Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 00:08:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617657.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_SRR617657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617657_1.fastq.gz SRR617657_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 00:08:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,218,467 / 94.43%
Unmapped reads	1,781,533 / 5.57%
Mapped paired reads	30,218,467 / 94.43%
Mapped reads, first in pair	15,292,901 / 47.79%
Mapped reads, second in pair	14,925,566 / 46.64%
Mapped reads, both in pair	29,488,294 / 92.15%
Mapped reads, singletons	730,173 / 2.28%
Secondary alignments	0
Supplementary alignments	170,795 / 0.53%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,920,180 / 21.63%
Duplication rate	10.66%
Clipped reads	6,564,980 / 20.52%

2.2. ACGT Content

Number/percentage of A's	869,790,303 / 29.79%
Number/percentage of C's	580,980,521 / 19.9%
Number/percentage of T's	868,448,819 / 29.75%
Number/percentage of G's	596,576,697 / 20.44%
Number/percentage of N's	3,494,798 / 0.12%

GC Percentage	40.34%

2.3. Coverage

Mean	0.9436
Standard Deviation	10.6497

2.4. Mapping Quality

Mean Mapping Quality	52.56

2.5. Insert size

Mean	43,077.76
Standard Deviation	1,916,090.64
P25/Median/P75	178 / 221 / 287

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	40,314,669
Insertions	459,799
Mapped reads with at least one insertion	1.49%
Deletions	1,072,265
Mapped reads with at least one deletion	3.47%
Homopolymer indels	47.64%

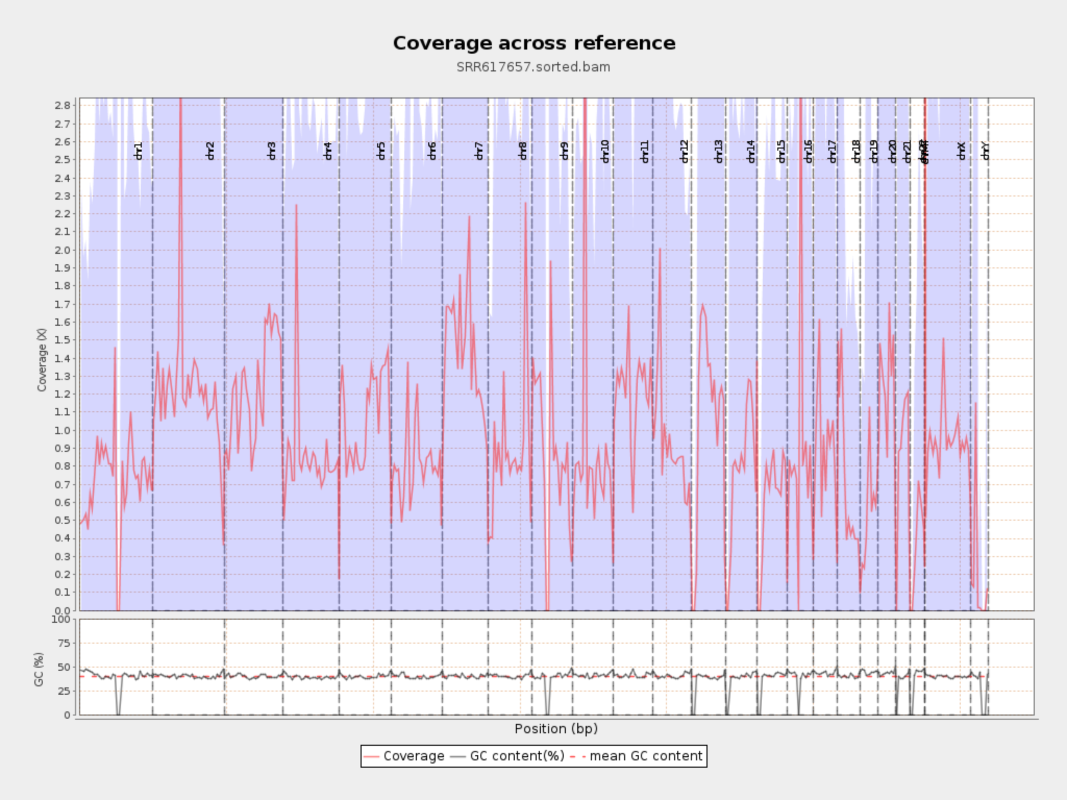
2.7. Chromosome stats

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

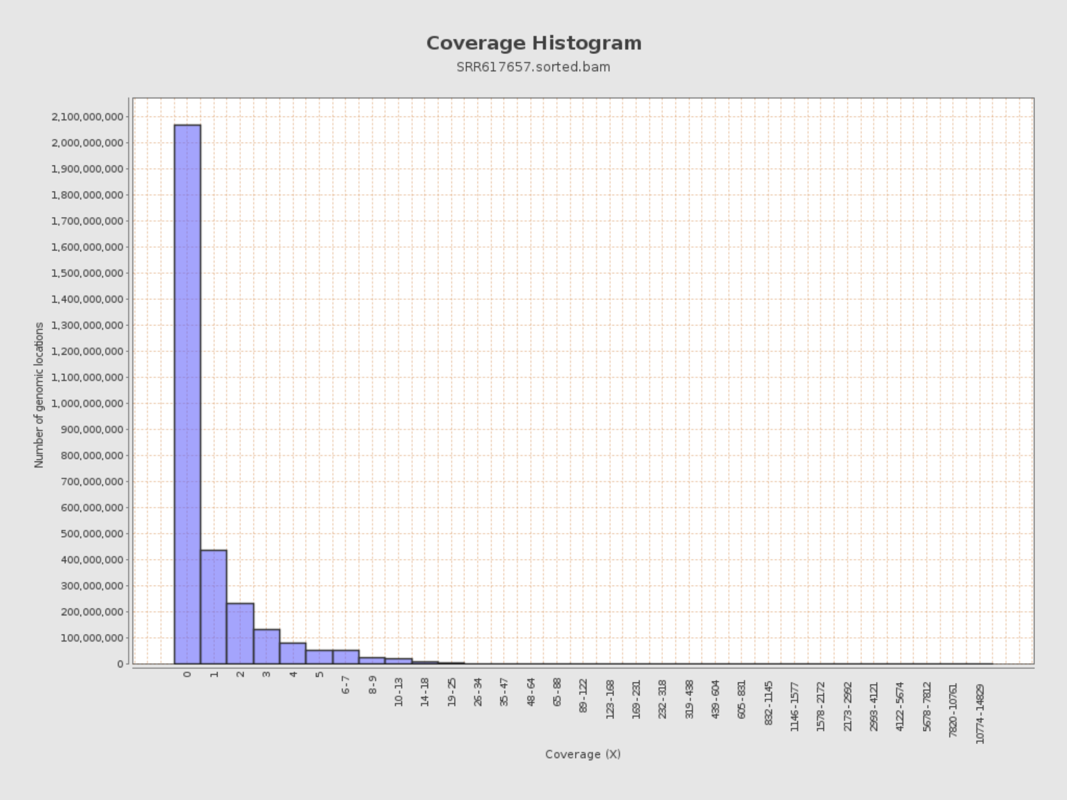
		bases	coverage	deviation
chr1	249250621	178991209	0.7181	10.1796
chr2	243199373	301489774	1.2397	12.2221
chr3	198022430	244337661	1.2339	2.4789
chr4	191154276	163281880	0.8542	8.4611
chr5	180915260	193493245	1.0695	2.3184
chr6	171115067	141454468	0.8267	5.7161
chr7	159138663	228691717	1.4371	13.3791
chr8	146364022	129785646	0.8867	4.1274
chr9	141213431	119918513	0.8492	20.5749
chr10	135534747	123773310	0.9132	21.6415
chr11	135006516	160749068	1.1907	12.1168
chr12	133851895	124637986	0.9312	2.164
chr13	115169878	125391885	1.0888	2.301
chr14	107349540	83439593	0.7773	2.4668
chr15	102531392	62482971	0.6094	1.667
chr16	90354753	81087675	0.8974	16.7394
chr17	81195210	72143849	0.8885	12.7867
chr18	78077248	53987977	0.6915	18.4703
chr19	59128983	31162963	0.527	6.1022
chr20	63025520	78934106	1.2524	3.0598
chr21	48129895	42597415	0.8851	4.3334
chr22	51304566	18858546	0.3676	1.2761
chrMT	16571	3076658	185.6652	129.7246
chrX	155270560	145414420	0.9365	4.344

chrY	59373566	11894416	0.2003	17.5397

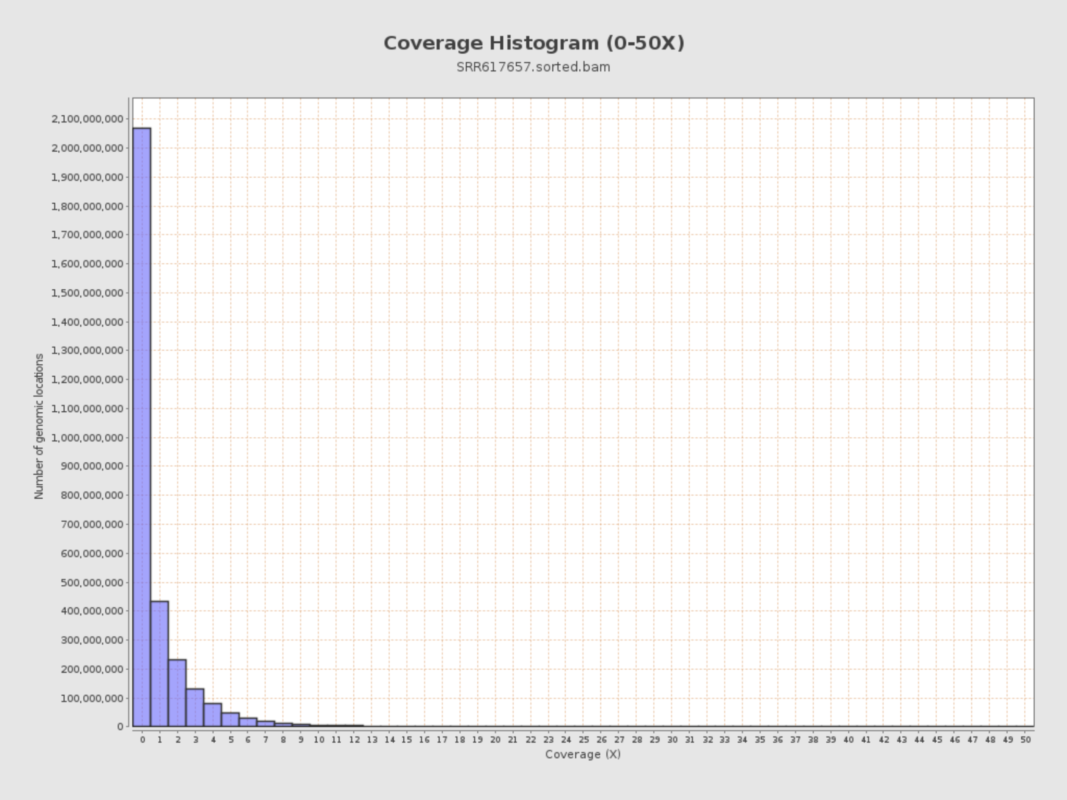
3. Results : Coverage across reference



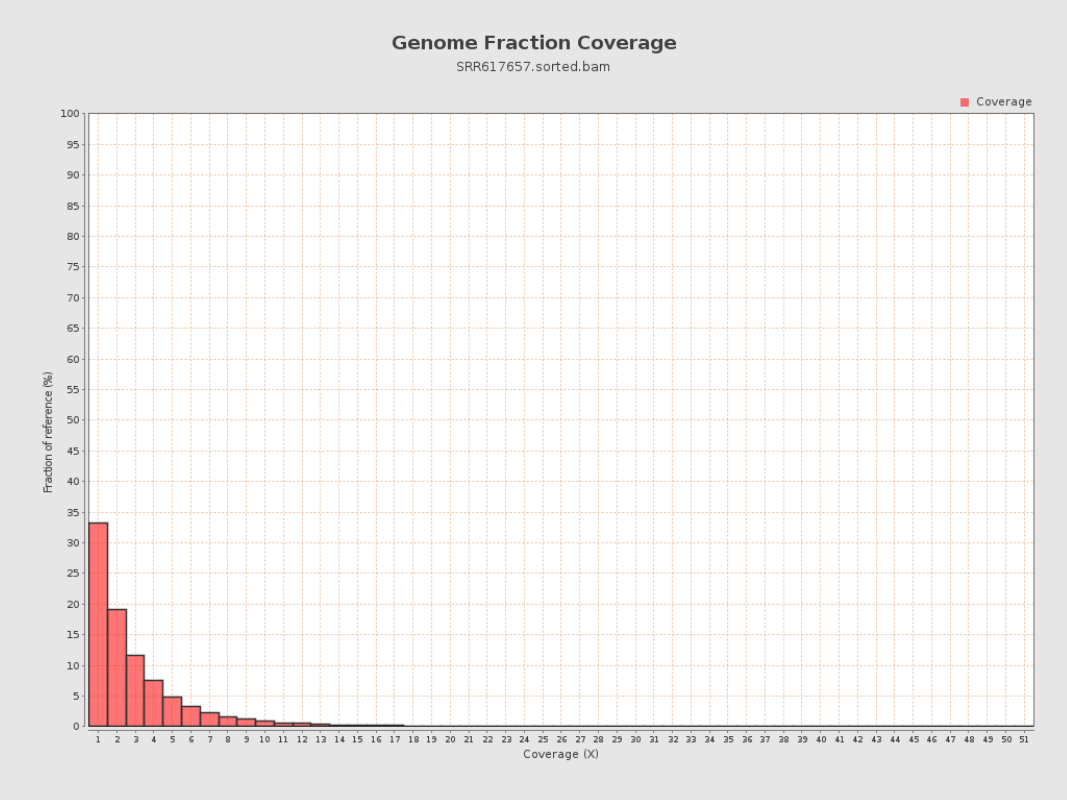
4. Results : Coverage Histogram



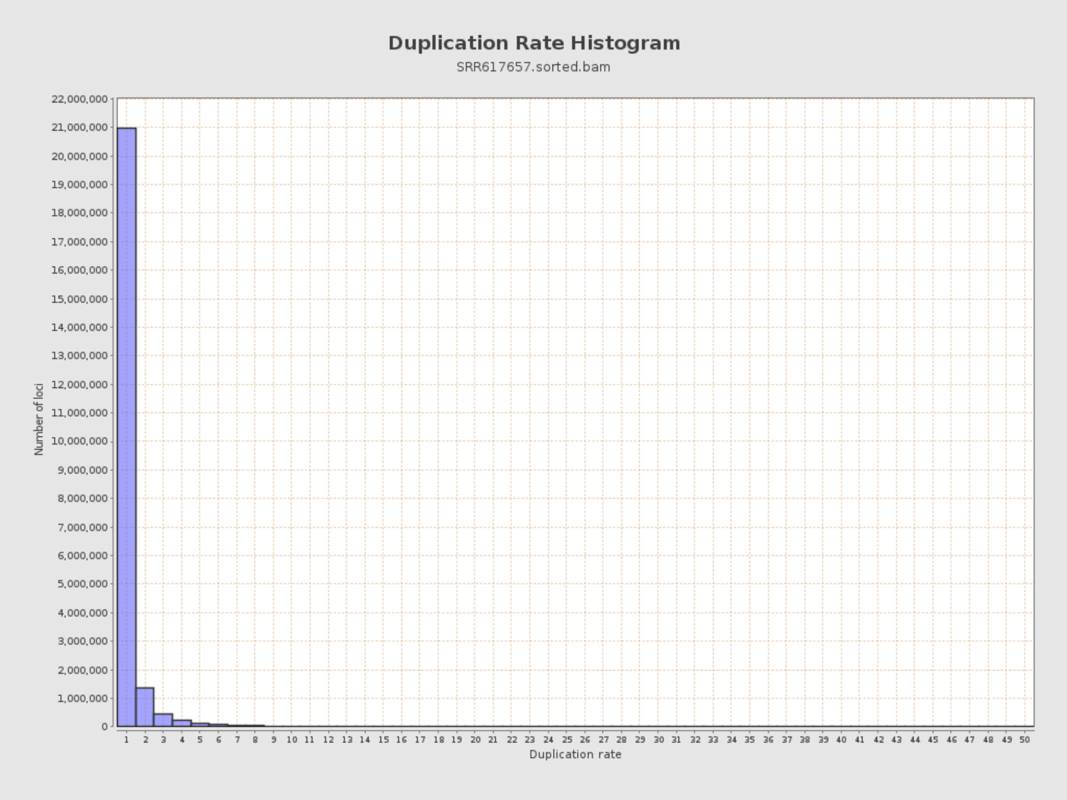
5. Results : Coverage Histogram (0-50X)



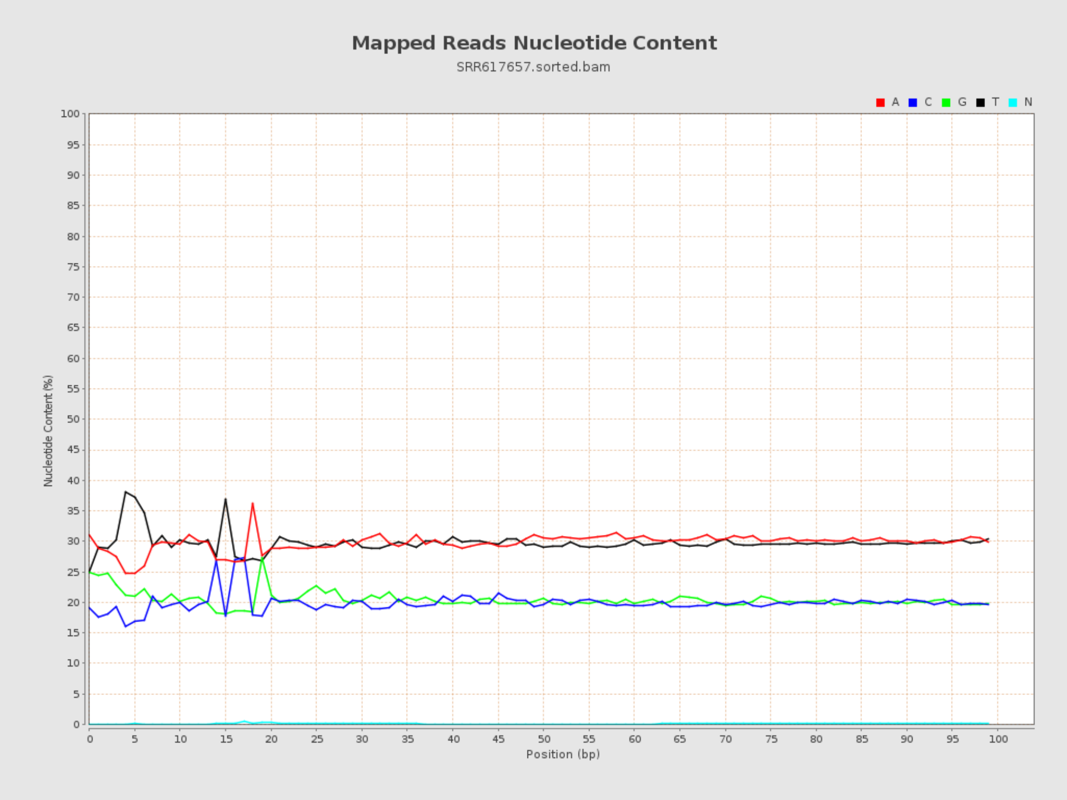
6. Results : Genome Fraction Coverage



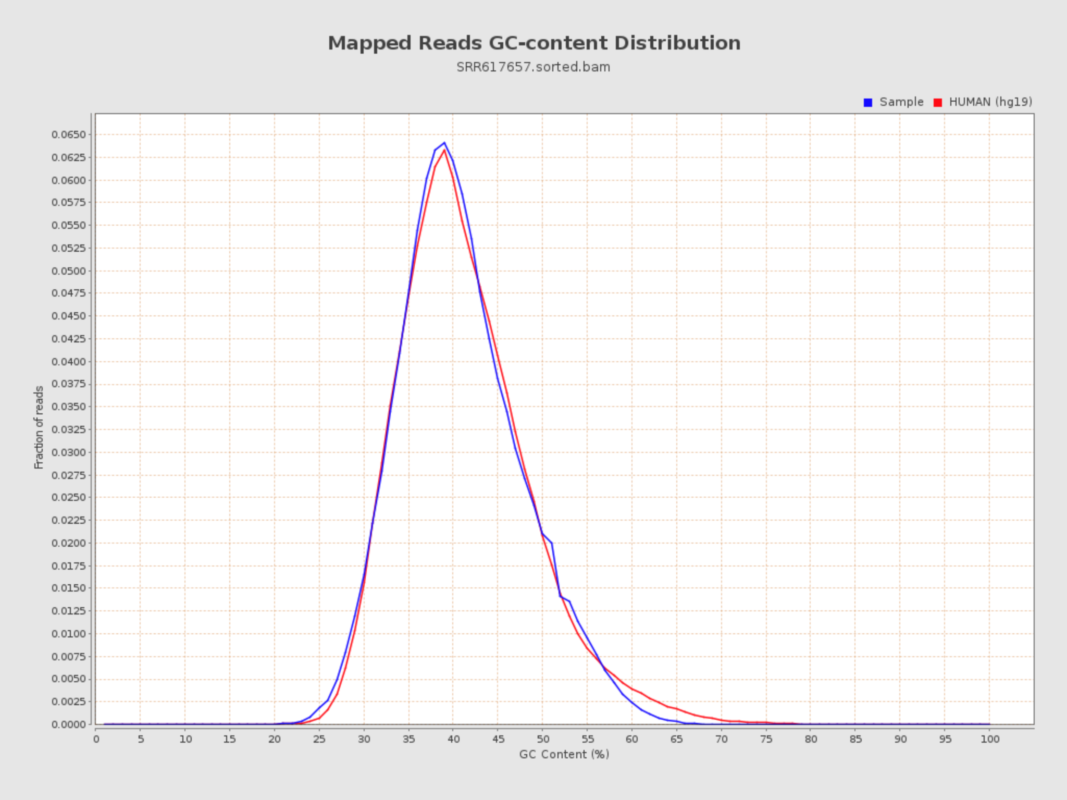
7. Results : Duplication Rate Histogram



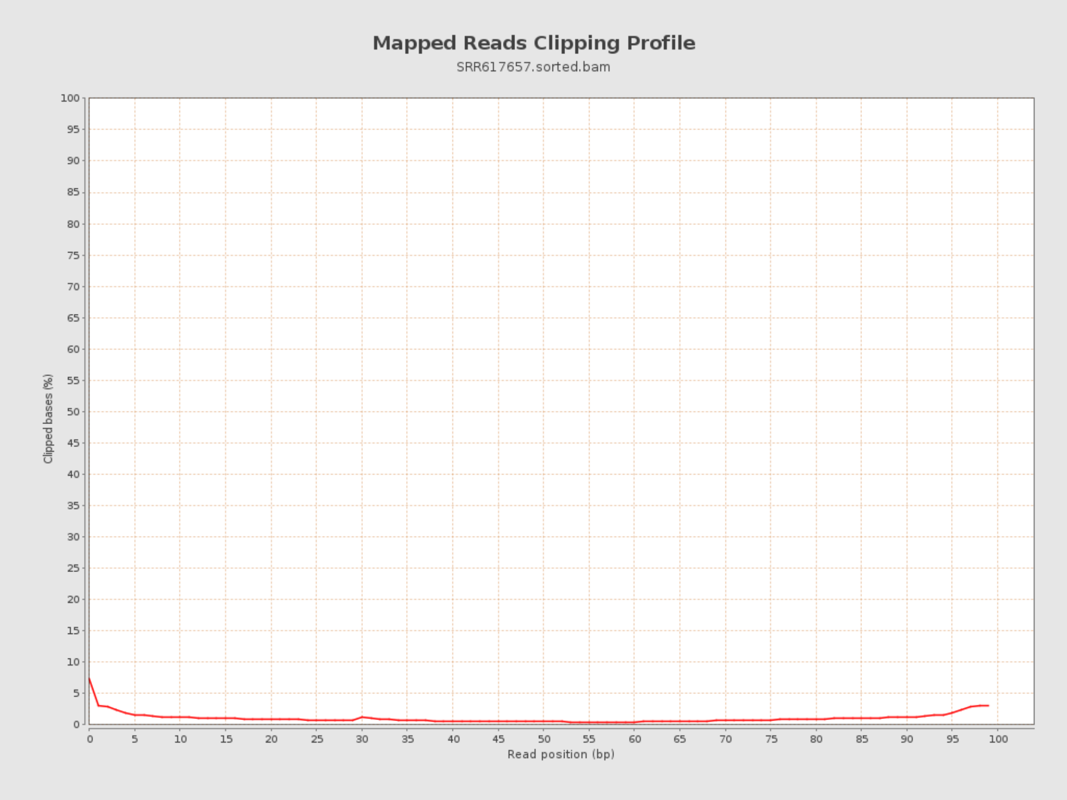
8. Results : Mapped Reads Nucleotide Content



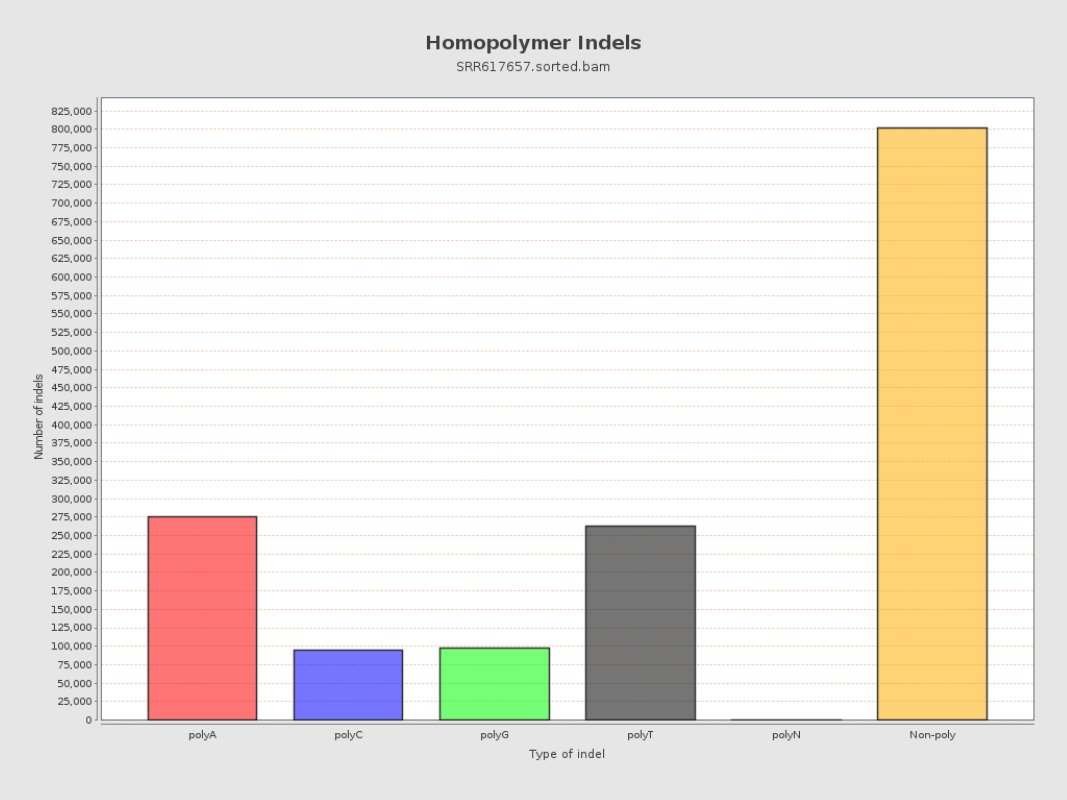
9. Results : Mapped Reads GC-content Distribution



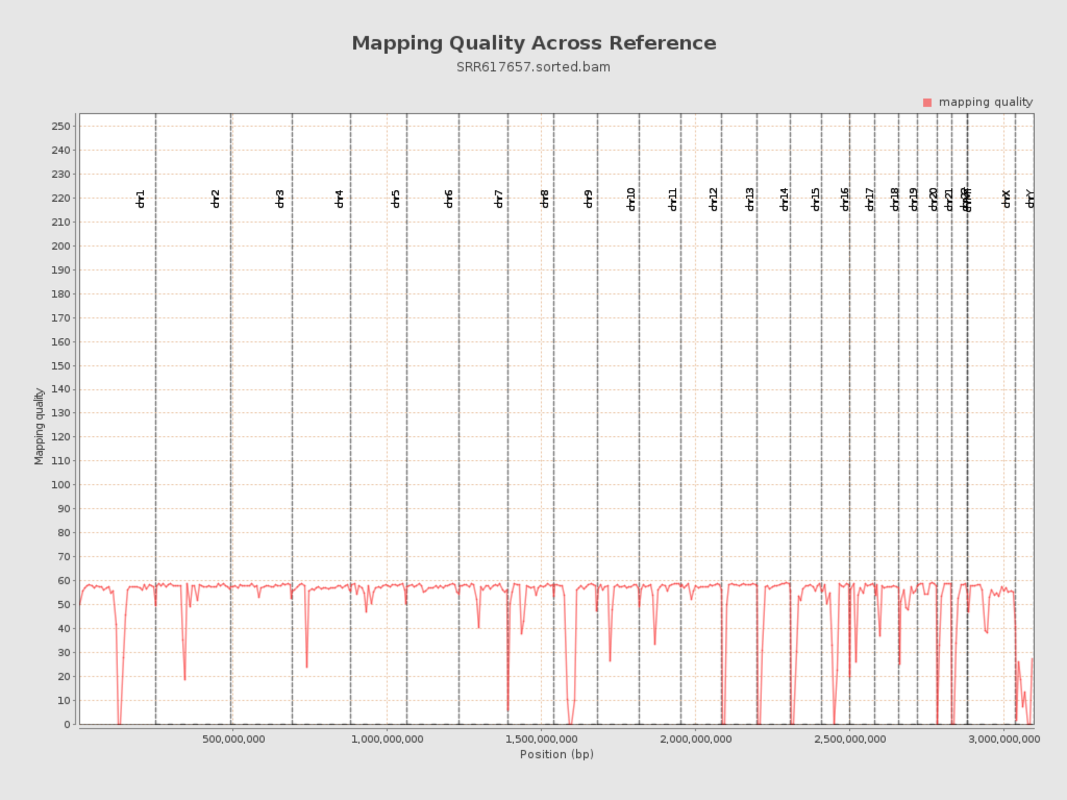
10. Results : Mapped Reads Clipping Profile



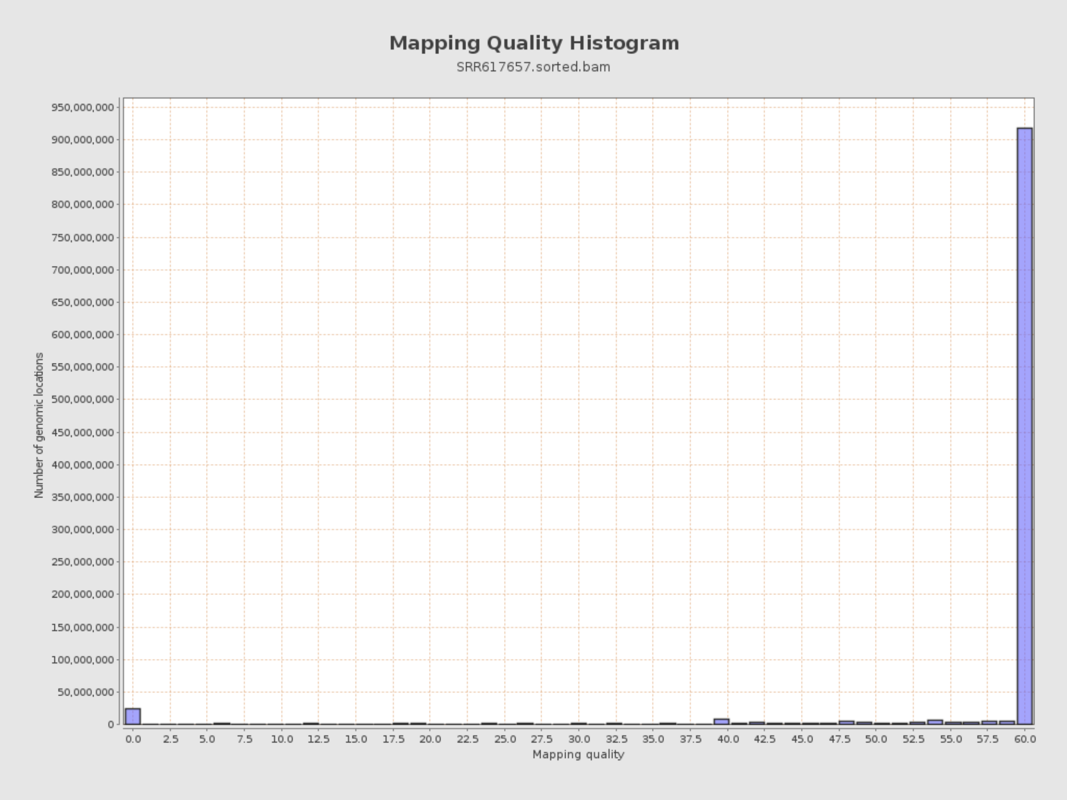
11. Results : Homopolymer Indels



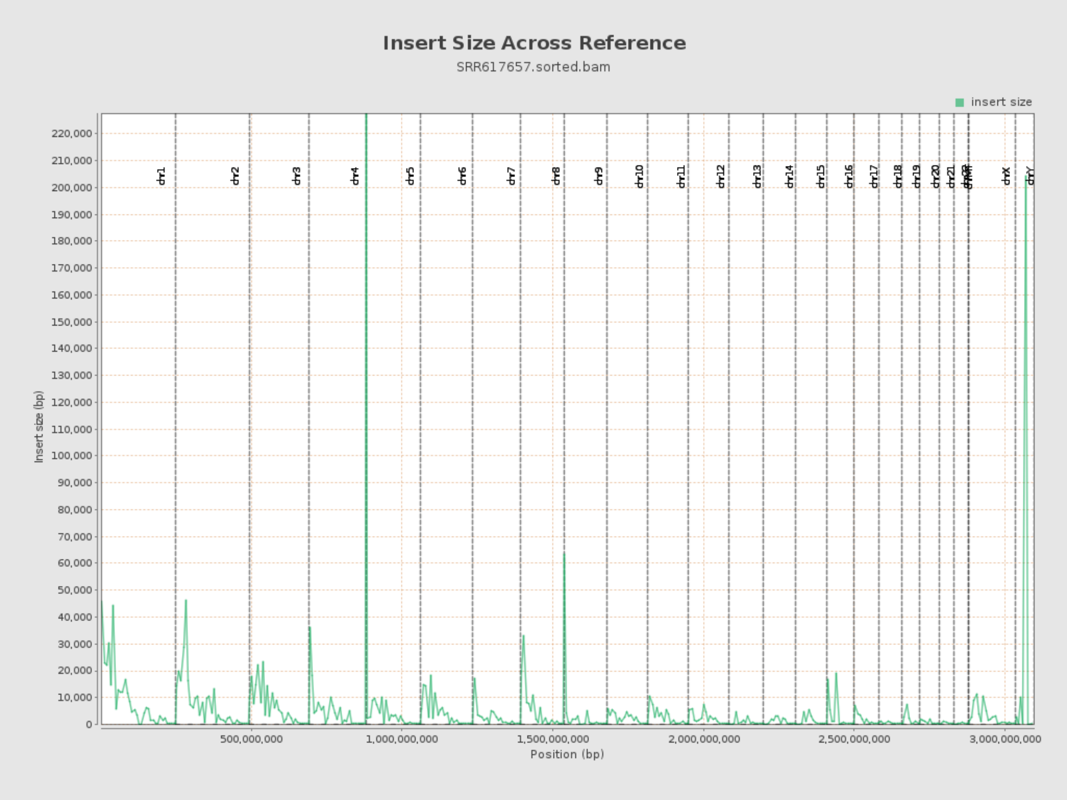
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram