

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 19:20:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432730.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_SRR6432730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432730_1.fastq.gz SRR6432730_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 19:20:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	371,336,068
Mapped reads	371,172,327 / 99.96%
Unmapped reads	163,741 / 0.04%
Mapped paired reads	371,172,327 / 99.96%
Mapped reads, first in pair	185,592,133 / 49.98%
Mapped reads, second in pair	185,580,194 / 49.98%
Mapped reads, both in pair	371,111,790 / 99.94%
Mapped reads, singletons	60,537 / 0.02%
Secondary alignments	0
Supplementary alignments	172,036 / 0.05%
Read min/max/mean length	30 / 150 / 140.62
Duplicated reads (estimated)	177,516,113 / 47.8%
Duplication rate	31.72%
Clipped reads	99,286,853 / 26.74%

2.2. ACGT Content

Number/percentage of A's	14,036,159,068 / 27.45%
Number/percentage of C's	11,056,213,173 / 21.62%
Number/percentage of T's	13,849,067,242 / 27.09%
Number/percentage of G's	12,188,436,595 / 23.84%
Number/percentage of N's	1,931,926 / 0%

GC Percentage	45.46%
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2.3. Coverage

Mean	16.5334
Standard Deviation	48.9405

2.4. Mapping Quality

Mean Mapping Quality	55.38
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2.5. Insert size

Mean	75,597.92
Standard Deviation	2,745,854.14
P25/Median/P75	291 / 309 / 327

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	521,999,498
Insertions	10,611,113
Mapped reads with at least one insertion	2.79%
Deletions	34,821,980
Mapped reads with at least one deletion	8.94%
Homopolymer indels	51.83%

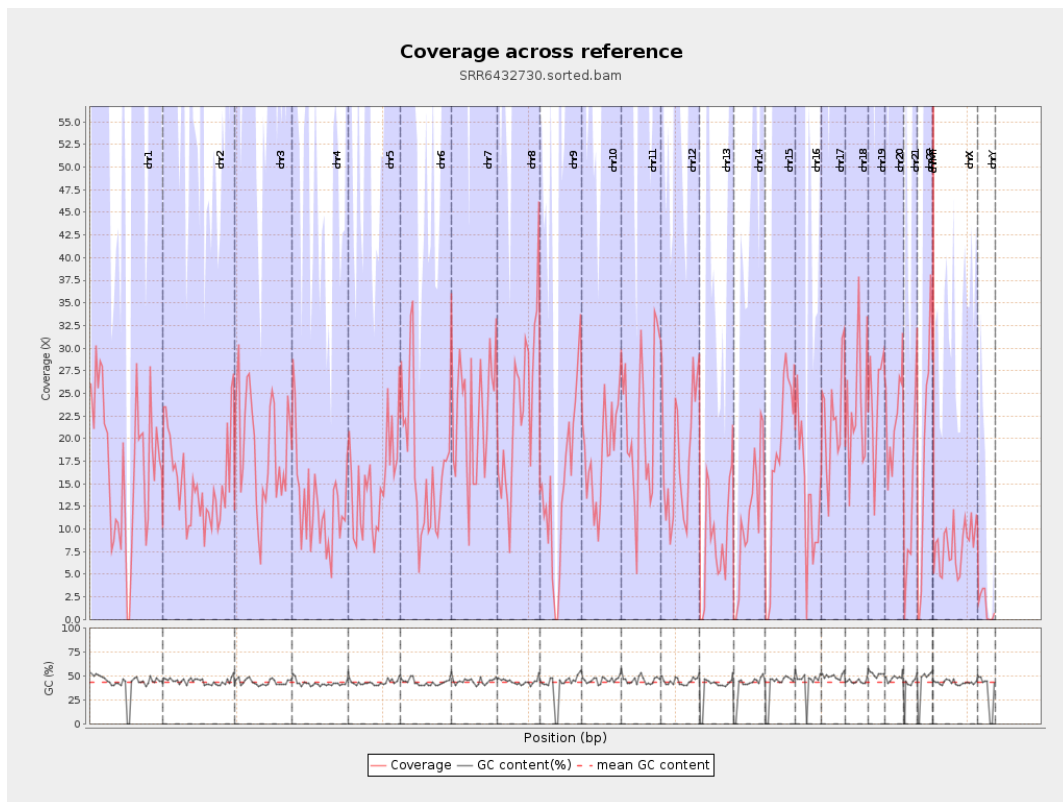
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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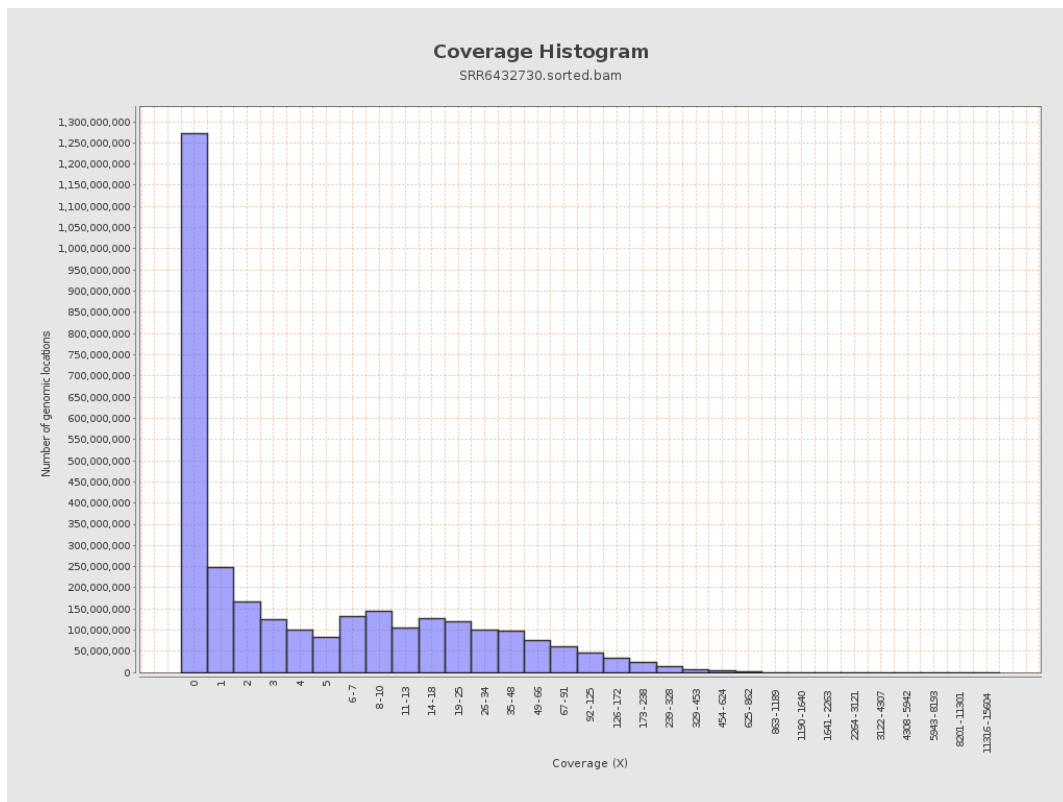
		bases	coverage	deviation
chr1	249250621	4226166618	16.9555	49.9739
chr2	243199373	3672577969	15.1011	47.0894
chr3	198022430	3687575883	18.622	49.6614
chr4	191154276	2437962807	12.7539	38.4714
chr5	180915260	2752250230	15.2129	42.9155
chr6	171115067	2849339122	16.6516	47.0274
chr7	159138663	3633547847	22.8326	60.2631
chr8	146364022	3401029614	23.2368	62.8021
chr9	141213431	2074249674	14.6888	48.2165
chr10	135534747	2466229030	18.1963	48.419
chr11	135006516	2937628533	21.7592	57.5398
chr12	133851895	2431568349	18.1661	49.9147
chr13	115169878	1023802518	8.8895	30.244
chr14	107349540	1210802884	11.2791	35.157
chr15	102531392	1807189718	17.6257	51.1091
chr16	90354753	1261392799	13.9604	48.2363
chr17	81195210	1797901510	22.143	57.9638
chr18	78077248	1794369230	22.982	62.833
chr19	59128983	1421008378	24.0323	65.1829
chr20	63025520	1373916160	21.7994	54.9298
chr21	48129895	619249786	12.8662	47.8354
chr22	51304566	942815721	18.3768	55.4403
chrMT	16571	3981899	240.2932	452.0817
chrX	155270560	1266286567	8.1554	24.872

chrY	59373566	89443052	1.5064	14.8917
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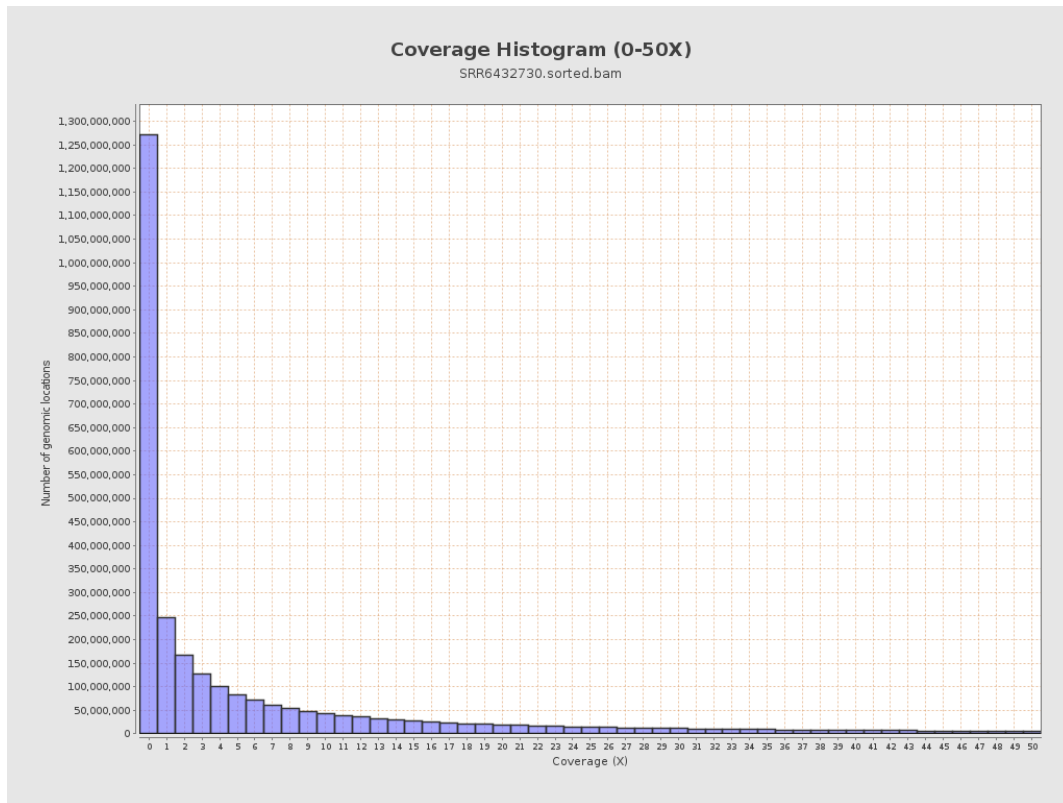
3. Results : Coverage across reference



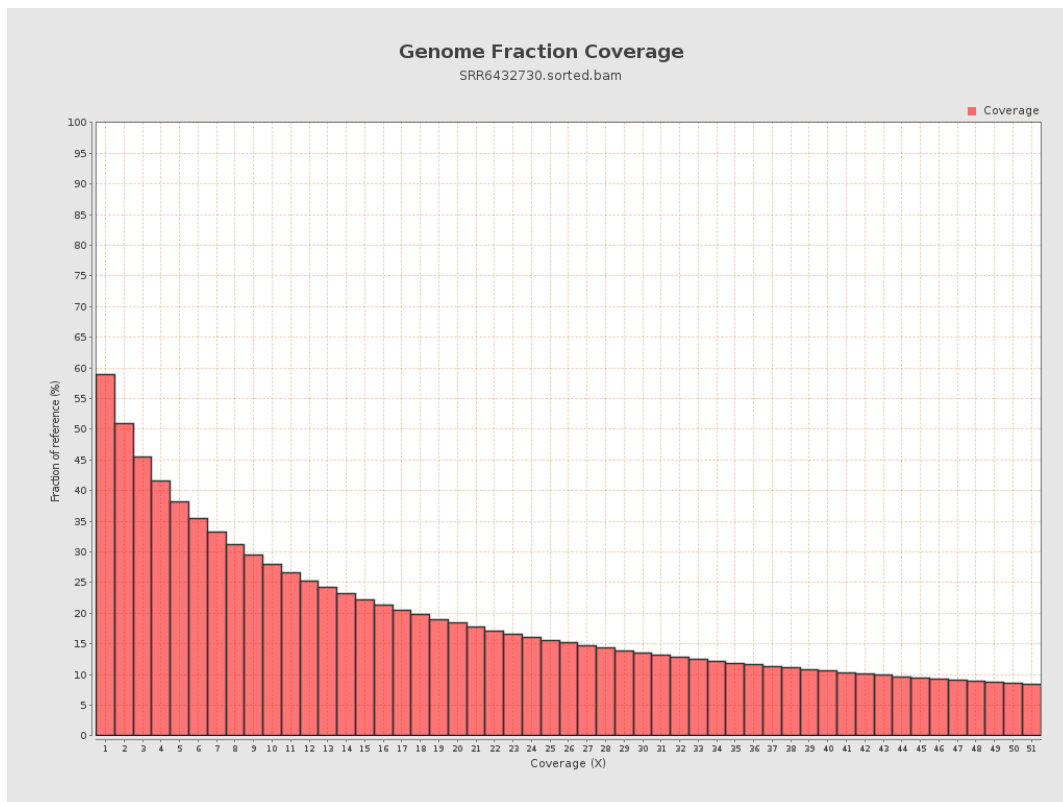
4. Results : Coverage Histogram



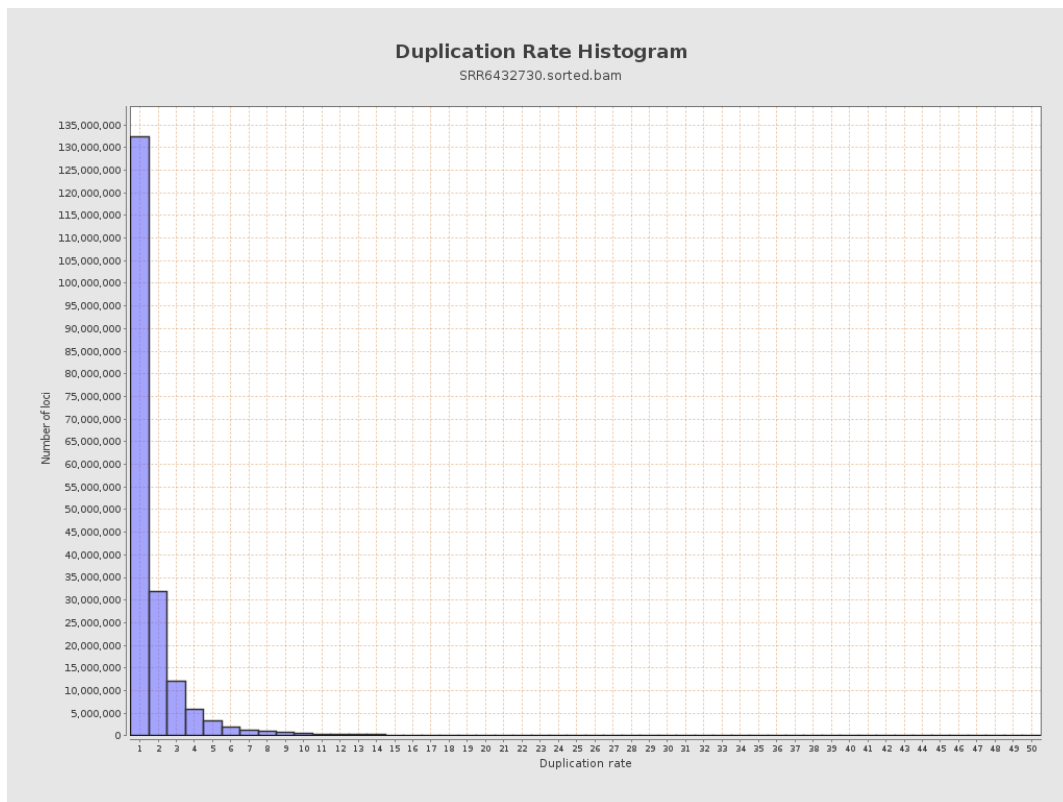
5. Results : Coverage Histogram (0-50X)



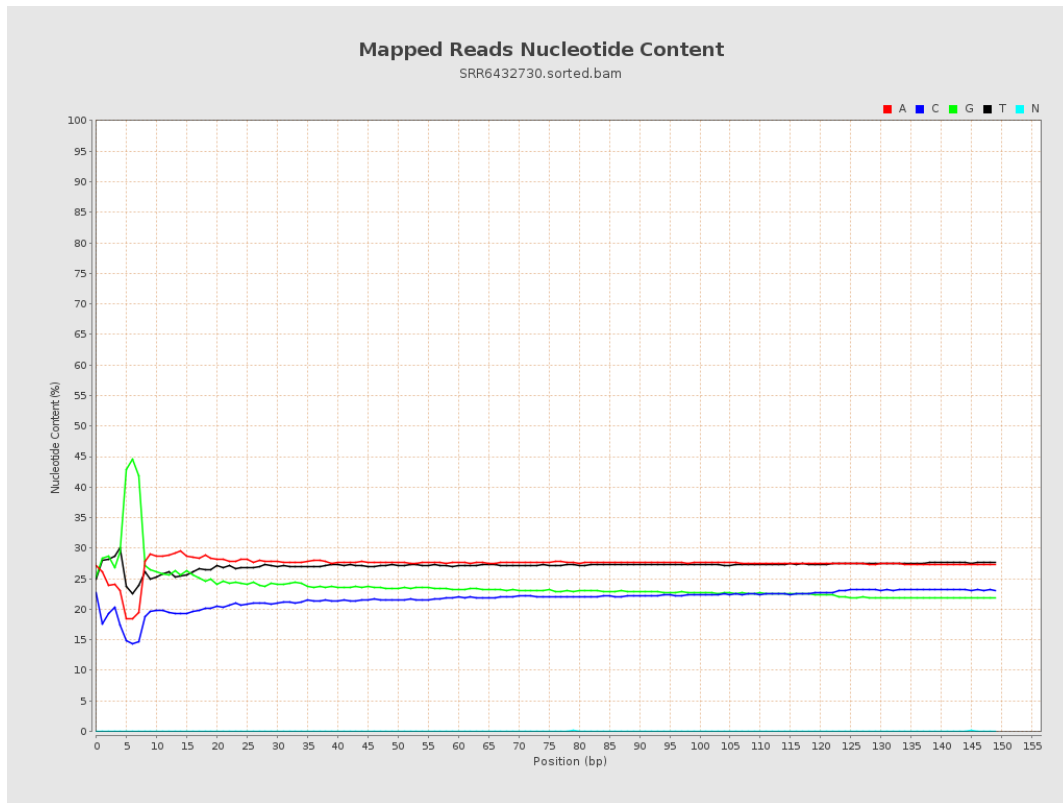
6. Results : Genome Fraction Coverage



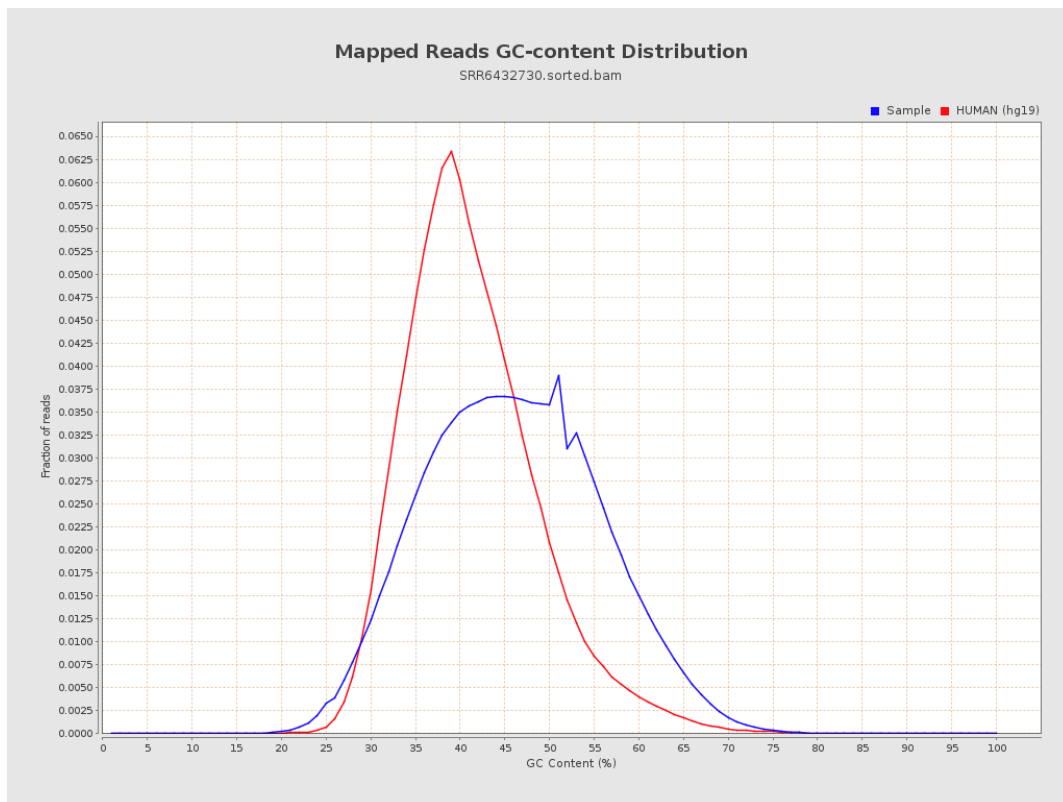
7. Results : Duplication Rate Histogram



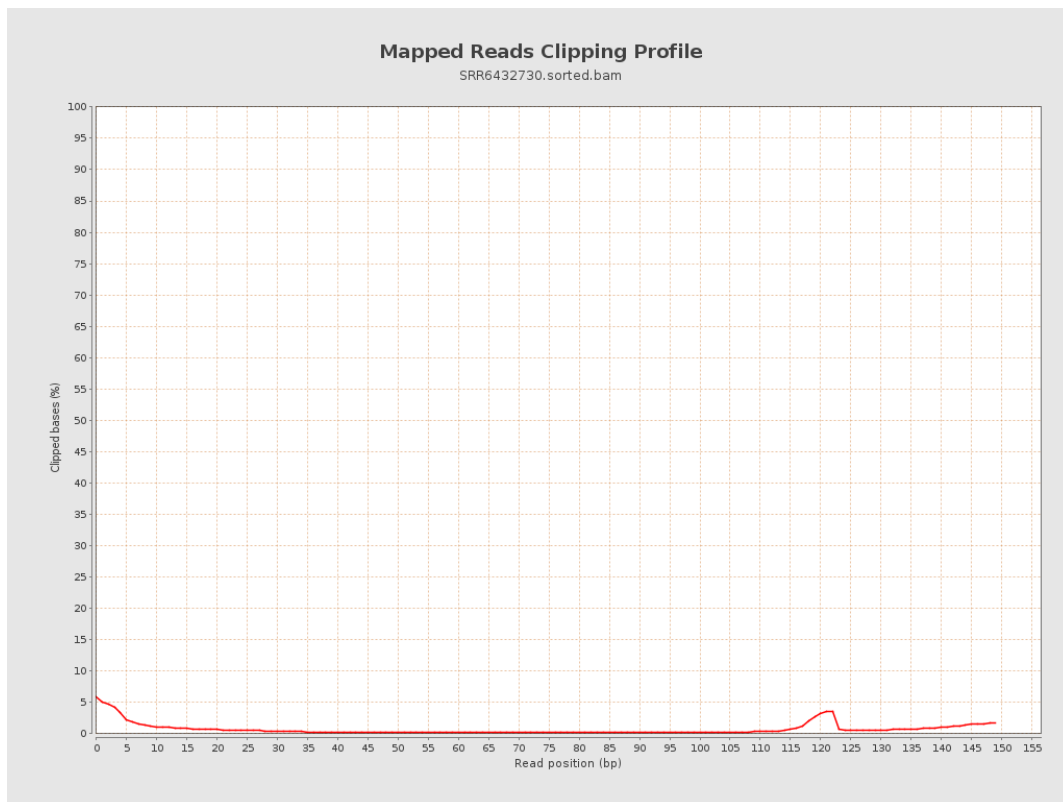
8. Results : Mapped Reads Nucleotide Content



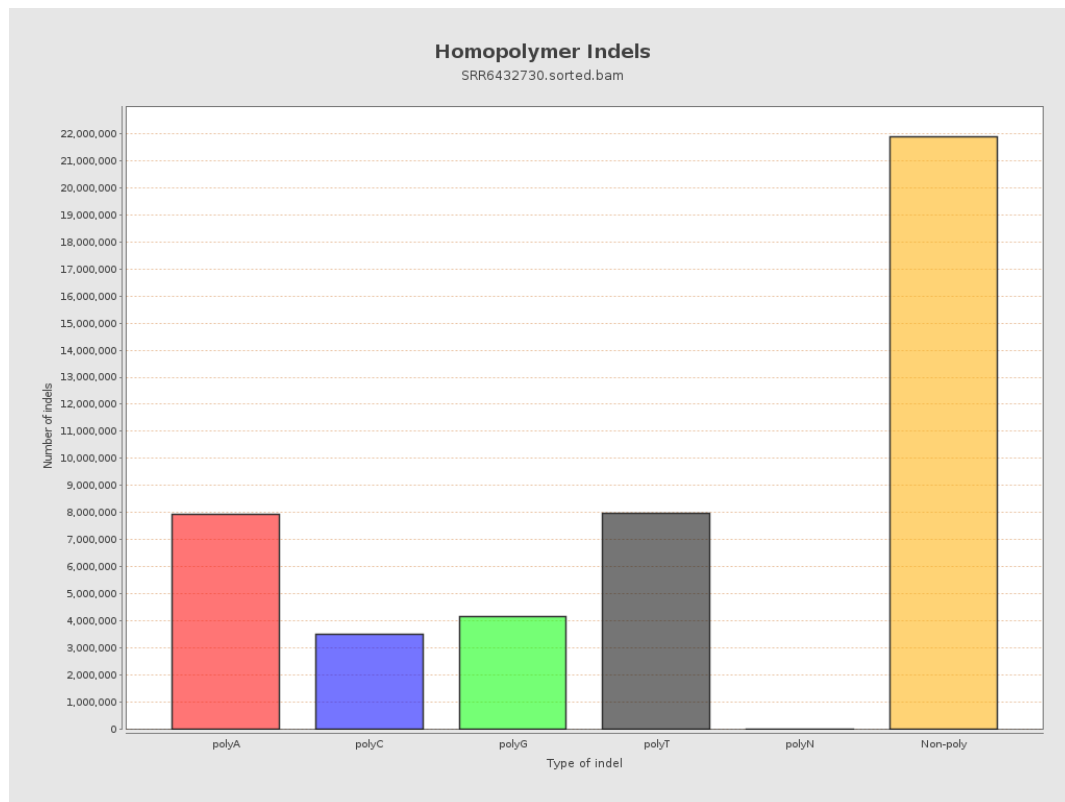
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



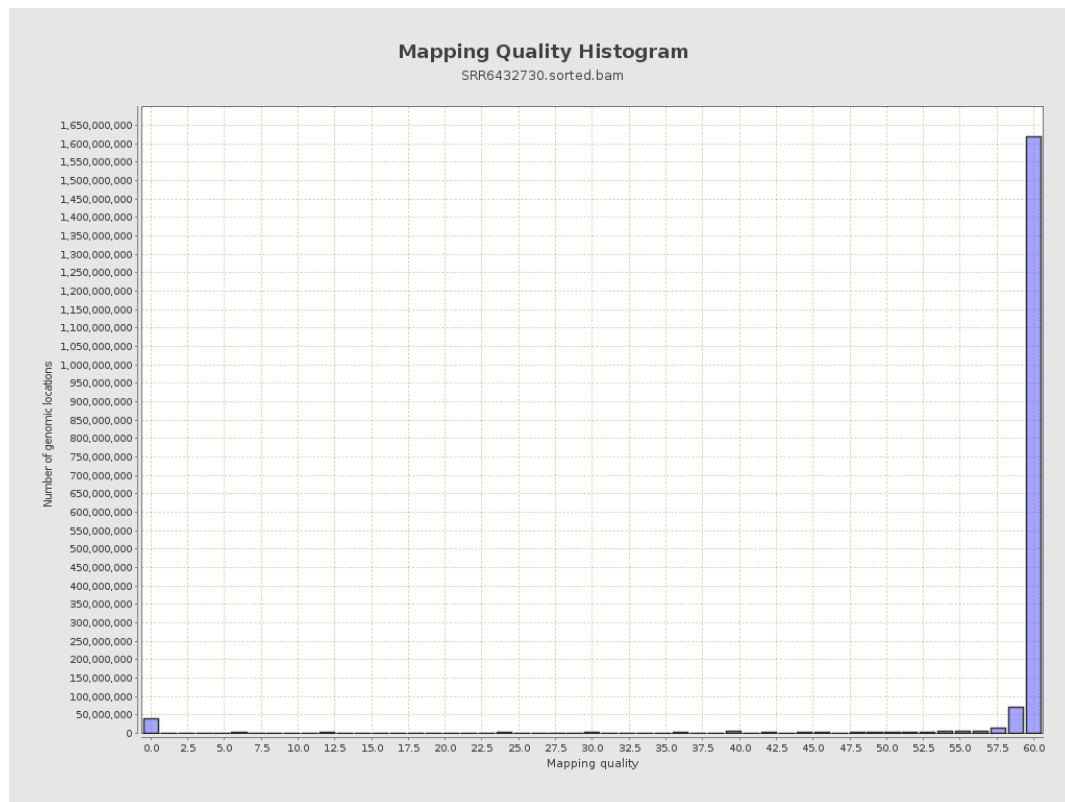
11. Results : Homopolymer Indels



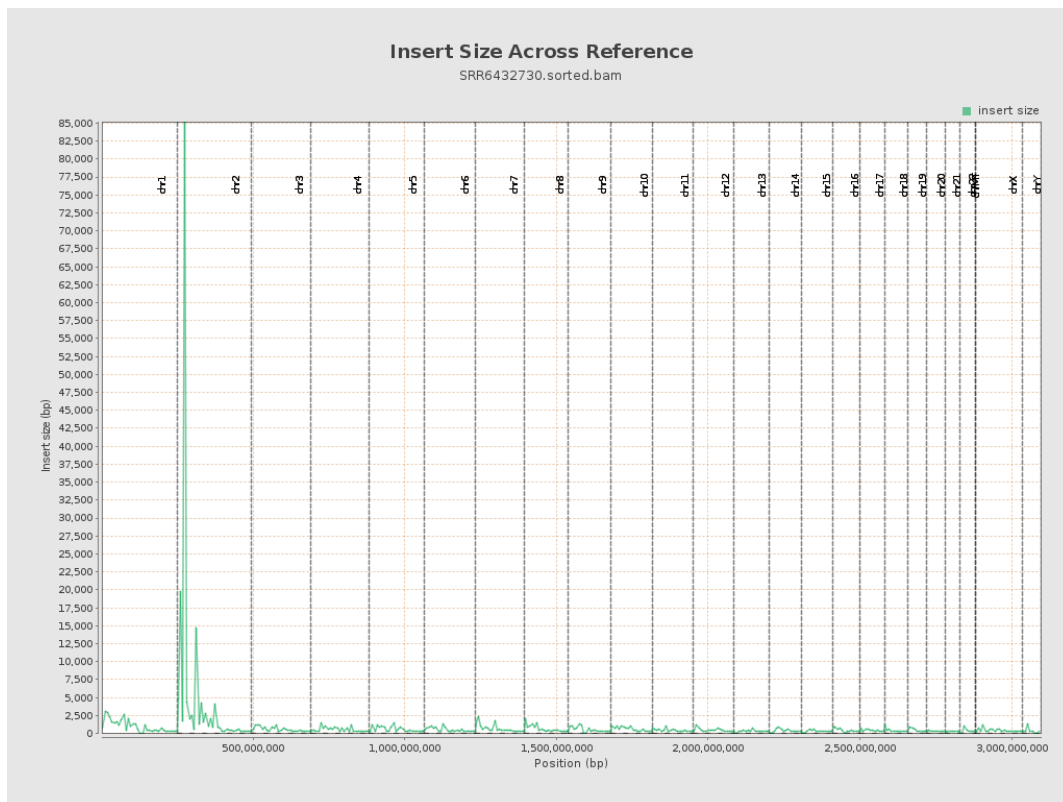
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

