Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 06:39:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124830.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_SRR3124830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124830_1.fastq.gz SRR3124830_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 06:39:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124830.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,641,394
Mapped reads	25,077,867 / 97.8%
Unmapped reads	563,527 / 2.2%
Mapped paired reads	25,077,867 / 97.8%
Mapped reads, first in pair	12,577,537 / 49.05%
Mapped reads, second in pair	12,500,330 / 48.75%
Mapped reads, both in pair	24,891,110 / 97.07%
Mapped reads, singletons	186,757 / 0.73%
Secondary alignments	0
Supplementary alignments	287,585 / 1.12%
Read min/max/mean length	30 / 101 / 101.45
Duplicated reads (estimated)	5,008,713 / 19.53%
Duplication rate	12.76%
Clipped reads	13,922,213 / 54.3%

2.2. ACGT Content

Number/percentage of A's	615,262,081 / 28.79%
Number/percentage of C's	388,150,844 / 18.16%
Number/percentage of T's	650,516,837 / 30.44%
Number/percentage of G's	482,876,067 / 22.6%
Number/percentage of N's	19,823 / 0%

GC Percentage	40.76%

2.3. Coverage

Mean	0.6906
Standard Deviation	8.4327

2.4. Mapping Quality

Mean Mapping Quality	52.31

2.5. Insert size

Mean	116,385.31
Standard Deviation	3,262,555.58
P25/Median/P75	127 / 174 / 245

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	16,987,612
Insertions	317,277
Mapped reads with at least one insertion	1.23%
Deletions	690,412
Mapped reads with at least one deletion	2.7%
Homopolymer indels	47.05%

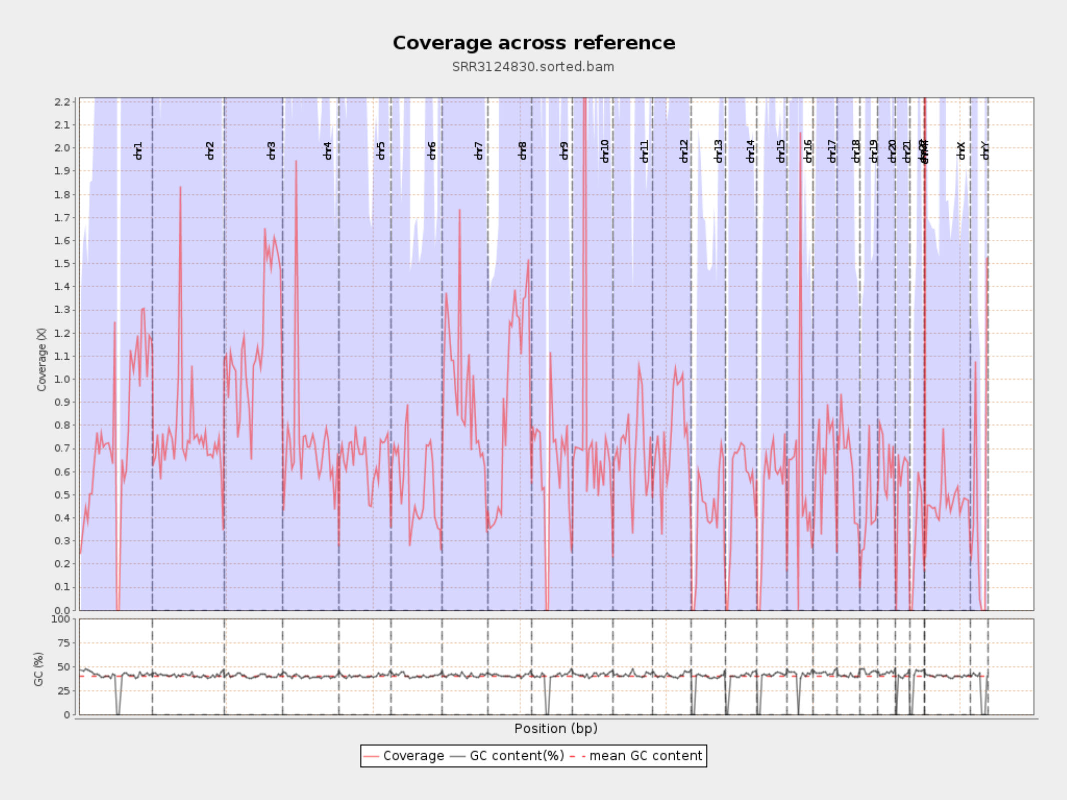
2.7. Chromosome stats

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

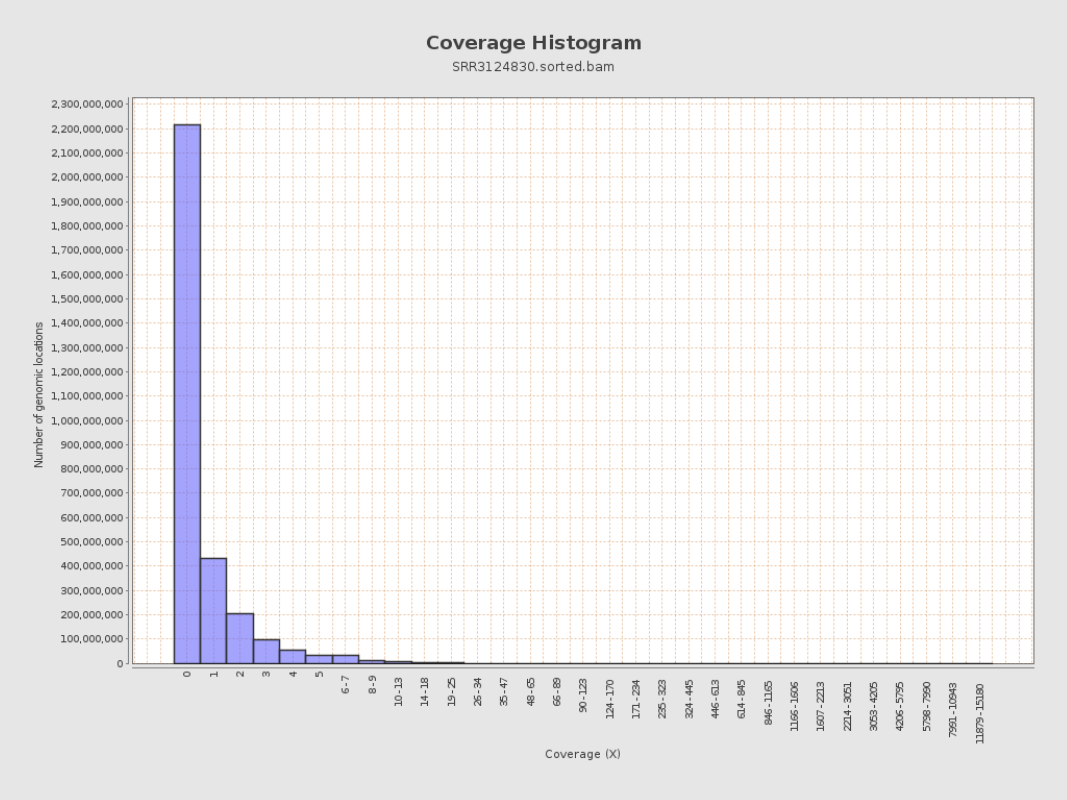
		bases	coverage	deviation
chr1	249250621	187689358	0.753	9.5999
chr2	243199373	184068194	0.7569	8.626
chr3	198022430	233641466	1.1799	2.4235
chr4	191154276	137110992	0.7173	6.507
chr5	180915260	117515269	0.6496	1.6664
chr6	171115067	93303891	0.5453	4.3896
chr7	159138663	146845241	0.9228	15.4147
chr8	146364022	134448299	0.9186	3.2578
chr9	141213431	84637519	0.5994	10.4154
chr10	135534747	109608435	0.8087	22.6025
chr11	135006516	92808564	0.6874	5.9062
chr12	133851895	100492514	0.7508	1.748
chr13	115169878	48365365	0.4199	1.1547
chr14	107349540	56128944	0.5229	2.6142
chr15	102531392	52670768	0.5137	1.5207
chr16	90354753	52848289	0.5849	11.3279
chr17	81195210	51467075	0.6339	5.9107
chr18	78077248	49560423	0.6348	10.5025
chr19	59128983	23334451	0.3946	5.4002
chr20	63025520	39378087	0.6248	2.2287
chr21	48129895	25627213	0.5325	3.5763
chr22	51304566	15083640	0.294	1.1964
chrMT	16571	2068380	124.8193	72.1706
chrX	155270560	72245698	0.4653	2.9873

chrY	59373566	27092201	0.4563	11.7748

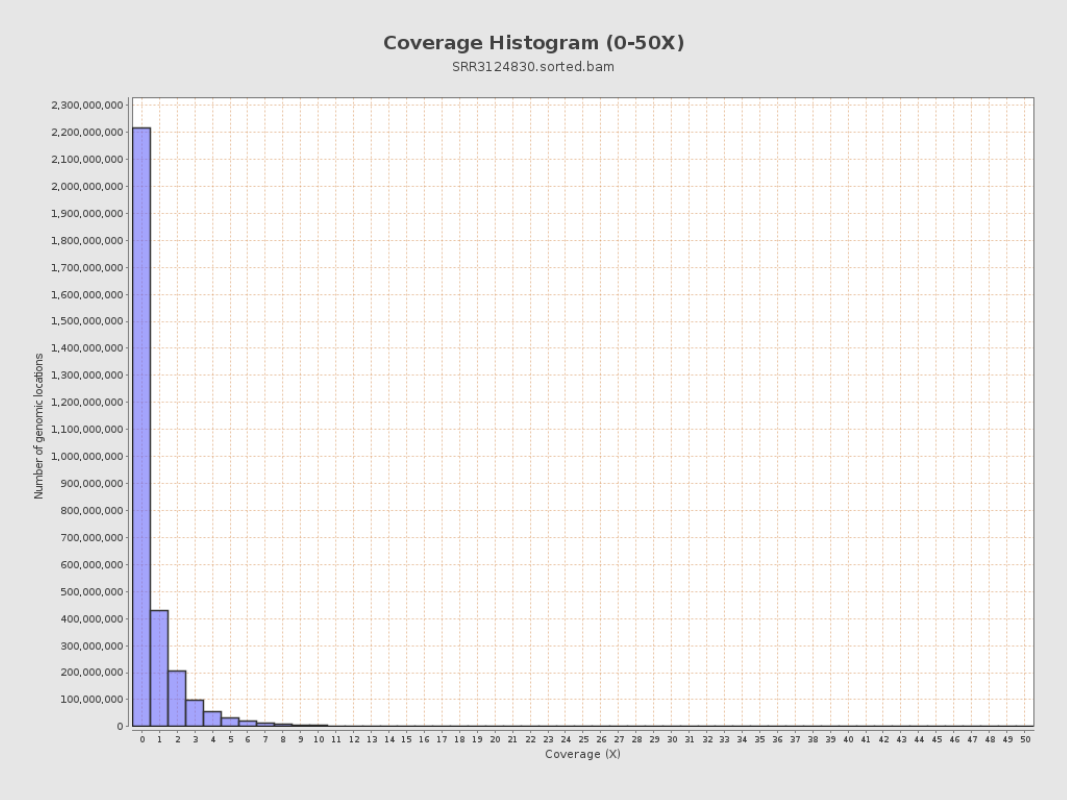
3. Results : Coverage across reference



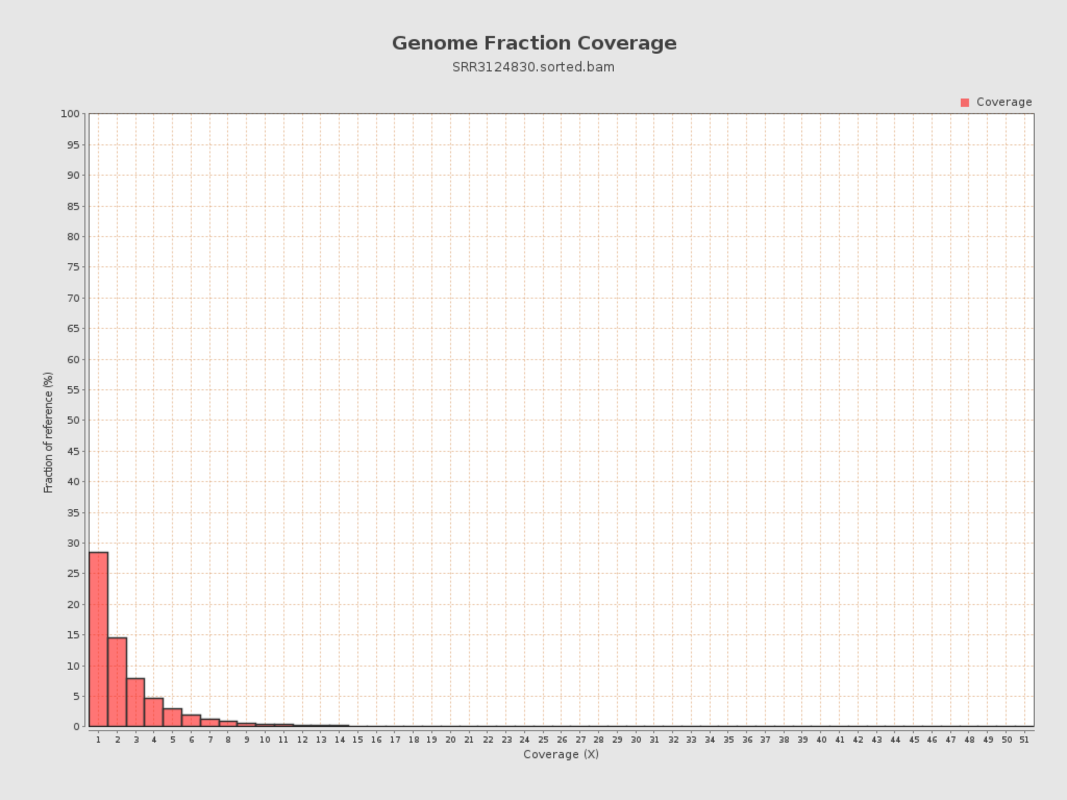
4. Results : Coverage Histogram



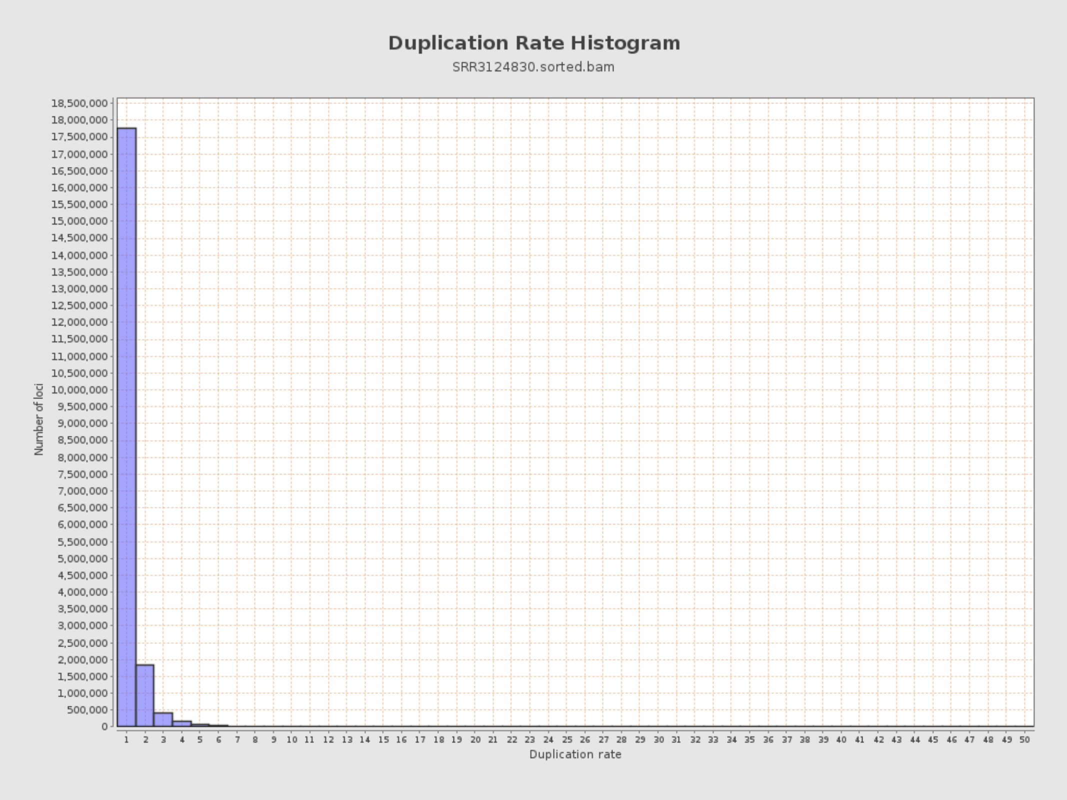
5. Results : Coverage Histogram (0-50X)



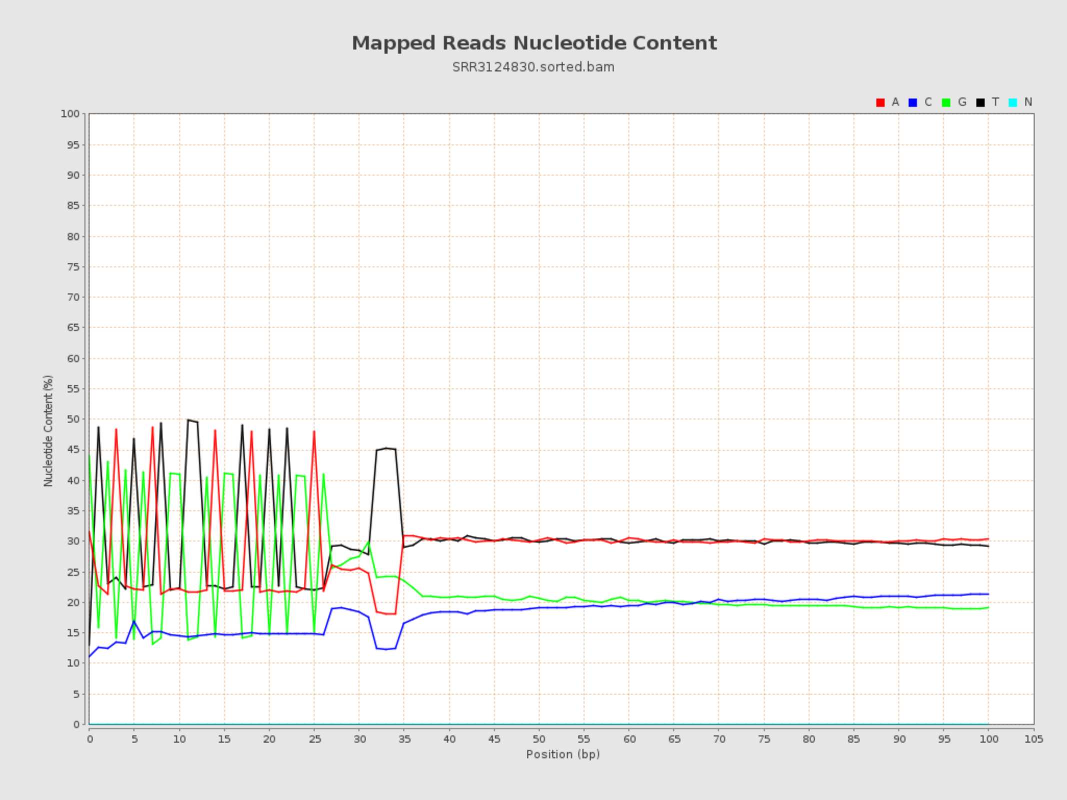
6. Results : Genome Fraction Coverage



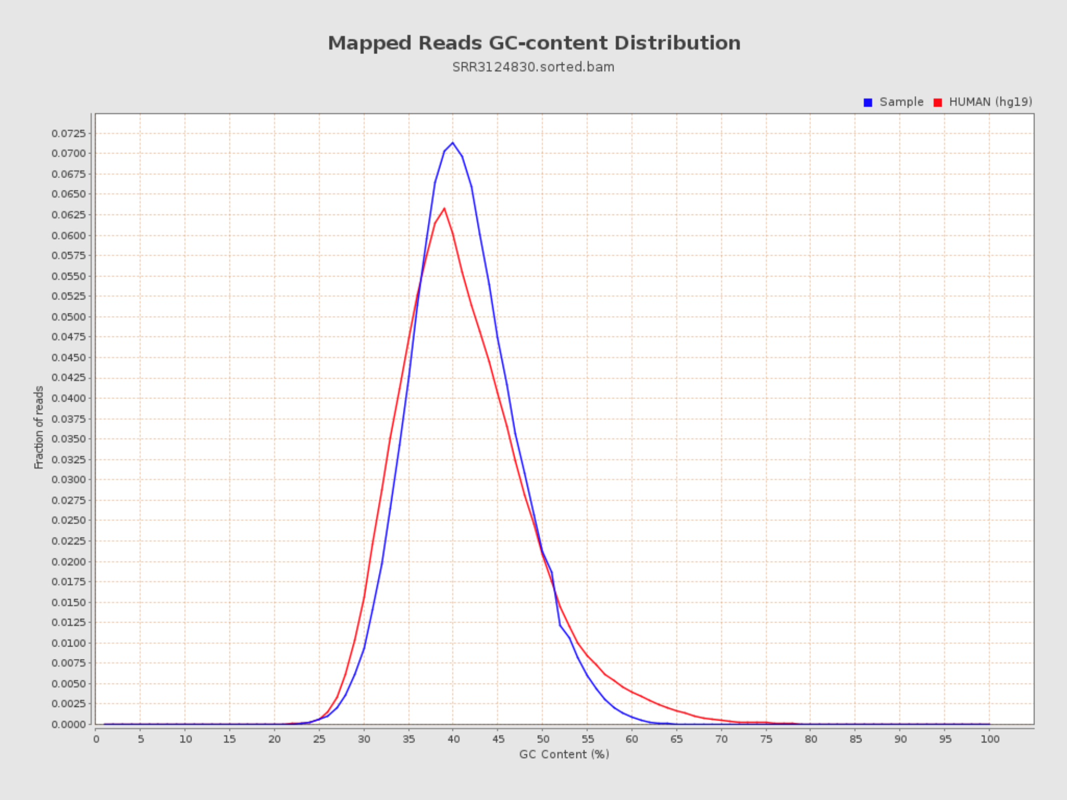
7. Results : Duplication Rate Histogram



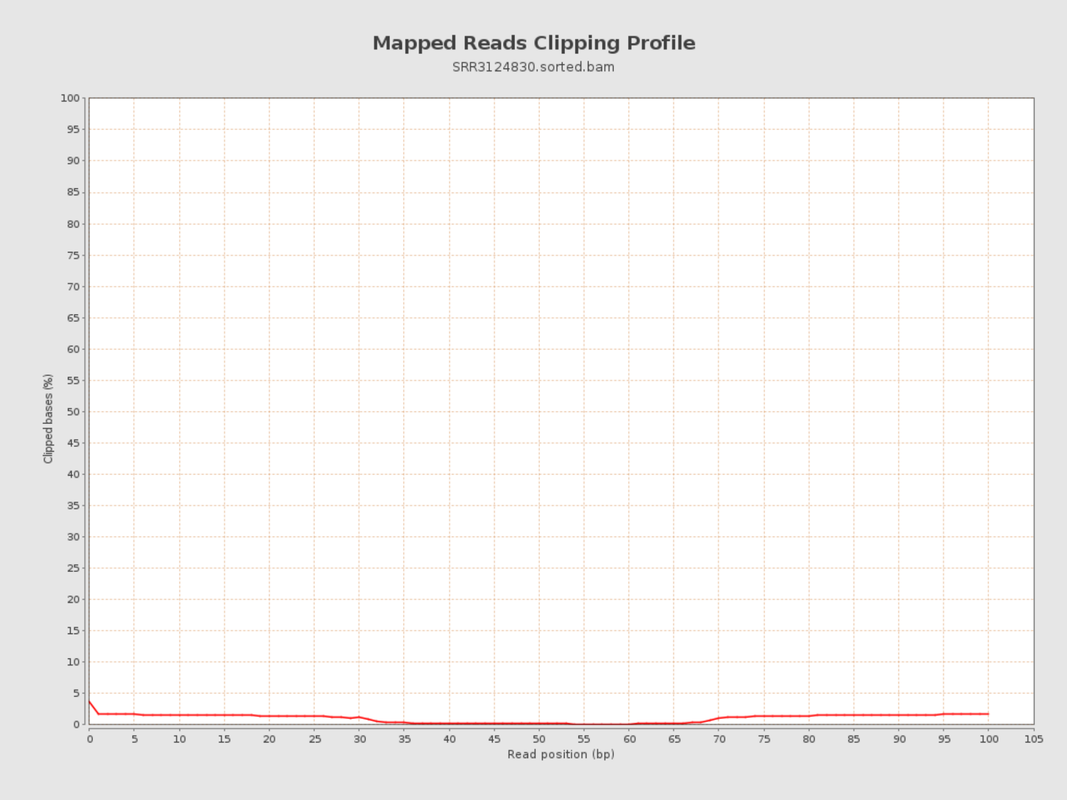
8. Results : Mapped Reads Nucleotide Content



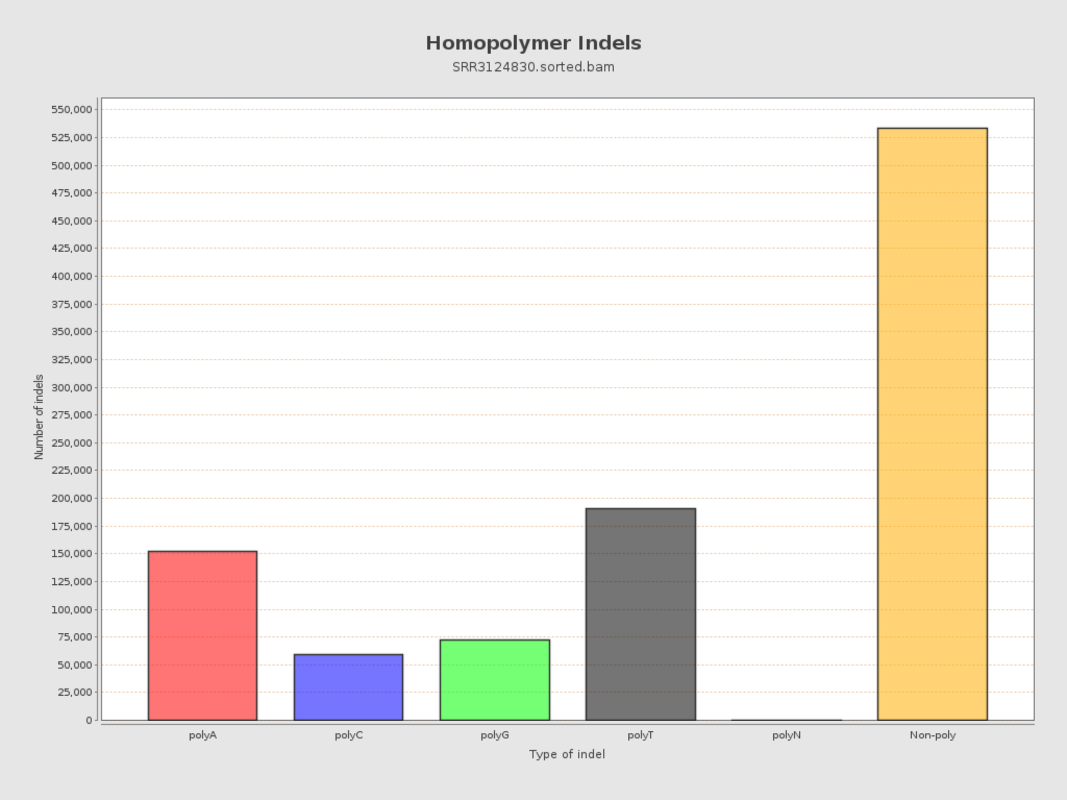
9. Results : Mapped Reads GC-content Distribution



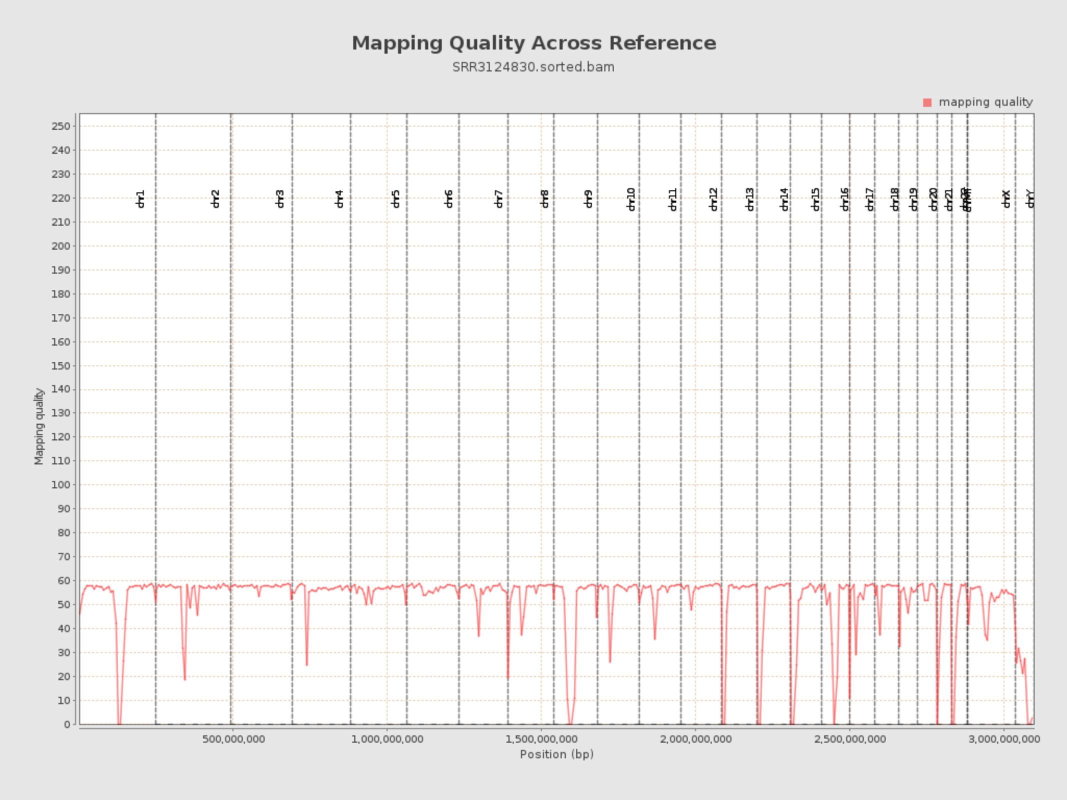
10. Results : Mapped Reads Clipping Profile



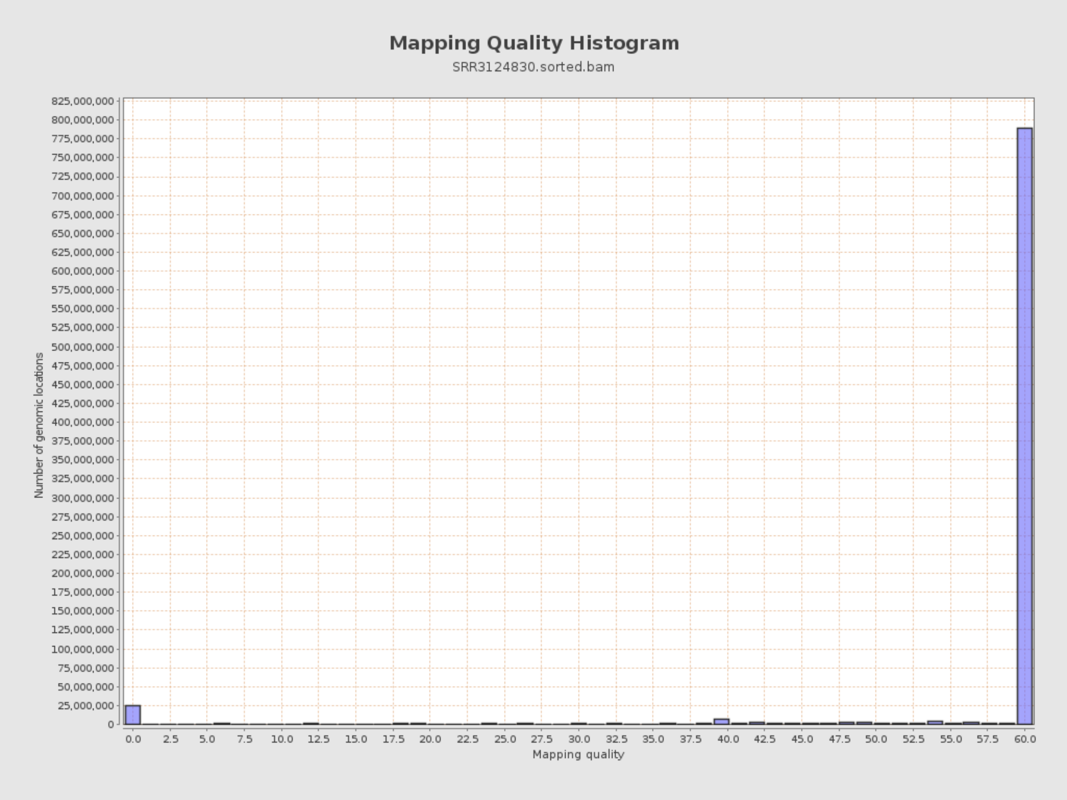
11. Results : Homopolymer Indels



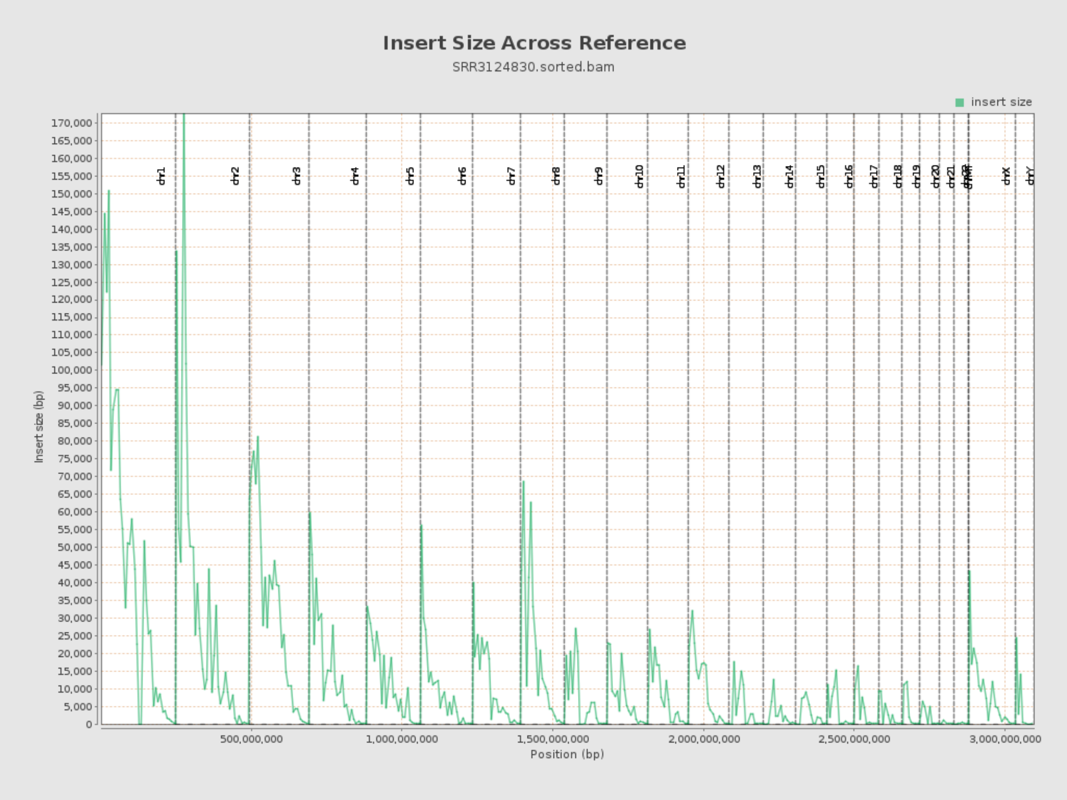
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram