Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 18:24:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472792.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_SRR3472792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472792_1.fastq.gz SRR3472792_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 18:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,038,992
Mapped reads	7,976,334 / 99.22%
Unmapped reads	62,658 / 0.78%
Mapped paired reads	7,976,334 / 99.22%
Mapped reads, first in pair	3,999,003 / 49.75%
Mapped reads, second in pair	3,977,331 / 49.48%
Mapped reads, both in pair	7,938,164 / 98.75%
Mapped reads, singletons	38,170 / 0.47%
Secondary alignments	0
Supplementary alignments	26,561 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	4,405,389 / 54.8%
Duplication rate	43.22%
Clipped reads	789,648 / 9.82%

2.2. ACGT Content

Number/percentage of A's	213,002,221 / 27.23%
Number/percentage of C's	179,442,955 / 22.94%
Number/percentage of T's	211,394,206 / 27.03%
Number/percentage of G's	178,177,807 / 22.78%
Number/percentage of N's	152,523 / 0.02%

GC Percentage	45.72%

2.3. Coverage

Mean	0.2527
Standard Deviation	9.6139

2.4. Mapping Quality

Mean Mapping Quality	55.26

2.5. Insert size

Mean	23,601.73
Standard Deviation	1,543,694.98
P25/Median/P75	155 / 221 / 304

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	4,456,841
Insertions	41,334
Mapped reads with at least one insertion	0.51%
Deletions	42,226
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.28%

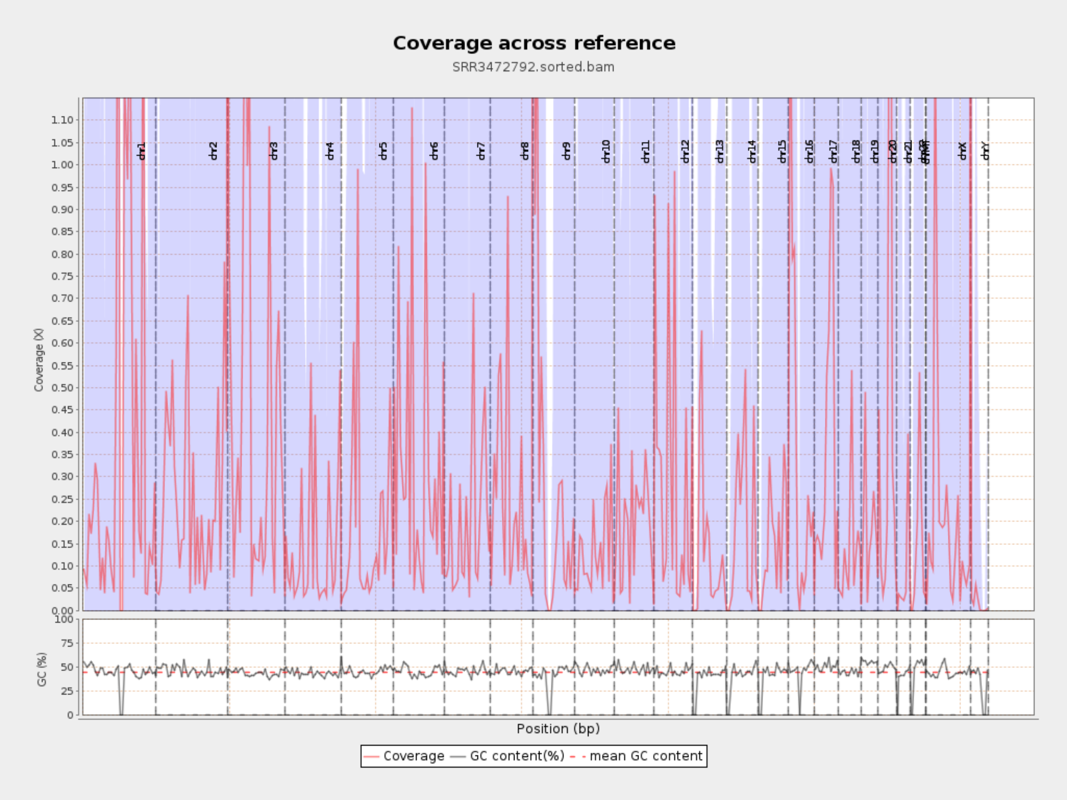
2.7. Chromosome stats

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

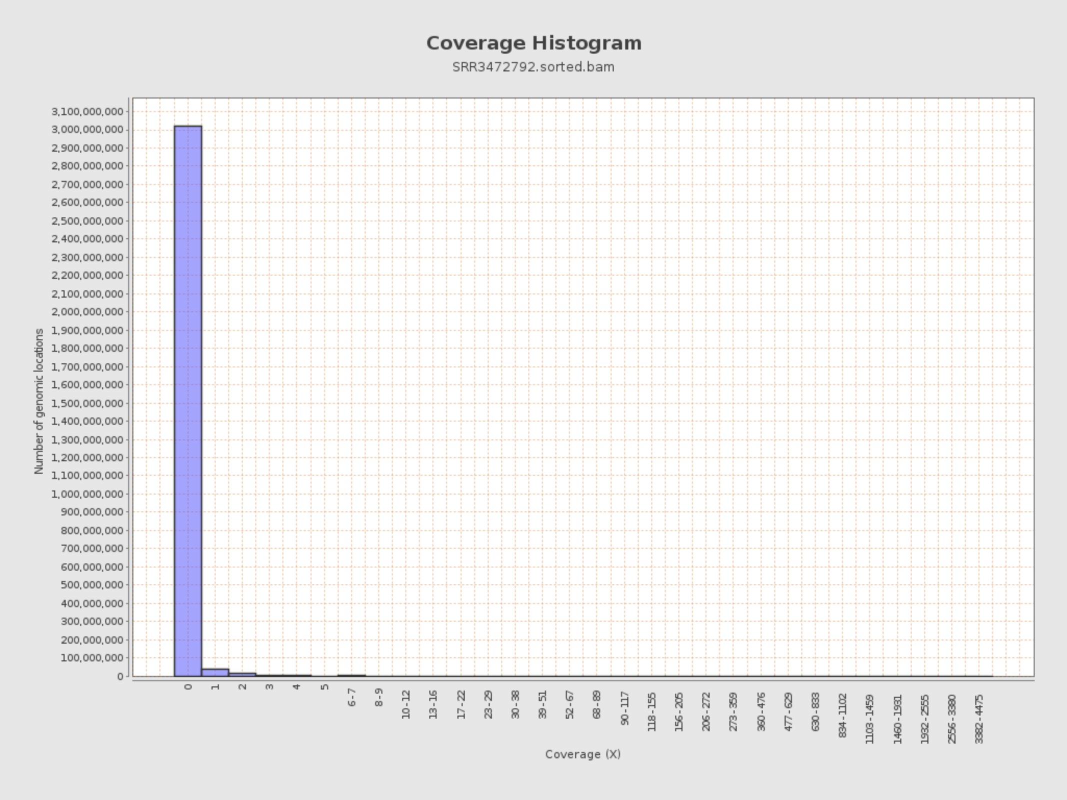
		bases	coverage	deviation
chr1	249250621	95929196	0.3849	15.0261
chr2	243199373	62685732	0.2578	10.431
chr3	198022430	92490338	0.4671	11.1323
chr4	191154276	28557440	0.1494	6.6105
chr5	180915260	34090817	0.1884	6.256
chr6	171115067	56418001	0.3297	11.0208
chr7	159138663	31968350	0.2009	6.5358
chr8	146364022	34744912	0.2374	8.047
chr9	141213431	41857616	0.2964	7.8997
chr10	135534747	18074733	0.1334	4.2714
chr11	135006516	27296307	0.2022	6.452
chr12	133851895	42607771	0.3183	12.3345
chr13	115169878	15719983	0.1365	4.8413
chr14	107349540	20166649	0.1879	9.76
chr15	102531392	14945897	0.1458	4.6407
chr16	90354753	31896408	0.353	13.6993
chr17	81195210	31468597	0.3876	11.5008
chr18	78077248	10438127	0.1337	5.4986
chr19	59128983	11130109	0.1882	4.7151
chr20	63025520	27944328	0.4434	21.3327
chr21	48129895	4388825	0.0912	4.5213
chr22	51304566	8164859	0.1591	5.5091
chrMT	16571	1207	0.0728	0.2833
chrX	155270560	38326580	0.2468	8.5253

chrY	59373566	963877	0.0162	0.7623

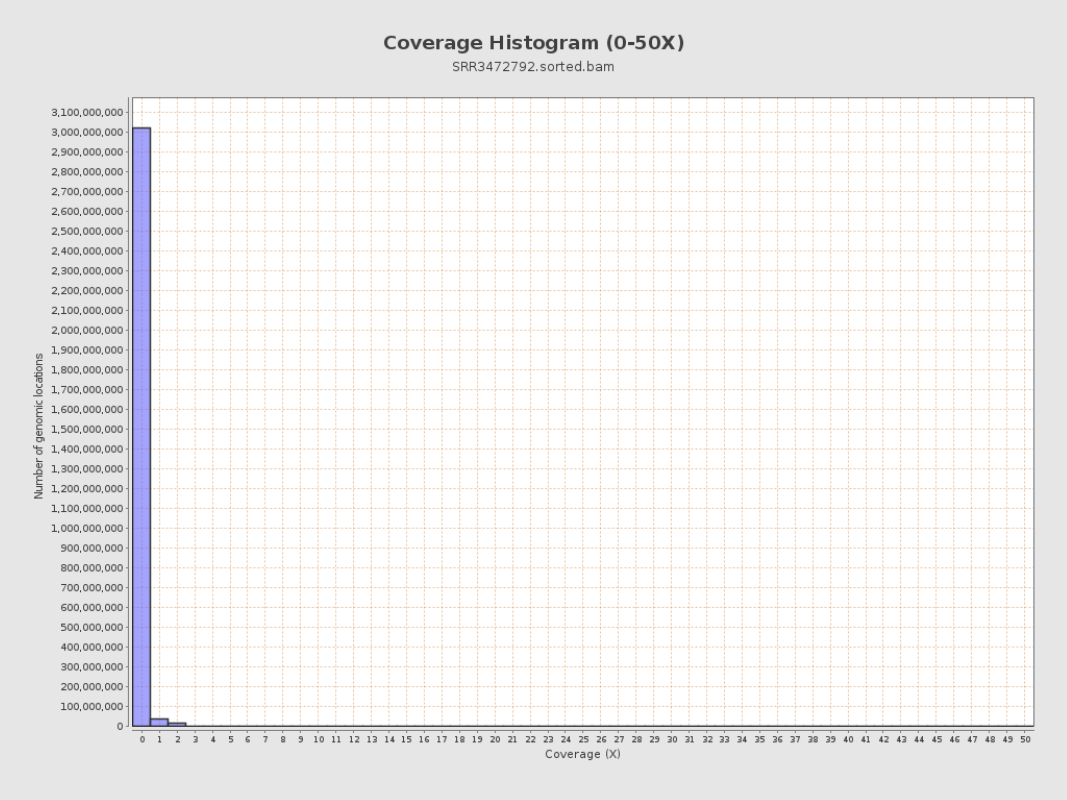
3. Results : Coverage across reference



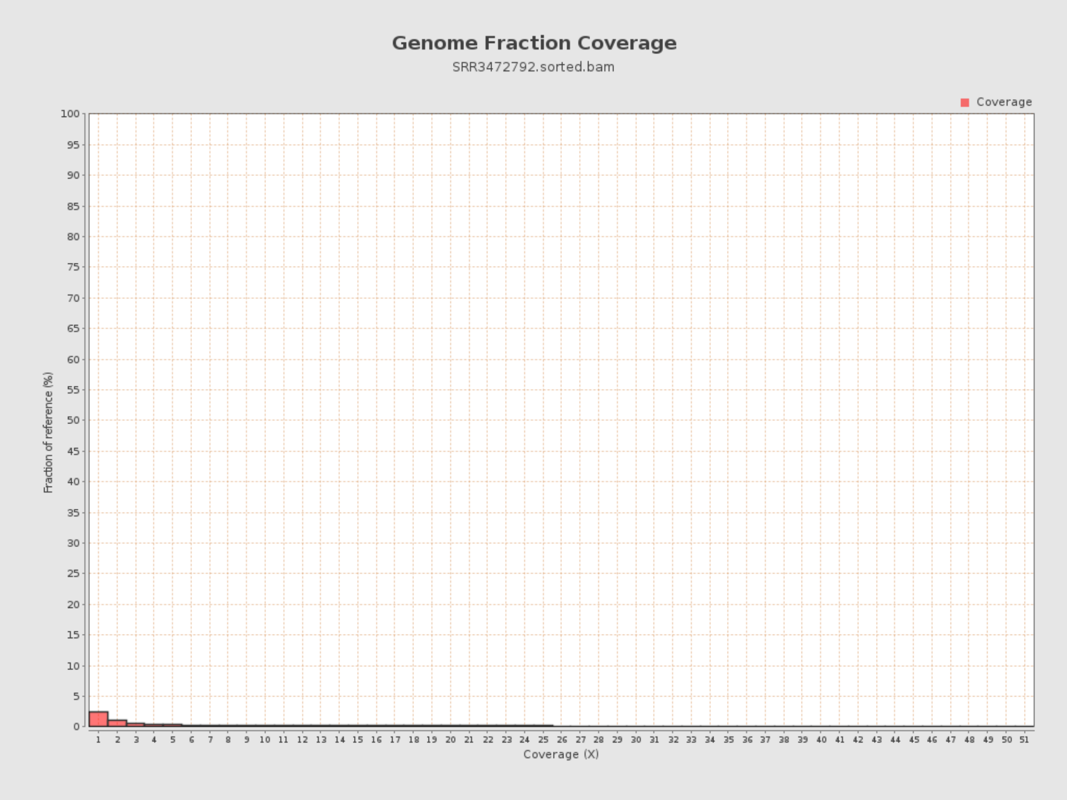
4. Results : Coverage Histogram



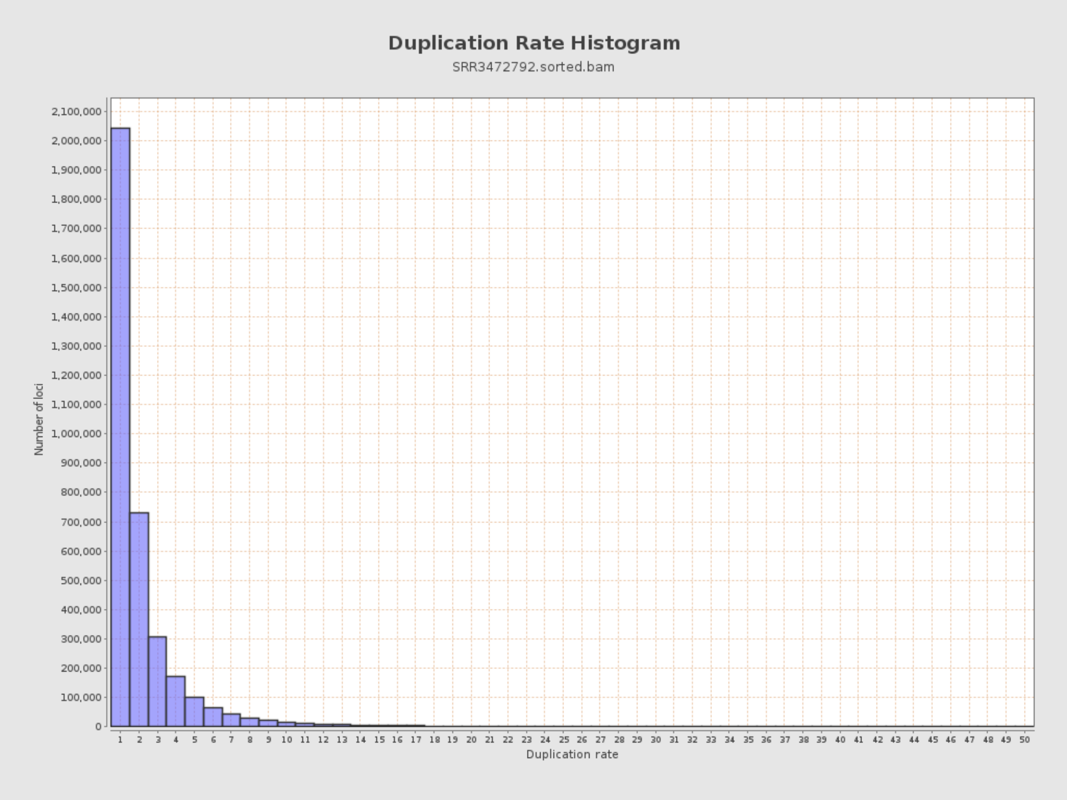
5. Results : Coverage Histogram (0-50X)



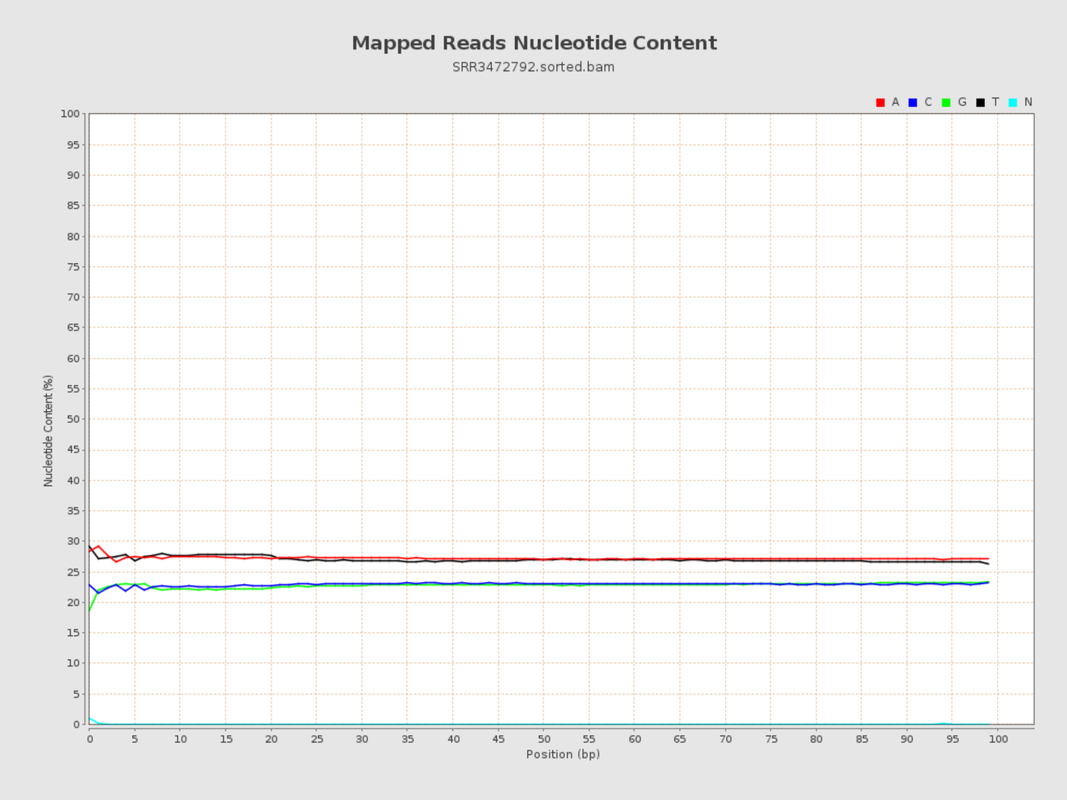
6. Results : Genome Fraction Coverage



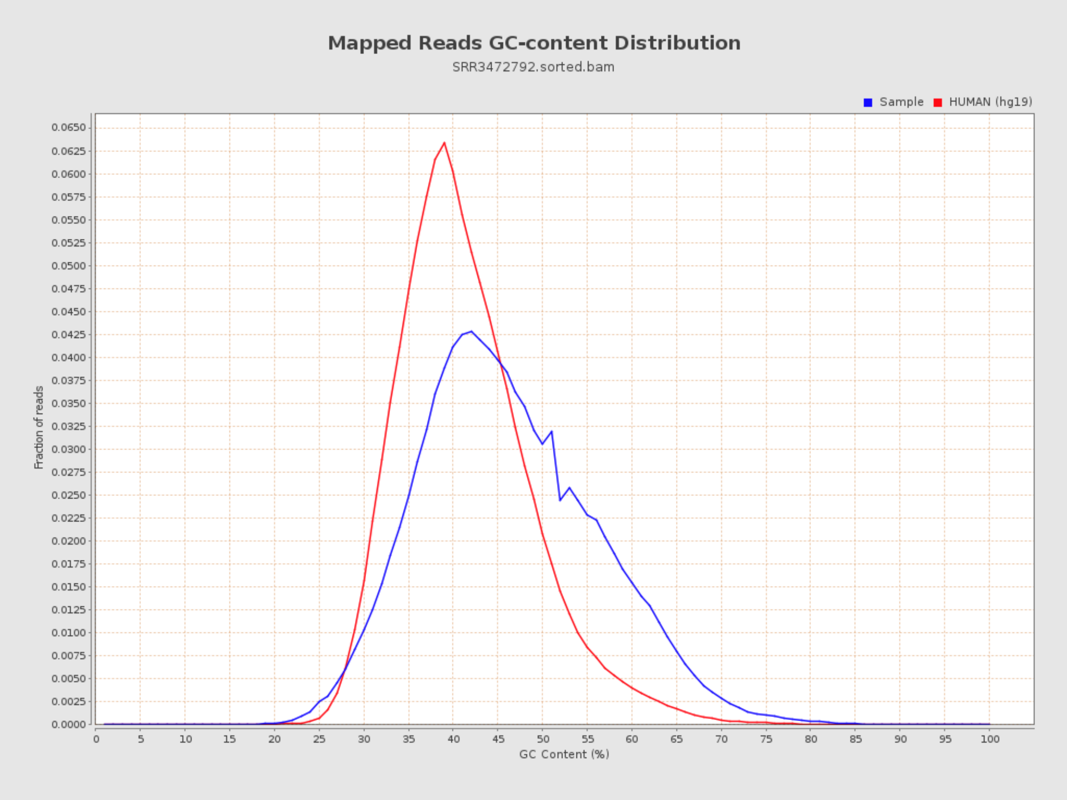
7. Results : Duplication Rate Histogram



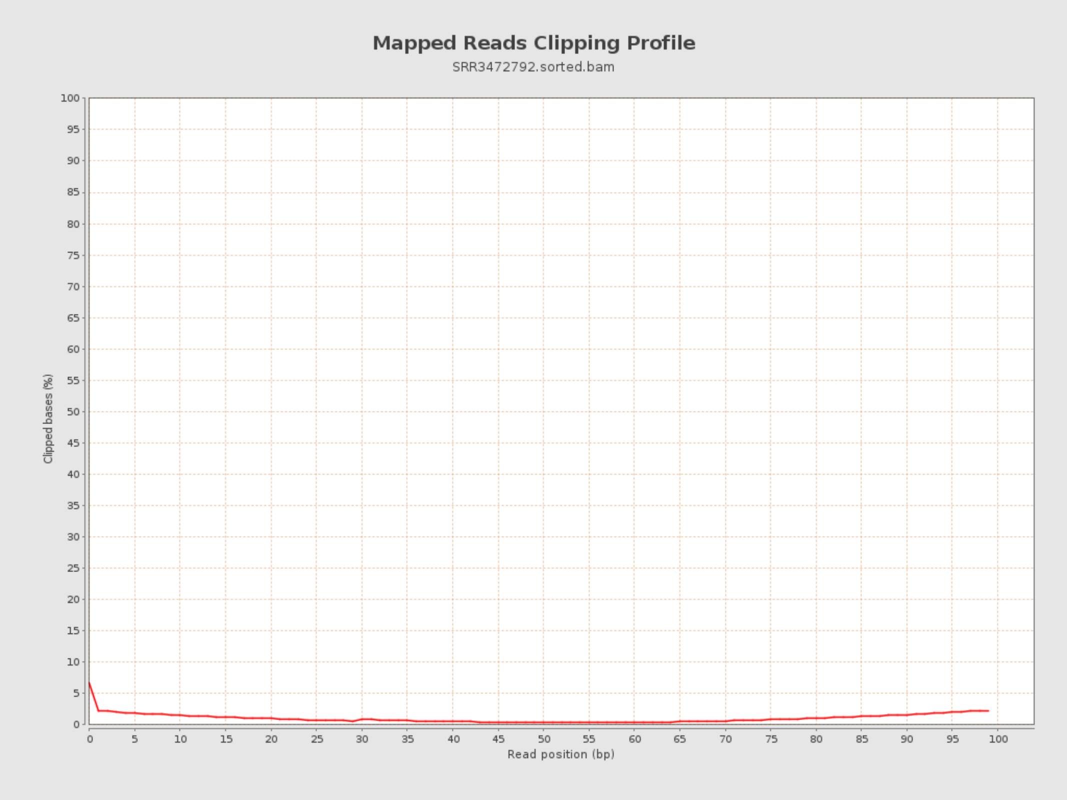
8. Results : Mapped Reads Nucleotide Content



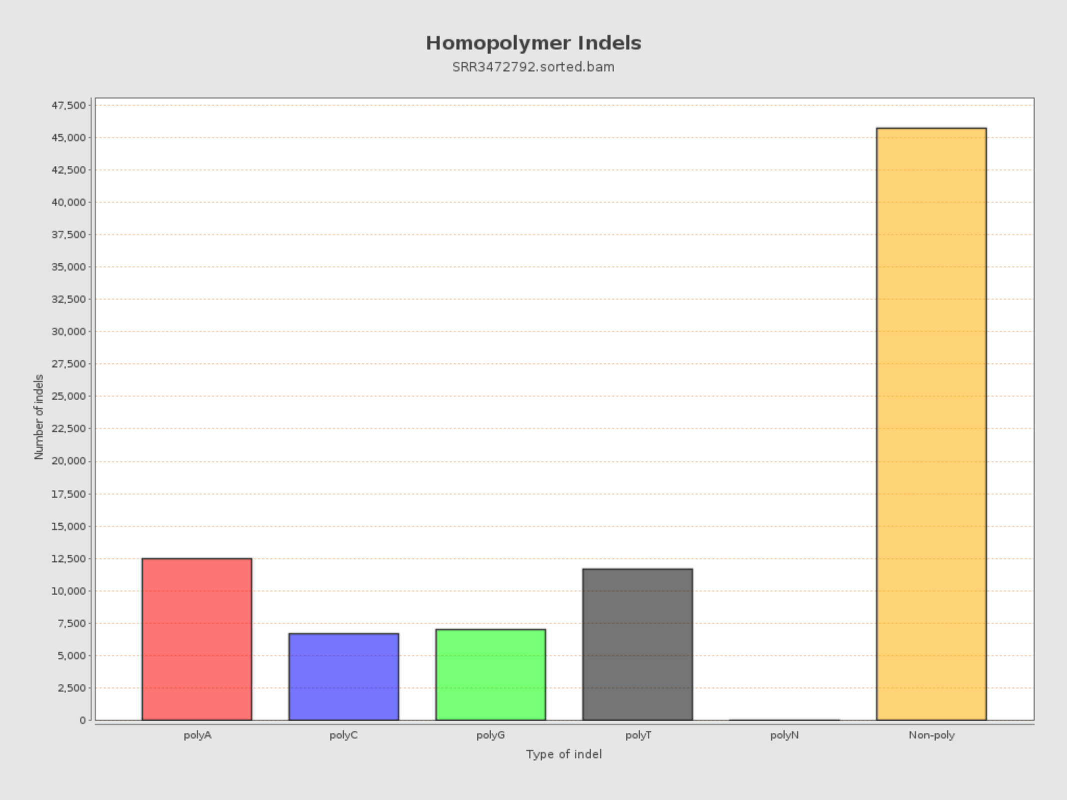
9. Results : Mapped Reads GC-content Distribution



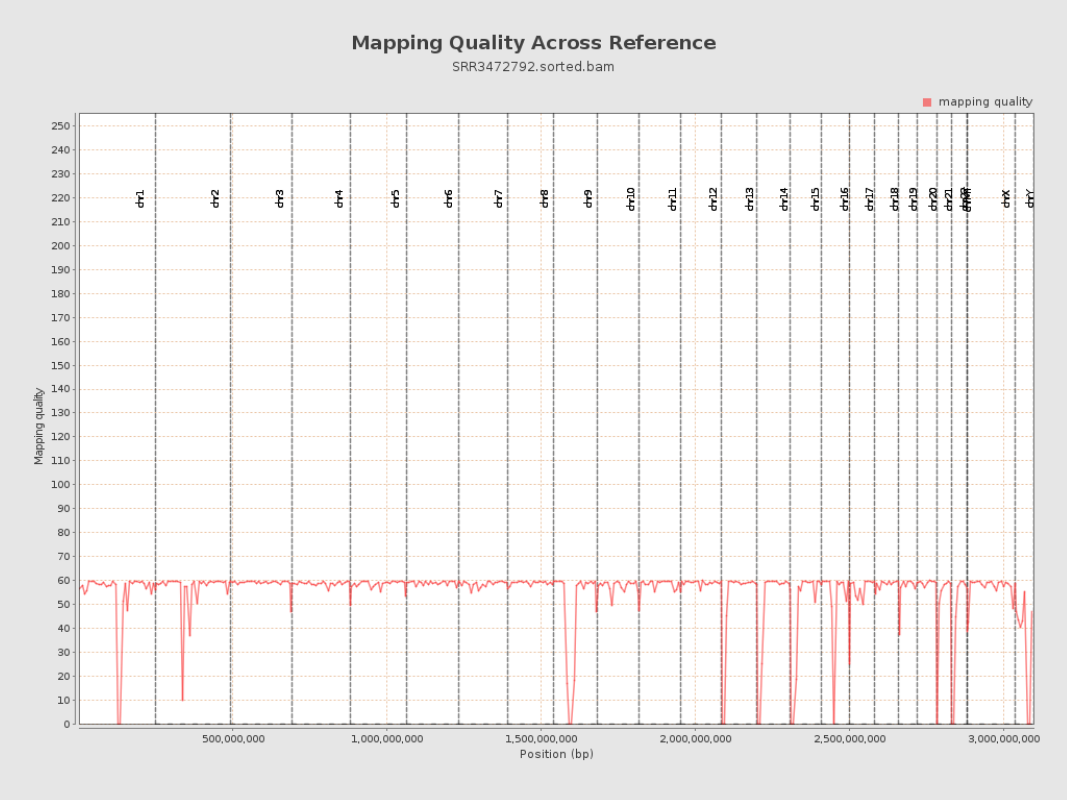
10. Results : Mapped Reads Clipping Profile



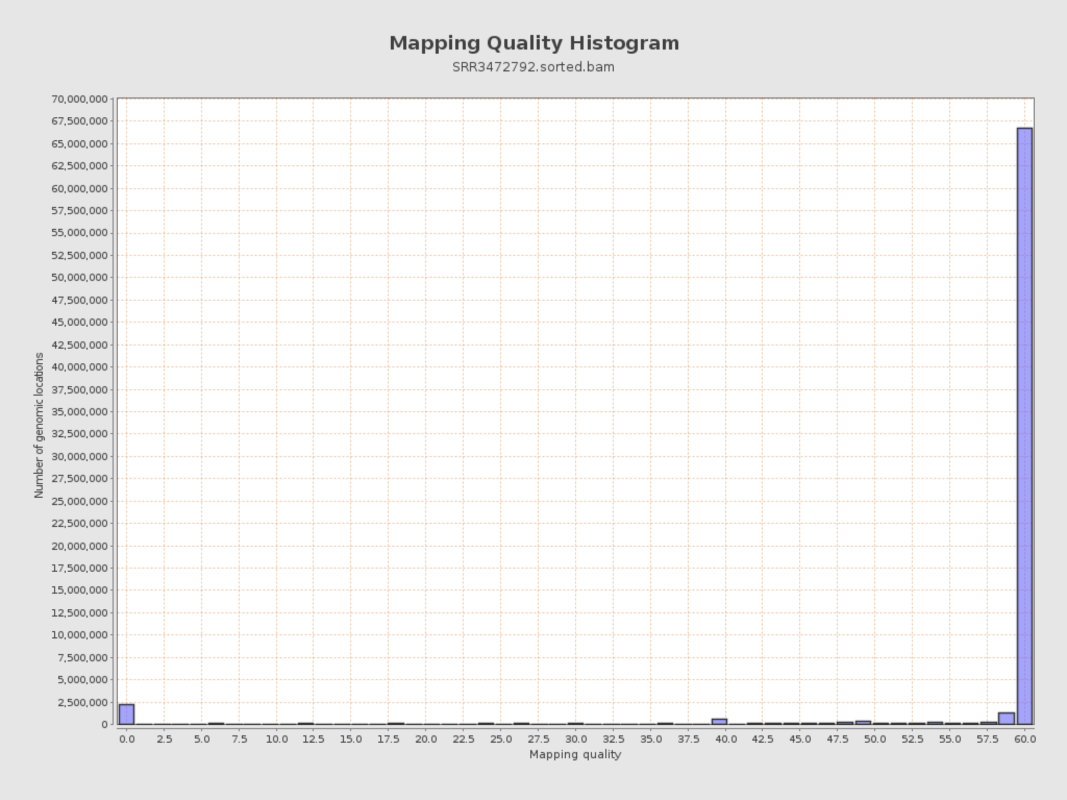
11. Results : Homopolymer Indels



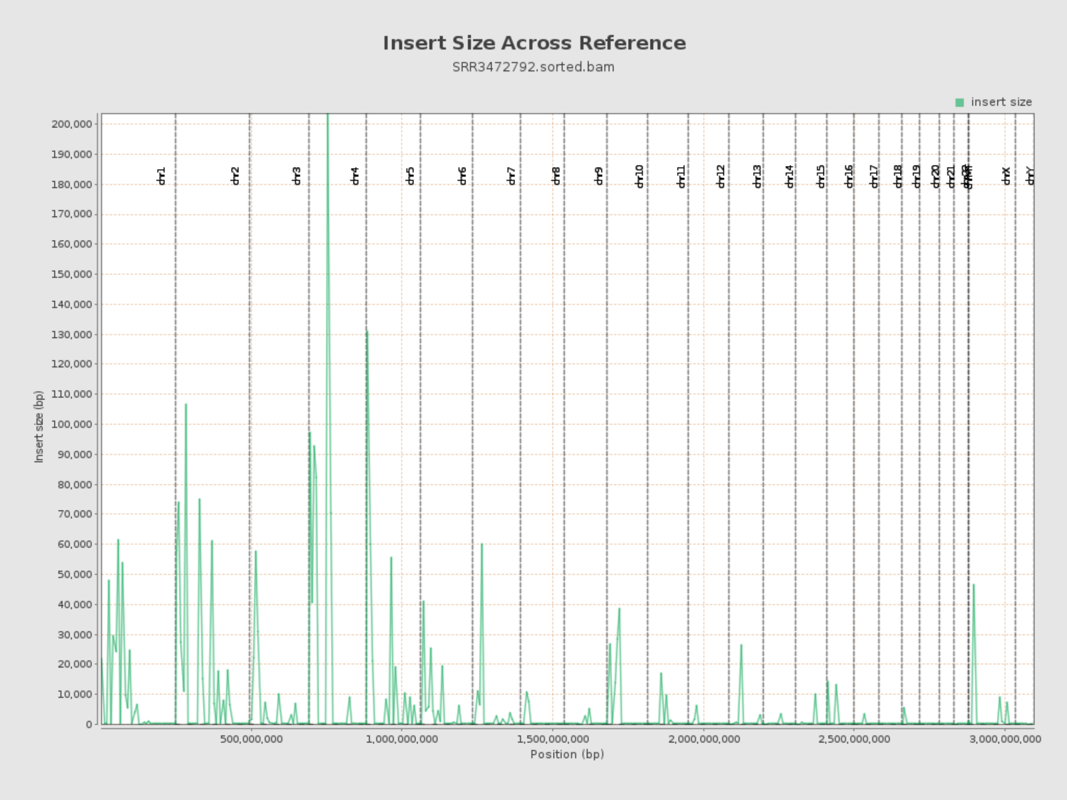
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram