Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 16:23:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617399.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_SRR617399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617399_1.fastq.gz SRR617399_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 16:23:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,632,280 / 92.6%
Unmapped reads	2,367,720 / 7.4%
Mapped paired reads	29,632,280 / 92.6%
Mapped reads, first in pair	14,958,640 / 46.75%
Mapped reads, second in pair	14,673,640 / 45.86%
Mapped reads, both in pair	29,020,774 / 90.69%
Mapped reads, singletons	611,506 / 1.91%
Secondary alignments	0
Supplementary alignments	471,376 / 1.47%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	1,379,218 / 4.31%
Duplication rate	4.16%
Clipped reads	3,676,246 / 11.49%

2.2. ACGT Content

Number/percentage of A's	867,110,657 / 29.81%
Number/percentage of C's	585,219,377 / 20.12%
Number/percentage of T's	859,083,208 / 29.53%
Number/percentage of G's	597,343,074 / 20.53%
Number/percentage of N's	473,137 / 0.02%

GC Percentage	40.65%

2.3. Coverage

Mean	0.94
Standard Deviation	2.8932

2.4. Mapping Quality

Mean Mapping Quality	53.83

2.5. Insert size

Mean	61,304.66
Standard Deviation	2,374,418.05
P25/Median/P75	172 / 212 / 277

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	30,462,655
Insertions	258,865
Mapped reads with at least one insertion	0.86%
Deletions	285,246
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.12%

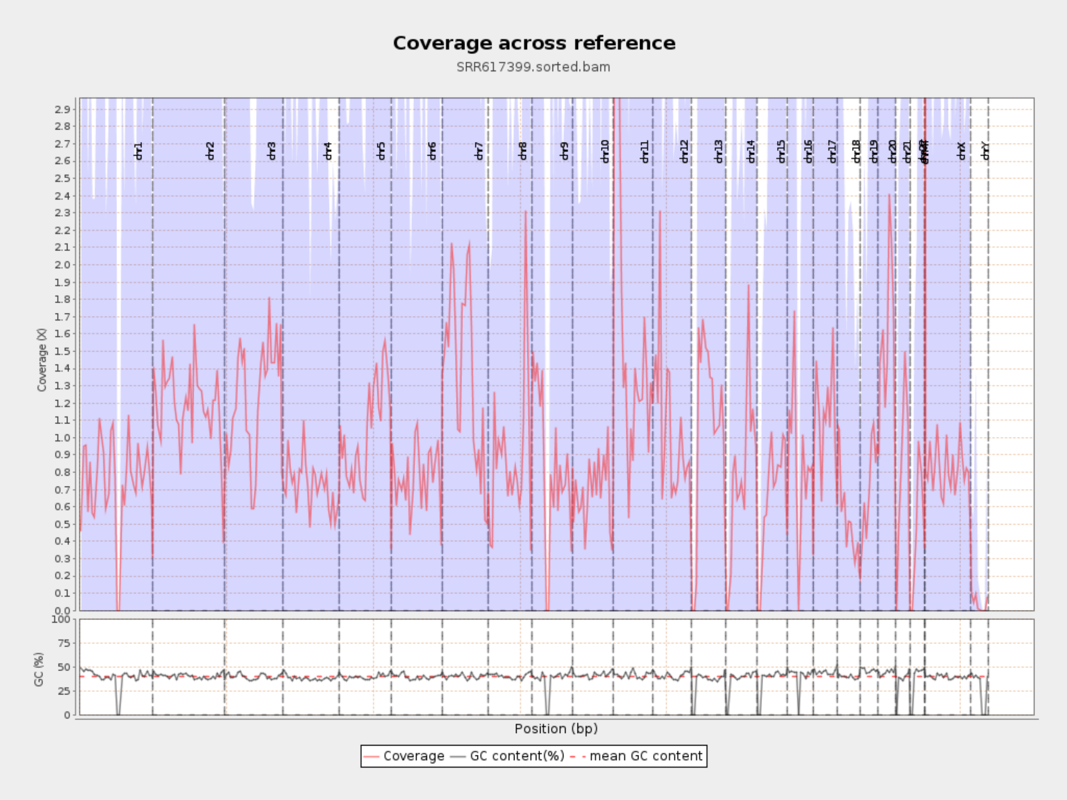
2.7. Chromosome stats

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

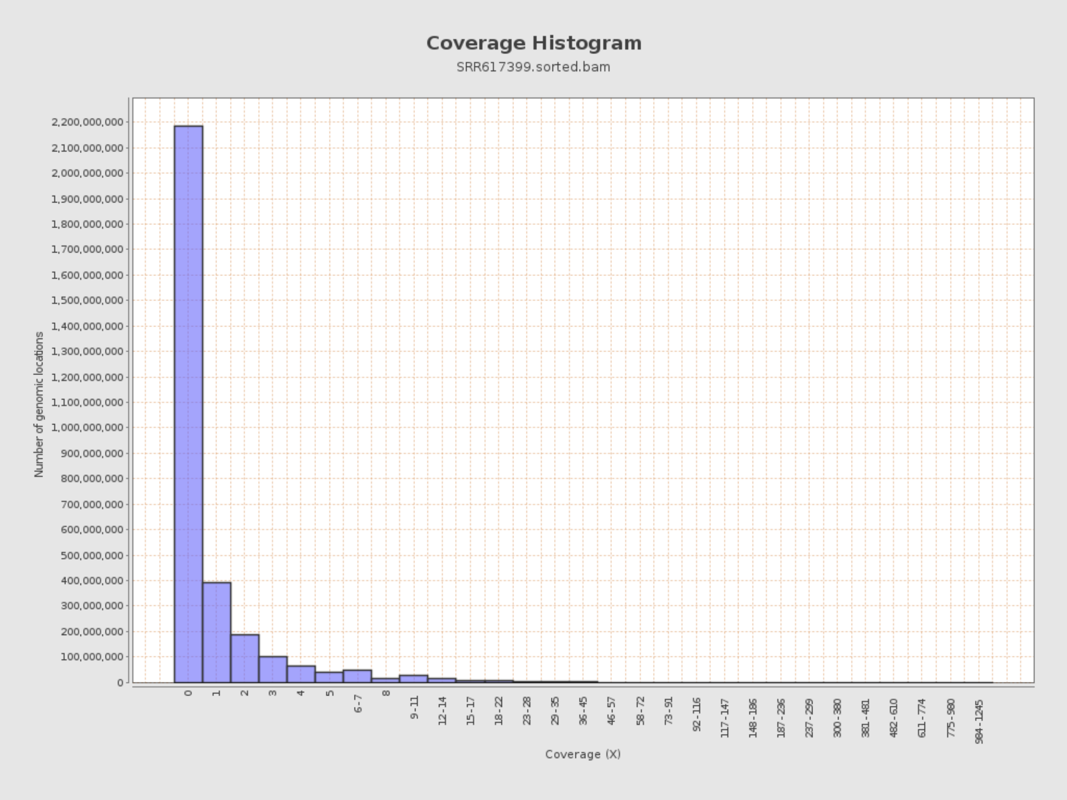
		bases	coverage	deviation
chr1	249250621	187208063	0.7511	2.7057
chr2	243199373	290168529	1.1931	3.0854
chr3	198022430	245337216	1.2389	3.3688
chr4	191154276	139338767	0.7289	2.2399
chr5	180915260	186054343	1.0284	2.8246
chr6	171115067	133183521	0.7783	2.5584
chr7	159138663	217984817	1.3698	3.1966
chr8	146364022	129107726	0.8821	3.2192
chr9	141213431	116033789	0.8217	2.5619
chr10	135534747	93298866	0.6884	2.3853
chr11	135006516	216160928	1.6011	3.7911
chr12	133851895	138474233	1.0345	2.7847
chr13	115169878	125776253	1.0921	2.7326
chr14	107349540	84386345	0.7861	2.8539
chr15	102531392	66832472	0.6518	2.3548
chr16	90354753	73611648	0.8147	3.2908
chr17	81195210	90314931	1.1123	3.6344
chr18	78077248	41611678	0.533	1.9794
chr19	59128983	41988254	0.7101	2.3217
chr20	63025520	99400065	1.5771	4.6991
chr21	48129895	39790639	0.8267	2.4852
chr22	51304566	23667864	0.4613	2.064
chrMT	16571	184378	11.1265	5.2356
chrX	155270560	127626696	0.822	2.531

chrY	59373566	2327925	0.0392	0.6084

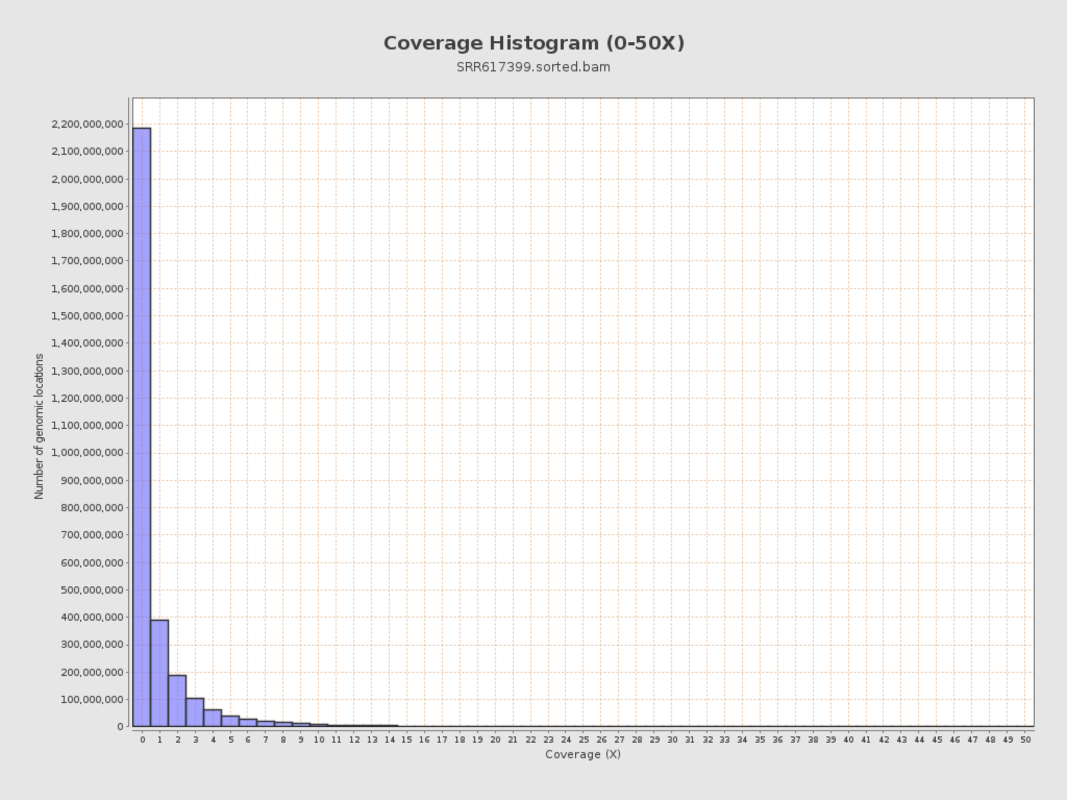
3. Results : Coverage across reference



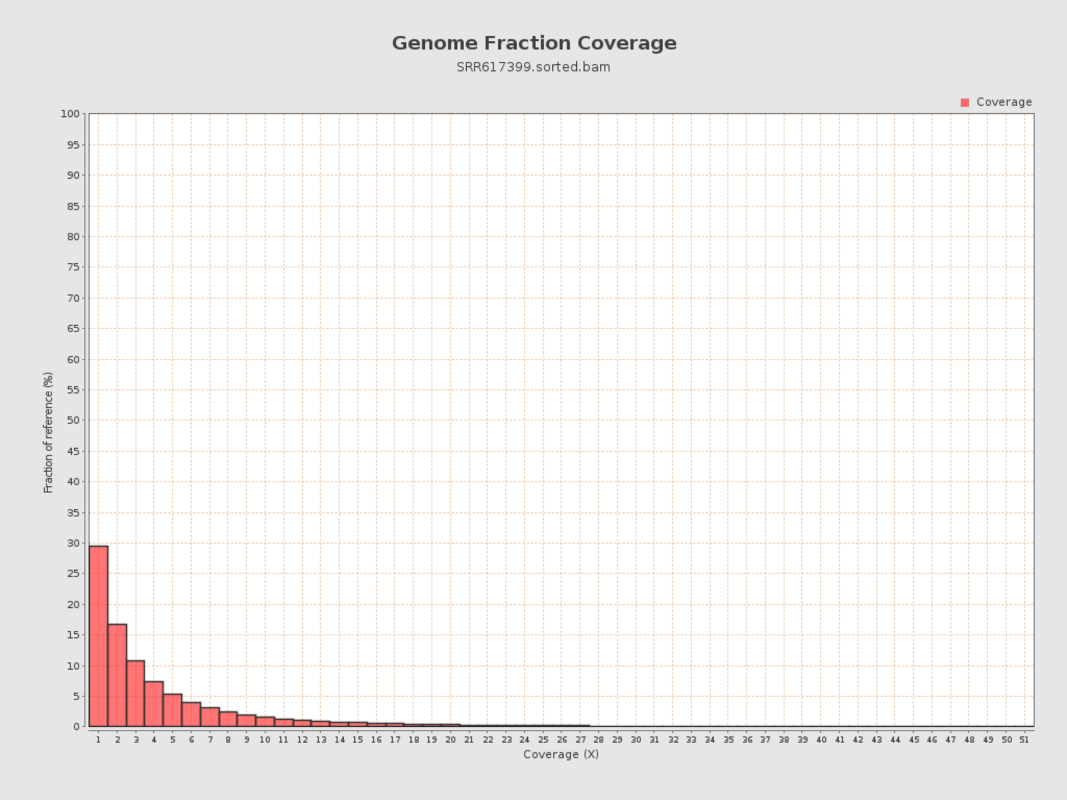
4. Results : Coverage Histogram



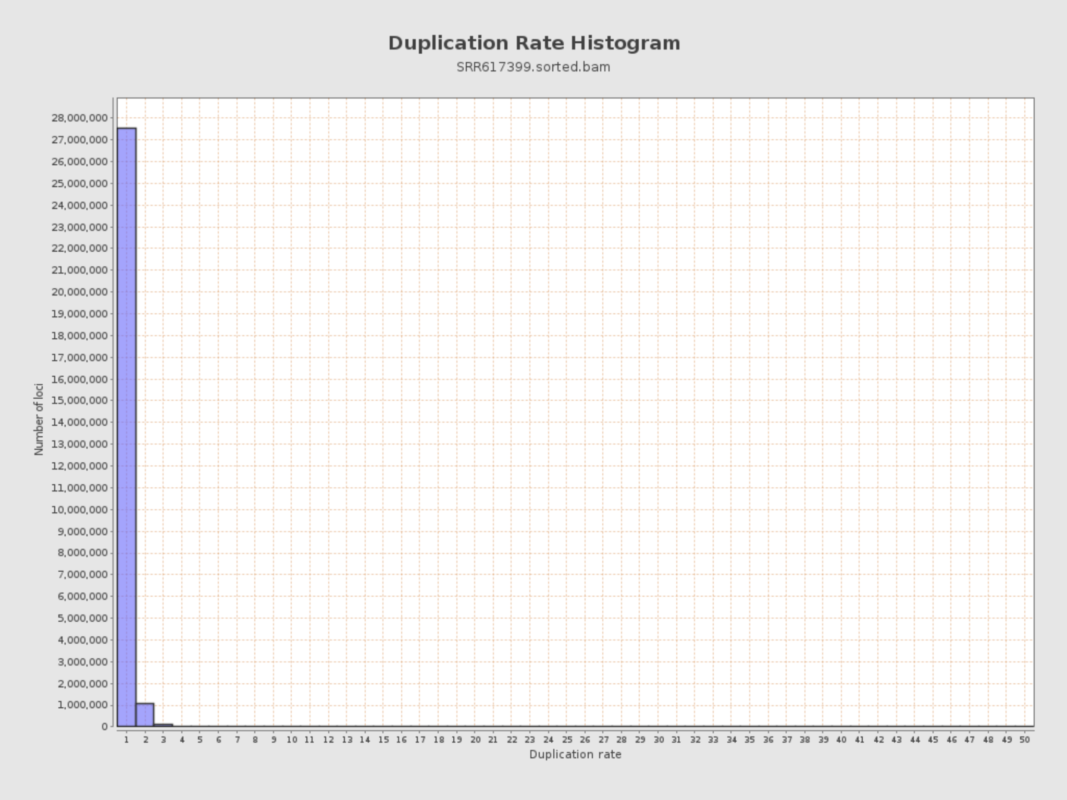
5. Results : Coverage Histogram (0-50X)



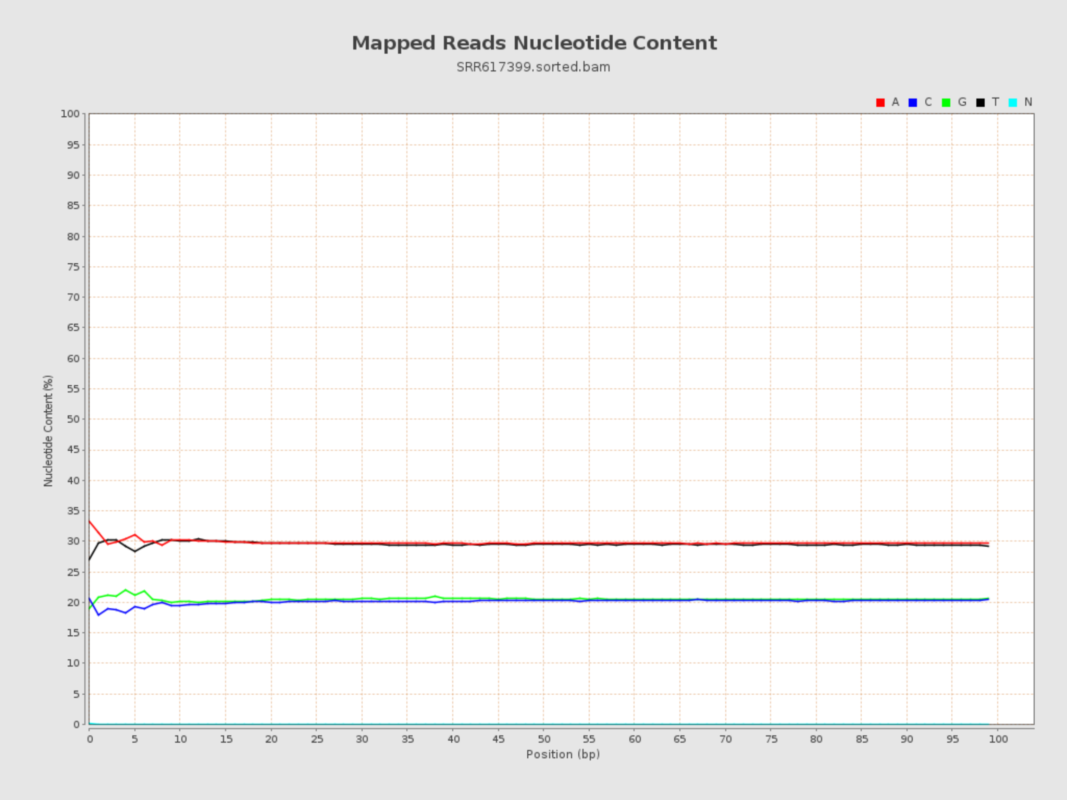
6. Results : Genome Fraction Coverage



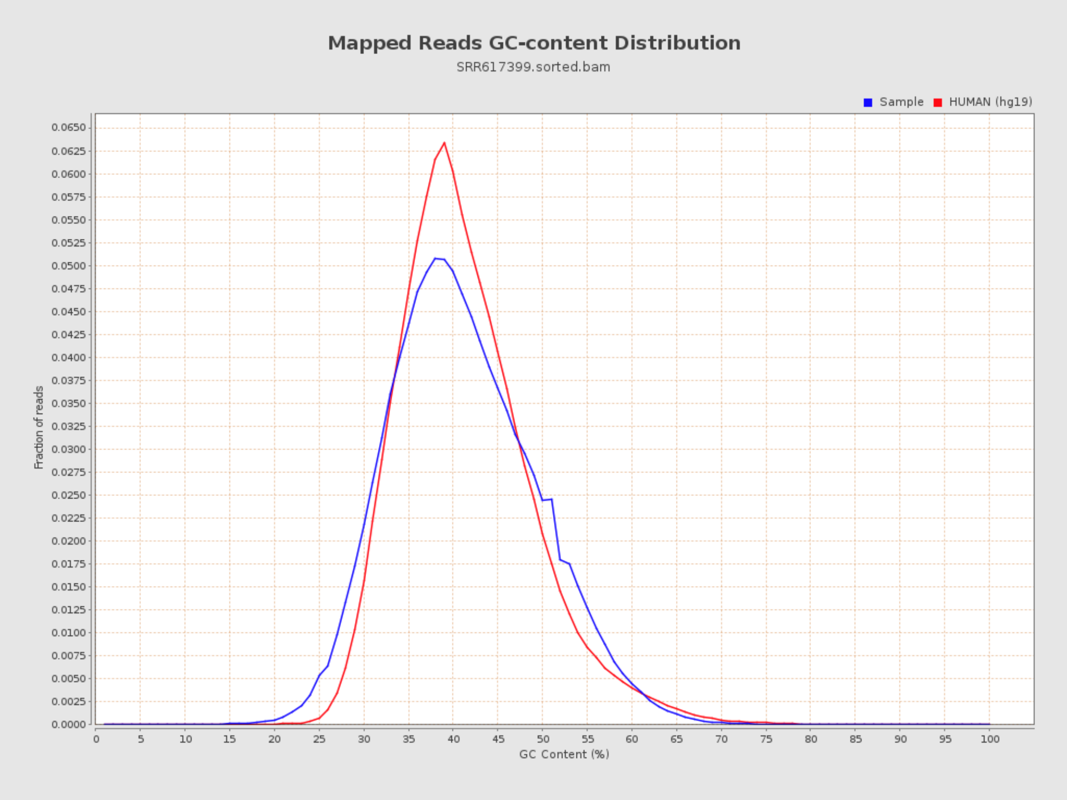
7. Results : Duplication Rate Histogram



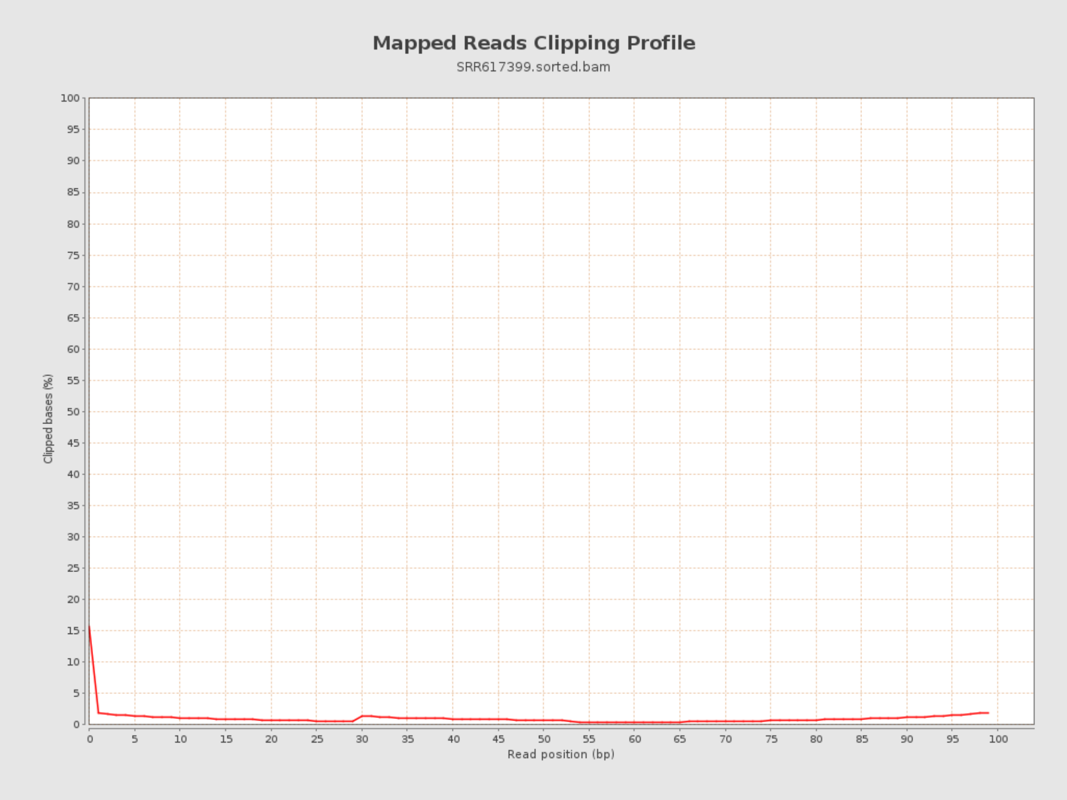
8. Results : Mapped Reads Nucleotide Content



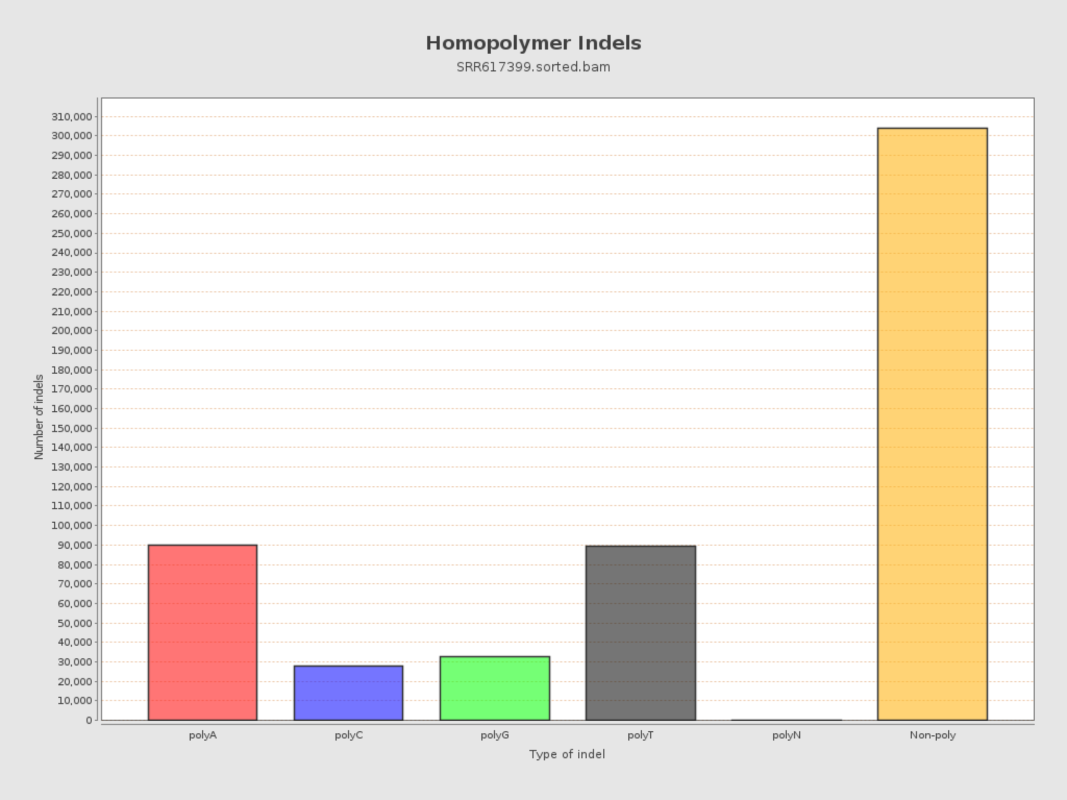
9. Results : Mapped Reads GC-content Distribution



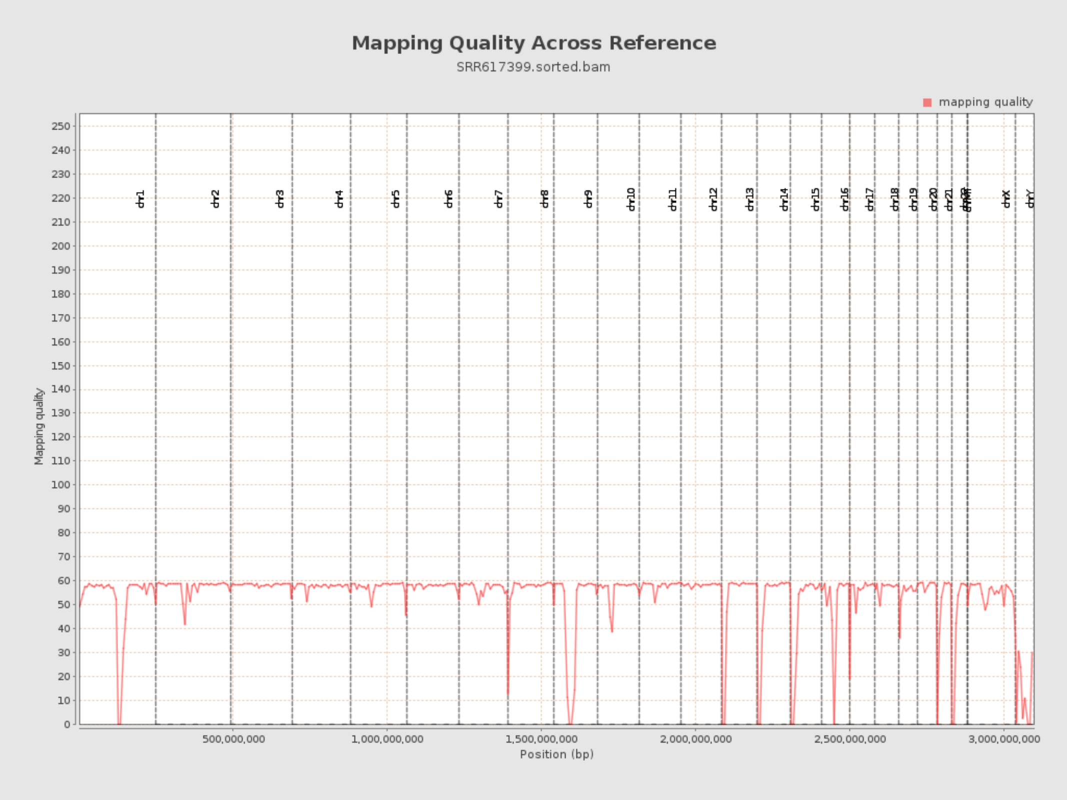
10. Results : Mapped Reads Clipping Profile



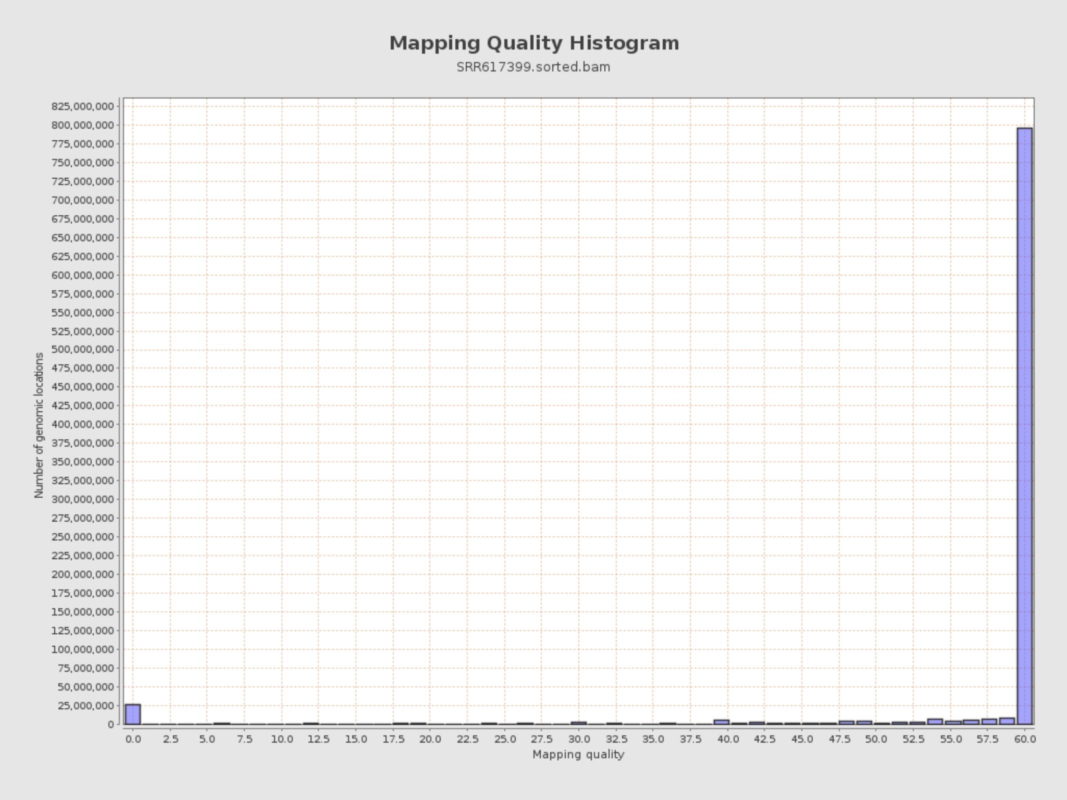
11. Results : Homopolymer Indels



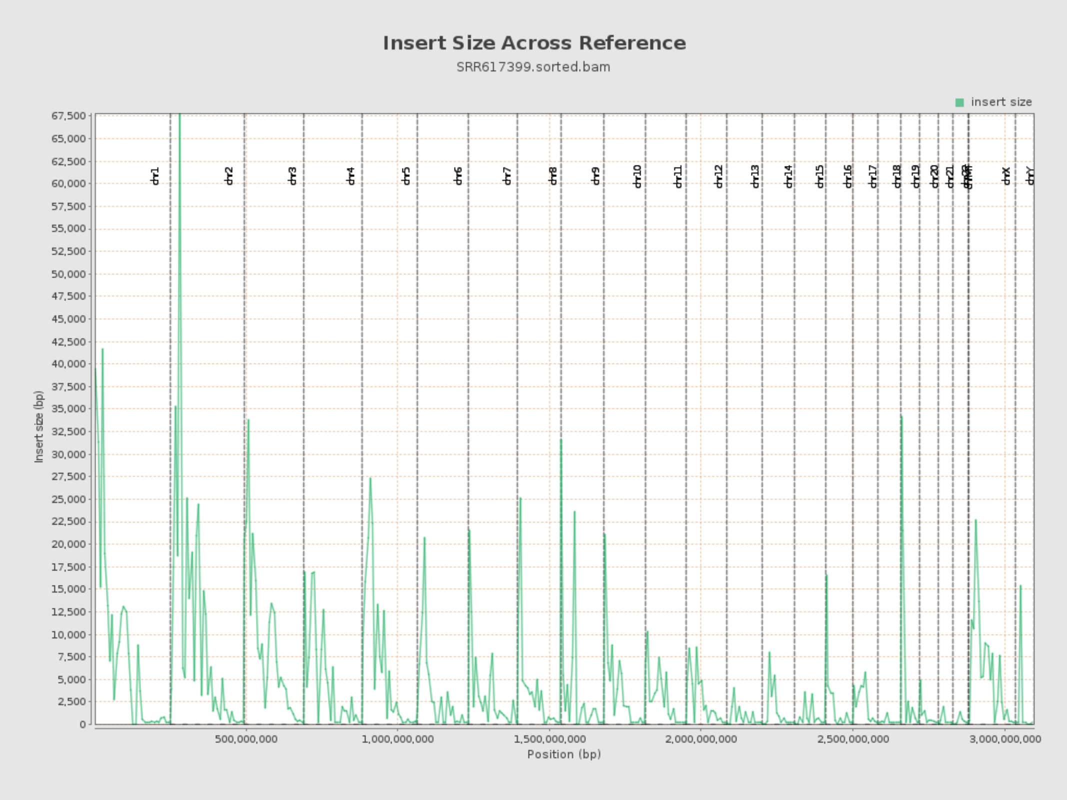
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram