Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 14:57:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006030.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_SRR1006030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006030_1.fastq.gz SRR1006030_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 14:57:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,914,010
Mapped reads	4,236,384 / 61.27%
Unmapped reads	2,677,626 / 38.73%
Mapped paired reads	4,236,384 / 61.27%
Mapped reads, first in pair	2,167,639 / 31.35%
Mapped reads, second in pair	2,068,745 / 29.92%
Mapped reads, both in pair	3,605,358 / 52.15%
Mapped reads, singletons	631,026 / 9.13%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	116,431 / 1.68%
Duplication rate	2.2%
Clipped reads	433,586 / 6.27%

2.2. ACGT Content

Number/percentage of A's	48,518,917 / 29.72%
Number/percentage of C's	33,424,539 / 20.47%
Number/percentage of T's	47,485,358 / 29.09%
Number/percentage of G's	33,773,106 / 20.69%
Number/percentage of N's	59,443 / 0.04%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0527
Standard Deviation	0.3652

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Insert size

Mean	74,958.25
Standard Deviation	2,641,037.1
P25/Median/P75	67 / 97 / 141

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	1,352,673
Insertions	5,207
Mapped reads with at least one insertion	0.12%
Deletions	14,159
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.89%

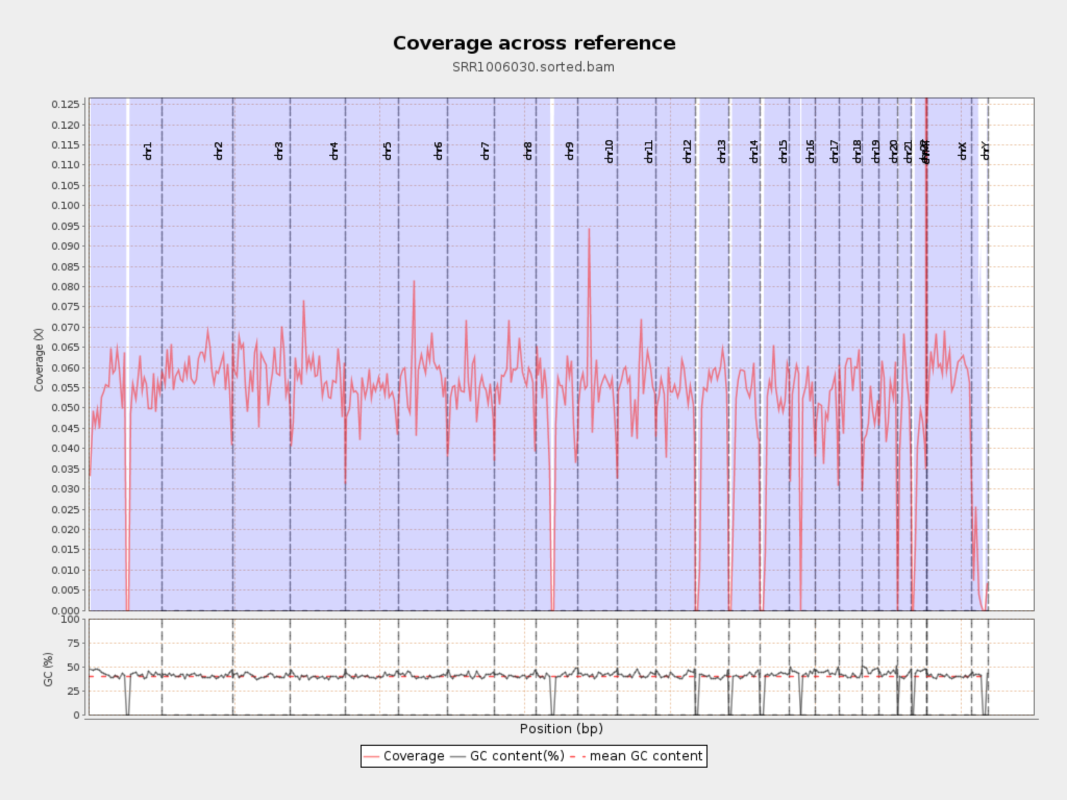
2.7. Chromosome stats

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

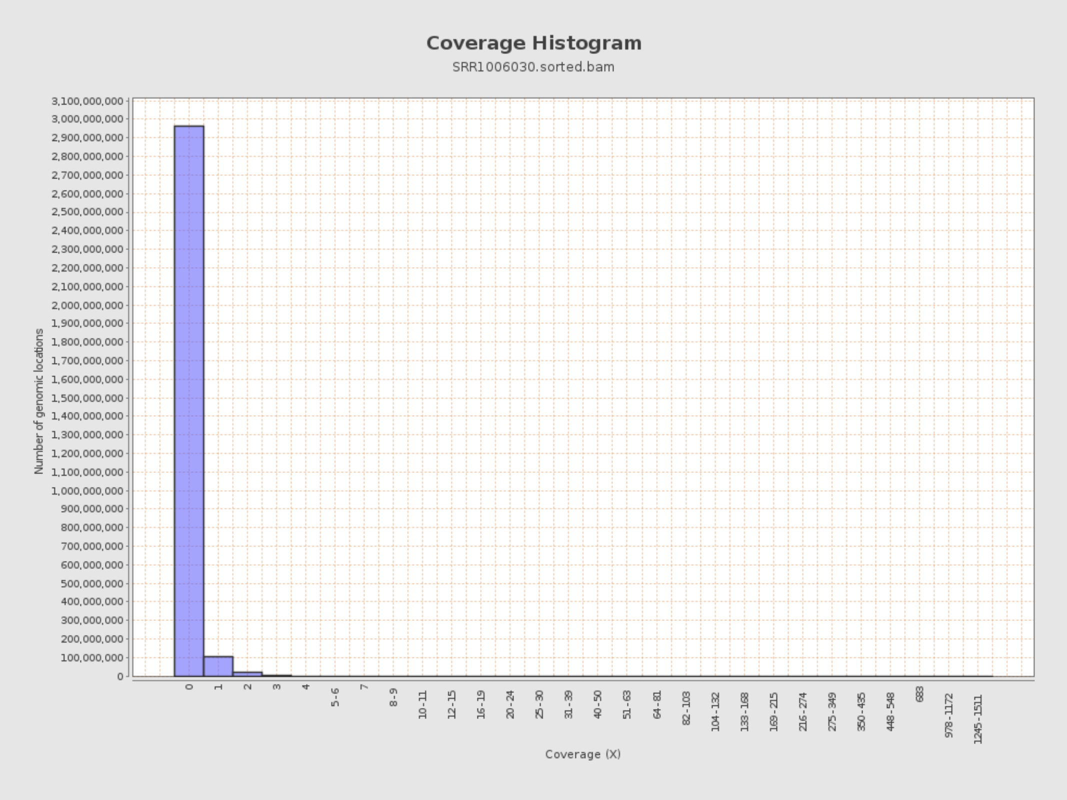
chr1	249250621	12662118	0.0508	0.4803
chr2	243199373	14446052	0.0594	0.3368
chr3	198022430	11763121	0.0594	0.2903
chr4	191154276	11030113	0.0577	0.311
chr5	180915260	9643044	0.0533	0.2743
chr6	171115067	10082997	0.0589	0.3633
chr7	159138663	8733445	0.0549	0.3823
chr8	146364022	8460740	0.0578	0.7861
chr9	141213431	6709225	0.0475	0.2885
chr10	135534747	7680069	0.0567	0.4068
chr11	135006516	7550718	0.0559	0.3069
chr12	133851895	7197260	0.0538	0.277
chr13	115169878	5491505	0.0477	0.2593
chr14	107349540	4850709	0.0452	0.263
chr15	102531392	4527183	0.0442	0.2493
chr16	90354753	4434178	0.0491	0.2984
chr17	81195210	3917976	0.0483	0.2676
chr18	78077248	4471808	0.0573	0.409
chr19	59128983	2772782	0.0469	0.3897
chr20	63025520	3296524	0.0523	0.2794
chr21	48129895	2235790	0.0465	0.2765
chr22	51304566	1567704	0.0306	0.2141
chrMT	16571	18900	1.1405	1.3579
chrX	155270560	9281980	0.0598	0.3095

chrY	59373566	453319	0.0076	0.1822

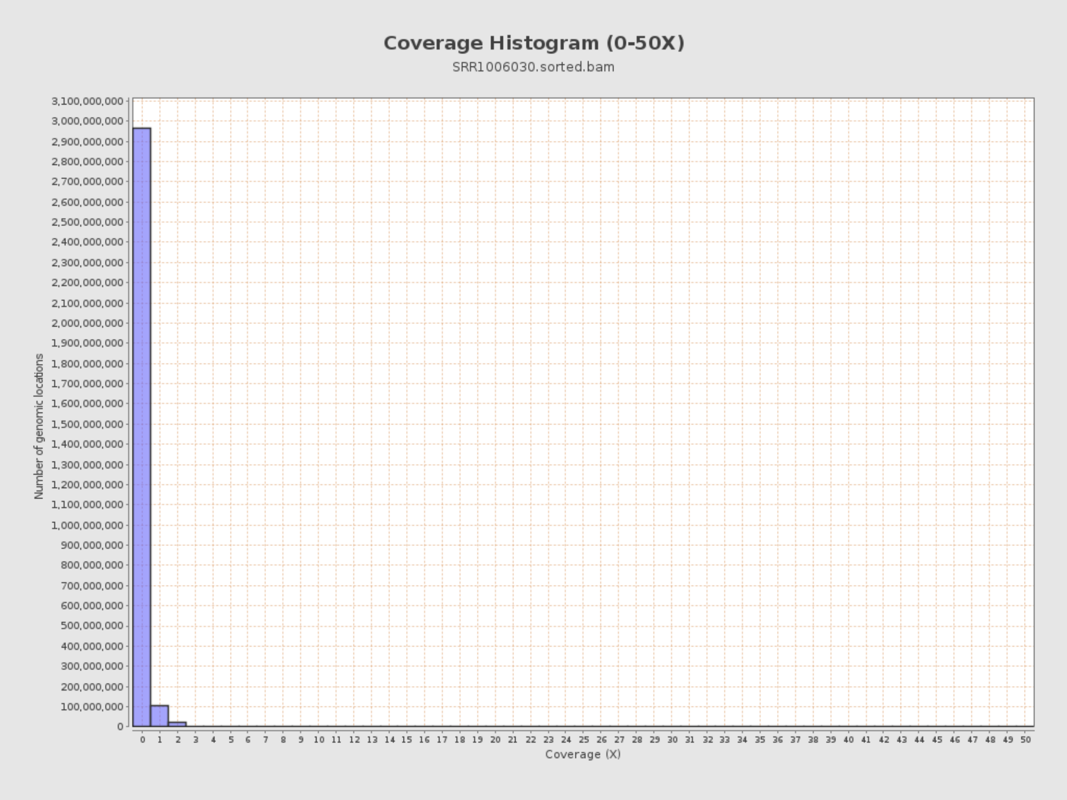
3. Results : Coverage across reference



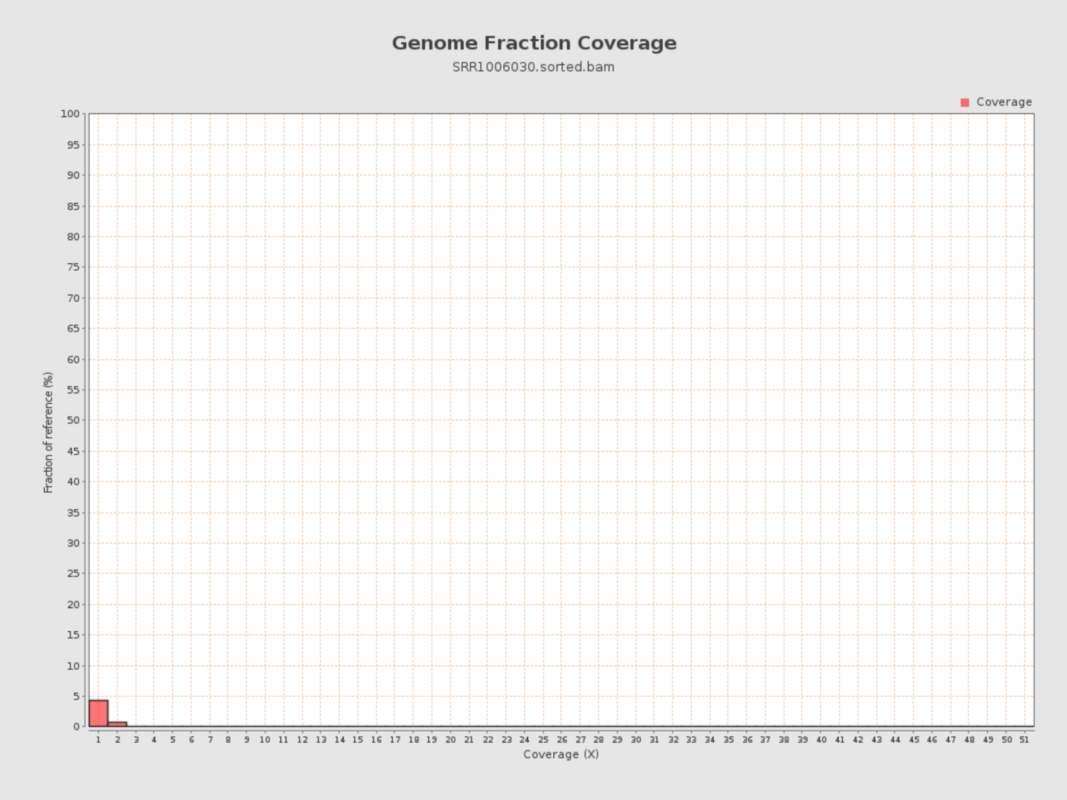
4. Results : Coverage Histogram



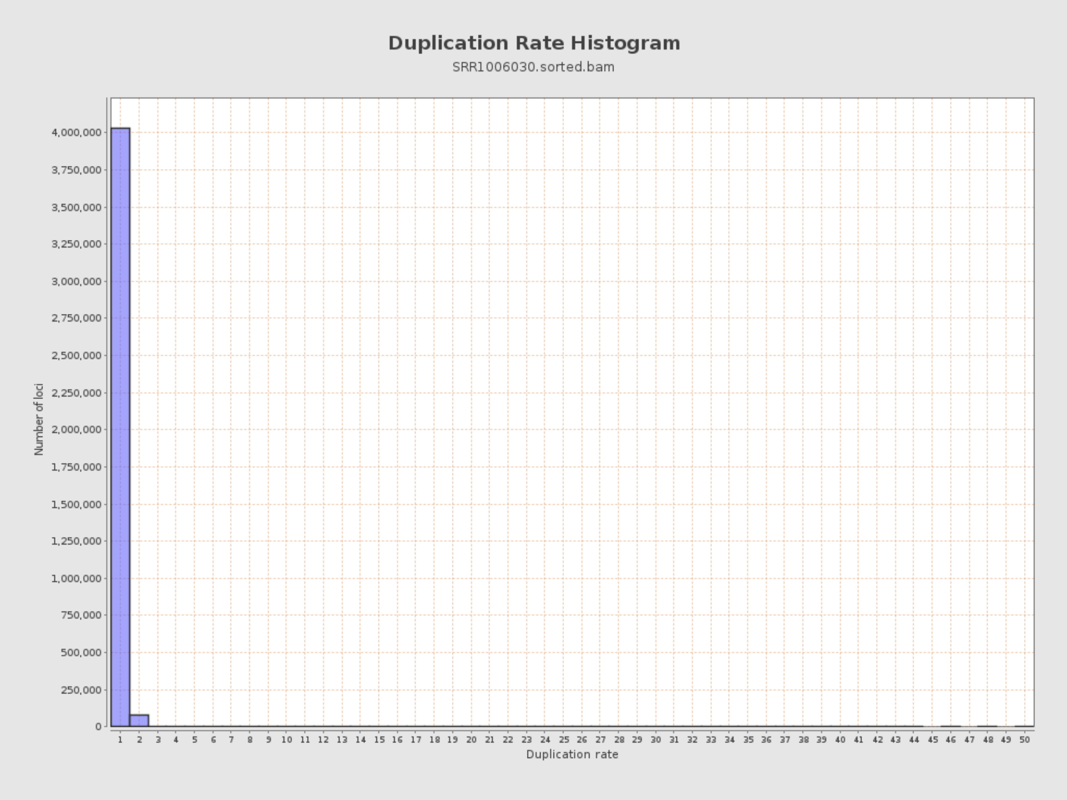
5. Results : Coverage Histogram (0-50X)



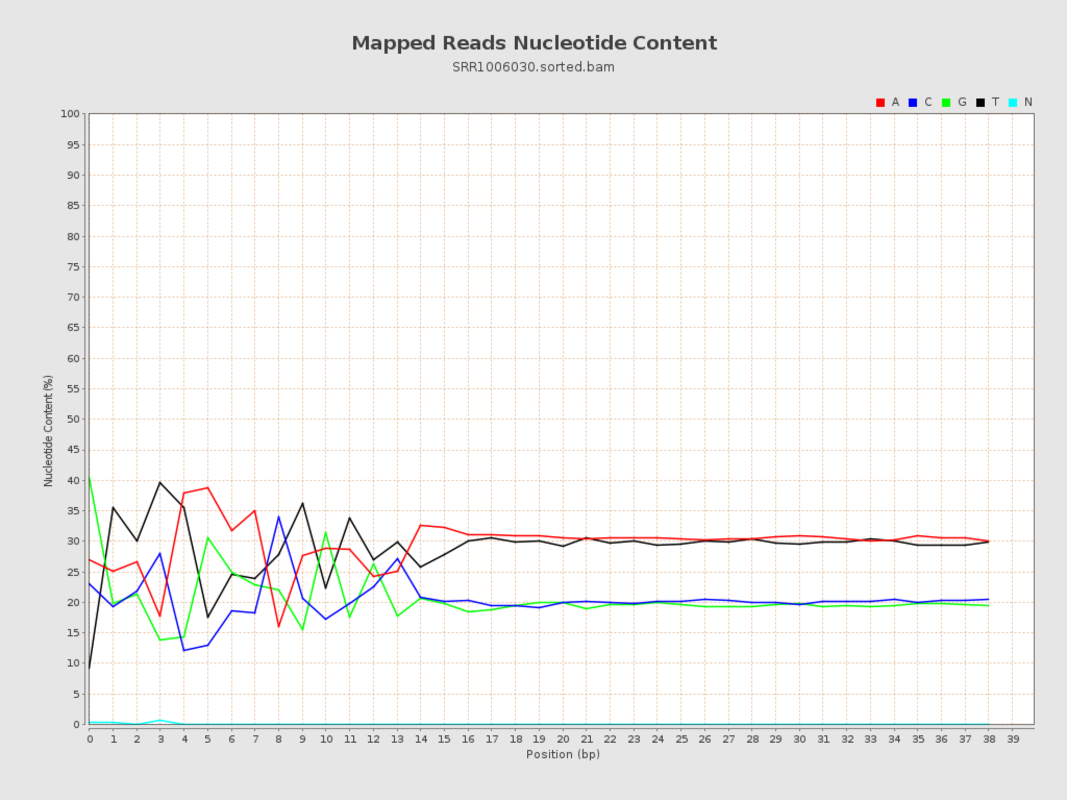
6. Results : Genome Fraction Coverage



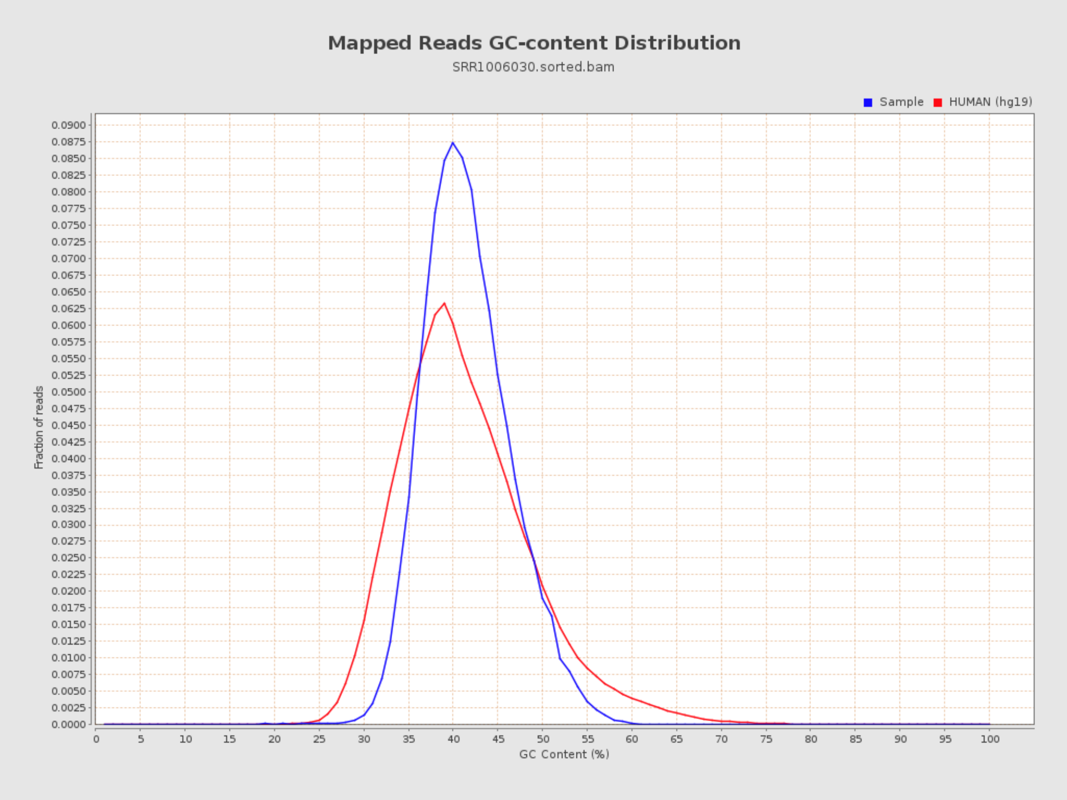
7. Results : Duplication Rate Histogram



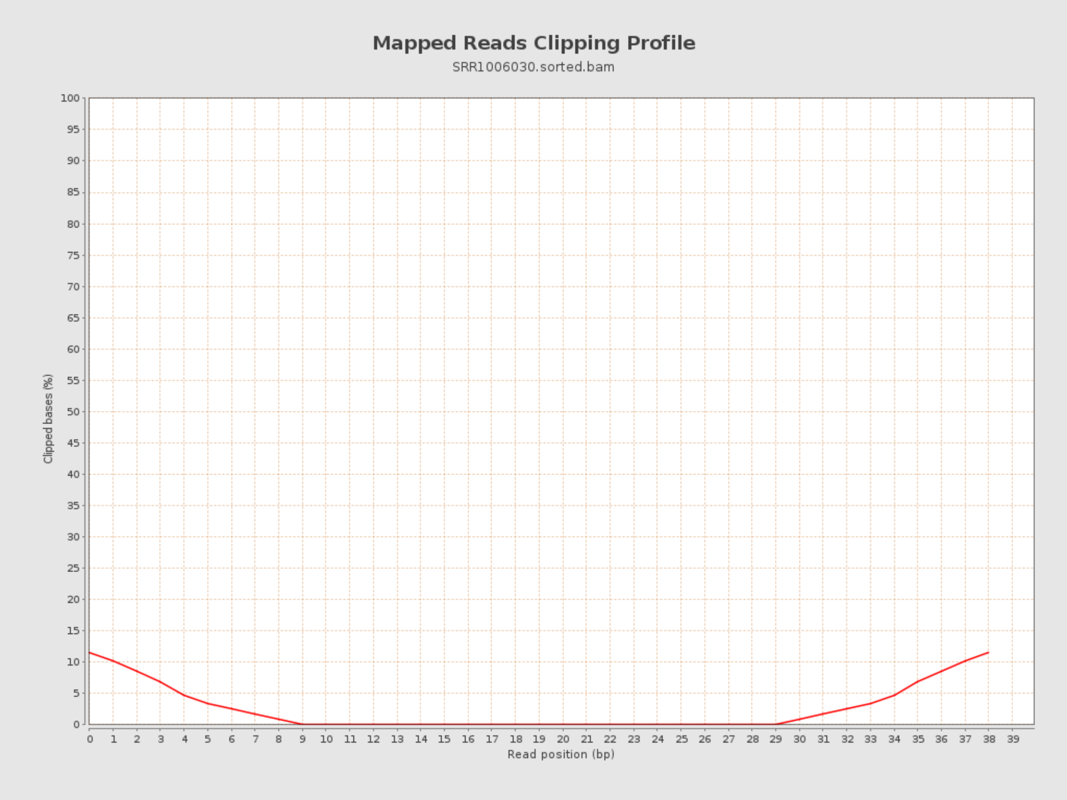
8. Results : Mapped Reads Nucleotide Content



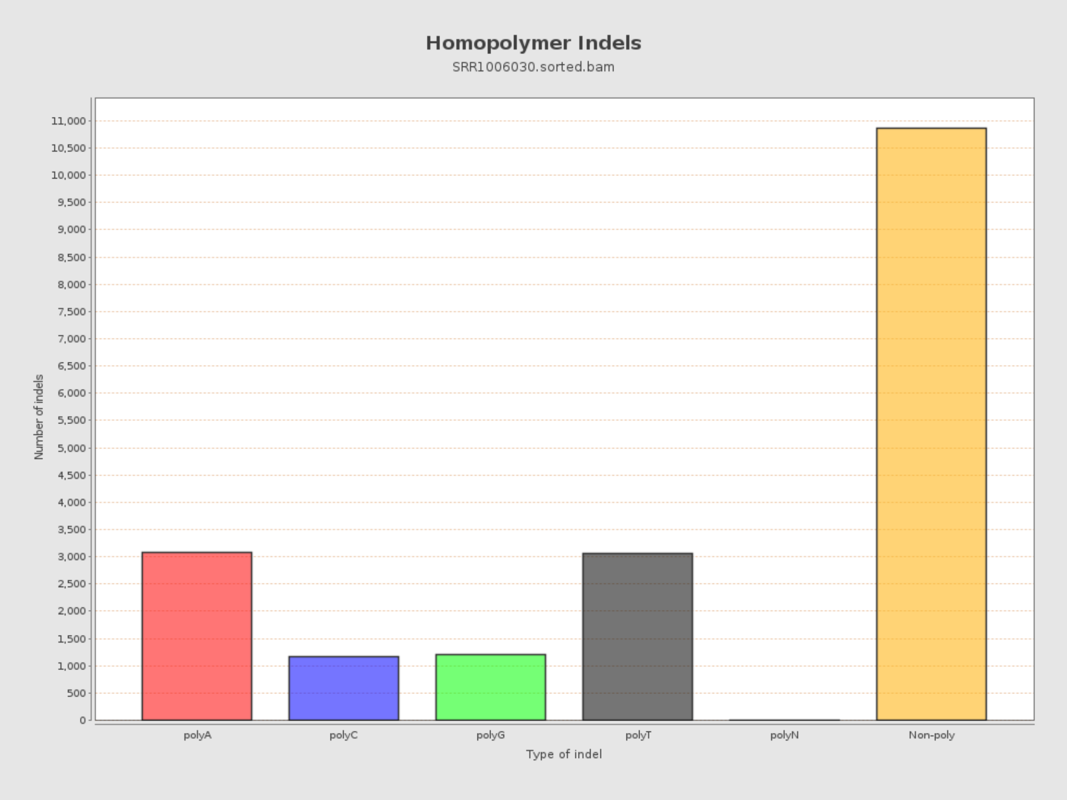
9. Results : Mapped Reads GC-content Distribution



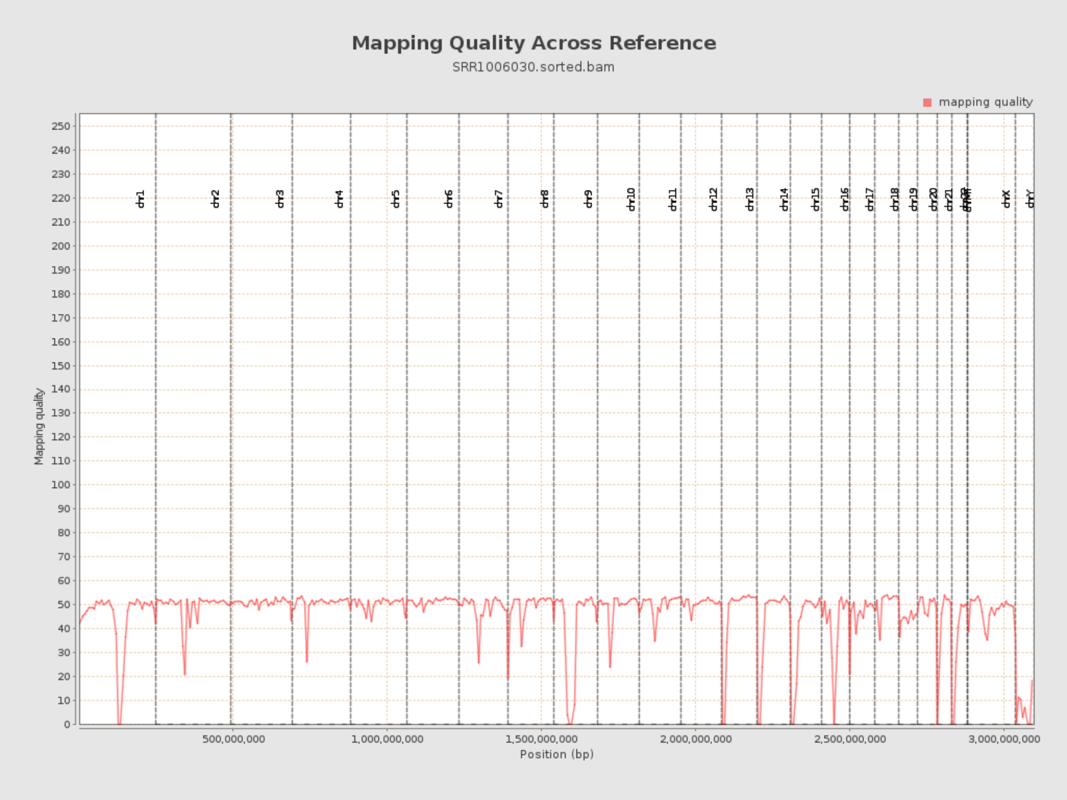
10. Results : Mapped Reads Clipping Profile



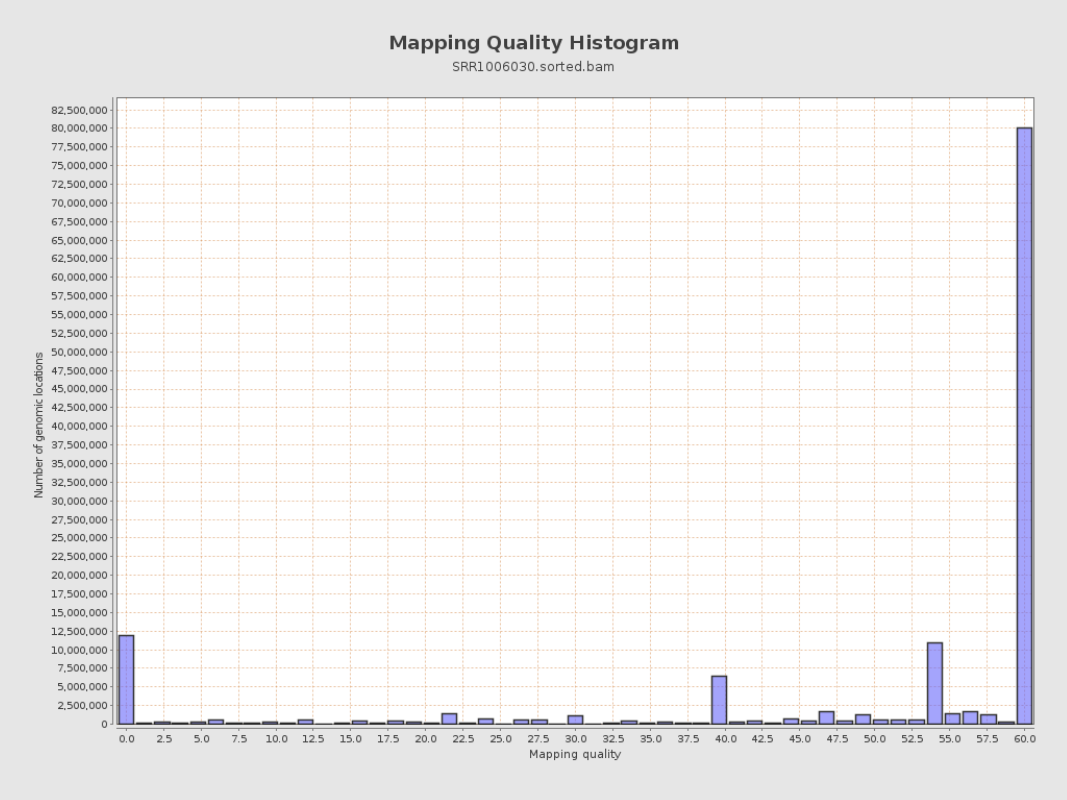
11. Results : Homopolymer Indels



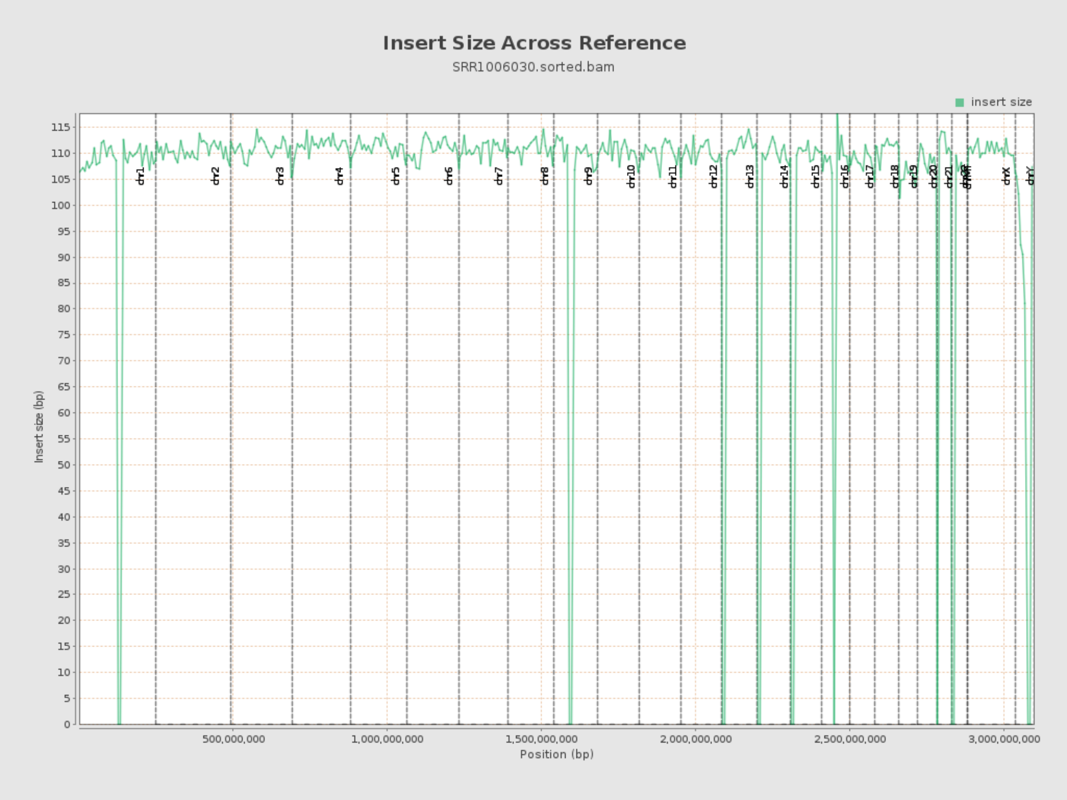
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram