

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:22:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124943.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_SRR3124943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124943_1.fastq.gz SRR3124943_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:22:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,430,976
Mapped reads	4,393,273 / 99.15%
Unmapped reads	37,703 / 0.85%
Mapped paired reads	4,393,273 / 99.15%
Mapped reads, first in pair	2,198,912 / 49.63%
Mapped reads, second in pair	2,194,361 / 49.52%
Mapped reads, both in pair	4,377,216 / 98.79%
Mapped reads, singletons	16,057 / 0.36%
Secondary alignments	0
Supplementary alignments	22,651 / 0.51%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	257,429 / 5.81%
Duplication rate	3.6%
Clipped reads	1,831,930 / 41.34%

2.2. ACGT Content

Number/percentage of A's	112,493,040 / 28.58%
Number/percentage of C's	74,883,365 / 19.03%
Number/percentage of T's	117,440,998 / 29.84%
Number/percentage of G's	88,749,772 / 22.55%
Number/percentage of N's	6,089 / 0%

GC Percentage	41.58%
---------------	--------

2.3. Coverage

Mean	0.1272
Standard Deviation	1.315

2.4. Mapping Quality

Mean Mapping Quality	53.16
----------------------	-------

2.5. Insert size

Mean	47,583.85
Standard Deviation	2,048,553.74
P25/Median/P75	145 / 192 / 263

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	2,868,916
Insertions	47,061
Mapped reads with at least one insertion	1.05%
Deletions	119,098
Mapped reads with at least one deletion	2.66%
Homopolymer indels	46.74%

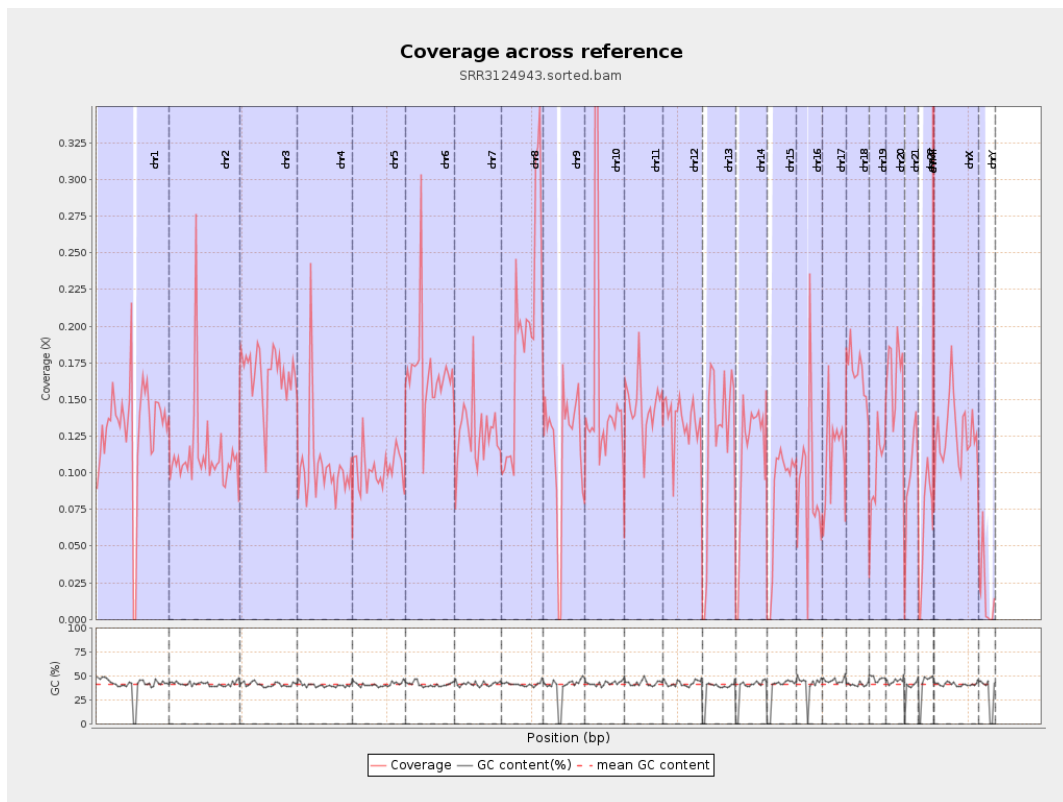
2.7. Chromosome stats

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

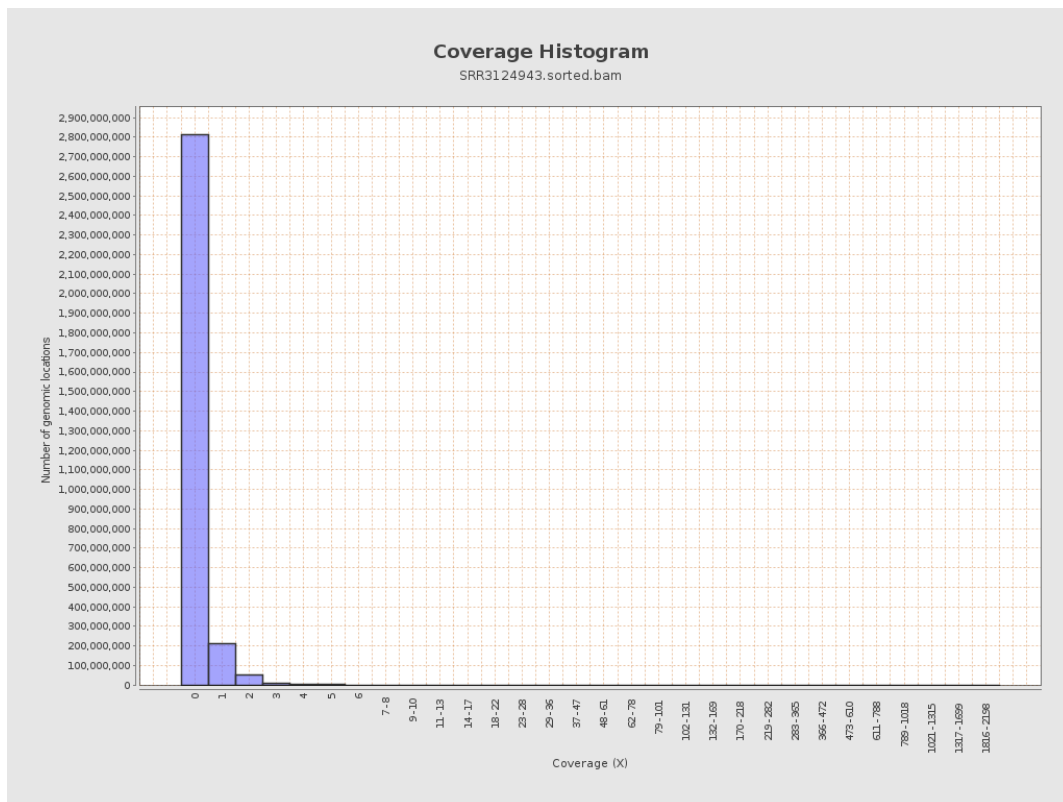
		bases	coverage	deviation
chr1	249250621	32252603	0.1294	1.2708
chr2	243199373	27384268	0.1126	1.1775
chr3	198022430	33166420	0.1675	0.5344
chr4	191154276	19840637	0.1038	0.9424
chr5	180915260	18585605	0.1027	0.4116
chr6	171115067	28750322	0.168	1.5384
chr7	159138663	20338331	0.1278	1.554
chr8	146364022	28011382	0.1914	0.7568
chr9	141213431	16757556	0.1187	1.5553
chr10	135534747	21229024	0.1566	3.7953
chr11	135006516	19341274	0.1433	1.4826
chr12	133851895	18036766	0.1348	0.4758
chr13	115169878	14063345	0.1221	0.4335
chr14	107349540	11867478	0.1105	0.4607
chr15	102531392	8681972	0.0847	0.3731
chr16	90354753	8101773	0.0897	1.1904
chr17	81195210	9005153	0.1109	1.5199
chr18	78077248	13172274	0.1687	1.8879
chr19	59128983	6107568	0.1033	0.8161
chr20	63025520	10430472	0.1655	0.5815
chr21	48129895	4695356	0.0976	0.5195
chr22	51304566	3247882	0.0633	0.3325
chrMT	16571	45546	2.7485	2.3444
chrX	155270560	19709131	0.1269	0.7204

chrY	59373566	945682	0.0159	0.8831
------	----------	--------	--------	--------

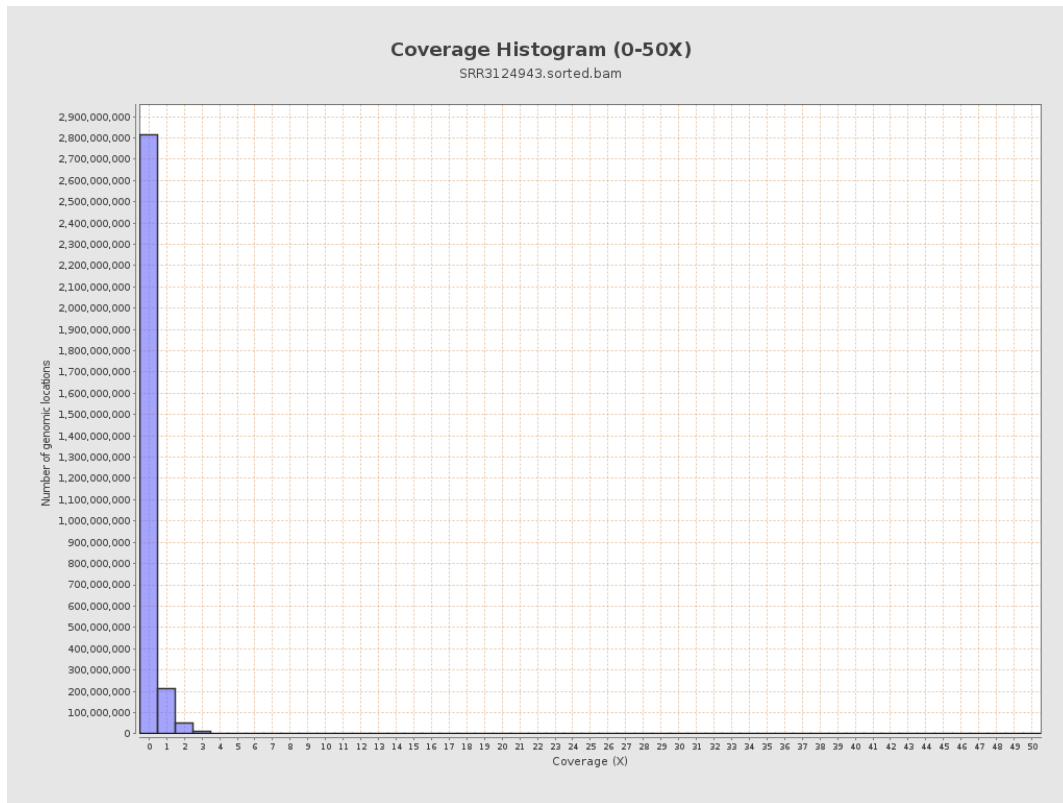
3. Results : Coverage across reference



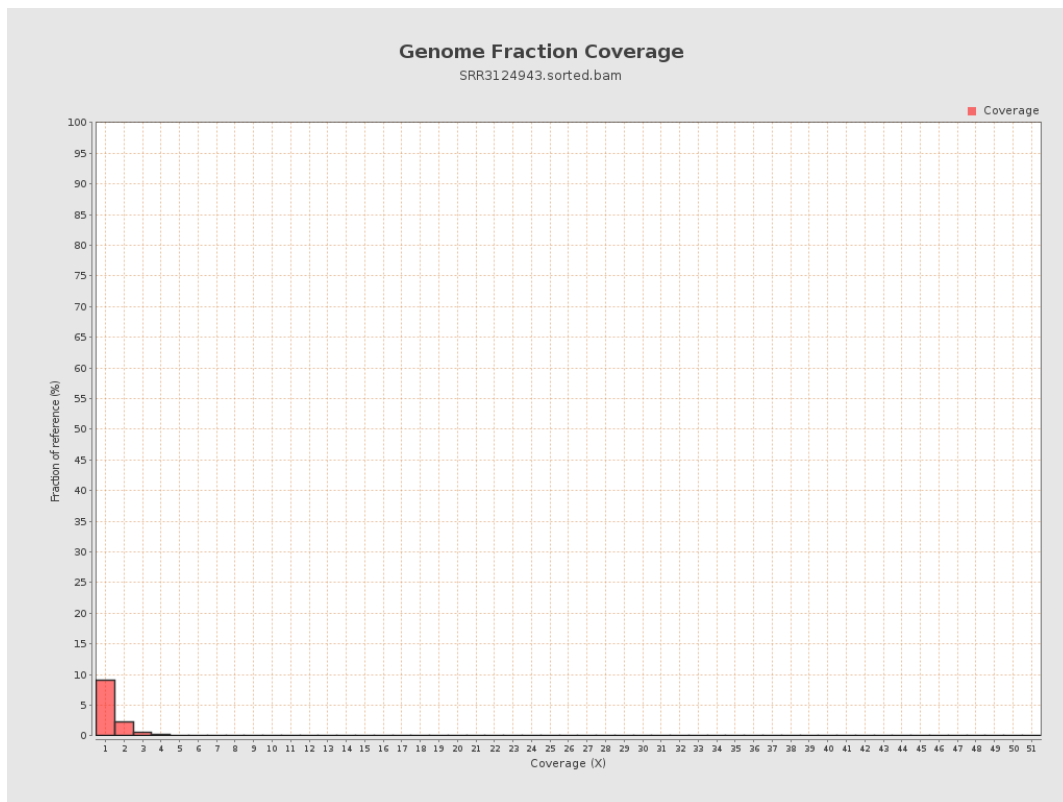
4. Results : Coverage Histogram



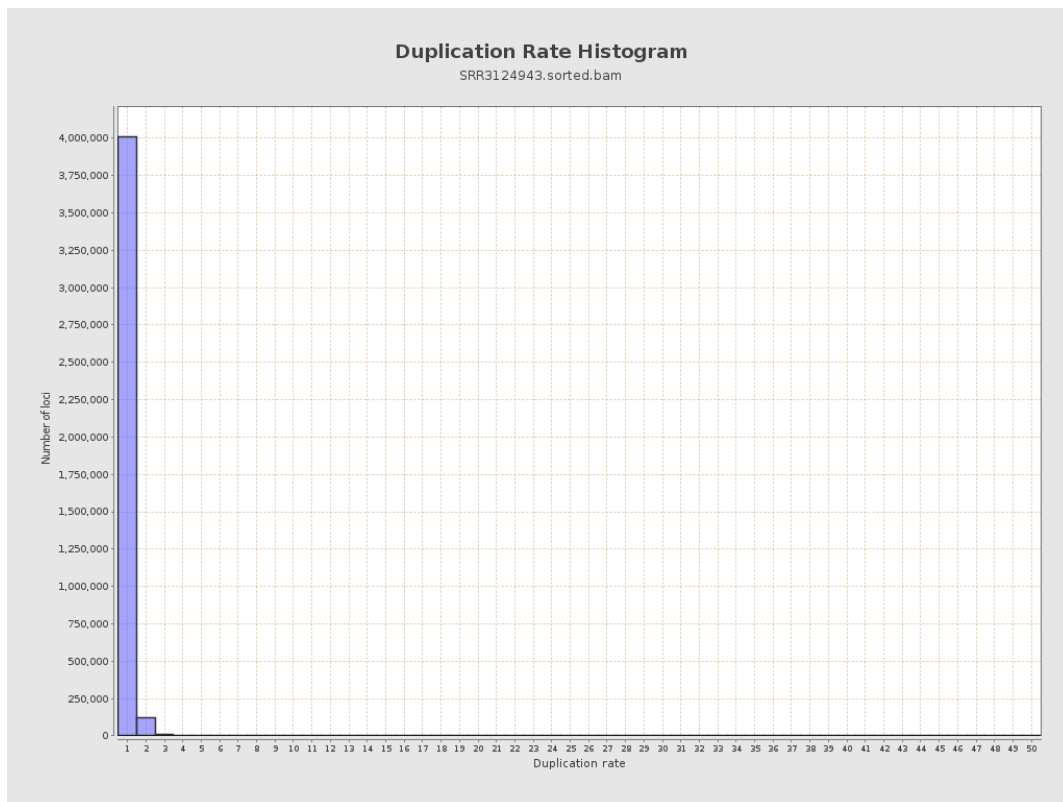
5. Results : Coverage Histogram (0-50X)



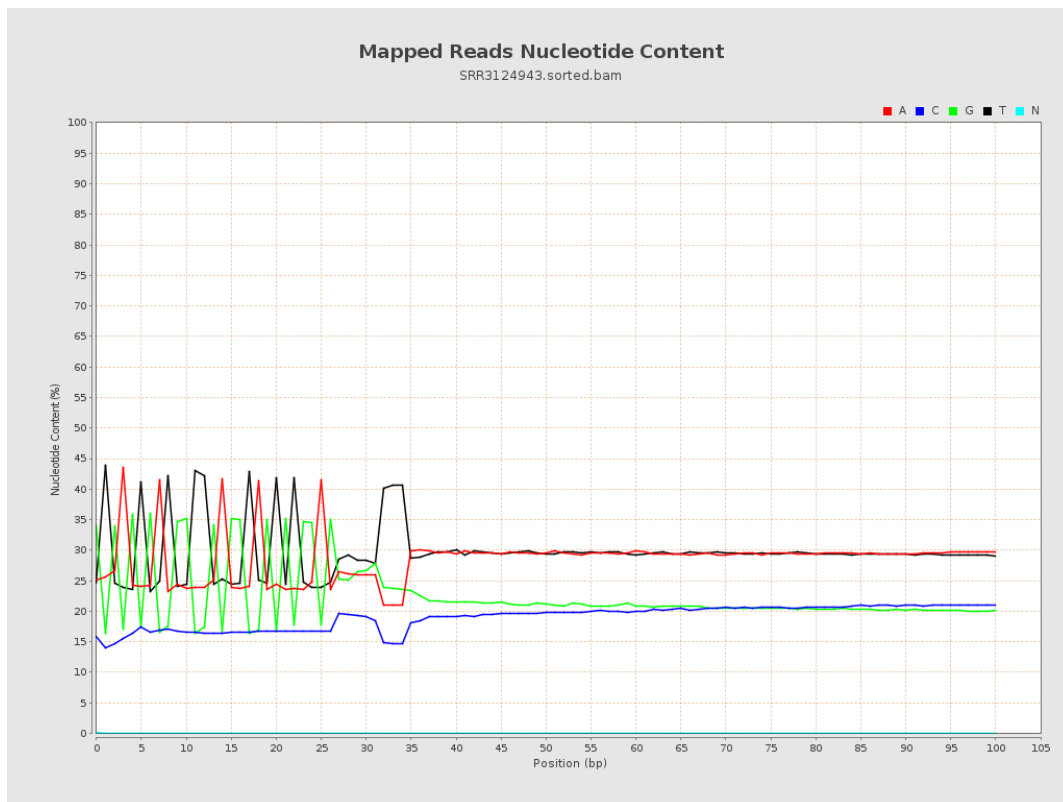
6. Results : Genome Fraction Coverage



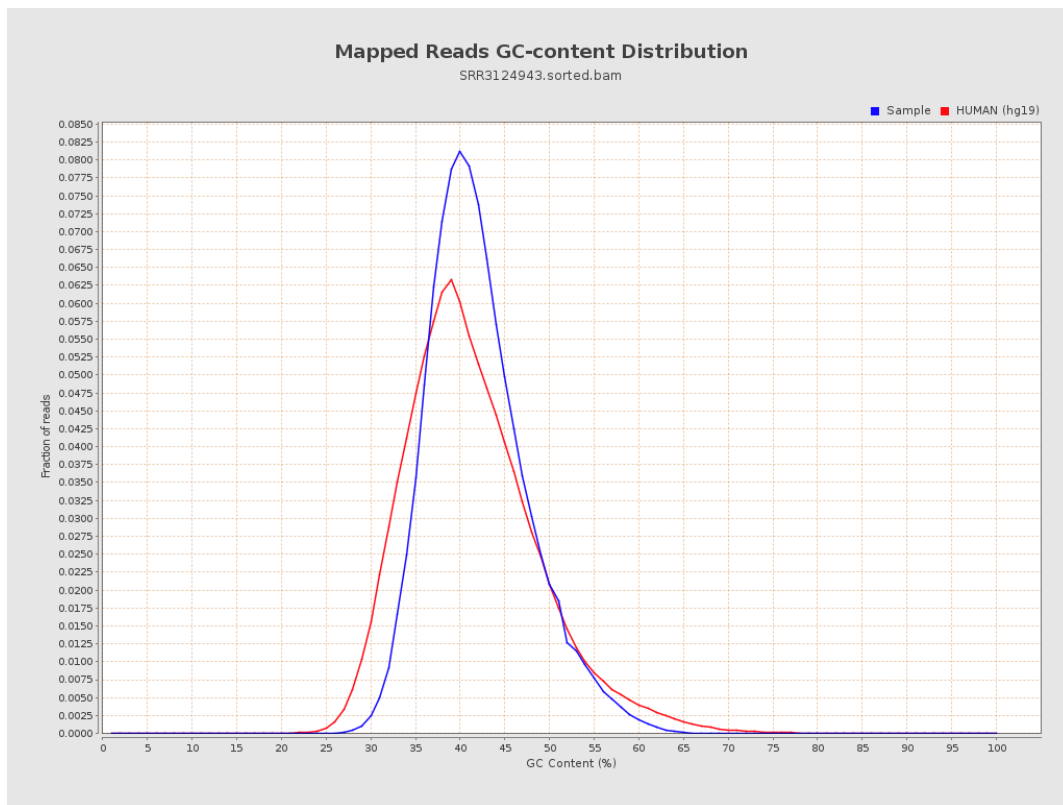
7. Results : Duplication Rate Histogram



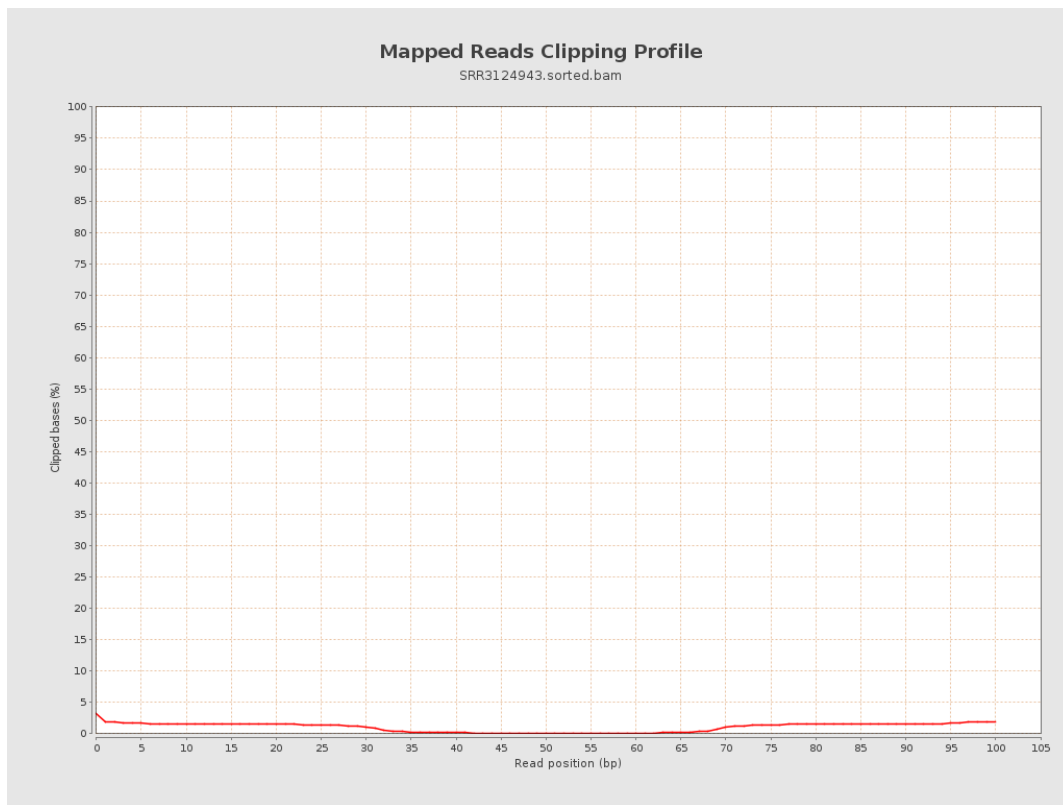
8. Results : Mapped Reads Nucleotide Content



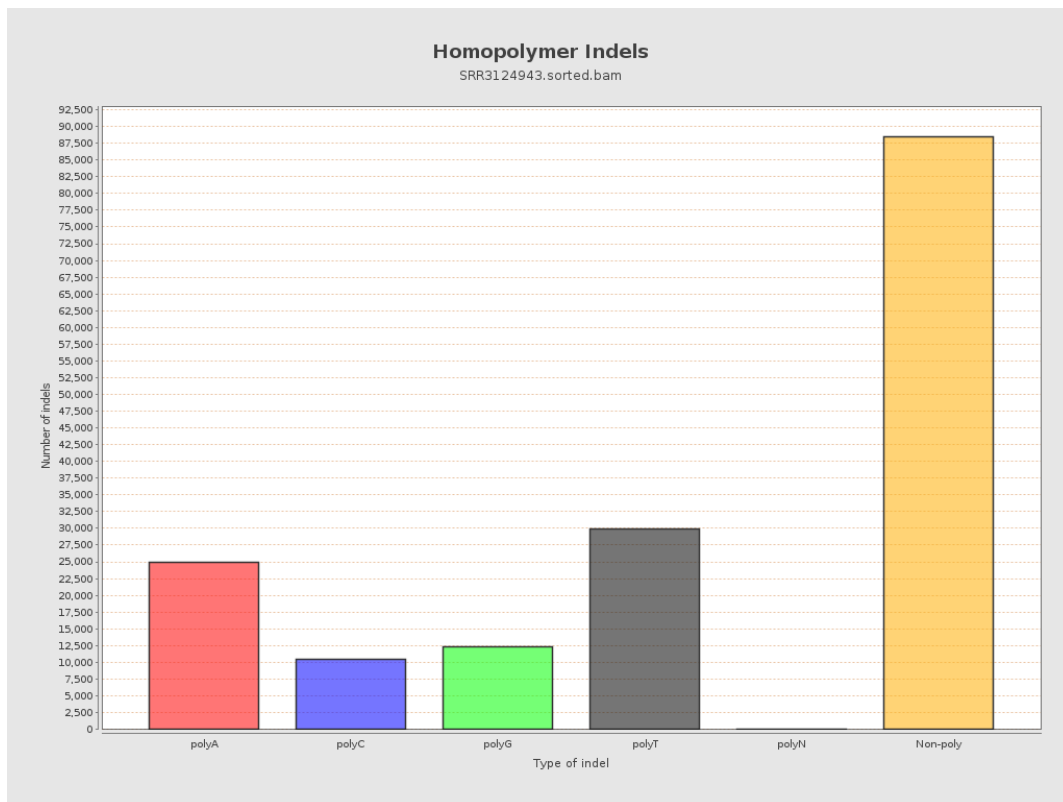
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



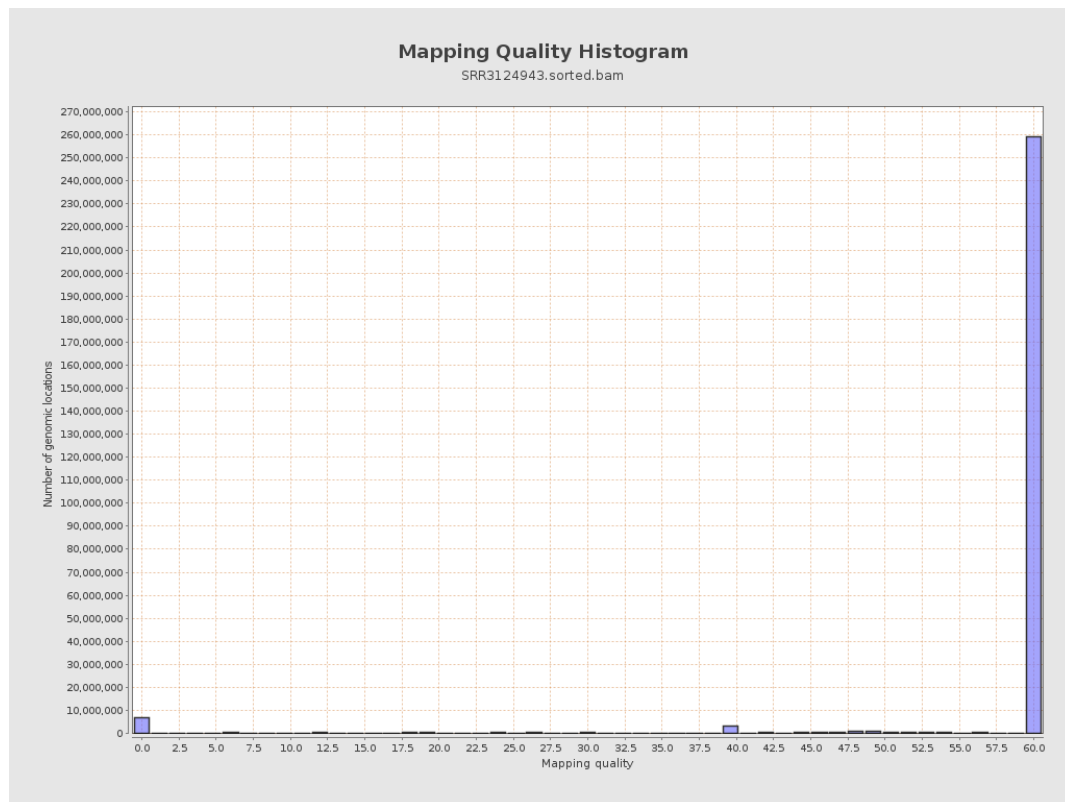
11. Results : Homopolymer Indels



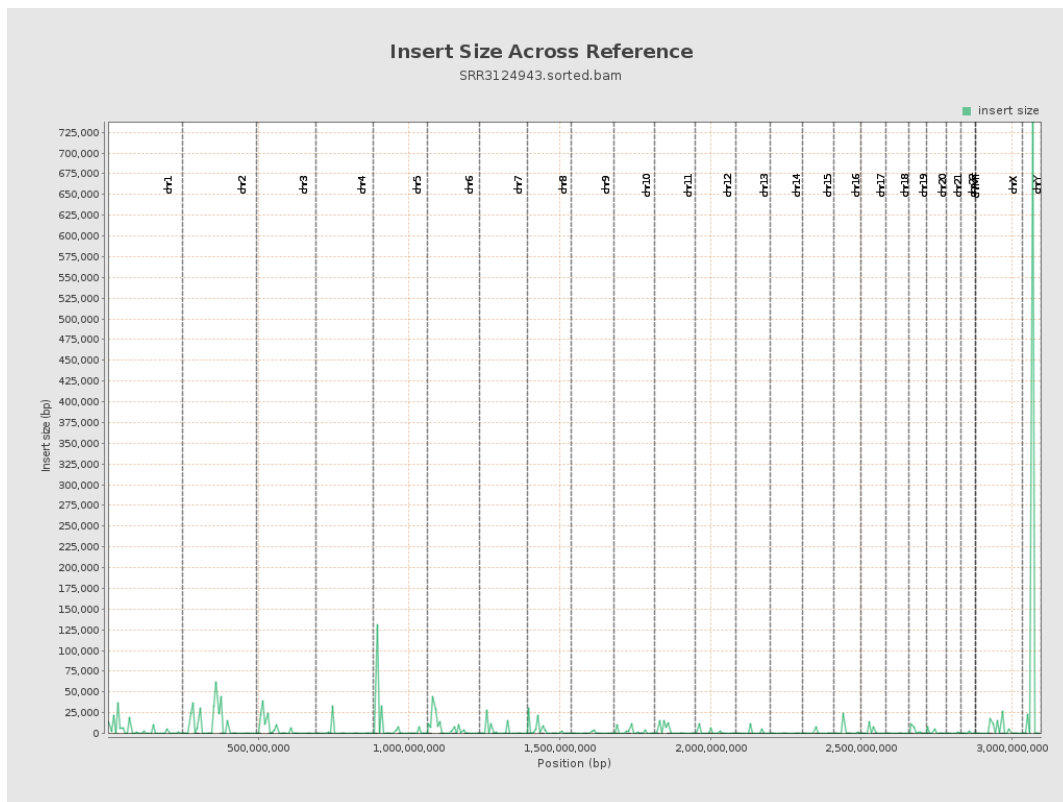
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

