Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:58:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124939.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_SRR3124939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124939_1.fastq.gz SRR3124939_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:58:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,284,810
Mapped reads	6,198,769 / 98.63%
Unmapped reads	86,041 / 1.37%
Mapped paired reads	6,198,769 / 98.63%
Mapped reads, first in pair	3,104,274 / 49.39%
Mapped reads, second in pair	3,094,495 / 49.24%
Mapped reads, both in pair	6,173,524 / 98.23%
Mapped reads, singletons	25,245 / 0.4%
Secondary alignments	0
Supplementary alignments	30,979 / 0.49%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	559,574 / 8.9%
Duplication rate	6.06%
Clipped reads	2,713,370 / 43.17%

2.2. ACGT Content

Number/percentage of A's	155,743,428 / 28.52%
Number/percentage of C's	100,987,836 / 18.49%
Number/percentage of T's	164,533,179 / 30.13%
Number/percentage of G's	124,786,723 / 22.85%
Number/percentage of N's	7,882 / 0%

GC Percentage	41.35%

2.3. Coverage

Mean	0.1765
Standard Deviation	1.7426

2.4. Mapping Quality

Mean Mapping Quality	52.7

2.5. Insert size

Mean	48,516.37
Standard Deviation	2,086,885.81
P25/Median/P75	151 / 203 / 280

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	3,995,090
Insertions	70,301
Mapped reads with at least one insertion	1.11%
Deletions	170,071
Mapped reads with at least one deletion	2.69%
Homopolymer indels	48.29%

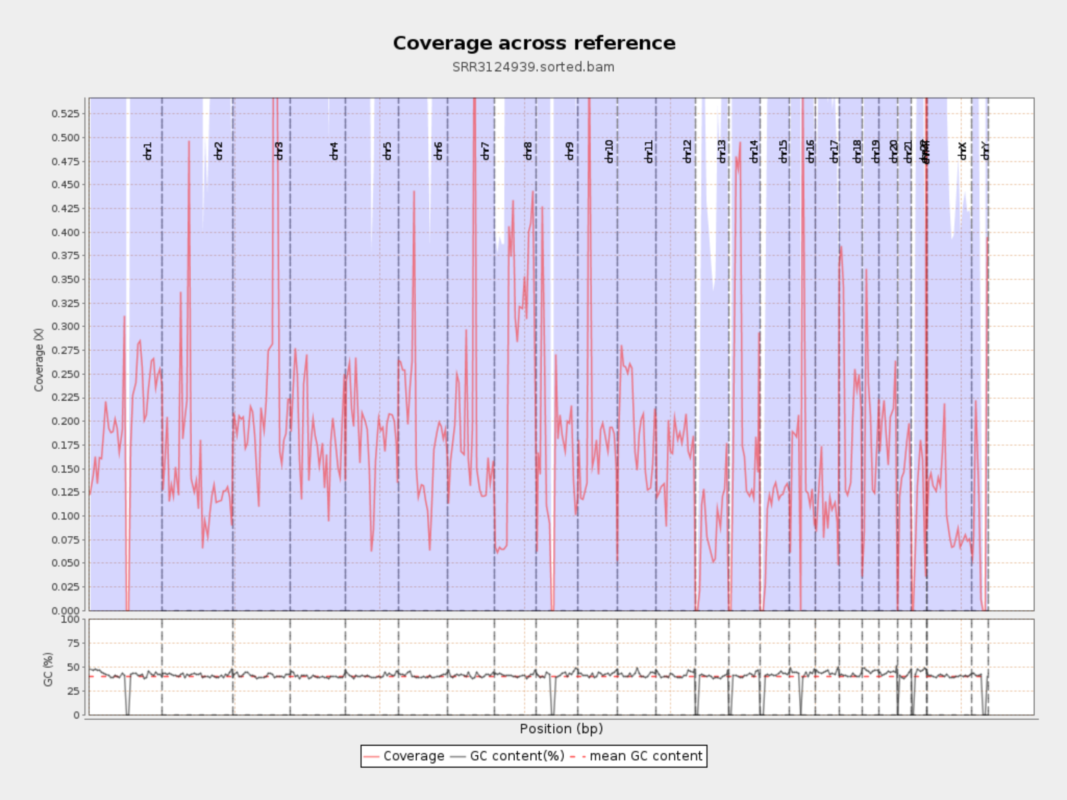
2.7. Chromosome stats

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

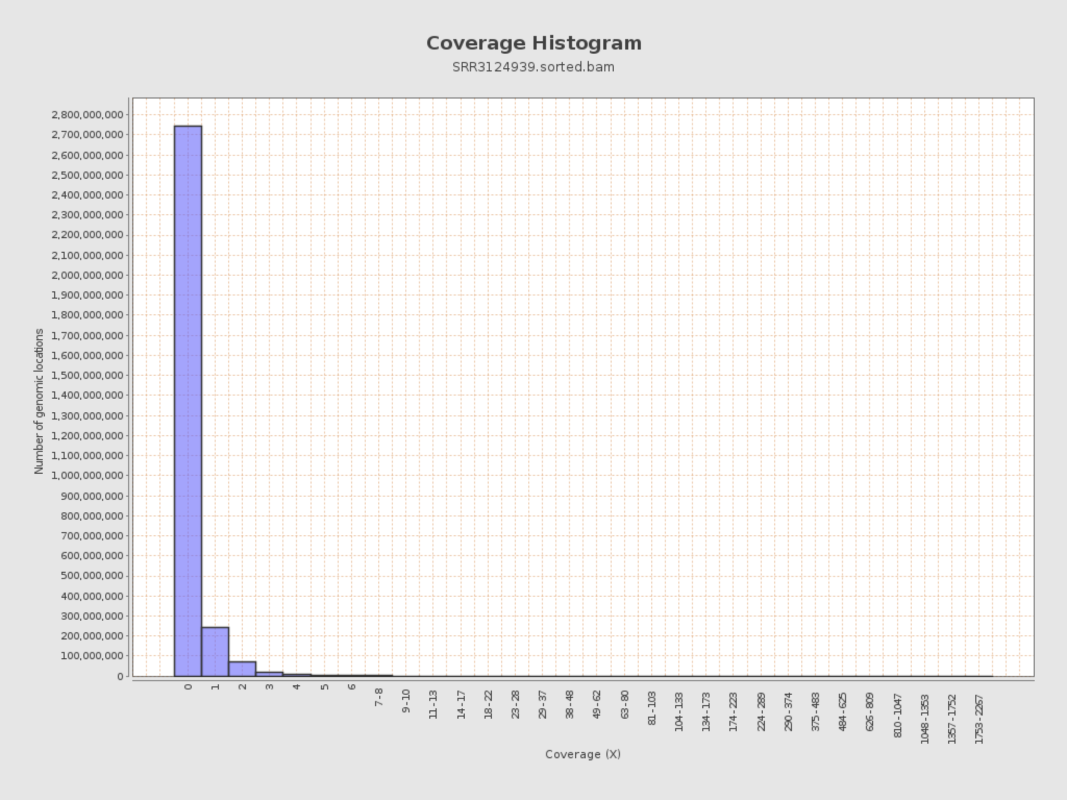
		bases	coverage	deviation
chr1	249250621	49203758	0.1974	1.9453
chr2	243199373	36728229	0.151	2.0338
chr3	198022430	48821226	0.2465	0.7677
chr4	191154276	35349809	0.1849	0.9592
chr5	180915260	34074174	0.1883	0.5942
chr6	171115067	32691651	0.1911	2.2562
chr7	159138663	31174625	0.1959	2.3095
chr8	146364022	38561331	0.2635	0.9449
chr9	141213431	24075787	0.1705	2.6599
chr10	135534747	25688312	0.1895	3.6623
chr11	135006516	26807341	0.1986	1.5184
chr12	133851895	21893074	0.1636	0.5473
chr13	115169878	9370995	0.0814	0.3651
chr14	107349540	21575288	0.201	0.7679
chr15	102531392	10130763	0.0988	0.4172
chr16	90354753	15167013	0.1679	2.8158
chr17	81195210	8623228	0.1062	1.2238
chr18	78077248	18257664	0.2338	2.7693
chr19	59128983	10907801	0.1845	1.3031
chr20	63025520	12475144	0.1979	0.6441
chr21	48129895	6585303	0.1368	0.6491
chr22	51304566	4715823	0.0919	0.4243
chrMT	16571	257507	15.5396	9.8595
chrX	155270560	16512636	0.1063	0.7651

chrY	59373566	6692062	0.1127	2.1845

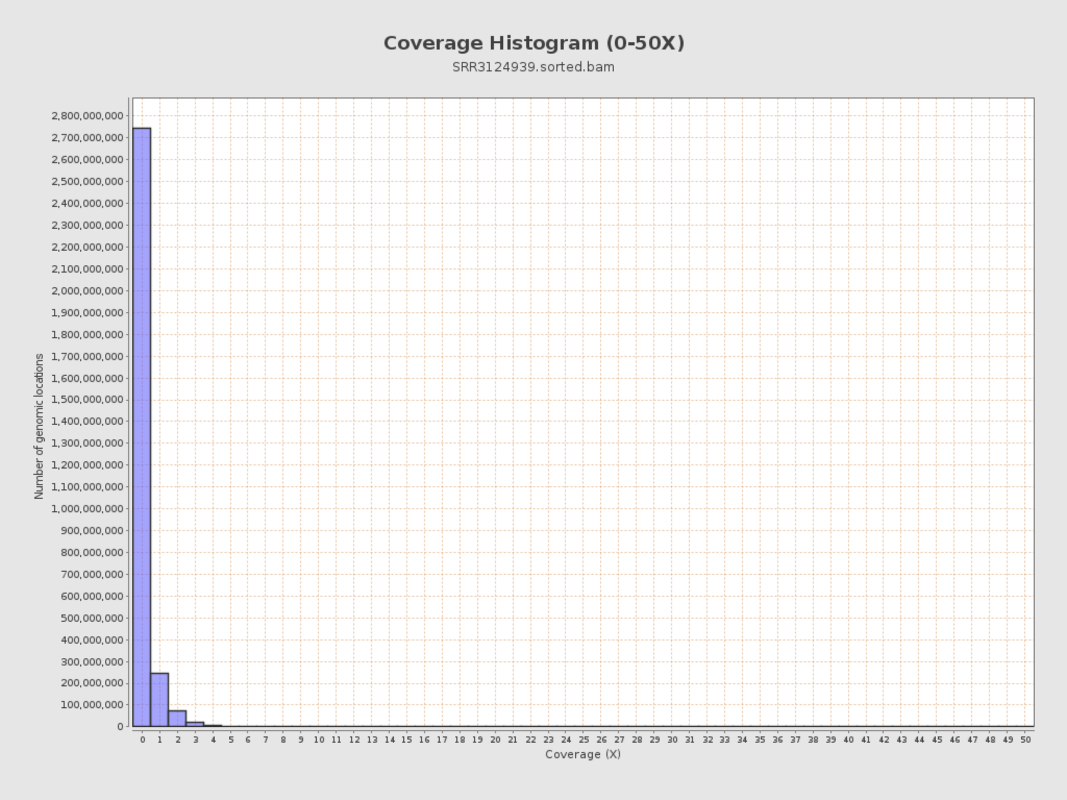
3. Results : Coverage across reference



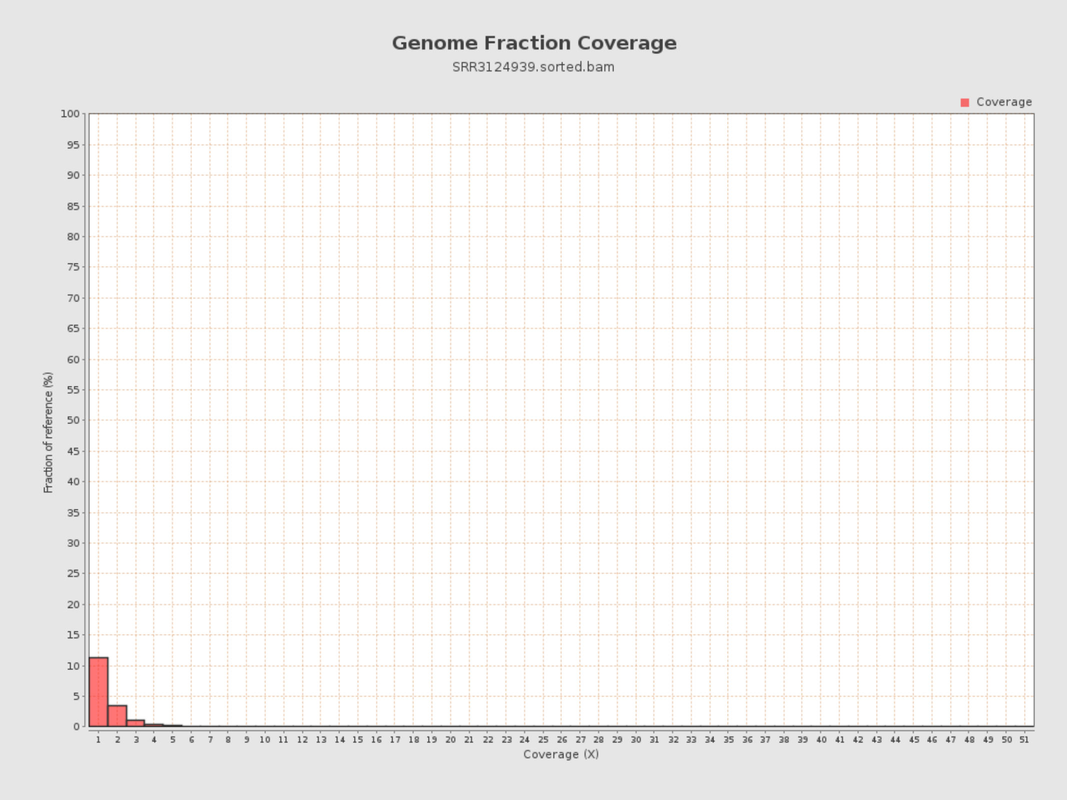
4. Results : Coverage Histogram



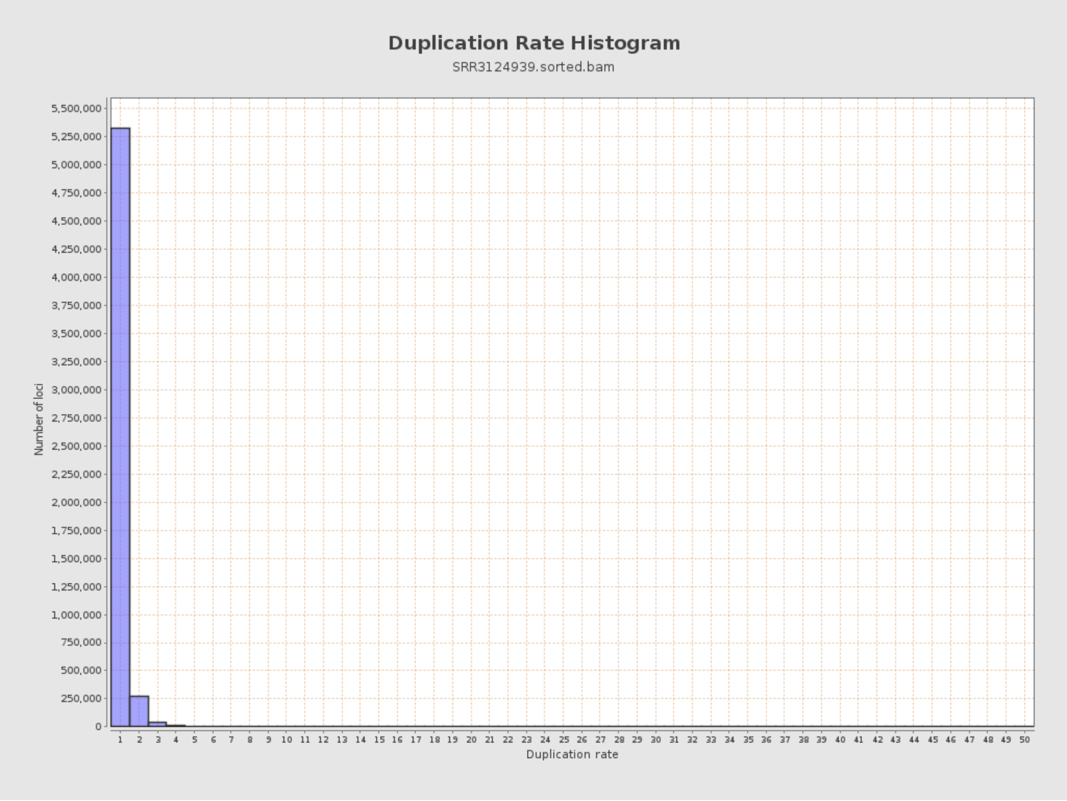
5. Results : Coverage Histogram (0-50X)



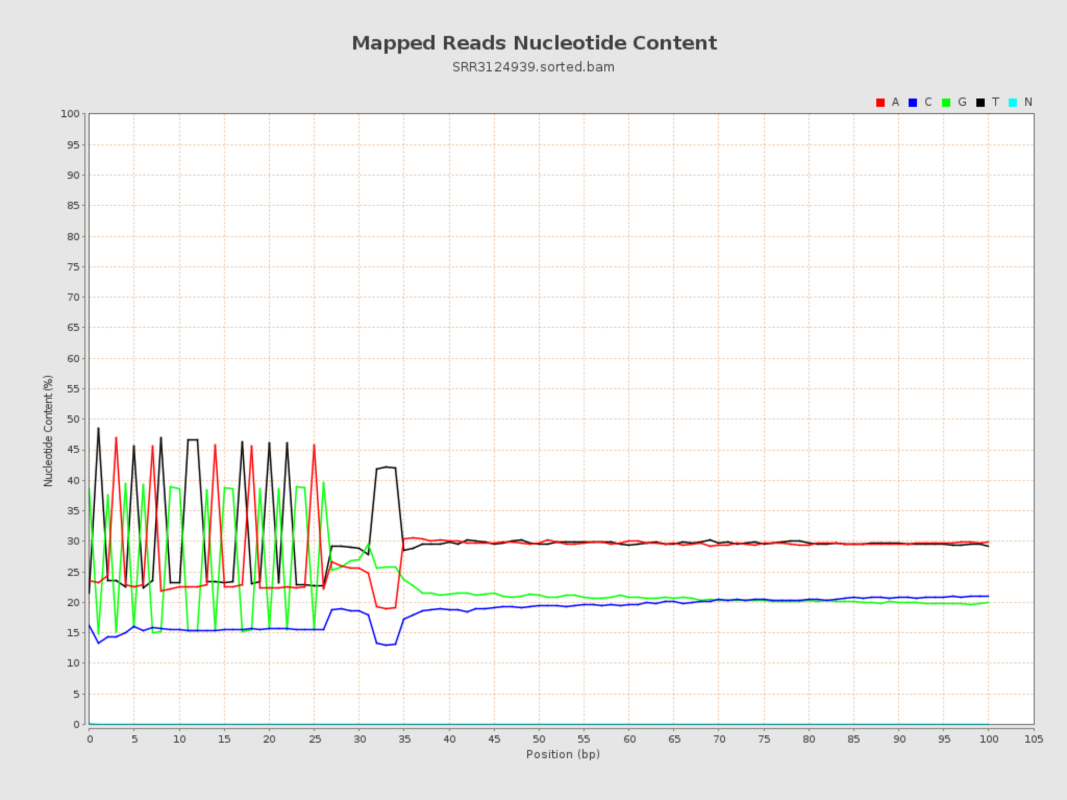
6. Results : Genome Fraction Coverage



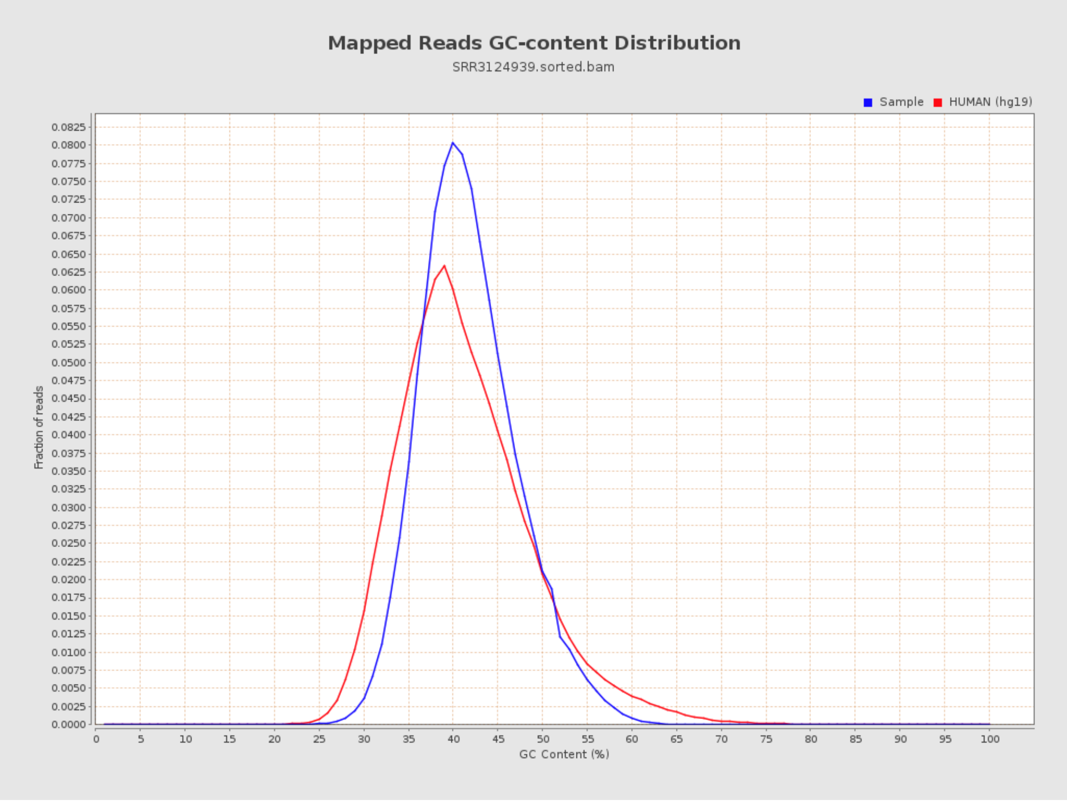
7. Results : Duplication Rate Histogram



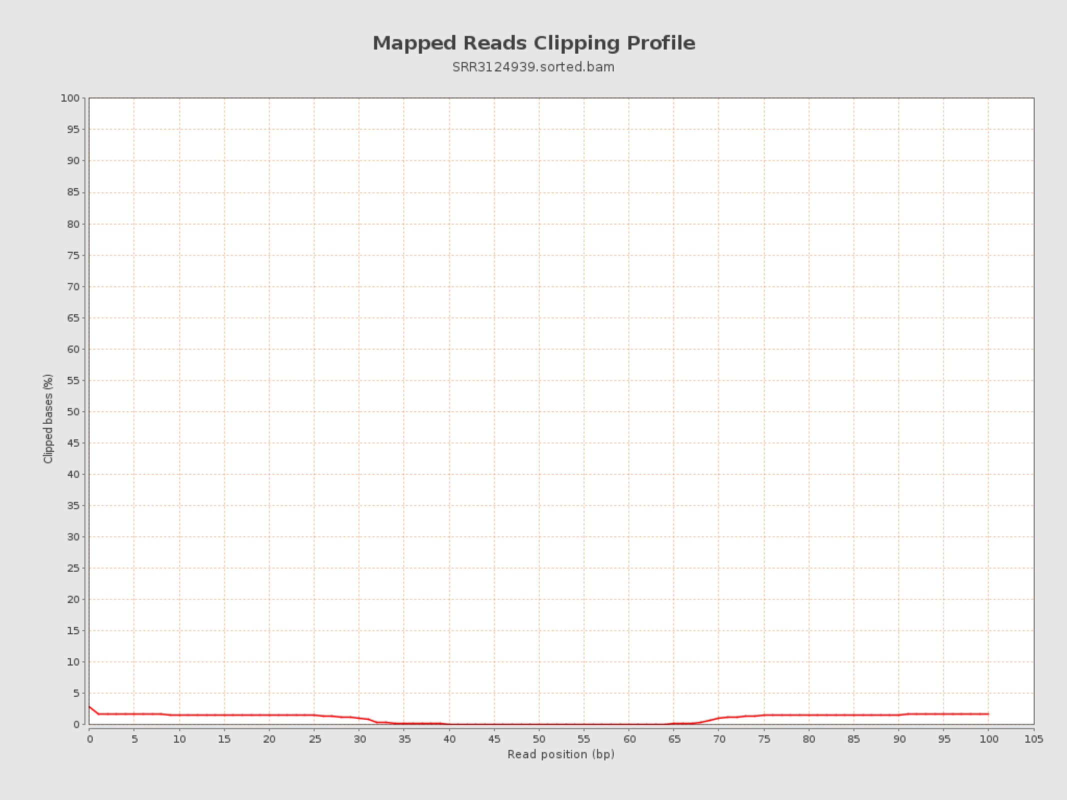
8. Results : Mapped Reads Nucleotide Content



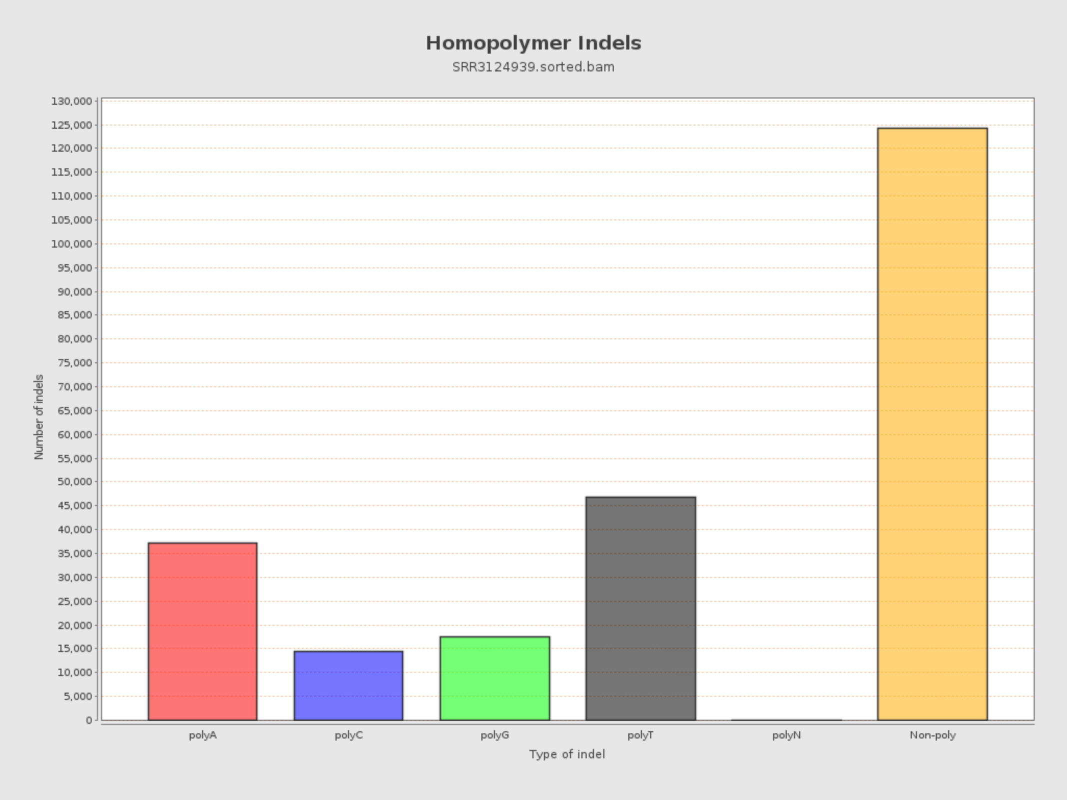
9. Results : Mapped Reads GC-content Distribution



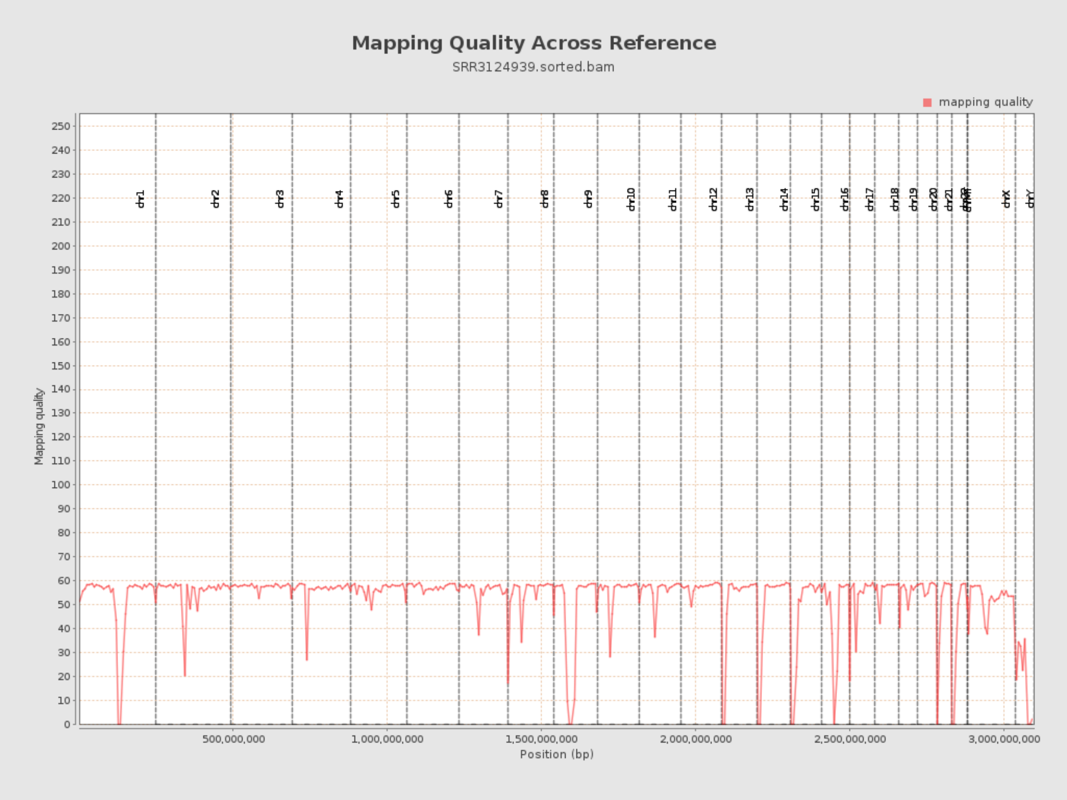
10. Results : Mapped Reads Clipping Profile



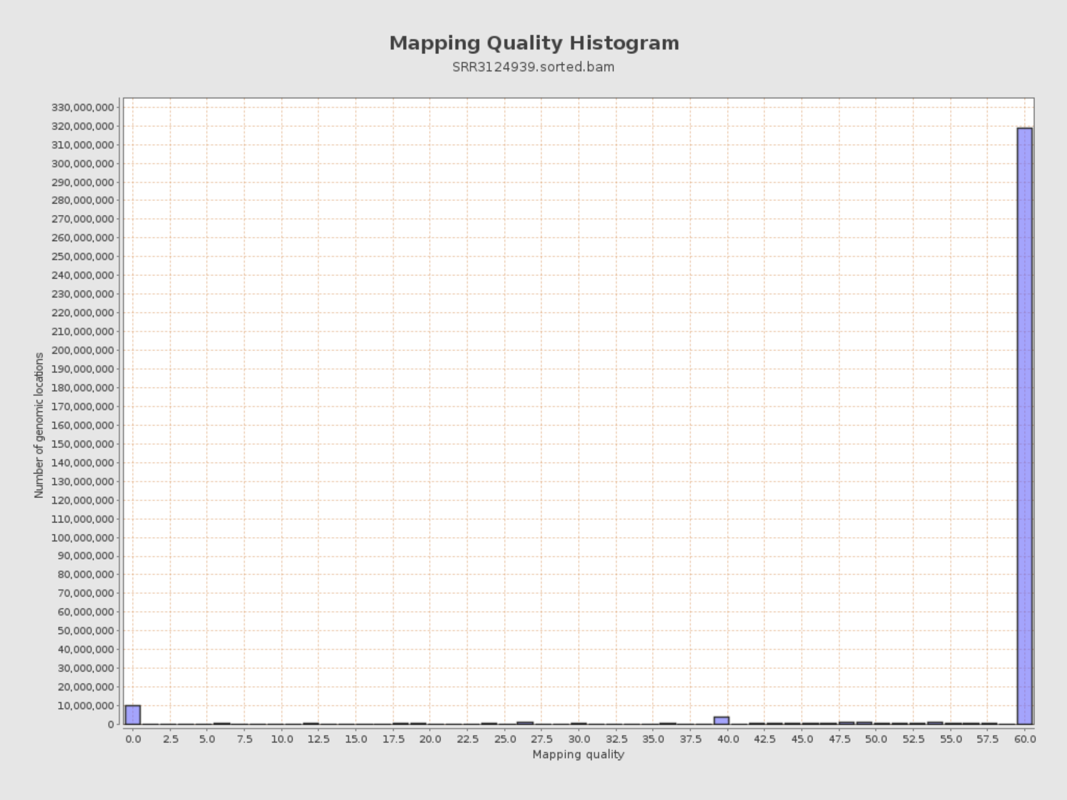
11. Results : Homopolymer Indels



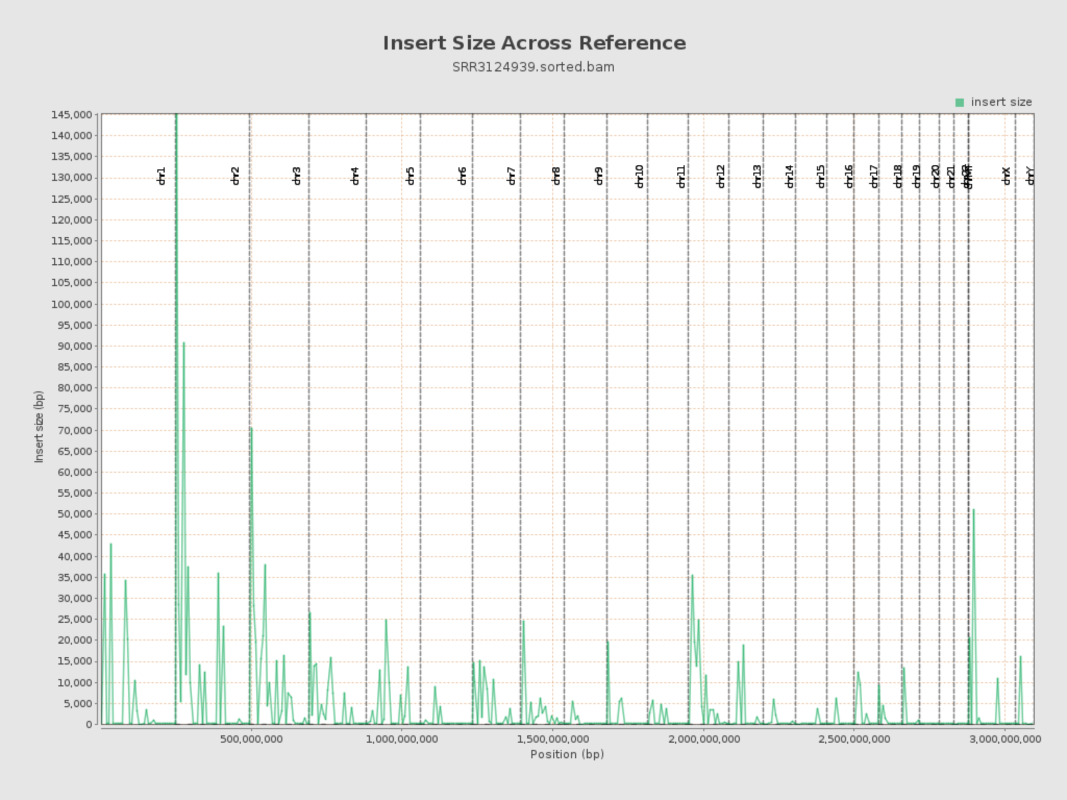
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram