

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 17:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124812.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_SRR3124812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124812_1.fastq.gz SRR3124812_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 17:40:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,204,902
Mapped reads	26,937,230 / 99.02%
Unmapped reads	267,672 / 0.98%
Mapped paired reads	26,937,230 / 99.02%
Mapped reads, first in pair	13,496,251 / 49.61%
Mapped reads, second in pair	13,440,979 / 49.41%
Mapped reads, both in pair	26,821,544 / 98.59%
Mapped reads, singletons	115,686 / 0.43%
Secondary alignments	0
Supplementary alignments	122,129 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	4,495,500 / 16.52%
Duplication rate	10.82%
Clipped reads	13,432,275 / 49.37%

2.2. ACGT Content

Number/percentage of A's	662,346,459 / 28.38%
Number/percentage of C's	425,845,183 / 18.25%
Number/percentage of T's	707,210,419 / 30.31%
Number/percentage of G's	538,058,611 / 23.06%
Number/percentage of N's	19,866 / 0%

GC Percentage	41.31%
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2.3. Coverage

Mean	0.7542
Standard Deviation	7.0596

2.4. Mapping Quality

Mean Mapping Quality	52.7
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2.5. Insert size

Mean	33,963.01
Standard Deviation	1,698,988.88
P25/Median/P75	147 / 196 / 271

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	18,506,355
Insertions	308,844
Mapped reads with at least one insertion	1.12%
Deletions	783,743
Mapped reads with at least one deletion	2.85%
Homopolymer indels	48.33%

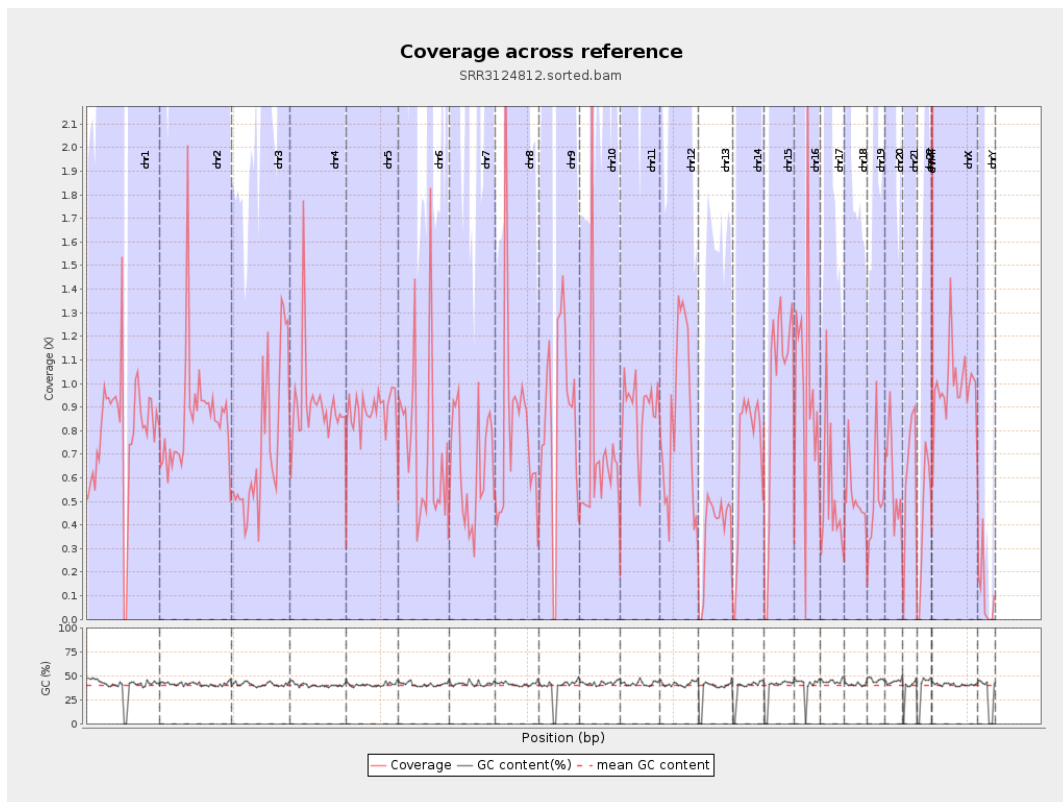
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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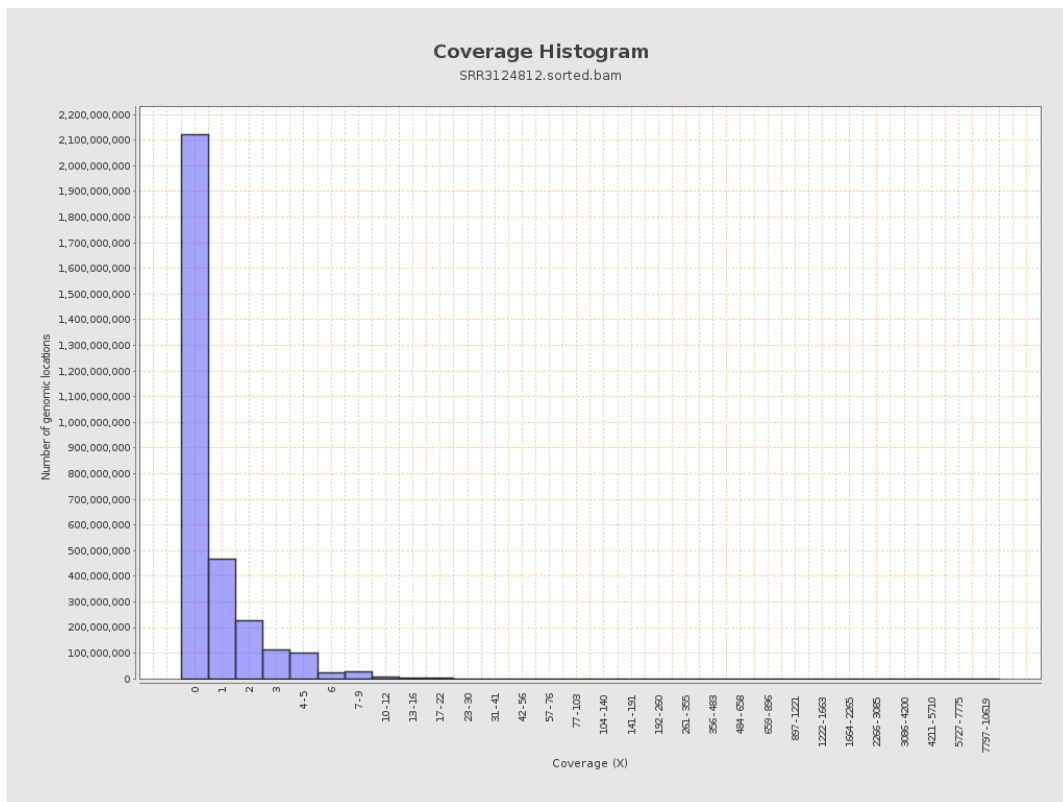
		bases	coverage	deviation
chr1	249250621	197704846	0.7932	10.7575
chr2	243199373	208296519	0.8565	8.2316
chr3	198022430	144401941	0.7292	1.6692
chr4	191154276	173150486	0.9058	5.6604
chr5	180915260	159008669	0.8789	1.8047
chr6	171115067	124395260	0.727	7.1271
chr7	159138663	102819437	0.6461	3.5259
chr8	146364022	117297641	0.8014	3.2128
chr9	141213431	118303303	0.8378	9.7351
chr10	135534747	93887282	0.6927	14.4176
chr11	135006516	117436390	0.8699	7.2033
chr12	133851895	112259925	0.8387	1.8055
chr13	115169878	43600510	0.3786	0.9914
chr14	107349540	75157892	0.7001	2.198
chr15	102531392	99486046	0.9703	2.0755
chr16	90354753	86731897	0.9599	11.326
chr17	81195210	41044406	0.5055	12.7625
chr18	78077248	40216914	0.5151	9.8157
chr19	59128983	29661786	0.5016	4.9272
chr20	63025520	36630669	0.5812	1.9767
chr21	48129895	31347319	0.6513	3.1182
chr22	51304566	21672569	0.4224	1.3033
chrMT	16571	286799	17.3073	12.056
chrX	155270560	153613673	0.9893	4.3108

chrY	59373566	6322369	0.1065	5.6261
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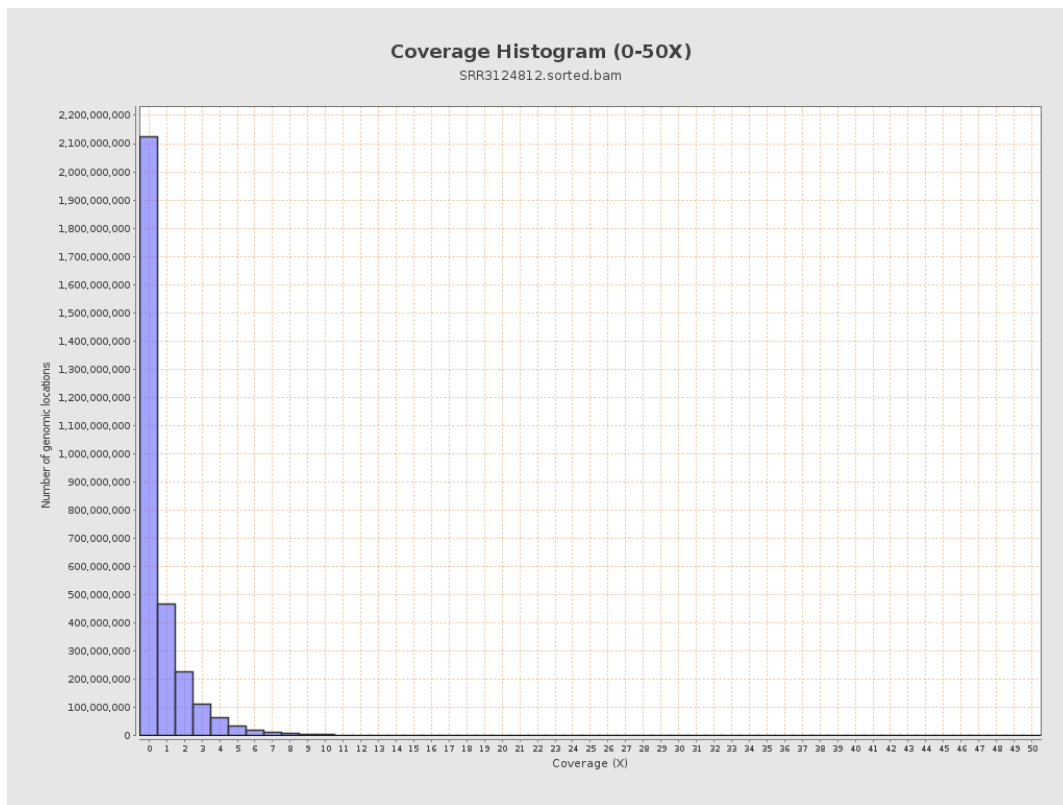
3. Results : Coverage across reference



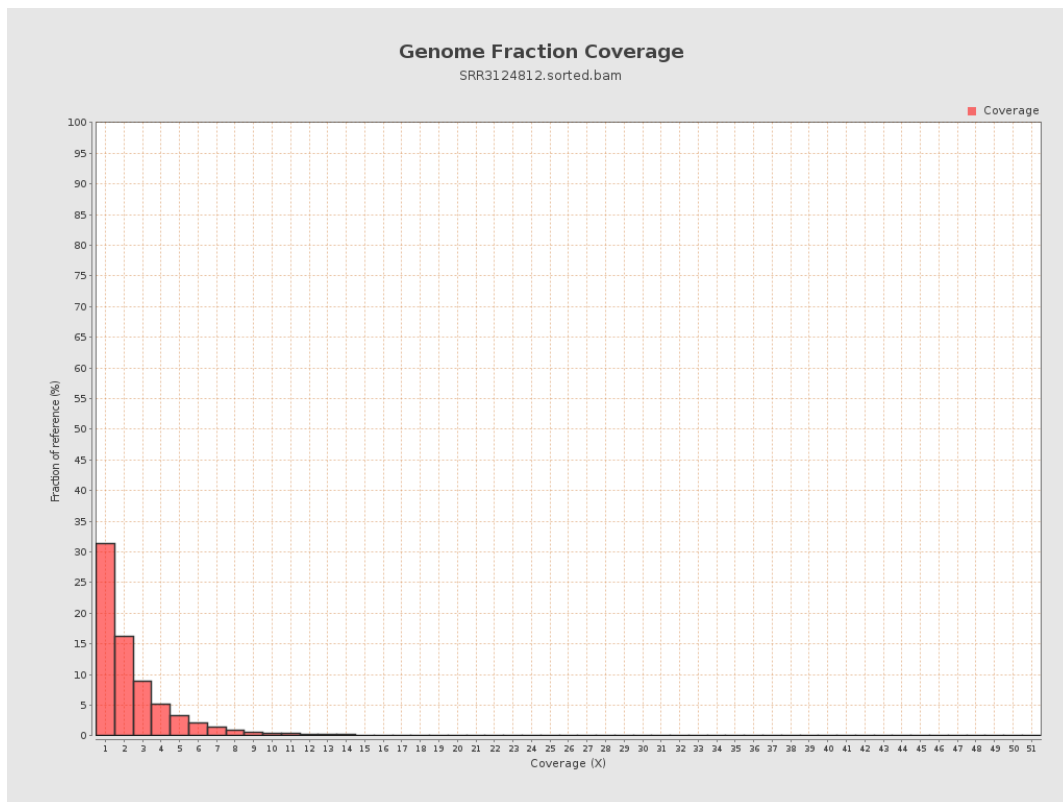
4. Results : Coverage Histogram



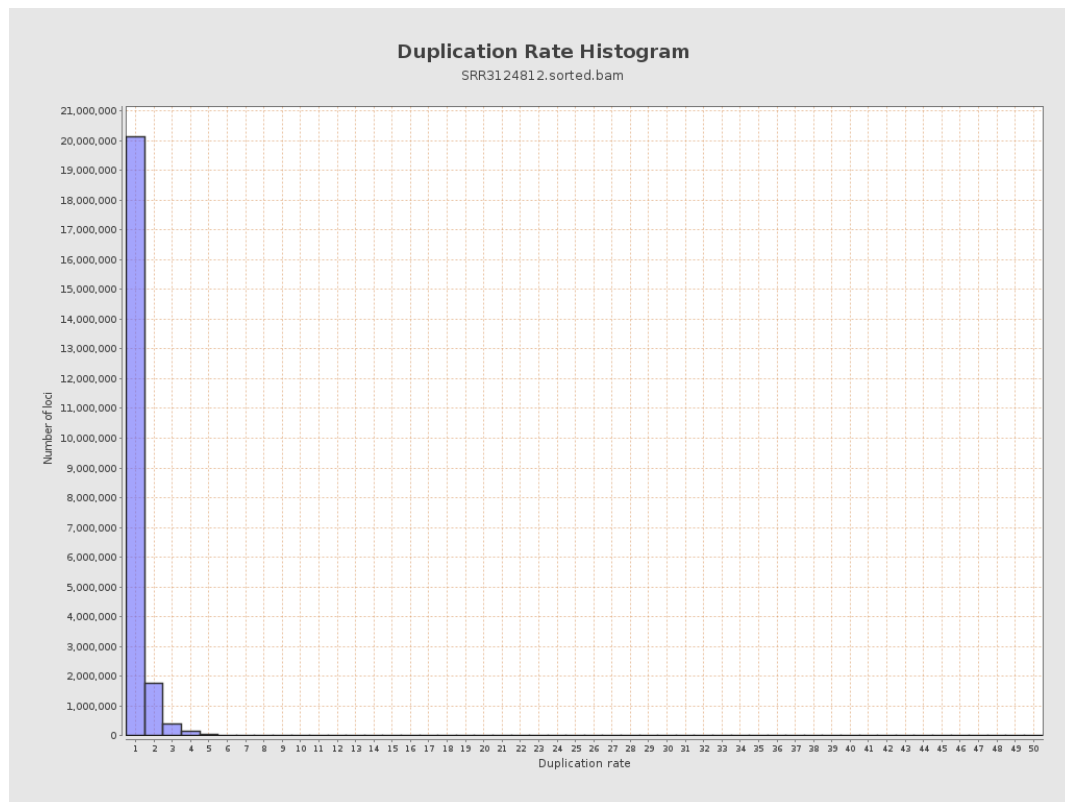
5. Results : Coverage Histogram (0-50X)



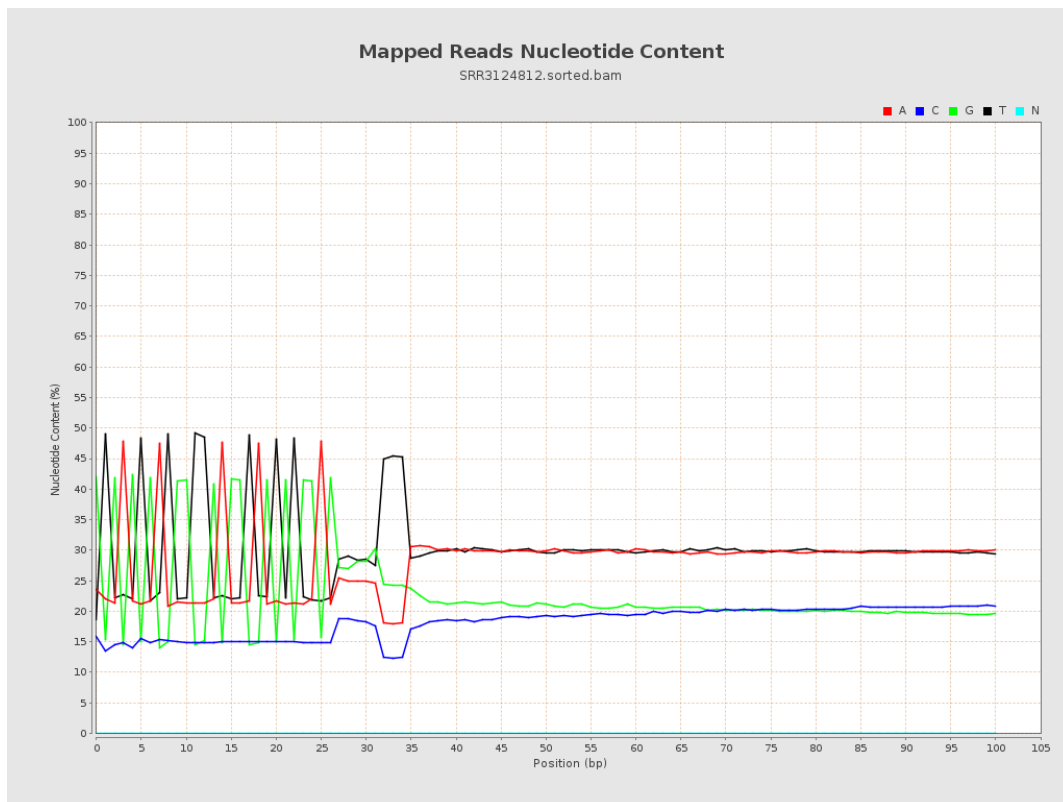
6. Results : Genome Fraction Coverage



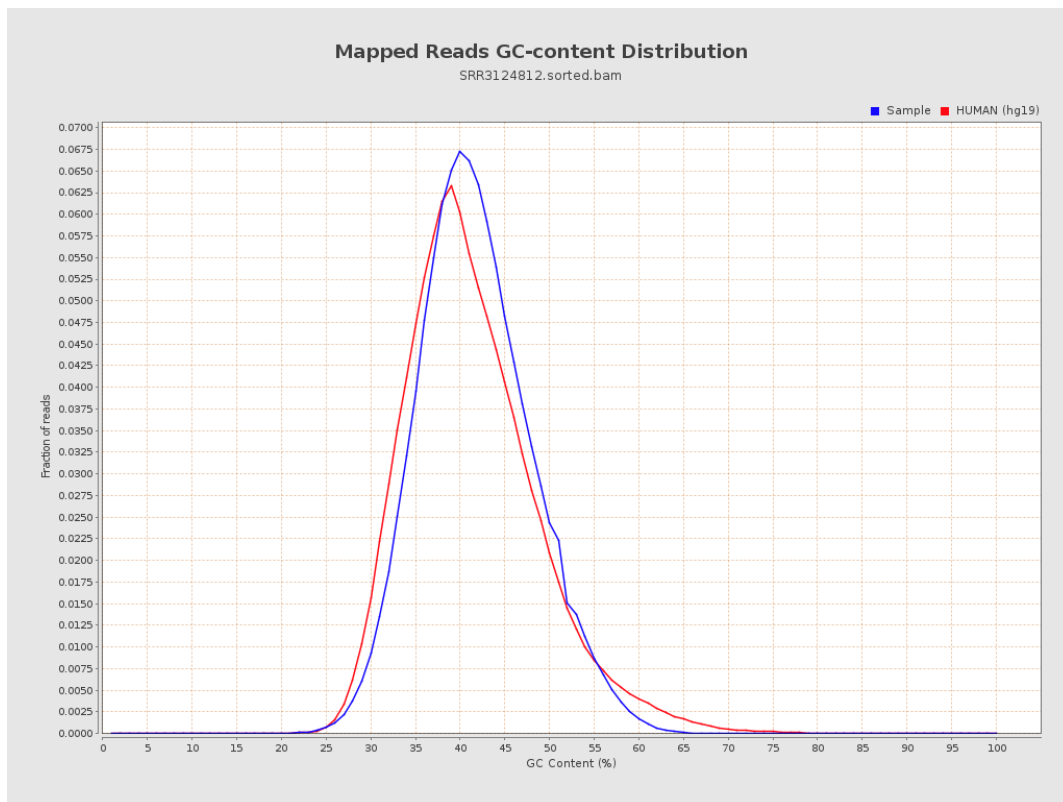
7. Results : Duplication Rate Histogram



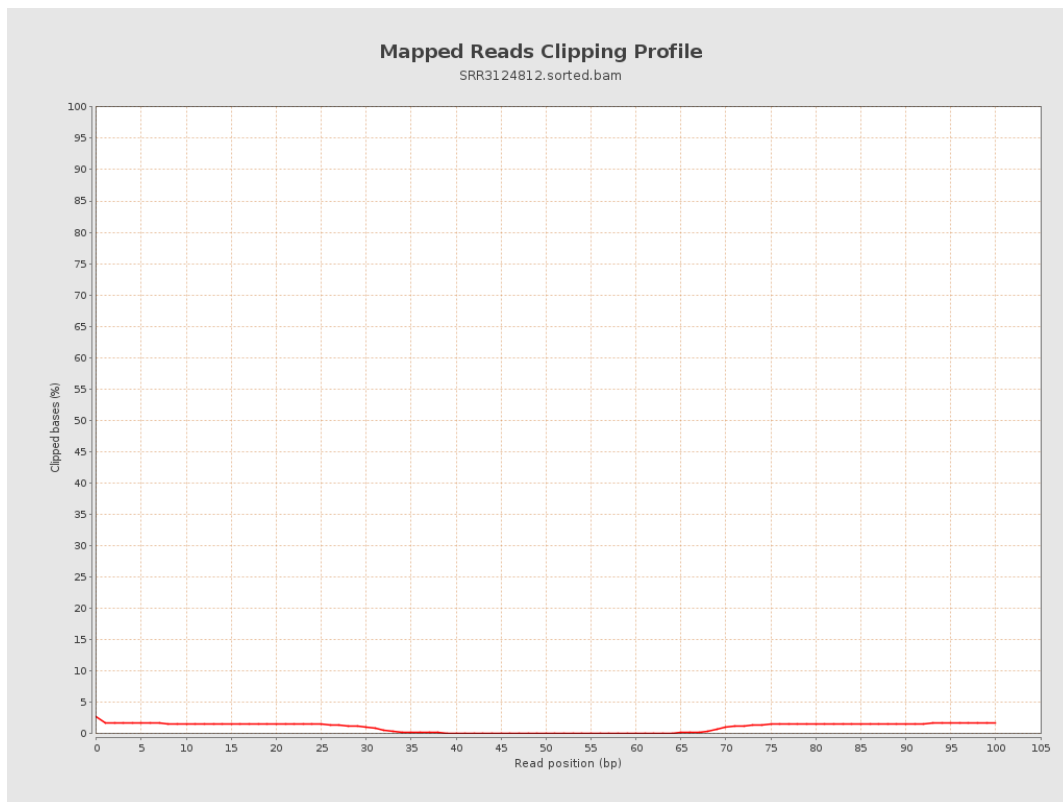
8. Results : Mapped Reads Nucleotide Content



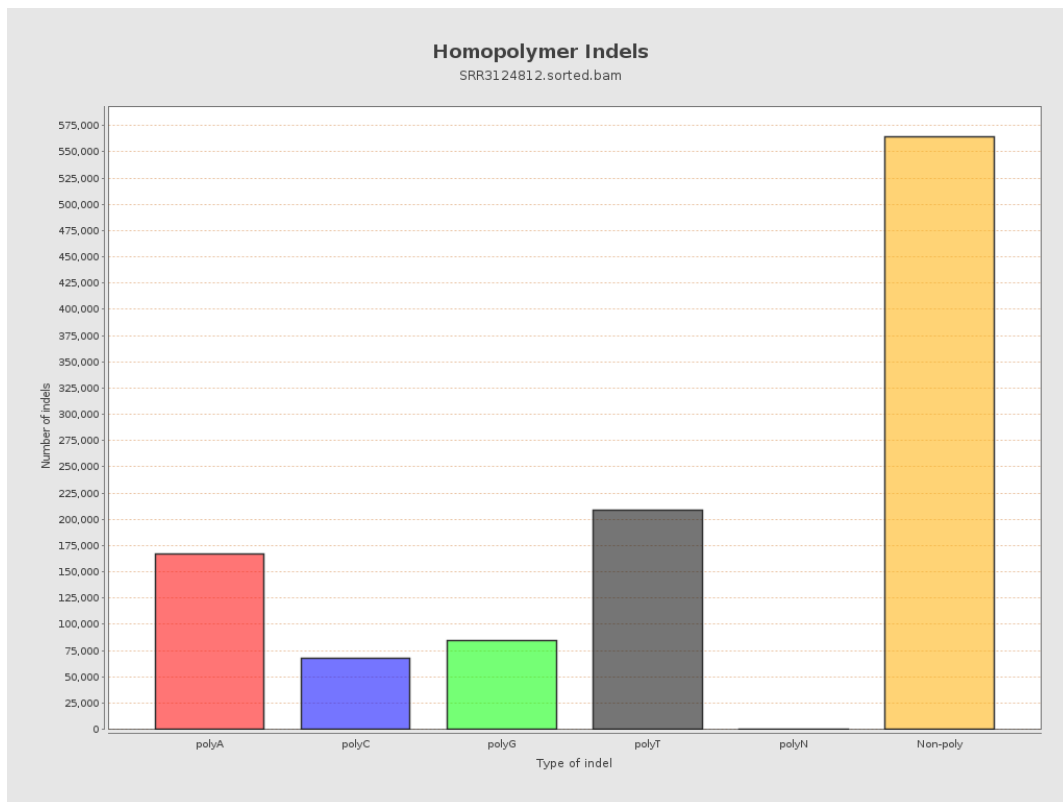
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



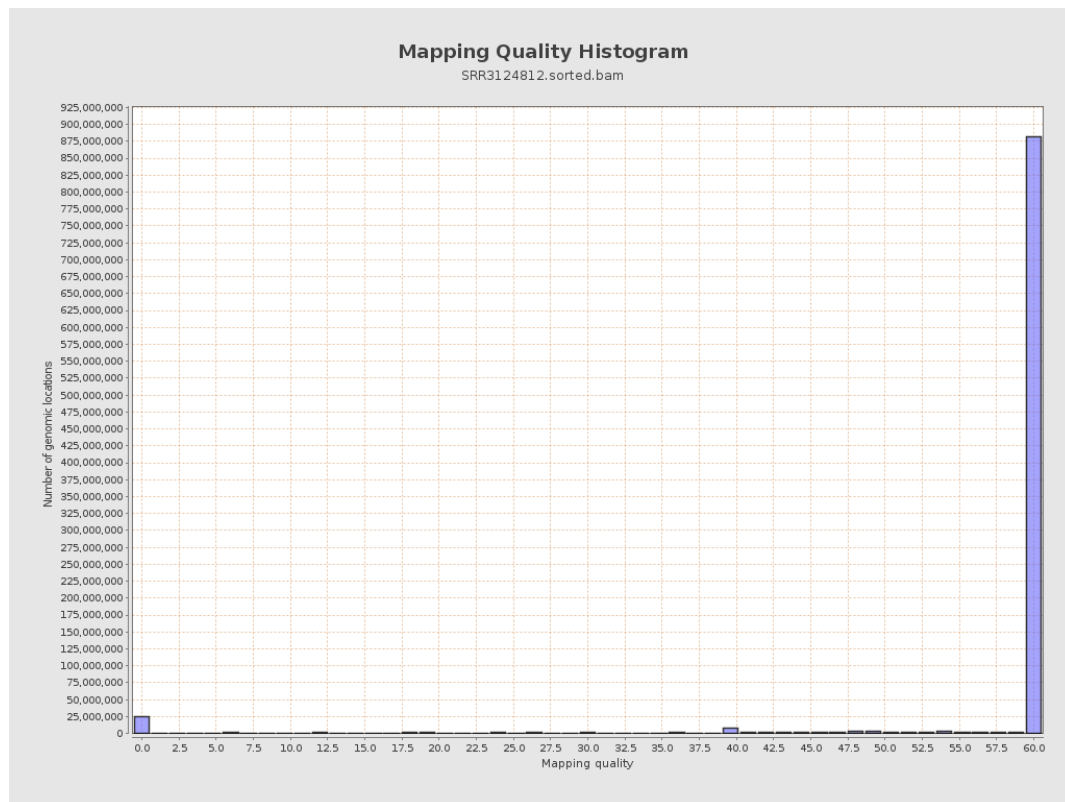
11. Results : Homopolymer Indels



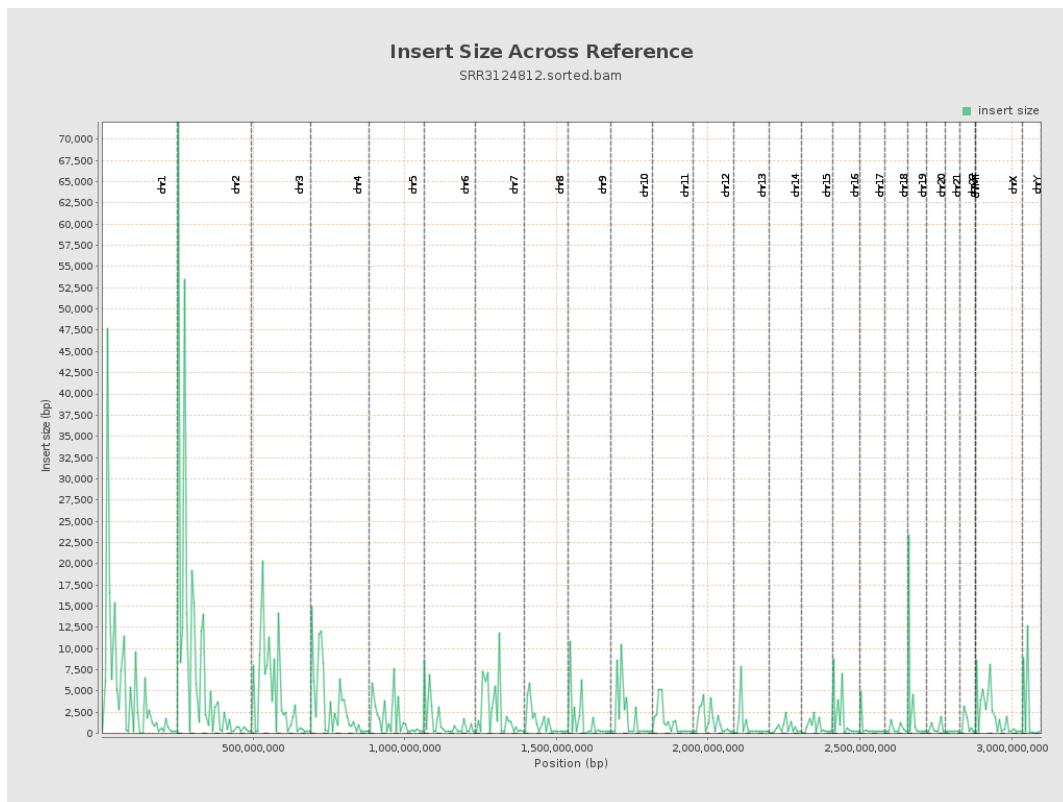
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

