Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 11:13:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472614.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_SRR3472614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472614_1.fastq.gz SRR3472614_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 11:13:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,078,684
Mapped reads	17,943,823 / 99.25%
Unmapped reads	134,861 / 0.75%
Mapped paired reads	17,943,823 / 99.25%
Mapped reads, first in pair	8,996,332 / 49.76%
Mapped reads, second in pair	8,947,491 / 49.49%
Mapped reads, both in pair	17,850,440 / 98.74%
Mapped reads, singletons	93,383 / 0.52%
Secondary alignments	0
Supplementary alignments	81,845 / 0.45%
Read min/max/mean length	30 / 101 / 99.76
Duplicated reads (estimated)	12,299,850 / 68.04%
Duplication rate	50.37%
Clipped reads	1,225,622 / 6.78%

2.2. ACGT Content

Number/percentage of A's	465,992,479 / 26.38%
Number/percentage of C's	419,879,479 / 23.77%
Number/percentage of T's	466,428,032 / 26.41%
Number/percentage of G's	413,760,659 / 23.42%
Number/percentage of N's	331,020 / 0.02%

GC Percentage	47.19%

2.3. Coverage

Mean	0.5707
Standard Deviation	23.9538

2.4. Mapping Quality

Mean Mapping Quality	54.94

2.5. Insert size

Mean	19,602.01
Standard Deviation	1,373,982.25
P25/Median/P75	162 / 222 / 295

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	10,929,533
Insertions	104,096
Mapped reads with at least one insertion	0.57%
Deletions	87,891
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.67%

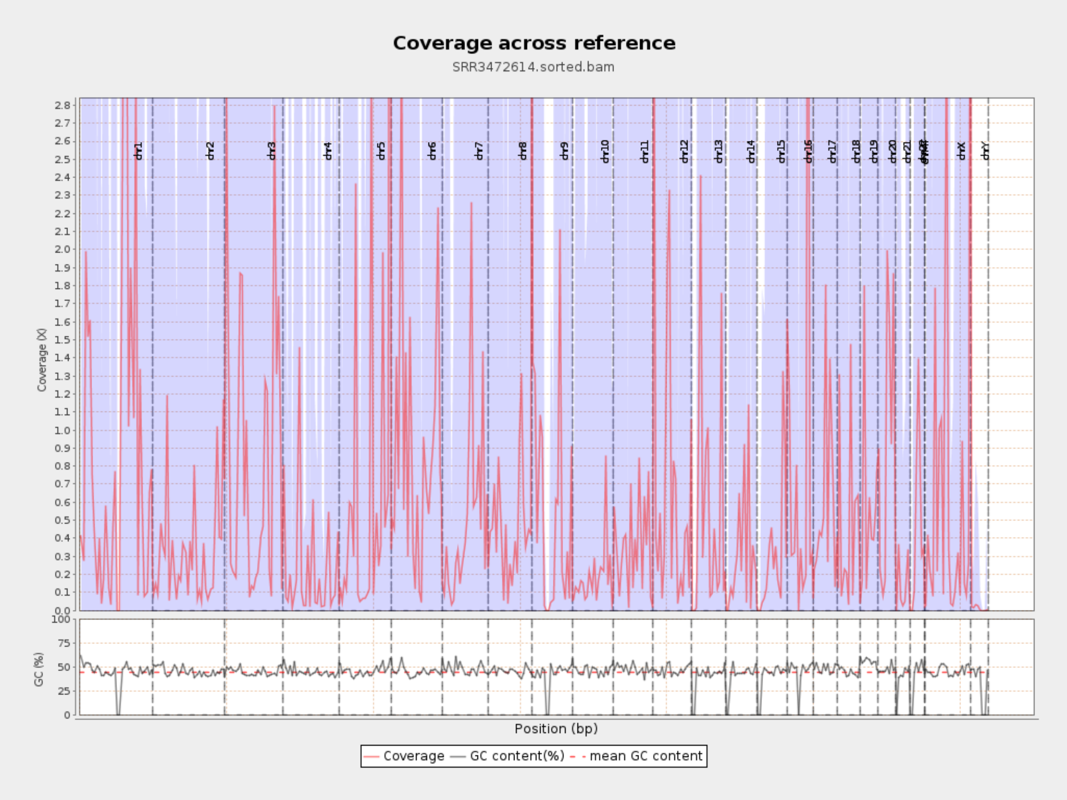
2.7. Chromosome stats

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

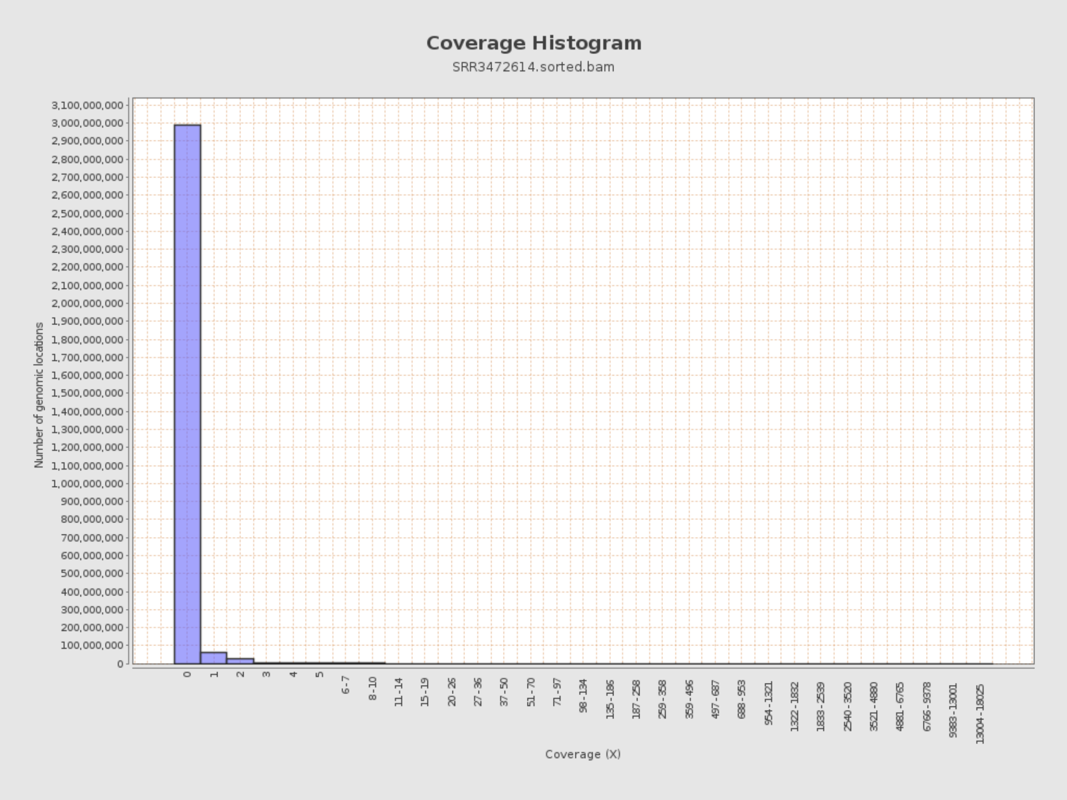
		bases	coverage	deviation
chr1	249250621	240976939	0.9668	29.0977
chr2	243199373	77427047	0.3184	13.0802
chr3	198022430	174889671	0.8832	27.28
chr4	191154276	42882175	0.2243	11.2334
chr5	180915260	158086325	0.8738	59.7609
chr6	171115067	150938703	0.8821	23.588
chr7	159138663	84191400	0.529	18.196
chr8	146364022	67764724	0.463	13.1333
chr9	141213431	82521306	0.5844	18.3246
chr10	135534747	26280908	0.1939	9.2033
chr11	135006516	48746878	0.3611	17.3562
chr12	133851895	97972340	0.7319	22.2917
chr13	115169878	65304157	0.567	21.3194
chr14	107349540	33278277	0.31	18.4094
chr15	102531392	32679690	0.3187	12.8863
chr16	90354753	76331892	0.8448	28.9748
chr17	81195210	49595788	0.6108	14.7265
chr18	78077248	38669761	0.4953	20.5575
chr19	59128983	33295676	0.5631	14.1181
chr20	63025520	59431804	0.943	26.3666
chr21	48129895	7085446	0.1472	7.6954
chr22	51304566	22878178	0.4459	17.6859
chrMT	16571	450	0.0272	0.1899
chrX	155270560	94621530	0.6094	19.633

chrY	59373566	756365	0.0127	0.4221

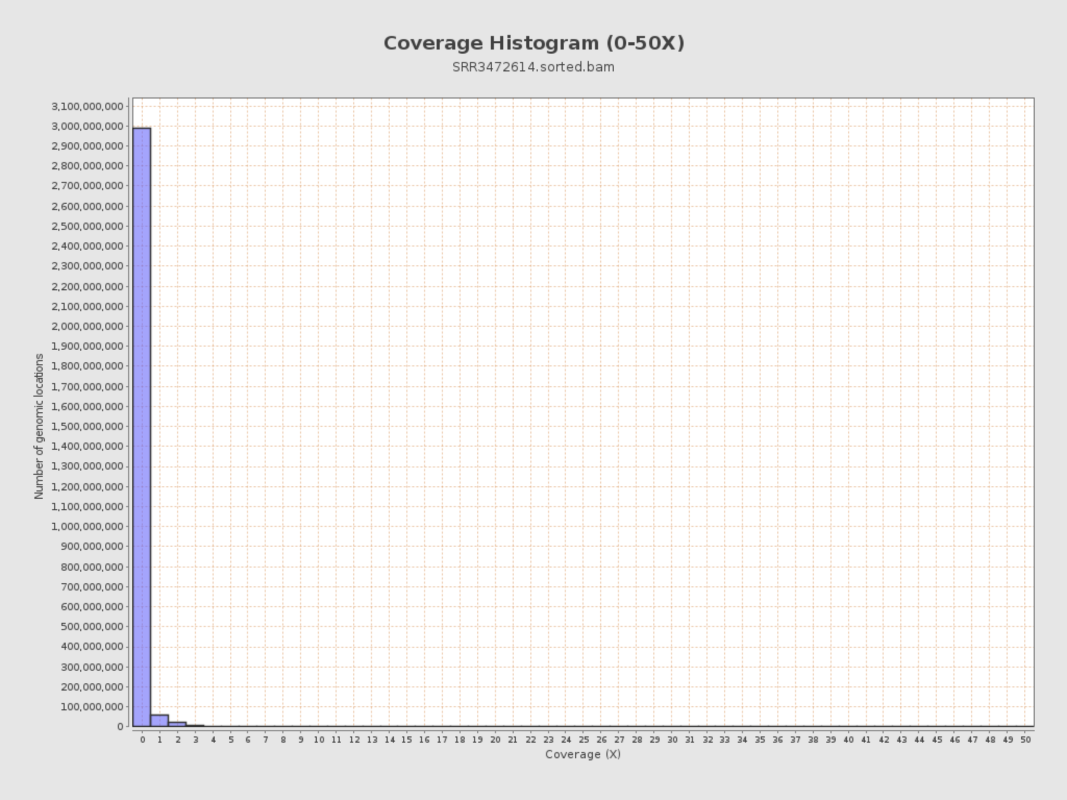
3. Results : Coverage across reference



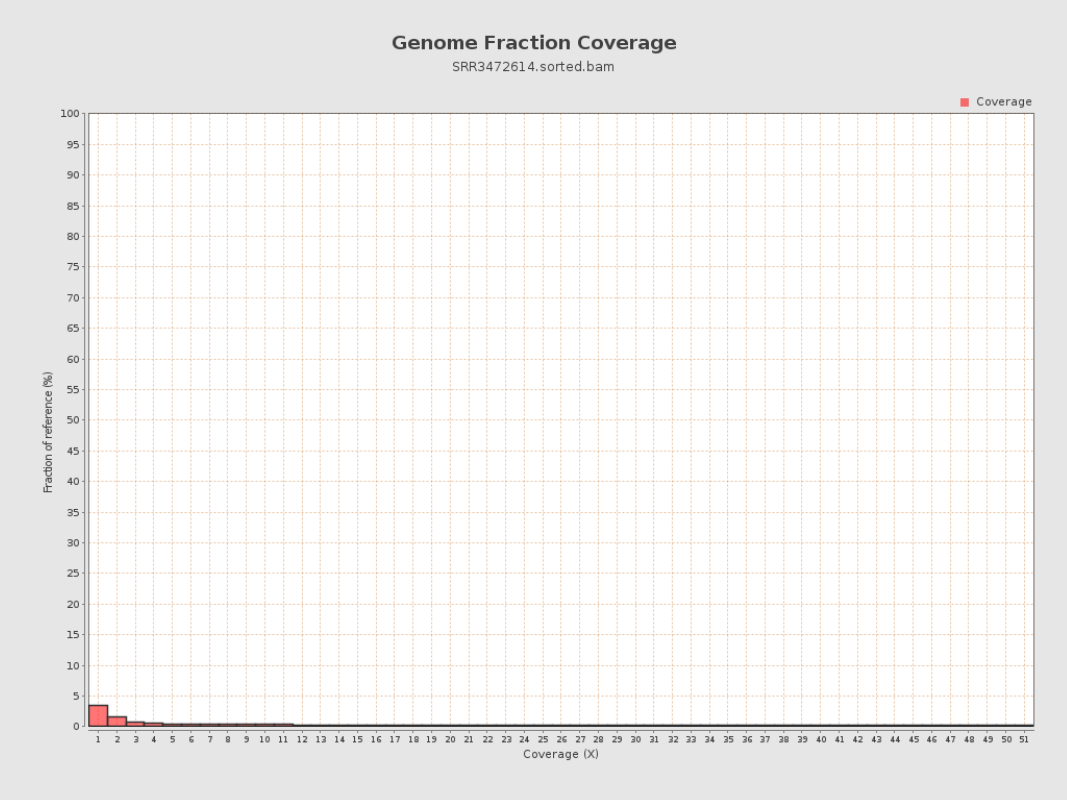
4. Results : Coverage Histogram



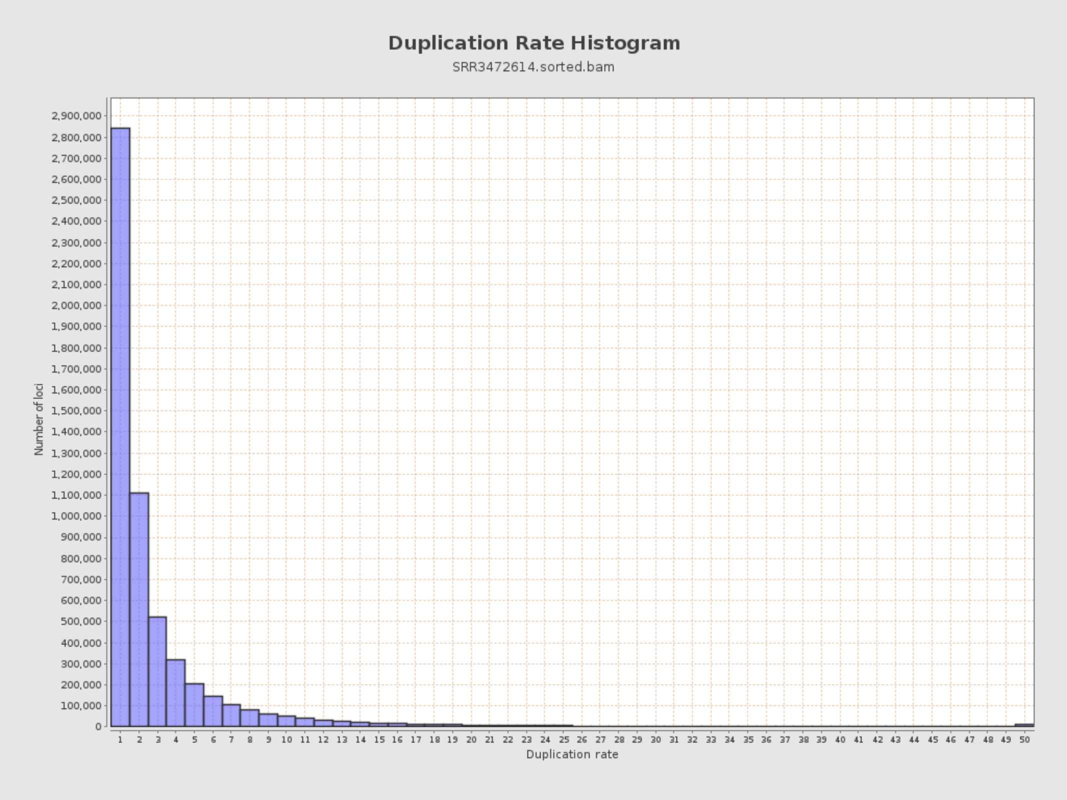
5. Results : Coverage Histogram (0-50X)



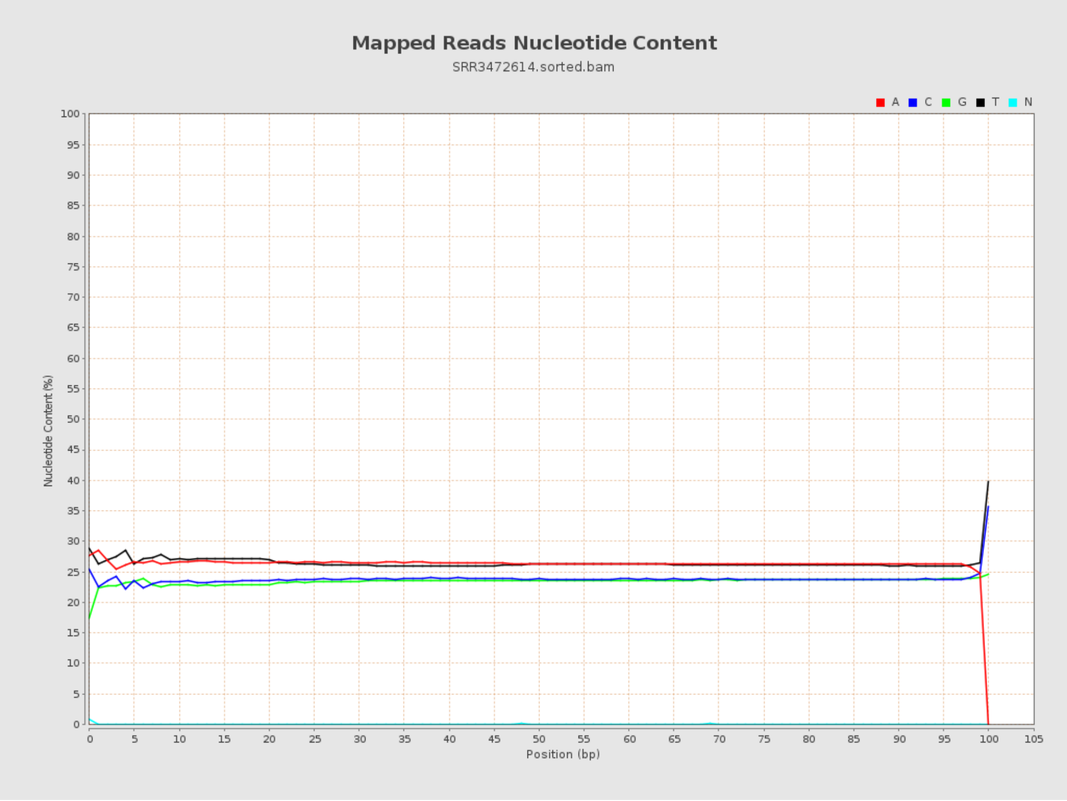
6. Results : Genome Fraction Coverage



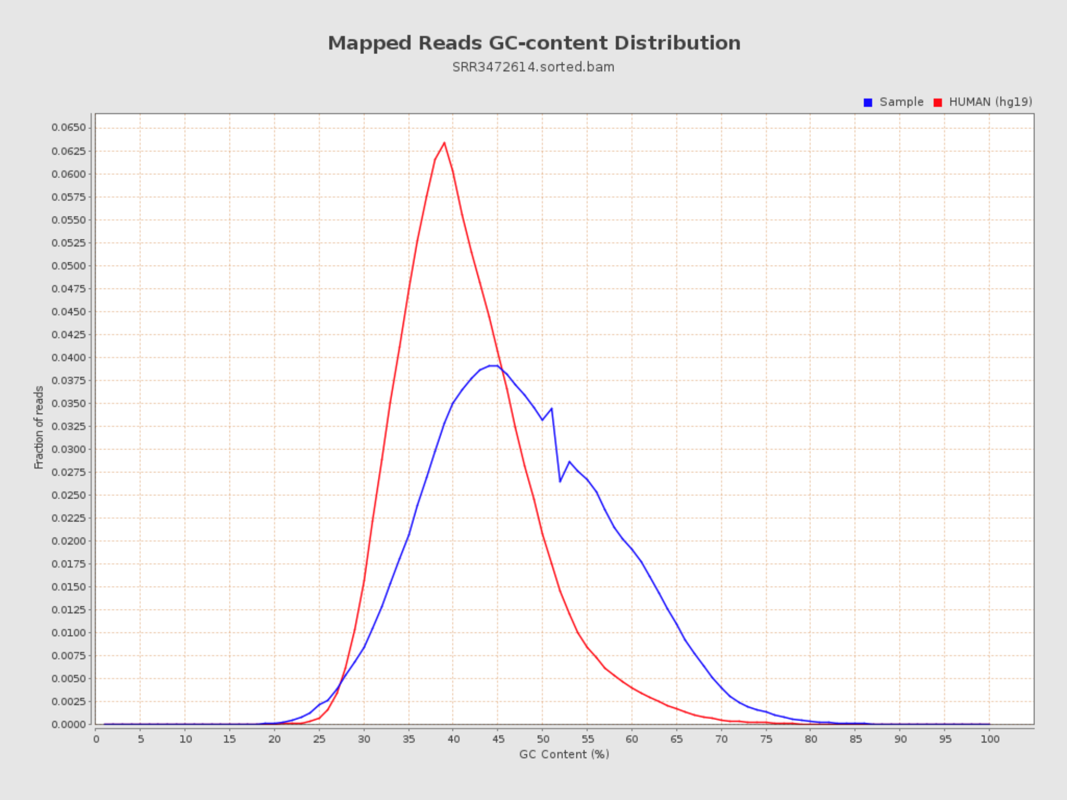
7. Results : Duplication Rate Histogram



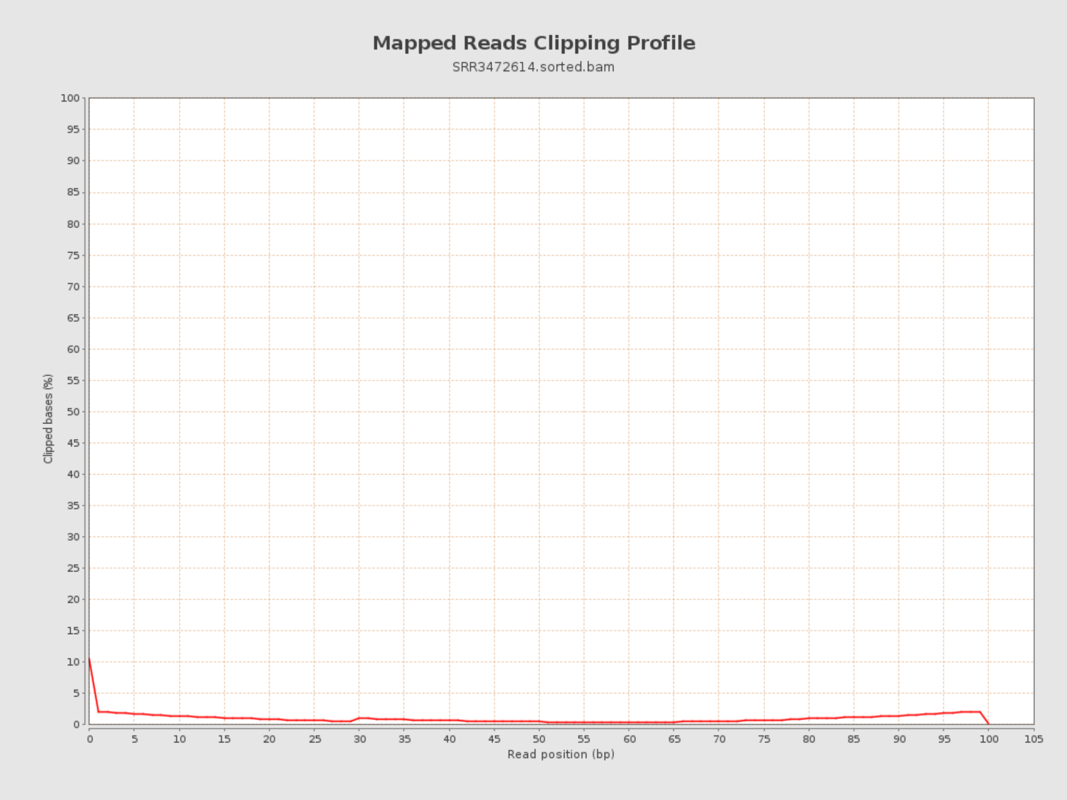
8. Results : Mapped Reads Nucleotide Content



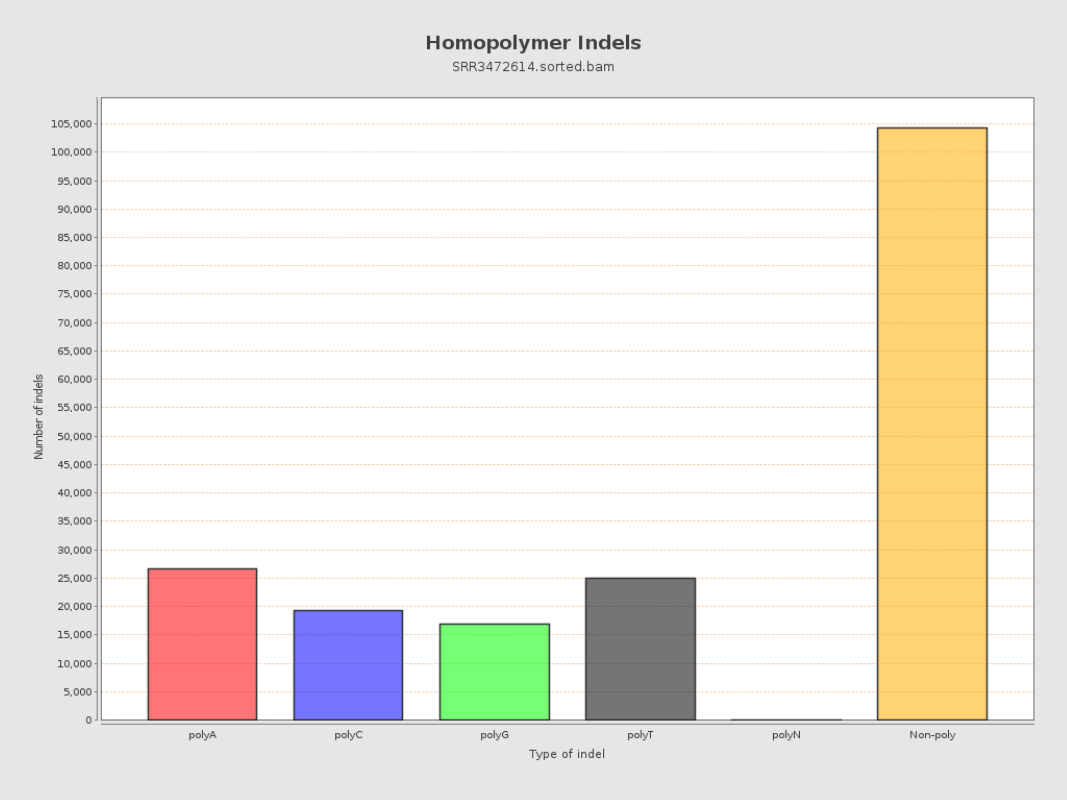
9. Results : Mapped Reads GC-content Distribution



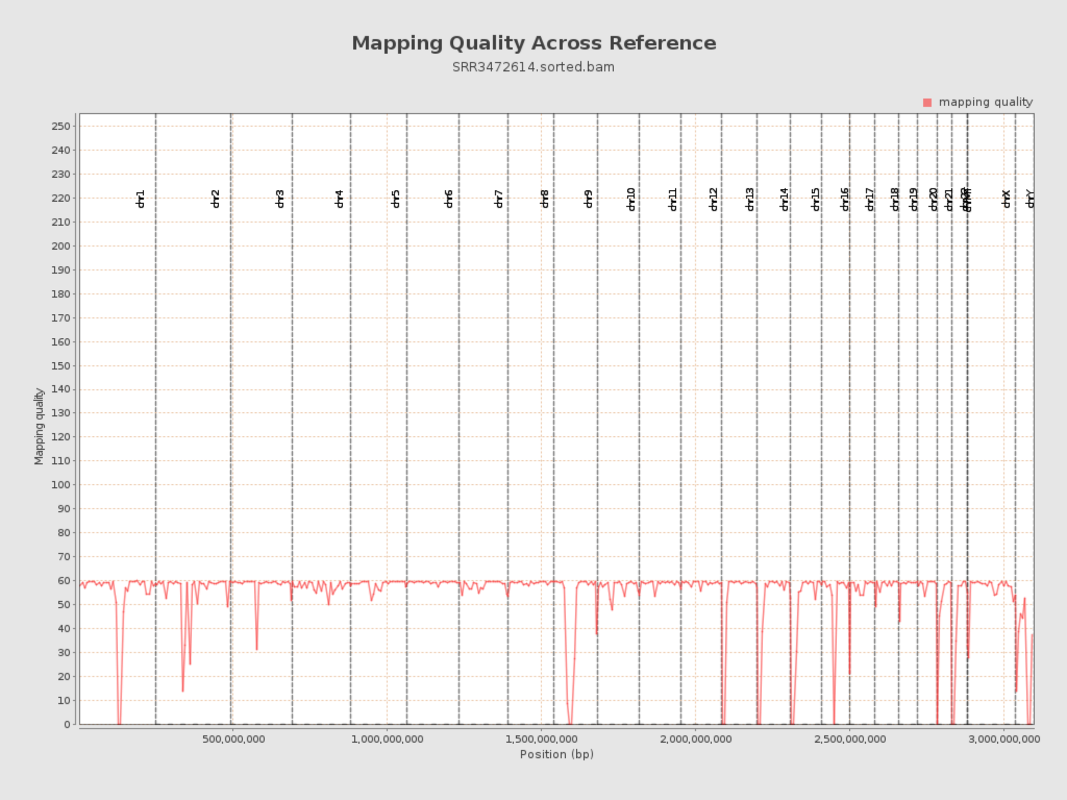
10. Results : Mapped Reads Clipping Profile



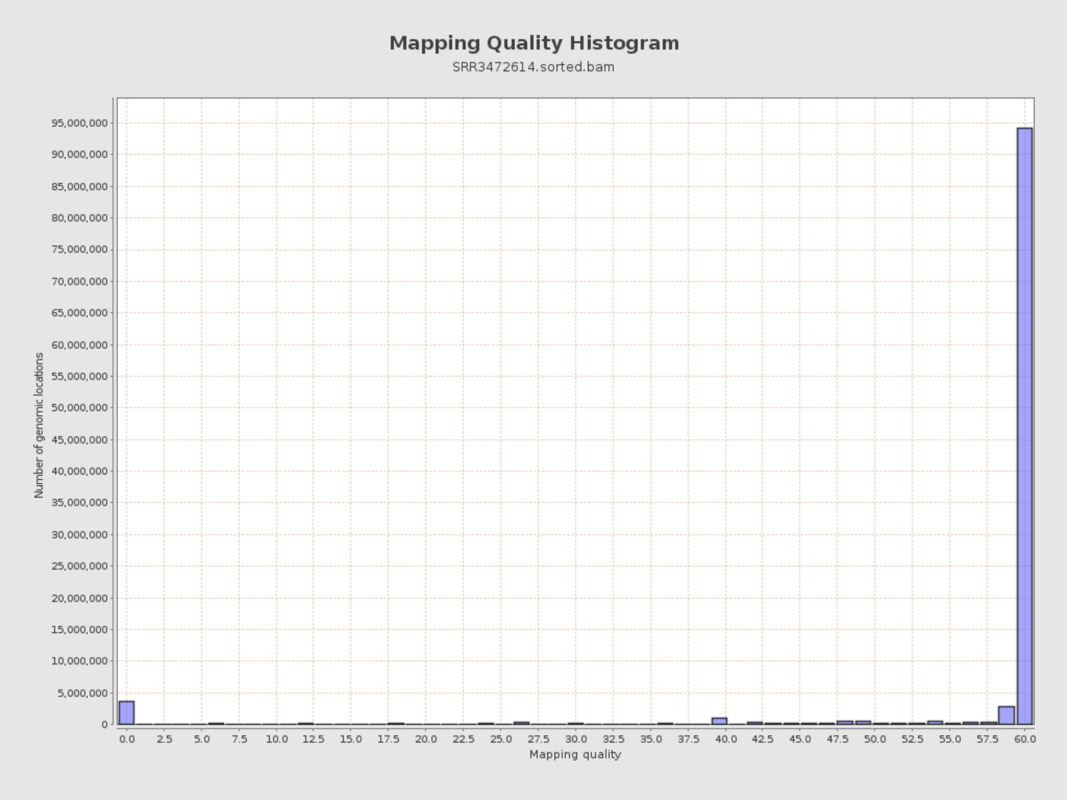
11. Results : Homopolymer Indels



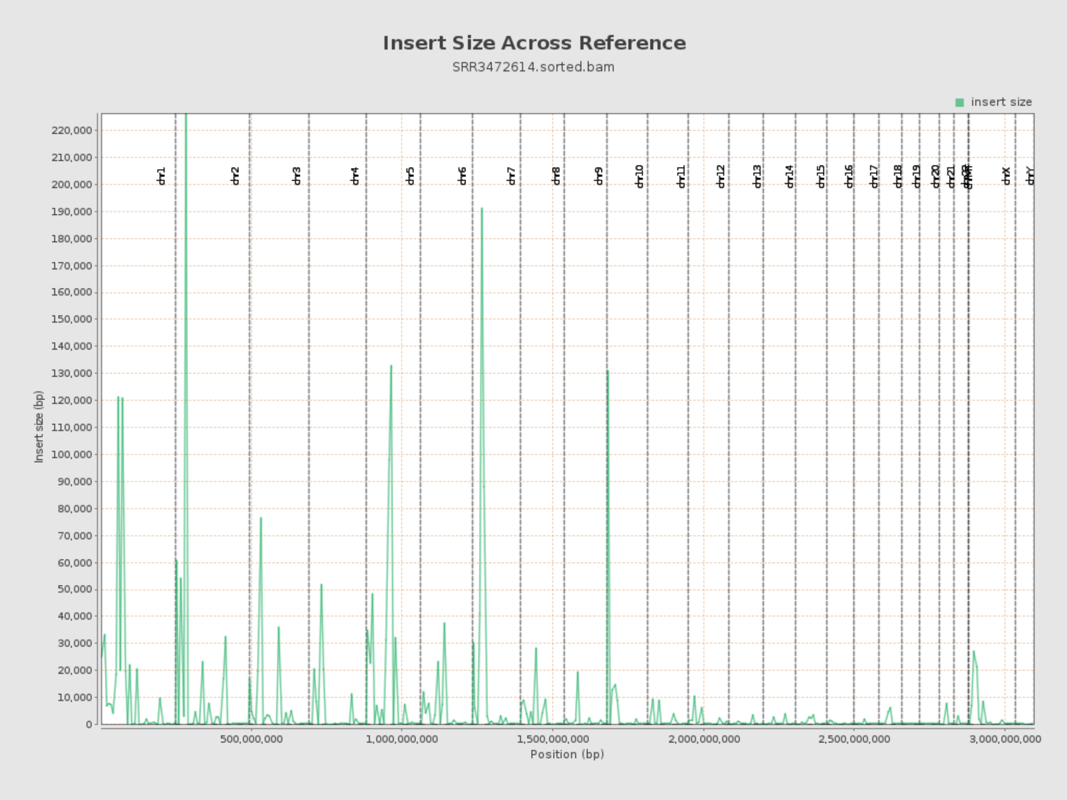
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram