Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/13 21:46:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365357.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_SRR5365357 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365357_1.fastq.gz SRR5365357_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Nov 13 21:46:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365357.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	546,294,286
Mapped reads	518,530,957 / 94.92%
Unmapped reads	27,763,329 / 5.08%
Mapped paired reads	518,530,957 / 94.92%
Mapped reads, first in pair	259,885,336 / 47.57%
Mapped reads, second in pair	258,645,621 / 47.35%
Mapped reads, both in pair	515,839,778 / 94.43%
Mapped reads, singletons	2,691,179 / 0.49%
Secondary alignments	0
Supplementary alignments	2,143,033 / 0.39%
Read min/max/mean length	30 / 125 / 125.16
Duplicated reads (estimated)	316,781,390 / 57.99%
Duplication rate	31.41%
Clipped reads	332,022,486 / 60.78%

2.2. ACGT Content

Number/percentage of A's	16,337,252,976 / 30.28%
Number/percentage of C's	10,483,925,217 / 19.43%
Number/percentage of T's	15,893,268,082 / 29.45%
Number/percentage of G's	11,235,967,596 / 20.82%
Number/percentage of N's	8,688,273 / 0.02%

GC Percentage	40.25%

2.3. Coverage

Mean	17.4362
Standard Deviation	183.9051

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	51,286.29
Standard Deviation	2,158,262.21
P25/Median/P75	113 / 163 / 231

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	315,240,791
Insertions	15,992,051
Mapped reads with at least one insertion	3.01%
Deletions	8,584,201
Mapped reads with at least one deletion	1.61%
Homopolymer indels	49.99%

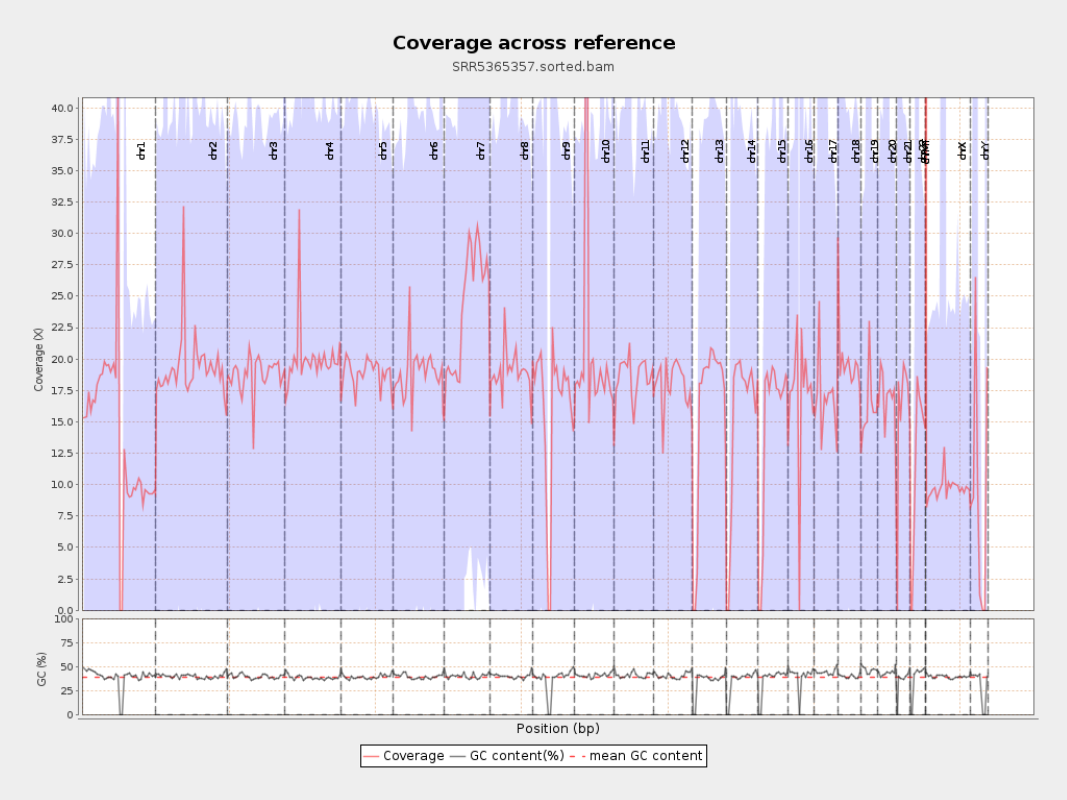
2.7. Chromosome stats

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

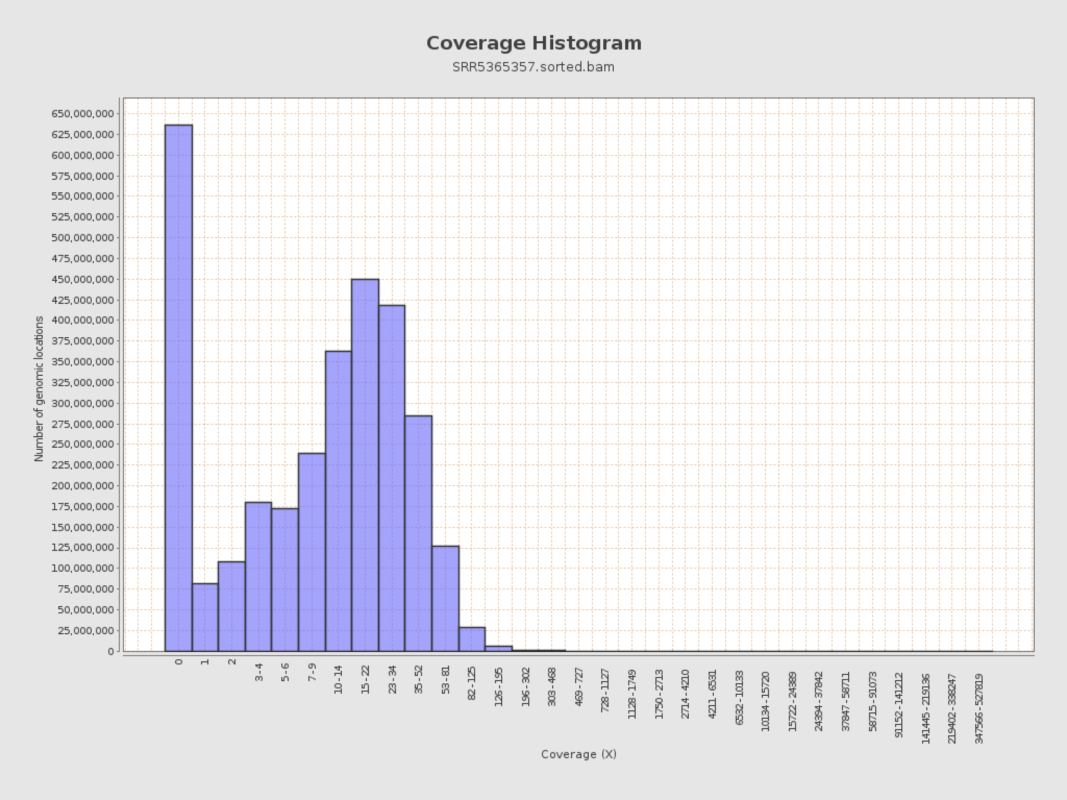
		bases	coverage	deviation
chr1	249250621	3466495500	13.9077	505.4847
chr2	243199373	4715301339	19.3886	107.2319
chr3	198022430	3719651542	18.784	29.5678
chr4	191154276	3830864561	20.0407	106.0745
chr5	180915260	3404380813	18.8175	23.2105
chr6	171115067	3242001173	18.9463	78.9955
chr7	159138663	3849773137	24.1913	119.4207
chr8	146364022	2772170111	18.9402	58.5386
chr9	141213431	2290027880	16.2168	138.8755
chr10	135534747	2789736996	20.5832	339.3021
chr11	135006516	2510410910	18.5947	117.9553
chr12	133851895	2415315184	18.0447	36.5574
chr13	115169878	1842646491	15.9994	19.2618
chr14	107349540	1653270104	15.4008	21.962
chr15	102531392	1492476161	14.5563	22.7826
chr16	90354753	1526479942	16.8943	68.9887
chr17	81195210	1374669819	16.9304	105.4638
chr18	78077248	1535300241	19.6639	176.9164
chr19	59128983	966494186	16.3455	257.8971
chr20	63025520	1075235466	17.0603	35.5664
chr21	48129895	769041864	15.9785	65.7882
chr22	51304566	598664049	11.6688	51.2589
chrMT	16571	74911208	4,520.6208	811.3363
chrX	155270560	1505933968	9.6988	46.9206

chrY	59373566	555997162	9.3644	208.0392

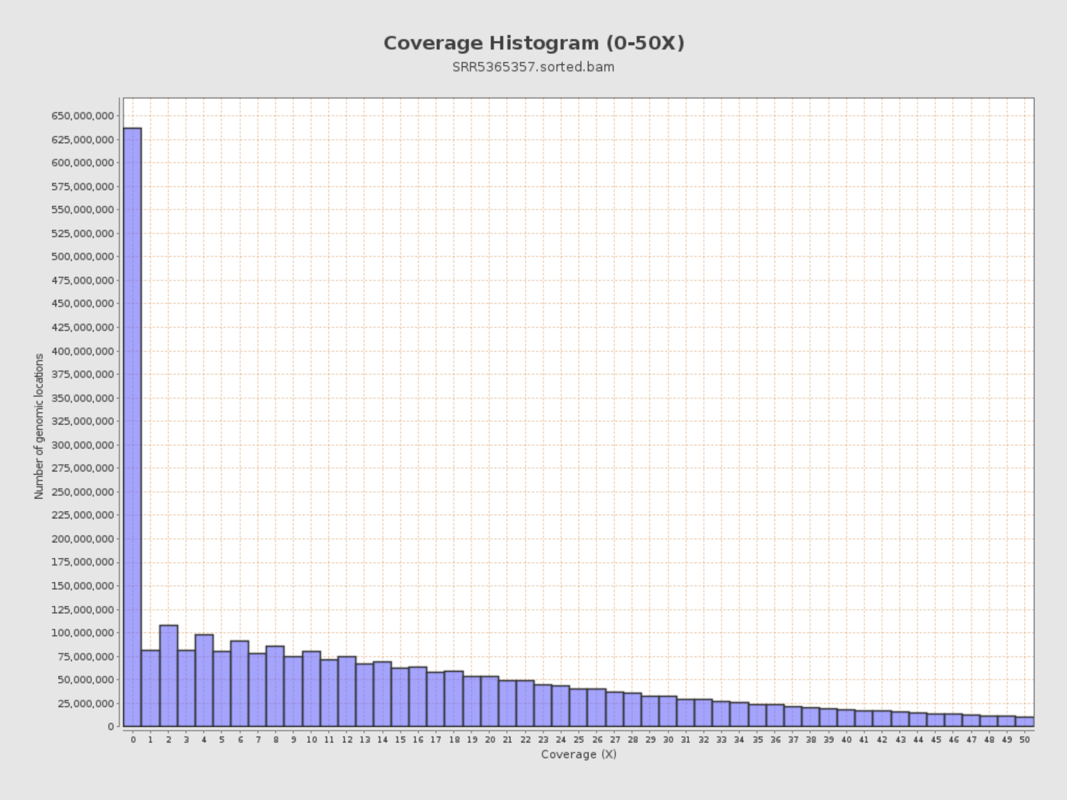
3. Results : Coverage across reference



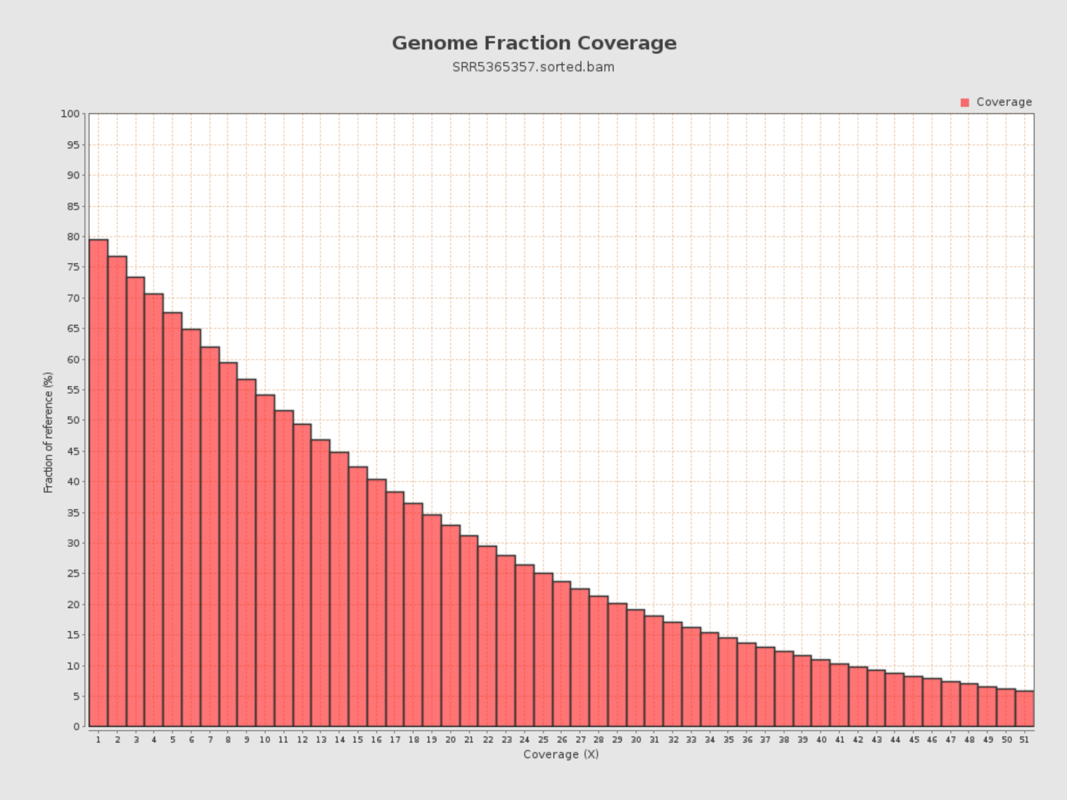
4. Results : Coverage Histogram



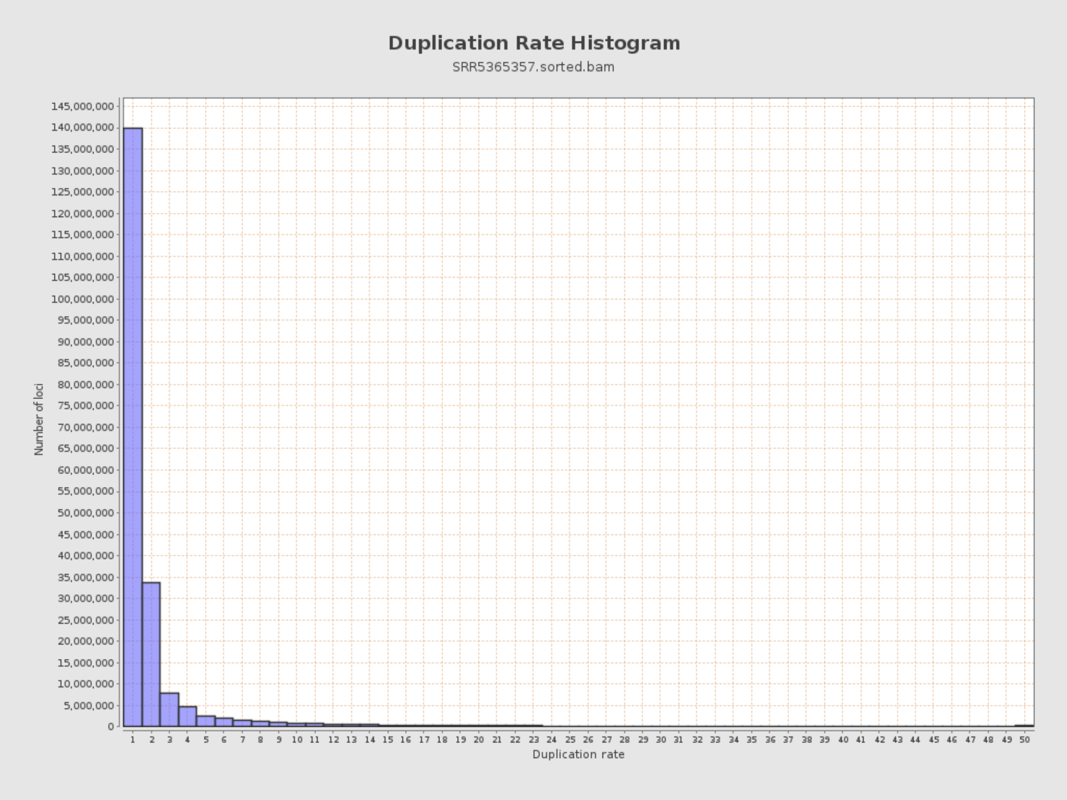
5. Results : Coverage Histogram (0-50X)



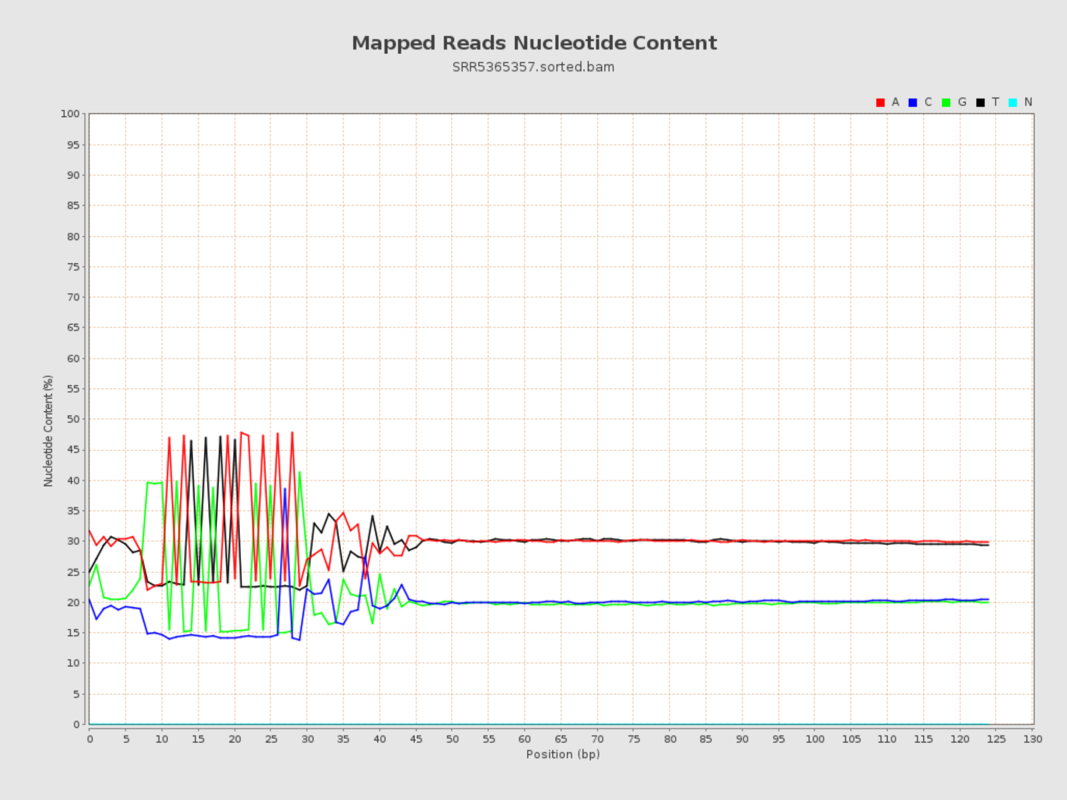
6. Results : Genome Fraction Coverage



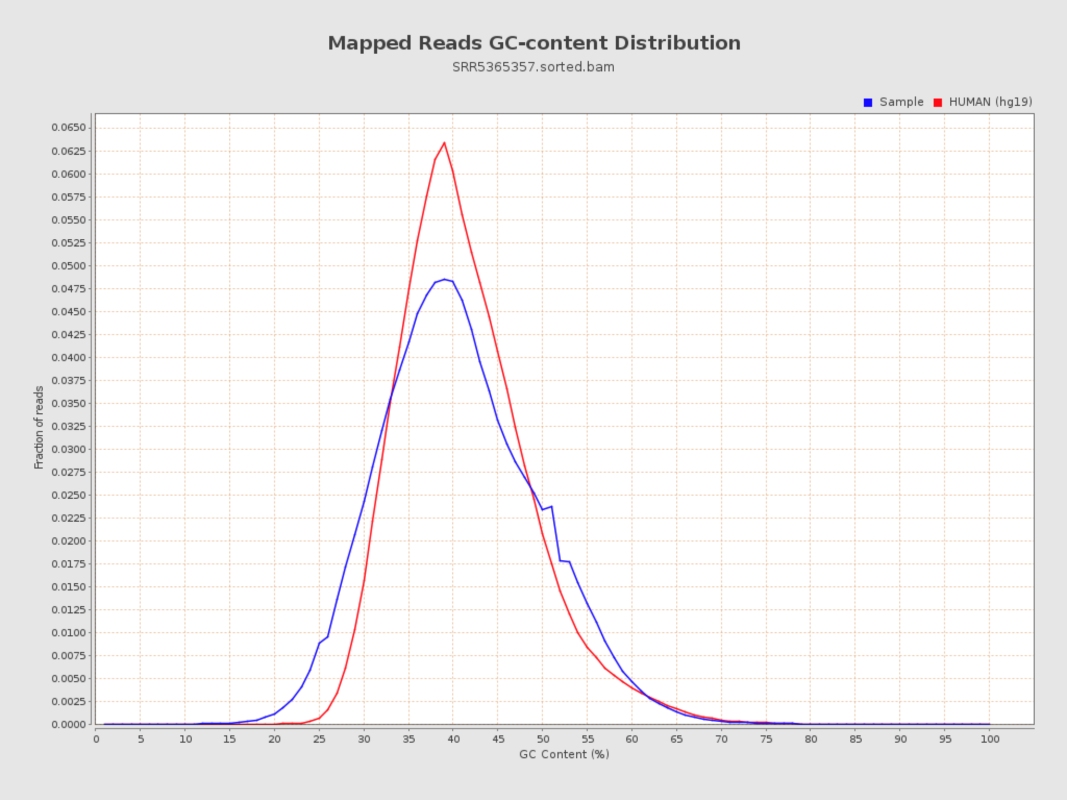
7. Results : Duplication Rate Histogram



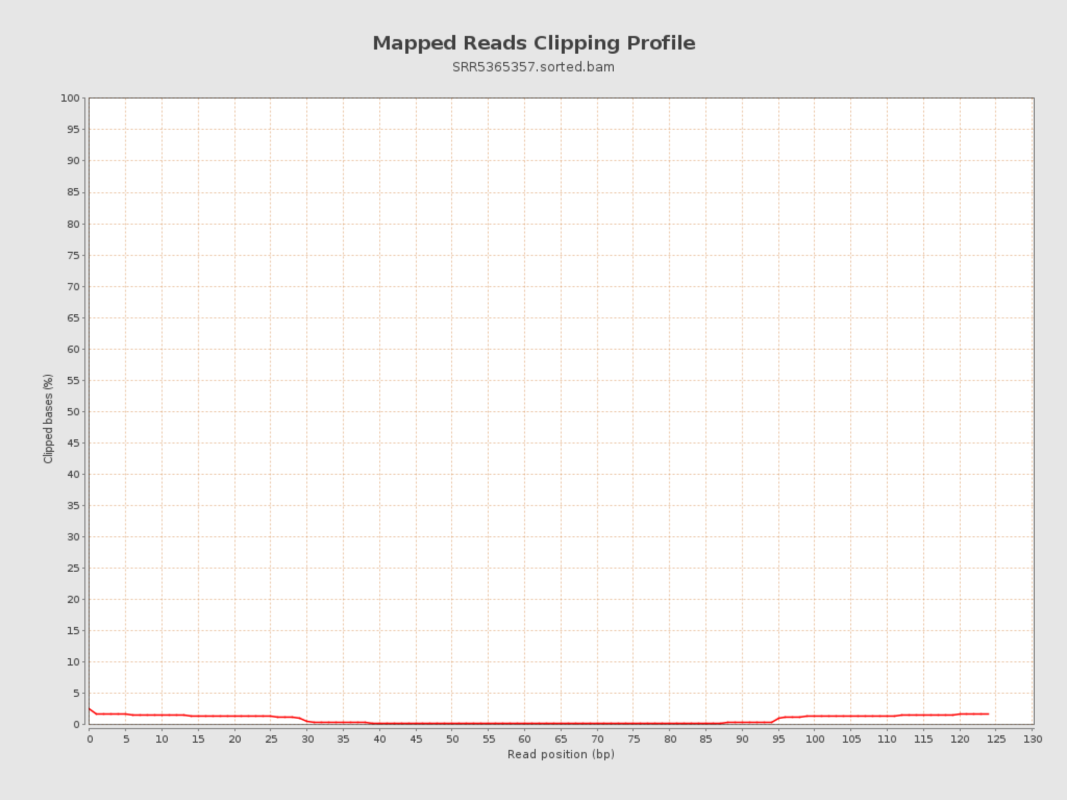
8. Results : Mapped Reads Nucleotide Content



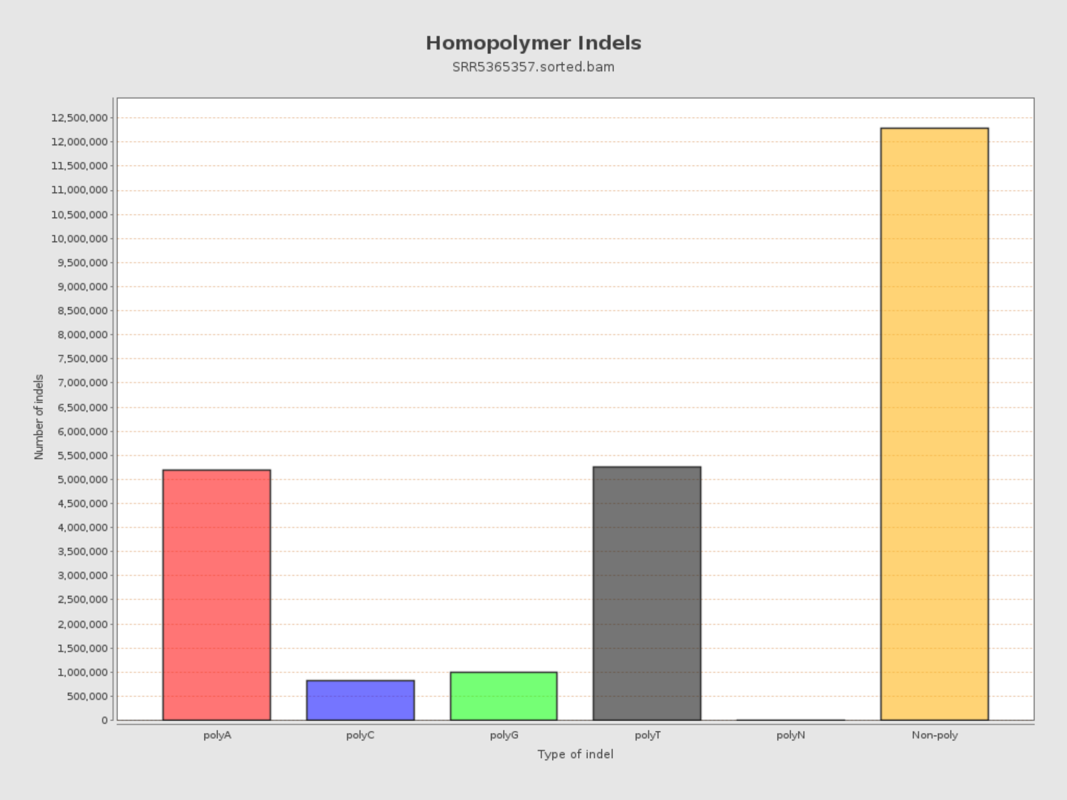
9. Results : Mapped Reads GC-content Distribution



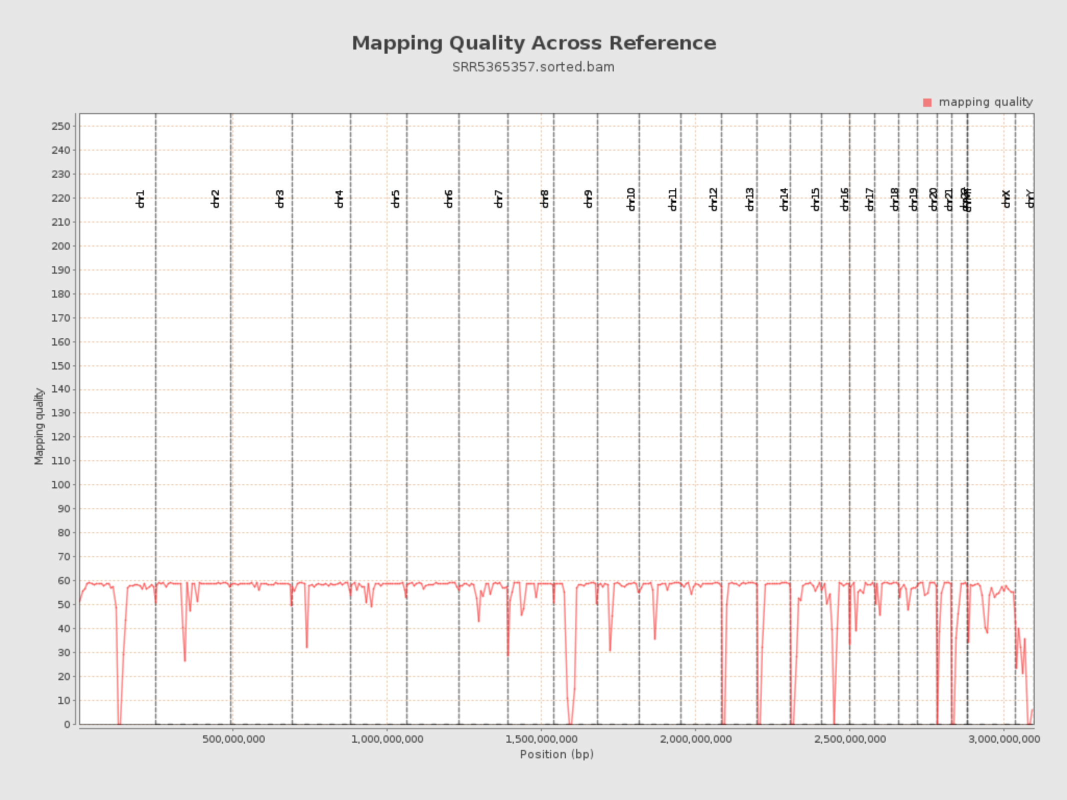
10. Results : Mapped Reads Clipping Profile



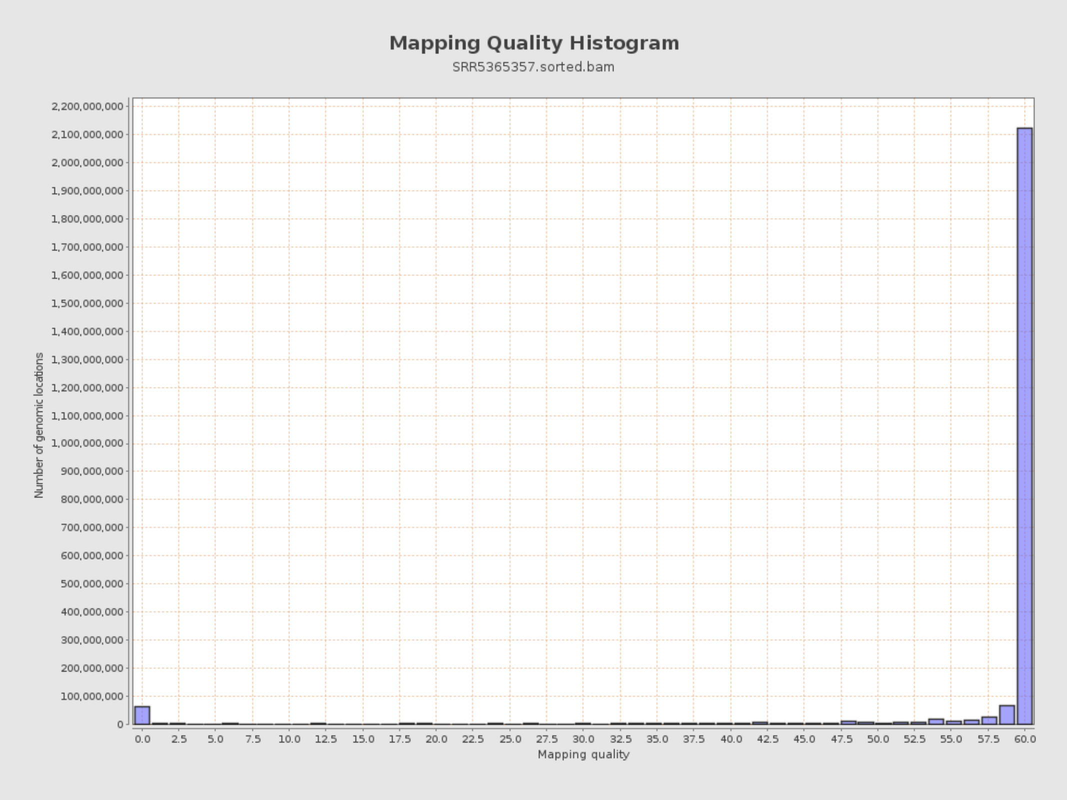
11. Results : Homopolymer Indels



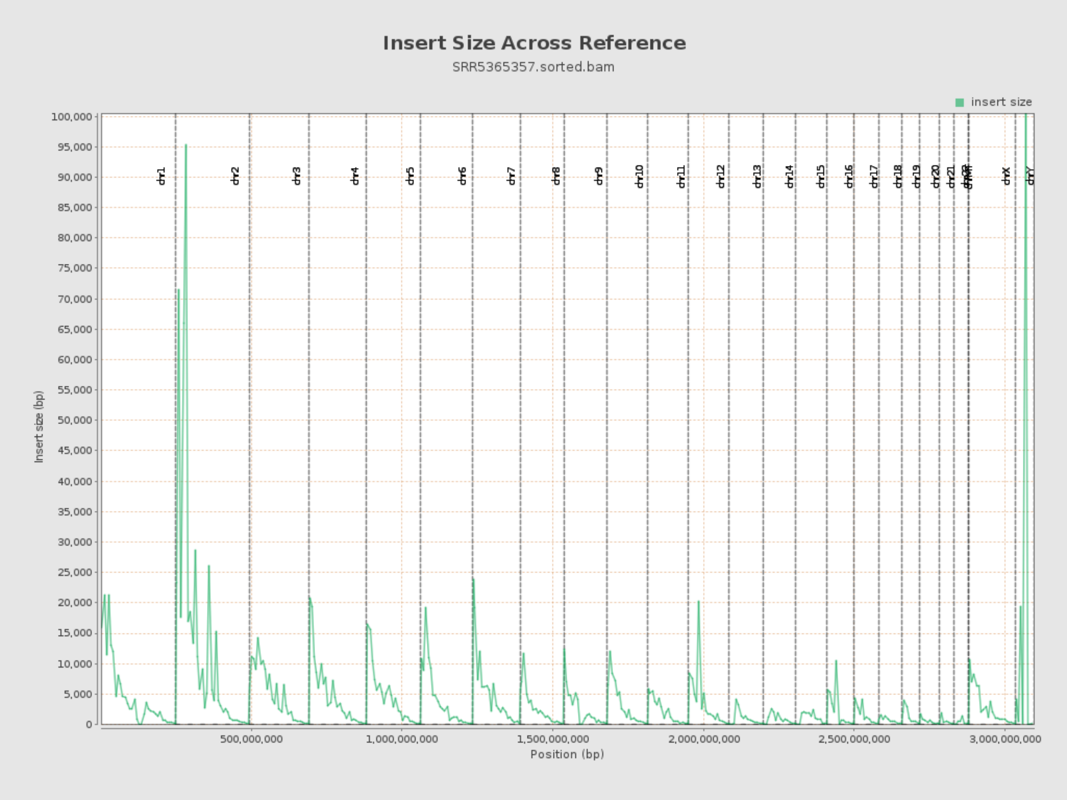
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram