

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:18:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173906.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_SRR10173906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173906_1.fastq.gz SRR10173906_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:18:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,562,038
Mapped reads	10,275,675 / 97.29%
Unmapped reads	286,363 / 2.71%
Mapped paired reads	10,275,675 / 97.29%
Mapped reads, first in pair	5,142,952 / 48.69%
Mapped reads, second in pair	5,132,723 / 48.6%
Mapped reads, both in pair	10,082,962 / 95.46%
Mapped reads, singletons	192,713 / 1.82%
Secondary alignments	0
Supplementary alignments	1,007,400 / 9.54%
Read min/max/mean length	30 / 133 / 128.12
Duplicated reads (estimated)	8,009,016 / 75.83%
Duplication rate	65.21%
Clipped reads	4,180,293 / 39.58%

2.2. ACGT Content

Number/percentage of A's	361,633,252 / 29.8%
Number/percentage of C's	241,373,534 / 19.89%
Number/percentage of T's	360,964,135 / 29.75%
Number/percentage of G's	249,373,876 / 20.55%
Number/percentage of N's	14,753 / 0%

GC Percentage	40.45%
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2.3. Coverage

Mean	0.3922
Standard Deviation	5.2885

2.4. Mapping Quality

Mean Mapping Quality	52.78
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2.5. Insert size

Mean	832,273.06
Standard Deviation	8,654,244.71
P25/Median/P75	146 / 204 / 290

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	12,404,337
Insertions	123,902
Mapped reads with at least one insertion	1.17%
Deletions	250,362
Mapped reads with at least one deletion	2.38%
Homopolymer indels	43.82%

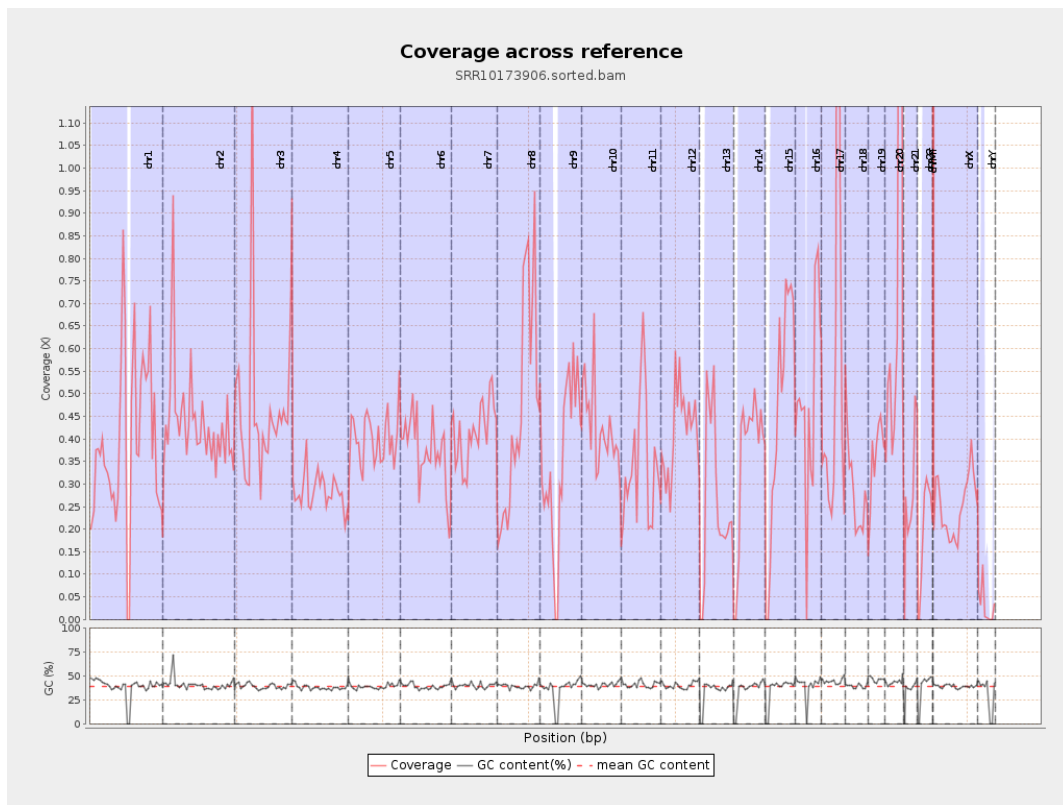
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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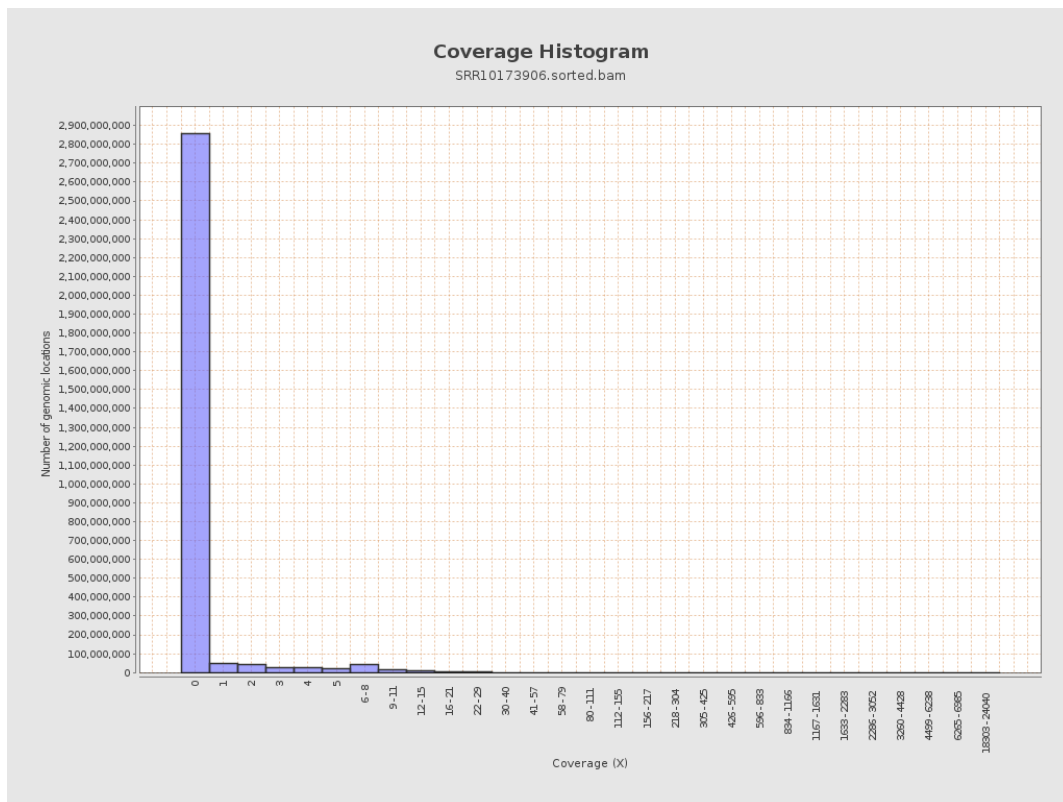
		bases	coverage	deviation
chr1	249250621	97094844	0.3895	3.3621
chr2	243199373	105767751	0.4349	16.8188
chr3	198022430	91571024	0.4624	2.033
chr4	191154276	54357733	0.2844	1.967
chr5	180915260	72505706	0.4008	1.8256
chr6	171115067	63875589	0.3733	2.1765
chr7	159138663	66165241	0.4158	2.8488
chr8	146364022	68330678	0.4669	2.9376
chr9	141213431	49352482	0.3495	2.2309
chr10	135534747	57577256	0.4248	4.0046
chr11	135006516	46223604	0.3424	1.7567
chr12	133851895	56329591	0.4208	1.9042
chr13	115169878	29882228	0.2595	1.472
chr14	107349540	38985177	0.3632	1.7664
chr15	102531392	46275690	0.4513	1.9685
chr16	90354753	42862847	0.4744	2.6549
chr17	81195210	55835272	0.6877	2.952
chr18	78077248	22428462	0.2873	3.2728
chr19	59128983	21390158	0.3618	2.4506
chr20	63025520	59956801	0.9513	3.4952
chr21	48129895	13491341	0.2803	1.6832
chr22	51304566	10162189	0.1981	1.2307
chrMT	16571	2728602	164.6613	127.0422
chrX	155270560	39001410	0.2512	1.4428

chrY	59373566	1831146	0.0308	1.1209
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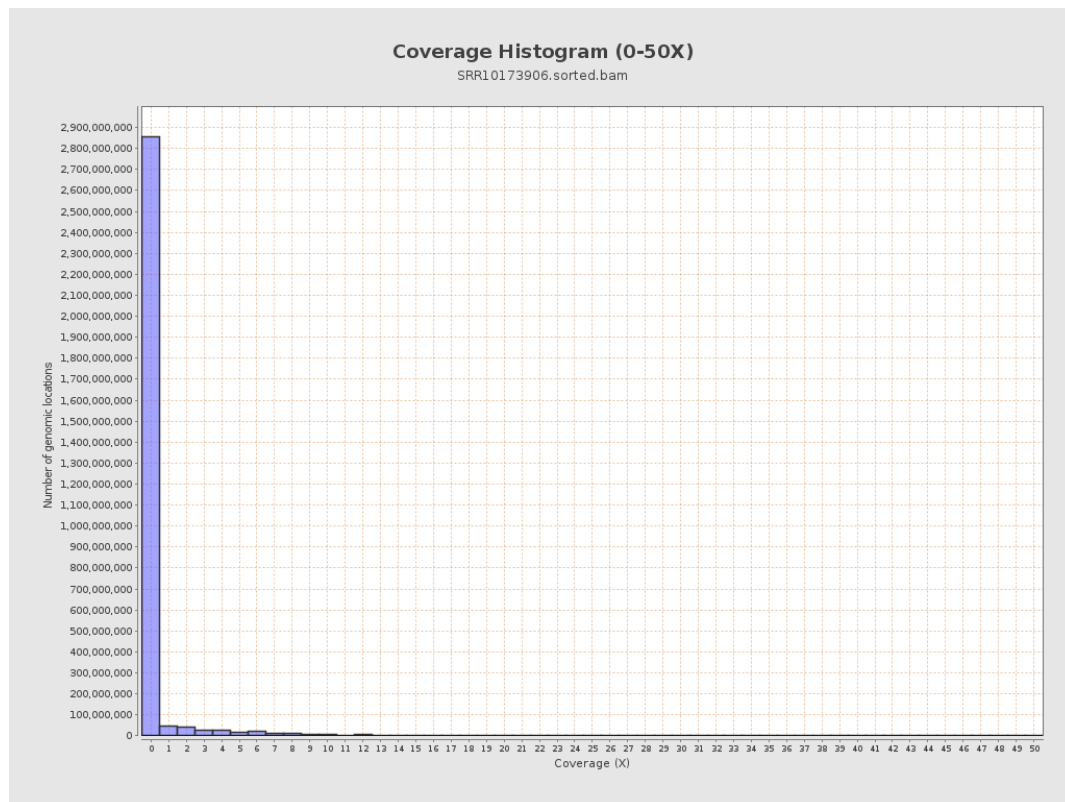
3. Results : Coverage across reference



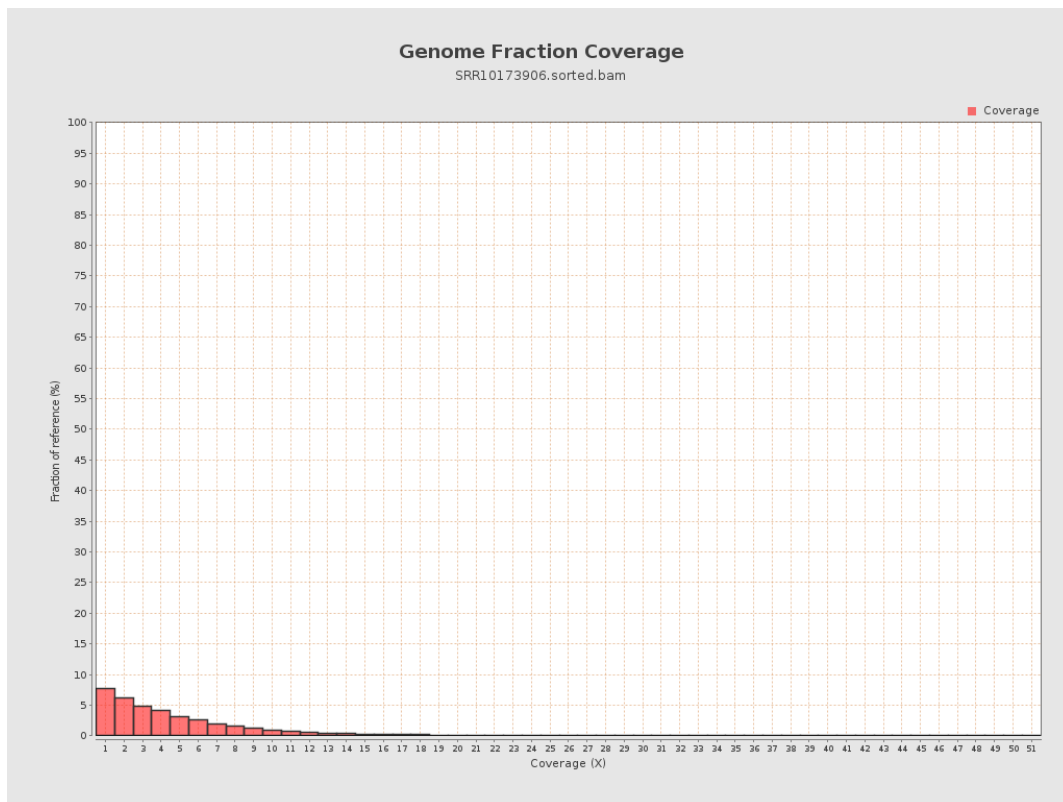
4. Results : Coverage Histogram



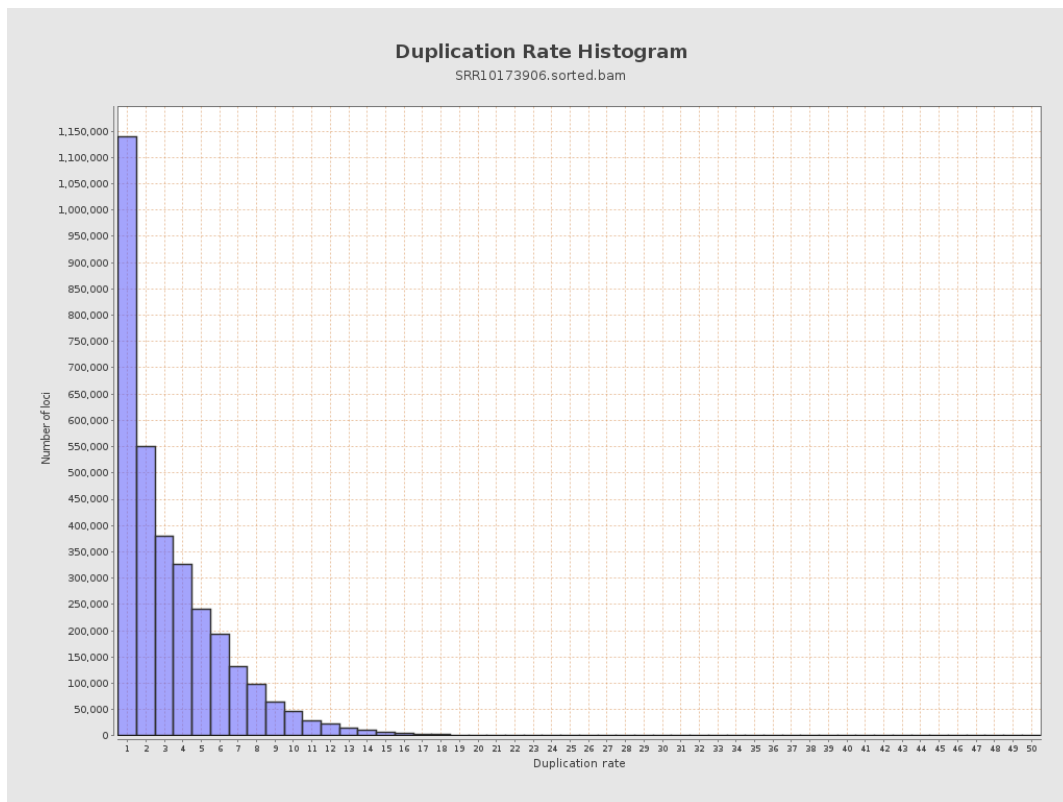
5. Results : Coverage Histogram (0-50X)



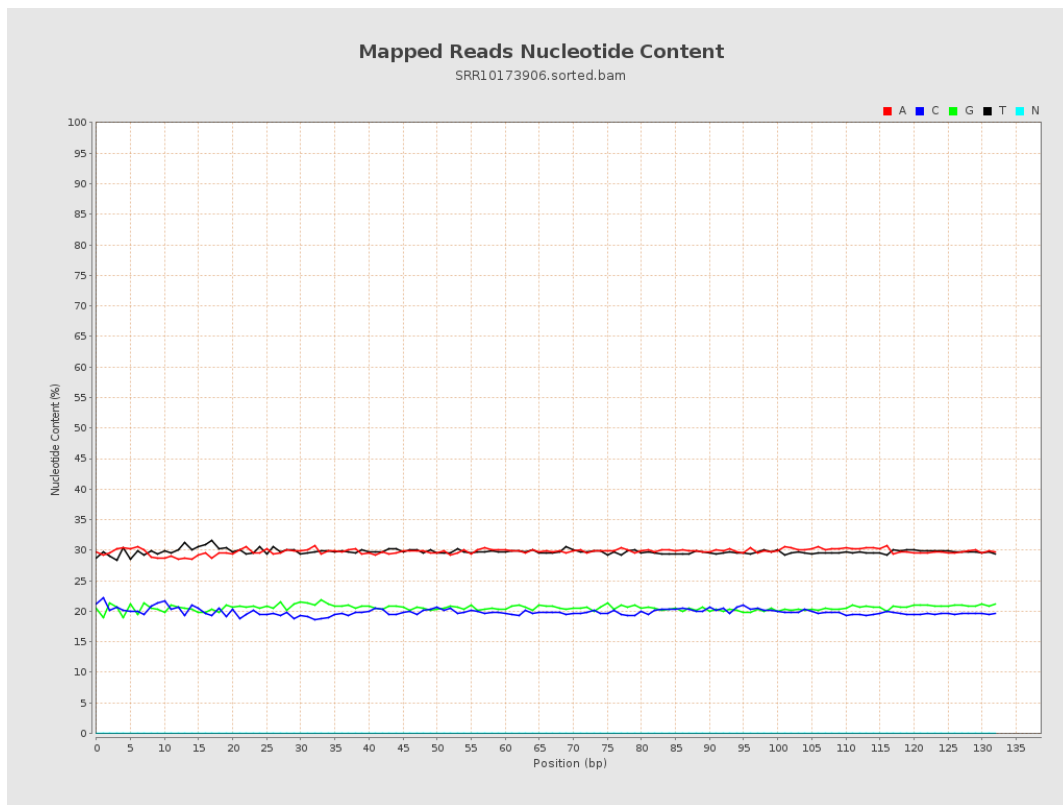
6. Results : Genome Fraction Coverage



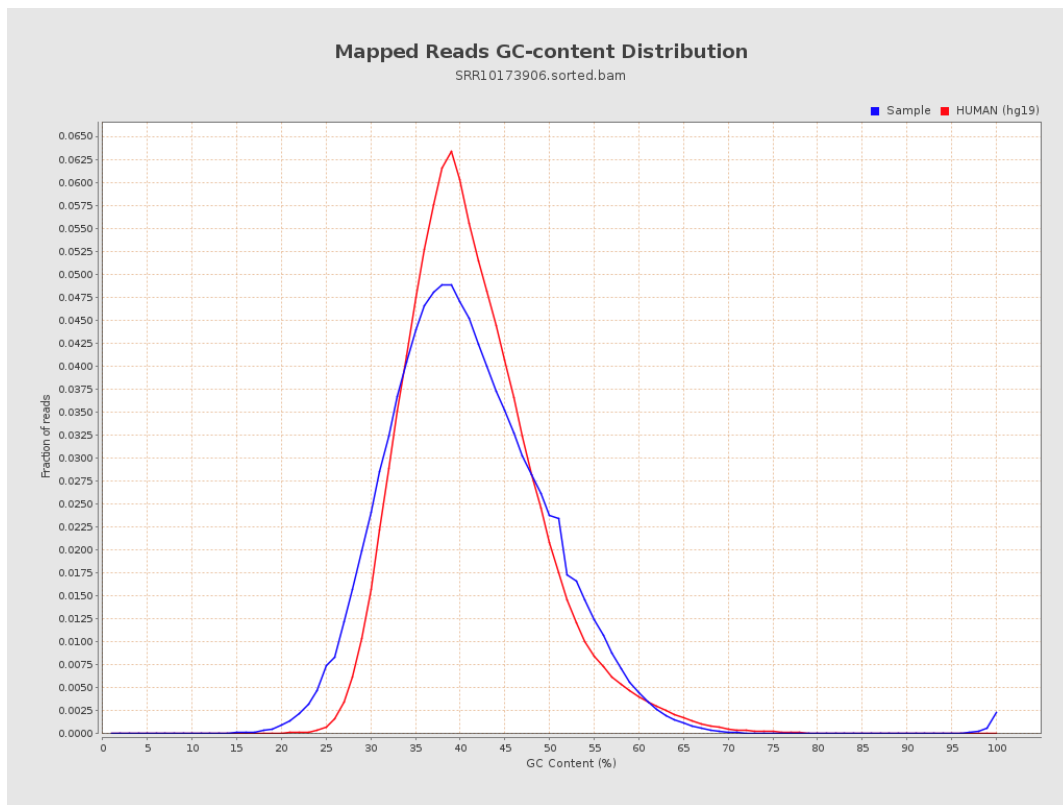
7. Results : Duplication Rate Histogram



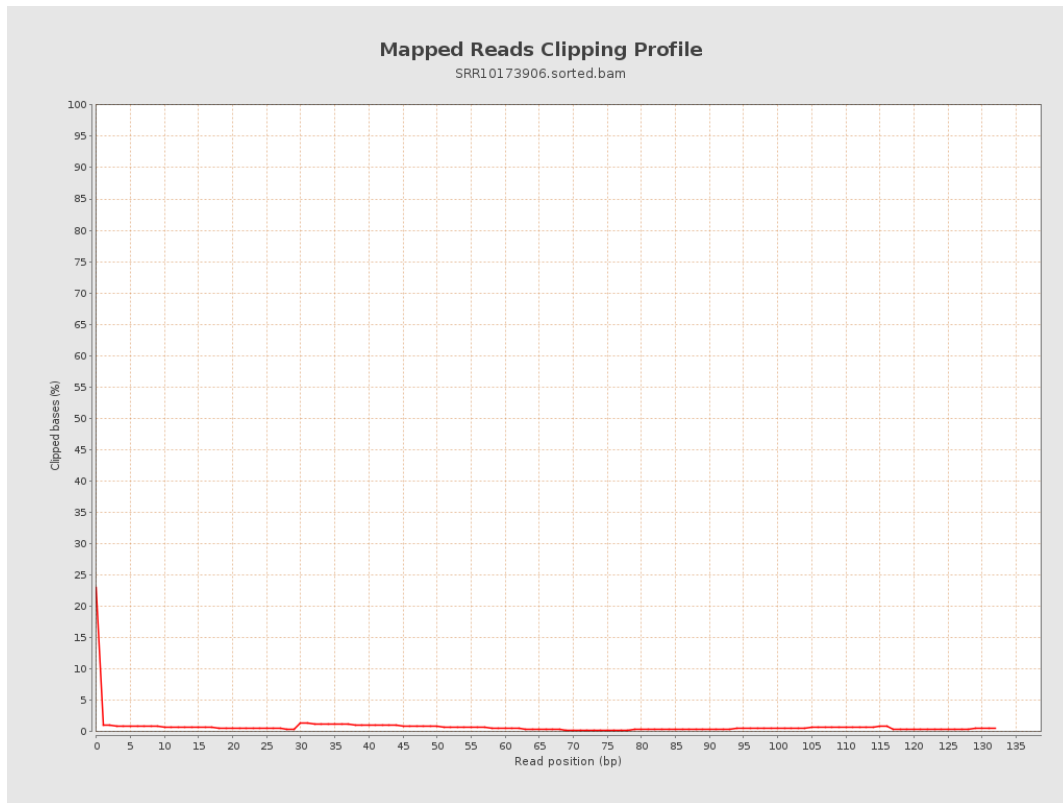
8. Results : Mapped Reads Nucleotide Content



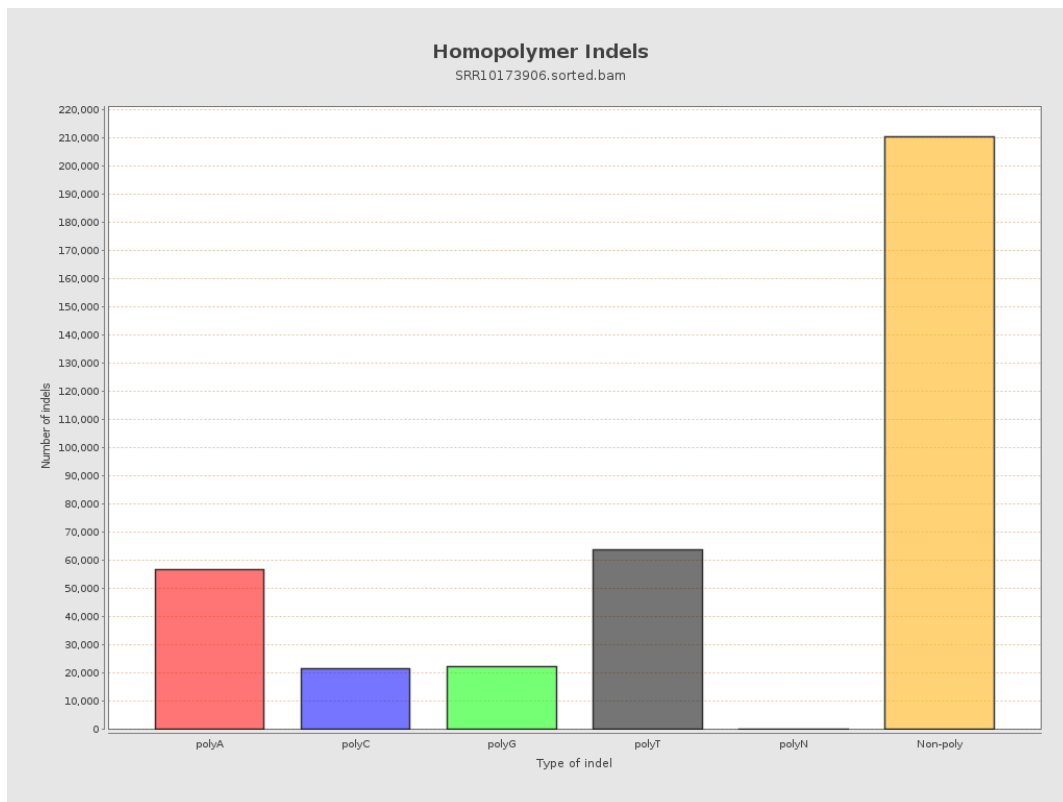
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



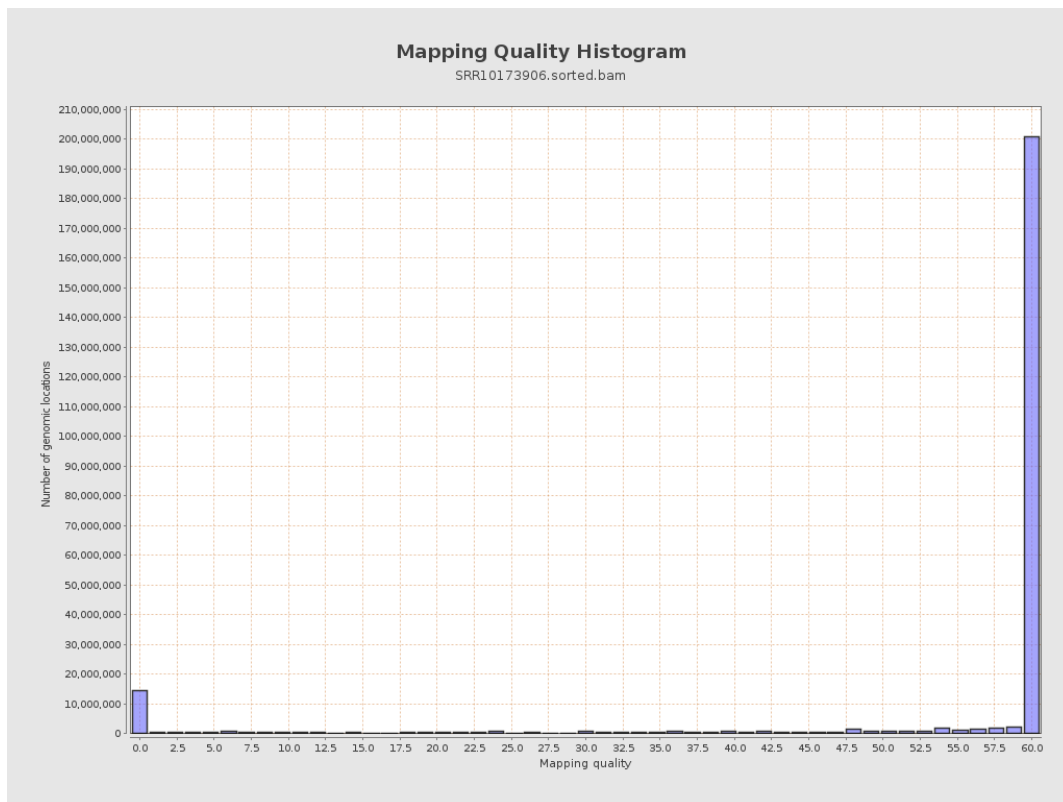
11. Results : Homopolymer Indels



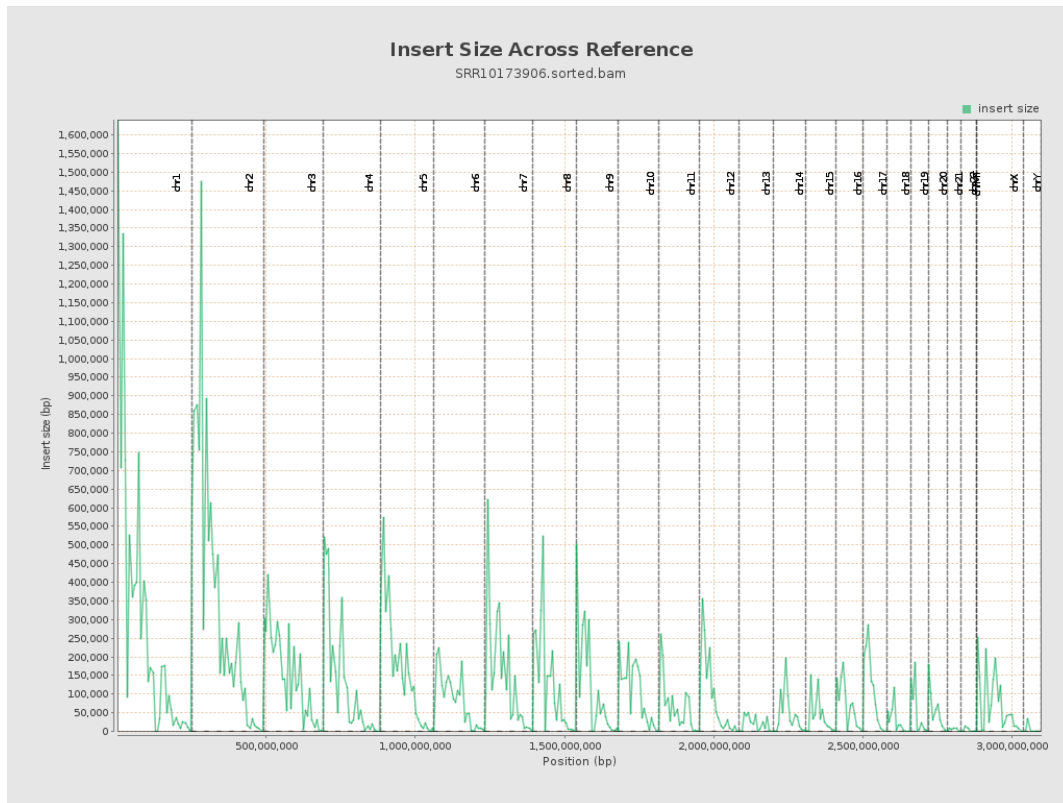
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

