Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 02:28:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617357.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_SRR617357 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617357_1.fastq.gz SRR617357_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 02:28:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617357.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,632,022 / 95.73%
Unmapped reads	1,367,978 / 4.27%
Mapped paired reads	30,632,022 / 95.73%
Mapped reads, first in pair	15,374,940 / 48.05%
Mapped reads, second in pair	15,257,082 / 47.68%
Mapped reads, both in pair	30,211,396 / 94.41%
Mapped reads, singletons	420,626 / 1.31%
Secondary alignments	0
Supplementary alignments	68,093 / 0.21%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	1,593,023 / 4.98%
Duplication rate	1.49%
Clipped reads	2,113,817 / 6.61%

2.2. ACGT Content

Number/percentage of A's	910,579,468 / 30.21%
Number/percentage of C's	600,333,646 / 19.91%
Number/percentage of T's	899,812,306 / 29.85%
Number/percentage of G's	603,151,602 / 20.01%
Number/percentage of N's	745,680 / 0.02%

GC Percentage	39.92%

2.3. Coverage

Mean	0.9741
Standard Deviation	9.916

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	58,481.87
Standard Deviation	2,306,839.4
P25/Median/P75	174 / 216 / 283

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	28,189,075
Insertions	307,056
Mapped reads with at least one insertion	0.97%
Deletions	372,694
Mapped reads with at least one deletion	1.18%
Homopolymer indels	41.28%

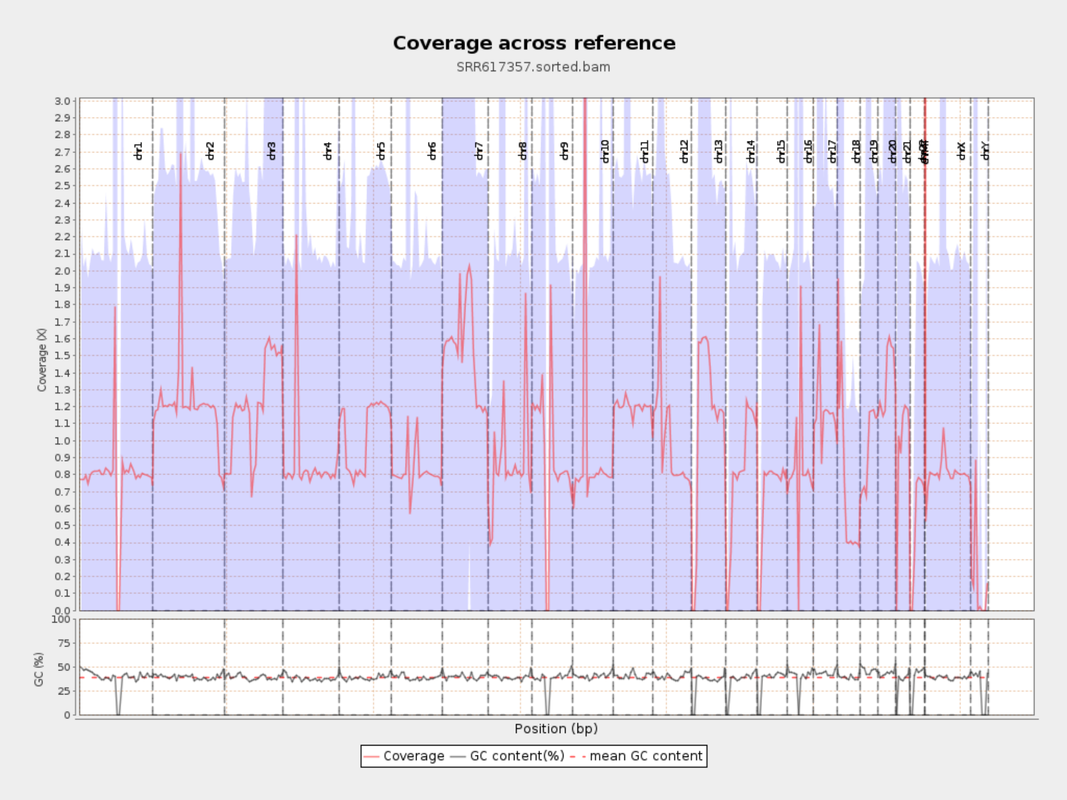
2.7. Chromosome stats

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

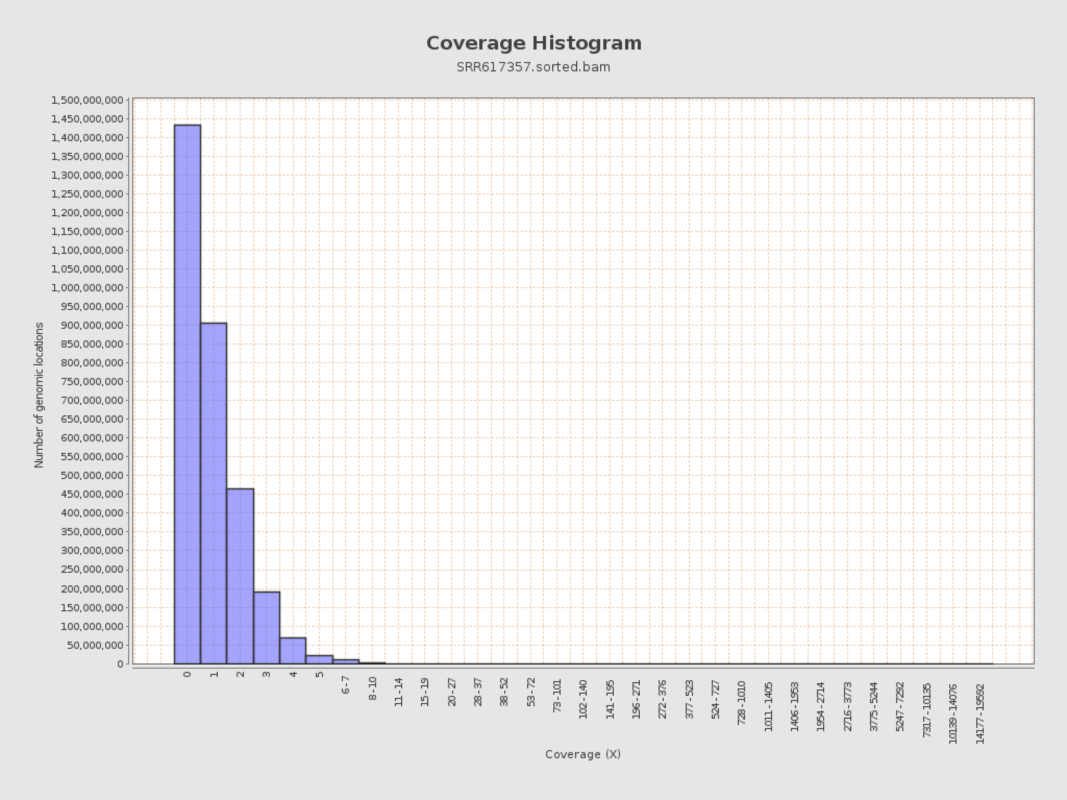
		bases	coverage	deviation
chr1	249250621	196159246	0.787	20.1074
chr2	243199373	297499834	1.2233	8.9588
chr3	198022430	239274734	1.2083	1.4758
chr4	191154276	164943913	0.8629	9.7494
chr5	180915260	189204483	1.0458	1.4624
chr6	171115067	140965431	0.8238	3.7298
chr7	159138663	244944633	1.5392	10.8788
chr8	146364022	126699647	0.8656	7.7471
chr9	141213431	127057550	0.8998	15.2558
chr10	135534747	126707719	0.9349	20.2176
chr11	135006516	161771982	1.1983	5.6233
chr12	133851895	132921443	0.993	1.3739
chr13	115169878	131167093	1.1389	1.3001
chr14	107349540	87041585	0.8108	1.3774
chr15	102531392	67966047	0.6629	0.9852
chr16	90354753	76101509	0.8423	7.9048
chr17	81195210	94523014	1.1641	7.3734
chr18	78077248	54573492	0.699	15.6455
chr19	59128983	56712341	0.9591	9.6181
chr20	63025520	86871892	1.3784	2.5065
chr21	48129895	47854847	0.9943	3.2318
chr22	51304566	27083785	0.5279	0.9263
chrMT	16571	2079567	125.4944	19.4011
chrX	155270560	125019096	0.8052	3.0493

chrY	59373566	10382193	0.1749	8.5503

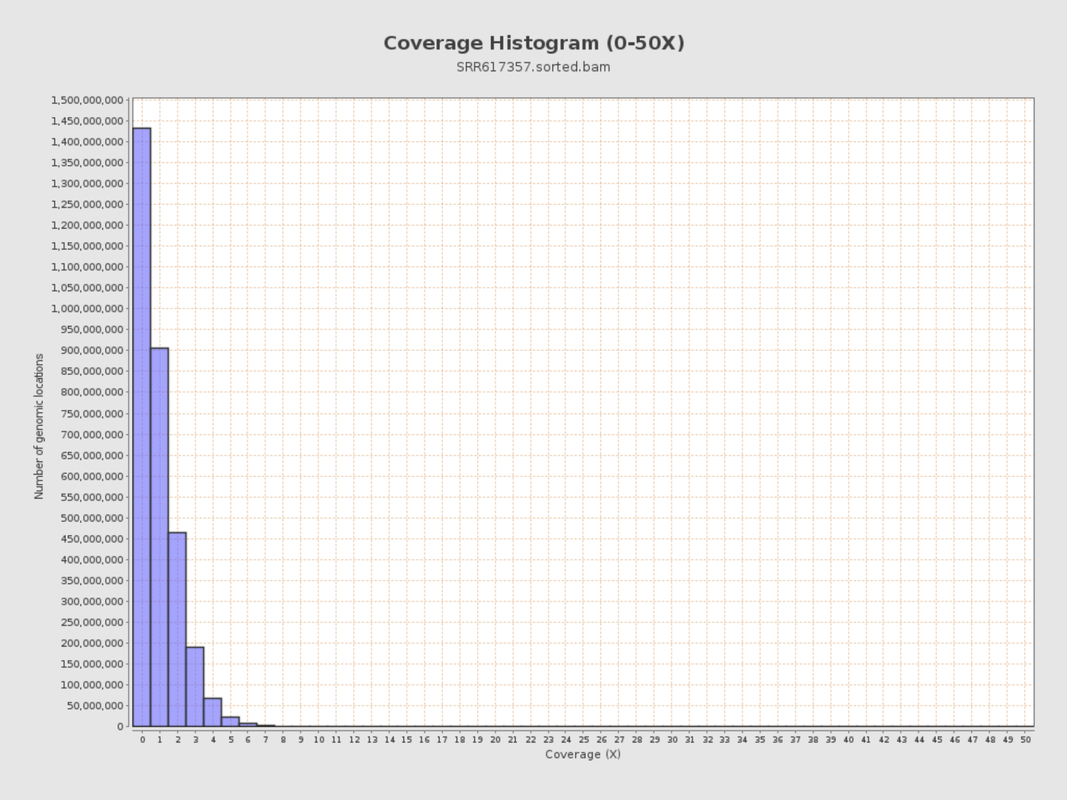
3. Results : Coverage across reference



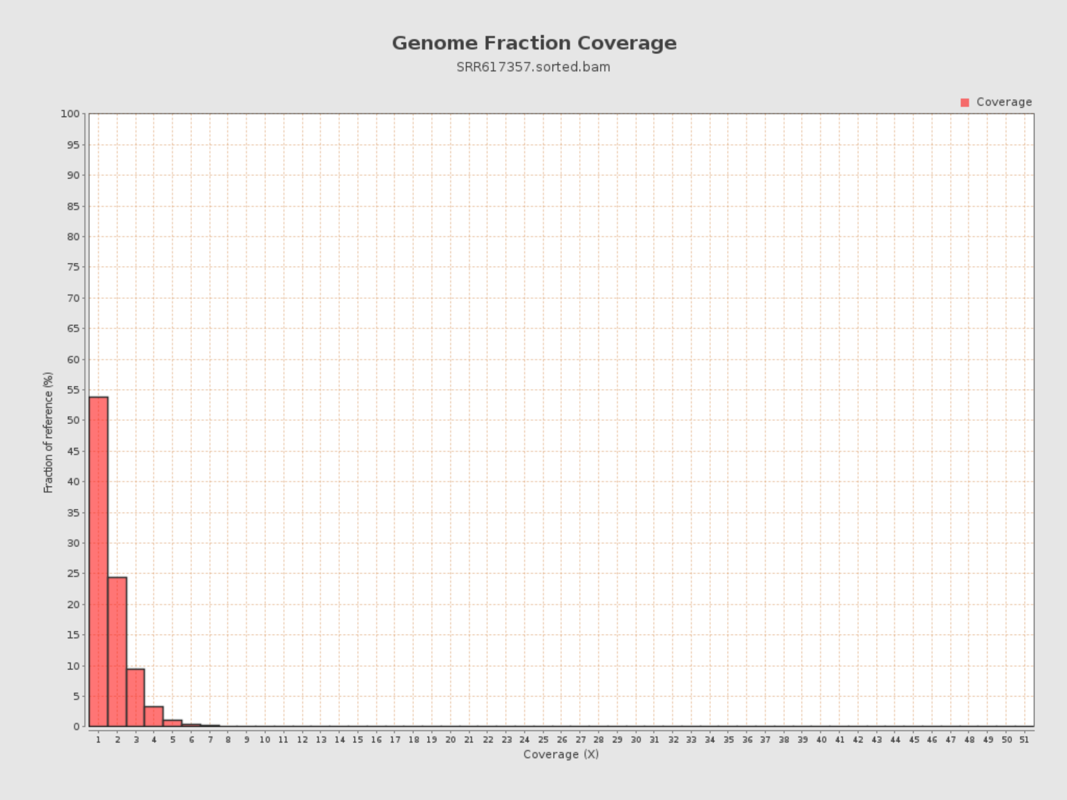
4. Results : Coverage Histogram



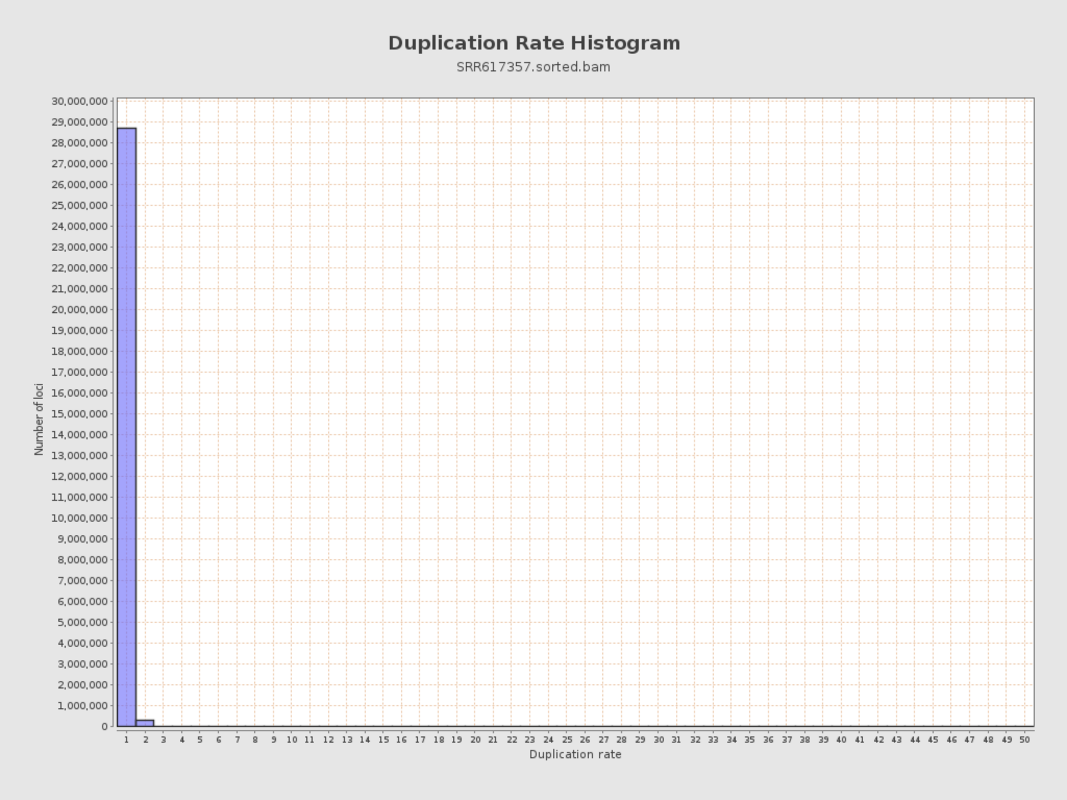
5. Results : Coverage Histogram (0-50X)



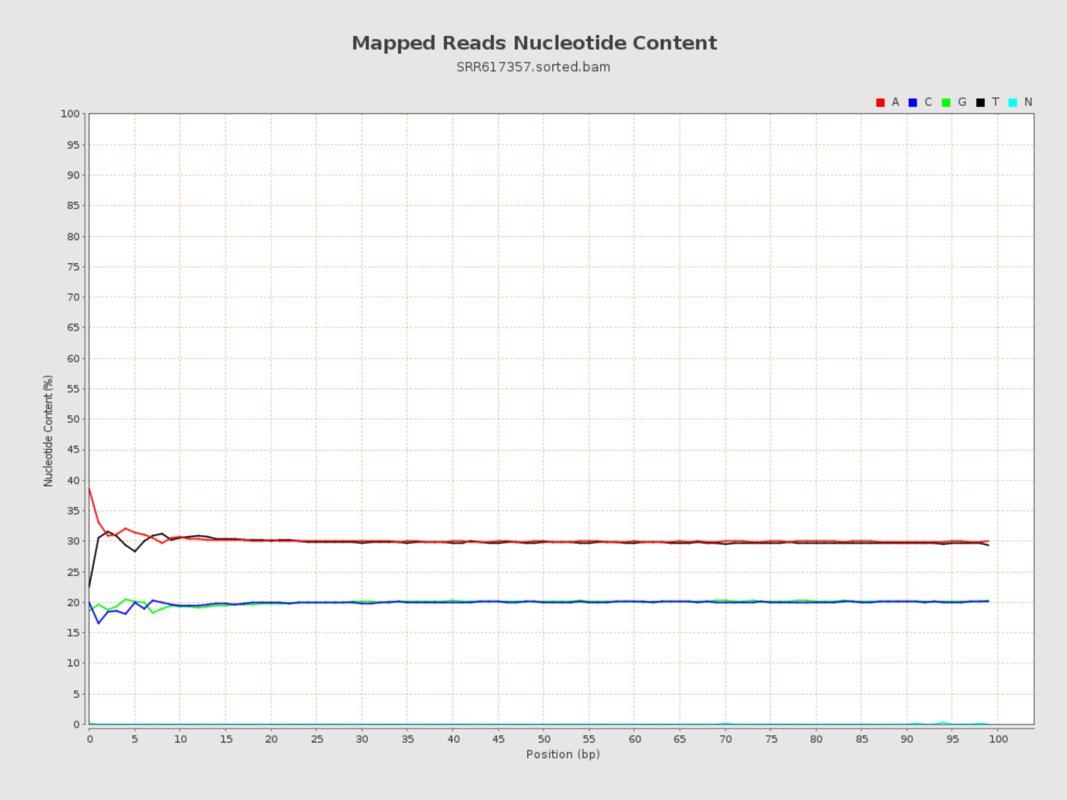
6. Results : Genome Fraction Coverage



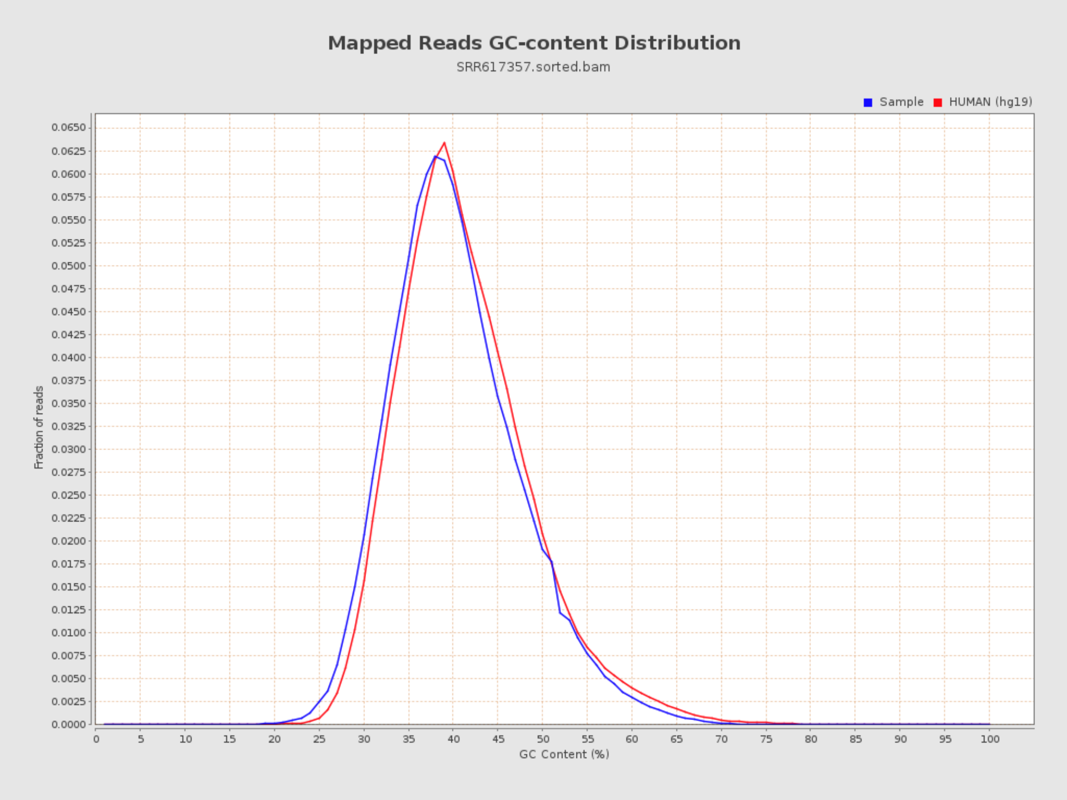
7. Results : Duplication Rate Histogram



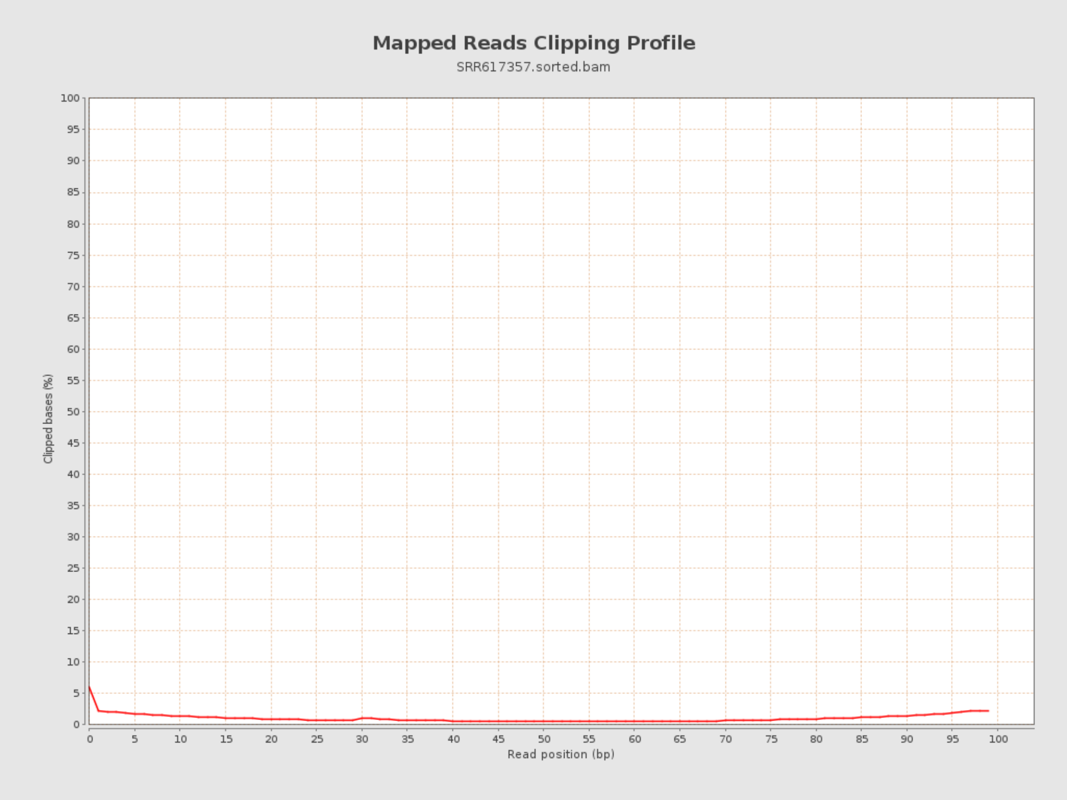
8. Results : Mapped Reads Nucleotide Content



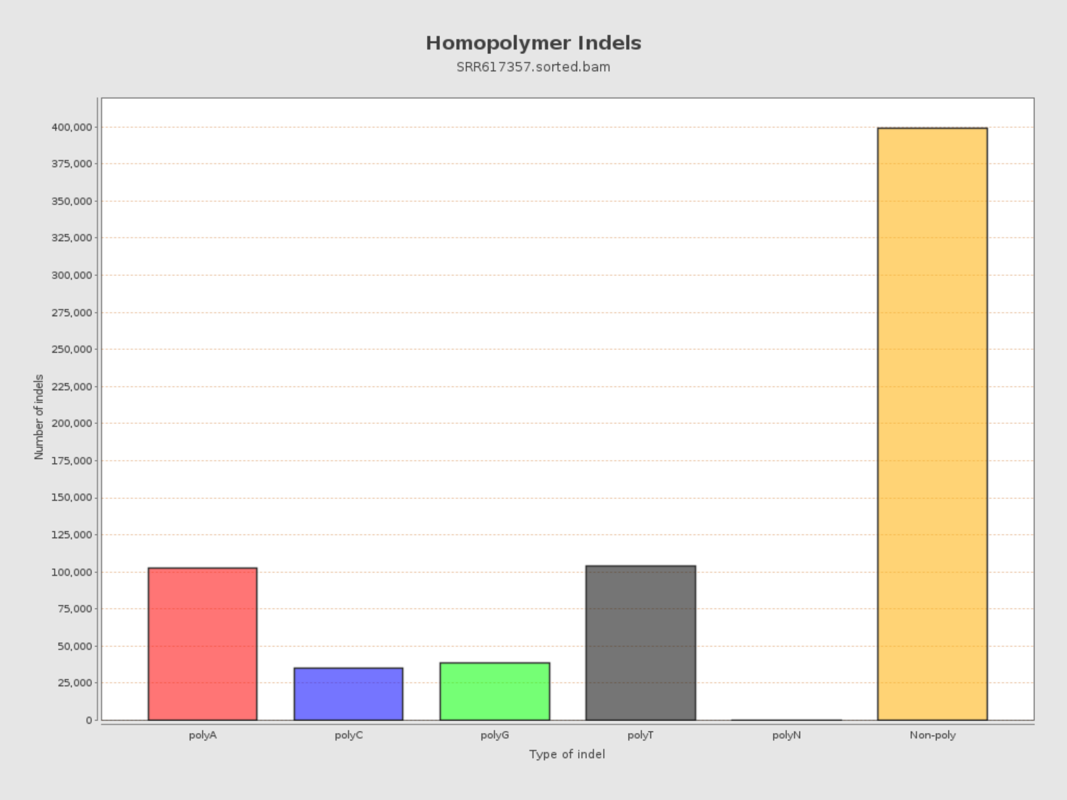
9. Results : Mapped Reads GC-content Distribution



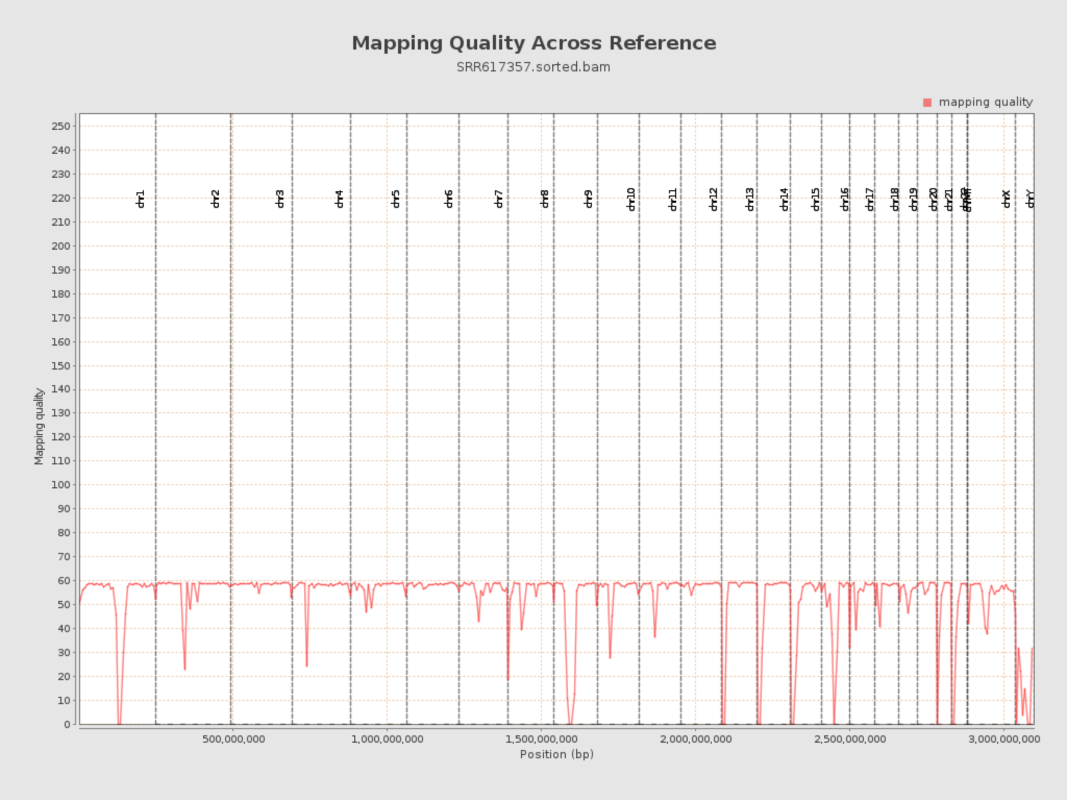
10. Results : Mapped Reads Clipping Profile



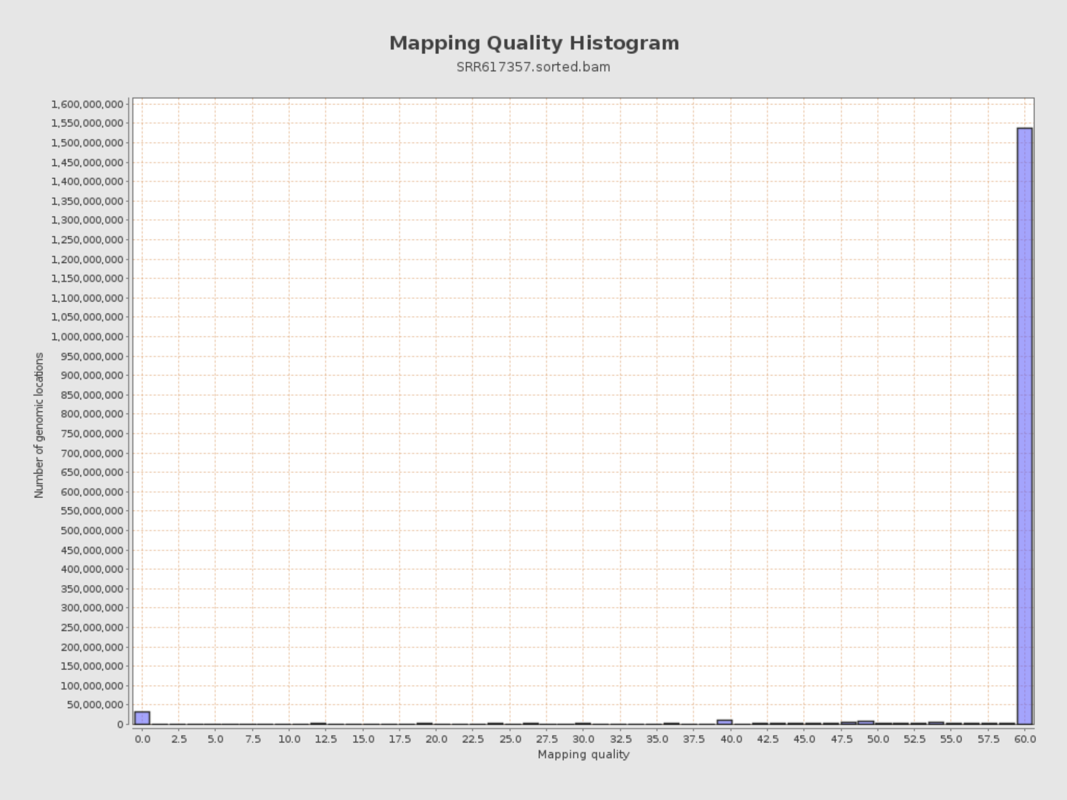
11. Results : Homopolymer Indels



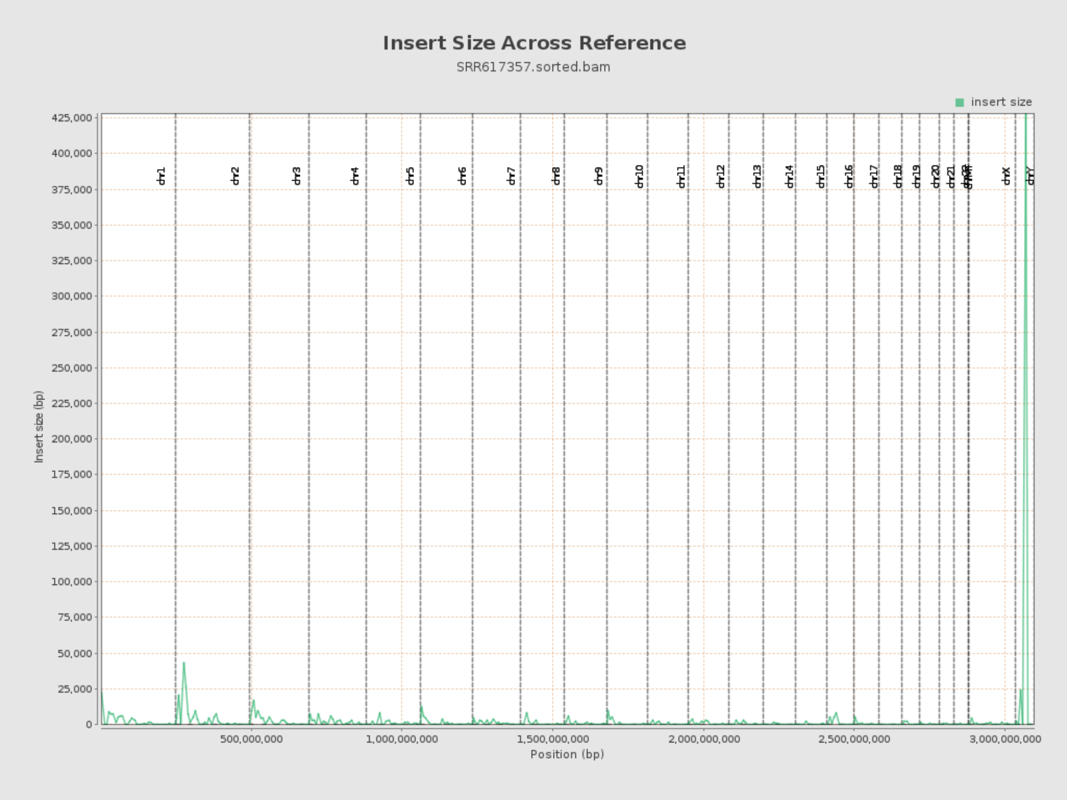
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram