Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/13 05:05:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR611492.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_SRR611492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR611492_1.fastq.gz SRR611492_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 13 05:05:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR611492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,091,314,268
Mapped reads	1,062,262,460 / 97.34%
Unmapped reads	29,051,808 / 2.66%
Mapped paired reads	1,062,262,460 / 97.34%
Mapped reads, first in pair	532,842,915 / 48.83%
Mapped reads, second in pair	529,419,545 / 48.51%
Mapped reads, both in pair	1,051,211,404 / 96.33%
Mapped reads, singletons	11,051,056 / 1.01%
Secondary alignments	0
Supplementary alignments	10,680,183 / 0.98%
Read min/max/mean length	30 / 90 / 90.38
Duplicated reads (estimated)	413,586,221 / 37.9%
Duplication rate	30.88%
Clipped reads	179,121,255 / 16.41%

2.2. ACGT Content

Number/percentage of A's	26,058,986,826 / 28.47%
Number/percentage of C's	19,120,551,081 / 20.89%
Number/percentage of T's	26,189,234,990 / 28.61%
Number/percentage of G's	20,161,920,252 / 22.02%
Number/percentage of N's	12,555,590 / 0.01%

GC Percentage	42.91%

2.3. Coverage

Mean	29.5947
Standard Deviation	359.8978

2.4. Mapping Quality

Mean Mapping Quality	52.16

2.5. Insert size

Mean	121,300.96
Standard Deviation	3,313,326.24
P25/Median/P75	166 / 176 / 184

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	970,883,304
Insertions	17,632,152
Mapped reads with at least one insertion	1.61%
Deletions	43,238,446
Mapped reads with at least one deletion	3.97%
Homopolymer indels	47.81%

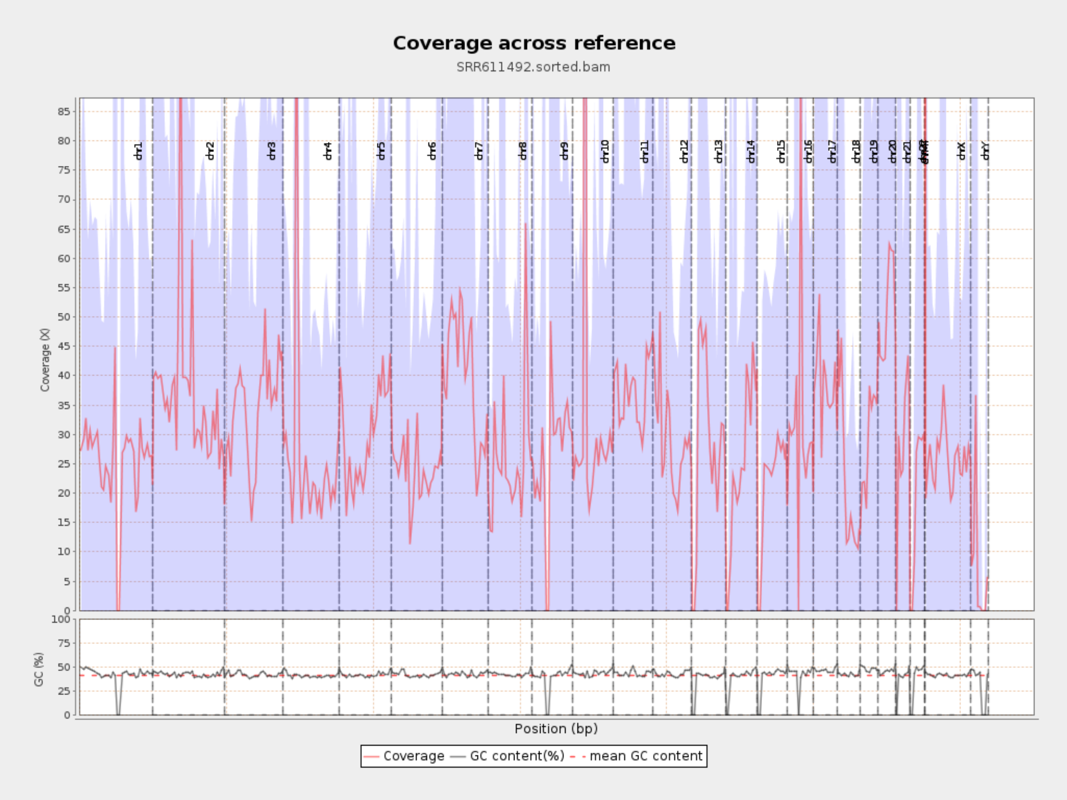
2.7. Chromosome stats

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

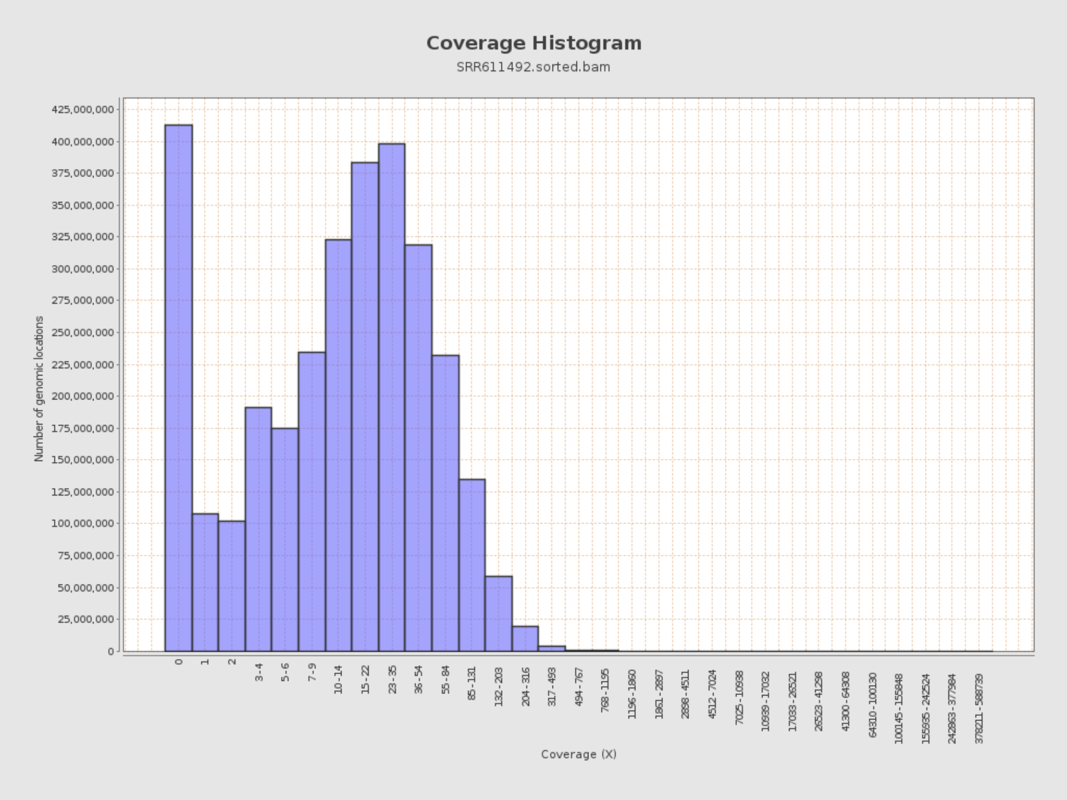
		bases	coverage	deviation
chr1	249250621	6326445480	25.3819	349.839
chr2	243199373	9177263073	37.7356	484.3766
chr3	198022430	6768625853	34.1811	62.0759
chr4	191154276	4828554279	25.26	361.4293
chr5	180915260	5446222121	30.1037	56.431
chr6	171115067	4077970127	23.8317	129.0625
chr7	159138663	6353691969	39.9255	304.2972
chr8	146364022	3773891631	25.7843	129.4849
chr9	141213431	3701788324	26.2141	411.5387
chr10	135534747	4530041368	33.4235	1,118.8871
chr11	135006516	4994616875	36.9954	217.1494
chr12	133851895	3921993179	29.301	50.9753
chr13	115169878	3285850356	28.5305	45.0072
chr14	107349540	2638692857	24.5804	66.9973
chr15	102531392	2171778861	21.1816	33.069
chr16	90354753	2898819637	32.0826	482.1594
chr17	81195210	3129992728	38.549	243.1759
chr18	78077248	1661064642	21.2746	427.4333
chr19	59128983	1713205766	28.974	201.6133
chr20	63025520	3272957885	51.9307	174.1799
chr21	48129895	1390962201	28.9002	202.3828
chr22	51304566	1003876359	19.567	55.2784
chrMT	16571	97222690	5,867.0382	2,199.6426
chrX	155270560	3997571438	25.7458	117.9348

chrY	59373566	453017322	7.6299	526.3874

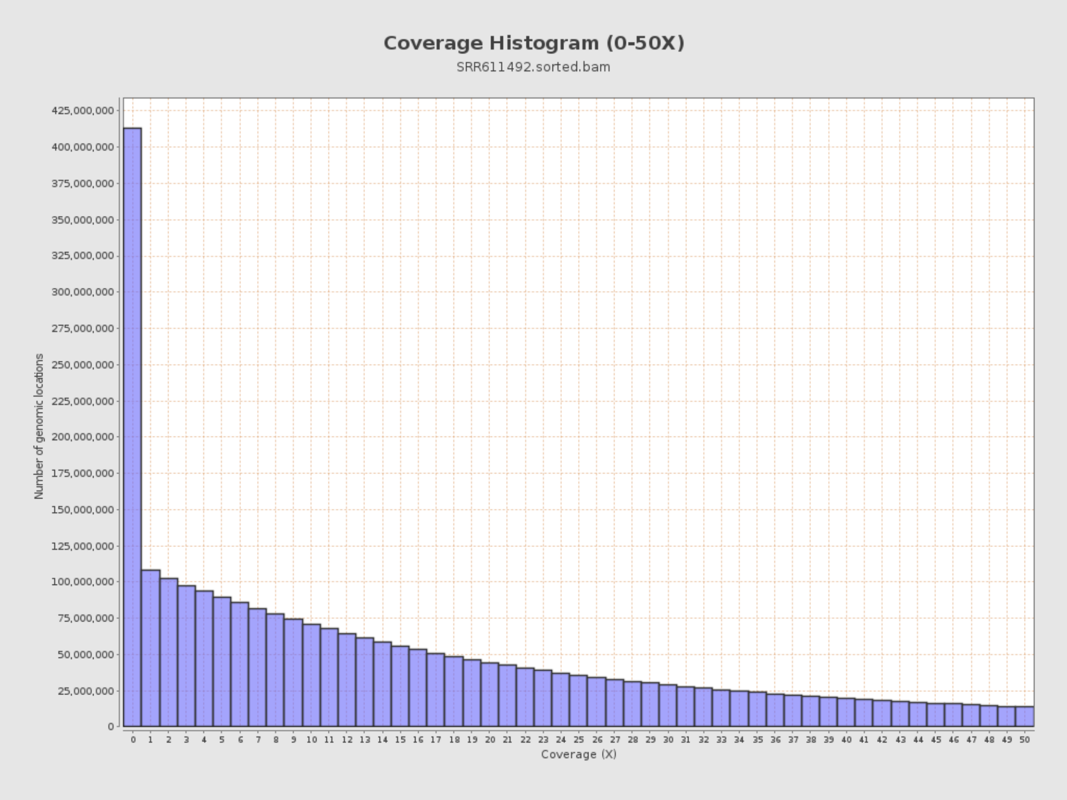
3. Results : Coverage across reference



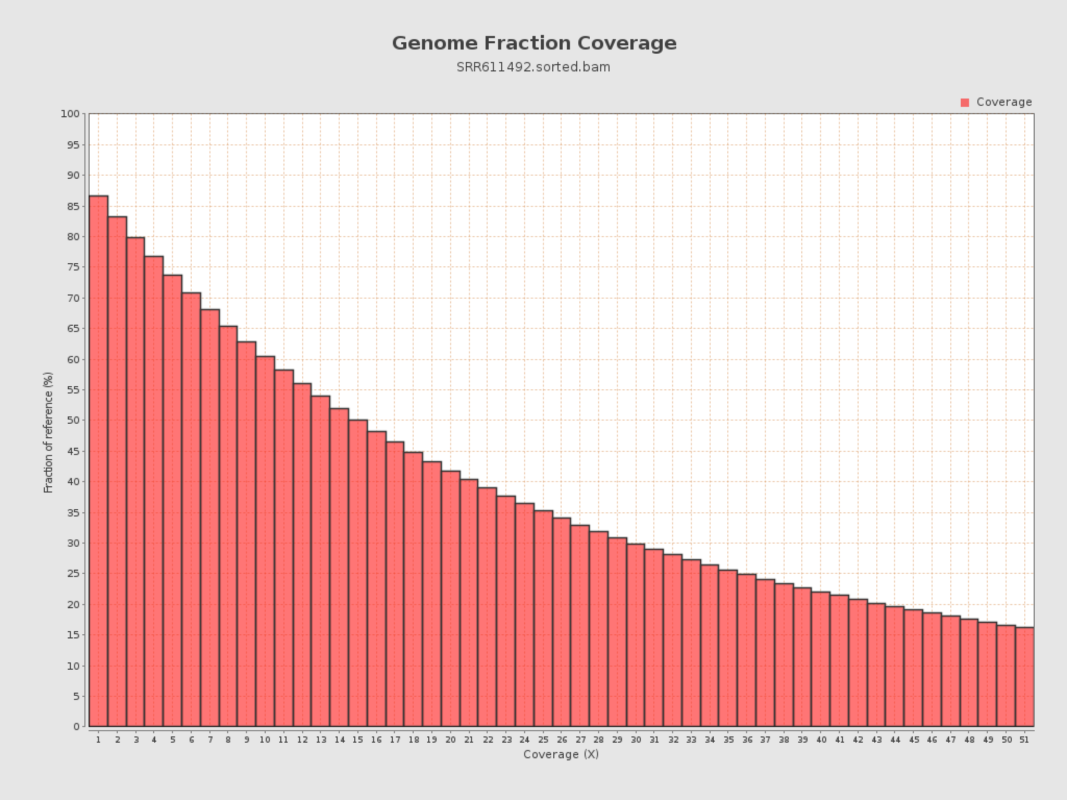
4. Results : Coverage Histogram



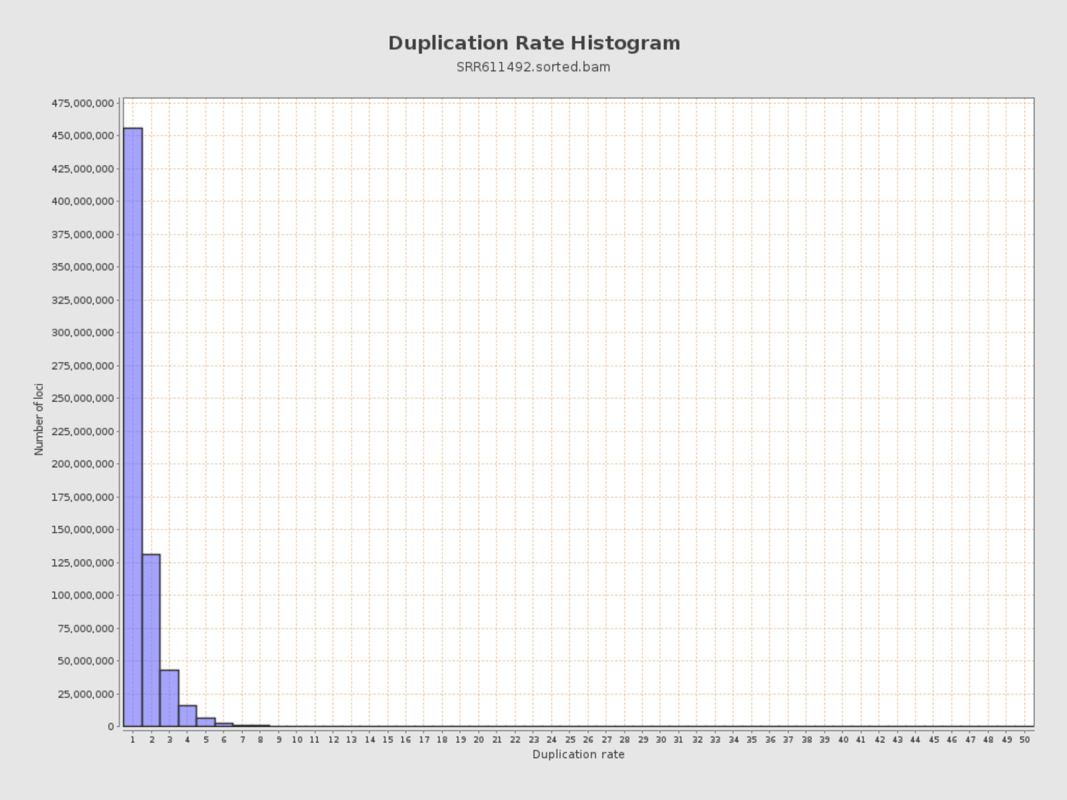
5. Results : Coverage Histogram (0-50X)



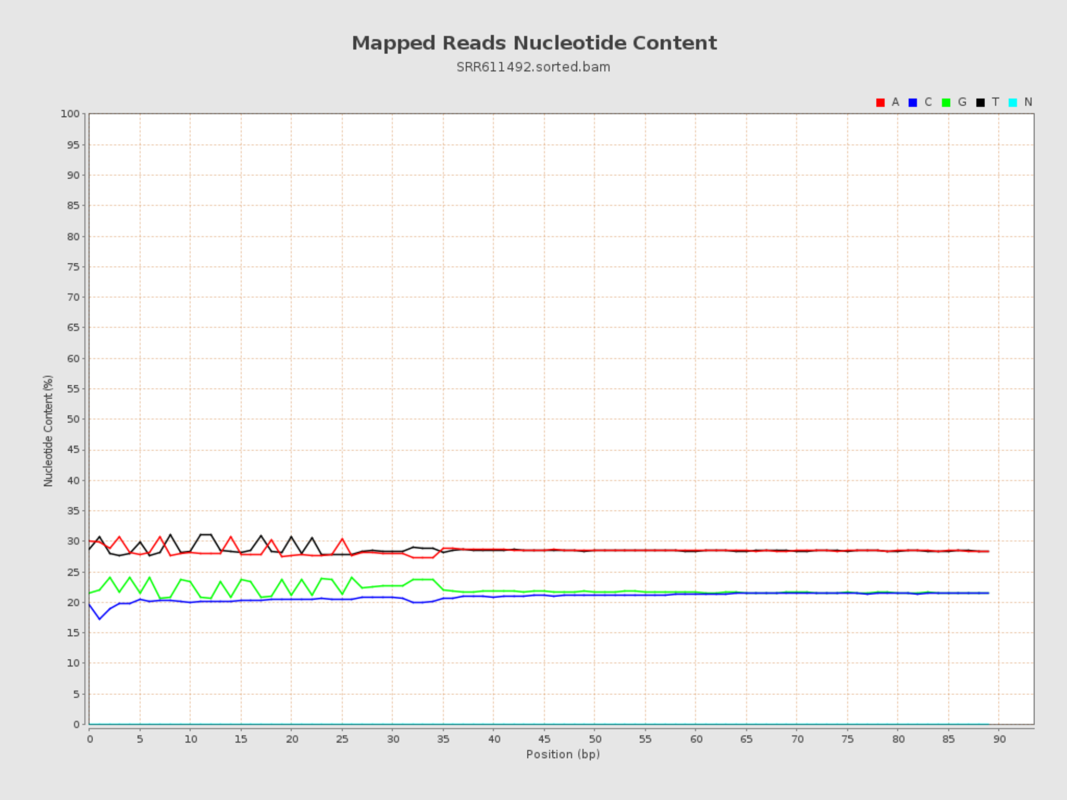
6. Results : Genome Fraction Coverage



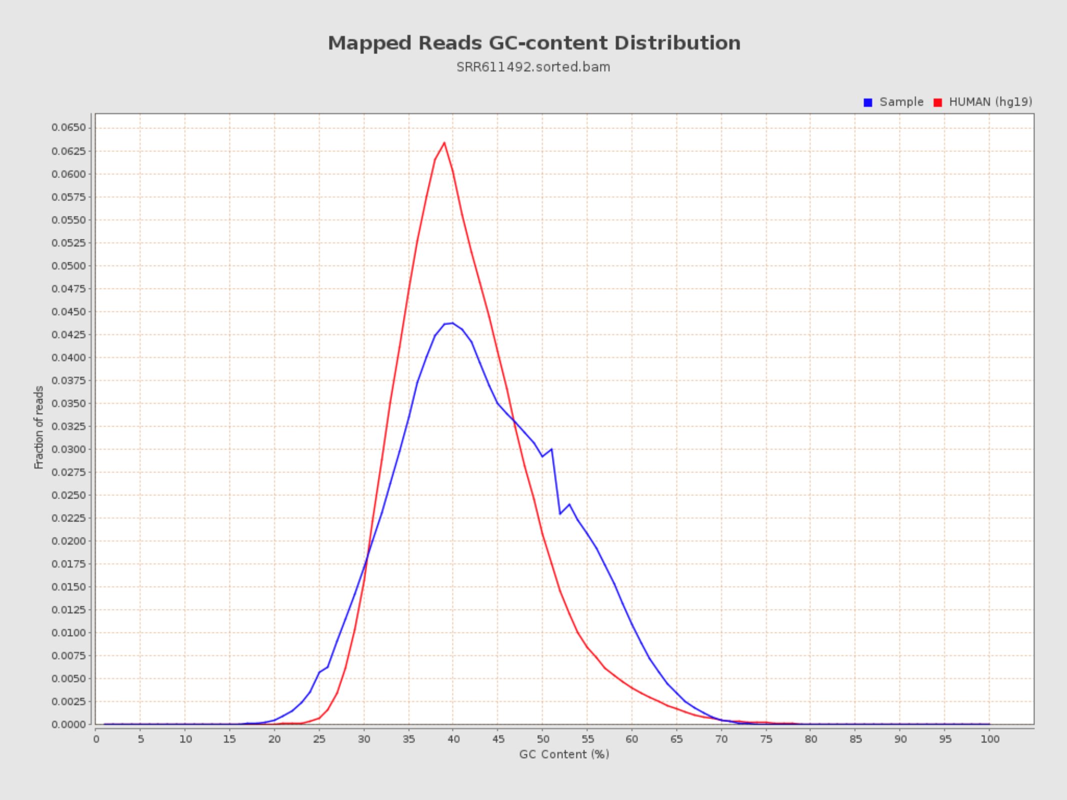
7. Results : Duplication Rate Histogram



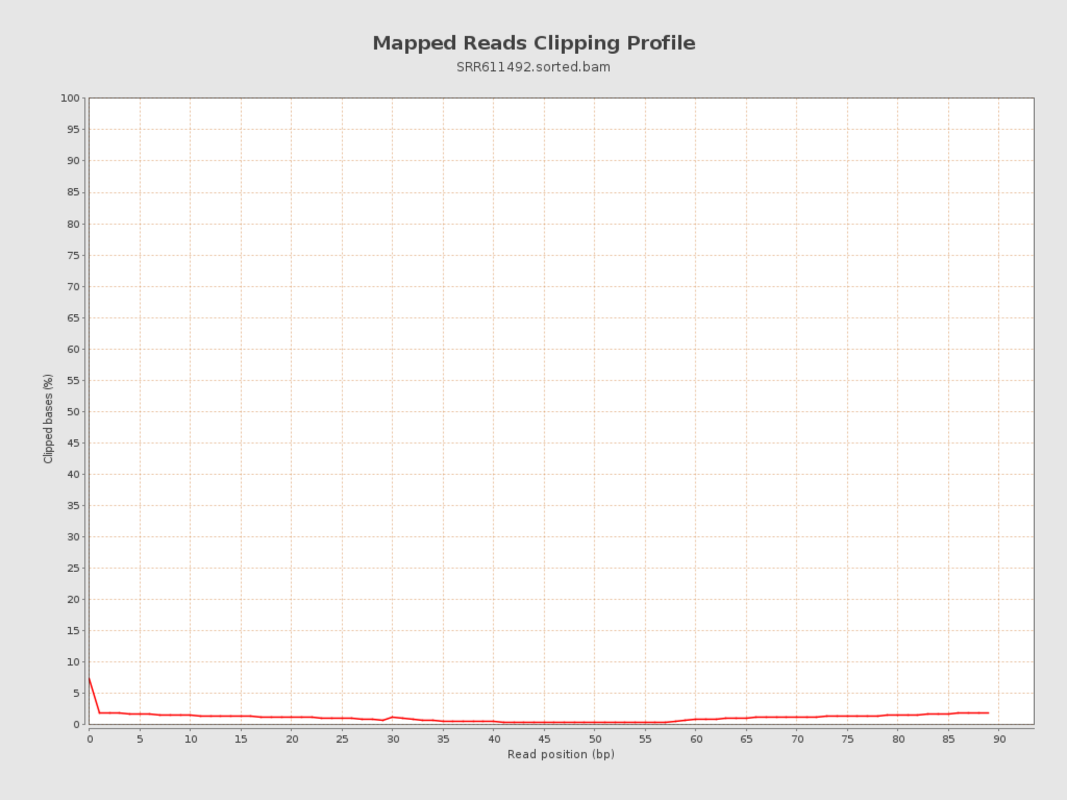
8. Results : Mapped Reads Nucleotide Content



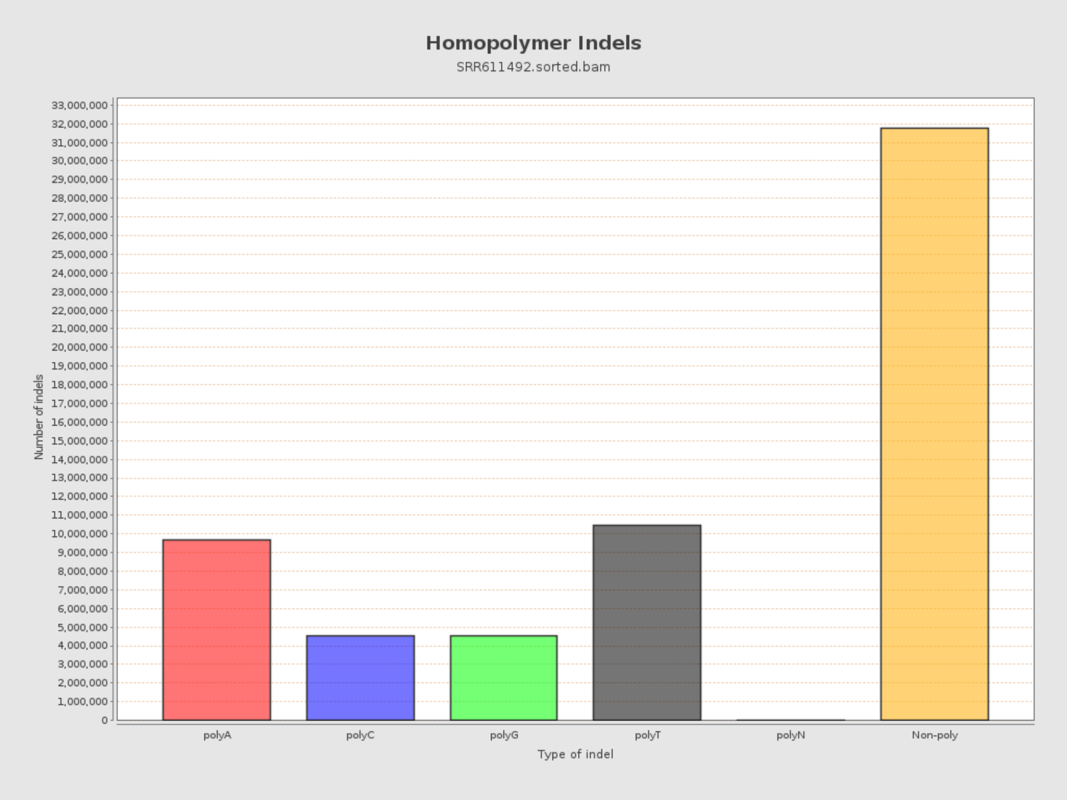
9. Results : Mapped Reads GC-content Distribution



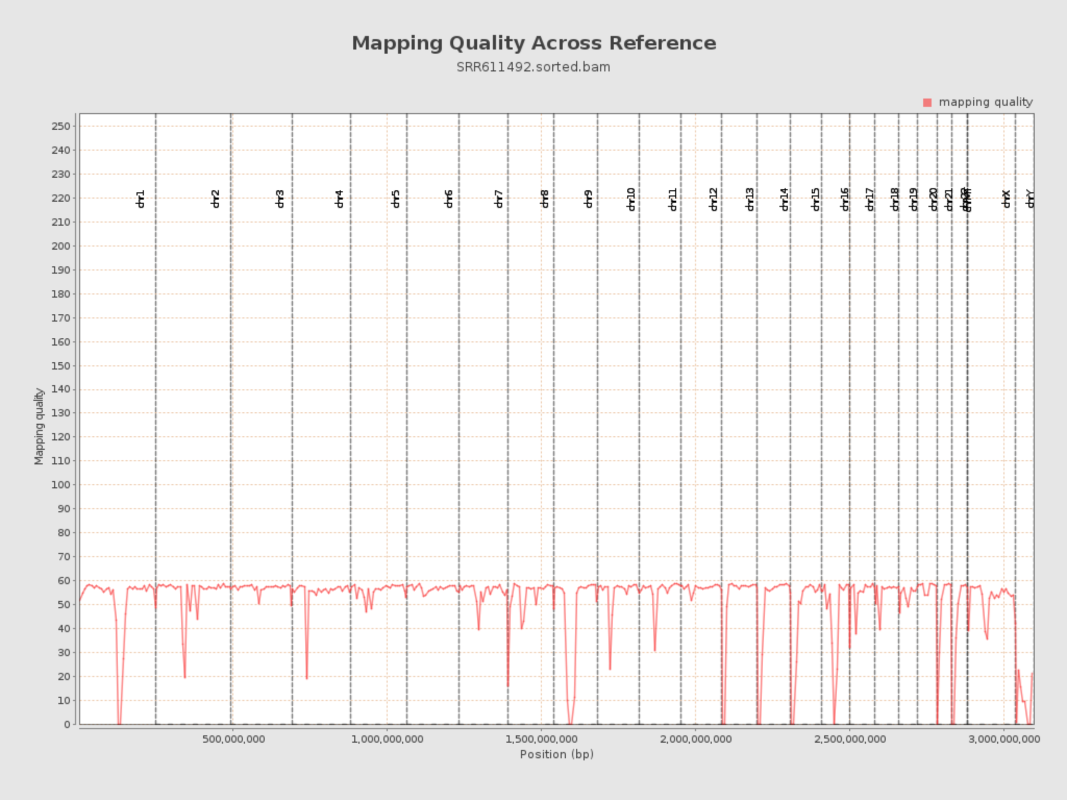
10. Results : Mapped Reads Clipping Profile



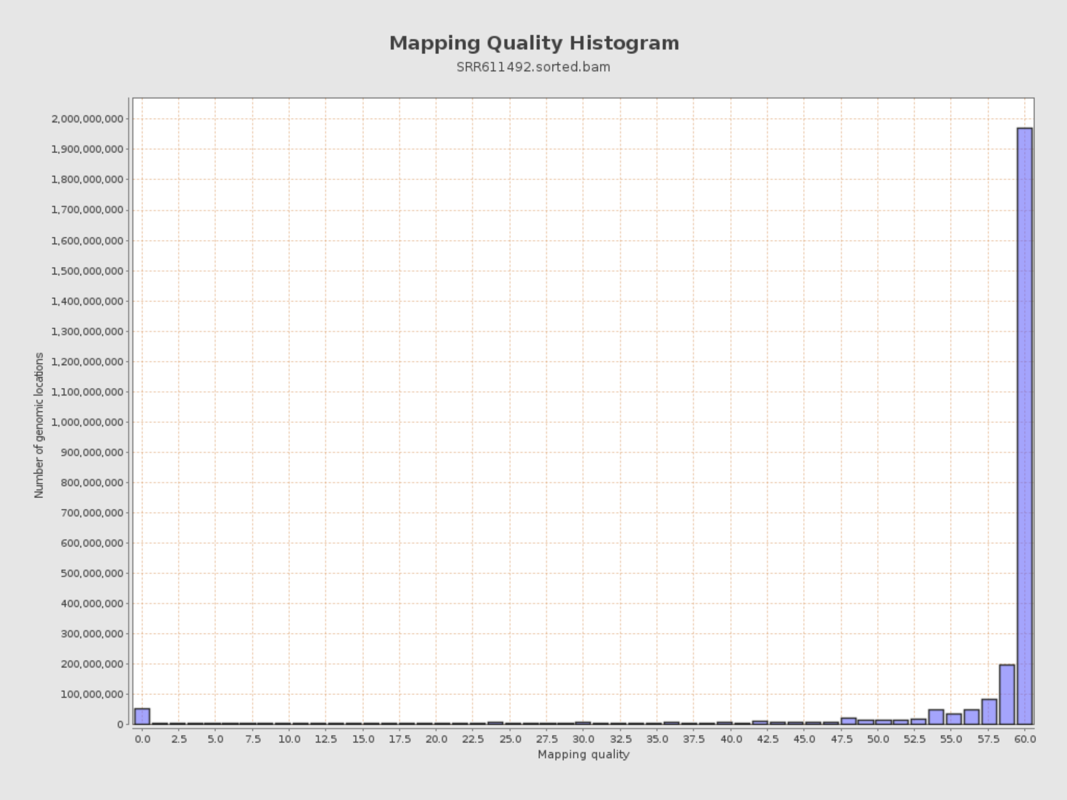
11. Results : Homopolymer Indels



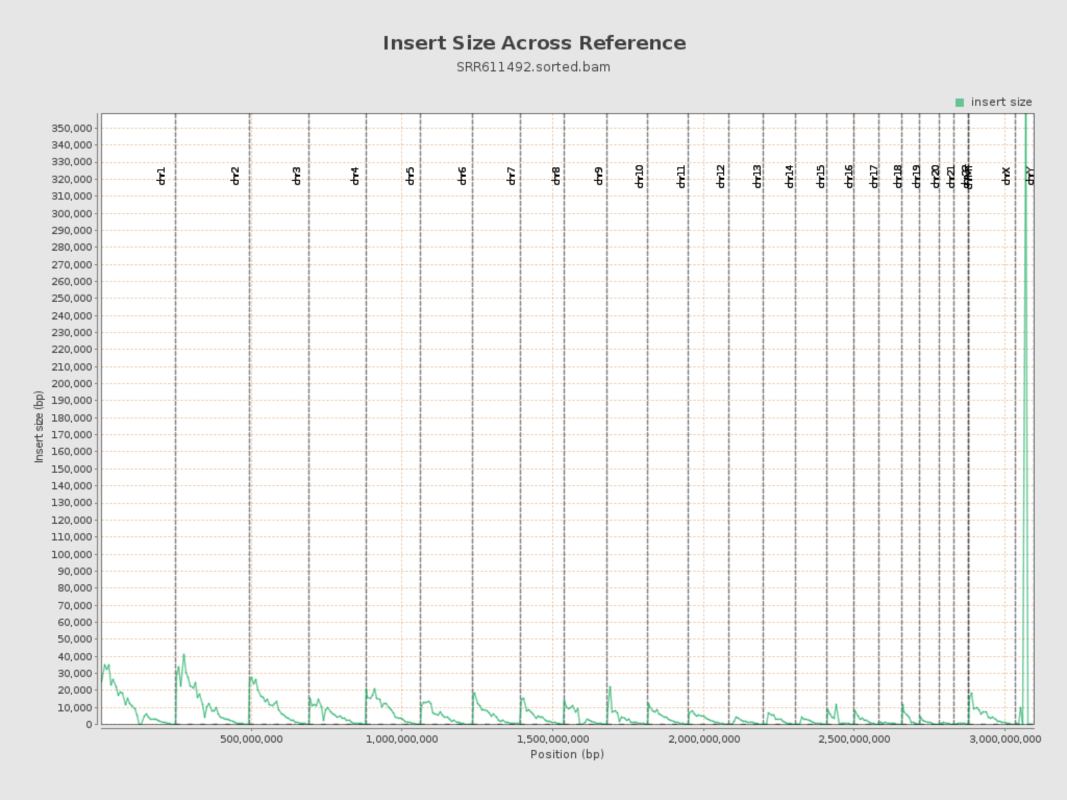
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram