Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 02:49:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617384.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_SRR617384 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617384_1.fastq.gz SRR617384_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 02:49:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617384.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,400,271 / 91.88%
Unmapped reads	2,599,729 / 8.12%
Mapped paired reads	29,400,271 / 91.88%
Mapped reads, first in pair	14,858,312 / 46.43%
Mapped reads, second in pair	14,541,959 / 45.44%
Mapped reads, both in pair	28,705,782 / 89.71%
Mapped reads, singletons	694,489 / 2.17%
Secondary alignments	0
Supplementary alignments	87,845 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,544,144 / 4.83%
Duplication rate	1.51%
Clipped reads	2,681,887 / 8.38%

2.2. ACGT Content

Number/percentage of A's	873,982,925 / 30.4%
Number/percentage of C's	567,930,680 / 19.75%
Number/percentage of T's	860,979,409 / 29.95%
Number/percentage of G's	571,242,472 / 19.87%
Number/percentage of N's	791,824 / 0.03%

GC Percentage	39.62%

2.3. Coverage

Mean	0.929
Standard Deviation	9.5446

2.4. Mapping Quality

Mean Mapping Quality	53.34

2.5. Insert size

Mean	56,098.31
Standard Deviation	2,259,200.42
P25/Median/P75	169 / 208 / 267

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	36,556,214
Insertions	289,173
Mapped reads with at least one insertion	0.95%
Deletions	345,766
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.1%

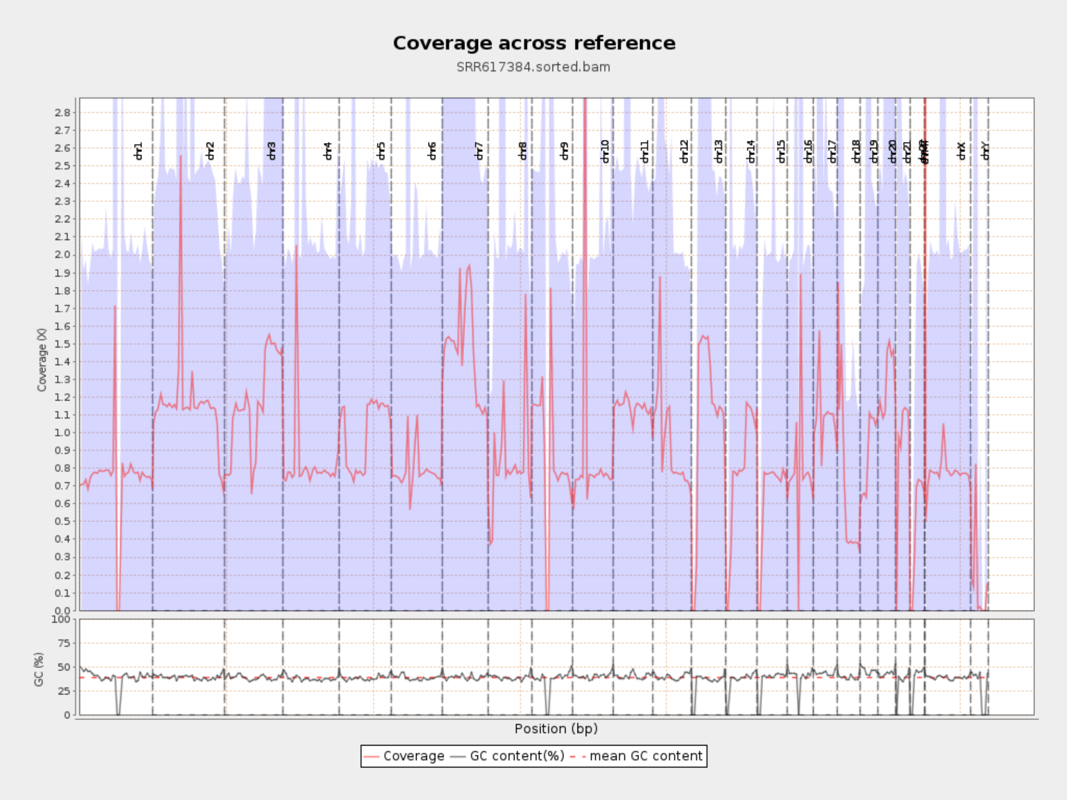
2.7. Chromosome stats

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

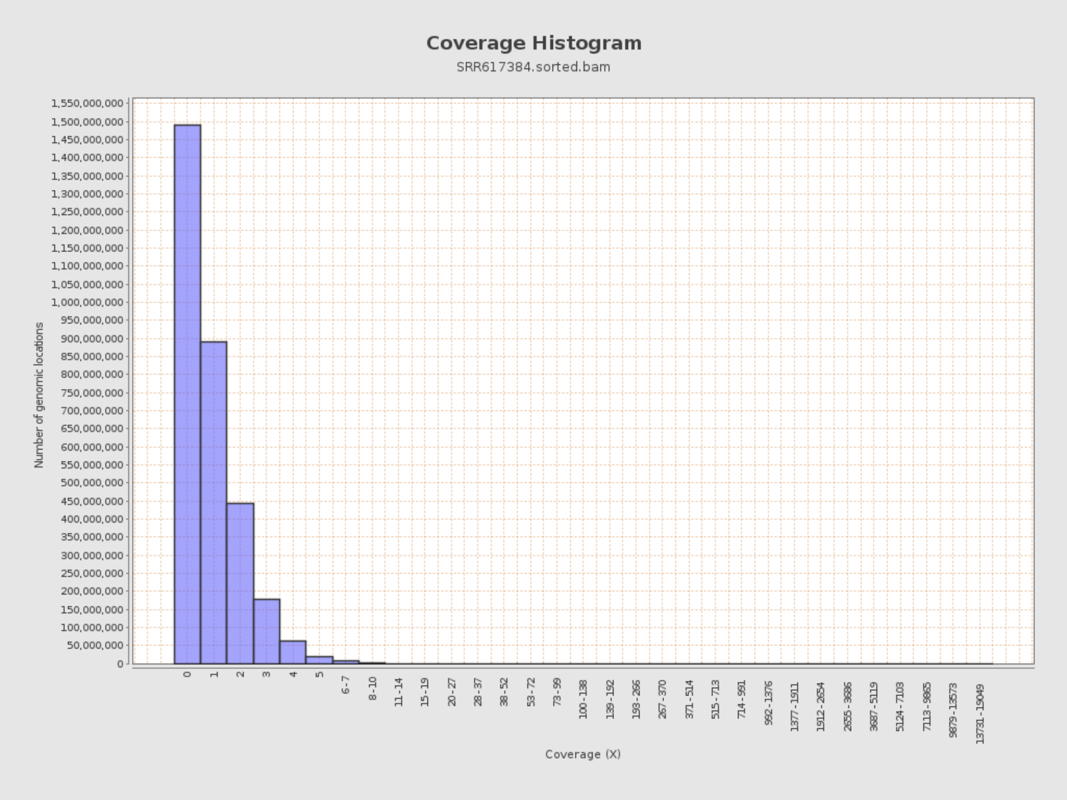
		bases	coverage	deviation
chr1	249250621	186023382	0.7463	19.4495
chr2	243199373	284165965	1.1684	8.4733
chr3	198022430	229442956	1.1587	1.4706
chr4	191154276	158096227	0.8271	8.7627
chr5	180915260	181145140	1.0013	1.467
chr6	171115067	135280285	0.7906	3.6105
chr7	159138663	233464156	1.467	10.8186
chr8	146364022	121134307	0.8276	7.4796
chr9	141213431	120961917	0.8566	14.3069
chr10	135534747	121402862	0.8957	19.9616
chr11	135006516	154002462	1.1407	5.4324
chr12	133851895	126673557	0.9464	1.3796
chr13	115169878	126110931	1.095	1.3118
chr14	107349540	83313642	0.7761	1.3624
chr15	102531392	64572008	0.6298	1.0869
chr16	90354753	72147369	0.7985	7.9229
chr17	81195210	88609389	1.0913	7.0619
chr18	78077248	51865229	0.6643	14.6913
chr19	59128983	52450567	0.8871	9.4176
chr20	63025520	81724639	1.2967	2.3672
chr21	48129895	45855205	0.9527	3.0769
chr22	51304566	25319942	0.4935	0.9084
chrMT	16571	1894899	114.3503	20.331
chrX	155270560	120393158	0.7754	2.9407

chrY	59373566	9706167	0.1635	7.8428

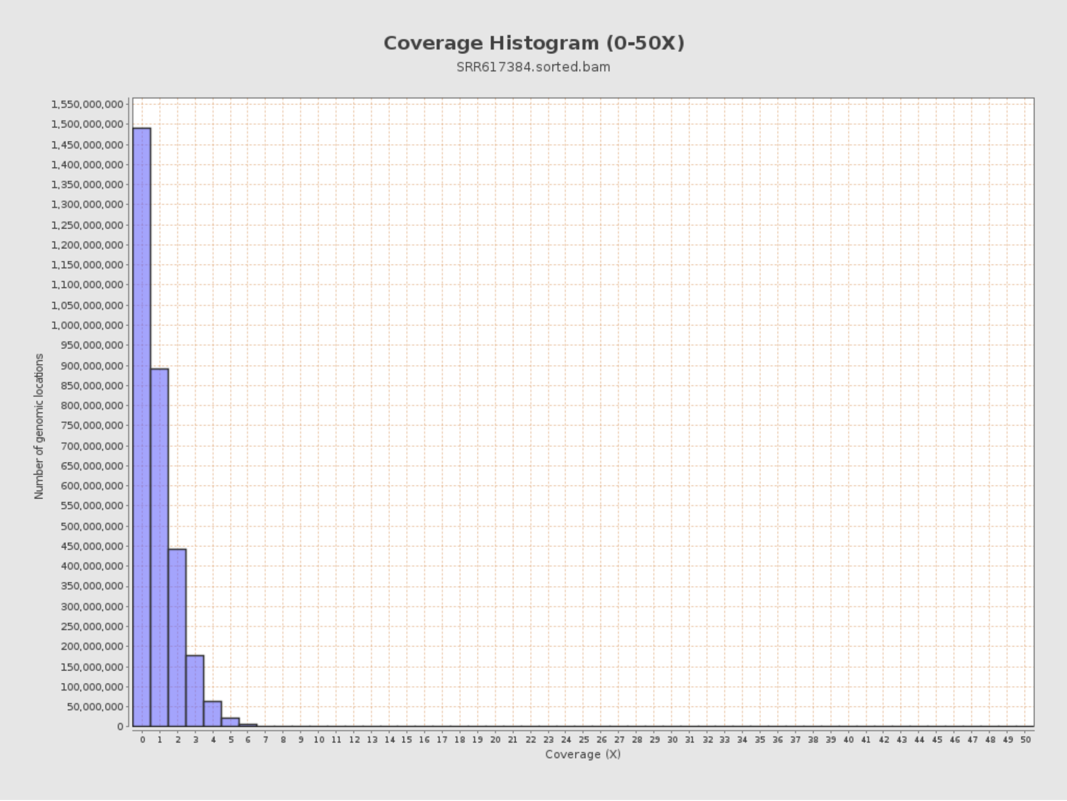
3. Results : Coverage across reference



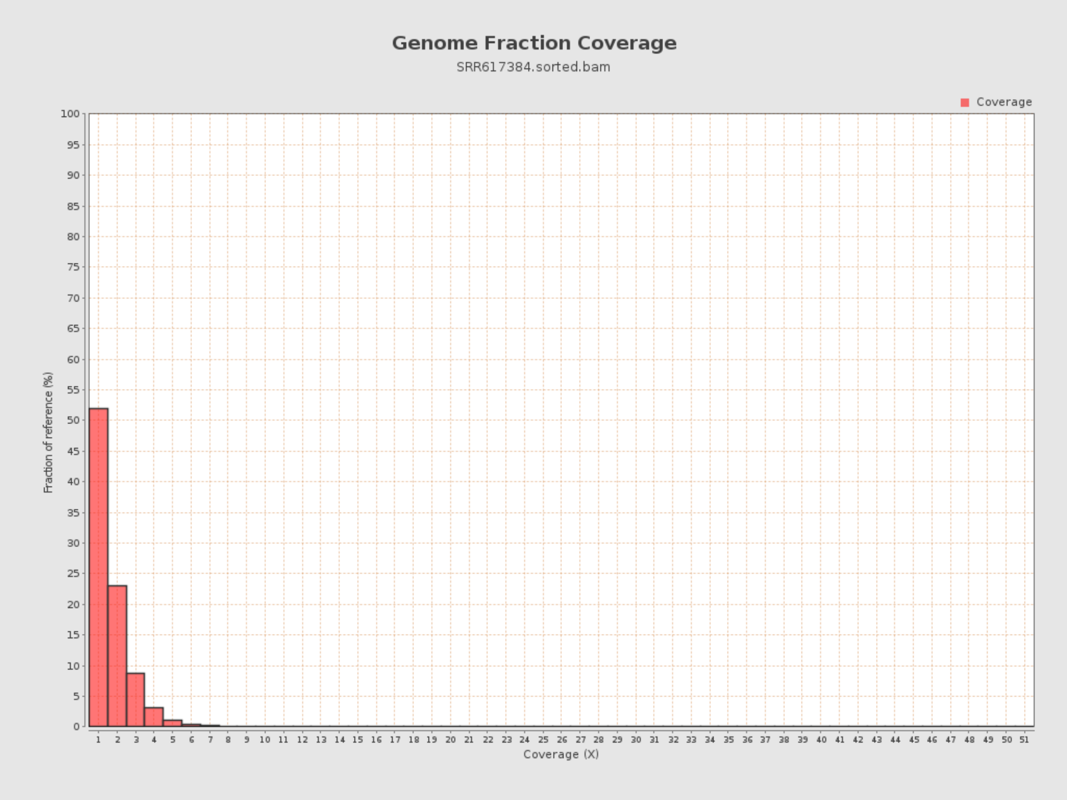
4. Results : Coverage Histogram



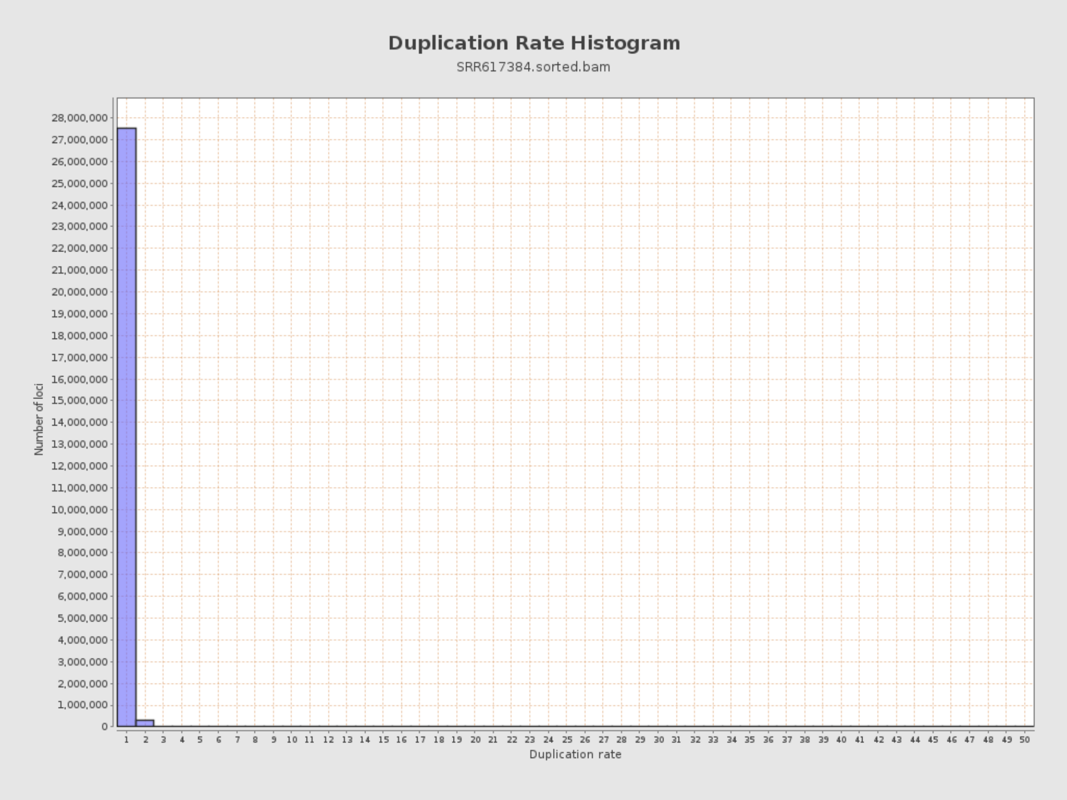
5. Results : Coverage Histogram (0-50X)



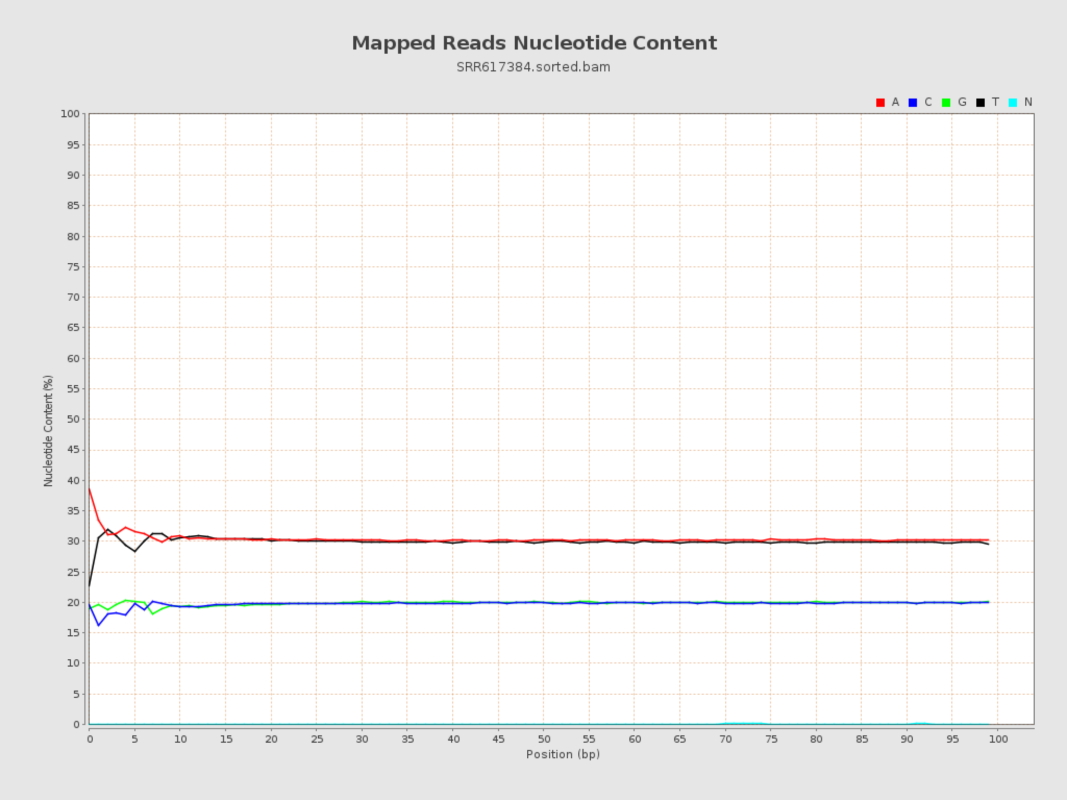
6. Results : Genome Fraction Coverage



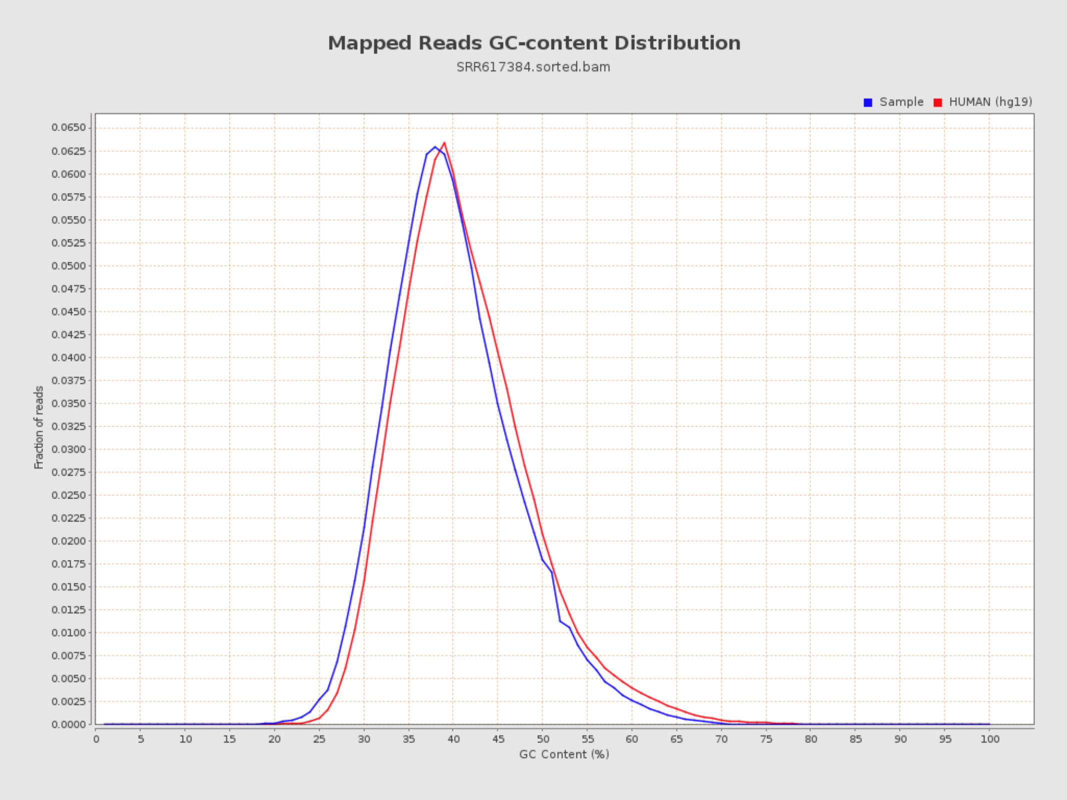
7. Results : Duplication Rate Histogram



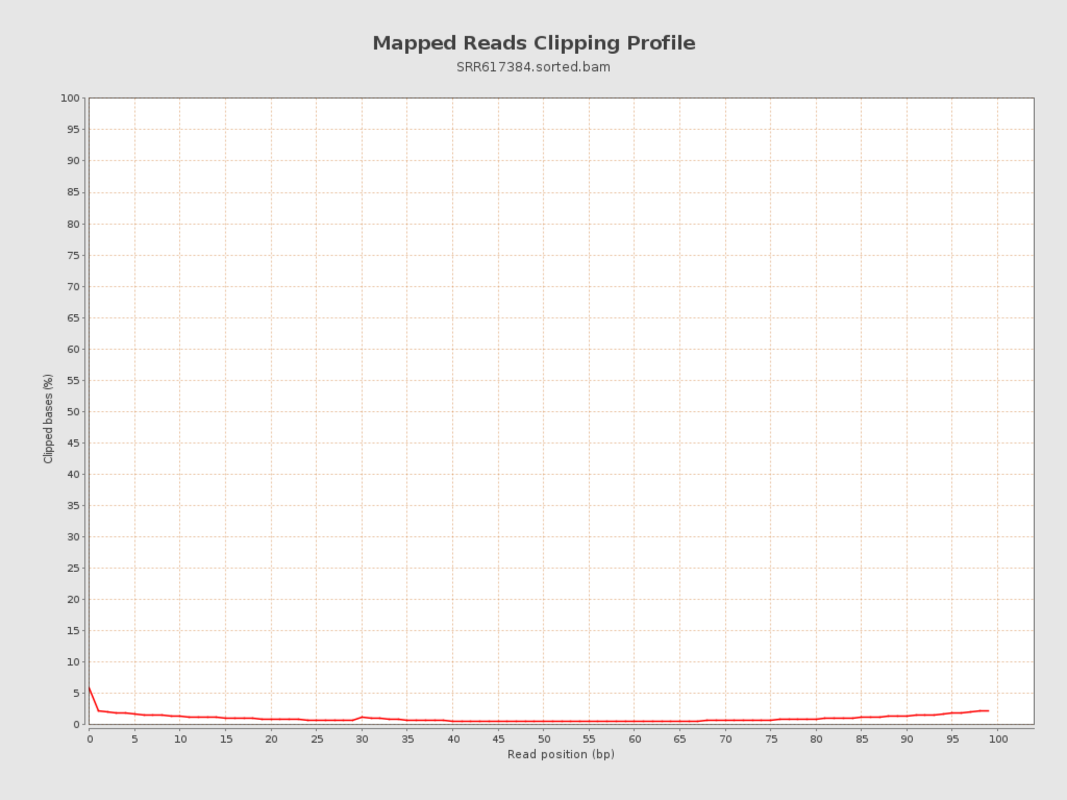
8. Results : Mapped Reads Nucleotide Content



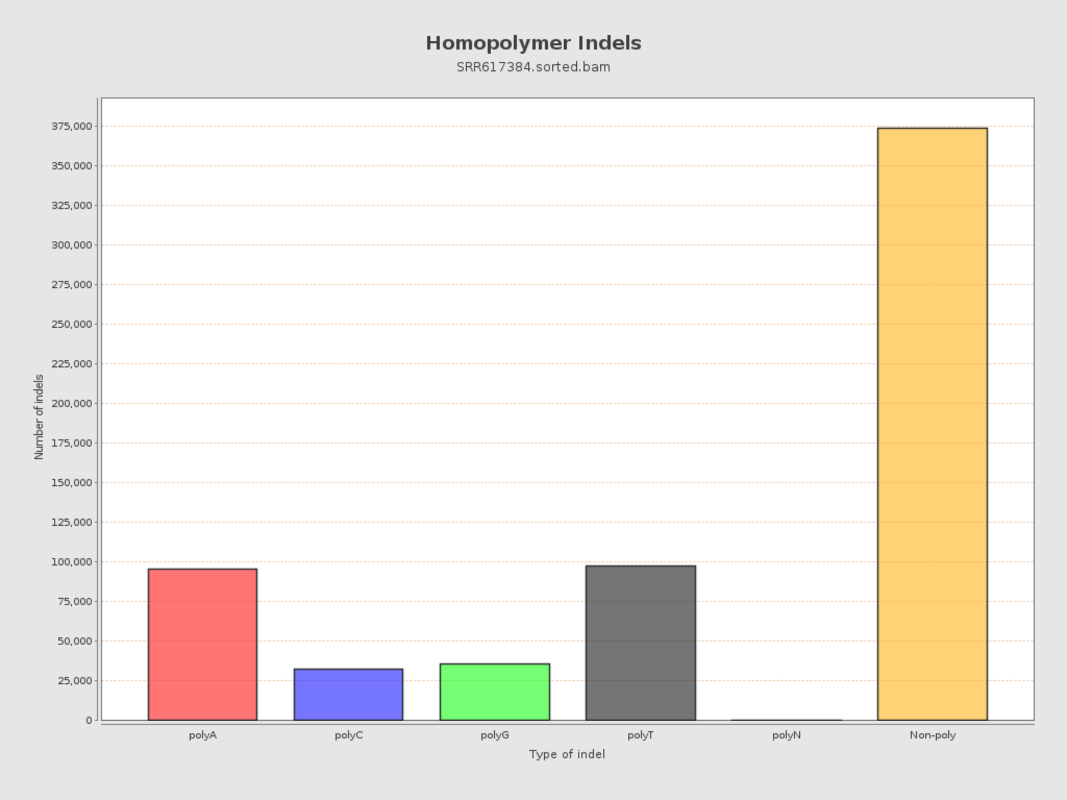
9. Results : Mapped Reads GC-content Distribution



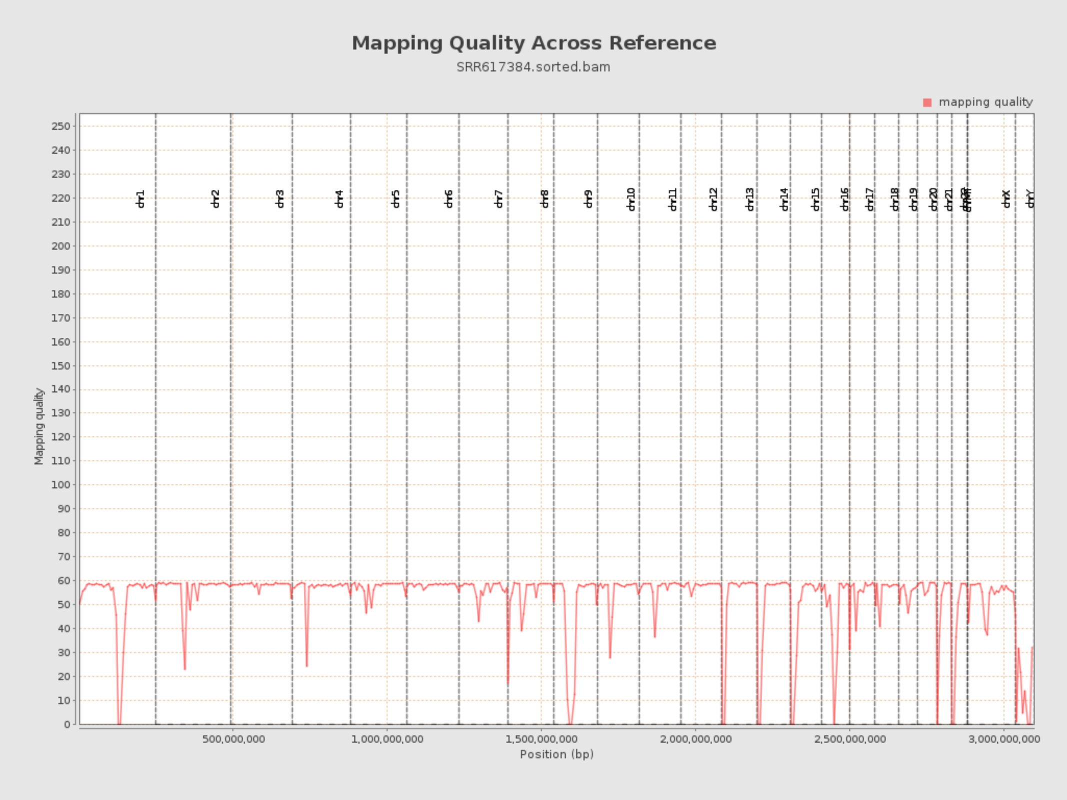
10. Results : Mapped Reads Clipping Profile



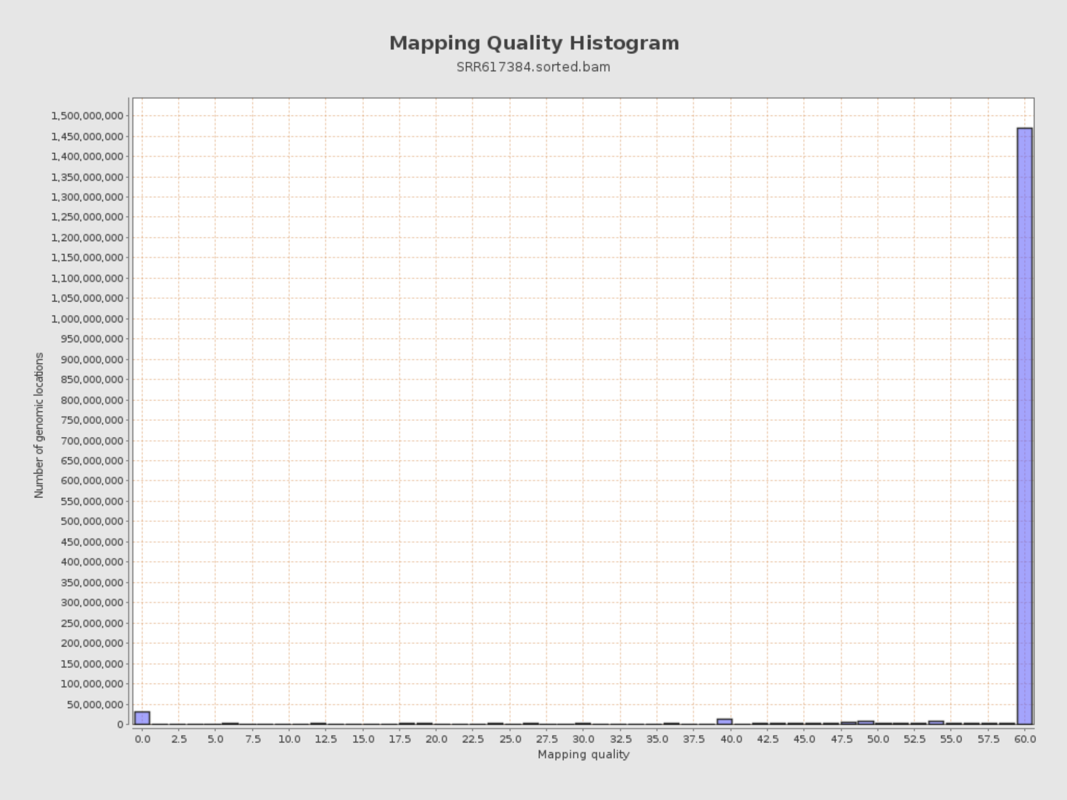
11. Results : Homopolymer Indels



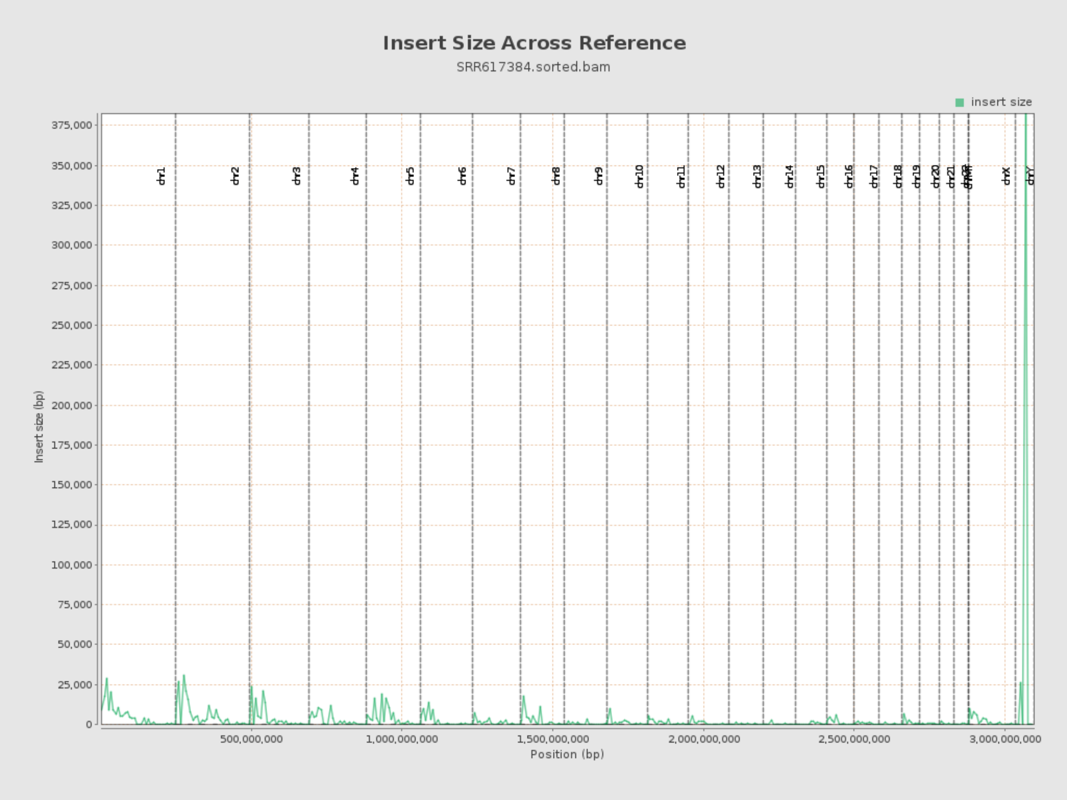
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram