Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:41:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006072.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_SRR1006072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006072_1.fastq.gz SRR1006072_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:41:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,395,092
Mapped reads	5,572,875 / 87.14%
Unmapped reads	822,217 / 12.86%
Mapped paired reads	5,572,875 / 87.14%
Mapped reads, first in pair	2,832,042 / 44.28%
Mapped reads, second in pair	2,740,833 / 42.86%
Mapped reads, both in pair	5,075,706 / 79.37%
Mapped reads, singletons	497,169 / 7.77%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	241,532 / 3.78%
Duplication rate	3.89%
Clipped reads	444,756 / 6.95%

2.2. ACGT Content

Number/percentage of A's	57,546,027 / 26.75%
Number/percentage of C's	47,651,108 / 22.15%
Number/percentage of T's	59,352,209 / 27.59%
Number/percentage of G's	50,601,087 / 23.52%
Number/percentage of N's	8,736 / 0%
GC Percentage	45.66%

2.3. Coverage

Mean	0.0695
Standard Deviation	0.4038

2.4. Mapping Quality

Mean Mapping Quality	47.01

2.5. Insert size

Mean	66,671.69
Standard Deviation	2,579,167.05
P25/Median/P75	74 / 105 / 137

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	1,017,006
Insertions	7,176
Mapped reads with at least one insertion	0.13%
Deletions	19,683
Mapped reads with at least one deletion	0.35%
Homopolymer indels	45.53%

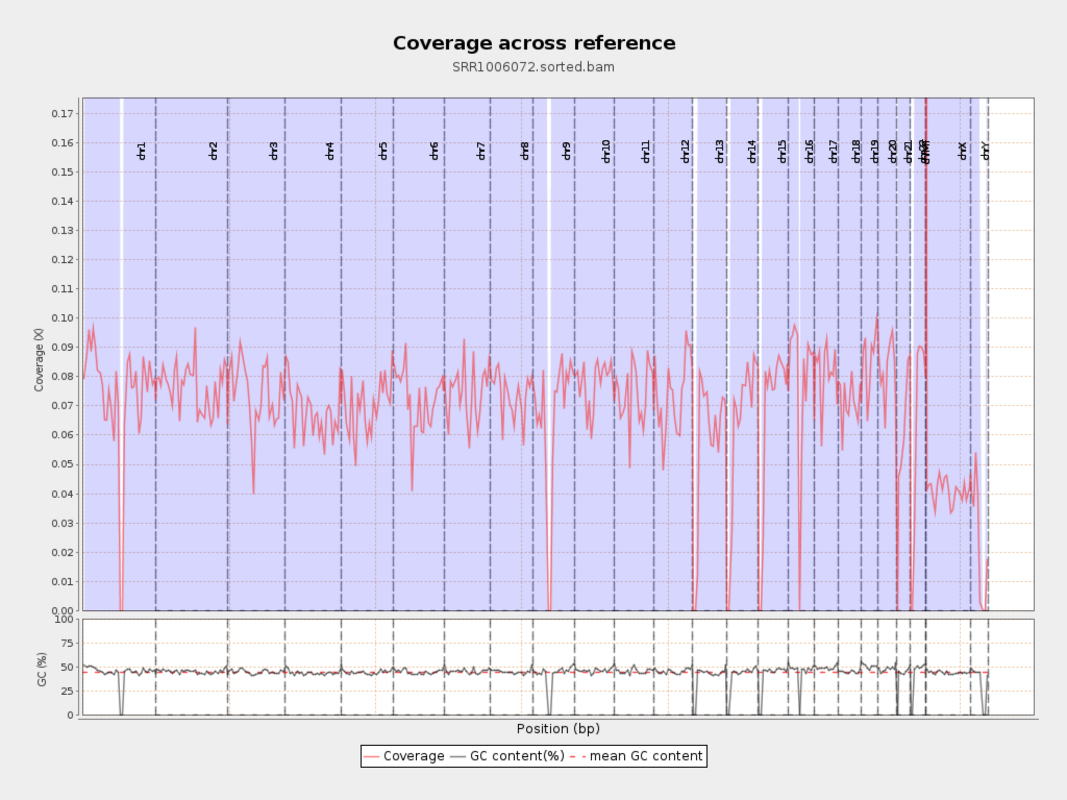
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

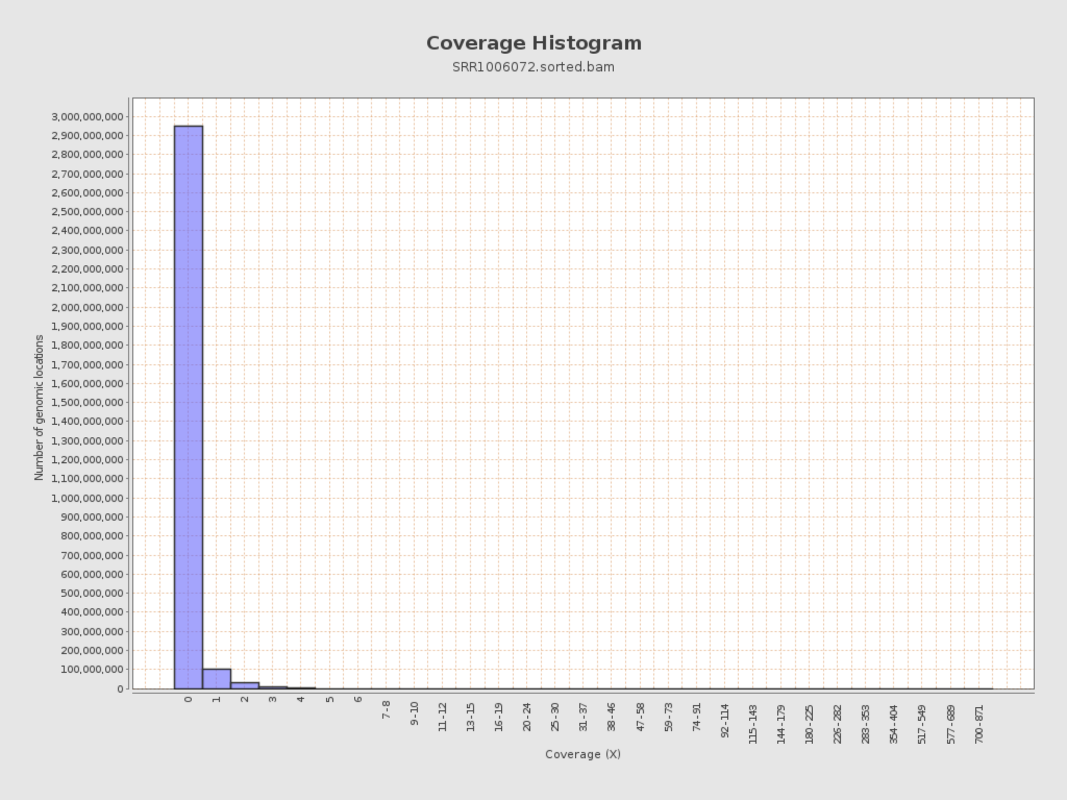
chr1	249250621	18292206	0.0734	0.4206
chr2	243199373	18603157	0.0765	0.4428
chr3	198022430	14634861	0.0739	0.3689
chr4	191154276	13033119	0.0682	0.3661
chr5	180915260	12772577	0.0706	0.3589
chr6	171115067	12284145	0.0718	0.398
chr7	159138663	11875506	0.0746	0.5038
chr8	146364022	10782585	0.0737	0.4284
chr9	141213431	9198168	0.0651	0.3735
chr10	135534747	10522546	0.0776	0.3959
chr11	135006516	10015223	0.0742	0.5849
chr12	133851895	9932936	0.0742	0.3733
chr13	115169878	6580848	0.0571	0.3245
chr14	107349540	6716753	0.0626	0.3486
chr15	102531392	6691288	0.0653	0.3508
chr16	90354753	7034452	0.0779	0.4157
chr17	81195210	6680121	0.0823	0.4292
chr18	78077248	5550093	0.0711	0.4482
chr19	59128983	5059465	0.0856	0.4819
chr20	63025520	5216842	0.0828	0.4011
chr21	48129895	2848954	0.0592	0.3612
chr22	51304566	3112978	0.0607	0.3671
chrMT	16571	21160	1.2769	1.8029
chrX	155270560	6358982	0.041	0.2811

chrY	59373566	1365566	0.023	0.2285

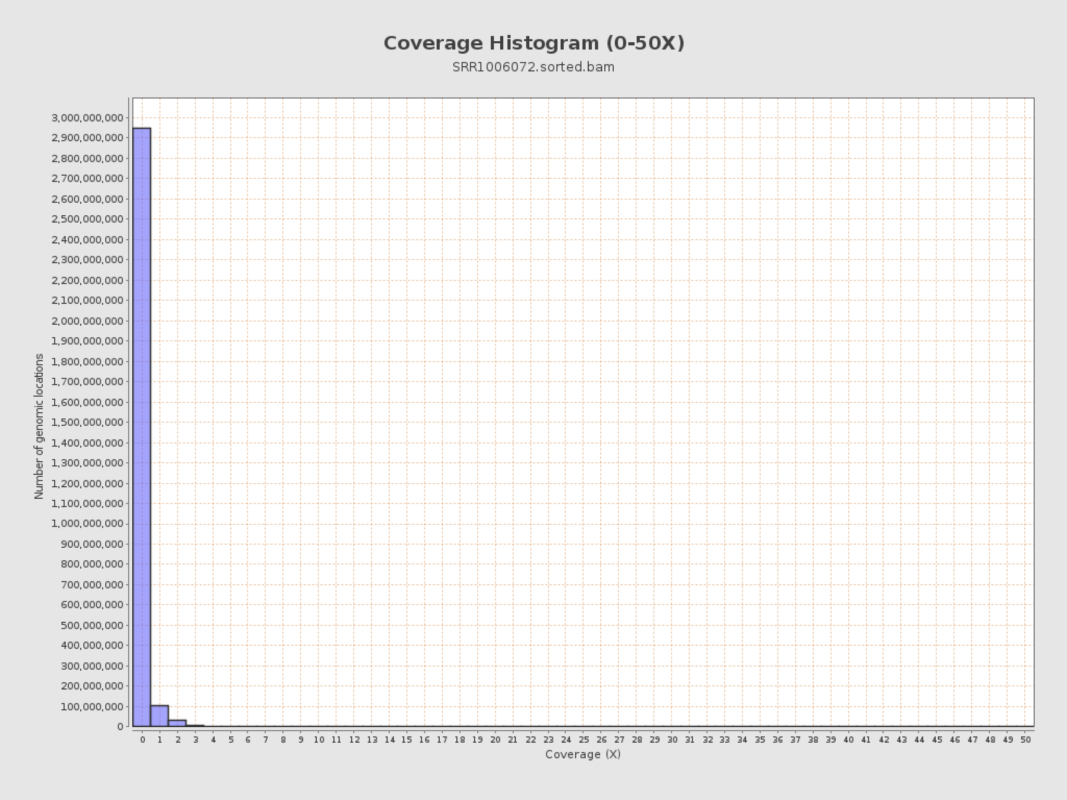
3. Results : Coverage across reference



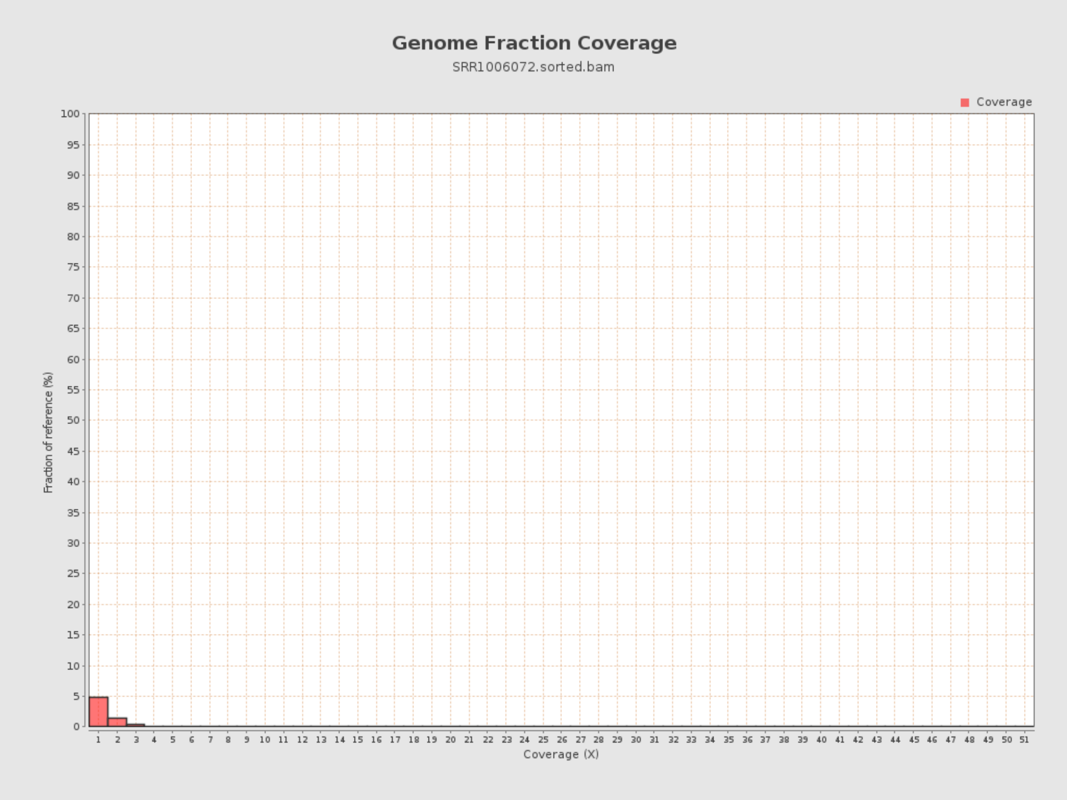
4. Results : Coverage Histogram



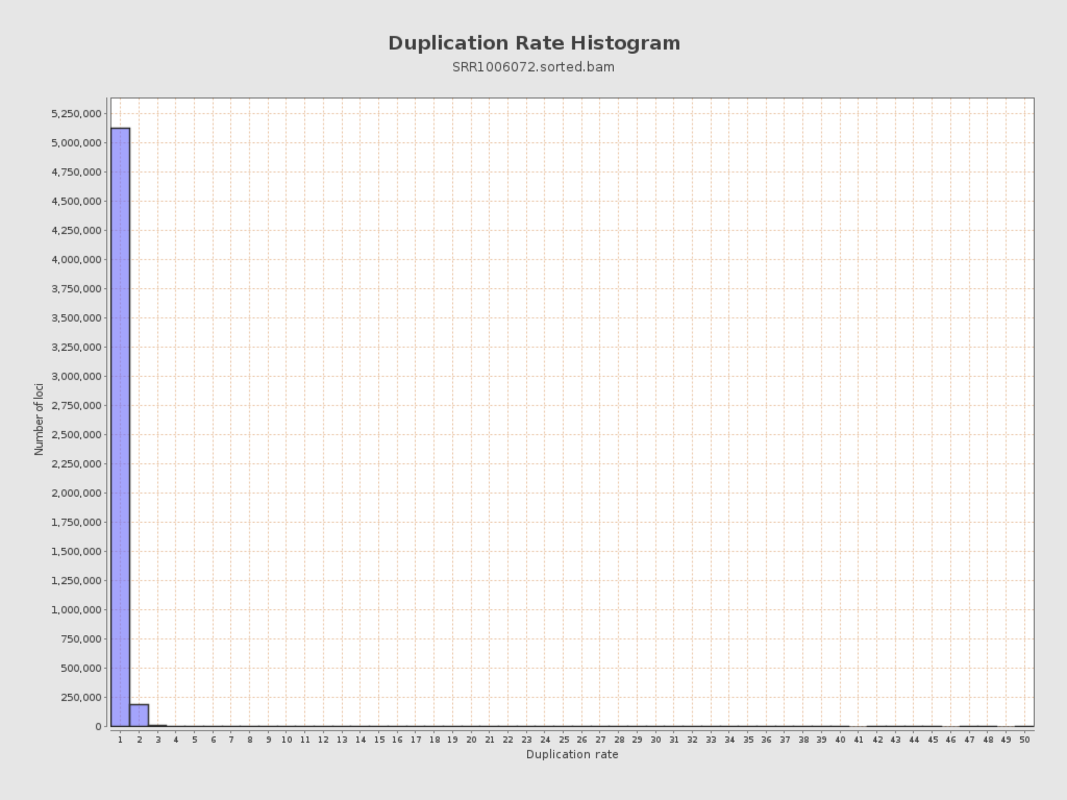
5. Results : Coverage Histogram (0-50X)



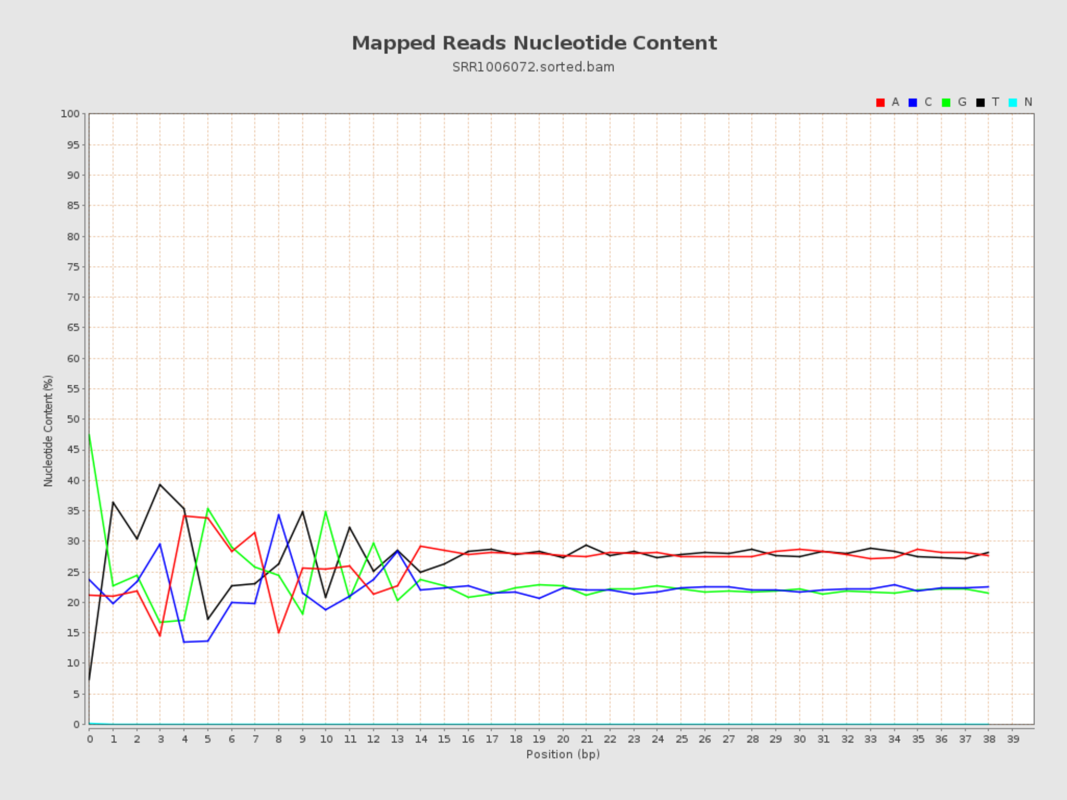
6. Results : Genome Fraction Coverage



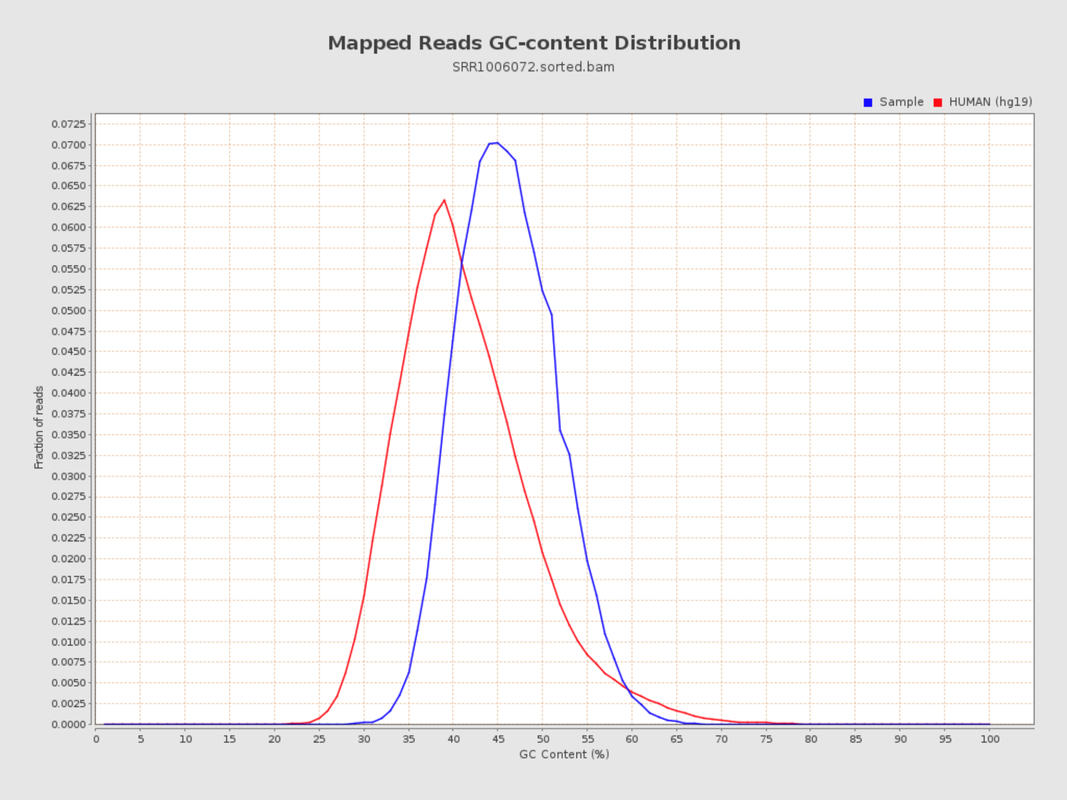
7. Results : Duplication Rate Histogram



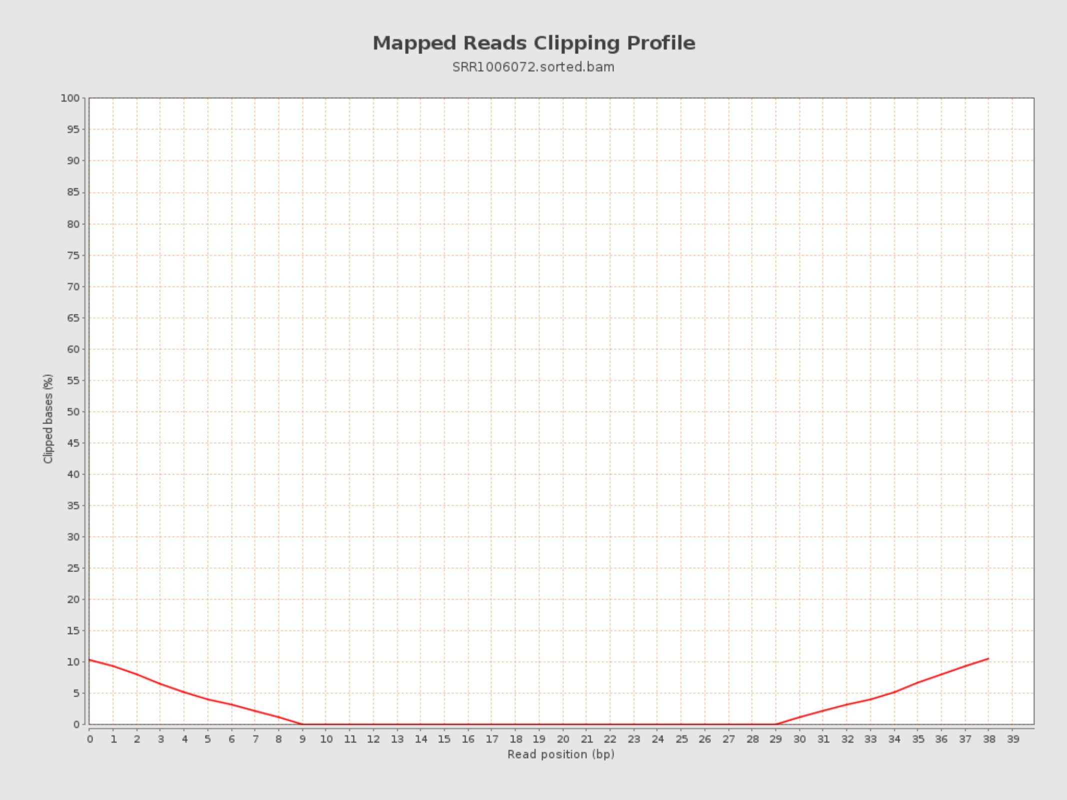
8. Results : Mapped Reads Nucleotide Content



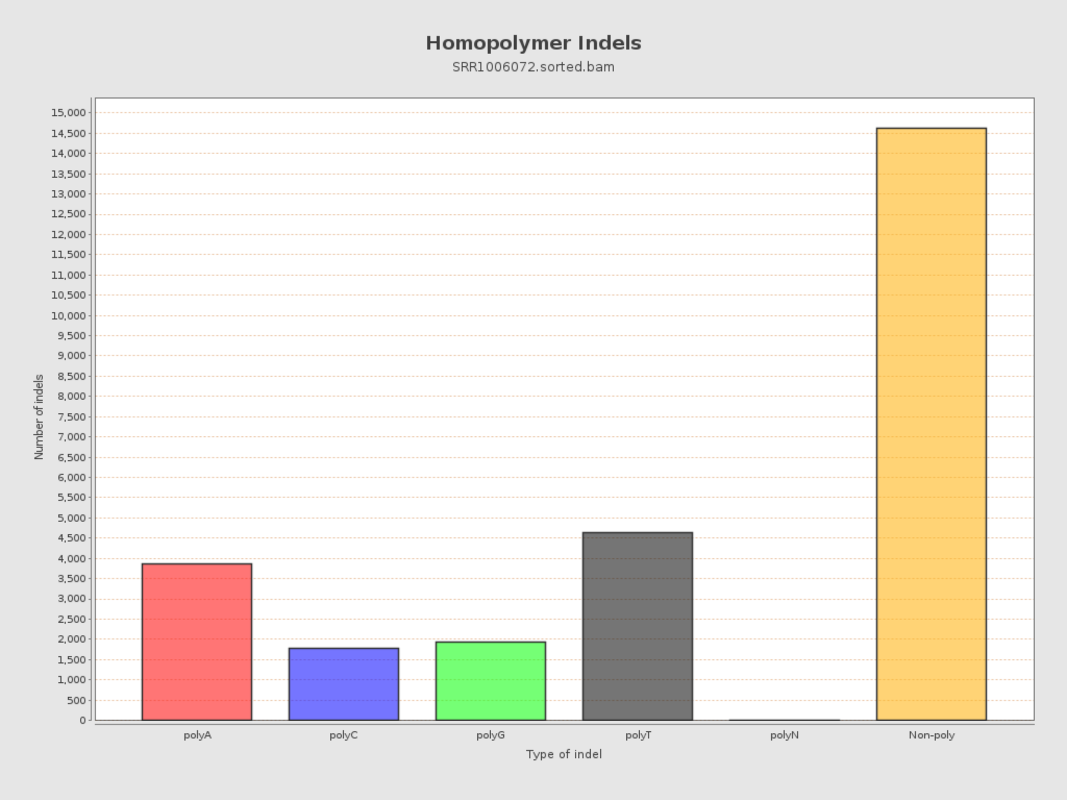
9. Results : Mapped Reads GC-content Distribution



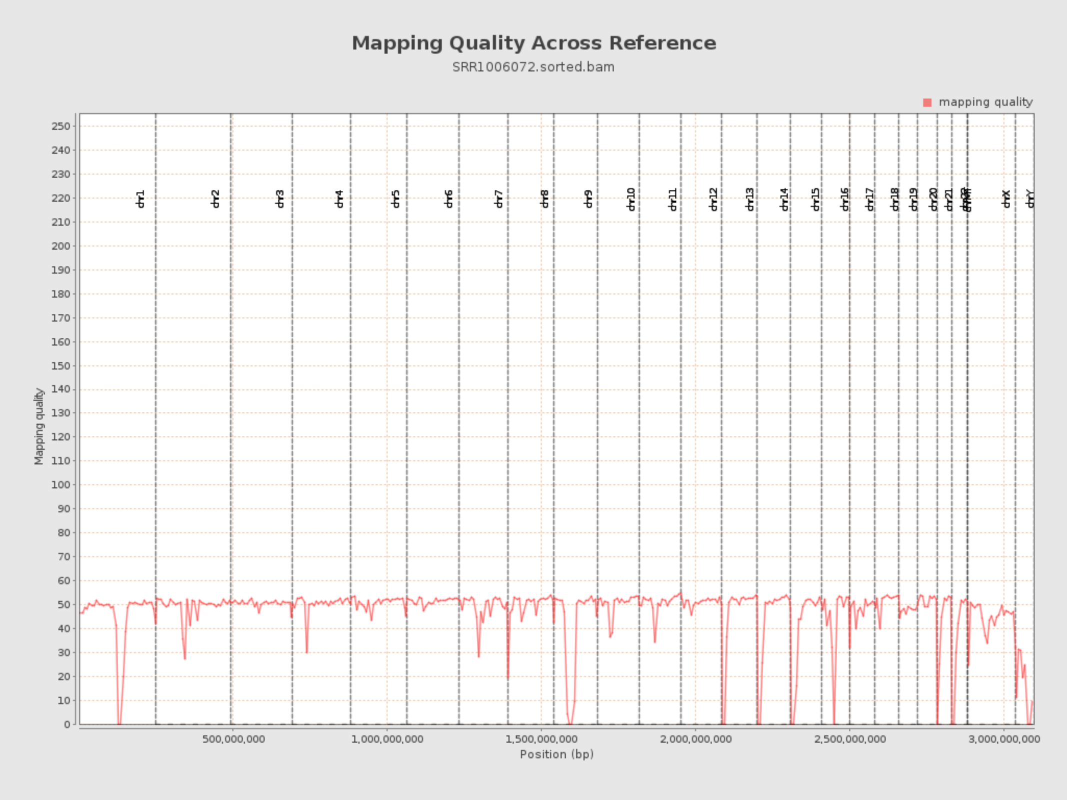
10. Results : Mapped Reads Clipping Profile



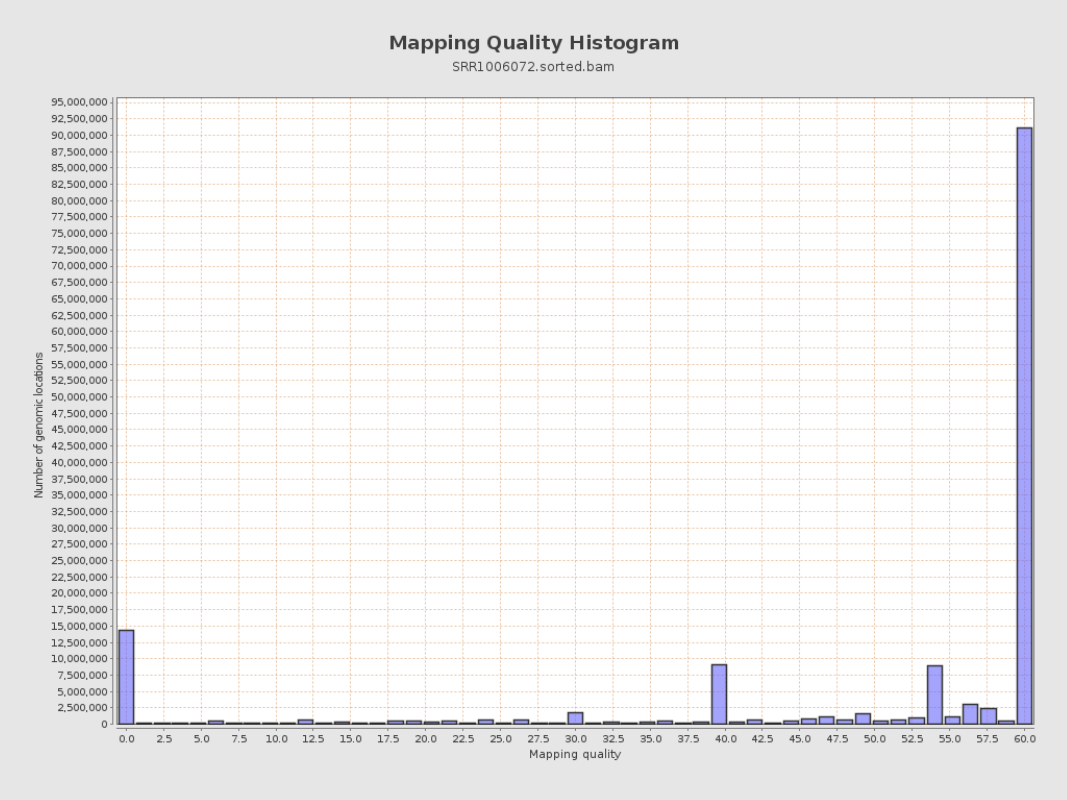
11. Results : Homopolymer Indels



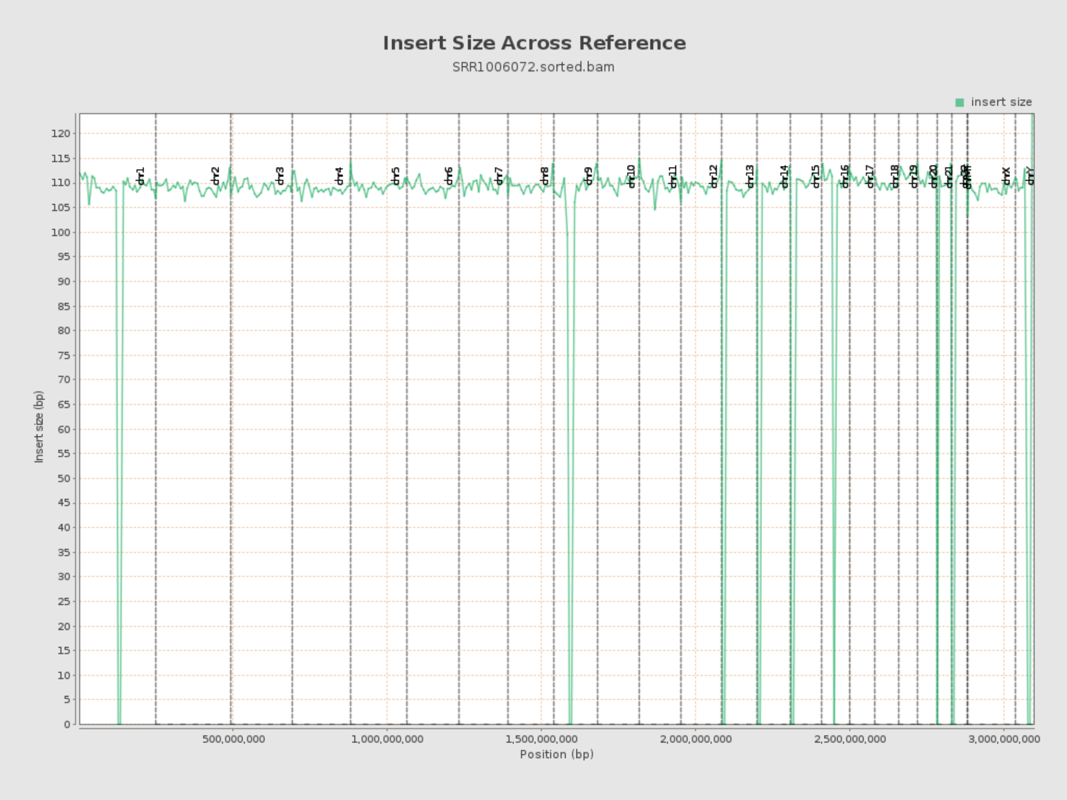
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram