Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 03:11:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124825.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_SRR3124825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124825_1.fastq.gz SRR3124825_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 03:11:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,917,774
Mapped reads	28,604,670 / 98.92%
Unmapped reads	313,104 / 1.08%
Mapped paired reads	28,604,670 / 98.92%
Mapped reads, first in pair	14,332,165 / 49.56%
Mapped reads, second in pair	14,272,505 / 49.36%
Mapped reads, both in pair	28,475,376 / 98.47%
Mapped reads, singletons	129,294 / 0.45%
Secondary alignments	0
Supplementary alignments	105,527 / 0.36%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	5,392,733 / 18.65%
Duplication rate	11.78%
Clipped reads	13,962,126 / 48.28%

2.2. ACGT Content

Number/percentage of A's	698,496,774 / 28.13%
Number/percentage of C's	462,865,500 / 18.64%
Number/percentage of T's	738,021,227 / 29.73%
Number/percentage of G's	583,285,201 / 23.49%
Number/percentage of N's	20,537 / 0%

GC Percentage	42.14%

2.3. Coverage

Mean	0.8024
Standard Deviation	7.4844

2.4. Mapping Quality

Mean Mapping Quality	52.73

2.5. Insert size

Mean	35,714.81
Standard Deviation	1,764,473.65
P25/Median/P75	150 / 202 / 280

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	18,697,778
Insertions	314,389
Mapped reads with at least one insertion	1.07%
Deletions	766,902
Mapped reads with at least one deletion	2.63%
Homopolymer indels	47.03%

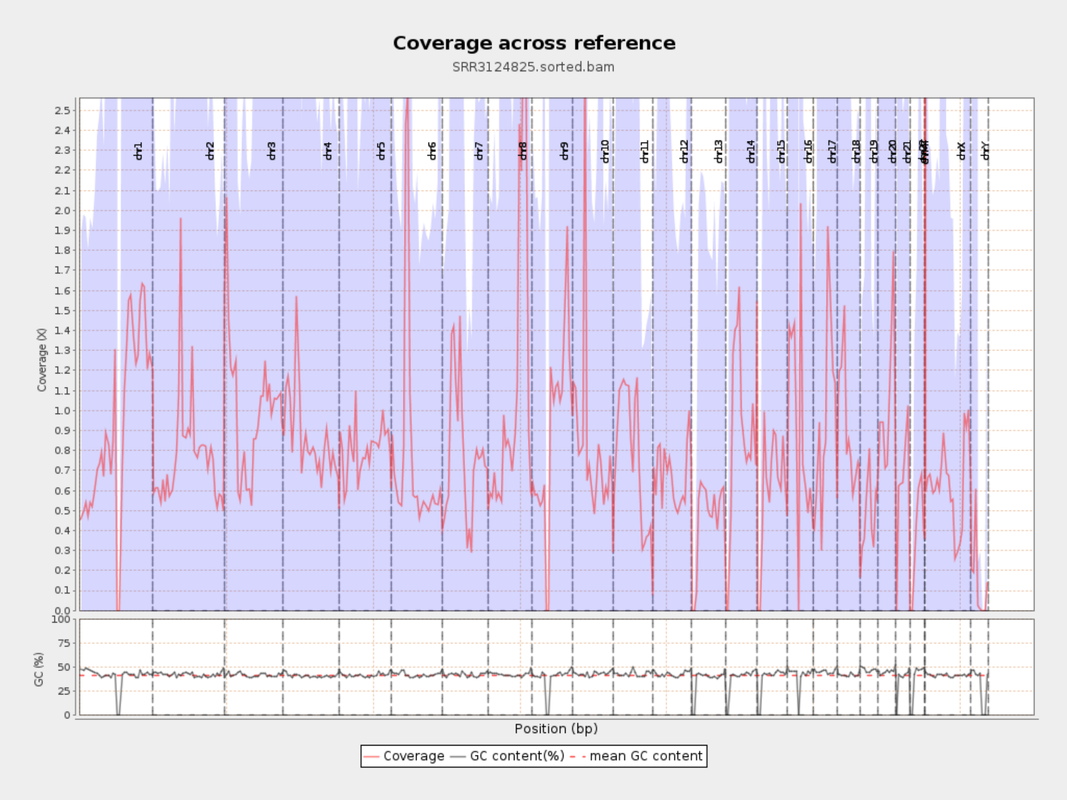
2.7. Chromosome stats

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

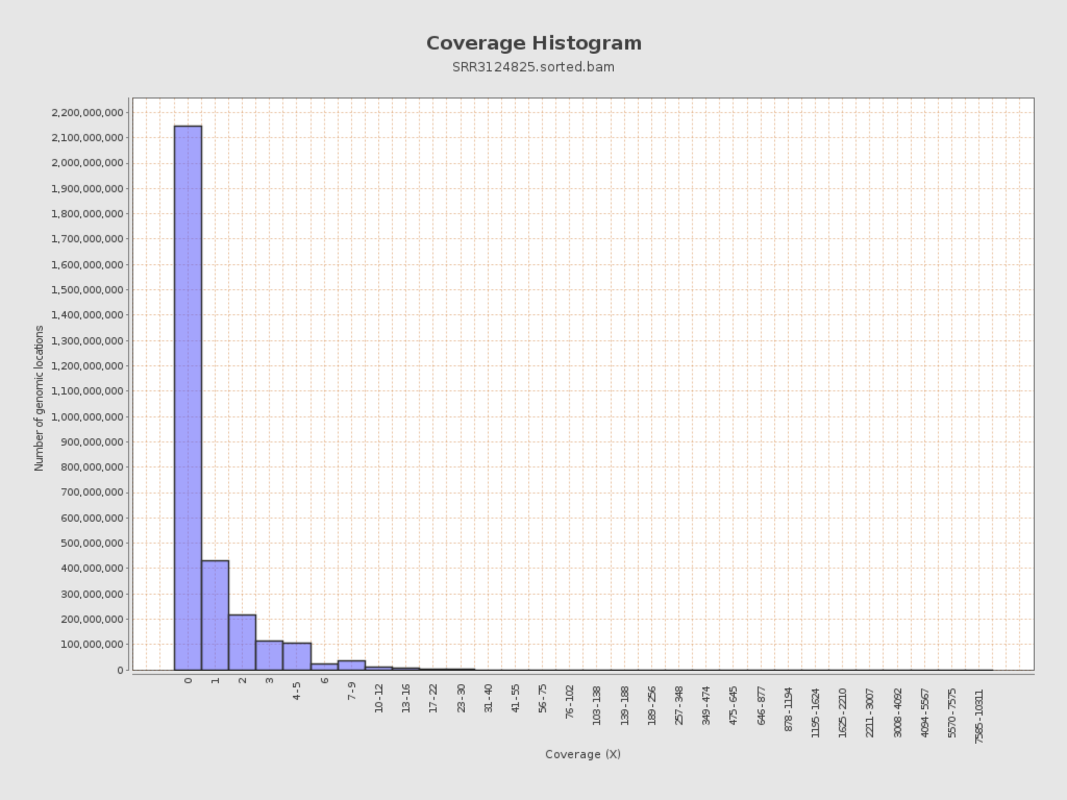
		bases	coverage	deviation
chr1	249250621	232155753	0.9314	7.547
chr2	243199373	188452463	0.7749	8.5672
chr3	198022430	199460832	1.0073	2.1221
chr4	191154276	166783169	0.8725	4.9743
chr5	180915260	145710584	0.8054	1.88
chr6	171115067	132983017	0.7772	10.3003
chr7	159138663	123483598	0.7759	12.0367
chr8	146364022	167235305	1.1426	3.4635
chr9	141213431	125186360	0.8865	10.394
chr10	135534747	116035778	0.8561	16.9062
chr11	135006516	104824379	0.7764	6.893
chr12	133851895	90602496	0.6769	1.6584
chr13	115169878	52838833	0.4588	1.223
chr14	107349540	94926655	0.8843	2.7293
chr15	102531392	62672905	0.6113	1.6374
chr16	90354753	80021384	0.8856	9.6793
chr17	81195210	77431365	0.9536	7.5768
chr18	78077248	71585631	0.9169	10.5893
chr19	59128983	27662310	0.4678	4.204
chr20	63025520	65681914	1.0421	2.5838
chr21	48129895	31476291	0.654	4.1486
chr22	51304566	19041361	0.3711	1.3633
chrMT	16571	551979	33.3099	21.0878
chrX	155270560	98611164	0.6351	3.0804

chrY	59373566	8559479	0.1442	8.4436

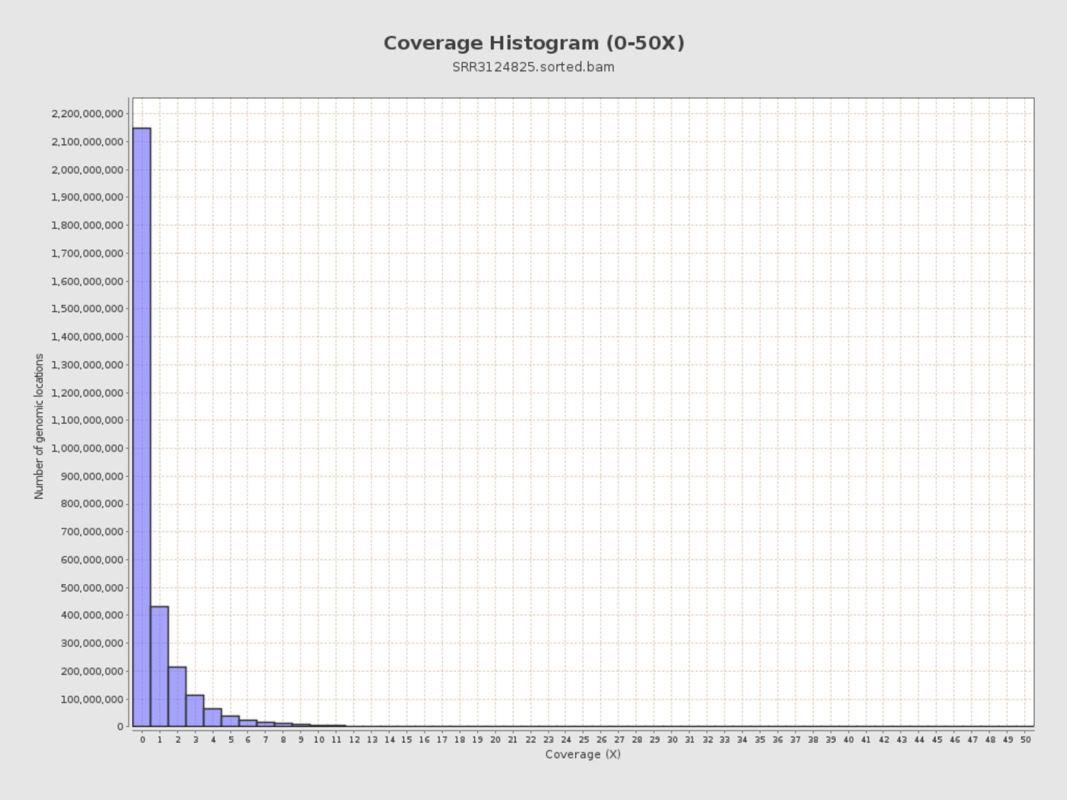
3. Results : Coverage across reference



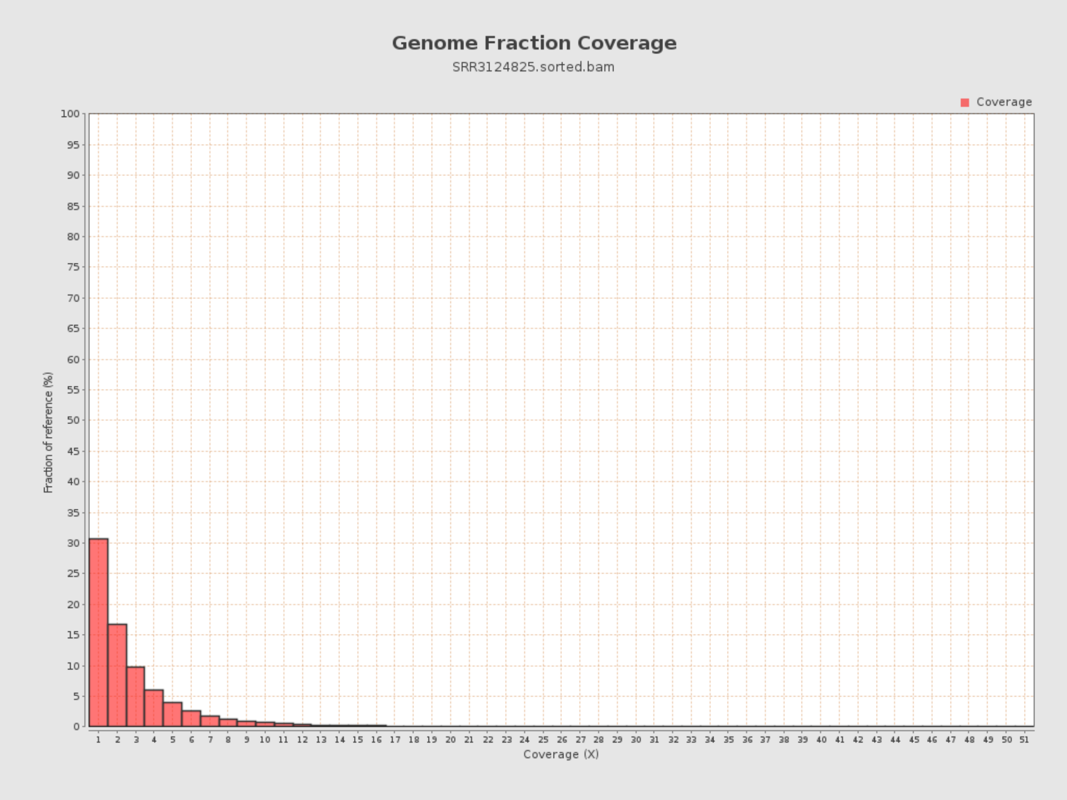
4. Results : Coverage Histogram



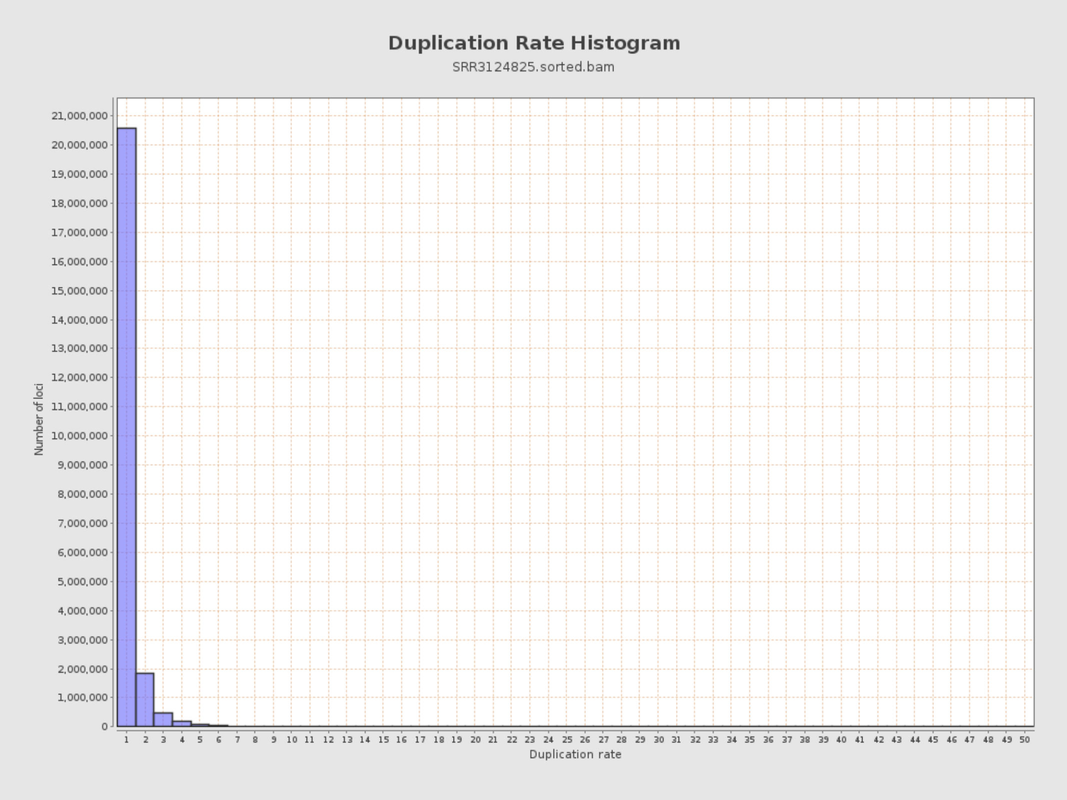
5. Results : Coverage Histogram (0-50X)



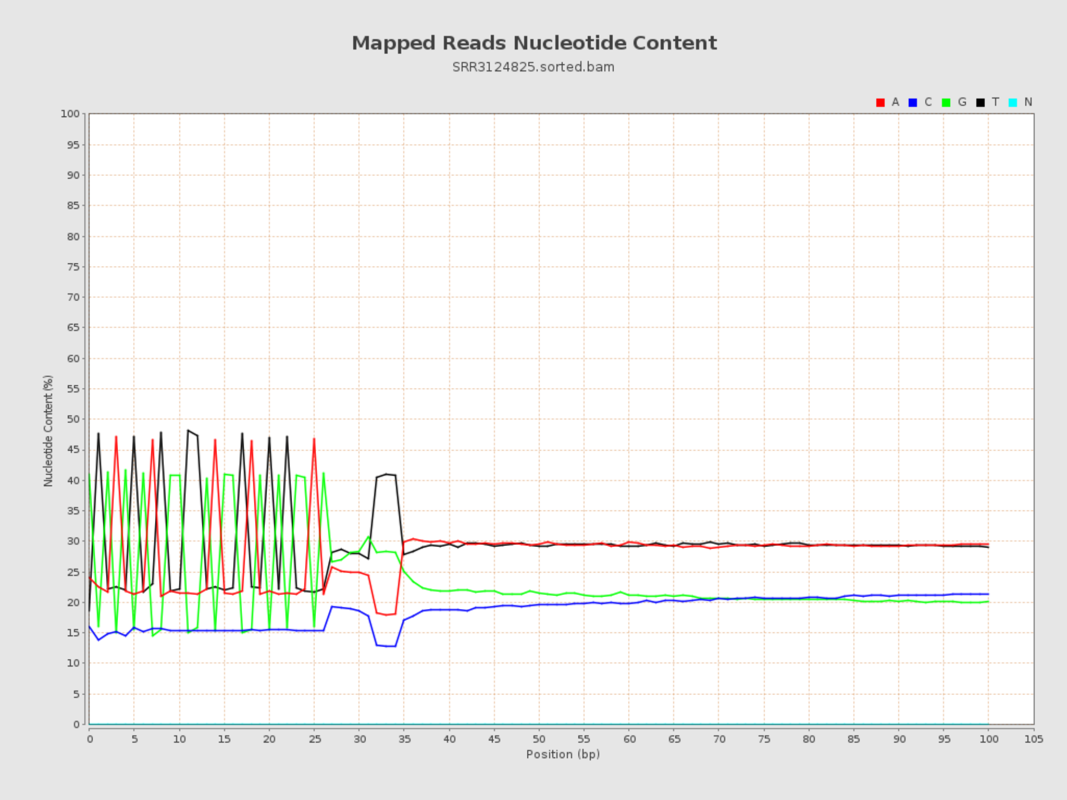
6. Results : Genome Fraction Coverage



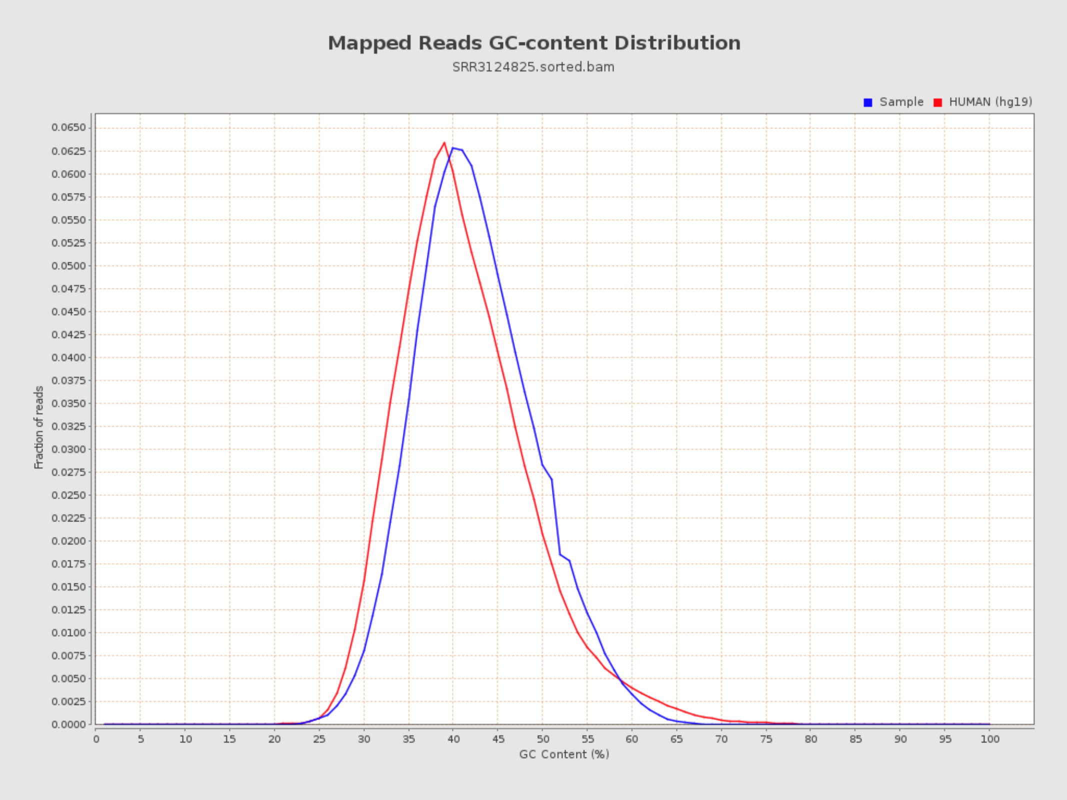
7. Results : Duplication Rate Histogram



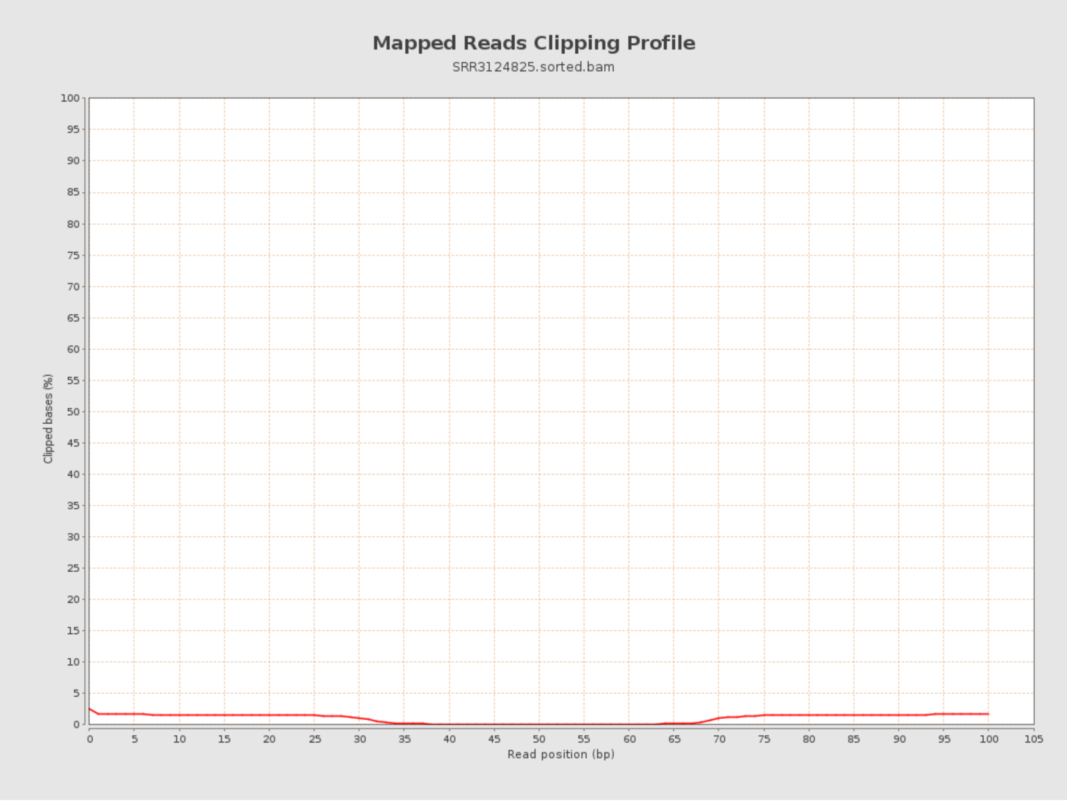
8. Results : Mapped Reads Nucleotide Content



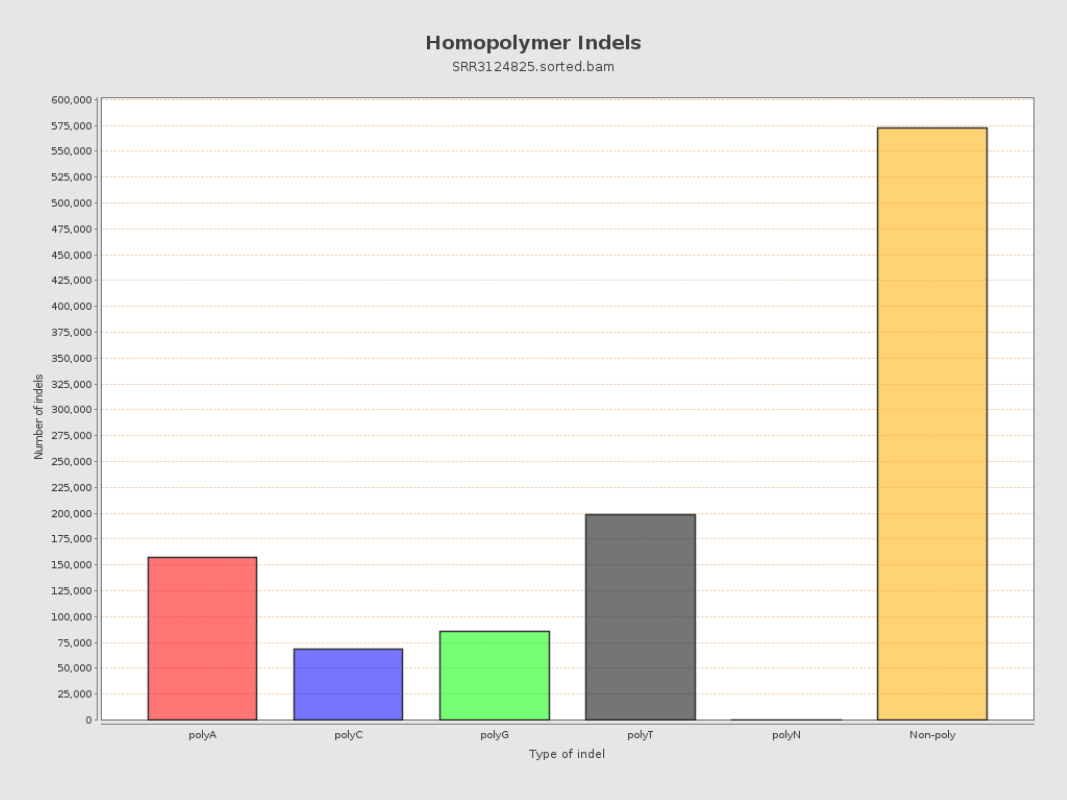
9. Results : Mapped Reads GC-content Distribution



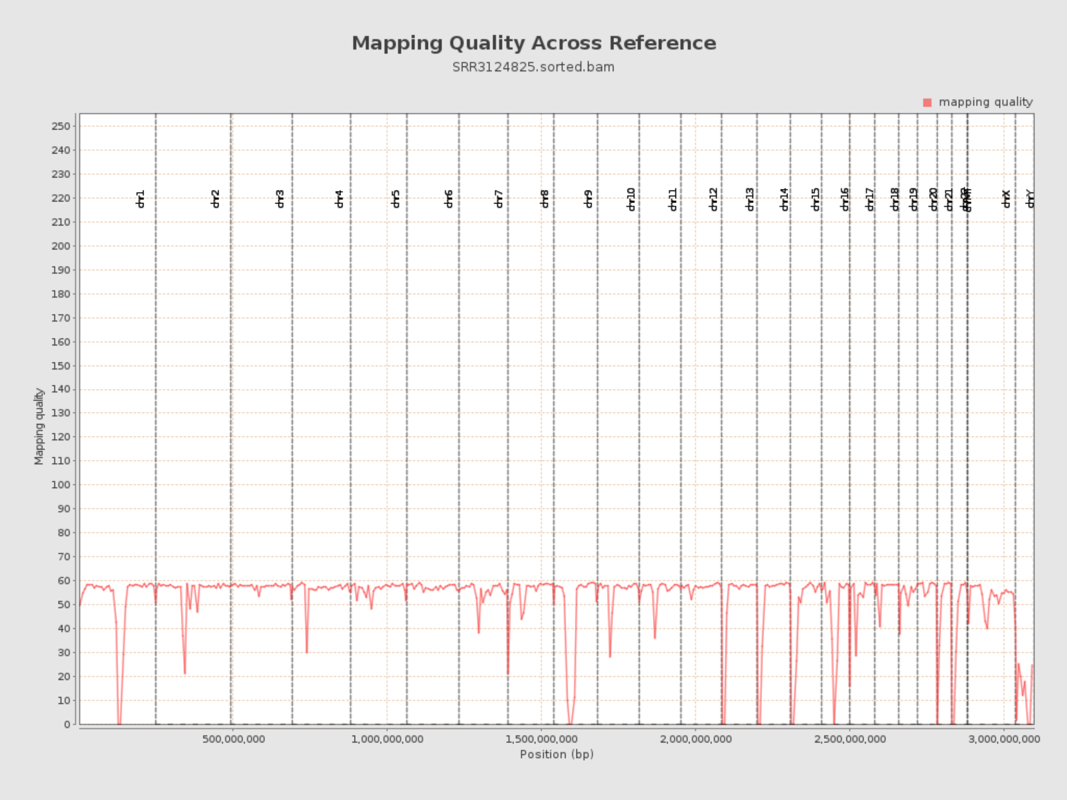
10. Results : Mapped Reads Clipping Profile



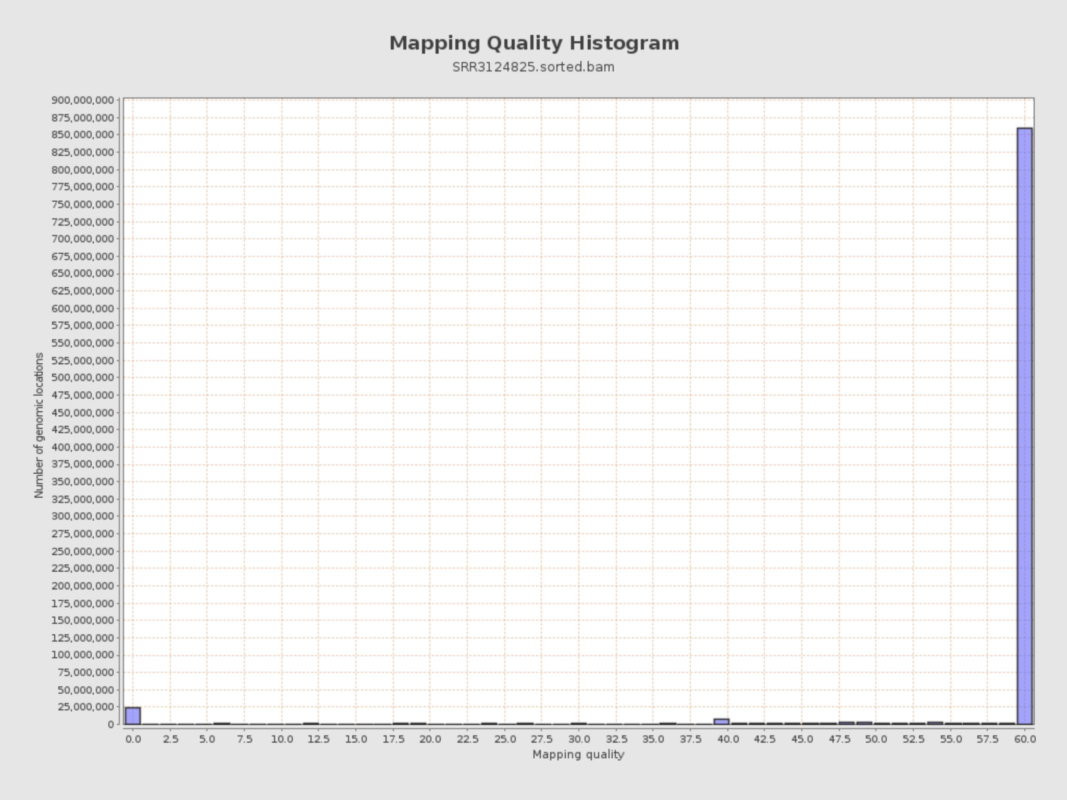
11. Results : Homopolymer Indels



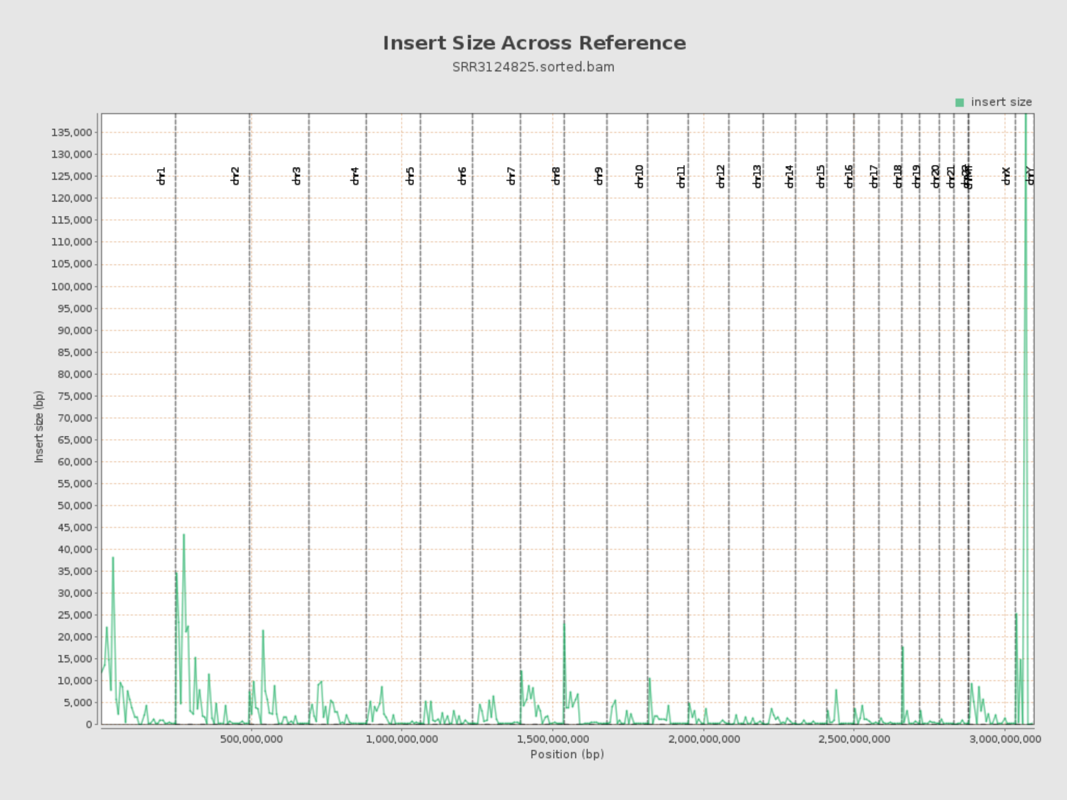
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram