Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 08:47:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617390.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_SRR617390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617390_1.fastq.gz SRR617390_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 08:47:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,236,032
Mapped reads	23,862,638 / 90.95%
Unmapped reads	2,373,394 / 9.05%
Mapped paired reads	23,862,638 / 90.95%
Mapped reads, first in pair	12,066,247 / 45.99%
Mapped reads, second in pair	11,796,391 / 44.96%
Mapped reads, both in pair	23,243,762 / 88.59%
Mapped reads, singletons	618,876 / 2.36%
Secondary alignments	0
Supplementary alignments	67,145 / 0.26%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	1,175,667 / 4.48%
Duplication rate	1.4%
Clipped reads	2,894,865 / 11.03%

2.2. ACGT Content

Number/percentage of A's	706,730,604 / 30.44%
Number/percentage of C's	457,906,078 / 19.72%
Number/percentage of T's	696,980,351 / 30.02%
Number/percentage of G's	459,658,406 / 19.8%
Number/percentage of N's	607,065 / 0.03%

GC Percentage	39.52%

2.3. Coverage

Mean	0.7503
Standard Deviation	7.6793

2.4. Mapping Quality

Mean Mapping Quality	53.28

2.5. Insert size

Mean	54,229.44
Standard Deviation	2,225,307.69
P25/Median/P75	168 / 205 / 263

2.6. Mismatches and indels

General error rate	1.52%
Mismatches	34,585,977
Insertions	235,901
Mapped reads with at least one insertion	0.96%
Deletions	281,131
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.84%

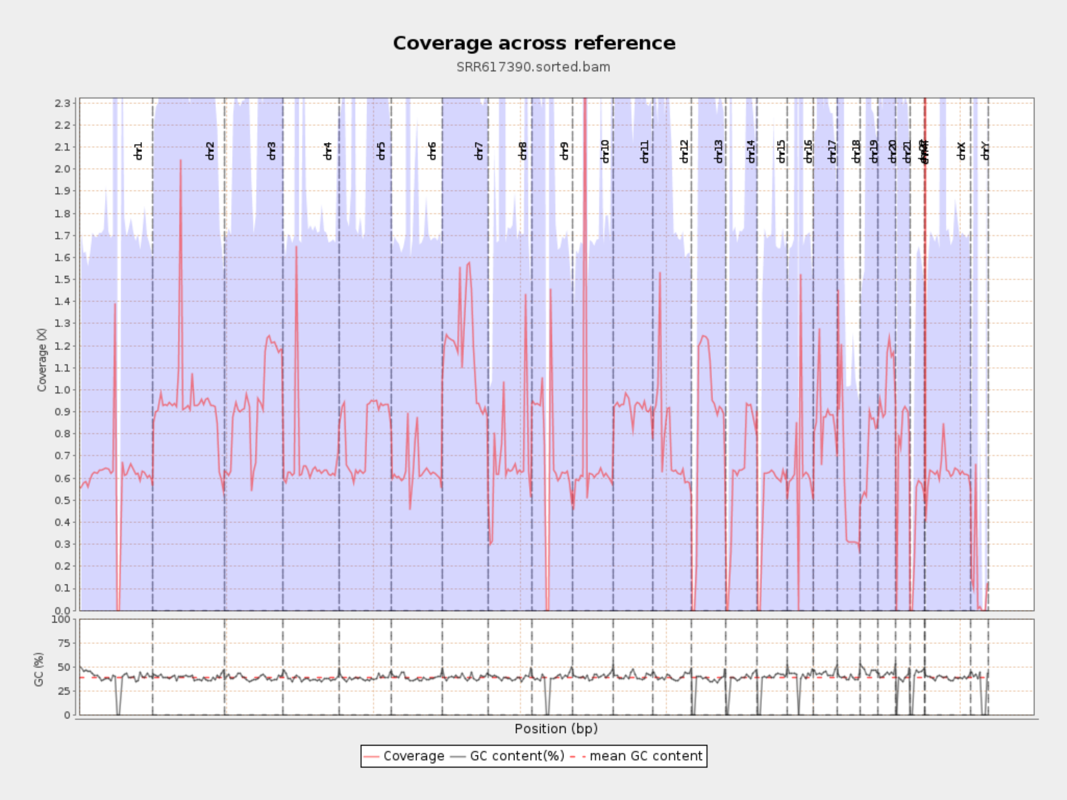
2.7. Chromosome stats

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

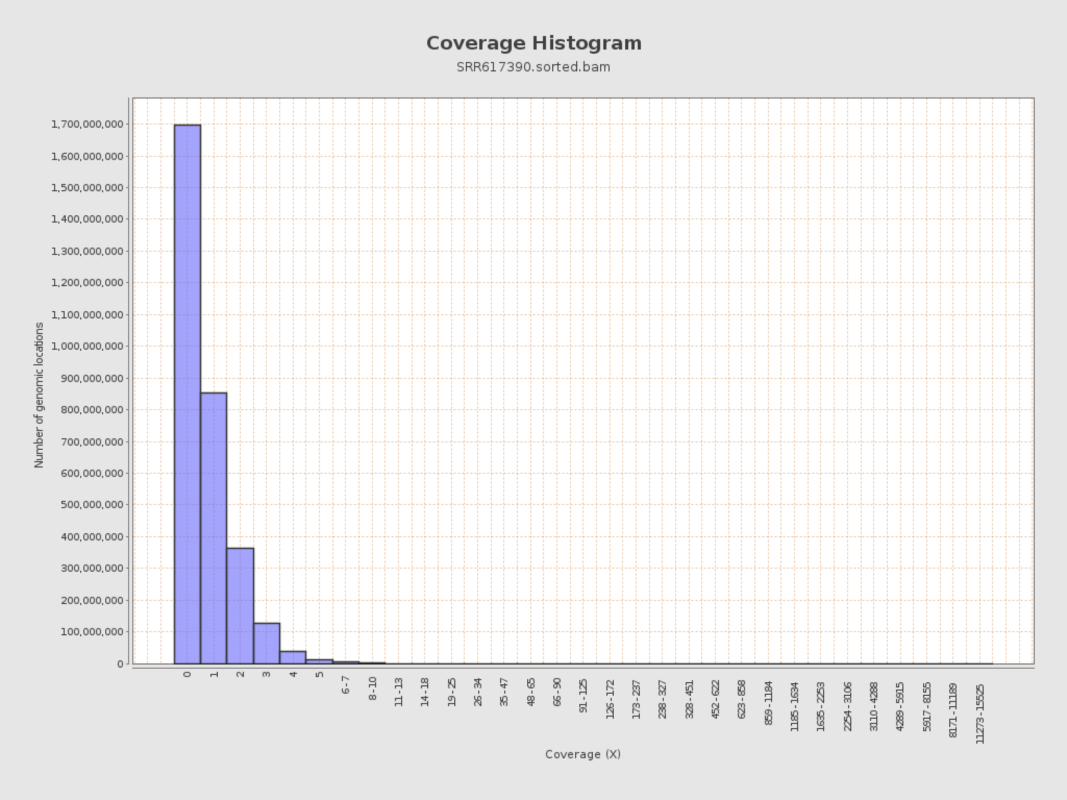
		bases	**coverage**	**deviation**
chr1	249250621	150405695	0.6034	15.8134
chr2	243199373	229670577	0.9444	6.7684
chr3	198022430	185847728	0.9385	1.2869
chr4	191154276	127914713	0.6692	6.8453
chr5	180915260	146466264	0.8096	1.249
chr6	171115067	109330081	0.6389	2.9399
chr7	159138663	188859965	1.1868	8.7868
chr8	146364022	98096327	0.6702	6.0079
chr9	141213431	97600453	0.6912	11.311
chr10	135534747	97802371	0.7216	16.049
chr11	135006516	124277573	0.9205	4.4086
chr12	133851895	102777325	0.7678	1.1794
chr13	115169878	101775750	0.8837	1.1404
chr14	107349540	67186650	0.6259	1.1754
chr15	102531392	52034533	0.5075	0.9142
chr16	90354753	57985067	0.6417	6.3842
chr17	81195210	71164009	0.8765	5.6064
chr18	78077248	41847200	0.536	11.6908
chr19	59128983	42143264	0.7127	7.5596
chr20	63025520	65733769	1.043	1.9577
chr21	48129895	36931627	0.7673	2.5734
chr22	51304566	20195628	0.3936	0.7851
chrMT	16571	1545962	93.2932	17.756
chrX	155270560	97163847	0.6258	2.3869

chrY	59373566	7789886	0.1312	6.1971

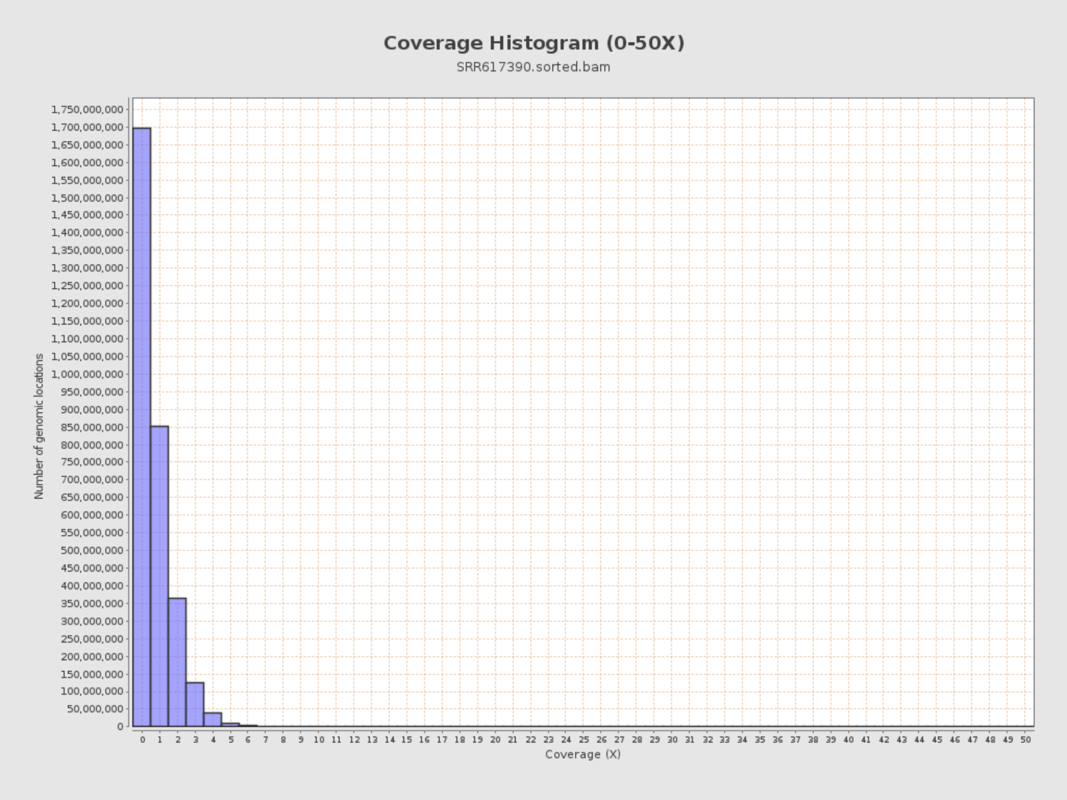
3. Results : Coverage across reference



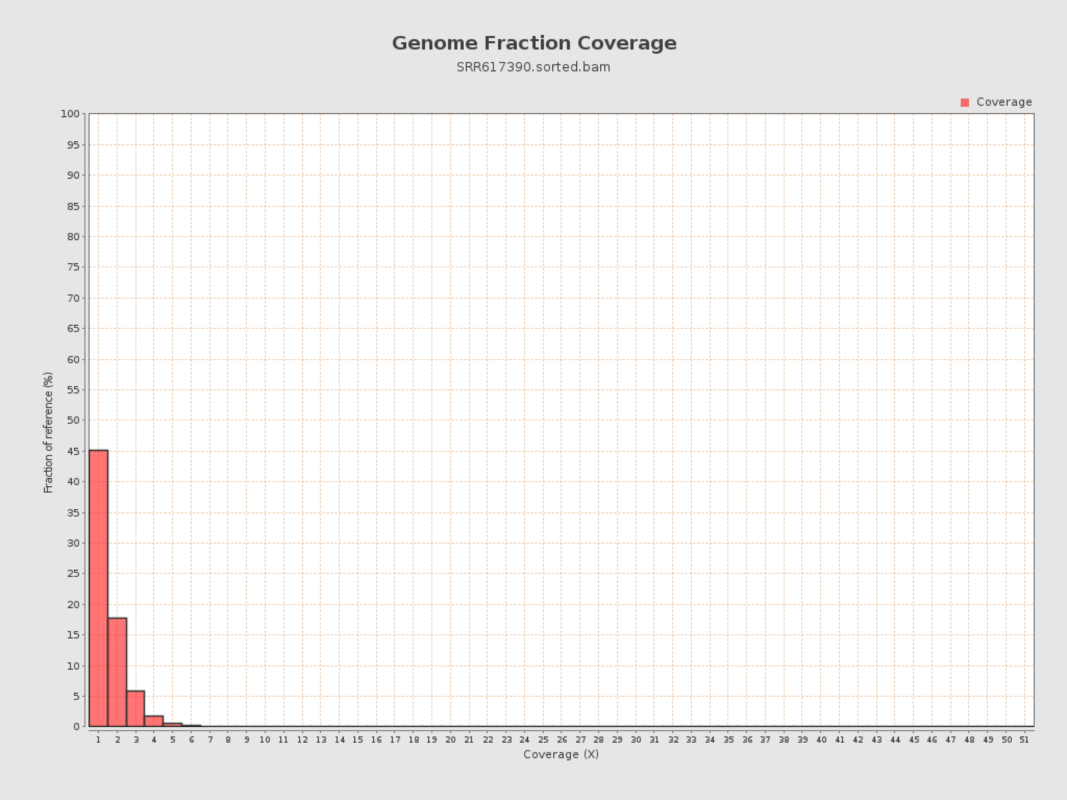
4. Results : Coverage Histogram



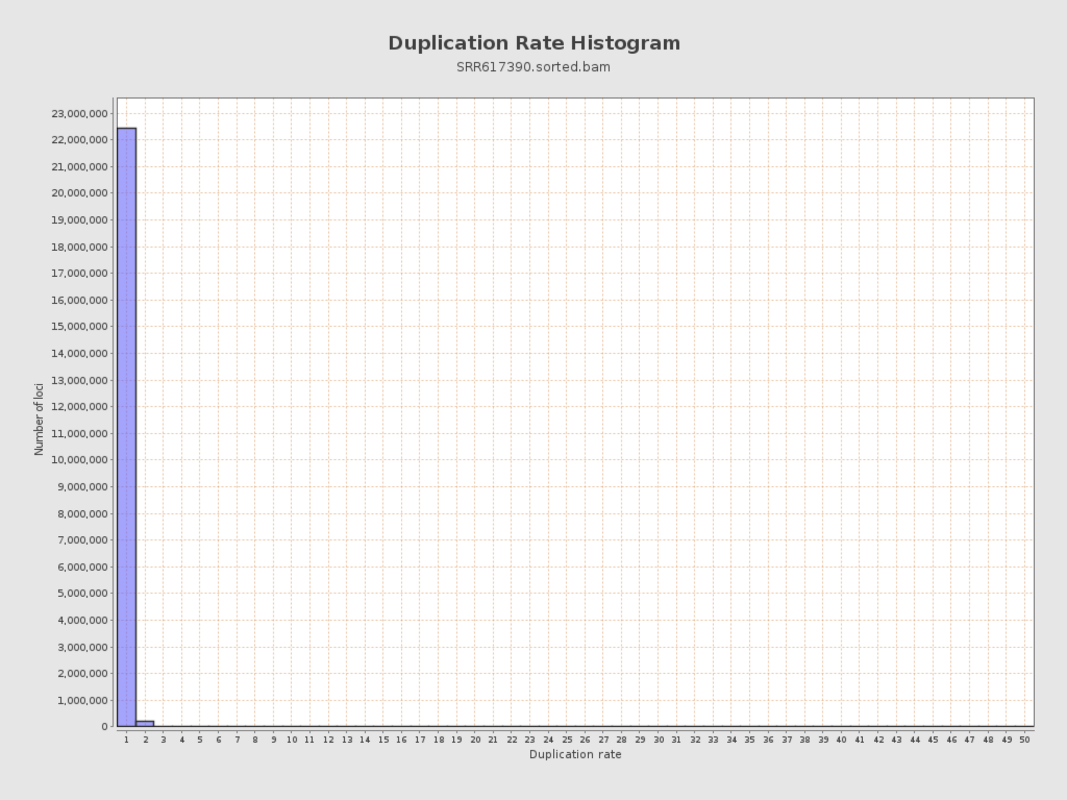
5. Results : Coverage Histogram (0-50X)



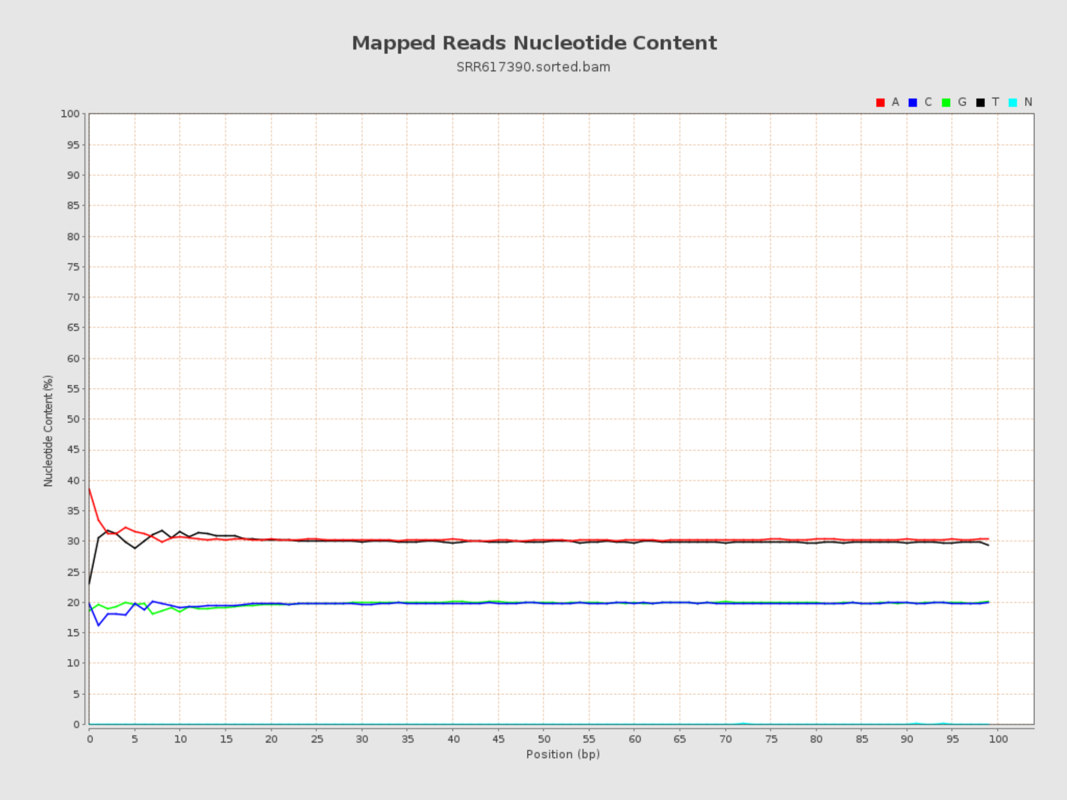
6. Results : Genome Fraction Coverage



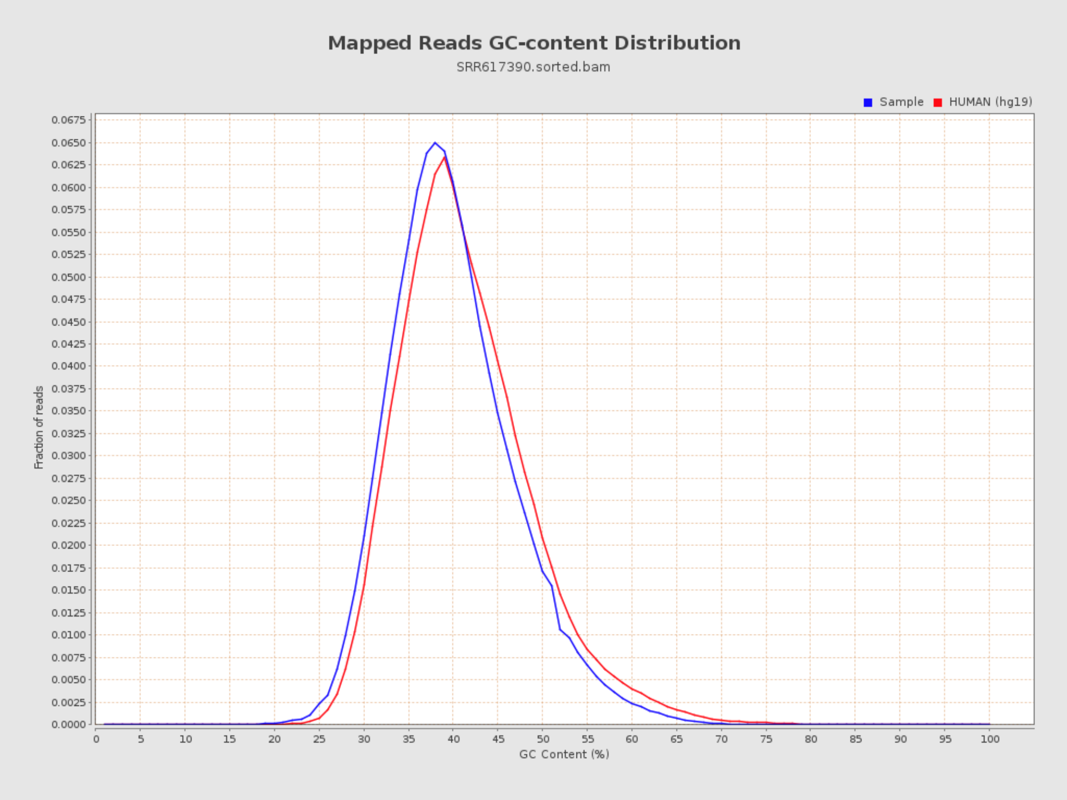
7. Results : Duplication Rate Histogram



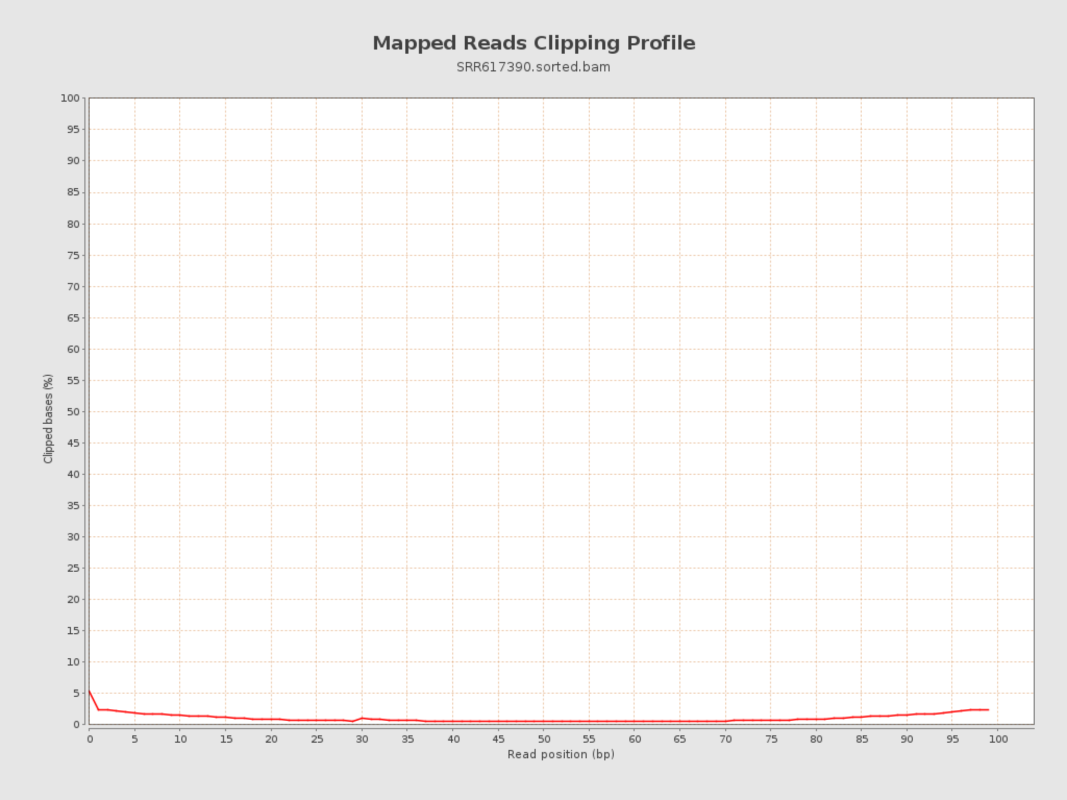
8. Results : Mapped Reads Nucleotide Content



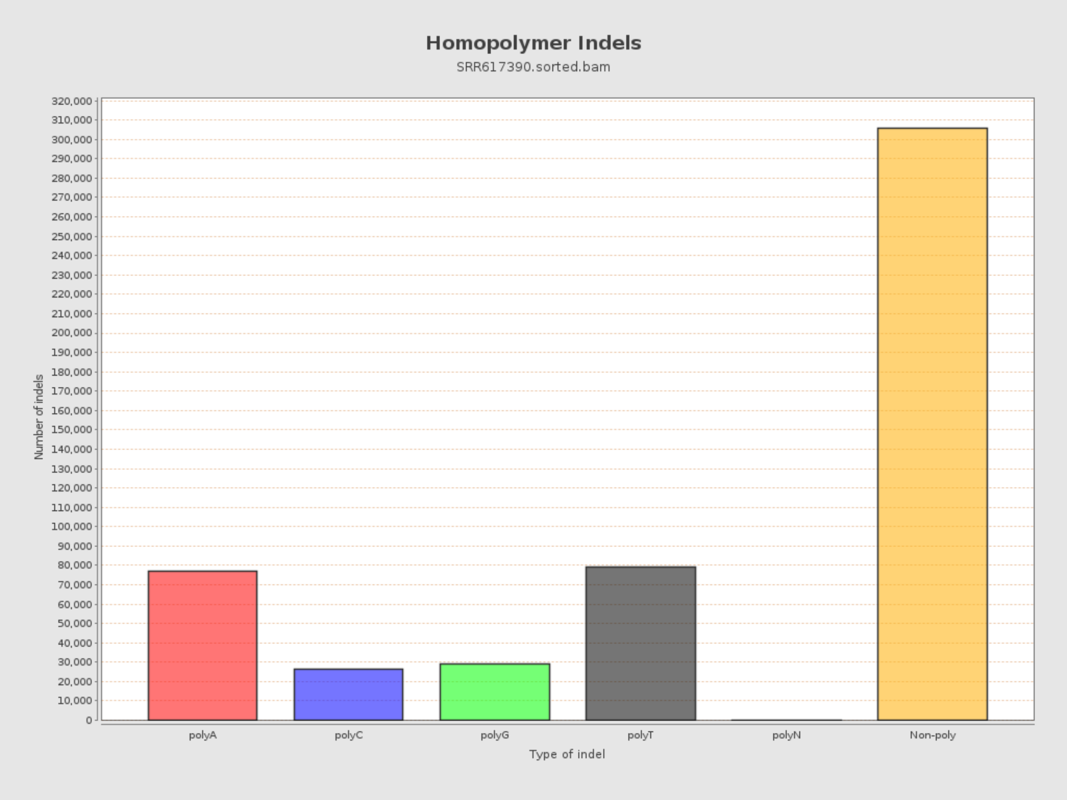
9. Results : Mapped Reads GC-content Distribution



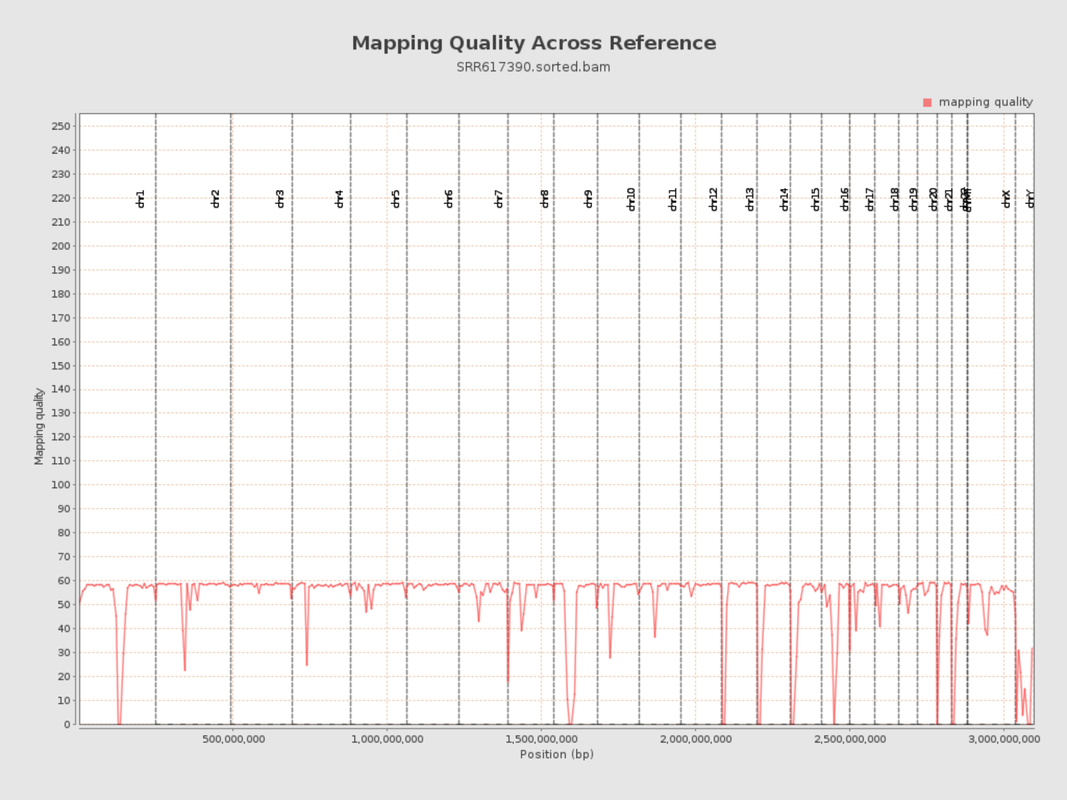
10. Results : Mapped Reads Clipping Profile



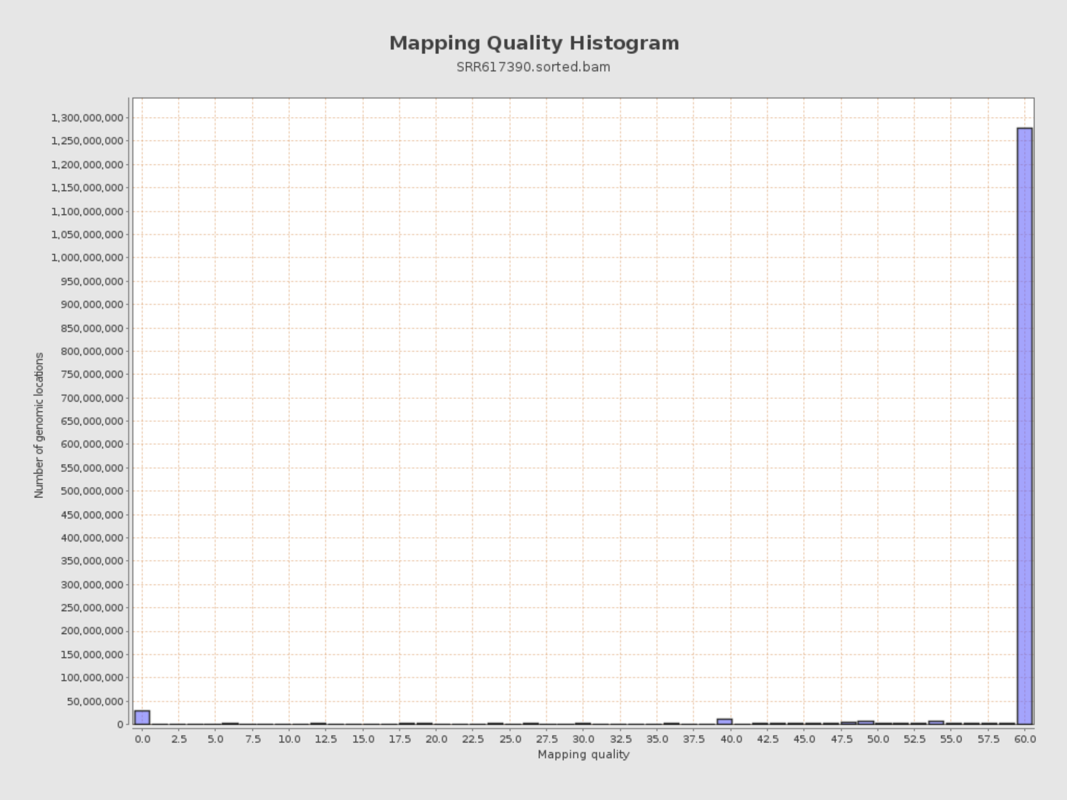
11. Results : Homopolymer Indels



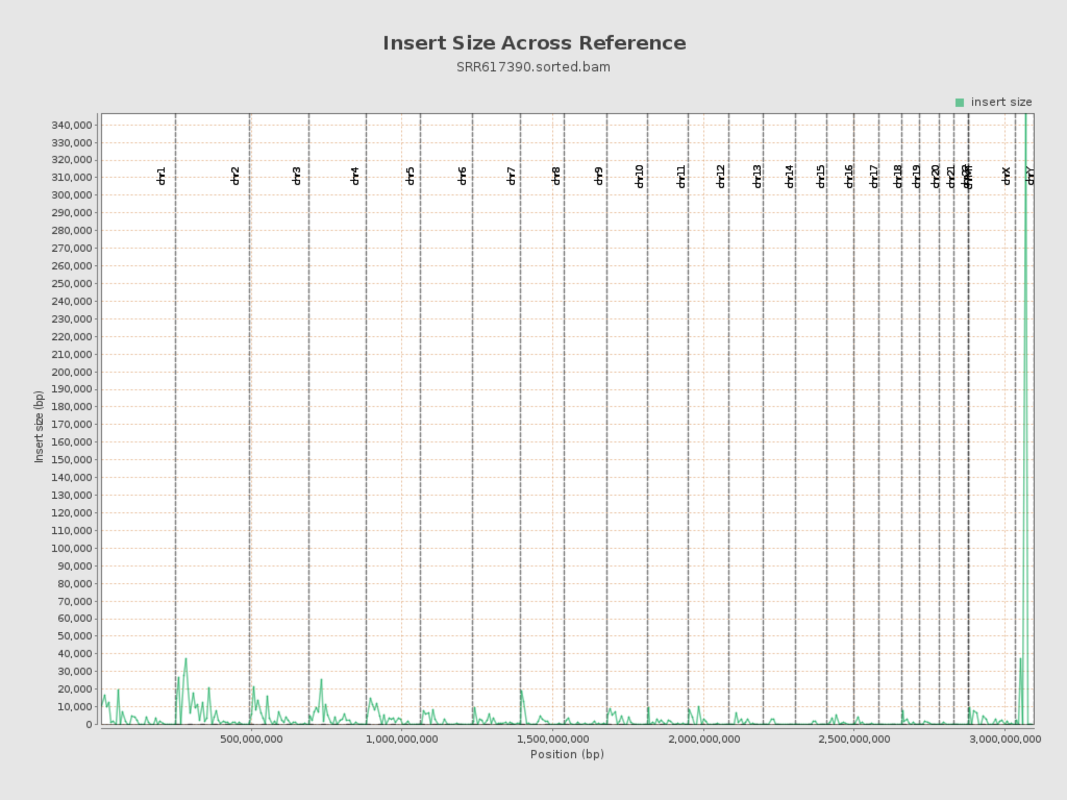
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram