Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:39:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617648.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_SRR617648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617648_1.fastq.gz SRR617648_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:39:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,055,665 / 93.92%
Unmapped reads	1,944,335 / 6.08%
Mapped paired reads	30,055,665 / 93.92%
Mapped reads, first in pair	15,058,712 / 47.06%
Mapped reads, second in pair	14,996,953 / 46.87%
Mapped reads, both in pair	29,417,256 / 91.93%
Mapped reads, singletons	638,409 / 2%
Secondary alignments	0
Supplementary alignments	140,158 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,877,273 / 21.49%
Duplication rate	10.71%
Clipped reads	6,422,979 / 20.07%

2.2. ACGT Content

Number/percentage of A's	867,947,484 / 29.78%
Number/percentage of C's	581,432,950 / 19.95%
Number/percentage of T's	865,955,524 / 29.71%
Number/percentage of G's	597,196,660 / 20.49%
Number/percentage of N's	1,973,119 / 0.07%

GC Percentage	40.44%

2.3. Coverage

Mean	0.942
Standard Deviation	10.51

2.4. Mapping Quality

Mean Mapping Quality	52.65

2.5. Insert size

Mean	34,024.95
Standard Deviation	1,698,200.3
P25/Median/P75	180 / 224 / 291

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	43,545,339
Insertions	453,681
Mapped reads with at least one insertion	1.48%
Deletions	1,068,370
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.77%

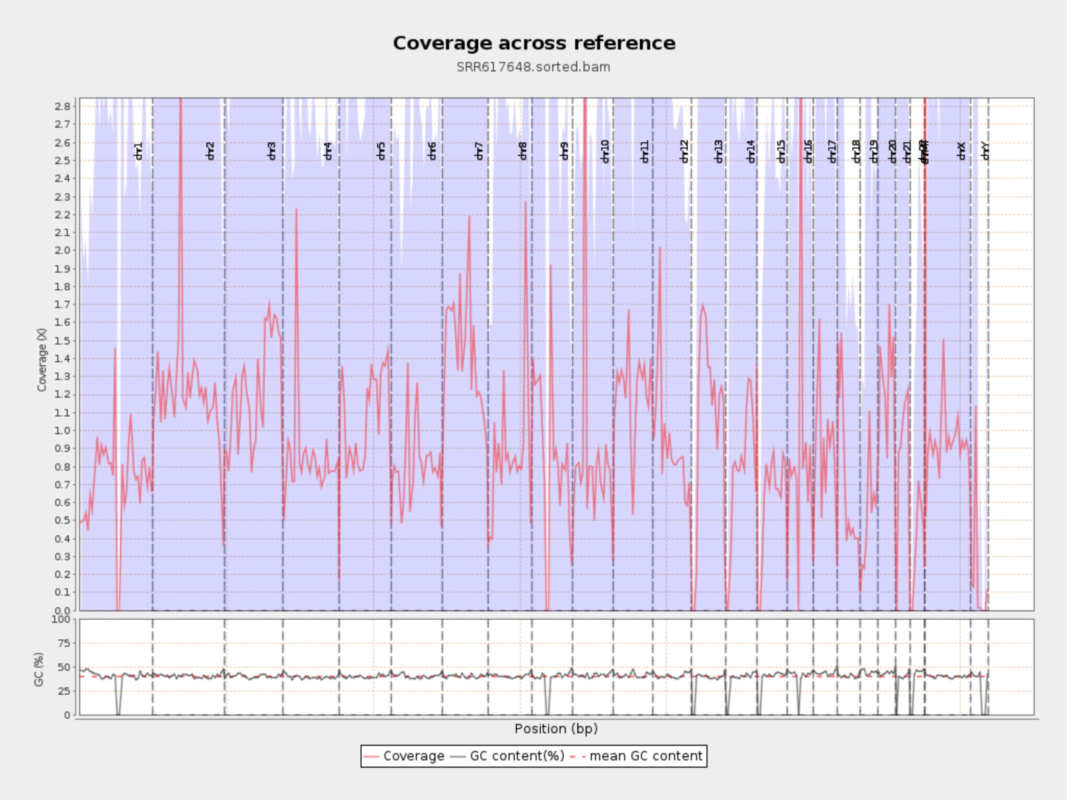
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

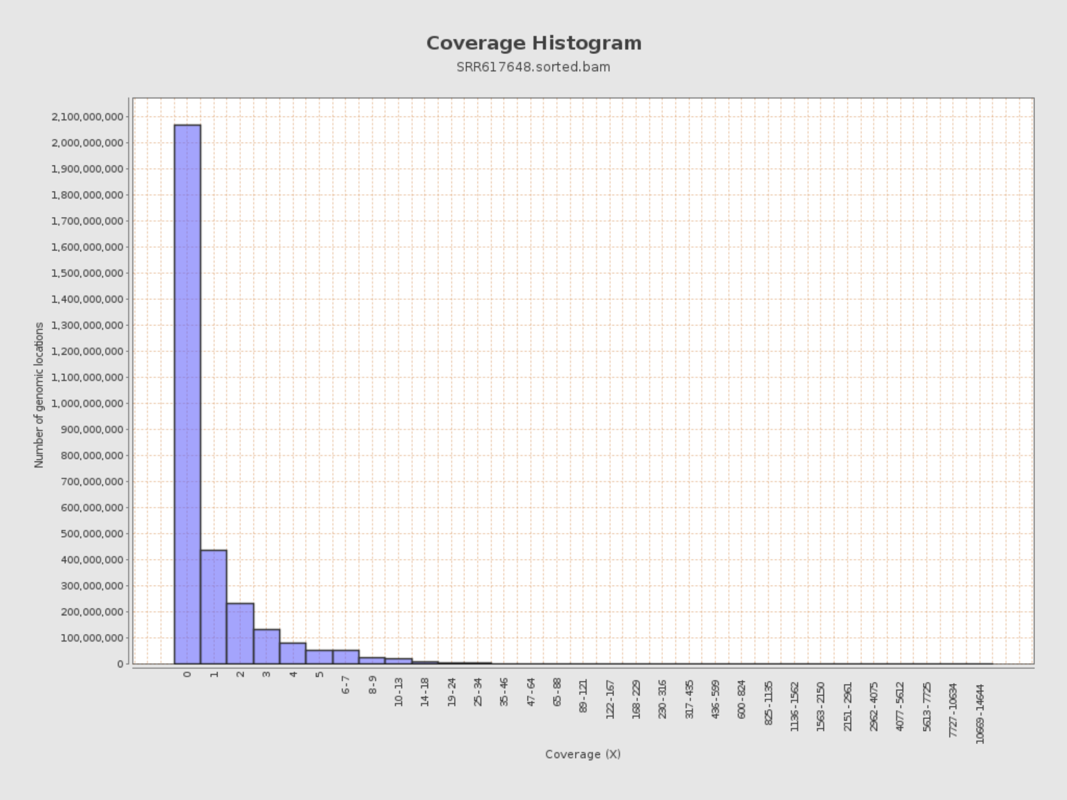
		bases	coverage	deviation
chr1	249250621	178840537	0.7175	10.067
chr2	243199373	301095843	1.2381	12.0191
chr3	198022430	244191700	1.2332	2.4607
chr4	191154276	163225929	0.8539	8.2598
chr5	180915260	193154909	1.0677	2.3186
chr6	171115067	141243838	0.8254	5.7406
chr7	159138663	228357740	1.435	13.4728
chr8	146364022	129862733	0.8873	4.0702
chr9	141213431	119610803	0.847	20.4393
chr10	135534747	123454408	0.9109	21.1911
chr11	135006516	160527581	1.189	11.737
chr12	133851895	124668788	0.9314	2.1353
chr13	115169878	125186981	1.087	2.272
chr14	107349540	83434534	0.7772	2.4663
chr15	102531392	62279675	0.6074	1.5753
chr16	90354753	80734165	0.8935	16.6435
chr17	81195210	71826246	0.8846	12.7458
chr18	78077248	53753196	0.6885	17.9903
chr19	59128983	30947289	0.5234	6.0651
chr20	63025520	78621505	1.2475	3.0449
chr21	48129895	42588736	0.8849	4.3477
chr22	51304566	18686122	0.3642	1.2532
chrMT	16571	3082729	186.0316	128.5017
chrX	155270560	145168333	0.9349	4.3368

chrY	59373566	11724571	0.1975	17.2335

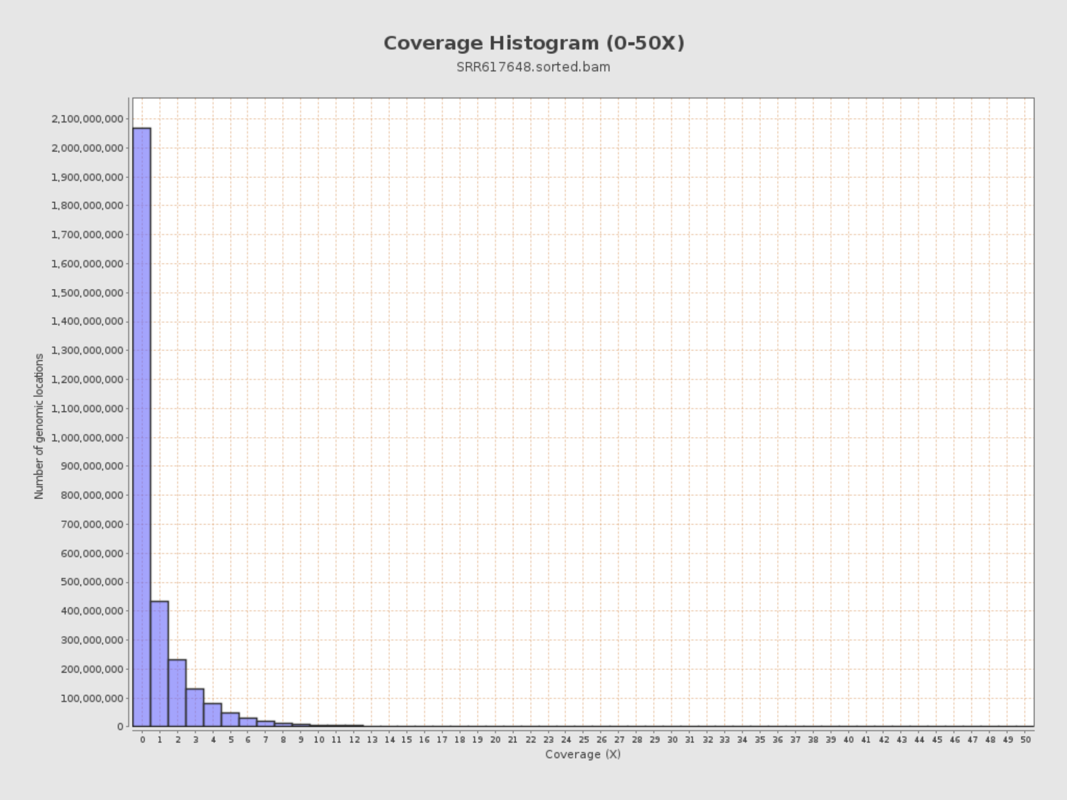
3. Results : Coverage across reference



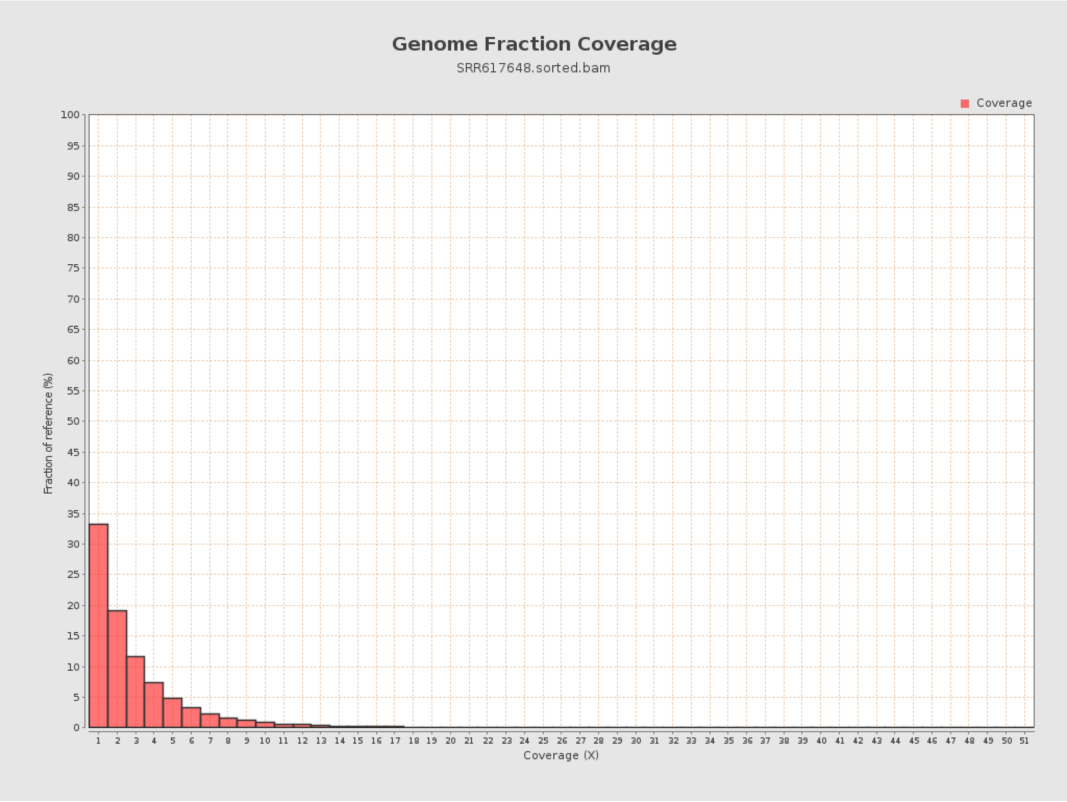
4. Results : Coverage Histogram



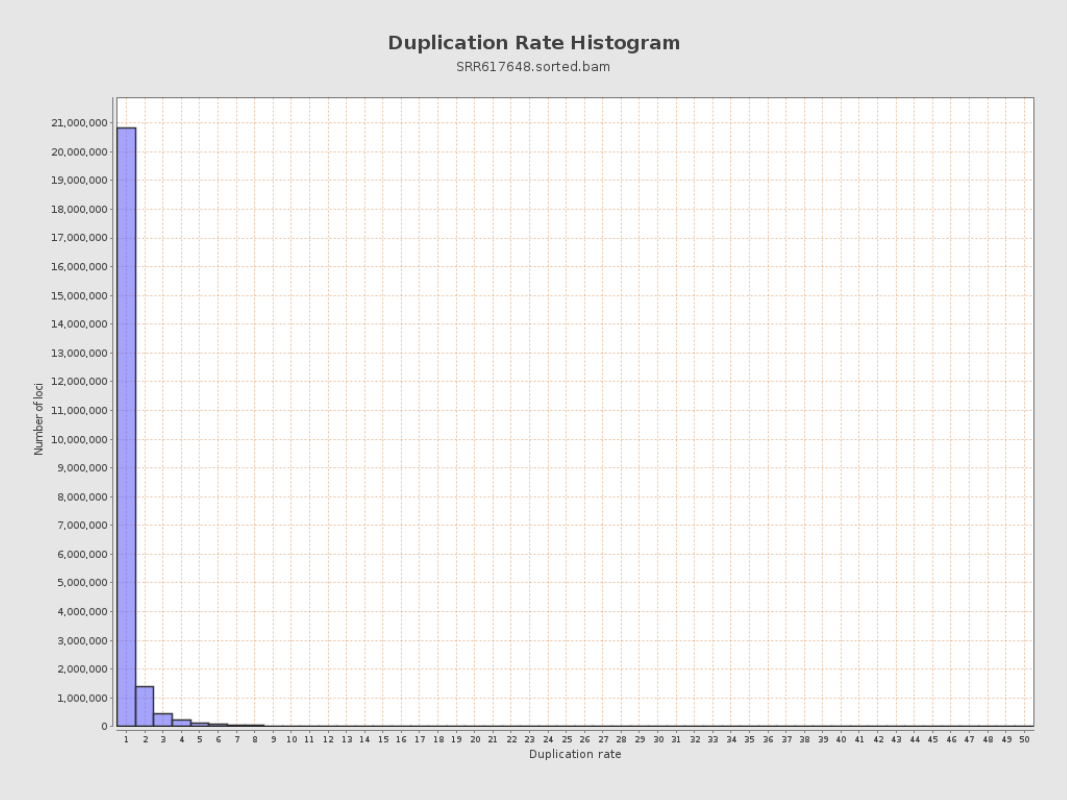
5. Results : Coverage Histogram (0-50X)



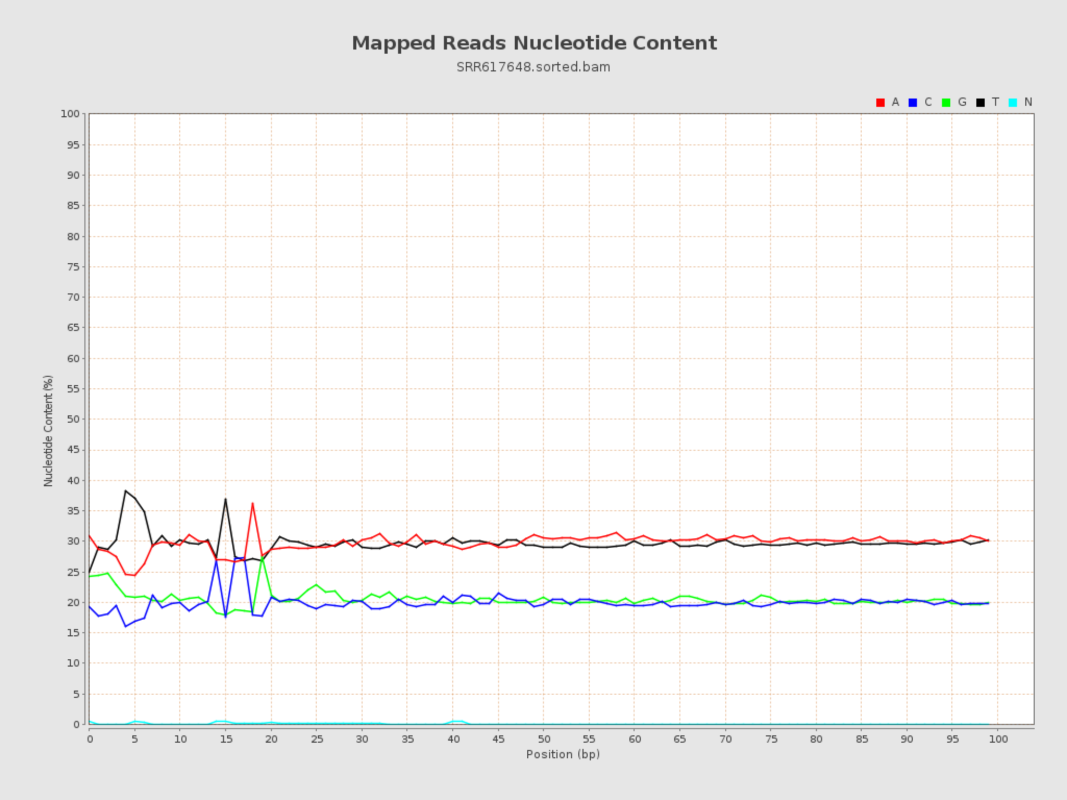
6. Results : Genome Fraction Coverage



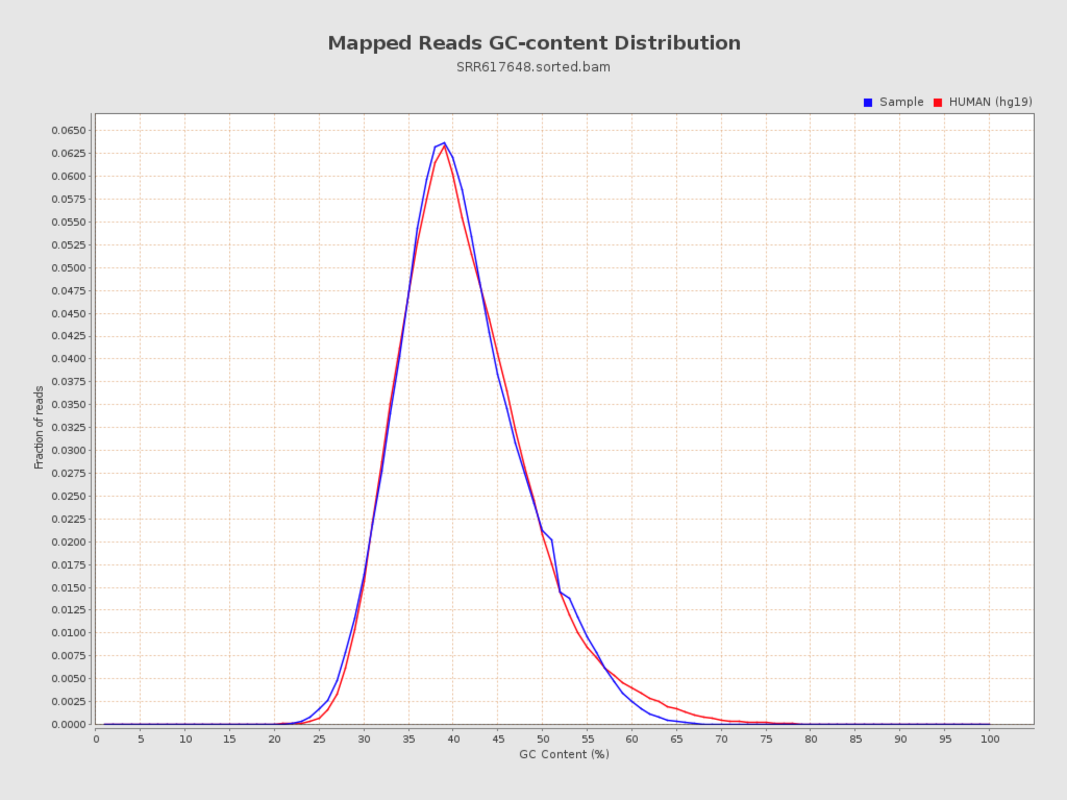
7. Results : Duplication Rate Histogram



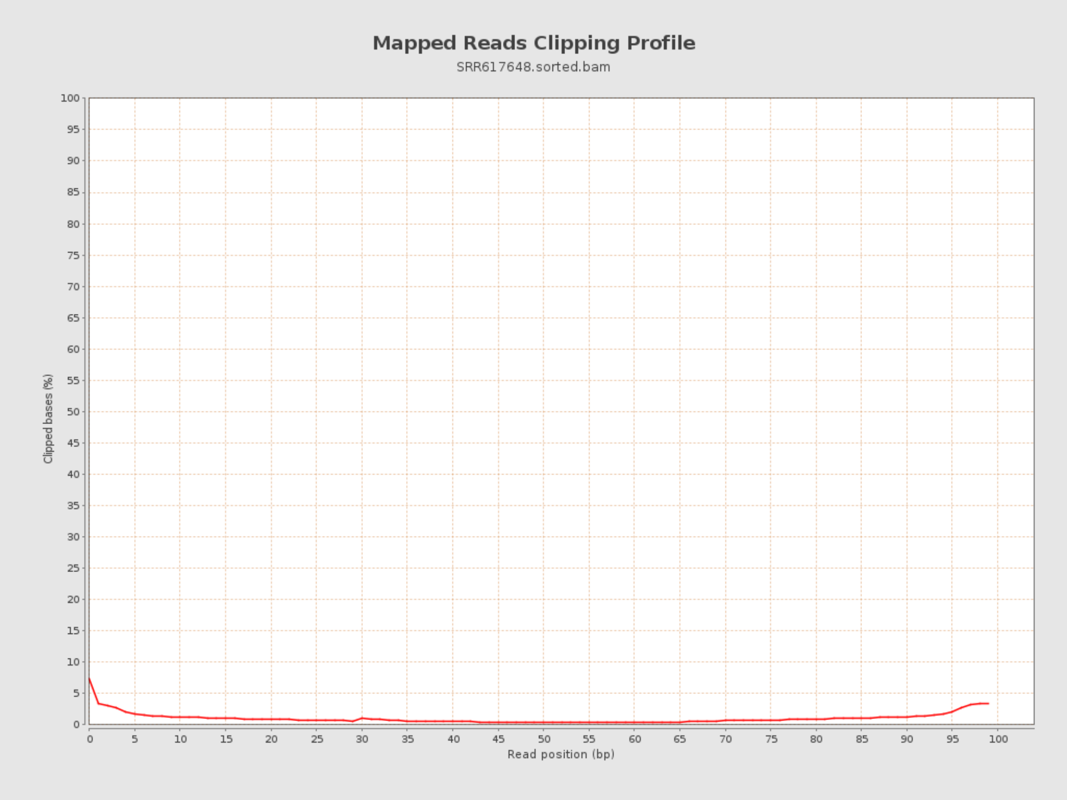
8. Results : Mapped Reads Nucleotide Content



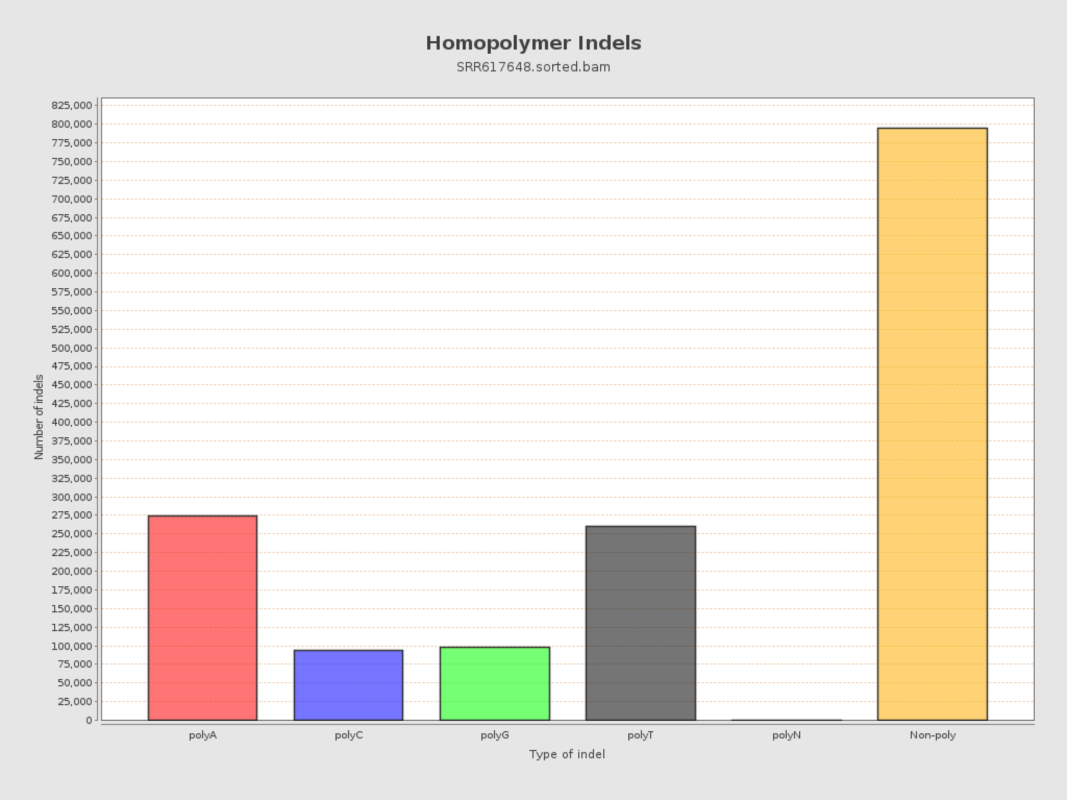
9. Results : Mapped Reads GC-content Distribution



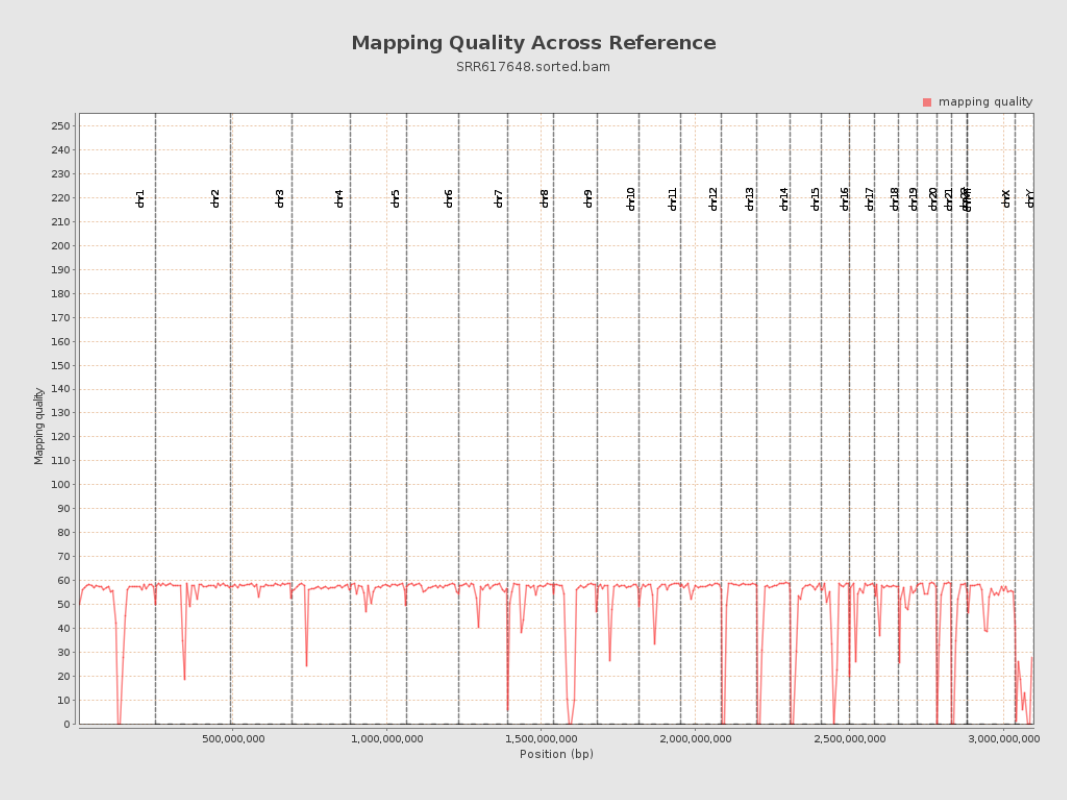
10. Results : Mapped Reads Clipping Profile



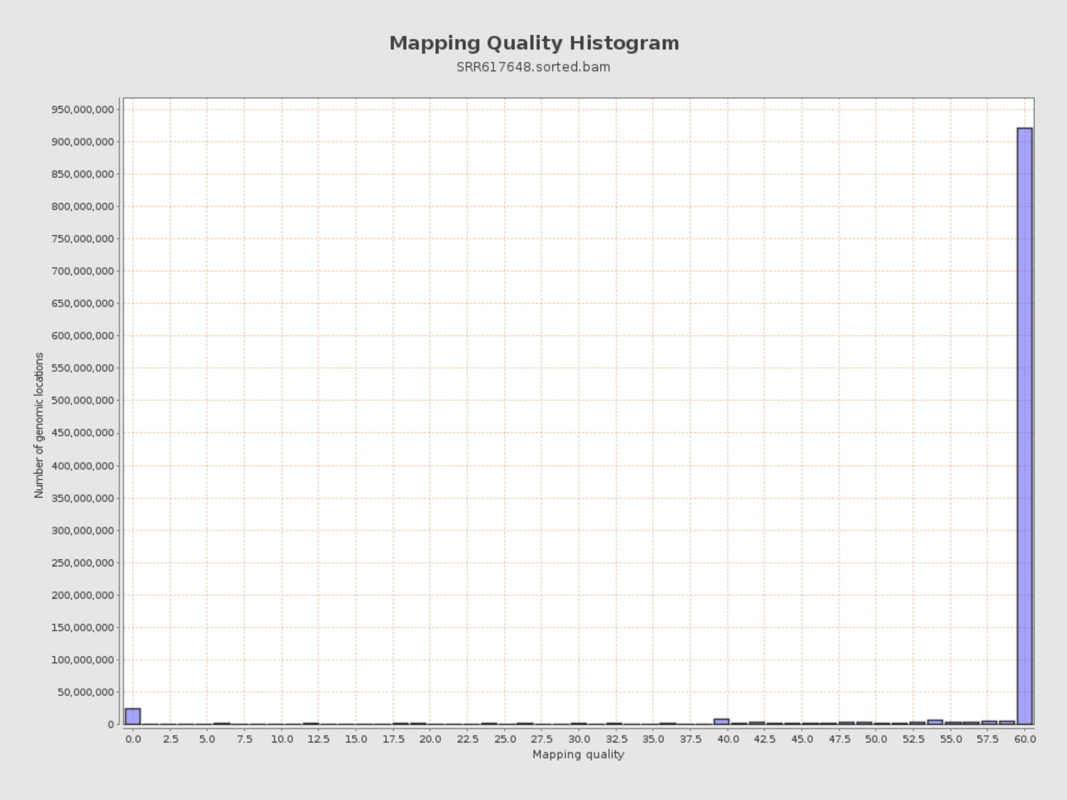
11. Results : Homopolymer Indels



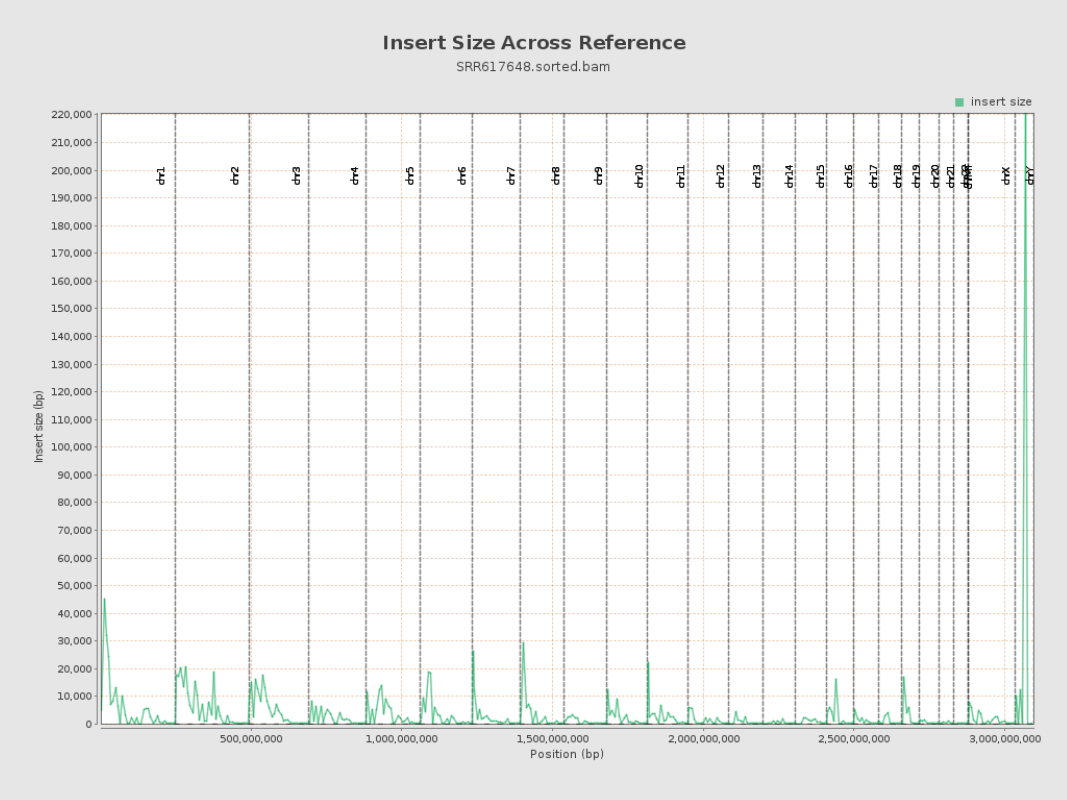
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram