

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 16:53:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124843.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_SRR3124843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124843_1.fastq.gz SRR3124843_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 16:53:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	83,864,376
Mapped reads	80,621,588 / 96.13%
Unmapped reads	3,242,788 / 3.87%
Mapped paired reads	80,621,588 / 96.13%
Mapped reads, first in pair	40,891,353 / 48.76%
Mapped reads, second in pair	39,730,235 / 47.37%
Mapped reads, both in pair	79,180,760 / 94.42%
Mapped reads, singletons	1,440,828 / 1.72%
Secondary alignments	0
Supplementary alignments	2,093,845 / 2.5%
Read min/max/mean length	30 / 150 / 151.18
Duplicated reads (estimated)	32,363,463 / 38.59%
Duplication rate	32.53%
Clipped reads	60,450,526 / 72.08%

2.2. ACGT Content

Number/percentage of A's	2,830,961,043 / 28.87%
Number/percentage of C's	1,963,664,893 / 20.02%
Number/percentage of T's	2,862,519,620 / 29.19%
Number/percentage of G's	2,149,122,691 / 21.92%
Number/percentage of N's	146,041 / 0%

GC Percentage	41.94%
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2.3. Coverage

Mean	3.1703
Standard Deviation	50.3723

2.4. Mapping Quality

Mean Mapping Quality	53.01
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2.5. Insert size

Mean	110,975.92
Standard Deviation	3,188,053.29
P25/Median/P75	116 / 158 / 217

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	112,119,582
Insertions	1,942,065
Mapped reads with at least one insertion	2.2%
Deletions	3,269,672
Mapped reads with at least one deletion	3.85%
Homopolymer indels	41.39%

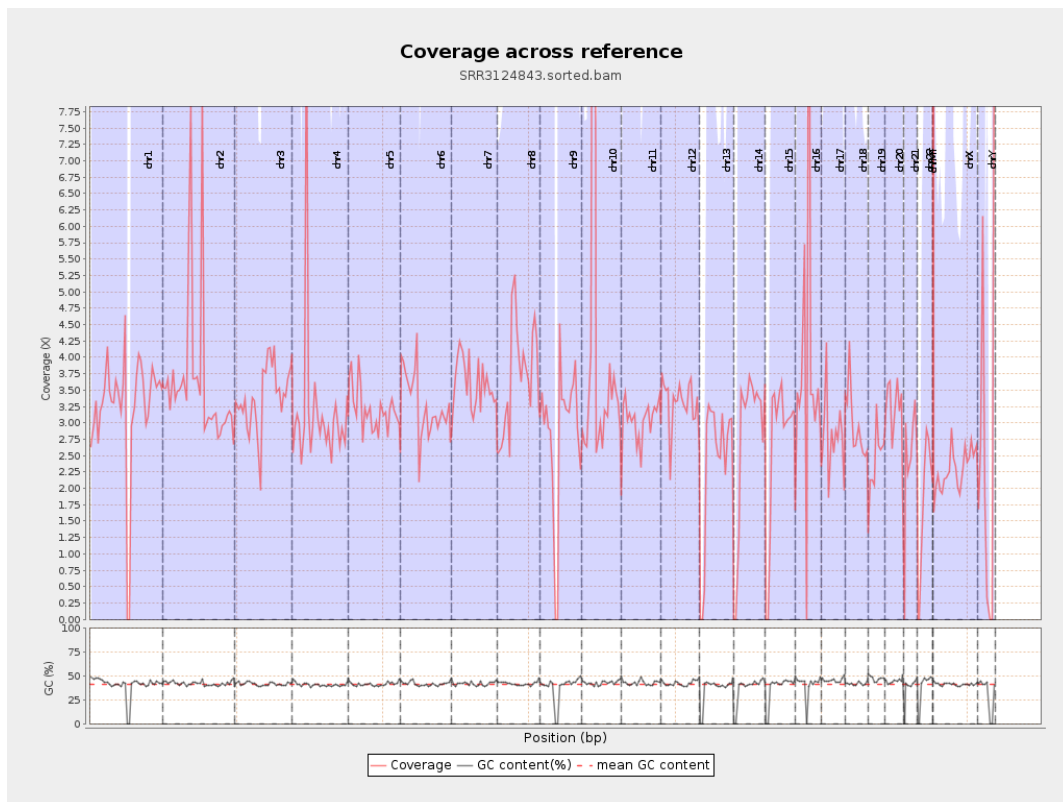
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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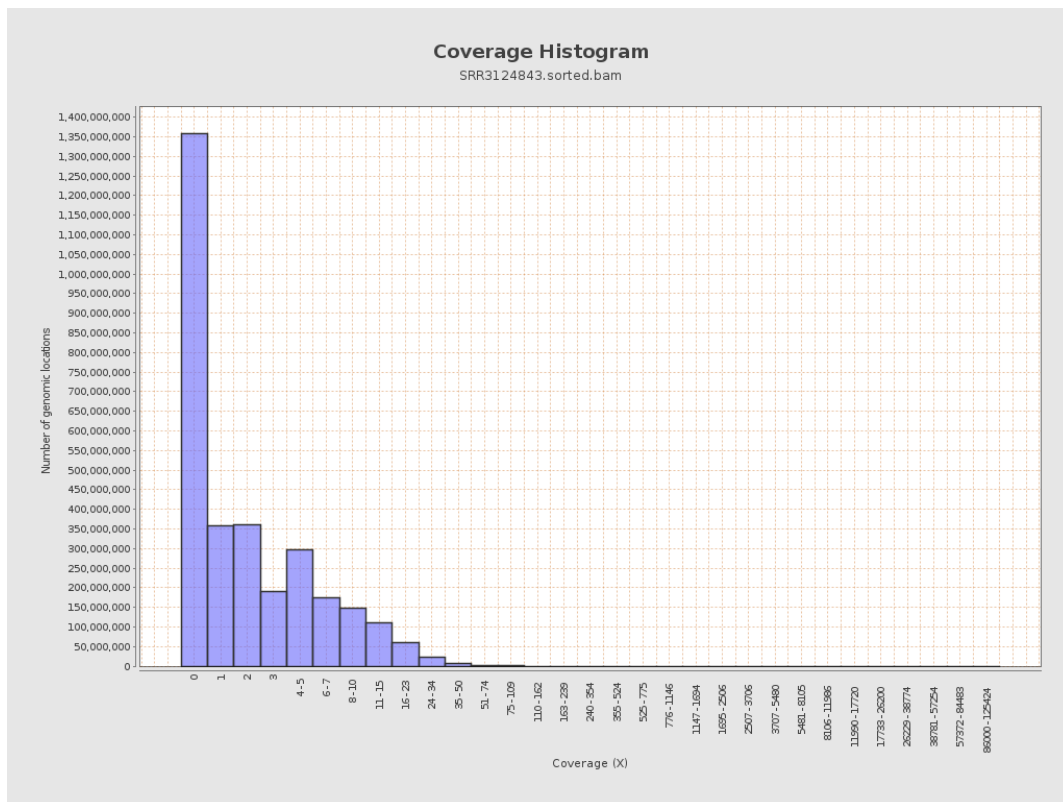
		bases	coverage	deviation
chr1	249250621	809746938	3.2487	25.399
chr2	243199373	891831687	3.6671	66.6724
chr3	198022430	670170298	3.3843	8.9052
chr4	191154276	609808901	3.1901	42.9017
chr5	180915260	578334907	3.1967	8.031
chr6	171115067	558659909	3.2648	12.7695
chr7	159138663	571054731	3.5884	21.7749
chr8	146364022	543221731	3.7114	10.7496
chr9	141213431	404333556	2.8633	38.7109
chr10	135534747	572952981	4.2274	186.6118
chr11	135006516	410184999	3.0383	14.6469
chr12	133851895	444842089	3.3234	6.2755
chr13	115169878	275343735	2.3908	4.8992
chr14	107349540	299550731	2.7904	8.5397
chr15	102531392	269354582	2.627	5.6869
chr16	90354753	354357719	3.9218	71.9206
chr17	81195210	230070493	2.8335	27.978
chr18	78077248	232521346	2.9781	41.8071
chr19	59128983	145197860	2.4556	15.047
chr20	63025520	203847312	3.2344	15.422
chr21	48129895	120624890	2.5062	23.3632
chr22	51304566	92317819	1.7994	7.9325
chrMT	16571	3018032	182.1273	98.3669
chrX	155270560	356028624	2.293	8.8363

chrY	59373566	166799278	2.8093	81.578
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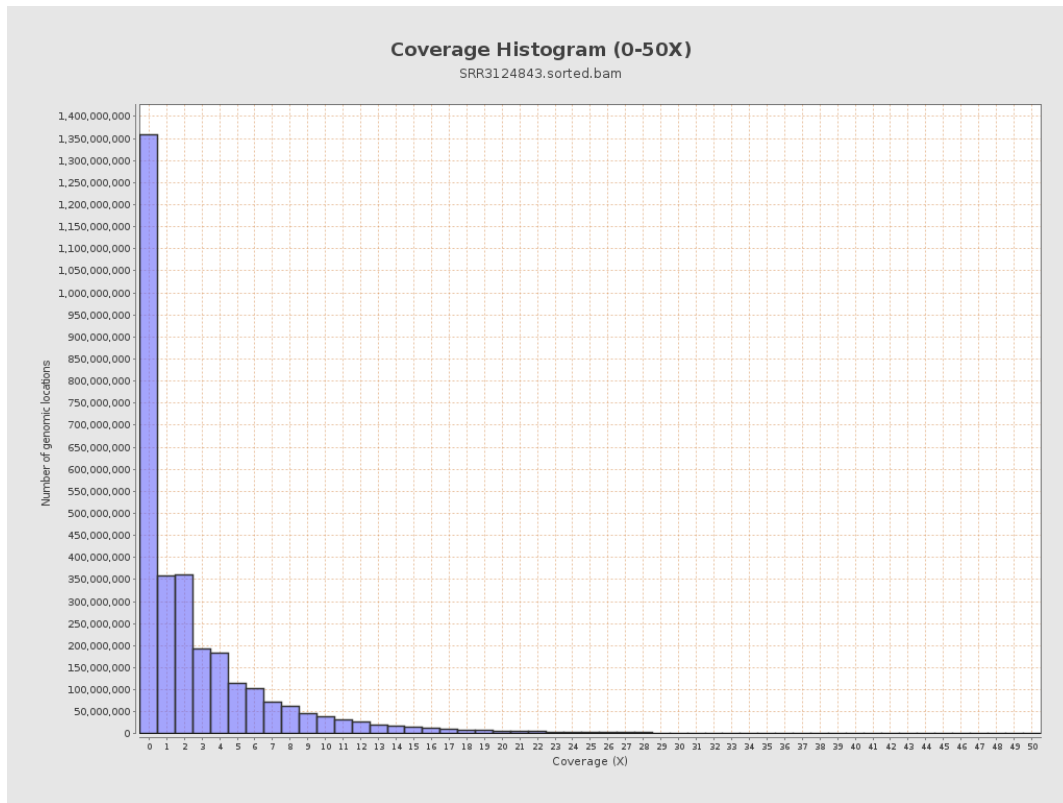
3. Results : Coverage across reference



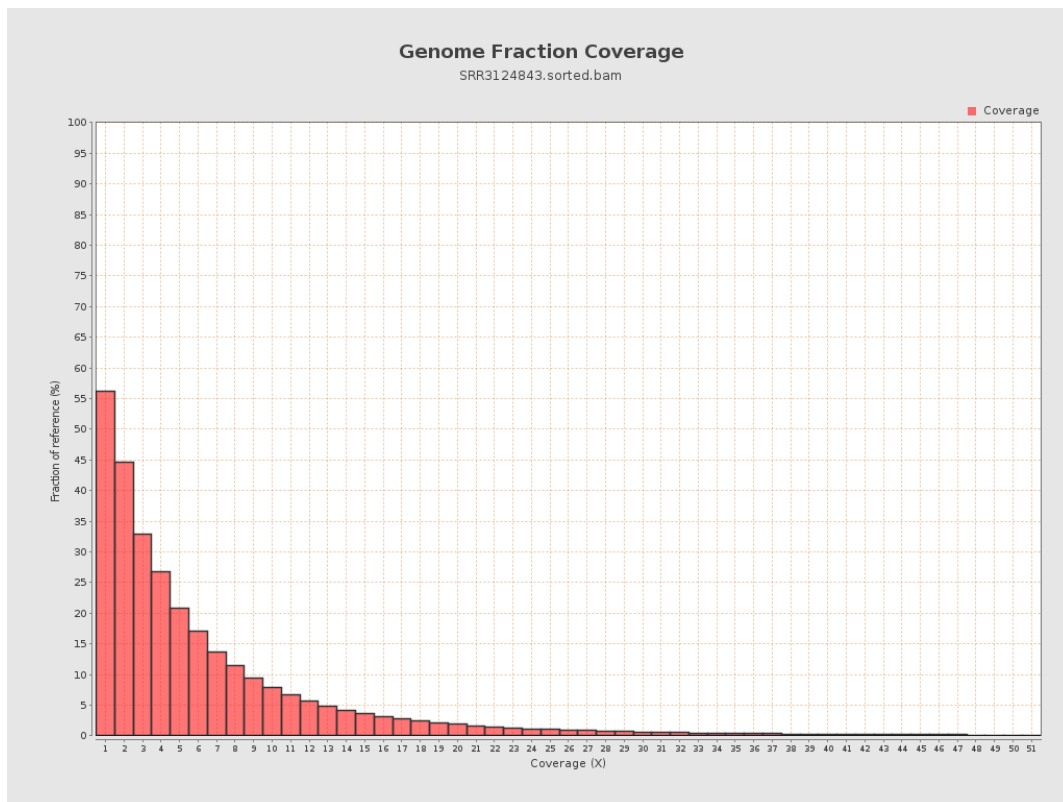
4. Results : Coverage Histogram



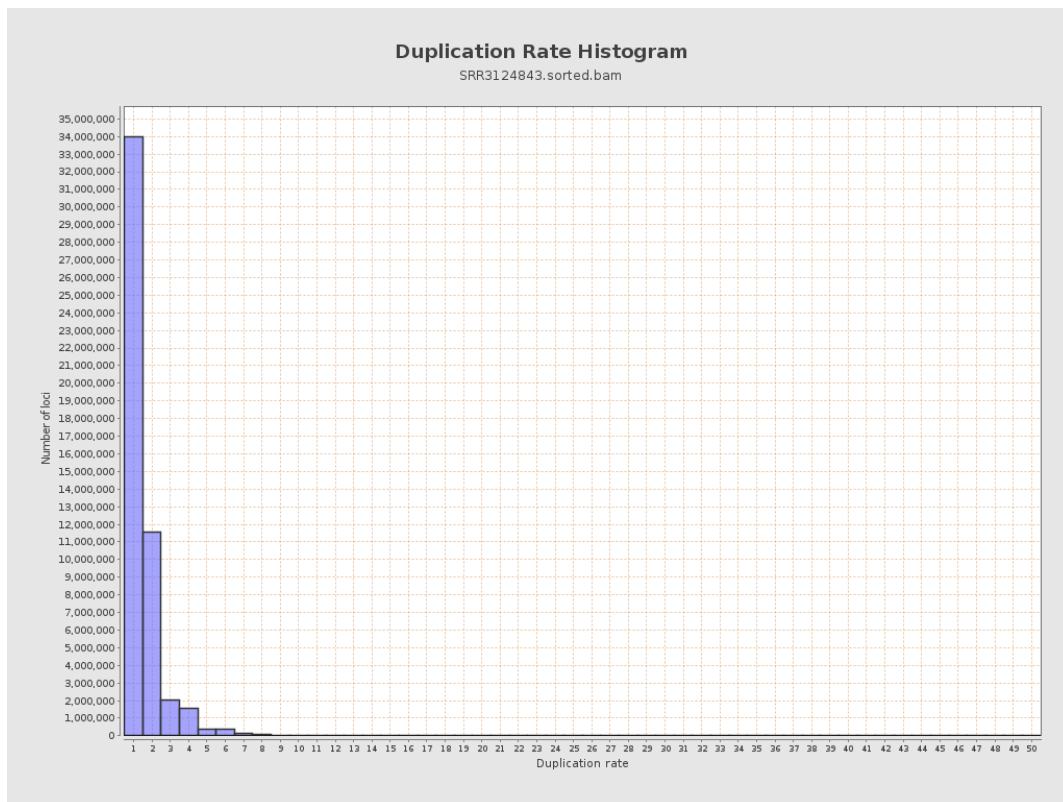
5. Results : Coverage Histogram (0-50X)



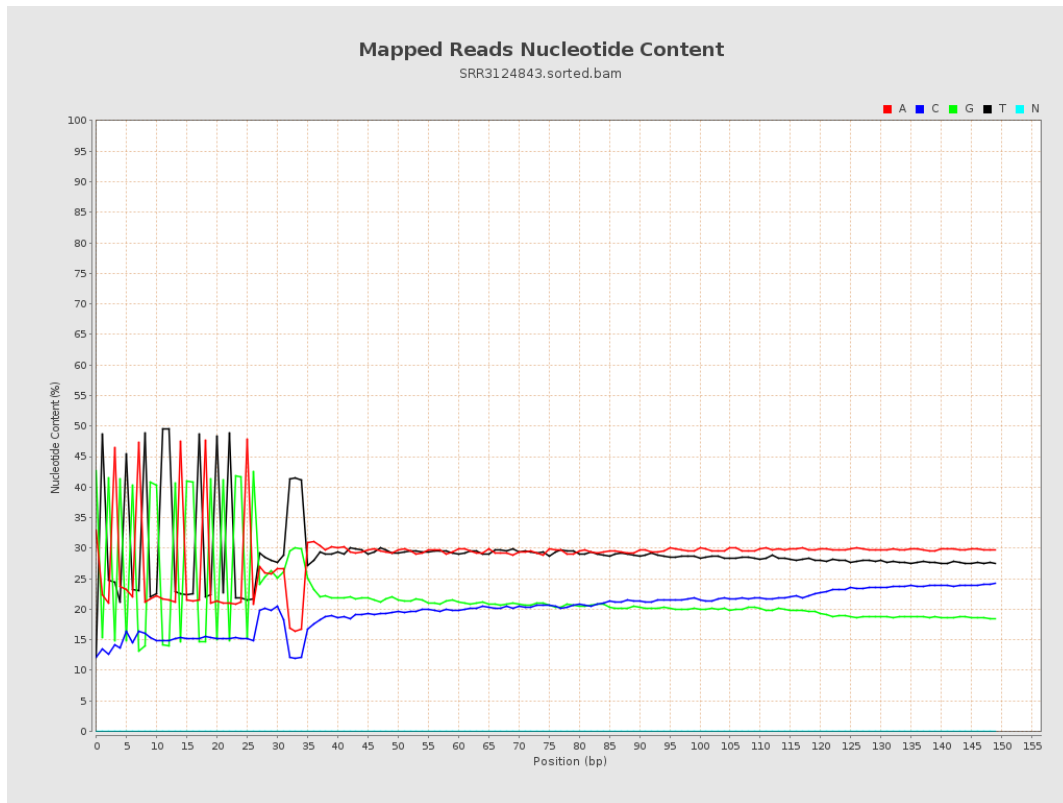
6. Results : Genome Fraction Coverage



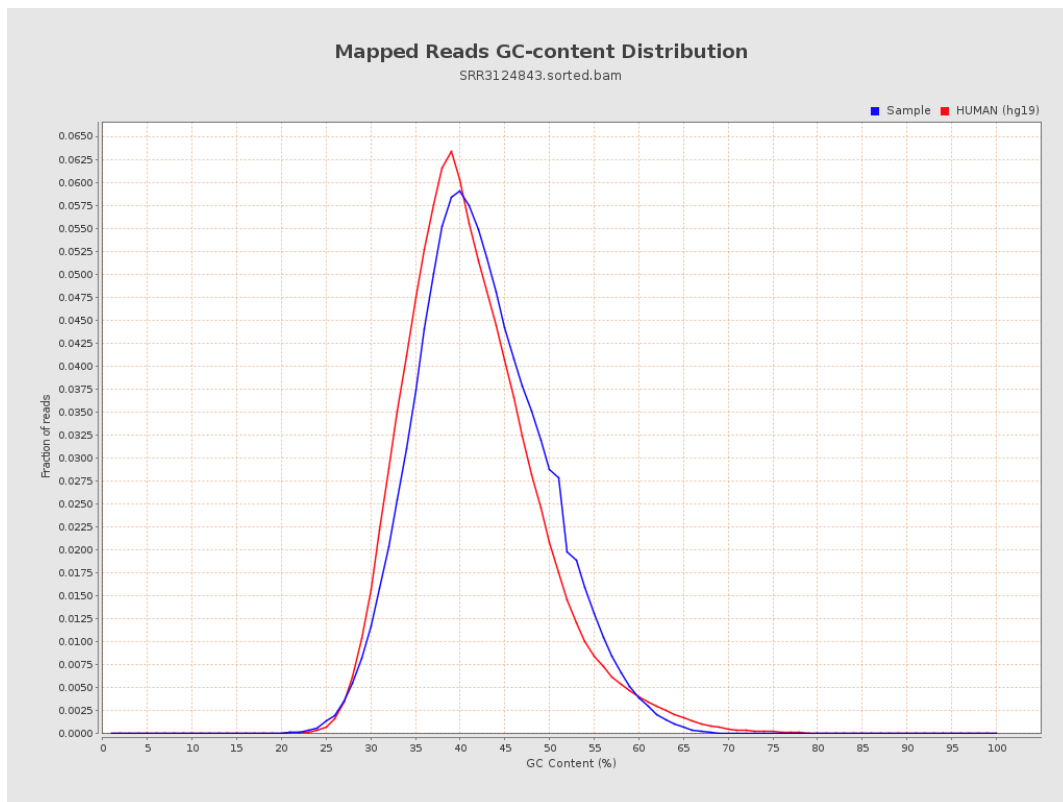
7. Results : Duplication Rate Histogram



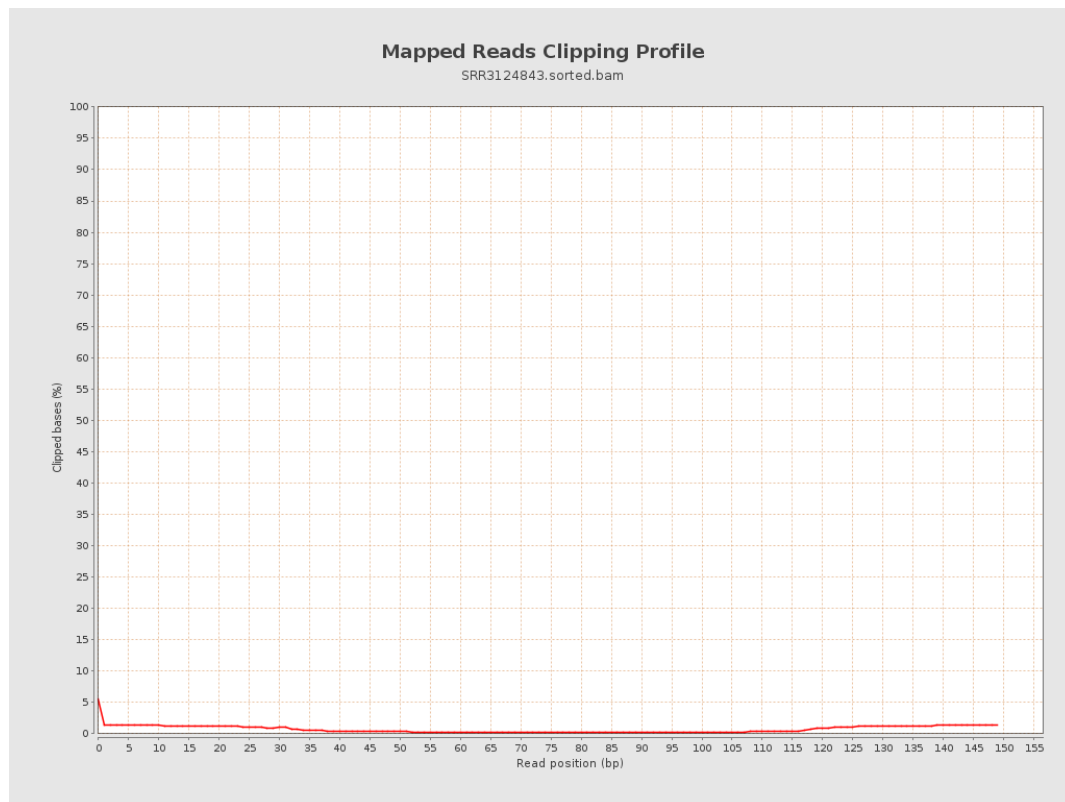
8. Results : Mapped Reads Nucleotide Content



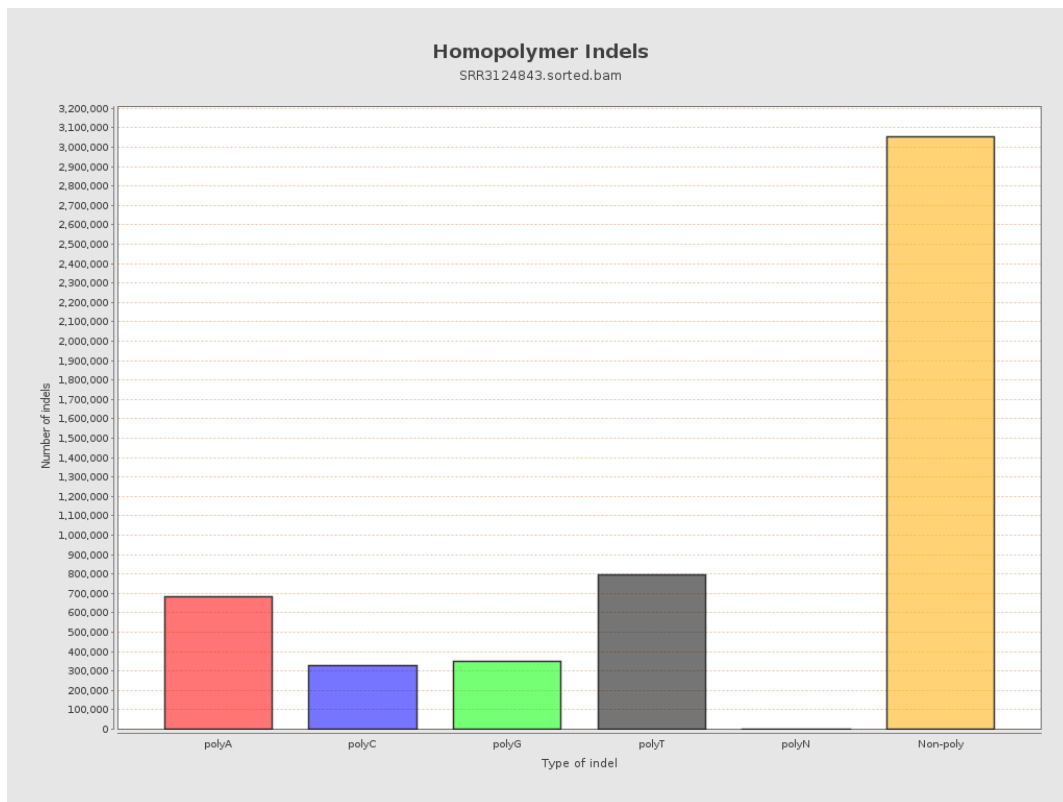
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



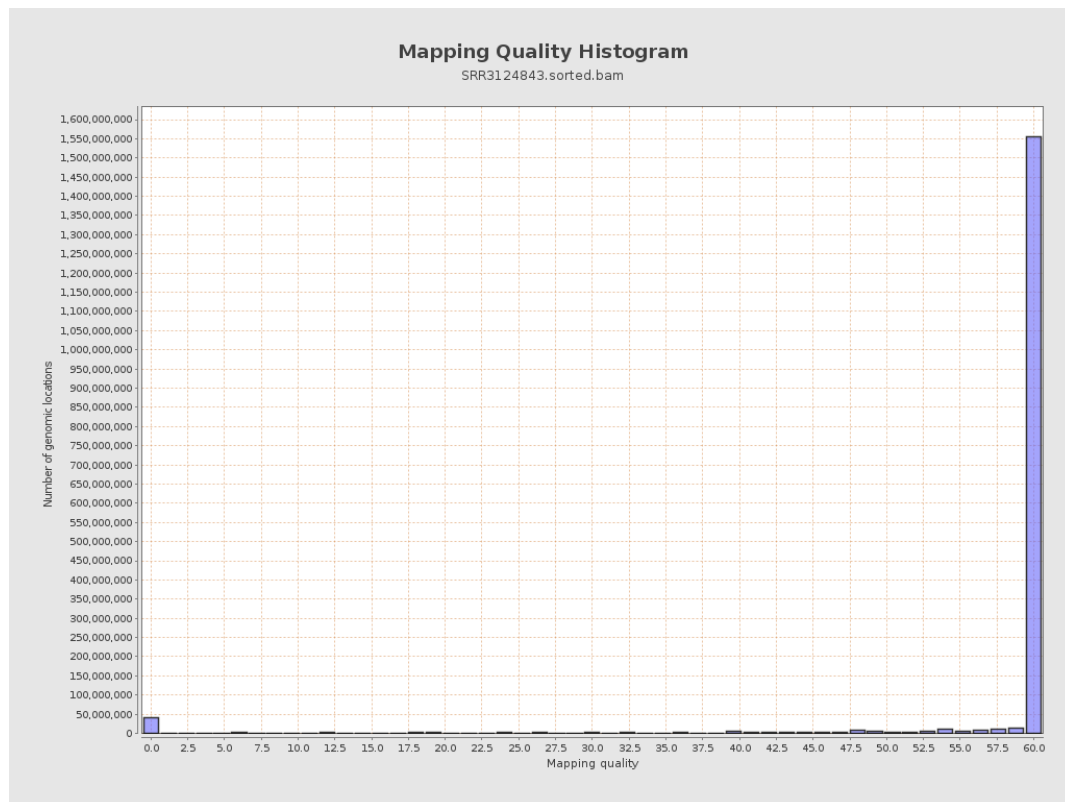
11. Results : Homopolymer Indels



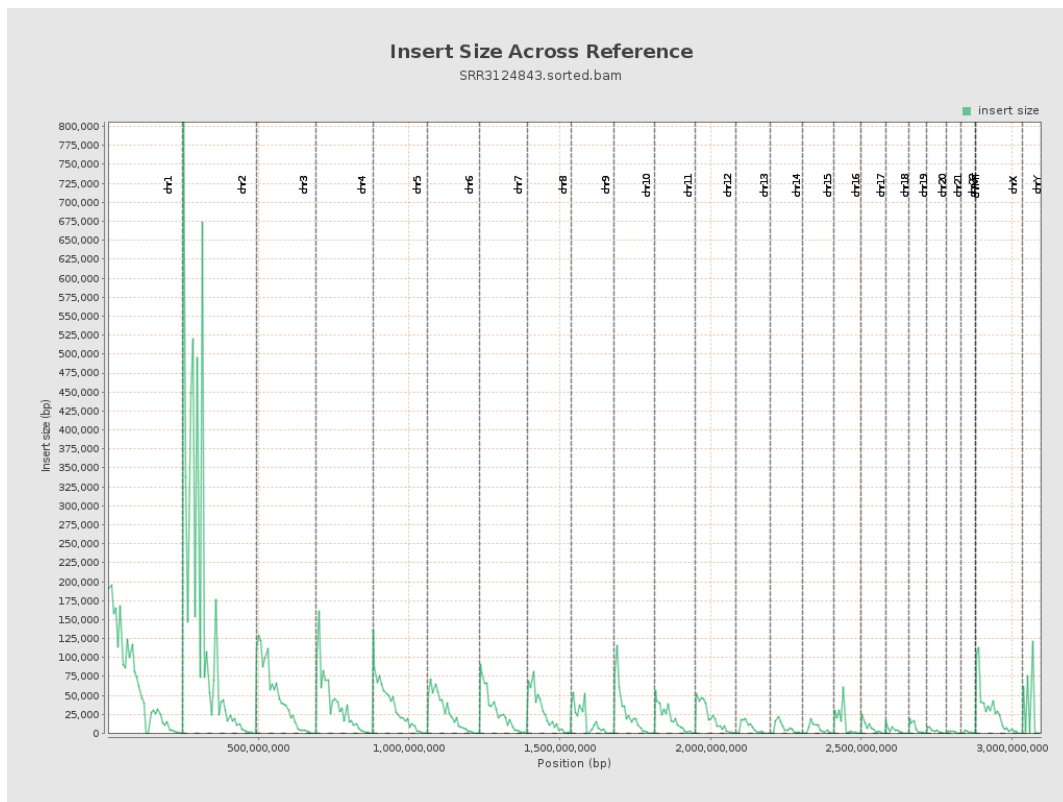
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

