Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 01:42:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618670.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_SRR618670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618670_1.fastq.gz SRR618670_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 01:42:43 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,244,357,534
Mapped reads	1,180,885,245 / 94.9%
Unmapped reads	63,472,289 / 5.1%
Mapped paired reads	1,180,885,245 / 94.9%
Mapped reads, first in pair	596,152,269 / 47.91%
Mapped reads, second in pair	584,732,976 / 46.99%
Mapped reads, both in pair	1,156,589,366 / 92.95%
Mapped reads, singletons	24,295,879 / 1.95%
Secondary alignments	0
Supplementary alignments	3,698,017 / 0.3%
Read min/max/mean length	30 / 101 / 101.12
Duplicated reads (estimated)	326,020,944 / 26.2%
Duplication rate	23.66%
Clipped reads	137,481,282 / 11.05%

2.2. ACGT Content

Number/percentage of A's	33,681,216,602 / 29%
Number/percentage of C's	24,304,636,617 / 20.93%
Number/percentage of T's	33,535,730,465 / 28.88%
Number/percentage of G's	24,409,594,019 / 21.02%
Number/percentage of N's	200,981,400 / 0.17%

GC Percentage	41.95%

2.3. Coverage

Mean	37.5246
Standard Deviation	386.1723

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	44,333.94
Standard Deviation	2,022,305.4
P25/Median/P75	165 / 173 / 181

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	1,243,899,460
Insertions	11,334,137
Mapped reads with at least one insertion	0.93%
Deletions	14,092,530
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.61%

2.7. Chromosome stats

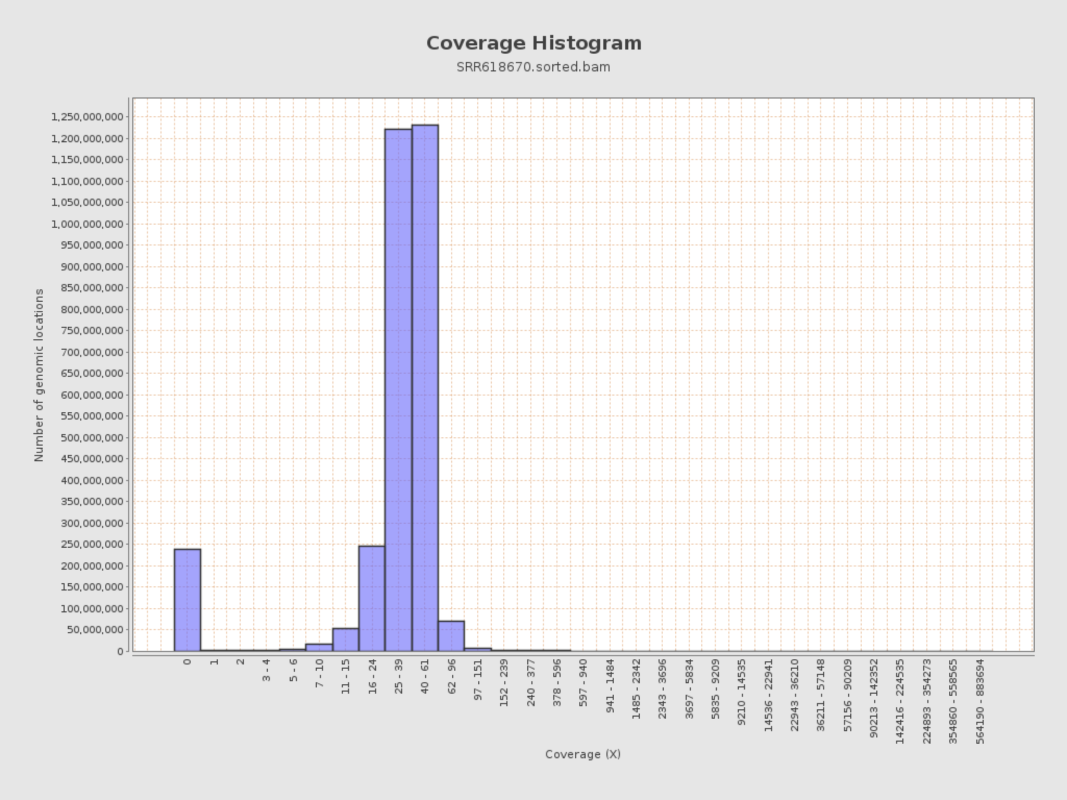
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	**coverage**	**deviation**
chr1	249250621	9624259767	38.6128	915.9013
chr2	243199373	9975035713	41.0159	262.0108
chr3	198022430	7670777522	38.7369	31.1576
chr4	191154276	7635526713	39.9443	201.8018
chr5	180915260	6985442558	38.6117	33.7179
chr6	171115067	6678242375	39.0278	174.2197
chr7	159138663	6320606743	39.7176	285.7924
chr8	146364022	5892882013	40.2618	392.7853
chr9	141213431	5023634181	35.5748	417.9815
chr10	135534747	6125701437	45.1965	853.5343
chr11	135006516	5413434924	40.0976	214.2629
chr12	133851895	5176465152	38.6731	30.4418
chr13	115169878	3680446108	31.9567	22.1513
chr14	107349540	3546802781	33.0398	37.1792
chr15	102531392	3376286788	32.9293	23.1305
chr16	90354753	3749621912	41.4989	271.8024
chr17	81195210	3345407250	41.202	184.5295
chr18	78077248	3272765248	41.917	534.2072
chr19	59128983	2456679023	41.5478	406.6107
chr20	63025520	2518644484	39.9623	105.8065
chr21	48129895	1645203692	34.1826	200.6359
chr22	51304566	1561497071	30.4358	179.4728
chrMT	16571	57286963	3,457.0613	551.9187
chrX	155270560	3108249301	20.0183	91.0928

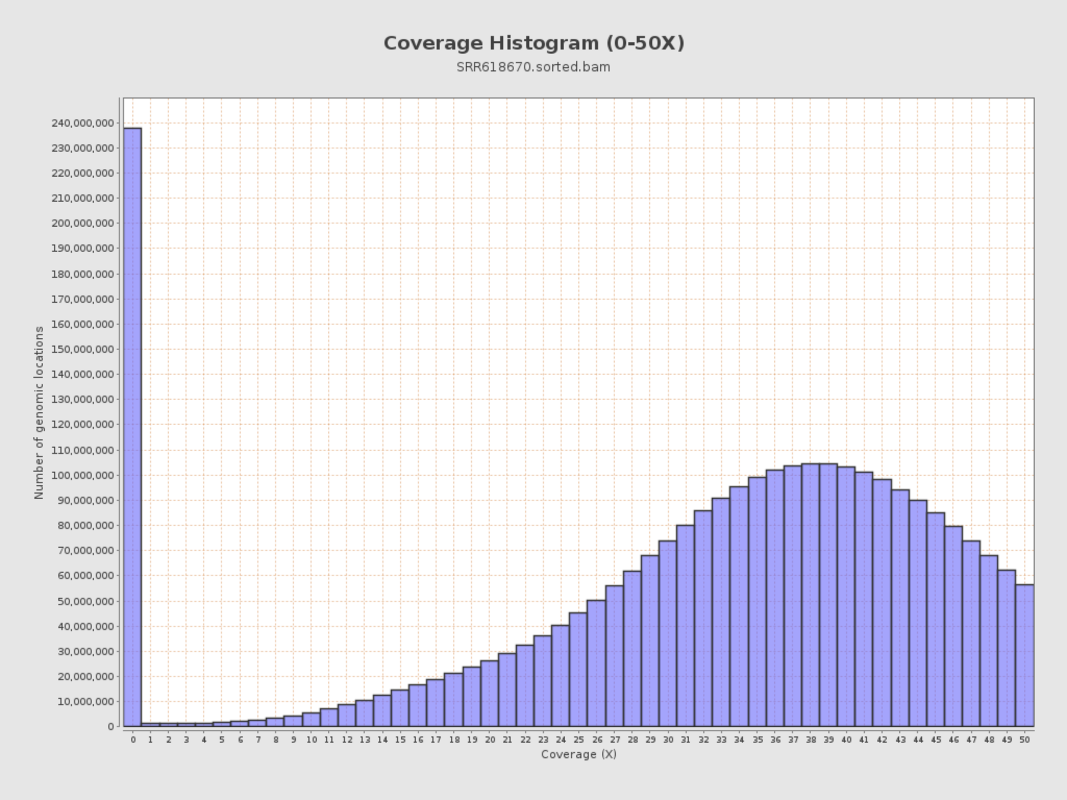
chrY	59373566	1323809232	22.2963	401.0469

3. Results : Coverage across reference

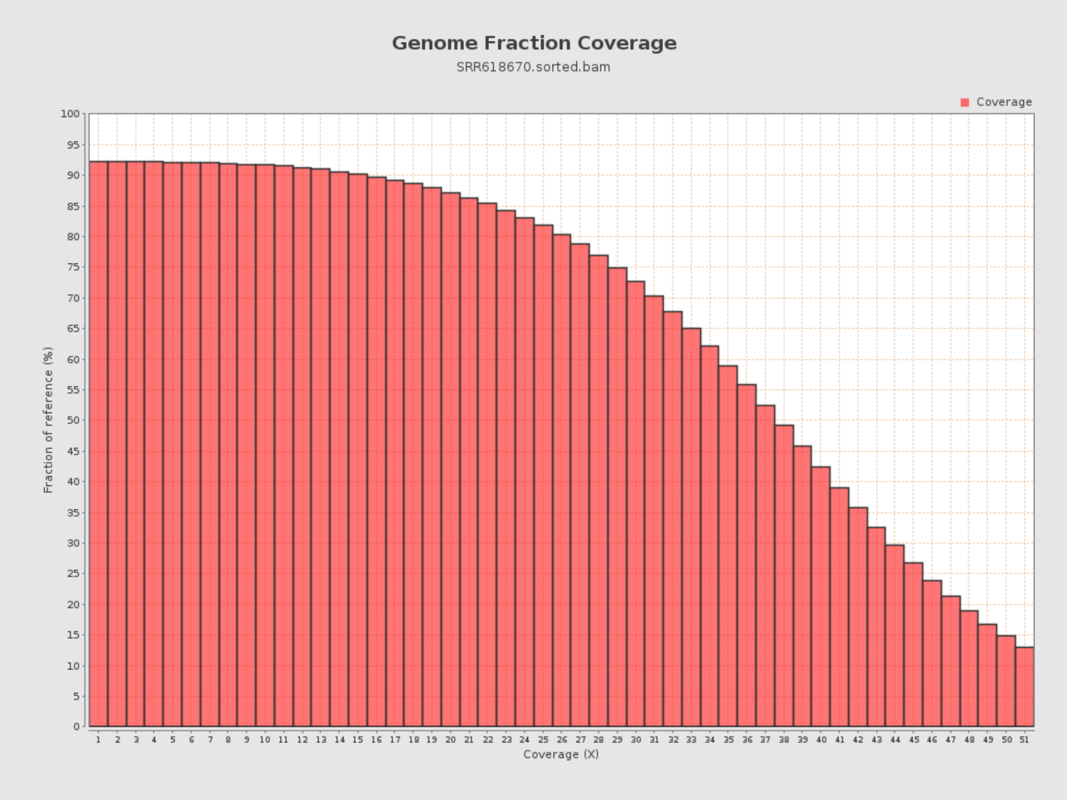
4. Results : Coverage Histogram



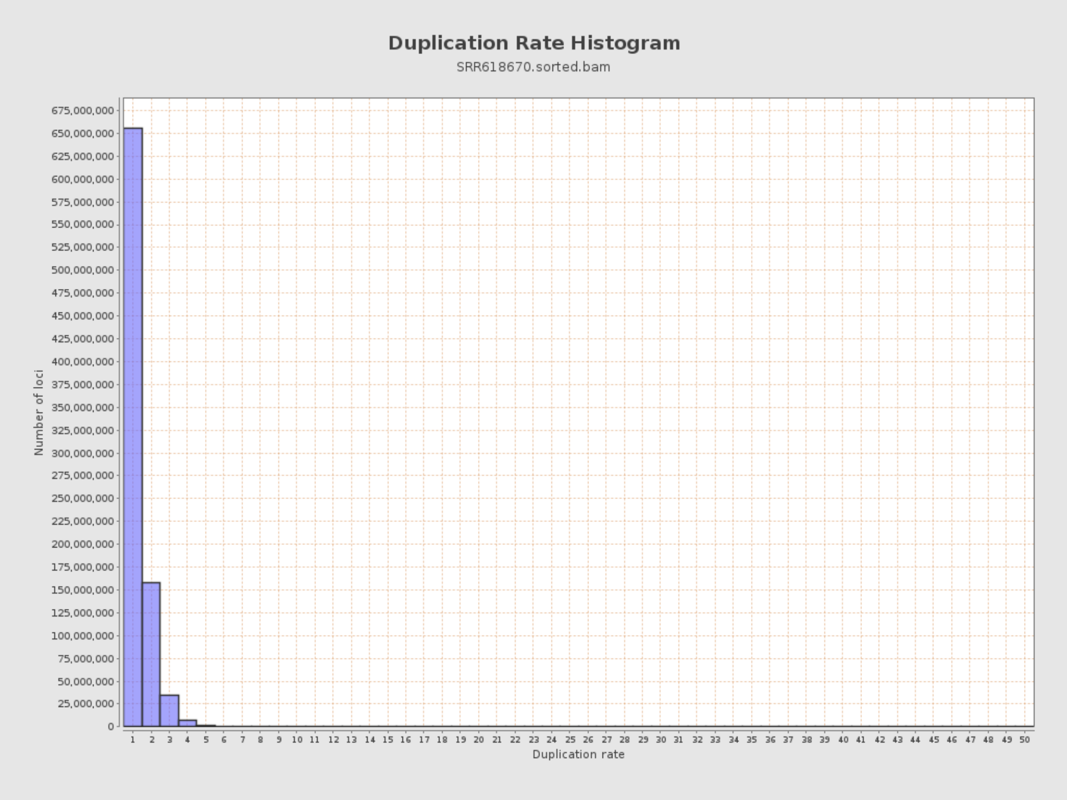
5. Results : Coverage Histogram (0-50X)



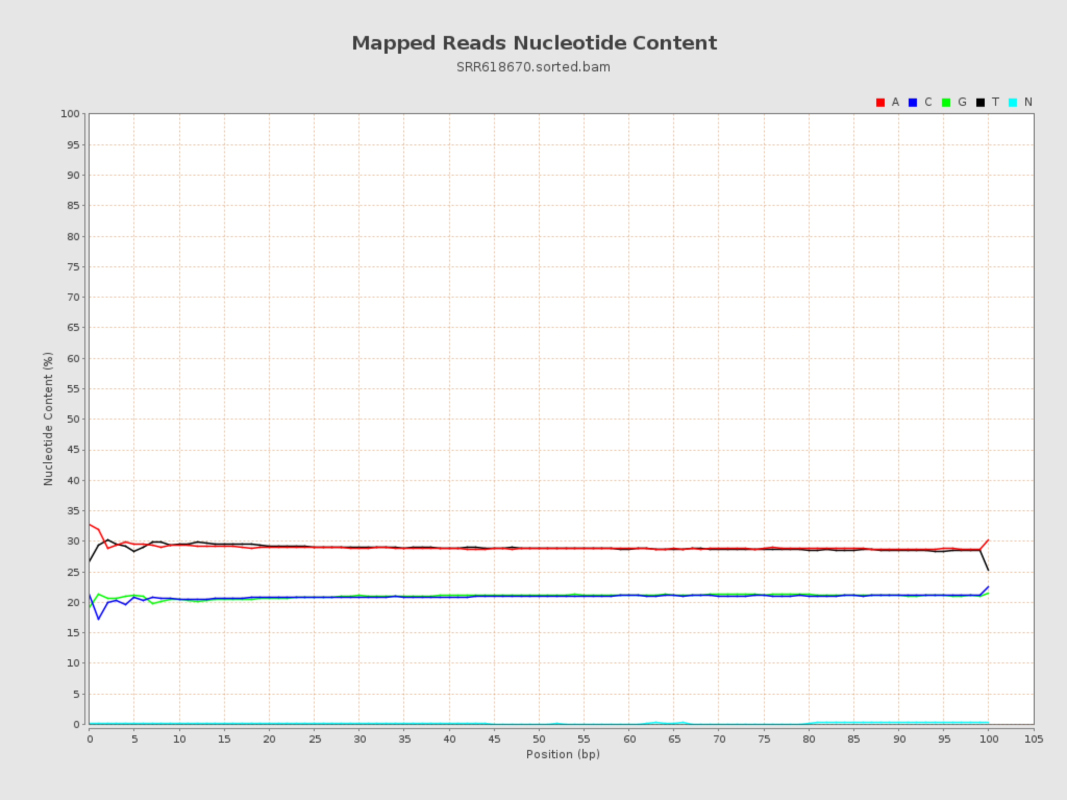
6. Results : Genome Fraction Coverage



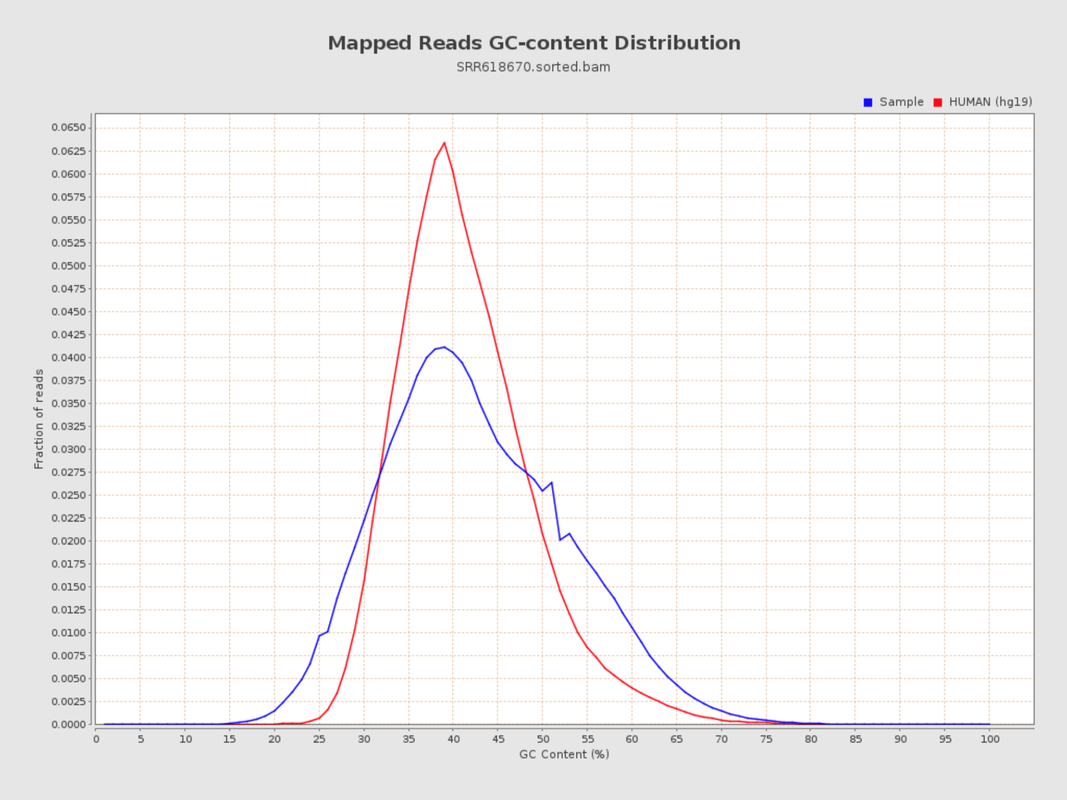
7. Results : Duplication Rate Histogram



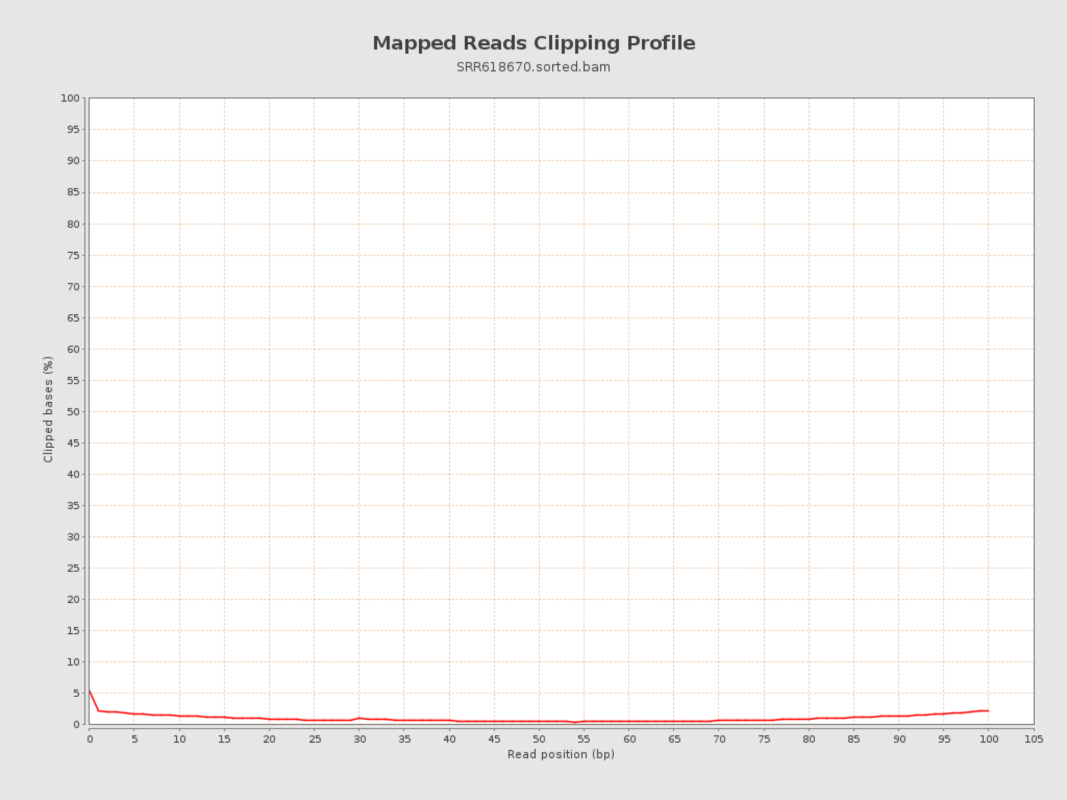
8. Results : Mapped Reads Nucleotide Content



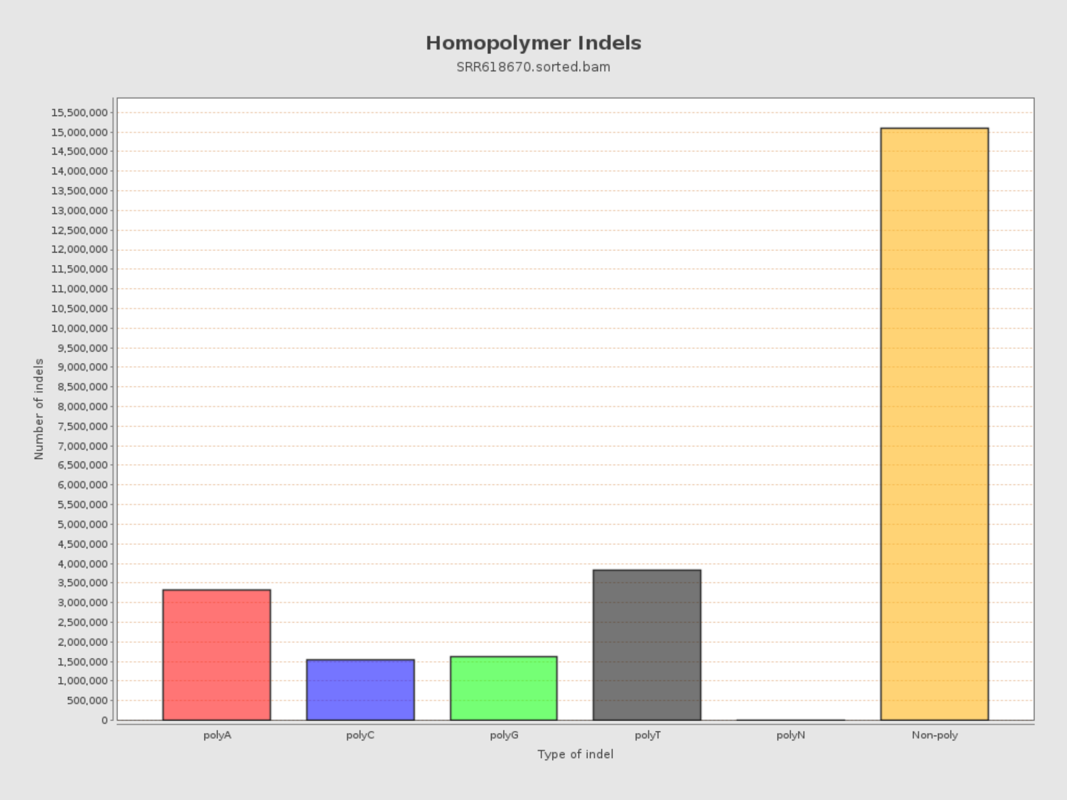
9. Results : Mapped Reads GC-content Distribution



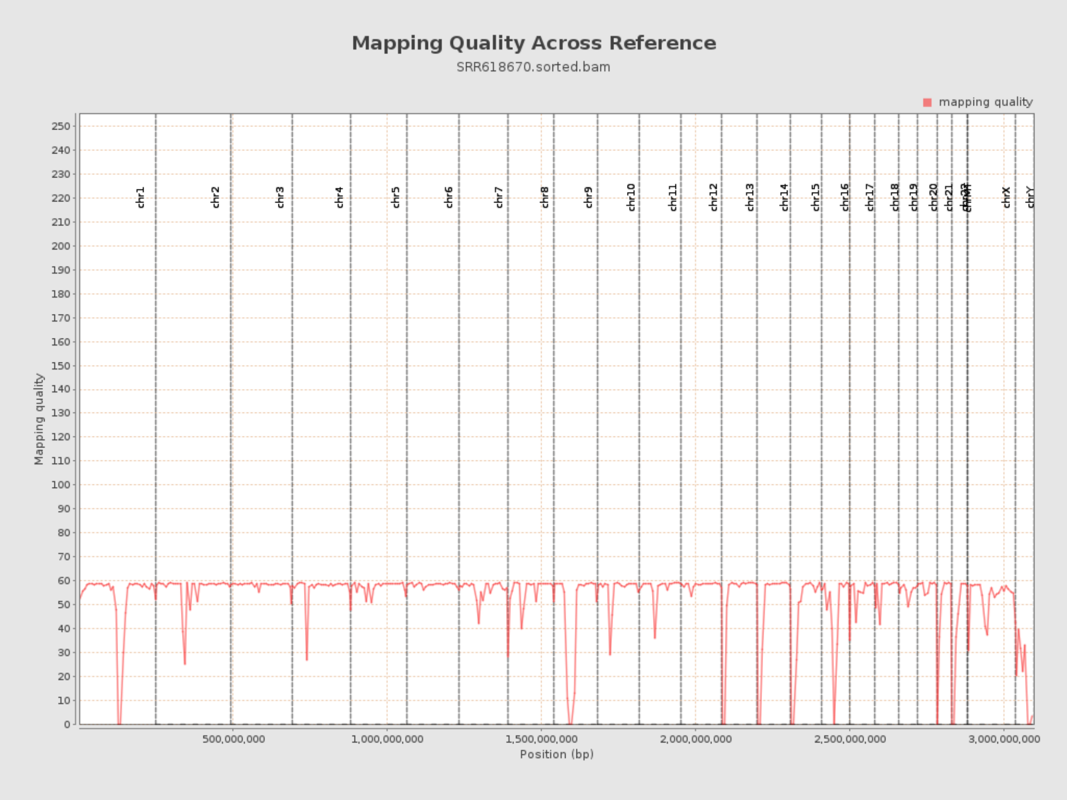
10. Results : Mapped Reads Clipping Profile



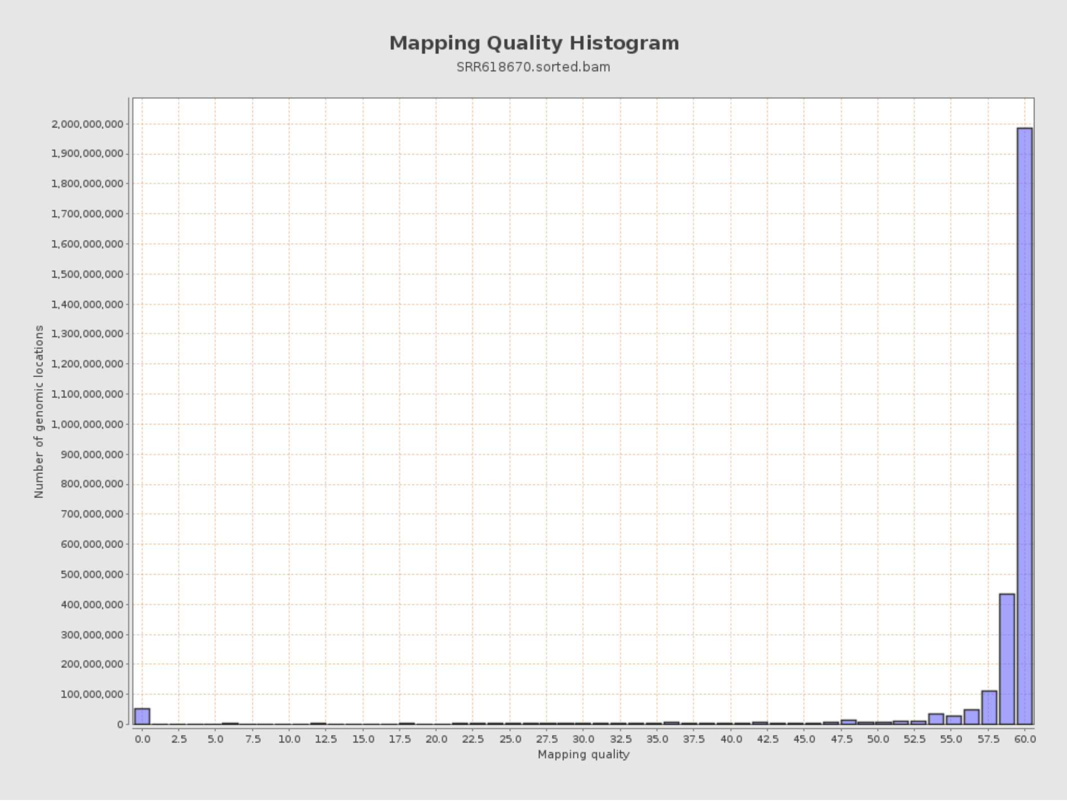
11. Results : Homopolymer Indels



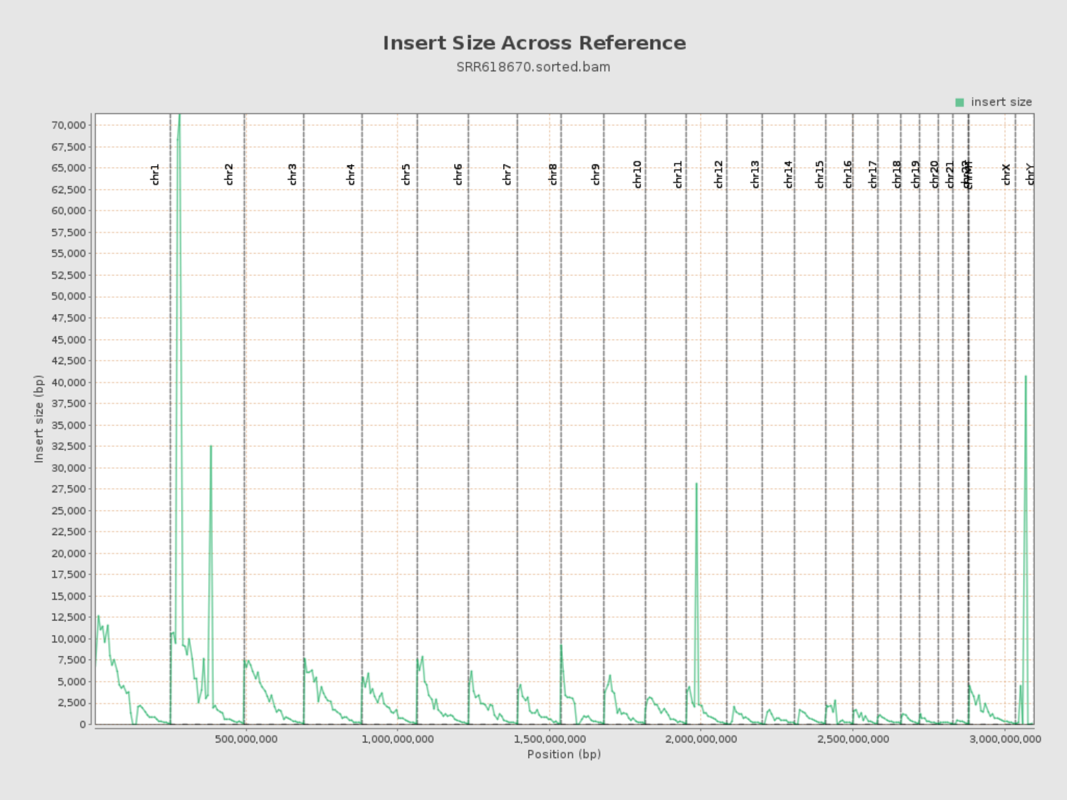
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram