Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 15:40:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617398.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_SRR617398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617398_1.fastq.gz SRR617398_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 15:40:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,204,957 / 91.27%
Unmapped reads	2,795,043 / 8.73%
Mapped paired reads	29,204,957 / 91.27%
Mapped reads, first in pair	14,725,944 / 46.02%
Mapped reads, second in pair	14,479,013 / 45.25%
Mapped reads, both in pair	28,600,472 / 89.38%
Mapped reads, singletons	604,485 / 1.89%
Secondary alignments	0
Supplementary alignments	422,632 / 1.32%
Read min/max/mean length	30 / 100 / 100.55
Duplicated reads (estimated)	1,289,899 / 4.03%
Duplication rate	4.04%
Clipped reads	3,918,500 / 12.25%

2.2. ACGT Content

Number/percentage of A's	856,326,439 / 29.91%
Number/percentage of C's	573,376,361 / 20.03%
Number/percentage of T's	845,475,564 / 29.54%
Number/percentage of G's	585,675,028 / 20.46%
Number/percentage of N's	1,766,398 / 0.06%

GC Percentage	40.49%

2.3. Coverage

Mean	0.9249
Standard Deviation	2.8231

2.4. Mapping Quality

Mean Mapping Quality	53.83

2.5. Insert size

Mean	47,564.15
Standard Deviation	2,074,007.56
P25/Median/P75	168 / 205 / 263

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	39,358,606
Insertions	233,246
Mapped reads with at least one insertion	0.79%
Deletions	272,754
Mapped reads with at least one deletion	0.91%
Homopolymer indels	44.17%

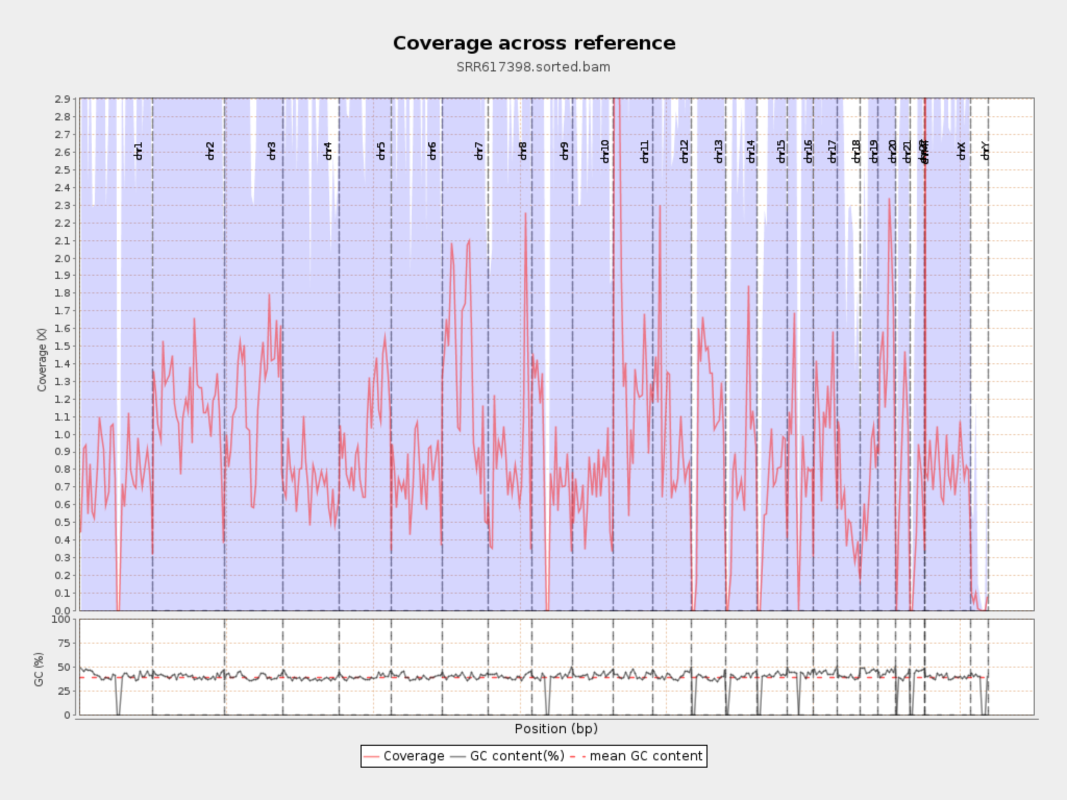
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

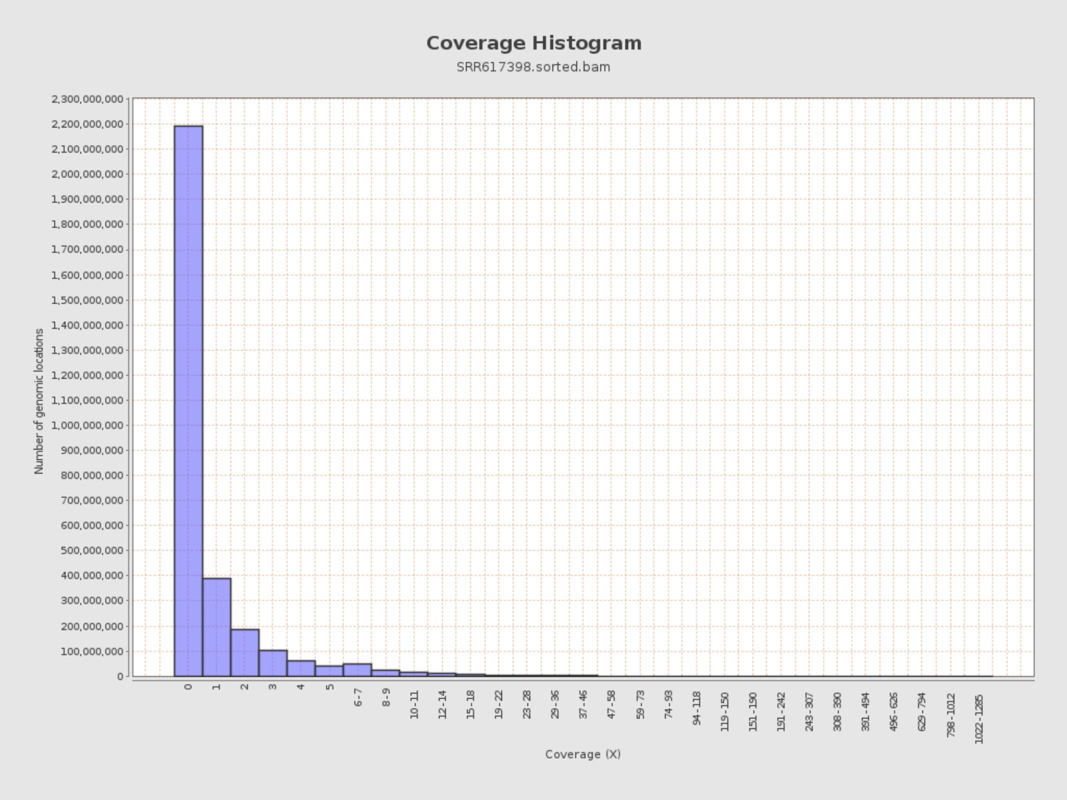
		bases	coverage	deviation
chr1	249250621	184427069	0.7399	2.644
chr2	243199373	285563746	1.1742	2.9683
chr3	198022430	241520276	1.2197	3.2873
chr4	191154276	138999903	0.7272	2.2281
chr5	180915260	183819461	1.0161	2.789
chr6	171115067	131642218	0.7693	2.5221
chr7	159138663	214633777	1.3487	3.1374
chr8	146364022	126752254	0.866	3.1187
chr9	141213431	114373306	0.8099	2.5181
chr10	135534747	91723019	0.6767	2.3257
chr11	135006516	212363973	1.573	3.7087
chr12	133851895	136110179	1.0169	2.6835
chr13	115169878	124690166	1.0827	2.6823
chr14	107349540	83014615	0.7733	2.7933
chr15	102531392	65673104	0.6405	2.286
chr16	90354753	71600020	0.7924	3.2013
chr17	81195210	87381848	1.0762	3.5403
chr18	78077248	41209211	0.5278	1.9393
chr19	59128983	40379763	0.6829	2.2291
chr20	63025520	96762033	1.5353	4.5155
chr21	48129895	39311273	0.8168	2.4552
chr22	51304566	22834584	0.4451	2.0039
chrMT	16571	167795	10.1258	5.3071
chrX	155270560	125978723	0.8113	2.4864

chrY	59373566	2295978	0.0387	0.5497

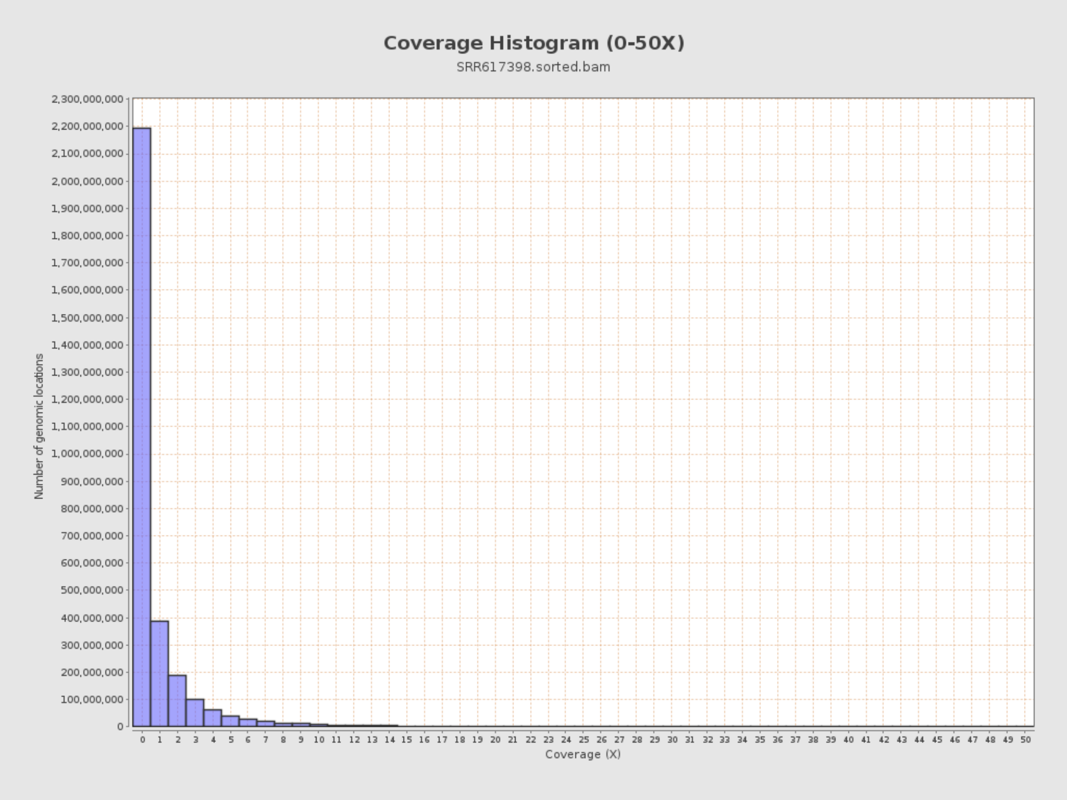
3. Results : Coverage across reference



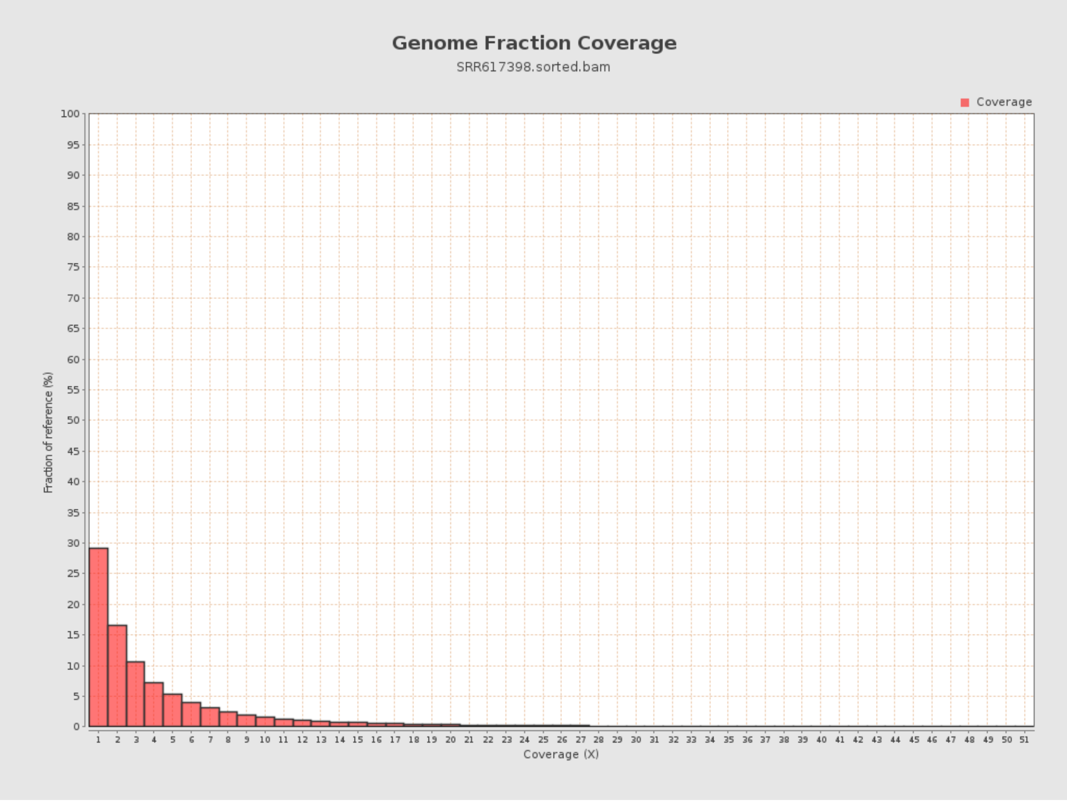
4. Results : Coverage Histogram



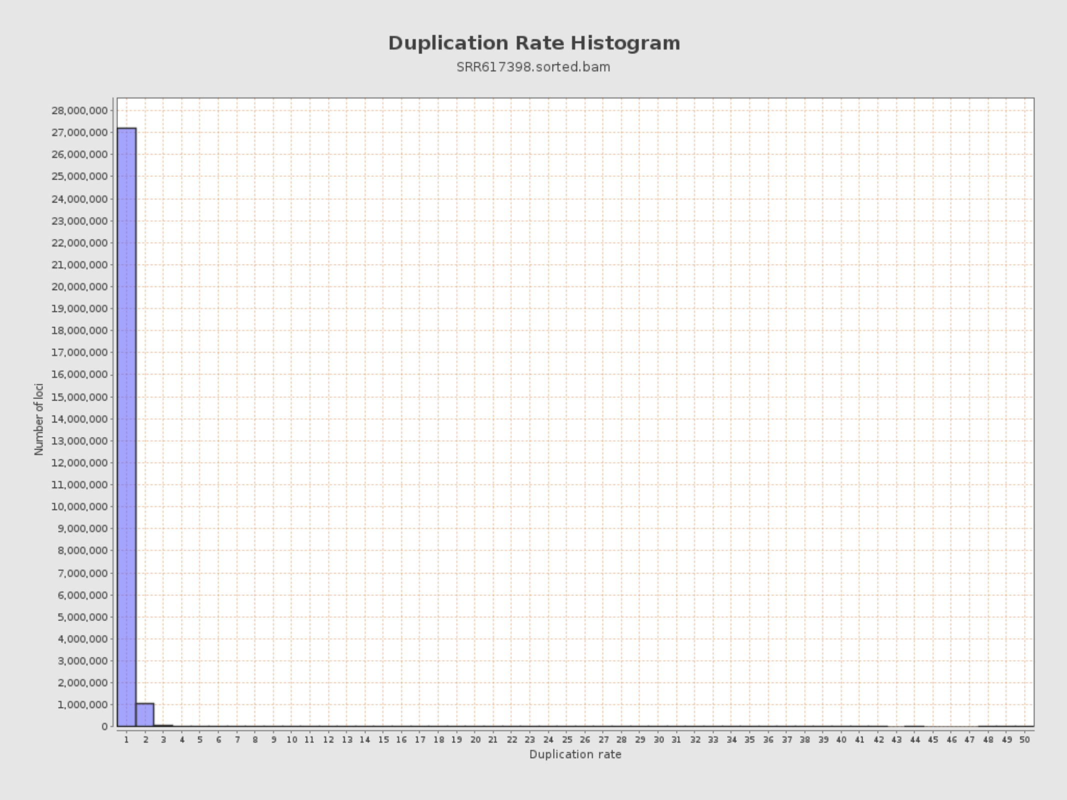
5. Results : Coverage Histogram (0-50X)



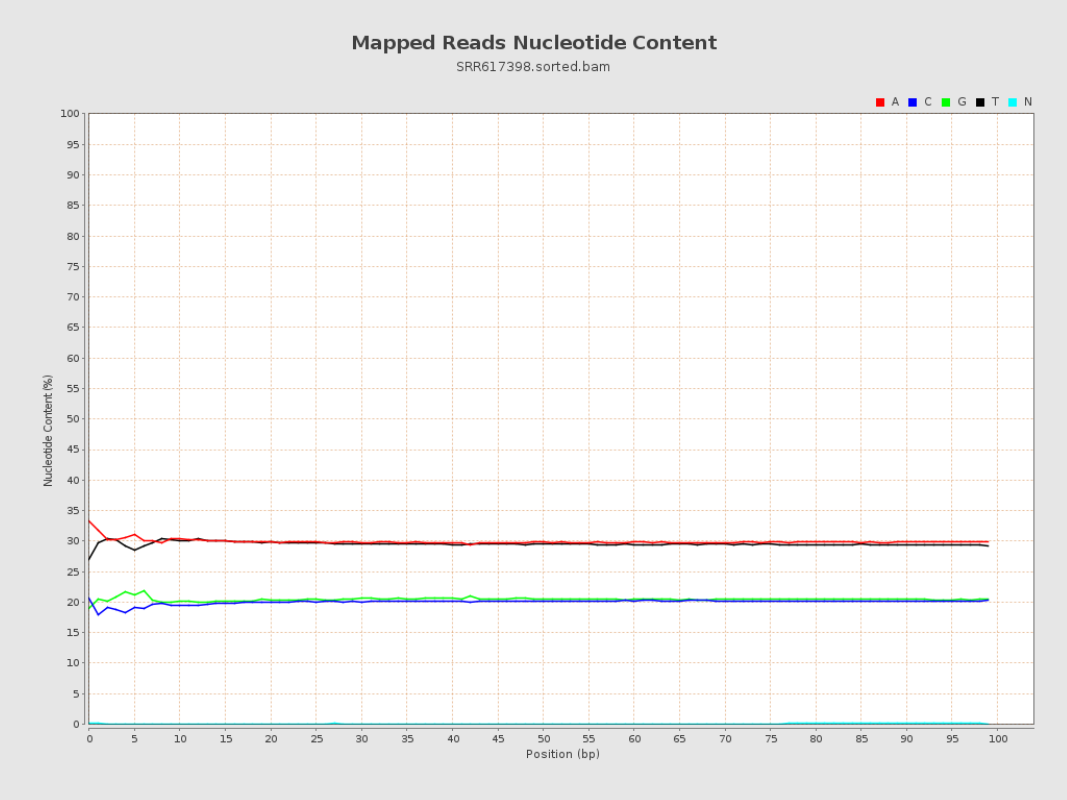
6. Results : Genome Fraction Coverage



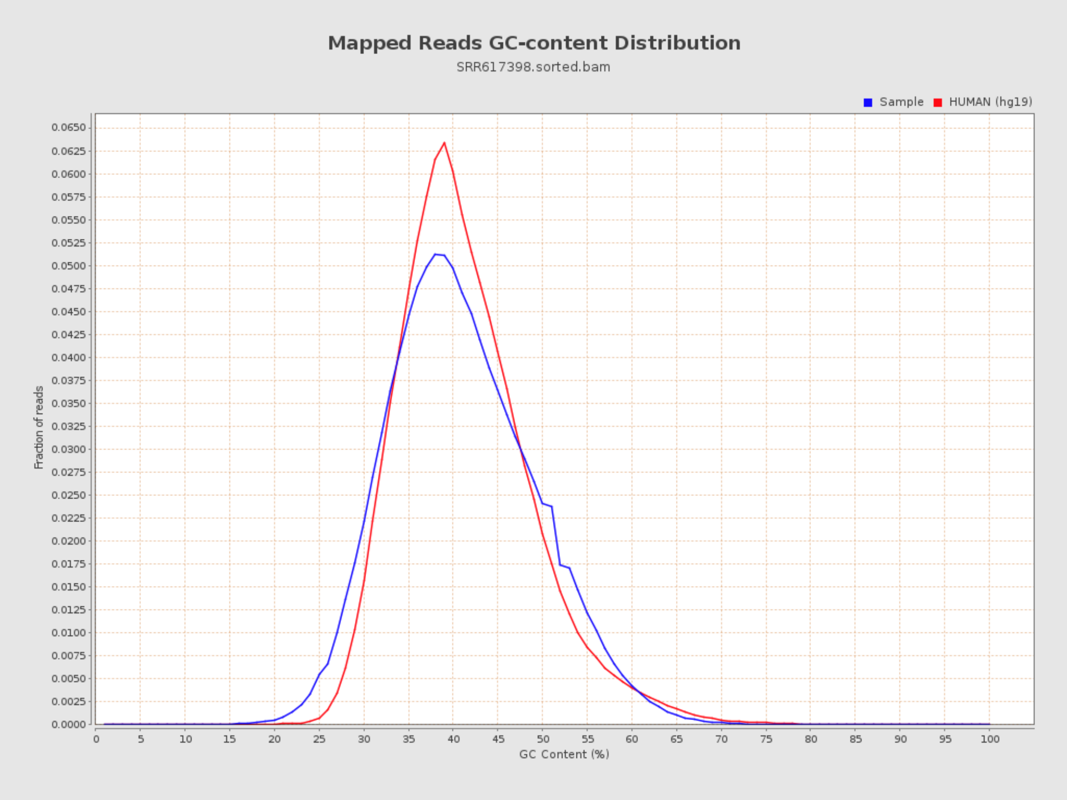
7. Results : Duplication Rate Histogram



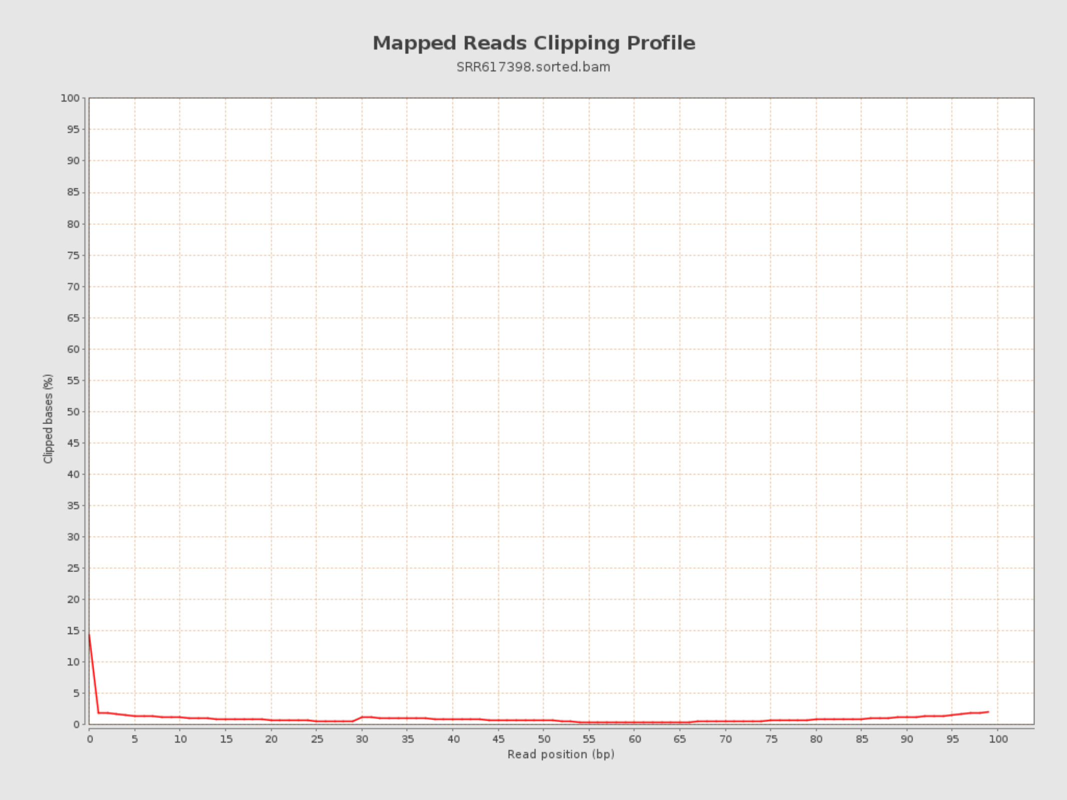
8. Results : Mapped Reads Nucleotide Content



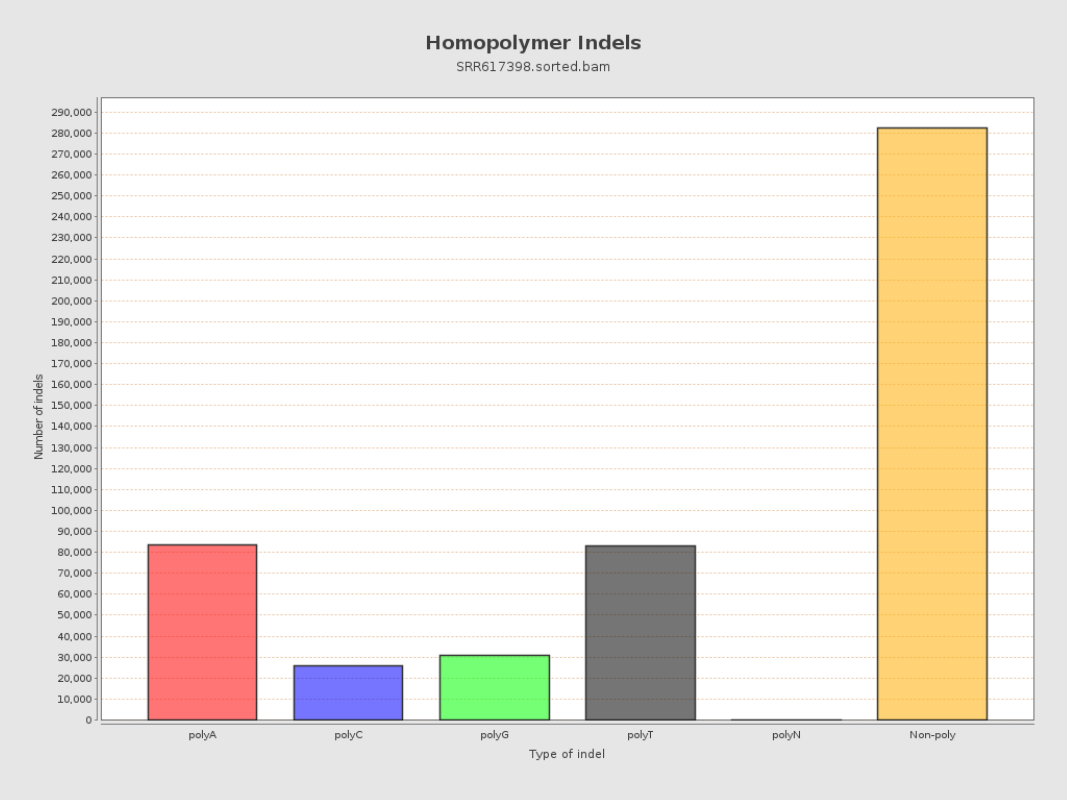
9. Results : Mapped Reads GC-content Distribution



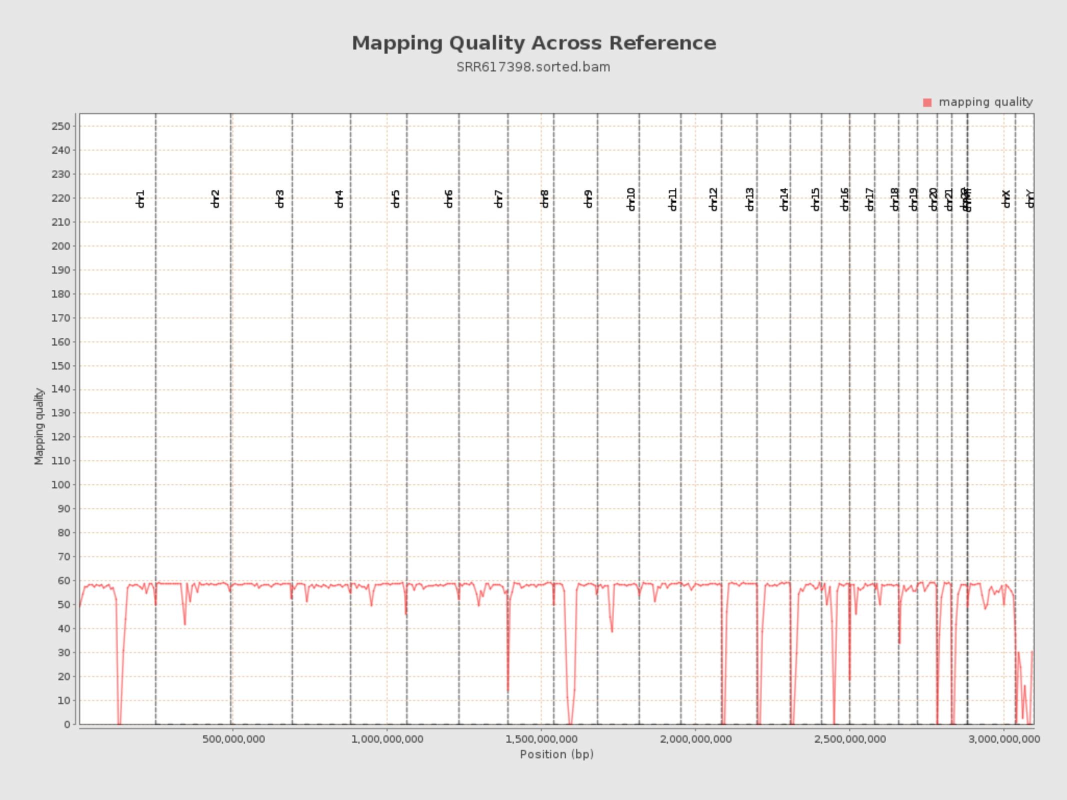
10. Results : Mapped Reads Clipping Profile



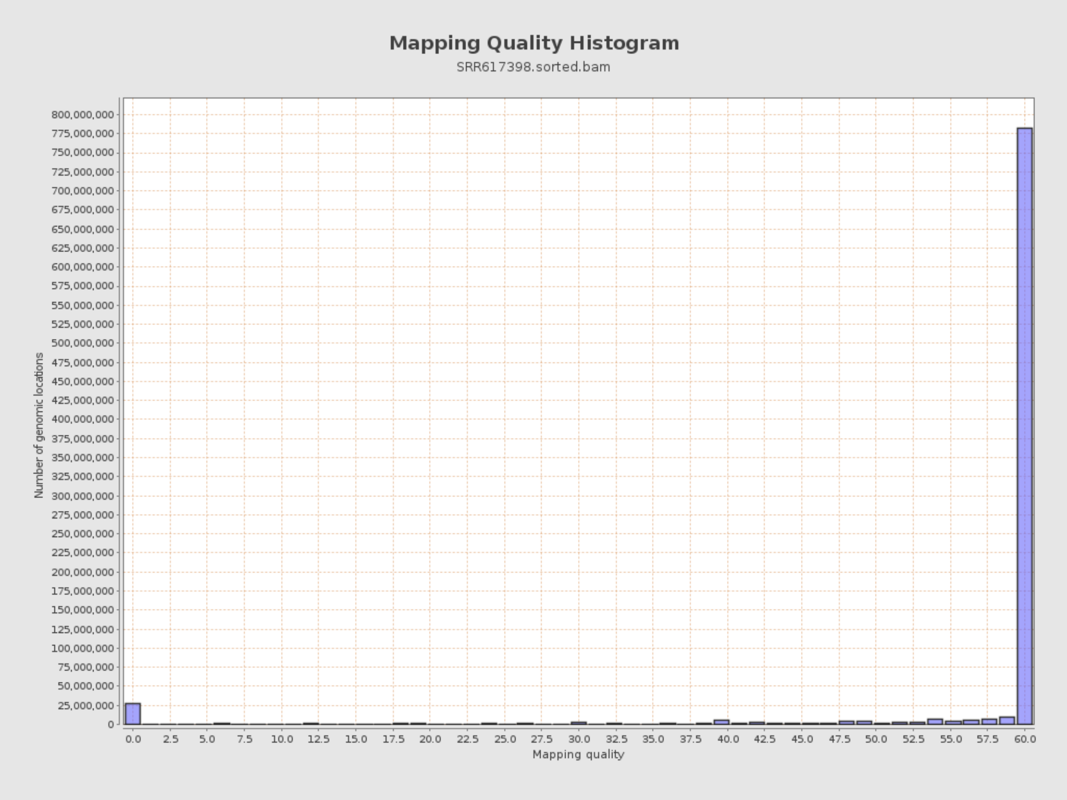
11. Results : Homopolymer Indels



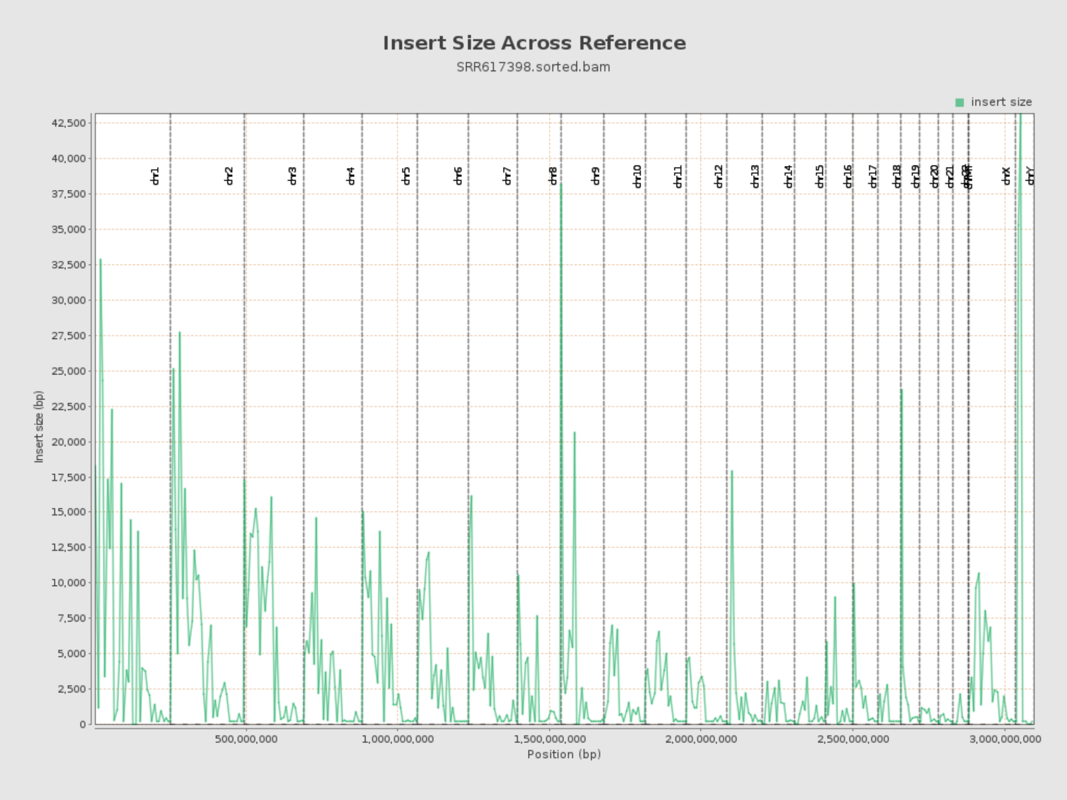
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram