

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/28 00:12:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365371.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_SRR5365371 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365371_1.fastq.gz SRR5365371_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 28 00:12:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365371.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	597,850,476
Mapped reads	570,889,125 / 95.49%
Unmapped reads	26,961,351 / 4.51%
Mapped paired reads	570,889,125 / 95.49%
Mapped reads, first in pair	285,778,771 / 47.8%
Mapped reads, second in pair	285,110,354 / 47.69%
Mapped reads, both in pair	568,200,476 / 95.04%
Mapped reads, singletons	2,688,649 / 0.45%
Secondary alignments	0
Supplementary alignments	13,075,796 / 2.19%
Read min/max/mean length	30 / 150 / 151.16
Duplicated reads (estimated)	214,667,014 / 35.91%
Duplication rate	35.57%
Clipped reads	161,244,779 / 26.97%

2.2. ACGT Content

Number/percentage of A's	22,189,311,995 / 27.02%
Number/percentage of C's	18,936,290,933 / 23.06%
Number/percentage of T's	21,702,580,841 / 26.43%
Number/percentage of G's	19,289,378,490 / 23.49%
Number/percentage of N's	863,782 / 0%

GC Percentage	46.55%
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2.3. Coverage

Mean	26.5323
Standard Deviation	53.2045

2.4. Mapping Quality

Mean Mapping Quality	54.68
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2.5. Insert size

Mean	87,953.48
Standard Deviation	2,977,367.47
P25/Median/P75	152 / 183 / 221

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	378,852,439
Insertions	7,570,057
Mapped reads with at least one insertion	1.29%
Deletions	6,009,015
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.19%

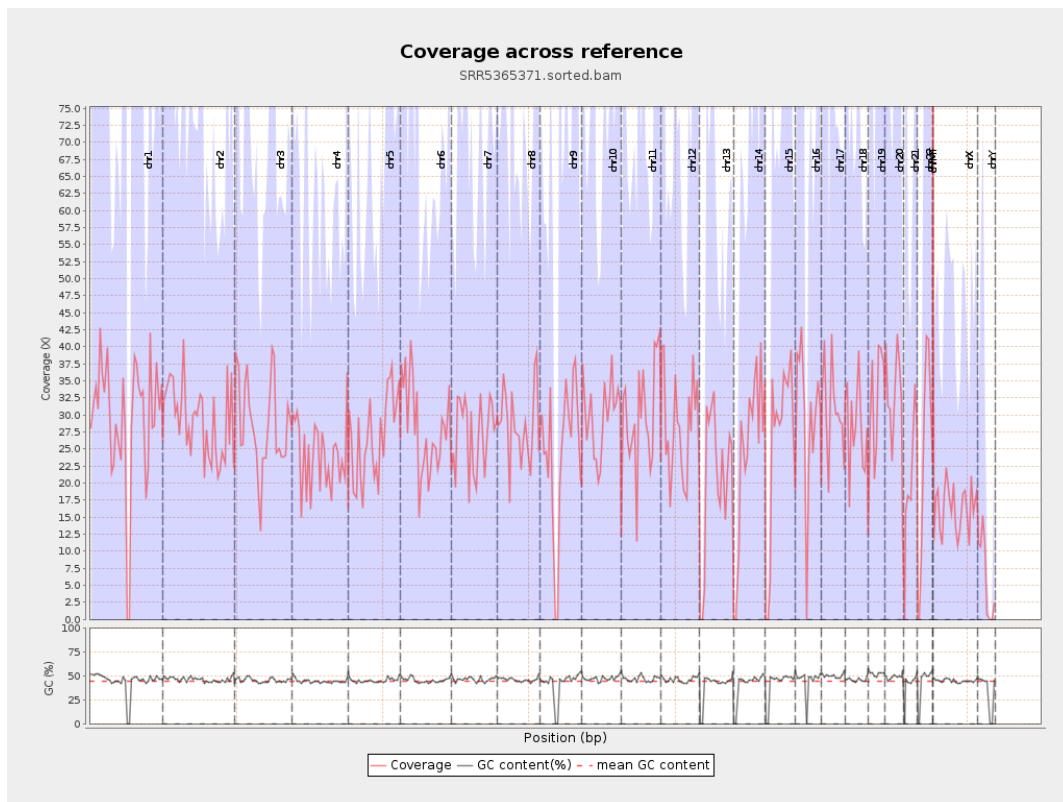
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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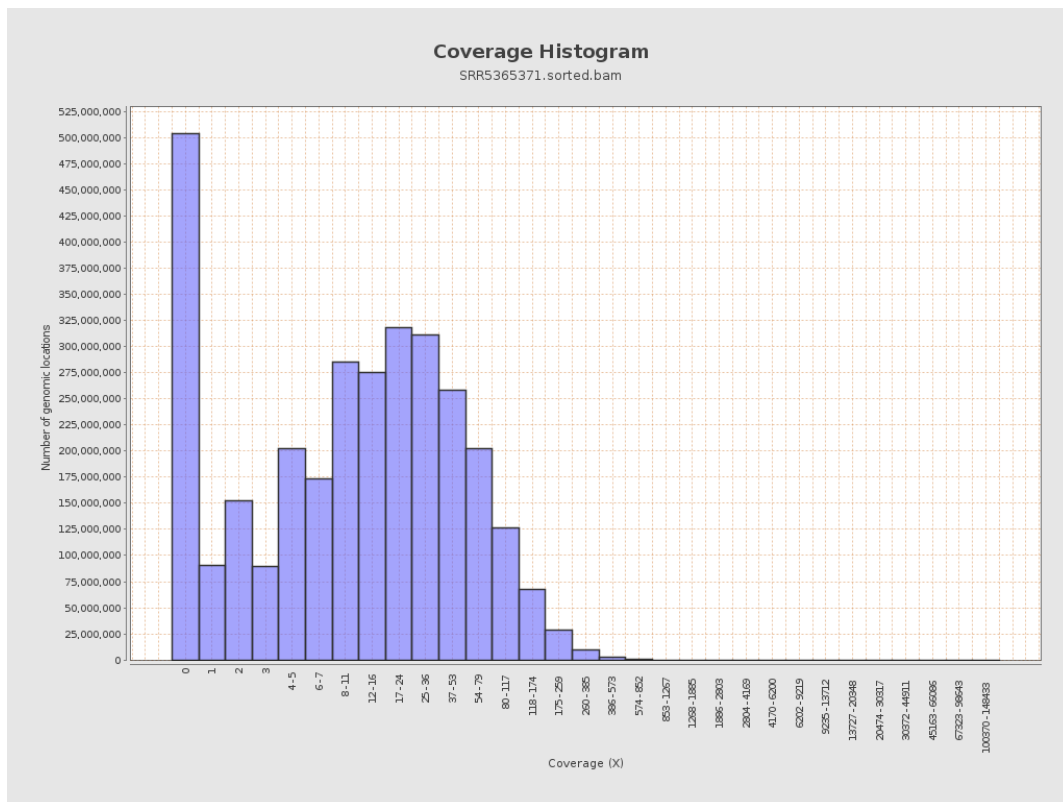
		bases	coverage	deviation
chr1	249250621	7321049643	29.3722	57.7072
chr2	243199373	7091811226	29.1605	108.4771
chr3	198022430	5620614196	28.3837	42.0815
chr4	191154276	4603346477	24.0818	38.6331
chr5	180915260	4860950132	26.8687	39.4915
chr6	171115067	4777152148	27.9178	45.9893
chr7	159138663	4314815173	27.1136	41.1731
chr8	146364022	4161765844	28.4344	45.2096
chr9	141213431	3471402784	24.5827	45.1828
chr10	135534747	4037368475	29.7884	48.7226
chr11	135006516	3994791148	29.5896	45.4818
chr12	133851895	3829943266	28.6133	44.1917
chr13	115169878	2364314310	20.5289	35.692
chr14	107349540	2671222677	24.8834	43.0528
chr15	102531392	2630640437	25.6569	42.1048
chr16	90354753	2616799687	28.9614	44.9166
chr17	81195210	2515589818	30.982	54.4439
chr18	78077248	2184749800	27.9819	60.4538
chr19	59128983	1891388652	31.9875	55.1678
chr20	63025520	2036223908	32.3079	51.4938
chr21	48129895	1008474628	20.9532	49.0099
chr22	51304566	1248118929	24.3276	48.3484
chrMT	16571	2119245	127.8888	55.0671
chrX	155270560	2513431300	16.1874	29.9589

chrY	59373566	367774275	6.1942	28.9435
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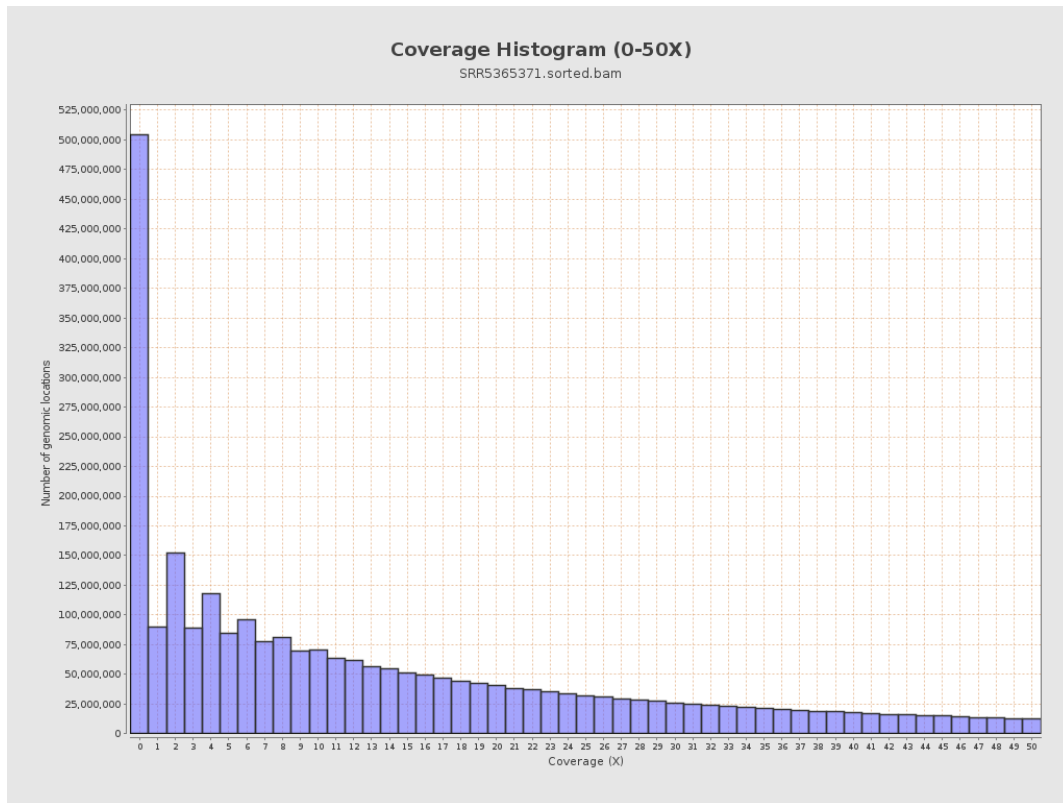
3. Results : Coverage across reference



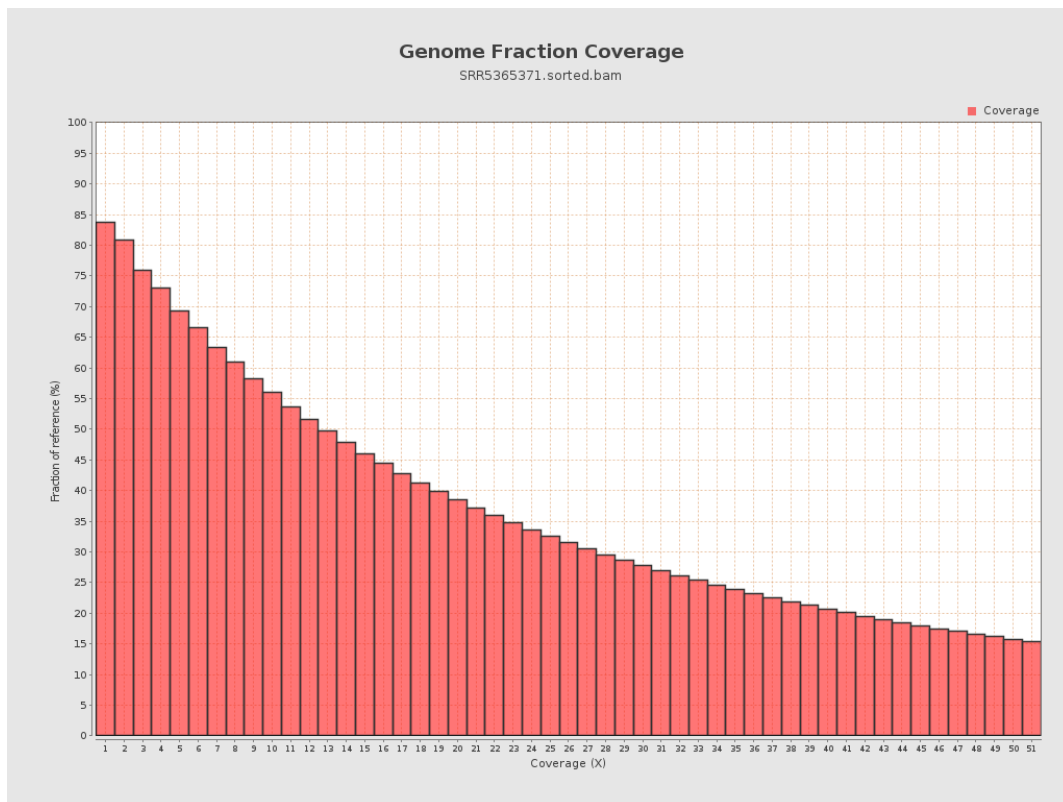
4. Results : Coverage Histogram



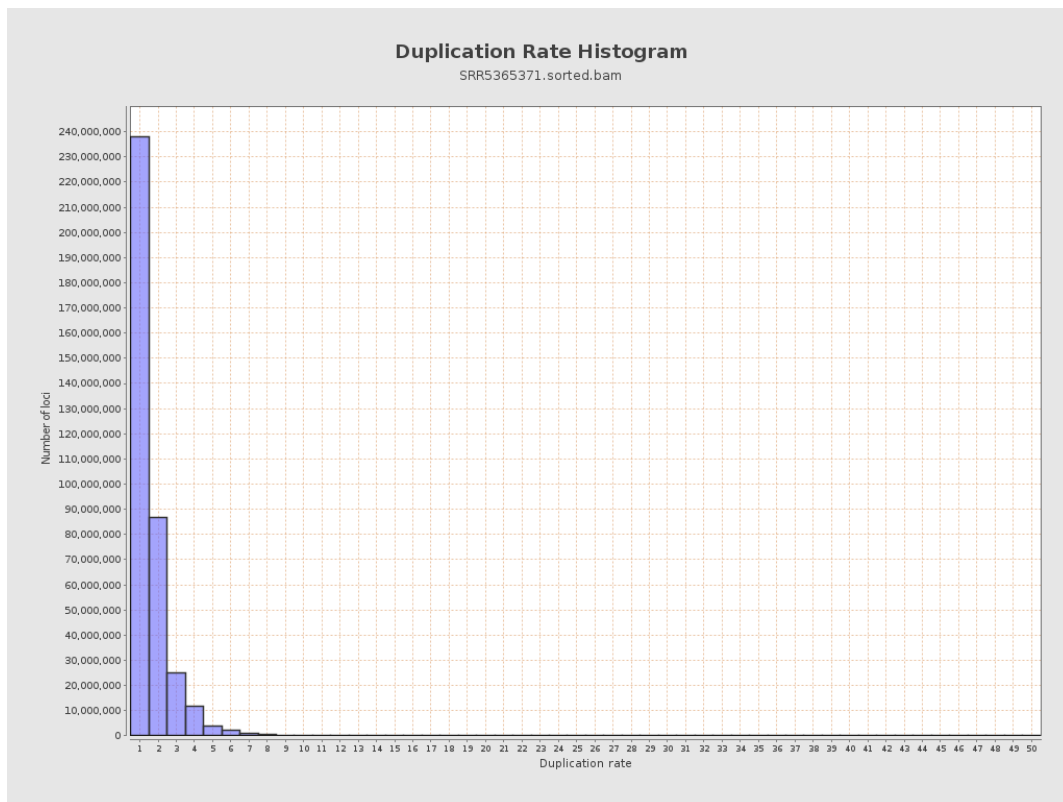
5. Results : Coverage Histogram (0-50X)



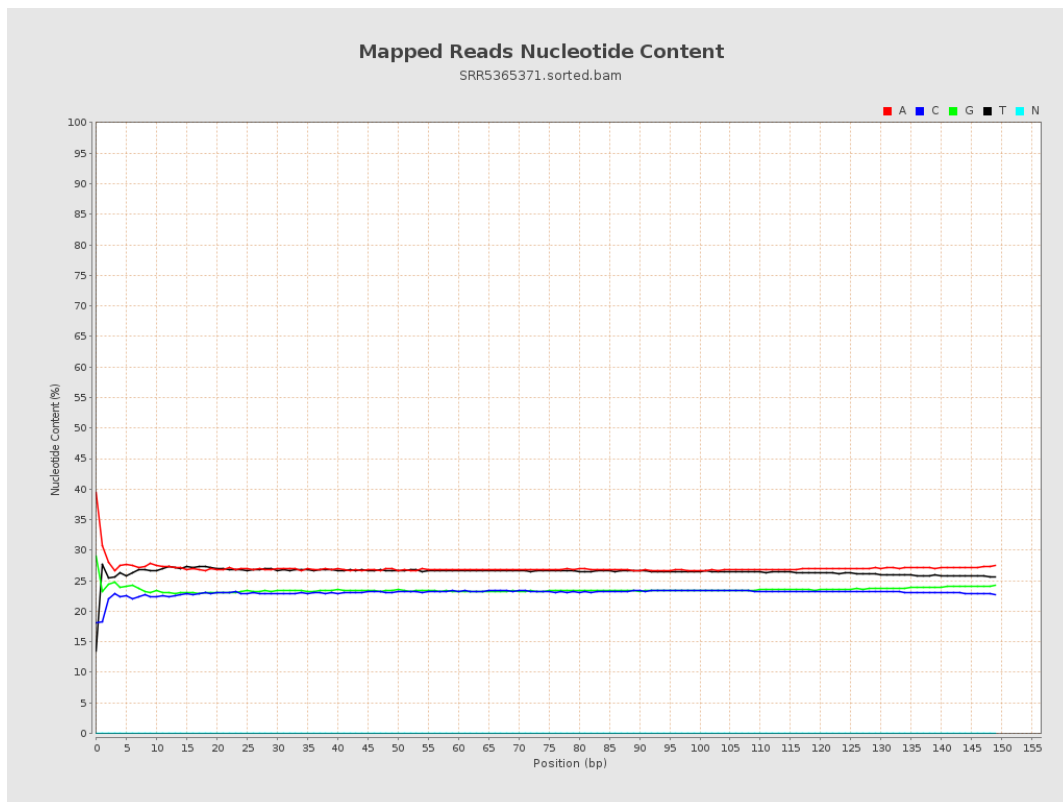
6. Results : Genome Fraction Coverage



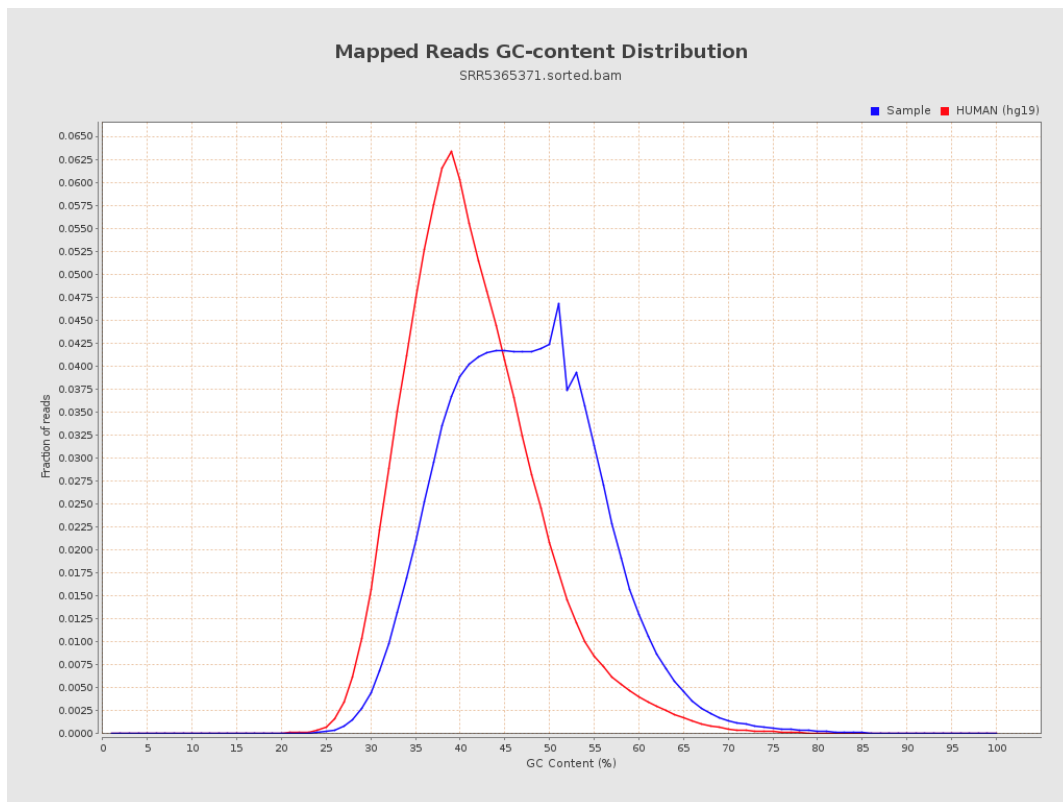
7. Results : Duplication Rate Histogram



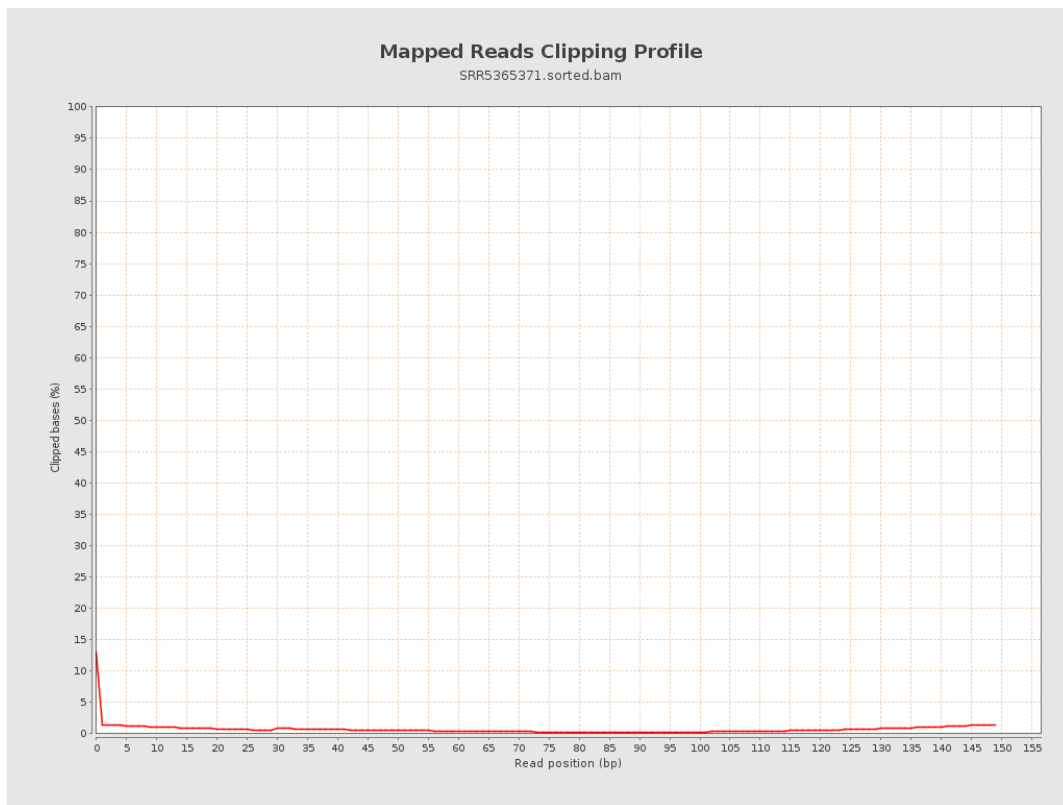
8. Results : Mapped Reads Nucleotide Content



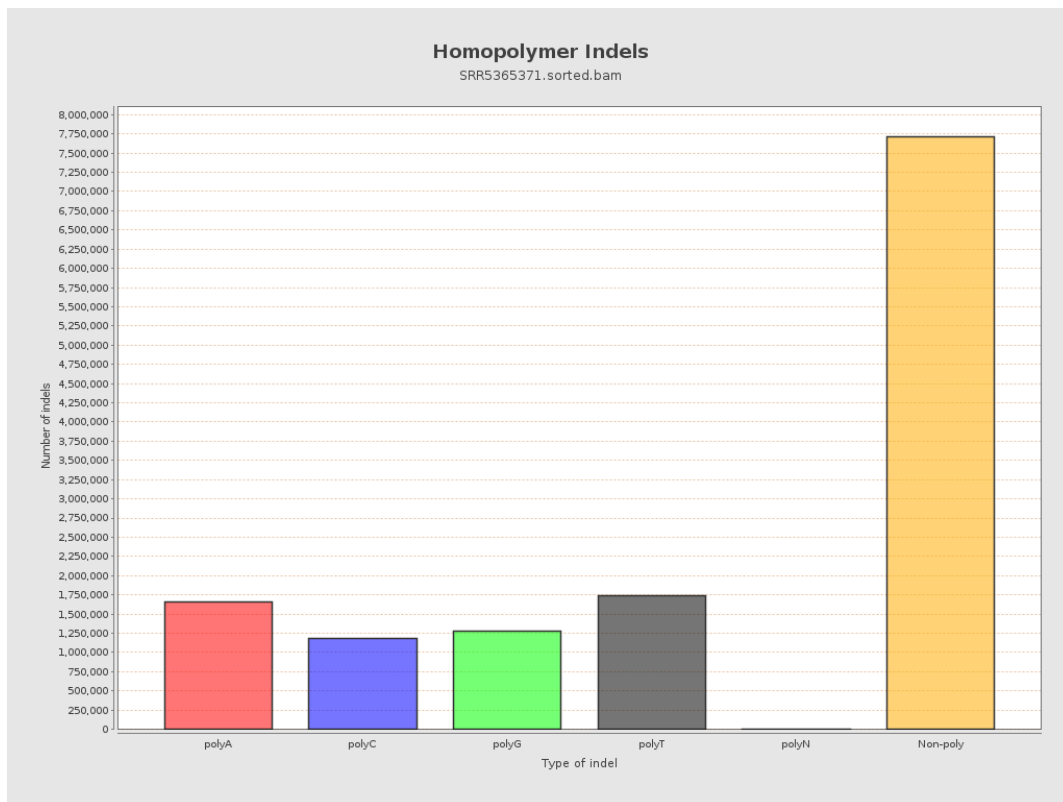
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



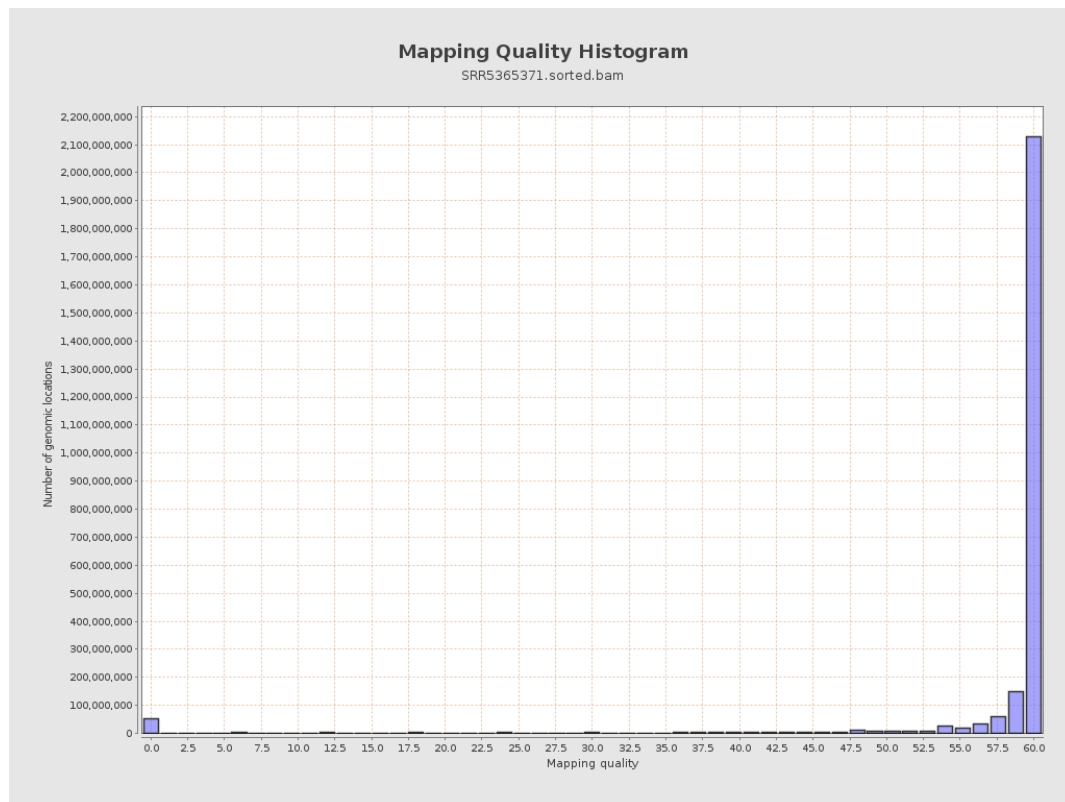
11. Results : Homopolymer Indels



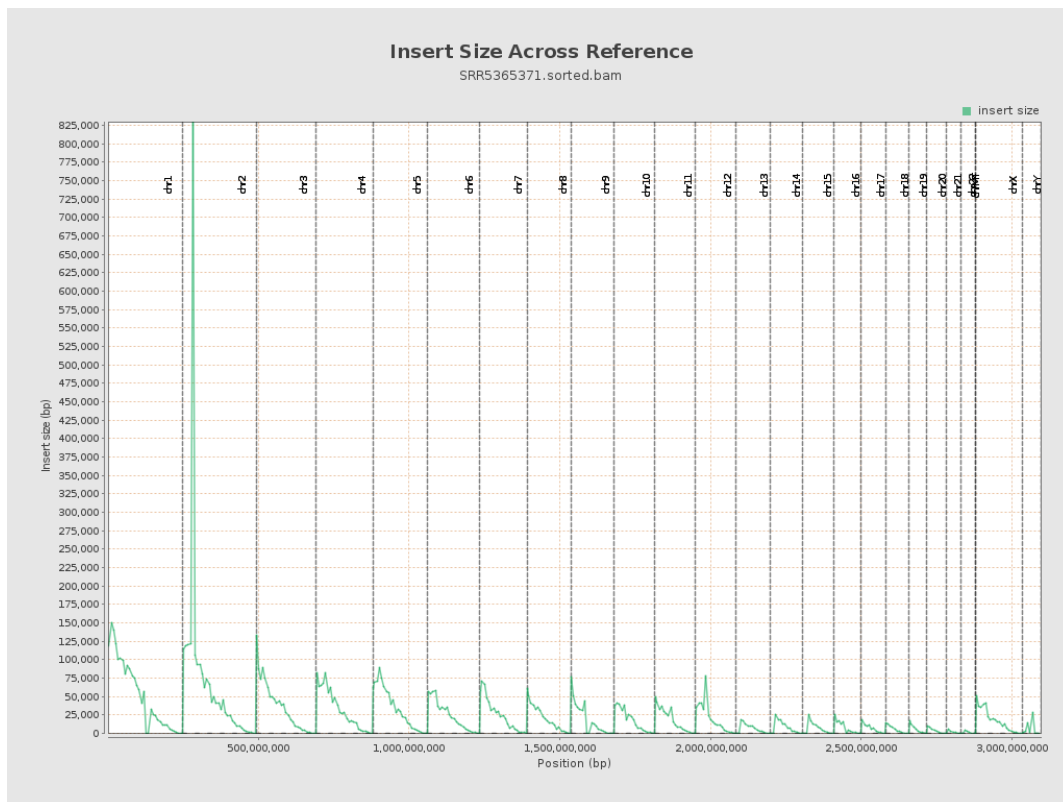
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

