

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/30 11:37:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365376.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_SRR5365376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365376_1.fastq.gz SRR5365376_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 30 11:37:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	686,238,352
Mapped reads	648,640,082 / 94.52%
Unmapped reads	37,598,270 / 5.48%
Mapped paired reads	648,640,082 / 94.52%
Mapped reads, first in pair	323,892,522 / 47.2%
Mapped reads, second in pair	324,747,560 / 47.32%
Mapped reads, both in pair	646,092,110 / 94.15%
Mapped reads, singletons	2,547,972 / 0.37%
Secondary alignments	0
Supplementary alignments	3,161,957 / 0.46%
Read min/max/mean length	30 / 125 / 125.19
Duplicated reads (estimated)	372,504,677 / 54.28%
Duplication rate	33.04%
Clipped reads	430,927,295 / 62.8%

2.2. ACGT Content

Number/percentage of A's	19,830,061,427 / 29.68%
Number/percentage of C's	13,414,613,577 / 20.08%
Number/percentage of T's	19,231,213,695 / 28.79%
Number/percentage of G's	14,296,096,535 / 21.4%
Number/percentage of N's	34,366,832 / 0.05%

GC Percentage	41.48%
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2.3. Coverage

Mean	21.5872
Standard Deviation	273.3837

2.4. Mapping Quality

Mean Mapping Quality	53.64
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2.5. Insert size

Mean	79,050.32
Standard Deviation	2,733,033.1
P25/Median/P75	105 / 144 / 199

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	331,111,736
Insertions	18,010,530
Mapped reads with at least one insertion	2.71%
Deletions	10,000,543
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.97%

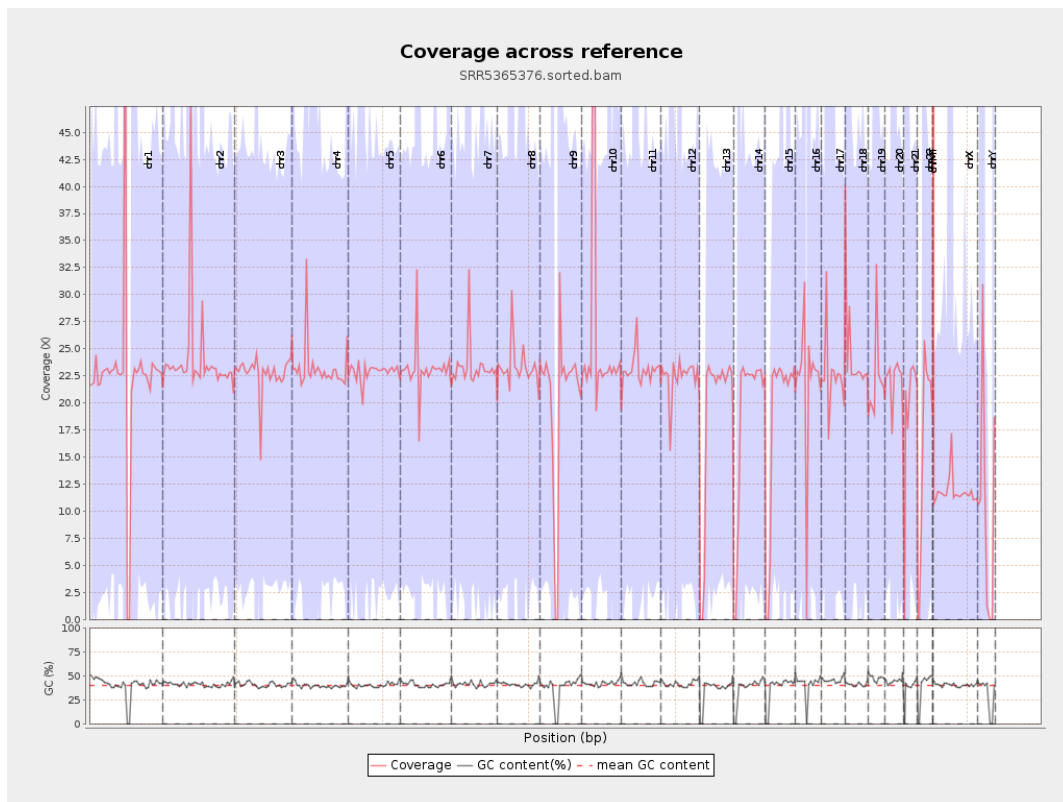
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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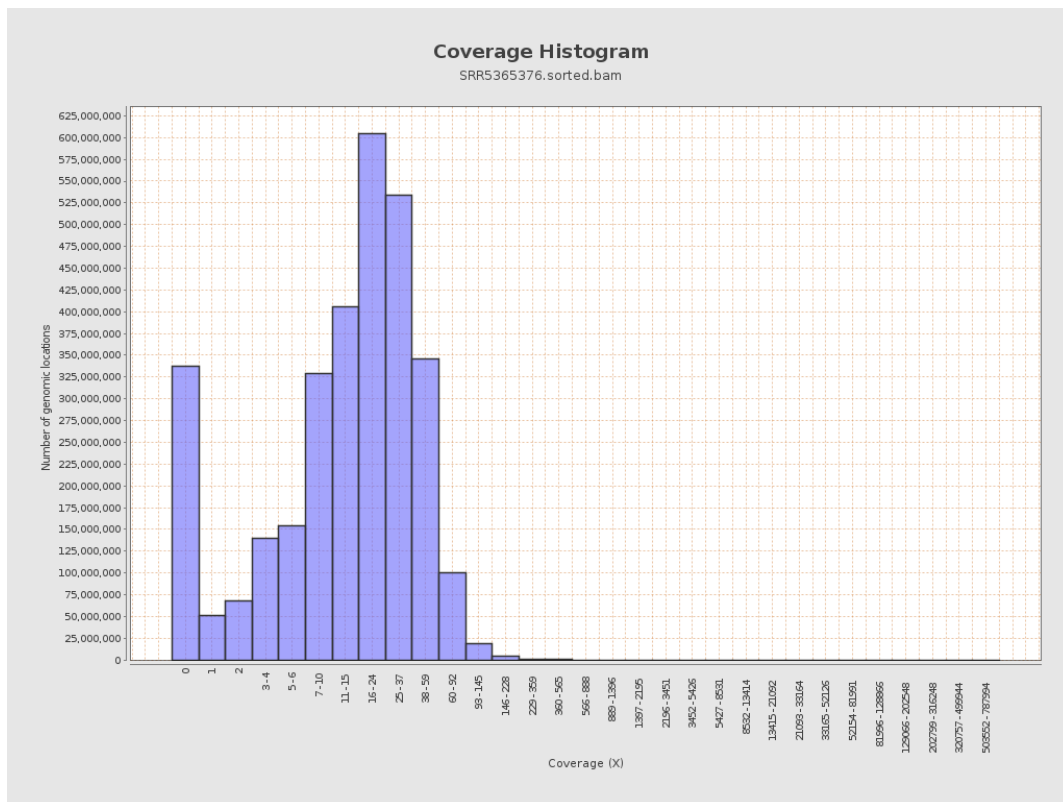
		bases	coverage	deviation
chr1	249250621	5602133921	22.4759	766.7641
chr2	243199373	5826371006	23.9572	166.2658
chr3	198022430	4505355474	22.7517	41.6521
chr4	191154276	4437491559	23.2142	97.528
chr5	180915260	4136189379	22.8626	27.8128
chr6	171115067	3961021718	23.1483	114.1214
chr7	159138663	3713423699	23.3345	205.1433
chr8	146364022	3408998414	23.2912	86.6572
chr9	141213431	2871847886	20.3369	239.0915
chr10	135534747	3521928327	25.9854	478.3441
chr11	135006516	3119056800	23.103	166.6783
chr12	133851895	3001431386	22.4235	58.4106
chr13	115169878	2172398480	18.8626	19.7049
chr14	107349540	2038907812	18.9932	28.8155
chr15	102531392	1852880755	18.0714	31.2463
chr16	90354753	1961621832	21.7102	77.2616
chr17	81195210	1838384401	22.6415	134.7396
chr18	78077248	1878402130	24.0583	298.2203
chr19	59128983	1316784241	22.2697	396.4467
chr20	63025520	1391512450	22.0786	38.7186
chr21	48129895	943754876	19.6085	78.295
chr22	51304566	821918305	16.0204	70.1353
chrMT	16571	37405129	2,257.2644	429.5013
chrX	155270560	1834718242	11.8163	70.0672

chrY	59373566	633397279	10.668	204.2245
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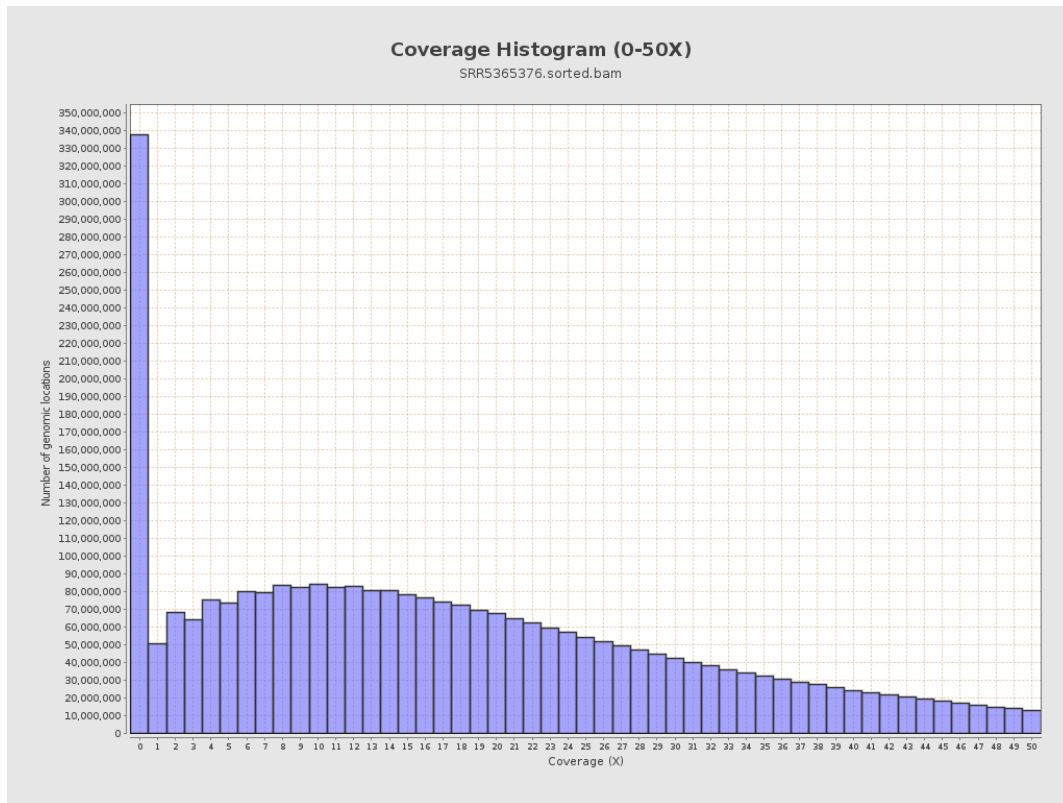
3. Results : Coverage across reference



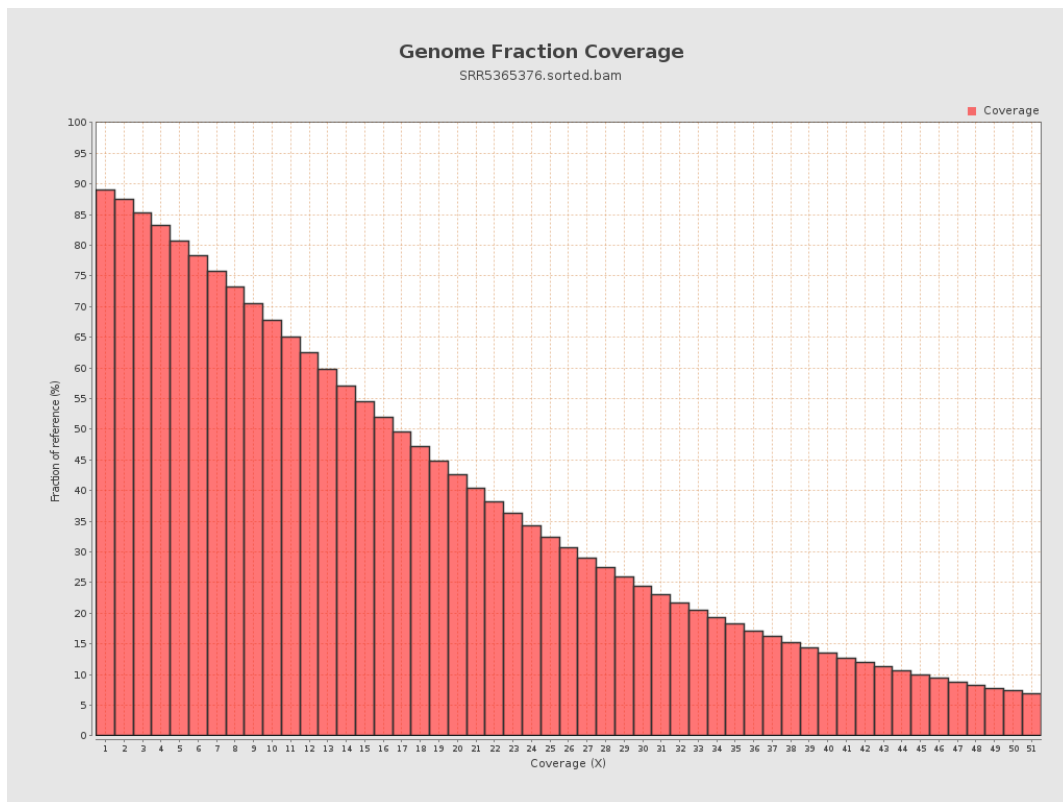
4. Results : Coverage Histogram



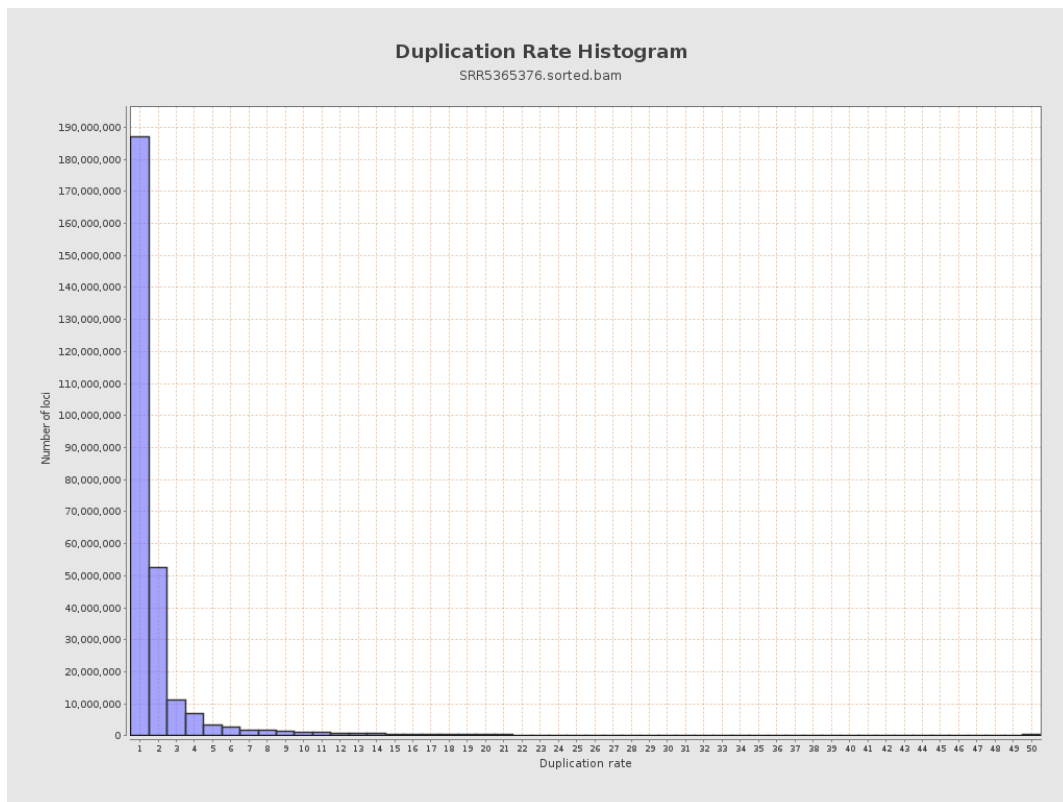
5. Results : Coverage Histogram (0-50X)



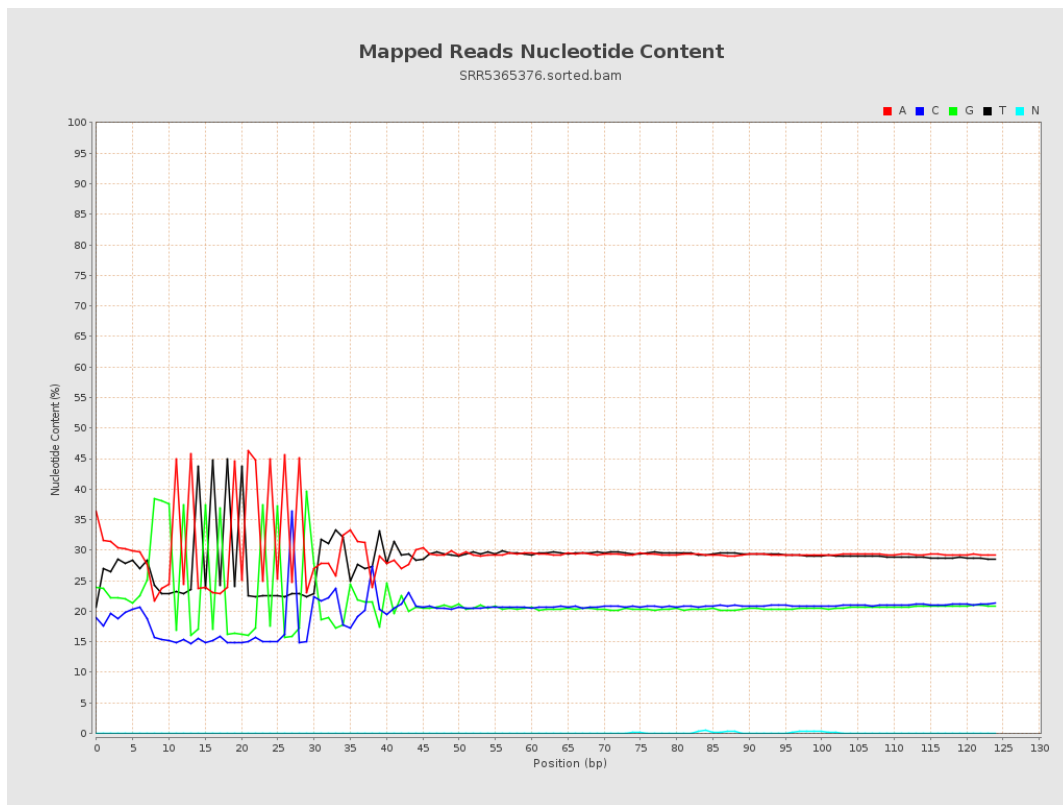
6. Results : Genome Fraction Coverage



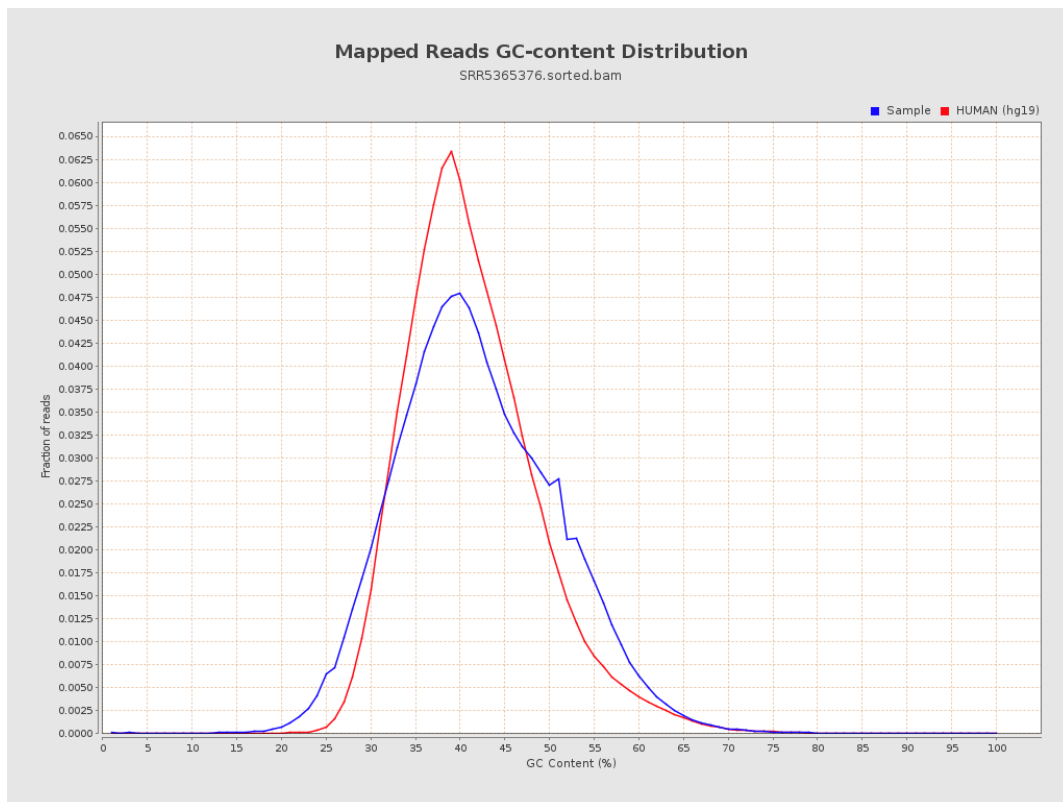
7. Results : Duplication Rate Histogram



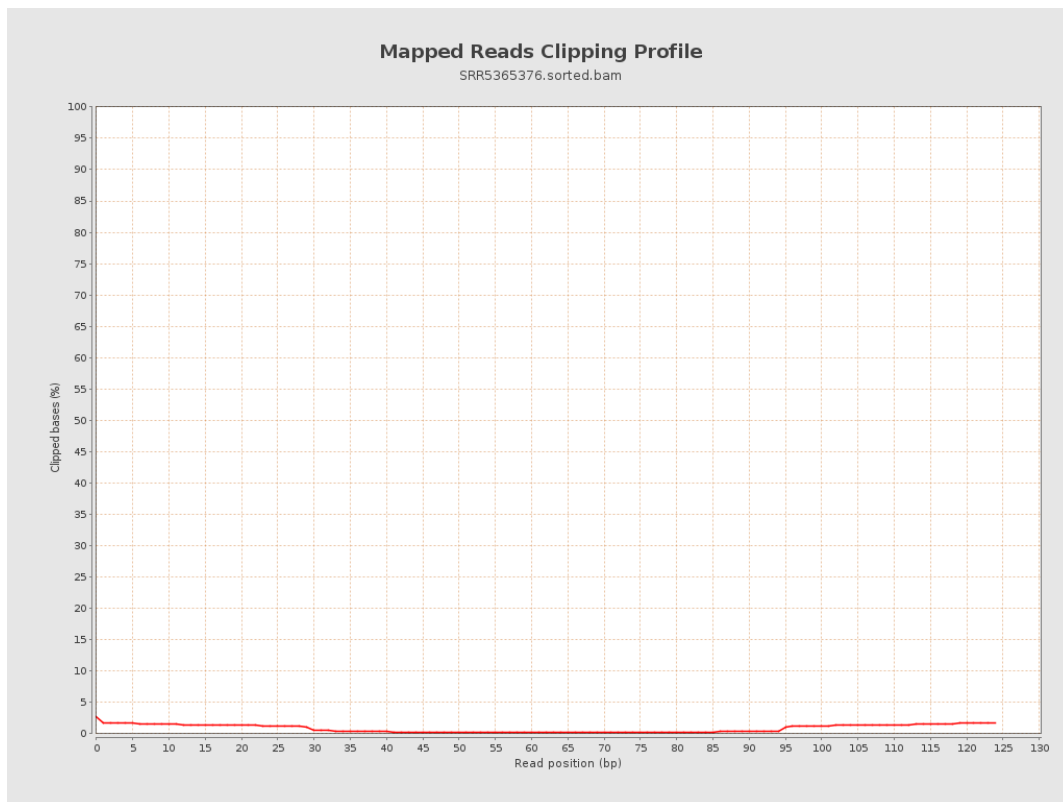
8. Results : Mapped Reads Nucleotide Content



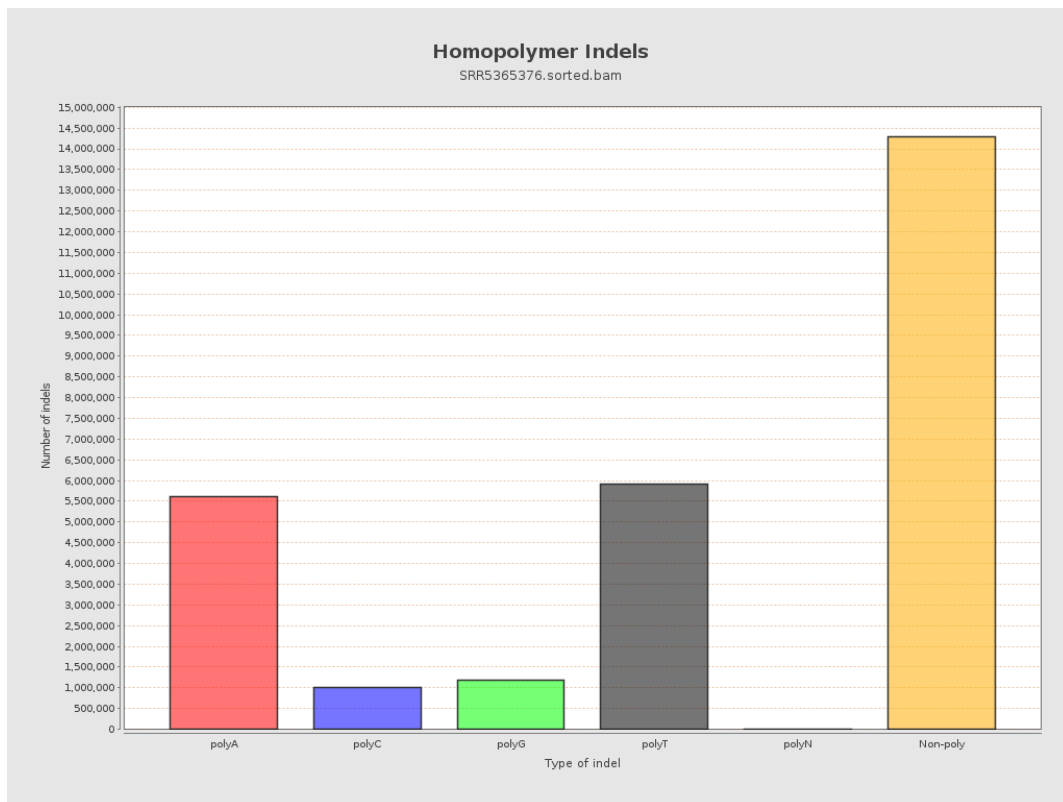
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



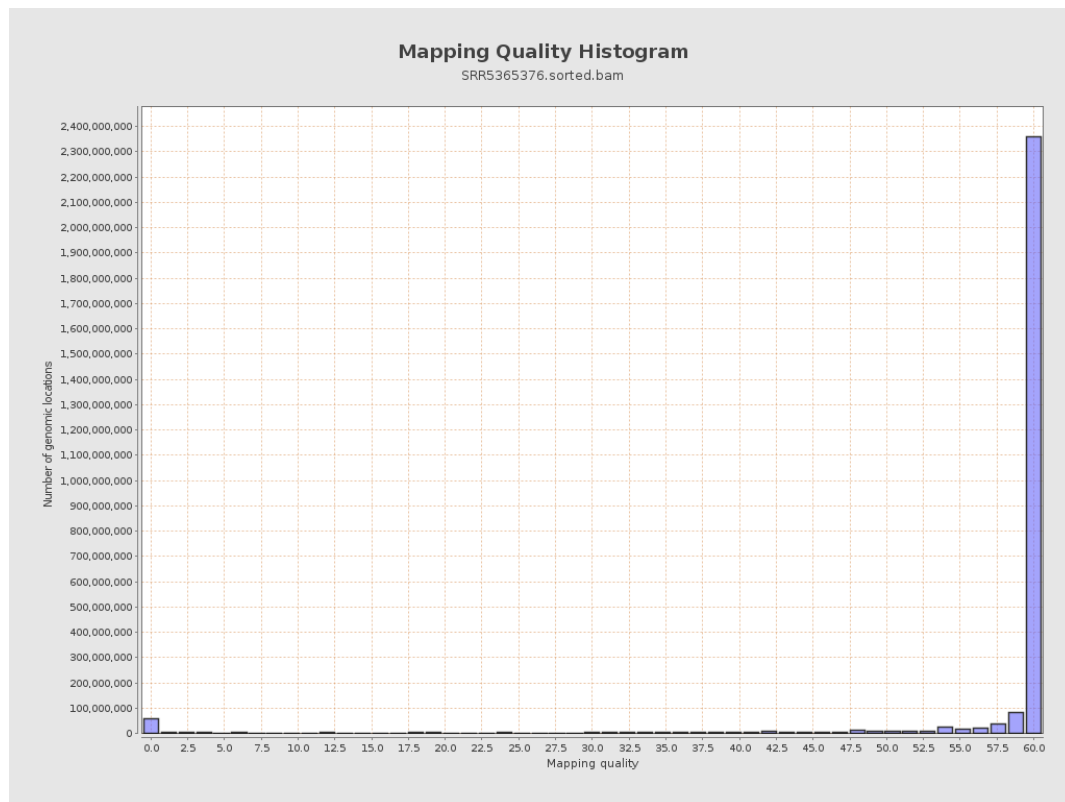
11. Results : Homopolymer Indels



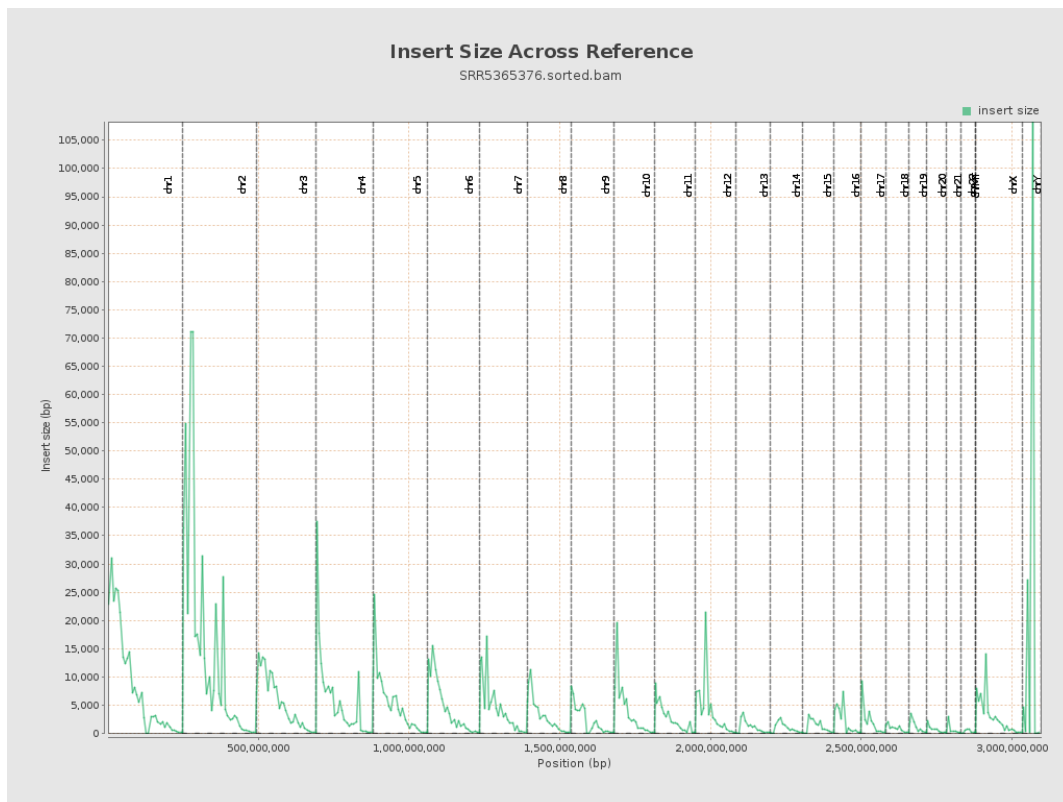
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

