Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 04:13:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124911.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_SRR3124911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124911_1.fastq.gz SRR3124911_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 04:13:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,918,832
Mapped reads	5,703,645 / 96.36%
Unmapped reads	215,187 / 3.64%
Mapped paired reads	5,703,645 / 96.36%
Mapped reads, first in pair	2,905,433 / 49.09%
Mapped reads, second in pair	2,798,212 / 47.28%
Mapped reads, both in pair	5,579,518 / 94.27%
Mapped reads, singletons	124,127 / 2.1%
Secondary alignments	0
Supplementary alignments	5,654 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	424,648 / 7.17%
Duplication rate	5.55%
Clipped reads	2,558,743 / 43.23%

2.2. ACGT Content

Number/percentage of A's	96,742,481 / 27.16%
Number/percentage of C's	64,812,301 / 18.2%
Number/percentage of T's	105,878,002 / 29.73%
Number/percentage of G's	88,735,121 / 24.91%
Number/percentage of N's	3,092 / 0%

GC Percentage	43.11%

2.3. Coverage

Mean	0.1151
Standard Deviation	0.7799

2.4. Mapping Quality

Mean Mapping Quality	51.97

2.5. Insert size

Mean	26,614.42
Standard Deviation	1,583,166.22
P25/Median/P75	143 / 192 / 267

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	2,422,796
Insertions	38,504
Mapped reads with at least one insertion	0.67%
Deletions	103,955
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.05%

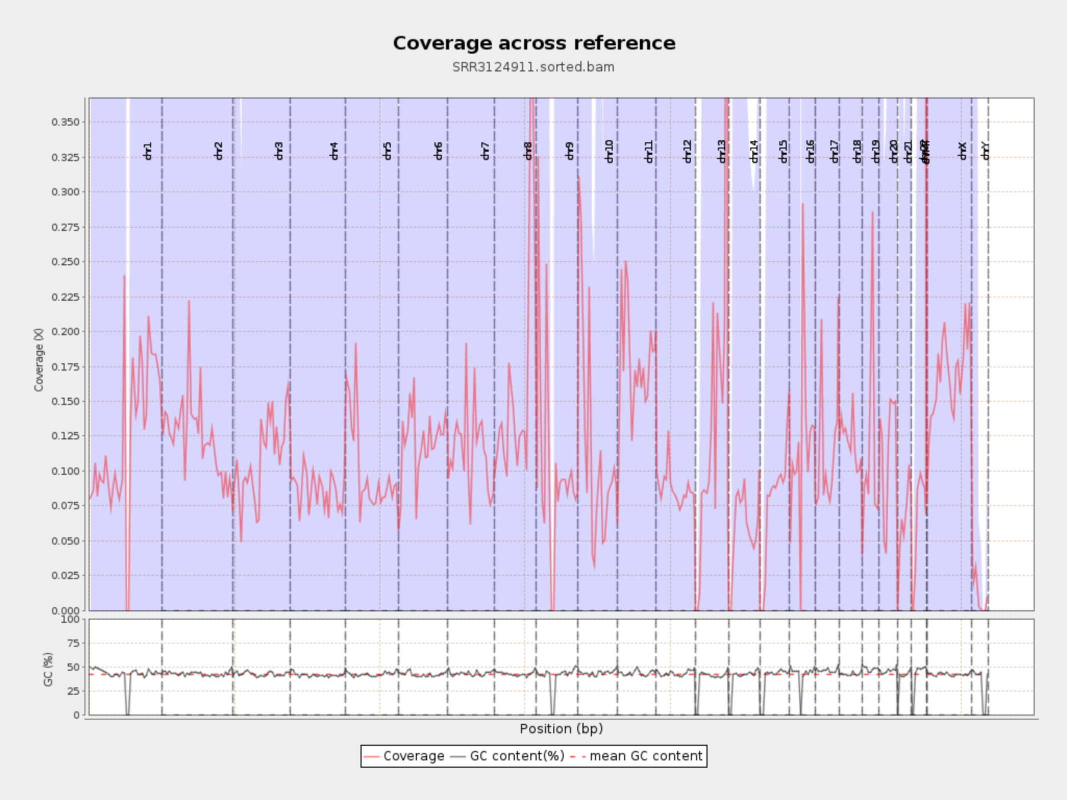
2.7. Chromosome stats

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

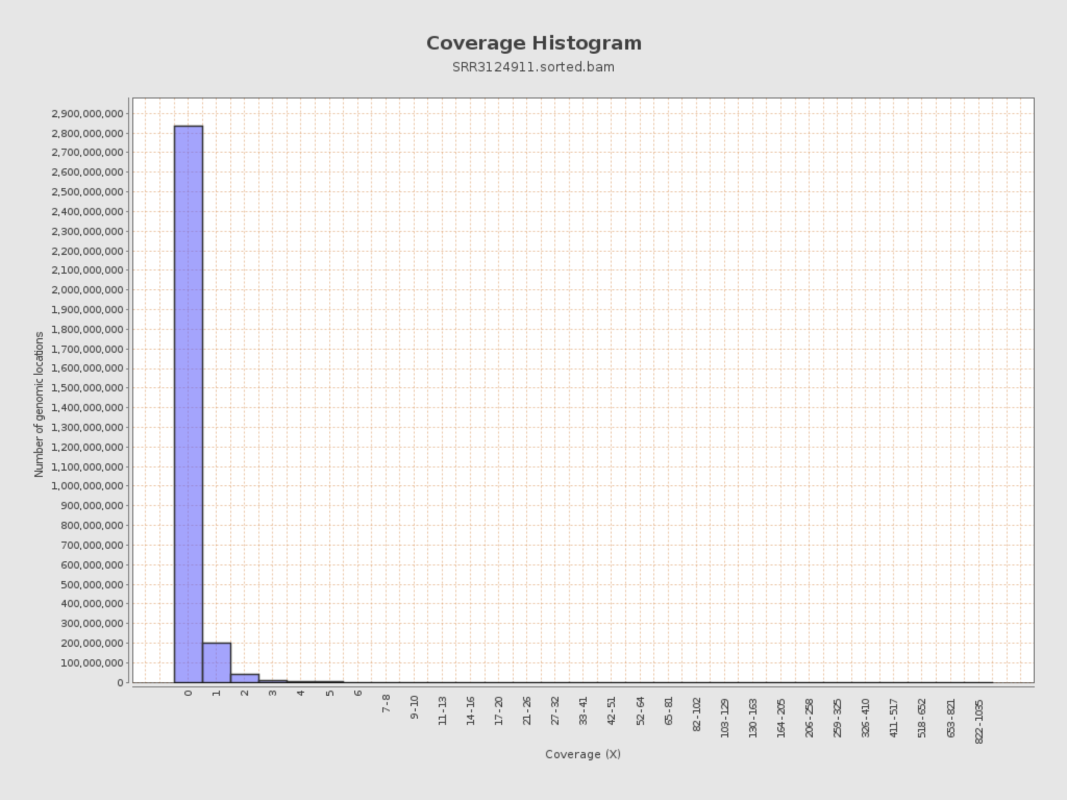
		bases	coverage	deviation
chr1	249250621	30817583	0.1236	0.9831
chr2	243199373	30277925	0.1245	0.9207
chr3	198022430	21471737	0.1084	0.4143
chr4	191154276	16464074	0.0861	0.4376
chr5	180915260	18250653	0.1009	0.4024
chr6	171115067	20641306	0.1206	0.6771
chr7	159138663	18407555	0.1157	0.9899
chr8	146364022	24298061	0.166	0.6226
chr9	141213431	14657584	0.1038	0.6896
chr10	135534747	16119252	0.1189	1.4613
chr11	135006516	23702244	0.1756	0.7146
chr12	133851895	11740442	0.0877	0.3713
chr13	115169878	18398303	0.1597	0.7214
chr14	107349540	6165005	0.0574	0.3375
chr15	102531392	7920172	0.0772	0.3608
chr16	90354753	10672798	0.1181	1.3336
chr17	81195210	9173942	0.113	1.0078
chr18	78077248	9512321	0.1218	1.0586
chr19	59128983	7089818	0.1199	0.8787
chr20	63025520	7144946	0.1134	0.4544
chr21	48129895	3095607	0.0643	0.345
chr22	51304566	3190966	0.0622	0.3117
chrMT	16571	364399	21.9902	16.1562
chrX	155270560	26072422	0.1679	0.7473

chrY	59373566	675366	0.0114	0.4686

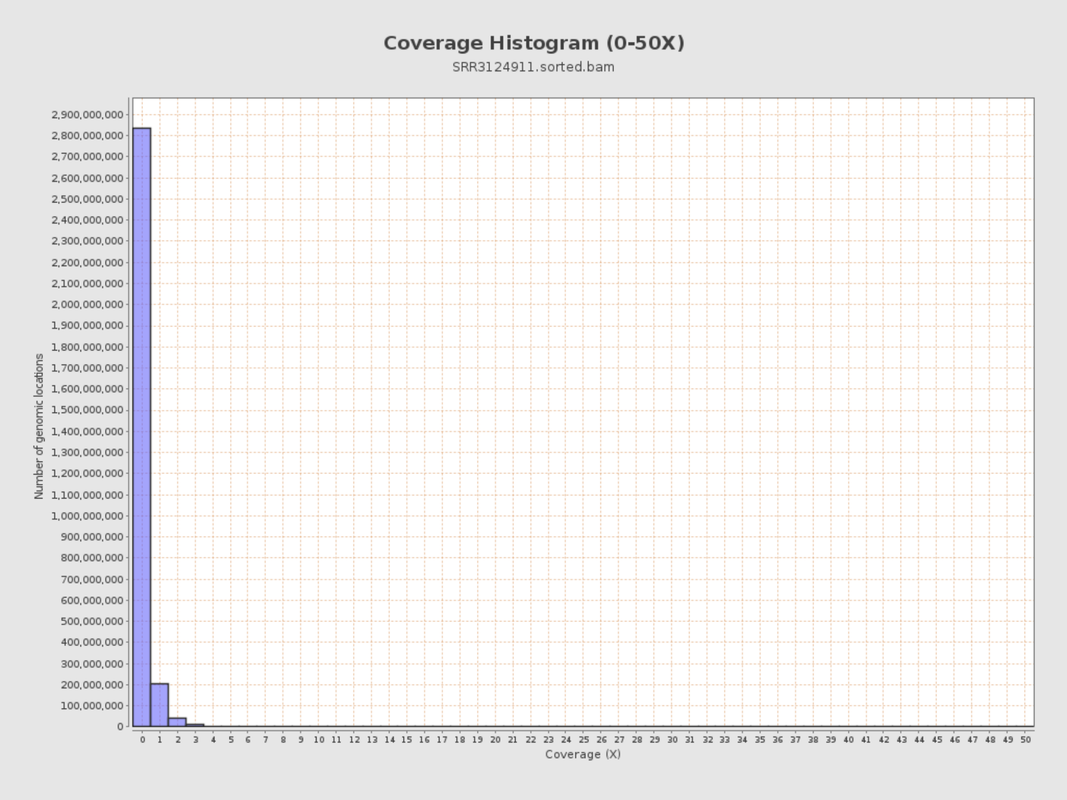
3. Results : Coverage across reference



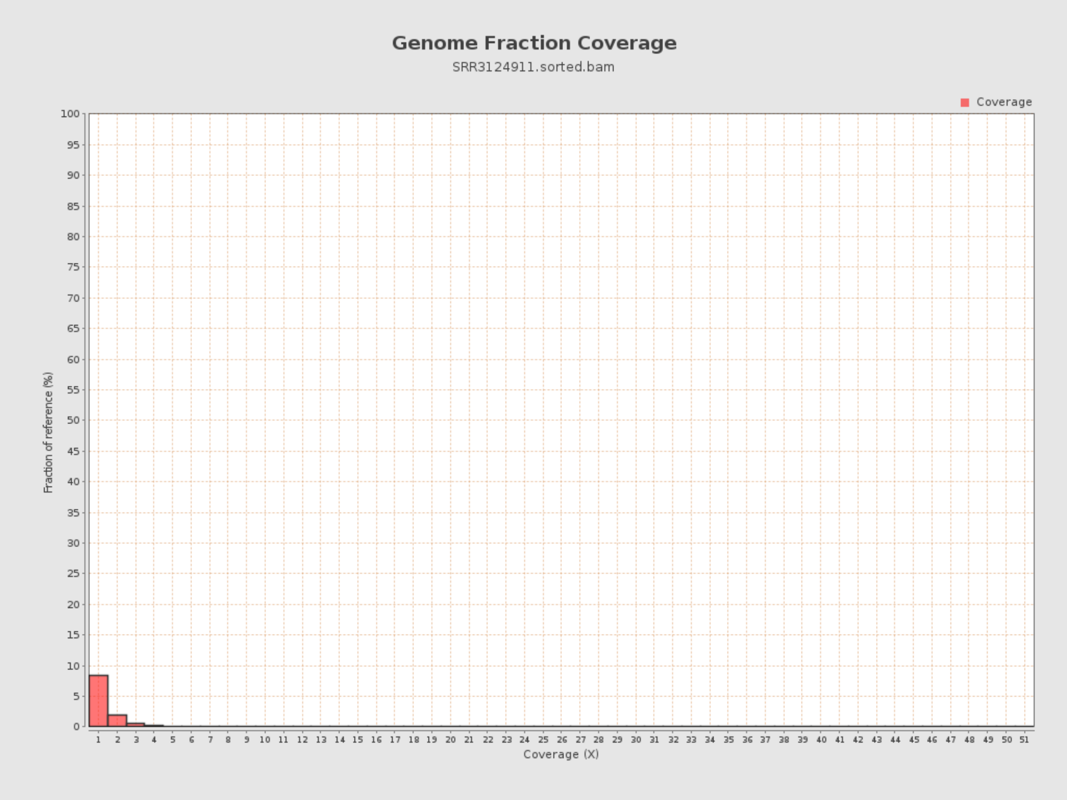
4. Results : Coverage Histogram



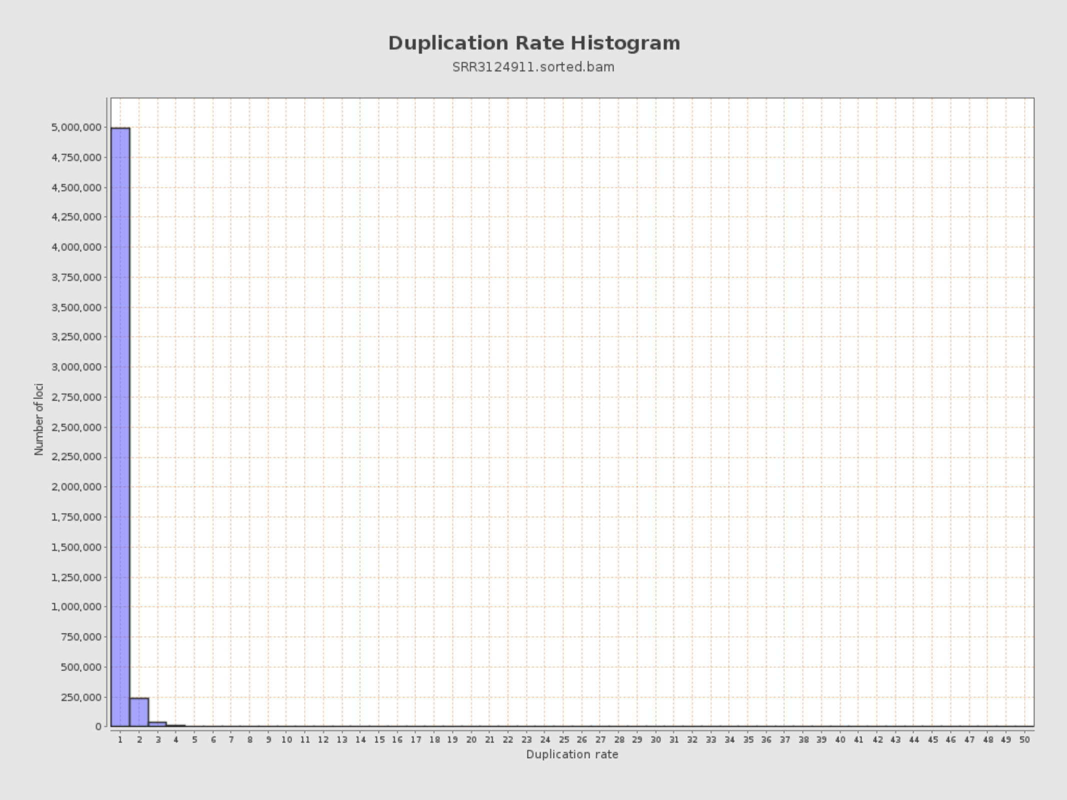
5. Results : Coverage Histogram (0-50X)



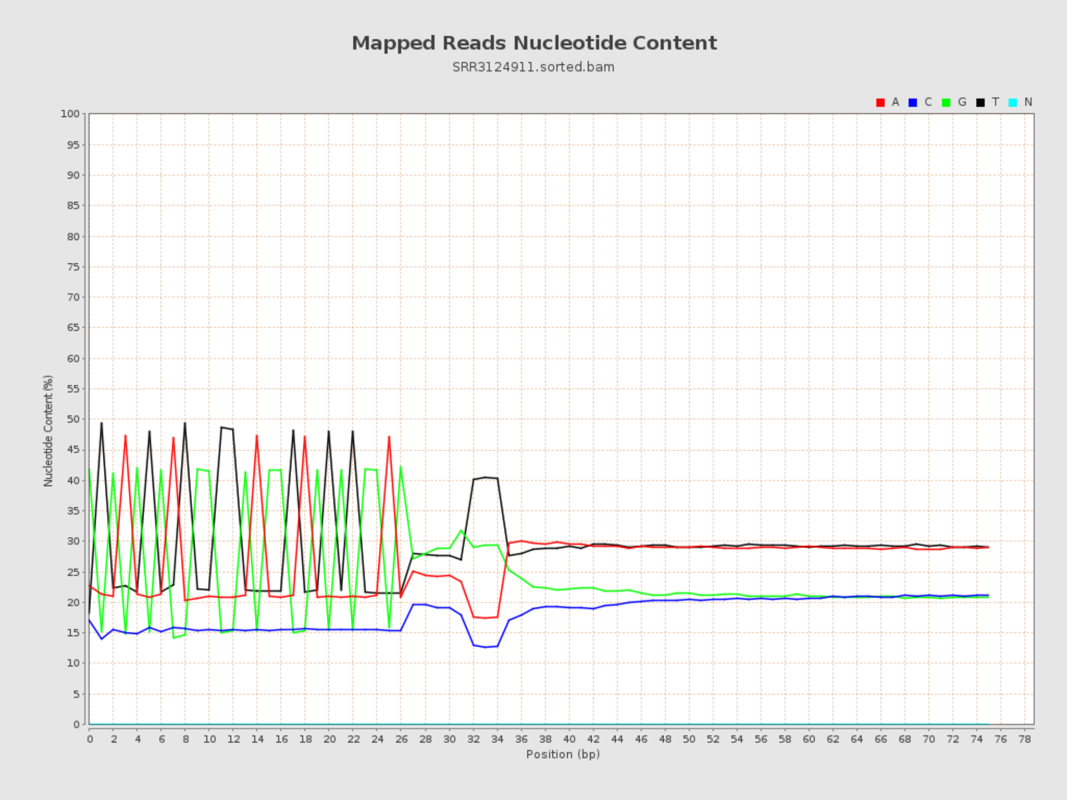
6. Results : Genome Fraction Coverage



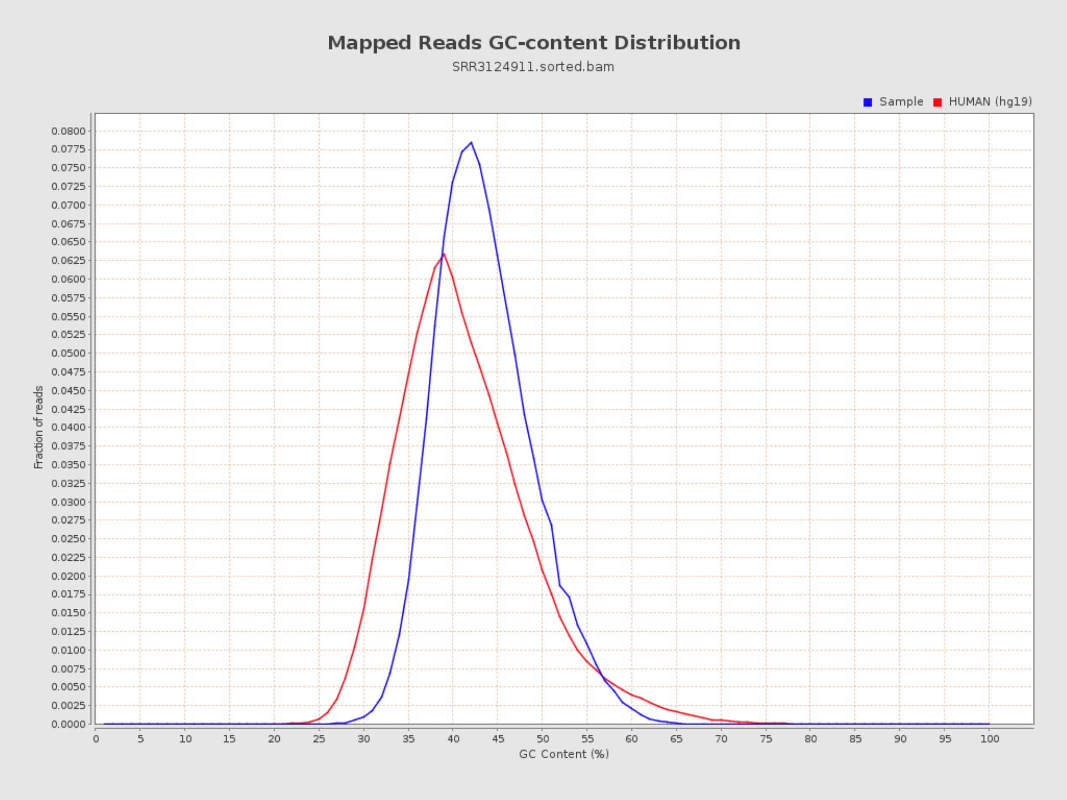
7. Results : Duplication Rate Histogram



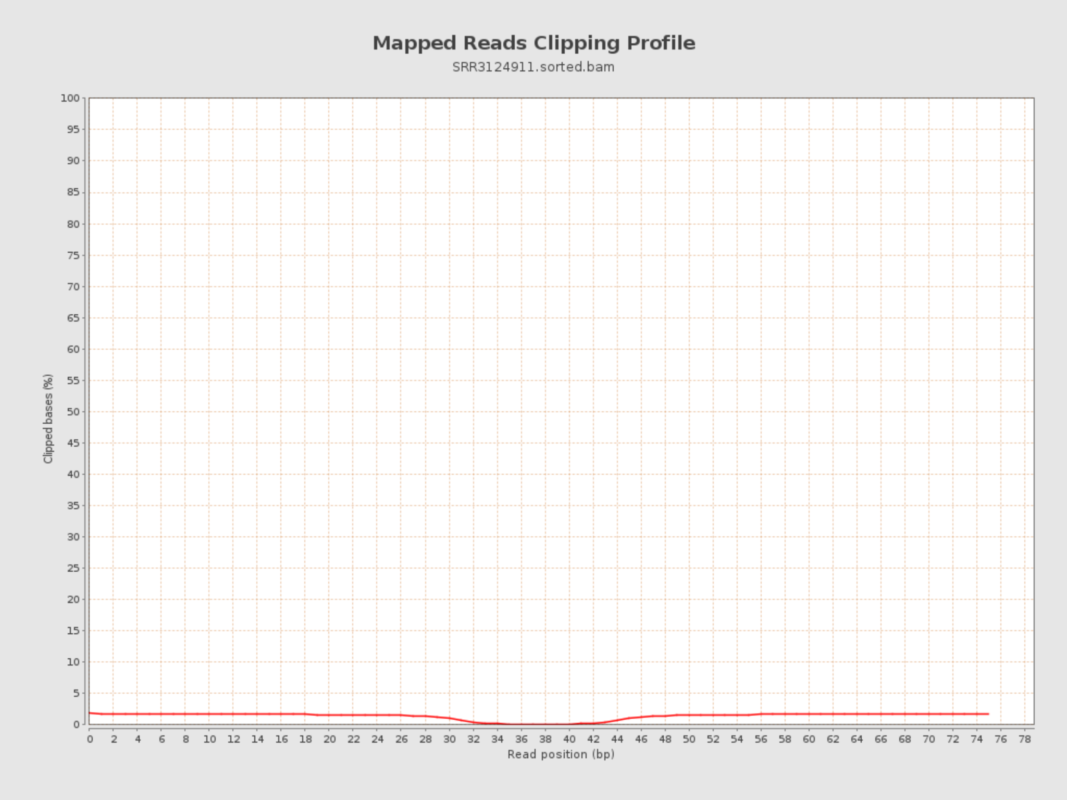
8. Results : Mapped Reads Nucleotide Content



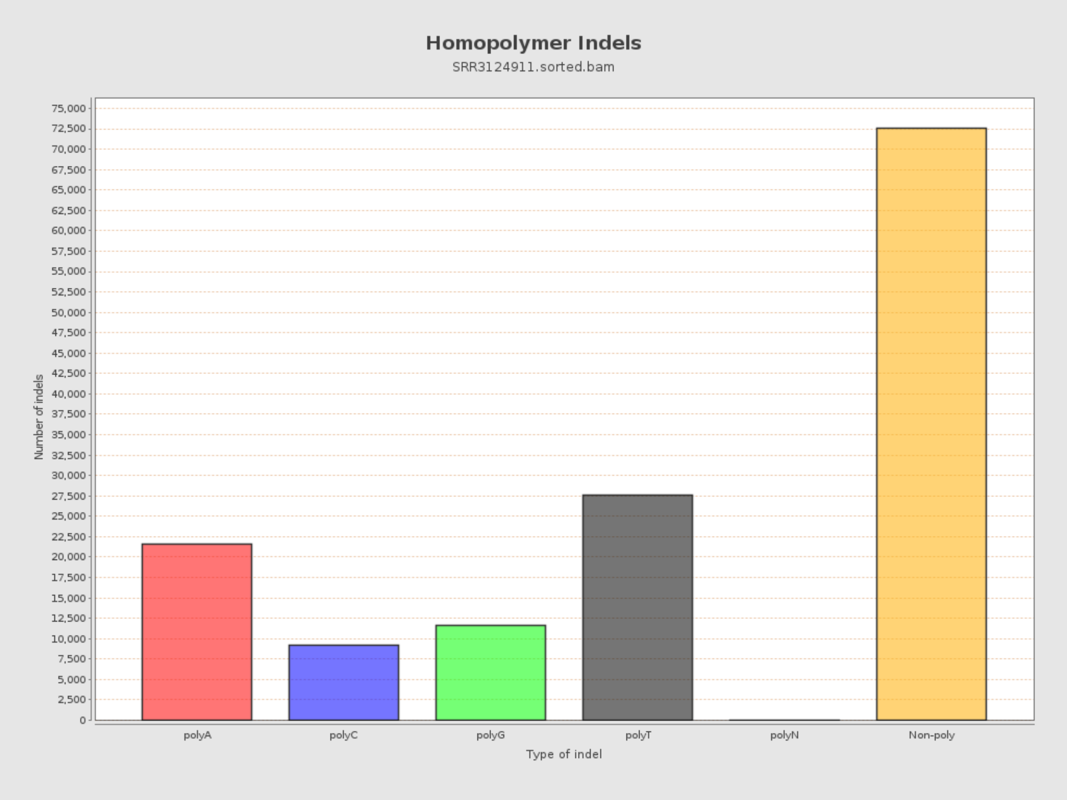
9. Results : Mapped Reads GC-content Distribution



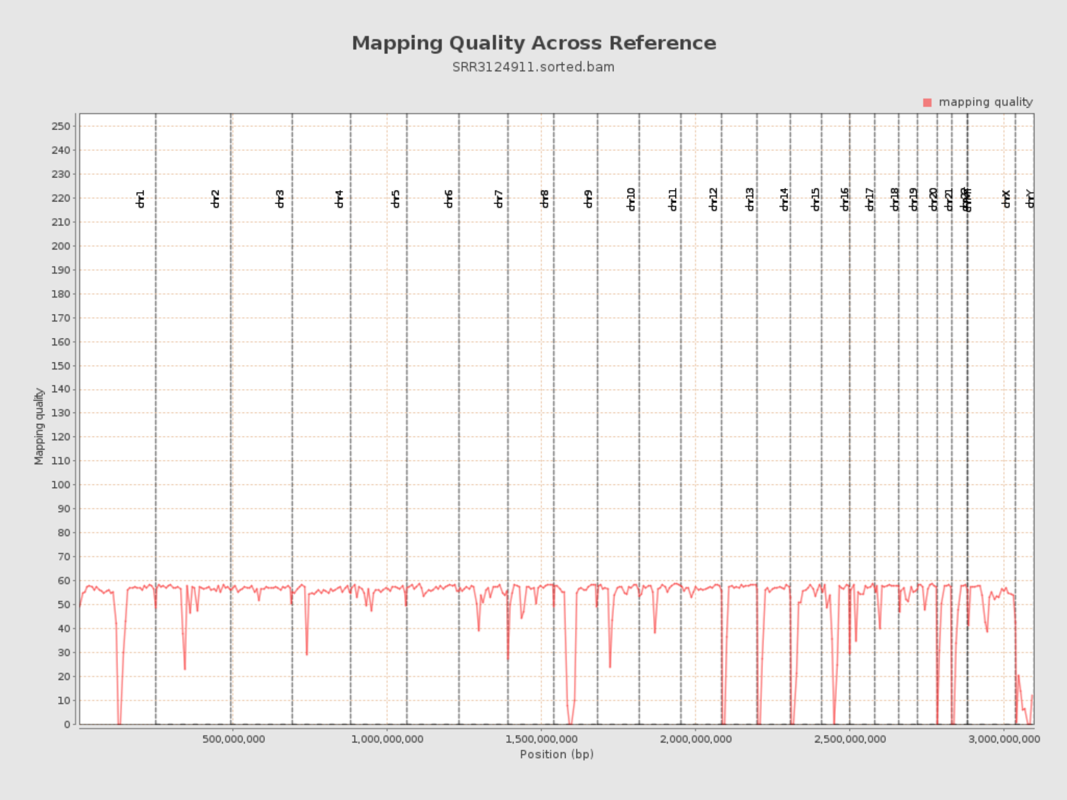
10. Results : Mapped Reads Clipping Profile



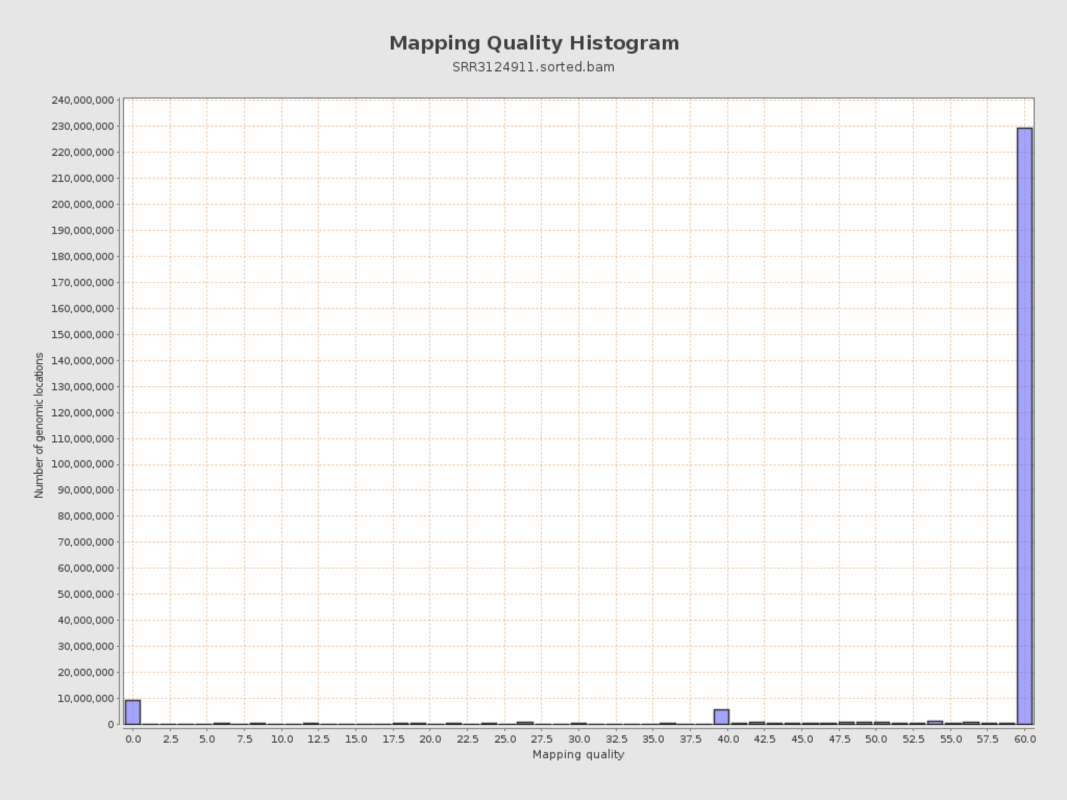
11. Results : Homopolymer Indels



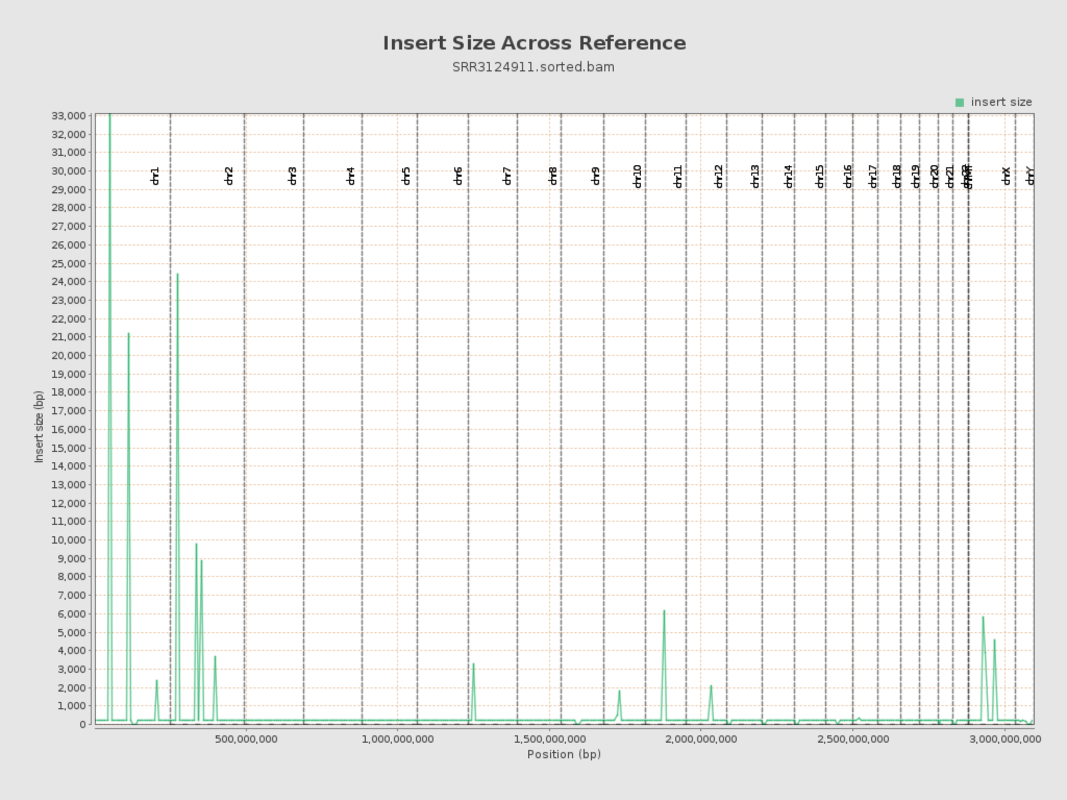
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram