Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:00:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472520.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_SRR3472520 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472520_1.fastq.gz SRR3472520_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:00:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472520.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,441,230
Mapped reads	14,213,509 / 98.42%
Unmapped reads	227,721 / 1.58%
Mapped paired reads	14,213,509 / 98.42%
Mapped reads, first in pair	7,136,544 / 49.42%
Mapped reads, second in pair	7,076,965 / 49.01%
Mapped reads, both in pair	14,105,814 / 97.68%
Mapped reads, singletons	107,695 / 0.75%
Secondary alignments	0
Supplementary alignments	54,220 / 0.38%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	8,596,914 / 59.53%
Duplication rate	45.2%
Clipped reads	1,100,095 / 7.62%

2.2. ACGT Content

Number/percentage of A's	391,350,453 / 27.95%
Number/percentage of C's	310,718,189 / 22.19%
Number/percentage of T's	389,324,626 / 27.81%
Number/percentage of G's	308,423,171 / 22.03%
Number/percentage of N's	216,376 / 0.02%

GC Percentage	44.22%

2.3. Coverage

Mean	0.4523
Standard Deviation	15.4741

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	28,785.55
Standard Deviation	1,694,195.93
P25/Median/P75	176 / 244 / 329

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	8,993,630
Insertions	81,524
Mapped reads with at least one insertion	0.57%
Deletions	74,261
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.3%

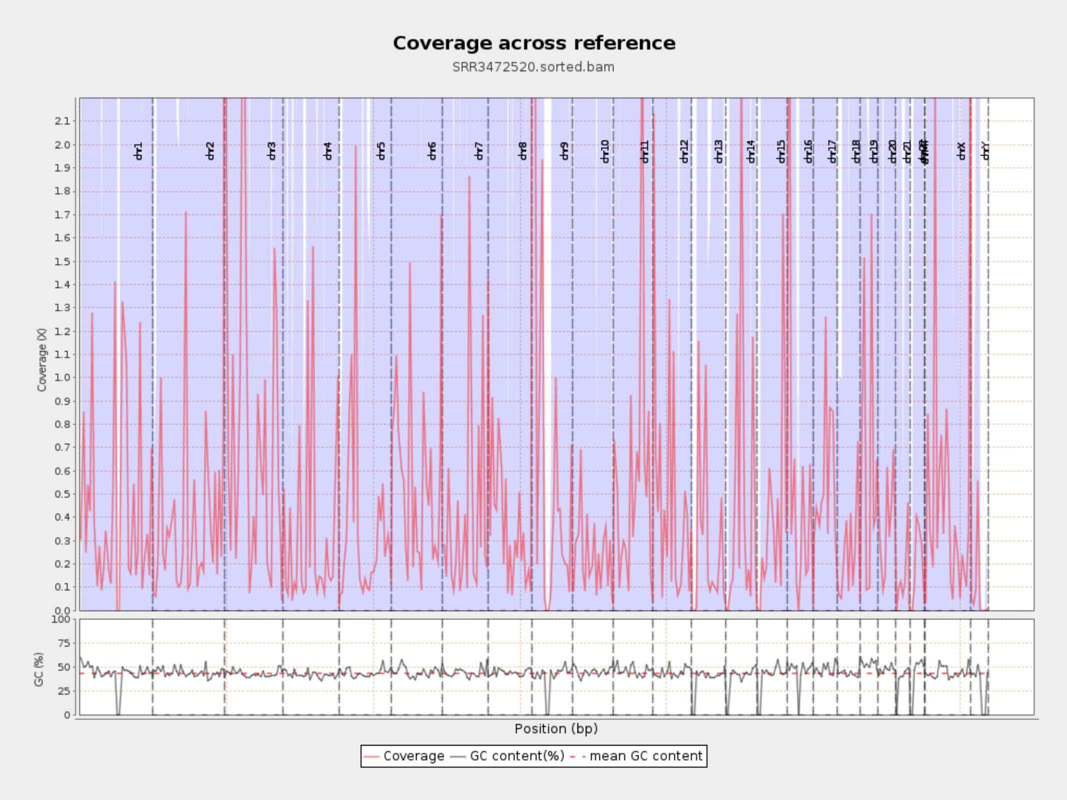
2.7. Chromosome stats

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

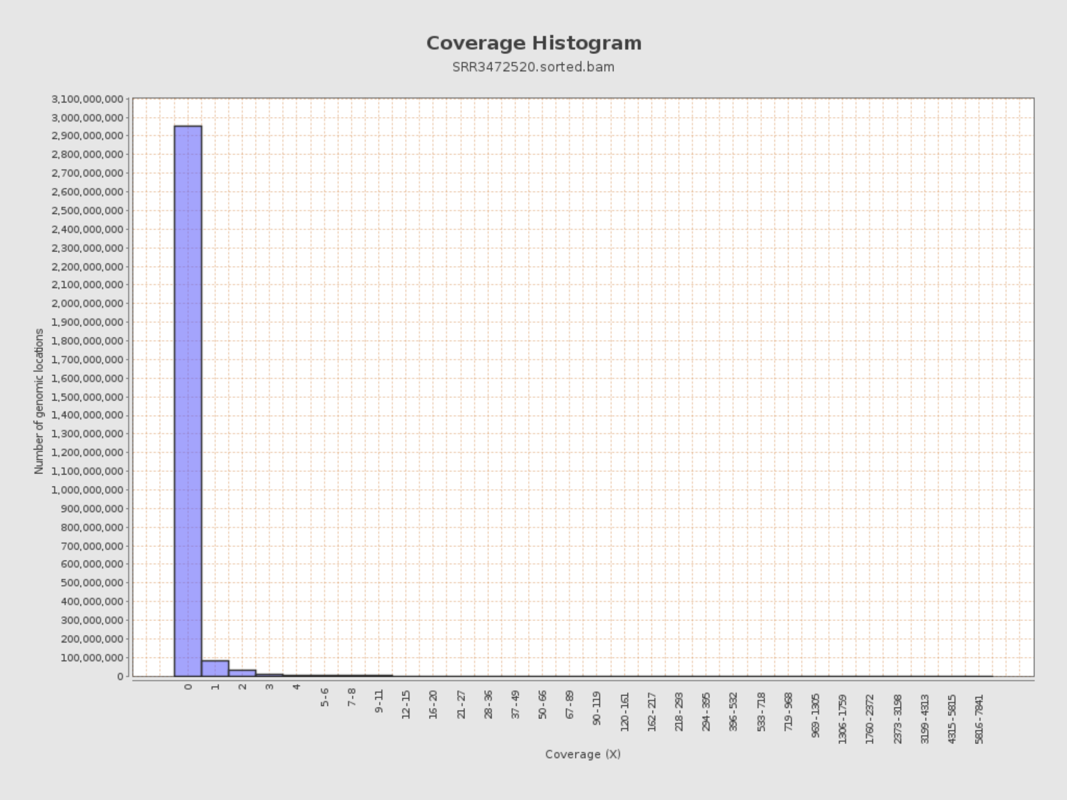
		bases	**coverage**	**deviation**
chr1	249250621	115737459	0.4643	14.0323
chr2	243199373	88237984	0.3628	12.5742
chr3	198022430	167597481	0.8464	23.019
chr4	191154276	63771860	0.3336	14.813
chr5	180915260	66971535	0.3702	10.7153
chr6	171115067	95161970	0.5561	15.163
chr7	159138663	66936712	0.4206	13.9624
chr8	146364022	52065838	0.3557	11.6698
chr9	141213431	99186207	0.7024	19.6038
chr10	135534747	33117127	0.2443	9.4924
chr11	135006516	78355223	0.5804	26.8242
chr12	133851895	68644598	0.5128	15.3323
chr13	115169878	32993172	0.2865	11.0939
chr14	107349540	51349371	0.4783	22.2039
chr15	102531392	42292278	0.4125	14.2003
chr16	90354753	52342169	0.5793	15.4392
chr17	81195210	44995950	0.5542	11.9182
chr18	78077248	19798595	0.2536	7.8384
chr19	59128983	40433801	0.6838	21.2952
chr20	63025520	23423492	0.3717	9.7349
chr21	48129895	6875425	0.1429	5.2923
chr22	51304566	9831538	0.1916	6.6689
chrMT	16571	3460	0.2088	0.6883
chrX	155270560	74530589	0.48	14.971

chrY	59373566	5556634	0.0936	7.9453

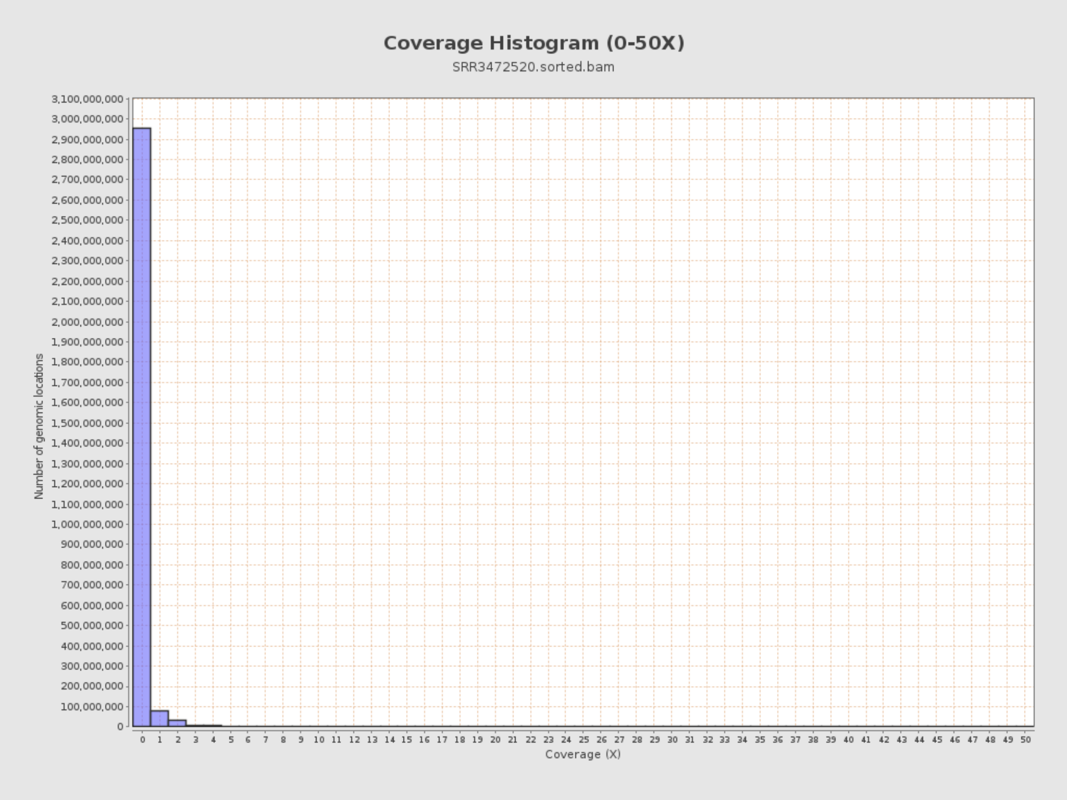
3. Results : Coverage across reference



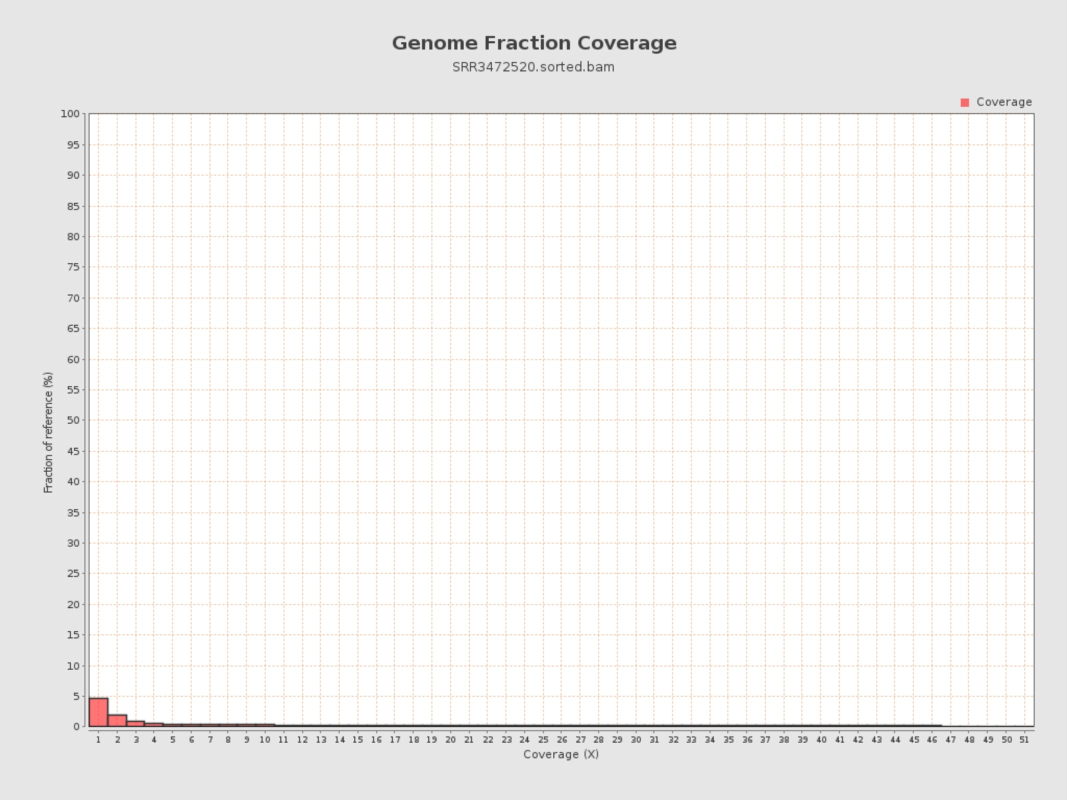
4. Results : Coverage Histogram



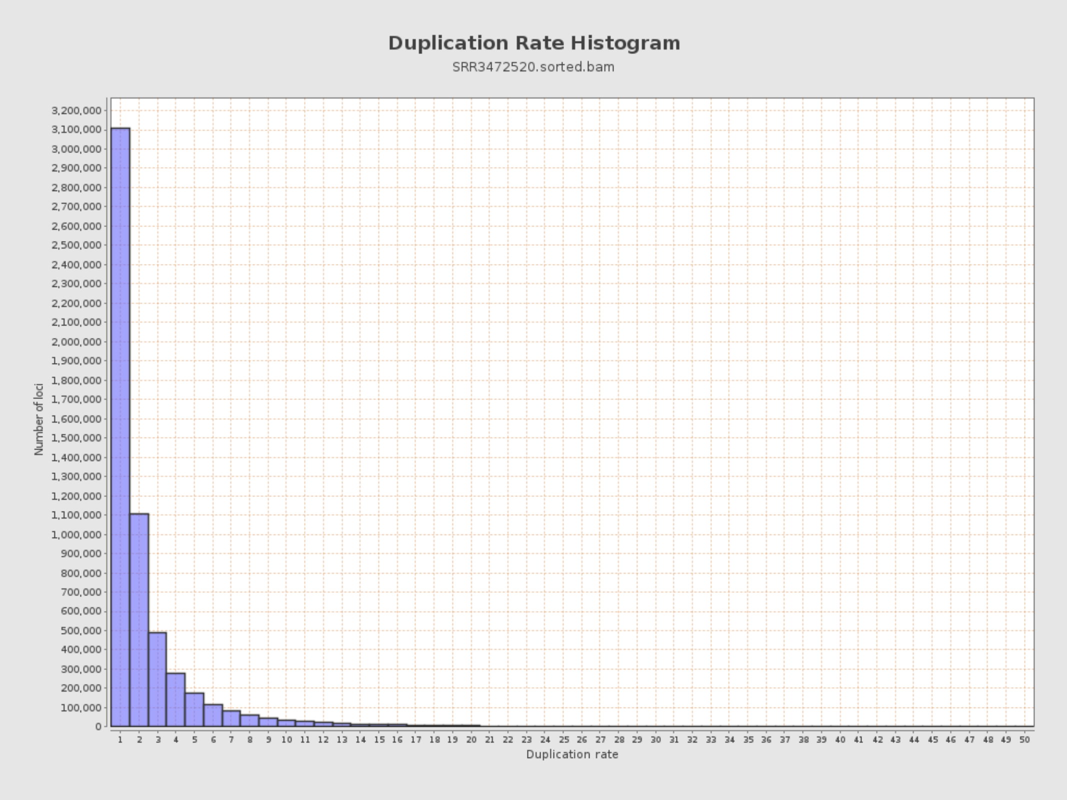
5. Results : Coverage Histogram (0-50X)



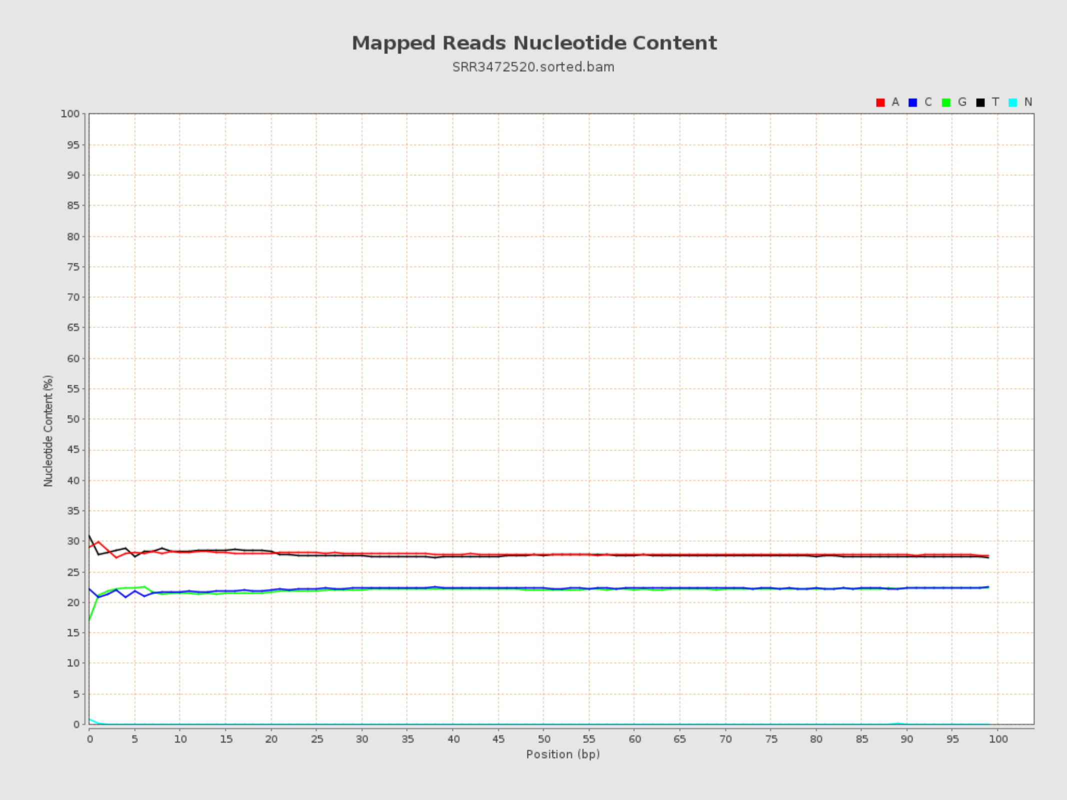
6. Results : Genome Fraction Coverage



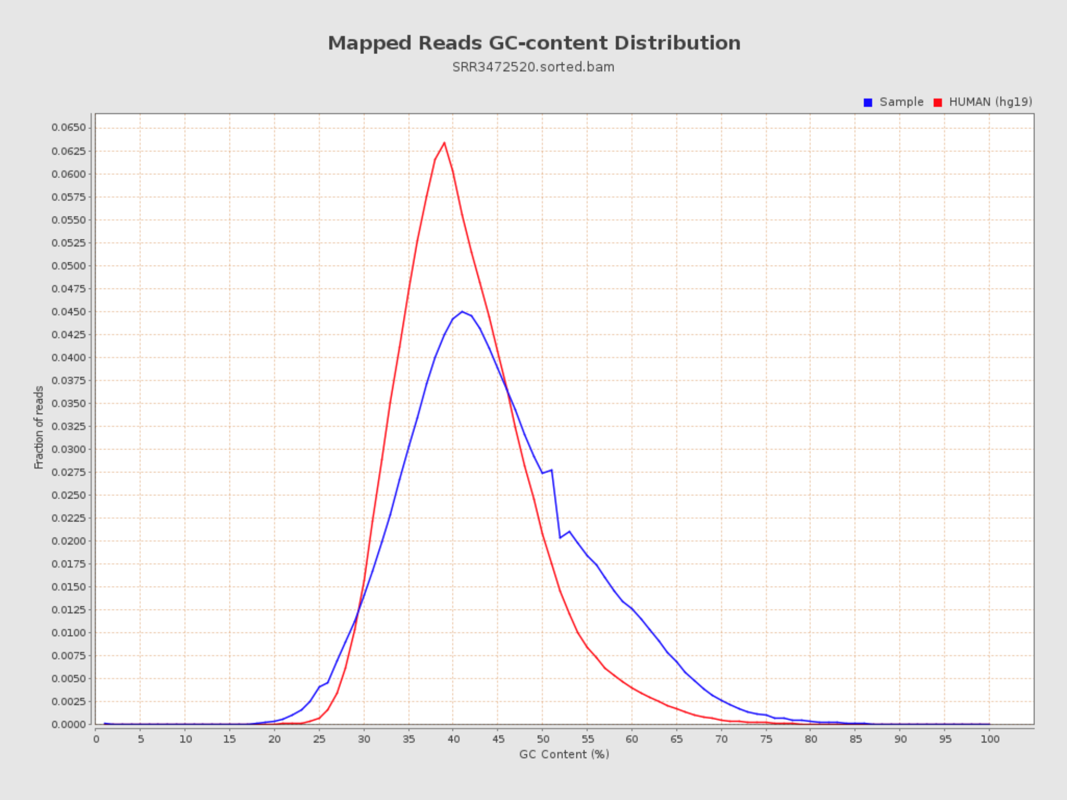
7. Results : Duplication Rate Histogram



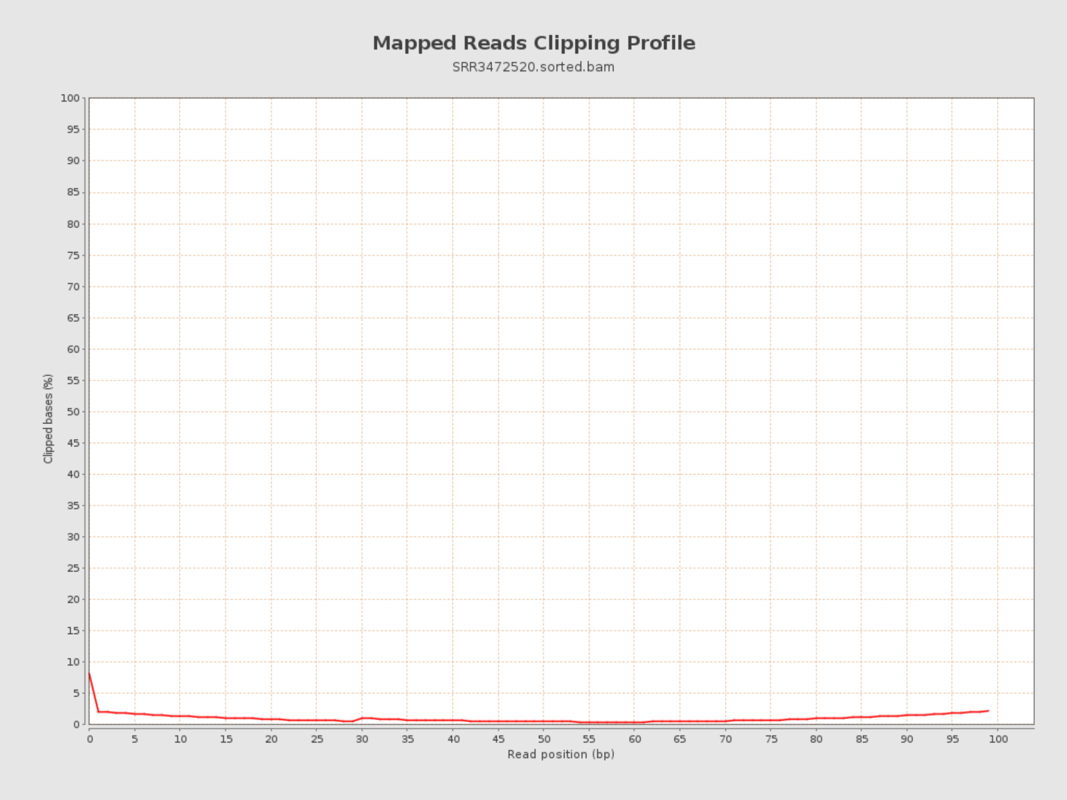
8. Results : Mapped Reads Nucleotide Content



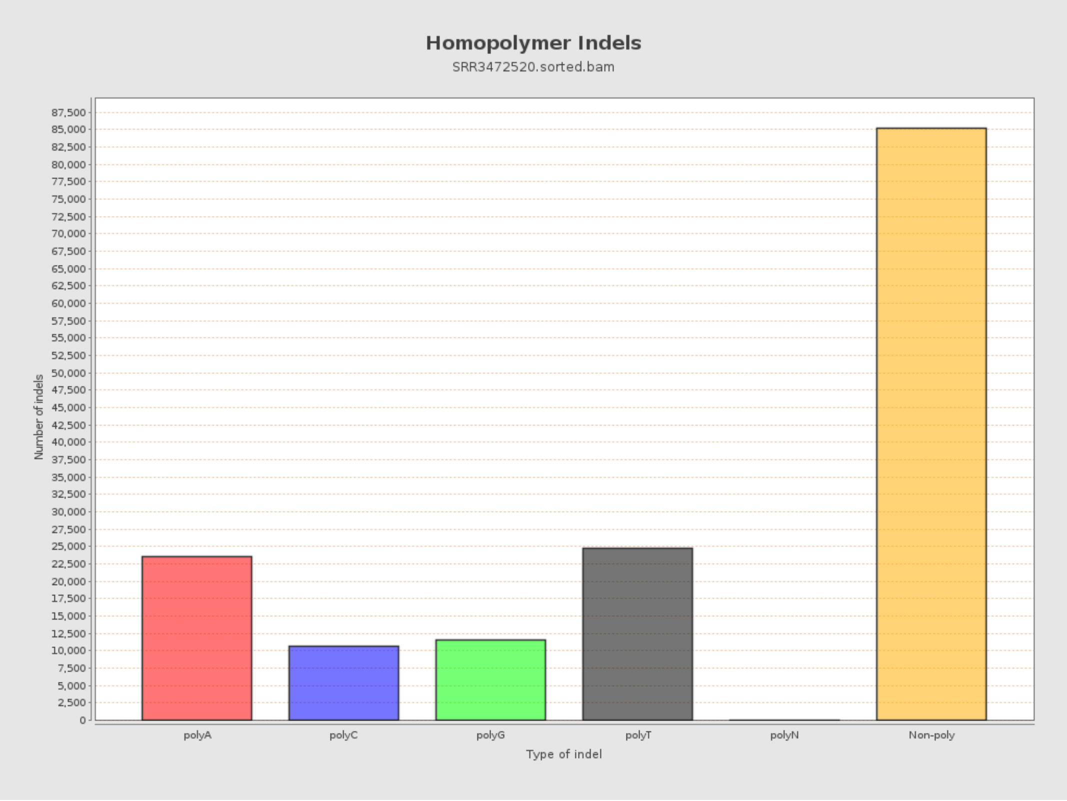
9. Results : Mapped Reads GC-content Distribution



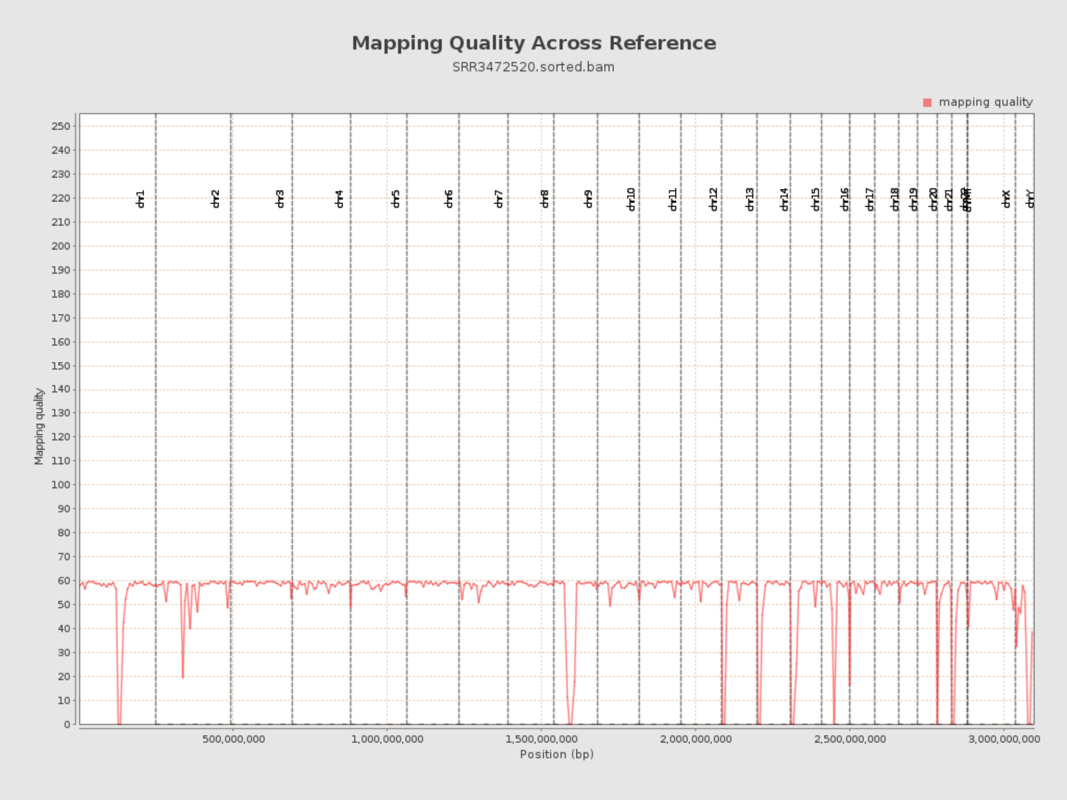
10. Results : Mapped Reads Clipping Profile



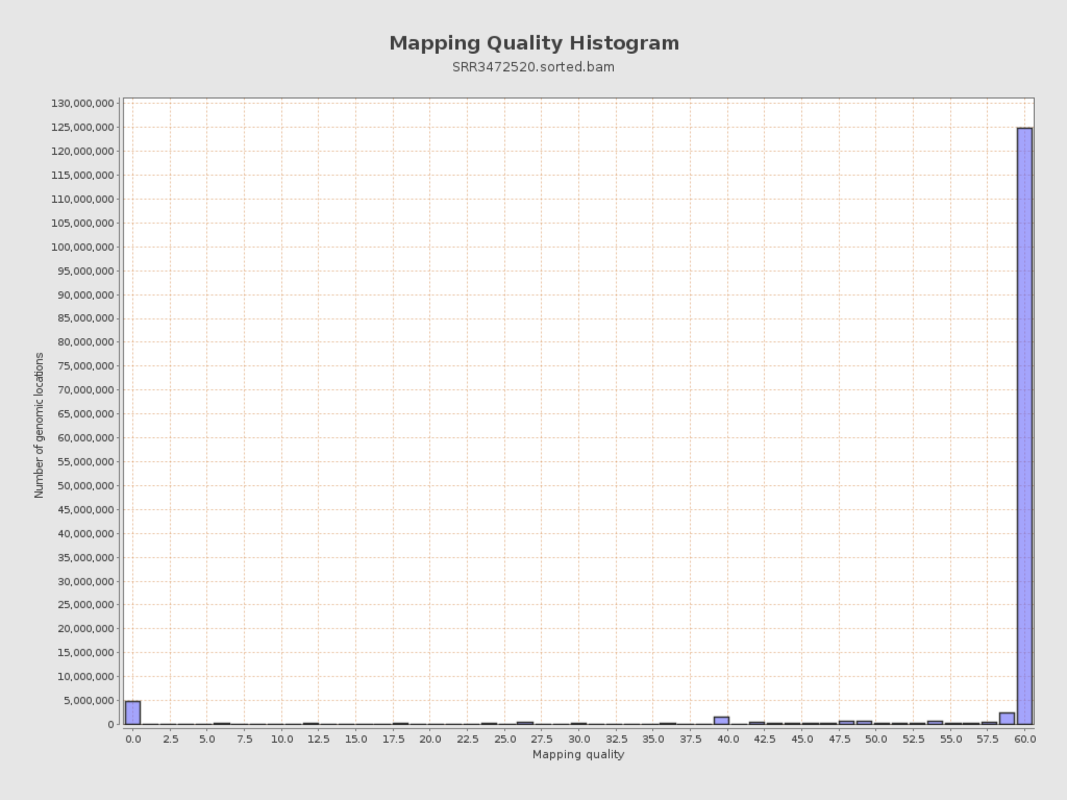
11. Results : Homopolymer Indels



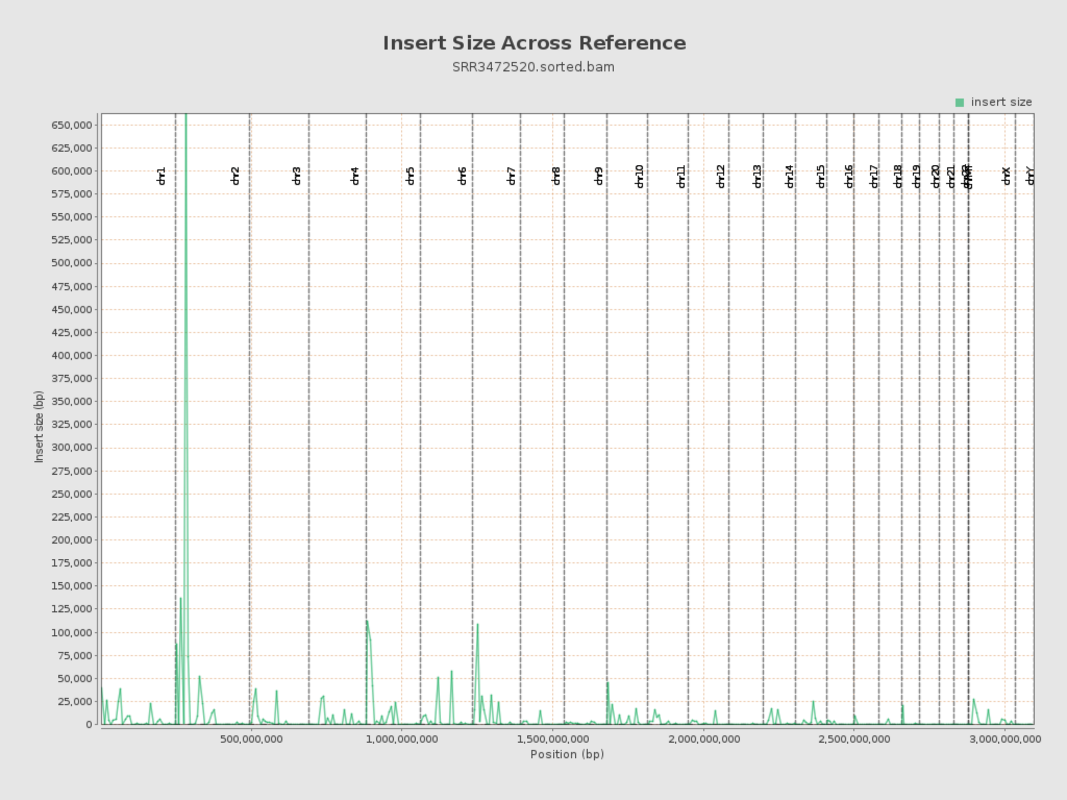
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram