Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:10:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124925.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_SRR3124925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124925_1.fastq.gz SRR3124925_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:10:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,685,944
Mapped reads	4,613,763 / 98.46%
Unmapped reads	72,181 / 1.54%
Mapped paired reads	4,613,763 / 98.46%
Mapped reads, first in pair	2,310,362 / 49.3%
Mapped reads, second in pair	2,303,401 / 49.16%
Mapped reads, both in pair	4,596,254 / 98.09%
Mapped reads, singletons	17,509 / 0.37%
Secondary alignments	0
Supplementary alignments	25,065 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	385,279 / 8.22%
Duplication rate	6.02%
Clipped reads	2,002,757 / 42.74%

2.2. ACGT Content

Number/percentage of A's	115,904,694 / 28.53%
Number/percentage of C's	75,238,333 / 18.52%
Number/percentage of T's	122,068,101 / 30.05%
Number/percentage of G's	93,060,525 / 22.91%
Number/percentage of N's	5,744 / 0%

GC Percentage	41.42%

2.3. Coverage

Mean	0.1313
Standard Deviation	1.167

2.4. Mapping Quality

Mean Mapping Quality	52.87

2.5. Insert size

Mean	52,184.37
Standard Deviation	2,171,286.09
P25/Median/P75	158 / 220 / 309

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	2,851,858
Insertions	55,441
Mapped reads with at least one insertion	1.17%
Deletions	132,175
Mapped reads with at least one deletion	2.81%
Homopolymer indels	48.93%

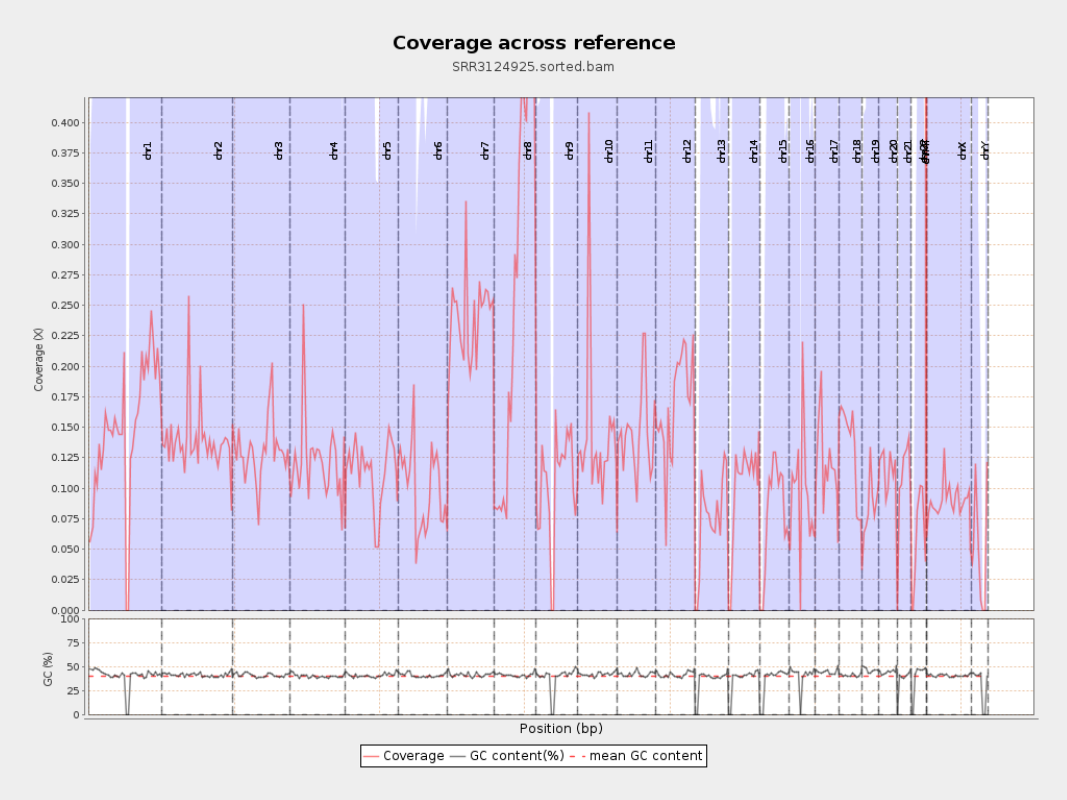
2.7. Chromosome stats

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

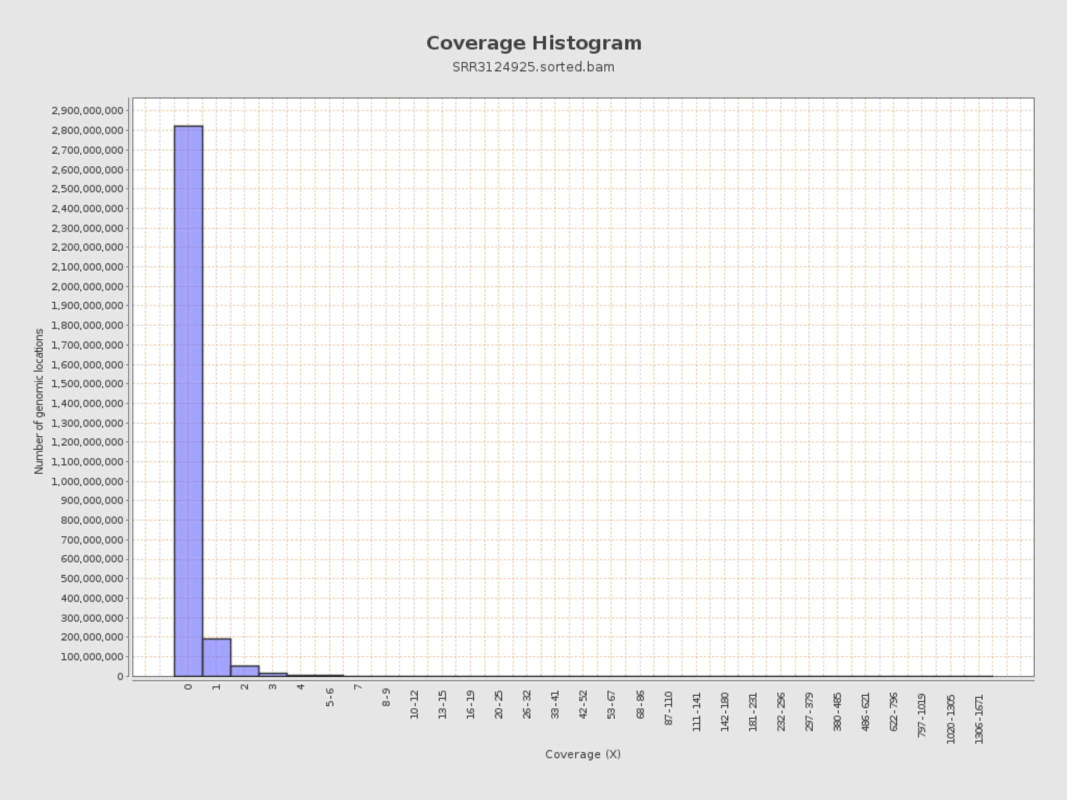
		bases	coverage	deviation
chr1	249250621	37004184	0.1485	1.413
chr2	243199373	33872623	0.1393	1.1839
chr3	198022430	26009948	0.1313	0.4855
chr4	191154276	23289133	0.1218	0.87
chr5	180915260	20589306	0.1138	0.4572
chr6	171115067	17222379	0.1006	0.9
chr7	159138663	38283203	0.2406	2.7514
chr8	146364022	40357406	0.2757	0.8258
chr9	141213431	14521378	0.1028	1.3989
chr10	135534747	19336215	0.1427	2.0943
chr11	135006516	19674111	0.1457	0.8869
chr12	133851895	22528779	0.1683	0.5567
chr13	115169878	8663668	0.0752	0.3578
chr14	107349540	10628469	0.099	0.4784
chr15	102531392	8155084	0.0795	0.3766
chr16	90354753	8540929	0.0945	1.1097
chr17	81195210	9646089	0.1188	1.2202
chr18	78077248	10513186	0.1347	1.5635
chr19	59128983	5050271	0.0854	0.775
chr20	63025520	7170731	0.1138	0.4813
chr21	48129895	5083141	0.1056	0.5354
chr22	51304566	3016483	0.0588	0.3296
chrMT	16571	581517	35.0925	20.9777
chrX	155270560	13865289	0.0893	0.5196

chrY	59373566	2895737	0.0488	1.032

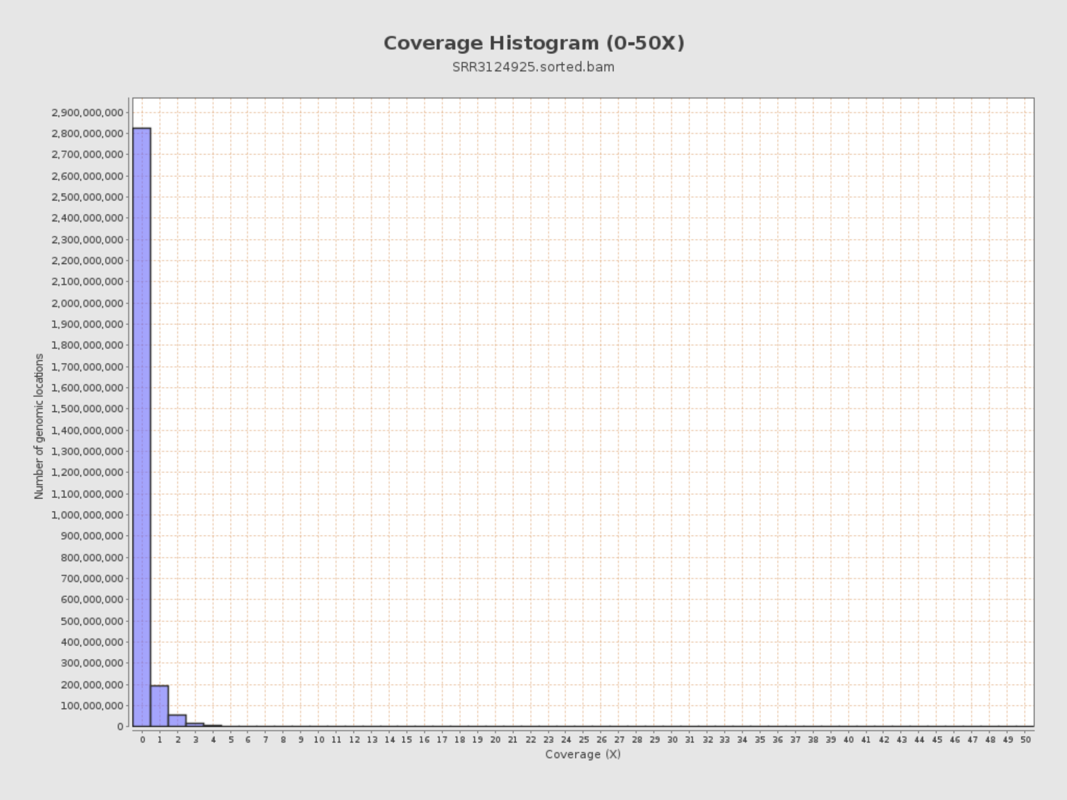
3. Results : Coverage across reference



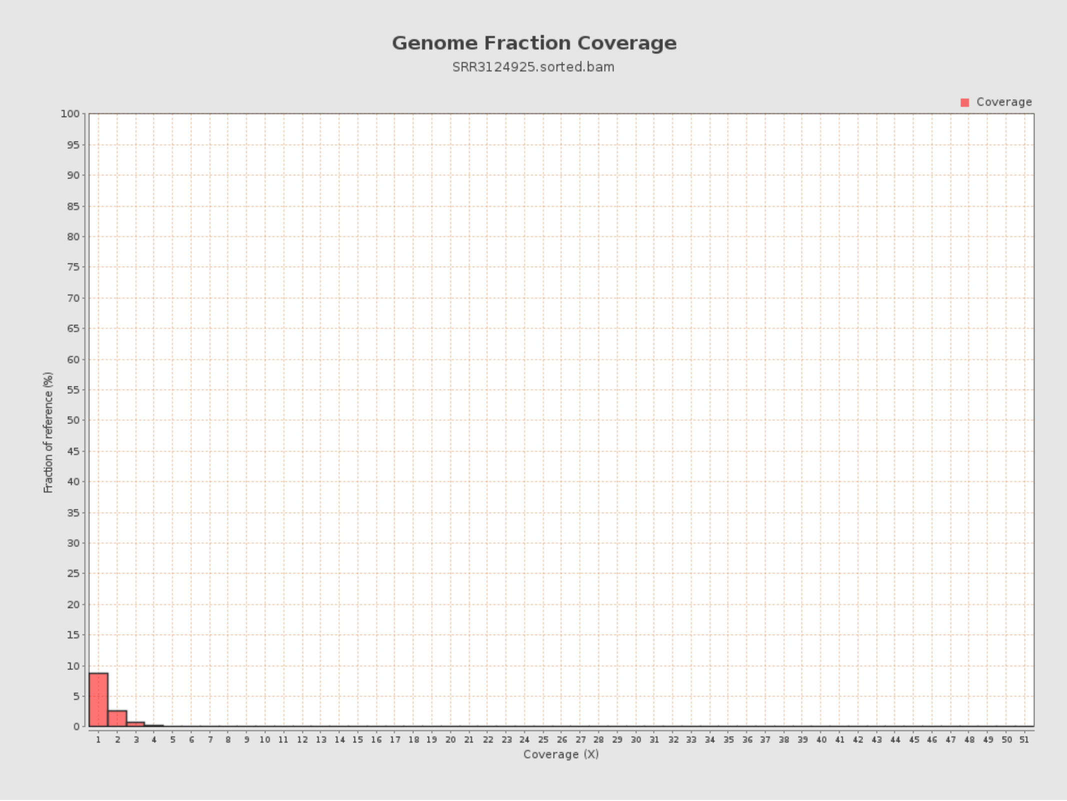
4. Results : Coverage Histogram



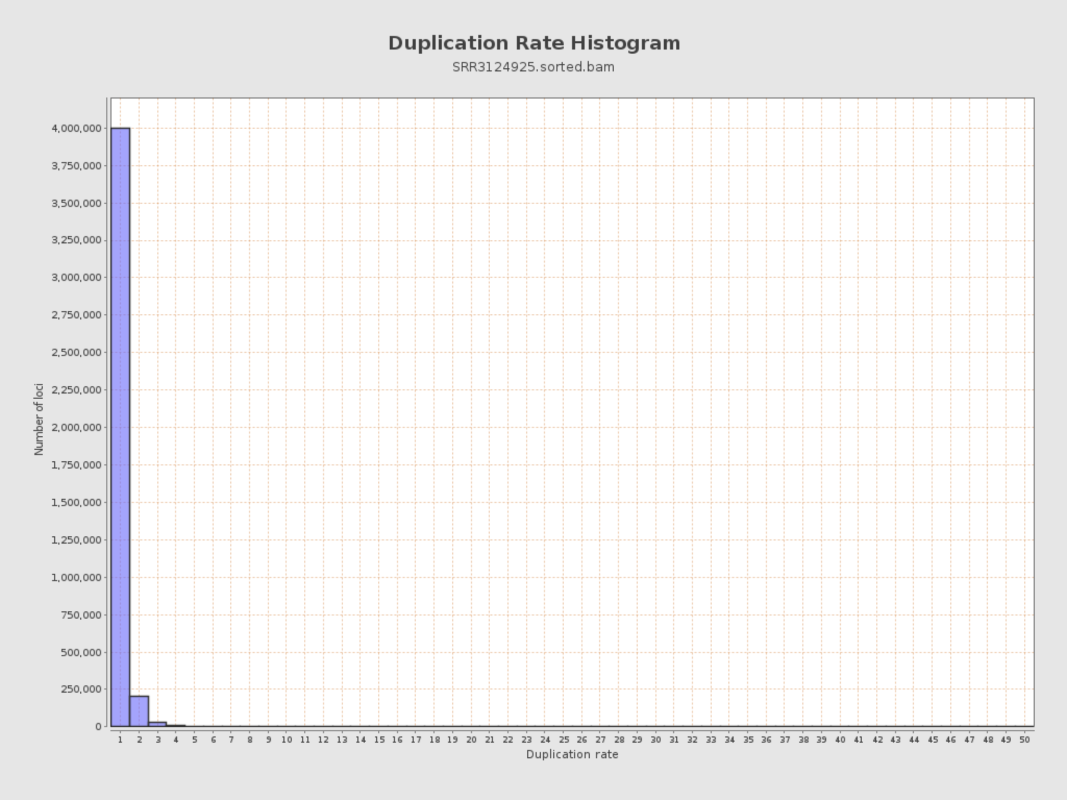
5. Results : Coverage Histogram (0-50X)



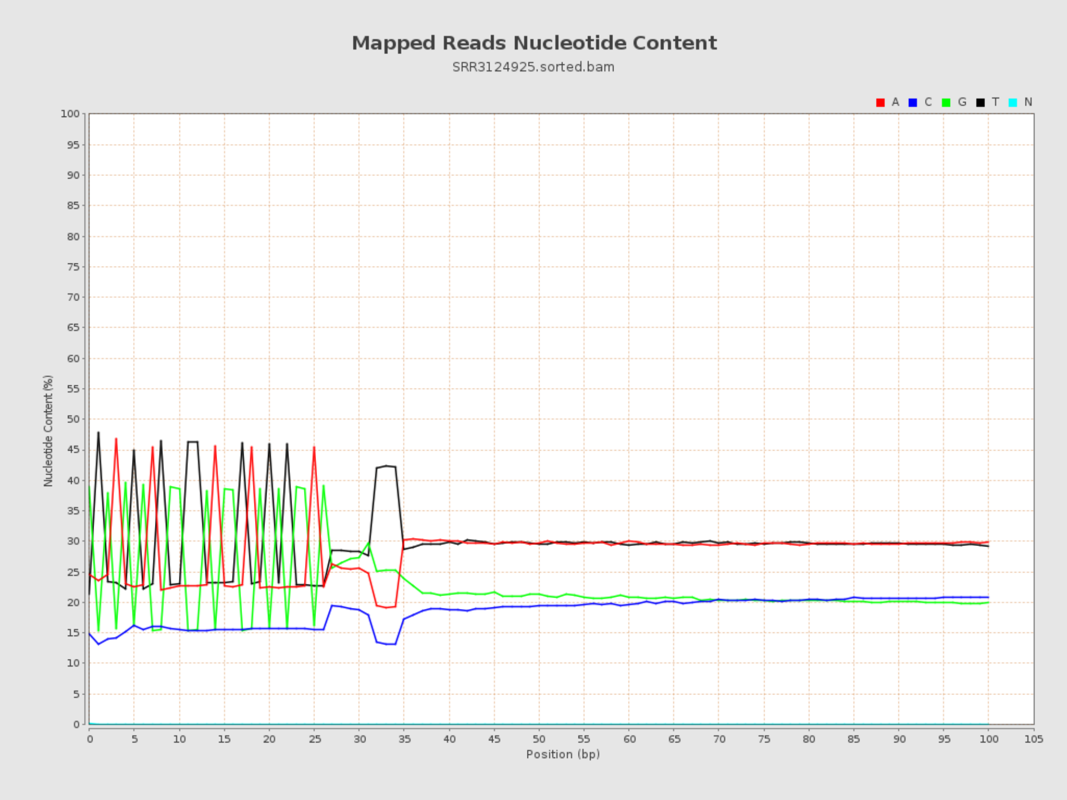
6. Results : Genome Fraction Coverage



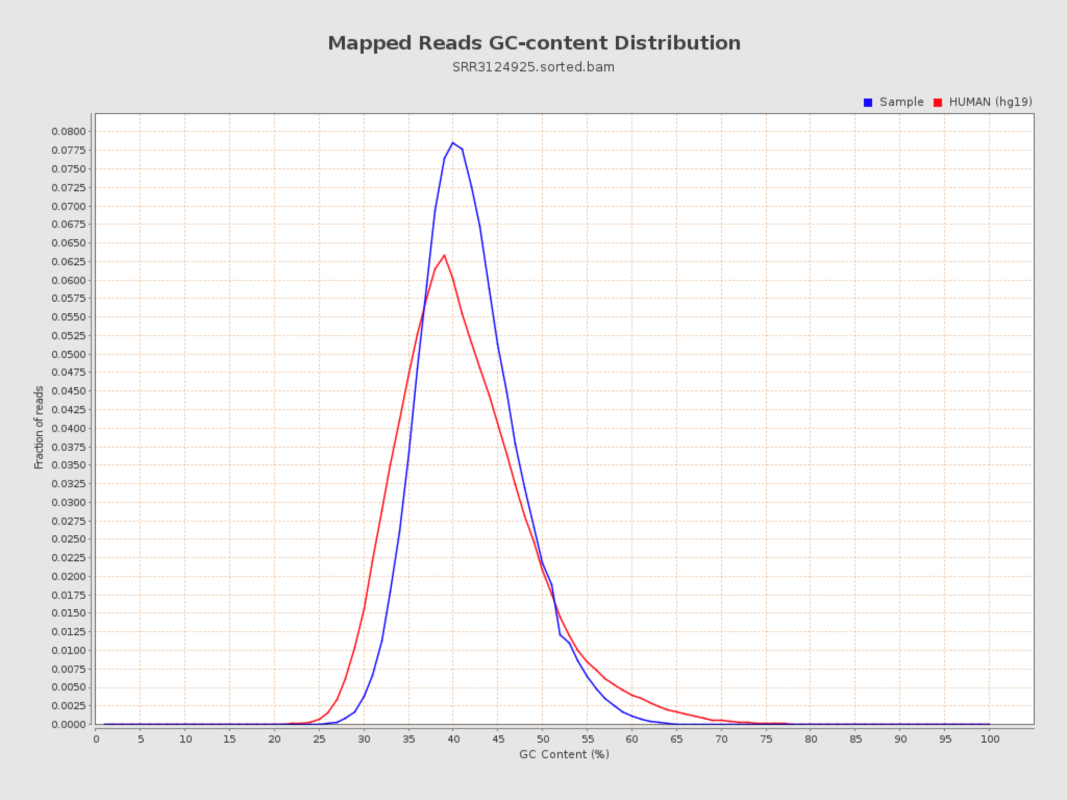
7. Results : Duplication Rate Histogram



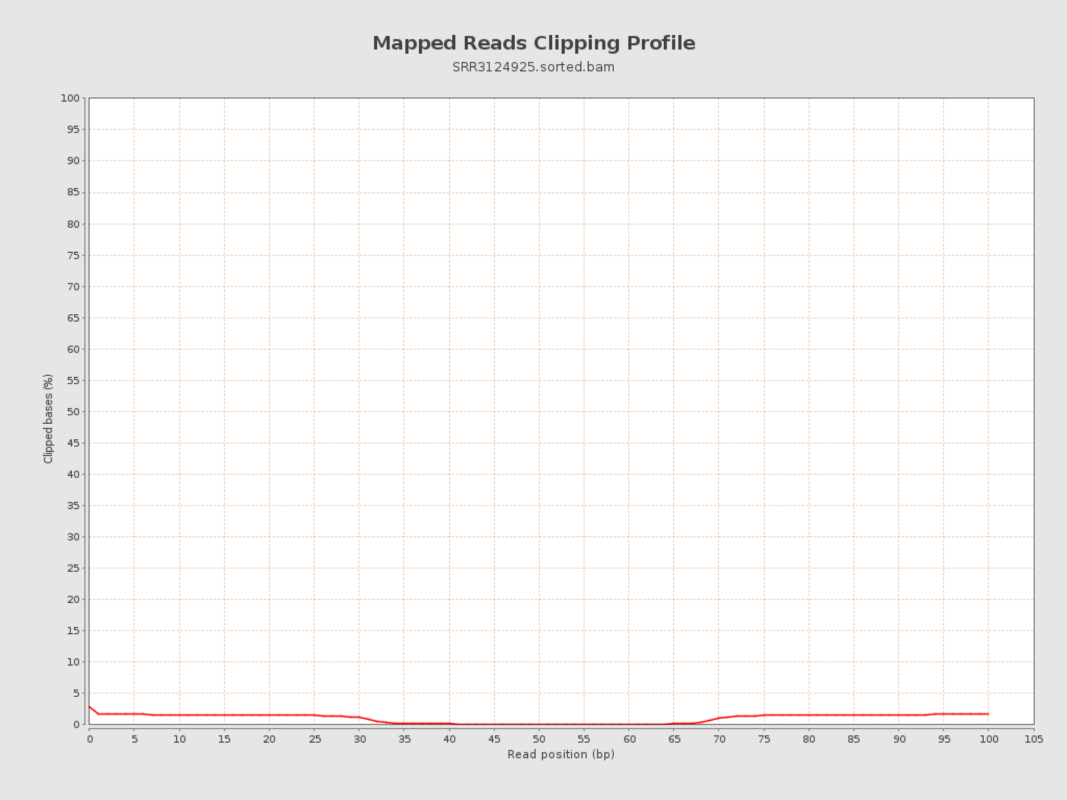
8. Results : Mapped Reads Nucleotide Content



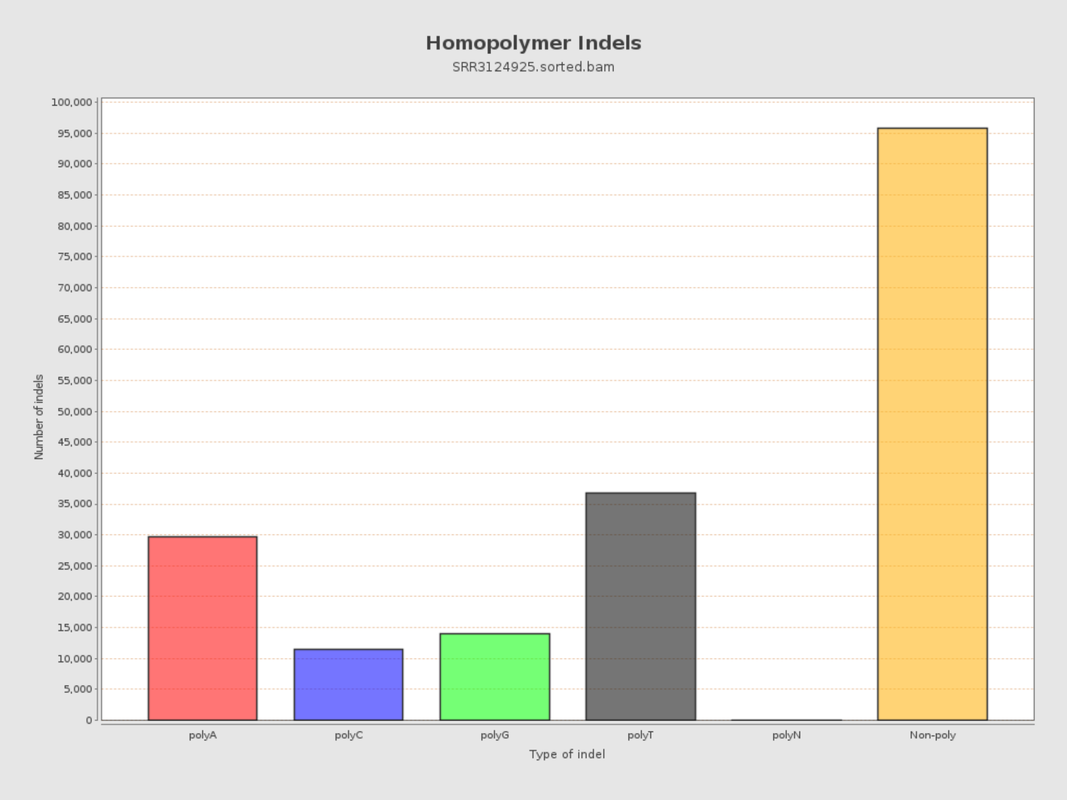
9. Results : Mapped Reads GC-content Distribution



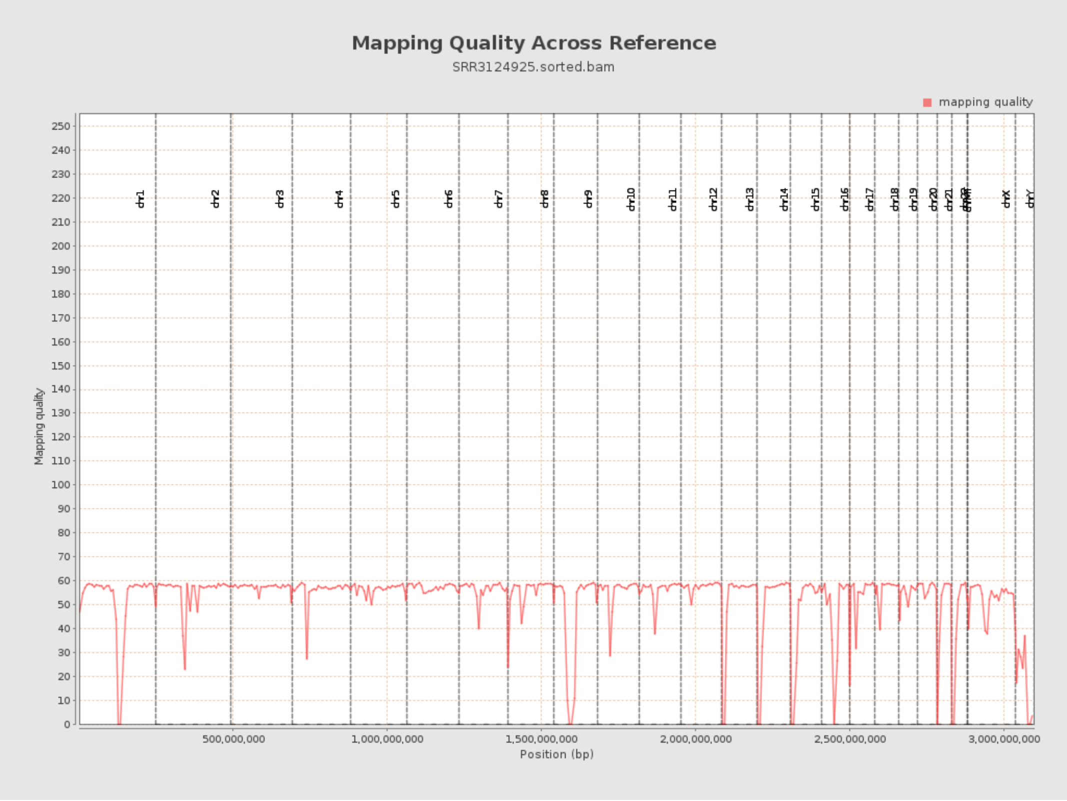
10. Results : Mapped Reads Clipping Profile



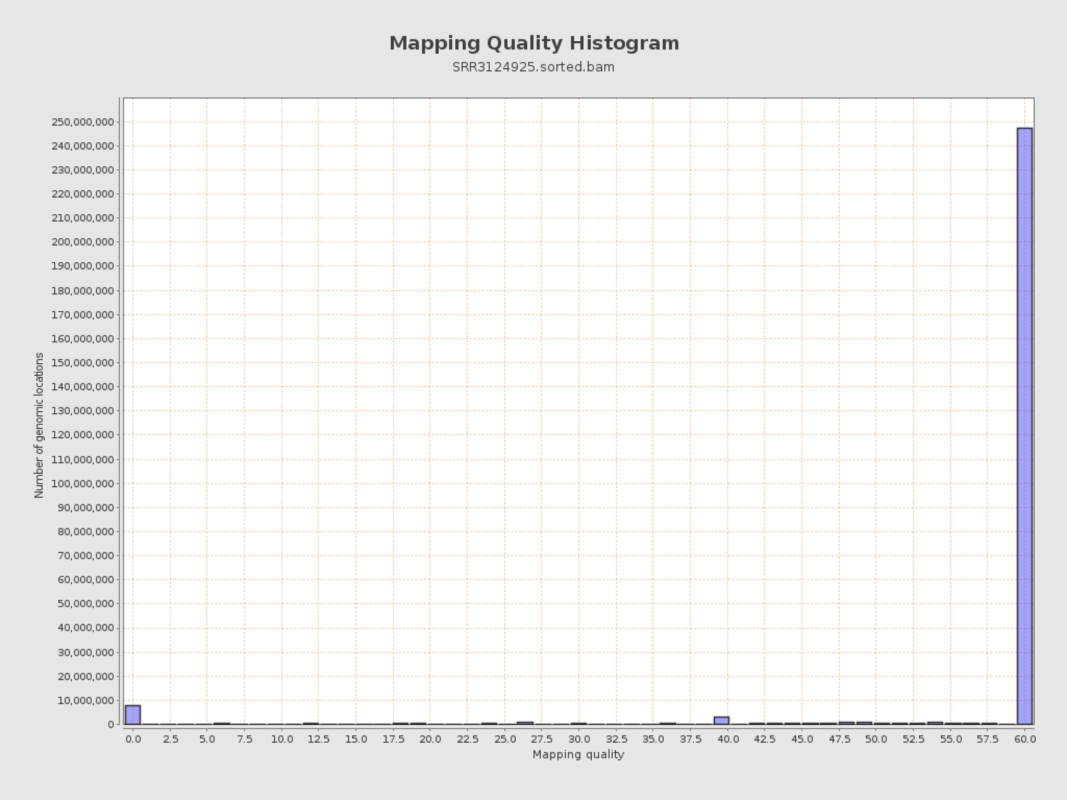
11. Results : Homopolymer Indels



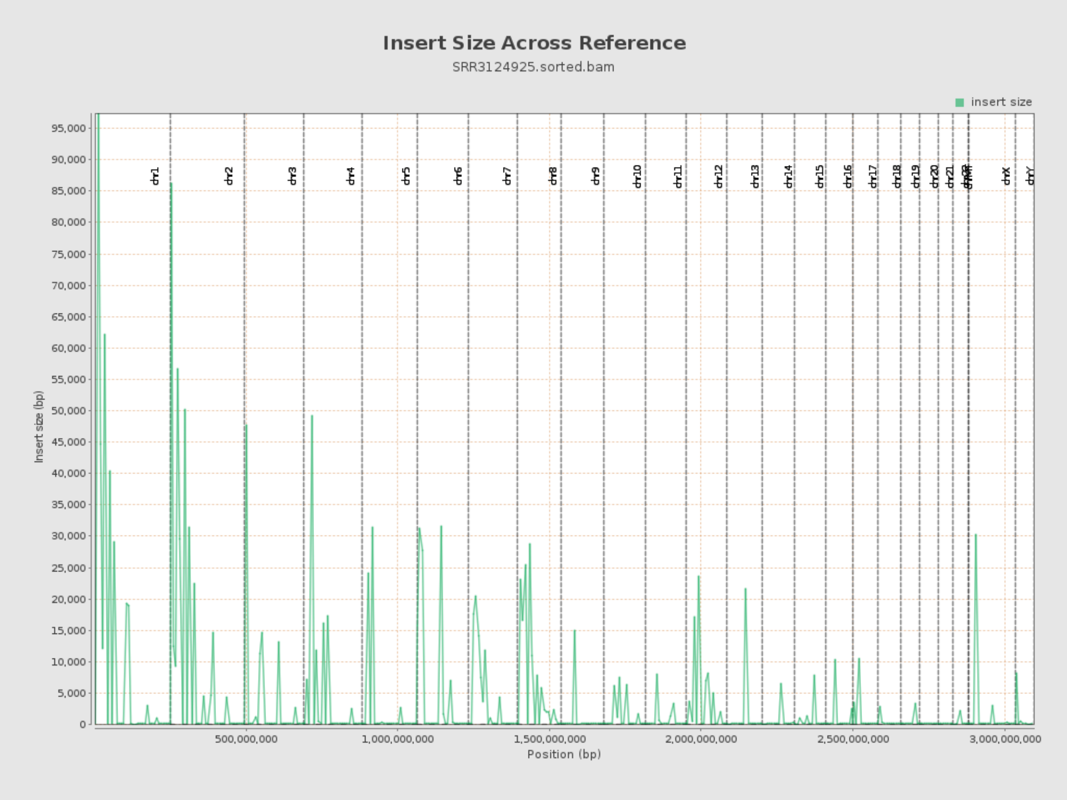
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram