Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/13 01:36:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365355.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_SRR5365355 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365355_1.fastq.gz SRR5365355_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Nov 13 01:36:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365355.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	543,114,166
Mapped reads	522,632,115 / 96.23%
Unmapped reads	20,482,051 / 3.77%
Mapped paired reads	522,632,115 / 96.23%
Mapped reads, first in pair	261,716,020 / 48.19%
Mapped reads, second in pair	260,916,095 / 48.04%
Mapped reads, both in pair	520,589,164 / 95.85%
Mapped reads, singletons	2,042,951 / 0.38%
Secondary alignments	0
Supplementary alignments	2,242,857 / 0.41%
Read min/max/mean length	30 / 125 / 125.17
Duplicated reads (estimated)	282,521,606 / 52.02%
Duplication rate	31.3%
Clipped reads	329,730,654 / 60.71%

2.2. ACGT Content

Number/percentage of A's	16,513,055,091 / 30.26%
Number/percentage of C's	10,598,308,370 / 19.42%
Number/percentage of T's	16,101,083,480 / 29.5%
Number/percentage of G's	11,357,705,267 / 20.81%
Number/percentage of N's	5,897,181 / 0.01%

GC Percentage	40.23%

2.3. Coverage

Mean	17.6355
Standard Deviation	115.4615

2.4. Mapping Quality

Mean Mapping Quality	53.88

2.5. Insert size

Mean	61,180.53
Standard Deviation	2,405,563.31
P25/Median/P75	112 / 161 / 228

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	256,864,608
Insertions	16,569,377
Mapped reads with at least one insertion	3.1%
Deletions	8,497,732
Mapped reads with at least one deletion	1.58%
Homopolymer indels	50.86%

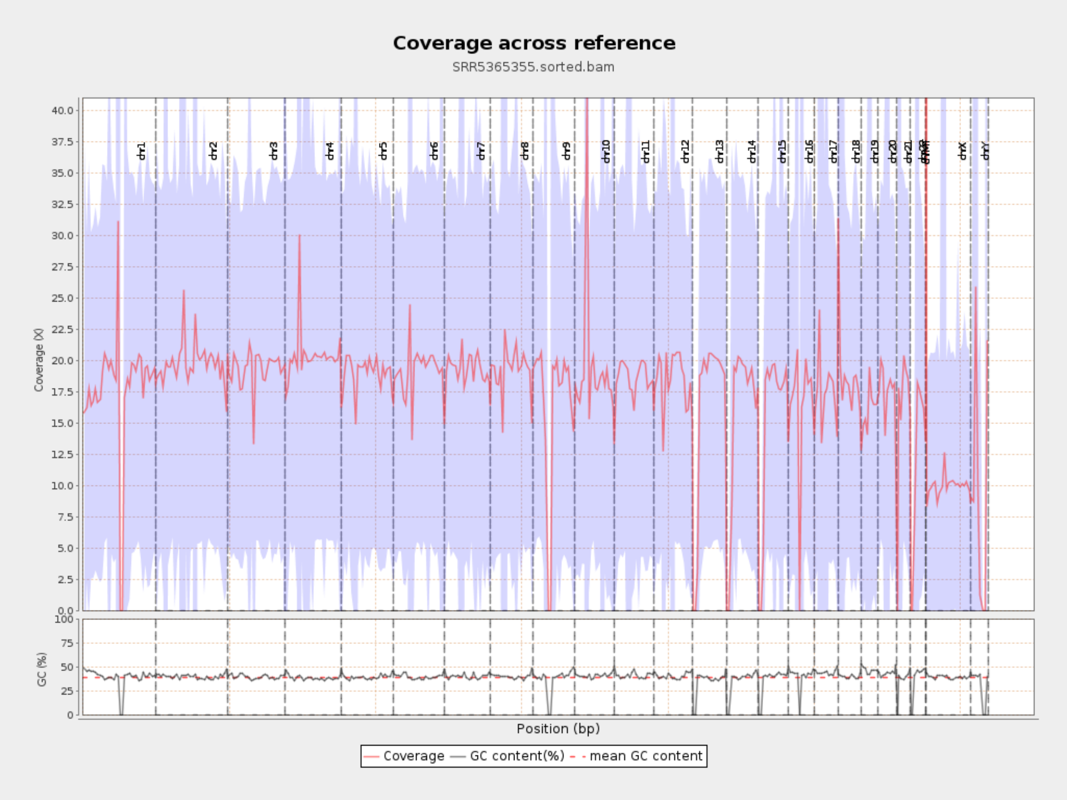
2.7. Chromosome stats

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

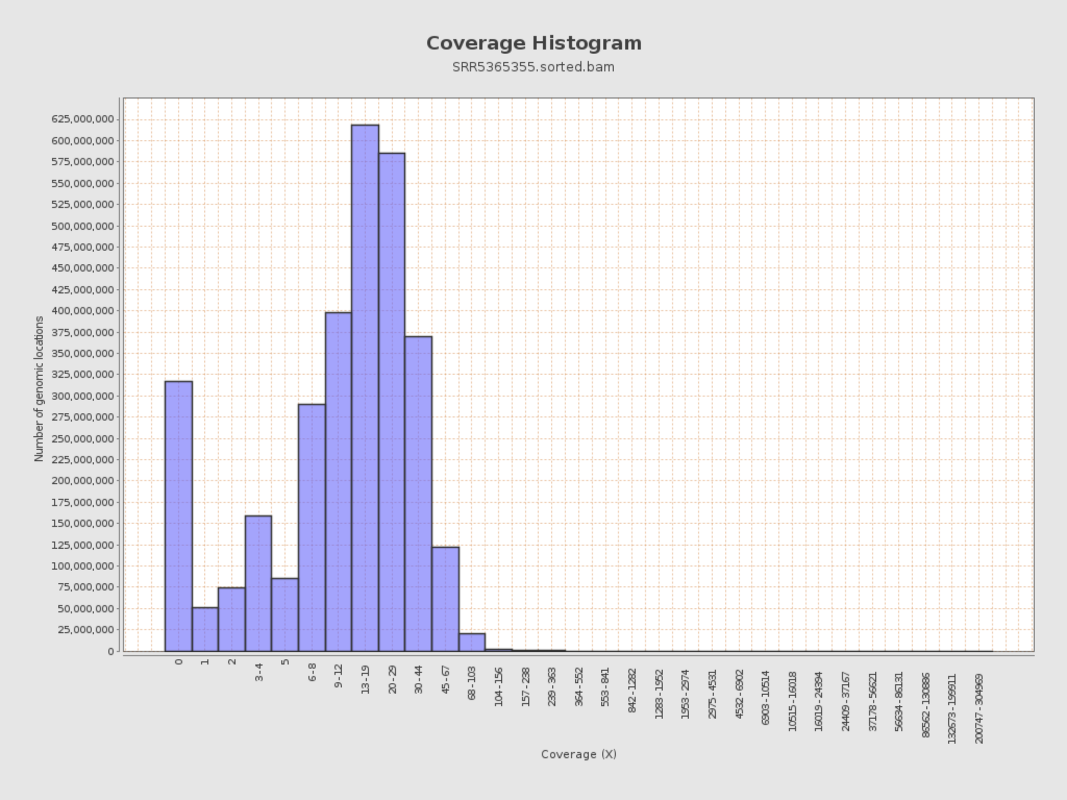
		bases	coverage	deviation
chr1	249250621	4415200915	17.7139	292.0022
chr2	243199373	4820448230	19.821	78.8749
chr3	198022430	3827807863	19.3302	18.8322
chr4	191154276	3904651237	20.4267	96.0377
chr5	180915260	3426292353	18.9387	17.4036
chr6	171115067	3297923704	19.2731	63.1638
chr7	159138663	3069176301	19.2862	109.1067
chr8	146364022	2815677976	19.2375	37.8455
chr9	141213431	2329810668	16.4985	83.7886
chr10	135534747	2620882197	19.3373	197.6189
chr11	135006516	2514409772	18.6244	72.1662
chr12	133851895	2481082605	18.536	33.1891
chr13	115169878	1883764239	16.3564	15.1001
chr14	107349540	1697103605	15.8091	16.6052
chr15	102531392	1532706512	14.9487	20.3656
chr16	90354753	1450780452	16.0565	43.7851
chr17	81195210	1433526256	17.6553	92.0623
chr18	78077248	1448051147	18.5464	133.2996
chr19	59128983	950910356	16.082	142.7921
chr20	63025520	1111181808	17.6307	30.1384
chr21	48129895	783249110	16.2737	62.986
chr22	51304566	610138773	11.8925	55.9698
chrMT	16571	51822859	3,127.3224	545.4529
chrX	155270560	1547763912	9.9682	34.0388

chrY	59373566	569717920	9.5955	199.615

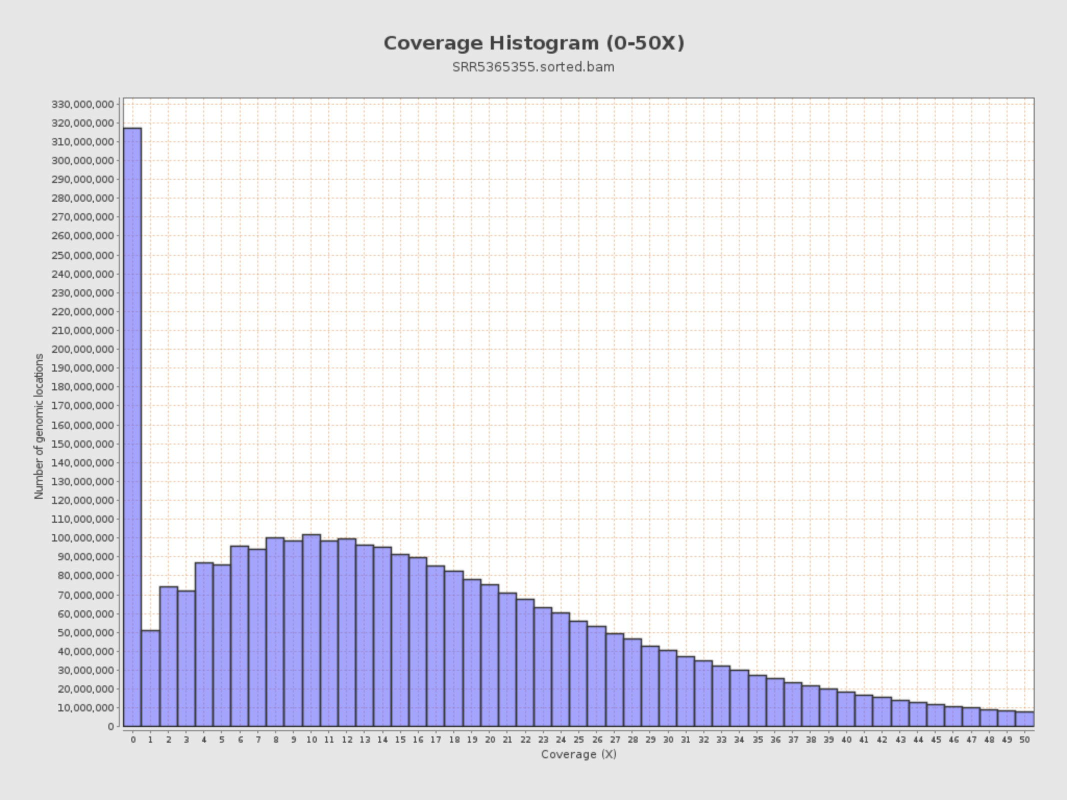
3. Results : Coverage across reference



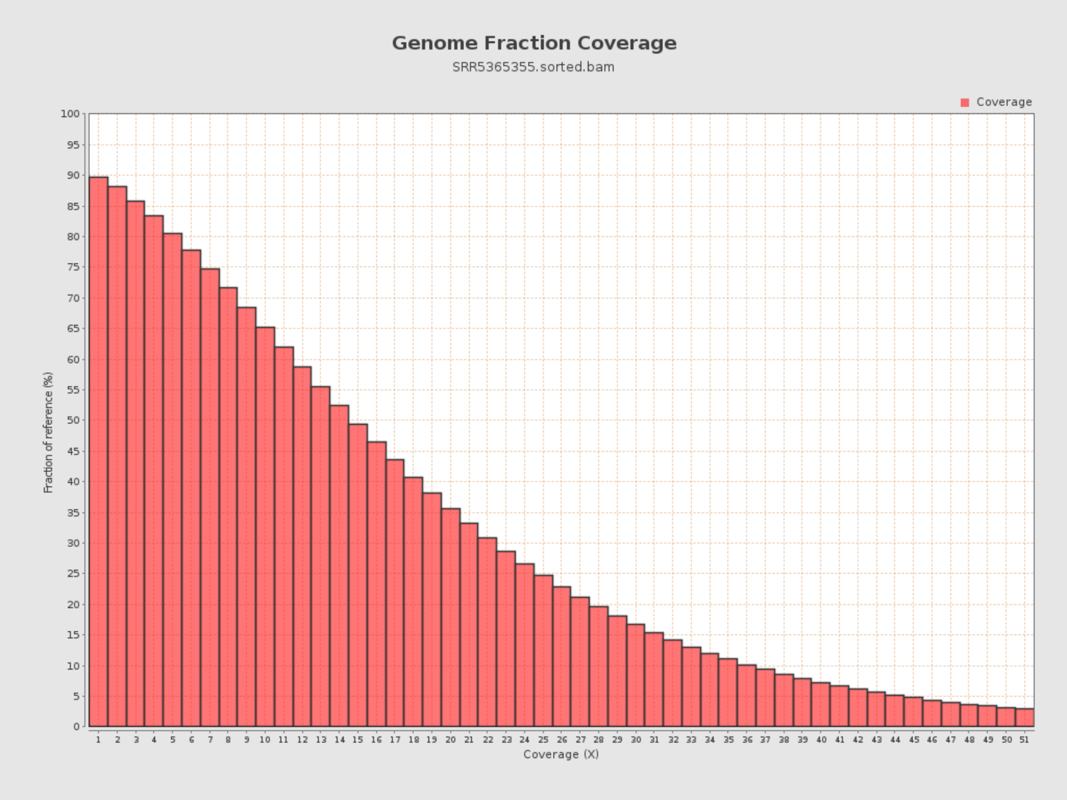
4. Results : Coverage Histogram



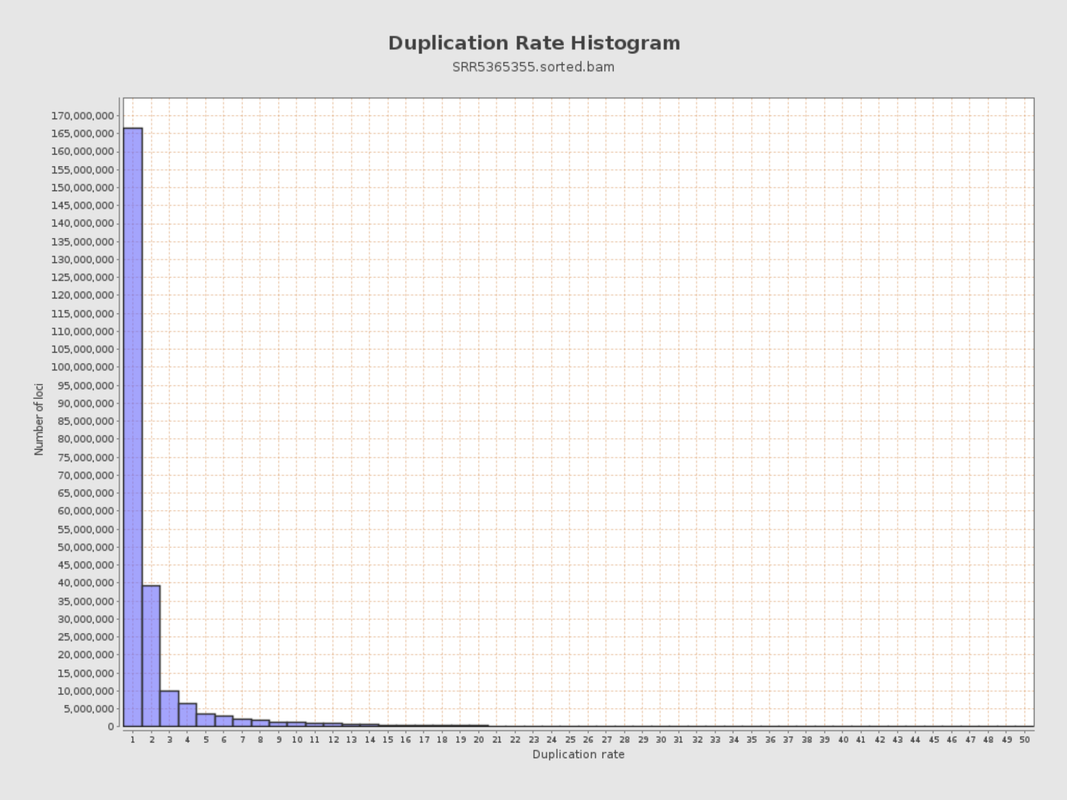
5. Results : Coverage Histogram (0-50X)



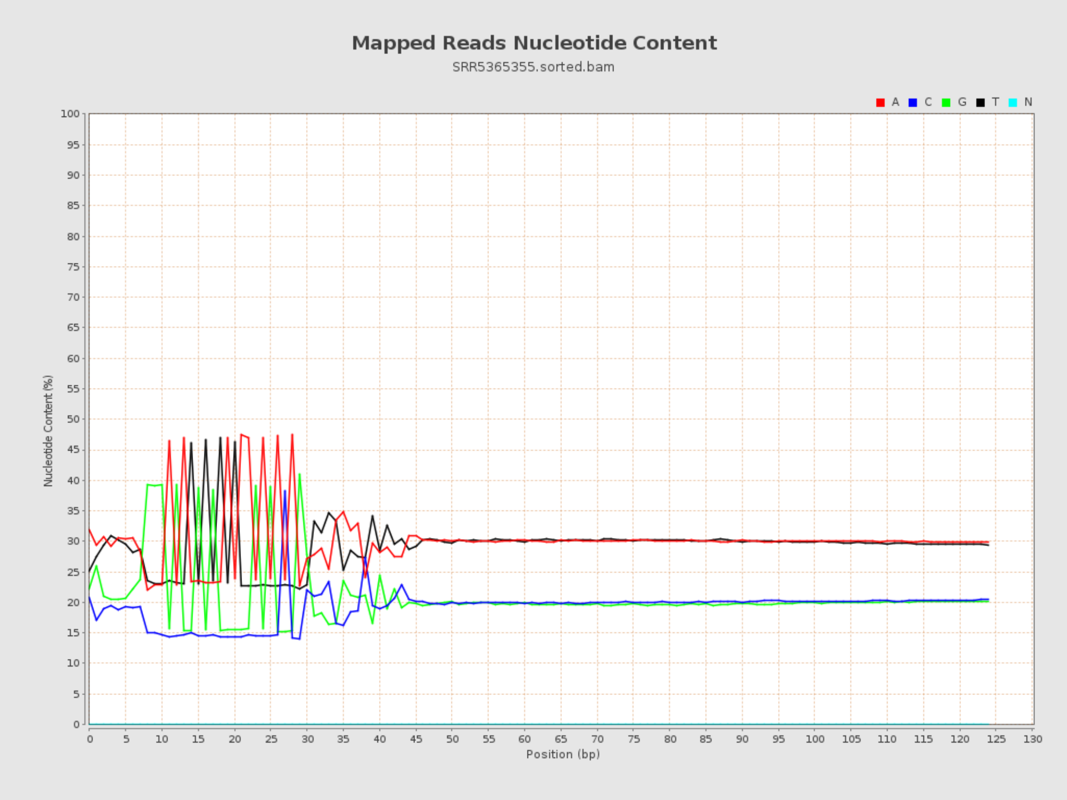
6. Results : Genome Fraction Coverage



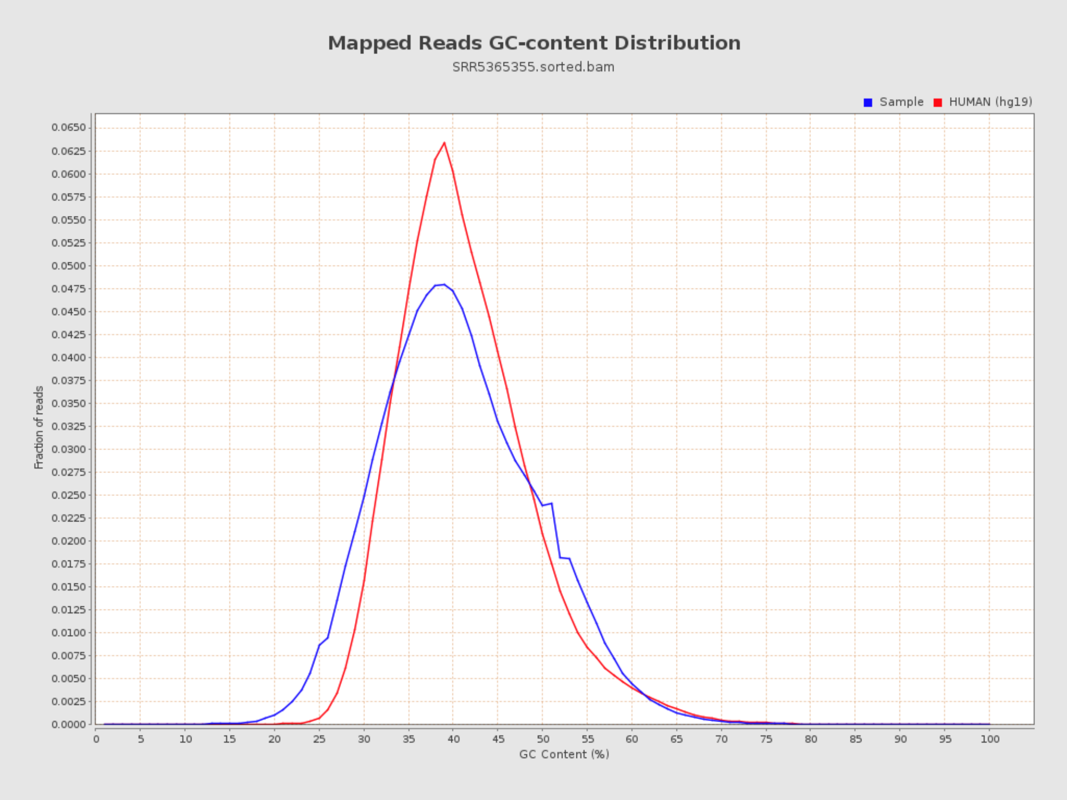
7. Results : Duplication Rate Histogram



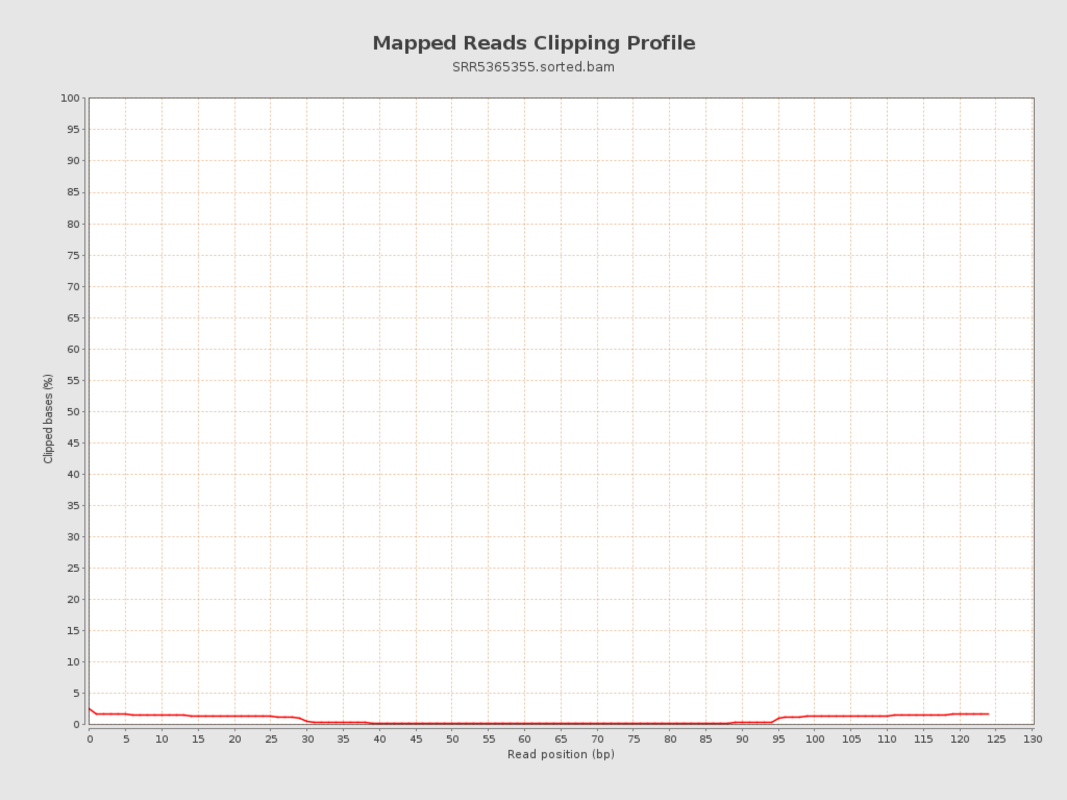
8. Results : Mapped Reads Nucleotide Content



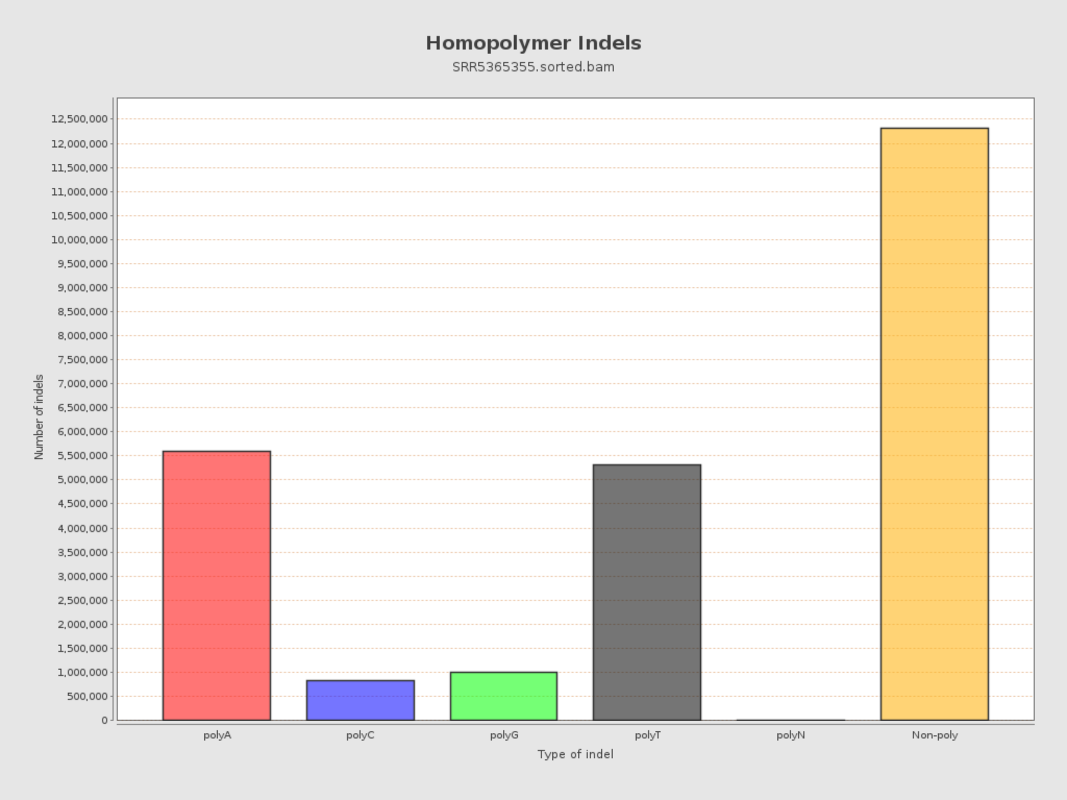
9. Results : Mapped Reads GC-content Distribution



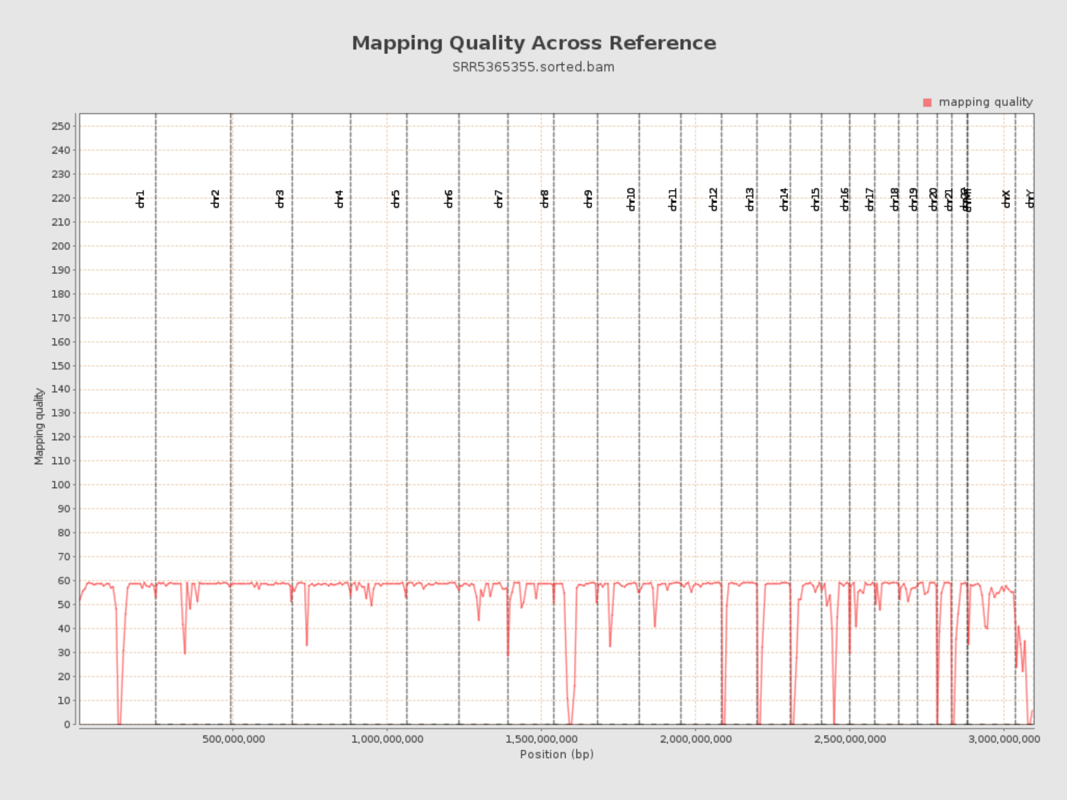
10. Results : Mapped Reads Clipping Profile



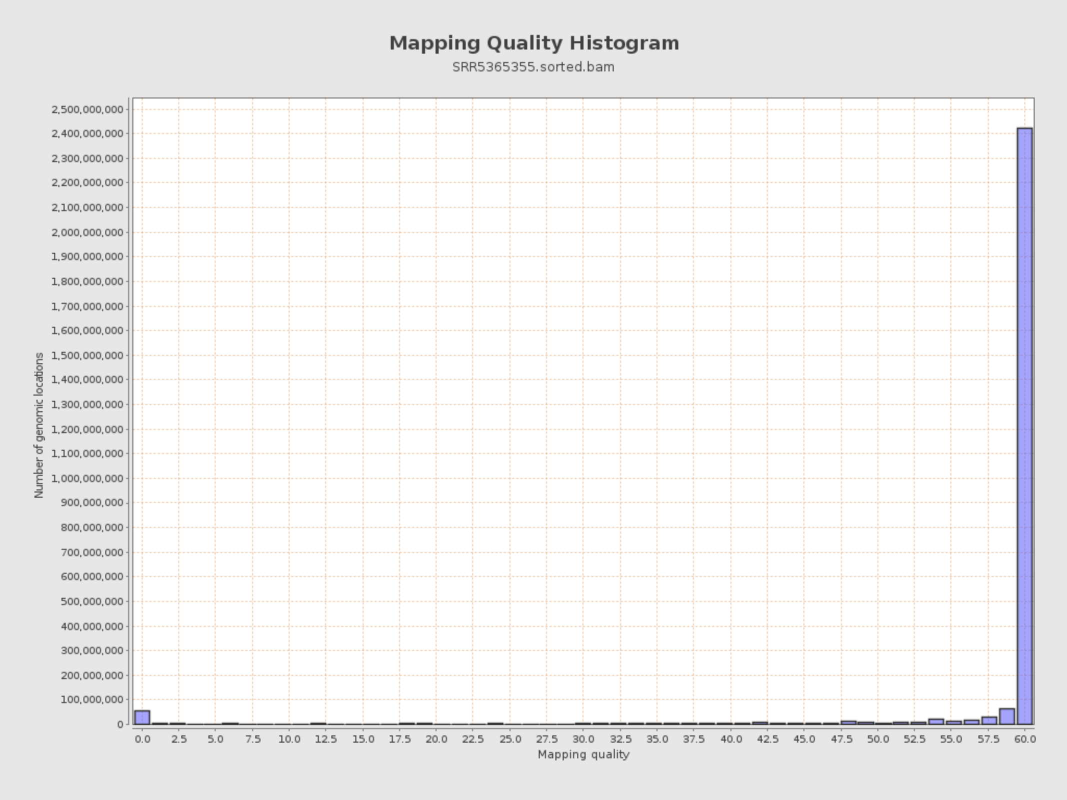
11. Results : Homopolymer Indels



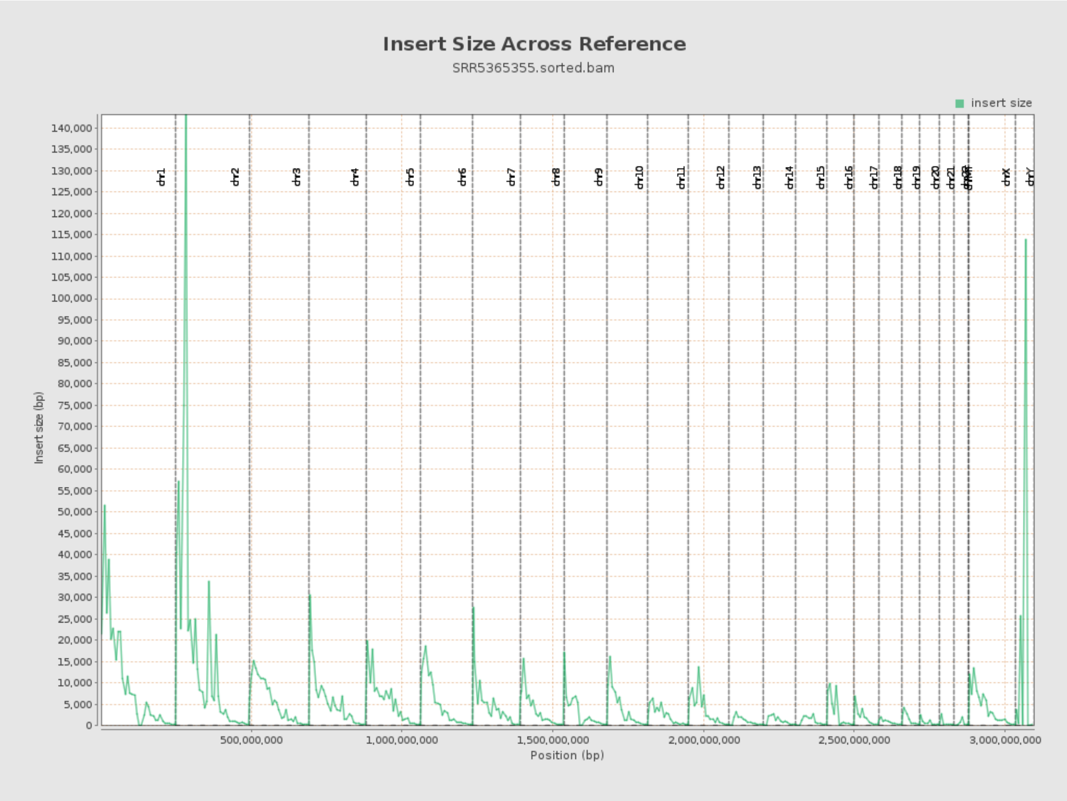
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram