Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 10:05:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472764.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_SRR3472764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472764_1.fastq.gz SRR3472764_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 10:05:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,493,204
Mapped reads	15,346,258 / 99.05%
Unmapped reads	146,946 / 0.95%
Mapped paired reads	15,346,258 / 99.05%
Mapped reads, first in pair	7,696,863 / 49.68%
Mapped reads, second in pair	7,649,395 / 49.37%
Mapped reads, both in pair	15,264,382 / 98.52%
Mapped reads, singletons	81,876 / 0.53%
Secondary alignments	0
Supplementary alignments	49,487 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	9,573,300 / 61.79%
Duplication rate	46.66%
Clipped reads	1,130,034 / 7.29%

2.2. ACGT Content

Number/percentage of A's	410,176,805 / 27.1%
Number/percentage of C's	348,589,222 / 23.03%
Number/percentage of T's	407,694,707 / 26.94%
Number/percentage of G's	346,617,716 / 22.9%
Number/percentage of N's	294,095 / 0.02%

GC Percentage	45.94%

2.3. Coverage

Mean	0.4889
Standard Deviation	17.4684

2.4. Mapping Quality

Mean Mapping Quality	55.16

2.5. Insert size

Mean	21,376.46
Standard Deviation	1,419,721.98
P25/Median/P75	177 / 246 / 329

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	9,321,511
Insertions	84,495
Mapped reads with at least one insertion	0.55%
Deletions	84,238
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.07%

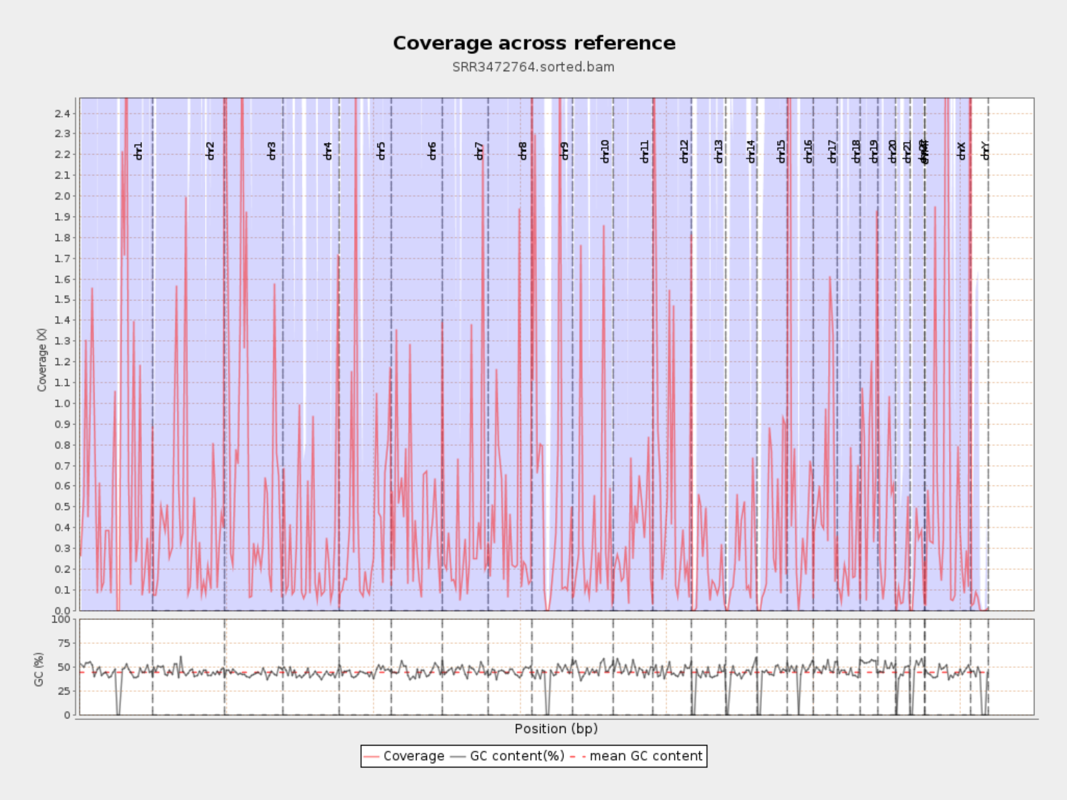
2.7. Chromosome stats

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

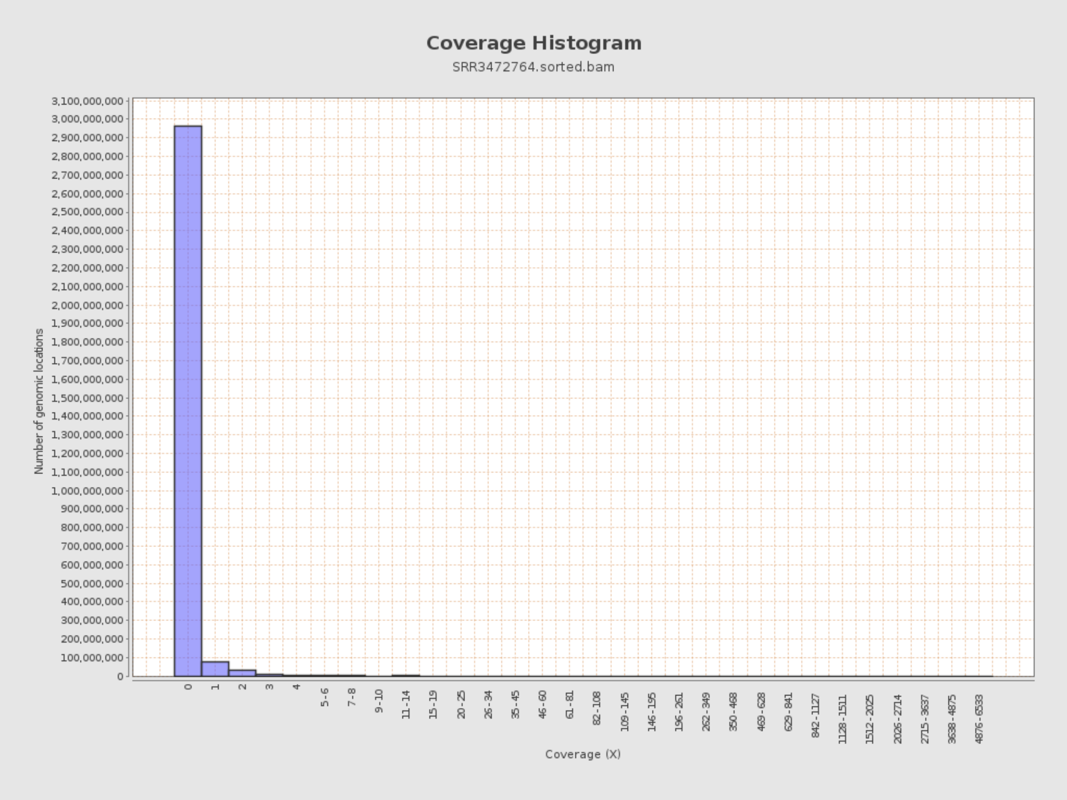
		bases	coverage	deviation
chr1	249250621	169621477	0.6805	21.6264
chr2	243199373	102240890	0.4204	15.8388
chr3	198022430	161226913	0.8142	17.2888
chr4	191154276	59896788	0.3133	10.2365
chr5	180915260	86687153	0.4792	18.4702
chr6	171115067	79336093	0.4636	13.6699
chr7	159138663	68795627	0.4323	16.5763
chr8	146364022	64766348	0.4425	16.9073
chr9	141213431	89567280	0.6343	19.0603
chr10	135534747	54676523	0.4034	26.3492
chr11	135006516	48821392	0.3616	10.4888
chr12	133851895	94745626	0.7078	26.3516
chr13	115169878	22876026	0.1986	6.4654
chr14	107349540	26827726	0.2499	10.7651
chr15	102531392	38560473	0.3761	10.543
chr16	90354753	71229949	0.7883	24.7282
chr17	81195210	52806023	0.6504	15.1622
chr18	78077248	20360230	0.2608	9.2132
chr19	59128983	43369845	0.7335	23.3723
chr20	63025520	30268901	0.4803	11.8831
chr21	48129895	7114766	0.1478	6.7057
chr22	51304566	11464869	0.2235	7.4611
chrMT	16571	4014	0.2422	0.8819
chrX	155270560	106678264	0.687	25.3517

chrY	59373566	1634073	0.0275	0.8326

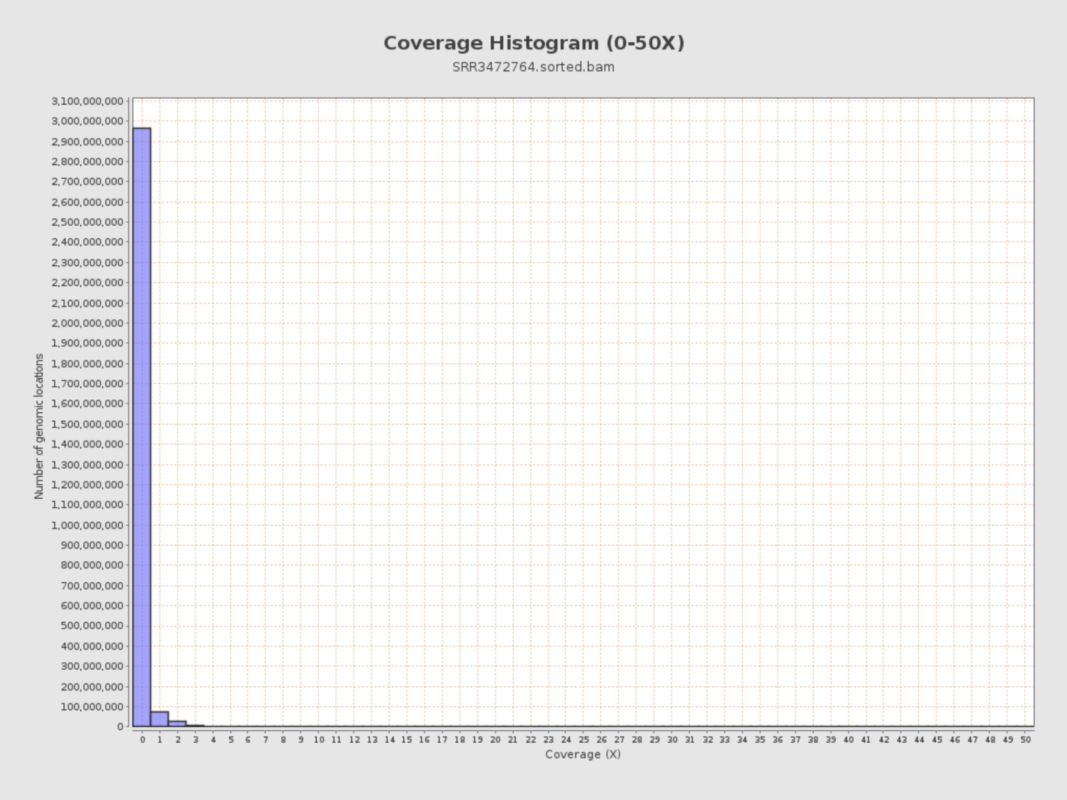
3. Results : Coverage across reference



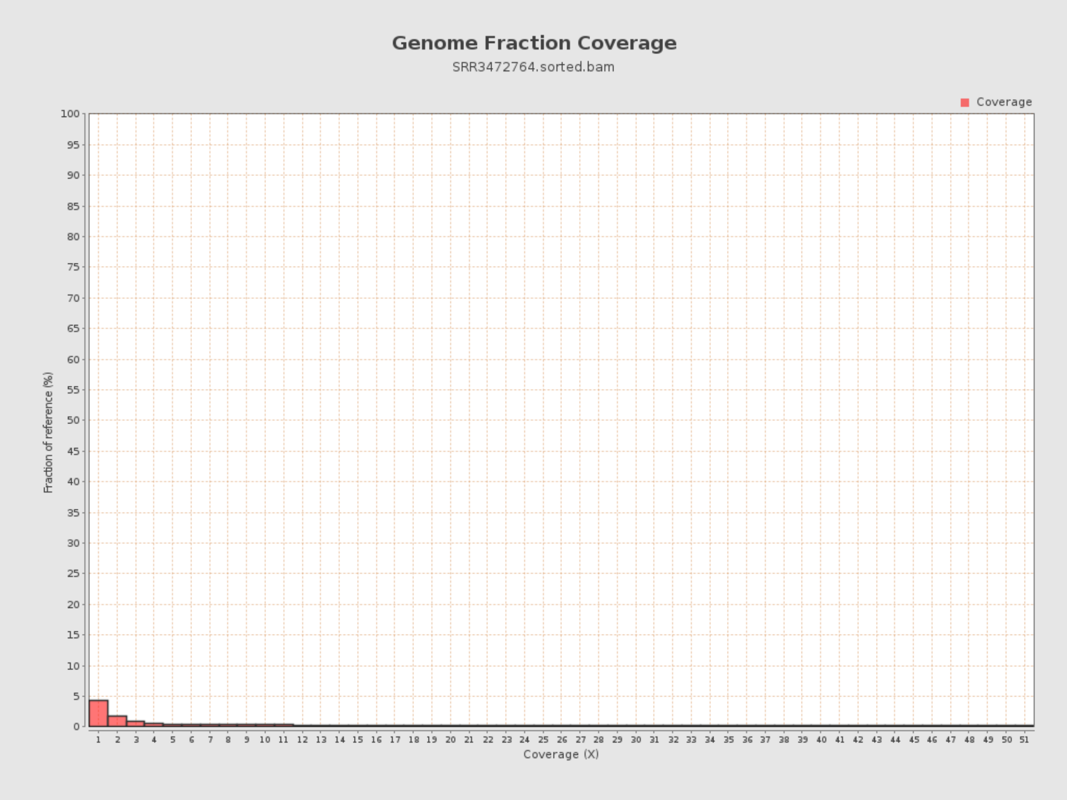
4. Results : Coverage Histogram



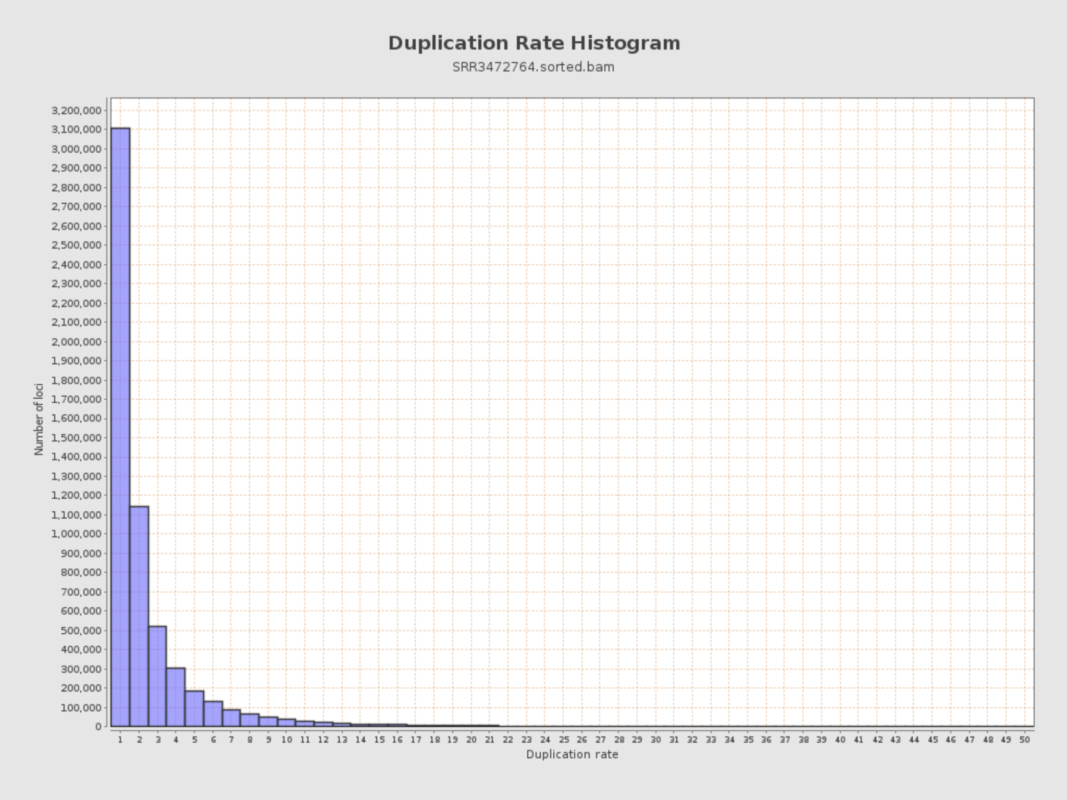
5. Results : Coverage Histogram (0-50X)



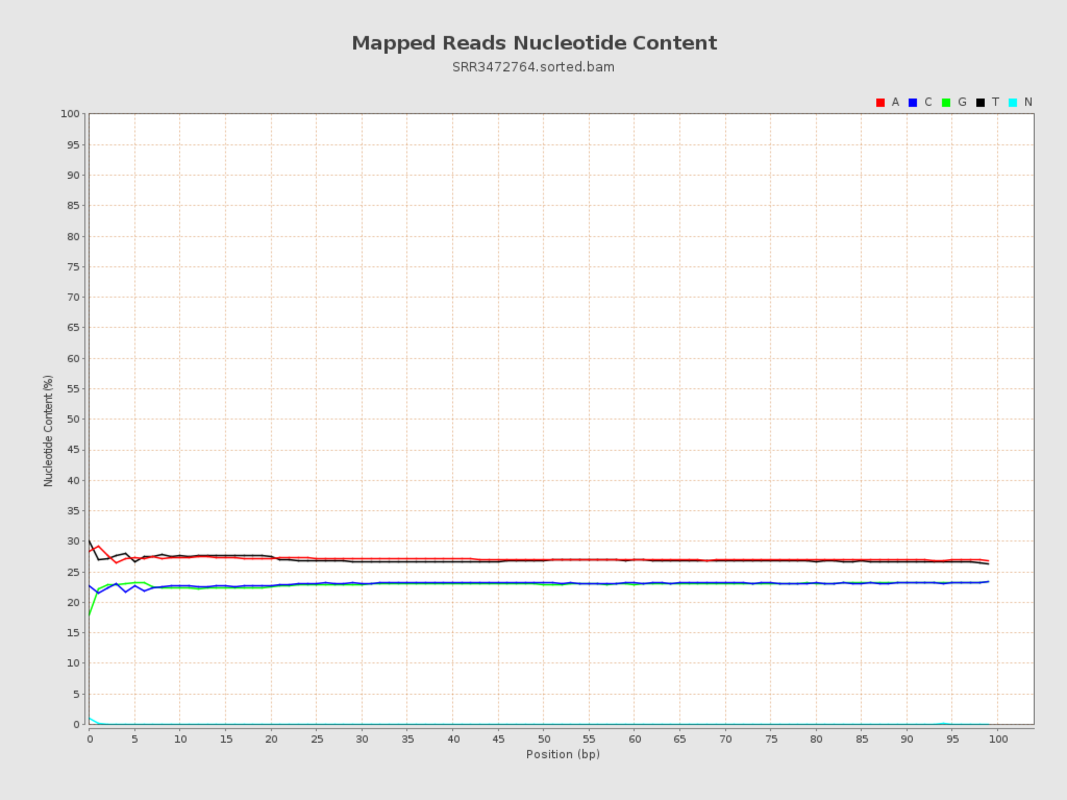
6. Results : Genome Fraction Coverage



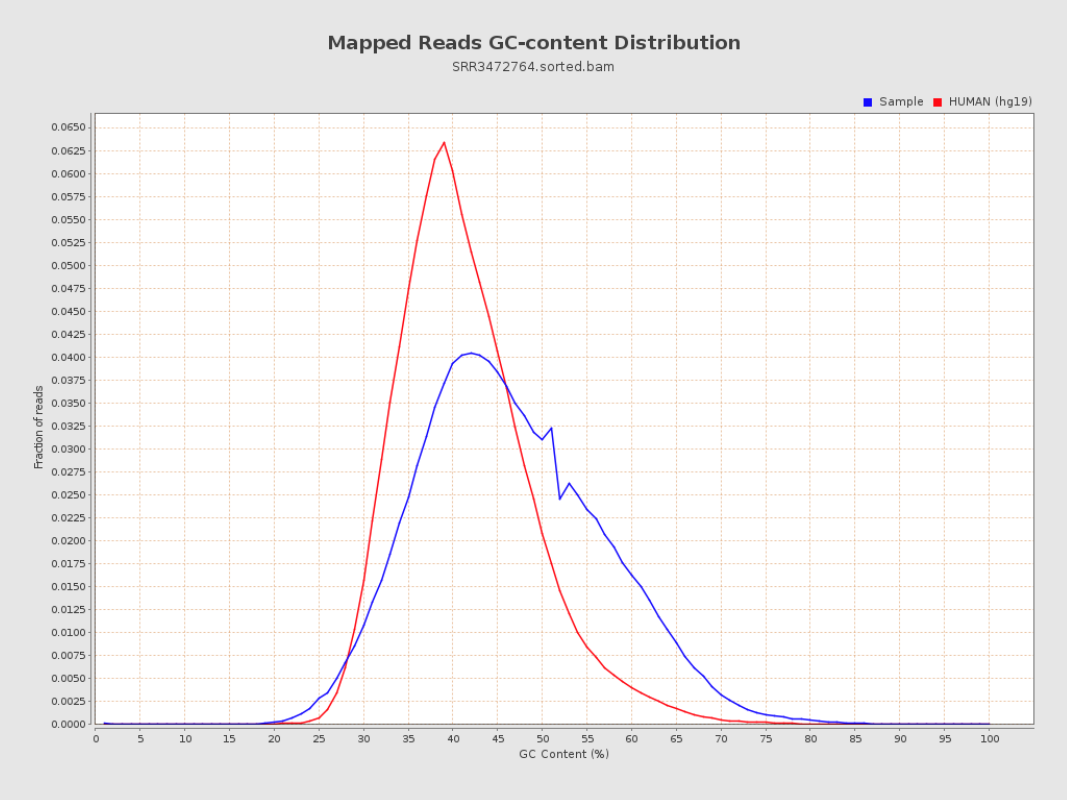
7. Results : Duplication Rate Histogram



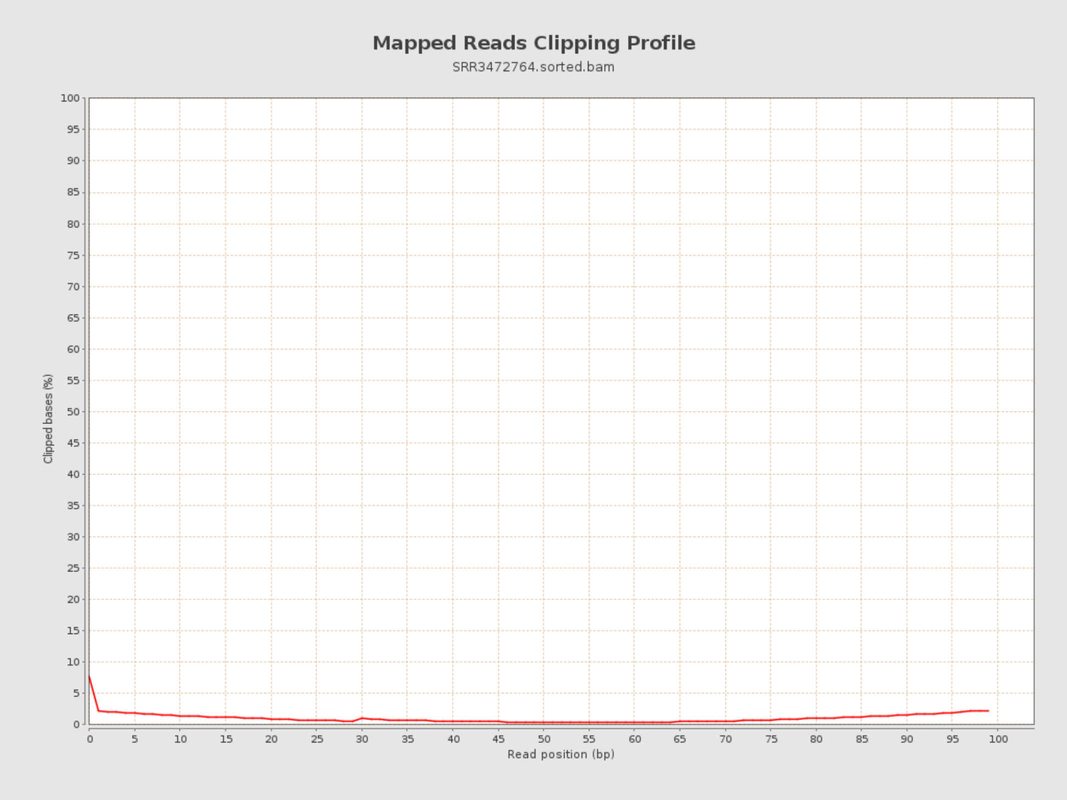
8. Results : Mapped Reads Nucleotide Content



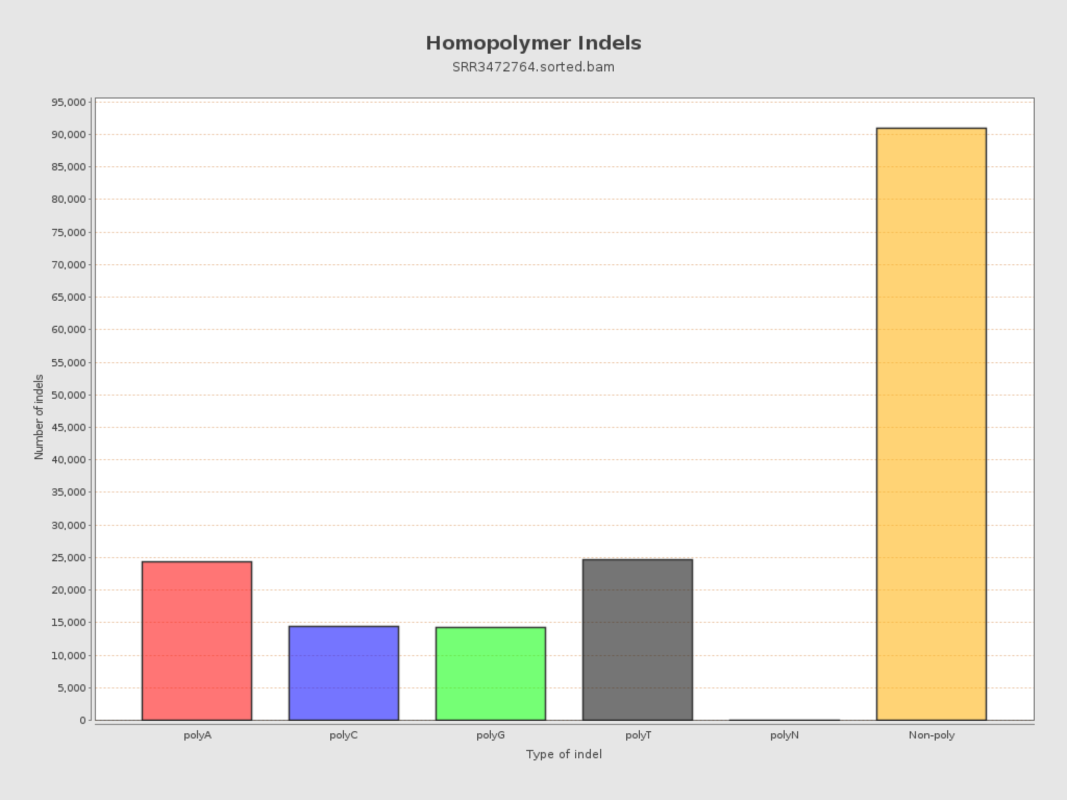
9. Results : Mapped Reads GC-content Distribution



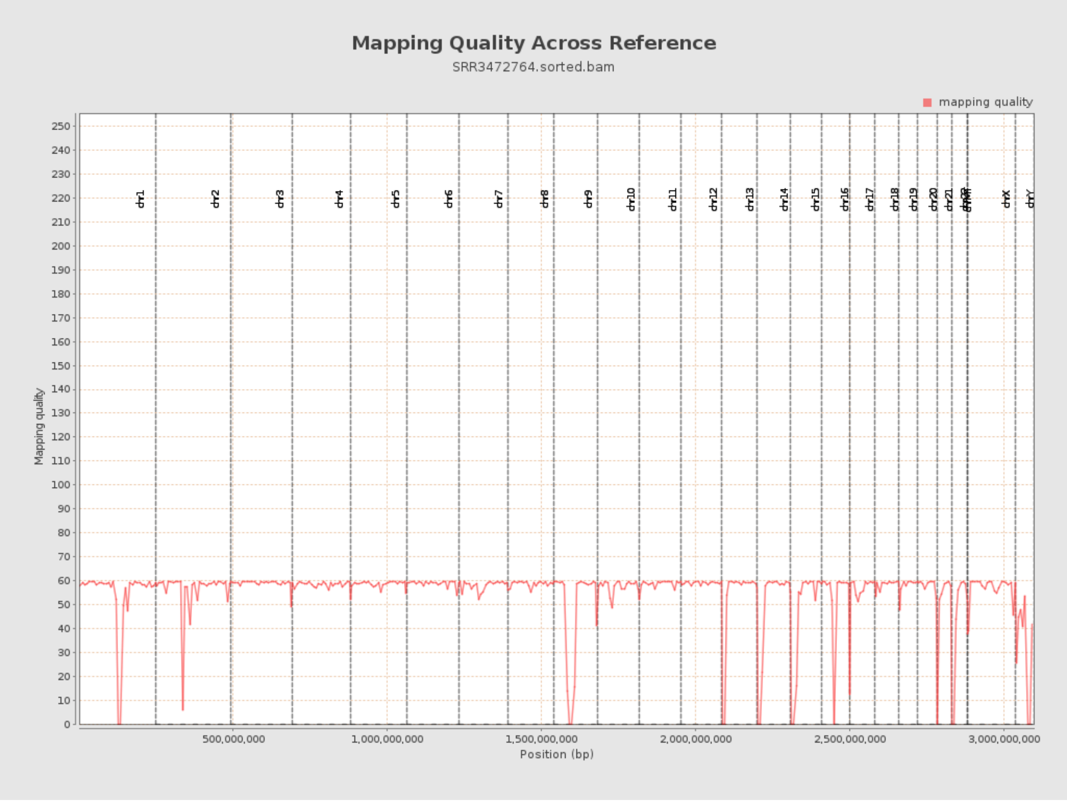
10. Results : Mapped Reads Clipping Profile



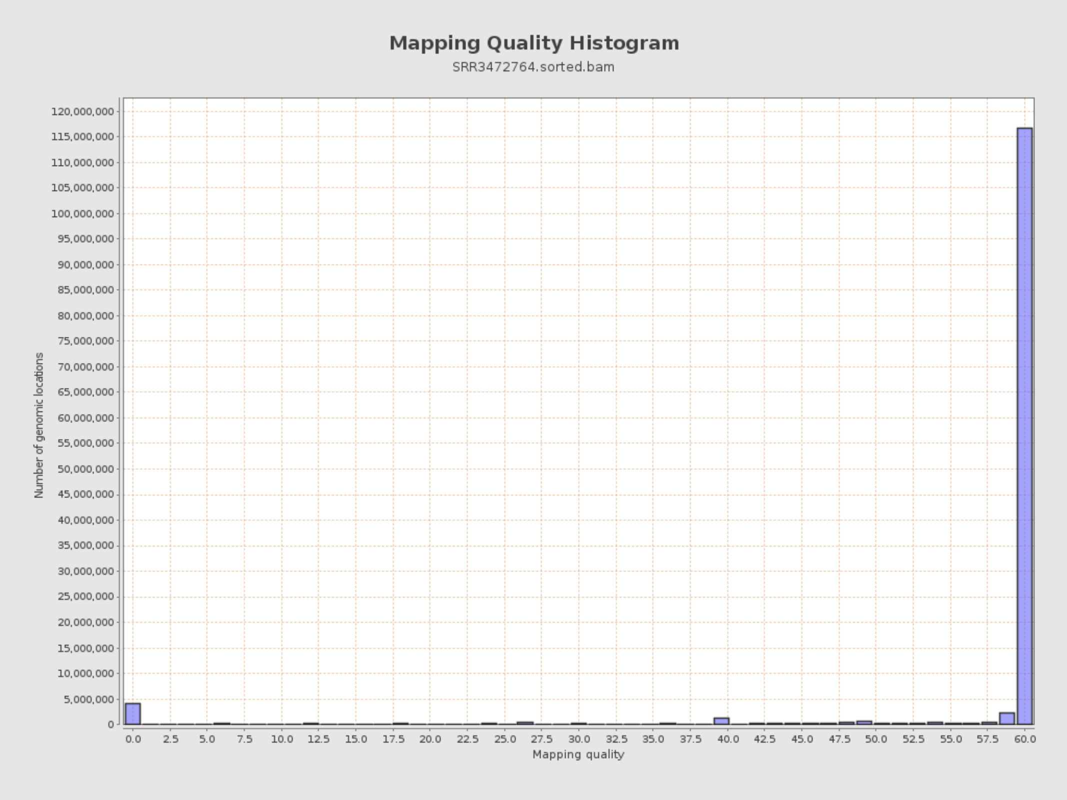
11. Results : Homopolymer Indels



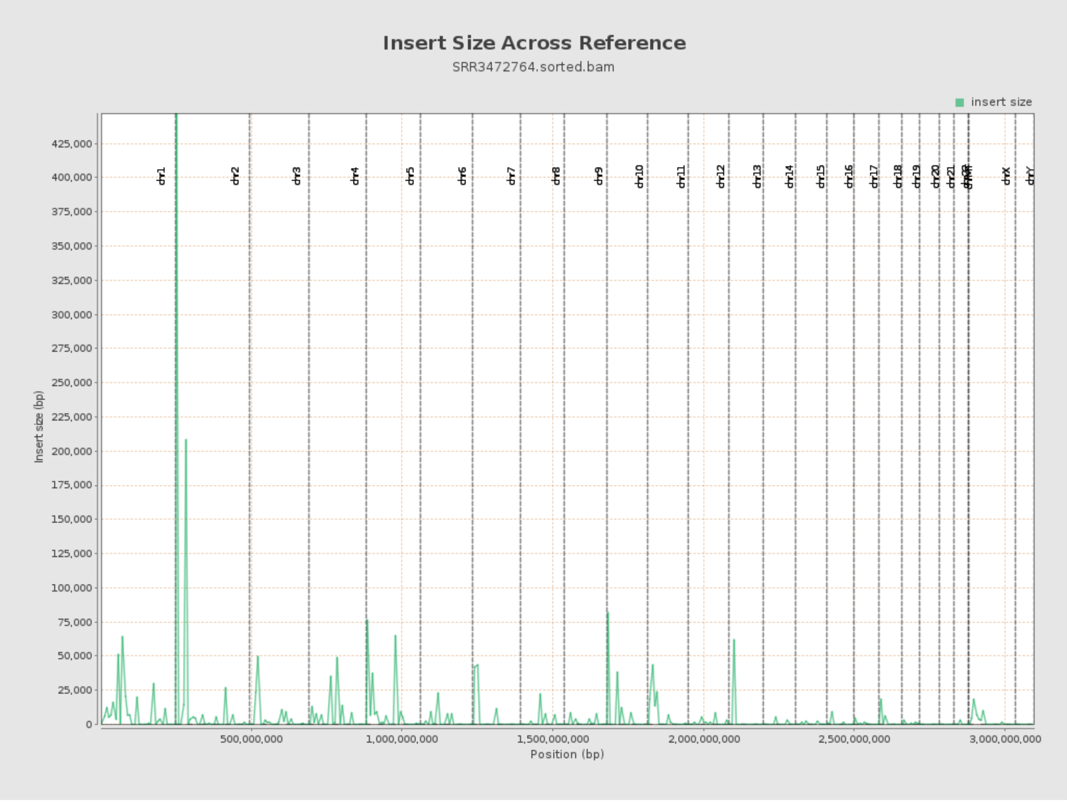
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram