

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:37:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174025.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_SRR10174025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174025_1.fastq.gz SRR10174025_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:37:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,581,030
Mapped reads	5,452,178 / 97.69%
Unmapped reads	128,852 / 2.31%
Mapped paired reads	5,452,178 / 97.69%
Mapped reads, first in pair	2,728,517 / 48.89%
Mapped reads, second in pair	2,723,661 / 48.8%
Mapped reads, both in pair	5,363,386 / 96.1%
Mapped reads, singletons	88,792 / 1.59%
Secondary alignments	0
Supplementary alignments	558,540 / 10.01%
Read min/max/mean length	30 / 133 / 128.29
Duplicated reads (estimated)	4,256,501 / 76.27%
Duplication rate	65.33%
Clipped reads	2,227,896 / 39.92%

2.2. ACGT Content

Number/percentage of A's	194,701,568 / 30.17%
Number/percentage of C's	125,906,648 / 19.51%
Number/percentage of T's	194,331,085 / 30.12%
Number/percentage of G's	130,344,503 / 20.2%
Number/percentage of N's	7,561 / 0%

GC Percentage	39.71%
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2.3. Coverage

Mean	0.2086
Standard Deviation	2.9685

2.4. Mapping Quality

Mean Mapping Quality	52.77
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2.5. Insert size

Mean	1,097,333.5
Standard Deviation	9,341,335.22
P25/Median/P75	145 / 202 / 291

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	6,450,044
Insertions	68,341
Mapped reads with at least one insertion	1.21%
Deletions	160,143
Mapped reads with at least one deletion	2.87%
Homopolymer indels	42.39%

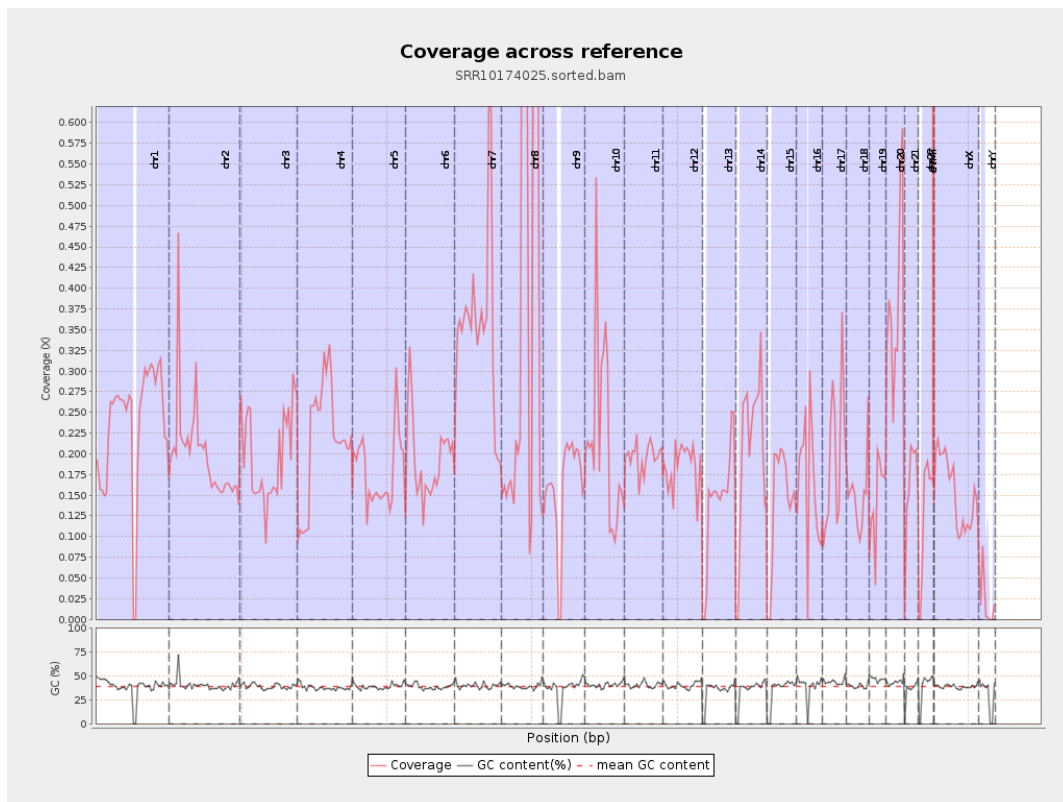
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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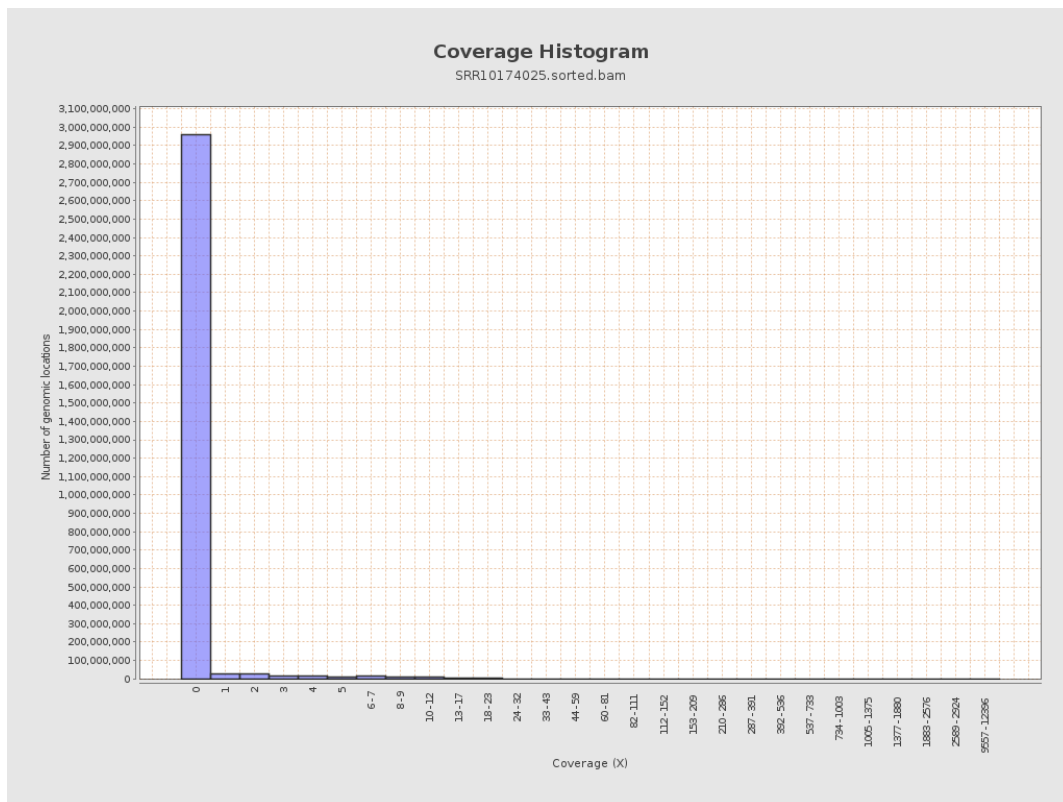
		bases	coverage	deviation
chr1	249250621	58563880	0.235	1.697
chr2	243199373	48597763	0.1998	8.6933
chr3	198022430	39159672	0.1978	1.2886
chr4	191154276	41315109	0.2161	1.7601
chr5	180915260	32422280	0.1792	1.2133
chr6	171115067	32752604	0.1914	1.3199
chr7	159138663	57132178	0.359	3.2114
chr8	146364022	63655355	0.4349	2.255
chr9	141213431	22527635	0.1595	1.4185
chr10	135534747	29742768	0.2194	3.5303
chr11	135006516	26477497	0.1961	1.2976
chr12	133851895	24846345	0.1856	1.242
chr13	115169878	16519345	0.1434	1.0955
chr14	107349540	21995711	0.2049	1.3079
chr15	102531392	14549465	0.1419	1.0681
chr16	90354753	14684392	0.1625	1.5417
chr17	81195210	16097766	0.1983	1.3646
chr18	78077248	11601187	0.1486	1.793
chr19	59128983	8615377	0.1457	1.3747
chr20	63025520	24066134	0.3818	1.7966
chr21	48129895	7701431	0.16	1.252
chr22	51304566	6342800	0.1236	0.9623
chrMT	16571	1219993	73.6222	54.4209
chrX	155270560	23862939	0.1537	1.1339

chrY	59373566	1239156	0.0209	0.9539
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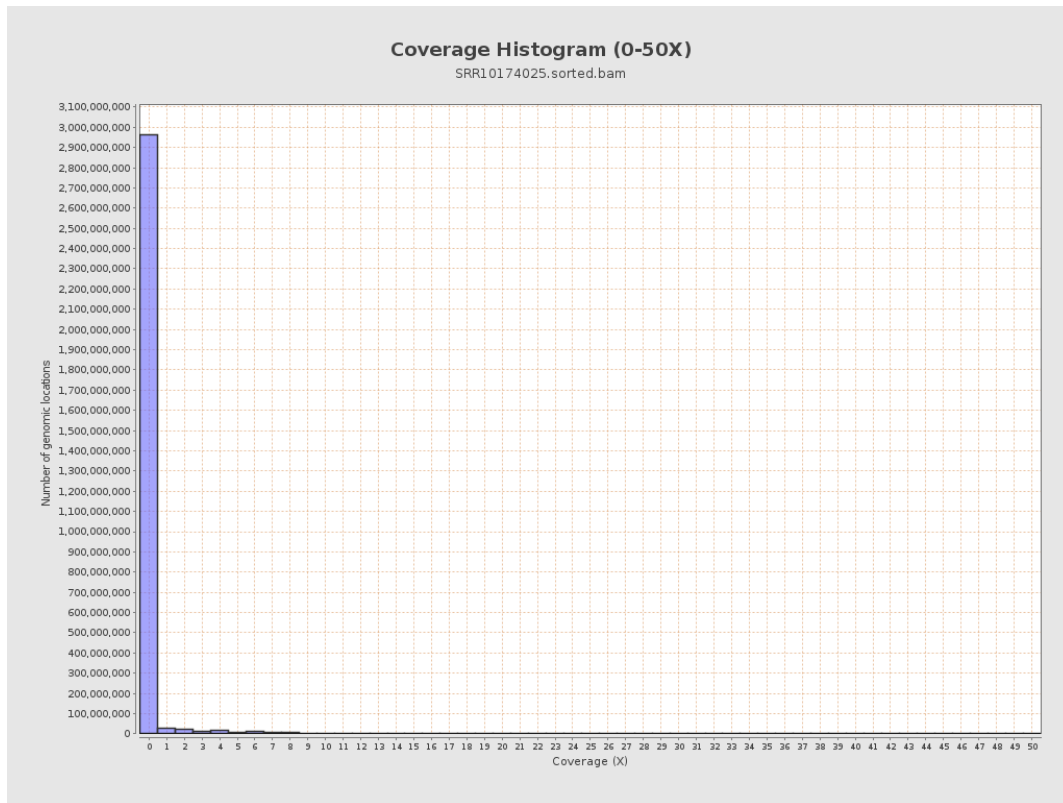
3. Results : Coverage across reference



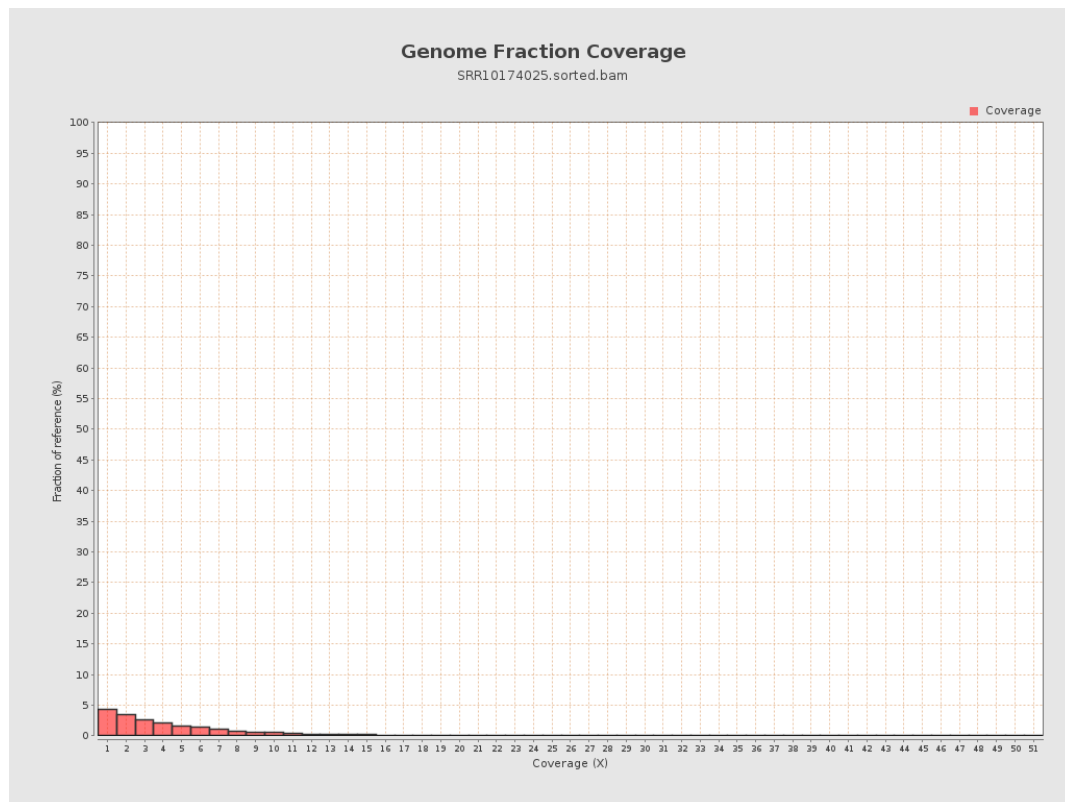
4. Results : Coverage Histogram



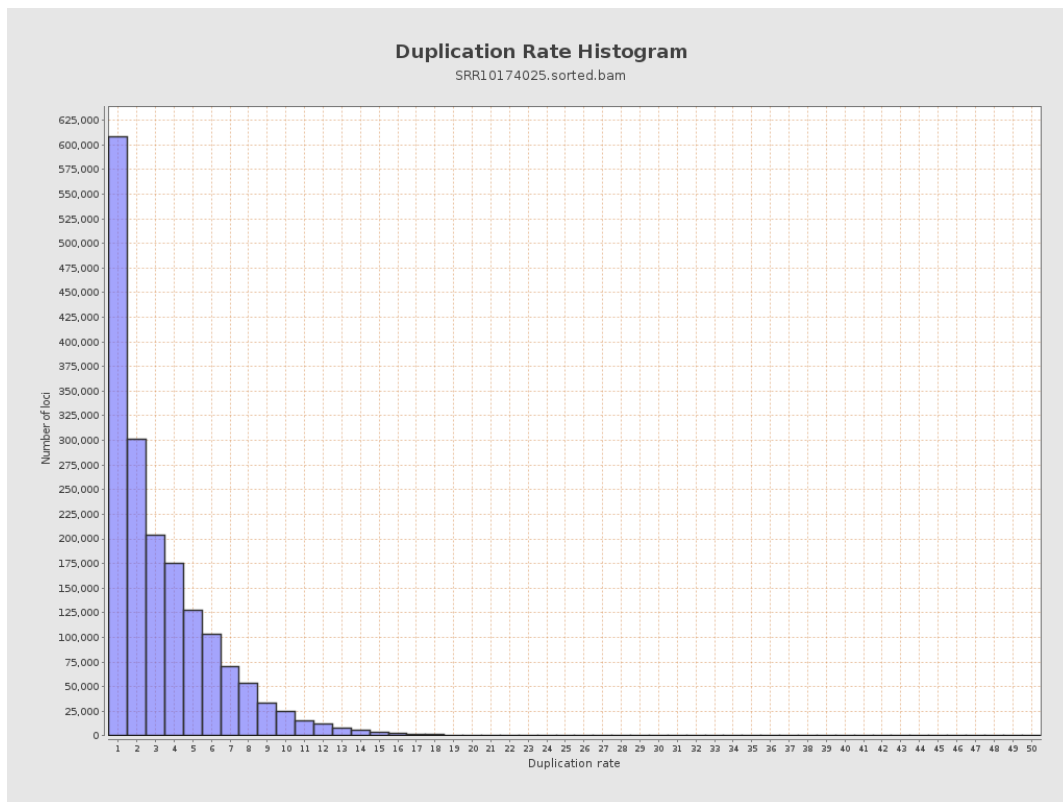
5. Results : Coverage Histogram (0-50X)



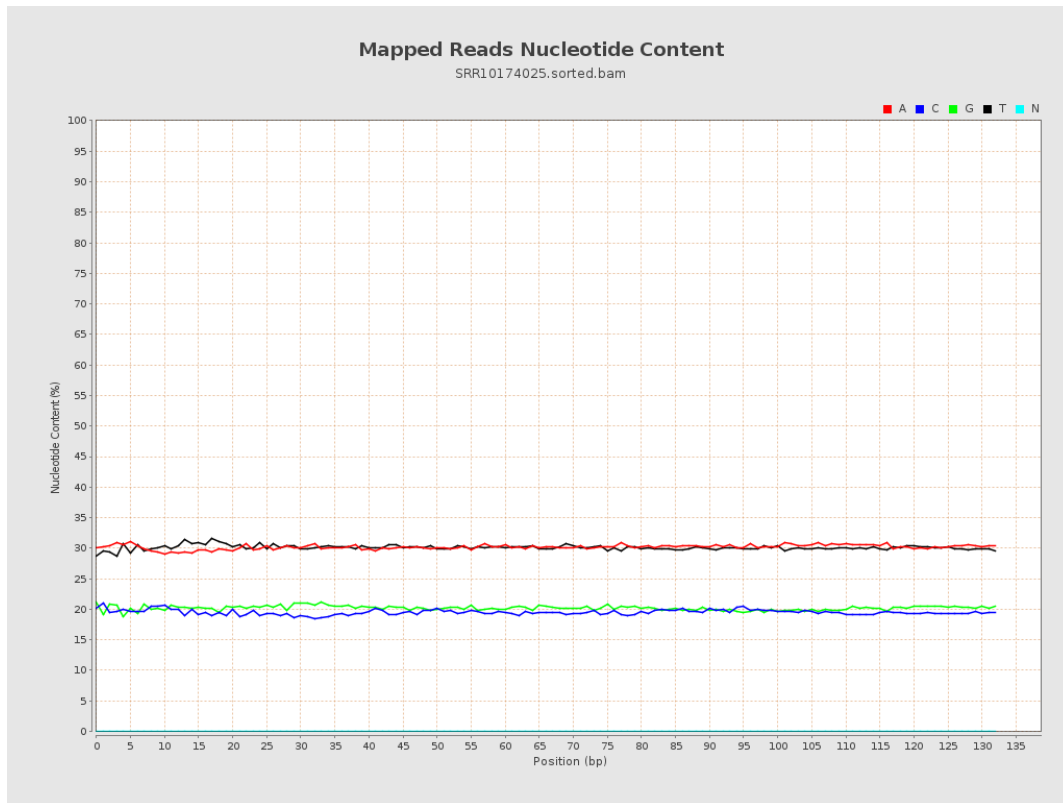
6. Results : Genome Fraction Coverage



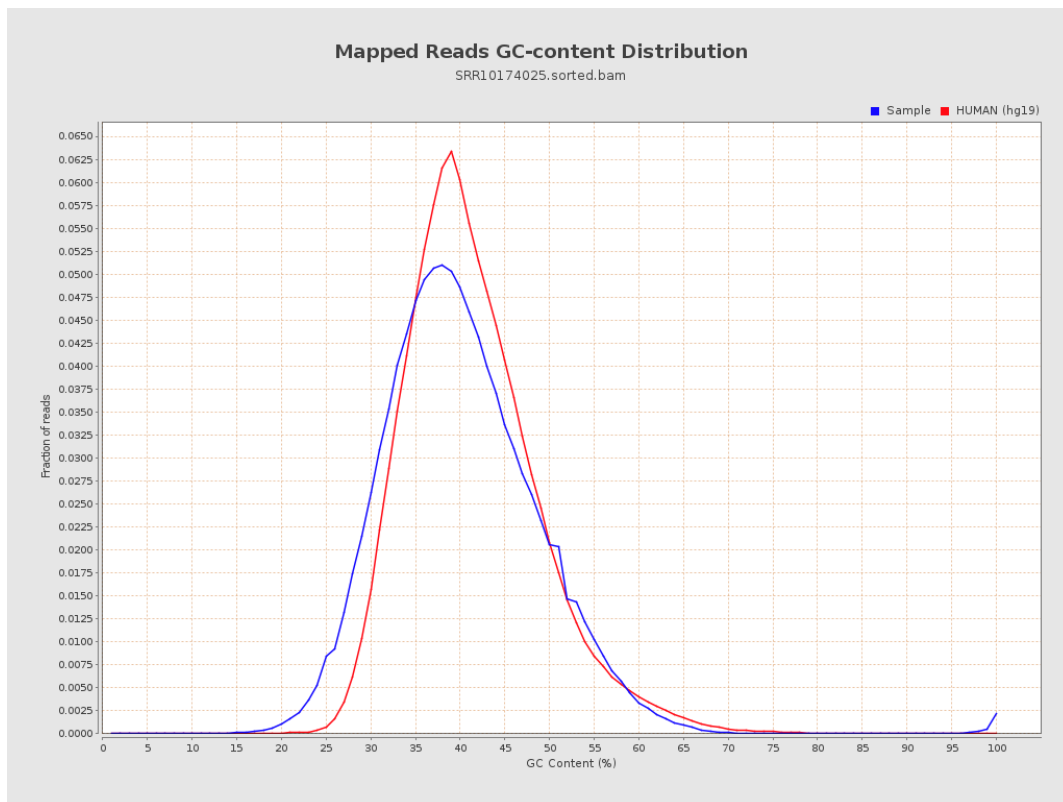
7. Results : Duplication Rate Histogram



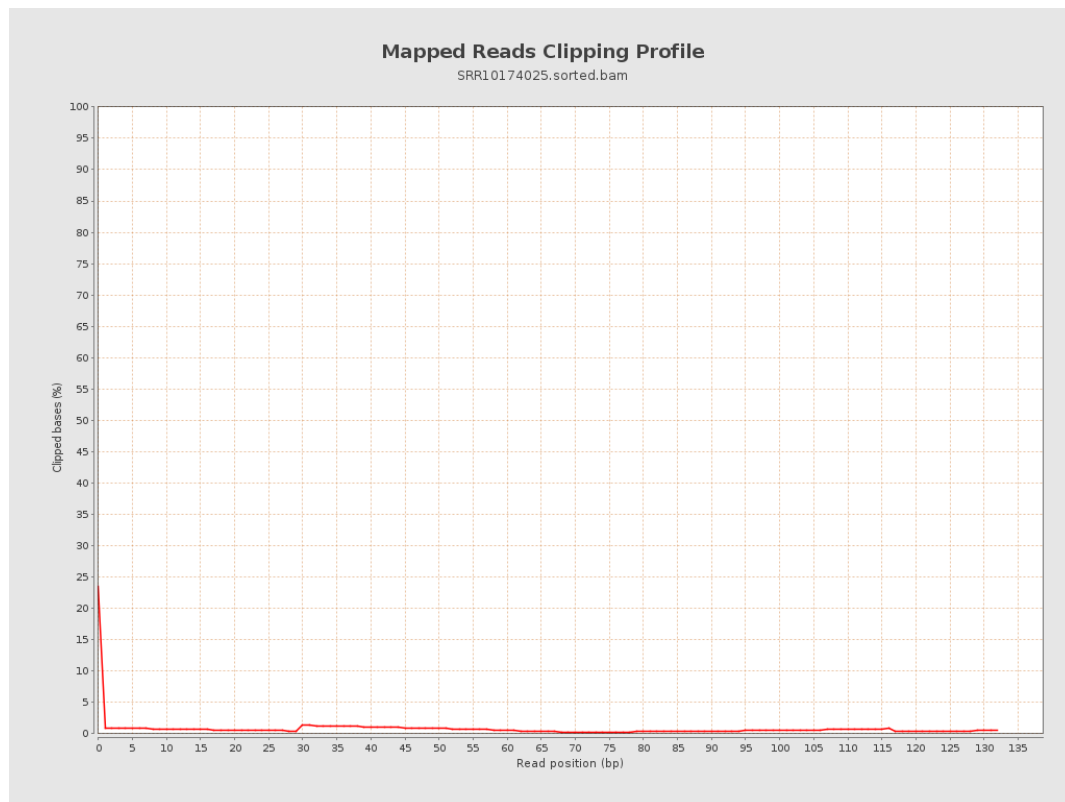
8. Results : Mapped Reads Nucleotide Content



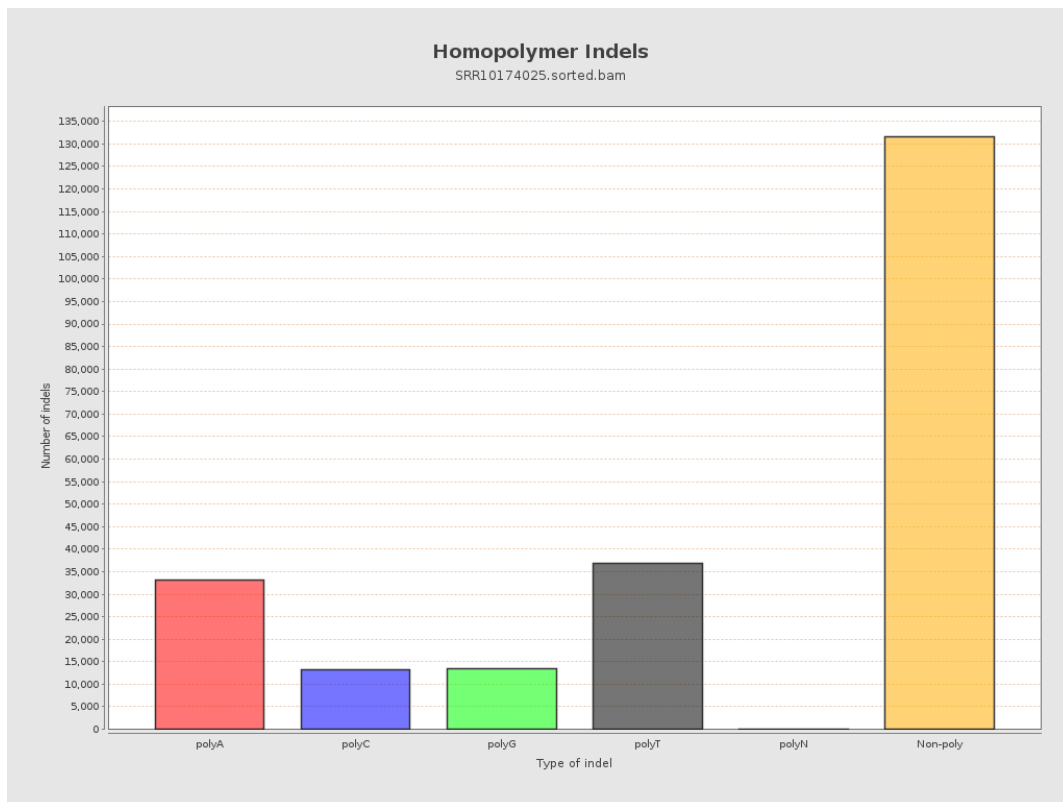
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



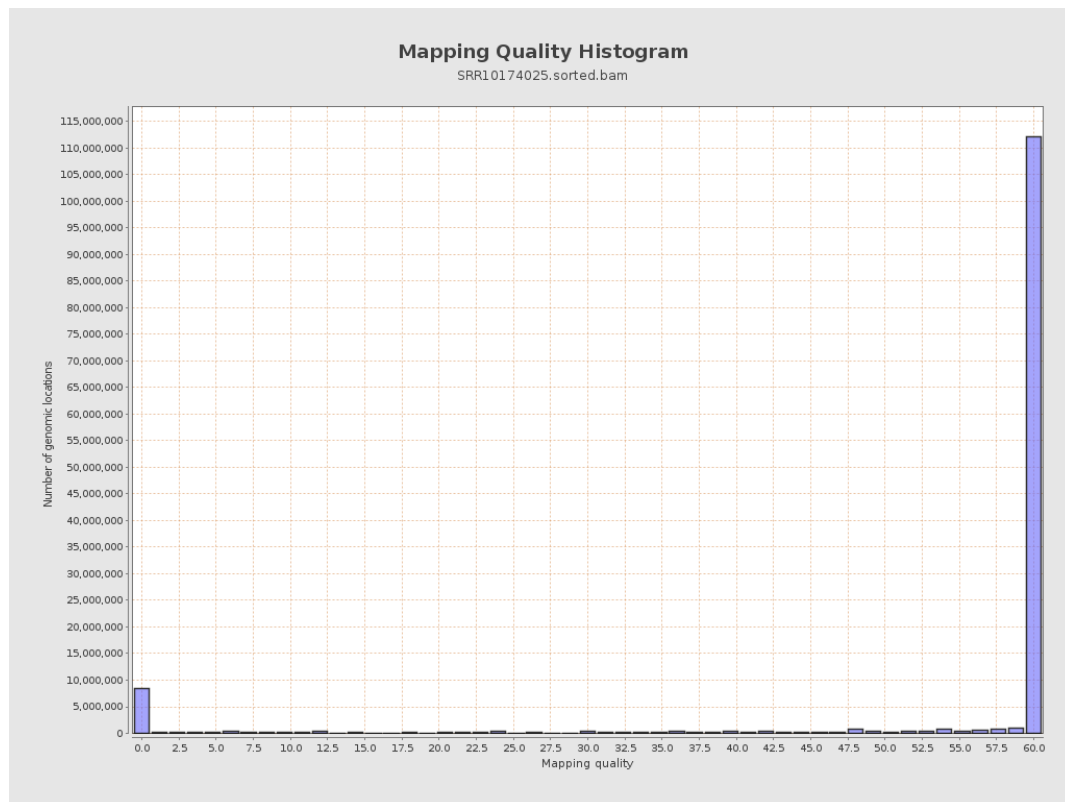
11. Results : Homopolymer Indels



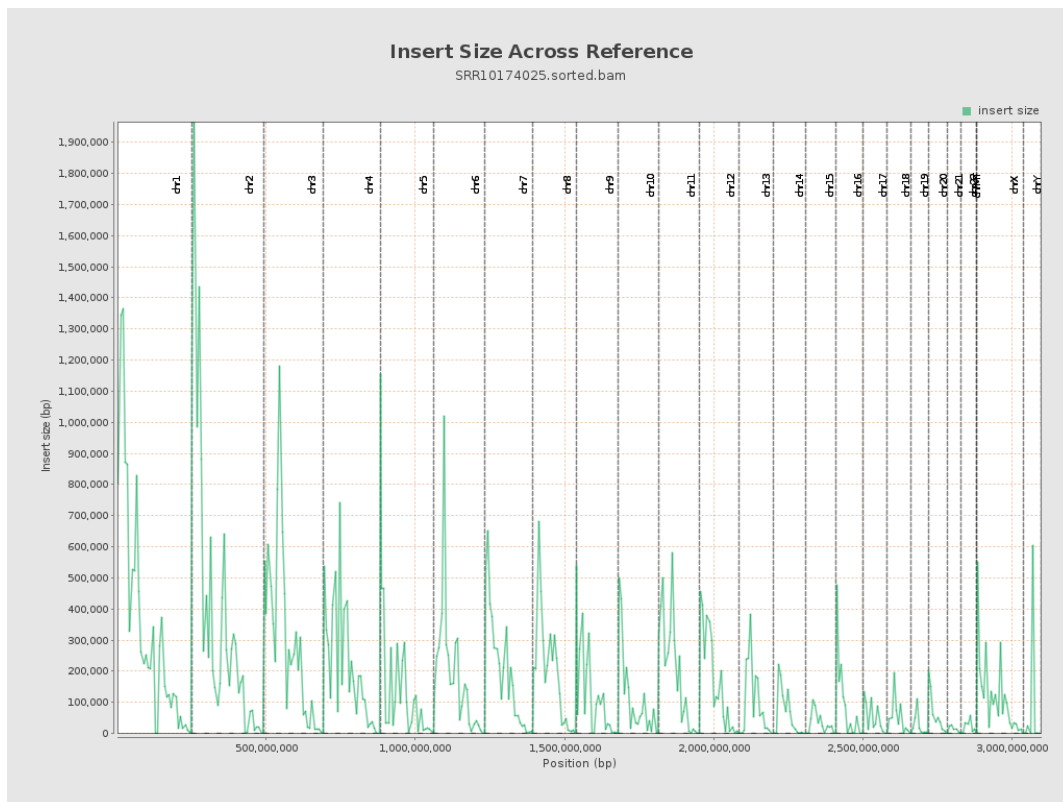
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

