Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/18 13:04:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365367.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_SRR5365367 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365367_1.fastq.gz SRR5365367_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 18 13:04:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365367.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	291,200,364
Mapped reads	266,965,642 / 91.68%
Unmapped reads	24,234,722 / 8.32%
Mapped paired reads	266,965,642 / 91.68%
Mapped reads, first in pair	133,834,382 / 45.96%
Mapped reads, second in pair	133,131,260 / 45.72%
Mapped reads, both in pair	261,902,612 / 89.94%
Mapped reads, singletons	5,063,030 / 1.74%
Secondary alignments	0
Supplementary alignments	11,082,382 / 3.81%
Read min/max/mean length	30 / 150 / 151.82
Duplicated reads (estimated)	161,046,915 / 55.3%
Duplication rate	38.6%
Clipped reads	196,481,884 / 67.47%

2.2. ACGT Content

Number/percentage of A's	9,512,492,142 / 27.99%
Number/percentage of C's	7,054,932,024 / 20.76%
Number/percentage of T's	9,754,638,918 / 28.7%
Number/percentage of G's	7,662,286,004 / 22.55%
Number/percentage of N's	1,401,746 / 0%

GC Percentage	43.3%

2.3. Coverage

Mean	10.9847
Standard Deviation	99.6522

2.4. Mapping Quality

Mean Mapping Quality	53.26

2.5. Insert size

Mean	139,092.32
Standard Deviation	3,627,427.38
P25/Median/P75	121 / 154 / 193

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	351,894,760
Insertions	3,330,680
Mapped reads with at least one insertion	1.19%
Deletions	9,205,454
Mapped reads with at least one deletion	3.35%
Homopolymer indels	43.32%

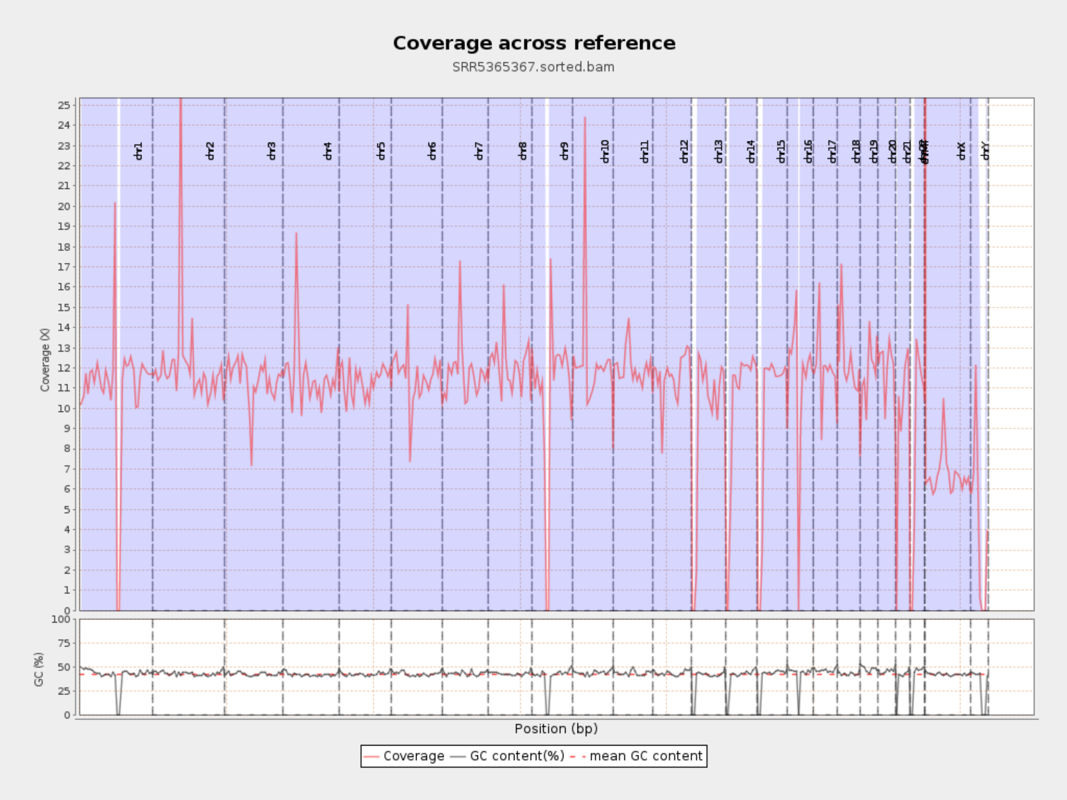
2.7. Chromosome stats

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

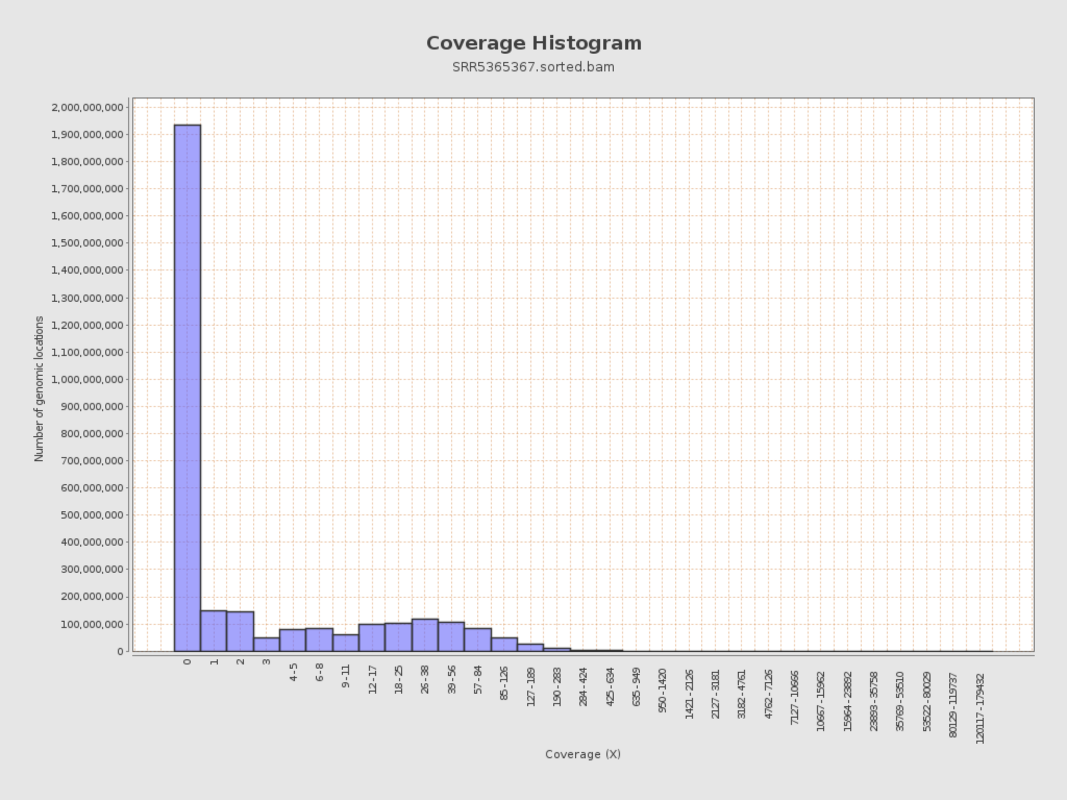
		bases	coverage	deviation
chr1	249250621	2750612659	11.0355	183.6359
chr2	243199373	2973324108	12.2259	127.3892
chr3	198022430	2260392430	11.4148	31.521
chr4	191154276	2217350864	11.5998	57.6992
chr5	180915260	2053093793	11.3484	34.5952
chr6	171115067	1985269769	11.602	56.6629
chr7	159138663	1875419443	11.7848	129.1211
chr8	146364022	1783128900	12.1828	59.8301
chr9	141213431	1493237827	10.5743	152.8104
chr10	135534747	1691615179	12.481	128.9019
chr11	135006516	1611977967	11.94	144.5254
chr12	133851895	1551112153	11.5883	32.3513
chr13	115169878	1081520784	9.3907	28.341
chr14	107349540	1067916774	9.948	53.788
chr15	102531392	974532989	9.5047	29.0067
chr16	90354753	1019084678	11.2787	44.1739
chr17	81195210	964733894	11.8817	82.4827
chr18	78077248	969240037	12.4139	170.9837
chr19	59128983	688777408	11.6487	109.9692
chr20	63025520	756494694	12.003	38.1405
chr21	48129895	477023040	9.9112	54.0458
chr22	51304566	429105176	8.3639	38.8839
chrMT	16571	25256045	1,524.1111	1,048.0379
chrX	155270560	1041503755	6.7077	42.4012

chrY	59373566	263451908	4.4372	62.9595

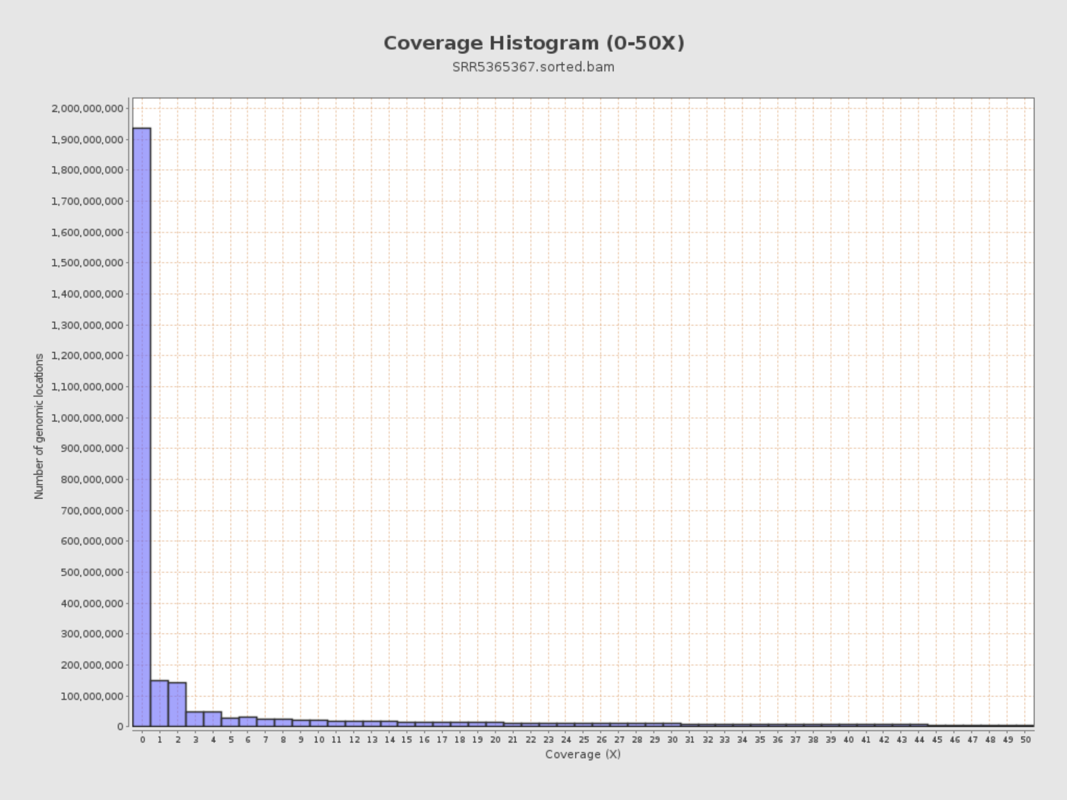
3. Results : Coverage across reference



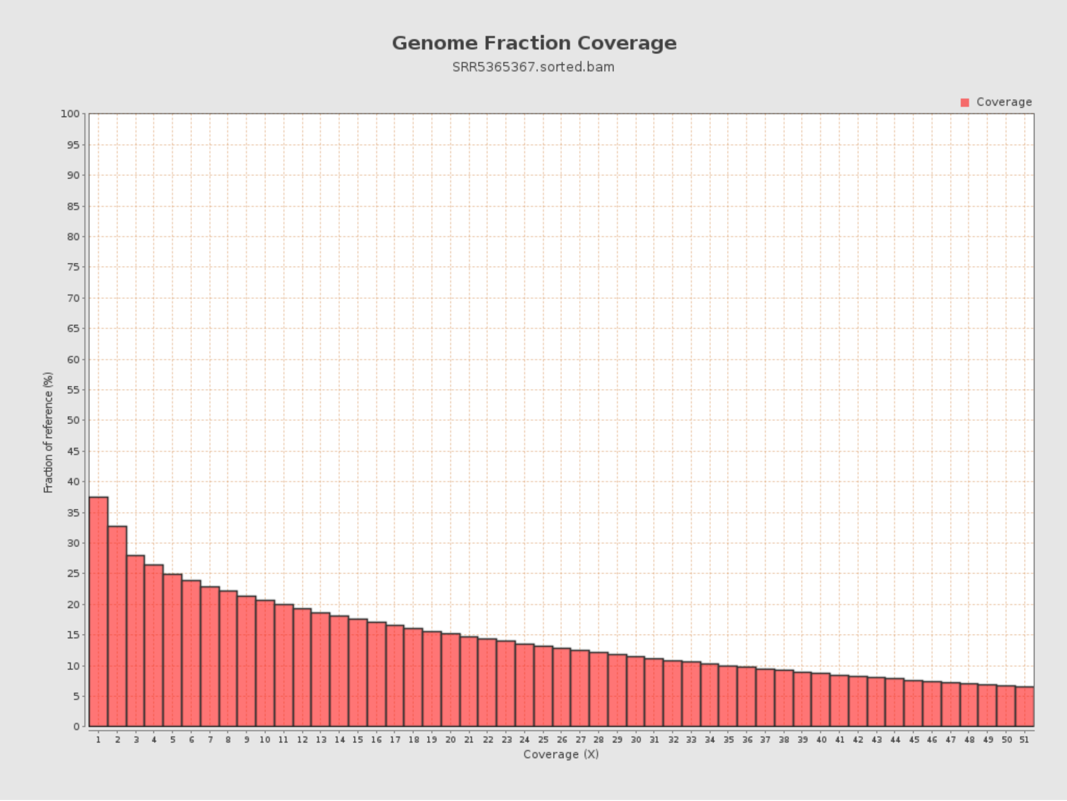
4. Results : Coverage Histogram



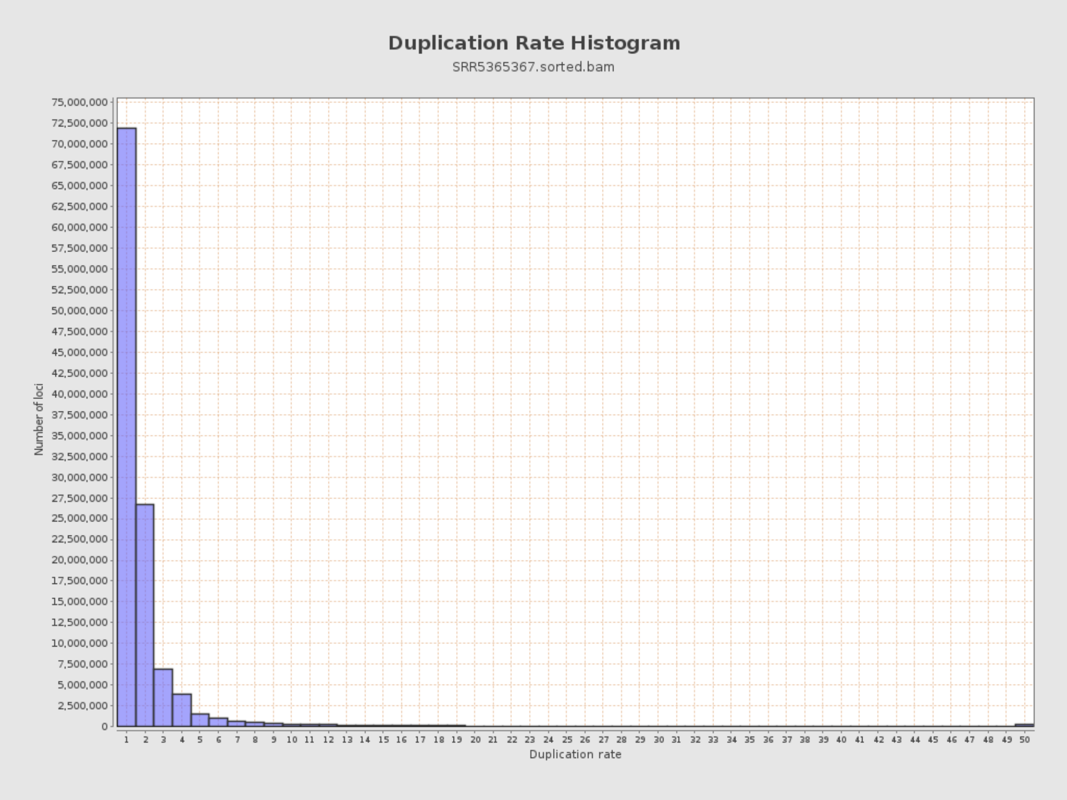
5. Results : Coverage Histogram (0-50X)



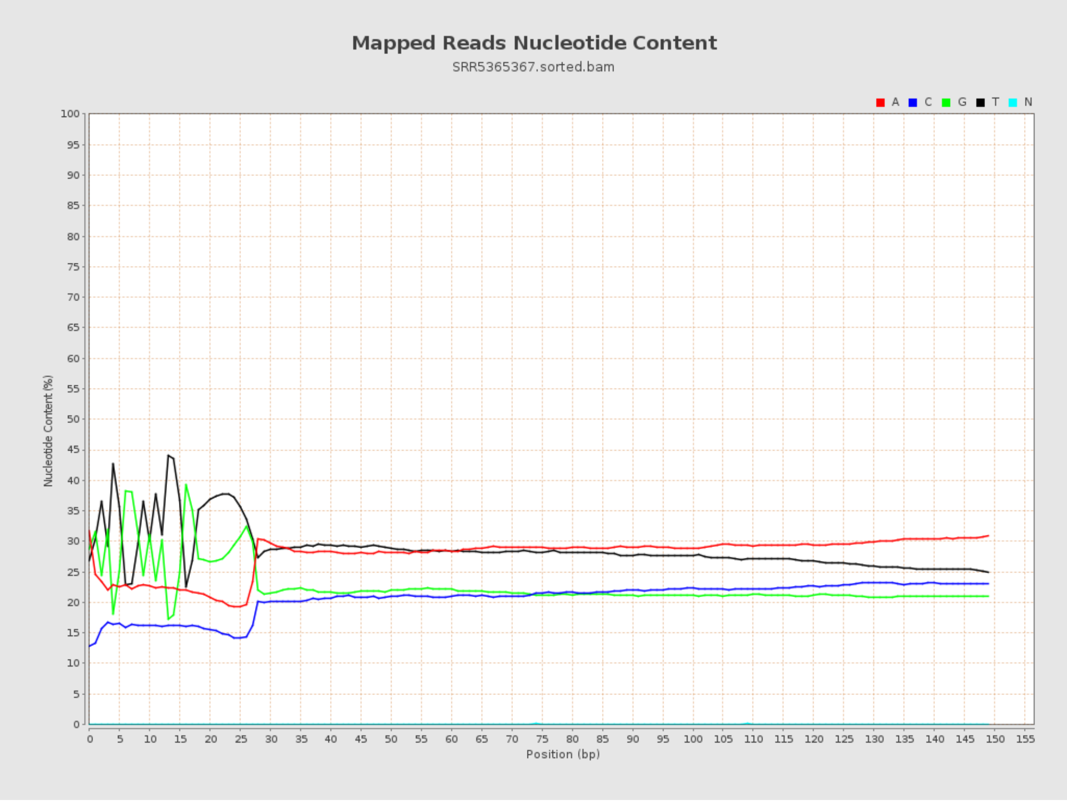
6. Results : Genome Fraction Coverage



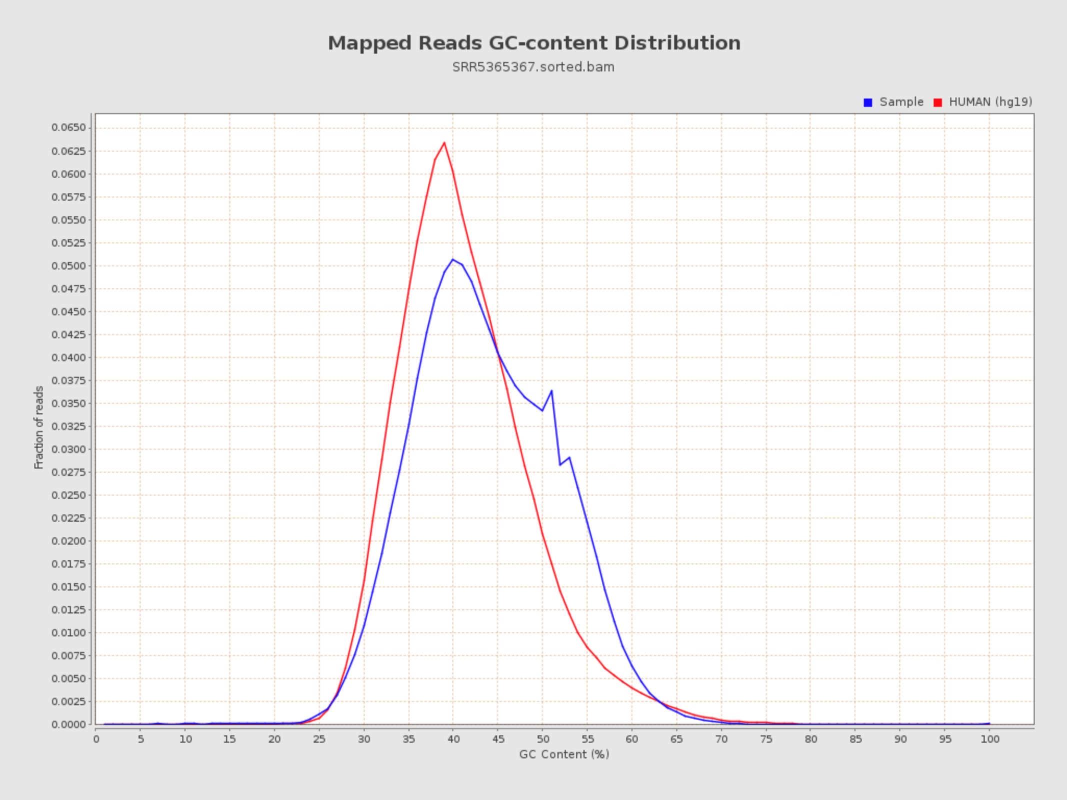
7. Results : Duplication Rate Histogram



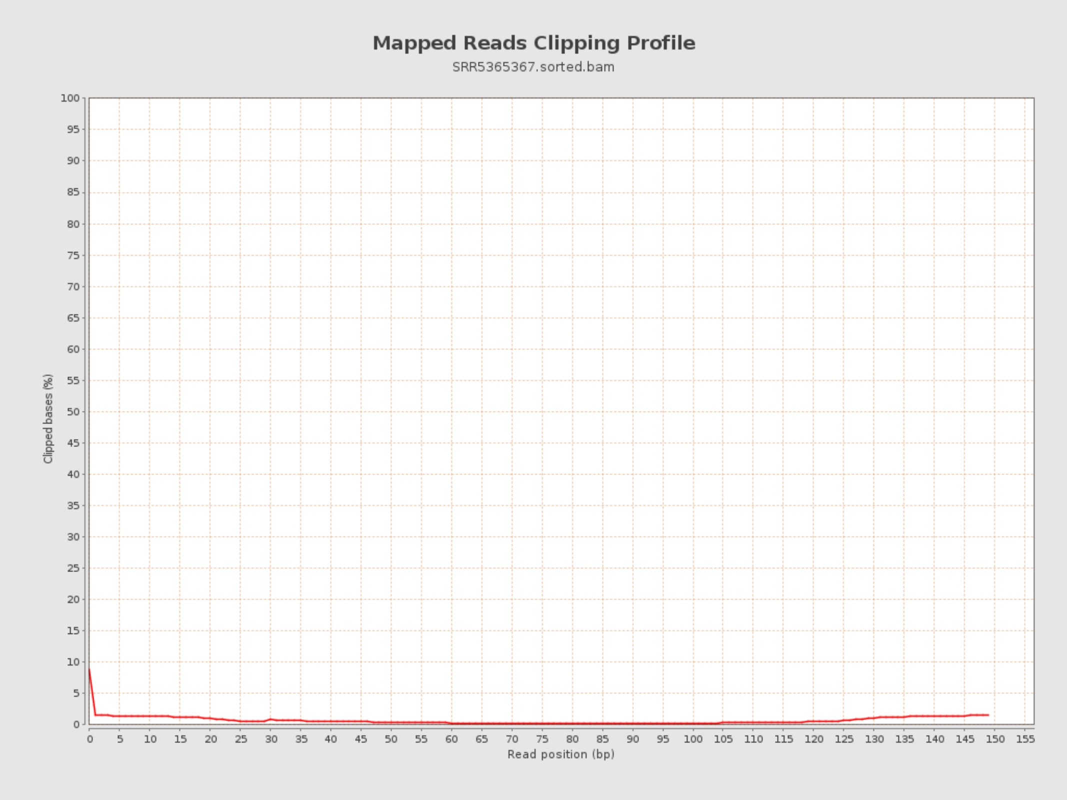
8. Results : Mapped Reads Nucleotide Content



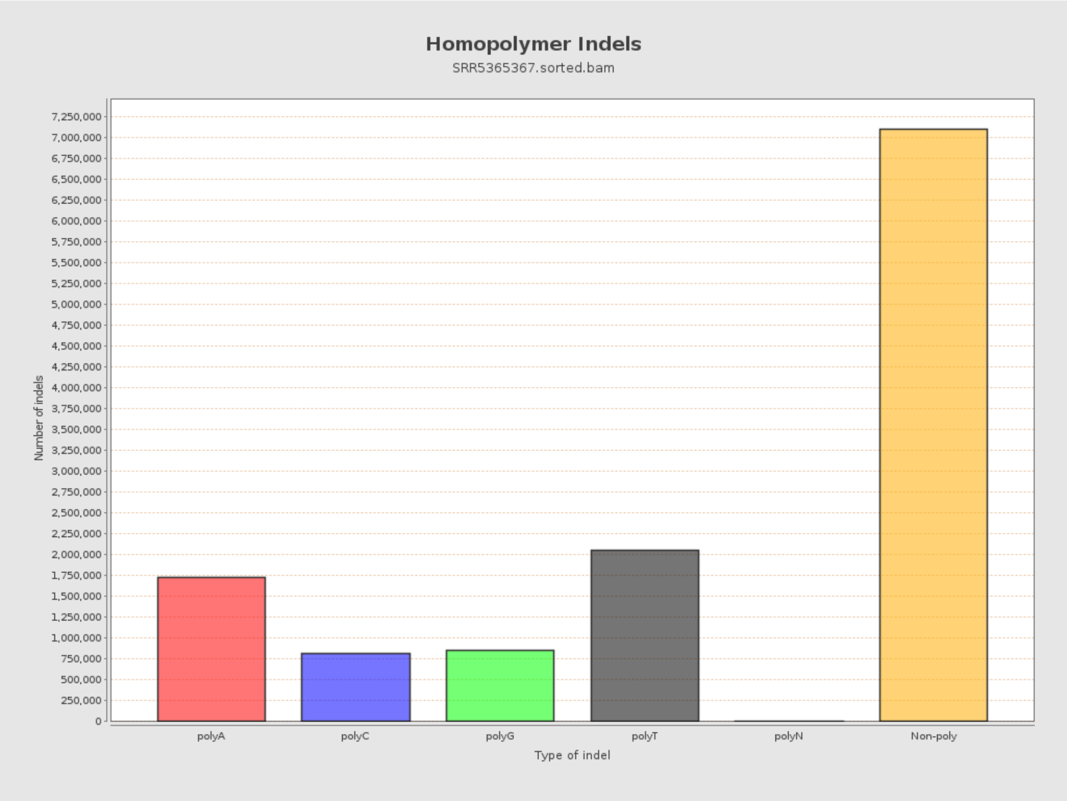
9. Results : Mapped Reads GC-content Distribution



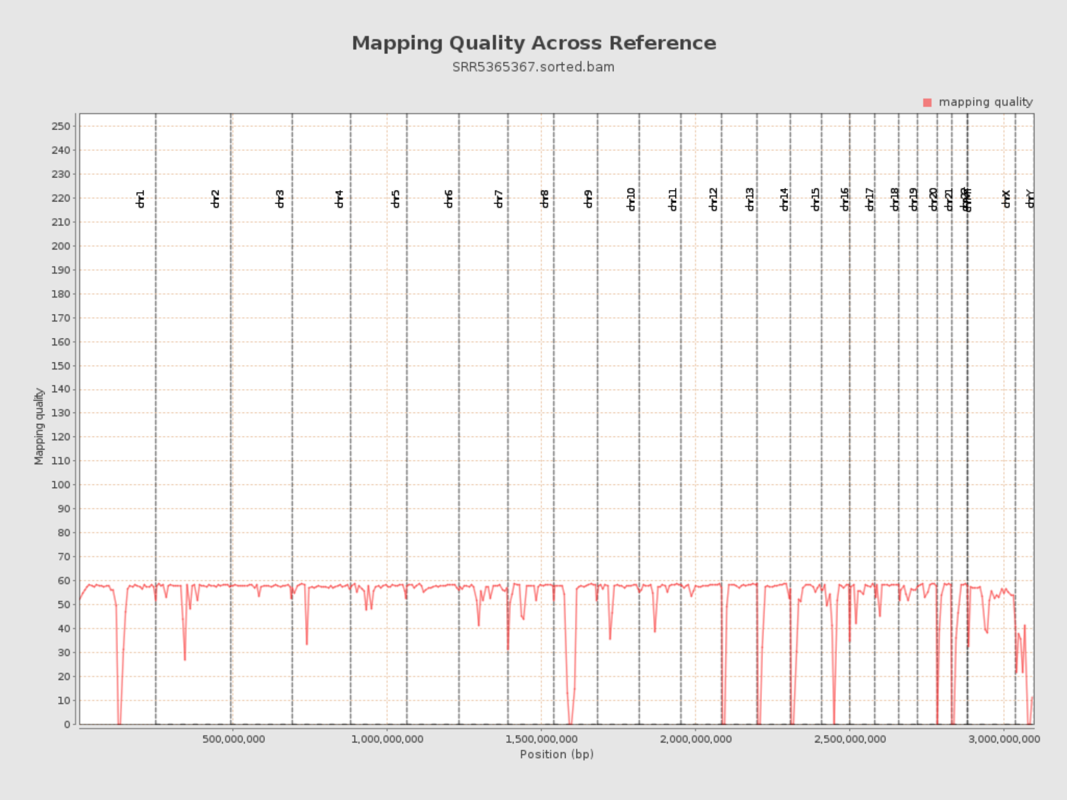
10. Results : Mapped Reads Clipping Profile



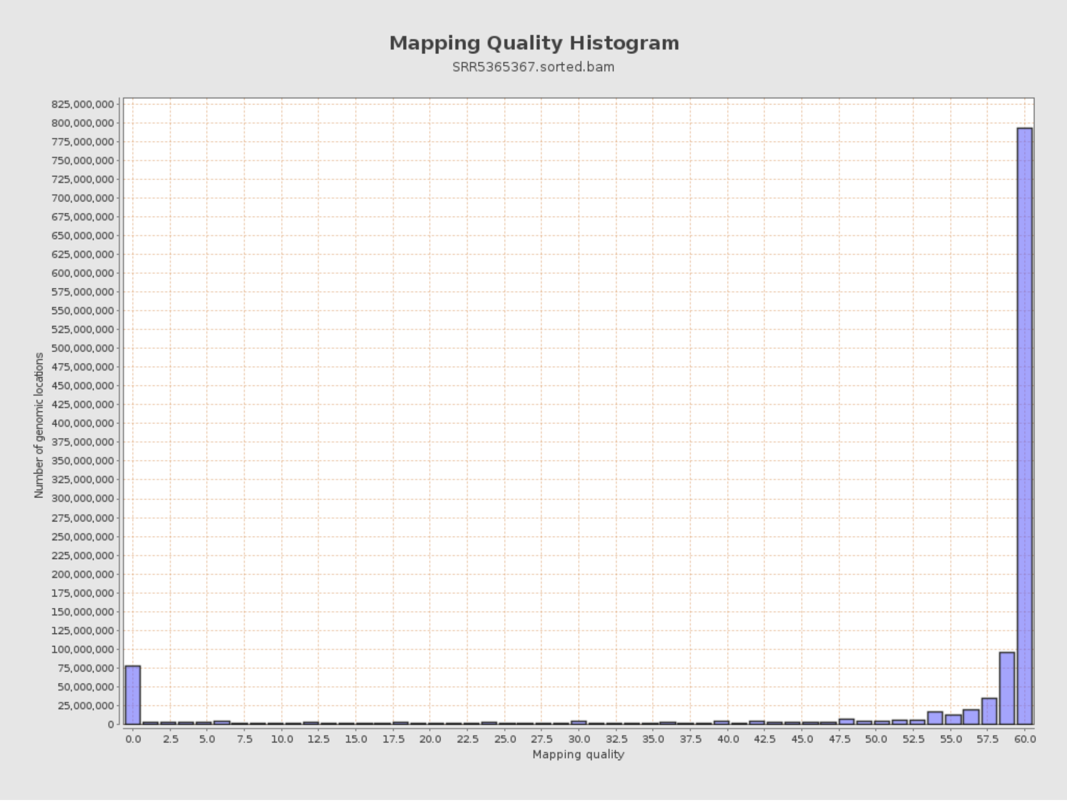
11. Results : Homopolymer Indels



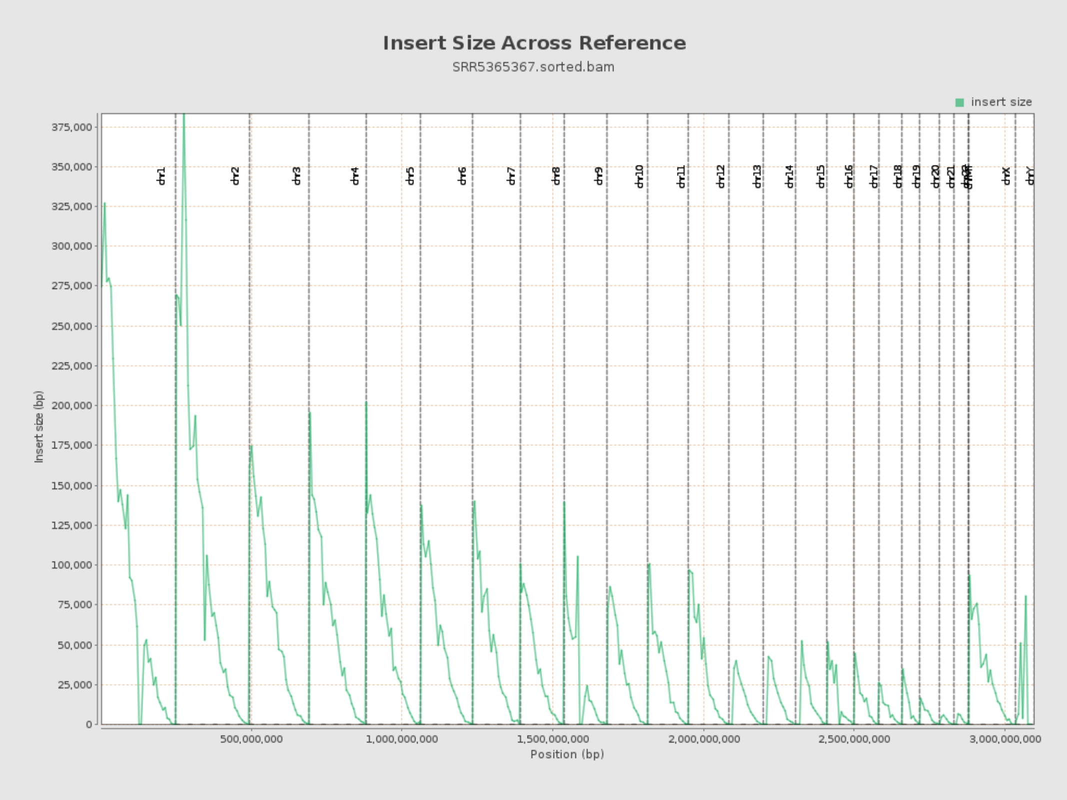
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram