Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 05:25:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124920.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_SRR3124920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124920_1.fastq.gz SRR3124920_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 05:25:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,792,336
Mapped reads	7,425,459 / 95.29%
Unmapped reads	366,877 / 4.71%
Mapped paired reads	7,425,459 / 95.29%
Mapped reads, first in pair	3,760,696 / 48.26%
Mapped reads, second in pair	3,664,763 / 47.03%
Mapped reads, both in pair	7,305,456 / 93.75%
Mapped reads, singletons	120,003 / 1.54%
Secondary alignments	0
Supplementary alignments	8,131 / 0.1%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	699,529 / 8.98%
Duplication rate	7.07%
Clipped reads	3,461,809 / 44.43%

2.2. ACGT Content

Number/percentage of A's	123,511,856 / 26.83%
Number/percentage of C's	84,213,038 / 18.3%
Number/percentage of T's	135,262,303 / 29.39%
Number/percentage of G's	117,285,883 / 25.48%
Number/percentage of N's	3,425 / 0%

GC Percentage	43.78%

2.3. Coverage

Mean	0.1488
Standard Deviation	0.9455

2.4. Mapping Quality

Mean Mapping Quality	52.03

2.5. Insert size

Mean	26,339.8
Standard Deviation	1,522,414.66
P25/Median/P75	145 / 194 / 269

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	3,083,635
Insertions	50,627
Mapped reads with at least one insertion	0.67%
Deletions	139,081
Mapped reads with at least one deletion	1.85%
Homopolymer indels	48.09%

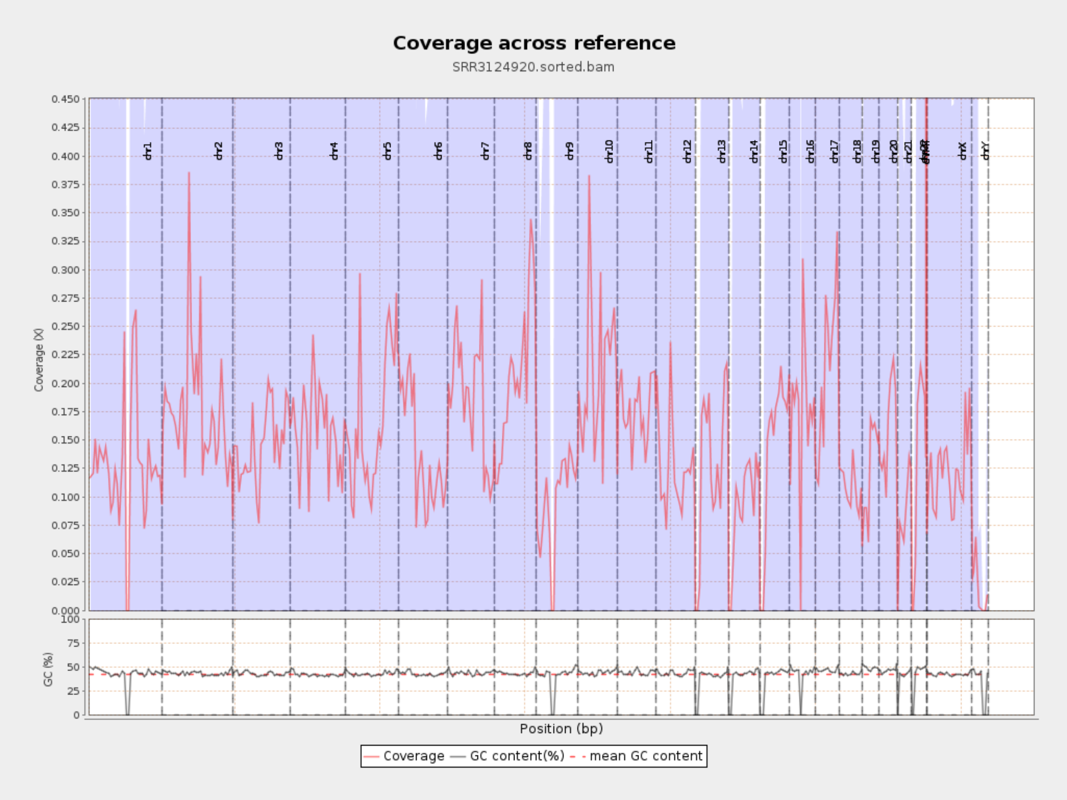
2.7. Chromosome stats

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

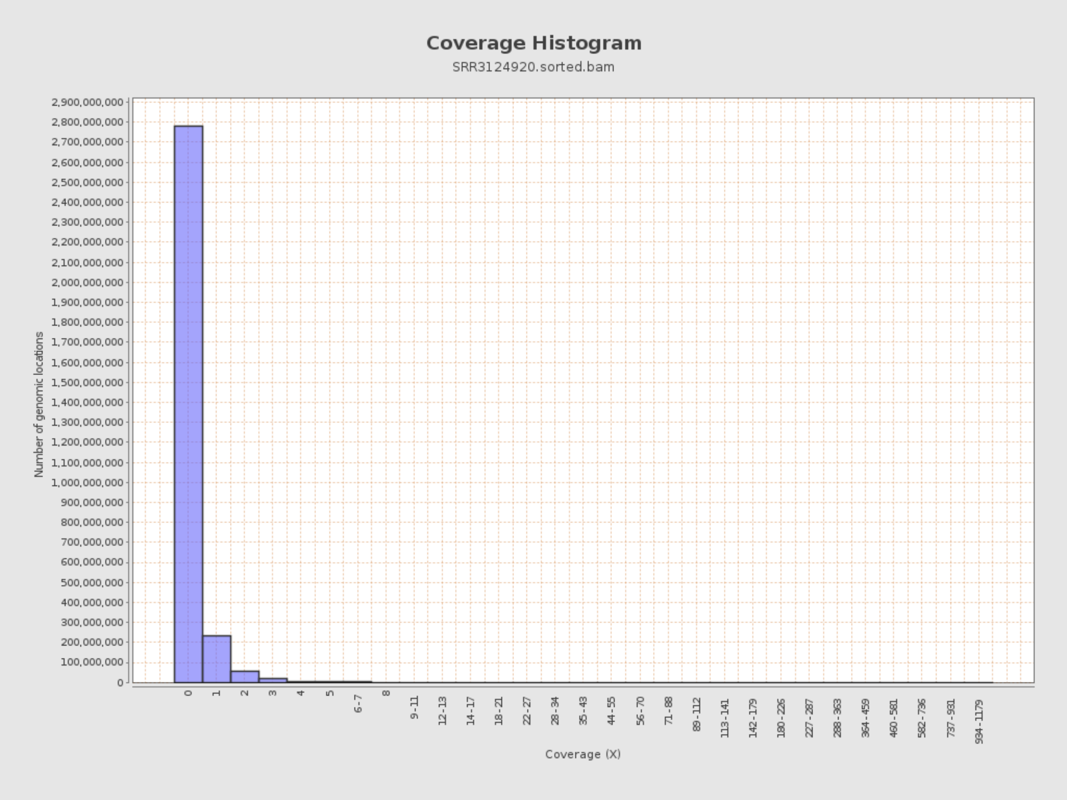
		bases	**coverage**	**deviation**
chr1	249250621	31493172	0.1264	0.966
chr2	243199373	43154012	0.1774	1.4844
chr3	198022430	28867669	0.1458	0.5108
chr4	191154276	30201326	0.158	0.6653
chr5	180915260	30061537	0.1662	0.5786
chr6	171115067	23856941	0.1394	0.7584
chr7	159138663	29801411	0.1873	1.2823
chr8	146364022	30396556	0.2077	0.7138
chr9	141213431	13265896	0.0939	0.7451
chr10	135534747	28573055	0.2108	1.7763
chr11	135006516	23802220	0.1763	0.7796
chr12	133851895	17102850	0.1278	0.4918
chr13	115169878	14643749	0.1271	0.4809
chr14	107349540	9707113	0.0904	0.4775
chr15	102531392	14777642	0.1441	0.5273
chr16	90354753	15815917	0.175	1.4553
chr17	81195210	17678693	0.2177	1.3057
chr18	78077248	8526828	0.1092	1.1373
chr19	59128983	7349512	0.1243	0.8265
chr20	63025520	10118091	0.1605	0.6464
chr21	48129895	4077896	0.0847	0.4926
chr22	51304566	6680400	0.1302	0.5195
chrMT	16571	471681	28.4642	20.8078
chrX	155270560	19001017	0.1224	0.5873

chrY	59373566	1060143	0.0179	1.0519

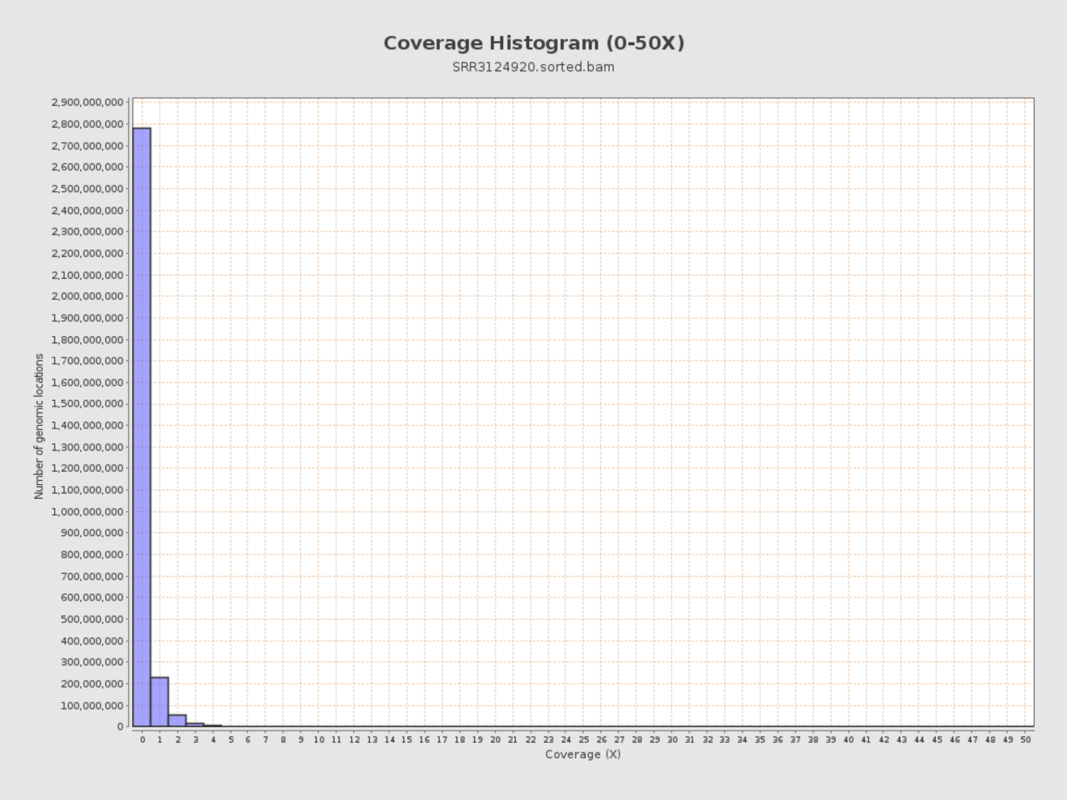
3. Results : Coverage across reference



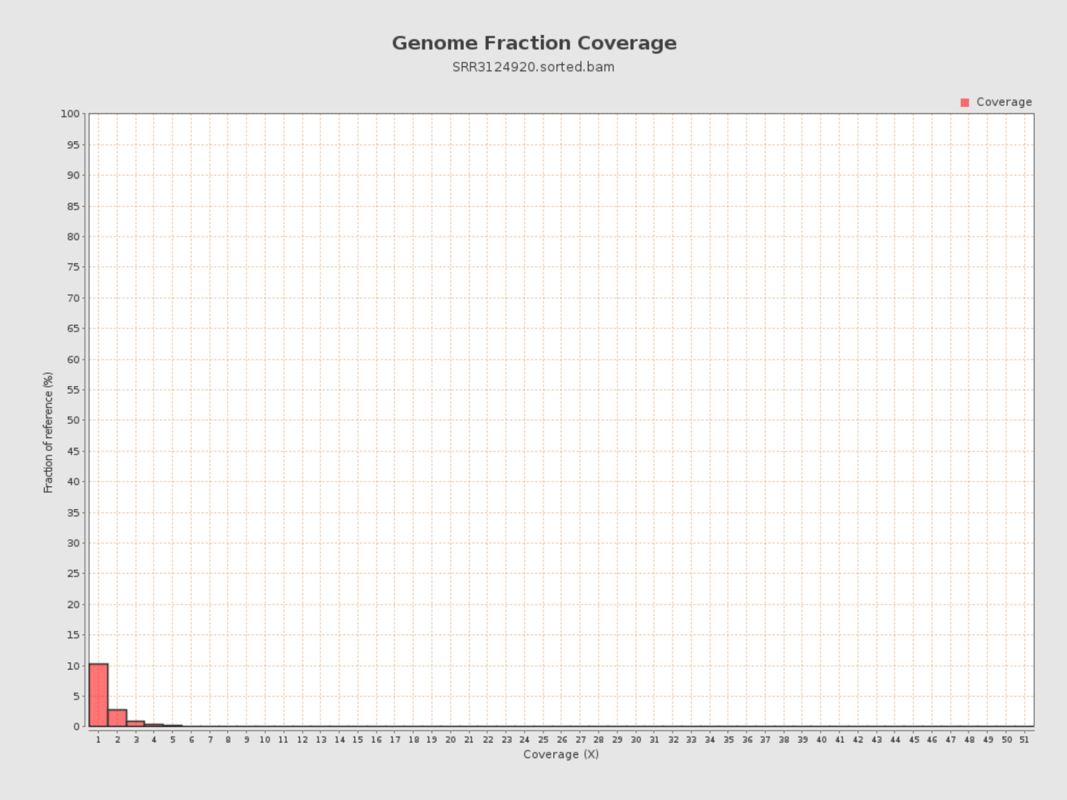
4. Results : Coverage Histogram



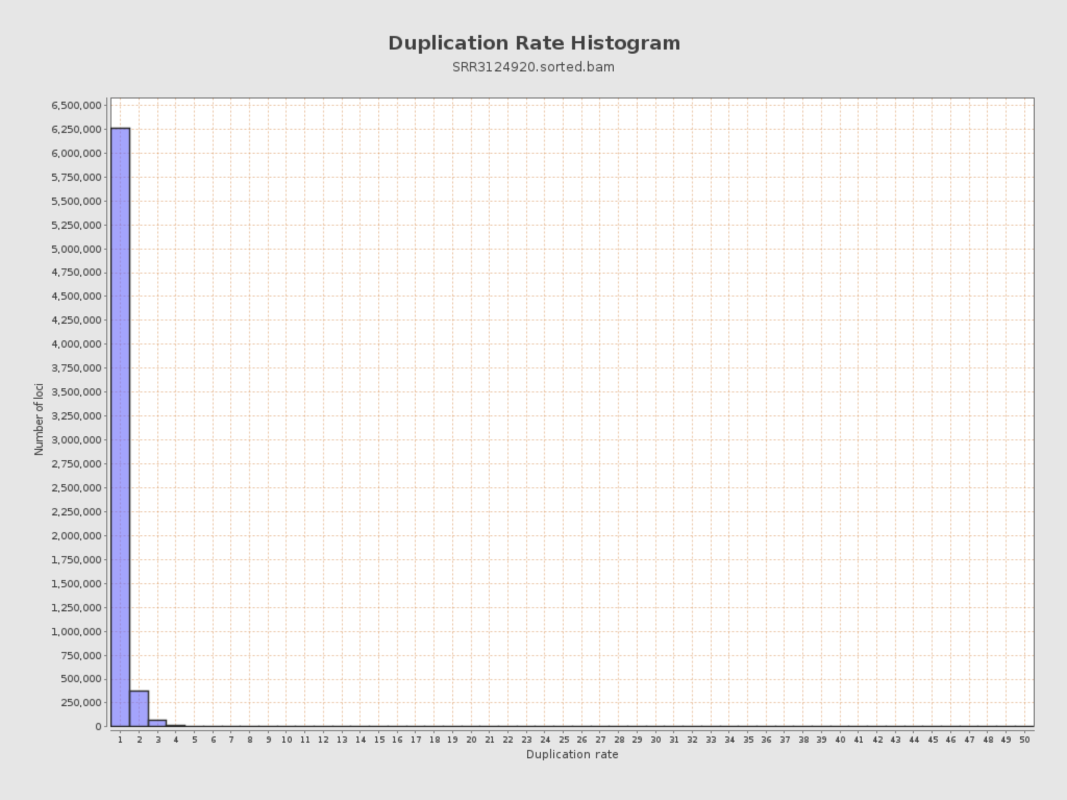
5. Results : Coverage Histogram (0-50X)



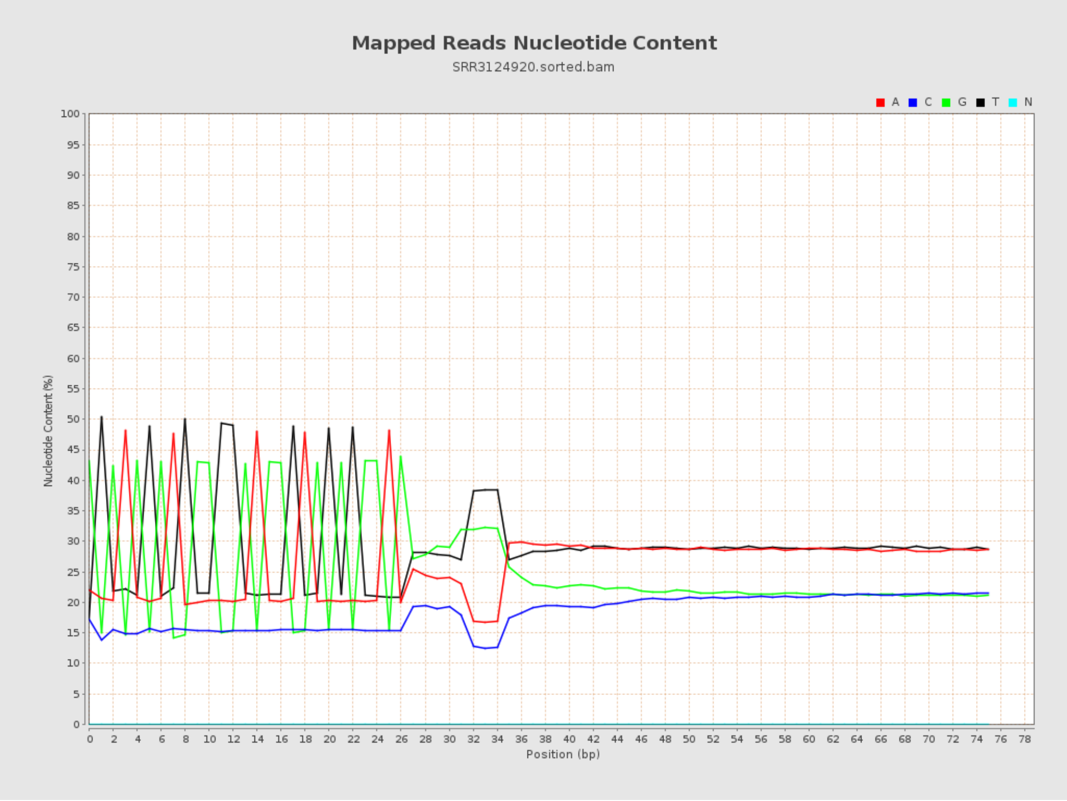
6. Results : Genome Fraction Coverage



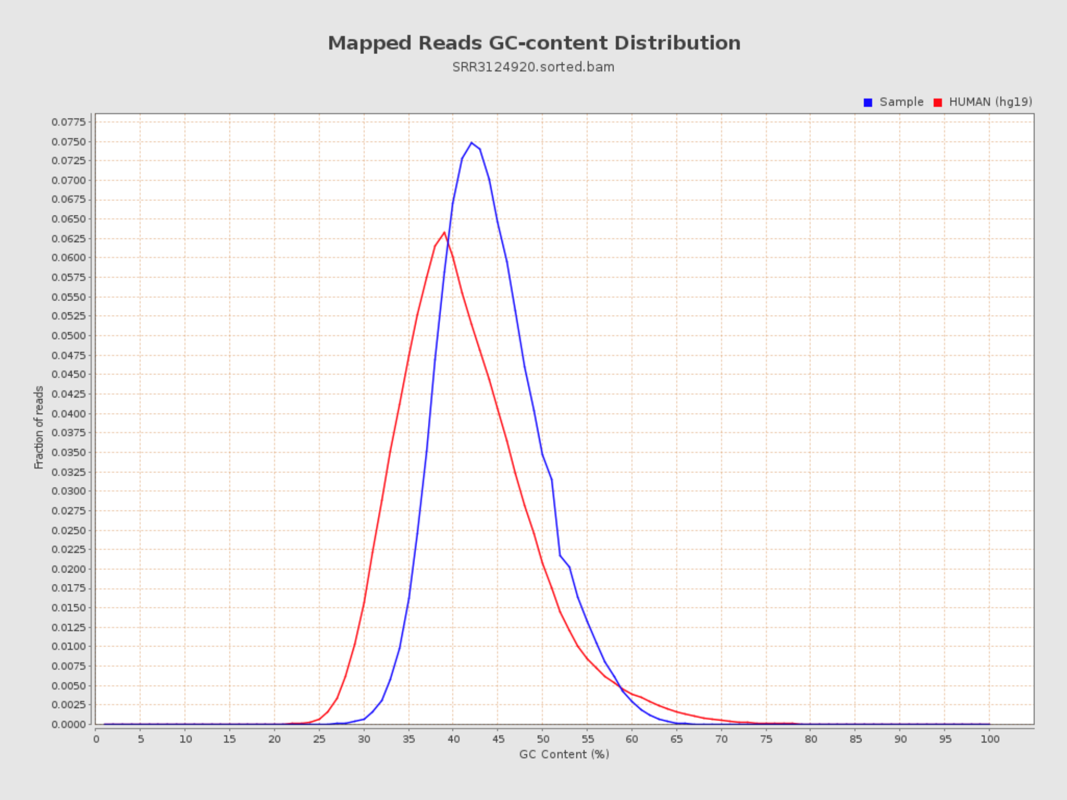
7. Results : Duplication Rate Histogram



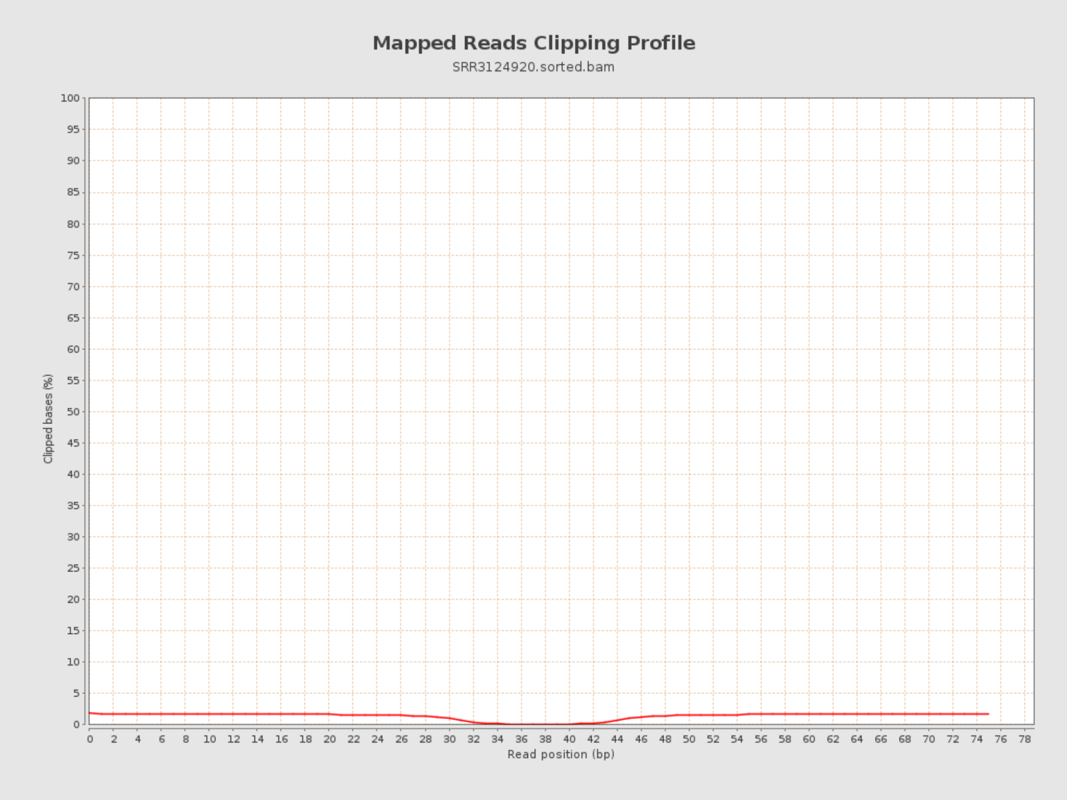
8. Results : Mapped Reads Nucleotide Content



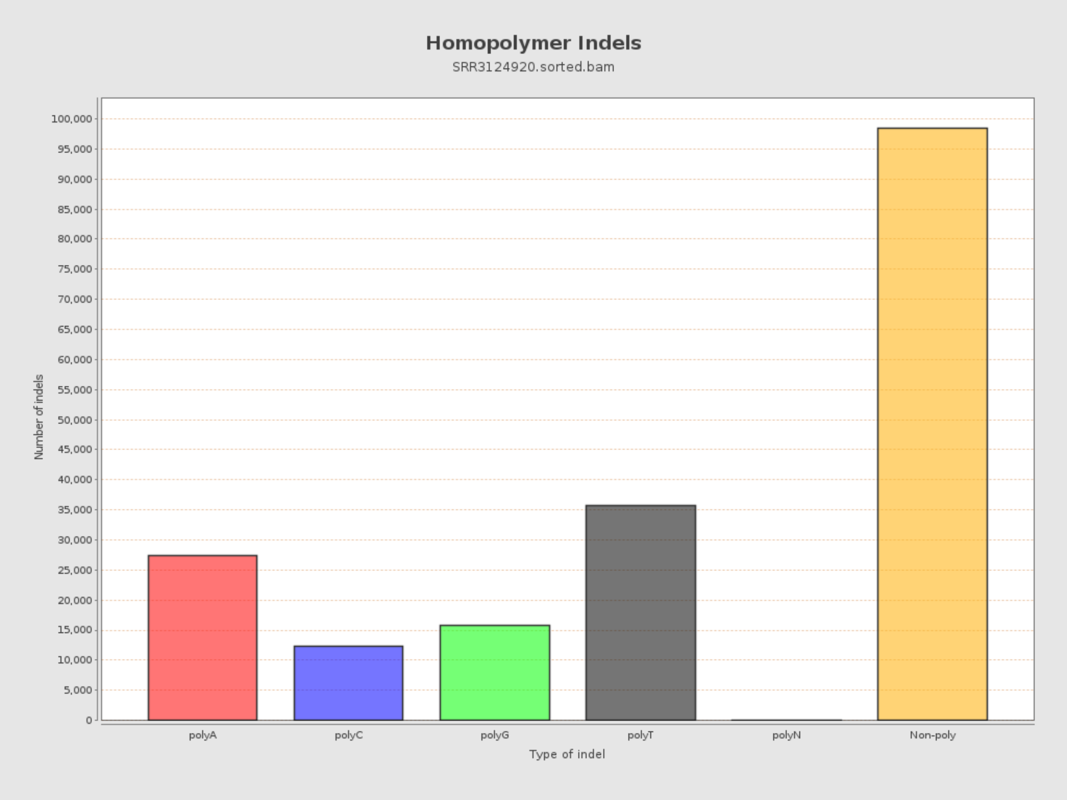
9. Results : Mapped Reads GC-content Distribution



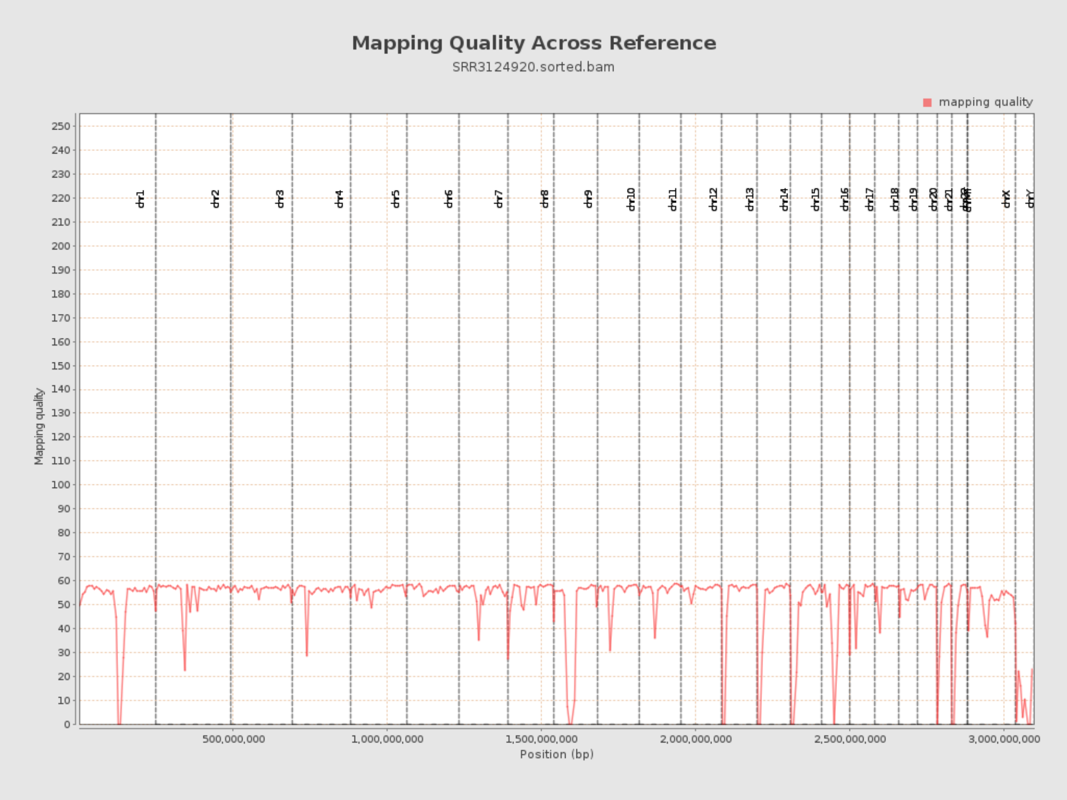
10. Results : Mapped Reads Clipping Profile



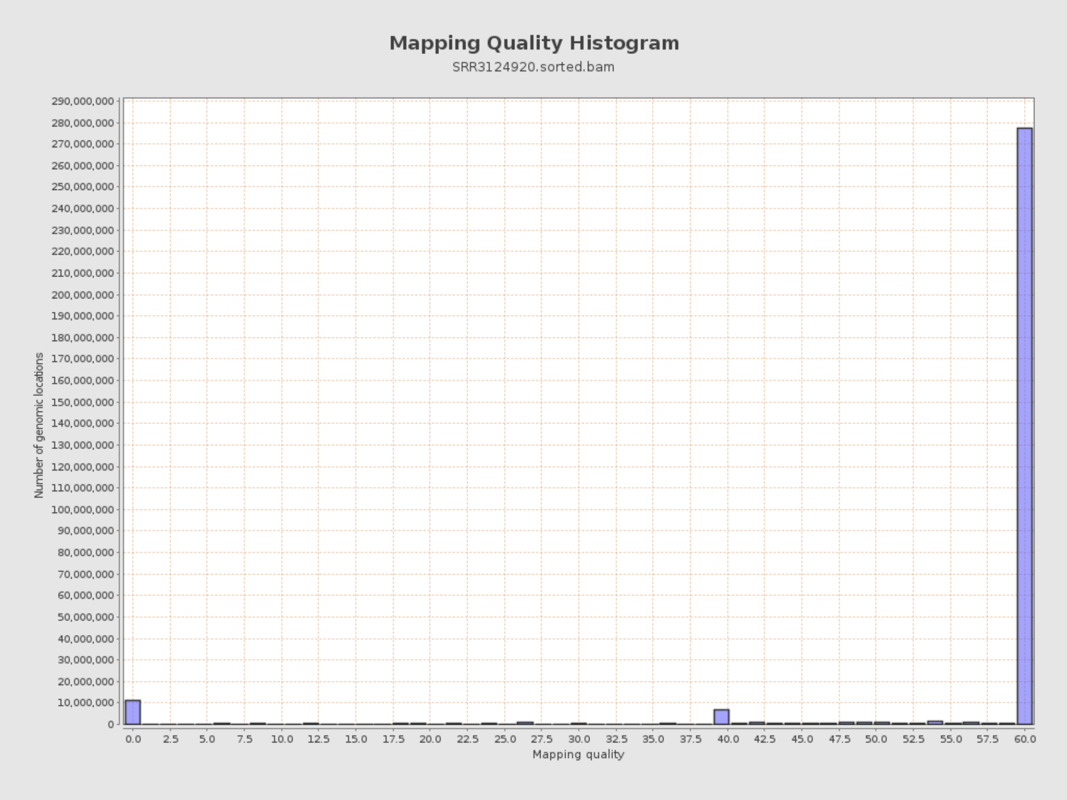
11. Results : Homopolymer Indels



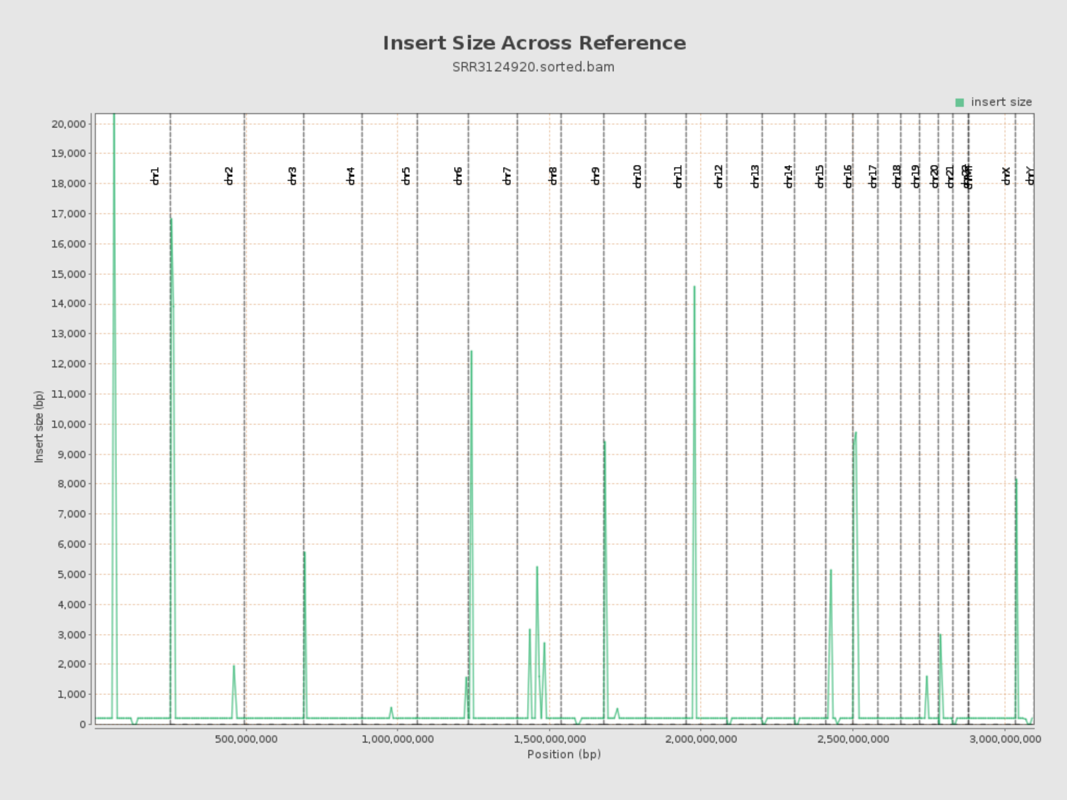
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram