Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/25 01:14:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365369.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_SRR5365369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365369_1.fastq.gz SRR5365369_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 25 01:14:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	637,397,960
Mapped reads	593,936,696 / 93.18%
Unmapped reads	43,461,264 / 6.82%
Mapped paired reads	593,936,696 / 93.18%
Mapped reads, first in pair	297,110,111 / 46.61%
Mapped reads, second in pair	296,826,585 / 46.57%
Mapped reads, both in pair	590,313,268 / 92.61%
Mapped reads, singletons	3,623,428 / 0.57%
Secondary alignments	0
Supplementary alignments	6,666,331 / 1.05%
Read min/max/mean length	30 / 150 / 150.53
Duplicated reads (estimated)	296,853,460 / 46.57%
Duplication rate	43.71%
Clipped reads	240,475,270 / 37.73%

2.2. ACGT Content

Number/percentage of A's	21,381,190,412 / 26.22%
Number/percentage of C's	19,149,094,083 / 23.48%
Number/percentage of T's	20,973,982,162 / 25.72%
Number/percentage of G's	20,038,668,020 / 24.57%
Number/percentage of N's	1,062,087 / 0%

GC Percentage	48.06%

2.3. Coverage

Mean	26.3602
Standard Deviation	87.4743

2.4. Mapping Quality

Mean Mapping Quality	54.51

2.5. Insert size

Mean	58,624.09
Standard Deviation	2,458,138.44
P25/Median/P75	142 / 178 / 221

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	780,404,775
Insertions	12,034,065
Mapped reads with at least one insertion	1.96%
Deletions	40,720,116
Mapped reads with at least one deletion	6.6%
Homopolymer indels	51.76%

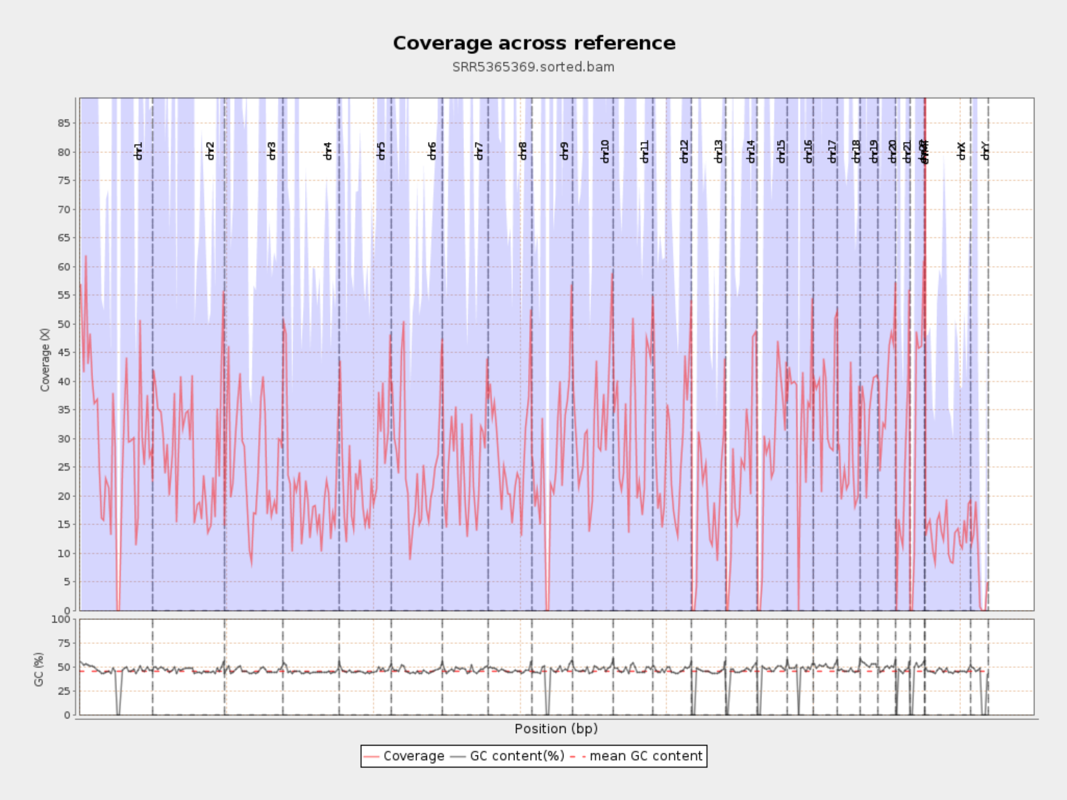
2.7. Chromosome stats

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

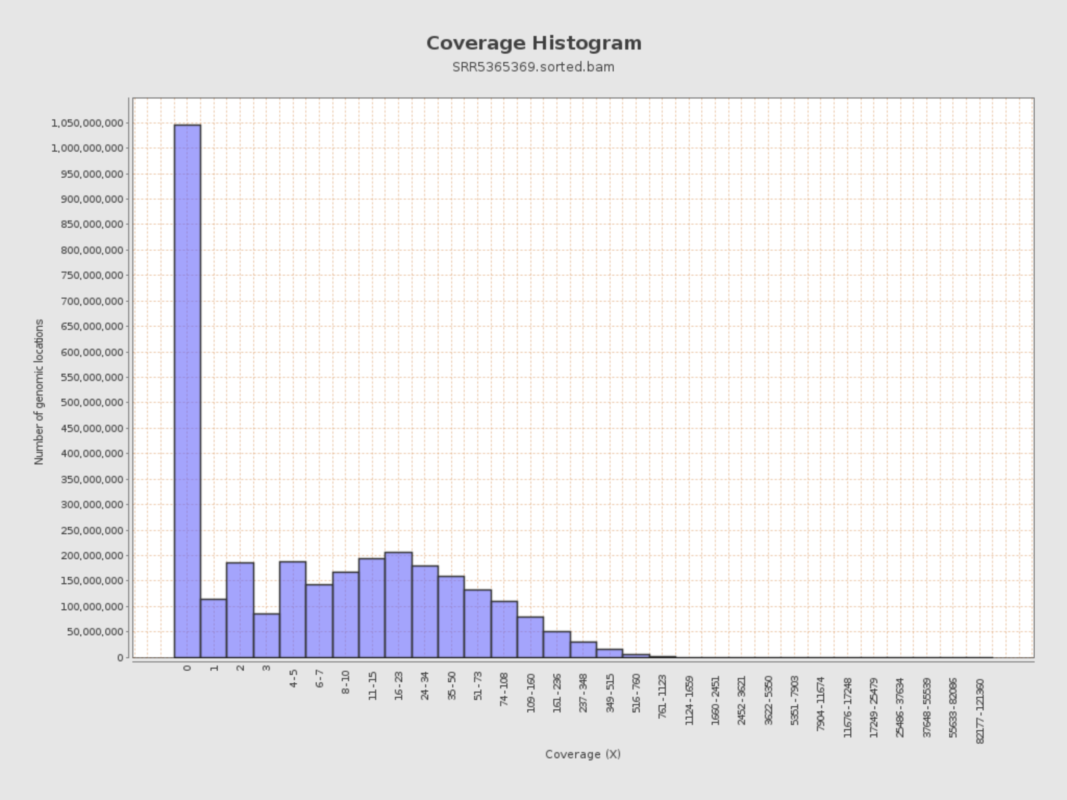
		bases	coverage	deviation
chr1	249250621	7495911278	30.0738	100.91
chr2	243199373	6841262159	28.1303	144.5771
chr3	198022430	5108842818	25.7993	60.7977
chr4	191154276	3941880613	20.6215	66.0896
chr5	180915260	4527523501	25.0257	61.0588
chr6	171115067	4268442821	24.9449	59.8443
chr7	159138663	4111122055	25.8336	64.4898
chr8	146364022	3959496048	27.0524	68.3868
chr9	141213431	3653744363	25.8739	98.1666
chr10	135534747	4268100242	31.4908	112.0565
chr11	135006516	4335479372	32.1131	89.2997
chr12	133851895	3734126905	27.8975	67.0472
chr13	115169878	2060791486	17.8935	47.6411
chr14	107349540	2522834342	23.5011	62.1412
chr15	102531392	2678777031	26.1264	65.0679
chr16	90354753	3132373505	34.6675	143.5096
chr17	81195210	3003984746	36.9971	88.14
chr18	78077248	2023186729	25.9126	106.5532
chr19	59128983	2099692051	35.5104	91.5696
chr20	63025520	2496062865	39.604	88.9791
chr21	48129895	1097093244	22.7944	99.7418
chr22	51304566	1730994552	33.7396	84.1453
chrMT	16571	6588005	397.5623	362.1741
chrX	155270560	2062715299	13.2847	36.6218

chrY	59373566	442167593	7.4472	89.475

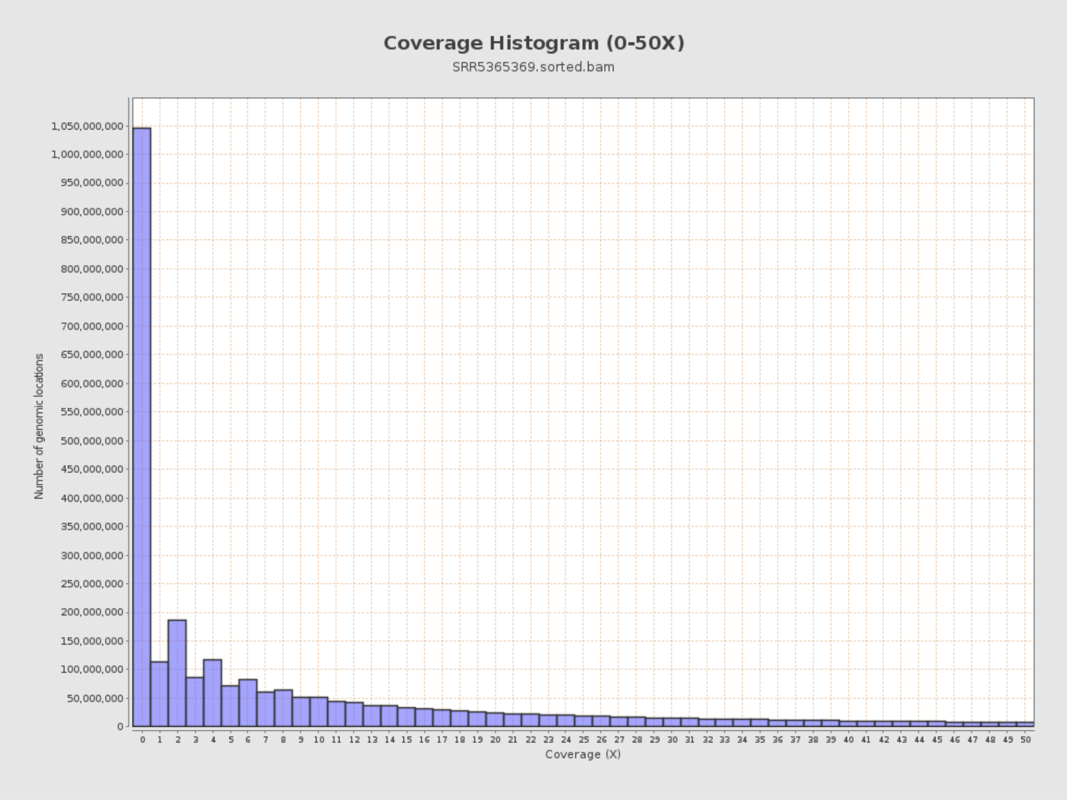
3. Results : Coverage across reference



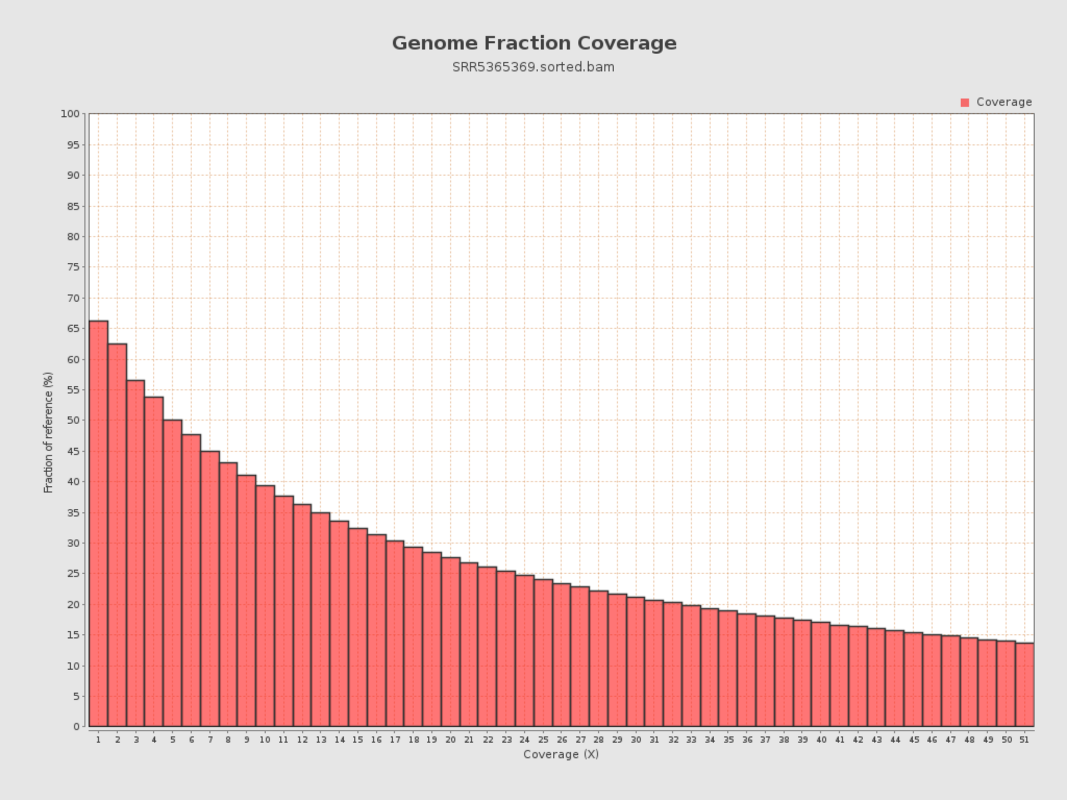
4. Results : Coverage Histogram



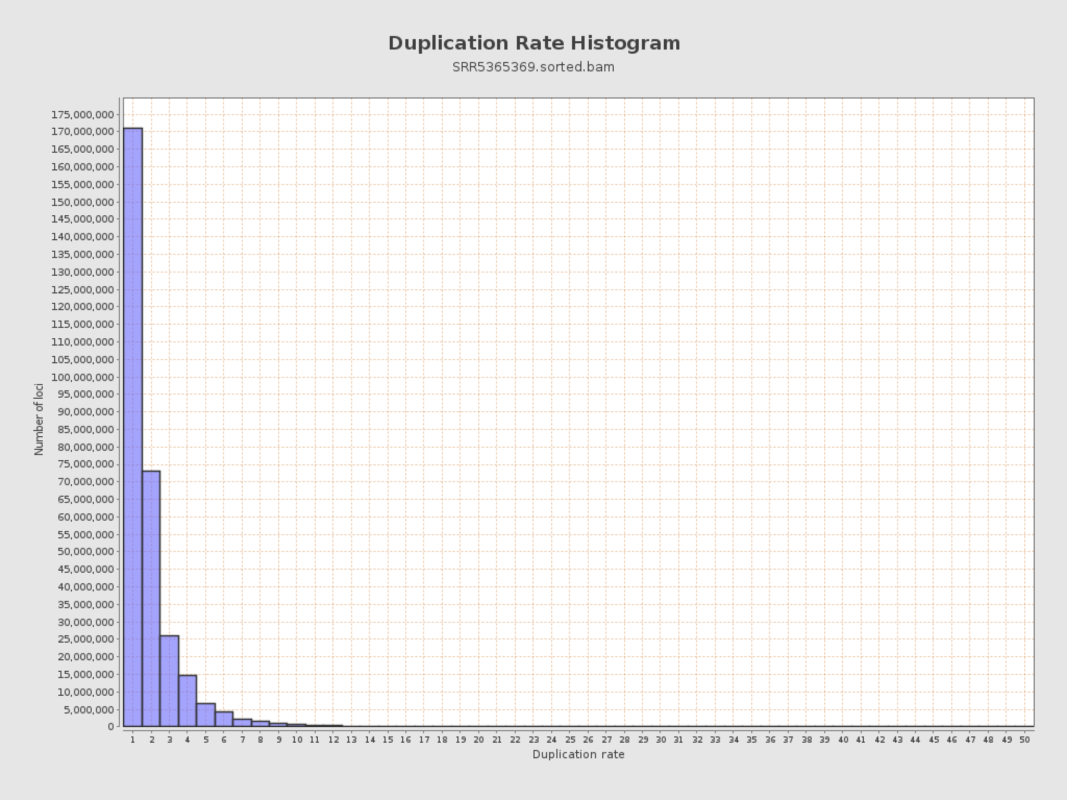
5. Results : Coverage Histogram (0-50X)



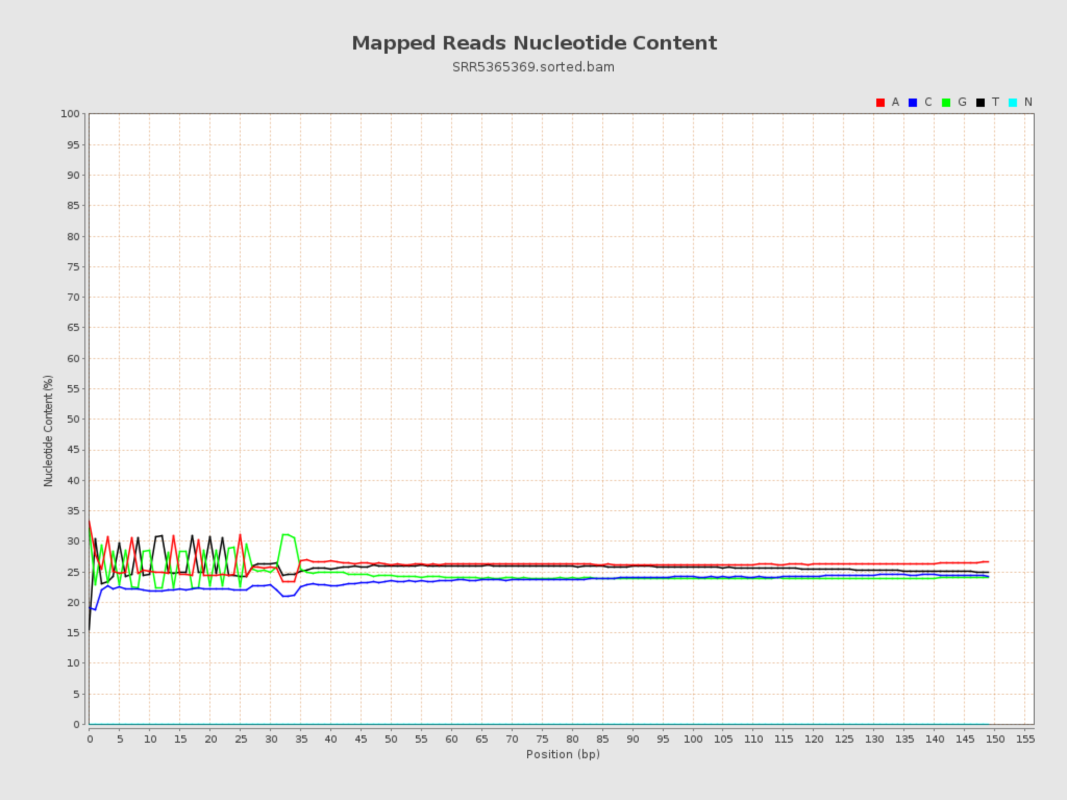
6. Results : Genome Fraction Coverage



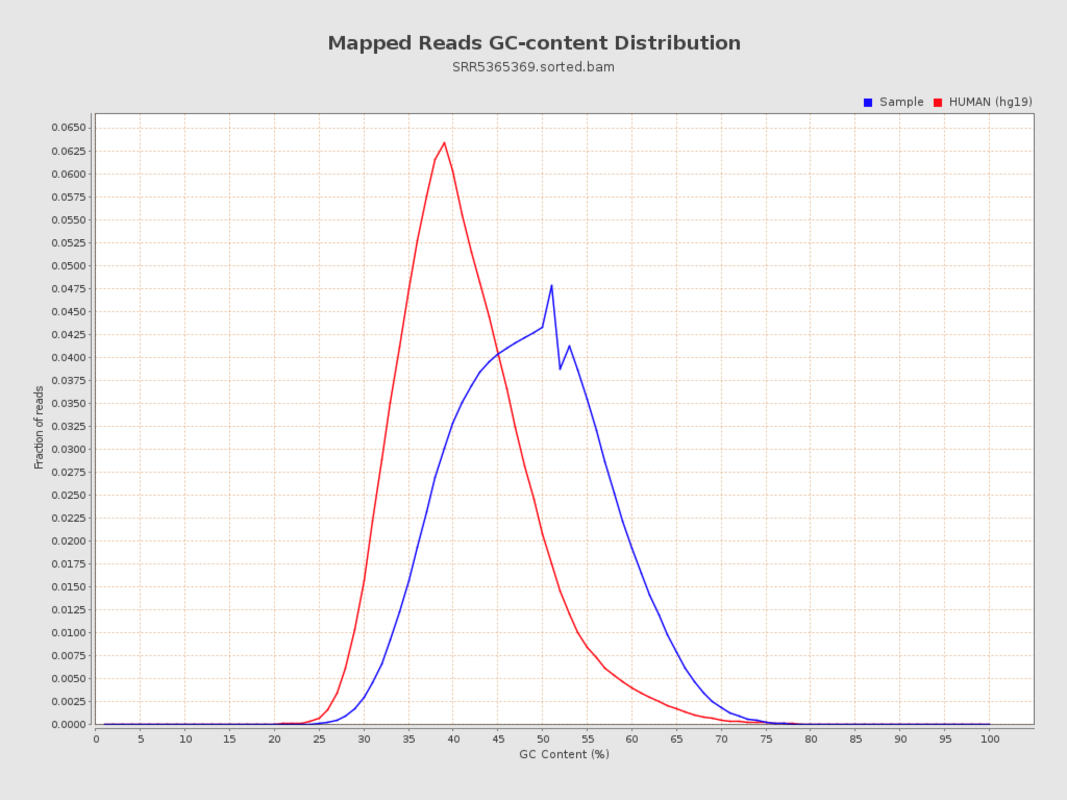
7. Results : Duplication Rate Histogram



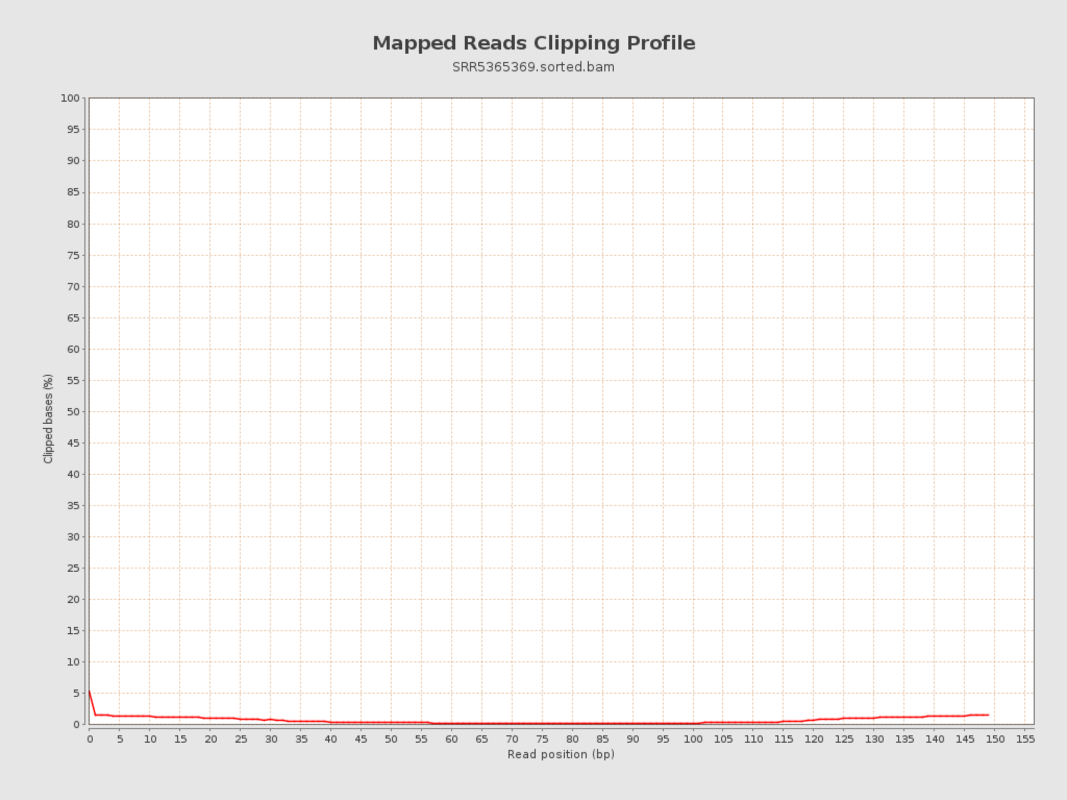
8. Results : Mapped Reads Nucleotide Content



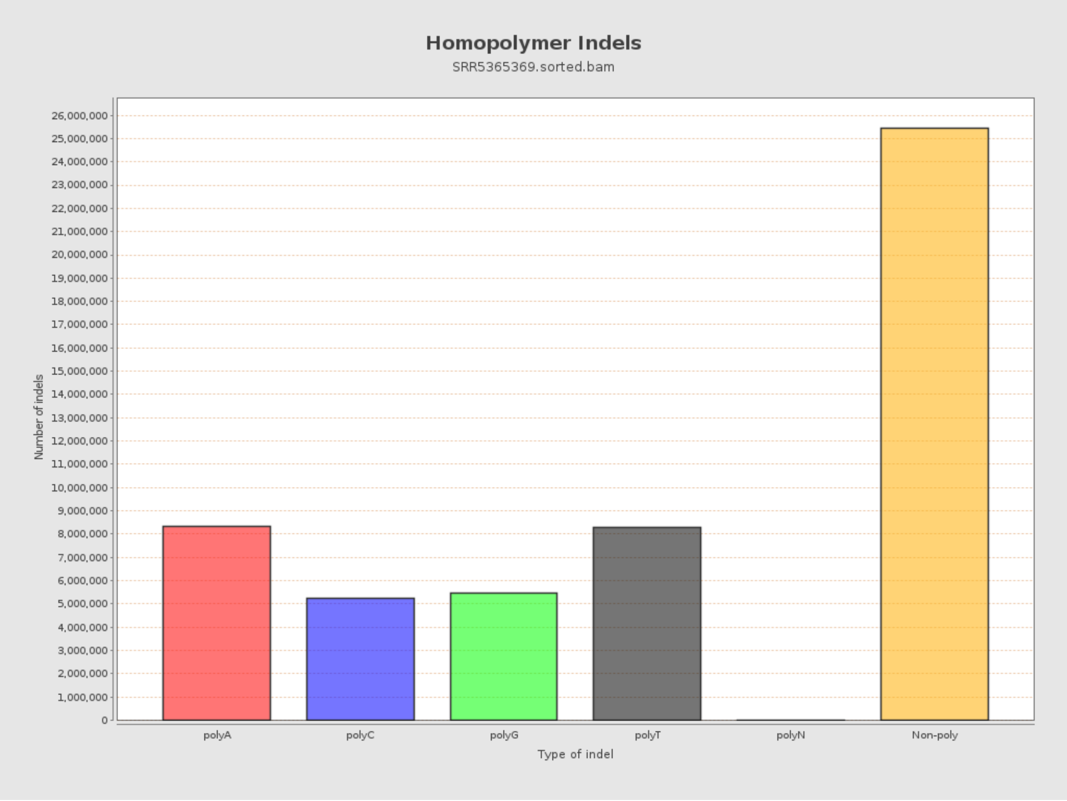
9. Results : Mapped Reads GC-content Distribution



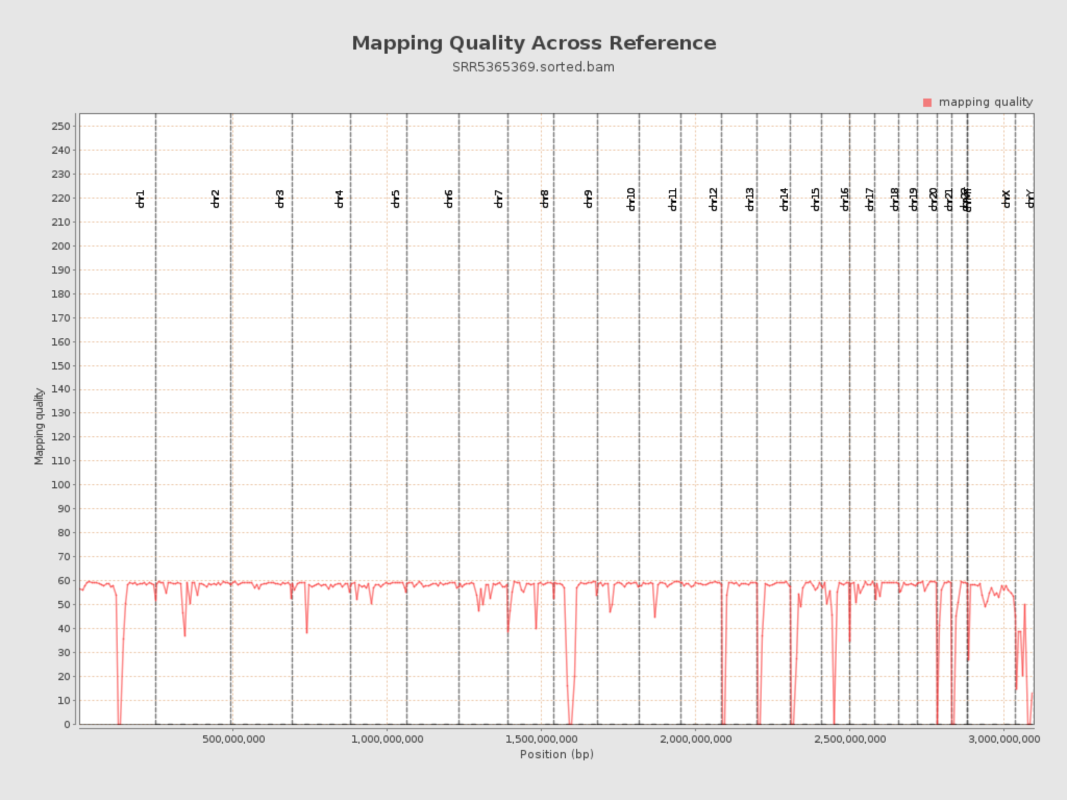
10. Results : Mapped Reads Clipping Profile



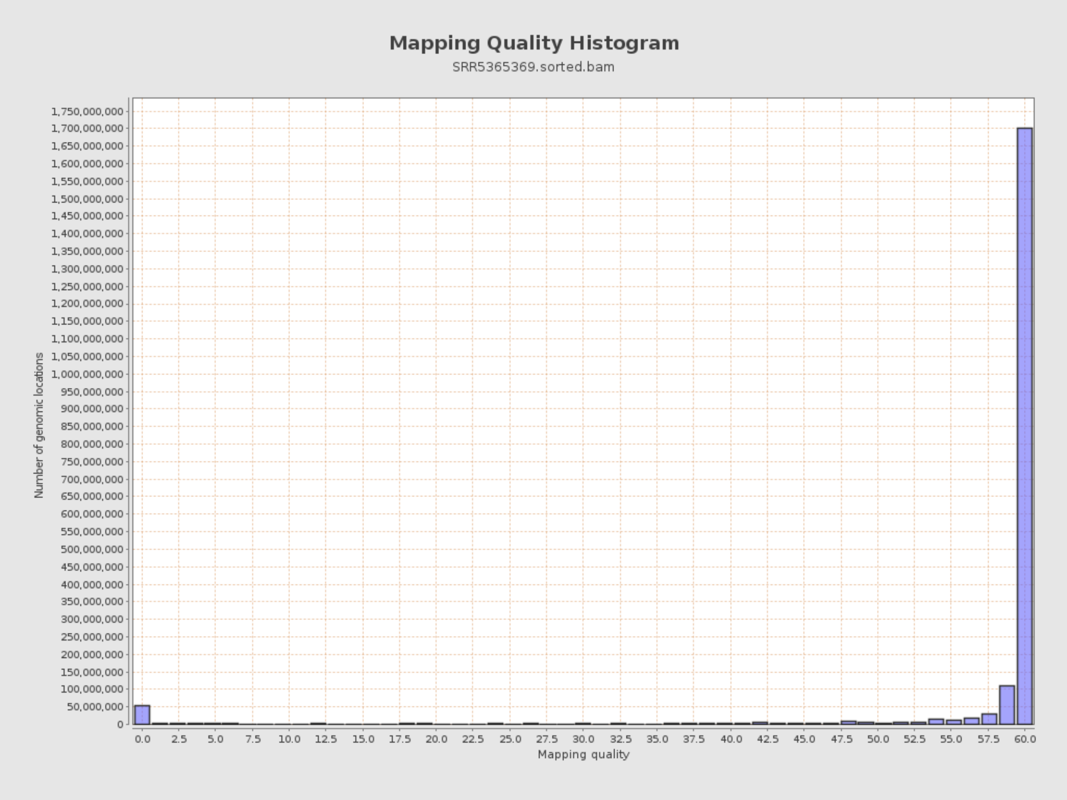
11. Results : Homopolymer Indels



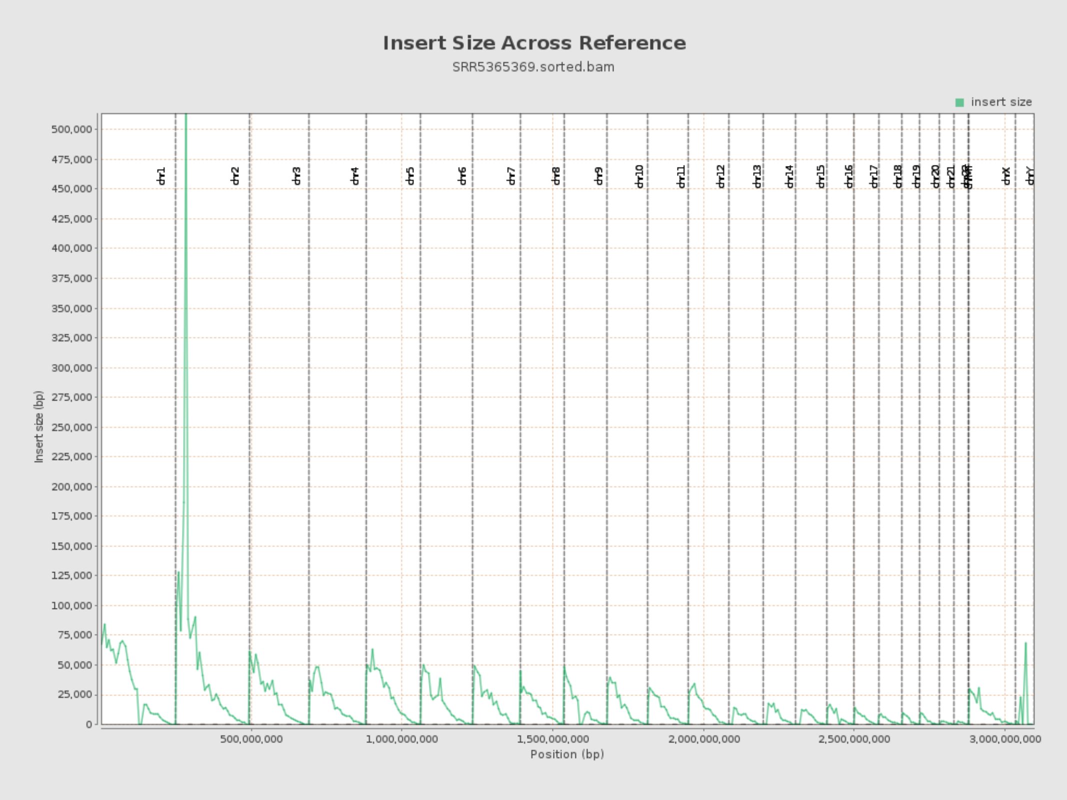
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram