Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 18:30:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617402.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_SRR617402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617402_1.fastq.gz SRR617402_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 18:30:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,136,727 / 94.18%
Unmapped reads	1,863,273 / 5.82%
Mapped paired reads	30,136,727 / 94.18%
Mapped reads, first in pair	15,213,153 / 47.54%
Mapped reads, second in pair	14,923,574 / 46.64%
Mapped reads, both in pair	29,596,864 / 92.49%
Mapped reads, singletons	539,863 / 1.69%
Secondary alignments	0
Supplementary alignments	495,109 / 1.55%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	1,432,212 / 4.48%
Duplication rate	4.25%
Clipped reads	3,045,142 / 9.52%

2.2. ACGT Content

Number/percentage of A's	883,644,492 / 29.75%
Number/percentage of C's	599,057,897 / 20.17%
Number/percentage of T's	877,450,342 / 29.54%
Number/percentage of G's	609,560,251 / 20.52%
Number/percentage of N's	618,998 / 0.02%

GC Percentage	40.69%

2.3. Coverage

Mean	0.9597
Standard Deviation	2.9573

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	60,205.22
Standard Deviation	2,349,030.5
P25/Median/P75	173 / 214 / 280

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	24,598,461
Insertions	249,029
Mapped reads with at least one insertion	0.81%
Deletions	297,580
Mapped reads with at least one deletion	0.97%
Homopolymer indels	44.95%

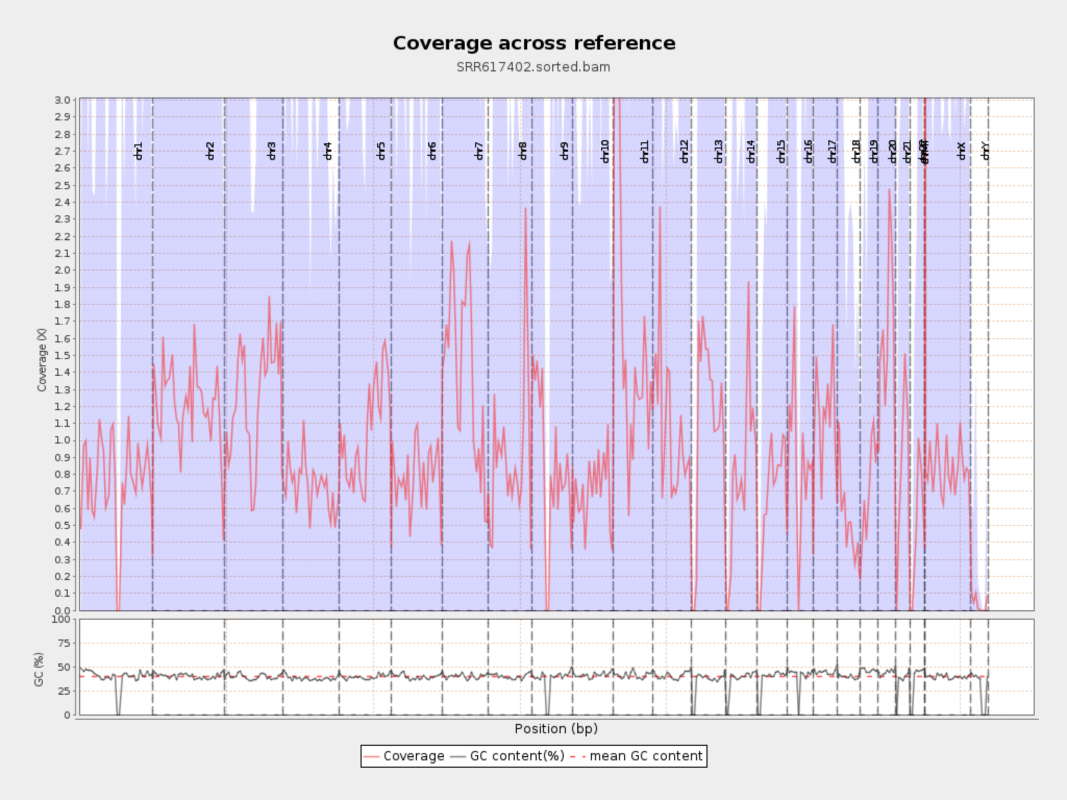
2.7. Chromosome stats

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

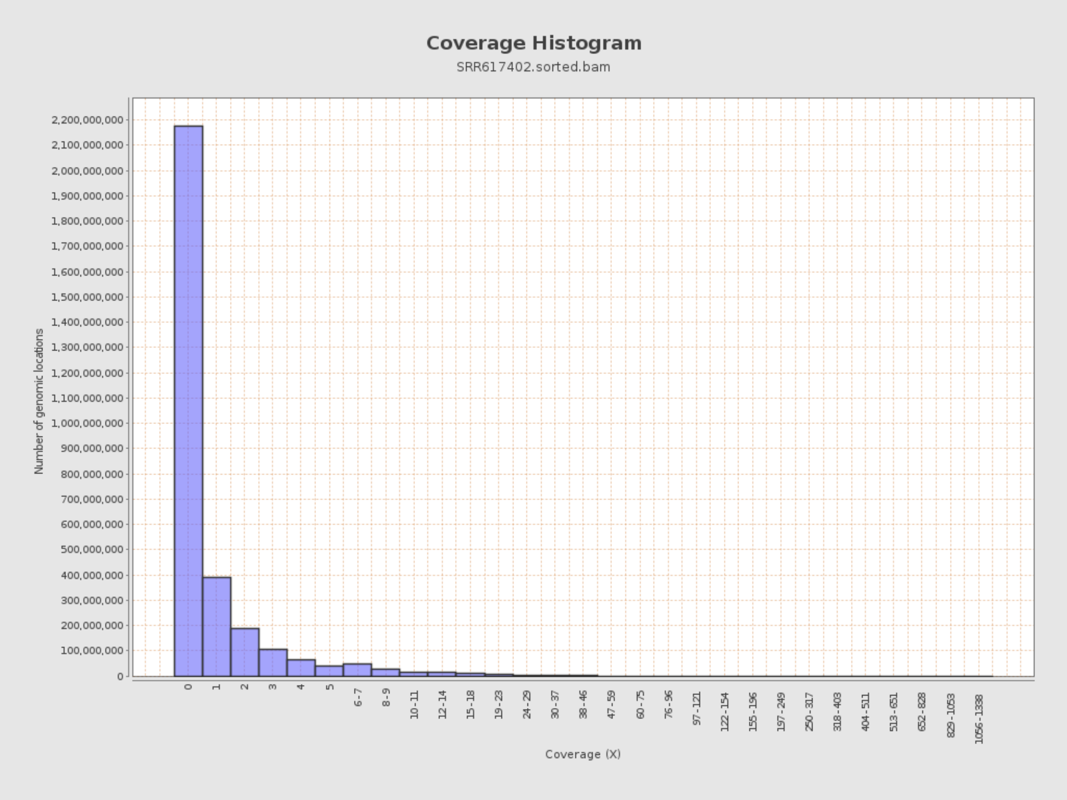
		bases	coverage	deviation
chr1	249250621	191208588	0.7671	2.7505
chr2	243199373	296079312	1.2174	3.1679
chr3	198022430	250288091	1.2639	3.4464
chr4	191154276	141292165	0.7392	2.2763
chr5	180915260	189566209	1.0478	2.8777
chr6	171115067	135793904	0.7936	2.6232
chr7	159138663	222265250	1.3967	3.2517
chr8	146364022	131195267	0.8964	3.2775
chr9	141213431	118580032	0.8397	2.6297
chr10	135534747	95389263	0.7038	2.449
chr11	135006516	220966586	1.6367	3.8698
chr12	133851895	141740015	1.0589	2.8268
chr13	115169878	128292329	1.1139	2.782
chr14	107349540	86282263	0.8038	2.9252
chr15	102531392	68407818	0.6672	2.3916
chr16	90354753	75916030	0.8402	3.3844
chr17	81195210	92964071	1.1449	3.7572
chr18	78077248	42388554	0.5429	2.02
chr19	59128983	43009656	0.7274	2.3776
chr20	63025520	102233880	1.6221	4.8309
chr21	48129895	40512602	0.8417	2.5288
chr22	51304566	24423774	0.4761	2.1295
chrMT	16571	192565	11.6206	5.5942
chrX	155270560	129591826	0.8346	2.5797

chrY	59373566	2423006	0.0408	0.6314

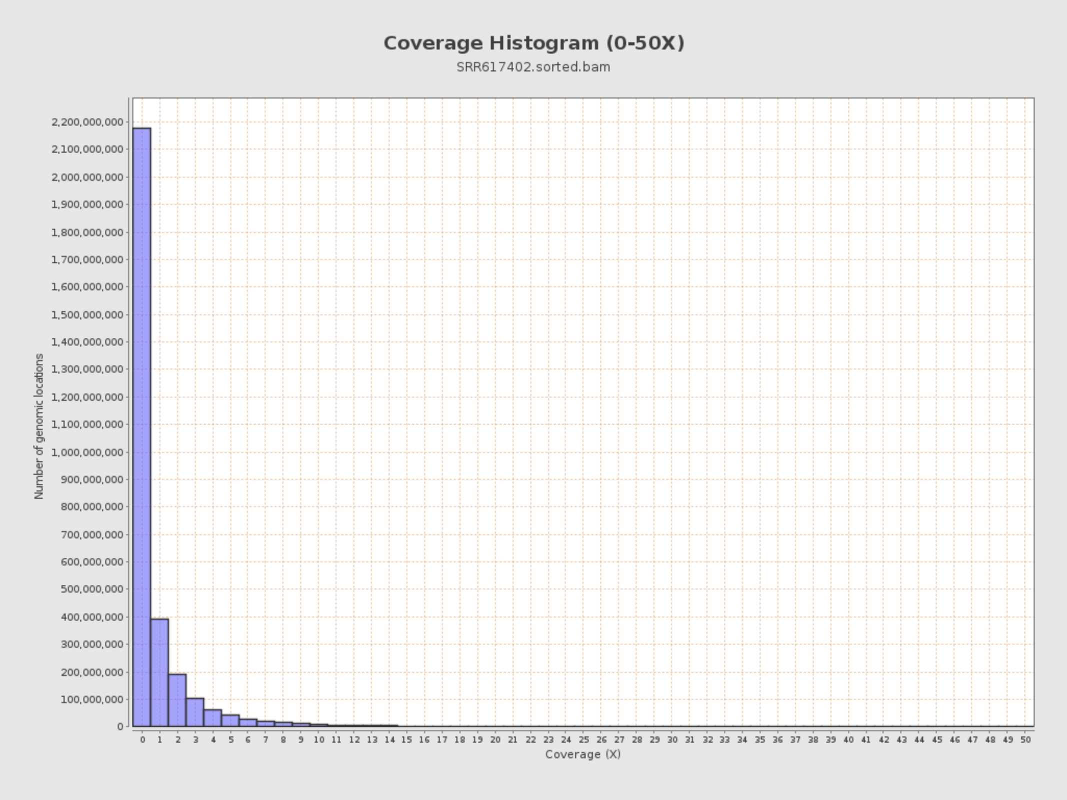
3. Results : Coverage across reference



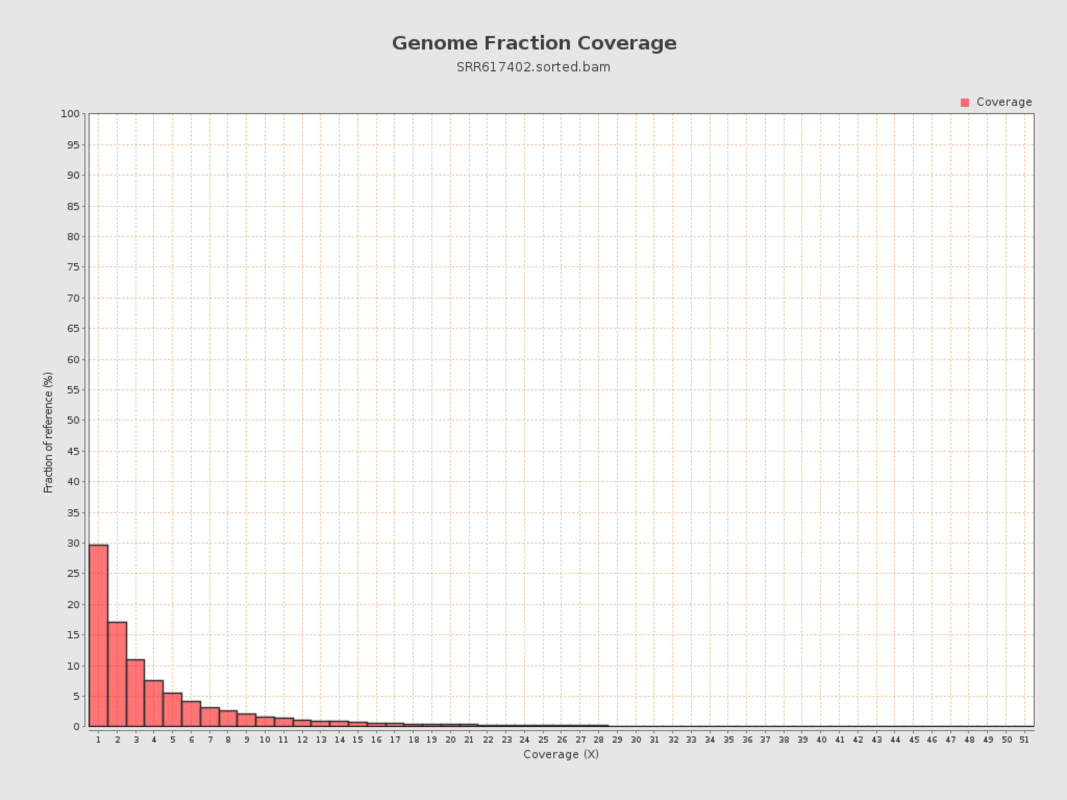
4. Results : Coverage Histogram



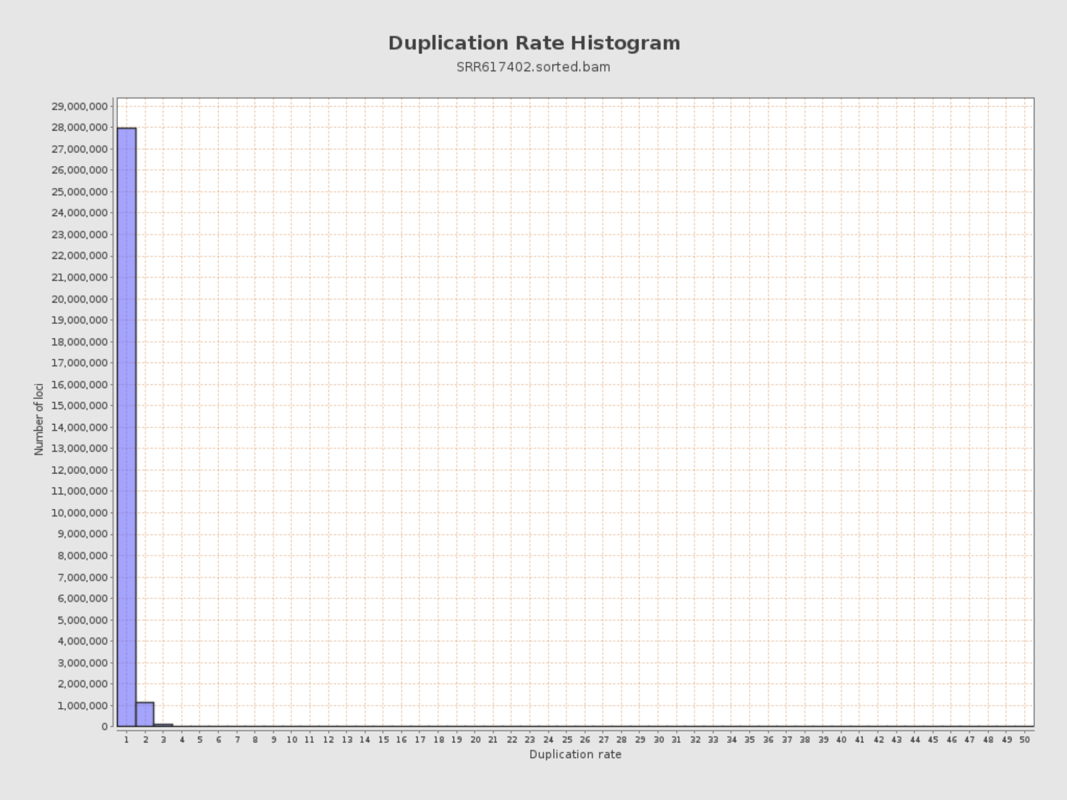
5. Results : Coverage Histogram (0-50X)



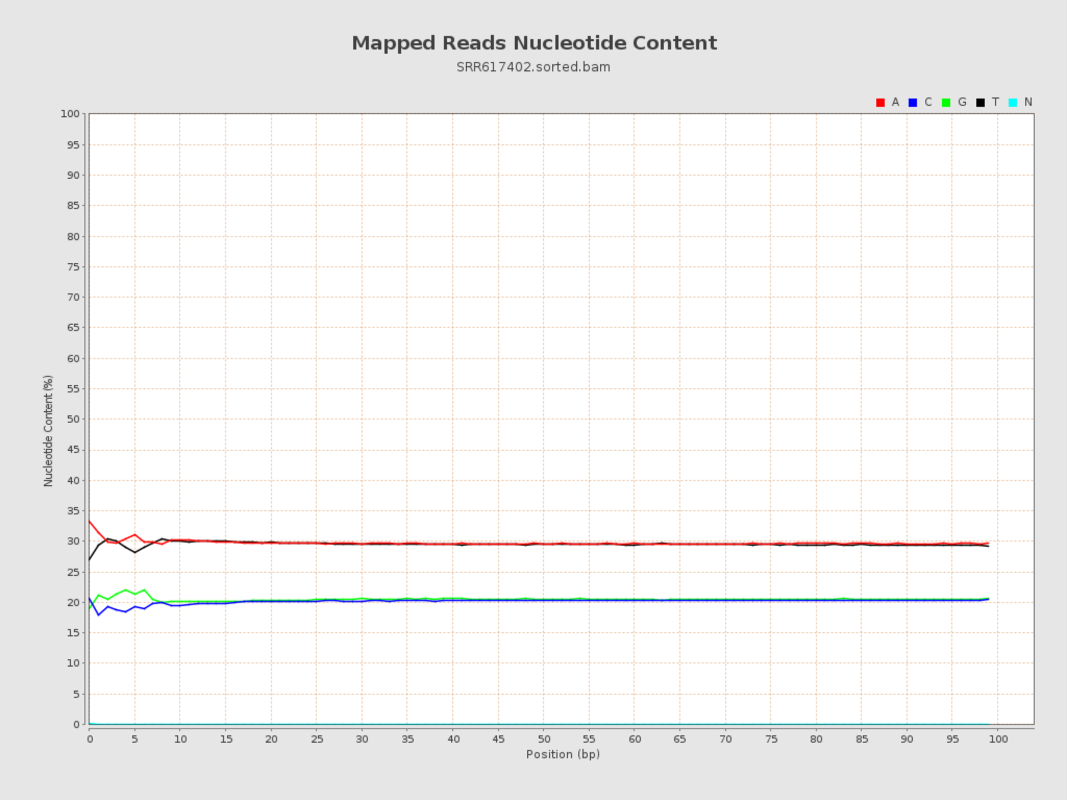
6. Results : Genome Fraction Coverage



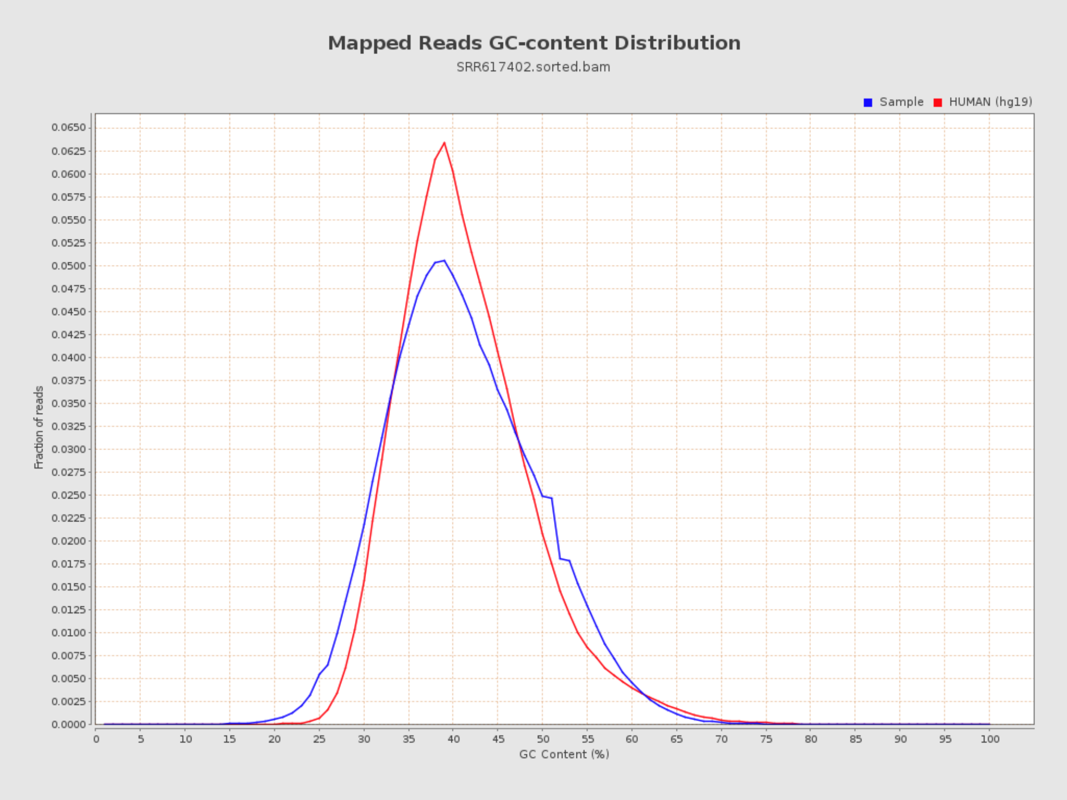
7. Results : Duplication Rate Histogram



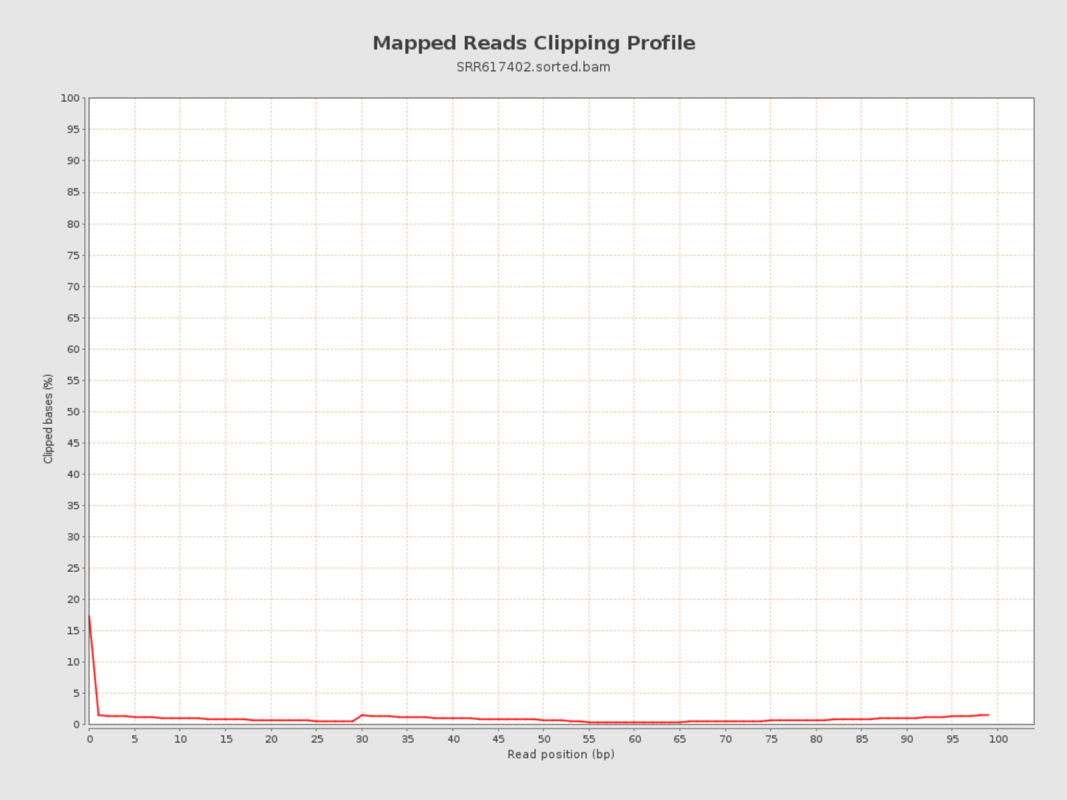
8. Results : Mapped Reads Nucleotide Content



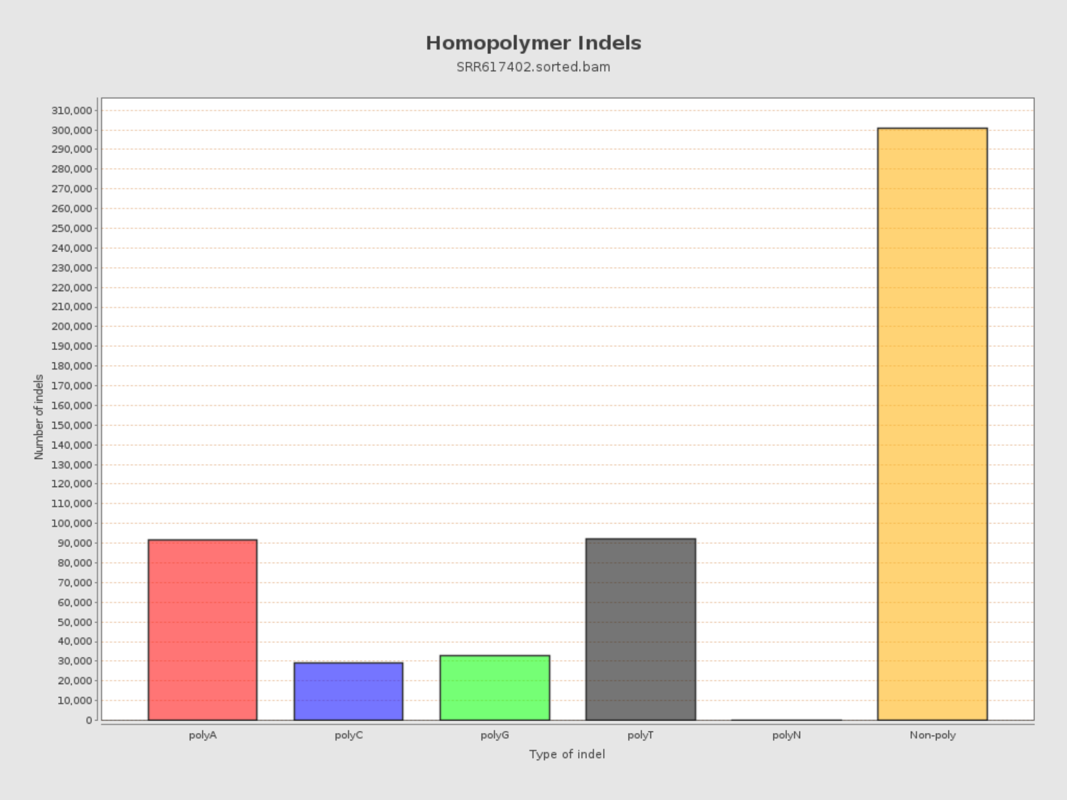
9. Results : Mapped Reads GC-content Distribution



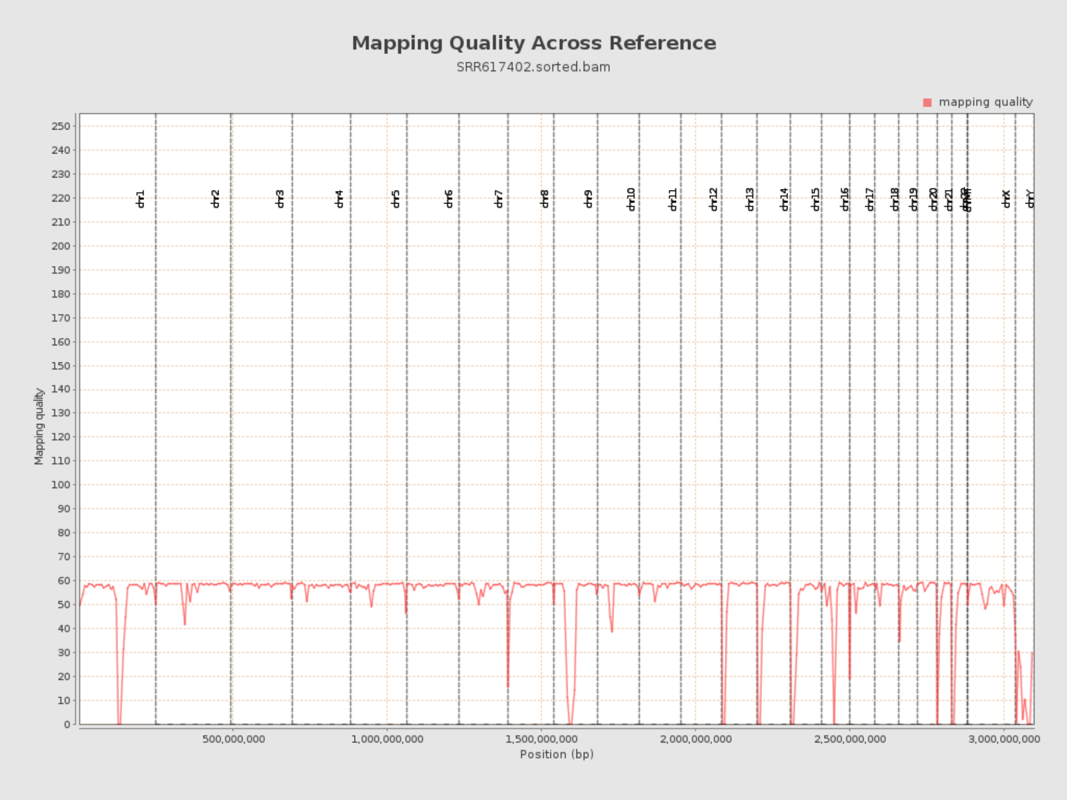
10. Results : Mapped Reads Clipping Profile



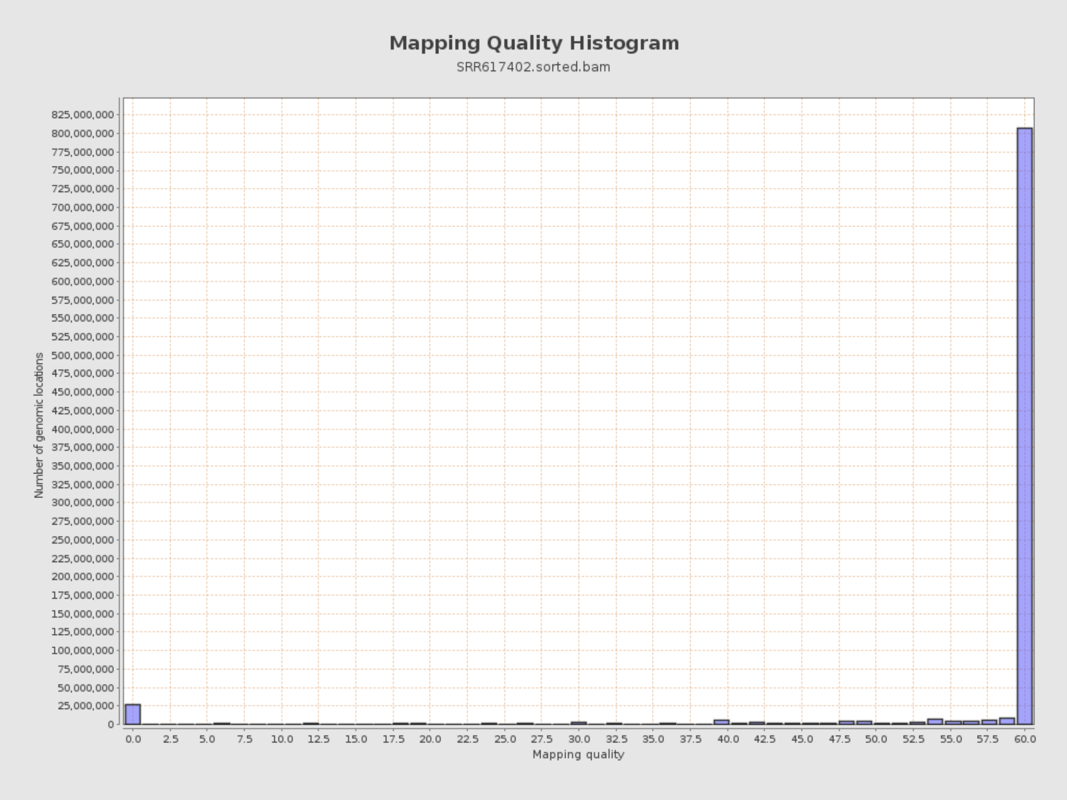
11. Results : Homopolymer Indels



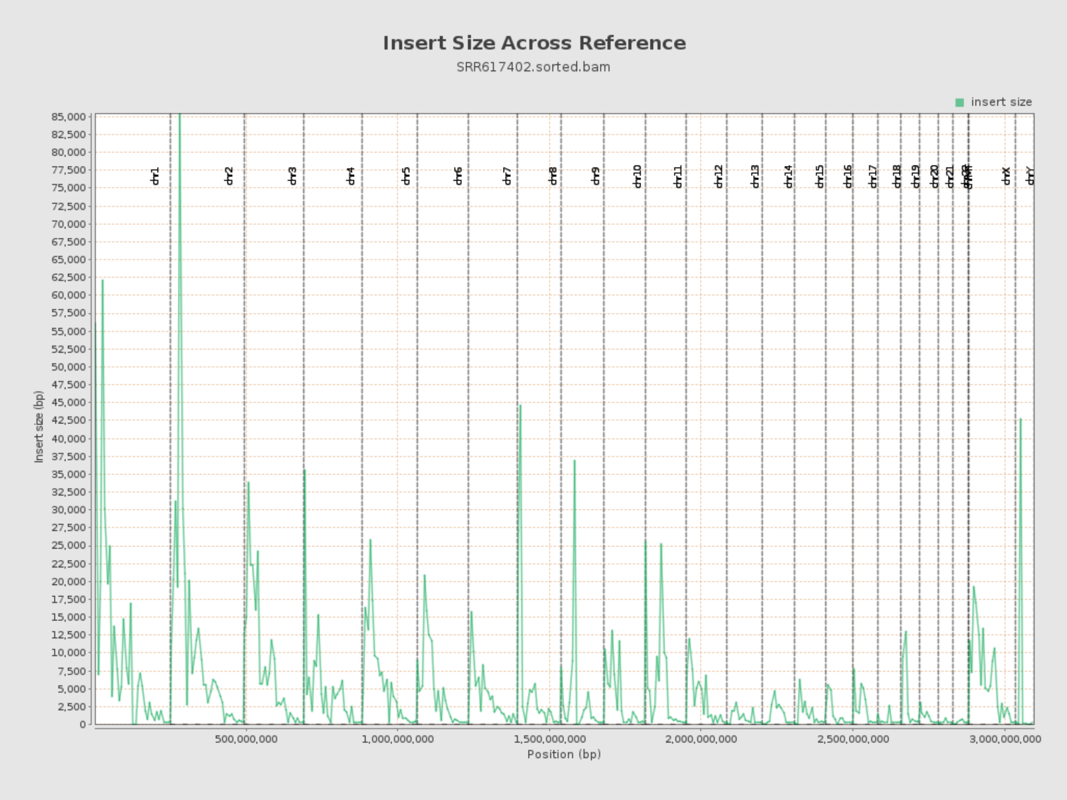
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram