

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/01 05:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352028.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_SRR16352028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352028_1.fastq.gz SRR16352028_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Feb 01 05:31:55 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,594,243,576
Mapped reads	1,549,291,278 / 97.18%
Unmapped reads	44,952,298 / 2.82%
Mapped paired reads	1,549,291,278 / 97.18%
Mapped reads, first in pair	776,192,274 / 48.69%
Mapped reads, second in pair	773,099,004 / 48.49%
Mapped reads, both in pair	1,534,909,976 / 96.28%
Mapped reads, singletons	14,381,302 / 0.9%
Secondary alignments	0
Supplementary alignments	35,069,329 / 2.2%
Read min/max/mean length	30 / 100 / 92.87
Duplicated reads (estimated)	590,326,322 / 37.03%
Duplication rate	34.43%
Clipped reads	222,885,305 / 13.98%

2.2. ACGT Content

Number/percentage of A's	40,770,017,711 / 29.13%
Number/percentage of C's	28,974,371,496 / 20.7%
Number/percentage of T's	40,360,414,656 / 28.84%
Number/percentage of G's	29,860,074,407 / 21.33%
Number/percentage of N's	2,894,883 / 0%

GC Percentage	42.03%
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2.3. Coverage

Mean	45.2425
Standard Deviation	429.0109

2.4. Mapping Quality

Mean Mapping Quality	52.9
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2.5. Insert size

Mean	162,209.5
Standard Deviation	3,936,033.43
P25/Median/P75	217 / 287 / 407

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	1,067,808,447
Insertions	18,043,753
Mapped reads with at least one insertion	1.14%
Deletions	59,042,305
Mapped reads with at least one deletion	3.73%
Homopolymer indels	45.11%

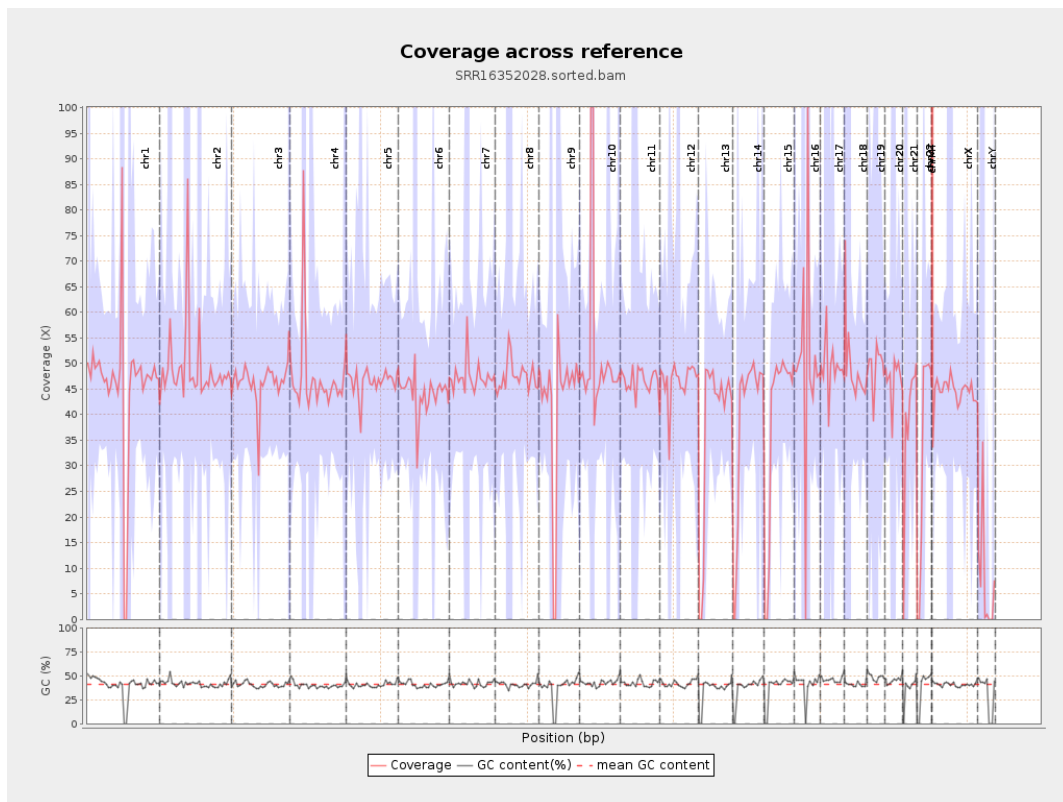
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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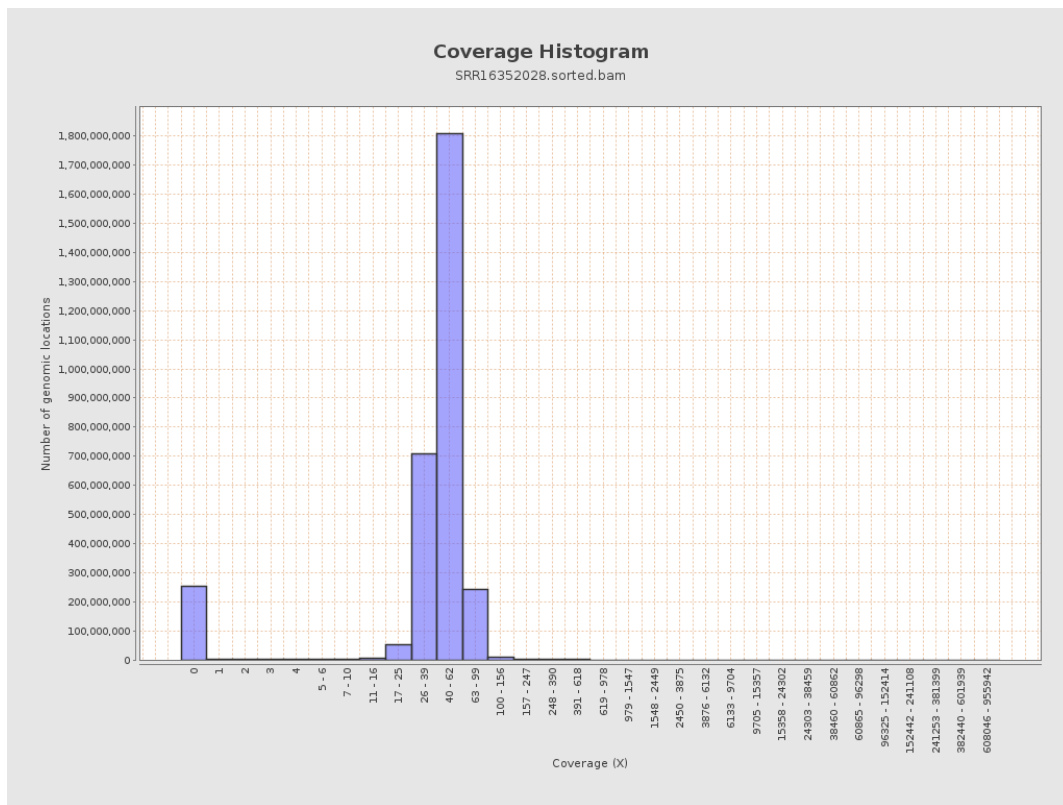
		bases	coverage	deviation
chr1	249250621	11472688660	46.0287	961.7458
chr2	243199373	11962576749	49.1884	472.248
chr3	198022430	9164769802	46.2815	38.1355
chr4	191154276	8956682070	46.8558	284.2339
chr5	180915260	8411511581	46.4942	30.4918
chr6	171115067	7551045907	44.1285	108.2162
chr7	159138663	7538147787	47.3684	286.3815
chr8	146364022	6953634828	47.5092	613.8154
chr9	141213431	5930829848	41.999	296.9757
chr10	135534747	7267768912	53.6229	908.0508
chr11	135006516	6320149646	46.8137	156.5158
chr12	133851895	6229329769	46.539	43.6282
chr13	115169878	4385249000	38.0764	25.1439
chr14	107349540	4186535076	38.9991	42.2418
chr15	102531392	3940112115	38.4283	27.7744
chr16	90354753	4569241458	50.57	369.7961
chr17	81195210	3992154098	49.1674	166.7679
chr18	78077248	3767860751	48.2581	486.9701
chr19	59128983	2933468435	49.6113	393.9569
chr20	63025520	2951053874	46.8232	52.895
chr21	48129895	1897044015	39.4151	98.3308
chr22	51304566	1746601916	34.0438	37.4482
chrMT	16571	569665998	34,377.2855	11,647.2236
chrX	155270560	6903212461	44.4592	80.7478

chrY	59373566	455638949	7.6741	285.4081
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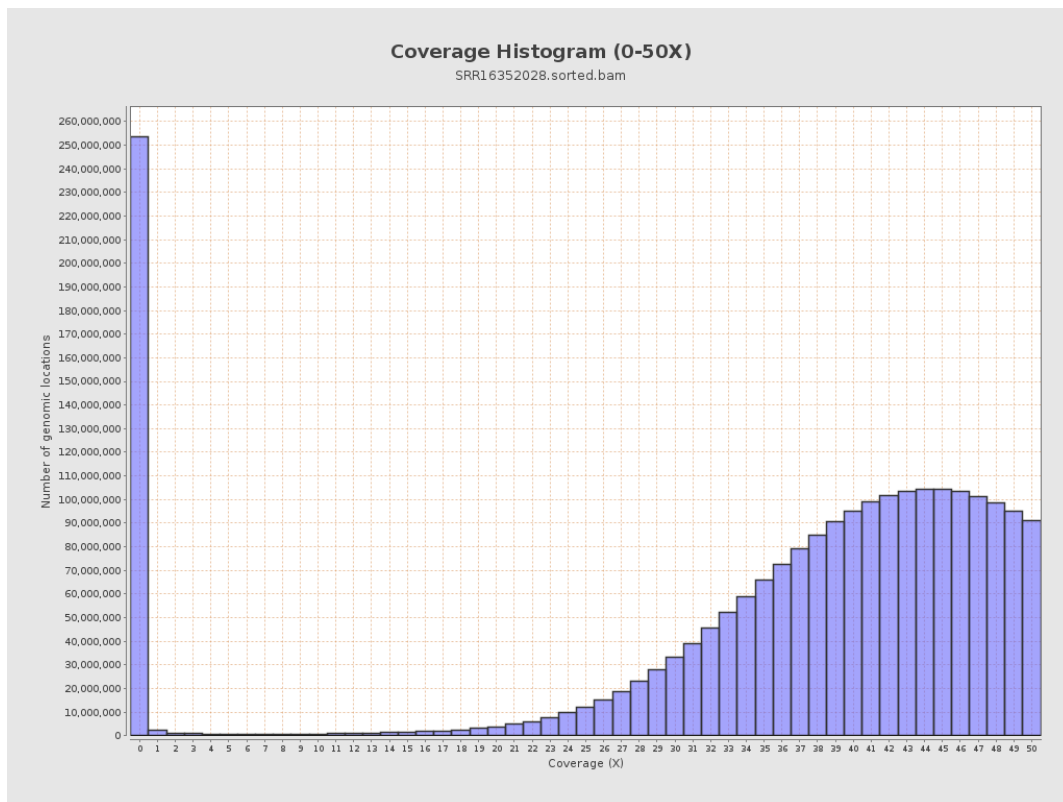
3. Results : Coverage across reference



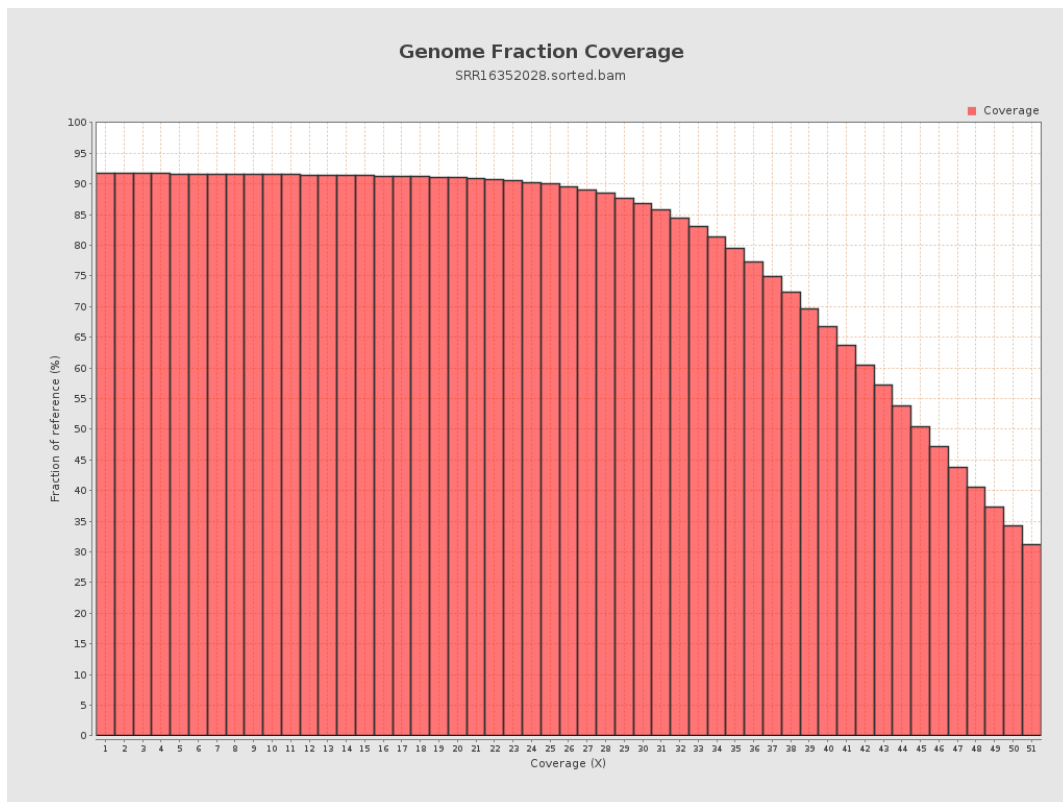
4. Results : Coverage Histogram



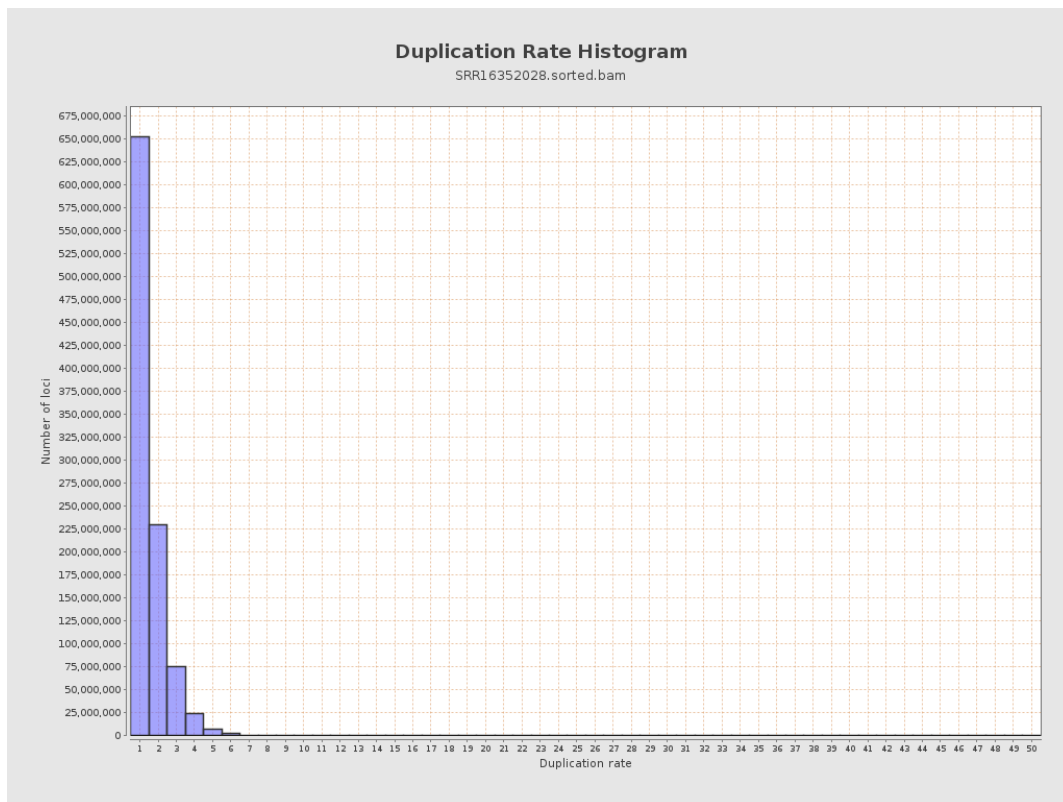
5. Results : Coverage Histogram (0-50X)



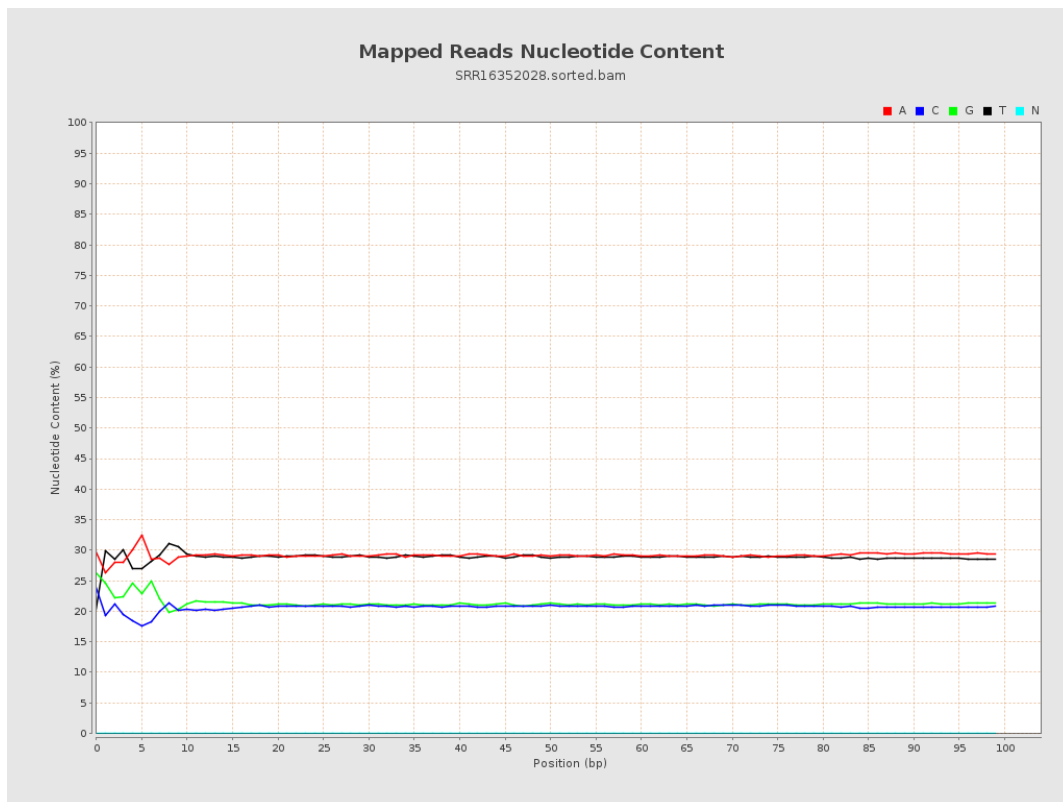
6. Results : Genome Fraction Coverage



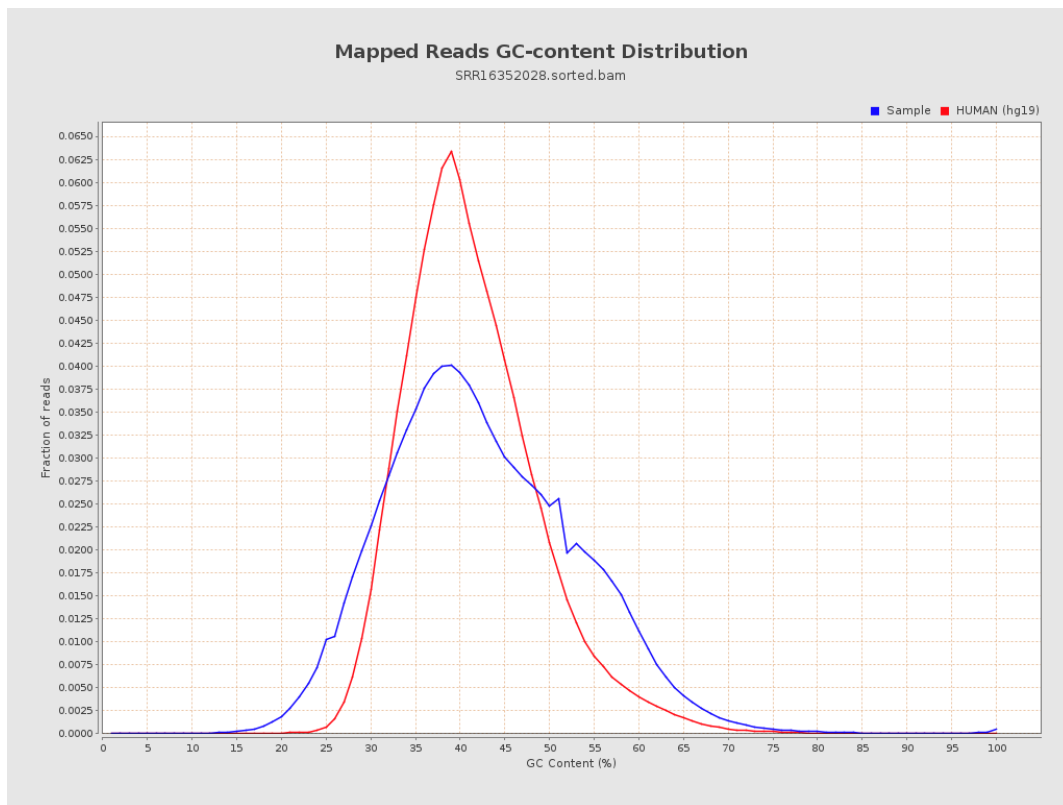
7. Results : Duplication Rate Histogram



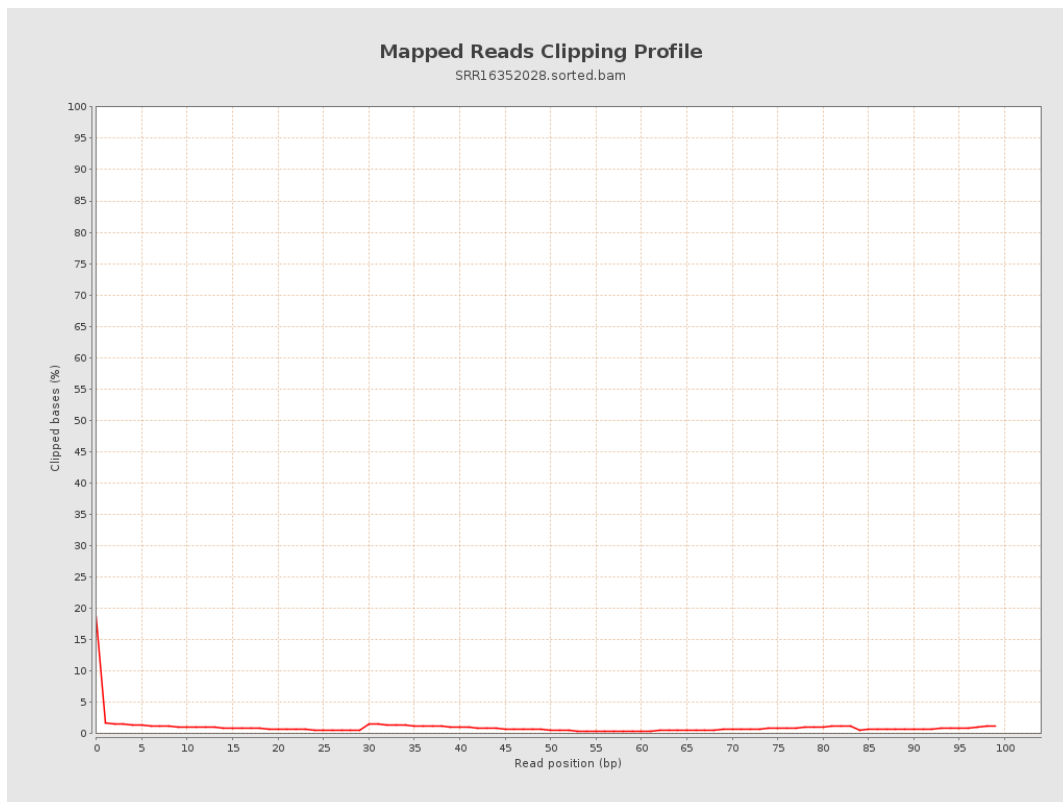
8. Results : Mapped Reads Nucleotide Content



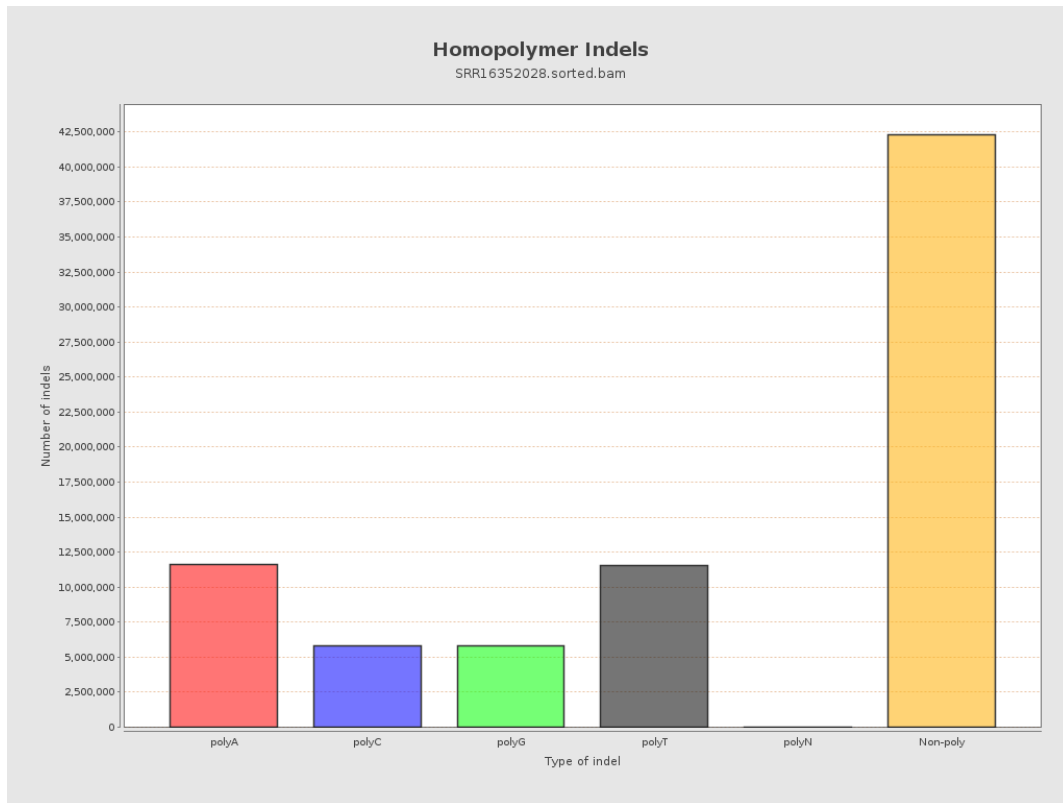
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



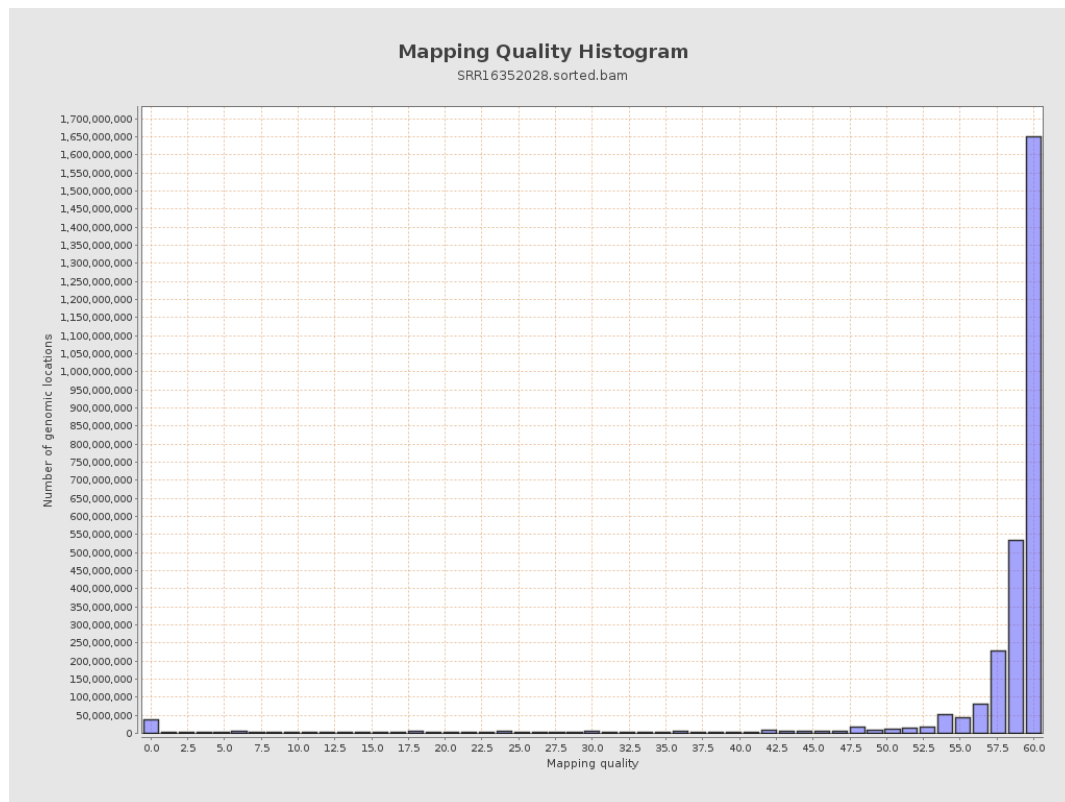
11. Results : Homopolymer Indels



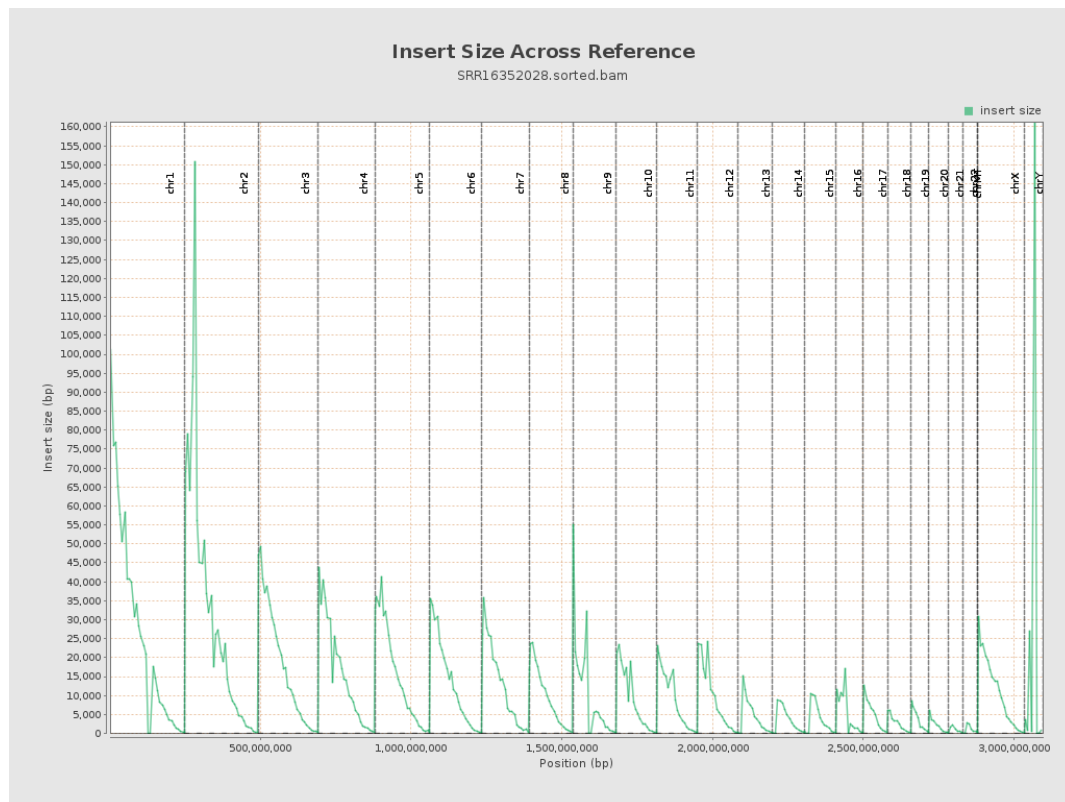
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

