Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:37:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617408.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_SRR617408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617408_1.fastq.gz SRR617408_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:37:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,298,478 / 94.68%
Unmapped reads	1,701,522 / 5.32%
Mapped paired reads	30,298,478 / 94.68%
Mapped reads, first in pair	15,232,269 / 47.6%
Mapped reads, second in pair	15,066,209 / 47.08%
Mapped reads, both in pair	29,845,546 / 93.27%
Mapped reads, singletons	452,932 / 1.42%
Secondary alignments	0
Supplementary alignments	464,003 / 1.45%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	1,403,606 / 4.39%
Duplication rate	4.21%
Clipped reads	3,143,290 / 9.82%

2.2. ACGT Content

Number/percentage of A's	888,637,808 / 29.77%
Number/percentage of C's	600,633,958 / 20.12%
Number/percentage of T's	880,169,699 / 29.48%
Number/percentage of G's	613,220,756 / 20.54%
Number/percentage of N's	2,655,650 / 0.09%

GC Percentage	40.66%

2.3. Coverage

Mean	0.9646
Standard Deviation	2.9543

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	48,089.38
Standard Deviation	2,072,468.9
P25/Median/P75	173 / 214 / 279

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	29,170,200
Insertions	243,446
Mapped reads with at least one insertion	0.79%
Deletions	291,457
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.76%

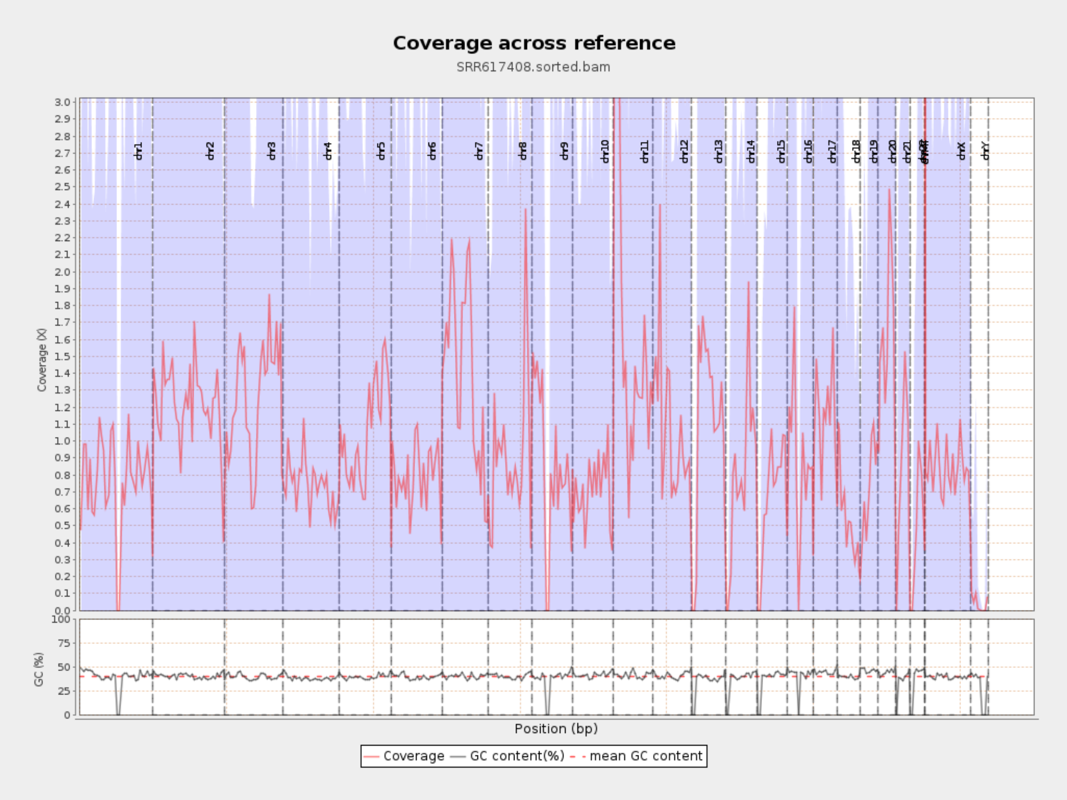
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

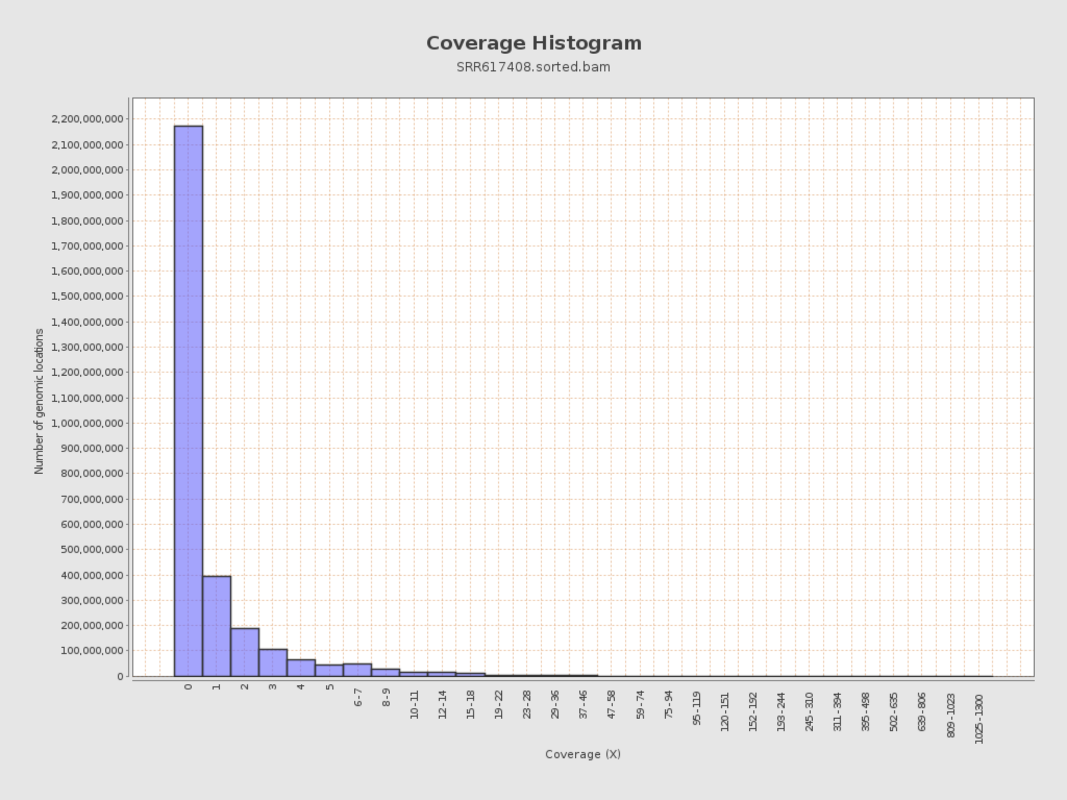
		bases	coverage	deviation
chr1	249250621	192331548	0.7716	2.7904
chr2	243199373	297350406	1.2227	3.0894
chr3	198022430	251783346	1.2715	3.4654
chr4	191154276	143053162	0.7484	2.291
chr5	180915260	190854112	1.0549	2.9036
chr6	171115067	136816005	0.7996	2.6184
chr7	159138663	223403494	1.4038	3.2481
chr8	146364022	132332457	0.9041	3.2858
chr9	141213431	119426826	0.8457	2.6303
chr10	135534747	95893741	0.7075	2.4363
chr11	135006516	221957444	1.644	3.8743
chr12	133851895	142165641	1.0621	2.8025
chr13	115169878	129011566	1.1202	2.7839
chr14	107349540	86631919	0.807	2.9293
chr15	102531392	68614623	0.6692	2.3743
chr16	90354753	75611298	0.8368	3.3763
chr17	81195210	92454398	1.1387	3.7142
chr18	78077248	42630799	0.546	2.0142
chr19	59128983	42804224	0.7239	2.3586
chr20	63025520	102525611	1.6267	4.8425
chr21	48129895	40920030	0.8502	2.5653
chr22	51304566	24230138	0.4723	2.1145
chrMT	16571	175597	10.5966	4.6014
chrX	155270560	130639777	0.8414	2.5778

chrY	59373566	2358267	0.0397	0.5728

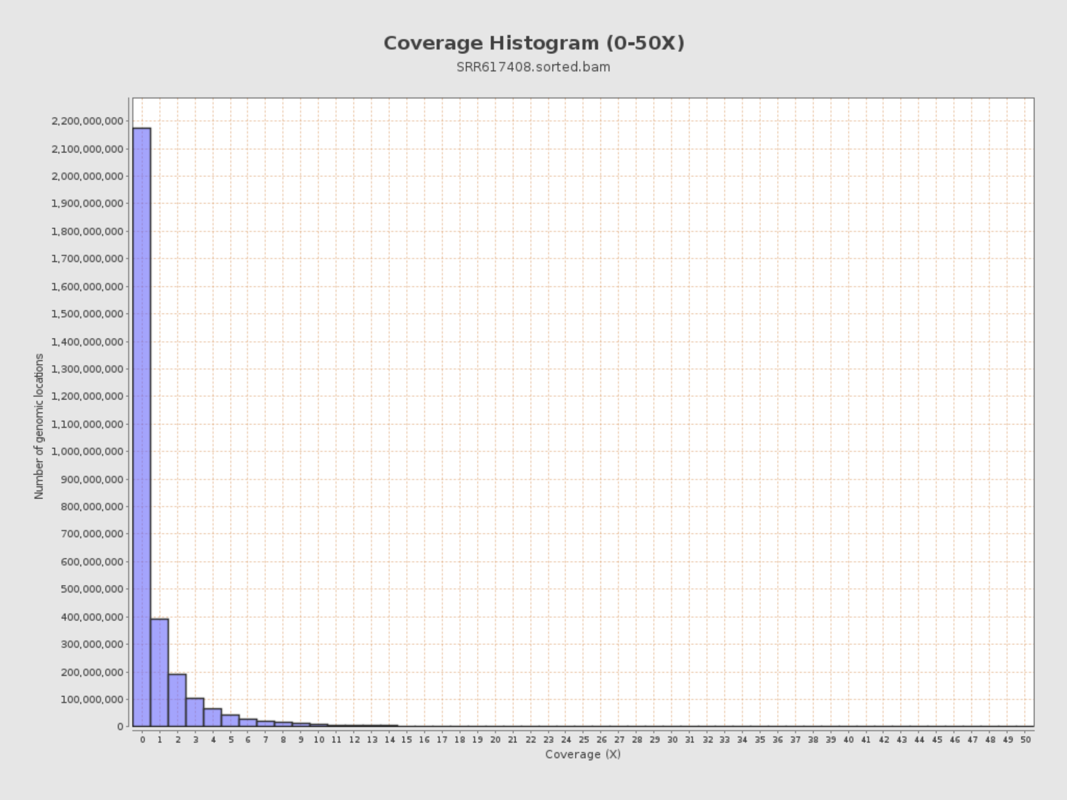
3. Results : Coverage across reference



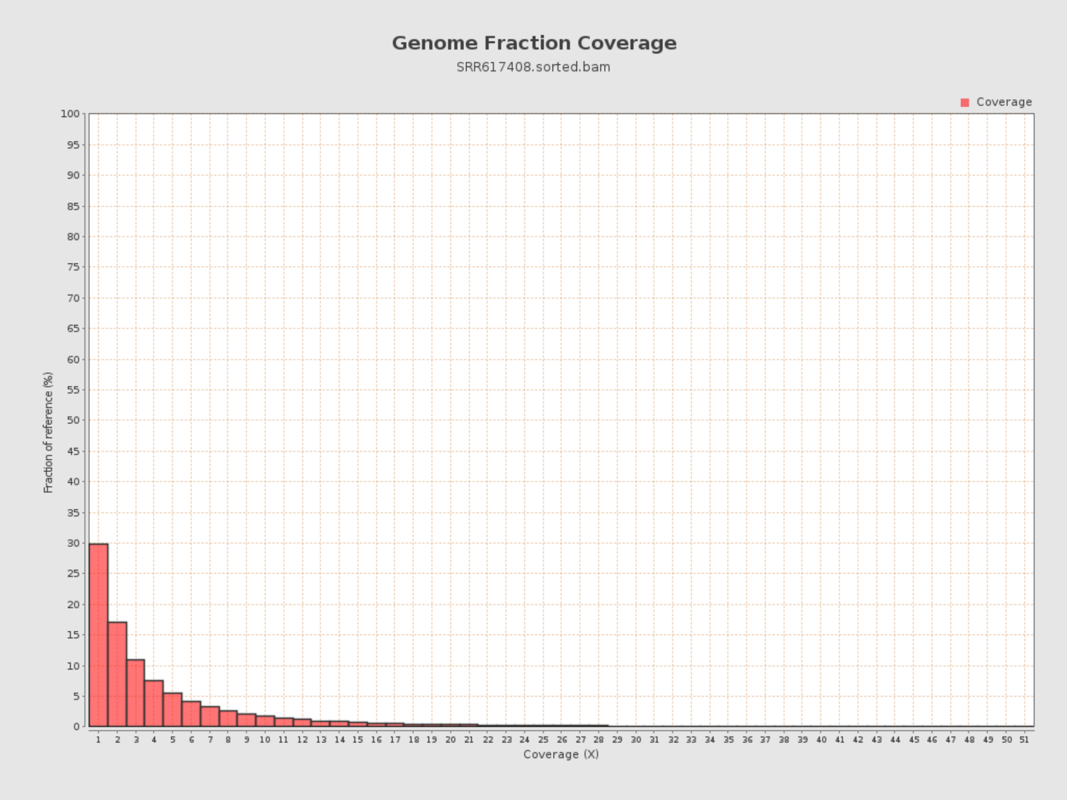
4. Results : Coverage Histogram



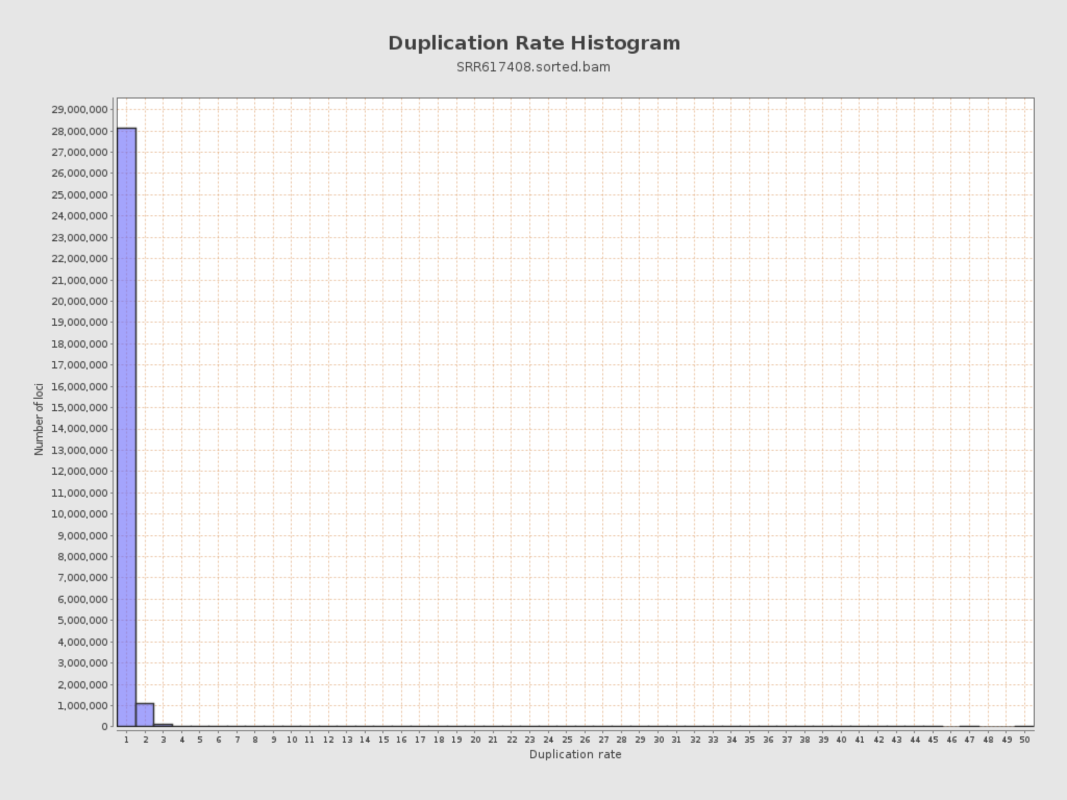
5. Results : Coverage Histogram (0-50X)



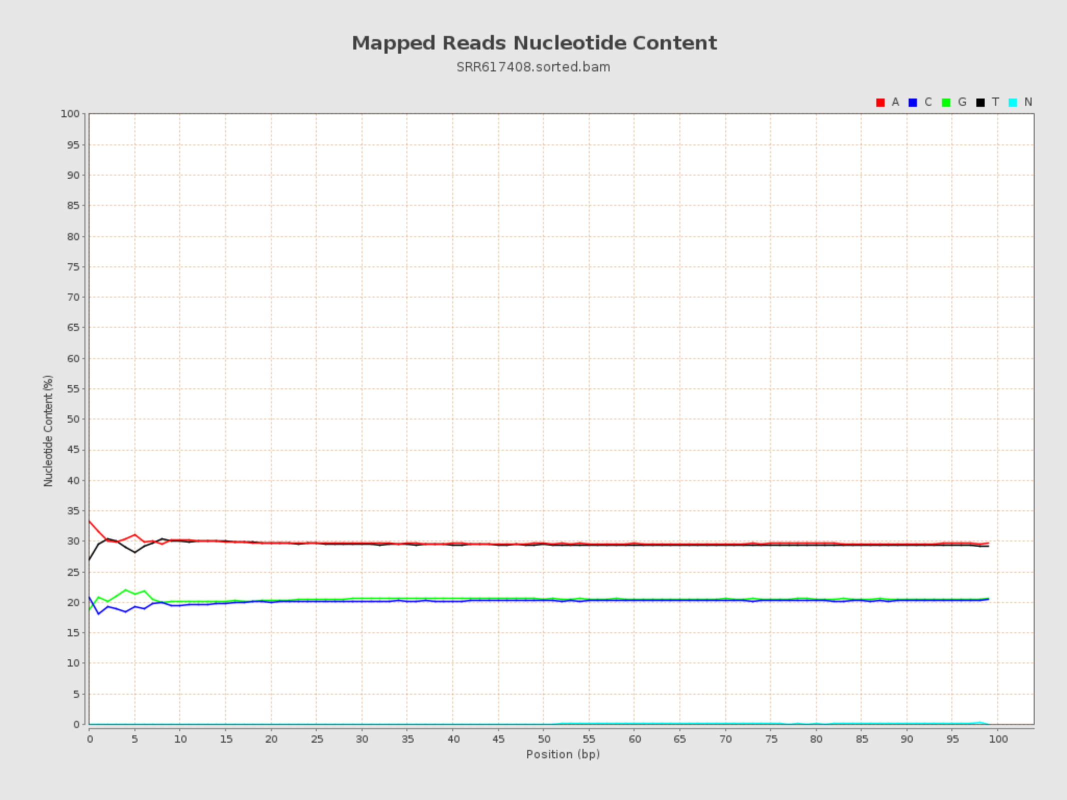
6. Results : Genome Fraction Coverage



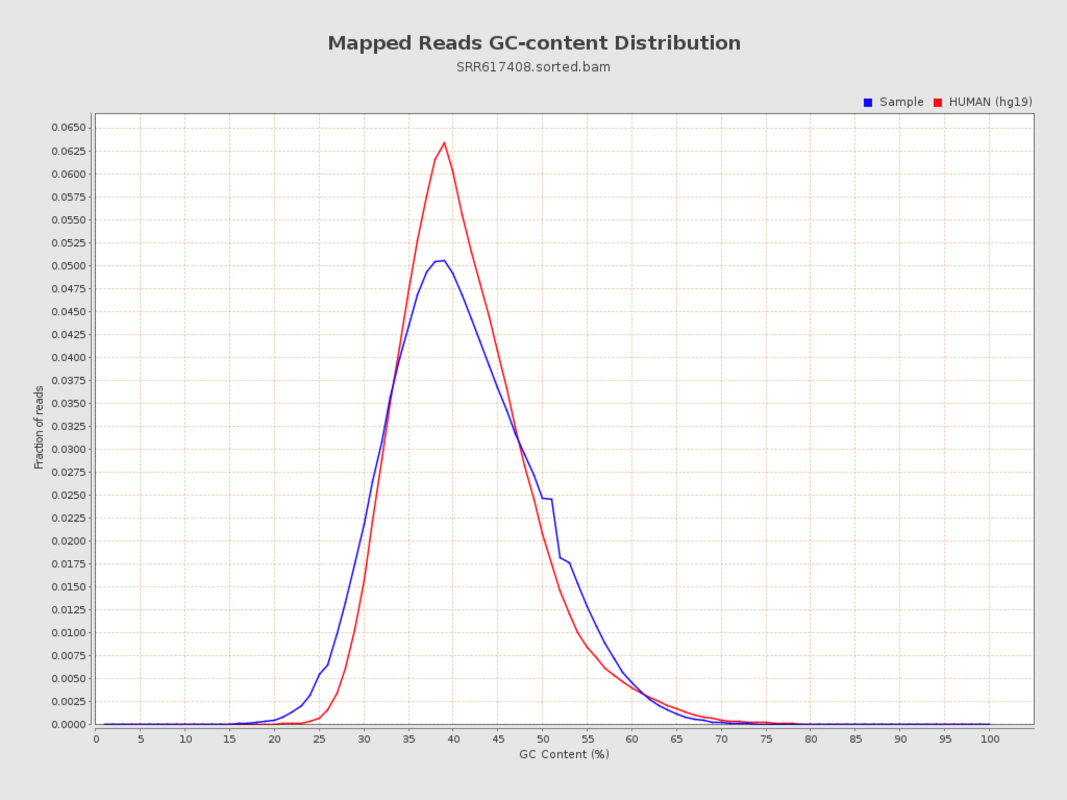
7. Results : Duplication Rate Histogram



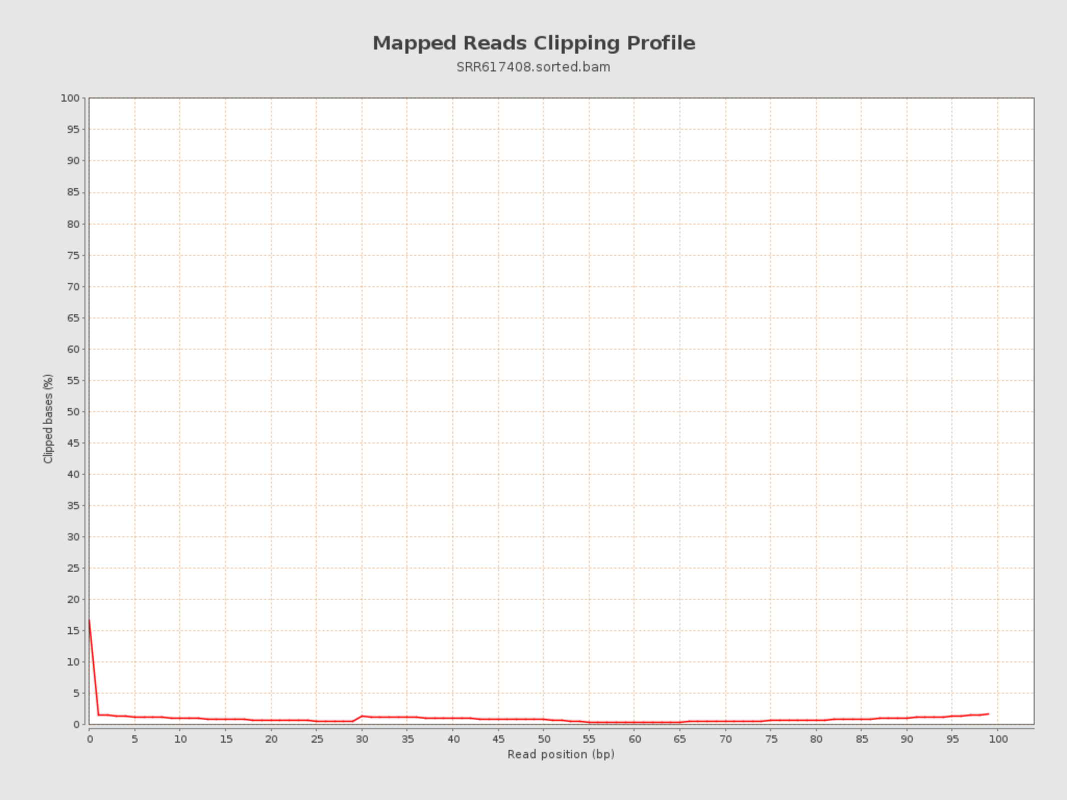
8. Results : Mapped Reads Nucleotide Content



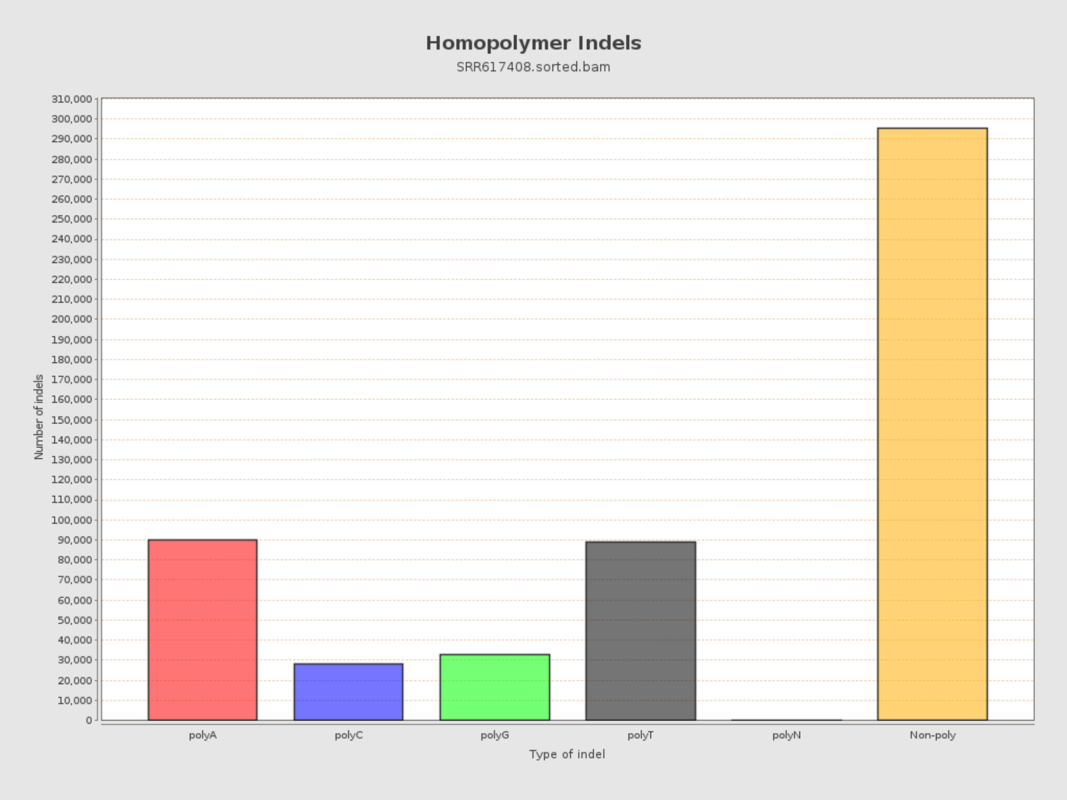
9. Results : Mapped Reads GC-content Distribution



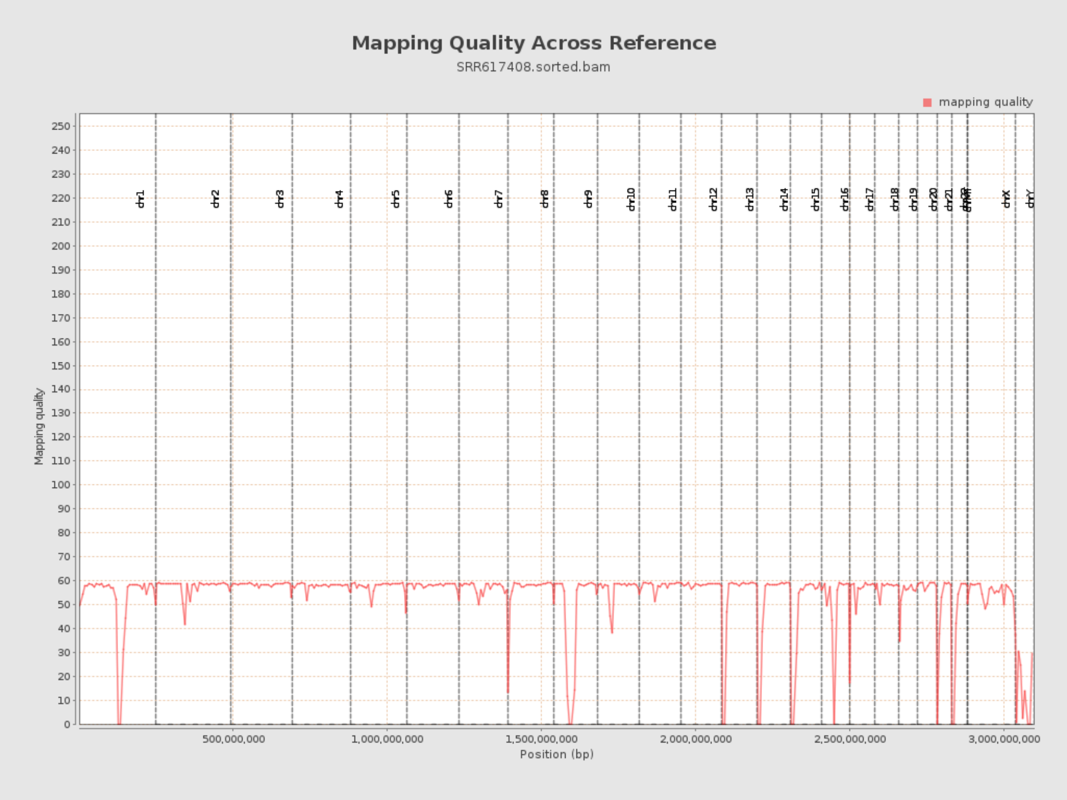
10. Results : Mapped Reads Clipping Profile



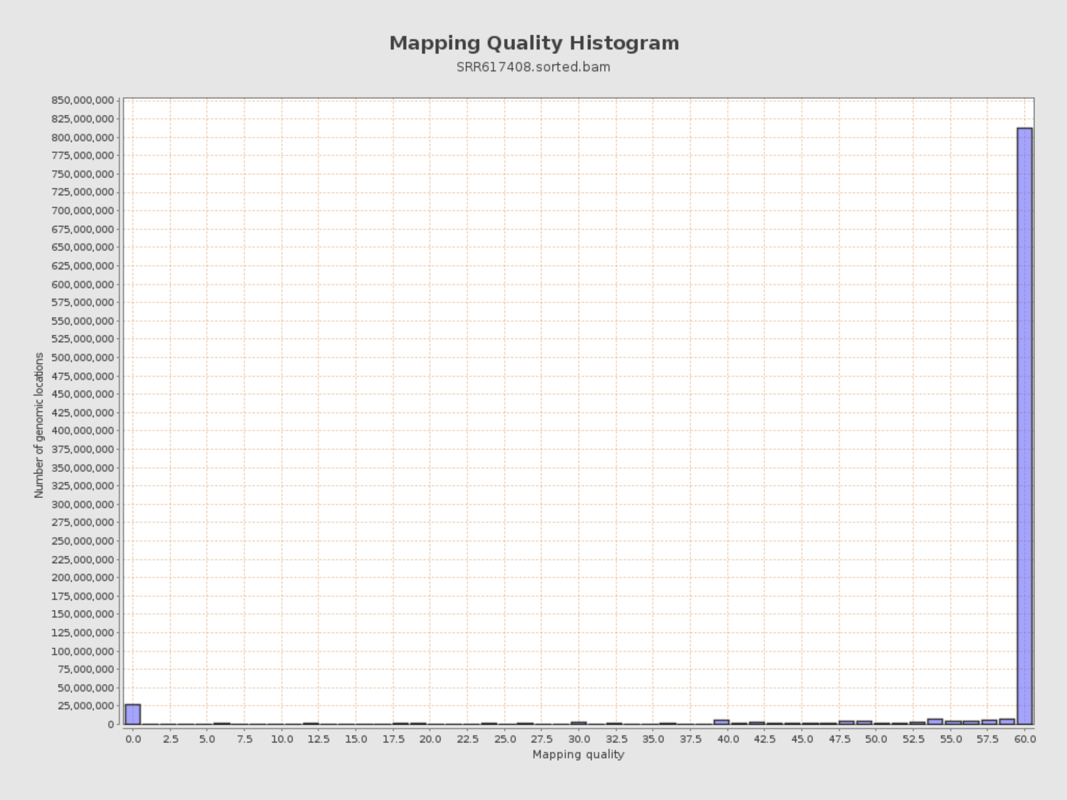
11. Results : Homopolymer Indels



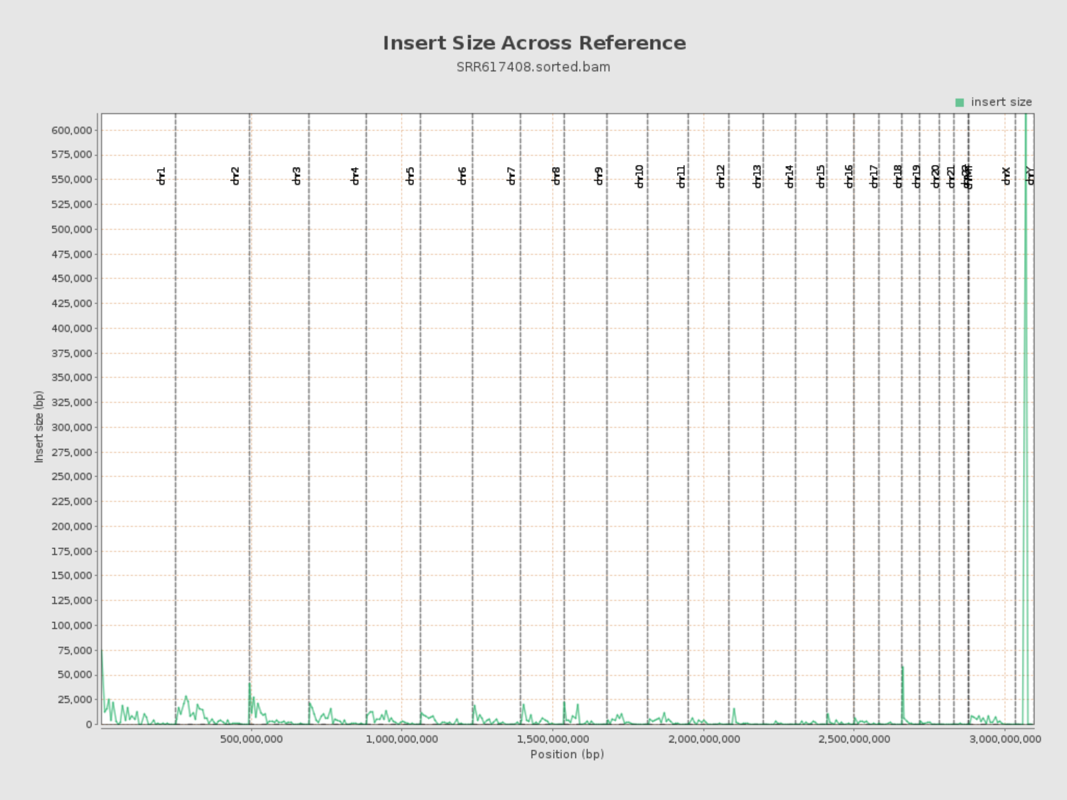
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram