Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 18:45:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124813.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_SRR3124813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124813_1.fastq.gz SRR3124813_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 18:44:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,954,254
Mapped reads	29,437,559 / 98.28%
Unmapped reads	516,695 / 1.72%
Mapped paired reads	29,437,559 / 98.28%
Mapped reads, first in pair	14,745,395 / 49.23%
Mapped reads, second in pair	14,692,164 / 49.05%
Mapped reads, both in pair	29,328,756 / 97.91%
Mapped reads, singletons	108,803 / 0.36%
Secondary alignments	0
Supplementary alignments	99,197 / 0.33%
Read min/max/mean length	30 / 101 / 101.13
Duplicated reads (estimated)	6,553,546 / 21.88%
Duplication rate	13.48%
Clipped reads	14,153,272 / 47.25%

2.2. ACGT Content

Number/percentage of A's	715,339,647 / 27.88%
Number/percentage of C's	487,218,112 / 18.99%
Number/percentage of T's	755,001,470 / 29.42%
Number/percentage of G's	608,507,974 / 23.71%
Number/percentage of N's	21,690 / 0%

GC Percentage	42.7%

2.3. Coverage

Mean	0.8294
Standard Deviation	6.3295

2.4. Mapping Quality

Mean Mapping Quality	52.83

2.5. Insert size

Mean	35,817.26
Standard Deviation	1,792,200.19
P25/Median/P75	146 / 197 / 276

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	18,942,495
Insertions	330,418
Mapped reads with at least one insertion	1.09%
Deletions	835,989
Mapped reads with at least one deletion	2.78%
Homopolymer indels	46.91%

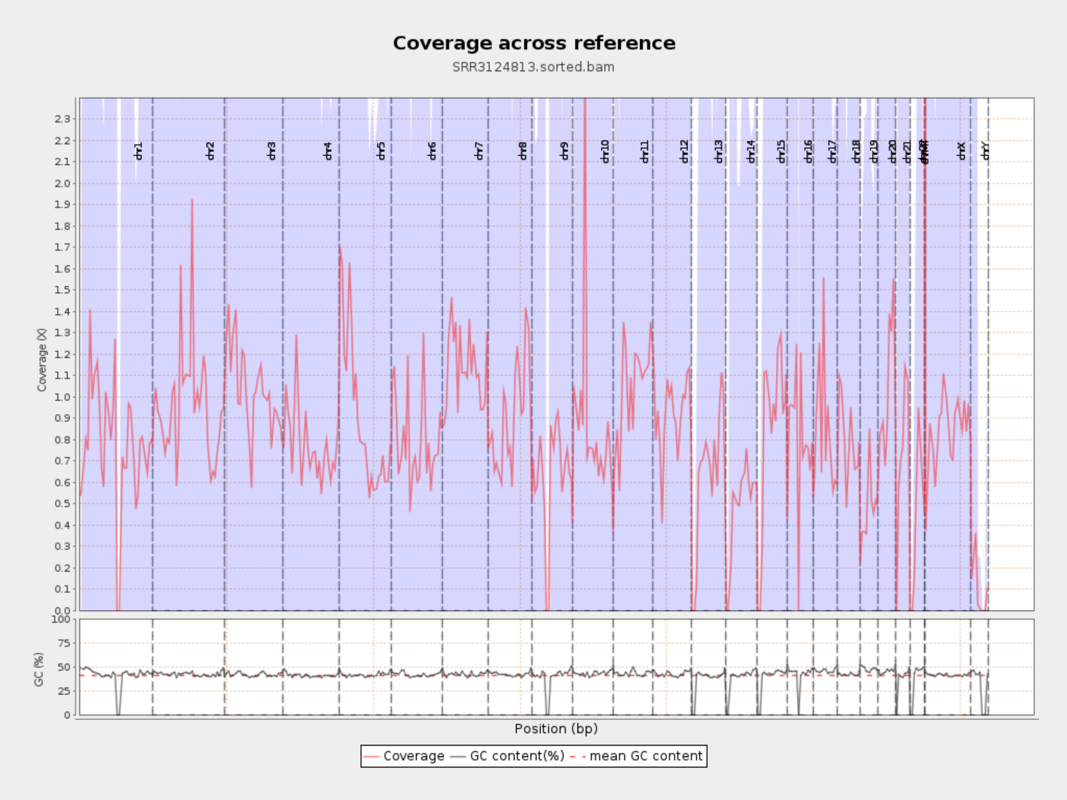
2.7. Chromosome stats

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

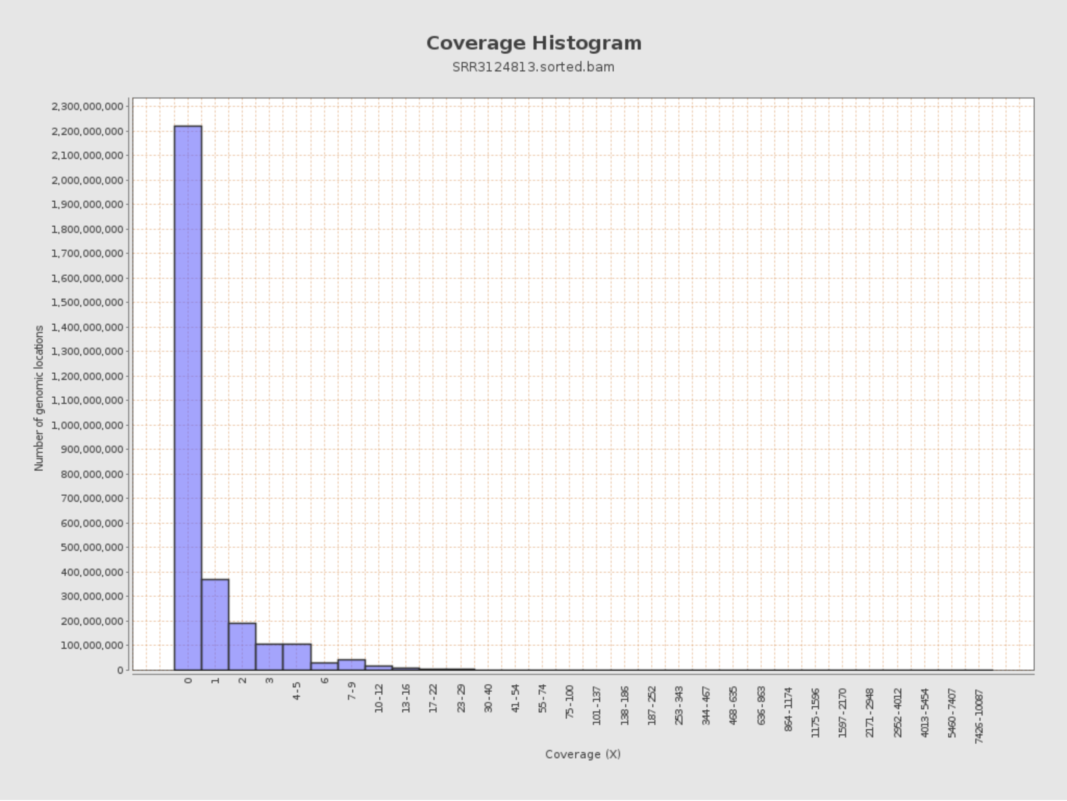
		bases	coverage	deviation
chr1	249250621	193751218	0.7773	6.5003
chr2	243199373	233018930	0.9581	8.9712
chr3	198022430	204488523	1.0327	2.4069
chr4	191154276	148172397	0.7751	4.3839
chr5	180915260	163776440	0.9053	2.4128
chr6	171115067	136370312	0.797	4.8426
chr7	159138663	180151769	1.132	9.4916
chr8	146364022	132475316	0.9051	2.9194
chr9	141213431	88376226	0.6258	6.7684
chr10	135534747	121465644	0.8962	16.0506
chr11	135006516	139048939	1.0299	4.7679
chr12	133851895	122896895	0.9182	2.2651
chr13	115169878	73790105	0.6407	1.8097
chr14	107349540	51812920	0.4827	2.0397
chr15	102531392	85223021	0.8312	2.281
chr16	90354753	72125398	0.7982	6.6466
chr17	81195210	68598722	0.8449	8.6476
chr18	78077248	62715600	0.8033	8.0606
chr19	59128983	28260425	0.4779	4.3086
chr20	63025520	64731771	1.0271	2.7942
chr21	48129895	36039712	0.7488	2.9328
chr22	51304566	23303195	0.4542	1.8973
chrMT	16571	527839	31.8532	21.1969
chrX	155270560	129775802	0.8358	3.3341

chrY	59373566	6597489	0.1111	6.8252

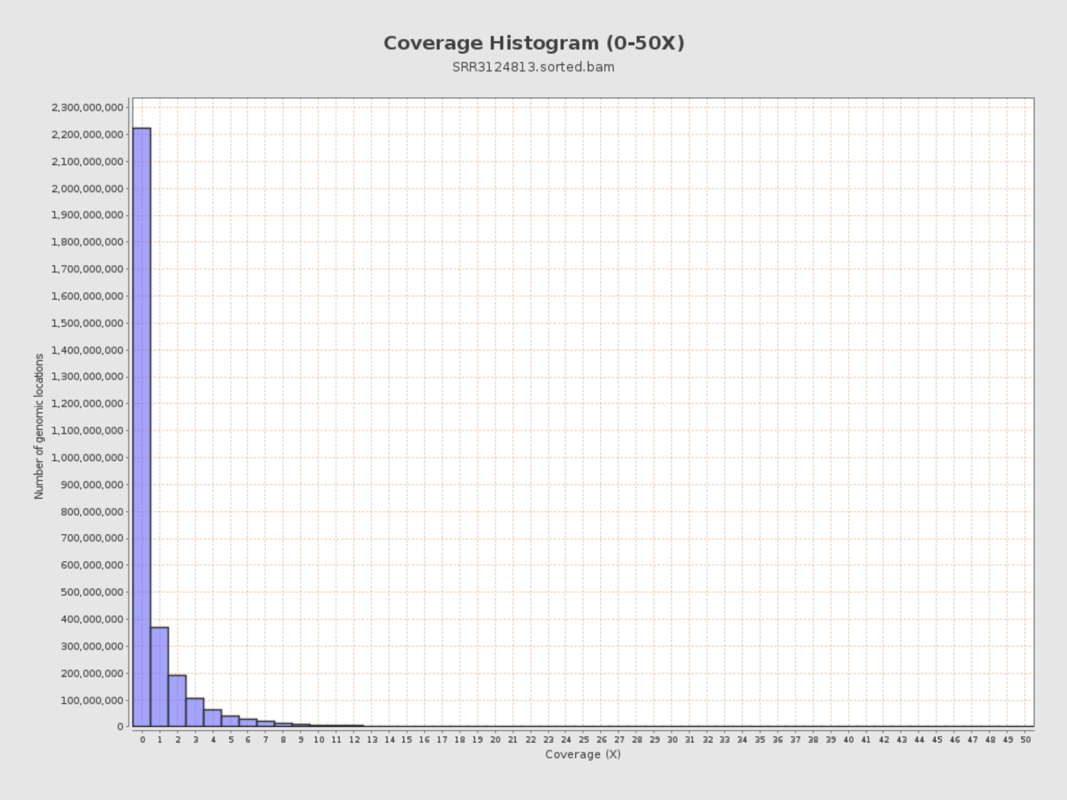
3. Results : Coverage across reference



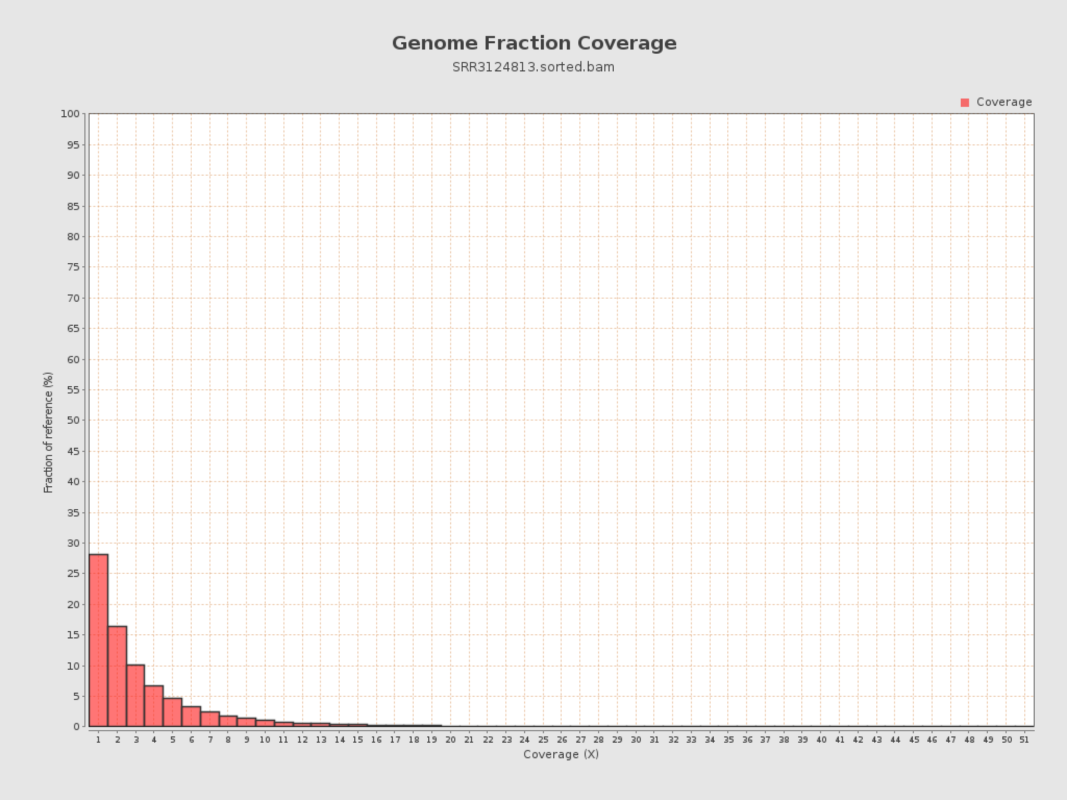
4. Results : Coverage Histogram



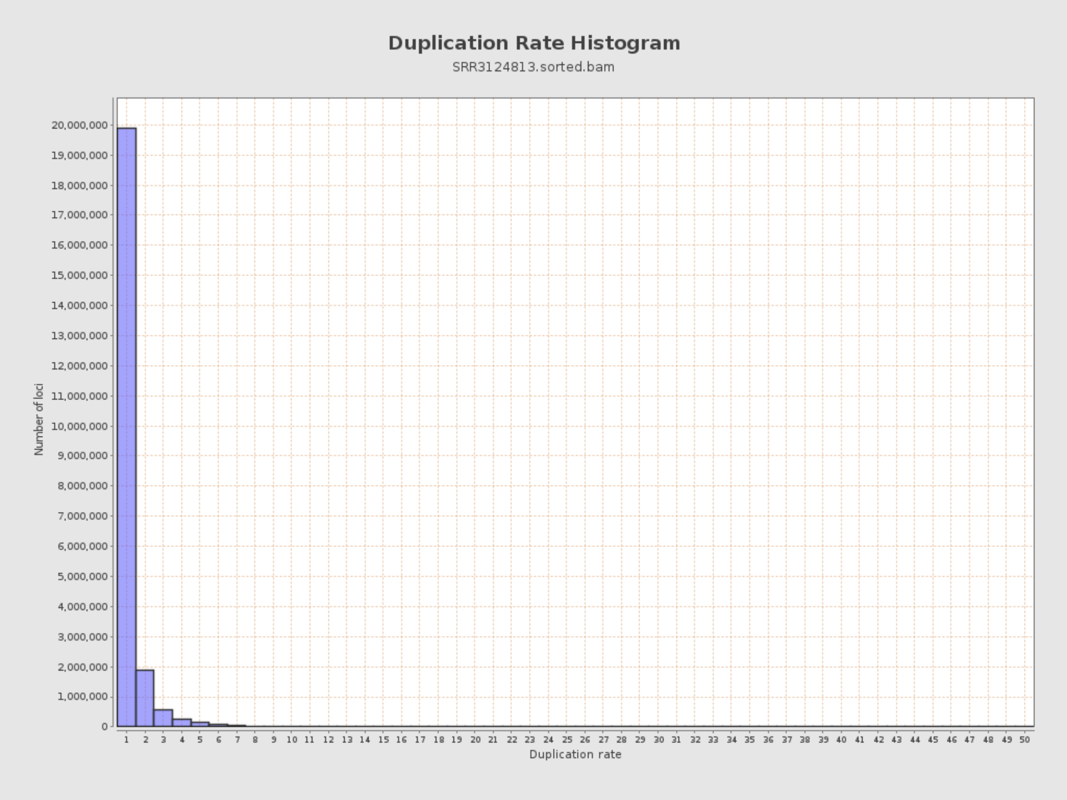
5. Results : Coverage Histogram (0-50X)



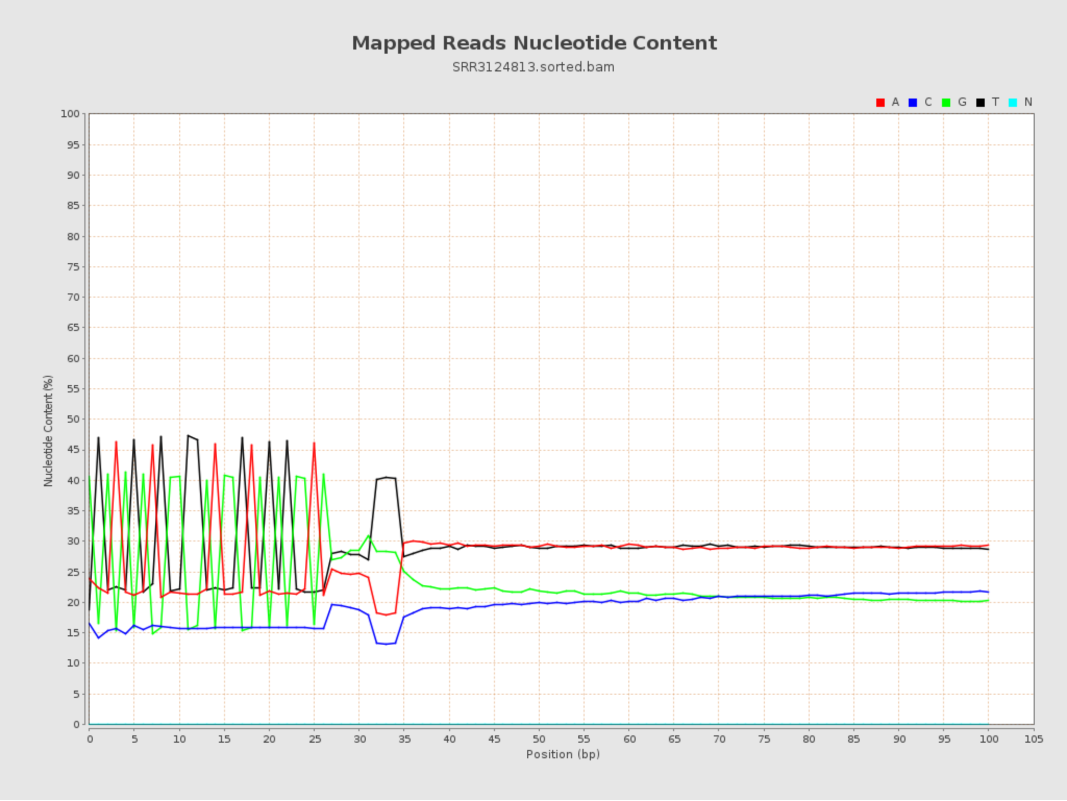
6. Results : Genome Fraction Coverage



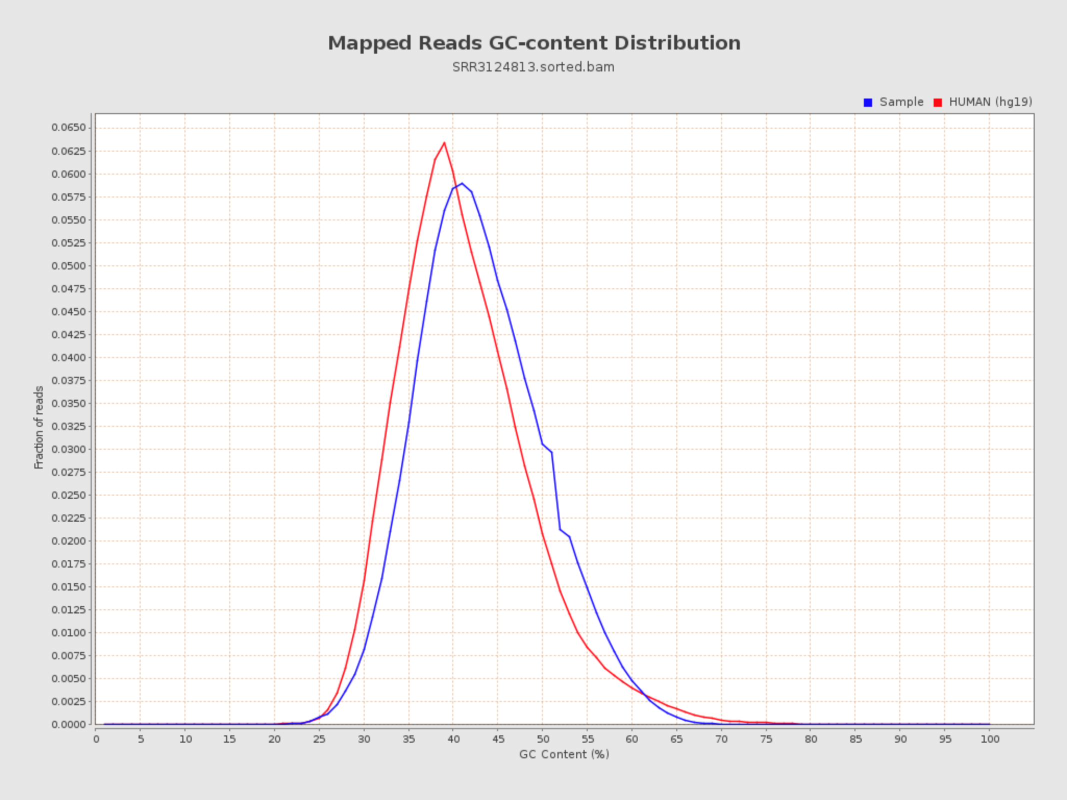
7. Results : Duplication Rate Histogram



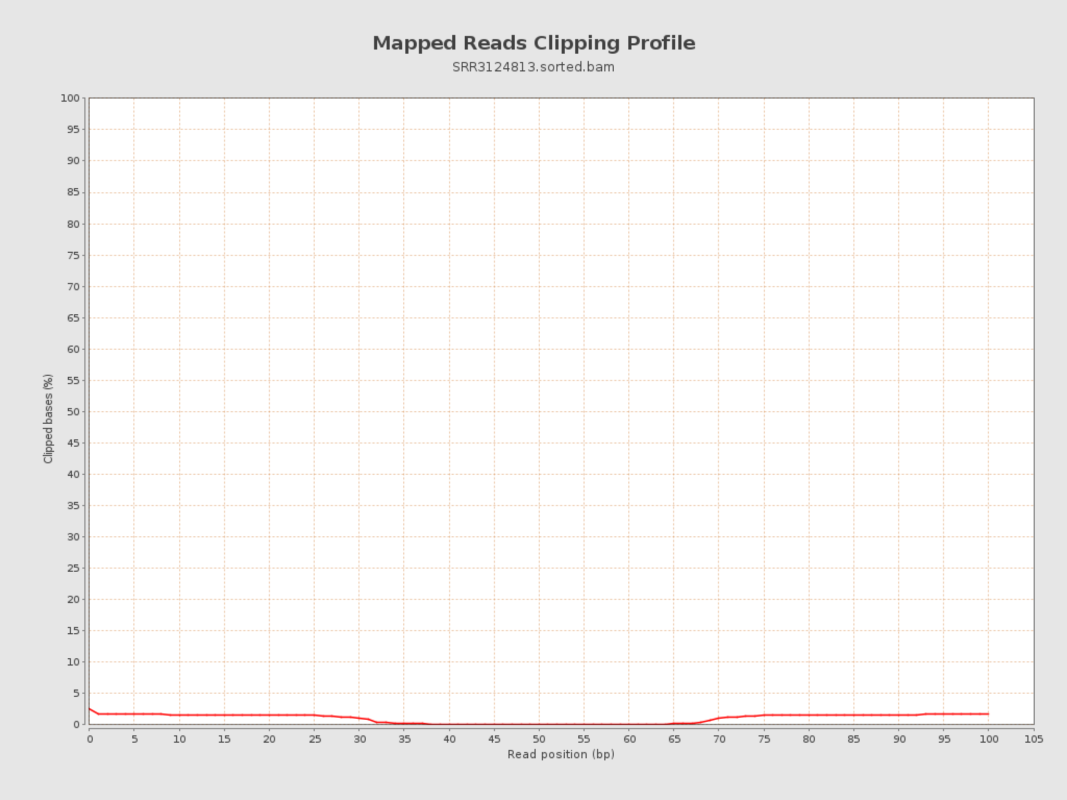
8. Results : Mapped Reads Nucleotide Content



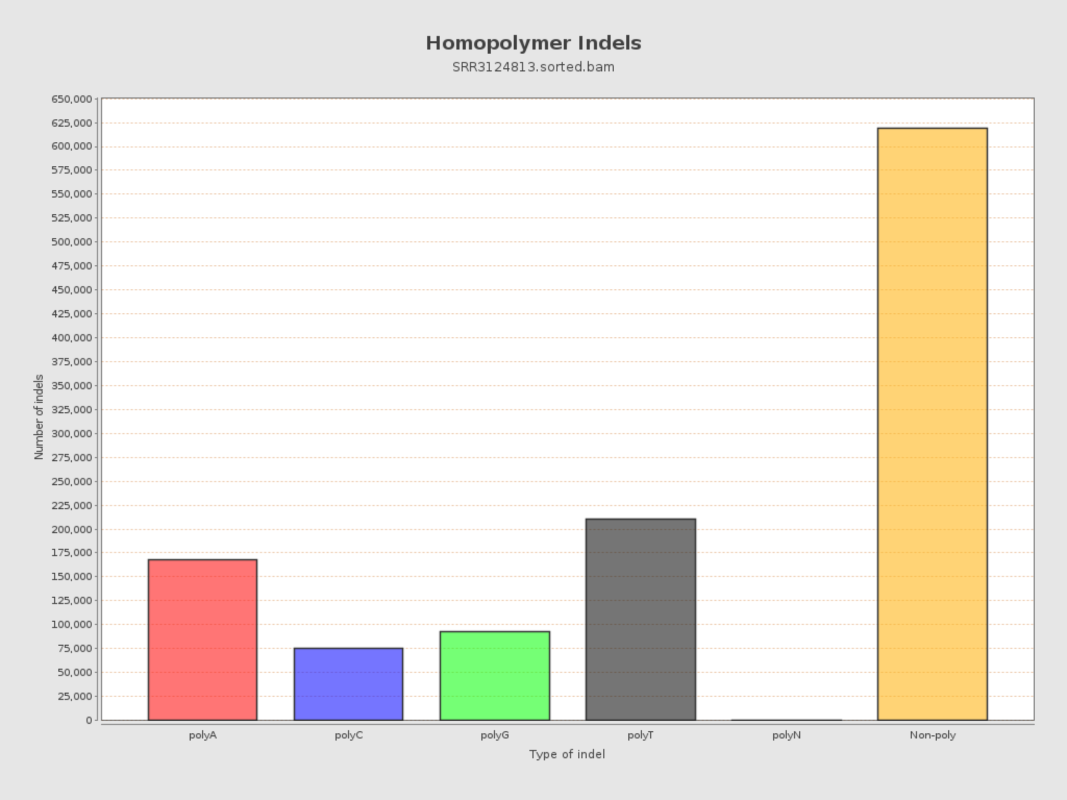
9. Results : Mapped Reads GC-content Distribution



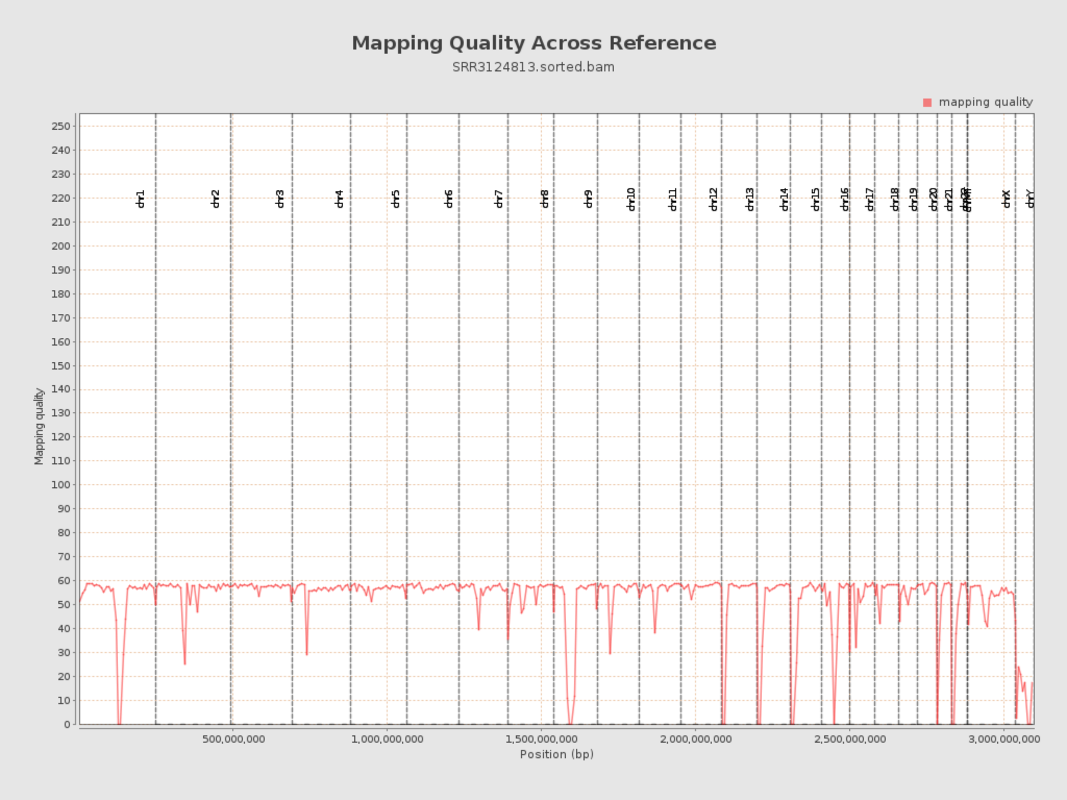
10. Results : Mapped Reads Clipping Profile



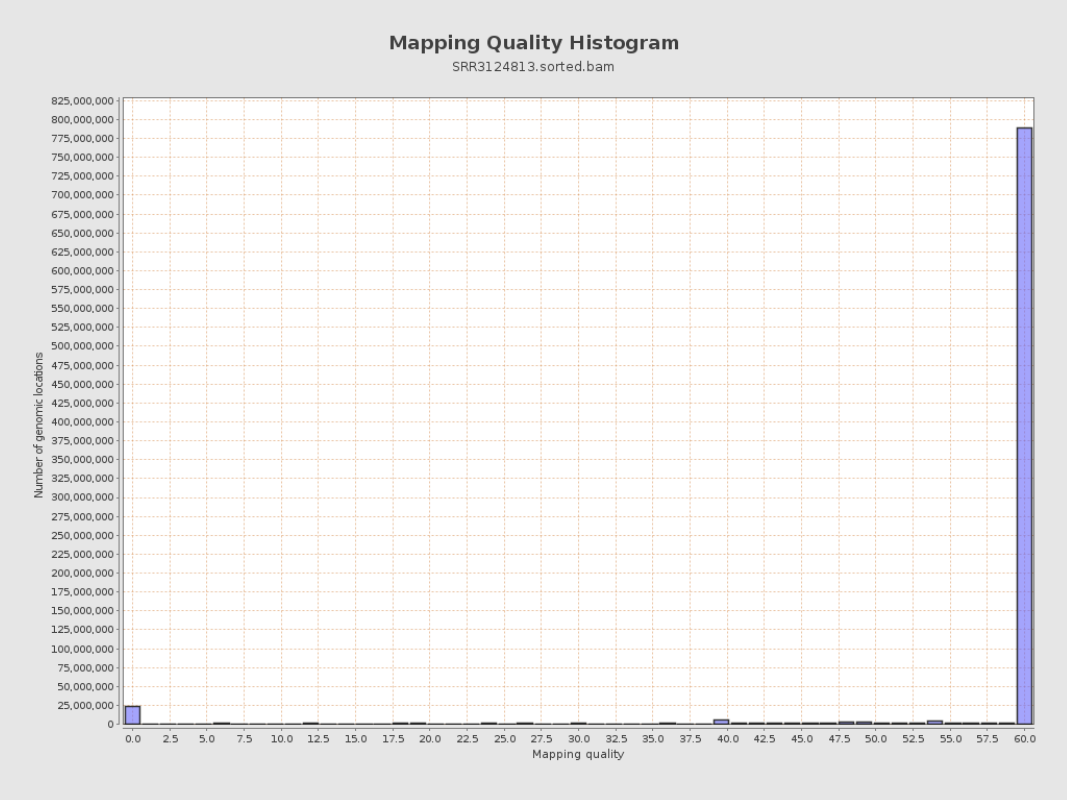
11. Results : Homopolymer Indels



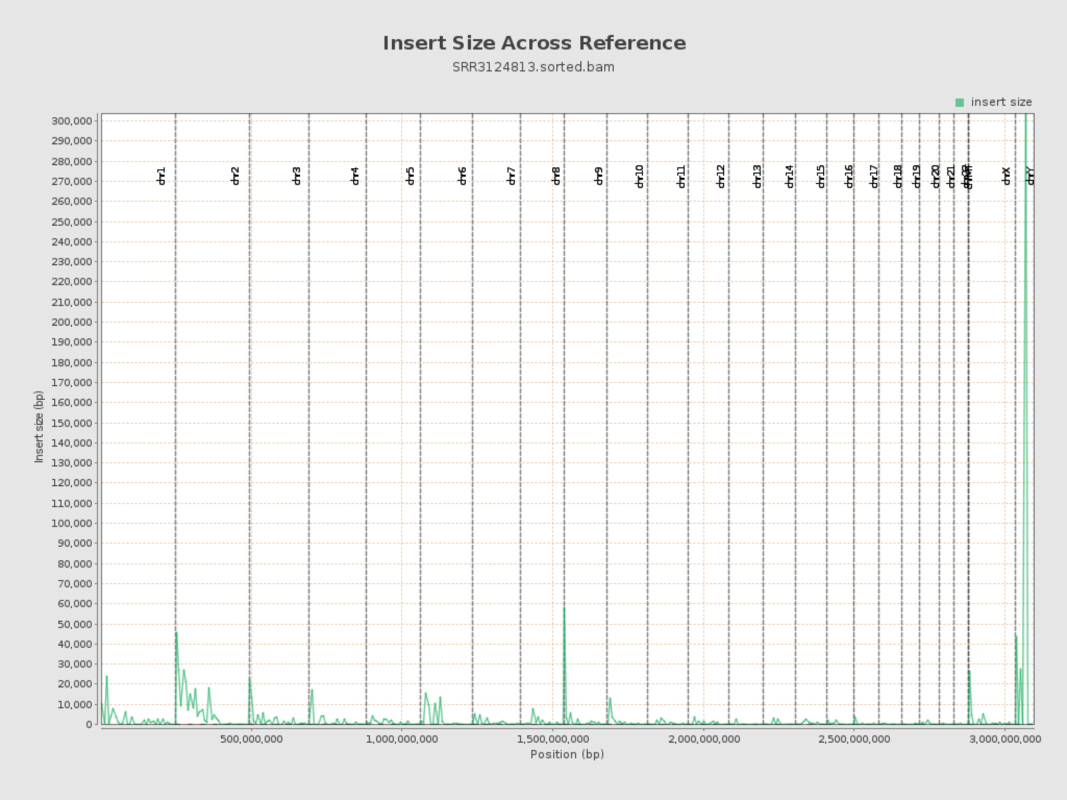
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram