Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 11:17:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617393.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_SRR617393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617393_1.fastq.gz SRR617393_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 11:17:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,743,712 / 86.7%
Unmapped reads	4,256,288 / 13.3%
Mapped paired reads	27,743,712 / 86.7%
Mapped reads, first in pair	14,081,403 / 44%
Mapped reads, second in pair	13,662,309 / 42.69%
Mapped reads, both in pair	26,967,420 / 84.27%
Mapped reads, singletons	776,292 / 2.43%
Secondary alignments	0
Supplementary alignments	378,337 / 1.18%
Read min/max/mean length	30 / 100 / 100.49
Duplicated reads (estimated)	1,174,940 / 3.67%
Duplication rate	3.89%
Clipped reads	3,687,681 / 11.52%

2.2. ACGT Content

Number/percentage of A's	812,369,850 / 29.94%
Number/percentage of C's	542,047,174 / 19.98%
Number/percentage of T's	801,248,965 / 29.53%
Number/percentage of G's	555,640,225 / 20.48%
Number/percentage of N's	1,995,585 / 0.07%

GC Percentage	40.46%

2.3. Coverage

Mean	0.8767
Standard Deviation	2.6798

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	48,123.59
Standard Deviation	2,095,551.58
P25/Median/P75	168 / 205 / 263

2.6. Mismatches and indels

General error rate	1.73%
Mismatches	46,490,639
Insertions	247,442
Mapped reads with at least one insertion	0.88%
Deletions	258,514
Mapped reads with at least one deletion	0.91%
Homopolymer indels	43.05%

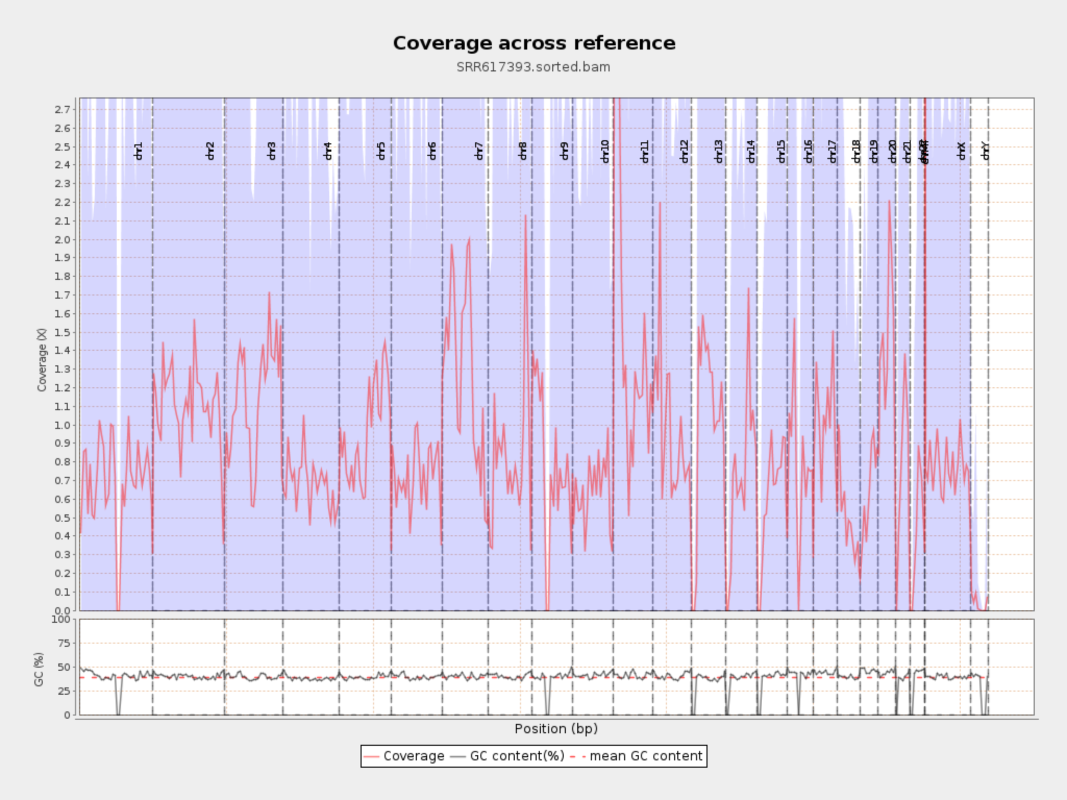
2.7. Chromosome stats

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

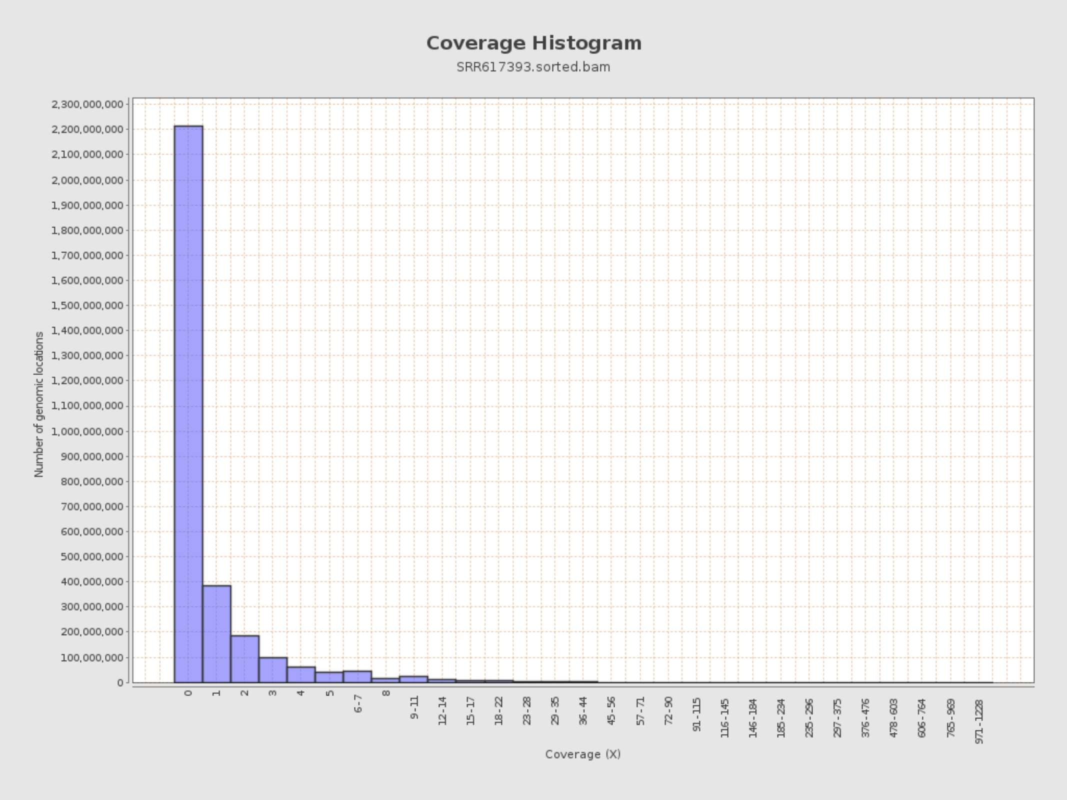
		bases	**coverage**	**deviation**
chr1	249250621	174208522	0.6989	2.5174
chr2	243199373	271375398	1.1159	2.8333
chr3	198022430	229440104	1.1587	3.1085
chr4	191154276	132084451	0.691	2.1199
chr5	180915260	174389116	0.9639	2.653
chr6	171115067	125076556	0.7309	2.3966
chr7	159138663	203208865	1.2769	2.9765
chr8	146364022	120467858	0.8231	2.9708
chr9	141213431	108443743	0.7679	2.3949
chr10	135534747	86752197	0.6401	2.1944
chr11	135006516	201012847	1.4889	3.5286
chr12	133851895	129291151	0.9659	2.5522
chr13	115169878	118681184	1.0305	2.5703
chr14	107349540	78598125	0.7322	2.6515
chr15	102531392	62105335	0.6057	2.1624
chr16	90354753	67593726	0.7481	3.0089
chr17	81195210	82434947	1.0153	3.3217
chr18	78077248	39087800	0.5006	1.8395
chr19	59128983	37816950	0.6396	2.0986
chr20	63025520	91139102	1.4461	4.2837
chr21	48129895	37082199	0.7705	2.3229
chr22	51304566	21465453	0.4184	1.8829
chrMT	16571	170462	10.2868	4.943
chrX	155270560	119753060	0.7713	2.3584

chrY	59373566	2194681	0.037	0.5046

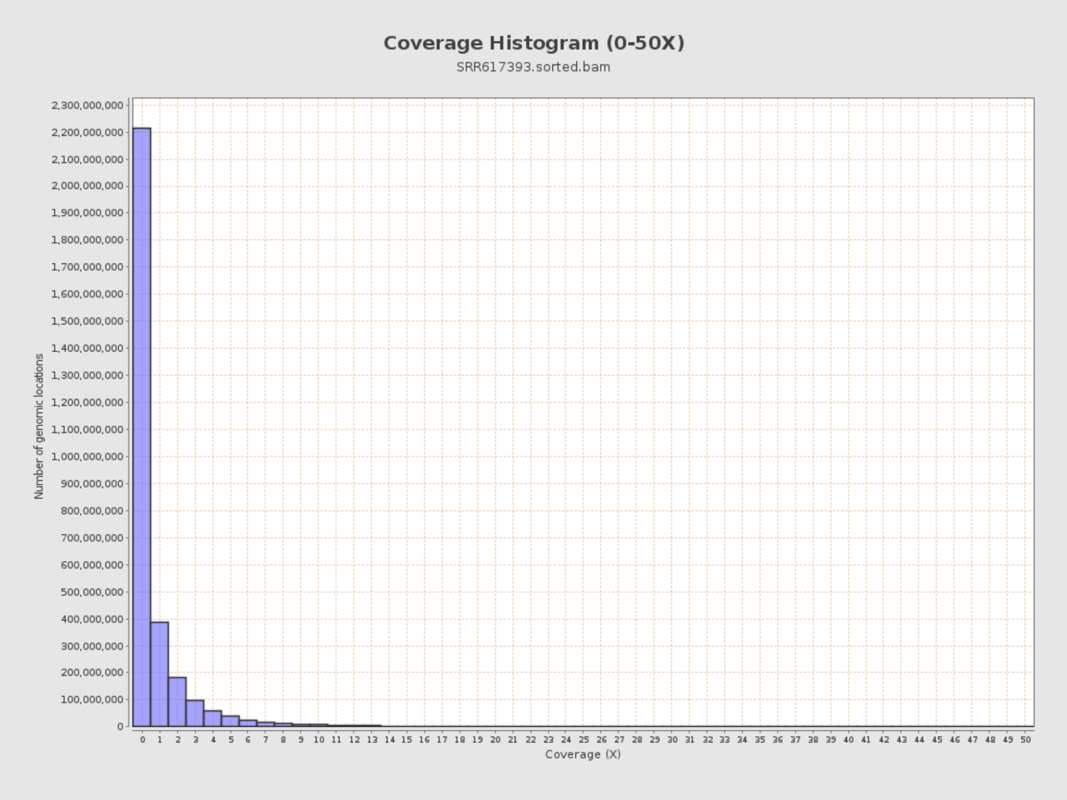
3. Results : Coverage across reference



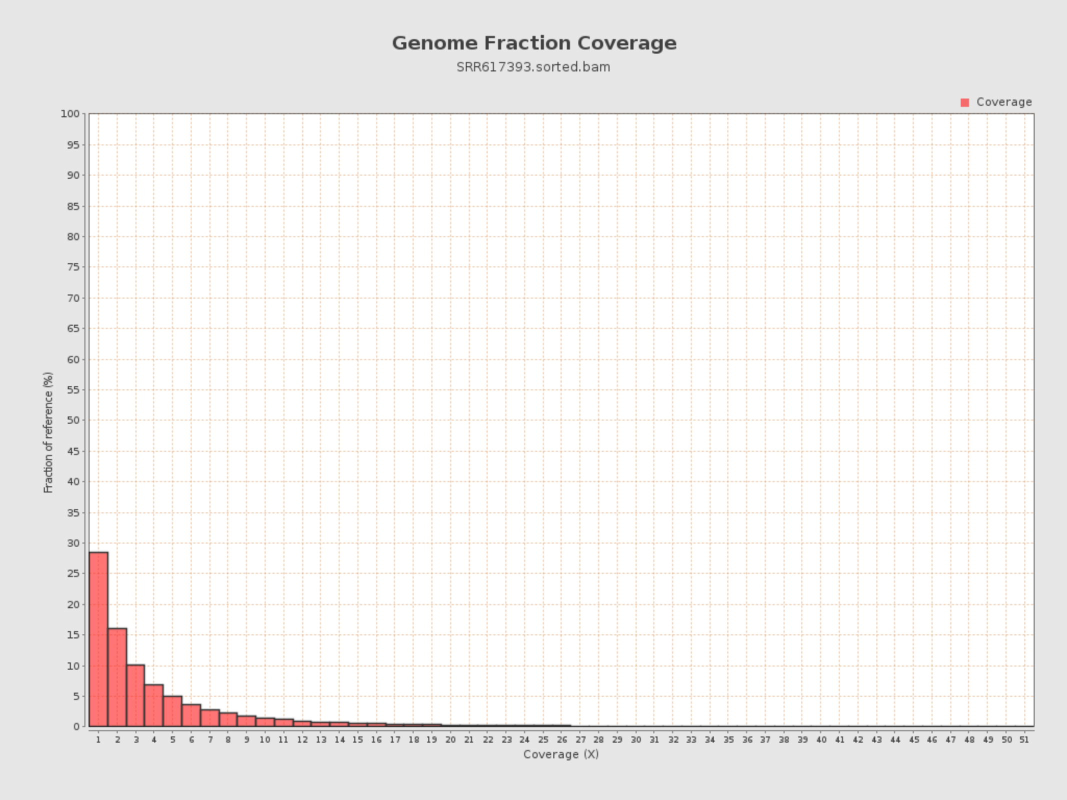
4. Results : Coverage Histogram



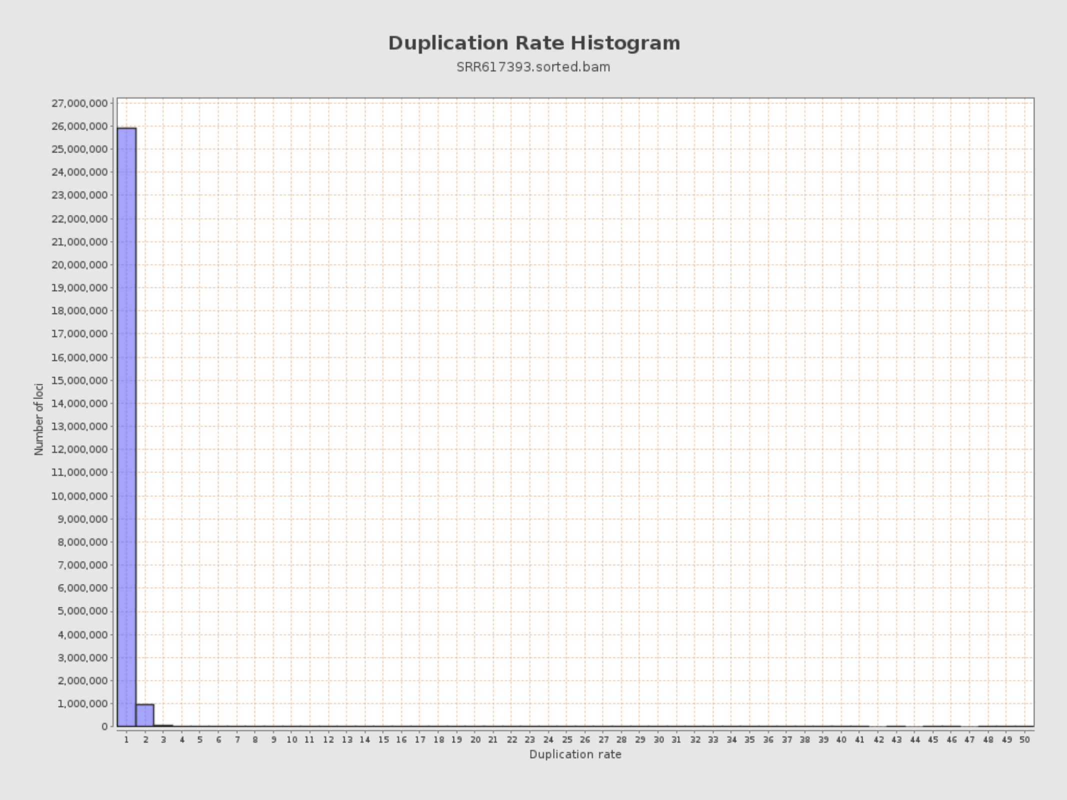
5. Results : Coverage Histogram (0-50X)



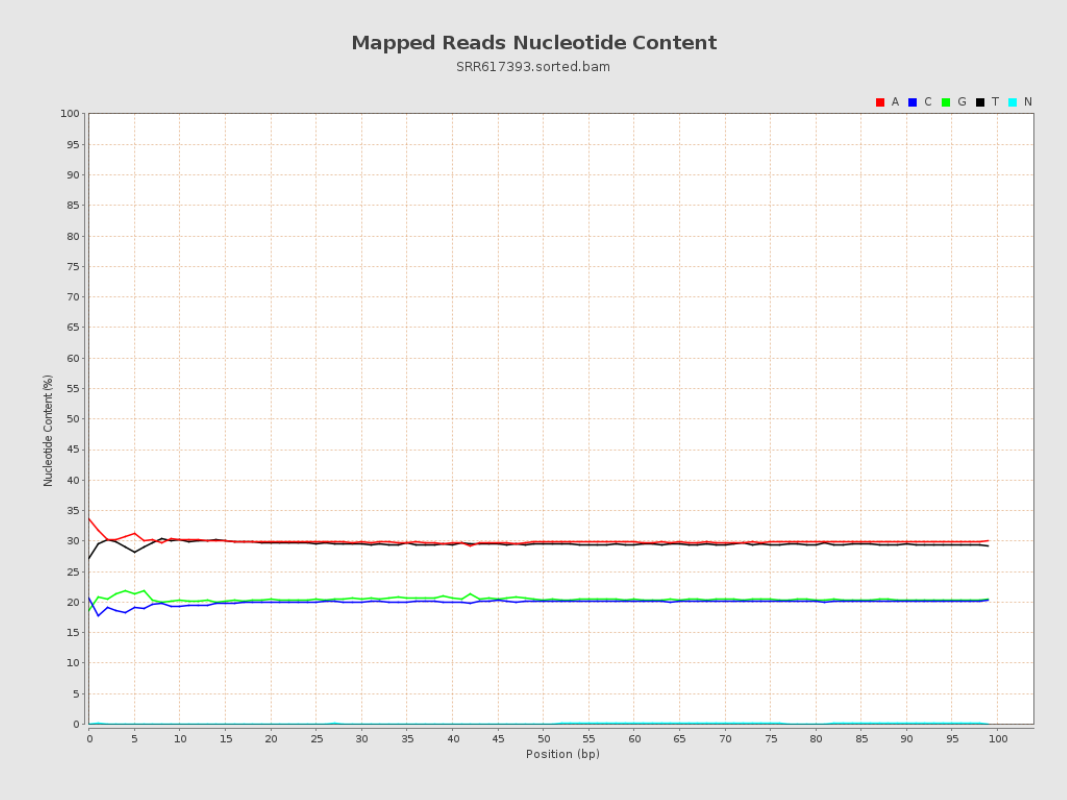
6. Results : Genome Fraction Coverage



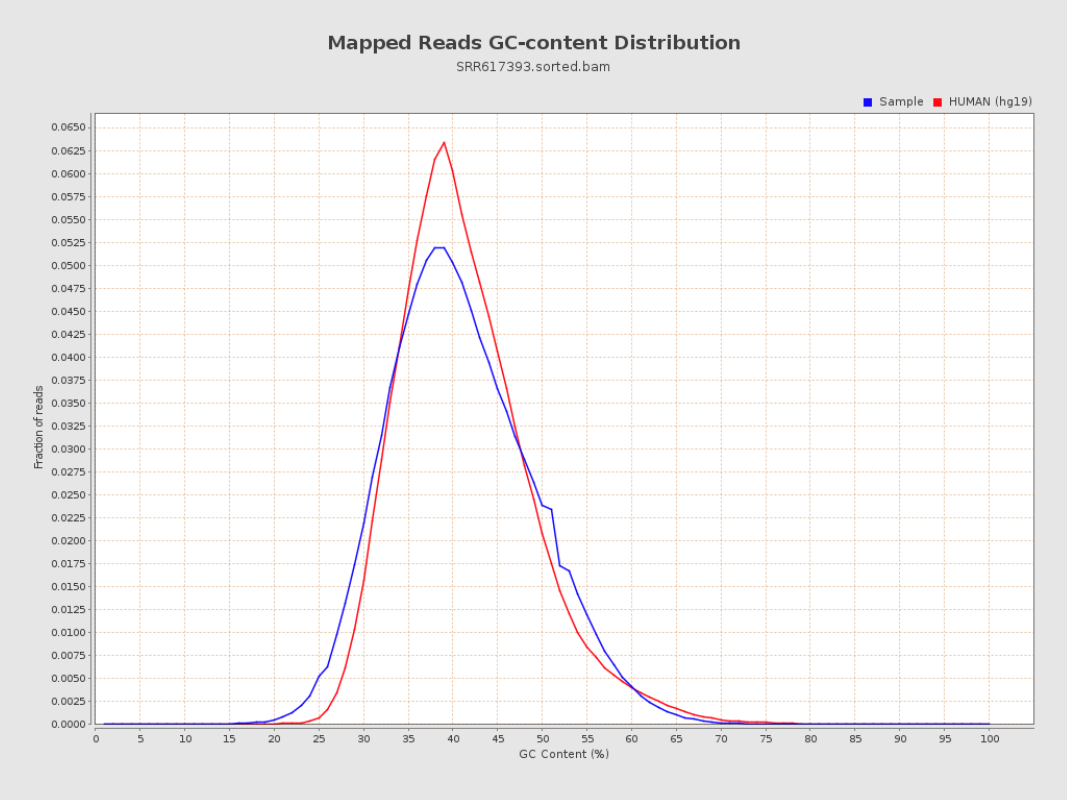
7. Results : Duplication Rate Histogram



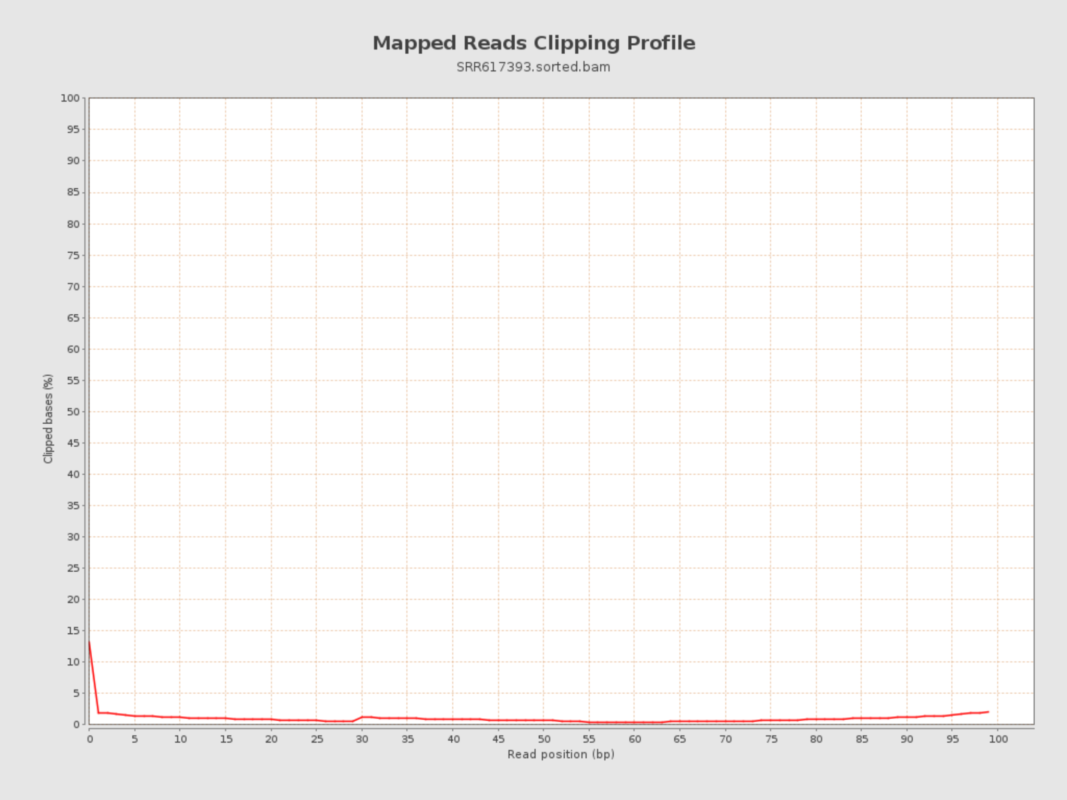
8. Results : Mapped Reads Nucleotide Content



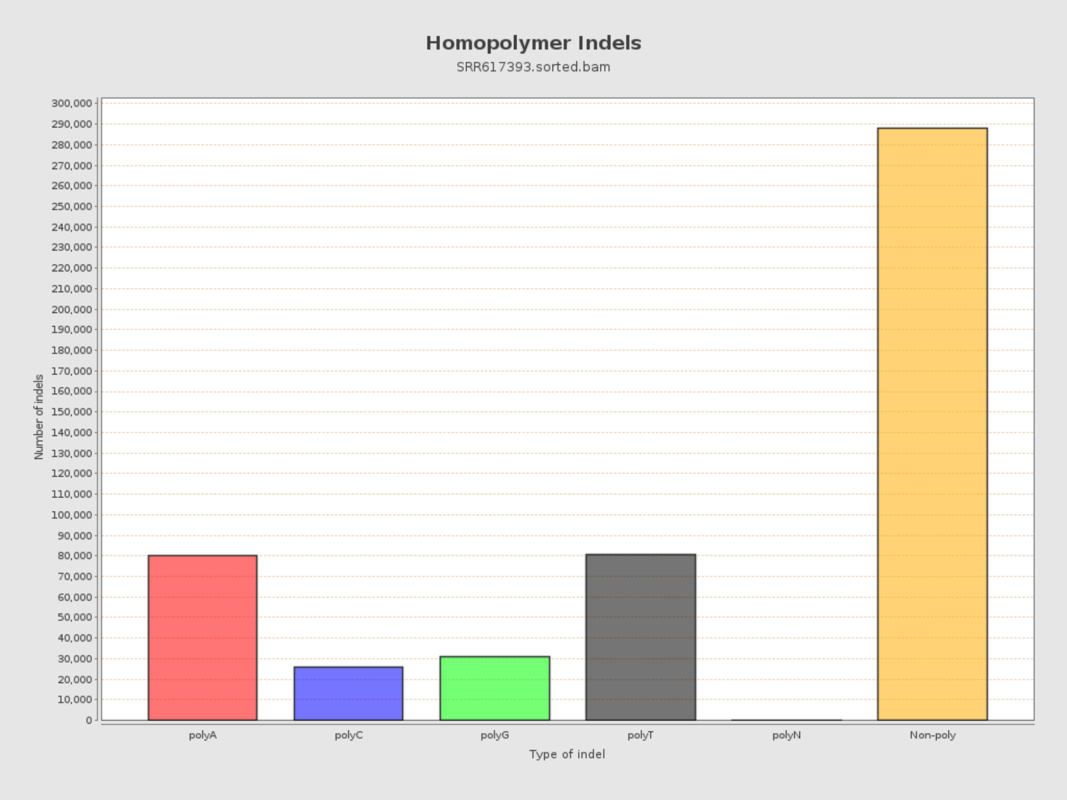
9. Results : Mapped Reads GC-content Distribution



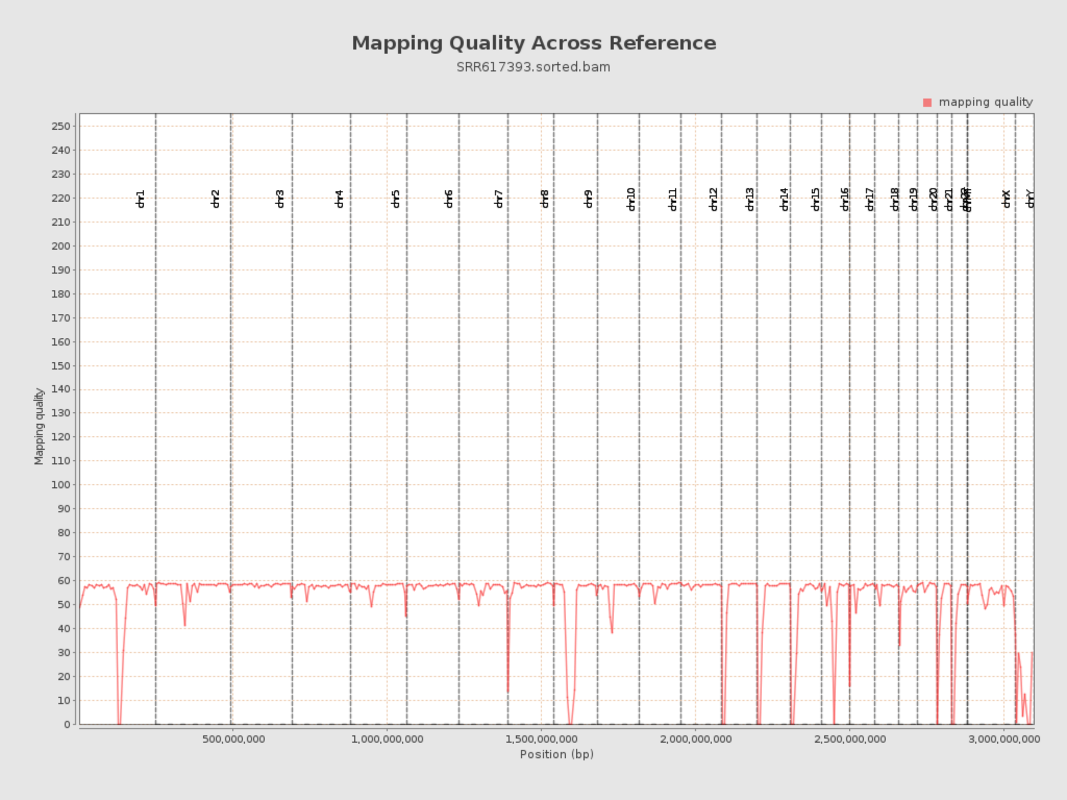
10. Results : Mapped Reads Clipping Profile



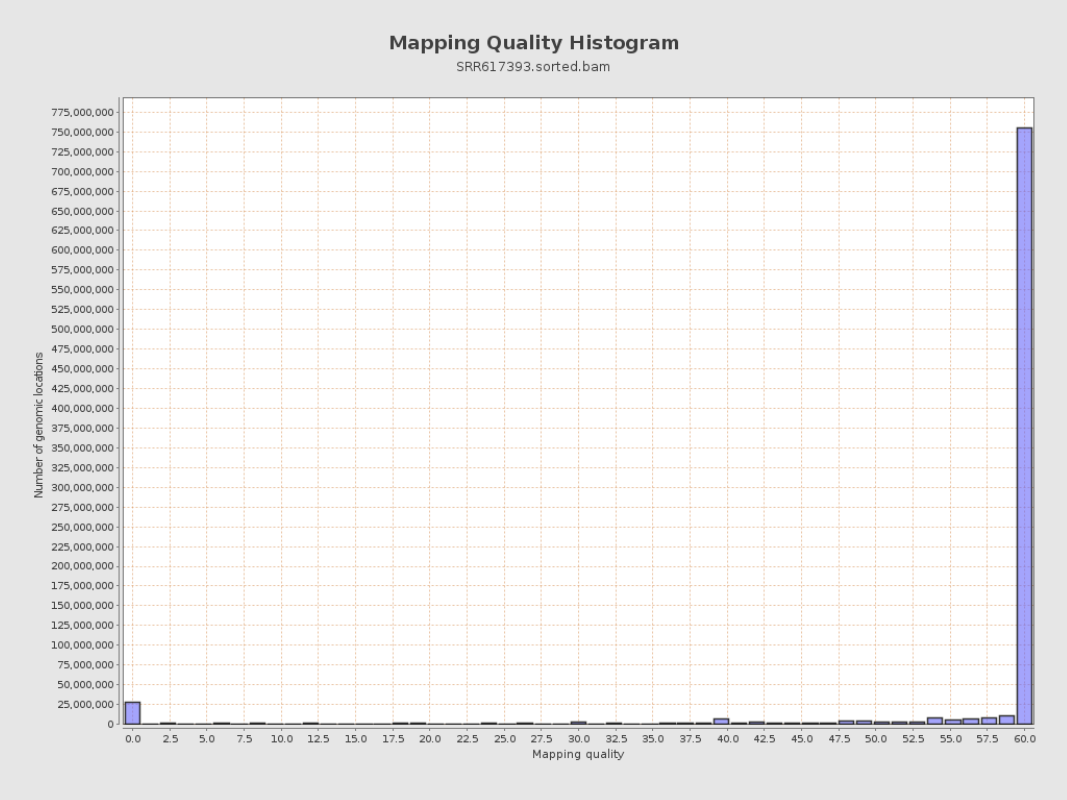
11. Results : Homopolymer Indels



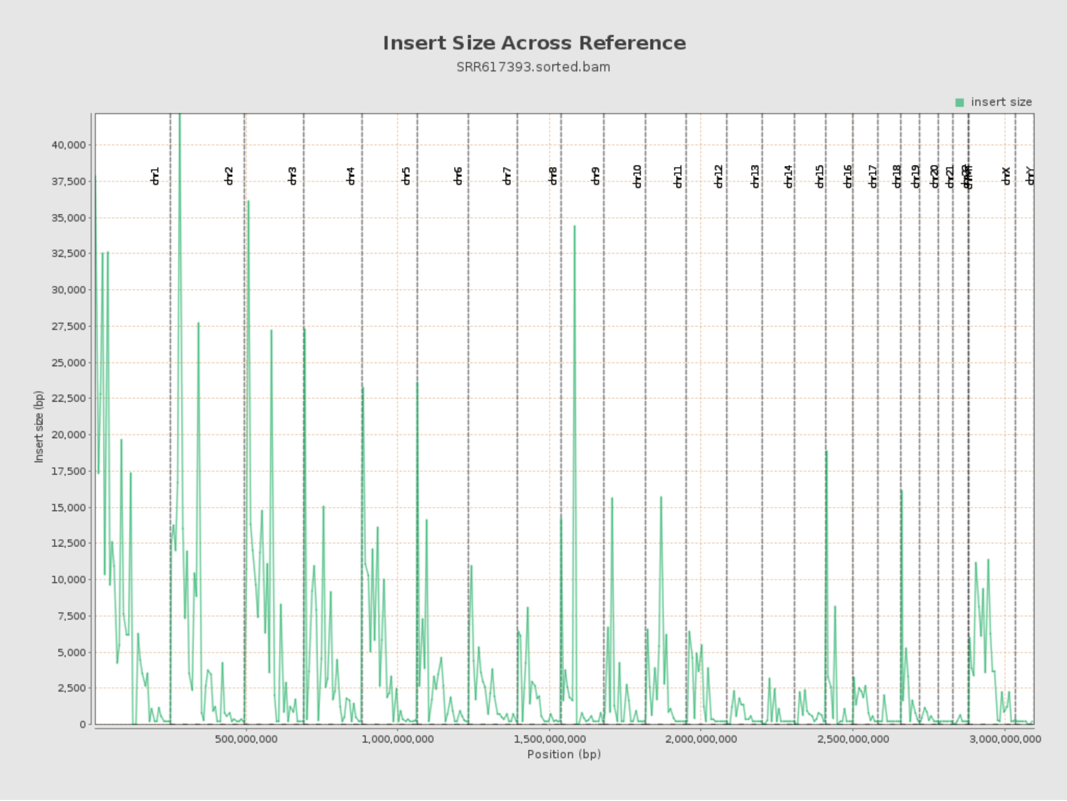
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram