

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 00:32:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174041.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_SRR10174041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174041_1.fastq.gz SRR10174041_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 00:32:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,208,436
Mapped reads	5,060,579 / 97.16%
Unmapped reads	147,857 / 2.84%
Mapped paired reads	5,060,579 / 97.16%
Mapped reads, first in pair	2,538,907 / 48.75%
Mapped reads, second in pair	2,521,672 / 48.42%
Mapped reads, both in pair	4,960,780 / 95.25%
Mapped reads, singletons	99,799 / 1.92%
Secondary alignments	0
Supplementary alignments	481,549 / 9.25%
Read min/max/mean length	30 / 133 / 127.72
Duplicated reads (estimated)	3,926,785 / 75.39%
Duplication rate	65.03%
Clipped reads	2,066,275 / 39.67%

2.2. ACGT Content

Number/percentage of A's	178,843,794 / 30.04%
Number/percentage of C's	117,024,664 / 19.66%
Number/percentage of T's	178,223,995 / 29.94%
Number/percentage of G's	121,168,048 / 20.36%
Number/percentage of N's	6,892 / 0%

GC Percentage	40.01%
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2.3. Coverage

Mean	0.1924
Standard Deviation	2.8803

2.4. Mapping Quality

Mean Mapping Quality	52.9
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2.5. Insert size

Mean	997,166.46
Standard Deviation	9,396,328.3
P25/Median/P75	142 / 199 / 285

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	6,208,707
Insertions	64,694
Mapped reads with at least one insertion	1.23%
Deletions	127,445
Mapped reads with at least one deletion	2.45%
Homopolymer indels	43.13%

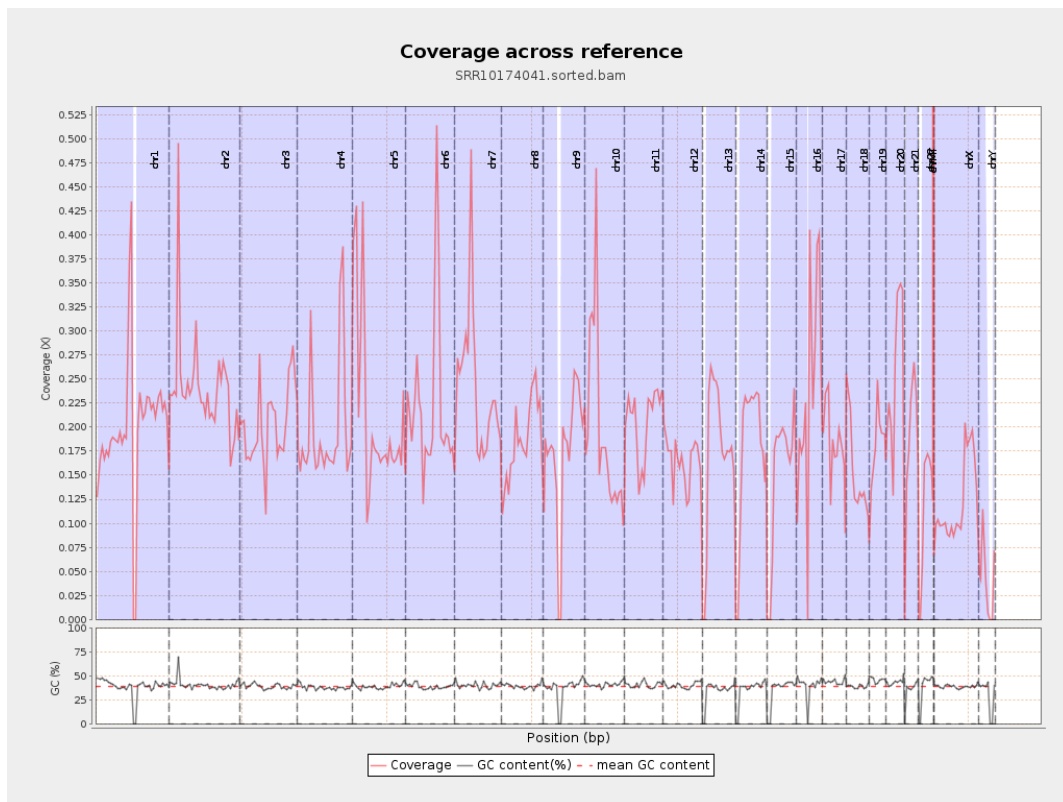
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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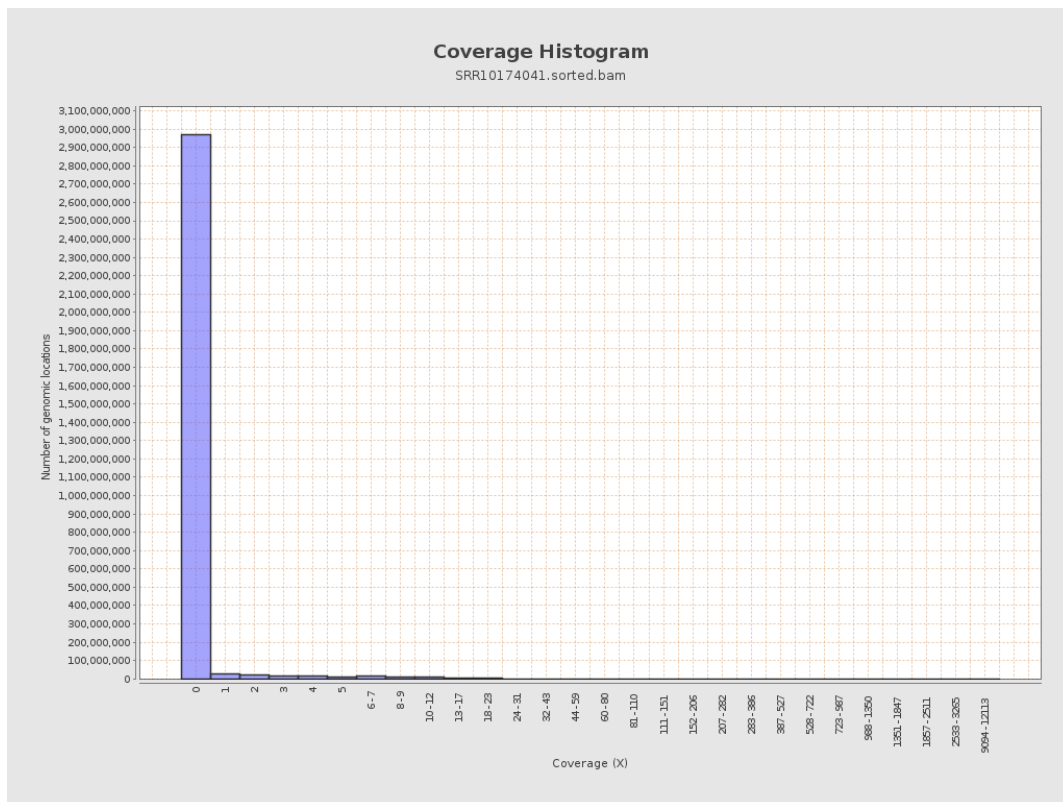
		bases	coverage	deviation
chr1	249250621	49705742	0.1994	2.1506
chr2	243199373	58477698	0.2405	8.4984
chr3	198022430	40112072	0.2026	1.3111
chr4	191154276	36941226	0.1933	1.7218
chr5	180915260	38623356	0.2135	1.3505
chr6	171115067	38246291	0.2235	1.4609
chr7	159138663	38433954	0.2415	2.3905
chr8	146364022	27308447	0.1866	1.6614
chr9	141213431	24850805	0.176	1.6143
chr10	135534747	26538164	0.1958	2.5636
chr11	135006516	27667318	0.2049	1.3561
chr12	133851895	21976578	0.1642	1.185
chr13	115169878	19702349	0.1711	1.2109
chr14	107349540	18916482	0.1762	1.2387
chr15	102531392	15541560	0.1516	1.123
chr16	90354753	21581127	0.2388	2.0006
chr17	81195210	14687636	0.1809	1.3808
chr18	78077248	12060352	0.1545	2.2774
chr19	59128983	10730779	0.1815	1.9398
chr20	63025520	16108962	0.2556	1.4895
chr21	48129895	8933740	0.1856	1.3549
chr22	51304566	5769111	0.1124	0.9502
chrMT	16571	1552994	93.7176	74.4399
chrX	155270560	18776922	0.1209	1.0145

chrY	59373566	2343590	0.0395	1.1032
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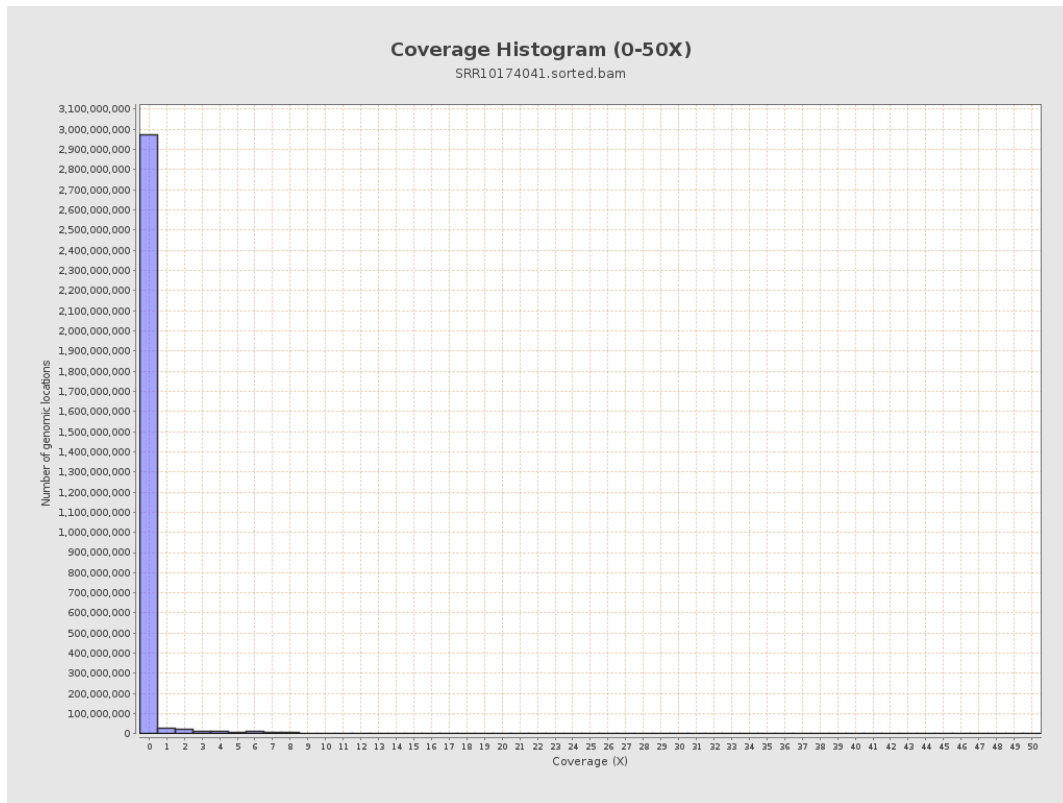
3. Results : Coverage across reference



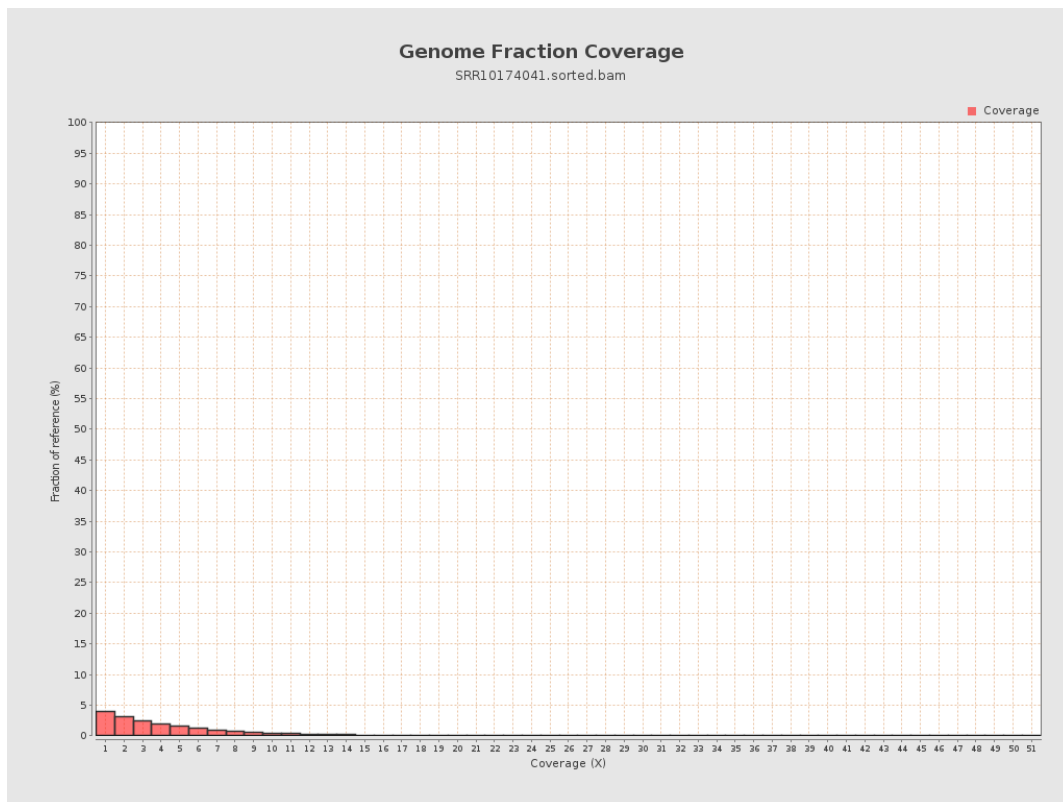
4. Results : Coverage Histogram



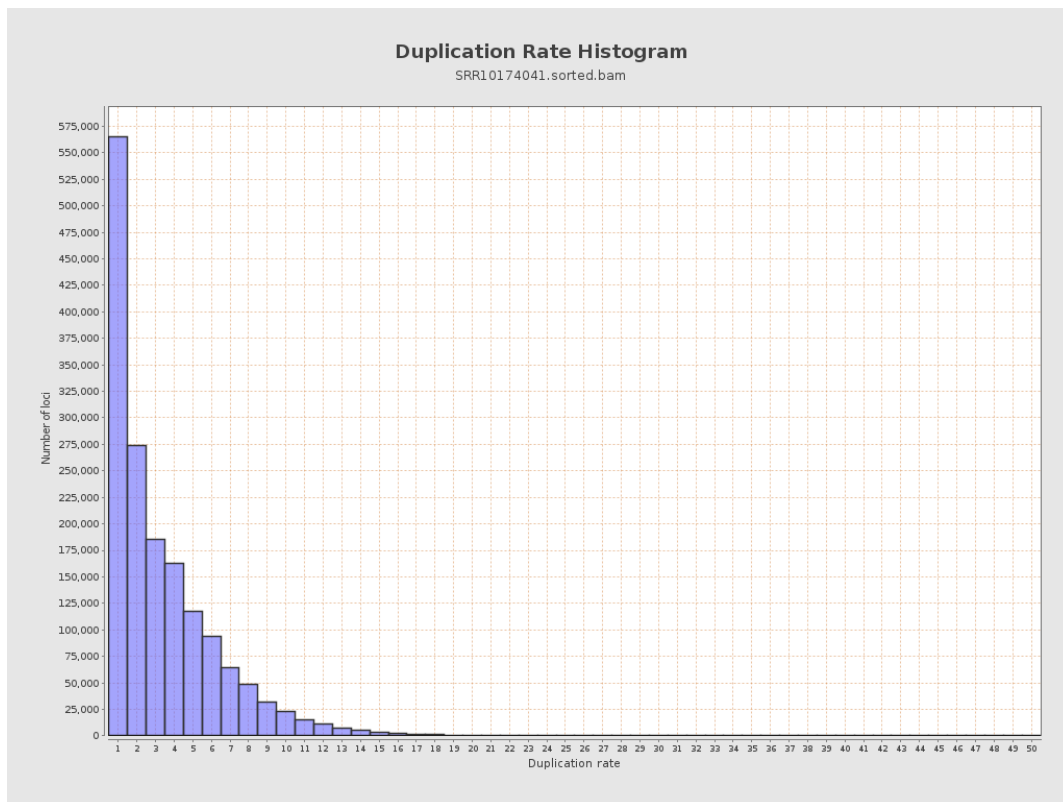
5. Results : Coverage Histogram (0-50X)



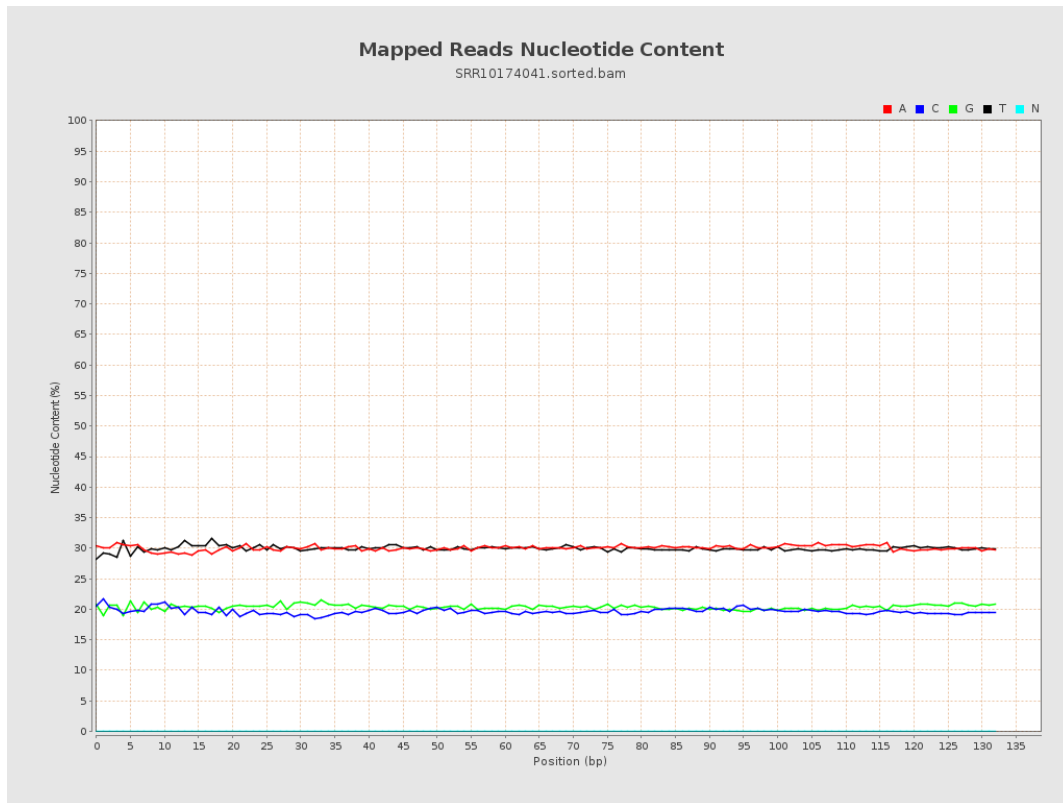
6. Results : Genome Fraction Coverage



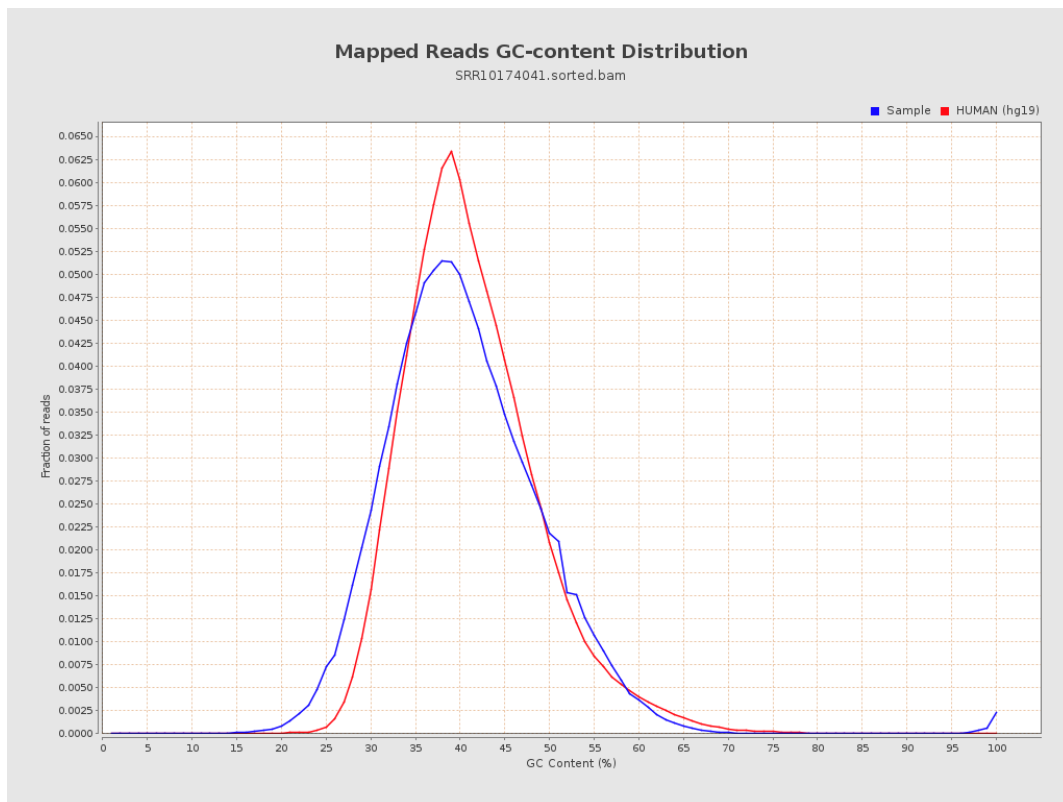
7. Results : Duplication Rate Histogram



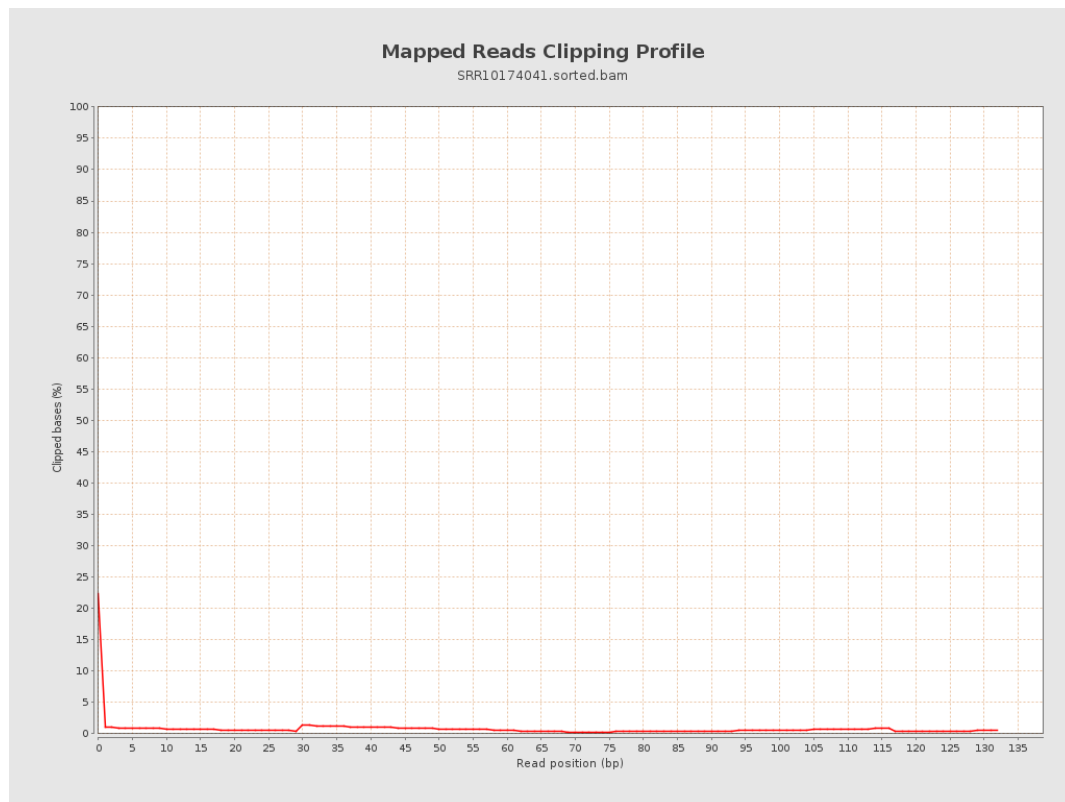
8. Results : Mapped Reads Nucleotide Content



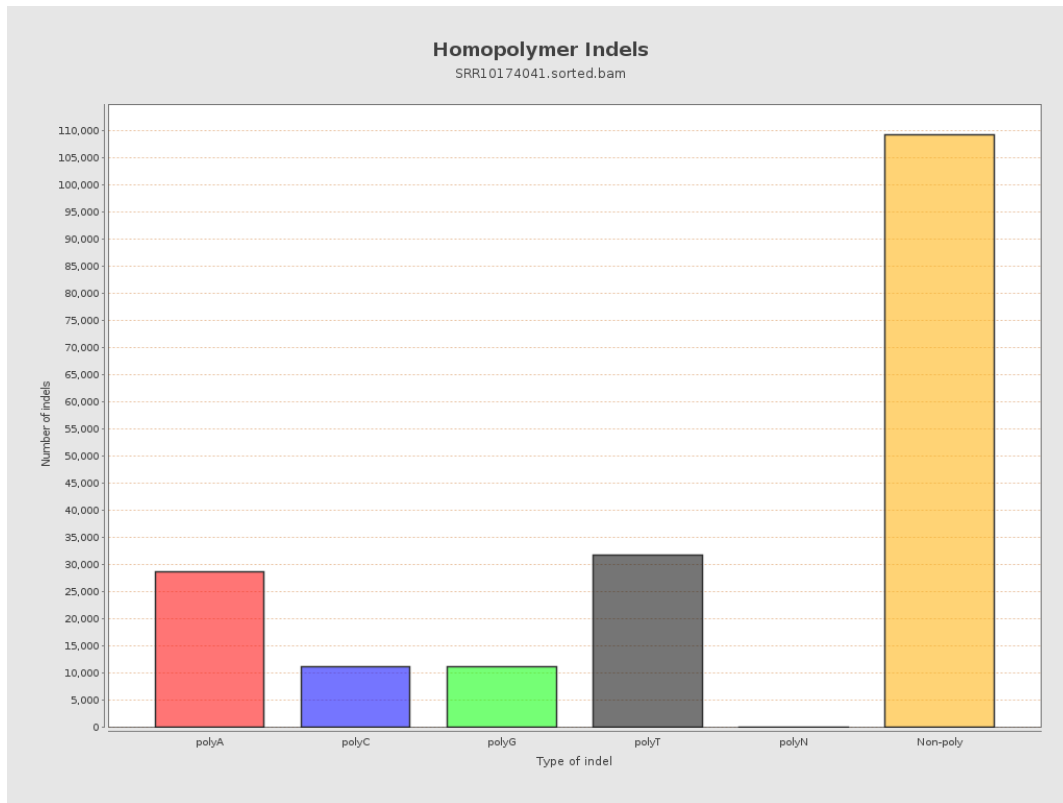
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



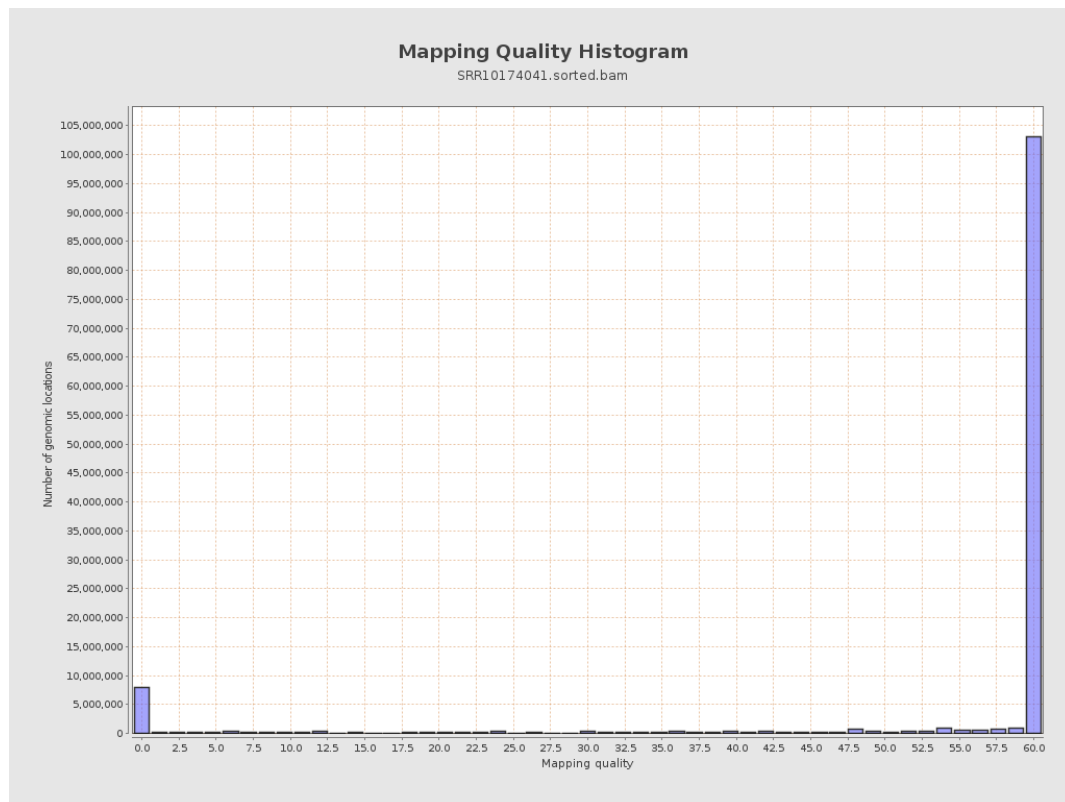
11. Results : Homopolymer Indels



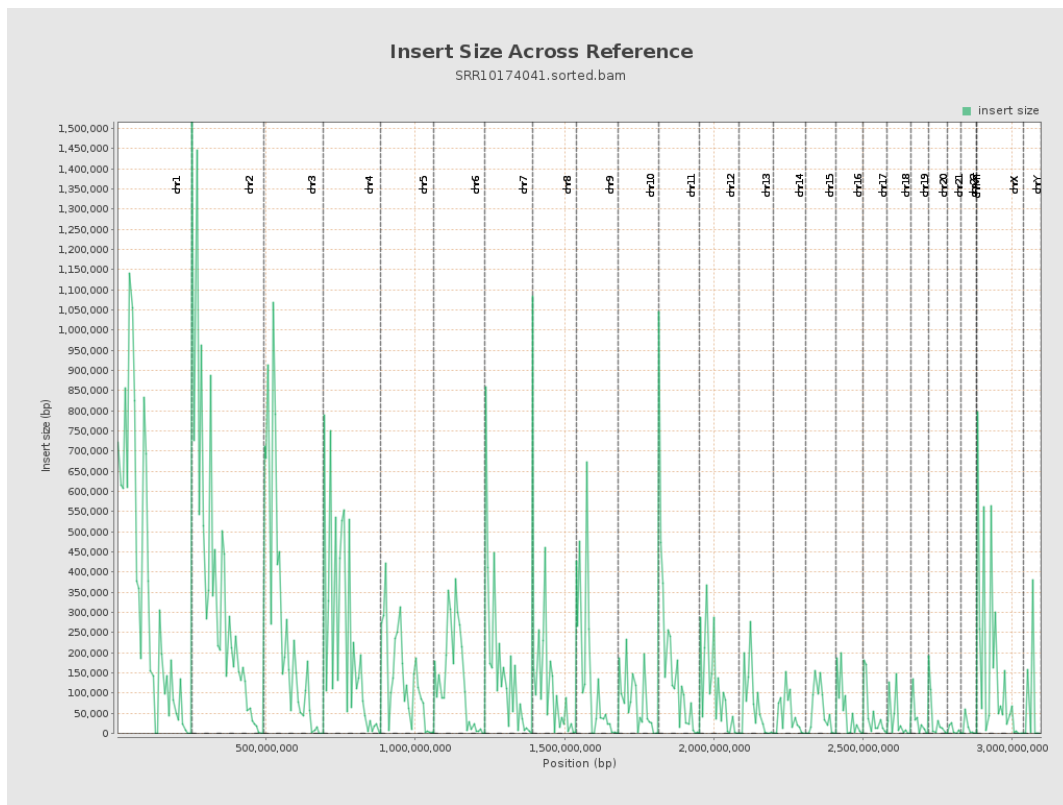
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

