

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 21:25:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104296.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_SRR26104296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104296_1.fastq.gz SRR26104296_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 21:25:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,522,045,848
Mapped reads	1,381,813,333 / 90.79%
Unmapped reads	140,232,515 / 9.21%
Mapped paired reads	1,381,813,333 / 90.79%
Mapped reads, first in pair	694,910,726 / 45.66%
Mapped reads, second in pair	686,902,607 / 45.13%
Mapped reads, both in pair	1,368,605,890 / 89.92%
Mapped reads, singletons	13,207,443 / 0.87%
Secondary alignments	0
Supplementary alignments	11,244 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	960,268,593 / 63.09%
Duplication rate	40.83%
Clipped reads	122,330,996 / 8.04%

2.2. ACGT Content

Number/percentage of A's	16,555,511,990 / 24.32%
Number/percentage of C's	17,525,025,539 / 25.74%
Number/percentage of T's	16,577,645,807 / 24.35%
Number/percentage of G's	17,414,978,269 / 25.58%
Number/percentage of N's	1,422,691 / 0%

GC Percentage	51.33%
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2.3. Coverage

Mean	21.9928
Standard Deviation	721.0528

2.4. Mapping Quality

Mean Mapping Quality	52.83
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2.5. Insert size

Mean	7,105.45
Standard Deviation	892,103.09
P25/Median/P75	74 / 149 / 208

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	191,275,503
Insertions	4,045,231
Mapped reads with at least one insertion	0.29%
Deletions	4,844,105
Mapped reads with at least one deletion	0.35%
Homopolymer indels	45.47%

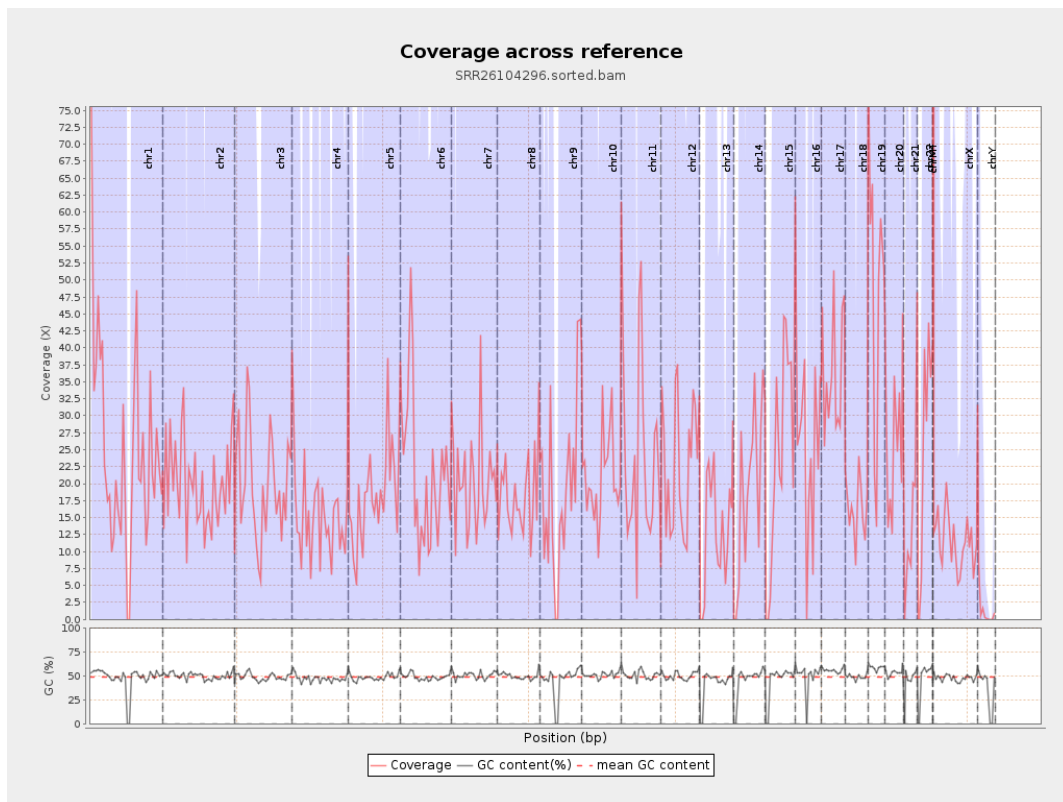
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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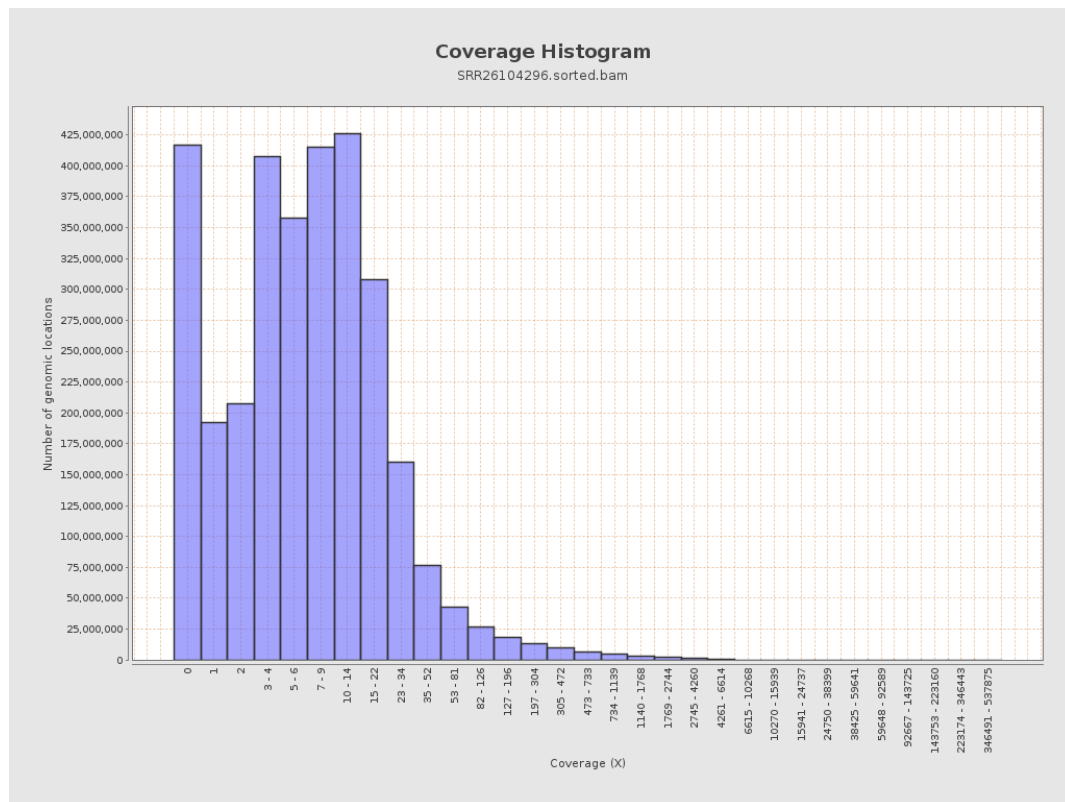
		bases	coverage	deviation
chr1	249250621	6232794635	25.0061	469.6661
chr2	243199373	4870206371	20.0256	150.337
chr3	198022430	3913247886	19.7616	115.174
chr4	191154276	2836113181	14.8368	89.2428
chr5	180915260	3383916665	18.7044	147.8271
chr6	171115067	3607614681	21.083	116.8546
chr7	159138663	3237653762	20.3449	138.8974
chr8	146364022	2632094786	17.9832	106.495
chr9	141213431	2662186715	18.8522	117.6908
chr10	135534747	2841058327	20.9618	114.6254
chr11	135006516	3197710606	23.6856	165.5144
chr12	133851895	3086559525	23.0595	132.0747
chr13	115169878	1484338698	12.8883	161.7449
chr14	107349540	2054268665	19.1363	122.7983
chr15	102531392	2400260203	23.41	139.5749
chr16	90354753	2360380371	26.1235	151.2489
chr17	81195210	2935921073	36.1588	223.4235
chr18	78077248	1260008317	16.138	96.8833
chr19	59128983	2799983212	47.3538	244.1508
chr20	63025520	1560258244	24.756	132.7294
chr21	48129895	708729047	14.7253	106.9715
chr22	51304566	1274634282	24.8445	143.612
chrMT	16571	4831515505	291,564.5106	75,714.2459
chrX	155270560	1840862755	11.8558	66.6215

chrY	59373566	70780567	1.1921	41.7211
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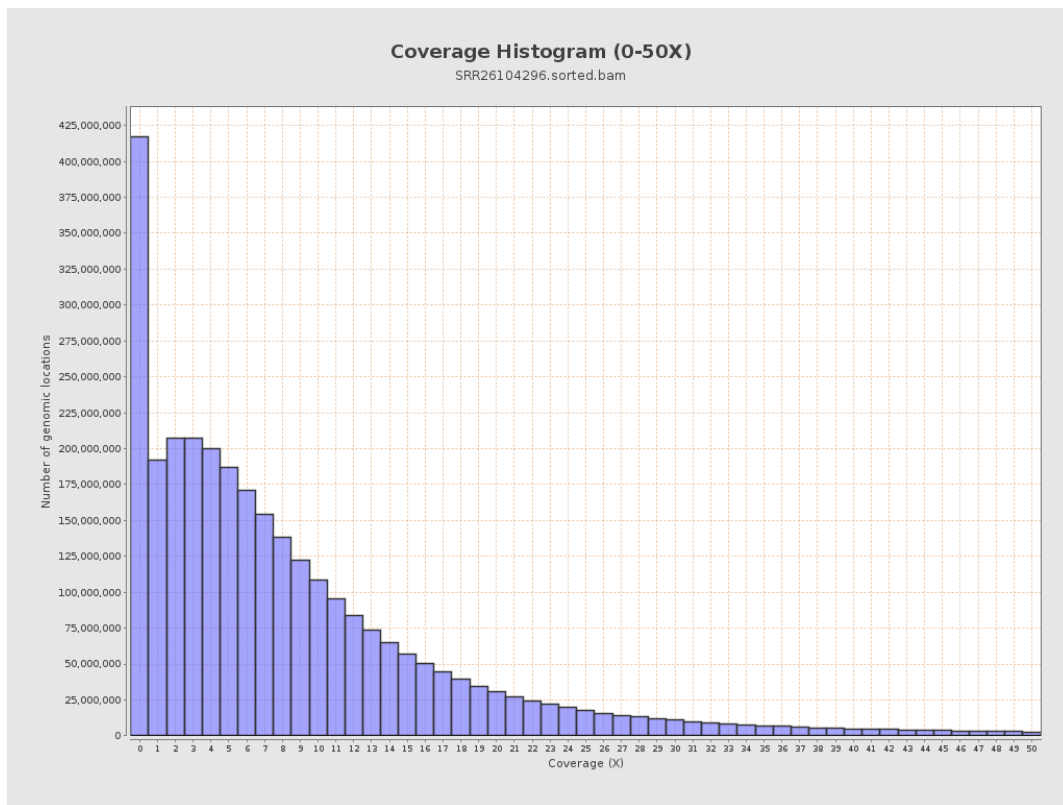
3. Results : Coverage across reference



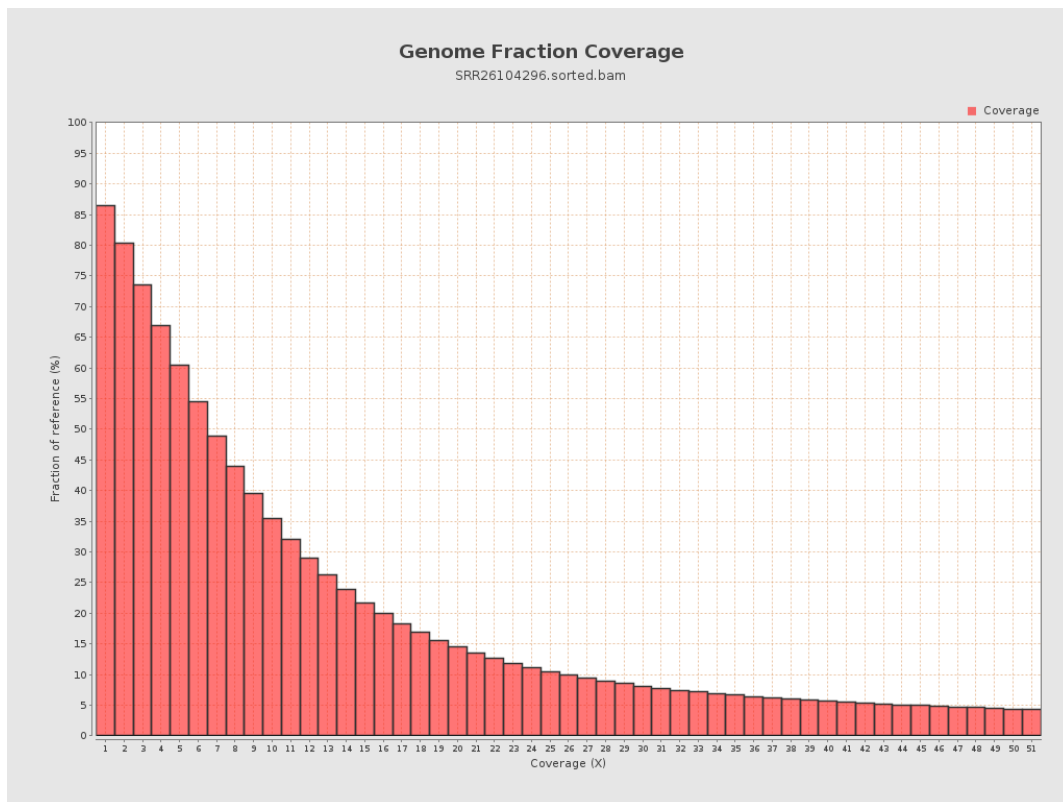
4. Results : Coverage Histogram



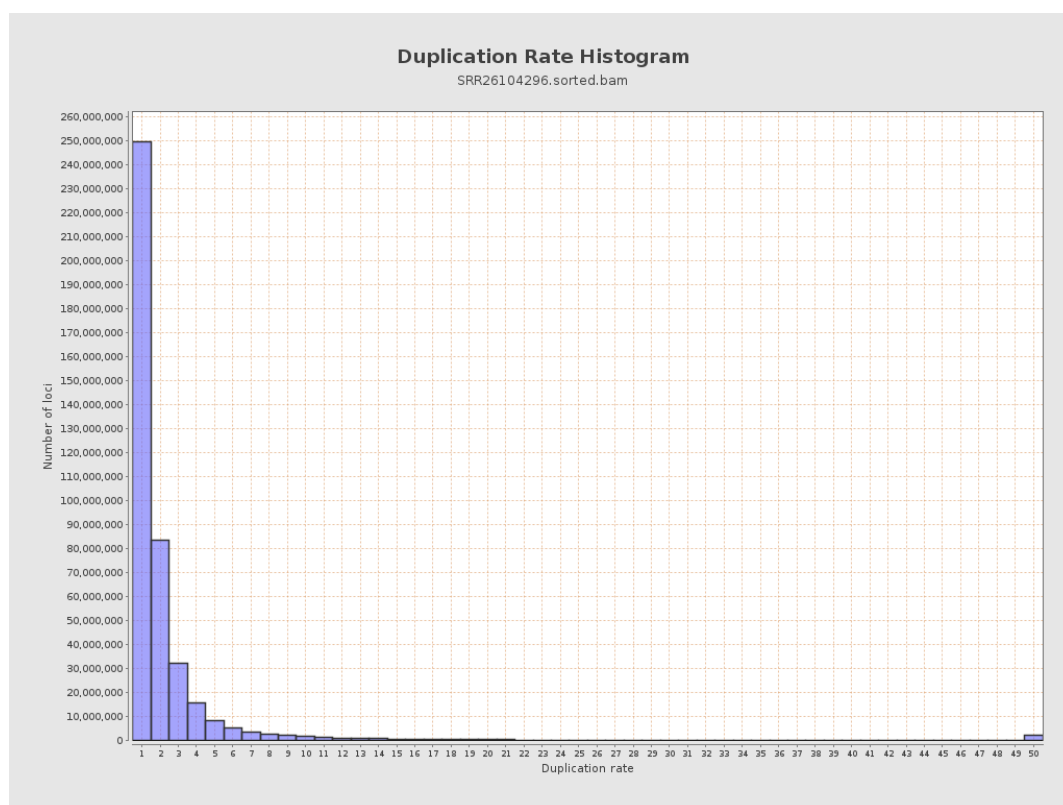
5. Results : Coverage Histogram (0-50X)



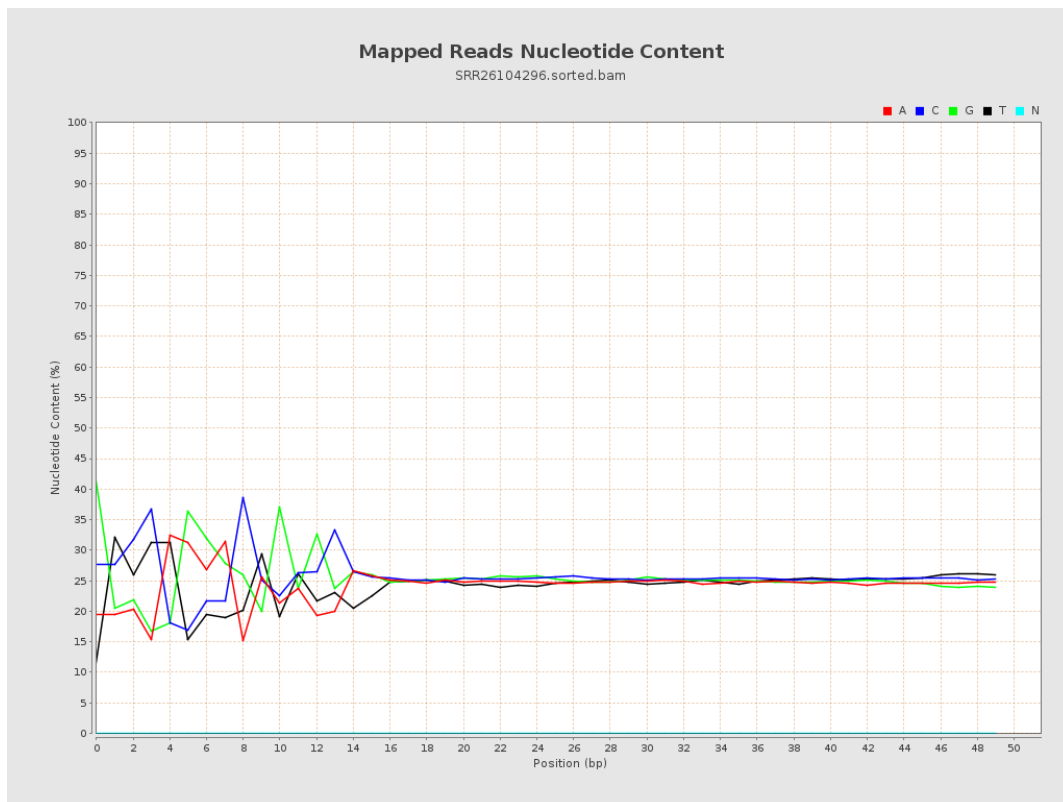
6. Results : Genome Fraction Coverage



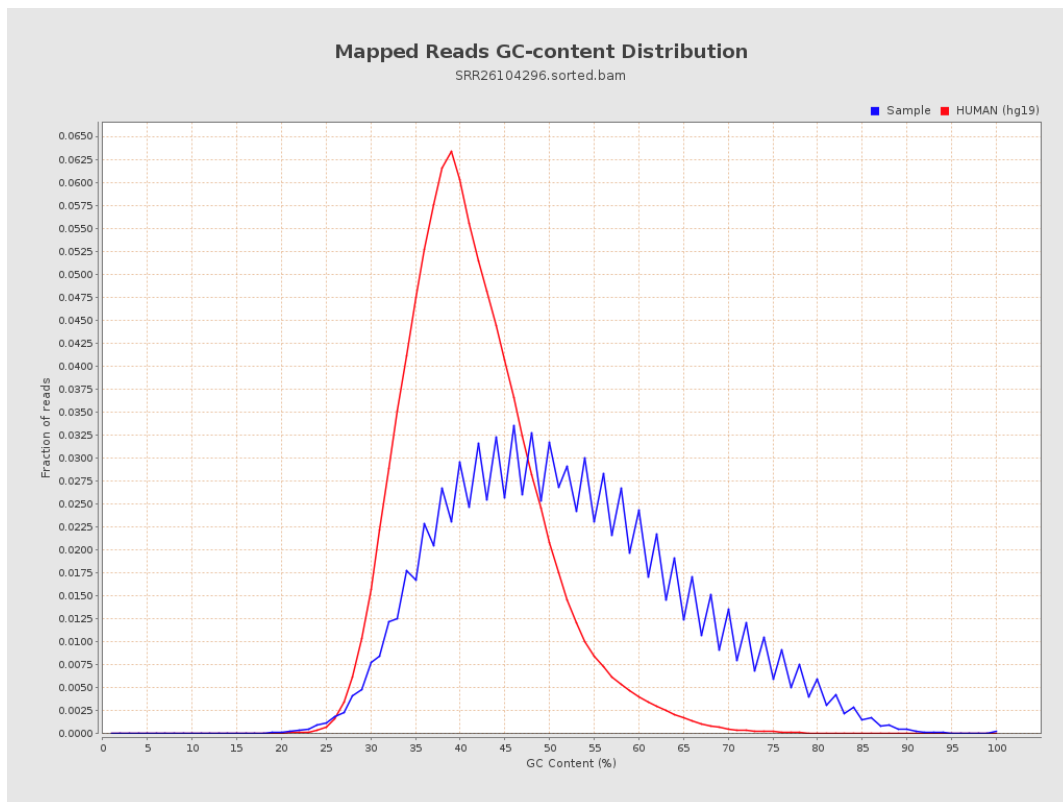
7. Results : Duplication Rate Histogram



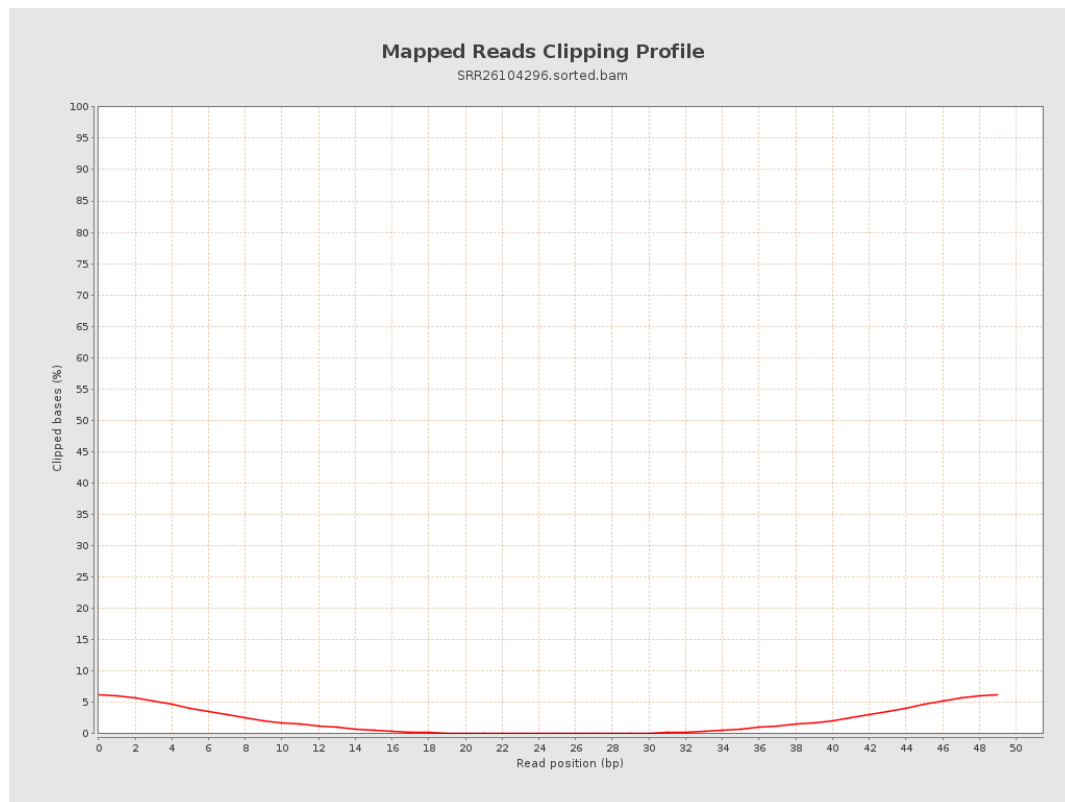
8. Results : Mapped Reads Nucleotide Content



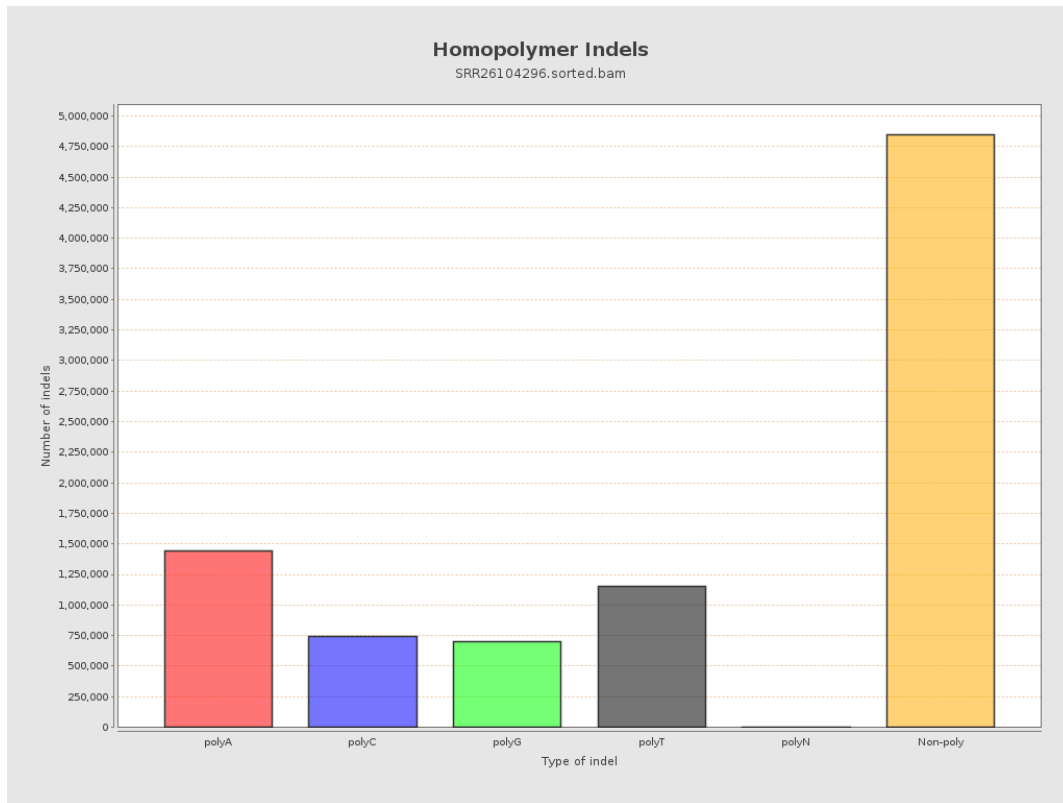
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



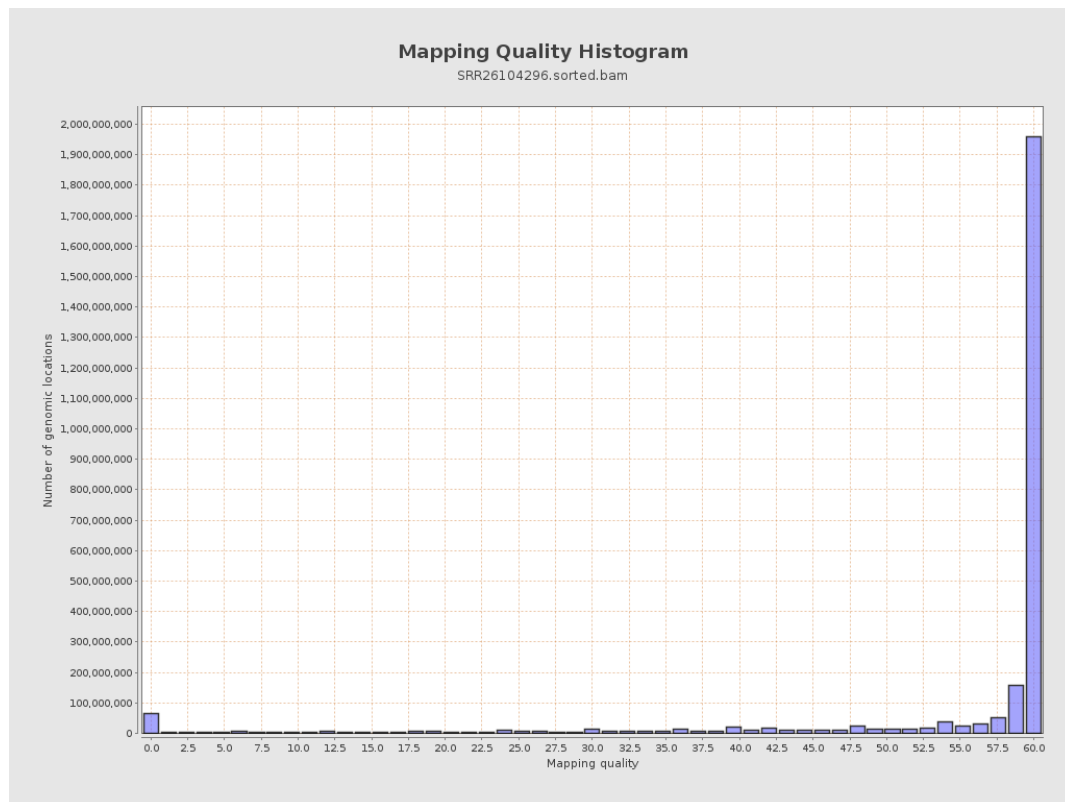
11. Results : Homopolymer Indels



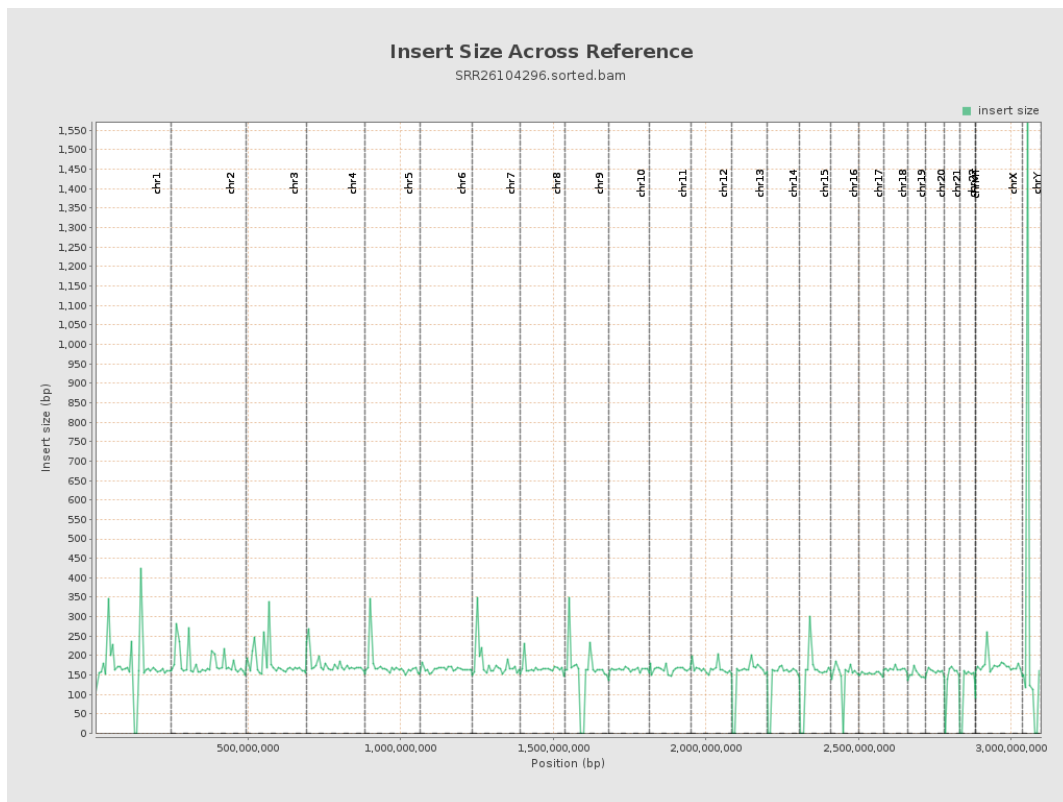
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

