Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 08:20:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617731.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_SRR8617731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617731_1.fastq.gz SRR8617731_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 08:20:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,333,562
Mapped reads	35,004,184 / 96.34%
Unmapped reads	1,329,378 / 3.66%
Mapped paired reads	35,004,184 / 96.34%
Mapped reads, first in pair	17,799,885 / 48.99%
Mapped reads, second in pair	17,204,299 / 47.35%
Mapped reads, both in pair	34,189,666 / 94.1%
Mapped reads, singletons	814,518 / 2.24%
Secondary alignments	0
Supplementary alignments	1,371,230 / 3.77%
Read min/max/mean length	30 / 150 / 151.88
Duplicated reads (estimated)	9,076,424 / 24.98%
Duplication rate	15.93%
Clipped reads	17,672,808 / 48.64%

2.2. ACGT Content

Number/percentage of A's	1,365,394,641 / 28.96%
Number/percentage of C's	919,043,510 / 19.49%
Number/percentage of T's	1,390,327,906 / 29.49%
Number/percentage of G's	1,040,077,389 / 22.06%
Number/percentage of N's	18,748 / 0%

GC Percentage	41.55%

2.3. Coverage

Mean	1.5243
Standard Deviation	19.9116

2.4. Mapping Quality

Mean Mapping Quality	52.83

2.5. Insert size

Mean	276,411.27
Standard Deviation	5,059,363.02
P25/Median/P75	218 / 277 / 351

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	64,387,719
Insertions	943,480
Mapped reads with at least one insertion	2.49%
Deletions	1,864,032
Mapped reads with at least one deletion	5.08%
Homopolymer indels	44.06%

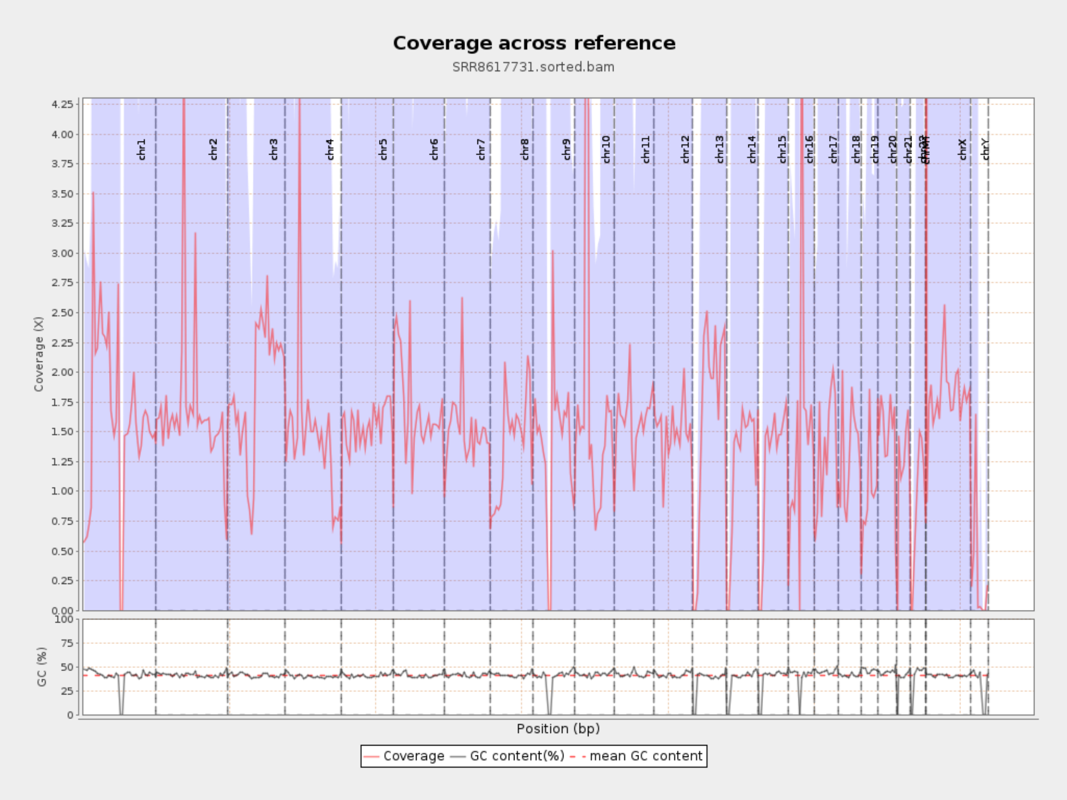
2.7. Chromosome stats

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

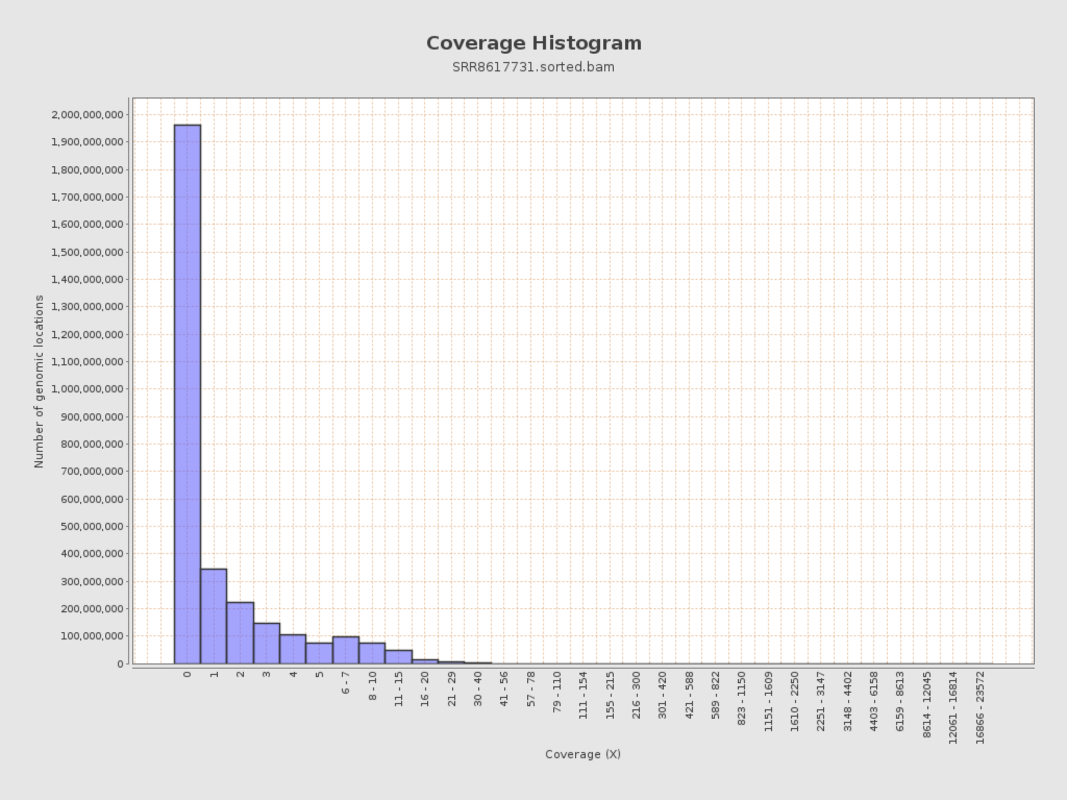
		bases	coverage	deviation
chr1	249250621	405784999	1.628	23.3813
chr2	243199373	415363766	1.7079	25.5788
chr3	198022430	368214611	1.8595	3.8848
chr4	191154276	284774170	1.4898	19.7586
chr5	180915260	280197315	1.5488	3.8264
chr6	171115067	292020180	1.7066	12.0614
chr7	159138663	241540331	1.5178	21.7739
chr8	146364022	205767111	1.4059	5.5706
chr9	141213431	201236561	1.4251	31.7137
chr10	135534747	239314645	1.7657	51.2969
chr11	135006516	216996880	1.6073	16.1625
chr12	133851895	202478333	1.5127	6.7926
chr13	115169878	190515841	1.6542	3.4402
chr14	107349540	133313298	1.2419	3.7672
chr15	102531392	125566910	1.2247	4.3891
chr16	90354753	139770669	1.5469	27.9622
chr17	81195210	111401651	1.372	15.4235
chr18	78077248	103447628	1.3249	24.5676
chr19	59128983	60034276	1.0153	11.5865
chr20	63025520	95987062	1.523	6.6645
chr21	48129895	58560665	1.2167	9.8711
chr22	51304566	45827401	0.8932	3.5598
chrMT	16571	2517851	151.9432	69.3683
chrX	155270560	278534356	1.7939	7.5257

chrY	59373566	19533286	0.329	25.705

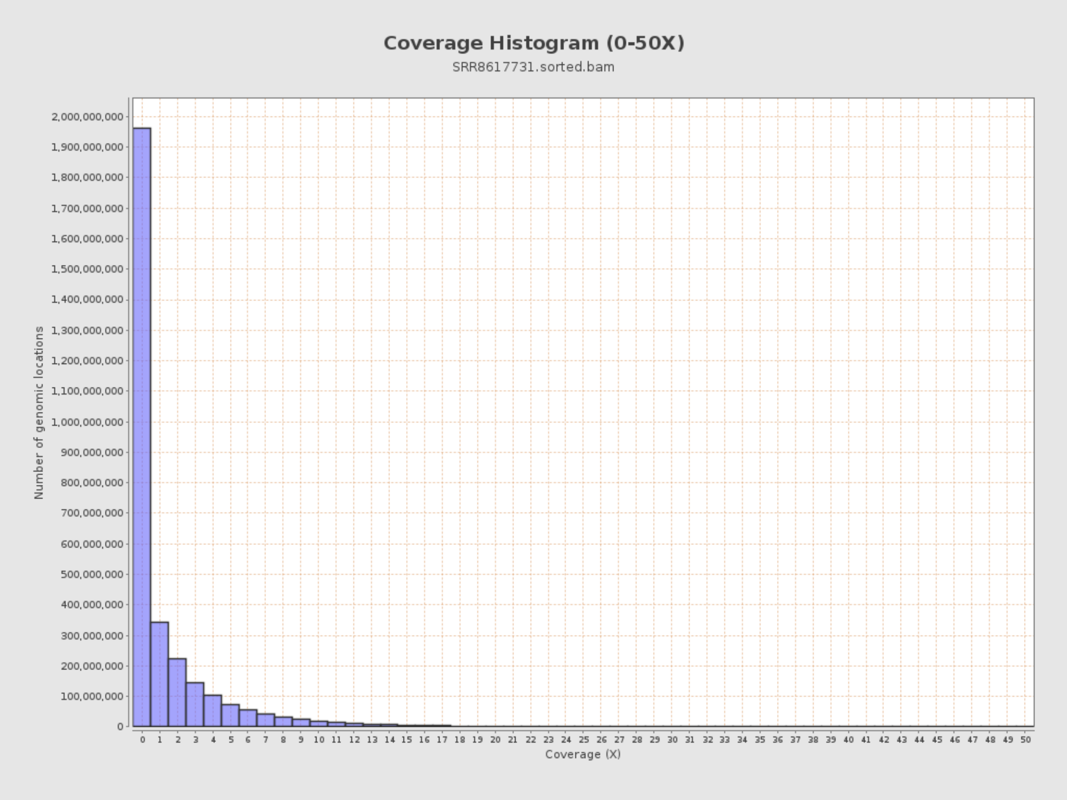
3. Results : Coverage across reference



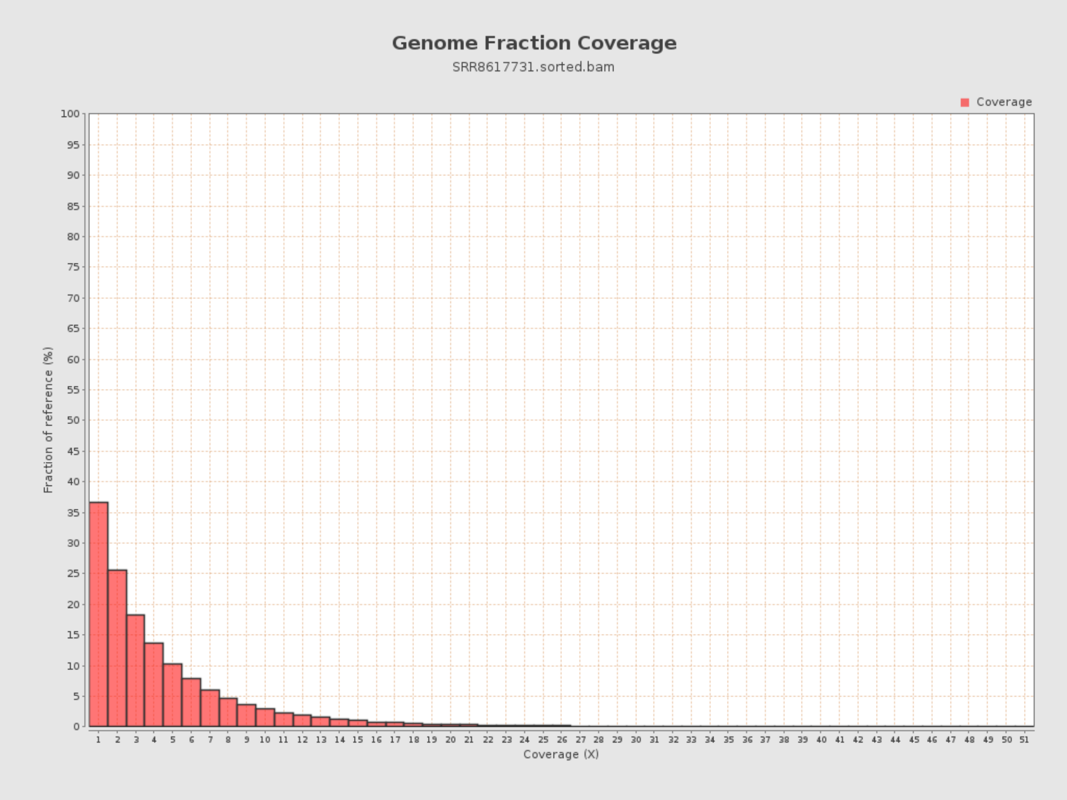
4. Results : Coverage Histogram



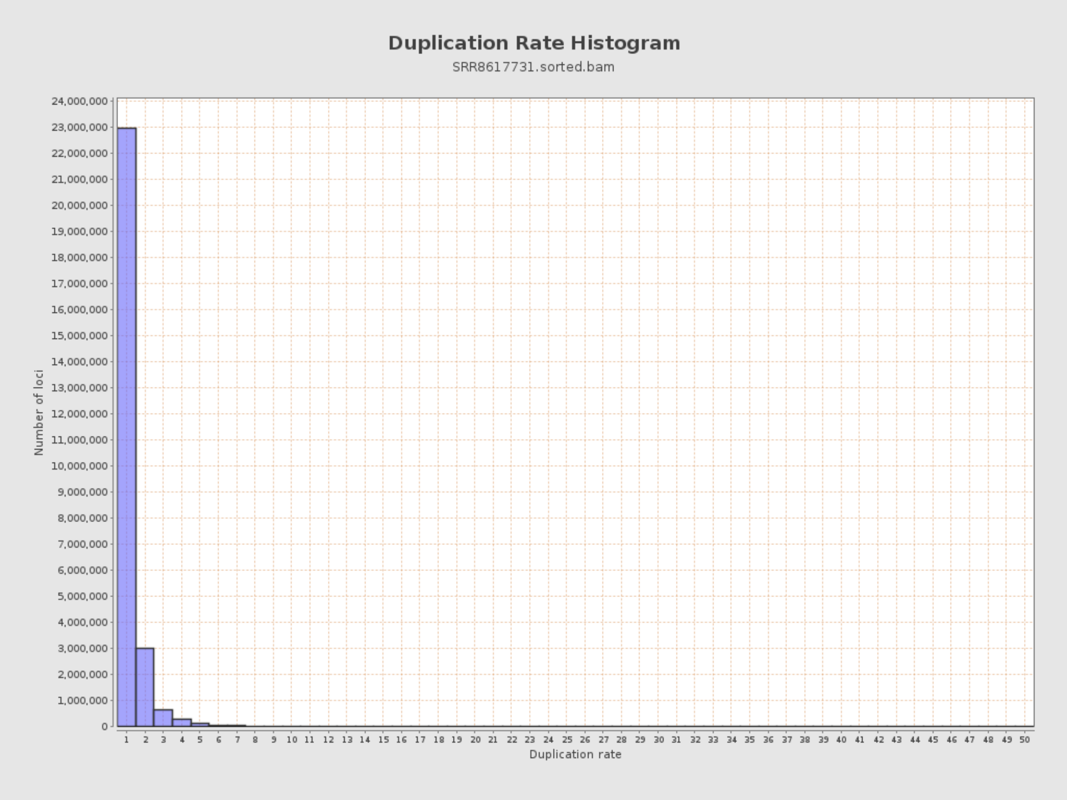
5. Results : Coverage Histogram (0-50X)



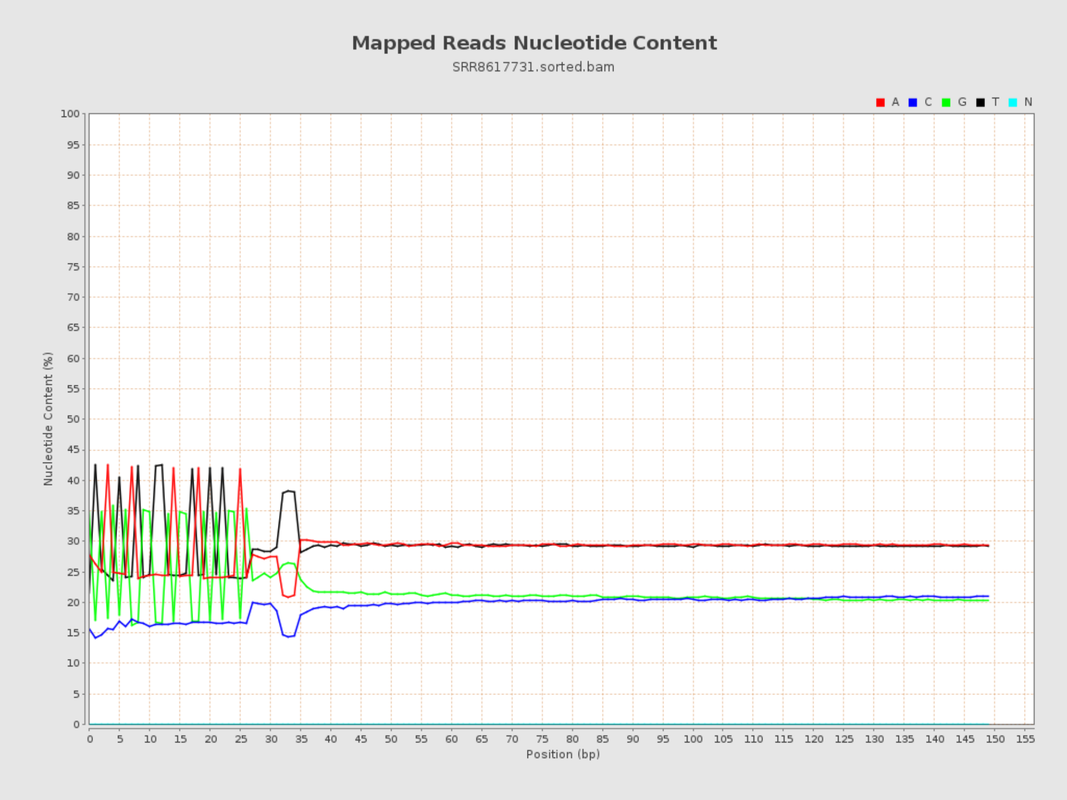
6. Results : Genome Fraction Coverage



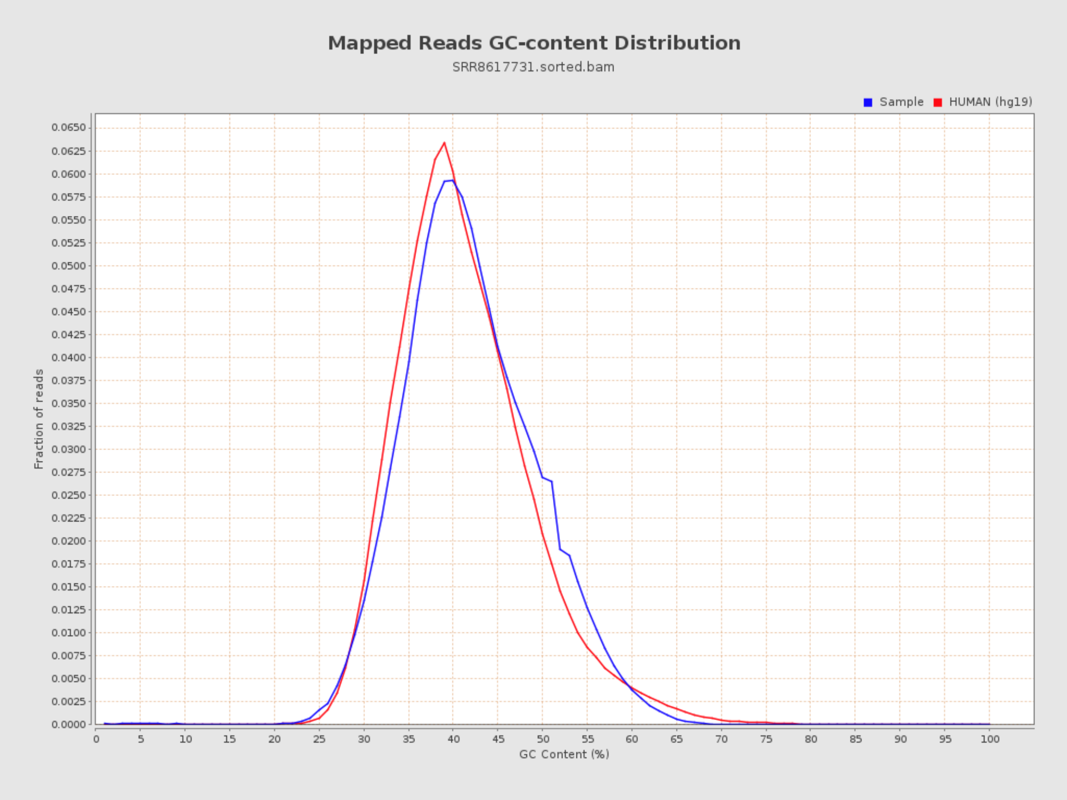
7. Results : Duplication Rate Histogram



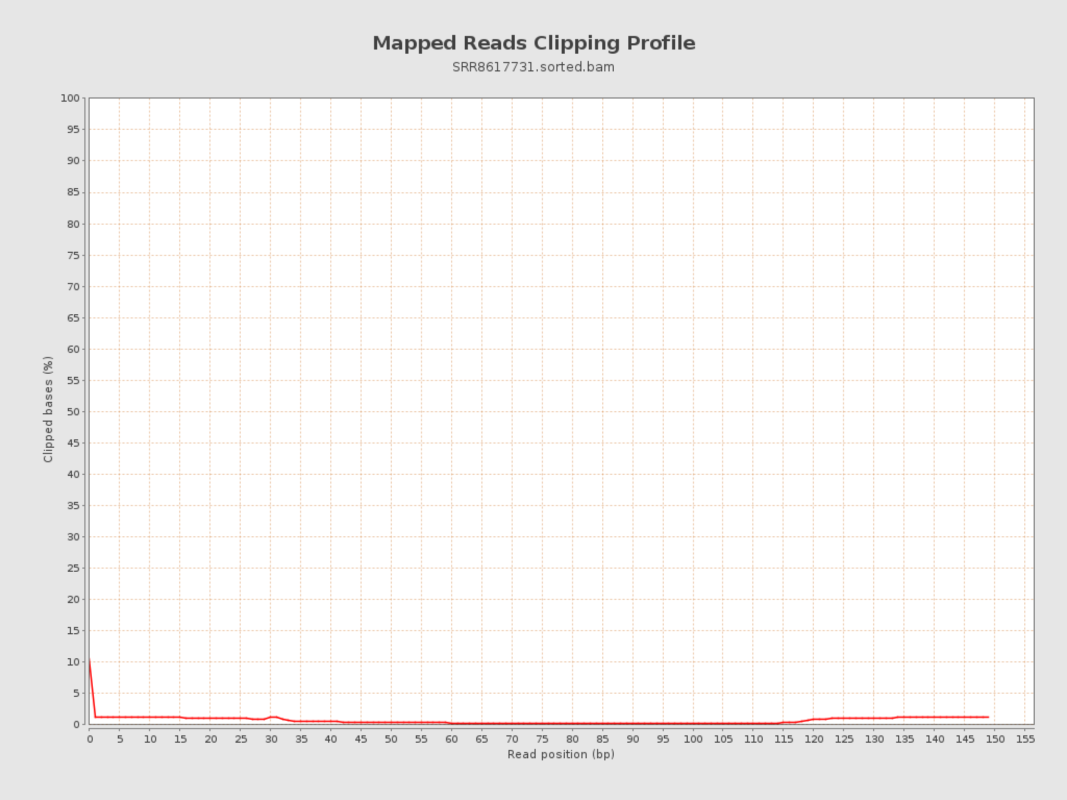
8. Results : Mapped Reads Nucleotide Content



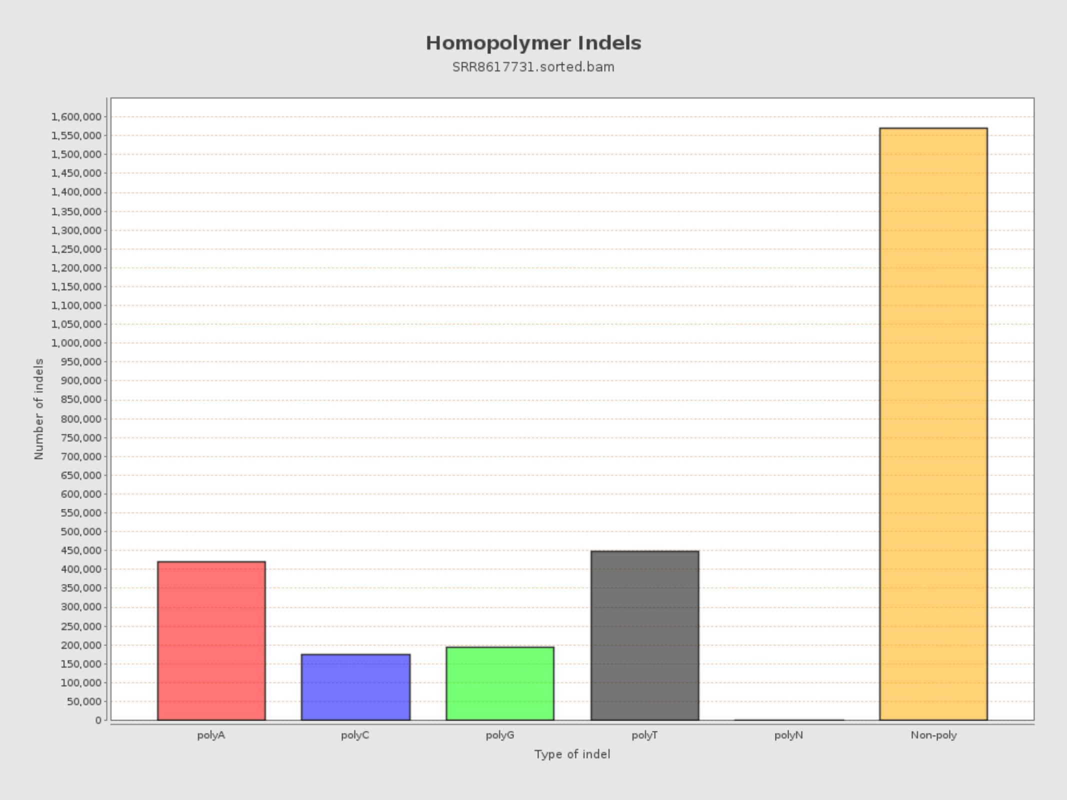
9. Results : Mapped Reads GC-content Distribution



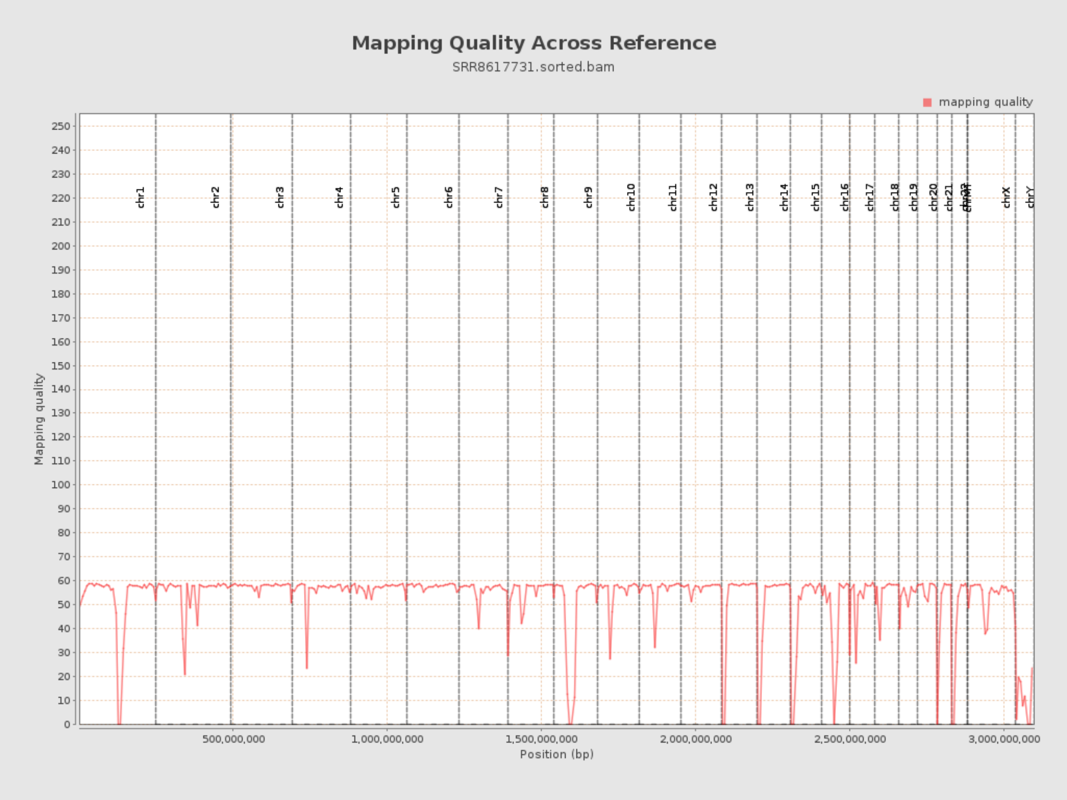
10. Results : Mapped Reads Clipping Profile



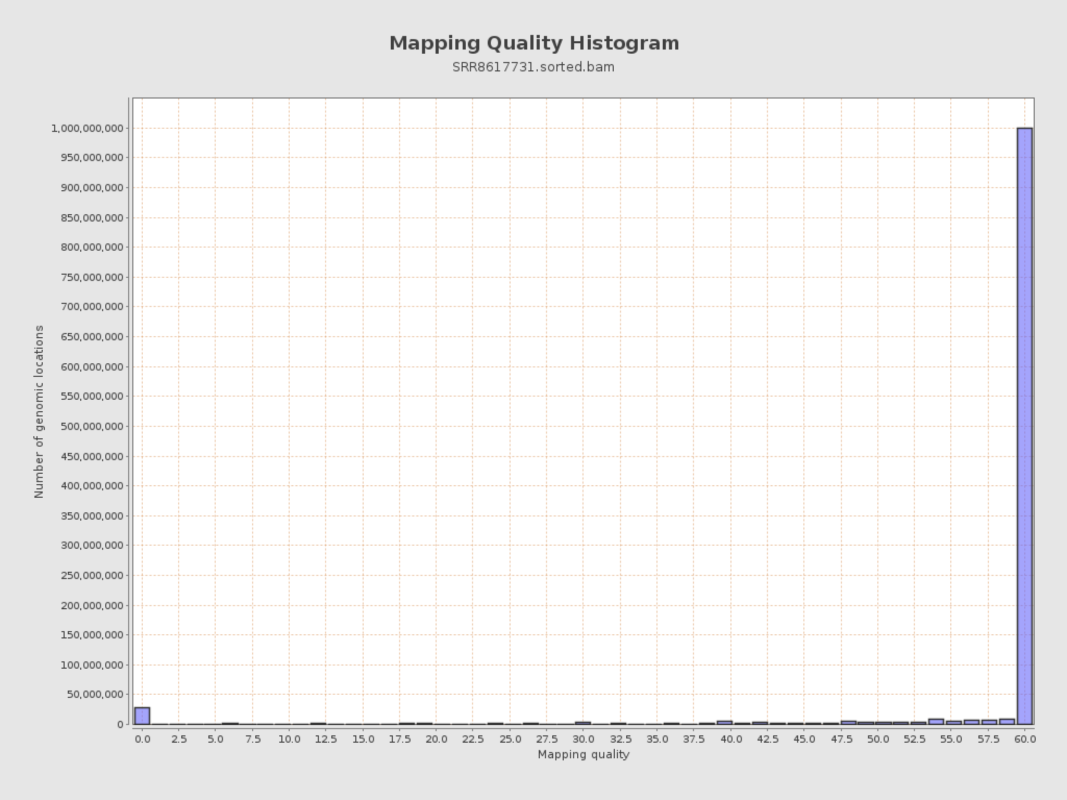
11. Results : Homopolymer Indels



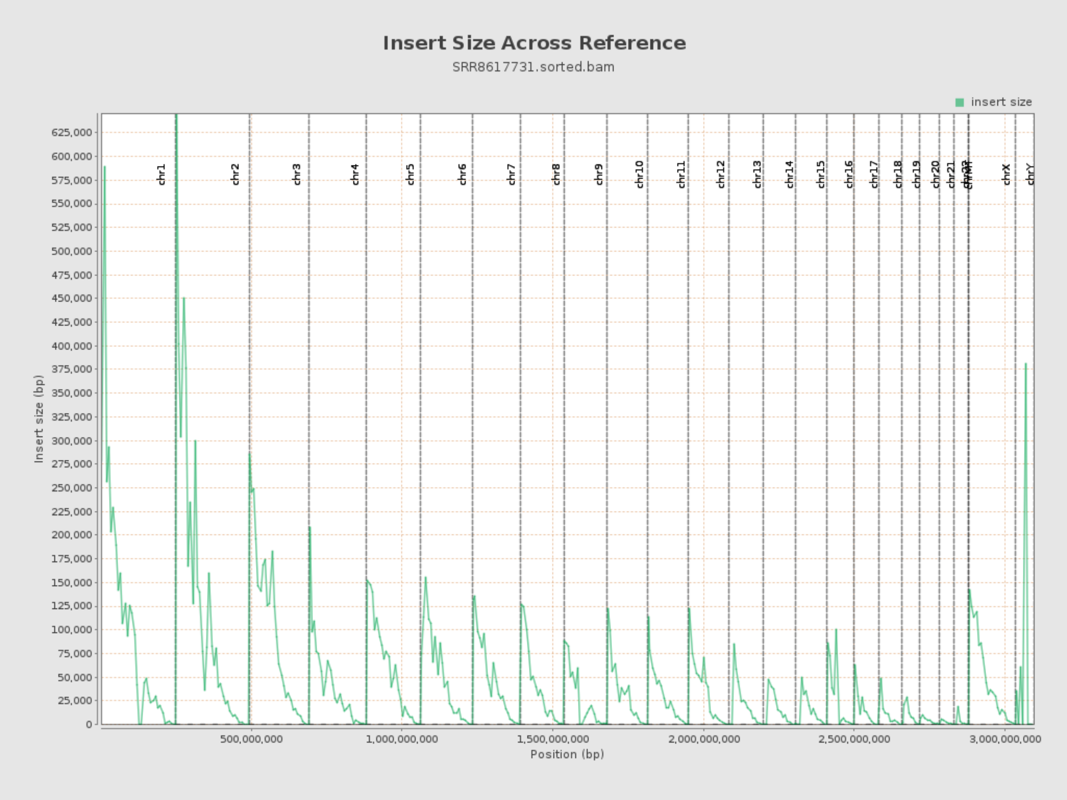
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram