

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:53:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124892.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_SRR3124892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124892_1.fastq.gz SRR3124892_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:53:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,740,286
Mapped reads	4,665,105 / 98.41%
Unmapped reads	75,181 / 1.59%
Mapped paired reads	4,665,105 / 98.41%
Mapped reads, first in pair	2,338,255 / 49.33%
Mapped reads, second in pair	2,326,850 / 49.09%
Mapped reads, both in pair	4,642,284 / 97.93%
Mapped reads, singletons	22,821 / 0.48%
Secondary alignments	0
Supplementary alignments	22,791 / 0.48%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	430,828 / 9.09%
Duplication rate	5.6%
Clipped reads	2,276,621 / 48.03%

2.2. ACGT Content

Number/percentage of A's	114,712,455 / 28.45%
Number/percentage of C's	74,169,458 / 18.4%
Number/percentage of T's	121,281,354 / 30.08%
Number/percentage of G's	92,877,384 / 23.04%
Number/percentage of N's	153,691 / 0.04%

GC Percentage	41.43%
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2.3. Coverage

Mean	0.1303
Standard Deviation	2.2375

2.4. Mapping Quality

Mean Mapping Quality	52.61
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2.5. Insert size

Mean	37,333.53
Standard Deviation	1,829,252.96
P25/Median/P75	142 / 192 / 267

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	3,308,251
Insertions	55,922
Mapped reads with at least one insertion	1.17%
Deletions	127,299
Mapped reads with at least one deletion	2.67%
Homopolymer indels	47.06%

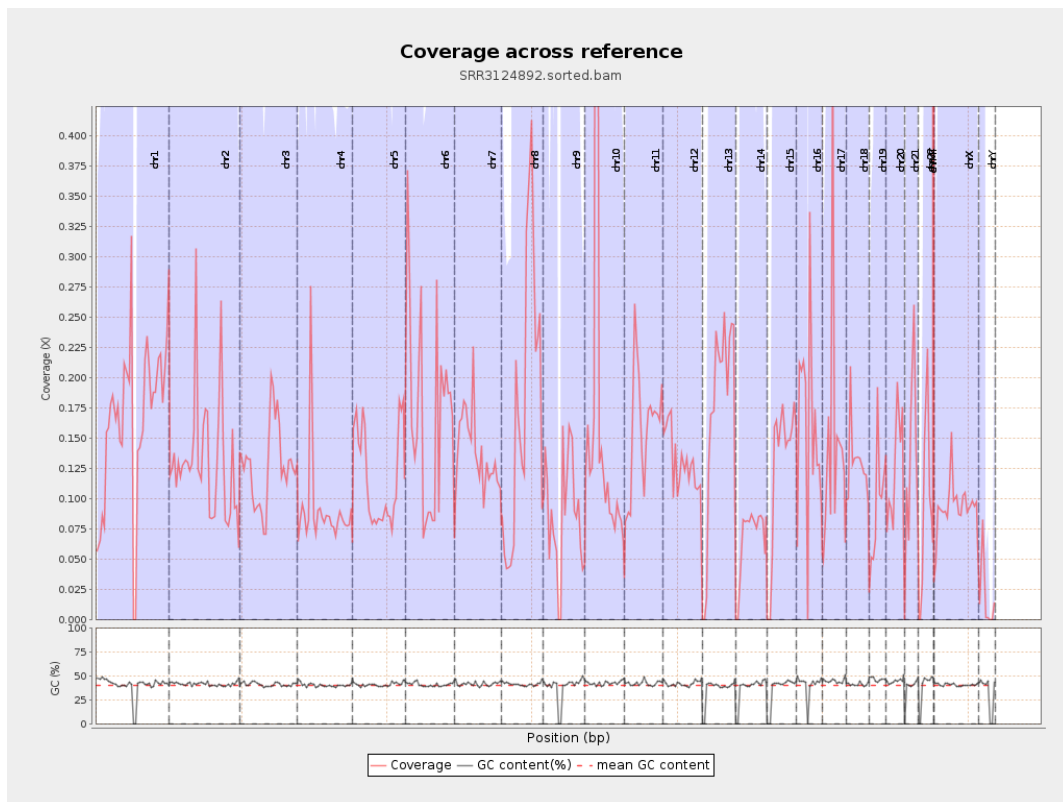
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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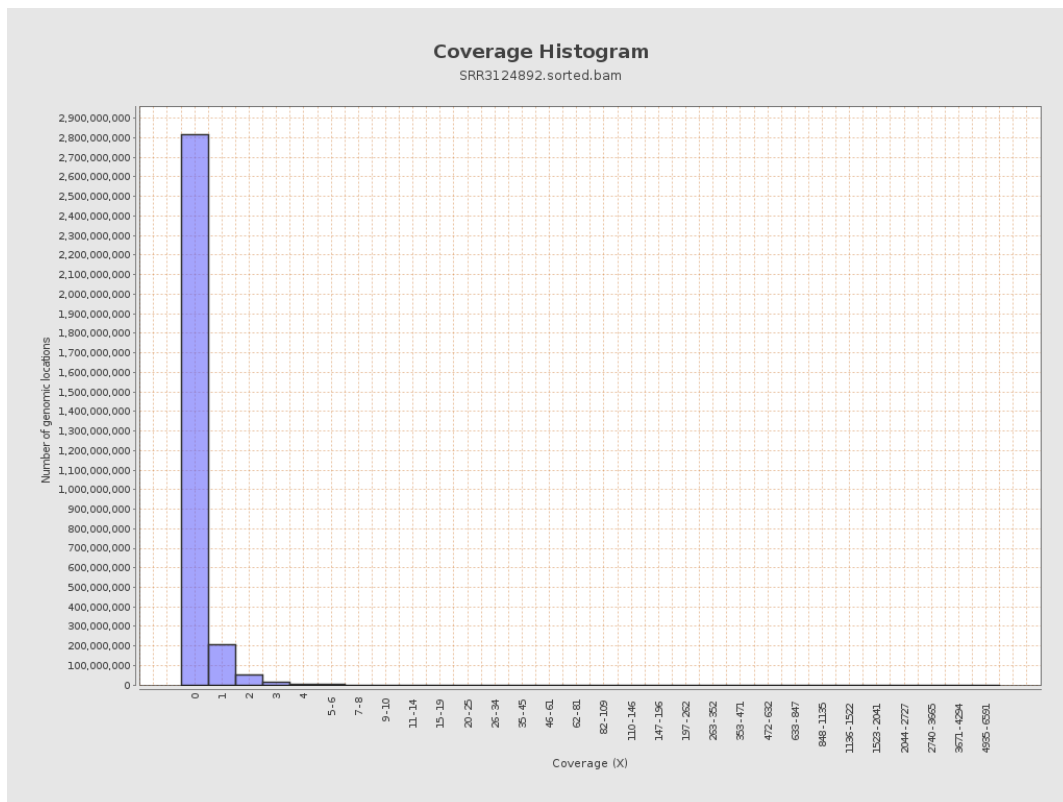
		bases	coverage	deviation
chr1	249250621	40899846	0.1641	1.9644
chr2	243199373	32192687	0.1324	1.4641
chr3	198022430	25123317	0.1269	0.5573
chr4	191154276	17080334	0.0894	0.9888
chr5	180915260	21322745	0.1179	0.4506
chr6	171115067	28991276	0.1694	1.3663
chr7	159138663	22220748	0.1396	1.6207
chr8	146364022	25613121	0.175	0.7654
chr9	141213431	12330803	0.0873	1.6879
chr10	135534747	22852276	0.1686	9.052
chr11	135006516	21260190	0.1575	1.3984
chr12	133851895	17186867	0.1284	0.4554
chr13	115169878	19852319	0.1724	0.5398
chr14	107349540	7144461	0.0666	0.383
chr15	102531392	13135235	0.1281	0.4653
chr16	90354753	14321729	0.1585	1.5922
chr17	81195210	11903736	0.1466	1.6431
chr18	78077248	10143924	0.1299	1.9556
chr19	59128983	5676869	0.096	1.2259
chr20	63025520	7776315	0.1234	0.5075
chr21	48129895	6100224	0.1267	0.6227
chr22	51304566	4674688	0.0911	0.4102
chrMT	16571	196320	11.8472	7.8328
chrX	155270560	14333198	0.0923	0.6381

chrY	59373566	1081087	0.0182	1.2084
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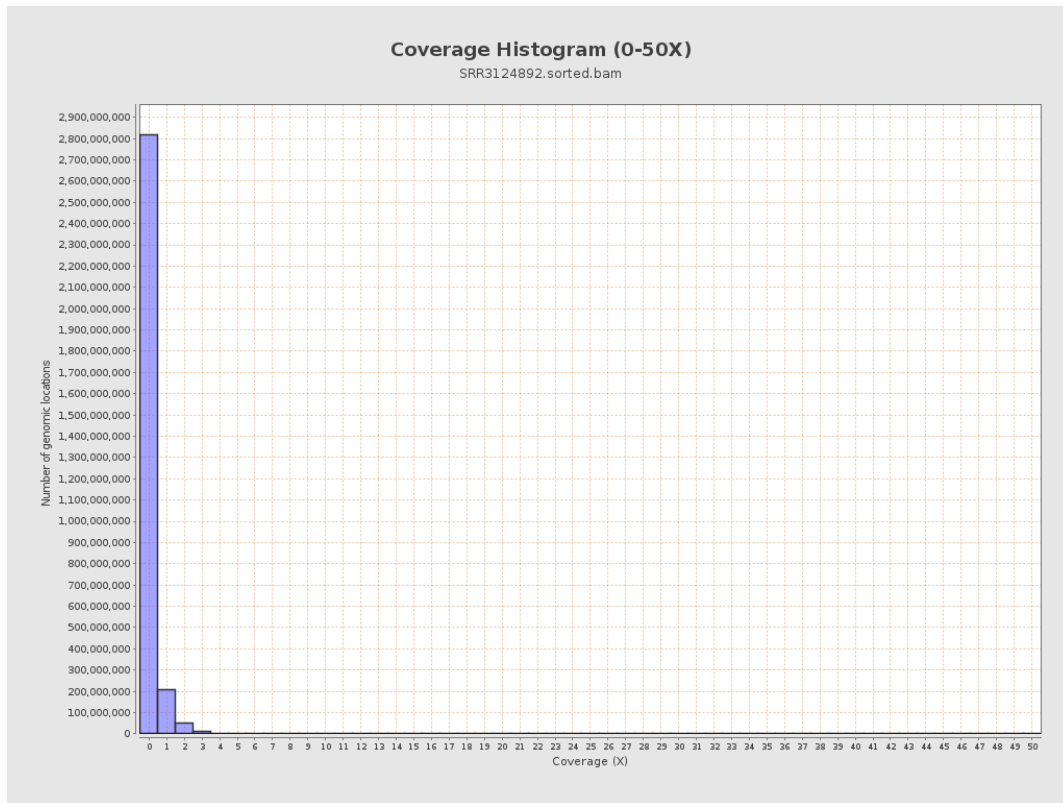
3. Results : Coverage across reference



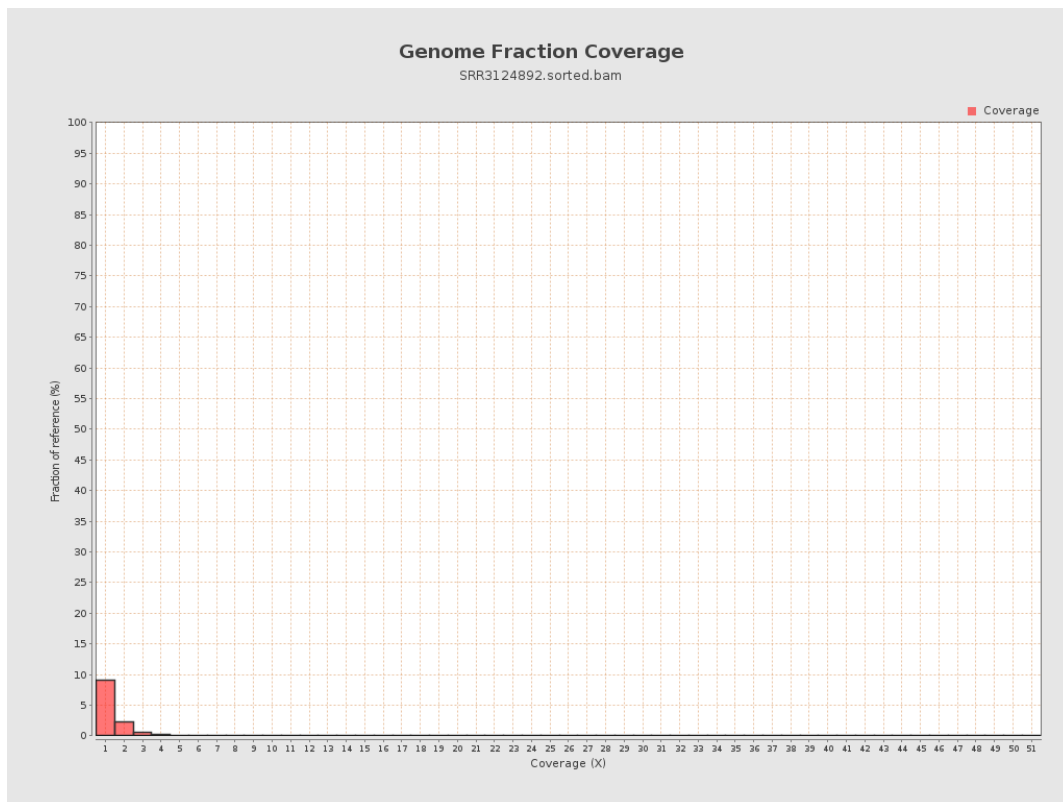
4. Results : Coverage Histogram



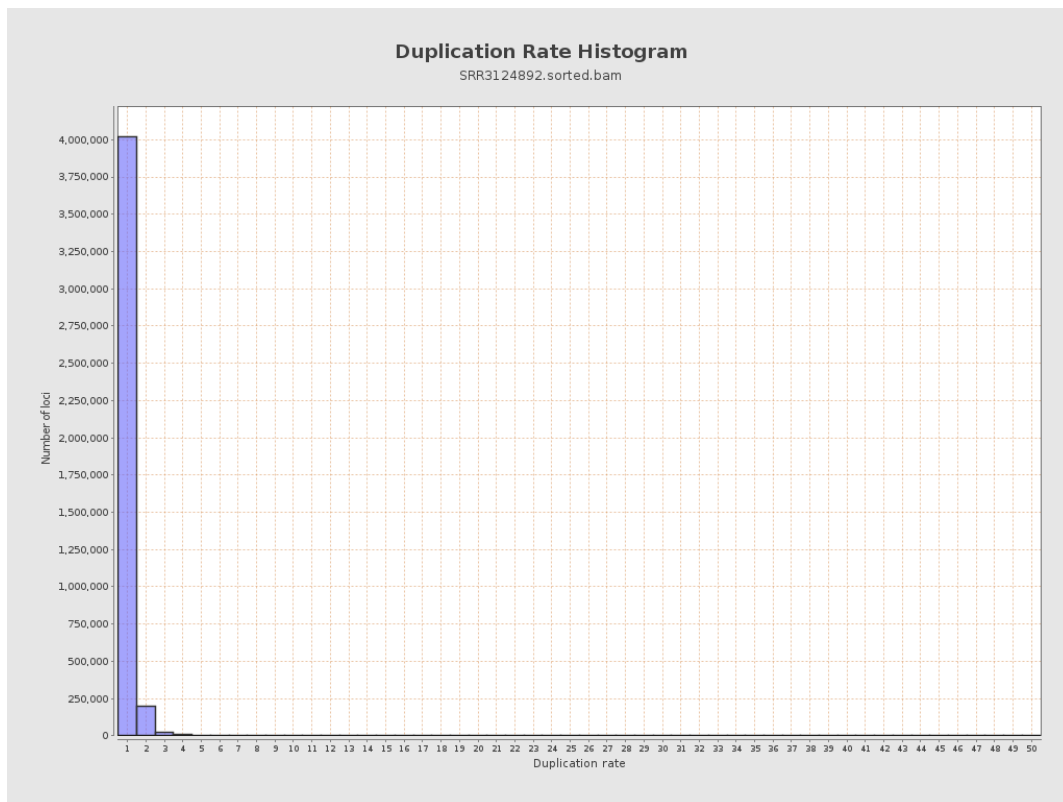
5. Results : Coverage Histogram (0-50X)



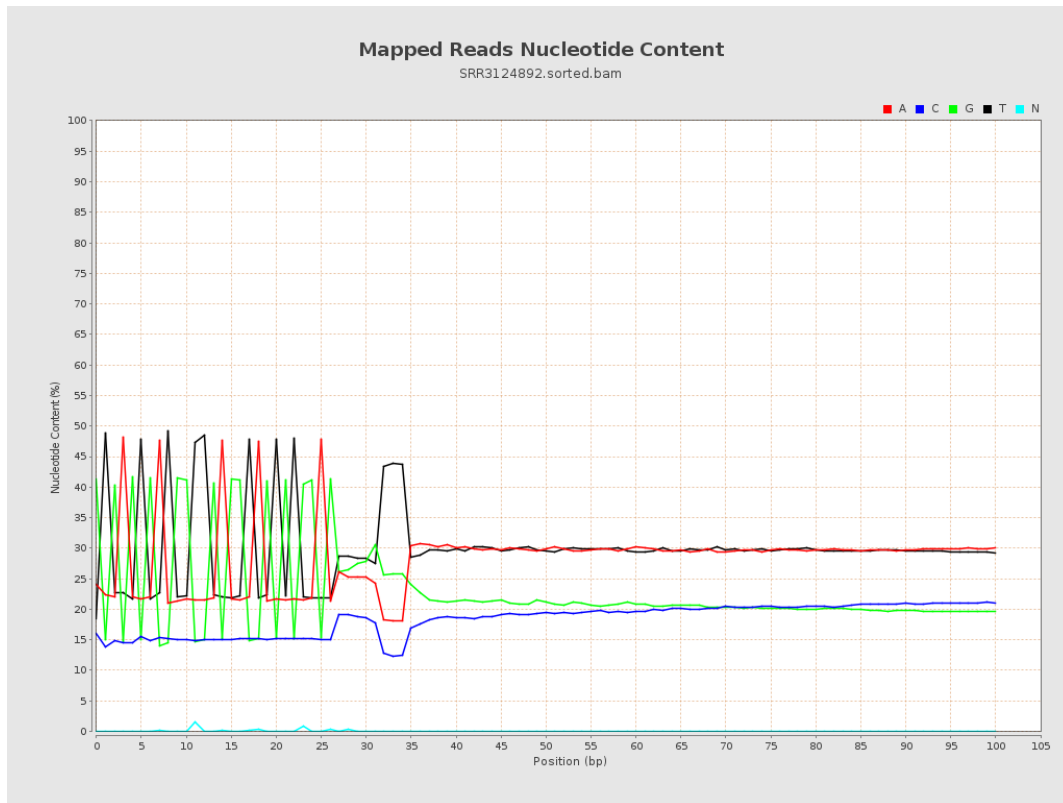
6. Results : Genome Fraction Coverage



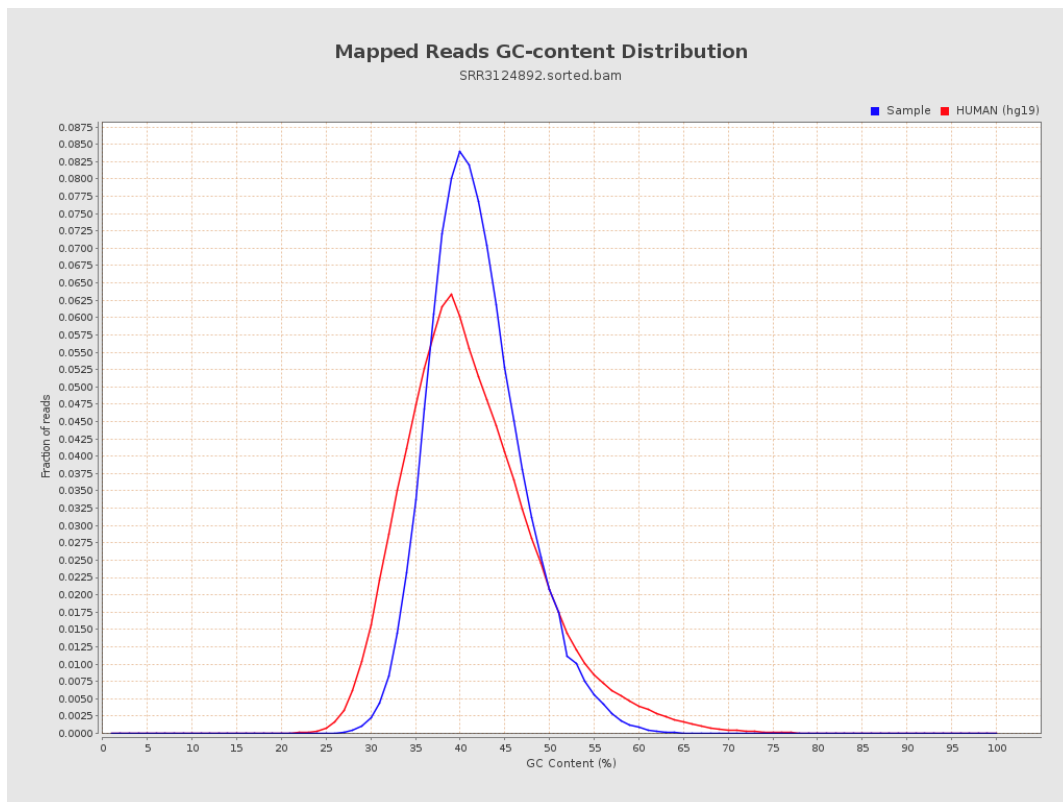
7. Results : Duplication Rate Histogram



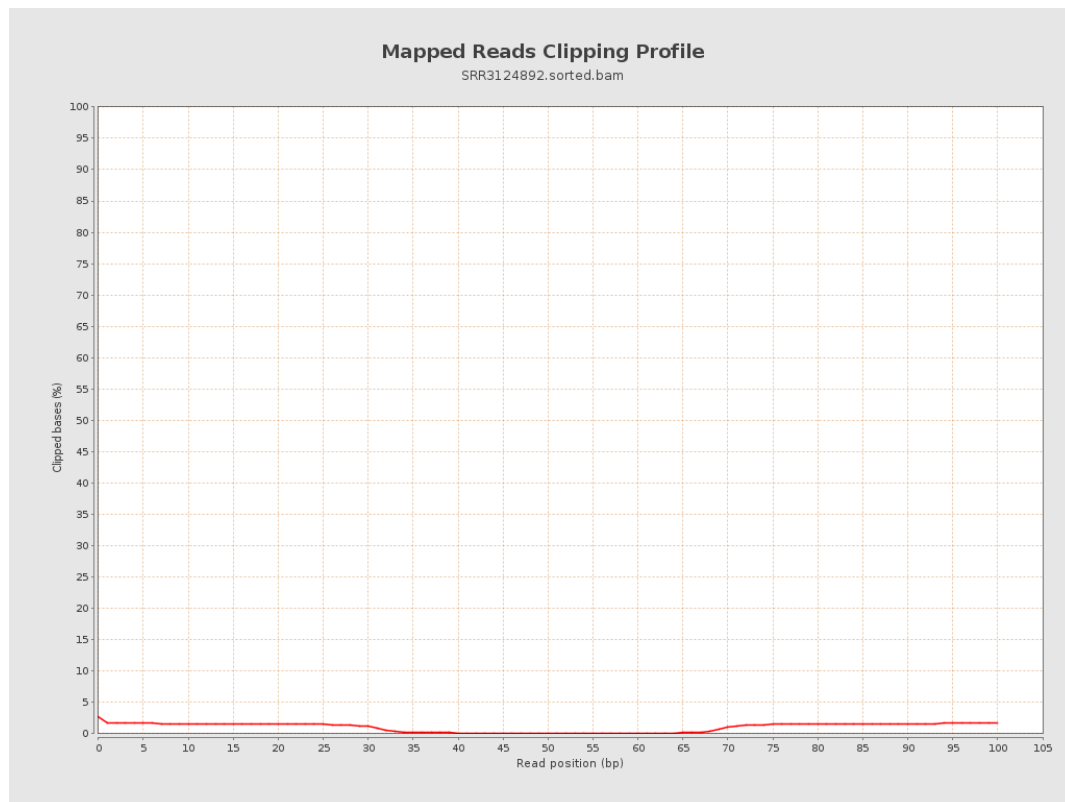
8. Results : Mapped Reads Nucleotide Content



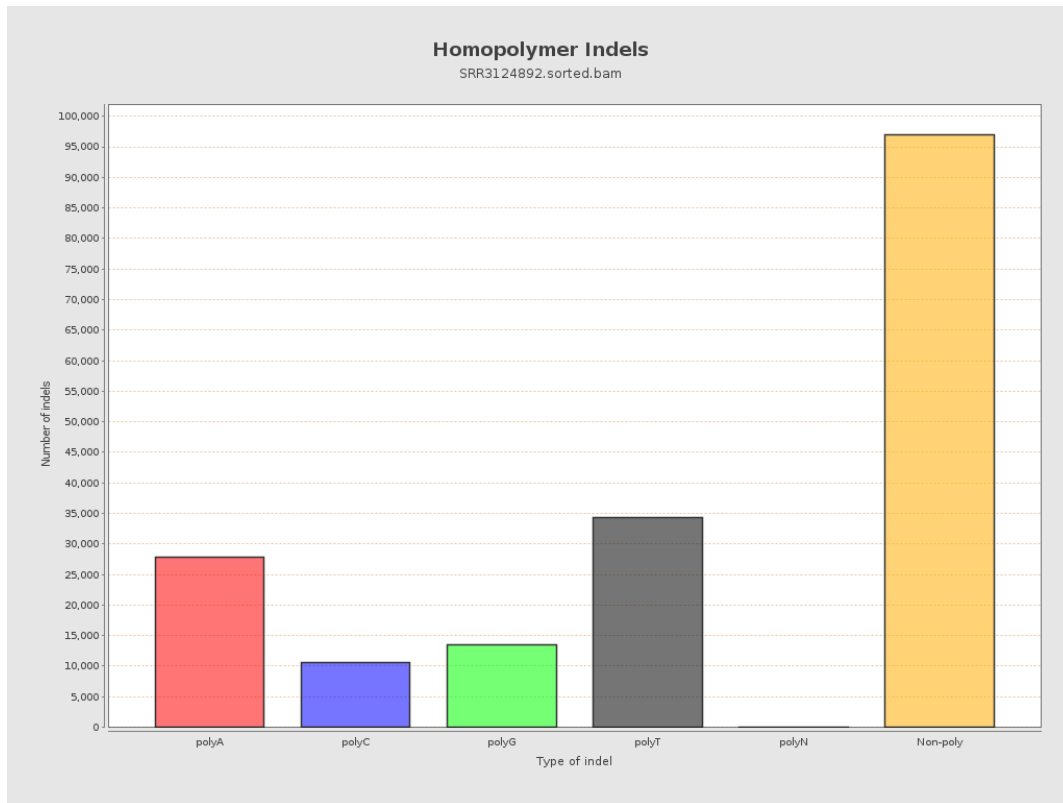
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



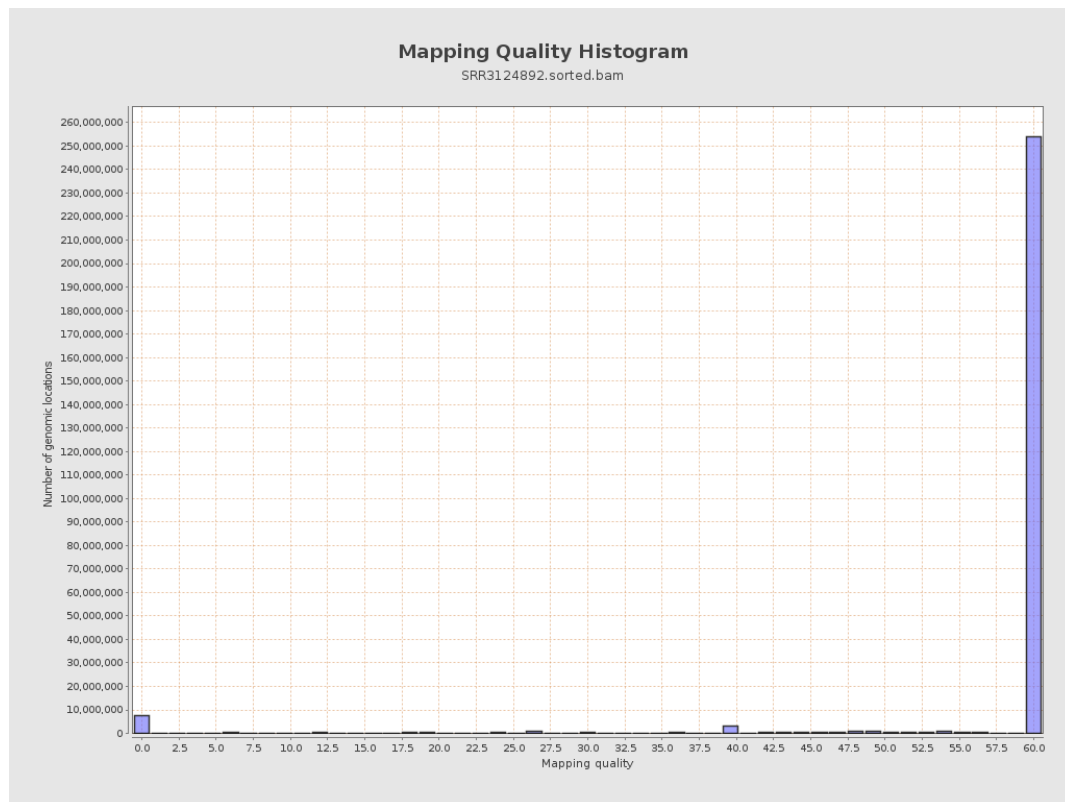
11. Results : Homopolymer Indels



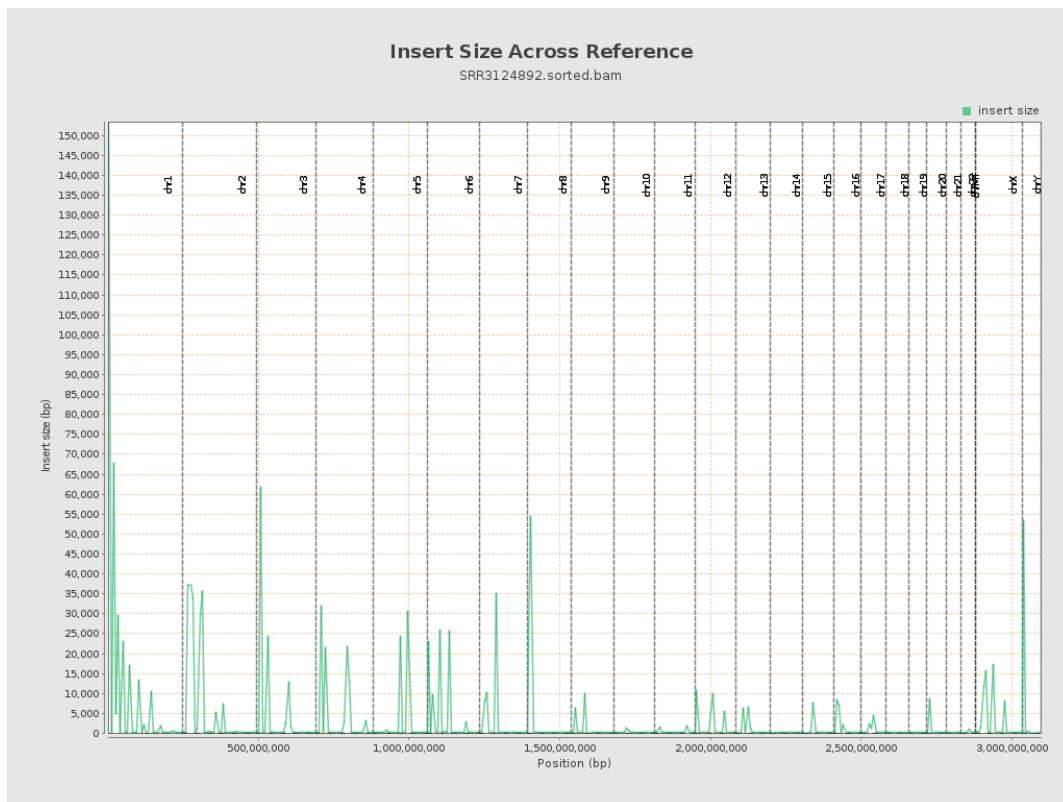
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

