Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 22:51:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124865.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_SRR3124865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124865_1.fastq.gz SRR3124865_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 22:51:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,081,964
Mapped reads	4,050,296 / 99.22%
Unmapped reads	31,668 / 0.78%
Mapped paired reads	4,050,296 / 99.22%
Mapped reads, first in pair	2,026,124 / 49.64%
Mapped reads, second in pair	2,024,172 / 49.59%
Mapped reads, both in pair	4,040,240 / 98.98%
Mapped reads, singletons	10,056 / 0.25%
Secondary alignments	0
Supplementary alignments	13,723 / 0.34%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	168,005 / 4.12%
Duplication rate	2.57%
Clipped reads	2,412,825 / 59.11%

2.2. ACGT Content

Number/percentage of A's	107,900,286 / 29.02%
Number/percentage of C's	73,249,033 / 19.7%
Number/percentage of T's	110,371,497 / 29.69%
Number/percentage of G's	79,994,507 / 21.52%
Number/percentage of N's	242,104 / 0.07%

GC Percentage	41.22%

2.3. Coverage

Mean	0.1201
Standard Deviation	1.1183

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	56,807.55
Standard Deviation	2,253,204.24
P25/Median/P75	135 / 168 / 213

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	2,942,564
Insertions	50,788
Mapped reads with at least one insertion	1.23%
Deletions	109,219
Mapped reads with at least one deletion	2.65%
Homopolymer indels	47.36%

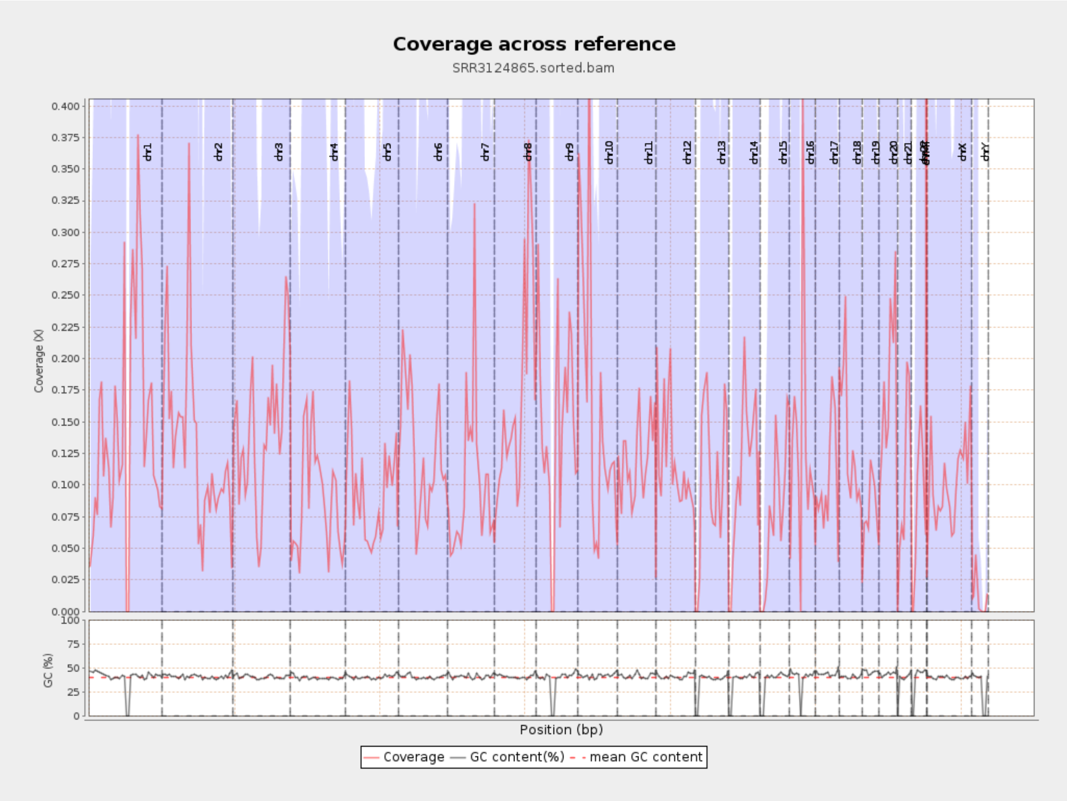
2.7. Chromosome stats

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

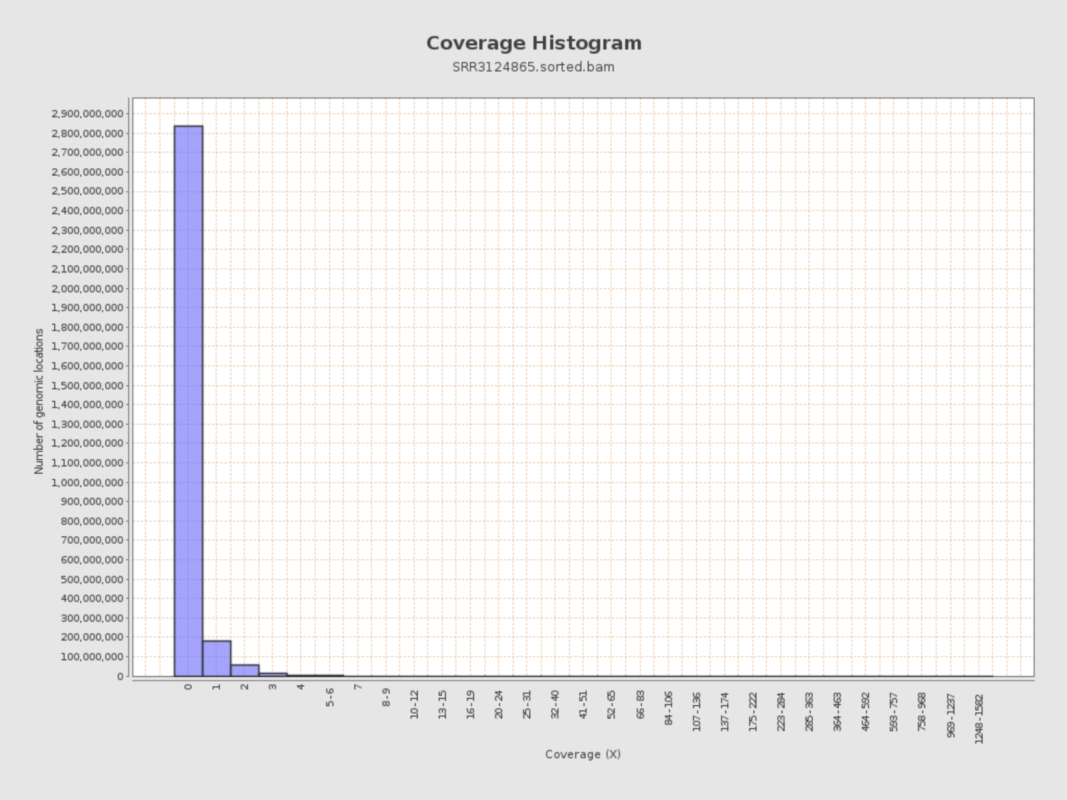
		bases	coverage	deviation
chr1	249250621	36172965	0.1451	1.0662
chr2	243199373	32389522	0.1332	1.3208
chr3	198022430	28116724	0.142	0.5093
chr4	191154276	16614355	0.0869	0.7828
chr5	180915260	16700233	0.0923	0.3852
chr6	171115067	21520412	0.1258	0.6089
chr7	159138663	16250492	0.1021	1.6188
chr8	146364022	25104965	0.1715	0.6627
chr9	141213431	20898631	0.148	1.5059
chr10	135534747	22520781	0.1662	3.1919
chr11	135006516	16275089	0.1206	0.5661
chr12	133851895	16020571	0.1197	0.4456
chr13	115169878	11962143	0.1039	0.4076
chr14	107349540	11825284	0.1102	0.4474
chr15	102531392	7655240	0.0747	0.3468
chr16	90354753	11640169	0.1288	1.8182
chr17	81195210	8337163	0.1027	0.598
chr18	78077248	10686713	0.1369	1.3562
chr19	59128983	4813068	0.0814	0.6796
chr20	63025520	11224735	0.1781	0.5748
chr21	48129895	4846972	0.1007	0.494
chr22	51304566	4113207	0.0802	0.3601
chrMT	16571	51628	3.1156	2.5414
chrX	155270560	15572627	0.1003	0.4539

chrY	59373566	622247	0.0105	0.6722

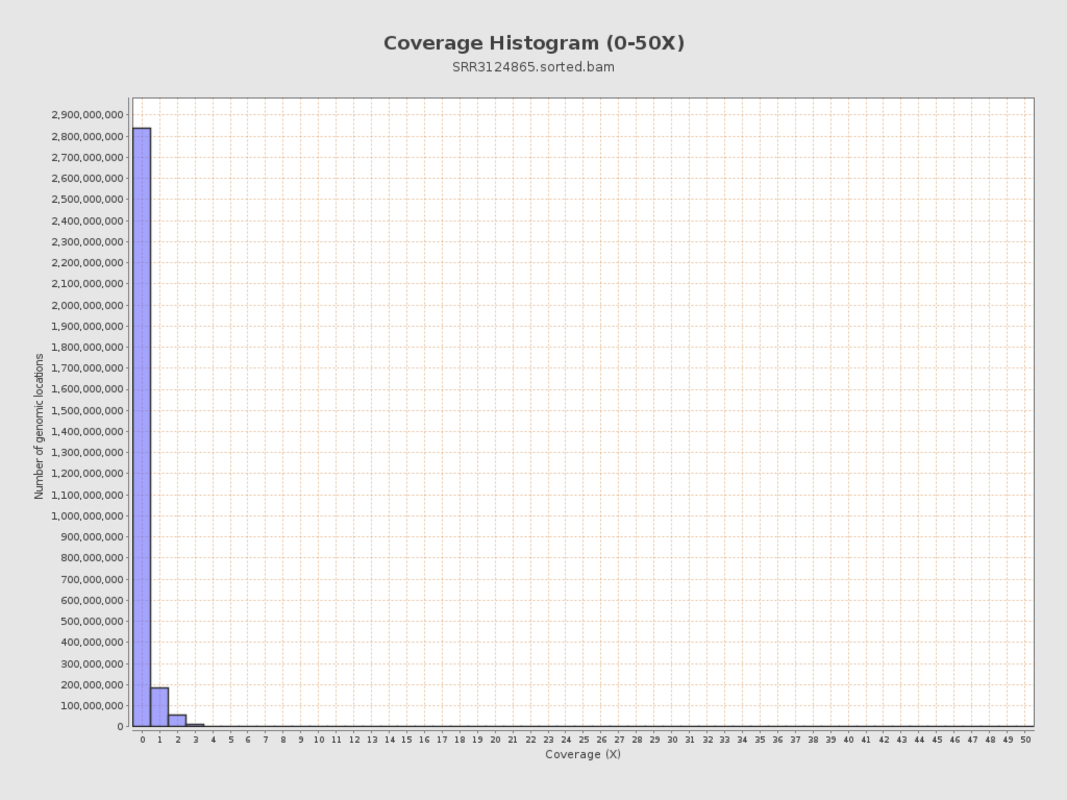
3. Results : Coverage across reference



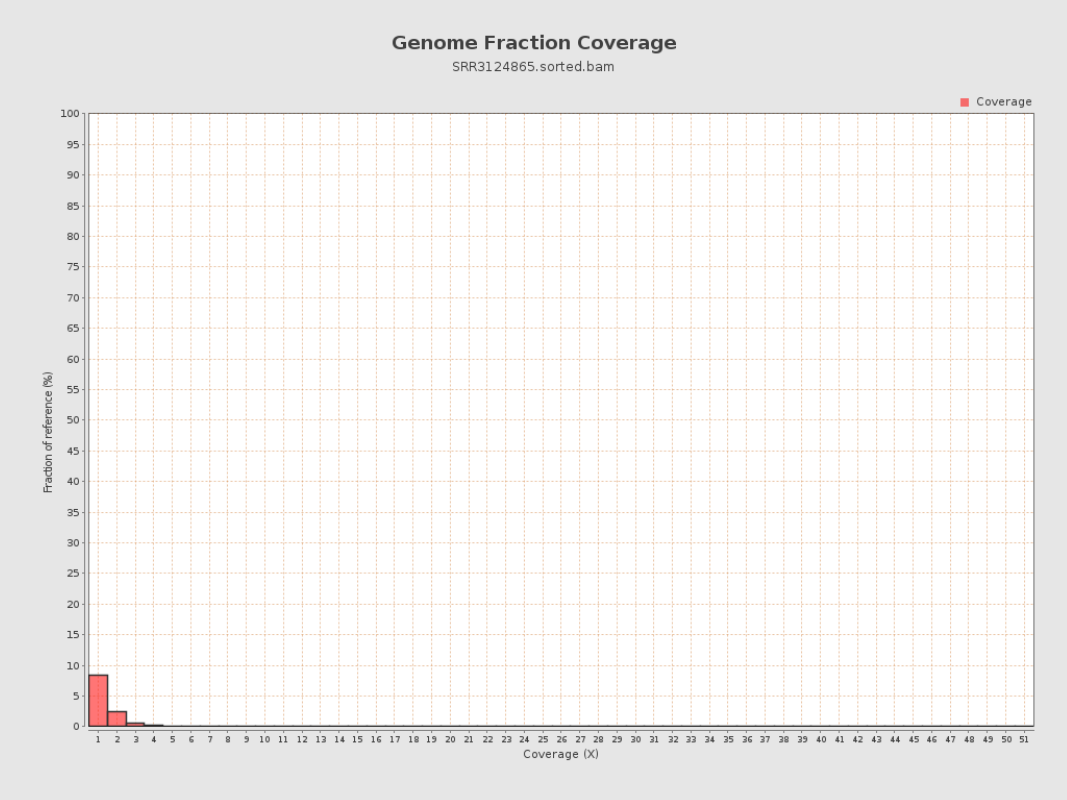
4. Results : Coverage Histogram



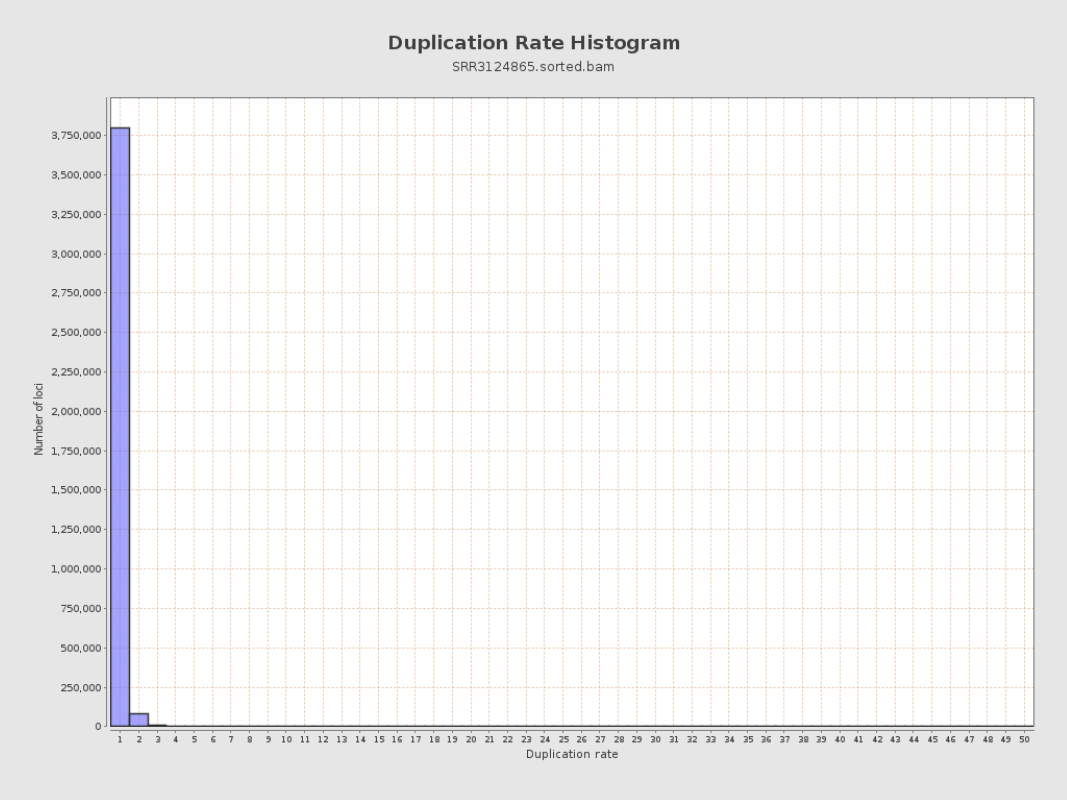
5. Results : Coverage Histogram (0-50X)



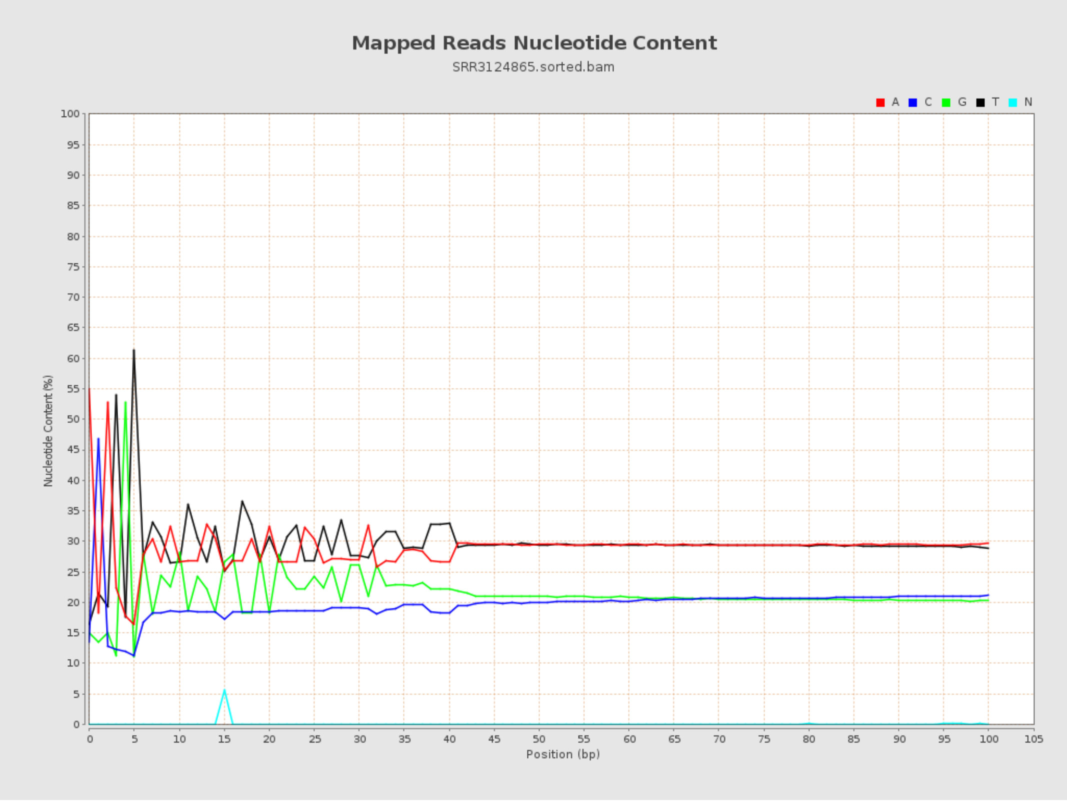
6. Results : Genome Fraction Coverage



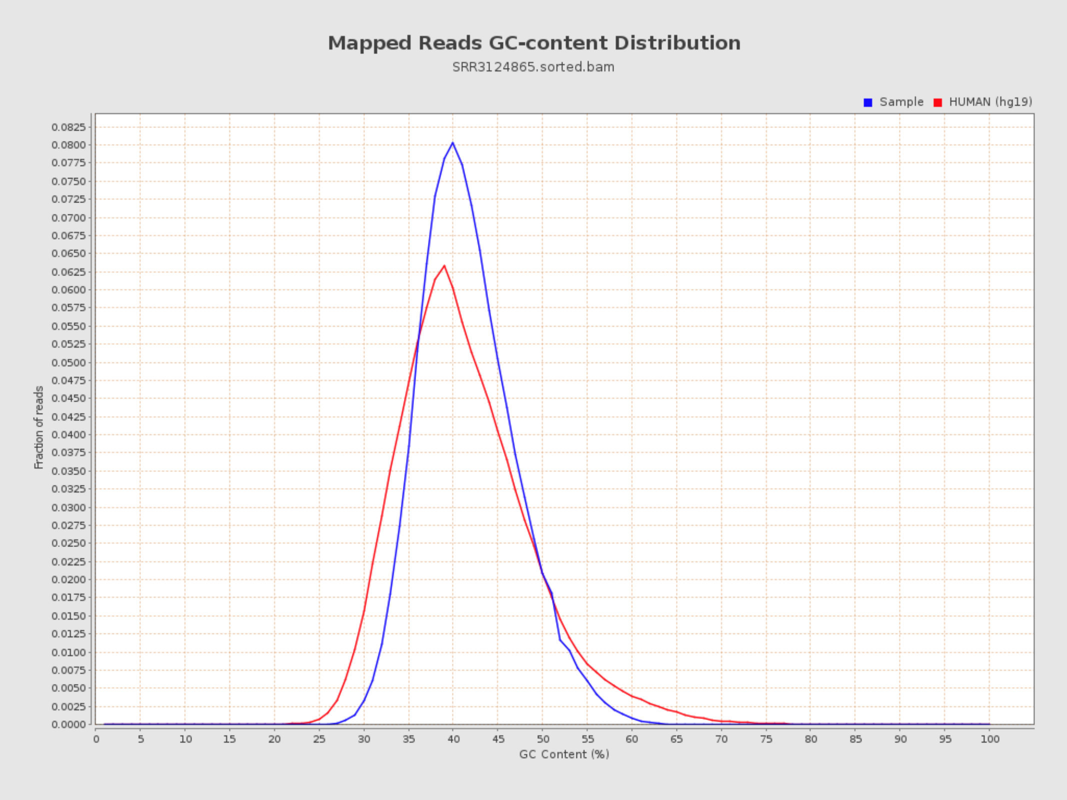
7. Results : Duplication Rate Histogram



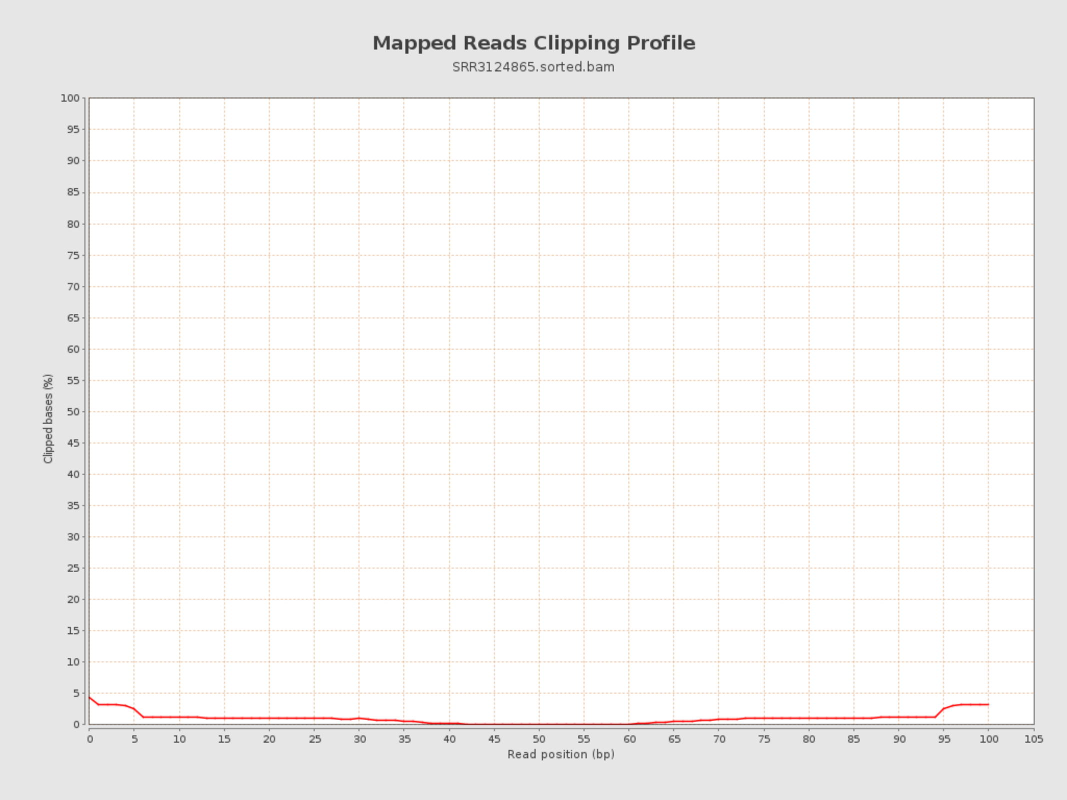
8. Results : Mapped Reads Nucleotide Content



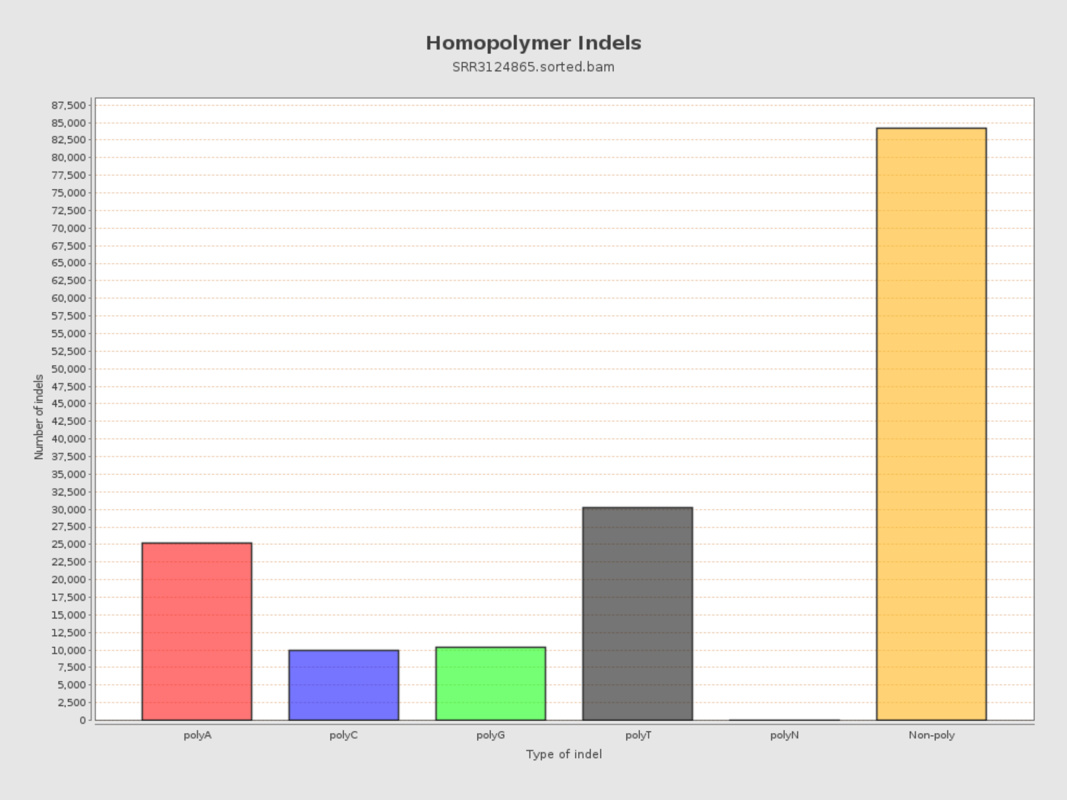
9. Results : Mapped Reads GC-content Distribution



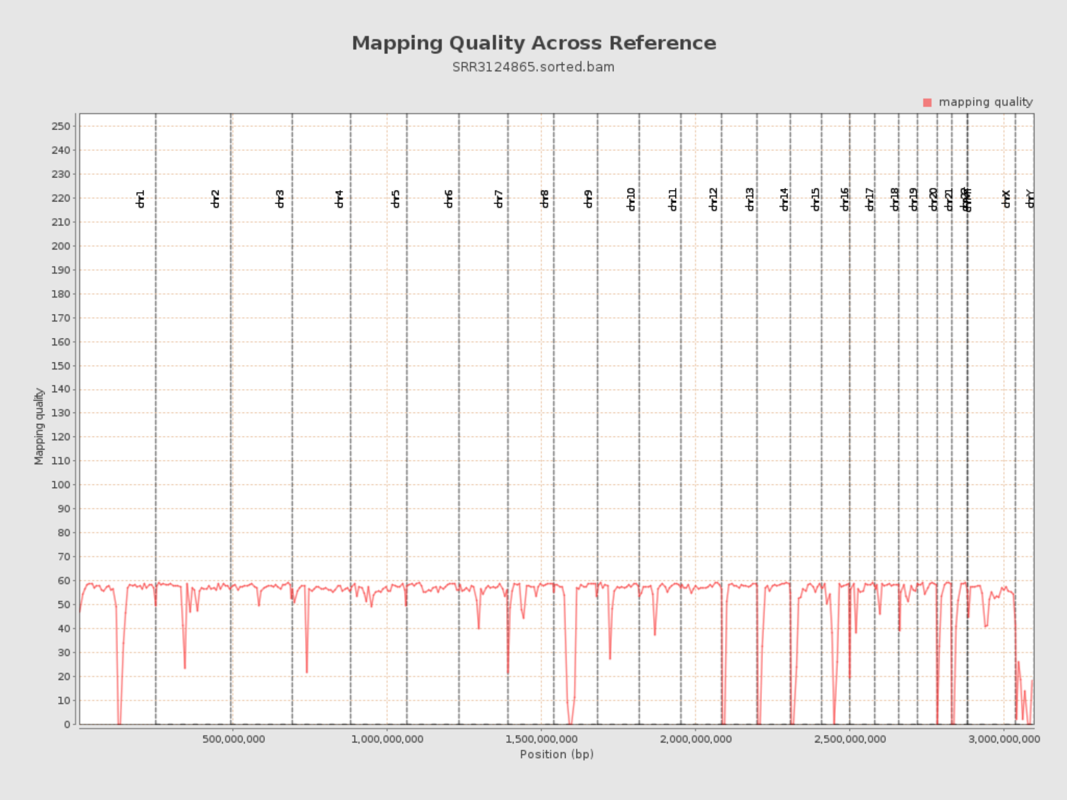
10. Results : Mapped Reads Clipping Profile



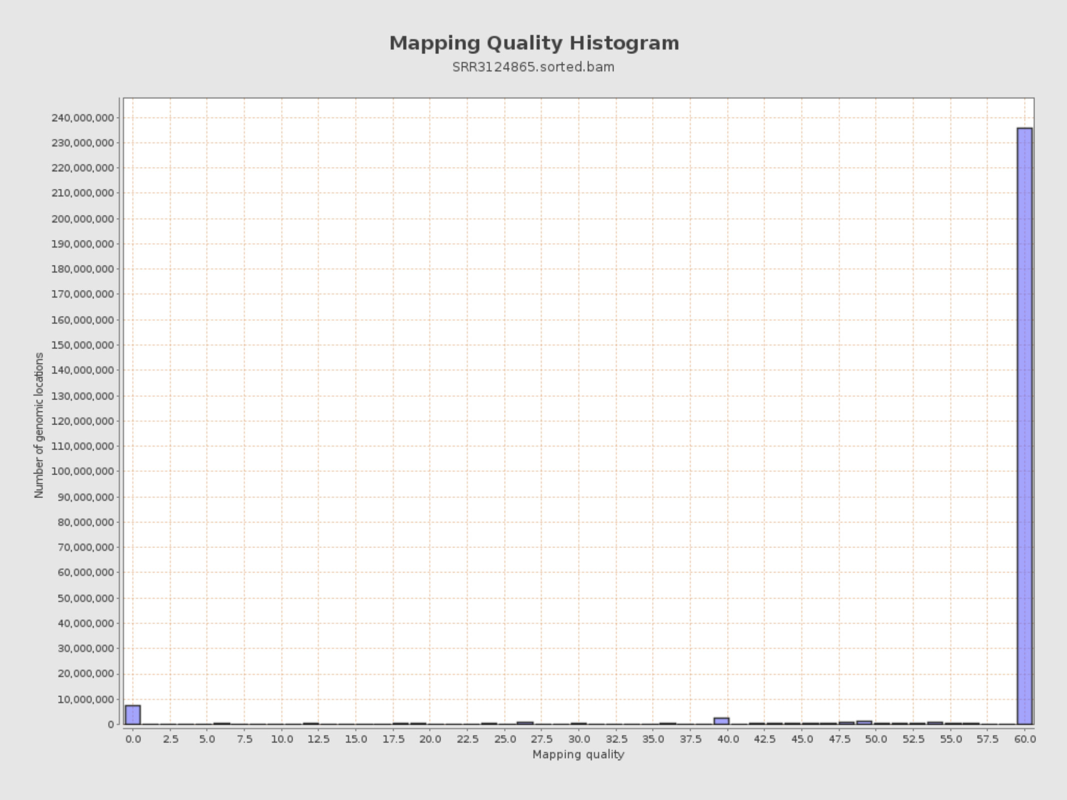
11. Results : Homopolymer Indels



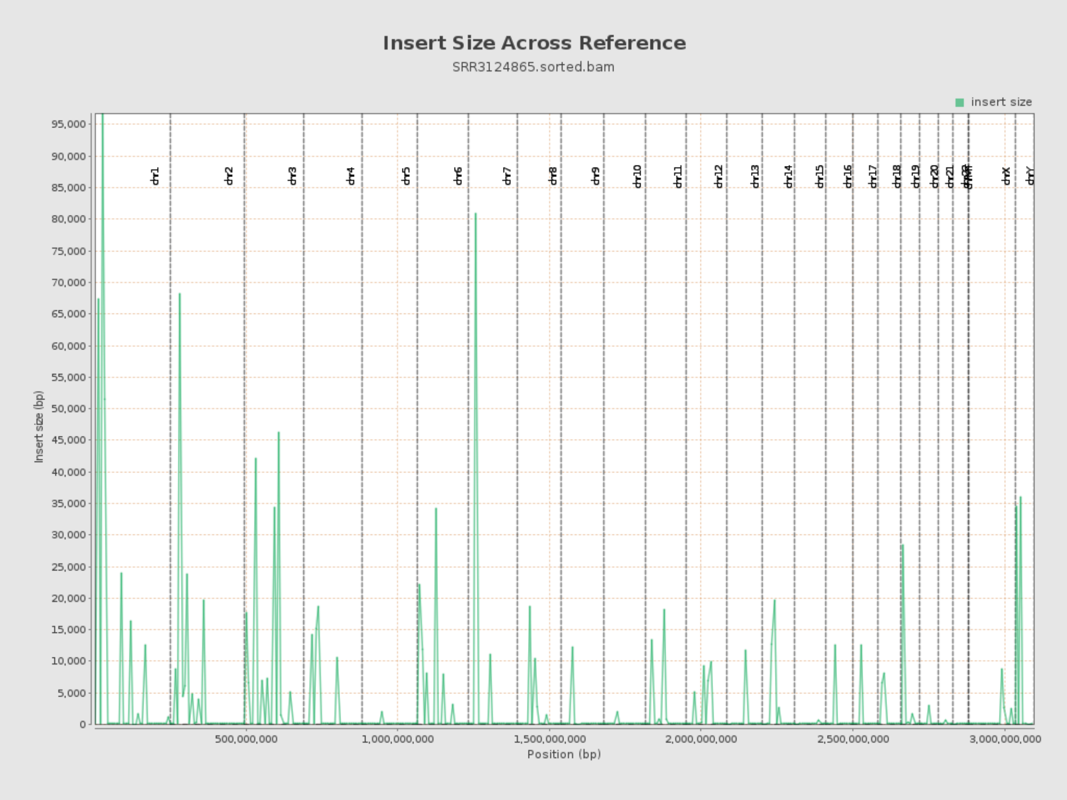
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram