Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 05:21:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617418.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_SRR617418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617418_1.fastq.gz SRR617418_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 05:21:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617418.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,153,437 / 84.85%
Unmapped reads	4,846,563 / 15.15%
Mapped paired reads	27,153,437 / 84.85%
Mapped reads, first in pair	14,181,414 / 44.32%
Mapped reads, second in pair	12,972,023 / 40.54%
Mapped reads, both in pair	25,664,688 / 80.2%
Mapped reads, singletons	1,488,749 / 4.65%
Secondary alignments	0
Supplementary alignments	381,000 / 1.19%
Read min/max/mean length	30 / 100 / 100.49
Duplicated reads (estimated)	1,137,225 / 3.55%
Duplication rate	3.79%
Clipped reads	4,251,019 / 13.28%

2.2. ACGT Content

Number/percentage of A's	787,929,323 / 29.93%
Number/percentage of C's	525,584,750 / 19.96%
Number/percentage of T's	782,510,645 / 29.72%
Number/percentage of G's	535,975,704 / 20.36%
Number/percentage of N's	583,834 / 0.02%

GC Percentage	40.32%

2.3. Coverage

Mean	0.8506
Standard Deviation	2.6121

2.4. Mapping Quality

Mean Mapping Quality	53.44

2.5. Insert size

Mean	56,042.17
Standard Deviation	2,263,755.3
P25/Median/P75	167 / 203 / 259

2.6. Mismatches and indels

General error rate	1.76%
Mismatches	45,786,313
Insertions	222,900
Mapped reads with at least one insertion	0.81%
Deletions	258,035
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.43%

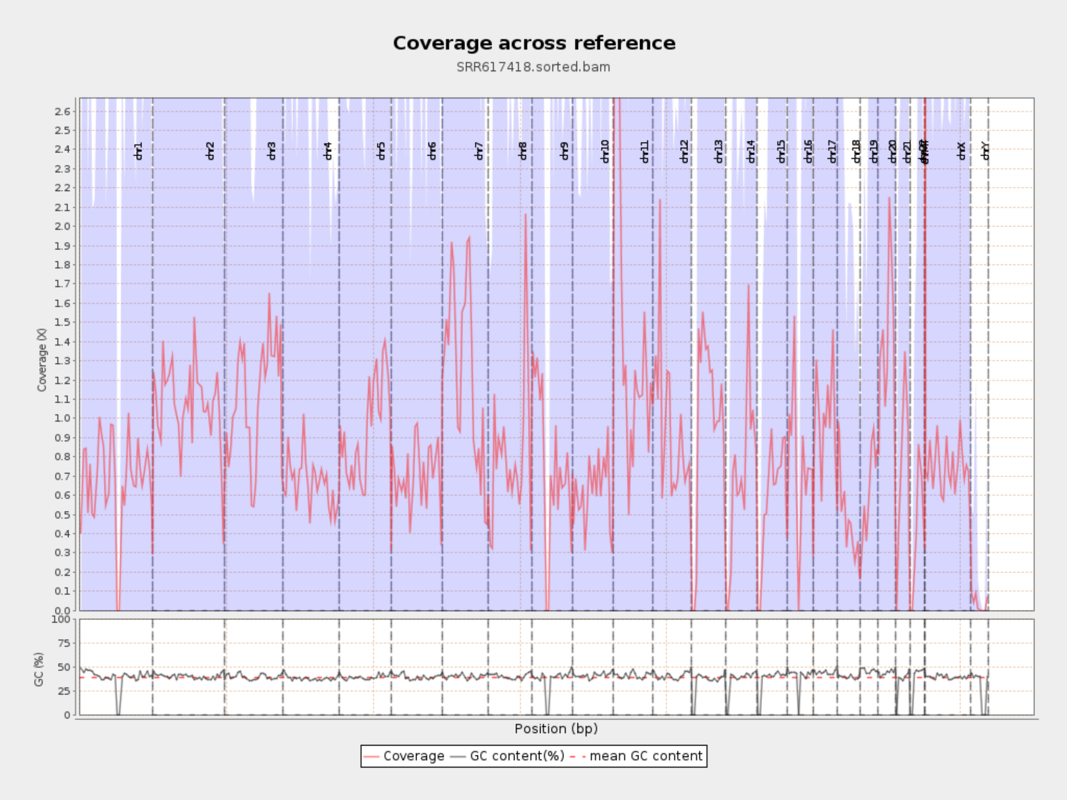
2.7. Chromosome stats

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

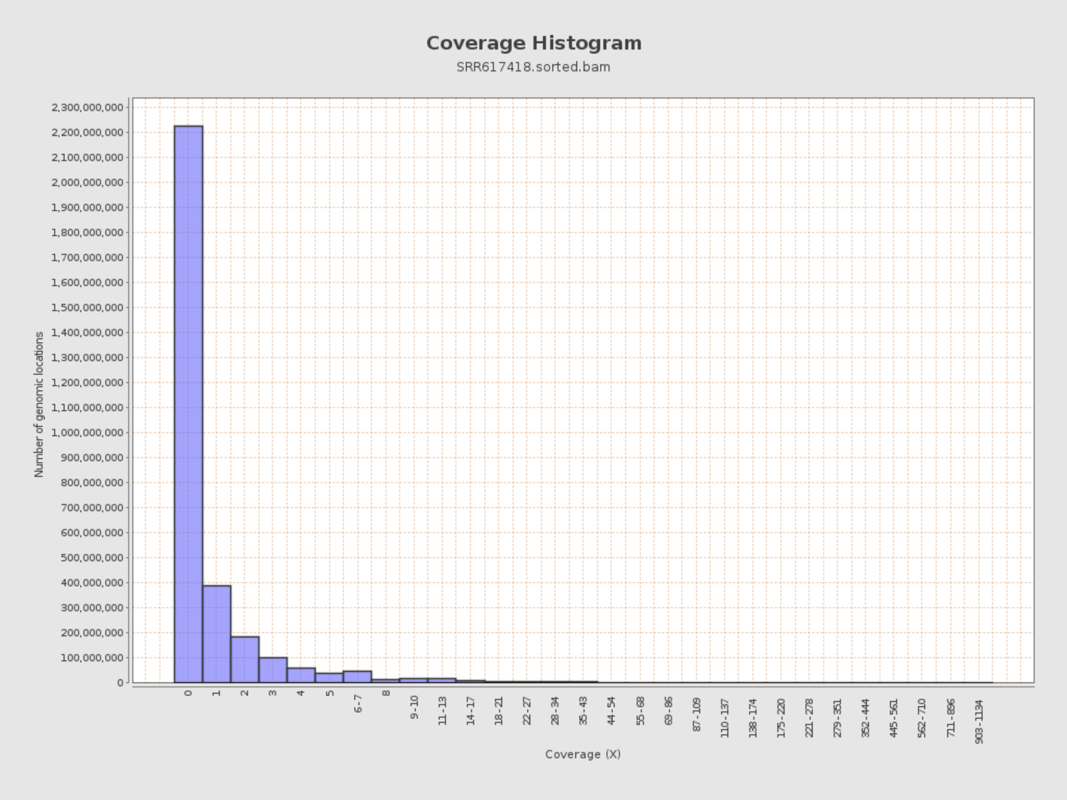
		bases	coverage	deviation
chr1	249250621	169318693	0.6793	2.4392
chr2	243199373	262657569	1.08	2.7974
chr3	198022430	222977473	1.126	3.041
chr4	191154276	128140270	0.6704	2.0647
chr5	180915260	169474094	0.9368	2.5872
chr6	171115067	121374372	0.7093	2.3455
chr7	159138663	196900421	1.2373	2.9082
chr8	146364022	116809040	0.7981	2.8667
chr9	141213431	105229925	0.7452	2.3298
chr10	135534747	84202199	0.6213	2.1387
chr11	135006516	194742899	1.4425	3.4162
chr12	133851895	125421538	0.937	2.5071
chr13	115169878	114887161	0.9975	2.5003
chr14	107349540	76314387	0.7109	2.5723
chr15	102531392	60210133	0.5872	2.1353
chr16	90354753	65532652	0.7253	2.9211
chr17	81195210	80232242	0.9881	3.2352
chr18	78077248	37772461	0.4838	1.7829
chr19	59128983	36734063	0.6213	2.0535
chr20	63025520	88638648	1.4064	4.126
chr21	48129895	36139171	0.7509	2.2777
chr22	51304566	20949258	0.4083	1.8413
chrMT	16571	172717	10.4228	5.1263
chrX	155270560	116206313	0.7484	2.3086

chrY	59373566	2118574	0.0357	0.5323

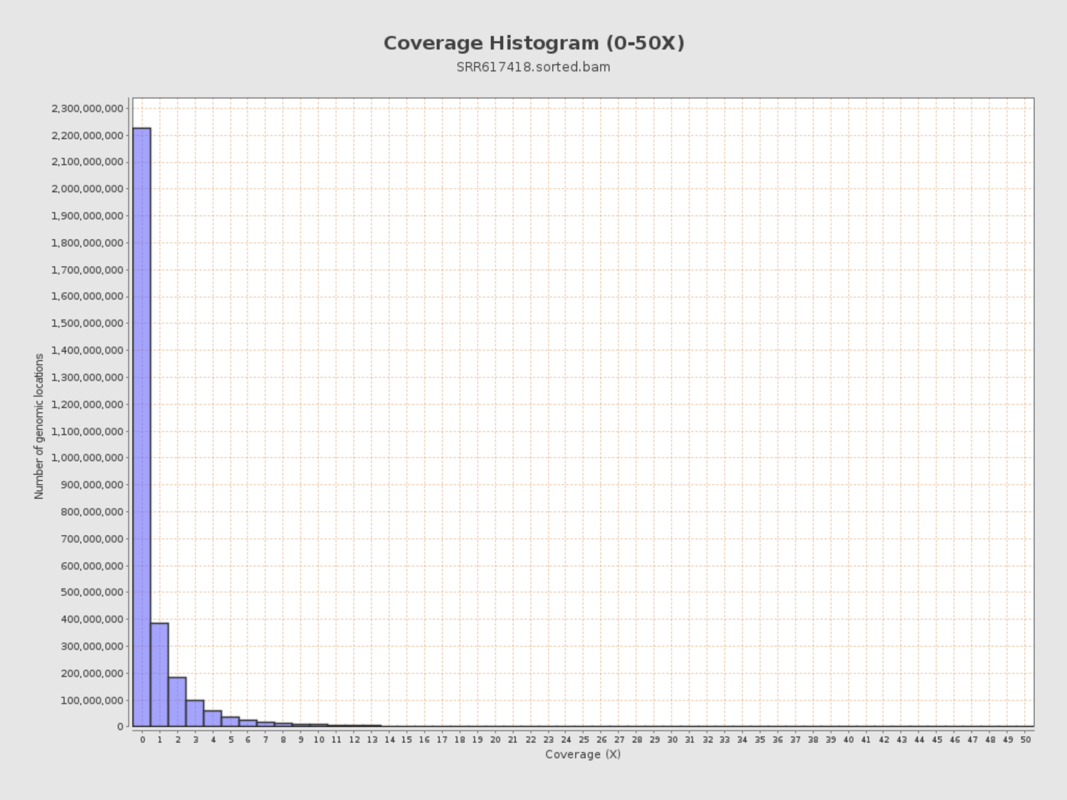
3. Results : Coverage across reference



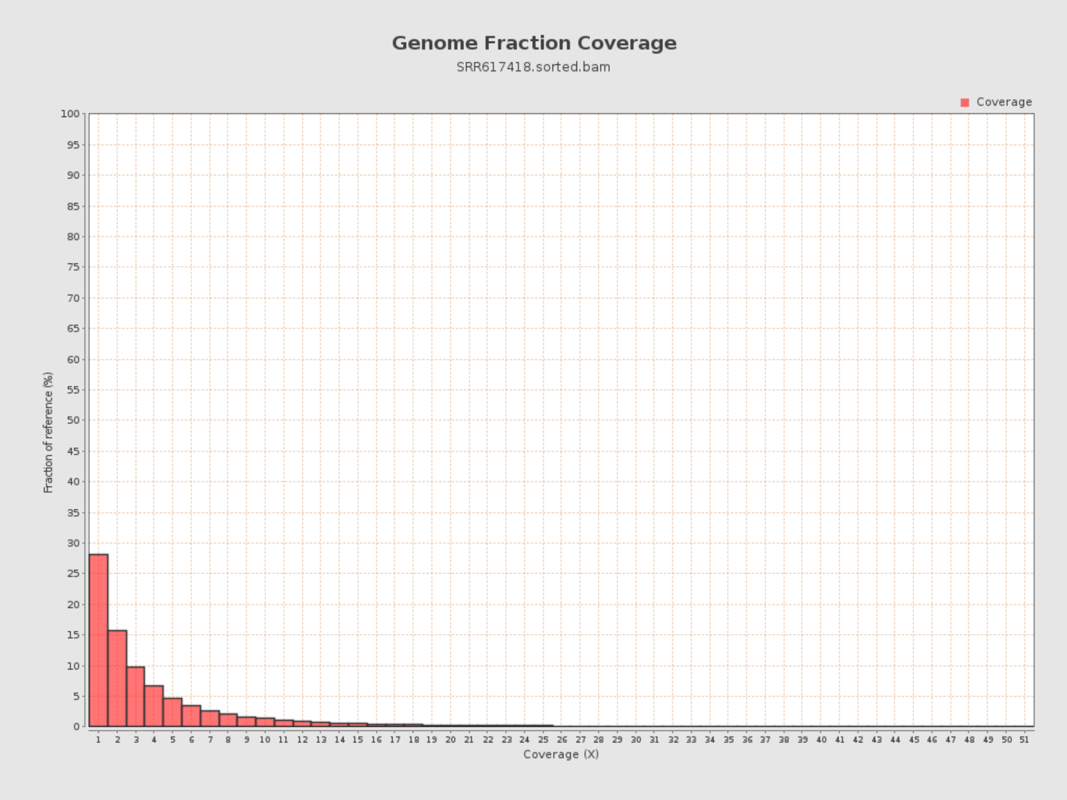
4. Results : Coverage Histogram



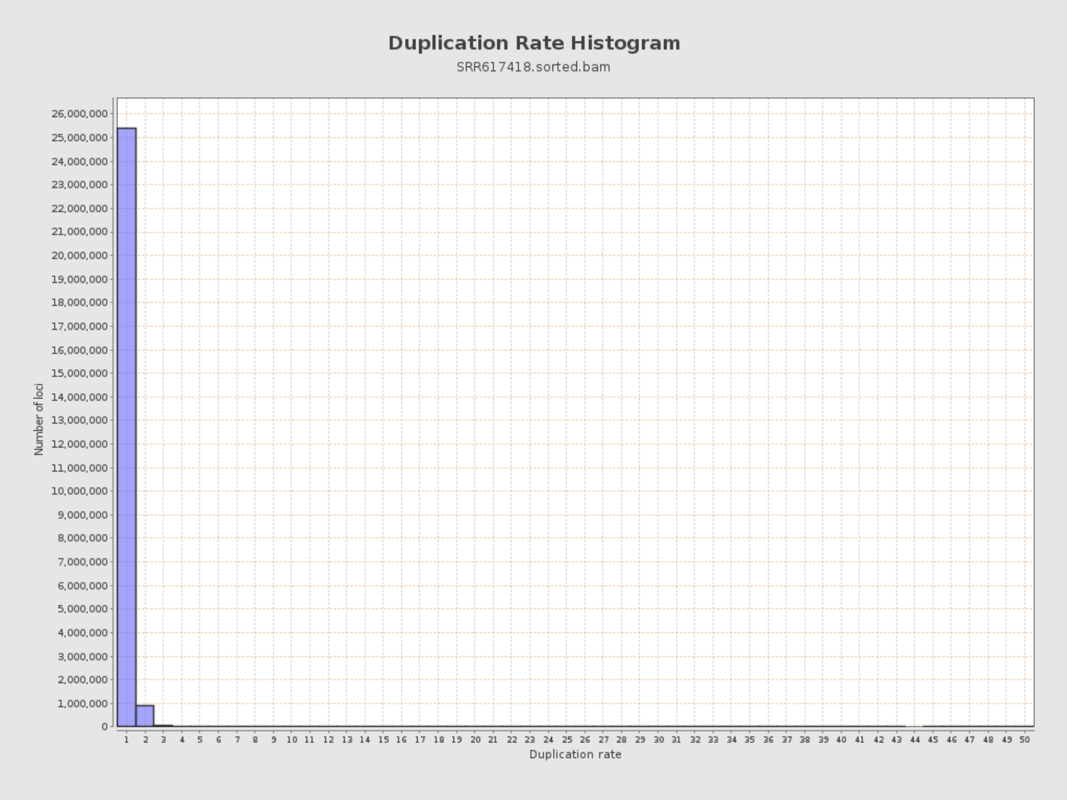
5. Results : Coverage Histogram (0-50X)



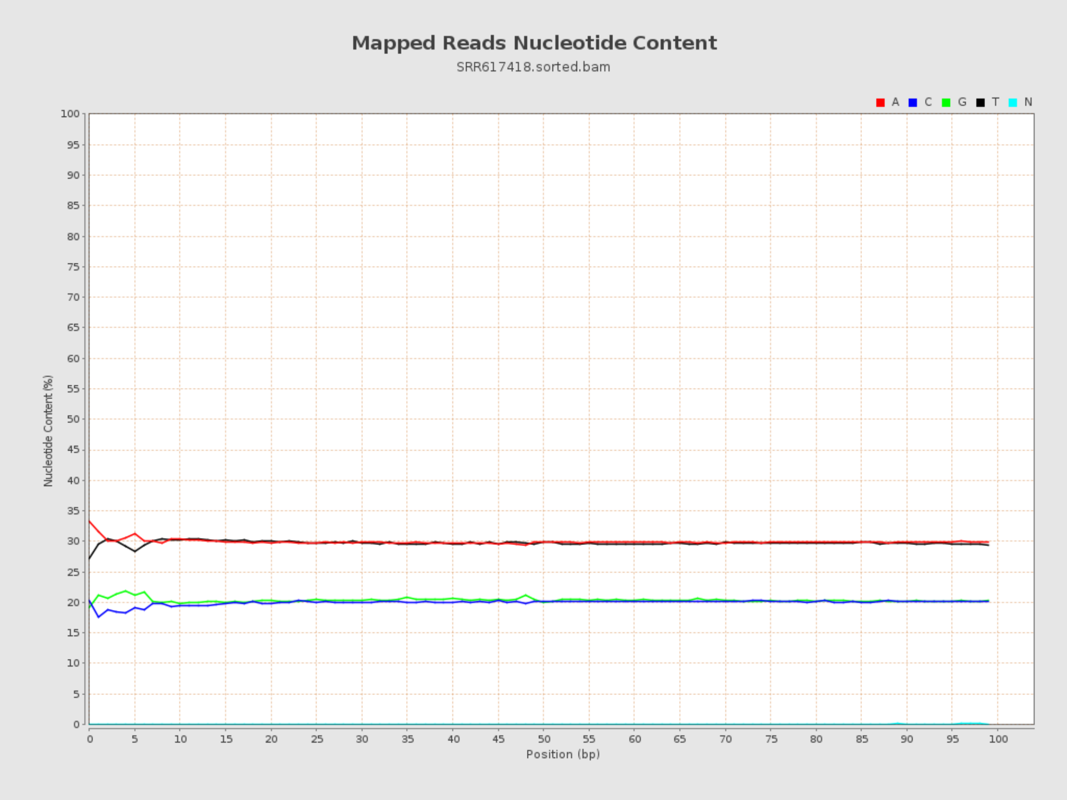
6. Results : Genome Fraction Coverage



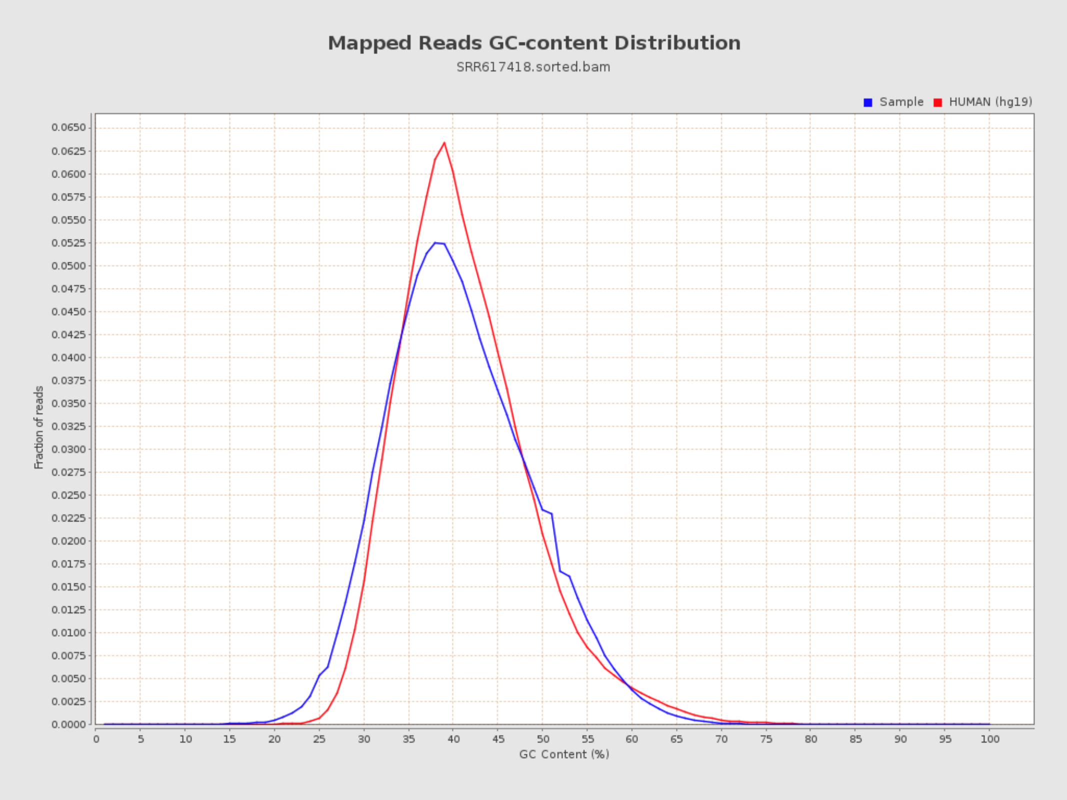
7. Results : Duplication Rate Histogram



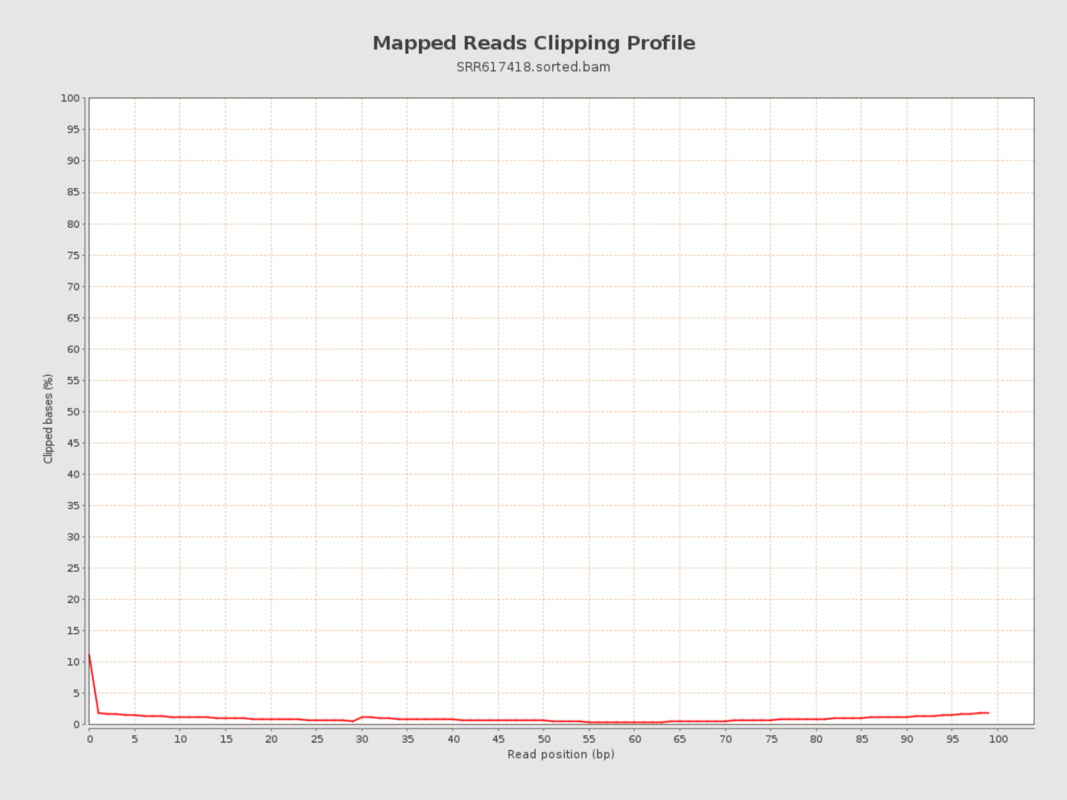
8. Results : Mapped Reads Nucleotide Content



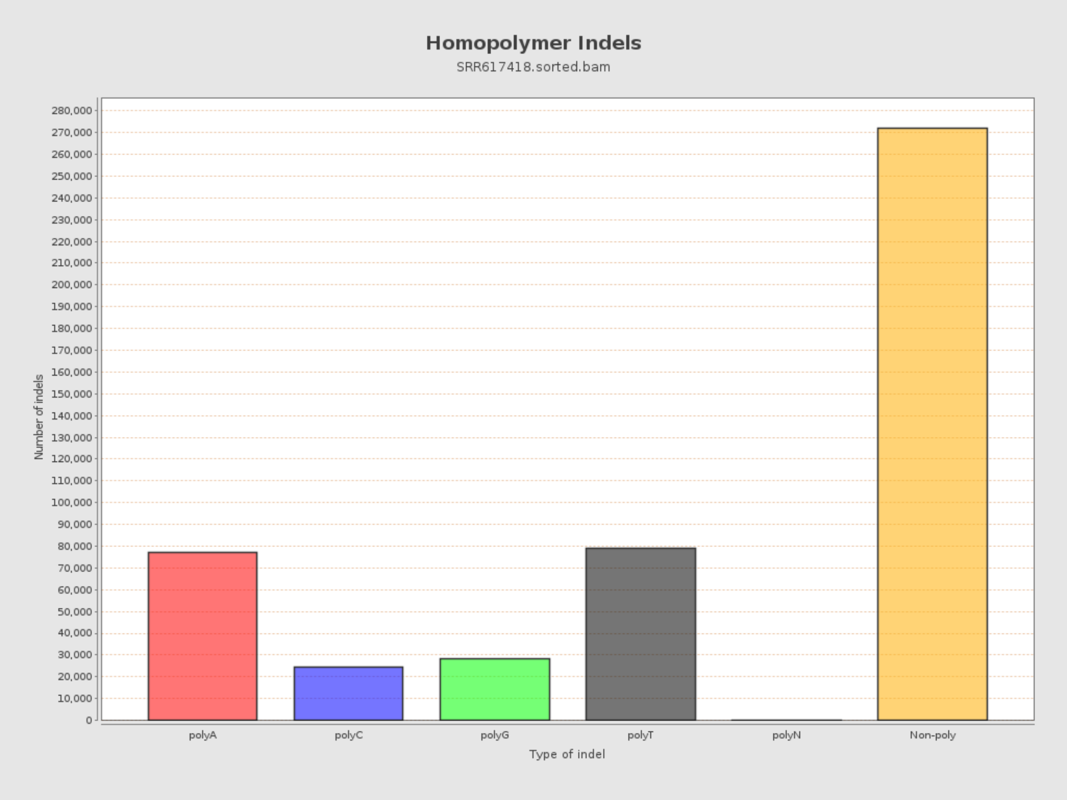
9. Results : Mapped Reads GC-content Distribution



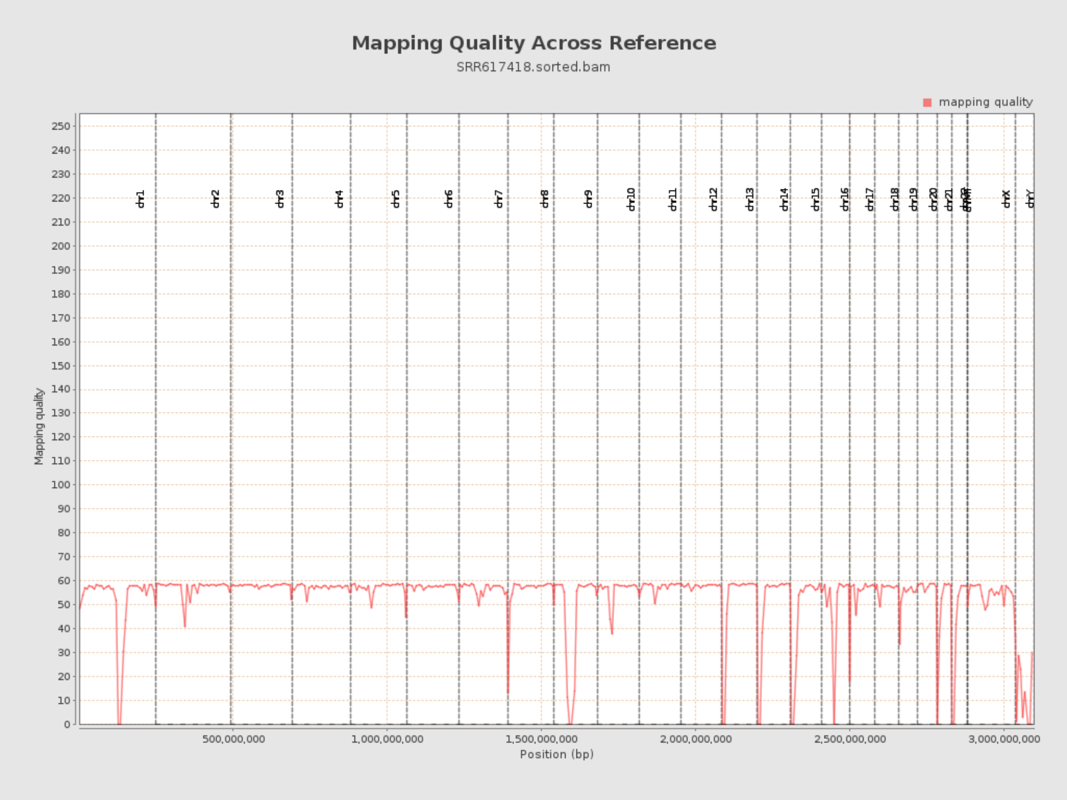
10. Results : Mapped Reads Clipping Profile



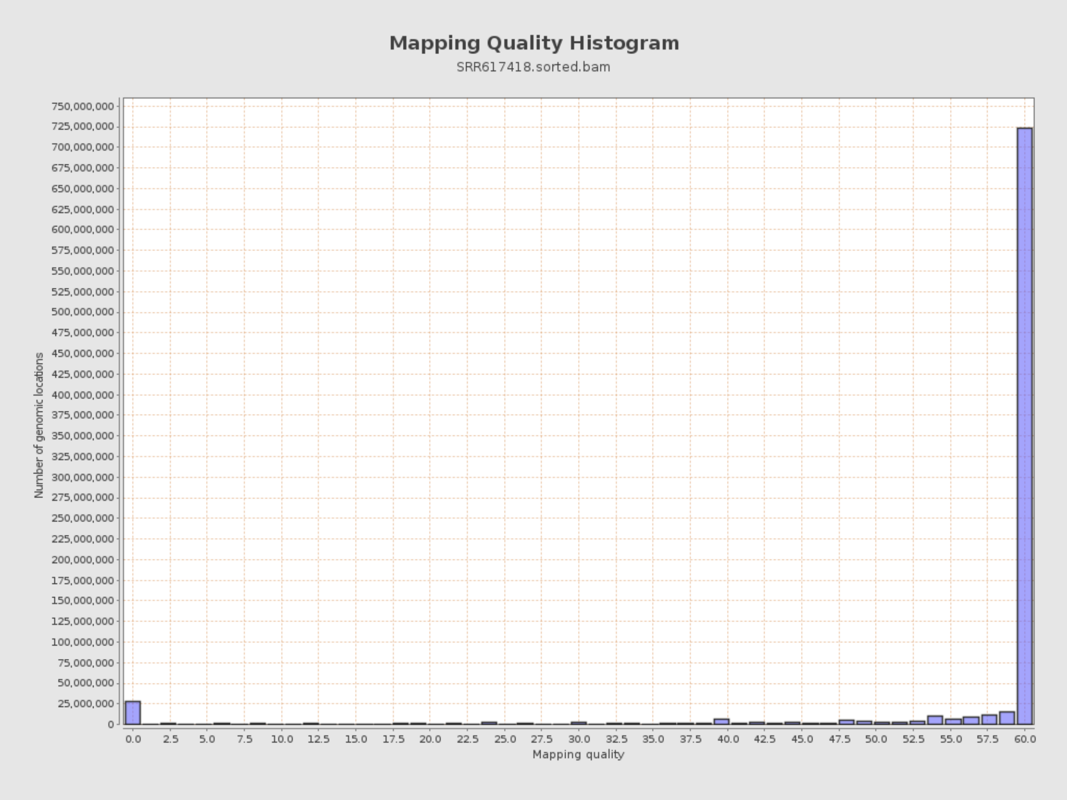
11. Results : Homopolymer Indels



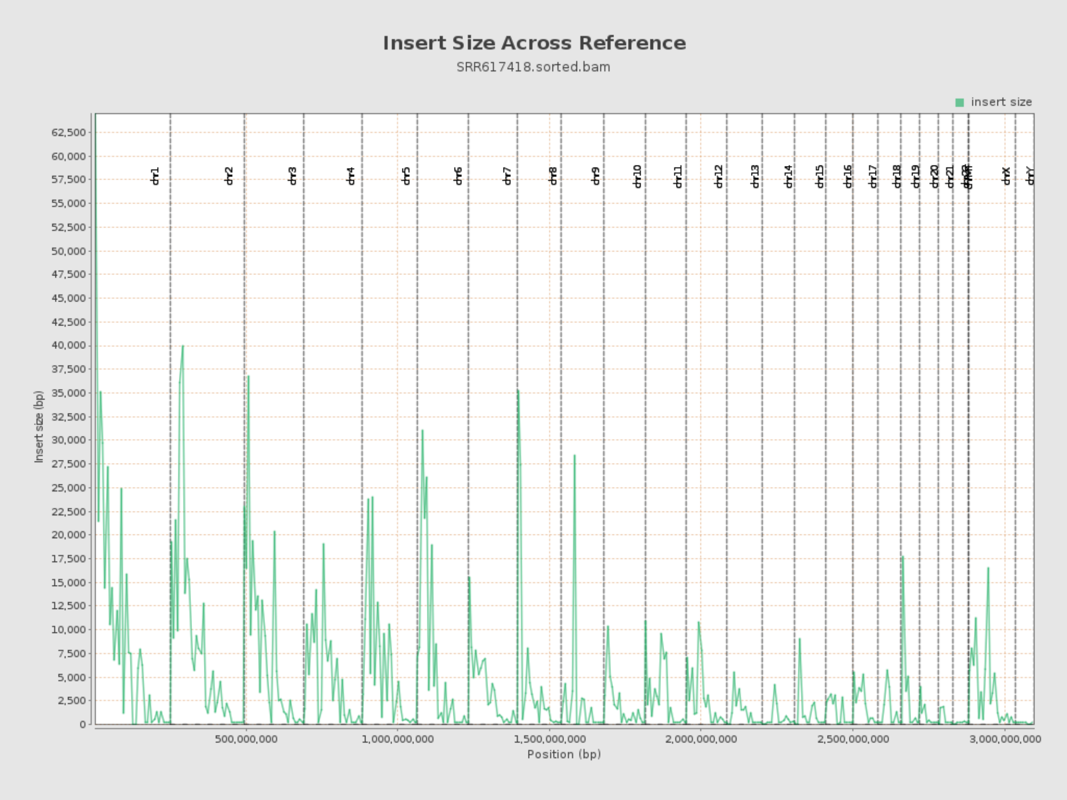
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram