Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 07:42:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124840.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_SRR3124840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124840_1.fastq.gz SRR3124840_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 07:42:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	160,877,568
Mapped reads	157,528,767 / 97.92%
Unmapped reads	3,348,801 / 2.08%
Mapped paired reads	157,528,767 / 97.92%
Mapped reads, first in pair	79,435,893 / 49.38%
Mapped reads, second in pair	78,092,874 / 48.54%
Mapped reads, both in pair	155,729,998 / 96.8%
Mapped reads, singletons	1,798,769 / 1.12%
Secondary alignments	0
Supplementary alignments	1,617,372 / 1.01%
Read min/max/mean length	30 / 150 / 150.49
Duplicated reads (estimated)	61,515,993 / 38.24%
Duplication rate	29.14%
Clipped reads	60,429,623 / 37.56%

2.2. ACGT Content

Number/percentage of A's	6,209,801,704 / 28.55%
Number/percentage of C's	4,383,244,351 / 20.15%
Number/percentage of T's	6,310,276,696 / 29.01%
Number/percentage of G's	4,847,656,169 / 22.29%
Number/percentage of N's	50,570 / 0%

GC Percentage	42.44%

2.3. Coverage

Mean	7.0311
Standard Deviation	71.6544

2.4. Mapping Quality

Mean Mapping Quality	53.81

2.5. Insert size

Mean	44,644.12
Standard Deviation	2,005,347.44
P25/Median/P75	205 / 265 / 336

2.6. Mismatches and indels

General error rate	1.23%
Mismatches	256,108,906
Insertions	3,658,659
Mapped reads with at least one insertion	2.16%
Deletions	7,533,082
Mapped reads with at least one deletion	4.58%
Homopolymer indels	45.67%

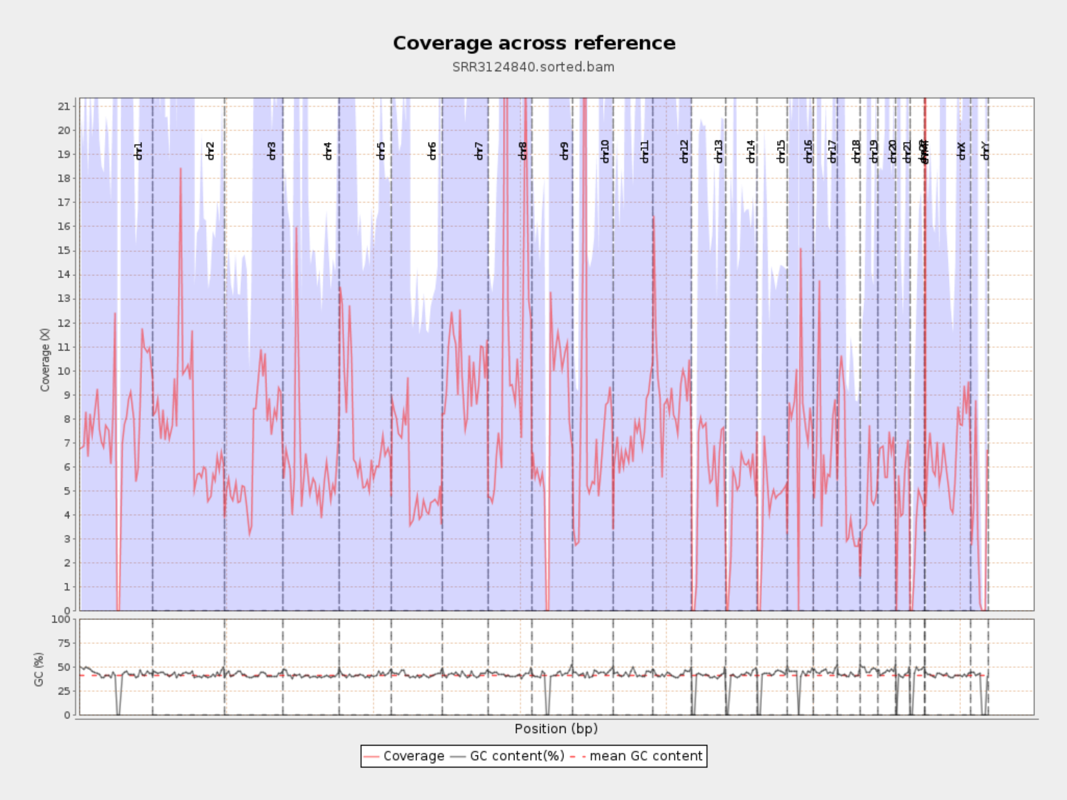
2.7. Chromosome stats

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

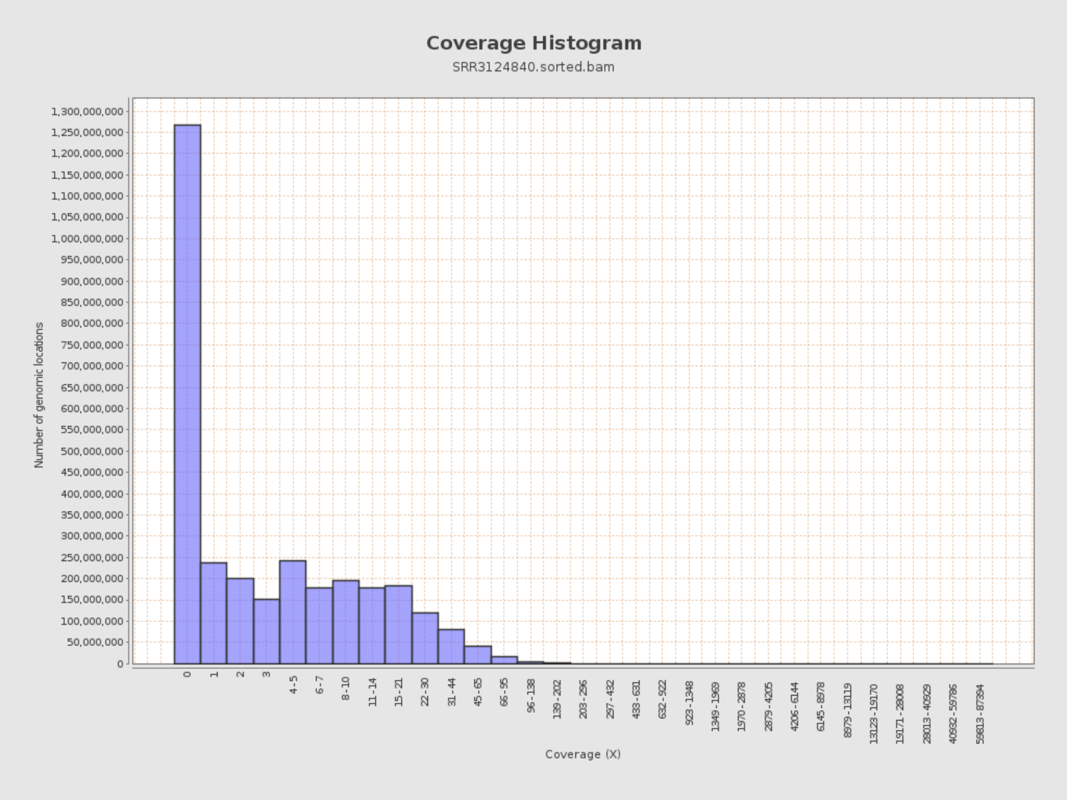
		bases	coverage	deviation
chr1	249250621	1930447161	7.745	81.8448
chr2	243199373	1900414506	7.8142	79.1104
chr3	198022430	1357285708	6.8542	12.2605
chr4	191154276	1134823807	5.9367	71.7143
chr5	180915260	1330694129	7.3553	14.295
chr6	171115067	964116551	5.6343	31.5804
chr7	159138663	1587650030	9.9765	92.368
chr8	146364022	1665058911	11.3761	36.998
chr9	141213431	1077871920	7.6329	128.9617
chr10	135534747	1076918207	7.9457	175.9105
chr11	135006516	969373515	7.1802	34.4867
chr12	133851895	1240854239	9.2704	15.4924
chr13	115169878	644477663	5.5959	10.6804
chr14	107349540	517092054	4.8169	11.9629
chr15	102531392	435714999	4.2496	9.0867
chr16	90354753	711549047	7.8751	68.5669
chr17	81195210	546874388	6.7353	124.0205
chr18	78077248	407932946	5.2247	90.6251
chr19	59128983	260357592	4.4032	44.0918
chr20	63025520	405183144	6.4289	23.8685
chr21	48129895	230882541	4.7971	34.9371
chr22	51304566	157720657	3.0742	9.1413
chrMT	16571	5903051	356.2278	162.3386
chrX	155270560	1014001626	6.5305	19.6529

chrY	59373566	192817774	3.2475	96.2935

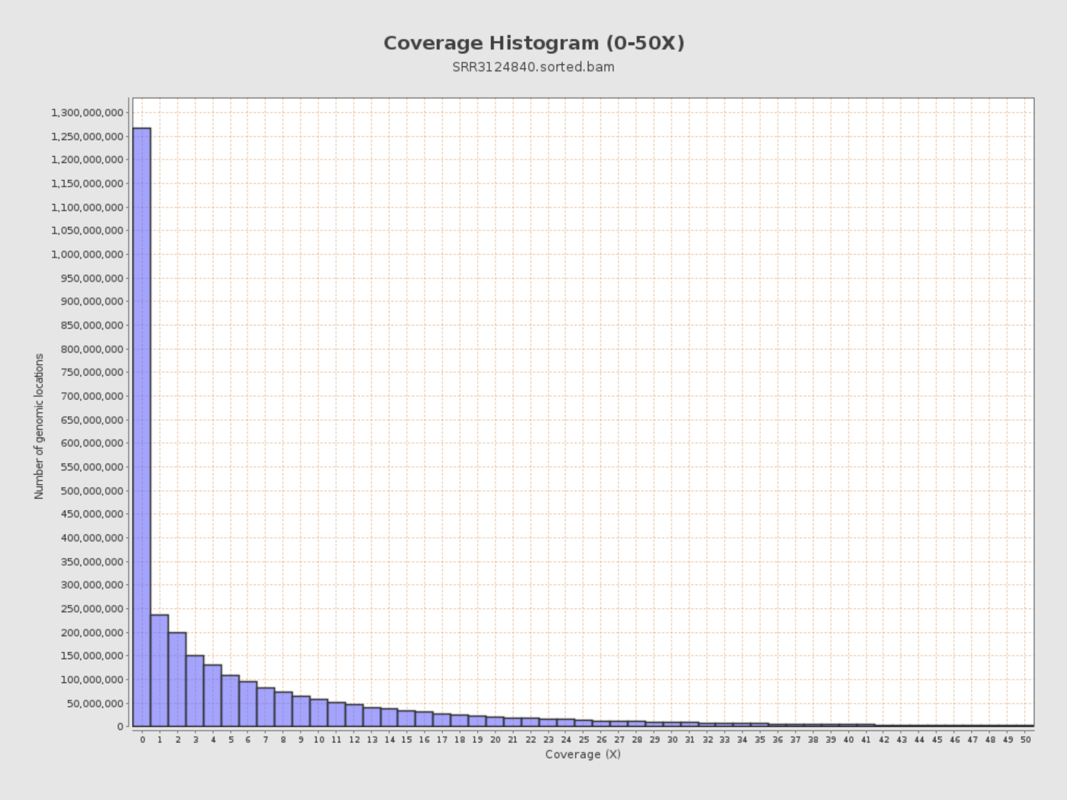
3. Results : Coverage across reference



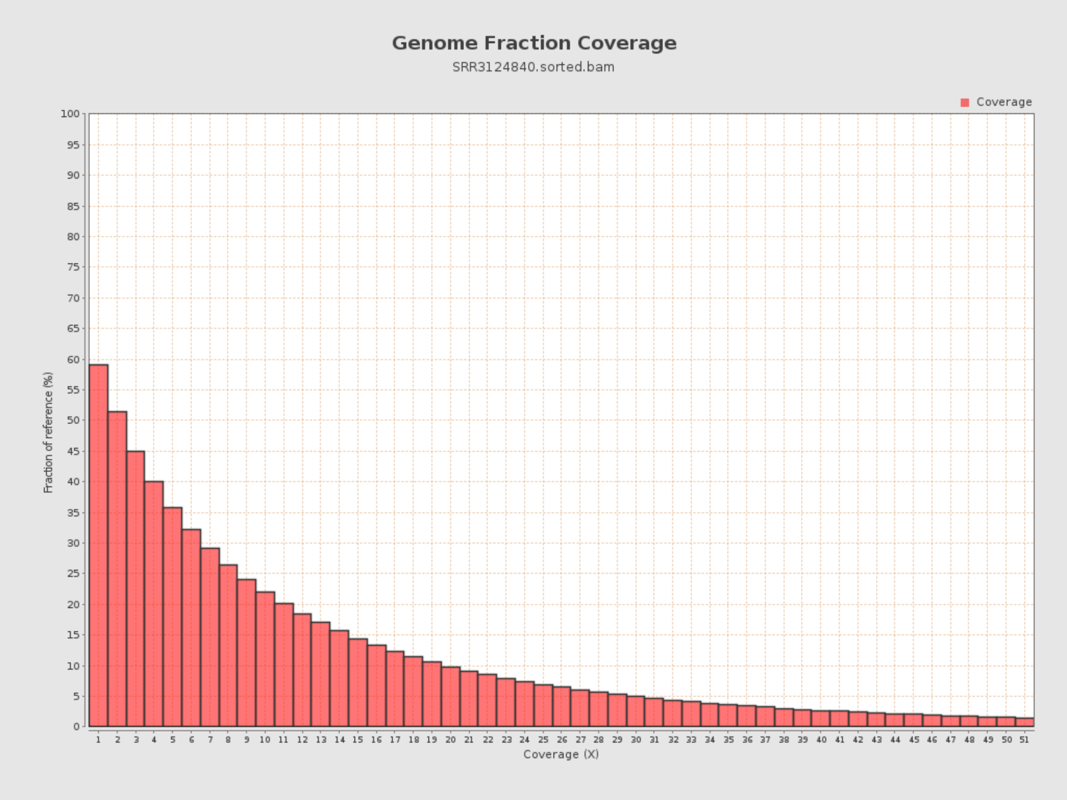
4. Results : Coverage Histogram



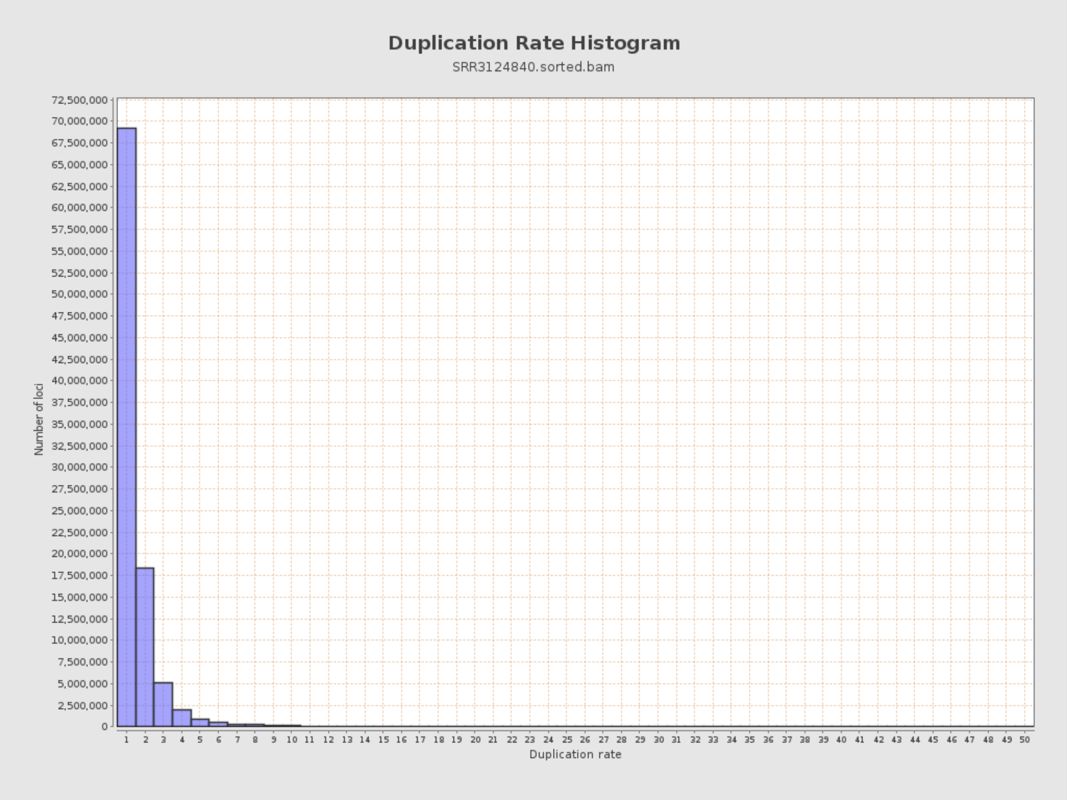
5. Results : Coverage Histogram (0-50X)



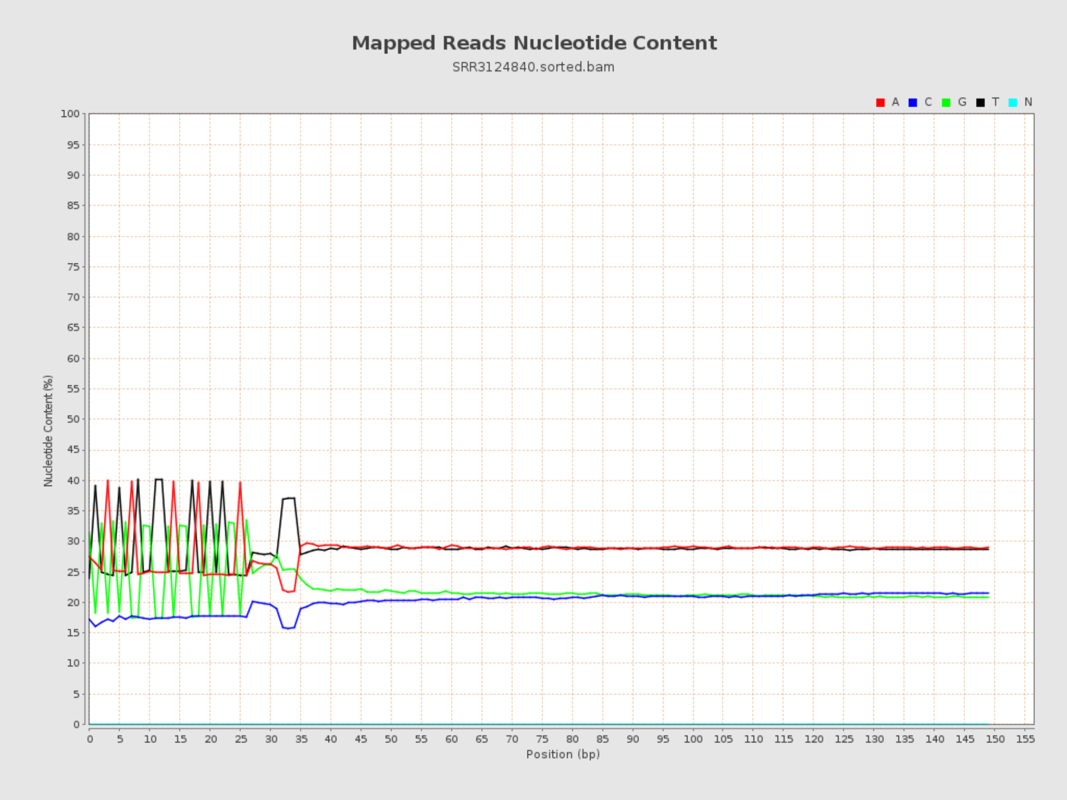
6. Results : Genome Fraction Coverage



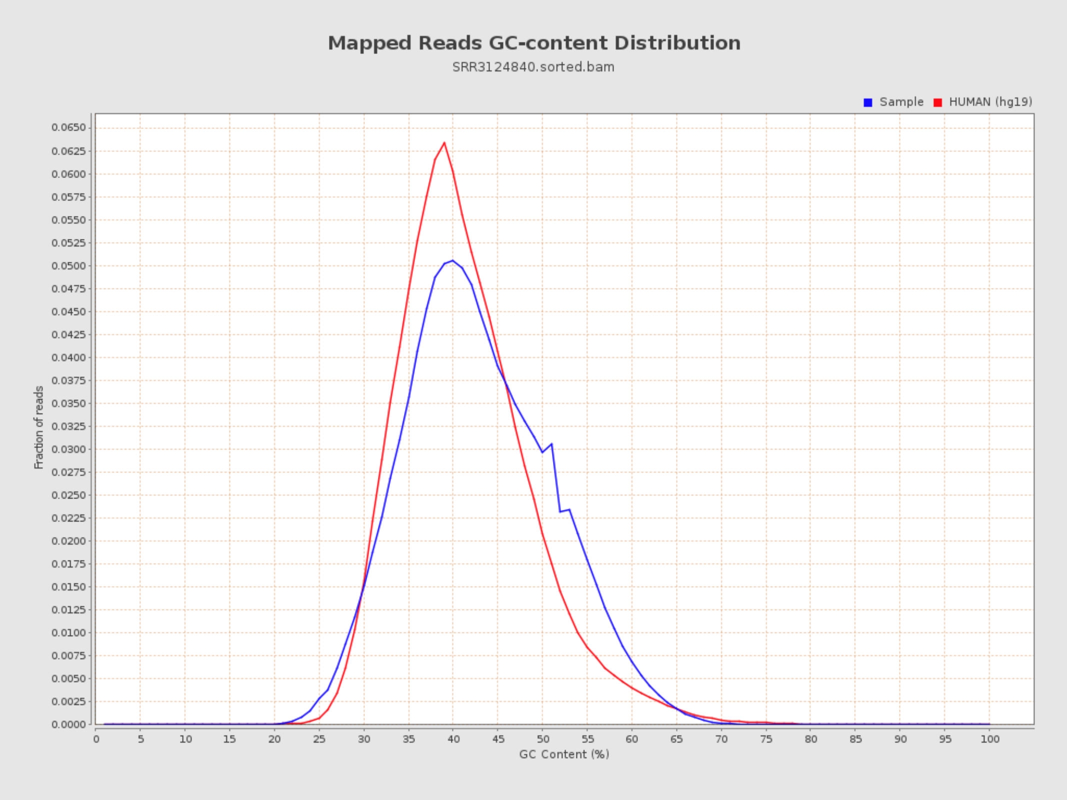
7. Results : Duplication Rate Histogram



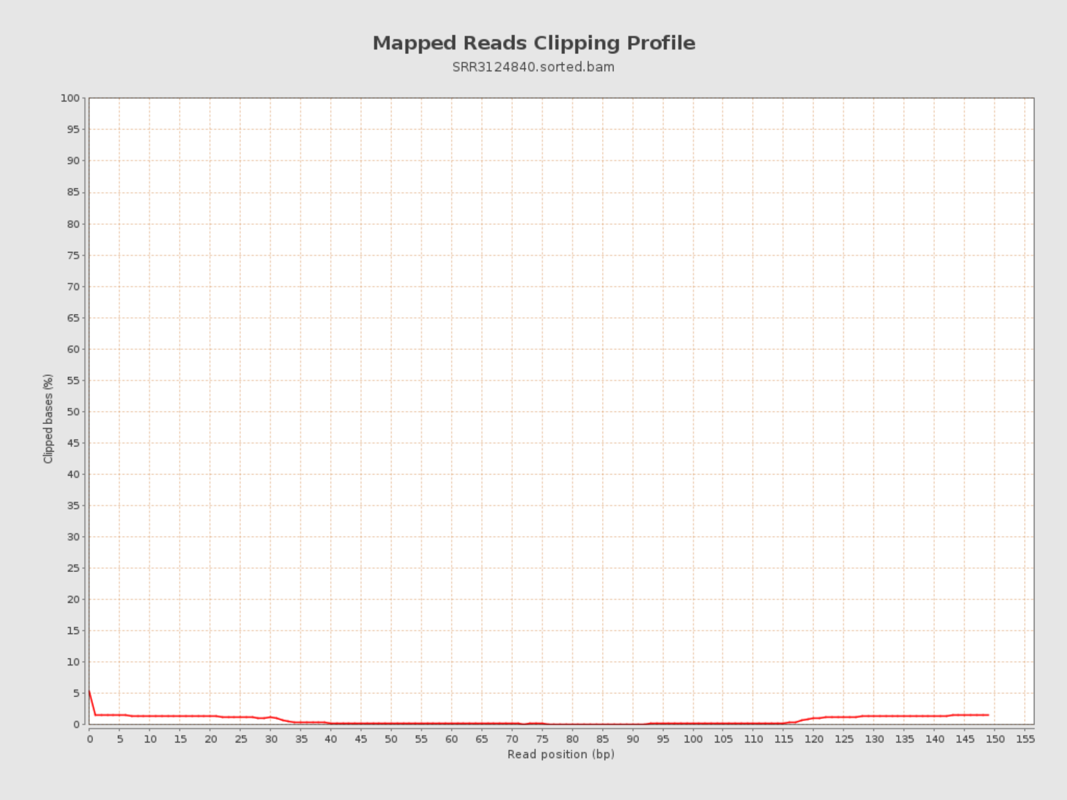
8. Results : Mapped Reads Nucleotide Content



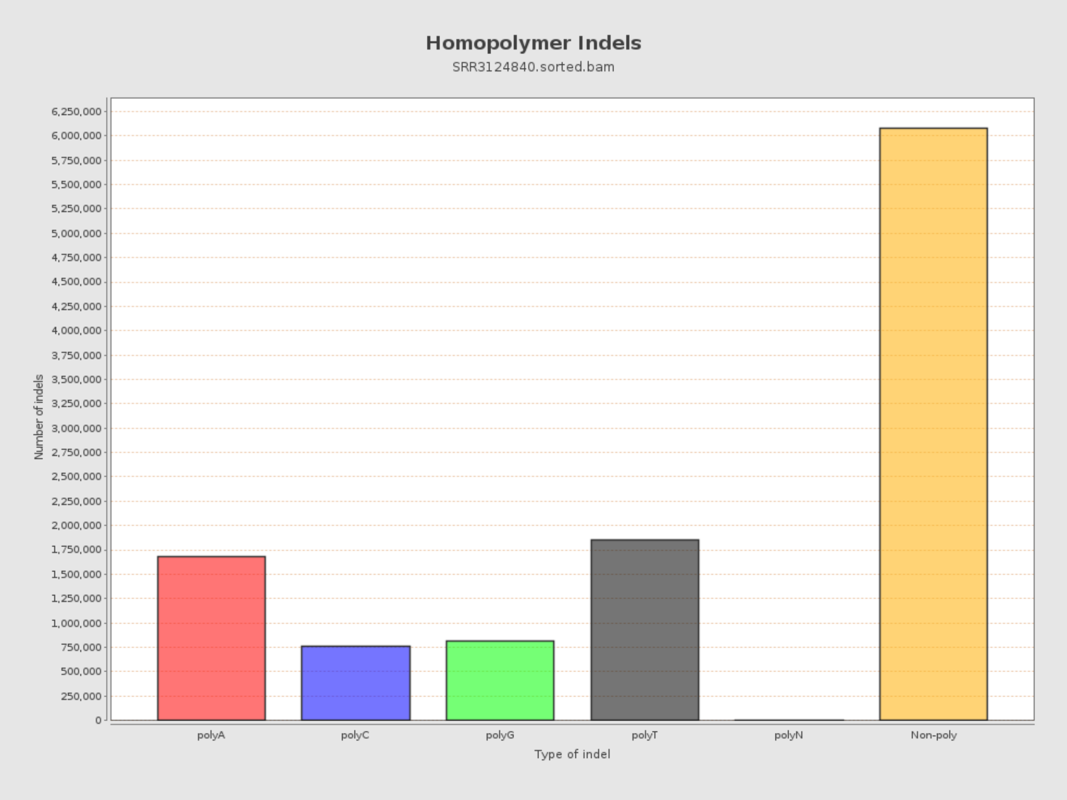
9. Results : Mapped Reads GC-content Distribution



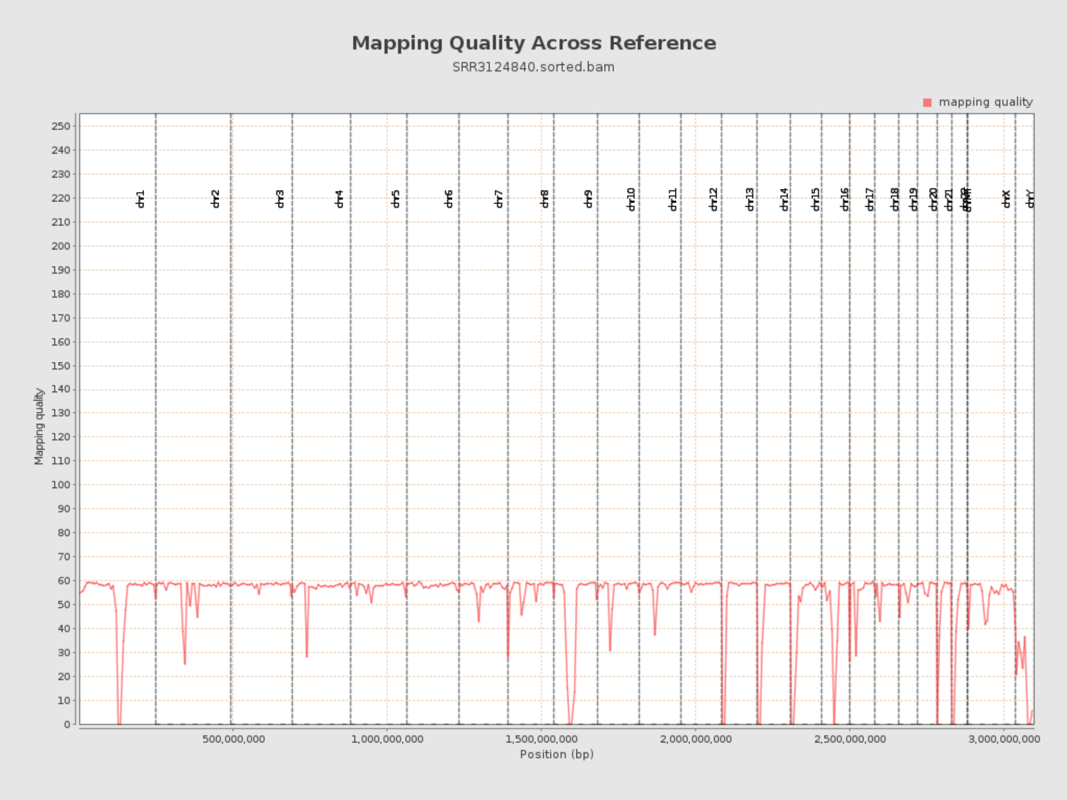
10. Results : Mapped Reads Clipping Profile



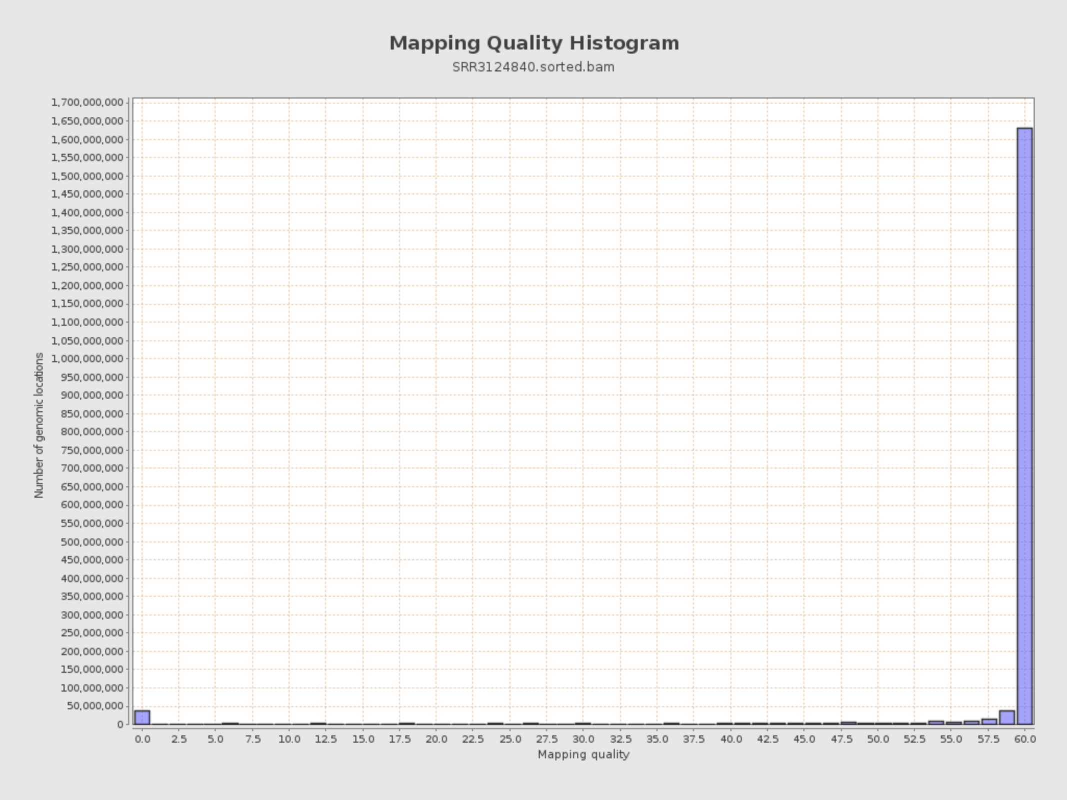
11. Results : Homopolymer Indels



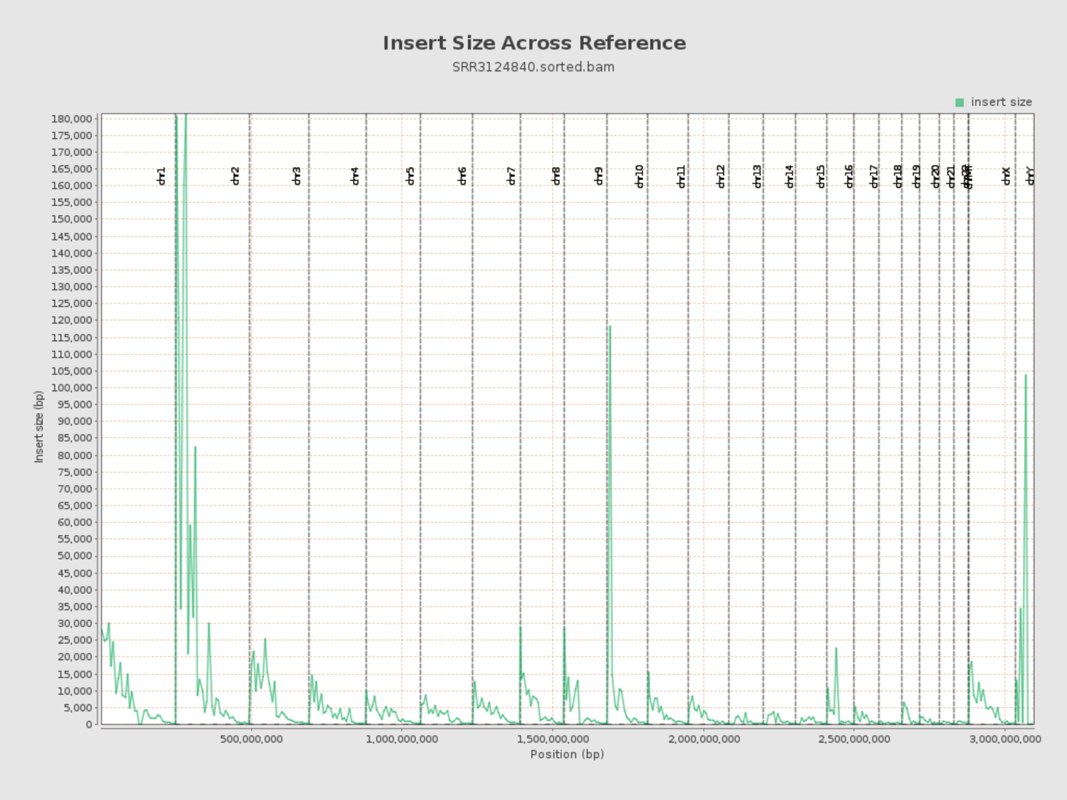
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram