

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/19 08:02:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362022.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_SRR16362022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362022_1.fastq.gz SRR16362022_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Feb 19 08:02:44 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16362022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	338,239,990
Mapped reads	326,323,285 / 96.48%
Unmapped reads	11,916,705 / 3.52%
Mapped paired reads	326,323,285 / 96.48%
Mapped reads, first in pair	164,444,821 / 48.62%
Mapped reads, second in pair	161,878,464 / 47.86%
Mapped reads, both in pair	322,987,202 / 95.49%
Mapped reads, singletons	3,336,083 / 0.99%
Secondary alignments	0
Supplementary alignments	15,023,600 / 4.44%
Read min/max/mean length	30 / 150 / 152.22
Duplicated reads (estimated)	121,245,062 / 35.85%
Duplication rate	31.76%
Clipped reads	214,436,541 / 63.4%

2.2. ACGT Content

Number/percentage of A's	13,081,422,440 / 28.88%
Number/percentage of C's	9,542,690,531 / 21.07%
Number/percentage of T's	13,014,437,604 / 28.73%
Number/percentage of G's	9,653,069,531 / 21.31%
Number/percentage of N's	3,395,341 / 0.01%

GC Percentage	42.38%
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2.3. Coverage

Mean	14.6444
Standard Deviation	153.035

2.4. Mapping Quality

Mean Mapping Quality	53.8
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2.5. Insert size

Mean	167,807.39
Standard Deviation	3,964,615.85
P25/Median/P75	193 / 257 / 364

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	419,308,724
Insertions	8,204,598
Mapped reads with at least one insertion	2.39%
Deletions	21,280,698
Mapped reads with at least one deletion	6.25%
Homopolymer indels	44.61%

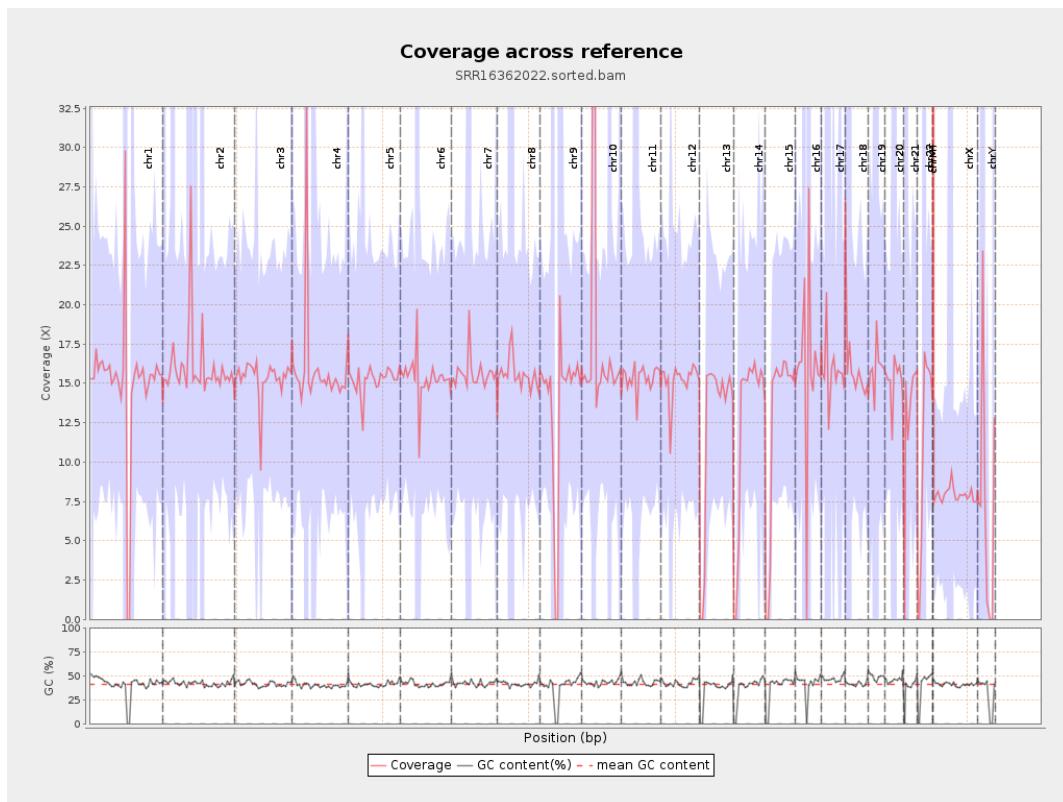
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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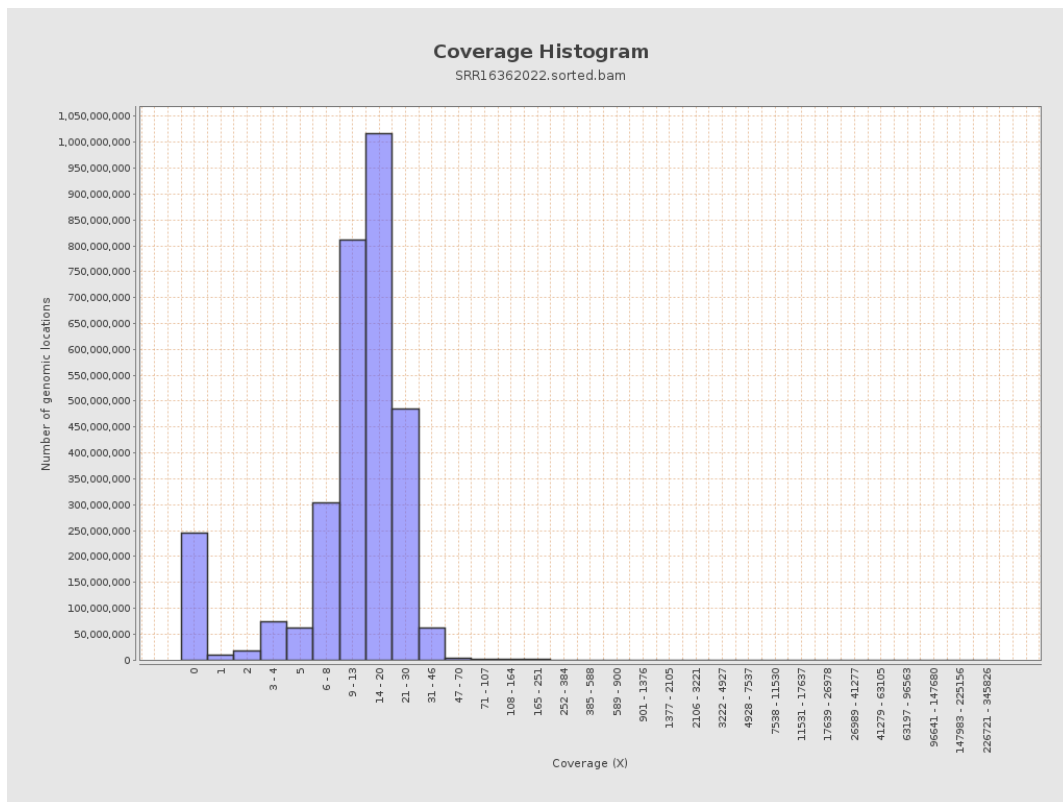
		bases	coverage	deviation
chr1	249250621	3742701241	15.0158	338.0351
chr2	243199373	3909559647	16.0755	116.2492
chr3	198022430	3033540934	15.3192	18.2467
chr4	191154276	3043119037	15.9197	150.9453
chr5	180915260	2757162035	15.2401	11.117
chr6	171115067	2622307965	15.3248	56.9403
chr7	159138663	2491205626	15.6543	108.594
chr8	146364022	2275865775	15.5494	153.5223
chr9	141213431	1941651210	13.7498	162.7443
chr10	135534747	2403774043	17.7355	344.9482
chr11	135006516	2069098522	15.3259	47.7377
chr12	133851895	2038514066	15.2296	9.8242
chr13	115169878	1440335062	12.5062	9.0168
chr14	107349540	1372427803	12.7847	12.0383
chr15	102531392	1283918567	12.5222	9.1798
chr16	90354753	1440152313	15.9389	99.9223
chr17	81195210	1284492860	15.8198	70.2651
chr18	78077248	1242893248	15.9188	158.5225
chr19	59128983	944267269	15.9696	196.399
chr20	63025520	951782687	15.1015	42.1609
chr21	48129895	632855431	13.1489	76.7074
chr22	51304566	564622257	11.0053	43.575
chrMT	16571	173943186	10,496.843	1,627.9715
chrX	155270560	1231964329	7.9343	21.8531

chrY	59373566	442288702	7.4493	192.2761
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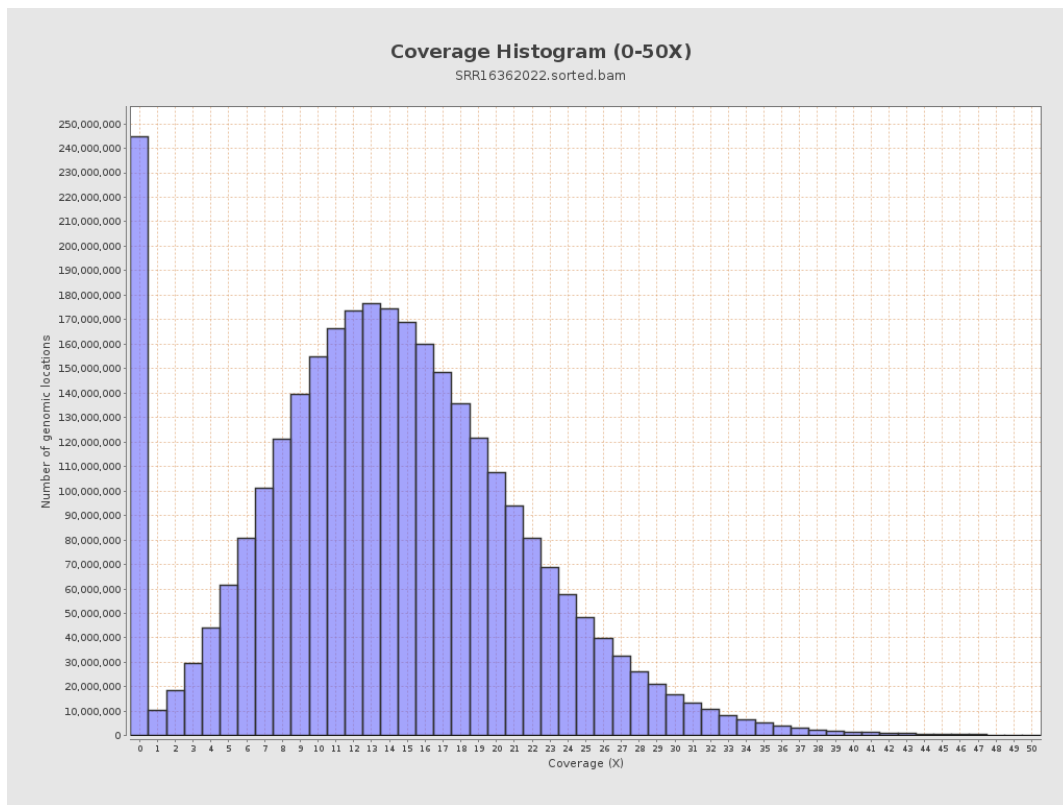
3. Results : Coverage across reference



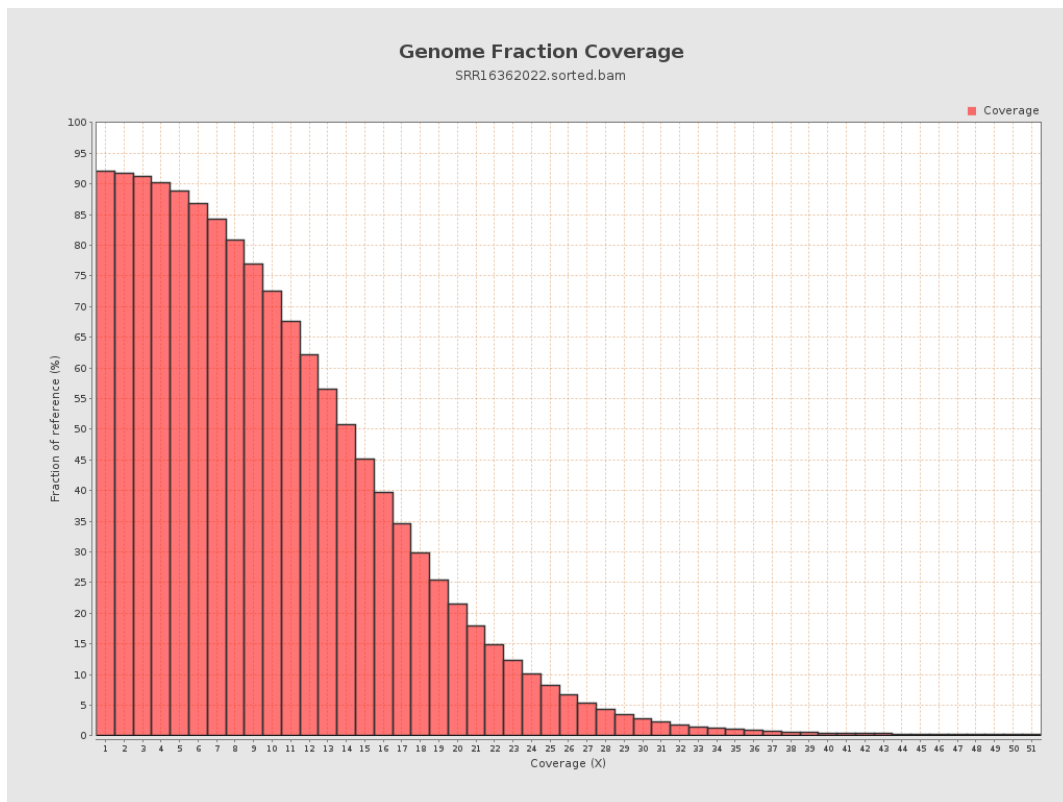
4. Results : Coverage Histogram



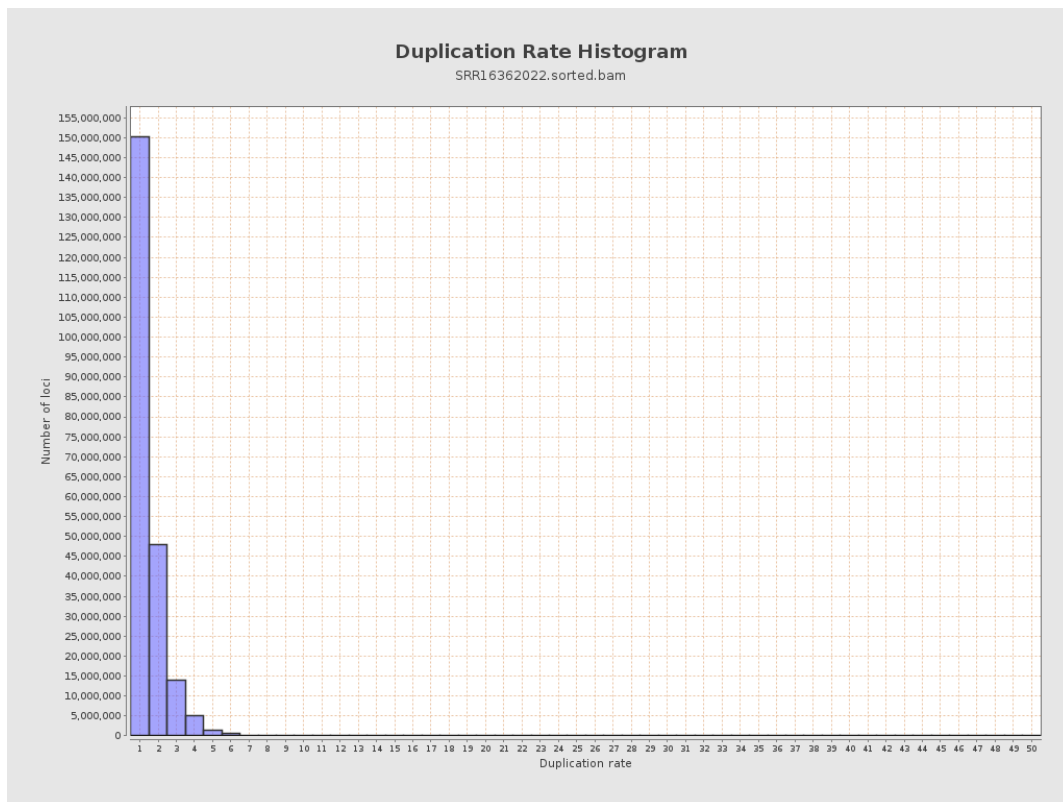
5. Results : Coverage Histogram (0-50X)



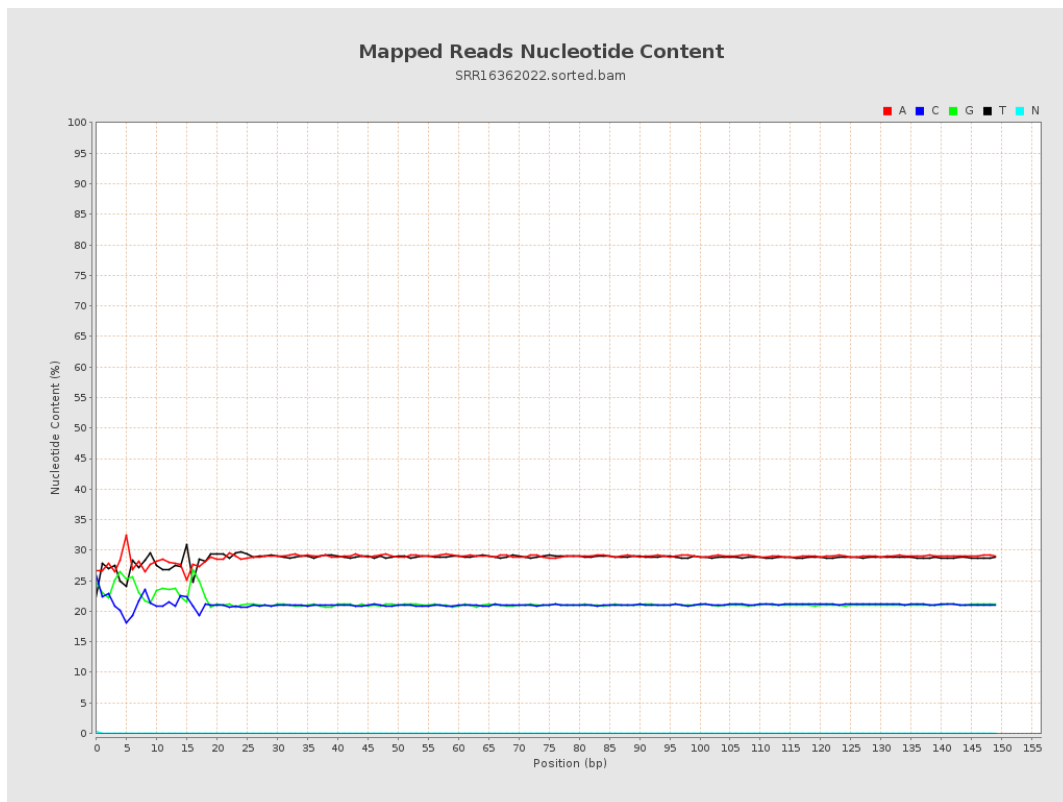
6. Results : Genome Fraction Coverage



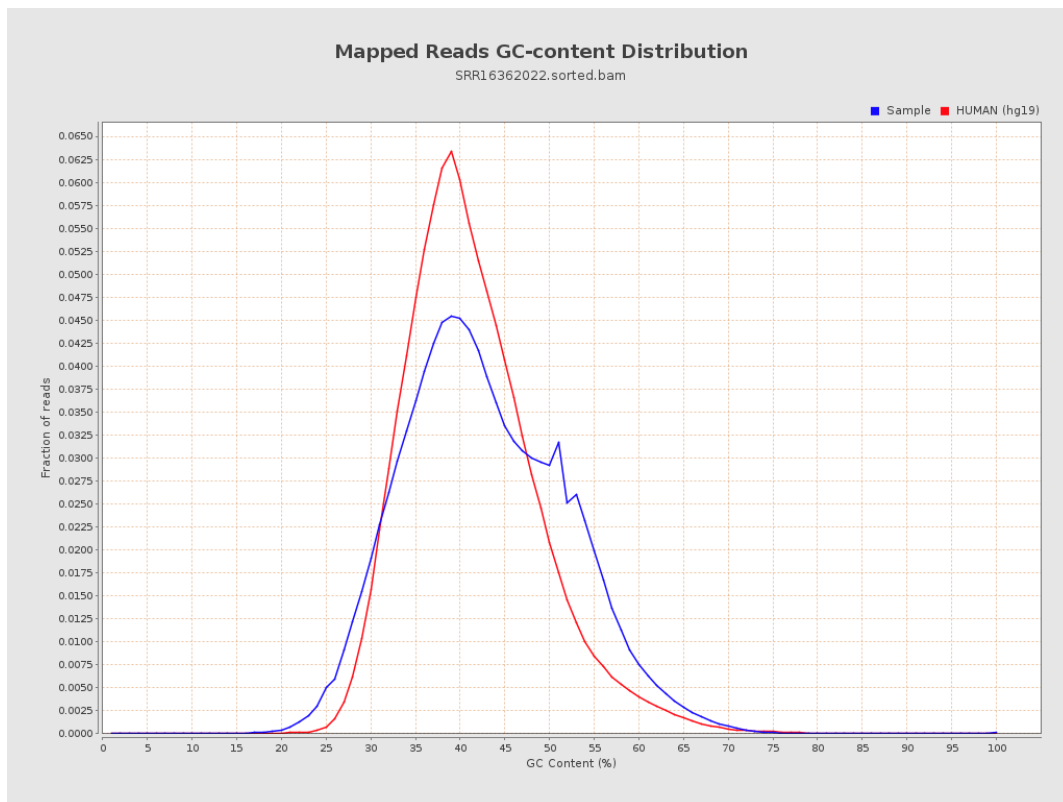
7. Results : Duplication Rate Histogram



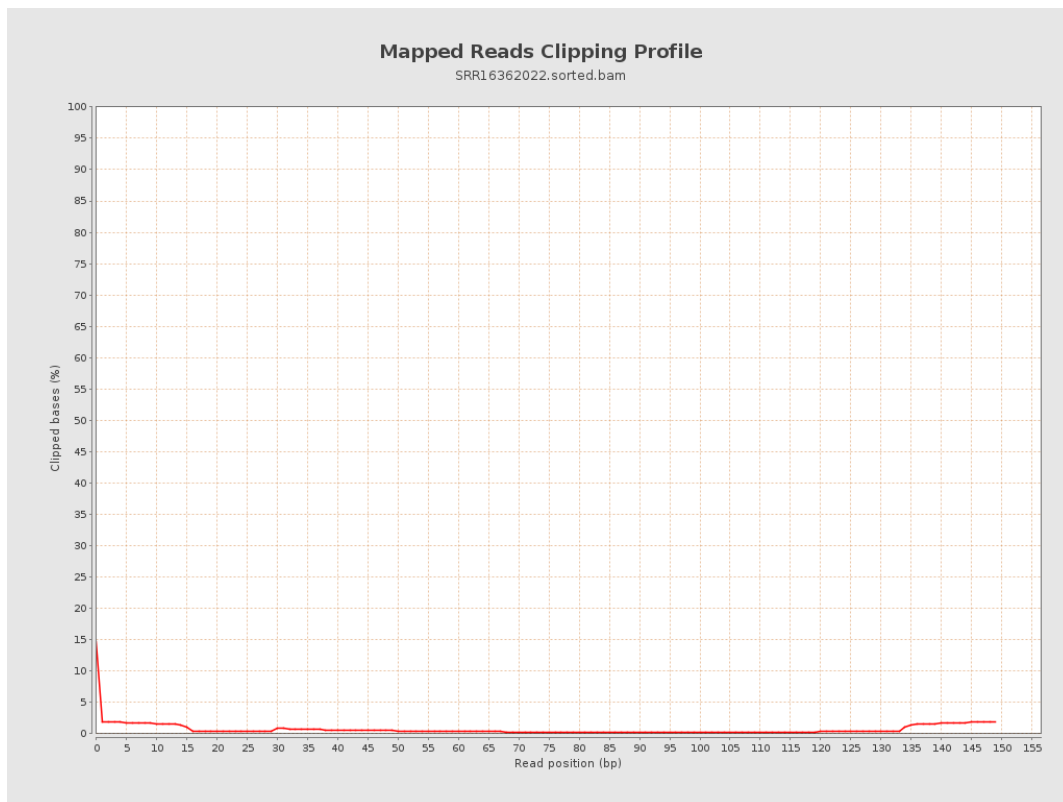
8. Results : Mapped Reads Nucleotide Content



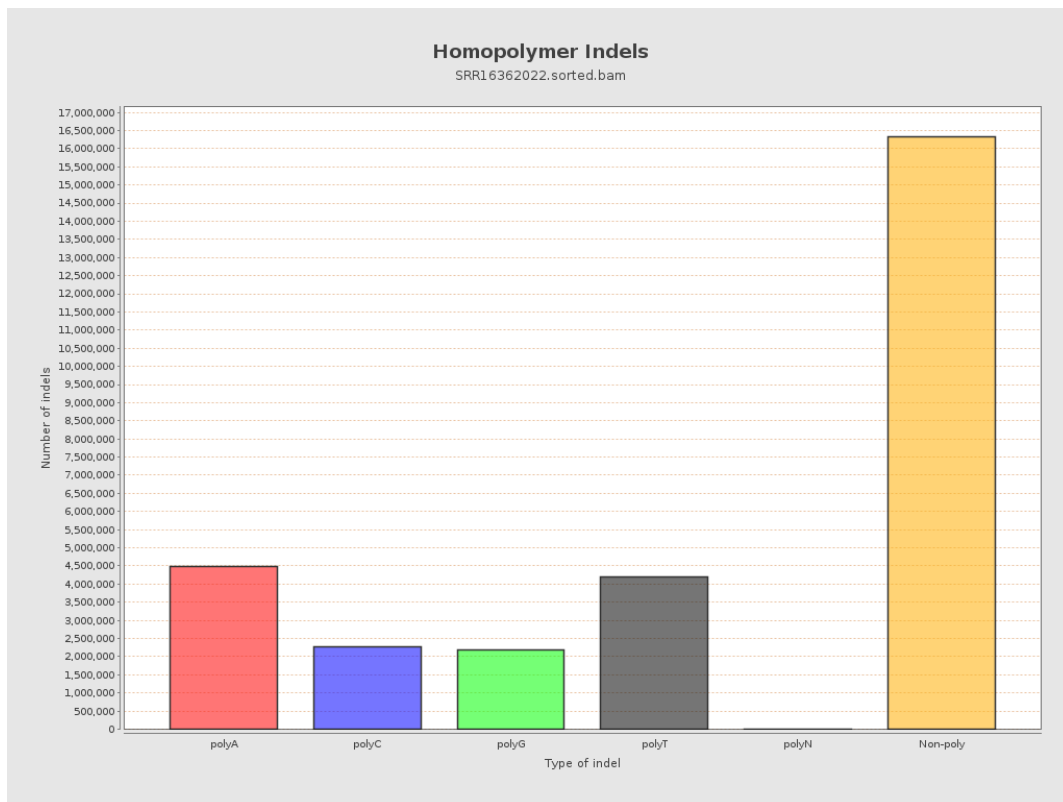
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



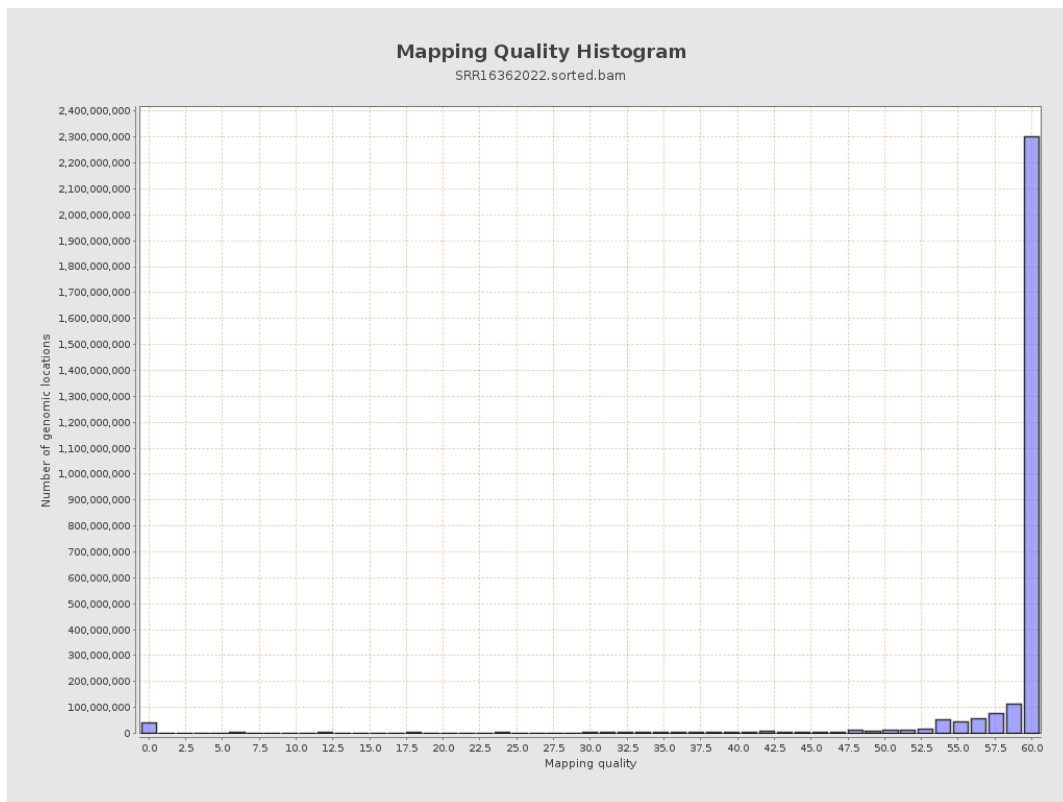
11. Results : Homopolymer Indels



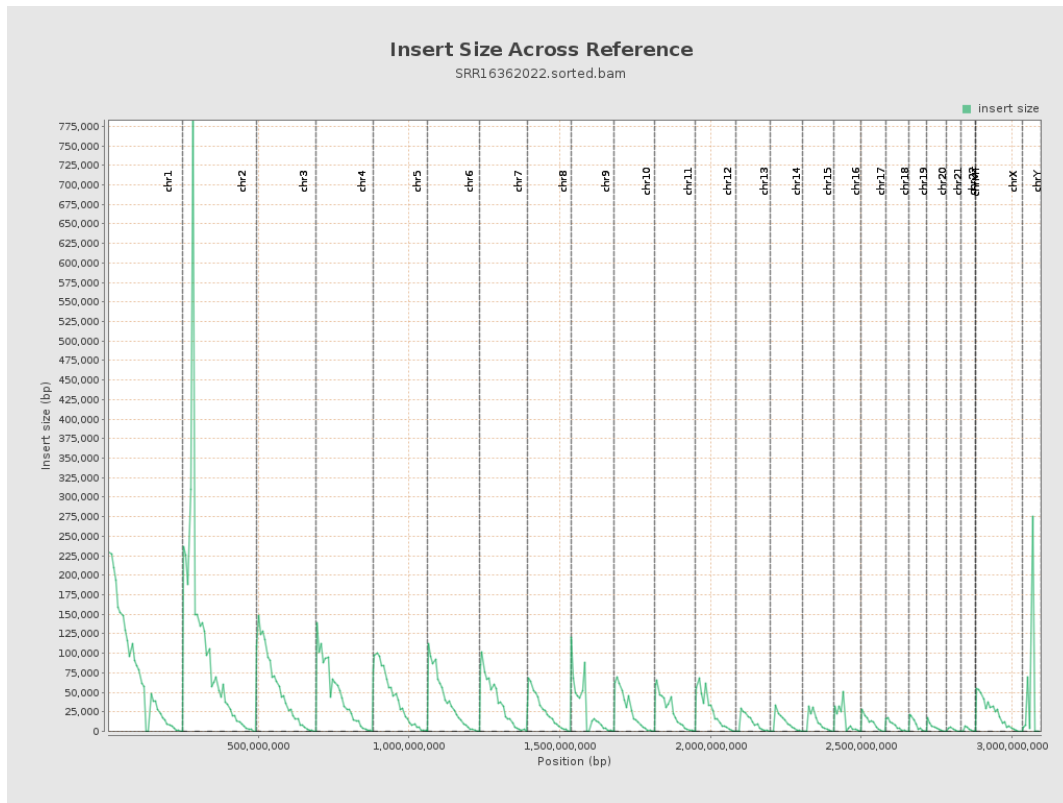
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

