Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:50:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124938.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_SRR3124938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124938_1.fastq.gz SRR3124938_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:50:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,010,204
Mapped reads	1,973,647 / 98.18%
Unmapped reads	36,557 / 1.82%
Mapped paired reads	1,973,647 / 98.18%
Mapped reads, first in pair	988,592 / 49.18%
Mapped reads, second in pair	985,055 / 49%
Mapped reads, both in pair	1,964,922 / 97.75%
Mapped reads, singletons	8,725 / 0.43%
Secondary alignments	0
Supplementary alignments	34,164 / 1.7%
Read min/max/mean length	30 / 151 / 151.8
Duplicated reads (estimated)	323,673 / 16.1%
Duplication rate	15.34%
Clipped reads	1,511,173 / 75.18%

2.2. ACGT Content

Number/percentage of A's	76,440,687 / 29.07%
Number/percentage of C's	53,265,777 / 20.26%
Number/percentage of T's	77,058,411 / 29.3%
Number/percentage of G's	56,172,393 / 21.36%
Number/percentage of N's	24,812 / 0.01%

GC Percentage	41.62%

2.3. Coverage

Mean	0.085
Standard Deviation	1.1021

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	78,496.2
Standard Deviation	2,625,894.76
P25/Median/P75	135 / 168 / 213

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	2,961,065
Insertions	59,399
Mapped reads with at least one insertion	2.77%
Deletions	104,640
Mapped reads with at least one deletion	5.04%
Homopolymer indels	44.35%

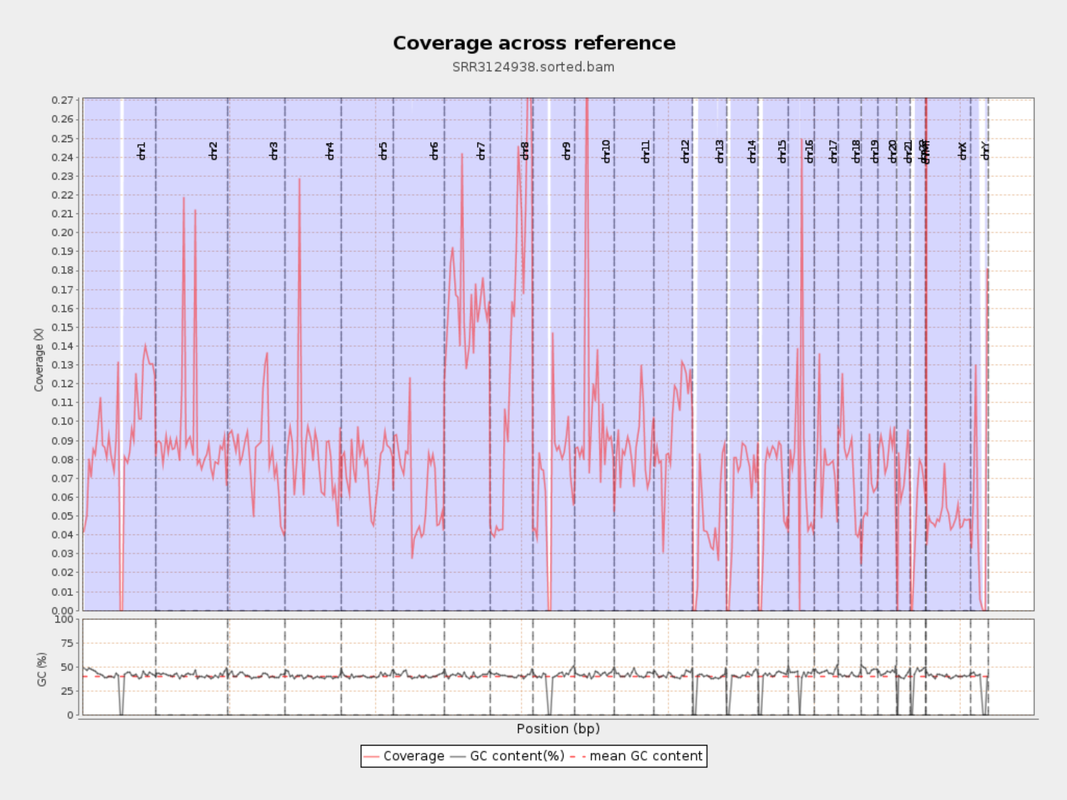
2.7. Chromosome stats

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

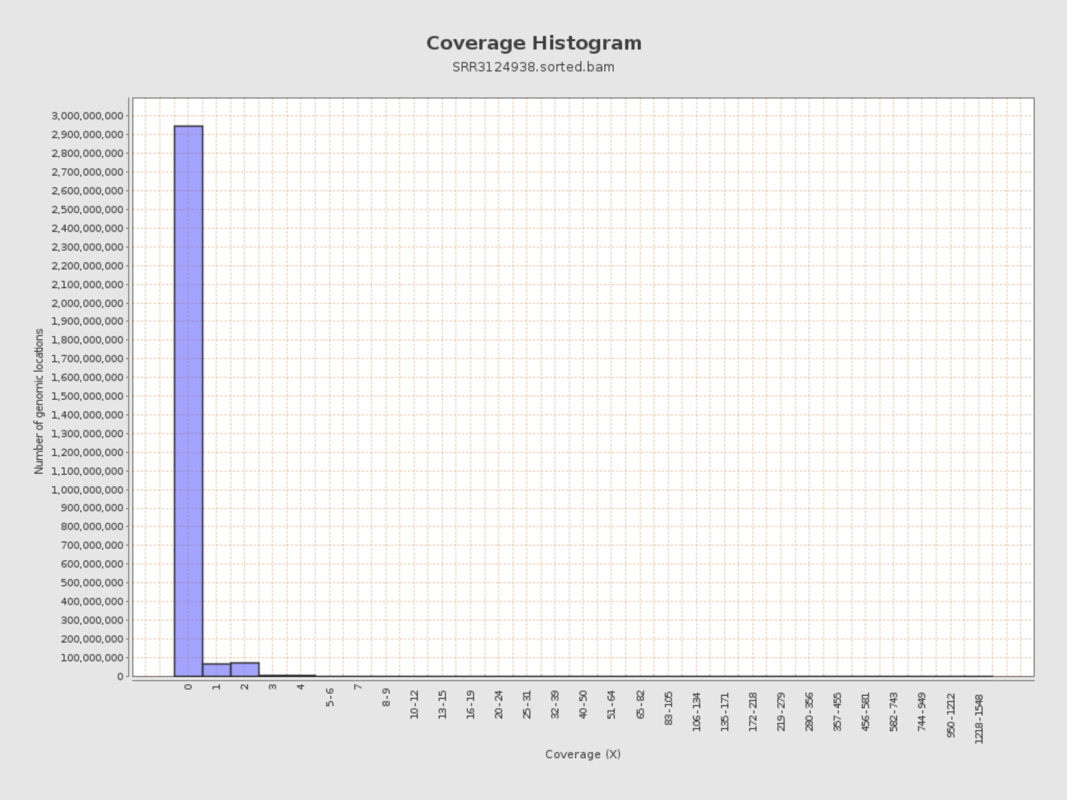
		bases	**coverage**	**deviation**
chr1	249250621	22549423	0.0905	0.9957
chr2	243199373	22645427	0.0931	1.6285
chr3	198022430	16589744	0.0838	0.4112
chr4	191154276	16374779	0.0857	0.9562
chr5	180915260	13793846	0.0762	0.4028
chr6	171115067	11192252	0.0654	0.6128
chr7	159138663	25750607	0.1618	2.1728
chr8	146364022	21061507	0.1439	0.595
chr9	141213431	9945205	0.0704	1.5602
chr10	135534747	14421770	0.1064	2.0879
chr11	135006516	11536665	0.0855	0.6922
chr12	133851895	13182879	0.0985	0.4447
chr13	115169878	5182382	0.045	0.2962
chr14	107349540	6949494	0.0647	0.4015
chr15	102531392	6317644	0.0616	0.3453
chr16	90354753	7305642	0.0809	1.5014
chr17	81195210	6380907	0.0786	0.9897
chr18	78077248	6031017	0.0772	1.4688
chr19	59128983	3625994	0.0613	0.5799
chr20	63025520	5345174	0.0848	0.5008
chr21	48129895	3273660	0.068	0.5728
chr22	51304566	2564227	0.05	0.3451
chrMT	16571	116625	7.0379	4.6373
chrX	155270560	7621320	0.0491	0.3761

chrY	59373566	3431972	0.0578	1.6553

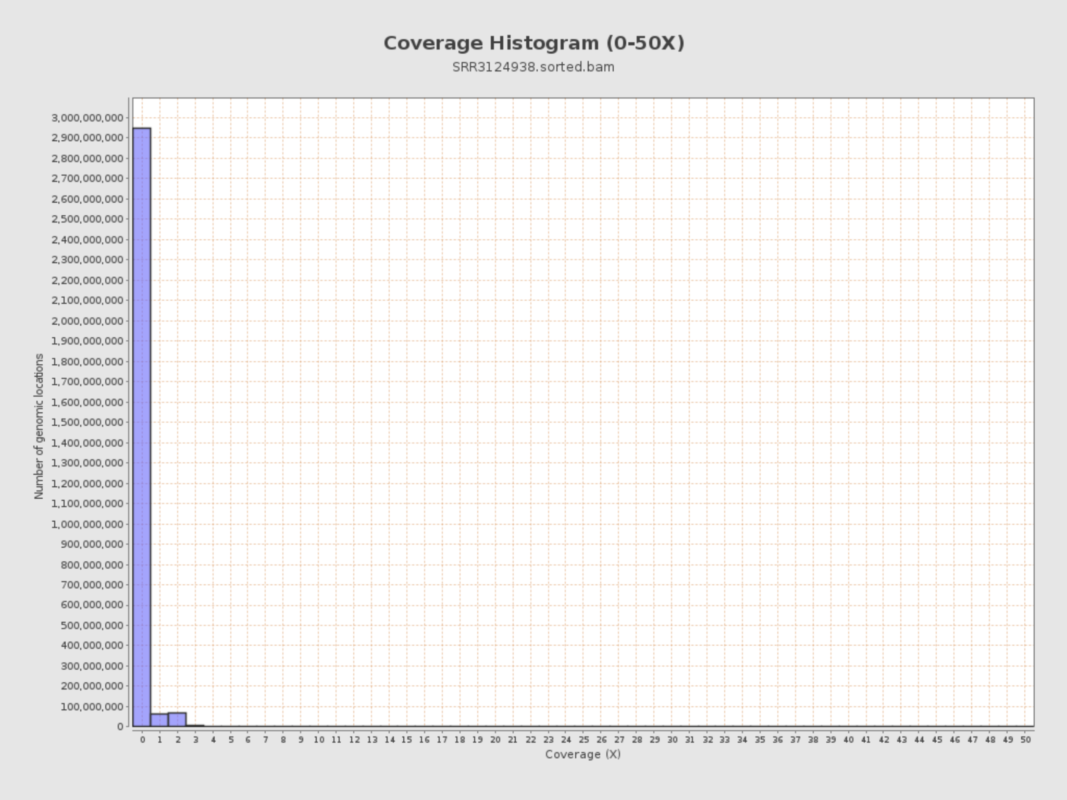
3. Results : Coverage across reference



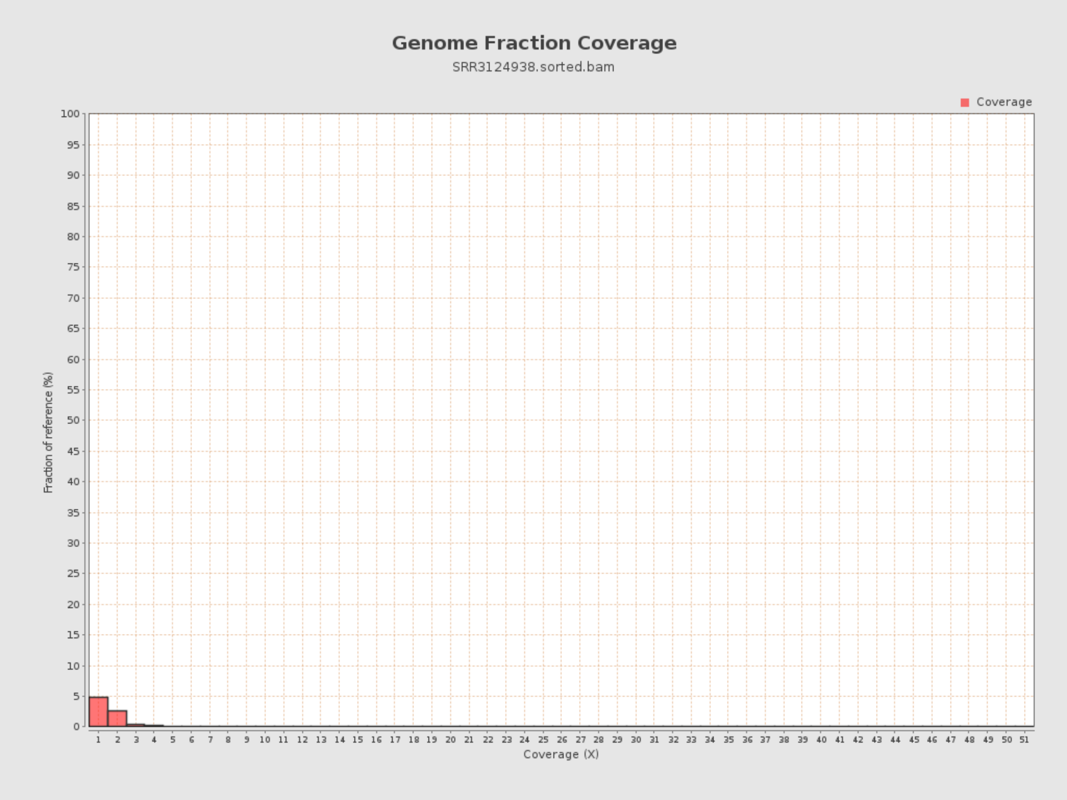
4. Results : Coverage Histogram



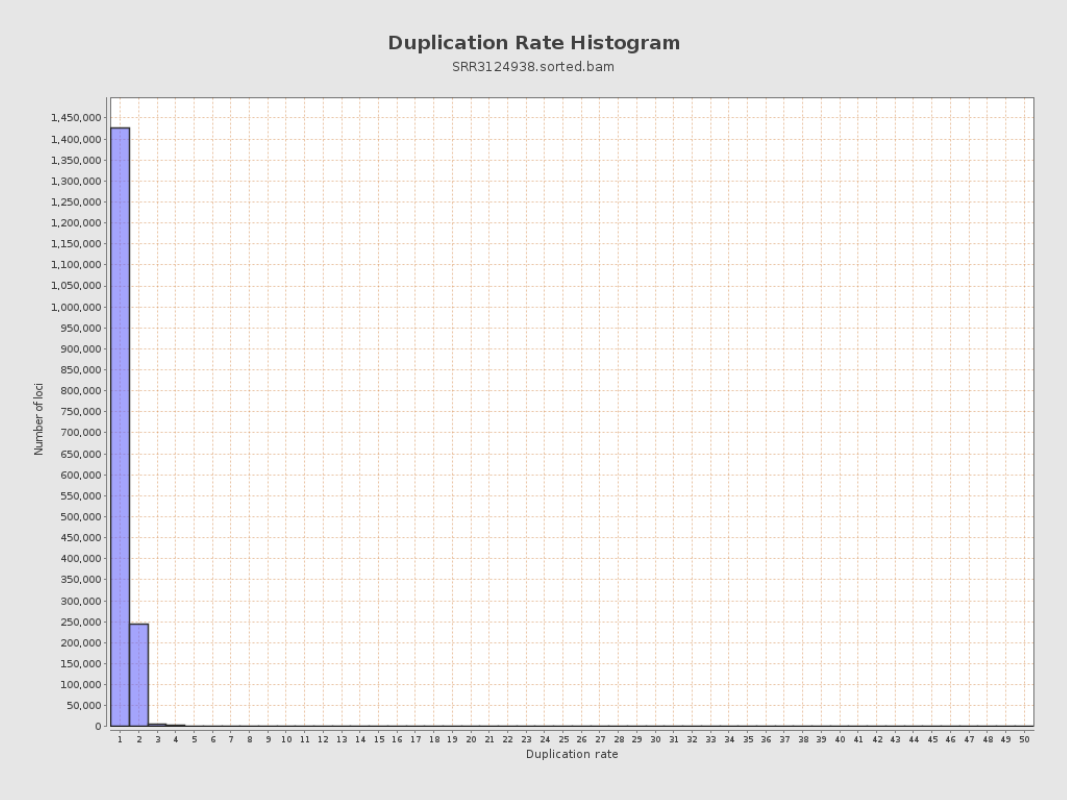
5. Results : Coverage Histogram (0-50X)



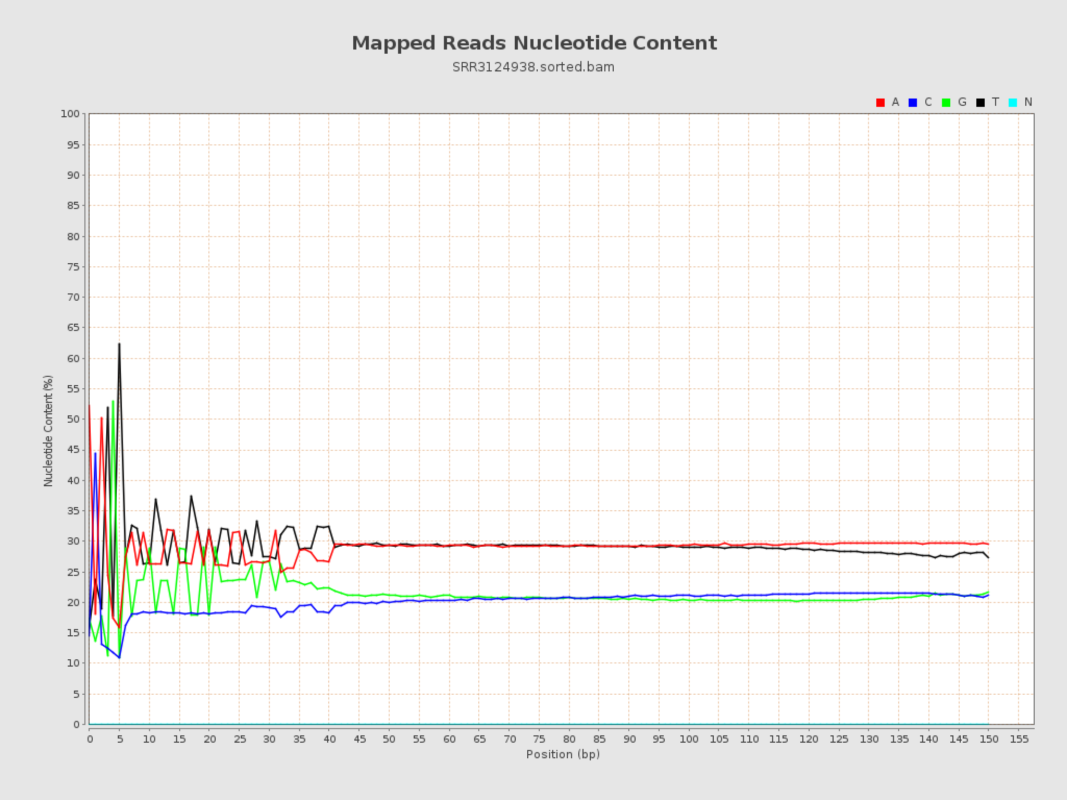
6. Results : Genome Fraction Coverage



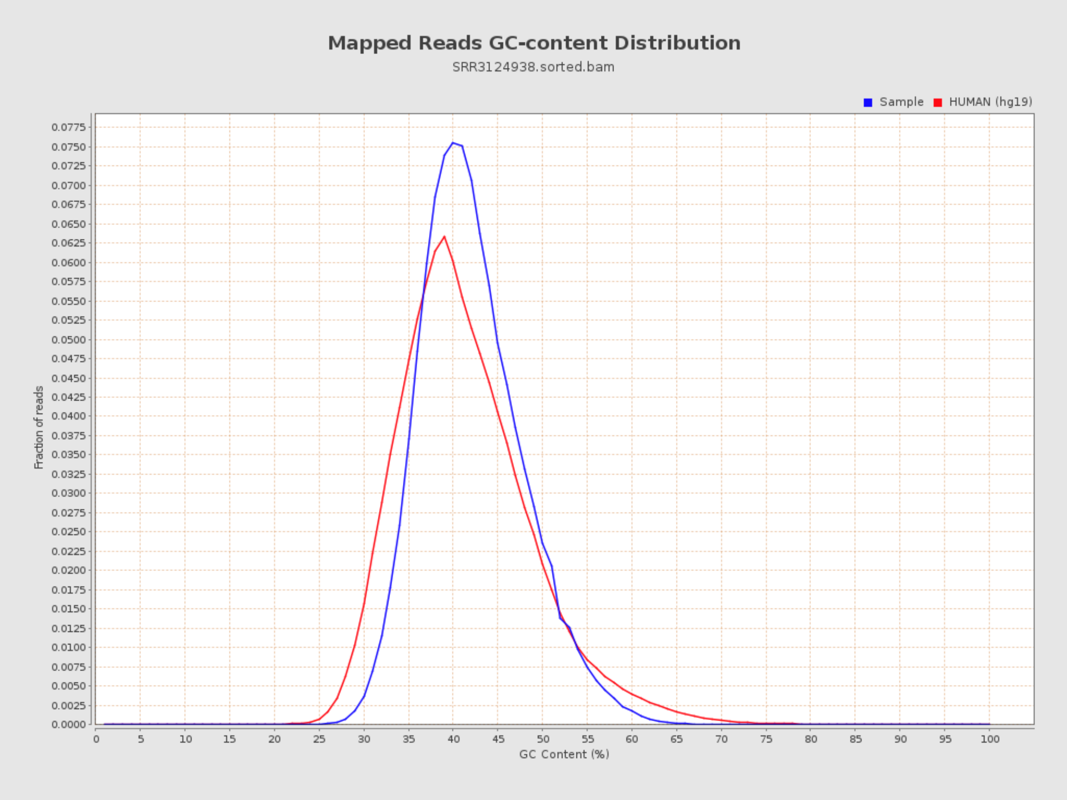
7. Results : Duplication Rate Histogram



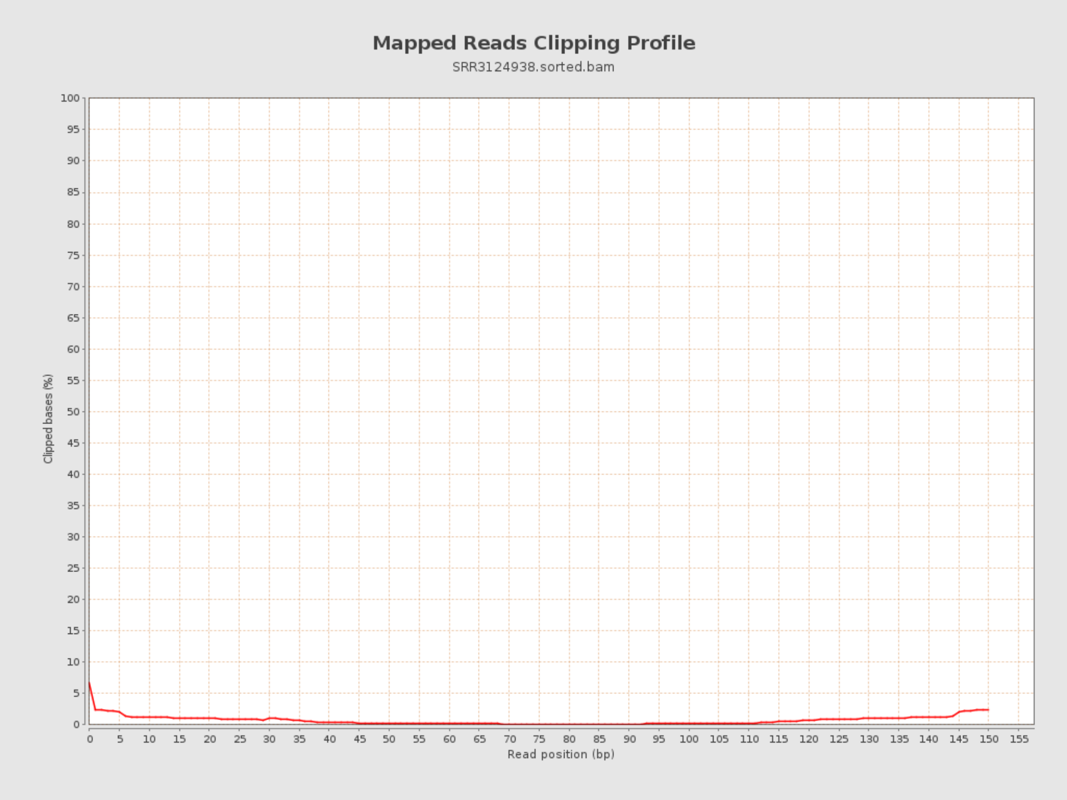
8. Results : Mapped Reads Nucleotide Content



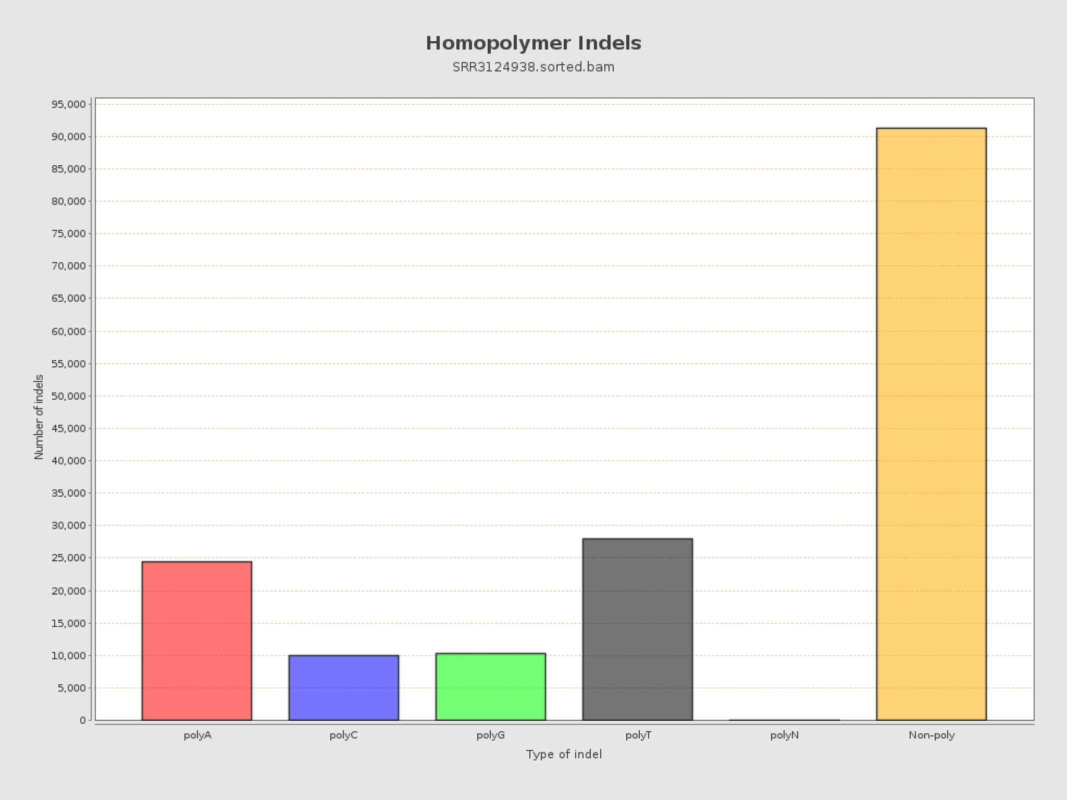
9. Results : Mapped Reads GC-content Distribution



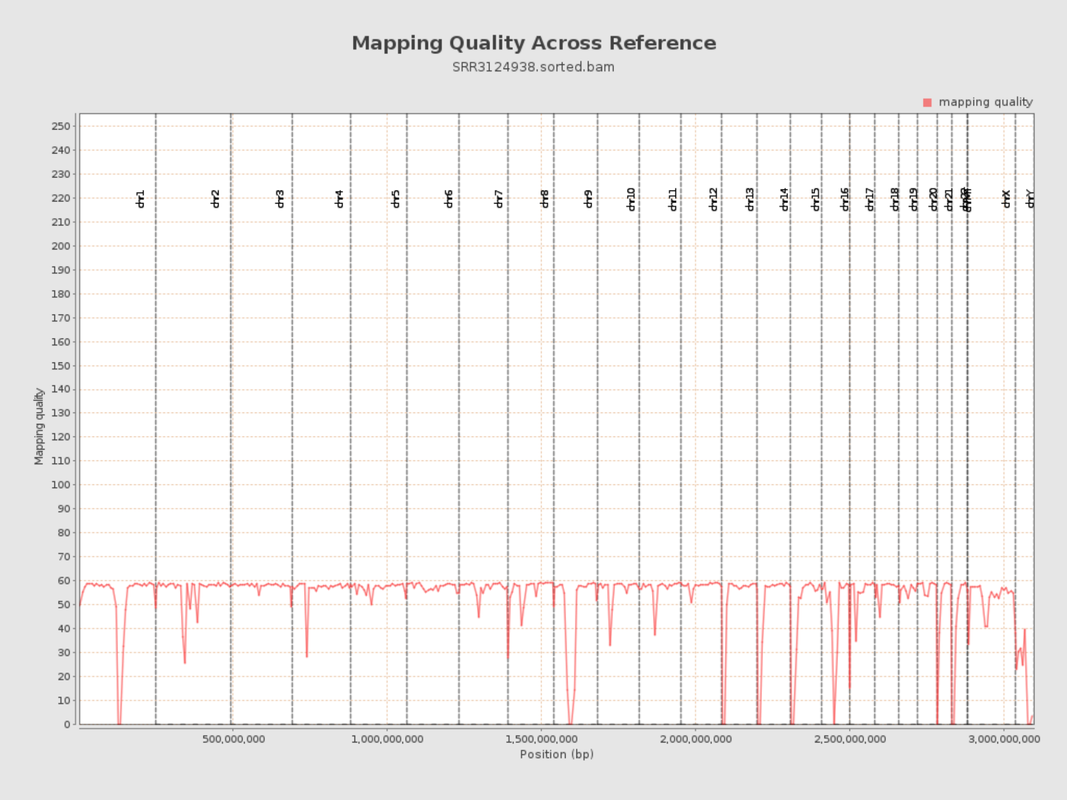
10. Results : Mapped Reads Clipping Profile



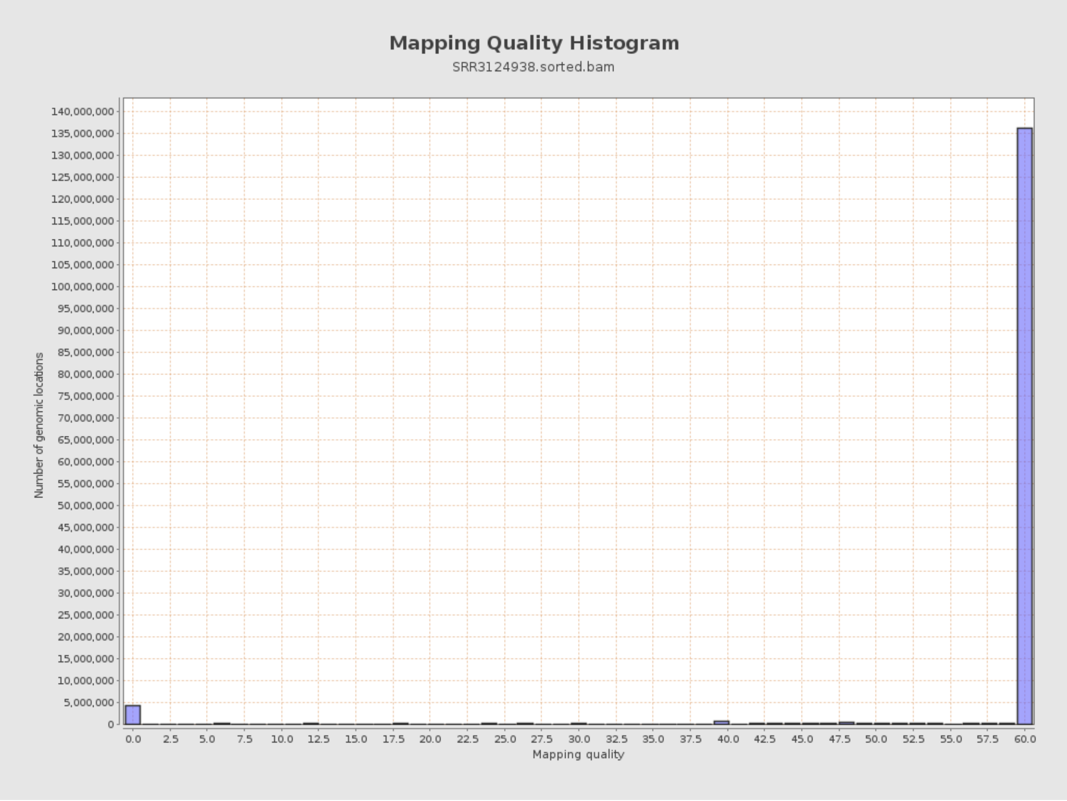
11. Results : Homopolymer Indels



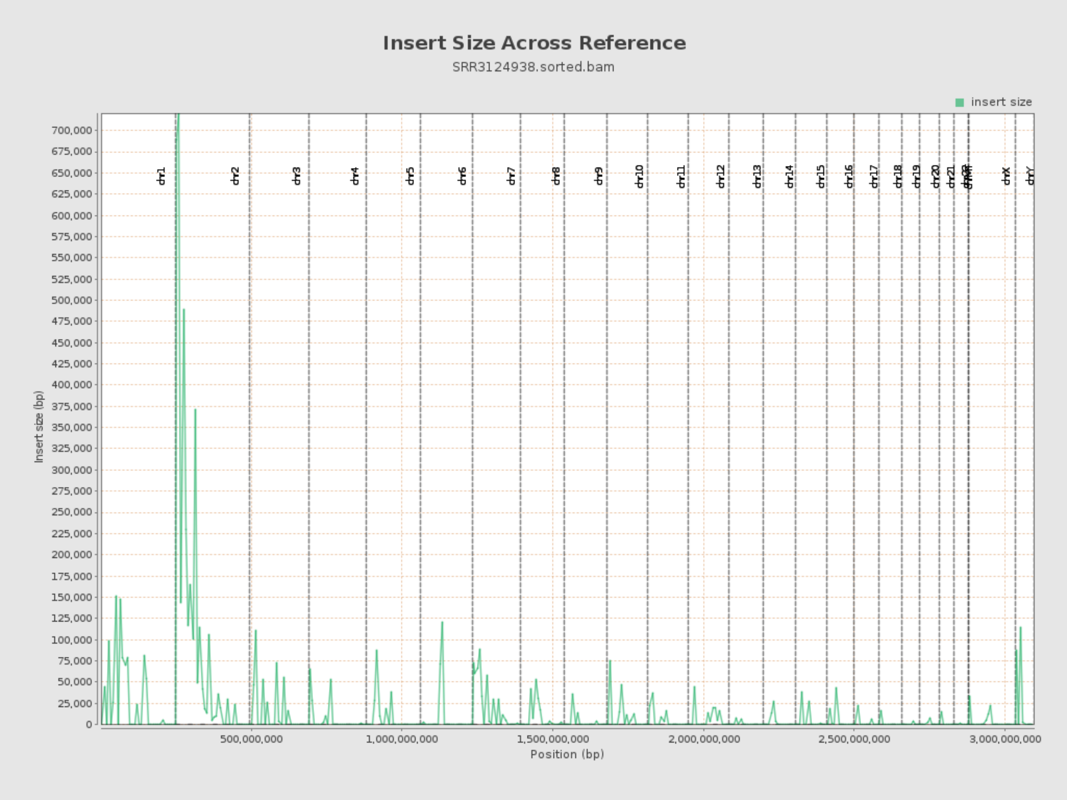
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram