Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/07 06:23:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365348.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_SRR5365348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365348_1.fastq.gz SRR5365348_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Nov 07 06:23:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	378,934,234
Mapped reads	349,266,910 / 92.17%
Unmapped reads	29,667,324 / 7.83%
Mapped paired reads	349,266,910 / 92.17%
Mapped reads, first in pair	174,972,350 / 46.17%
Mapped reads, second in pair	174,294,560 / 46%
Mapped reads, both in pair	347,293,126 / 91.65%
Mapped reads, singletons	1,973,784 / 0.52%
Secondary alignments	0
Supplementary alignments	1,662,254 / 0.44%
Read min/max/mean length	30 / 125 / 125.18
Duplicated reads (estimated)	250,360,954 / 66.07%
Duplication rate	42.57%
Clipped reads	250,323,497 / 66.06%

2.2. ACGT Content

Number/percentage of A's	10,675,451,041 / 30.07%
Number/percentage of C's	6,918,441,719 / 19.49%
Number/percentage of T's	10,315,839,291 / 29.05%
Number/percentage of G's	7,594,190,995 / 21.39%
Number/percentage of N's	1,860,328 / 0.01%

GC Percentage	40.87%

2.3. Coverage

Mean	11.4734
Standard Deviation	136.5197

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	76,118.55
Standard Deviation	2,659,798.32
P25/Median/P75	123 / 192 / 295

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	207,212,673
Insertions	10,776,188
Mapped reads with at least one insertion	3.01%
Deletions	5,787,786
Mapped reads with at least one deletion	1.61%
Homopolymer indels	49.34%

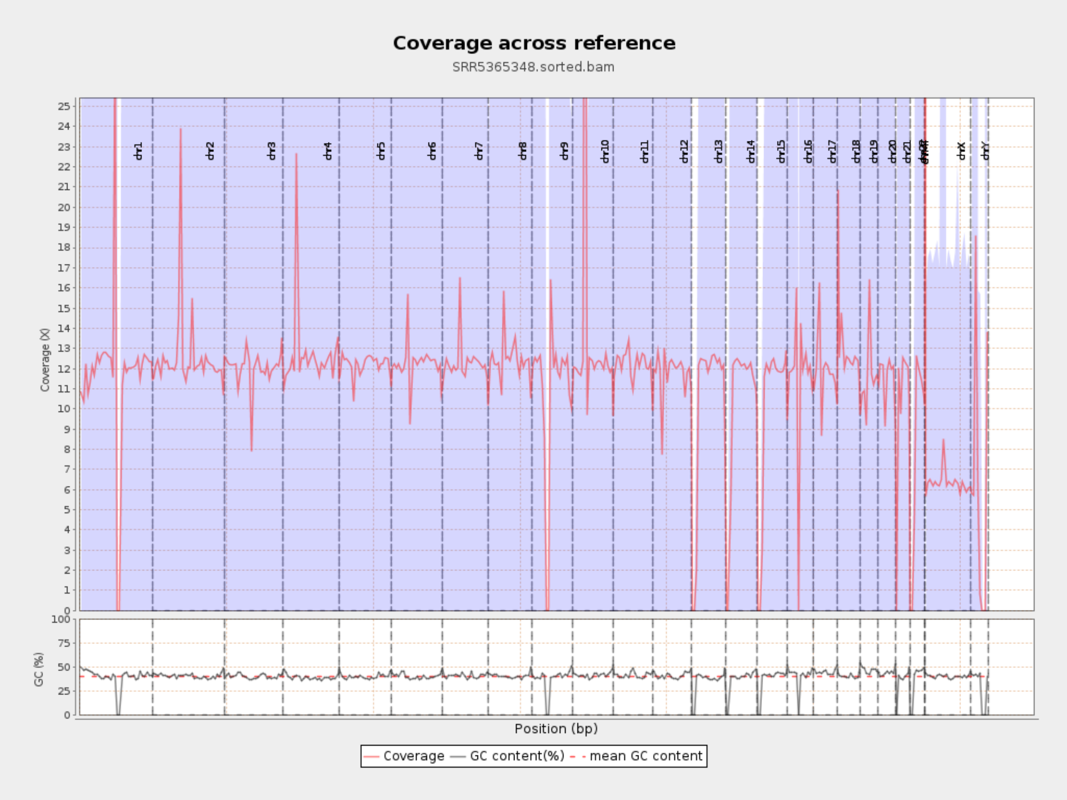
2.7. Chromosome stats

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

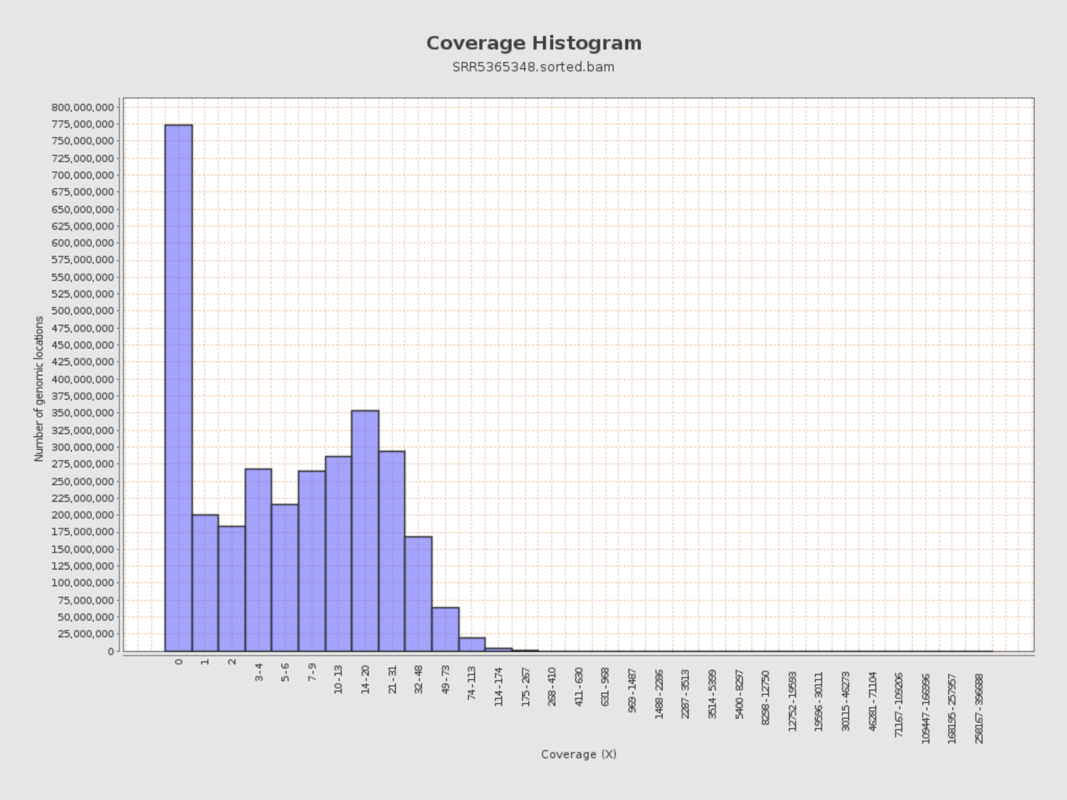
		bases	coverage	deviation
chr1	249250621	2947819892	11.8267	372.7698
chr2	243199373	3067773102	12.6142	80.4813
chr3	198022430	2374461406	11.9909	22.4585
chr4	191154276	2424097443	12.6814	83.6815
chr5	180915260	2205916334	12.1931	17.4146
chr6	171115067	2102158329	12.2851	48.1191
chr7	159138663	1960049739	12.3166	98.2072
chr8	146364022	1823388348	12.4579	45.5482
chr9	141213431	1507695483	10.6767	120.0673
chr10	135534747	1899970764	14.0183	262.4433
chr11	135006516	1648103171	12.2076	71.1061
chr12	133851895	1577595359	11.7861	25.3507
chr13	115169878	1178456333	10.2323	14.8498
chr14	107349540	1080877226	10.0688	17.768
chr15	102531392	991940973	9.6745	16.9877
chr16	90354753	1022835606	11.3202	44.3319
chr17	81195210	961385501	11.8404	62.2186
chr18	78077248	1012076885	12.9625	143.7195
chr19	59128983	685159627	11.5875	178.2023
chr20	63025520	727148426	11.5374	25.769
chr21	48129895	506004977	10.5133	44.9465
chr22	51304566	417552457	8.1387	31.7396
chrMT	16571	31731463	1,914.8792	401.1776
chrX	155270560	983711397	6.3355	27.5495

chrY	59373566	380260671	6.4045	140.1691

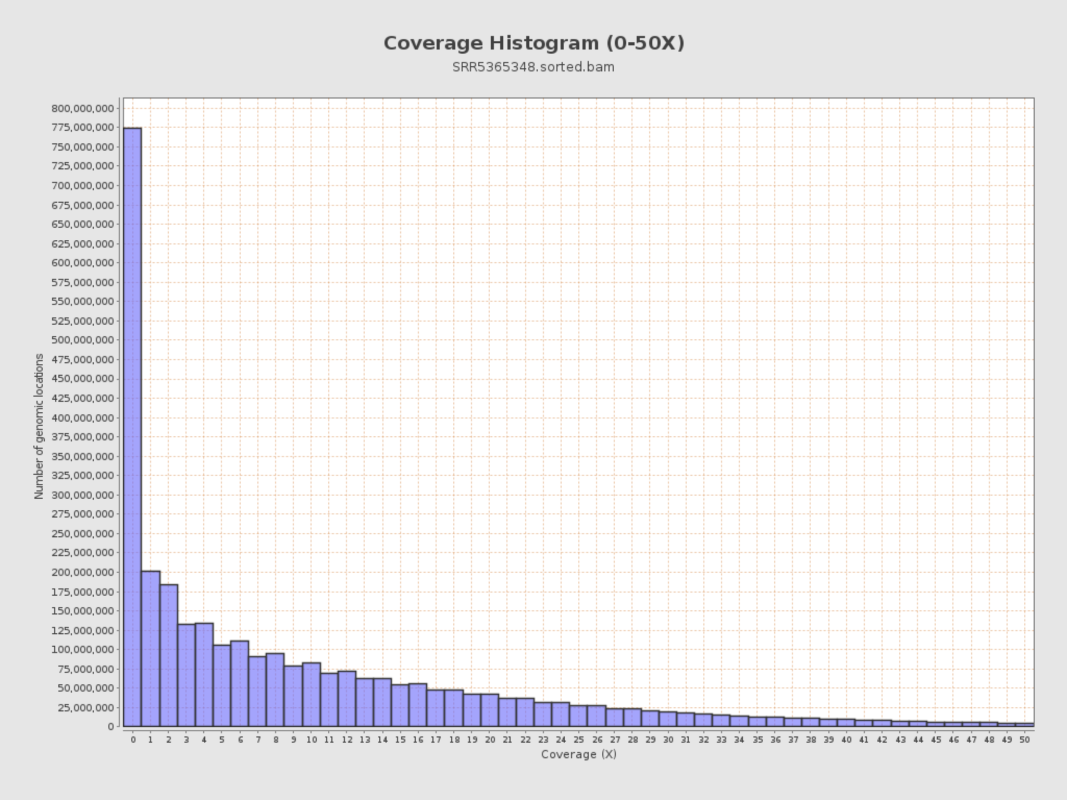
3. Results : Coverage across reference



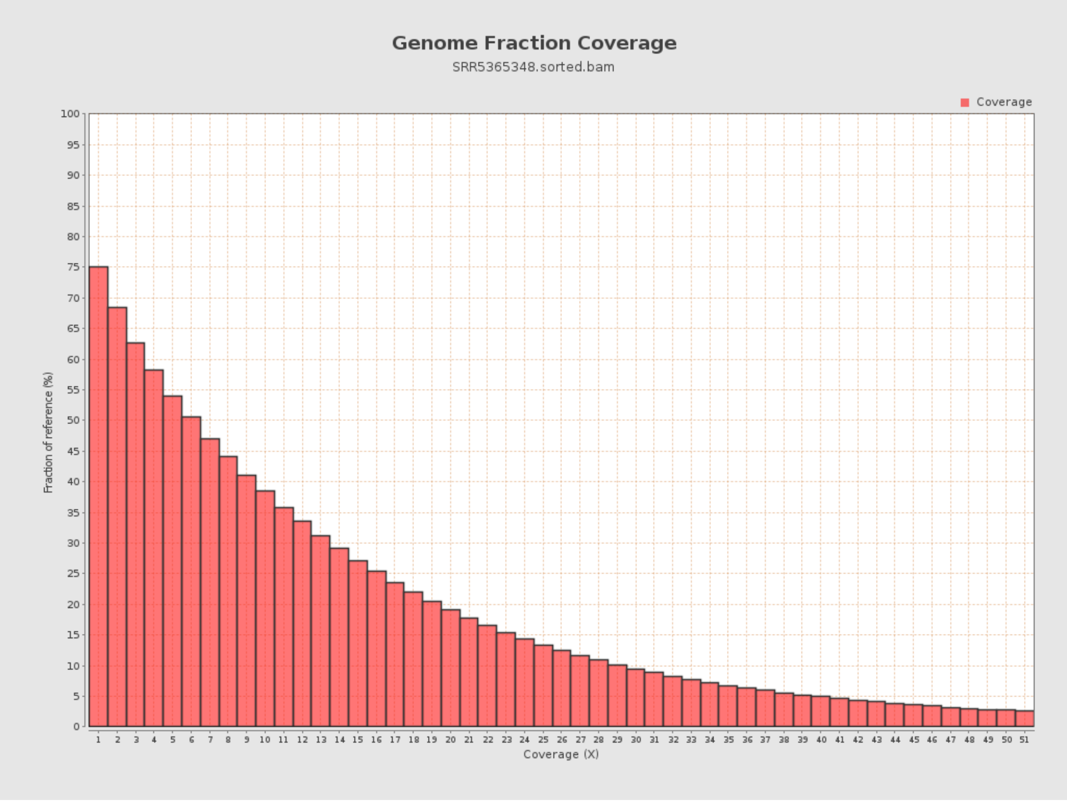
4. Results : Coverage Histogram



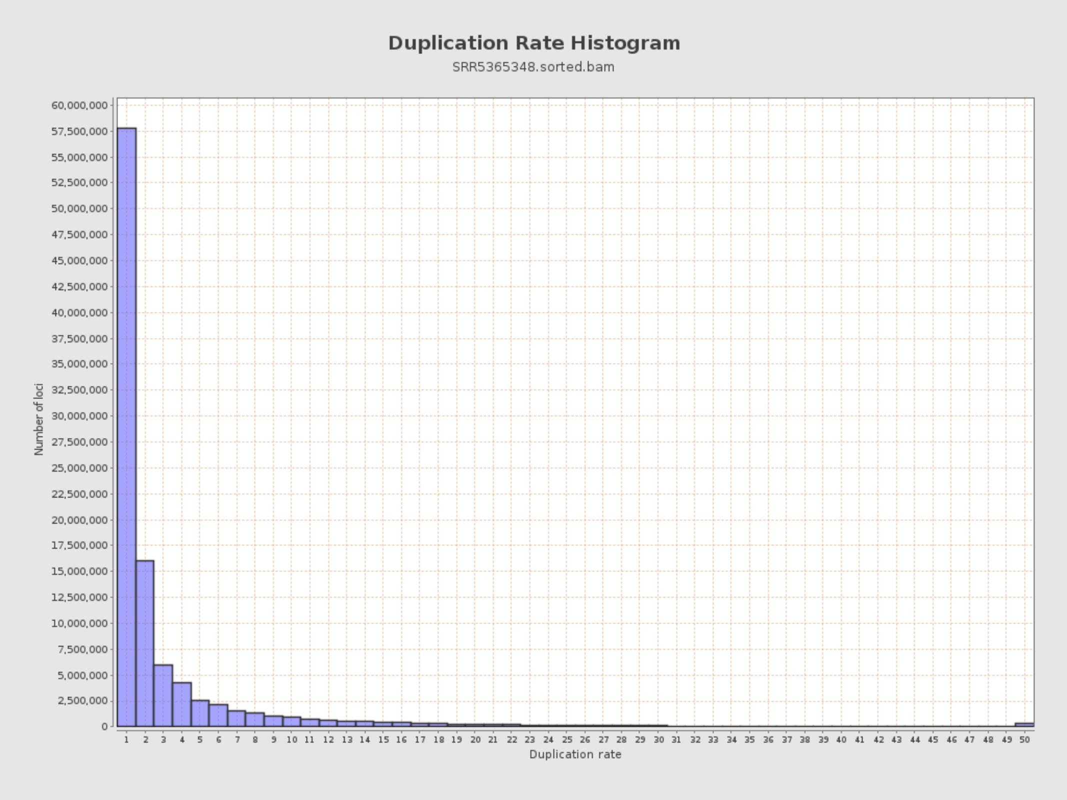
5. Results : Coverage Histogram (0-50X)



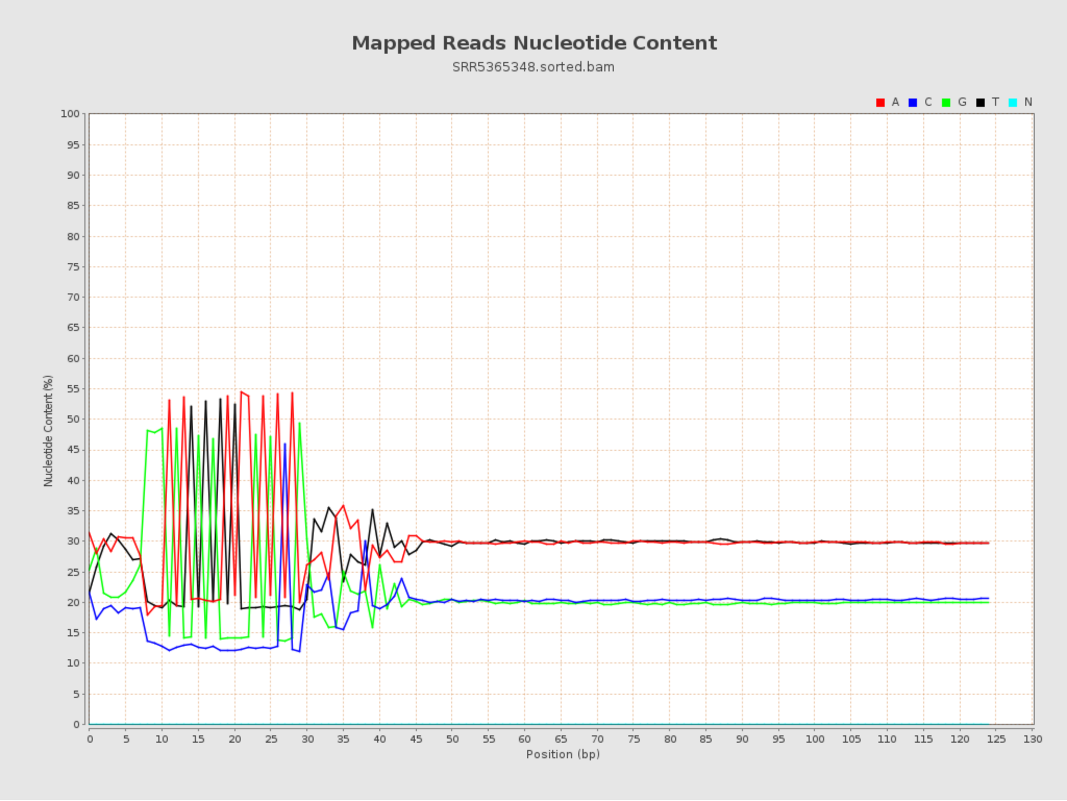
6. Results : Genome Fraction Coverage



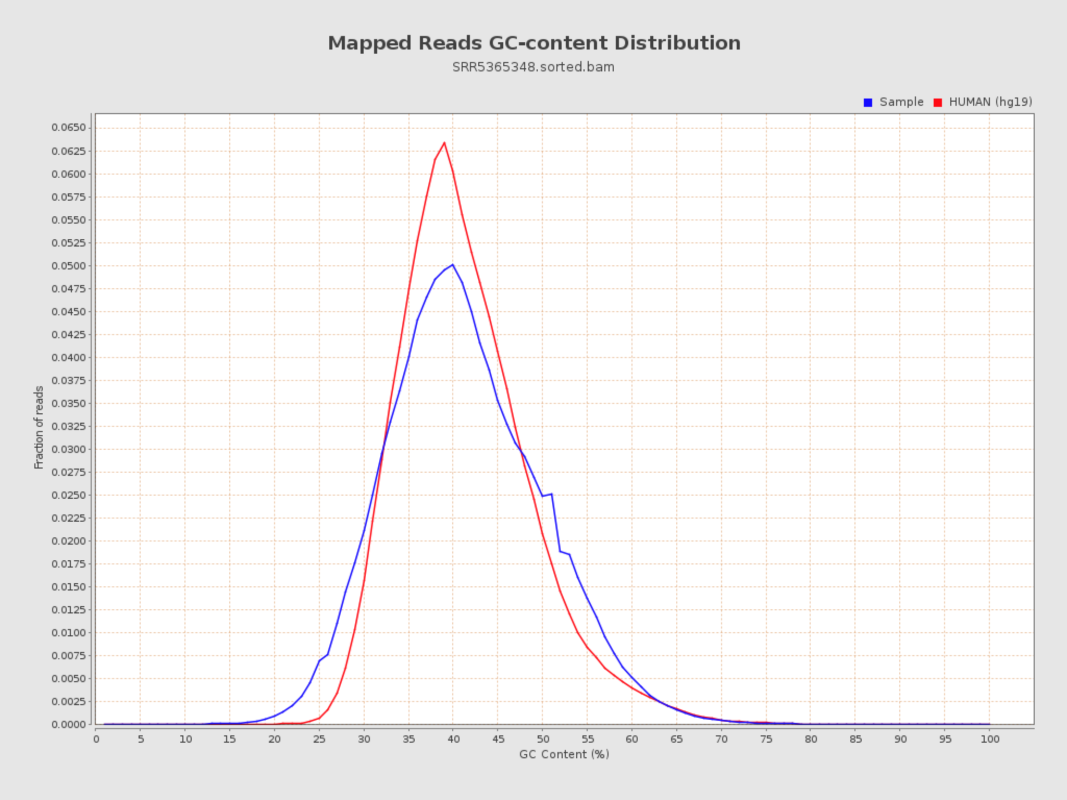
7. Results : Duplication Rate Histogram



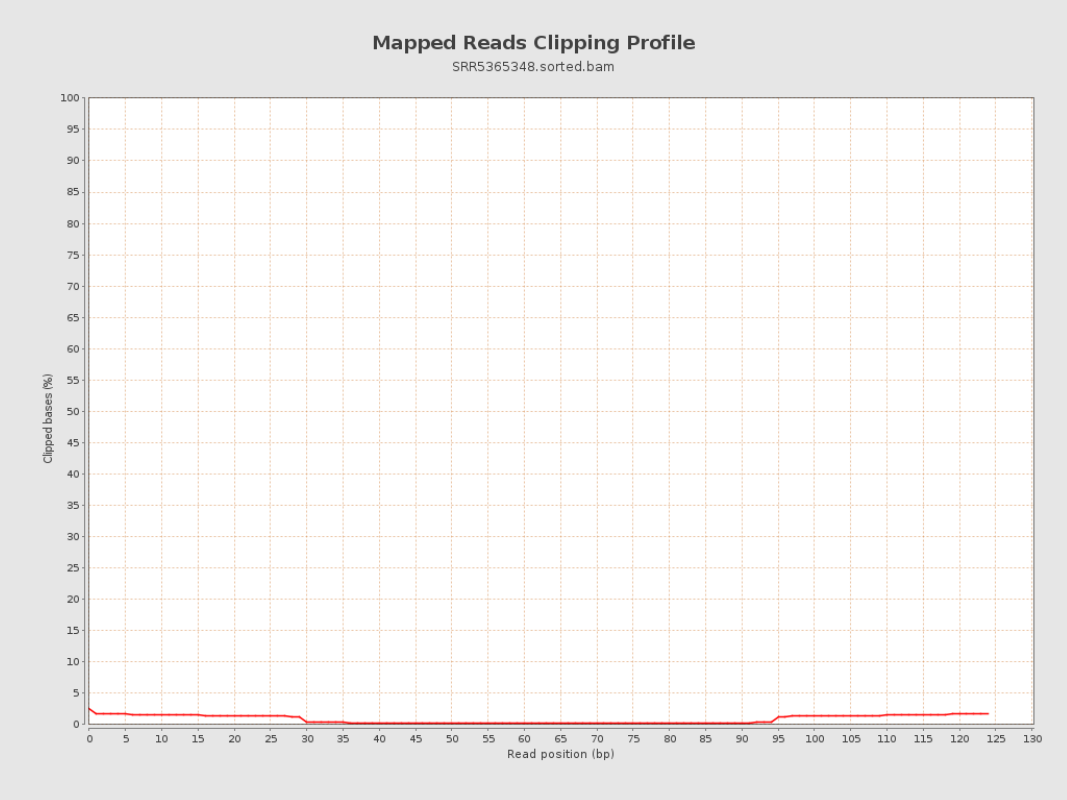
8. Results : Mapped Reads Nucleotide Content



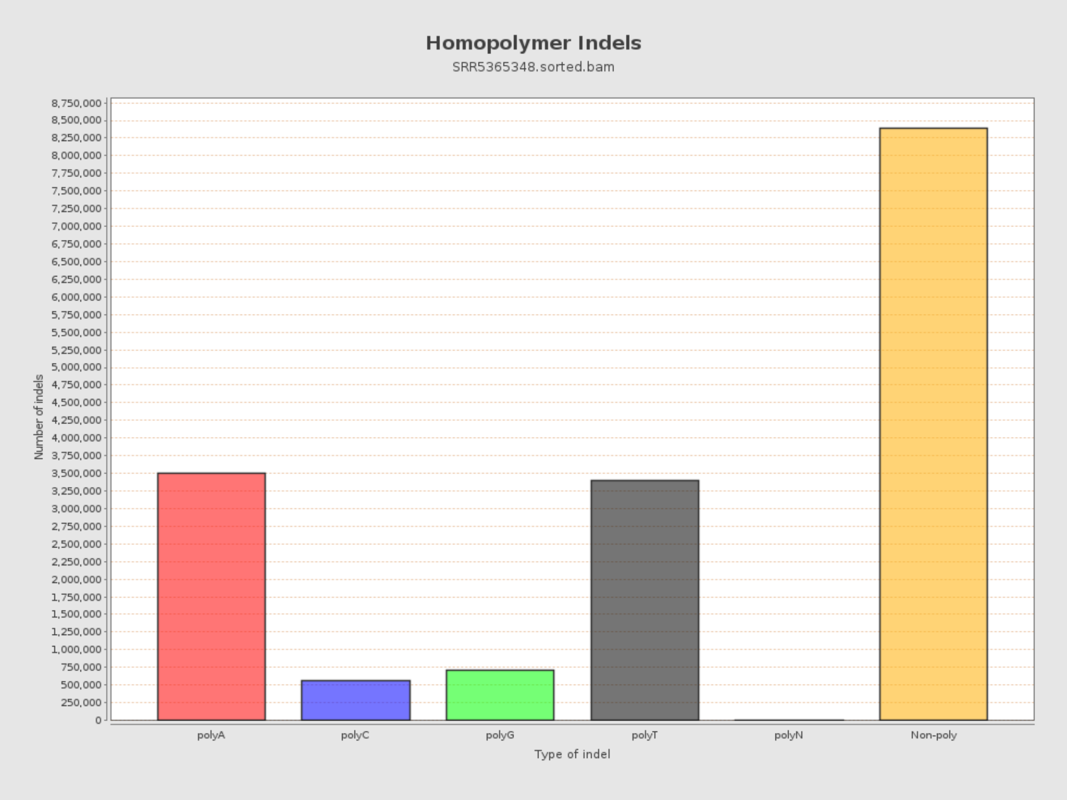
9. Results : Mapped Reads GC-content Distribution



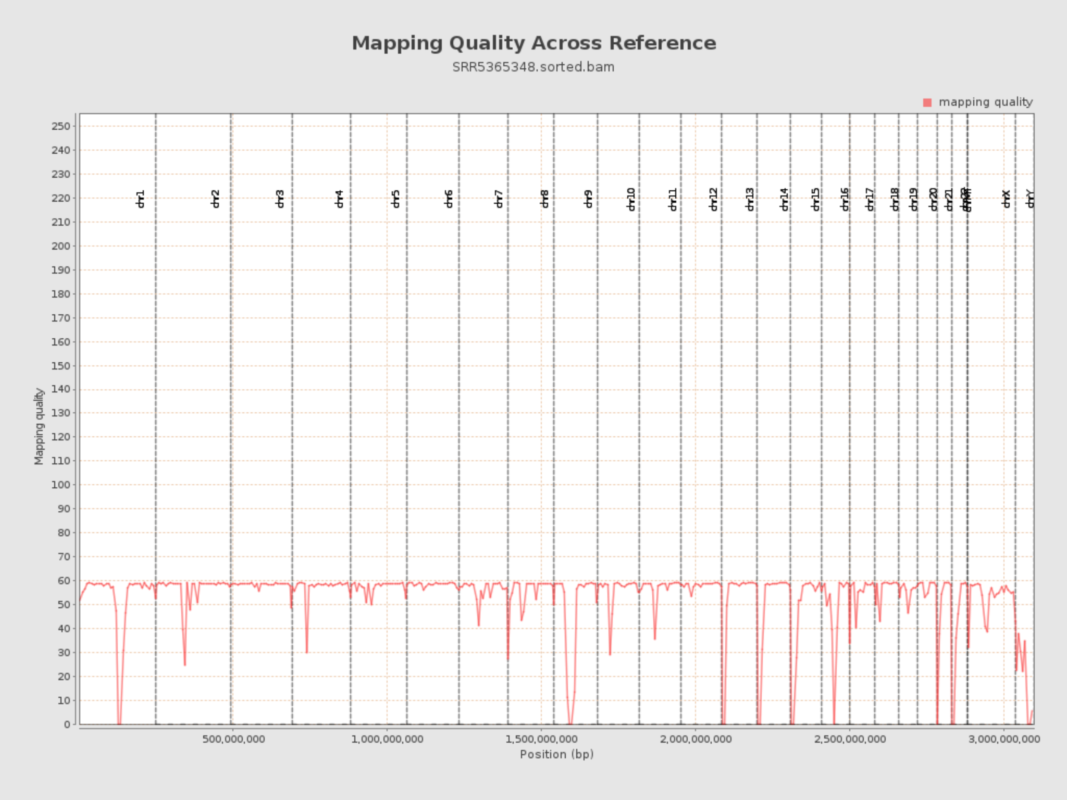
10. Results : Mapped Reads Clipping Profile



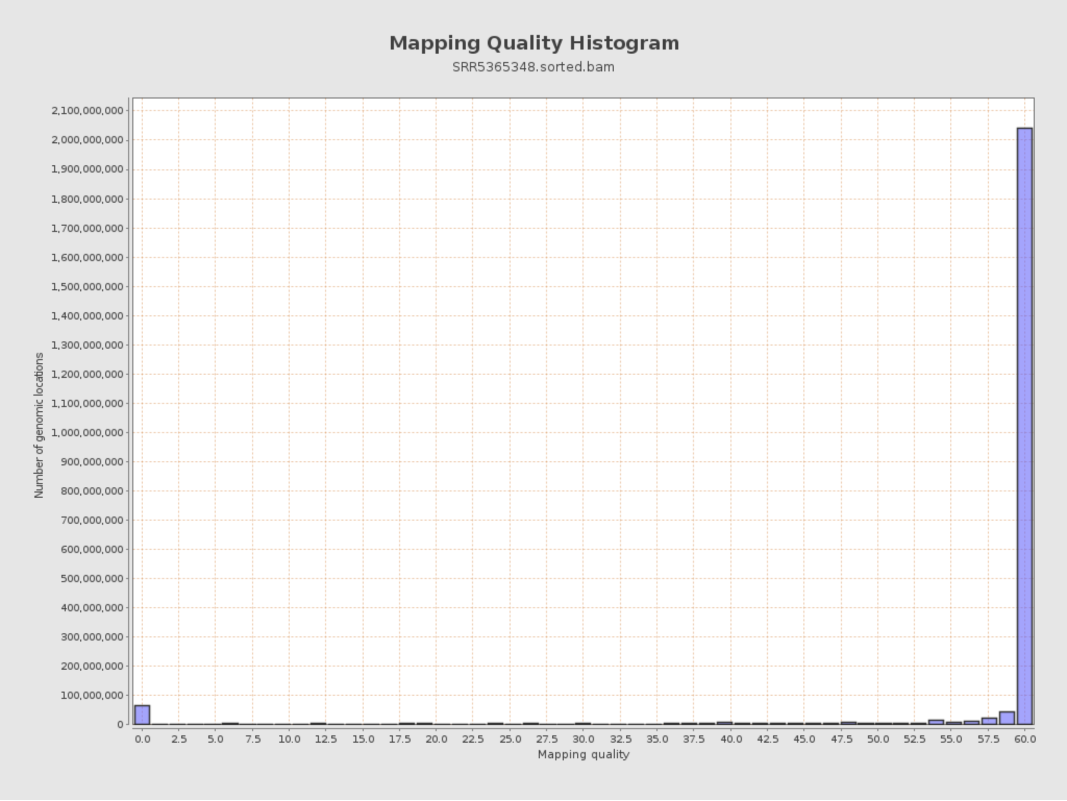
11. Results : Homopolymer Indels



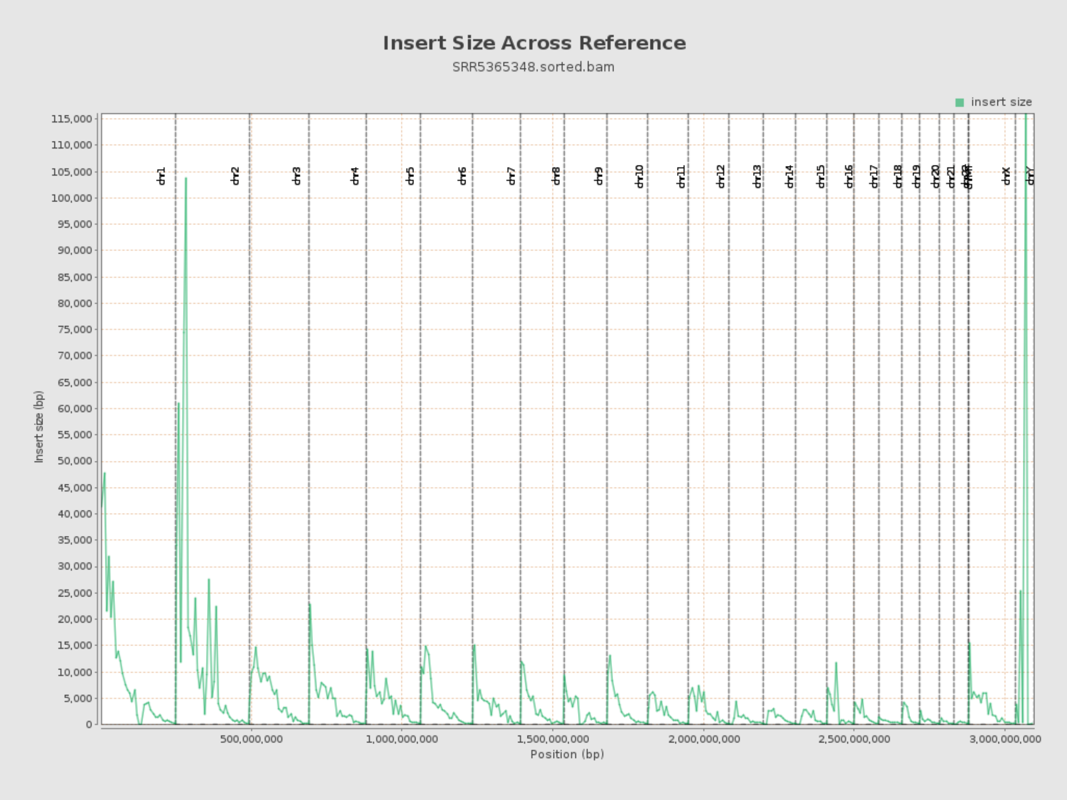
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram