Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 15:16:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472626.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_SRR3472626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472626_1.fastq.gz SRR3472626_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 15:16:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,724,004
Mapped reads	18,573,711 / 99.2%
Unmapped reads	150,293 / 0.8%
Mapped paired reads	18,573,711 / 99.2%
Mapped reads, first in pair	9,317,444 / 49.76%
Mapped reads, second in pair	9,256,267 / 49.44%
Mapped reads, both in pair	18,470,340 / 98.65%
Mapped reads, singletons	103,371 / 0.55%
Secondary alignments	0
Supplementary alignments	82,505 / 0.44%
Read min/max/mean length	30 / 101 / 99.52
Duplicated reads (estimated)	13,085,020 / 69.88%
Duplication rate	50.6%
Clipped reads	1,334,122 / 7.13%

2.2. ACGT Content

Number/percentage of A's	488,678,512 / 26.82%
Number/percentage of C's	424,069,917 / 23.27%
Number/percentage of T's	489,784,456 / 26.88%
Number/percentage of G's	419,335,935 / 23.01%
Number/percentage of N's	346,487 / 0.02%

GC Percentage	46.28%

2.3. Coverage

Mean	0.5887
Standard Deviation	25.8406

2.4. Mapping Quality

Mean Mapping Quality	54.75

2.5. Insert size

Mean	19,339.64
Standard Deviation	1,404,037.17
P25/Median/P75	146 / 200 / 266

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	10,369,858
Insertions	95,731
Mapped reads with at least one insertion	0.51%
Deletions	92,922
Mapped reads with at least one deletion	0.49%
Homopolymer indels	47.19%

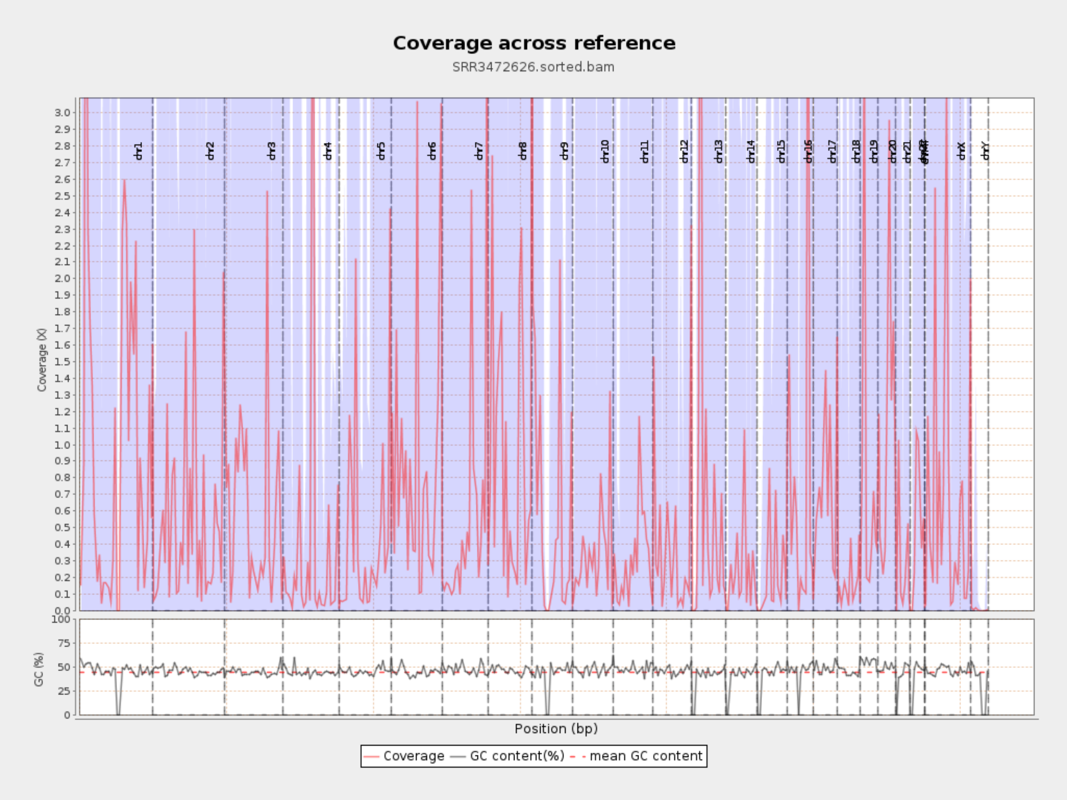
2.7. Chromosome stats

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

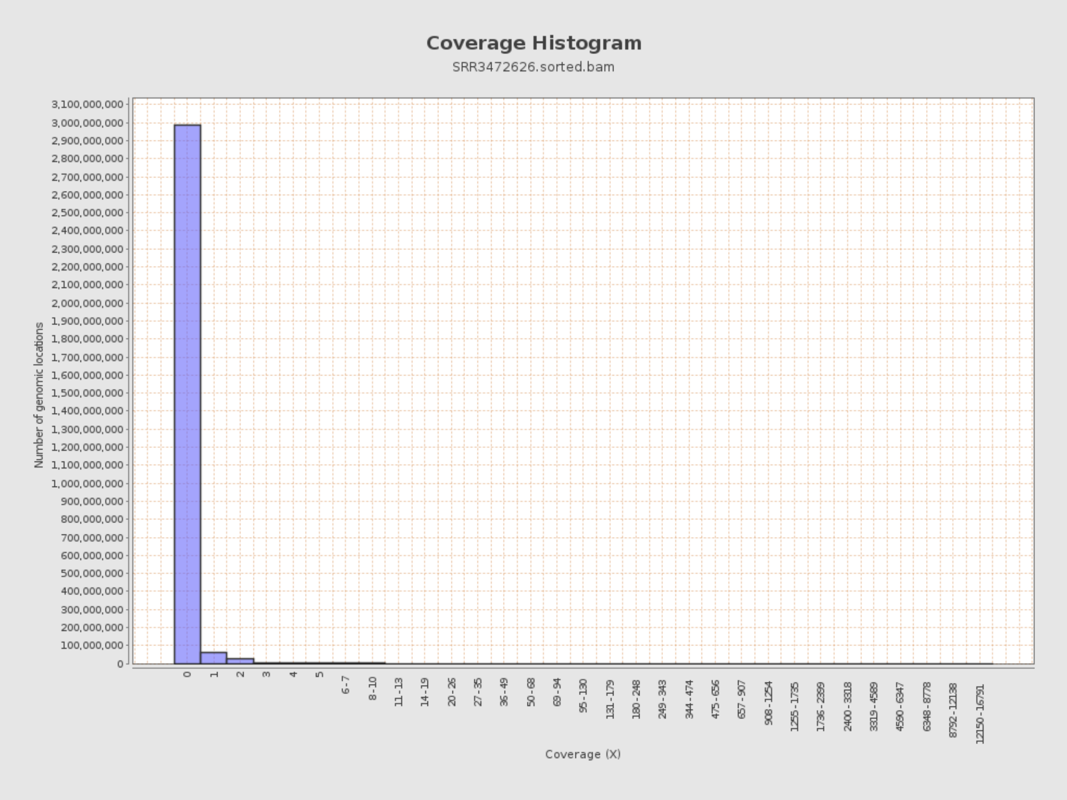
		bases	coverage	deviation
chr1	249250621	257575015	1.0334	36.7735
chr2	243199373	126244219	0.5191	20.8453
chr3	198022430	123350510	0.6229	21.2542
chr4	191154276	68771035	0.3598	32.6686
chr5	180915260	85239239	0.4712	19.5979
chr6	171115067	151179996	0.8835	31.0099
chr7	159138663	97785701	0.6145	31.862
chr8	146364022	137059100	0.9364	37.9332
chr9	141213431	87035716	0.6163	22.7069
chr10	135534747	47532310	0.3507	15.3758
chr11	135006516	42970707	0.3183	14.5308
chr12	133851895	48735206	0.3641	12.595
chr13	115169878	84858451	0.7368	42.2269
chr14	107349540	24833025	0.2313	9.4476
chr15	102531392	21967480	0.2143	14.4887
chr16	90354753	76421799	0.8458	30.9983
chr17	81195210	59855595	0.7372	17.3859
chr18	78077248	12528625	0.1605	7.6902
chr19	59128983	49748511	0.8414	27.072
chr20	63025520	73979236	1.1738	30.9476
chr21	48129895	14658117	0.3046	20.296
chr22	51304566	25211450	0.4914	18.6302
chrMT	16571	4950	0.2987	0.8562
chrX	155270560	104551828	0.6734	22.1385

chrY	59373566	348693	0.0059	0.5364

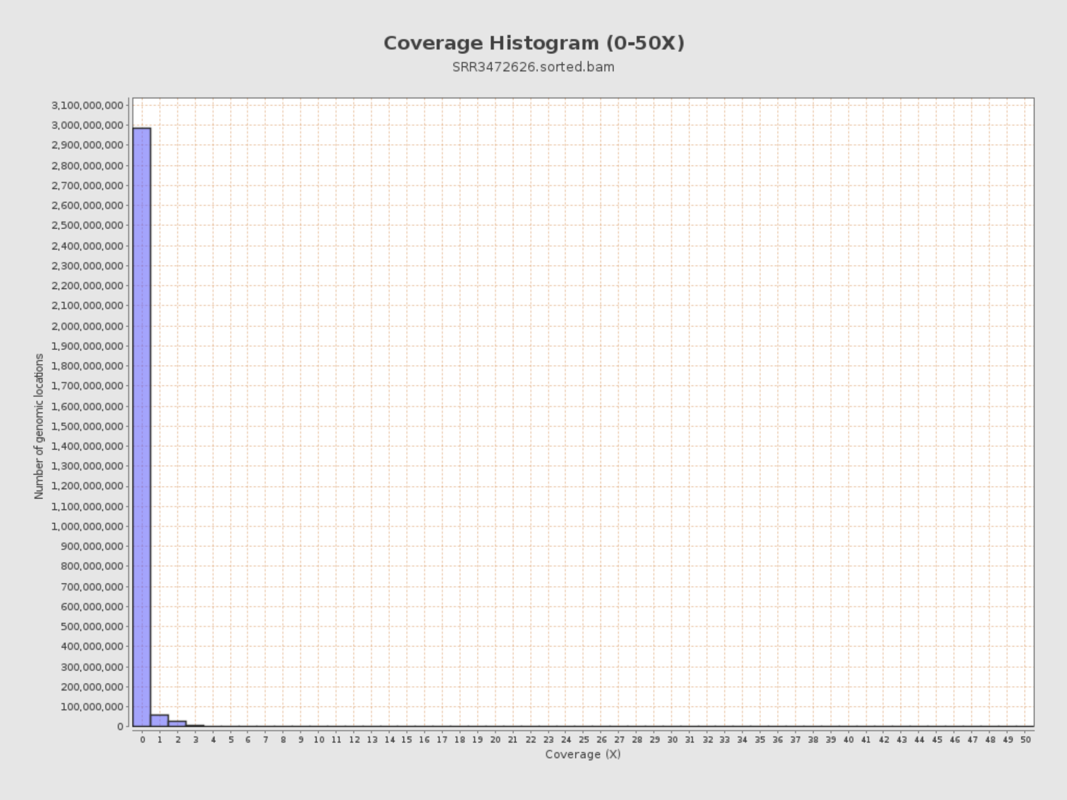
3. Results : Coverage across reference



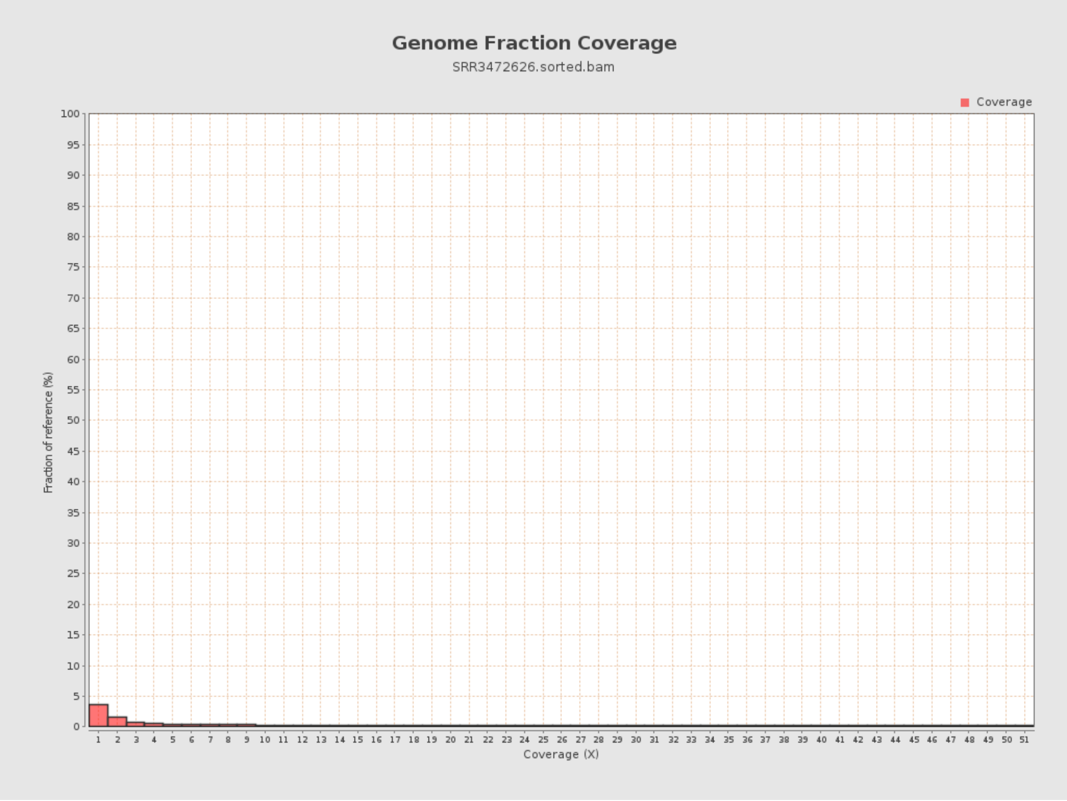
4. Results : Coverage Histogram



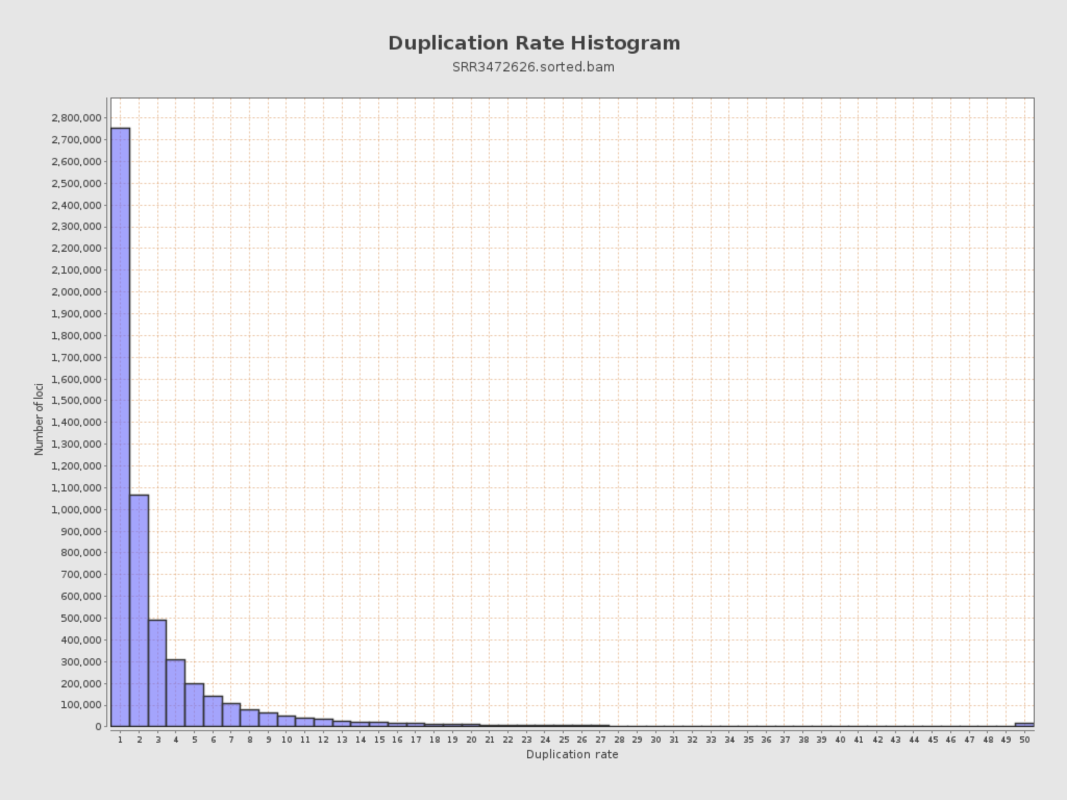
5. Results : Coverage Histogram (0-50X)



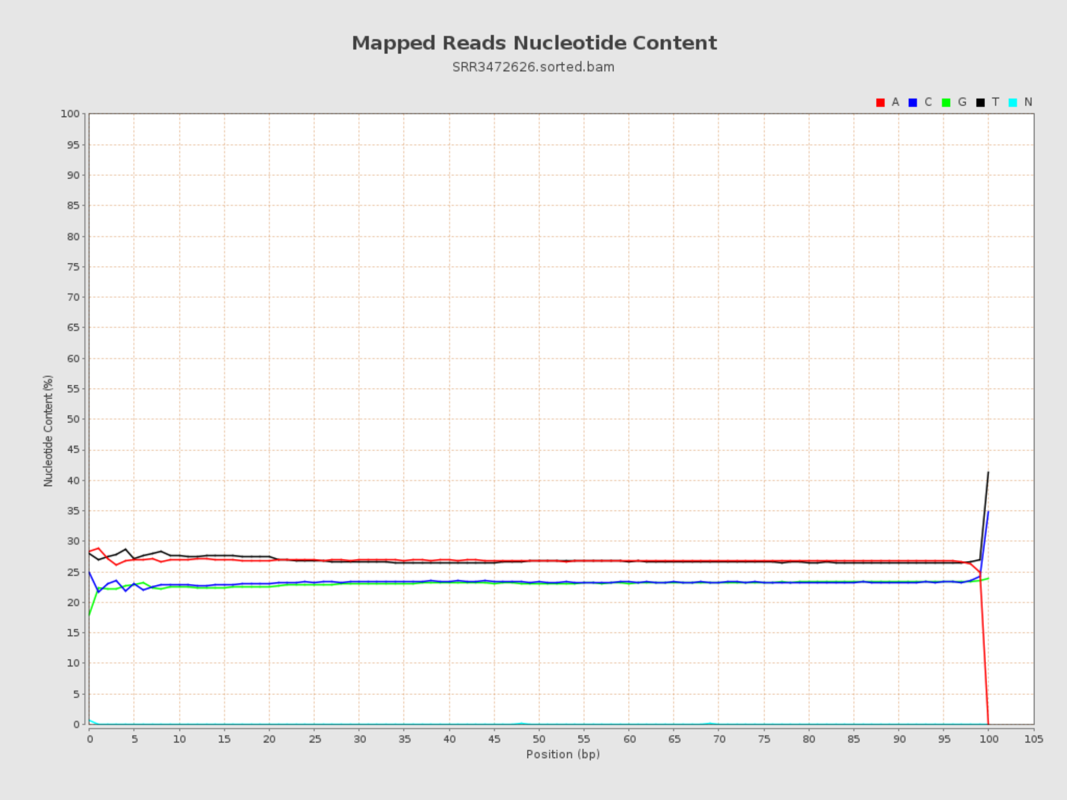
6. Results : Genome Fraction Coverage



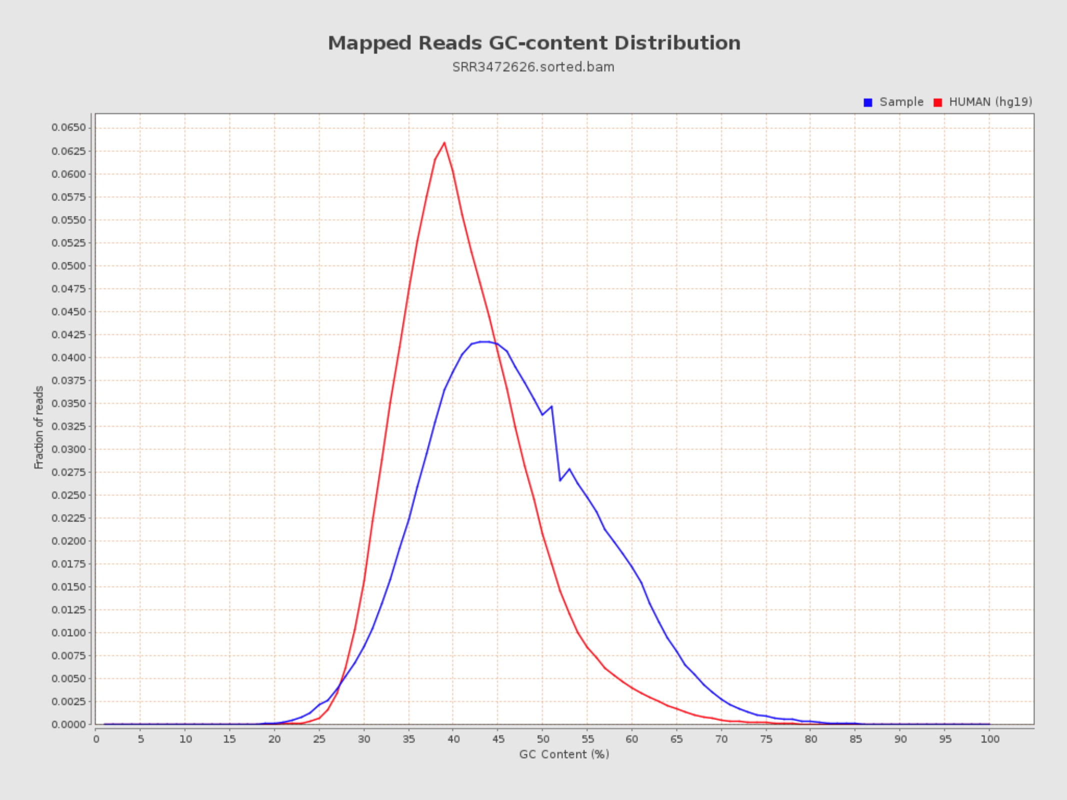
7. Results : Duplication Rate Histogram



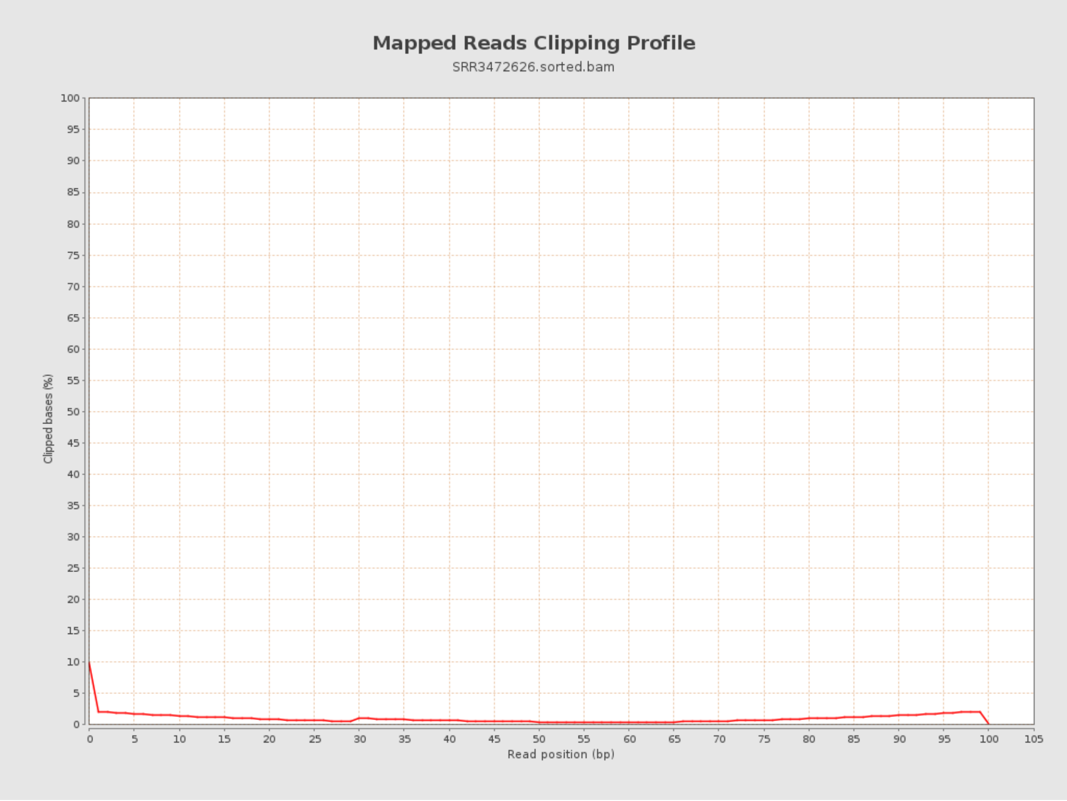
8. Results : Mapped Reads Nucleotide Content



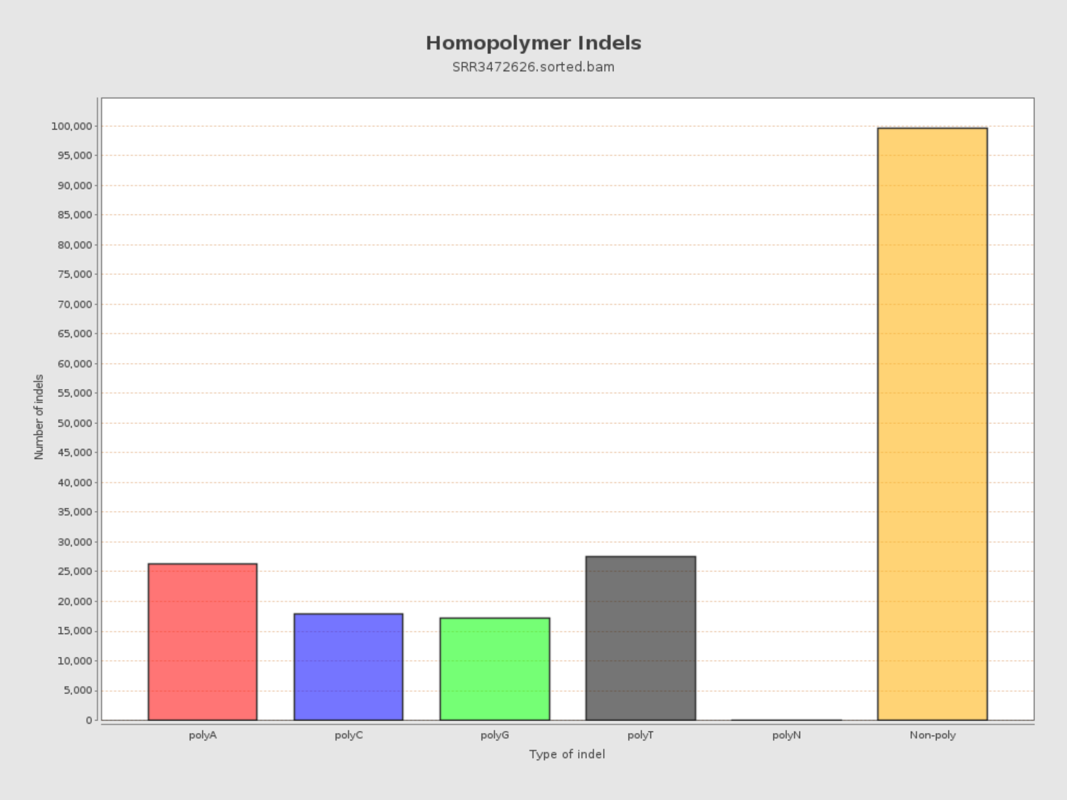
9. Results : Mapped Reads GC-content Distribution



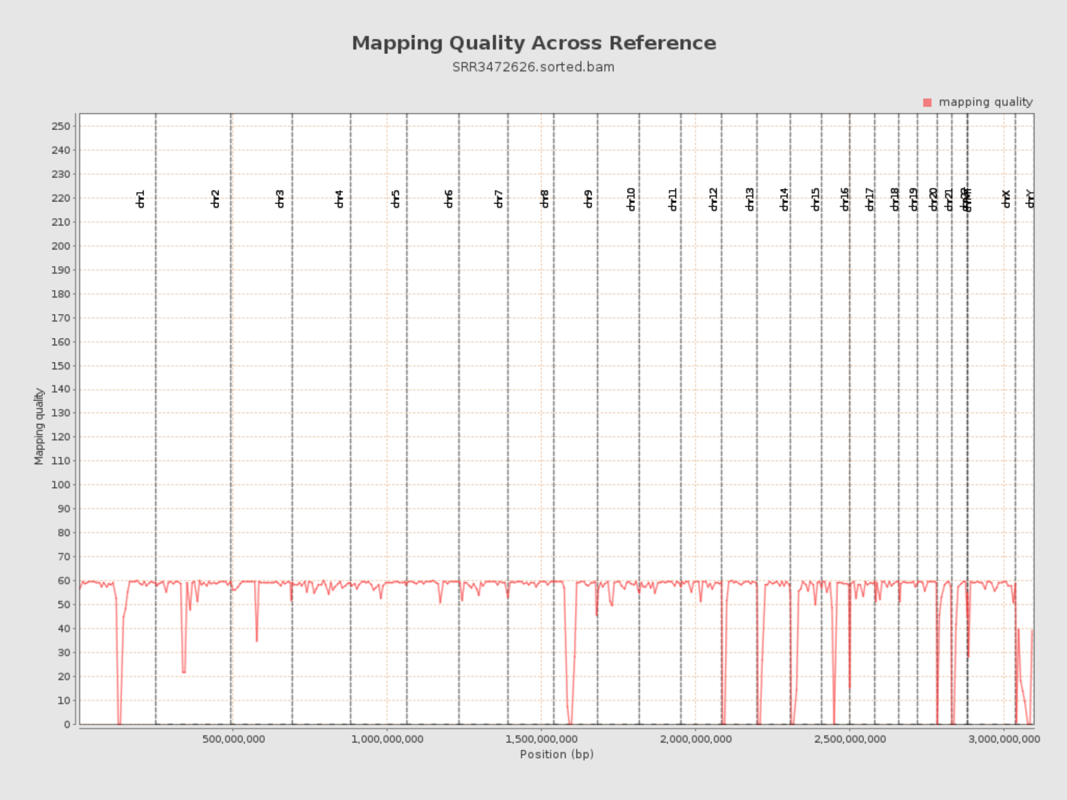
10. Results : Mapped Reads Clipping Profile



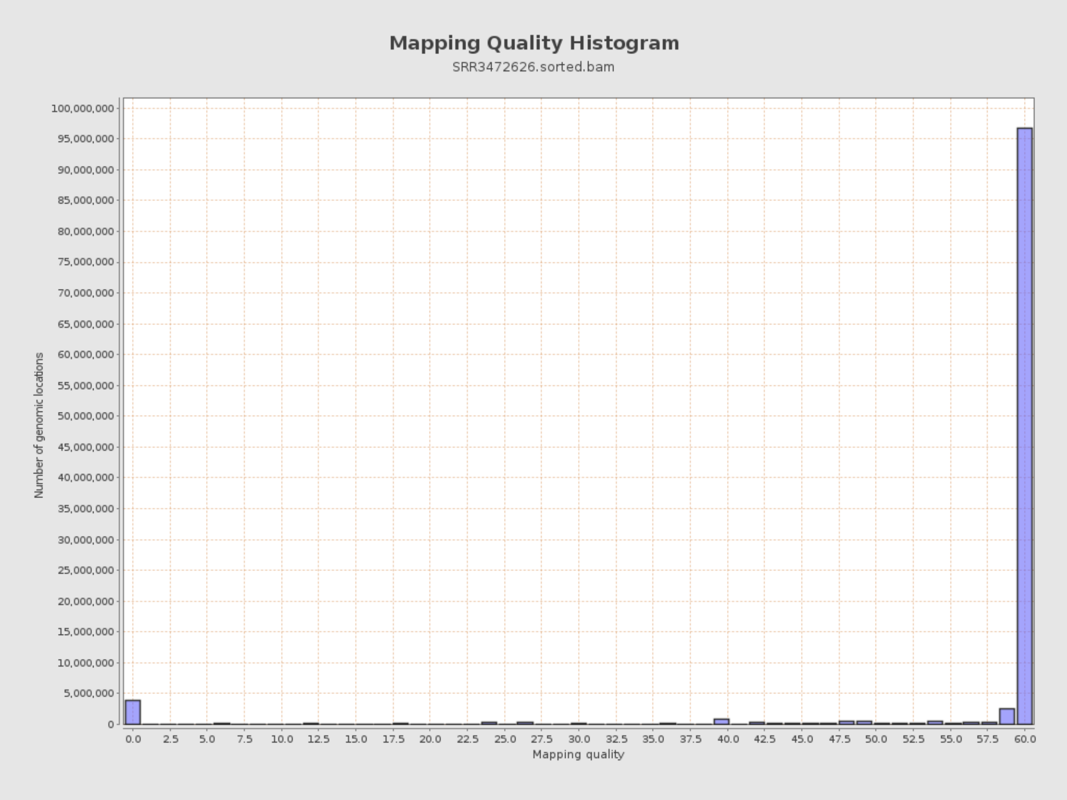
11. Results : Homopolymer Indels



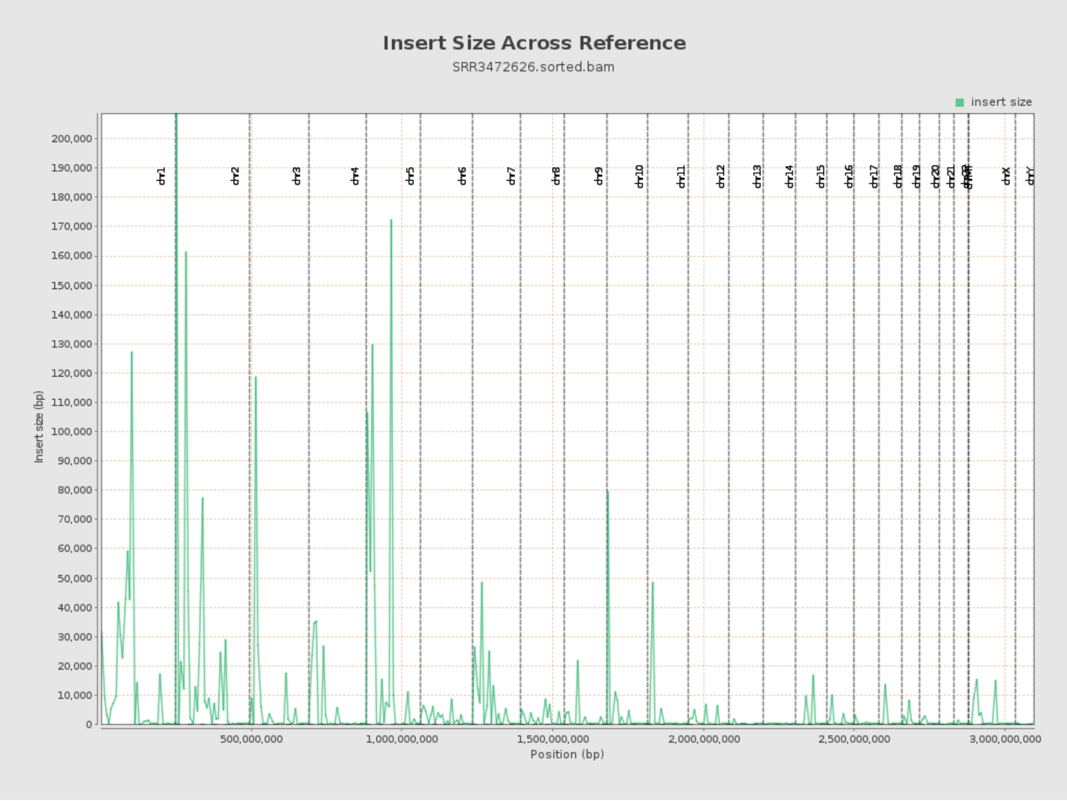
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram