

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:06:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174046.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_SRR10174046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174046_1.fastq.gz SRR10174046_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:06:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,913,870
Mapped reads	1,865,652 / 97.48%
Unmapped reads	48,218 / 2.52%
Mapped paired reads	1,865,652 / 97.48%
Mapped reads, first in pair	933,647 / 48.78%
Mapped reads, second in pair	932,005 / 48.7%
Mapped reads, both in pair	1,835,258 / 95.89%
Mapped reads, singletons	30,394 / 1.59%
Secondary alignments	0
Supplementary alignments	175,121 / 9.15%
Read min/max/mean length	30 / 133 / 128
Duplicated reads (estimated)	1,392,573 / 72.76%
Duplication rate	64.02%
Clipped reads	707,305 / 36.96%

2.2. ACGT Content

Number/percentage of A's	66,763,196 / 30.17%
Number/percentage of C's	43,347,438 / 19.59%
Number/percentage of T's	66,447,253 / 30.02%
Number/percentage of G's	44,757,496 / 20.22%
Number/percentage of N's	2,799 / 0%

GC Percentage	39.81%
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2.3. Coverage

Mean	0.0715
Standard Deviation	1.1511

2.4. Mapping Quality

Mean Mapping Quality	53.08
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2.5. Insert size

Mean	1,238,424.5
Standard Deviation	10,479,512.62
P25/Median/P75	147 / 201 / 286

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	2,254,606
Insertions	24,651
Mapped reads with at least one insertion	1.27%
Deletions	45,805
Mapped reads with at least one deletion	2.4%
Homopolymer indels	43.63%

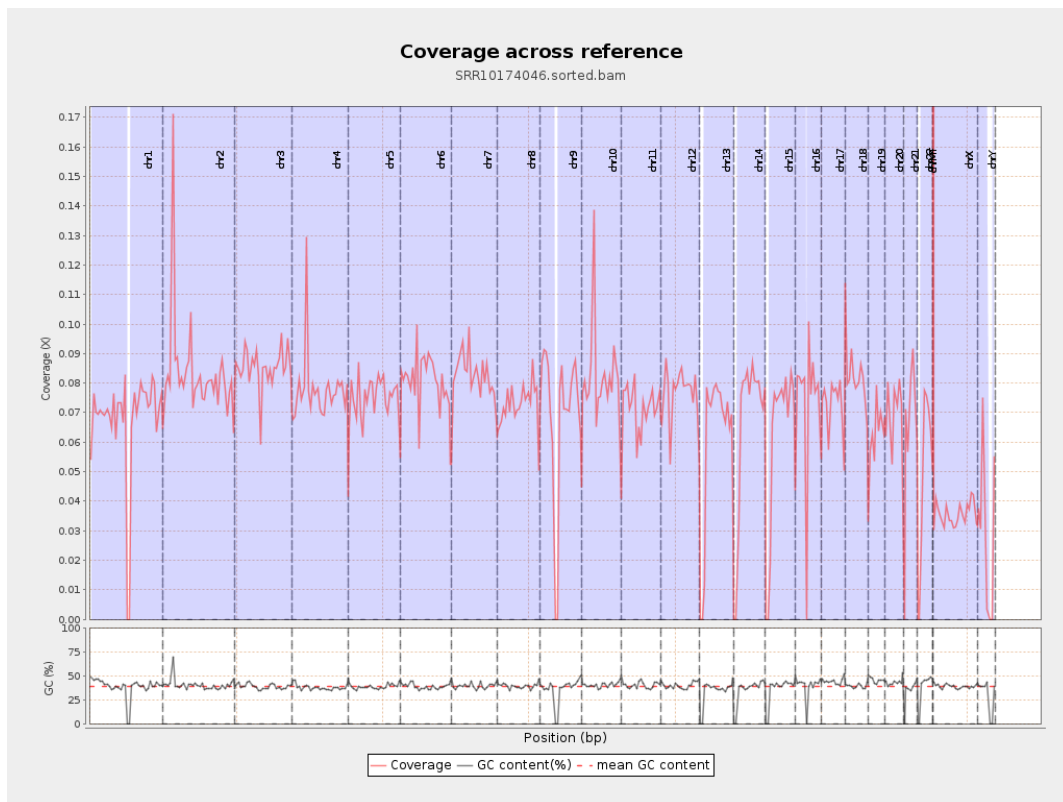
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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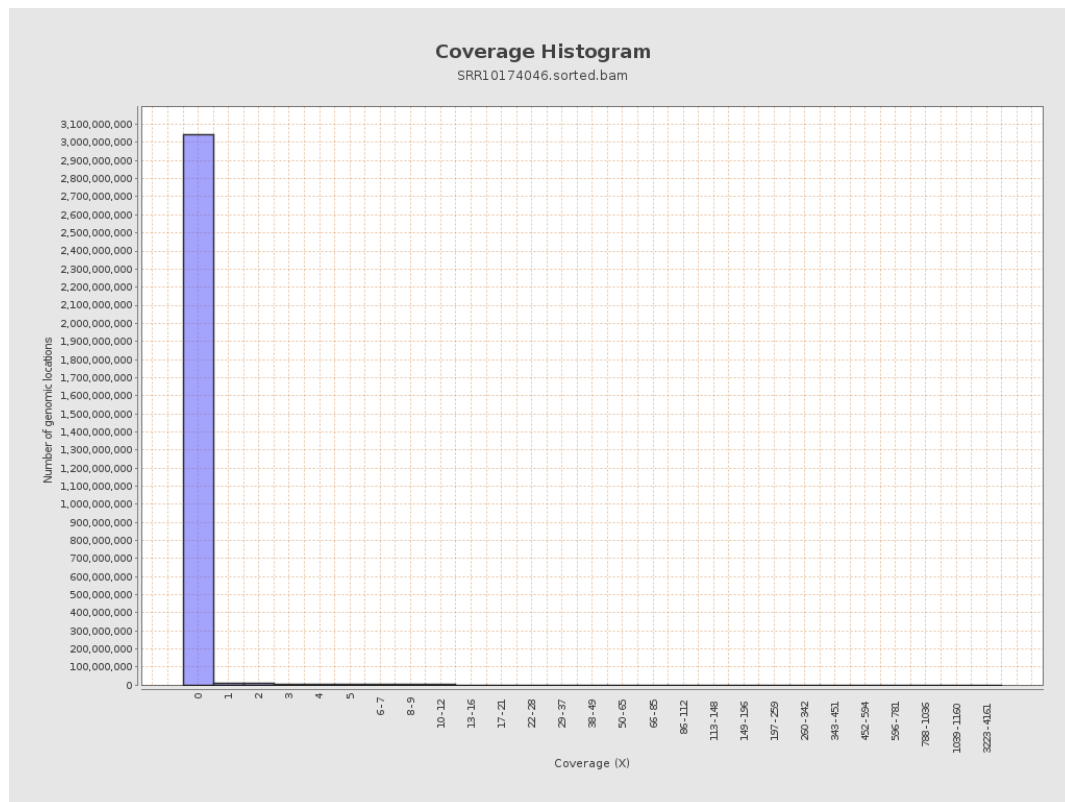
		bases	coverage	deviation
chr1	249250621	16826597	0.0675	0.9072
chr2	243199373	20202441	0.0831	3.0073
chr3	198022430	16832120	0.085	0.7961
chr4	191154276	14876498	0.0778	0.9019
chr5	180915260	13535959	0.0748	0.7418
chr6	171115067	13858427	0.081	0.8291
chr7	159138663	13062178	0.0821	0.9539
chr8	146364022	10672776	0.0729	0.9848
chr9	141213431	9818047	0.0695	0.8273
chr10	135534747	11115613	0.082	1.0358
chr11	135006516	9643740	0.0714	0.7305
chr12	133851895	10300054	0.077	0.7521
chr13	115169878	7009933	0.0609	0.677
chr14	107349540	7098492	0.0661	0.7023
chr15	102531392	6231634	0.0608	0.6605
chr16	90354753	6499122	0.0719	0.7938
chr17	81195210	5940755	0.0732	0.7434
chr18	78077248	6419494	0.0822	1.0369
chr19	59128983	3724631	0.063	0.7125
chr20	63025520	4397176	0.0698	0.7191
chr21	48129895	3211069	0.0667	0.8316
chr22	51304566	2540236	0.0495	0.6387
chrMT	16571	313132	18.8964	17.5489
chrX	155270560	5528029	0.0356	0.5066

chrY	59373566	1778193	0.0299	0.5531
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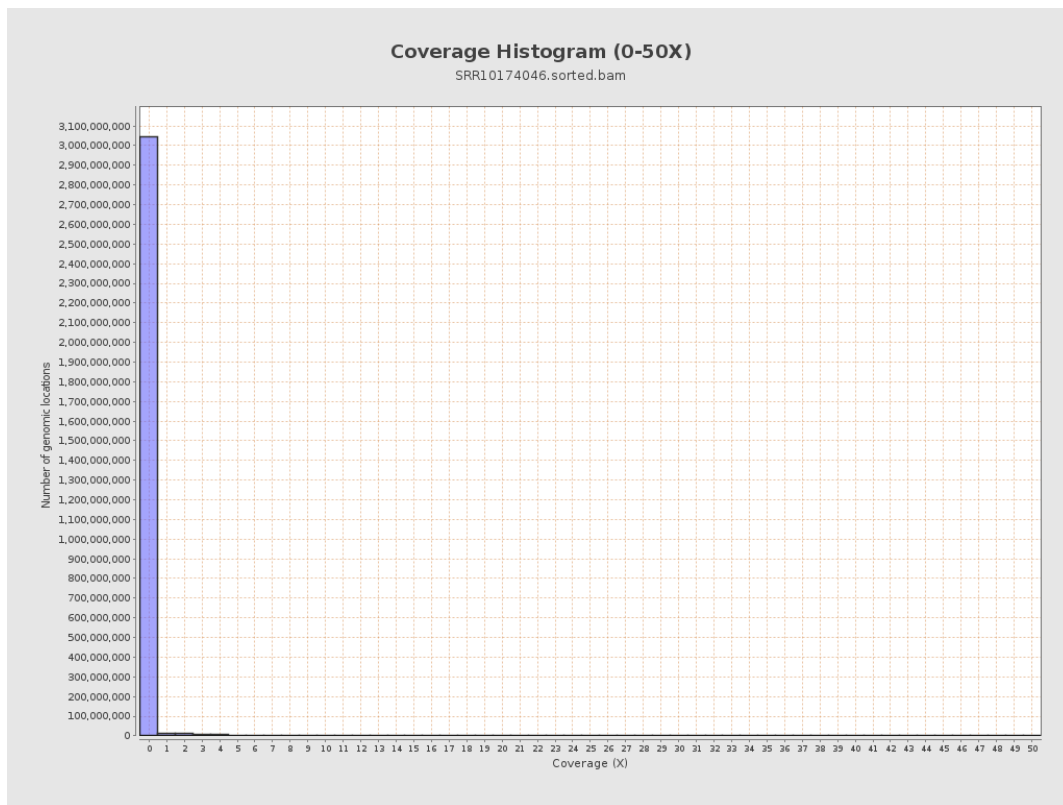
3. Results : Coverage across reference



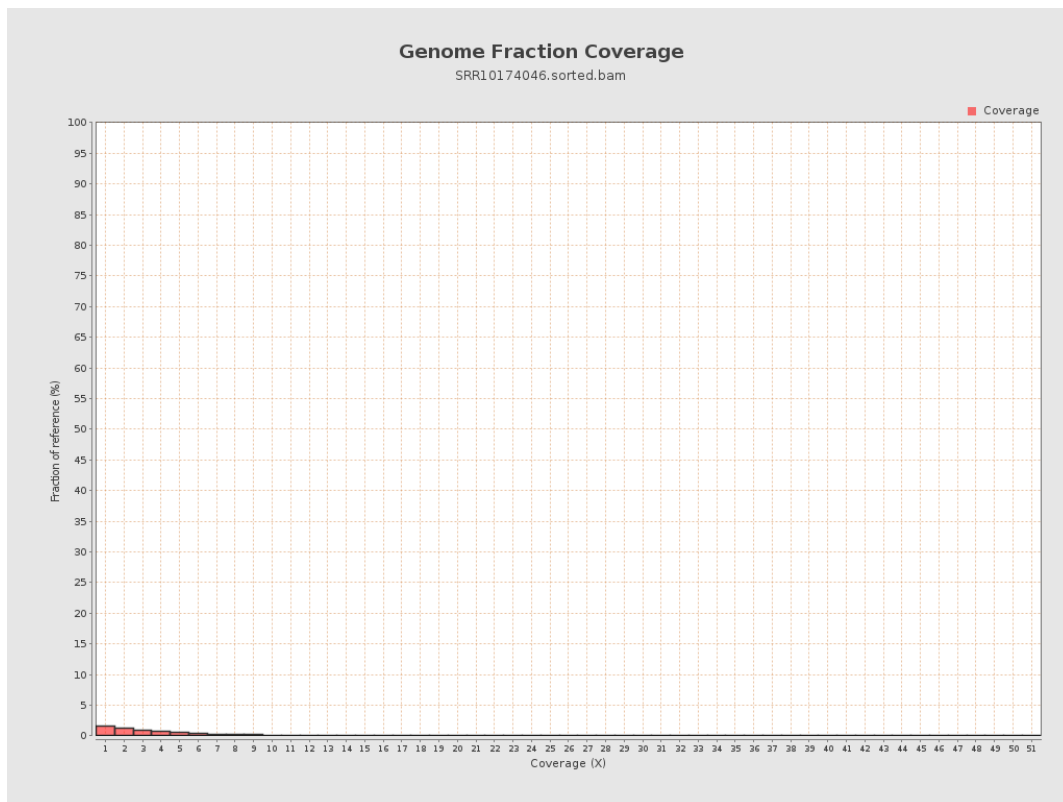
4. Results : Coverage Histogram



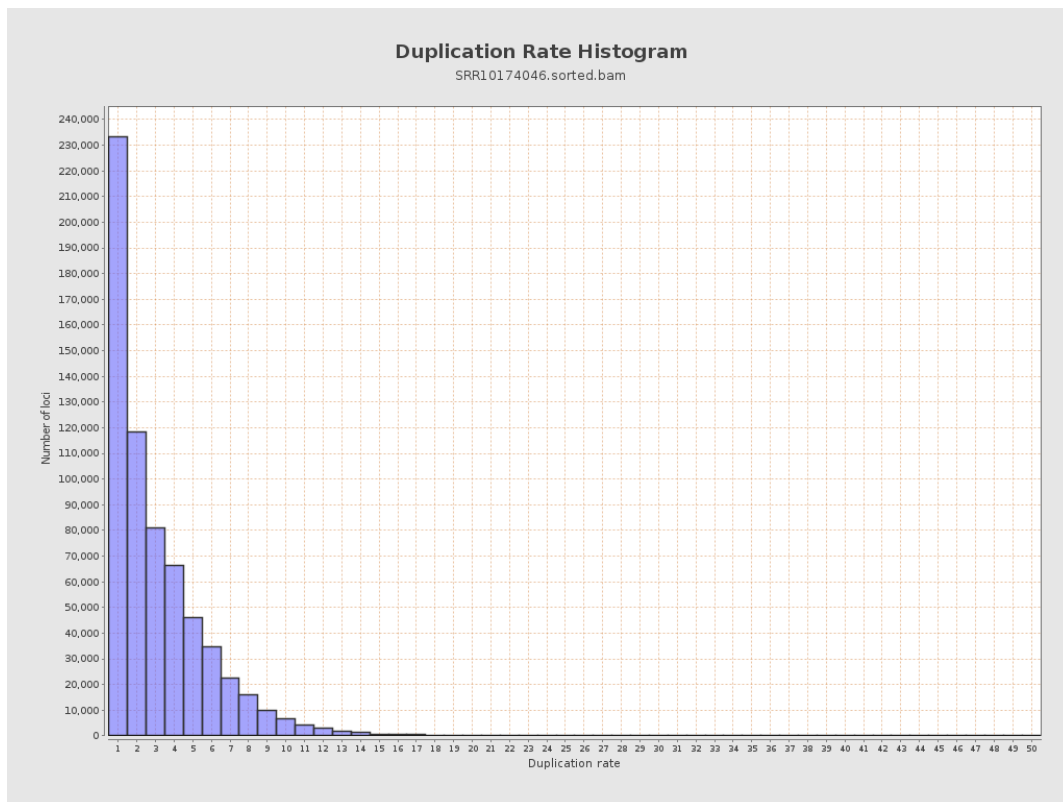
5. Results : Coverage Histogram (0-50X)



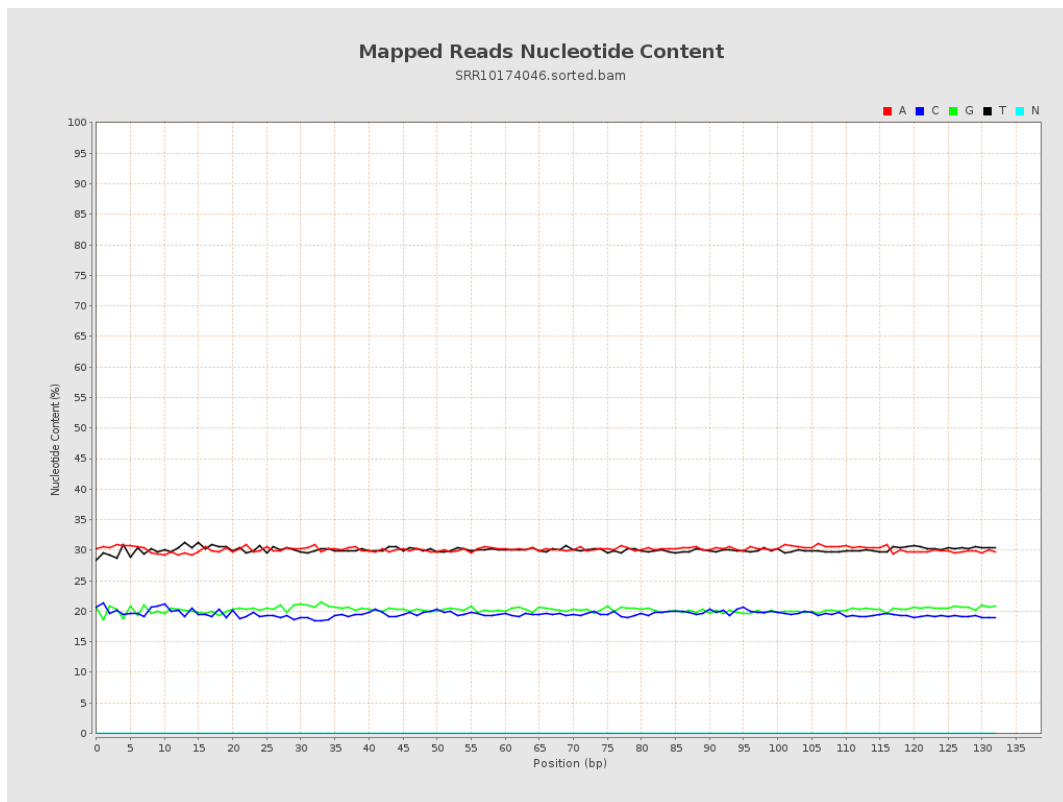
6. Results : Genome Fraction Coverage



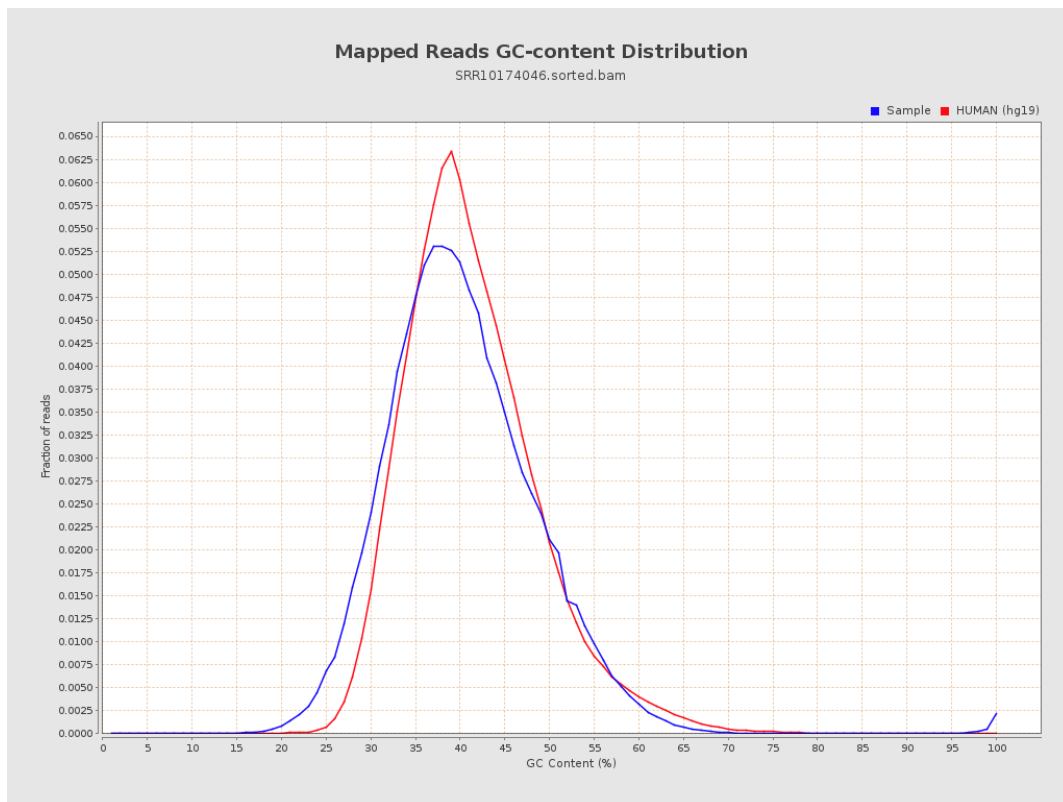
7. Results : Duplication Rate Histogram



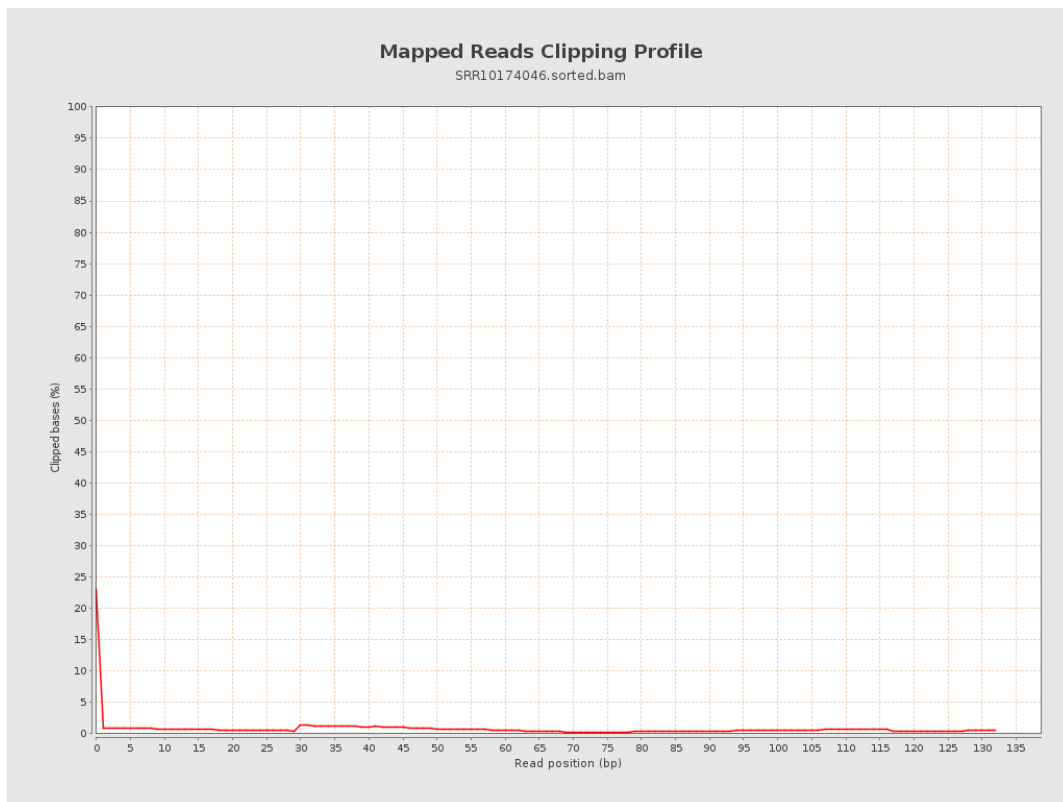
8. Results : Mapped Reads Nucleotide Content



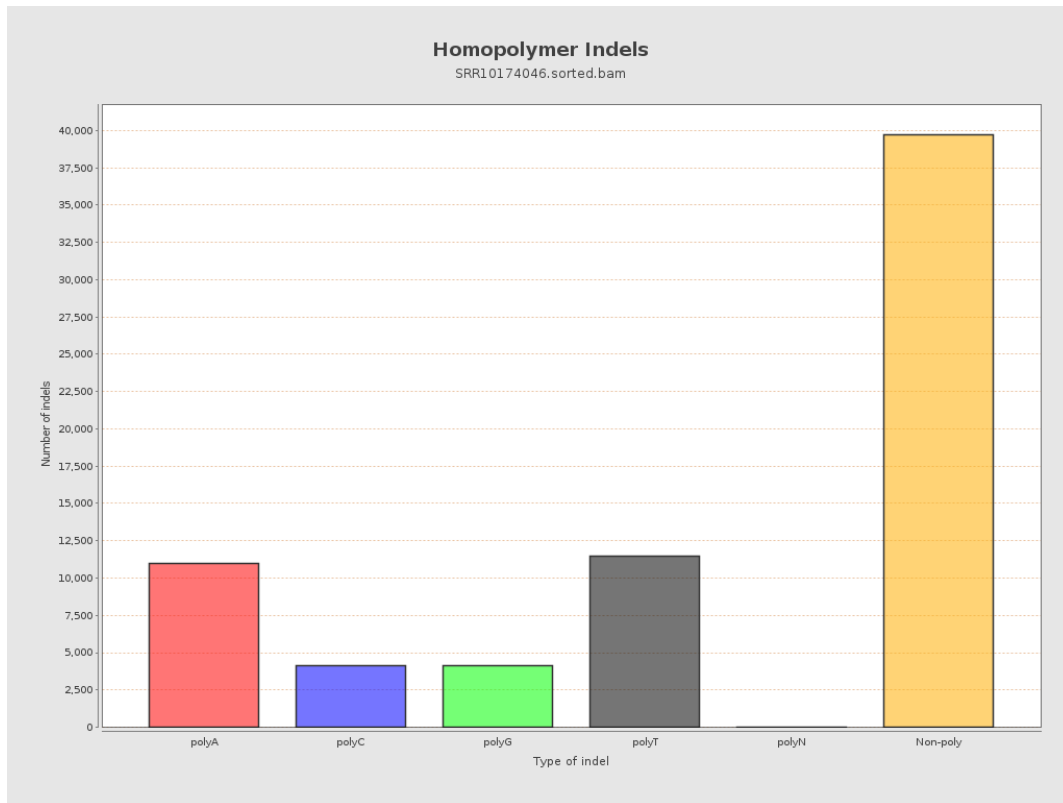
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



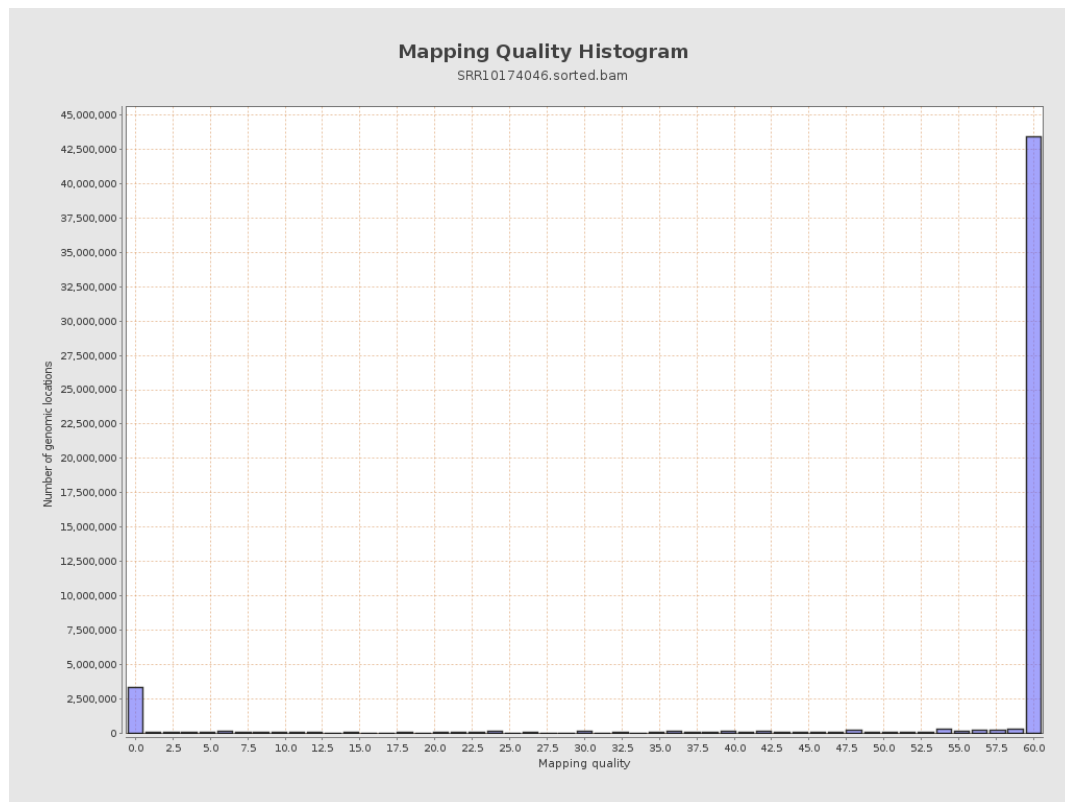
11. Results : Homopolymer Indels



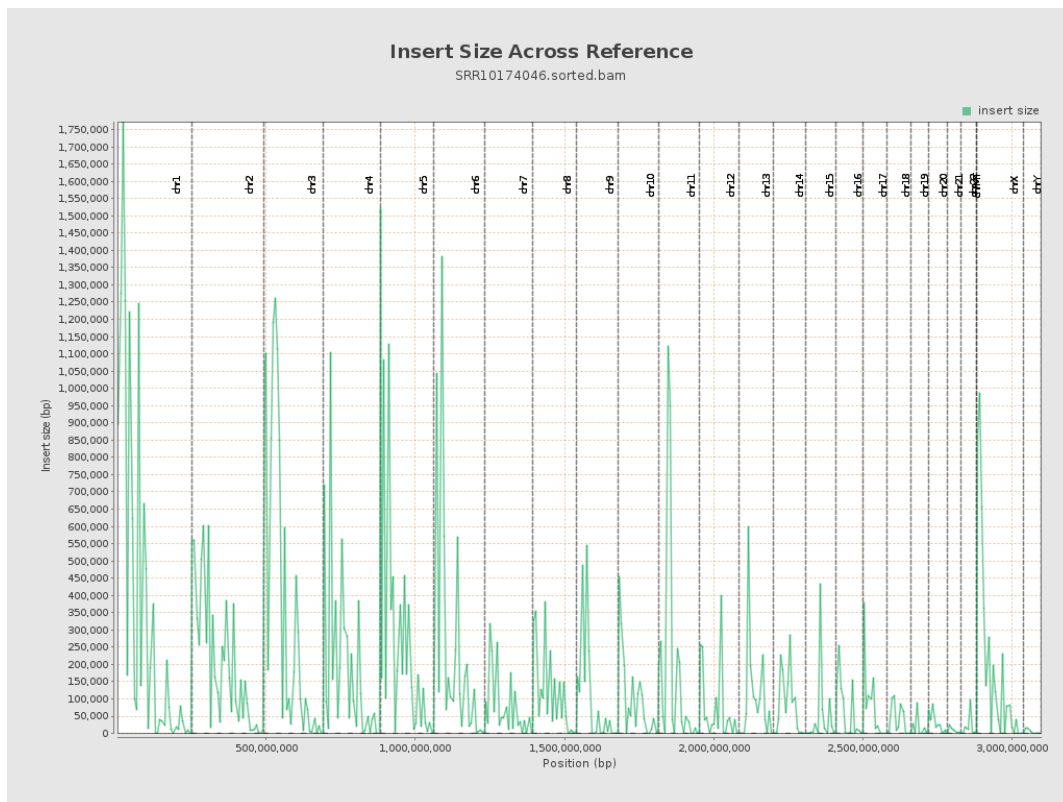
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

