Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 04:37:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124914.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_SRR3124914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124914_1.fastq.gz SRR3124914_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 04:37:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,587,714
Mapped reads	4,491,725 / 97.91%
Unmapped reads	95,989 / 2.09%
Mapped paired reads	4,491,725 / 97.91%
Mapped reads, first in pair	2,250,752 / 49.06%
Mapped reads, second in pair	2,240,973 / 48.85%
Mapped reads, both in pair	4,469,684 / 97.43%
Mapped reads, singletons	22,041 / 0.48%
Secondary alignments	0
Supplementary alignments	22,439 / 0.49%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	336,106 / 7.33%
Duplication rate	4.52%
Clipped reads	2,205,340 / 48.07%

2.2. ACGT Content

Number/percentage of A's	111,039,966 / 28.16%
Number/percentage of C's	74,819,048 / 18.97%
Number/percentage of T's	116,997,754 / 29.67%
Number/percentage of G's	91,497,546 / 23.2%
Number/percentage of N's	11,741 / 0%

GC Percentage	42.17%

2.3. Coverage

Mean	0.1275
Standard Deviation	1.3794

2.4. Mapping Quality

Mean Mapping Quality	52.79

2.5. Insert size

Mean	42,398.68
Standard Deviation	1,871,436.91
P25/Median/P75	146 / 193 / 265

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	2,872,650
Insertions	58,112
Mapped reads with at least one insertion	1.25%
Deletions	120,415
Mapped reads with at least one deletion	2.62%
Homopolymer indels	45.89%

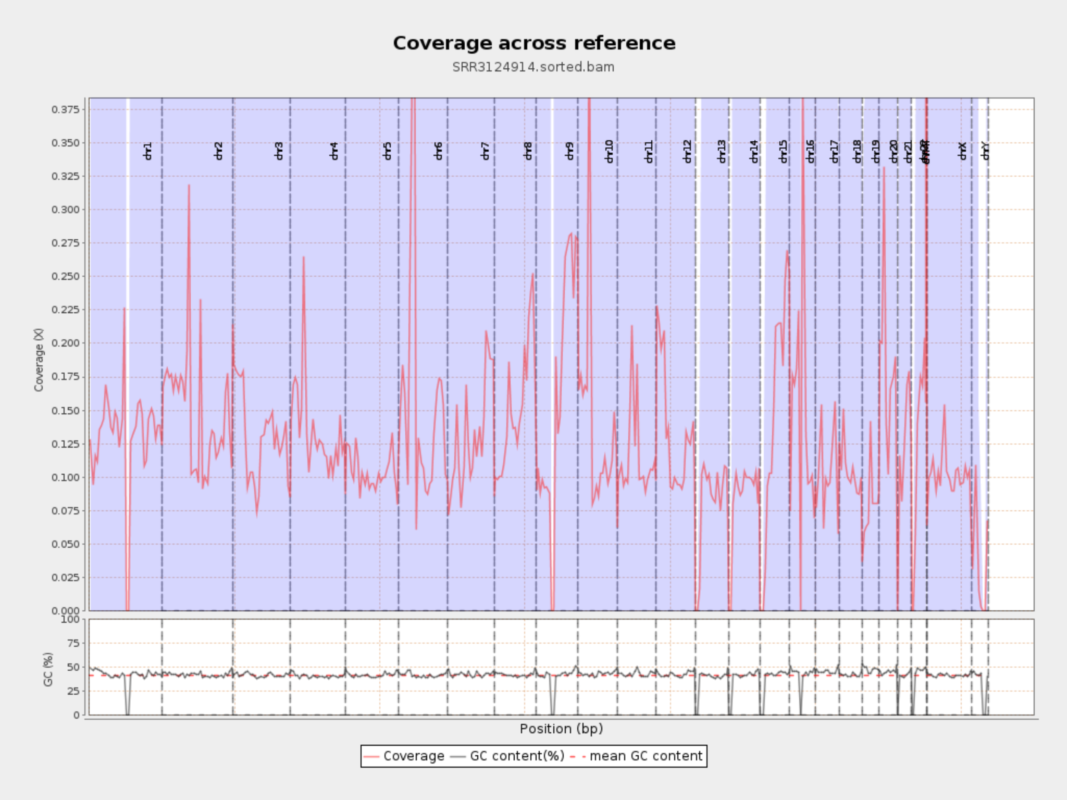
2.7. Chromosome stats

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

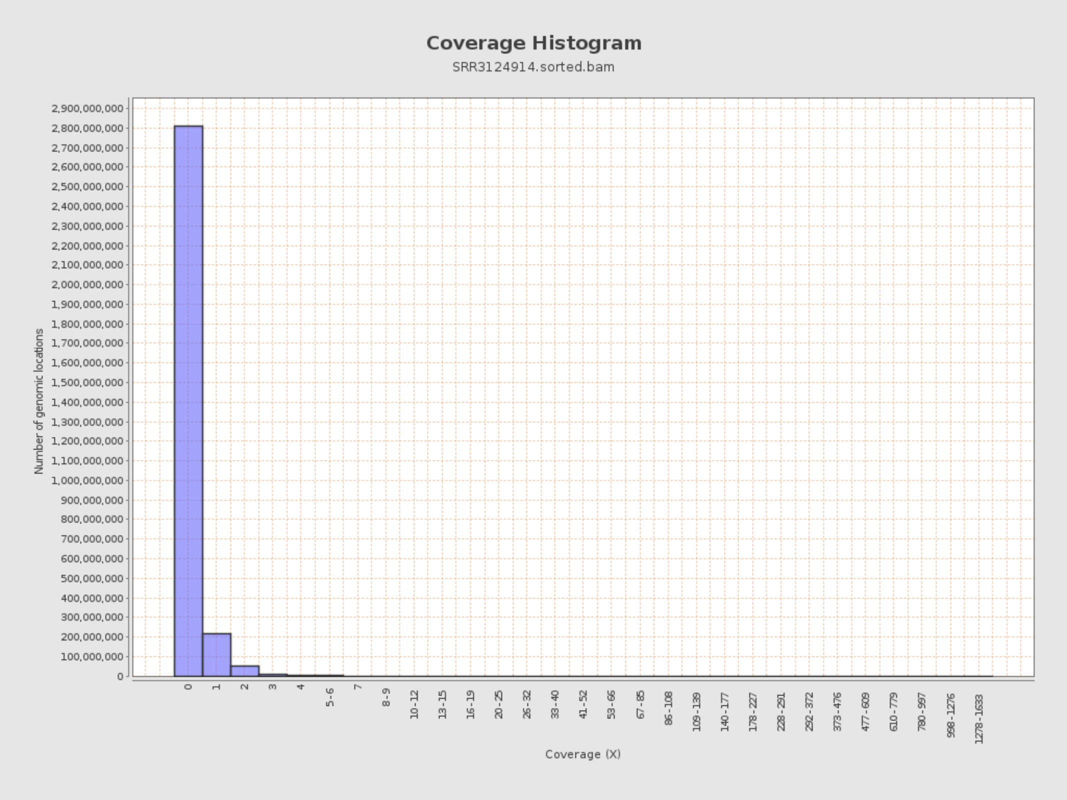
		bases	**coverage**	**deviation**
chr1	249250621	32458379	0.1302	1.4778
chr2	243199373	36449064	0.1499	1.6397
chr3	198022430	26120208	0.1319	0.4646
chr4	191154276	25796432	0.135	0.9611
chr5	180915260	18751994	0.1037	0.462
chr6	171115067	27871294	0.1629	2.8637
chr7	159138663	20942268	0.1316	1.1679
chr8	146364022	22482393	0.1536	0.6408
chr9	141213431	22376079	0.1585	1.6891
chr10	135534747	19092717	0.1409	2.6792
chr11	135006516	15493688	0.1148	1.3339
chr12	133851895	17991021	0.1344	0.5209
chr13	115169878	9163720	0.0796	0.3434
chr14	107349540	8863550	0.0826	0.4398
chr15	102531392	14825943	0.1446	0.4888
chr16	90354753	13124429	0.1453	2.076
chr17	81195210	8285739	0.102	0.999
chr18	78077248	8234121	0.1055	1.6512
chr19	59128983	4686471	0.0793	1.0237
chr20	63025520	11576927	0.1837	0.6065
chr21	48129895	5748366	0.1194	0.7098
chr22	51304566	6081097	0.1185	0.461
chrMT	16571	201477	12.1584	6.5785
chrX	155270560	15875134	0.1022	0.631

chrY	59373566	2089876	0.0352	1.6984

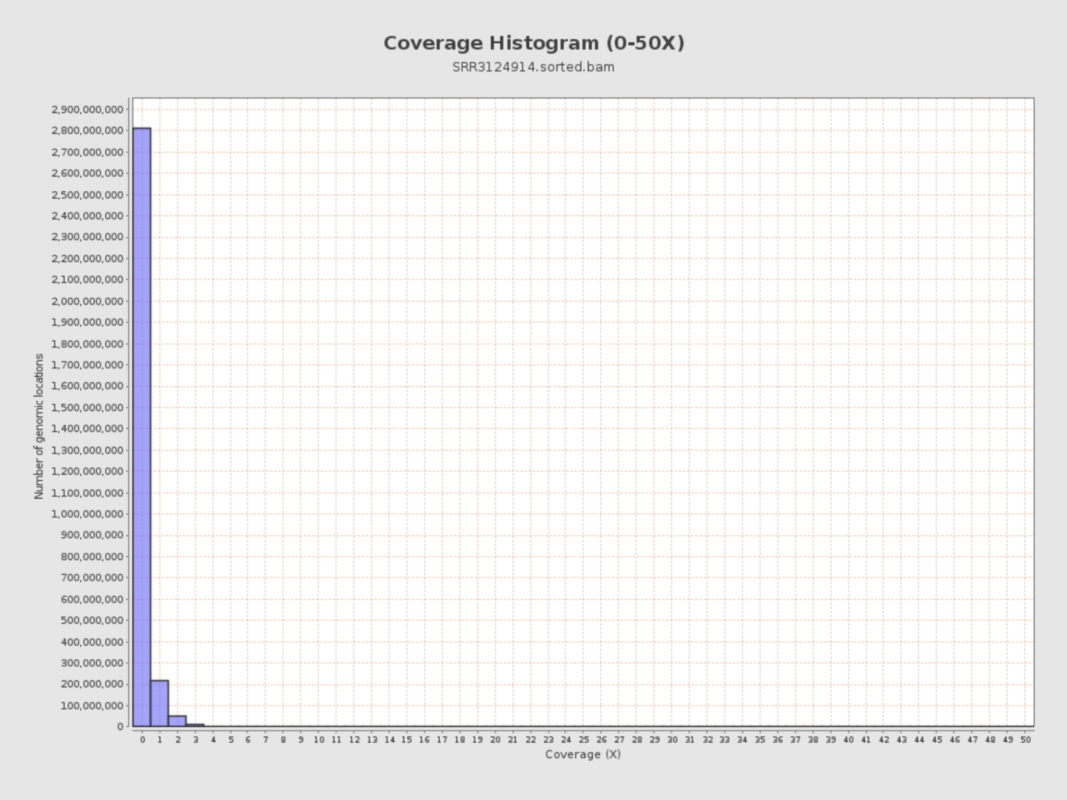
3. Results : Coverage across reference



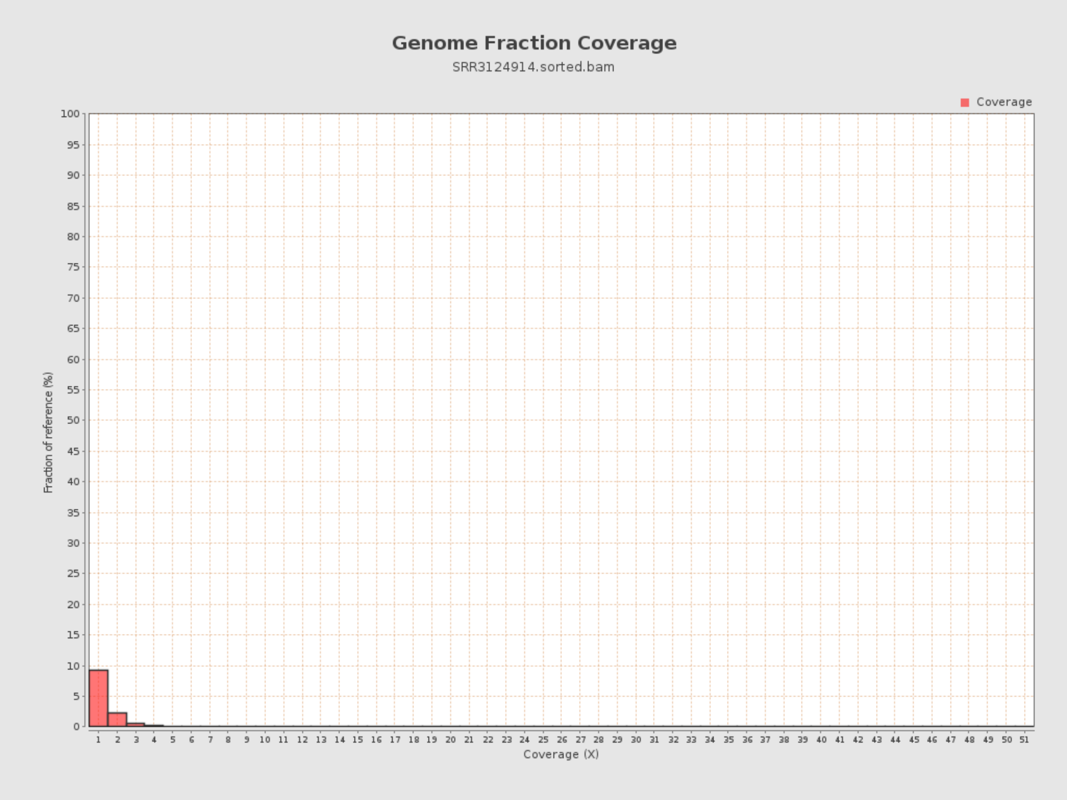
4. Results : Coverage Histogram



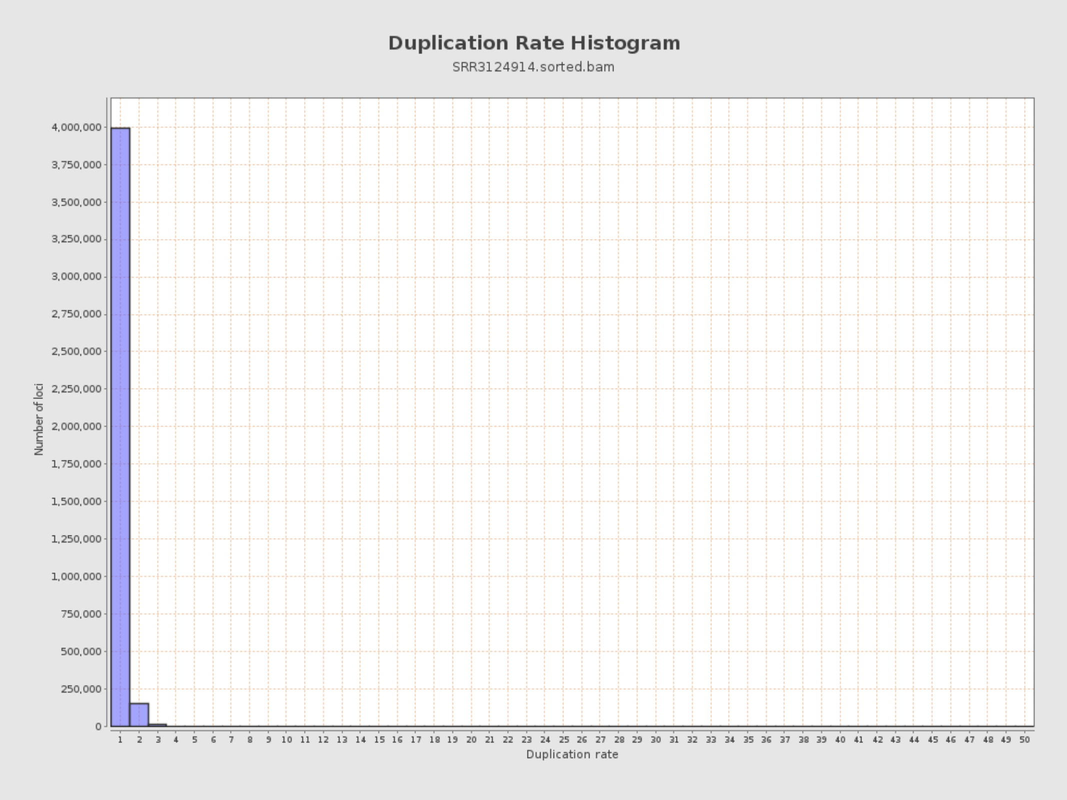
5. Results : Coverage Histogram (0-50X)



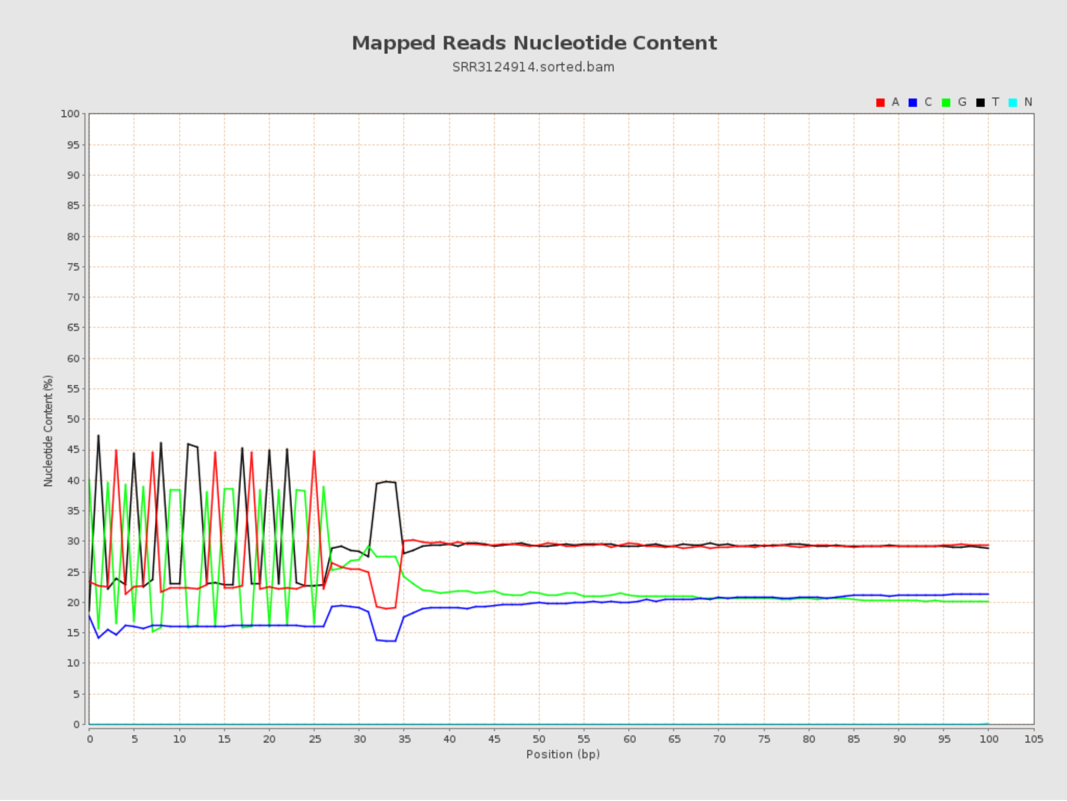
6. Results : Genome Fraction Coverage



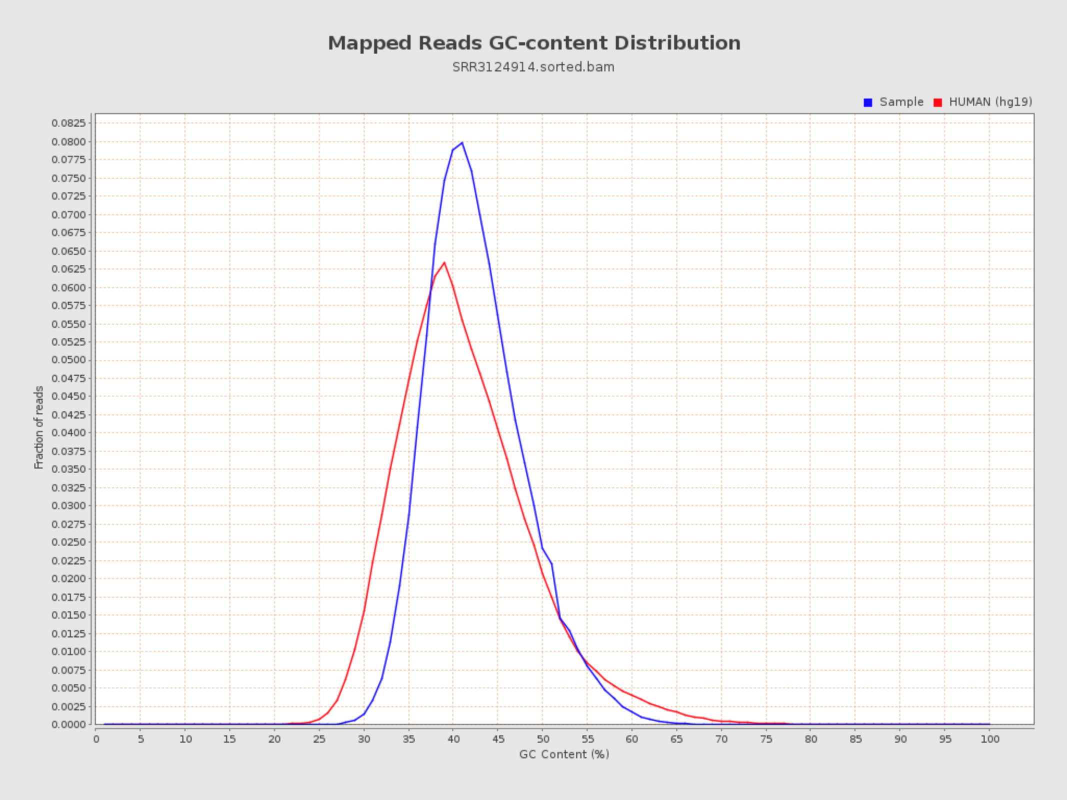
7. Results : Duplication Rate Histogram



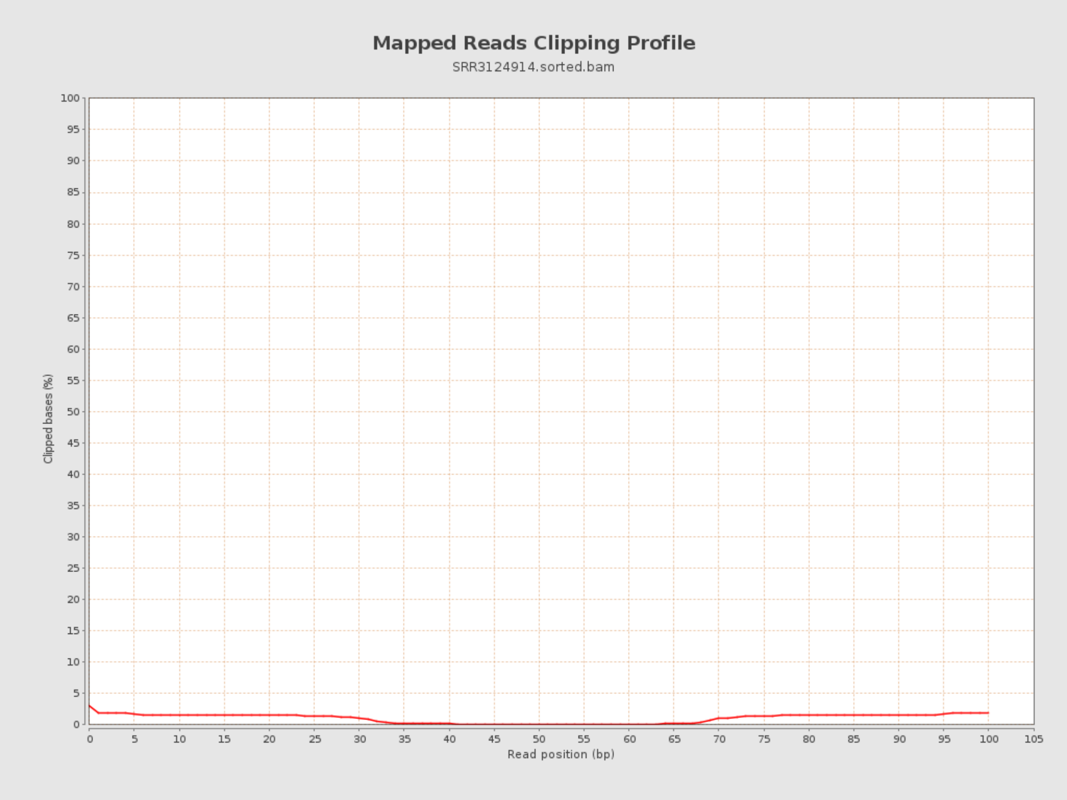
8. Results : Mapped Reads Nucleotide Content



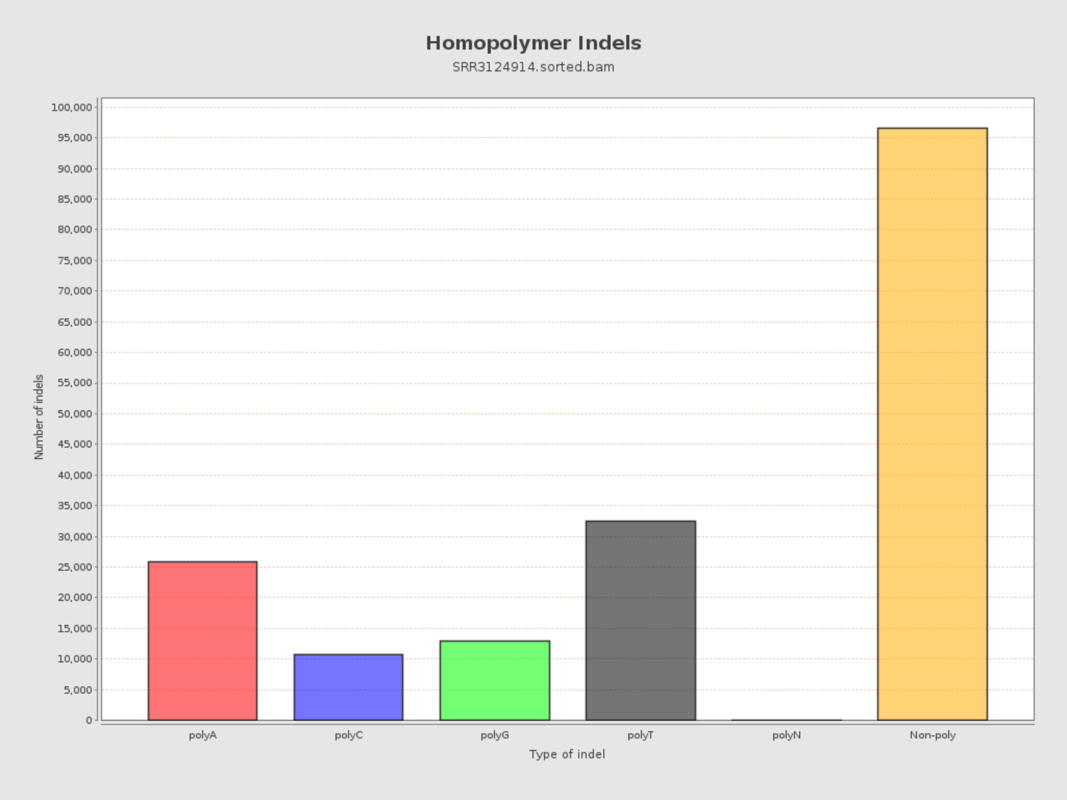
9. Results : Mapped Reads GC-content Distribution



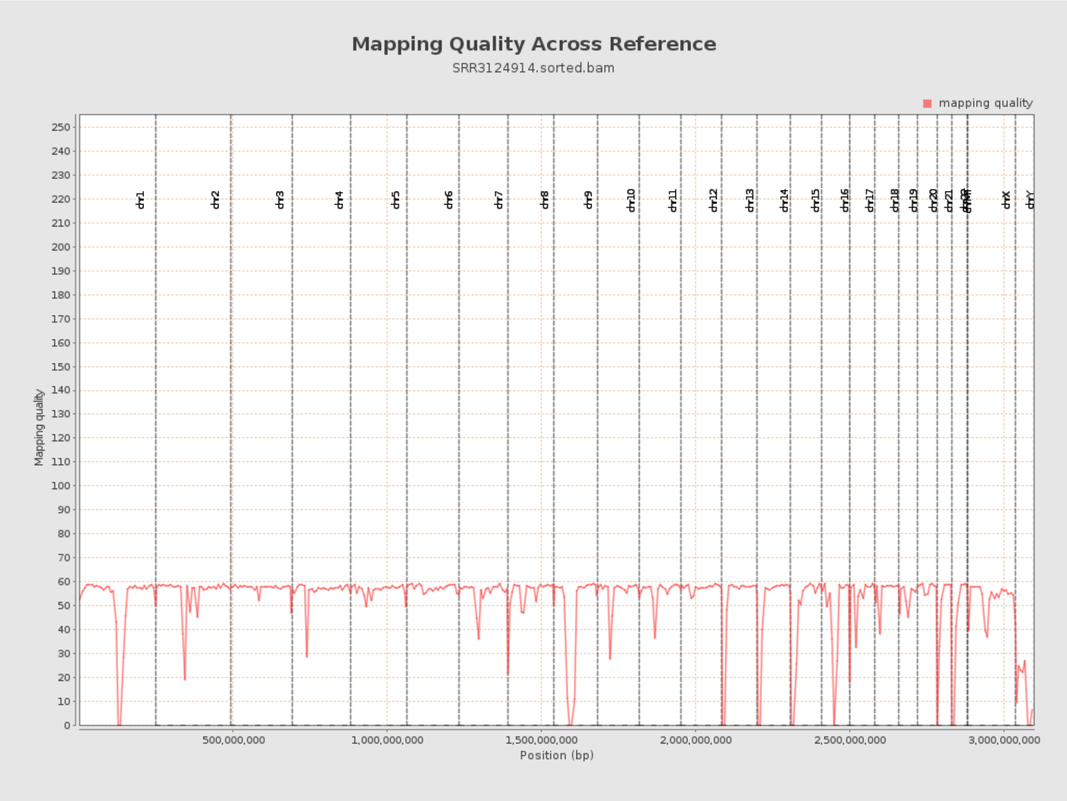
10. Results : Mapped Reads Clipping Profile



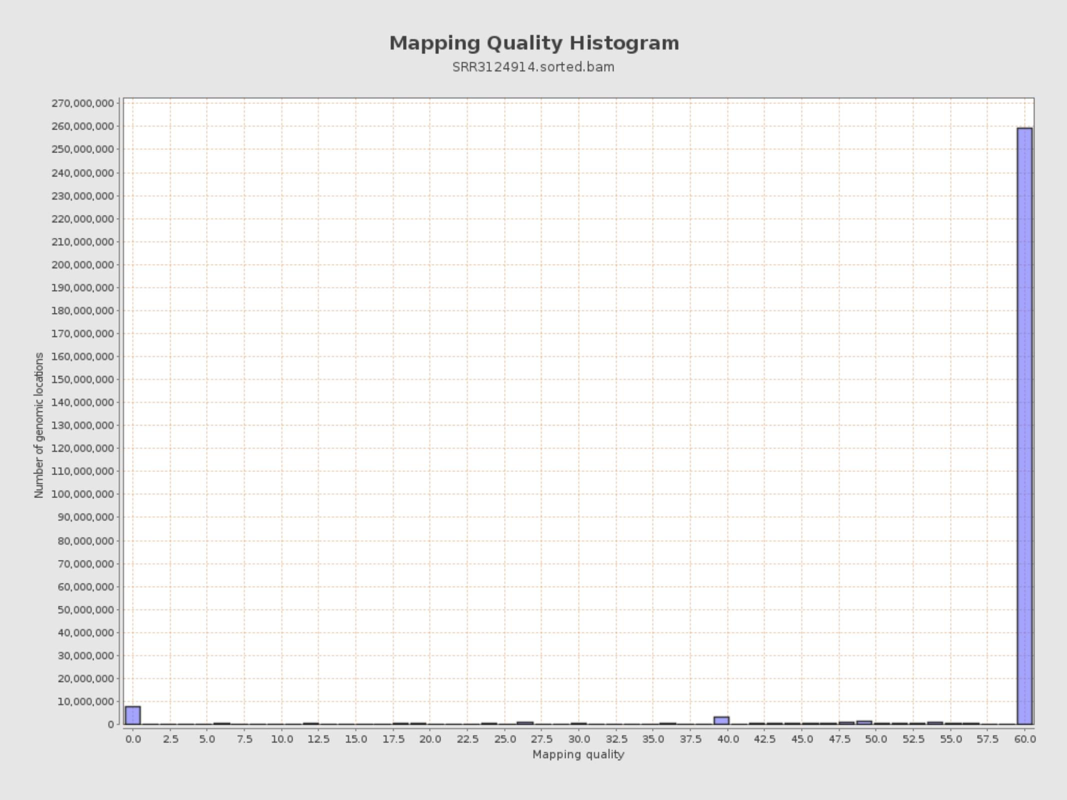
11. Results : Homopolymer Indels



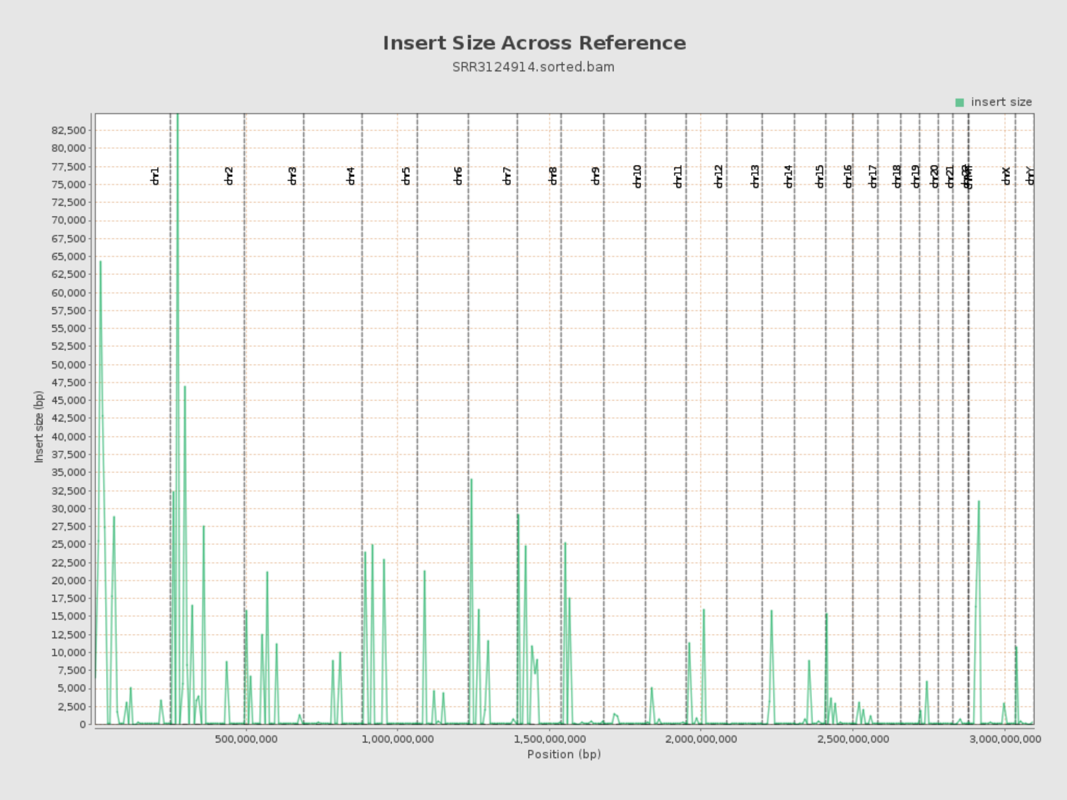
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram