Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:28:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124905.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_SRR3124905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124905_1.fastq.gz SRR3124905_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:28:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,566,480
Mapped reads	3,520,600 / 98.71%
Unmapped reads	45,880 / 1.29%
Mapped paired reads	3,520,600 / 98.71%
Mapped reads, first in pair	1,764,546 / 49.48%
Mapped reads, second in pair	1,756,054 / 49.24%
Mapped reads, both in pair	3,505,722 / 98.3%
Mapped reads, singletons	14,878 / 0.42%
Secondary alignments	0
Supplementary alignments	38,776 / 1.09%
Read min/max/mean length	30 / 151 / 151.53
Duplicated reads (estimated)	521,184 / 14.61%
Duplication rate	14.13%
Clipped reads	2,550,629 / 71.52%

2.2. ACGT Content

Number/percentage of A's	137,918,610 / 29.12%
Number/percentage of C's	95,800,499 / 20.23%
Number/percentage of T's	139,284,191 / 29.41%
Number/percentage of G's	100,529,292 / 21.23%
Number/percentage of N's	20,409 / 0%

GC Percentage	41.46%

2.3. Coverage

Mean	0.1531
Standard Deviation	1.909

2.4. Mapping Quality

Mean Mapping Quality	53.7

2.5. Insert size

Mean	73,982.21
Standard Deviation	2,631,864.35
P25/Median/P75	136 / 167 / 210

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	6,390,558
Insertions	80,700
Mapped reads with at least one insertion	2.2%
Deletions	163,756
Mapped reads with at least one deletion	4.5%
Homopolymer indels	46.74%

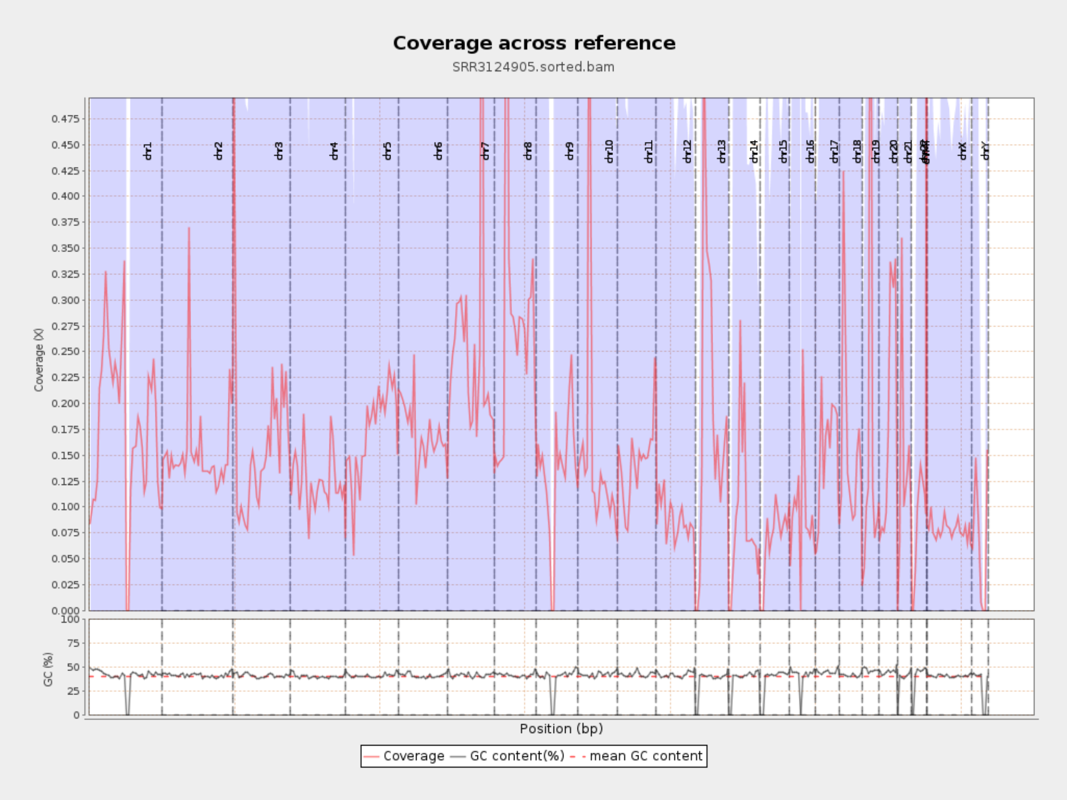
2.7. Chromosome stats

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

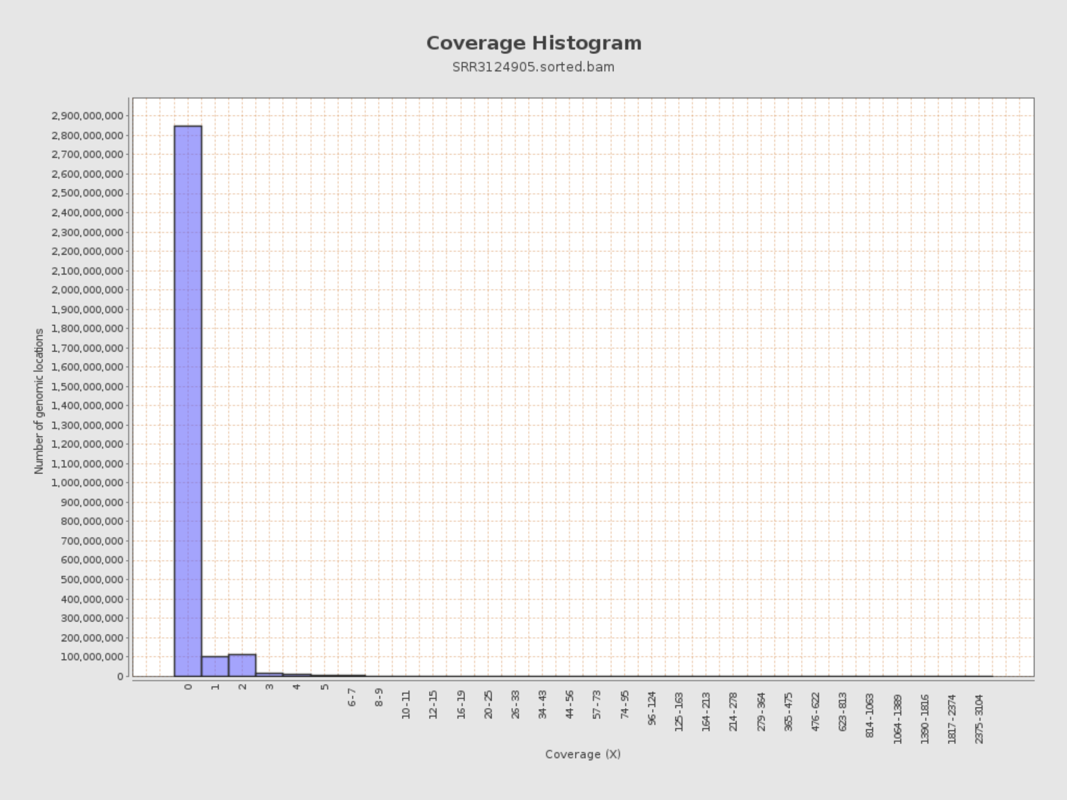
		bases	**coverage**	**deviation**
chr1	249250621	44751931	0.1795	2.9473
chr2	243199373	37094410	0.1525	1.6324
chr3	198022430	32255700	0.1629	0.6559
chr4	191154276	23762351	0.1243	0.7938
chr5	180915260	31254292	0.1728	0.6042
chr6	171115067	29351690	0.1715	1.2381
chr7	159138663	41722366	0.2622	2.7238
chr8	146364022	40250480	0.275	1.1019
chr9	141213431	19348527	0.137	2.0991
chr10	135534747	20571628	0.1518	5.6166
chr11	135006516	19002103	0.1407	1.2403
chr12	133851895	11758083	0.0878	0.4258
chr13	115169878	21782552	0.1891	0.672
chr14	107349540	9774417	0.0911	0.4744
chr15	102531392	7085613	0.0691	0.3809
chr16	90354753	8490791	0.094	1.2827
chr17	81195210	12580471	0.1549	2.2484
chr18	78077248	12886213	0.165	2.3091
chr19	59128983	11014000	0.1863	1.6708
chr20	63025520	11903772	0.1889	0.6942
chr21	48129895	6769815	0.1407	0.6889
chr22	51304566	4200760	0.0819	0.4141
chrMT	16571	33730	2.0355	2.2482
chrX	155270560	12262542	0.079	0.5608

chrY	59373566	3944804	0.0664	1.2659

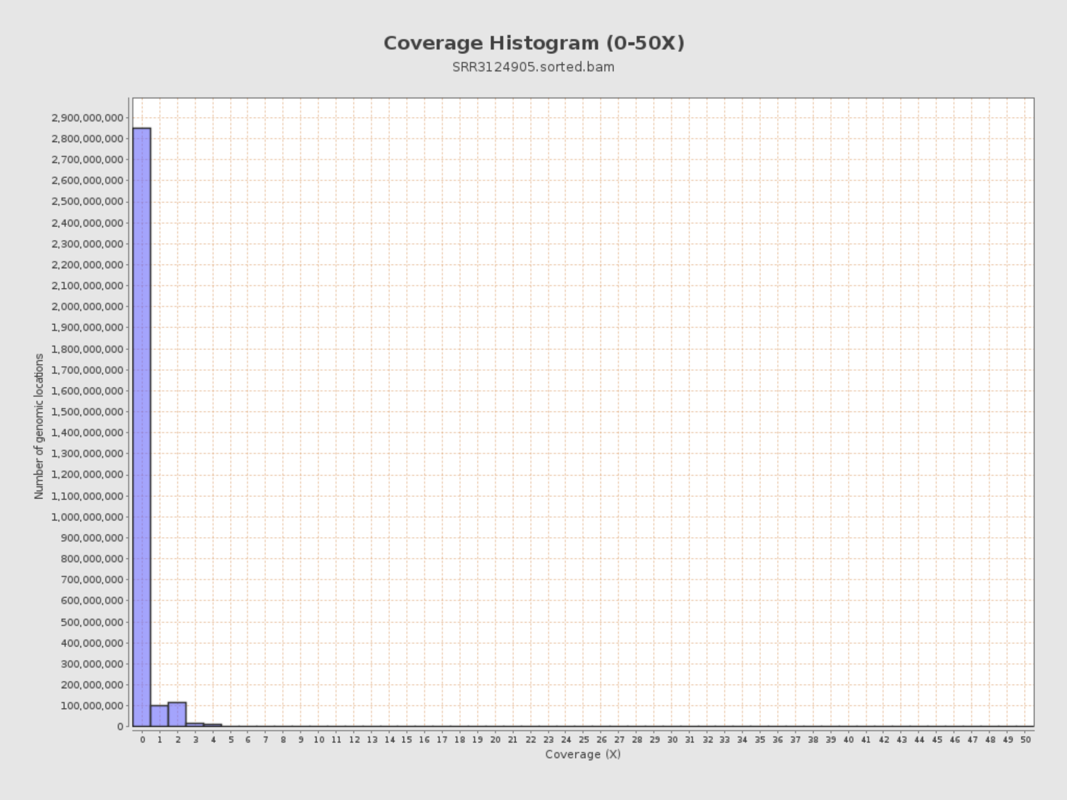
3. Results : Coverage across reference



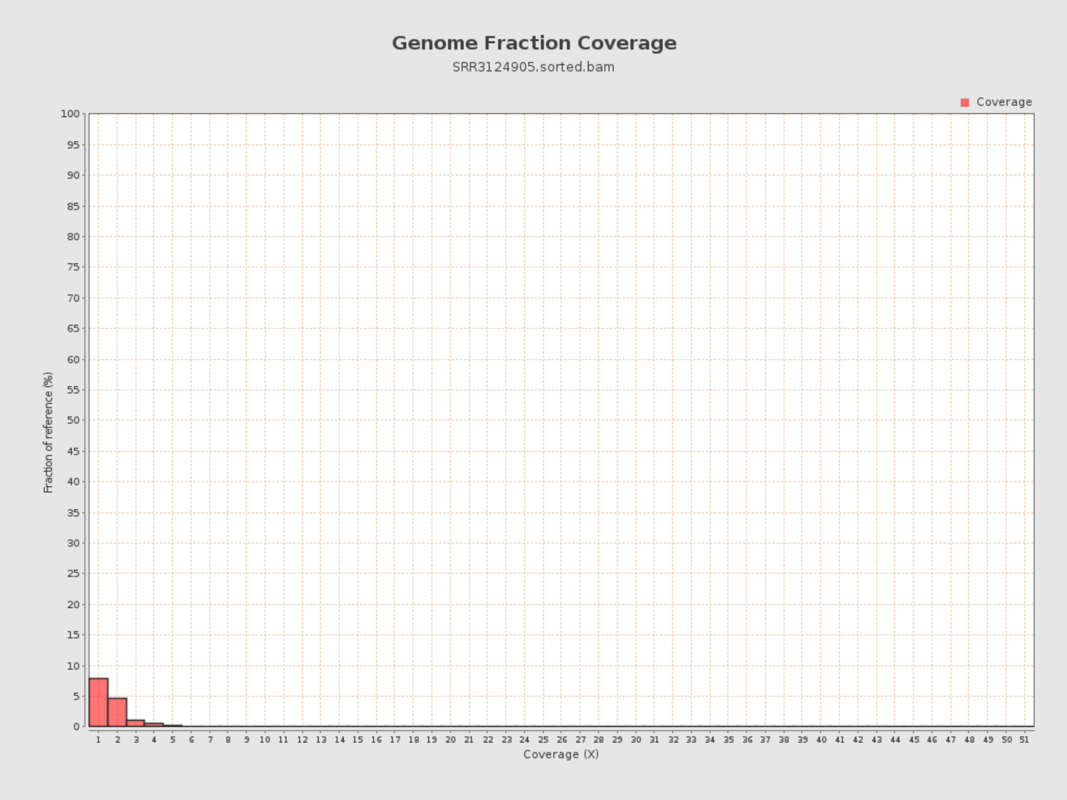
4. Results : Coverage Histogram



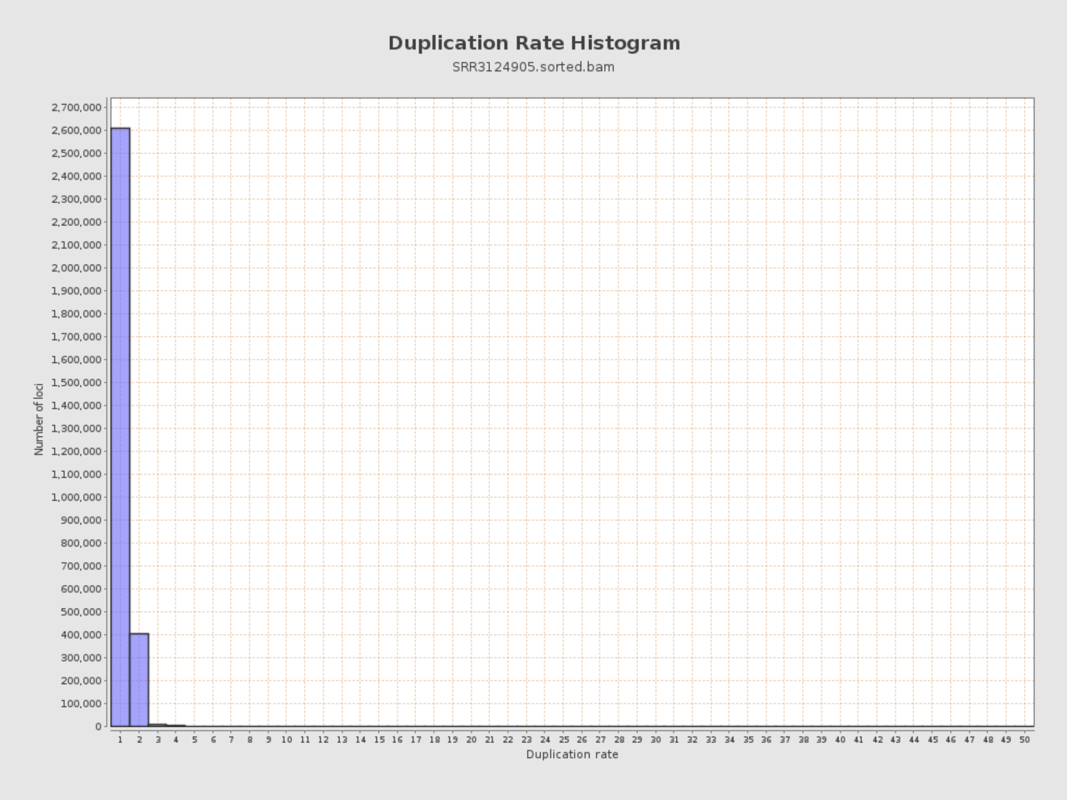
5. Results : Coverage Histogram (0-50X)



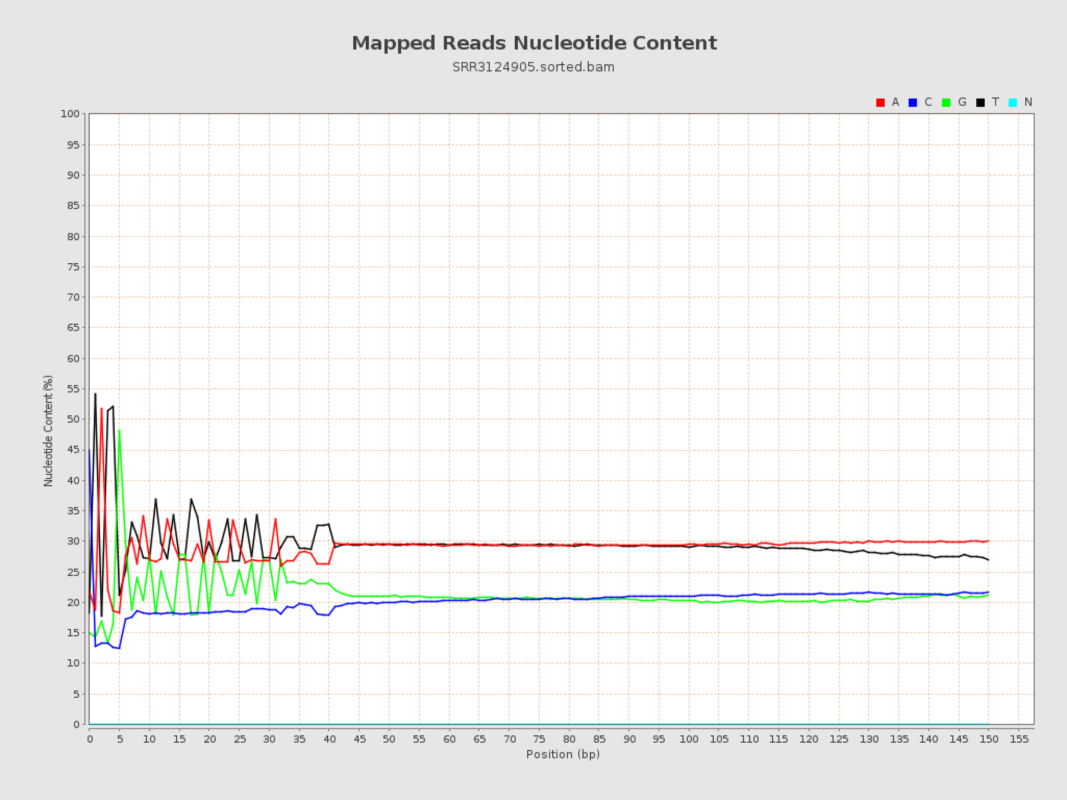
6. Results : Genome Fraction Coverage



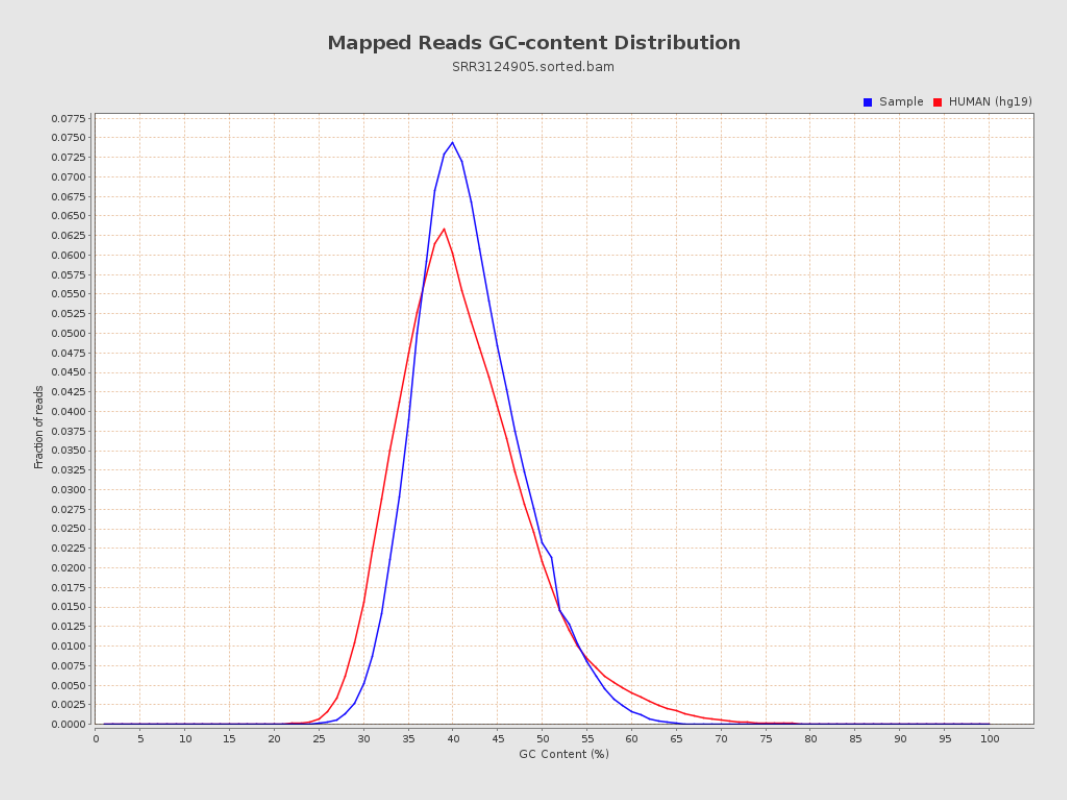
7. Results : Duplication Rate Histogram



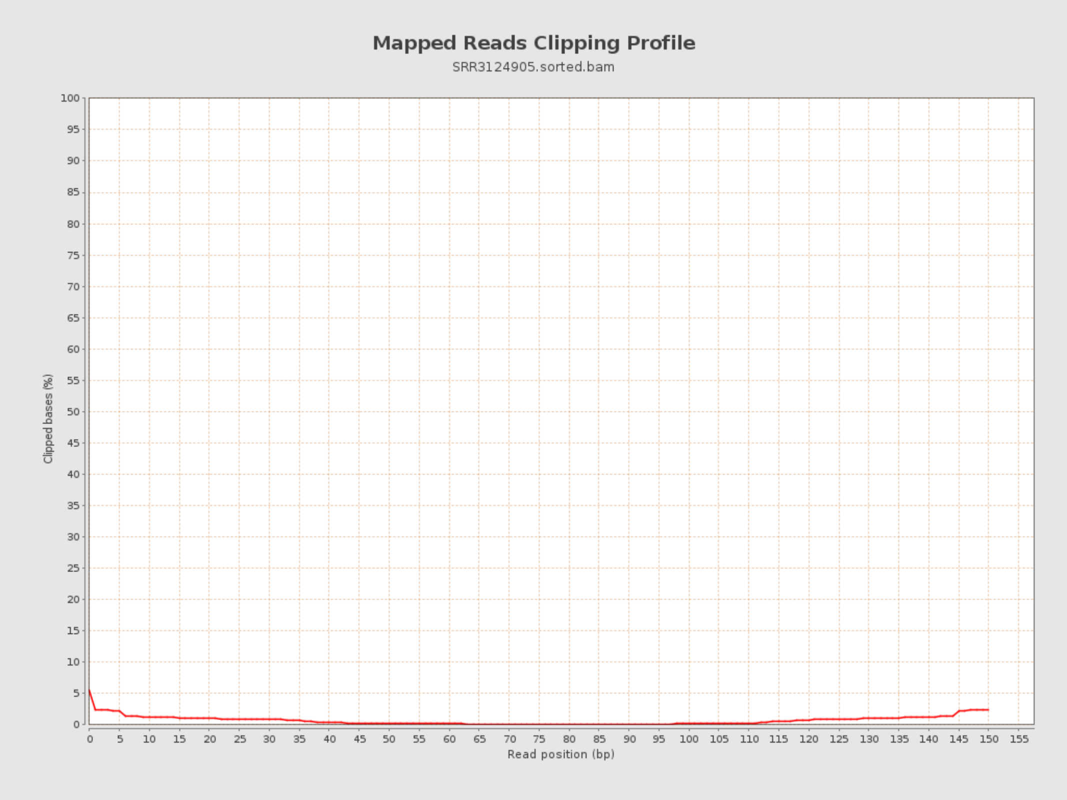
8. Results : Mapped Reads Nucleotide Content



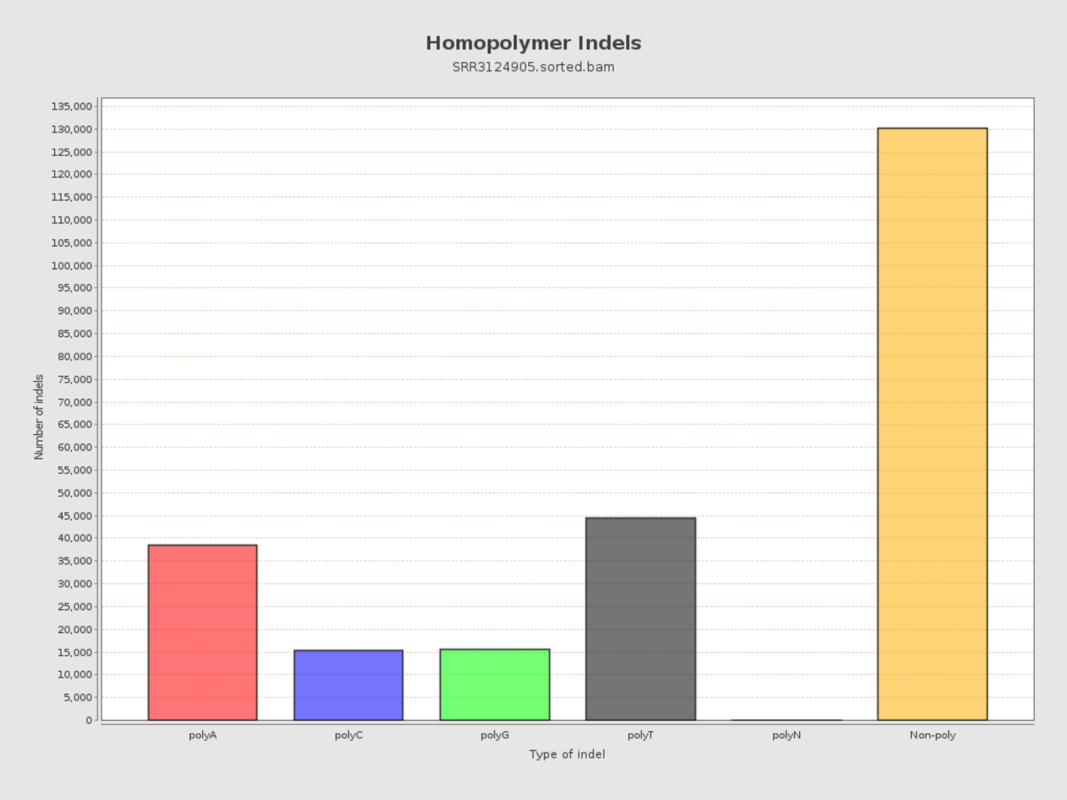
9. Results : Mapped Reads GC-content Distribution



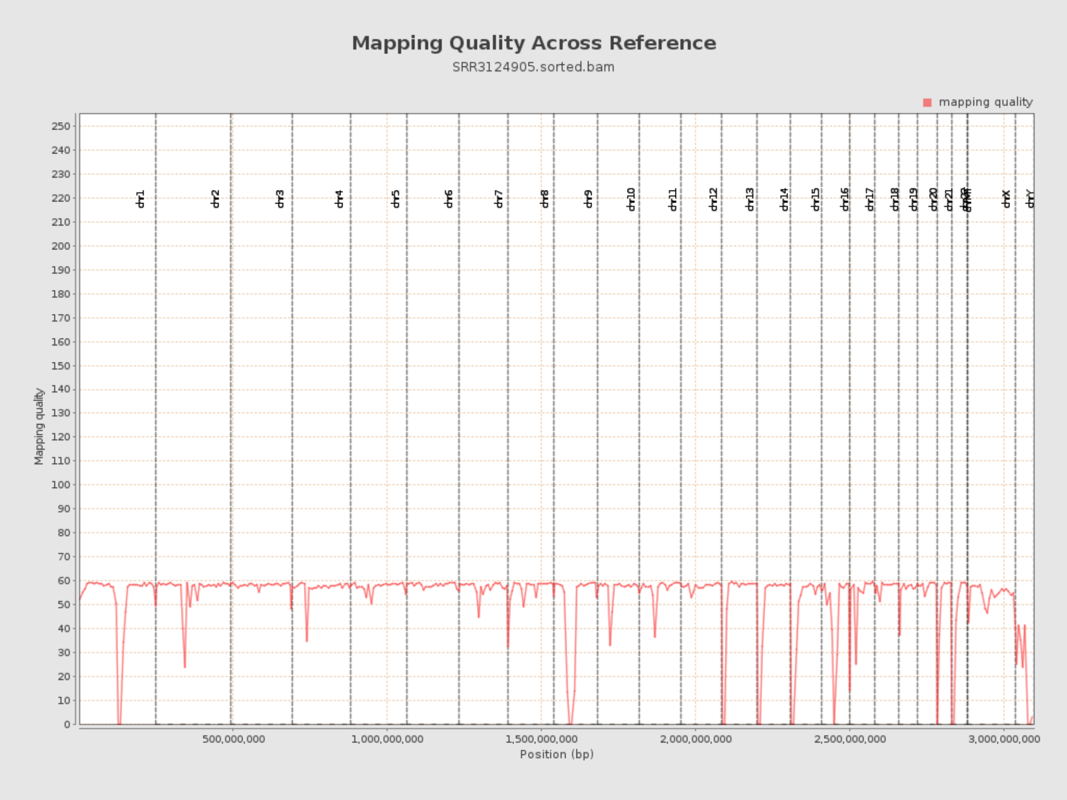
10. Results : Mapped Reads Clipping Profile



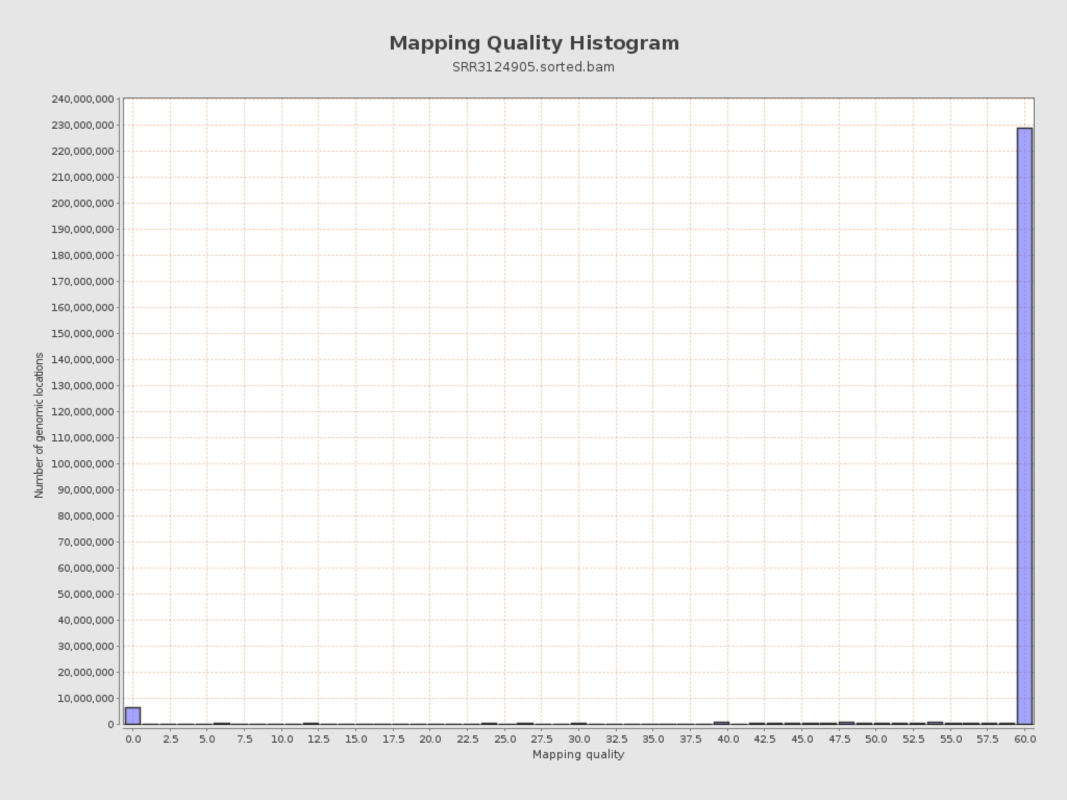
11. Results : Homopolymer Indels



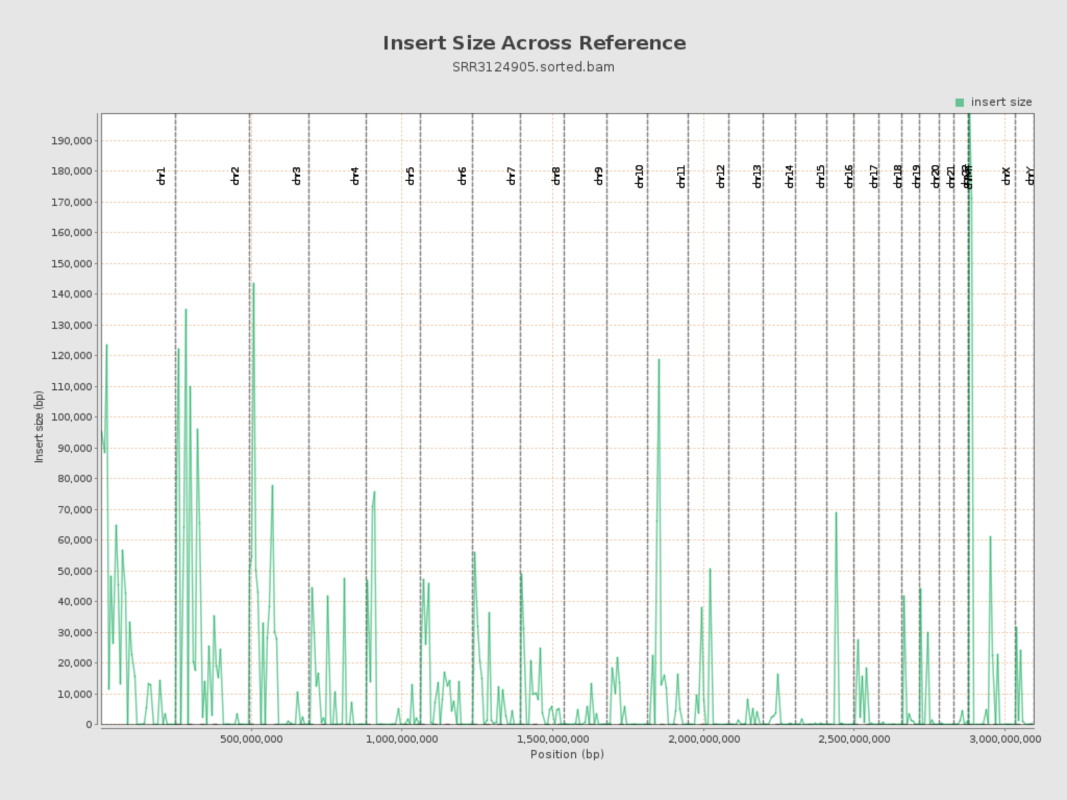
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram