

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 04:22:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124912.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_SRR3124912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124912_1.fastq.gz SRR3124912_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 04:22:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,567,640
Mapped reads	4,535,660 / 99.3%
Unmapped reads	31,980 / 0.7%
Mapped paired reads	4,535,660 / 99.3%
Mapped reads, first in pair	2,272,358 / 49.75%
Mapped reads, second in pair	2,263,302 / 49.55%
Mapped reads, both in pair	4,523,544 / 99.03%
Mapped reads, singletons	12,116 / 0.27%
Secondary alignments	0
Supplementary alignments	75,117 / 1.64%
Read min/max/mean length	30 / 151 / 151.85
Duplicated reads (estimated)	687,140 / 15.04%
Duplication rate	12.65%
Clipped reads	1,911,321 / 41.84%

2.2. ACGT Content

Number/percentage of A's	190,370,713 / 29.62%
Number/percentage of C's	129,274,798 / 20.11%
Number/percentage of T's	189,523,127 / 29.48%
Number/percentage of G's	133,600,110 / 20.78%
Number/percentage of N's	37,944 / 0.01%

GC Percentage	40.89%
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2.3. Coverage

Mean	0.2078
Standard Deviation	2.763

2.4. Mapping Quality

Mean Mapping Quality	53.75
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2.5. Insert size

Mean	55,338.06
Standard Deviation	2,253,472.5
P25/Median/P75	145 / 180 / 234

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	7,292,097
Insertions	124,117
Mapped reads with at least one insertion	2.61%
Deletions	270,171
Mapped reads with at least one deletion	5.73%
Homopolymer indels	48.48%

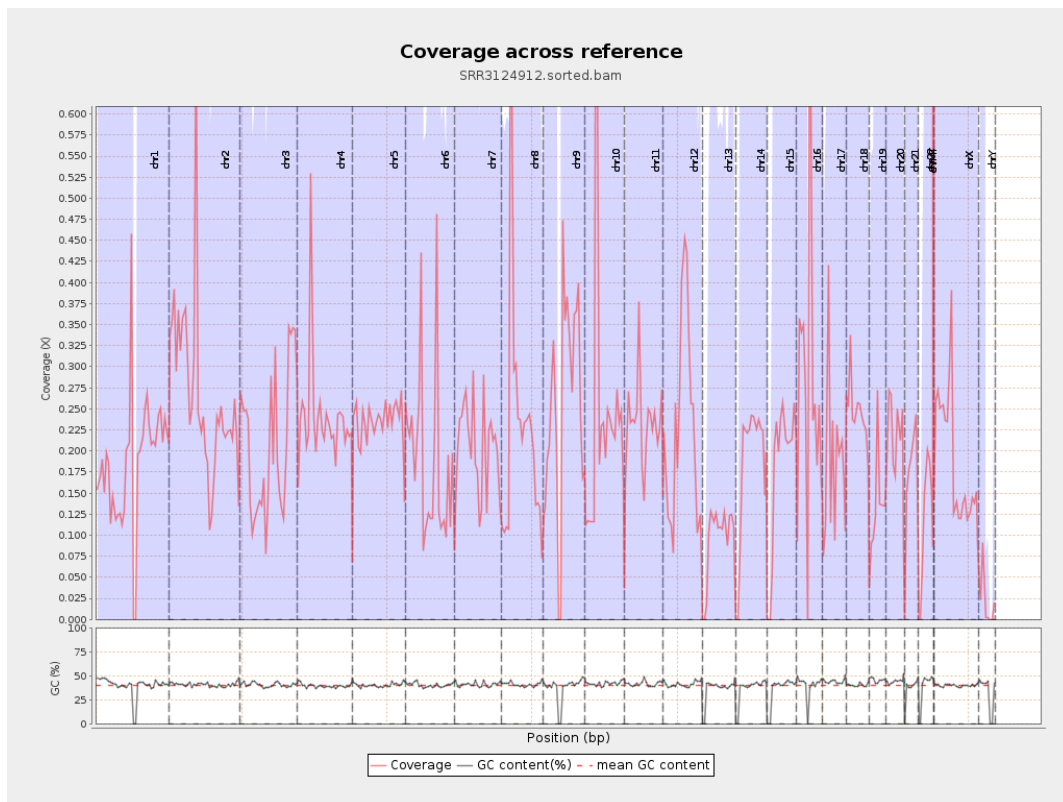
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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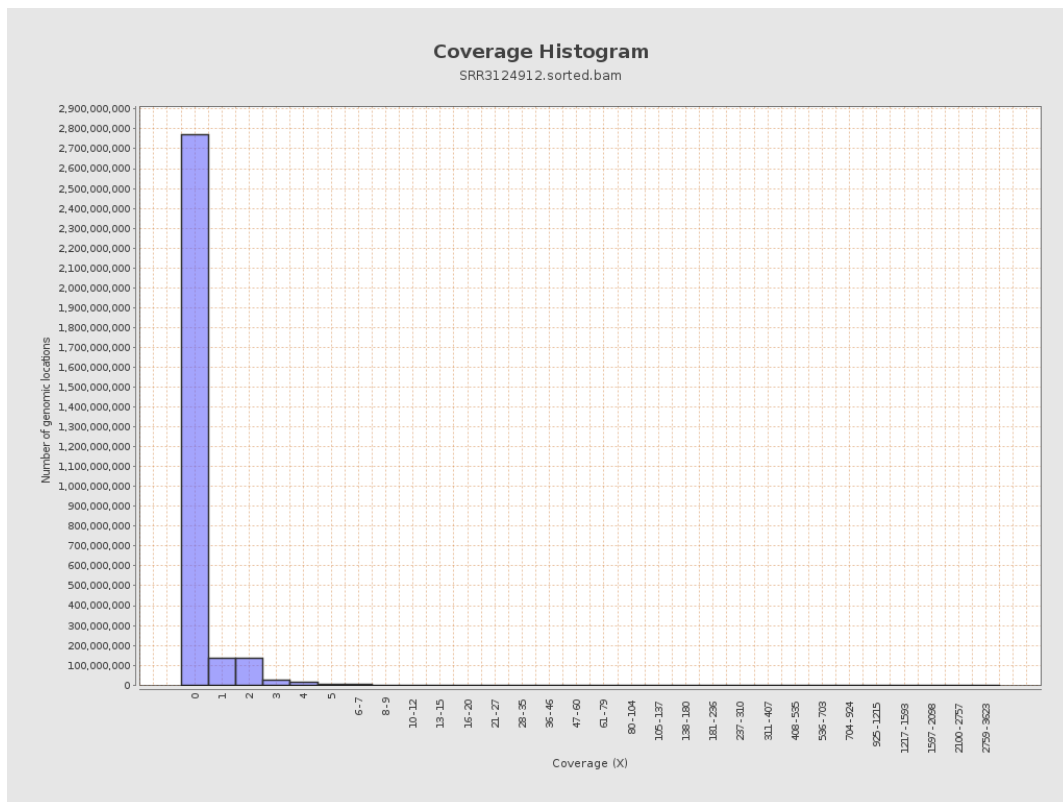
		bases	coverage	deviation
chr1	249250621	46309147	0.1858	3.6883
chr2	243199373	65241103	0.2683	2.888
chr3	198022430	40841267	0.2062	0.743
chr4	191154276	45453327	0.2378	2.168
chr5	180915260	42364311	0.2342	0.7372
chr6	171115067	32433845	0.1895	2.4153
chr7	159138663	32779746	0.206	2.3452
chr8	146364022	32176099	0.2198	1.1912
chr9	141213431	36698367	0.2599	4.6962
chr10	135534747	32154291	0.2372	6.2839
chr11	135006516	30863570	0.2286	2.9489
chr12	133851895	30670517	0.2291	0.7371
chr13	115169878	10853288	0.0942	0.4406
chr14	107349540	19739621	0.1839	0.6844
chr15	102531392	18431048	0.1798	0.6379
chr16	90354753	25470329	0.2819	3.9885
chr17	81195210	14714907	0.1812	4.8242
chr18	78077248	19418557	0.2487	3.5047
chr19	59128983	8082224	0.1367	2.0944
chr20	63025520	13768623	0.2185	1.0498
chr21	48129895	8067326	0.1676	1.2956
chr22	51304566	5990543	0.1168	0.5186
chrMT	16571	99320	5.9936	4.4726
chrX	155270560	29420420	0.1895	1.2982

chrY	59373566	1260964	0.0212	1.9245
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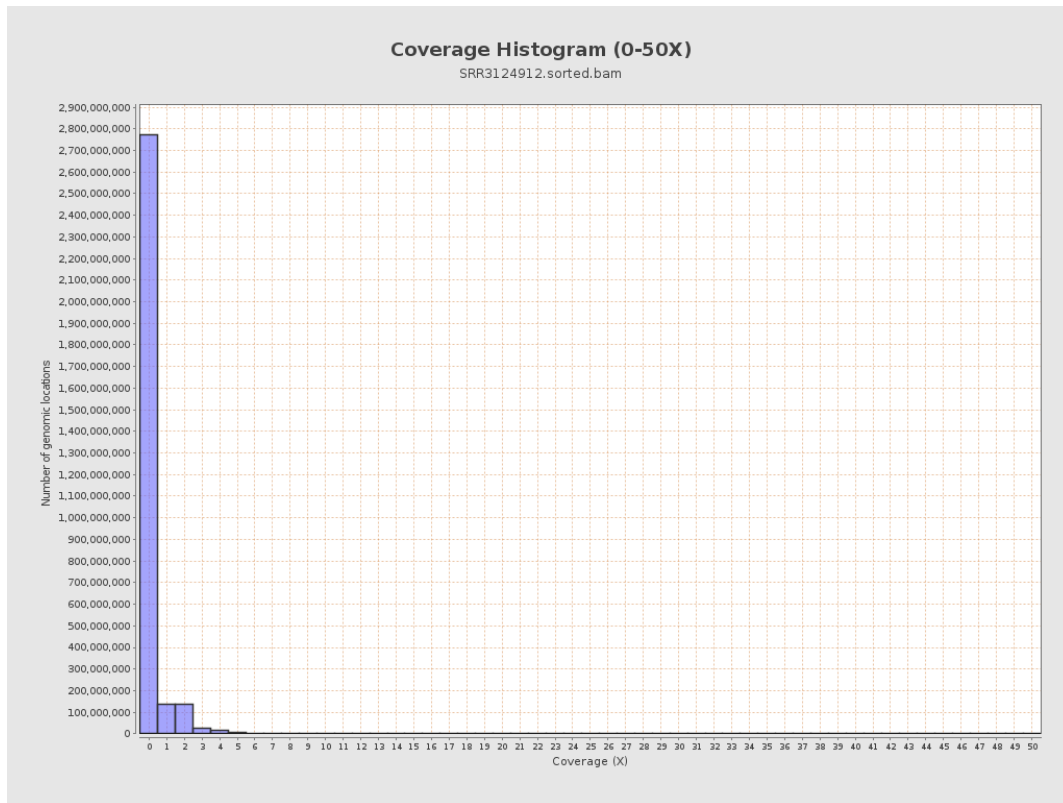
3. Results : Coverage across reference



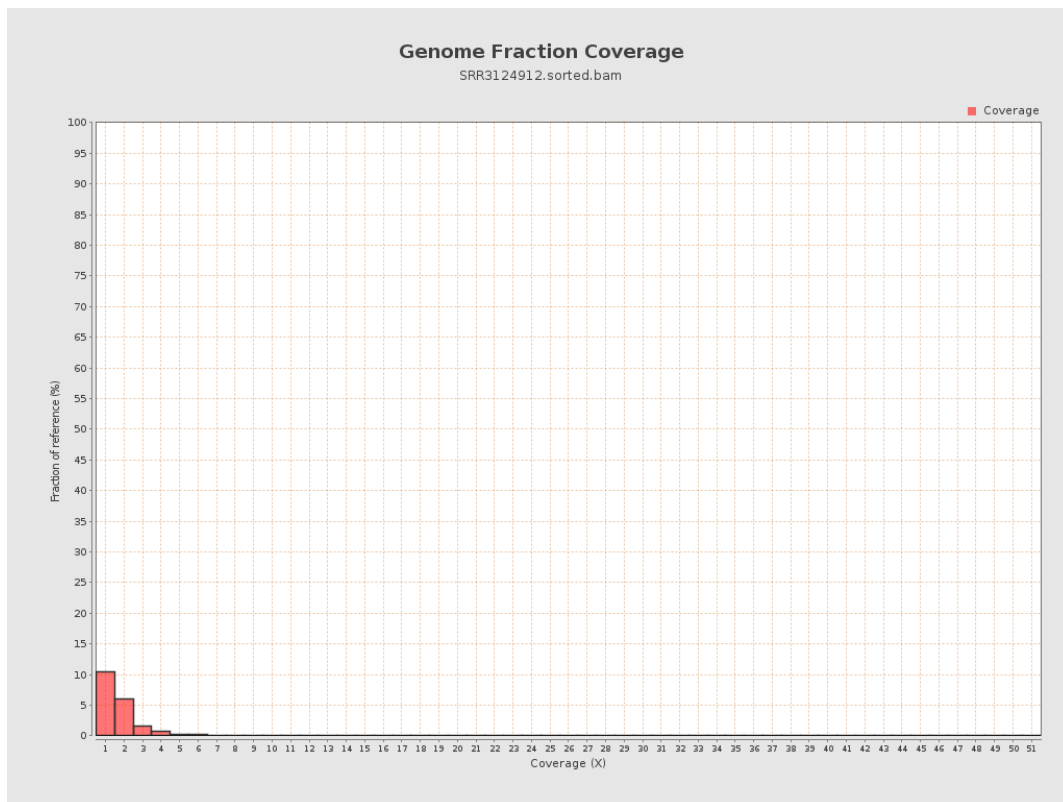
4. Results : Coverage Histogram



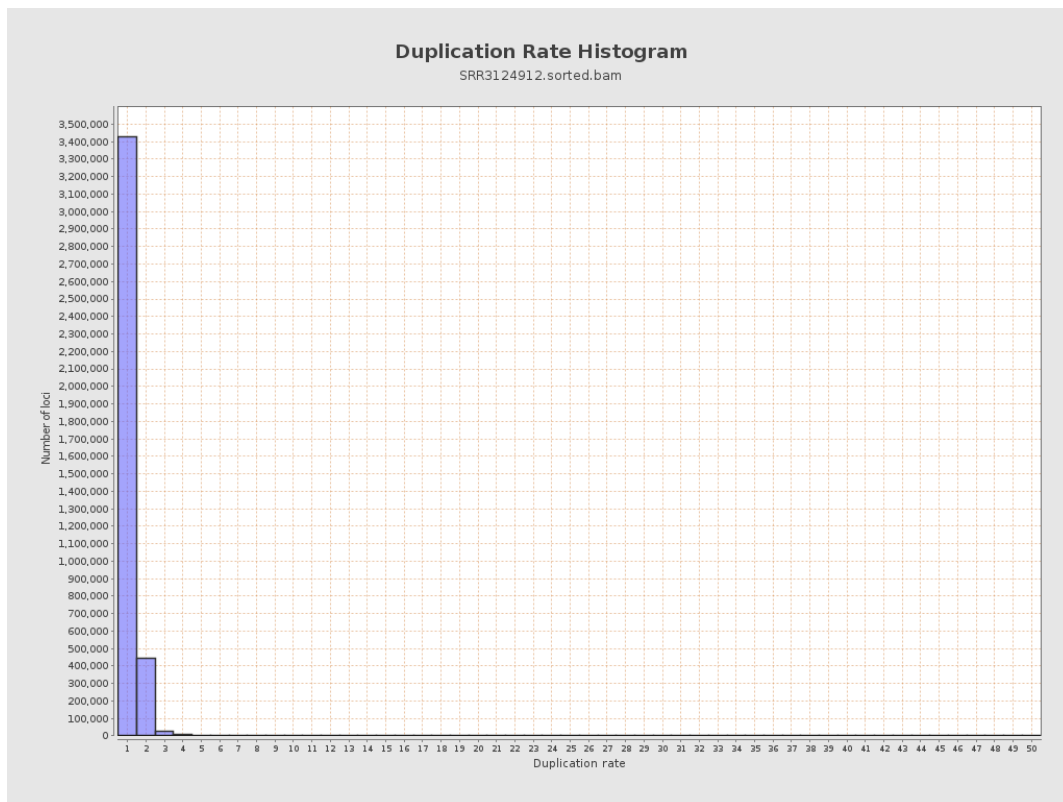
5. Results : Coverage Histogram (0-50X)



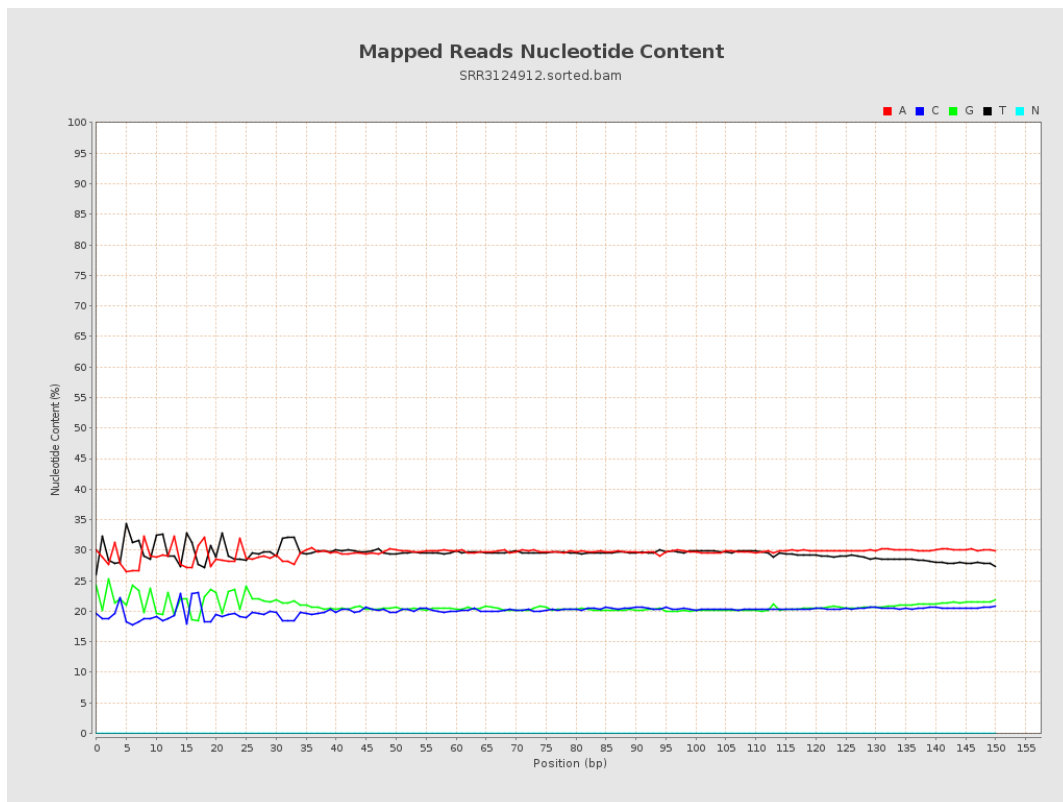
6. Results : Genome Fraction Coverage



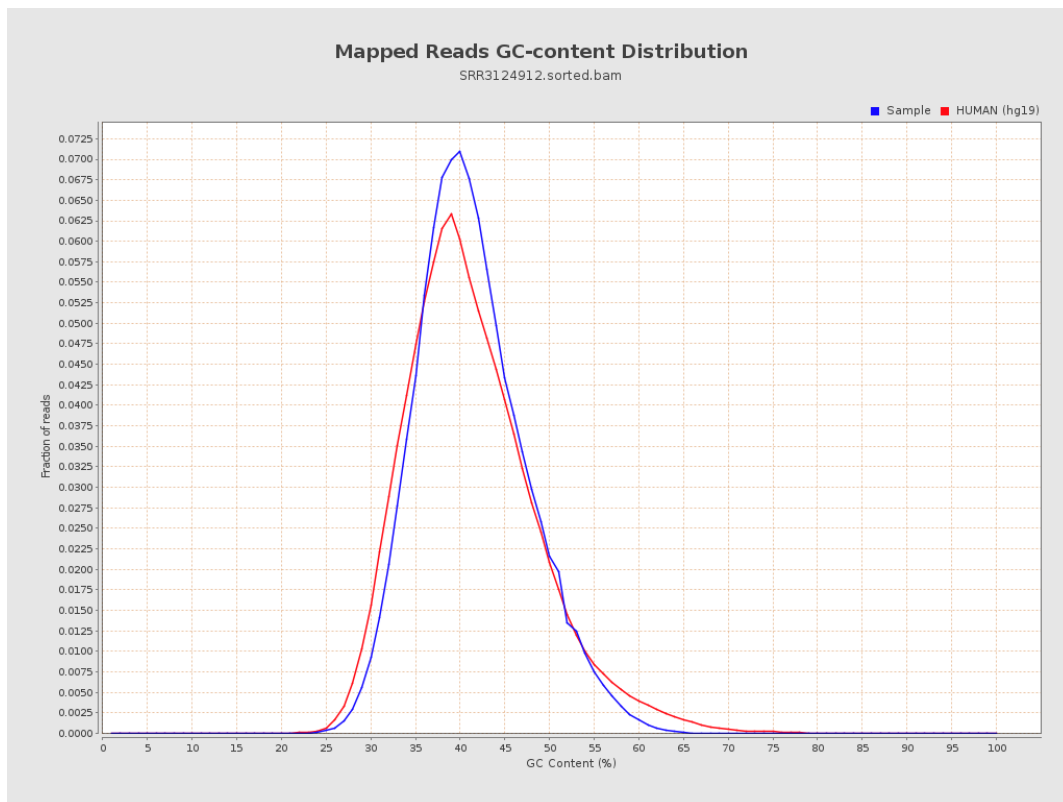
7. Results : Duplication Rate Histogram



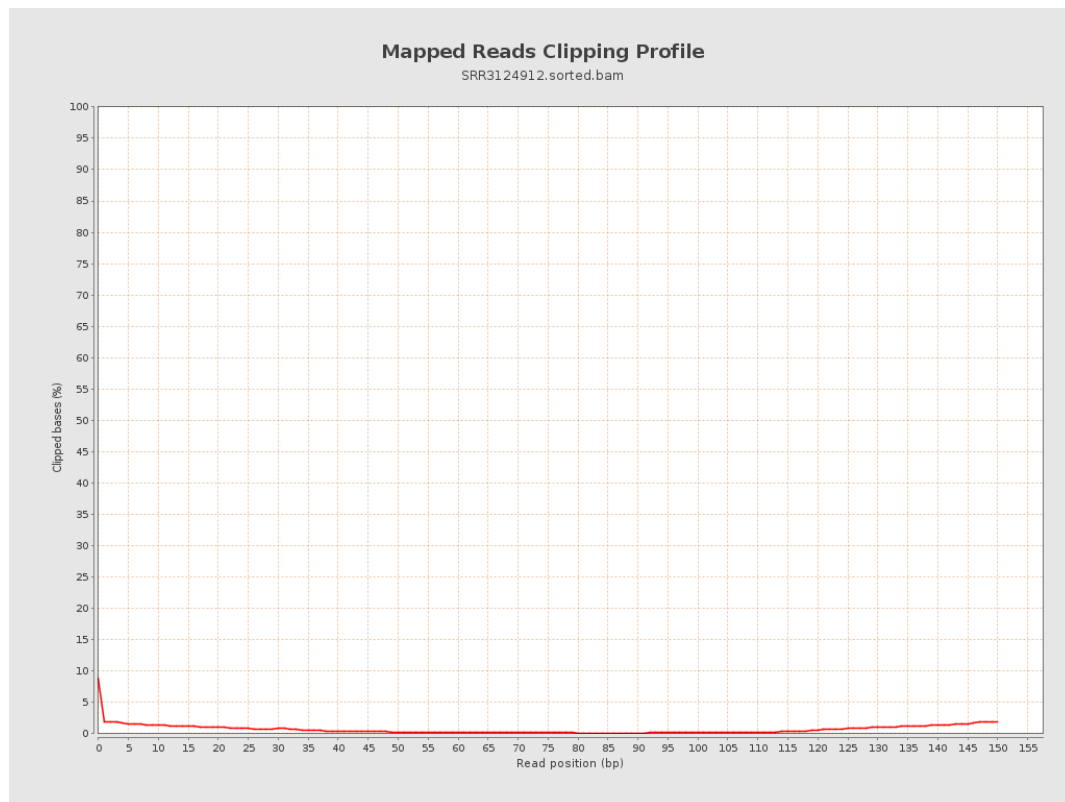
8. Results : Mapped Reads Nucleotide Content



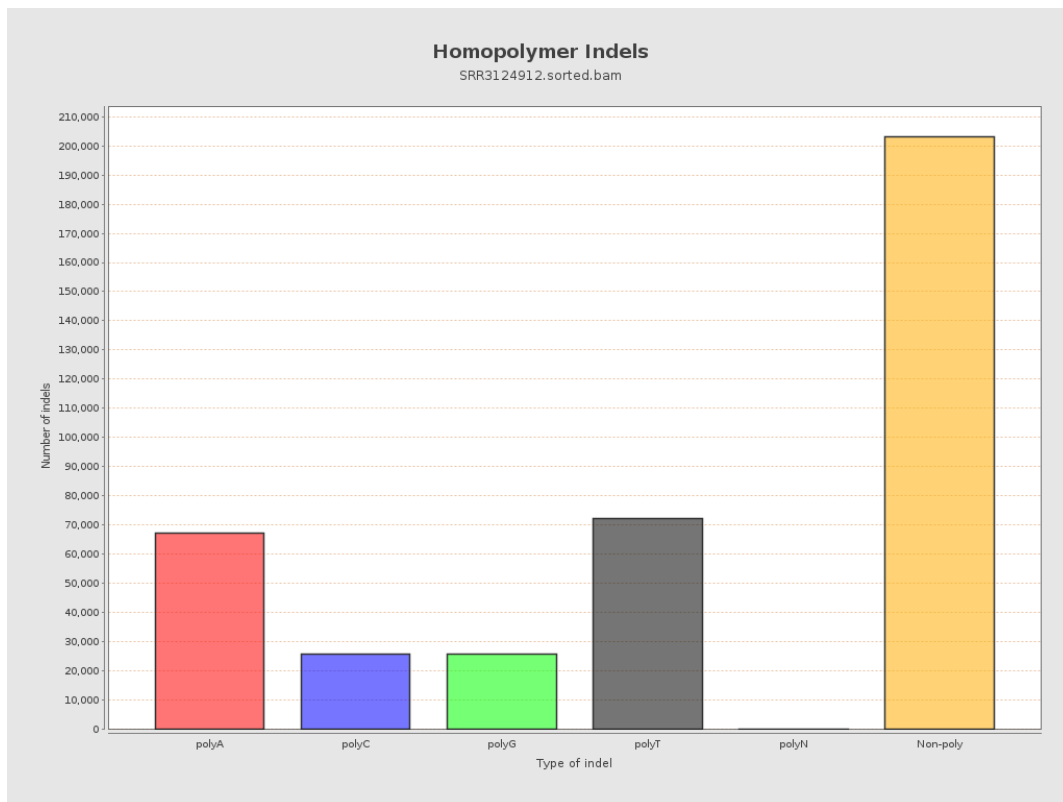
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



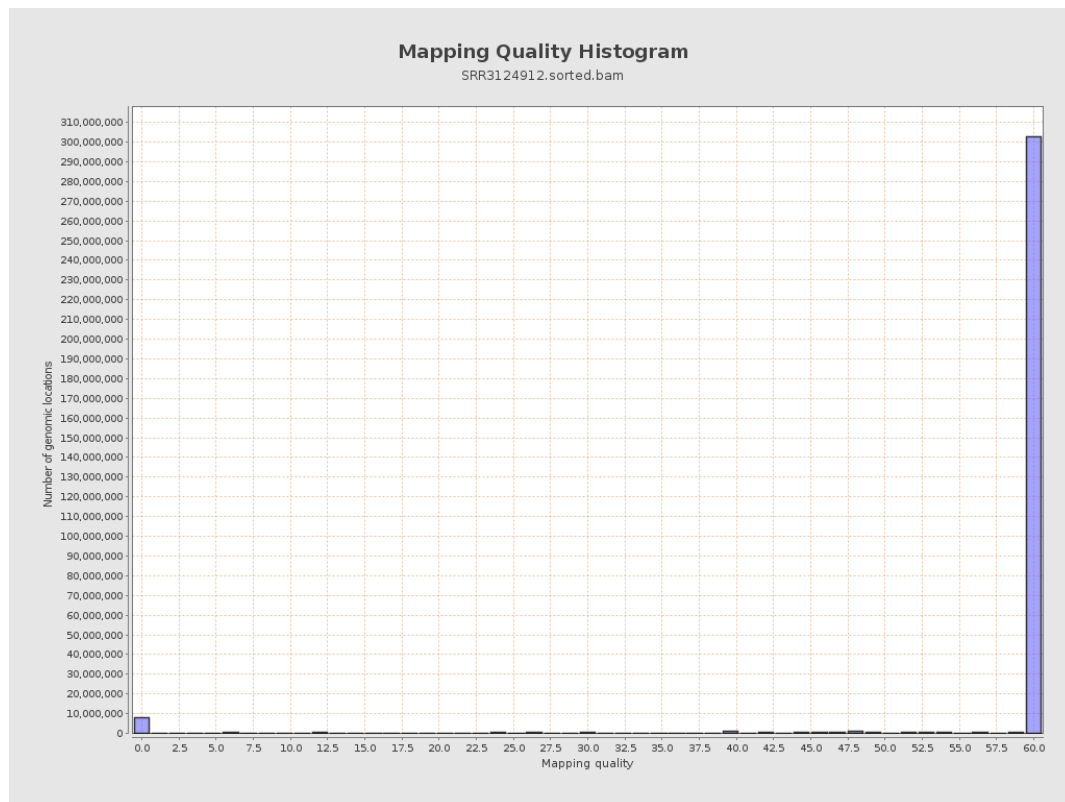
11. Results : Homopolymer Indels



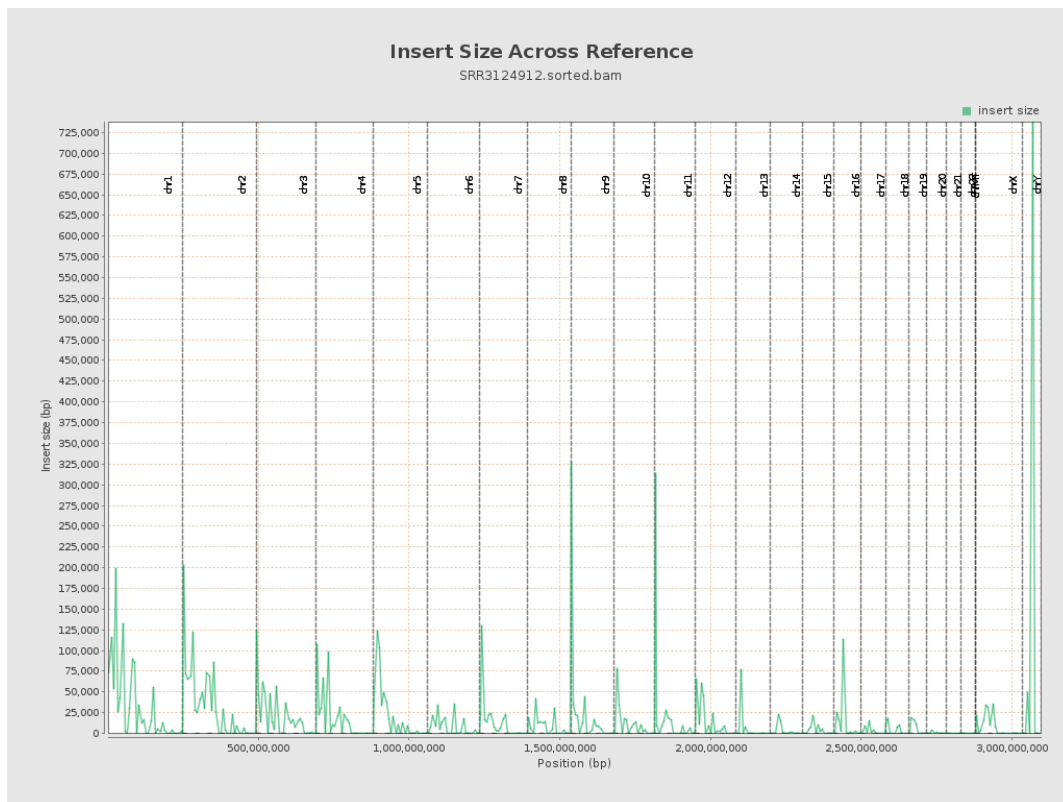
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

