

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 00:25:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432720.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_SRR6432720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432720_1.fastq.gz SRR6432720_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 00:25:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	382,757,346
Mapped reads	382,645,028 / 99.97%
Unmapped reads	112,318 / 0.03%
Mapped paired reads	382,645,028 / 99.97%
Mapped reads, first in pair	191,325,333 / 49.99%
Mapped reads, second in pair	191,319,695 / 49.98%
Mapped reads, both in pair	382,606,168 / 99.96%
Mapped reads, singletons	38,860 / 0.01%
Secondary alignments	0
Supplementary alignments	4,716,030 / 1.23%
Read min/max/mean length	30 / 150 / 141.5
Duplicated reads (estimated)	190,398,768 / 49.74%
Duplication rate	32.6%
Clipped reads	97,275,839 / 25.41%

2.2. ACGT Content

Number/percentage of A's	14,823,456,611 / 27.91%
Number/percentage of C's	11,238,485,284 / 21.16%
Number/percentage of T's	14,655,606,677 / 27.59%
Number/percentage of G's	12,388,004,270 / 23.32%
Number/percentage of N's	10,111,713 / 0.02%

GC Percentage	44.48%
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2.3. Coverage

Mean	17.1757
Standard Deviation	50.0662

2.4. Mapping Quality

Mean Mapping Quality	57.41
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2.5. Insert size

Mean	58,869.54
Standard Deviation	2,469,976.21
P25/Median/P75	290 / 310 / 328

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	424,862,078
Insertions	11,899,385
Mapped reads with at least one insertion	3.05%
Deletions	38,255,415
Mapped reads with at least one deletion	9.51%
Homopolymer indels	53.12%

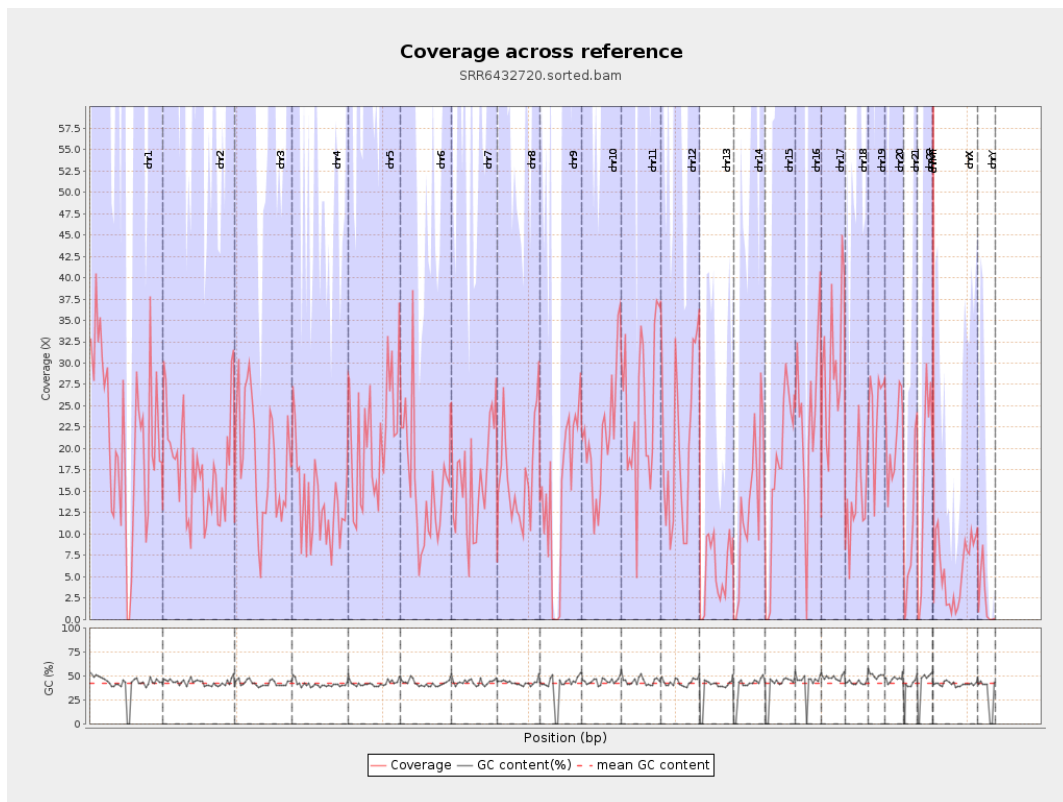
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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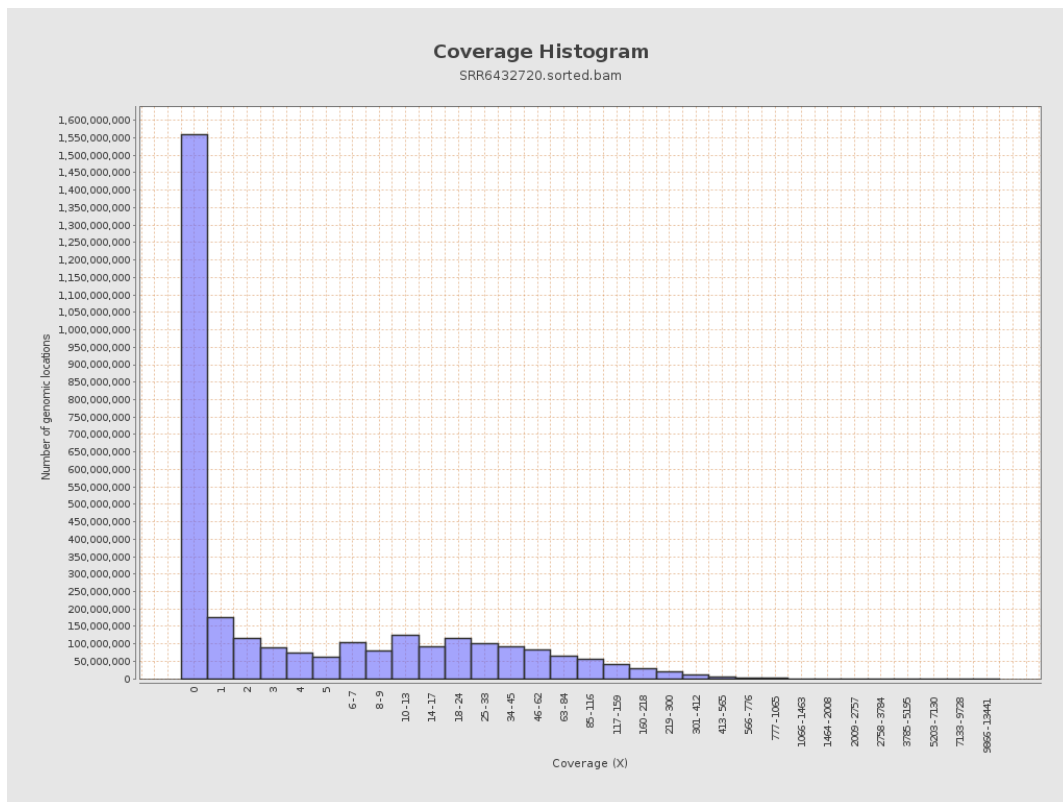
		bases	coverage	deviation
chr1	249250621	5279079598	21.1798	58.1785
chr2	243199373	4287565185	17.6298	50.8866
chr3	198022430	3646078281	18.4125	49.5433
chr4	191154276	2575154061	13.4716	38.9555
chr5	180915260	3873082102	21.4083	56.5142
chr6	171115067	2667778930	15.5906	45.6084
chr7	159138663	2616210148	16.4398	45.7845
chr8	146364022	2490607515	17.0165	46.7142
chr9	141213431	2058550462	14.5776	44.3525
chr10	135534747	2886385570	21.2963	55.3059
chr11	135006516	3356431670	24.8613	63.0524
chr12	133851895	2795835575	20.8875	56.2765
chr13	115169878	641329926	5.5686	21.8481
chr14	107349540	1424225858	13.2672	40.8523
chr15	102531392	1750939111	17.0771	49.5625
chr16	90354753	2161468862	23.922	65.838
chr17	81195210	2433752562	29.9741	74.3059
chr18	78077248	1064830150	13.6382	39.6786
chr19	59128983	1453389604	24.58	65.2606
chr20	63025520	1328637840	21.081	53.546
chr21	48129895	470474880	9.7751	34.0752
chr22	51304566	857035277	16.7049	50.6039
chrMT	16571	5650538	340.9896	411.2866
chrX	155270560	901293556	5.8047	22.1389

chrY	59373566	144908023	2.4406	19.3355
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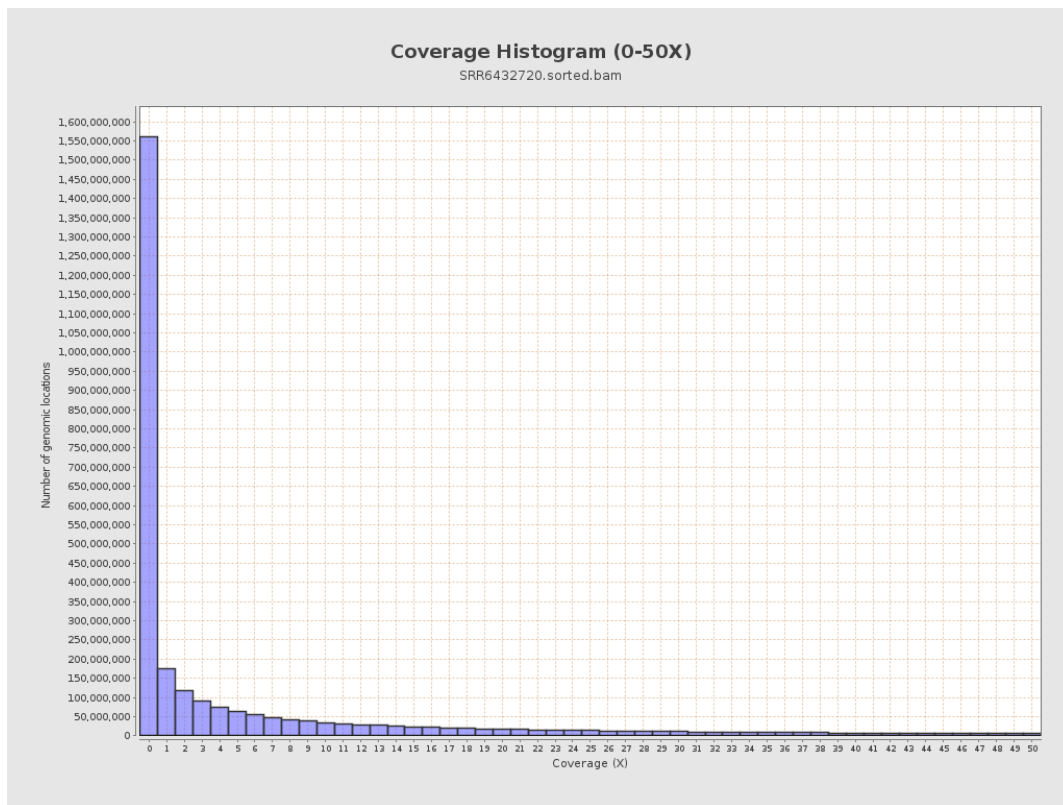
3. Results : Coverage across reference



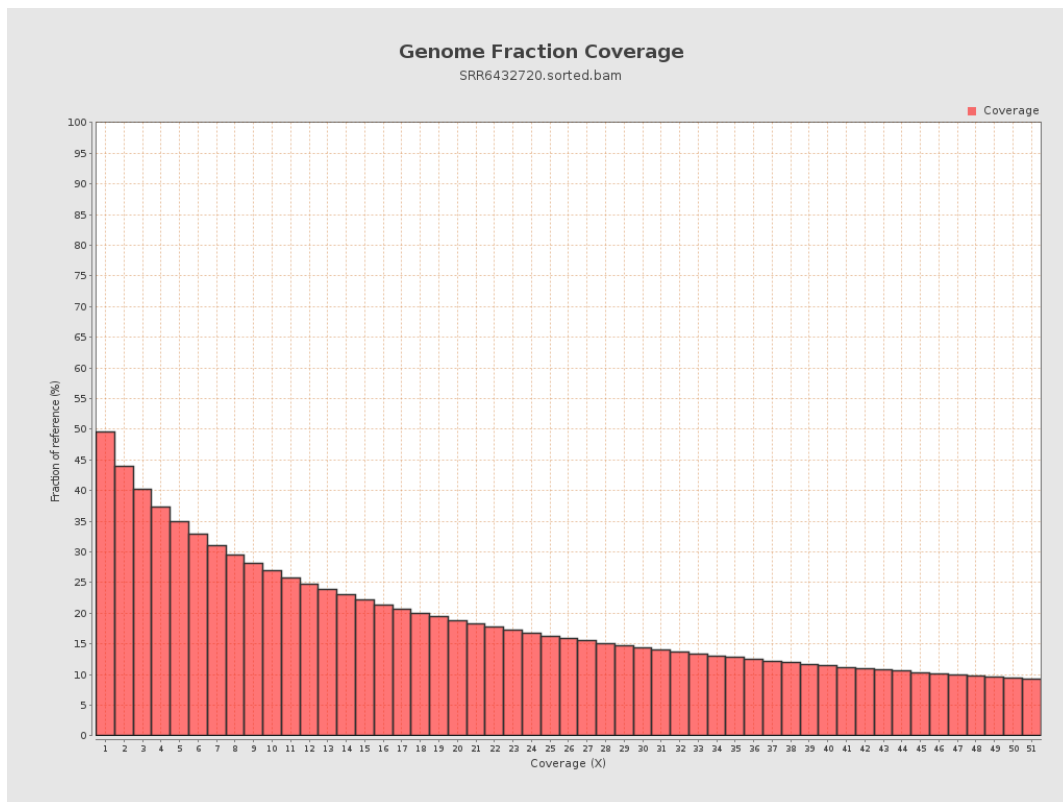
4. Results : Coverage Histogram



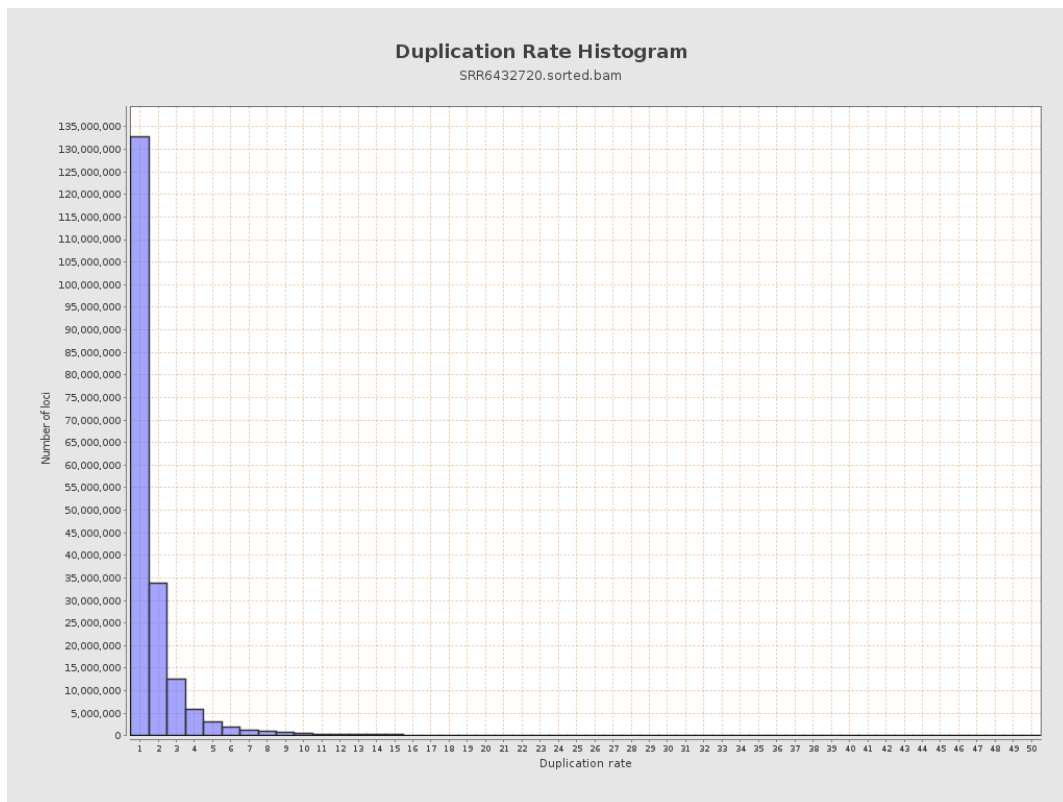
5. Results : Coverage Histogram (0-50X)



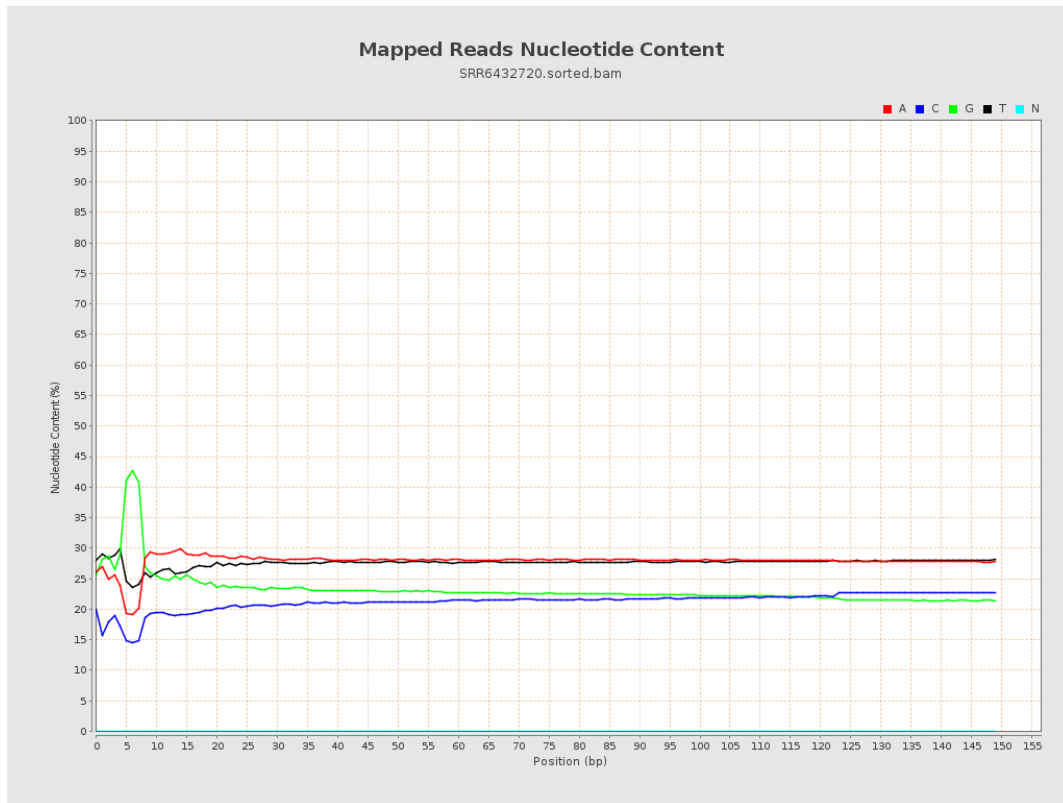
6. Results : Genome Fraction Coverage



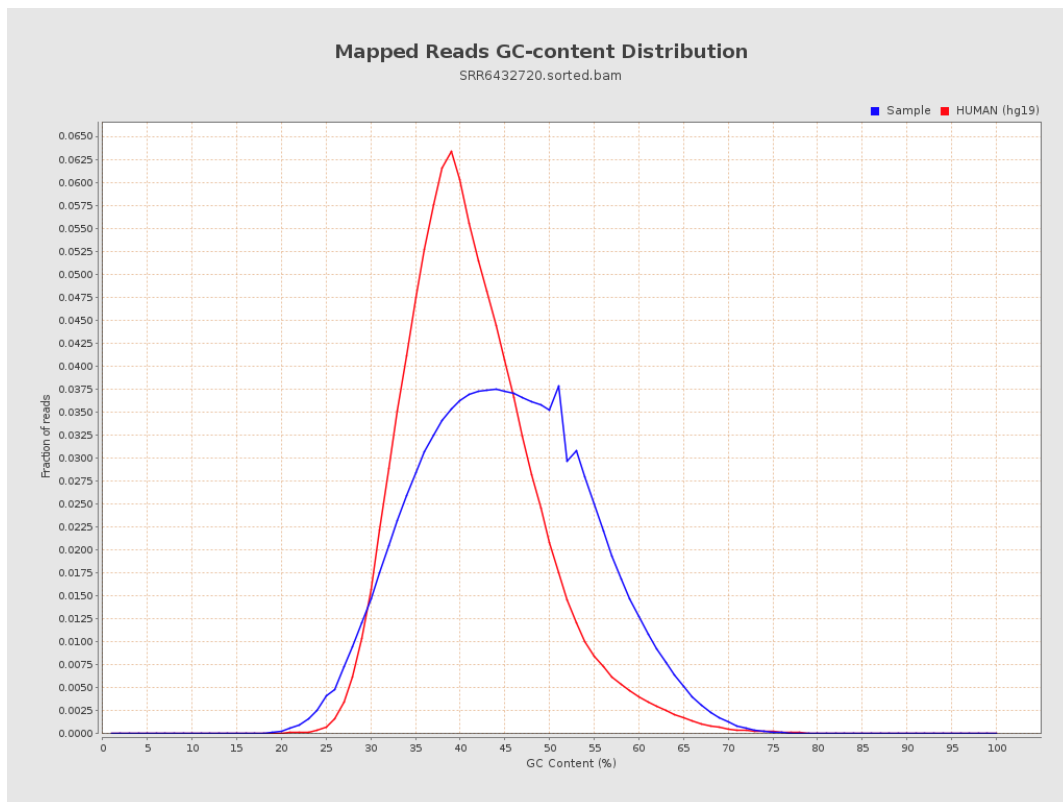
7. Results : Duplication Rate Histogram



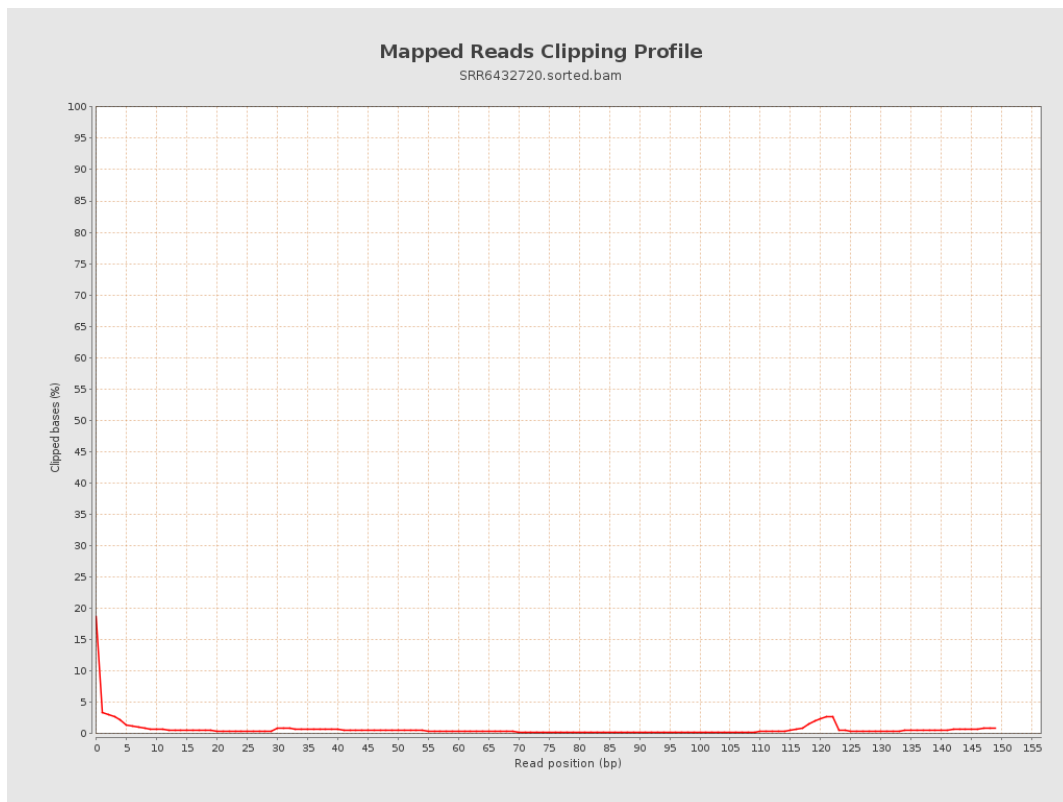
8. Results : Mapped Reads Nucleotide Content



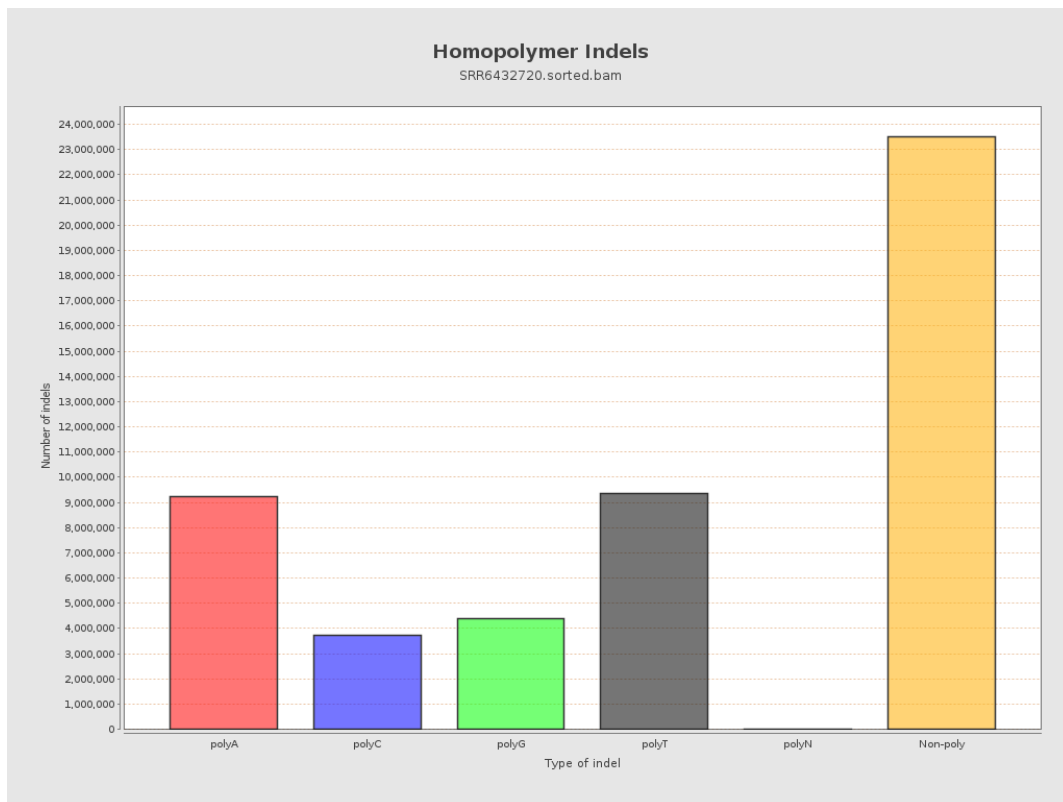
9. Results : Mapped Reads GC-content Distribution



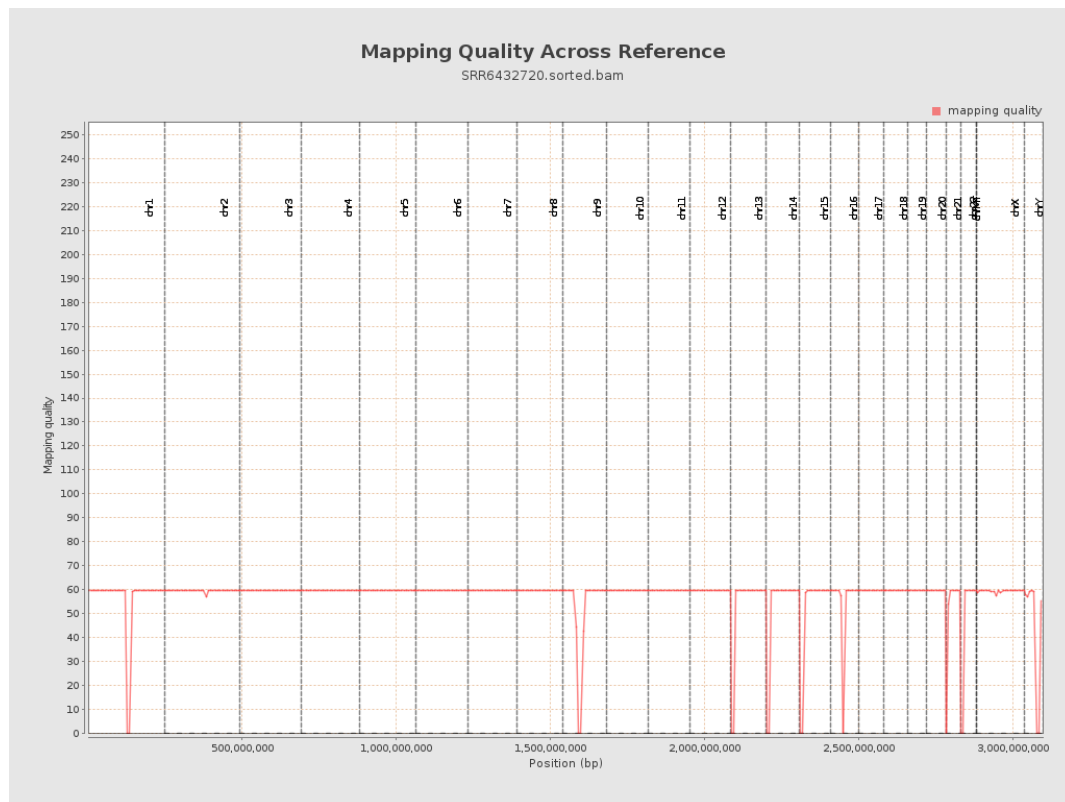
10. Results : Mapped Reads Clipping Profile



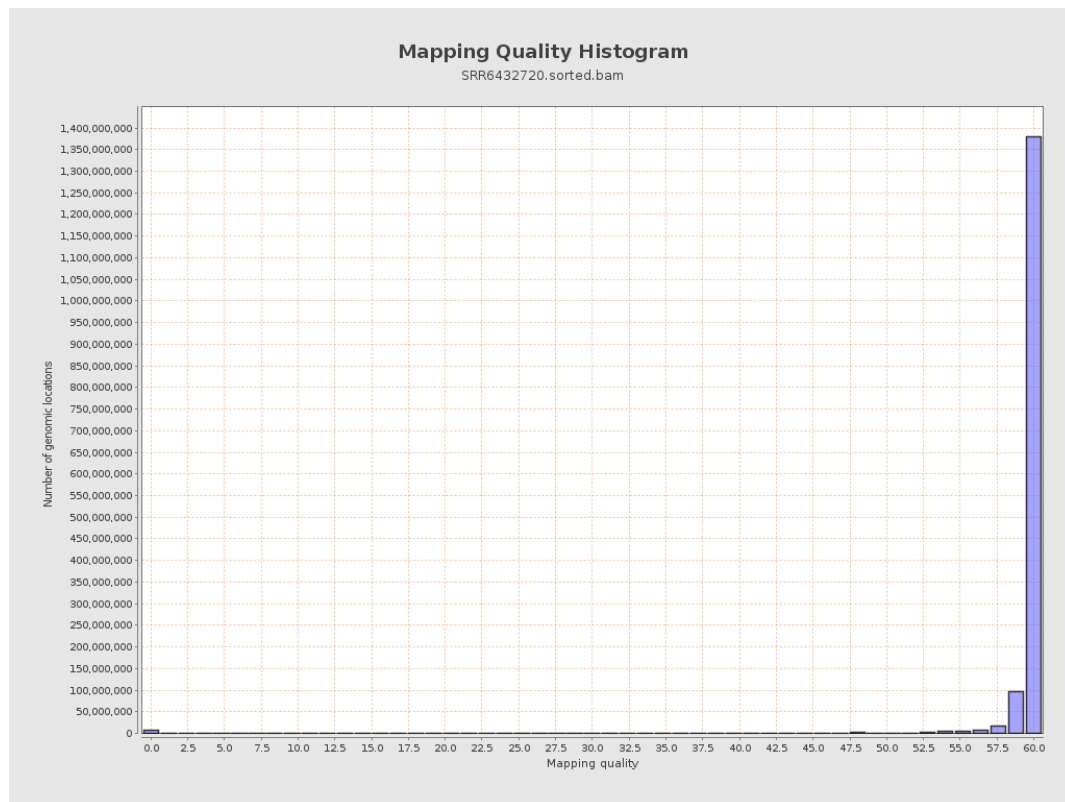
11. Results : Homopolymer Indels



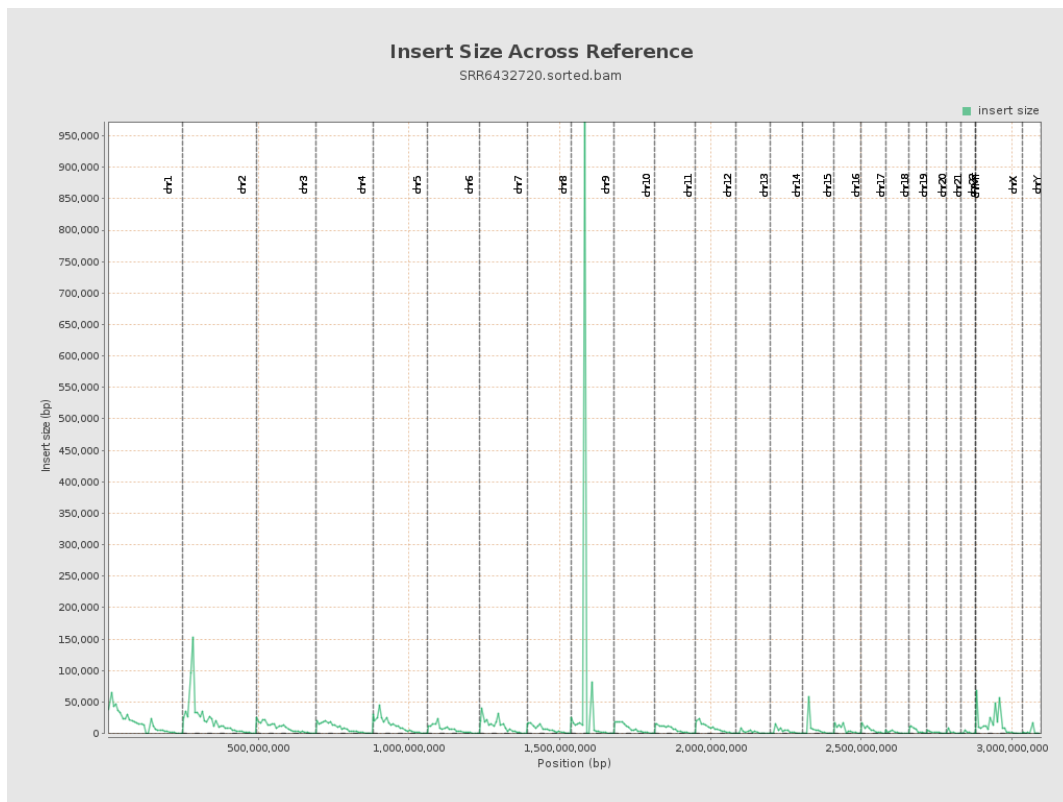
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

