

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/29 10:33:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365374.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_SRR5365374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365374_1.fastq.gz SRR5365374_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Nov 29 10:33:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	518,060,238
Mapped reads	450,078,614 / 86.88%
Unmapped reads	67,981,624 / 13.12%
Mapped paired reads	450,078,614 / 86.88%
Mapped reads, first in pair	224,389,397 / 43.31%
Mapped reads, second in pair	225,689,217 / 43.56%
Mapped reads, both in pair	446,343,208 / 86.16%
Mapped reads, singletons	3,735,406 / 0.72%
Secondary alignments	0
Supplementary alignments	2,099,527 / 0.41%
Read min/max/mean length	30 / 125 / 125.16
Duplicated reads (estimated)	231,160,140 / 44.62%
Duplication rate	29.02%
Clipped reads	384,765,178 / 74.27%

2.2. ACGT Content

Number/percentage of A's	12,620,184,892 / 29.17%
Number/percentage of C's	8,608,435,324 / 19.9%
Number/percentage of T's	12,210,543,886 / 28.22%
Number/percentage of G's	9,070,577,753 / 20.96%
Number/percentage of N's	757,381,998 / 1.75%

GC Percentage	40.86%
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2.3. Coverage

Mean	13.9806
Standard Deviation	177.1795

2.4. Mapping Quality

Mean Mapping Quality	53.42
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2.5. Insert size

Mean	63,144.68
Standard Deviation	2,431,888.65
P25/Median/P75	103 / 141 / 194

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	209,787,779
Insertions	11,102,803
Mapped reads with at least one insertion	2.42%
Deletions	6,147,904
Mapped reads with at least one deletion	1.34%
Homopolymer indels	48.88%

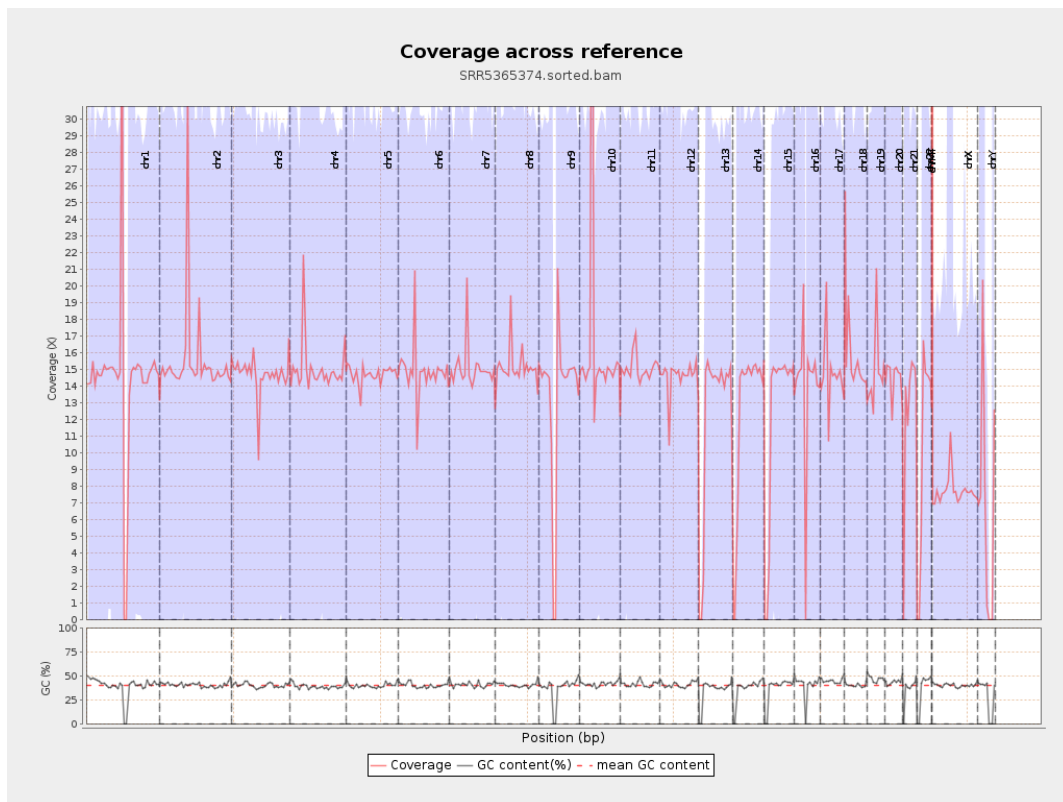
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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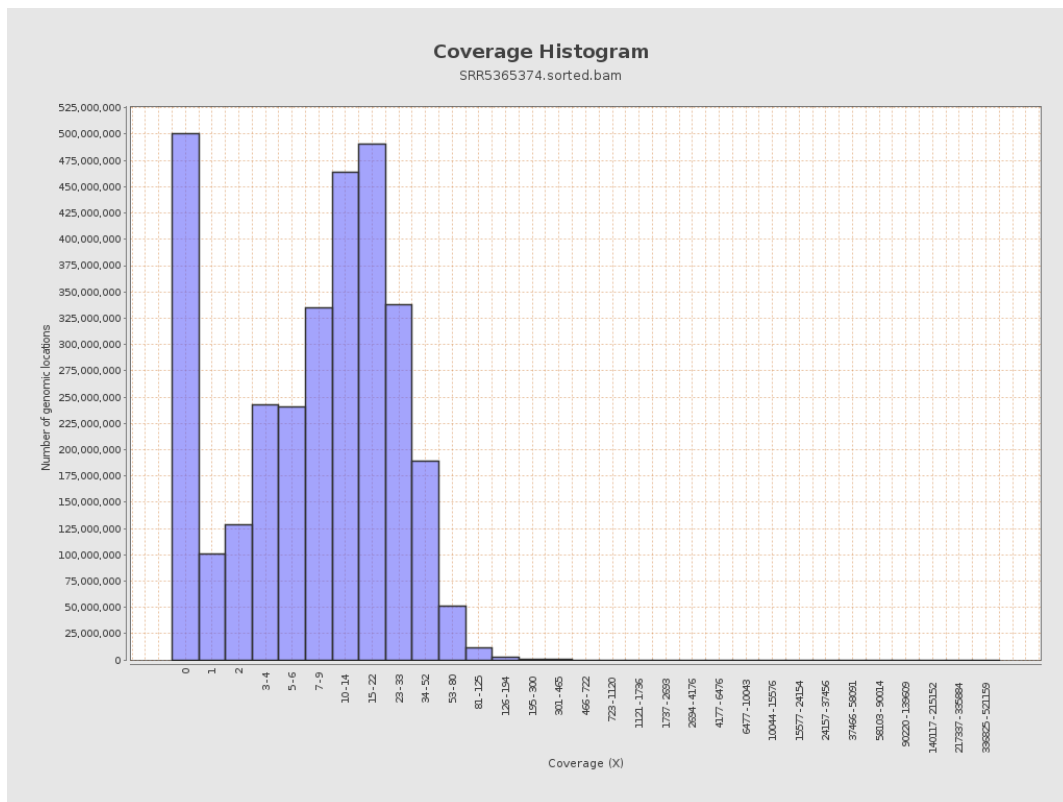
		bases	coverage	deviation
chr1	249250621	3631572160	14.57	502.7981
chr2	243199373	3773176230	15.5147	110.295
chr3	198022430	2893644832	14.6127	28.9369
chr4	191154276	2863874671	14.982	63.7068
chr5	180915260	2651591057	14.6565	20.2237
chr6	171115067	2550244307	14.9037	72.9823
chr7	159138663	2393204944	15.0385	122.6372
chr8	146364022	2221692261	15.1792	73.3939
chr9	141213431	1863927758	13.1994	156.47
chr10	135534747	2267865182	16.7327	294.8672
chr11	135006516	2023680475	14.9895	100.6962
chr12	133851895	1946812788	14.5445	33.3466
chr13	115169878	1406235481	12.2101	14.7033
chr14	107349540	1332418856	12.412	21.2312
chr15	102531392	1225071448	11.9483	19.9425
chr16	90354753	1253947734	13.878	47.9236
chr17	81195210	1188458025	14.637	78.3739
chr18	78077248	1224466608	15.6828	201.6396
chr19	59128983	875396906	14.8049	247.8343
chr20	63025520	909732083	14.4343	31.072
chr21	48129895	612863047	12.7335	49.9499
chr22	51304566	533936397	10.4072	42.8263
chrMT	16571	25578844	1,543.5909	282.5562
chrX	155270560	1194557859	7.6934	44.2741

chrY	59373566	415757013	7.0024	135.0529
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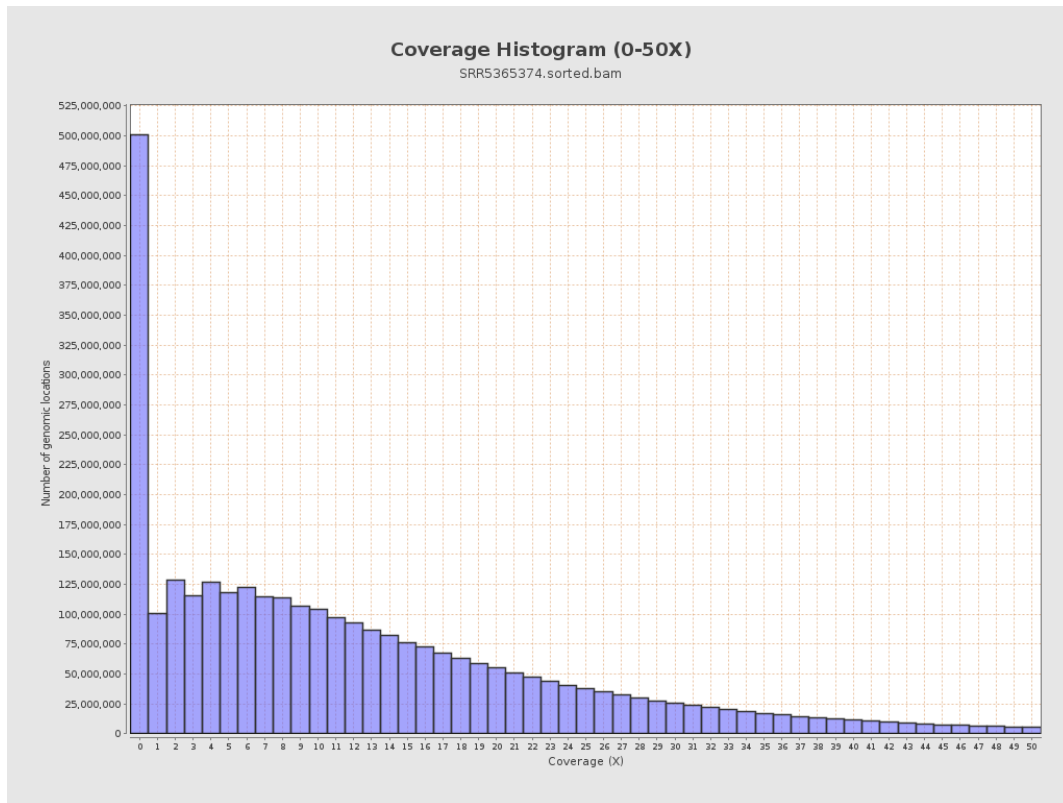
3. Results : Coverage across reference



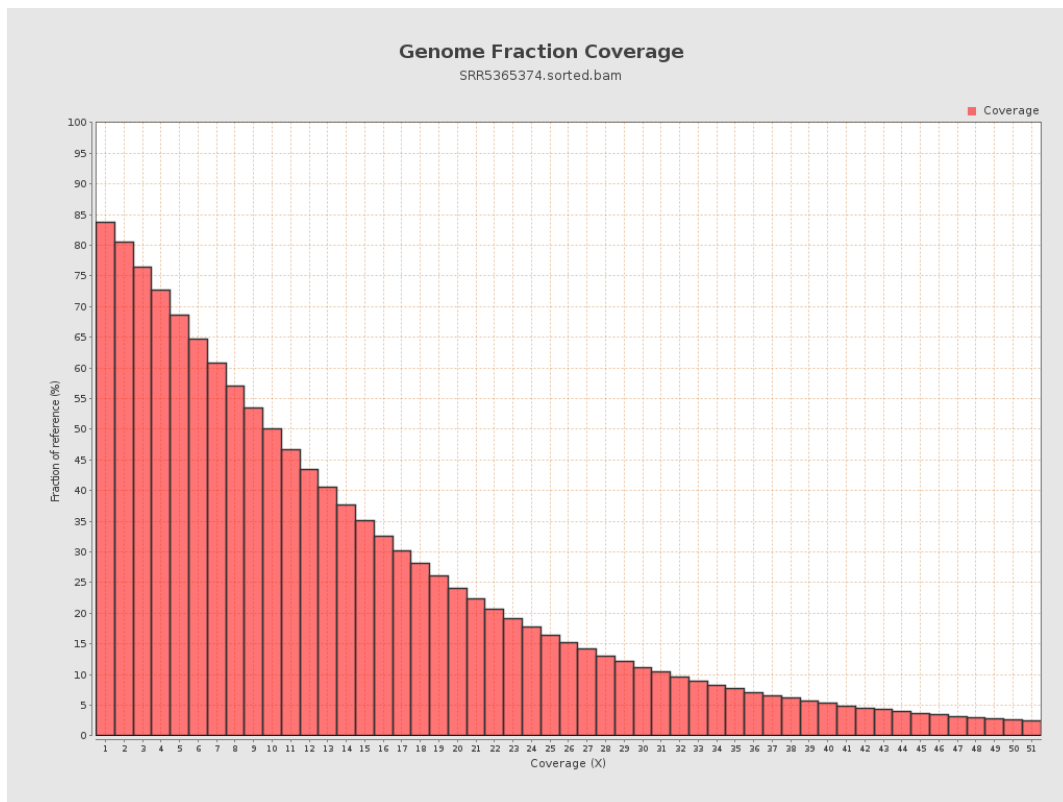
4. Results : Coverage Histogram



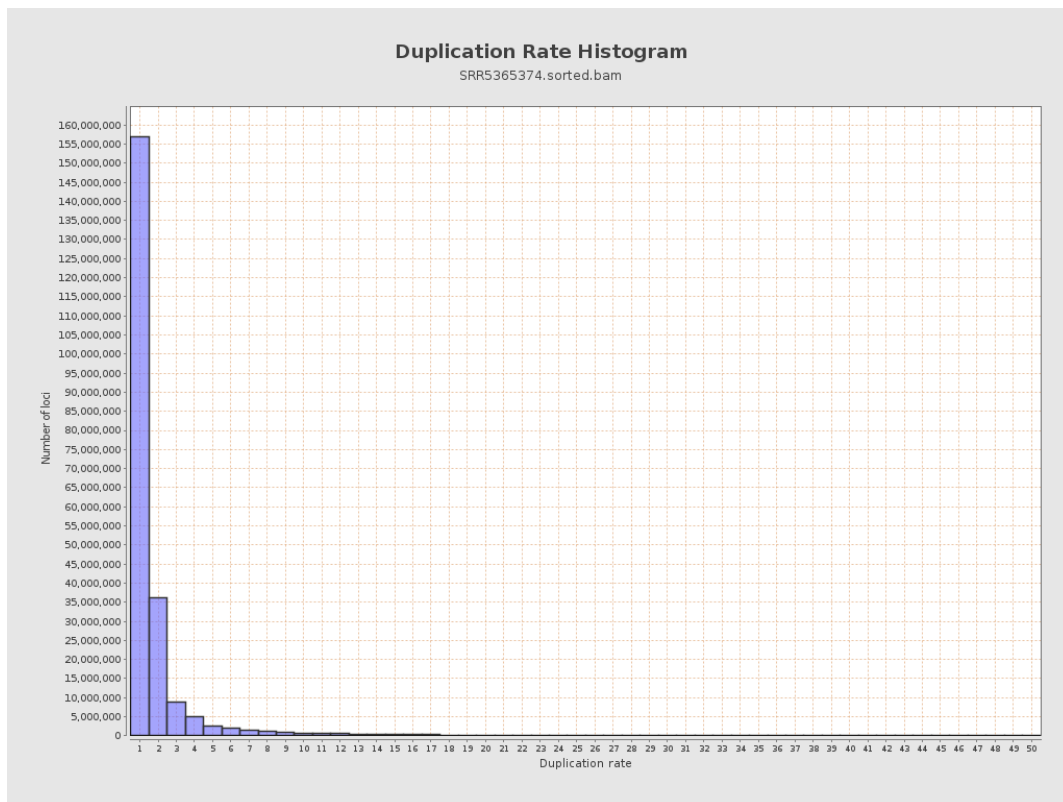
5. Results : Coverage Histogram (0-50X)



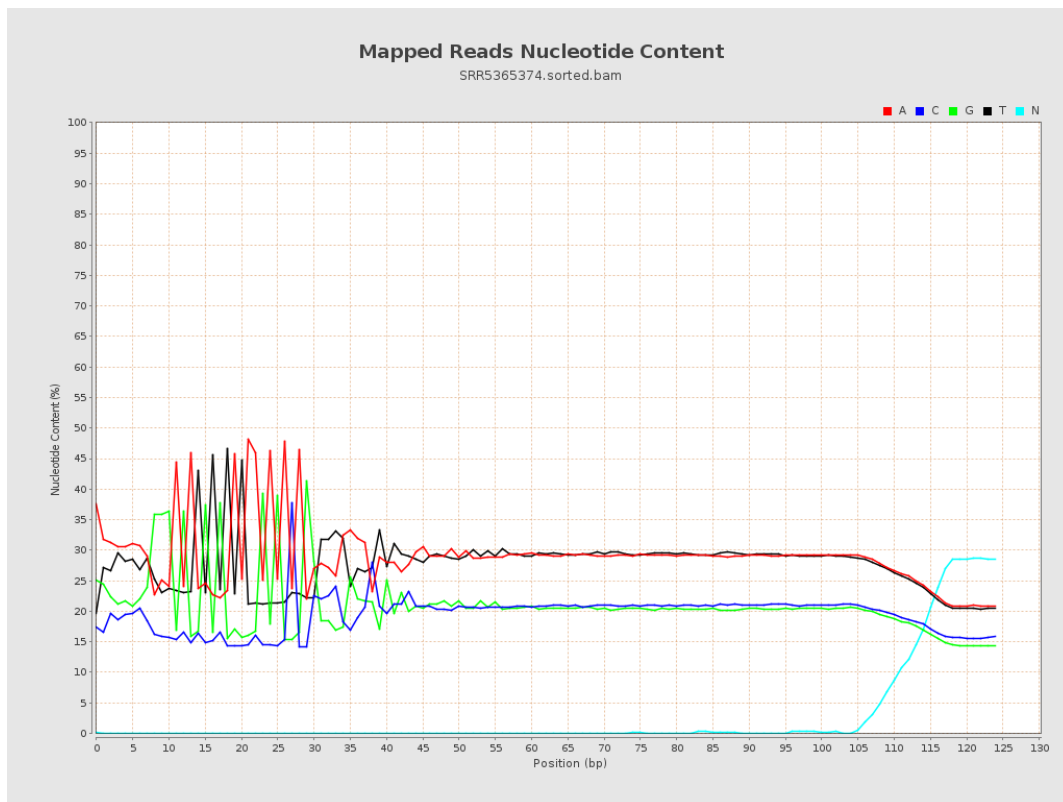
6. Results : Genome Fraction Coverage



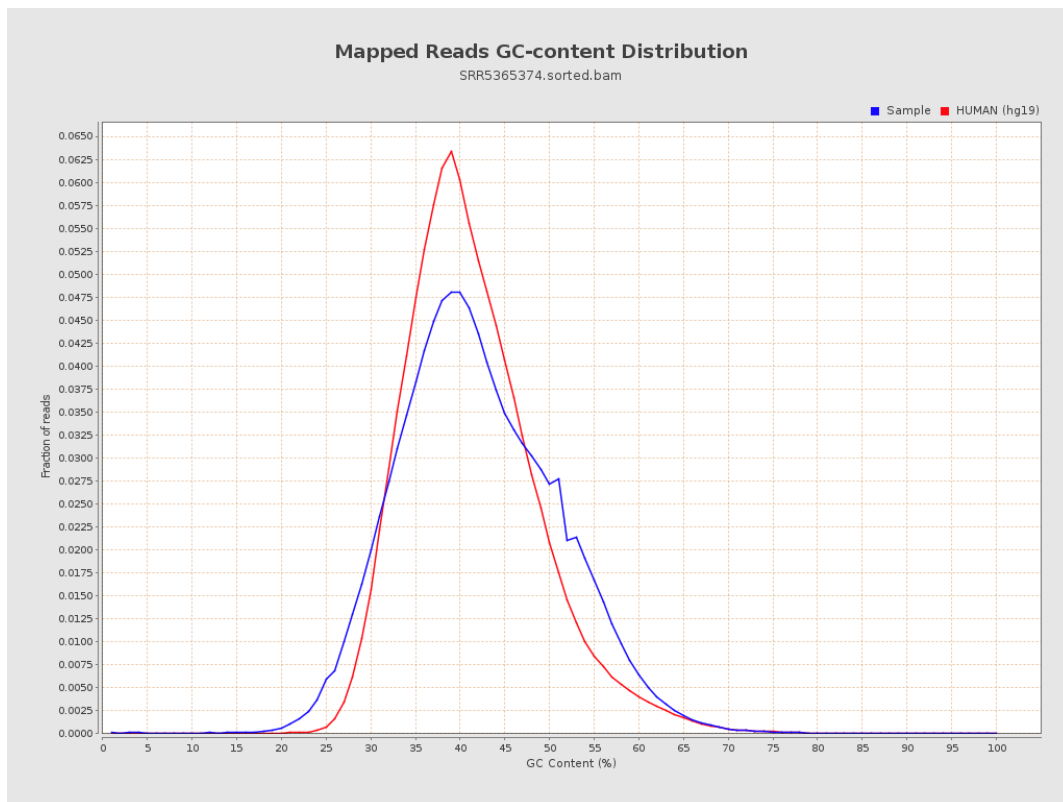
7. Results : Duplication Rate Histogram



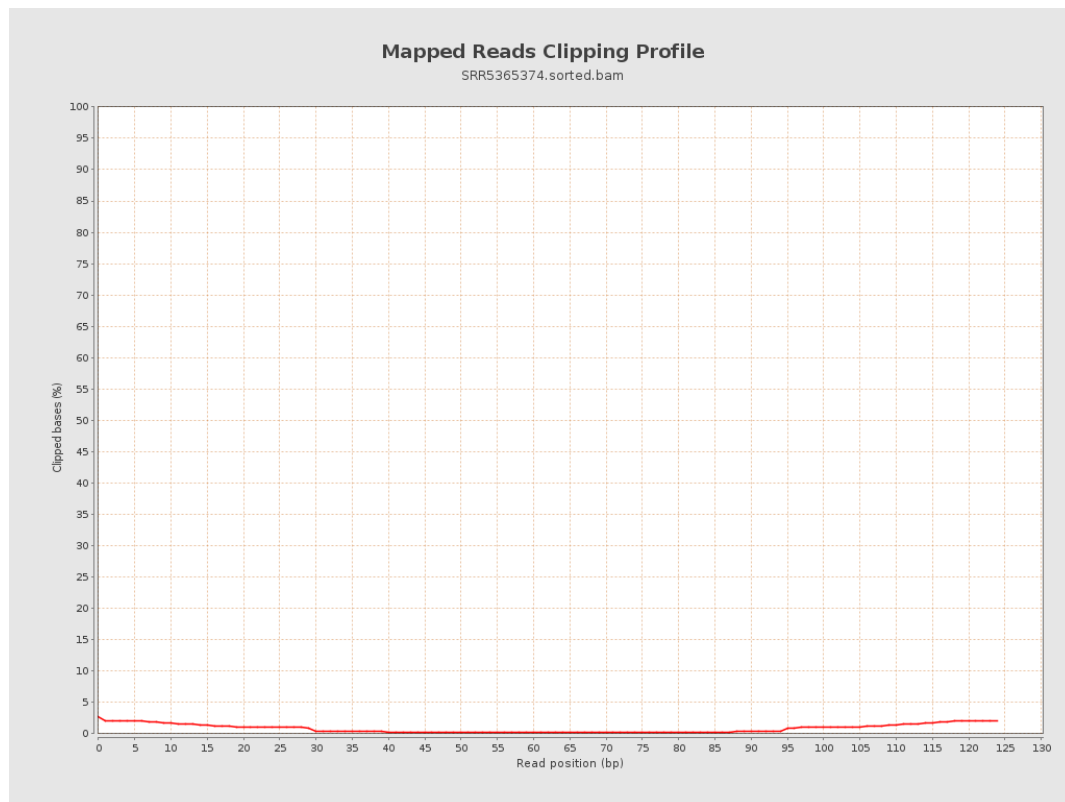
8. Results : Mapped Reads Nucleotide Content



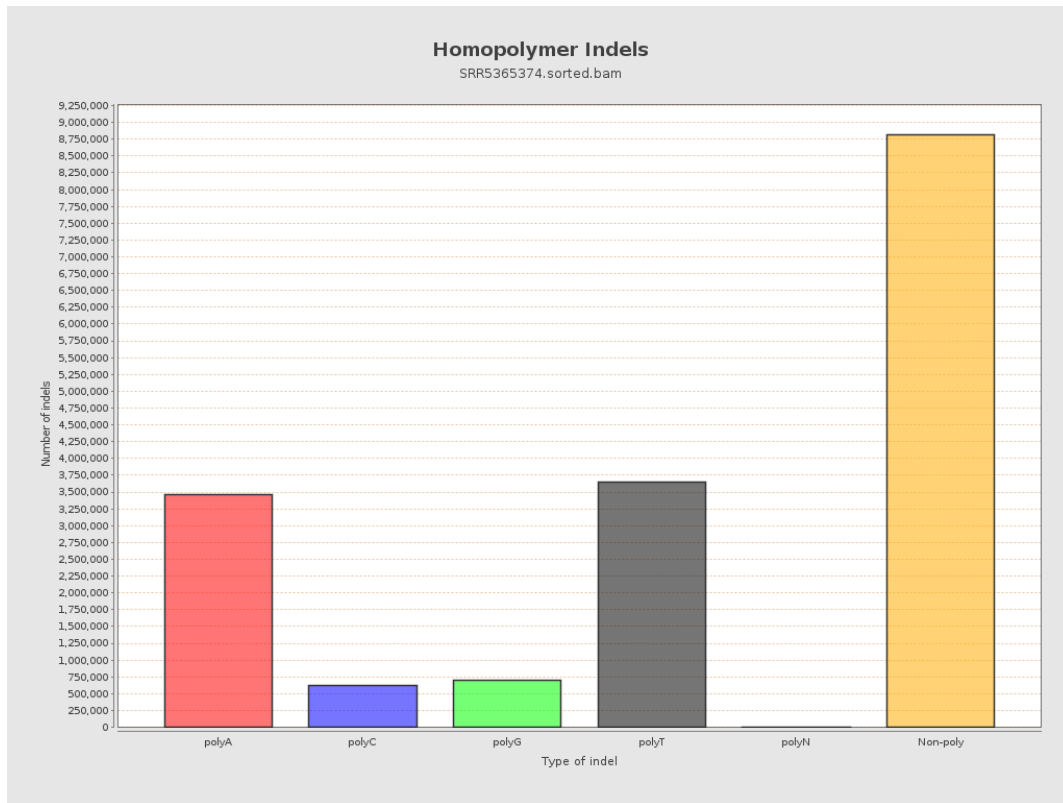
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



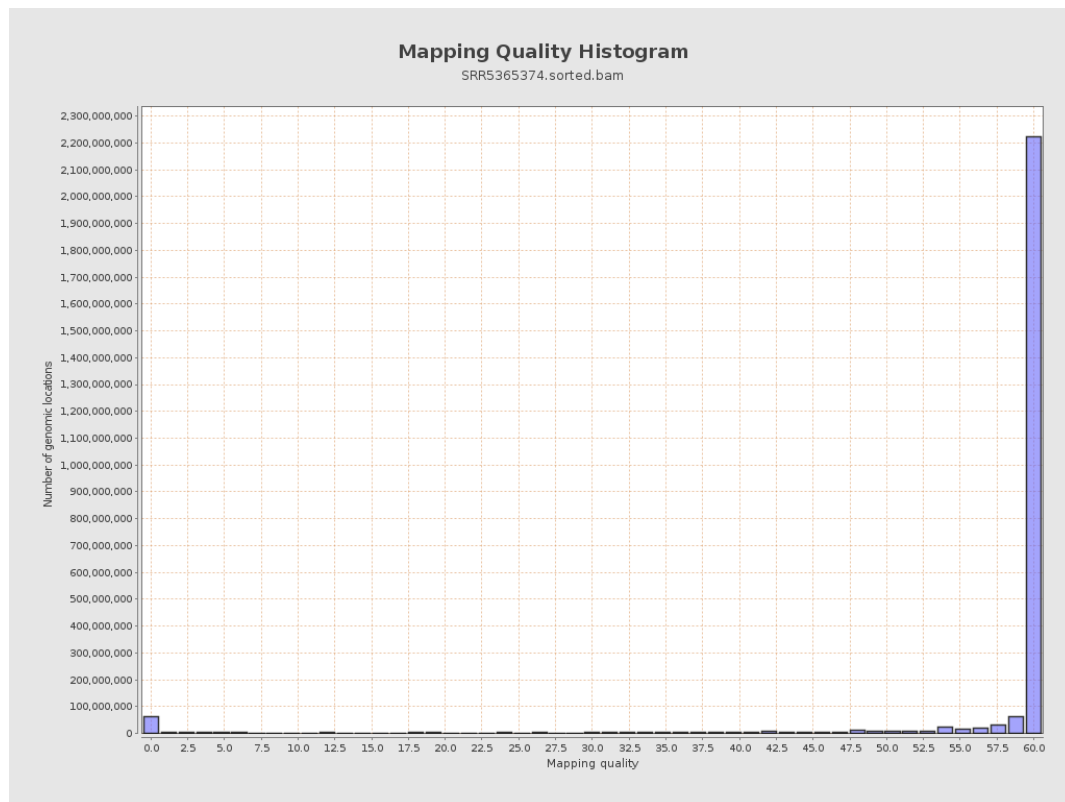
11. Results : Homopolymer Indels



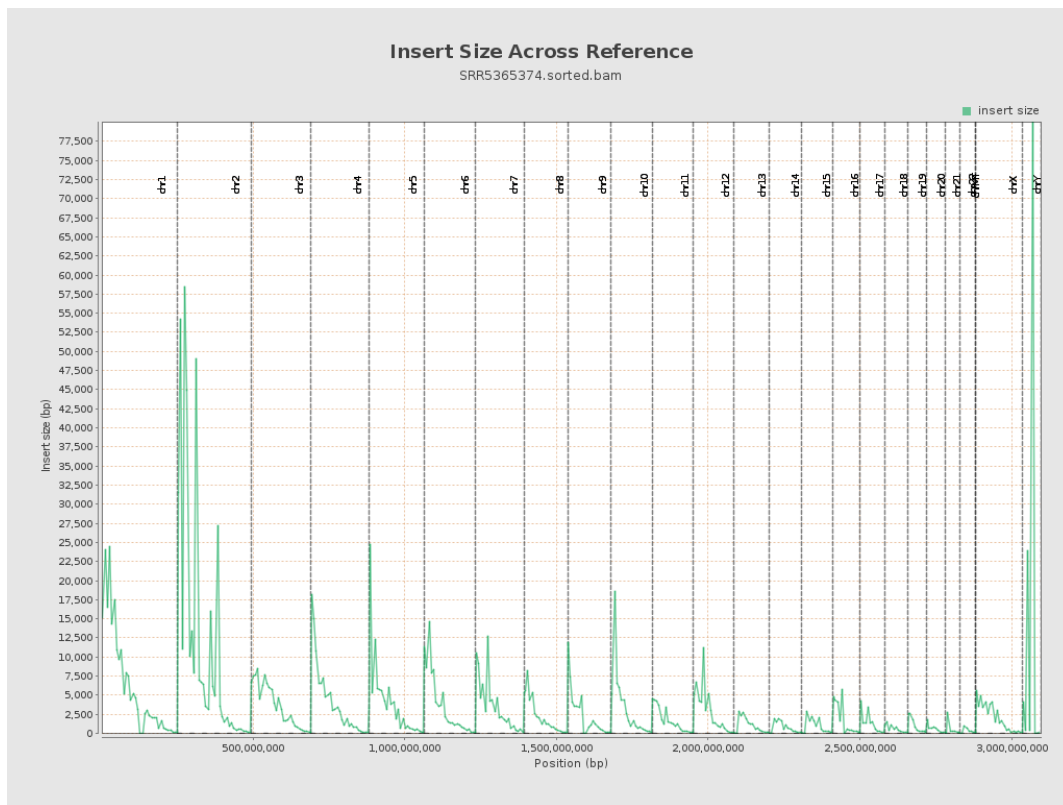
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

