Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472398.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_SRR3472398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472398_1.fastq.gz SRR3472398_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:04:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,818,552
Mapped reads	18,547,970 / 98.56%
Unmapped reads	270,582 / 1.44%
Mapped paired reads	18,547,970 / 98.56%
Mapped reads, first in pair	9,328,893 / 49.57%
Mapped reads, second in pair	9,219,077 / 48.99%
Mapped reads, both in pair	18,374,774 / 97.64%
Mapped reads, singletons	173,196 / 0.92%
Secondary alignments	0
Supplementary alignments	83,469 / 0.44%
Read min/max/mean length	30 / 100 / 99.48
Duplicated reads (estimated)	11,240,547 / 59.73%
Duplication rate	46.46%
Clipped reads	1,315,294 / 6.99%

2.2. ACGT Content

Number/percentage of A's	498,684,154 / 27.4%
Number/percentage of C's	413,241,990 / 22.71%
Number/percentage of T's	498,037,627 / 27.36%
Number/percentage of G's	409,827,444 / 22.52%
Number/percentage of N's	217,396 / 0.01%

GC Percentage	45.22%

2.3. Coverage

Mean	0.588
Standard Deviation	16.3732

2.4. Mapping Quality

Mean Mapping Quality	54.79

2.5. Insert size

Mean	26,127.64
Standard Deviation	1,584,666.08
P25/Median/P75	183 / 263 / 361

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	12,149,743
Insertions	113,334
Mapped reads with at least one insertion	0.6%
Deletions	92,681
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.08%

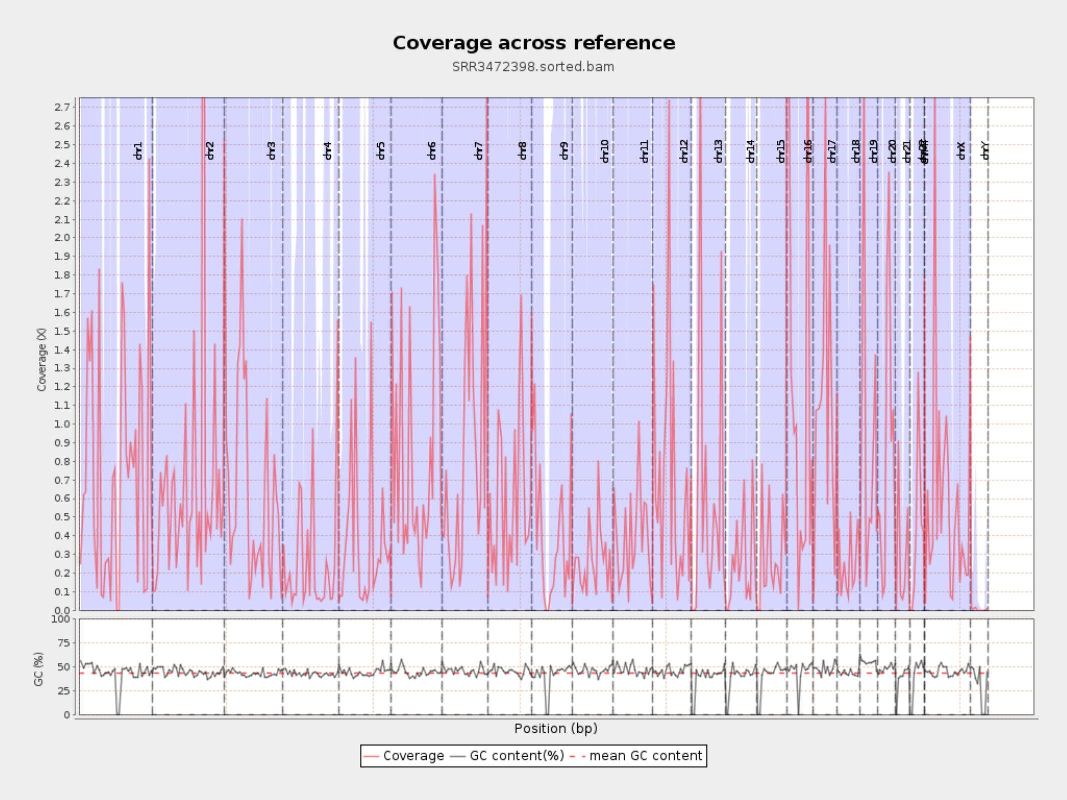
2.7. Chromosome stats

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

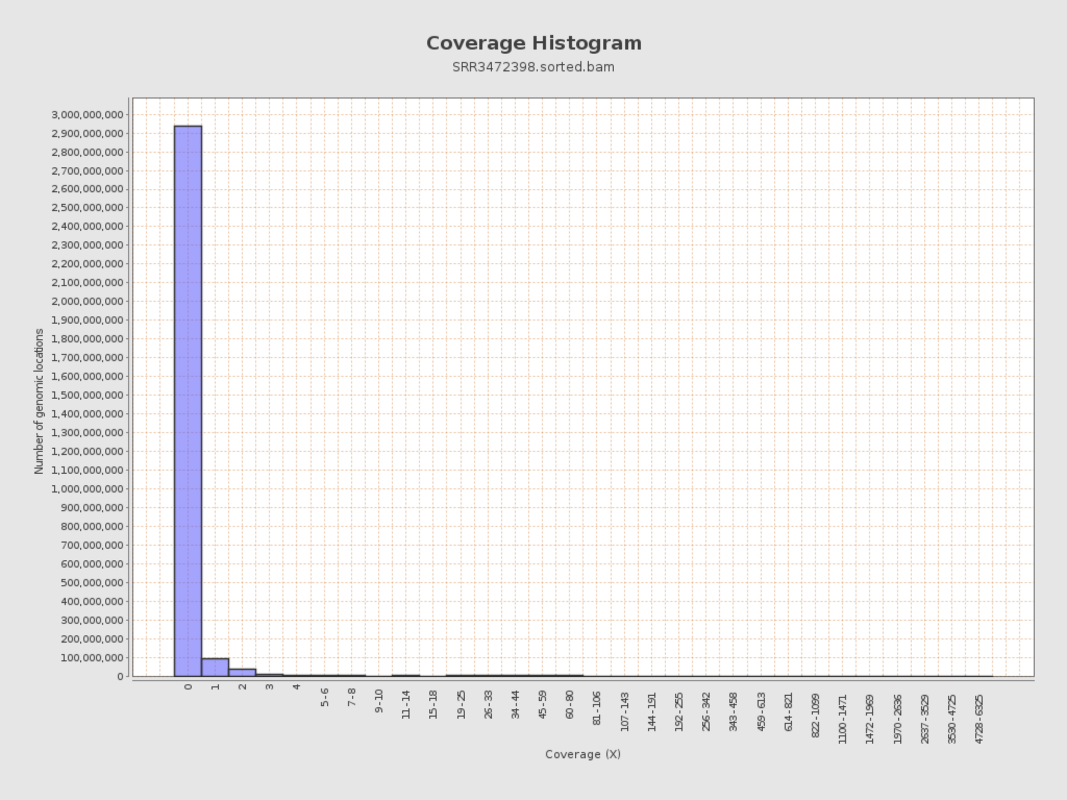
		bases	**coverage**	**deviation**
chr1	249250621	187356019	0.7517	20.231
chr2	243199373	171438285	0.7049	19.9626
chr3	198022430	132036095	0.6668	13.6227
chr4	191154276	50385715	0.2636	9.9551
chr5	180915260	69596766	0.3847	11.9187
chr6	171115067	141787902	0.8286	21.6709
chr7	159138663	140306868	0.8817	22.4664
chr8	146364022	87778276	0.5997	14.5973
chr9	141213431	57941743	0.4103	9.781
chr10	135534747	36033865	0.2659	9.7261
chr11	135006516	52759726	0.3908	10.8087
chr12	133851895	97840777	0.731	17.7291
chr13	115169878	72338351	0.6281	21.8285
chr14	107349540	26166303	0.2437	6.975
chr15	102531392	28991154	0.2828	8.0637
chr16	90354753	115987571	1.2837	28.5663
chr17	81195210	90656647	1.1165	22.7296
chr18	78077248	20016610	0.2564	7.0058
chr19	59128983	59580884	1.0076	19.4333
chr20	63025520	57349522	0.9099	20.0184
chr21	48129895	14084861	0.2926	13.4957
chr22	51304566	20992680	0.4092	11.6048
chrMT	16571	29607	1.7867	2.0808
chrX	155270560	88473348	0.5698	12.3671

chrY	59373566	302624	0.0051	0.3636

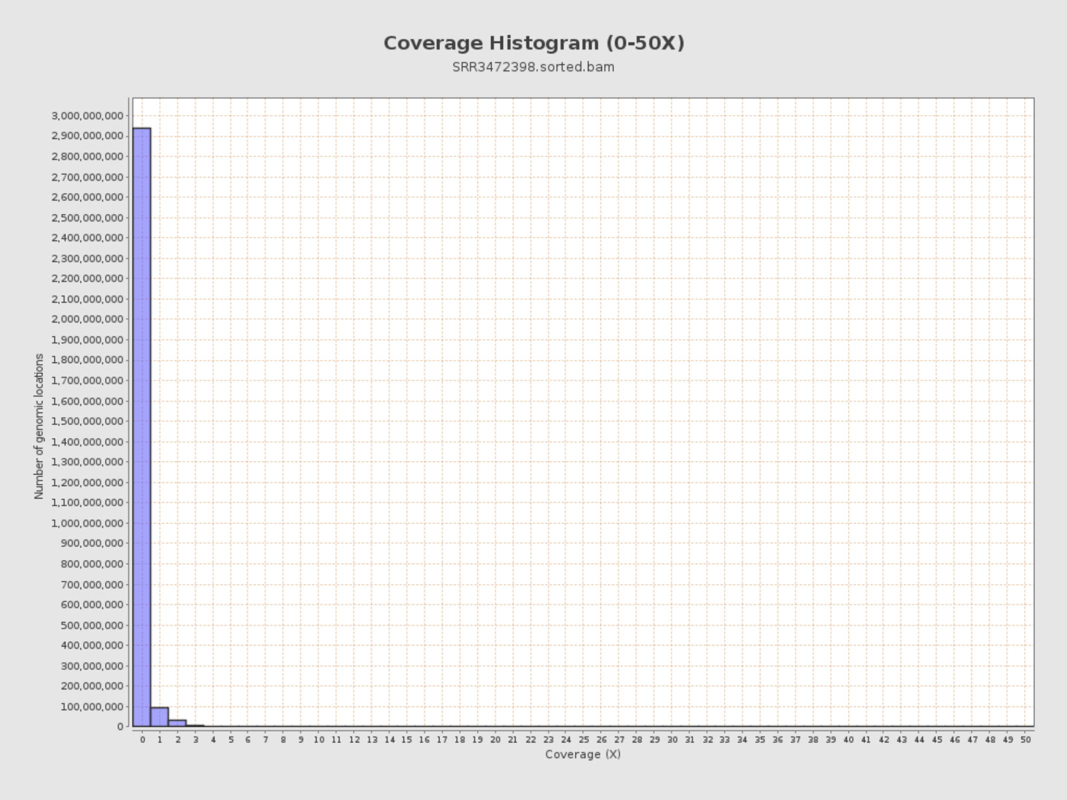
3. Results : Coverage across reference



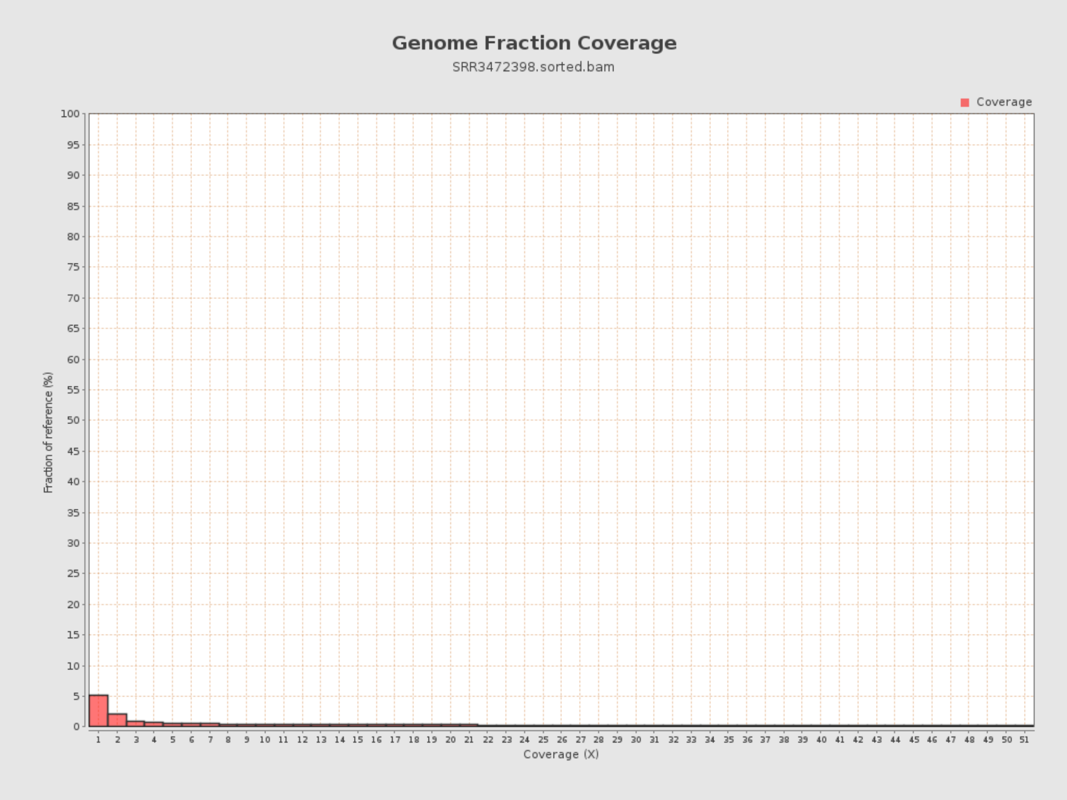
4. Results : Coverage Histogram



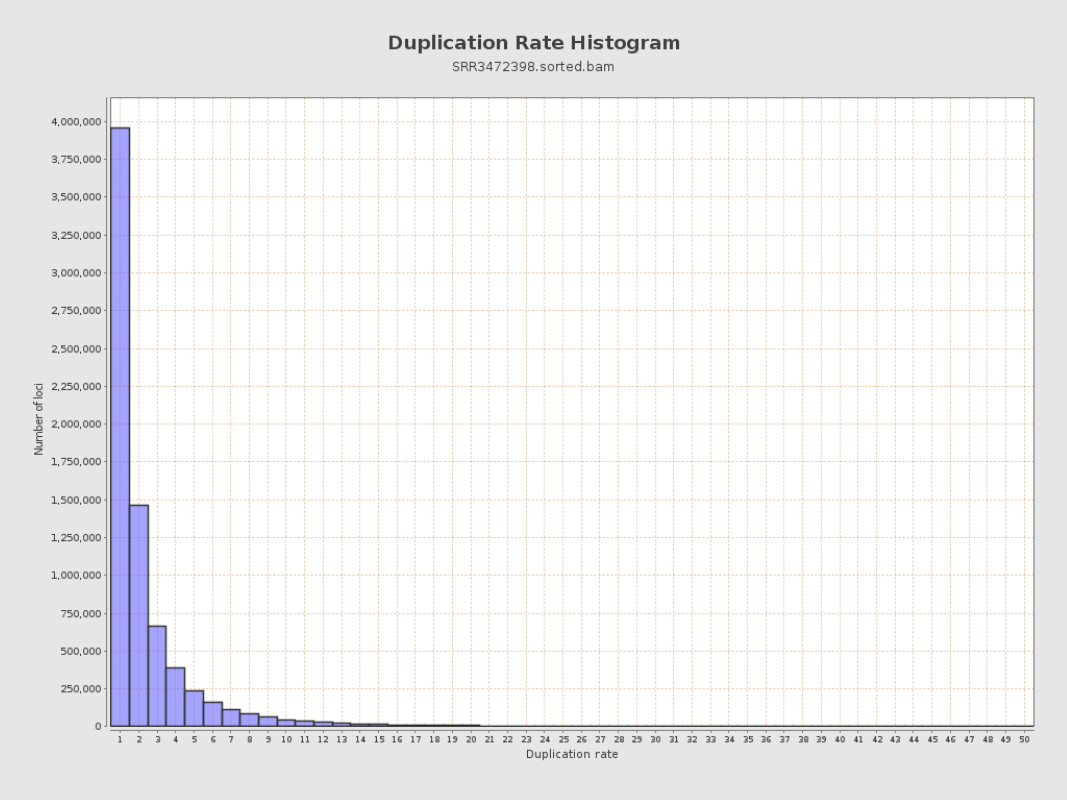
5. Results : Coverage Histogram (0-50X)



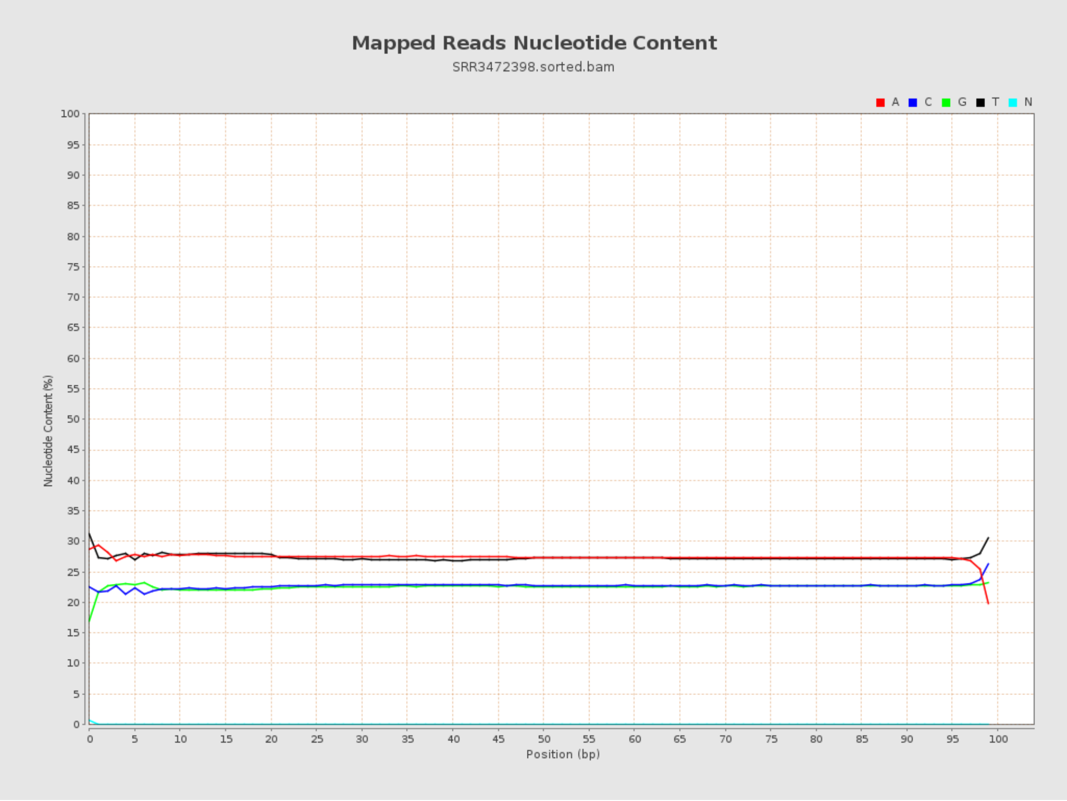
6. Results : Genome Fraction Coverage



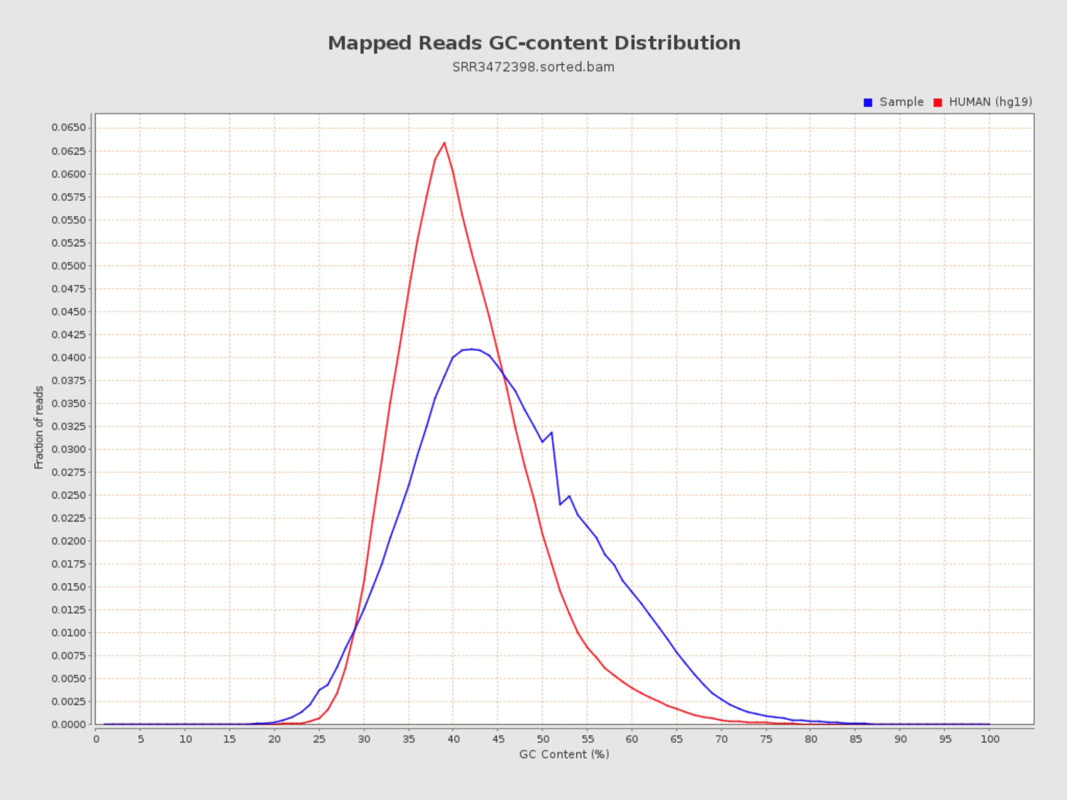
7. Results : Duplication Rate Histogram



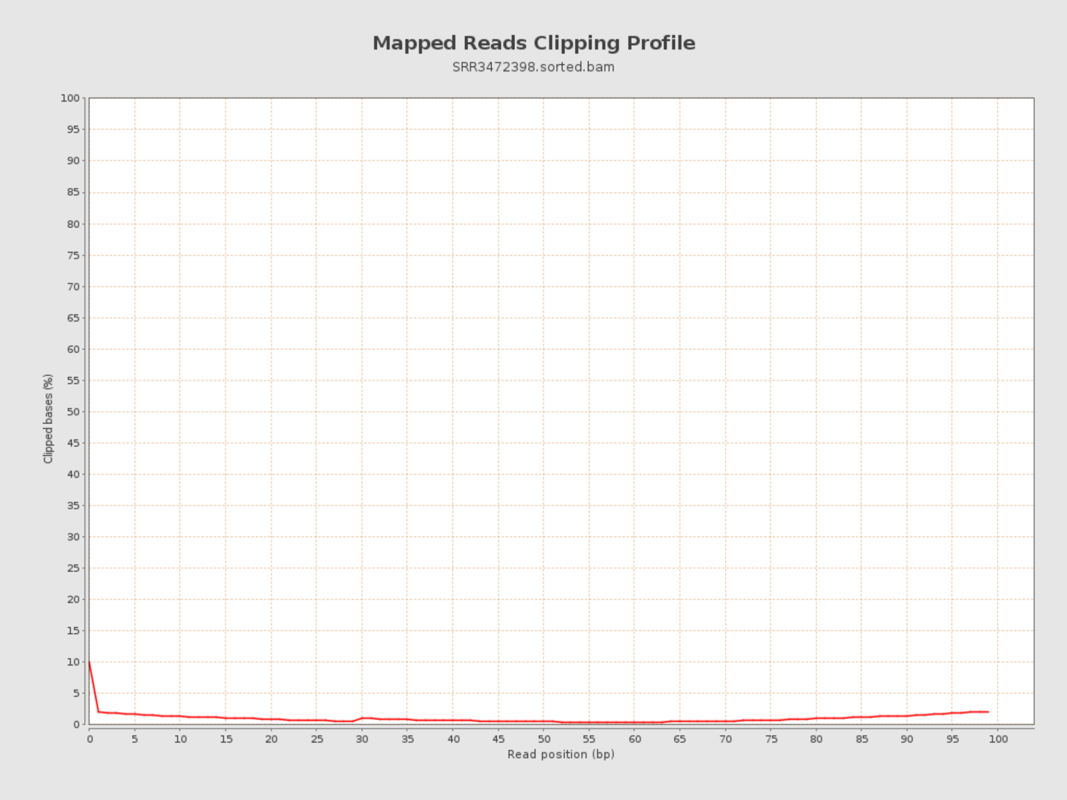
8. Results : Mapped Reads Nucleotide Content



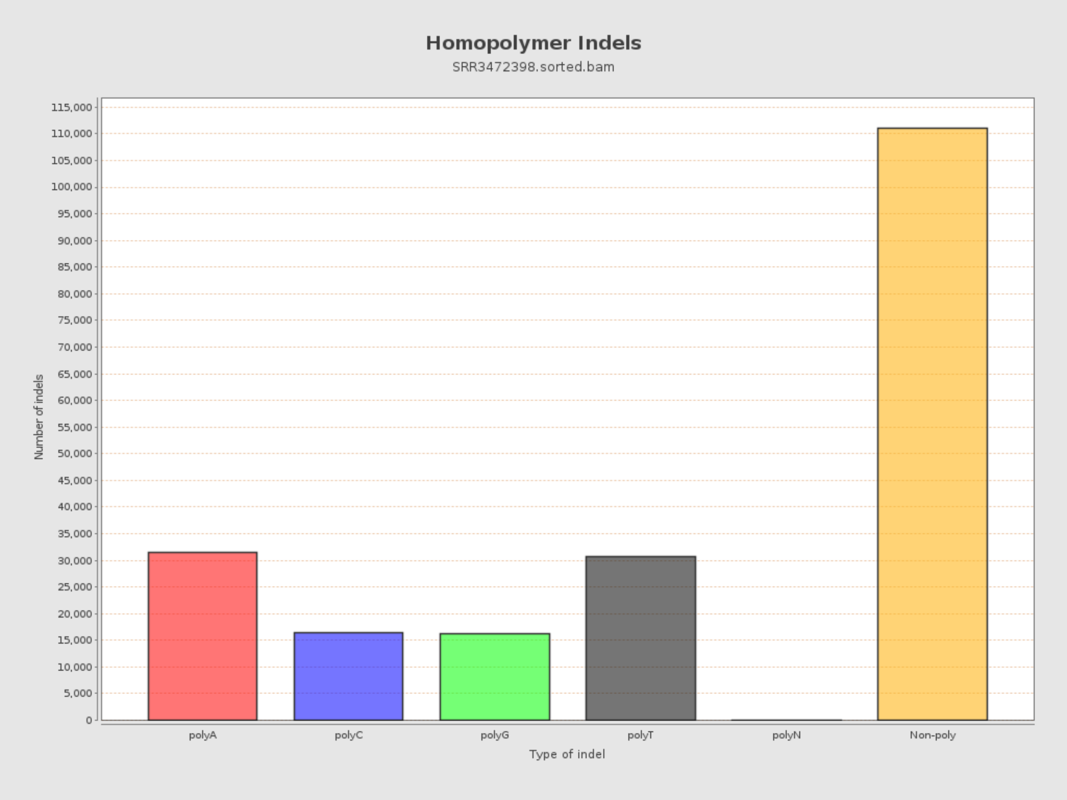
9. Results : Mapped Reads GC-content Distribution



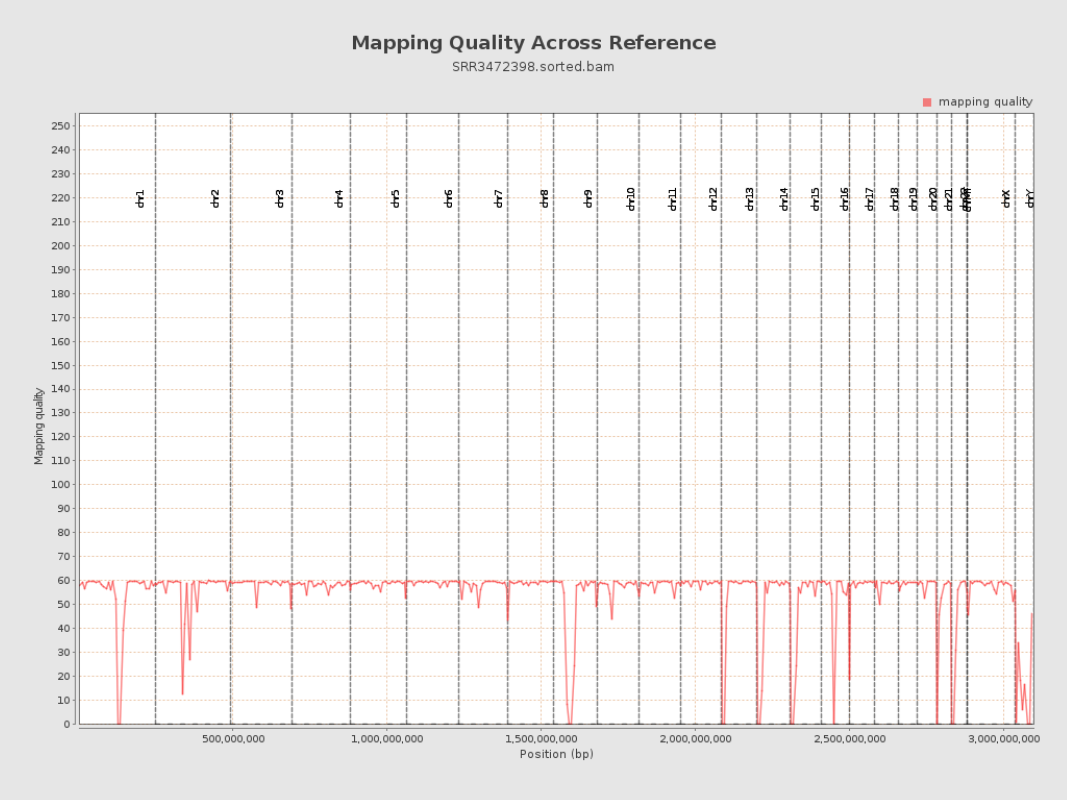
10. Results : Mapped Reads Clipping Profile



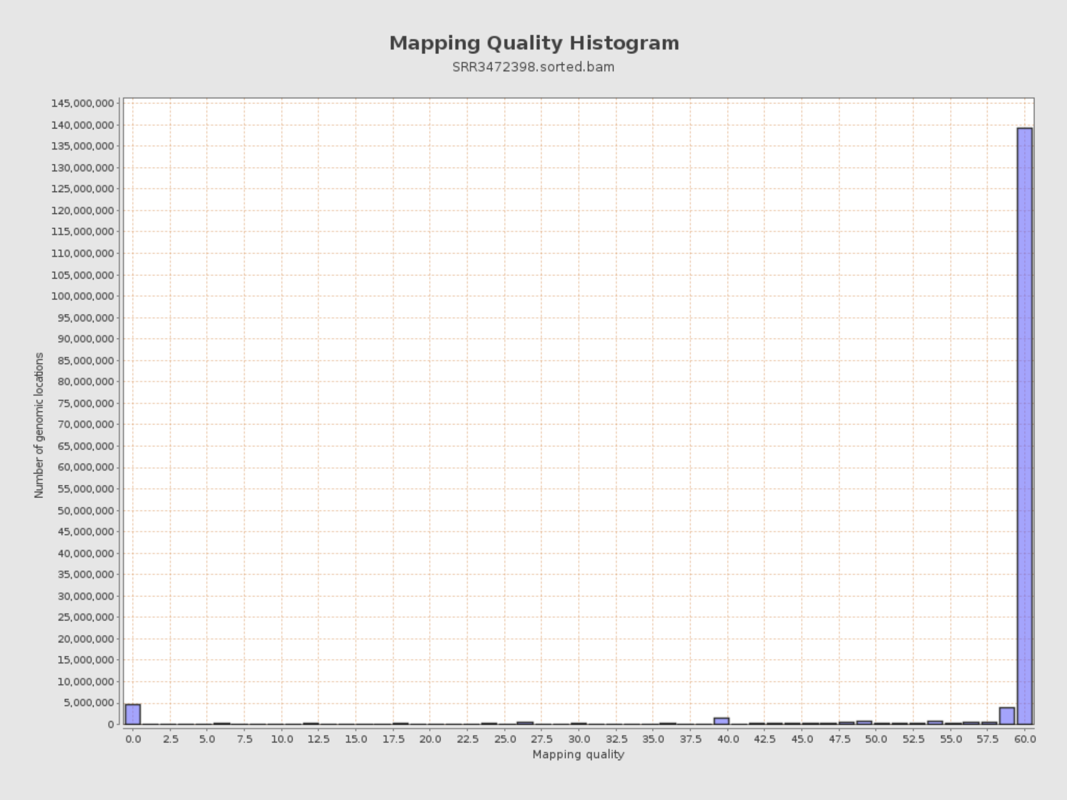
11. Results : Homopolymer Indels



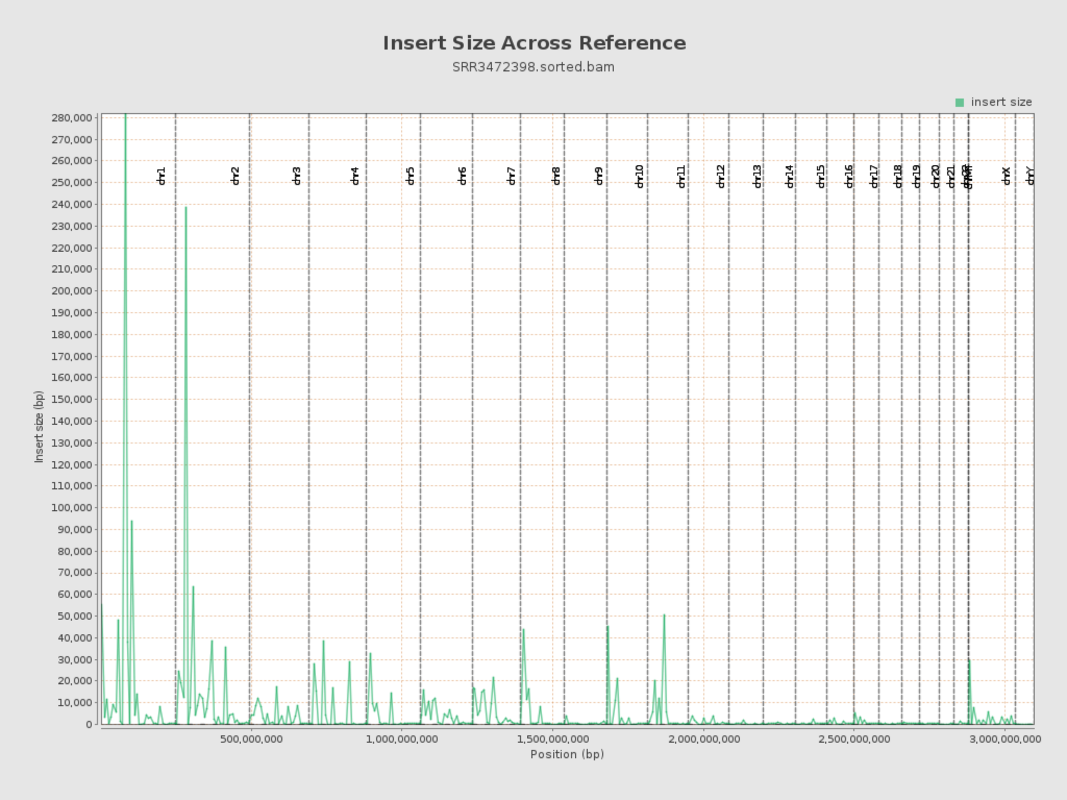
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram