

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124935.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_SRR3124935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124935_1.fastq.gz SRR3124935_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:25:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,840,704
Mapped reads	6,543,398 / 95.65%
Unmapped reads	297,306 / 4.35%
Mapped paired reads	6,543,398 / 95.65%
Mapped reads, first in pair	3,310,289 / 48.39%
Mapped reads, second in pair	3,233,109 / 47.26%
Mapped reads, both in pair	6,446,636 / 94.24%
Mapped reads, singletons	96,762 / 1.41%
Secondary alignments	0
Supplementary alignments	7,478 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	549,222 / 8.03%
Duplication rate	6.44%
Clipped reads	3,028,283 / 44.27%

2.2. ACGT Content

Number/percentage of A's	109,424,446 / 26.93%
Number/percentage of C's	74,621,793 / 18.36%
Number/percentage of T's	118,335,965 / 29.12%
Number/percentage of G's	104,007,199 / 25.59%
Number/percentage of N's	3,274 / 0%

GC Percentage	43.95%
---------------	--------

2.3. Coverage

Mean	0.1313
Standard Deviation	0.7958

2.4. Mapping Quality

Mean Mapping Quality	52.2
----------------------	------

2.5. Insert size

Mean	27,095.76
Standard Deviation	1,557,799.5
P25/Median/P75	142 / 194 / 272

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	2,707,980
Insertions	43,795
Mapped reads with at least one insertion	0.66%
Deletions	122,439
Mapped reads with at least one deletion	1.85%
Homopolymer indels	48.05%

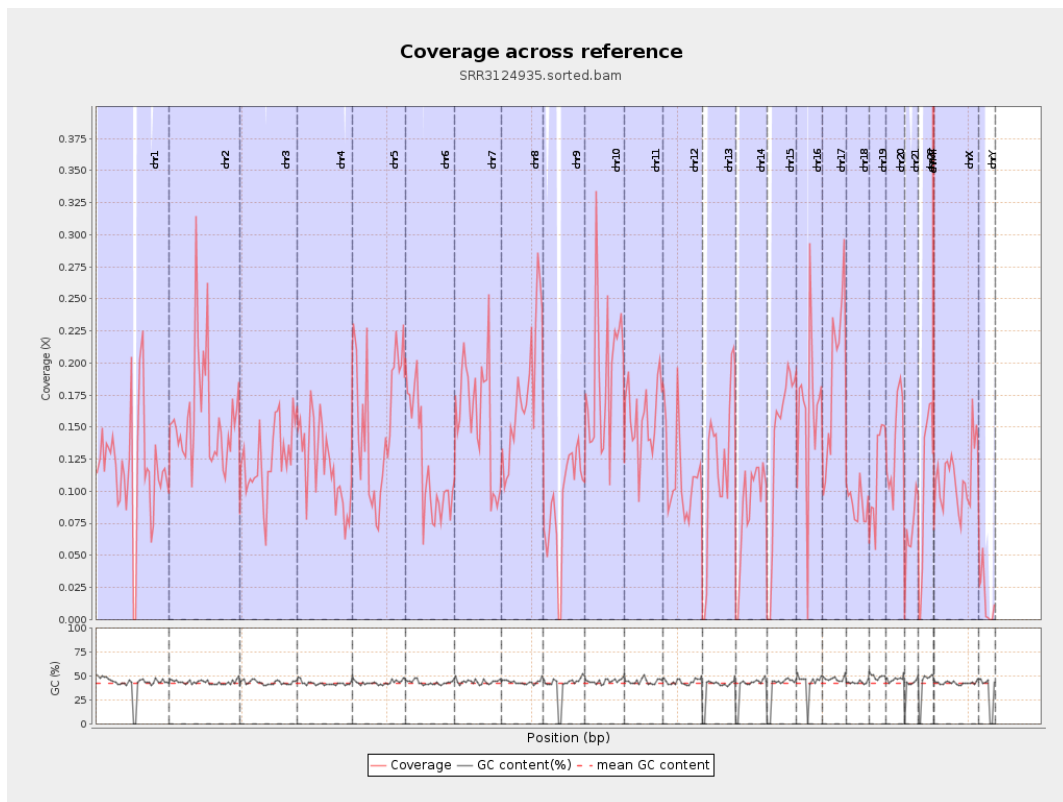
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

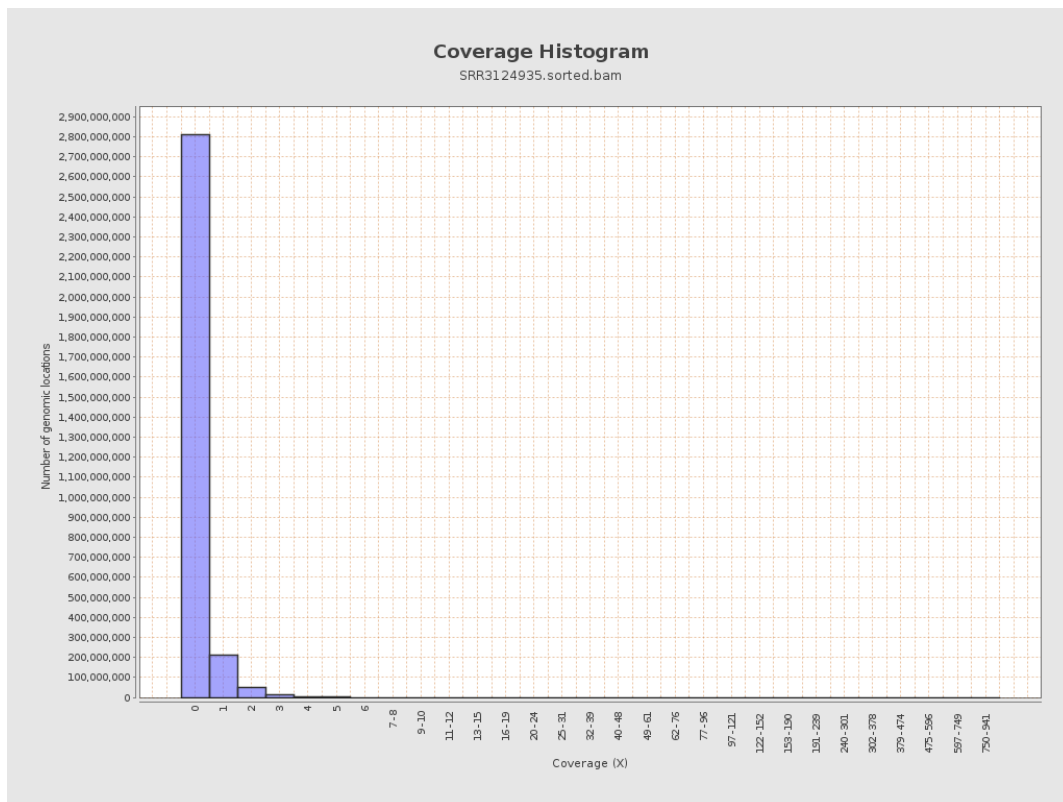
		bases	coverage	deviation
chr1	249250621	29069189	0.1166	0.7604
chr2	243199373	38426858	0.158	1.2272
chr3	198022430	24694429	0.1247	0.4631
chr4	191154276	22811110	0.1193	0.572
chr5	180915260	27701839	0.1531	0.5343
chr6	171115067	20569907	0.1202	0.6097
chr7	159138663	25290378	0.1589	1.0535
chr8	146364022	25823590	0.1764	0.6149
chr9	141213431	12822032	0.0908	0.6631
chr10	135534747	25476742	0.188	1.5427
chr11	135006516	21250721	0.1574	0.6375
chr12	133851895	15177586	0.1134	0.4487
chr13	115169878	13673555	0.1187	0.4546
chr14	107349540	9262156	0.0863	0.4319
chr15	102531392	14384908	0.1403	0.5047
chr16	90354753	14652329	0.1622	1.3077
chr17	81195210	15679990	0.1931	0.9486
chr18	78077248	7058177	0.0904	0.9549
chr19	59128983	6801018	0.115	0.6715
chr20	63025520	8657615	0.1374	0.5602
chr21	48129895	3354054	0.0697	0.4284
chr22	51304566	5488625	0.107	0.4571
chrMT	16571	351420	21.2069	14.6259
chrX	155270560	17185715	0.1107	0.5049

chrY	59373566	912162	0.0154	0.85
------	----------	--------	--------	------

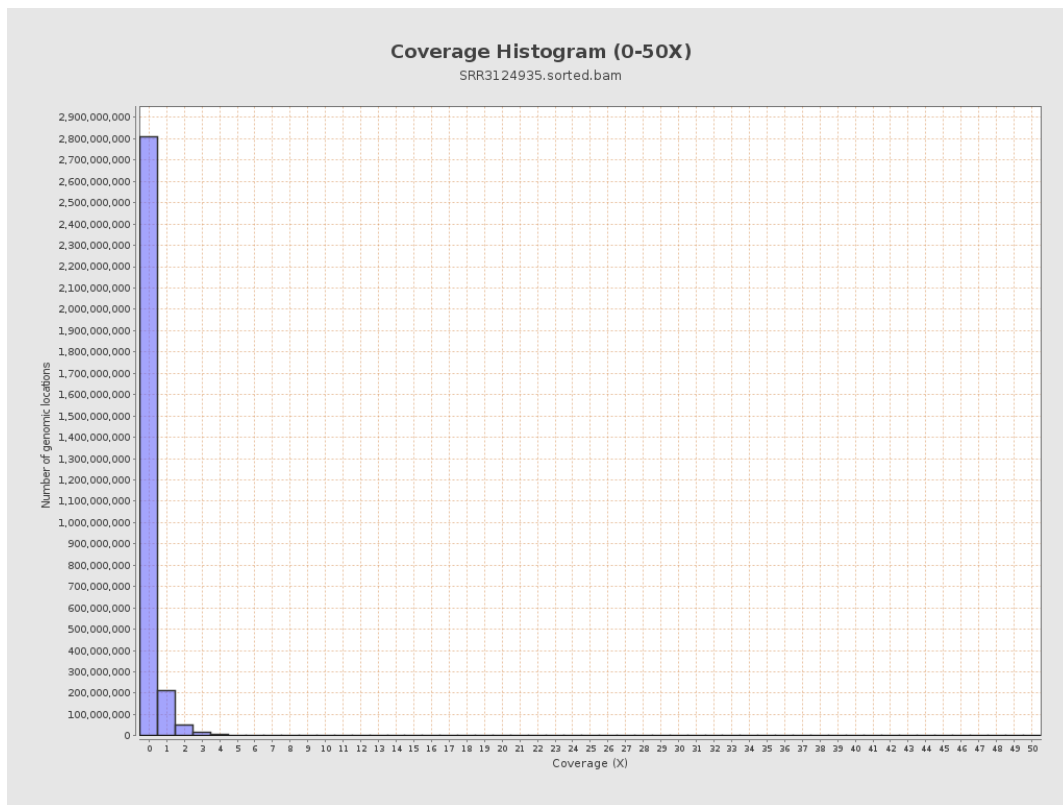
3. Results : Coverage across reference



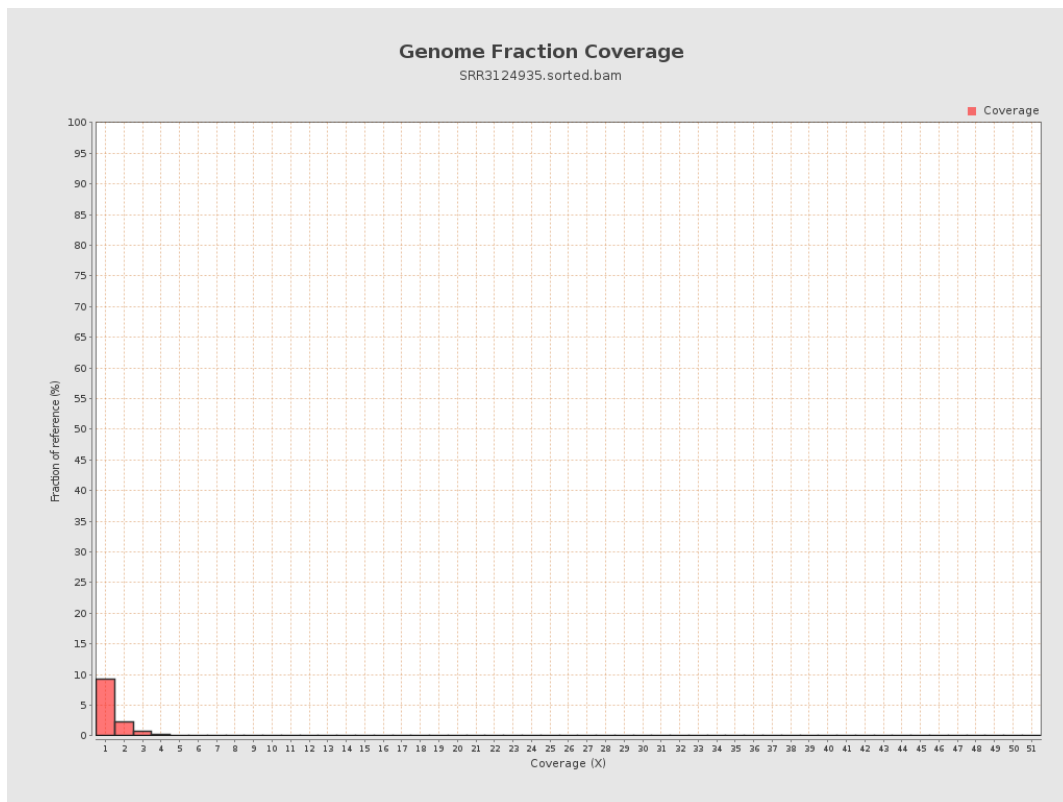
4. Results : Coverage Histogram



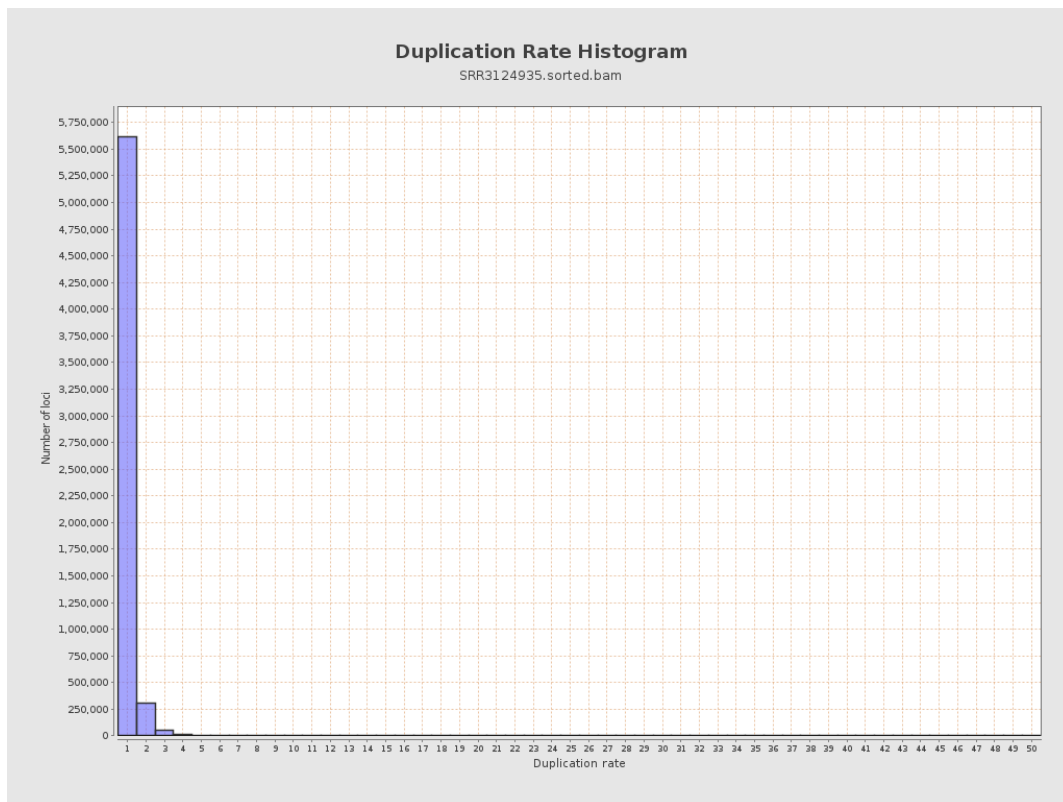
5. Results : Coverage Histogram (0-50X)



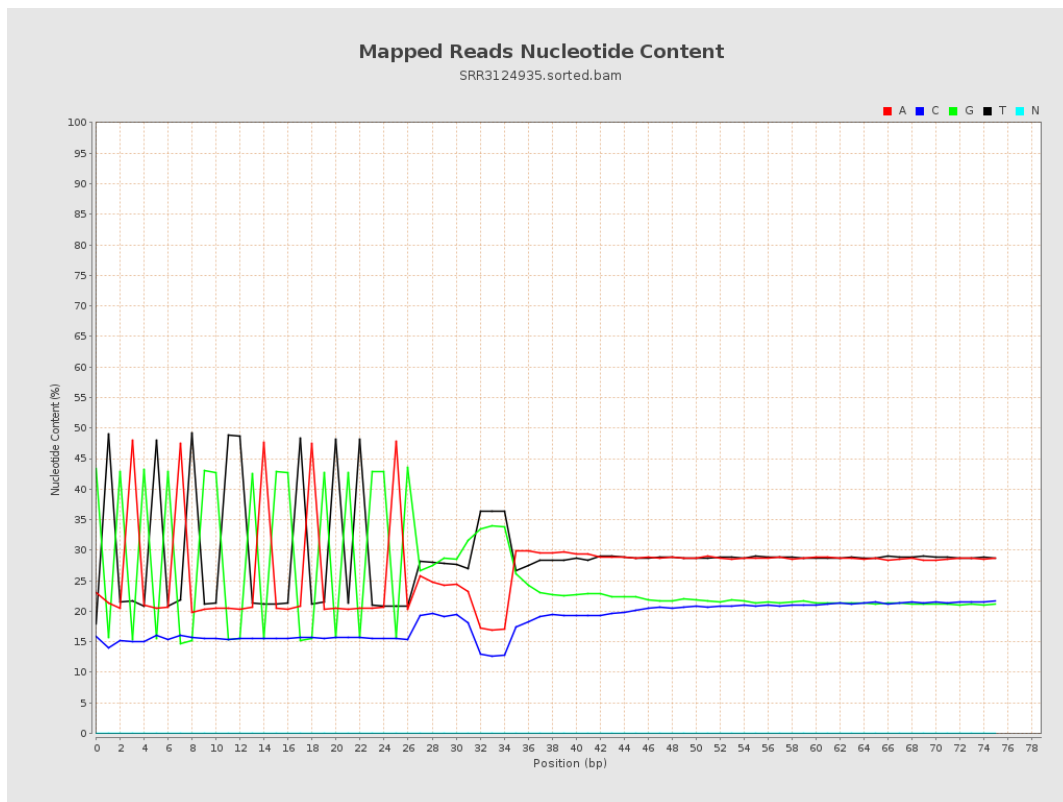
6. Results : Genome Fraction Coverage



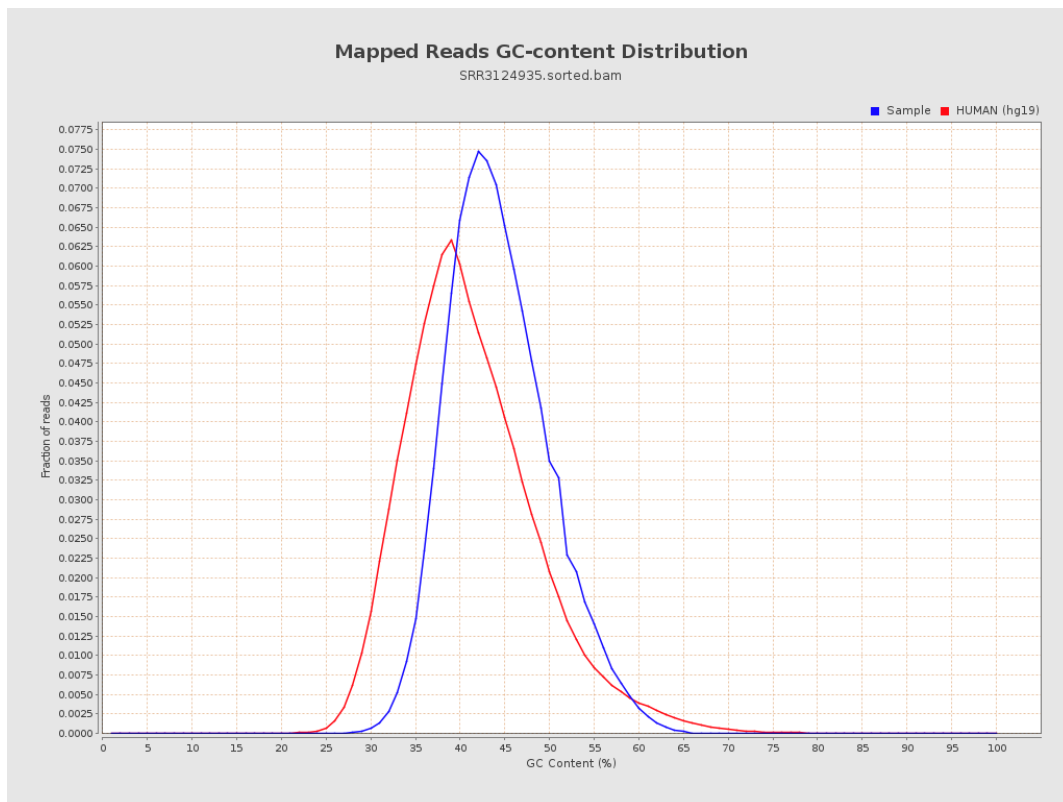
7. Results : Duplication Rate Histogram



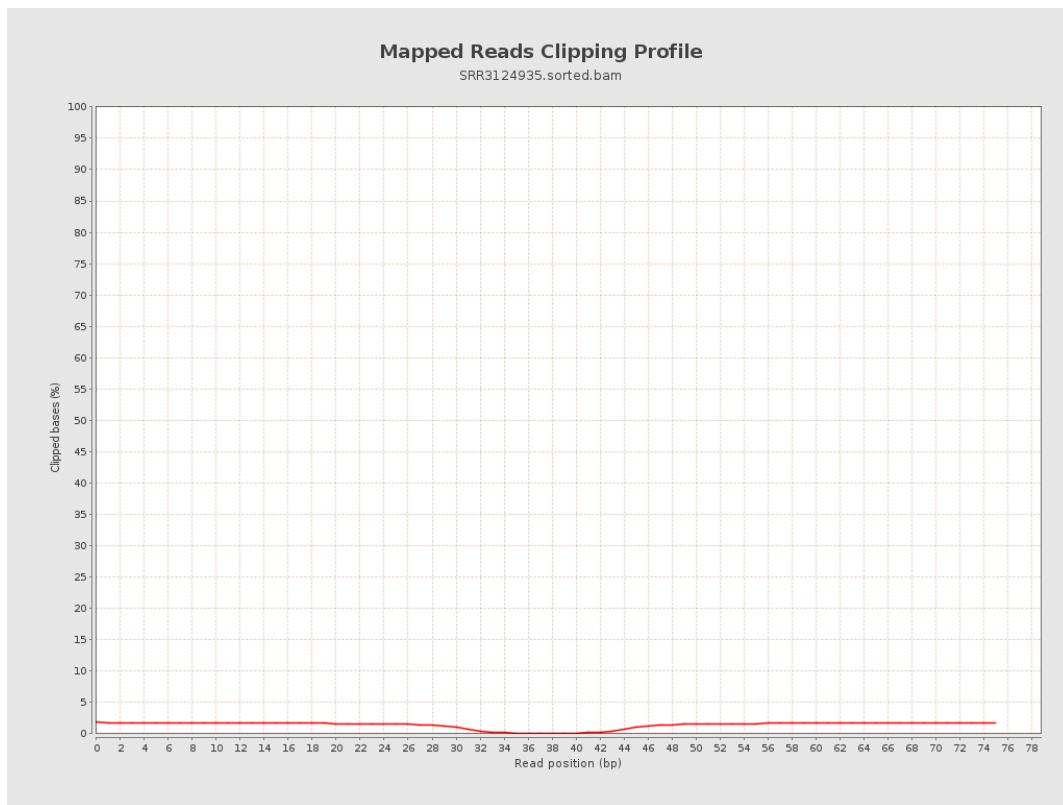
8. Results : Mapped Reads Nucleotide Content



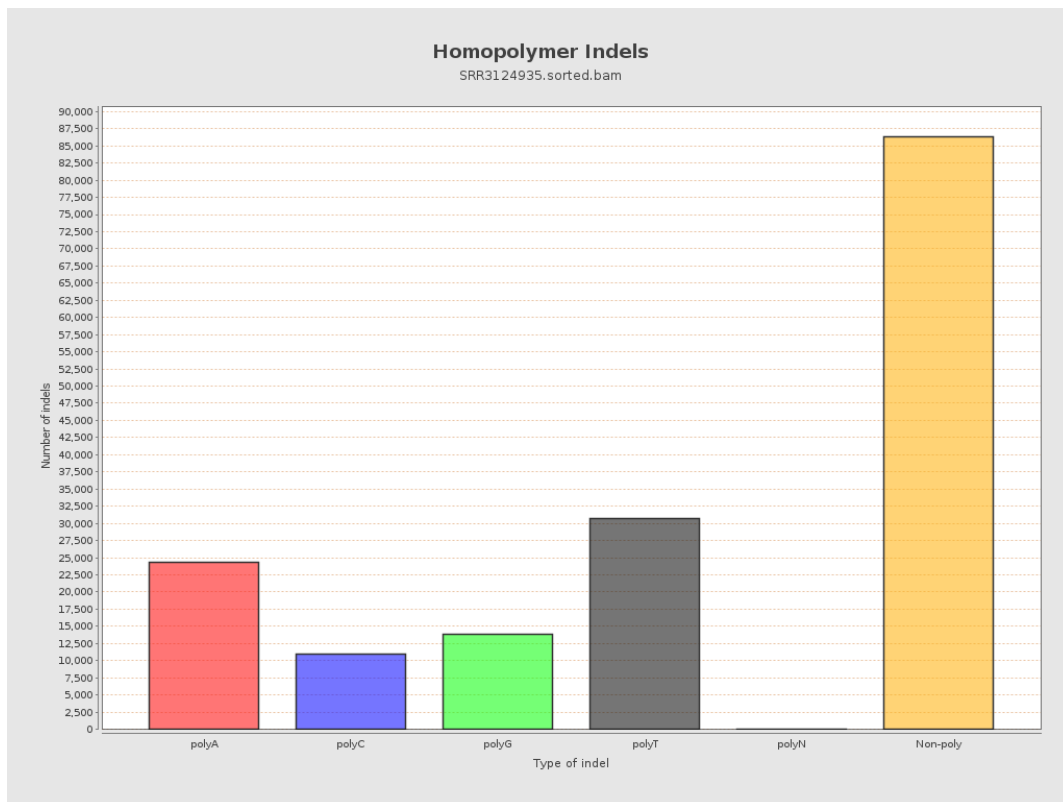
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



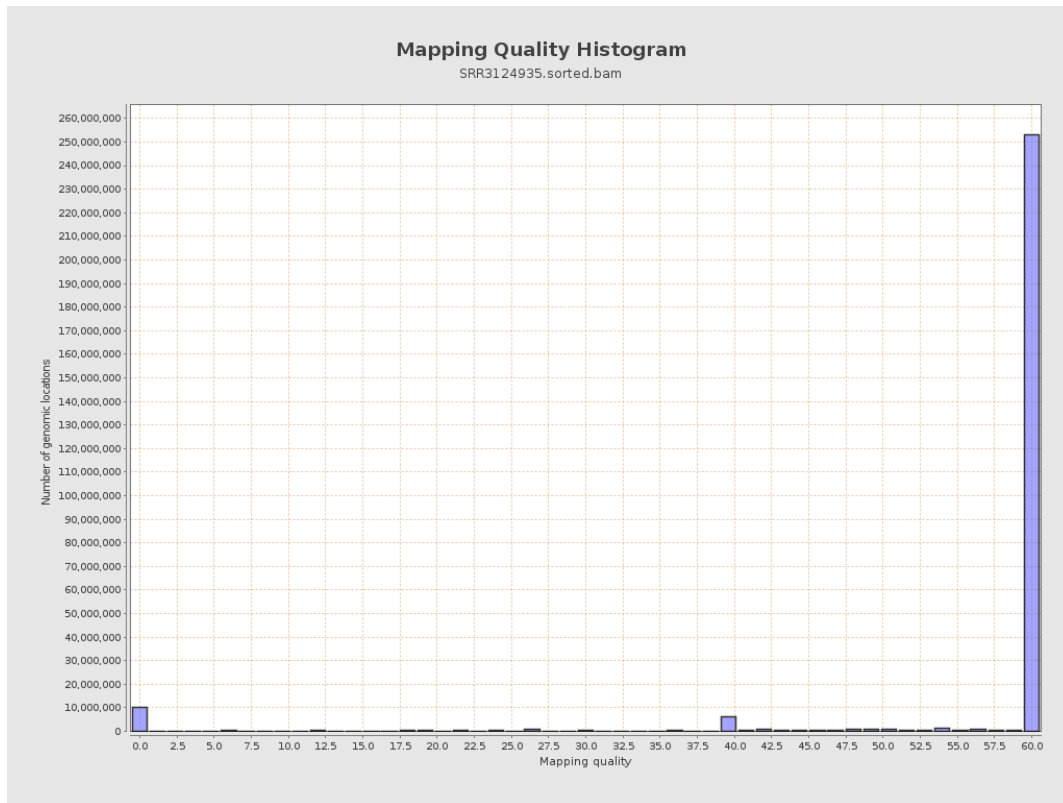
11. Results : Homopolymer Indels



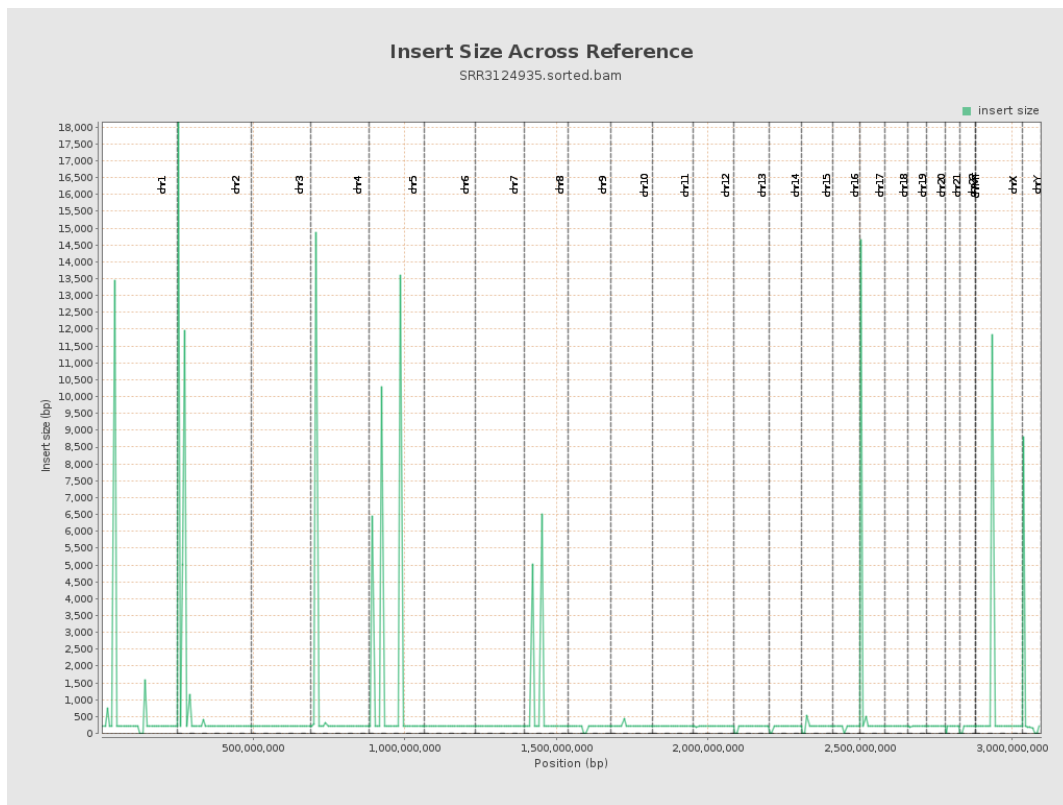
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

