Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 17:37:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472788.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_SRR3472788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472788_1.fastq.gz SRR3472788_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 17:37:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,040,566
Mapped reads	10,938,023 / 99.07%
Unmapped reads	102,543 / 0.93%
Mapped paired reads	10,938,023 / 99.07%
Mapped reads, first in pair	5,488,585 / 49.71%
Mapped reads, second in pair	5,449,438 / 49.36%
Mapped reads, both in pair	10,874,190 / 98.49%
Mapped reads, singletons	63,833 / 0.58%
Secondary alignments	0
Supplementary alignments	45,843 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,863,019 / 62.16%
Duplication rate	44.21%
Clipped reads	1,045,619 / 9.47%

2.2. ACGT Content

Number/percentage of A's	297,146,219 / 27.67%
Number/percentage of C's	241,570,074 / 22.5%
Number/percentage of T's	294,873,683 / 27.46%
Number/percentage of G's	239,923,876 / 22.35%
Number/percentage of N's	205,505 / 0.02%

GC Percentage	44.84%

2.3. Coverage

Mean	0.3469
Standard Deviation	16.9557

2.4. Mapping Quality

Mean Mapping Quality	54.9

2.5. Insert size

Mean	24,661.98
Standard Deviation	1,530,152.19
P25/Median/P75	163 / 232 / 317

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	6,678,975
Insertions	71,759
Mapped reads with at least one insertion	0.65%
Deletions	57,904
Mapped reads with at least one deletion	0.52%
Homopolymer indels	43.3%

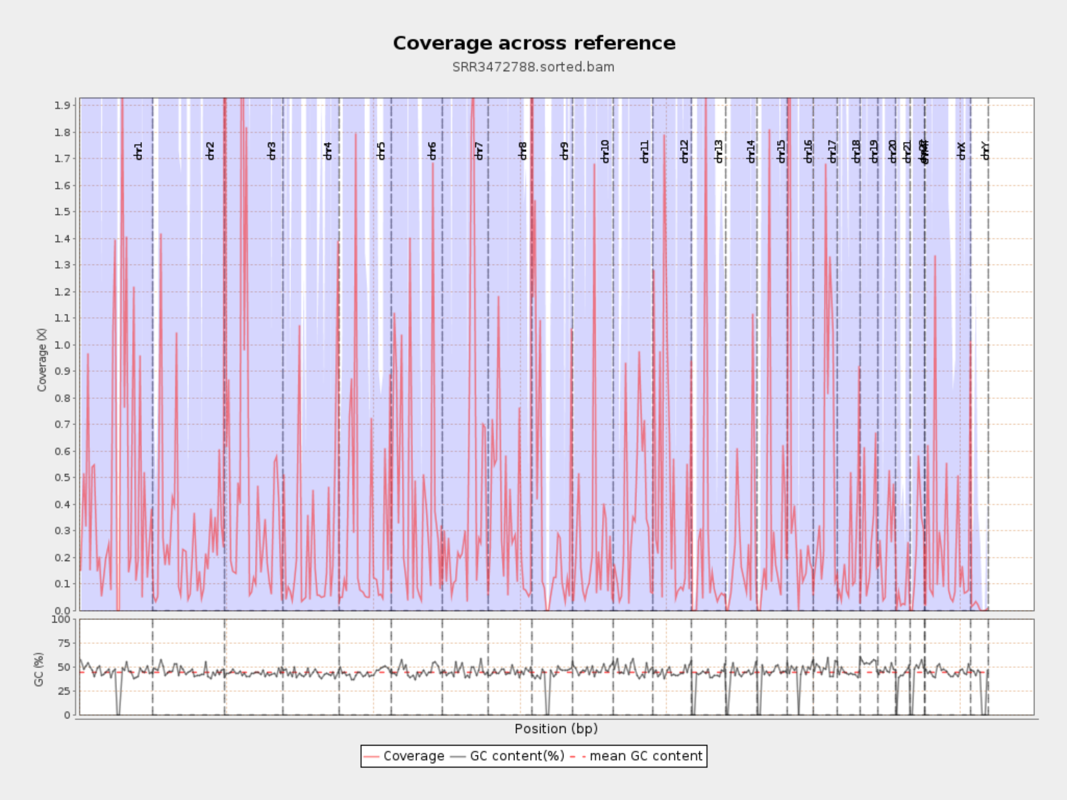
2.7. Chromosome stats

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

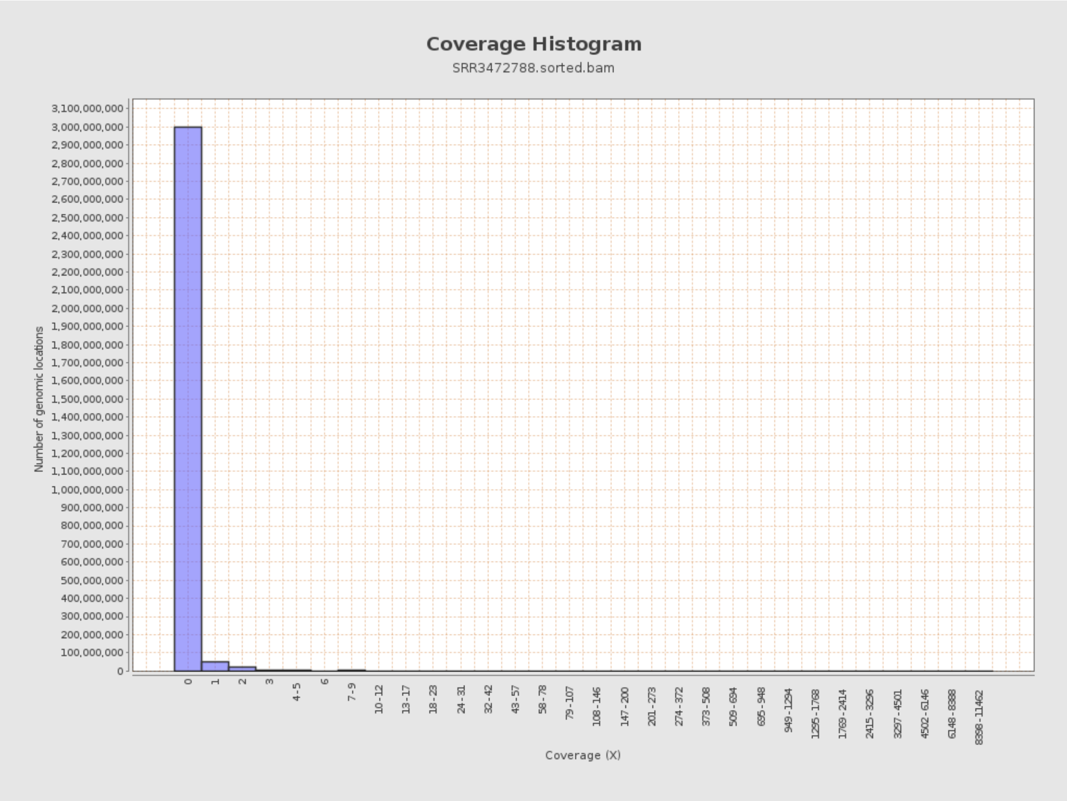
		bases	coverage	deviation
chr1	249250621	116948052	0.4692	22.8205
chr2	243199373	65863988	0.2708	12.8822
chr3	198022430	106753434	0.5391	15.2781
chr4	191154276	46515954	0.2433	11.7994
chr5	180915260	55759738	0.3082	15.4109
chr6	171115067	77382725	0.4522	28.3206
chr7	159138663	68564275	0.4308	23.5416
chr8	146364022	51216255	0.3499	12.5125
chr9	141213431	60944155	0.4316	13.6082
chr10	135534747	35437663	0.2615	20.3489
chr11	135006516	46998558	0.3481	14.8722
chr12	133851895	63924580	0.4776	17.7413
chr13	115169878	26600490	0.231	17.8909
chr14	107349540	25331422	0.236	9.1966
chr15	102531392	31102118	0.3033	21.4463
chr16	90354753	41295557	0.457	15.5424
chr17	81195210	46712025	0.5753	25.637
chr18	78077248	17386824	0.2227	11.9712
chr19	59128983	18138658	0.3068	7.4968
chr20	63025520	16711971	0.2652	8.3987
chr21	48129895	3382148	0.0703	3.4684
chr22	51304566	12157705	0.237	7.4995
chrMT	16571	4022	0.2427	0.6879
chrX	155270560	37996262	0.2447	8.2765

chrY	59373566	739527	0.0125	0.498

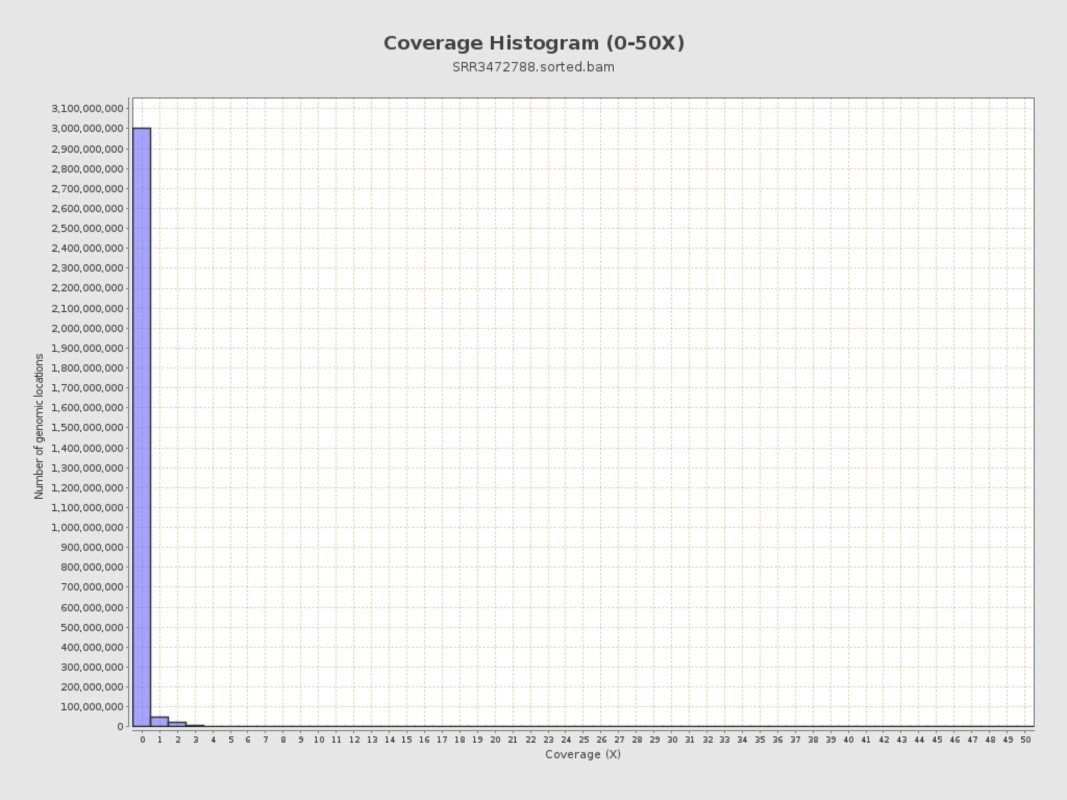
3. Results : Coverage across reference



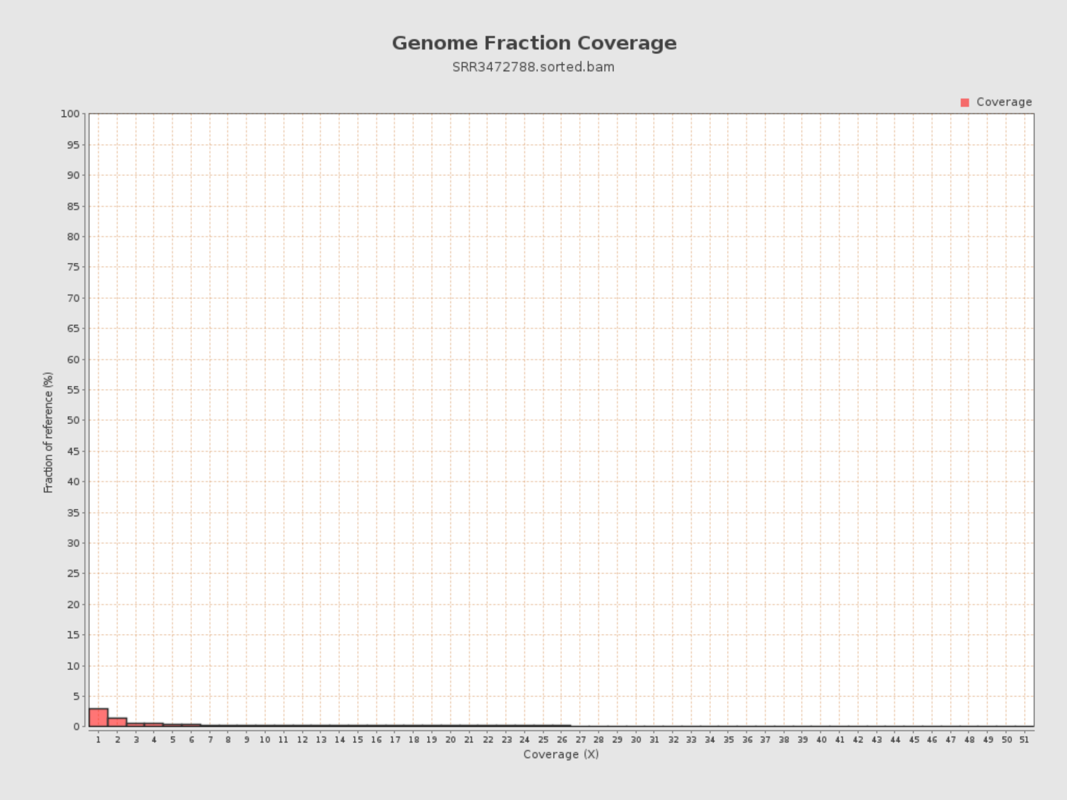
4. Results : Coverage Histogram



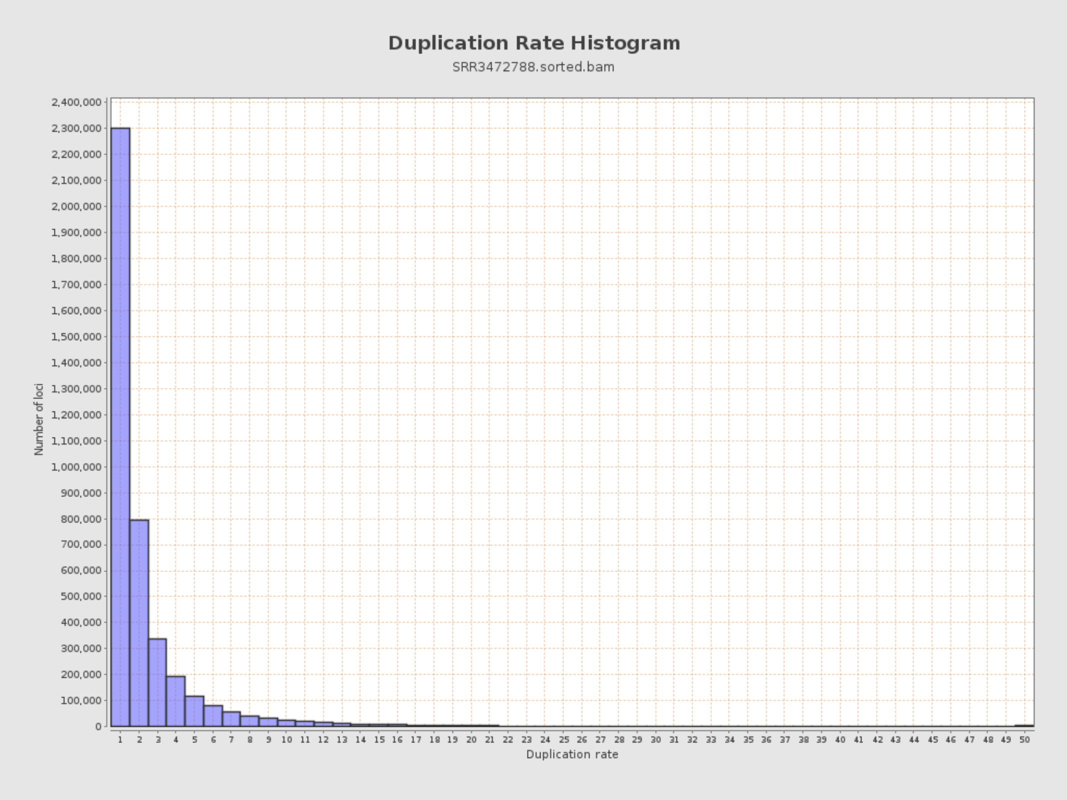
5. Results : Coverage Histogram (0-50X)



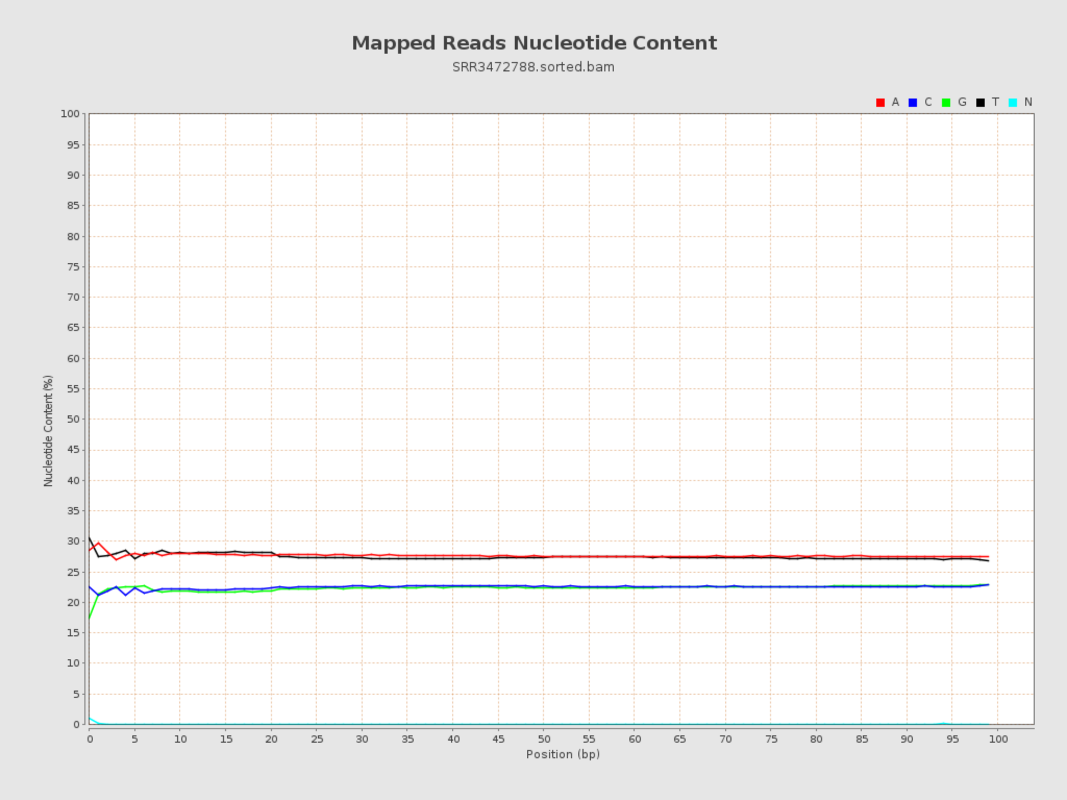
6. Results : Genome Fraction Coverage



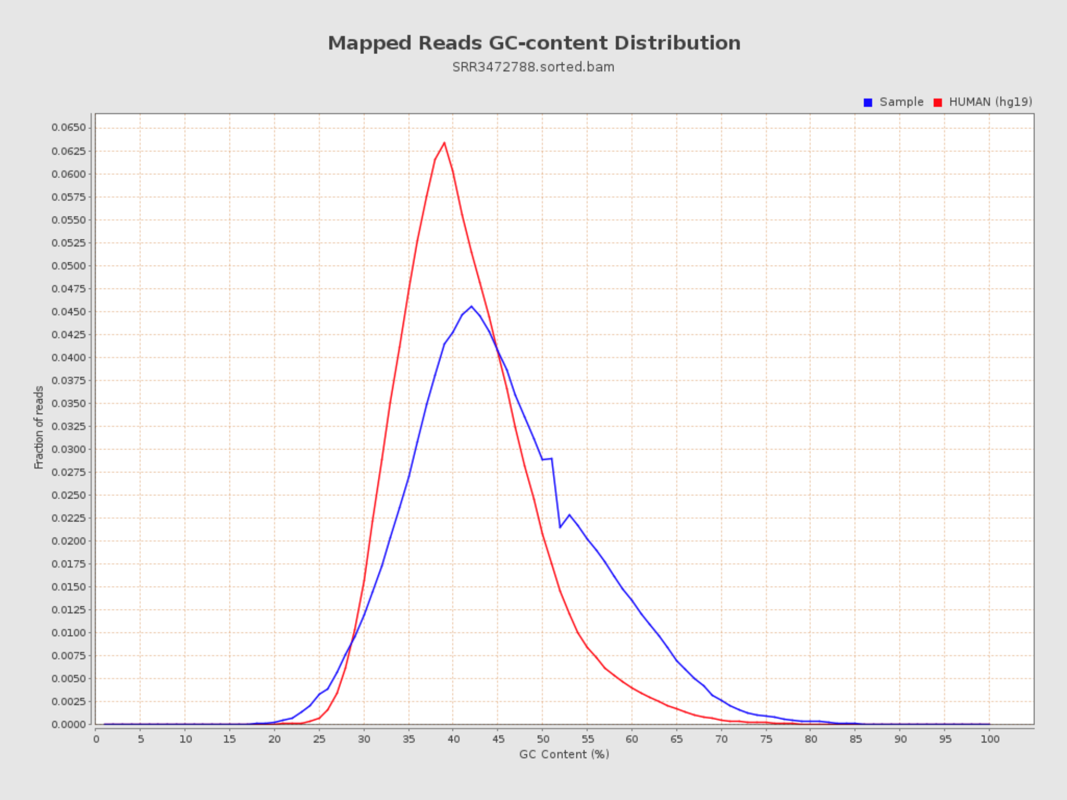
7. Results : Duplication Rate Histogram



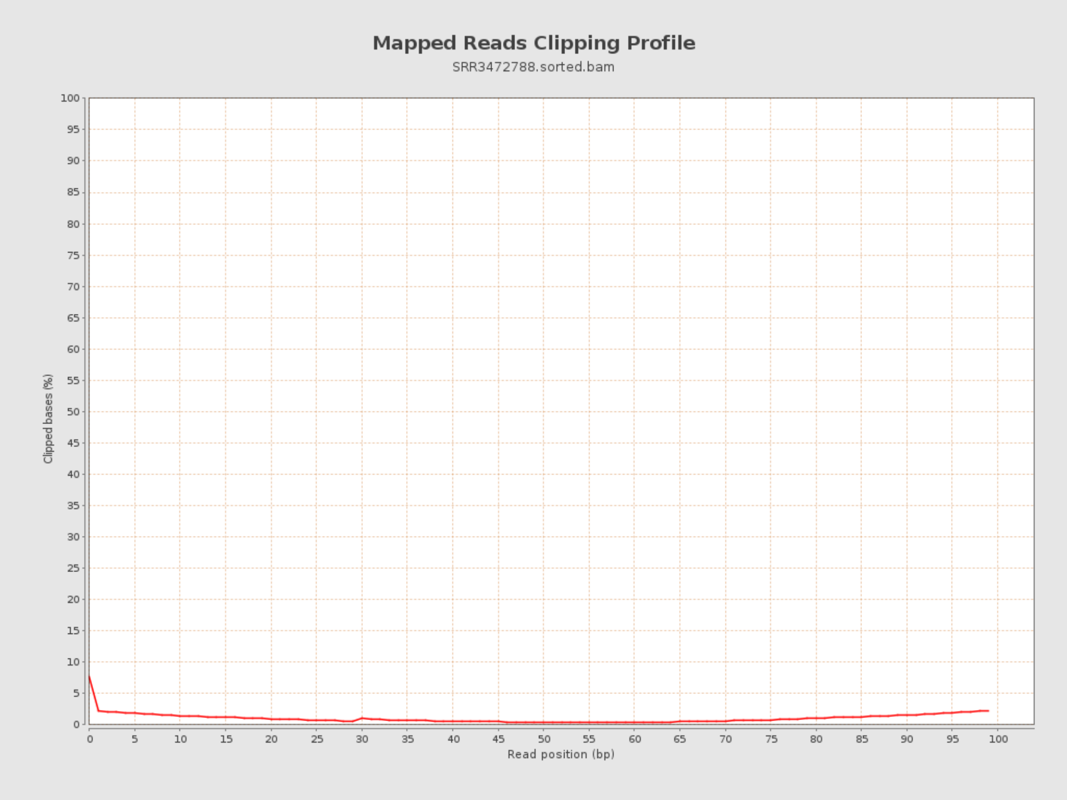
8. Results : Mapped Reads Nucleotide Content



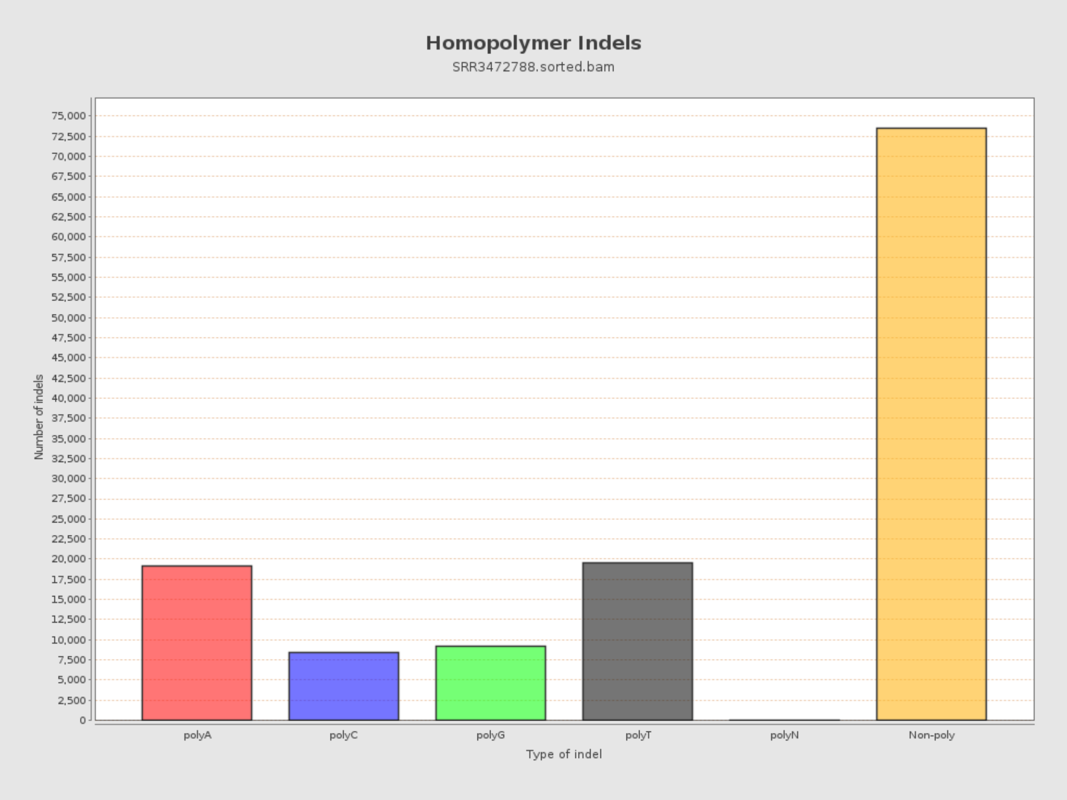
9. Results : Mapped Reads GC-content Distribution



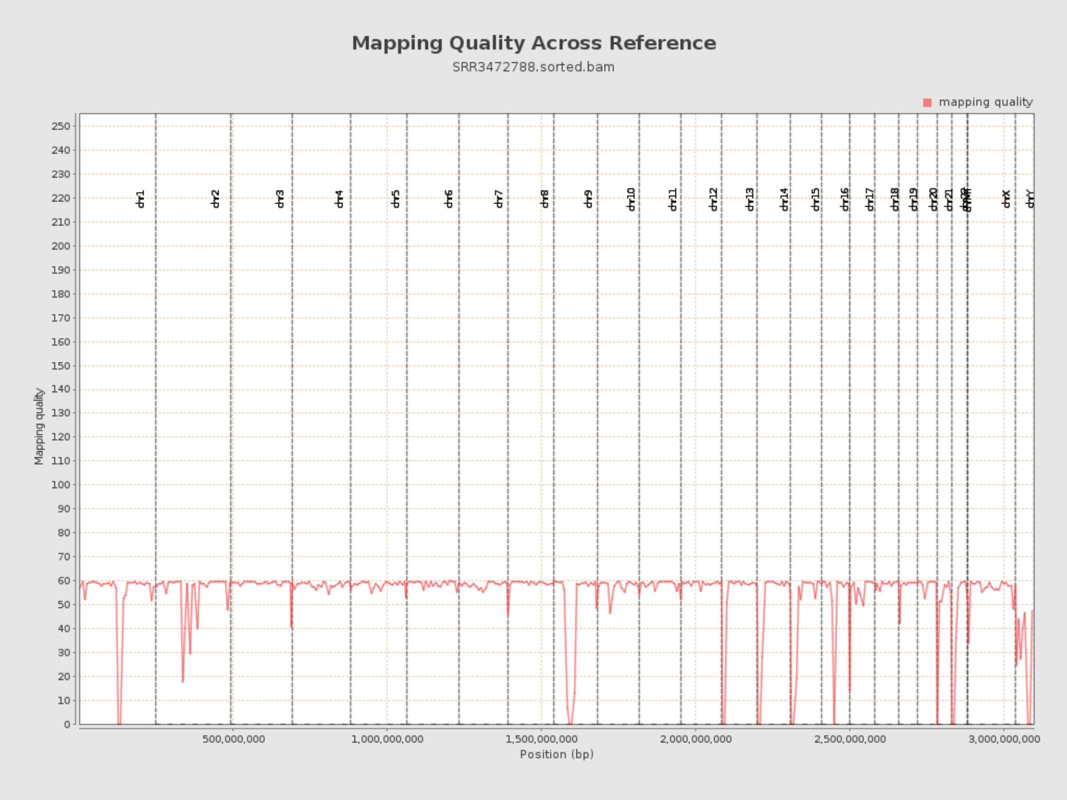
10. Results : Mapped Reads Clipping Profile



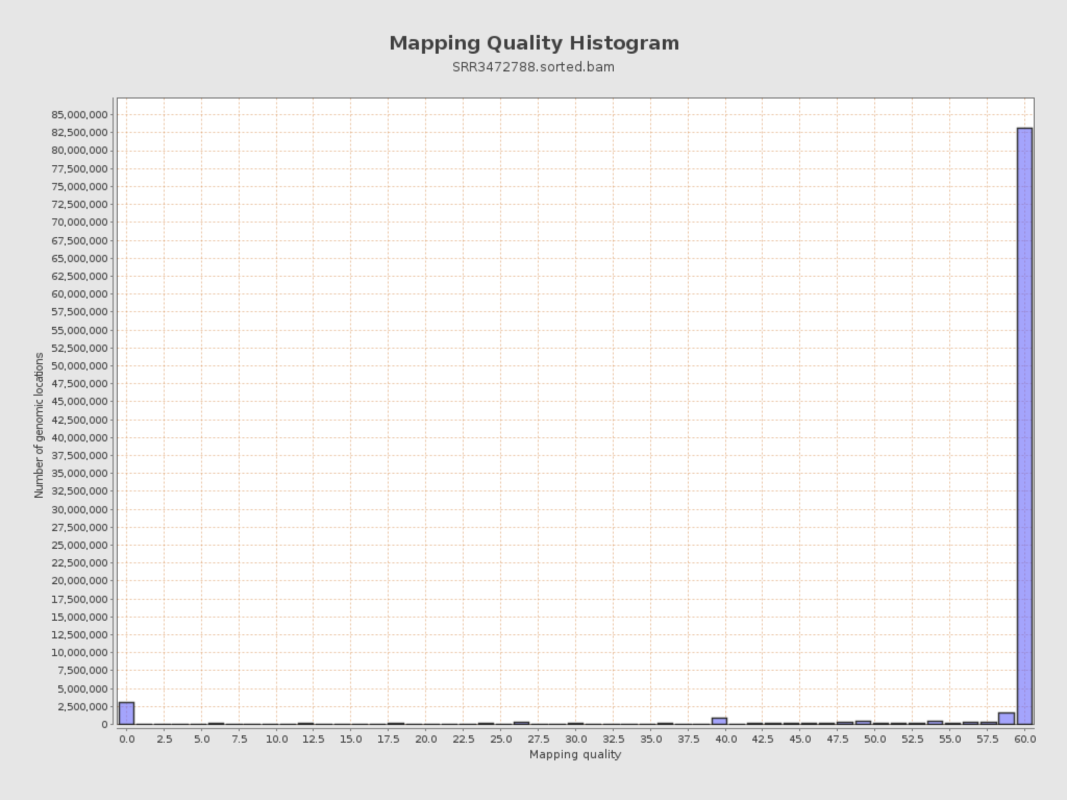
11. Results : Homopolymer Indels



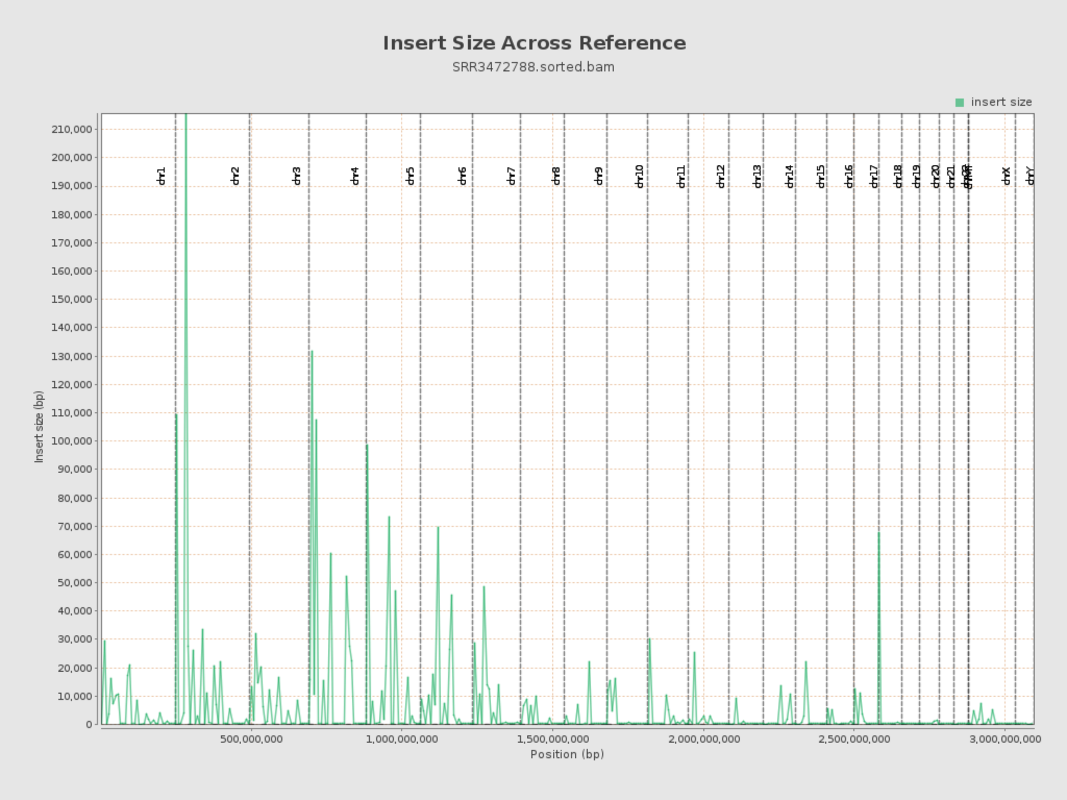
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram