

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:02:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124867.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_SRR3124867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124867_1.fastq.gz SRR3124867_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:02:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,838,788
Mapped reads	3,807,348 / 99.18%
Unmapped reads	31,440 / 0.82%
Mapped paired reads	3,807,348 / 99.18%
Mapped reads, first in pair	1,906,306 / 49.66%
Mapped reads, second in pair	1,901,042 / 49.52%
Mapped reads, both in pair	3,797,240 / 98.92%
Mapped reads, singletons	10,108 / 0.26%
Secondary alignments	0
Supplementary alignments	13,188 / 0.34%
Read min/max/mean length	30 / 101 / 101.13
Duplicated reads (estimated)	211,880 / 5.52%
Duplication rate	4.35%
Clipped reads	1,842,884 / 48.01%

2.2. ACGT Content

Number/percentage of A's	92,093,873 / 27.91%
Number/percentage of C's	61,972,445 / 18.78%
Number/percentage of T's	97,165,540 / 29.45%
Number/percentage of G's	78,625,799 / 23.83%
Number/percentage of N's	124,626 / 0.04%

GC Percentage	42.61%
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2.3. Coverage

Mean	0.1066
Standard Deviation	0.7256

2.4. Mapping Quality

Mean Mapping Quality	52.93
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2.5. Insert size

Mean	24,072.8
Standard Deviation	1,458,399.59
P25/Median/P75	143 / 193 / 267

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	2,189,831
Insertions	40,265
Mapped reads with at least one insertion	1.03%
Deletions	99,450
Mapped reads with at least one deletion	2.56%
Homopolymer indels	48.39%

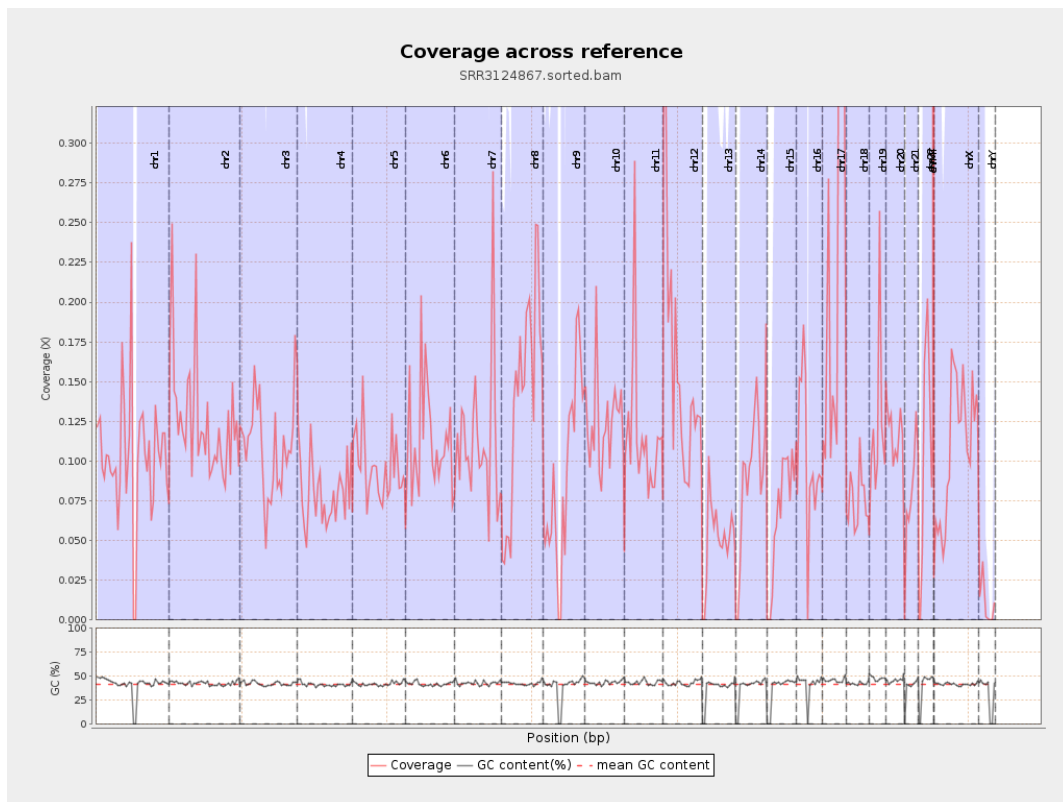
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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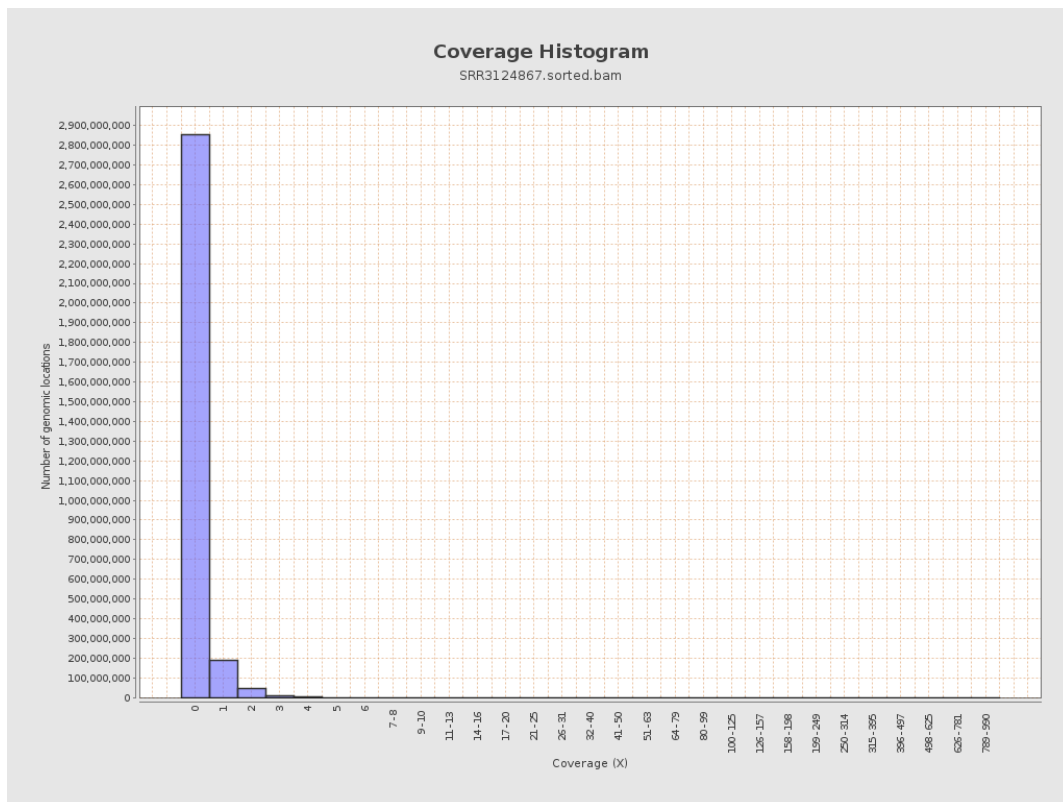
		bases	coverage	deviation
chr1	249250621	25382542	0.1018	0.9431
chr2	243199373	30595853	0.1258	0.866
chr3	198022430	21578292	0.109	0.4035
chr4	191154276	15159210	0.0793	0.4593
chr5	180915260	17333906	0.0958	0.3788
chr6	171115067	19038674	0.1113	0.6962
chr7	159138663	18200798	0.1144	1.0144
chr8	146364022	20442742	0.1397	0.6489
chr9	141213431	12887927	0.0913	0.8079
chr10	135534747	16737559	0.1235	1.1796
chr11	135006516	15652280	0.1159	0.7206
chr12	133851895	21383288	0.1598	0.5217
chr13	115169878	5872530	0.051	0.268
chr14	107349540	9401989	0.0876	0.3752
chr15	102531392	6877828	0.0671	0.3184
chr16	90354753	9342122	0.1034	0.588
chr17	81195210	17284105	0.2129	1.5739
chr18	78077248	5976361	0.0765	0.8719
chr19	59128983	7279996	0.1231	0.5996
chr20	63025520	7232662	0.1148	0.4269
chr21	48129895	3847838	0.0799	0.3998
chr22	51304566	5179914	0.101	0.4111
chrMT	16571	116742	7.045	5.4966
chrX	155270560	16738990	0.1078	0.4731

chrY	59373566	601630	0.0101	0.548
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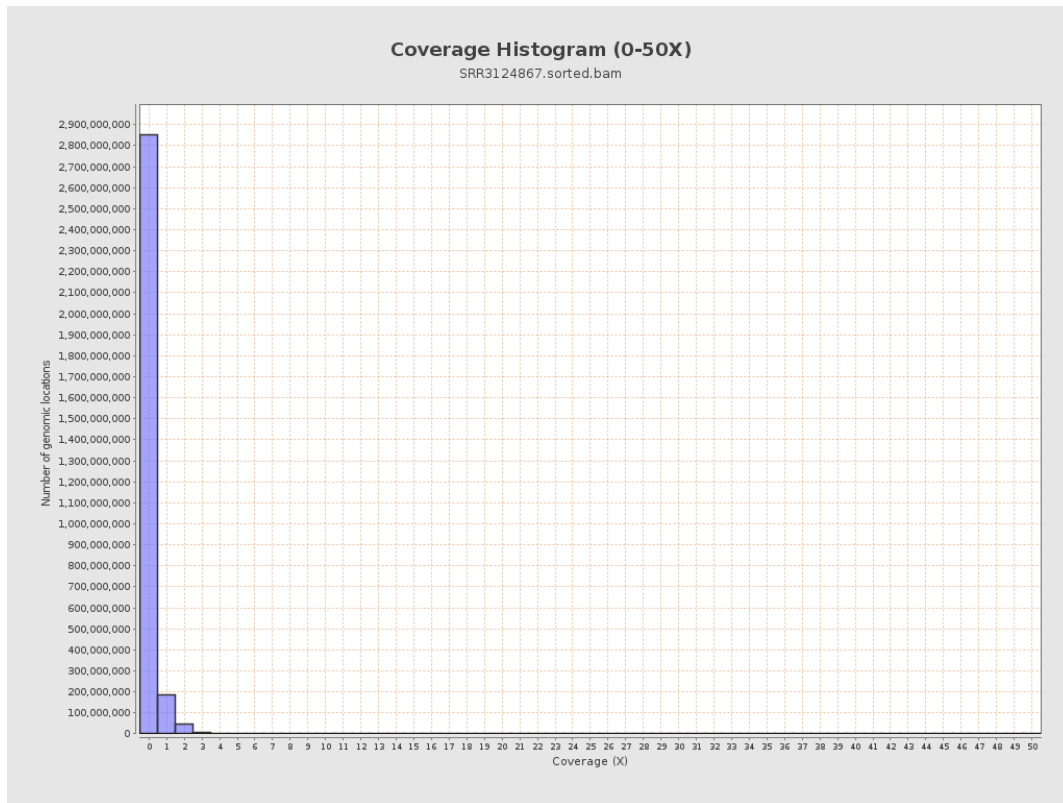
3. Results : Coverage across reference



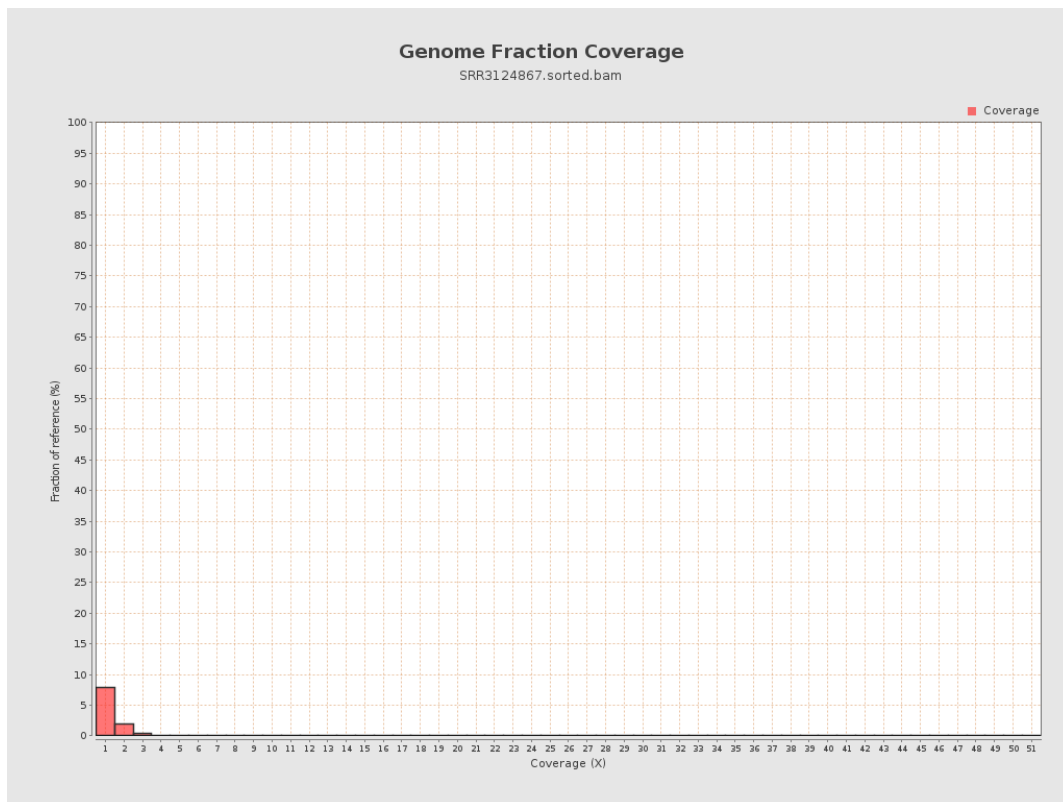
4. Results : Coverage Histogram



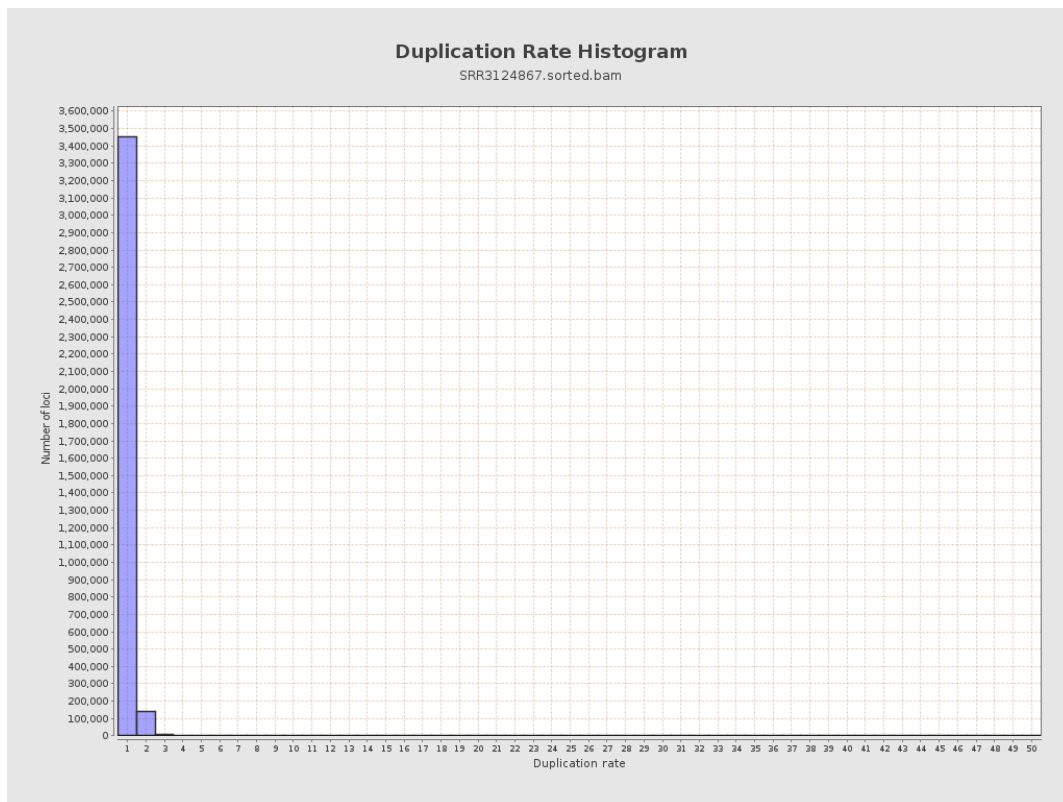
5. Results : Coverage Histogram (0-50X)



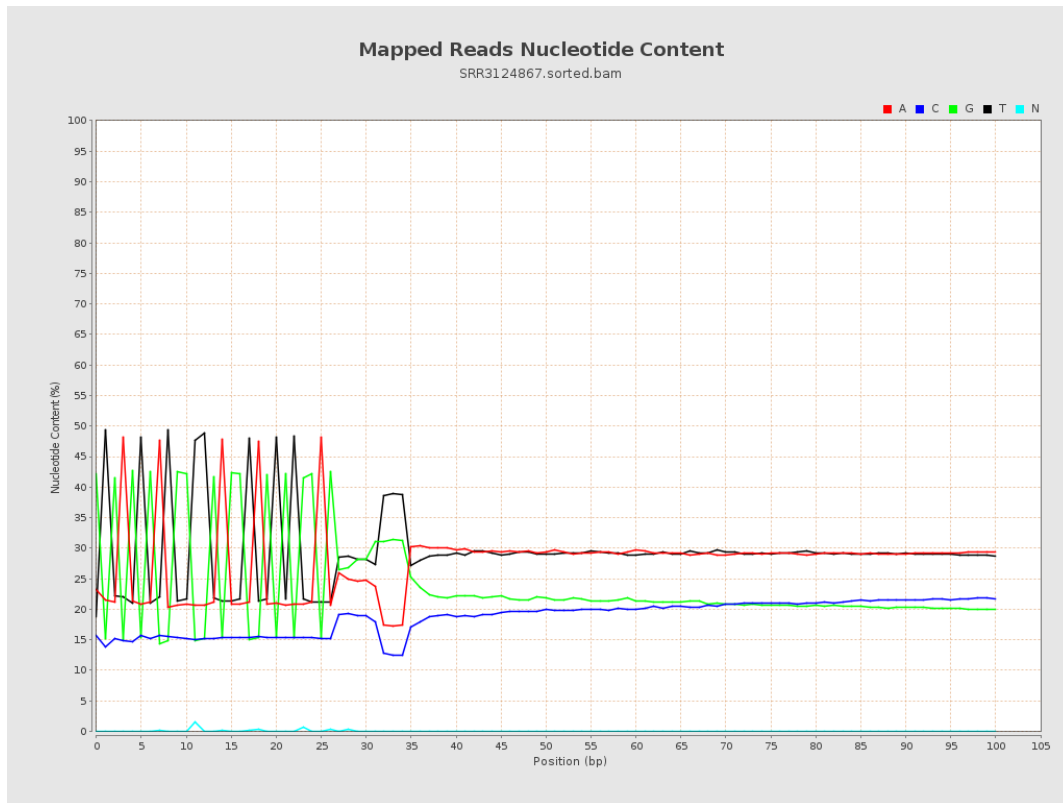
6. Results : Genome Fraction Coverage



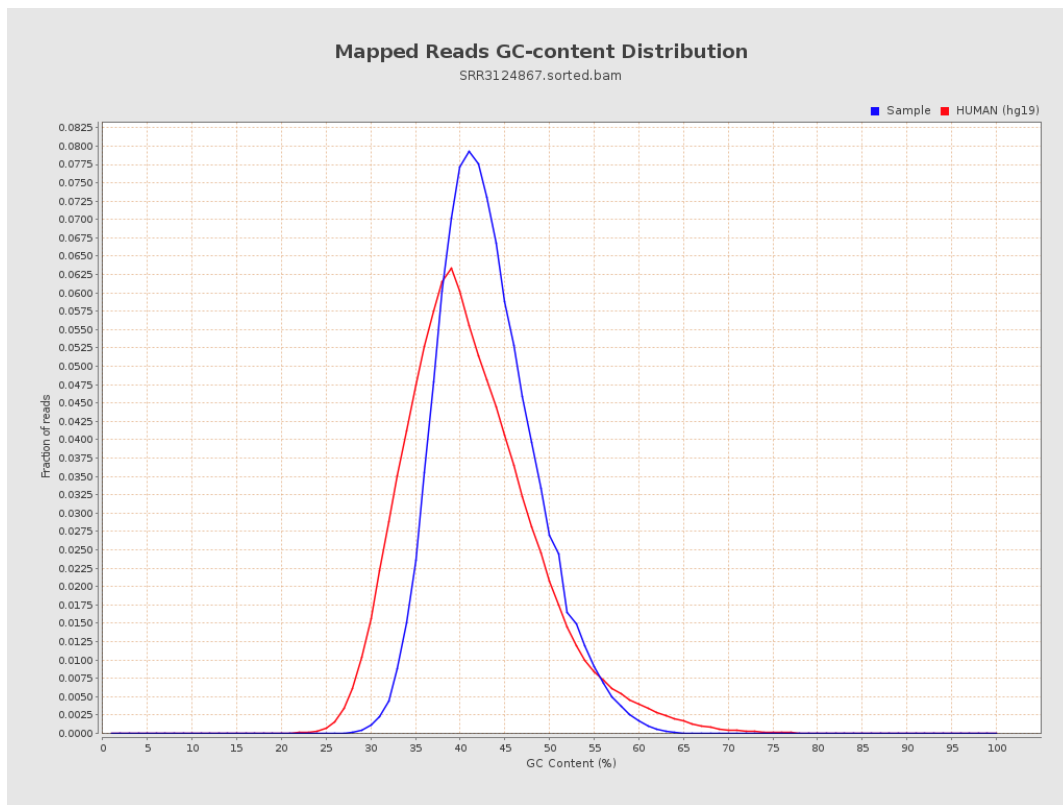
7. Results : Duplication Rate Histogram



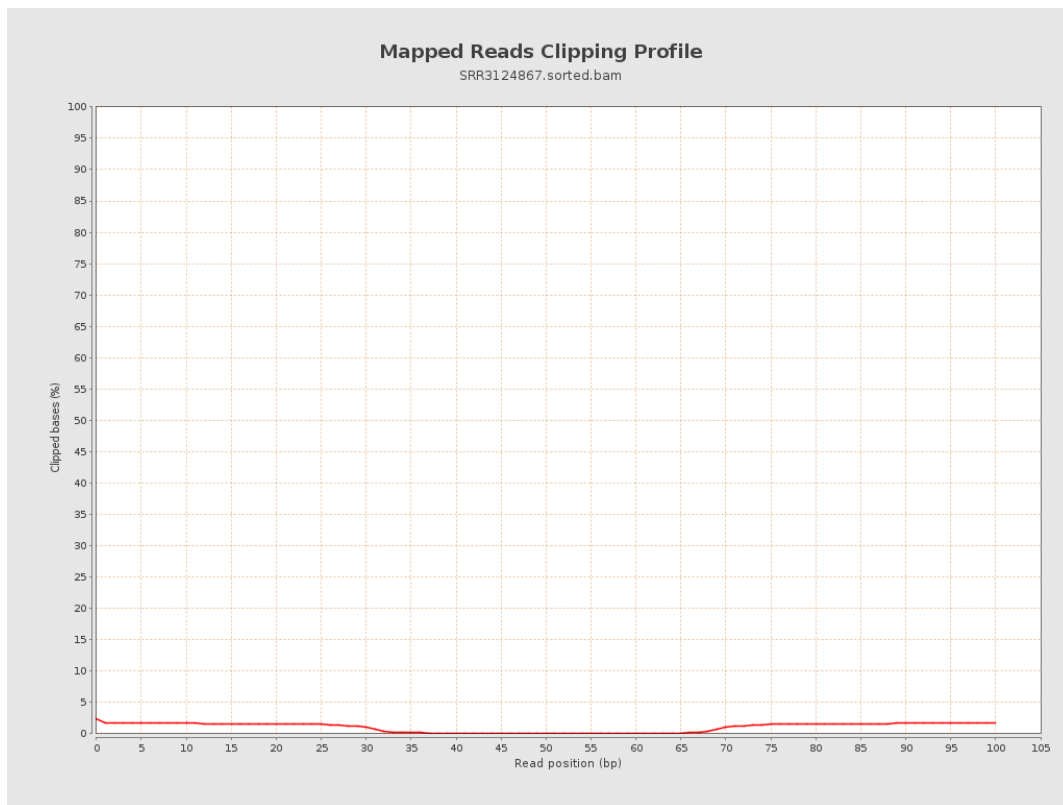
8. Results : Mapped Reads Nucleotide Content



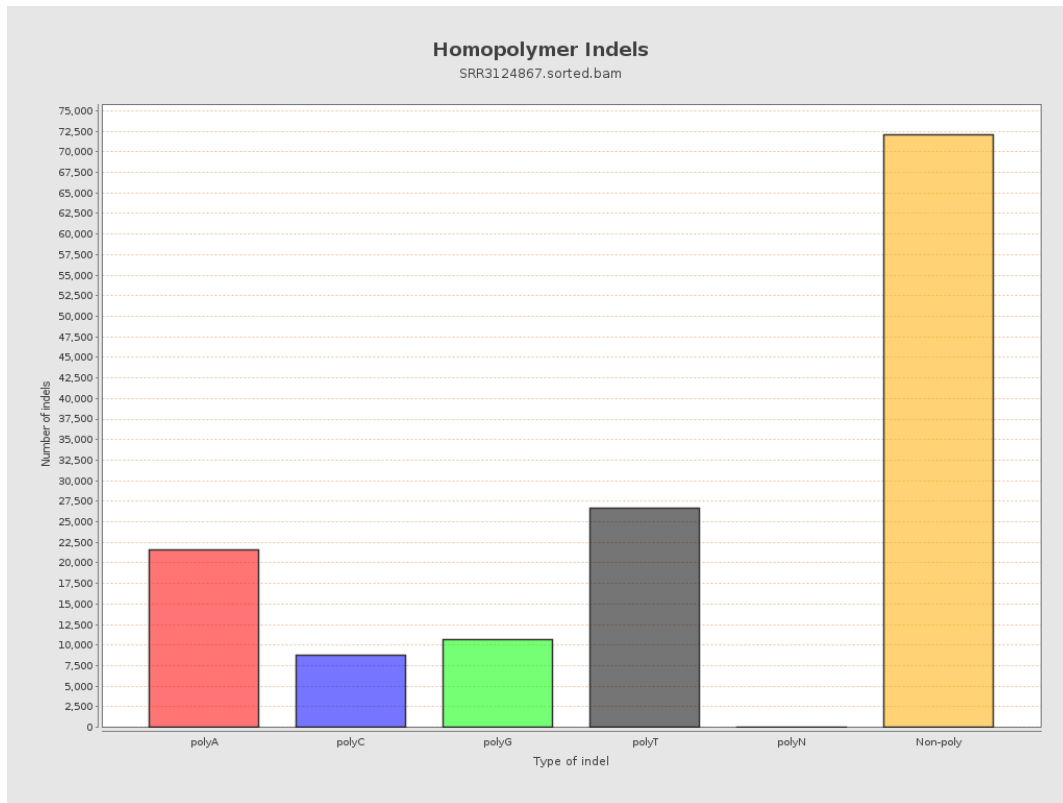
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



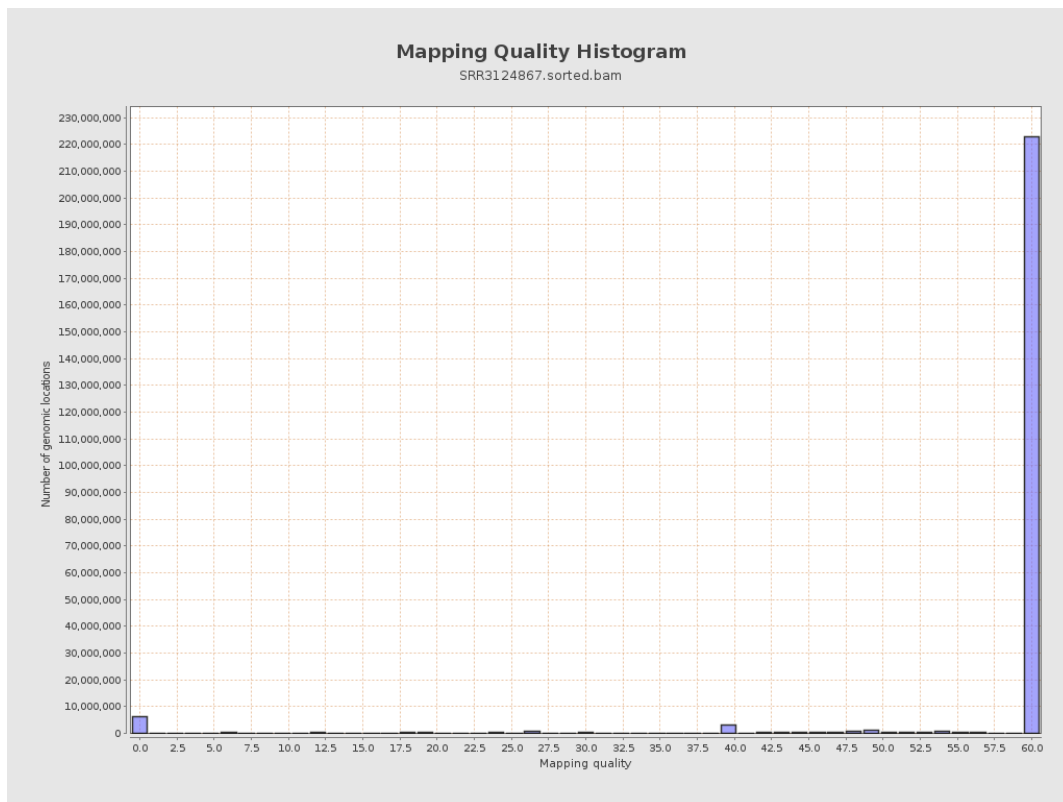
11. Results : Homopolymer Indels



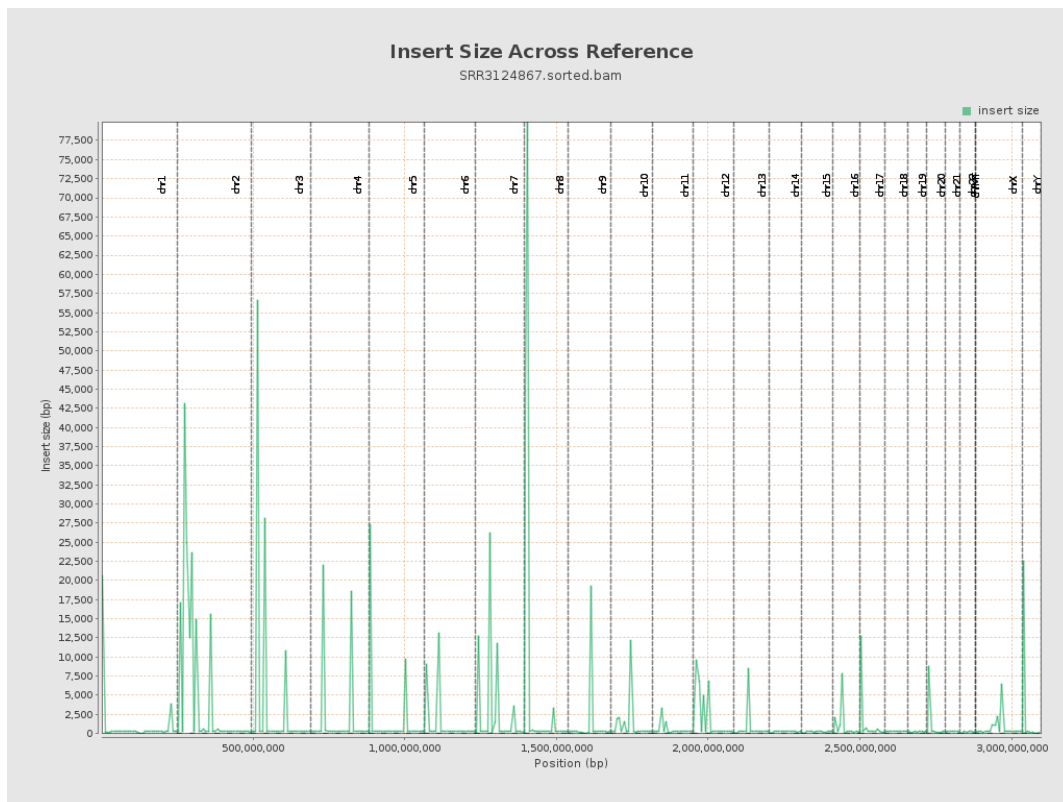
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

