Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:09:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124941.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_SRR3124941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124941_1.fastq.gz SRR3124941_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:09:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,877,382
Mapped reads	1,846,576 / 98.36%
Unmapped reads	30,806 / 1.64%
Mapped paired reads	1,846,576 / 98.36%
Mapped reads, first in pair	924,050 / 49.22%
Mapped reads, second in pair	922,526 / 49.14%
Mapped reads, both in pair	1,840,820 / 98.05%
Mapped reads, singletons	5,756 / 0.31%
Secondary alignments	0
Supplementary alignments	12,981 / 0.69%
Read min/max/mean length	30 / 151 / 151.34
Duplicated reads (estimated)	260,908 / 13.9%
Duplication rate	14.21%
Clipped reads	1,316,326 / 70.11%

2.2. ACGT Content

Number/percentage of A's	72,992,195 / 29.08%
Number/percentage of C's	50,795,421 / 20.24%
Number/percentage of T's	73,795,211 / 29.4%
Number/percentage of G's	53,401,280 / 21.27%
Number/percentage of N's	21,520 / 0.01%

GC Percentage	41.51%

2.3. Coverage

Mean	0.0811
Standard Deviation	0.8497

2.4. Mapping Quality

Mean Mapping Quality	53.8

2.5. Insert size

Mean	59,657.09
Standard Deviation	2,349,132.46
P25/Median/P75	142 / 176 / 224

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	2,816,326
Insertions	43,509
Mapped reads with at least one insertion	2.29%
Deletions	87,274
Mapped reads with at least one deletion	4.59%
Homopolymer indels	47.91%

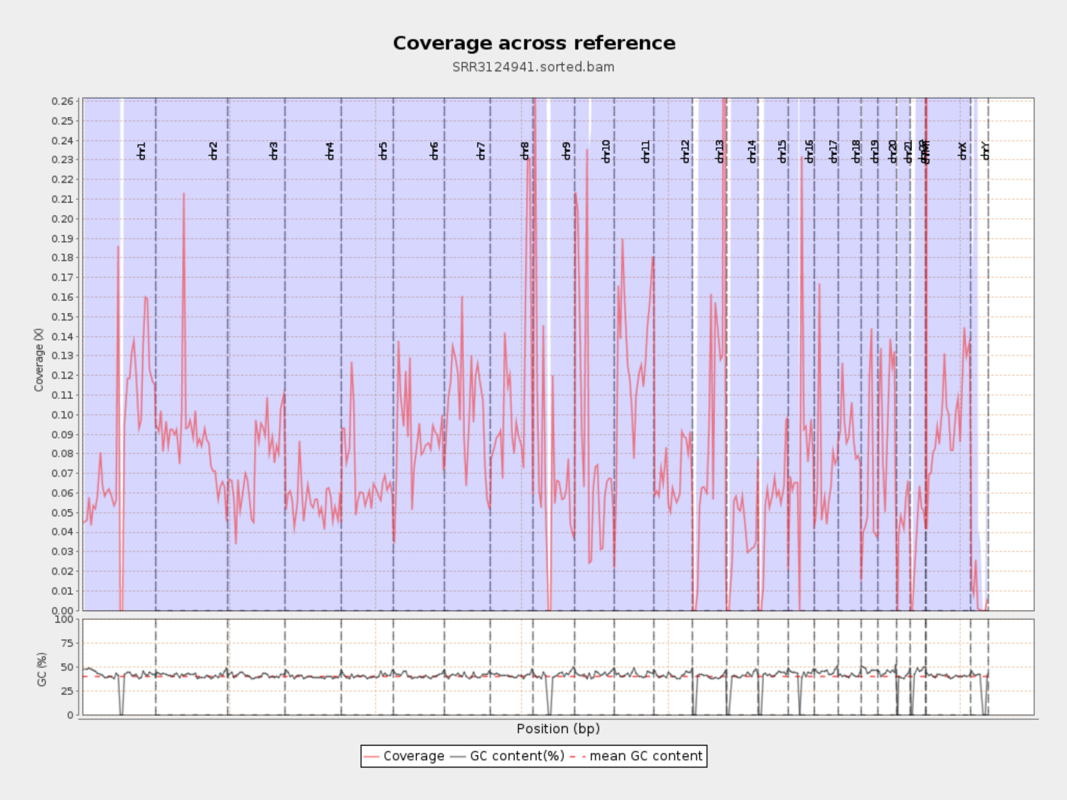
2.7. Chromosome stats

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

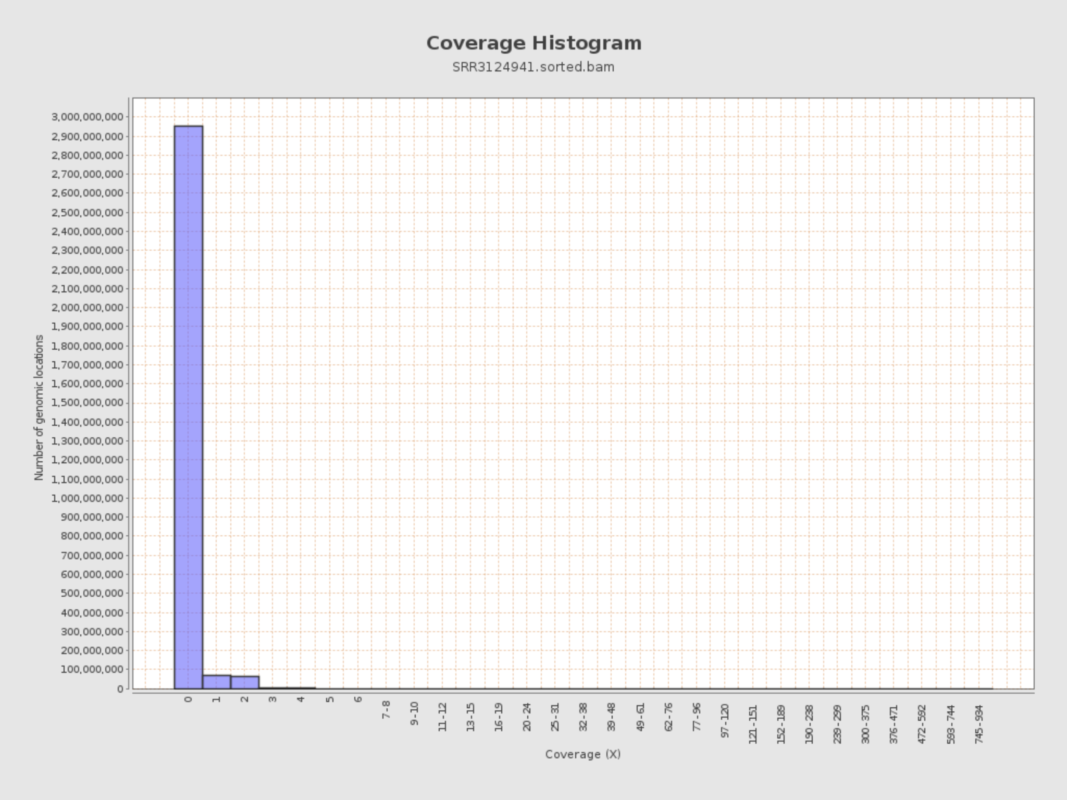
		bases	coverage	deviation
chr1	249250621	21522908	0.0864	1.0644
chr2	243199373	21476871	0.0883	0.8677
chr3	198022430	14852106	0.075	0.3779
chr4	191154276	10665198	0.0558	0.4439
chr5	180915260	12409397	0.0686	0.3622
chr6	171115067	15328139	0.0896	0.6246
chr7	159138663	16495584	0.1037	1.3159
chr8	146364022	16343819	0.1117	0.5375
chr9	141213431	10536980	0.0746	1.1606
chr10	135534747	11939503	0.0881	1.8888
chr11	135006516	17318278	0.1283	0.8148
chr12	133851895	9265236	0.0692	0.3626
chr13	115169878	13485584	0.1171	0.5894
chr14	107349540	3943263	0.0367	0.2682
chr15	102531392	5265075	0.0514	0.313
chr16	90354753	7314479	0.081	1.0893
chr17	81195210	5698765	0.0702	1.1968
chr18	78077248	7152994	0.0916	1.3008
chr19	59128983	3785620	0.064	0.6397
chr20	63025520	6529717	0.1036	0.4654
chr21	48129895	2131473	0.0443	0.3348
chr22	51304566	1880822	0.0367	0.2628
chrMT	16571	175358	10.5822	7.0832
chrX	155270560	15248851	0.0982	0.5146

chrY	59373566	389653	0.0066	0.3787

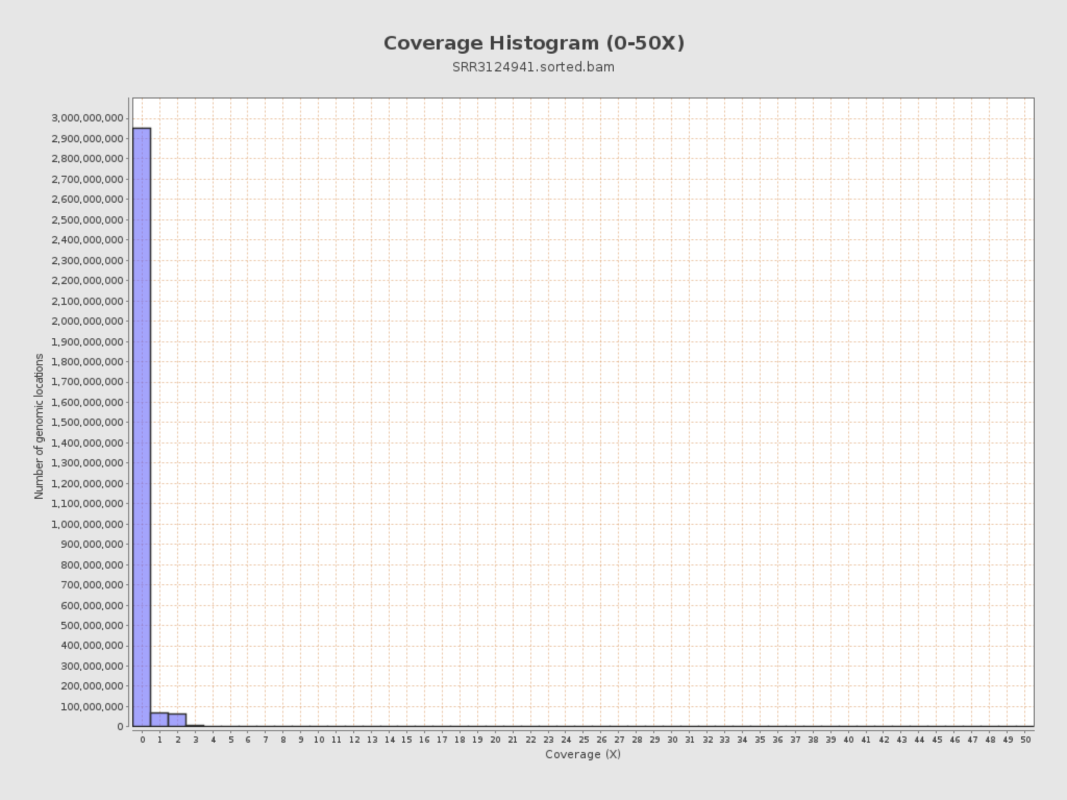
3. Results : Coverage across reference



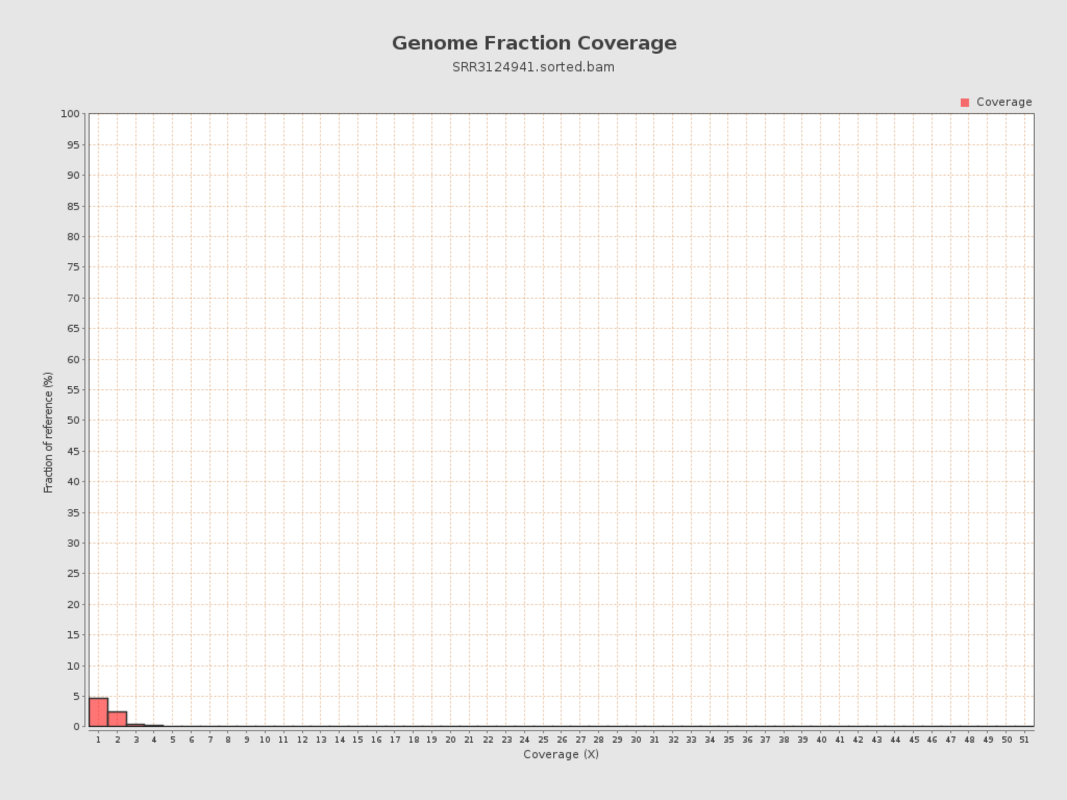
4. Results : Coverage Histogram



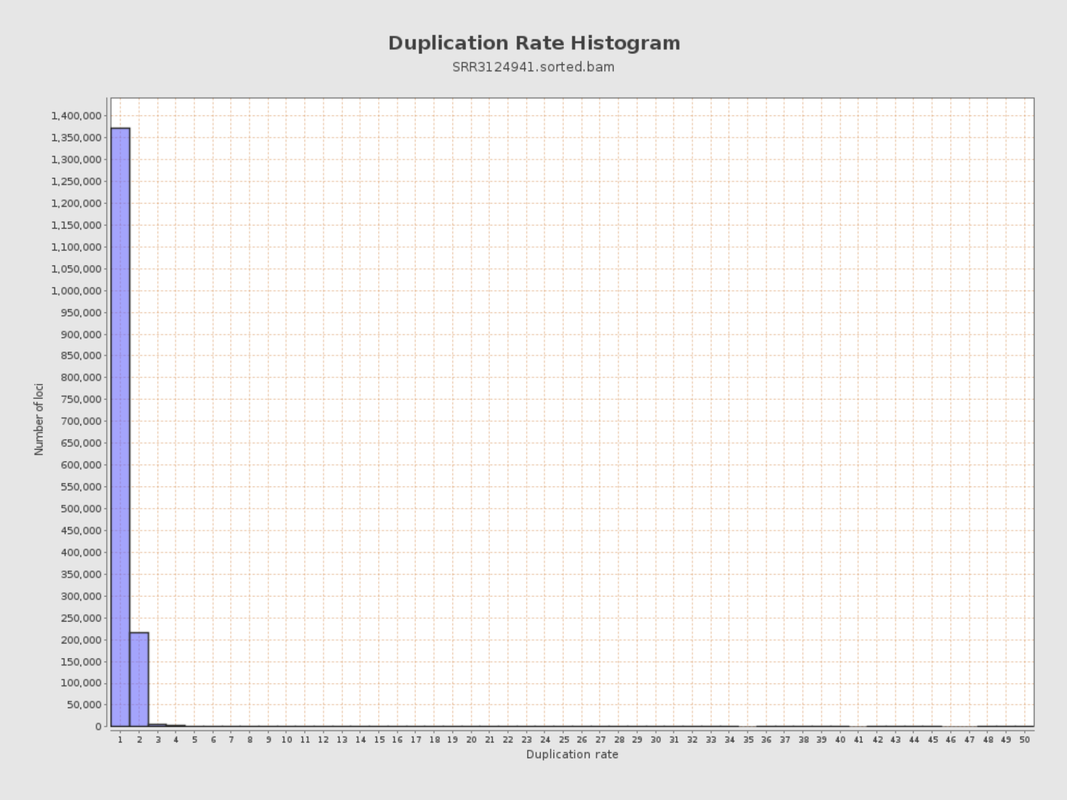
5. Results : Coverage Histogram (0-50X)



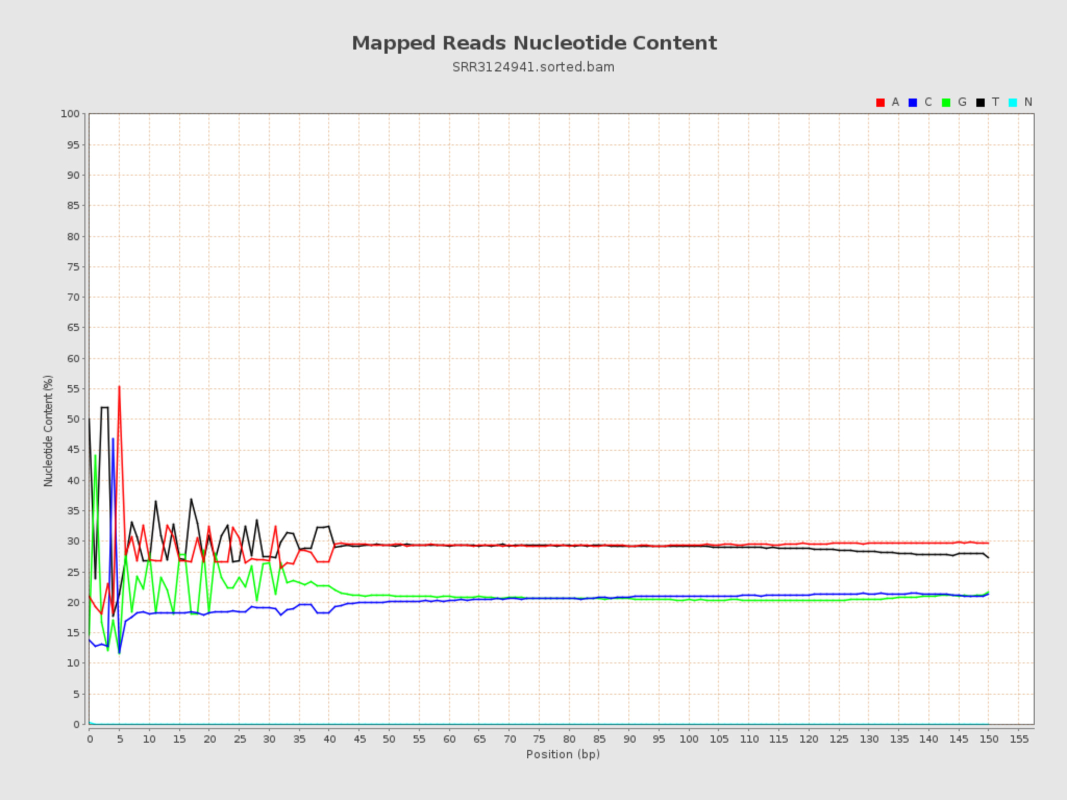
6. Results : Genome Fraction Coverage



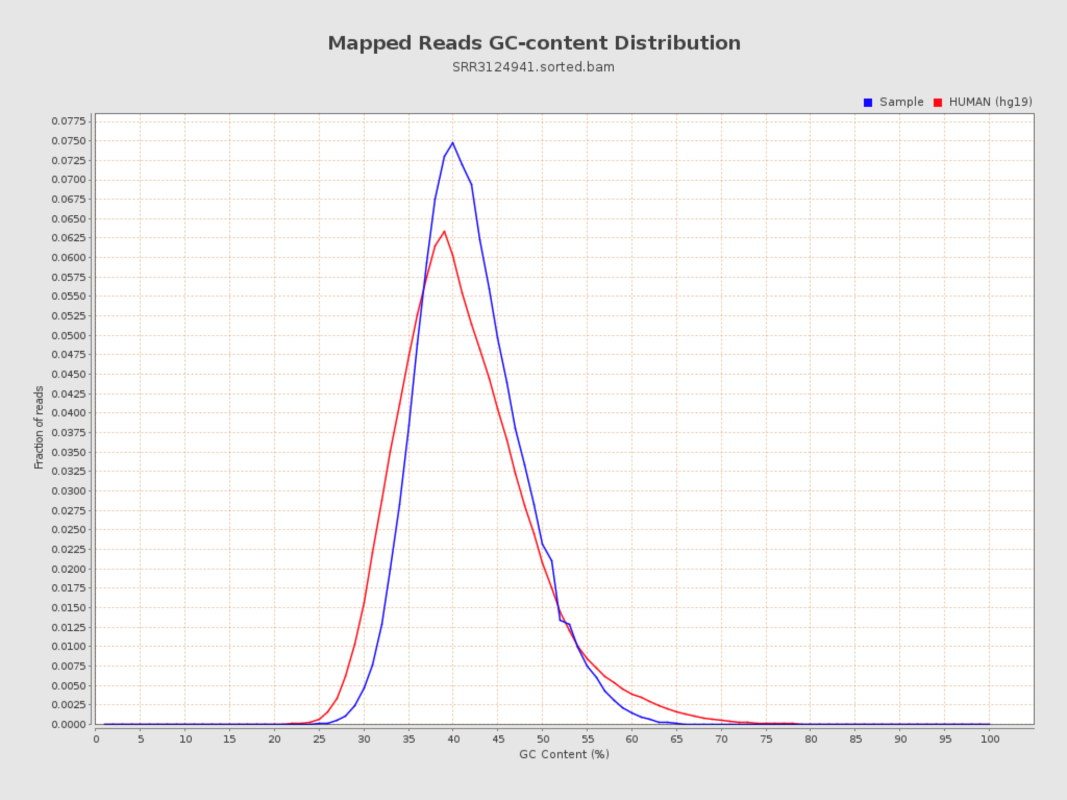
7. Results : Duplication Rate Histogram



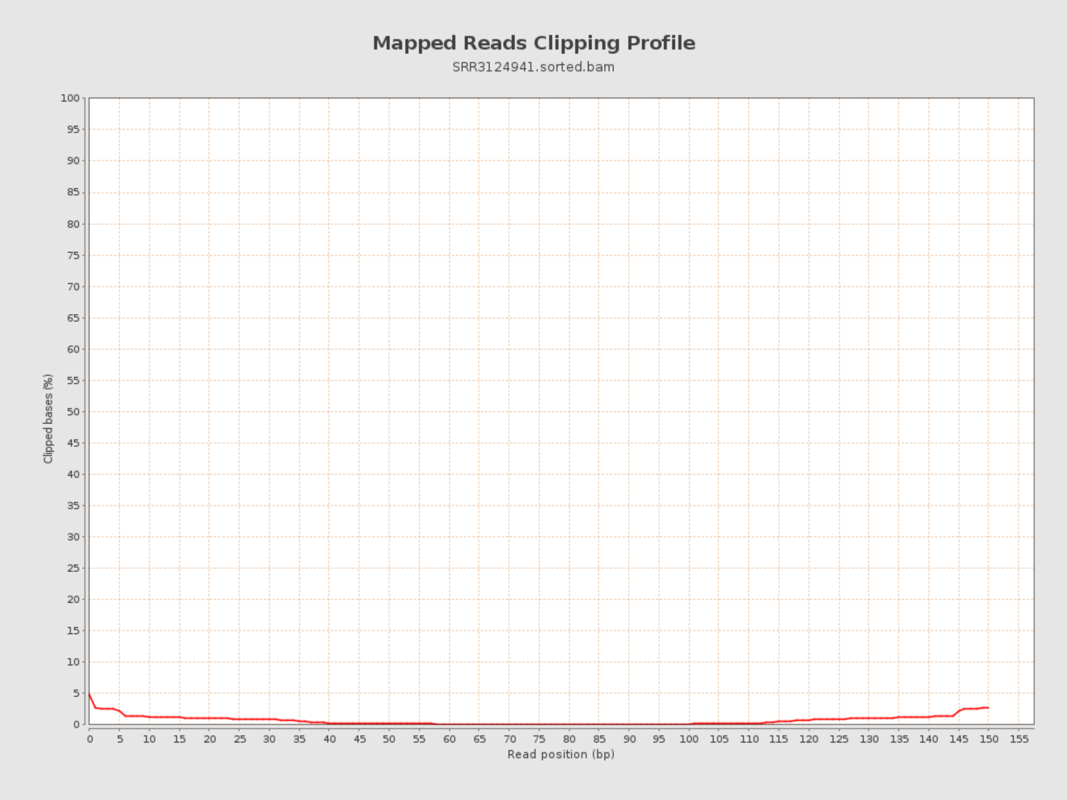
8. Results : Mapped Reads Nucleotide Content



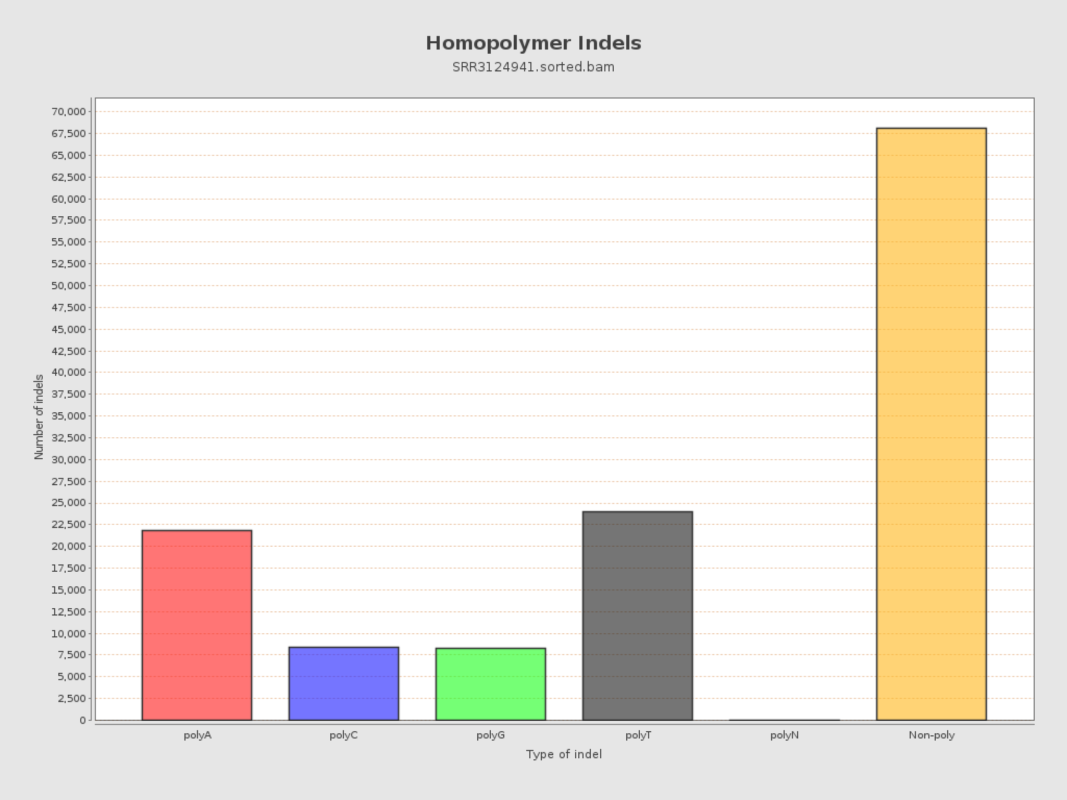
9. Results : Mapped Reads GC-content Distribution



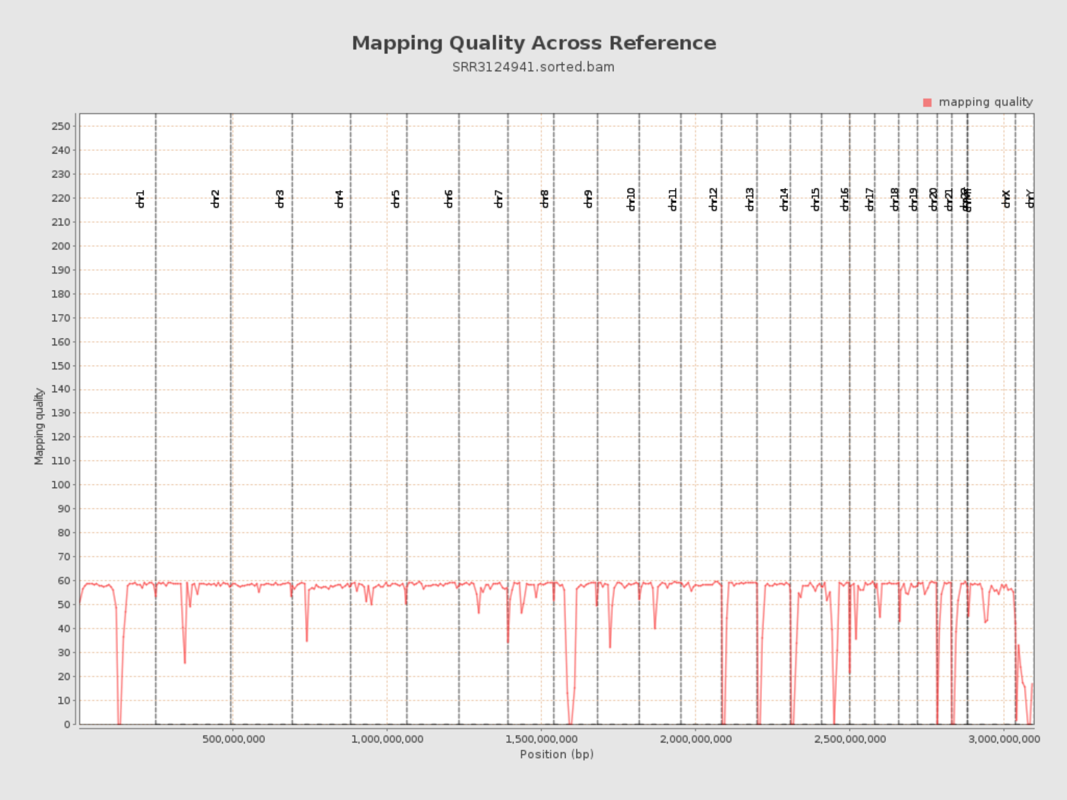
10. Results : Mapped Reads Clipping Profile



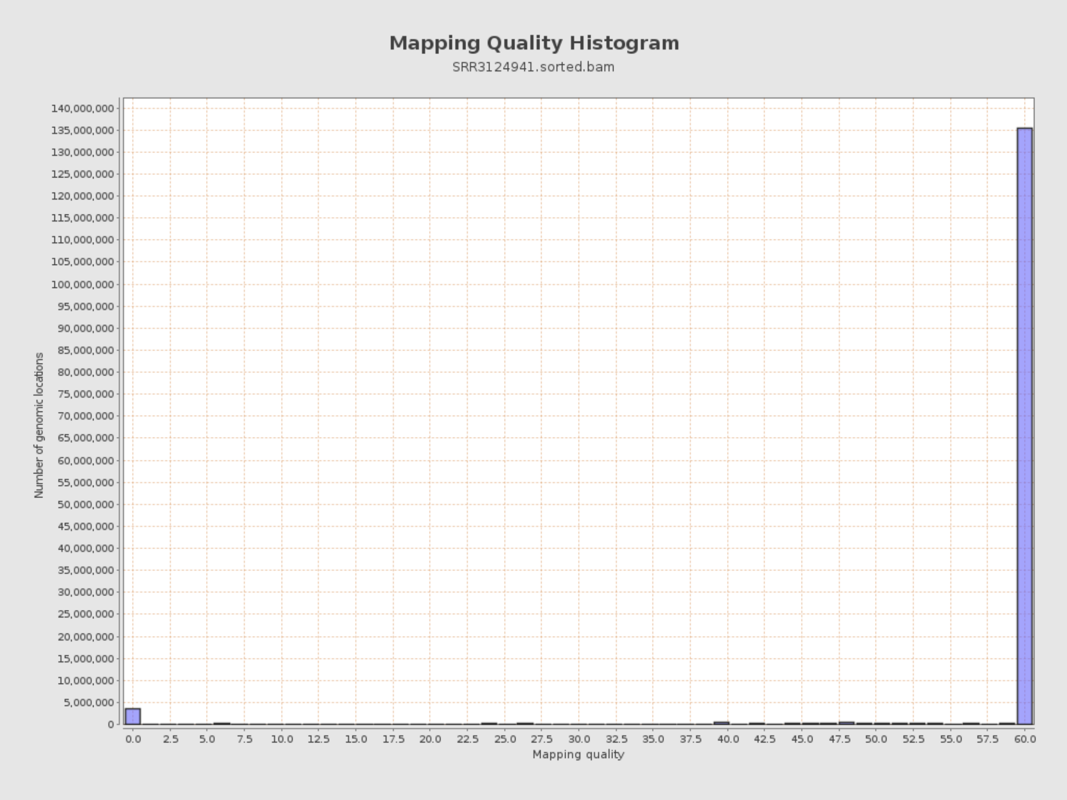
11. Results : Homopolymer Indels



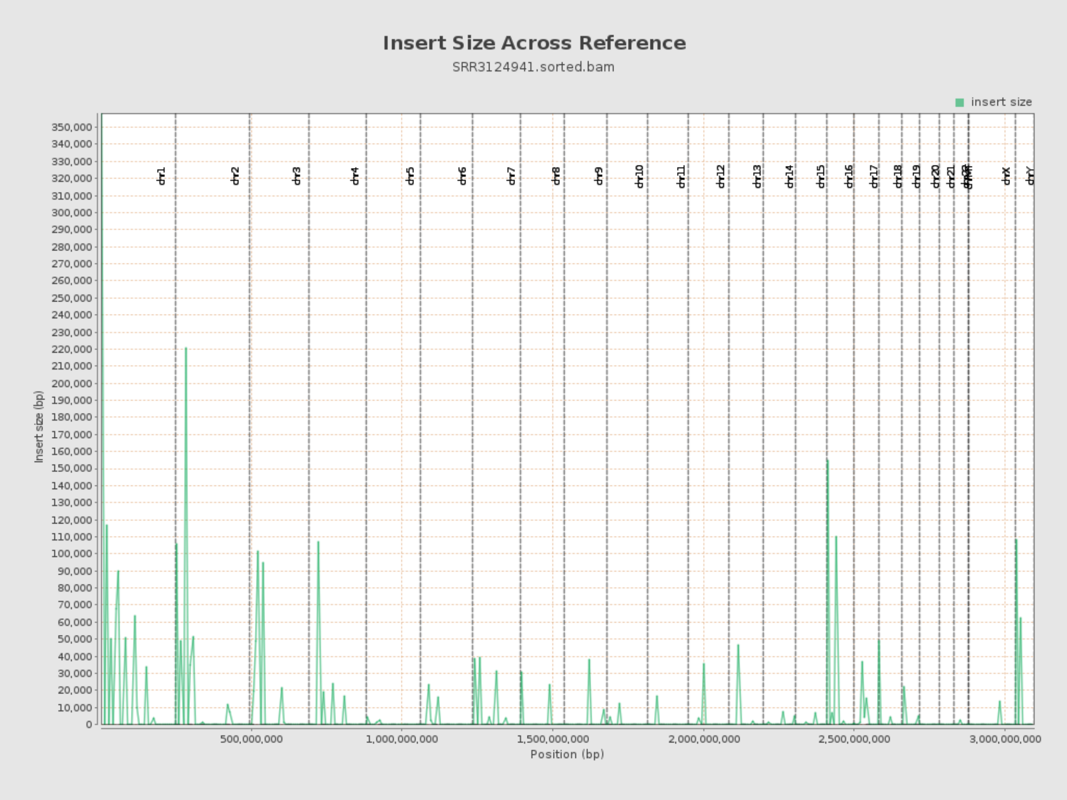
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram