Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 02:57:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617700.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_SRR8617700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617700_1.fastq.gz SRR8617700_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 02:57:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,418,896
Mapped reads	43,762,570 / 98.52%
Unmapped reads	656,326 / 1.48%
Mapped paired reads	43,762,570 / 98.52%
Mapped reads, first in pair	22,065,291 / 49.68%
Mapped reads, second in pair	21,697,279 / 48.85%
Mapped reads, both in pair	43,299,270 / 97.48%
Mapped reads, singletons	463,300 / 1.04%
Secondary alignments	0
Supplementary alignments	1,405,384 / 3.16%
Read min/max/mean length	30 / 150 / 151.58
Duplicated reads (estimated)	14,254,687 / 32.09%
Duplication rate	22.77%
Clipped reads	24,798,535 / 55.83%

2.2. ACGT Content

Number/percentage of A's	1,702,634,333 / 29.24%
Number/percentage of C's	1,085,897,562 / 18.65%
Number/percentage of T's	1,766,036,458 / 30.33%
Number/percentage of G's	1,268,423,453 / 21.78%
Number/percentage of N's	225,518 / 0%

GC Percentage	40.43%

2.3. Coverage

Mean	1.8824
Standard Deviation	25.1517

2.4. Mapping Quality

Mean Mapping Quality	53.29

2.5. Insert size

Mean	213,414.72
Standard Deviation	4,392,737.29
P25/Median/P75	210 / 263 / 331

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	66,548,460
Insertions	962,279
Mapped reads with at least one insertion	2.09%
Deletions	2,038,707
Mapped reads with at least one deletion	4.49%
Homopolymer indels	46.84%

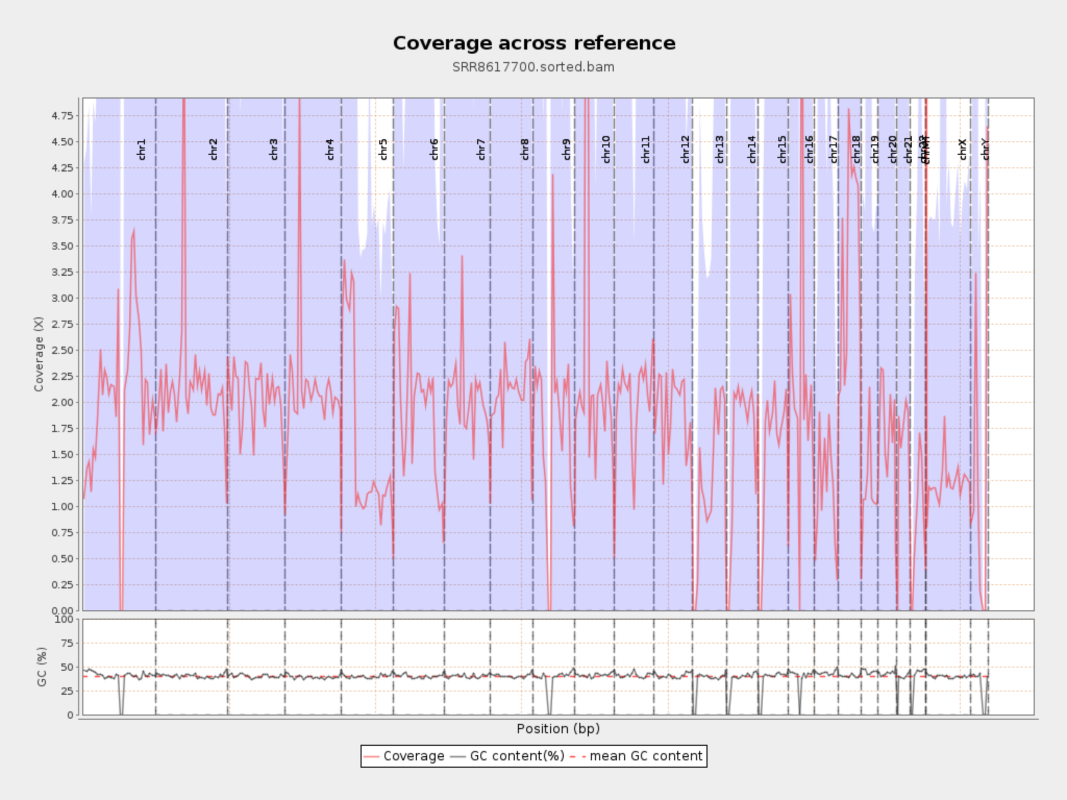
2.7. Chromosome stats

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

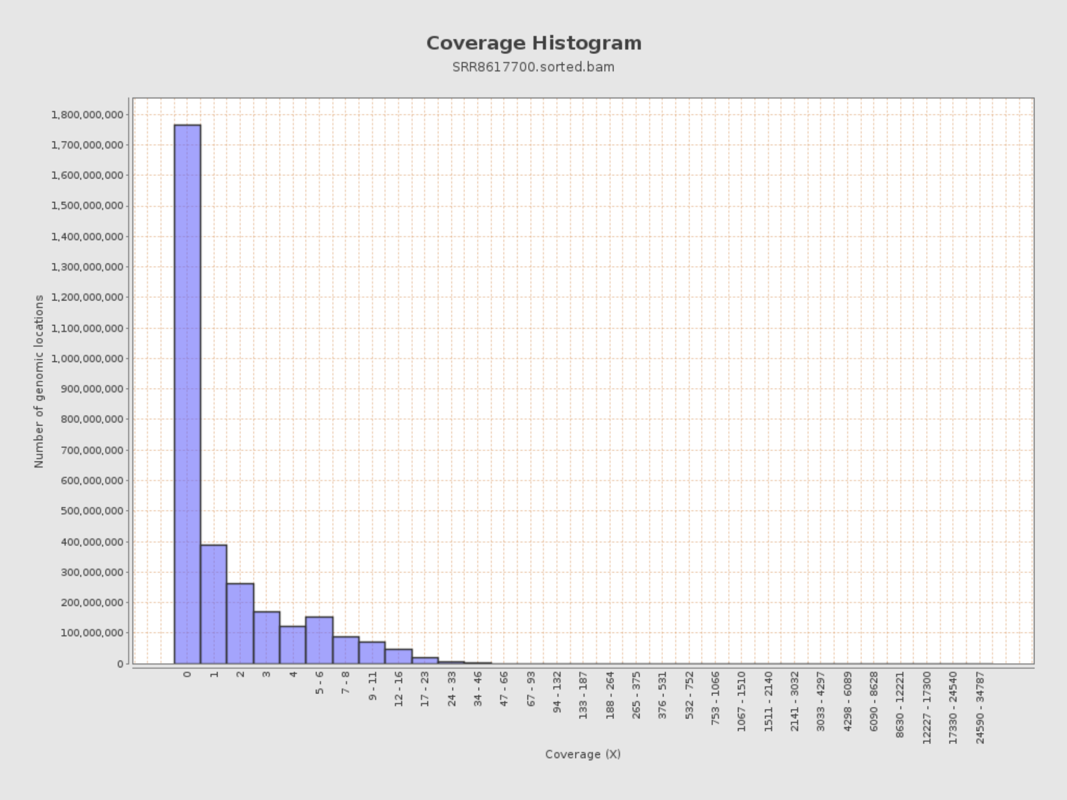
		bases	coverage	deviation
chr1	249250621	501540530	2.0122	22.0796
chr2	243199373	535604328	2.2023	25.9057
chr3	198022430	404726363	2.0438	4.0972
chr4	191154276	412516993	2.158	19.8725
chr5	180915260	286533620	1.5838	3.7764
chr6	171115067	337604711	1.973	13.2537
chr7	159138663	320126478	2.0116	28.5575
chr8	146364022	306798223	2.0961	7.3017
chr9	141213431	253035802	1.7919	50.5003
chr10	135534747	325180311	2.3992	68.518
chr11	135006516	273920138	2.0289	13.7288
chr12	133851895	255494605	1.9088	8.265
chr13	115169878	143721369	1.2479	2.8376
chr14	107349540	172785297	1.6096	3.9187
chr15	102531392	155410843	1.5157	4.6516
chr16	90354753	202561359	2.2418	37.0264
chr17	81195210	95726344	1.179	16.6599
chr18	78077248	268007756	3.4326	42.6198
chr19	59128983	70678288	1.1953	12.141
chr20	63025520	112413656	1.7836	6.7971
chr21	48129895	74601577	1.55	10.2923
chr22	51304566	44555510	0.8685	2.6678
chrMT	16571	881982	53.2244	28.5988
chrX	155270560	189611185	1.2212	5.3694

chrY	59373566	83145358	1.4004	36.3238

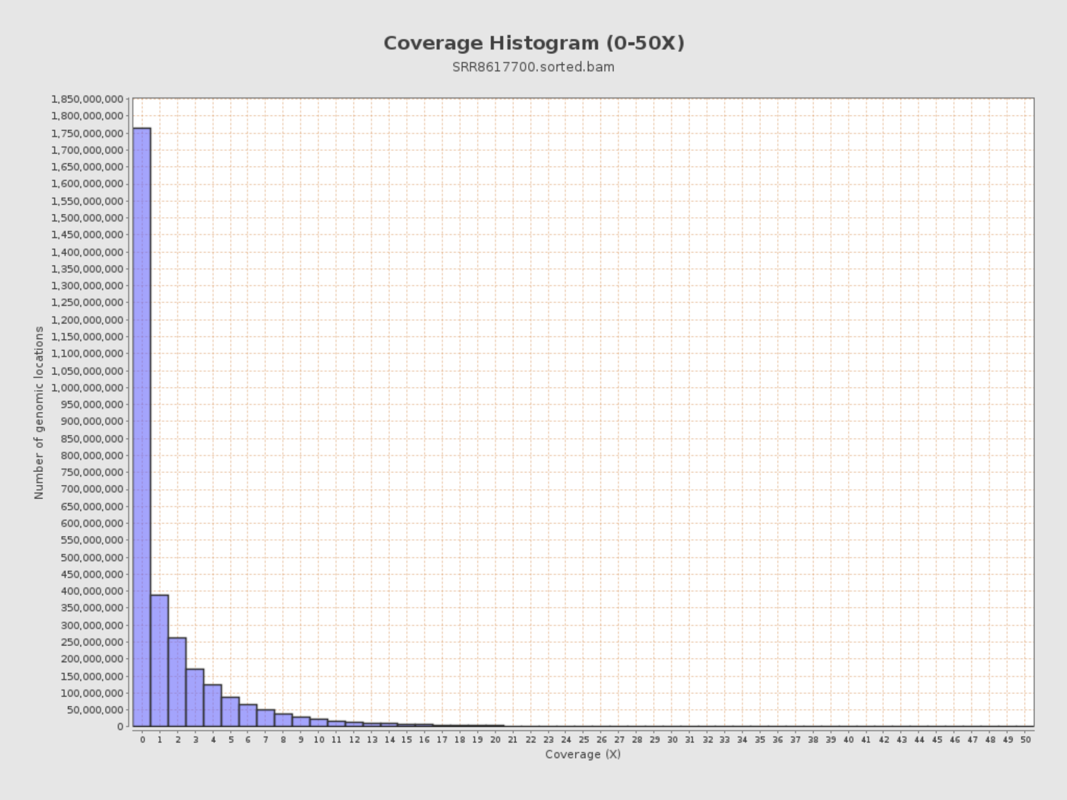
3. Results : Coverage across reference



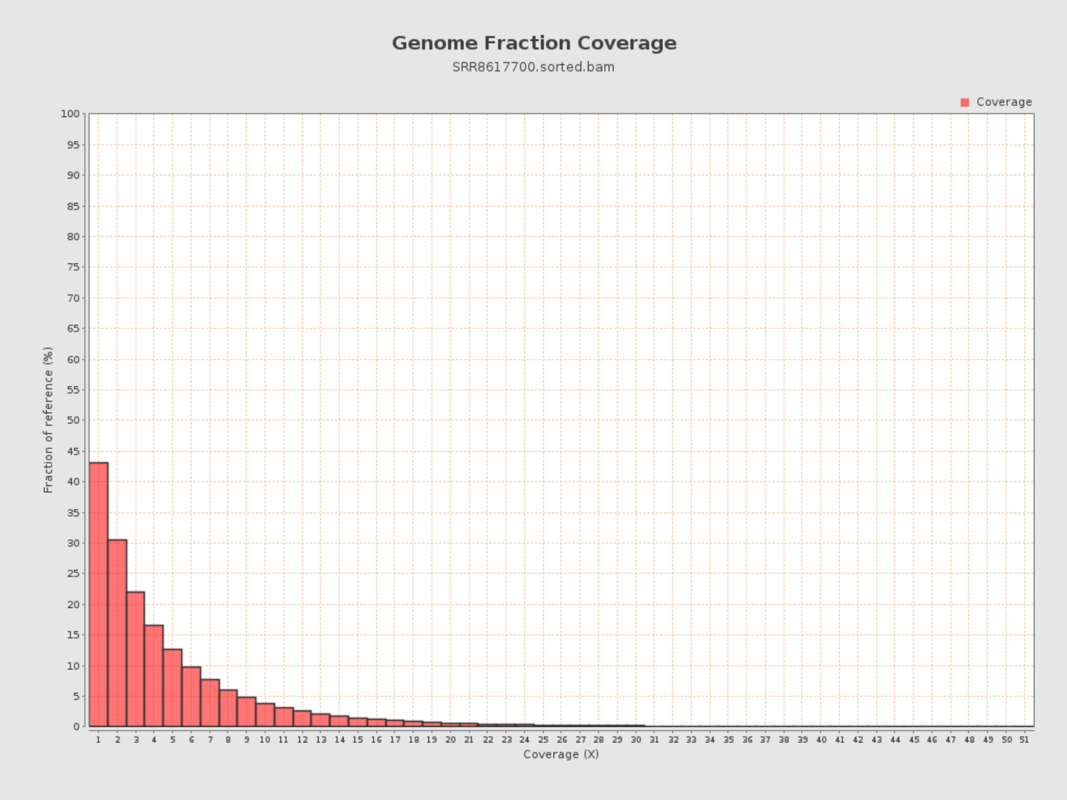
4. Results : Coverage Histogram



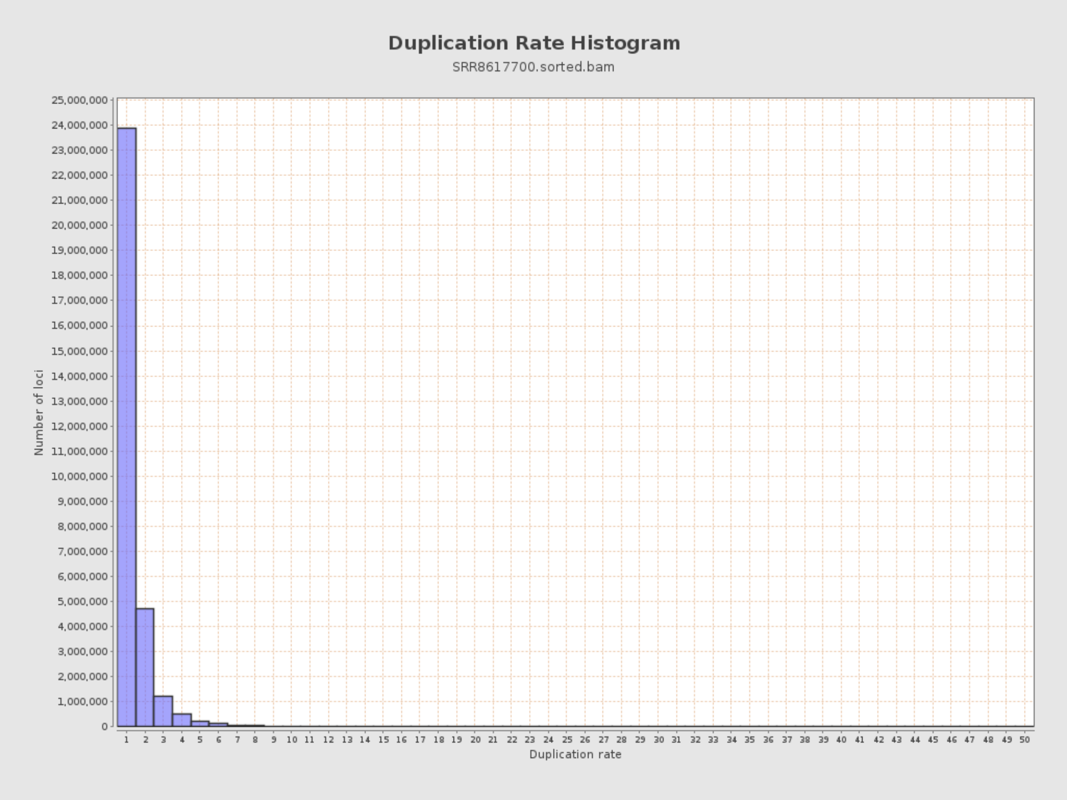
5. Results : Coverage Histogram (0-50X)



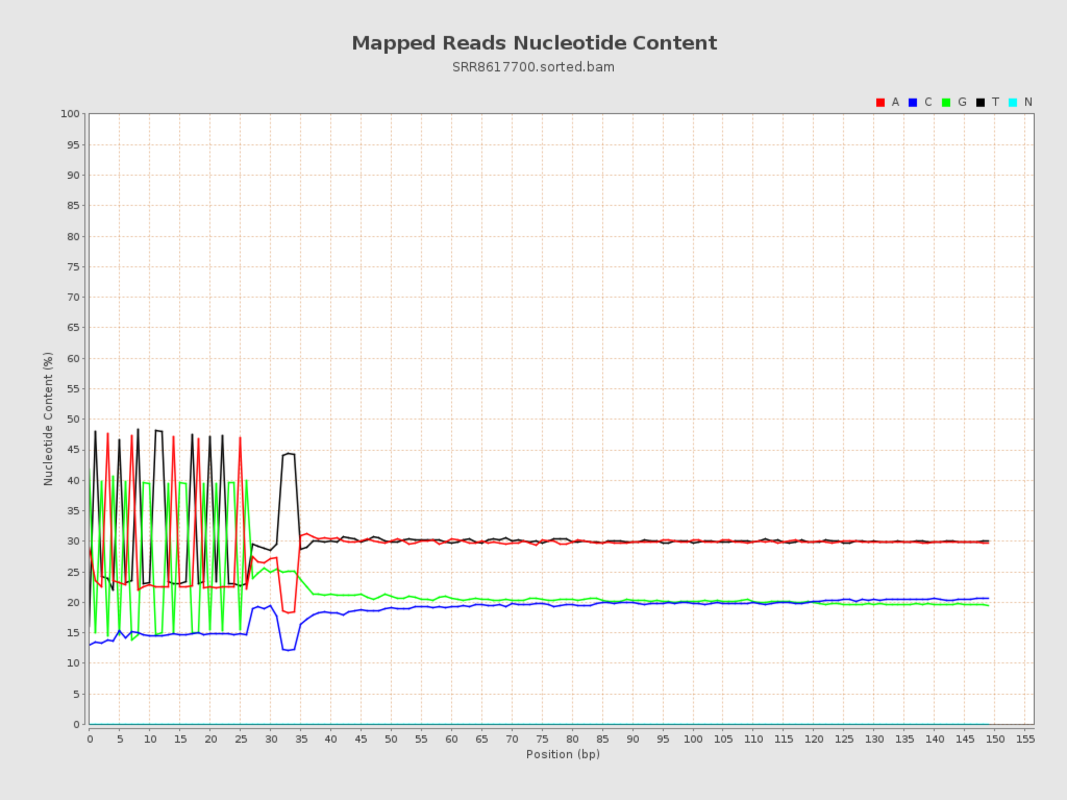
6. Results : Genome Fraction Coverage



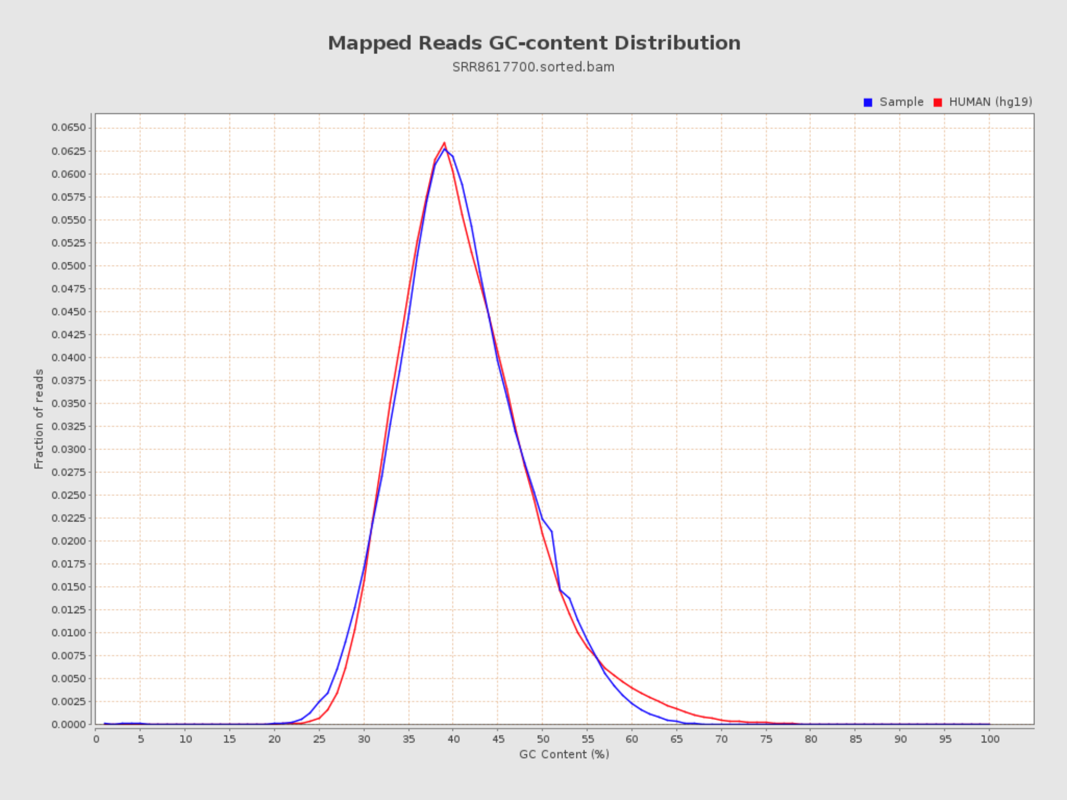
7. Results : Duplication Rate Histogram



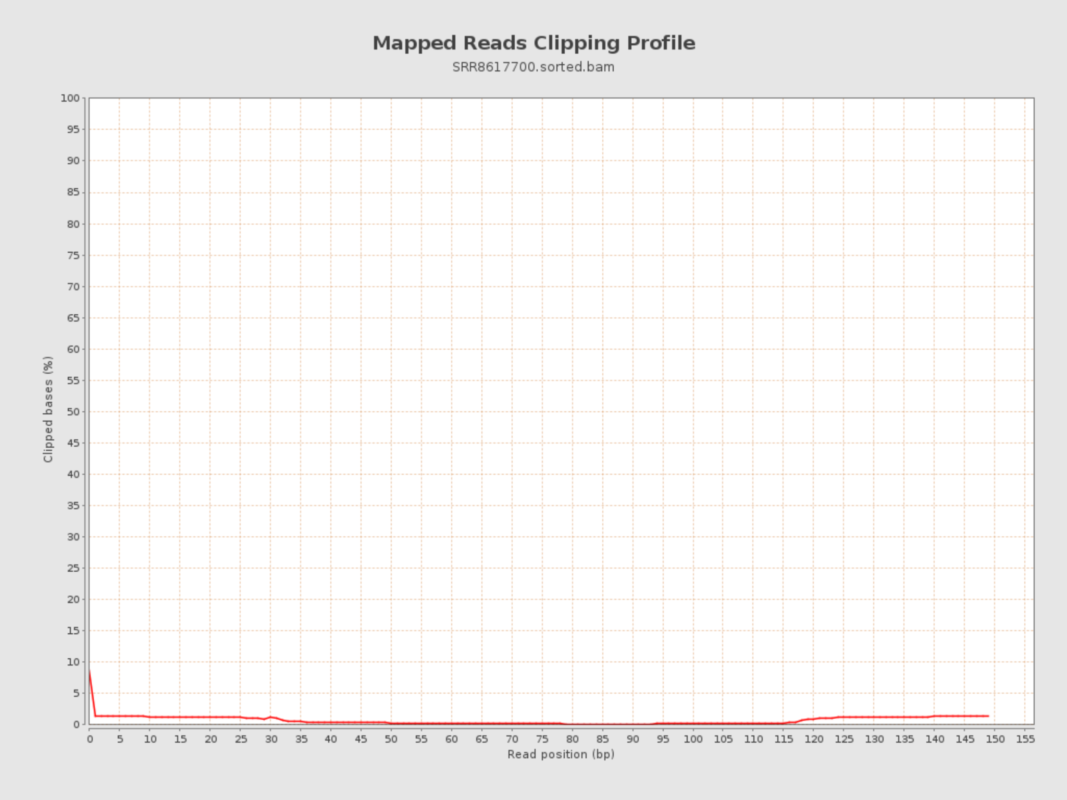
8. Results : Mapped Reads Nucleotide Content



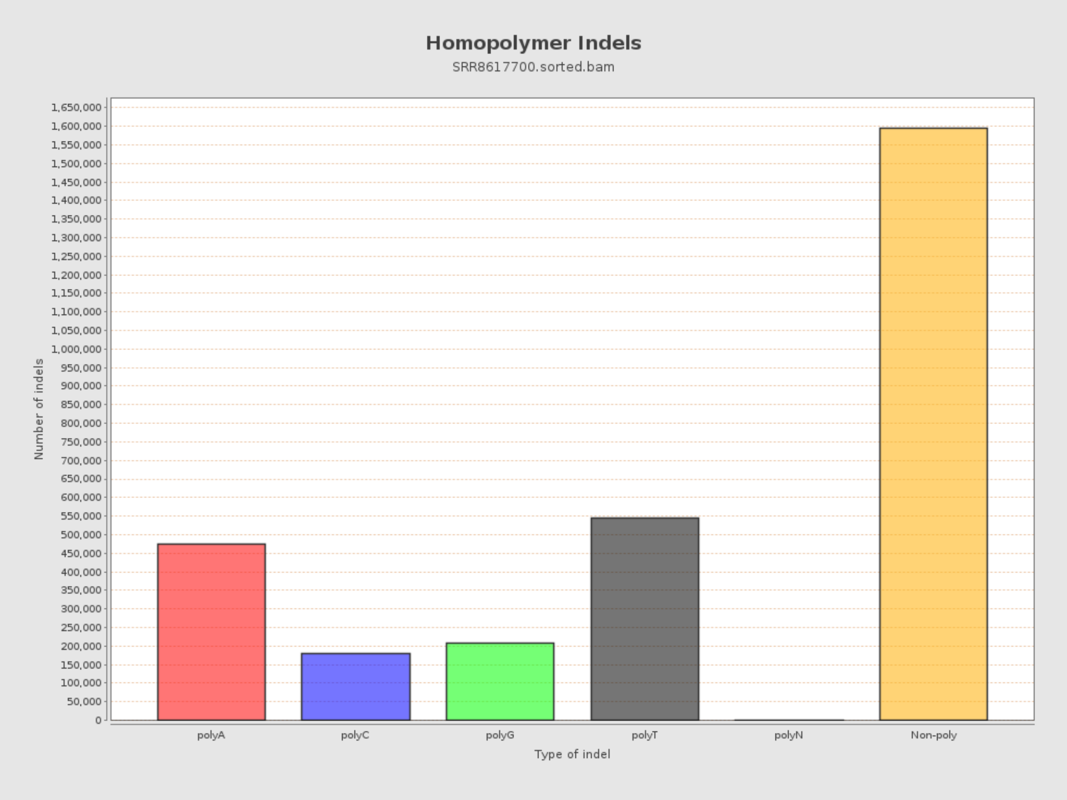
9. Results : Mapped Reads GC-content Distribution



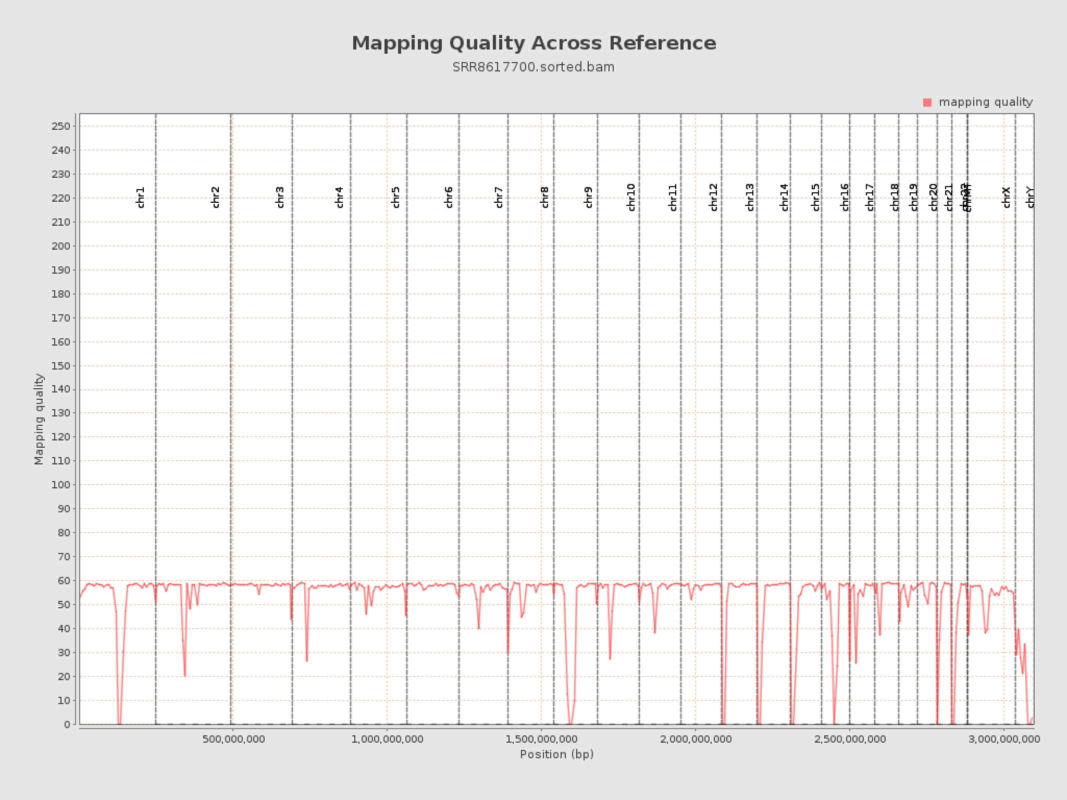
10. Results : Mapped Reads Clipping Profile



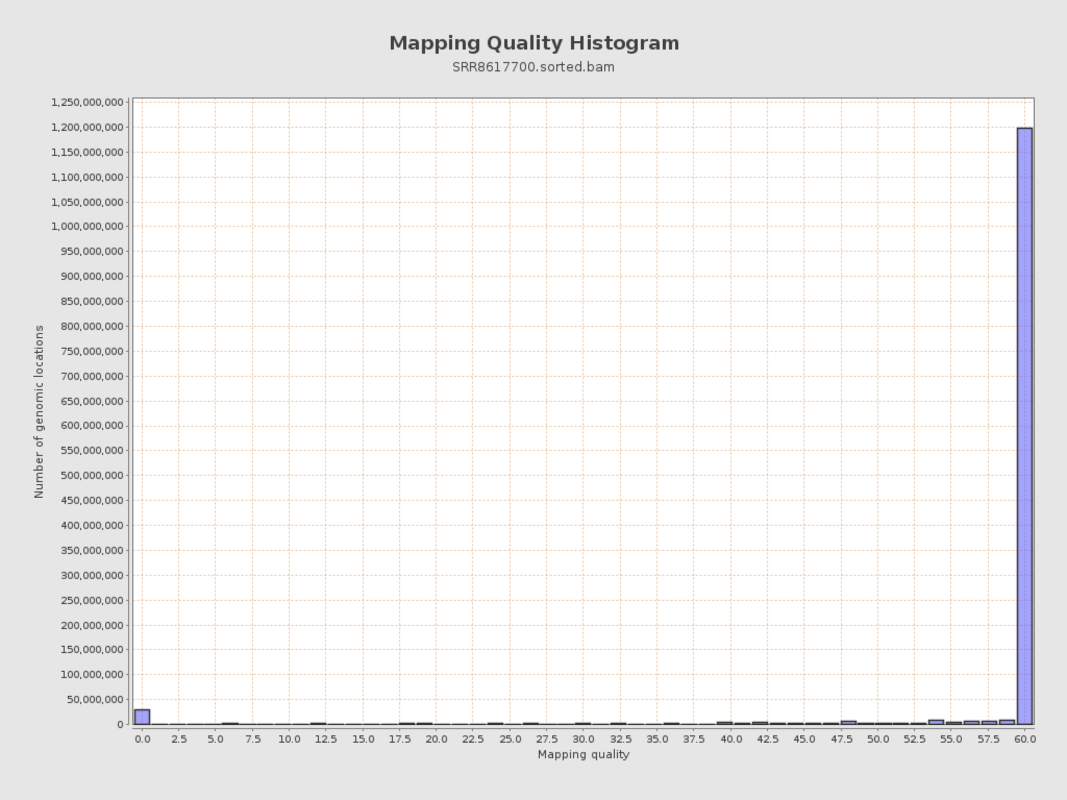
11. Results : Homopolymer Indels



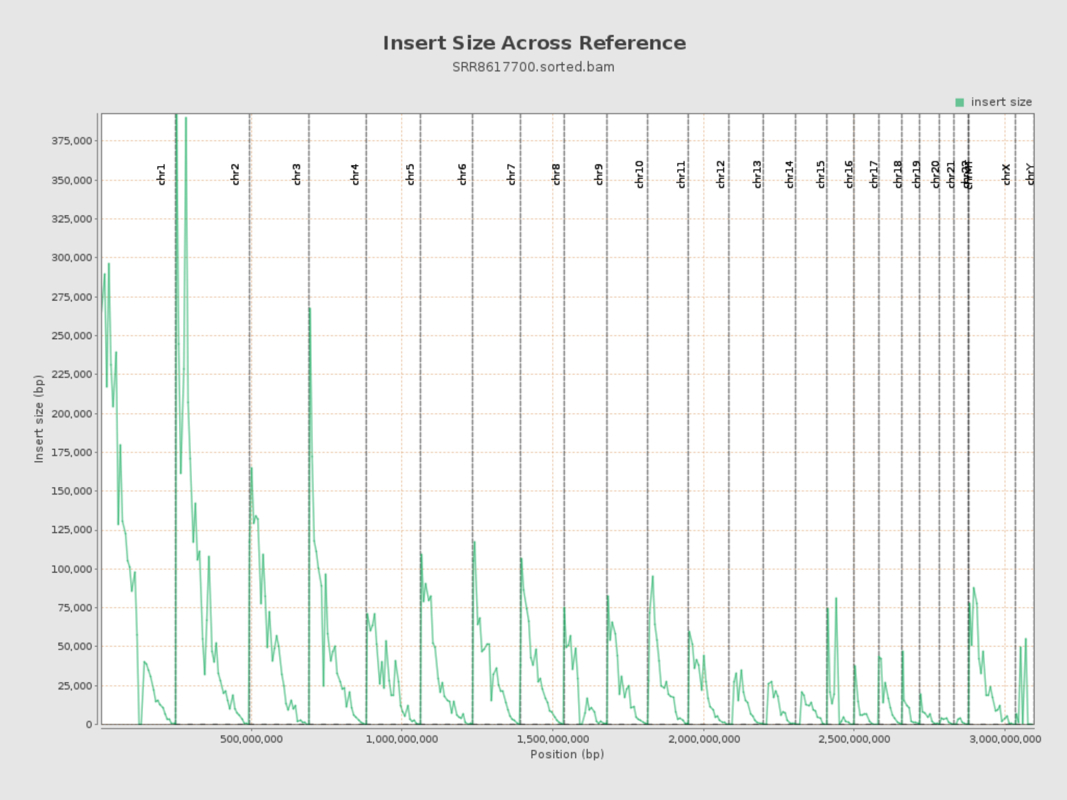
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram