Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 23:56:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617410.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_SRR617410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617410_1.fastq.gz SRR617410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 23:56:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,925,550 / 87.27%
Unmapped reads	4,074,450 / 12.73%
Mapped paired reads	27,925,550 / 87.27%
Mapped reads, first in pair	14,291,846 / 44.66%
Mapped reads, second in pair	13,633,704 / 42.61%
Mapped reads, both in pair	26,906,080 / 84.08%
Mapped reads, singletons	1,019,470 / 3.19%
Secondary alignments	0
Supplementary alignments	388,408 / 1.21%
Read min/max/mean length	30 / 100 / 100.5
Duplicated reads (estimated)	1,178,656 / 3.68%
Duplication rate	3.87%
Clipped reads	3,832,296 / 11.98%

2.2. ACGT Content

Number/percentage of A's	817,580,436 / 29.94%
Number/percentage of C's	546,500,650 / 20.01%
Number/percentage of T's	806,627,909 / 29.54%
Number/percentage of G's	558,096,006 / 20.44%
Number/percentage of N's	1,710,566 / 0.06%

GC Percentage	40.45%

2.3. Coverage

Mean	0.8822
Standard Deviation	2.6965

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	48,556.33
Standard Deviation	2,099,312.75
P25/Median/P75	169 / 206 / 264

2.6. Mismatches and indels

General error rate	1.61%
Mismatches	43,445,523
Insertions	222,170
Mapped reads with at least one insertion	0.78%
Deletions	260,304
Mapped reads with at least one deletion	0.91%
Homopolymer indels	43.96%

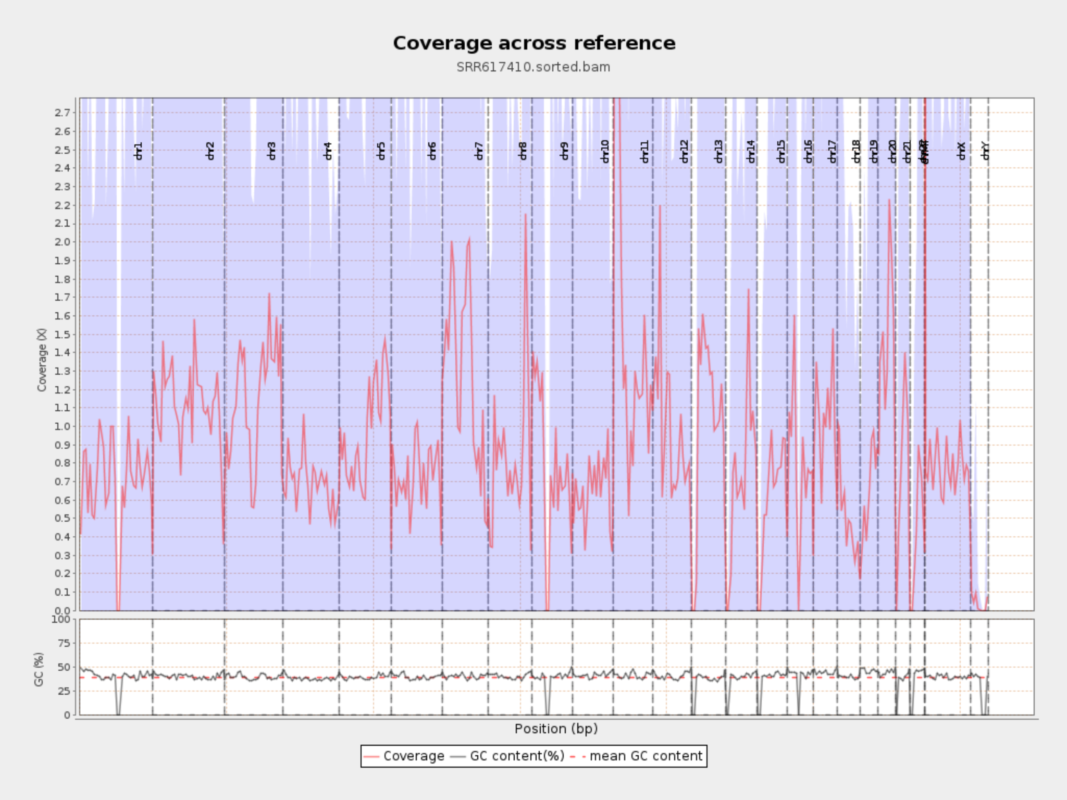
2.7. Chromosome stats

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

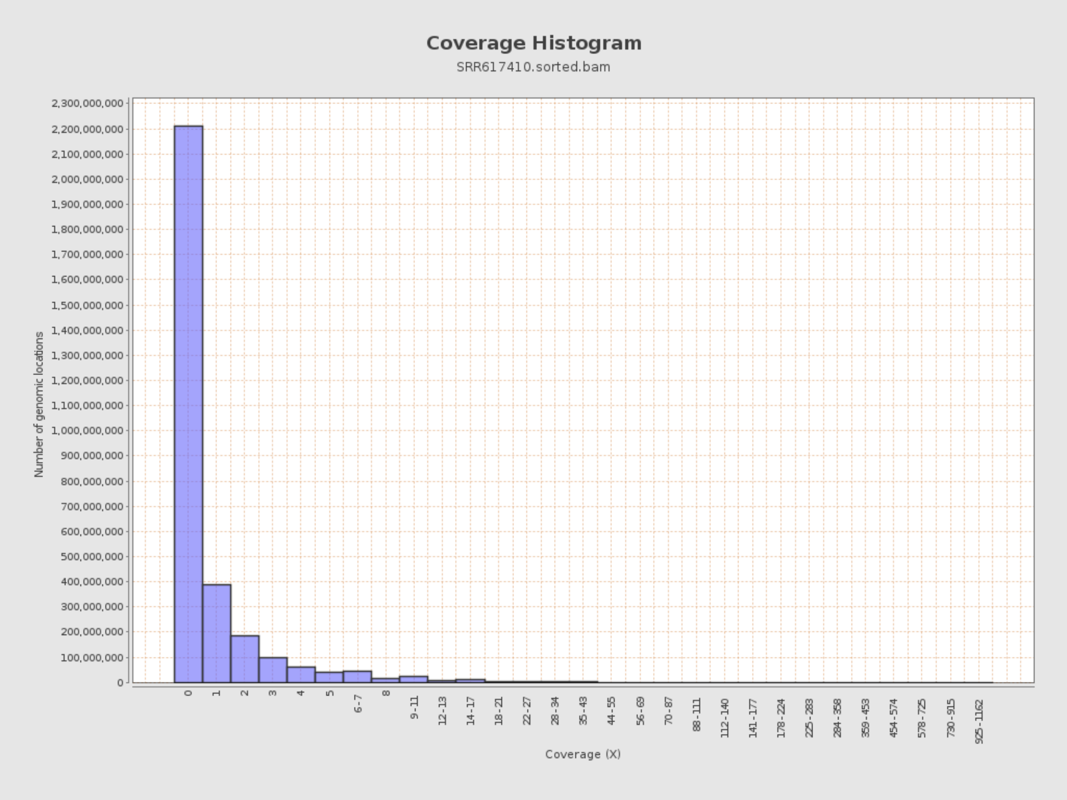
		bases	coverage	deviation
chr1	249250621	175195906	0.7029	2.5261
chr2	243199373	273090976	1.1229	2.8446
chr3	198022430	231014660	1.1666	3.1518
chr4	191154276	132669077	0.694	2.1305
chr5	180915260	175389887	0.9695	2.6683
chr6	171115067	125829582	0.7354	2.4185
chr7	159138663	204471268	1.2849	2.9997
chr8	146364022	120867385	0.8258	2.9901
chr9	141213431	108984011	0.7718	2.4003
chr10	135534747	87552953	0.646	2.2125
chr11	135006516	202140692	1.4973	3.5395
chr12	133851895	130260524	0.9732	2.5746
chr13	115169878	119208934	1.0351	2.5852
chr14	107349540	78980296	0.7357	2.649
chr15	102531392	62489297	0.6095	2.1717
chr16	90354753	67950750	0.752	3.0269
chr17	81195210	83313876	1.0261	3.3495
chr18	78077248	39449474	0.5053	1.8553
chr19	59128983	38198522	0.646	2.1204
chr20	63025520	91993291	1.4596	4.2944
chr21	48129895	37524879	0.7797	2.3505
chr22	51304566	21599191	0.421	1.8825
chrMT	16571	166303	10.0358	4.9132
chrX	155270560	120537504	0.7763	2.3771

chrY	59373566	2214018	0.0373	0.5264

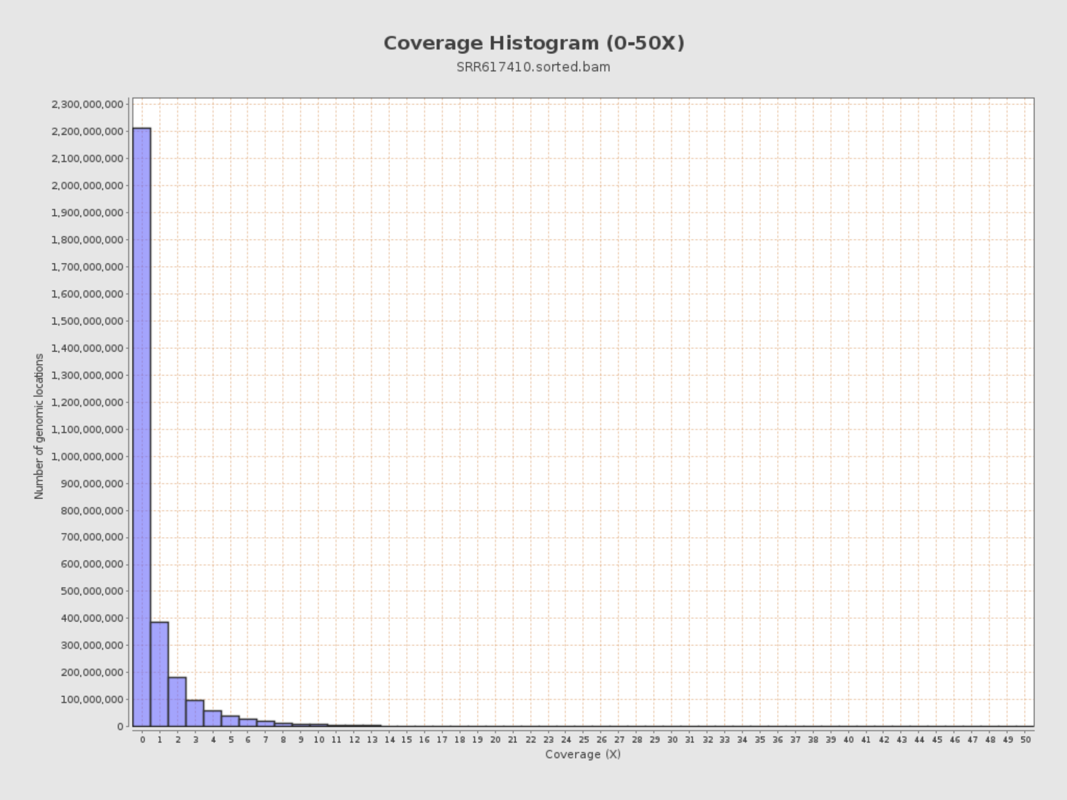
3. Results : Coverage across reference



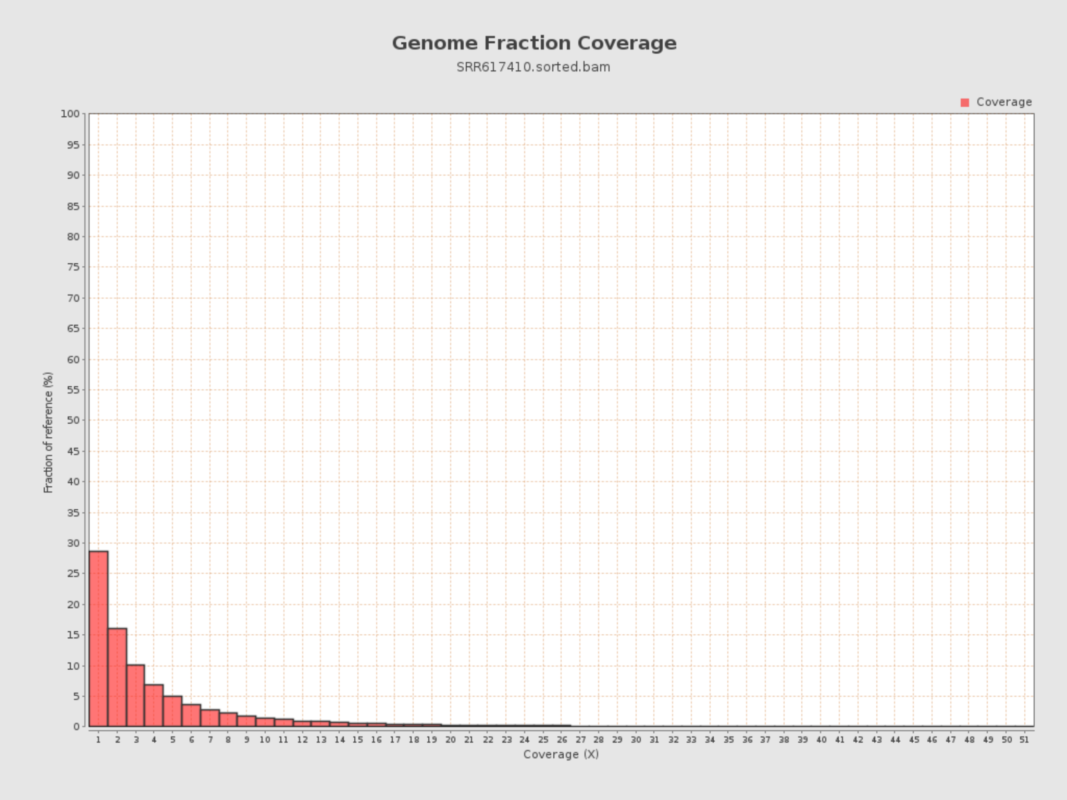
4. Results : Coverage Histogram



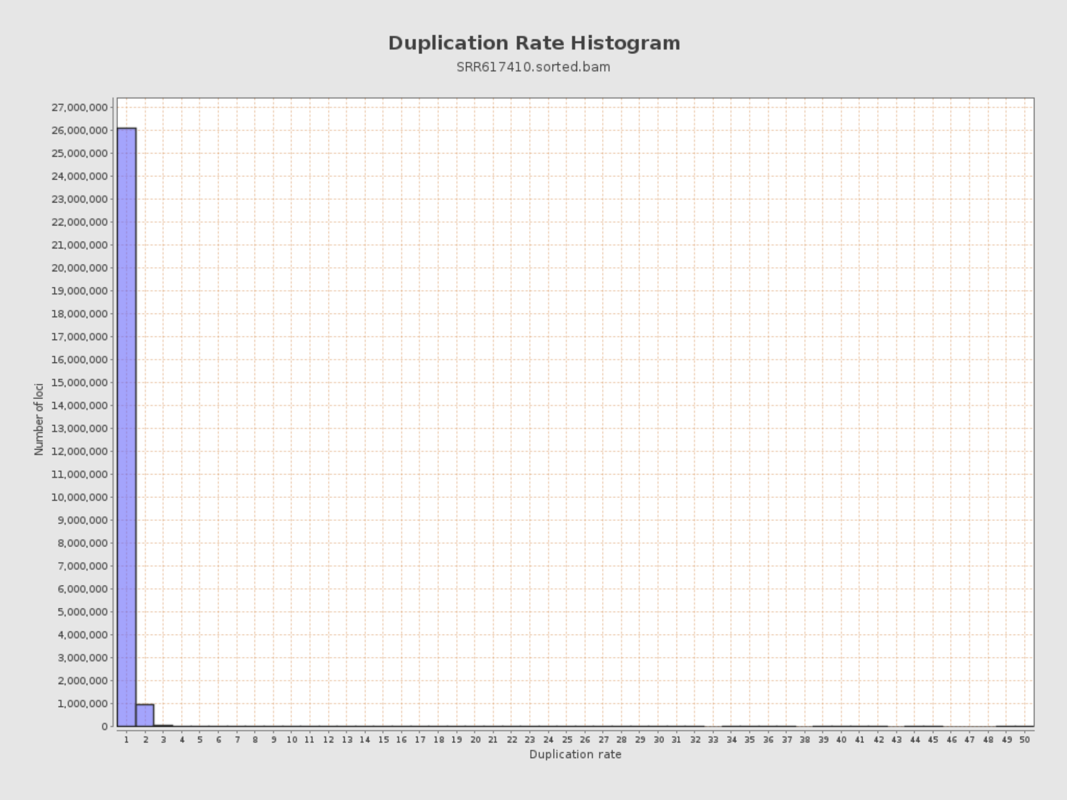
5. Results : Coverage Histogram (0-50X)



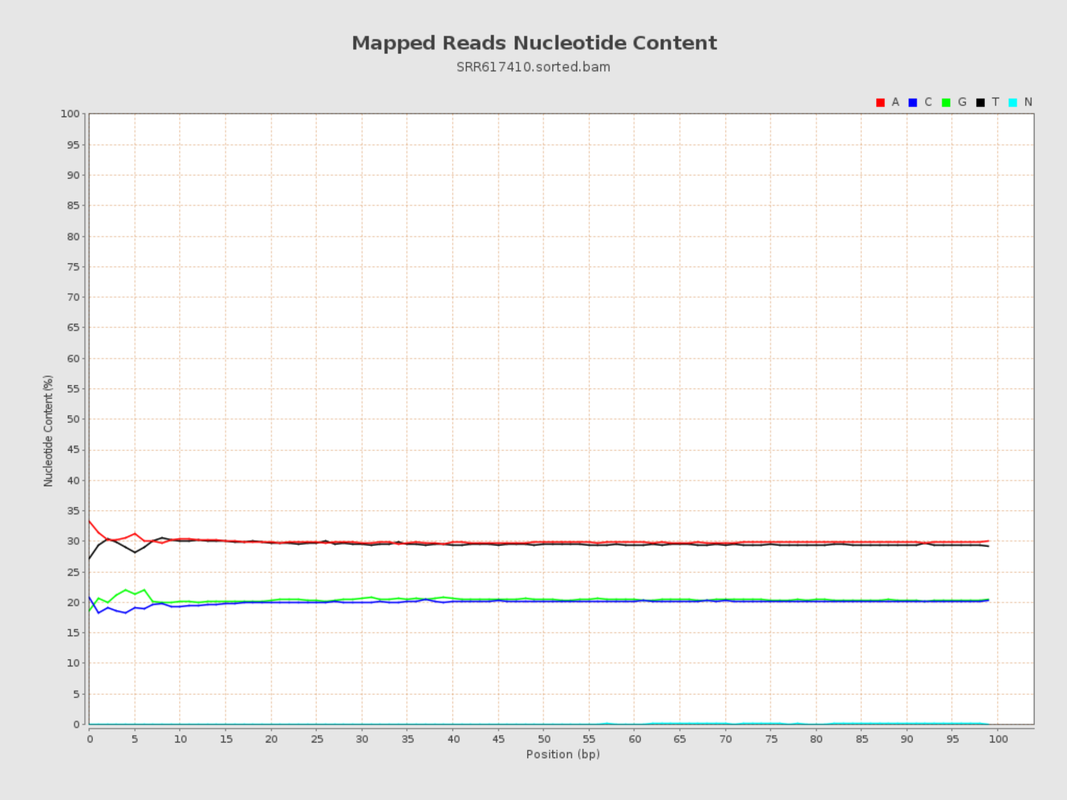
6. Results : Genome Fraction Coverage



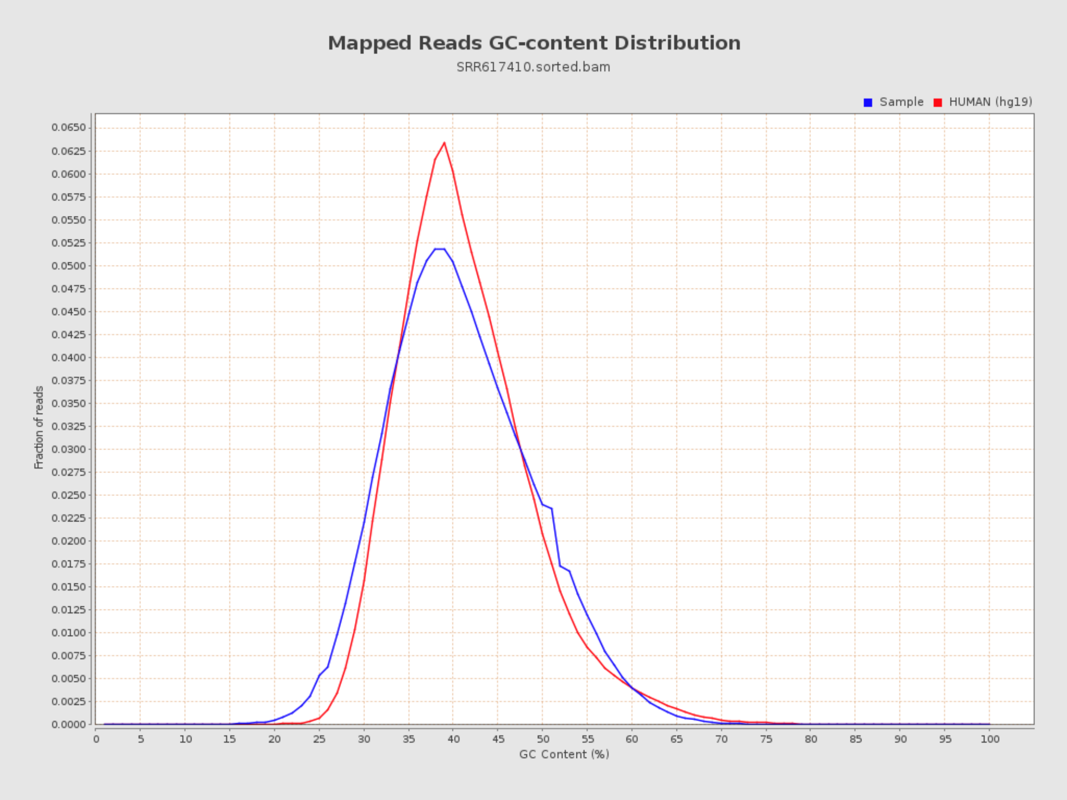
7. Results : Duplication Rate Histogram



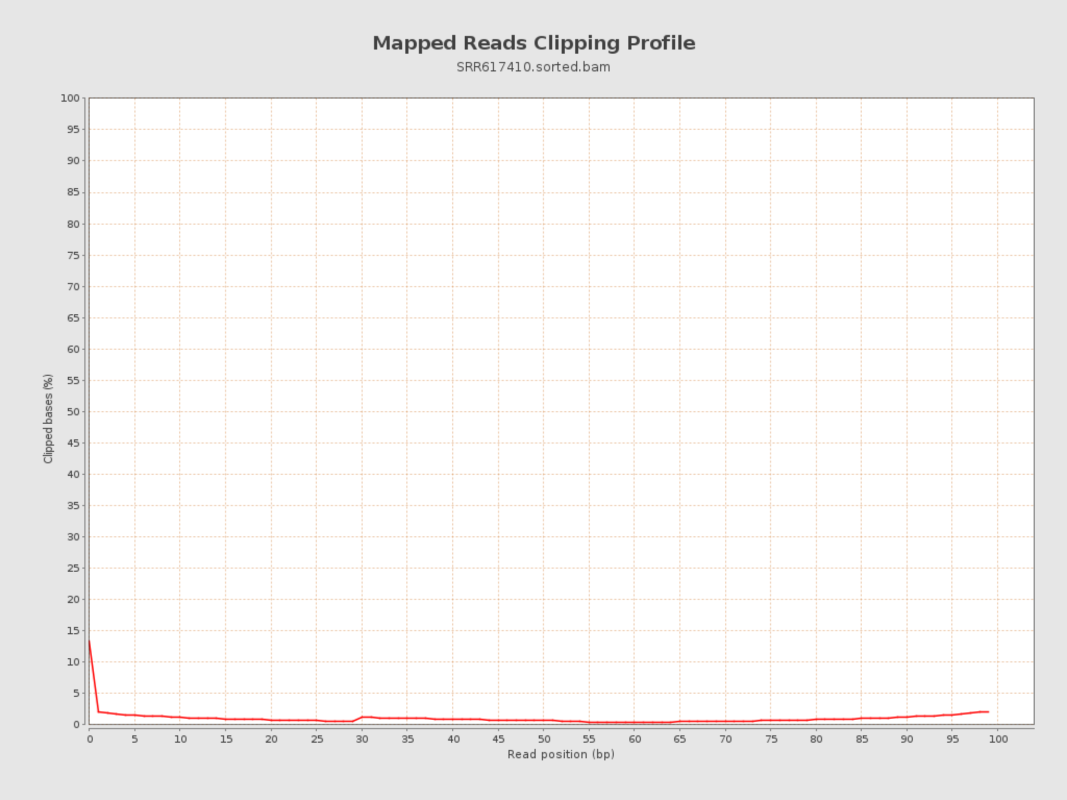
8. Results : Mapped Reads Nucleotide Content



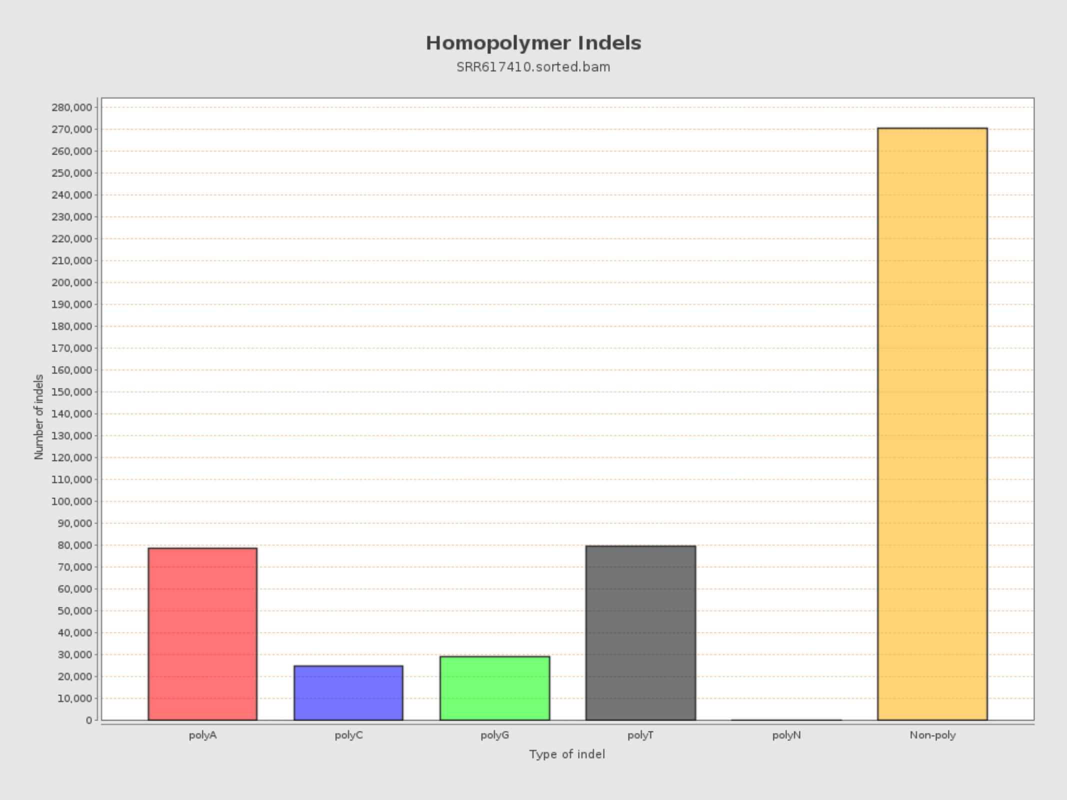
9. Results : Mapped Reads GC-content Distribution



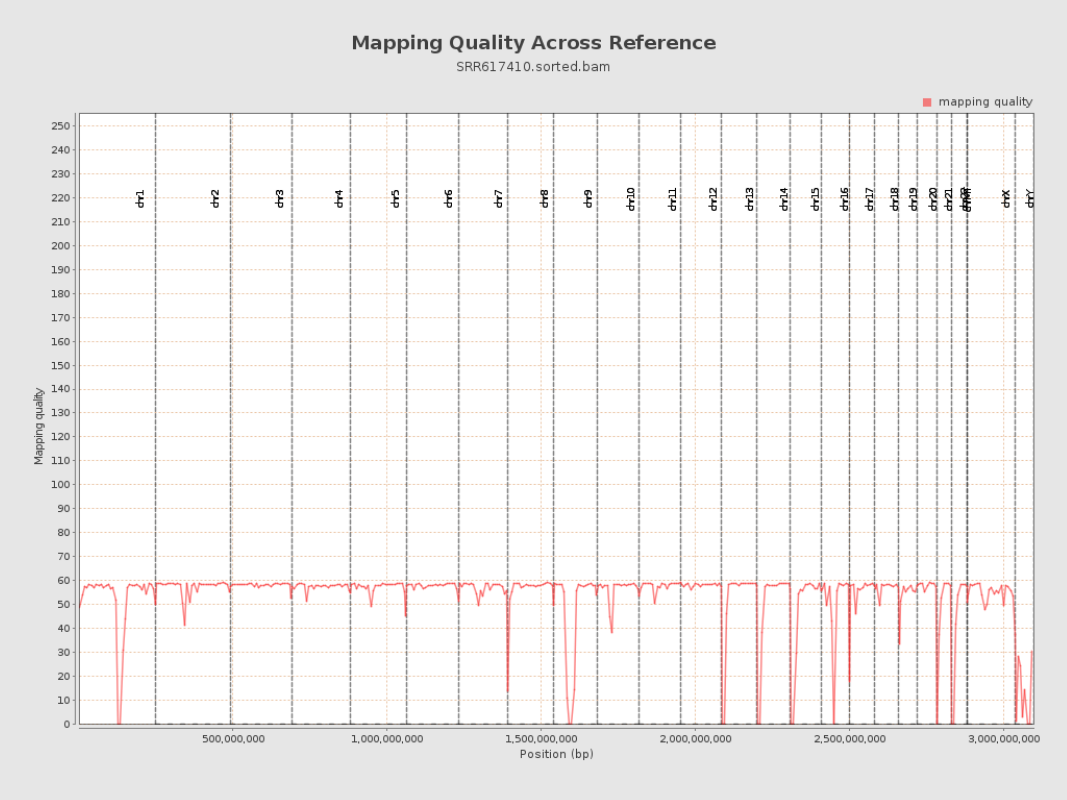
10. Results : Mapped Reads Clipping Profile



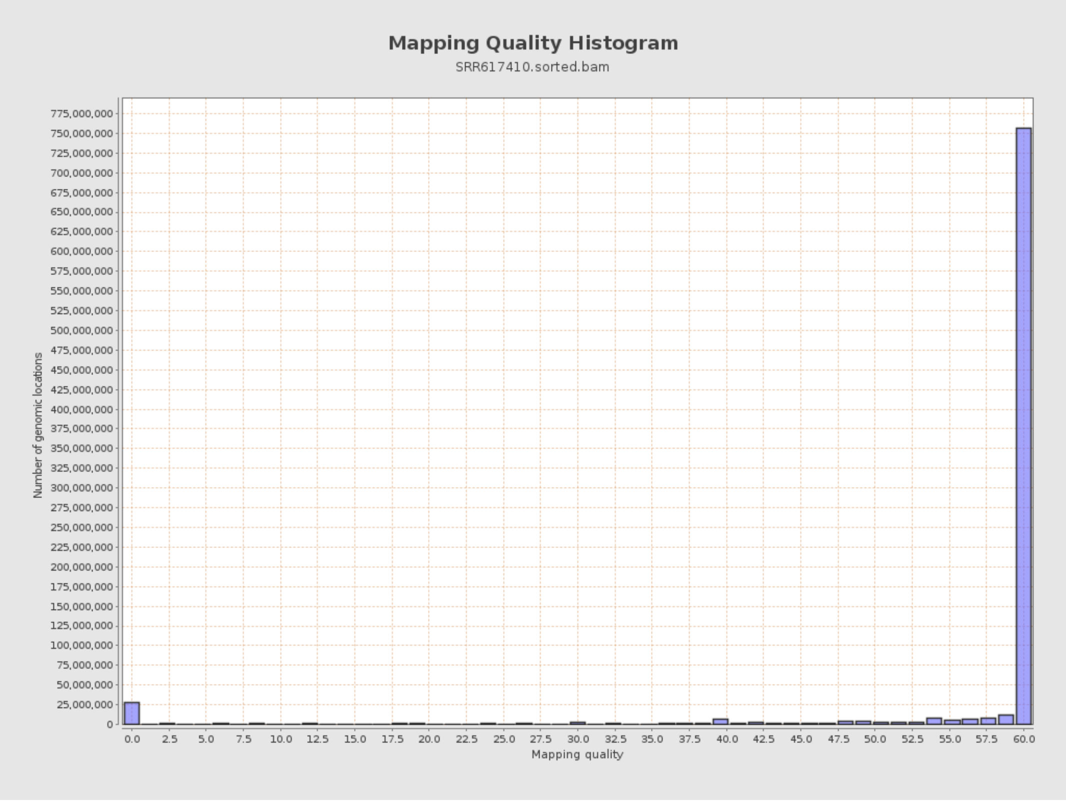
11. Results : Homopolymer Indels



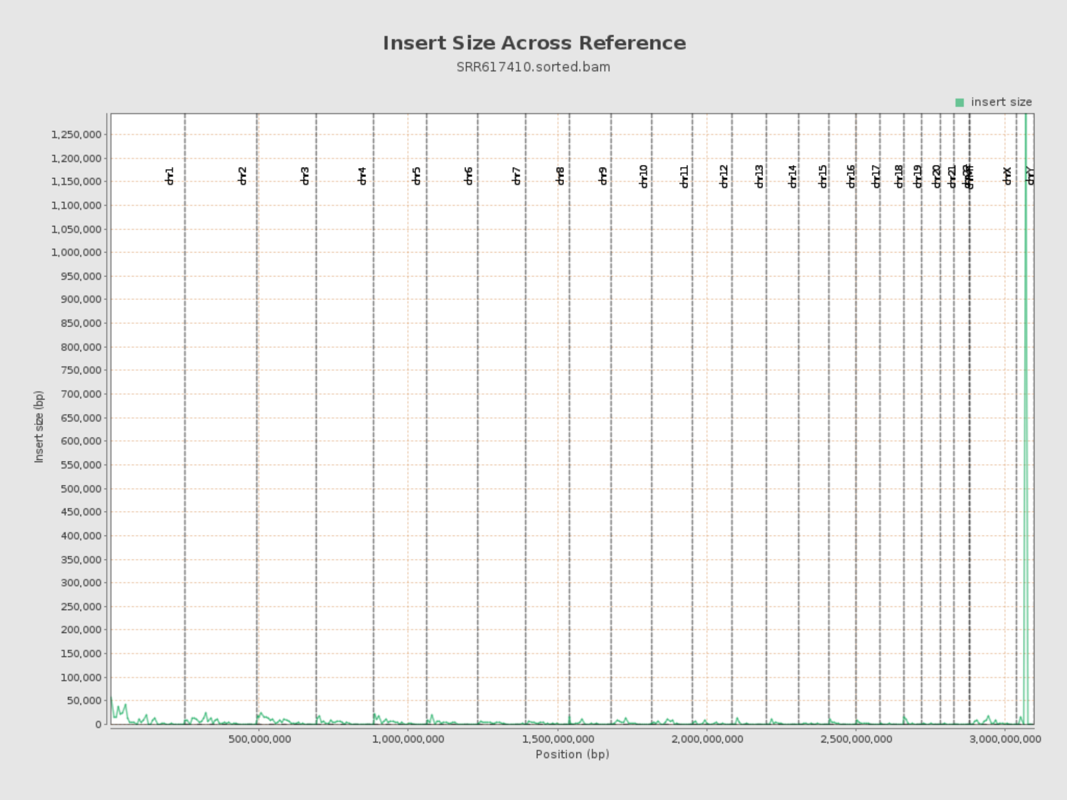
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram