

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:33:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174034.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_SRR10174034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174034_1.fastq.gz SRR10174034_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:33:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,876,646
Mapped reads	3,763,868 / 97.09%
Unmapped reads	112,778 / 2.91%
Mapped paired reads	3,763,868 / 97.09%
Mapped reads, first in pair	1,888,008 / 48.7%
Mapped reads, second in pair	1,875,860 / 48.39%
Mapped reads, both in pair	3,687,138 / 95.11%
Mapped reads, singletons	76,730 / 1.98%
Secondary alignments	0
Supplementary alignments	377,713 / 9.74%
Read min/max/mean length	30 / 133 / 128.27
Duplicated reads (estimated)	2,874,686 / 74.15%
Duplication rate	63.74%
Clipped reads	1,570,738 / 40.52%

2.2. ACGT Content

Number/percentage of A's	133,714,672 / 30.13%
Number/percentage of C's	86,766,695 / 19.55%
Number/percentage of T's	133,493,216 / 30.08%
Number/percentage of G's	89,878,558 / 20.25%
Number/percentage of N's	5,111 / 0%

GC Percentage	39.8%
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2.3. Coverage

Mean	0.1435
Standard Deviation	2.1886

2.4. Mapping Quality

Mean Mapping Quality	52.6
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2.5. Insert size

Mean	876,602.22
Standard Deviation	8,483,539.49
P25/Median/P75	146 / 203 / 292

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	4,655,336
Insertions	46,258
Mapped reads with at least one insertion	1.18%
Deletions	96,010
Mapped reads with at least one deletion	2.49%
Homopolymer indels	43.63%

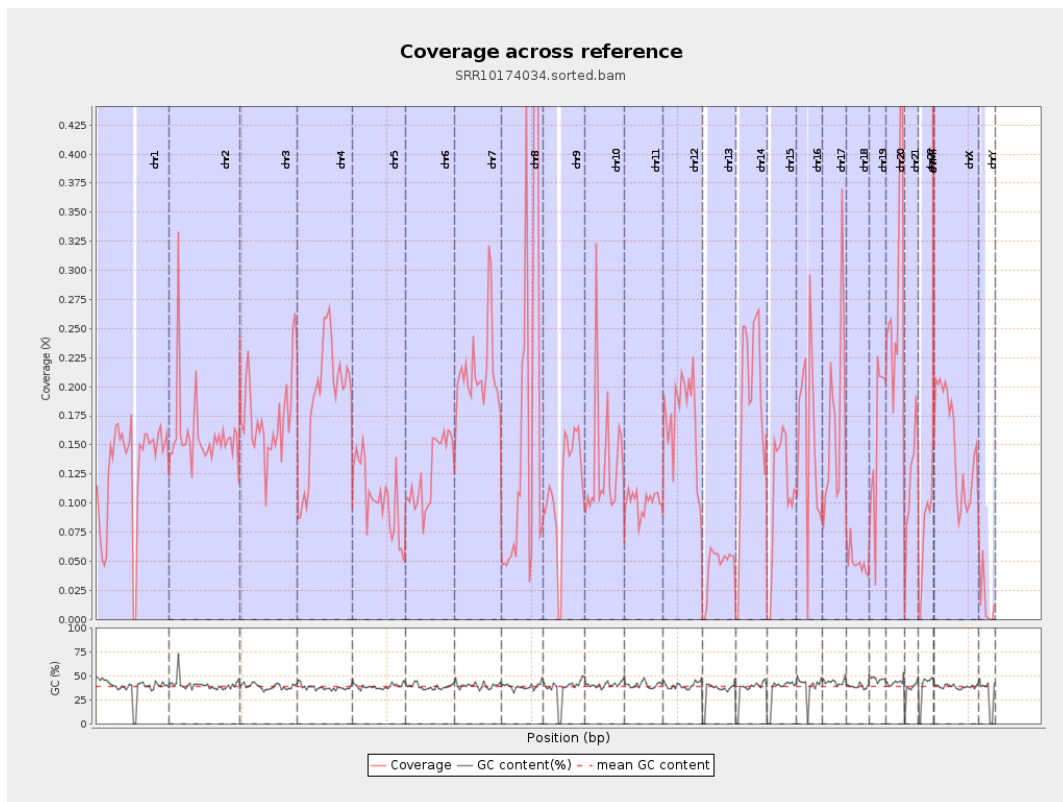
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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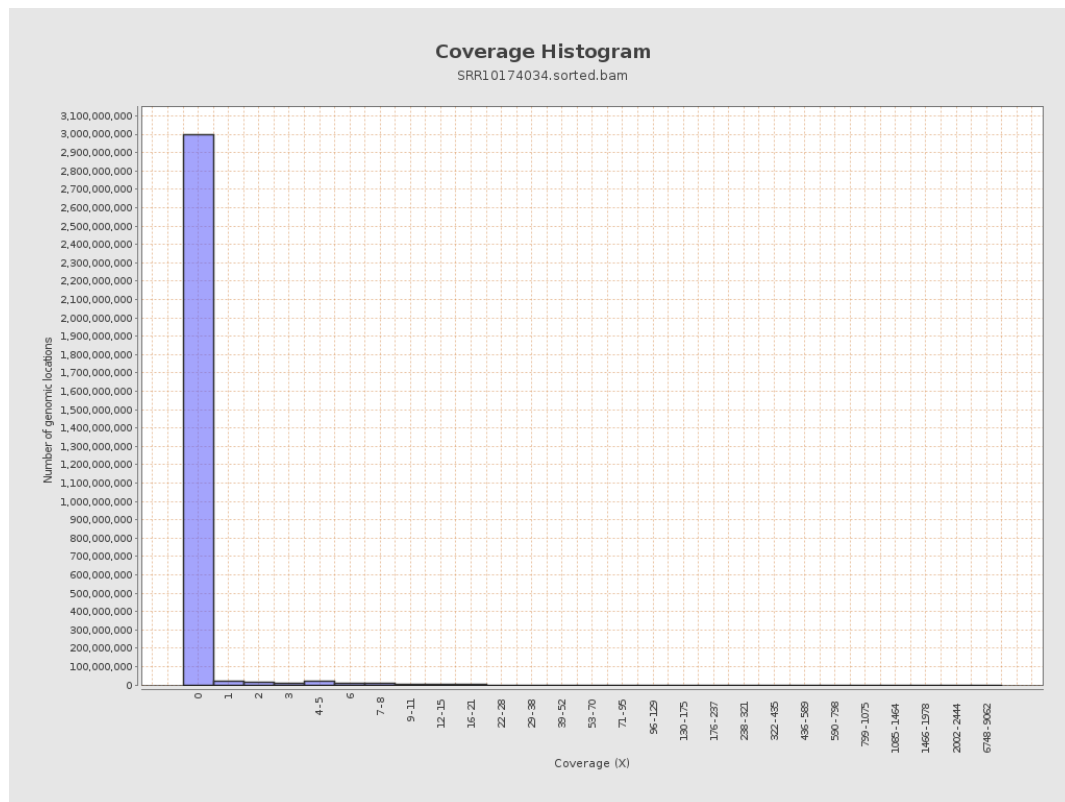
		bases	coverage	deviation
chr1	249250621	32181257	0.1291	1.3085
chr2	243199373	38557927	0.1585	6.3407
chr3	198022430	34715676	0.1753	1.1829
chr4	191154276	35712739	0.1868	1.4462
chr5	180915260	18709699	0.1034	0.9021
chr6	171115067	21634191	0.1264	1.0286
chr7	159138663	34154333	0.2146	2.0427
chr8	146364022	28072386	0.1918	1.5152
chr9	141213431	16223009	0.1149	1.1343
chr10	135534747	18044191	0.1331	2.2985
chr11	135006516	13589389	0.1007	0.9081
chr12	133851895	23274015	0.1739	1.1811
chr13	115169878	5168746	0.0449	0.6011
chr14	107349540	19174300	0.1786	1.1974
chr15	102531392	11069875	0.108	0.9139
chr16	90354753	14023499	0.1552	1.5891
chr17	81195210	13891717	0.1711	1.203
chr18	78077248	3899967	0.05	1.2183
chr19	59128983	9274523	0.1569	1.3082
chr20	63025520	17927956	0.2845	1.5251
chr21	48129895	5692280	0.1183	1.0073
chr22	51304566	3689503	0.0719	0.7229
chrMT	16571	1199133	72.3633	54.5521
chrX	155270560	23302264	0.1501	1.1048

chrY	59373566	913525	0.0154	0.6448
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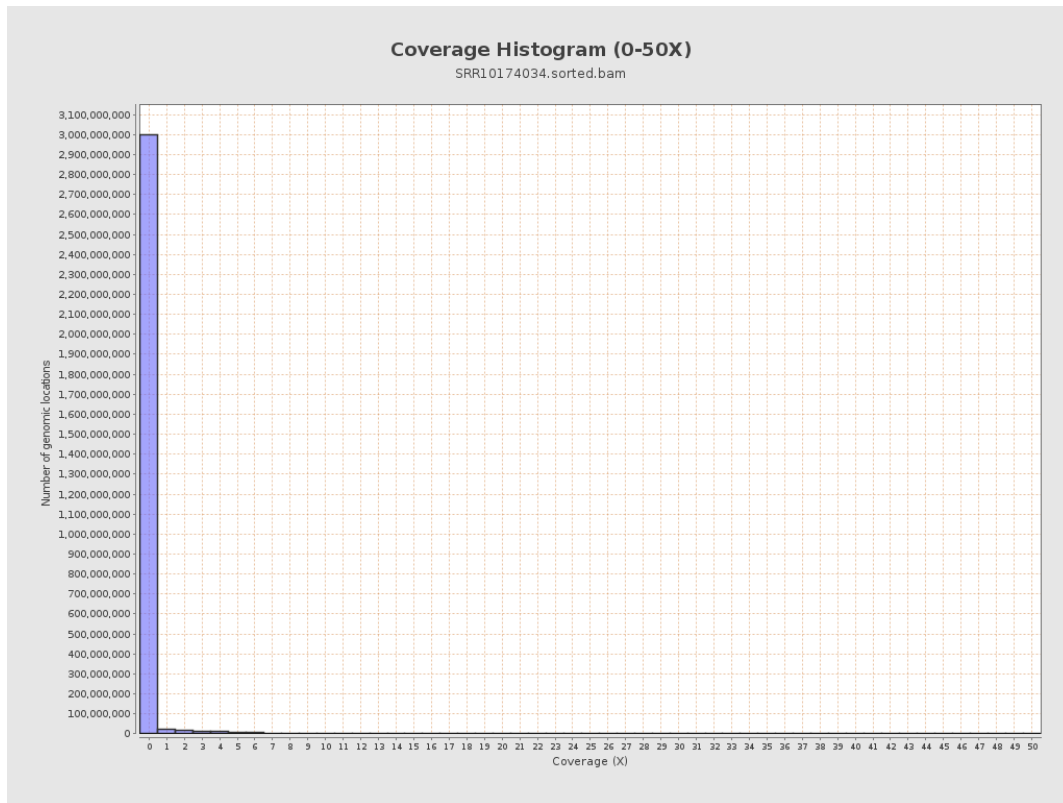
3. Results : Coverage across reference



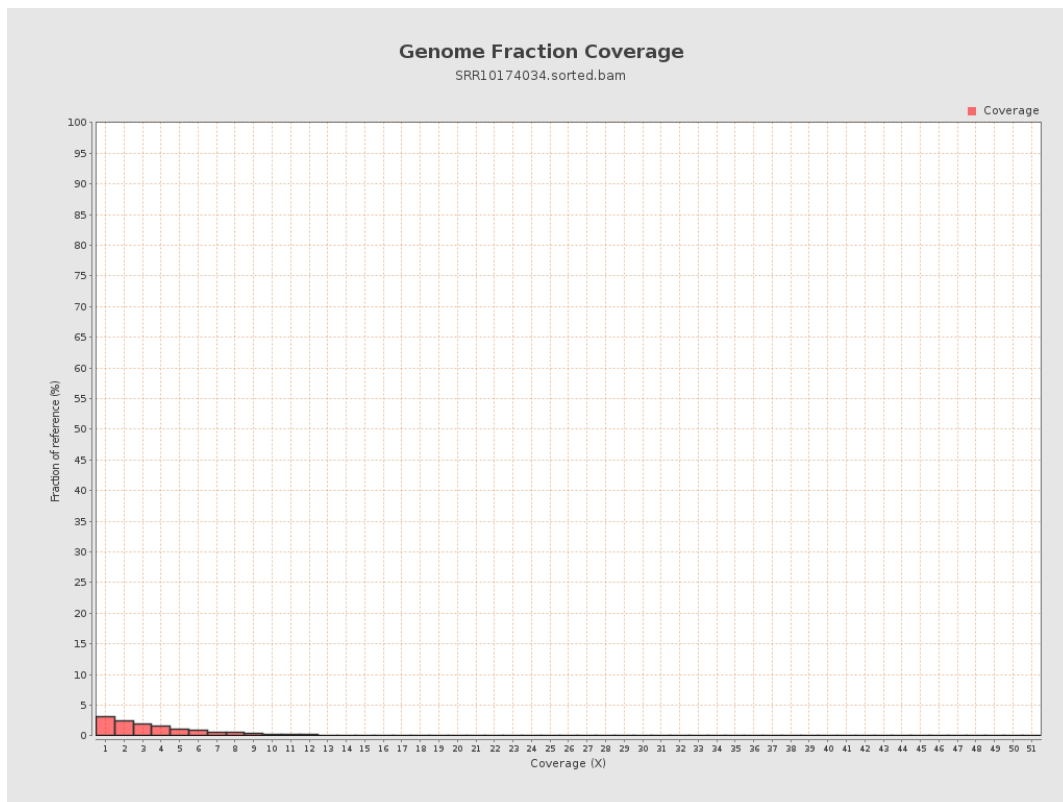
4. Results : Coverage Histogram



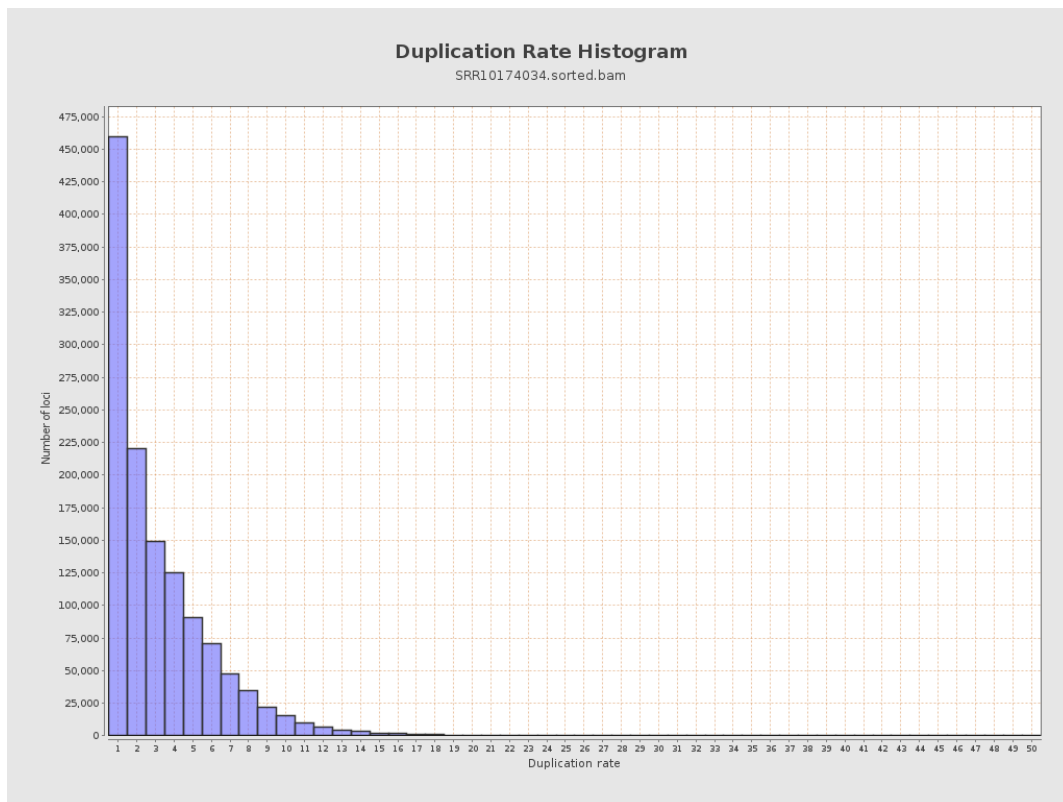
5. Results : Coverage Histogram (0-50X)



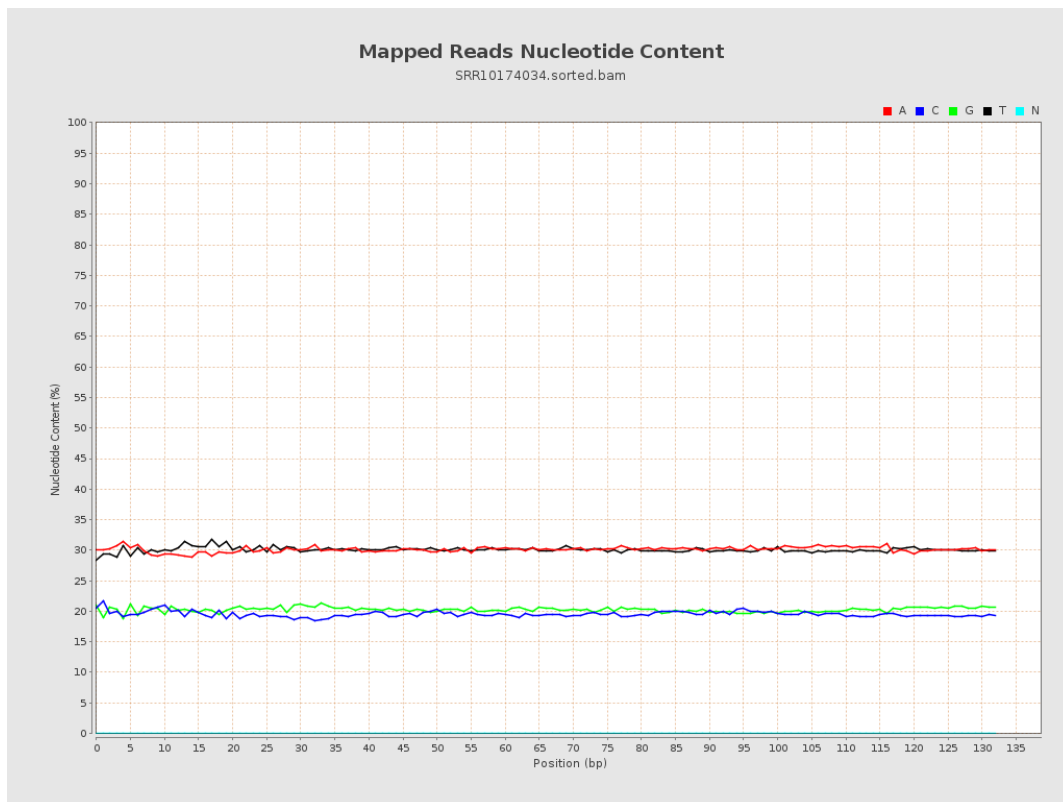
6. Results : Genome Fraction Coverage



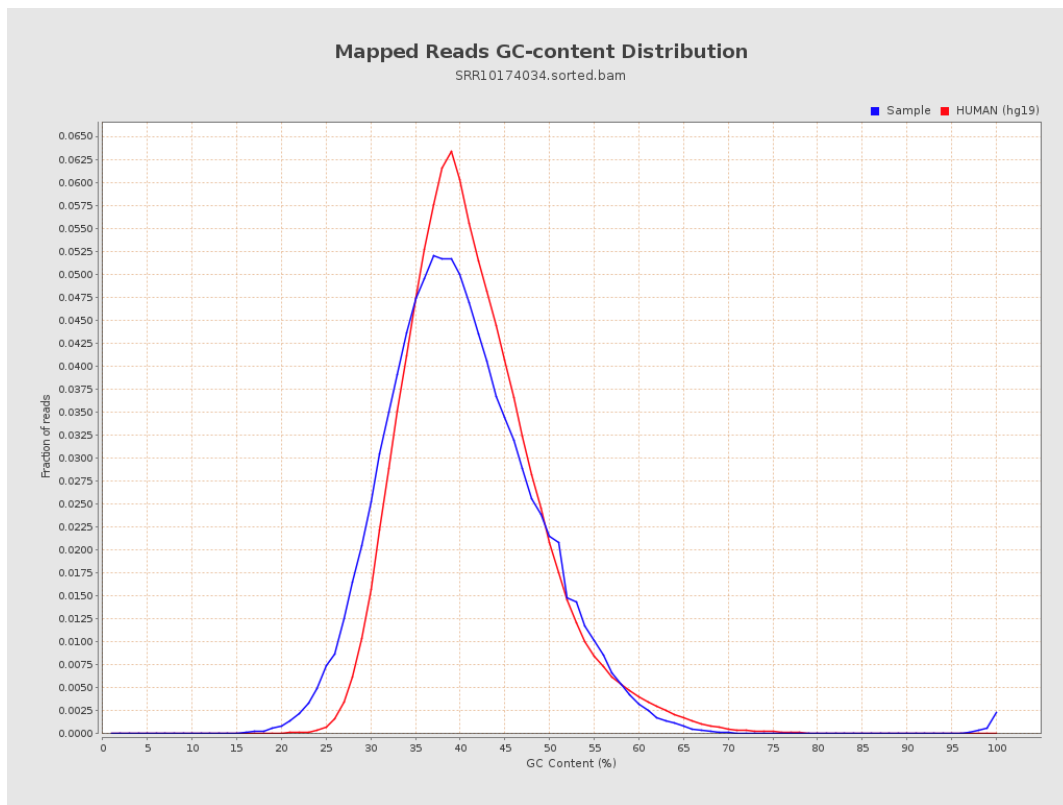
7. Results : Duplication Rate Histogram



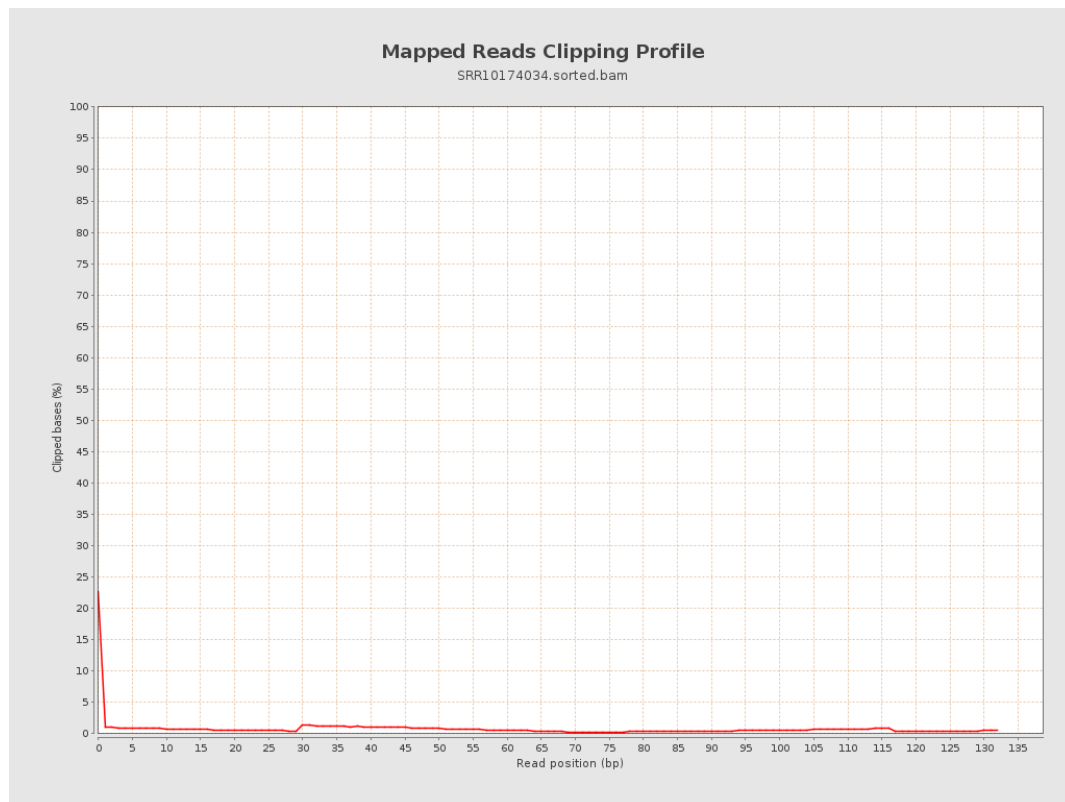
8. Results : Mapped Reads Nucleotide Content



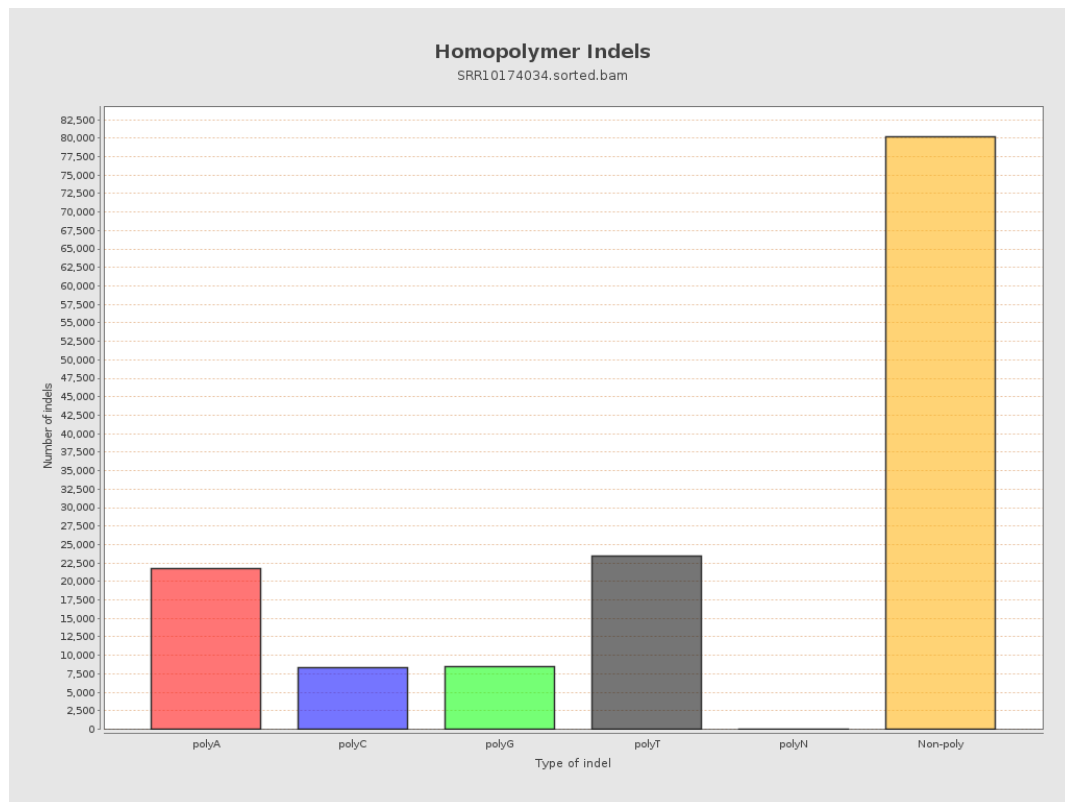
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



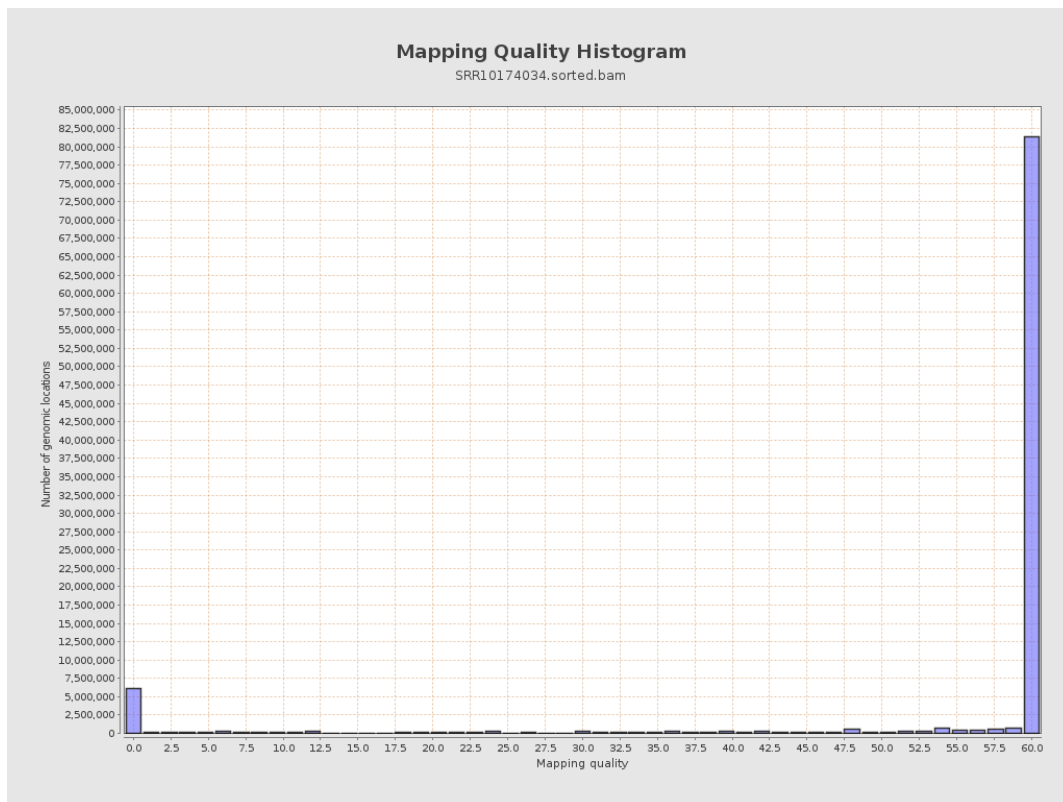
11. Results : Homopolymer Indels



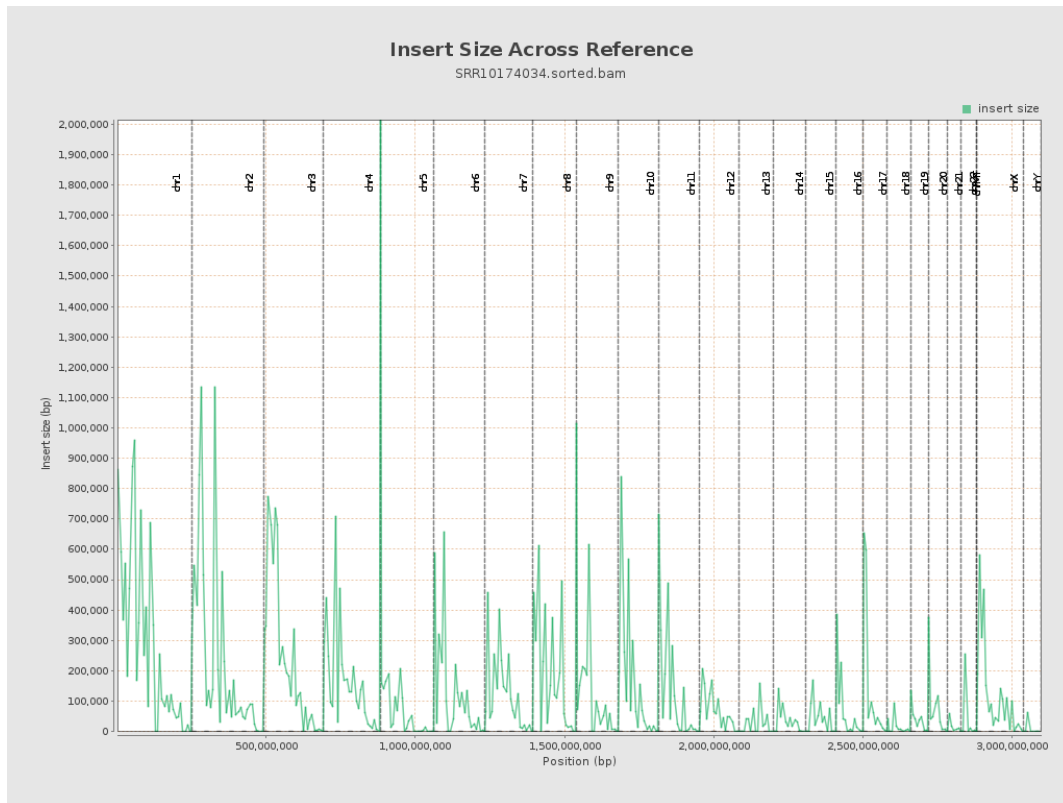
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

