

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 22:53:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124818.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_SRR3124818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124818_1.fastq.gz SRR3124818_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 22:53:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,441,724
Mapped reads	27,089,249 / 98.72%
Unmapped reads	352,475 / 1.28%
Mapped paired reads	27,089,249 / 98.72%
Mapped reads, first in pair	13,551,762 / 49.38%
Mapped reads, second in pair	13,537,487 / 49.33%
Mapped reads, both in pair	27,000,338 / 98.39%
Mapped reads, singletons	88,911 / 0.32%
Secondary alignments	0
Supplementary alignments	123,304 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	2,375,526 / 8.66%
Duplication rate	4.88%
Clipped reads	16,261,958 / 59.26%

2.2. ACGT Content

Number/percentage of A's	709,655,166 / 28.62%
Number/percentage of C's	491,085,899 / 19.8%
Number/percentage of T's	732,410,388 / 29.54%
Number/percentage of G's	546,548,090 / 22.04%
Number/percentage of N's	18,339 / 0%

GC Percentage	41.84%
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2.3. Coverage

Mean	0.8017
Standard Deviation	7.0166

2.4. Mapping Quality

Mean Mapping Quality	52.9
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2.5. Insert size

Mean	64,967.57
Standard Deviation	2,421,502.32
P25/Median/P75	138 / 169 / 213

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	18,389,910
Insertions	400,490
Mapped reads with at least one insertion	1.44%
Deletions	1,039,725
Mapped reads with at least one deletion	3.75%
Homopolymer indels	47.03%

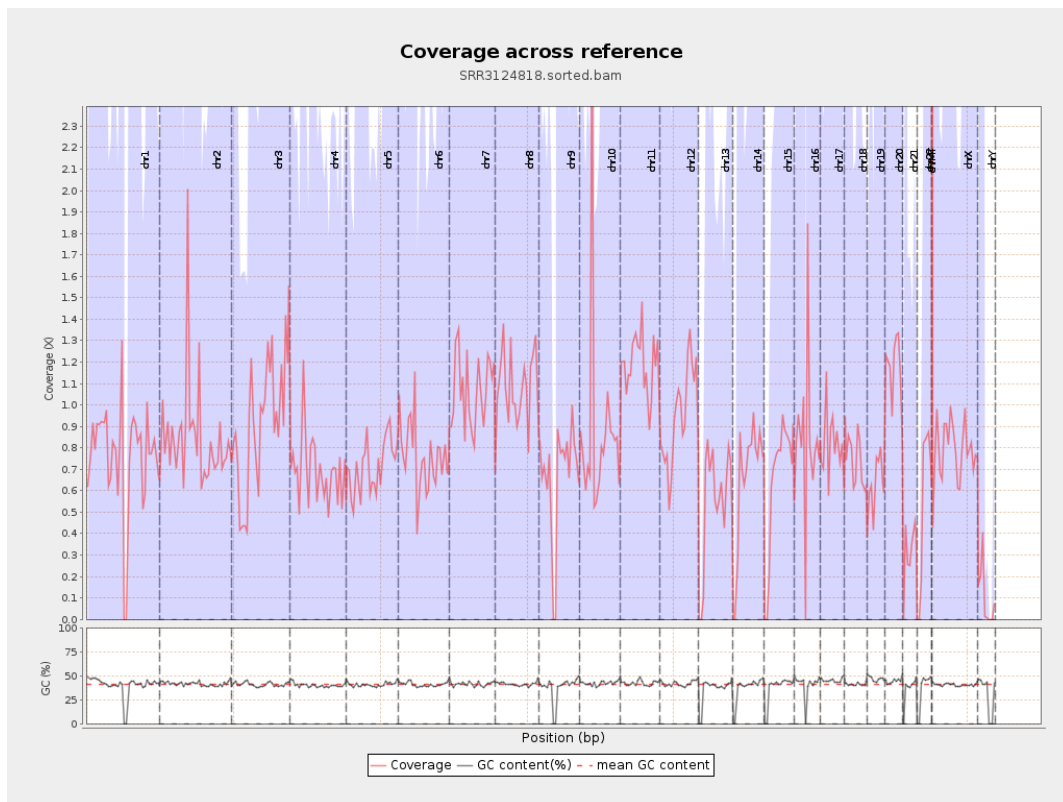
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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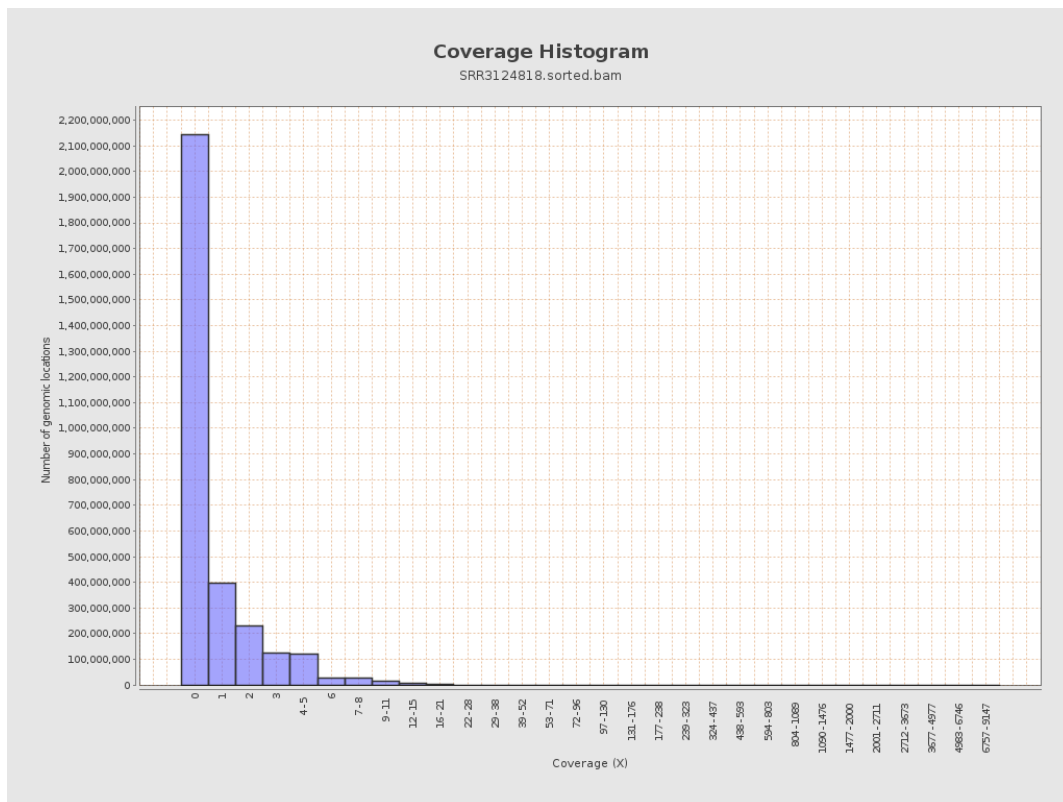
		bases	coverage	deviation
chr1	249250621	190523257	0.7644	7.1446
chr2	243199373	205866548	0.8465	9.3603
chr3	198022430	180195096	0.91	2.1488
chr4	191154276	132621496	0.6938	3.9864
chr5	180915260	129781372	0.7174	1.7231
chr6	171115067	129899466	0.7591	4.6436
chr7	159138663	169623553	1.0659	8.3767
chr8	146364022	160080219	1.0937	3.4683
chr9	141213431	93570028	0.6626	8.5021
chr10	135534747	119523434	0.8819	19.2926
chr11	135006516	159936602	1.1847	9.3926
chr12	133851895	127064835	0.9493	1.9617
chr13	115169878	63493273	0.5513	1.3653
chr14	107349540	70024903	0.6523	1.9174
chr15	102531392	65463008	0.6385	1.5149
chr16	90354753	75018213	0.8303	8.9968
chr17	81195210	65857385	0.8111	6.6738
chr18	78077248	57867718	0.7412	8.5716
chr19	59128983	37715911	0.6379	3.8184
chr20	63025520	74513102	1.1823	2.449
chr21	48129895	15629126	0.3247	2.0457
chr22	51304566	27940048	0.5446	1.7275
chrMT	16571	1256685	75.8364	43.2933
chrX	155270560	121936351	0.7853	3.8117

chrY	59373566	6268480	0.1056	6.5959
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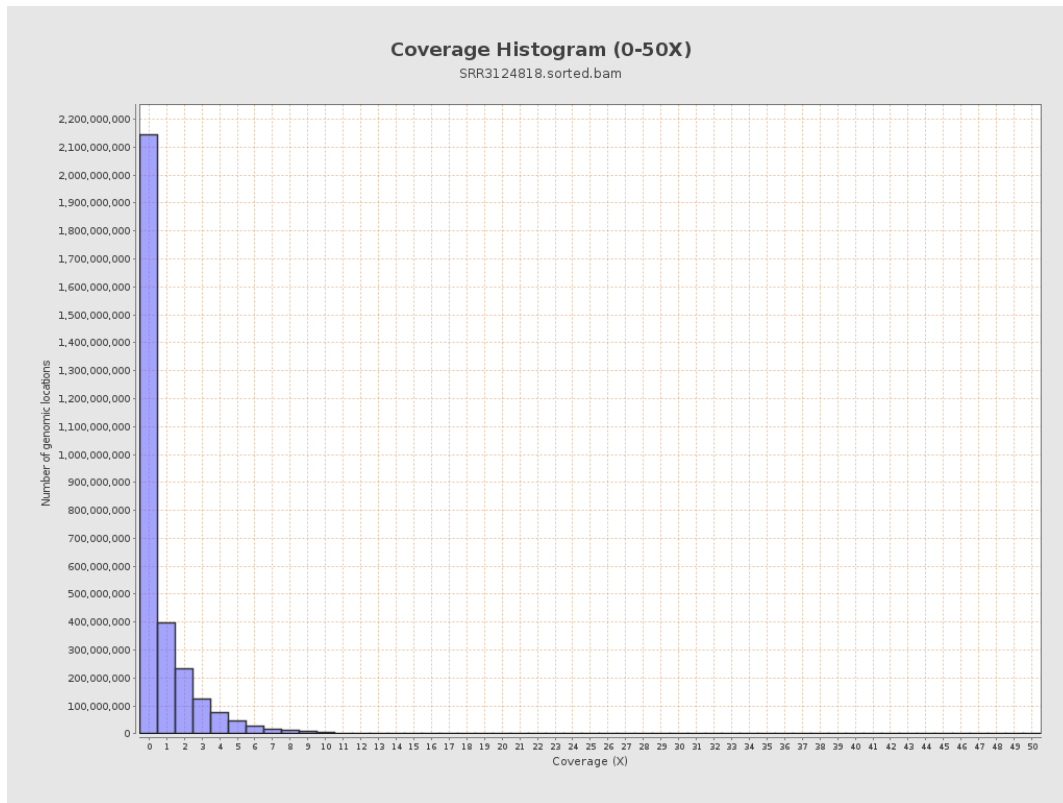
3. Results : Coverage across reference



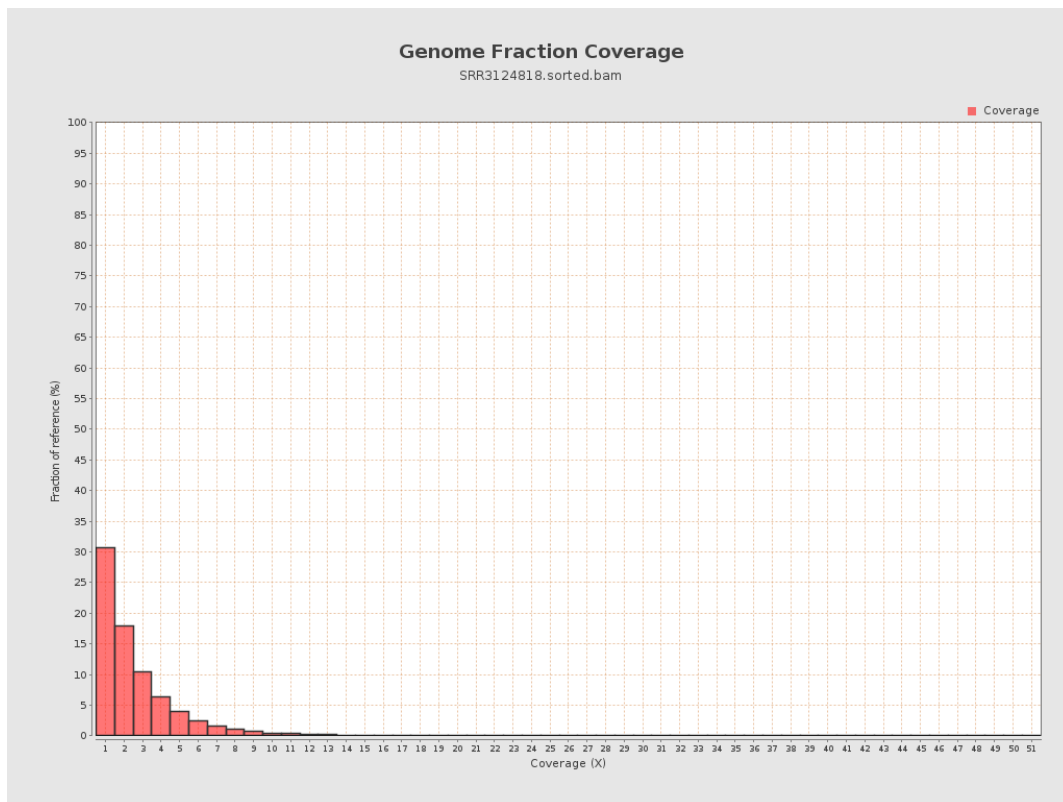
4. Results : Coverage Histogram



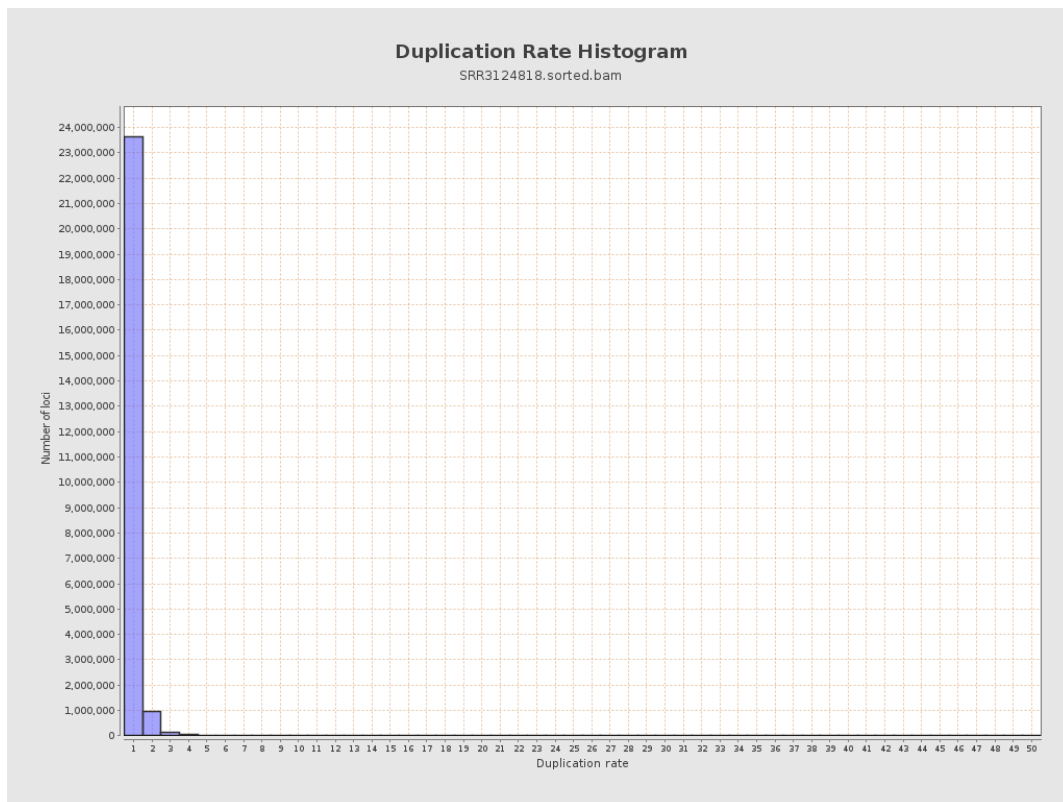
5. Results : Coverage Histogram (0-50X)



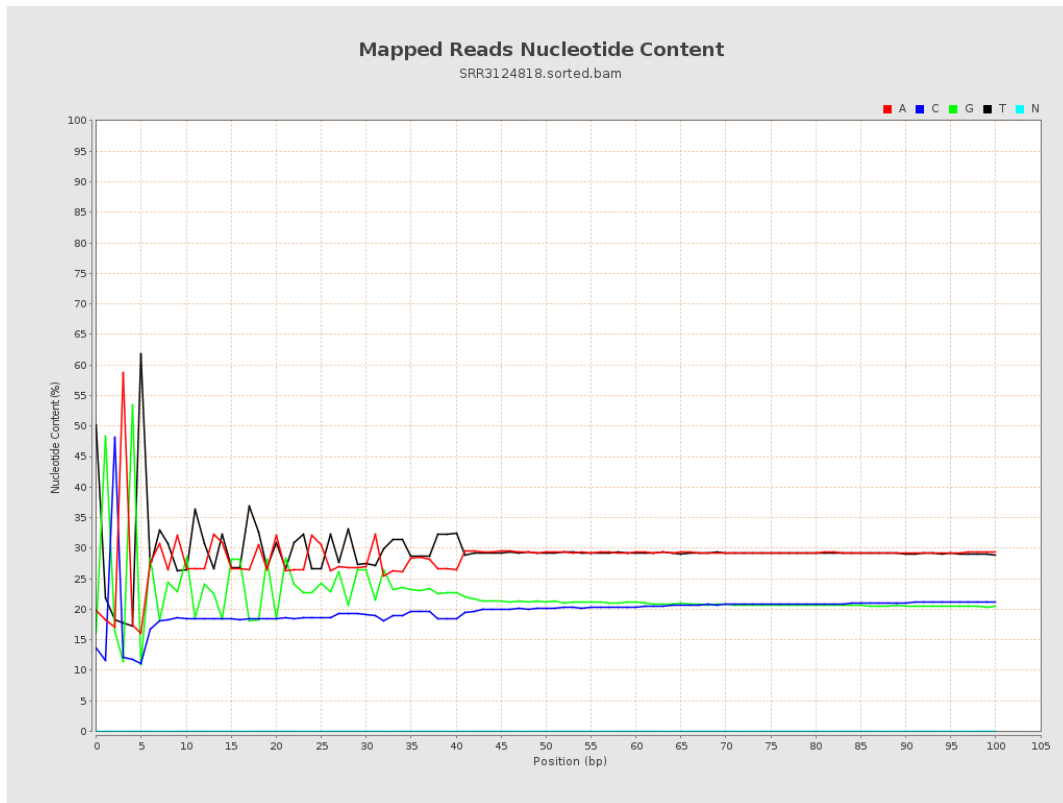
6. Results : Genome Fraction Coverage



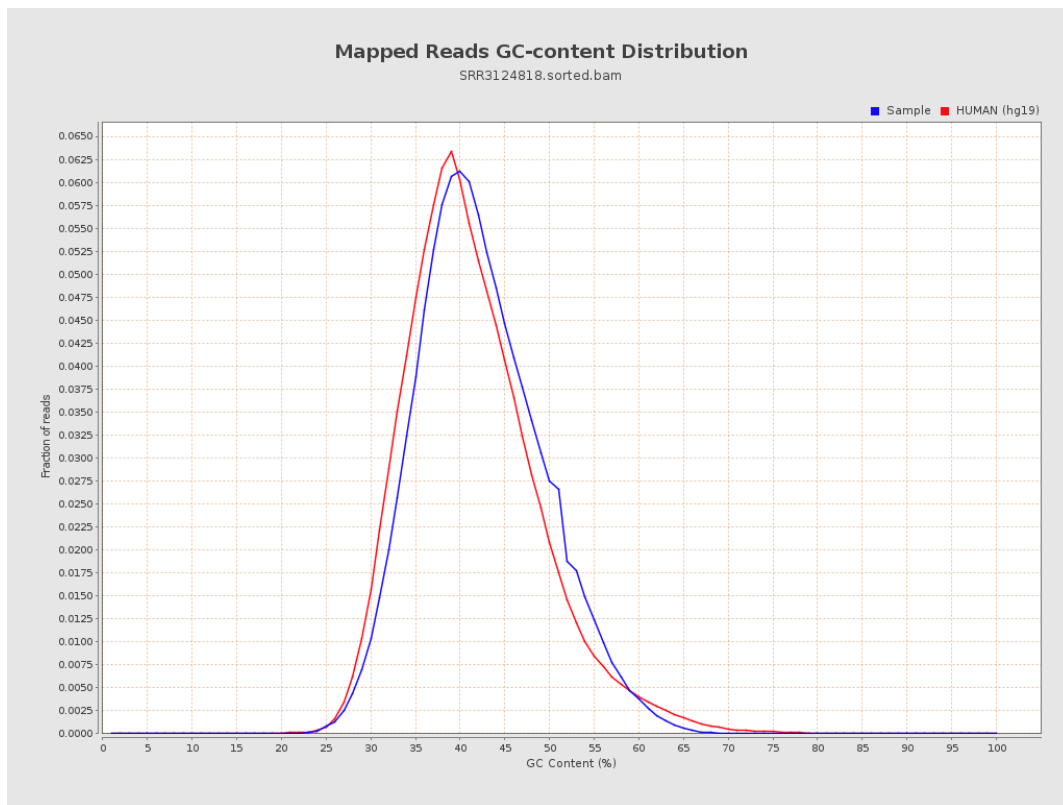
7. Results : Duplication Rate Histogram



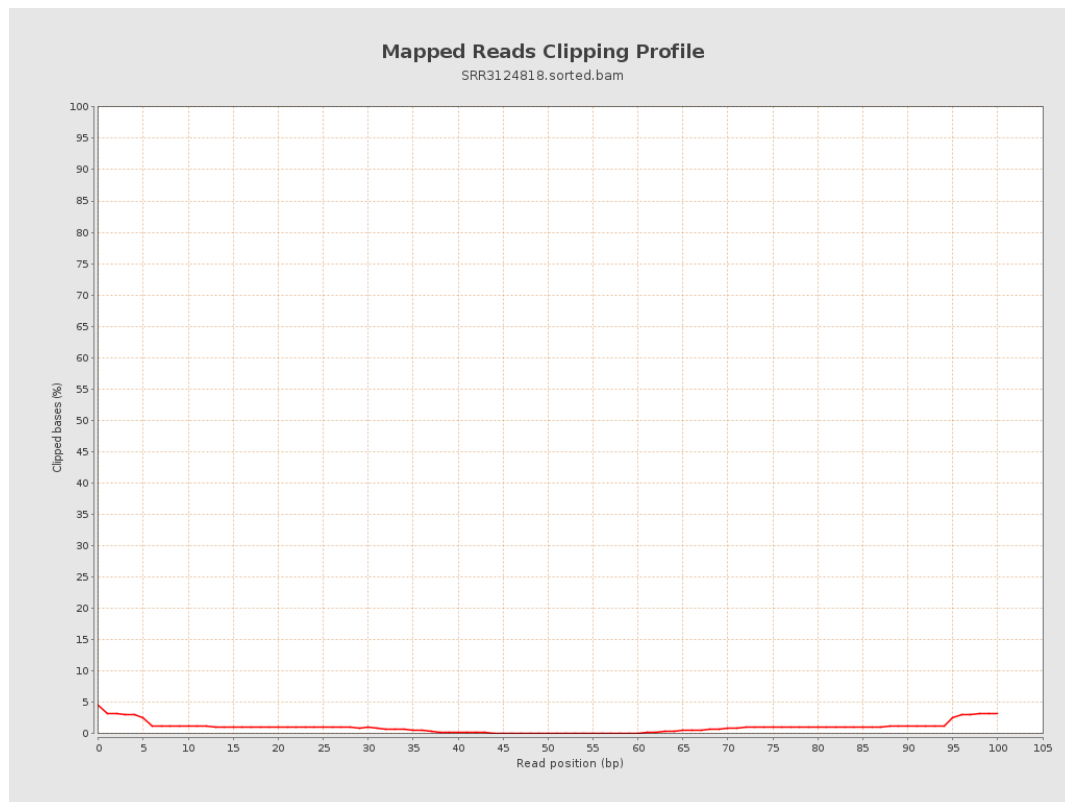
8. Results : Mapped Reads Nucleotide Content



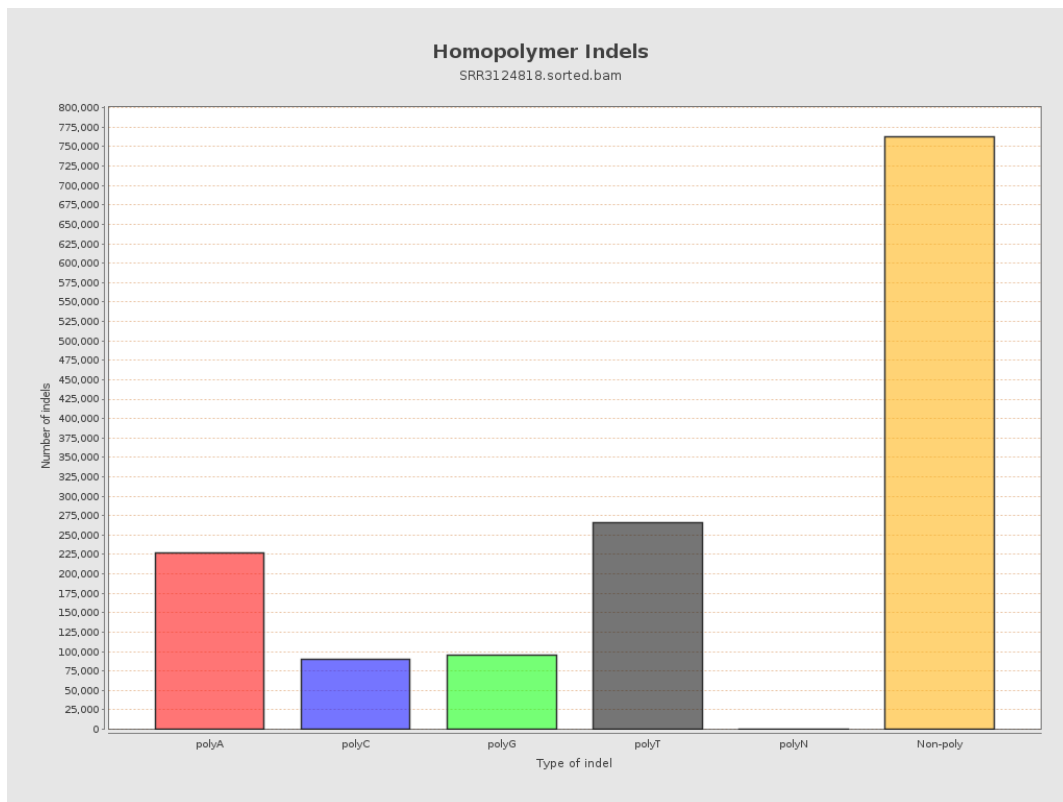
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



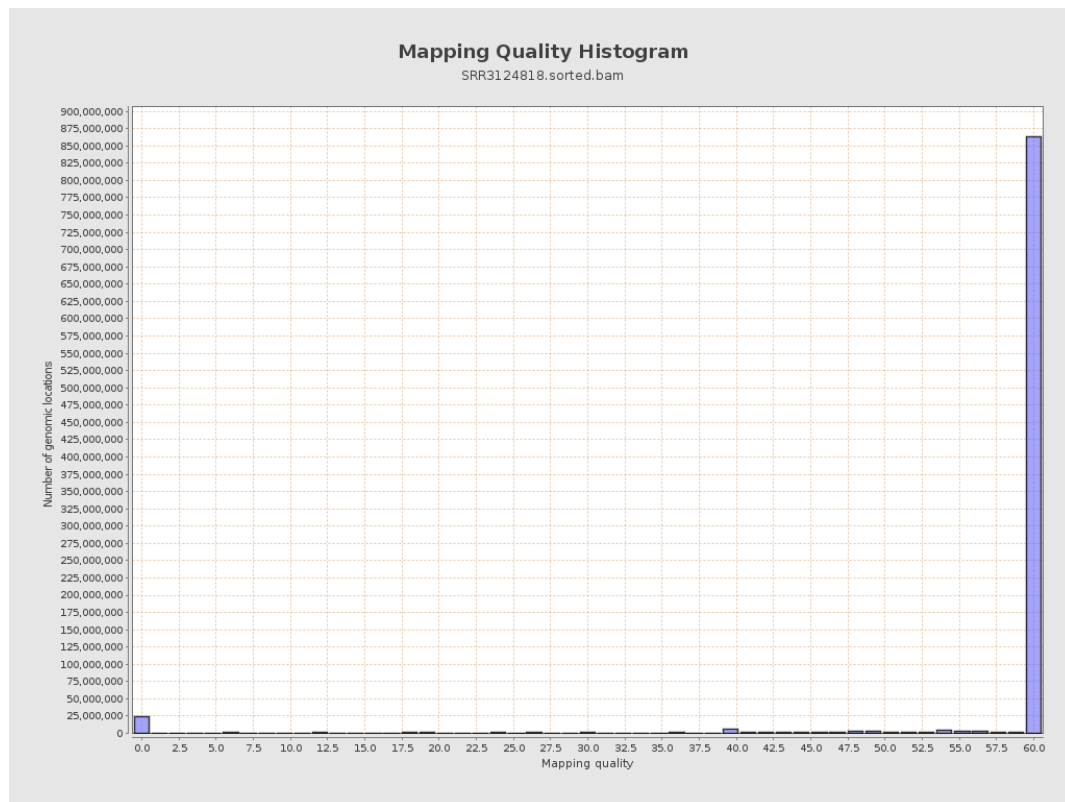
11. Results : Homopolymer Indels



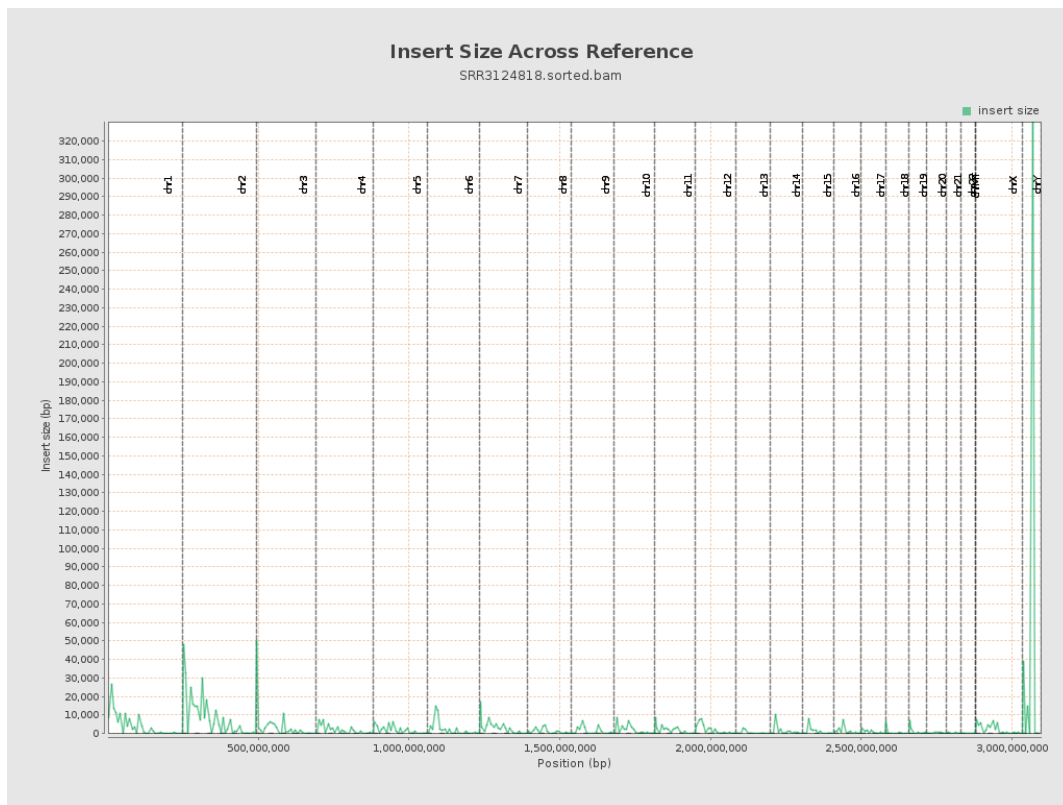
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

