Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 23:55:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124846.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_SRR3124846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124846_1.fastq.gz SRR3124846_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 23:55:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	88,870,426
Mapped reads	84,415,516 / 94.99%
Unmapped reads	4,454,910 / 5.01%
Mapped paired reads	84,415,516 / 94.99%
Mapped reads, first in pair	43,454,945 / 48.9%
Mapped reads, second in pair	40,960,571 / 46.09%
Mapped reads, both in pair	81,503,164 / 91.71%
Mapped reads, singletons	2,912,352 / 3.28%
Secondary alignments	0
Supplementary alignments	2,732,501 / 3.07%
Read min/max/mean length	30 / 150 / 151.44
Duplicated reads (estimated)	31,420,523 / 35.36%
Duplication rate	21.42%
Clipped reads	51,678,799 / 58.15%

2.2. ACGT Content

Number/percentage of A's	3,129,666,812 / 28.73%
Number/percentage of C's	2,108,387,155 / 19.35%
Number/percentage of T's	3,235,827,207 / 29.7%
Number/percentage of G's	2,421,098,407 / 22.22%
Number/percentage of N's	184,032 / 0%

GC Percentage	41.57%

2.3. Coverage

Mean	3.5228
Standard Deviation	65.9093

2.4. Mapping Quality

Mean Mapping Quality	52.83

2.5. Insert size

Mean	191,553.9
Standard Deviation	4,153,181.62
P25/Median/P75	189 / 254 / 327

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	149,705,195
Insertions	2,698,144
Mapped reads with at least one insertion	2.89%
Deletions	4,257,972
Mapped reads with at least one deletion	4.76%
Homopolymer indels	42.03%

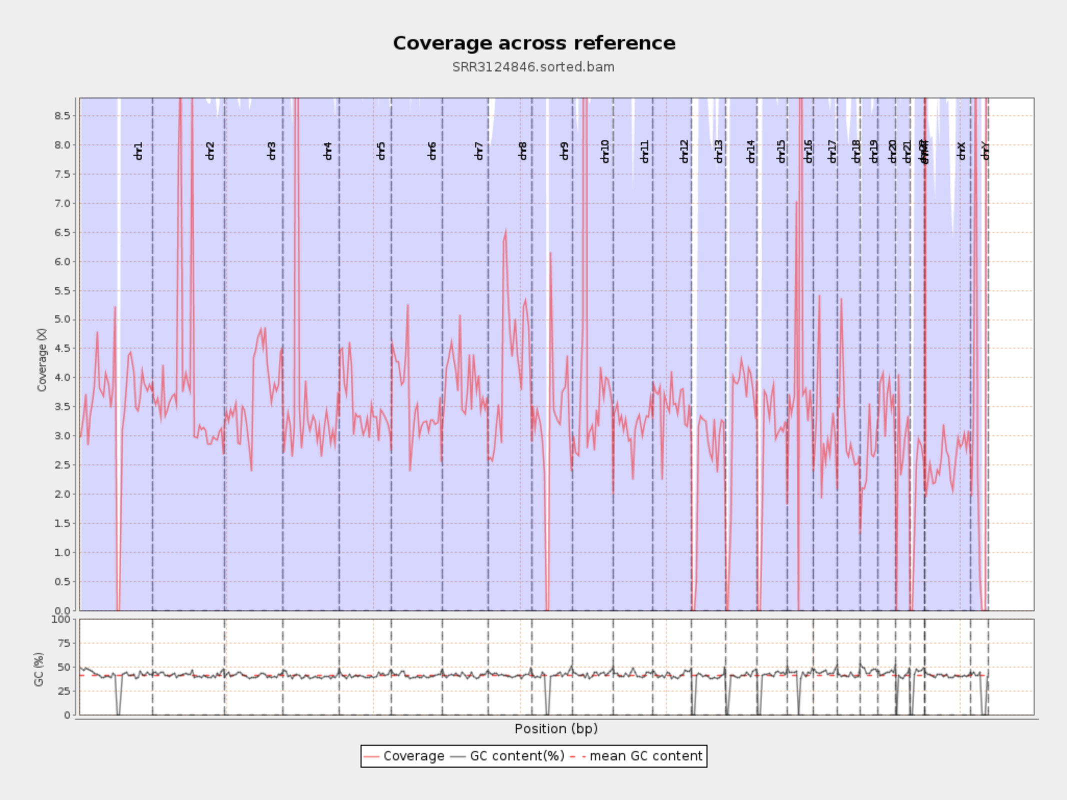
2.7. Chromosome stats

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

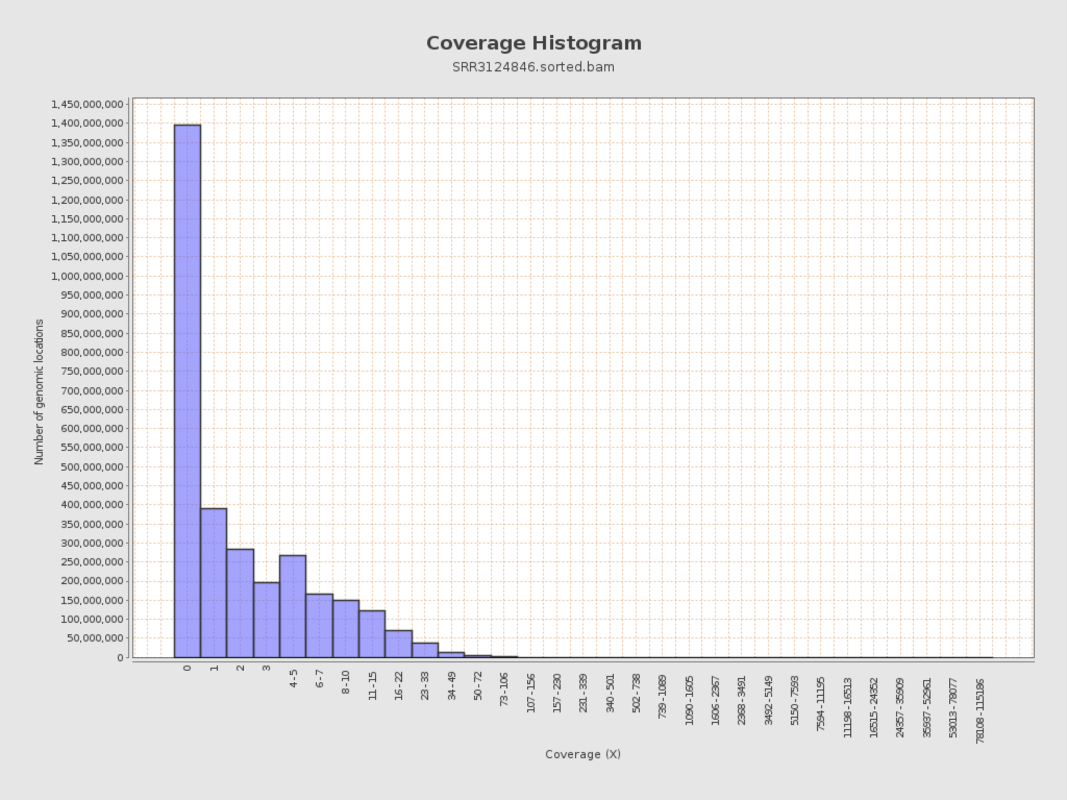
		bases	**coverage**	**deviation**
chr1	249250621	885257723	3.5517	28.8599
chr2	243199373	942114485	3.8738	79.6522
chr3	198022430	741124136	3.7426	8.7152
chr4	191154276	709189977	3.71	87.7529
chr5	180915260	630404464	3.4845	9.5836
chr6	171115067	615293065	3.5958	15.8409
chr7	159138663	623690098	3.9192	26.9425
chr8	146364022	628694254	4.2954	12.7862
chr9	141213431	434858400	3.0794	61.976
chr10	135534747	675309180	4.9826	220.2992
chr11	135006516	427663063	3.1677	15.3966
chr12	133851895	471928174	3.5257	21.0307
chr13	115169878	290997924	2.5267	5.5376
chr14	107349540	350366449	3.2638	9.9967
chr15	102531392	283412803	2.7642	10.3888
chr16	90354753	415264590	4.5959	99.4192
chr17	81195210	244957497	3.0169	43.5312
chr18	78077248	244752054	3.1347	54.95
chr19	59128983	150409386	2.5438	16.9211
chr20	63025520	226961056	3.6011	29.3067
chr21	48129895	130943562	2.7206	43.3733
chr22	51304566	97491052	1.9002	9.778
chrMT	16571	3484933	210.3031	113.7531
chrX	155270560	399790651	2.5748	10.5962

chrY	59373566	281276901	4.7374	148.2955

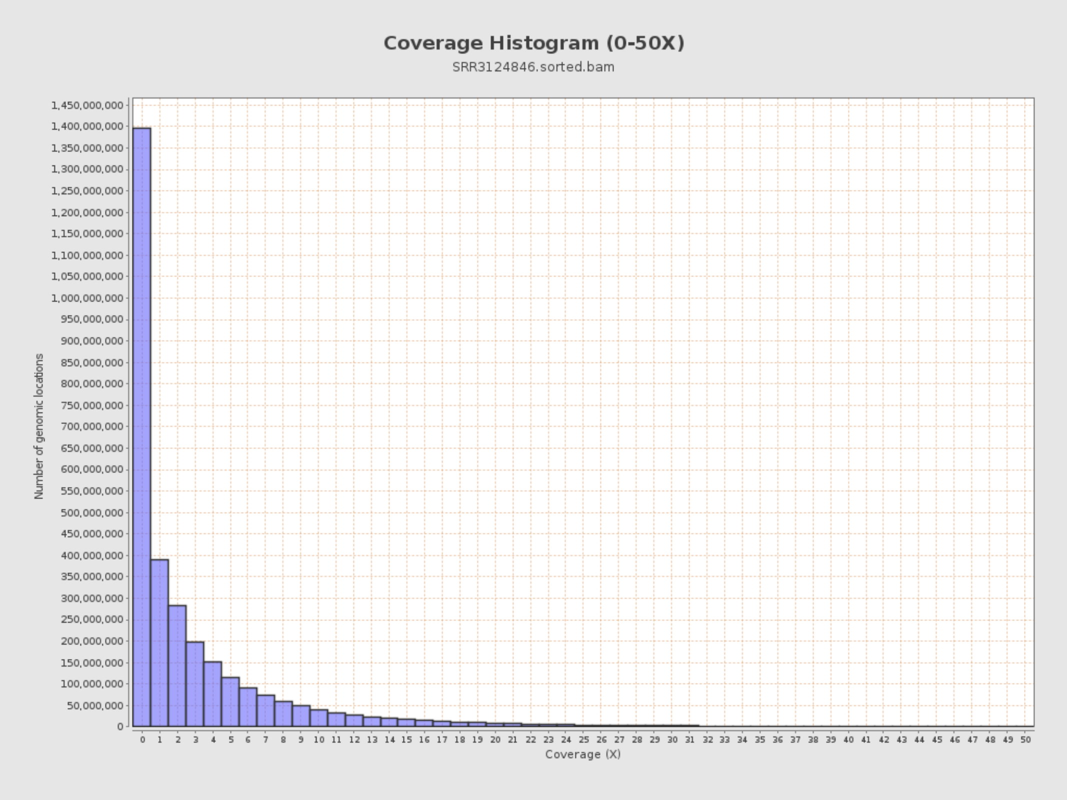
3. Results : Coverage across reference



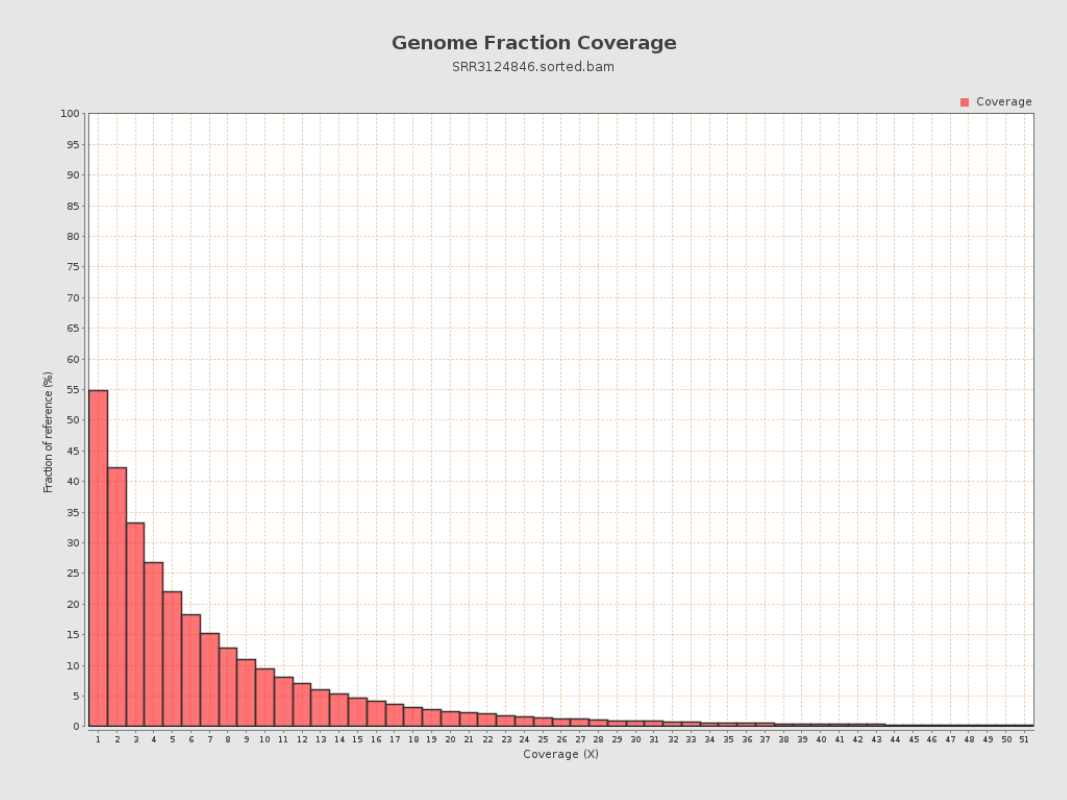
4. Results : Coverage Histogram



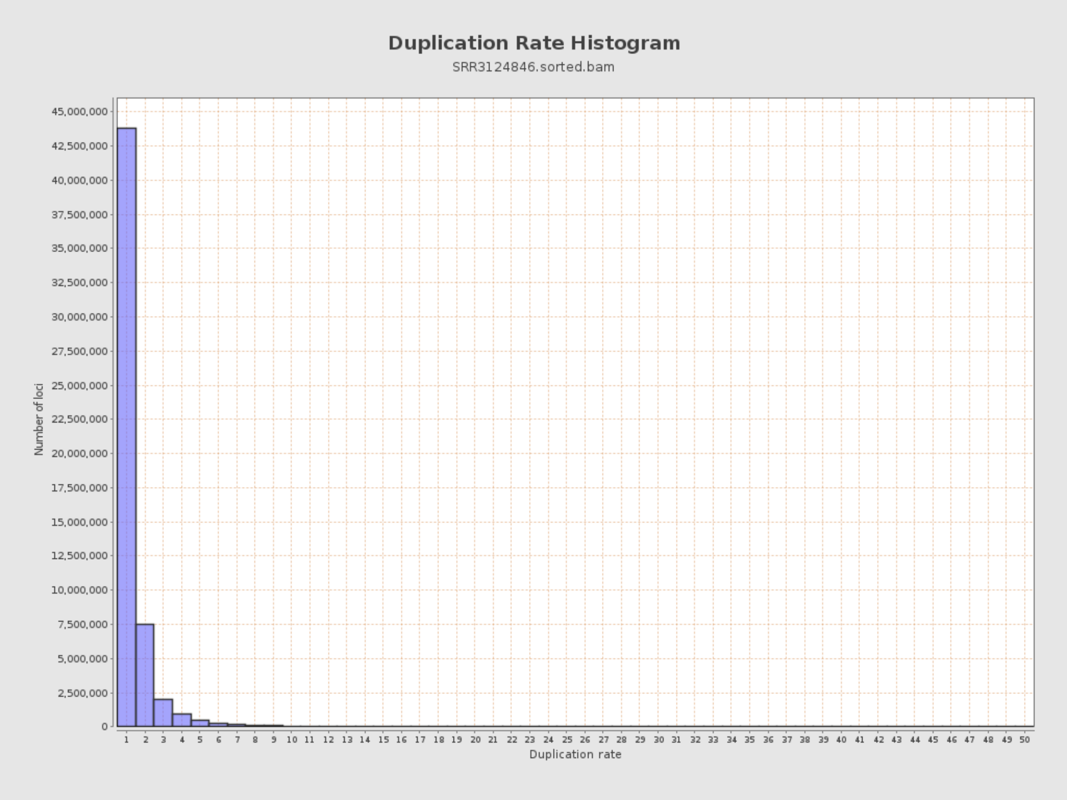
5. Results : Coverage Histogram (0-50X)



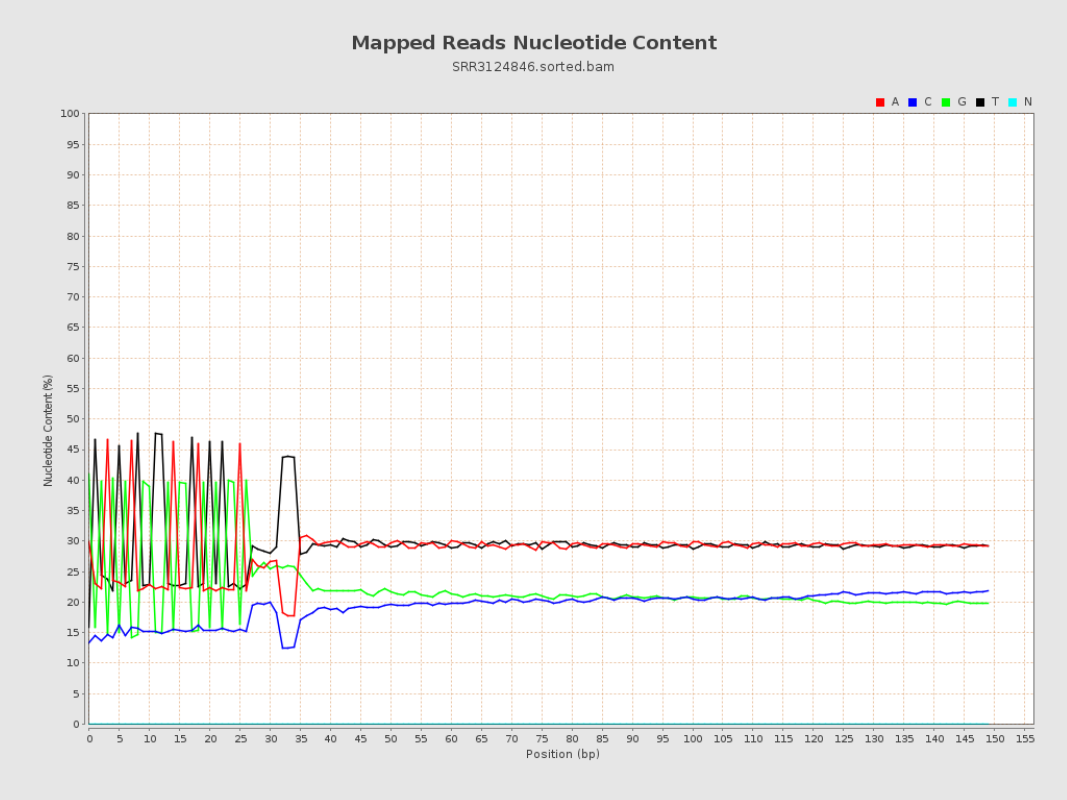
6. Results : Genome Fraction Coverage



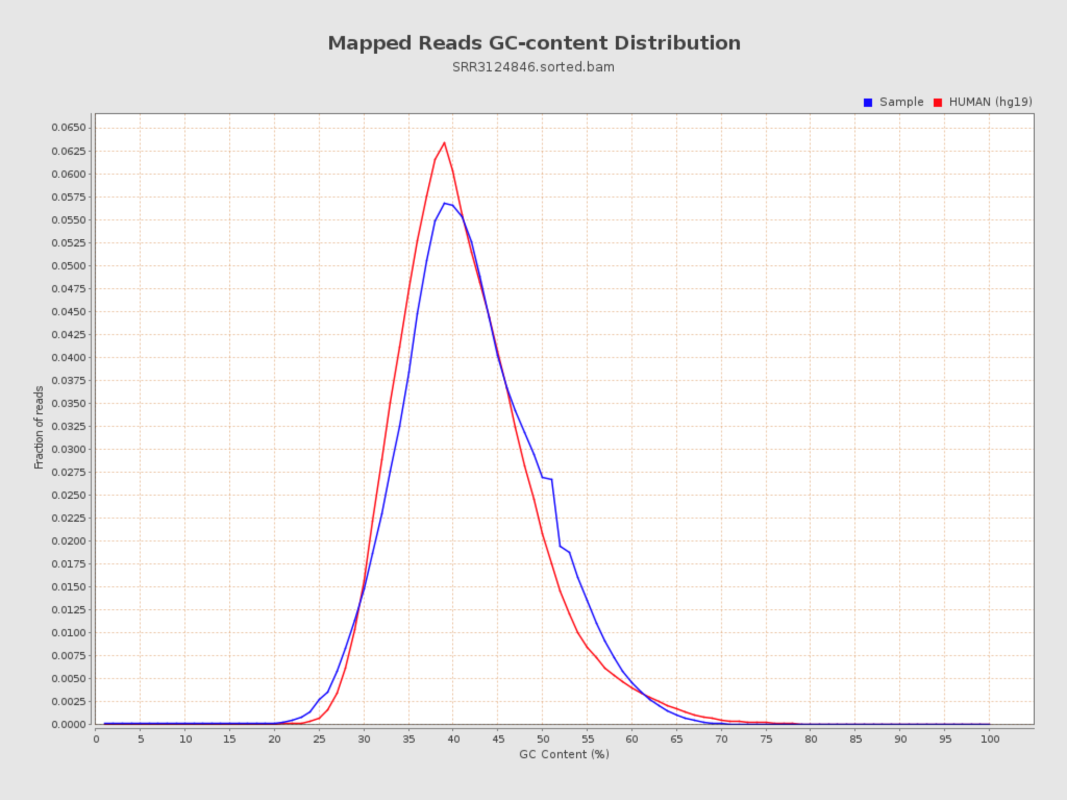
7. Results : Duplication Rate Histogram



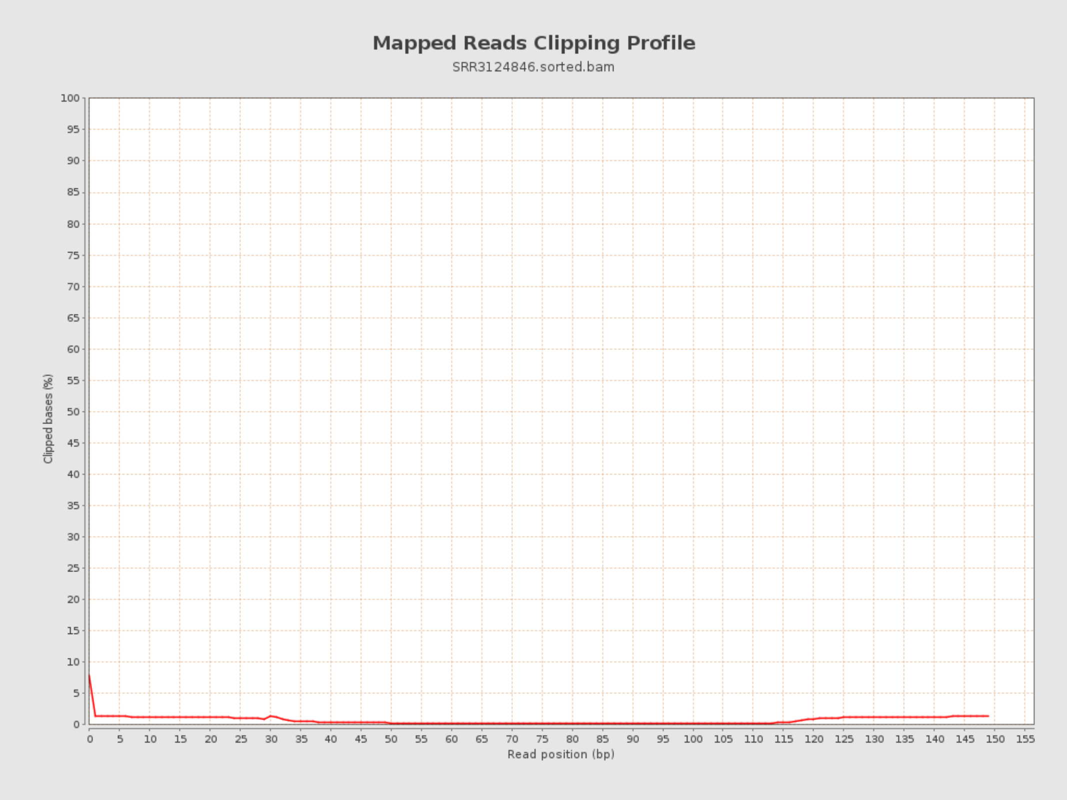
8. Results : Mapped Reads Nucleotide Content



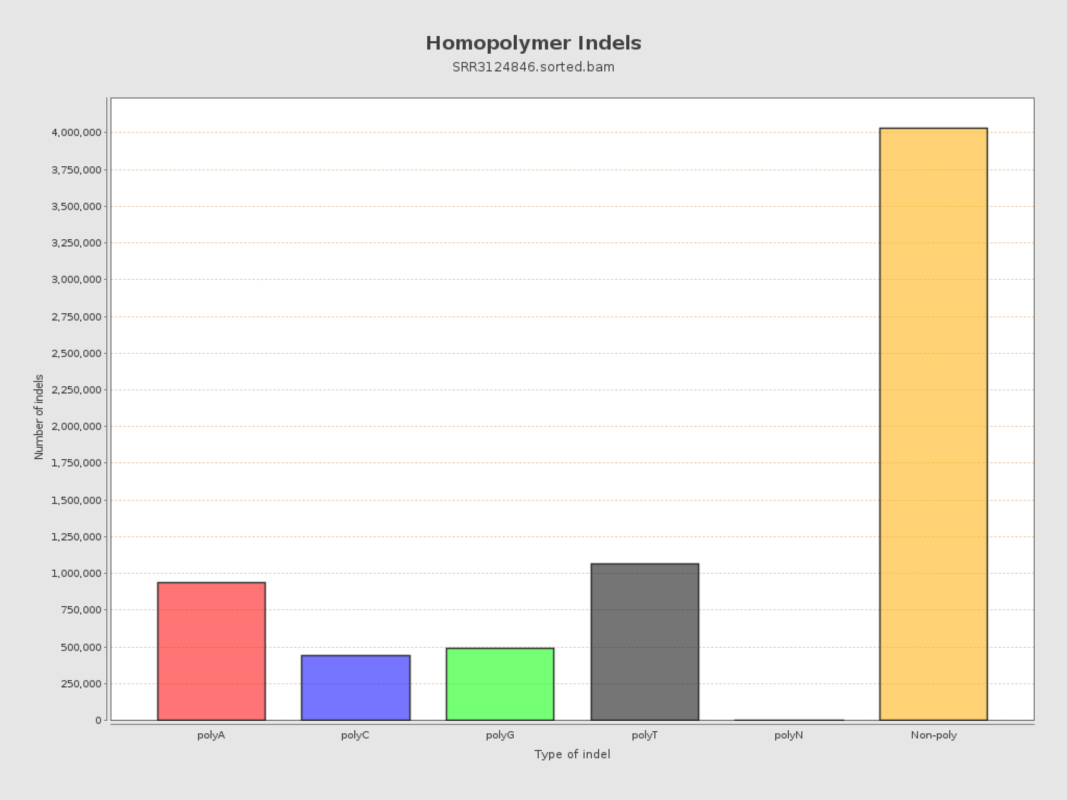
9. Results : Mapped Reads GC-content Distribution



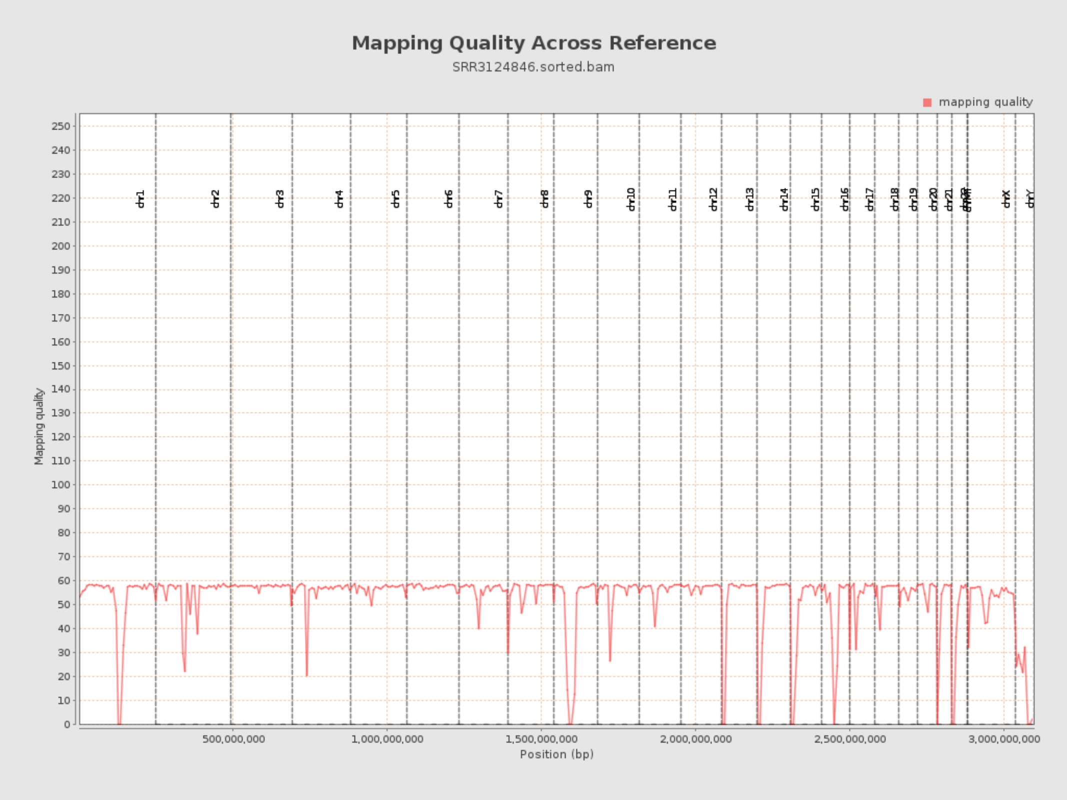
10. Results : Mapped Reads Clipping Profile



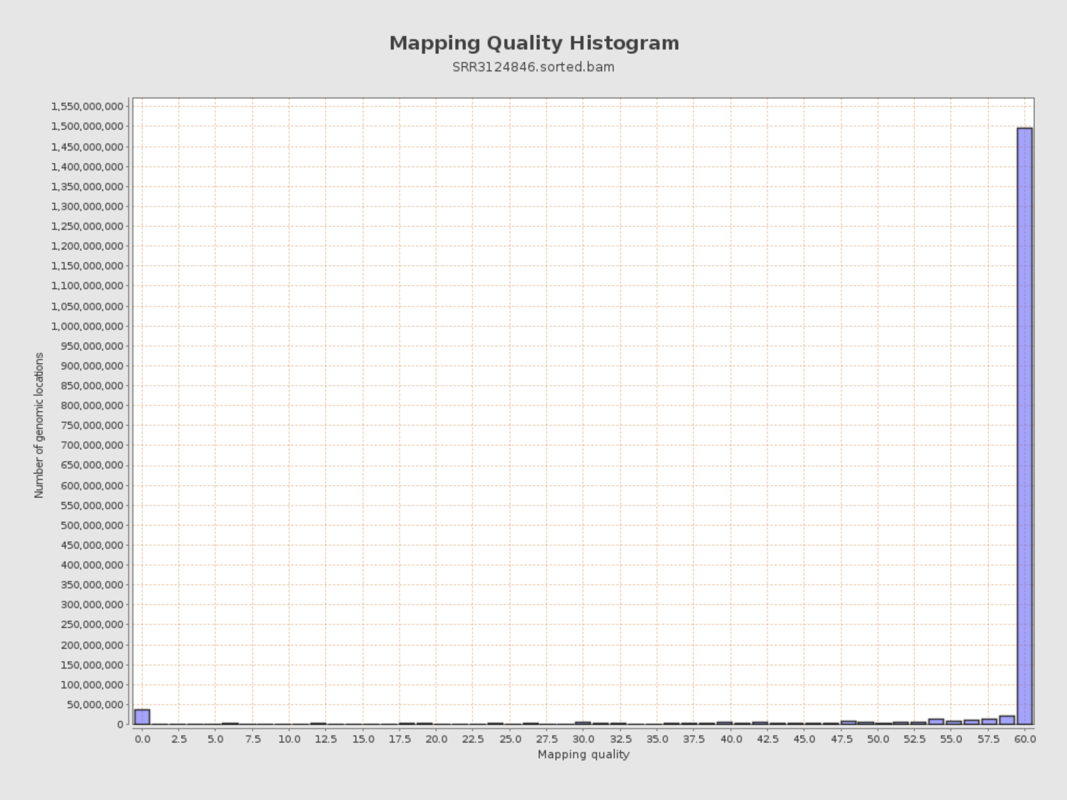
11. Results : Homopolymer Indels



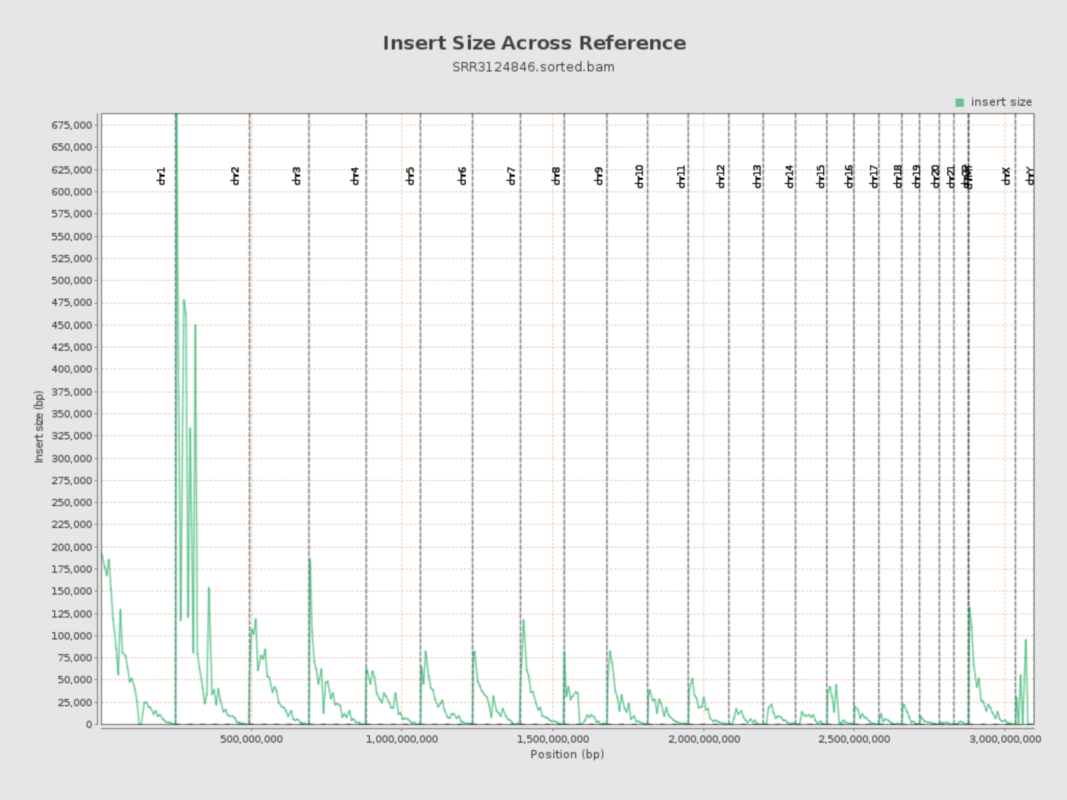
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram