Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:05:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472524.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_SRR3472524 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472524_1.fastq.gz SRR3472524_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:05:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472524.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,066,932
Mapped reads	17,884,646 / 98.99%
Unmapped reads	182,286 / 1.01%
Mapped paired reads	17,884,646 / 98.99%
Mapped reads, first in pair	8,966,117 / 49.63%
Mapped reads, second in pair	8,918,529 / 49.36%
Mapped reads, both in pair	17,789,546 / 98.46%
Mapped reads, singletons	95,100 / 0.53%
Secondary alignments	0
Supplementary alignments	71,679 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	11,503,469 / 63.67%
Duplication rate	47.75%
Clipped reads	1,610,932 / 8.92%

2.2. ACGT Content

Number/percentage of A's	484,568,882 / 27.57%
Number/percentage of C's	397,250,723 / 22.6%
Number/percentage of T's	481,788,894 / 27.41%
Number/percentage of G's	393,776,384 / 22.4%
Number/percentage of N's	275,236 / 0.02%

GC Percentage	45%

2.3. Coverage

Mean	0.5679
Standard Deviation	19.1601

2.4. Mapping Quality

Mean Mapping Quality	55.01

2.5. Insert size

Mean	28,328.13
Standard Deviation	1,631,160.25
P25/Median/P75	162 / 228 / 308

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,169,227
Insertions	92,689
Mapped reads with at least one insertion	0.51%
Deletions	87,256
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.97%

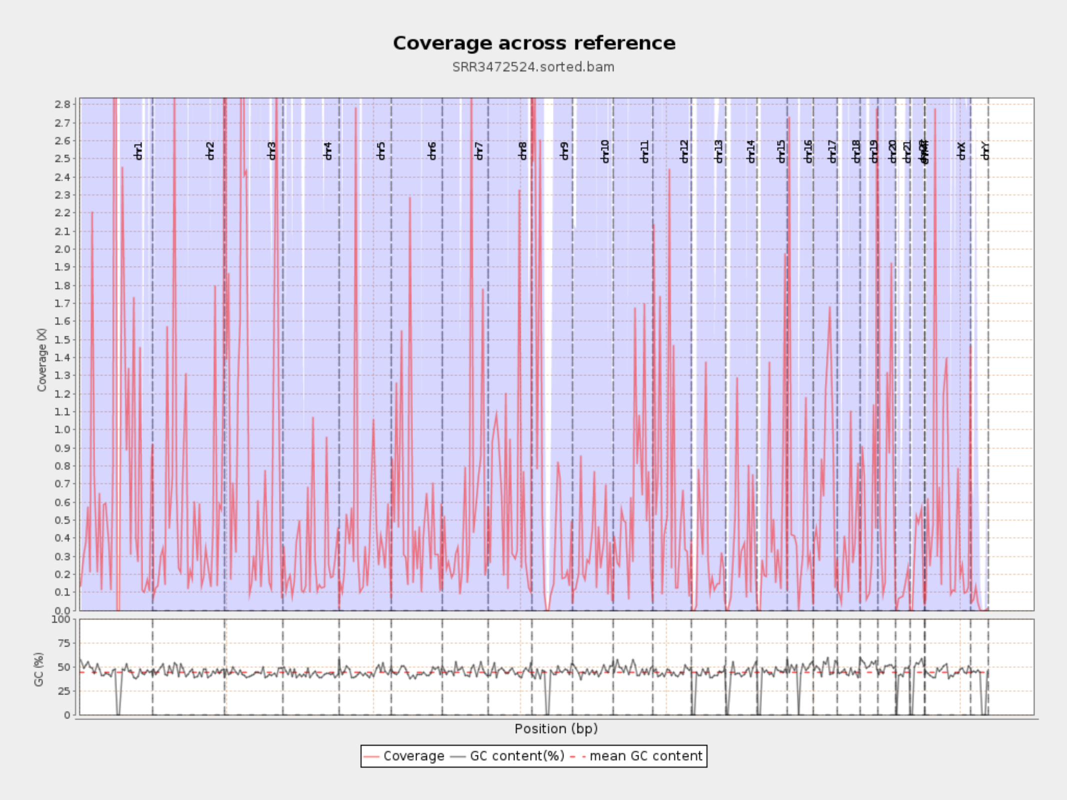
2.7. Chromosome stats

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

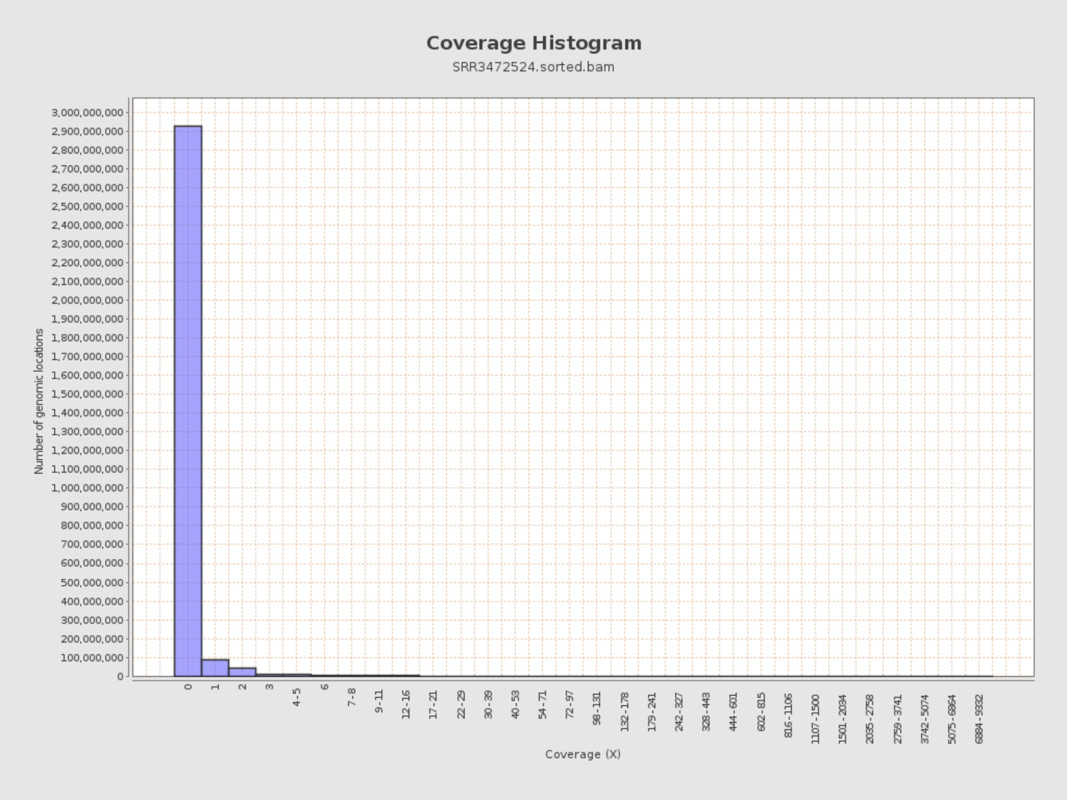
		bases	coverage	deviation
chr1	249250621	197599622	0.7928	27.8905
chr2	243199373	134459460	0.5529	21.0948
chr3	198022430	220452492	1.1133	25.3506
chr4	191154276	55169551	0.2886	10.1937
chr5	180915260	82514706	0.4561	15.0824
chr6	171115067	94483314	0.5522	17.8985
chr7	159138663	89737404	0.5639	17.0028
chr8	146364022	93840220	0.6411	20.1565
chr9	141213431	103060329	0.7298	18.5446
chr10	135534747	44984710	0.3319	13.6707
chr11	135006516	83904287	0.6215	20.3155
chr12	133851895	96474700	0.7208	21.9777
chr13	115169878	35394793	0.3073	12.3555
chr14	107349540	38240532	0.3562	16.1355
chr15	102531392	50167059	0.4893	16.1597
chr16	90354753	49288371	0.5455	17.7234
chr17	81195210	63131921	0.7775	18.7226
chr18	78077248	29238816	0.3745	11.644
chr19	59128983	34326773	0.5805	18.1759
chr20	63025520	54329669	0.862	34.5049
chr21	48129895	5150599	0.107	2.5272
chr22	51304566	14952814	0.2915	10.6533
chrMT	16571	2574	0.1553	0.6434
chrX	155270560	84807457	0.5462	18.0976

chrY	59373566	2186046	0.0368	1.0743

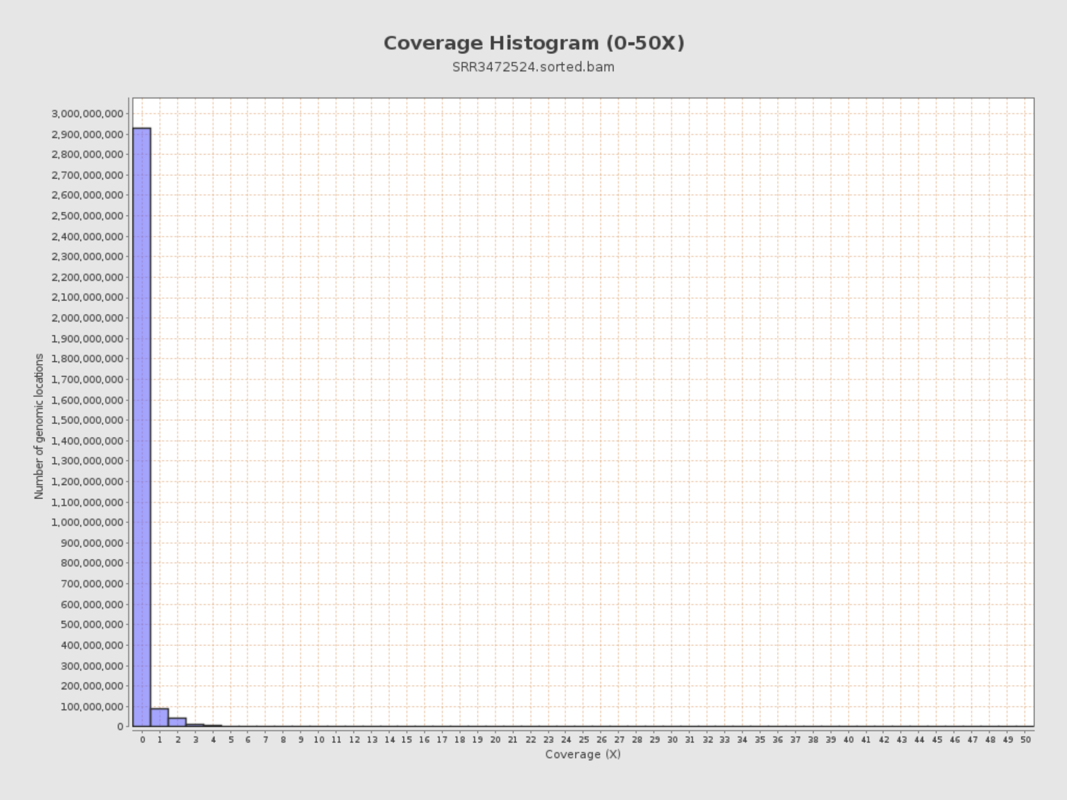
3. Results : Coverage across reference



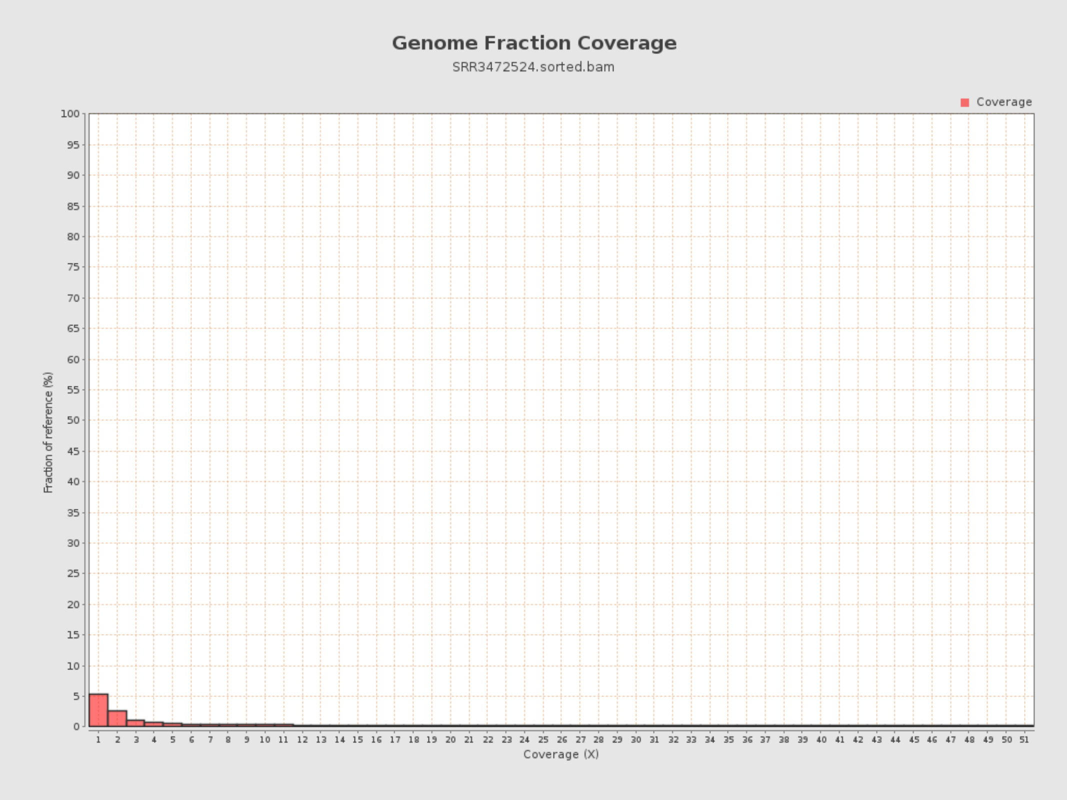
4. Results : Coverage Histogram



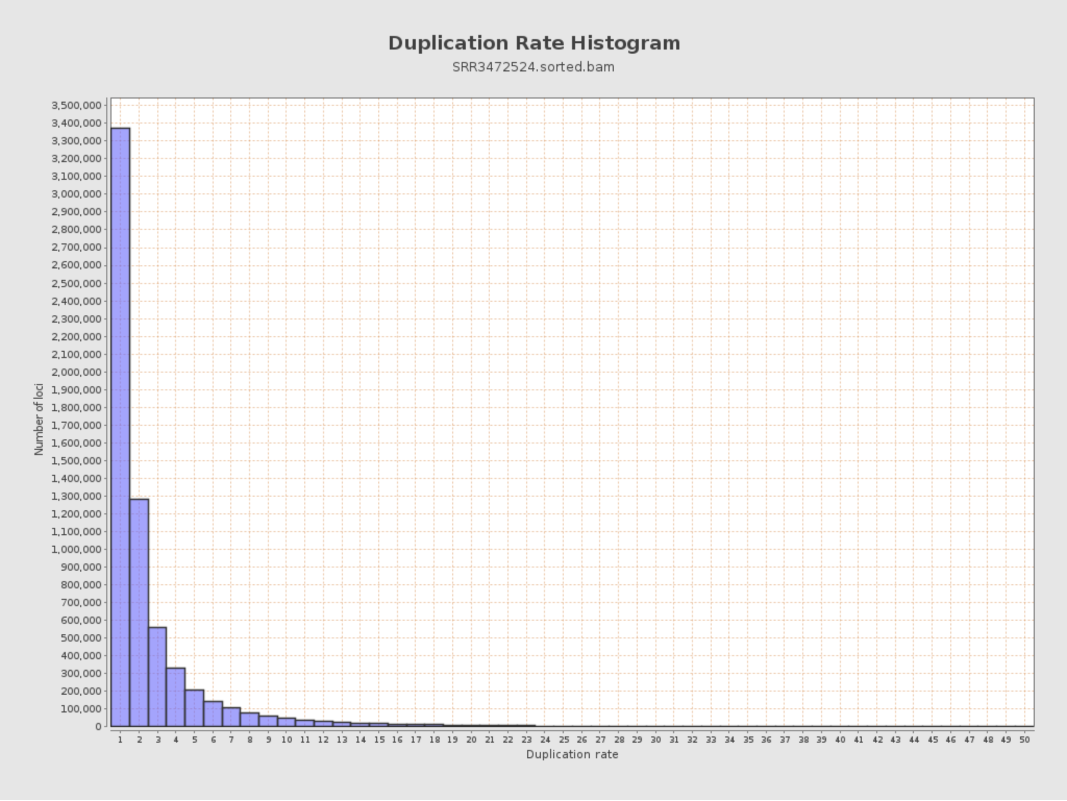
5. Results : Coverage Histogram (0-50X)



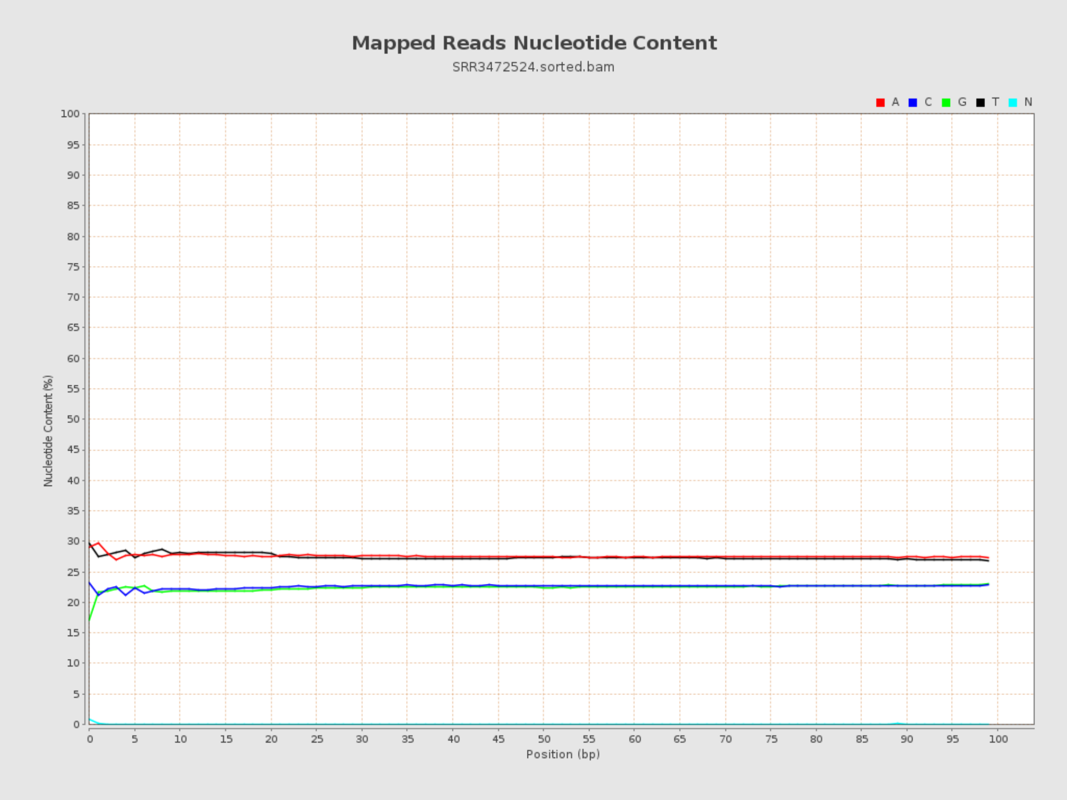
6. Results : Genome Fraction Coverage



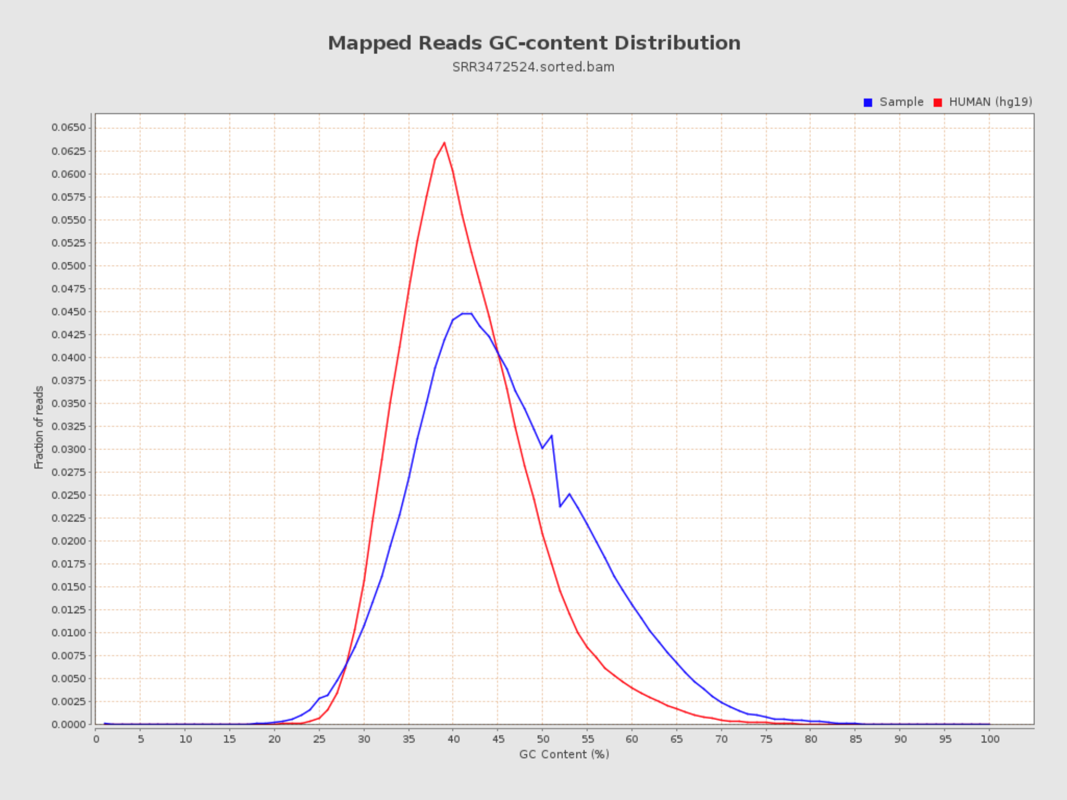
7. Results : Duplication Rate Histogram



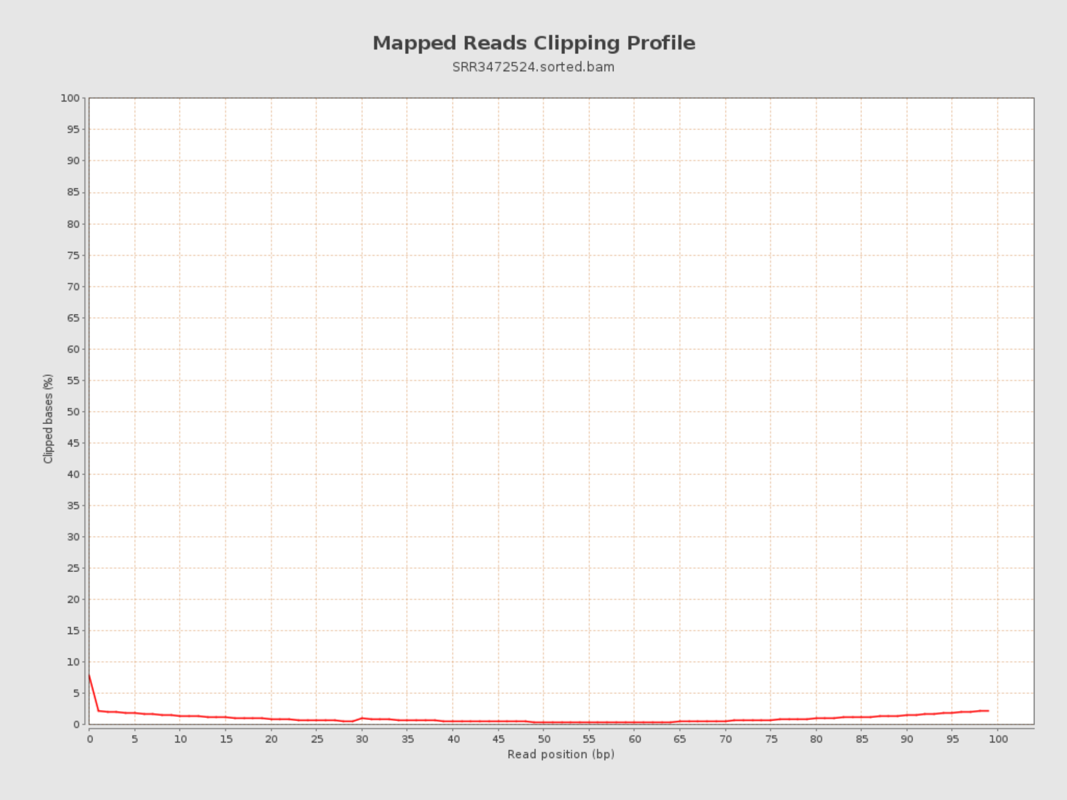
8. Results : Mapped Reads Nucleotide Content



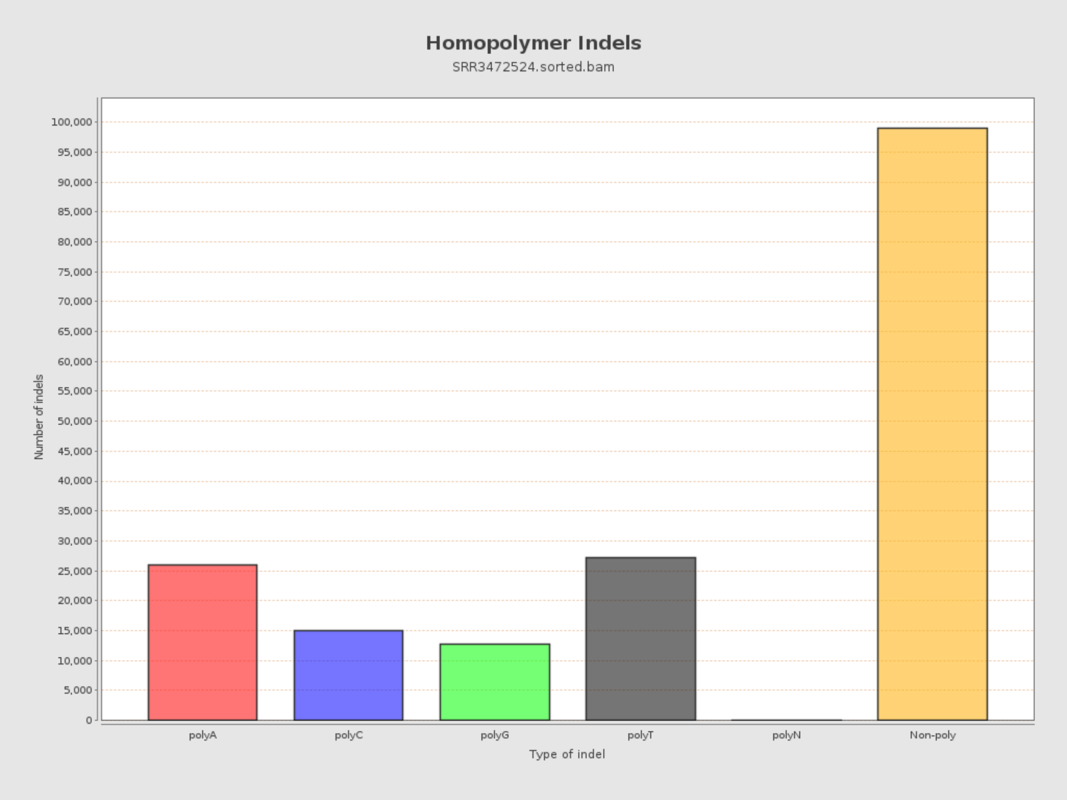
9. Results : Mapped Reads GC-content Distribution



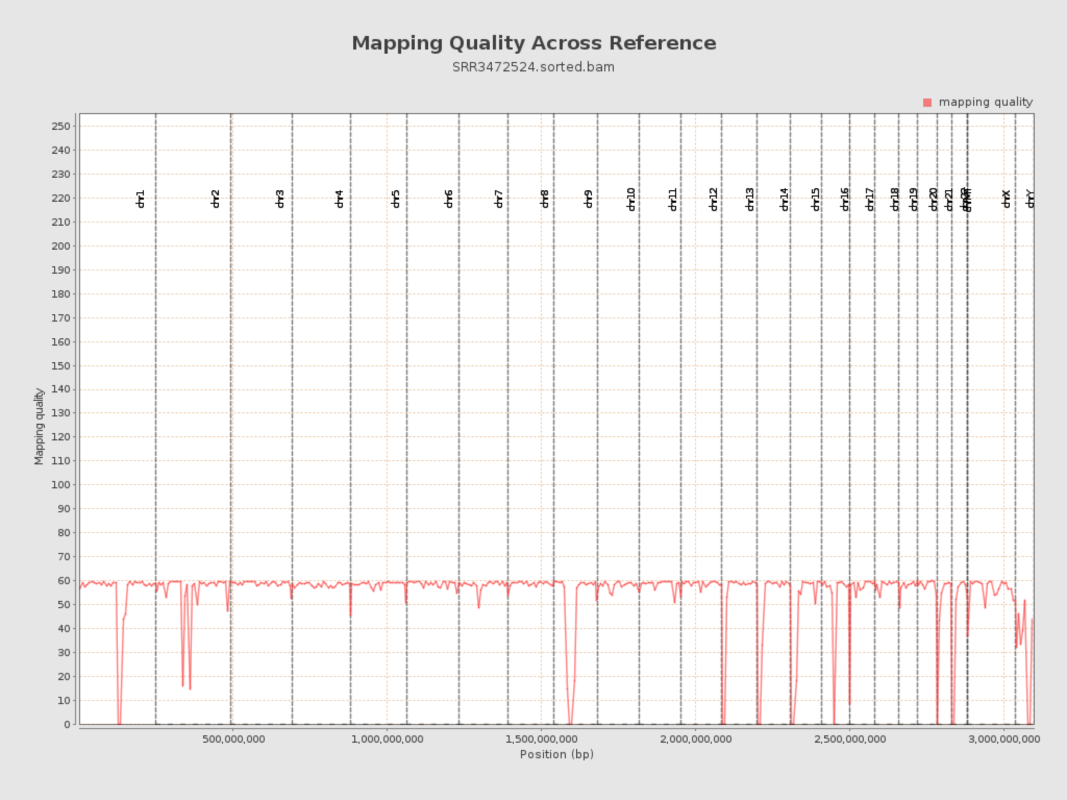
10. Results : Mapped Reads Clipping Profile



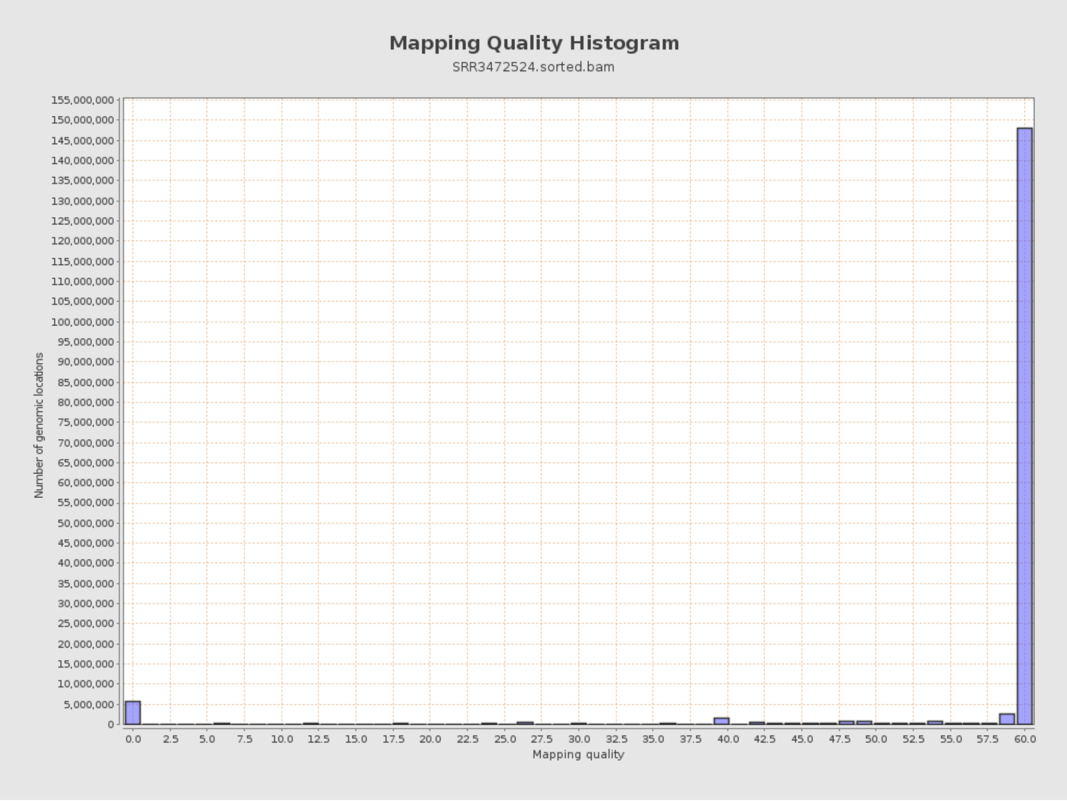
11. Results : Homopolymer Indels



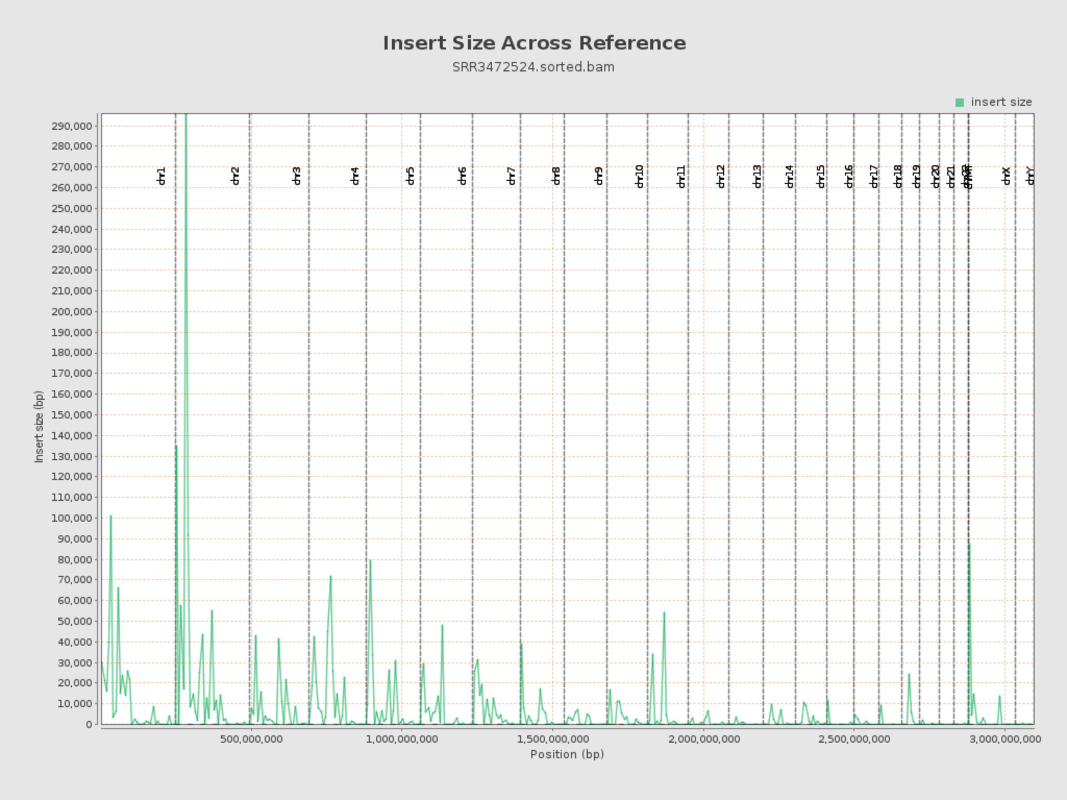
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram