Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:49:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124955.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_SRR3124955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124955_1.fastq.gz SRR3124955_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:49:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,387,544
Mapped reads	2,348,953 / 98.38%
Unmapped reads	38,591 / 1.62%
Mapped paired reads	2,348,953 / 98.38%
Mapped reads, first in pair	1,176,695 / 49.28%
Mapped reads, second in pair	1,172,258 / 49.1%
Mapped reads, both in pair	2,338,038 / 97.93%
Mapped reads, singletons	10,915 / 0.46%
Secondary alignments	0
Supplementary alignments	41,015 / 1.72%
Read min/max/mean length	30 / 151 / 151.83
Duplicated reads (estimated)	383,072 / 16.04%
Duplication rate	14.86%
Clipped reads	1,788,057 / 74.89%

2.2. ACGT Content

Number/percentage of A's	91,551,842 / 29.14%
Number/percentage of C's	63,649,139 / 20.26%
Number/percentage of T's	92,030,794 / 29.29%
Number/percentage of G's	66,956,935 / 21.31%
Number/percentage of N's	34,092 / 0.01%

GC Percentage	41.56%

2.3. Coverage

Mean	0.1016
Standard Deviation	1.4243

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	100,194.04
Standard Deviation	3,055,908.46
P25/Median/P75	136 / 169 / 214

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	3,572,099
Insertions	68,869
Mapped reads with at least one insertion	2.74%
Deletions	117,135
Mapped reads with at least one deletion	4.77%
Homopolymer indels	44.59%

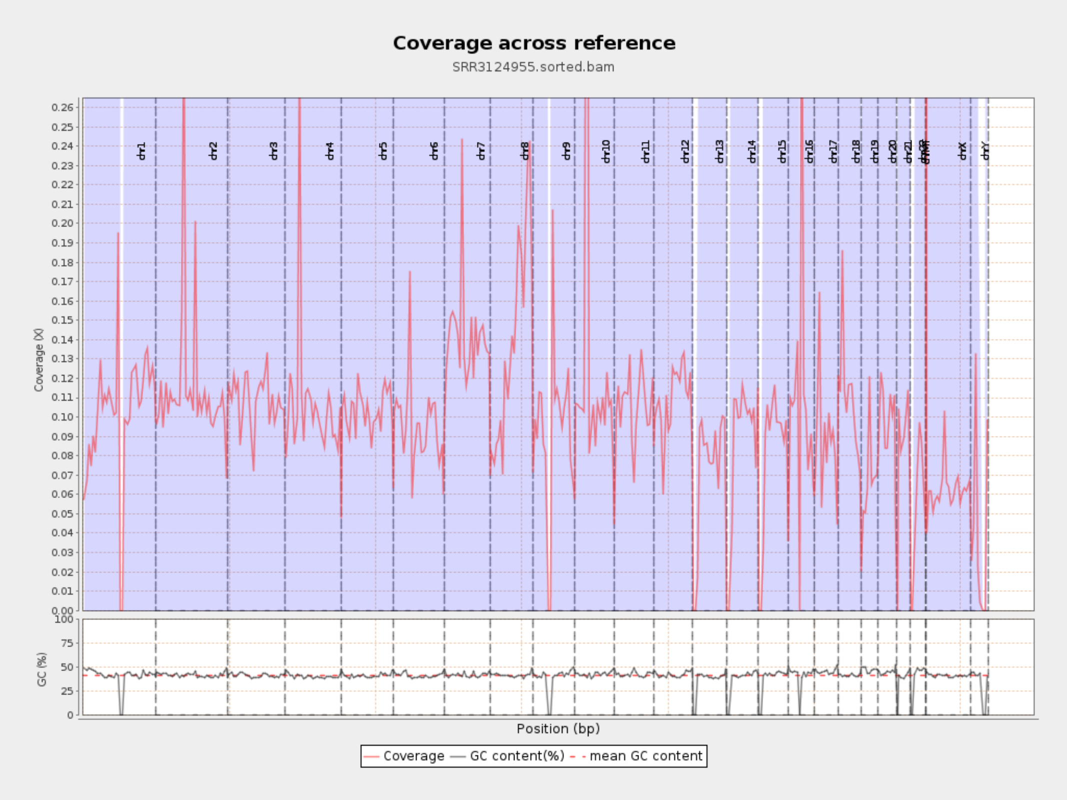
2.7. Chromosome stats

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

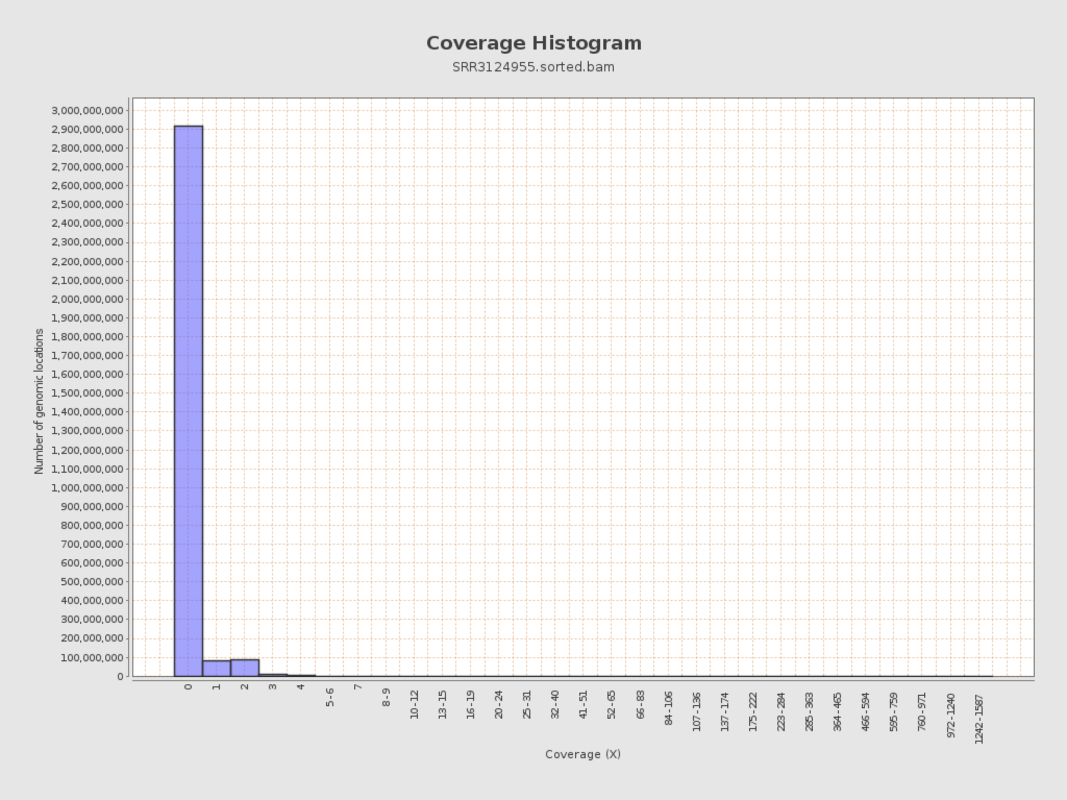
		bases	coverage	deviation
chr1	249250621	25415390	0.102	1.6297
chr2	243199373	28279446	0.1163	1.6548
chr3	198022430	21474255	0.1084	0.4765
chr4	191154276	20668785	0.1081	1.2297
chr5	180915260	18649841	0.1031	0.4567
chr6	171115067	16560003	0.0968	0.9045
chr7	159138663	22554445	0.1417	2.265
chr8	146364022	20635844	0.141	0.6197
chr9	141213431	13280278	0.094	2.3458
chr10	135534747	16911701	0.1248	3.2428
chr11	135006516	14283937	0.1058	0.9829
chr12	133851895	14665872	0.1096	0.4594
chr13	115169878	8315369	0.0722	0.3667
chr14	107349540	9121802	0.085	0.4423
chr15	102531392	8151891	0.0795	0.3883
chr16	90354753	9965113	0.1103	1.8817
chr17	81195210	7355487	0.0906	1.3176
chr18	78077248	8651364	0.1108	2.1911
chr19	59128983	4005363	0.0677	0.8112
chr20	63025520	6313457	0.1002	0.5645
chr21	48129895	4091429	0.085	0.7378
chr22	51304566	2803857	0.0547	0.3387
chrMT	16571	186712	11.2674	7.1386
chrX	155270560	9669832	0.0623	0.4728

chrY	59373566	2460066	0.0414	1.7827

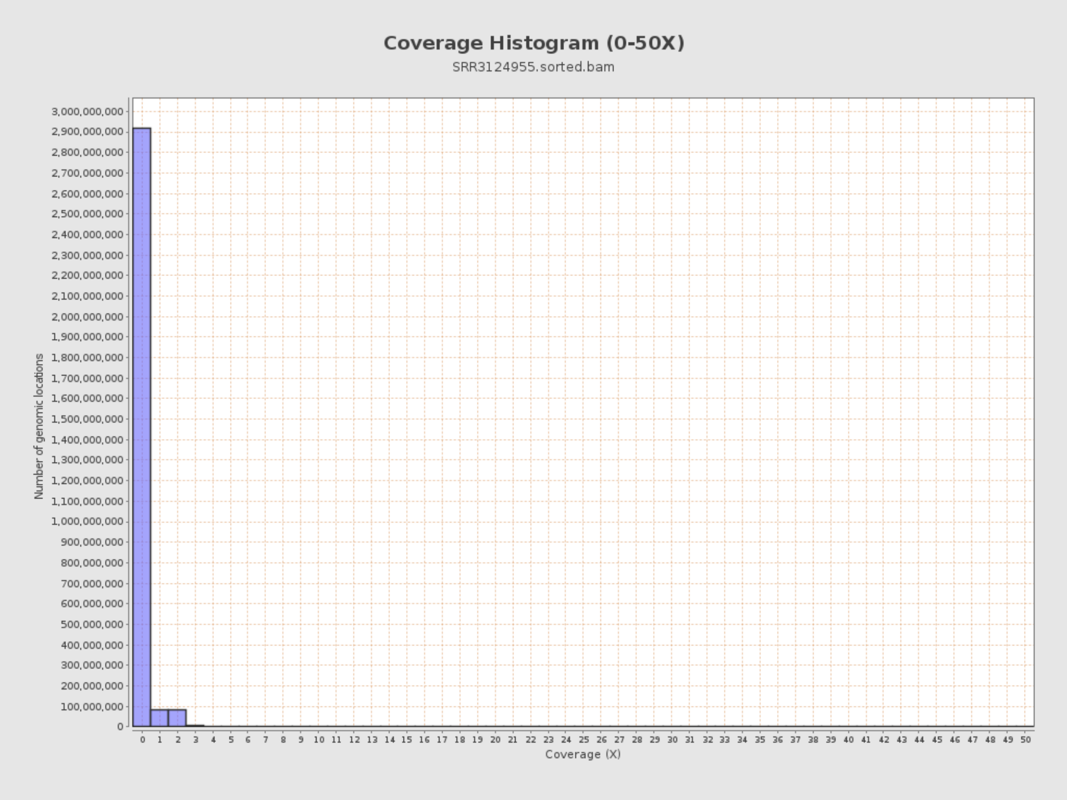
3. Results : Coverage across reference



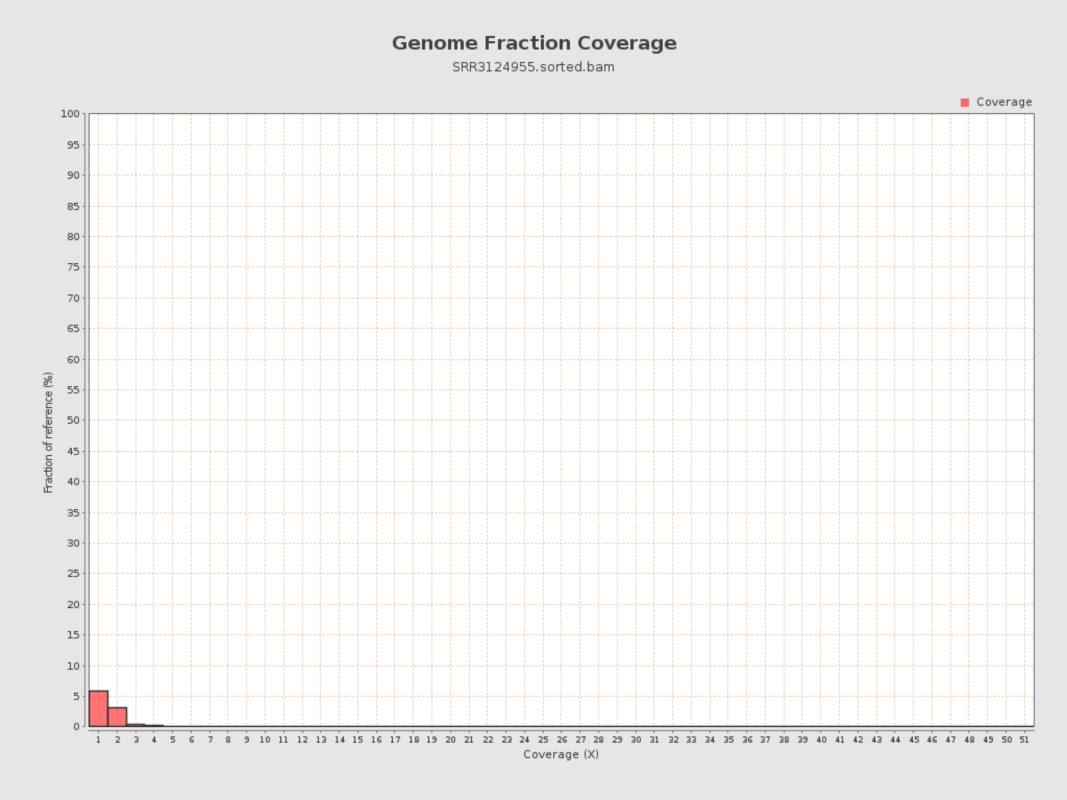
4. Results : Coverage Histogram



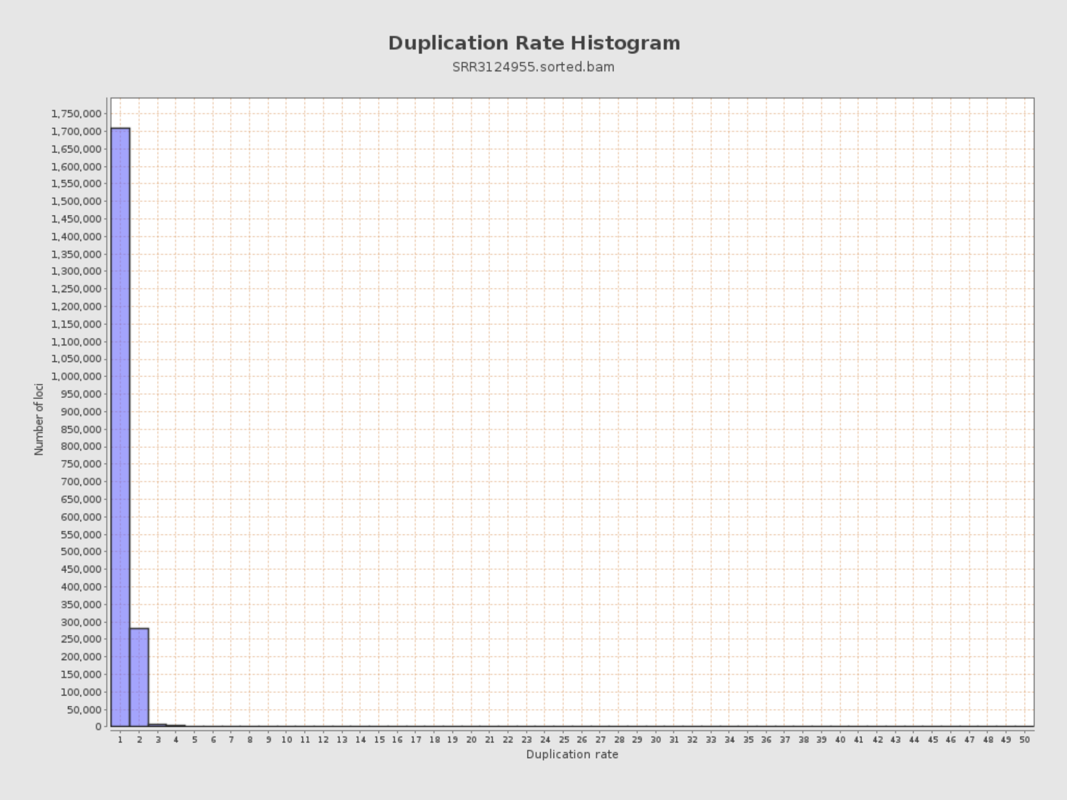
5. Results : Coverage Histogram (0-50X)



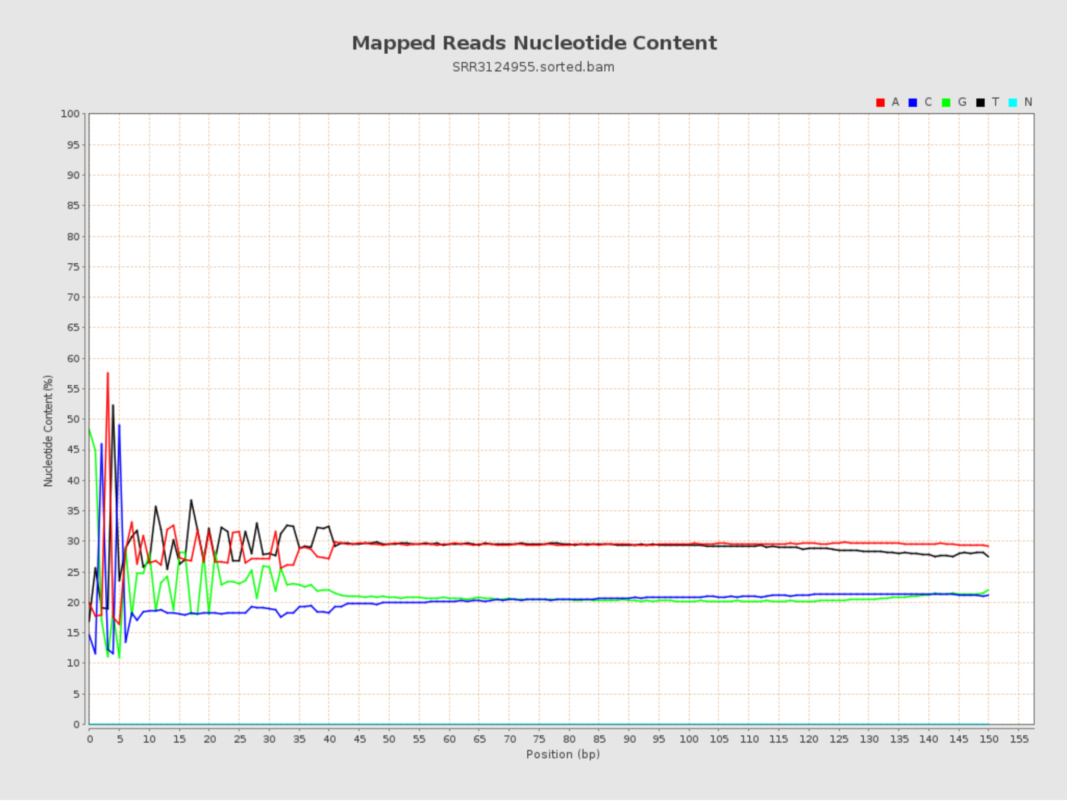
6. Results : Genome Fraction Coverage



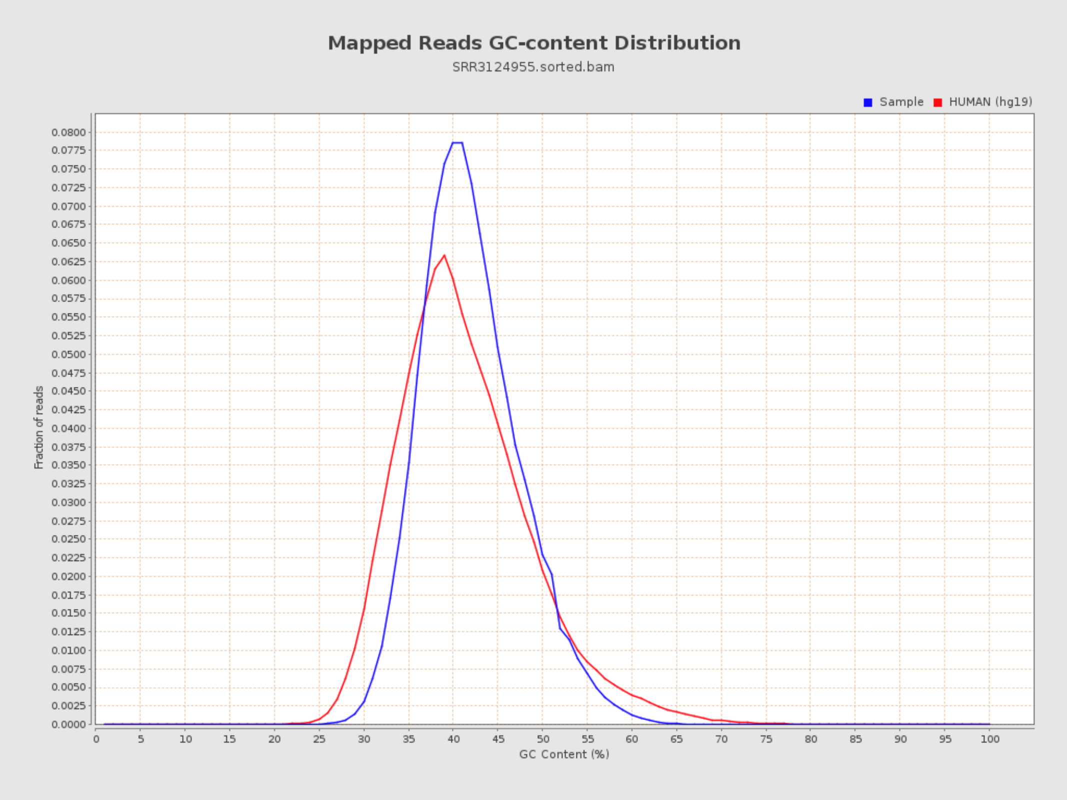
7. Results : Duplication Rate Histogram



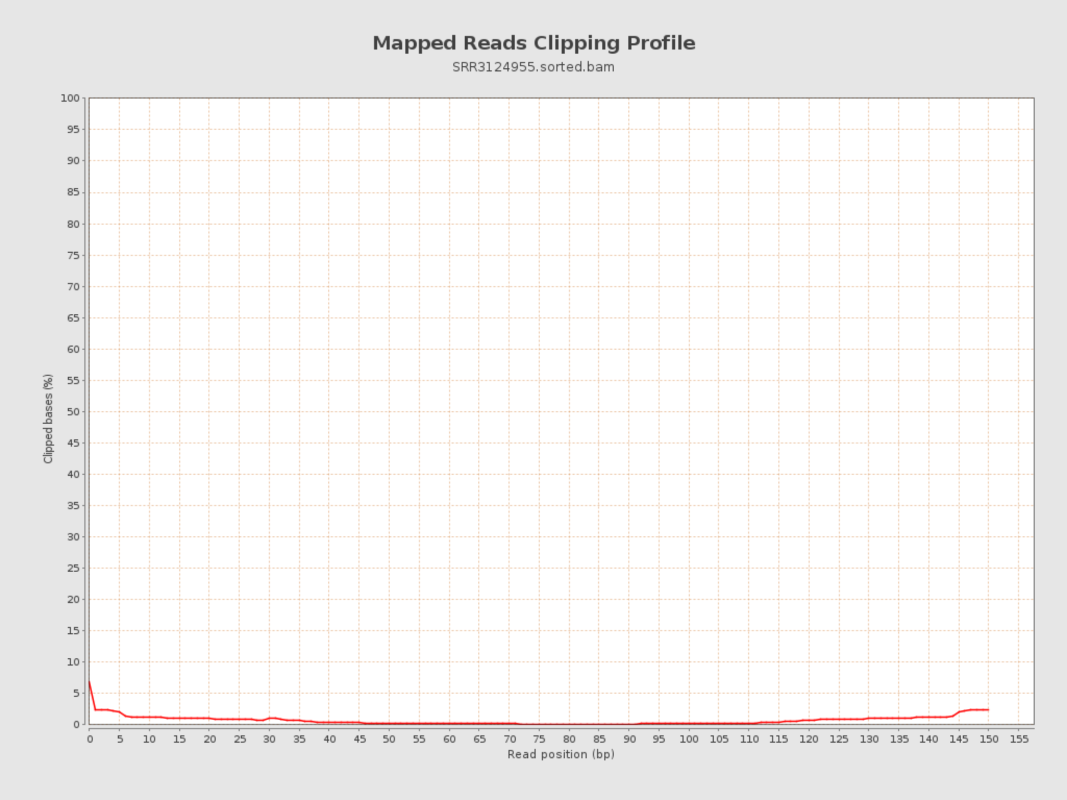
8. Results : Mapped Reads Nucleotide Content



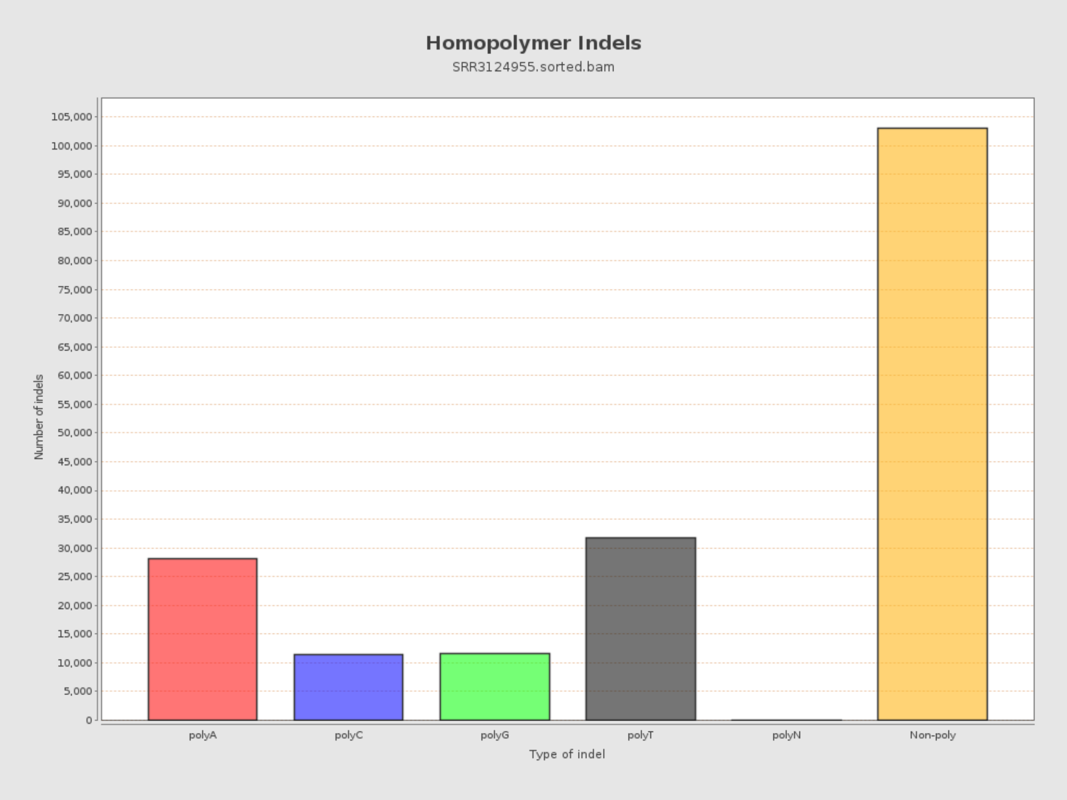
9. Results : Mapped Reads GC-content Distribution



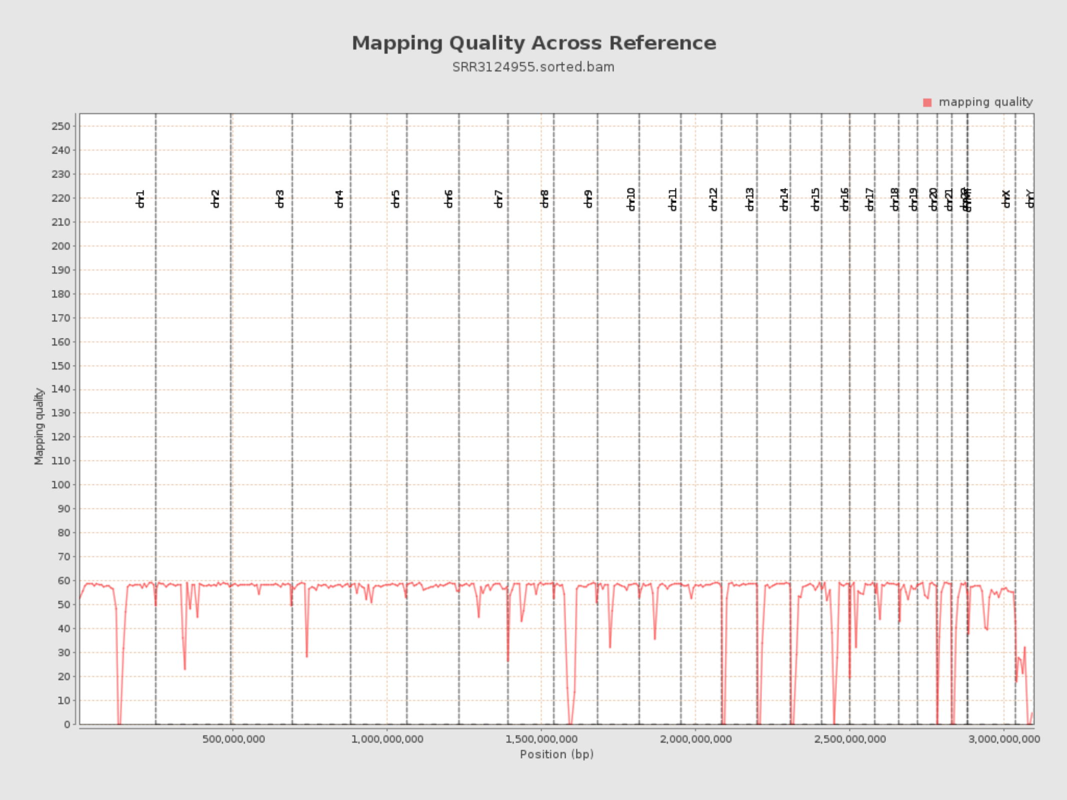
10. Results : Mapped Reads Clipping Profile



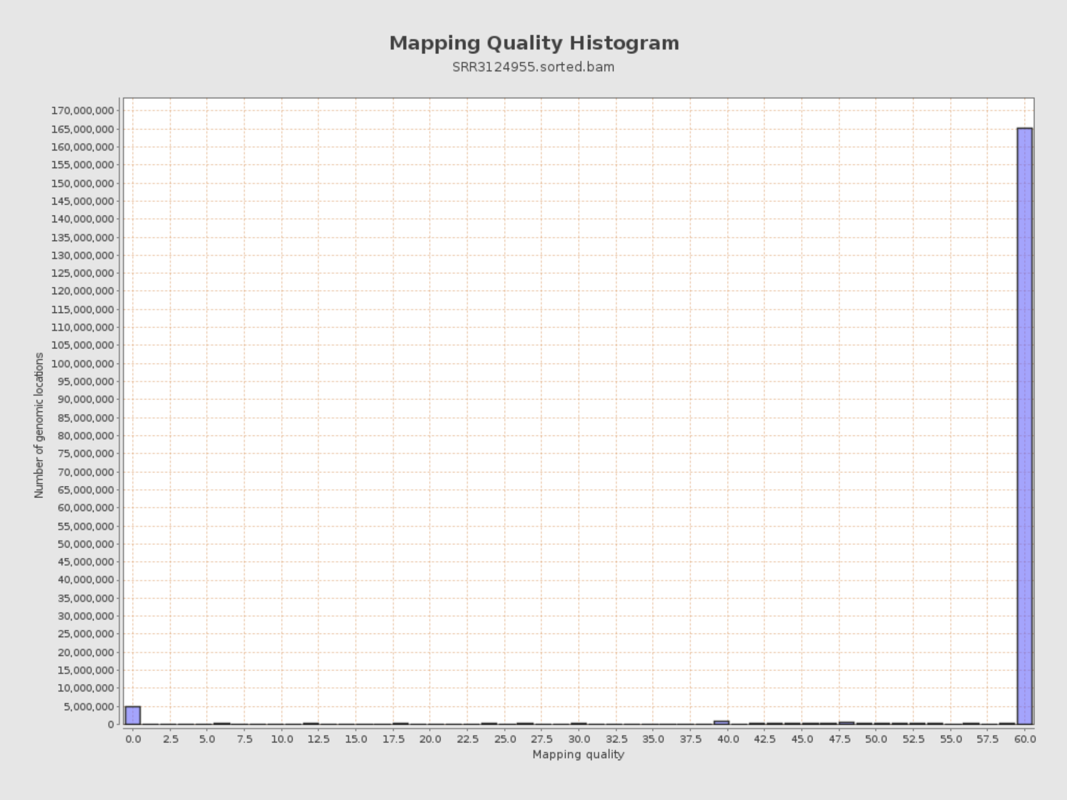
11. Results : Homopolymer Indels



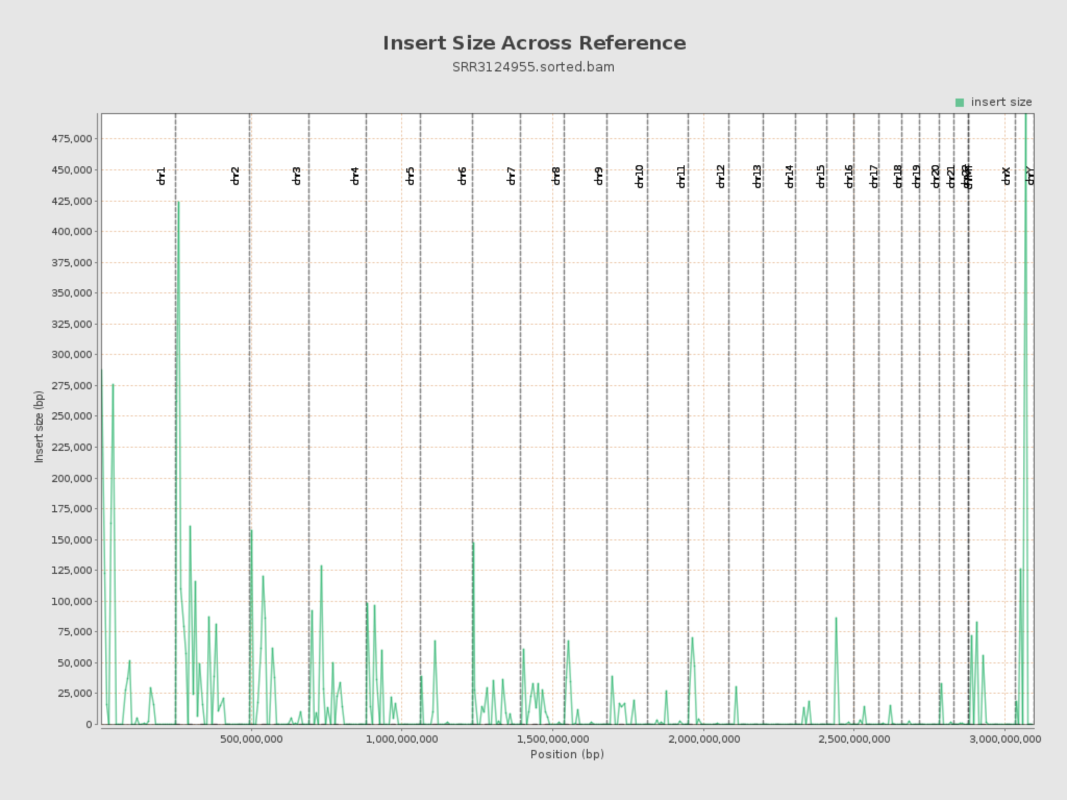
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram