Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/02 11:43:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365336.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_SRR5365336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365336_1.fastq.gz SRR5365336_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Nov 02 11:43:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	144,680,966
Mapped reads	142,032,397 / 98.17%
Unmapped reads	2,648,569 / 1.83%
Mapped paired reads	142,032,397 / 98.17%
Mapped reads, first in pair	71,286,512 / 49.27%
Mapped reads, second in pair	70,745,885 / 48.9%
Mapped reads, both in pair	141,255,144 / 97.63%
Mapped reads, singletons	777,253 / 0.54%
Secondary alignments	0
Supplementary alignments	1,201,693 / 0.83%
Read min/max/mean length	30 / 151 / 151.37
Duplicated reads (estimated)	67,045,914 / 46.34%
Duplication rate	30.45%
Clipped reads	84,653,977 / 58.51%

2.2. ACGT Content

Number/percentage of A's	5,545,374,676 / 29.65%
Number/percentage of C's	3,756,584,941 / 20.09%
Number/percentage of T's	5,455,273,271 / 29.17%
Number/percentage of G's	3,945,366,076 / 21.09%
Number/percentage of N's	669,621 / 0%

GC Percentage	41.18%

2.3. Coverage

Mean	6.0439
Standard Deviation	62.584

2.4. Mapping Quality

Mean Mapping Quality	54.23

2.5. Insert size

Mean	81,853.47
Standard Deviation	2,828,064.9
P25/Median/P75	150 / 206 / 283

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	135,635,727
Insertions	5,458,247
Mapped reads with at least one insertion	3.73%
Deletions	2,893,726
Mapped reads with at least one deletion	1.97%
Homopolymer indels	50%

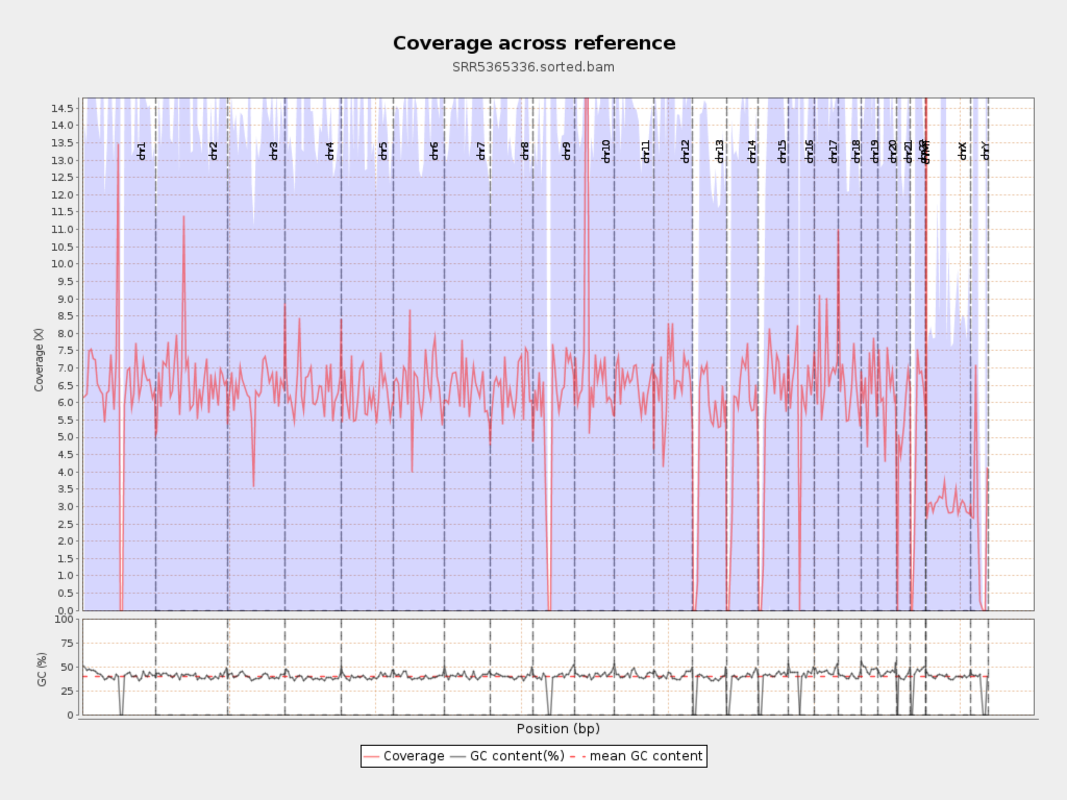
2.7. Chromosome stats

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

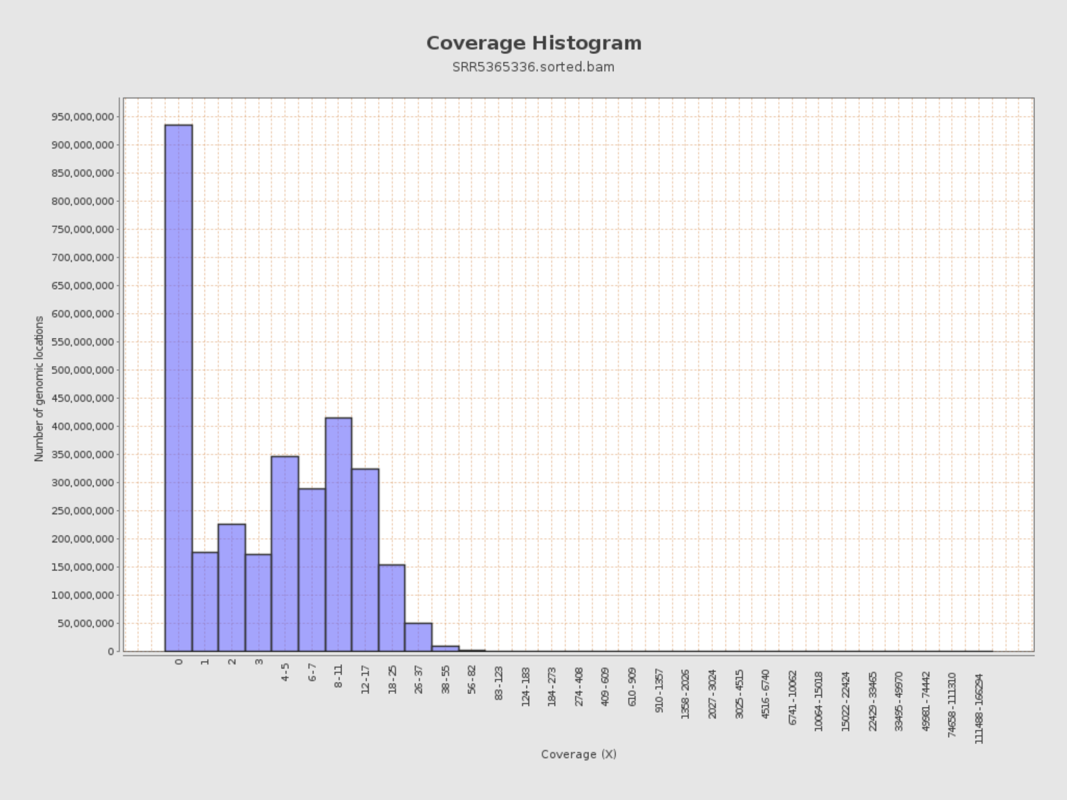
		bases	coverage	deviation
chr1	249250621	1596122767	6.4037	164.5149
chr2	243199373	1635938706	6.7267	38.0506
chr3	198022430	1257154406	6.3485	8.9355
chr4	191154276	1222435099	6.395	28.7995
chr5	180915260	1123281968	6.2089	8.1792
chr6	171115067	1112912679	6.5039	25.6764
chr7	159138663	1013663903	6.3697	45.5841
chr8	146364022	939204924	6.4169	20.5467
chr9	141213431	810858518	5.7421	63.0461
chr10	135534747	992374088	7.3219	130.3606
chr11	135006516	883011220	6.5405	39.9748
chr12	133851895	896541327	6.698	33.6111
chr13	115169878	581645858	5.0503	6.5737
chr14	107349540	574470005	5.3514	7.4148
chr15	102531392	546358663	5.3287	17.5702
chr16	90354753	551711294	6.1061	19.8589
chr17	81195210	569297354	7.0115	31.0291
chr18	78077248	511794377	6.555	63.4294
chr19	59128983	378853826	6.4072	82.9395
chr20	63025520	399100376	6.3324	12.3009
chr21	48129895	248521886	5.1636	20.6478
chr22	51304566	240321643	4.6842	18.2657
chrMT	16571	6631942	400.2137	89.4131
chrX	155270560	473857870	3.0518	13.0285

chrY	59373566	144027008	2.4258	49.7638

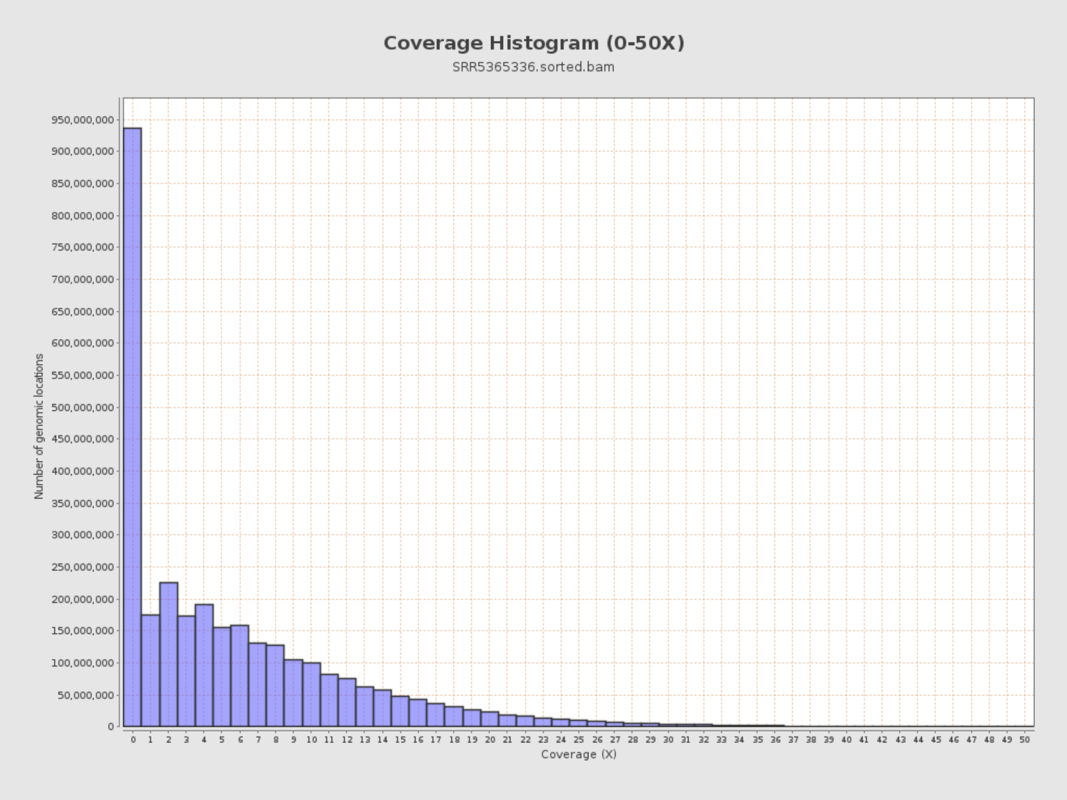
3. Results : Coverage across reference



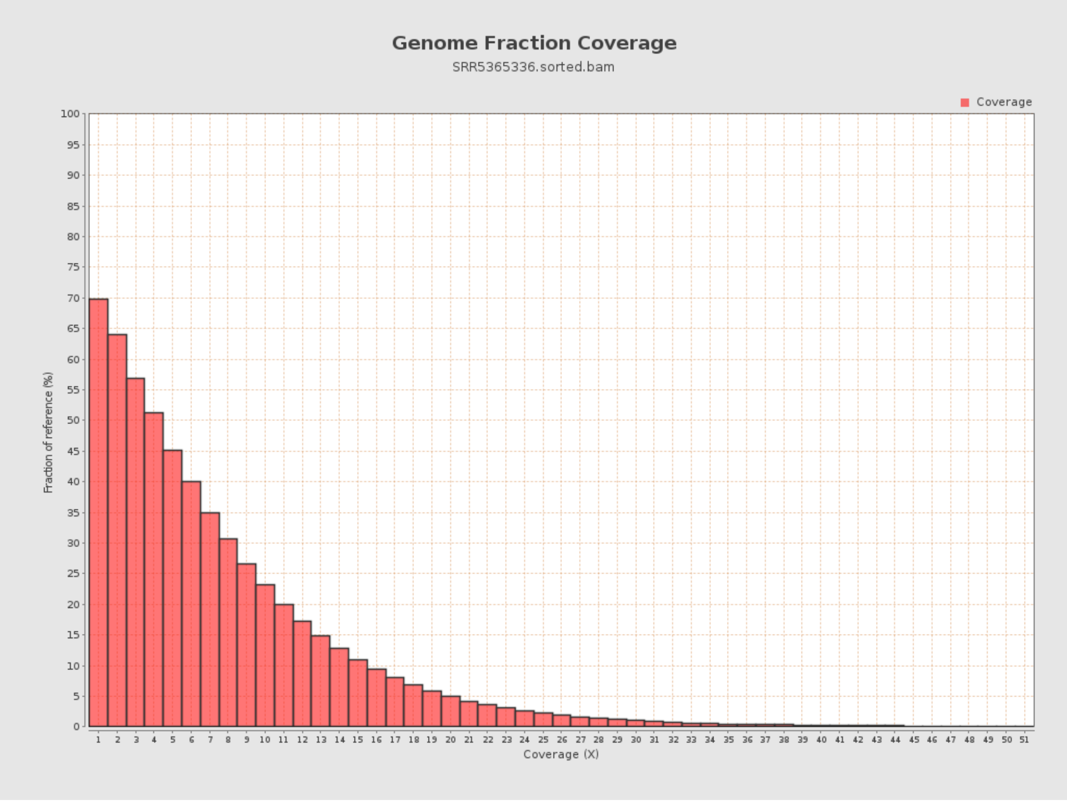
4. Results : Coverage Histogram



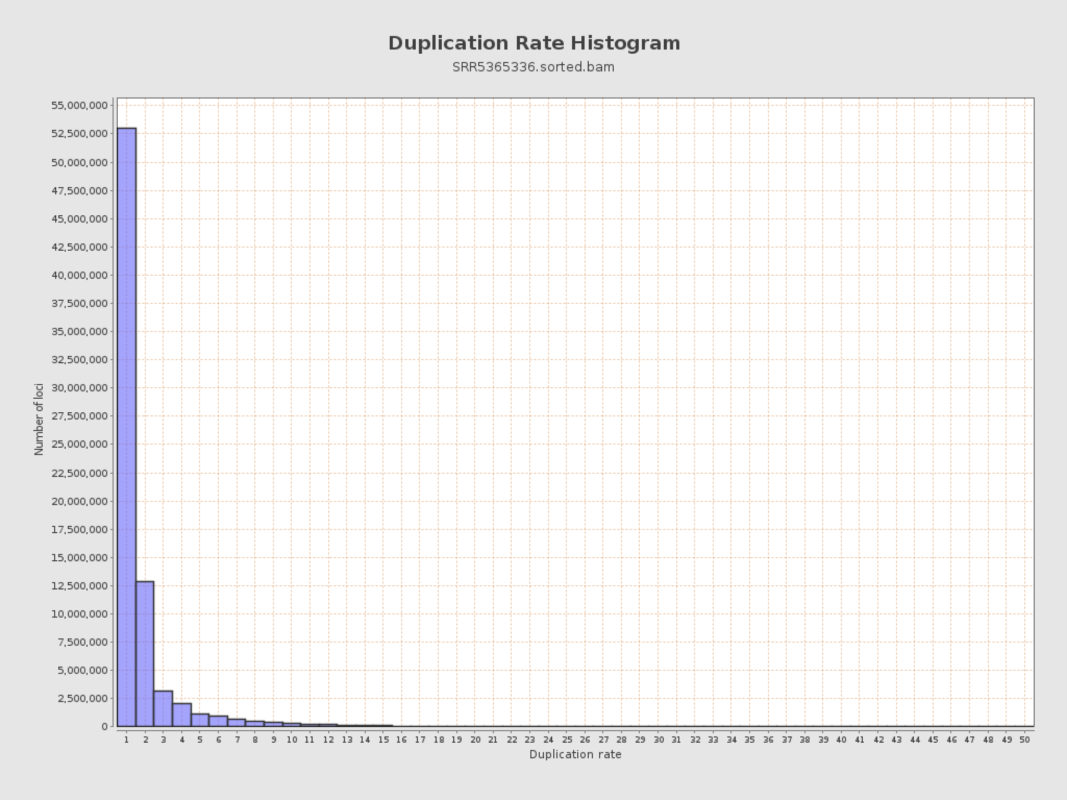
5. Results : Coverage Histogram (0-50X)



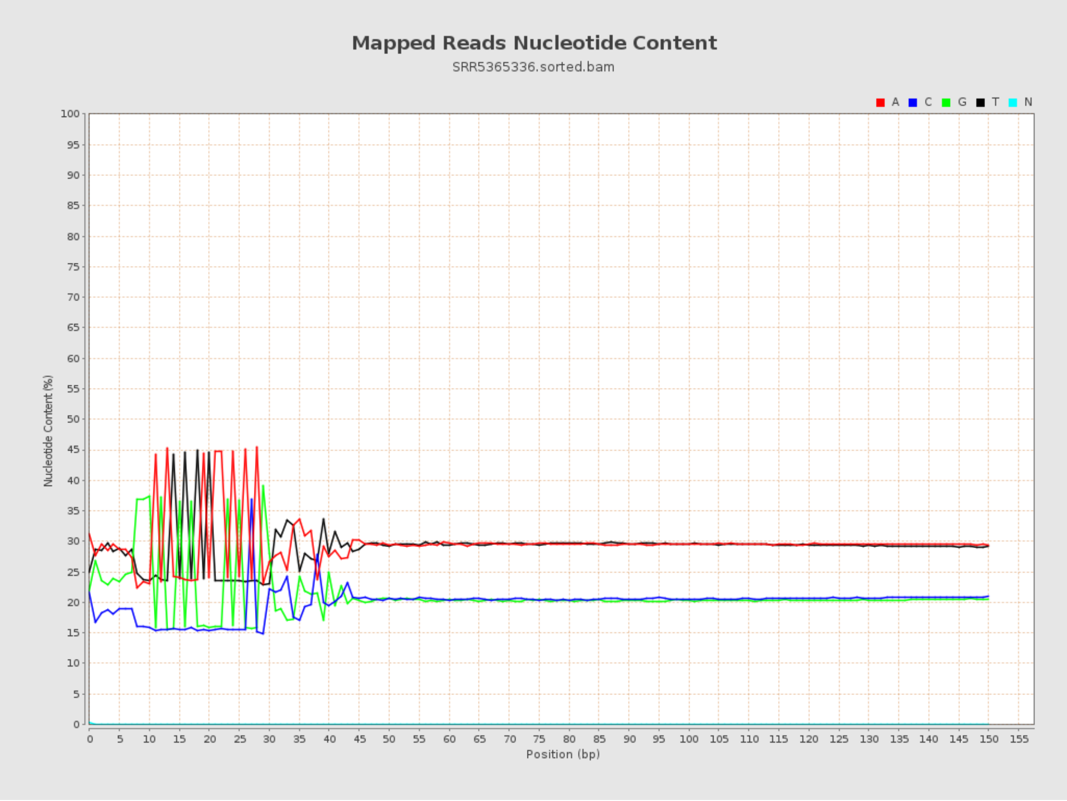
6. Results : Genome Fraction Coverage



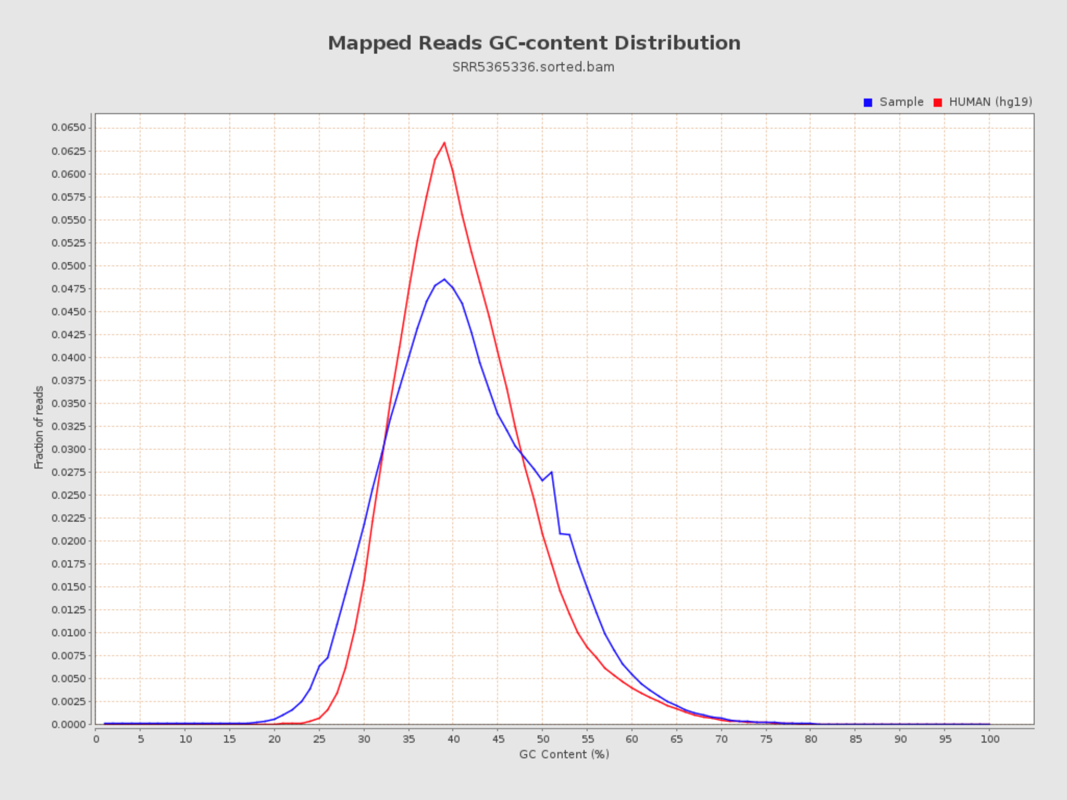
7. Results : Duplication Rate Histogram



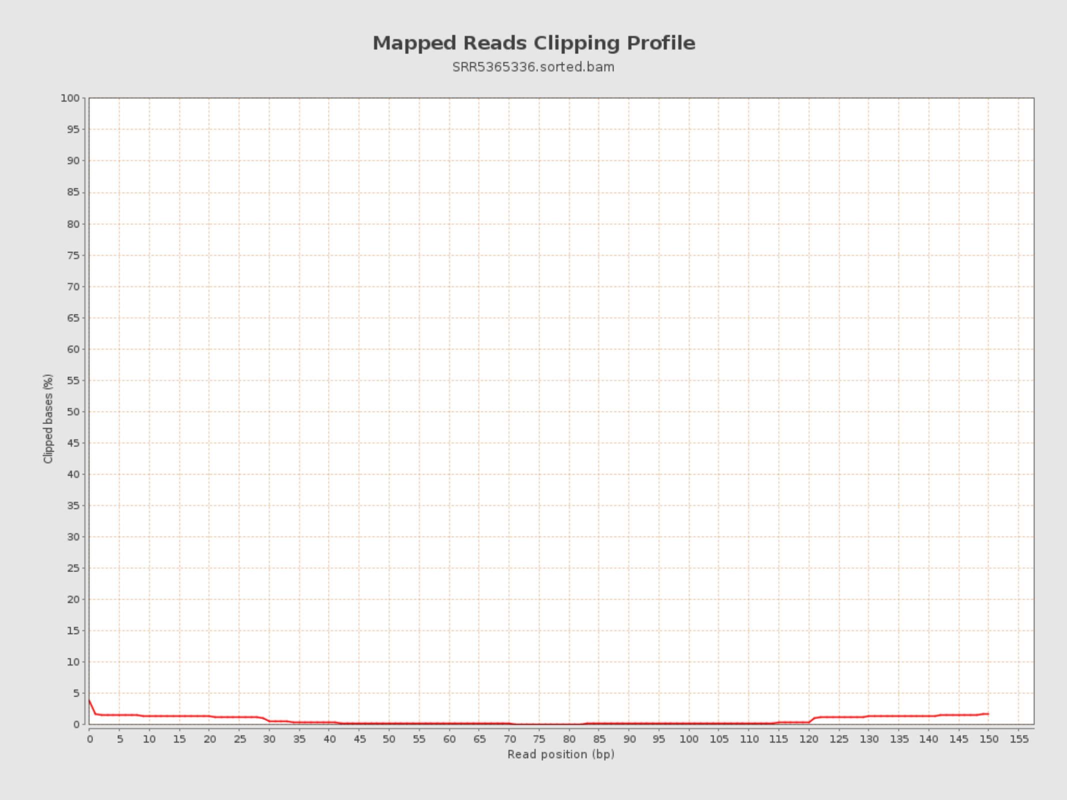
8. Results : Mapped Reads Nucleotide Content



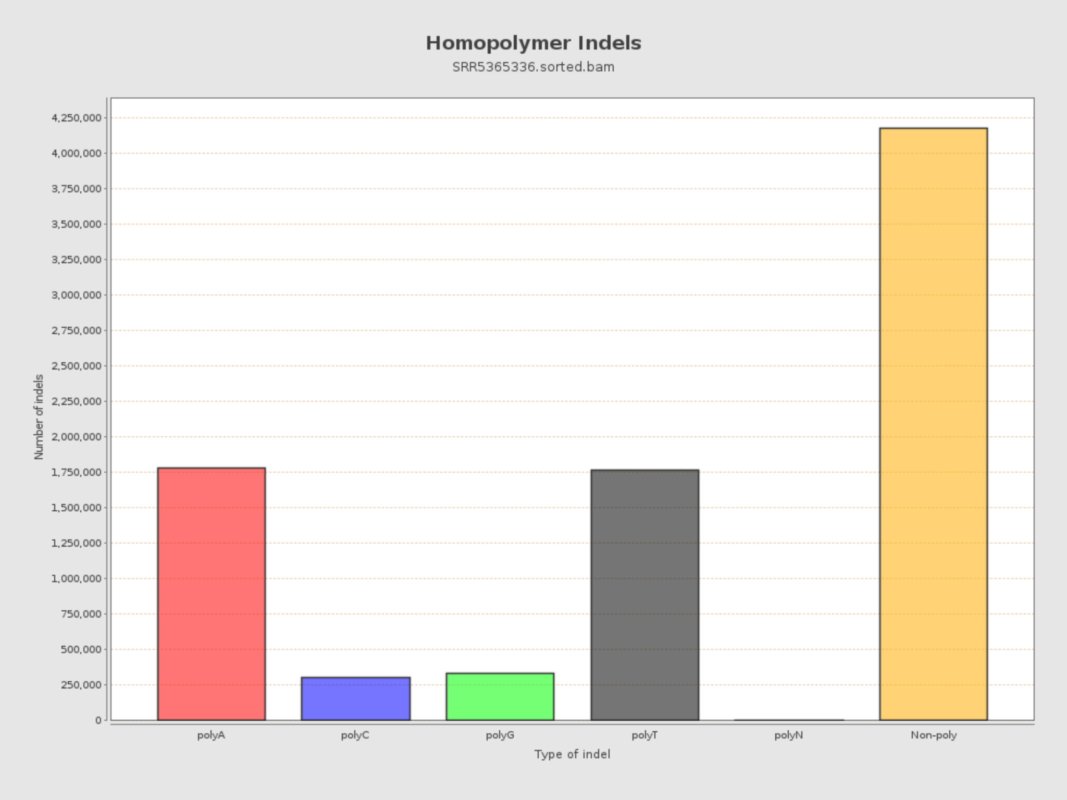
9. Results : Mapped Reads GC-content Distribution



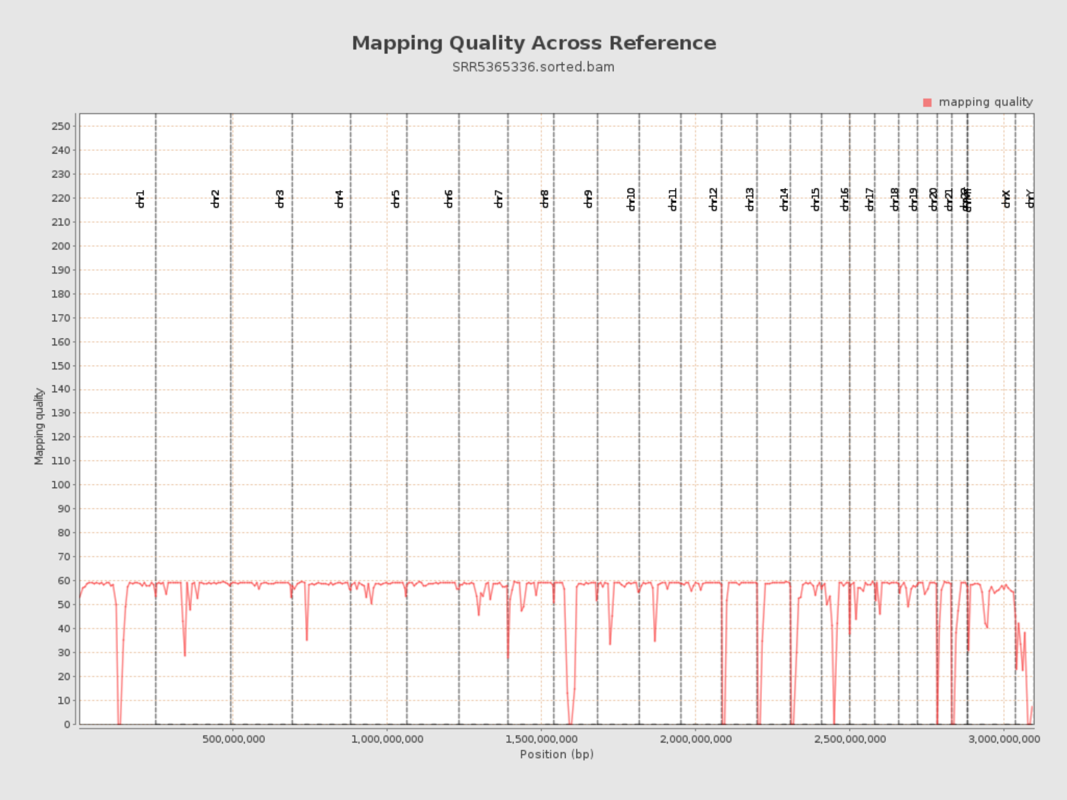
10. Results : Mapped Reads Clipping Profile



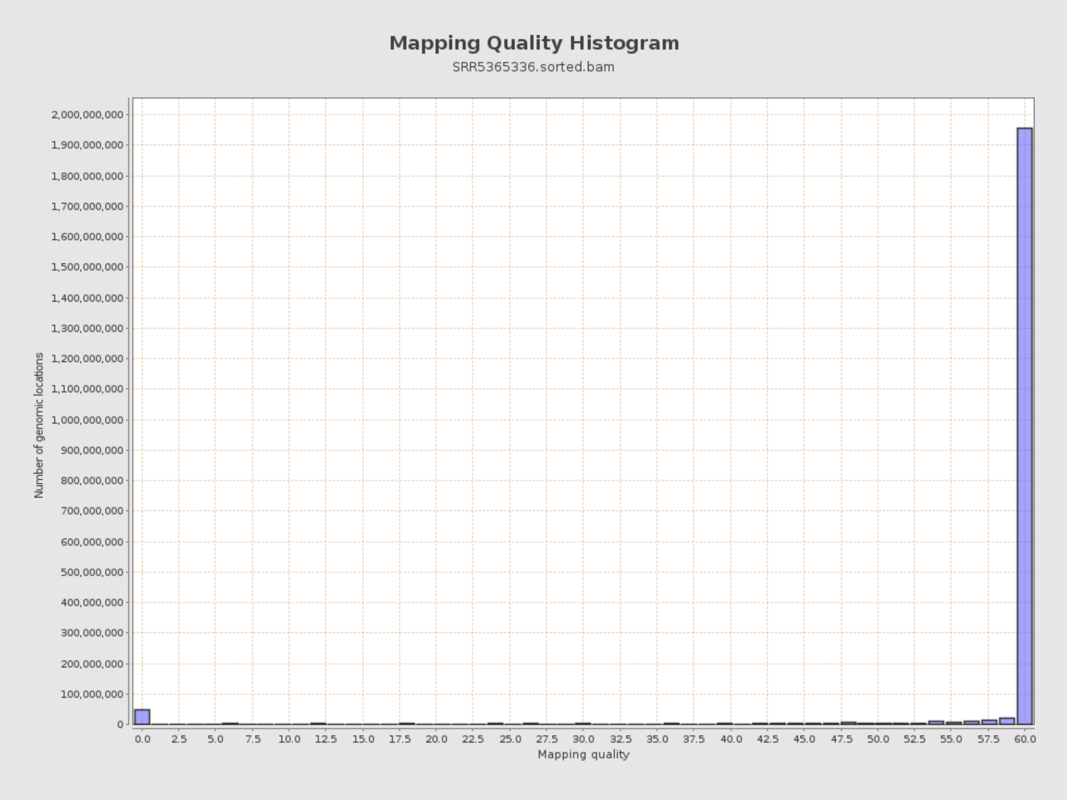
11. Results : Homopolymer Indels



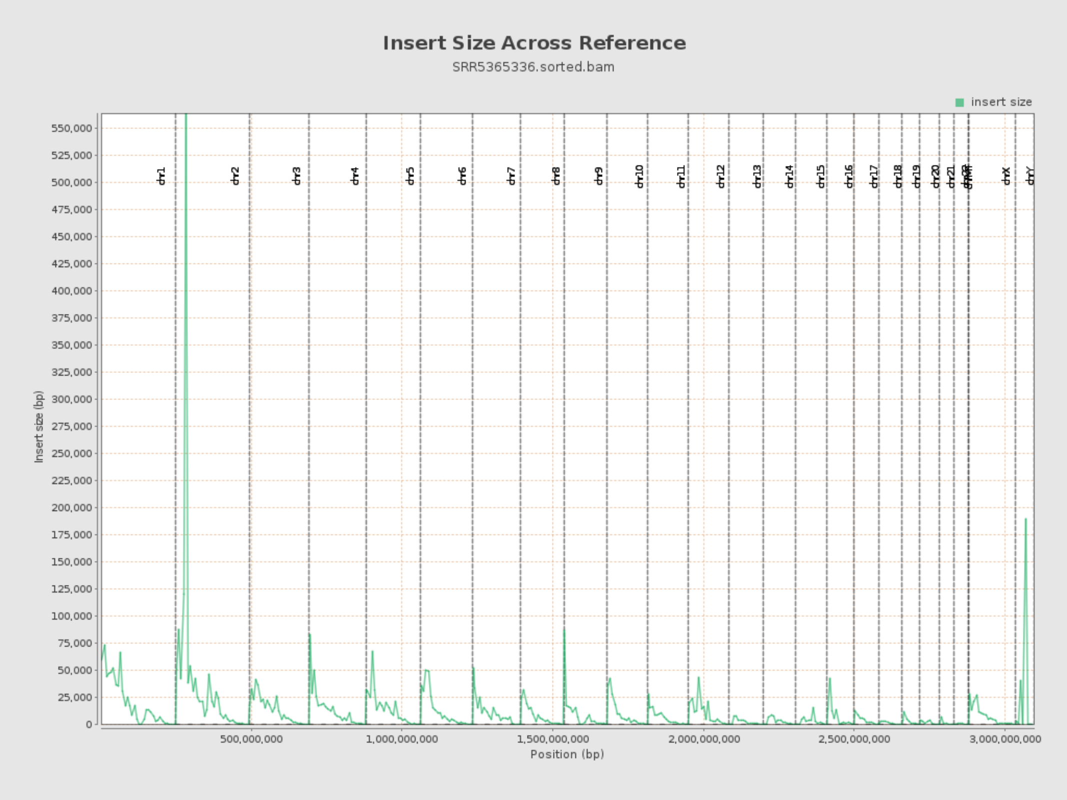
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram