Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 14:31:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124842.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_SRR3124842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124842_1.fastq.gz SRR3124842_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 14:31:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	100,518,680
Mapped reads	97,267,480 / 96.77%
Unmapped reads	3,251,200 / 3.23%
Mapped paired reads	97,267,480 / 96.77%
Mapped reads, first in pair	49,938,052 / 49.68%
Mapped reads, second in pair	47,329,428 / 47.09%
Mapped reads, both in pair	94,504,170 / 94.02%
Mapped reads, singletons	2,763,310 / 2.75%
Secondary alignments	0
Supplementary alignments	1,877,039 / 1.87%
Read min/max/mean length	30 / 150 / 150.89
Duplicated reads (estimated)	30,562,085 / 30.4%
Duplication rate	19.56%
Clipped reads	47,598,061 / 47.35%

2.2. ACGT Content

Number/percentage of A's	3,775,779,421 / 28.89%
Number/percentage of C's	2,525,710,371 / 19.33%
Number/percentage of T's	3,884,284,131 / 29.72%
Number/percentage of G's	2,883,206,317 / 22.06%
Number/percentage of N's	235,569 / 0%

GC Percentage	41.39%

2.3. Coverage

Mean	4.2246
Standard Deviation	44.7641

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	115,403.46
Standard Deviation	3,230,025.55
P25/Median/P75	211 / 267 / 334

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	163,502,894
Insertions	2,095,678
Mapped reads with at least one insertion	2.03%
Deletions	4,562,272
Mapped reads with at least one deletion	4.51%
Homopolymer indels	46.02%

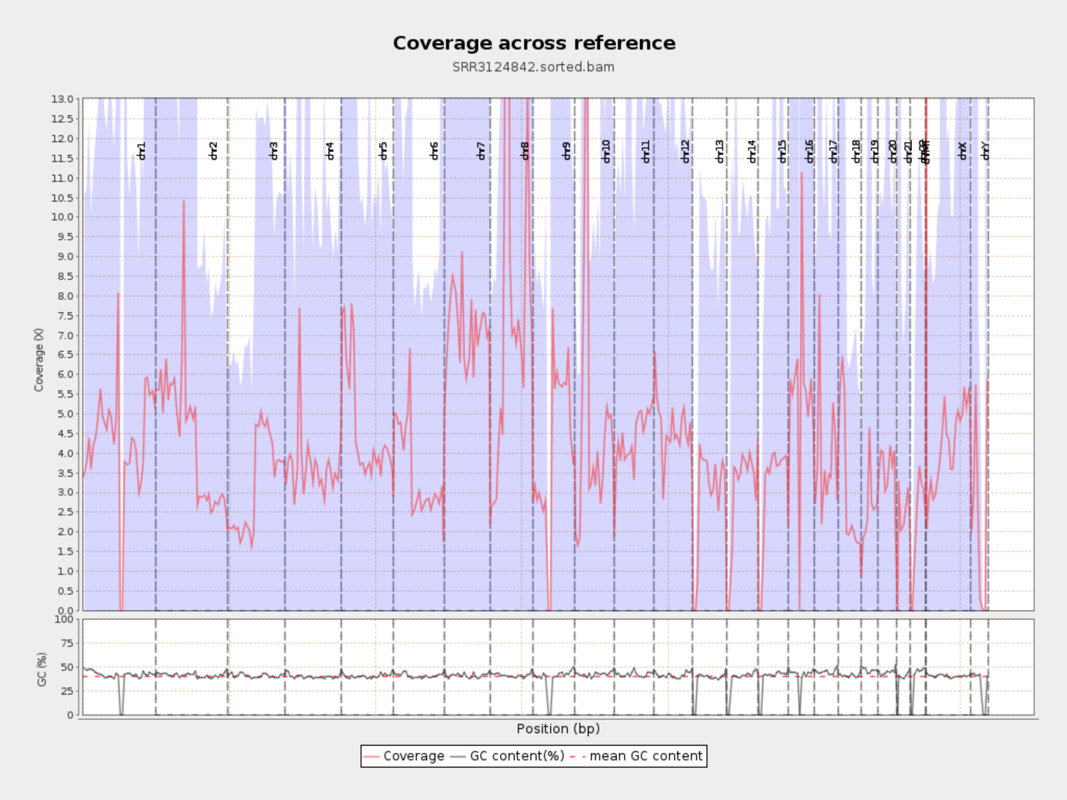
2.7. Chromosome stats

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

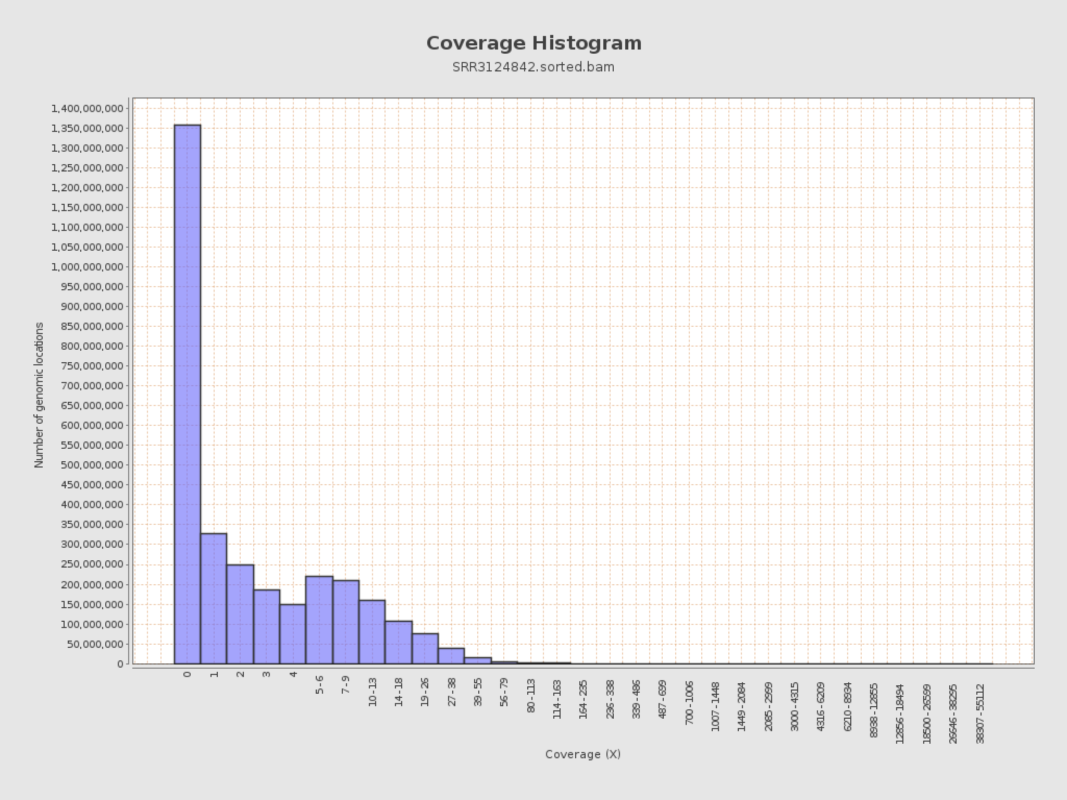
		bases	coverage	deviation
chr1	249250621	1076499872	4.3189	56.6722
chr2	243199373	1080128270	4.4413	43.5382
chr3	198022430	632772977	3.1955	6.3179
chr4	191154276	705664453	3.6916	31.8666
chr5	180915260	840107514	4.6437	8.6005
chr6	171115067	603891388	3.5292	22.4052
chr7	159138663	1137916135	7.1505	67.828
chr8	146364022	1124269545	7.6813	27.521
chr9	141213431	581390263	4.1171	75.6323
chr10	135534747	642600092	4.7412	110.846
chr11	135006516	592177118	4.3863	25.3016
chr12	133851895	622674771	4.652	18.0393
chr13	115169878	334929828	2.9081	5.6158
chr14	107349540	320299015	2.9837	6.7294
chr15	102531392	311986077	3.0428	9.6089
chr16	90354753	489009442	5.4121	50.0631
chr17	81195210	318460045	3.9222	75.2899
chr18	78077248	250871031	3.2131	53.6513
chr19	59128983	153909567	2.6029	31.9742
chr20	63025520	229217184	3.6369	11.4371
chr21	48129895	112811651	2.3439	15.9823
chr22	51304566	112737473	2.1974	5.9509
chrMT	16571	6772199	408.6778	222.4082
chrX	155270560	650572353	4.1899	14.5293

chrY	59373566	146382323	2.4654	48.6951

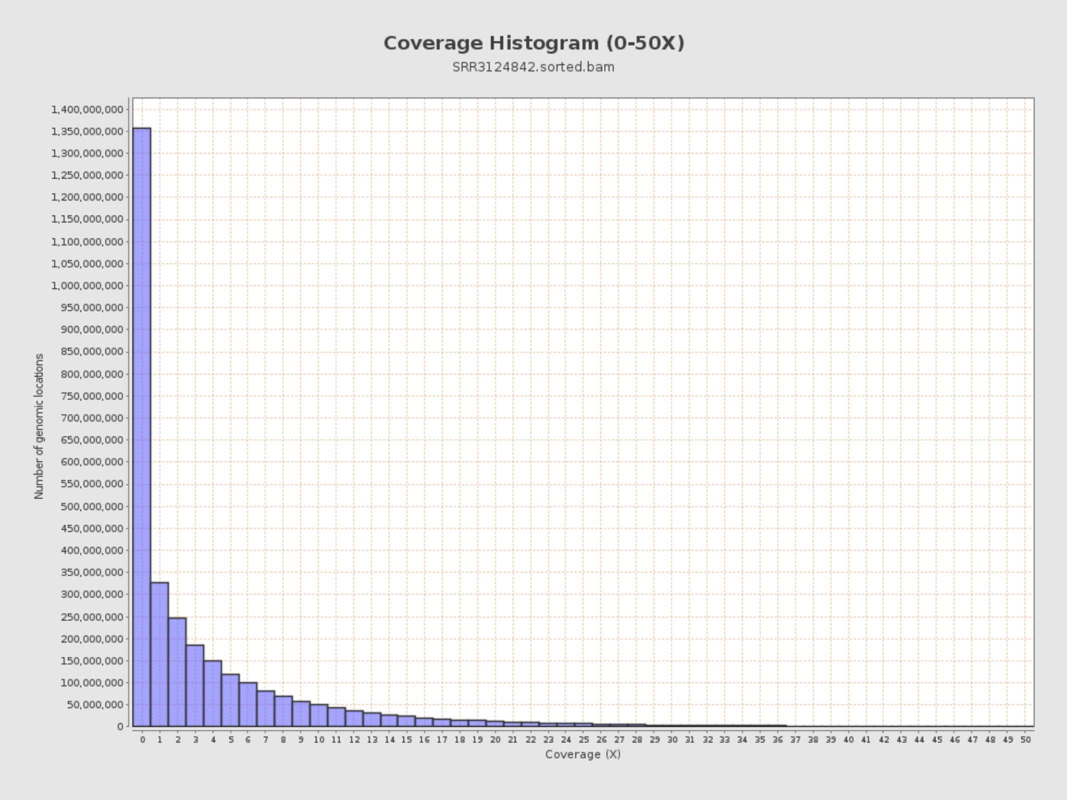
3. Results : Coverage across reference



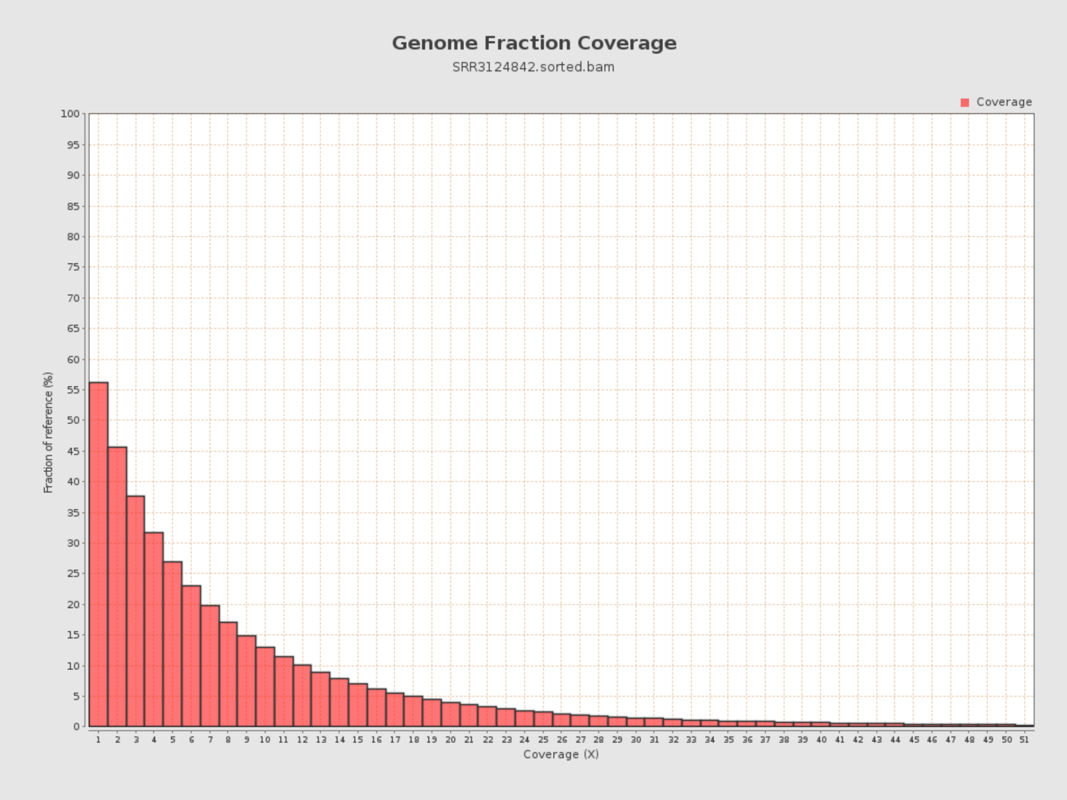
4. Results : Coverage Histogram



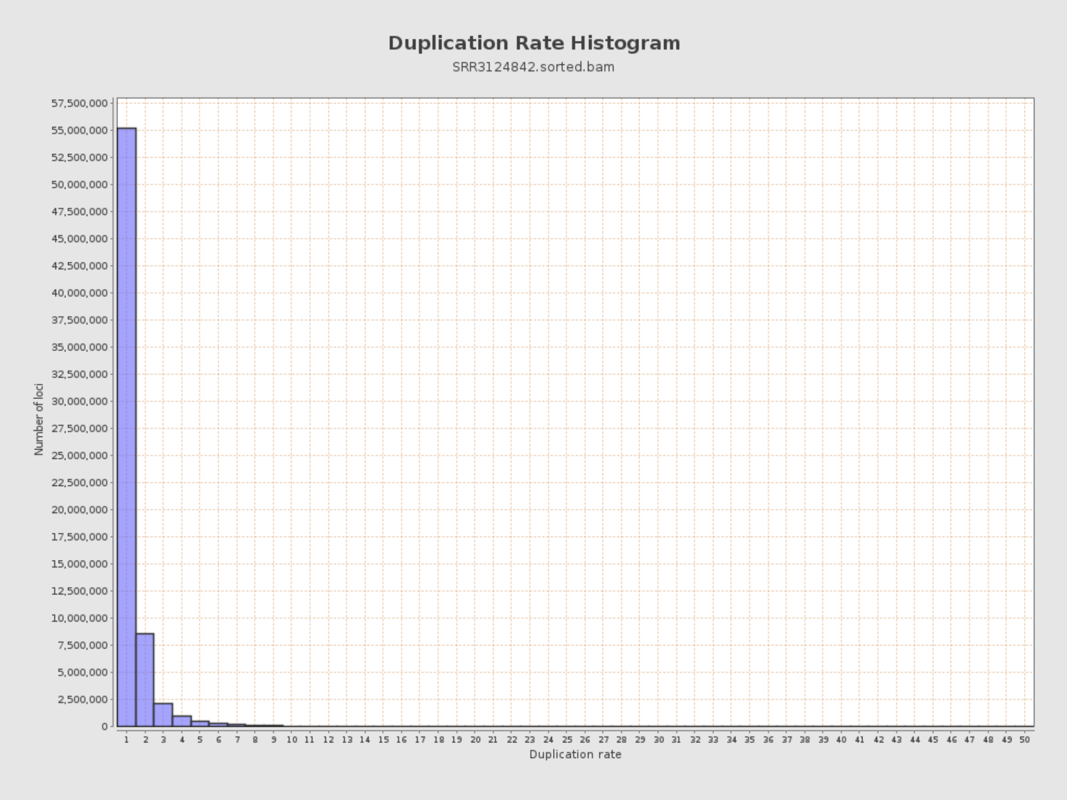
5. Results : Coverage Histogram (0-50X)



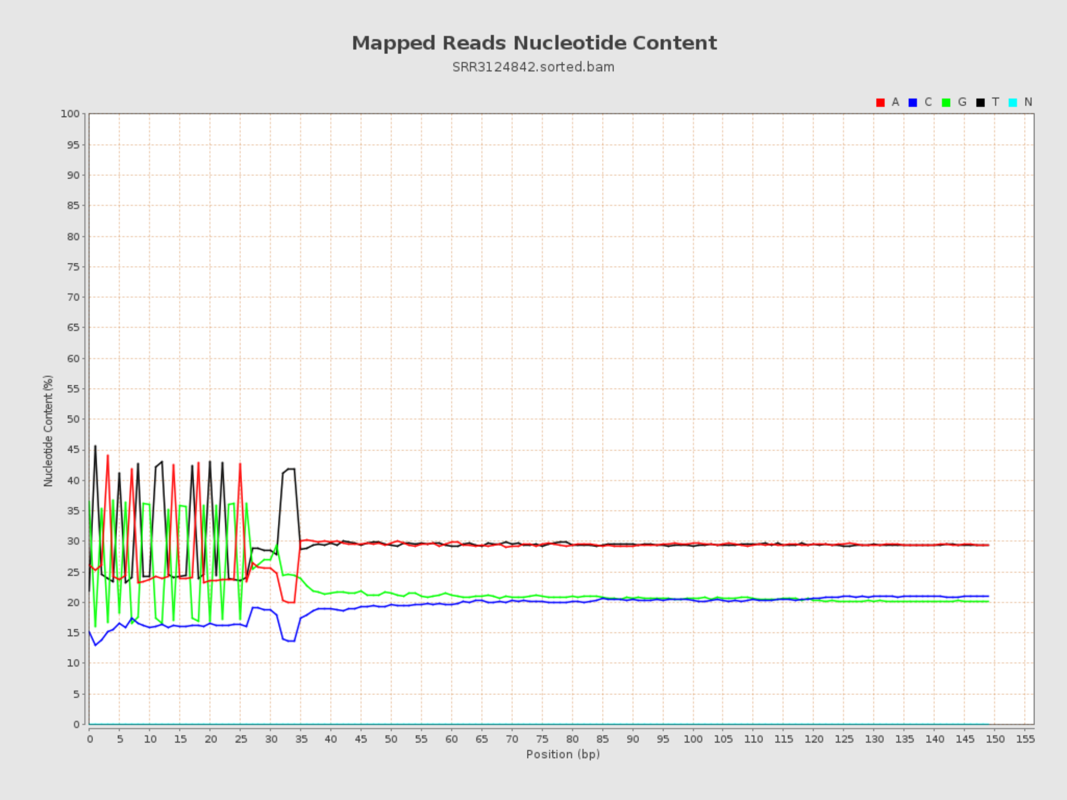
6. Results : Genome Fraction Coverage



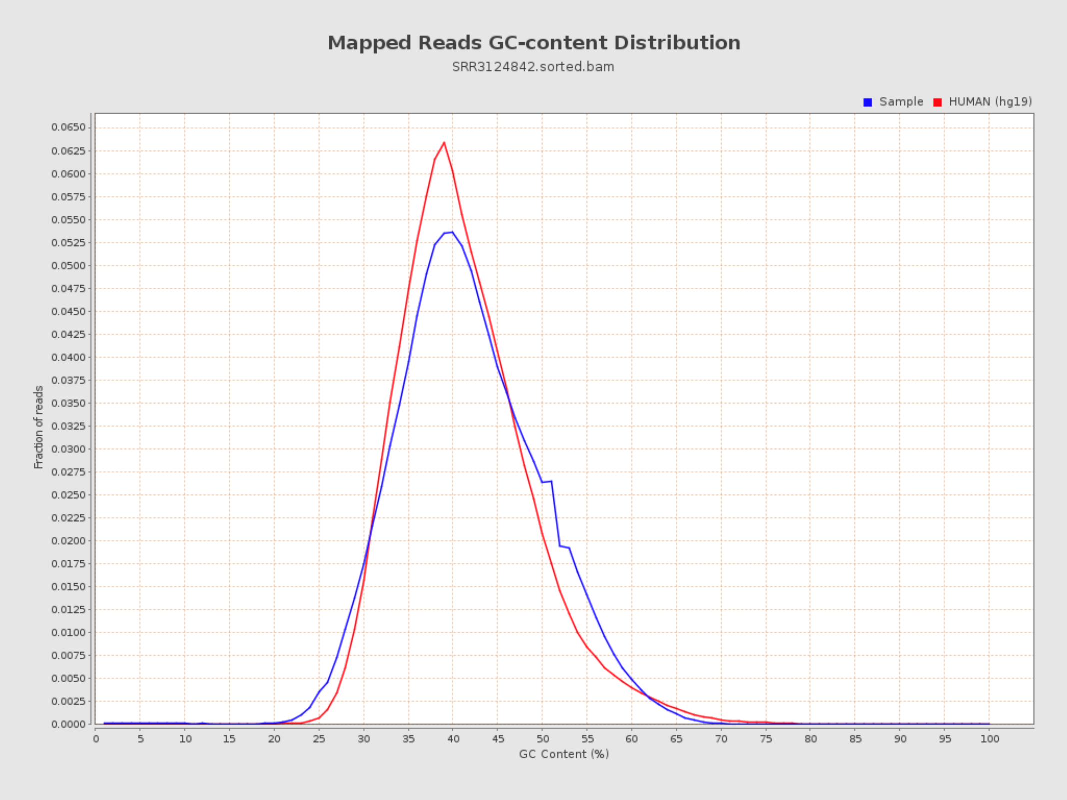
7. Results : Duplication Rate Histogram



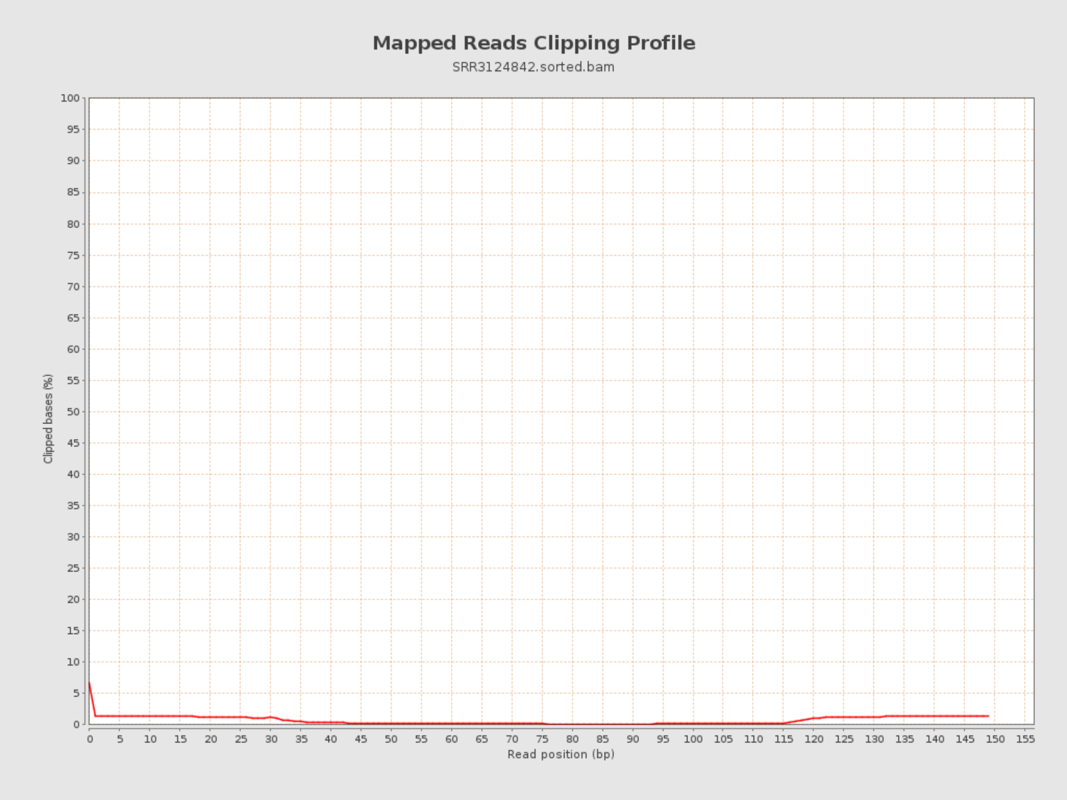
8. Results : Mapped Reads Nucleotide Content



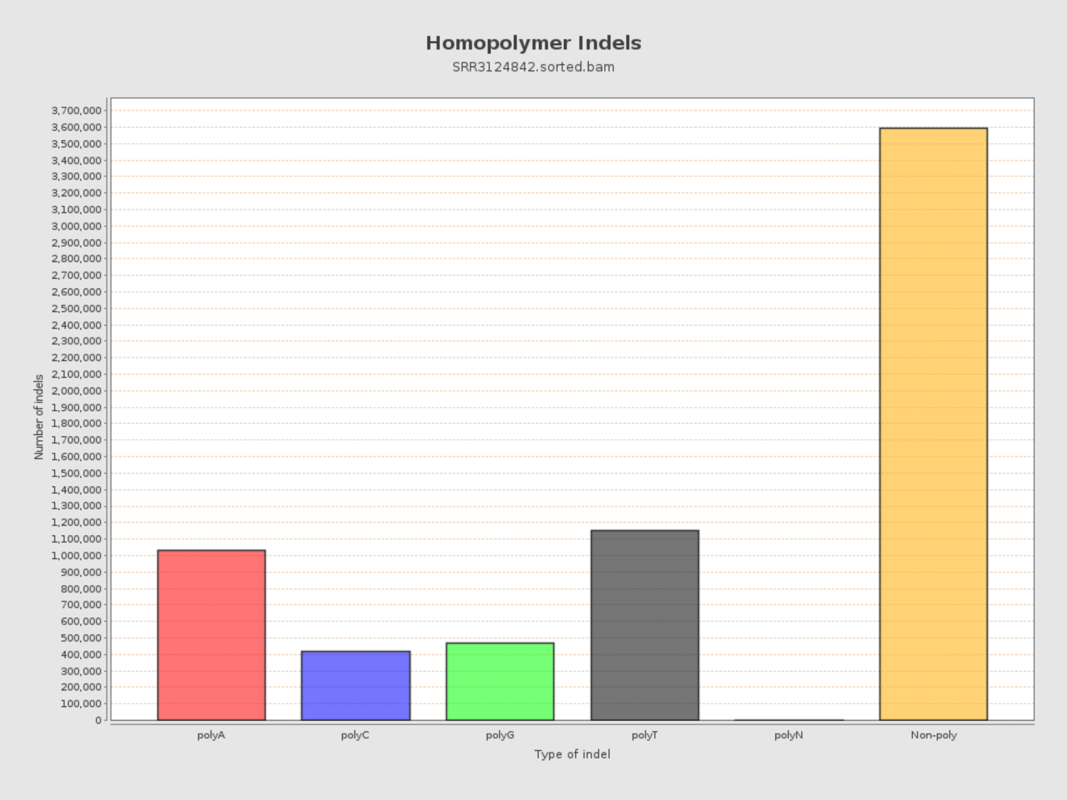
9. Results : Mapped Reads GC-content Distribution



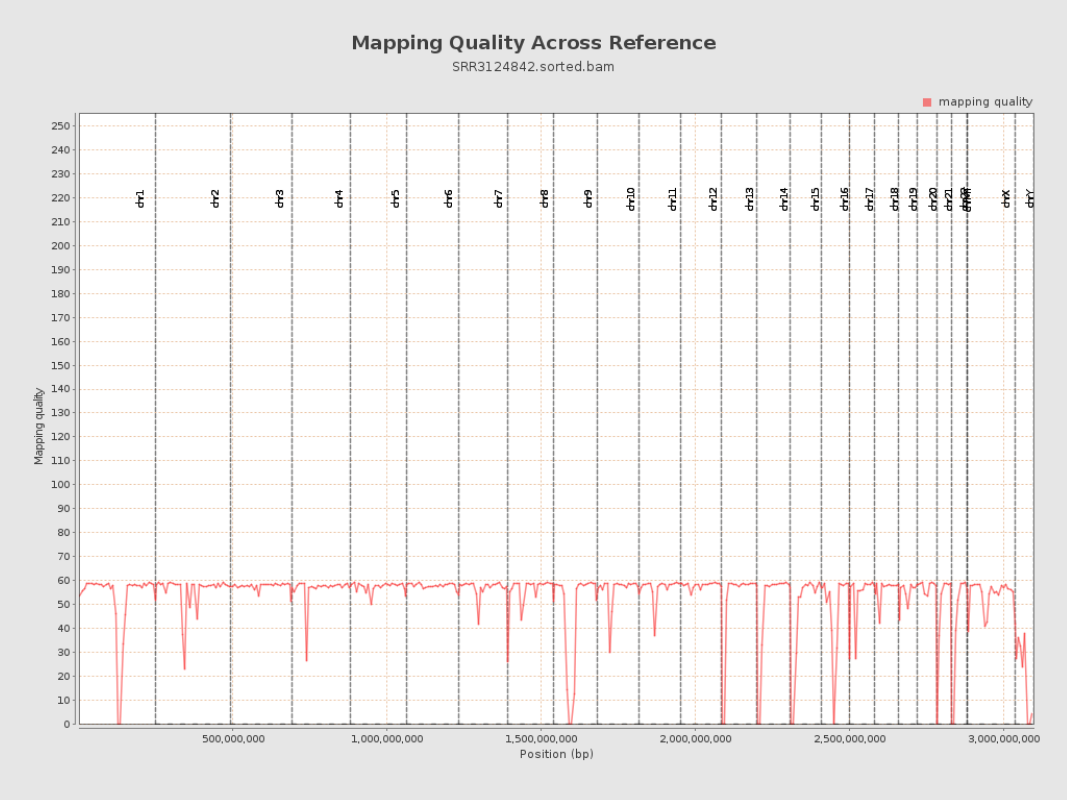
10. Results : Mapped Reads Clipping Profile



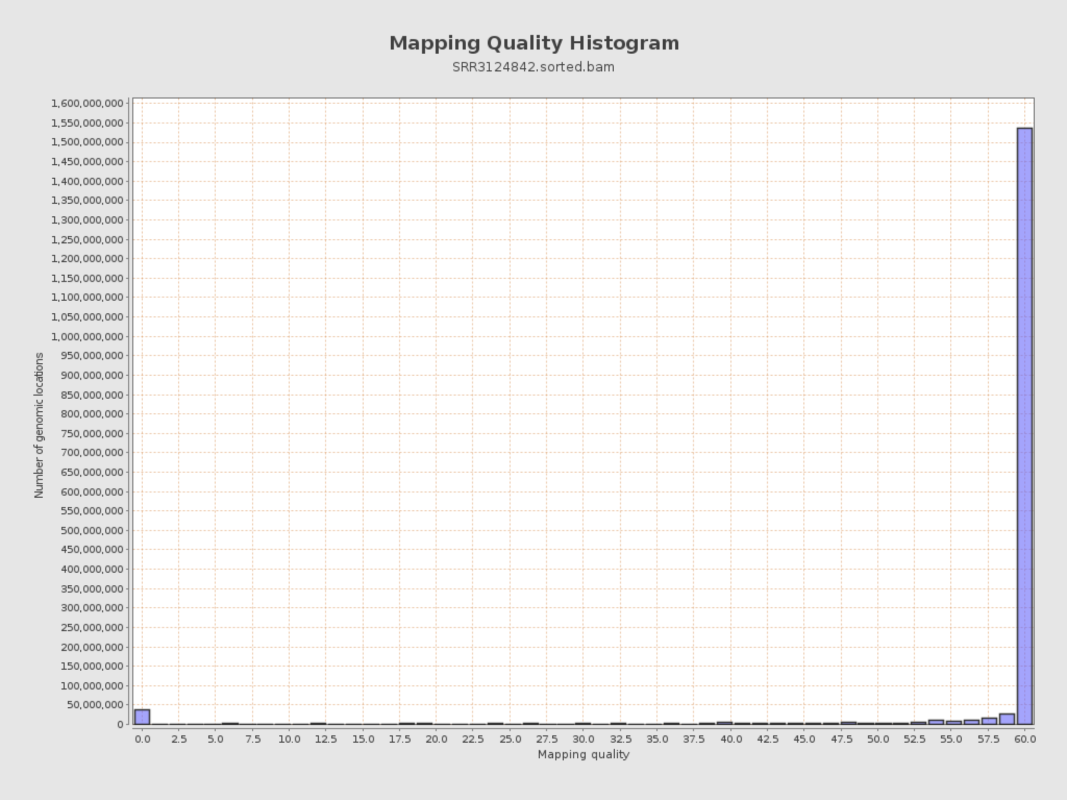
11. Results : Homopolymer Indels



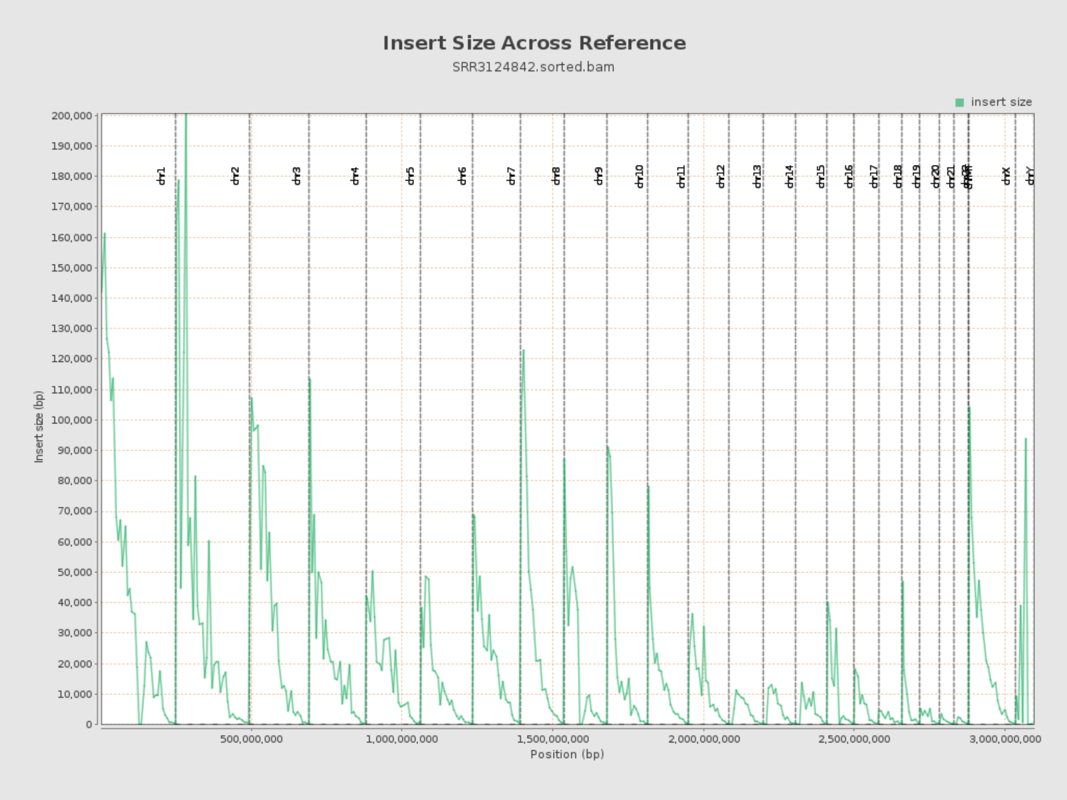
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram