Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 20:35:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617653.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_SRR617653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617653_1.fastq.gz SRR617653_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 20:35:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,226,293 / 94.46%
Unmapped reads	1,773,707 / 5.54%
Mapped paired reads	30,226,293 / 94.46%
Mapped reads, first in pair	15,230,238 / 47.59%
Mapped reads, second in pair	14,996,055 / 46.86%
Mapped reads, both in pair	29,580,764 / 92.44%
Mapped reads, singletons	645,529 / 2.02%
Secondary alignments	0
Supplementary alignments	158,842 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,949,475 / 21.72%
Duplication rate	10.79%
Clipped reads	6,597,921 / 20.62%

2.2. ACGT Content

Number/percentage of A's	869,649,148 / 29.73%
Number/percentage of C's	582,120,056 / 19.9%
Number/percentage of T's	869,525,115 / 29.73%
Number/percentage of G's	599,779,761 / 20.51%
Number/percentage of N's	3,686,468 / 0.13%

GC Percentage	40.41%

2.3. Coverage

Mean	0.9454
Standard Deviation	10.4183

2.4. Mapping Quality

Mean Mapping Quality	52.58

2.5. Insert size

Mean	40,885.79
Standard Deviation	1,880,251.27
P25/Median/P75	180 / 225 / 293

2.6. Mismatches and indels

General error rate	1.59%
Mismatches	45,598,898
Insertions	458,255
Mapped reads with at least one insertion	1.49%
Deletions	1,072,346
Mapped reads with at least one deletion	3.47%
Homopolymer indels	47.5%

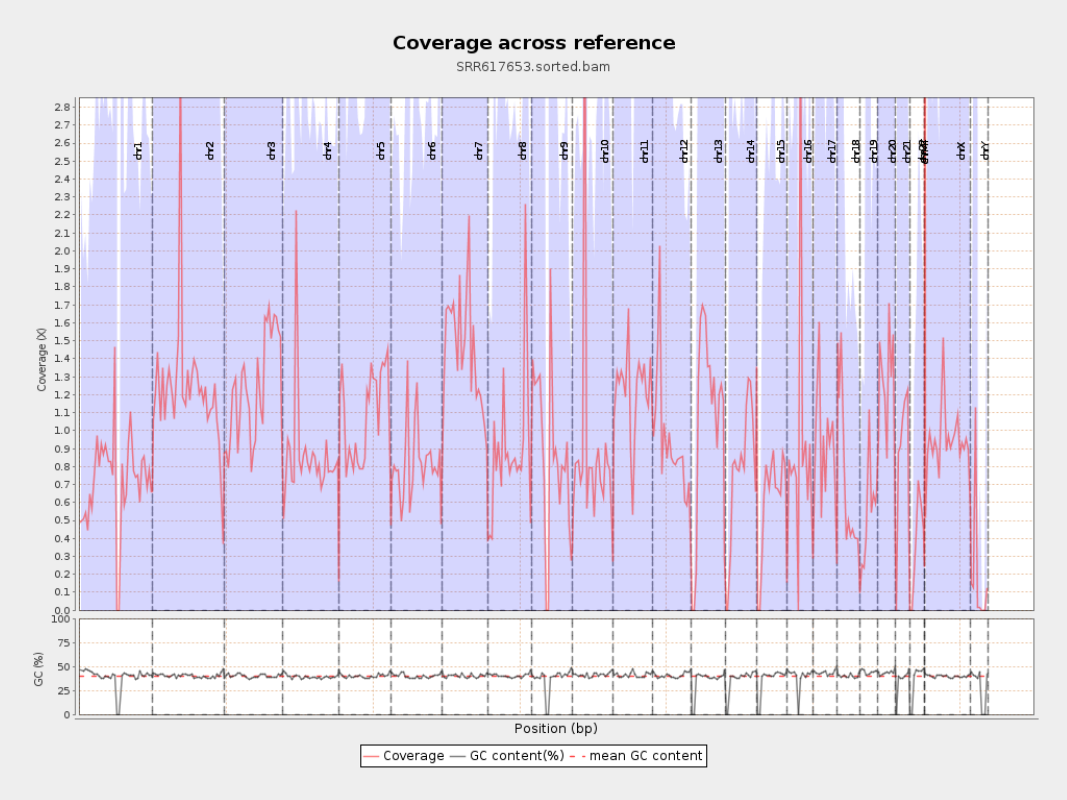
2.7. Chromosome stats

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

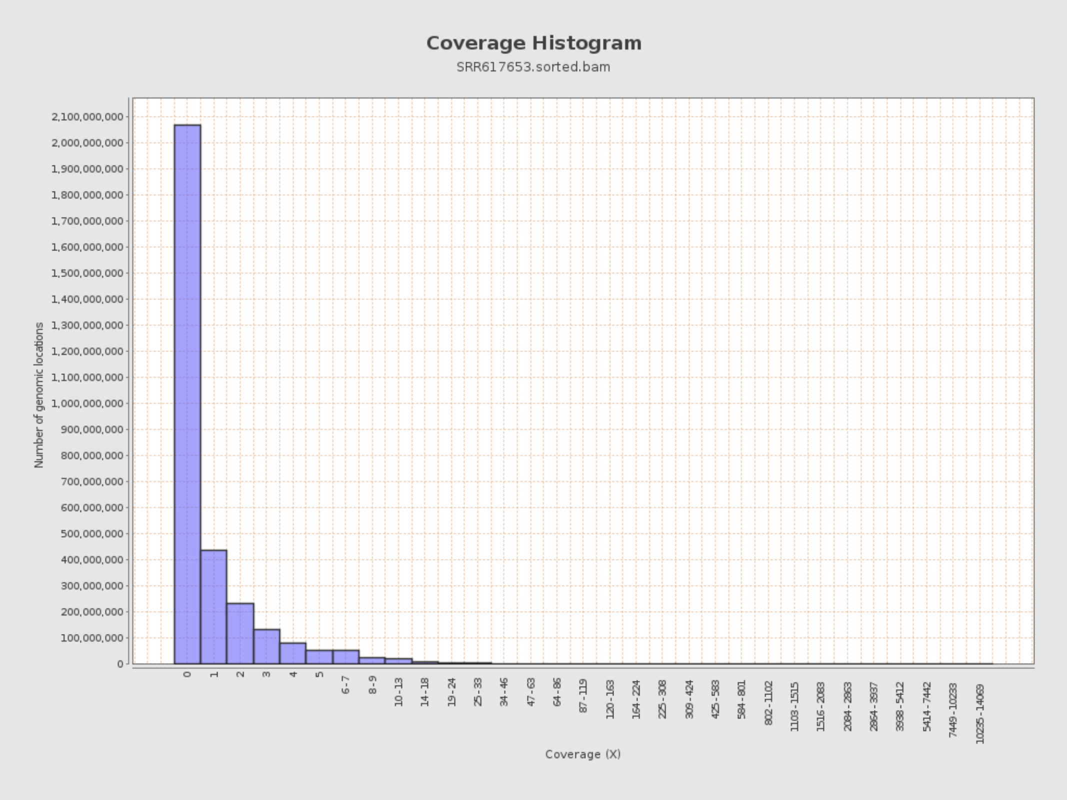
		bases	coverage	deviation
chr1	249250621	179687444	0.7209	10.0902
chr2	243199373	301781066	1.2409	11.9964
chr3	198022430	245437897	1.2394	2.4819
chr4	191154276	163679373	0.8563	8.1647
chr5	180915260	193800697	1.0712	2.3271
chr6	171115067	141962617	0.8296	5.8049
chr7	159138663	228613432	1.4366	13.2919
chr8	146364022	130172155	0.8894	4.0593
chr9	141213431	119619256	0.8471	19.7426
chr10	135534747	124117014	0.9158	21.2168
chr11	135006516	161001800	1.1925	11.786
chr12	133851895	125199148	0.9354	2.1715
chr13	115169878	125725179	1.0916	2.2989
chr14	107349540	83811651	0.7807	2.4548
chr15	102531392	62430490	0.6089	1.6532
chr16	90354753	81258081	0.8993	16.634
chr17	81195210	72141215	0.8885	12.5249
chr18	78077248	53765156	0.6886	17.9944
chr19	59128983	31049950	0.5251	6.0372
chr20	63025520	79130439	1.2555	3.0188
chr21	48129895	42709736	0.8874	4.339
chr22	51304566	18871931	0.3678	1.2681
chrMT	16571	3149678	190.0717	130.9137
chrX	155270560	145794695	0.939	4.3176

chrY	59373566	11624437	0.1958	16.7804

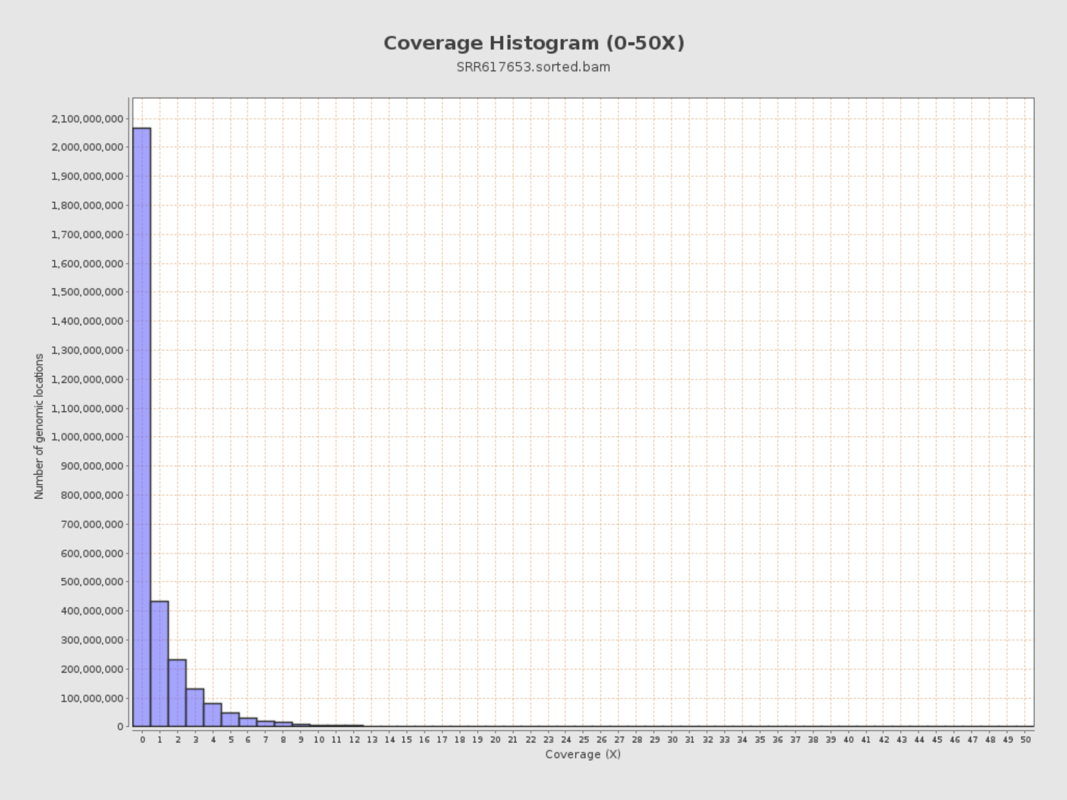
3. Results : Coverage across reference



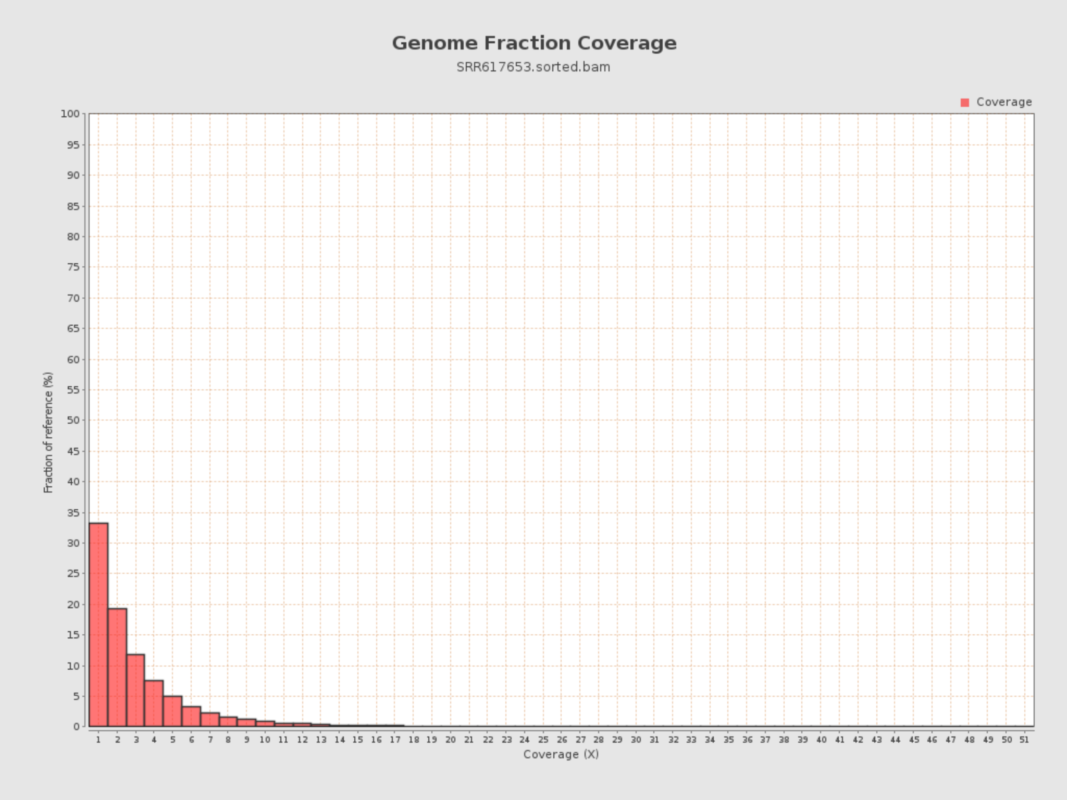
4. Results : Coverage Histogram



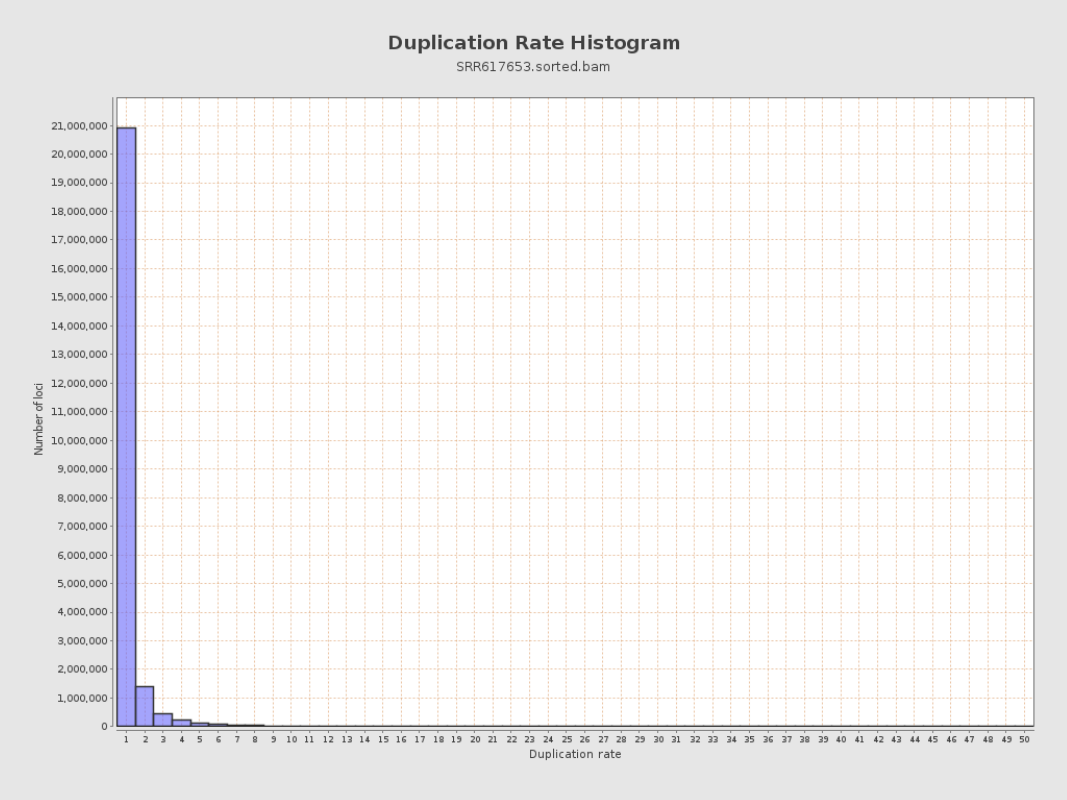
5. Results : Coverage Histogram (0-50X)



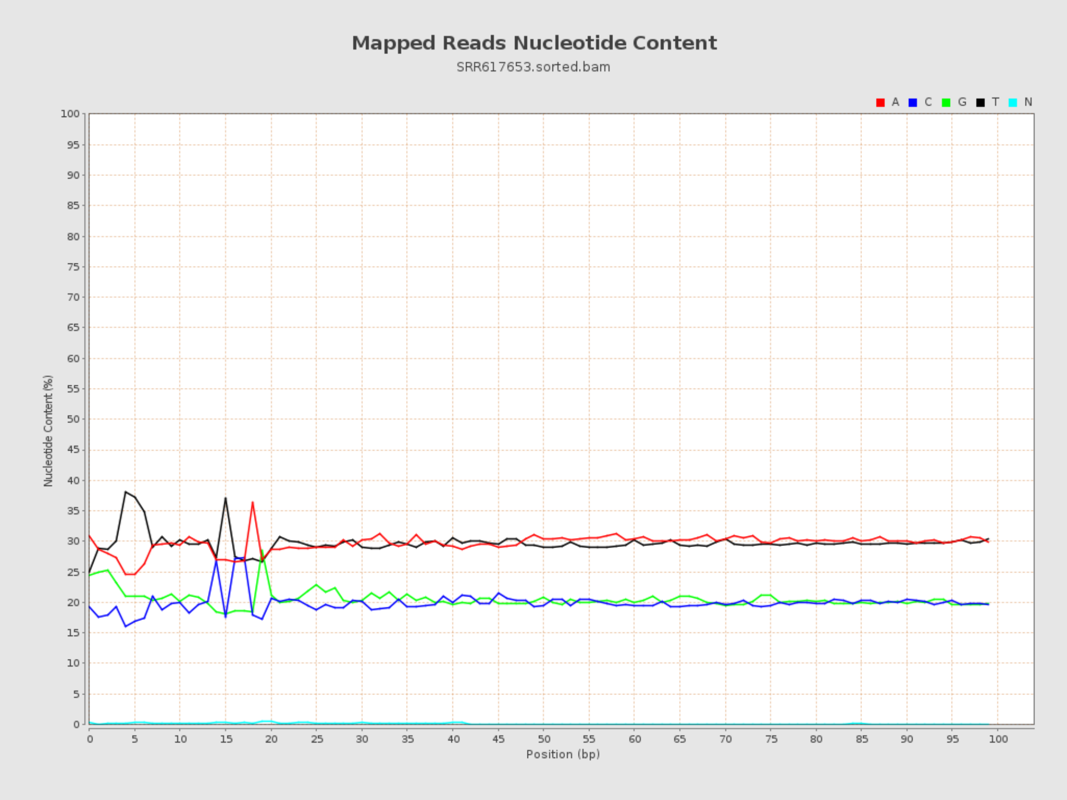
6. Results : Genome Fraction Coverage



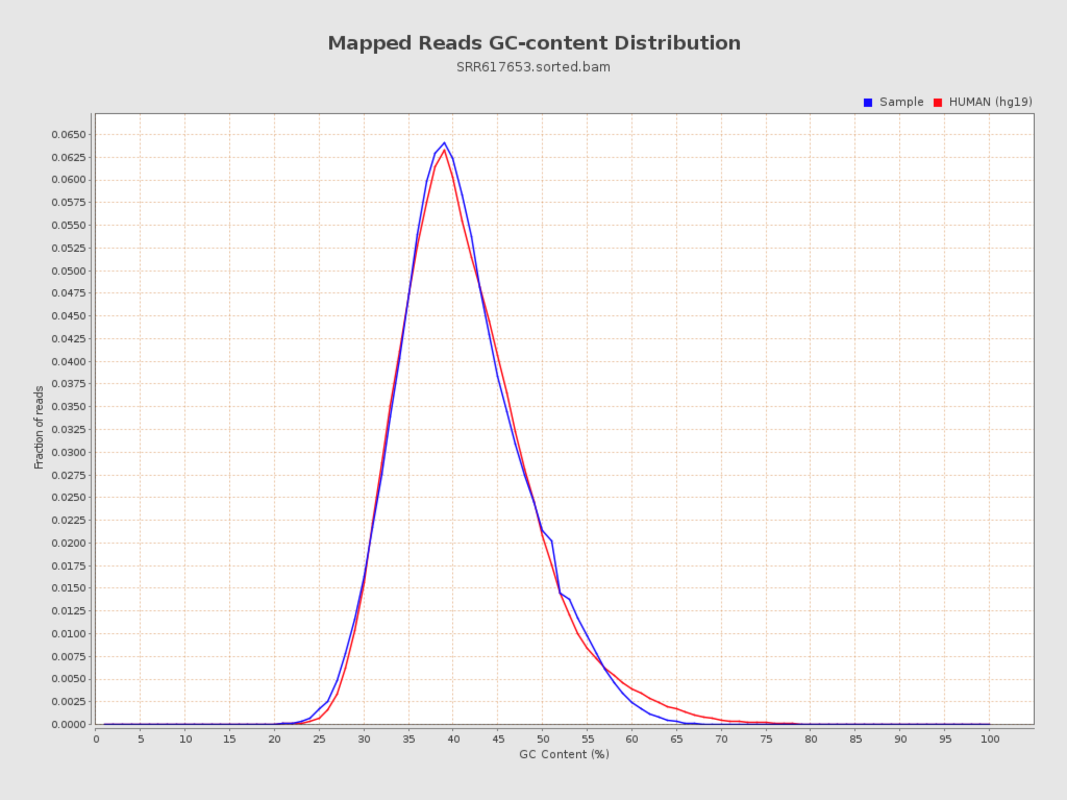
7. Results : Duplication Rate Histogram



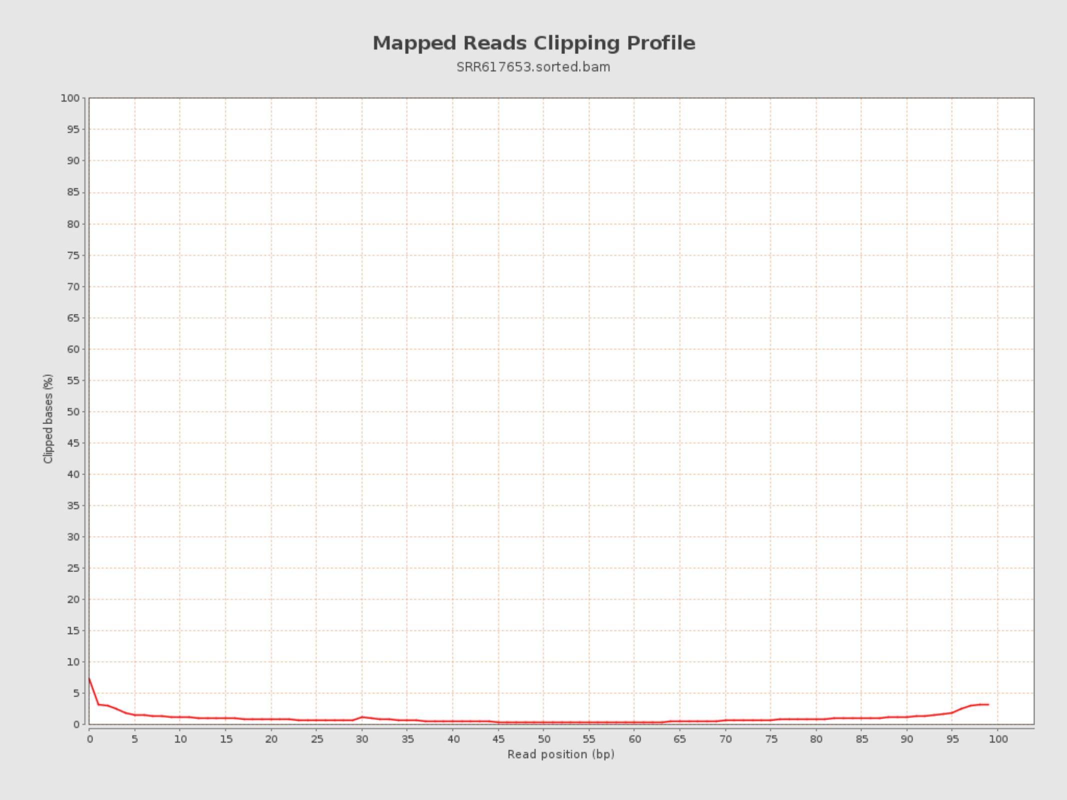
8. Results : Mapped Reads Nucleotide Content



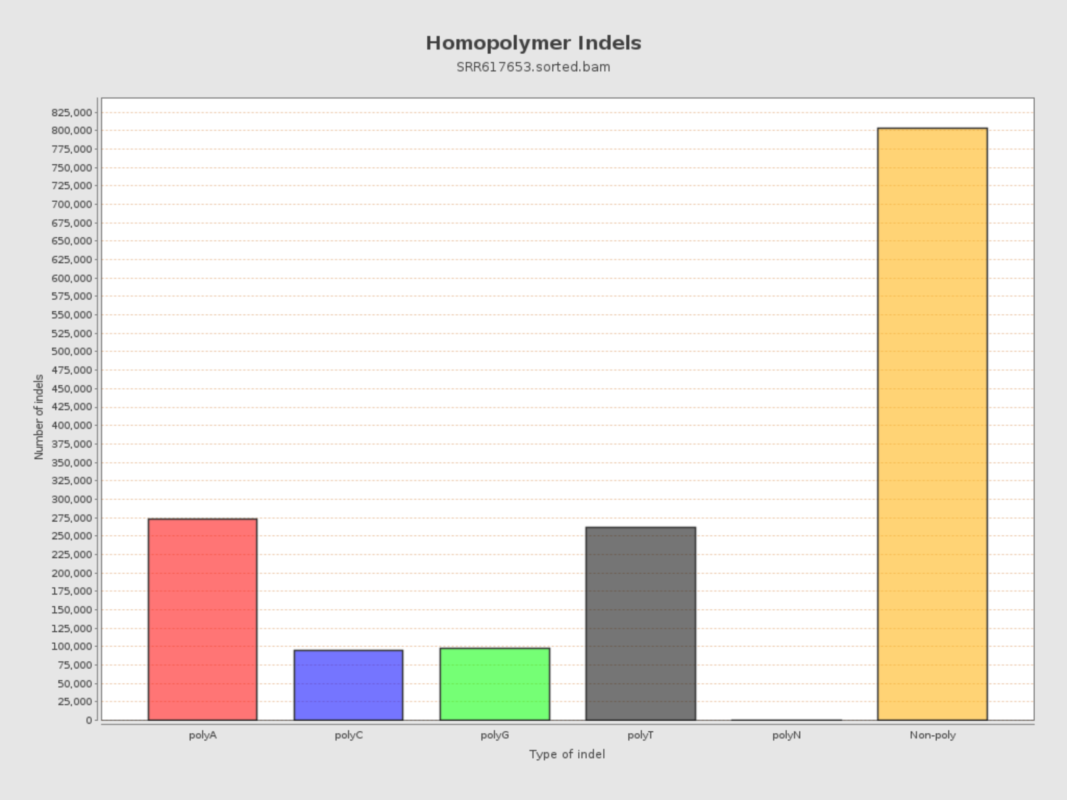
9. Results : Mapped Reads GC-content Distribution



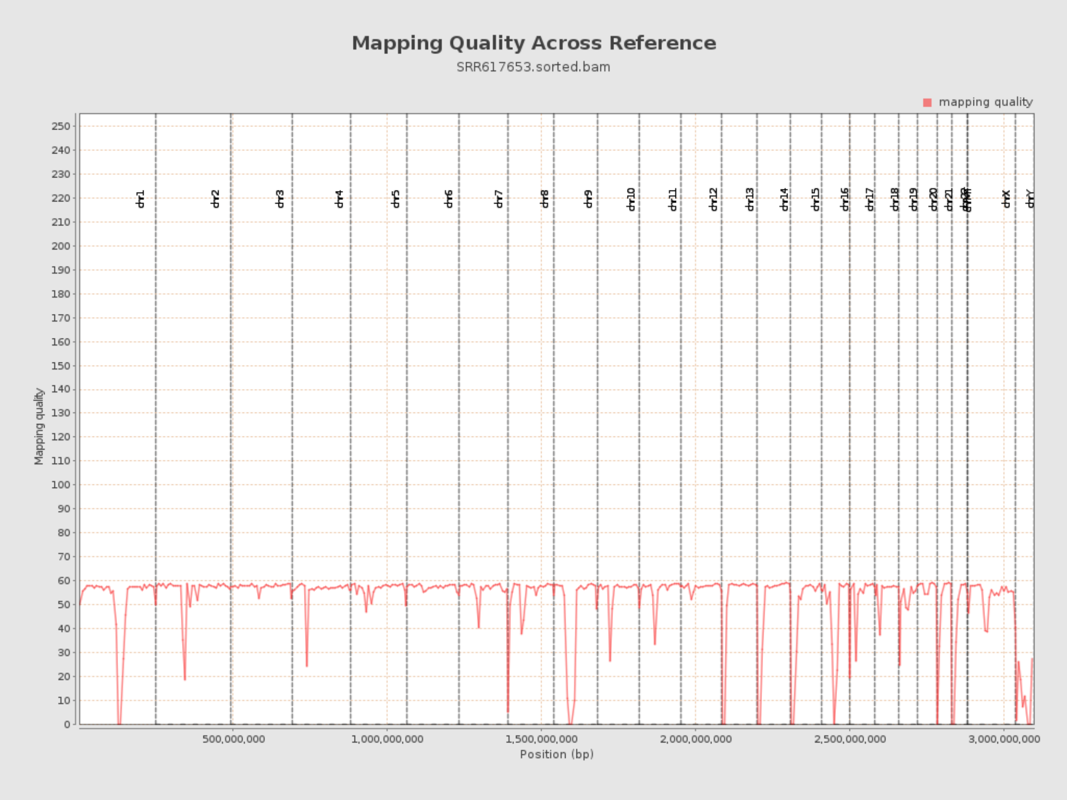
10. Results : Mapped Reads Clipping Profile



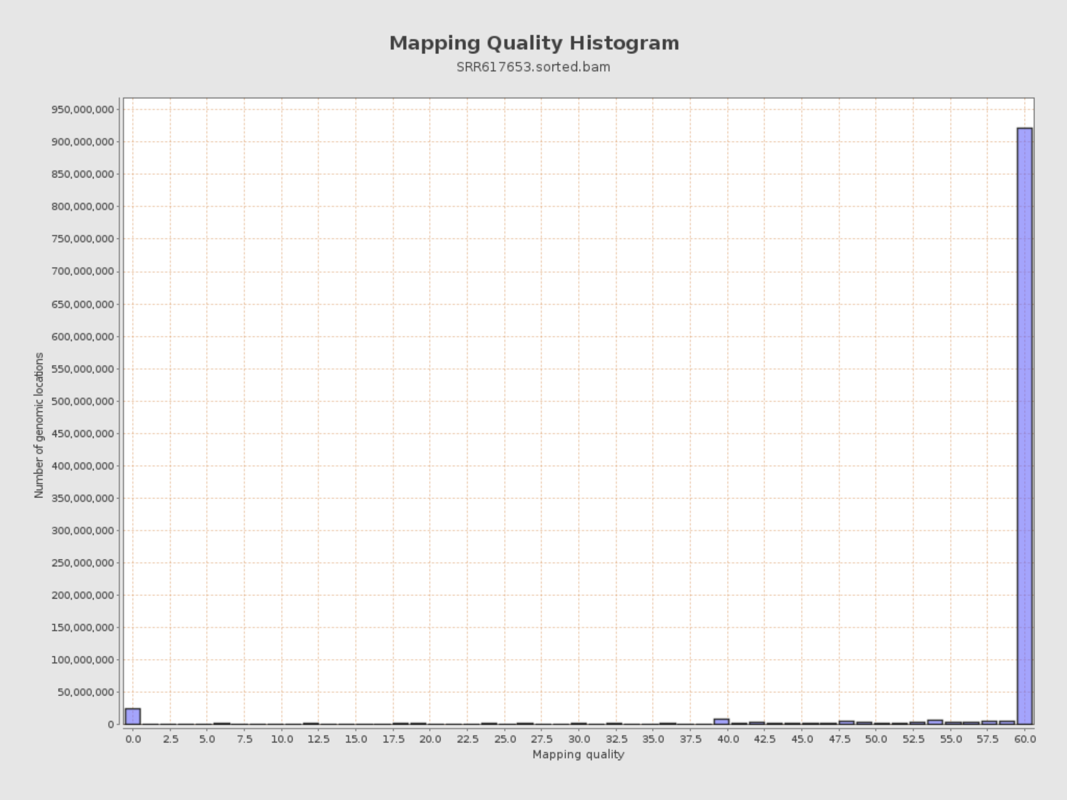
11. Results : Homopolymer Indels



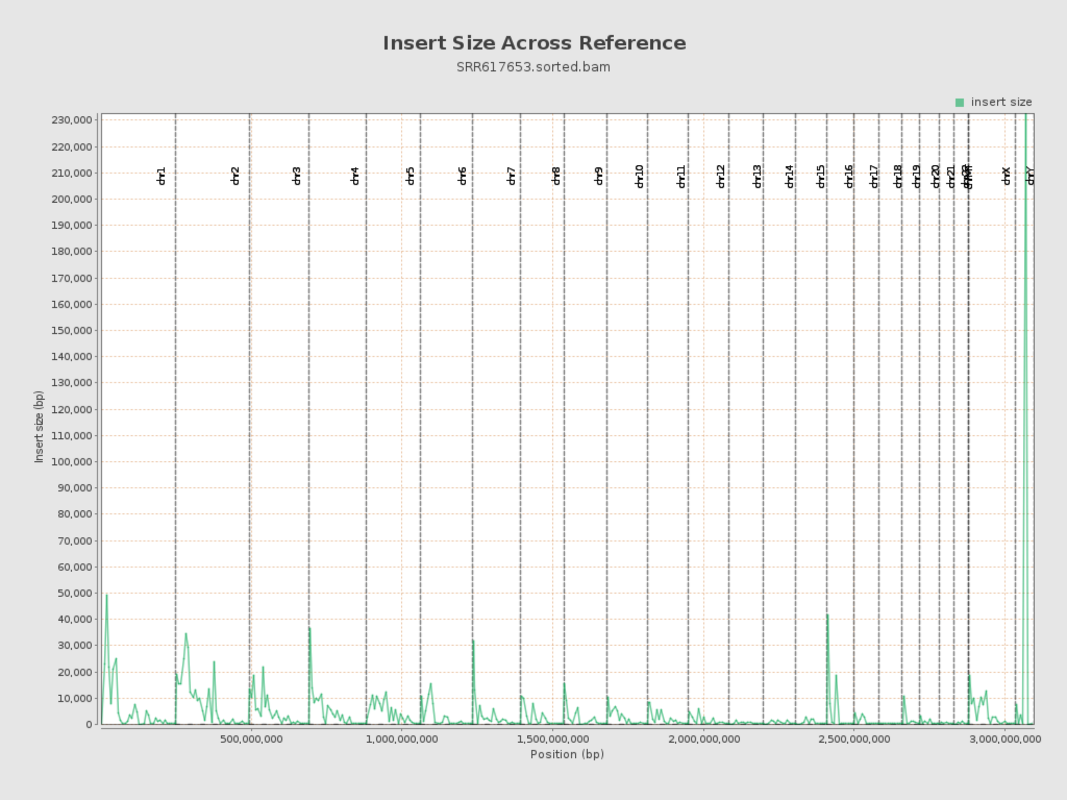
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram