Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:03:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124974.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_SRR3124974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124974_1.fastq.gz SRR3124974_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:03:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,521,208
Mapped reads	2,476,223 / 98.22%
Unmapped reads	44,985 / 1.78%
Mapped paired reads	2,476,223 / 98.22%
Mapped reads, first in pair	1,245,668 / 49.41%
Mapped reads, second in pair	1,230,555 / 48.81%
Mapped reads, both in pair	2,458,658 / 97.52%
Mapped reads, singletons	17,565 / 0.7%
Secondary alignments	0
Supplementary alignments	55,877 / 2.22%
Read min/max/mean length	30 / 151 / 152.08
Duplicated reads (estimated)	475,799 / 18.87%
Duplication rate	16.56%
Clipped reads	1,750,912 / 69.45%

2.2. ACGT Content

Number/percentage of A's	90,546,674 / 28.99%
Number/percentage of C's	61,795,683 / 19.79%
Number/percentage of T's	92,088,033 / 29.49%
Number/percentage of G's	67,878,286 / 21.73%
Number/percentage of N's	2,422 / 0%

GC Percentage	41.52%

2.3. Coverage

Mean	0.101
Standard Deviation	1.7495

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	85,986.4
Standard Deviation	2,733,017.03
P25/Median/P75	125 / 170 / 240

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	3,188,429
Insertions	67,086
Mapped reads with at least one insertion	2.52%
Deletions	118,582
Mapped reads with at least one deletion	4.58%
Homopolymer indels	45.07%

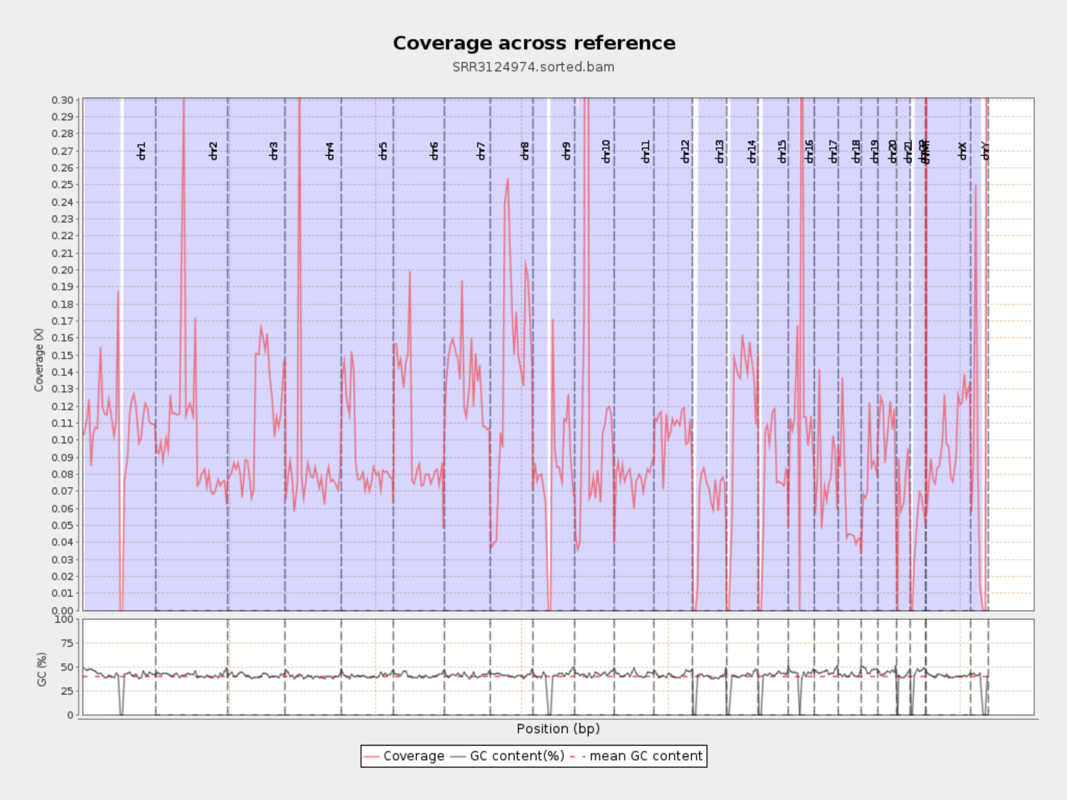
2.7. Chromosome stats

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

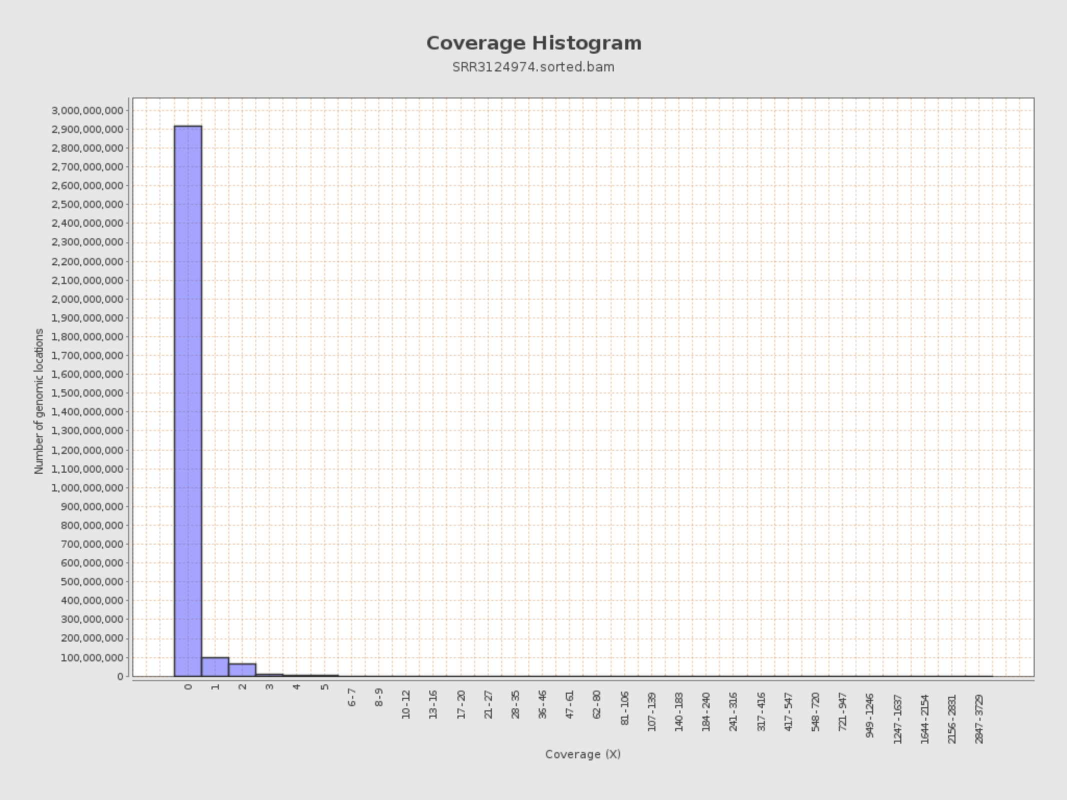
		bases	coverage	deviation
chr1	249250621	26674950	0.107	1.4506
chr2	243199373	25631524	0.1054	1.6256
chr3	198022430	21712628	0.1096	0.5138
chr4	191154276	16540328	0.0865	1.7868
chr5	180915260	16841264	0.0931	0.4384
chr6	171115067	17865236	0.1044	0.7868
chr7	159138663	21621897	0.1359	1.3427
chr8	146364022	21125475	0.1443	0.7023
chr9	141213431	11572785	0.082	1.6747
chr10	135534747	17032335	0.1257	5.9068
chr11	135006516	10502064	0.0778	0.66
chr12	133851895	14385397	0.1075	0.4647
chr13	115169878	6945147	0.0603	0.3411
chr14	107349540	12672297	0.118	0.5149
chr15	102531392	7769717	0.0758	0.3934
chr16	90354753	11912135	0.1318	2.6593
chr17	81195210	6507722	0.0801	1.2375
chr18	78077248	4927913	0.0631	1.612
chr19	59128983	4784221	0.0809	0.8443
chr20	63025520	6872891	0.109	0.7335
chr21	48129895	3287049	0.0683	1.0321
chr22	51304566	2261731	0.0441	0.3242
chrMT	16571	415413	25.0687	14.8668
chrX	155270560	15376646	0.099	0.5472

chrY	59373566	7336968	0.1236	3.4695

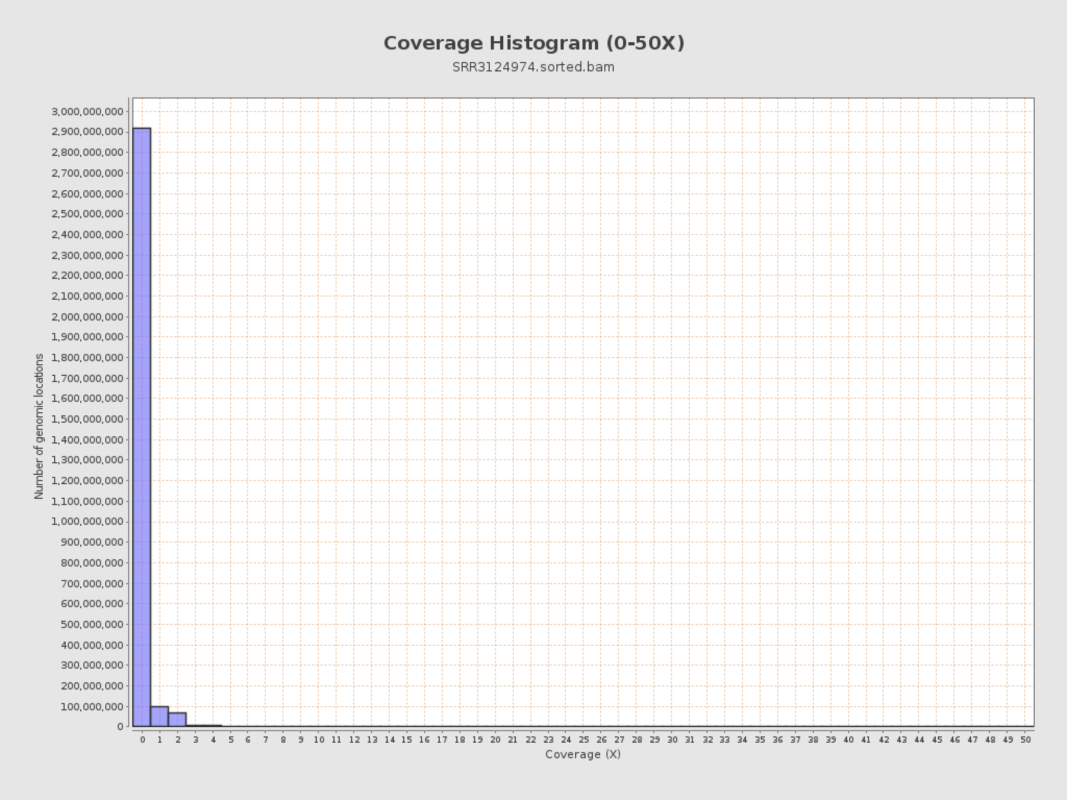
3. Results : Coverage across reference



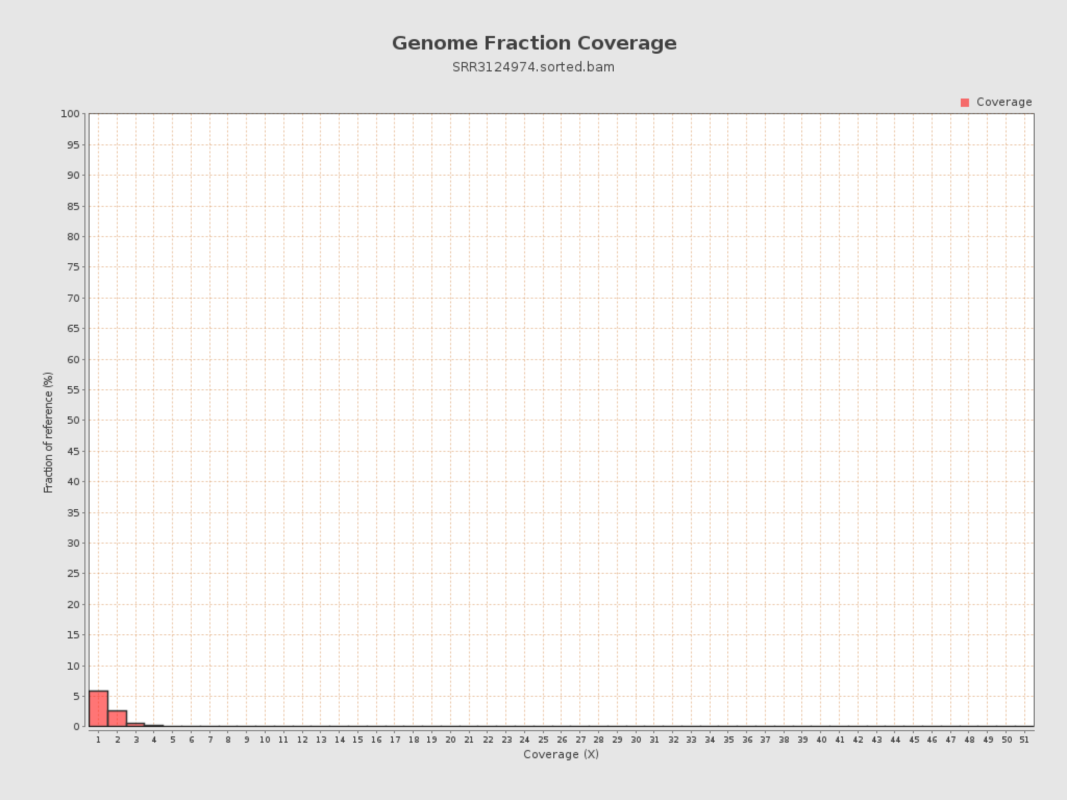
4. Results : Coverage Histogram



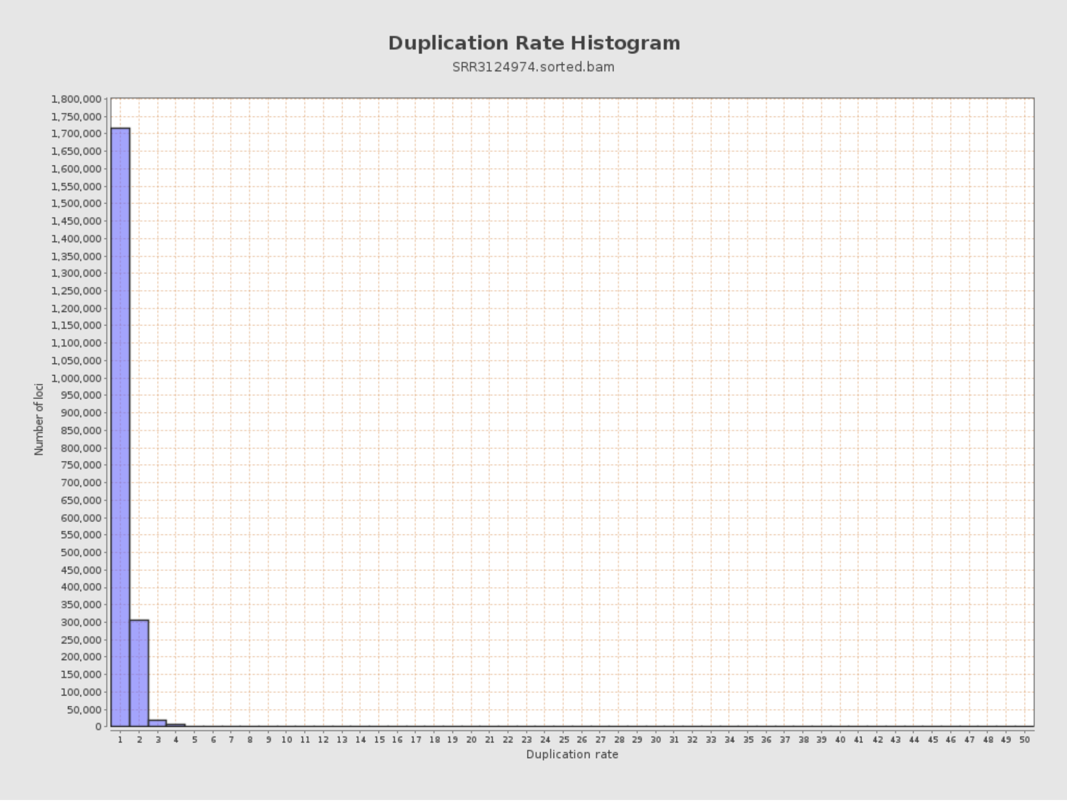
5. Results : Coverage Histogram (0-50X)



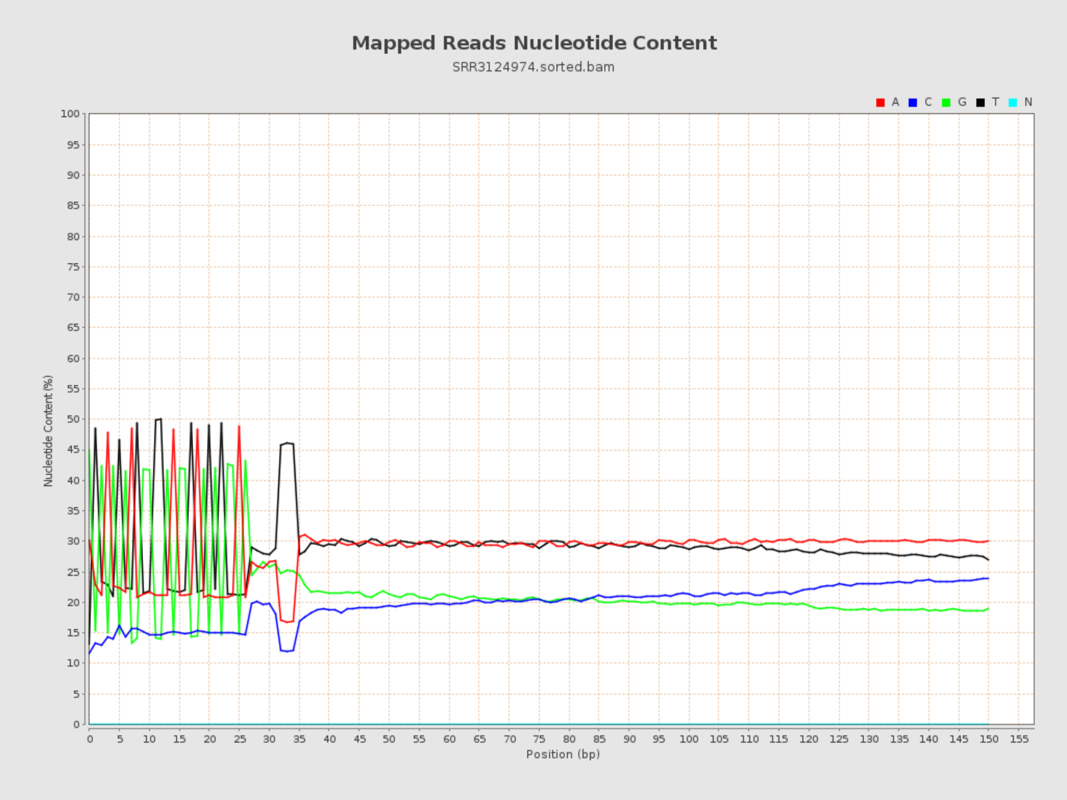
6. Results : Genome Fraction Coverage



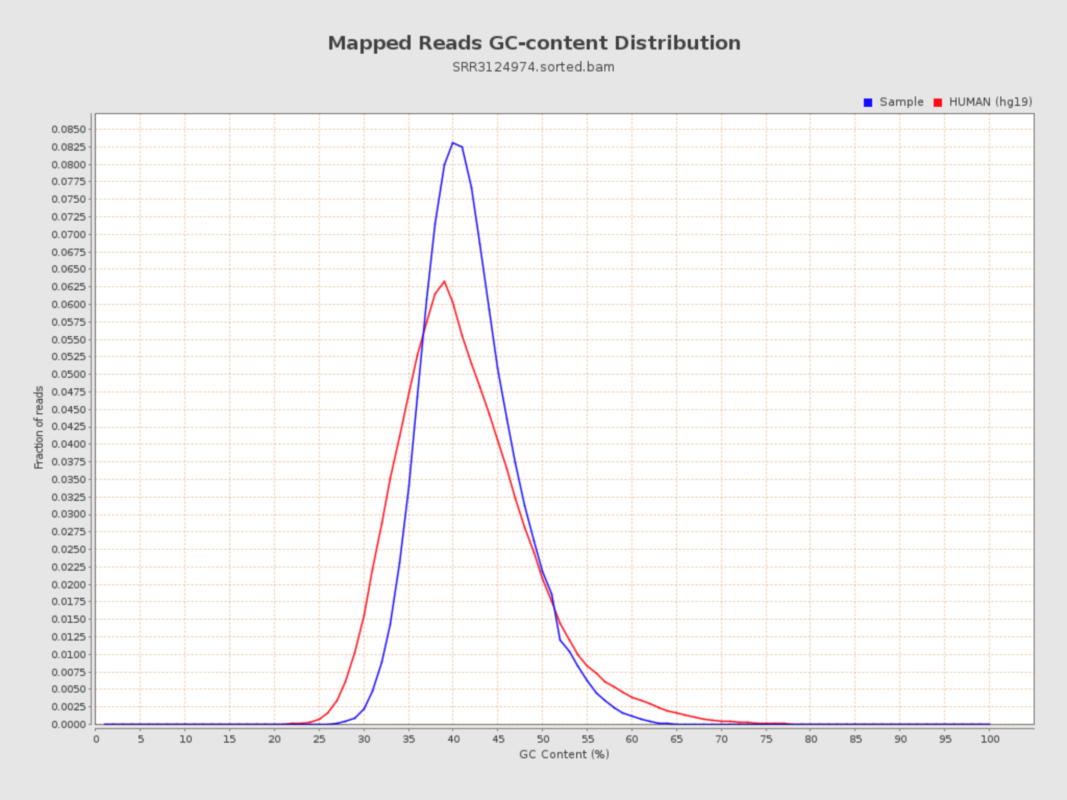
7. Results : Duplication Rate Histogram



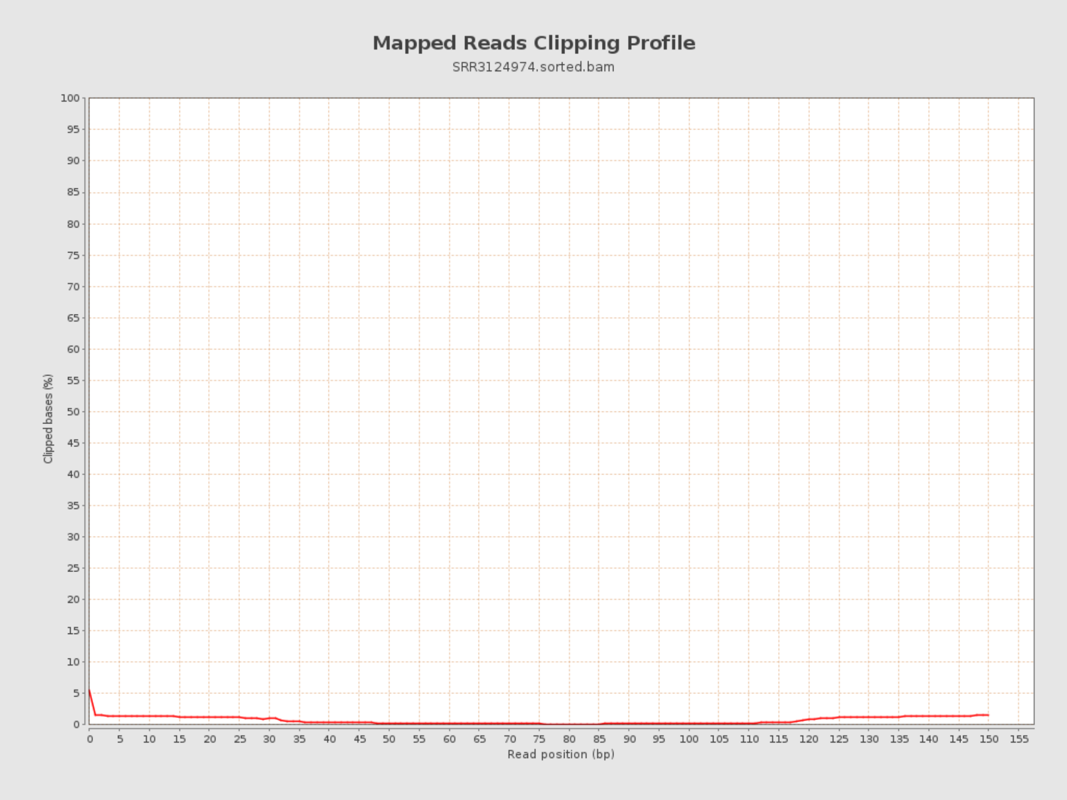
8. Results : Mapped Reads Nucleotide Content



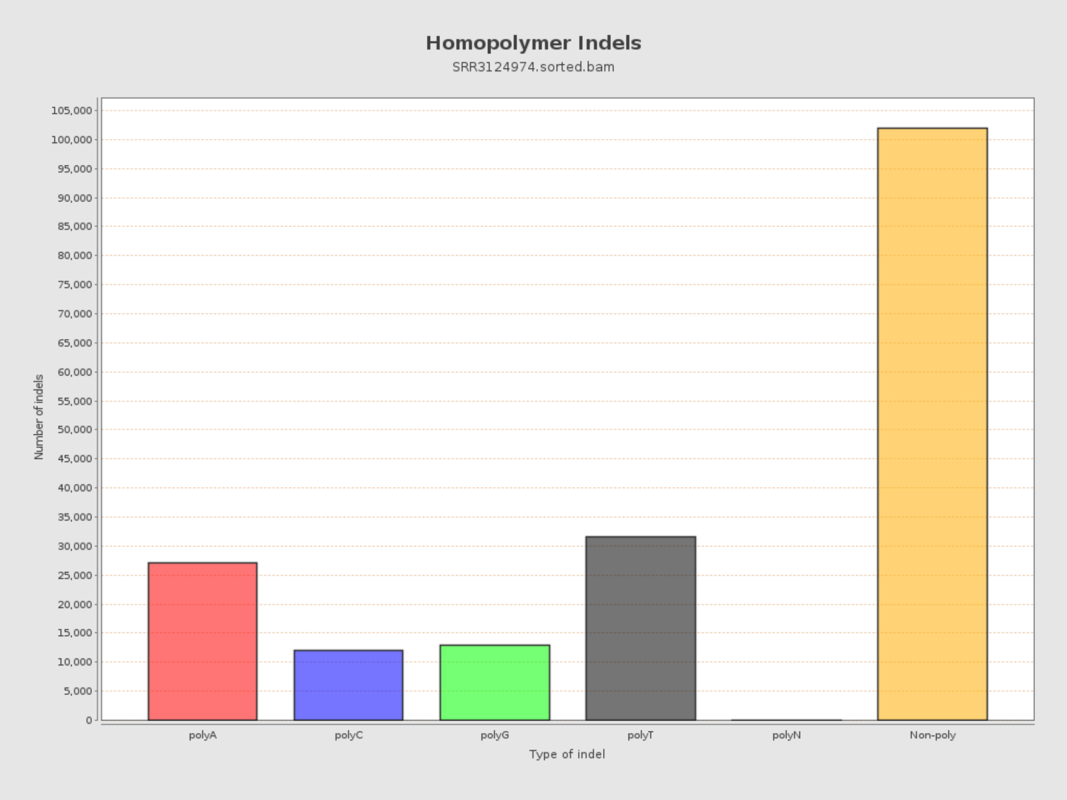
9. Results : Mapped Reads GC-content Distribution



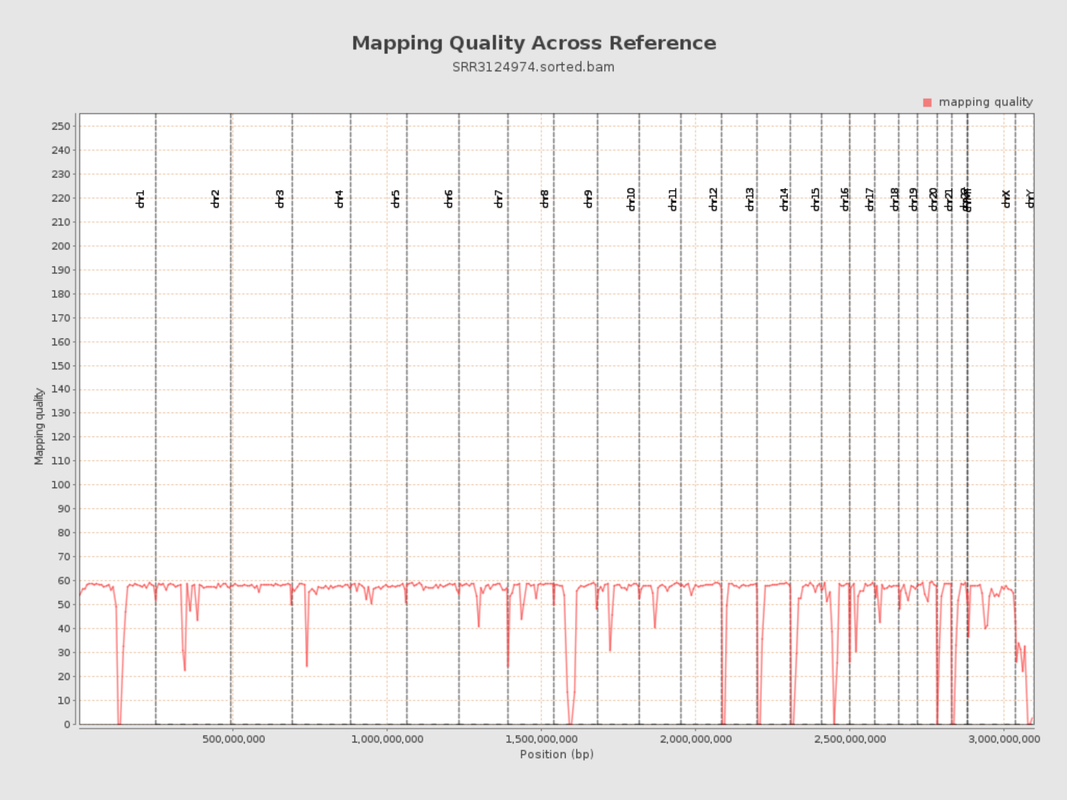
10. Results : Mapped Reads Clipping Profile



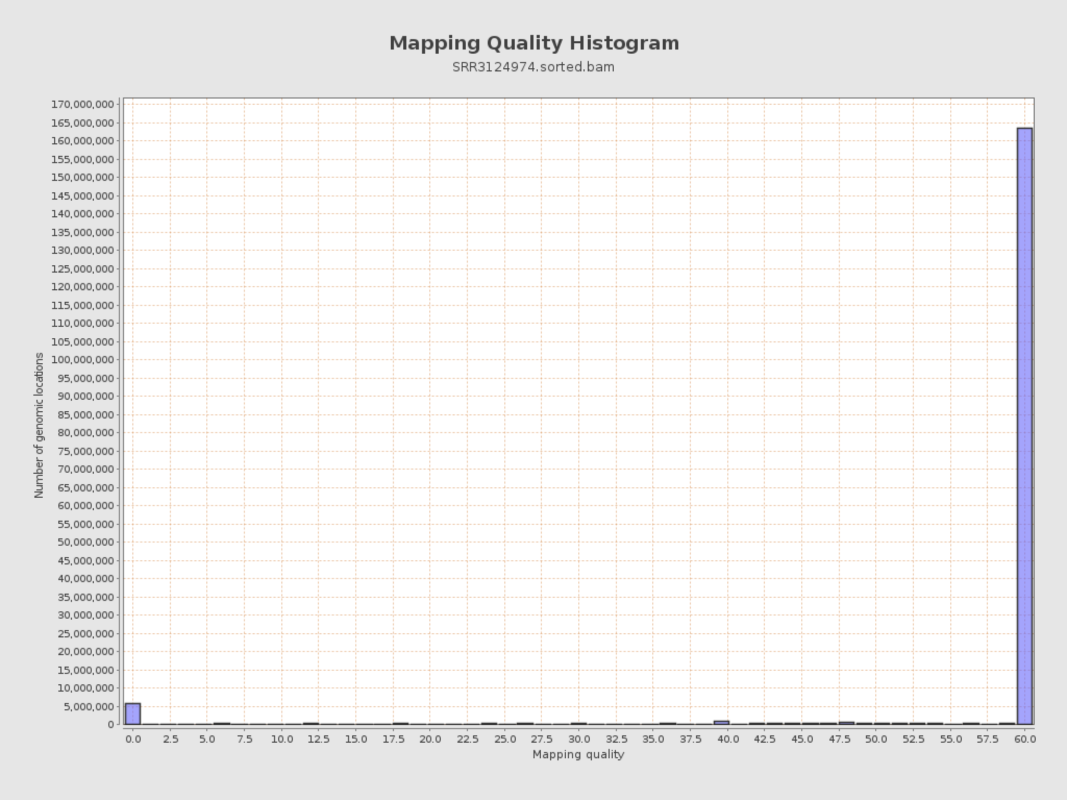
11. Results : Homopolymer Indels



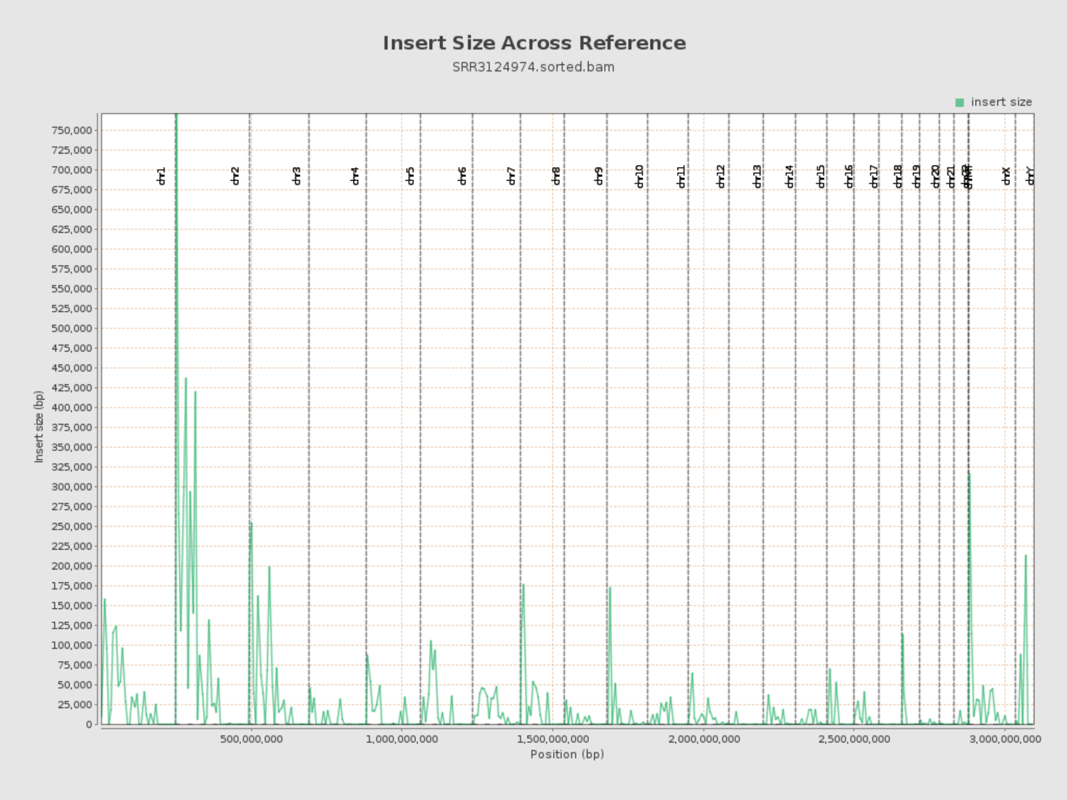
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram