

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:13:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124903.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_SRR3124903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124903_1.fastq.gz SRR3124903_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:13:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,884,712
Mapped reads	3,842,781 / 98.92%
Unmapped reads	41,931 / 1.08%
Mapped paired reads	3,842,781 / 98.92%
Mapped reads, first in pair	1,922,663 / 49.49%
Mapped reads, second in pair	1,920,118 / 49.43%
Mapped reads, both in pair	3,830,248 / 98.6%
Mapped reads, singletons	12,533 / 0.32%
Secondary alignments	0
Supplementary alignments	16,676 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	182,848 / 4.71%
Duplication rate	2.57%
Clipped reads	2,287,658 / 58.89%

2.2. ACGT Content

Number/percentage of A's	102,351,984 / 29%
Number/percentage of C's	71,920,015 / 20.38%
Number/percentage of T's	103,474,240 / 29.32%
Number/percentage of G's	74,939,720 / 21.23%
Number/percentage of N's	230,766 / 0.07%

GC Percentage	41.61%
---------------	--------

2.3. Coverage

Mean	0.1141
Standard Deviation	1.2673

2.4. Mapping Quality

Mean Mapping Quality	52.56
----------------------	-------

2.5. Insert size

Mean	63,259.42
Standard Deviation	2,467,740.76
P25/Median/P75	138 / 169 / 212

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,030,160
Insertions	51,337
Mapped reads with at least one insertion	1.31%
Deletions	112,353
Mapped reads with at least one deletion	2.86%
Homopolymer indels	46.45%

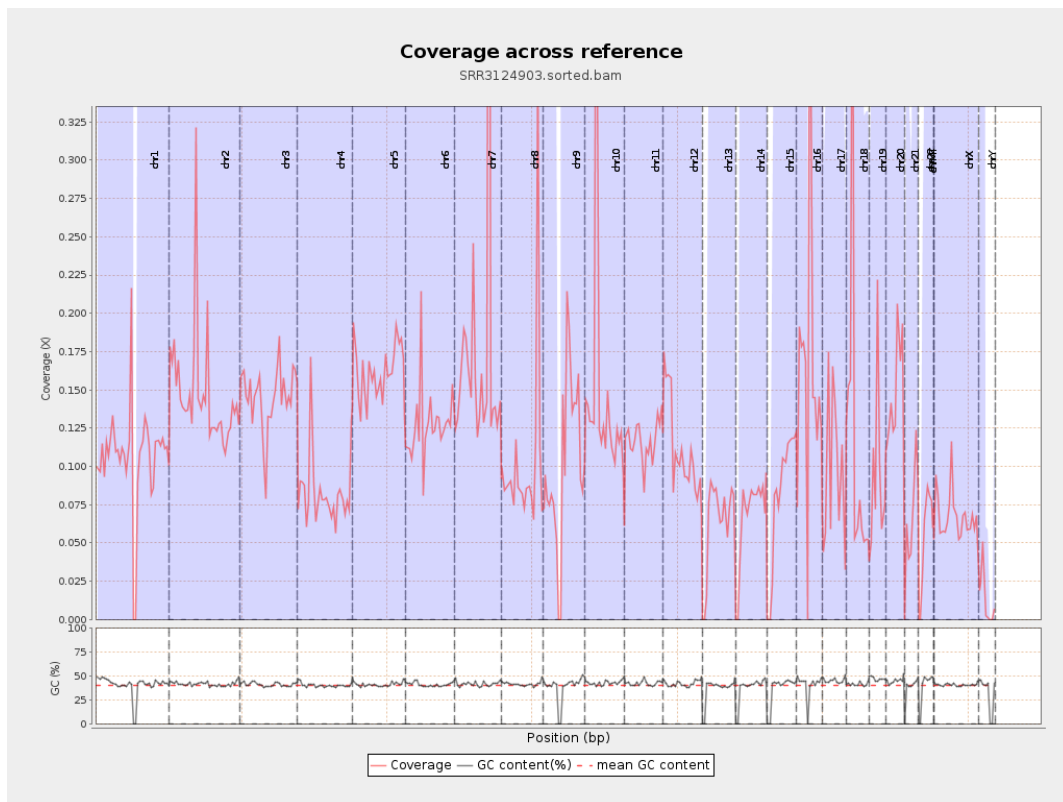
2.7. Chromosome stats

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

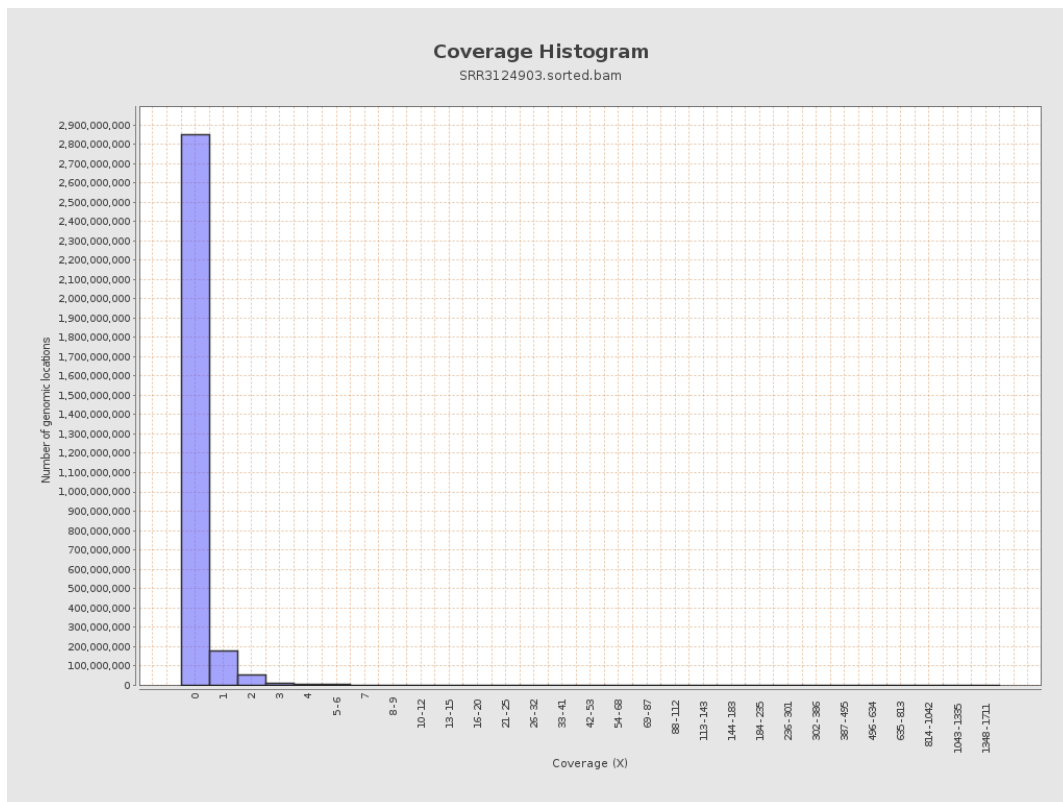
		bases	coverage	deviation
chr1	249250621	26440618	0.1061	1.7614
chr2	243199373	35875661	0.1475	1.2431
chr3	198022430	28728933	0.1451	0.5105
chr4	191154276	15744557	0.0824	0.7238
chr5	180915260	29216605	0.1615	0.5187
chr6	171115067	21832901	0.1276	1.0935
chr7	159138663	28206882	0.1772	2.0844
chr8	146364022	15032996	0.1027	0.5482
chr9	141213431	14546228	0.103	1.5309
chr10	135534747	19650426	0.145	2.9654
chr11	135006516	15590444	0.1155	0.7998
chr12	133851895	14817161	0.1107	0.4261
chr13	115169878	7272952	0.0631	0.3087
chr14	107349540	7180203	0.0669	0.372
chr15	102531392	8297500	0.0809	0.3573
chr16	90354753	14917895	0.1651	2.2998
chr17	81195210	7842931	0.0966	1.5059
chr18	78077248	9671590	0.1239	1.5424
chr19	59128983	5699733	0.0964	0.967
chr20	63025520	9381804	0.1489	0.5223
chr21	48129895	3179725	0.0661	0.4103
chr22	51304566	2734766	0.0533	0.3027
chrMT	16571	1201	0.0725	0.2933
chrX	155270560	10489281	0.0676	0.4873

chrY	59373566	754126	0.0127	0.773
------	----------	--------	--------	-------

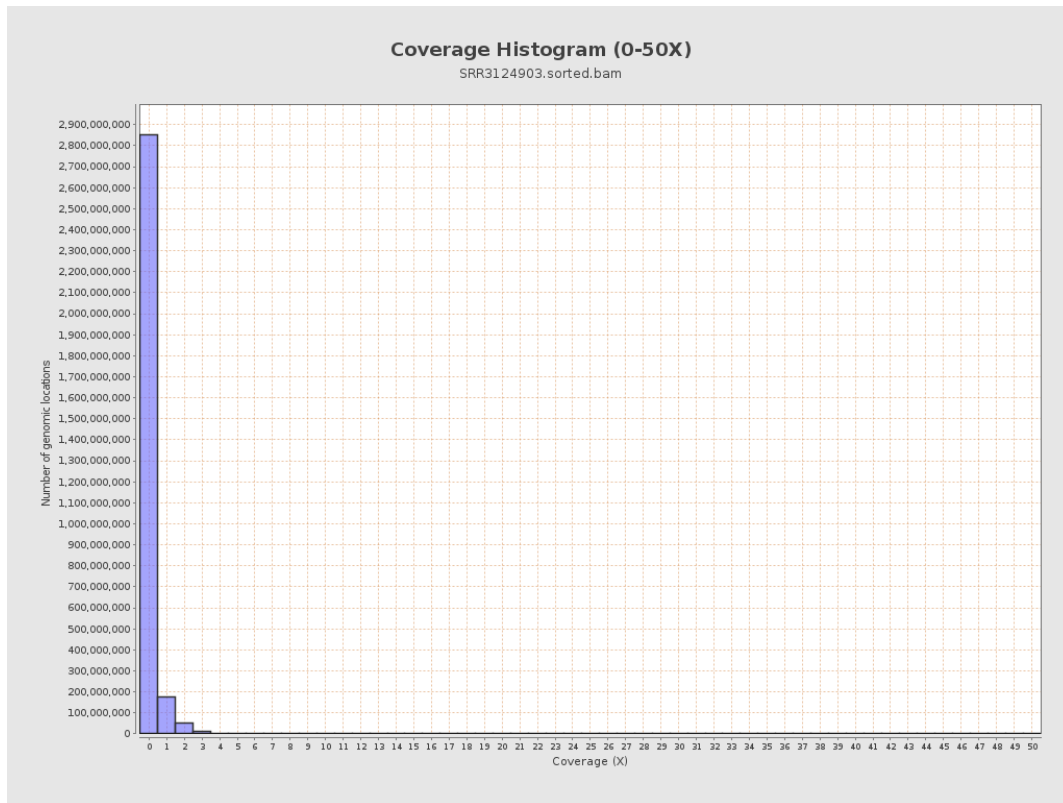
3. Results : Coverage across reference



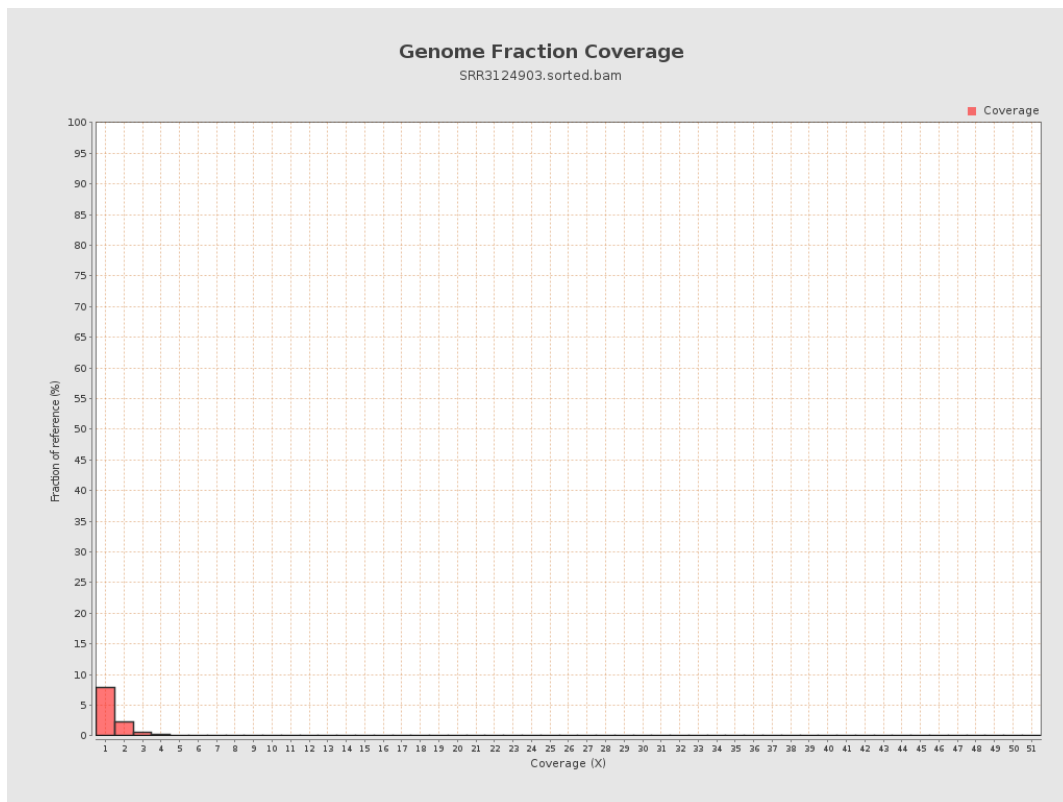
4. Results : Coverage Histogram



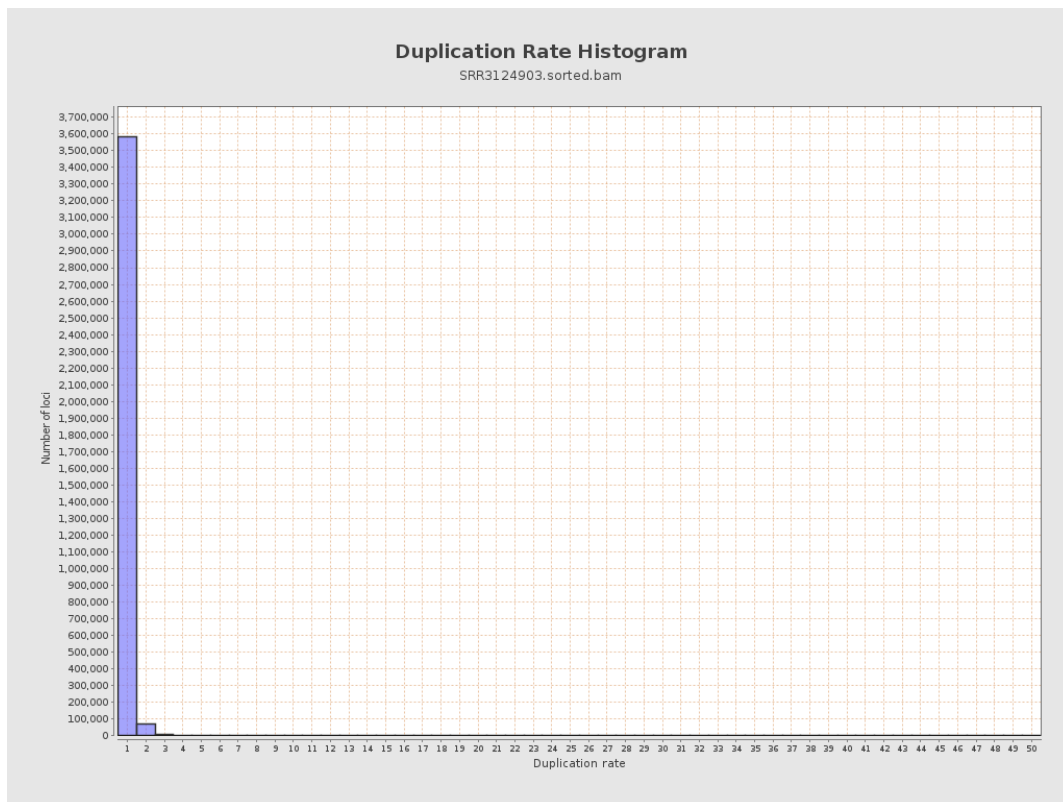
5. Results : Coverage Histogram (0-50X)



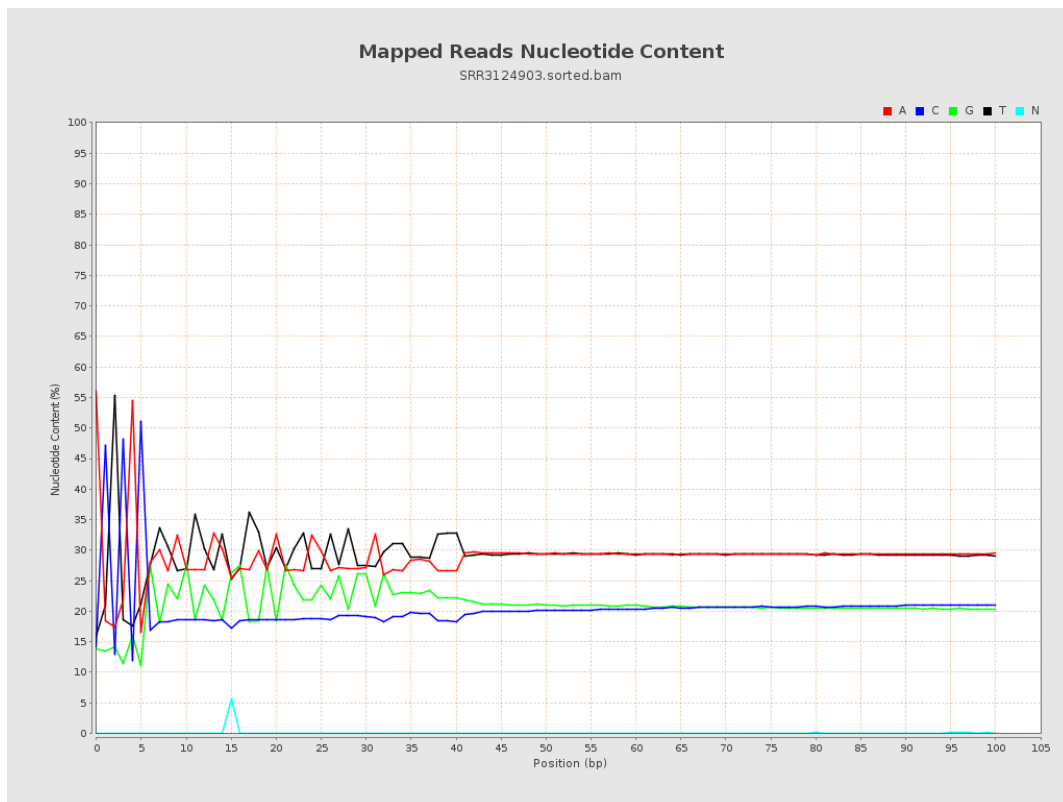
6. Results : Genome Fraction Coverage



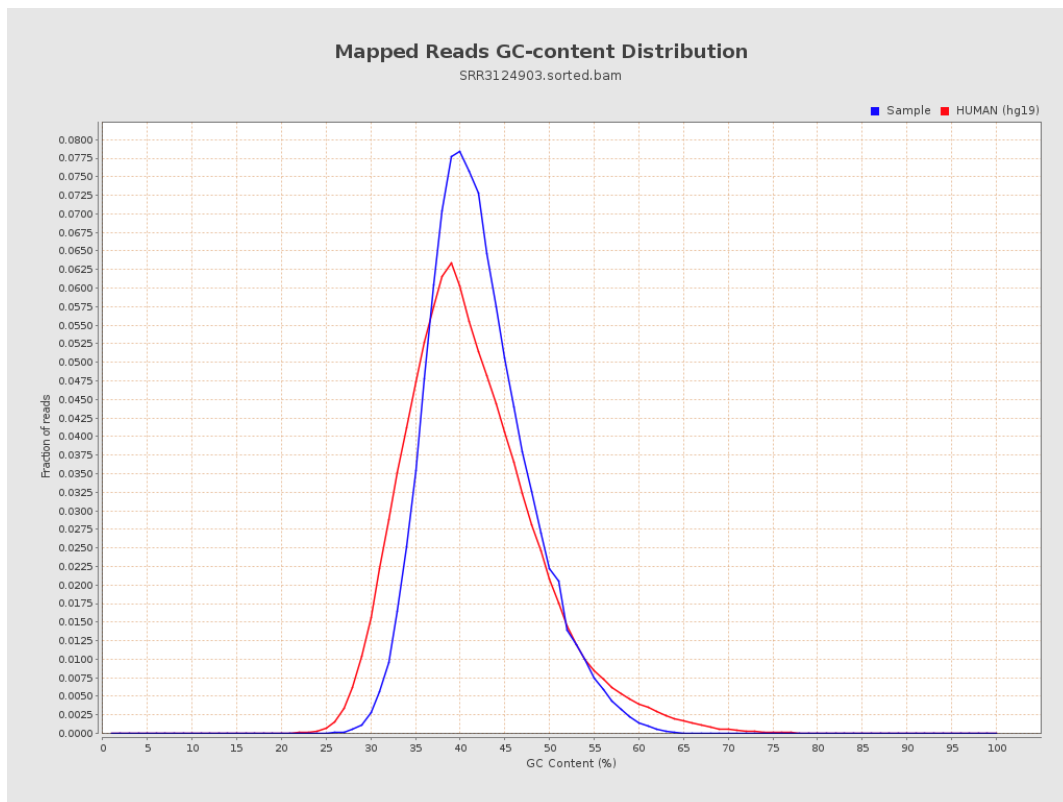
7. Results : Duplication Rate Histogram



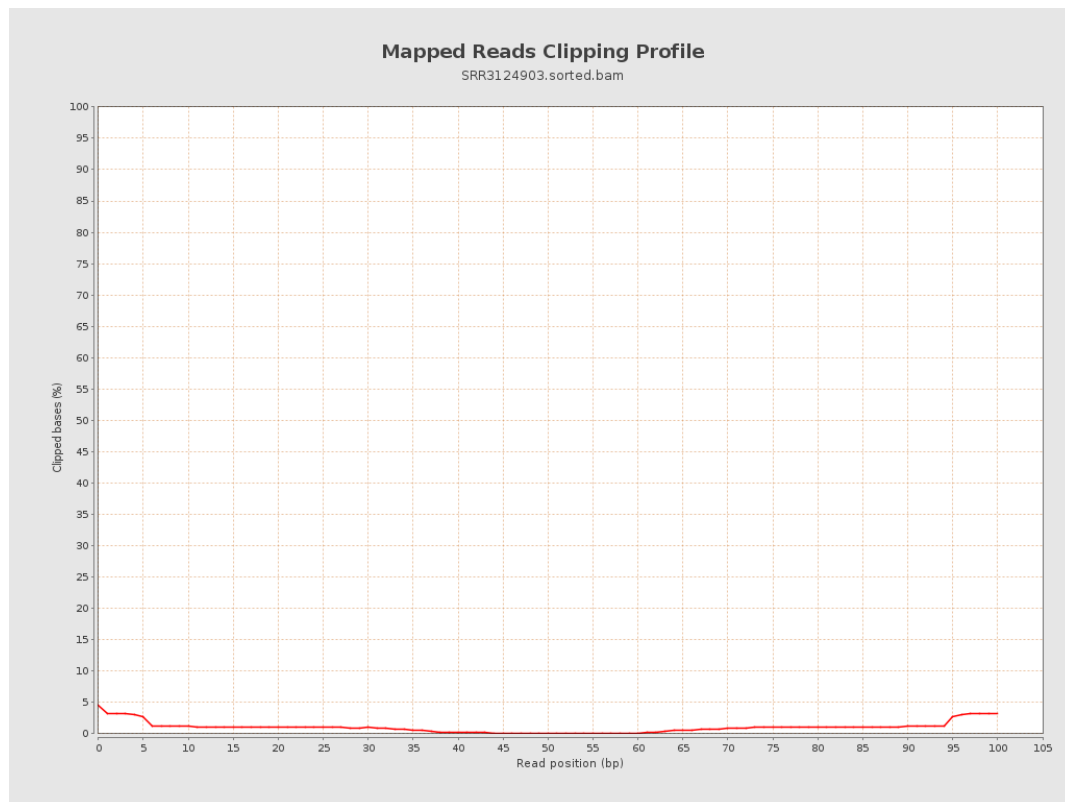
8. Results : Mapped Reads Nucleotide Content



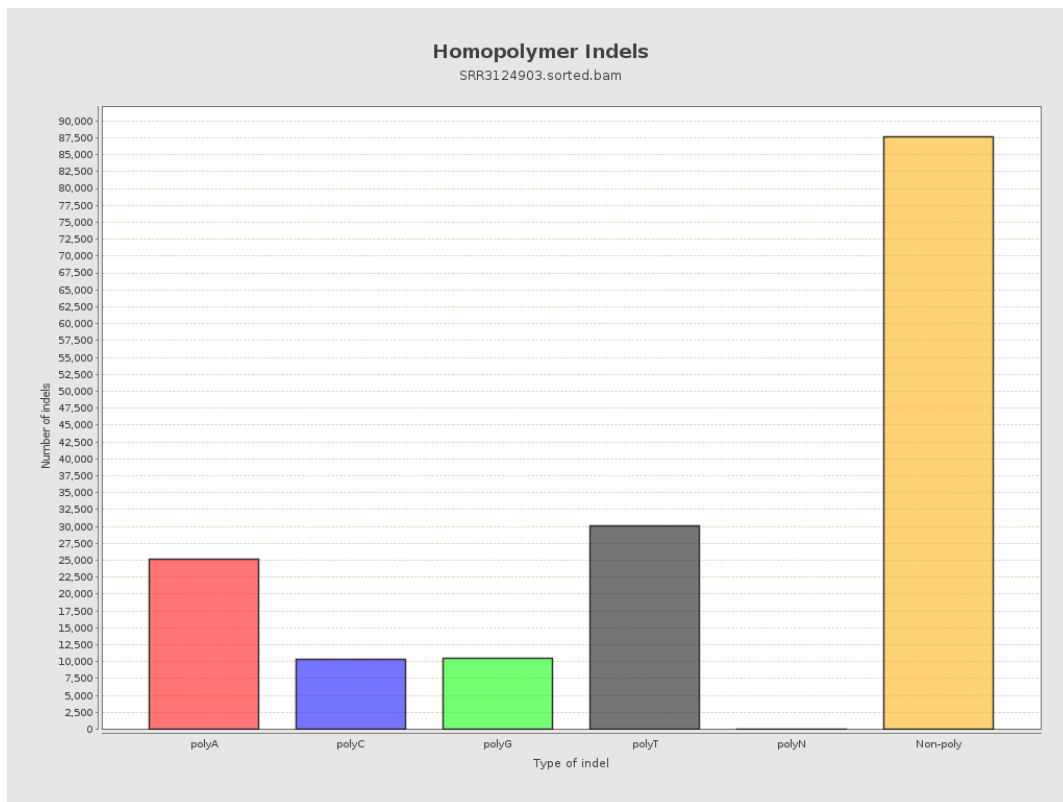
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



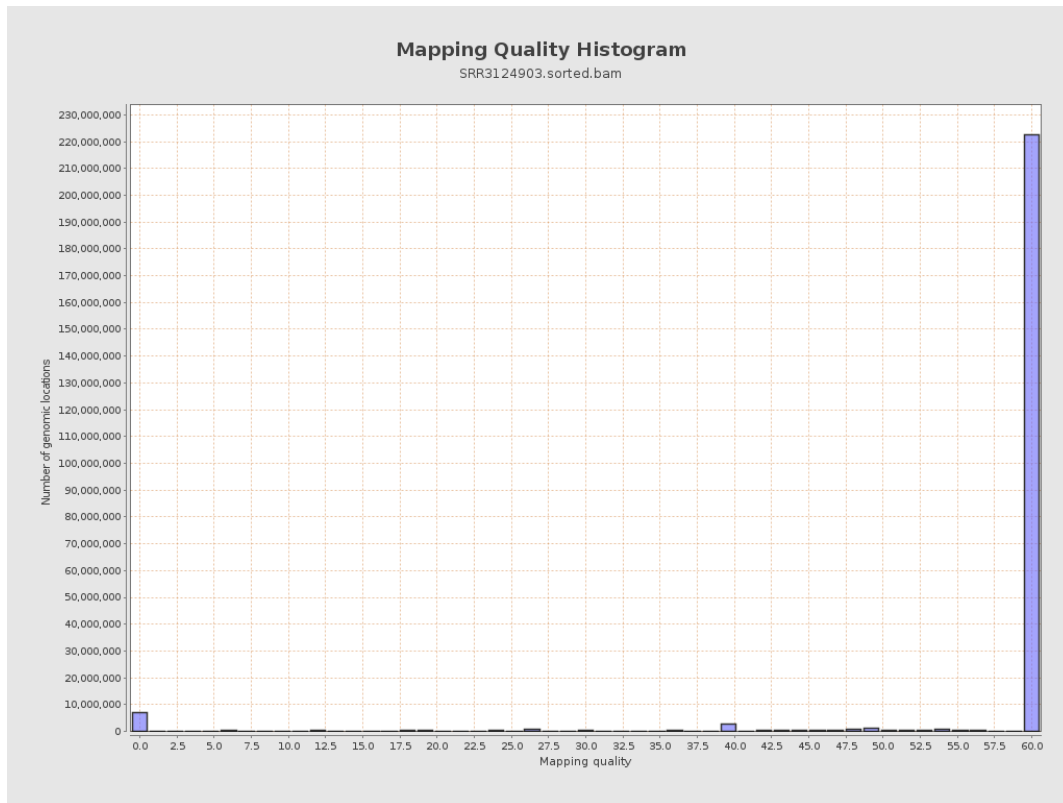
11. Results : Homopolymer Indels



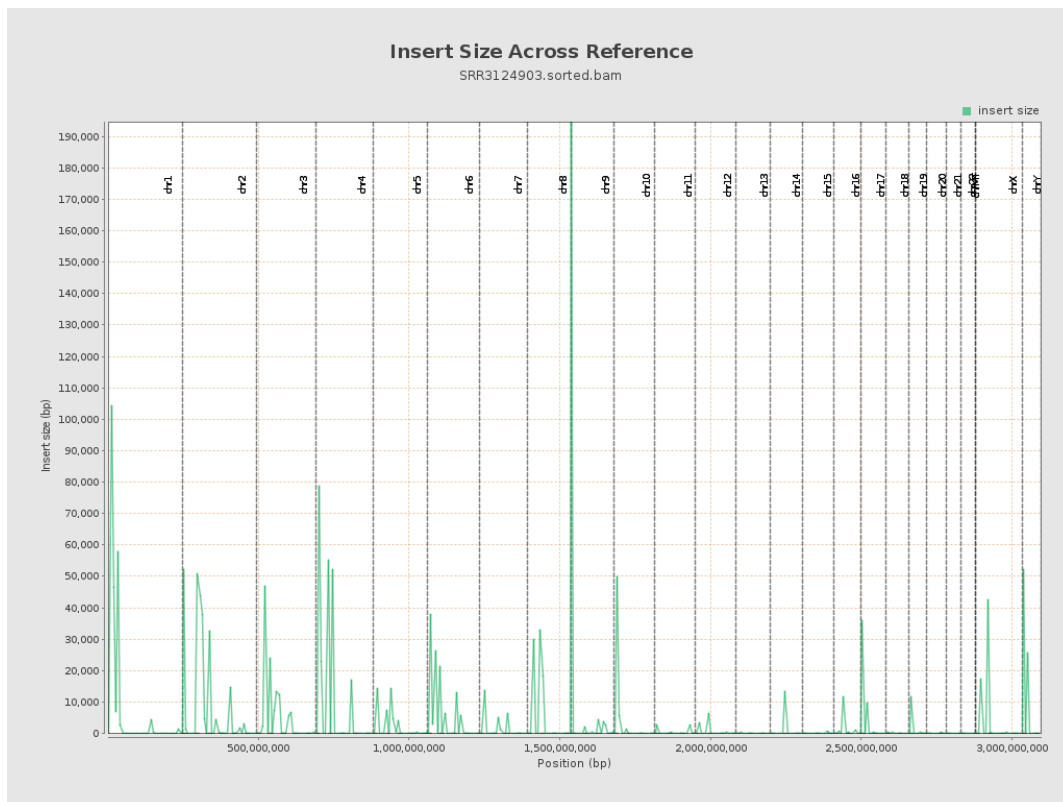
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

