

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/21 18:43:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365361.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_SRR5365361 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365361_1.fastq.gz SRR5365361_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 21 18:43:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365361.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	543,506,528
Mapped reads	484,600,078 / 89.16%
Unmapped reads	58,906,450 / 10.84%
Mapped paired reads	484,600,078 / 89.16%
Mapped reads, first in pair	242,079,239 / 44.54%
Mapped reads, second in pair	242,520,839 / 44.62%
Mapped reads, both in pair	475,216,138 / 87.44%
Mapped reads, singletons	9,383,940 / 1.73%
Secondary alignments	0
Supplementary alignments	12,282,365 / 2.26%
Read min/max/mean length	30 / 150 / 151.1
Duplicated reads (estimated)	287,117,375 / 52.83%
Duplication rate	46.31%
Clipped reads	357,827,832 / 65.84%

2.2. ACGT Content

Number/percentage of A's	15,711,642,042 / 25.83%
Number/percentage of C's	14,086,808,965 / 23.16%
Number/percentage of T's	15,817,576,450 / 26.01%
Number/percentage of G's	15,205,850,959 / 25%
Number/percentage of N's	2,285,107 / 0%

GC Percentage	48.16%
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2.3. Coverage

Mean	19.6581
Standard Deviation	150.3529

2.4. Mapping Quality

Mean Mapping Quality	52.91
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2.5. Insert size

Mean	116,567.37
Standard Deviation	3,423,485.63
P25/Median/P75	119 / 148 / 183

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	692,994,888
Insertions	7,458,986
Mapped reads with at least one insertion	1.45%
Deletions	16,926,072
Mapped reads with at least one deletion	3.38%
Homopolymer indels	40.3%

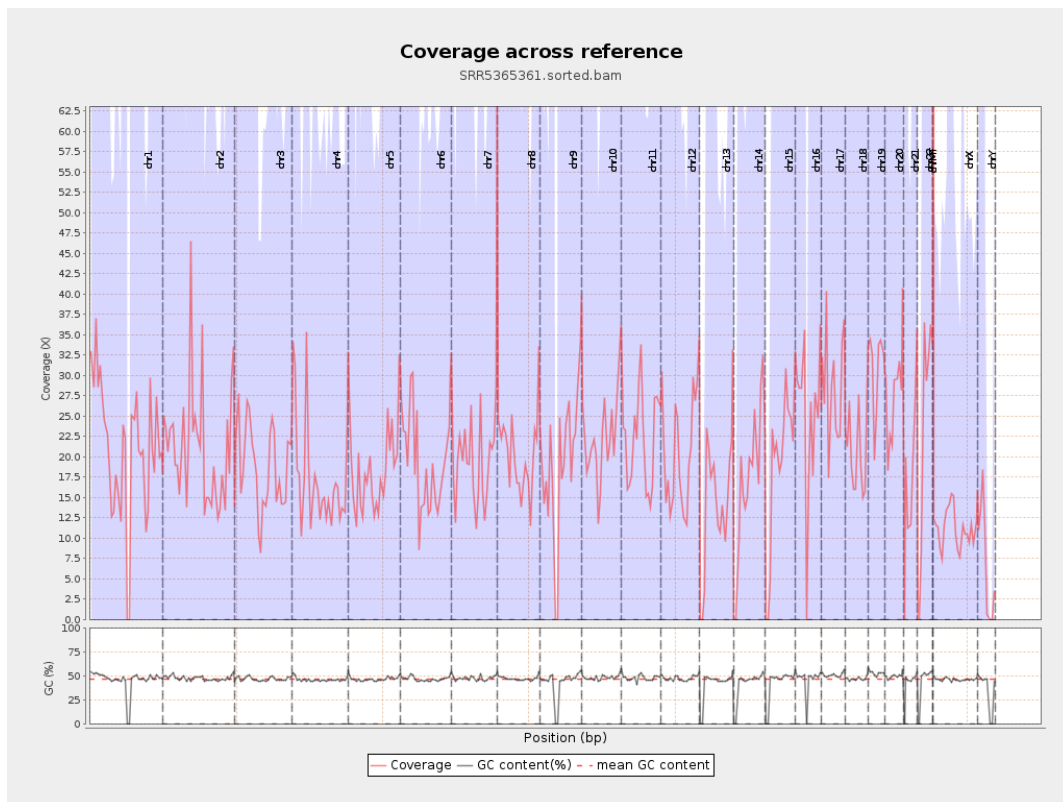
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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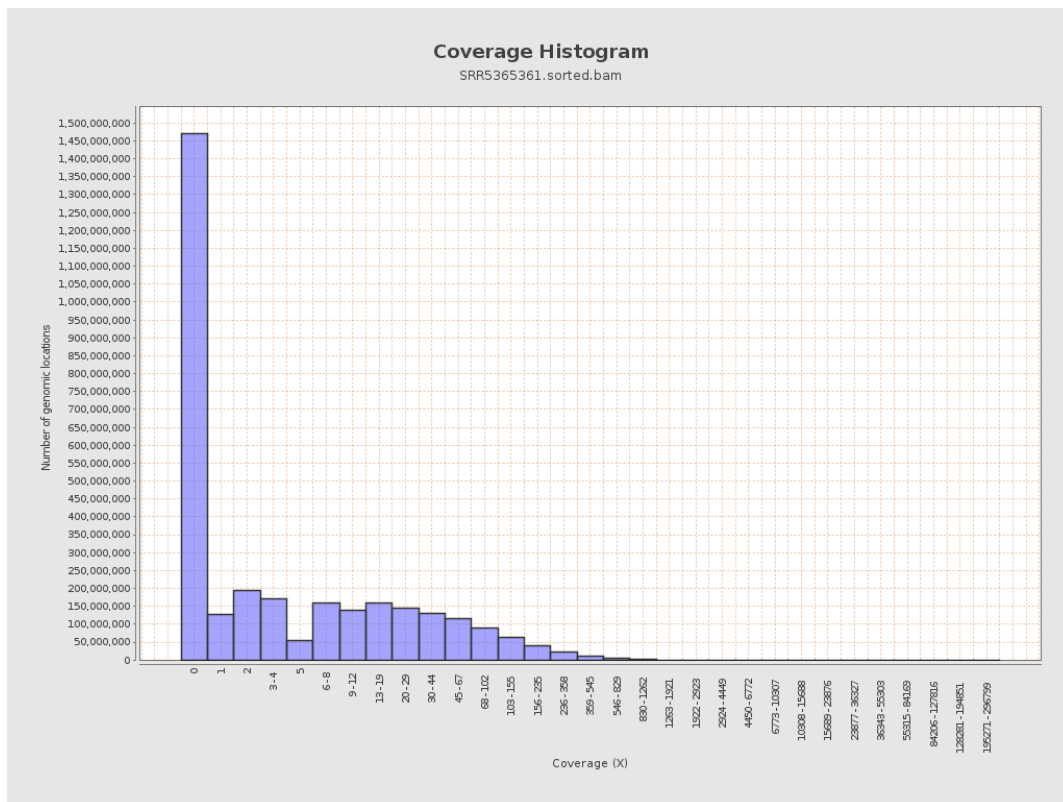
		bases	coverage	deviation
chr1	249250621	5208240926	20.8956	129.0647
chr2	243199373	5140077932	21.1352	264.8587
chr3	198022430	3713715476	18.754	57.7238
chr4	191154276	3302201517	17.2751	114.5021
chr5	180915260	3373502265	18.6469	62.8513
chr6	171115067	3274957121	19.1389	144.9193
chr7	159138663	3138487363	19.7217	113.0867
chr8	146364022	2960225017	20.2251	105.6655
chr9	141213431	2690474898	19.0525	196.3778
chr10	135534747	2997492677	22.116	82.0766
chr11	135006516	3012099106	22.3108	281.5501
chr12	133851895	2755490842	20.5861	61.3127
chr13	115169878	1626300676	14.1209	50.6393
chr14	107349540	1858469870	17.3123	64.5745
chr15	102531392	1898180255	18.5132	57.2706
chr16	90354753	2276836616	25.1989	121.0737
chr17	81195210	2308837566	28.4356	271.1417
chr18	78077248	1587636084	20.3342	294.6808
chr19	59128983	1805149841	30.529	101.0585
chr20	63025520	1701659358	26.9995	83.894
chr21	48129895	865065062	17.9735	176.1505
chr22	51304566	1172780234	22.8592	100.7035
chrMT	16571	20305733	1,225.3776	3,371.3819
chrX	155270560	1742004903	11.2192	70.1643

chrY	59373566	425204771	7.1615	117.5971
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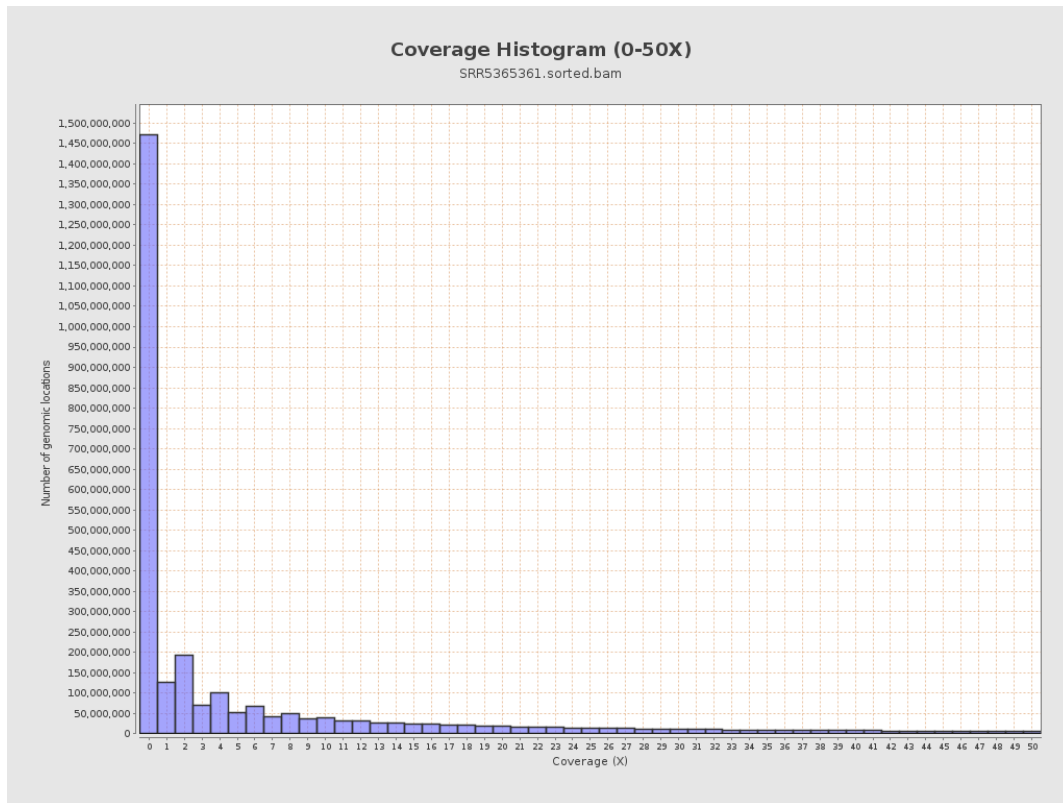
3. Results : Coverage across reference



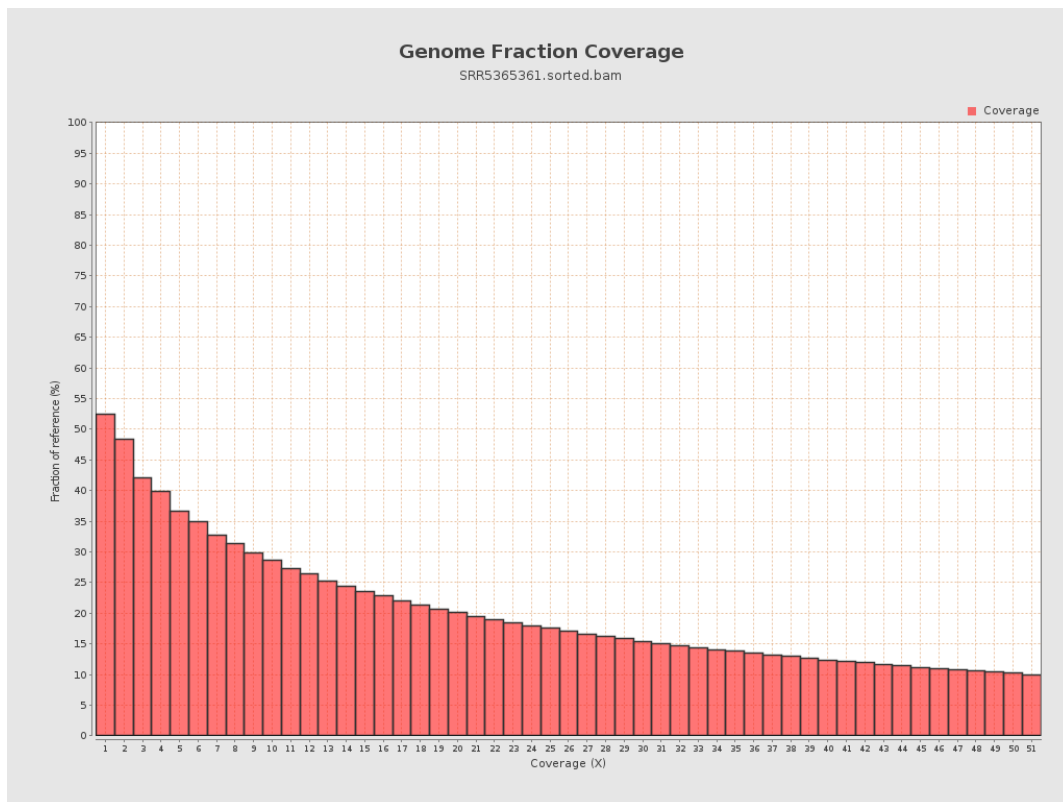
4. Results : Coverage Histogram



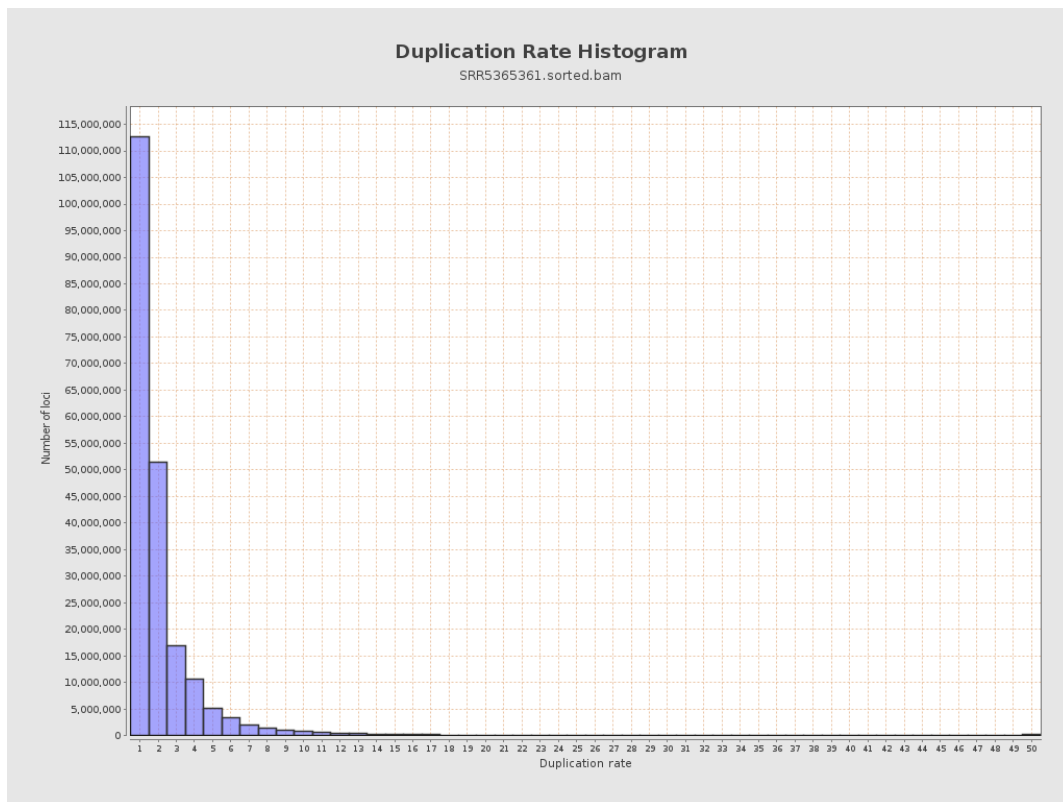
5. Results : Coverage Histogram (0-50X)



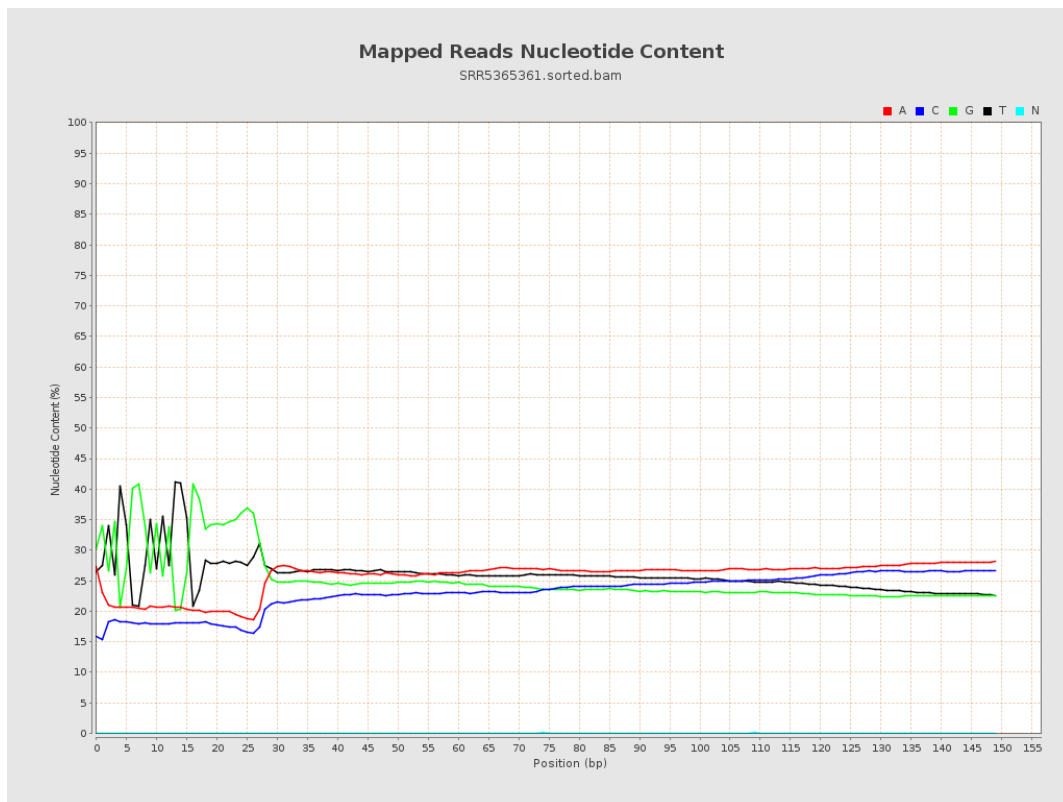
6. Results : Genome Fraction Coverage



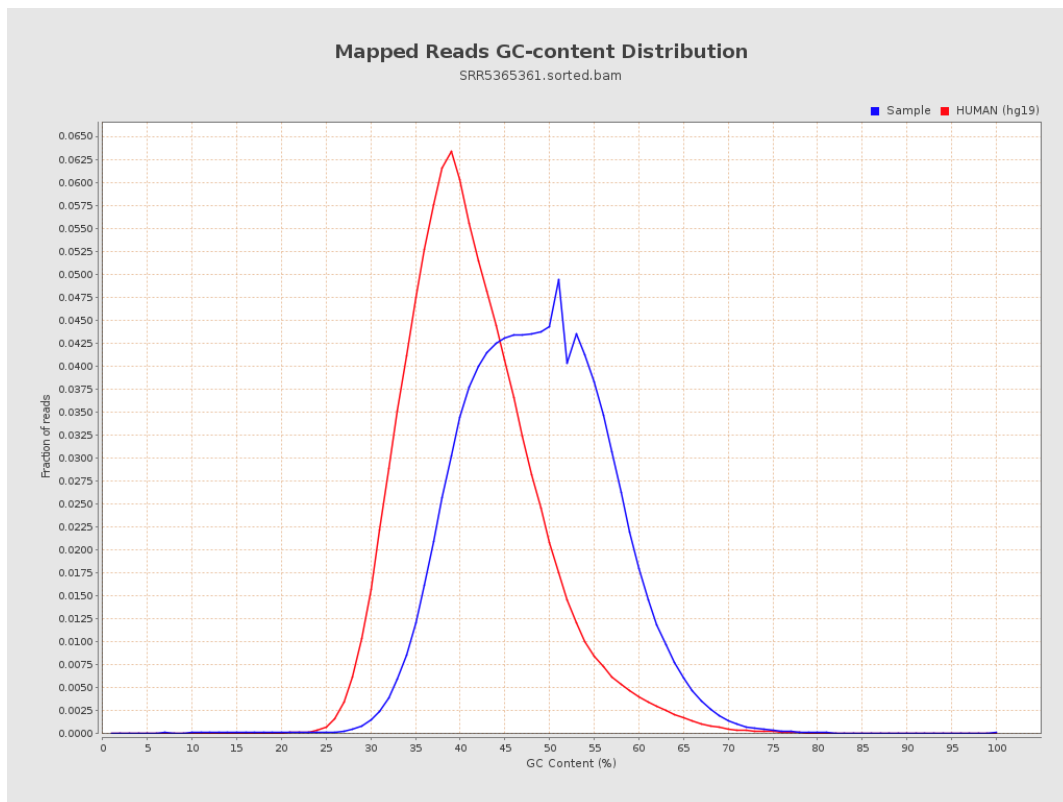
7. Results : Duplication Rate Histogram



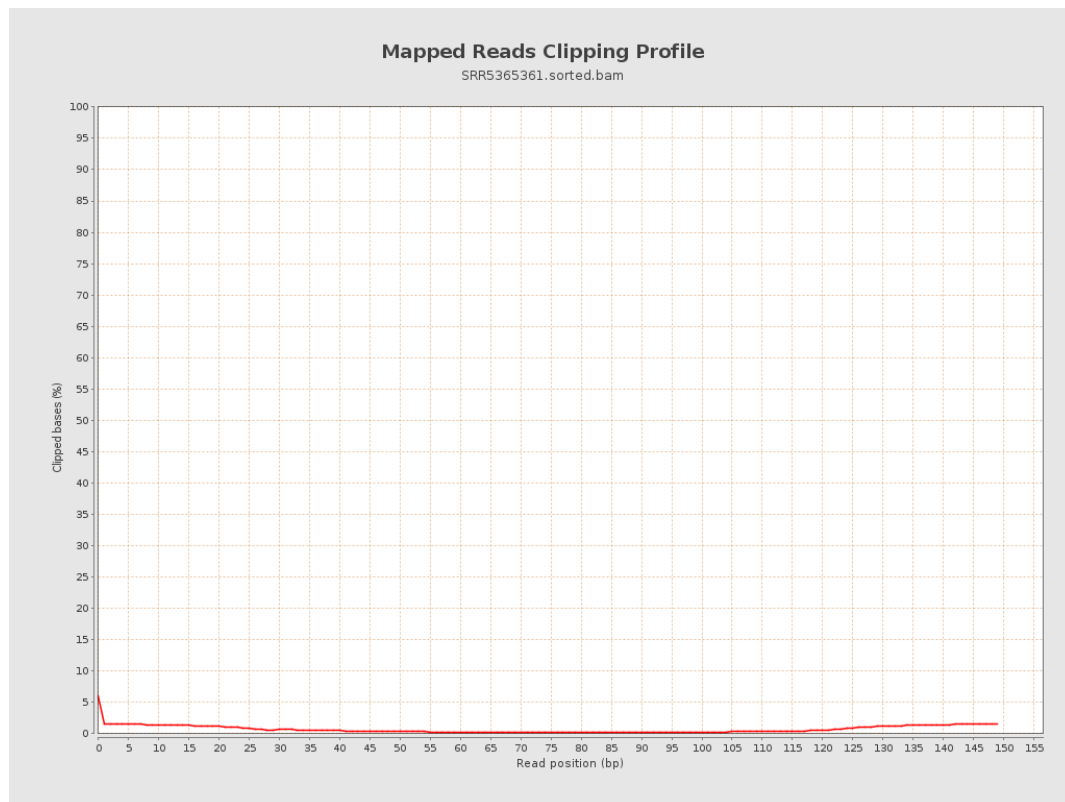
8. Results : Mapped Reads Nucleotide Content



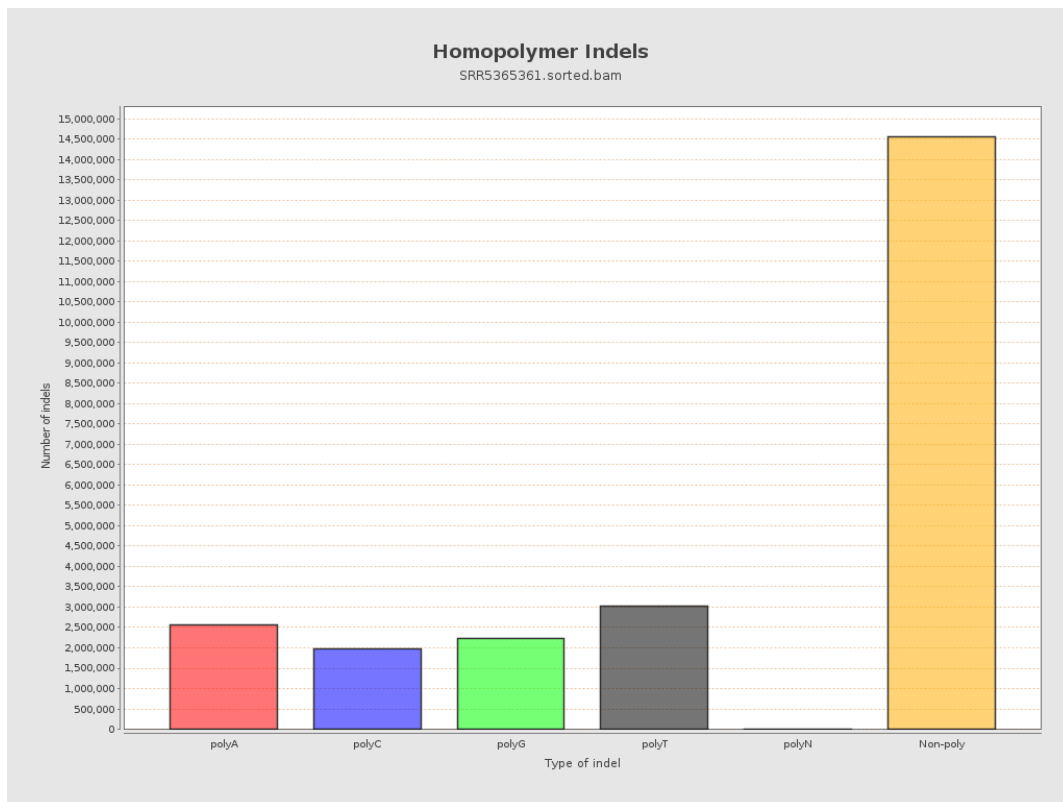
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



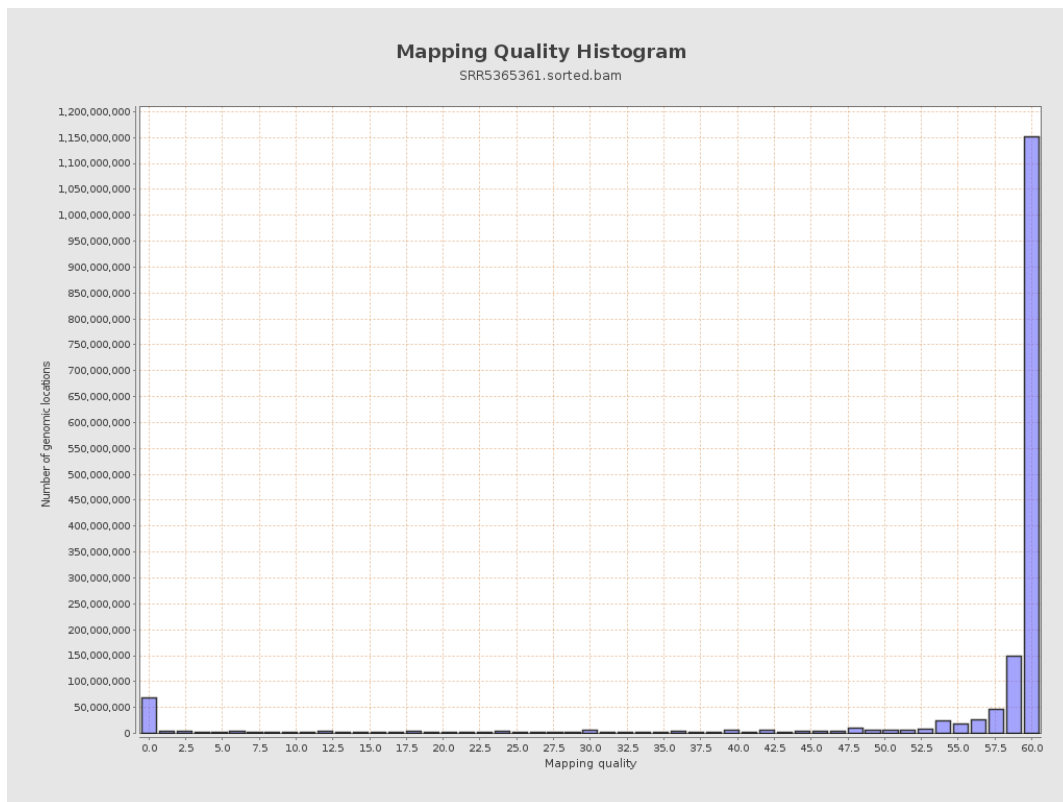
11. Results : Homopolymer Indels



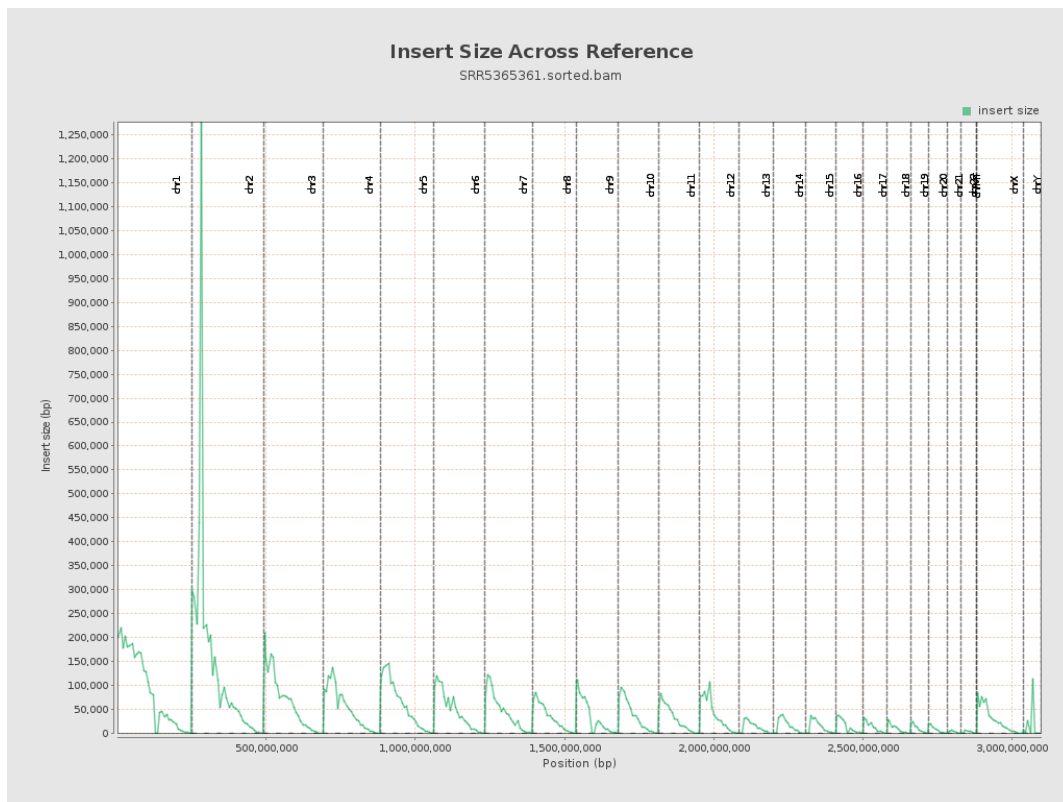
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

