Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/08 17:44:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365353.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_SRR5365353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365353_1.fastq.gz SRR5365353_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Nov 08 17:44:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	556,620,444
Mapped reads	537,586,567 / 96.58%
Unmapped reads	19,033,877 / 3.42%
Mapped paired reads	537,586,567 / 96.58%
Mapped reads, first in pair	269,306,503 / 48.38%
Mapped reads, second in pair	268,280,064 / 48.2%
Mapped reads, both in pair	535,231,272 / 96.16%
Mapped reads, singletons	2,355,295 / 0.42%
Secondary alignments	0
Supplementary alignments	2,378,614 / 0.43%
Read min/max/mean length	30 / 125 / 125.18
Duplicated reads (estimated)	328,396,002 / 59%
Duplication rate	31.98%
Clipped reads	344,584,227 / 61.91%

2.2. ACGT Content

Number/percentage of A's	16,670,234,606 / 29.78%
Number/percentage of C's	11,143,411,134 / 19.91%
Number/percentage of T's	16,191,102,822 / 28.92%
Number/percentage of G's	11,971,106,012 / 21.38%
Number/percentage of N's	6,541,789 / 0.01%

GC Percentage	41.29%

2.3. Coverage

Mean	18.0899
Standard Deviation	160.1927

2.4. Mapping Quality

Mean Mapping Quality	53.85

2.5. Insert size

Mean	56,821.09
Standard Deviation	2,341,332.2
P25/Median/P75	113 / 161 / 229

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	274,127,294
Insertions	16,062,270
Mapped reads with at least one insertion	2.92%
Deletions	8,796,880
Mapped reads with at least one deletion	1.6%
Homopolymer indels	50.42%

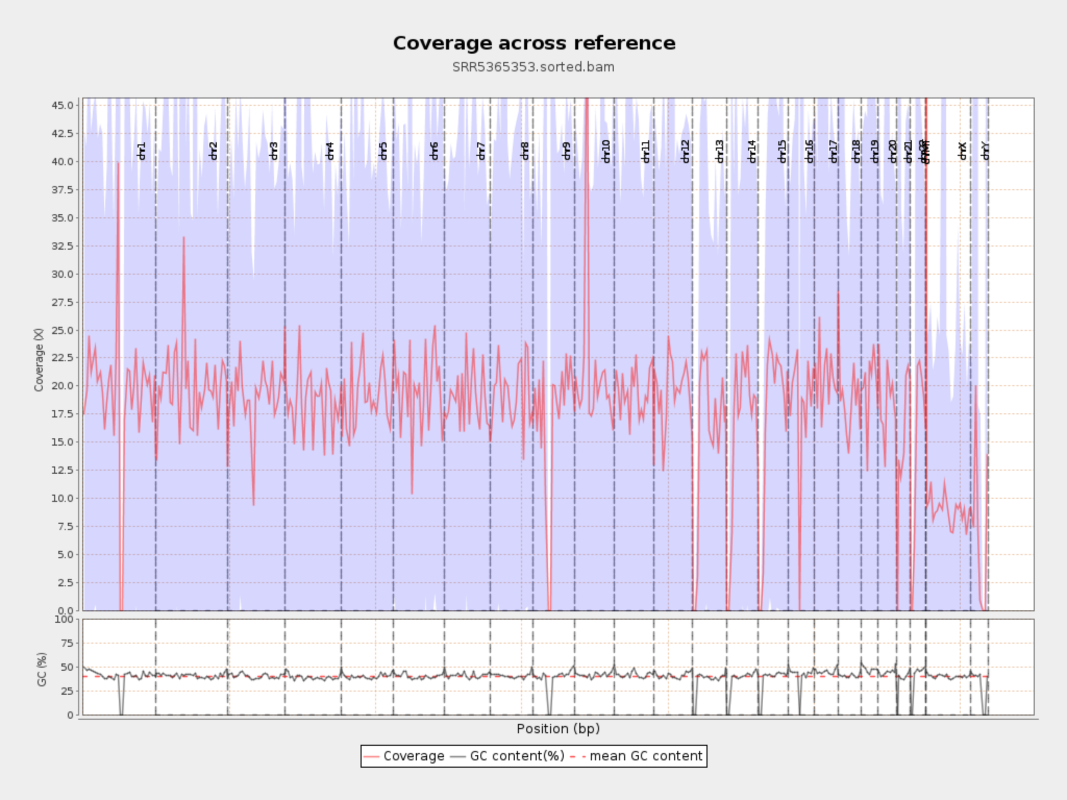
2.7. Chromosome stats

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

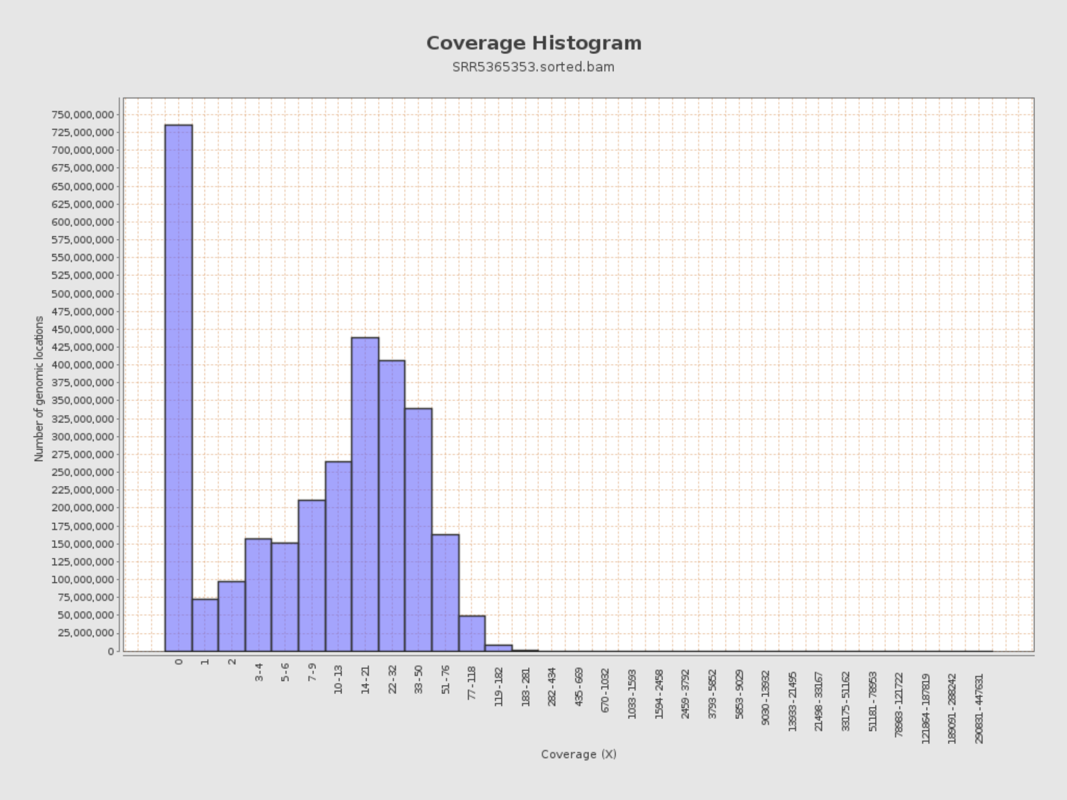
		bases	coverage	deviation
chr1	249250621	4841113330	19.4227	432.2276
chr2	243199373	4916946946	20.2178	104.549
chr3	198022430	3765831668	19.0172	30.8057
chr4	191154276	3550444732	18.5737	80.1838
chr5	180915260	3458111908	19.1145	23.0881
chr6	171115067	3347789950	19.5646	55.6106
chr7	159138663	3017482085	18.9613	115.9553
chr8	146364022	2824669988	19.2989	48.3208
chr9	141213431	2379511333	16.8505	136.7079
chr10	135534747	2912771016	21.491	321.0196
chr11	135006516	2626355644	19.4535	90.3697
chr12	133851895	2647981614	19.7829	37.3752
chr13	115169878	1784209406	15.492	20.0695
chr14	107349540	1758398357	16.3801	24.2337
chr15	102531392	1687090494	16.4544	25.6762
chr16	90354753	1630491447	18.0454	56.1704
chr17	81195210	1695521862	20.882	72.1637
chr18	78077248	1465073912	18.7644	157.8118
chr19	59128983	1183076042	20.0084	221.4068
chr20	63025520	1163447293	18.4599	31.395
chr21	48129895	736510641	15.3026	51.3331
chr22	51304566	725280618	14.1368	41.0251
chrMT	16571	61740612	3,725.8229	705.9983
chrX	155270560	1390708431	8.9567	36.4237

chrY	59373566	430358131	7.2483	149.3057

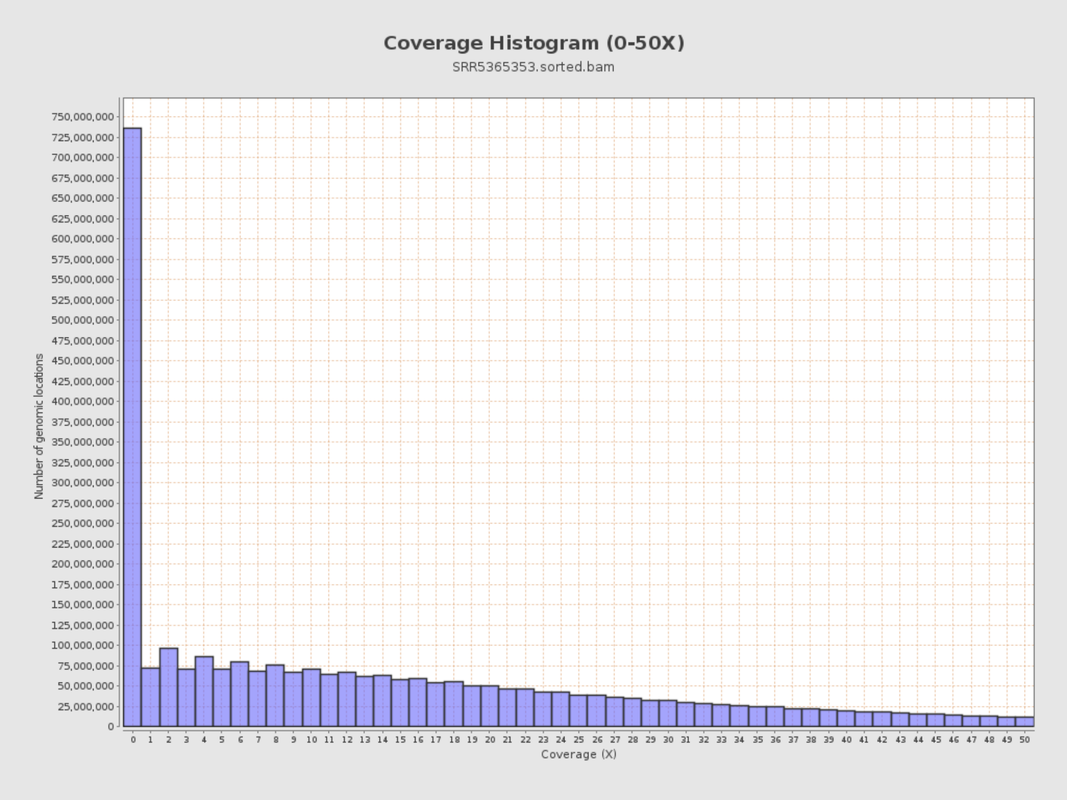
3. Results : Coverage across reference



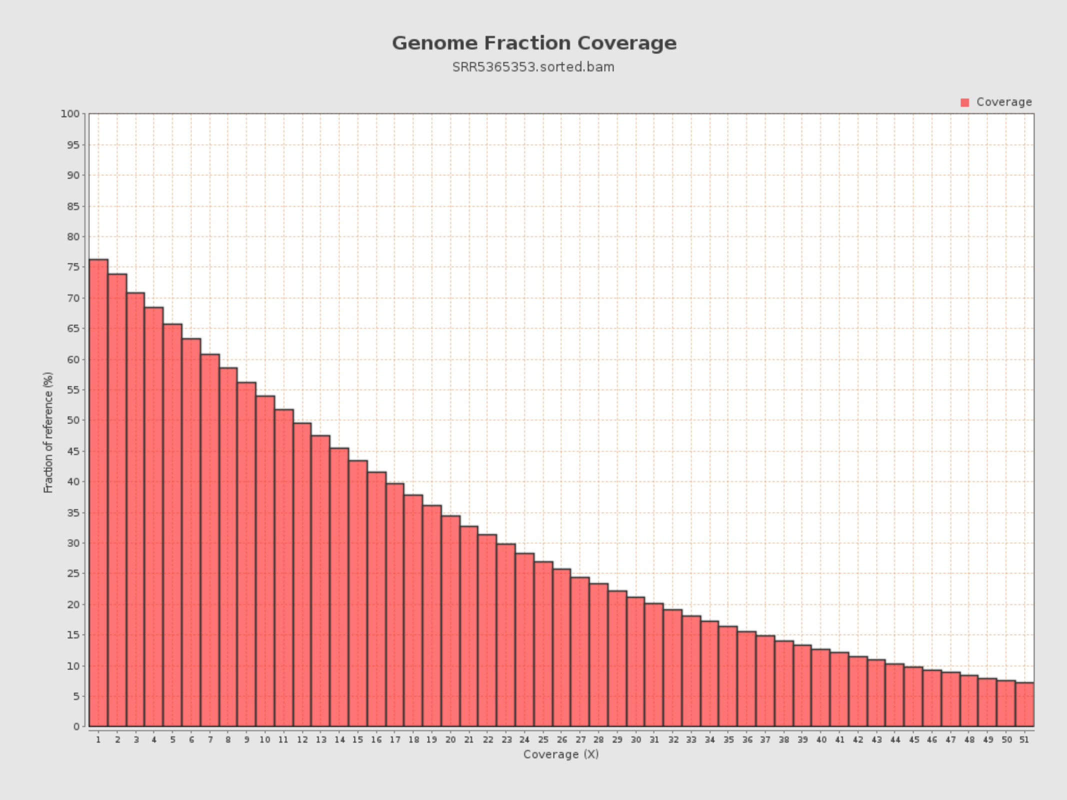
4. Results : Coverage Histogram



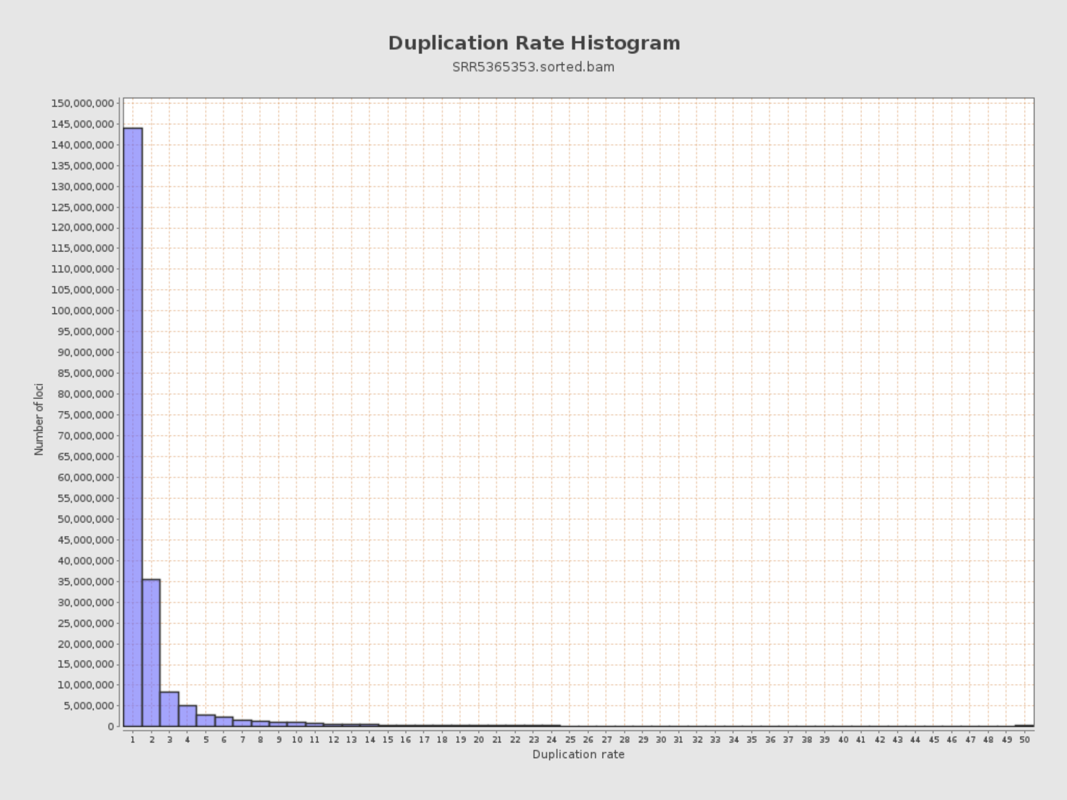
5. Results : Coverage Histogram (0-50X)



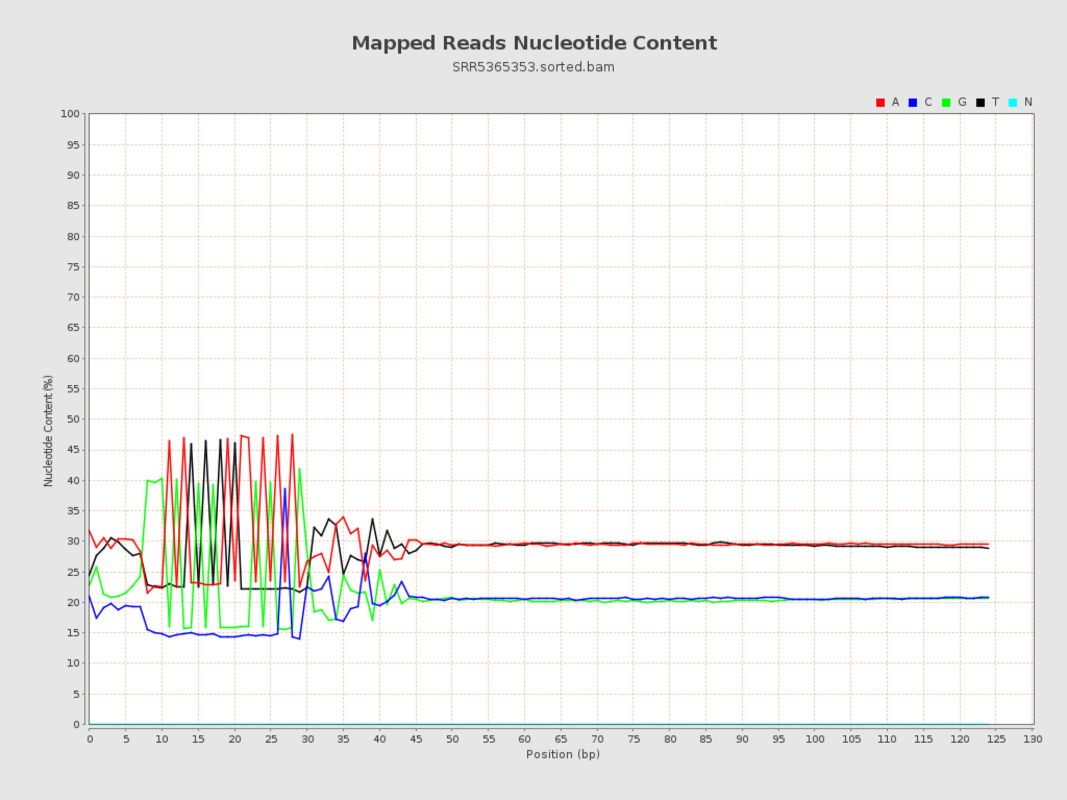
6. Results : Genome Fraction Coverage



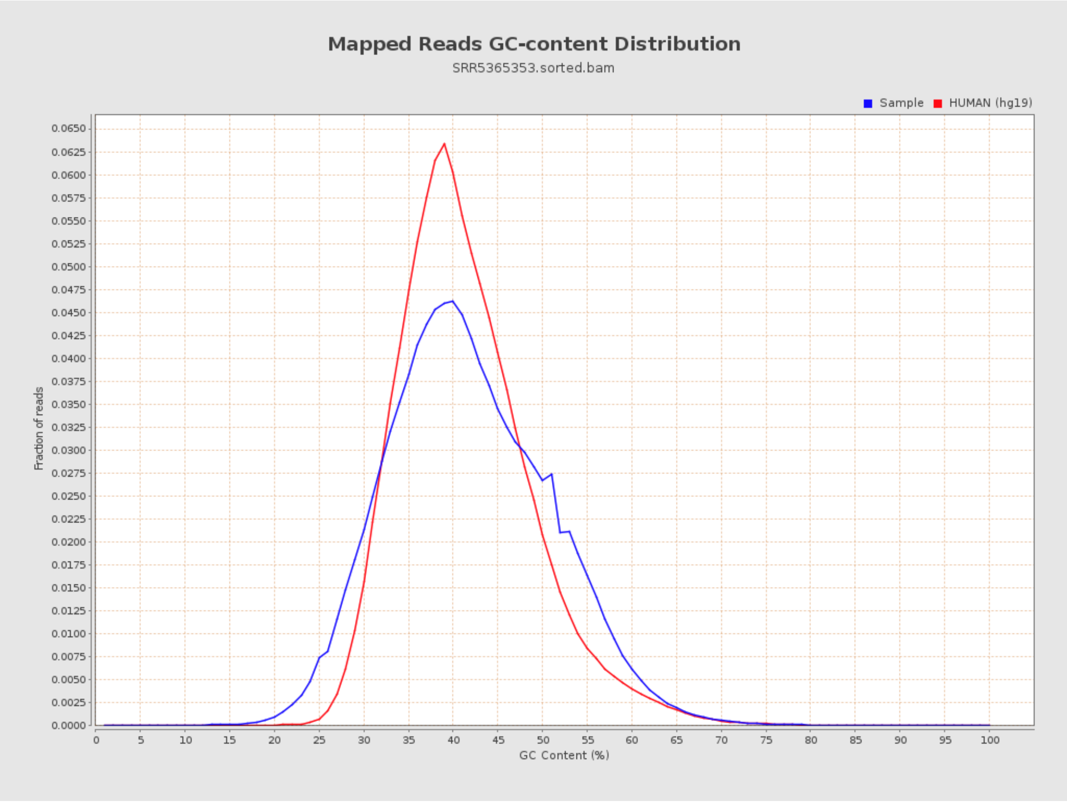
7. Results : Duplication Rate Histogram



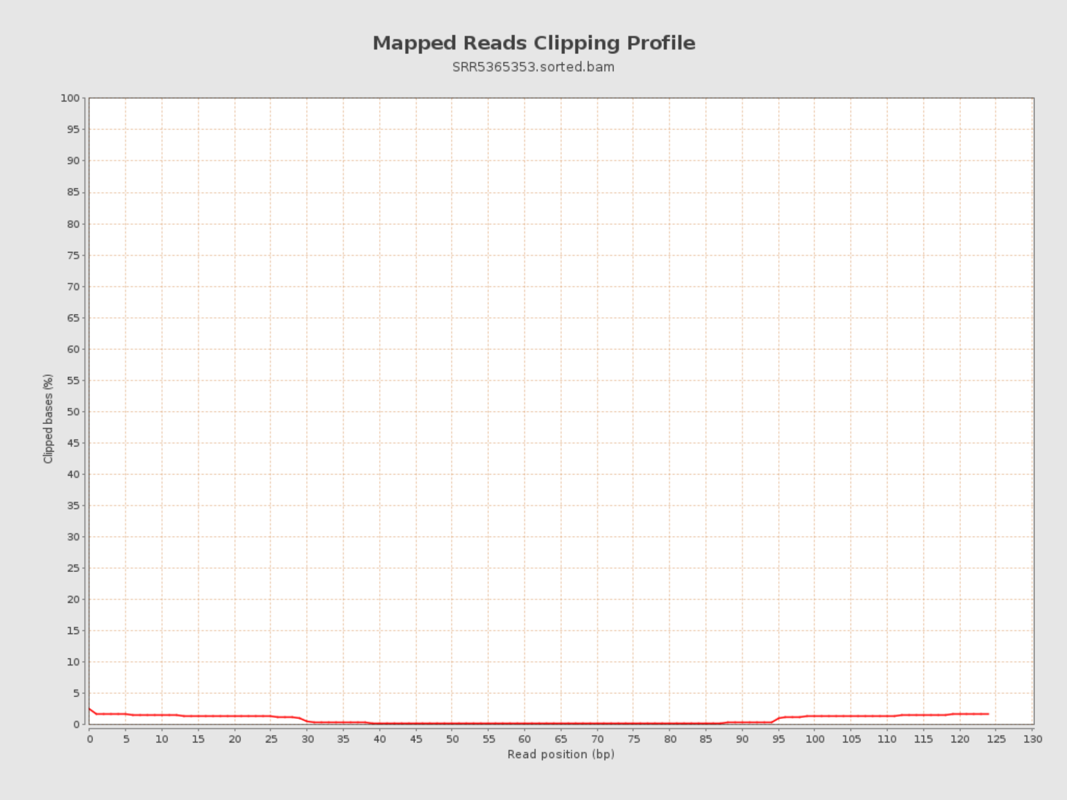
8. Results : Mapped Reads Nucleotide Content



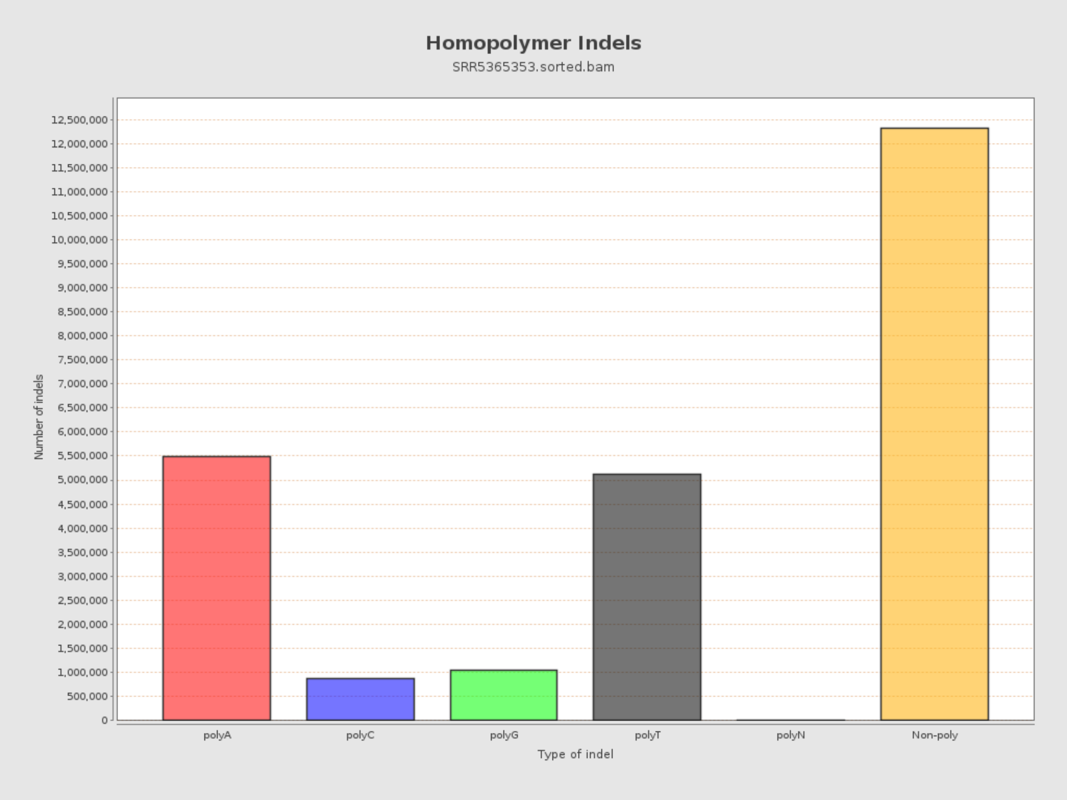
9. Results : Mapped Reads GC-content Distribution



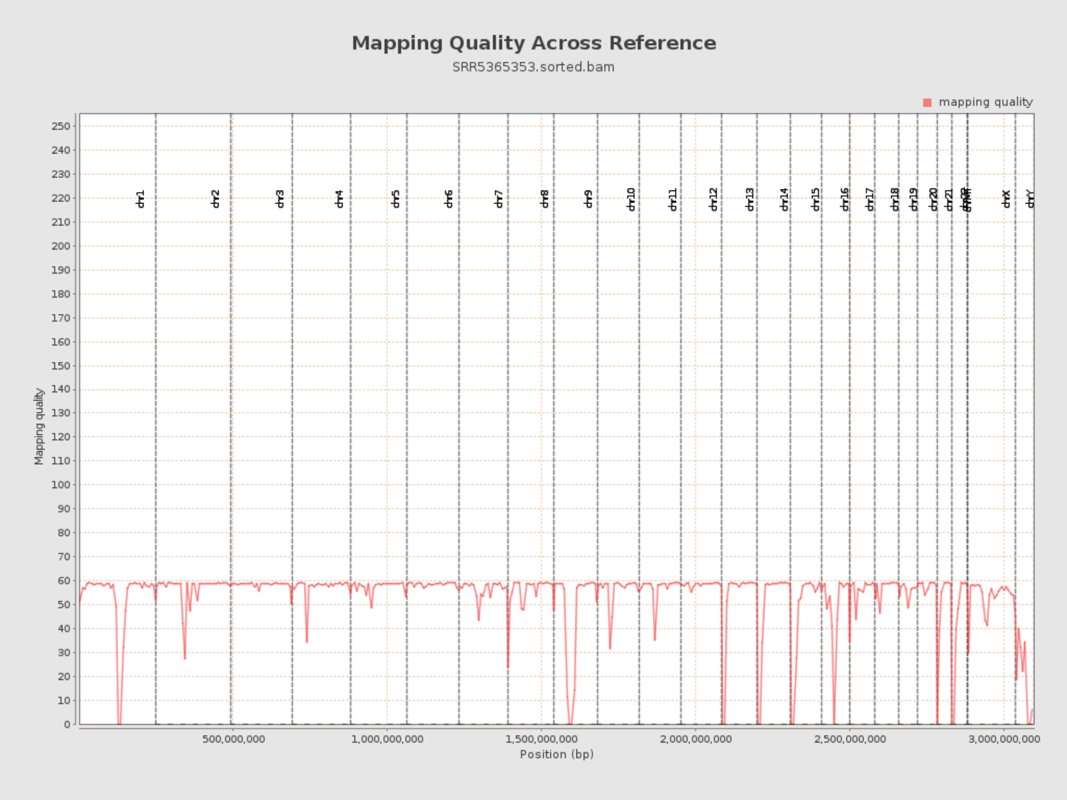
10. Results : Mapped Reads Clipping Profile



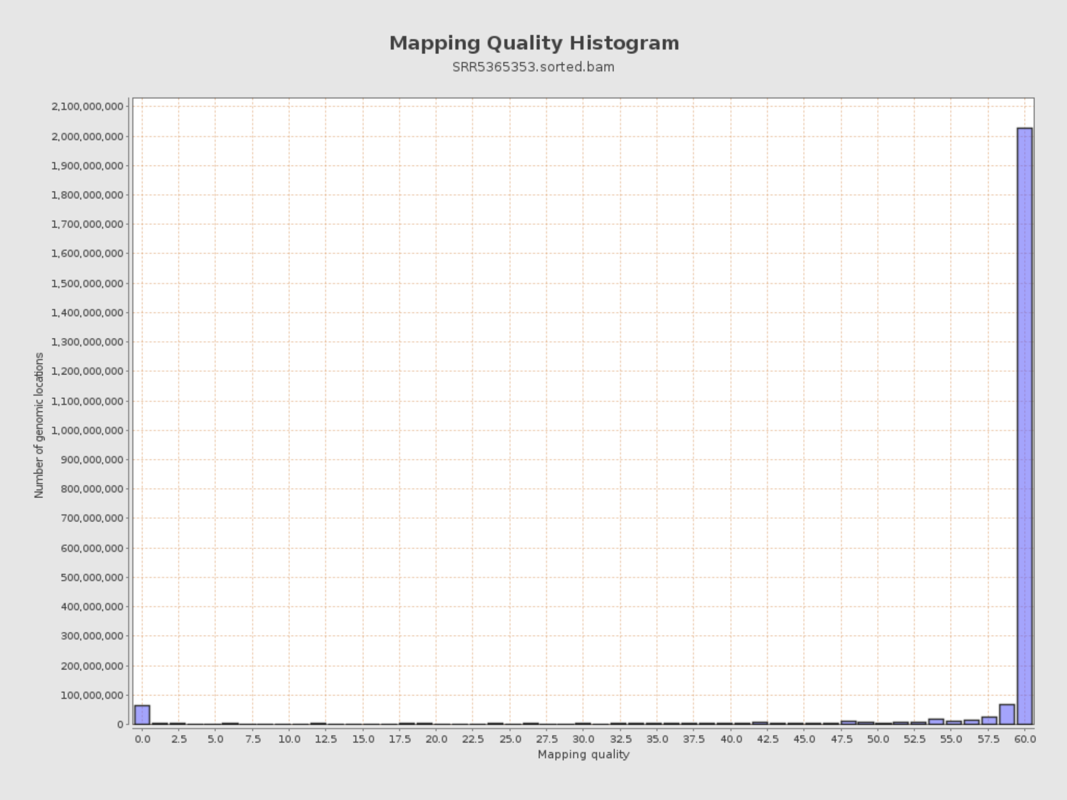
11. Results : Homopolymer Indels



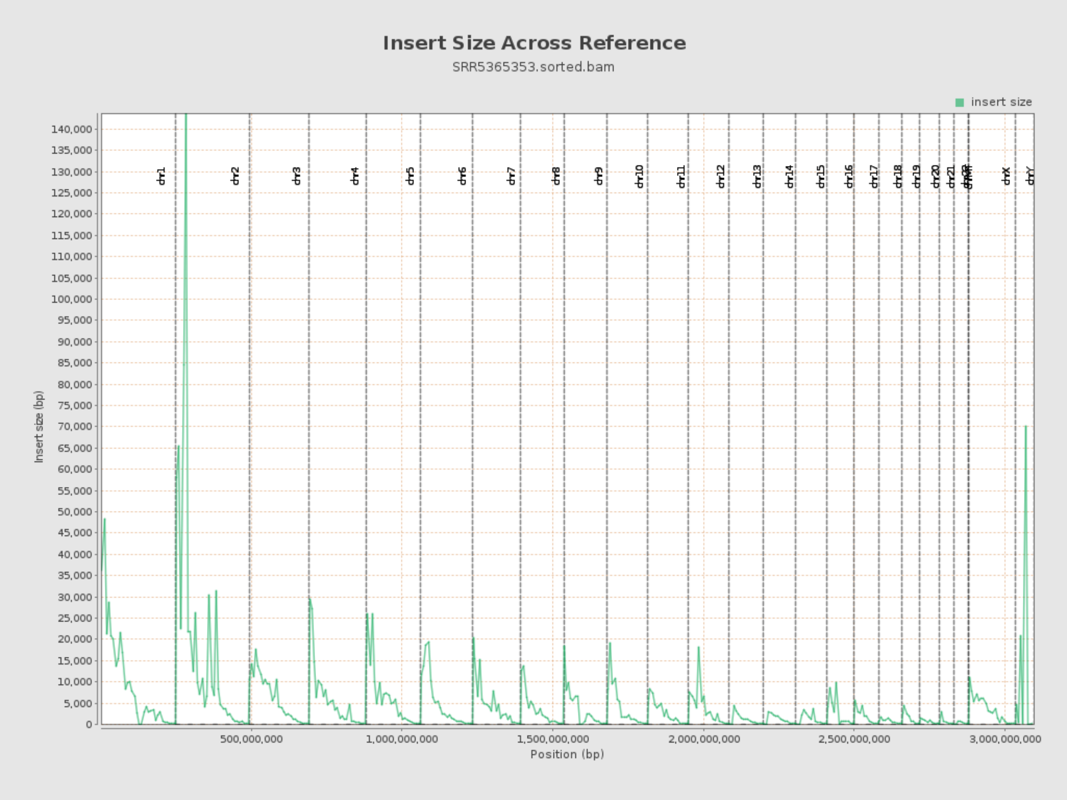
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram