

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 14:37:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365337.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_SRR5365337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365337_1.fastq.gz SRR5365337_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 14:37:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	132,362,592
Mapped reads	129,853,220 / 98.1%
Unmapped reads	2,509,372 / 1.9%
Mapped paired reads	129,853,220 / 98.1%
Mapped reads, first in pair	65,236,026 / 49.29%
Mapped reads, second in pair	64,617,194 / 48.82%
Mapped reads, both in pair	129,039,218 / 97.49%
Mapped reads, singletons	814,002 / 0.61%
Secondary alignments	0
Supplementary alignments	1,058,467 / 0.8%
Read min/max/mean length	30 / 151 / 151.36
Duplicated reads (estimated)	58,219,185 / 43.98%
Duplication rate	30.49%
Clipped reads	76,452,718 / 57.76%

2.2. ACGT Content

Number/percentage of A's	5,112,363,595 / 29.75%
Number/percentage of C's	3,419,910,447 / 19.9%
Number/percentage of T's	5,050,644,192 / 29.39%
Number/percentage of G's	3,600,621,794 / 20.95%
Number/percentage of N's	622,748 / 0%

GC Percentage	40.85%
---------------	--------

2.3. Coverage

Mean	5.5531
Standard Deviation	36.4878

2.4. Mapping Quality

Mean Mapping Quality	54.34
----------------------	-------

2.5. Insert size

Mean	90,754.68
Standard Deviation	2,972,243.56
P25/Median/P75	153 / 207 / 280

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	116,443,863
Insertions	5,175,402
Mapped reads with at least one insertion	3.87%
Deletions	2,623,568
Mapped reads with at least one deletion	1.96%
Homopolymer indels	50.75%

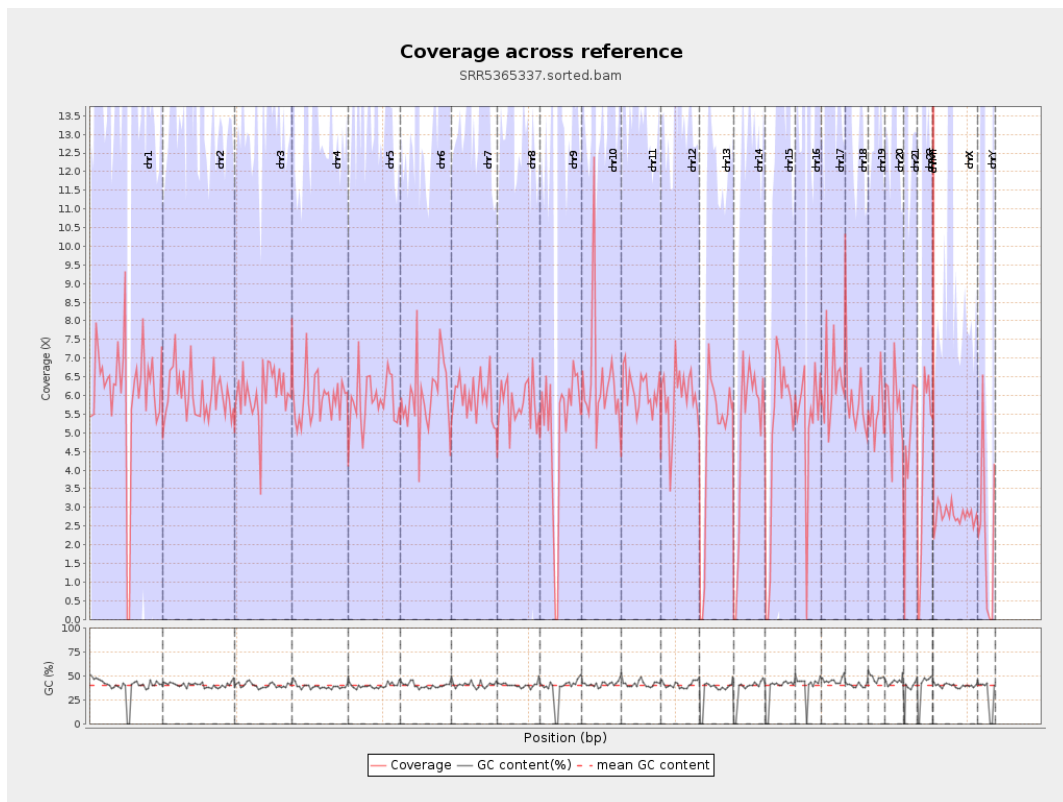
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

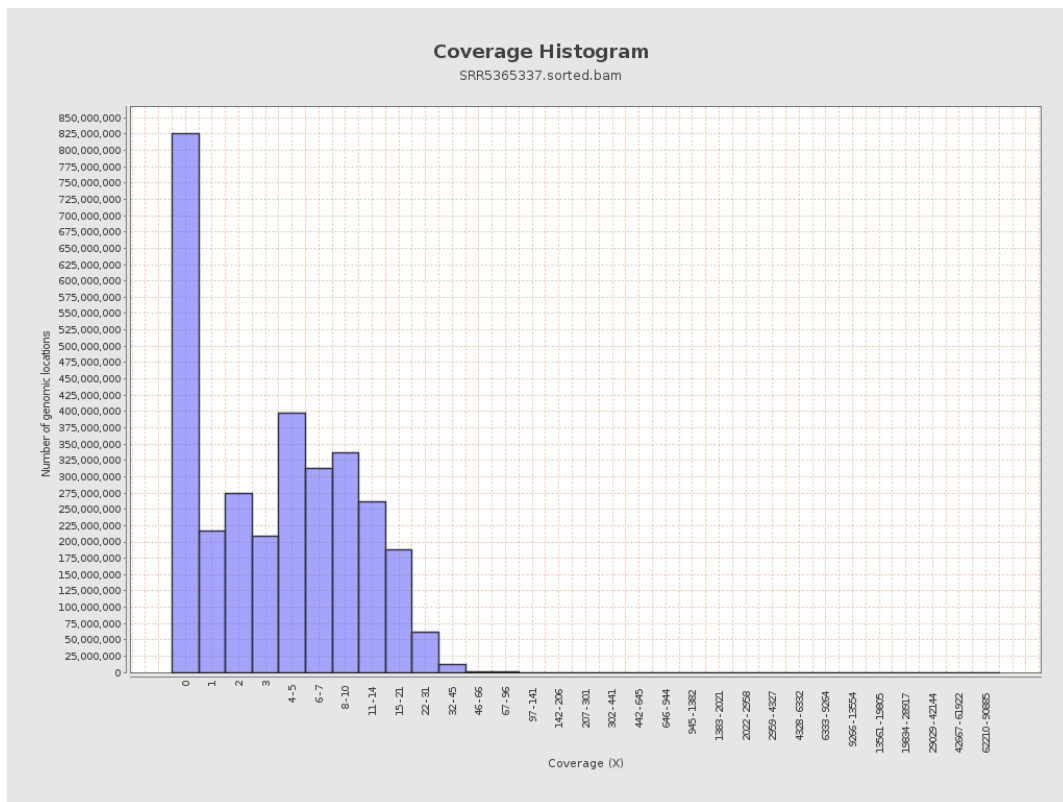
		bases	coverage	deviation
chr1	249250621	1522506141	6.1083	90.3292
chr2	243199373	1466973483	6.032	25.3541
chr3	198022430	1200418573	6.062	7.0657
chr4	191154276	1127992453	5.901	26.2431
chr5	180915260	1063227783	5.8769	7.1074
chr6	171115067	1027849459	6.0068	22.8767
chr7	159138663	943467263	5.9286	22.8968
chr8	146364022	846740600	5.7852	12.093
chr9	141213431	730102243	5.1702	34.3547
chr10	135534747	859287373	6.34	65.8954
chr11	135006516	825032608	6.1111	29.0153
chr12	133851895	801701742	5.9895	30.0871
chr13	115169878	555798554	4.8259	5.9719
chr14	107349540	543858922	5.0662	6.4485
chr15	102531392	499339328	4.8701	15.2721
chr16	90354753	487189448	5.392	14.0746
chr17	81195210	515962382	6.3546	26.6109
chr18	78077248	456721116	5.8496	43.5844
chr19	59128983	326702808	5.5253	47.1826
chr20	63025520	357154921	5.6668	11.1459
chr21	48129895	233602228	4.8536	19.724
chr22	51304566	217792447	4.2451	17.1059
chrMT	16571	11310597	682.5537	153.8739
chrX	155270560	433318613	2.7907	10.6296

chrY	59373566	136573339	2.3002	48.3578
------	----------	-----------	--------	---------

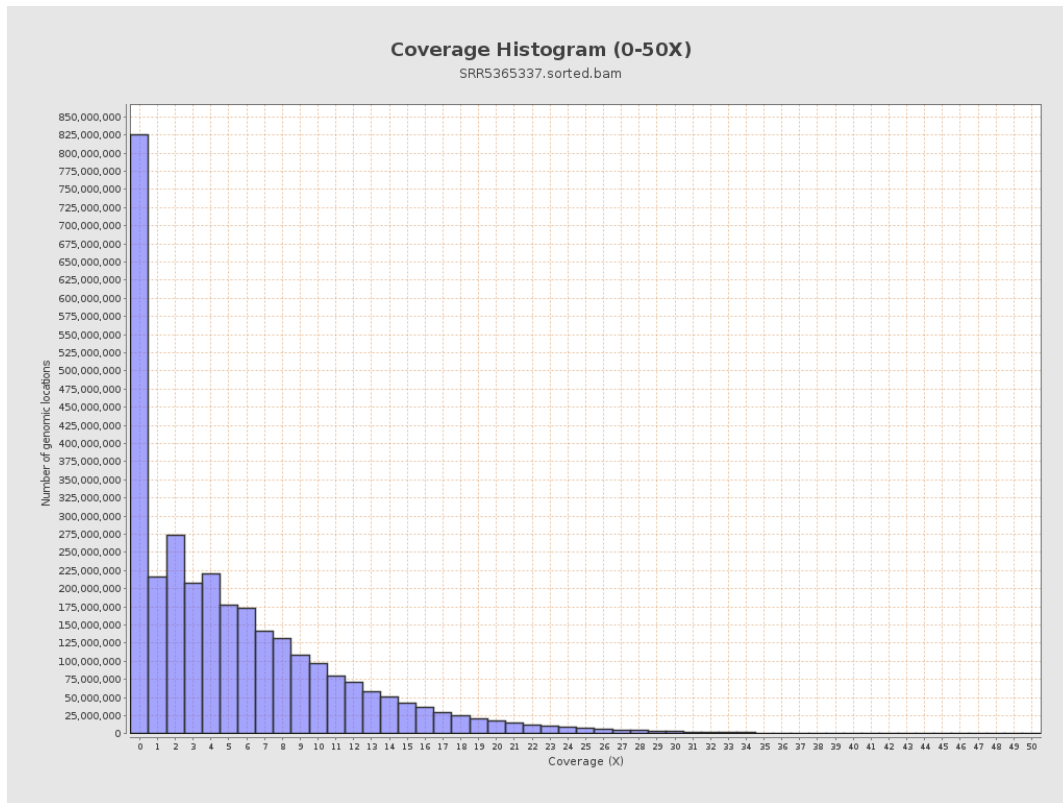
3. Results : Coverage across reference



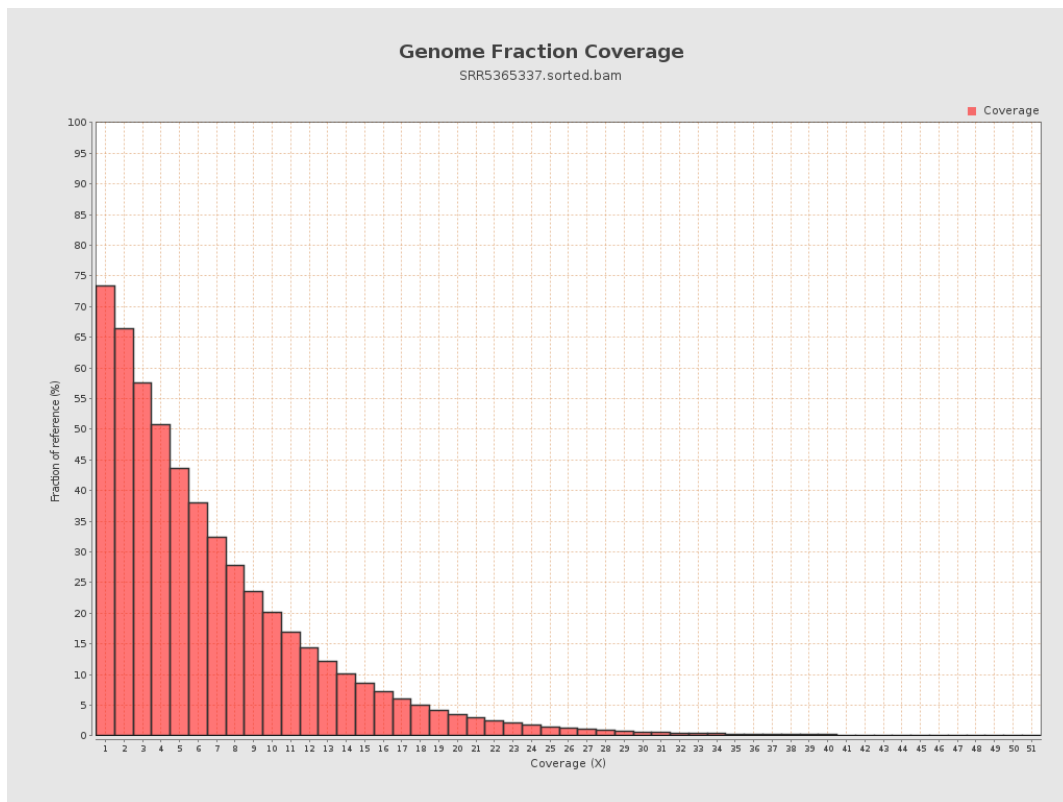
4. Results : Coverage Histogram



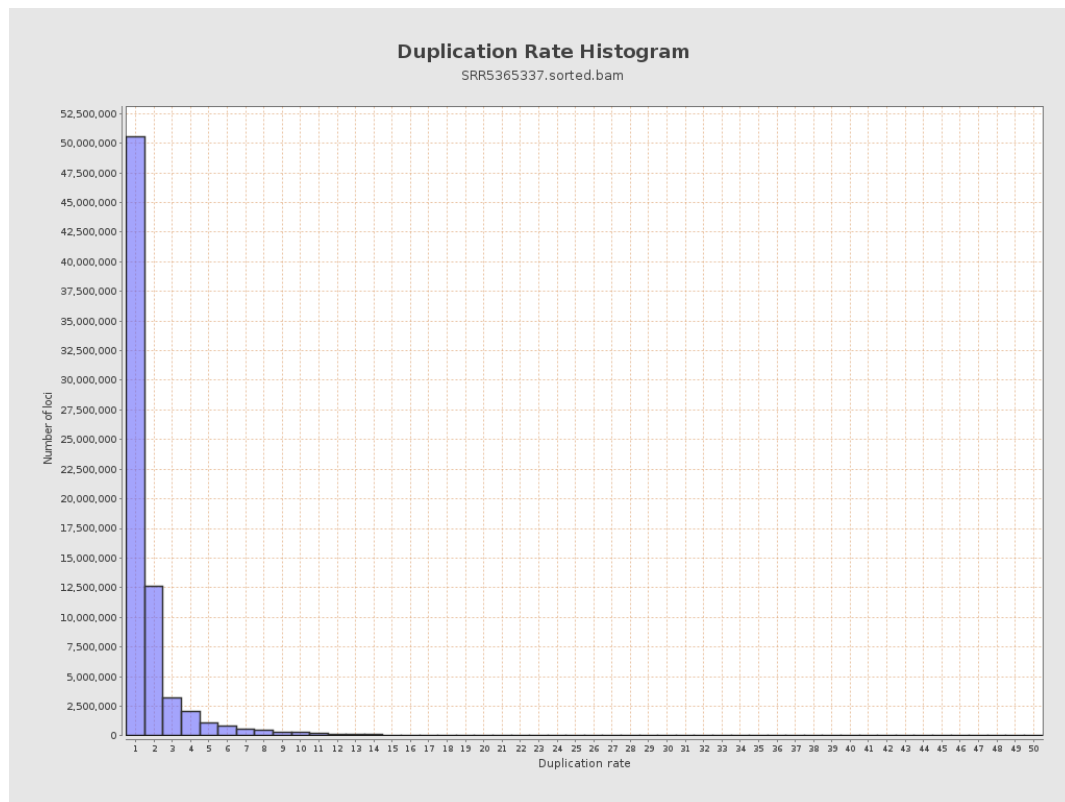
5. Results : Coverage Histogram (0-50X)



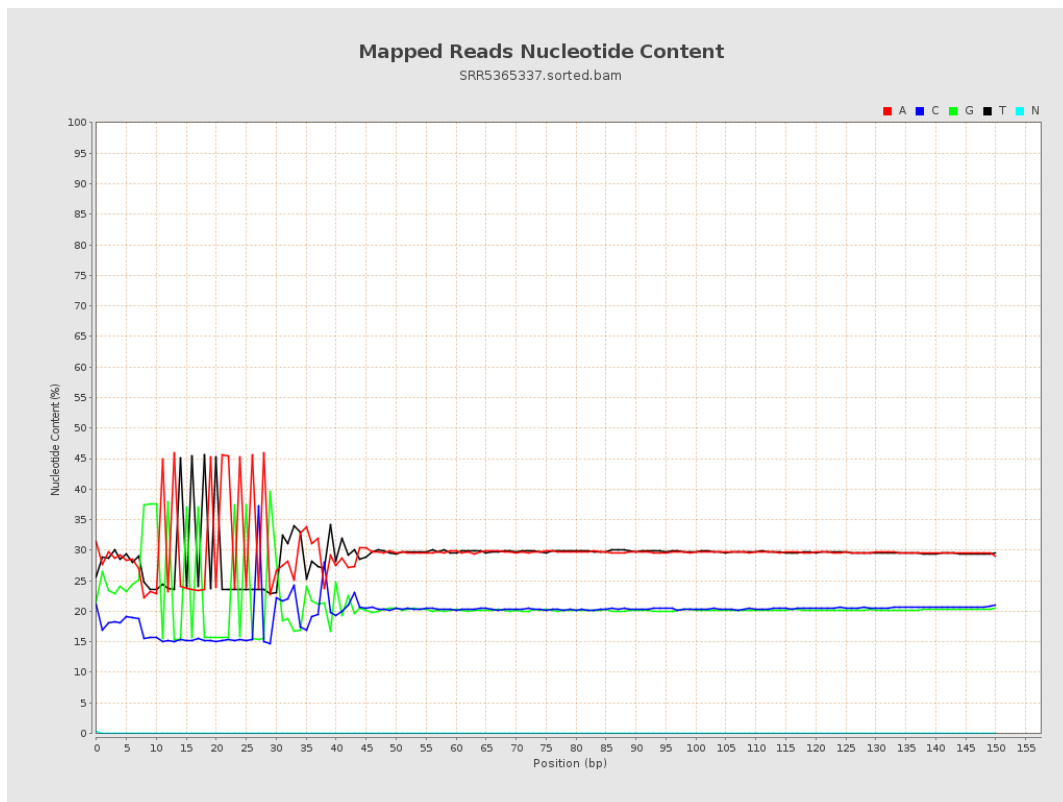
6. Results : Genome Fraction Coverage



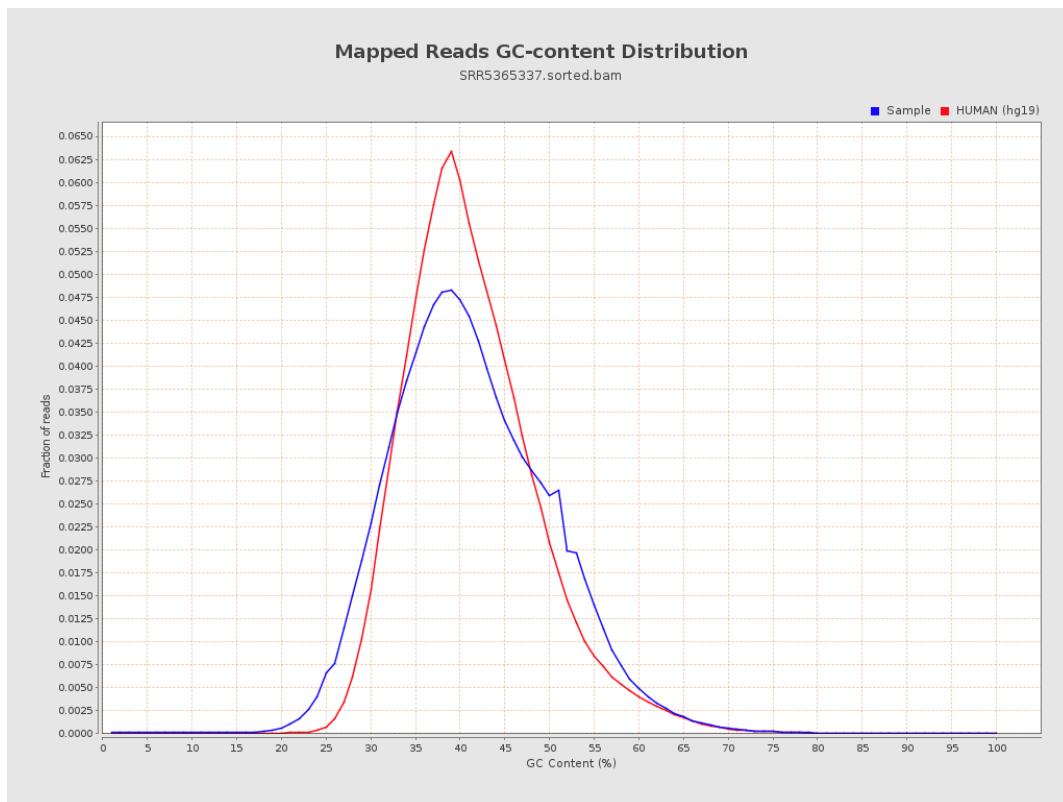
7. Results : Duplication Rate Histogram



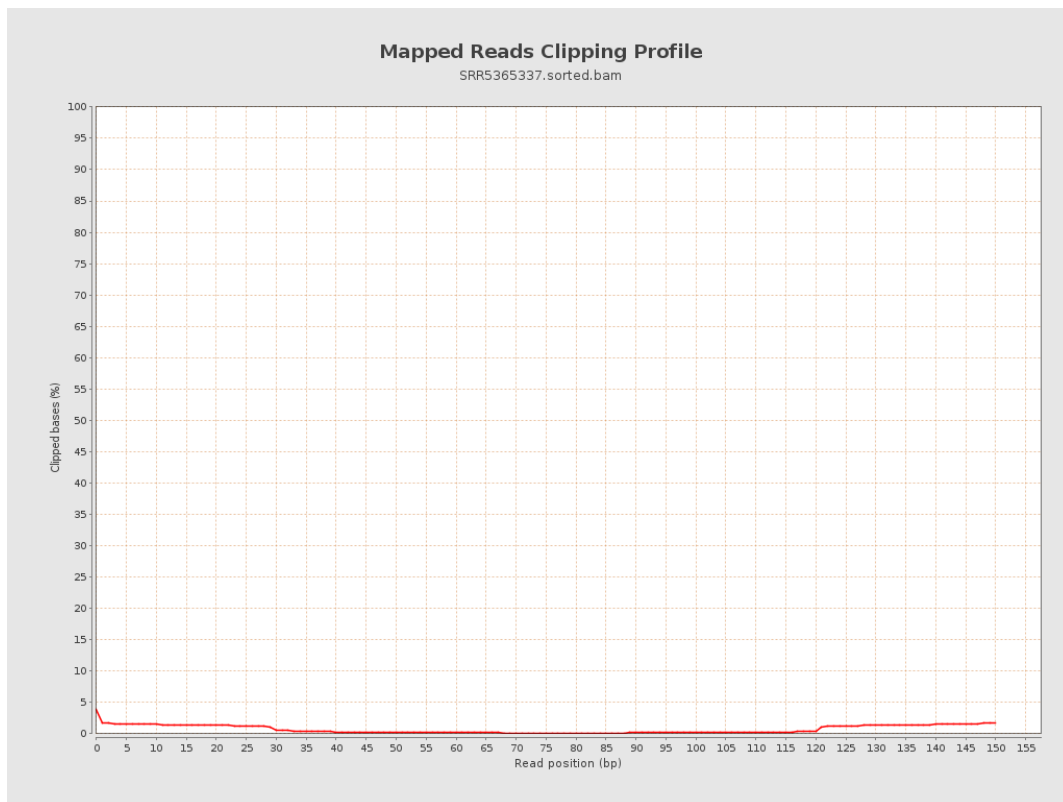
8. Results : Mapped Reads Nucleotide Content



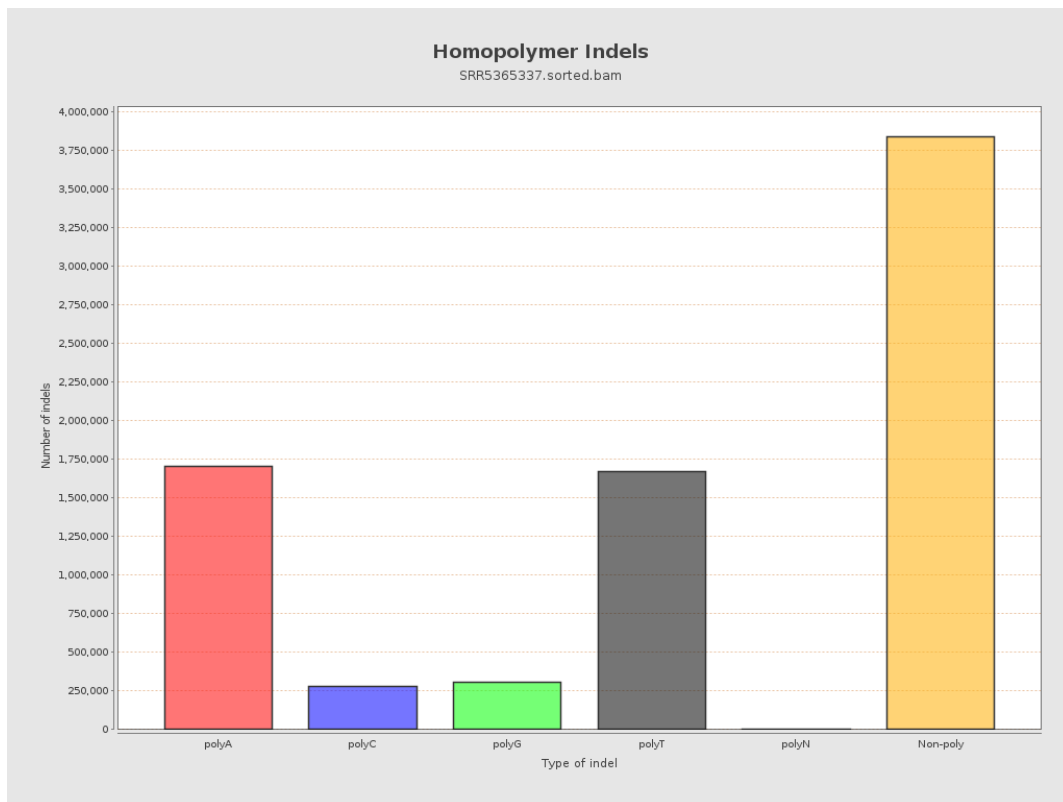
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



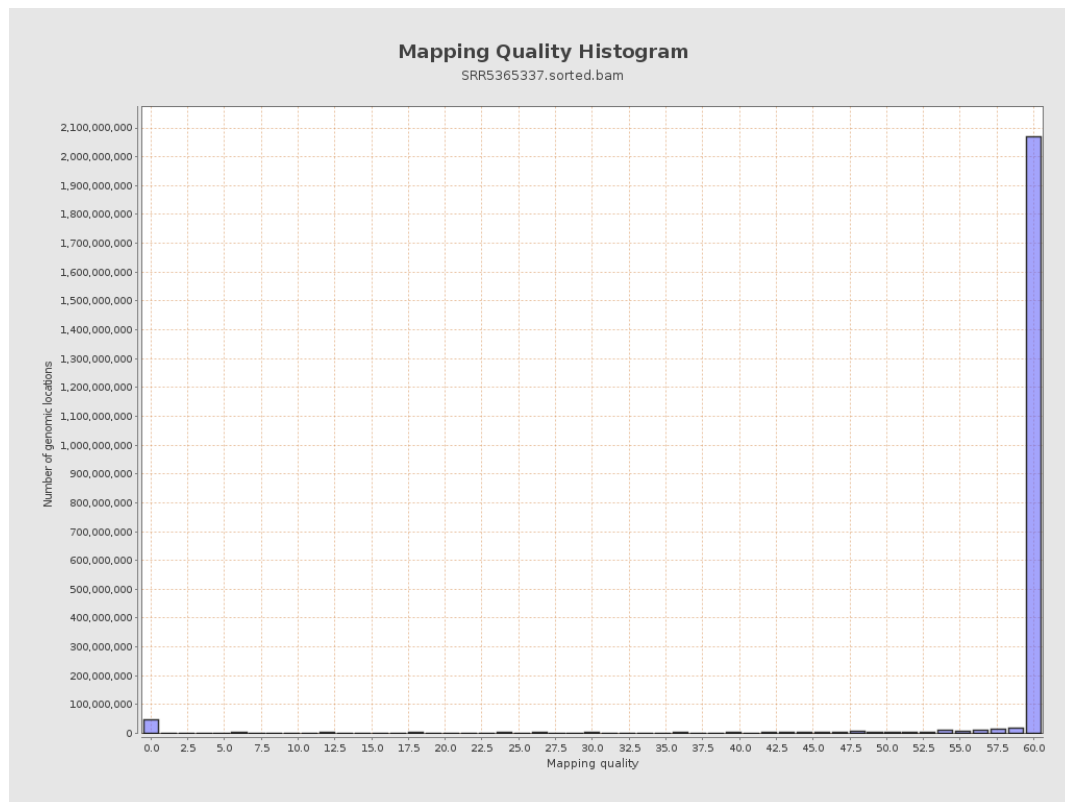
11. Results : Homopolymer Indels



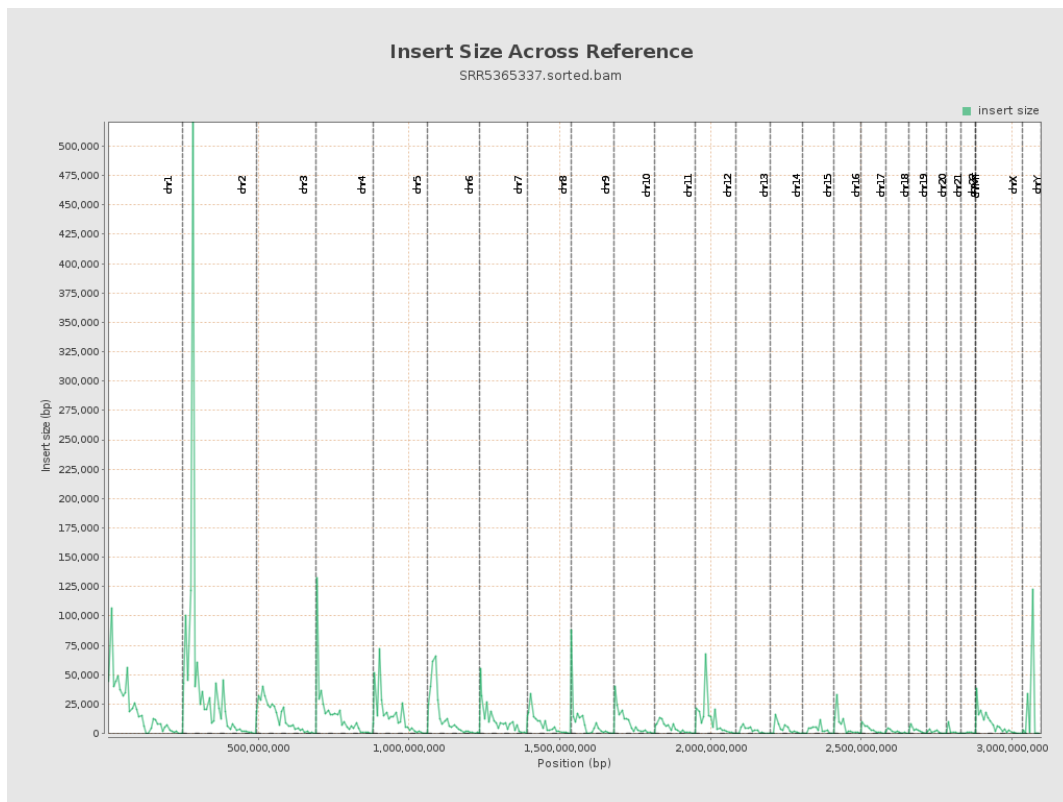
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

