

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/05 16:01:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352033.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_SRR16352033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352033_1.fastq.gz SRR16352033_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Feb 05 16:01:52 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,377,826,506
Mapped reads	1,337,738,496 / 97.09%
Unmapped reads	40,088,010 / 2.91%
Mapped paired reads	1,337,738,496 / 97.09%
Mapped reads, first in pair	669,606,424 / 48.6%
Mapped reads, second in pair	668,132,072 / 48.49%
Mapped reads, both in pair	1,326,143,868 / 96.25%
Mapped reads, singletons	11,594,628 / 0.84%
Secondary alignments	0
Supplementary alignments	29,654,945 / 2.15%
Read min/max/mean length	30 / 100 / 92.85
Duplicated reads (estimated)	470,335,212 / 34.14%
Duplication rate	31.28%
Clipped reads	196,151,657 / 14.24%

2.2. ACGT Content

Number/percentage of A's	35,056,797,032 / 29.01%
Number/percentage of C's	25,136,543,834 / 20.8%
Number/percentage of T's	34,778,073,552 / 28.78%
Number/percentage of G's	25,866,593,298 / 21.41%
Number/percentage of N's	2,535,208 / 0%

GC Percentage	42.21%
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2.3. Coverage

Mean	39.0607
Standard Deviation	370.3229

2.4. Mapping Quality

Mean Mapping Quality	52.93
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2.5. Insert size

Mean	130,699.05
Standard Deviation	3,511,771.75
P25/Median/P75	213 / 282 / 398

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	903,156,853
Insertions	16,152,958
Mapped reads with at least one insertion	1.18%
Deletions	53,259,770
Mapped reads with at least one deletion	3.9%
Homopolymer indels	45.5%

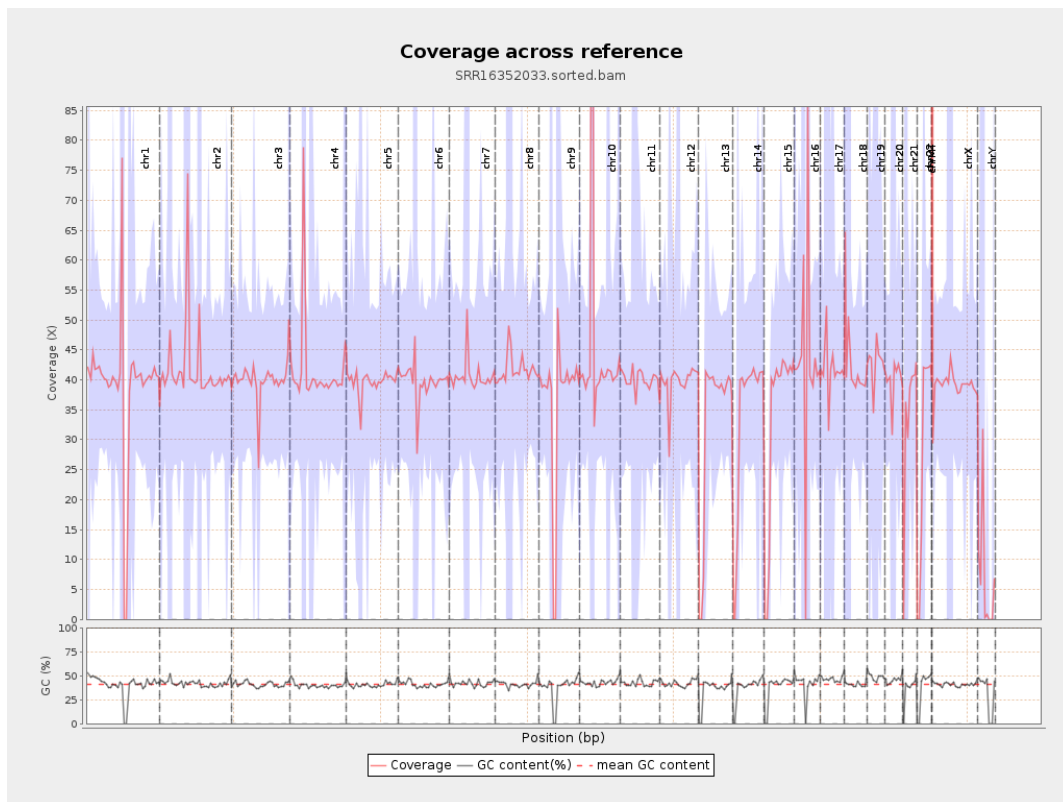
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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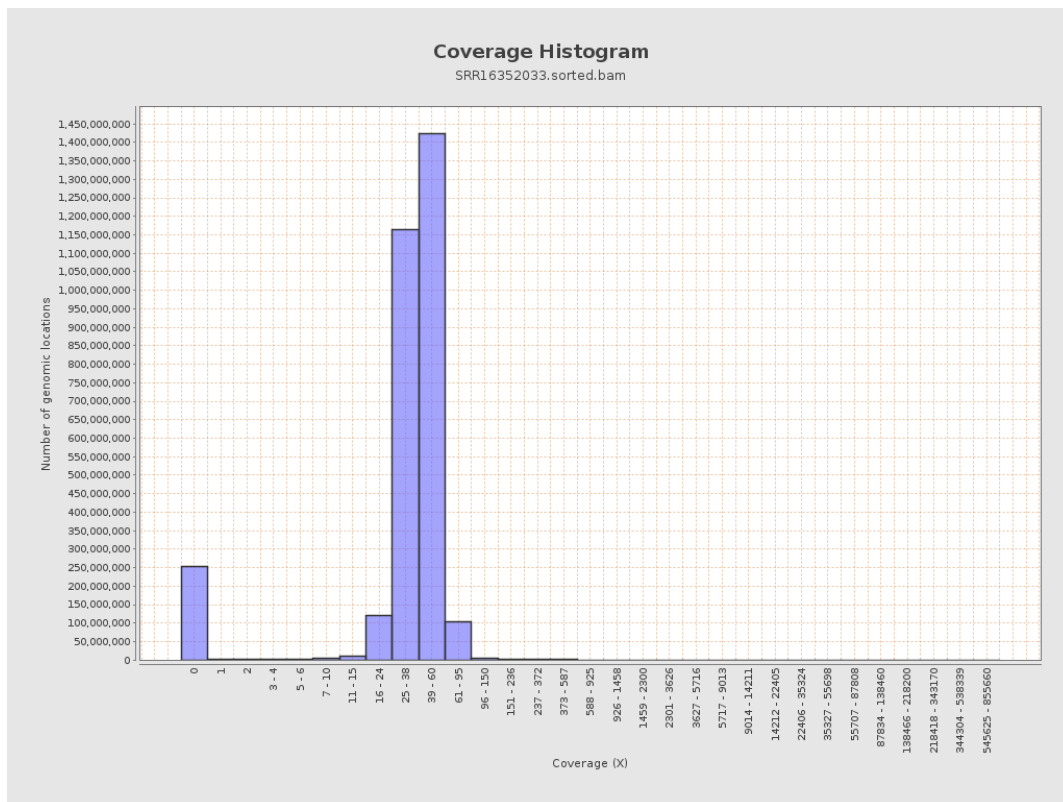
		bases	coverage	deviation
chr1	249250621	9786452723	39.2635	844.8432
chr2	243199373	10209775340	41.9811	361.9948
chr3	198022430	7886643638	39.827	36.3593
chr4	191154276	7900012729	41.3279	260.4401
chr5	180915260	7185551145	39.7178	27.7495
chr6	171115067	6801948038	39.7507	100.2975
chr7	159138663	6473034603	40.6754	253.3098
chr8	146364022	6113215549	41.7672	561.49
chr9	141213431	5121628328	36.2687	259.0984
chr10	135534747	6278392480	46.3231	780.5242
chr11	135006516	5417912734	40.1307	128.9388
chr12	133851895	5306881861	39.6474	38.8065
chr13	115169878	3814545916	33.121	22.5852
chr14	107349540	3594704313	33.486	36.0116
chr15	102531392	3399451648	33.1552	24.4352
chr16	90354753	3936994368	43.5726	318.6051
chr17	81195210	3378584026	41.6106	148.5413
chr18	78077248	3274385510	41.9378	465.2093
chr19	59128983	2538072408	42.9243	353.2649
chr20	63025520	2513899402	39.887	48.072
chr21	48129895	1657427827	34.4366	88.5638
chr22	51304566	1495331842	29.1462	34.3625
chrMT	16571	357050255	21,546.6933	3,640.9494
chrX	155270560	6066862496	39.0728	75.8164

chrY	59373566	411273177	6.9269	255.5127
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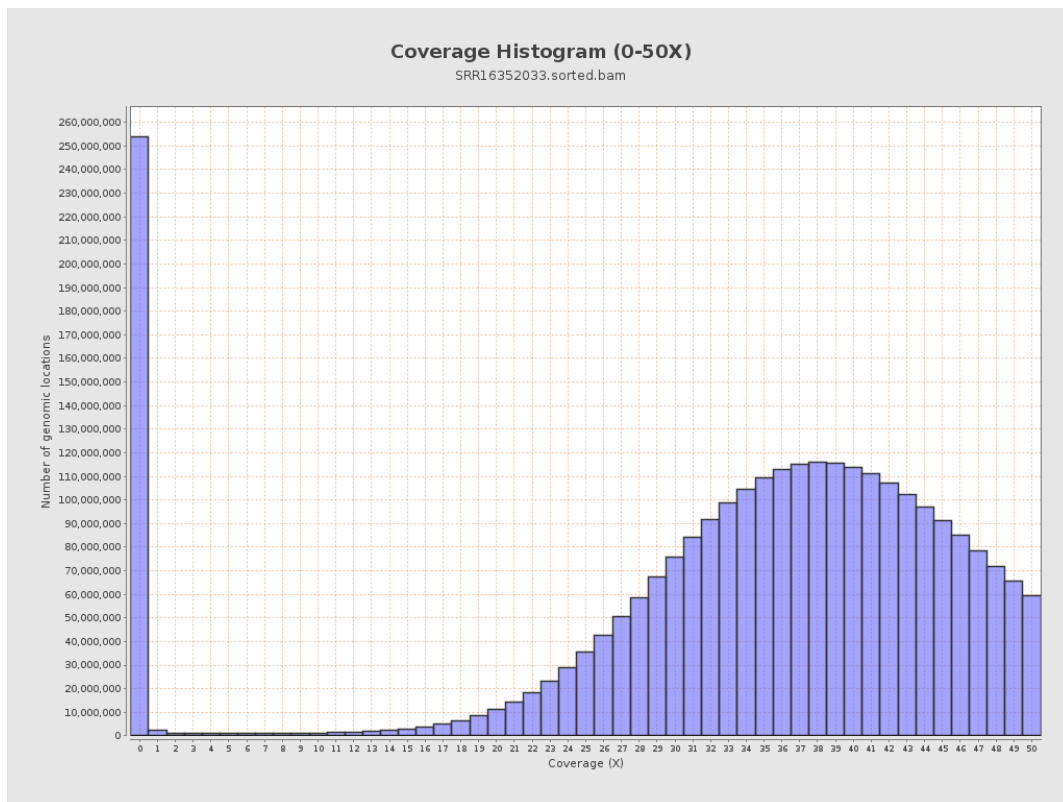
3. Results : Coverage across reference



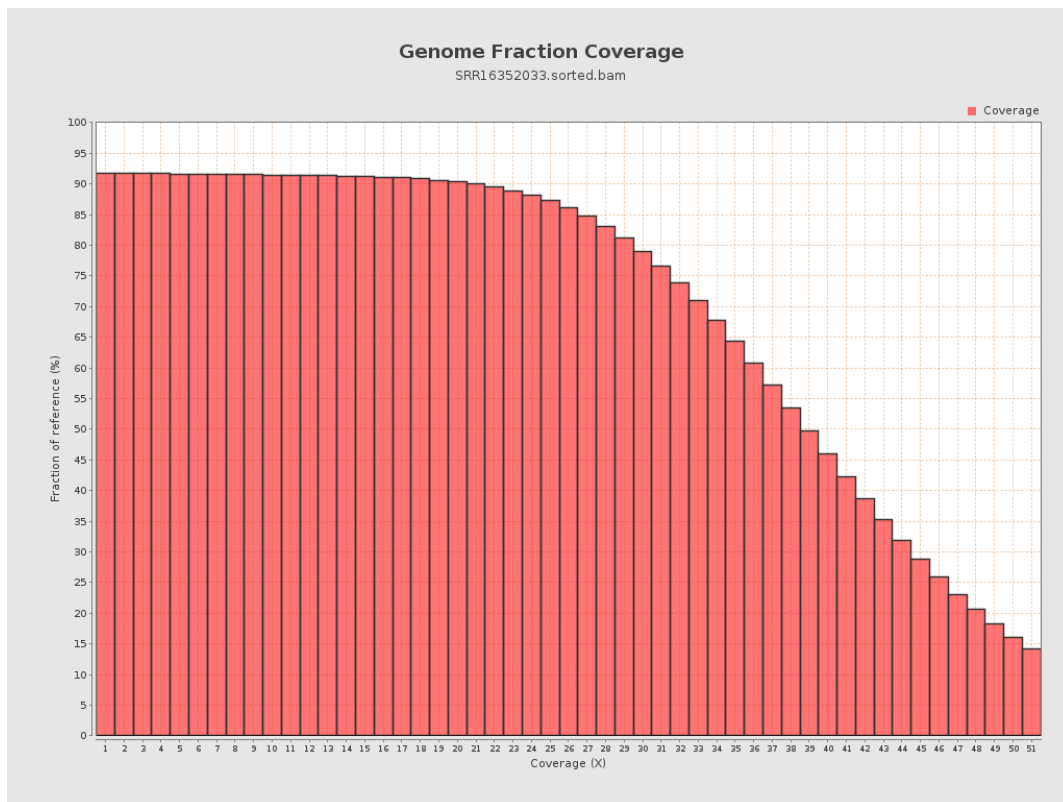
4. Results : Coverage Histogram



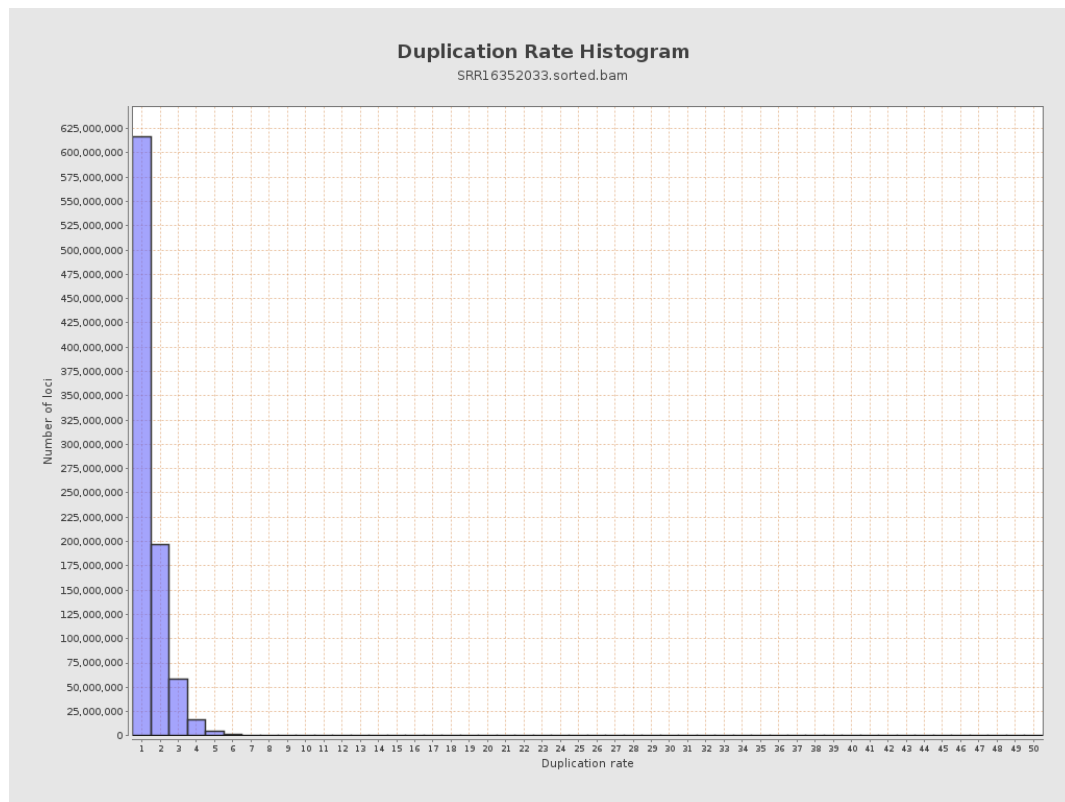
5. Results : Coverage Histogram (0-50X)



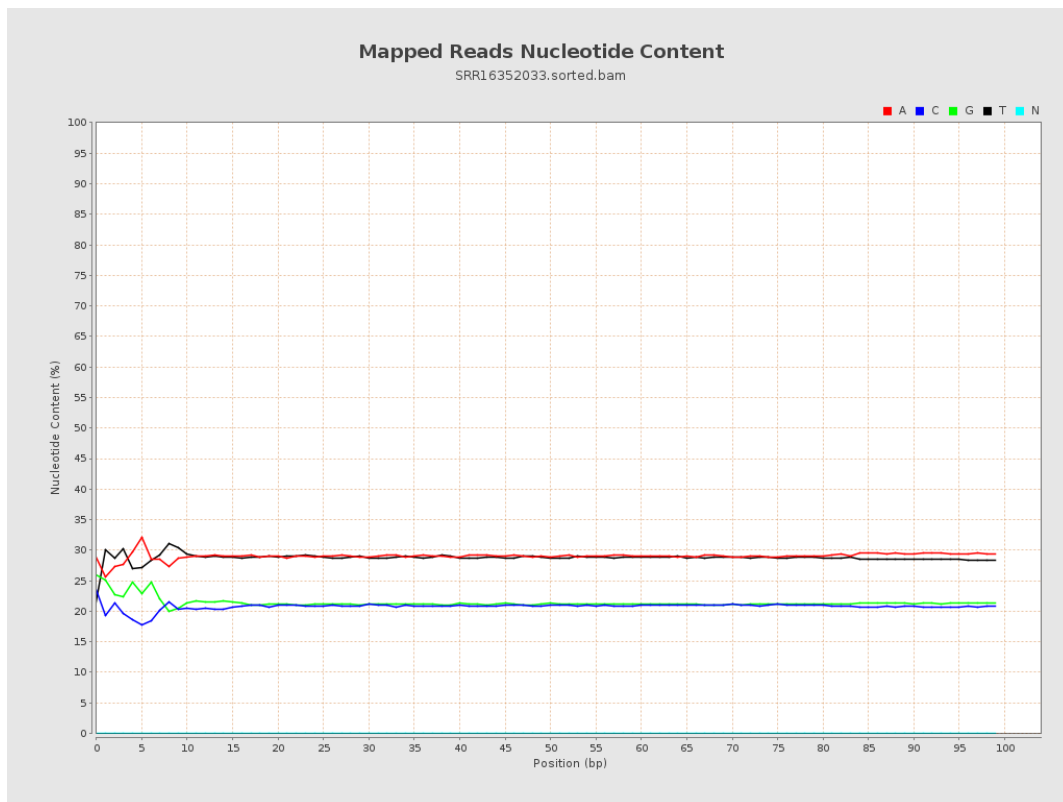
6. Results : Genome Fraction Coverage



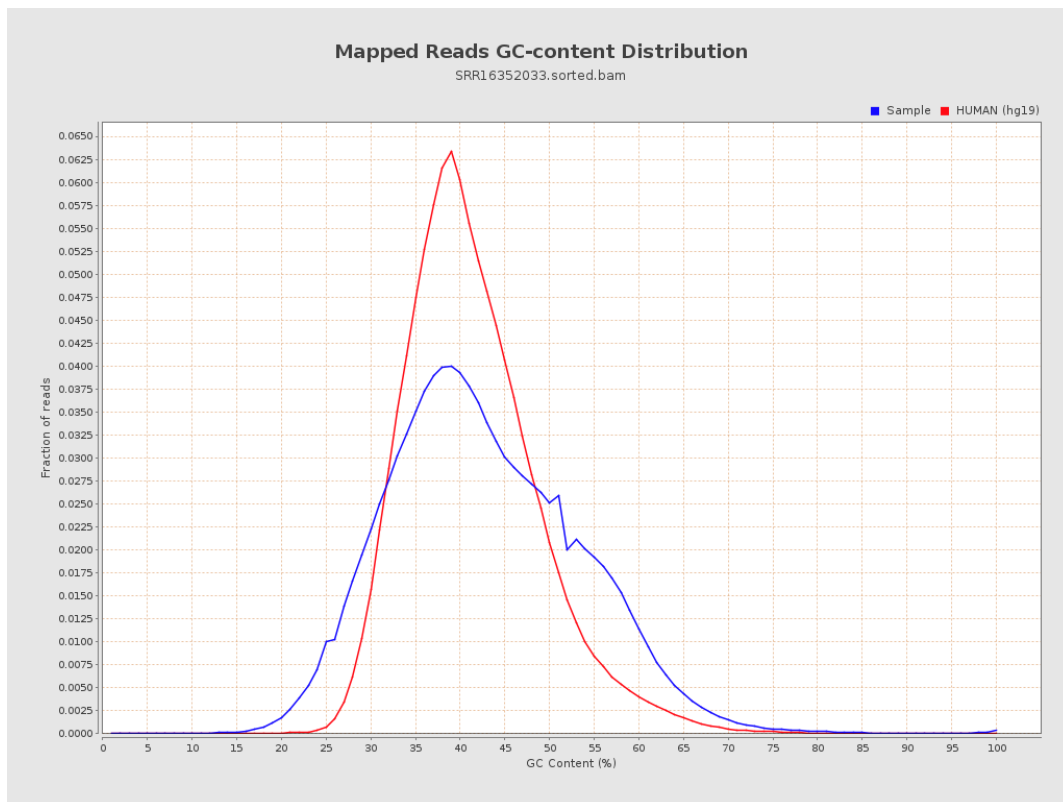
7. Results : Duplication Rate Histogram



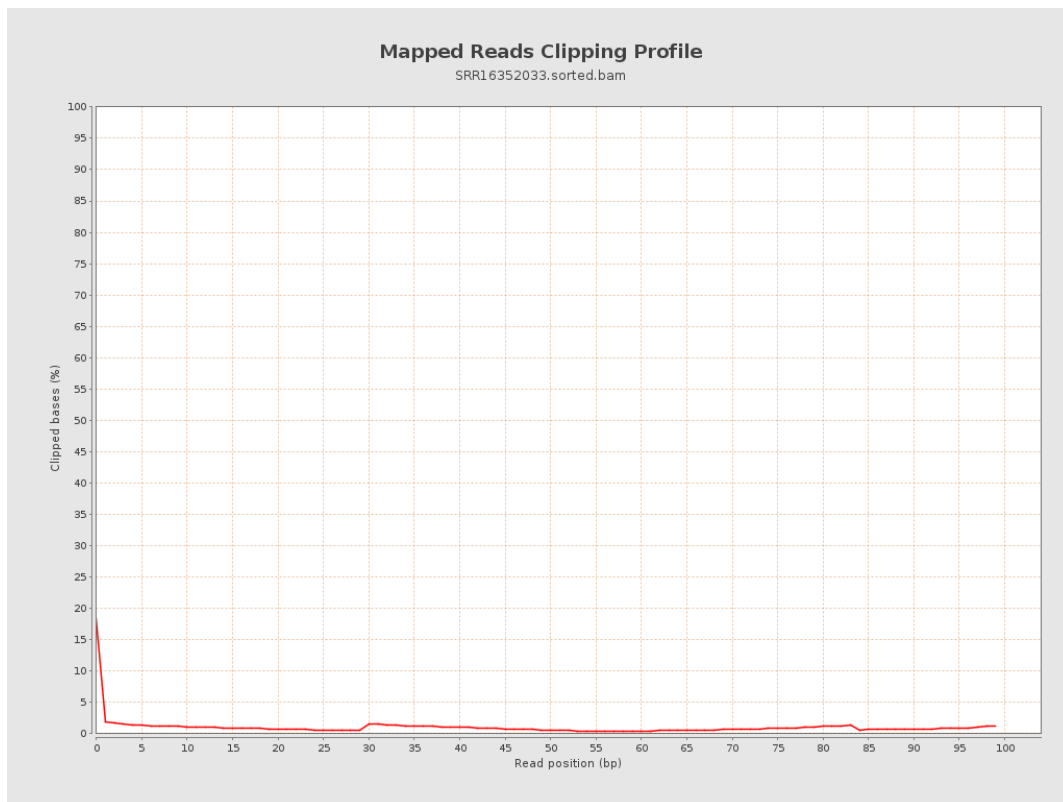
8. Results : Mapped Reads Nucleotide Content



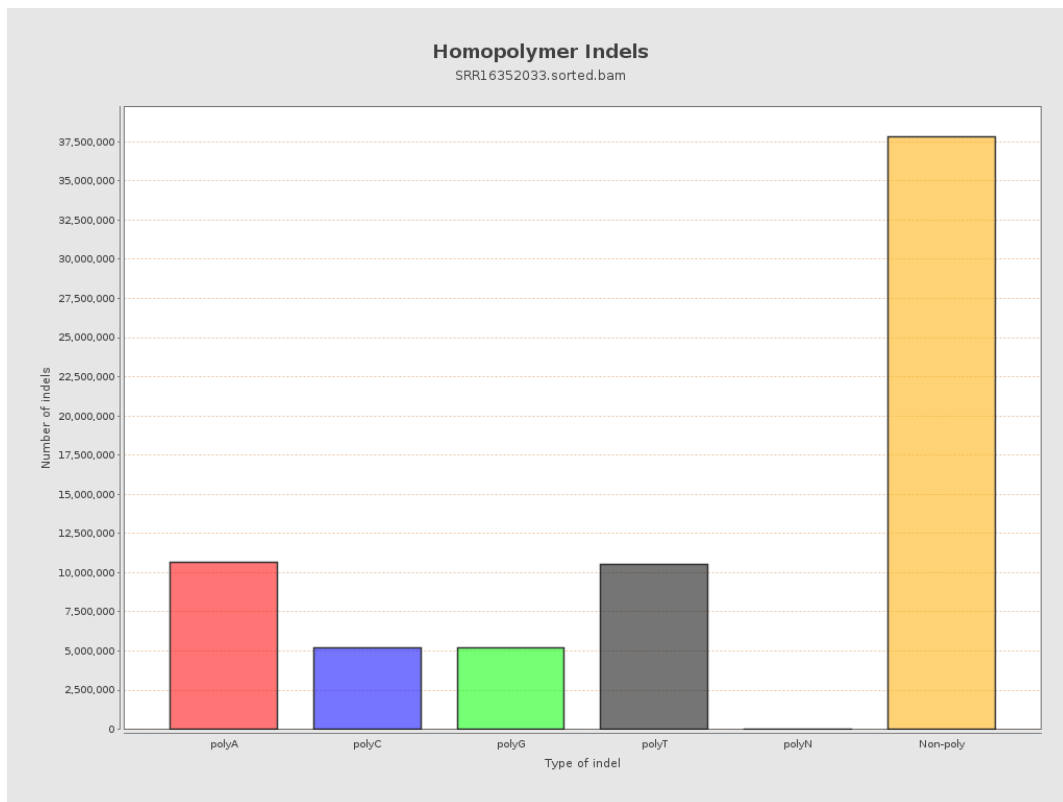
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



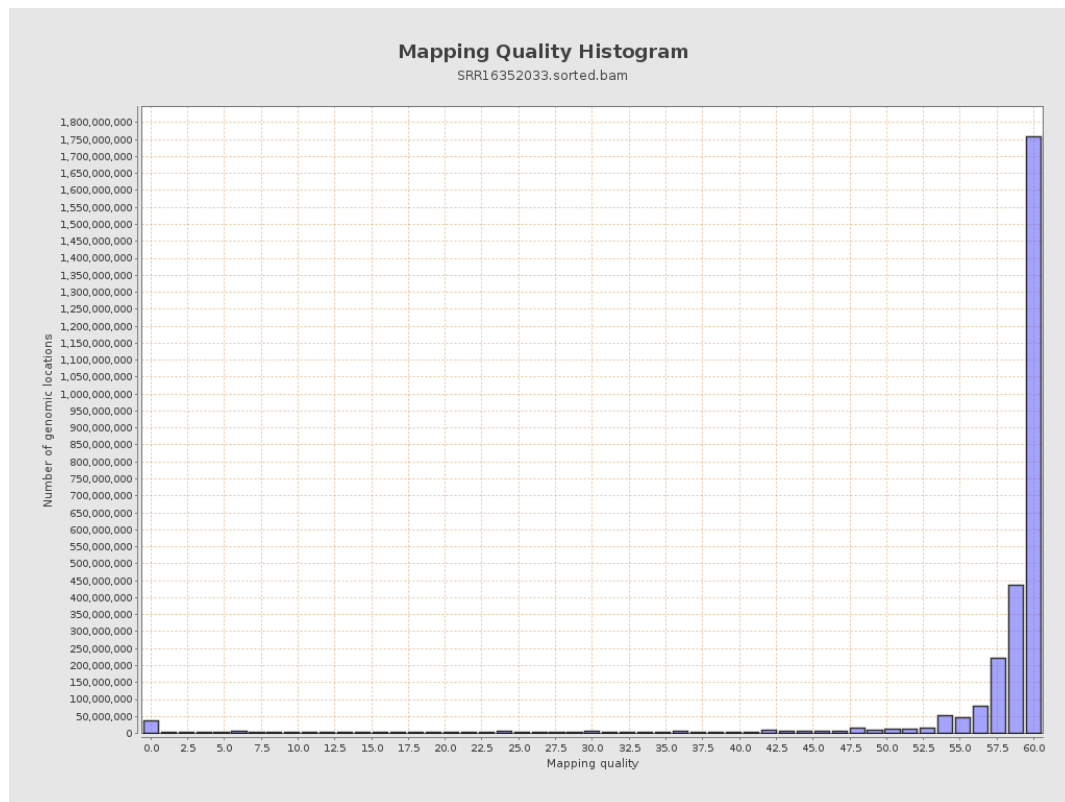
11. Results : Homopolymer Indels



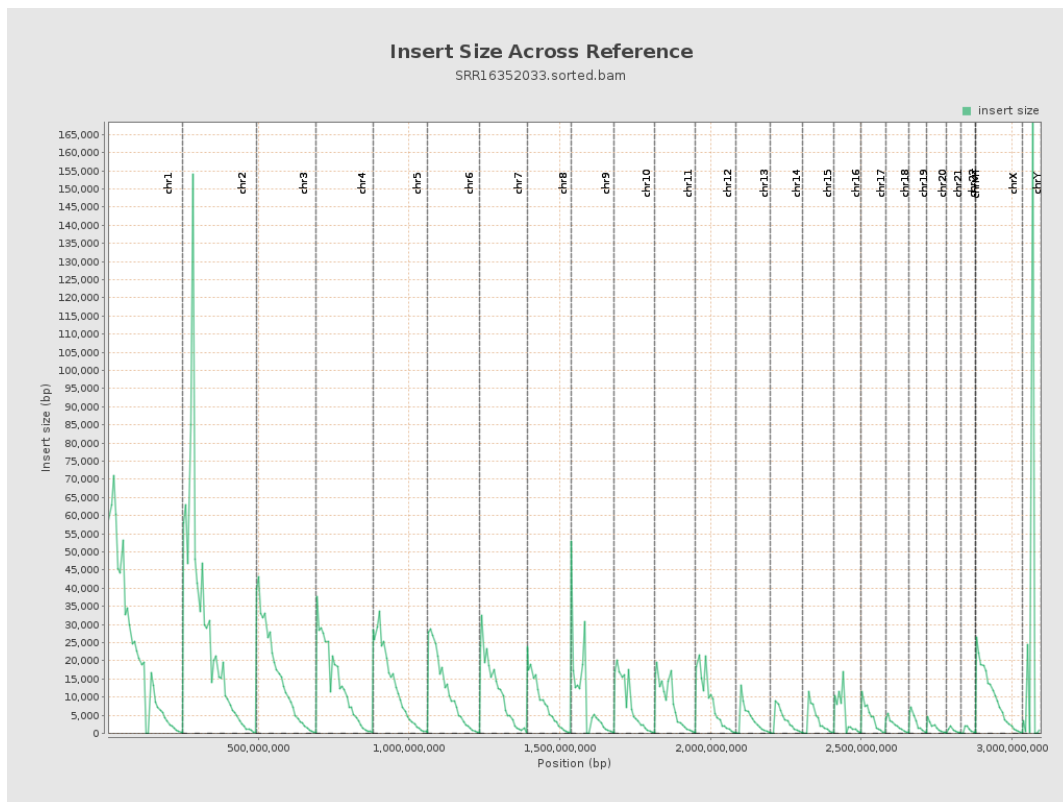
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

