Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 02:29:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124847.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_SRR3124847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124847_1.fastq.gz SRR3124847_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 02:29:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	100,061,340
Mapped reads	96,584,022 / 96.52%
Unmapped reads	3,477,318 / 3.48%
Mapped paired reads	96,584,022 / 96.52%
Mapped reads, first in pair	49,652,754 / 49.62%
Mapped reads, second in pair	46,931,268 / 46.9%
Mapped reads, both in pair	93,663,754 / 93.61%
Mapped reads, singletons	2,920,268 / 2.92%
Secondary alignments	0
Supplementary alignments	3,011,773 / 3.01%
Read min/max/mean length	30 / 150 / 151.43
Duplicated reads (estimated)	31,691,541 / 31.67%
Duplication rate	21.17%
Clipped reads	57,661,622 / 57.63%

2.2. ACGT Content

Number/percentage of A's	3,633,991,813 / 28.78%
Number/percentage of C's	2,422,668,640 / 19.19%
Number/percentage of T's	3,755,232,619 / 29.74%
Number/percentage of G's	2,815,152,313 / 22.29%
Number/percentage of N's	218,681 / 0%

GC Percentage	41.48%

2.3. Coverage

Mean	4.0826
Standard Deviation	57.417

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	177,686.22
Standard Deviation	4,017,976.12
P25/Median/P75	195 / 247 / 310

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	156,011,990
Insertions	2,796,101
Mapped reads with at least one insertion	2.65%
Deletions	4,882,230
Mapped reads with at least one deletion	4.81%
Homopolymer indels	43.74%

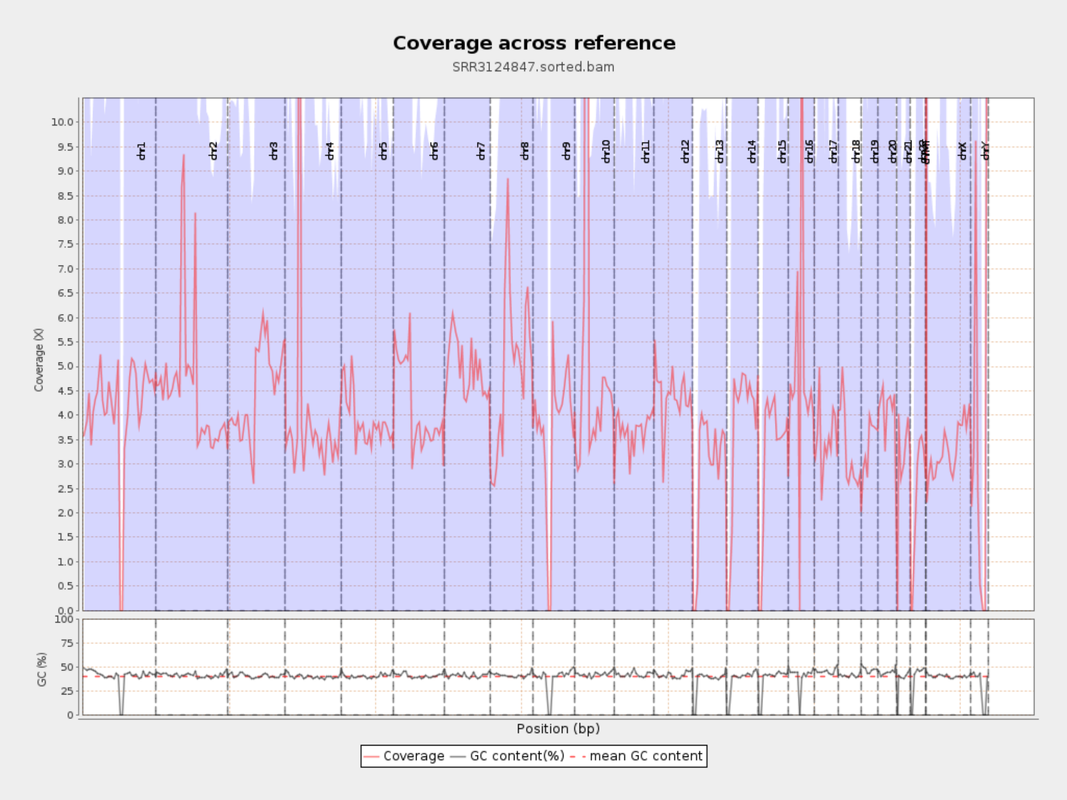
2.7. Chromosome stats

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

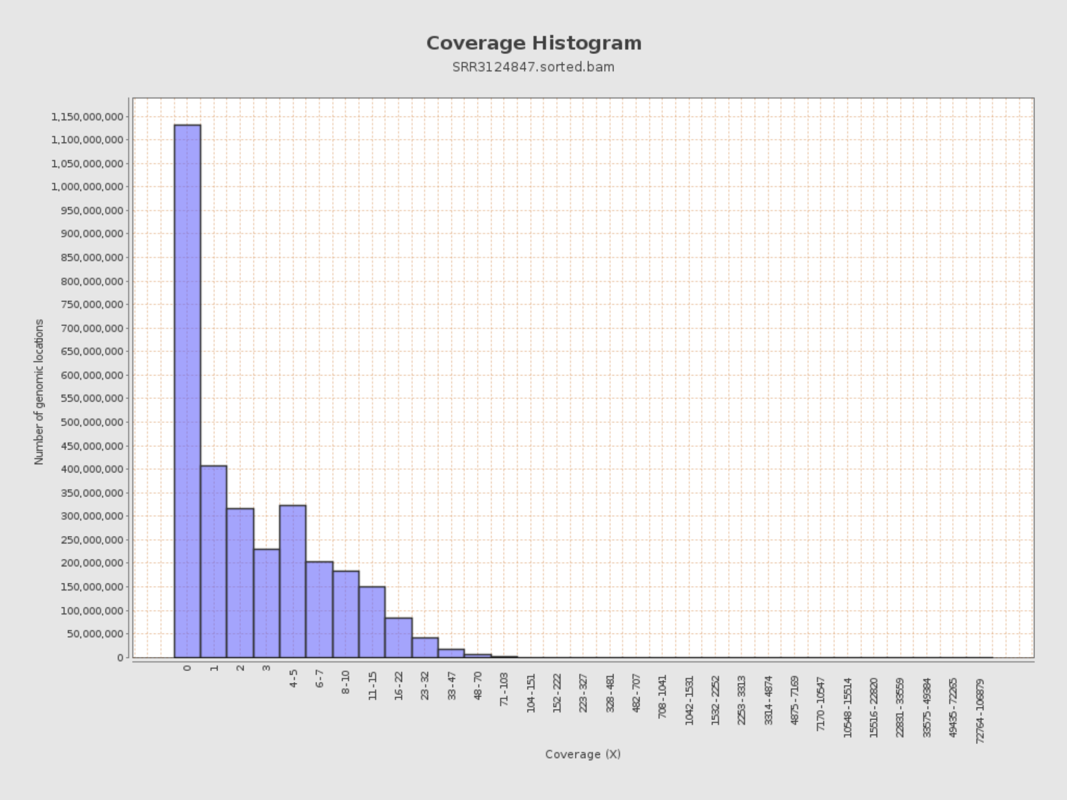
		bases	coverage	deviation
chr1	249250621	1027762256	4.1234	24.1477
chr2	243199373	1117236219	4.5939	61.2752
chr3	198022430	886502707	4.4768	8.1736
chr4	191154276	774511591	4.0518	98.2165
chr5	180915260	706057081	3.9027	8.002
chr6	171115067	714166376	4.1736	14.283
chr7	159138663	787159434	4.9464	25.2915
chr8	146364022	731474267	4.9976	11.7421
chr9	141213431	529760423	3.7515	51.3185
chr10	135534747	726383140	5.3594	183.0269
chr11	135006516	495985520	3.6738	12.8606
chr12	133851895	592067806	4.4233	23.8168
chr13	115169878	332256516	2.8849	5.3983
chr14	107349540	397193345	3.7	8.2421
chr15	102531392	325176138	3.1715	11.6289
chr16	90354753	451442697	4.9963	78.2509
chr17	81195210	287210939	3.5373	31.562
chr18	78077248	257571535	3.2989	42.1733
chr19	59128983	199790534	3.3789	14.0454
chr20	63025520	260523925	4.1336	32.8032
chr21	48129895	149367593	3.1034	47.3924
chr22	51304566	118532983	2.3104	7.792
chrMT	16571	5234622	315.8905	167.6291
chrX	155270560	512117821	3.2982	9.2757

chrY	59373566	253033576	4.2617	136.4876

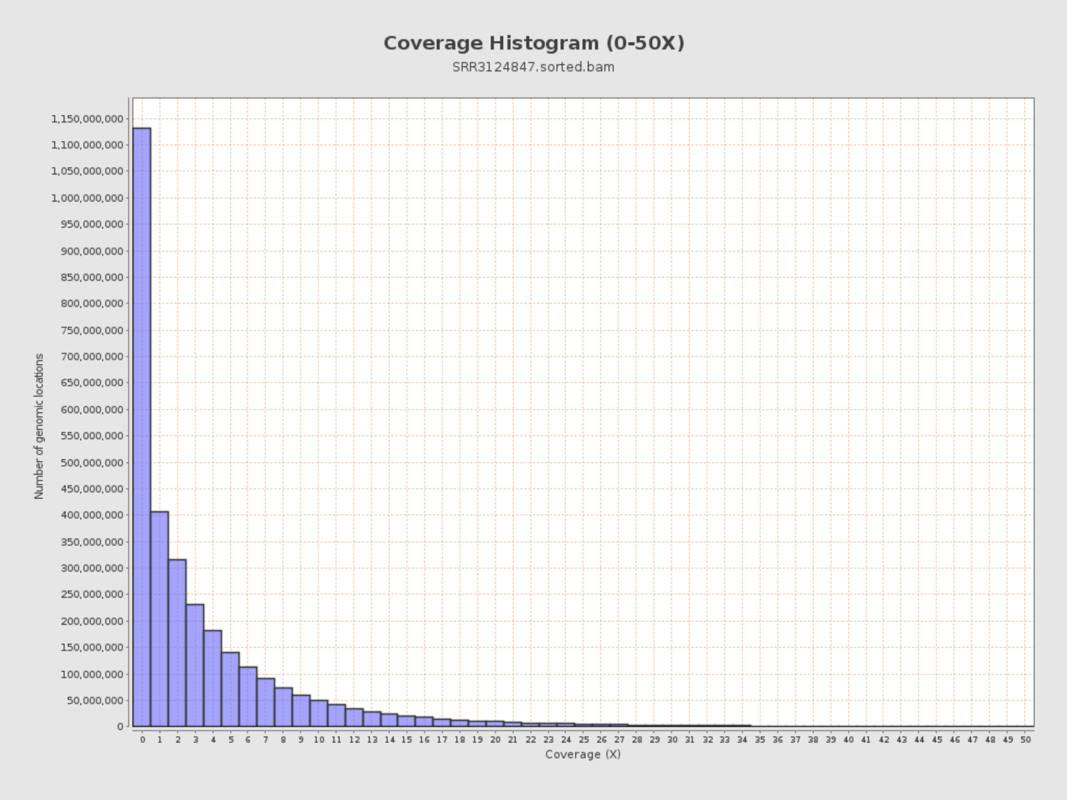
3. Results : Coverage across reference



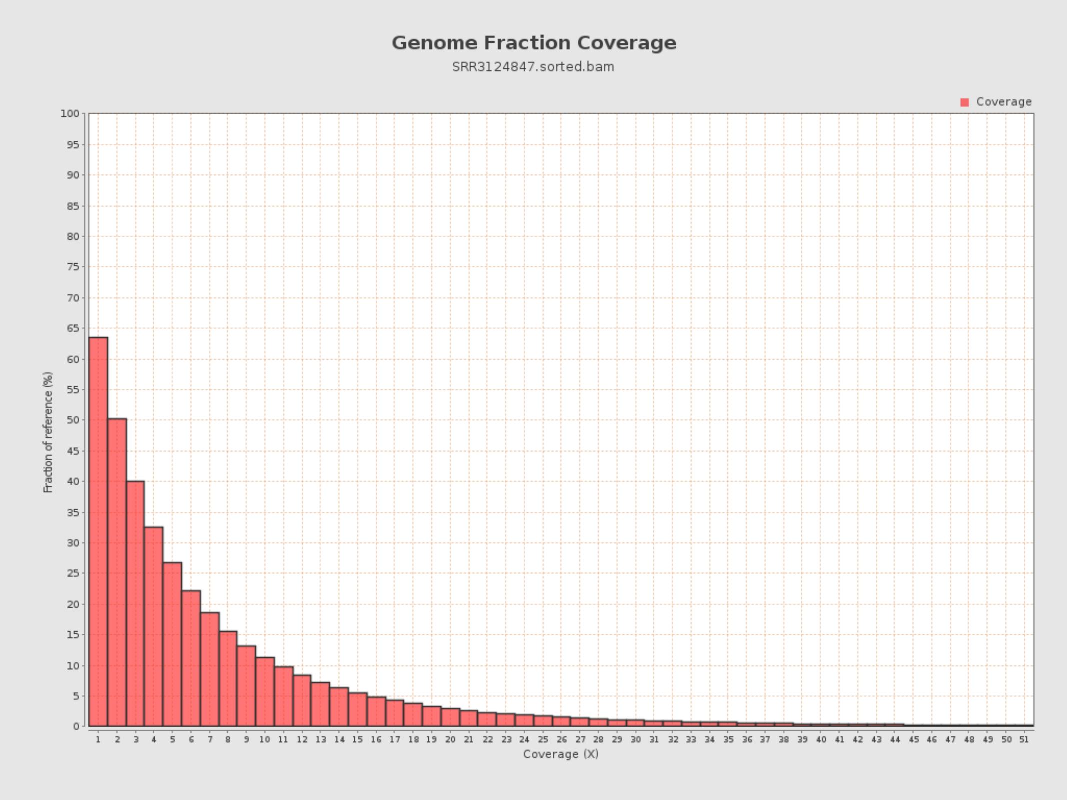
4. Results : Coverage Histogram



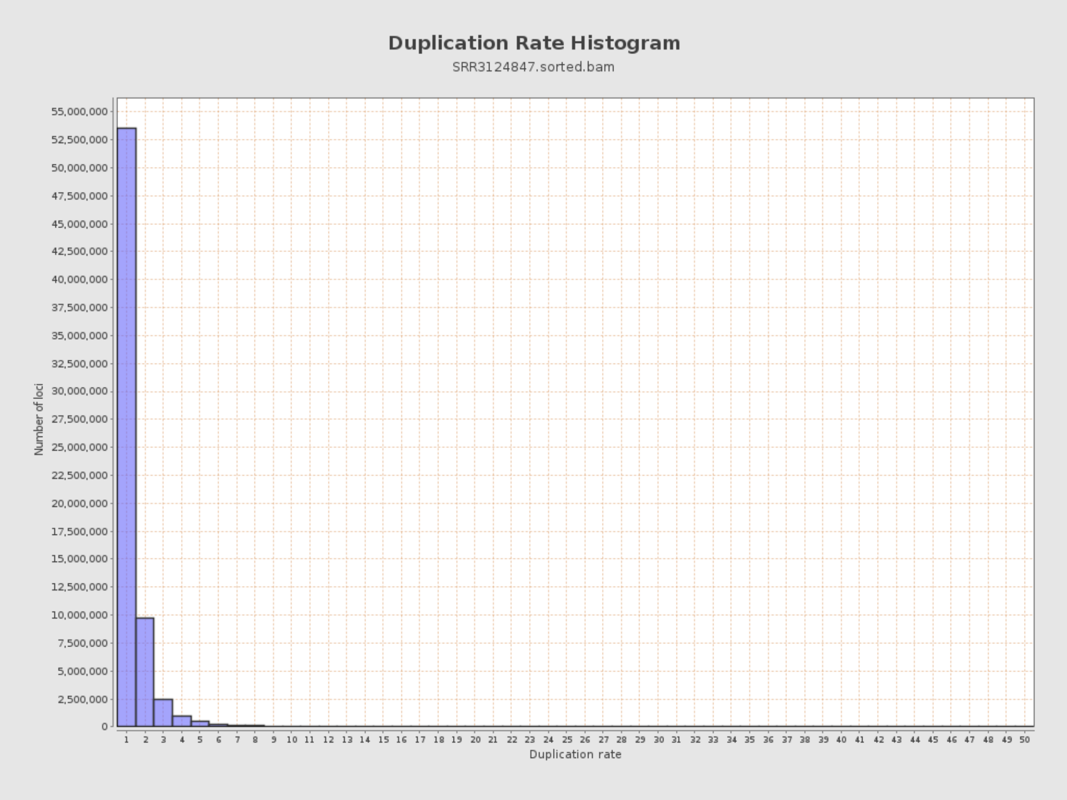
5. Results : Coverage Histogram (0-50X)



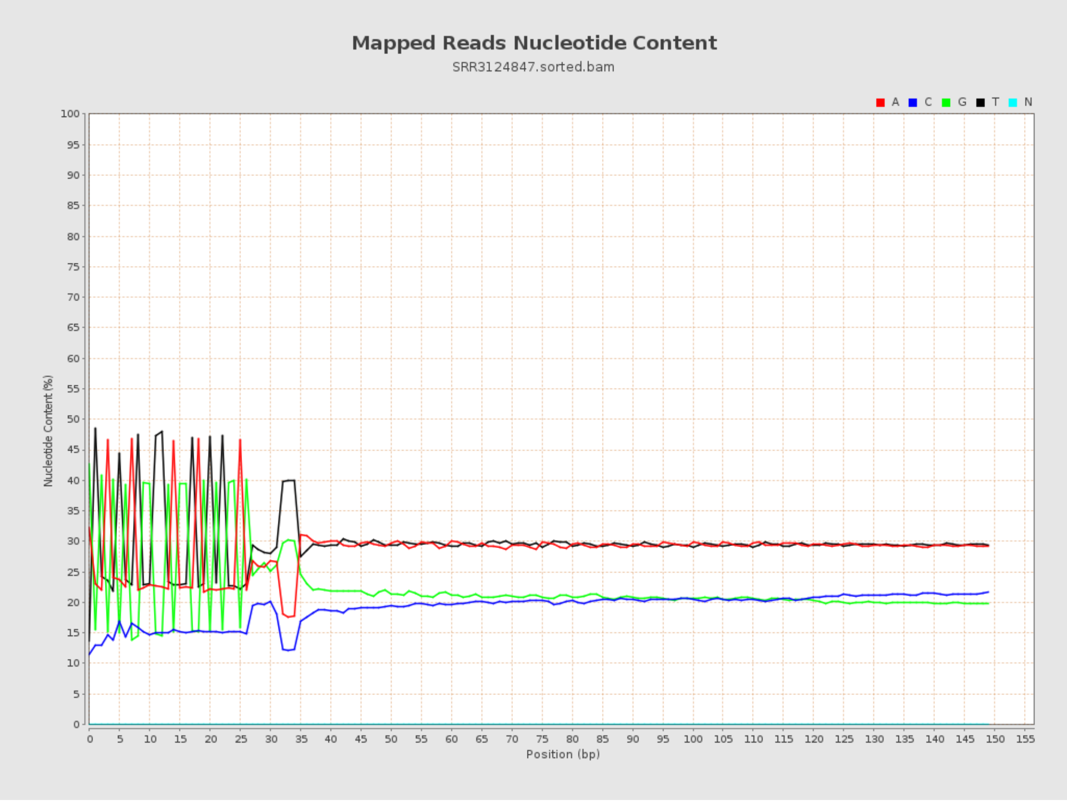
6. Results : Genome Fraction Coverage



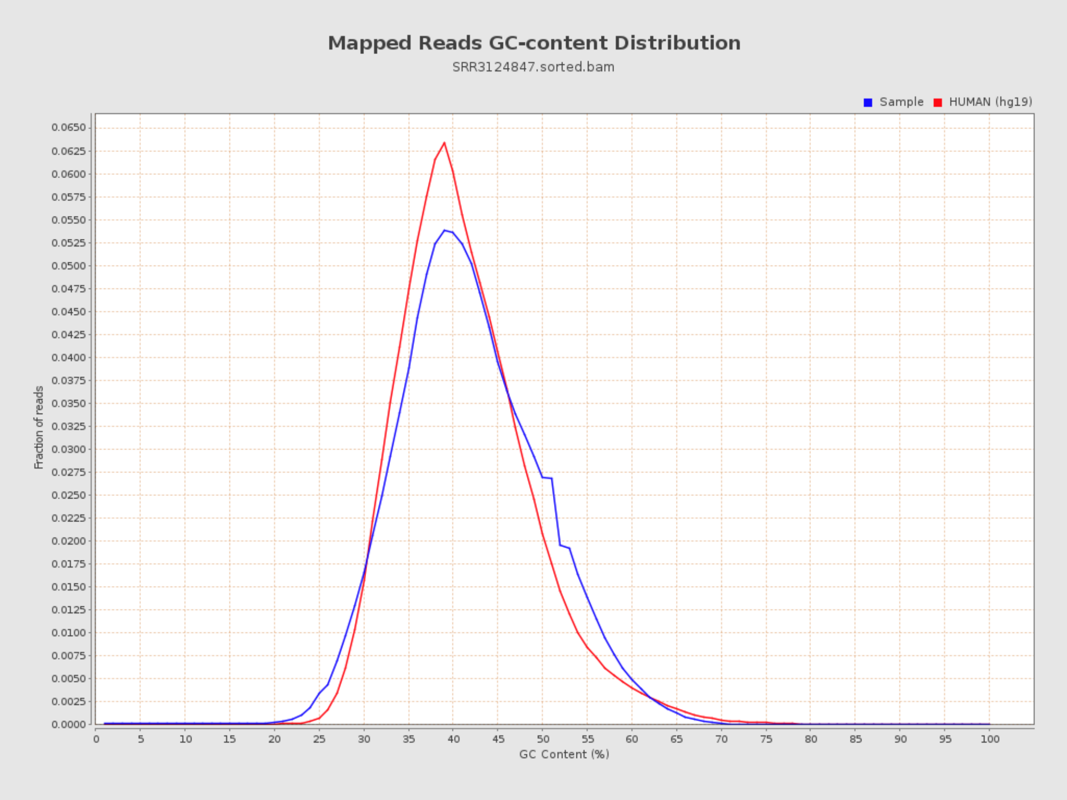
7. Results : Duplication Rate Histogram



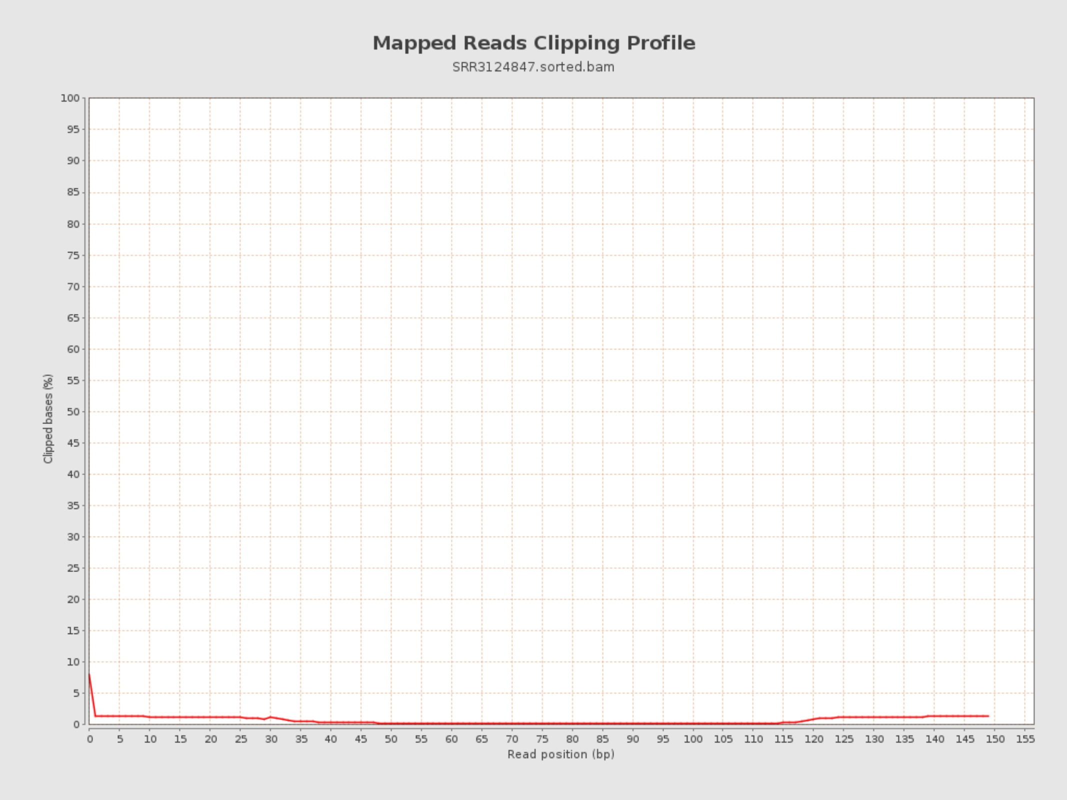
8. Results : Mapped Reads Nucleotide Content



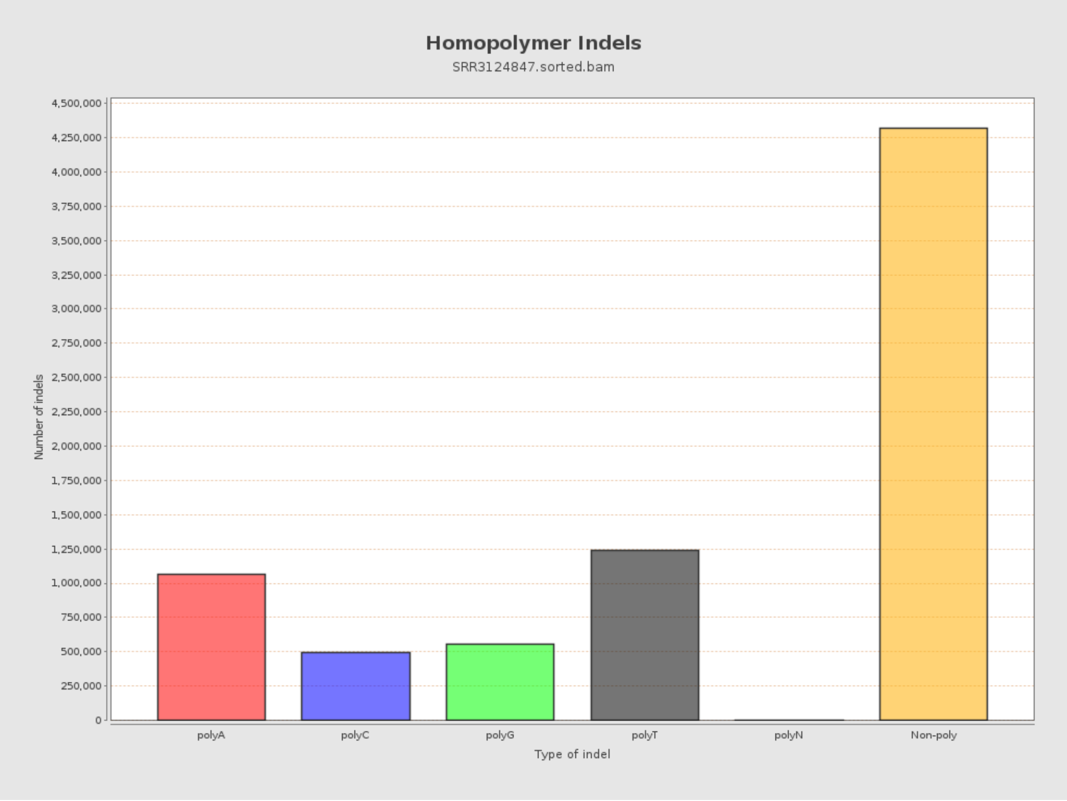
9. Results : Mapped Reads GC-content Distribution



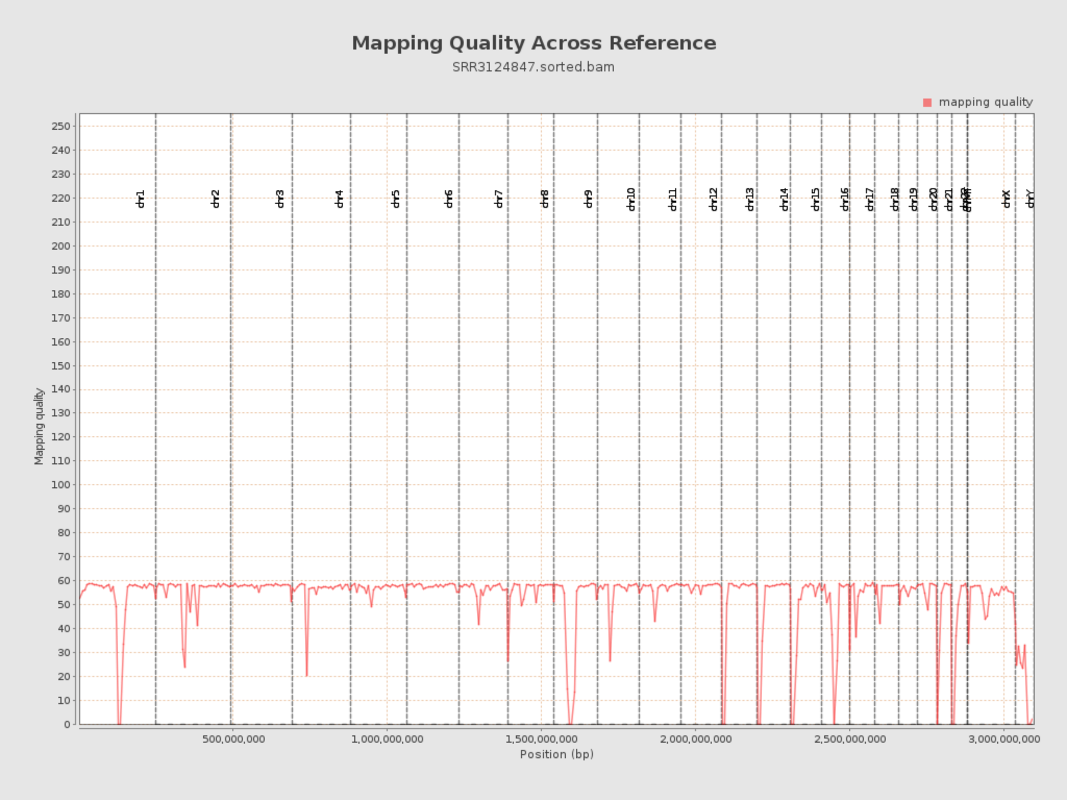
10. Results : Mapped Reads Clipping Profile



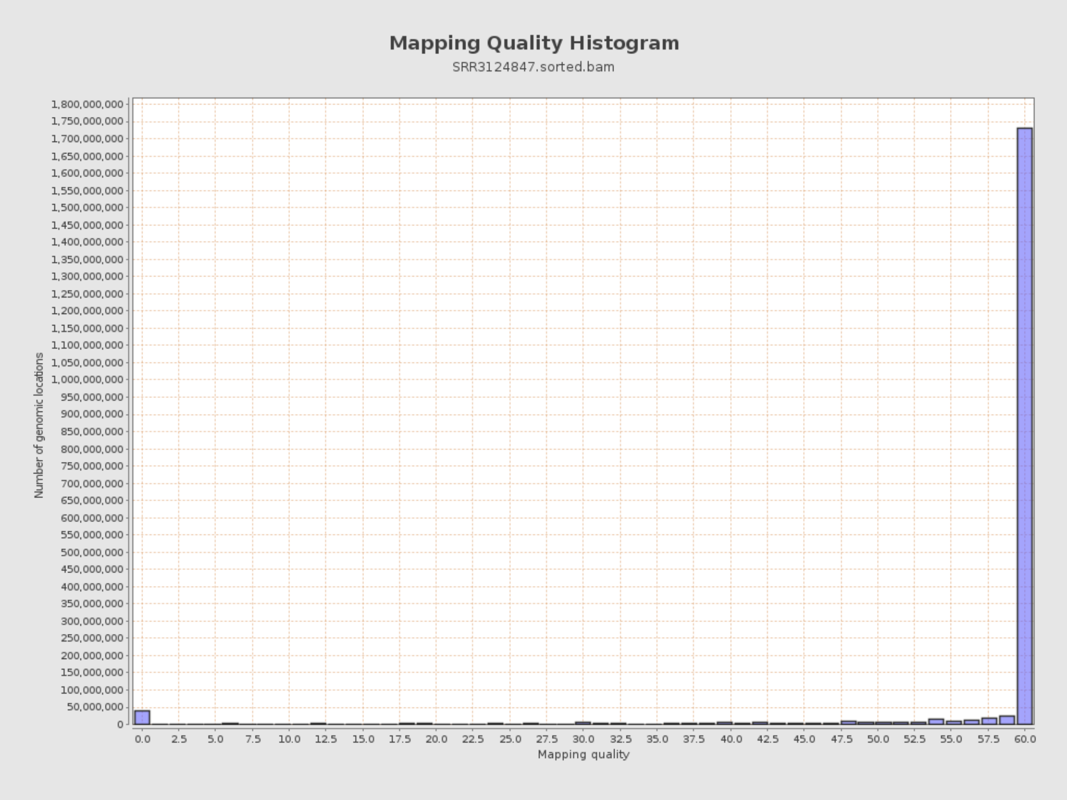
11. Results : Homopolymer Indels



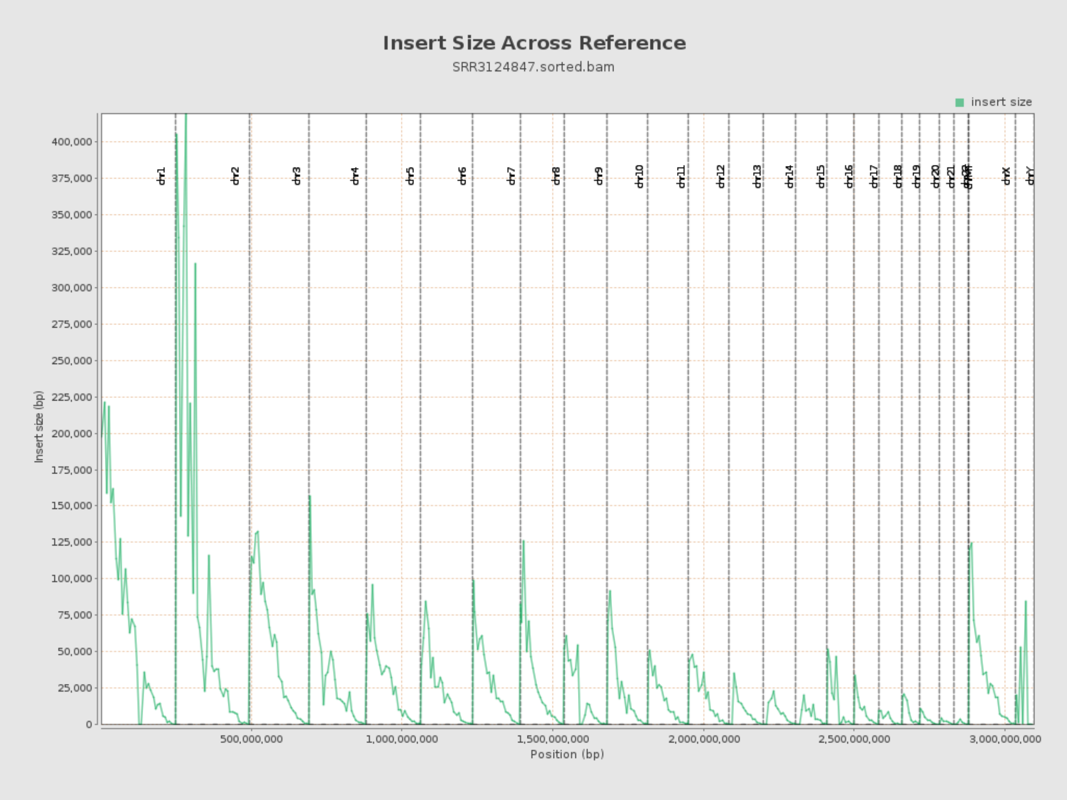
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram