Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:26:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124952.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_SRR3124952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124952_1.fastq.gz SRR3124952_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:26:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,319,778
Mapped reads	4,252,929 / 98.45%
Unmapped reads	66,849 / 1.55%
Mapped paired reads	4,252,929 / 98.45%
Mapped reads, first in pair	2,130,987 / 49.33%
Mapped reads, second in pair	2,121,942 / 49.12%
Mapped reads, both in pair	4,233,606 / 98.01%
Mapped reads, singletons	19,323 / 0.45%
Secondary alignments	0
Supplementary alignments	19,598 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	352,184 / 8.15%
Duplication rate	5.51%
Clipped reads	2,008,080 / 46.49%

2.2. ACGT Content

Number/percentage of A's	104,884,552 / 28.36%
Number/percentage of C's	67,750,881 / 18.32%
Number/percentage of T's	111,992,081 / 30.28%
Number/percentage of G's	85,209,829 / 23.04%
Number/percentage of N's	5,595 / 0%

GC Percentage	41.36%

2.3. Coverage

Mean	0.1195
Standard Deviation	1.2624

2.4. Mapping Quality

Mean Mapping Quality	52.64

2.5. Insert size

Mean	38,479.94
Standard Deviation	1,809,689.27
P25/Median/P75	149 / 203 / 284

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,773,802
Insertions	49,621
Mapped reads with at least one insertion	1.14%
Deletions	120,471
Mapped reads with at least one deletion	2.78%
Homopolymer indels	47.97%

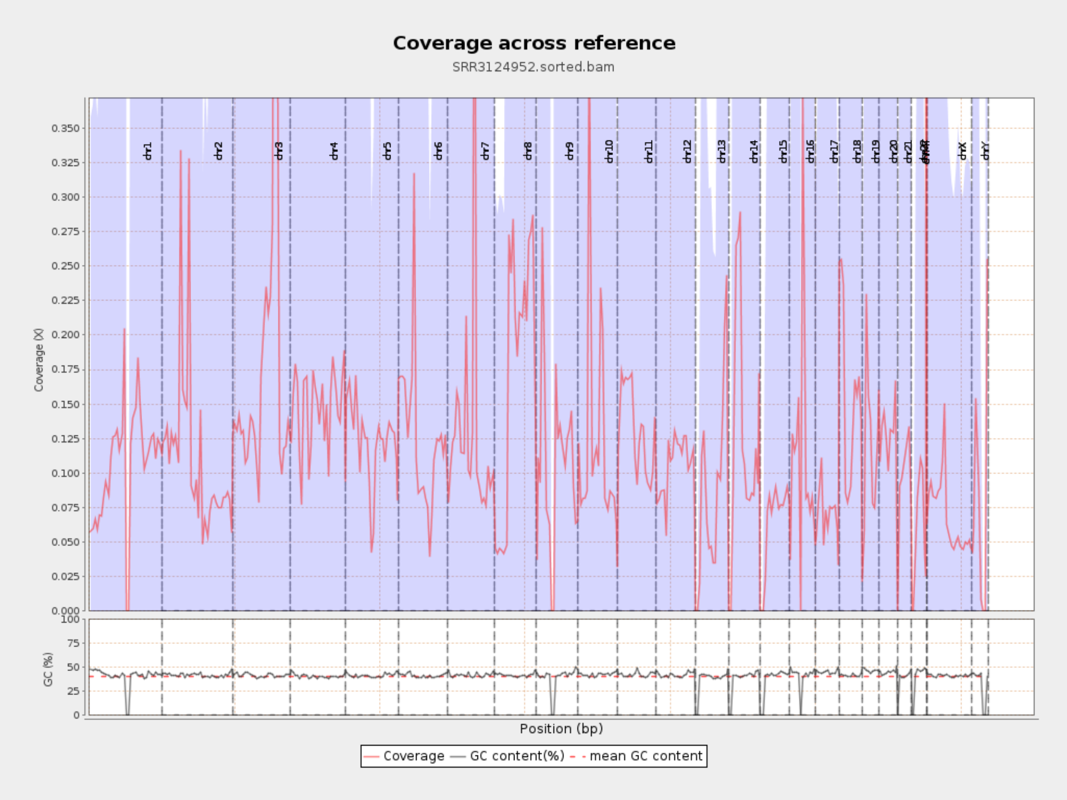
2.7. Chromosome stats

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

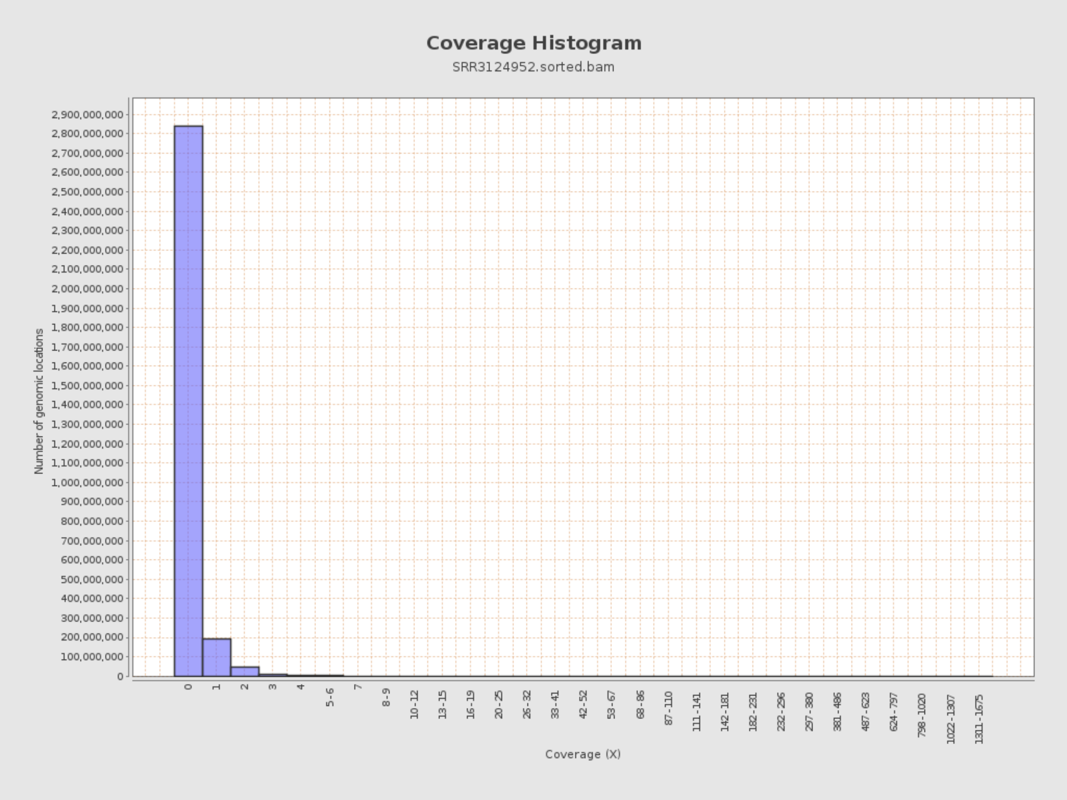
		bases	coverage	deviation
chr1	249250621	26418507	0.106	1.4114
chr2	243199373	27465664	0.1129	1.4703
chr3	198022430	37043350	0.1871	0.6408
chr4	191154276	28069978	0.1468	0.697
chr5	180915260	22142337	0.1224	0.4566
chr6	171115067	21576738	0.1261	1.7755
chr7	159138663	21562964	0.1355	1.726
chr8	146364022	25683640	0.1755	0.6981
chr9	141213431	15770827	0.1117	1.8156
chr10	135534747	16832439	0.1242	2.5844
chr11	135006516	17570415	0.1301	1.081
chr12	133851895	14078186	0.1052	0.4155
chr13	115169878	10020793	0.087	0.3827
chr14	107349540	13114714	0.1222	0.553
chr15	102531392	6566163	0.064	0.325
chr16	90354753	10109748	0.1119	2.0093
chr17	81195210	5622917	0.0693	0.7742
chr18	78077248	12167995	0.1558	1.9679
chr19	59128983	7073523	0.1196	0.9699
chr20	63025520	8081122	0.1282	0.4901
chr21	48129895	4612903	0.0958	0.4925
chr22	51304566	2948801	0.0575	0.3195
chrMT	16571	174789	10.5479	8.0173
chrX	155270560	10744650	0.0692	0.5861

chrY	59373566	4589414	0.0773	1.5323

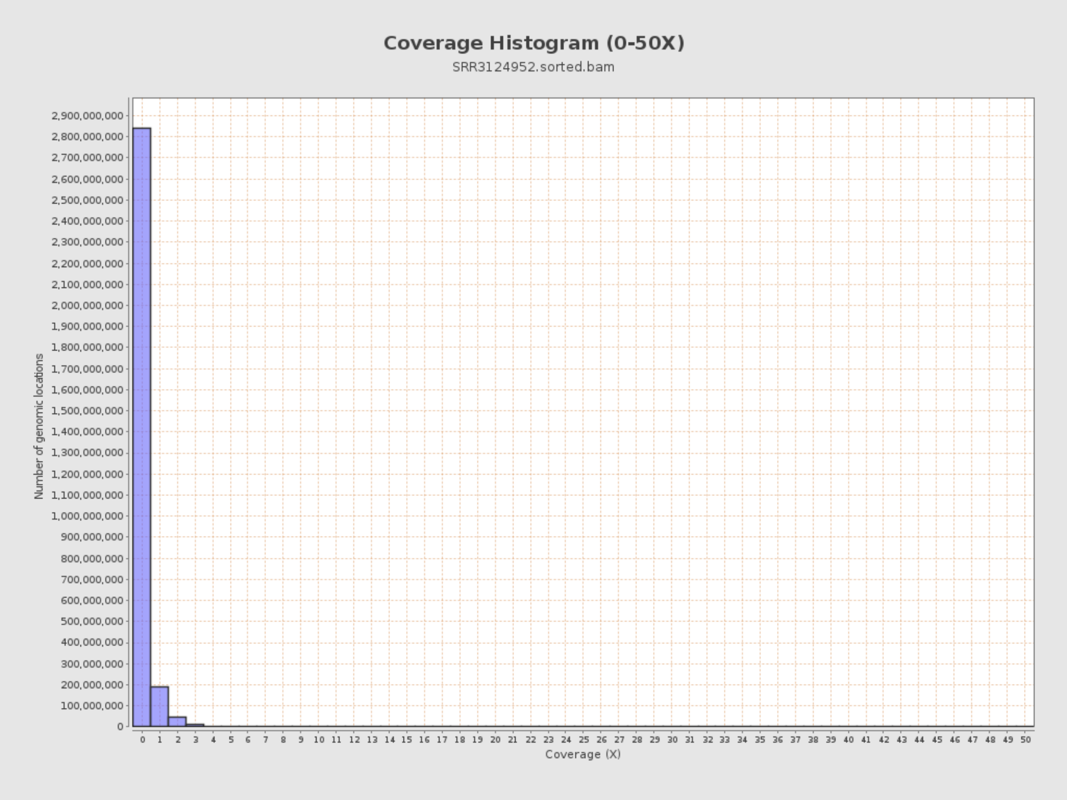
3. Results : Coverage across reference



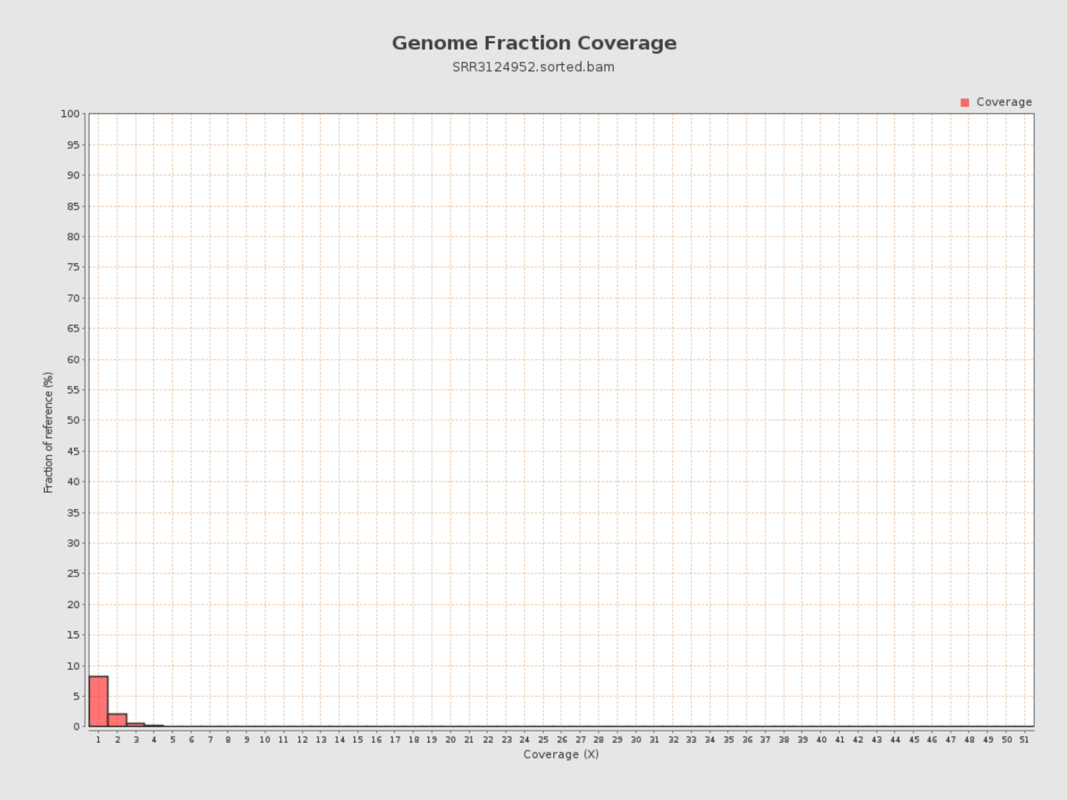
4. Results : Coverage Histogram



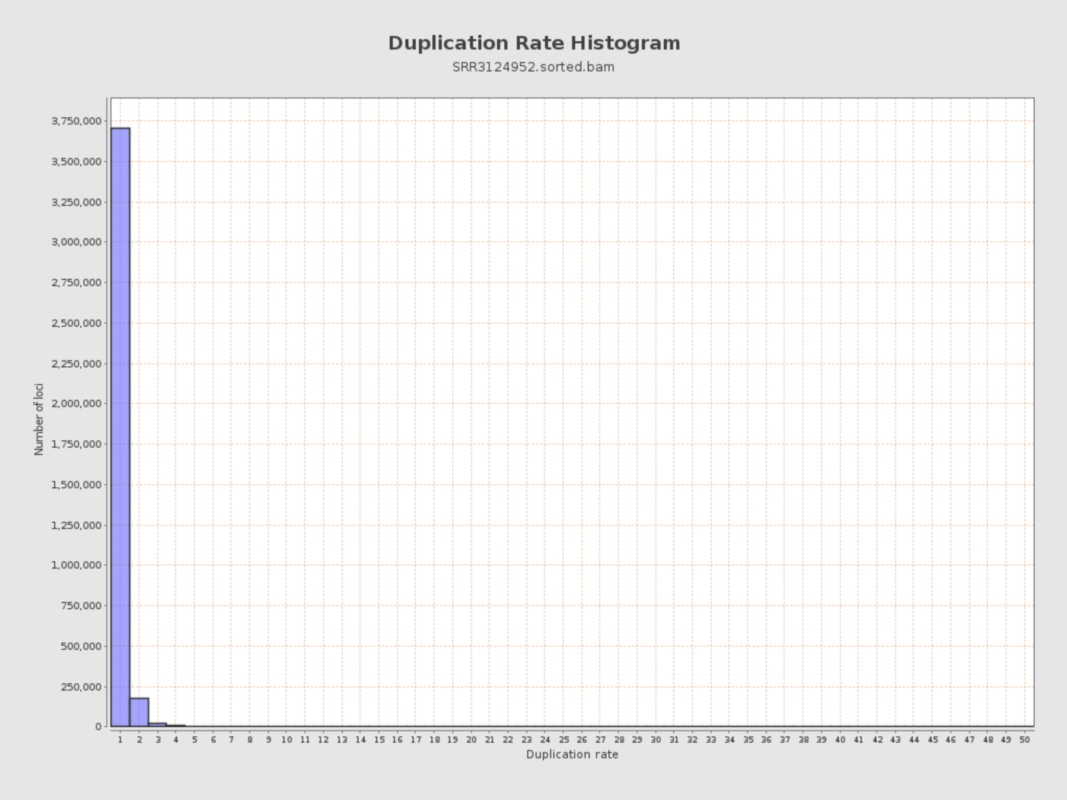
5. Results : Coverage Histogram (0-50X)



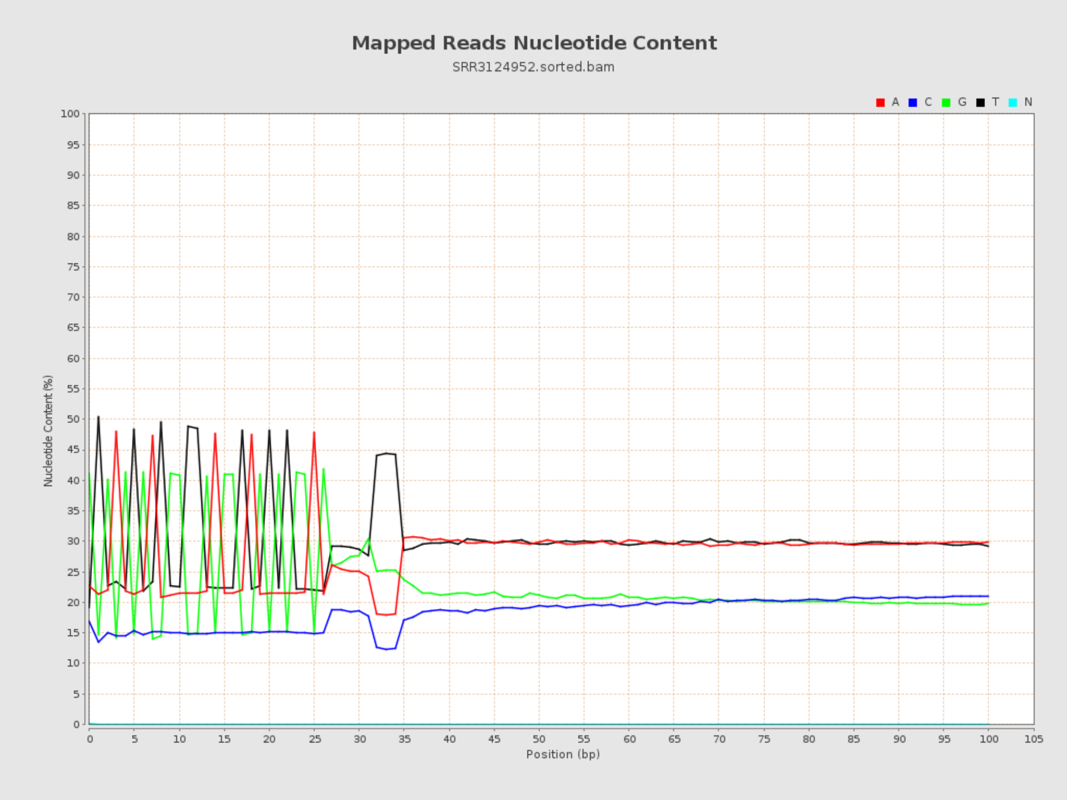
6. Results : Genome Fraction Coverage



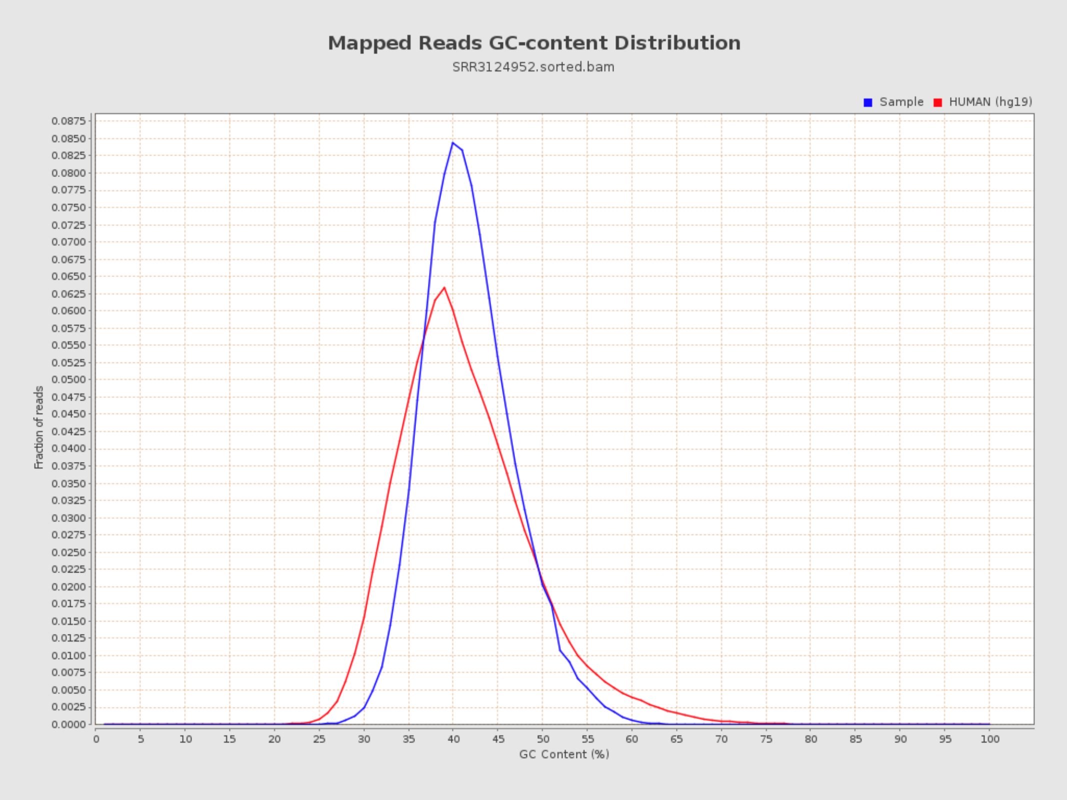
7. Results : Duplication Rate Histogram



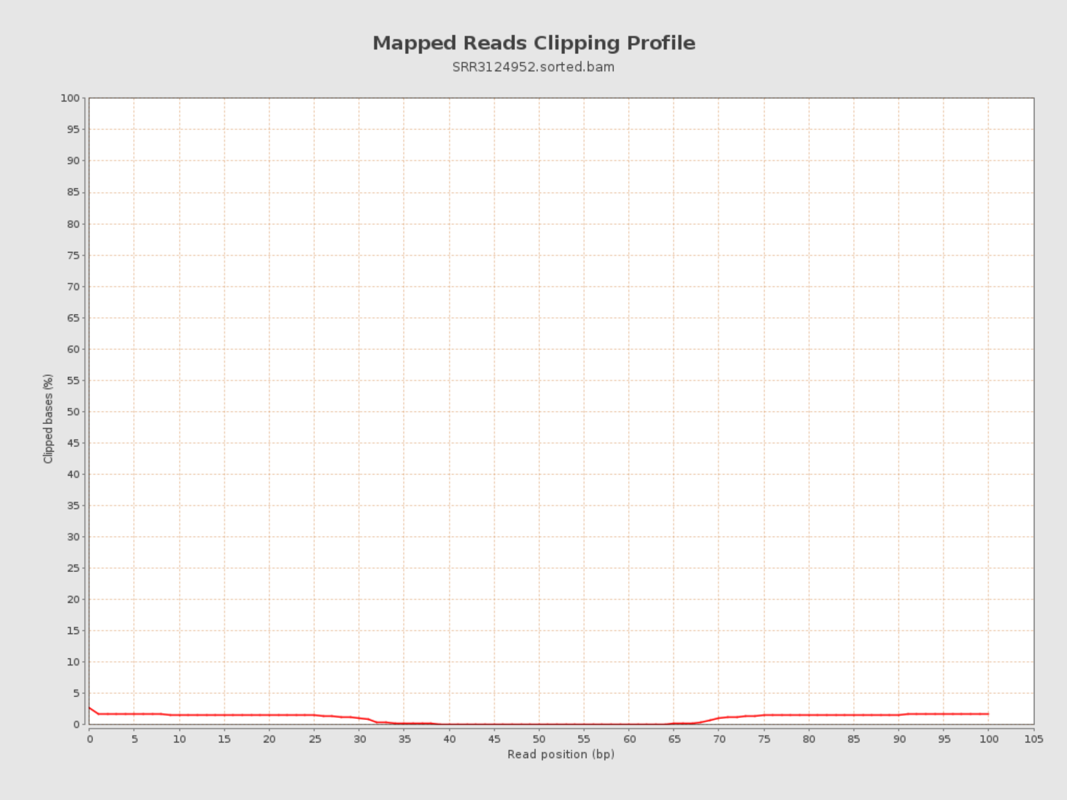
8. Results : Mapped Reads Nucleotide Content



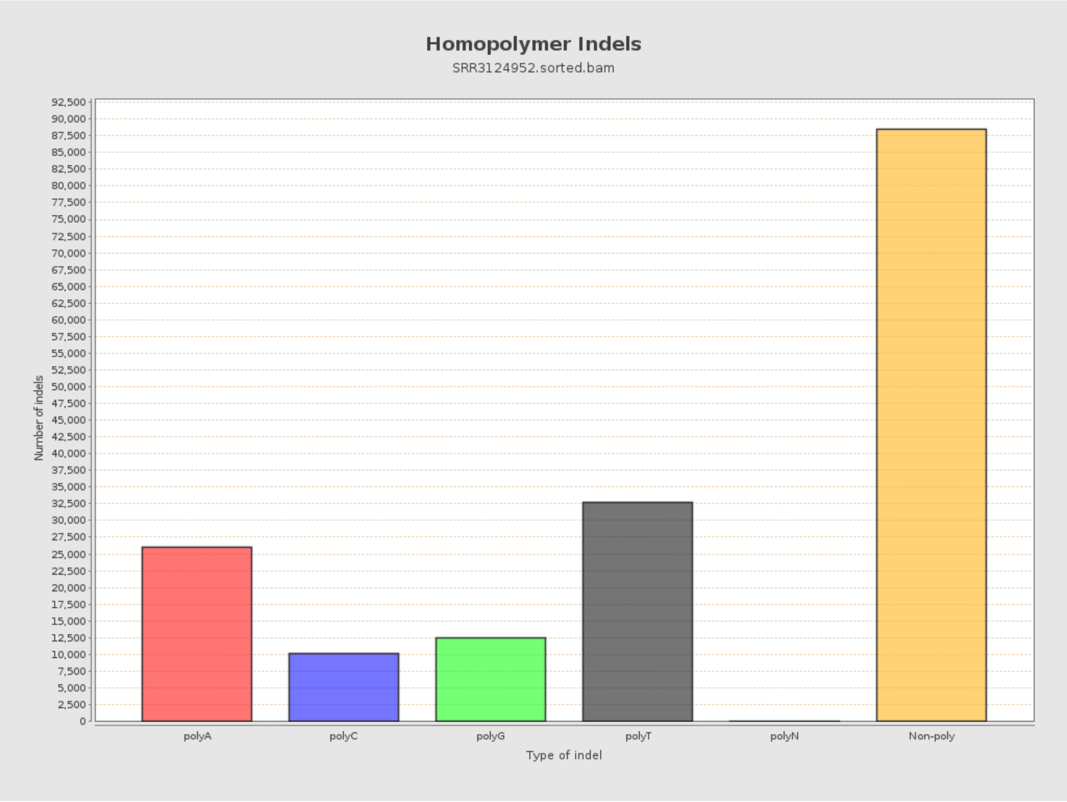
9. Results : Mapped Reads GC-content Distribution



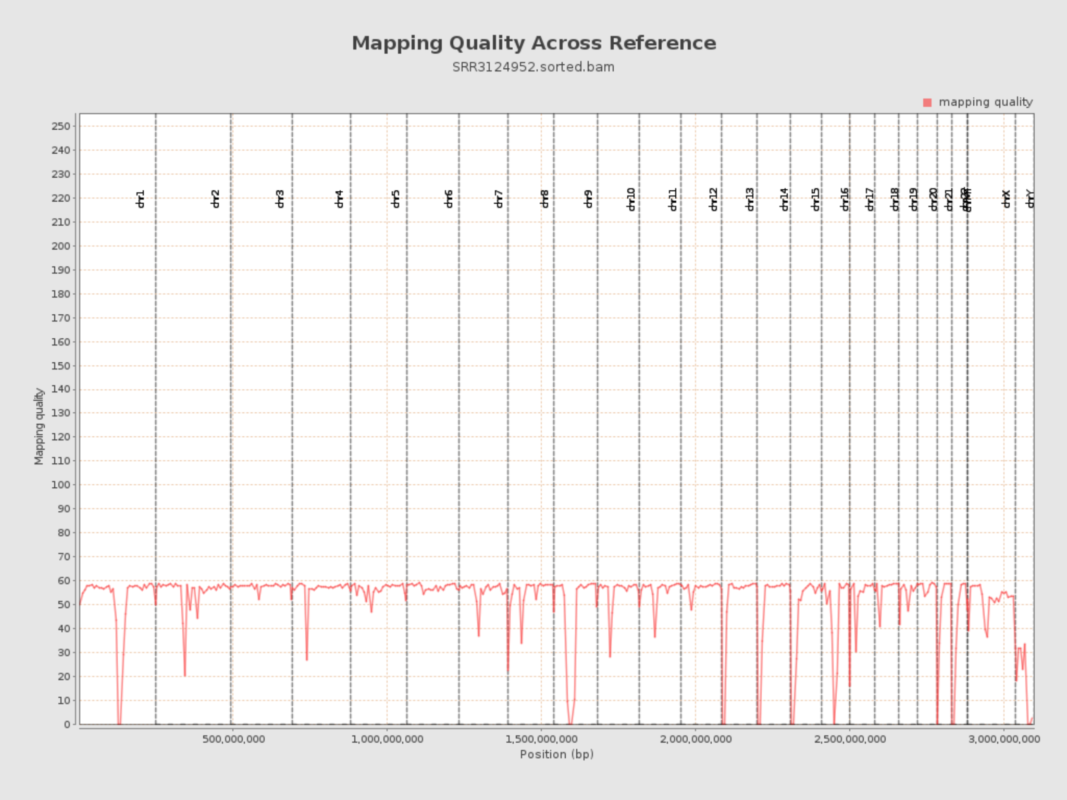
10. Results : Mapped Reads Clipping Profile



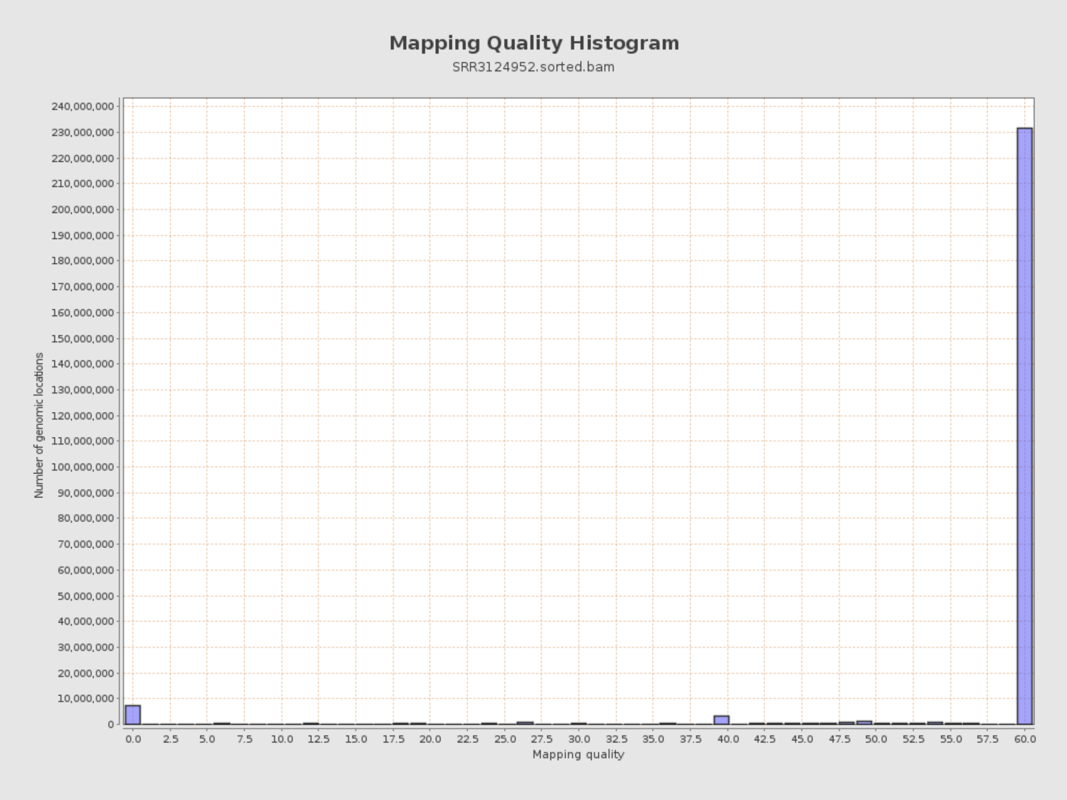
11. Results : Homopolymer Indels



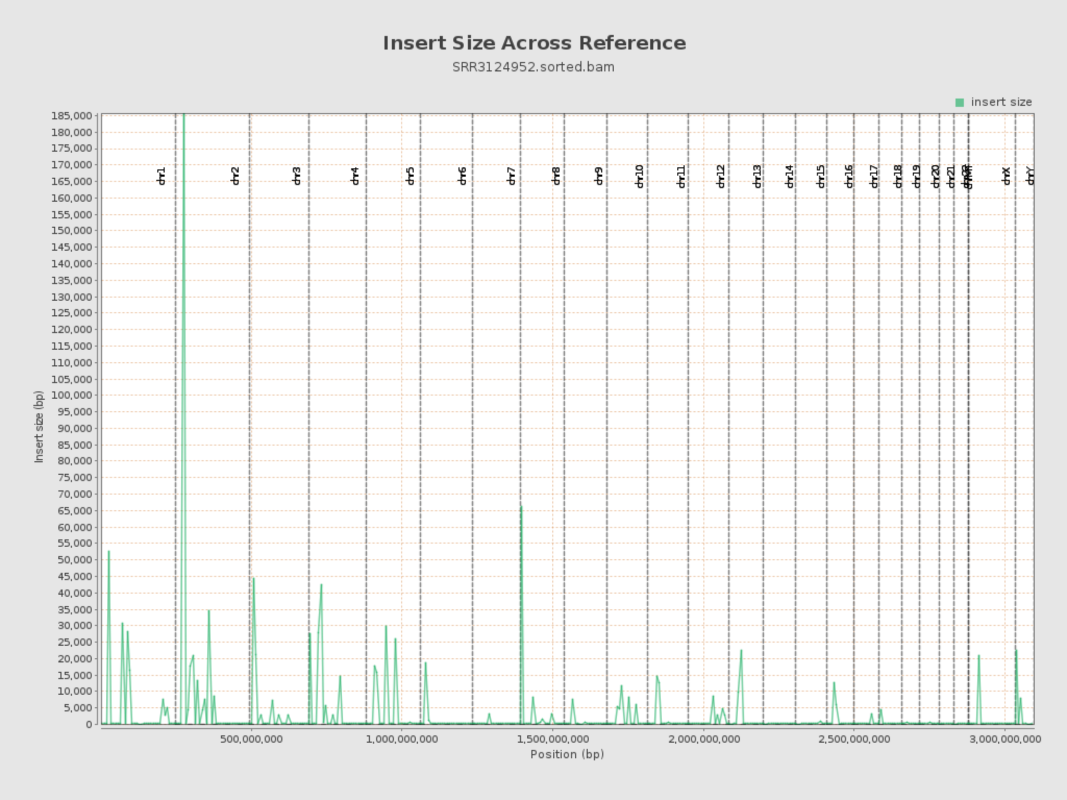
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram