Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 06:46:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617703.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_SRR8617703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617703_1.fastq.gz SRR8617703_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 06:46:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	49,066,826
Mapped reads	48,404,906 / 98.65%
Unmapped reads	661,920 / 1.35%
Mapped paired reads	48,404,906 / 98.65%
Mapped reads, first in pair	24,308,469 / 49.54%
Mapped reads, second in pair	24,096,437 / 49.11%
Mapped reads, both in pair	48,040,358 / 97.91%
Mapped reads, singletons	364,548 / 0.74%
Secondary alignments	0
Supplementary alignments	859,304 / 1.75%
Read min/max/mean length	30 / 150 / 150.81
Duplicated reads (estimated)	14,913,094 / 30.39%
Duplication rate	20.48%
Clipped reads	23,494,551 / 47.88%

2.2. ACGT Content

Number/percentage of A's	1,930,454,332 / 29.67%
Number/percentage of C's	1,209,399,789 / 18.59%
Number/percentage of T's	1,970,821,033 / 30.29%
Number/percentage of G's	1,395,265,606 / 21.45%
Number/percentage of N's	242,692 / 0%

GC Percentage	40.03%

2.3. Coverage

Mean	2.1031
Standard Deviation	28.7287

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	98,358.52
Standard Deviation	3,010,115.8
P25/Median/P75	214 / 276 / 352

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	75,906,269
Insertions	1,149,768
Mapped reads with at least one insertion	2.23%
Deletions	2,081,666
Mapped reads with at least one deletion	4.13%
Homopolymer indels	45.25%

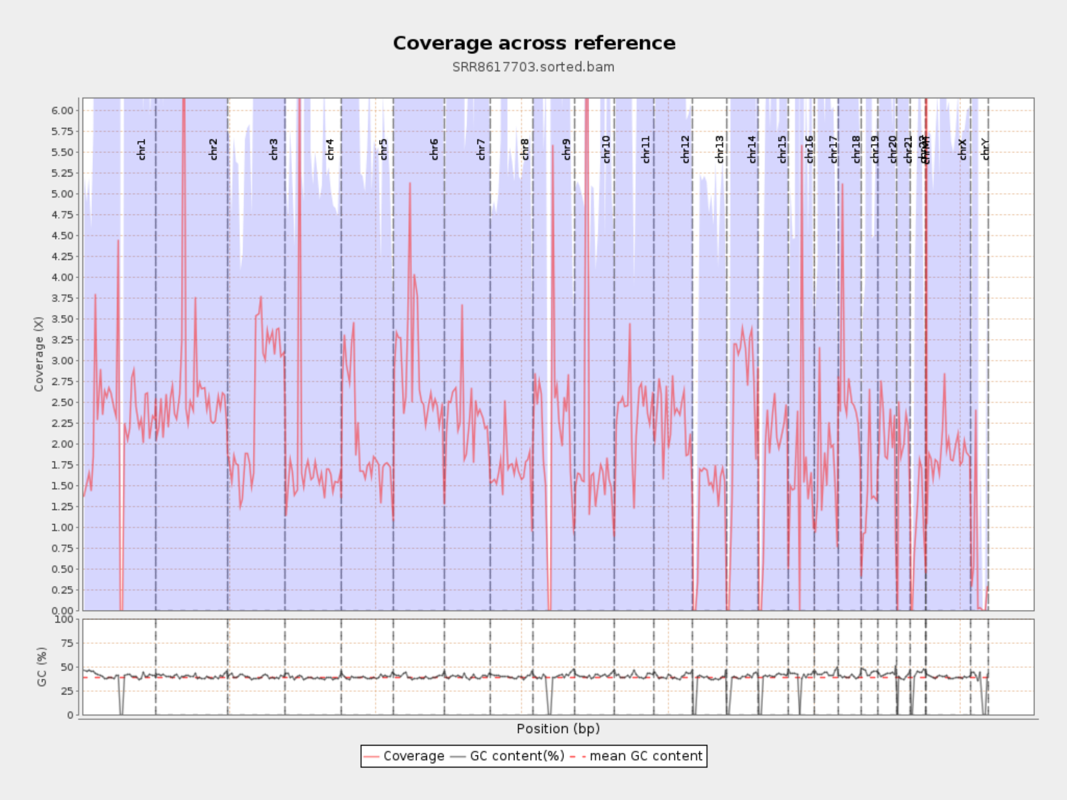
2.7. Chromosome stats

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

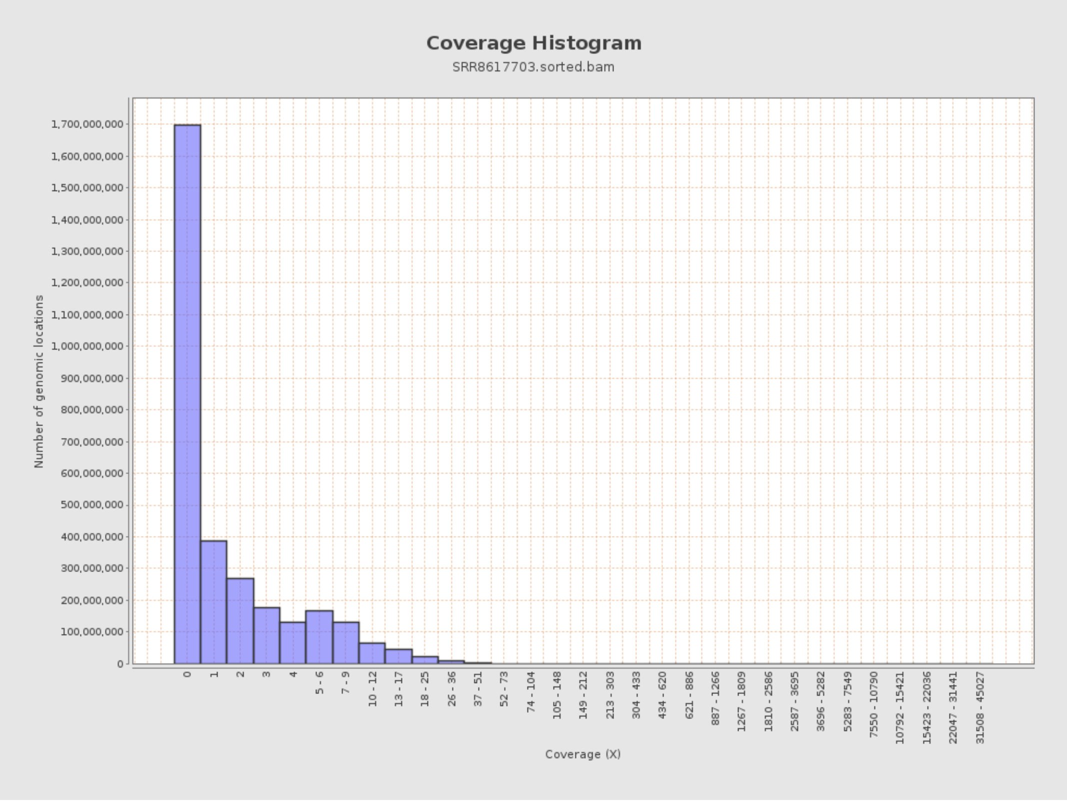
		bases	coverage	deviation
chr1	249250621	559906230	2.2464	36.2005
chr2	243199373	653497141	2.6871	34.7464
chr3	198022430	495999732	2.5048	4.6562
chr4	191154276	341471205	1.7864	29.7956
chr5	180915260	370453743	2.0477	4.3923
chr6	171115067	492029011	2.8754	21.9812
chr7	159138663	366776337	2.3048	25.5518
chr8	146364022	246701554	1.6855	8.0978
chr9	141213431	308368661	2.1837	66.3897
chr10	135534747	262681380	1.9381	50.5043
chr11	135006516	322140933	2.3861	23.7517
chr12	133851895	305054403	2.279	8.0279
chr13	115169878	151986548	1.3197	2.9519
chr14	107349540	268858706	2.5045	5.3808
chr15	102531392	181363032	1.7689	4.9688
chr16	90354753	155785609	1.7242	29.0084
chr17	81195210	139813879	1.7219	26.0585
chr18	78077248	210216745	2.6924	57.5972
chr19	59128983	82283782	1.3916	18.0749
chr20	63025520	133718614	2.1217	9.0552
chr21	48129895	90264075	1.8754	13.8185
chr22	51304566	50684544	0.9879	3.3083
chrMT	16571	1643140	99.1576	57.9868
chrX	155270560	291954231	1.8803	8.1035

chrY	59373566	26903989	0.4531	33.3399

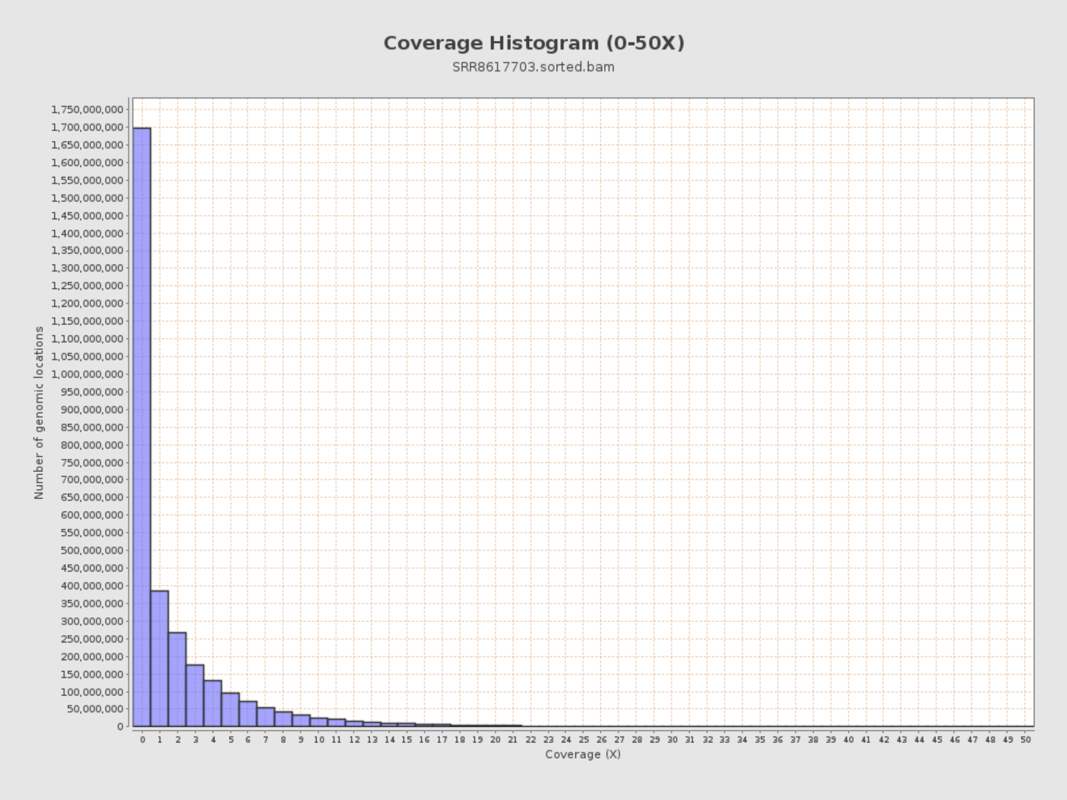
3. Results : Coverage across reference



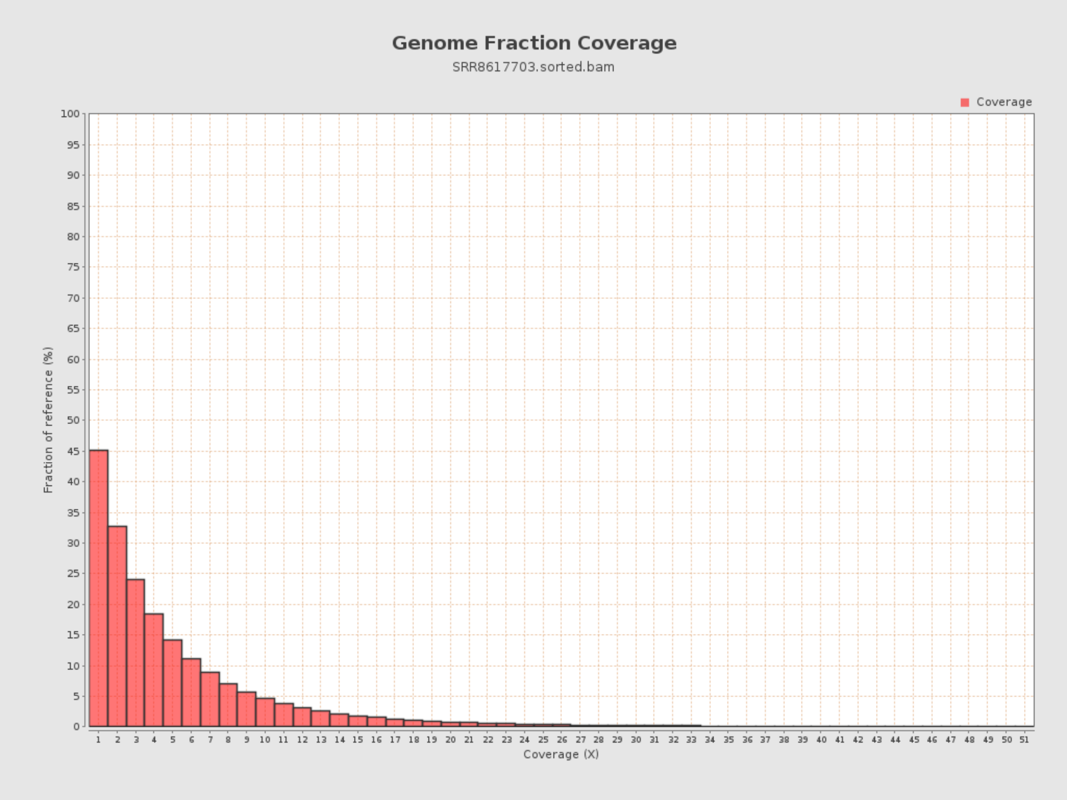
4. Results : Coverage Histogram



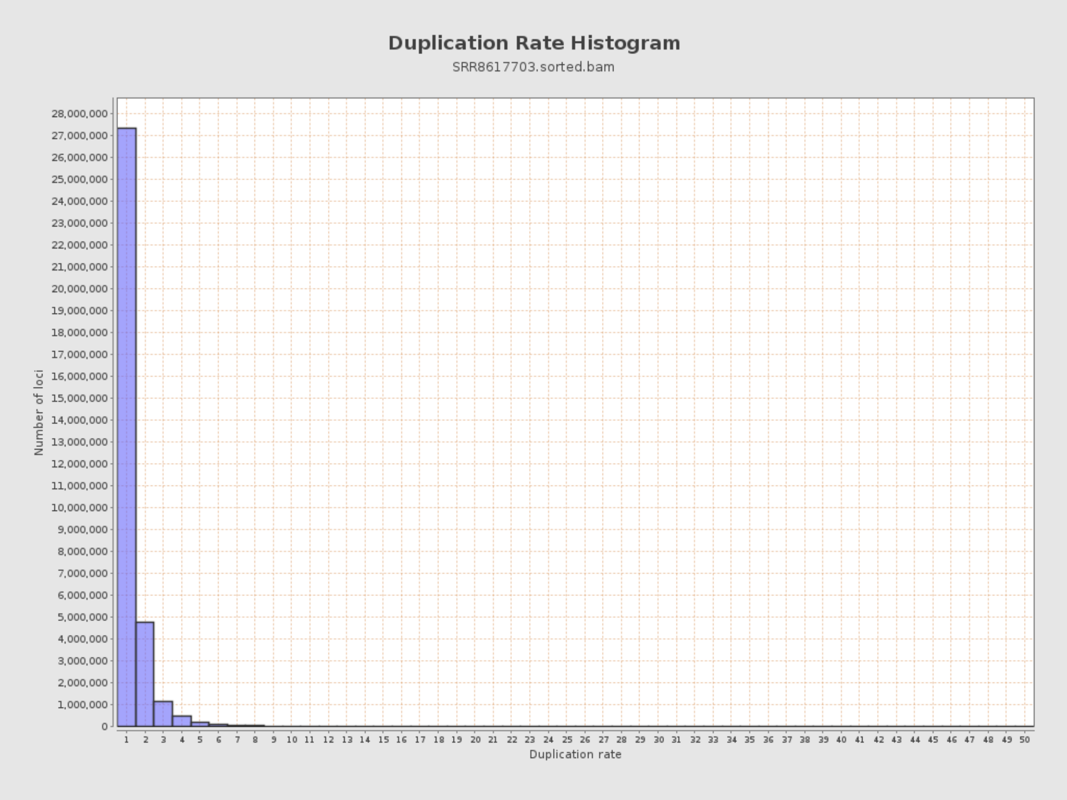
5. Results : Coverage Histogram (0-50X)



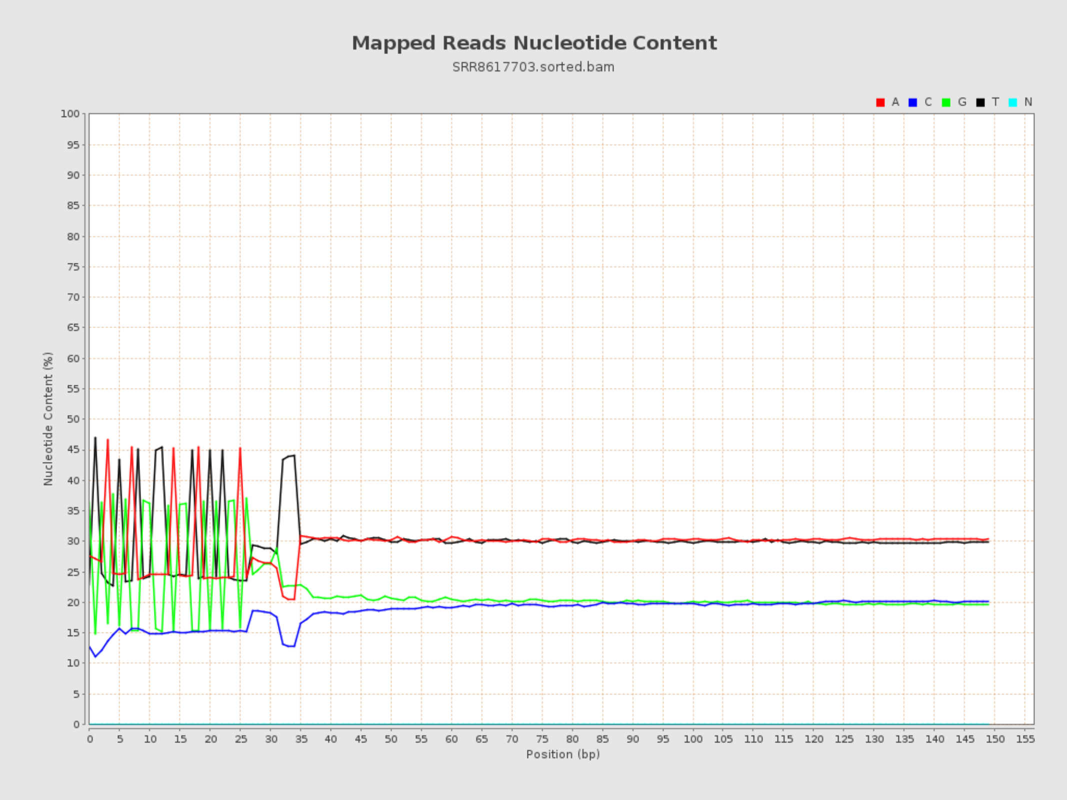
6. Results : Genome Fraction Coverage



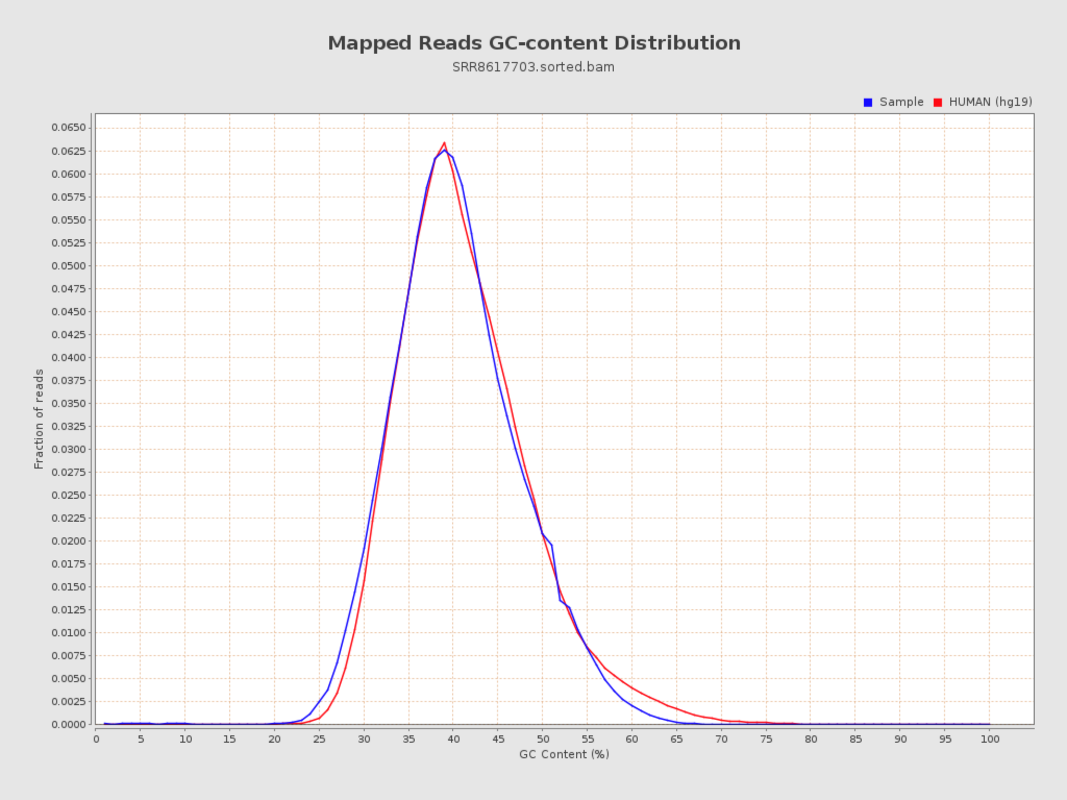
7. Results : Duplication Rate Histogram



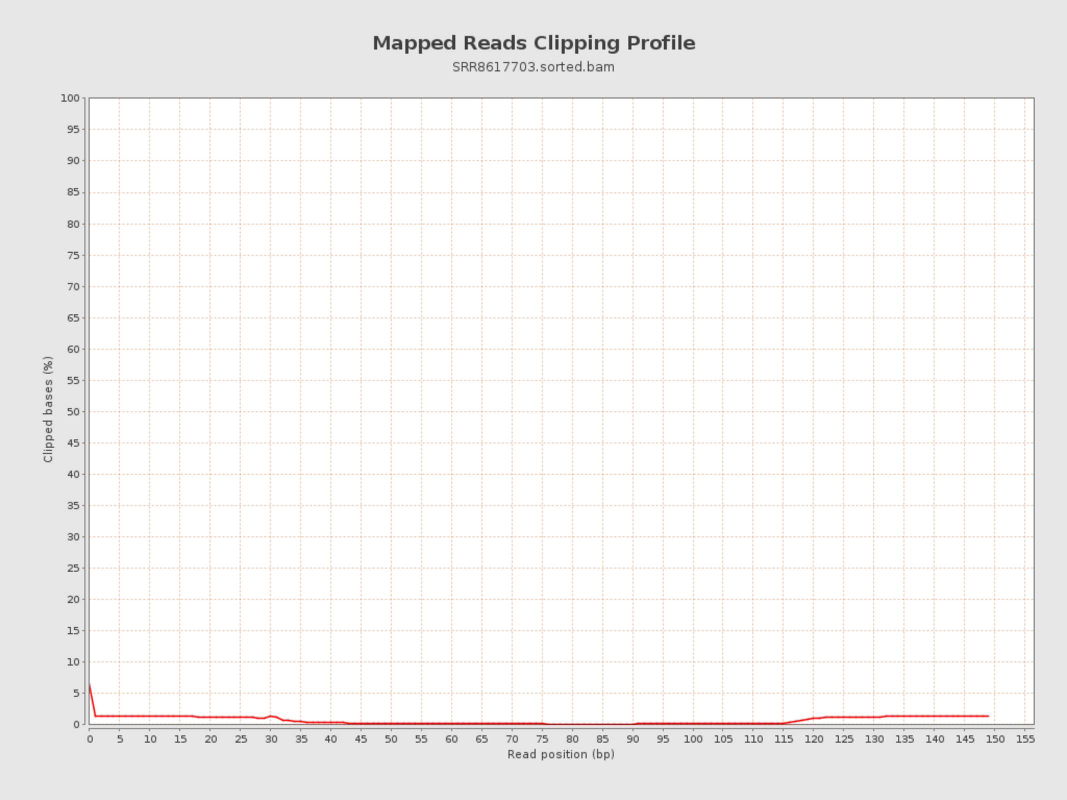
8. Results : Mapped Reads Nucleotide Content



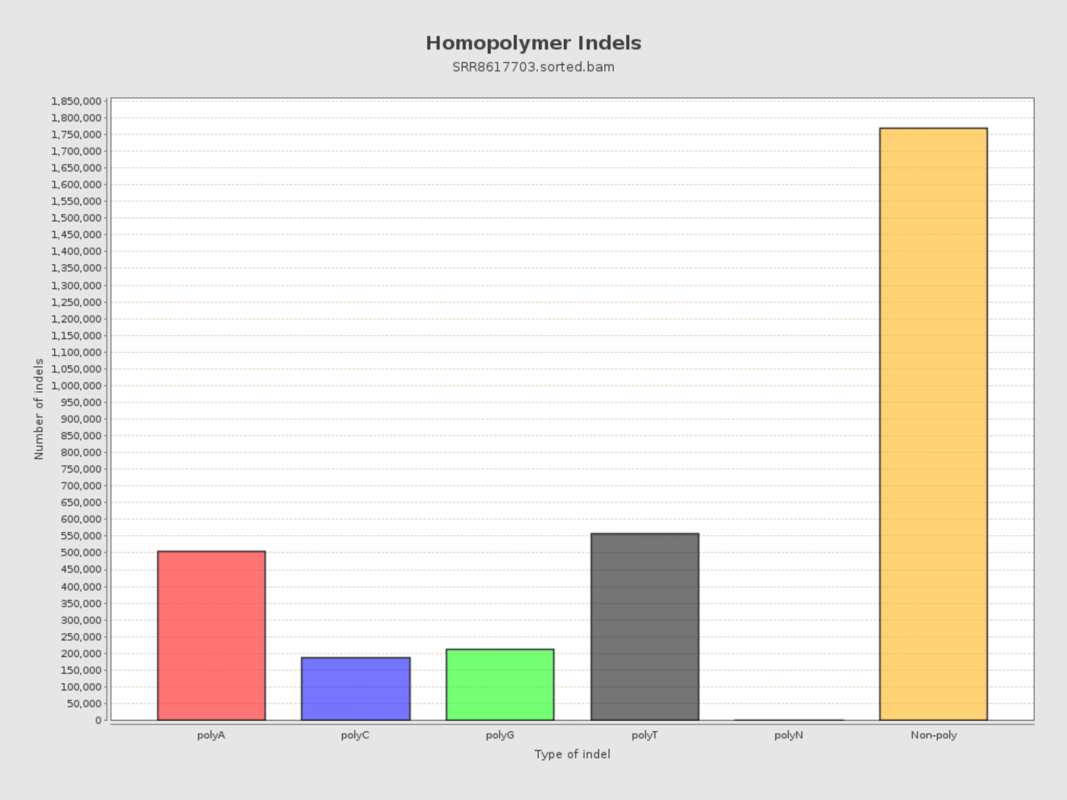
9. Results : Mapped Reads GC-content Distribution



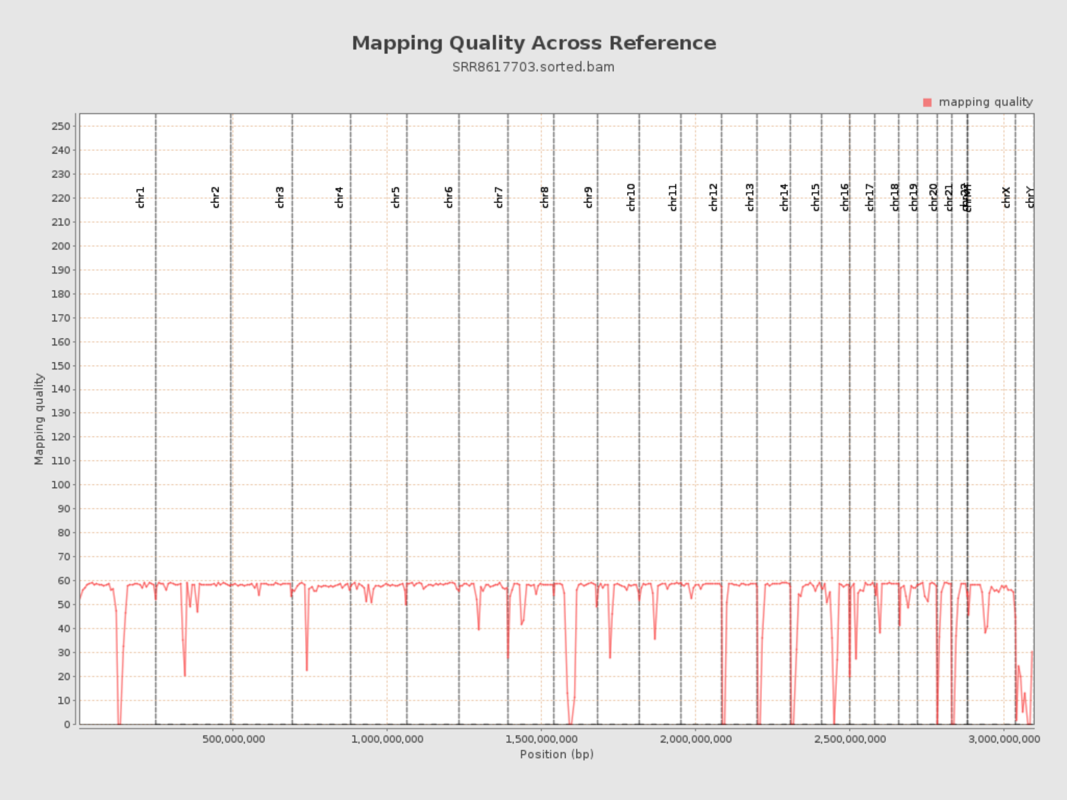
10. Results : Mapped Reads Clipping Profile



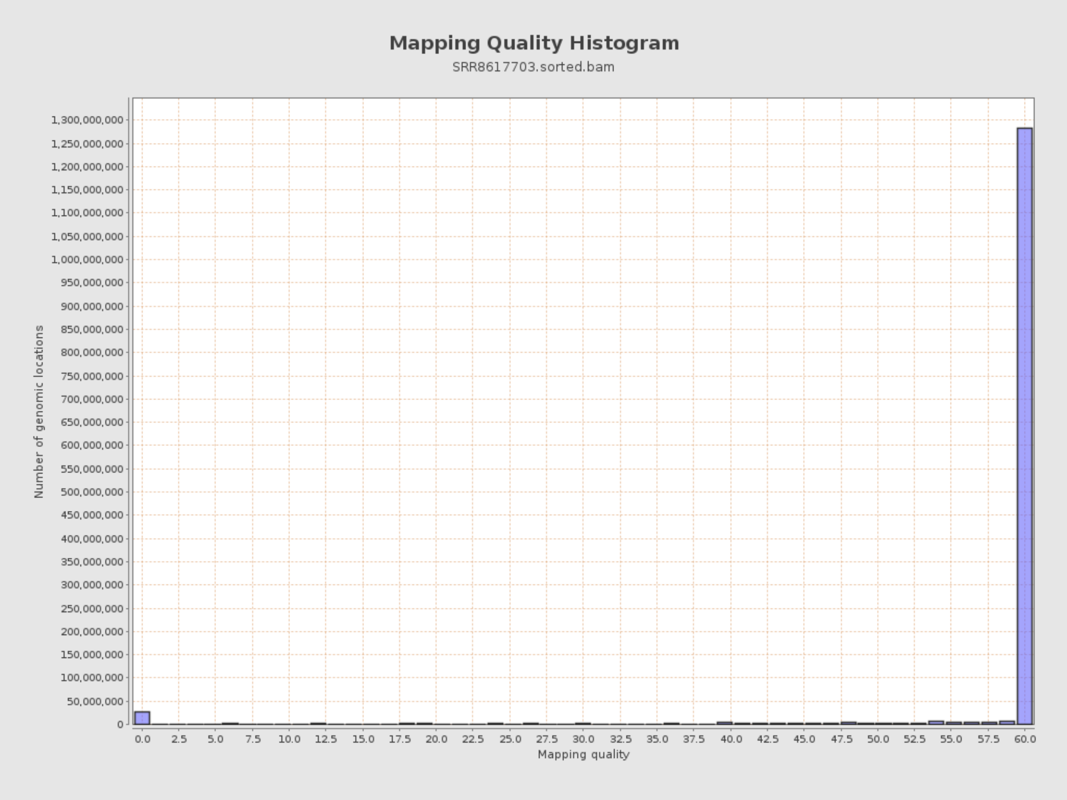
11. Results : Homopolymer Indels



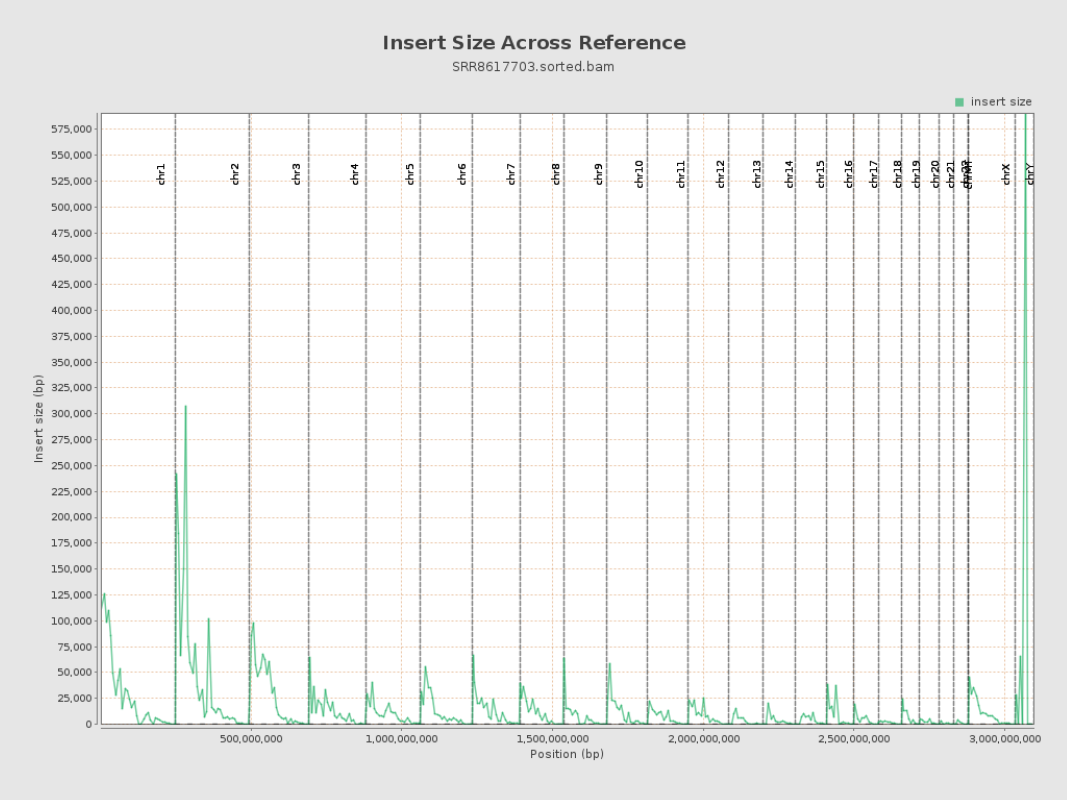
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram