Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 18:02:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472790.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_SRR3472790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472790_1.fastq.gz SRR3472790_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 18:02:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,671,470
Mapped reads	12,557,856 / 99.1%
Unmapped reads	113,614 / 0.9%
Mapped paired reads	12,557,856 / 99.1%
Mapped reads, first in pair	6,298,321 / 49.7%
Mapped reads, second in pair	6,259,535 / 49.4%
Mapped reads, both in pair	12,493,168 / 98.59%
Mapped reads, singletons	64,688 / 0.51%
Secondary alignments	0
Supplementary alignments	41,468 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	7,598,821 / 59.97%
Duplication rate	46.23%
Clipped reads	1,144,155 / 9.03%

2.2. ACGT Content

Number/percentage of A's	334,041,657 / 27.08%
Number/percentage of C's	284,532,054 / 23.07%
Number/percentage of T's	331,407,191 / 26.87%
Number/percentage of G's	283,344,962 / 22.97%
Number/percentage of N's	241,412 / 0.02%

GC Percentage	46.04%

2.3. Coverage

Mean	0.3985
Standard Deviation	14.4932

2.4. Mapping Quality

Mean Mapping Quality	55.16

2.5. Insert size

Mean	22,245.13
Standard Deviation	1,489,937.36
P25/Median/P75	161 / 227 / 307

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	7,347,231
Insertions	65,984
Mapped reads with at least one insertion	0.52%
Deletions	68,116
Mapped reads with at least one deletion	0.54%
Homopolymer indels	44.64%

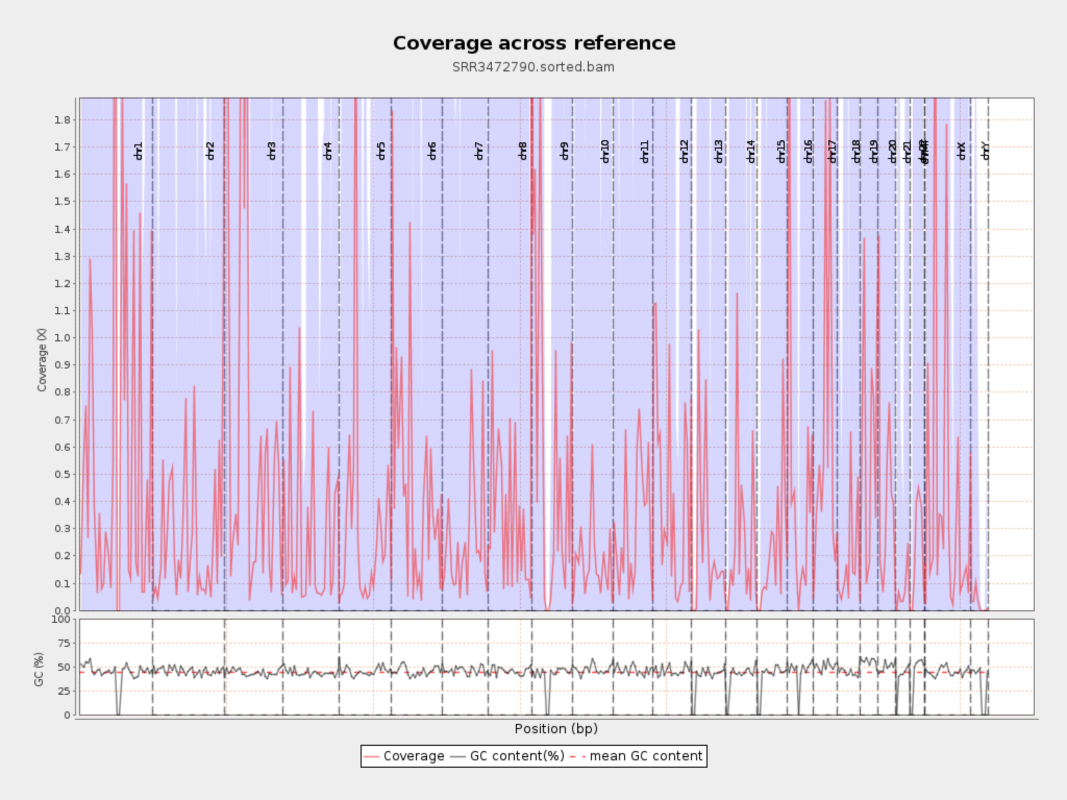
2.7. Chromosome stats

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

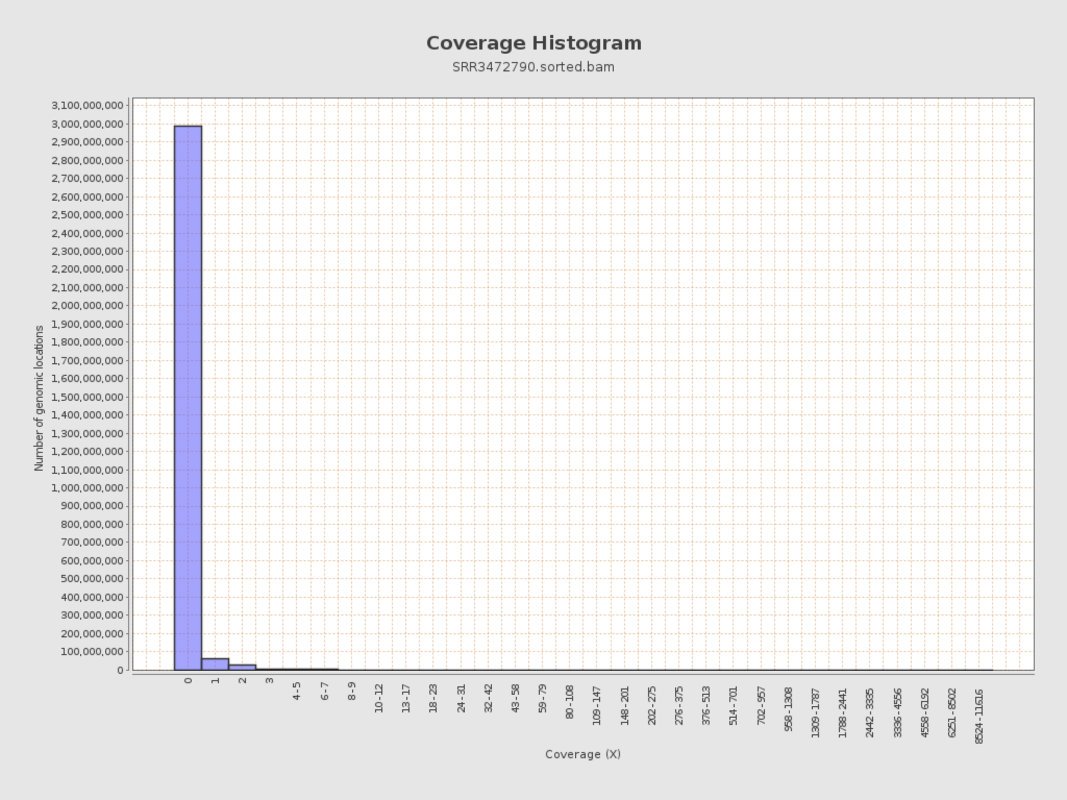
		bases	coverage	deviation
chr1	249250621	149849982	0.6012	25.3322
chr2	243199373	64225498	0.2641	9.2705
chr3	198022430	188866978	0.9538	24.9699
chr4	191154276	50885143	0.2662	11.2529
chr5	180915260	59204943	0.3273	11.7167
chr6	171115067	78309489	0.4576	13.0441
chr7	159138663	41681021	0.2619	8.1852
chr8	146364022	50465550	0.3448	11.8707
chr9	141213431	85783227	0.6075	16.2098
chr10	135534747	24497582	0.1807	9.9952
chr11	135006516	42369806	0.3138	10.5514
chr12	133851895	59366427	0.4435	15.9701
chr13	115169878	28309963	0.2458	10.6678
chr14	107349540	27318471	0.2545	8.355
chr15	102531392	23742030	0.2316	7.1374
chr16	90354753	42223168	0.4673	12.258
chr17	81195210	52875342	0.6512	20.7322
chr18	78077248	15333131	0.1964	7.527
chr19	59128983	35975308	0.6084	15.1004
chr20	63025520	28104892	0.4459	13.7356
chr21	48129895	3825883	0.0795	3.0074
chr22	51304566	11145674	0.2172	6.0599
chrMT	16571	2893	0.1746	0.6368
chrX	155270560	67782338	0.4365	13.917

chrY	59373566	1584329	0.0267	1.0579

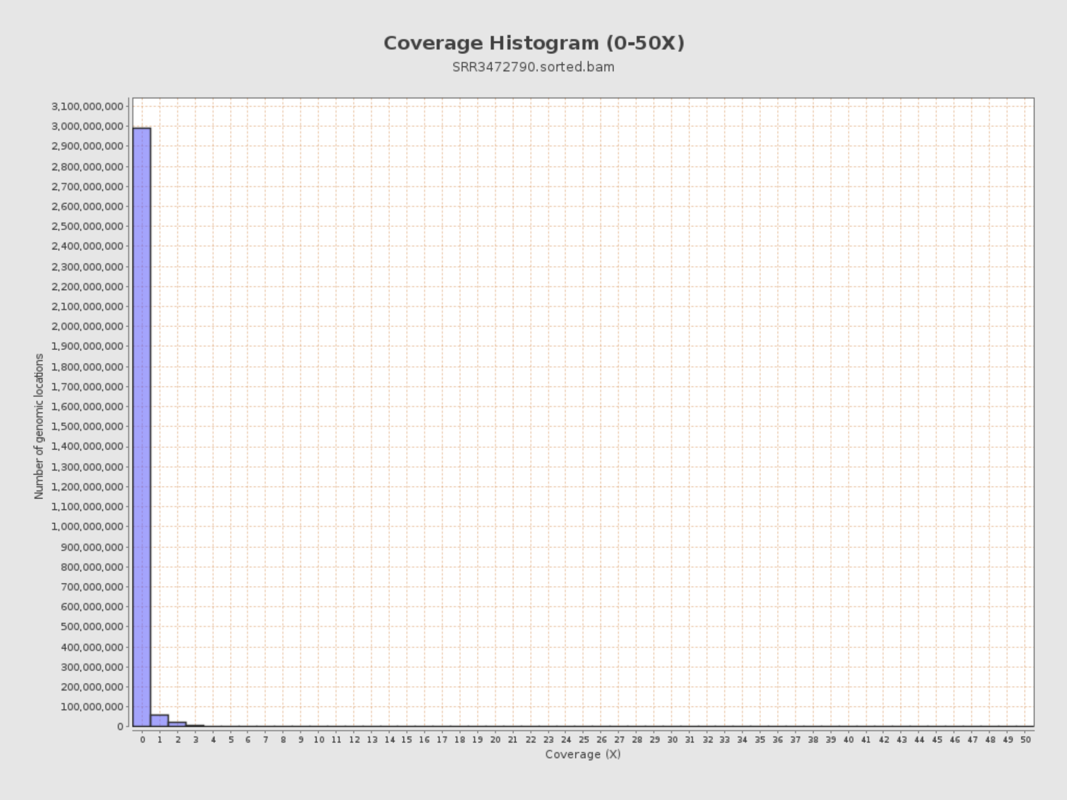
3. Results : Coverage across reference



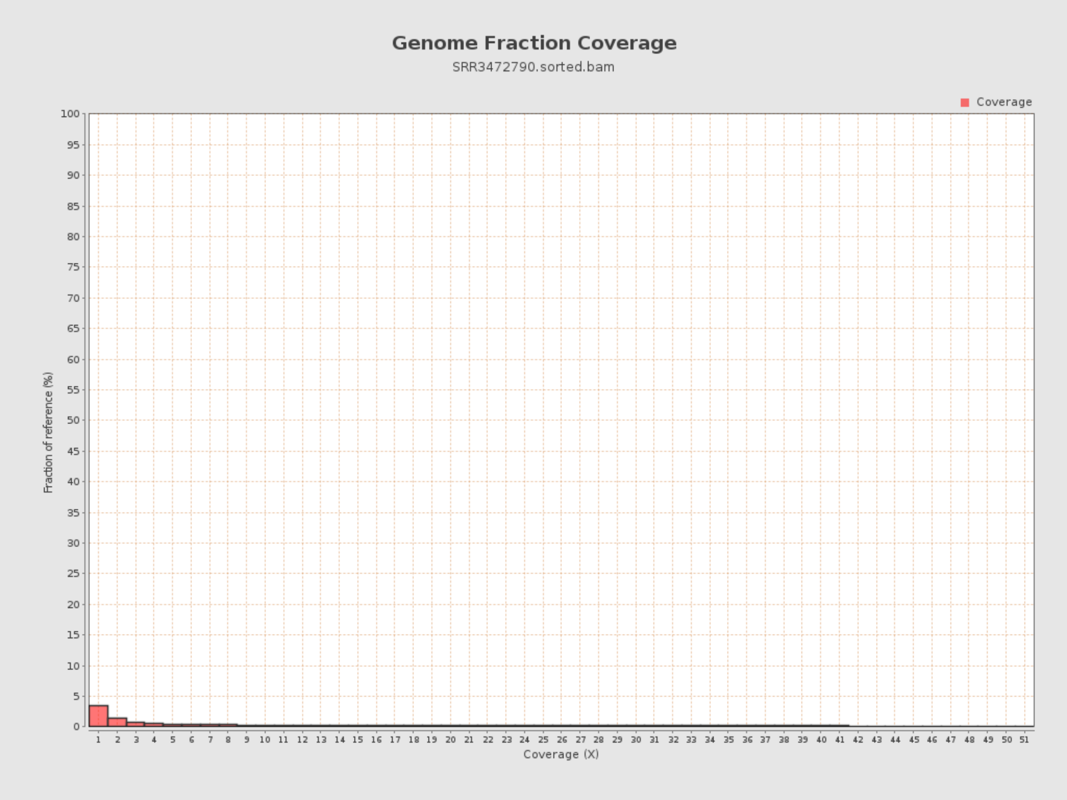
4. Results : Coverage Histogram



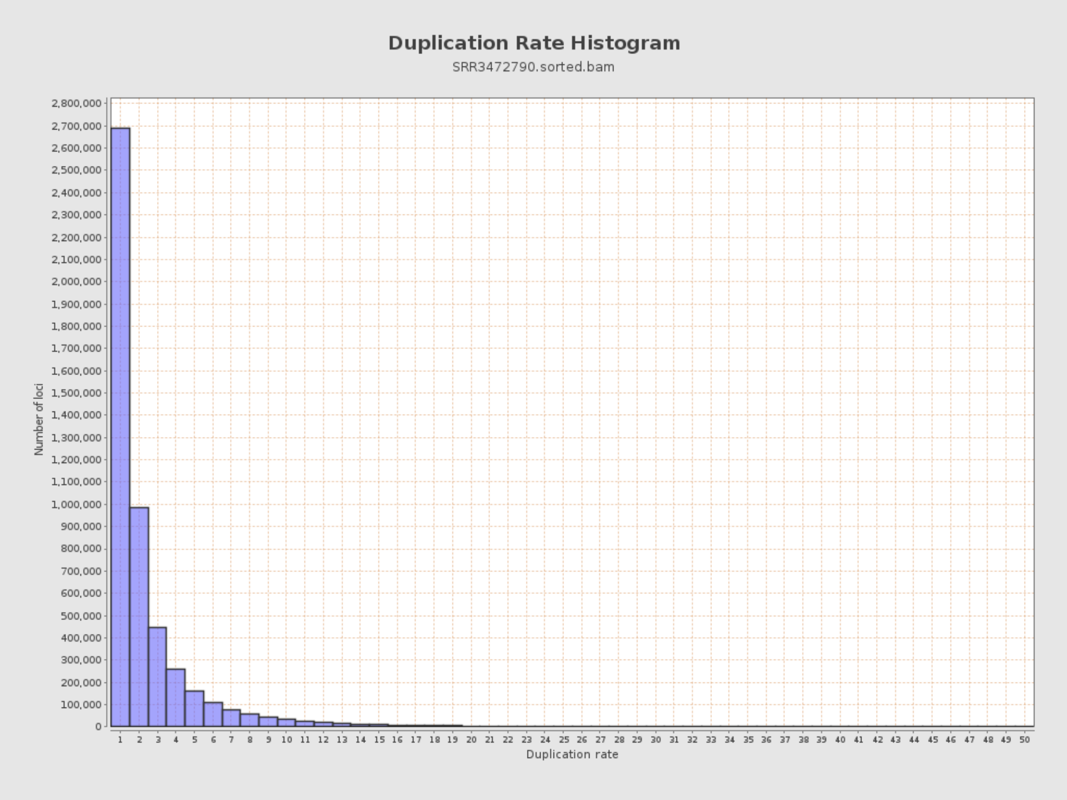
5. Results : Coverage Histogram (0-50X)



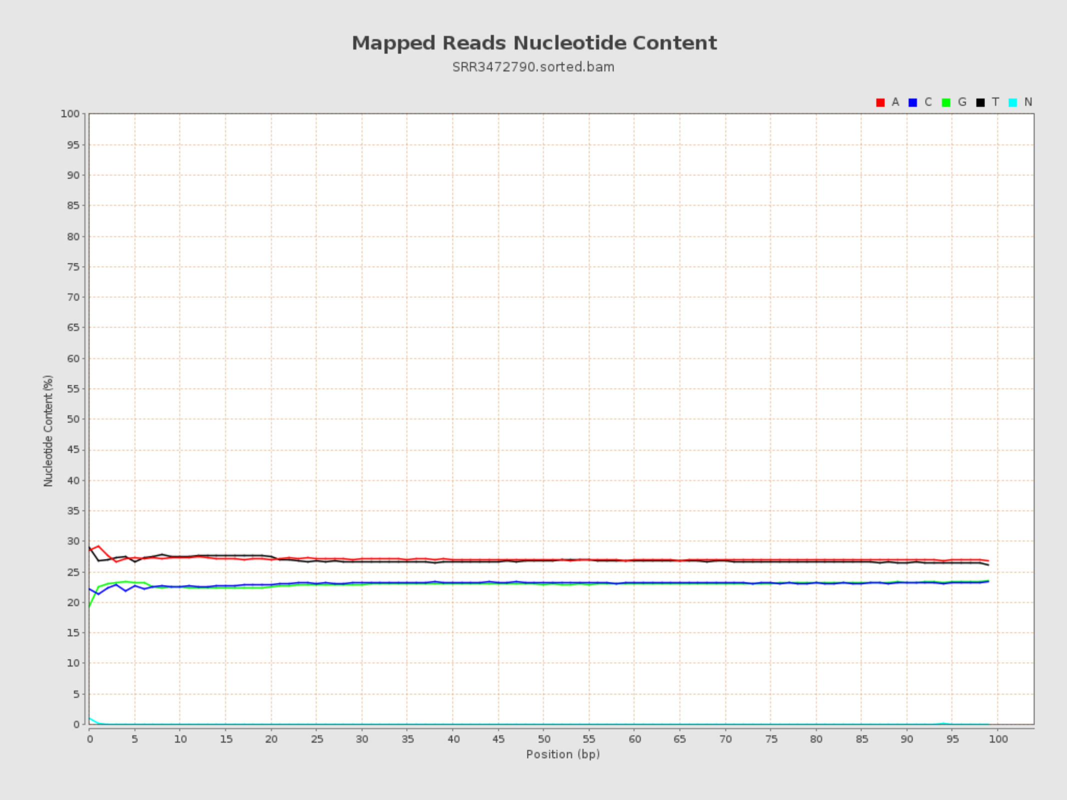
6. Results : Genome Fraction Coverage



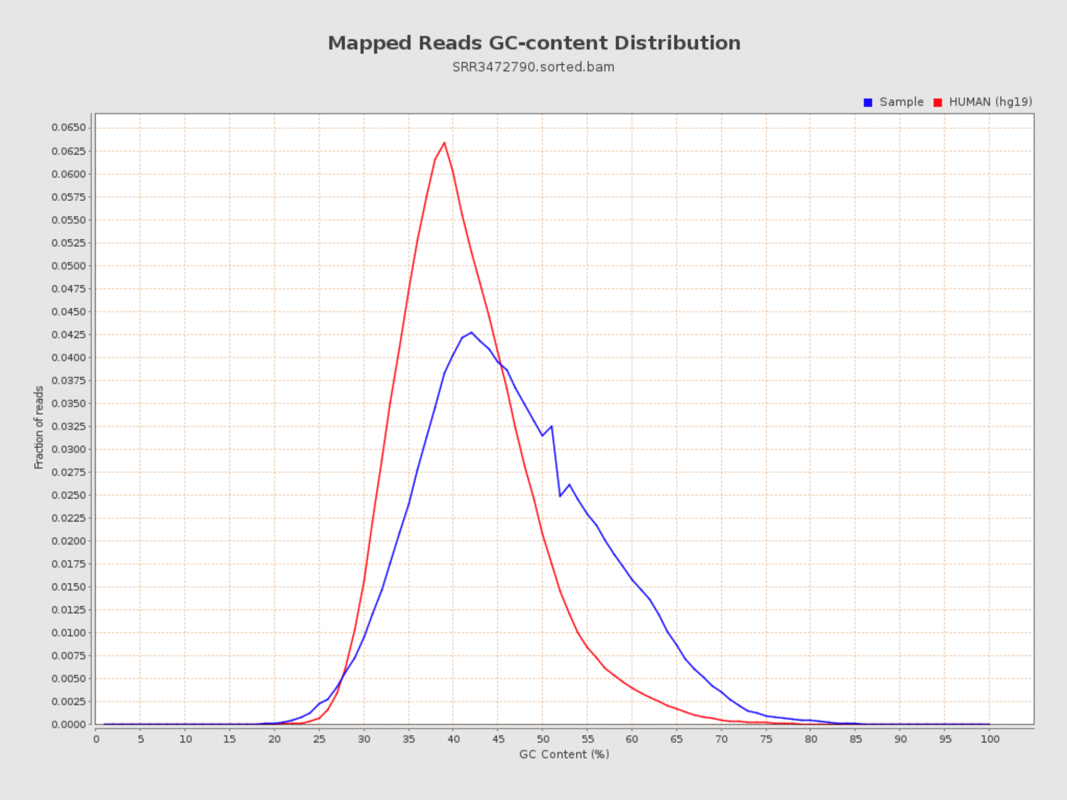
7. Results : Duplication Rate Histogram



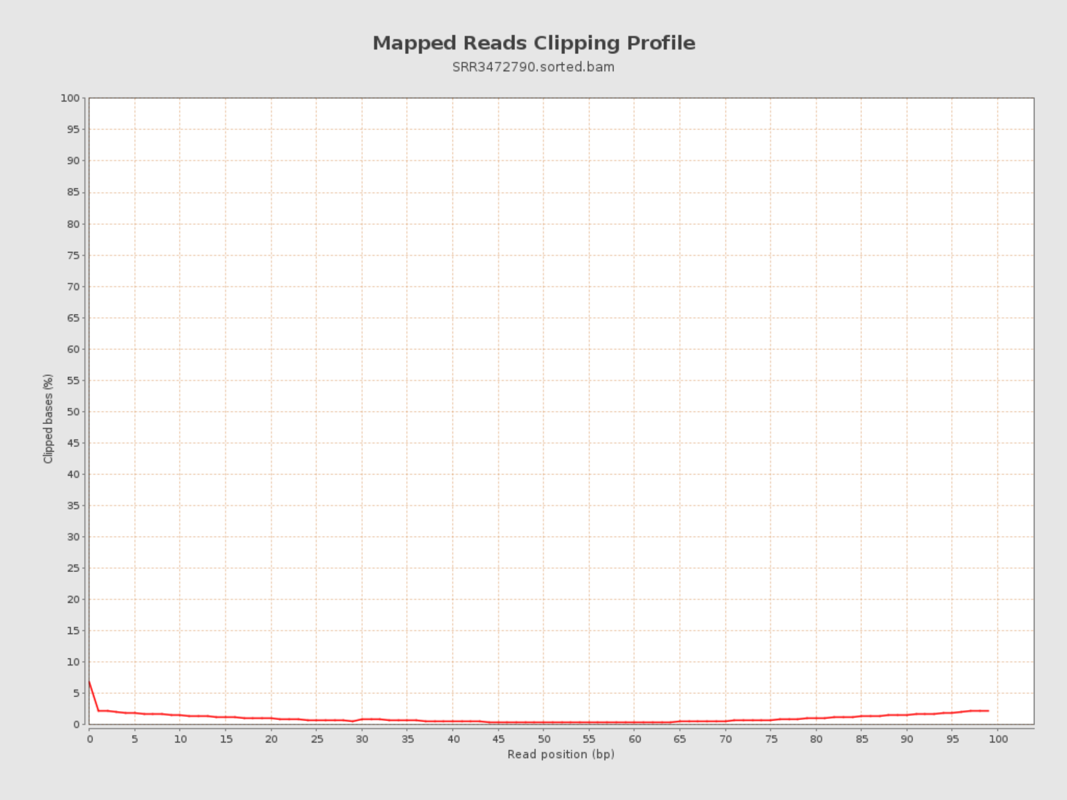
8. Results : Mapped Reads Nucleotide Content



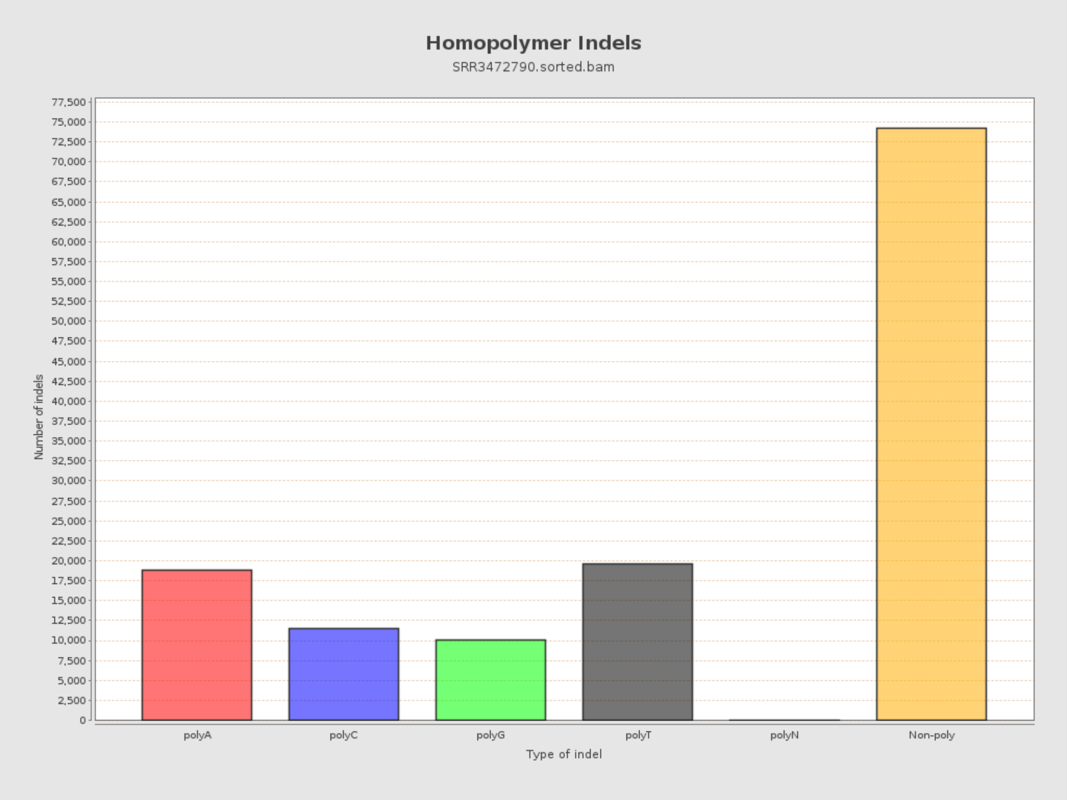
9. Results : Mapped Reads GC-content Distribution



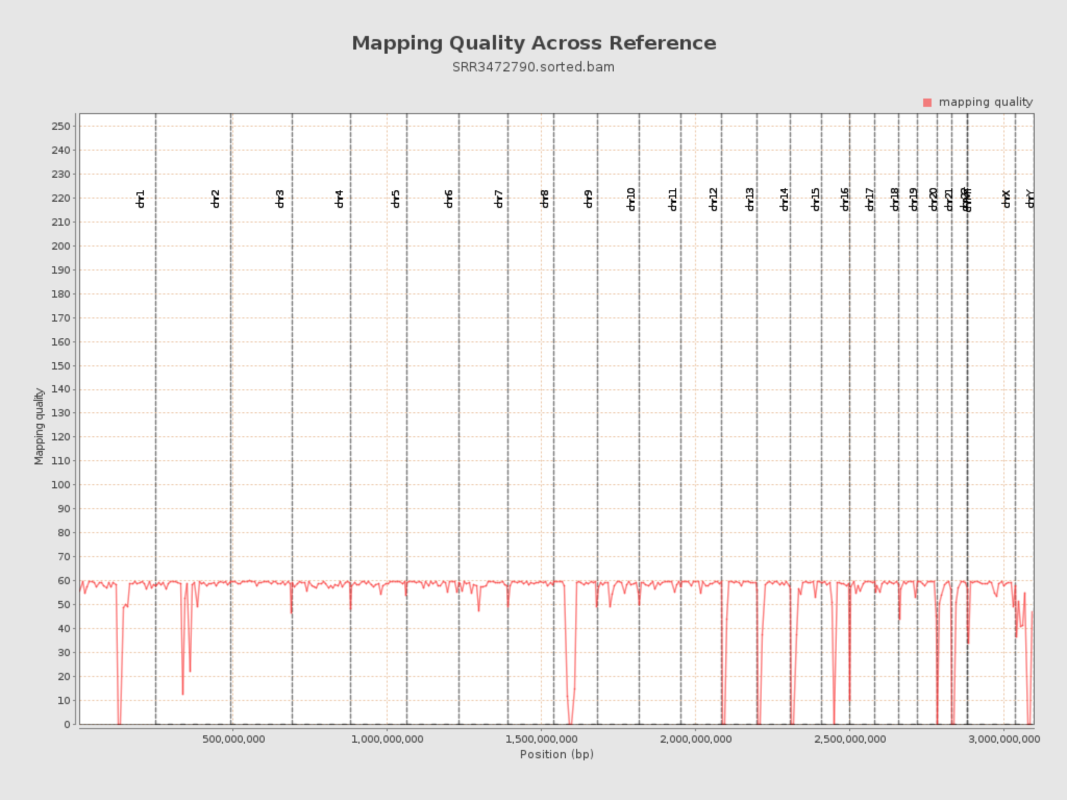
10. Results : Mapped Reads Clipping Profile



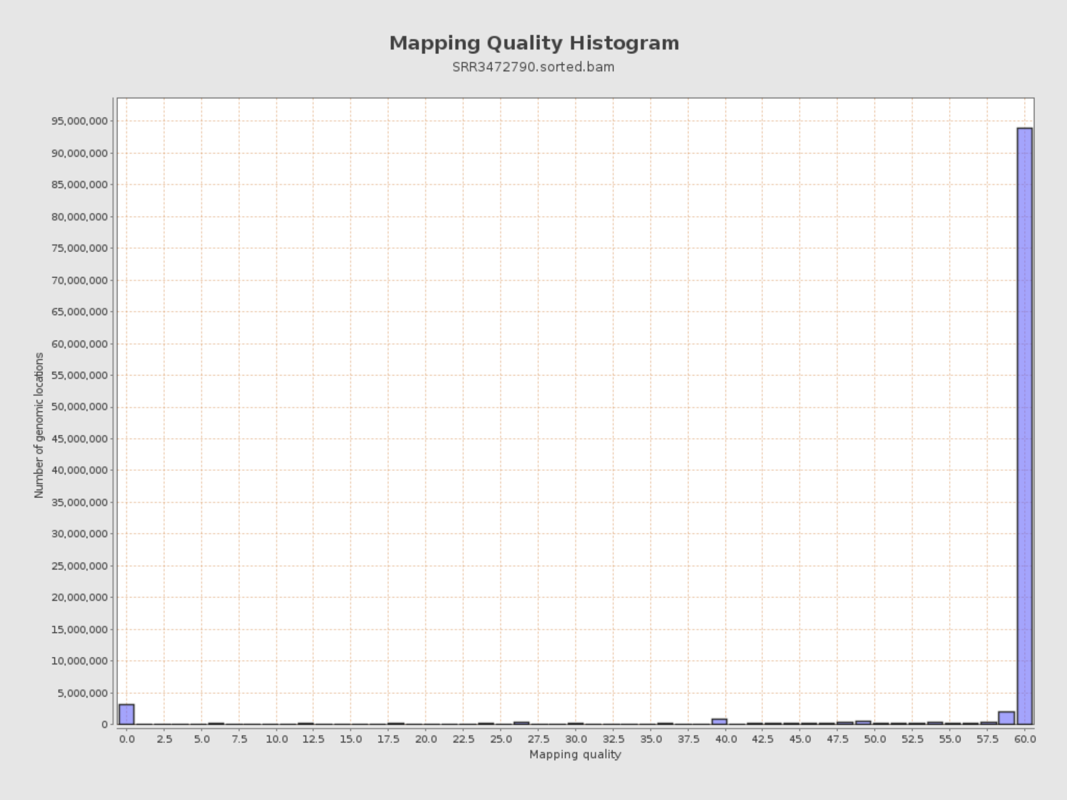
11. Results : Homopolymer Indels



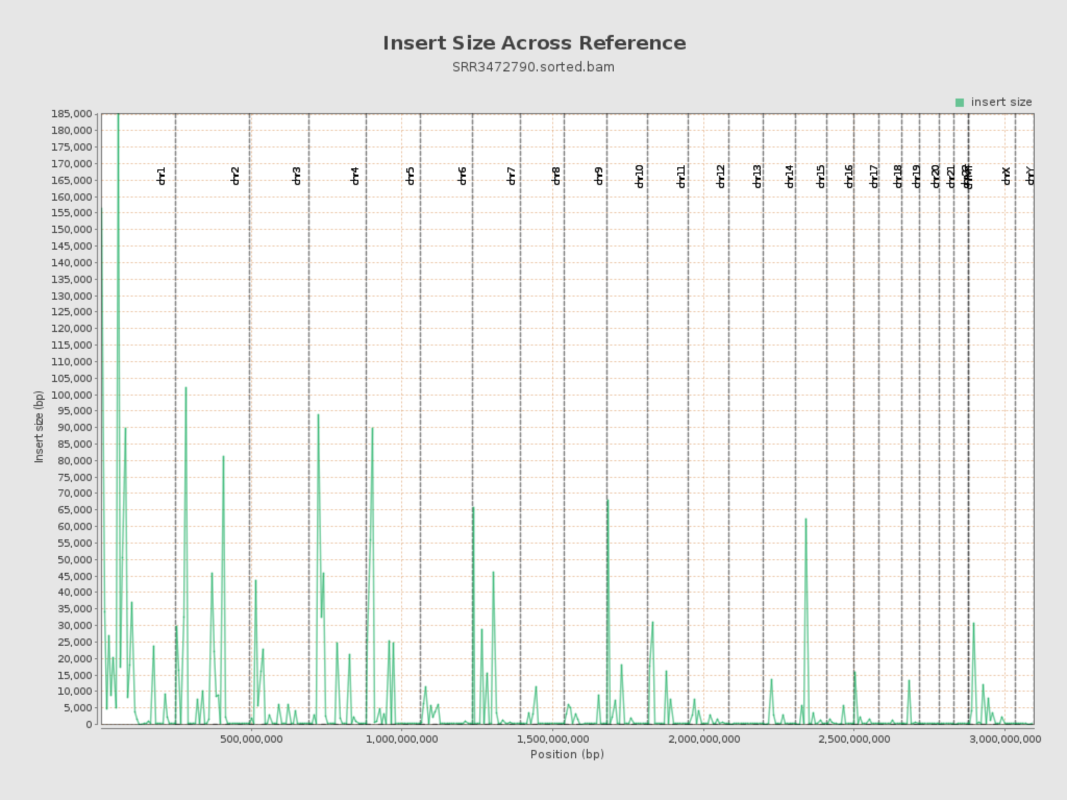
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram