Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 11:25:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617672.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_SRR617672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617672_1.fastq.gz SRR617672_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 11:25:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,059,447 / 93.94%
Unmapped reads	1,940,553 / 6.06%
Mapped paired reads	30,059,447 / 93.94%
Mapped reads, first in pair	15,276,011 / 47.74%
Mapped reads, second in pair	14,783,436 / 46.2%
Mapped reads, both in pair	29,208,448 / 91.28%
Mapped reads, singletons	850,999 / 2.66%
Secondary alignments	0
Supplementary alignments	165,242 / 0.52%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,760,565 / 21.13%
Duplication rate	10.44%
Clipped reads	6,693,989 / 20.92%

2.2. ACGT Content

Number/percentage of A's	862,009,200 / 29.76%
Number/percentage of C's	574,789,429 / 19.84%
Number/percentage of T's	860,749,390 / 29.71%
Number/percentage of G's	596,291,666 / 20.58%
Number/percentage of N's	3,088,169 / 0.11%

GC Percentage	40.42%

2.3. Coverage

Mean	0.9364
Standard Deviation	10.3228

2.4. Mapping Quality

Mean Mapping Quality	52.49

2.5. Insert size

Mean	45,696.31
Standard Deviation	1,996,448.99
P25/Median/P75	178 / 221 / 287

2.6. Mismatches and indels

General error rate	1.69%
Mismatches	47,980,981
Insertions	453,176
Mapped reads with at least one insertion	1.48%
Deletions	1,057,249
Mapped reads with at least one deletion	3.44%
Homopolymer indels	47.43%

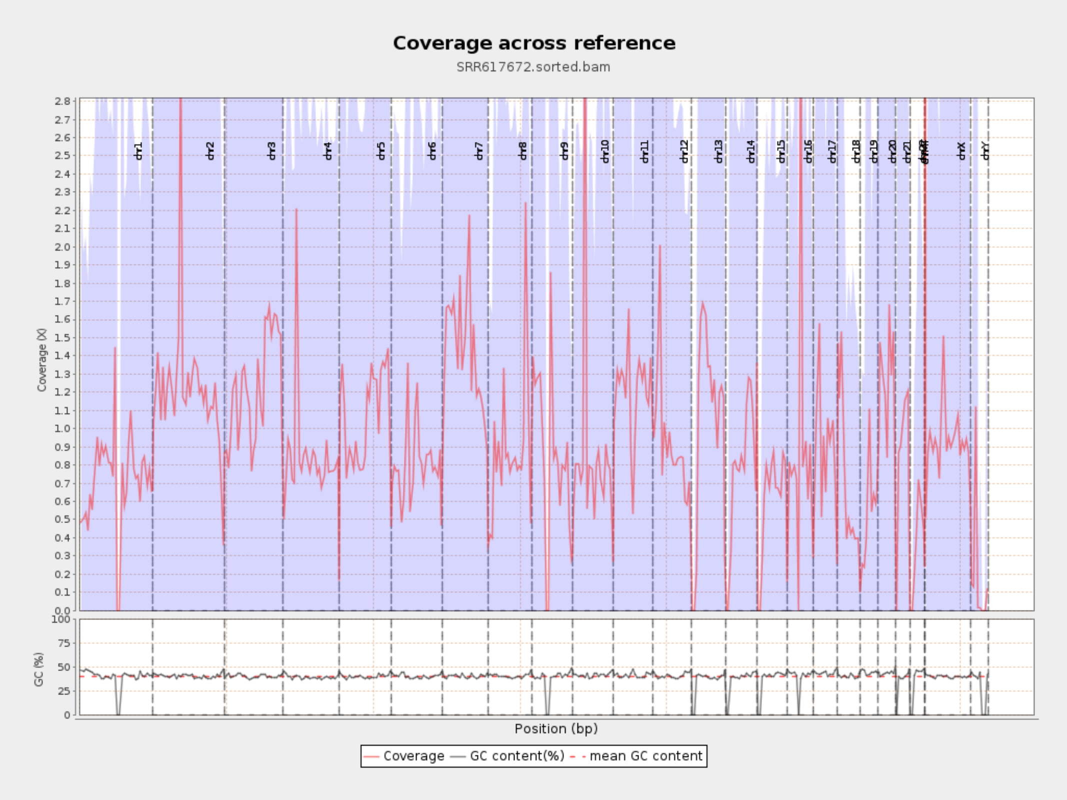
2.7. Chromosome stats

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

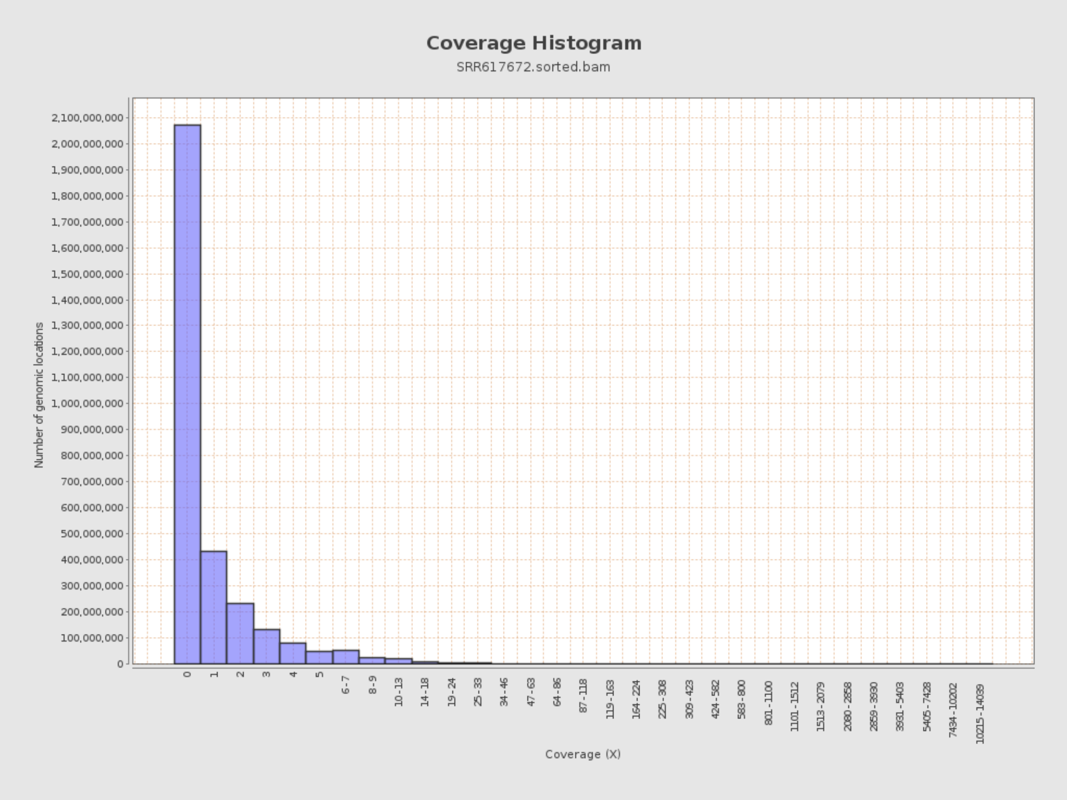
		bases	coverage	deviation
chr1	249250621	177738490	0.7131	9.959
chr2	243199373	299195740	1.2302	11.8908
chr3	198022430	243133806	1.2278	2.4672
chr4	191154276	162084234	0.8479	8.0678
chr5	180915260	192052635	1.0616	2.3157
chr6	171115067	140302698	0.8199	5.7006
chr7	159138663	226581041	1.4238	13.1051
chr8	146364022	128959555	0.8811	4.0644
chr9	141213431	118617652	0.84	19.414
chr10	135534747	122591895	0.9045	21.1058
chr11	135006516	159326793	1.1801	11.8688
chr12	133851895	123895789	0.9256	2.164
chr13	115169878	124542066	1.0814	2.3057
chr14	107349540	83047132	0.7736	2.4828
chr15	102531392	61955486	0.6043	1.6977
chr16	90354753	80356955	0.8893	16.5779
chr17	81195210	71348747	0.8787	12.3563
chr18	78077248	53475368	0.6849	17.9935
chr19	59128983	30844522	0.5216	5.9389
chr20	63025520	78566384	1.2466	3.0314
chr21	48129895	42261656	0.8781	4.3089
chr22	51304566	18638238	0.3633	1.268
chrMT	16571	3100049	187.0768	131.0265
chrX	155270560	144418414	0.9301	4.2623

chrY	59373566	11639972	0.196	16.4217

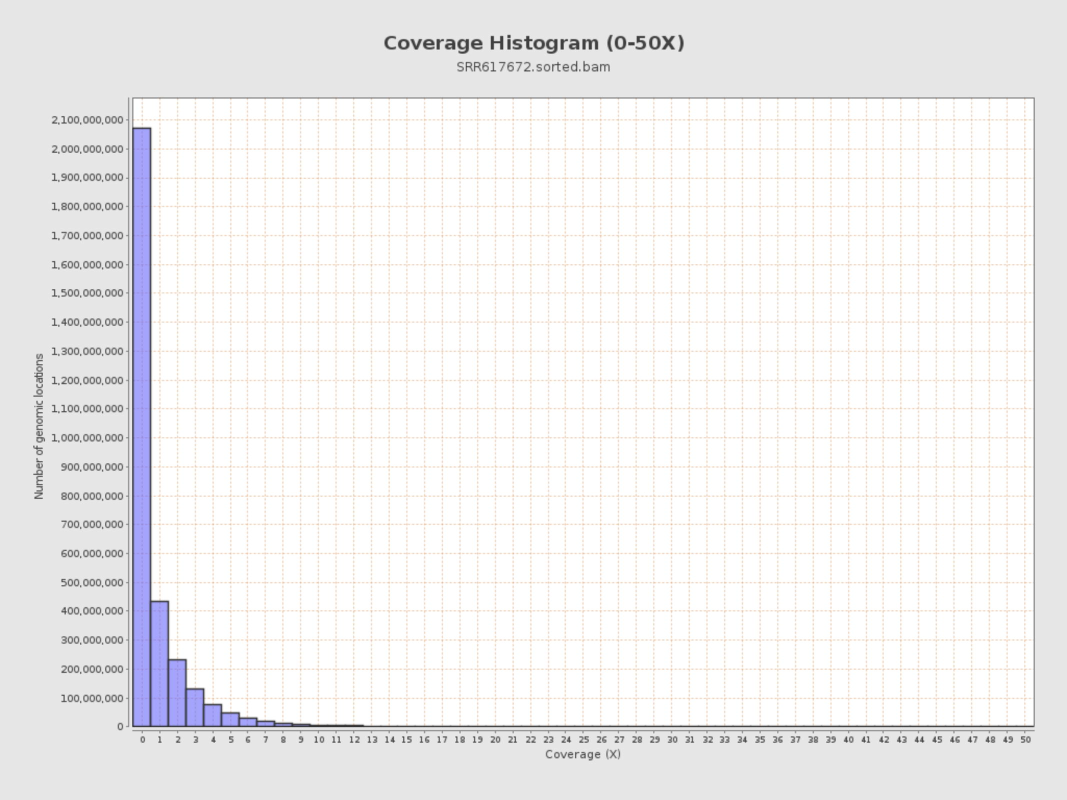
3. Results : Coverage across reference



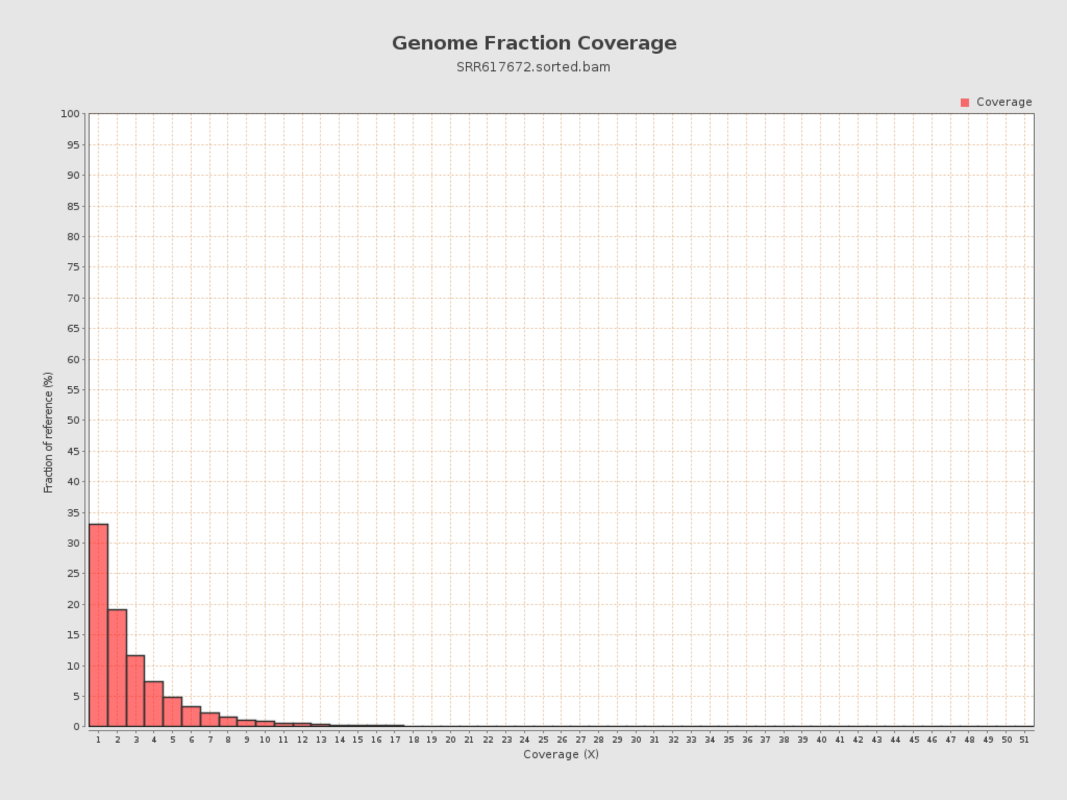
4. Results : Coverage Histogram



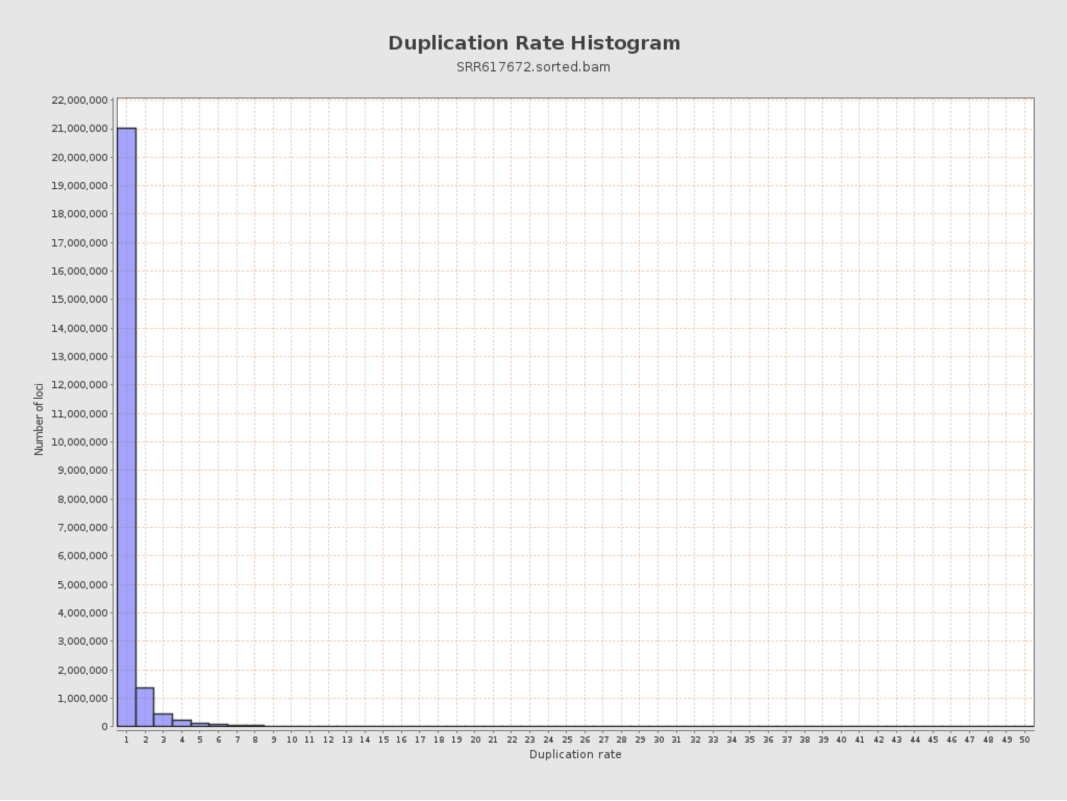
5. Results : Coverage Histogram (0-50X)



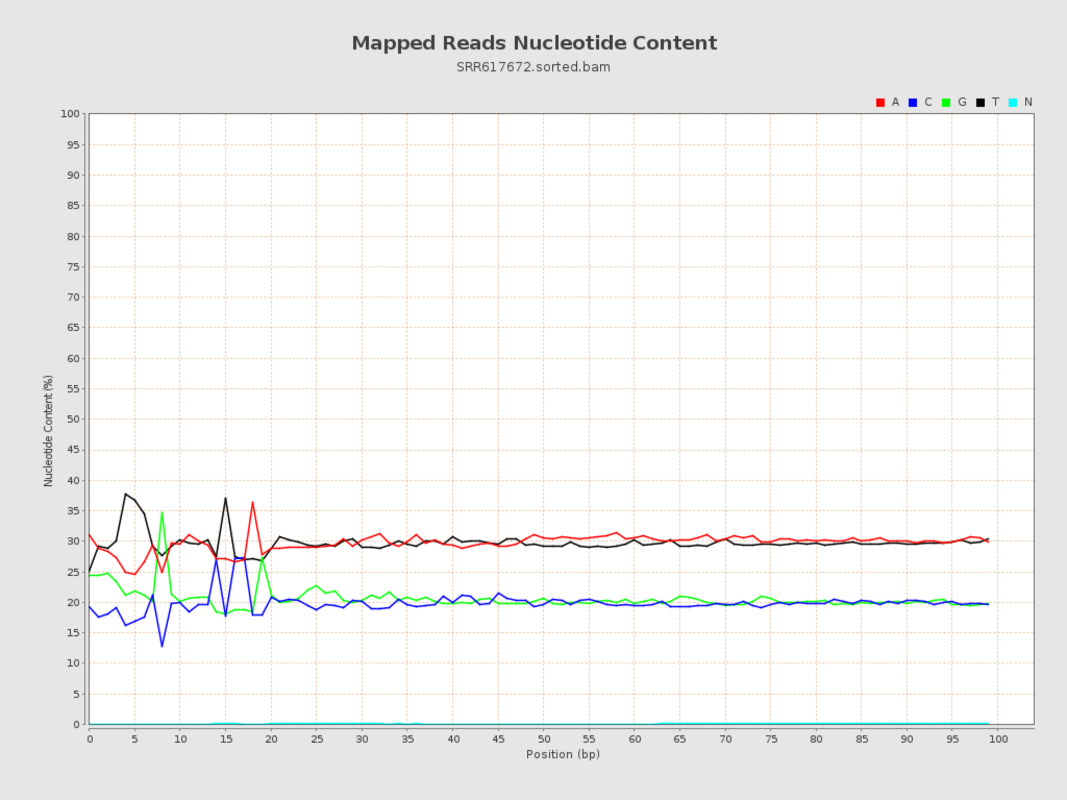
6. Results : Genome Fraction Coverage



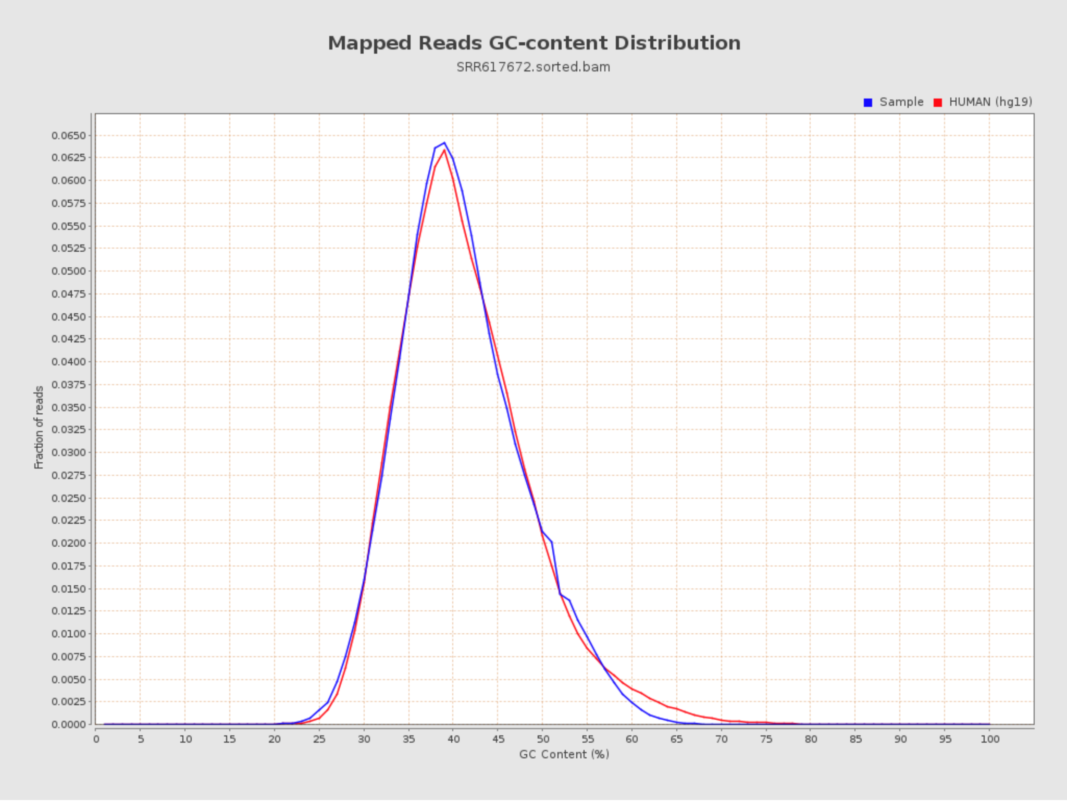
7. Results : Duplication Rate Histogram



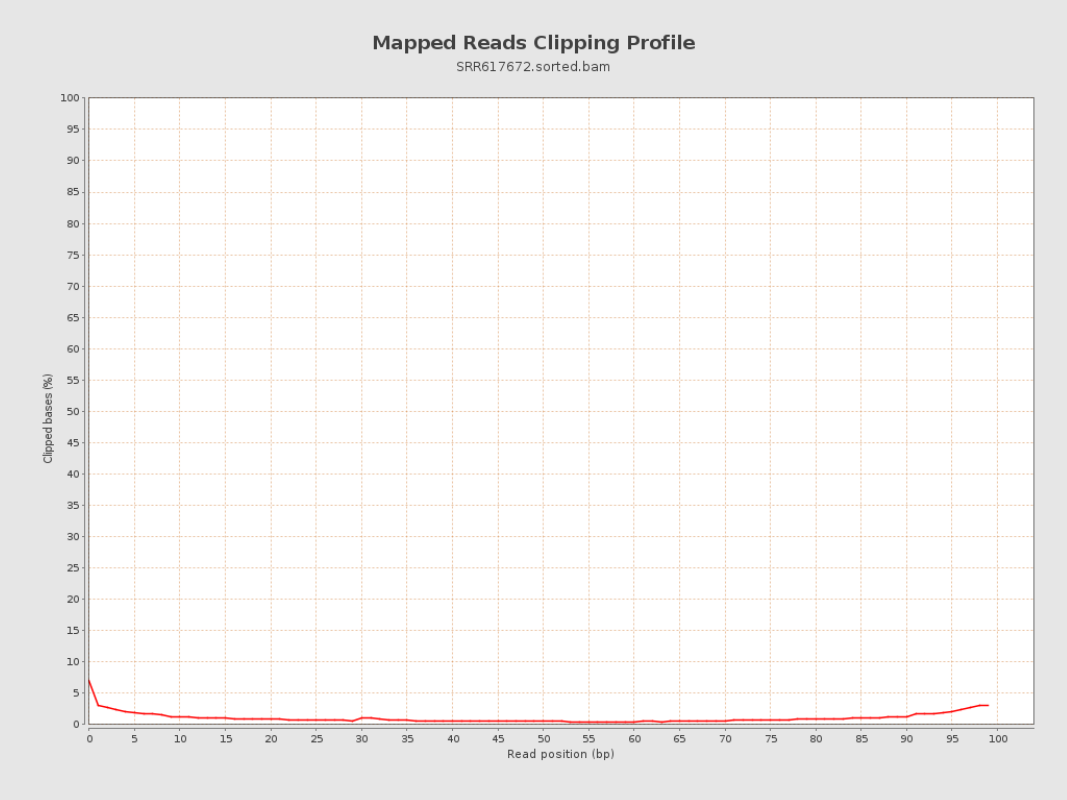
8. Results : Mapped Reads Nucleotide Content



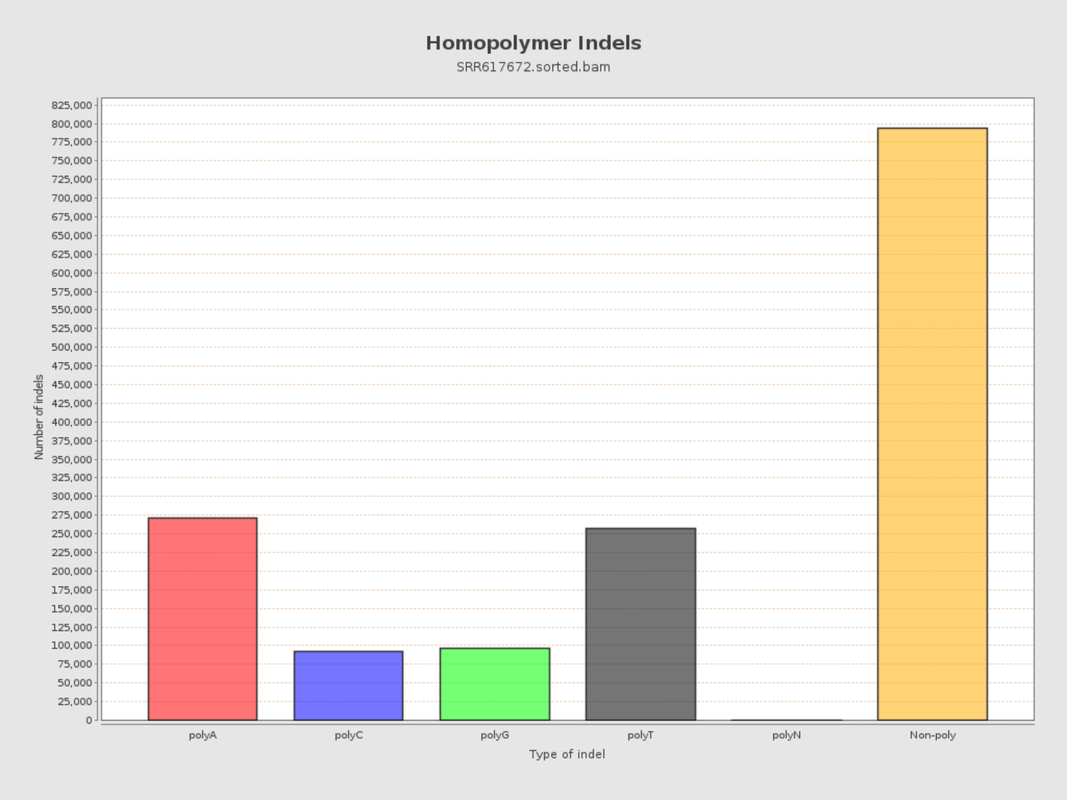
9. Results : Mapped Reads GC-content Distribution



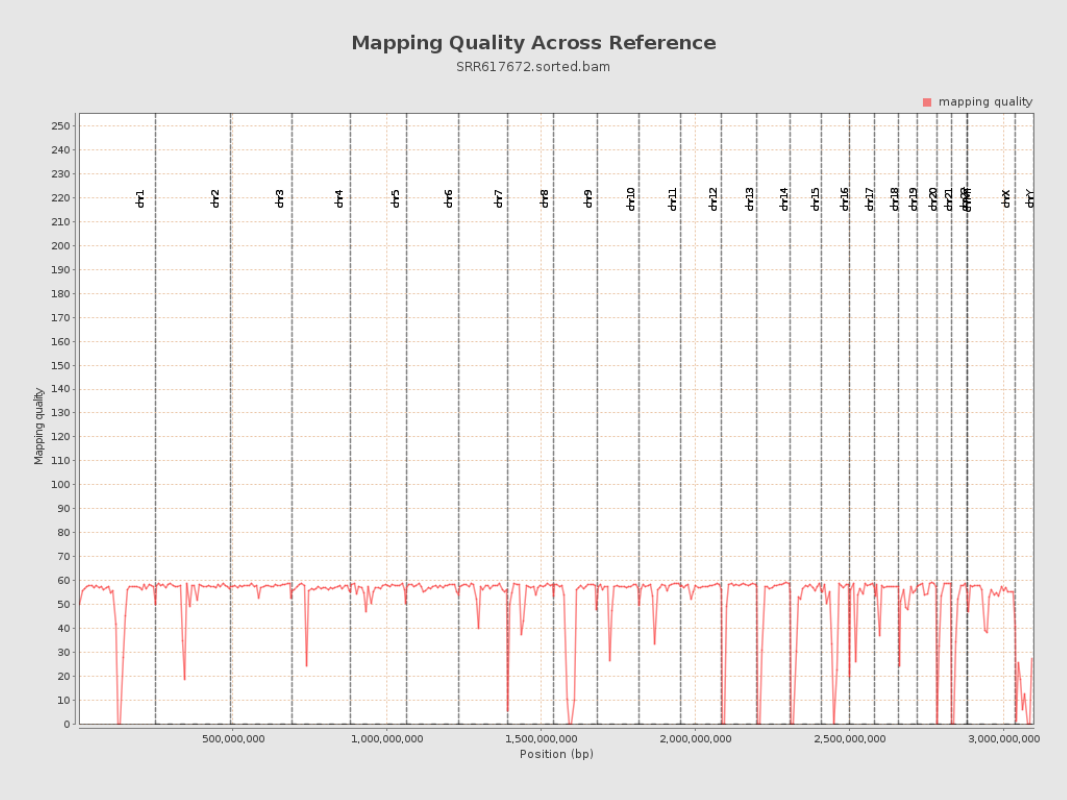
10. Results : Mapped Reads Clipping Profile



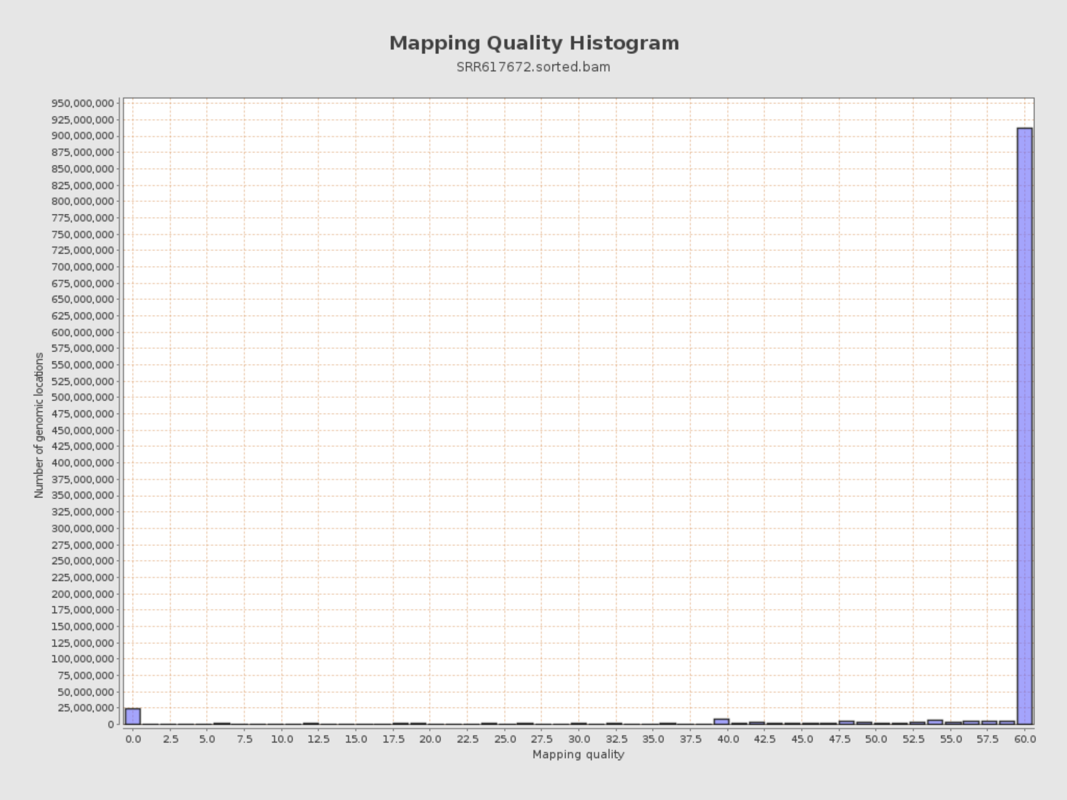
11. Results : Homopolymer Indels



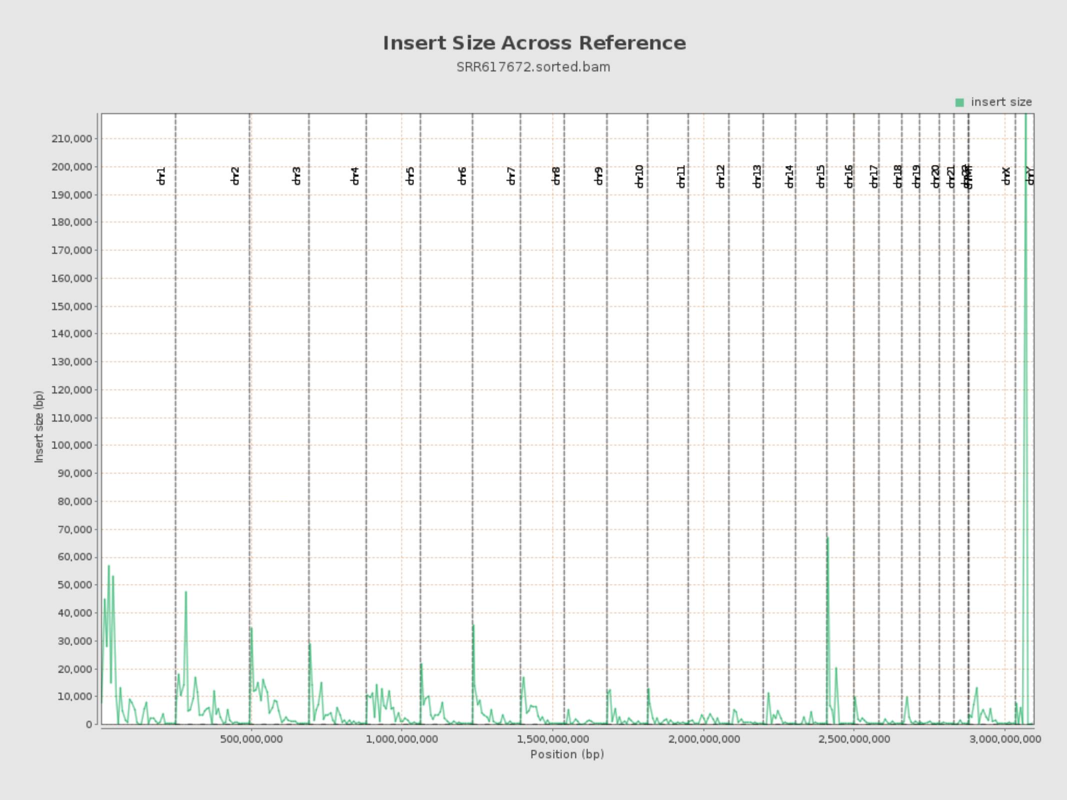
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram