

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/02 04:29:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352029.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_SRR16352029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352029_1.fastq.gz SRR16352029_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Feb 02 04:29:40 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,630,933,214
Mapped reads	1,584,553,489 / 97.16%
Unmapped reads	46,379,725 / 2.84%
Mapped paired reads	1,584,553,489 / 97.16%
Mapped reads, first in pair	793,733,390 / 48.67%
Mapped reads, second in pair	790,820,099 / 48.49%
Mapped reads, both in pair	1,569,480,450 / 96.23%
Mapped reads, singletons	15,073,039 / 0.92%
Secondary alignments	0
Supplementary alignments	38,228,138 / 2.34%
Read min/max/mean length	30 / 100 / 92.93
Duplicated reads (estimated)	618,975,524 / 37.95%
Duplication rate	35.39%
Clipped reads	236,659,663 / 14.51%

2.2. ACGT Content

Number/percentage of A's	41,362,151,013 / 28.91%
Number/percentage of C's	29,909,683,103 / 20.91%
Number/percentage of T's	40,946,778,143 / 28.62%
Number/percentage of G's	30,833,837,044 / 21.55%
Number/percentage of N's	2,954,488 / 0%

GC Percentage	42.46%
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2.3. Coverage

Mean	46.2402
Standard Deviation	401.4303

2.4. Mapping Quality

Mean Mapping Quality	52.89
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2.5. Insert size

Mean	165,747.85
Standard Deviation	3,990,753.44
P25/Median/P75	212 / 281 / 398

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	1,080,219,773
Insertions	18,411,998
Mapped reads with at least one insertion	1.14%
Deletions	59,101,560
Mapped reads with at least one deletion	3.65%
Homopolymer indels	45.15%

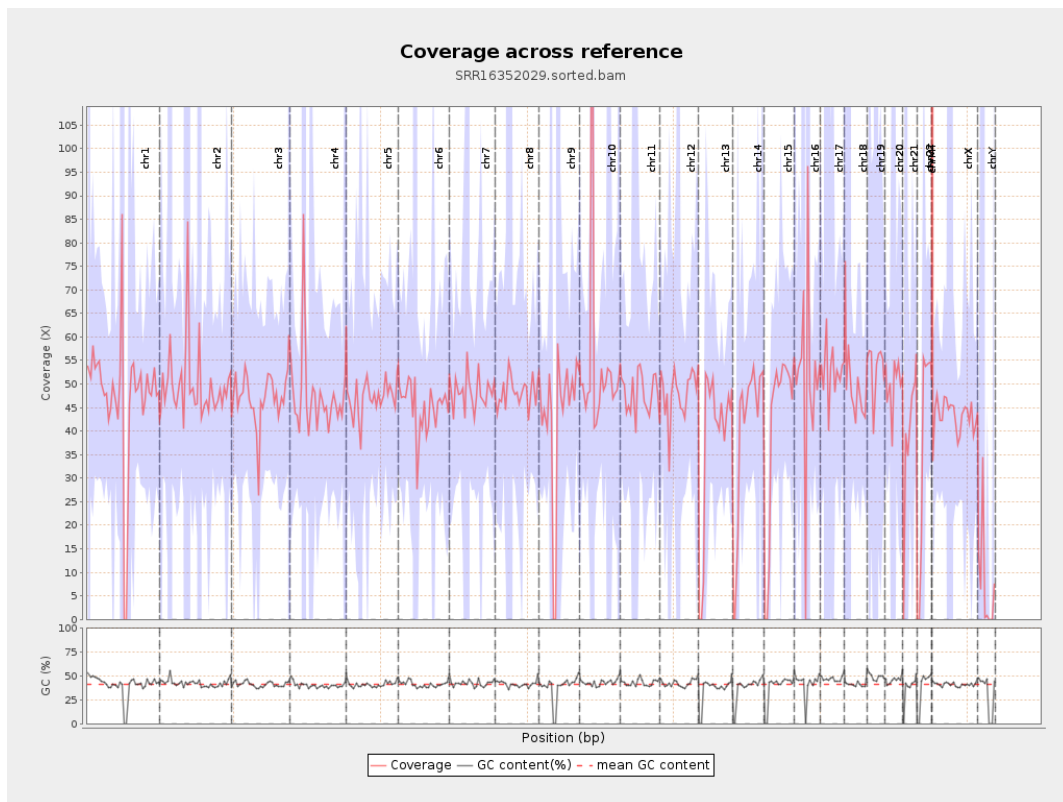
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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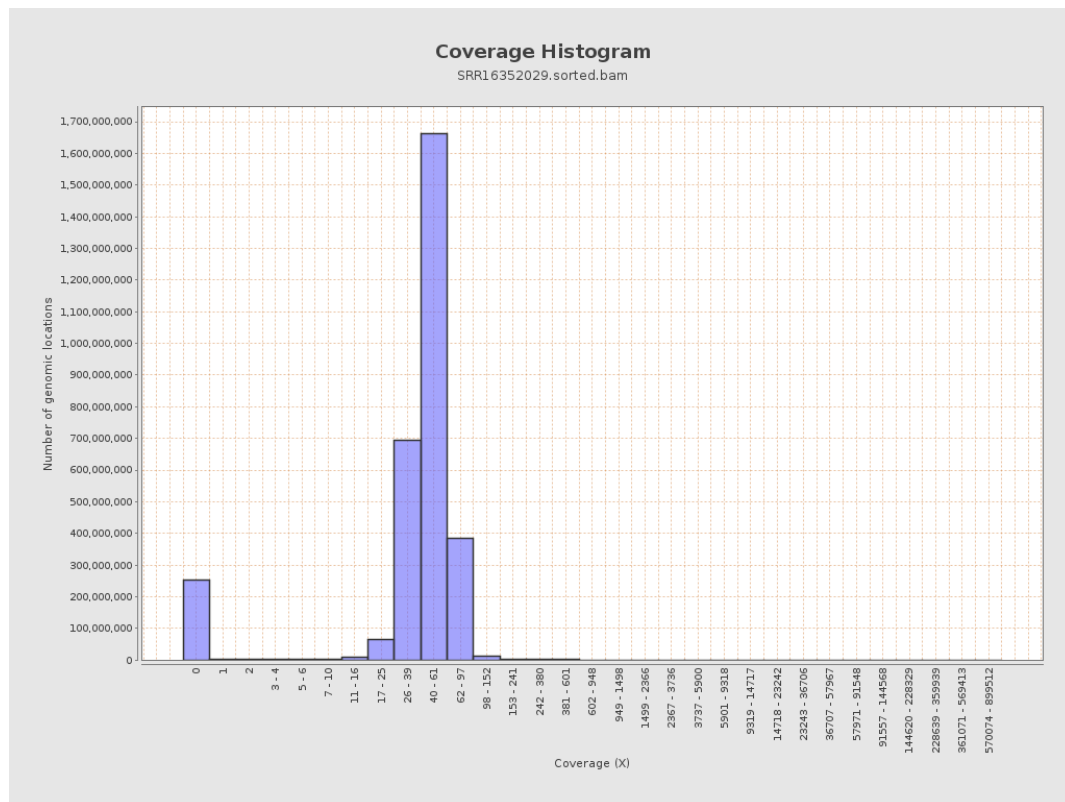
		bases	coverage	deviation
chr1	249250621	11878249796	47.6558	897.1065
chr2	243199373	12139938590	49.9176	505.9349
chr3	198022430	9331463397	47.1233	37.7272
chr4	191154276	8998929576	47.0768	273.3153
chr5	180915260	8542083524	47.2159	32.9851
chr6	171115067	7698899630	44.9925	103.5541
chr7	159138663	7683974364	48.2848	263.8312
chr8	146364022	7058597690	48.2263	556.0394
chr9	141213431	6113391762	43.2919	275.4313
chr10	135534747	7413741596	54.6999	814.3791
chr11	135006516	6515444124	48.2602	156.0082
chr12	133851895	6419231764	47.9577	45.5916
chr13	115169878	4384902000	38.0733	28.9397
chr14	107349540	4285933613	39.925	44.8239
chr15	102531392	4155231548	40.5264	31.2533
chr16	90354753	4707672112	52.1021	337.4827
chr17	81195210	4268516399	52.571	159.442
chr18	78077248	3817509989	48.894	511.9019
chr19	59128983	3176441349	53.7205	371.2542
chr20	63025520	3130451877	49.6696	55.3088
chr21	48129895	1928460725	40.0678	98.215
chr22	51304566	1922760416	37.4774	40.5408
chrMT	16571	422924892	25,521.9897	6,211.41
chrX	155270560	6693444972	43.1083	75.2965

chrY	59373566	457385539	7.7035	272.1806
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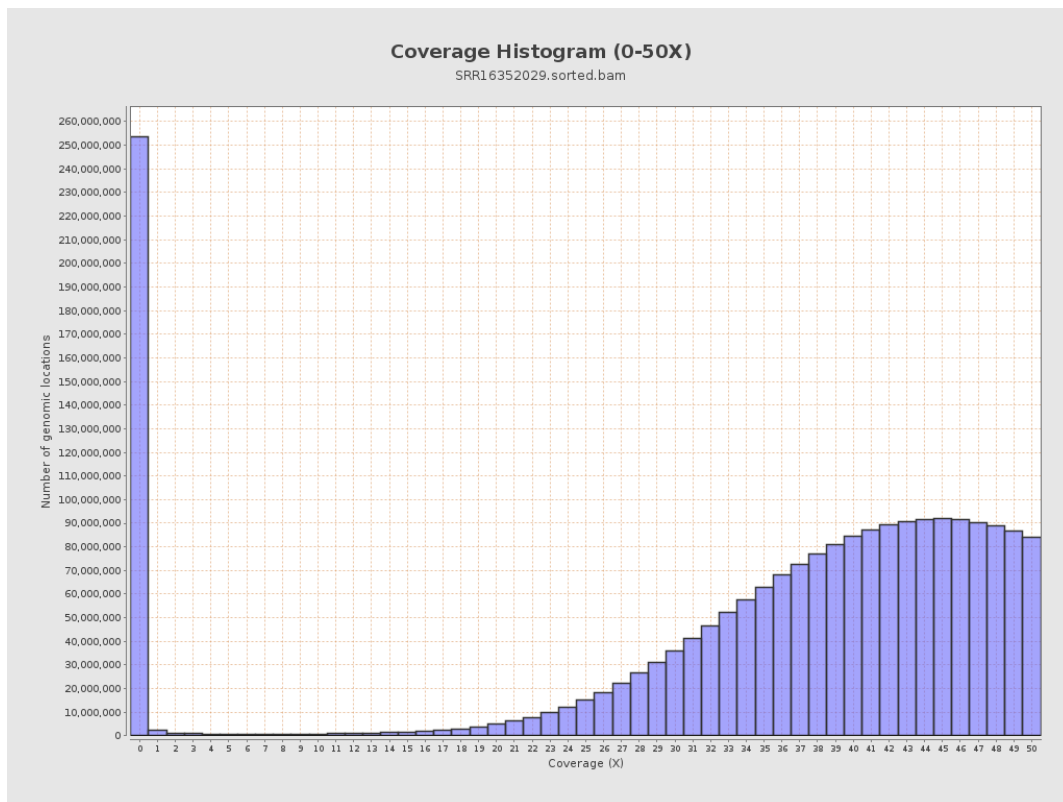
3. Results : Coverage across reference



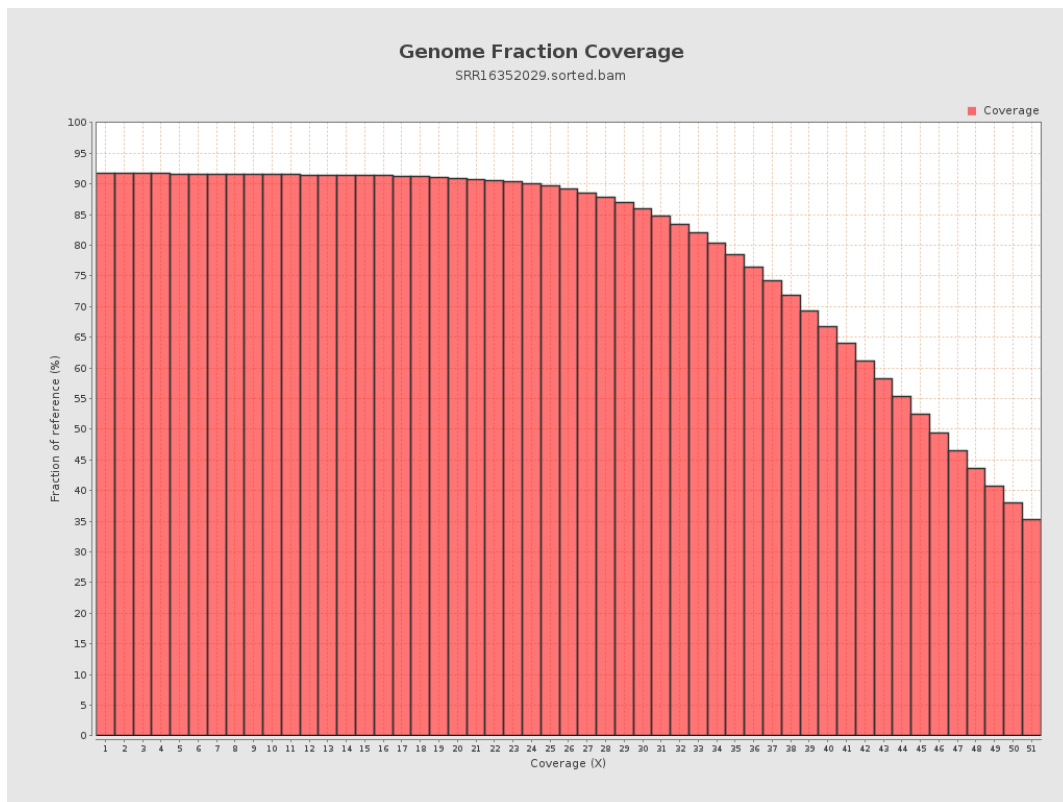
4. Results : Coverage Histogram



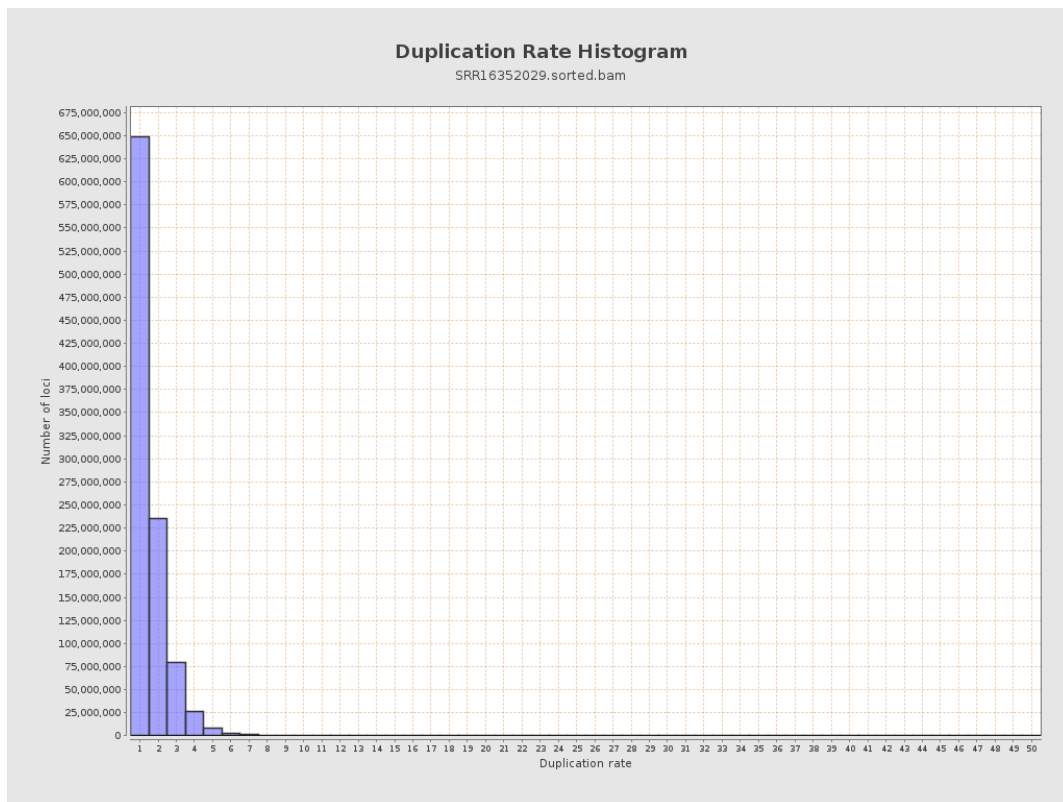
5. Results : Coverage Histogram (0-50X)



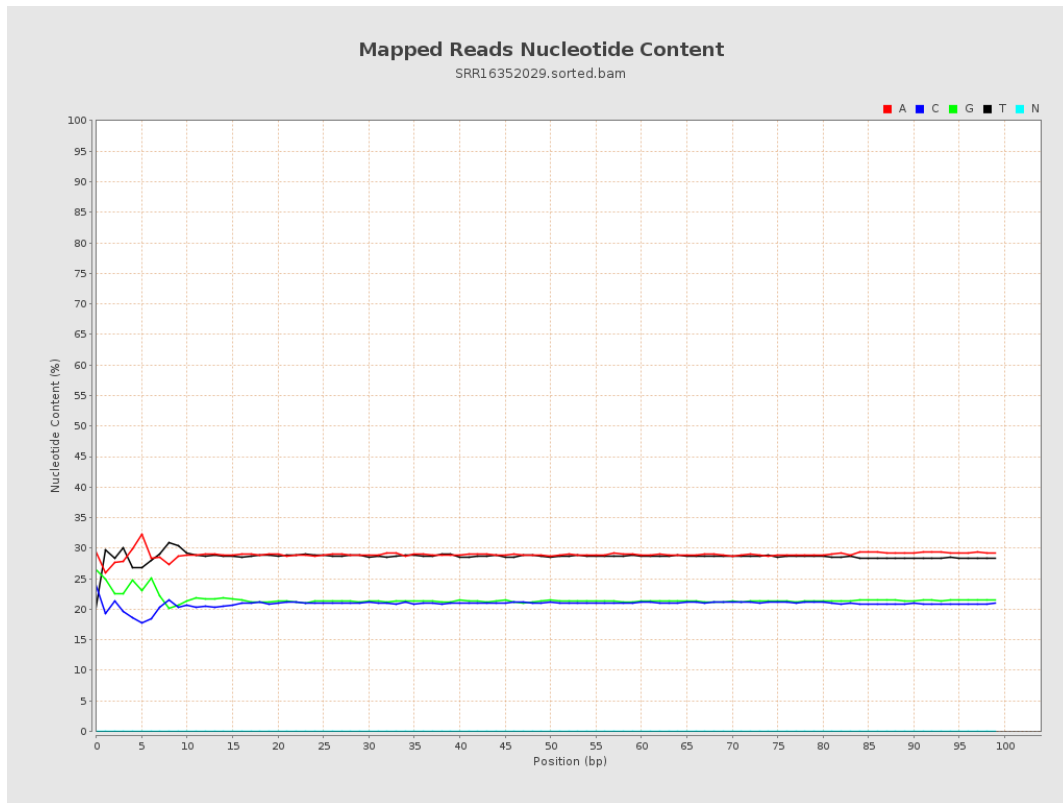
6. Results : Genome Fraction Coverage



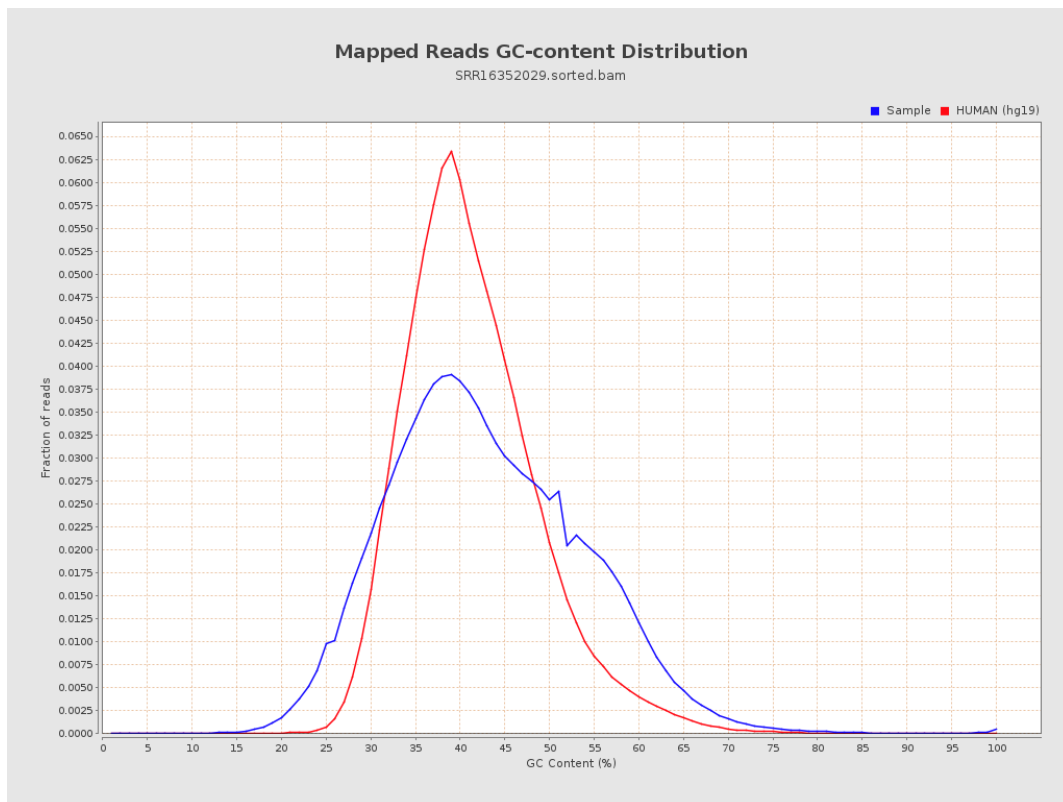
7. Results : Duplication Rate Histogram



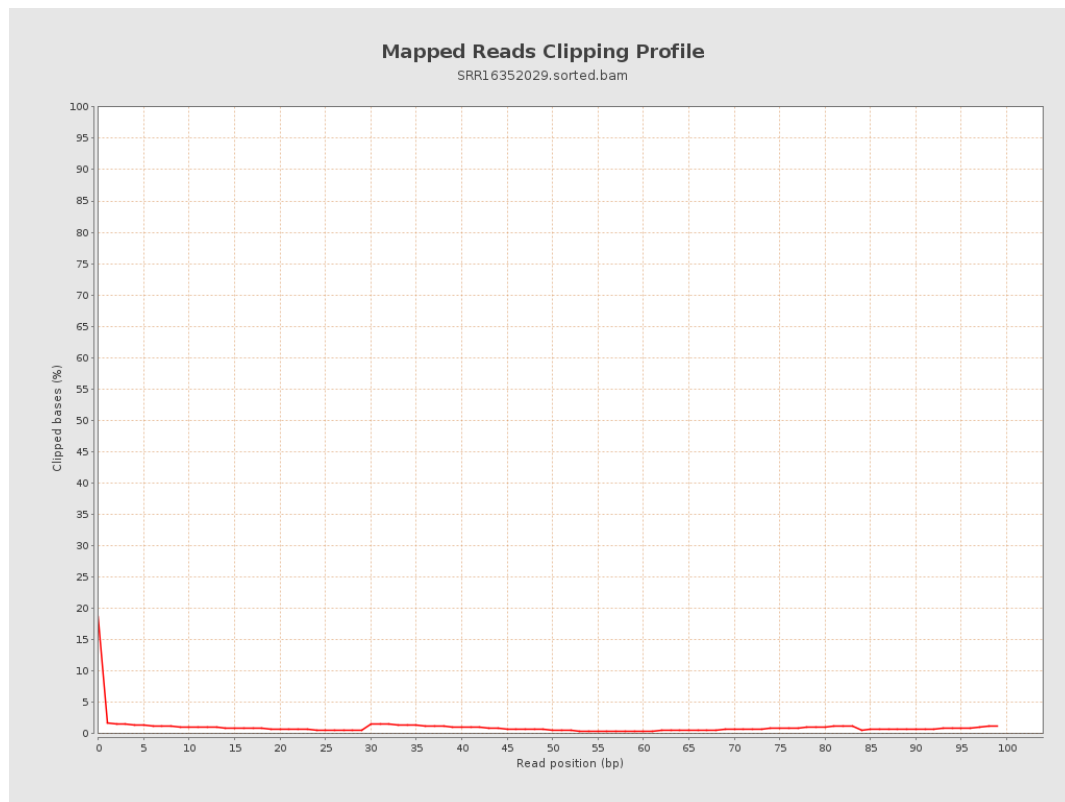
8. Results : Mapped Reads Nucleotide Content



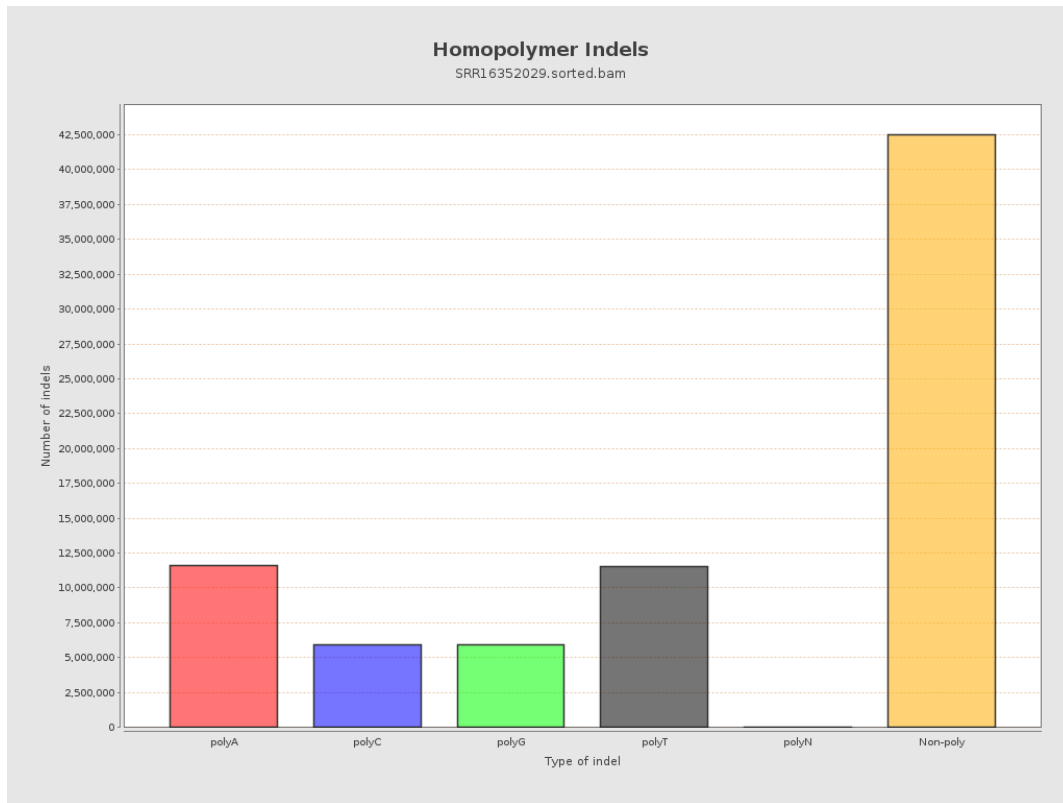
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



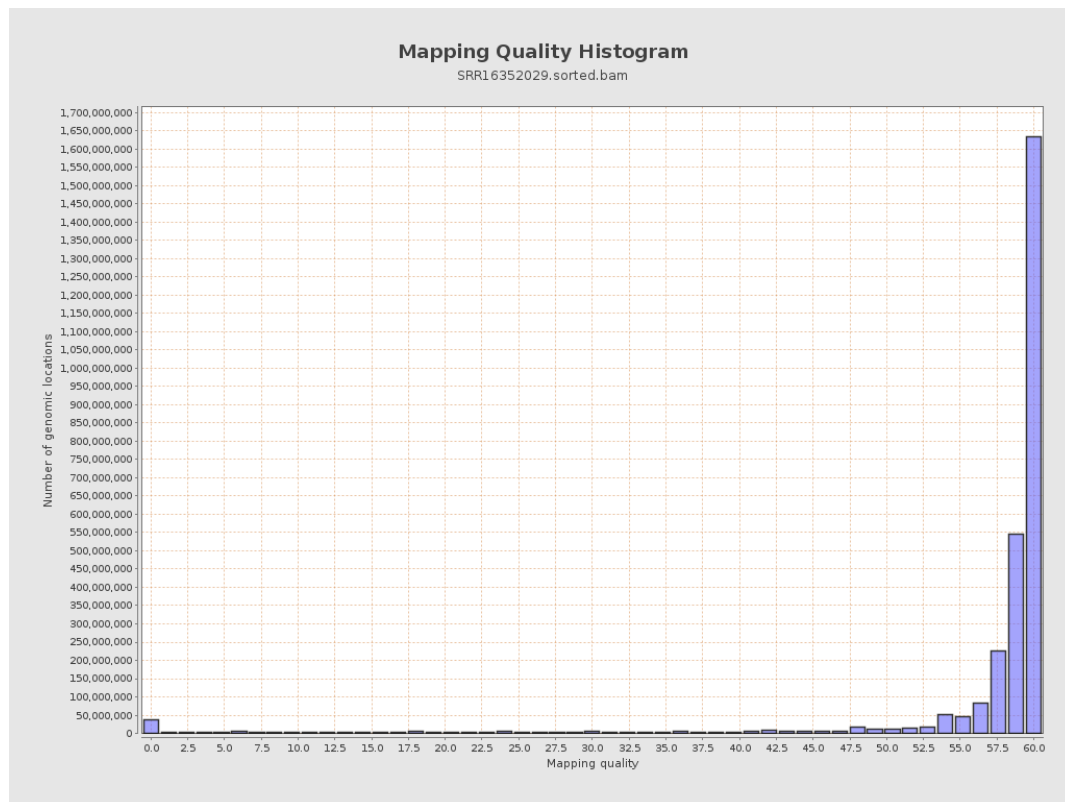
11. Results : Homopolymer Indels



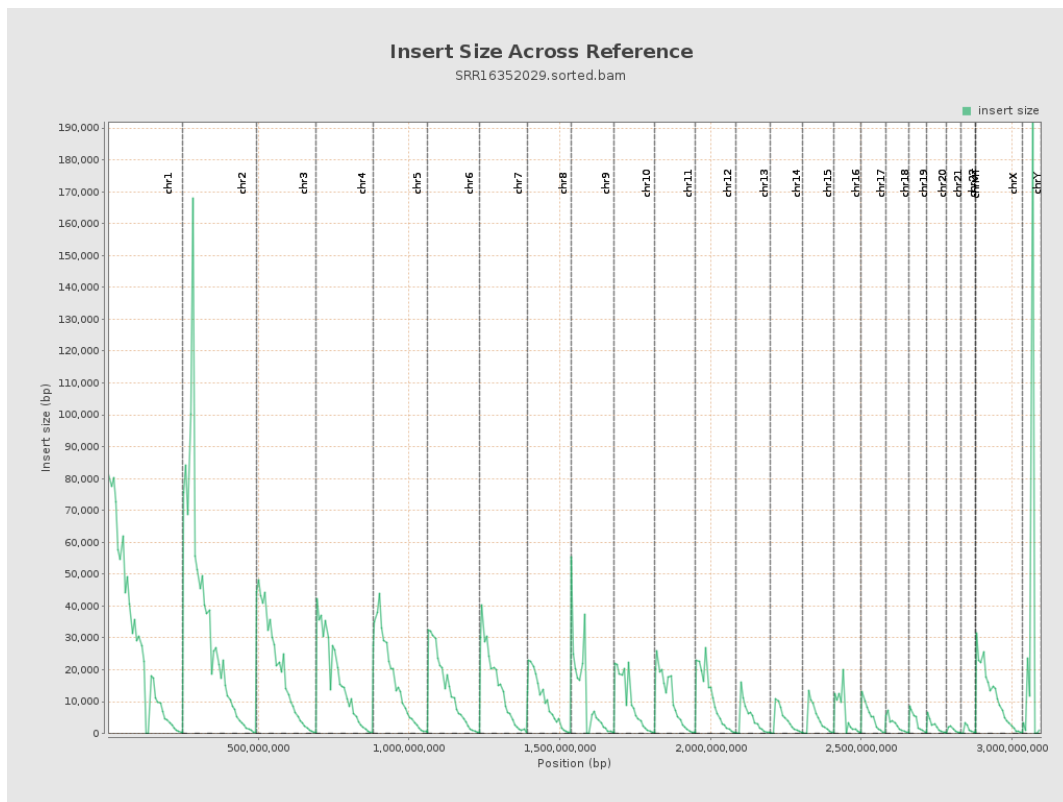
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

