Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 03:21:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617661.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_SRR617661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617661_1.fastq.gz SRR617661_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 03:21:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,745,931 / 96.08%
Unmapped reads	1,254,069 / 3.92%
Mapped paired reads	30,745,931 / 96.08%
Mapped reads, first in pair	15,362,565 / 48.01%
Mapped reads, second in pair	15,383,366 / 48.07%
Mapped reads, both in pair	30,258,138 / 94.56%
Mapped reads, singletons	487,793 / 1.52%
Secondary alignments	0
Supplementary alignments	142,556 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,208,961 / 22.53%
Duplication rate	10.93%
Clipped reads	6,170,405 / 19.28%

2.2. ACGT Content

Number/percentage of A's	890,236,466 / 29.72%
Number/percentage of C's	598,408,698 / 19.98%
Number/percentage of T's	889,882,397 / 29.71%
Number/percentage of G's	614,584,770 / 20.52%
Number/percentage of N's	2,080,381 / 0.07%

GC Percentage	40.5%

2.3. Coverage

Mean	0.9681
Standard Deviation	10.9033

2.4. Mapping Quality

Mean Mapping Quality	52.76

2.5. Insert size

Mean	30,903.44
Standard Deviation	1,609,198.6
P25/Median/P75	181 / 227 / 296

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	40,512,244
Insertions	466,526
Mapped reads with at least one insertion	1.49%
Deletions	1,106,182
Mapped reads with at least one deletion	3.52%
Homopolymer indels	47.75%

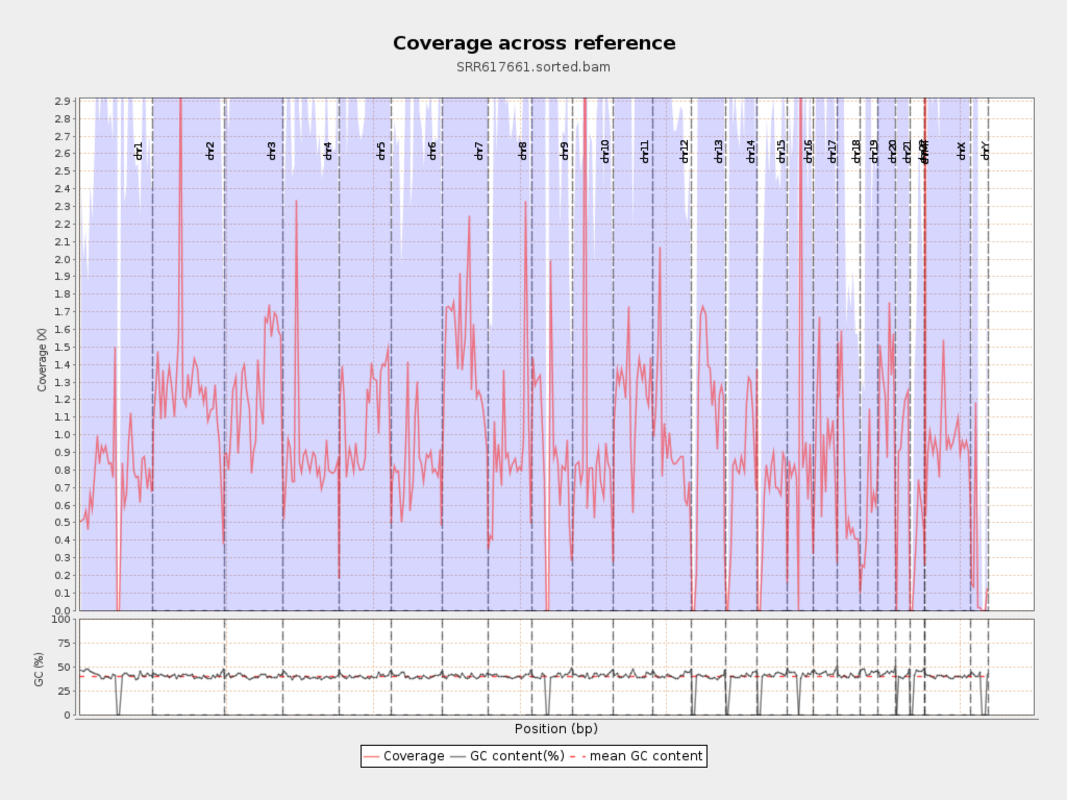
2.7. Chromosome stats

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

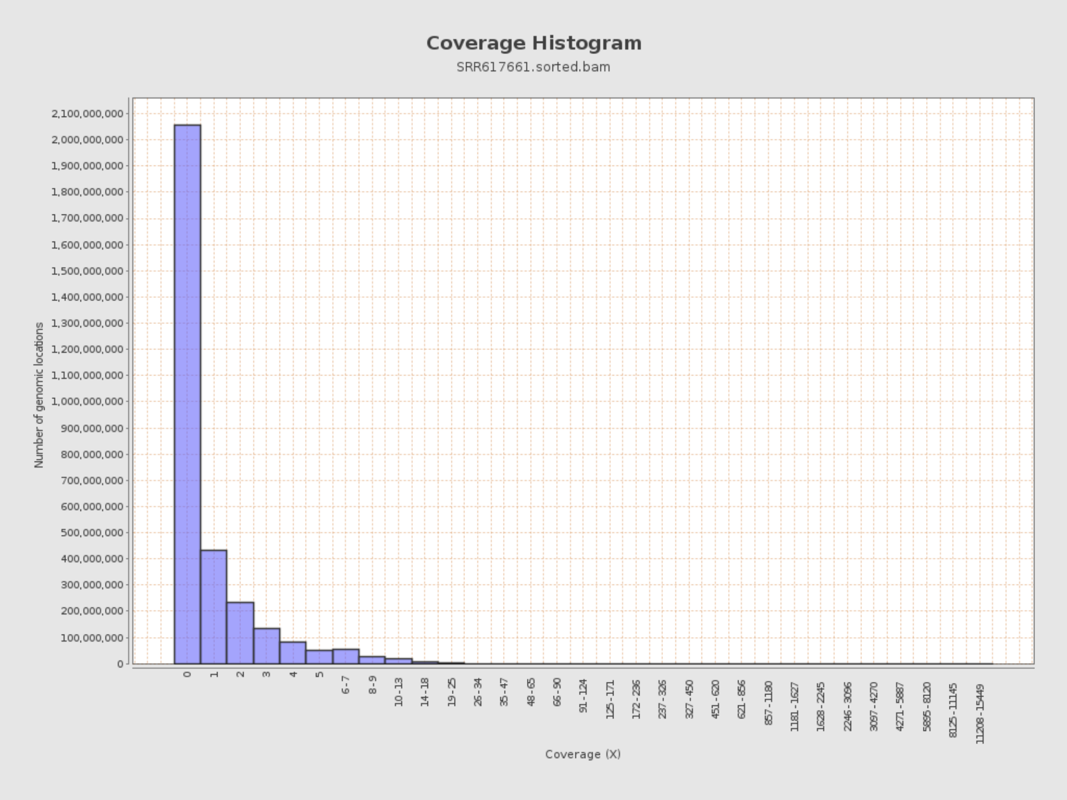
		bases	coverage	deviation
chr1	249250621	183915539	0.7379	10.389
chr2	243199373	309813898	1.2739	12.529
chr3	198022430	250682709	1.2659	2.5137
chr4	191154276	167600793	0.8768	8.8735
chr5	180915260	198192746	1.0955	2.357
chr6	171115067	145096689	0.8479	5.8348
chr7	159138663	234567214	1.474	13.7624
chr8	146364022	133104208	0.9094	4.1755
chr9	141213431	123102356	0.8717	21.2881
chr10	135534747	127066626	0.9375	21.9754
chr11	135006516	165161125	1.2234	12.28
chr12	133851895	127900191	0.9555	2.1784
chr13	115169878	128440746	1.1152	2.3179
chr14	107349540	85695699	0.7983	2.488
chr15	102531392	63950058	0.6237	1.5954
chr16	90354753	82963608	0.9182	16.9807
chr17	81195210	74204962	0.9139	13.2004
chr18	78077248	55298664	0.7083	18.7347
chr19	59128983	31845327	0.5386	6.225
chr20	63025520	81057055	1.2861	3.1083
chr21	48129895	43678884	0.9075	4.5672
chr22	51304566	19354815	0.3773	1.2913
chrMT	16571	3195723	192.8503	137.8623
chrX	155270560	149002496	0.9596	4.4432

chrY	59373566	12139023	0.2045	18.049

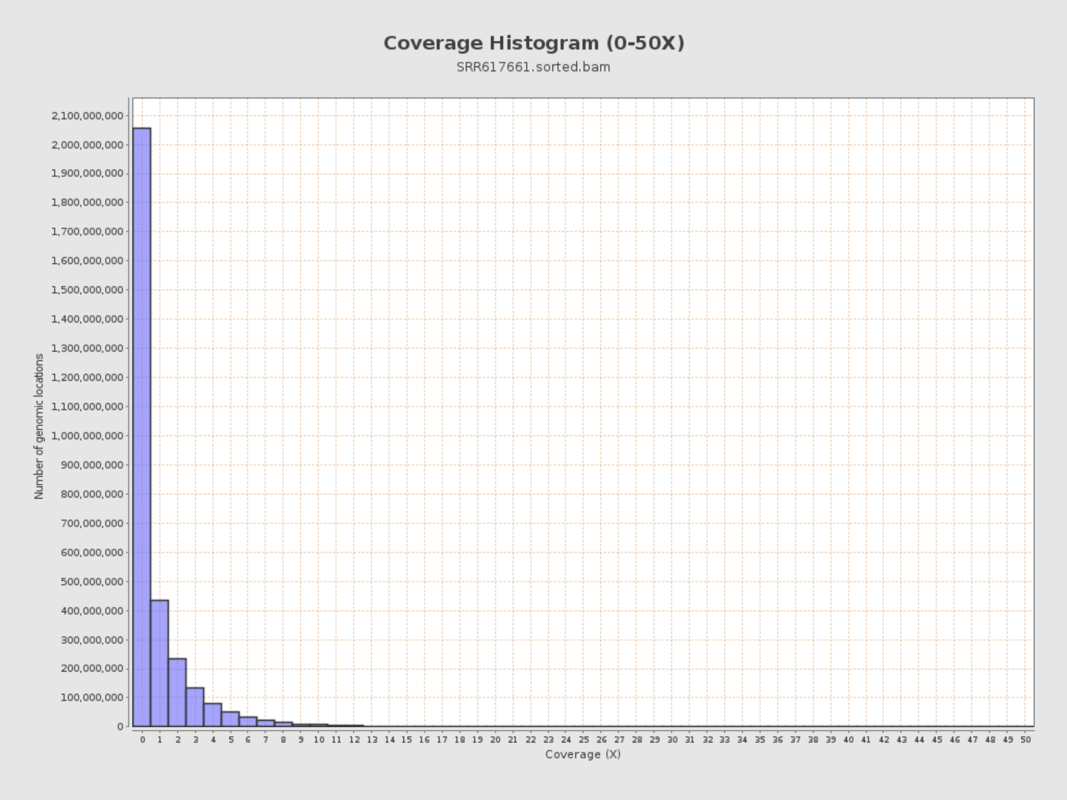
3. Results : Coverage across reference



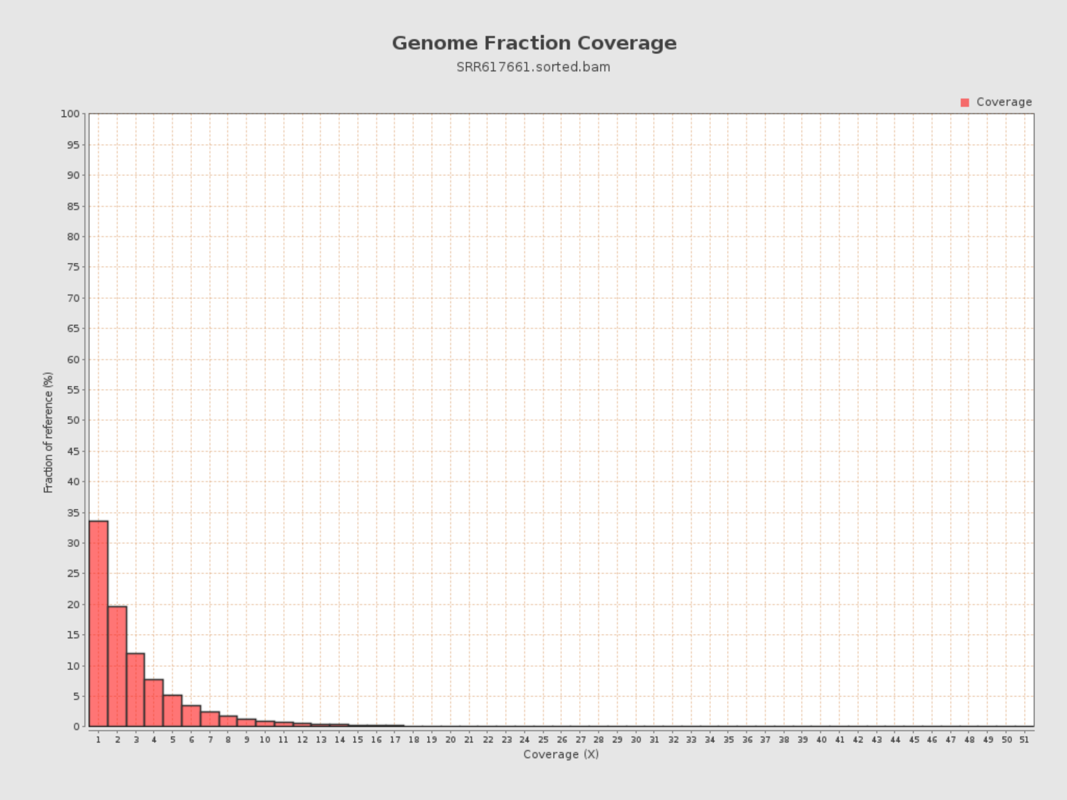
4. Results : Coverage Histogram



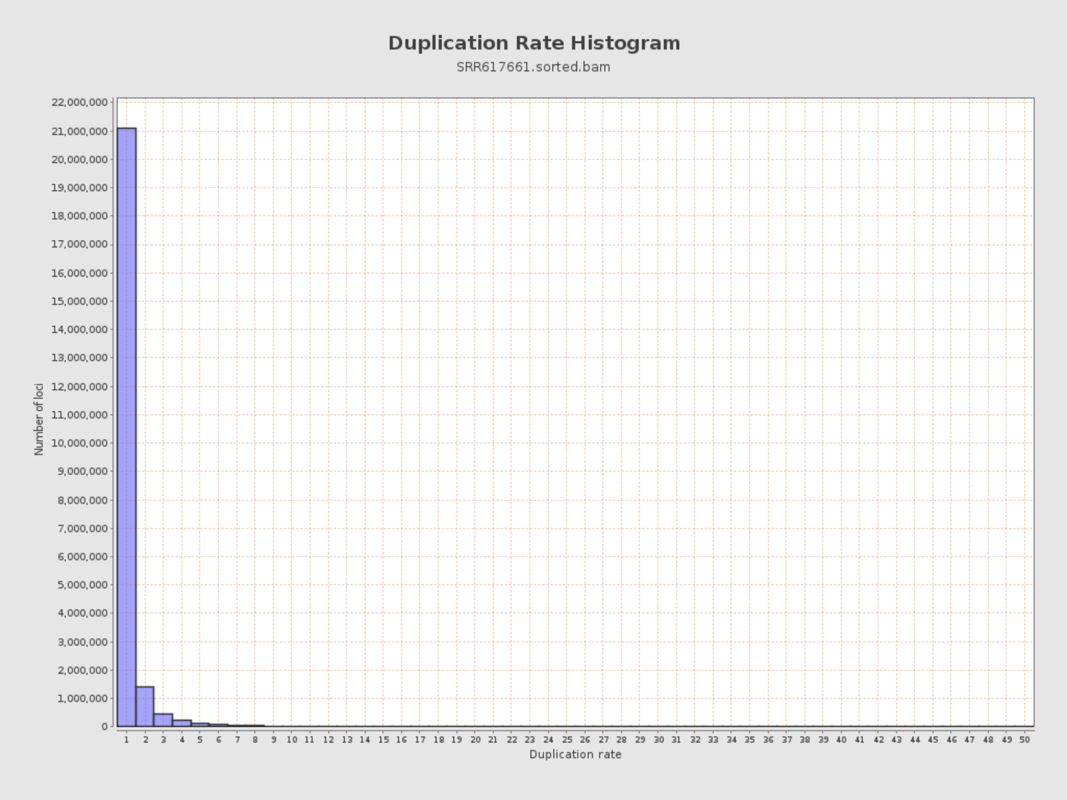
5. Results : Coverage Histogram (0-50X)



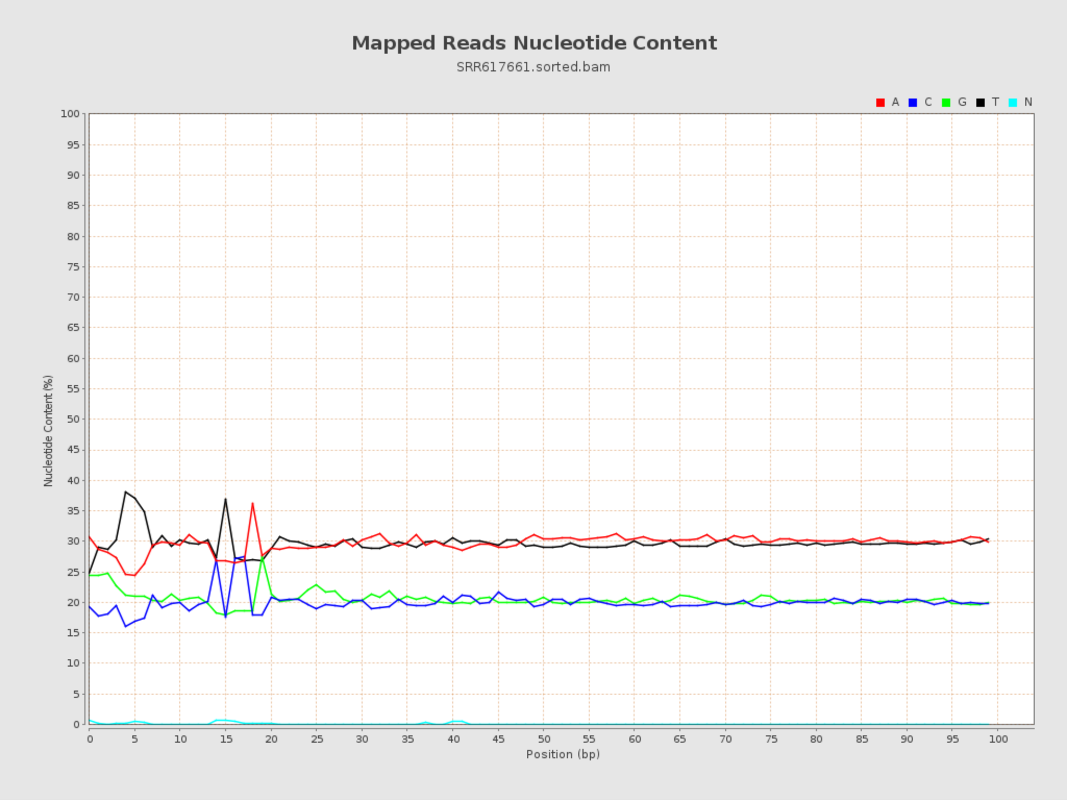
6. Results : Genome Fraction Coverage



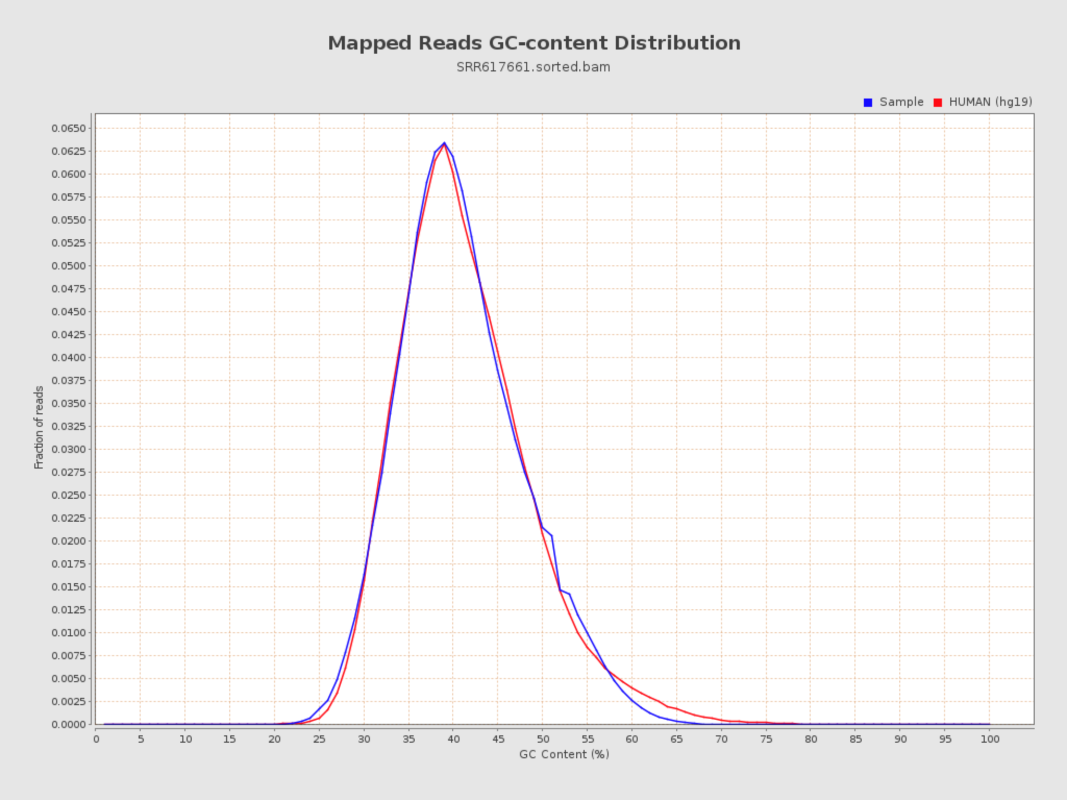
7. Results : Duplication Rate Histogram



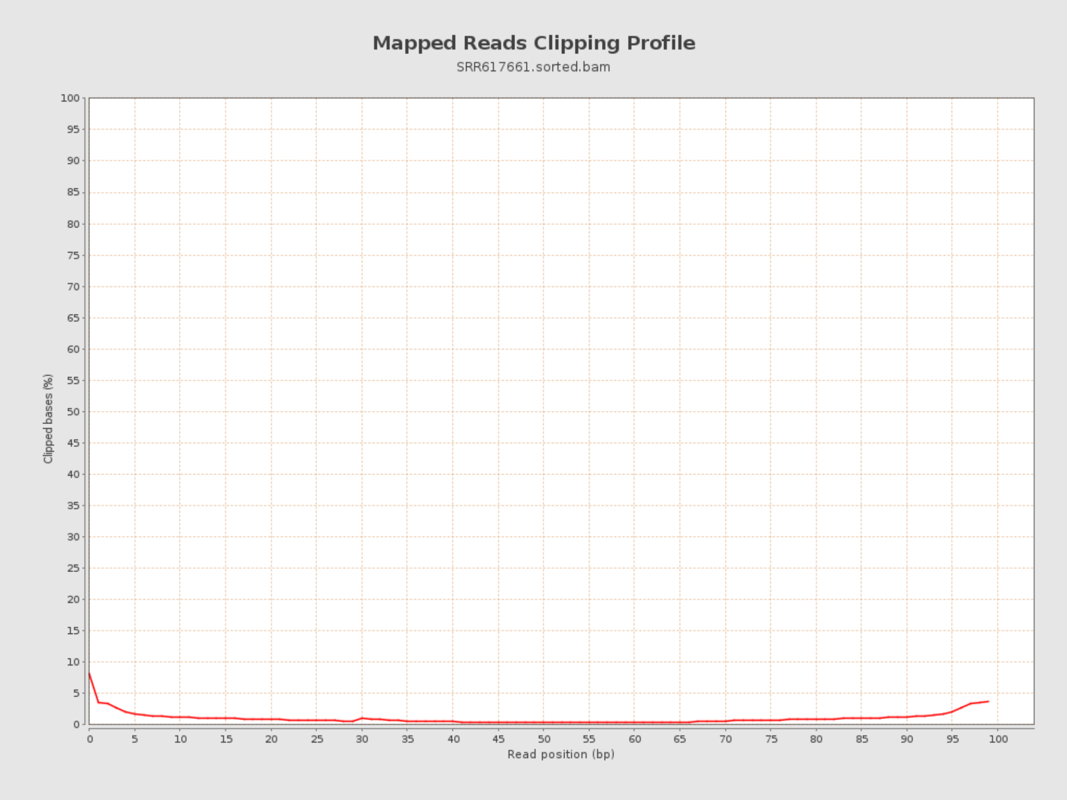
8. Results : Mapped Reads Nucleotide Content



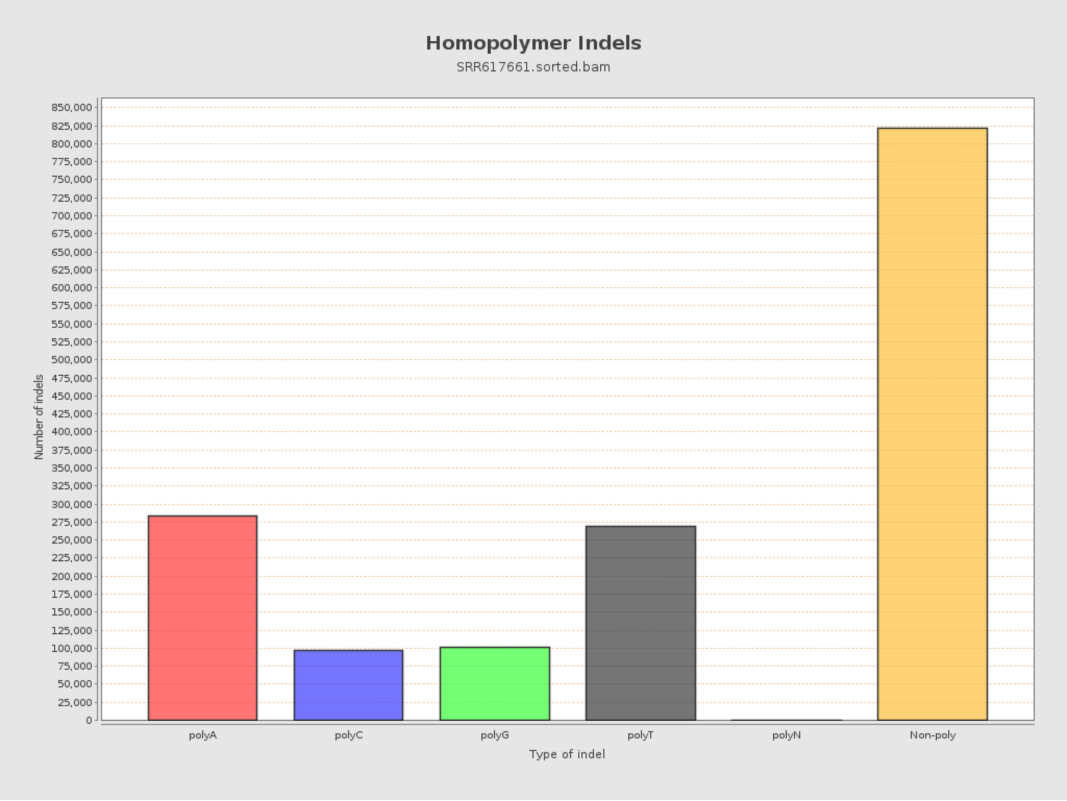
9. Results : Mapped Reads GC-content Distribution



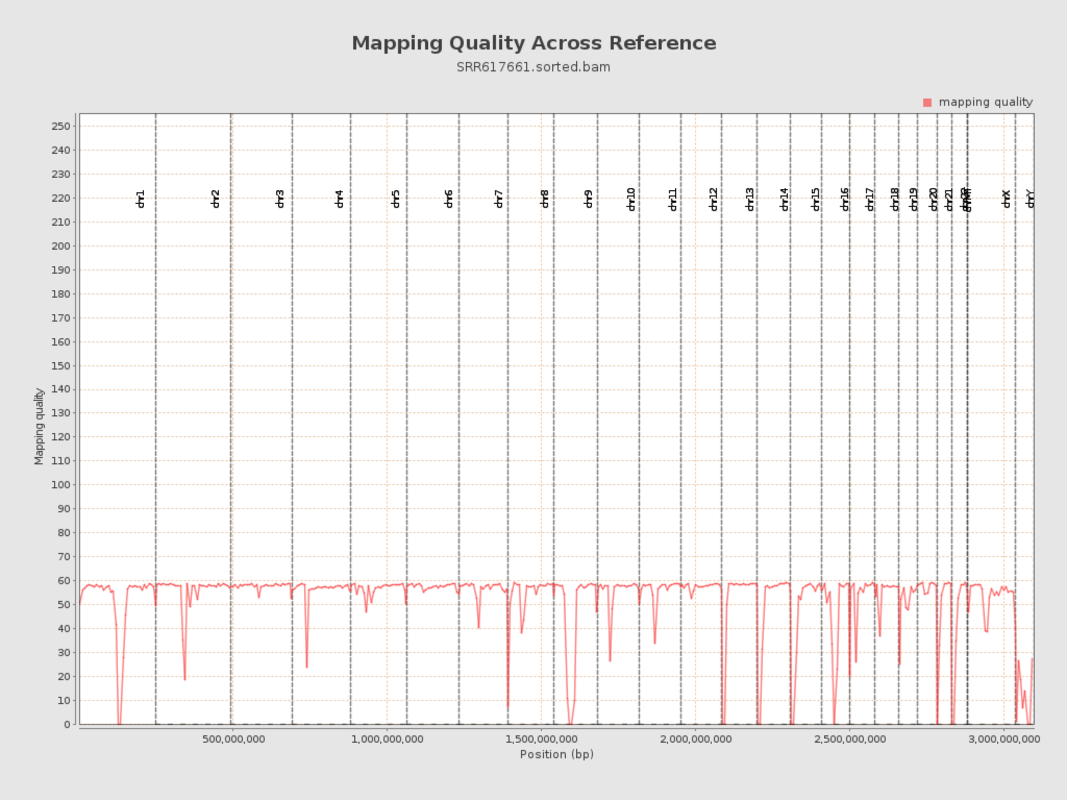
10. Results : Mapped Reads Clipping Profile



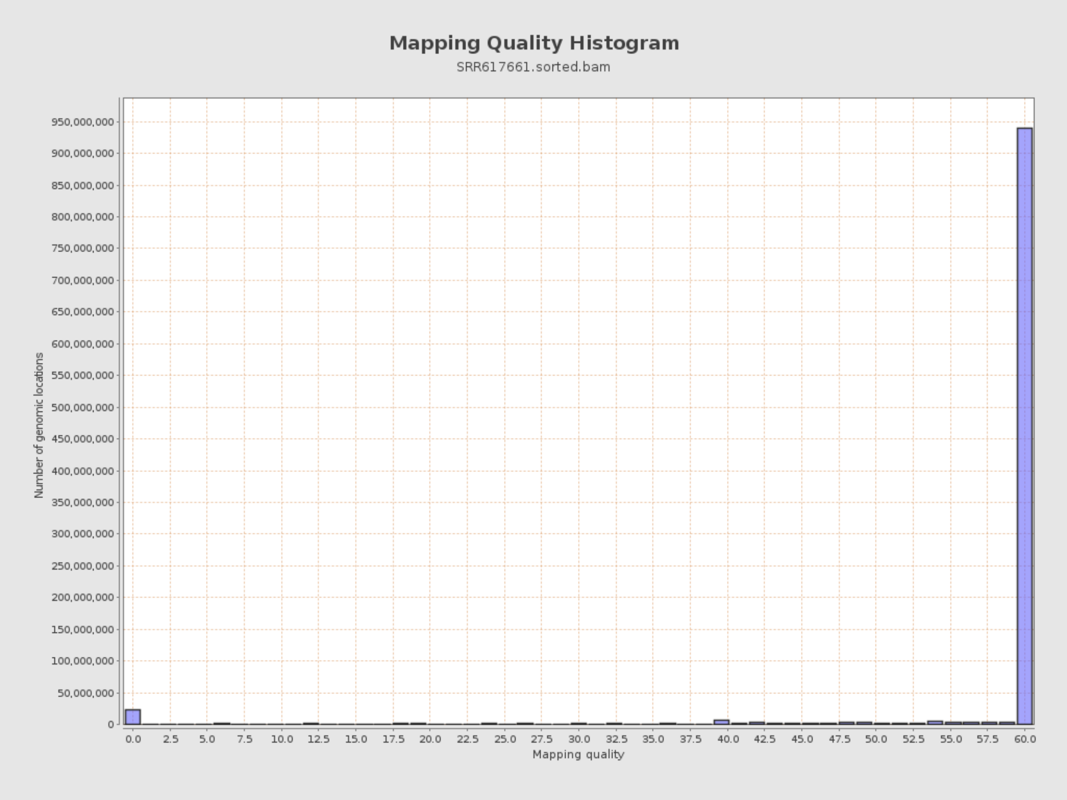
11. Results : Homopolymer Indels



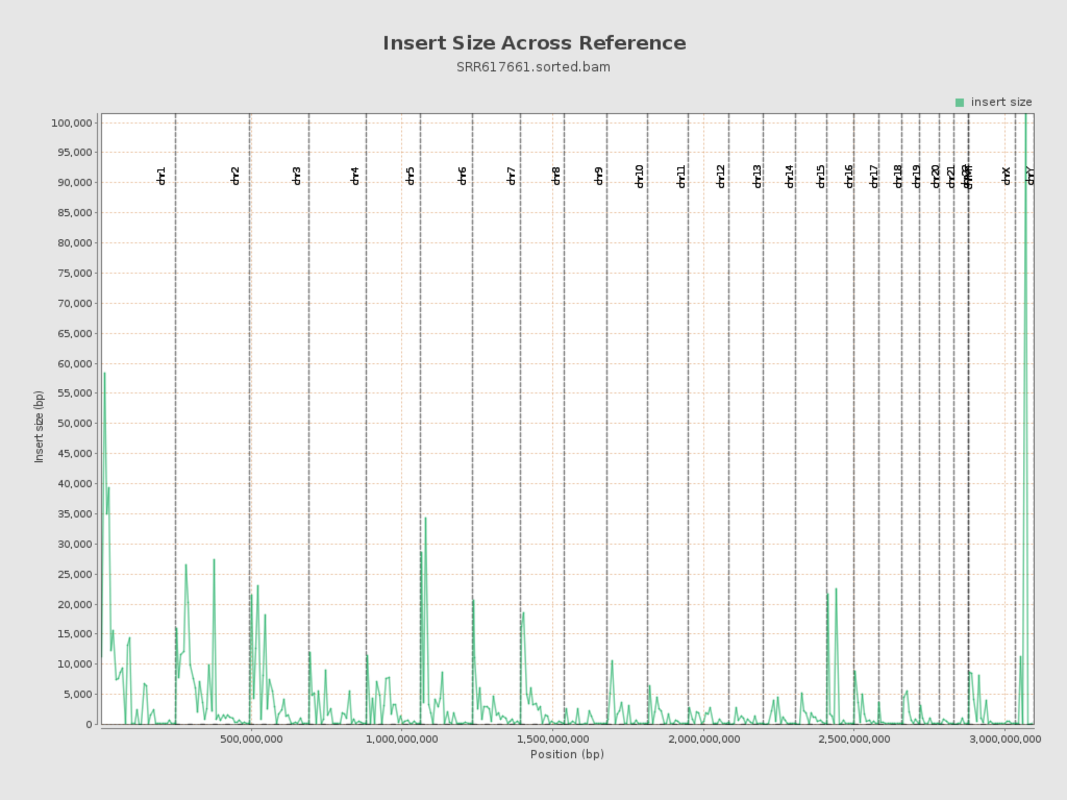
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram