Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:15:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124942.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_SRR3124942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124942_1.fastq.gz SRR3124942_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:15:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,141,120
Mapped reads	5,097,637 / 99.15%
Unmapped reads	43,483 / 0.85%
Mapped paired reads	5,097,637 / 99.15%
Mapped reads, first in pair	2,551,335 / 49.63%
Mapped reads, second in pair	2,546,302 / 49.53%
Mapped reads, both in pair	5,080,282 / 98.82%
Mapped reads, singletons	17,355 / 0.34%
Secondary alignments	0
Supplementary alignments	32,231 / 0.63%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	338,607 / 6.59%
Duplication rate	4.43%
Clipped reads	2,237,998 / 43.53%

2.2. ACGT Content

Number/percentage of A's	129,336,356 / 28.44%
Number/percentage of C's	86,866,927 / 19.1%
Number/percentage of T's	135,224,708 / 29.74%
Number/percentage of G's	103,310,459 / 22.72%
Number/percentage of N's	6,713 / 0%

GC Percentage	41.82%

2.3. Coverage

Mean	0.147
Standard Deviation	1.3632

2.4. Mapping Quality

Mean Mapping Quality	53.22

2.5. Insert size

Mean	60,672.04
Standard Deviation	2,309,398.98
P25/Median/P75	147 / 192 / 261

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	3,308,779
Insertions	57,466
Mapped reads with at least one insertion	1.1%
Deletions	140,985
Mapped reads with at least one deletion	2.71%
Homopolymer indels	47.28%

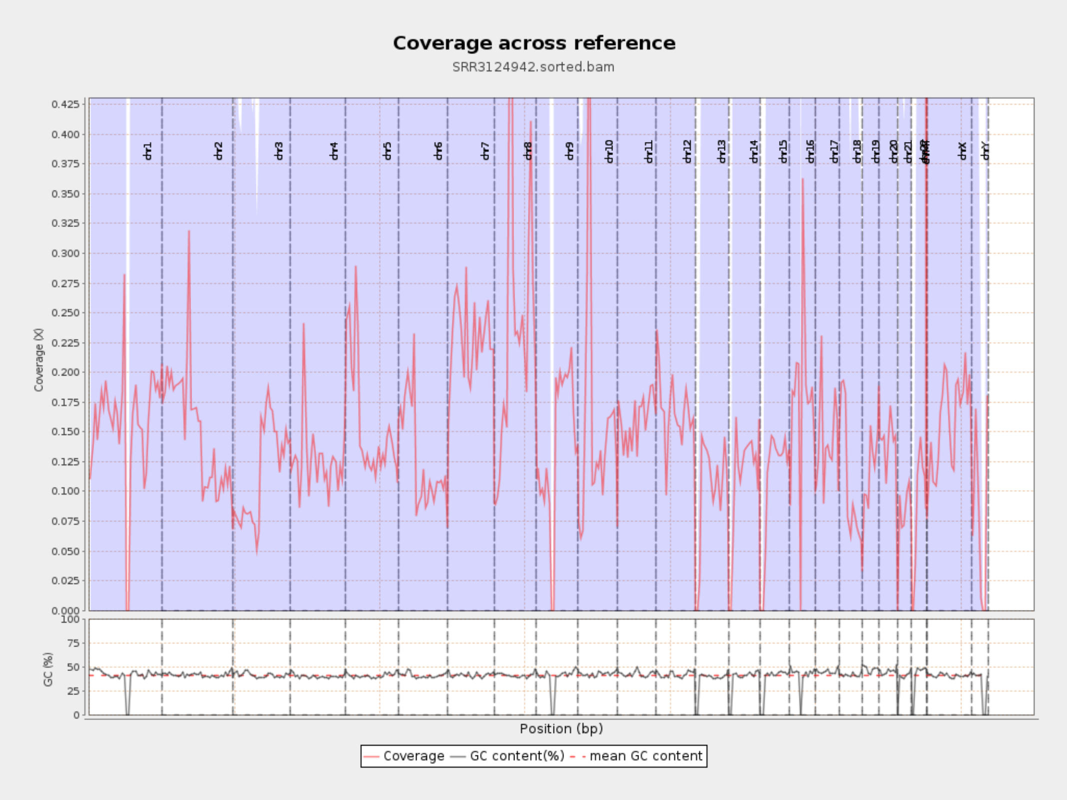
2.7. Chromosome stats

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

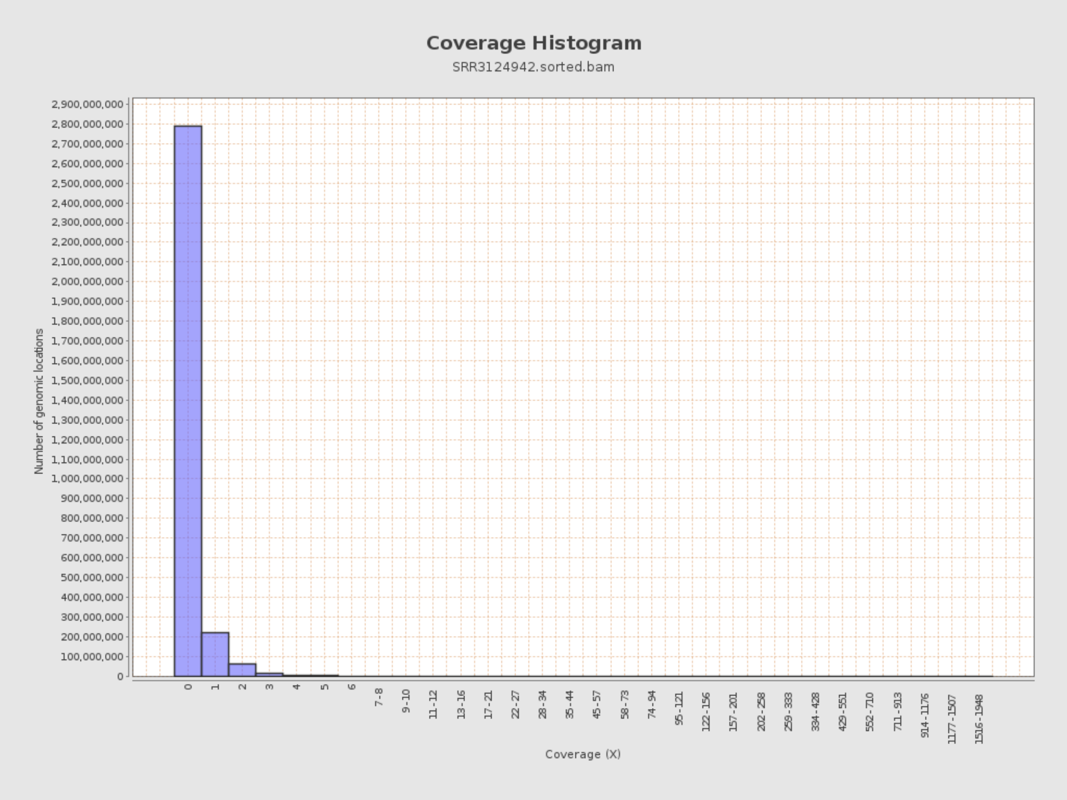
		bases	coverage	deviation
chr1	249250621	38937030	0.1562	1.8742
chr2	243199373	37413718	0.1538	1.2496
chr3	198022430	22816752	0.1152	0.4724
chr4	191154276	23867327	0.1249	0.923
chr5	180915260	28396302	0.157	0.5433
chr6	171115067	21931435	0.1282	0.8653
chr7	159138663	36694310	0.2306	2.1263
chr8	146364022	36436903	0.2489	0.9979
chr9	141213431	19626242	0.139	1.5681
chr10	135534747	21502386	0.1586	3.3913
chr11	135006516	21386355	0.1584	0.9413
chr12	133851895	22420873	0.1675	0.5722
chr13	115169878	11473373	0.0996	0.4123
chr14	107349540	11628763	0.1083	0.4984
chr15	102531392	11067321	0.1079	0.4497
chr16	90354753	16055247	0.1777	1.6346
chr17	81195210	11449029	0.141	1.9898
chr18	78077248	8638730	0.1106	1.6369
chr19	59128983	7003875	0.1185	1.2285
chr20	63025520	8824417	0.14	0.6024
chr21	48129895	3866124	0.0803	0.5138
chr22	51304566	4285718	0.0835	0.4216
chrMT	16571	214638	12.9526	7.9033
chrX	155270560	24607487	0.1585	0.7599

chrY	59373566	4434544	0.0747	1.3152

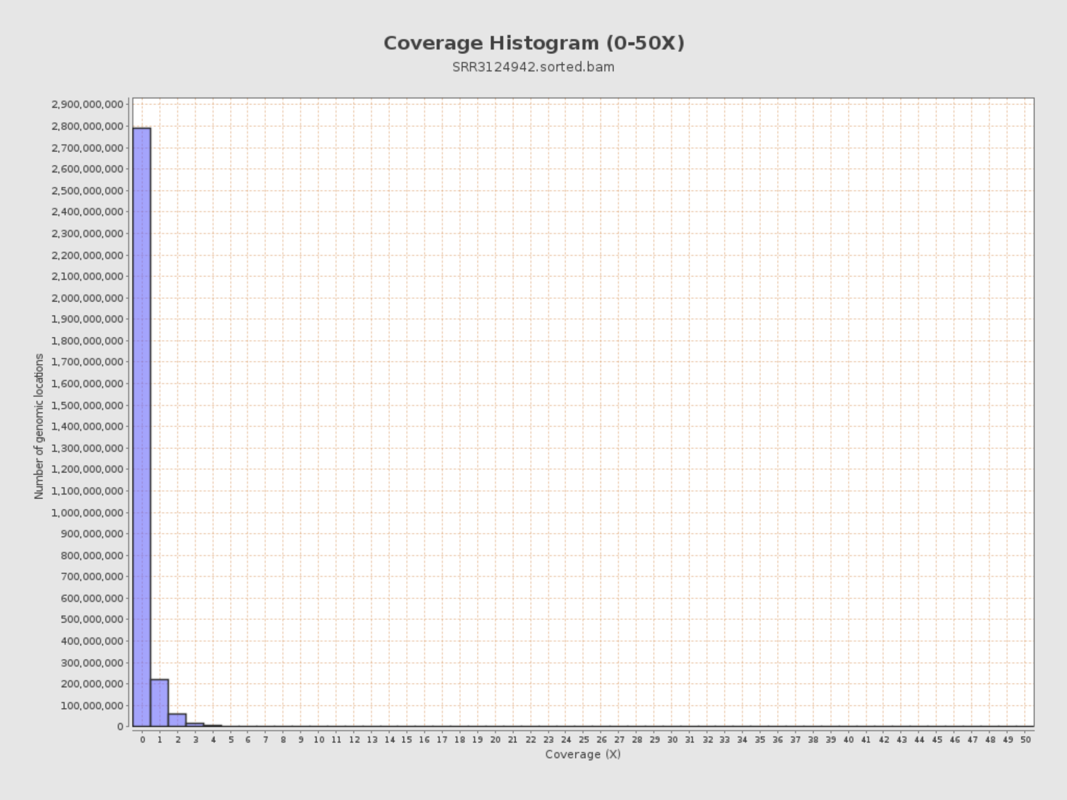
3. Results : Coverage across reference



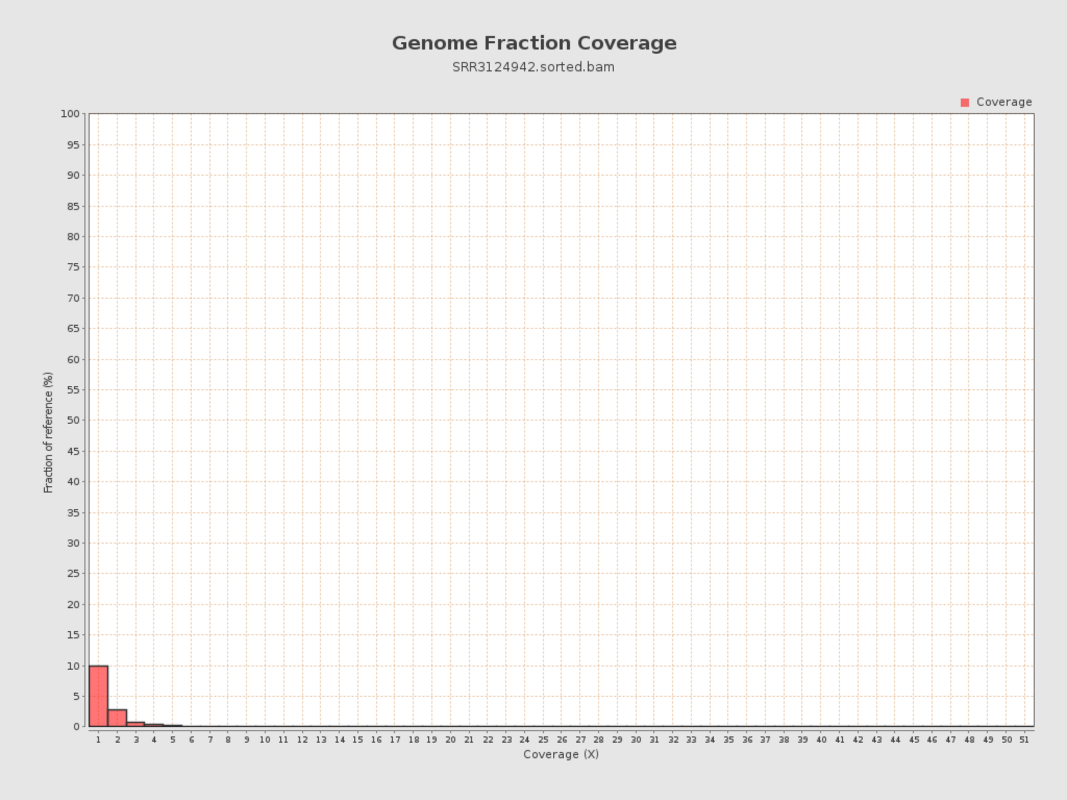
4. Results : Coverage Histogram



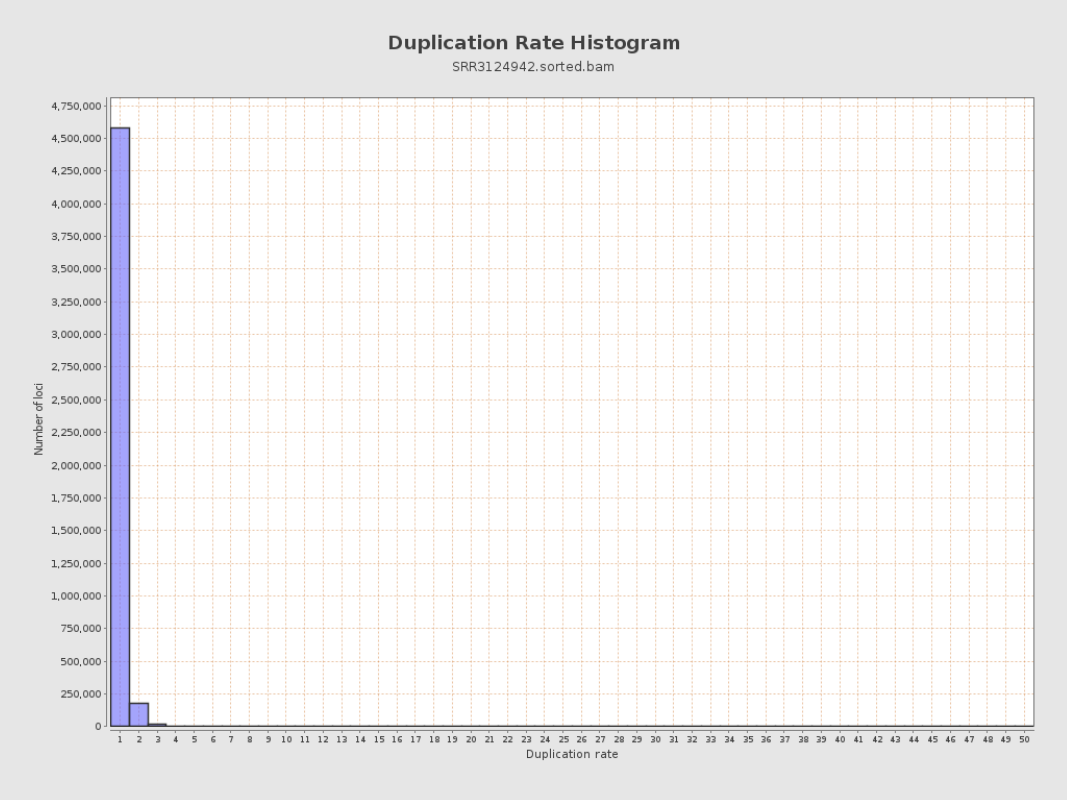
5. Results : Coverage Histogram (0-50X)



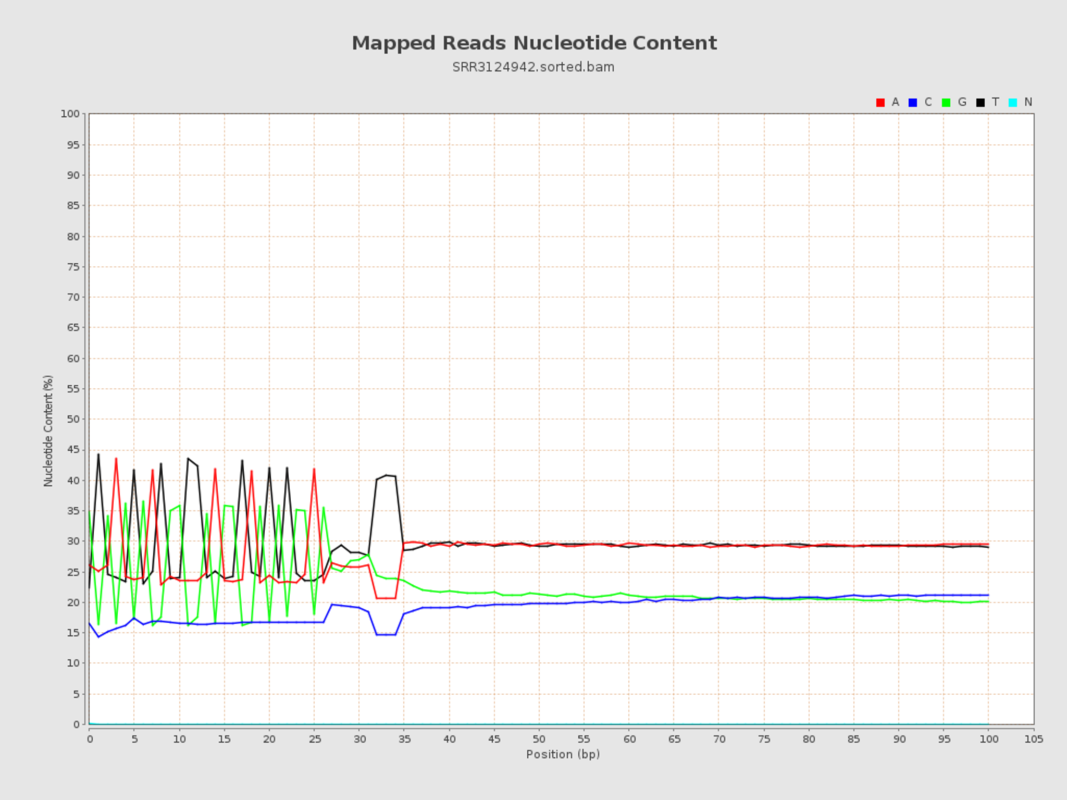
6. Results : Genome Fraction Coverage



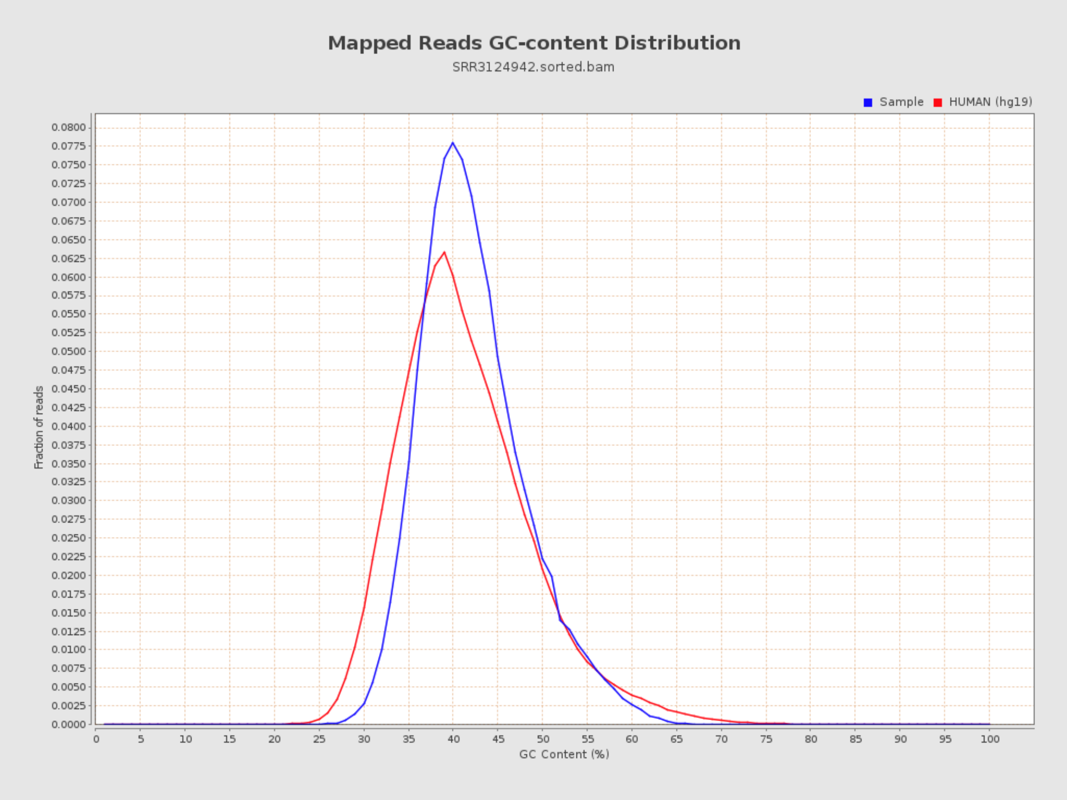
7. Results : Duplication Rate Histogram



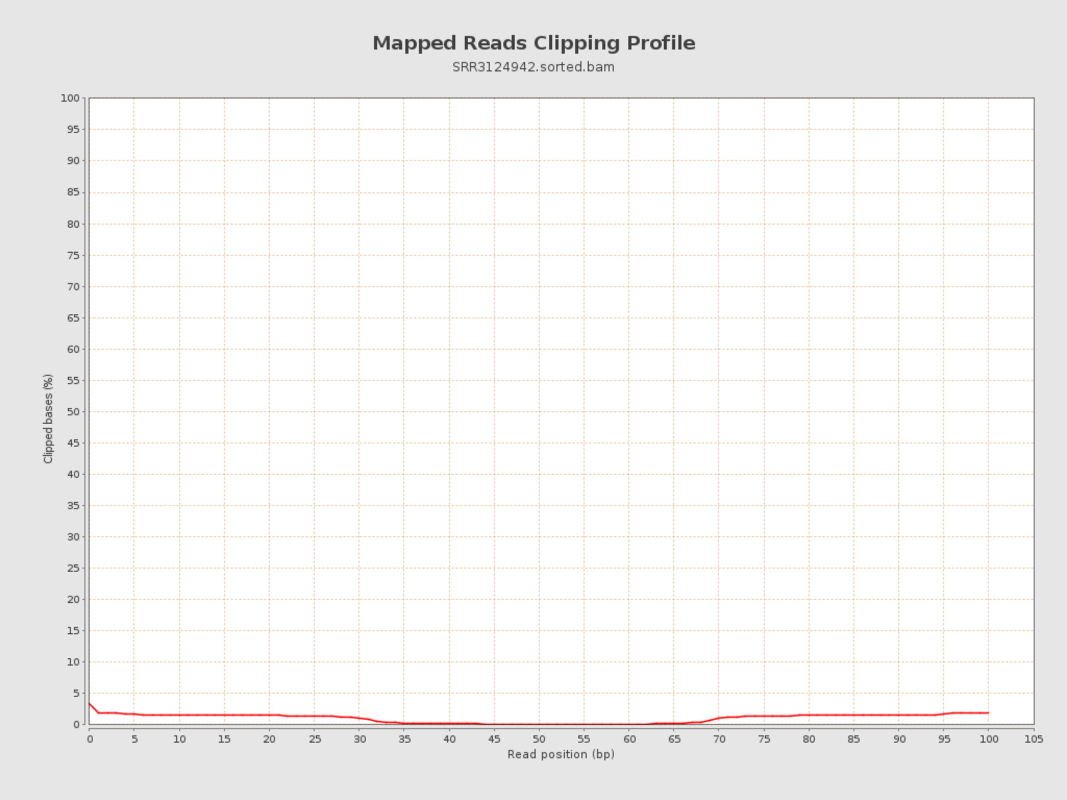
8. Results : Mapped Reads Nucleotide Content



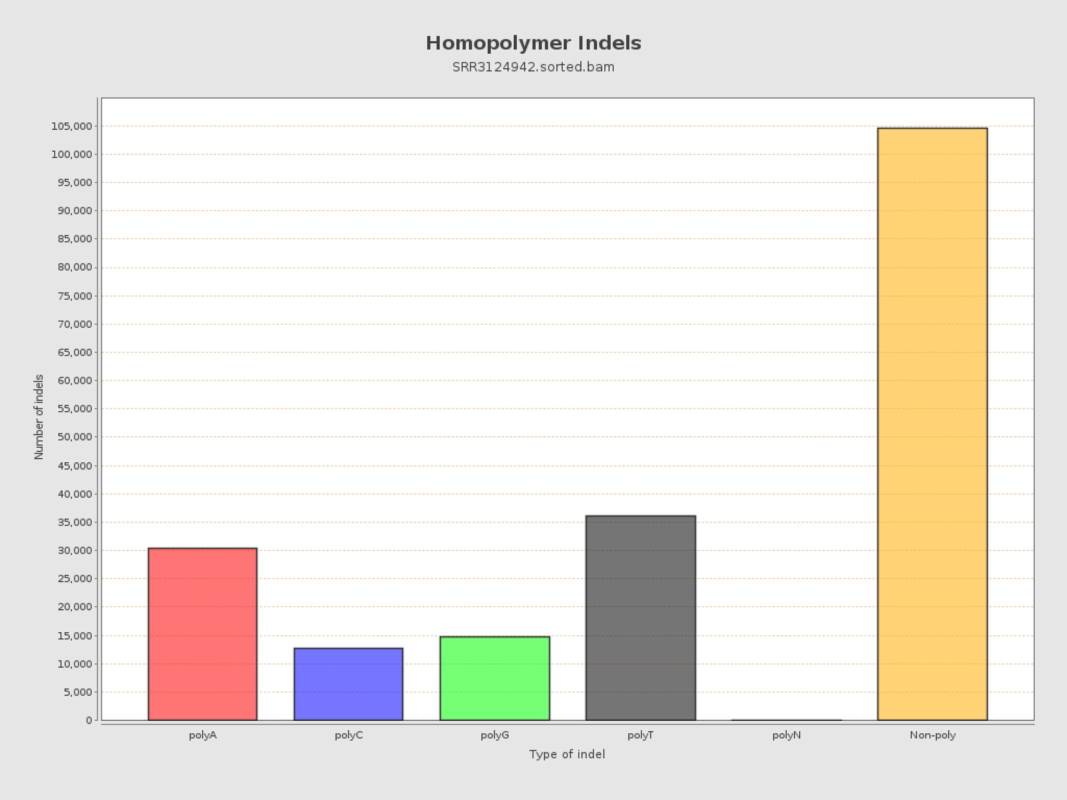
9. Results : Mapped Reads GC-content Distribution



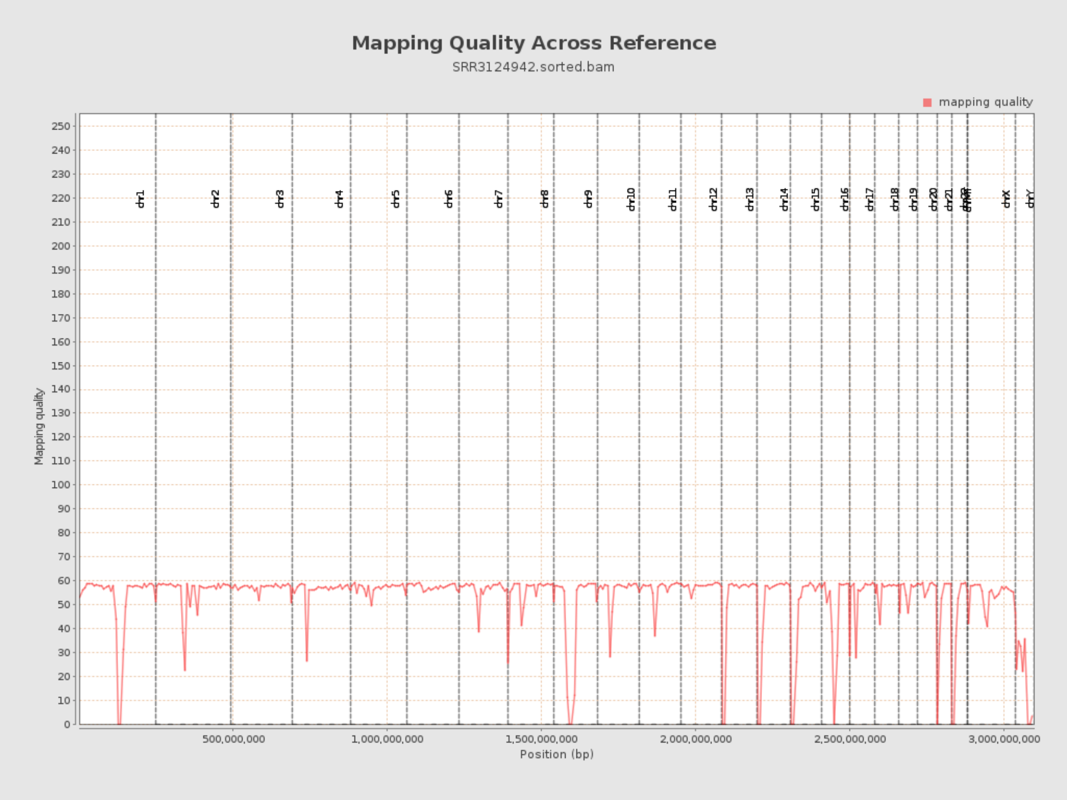
10. Results : Mapped Reads Clipping Profile



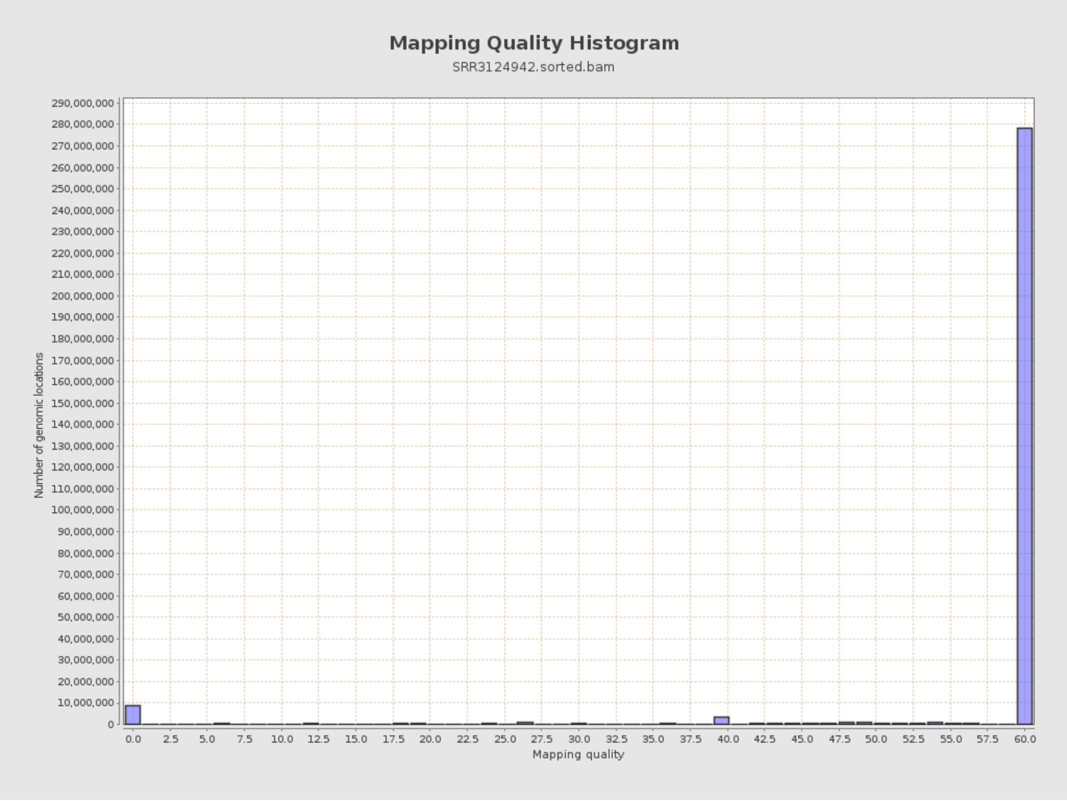
11. Results : Homopolymer Indels



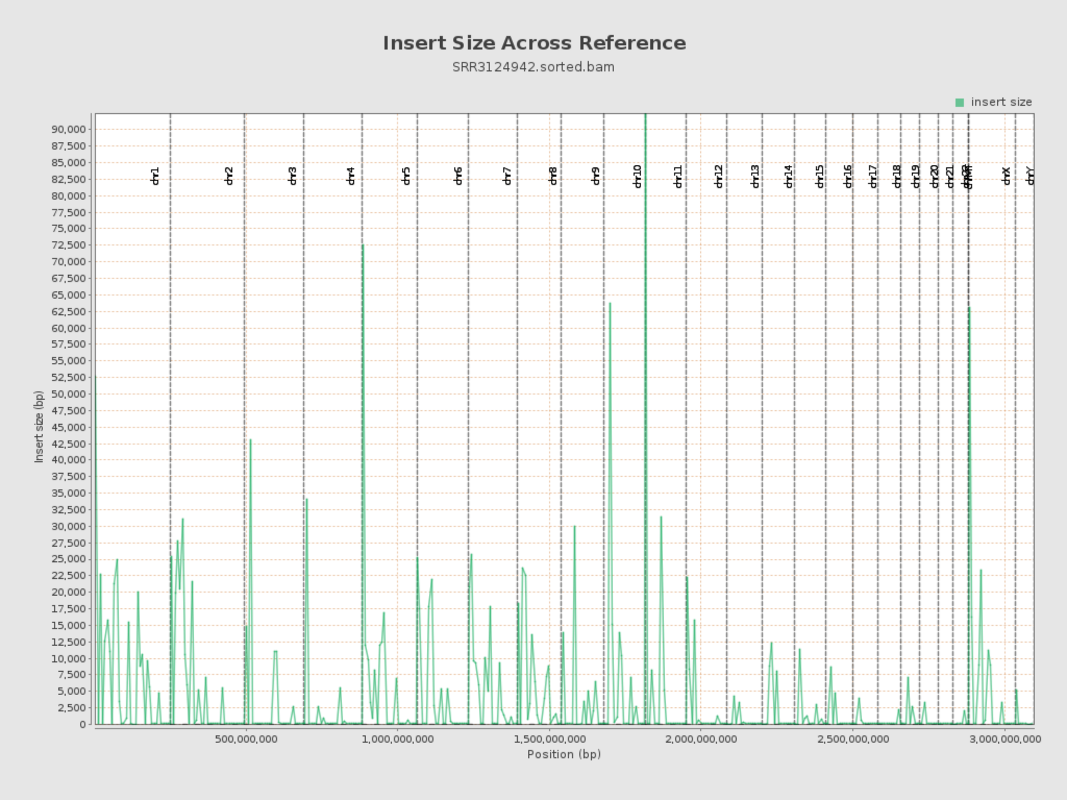
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram