Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 07:57:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617363.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_SRR617363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617363_1.fastq.gz SRR617363_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 07:57:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,315,296 / 94.74%
Unmapped reads	1,684,704 / 5.26%
Mapped paired reads	30,315,296 / 94.74%
Mapped reads, first in pair	15,226,299 / 47.58%
Mapped reads, second in pair	15,088,997 / 47.15%
Mapped reads, both in pair	29,779,640 / 93.06%
Mapped reads, singletons	535,656 / 1.67%
Secondary alignments	0
Supplementary alignments	66,855 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,572,369 / 4.91%
Duplication rate	1.5%
Clipped reads	2,497,757 / 7.81%

2.2. ACGT Content

Number/percentage of A's	899,497,604 / 30.24%
Number/percentage of C's	591,425,160 / 19.88%
Number/percentage of T's	887,363,449 / 29.83%
Number/percentage of G's	594,279,825 / 19.98%
Number/percentage of N's	2,174,959 / 0.07%

GC Percentage	39.86%

2.3. Coverage

Mean	0.9612
Standard Deviation	9.8008

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	52,668.4
Standard Deviation	2,189,544.52
P25/Median/P75	171 / 212 / 275

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	33,161,333
Insertions	299,335
Mapped reads with at least one insertion	0.96%
Deletions	365,470
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.29%

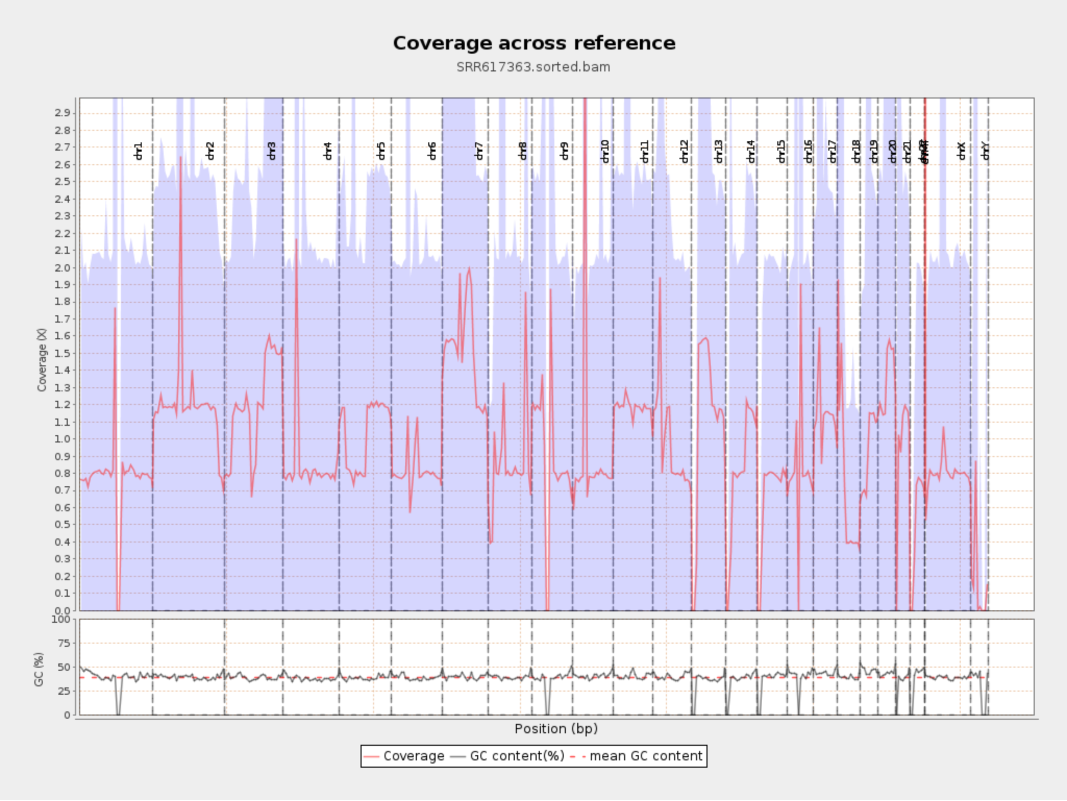
2.7. Chromosome stats

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

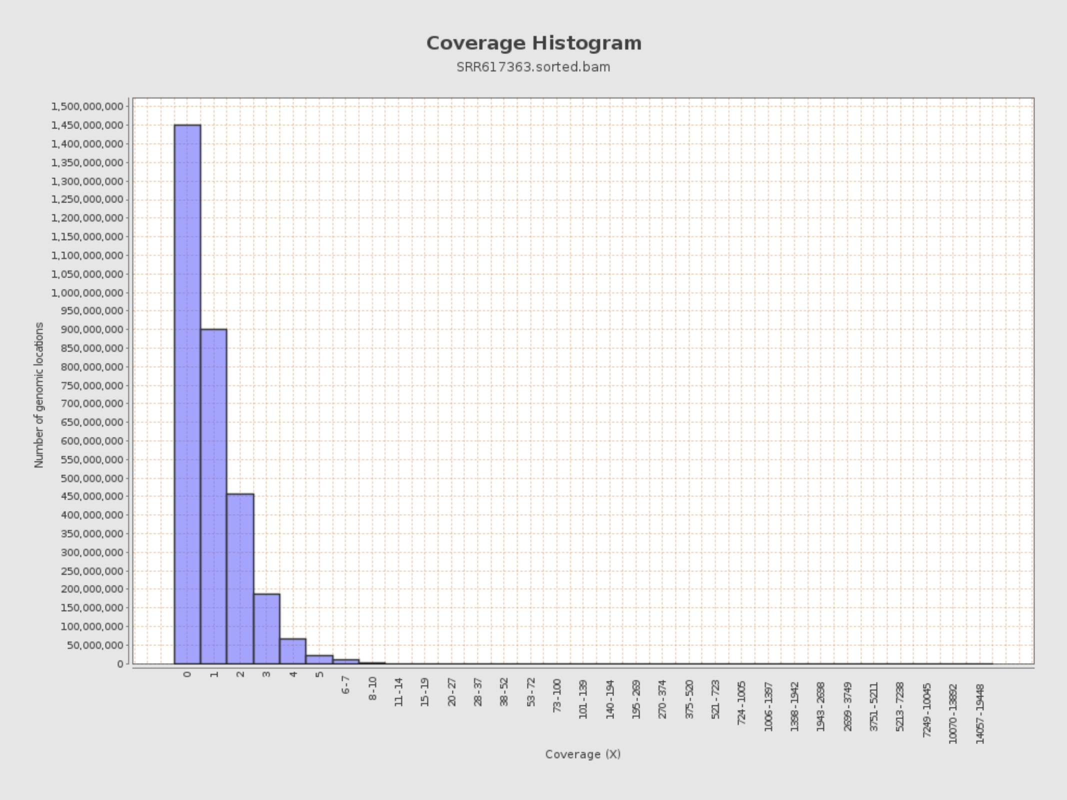
		bases	coverage	deviation
chr1	249250621	193511757	0.7764	20.0308
chr2	243199373	293335480	1.2062	8.8311
chr3	198022430	236536152	1.1945	1.452
chr4	191154276	162697551	0.8511	9.4788
chr5	180915260	186882302	1.033	1.4608
chr6	171115067	139874485	0.8174	3.6863
chr7	159138663	241414850	1.517	10.8645
chr8	146364022	125273475	0.8559	7.4747
chr9	141213431	125275476	0.8871	14.7713
chr10	135534747	125307117	0.9245	20.1524
chr11	135006516	159848421	1.184	5.5838
chr12	133851895	131413036	0.9818	1.3566
chr13	115169878	129638818	1.1256	1.2933
chr14	107349540	86080505	0.8019	1.3735
chr15	102531392	66886882	0.6524	0.9778
chr16	90354753	74698636	0.8267	7.9217
chr17	81195210	92596124	1.1404	7.0595
chr18	78077248	53809213	0.6892	15.3263
chr19	59128983	55272706	0.9348	9.5145
chr20	63025520	85380383	1.3547	2.4498
chr21	48129895	47350741	0.9838	3.2473
chr22	51304566	26548893	0.5175	0.9209
chrMT	16571	2052538	123.8633	20.1005
chrX	155270560	123770007	0.7971	3.0437

chrY	59373566	10164725	0.1712	8.3082

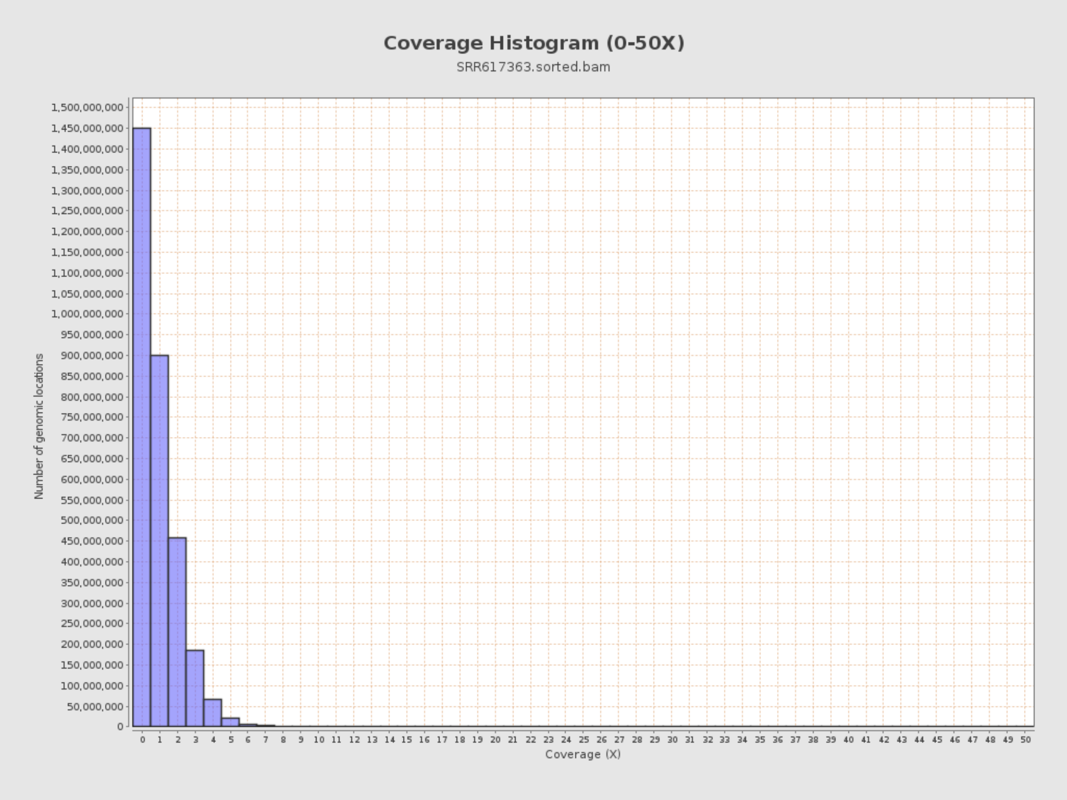
3. Results : Coverage across reference



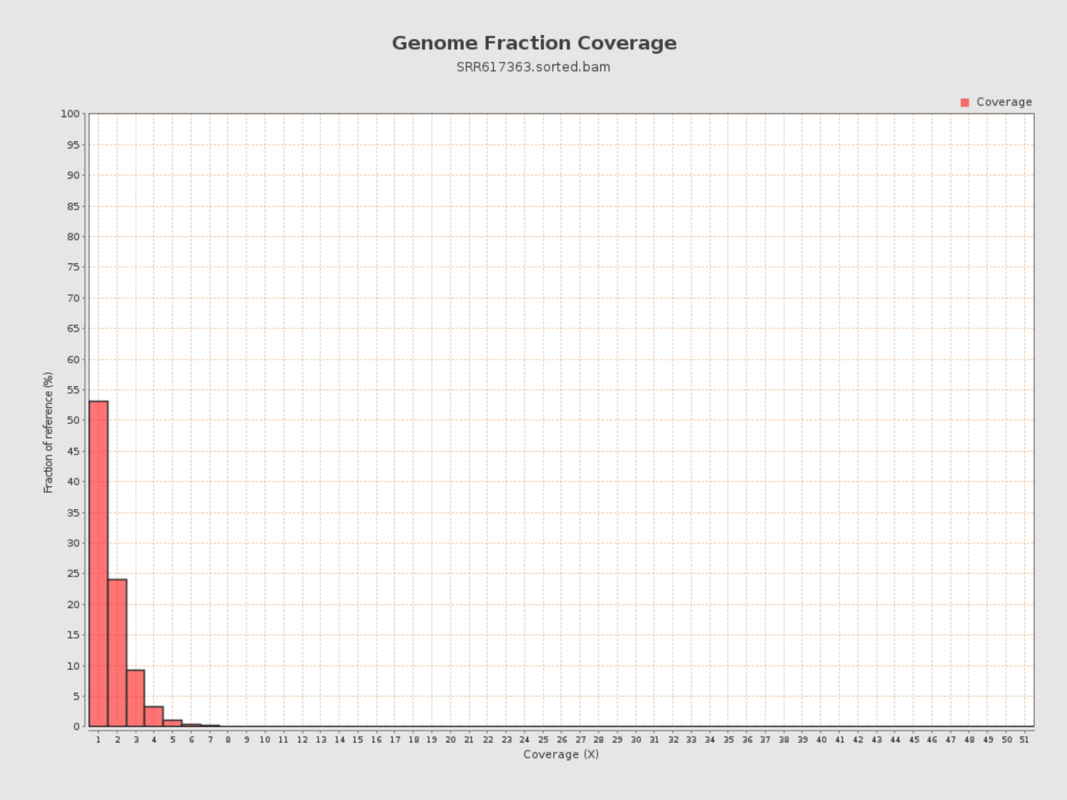
4. Results : Coverage Histogram



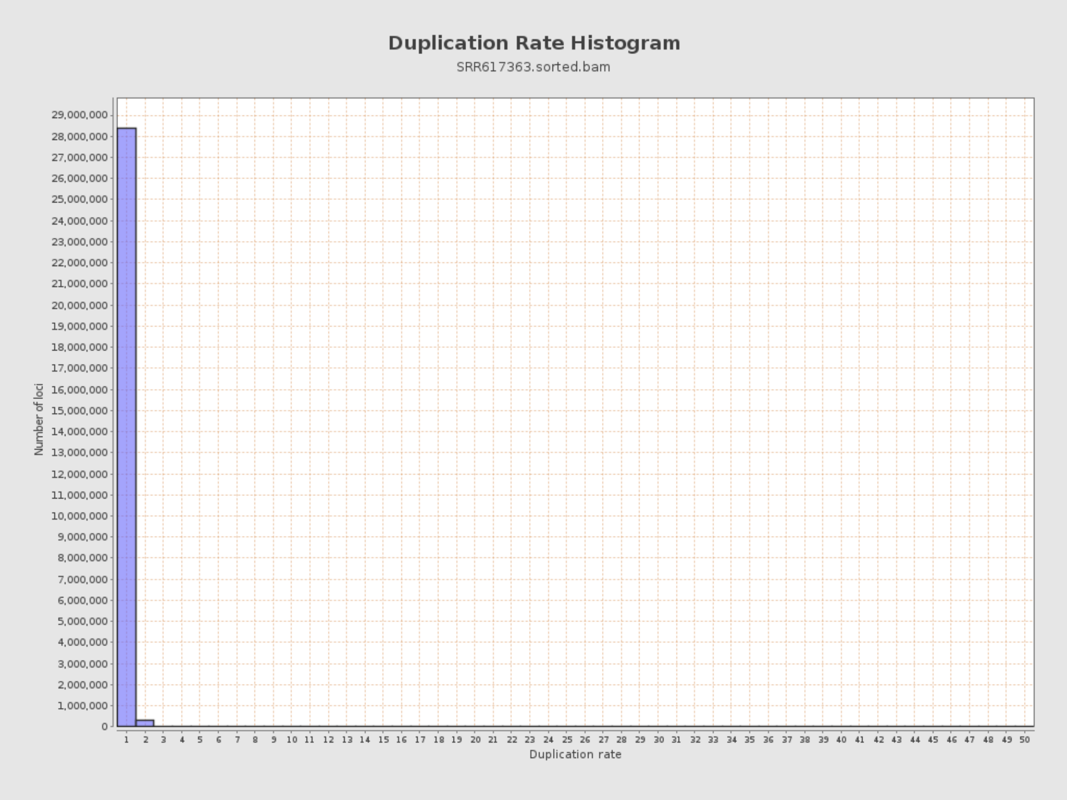
5. Results : Coverage Histogram (0-50X)



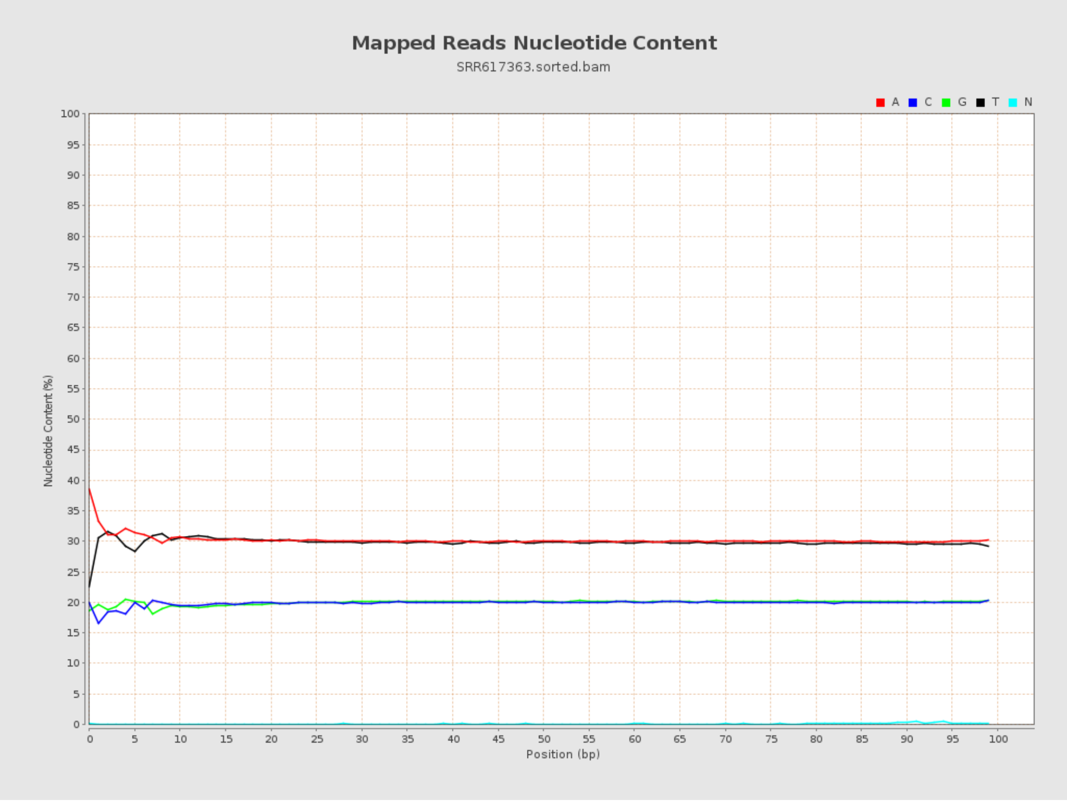
6. Results : Genome Fraction Coverage



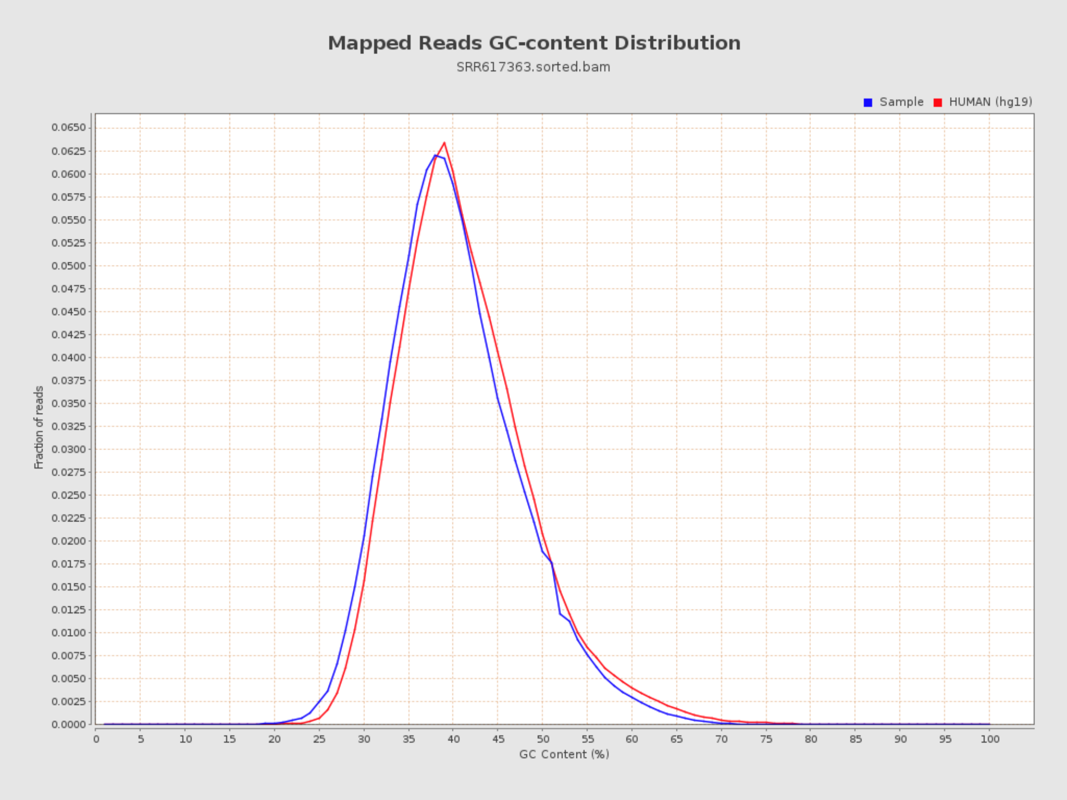
7. Results : Duplication Rate Histogram



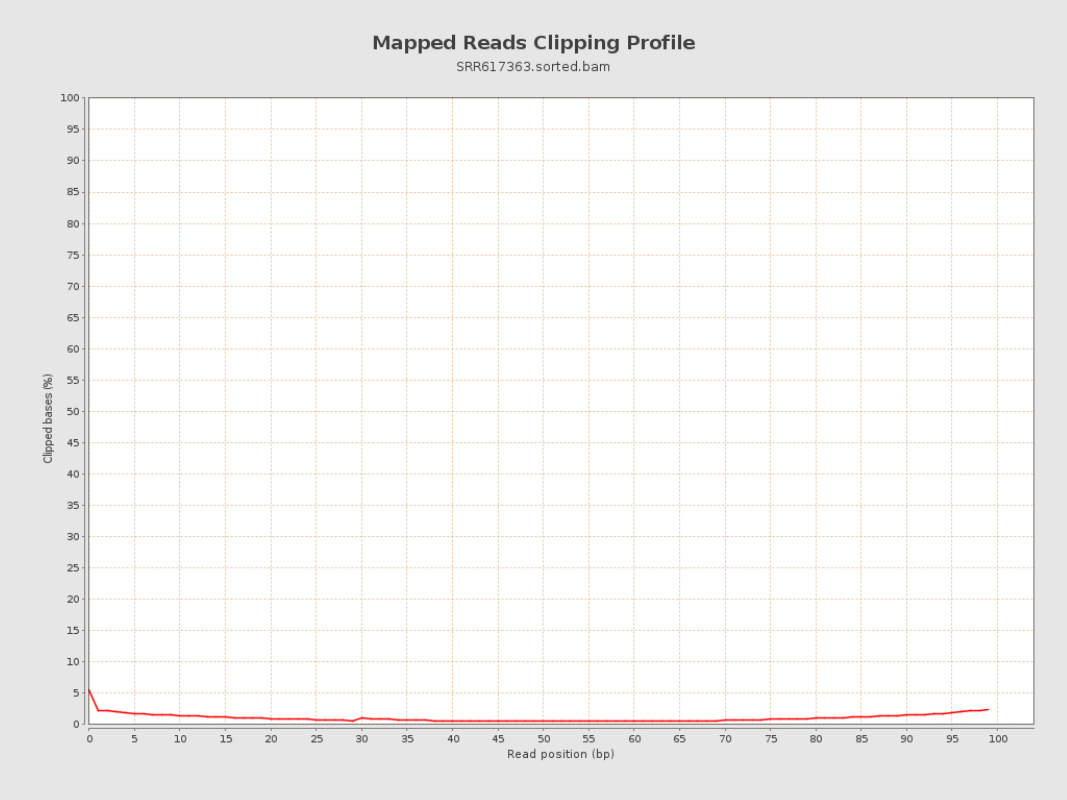
8. Results : Mapped Reads Nucleotide Content



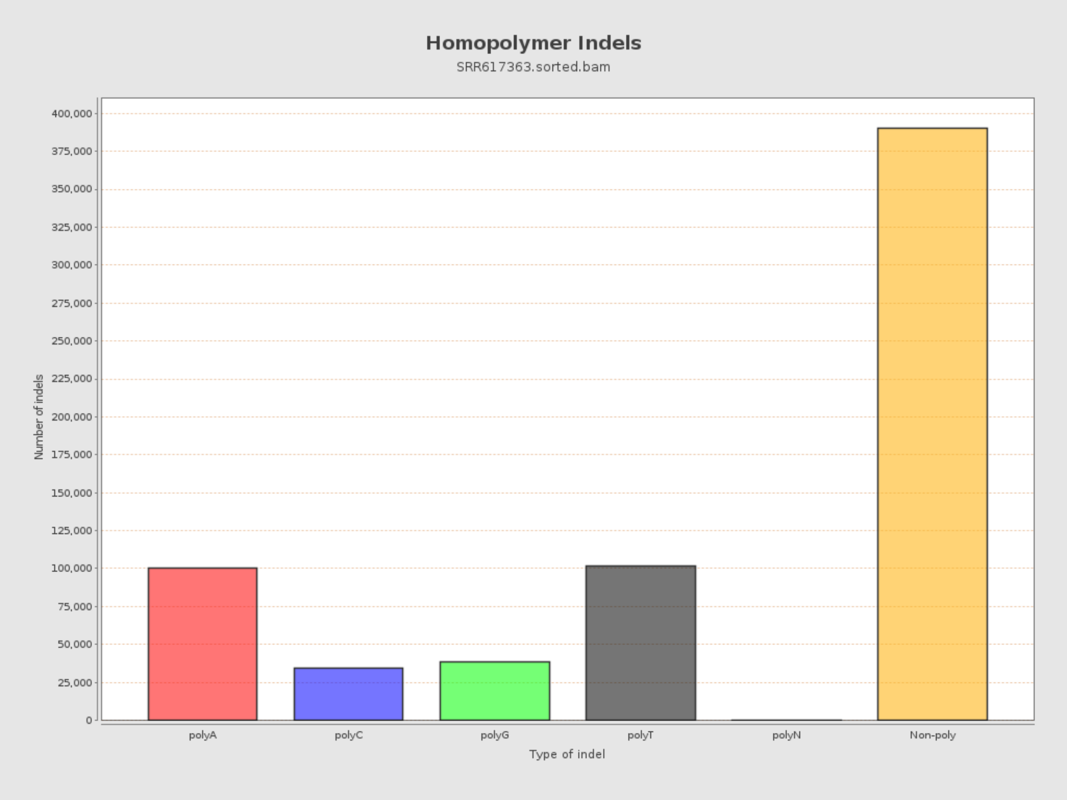
9. Results : Mapped Reads GC-content Distribution



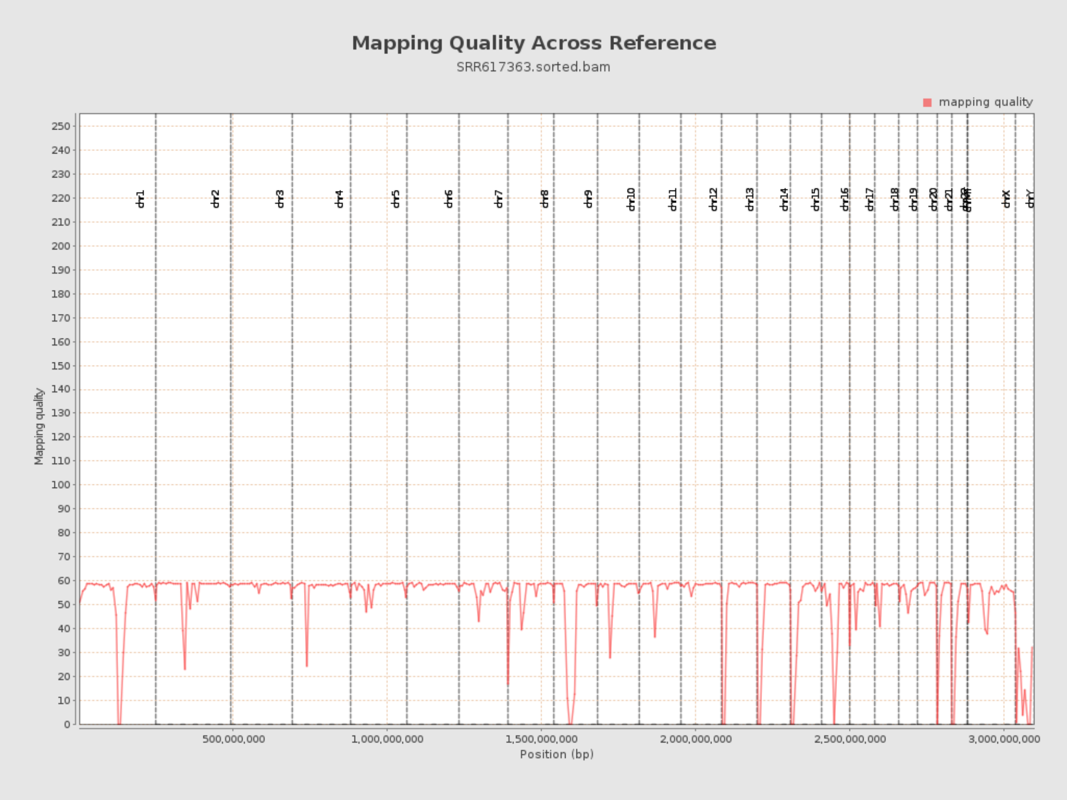
10. Results : Mapped Reads Clipping Profile



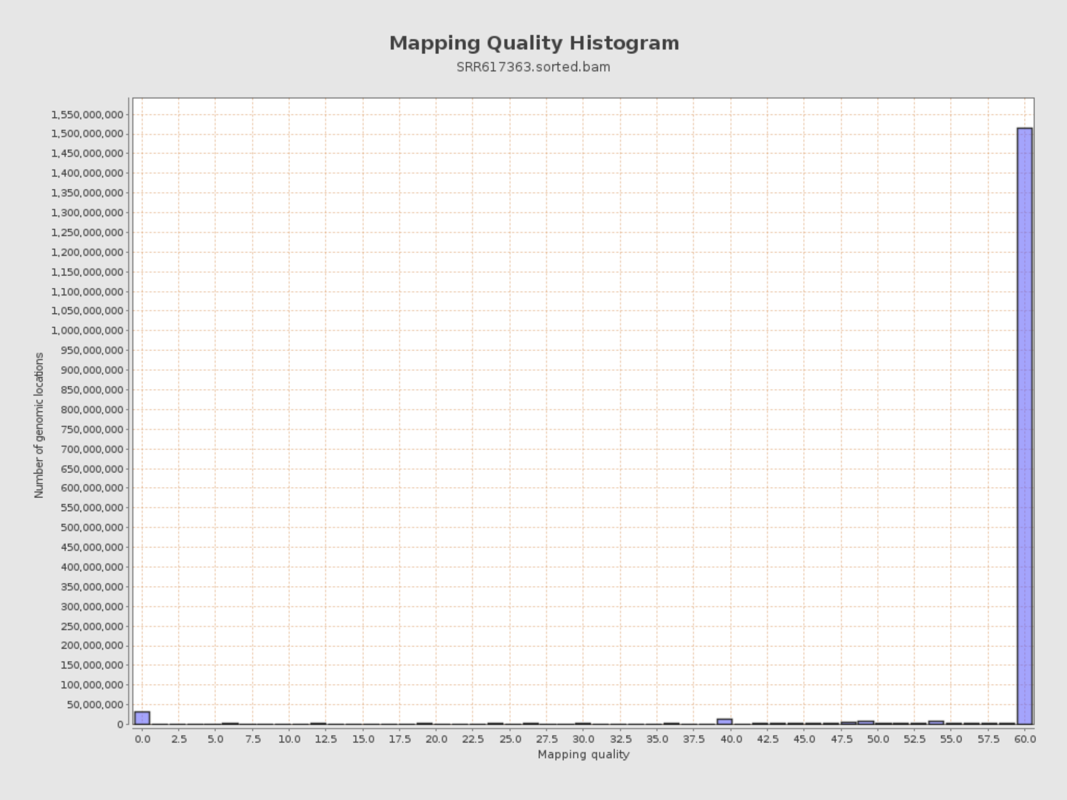
11. Results : Homopolymer Indels



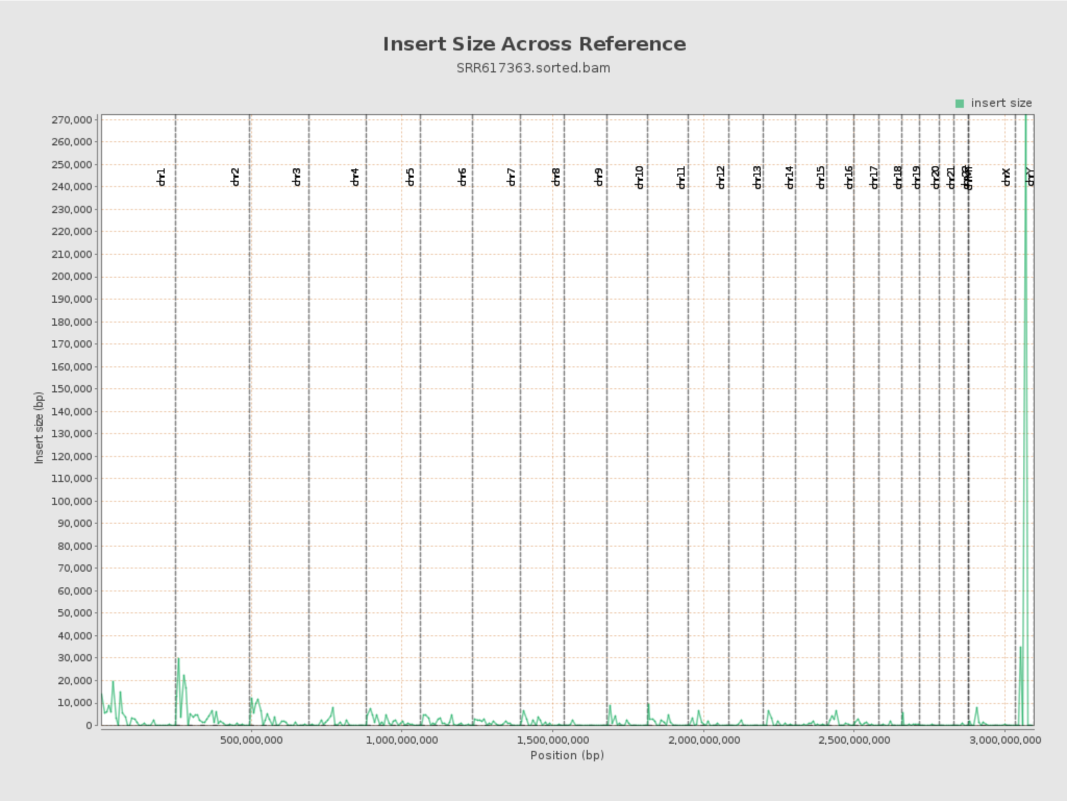
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram