

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 15:30:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432722.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_SRR6432722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432722_1.fastq.gz SRR6432722_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 15:30:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	373,729,990
Mapped reads	373,591,062 / 99.96%
Unmapped reads	138,928 / 0.04%
Mapped paired reads	373,591,062 / 99.96%
Mapped reads, first in pair	186,799,832 / 49.98%
Mapped reads, second in pair	186,791,230 / 49.98%
Mapped reads, both in pair	373,539,690 / 99.95%
Mapped reads, singletons	51,372 / 0.01%
Secondary alignments	0
Supplementary alignments	2,837,477 / 0.76%
Read min/max/mean length	30 / 150 / 139.65
Duplicated reads (estimated)	190,052,382 / 50.85%
Duplication rate	32.27%
Clipped reads	103,384,138 / 27.66%

2.2. ACGT Content

Number/percentage of A's	14,134,346,348 / 27.61%
Number/percentage of C's	10,838,130,955 / 21.17%
Number/percentage of T's	13,932,782,397 / 27.22%
Number/percentage of G's	12,274,211,192 / 23.98%
Number/percentage of N's	9,307,526 / 0.02%

GC Percentage	45.15%
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2.3. Coverage

Mean	16.5515
Standard Deviation	47.394

2.4. Mapping Quality

Mean Mapping Quality	57.42
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2.5. Insert size

Mean	74,905.04
Standard Deviation	2,789,069.58
P25/Median/P75	299 / 317 / 335

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	456,436,237
Insertions	10,635,356
Mapped reads with at least one insertion	2.79%
Deletions	34,716,048
Mapped reads with at least one deletion	8.87%
Homopolymer indels	52.35%

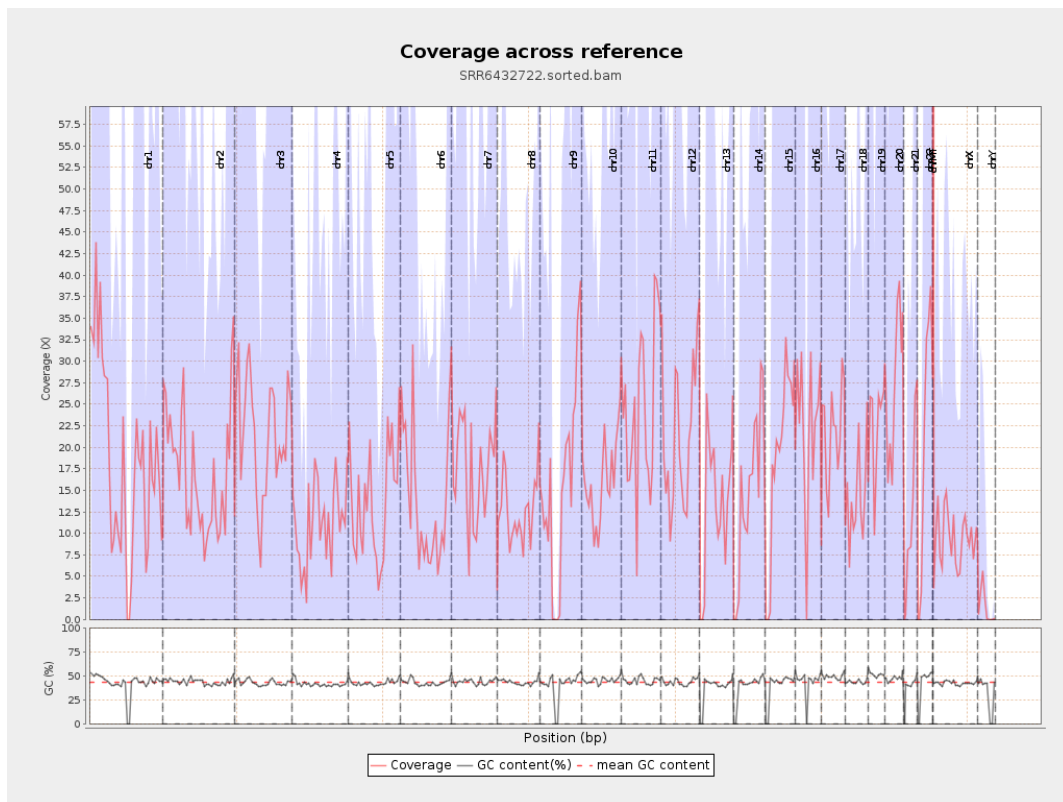
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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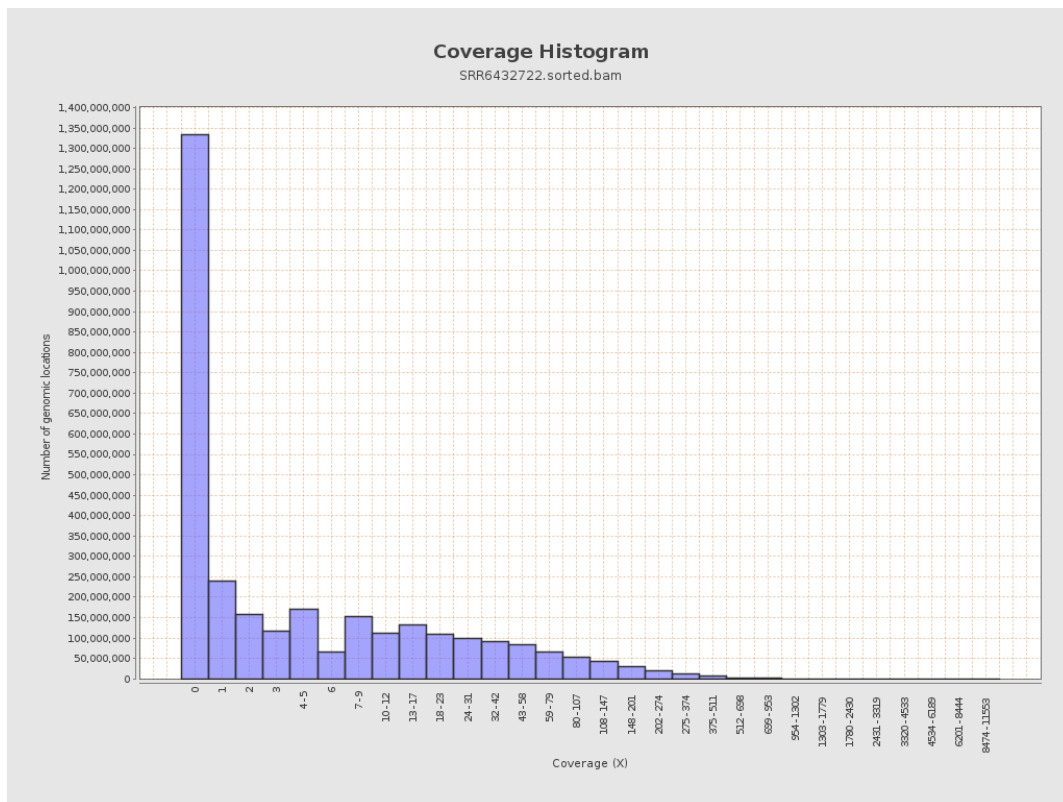
		bases	coverage	deviation
chr1	249250621	4543287010	18.2278	52.2329
chr2	243199373	4137488215	17.0127	48.7515
chr3	198022430	4215160525	21.2863	54.207
chr4	191154276	2144267957	11.2175	33.5398
chr5	180915260	2521602580	13.938	39.7571
chr6	171115067	2333620521	13.6377	40.6859
chr7	159138663	2824832697	17.7508	47.6634
chr8	146364022	1857725054	12.6925	35.6311
chr9	141213431	2160625352	15.3004	46.2298
chr10	135534747	2162193759	15.9531	42.205
chr11	135006516	3289212160	24.3634	61.4072
chr12	133851895	2898333206	21.6533	55.7521
chr13	115169878	1551644922	13.4727	41.0037
chr14	107349540	1604589859	14.9473	43.7335
chr15	102531392	1907114690	18.6003	52.3436
chr16	90354753	1994859676	22.0781	60.8265
chr17	81195210	1783627897	21.9672	55.4293
chr18	78077248	1070423167	13.7098	38.8211
chr19	59128983	1323747403	22.3875	58.3103
chr20	63025520	1700110930	26.975	63.852
chr21	48129895	579313005	12.0364	39.1161
chr22	51304566	1080955201	21.0694	60.0634
chrMT	16571	7637461	460.8932	634.8582
chrX	155270560	1453361189	9.3602	28.4938

chrY	59373566	92572232	1.5591	14.3295
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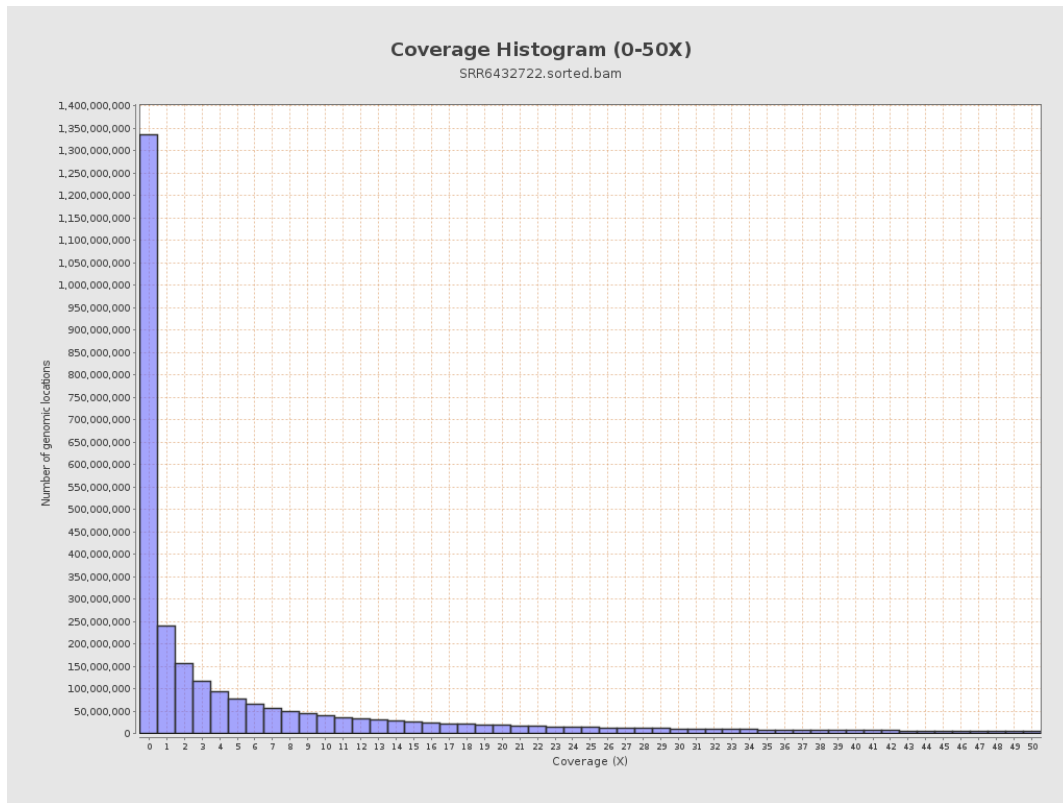
3. Results : Coverage across reference



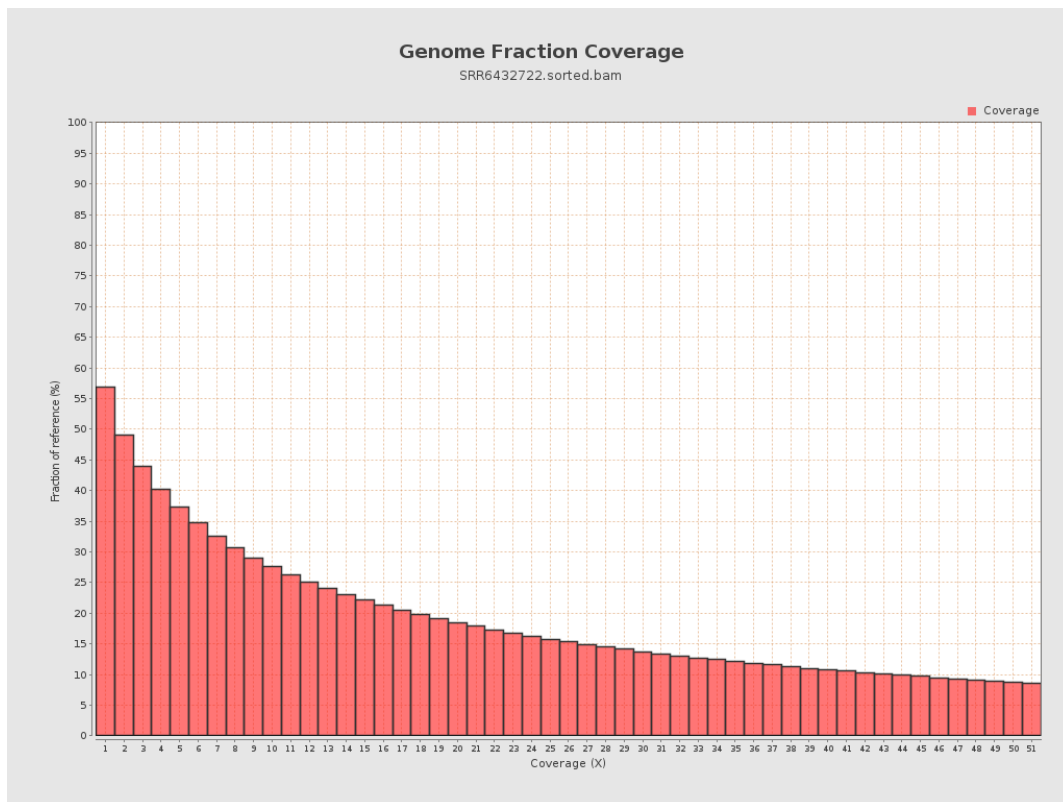
4. Results : Coverage Histogram



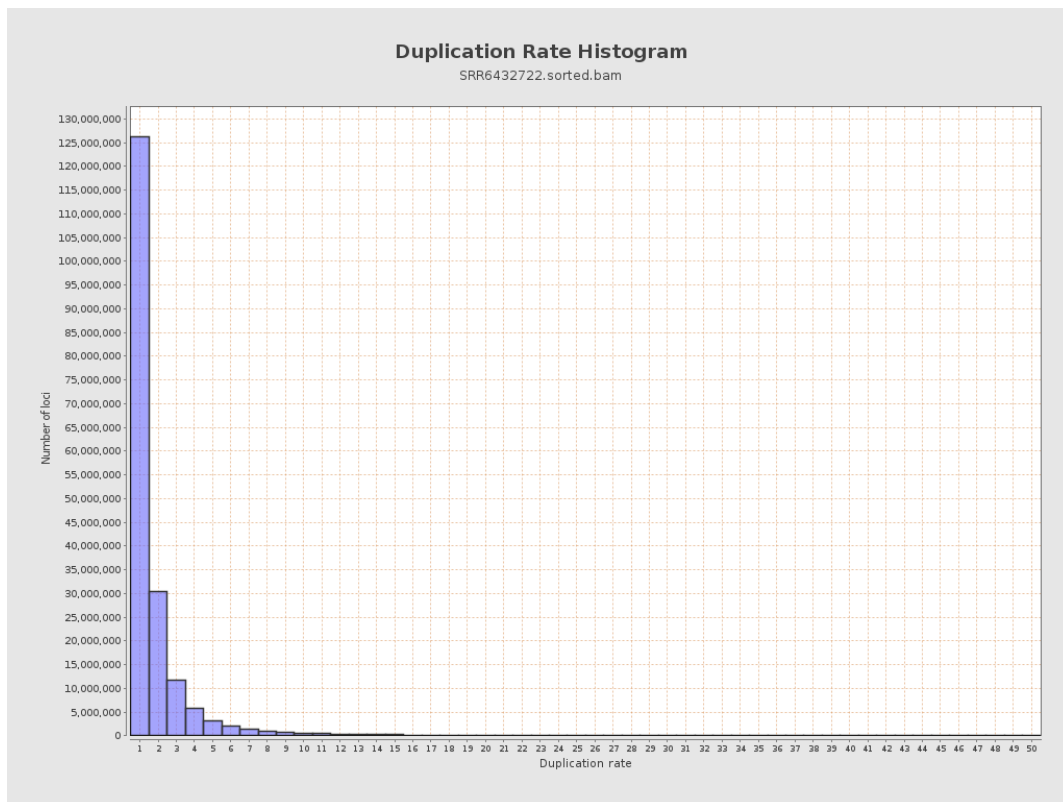
5. Results : Coverage Histogram (0-50X)



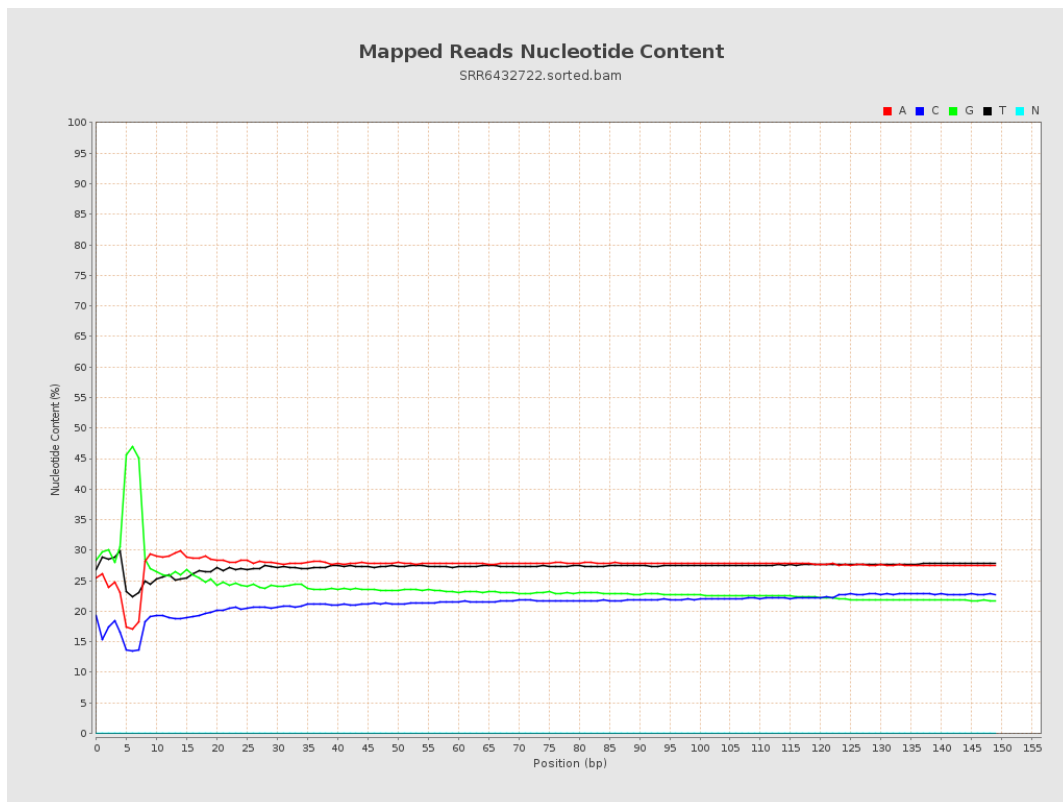
6. Results : Genome Fraction Coverage



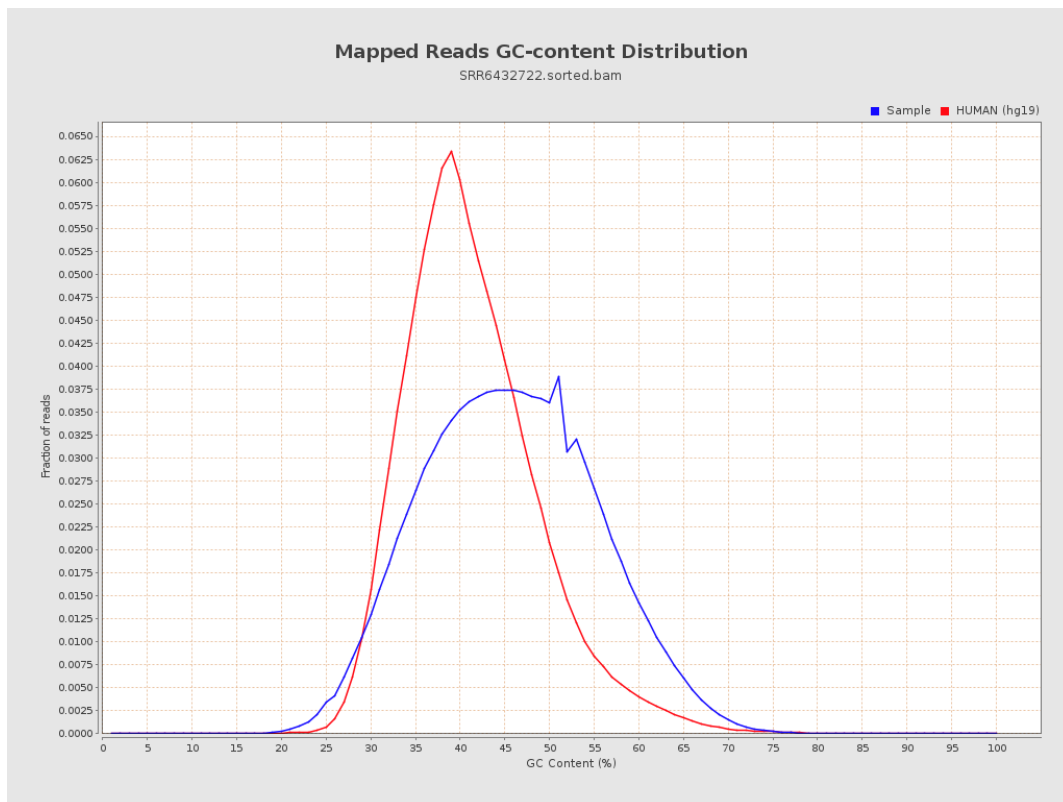
7. Results : Duplication Rate Histogram



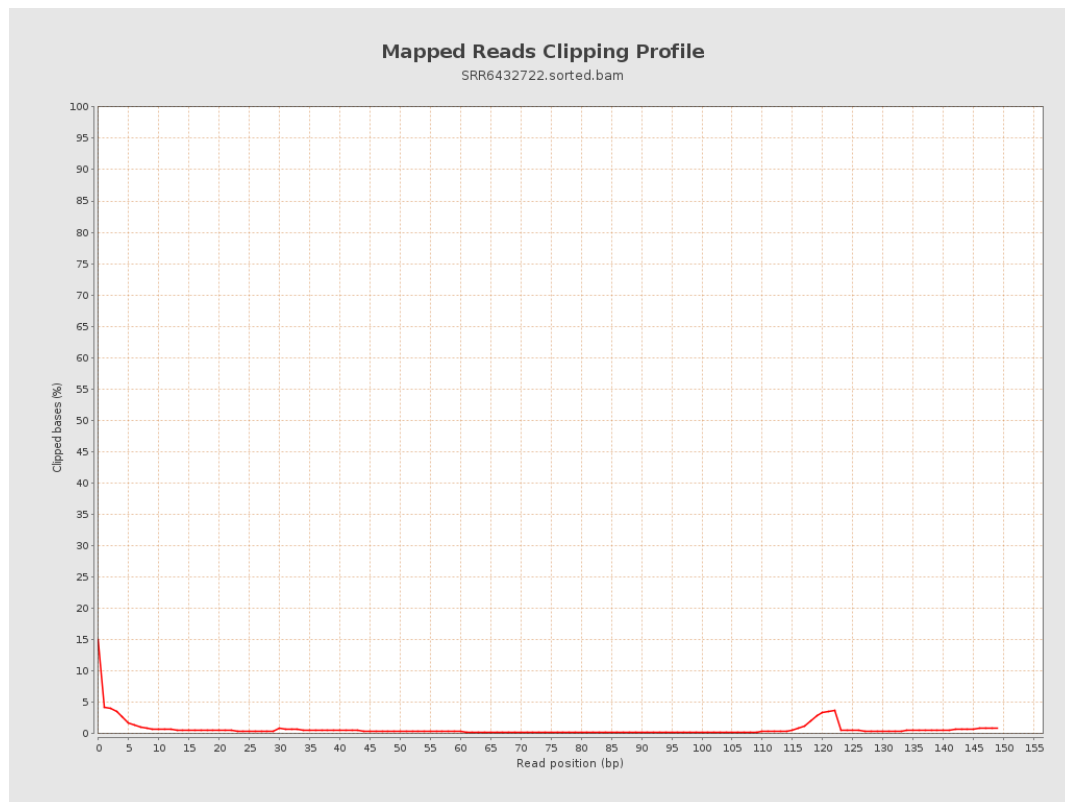
8. Results : Mapped Reads Nucleotide Content



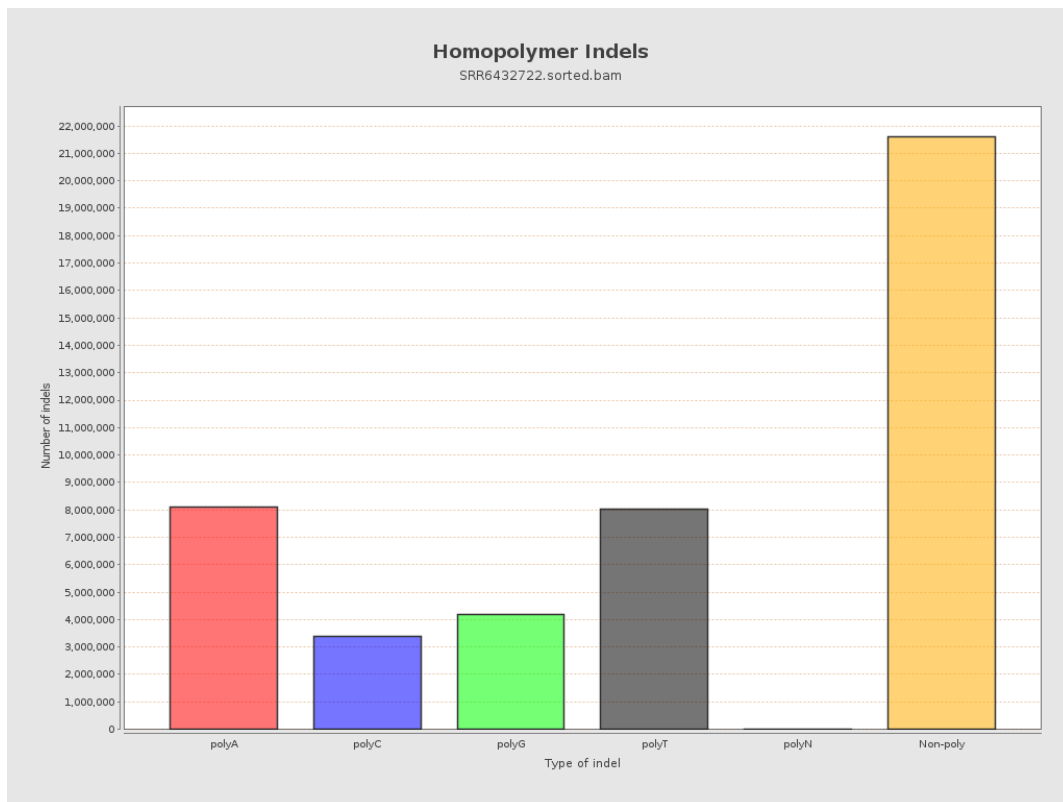
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



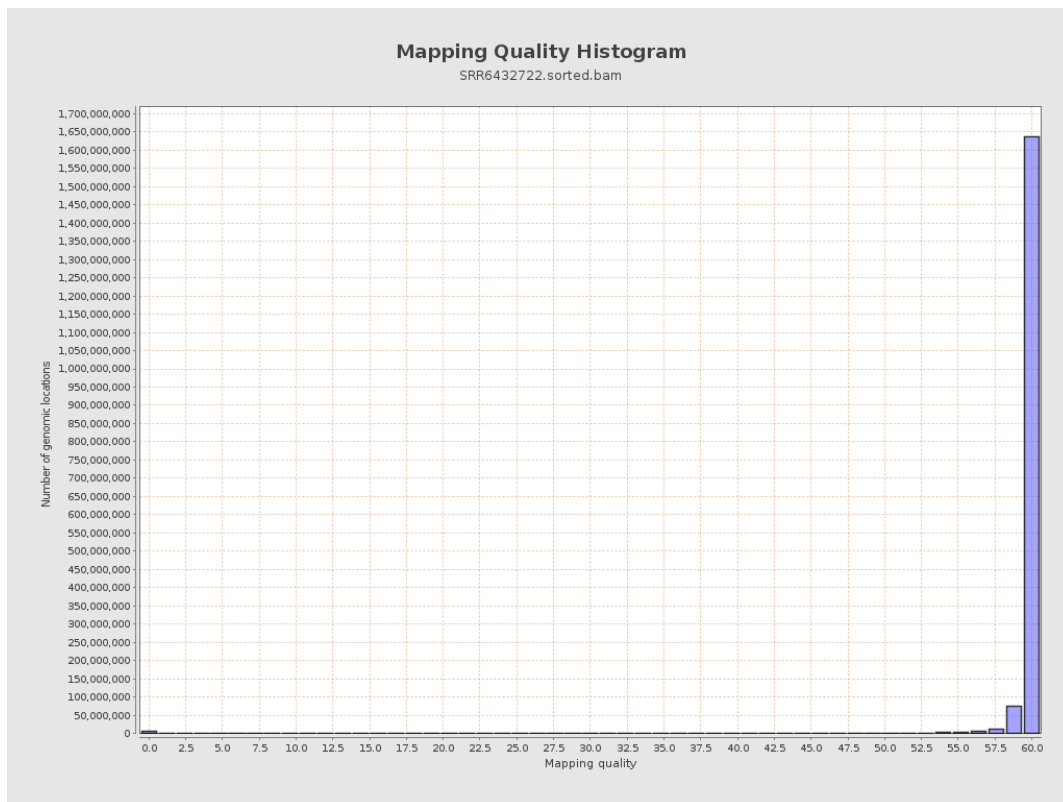
11. Results : Homopolymer Indels



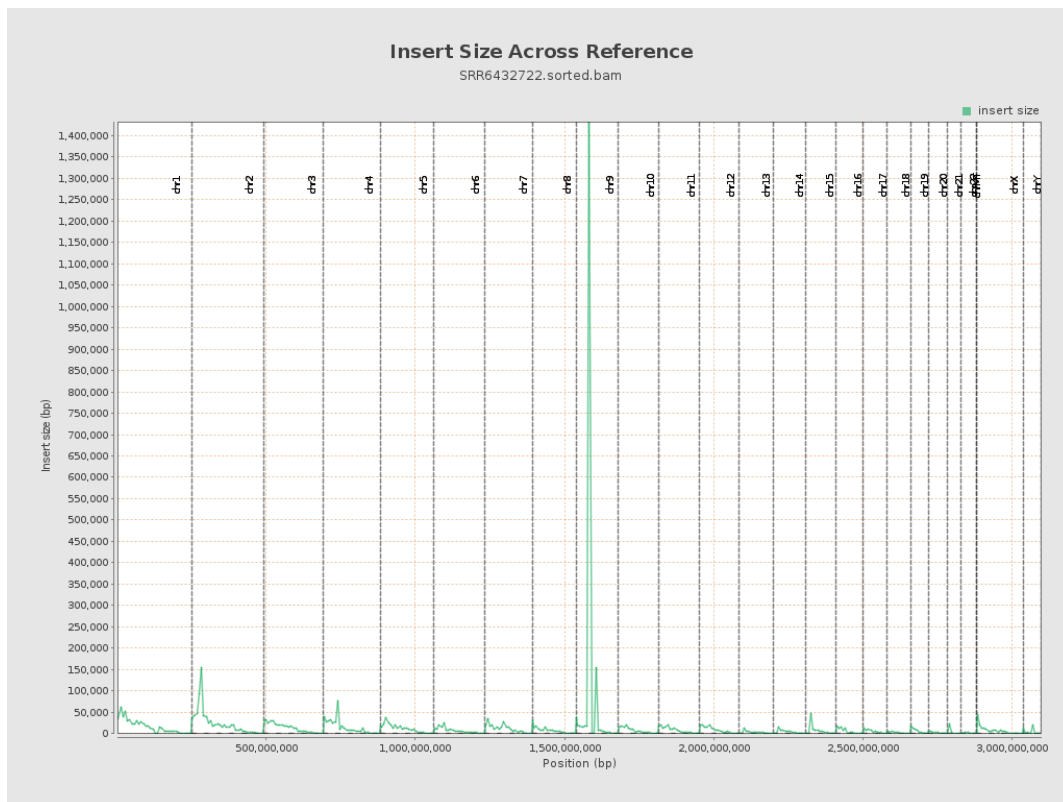
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

