Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 15:09:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006034.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_SRR1006034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006034_1.fastq.gz SRR1006034_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 15:09:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,423,480
Mapped reads	18,593,645 / 73.14%
Unmapped reads	6,829,835 / 26.86%
Mapped paired reads	18,593,645 / 73.14%
Mapped reads, first in pair	9,325,852 / 36.68%
Mapped reads, second in pair	9,267,793 / 36.45%
Mapped reads, both in pair	16,668,012 / 65.56%
Mapped reads, singletons	1,925,633 / 7.57%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,110,695 / 4.37%
Duplication rate	5.13%
Clipped reads	1,466,134 / 5.77%

2.2. ACGT Content

Number/percentage of A's	205,295,746 / 28.59%
Number/percentage of C's	151,776,313 / 21.13%
Number/percentage of T's	206,255,337 / 28.72%
Number/percentage of G's	154,743,195 / 21.55%
Number/percentage of N's	85,288 / 0.01%
GC Percentage	42.68%

2.3. Coverage

Mean	0.232
Standard Deviation	1.0678

2.4. Mapping Quality

Mean Mapping Quality	47.14

2.5. Insert size

Mean	70,466.93
Standard Deviation	2,566,275.44
P25/Median/P75	64 / 90 / 129

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	4,096,055
Insertions	21,688
Mapped reads with at least one insertion	0.12%
Deletions	64,264
Mapped reads with at least one deletion	0.35%
Homopolymer indels	44.19%

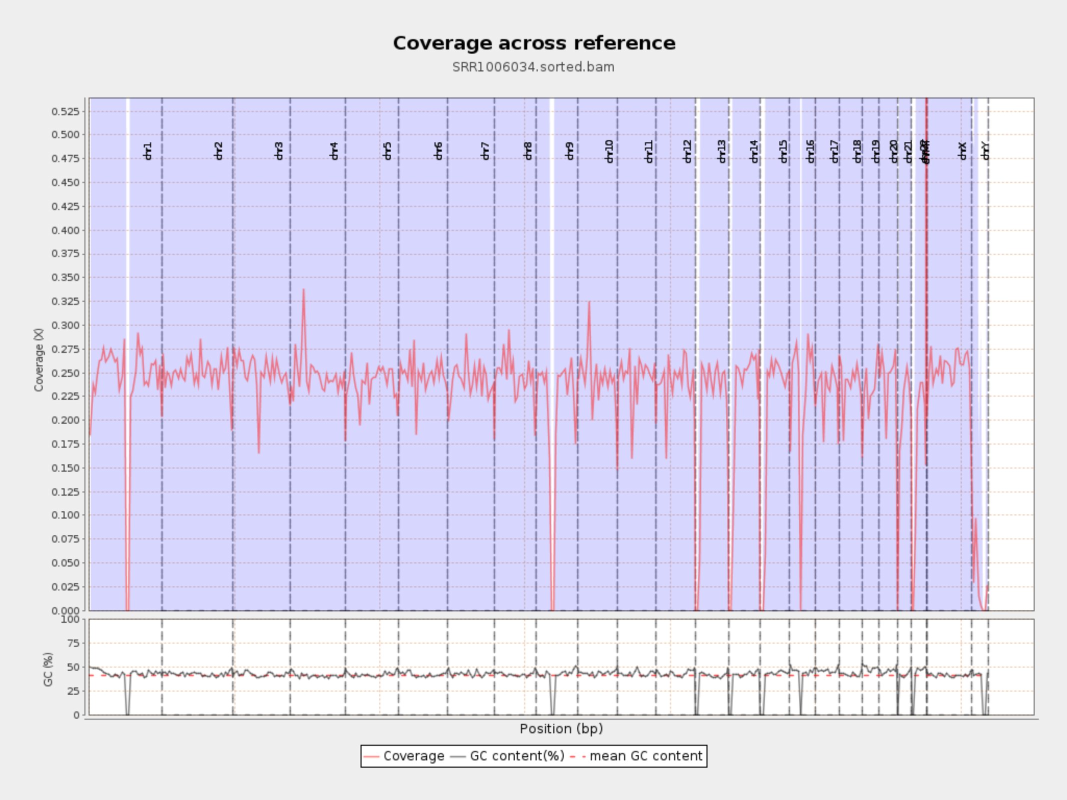
2.7. Chromosome stats

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

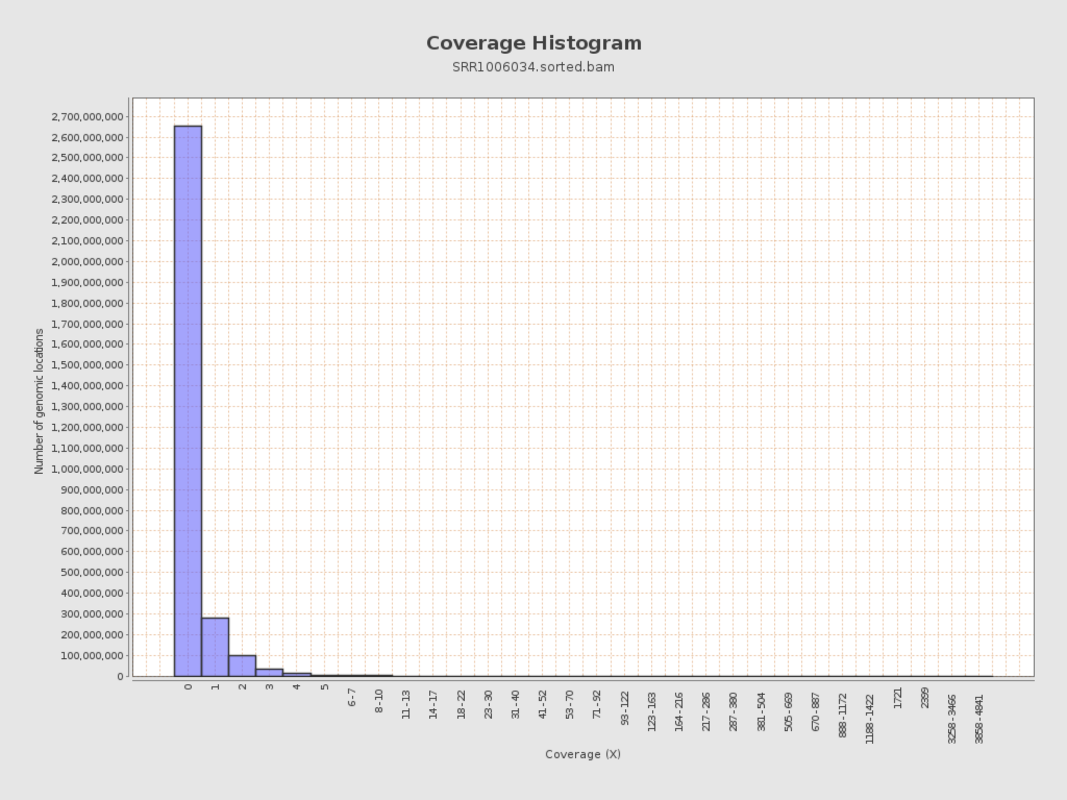
chr1	249250621	59129771	0.2372	1.3859
chr2	243199373	60867865	0.2503	0.9728
chr3	198022430	49494127	0.2499	0.7225
chr4	191154276	47578154	0.2489	0.8797
chr5	180915260	43513163	0.2405	0.7122
chr6	171115067	42257323	0.247	1.05
chr7	159138663	38657492	0.2429	1.353
chr8	146364022	36115316	0.2467	2.4681
chr9	141213431	29329533	0.2077	0.7908
chr10	135534747	33436825	0.2467	1.1461
chr11	135006516	32982101	0.2443	0.8123
chr12	133851895	32276442	0.2411	0.718
chr13	115169878	23434273	0.2035	0.6584
chr14	107349540	22526856	0.2098	0.7104
chr15	102531392	20611703	0.201	0.6547
chr16	90354753	20570061	0.2277	0.8209
chr17	81195210	18800700	0.2315	0.7561
chr18	78077248	18728436	0.2399	1.1936
chr19	59128983	13810517	0.2336	1.3209
chr20	63025520	15357232	0.2437	0.7677
chr21	48129895	9415717	0.1956	0.7642
chr22	51304566	7954668	0.155	0.634
chrMT	16571	42440	2.5611	2.5601
chrX	155270560	39521130	0.2545	0.802

chrY	59373566	1827287	0.0308	0.6158

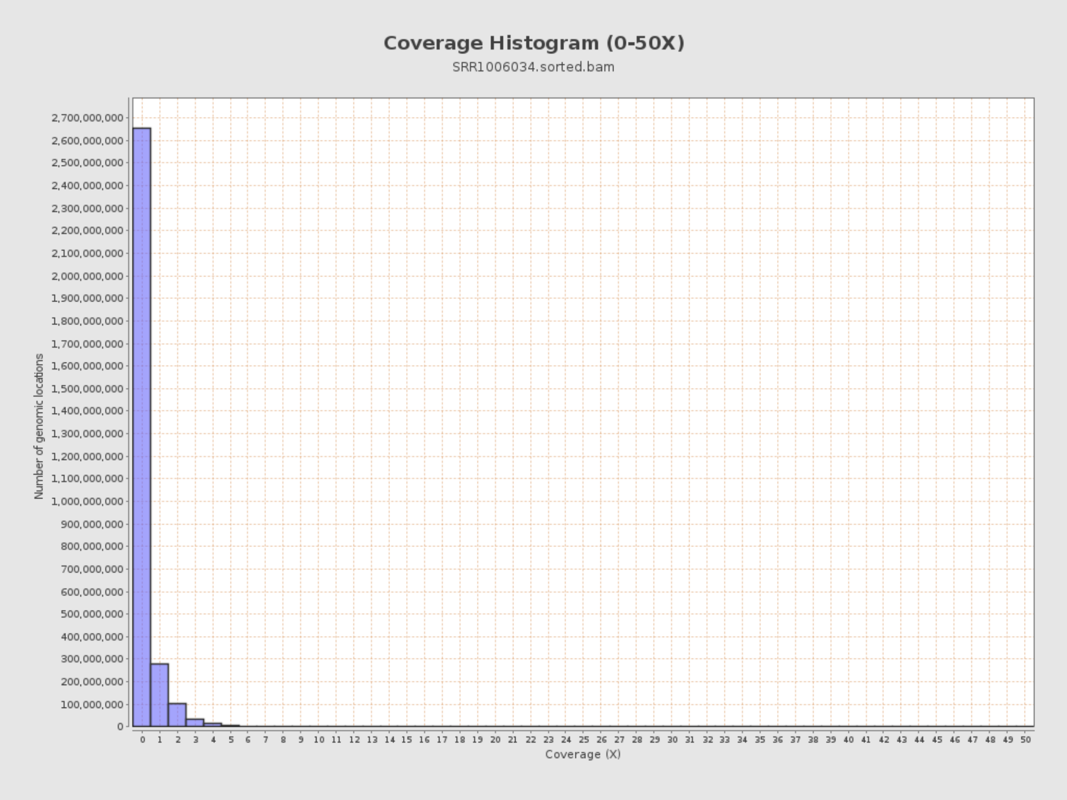
3. Results : Coverage across reference



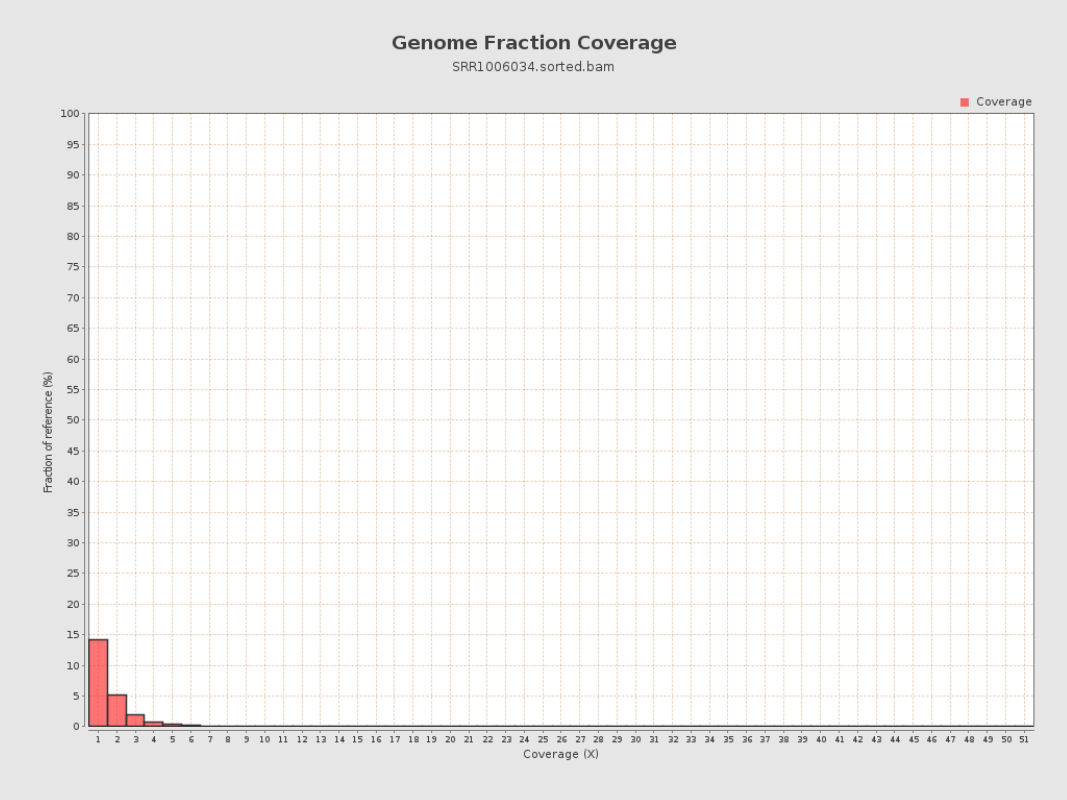
4. Results : Coverage Histogram



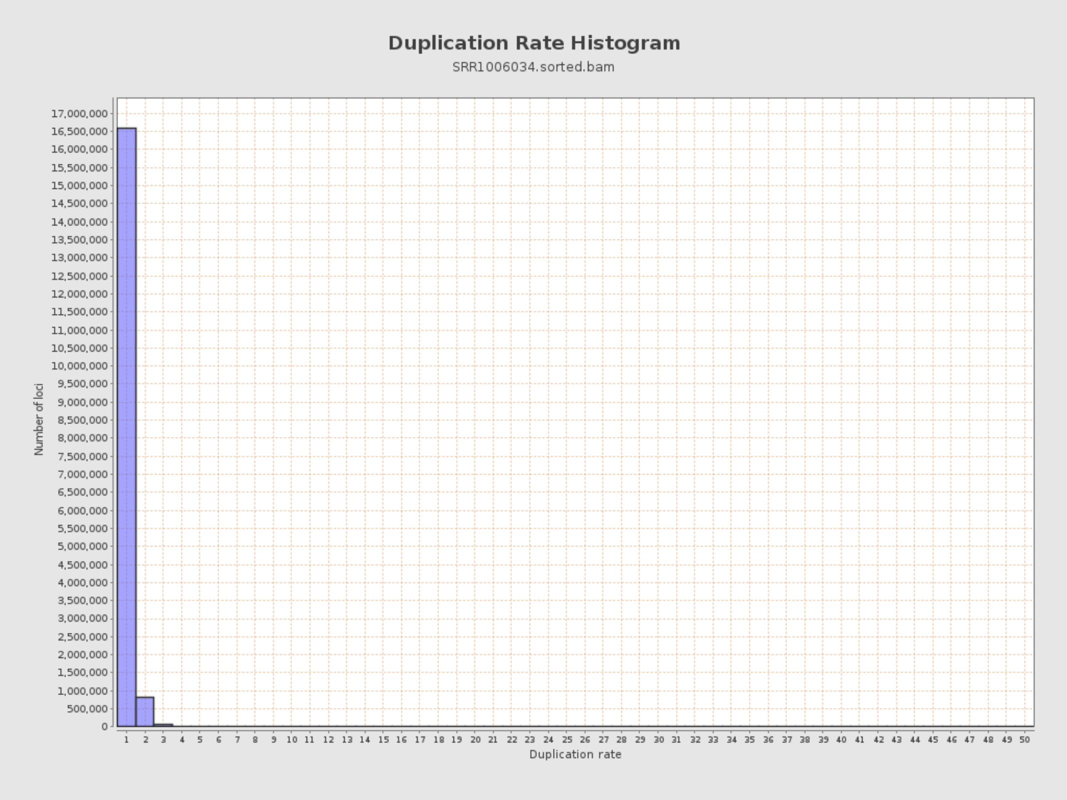
5. Results : Coverage Histogram (0-50X)



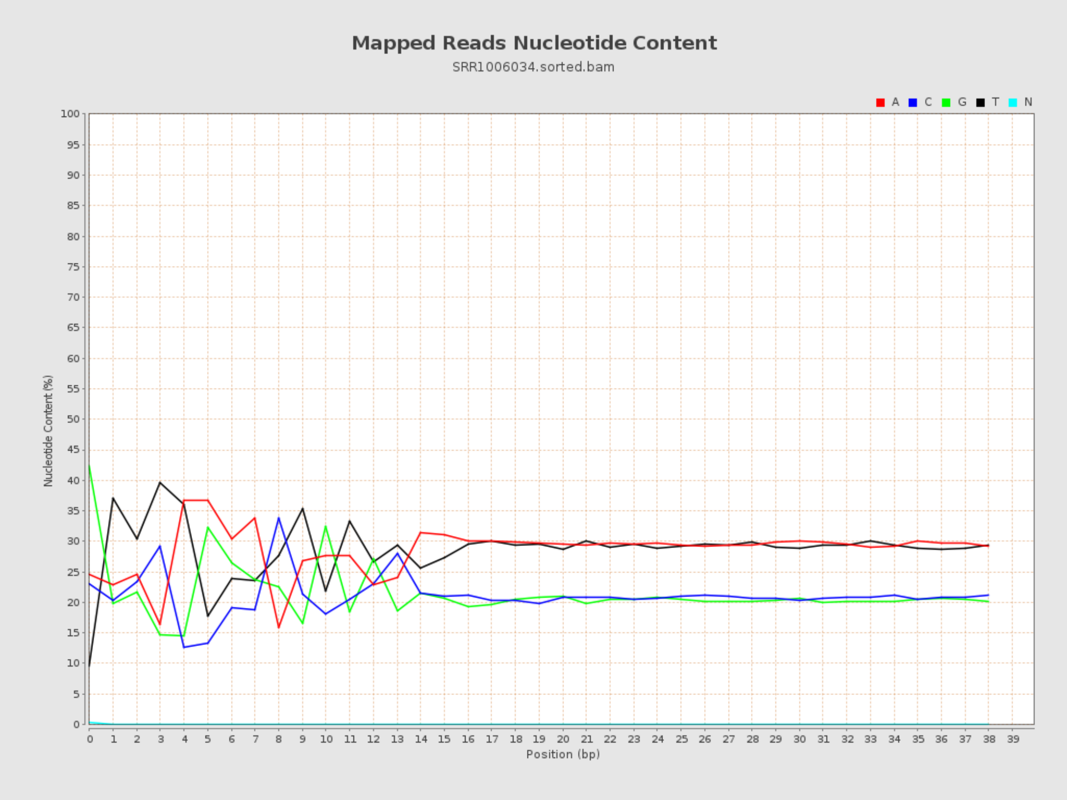
6. Results : Genome Fraction Coverage



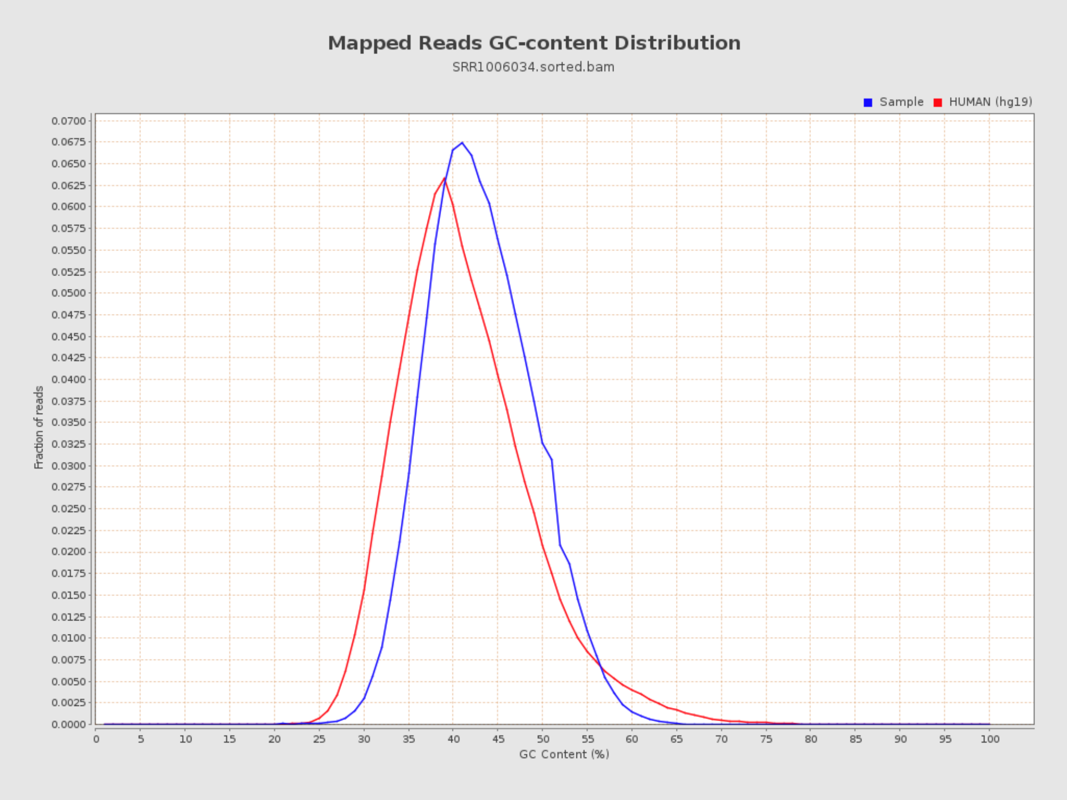
7. Results : Duplication Rate Histogram



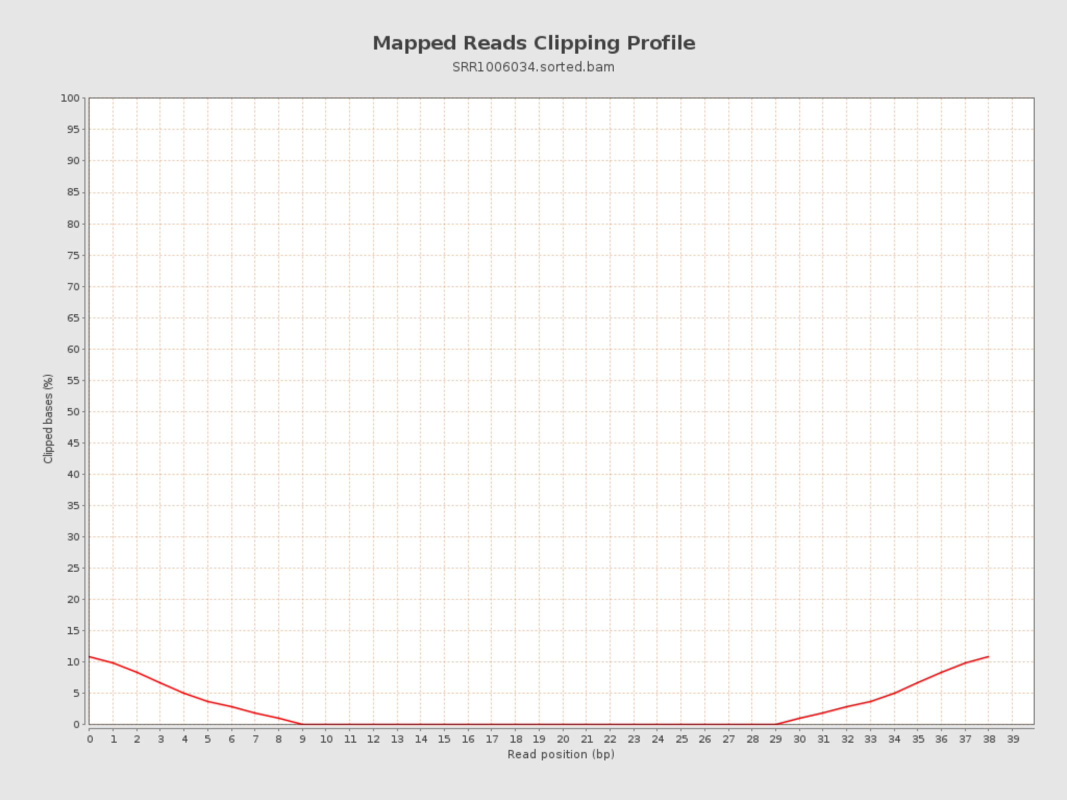
8. Results : Mapped Reads Nucleotide Content



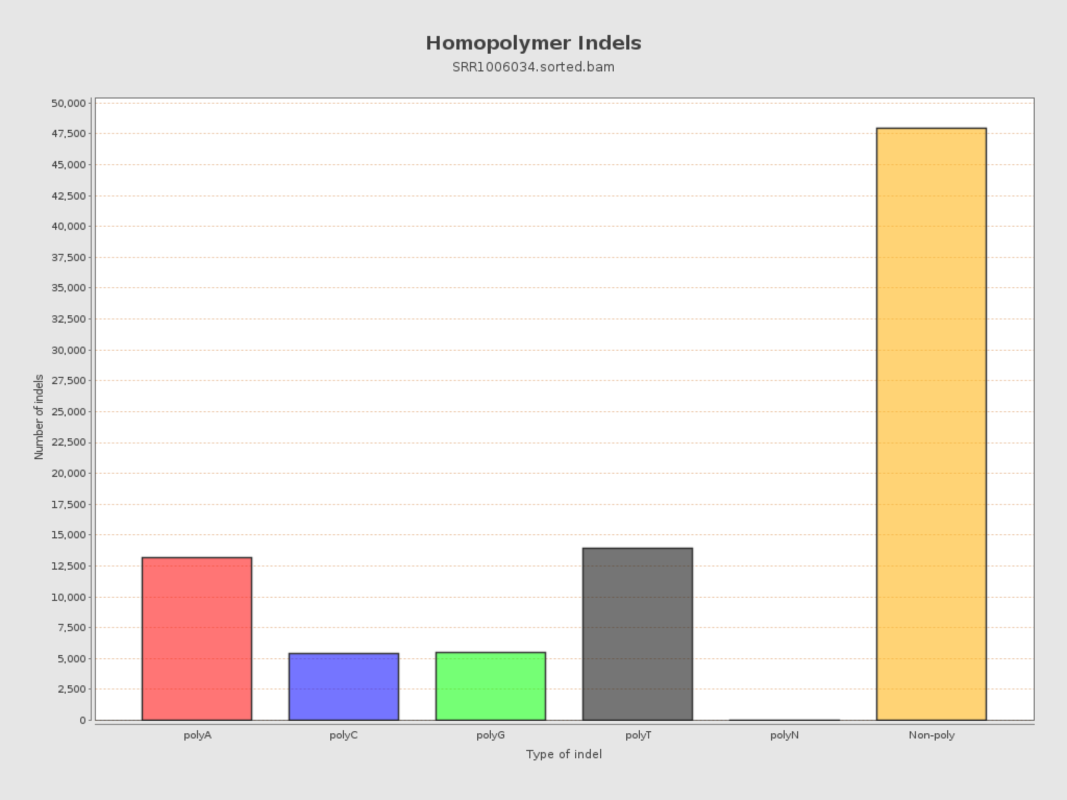
9. Results : Mapped Reads GC-content Distribution



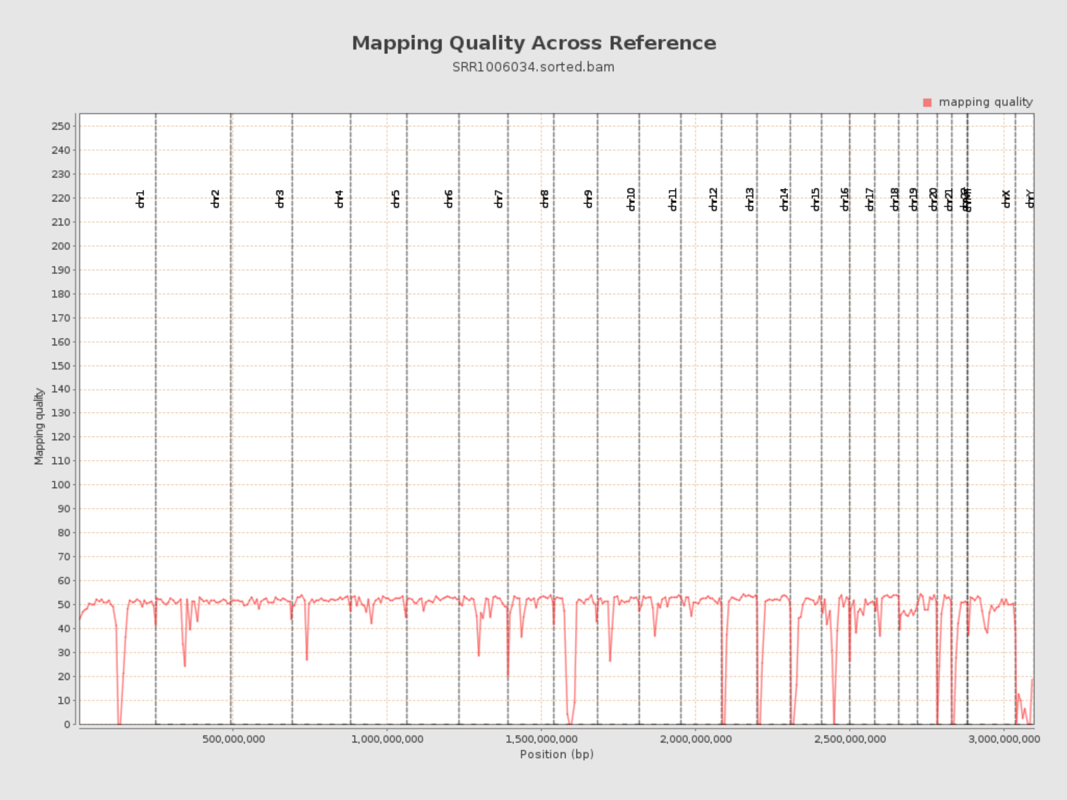
10. Results : Mapped Reads Clipping Profile



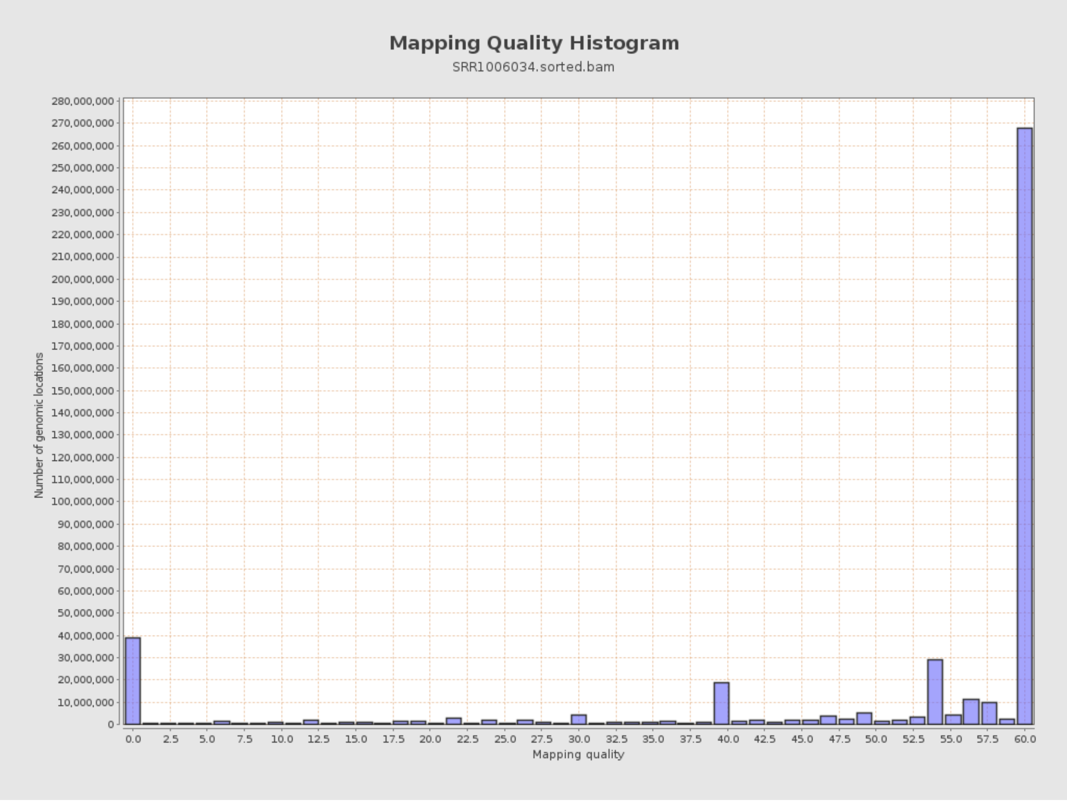
11. Results : Homopolymer Indels



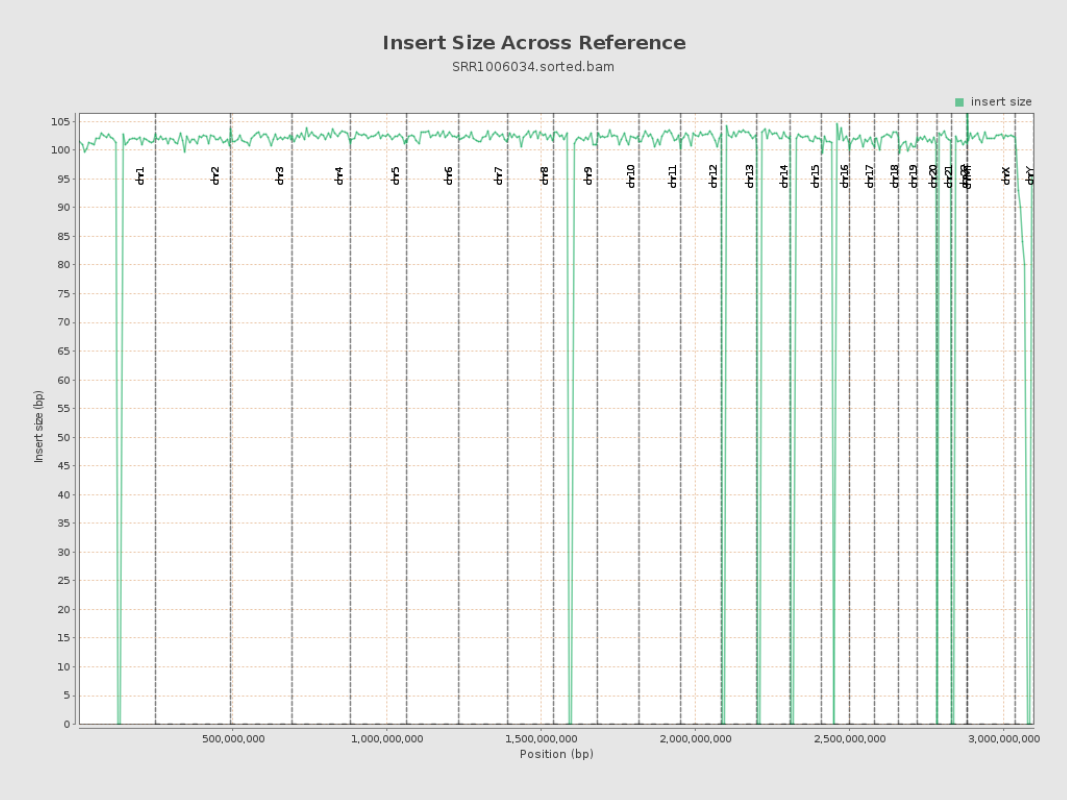
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram