Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:16:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124976.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_SRR3124976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124976_1.fastq.gz SRR3124976_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:16:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,887,262
Mapped reads	2,724,390 / 94.36%
Unmapped reads	162,872 / 5.64%
Mapped paired reads	2,724,390 / 94.36%
Mapped reads, first in pair	1,385,392 / 47.98%
Mapped reads, second in pair	1,338,998 / 46.38%
Mapped reads, both in pair	2,662,242 / 92.21%
Mapped reads, singletons	62,148 / 2.15%
Secondary alignments	0
Supplementary alignments	9,613 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	168,499 / 5.84%
Duplication rate	4.19%
Clipped reads	1,429,971 / 49.53%

2.2. ACGT Content

Number/percentage of A's	46,648,162 / 28.06%
Number/percentage of C's	29,338,307 / 17.65%
Number/percentage of T's	50,028,981 / 30.09%
Number/percentage of G's	40,246,786 / 24.21%
Number/percentage of N's	0 / 0%

GC Percentage	41.85%

2.3. Coverage

Mean	0.0537
Standard Deviation	0.6091

2.4. Mapping Quality

Mean Mapping Quality	51.57

2.5. Insert size

Mean	71,119
Standard Deviation	2,490,242.59
P25/Median/P75	116 / 158 / 220

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	1,317,403
Insertions	21,180
Mapped reads with at least one insertion	0.77%
Deletions	51,467
Mapped reads with at least one deletion	1.87%
Homopolymer indels	46.27%

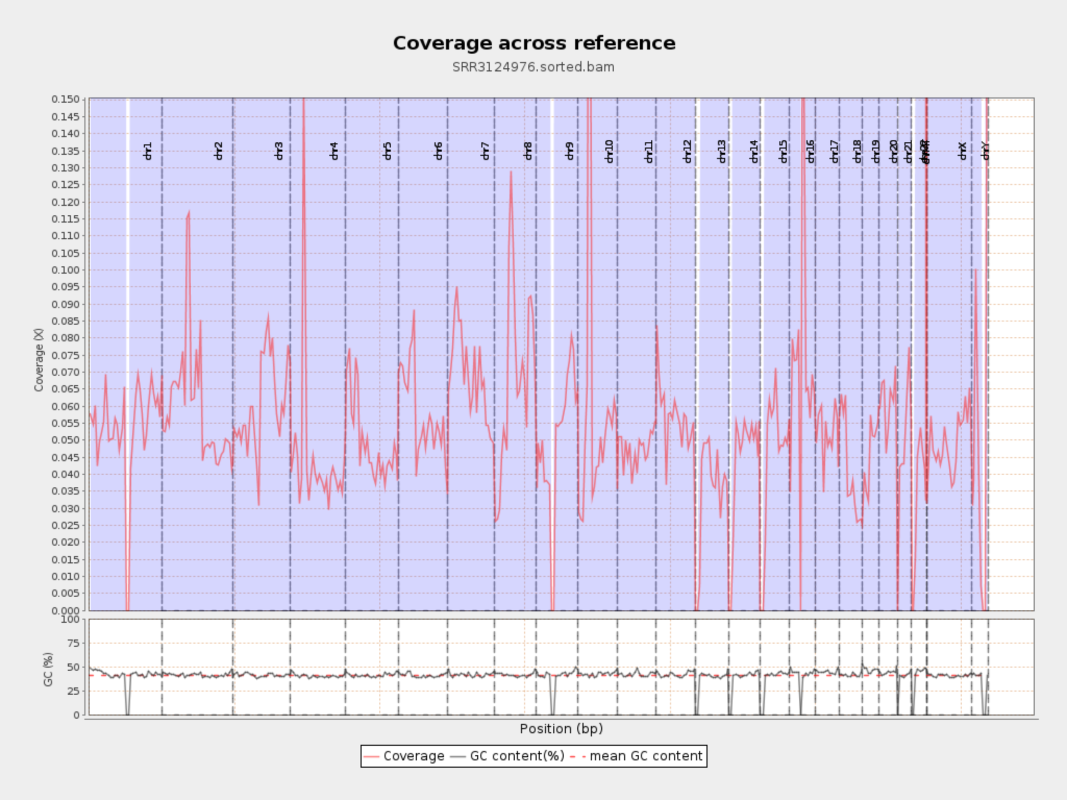
2.7. Chromosome stats

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

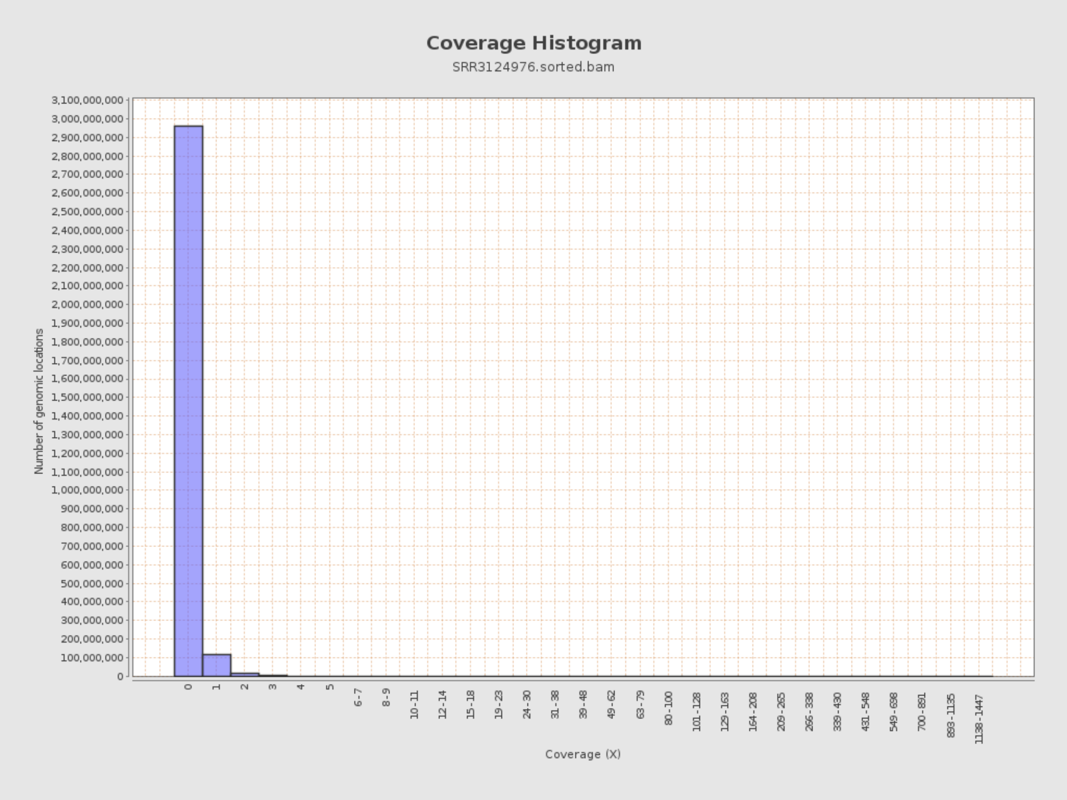
		bases	coverage	deviation
chr1	249250621	13178201	0.0529	0.4034
chr2	243199373	14722848	0.0605	0.6856
chr3	198022430	12010443	0.0607	0.3148
chr4	191154276	8414430	0.044	0.552
chr5	180915260	8992939	0.0497	0.262
chr6	171115067	10012089	0.0585	0.3214
chr7	159138663	11039803	0.0694	0.4886
chr8	146364022	10133680	0.0692	0.3388
chr9	141213431	7030313	0.0498	0.365
chr10	135534747	8194387	0.0605	1.9518
chr11	135006516	6377286	0.0472	0.2905
chr12	133851895	7608067	0.0568	0.2762
chr13	115169878	3945776	0.0343	0.2098
chr14	107349540	4577187	0.0426	0.2587
chr15	102531392	4554685	0.0444	0.2436
chr16	90354753	6720320	0.0744	1.0909
chr17	81195210	4205003	0.0518	0.3647
chr18	78077248	3224757	0.0413	0.4891
chr19	59128983	2693009	0.0455	0.3573
chr20	63025520	3823372	0.0607	0.3297
chr21	48129895	2358310	0.049	0.3643
chr22	51304566	1634156	0.0319	0.2274
chrMT	16571	126491	7.6333	5.2986
chrX	155270560	7623637	0.0491	0.2883

chrY	59373566	3142825	0.0529	1.1651

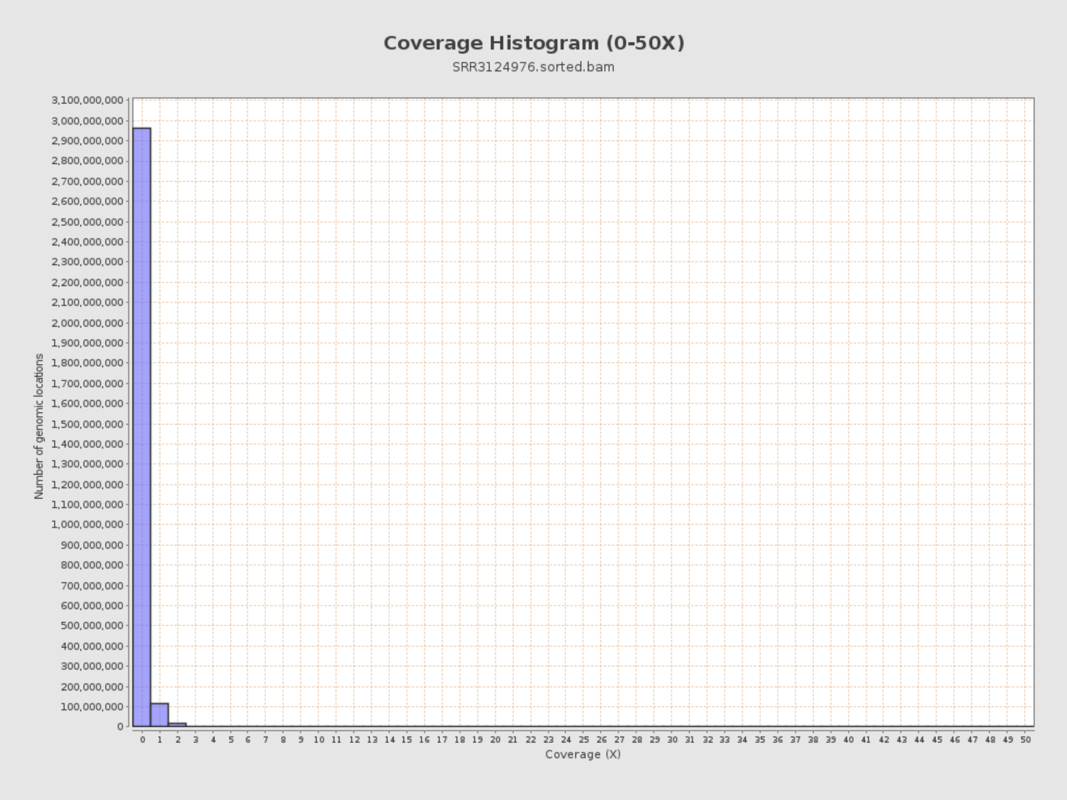
3. Results : Coverage across reference



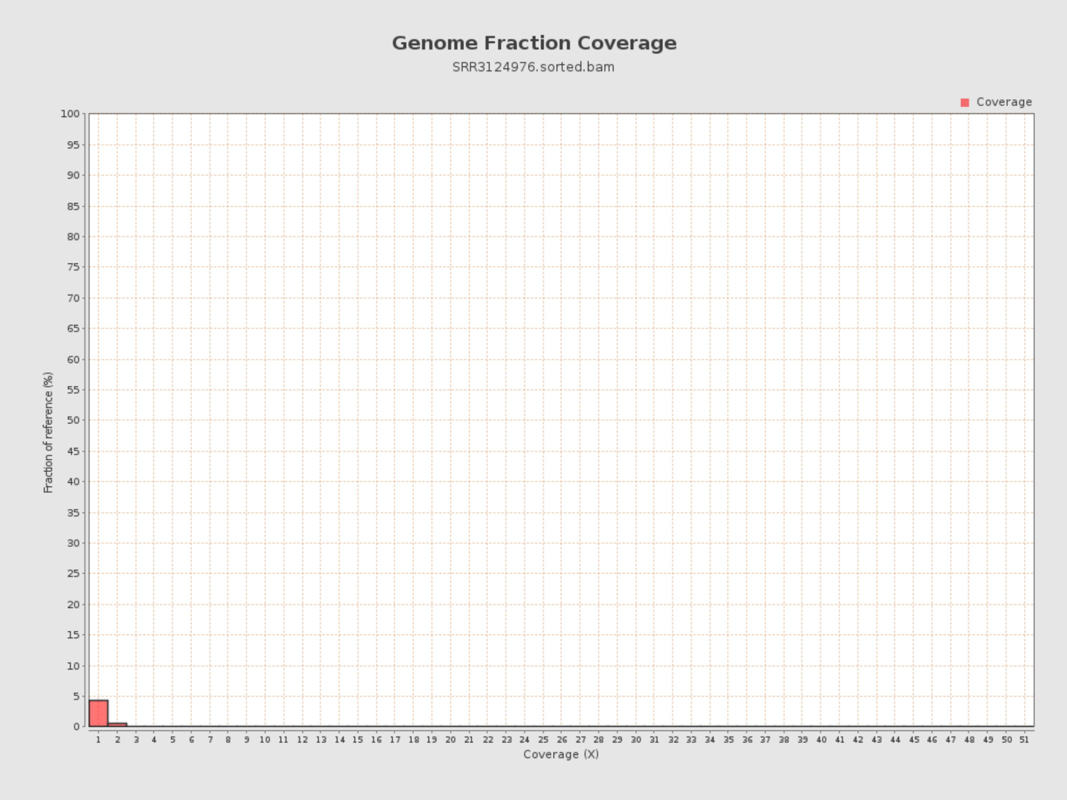
4. Results : Coverage Histogram



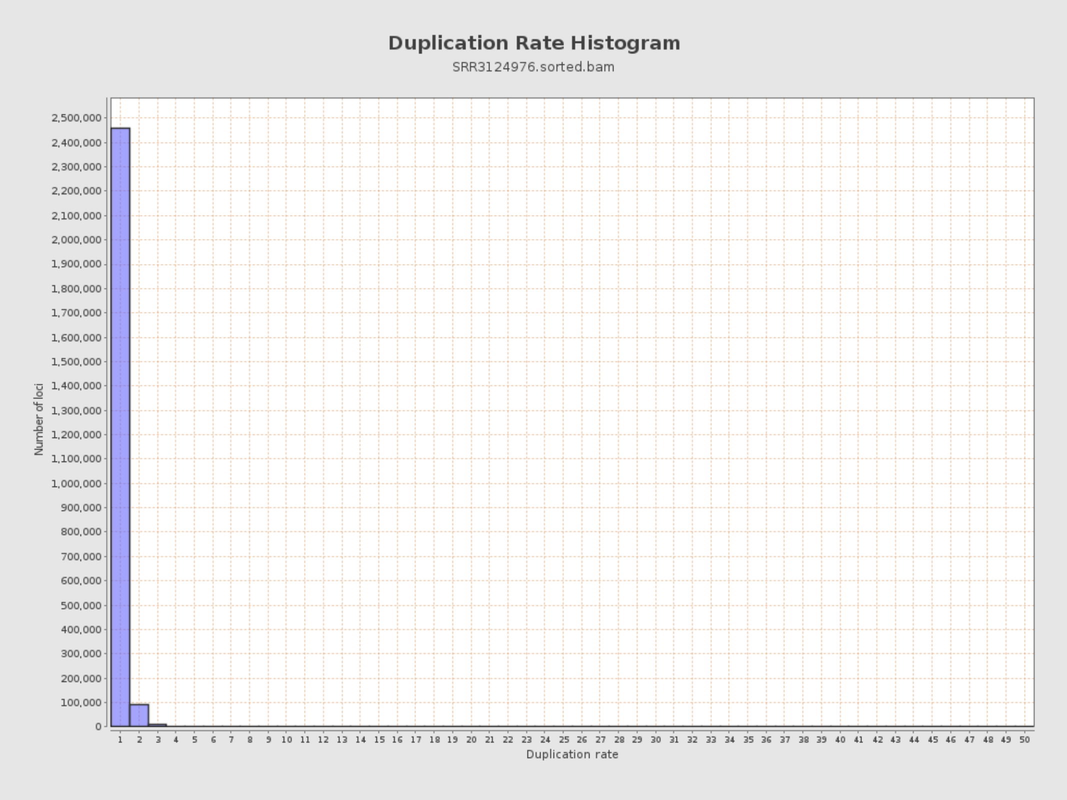
5. Results : Coverage Histogram (0-50X)



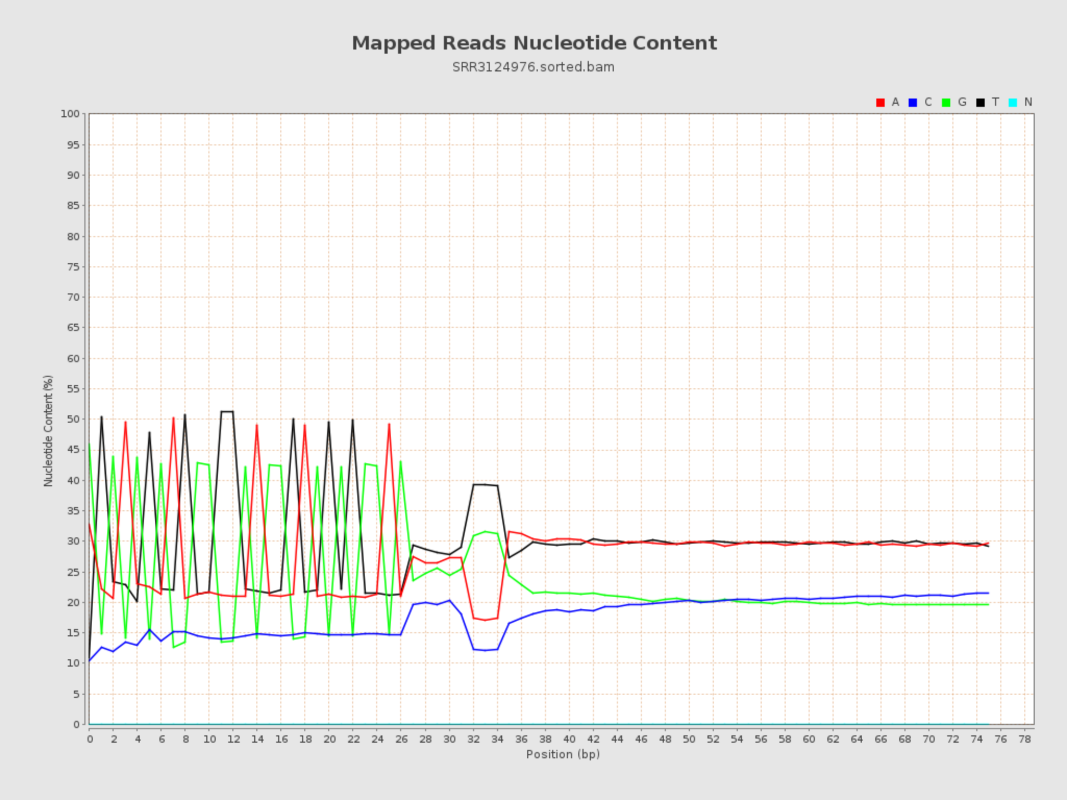
6. Results : Genome Fraction Coverage



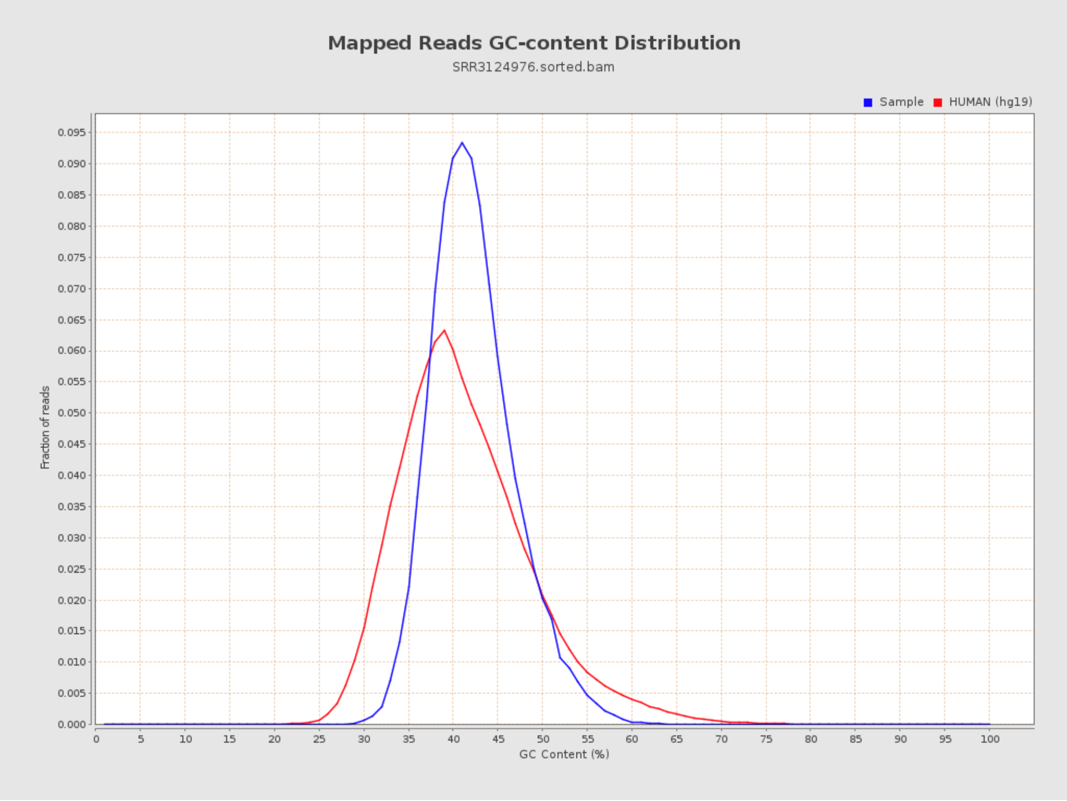
7. Results : Duplication Rate Histogram



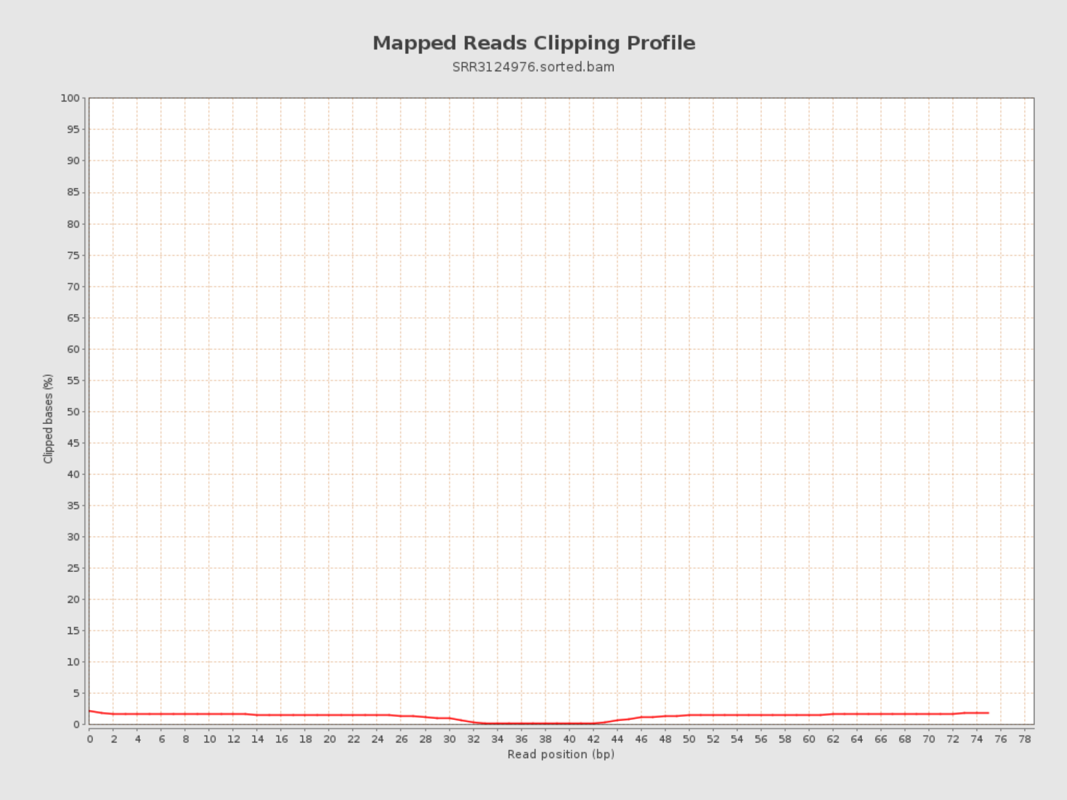
8. Results : Mapped Reads Nucleotide Content



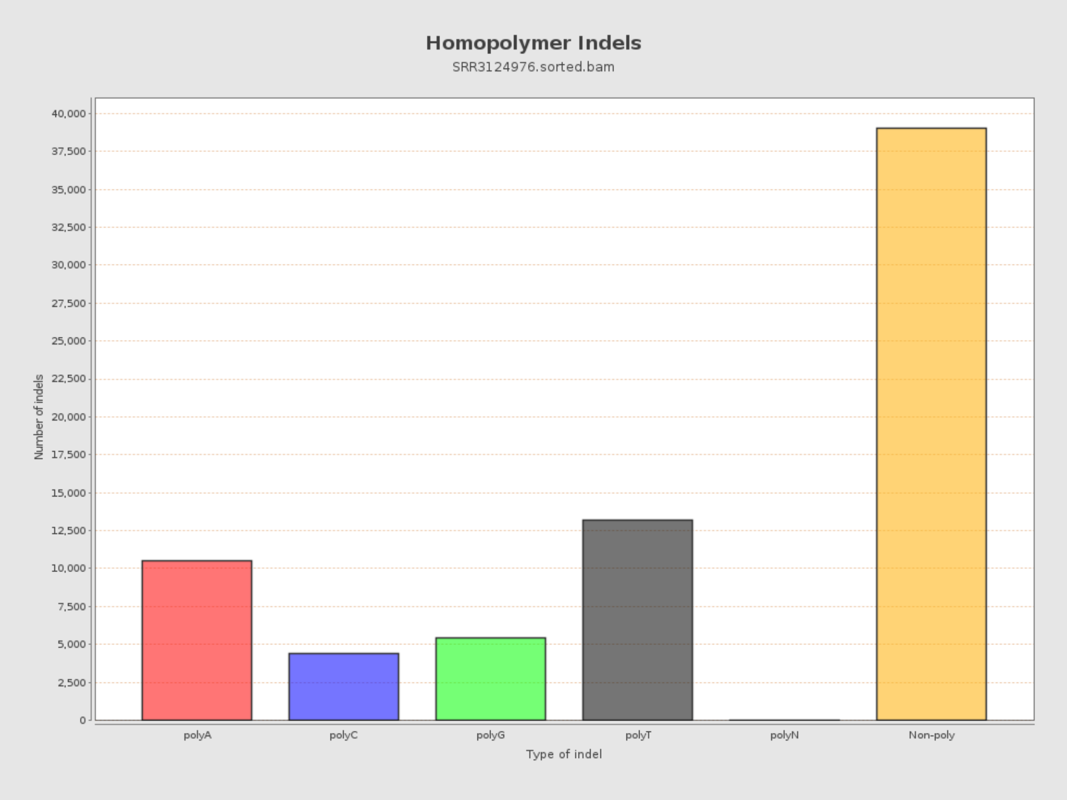
9. Results : Mapped Reads GC-content Distribution



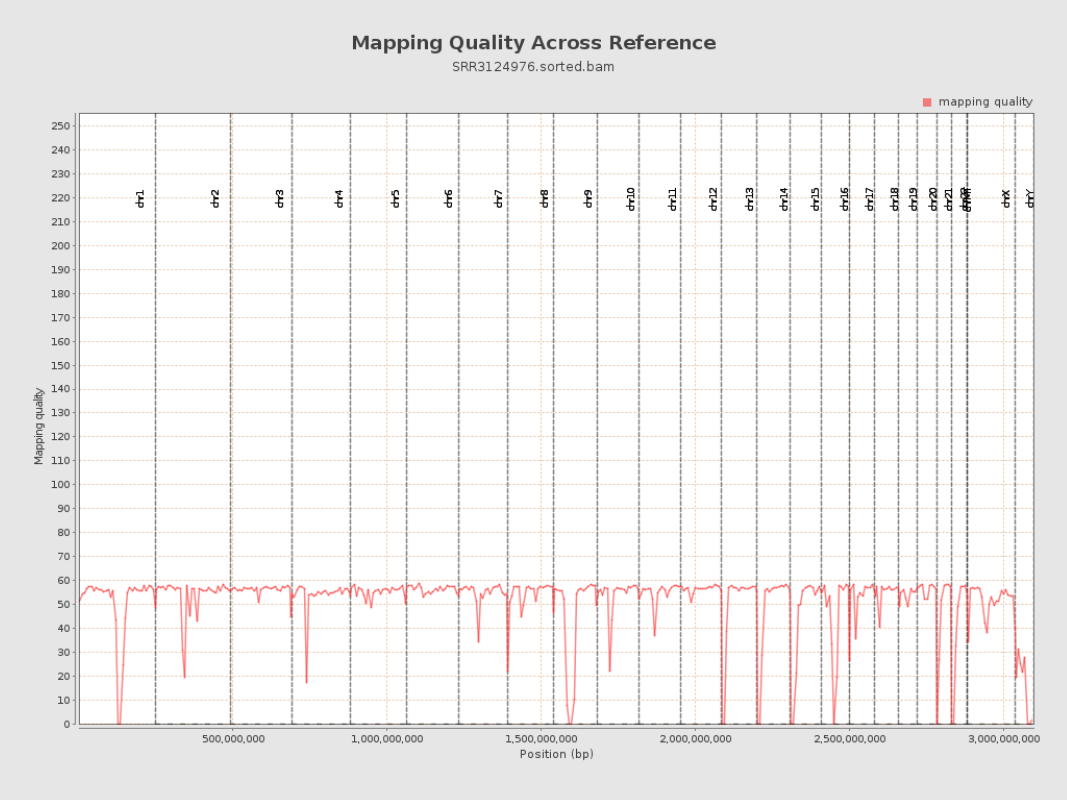
10. Results : Mapped Reads Clipping Profile



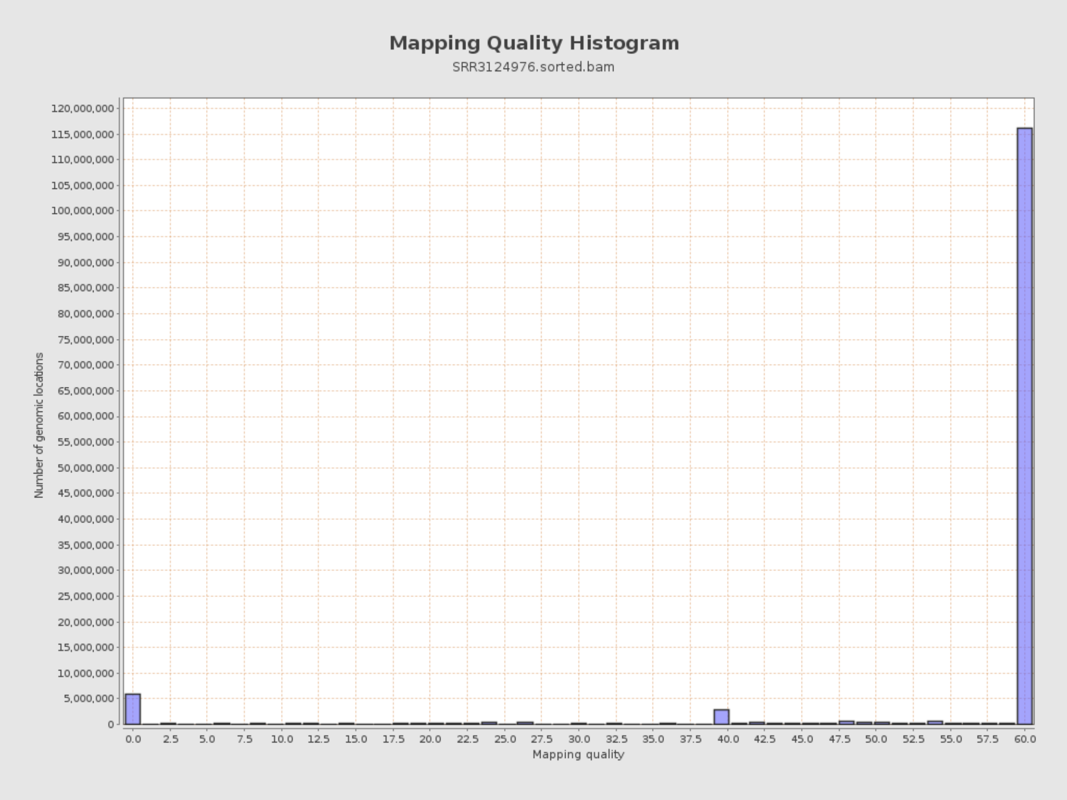
11. Results : Homopolymer Indels



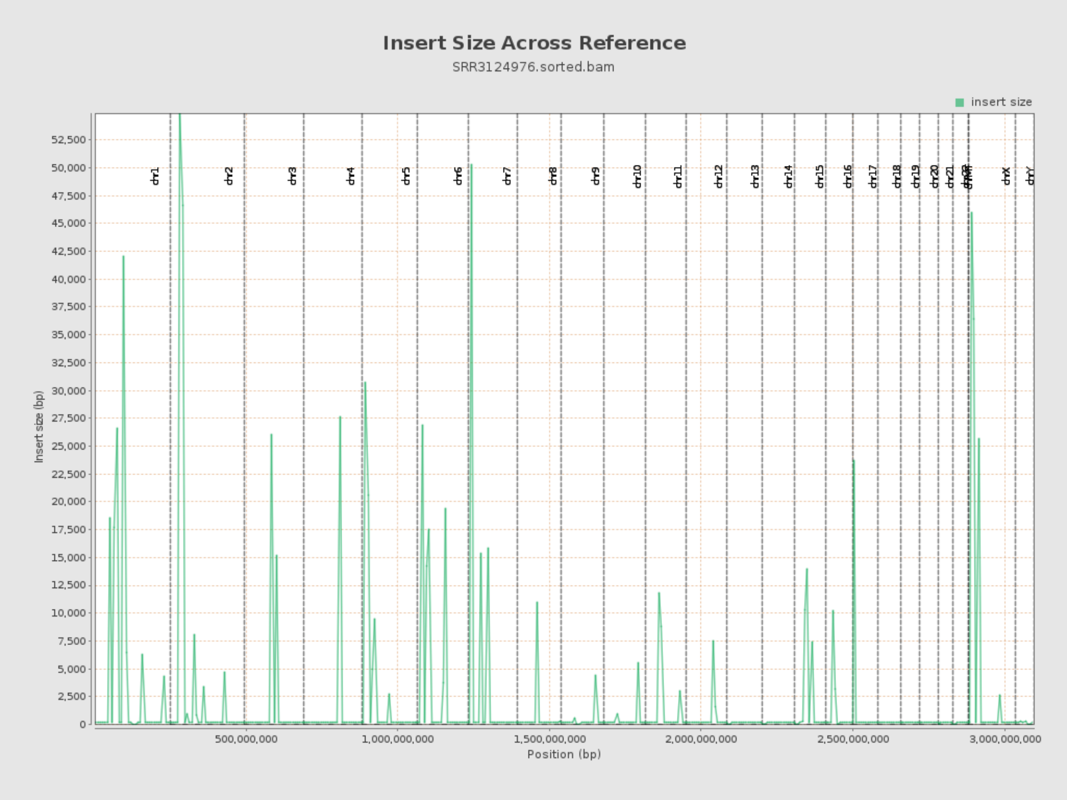
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram