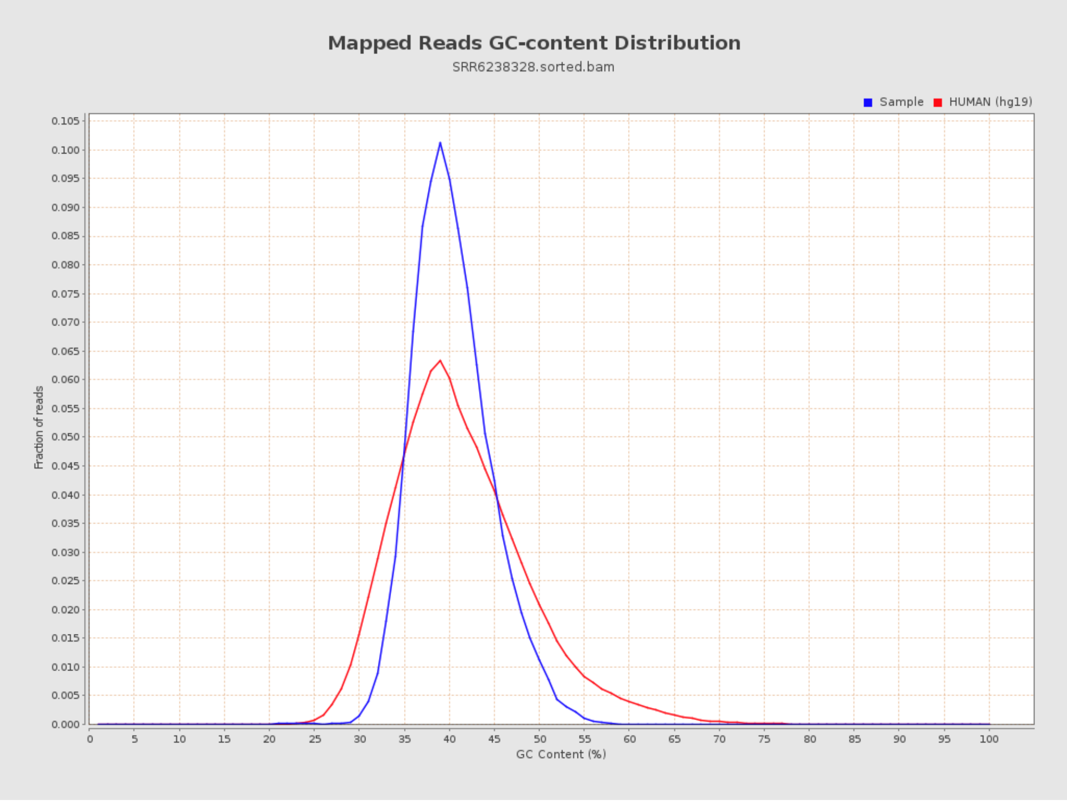
7. Results : Duplication Rate Histogram



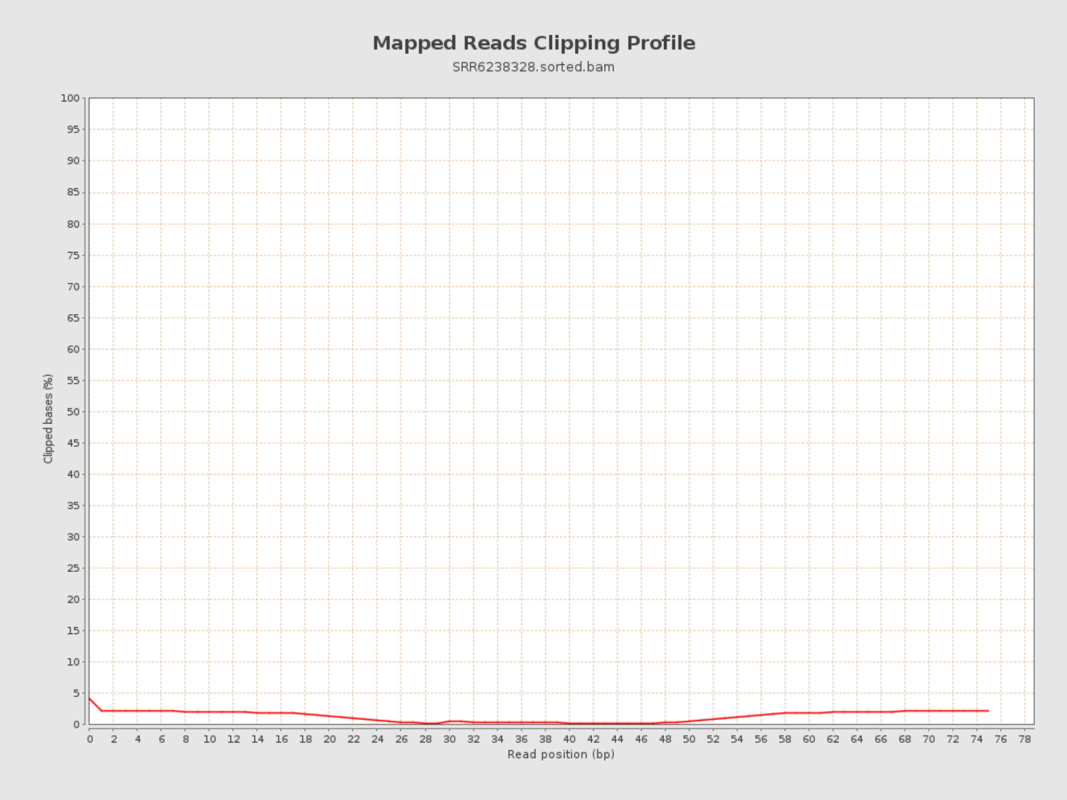
8. Results : Mapped Reads Nucleotide Content



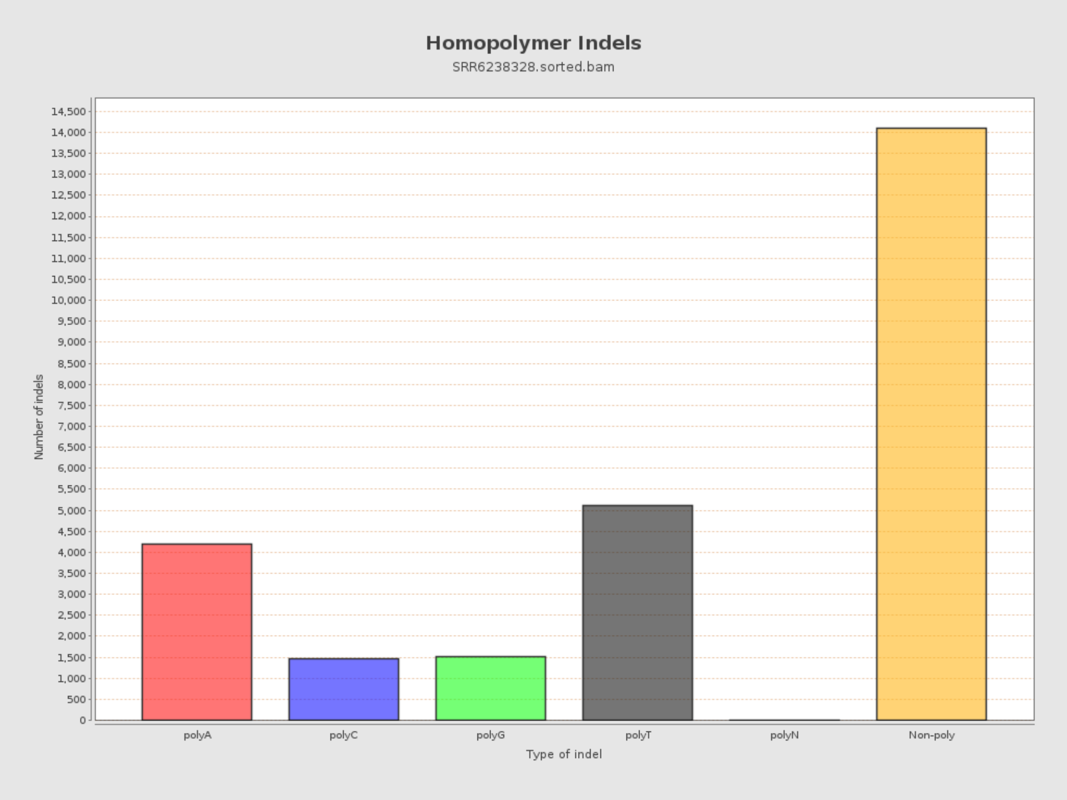
9. Results : Mapped Reads GC-content Distribution



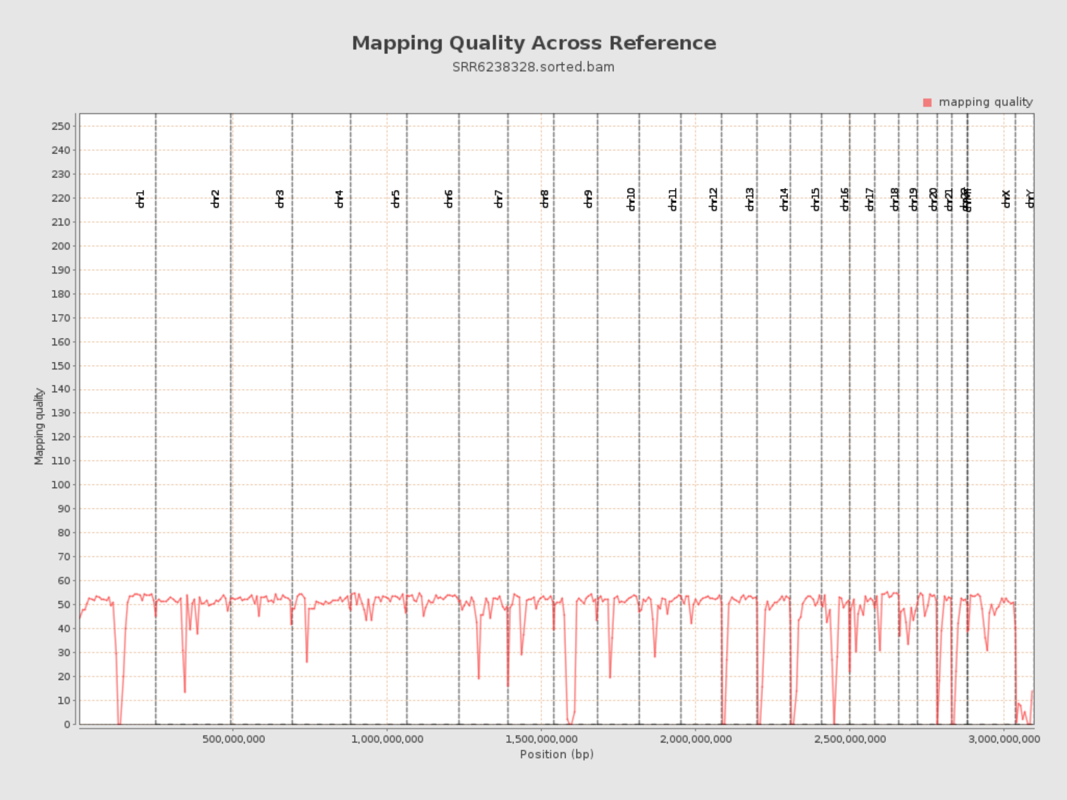
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram