Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 20:43:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617602.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_SRR8617602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617602_1.fastq.gz SRR8617602_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 20:43:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,023,314
Mapped reads	47,100,633 / 98.08%
Unmapped reads	922,681 / 1.92%
Mapped paired reads	47,100,633 / 98.08%
Mapped reads, first in pair	23,775,172 / 49.51%
Mapped reads, second in pair	23,325,461 / 48.57%
Mapped reads, both in pair	46,525,248 / 96.88%
Mapped reads, singletons	575,385 / 1.2%
Secondary alignments	0
Supplementary alignments	647,907 / 1.35%
Read min/max/mean length	30 / 150 / 150.64
Duplicated reads (estimated)	15,008,219 / 31.25%
Duplication rate	23.74%
Clipped reads	22,548,146 / 46.95%

2.2. ACGT Content

Number/percentage of A's	1,834,459,430 / 28.94%
Number/percentage of C's	1,209,199,805 / 19.07%
Number/percentage of T's	1,878,447,614 / 29.63%
Number/percentage of G's	1,416,968,200 / 22.35%
Number/percentage of N's	258,912 / 0%

GC Percentage	41.43%

2.3. Coverage

Mean	2.0492
Standard Deviation	28.9644

2.4. Mapping Quality

Mean Mapping Quality	53.51

2.5. Insert size

Mean	78,558.11
Standard Deviation	2,662,559.01
P25/Median/P75	223 / 279 / 351

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	71,033,680
Insertions	1,070,659
Mapped reads with at least one insertion	2.15%
Deletions	2,249,411
Mapped reads with at least one deletion	4.6%
Homopolymer indels	47.84%

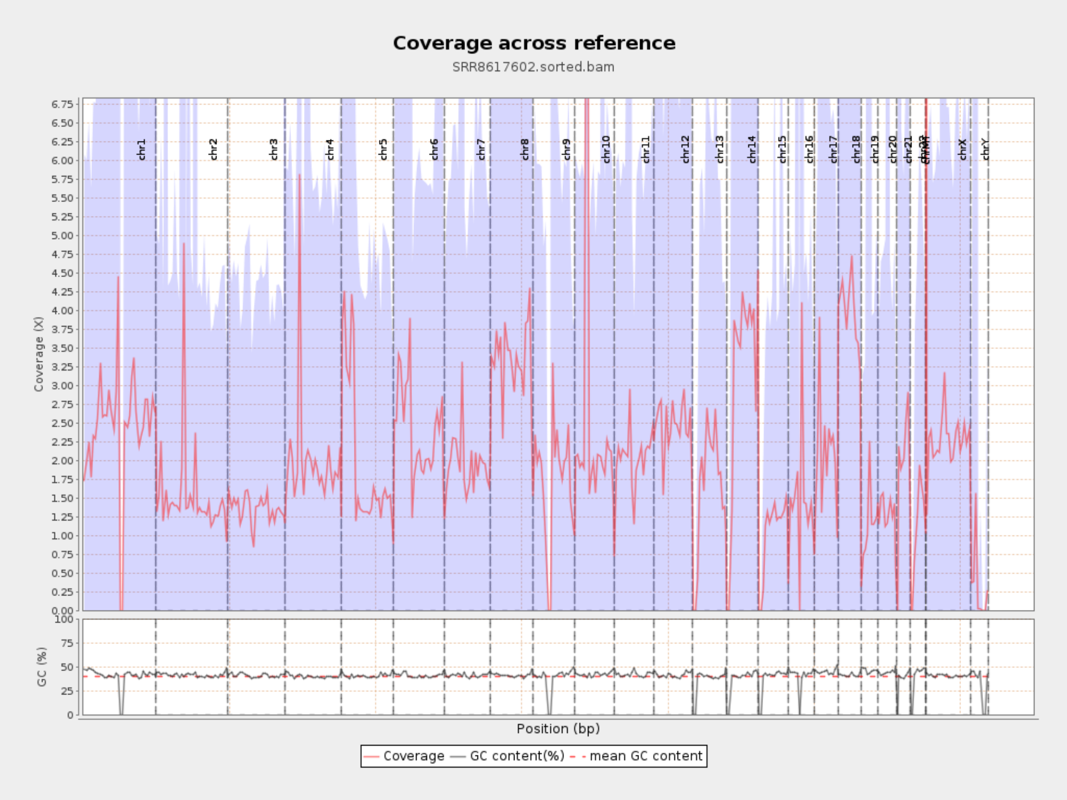
2.7. Chromosome stats

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

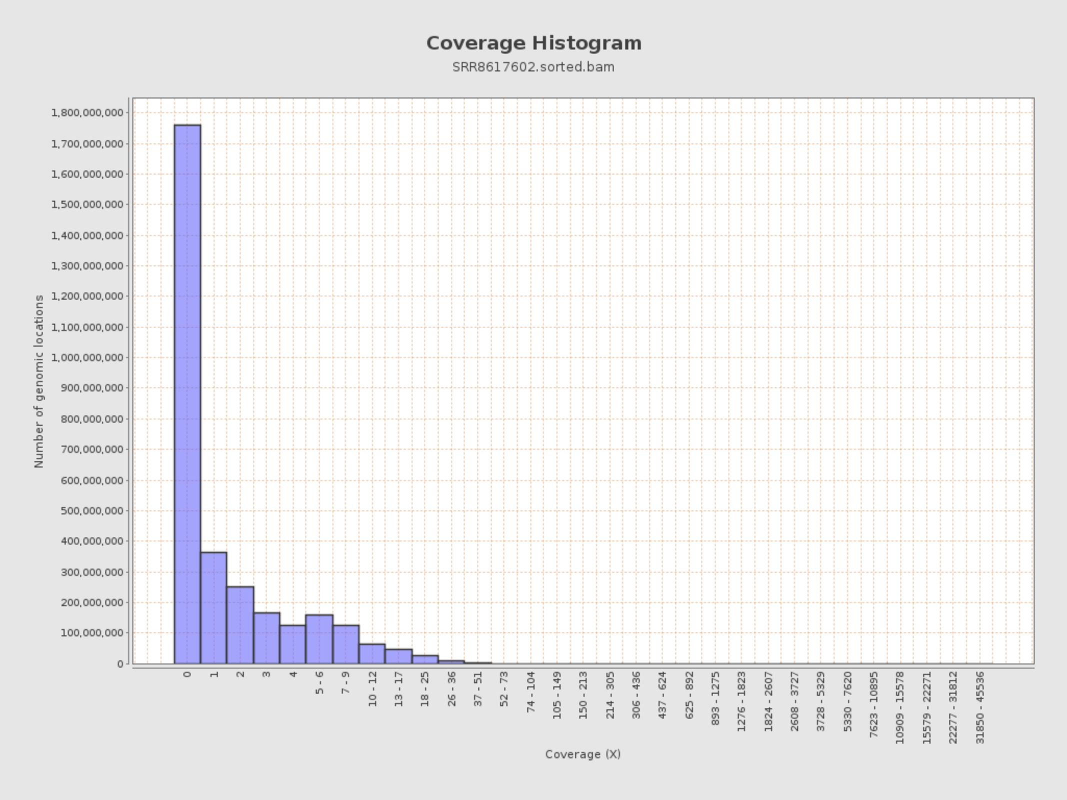
		bases	coverage	deviation
chr1	249250621	612821436	2.4587	26.8691
chr2	243199373	374348832	1.5393	23.7916
chr3	198022430	268895869	1.3579	3.5326
chr4	191154276	388680797	2.0333	24.7459
chr5	180915260	360845547	1.9946	4.3116
chr6	171115067	413898411	2.4188	21.6929
chr7	159138663	308518230	1.9387	29.5565
chr8	146364022	490782132	3.3532	9.3179
chr9	141213431	246297554	1.7442	37.4049
chr10	135534747	346184775	2.5542	99.0089
chr11	135006516	274378452	2.0323	23.9457
chr12	133851895	332006365	2.4804	7.2608
chr13	115169878	190445031	1.6536	3.5292
chr14	107349540	334106718	3.1123	5.9954
chr15	102531392	105994079	1.0338	3.5505
chr16	90354753	132208630	1.4632	20.7042
chr17	81195210	172842409	2.1287	34.1365
chr18	78077248	313887296	4.0202	36.9437
chr19	59128983	68815104	1.1638	13.4004
chr20	63025520	82123332	1.303	7.5688
chr21	48129895	96379973	2.0025	11.7627
chr22	51304566	56673149	1.1046	3.126
chrMT	16571	1438219	86.7913	49.4311
chrX	155270560	351674329	2.2649	8.91

chrY	59373566	19364865	0.3262	23.1678

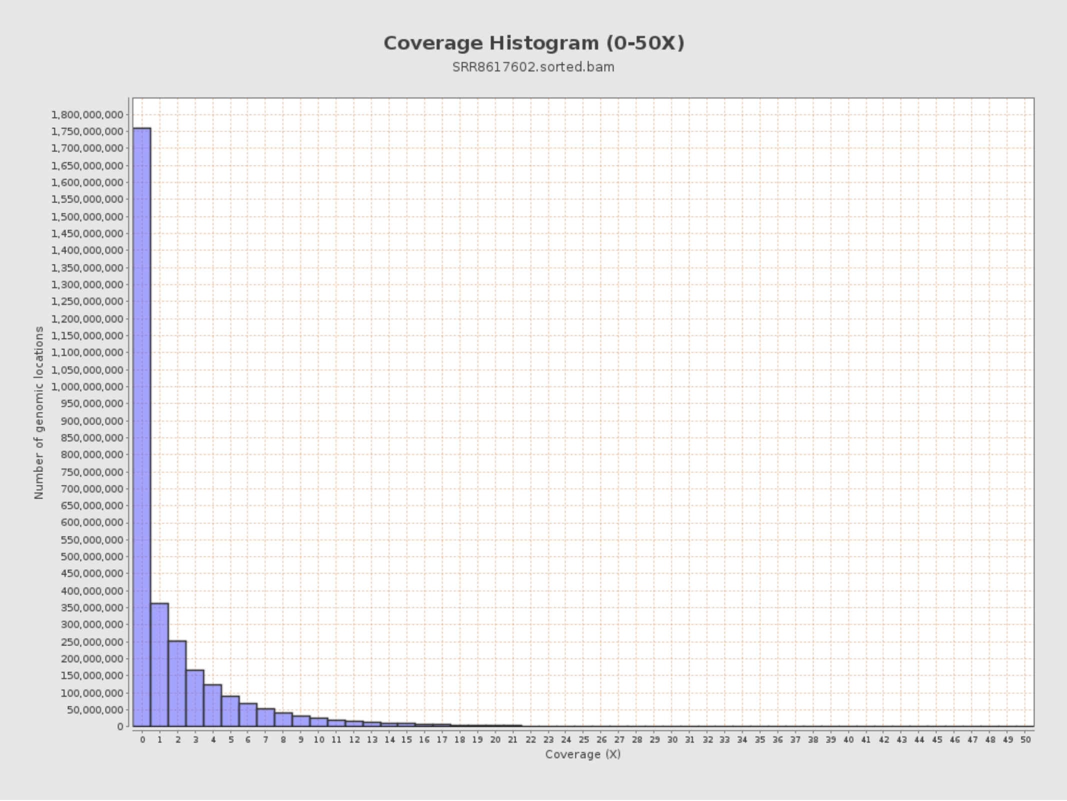
3. Results : Coverage across reference



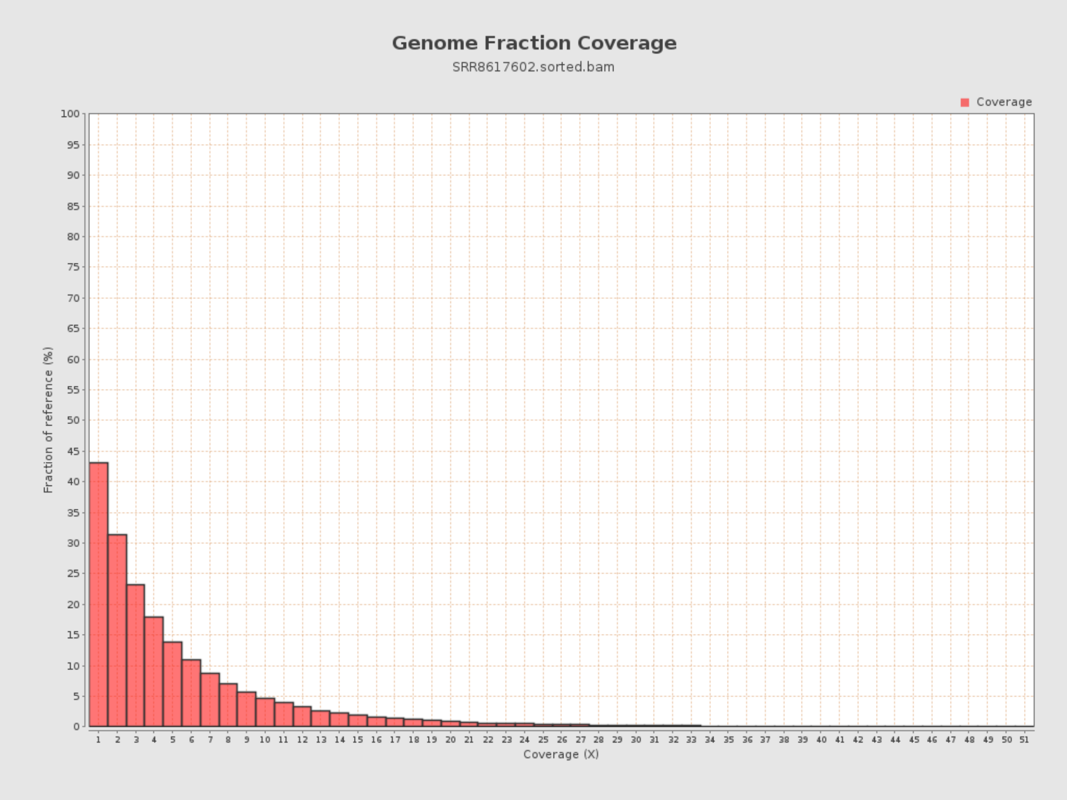
4. Results : Coverage Histogram



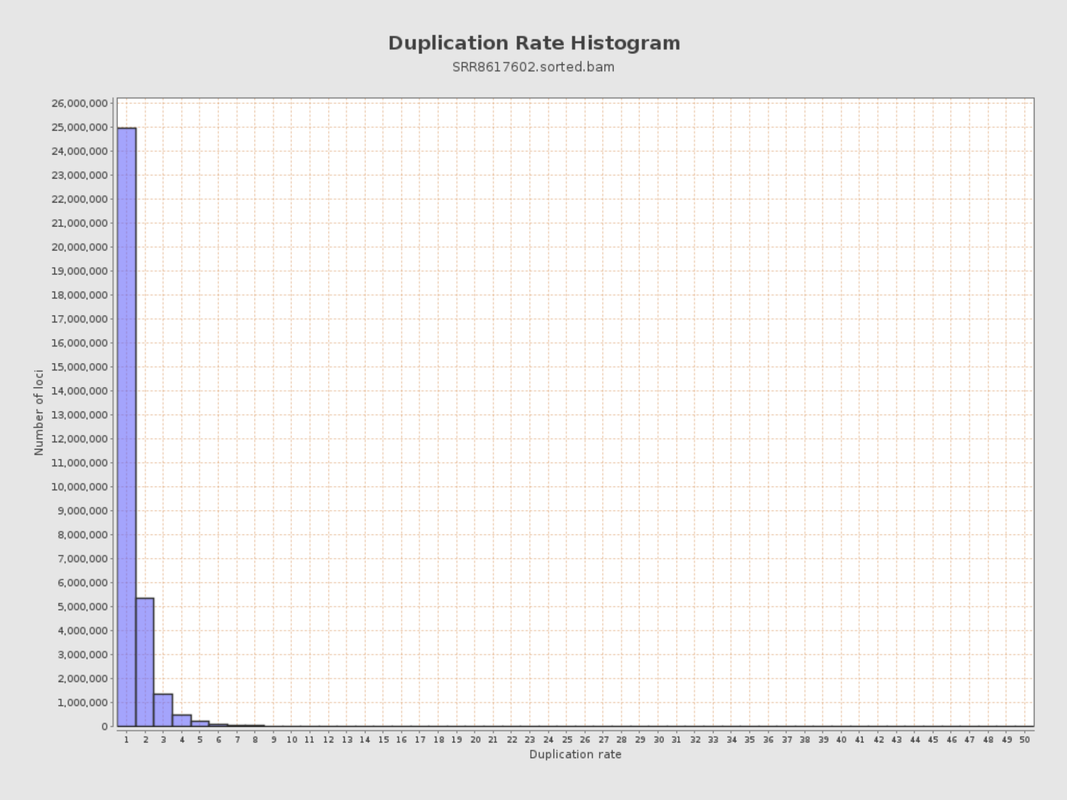
5. Results : Coverage Histogram (0-50X)



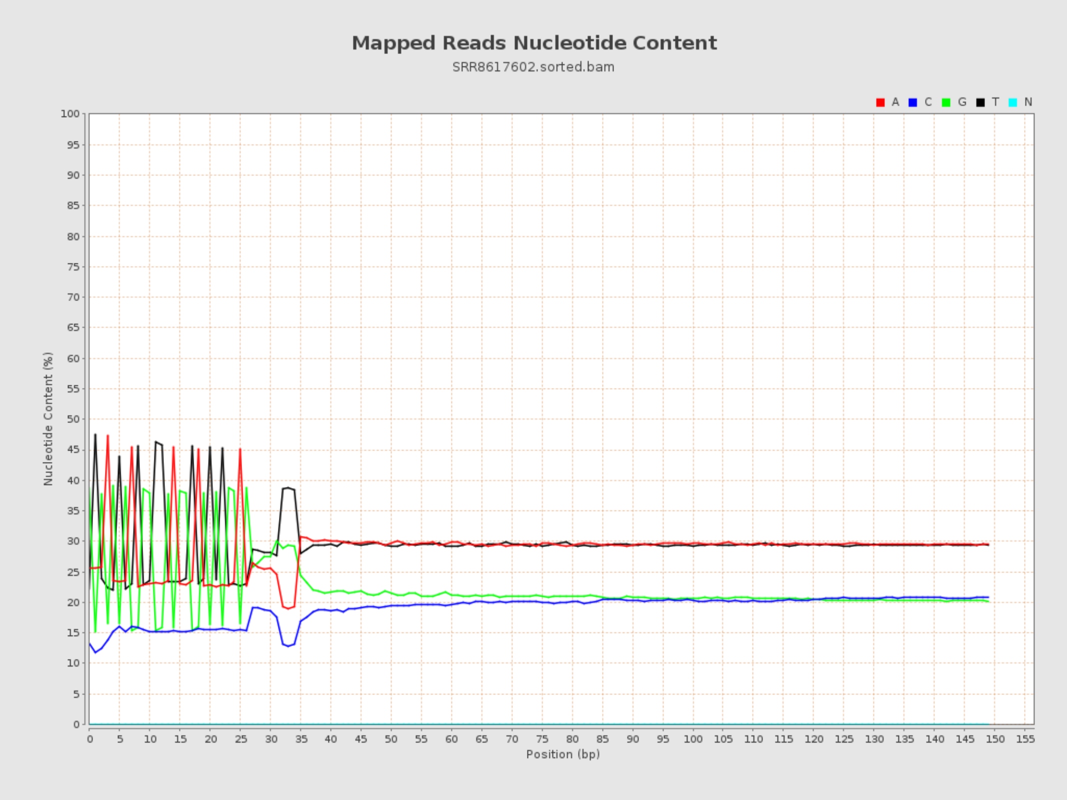
6. Results : Genome Fraction Coverage



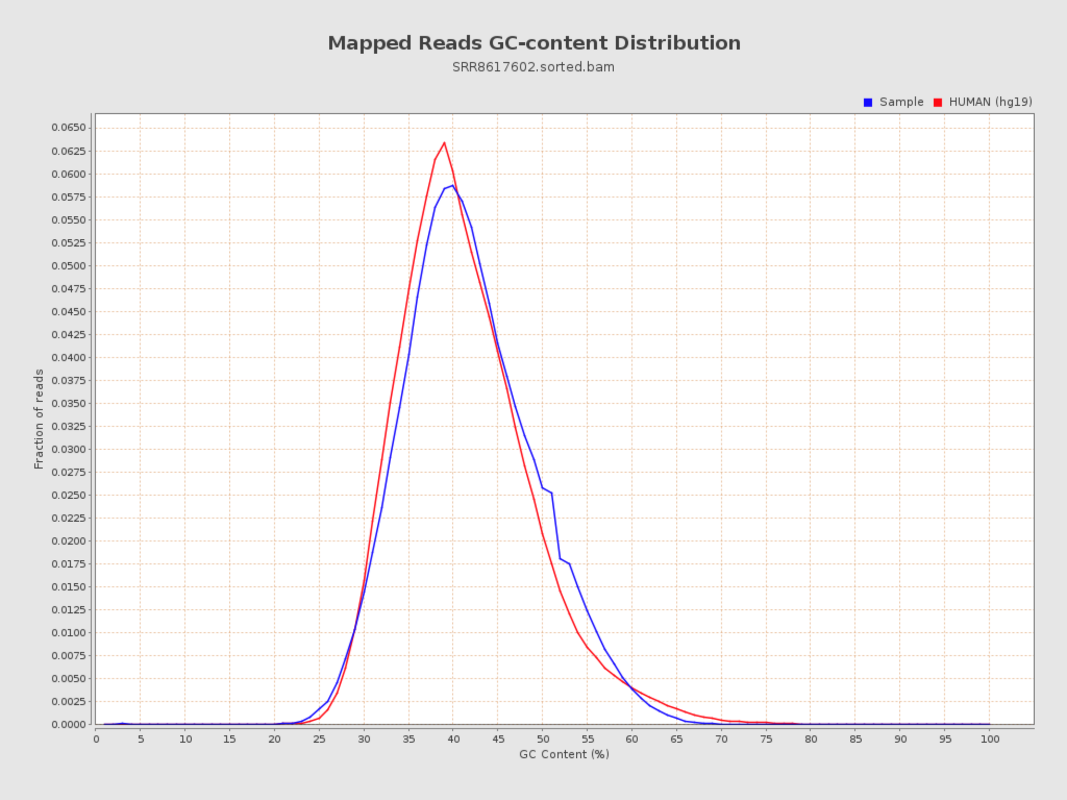
7. Results : Duplication Rate Histogram



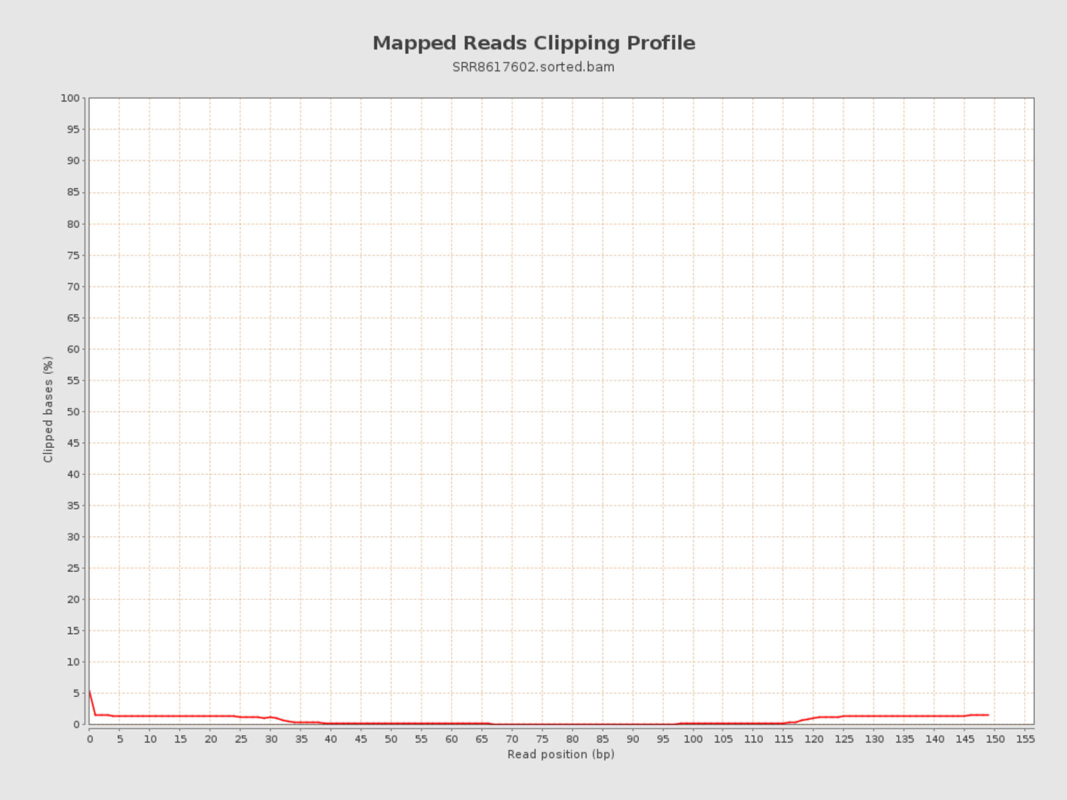
8. Results : Mapped Reads Nucleotide Content



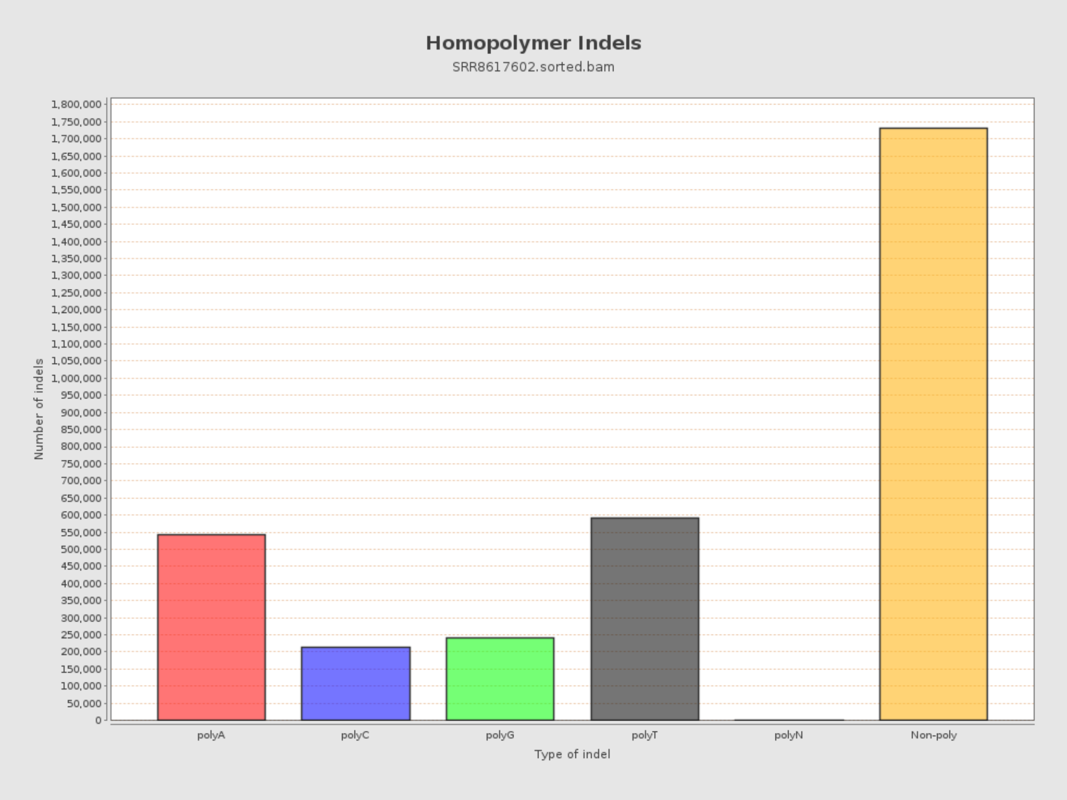
9. Results : Mapped Reads GC-content Distribution



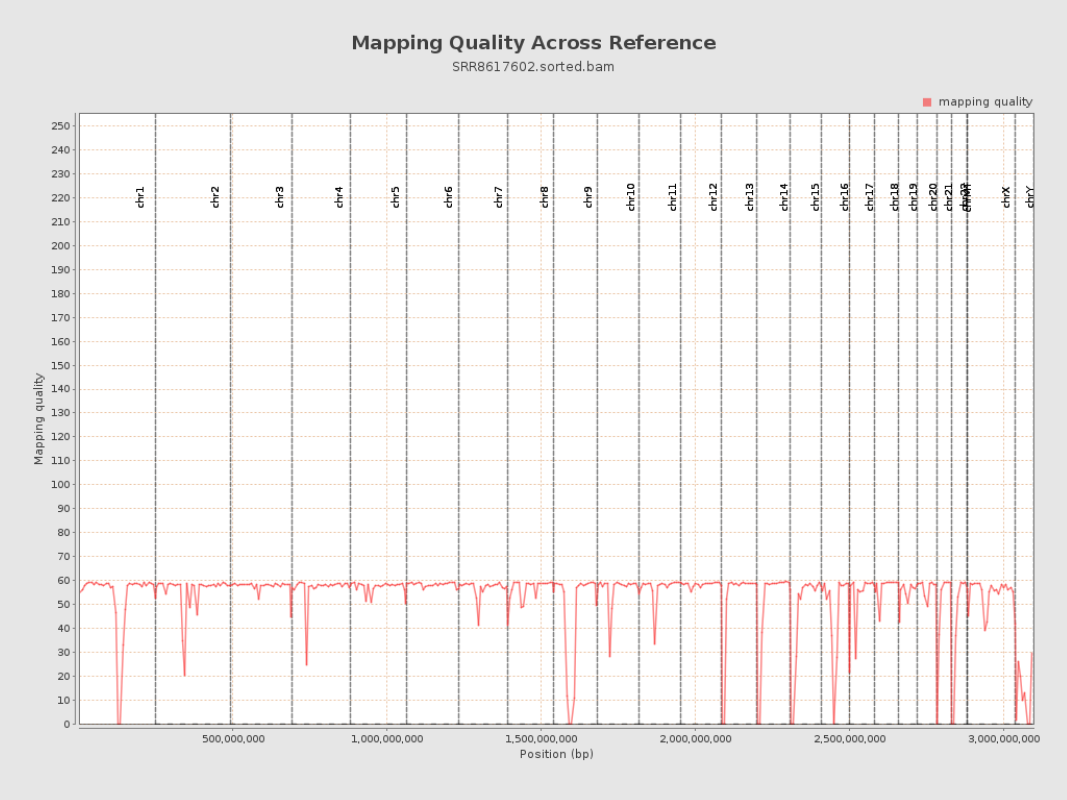
10. Results : Mapped Reads Clipping Profile



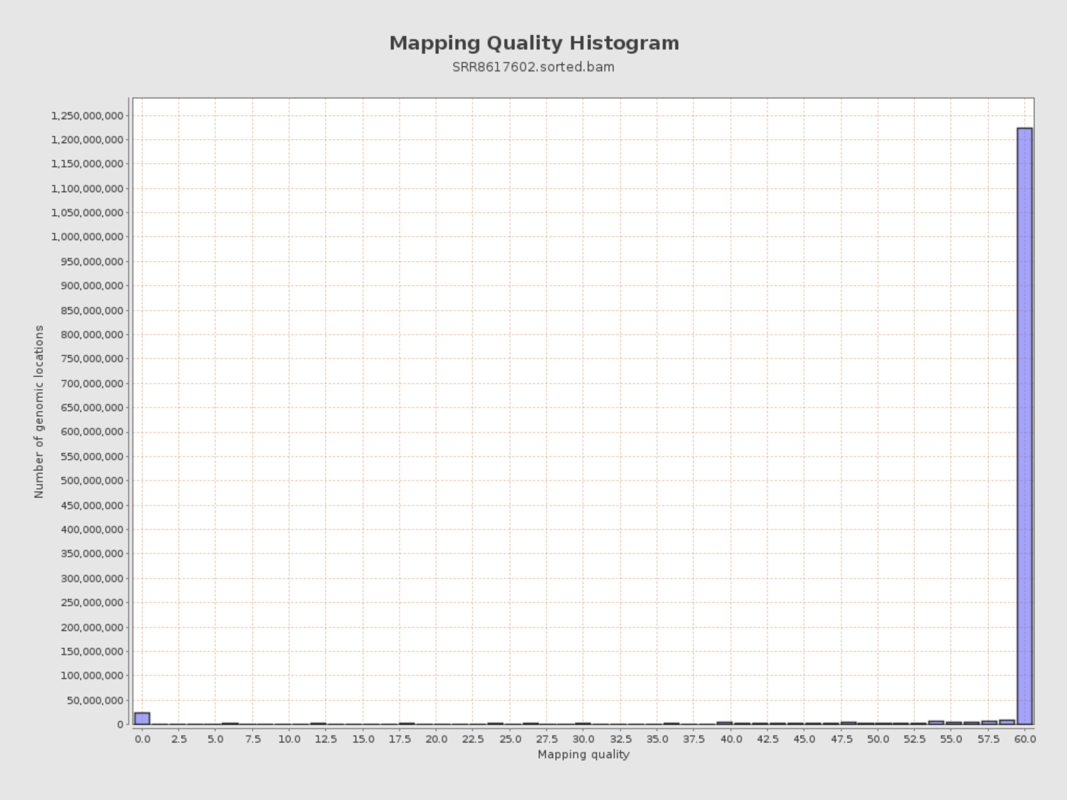
11. Results : Homopolymer Indels



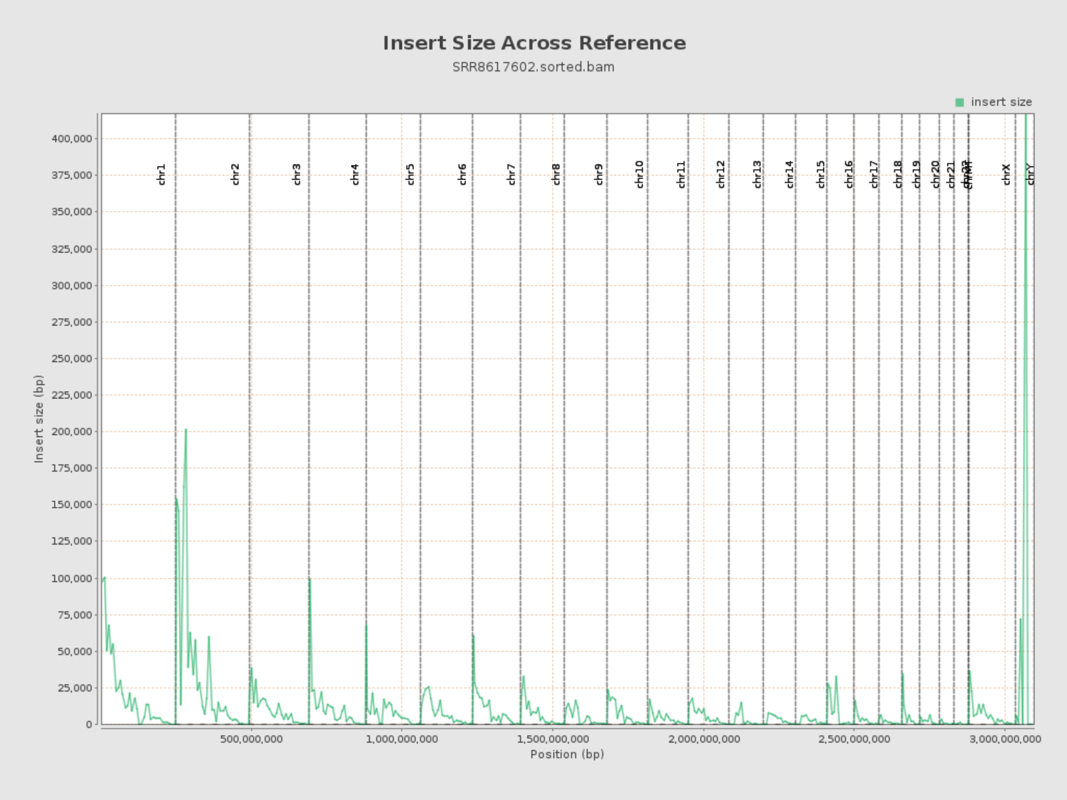
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram