Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 18:12:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617650.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_SRR617650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617650_1.fastq.gz SRR617650_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 18:12:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,922,801 / 93.51%
Unmapped reads	2,077,199 / 6.49%
Mapped paired reads	29,922,801 / 93.51%
Mapped reads, first in pair	15,008,801 / 46.9%
Mapped reads, second in pair	14,914,000 / 46.61%
Mapped reads, both in pair	29,292,516 / 91.54%
Mapped reads, singletons	630,285 / 1.97%
Secondary alignments	0
Supplementary alignments	140,790 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,761,182 / 21.13%
Duplication rate	10.55%
Clipped reads	6,493,798 / 20.29%

2.2. ACGT Content

Number/percentage of A's	864,723,437 / 29.83%
Number/percentage of C's	577,354,765 / 19.92%
Number/percentage of T's	862,115,426 / 29.74%
Number/percentage of G's	592,295,574 / 20.44%
Number/percentage of N's	1,899,629 / 0.07%

GC Percentage	40.36%

2.3. Coverage

Mean	0.9368
Standard Deviation	10.5236

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Insert size

Mean	32,428.56
Standard Deviation	1,638,816.09
P25/Median/P75	178 / 220 / 285

2.6. Mismatches and indels

General error rate	1.58%
Mismatches	44,877,054
Insertions	451,975
Mapped reads with at least one insertion	1.48%
Deletions	1,059,204
Mapped reads with at least one deletion	3.47%
Homopolymer indels	47.66%

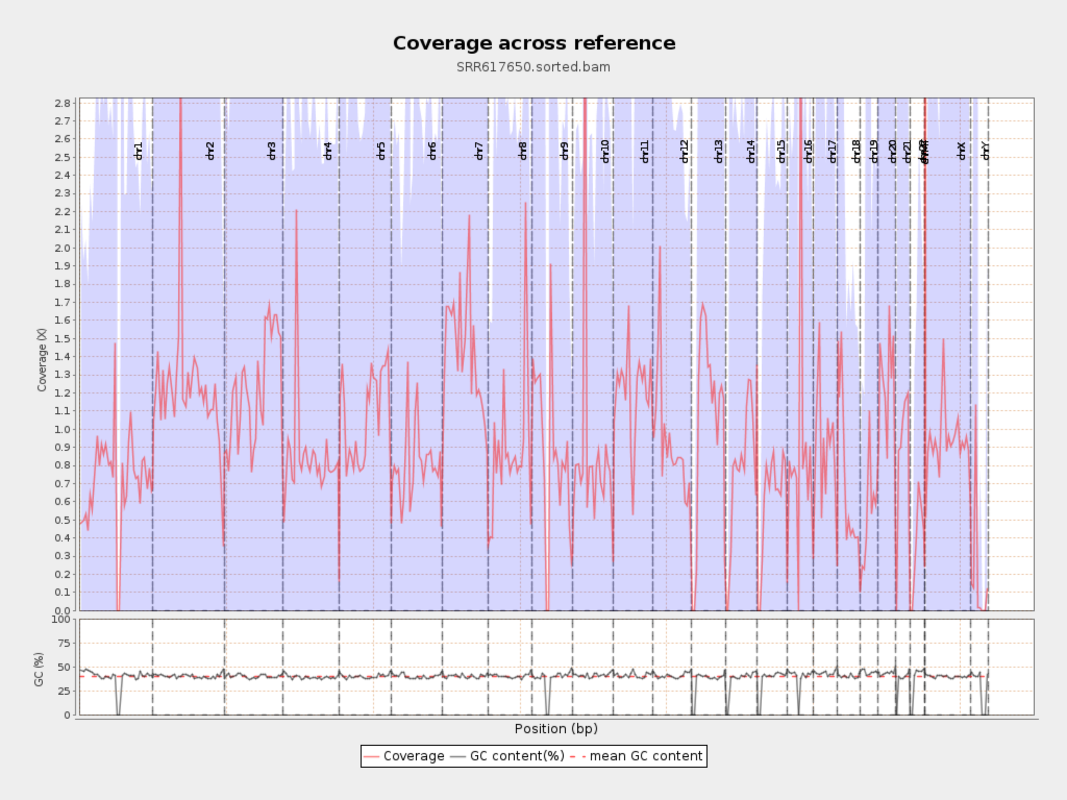
2.7. Chromosome stats

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

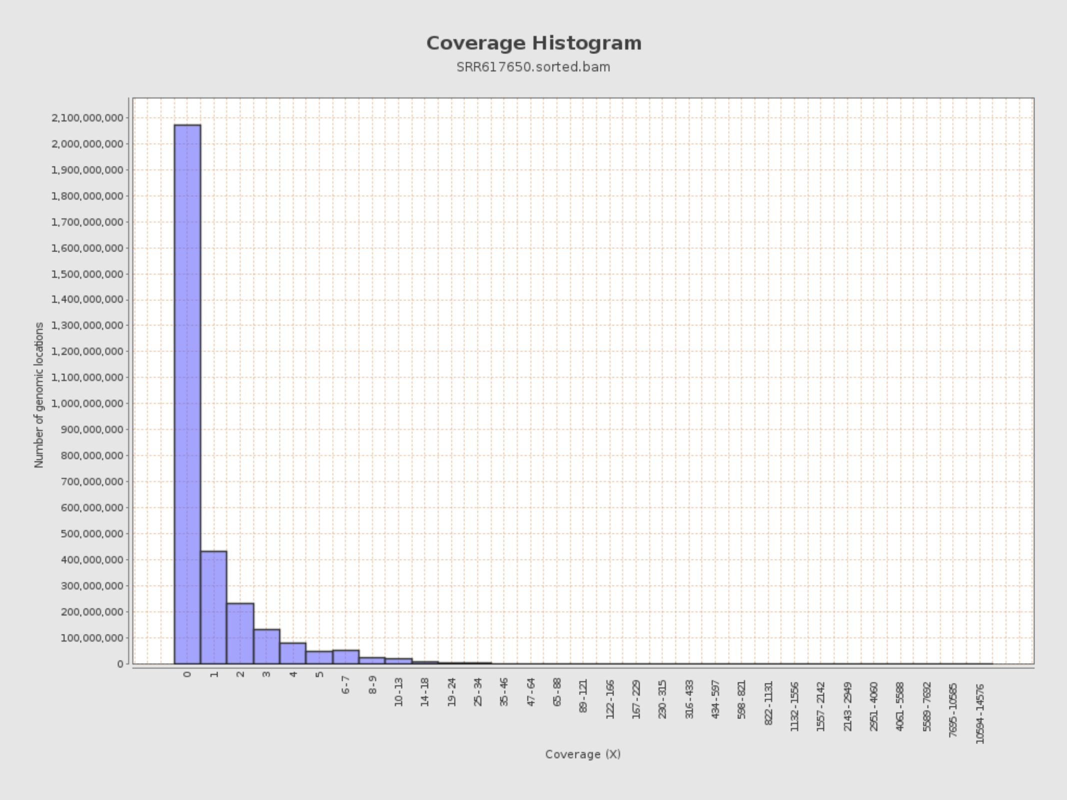
		bases	coverage	deviation
chr1	249250621	177708820	0.713	10.2038
chr2	243199373	299730177	1.2324	11.9888
chr3	198022430	242997521	1.2271	2.4522
chr4	191154276	162666510	0.851	8.2425
chr5	180915260	192087834	1.0618	2.3034
chr6	171115067	140911646	0.8235	5.7121
chr7	159138663	226701239	1.4246	13.1658
chr8	146364022	129130492	0.8823	4.0807
chr9	141213431	119200626	0.8441	20.2525
chr10	135534747	122839248	0.9063	21.5302
chr11	135006516	159216991	1.1793	11.8905
chr12	133851895	123793934	0.9249	2.1173
chr13	115169878	124791947	1.0835	2.2582
chr14	107349540	82700053	0.7704	2.4287
chr15	102531392	61881793	0.6035	1.562
chr16	90354753	80487636	0.8908	16.8926
chr17	81195210	70982992	0.8742	12.5225
chr18	78077248	53606623	0.6866	18.0757
chr19	59128983	30537033	0.5164	6.047
chr20	63025520	78058058	1.2385	3.0166
chr21	48129895	42238370	0.8776	4.3593
chr22	51304566	18458234	0.3598	1.2428
chrMT	16571	3072673	185.4247	128.5511
chrX	155270560	144651969	0.9316	4.3093

chrY	59373566	11685072	0.1968	17.2241

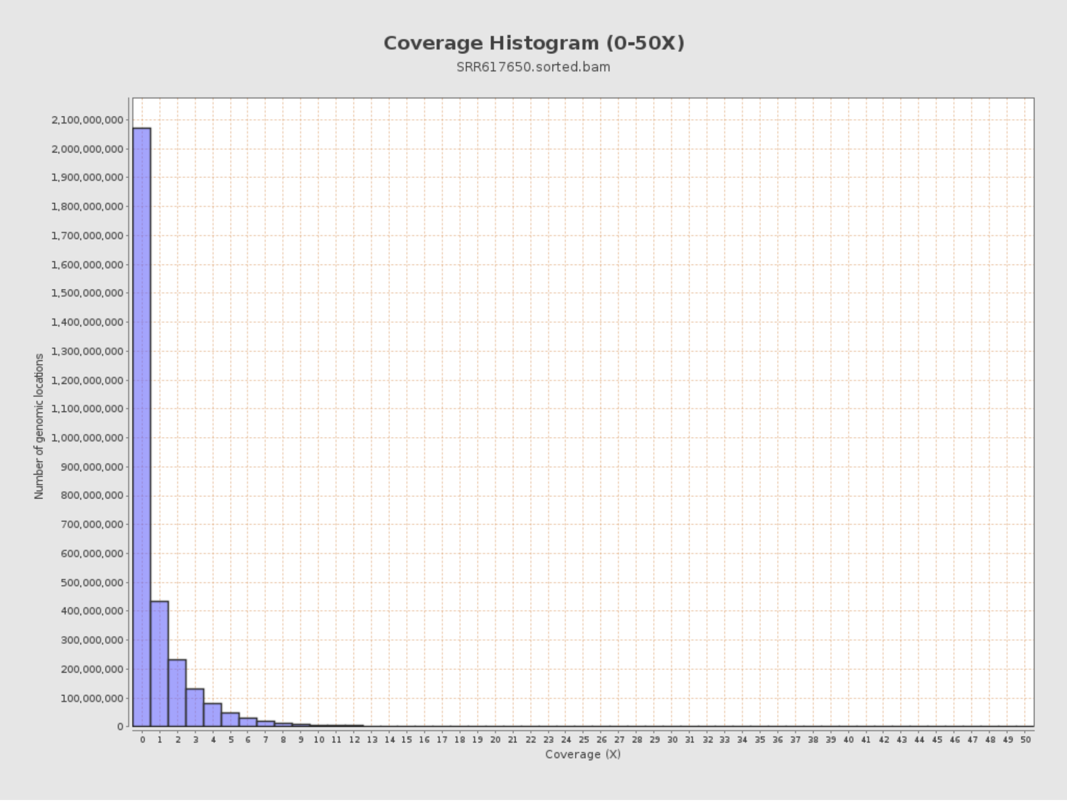
3. Results : Coverage across reference



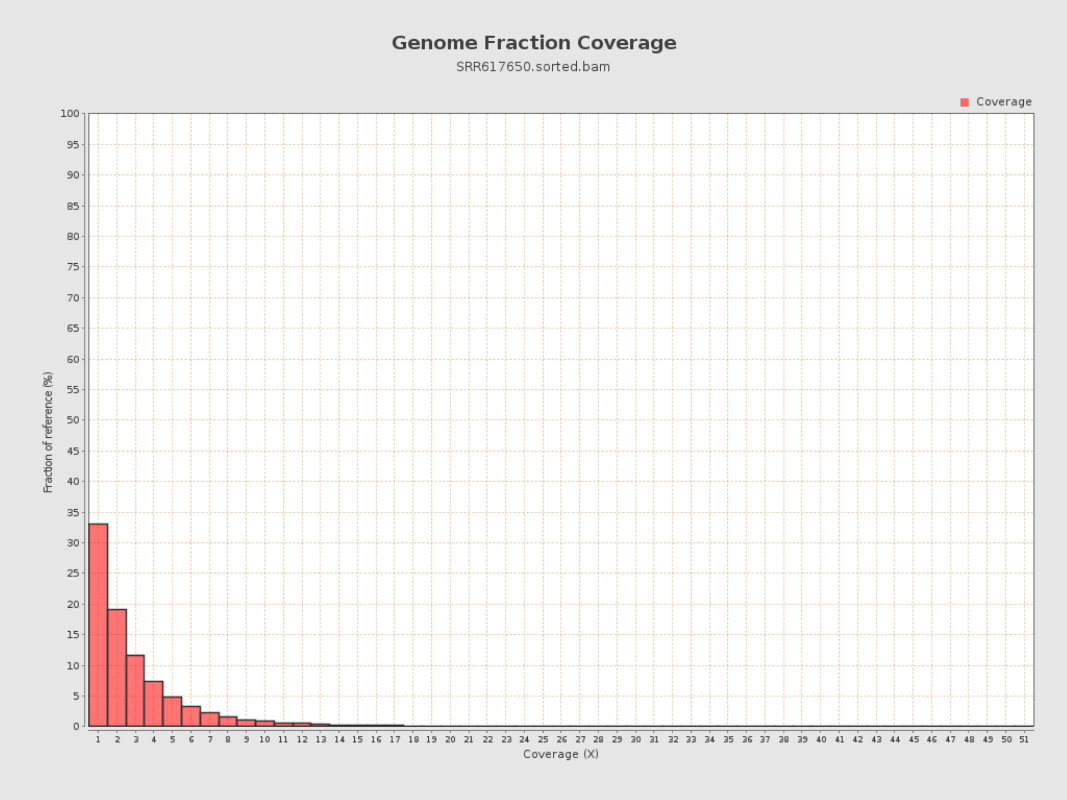
4. Results : Coverage Histogram



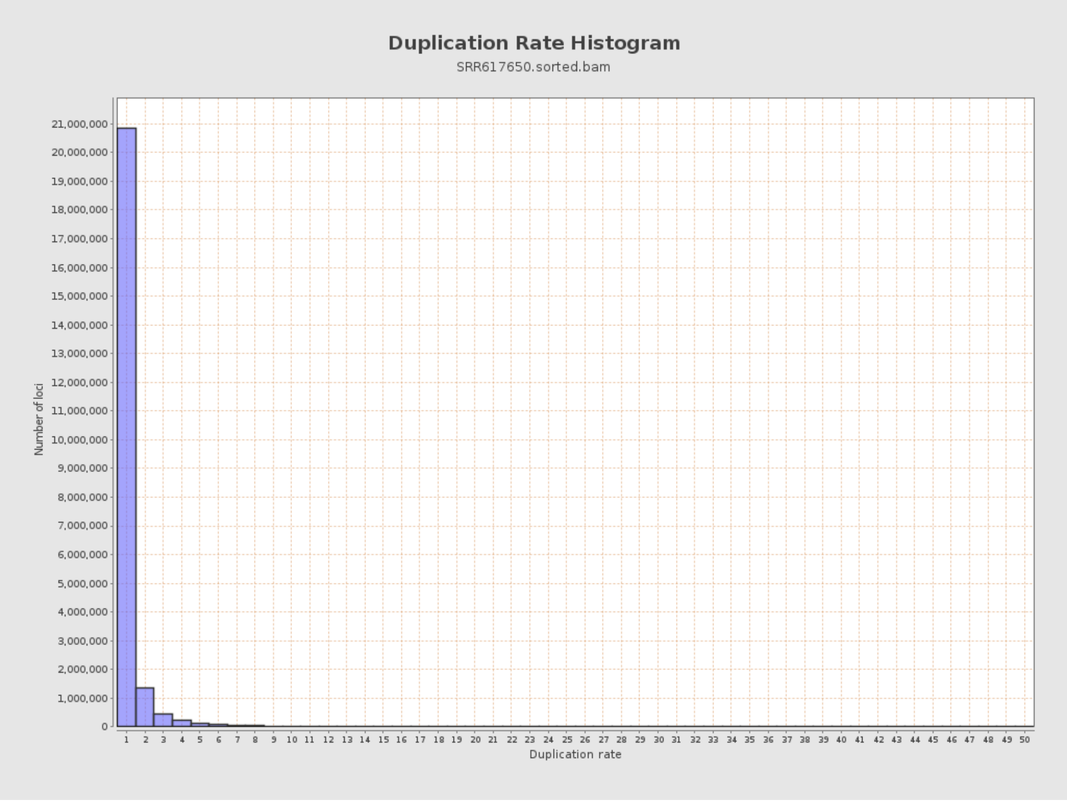
5. Results : Coverage Histogram (0-50X)



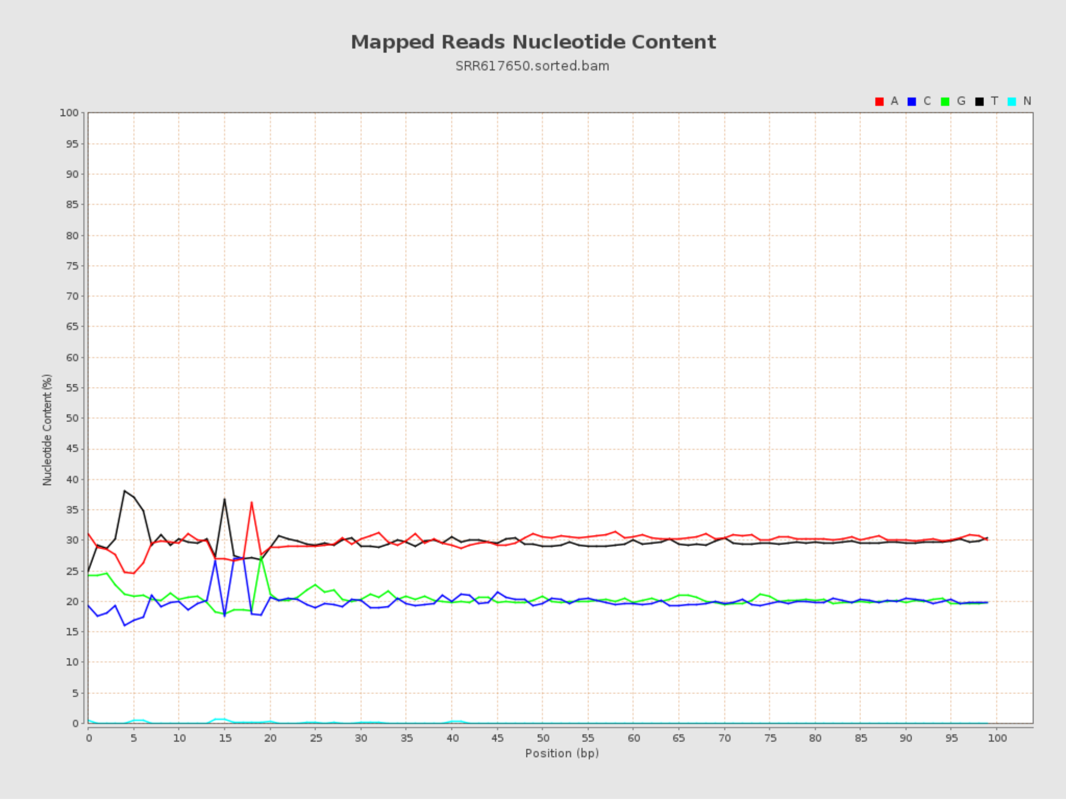
6. Results : Genome Fraction Coverage



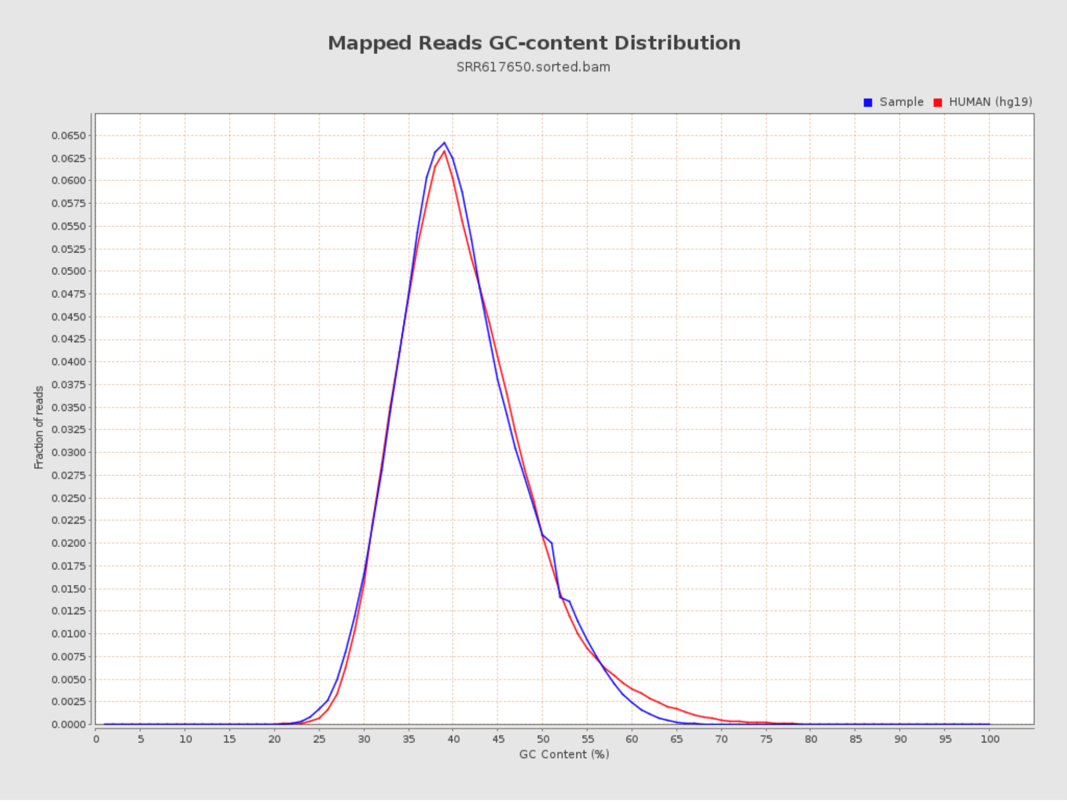
7. Results : Duplication Rate Histogram



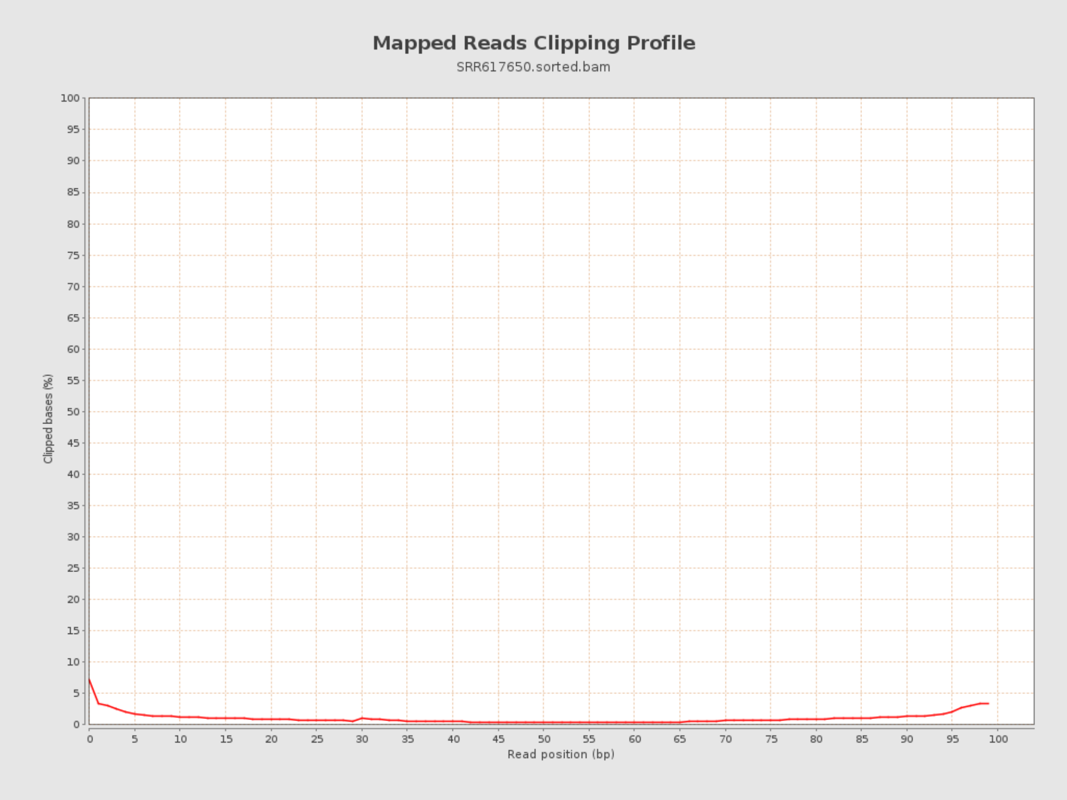
8. Results : Mapped Reads Nucleotide Content



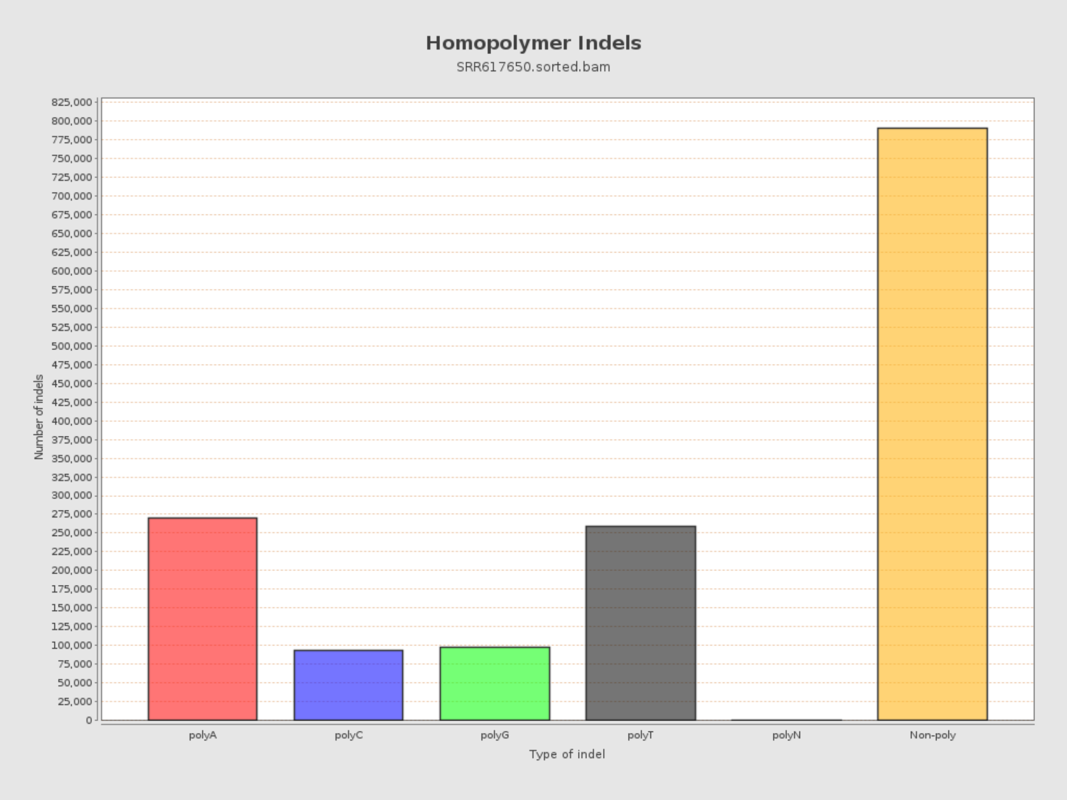
9. Results : Mapped Reads GC-content Distribution



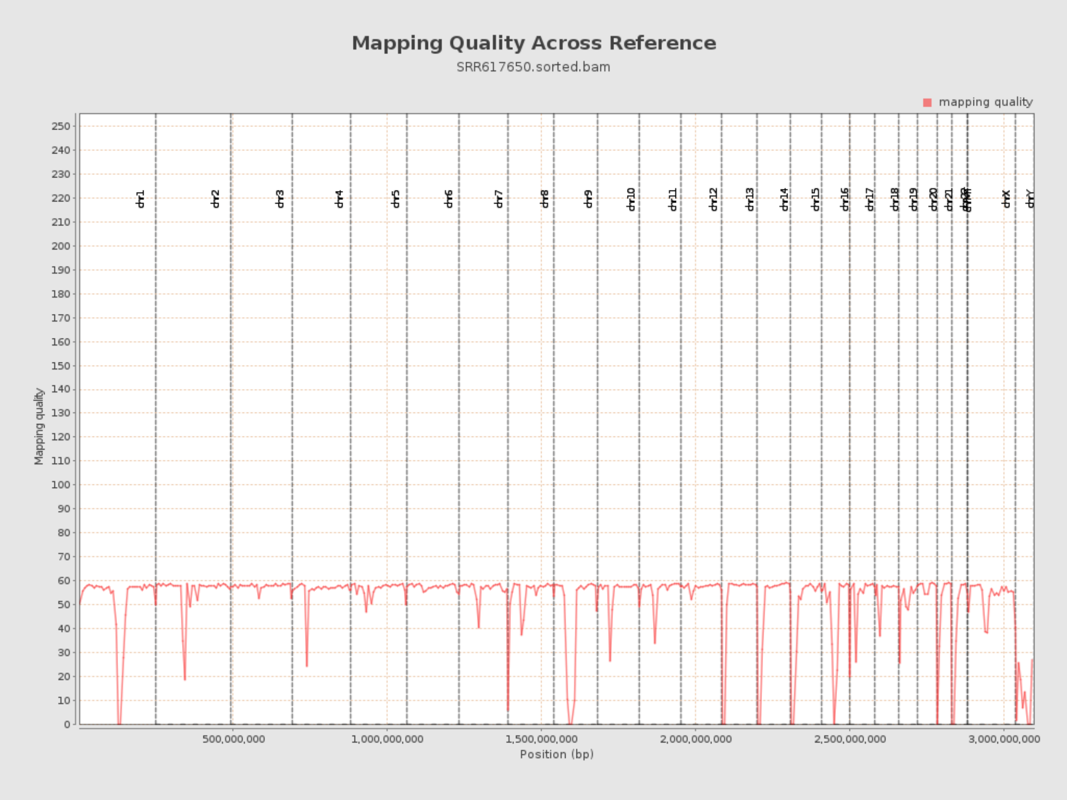
10. Results : Mapped Reads Clipping Profile



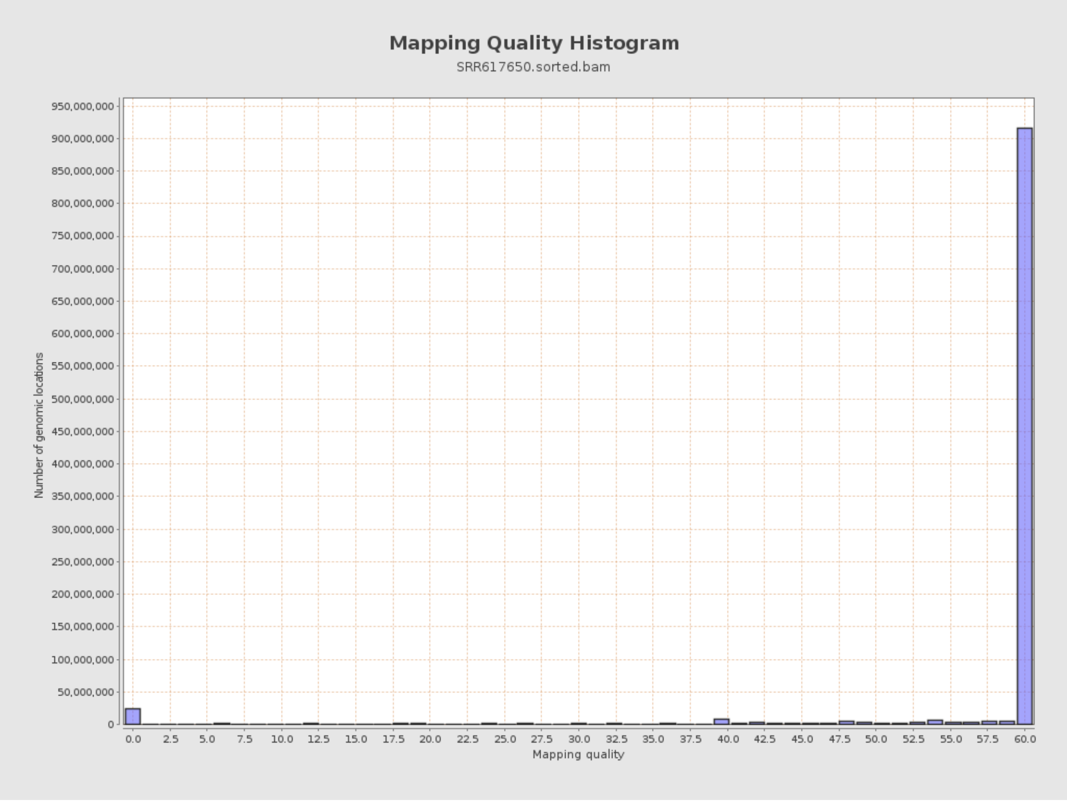
11. Results : Homopolymer Indels



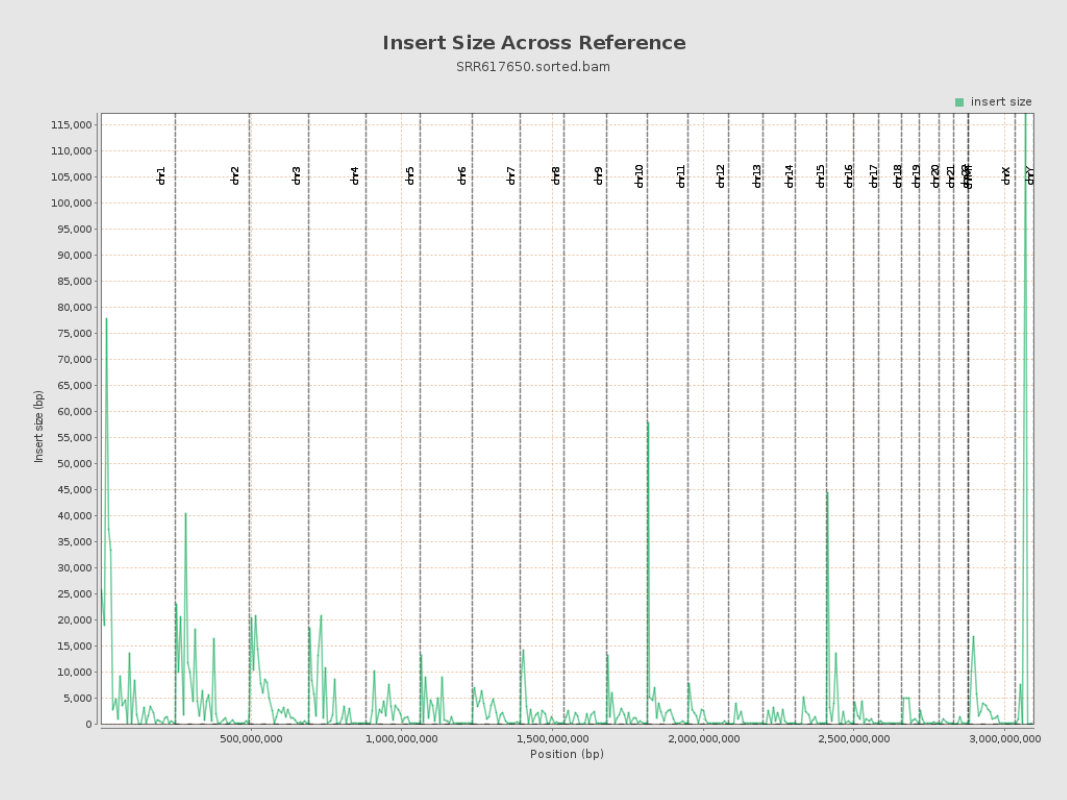
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram