Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 19:00:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006094.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_SRR1006094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006094_1.fastq.gz SRR1006094_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 19:00:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,136,998
Mapped reads	4,555,689 / 88.68%
Unmapped reads	581,309 / 11.32%
Mapped paired reads	4,555,689 / 88.68%
Mapped reads, first in pair	2,299,273 / 44.76%
Mapped reads, second in pair	2,256,416 / 43.92%
Mapped reads, both in pair	4,244,370 / 82.62%
Mapped reads, singletons	311,319 / 6.06%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	152,723 / 2.97%
Duplication rate	2.98%
Clipped reads	338,147 / 6.58%

2.2. ACGT Content

Number/percentage of A's	46,921,169 / 26.65%
Number/percentage of C's	39,613,724 / 22.5%
Number/percentage of T's	48,170,381 / 27.36%
Number/percentage of G's	41,359,899 / 23.49%
Number/percentage of N's	7,460 / 0%
GC Percentage	45.99%

2.3. Coverage

Mean	0.0569
Standard Deviation	0.3326

2.4. Mapping Quality

Mean Mapping Quality	47.11

2.5. Insert size

Mean	54,607.72
Standard Deviation	2,254,097.99
P25/Median/P75	67 / 94 / 128

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	803,014
Insertions	5,594
Mapped reads with at least one insertion	0.12%
Deletions	14,539
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.64%

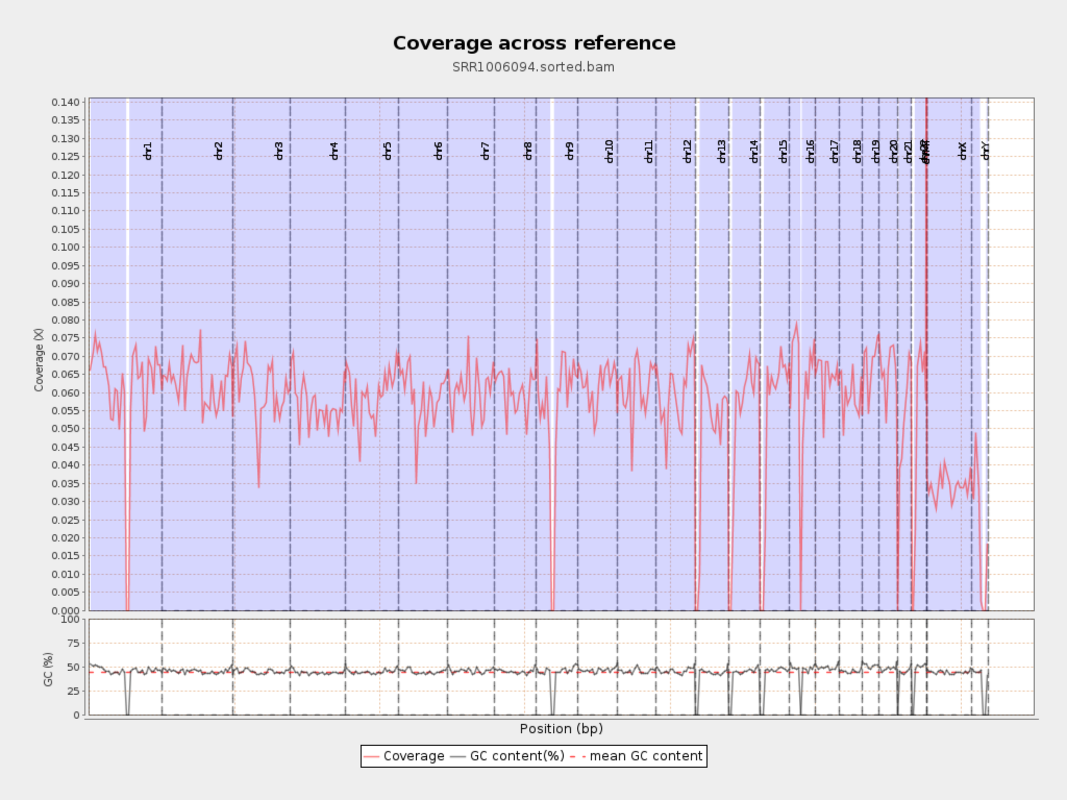
2.7. Chromosome stats

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

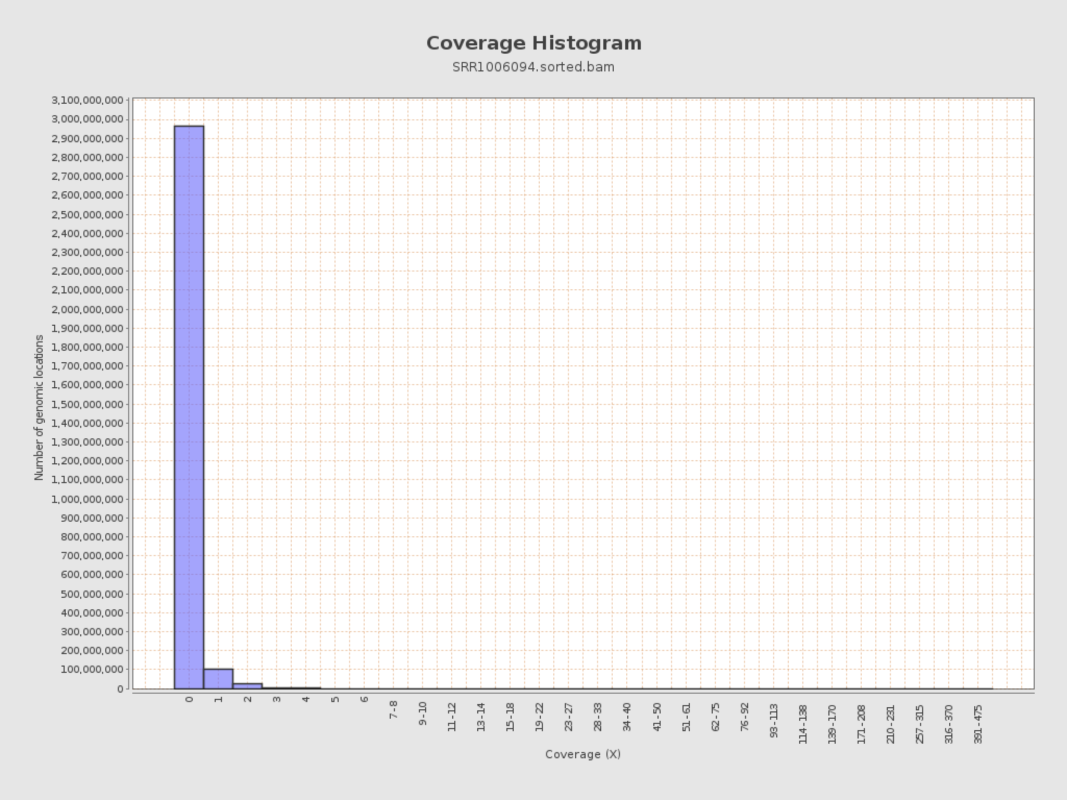
chr1	249250621	15032892	0.0603	0.3636
chr2	243199373	15361175	0.0632	0.3688
chr3	198022430	11989346	0.0605	0.3081
chr4	191154276	10807479	0.0565	0.3106
chr5	180915260	10680972	0.059	0.3054
chr6	171115067	10103347	0.059	0.3189
chr7	159138663	9541916	0.06	0.3967
chr8	146364022	8826004	0.0603	0.3575
chr9	141213431	7550264	0.0535	0.3149
chr10	135534747	8445253	0.0623	0.3294
chr11	135006516	8271987	0.0613	0.4002
chr12	133851895	8043688	0.0601	0.3094
chr13	115169878	5476275	0.0475	0.2744
chr14	107349540	5572130	0.0519	0.294
chr15	102531392	5402517	0.0527	0.2917
chr16	90354753	5606479	0.062	0.3594
chr17	81195210	5236631	0.0645	0.3392
chr18	78077248	4609249	0.059	0.3897
chr19	59128983	3994715	0.0676	0.3991
chr20	63025520	4172087	0.0662	0.3315
chr21	48129895	2383288	0.0495	0.3141
chr22	51304566	2440449	0.0476	0.3244
chrMT	16571	5812	0.3507	0.8861
chrX	155270560	5332222	0.0343	0.2402

chrY	59373566	1205161	0.0203	0.2154

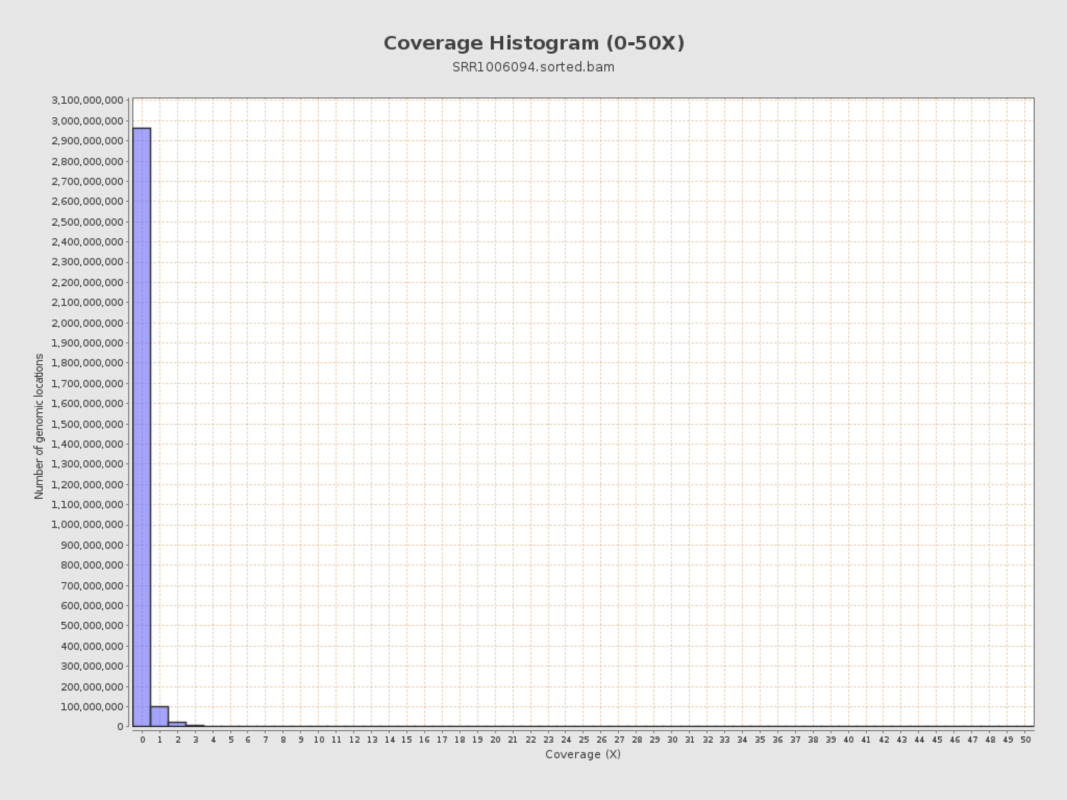
3. Results : Coverage across reference



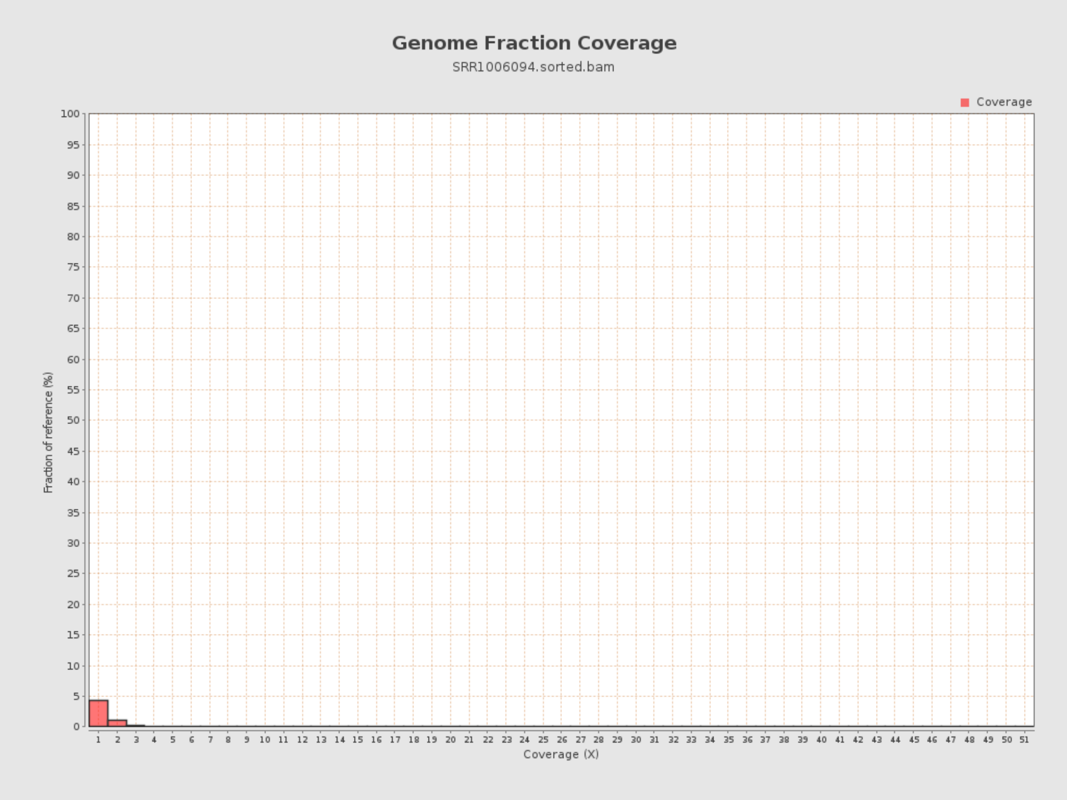
4. Results : Coverage Histogram



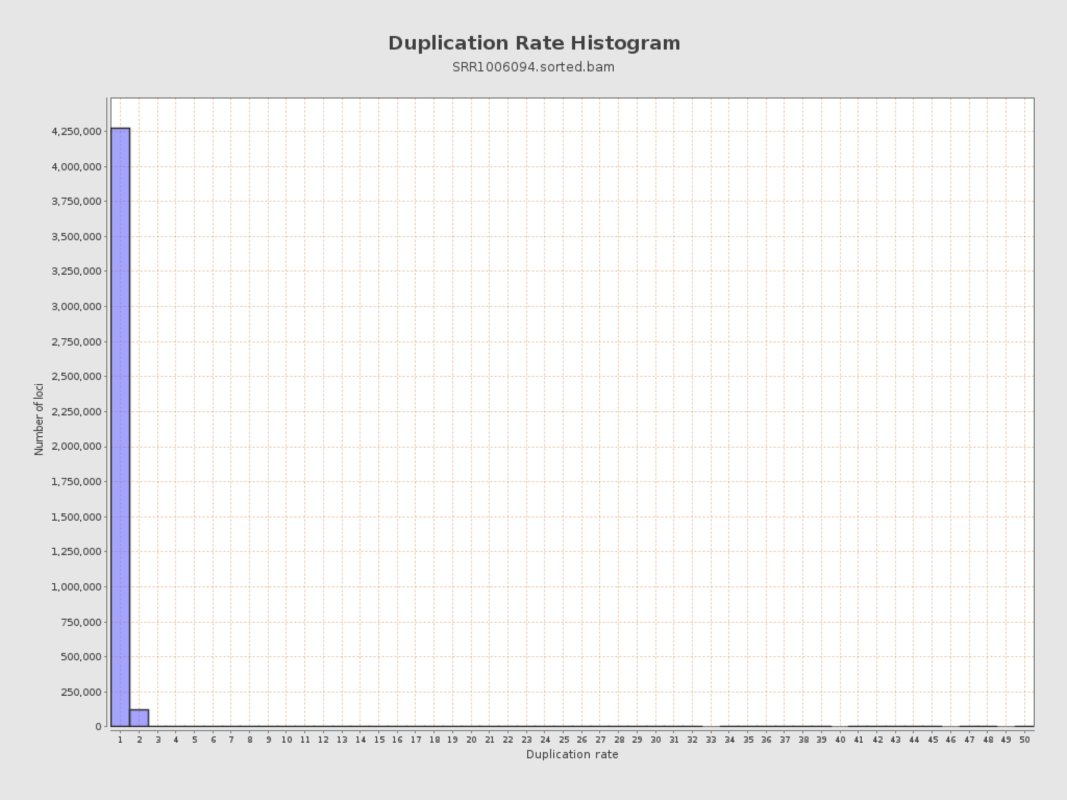
5. Results : Coverage Histogram (0-50X)



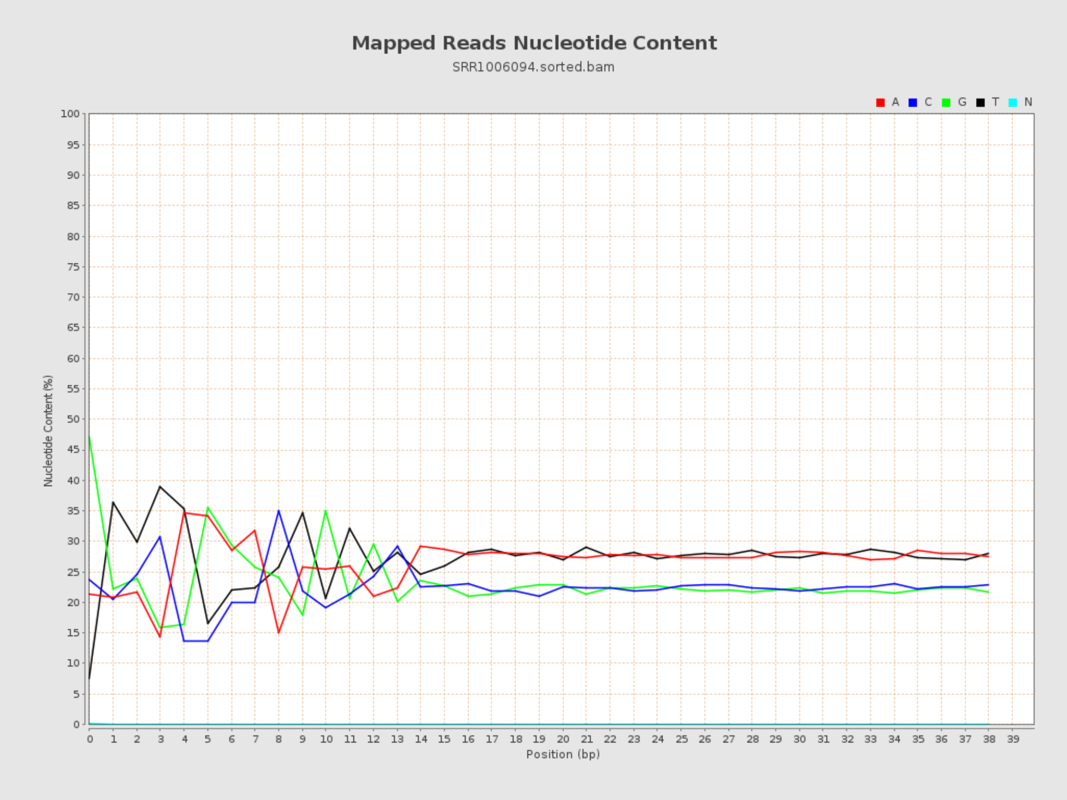
6. Results : Genome Fraction Coverage



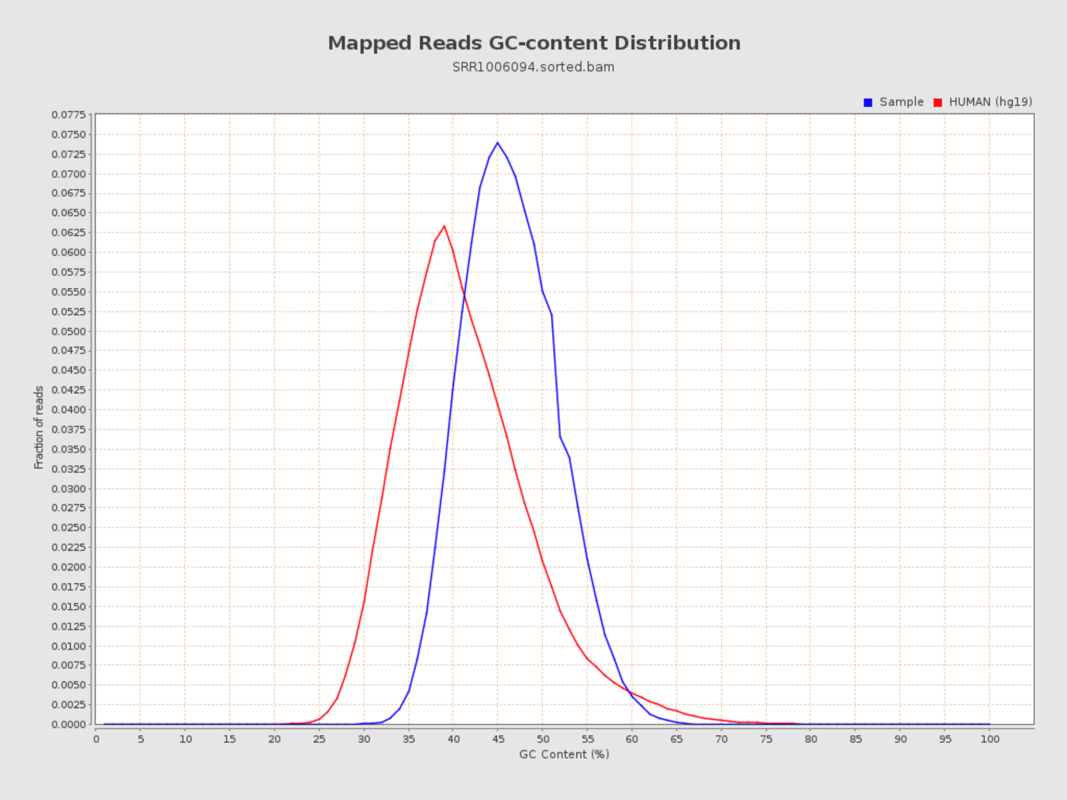
7. Results : Duplication Rate Histogram



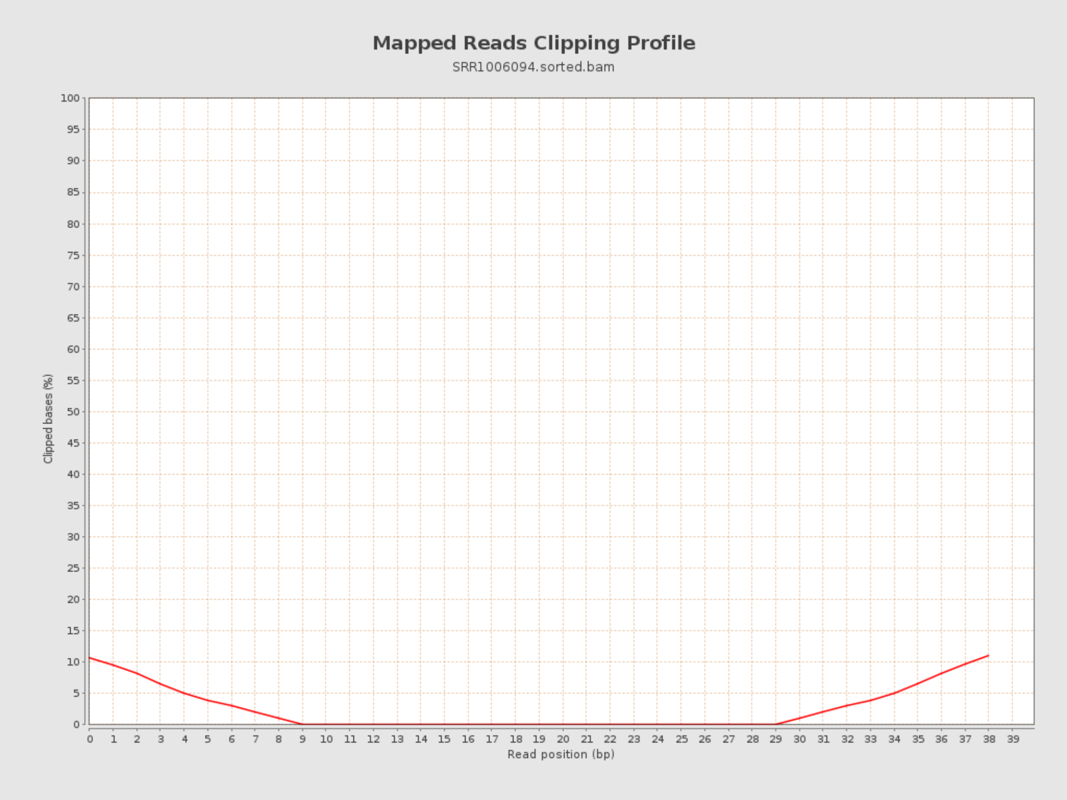
8. Results : Mapped Reads Nucleotide Content



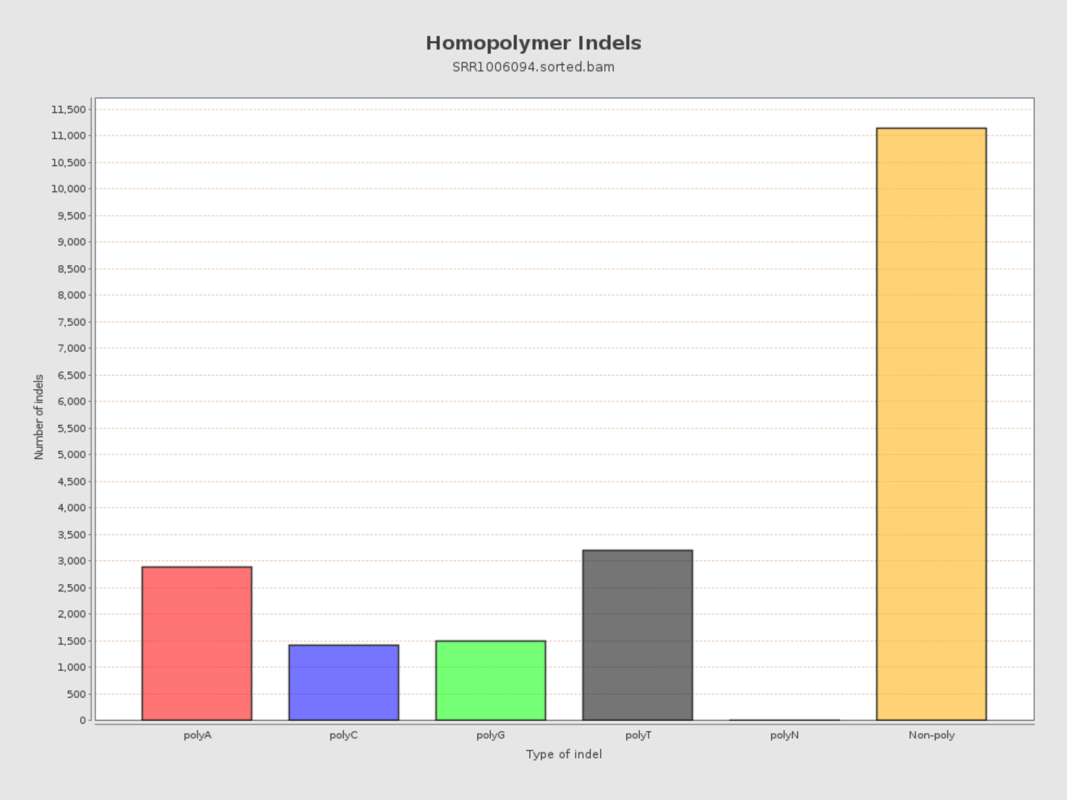
9. Results : Mapped Reads GC-content Distribution



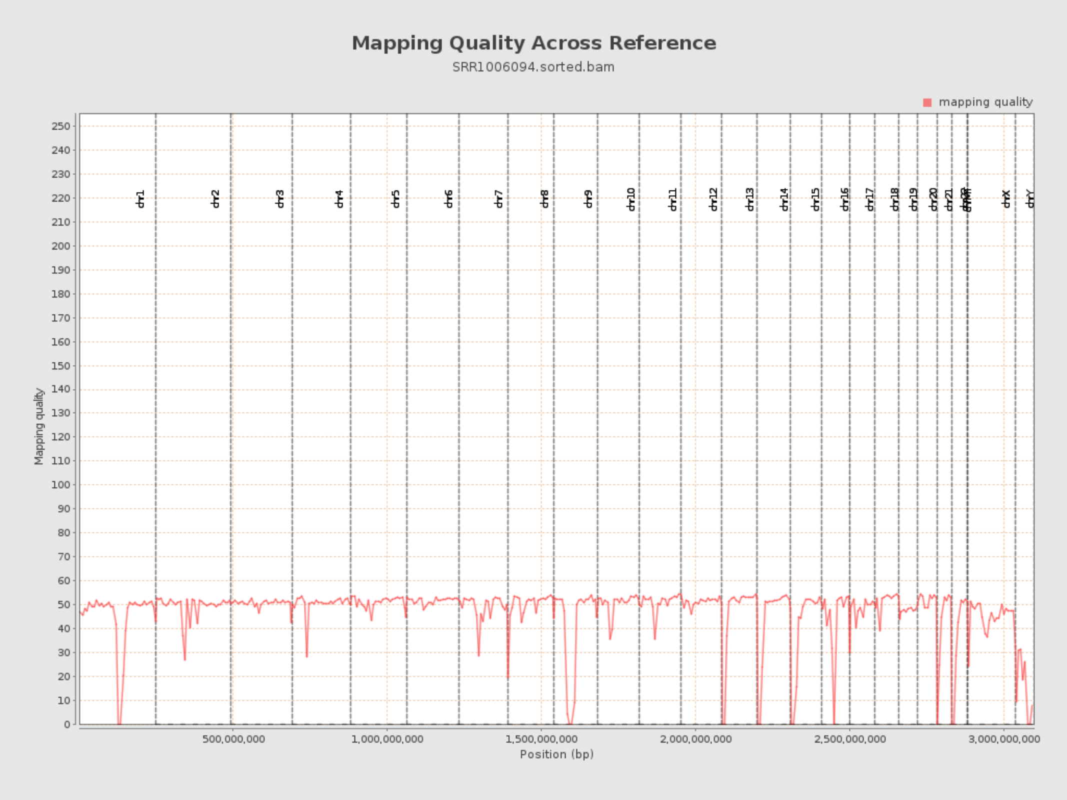
10. Results : Mapped Reads Clipping Profile



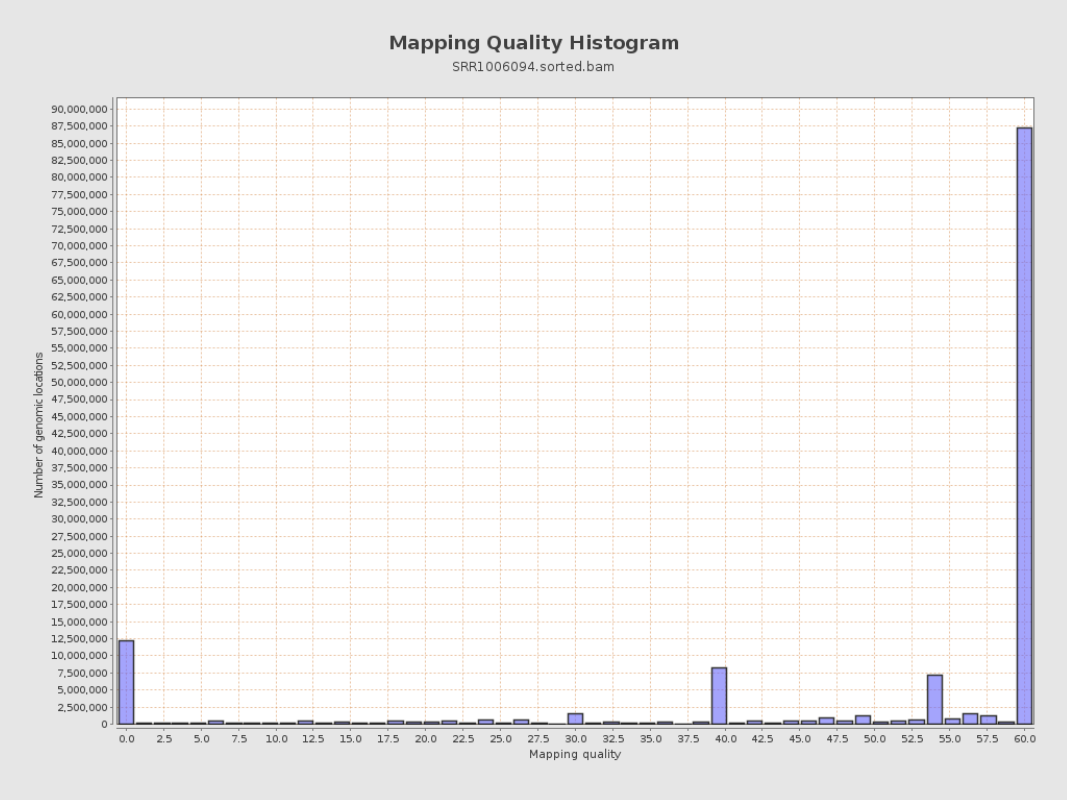
11. Results : Homopolymer Indels



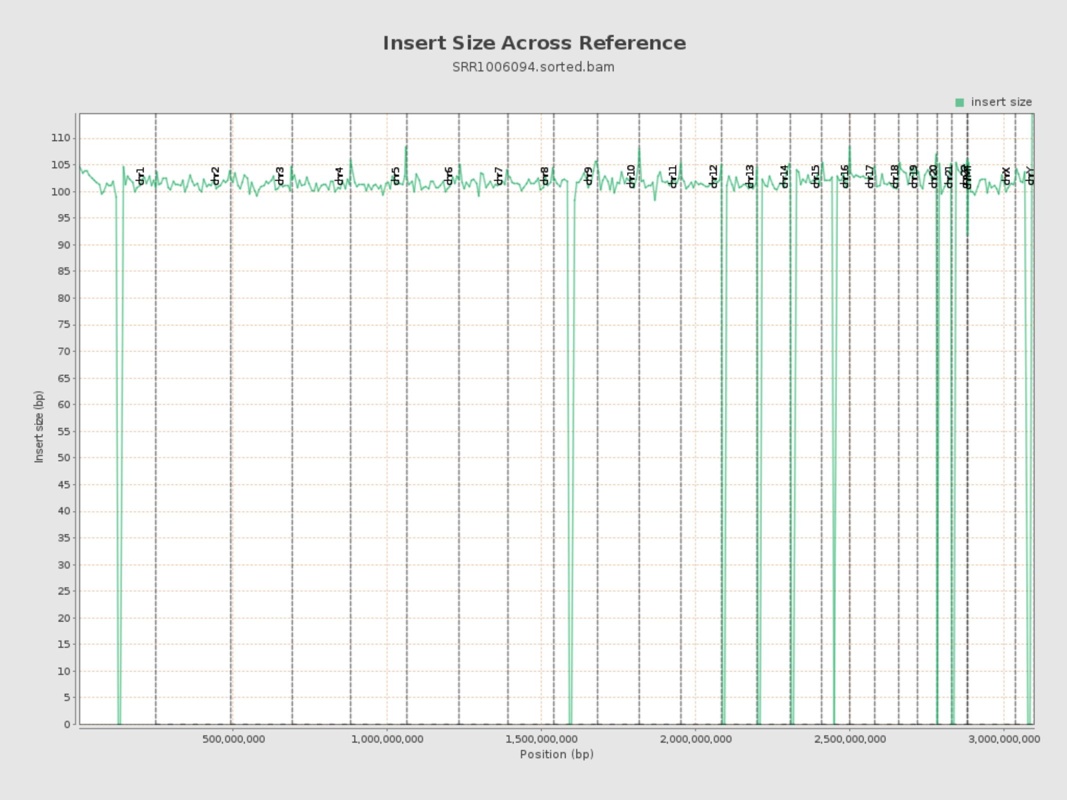
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram