Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:31:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124944.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_SRR3124944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124944_1.fastq.gz SRR3124944_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:31:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,531,598
Mapped reads	4,396,442 / 97.02%
Unmapped reads	135,156 / 2.98%
Mapped paired reads	4,396,442 / 97.02%
Mapped reads, first in pair	2,225,418 / 49.11%
Mapped reads, second in pair	2,171,024 / 47.91%
Mapped reads, both in pair	4,326,886 / 95.48%
Mapped reads, singletons	69,556 / 1.53%
Secondary alignments	0
Supplementary alignments	5,879 / 0.13%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	222,197 / 4.9%
Duplication rate	3.59%
Clipped reads	2,024,004 / 44.66%

2.2. ACGT Content

Number/percentage of A's	74,283,002 / 27.19%
Number/percentage of C's	49,578,066 / 18.15%
Number/percentage of T's	80,296,761 / 29.39%
Number/percentage of G's	69,027,223 / 25.27%
Number/percentage of N's	2,339 / 0%

GC Percentage	43.42%

2.3. Coverage

Mean	0.0883
Standard Deviation	0.6375

2.4. Mapping Quality

Mean Mapping Quality	51.91

2.5. Insert size

Mean	31,147.29
Standard Deviation	1,656,087.38
P25/Median/P75	144 / 193 / 267

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	1,780,734
Insertions	29,704
Mapped reads with at least one insertion	0.67%
Deletions	78,763
Mapped reads with at least one deletion	1.77%
Homopolymer indels	47.7%

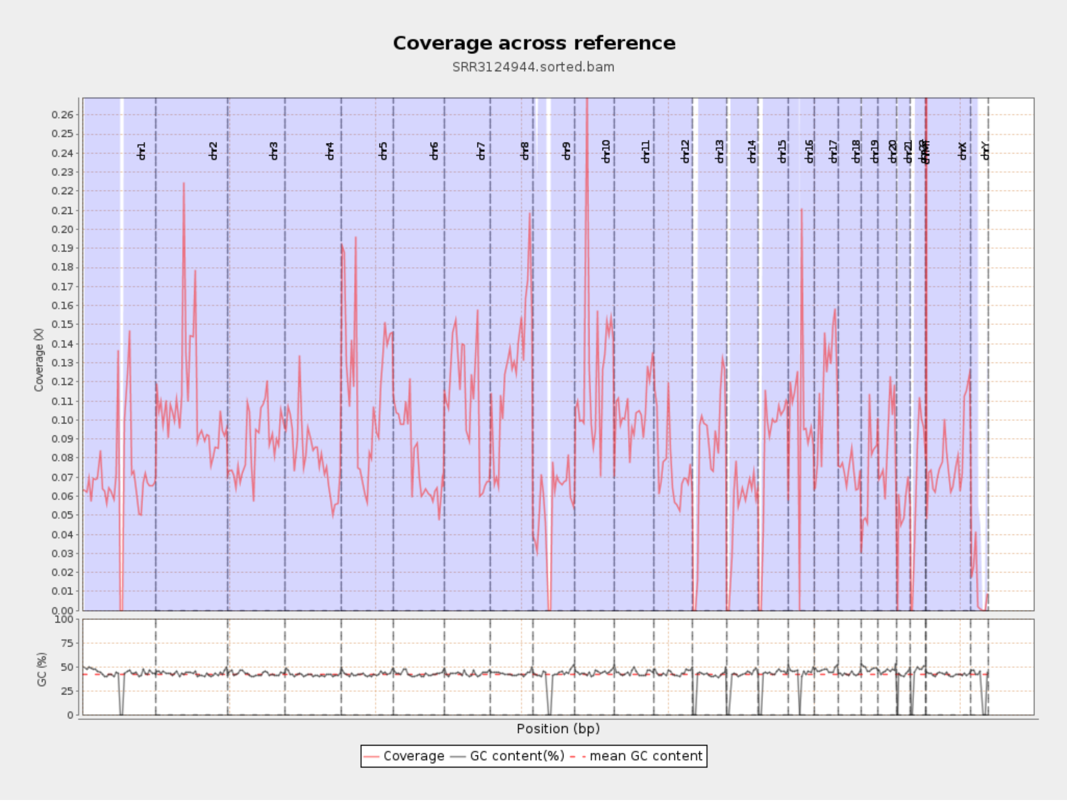
2.7. Chromosome stats

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

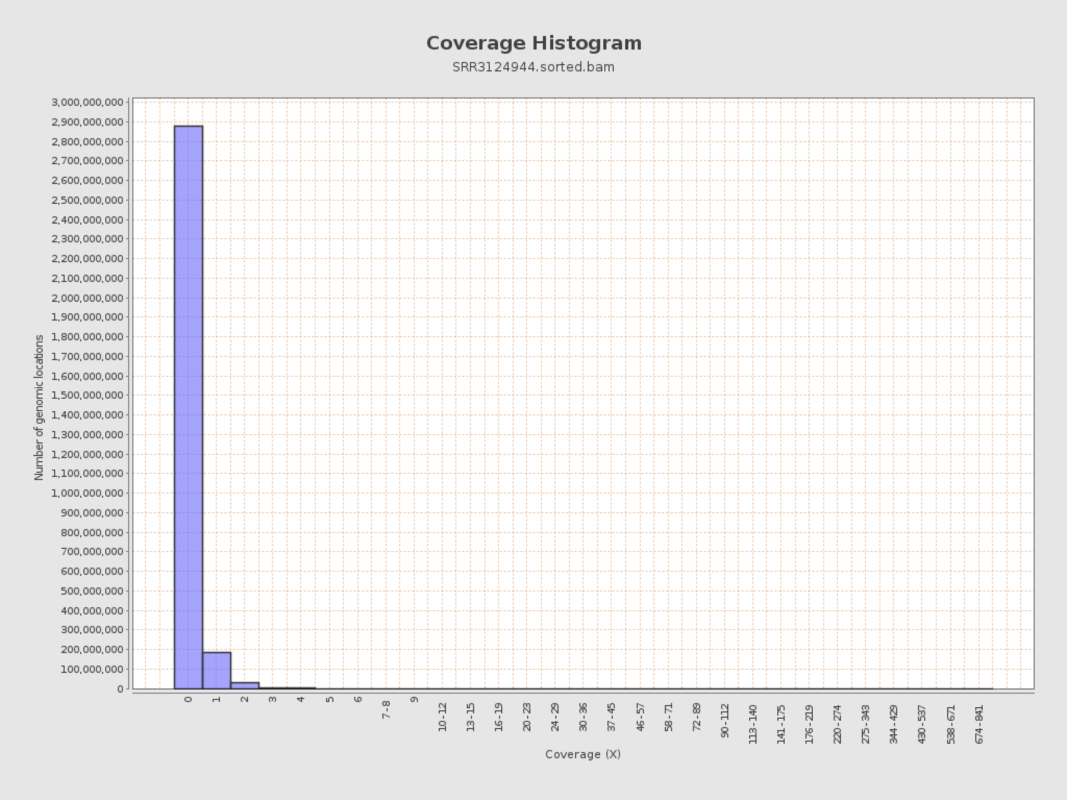
		bases	coverage	deviation
chr1	249250621	17169128	0.0689	0.605
chr2	243199373	26311392	0.1082	0.9371
chr3	198022430	17372141	0.0877	0.3464
chr4	191154276	15712750	0.0822	0.4285
chr5	180915260	21171388	0.117	0.4207
chr6	171115067	13498559	0.0789	0.4767
chr7	159138663	17557902	0.1103	0.9156
chr8	146364022	18687111	0.1277	0.4687
chr9	141213431	7618314	0.0539	0.4913
chr10	135534747	17139560	0.1265	1.4004
chr11	135006516	14099861	0.1044	0.4804
chr12	133851895	10092564	0.0754	0.3267
chr13	115169878	9444070	0.082	0.3363
chr14	107349540	5735105	0.0534	0.3062
chr15	102531392	8610329	0.084	0.3466
chr16	90354753	9141141	0.1012	1.0436
chr17	81195210	9579366	0.118	0.7251
chr18	78077248	5653678	0.0724	0.7611
chr19	59128983	4234322	0.0716	0.5407
chr20	63025520	5515359	0.0875	0.4128
chr21	48129895	2487275	0.0517	0.339
chr22	51304566	3457719	0.0674	0.3249
chrMT	16571	50852	3.0687	2.778
chrX	155270560	12285476	0.0791	0.3863

chrY	59373566	682981	0.0115	0.6696

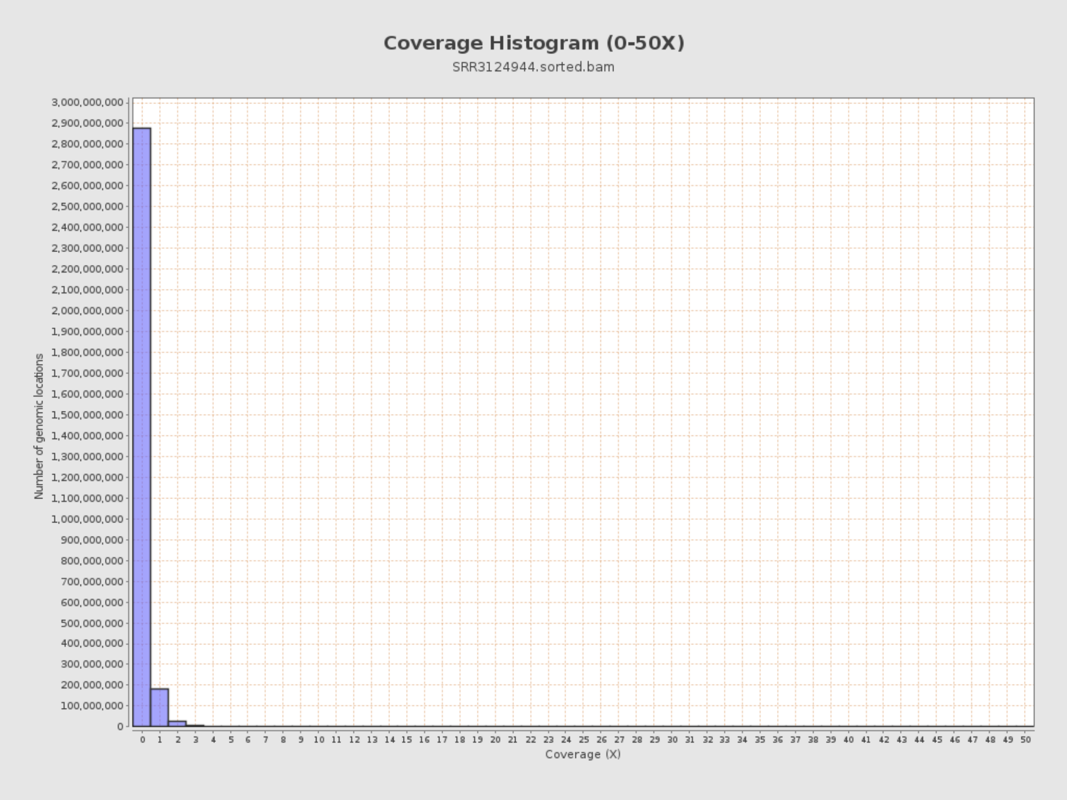
3. Results : Coverage across reference



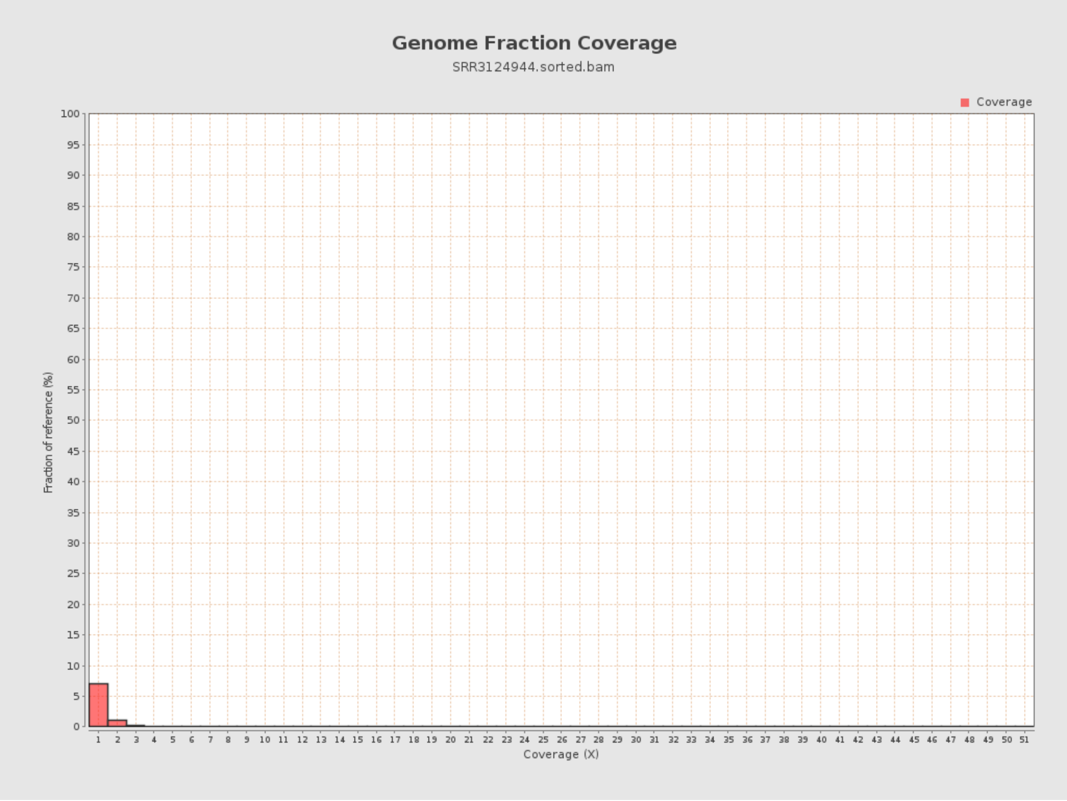
4. Results : Coverage Histogram



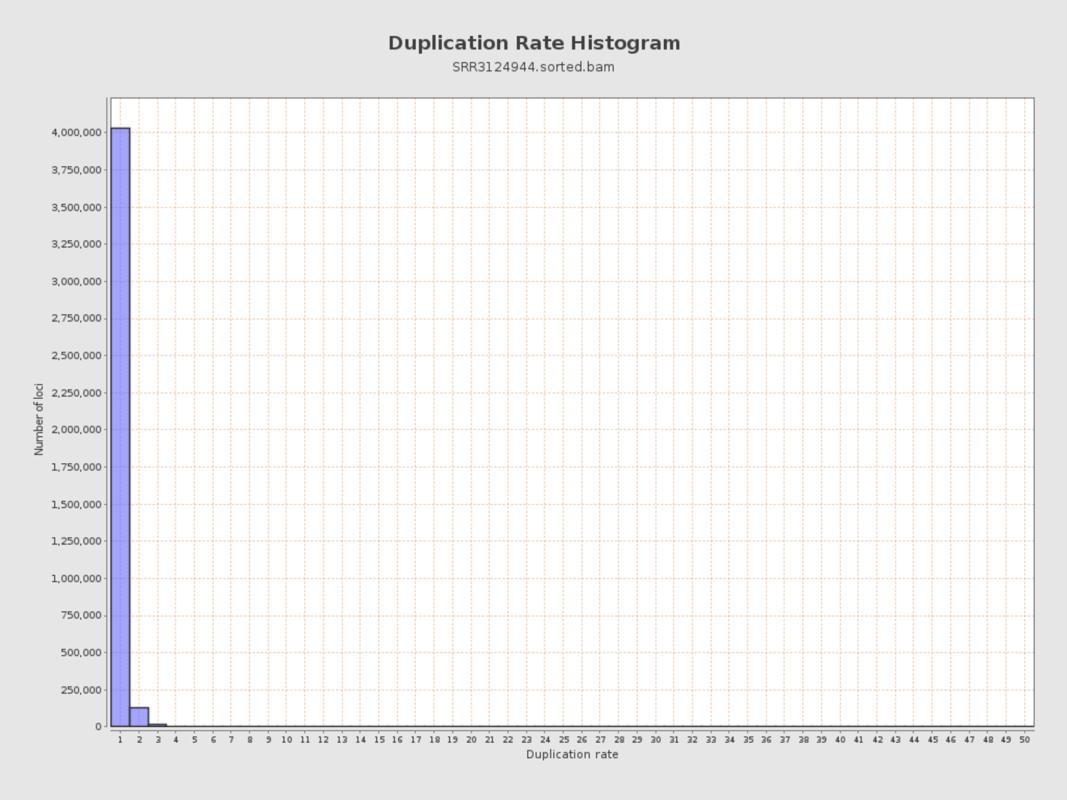
5. Results : Coverage Histogram (0-50X)



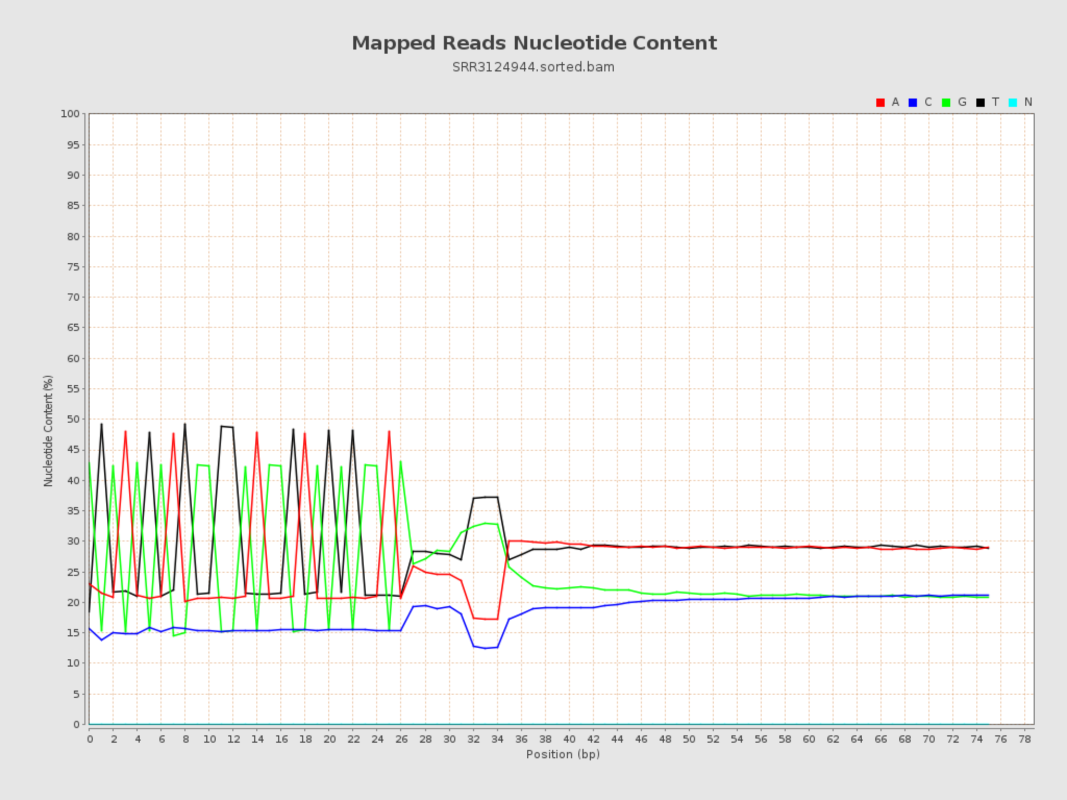
6. Results : Genome Fraction Coverage



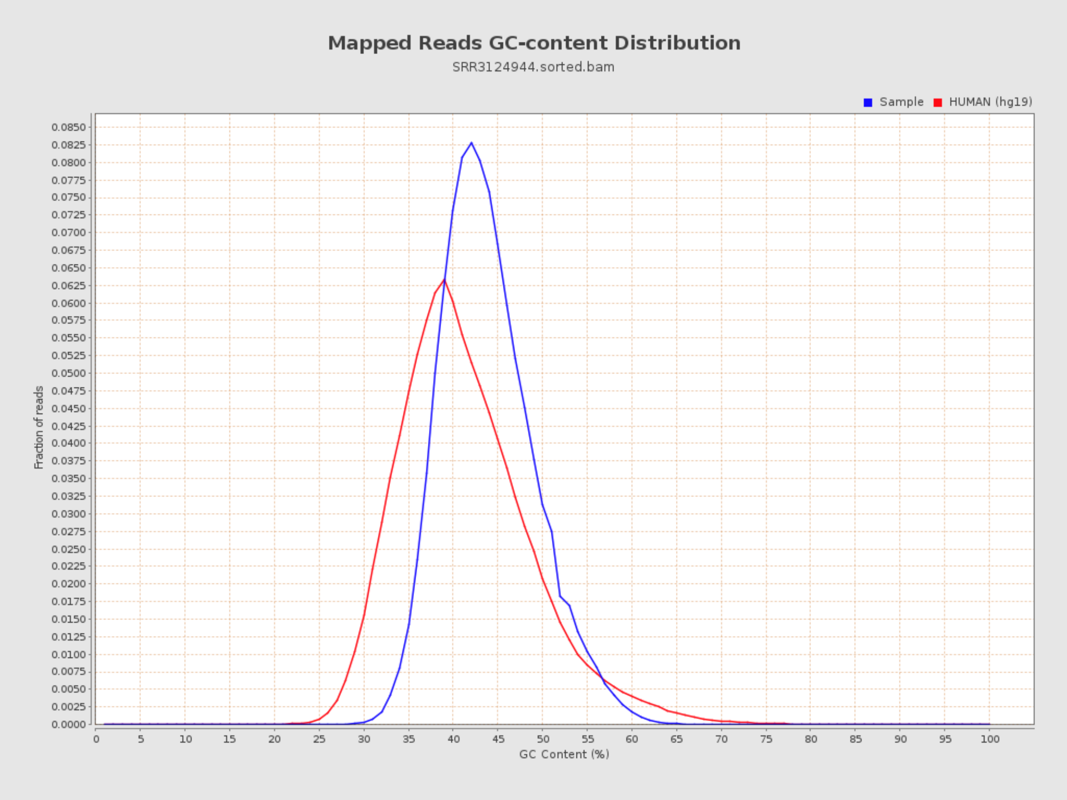
7. Results : Duplication Rate Histogram



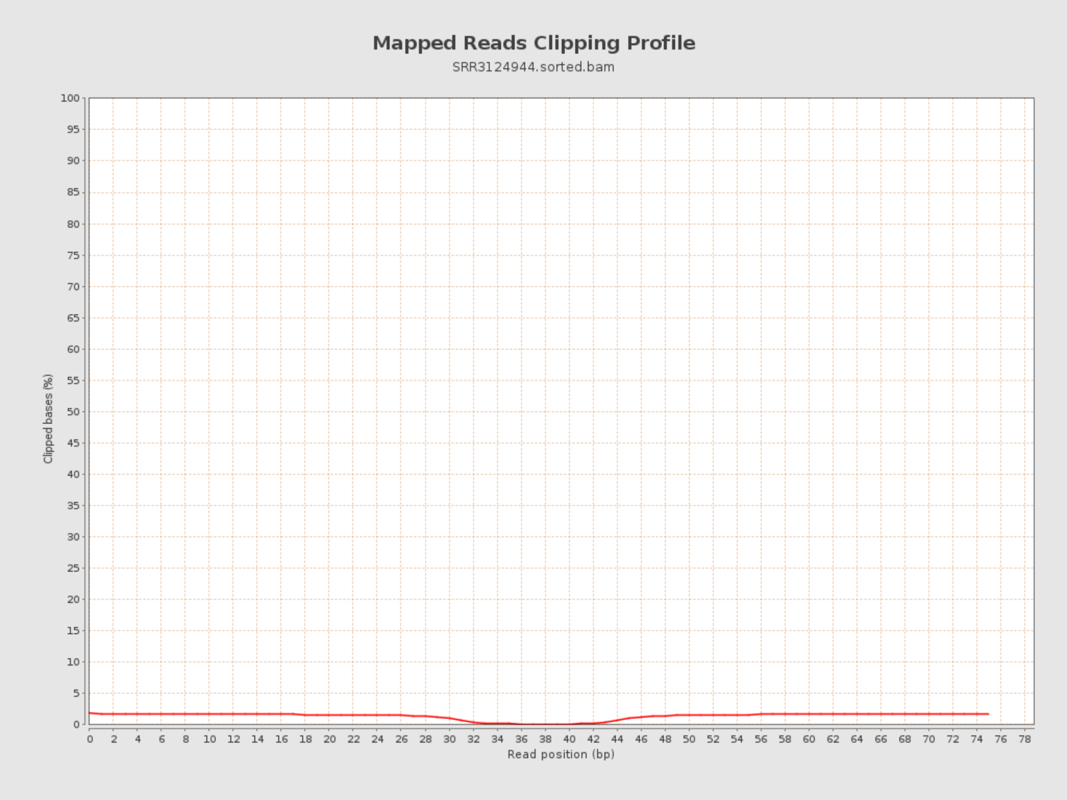
8. Results : Mapped Reads Nucleotide Content



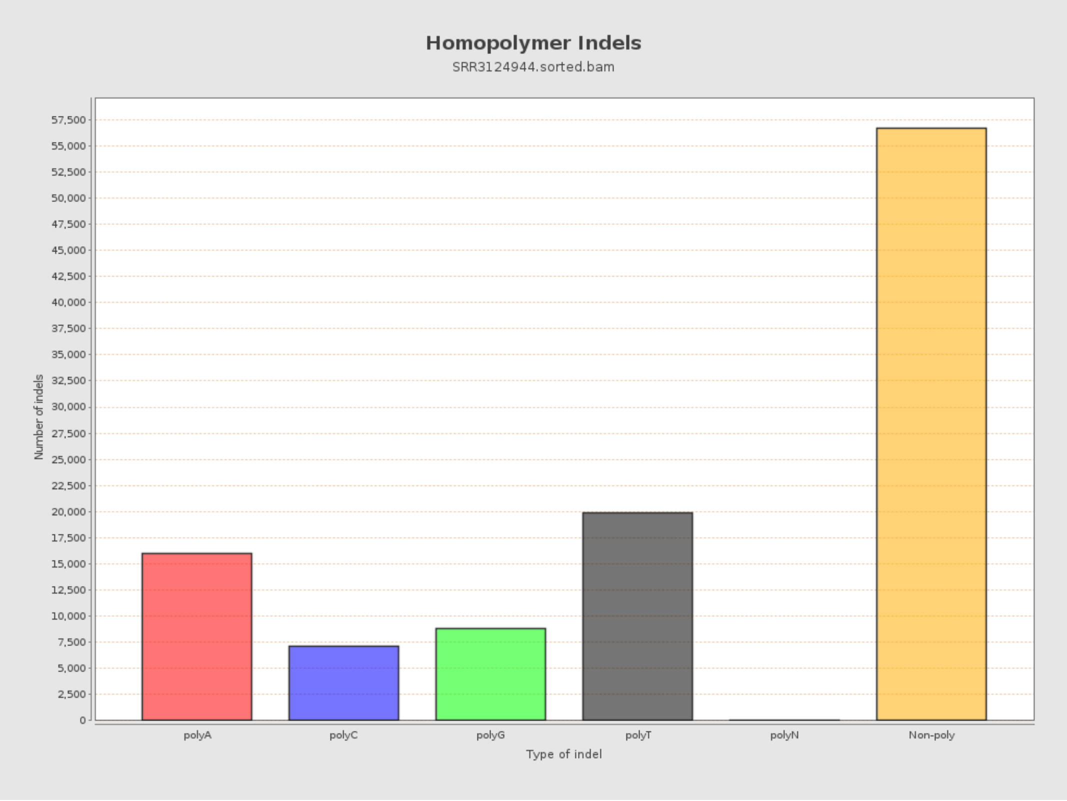
9. Results : Mapped Reads GC-content Distribution



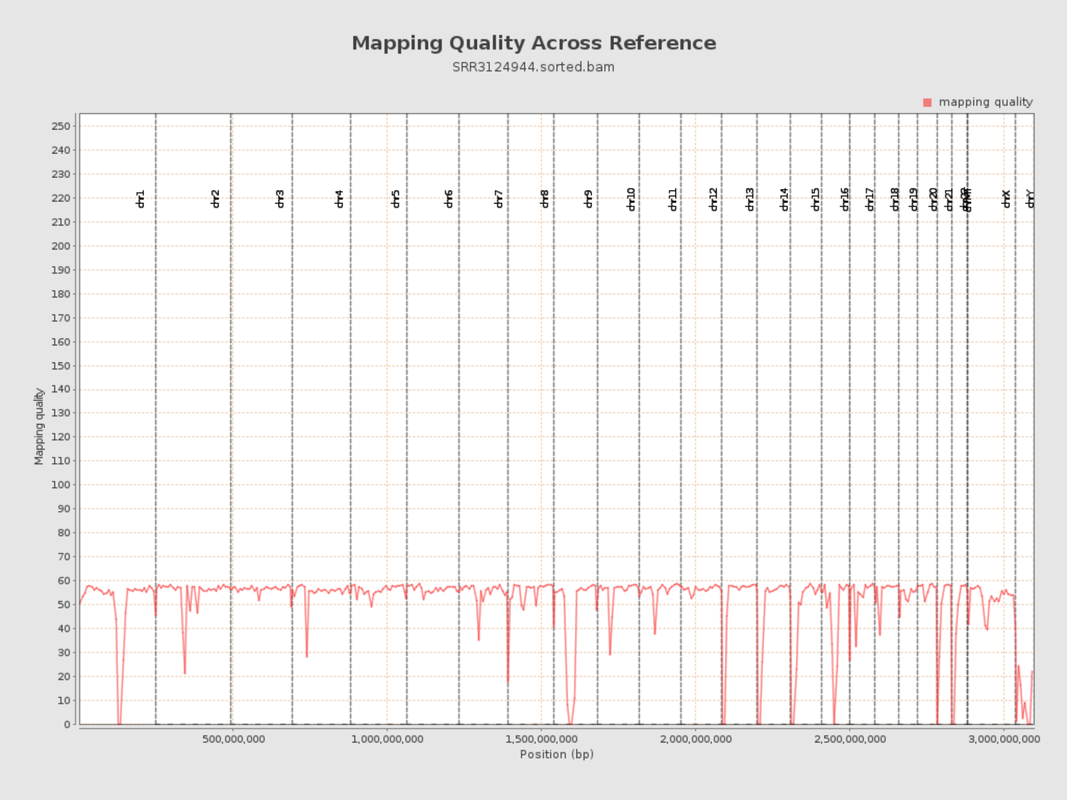
10. Results : Mapped Reads Clipping Profile



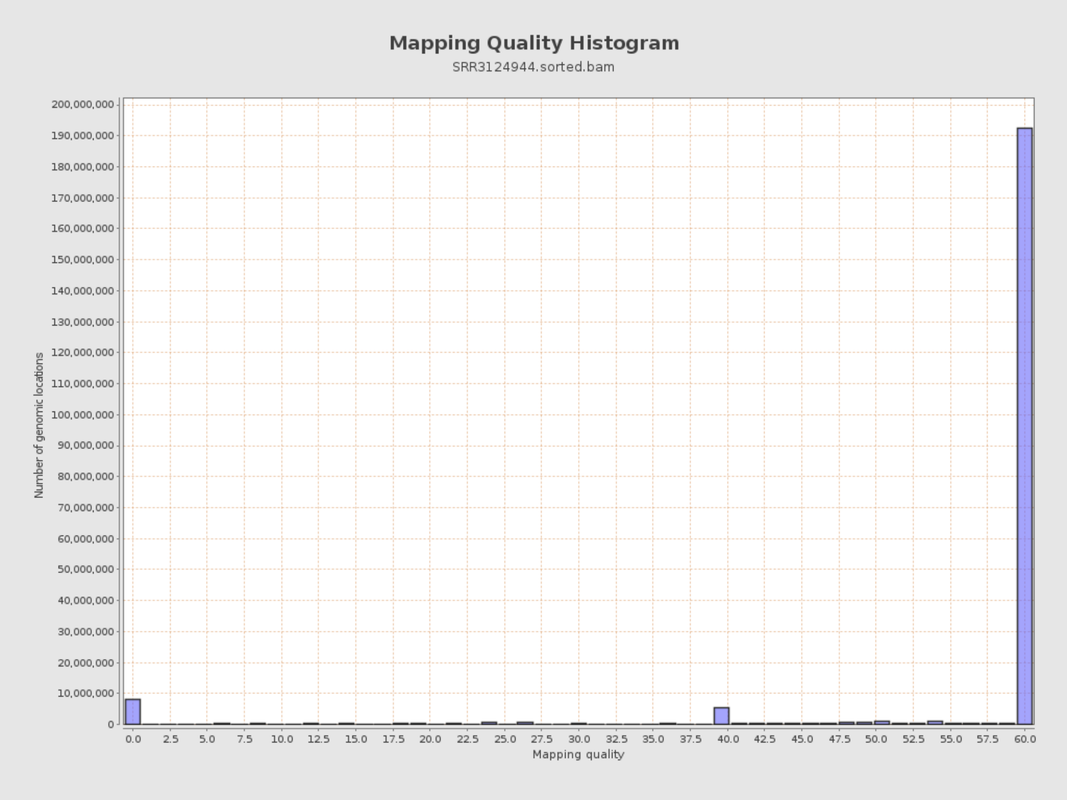
11. Results : Homopolymer Indels



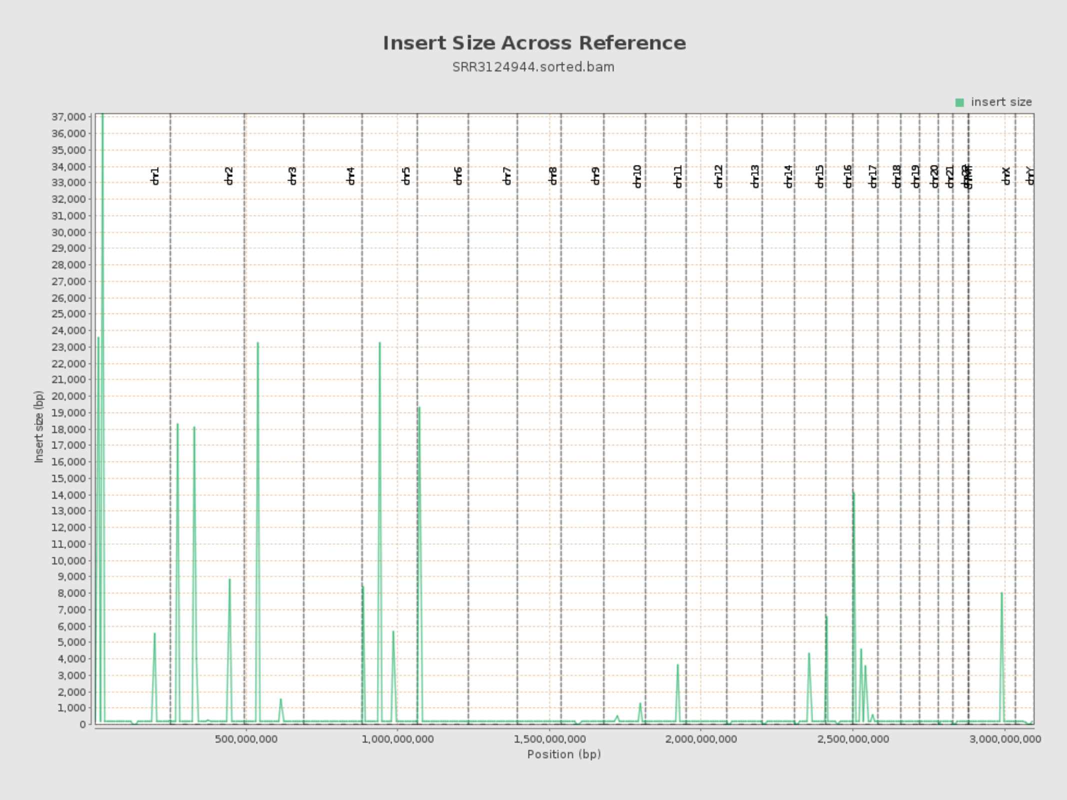
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram