Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:04:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124940.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_SRR3124940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124940_1.fastq.gz SRR3124940_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:04:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,092,458
Mapped reads	2,057,439 / 98.33%
Unmapped reads	35,019 / 1.67%
Mapped paired reads	2,057,439 / 98.33%
Mapped reads, first in pair	1,029,286 / 49.19%
Mapped reads, second in pair	1,028,153 / 49.14%
Mapped reads, both in pair	2,046,388 / 97.8%
Mapped reads, singletons	11,051 / 0.53%
Secondary alignments	0
Supplementary alignments	33,913 / 1.62%
Read min/max/mean length	30 / 151 / 151.78
Duplicated reads (estimated)	329,347 / 15.74%
Duplication rate	15.61%
Clipped reads	1,580,509 / 75.53%

2.2. ACGT Content

Number/percentage of A's	80,284,173 / 29.23%
Number/percentage of C's	55,211,640 / 20.1%
Number/percentage of T's	80,597,719 / 29.34%
Number/percentage of G's	58,586,490 / 21.33%
Number/percentage of N's	20,335 / 0.01%

GC Percentage	41.43%

2.3. Coverage

Mean	0.0888
Standard Deviation	0.9983

2.4. Mapping Quality

Mean Mapping Quality	53.54

2.5. Insert size

Mean	82,152.97
Standard Deviation	2,725,616.59
P25/Median/P75	134 / 167 / 211

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	3,105,646
Insertions	57,109
Mapped reads with at least one insertion	2.62%
Deletions	108,823
Mapped reads with at least one deletion	5.07%
Homopolymer indels	45.4%

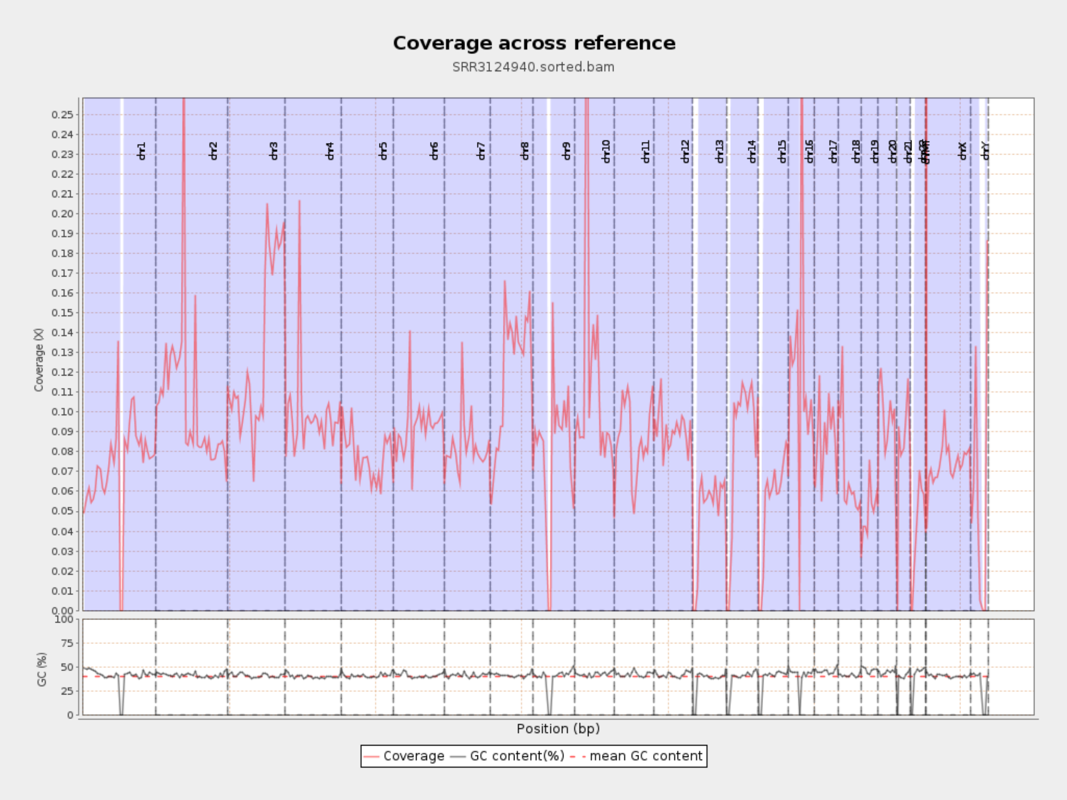
2.7. Chromosome stats

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

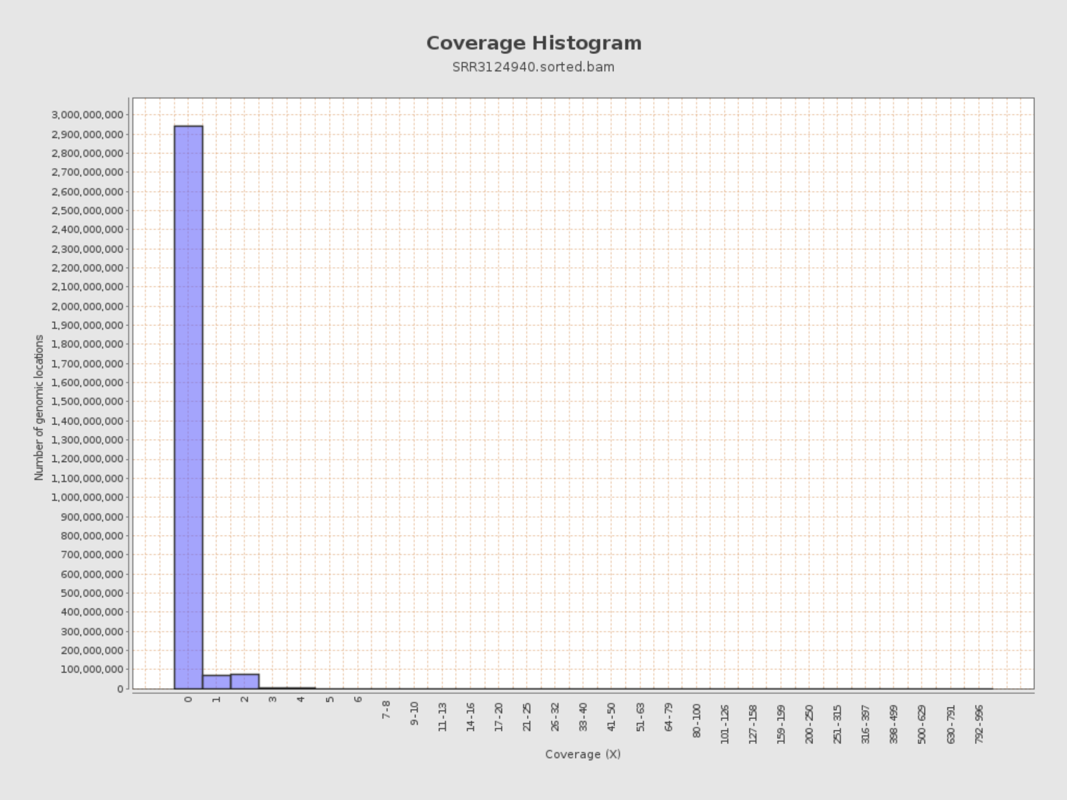
		bases	coverage	deviation
chr1	249250621	18194867	0.073	0.8508
chr2	243199373	25784731	0.106	1.5048
chr3	198022430	25962104	0.1311	0.5134
chr4	191154276	18901249	0.0989	0.8182
chr5	180915260	14077835	0.0778	0.3905
chr6	171115067	15896552	0.0929	0.7026
chr7	159138663	13166200	0.0827	0.9196
chr8	146364022	17708757	0.121	0.5839
chr9	141213431	11429323	0.0809	1.5381
chr10	135534747	15609919	0.1152	2.2965
chr11	135006516	11660368	0.0864	0.7596
chr12	133851895	12155432	0.0908	0.4177
chr13	115169878	5733907	0.0498	0.3044
chr14	107349540	9223022	0.0859	0.4232
chr15	102531392	5490094	0.0535	0.3173
chr16	90354753	10833844	0.1199	1.6595
chr17	81195210	7075748	0.0871	0.8065
chr18	78077248	5474341	0.0701	1.4481
chr19	59128983	2984454	0.0505	0.6277
chr20	63025520	6185659	0.0981	0.4821
chr21	48129895	4008720	0.0833	0.5725
chr22	51304566	2118040	0.0413	0.2931
chrMT	16571	187555	11.3183	7.0564
chrX	155270560	11445825	0.0737	0.4431

chrY	59373566	3610572	0.0608	1.4728

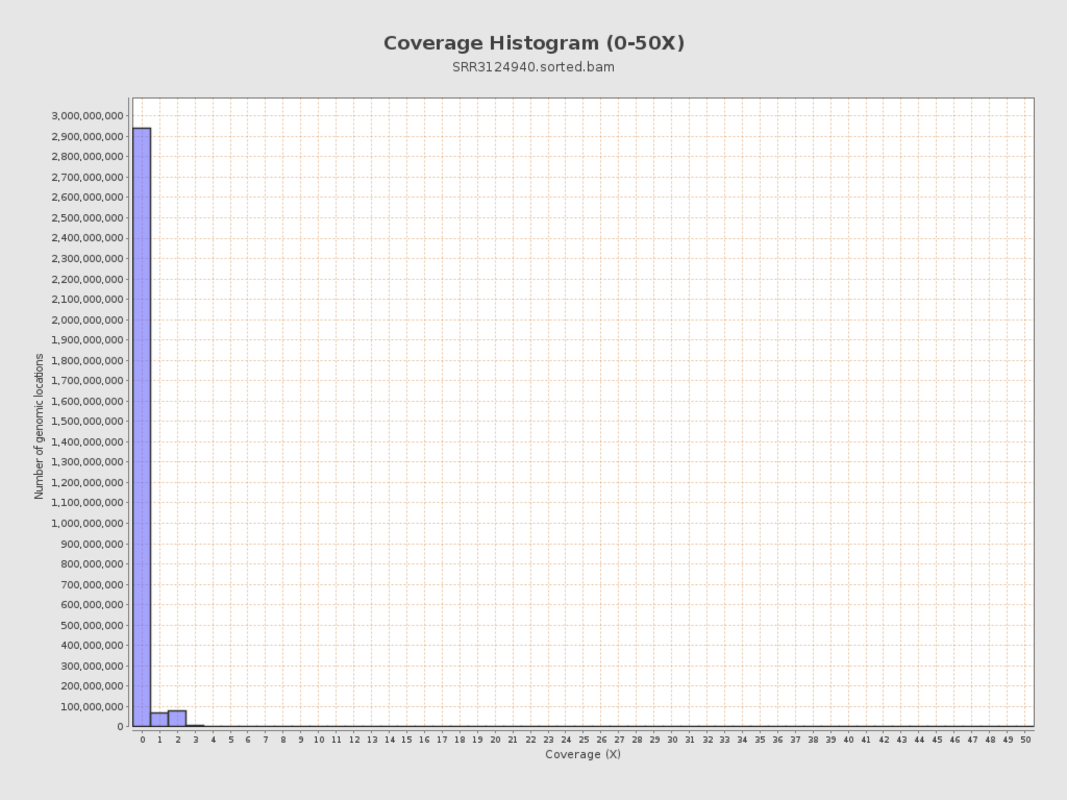
3. Results : Coverage across reference



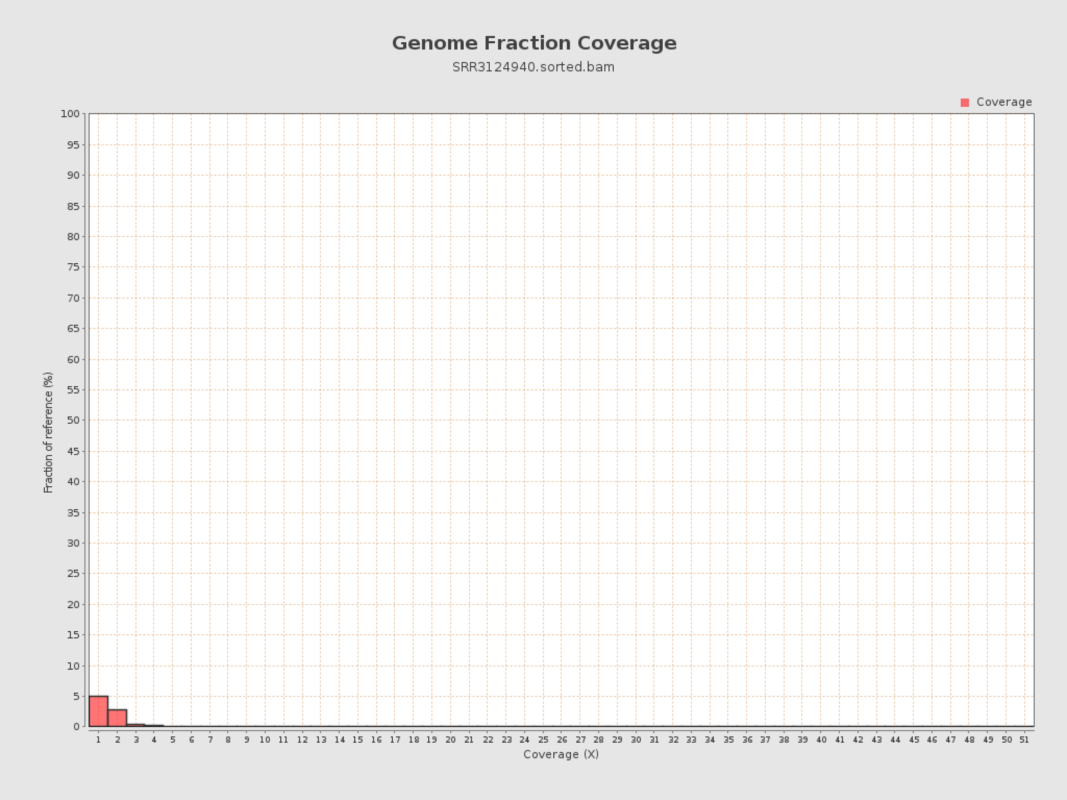
4. Results : Coverage Histogram



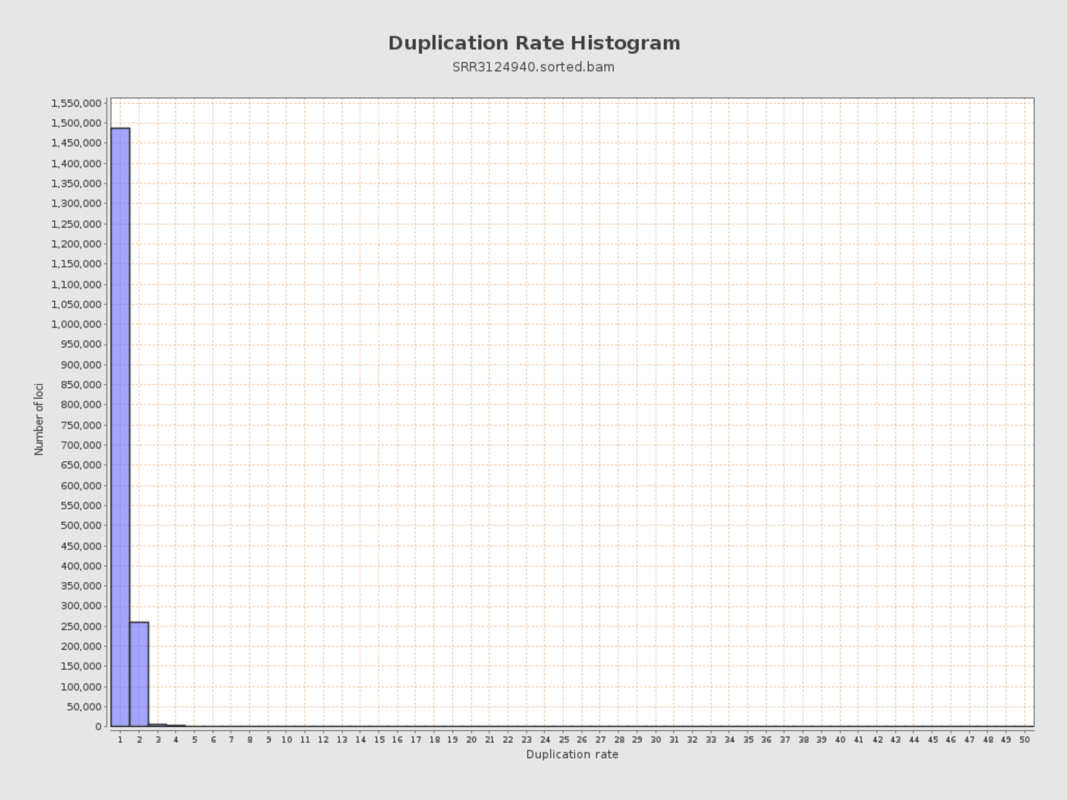
5. Results : Coverage Histogram (0-50X)



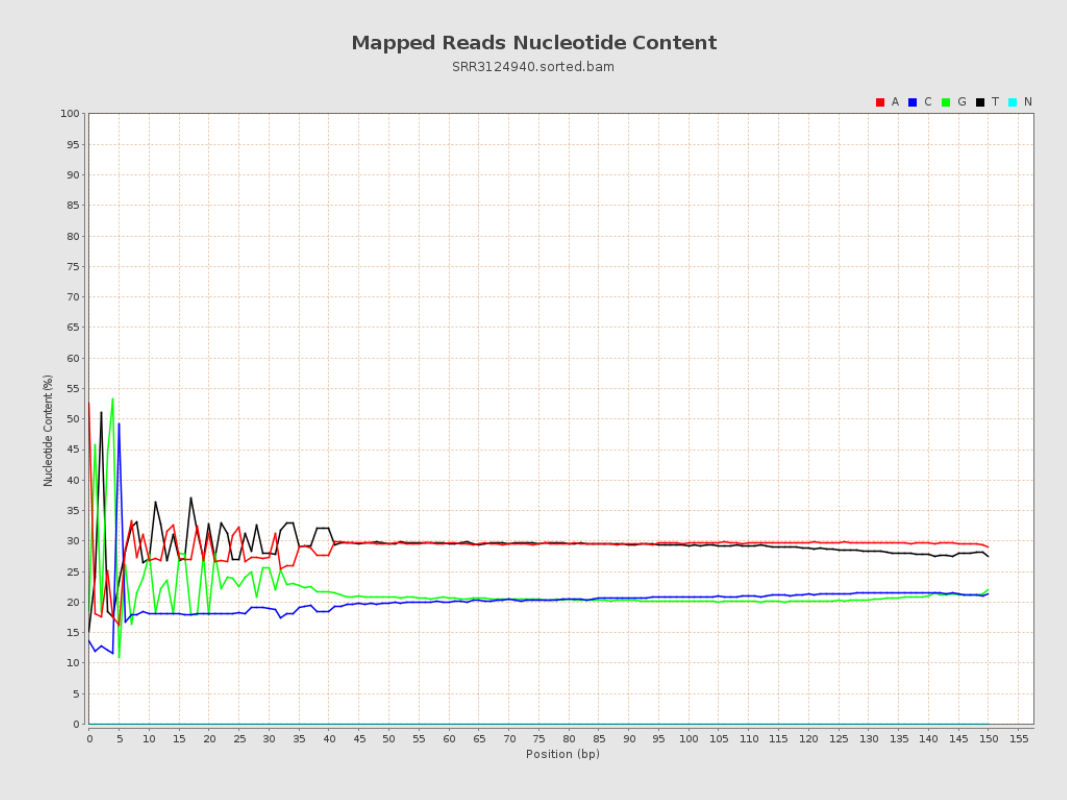
6. Results : Genome Fraction Coverage



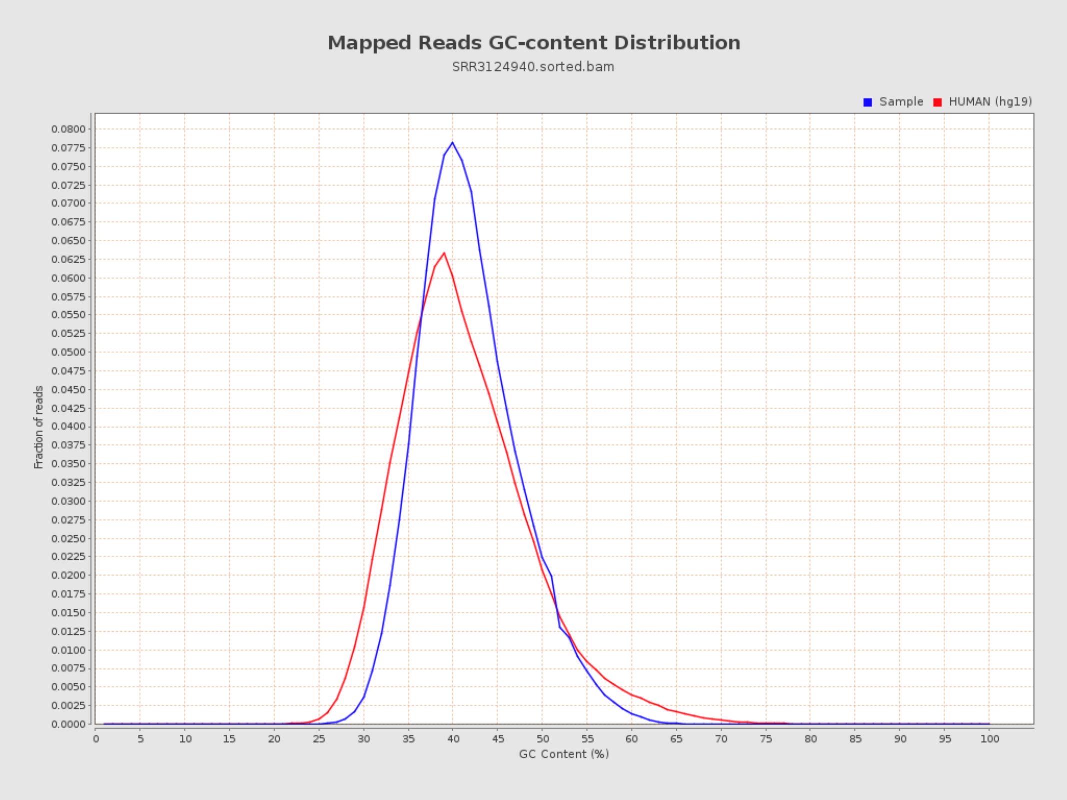
7. Results : Duplication Rate Histogram



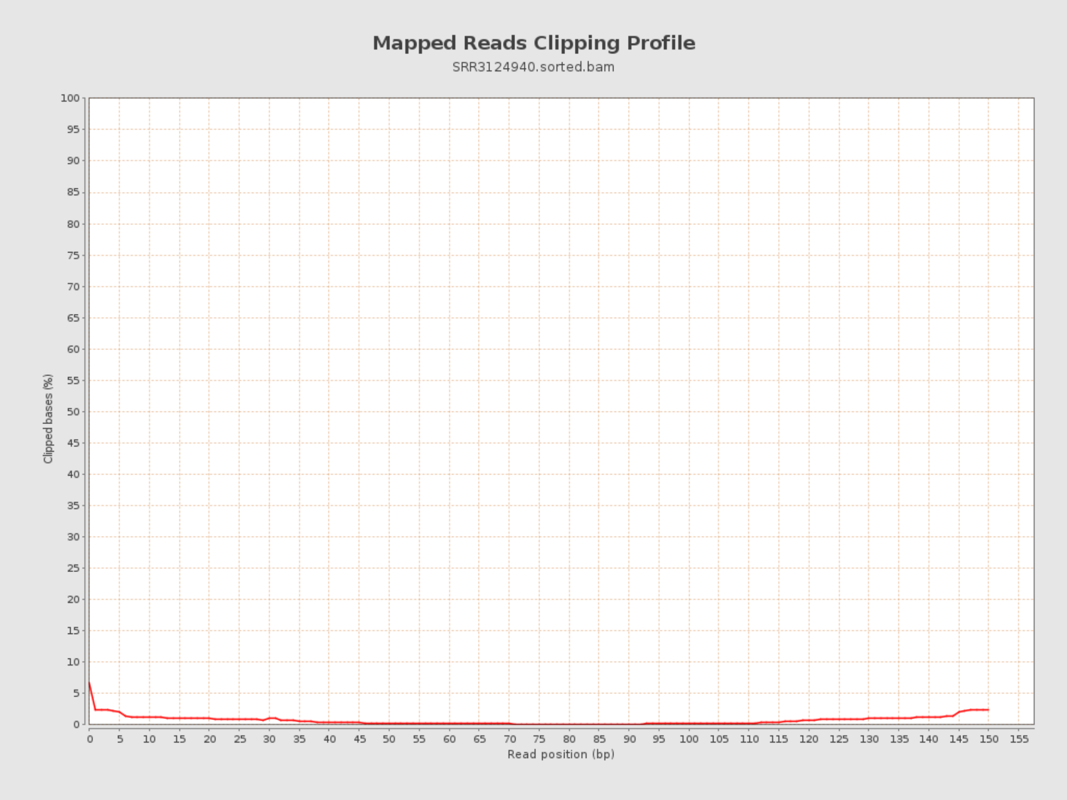
8. Results : Mapped Reads Nucleotide Content



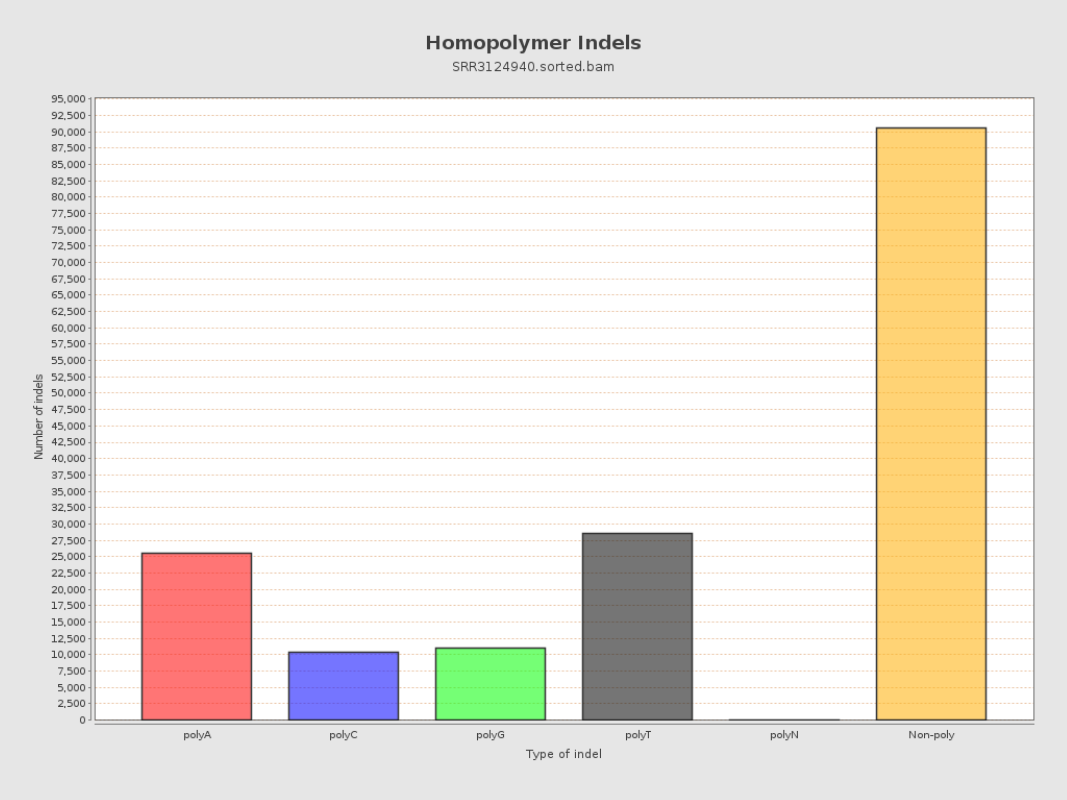
9. Results : Mapped Reads GC-content Distribution



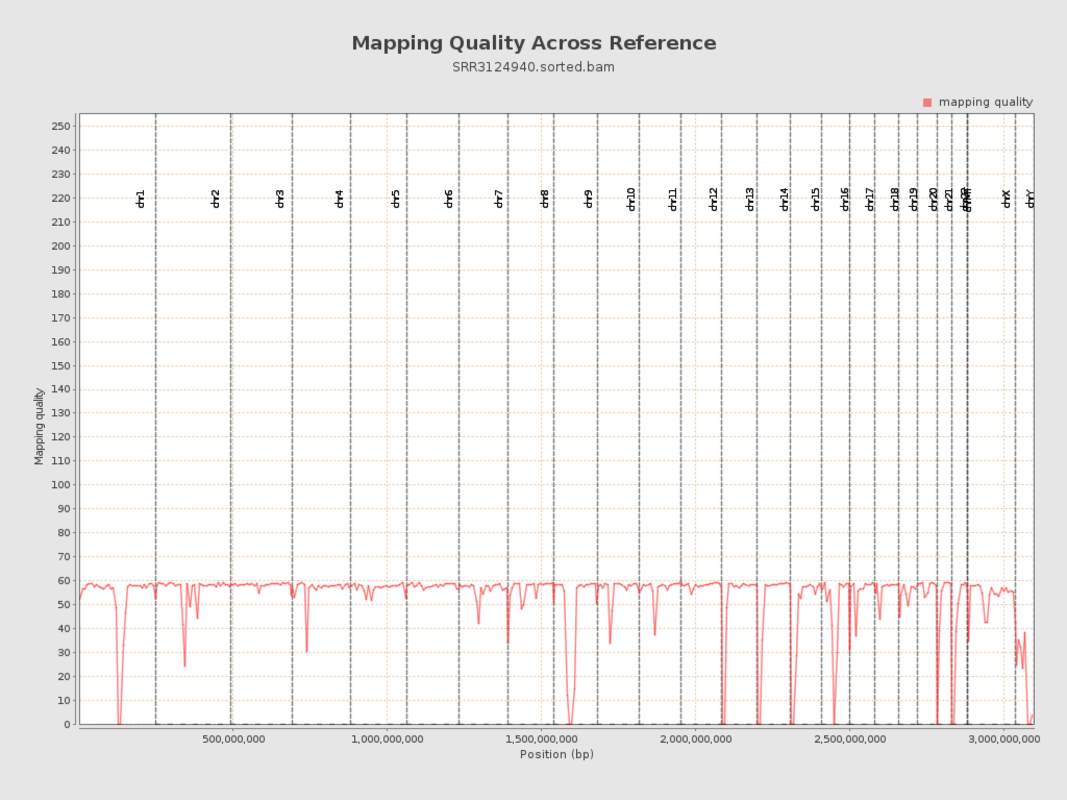
10. Results : Mapped Reads Clipping Profile



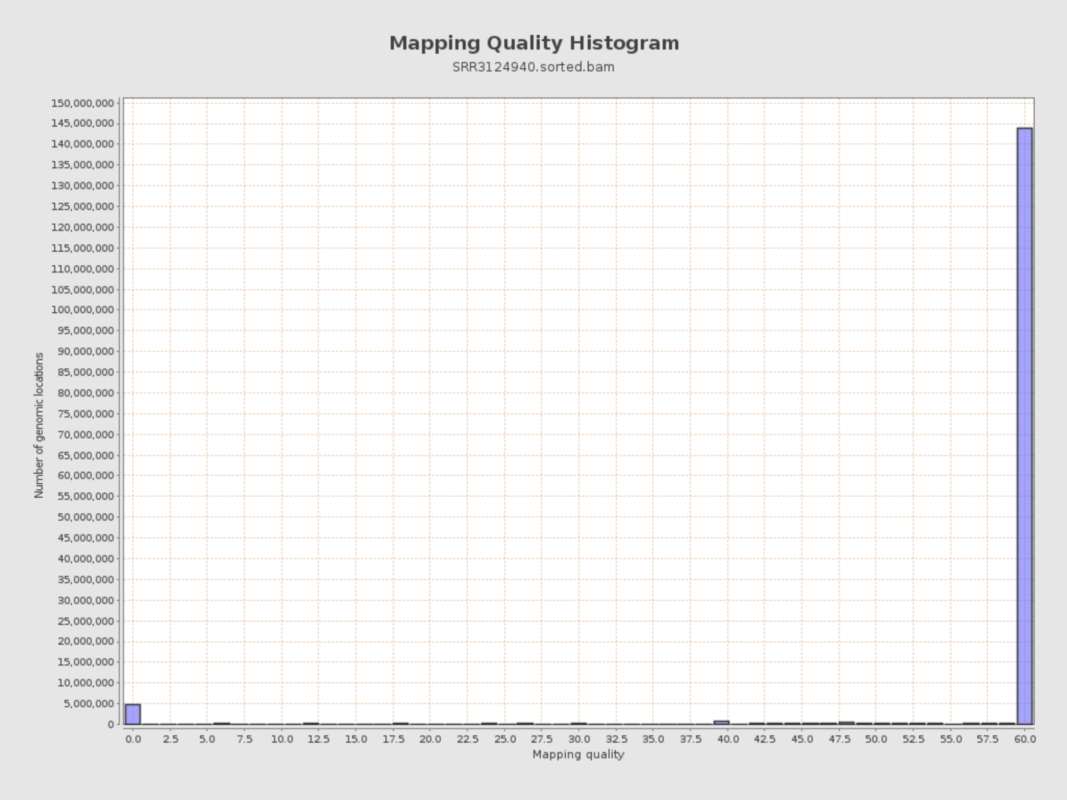
11. Results : Homopolymer Indels



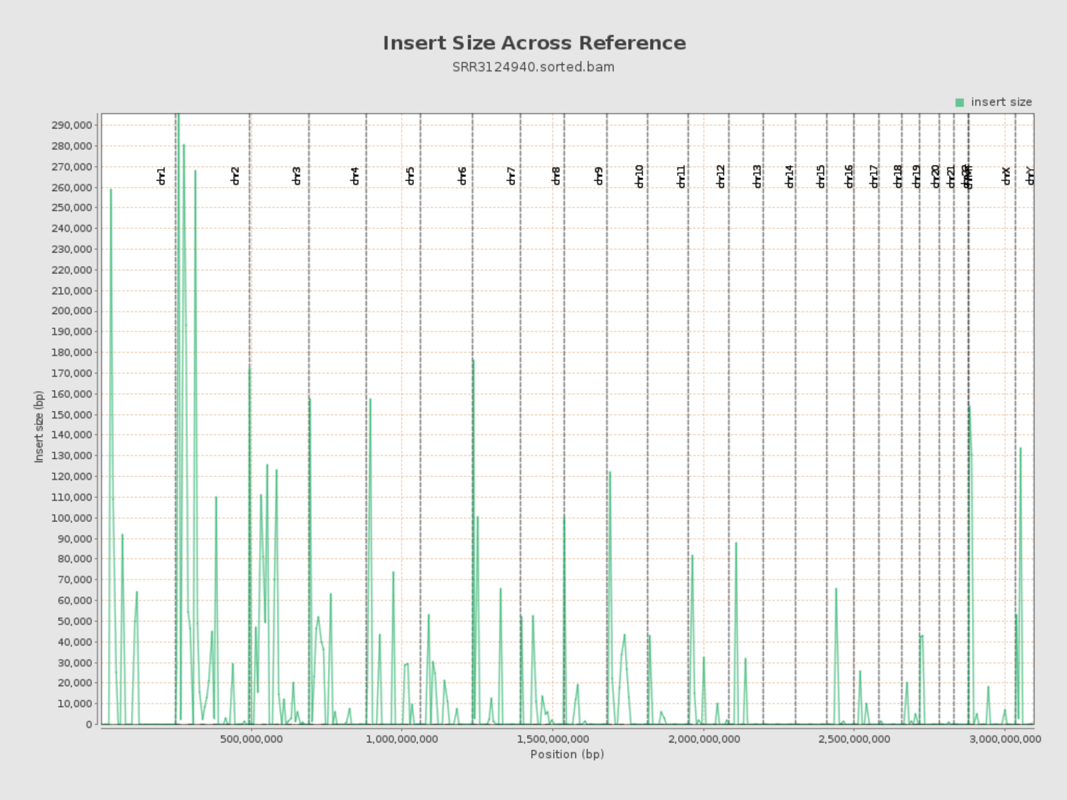
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram