Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/06 17:07:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365346.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_SRR5365346 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365346_1.fastq.gz SRR5365346_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Nov 06 17:07:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365346.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	535,286,226
Mapped reads	509,738,309 / 95.23%
Unmapped reads	25,547,917 / 4.77%
Mapped paired reads	509,738,309 / 95.23%
Mapped reads, first in pair	255,340,514 / 47.7%
Mapped reads, second in pair	254,397,795 / 47.53%
Mapped reads, both in pair	506,826,152 / 94.68%
Mapped reads, singletons	2,912,157 / 0.54%
Secondary alignments	0
Supplementary alignments	2,238,897 / 0.42%
Read min/max/mean length	30 / 125 / 125.17
Duplicated reads (estimated)	357,759,498 / 66.84%
Duplication rate	43.01%
Clipped reads	371,272,490 / 69.36%

2.2. ACGT Content

Number/percentage of A's	15,516,523,661 / 29.96%
Number/percentage of C's	10,130,201,690 / 19.56%
Number/percentage of T's	15,015,862,678 / 28.99%
Number/percentage of G's	11,104,943,532 / 21.44%
Number/percentage of N's	20,556,661 / 0.04%

GC Percentage	41%

2.3. Coverage

Mean	16.7346
Standard Deviation	137.5103

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	80,711.8
Standard Deviation	2,760,225.91
P25/Median/P75	123 / 191 / 294

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	300,592,188
Insertions	15,731,460
Mapped reads with at least one insertion	3.02%
Deletions	8,194,453
Mapped reads with at least one deletion	1.57%
Homopolymer indels	50.02%

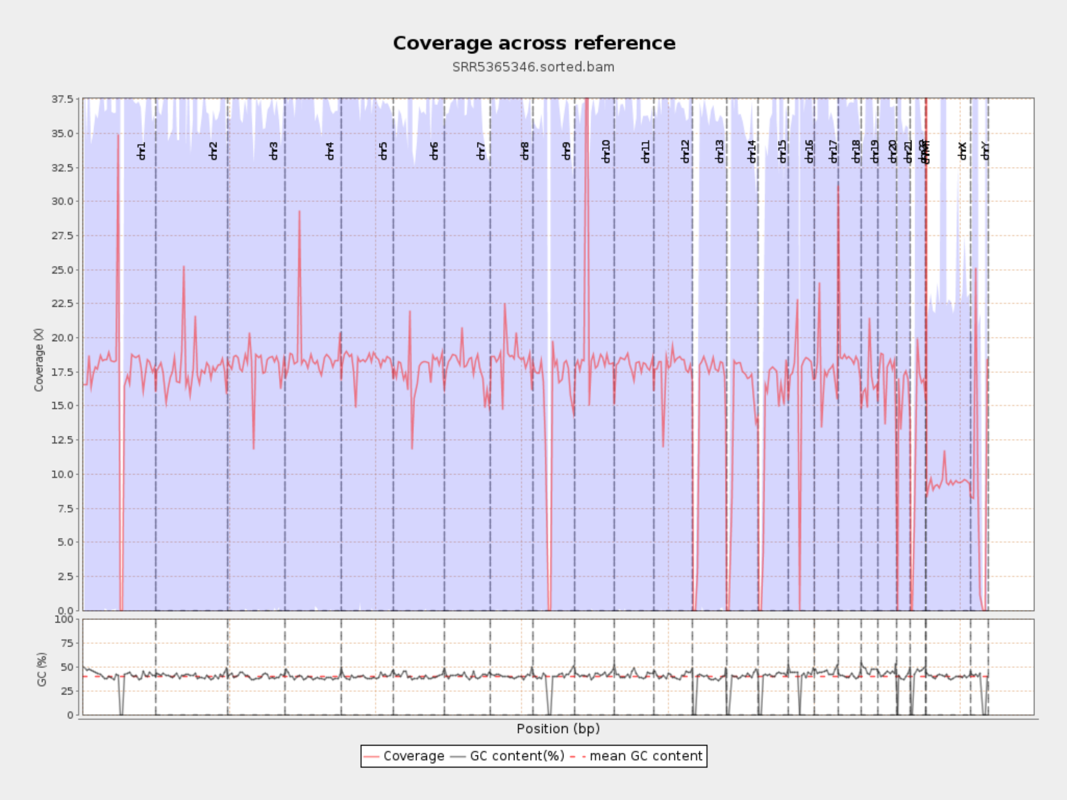
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

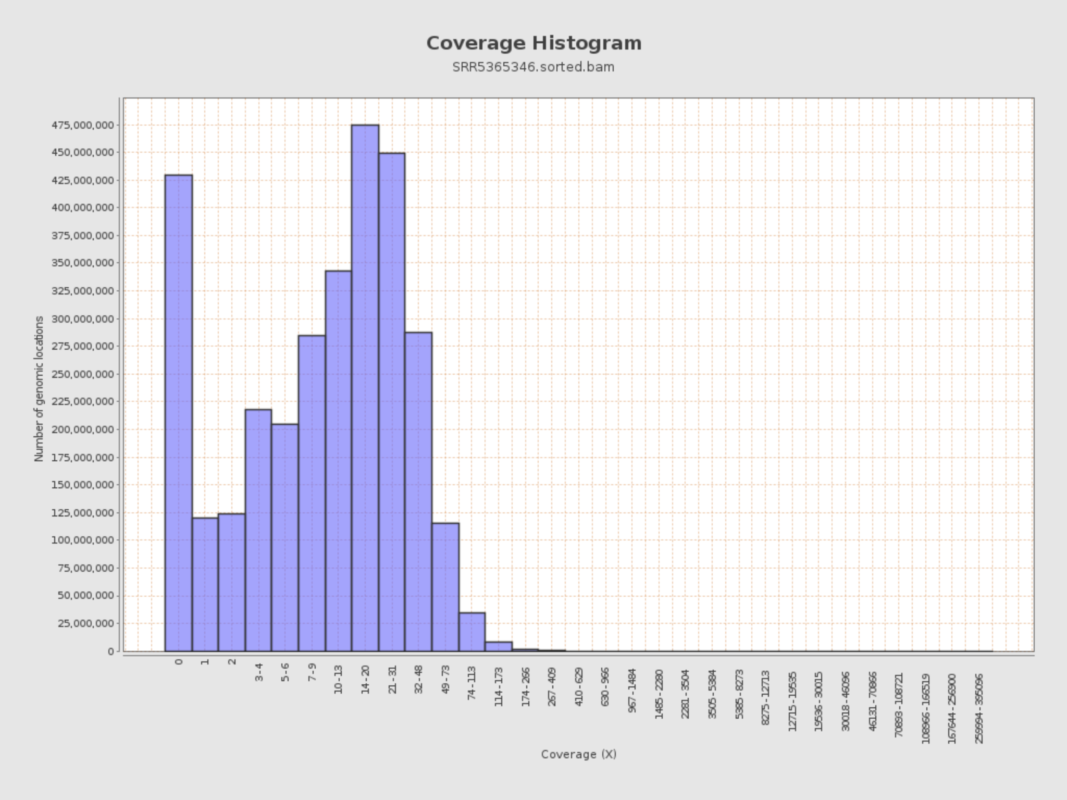
		bases	coverage	deviation
chr1	249250621	4296787386	17.2388	370.8911
chr2	243199373	4320634253	17.7658	83.7293
chr3	198022430	3570494120	18.0308	23.3854
chr4	191154276	3582104755	18.7393	96.6885
chr5	180915260	3299585879	18.2383	20.6565
chr6	171115067	3016764877	17.63	68.1769
chr7	159138663	2834957285	17.8144	99.1828
chr8	146364022	2712223579	18.5307	47.0873
chr9	141213431	2153932135	15.253	111.8757
chr10	135534747	2676945401	19.751	230.2017
chr11	135006516	2428745606	17.9898	87.4335
chr12	133851895	2382744063	17.8013	37.0927
chr13	115169878	1718806807	14.9241	17.6846
chr14	107349540	1535580518	14.3045	19.7425
chr15	102531392	1388482552	13.542	23.245
chr16	90354753	1506656908	16.6749	48.0842
chr17	81195210	1433036138	17.6493	89.1069
chr18	78077248	1480811403	18.966	159.9479
chr19	59128983	992588041	16.7868	186.6139
chr20	63025520	1102758530	17.497	30.7936
chr21	48129895	703005172	14.6064	59.1391
chr22	51304566	628384871	12.2481	48.0377
chrMT	16571	53318794	3,217.5966	582.1572
chrX	155270560	1460151753	9.4039	35.201

chrY	59373566	525823988	8.8562	180.8879

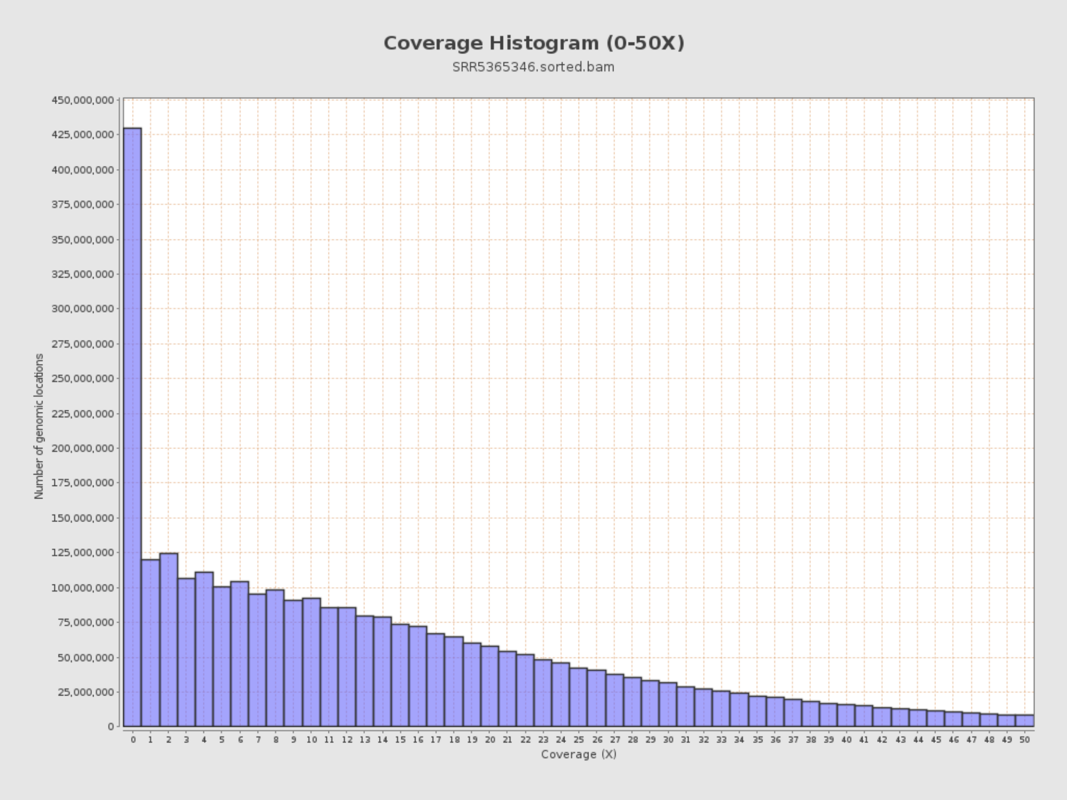
3. Results : Coverage across reference



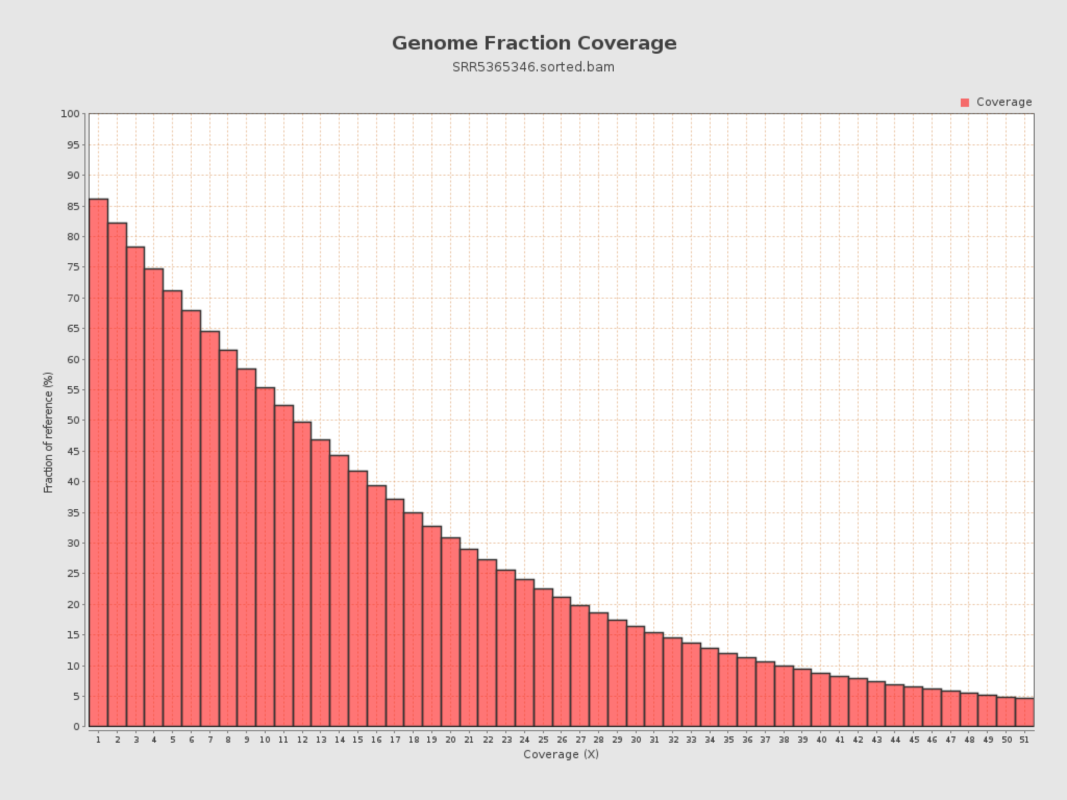
4. Results : Coverage Histogram



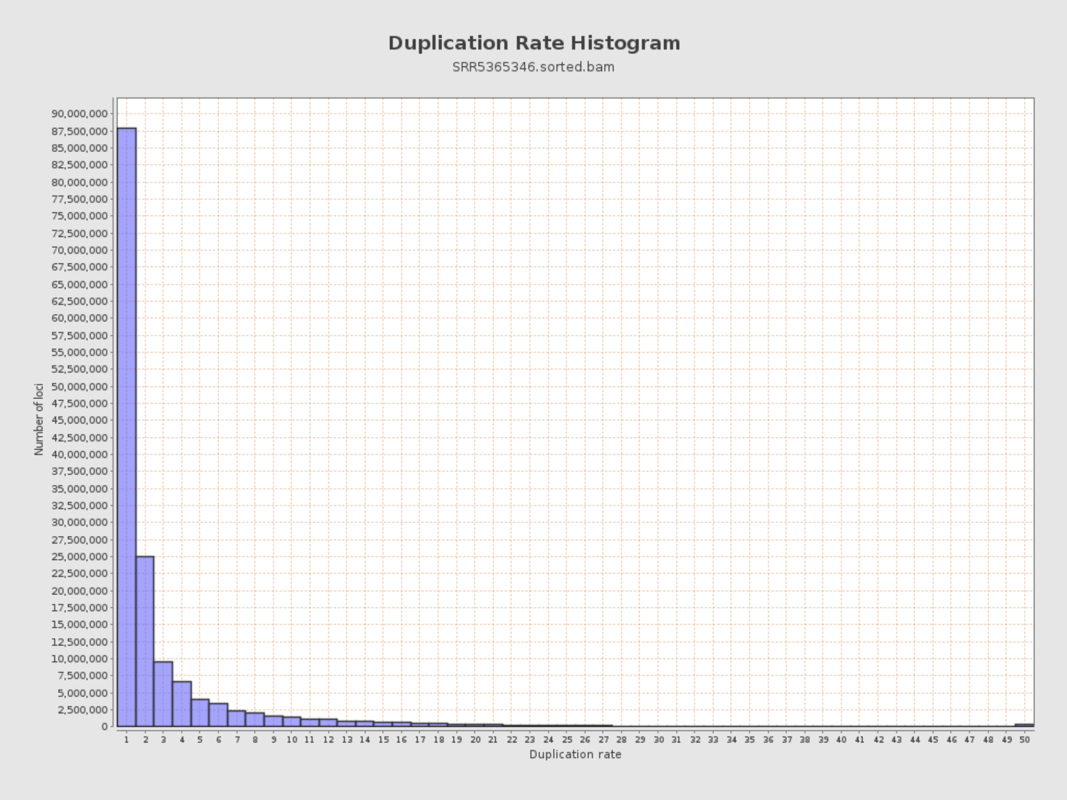
5. Results : Coverage Histogram (0-50X)



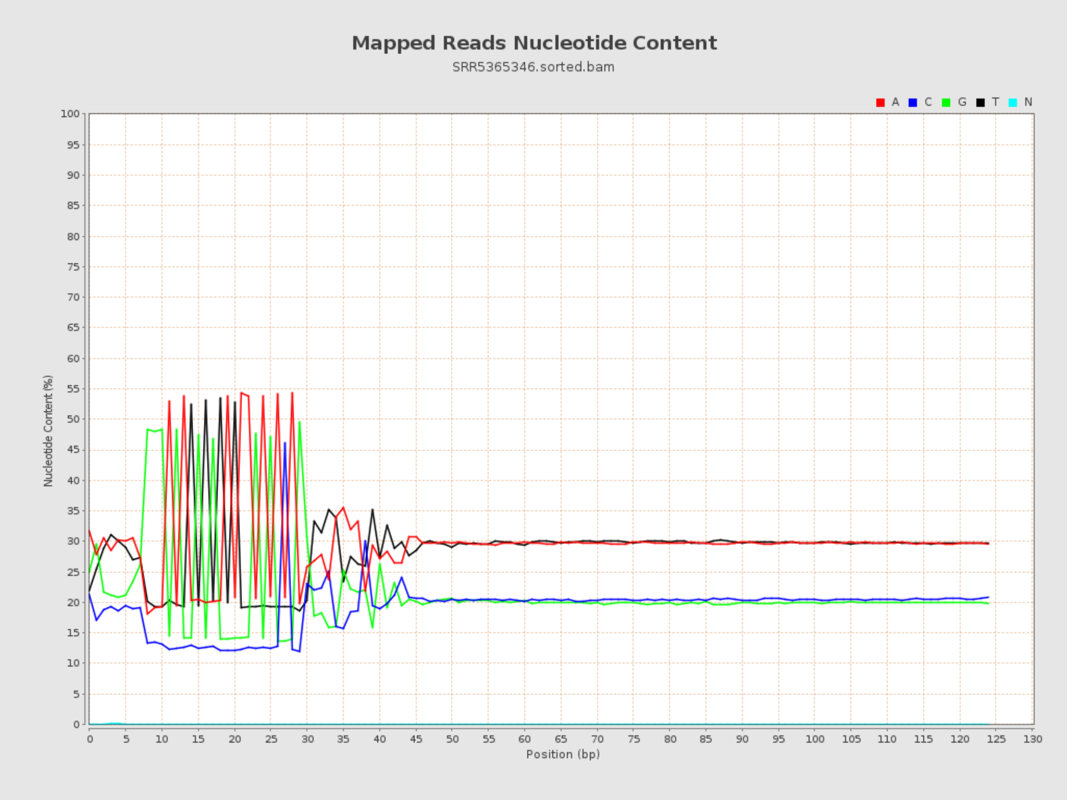
6. Results : Genome Fraction Coverage



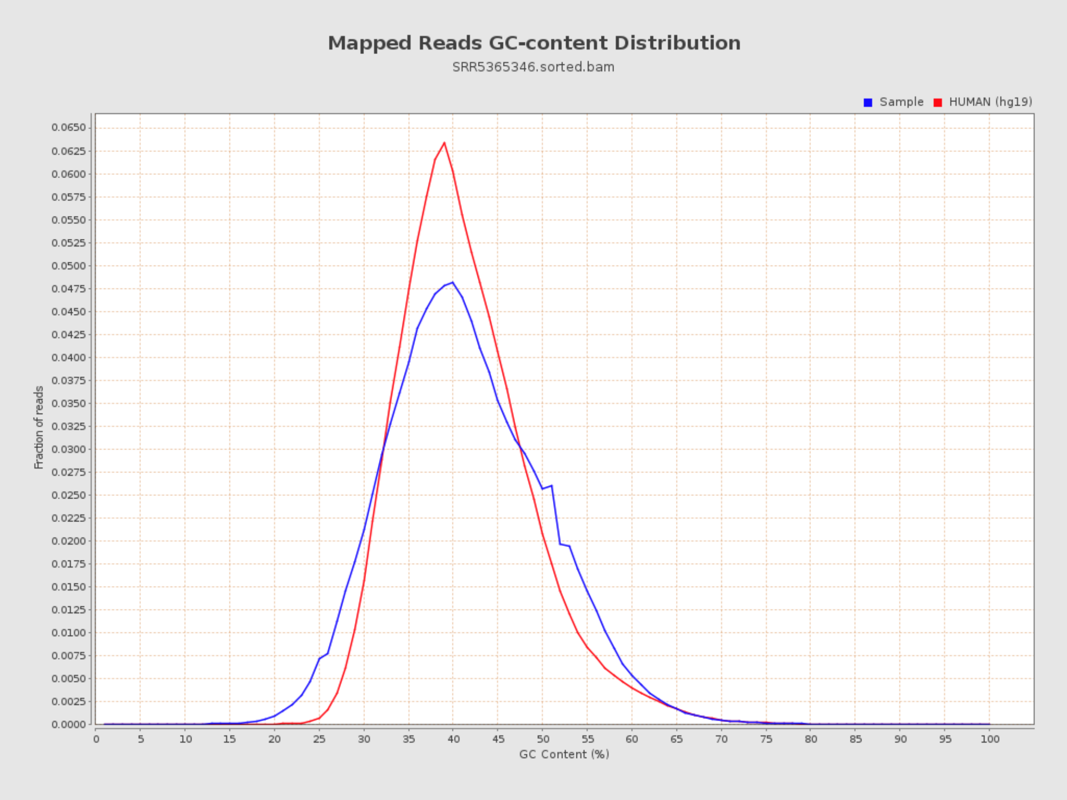
7. Results : Duplication Rate Histogram



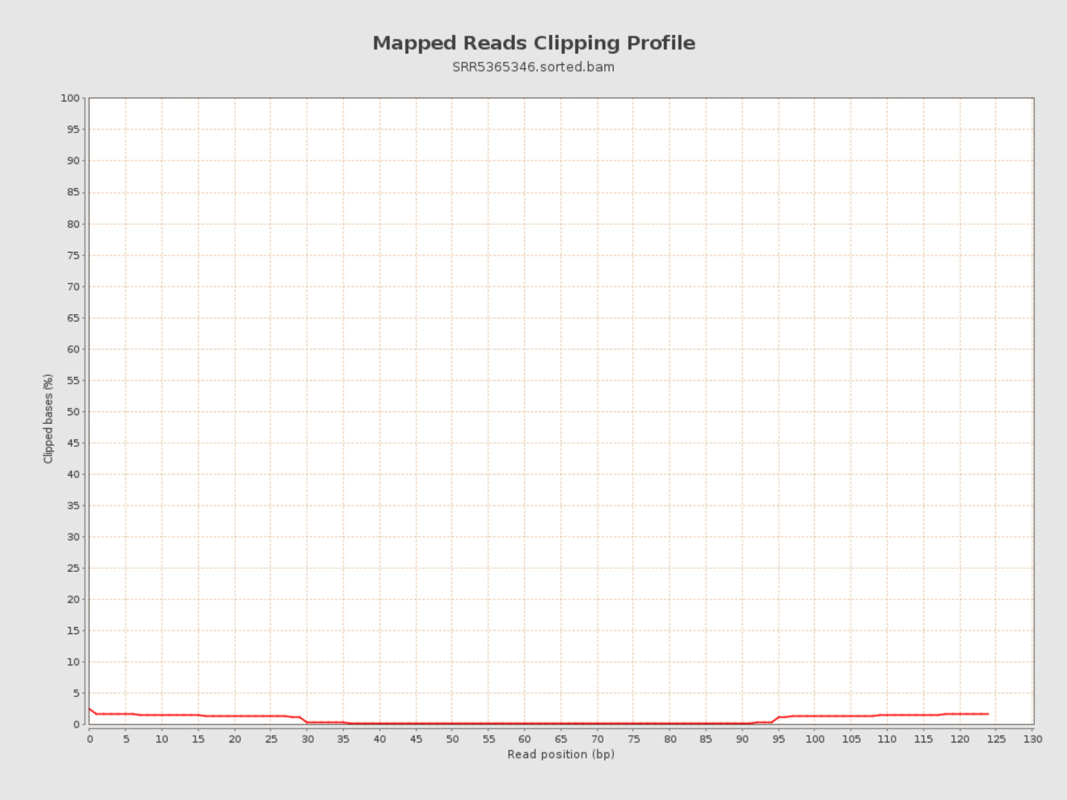
8. Results : Mapped Reads Nucleotide Content



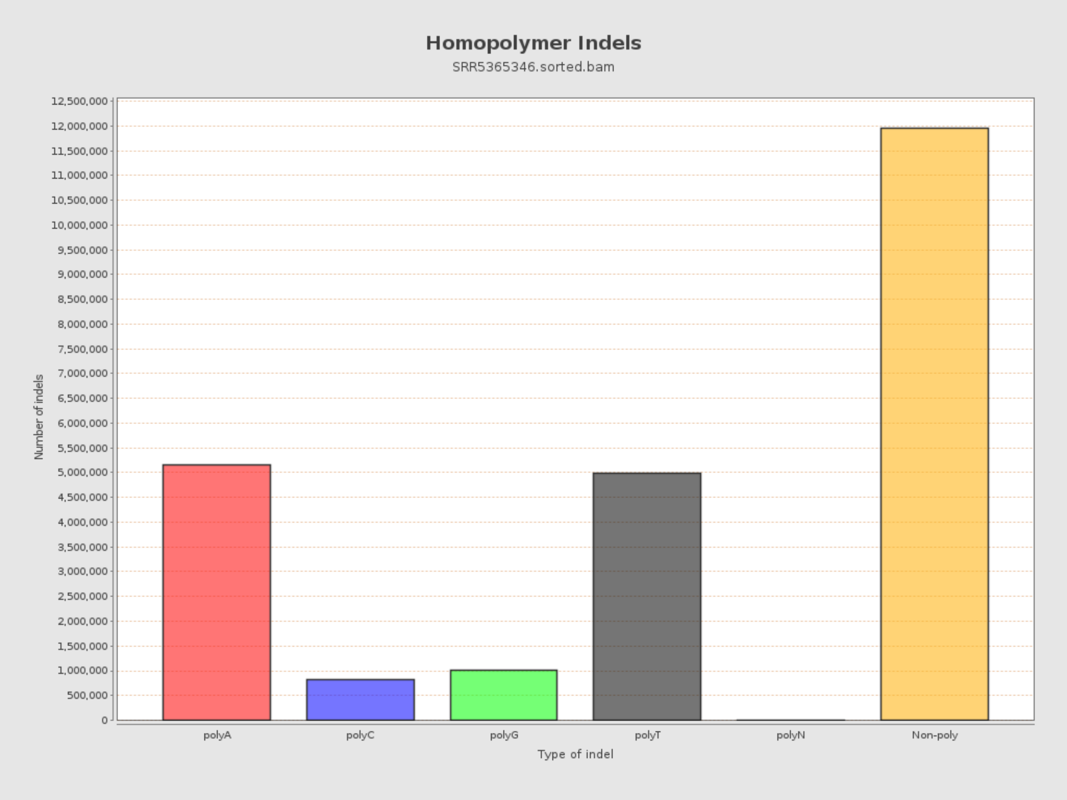
9. Results : Mapped Reads GC-content Distribution



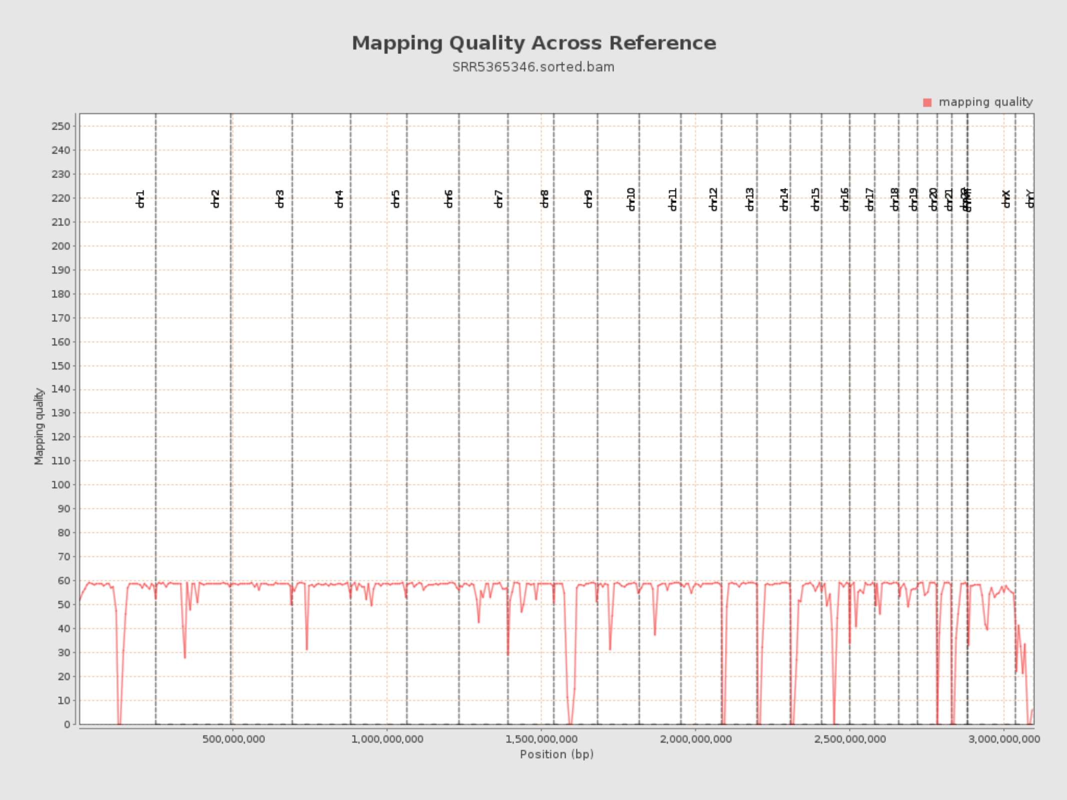
10. Results : Mapped Reads Clipping Profile



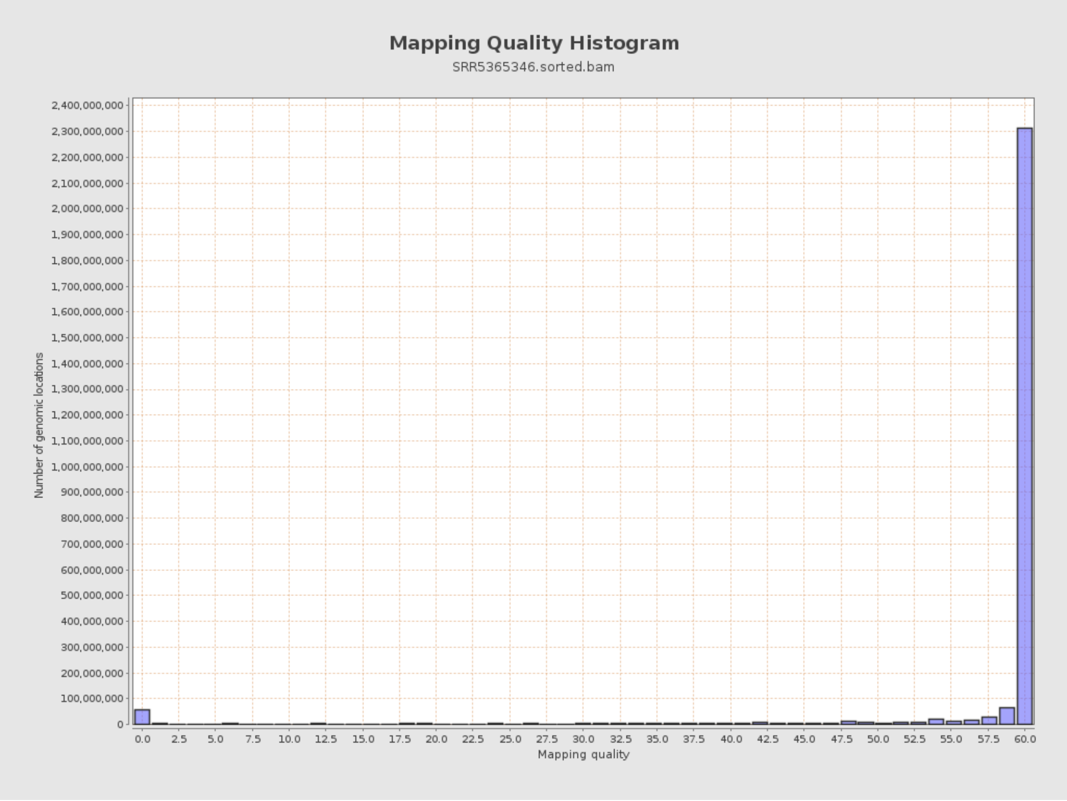
11. Results : Homopolymer Indels



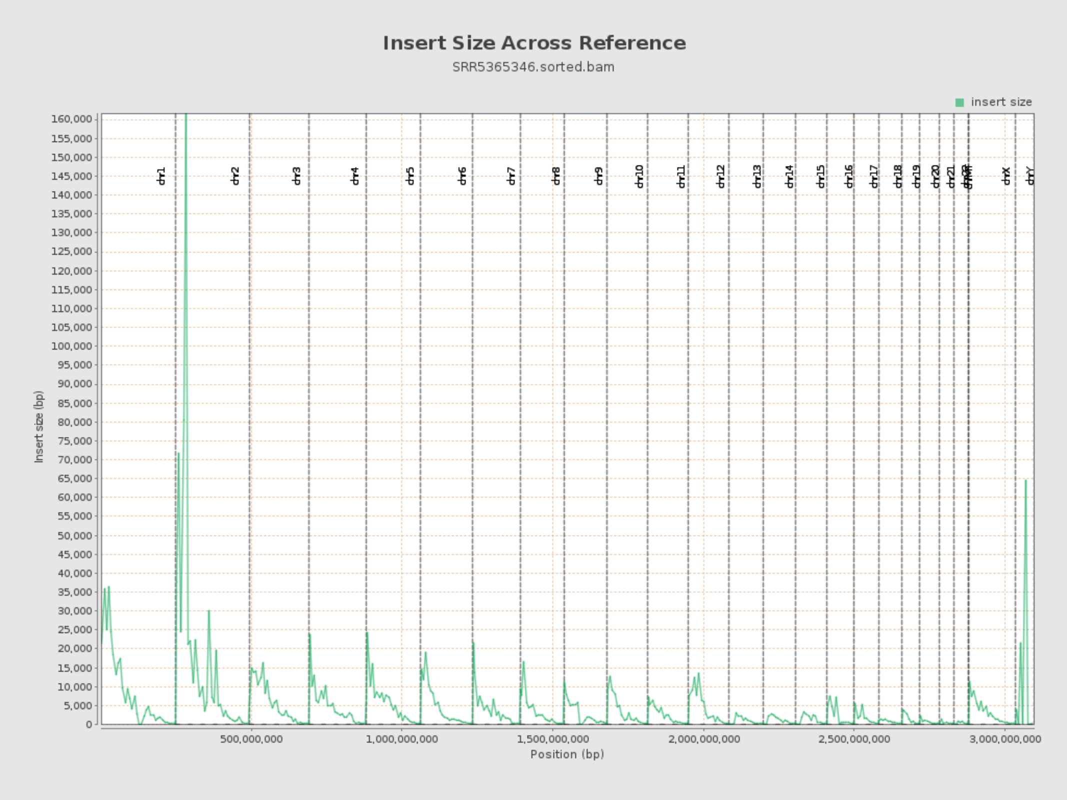
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram