

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 00:18:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104294.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_SRR26104294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104294_1.fastq.gz SRR26104294_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 00:18:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	873,135,994
Mapped reads	834,310,901 / 95.55%
Unmapped reads	38,825,093 / 4.45%
Mapped paired reads	834,310,901 / 95.55%
Mapped reads, first in pair	428,031,485 / 49.02%
Mapped reads, second in pair	406,279,416 / 46.53%
Mapped reads, both in pair	810,588,086 / 92.84%
Mapped reads, singletons	23,722,815 / 2.72%
Secondary alignments	0
Supplementary alignments	741,329 / 0.08%
Read min/max/mean length	30 / 97 / 91.03
Duplicated reads (estimated)	314,272,469 / 35.99%
Duplication rate	32.94%
Clipped reads	344,565,542 / 39.46%

2.2. ACGT Content

Number/percentage of A's	18,858,013,311 / 29.5%
Number/percentage of C's	13,269,650,619 / 20.75%
Number/percentage of T's	19,073,802,560 / 29.83%
Number/percentage of G's	12,722,027,469 / 19.9%
Number/percentage of N's	12,328,502 / 0.02%

GC Percentage	40.65%
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2.3. Coverage

Mean	20.6581
Standard Deviation	194.0521

2.4. Mapping Quality

Mean Mapping Quality	52.31
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2.5. Insert size

Mean	13,861.4
Standard Deviation	1,071,115.45
P25/Median/P75	61 / 120 / 209

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	396,113,369
Insertions	6,055,480
Mapped reads with at least one insertion	0.72%
Deletions	6,852,485
Mapped reads with at least one deletion	0.81%
Homopolymer indels	43.81%

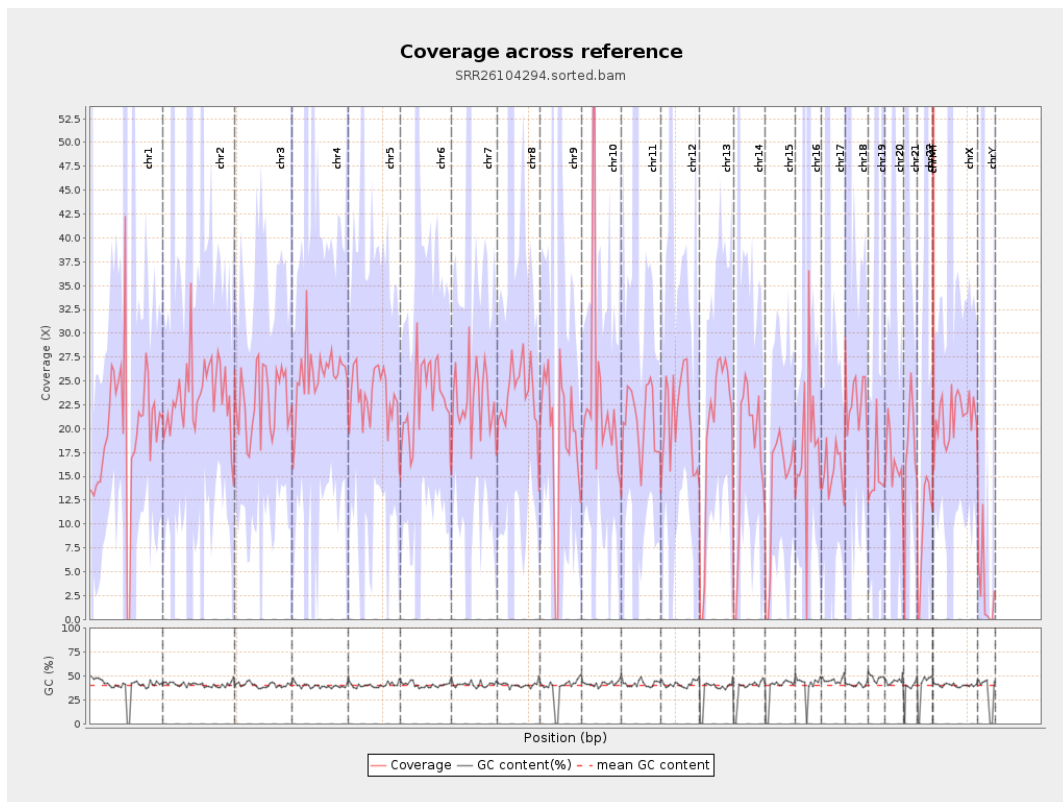
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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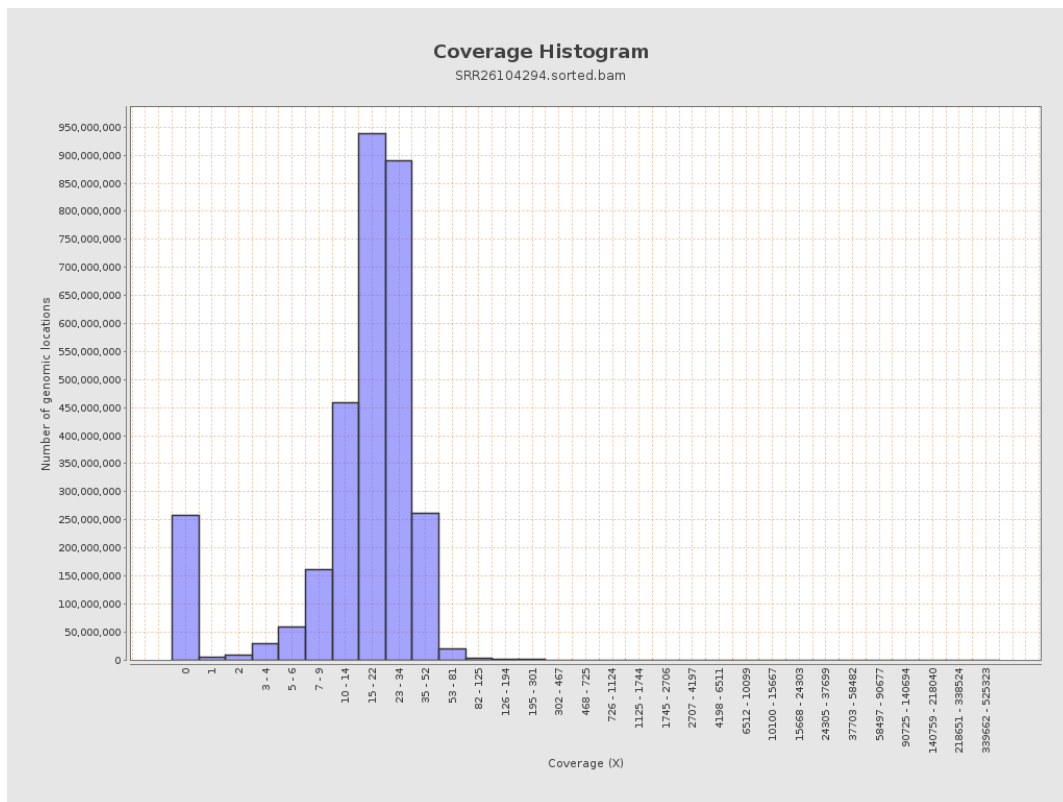
		bases	coverage	deviation
chr1	249250621	4905508636	19.681	475.7339
chr2	243199373	5705150880	23.4587	114.9945
chr3	198022430	4537661945	22.9149	43.2518
chr4	191154276	4903240496	25.6507	82.8666
chr5	180915260	4190675400	23.1637	20.7402
chr6	171115067	3971859887	23.2116	68.4219
chr7	159138663	3620440843	22.7502	179.3367
chr8	146364022	3451970204	23.5848	306.4013
chr9	141213431	2729418733	19.3283	130.6012
chr10	135534747	3112317427	22.9632	355.1298
chr11	135006516	2824271934	20.9195	72.9689
chr12	133851895	2808970273	20.9857	22.7289
chr13	115169878	2287661350	19.8634	14.9548
chr14	107349540	1872629441	17.4442	27.7524
chr15	102531392	1427374735	13.9213	12.7825
chr16	90354753	1618265181	17.9101	135.8504
chr17	81195210	1274868318	15.7013	56.4241
chr18	78077248	1796749930	23.0125	183.6598
chr19	59128983	887135554	15.0034	322.8898
chr20	63025520	1050733163	16.6716	26.0123
chr21	48129895	838804221	17.4279	47.2513
chr22	51304566	504507427	9.8336	154.9135
chrMT	16571	171391594	10,342.8637	3,884.1215
chrX	155270560	3288341012	21.1781	41.609

chrY	59373566	171061653	2.8811	106.1246
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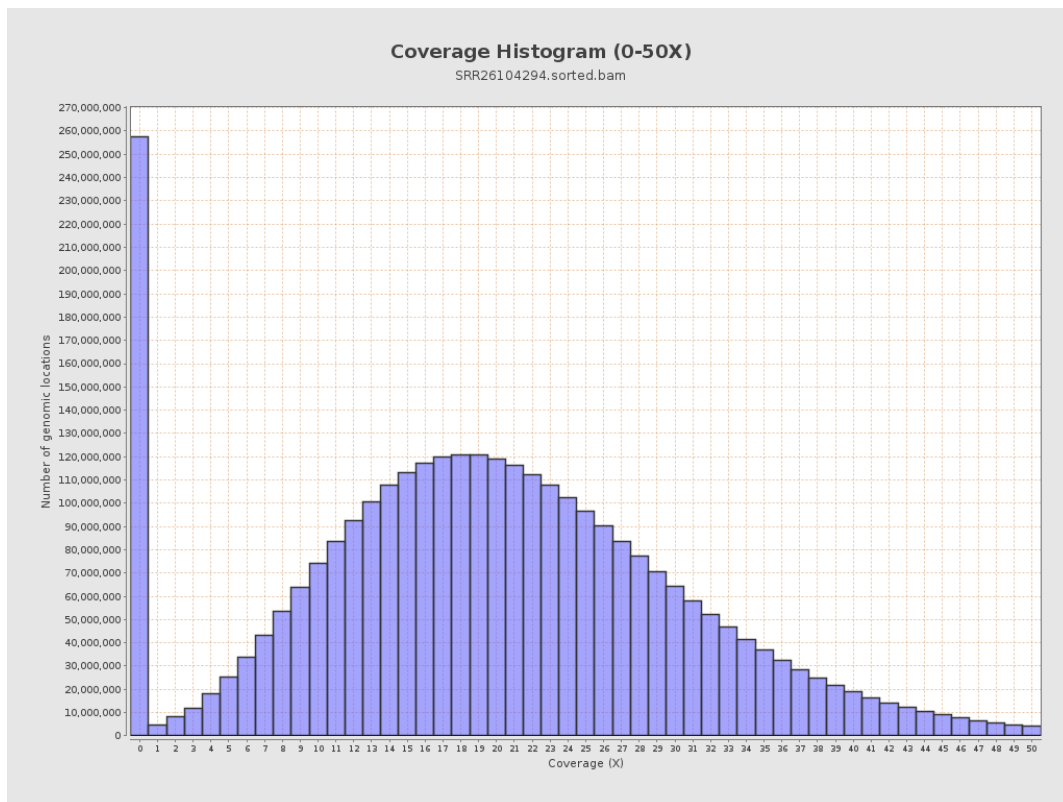
3. Results : Coverage across reference



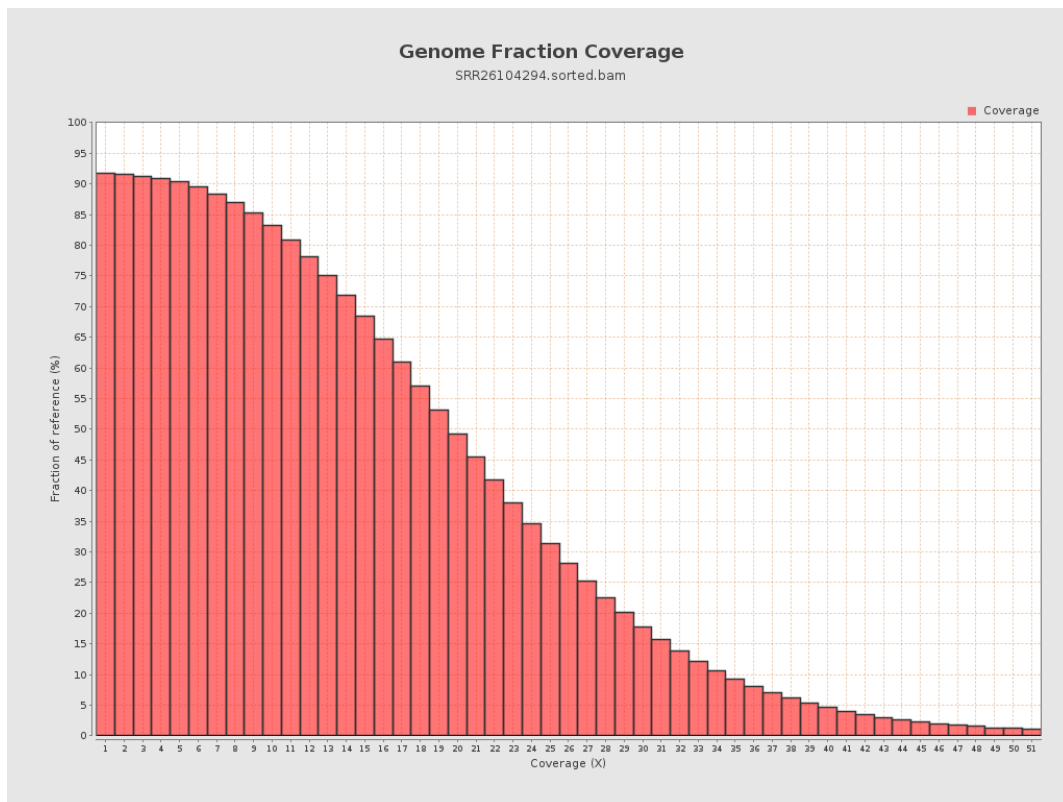
4. Results : Coverage Histogram



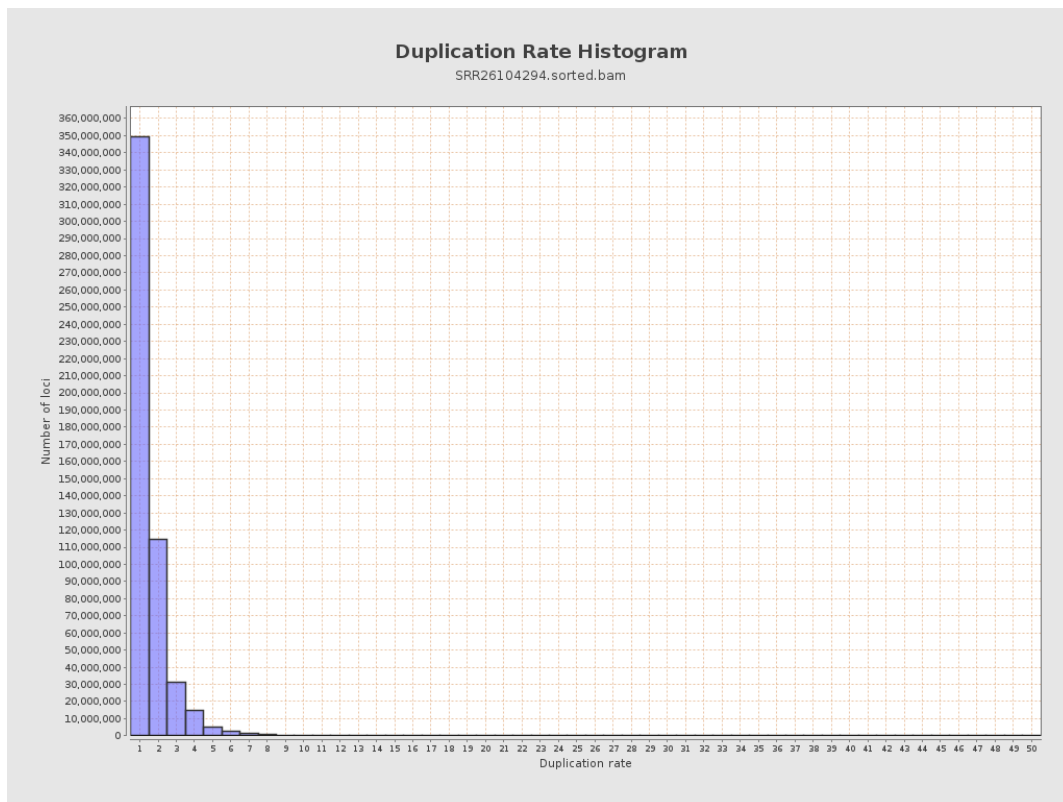
5. Results : Coverage Histogram (0-50X)



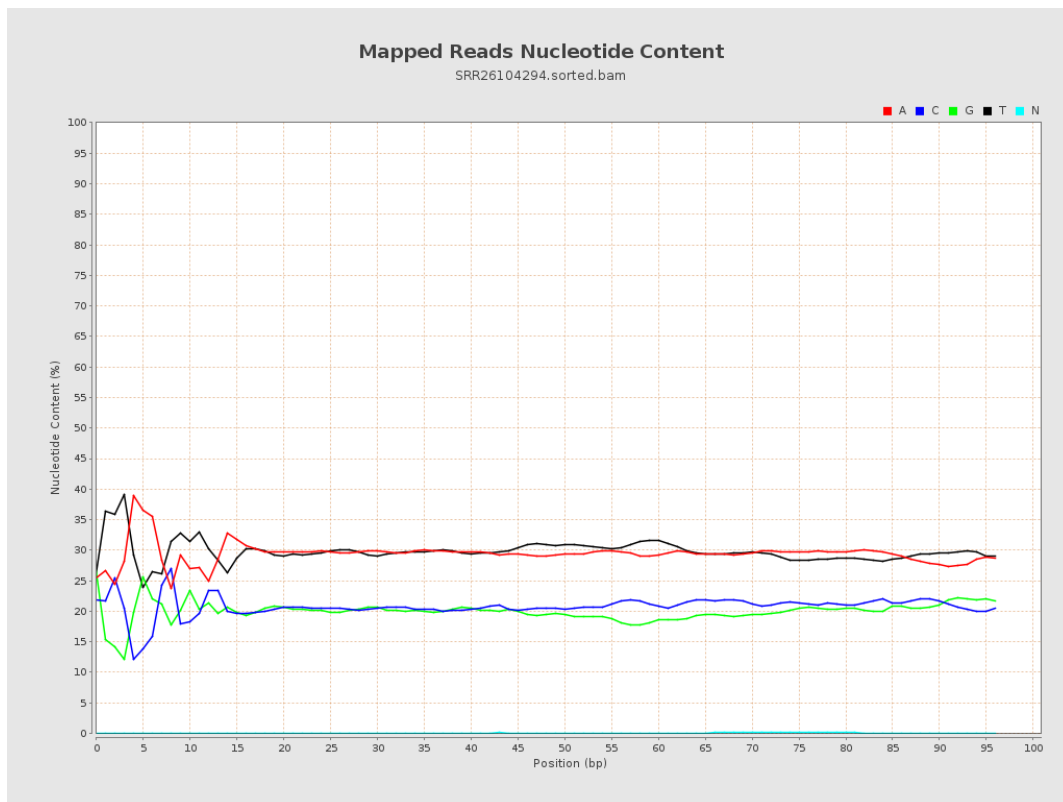
6. Results : Genome Fraction Coverage



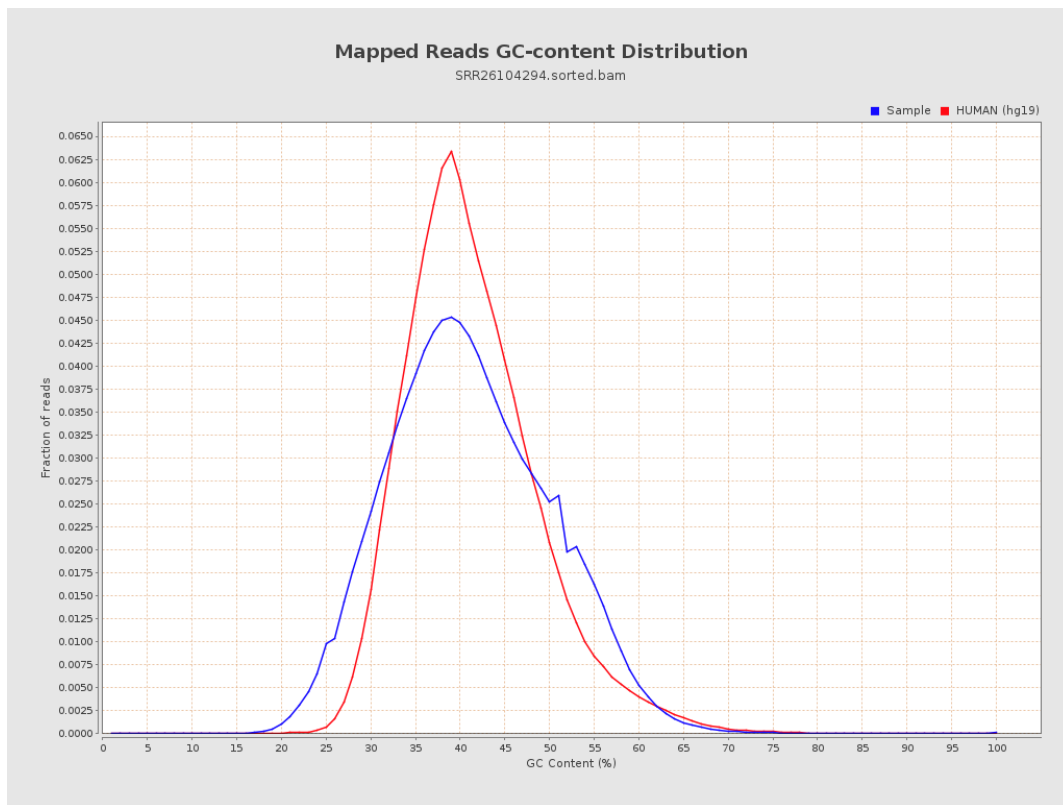
7. Results : Duplication Rate Histogram



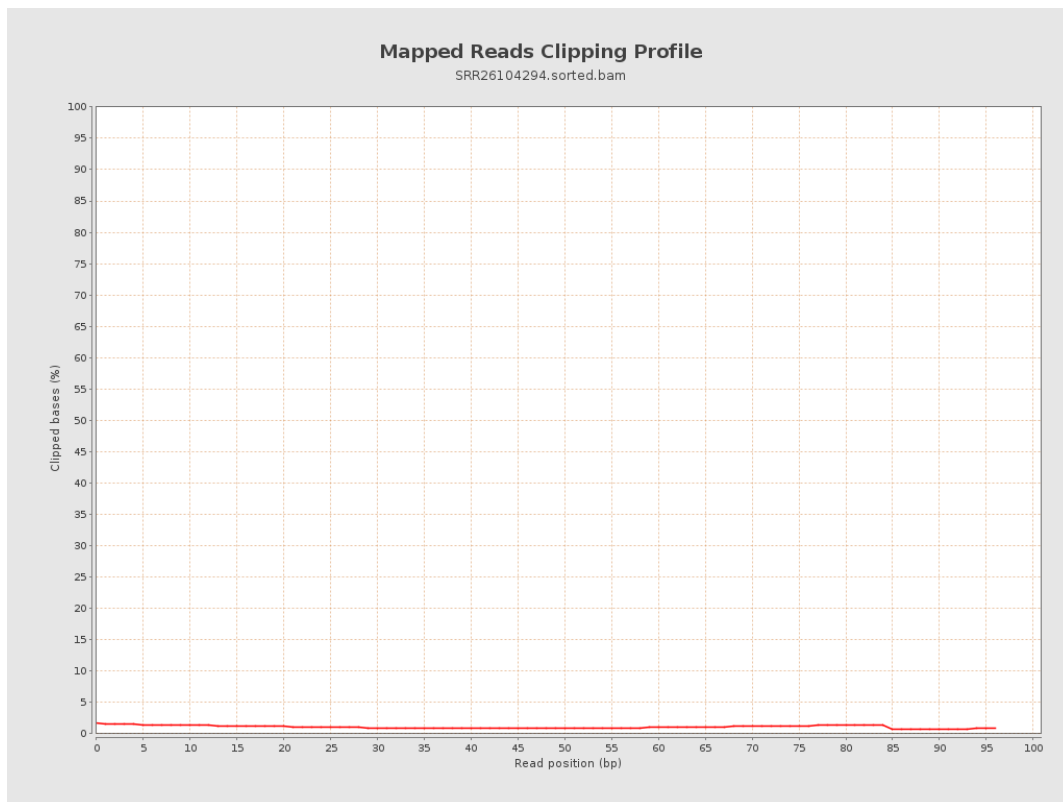
8. Results : Mapped Reads Nucleotide Content



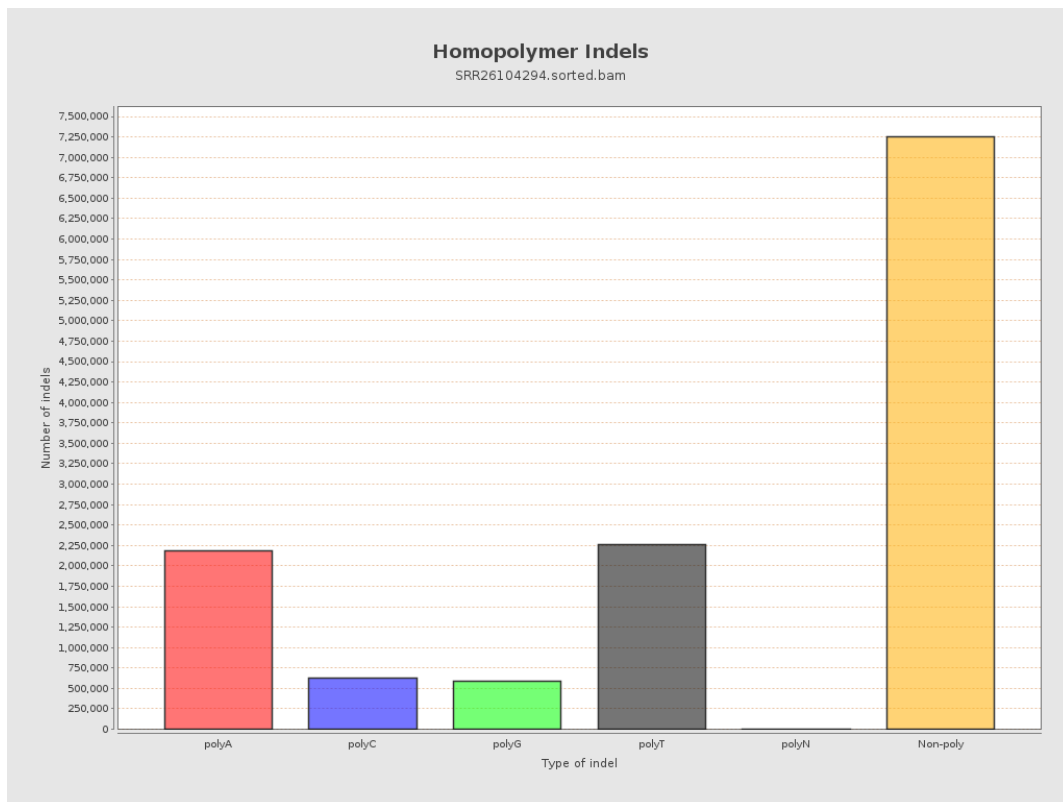
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



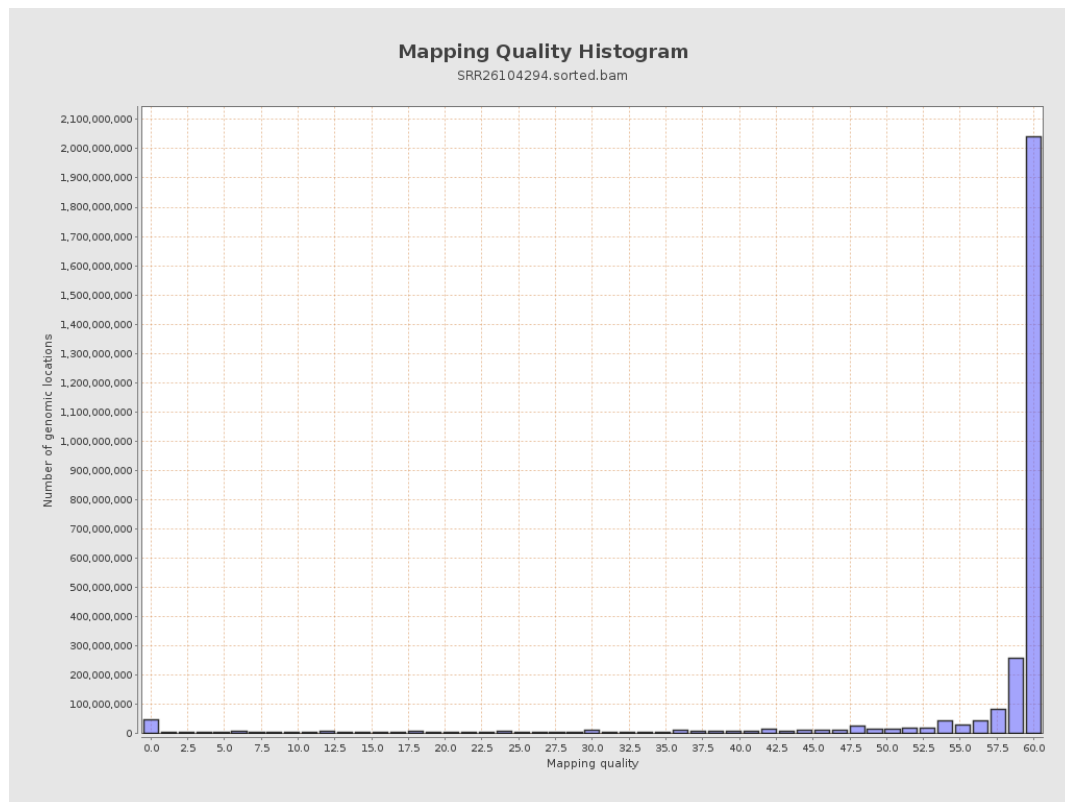
11. Results : Homopolymer Indels



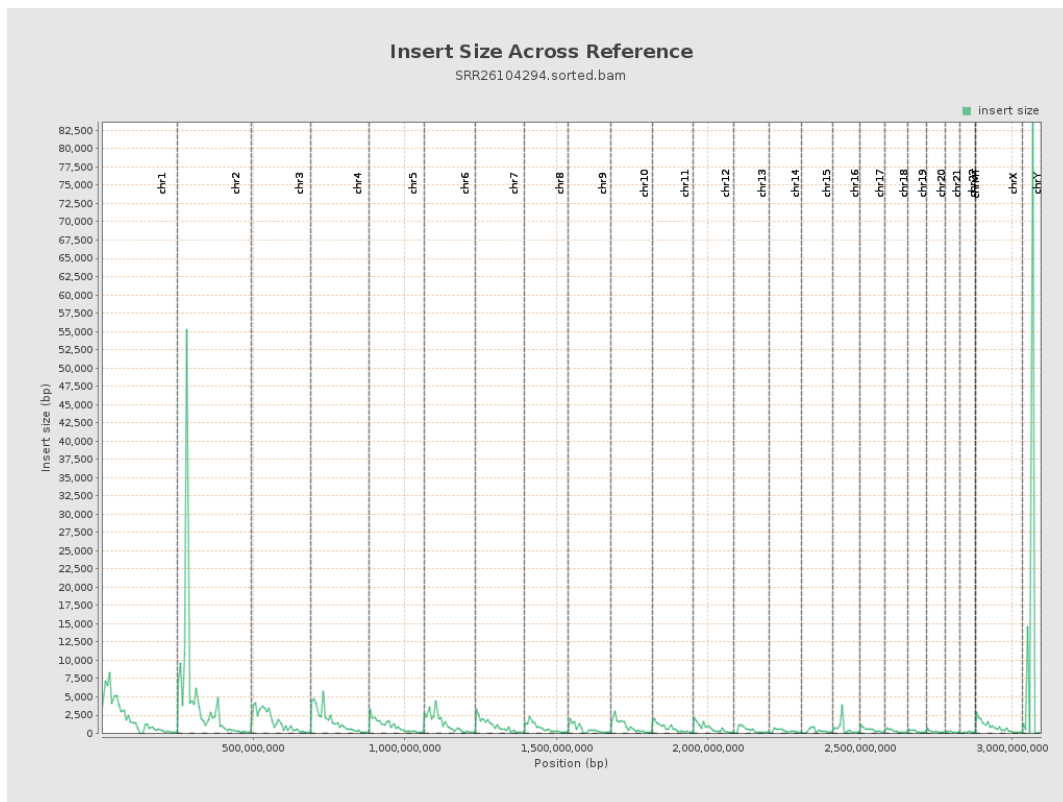
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

