Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 14:05:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472702.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_SRR3472702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472702_1.fastq.gz SRR3472702_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 14:05:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,230,318
Mapped reads	15,092,324 / 99.09%
Unmapped reads	137,994 / 0.91%
Mapped paired reads	15,092,324 / 99.09%
Mapped reads, first in pair	7,568,083 / 49.69%
Mapped reads, second in pair	7,524,241 / 49.4%
Mapped reads, both in pair	15,014,222 / 98.58%
Mapped reads, singletons	78,102 / 0.51%
Secondary alignments	0
Supplementary alignments	50,924 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,246,927 / 60.71%
Duplication rate	45.81%
Clipped reads	1,451,257 / 9.53%

2.2. ACGT Content

Number/percentage of A's	394,771,417 / 26.67%
Number/percentage of C's	348,124,881 / 23.51%
Number/percentage of T's	392,164,996 / 26.49%
Number/percentage of G's	345,122,267 / 23.31%
Number/percentage of N's	288,028 / 0.02%

GC Percentage	46.83%

2.3. Coverage

Mean	0.4783
Standard Deviation	16.053

2.4. Mapping Quality

Mean Mapping Quality	55.05

2.5. Insert size

Mean	23,145.44
Standard Deviation	1,513,489.32
P25/Median/P75	157 / 219 / 296

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	8,484,667
Insertions	86,438
Mapped reads with at least one insertion	0.56%
Deletions	78,307
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.2%

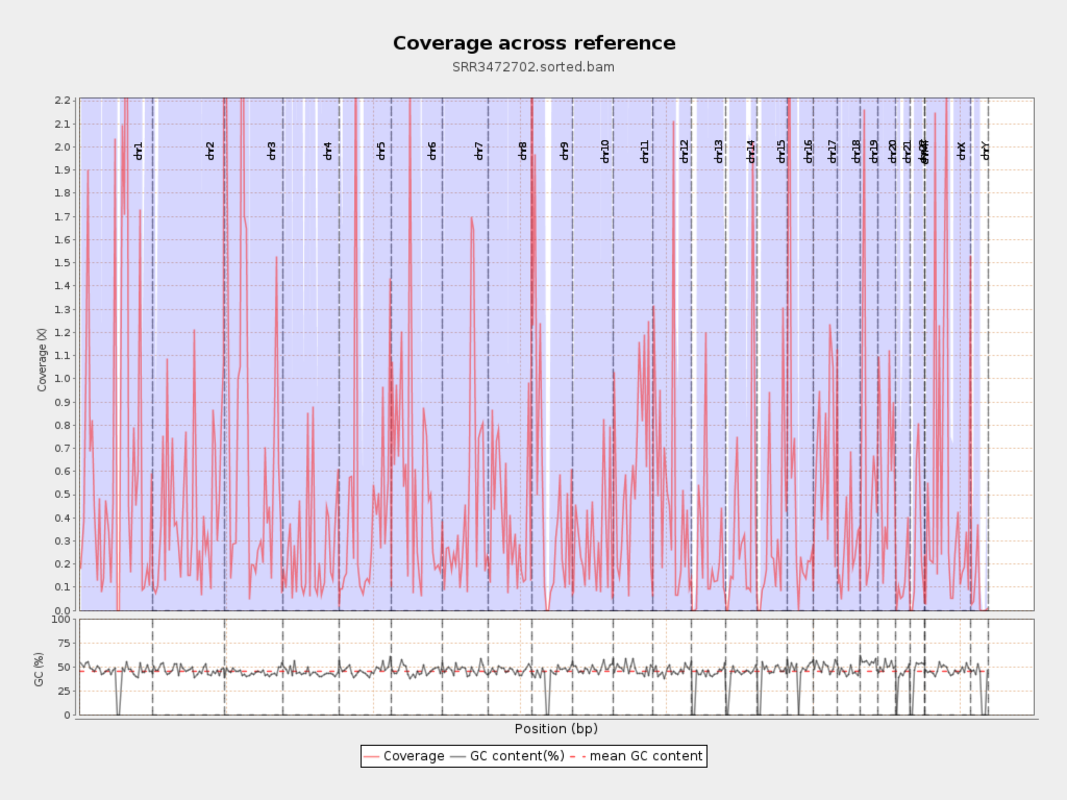
2.7. Chromosome stats

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

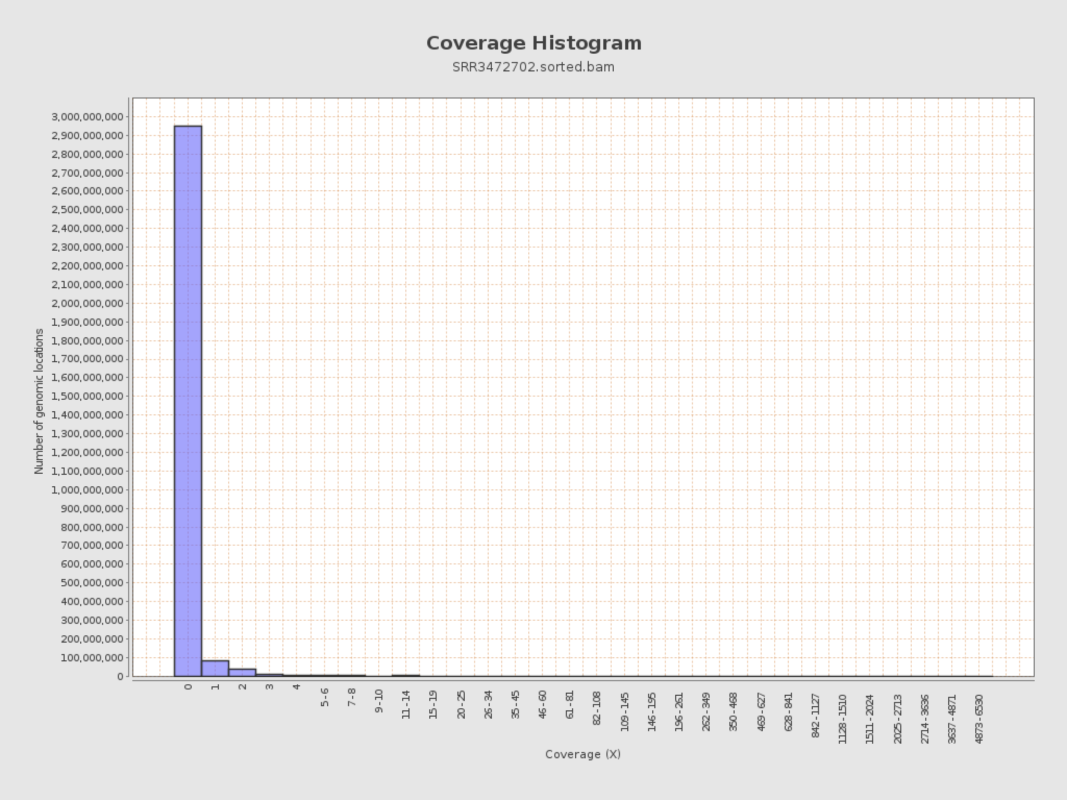
		bases	coverage	deviation
chr1	249250621	175377747	0.7036	24.5756
chr2	243199373	102074270	0.4197	14.1867
chr3	198022430	166464774	0.8406	18.4549
chr4	191154276	50089551	0.262	10.2812
chr5	180915260	81502093	0.4505	16.273
chr6	171115067	96858199	0.566	15.0696
chr7	159138663	73759334	0.4635	15.9007
chr8	146364022	55644236	0.3802	14.7451
chr9	141213431	70881137	0.5019	12.6126
chr10	135534747	40803367	0.3011	10.5131
chr11	135006516	80313621	0.5949	18.6652
chr12	133851895	72289588	0.5401	19.1797
chr13	115169878	28419123	0.2468	9.212
chr14	107349540	38783521	0.3613	16.0338
chr15	102531392	33708819	0.3288	9.5818
chr16	90354753	47125376	0.5216	14.288
chr17	81195210	55034913	0.6778	14.369
chr18	78077248	21684389	0.2777	10.3096
chr19	59128983	41754322	0.7062	20.0107
chr20	63025520	40332127	0.6399	26.9505
chr21	48129895	6428858	0.1336	5.0065
chr22	51304566	14363092	0.28	9.3071
chrMT	16571	4003	0.2416	0.6362
chrX	155270560	82308772	0.5301	18.0207

chrY	59373566	4658427	0.0785	6.0338

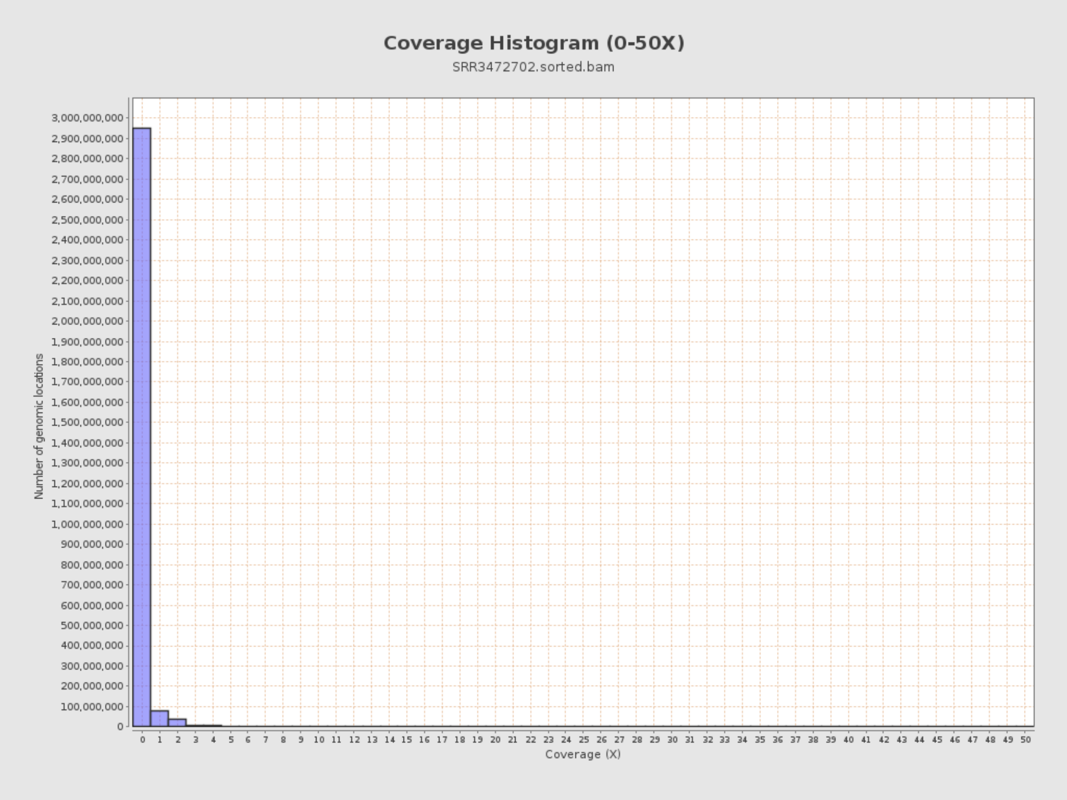
3. Results : Coverage across reference



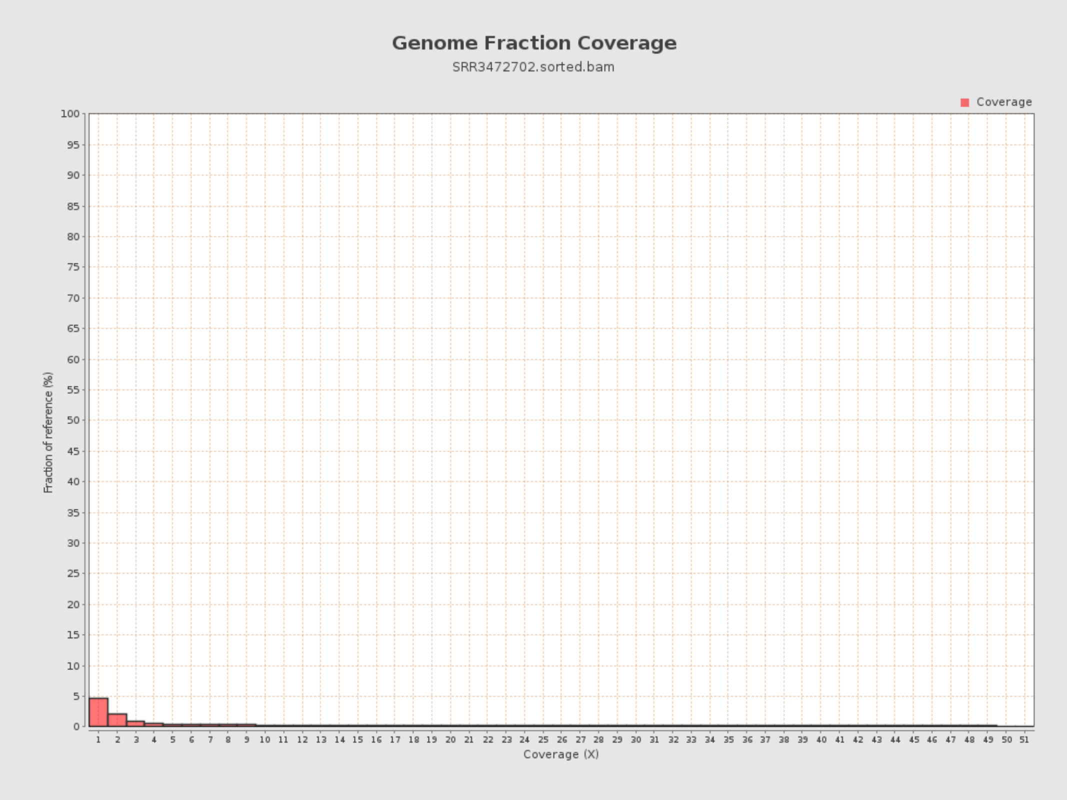
4. Results : Coverage Histogram



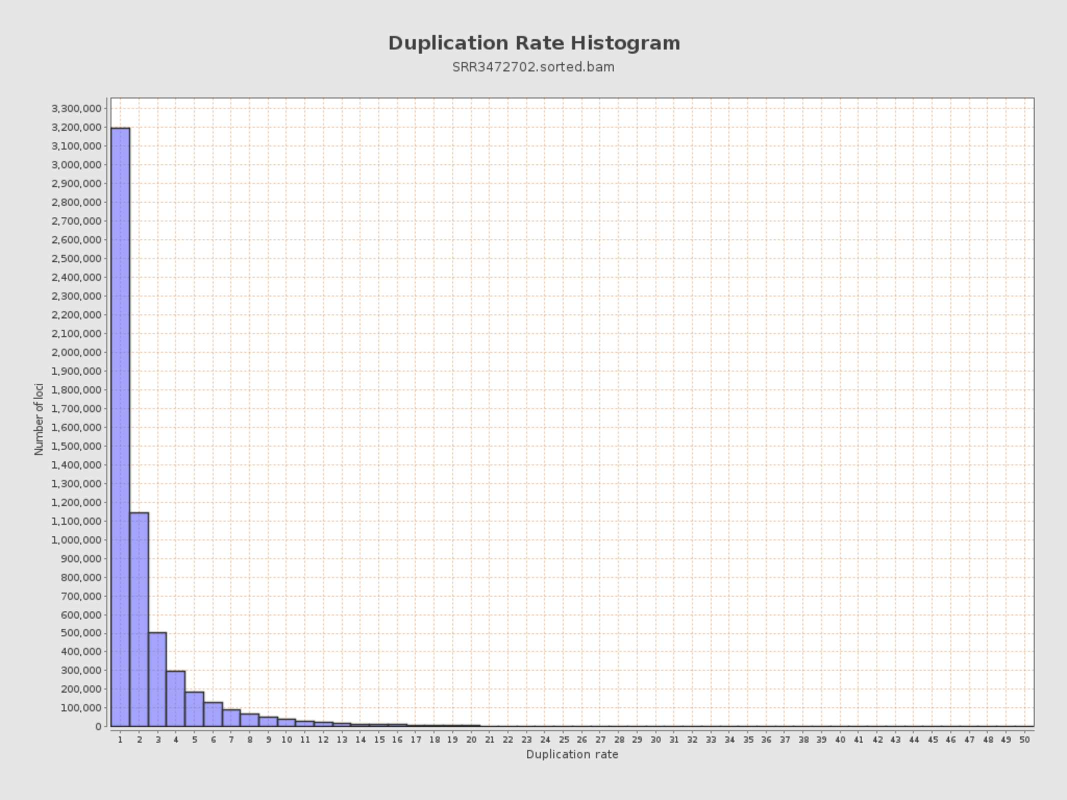
5. Results : Coverage Histogram (0-50X)



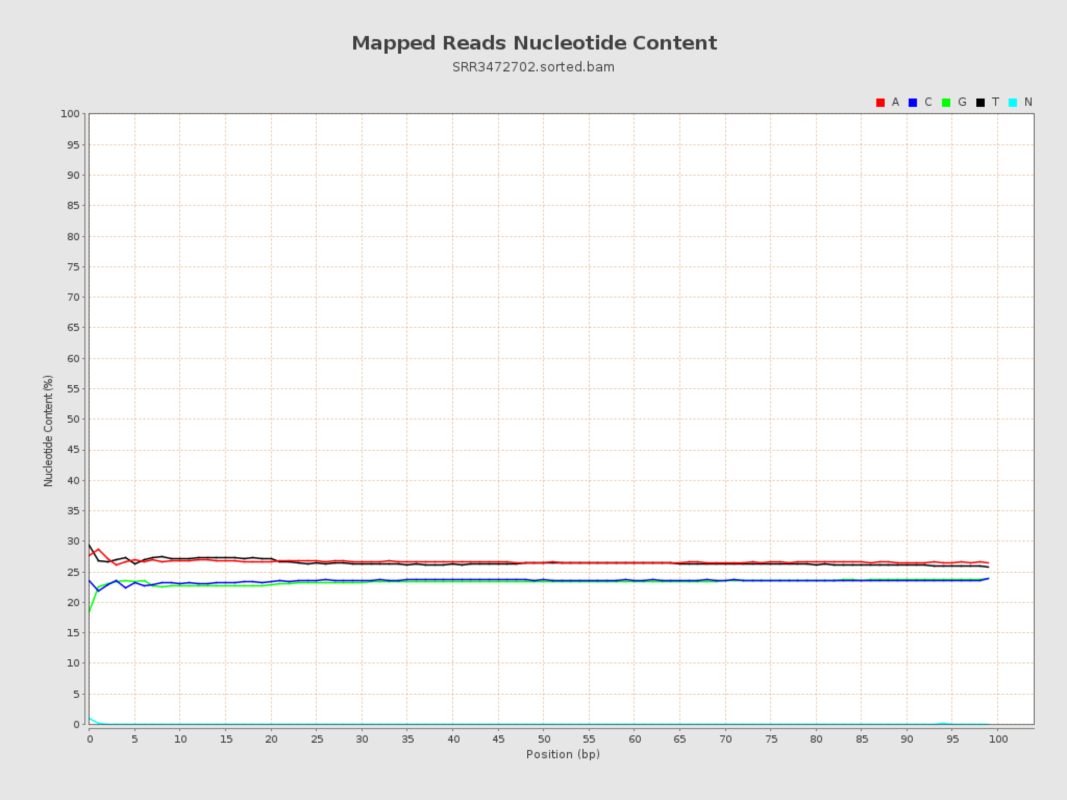
6. Results : Genome Fraction Coverage



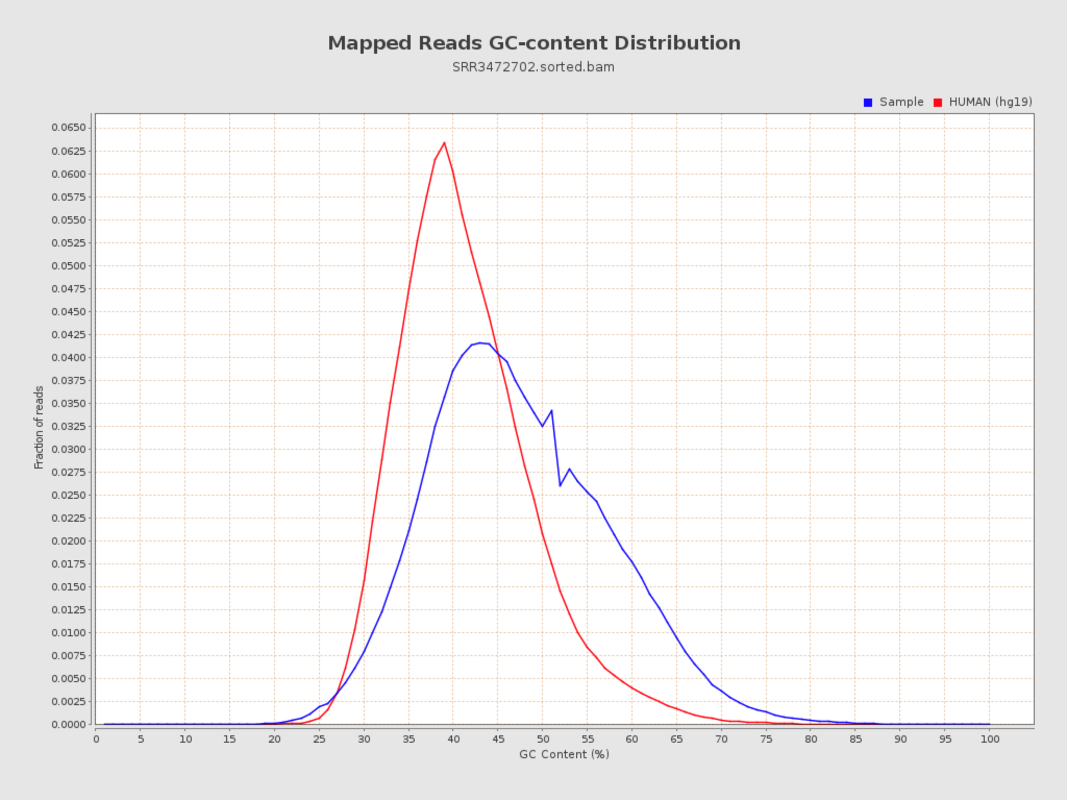
7. Results : Duplication Rate Histogram



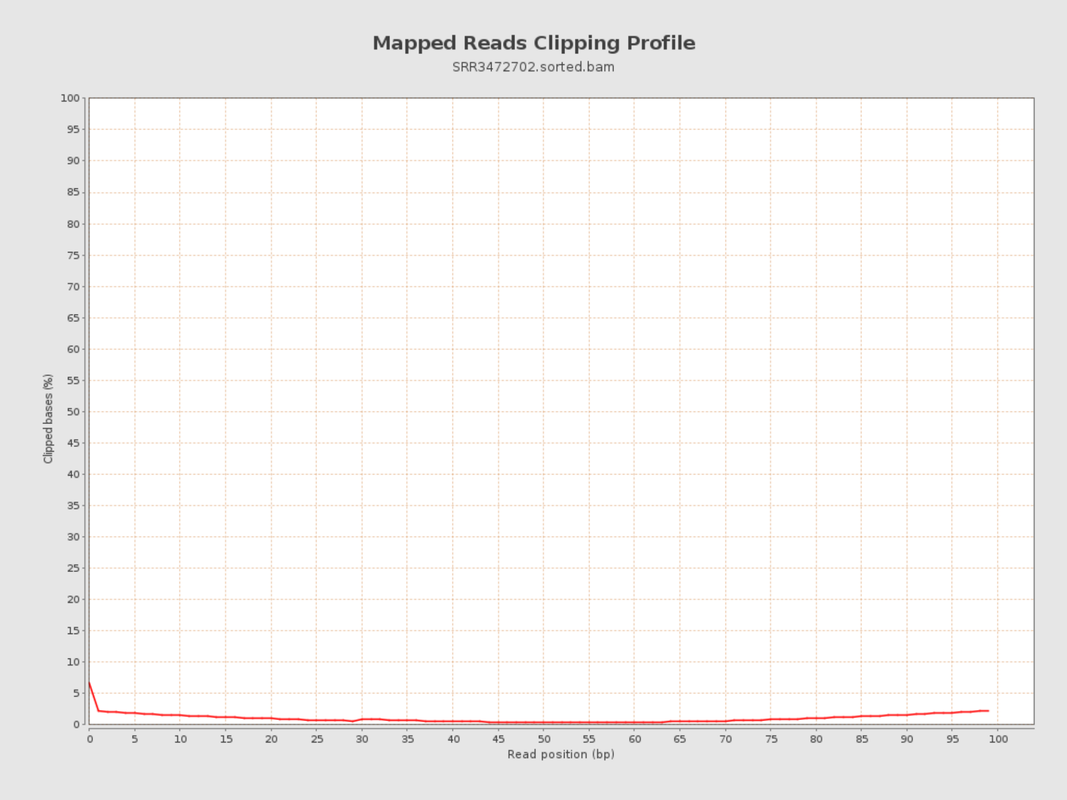
8. Results : Mapped Reads Nucleotide Content



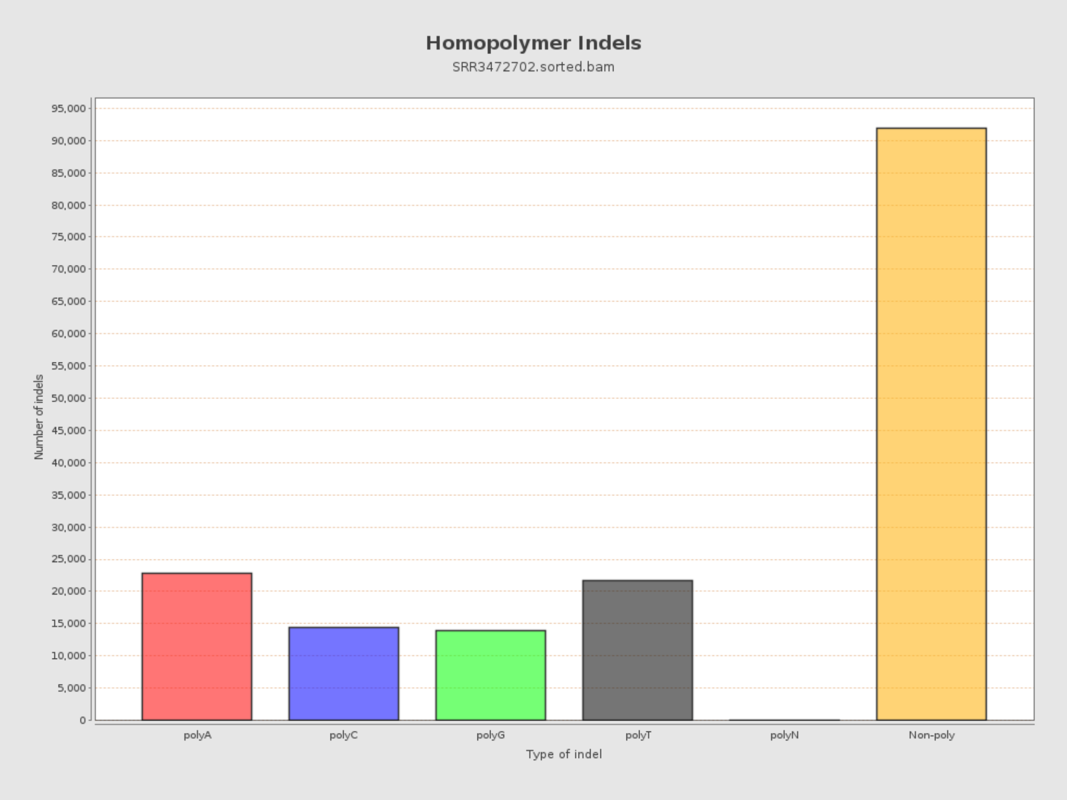
9. Results : Mapped Reads GC-content Distribution



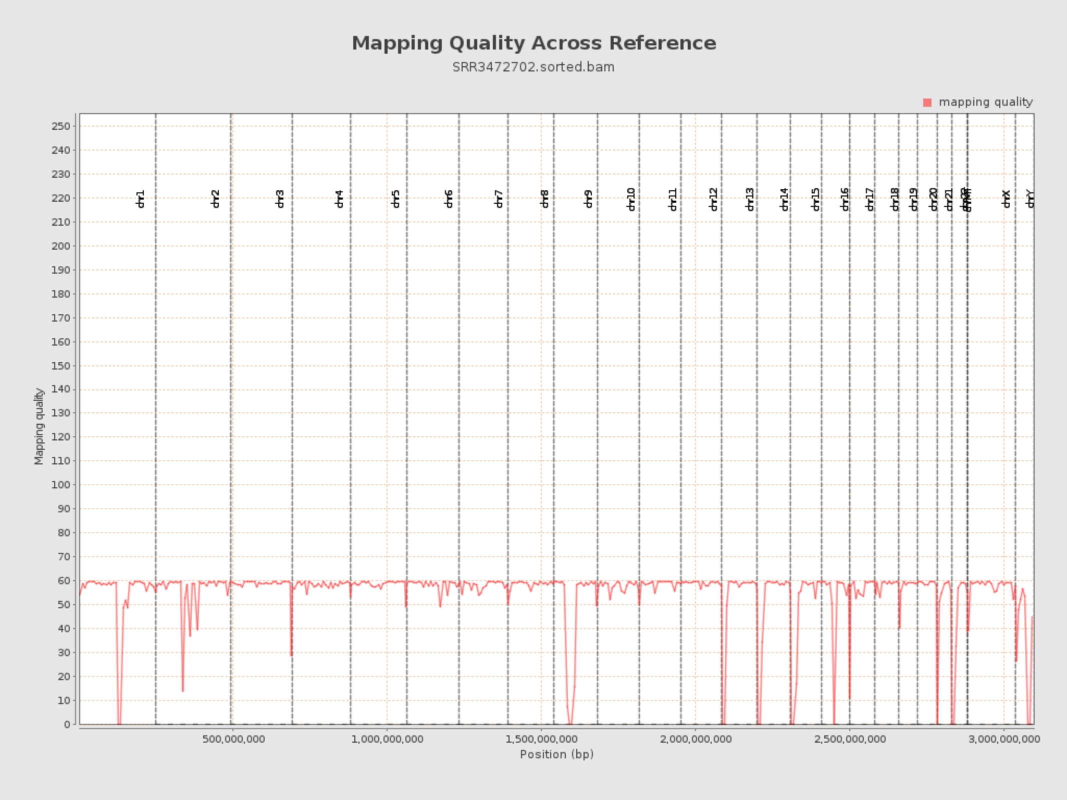
10. Results : Mapped Reads Clipping Profile



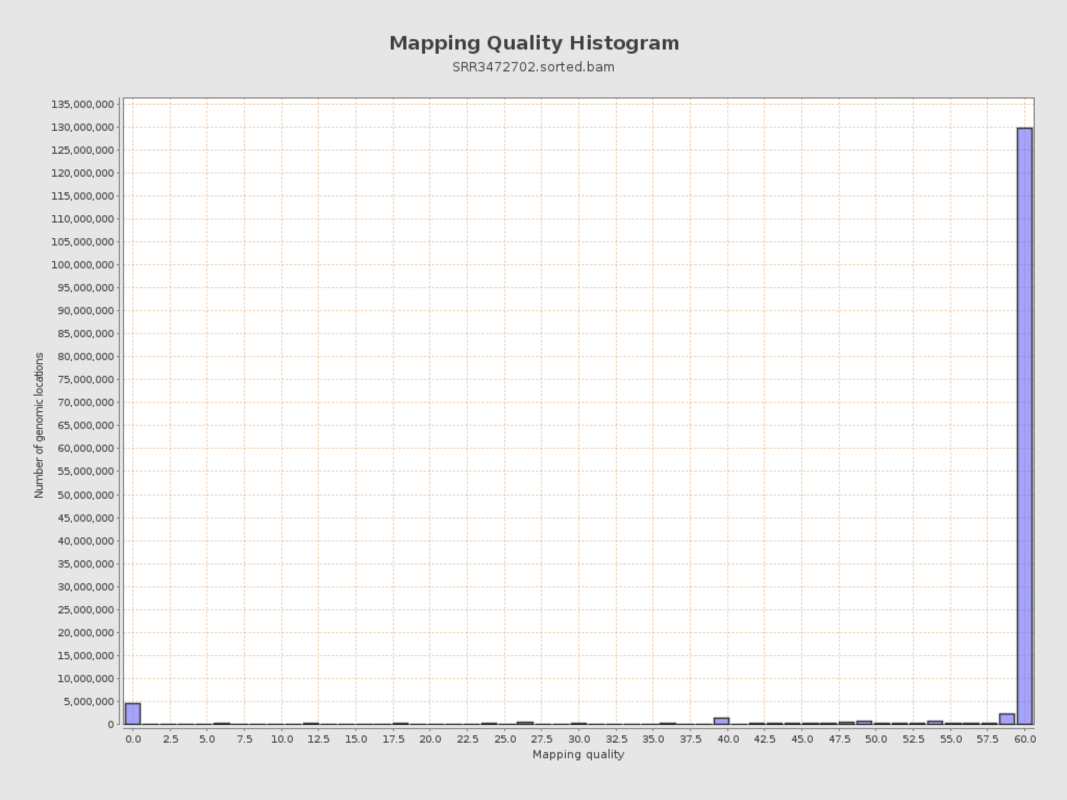
11. Results : Homopolymer Indels



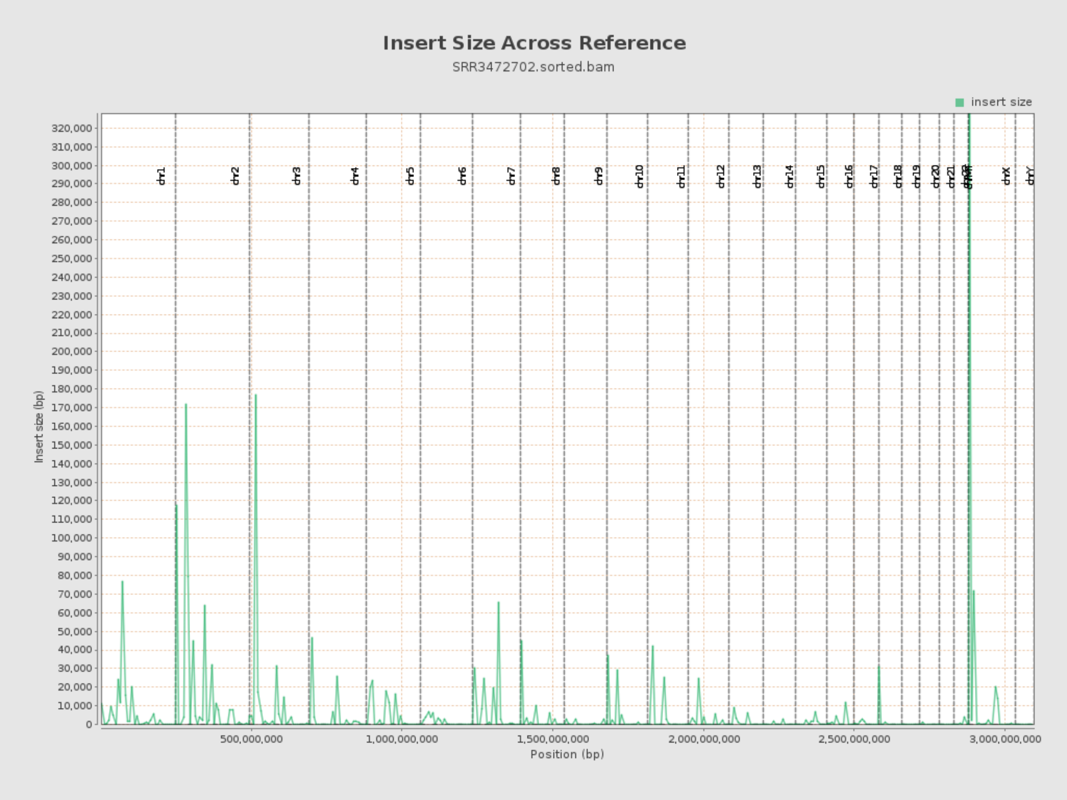
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram