Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:30:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006403.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_SRR1006403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006403_1.fastq.gz SRR1006403_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:30:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,620,112
Mapped reads	4,965,056 / 88.34%
Unmapped reads	655,056 / 11.66%
Mapped paired reads	4,965,056 / 88.34%
Mapped reads, first in pair	2,498,029 / 44.45%
Mapped reads, second in pair	2,467,027 / 43.9%
Mapped reads, both in pair	4,584,612 / 81.58%
Mapped reads, singletons	380,444 / 6.77%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	145,307 / 2.59%
Duplication rate	2.44%
Clipped reads	270,083 / 4.81%

2.2. ACGT Content

Number/percentage of A's	52,511,946 / 27.32%
Number/percentage of C's	42,302,690 / 22.01%
Number/percentage of T's	53,574,468 / 27.87%
Number/percentage of G's	43,821,583 / 22.8%
Number/percentage of N's	8,363 / 0%
GC Percentage	44.81%

2.3. Coverage

Mean	0.0621
Standard Deviation	0.3631

2.4. Mapping Quality

Mean Mapping Quality	48.07

2.5. Insert size

Mean	74,086.84
Standard Deviation	2,586,465.86
P25/Median/P75	94 / 133 / 183

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	578,534
Insertions	5,337
Mapped reads with at least one insertion	0.11%
Deletions	17,801
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.07%

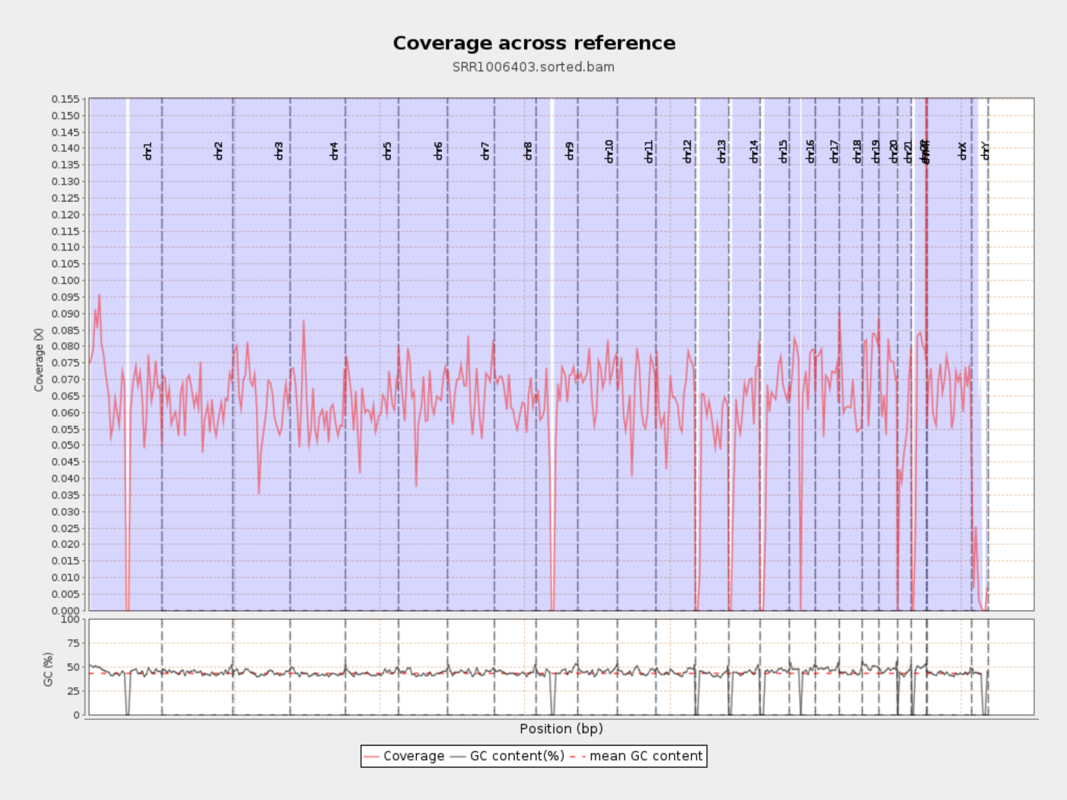
2.7. Chromosome stats

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

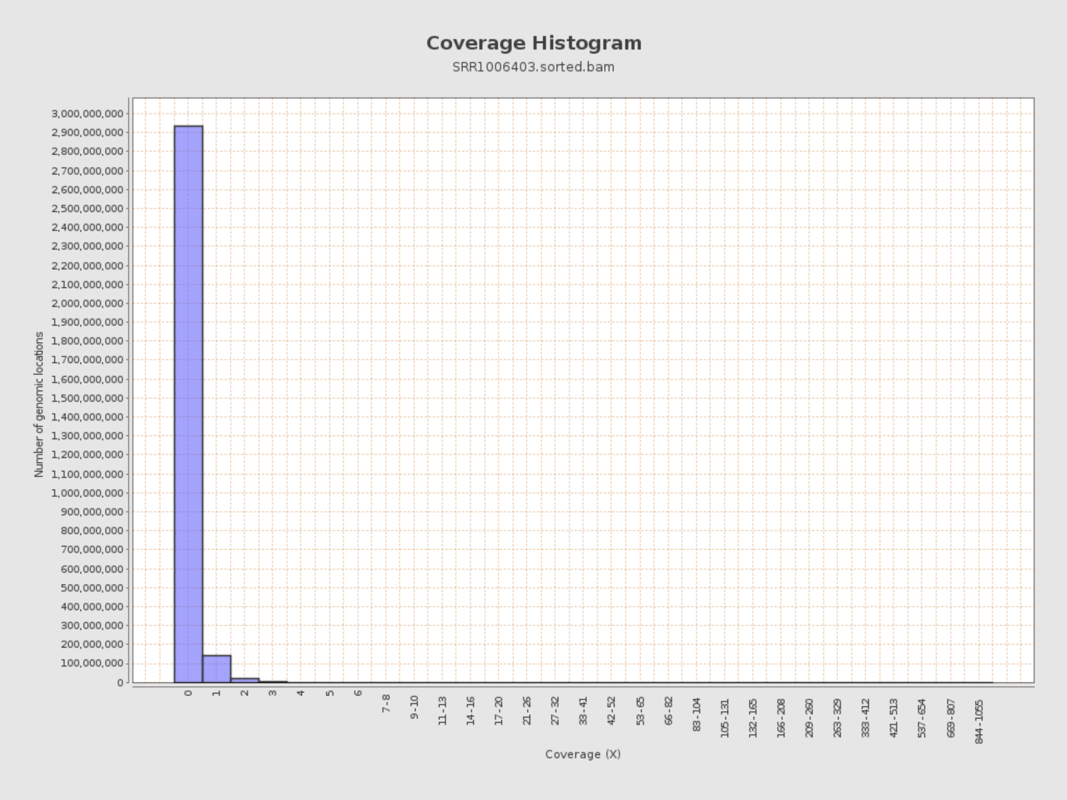
chr1	249250621	16225997	0.0651	0.4334
chr2	243199373	15195811	0.0625	0.3388
chr3	198022430	12694953	0.0641	0.2891
chr4	191154276	11646528	0.0609	0.3131
chr5	180915260	11210770	0.062	0.2845
chr6	171115067	11128988	0.065	0.3157
chr7	159138663	10648141	0.0669	0.3964
chr8	146364022	9384953	0.0641	0.5932
chr9	141213431	8192211	0.058	0.31
chr10	135534747	9582060	0.0707	0.3746
chr11	135006516	8757838	0.0649	0.3314
chr12	133851895	8602547	0.0643	0.2904
chr13	115169878	5713167	0.0496	0.2525
chr14	107349540	5828692	0.0543	0.6191
chr15	102531392	5568986	0.0543	0.2661
chr16	90354753	6119922	0.0677	0.3294
chr17	81195210	5763517	0.071	0.3157
chr18	78077248	4940400	0.0633	0.4554
chr19	59128983	4503185	0.0762	0.3881
chr20	63025520	4368851	0.0693	0.3149
chr21	48129895	2361655	0.0491	0.2961
chr22	51304566	2855315	0.0557	0.2819
chrMT	16571	8791	0.5305	0.8121
chrX	155270560	10477773	0.0675	0.3133

chrY	59373566	461626	0.0078	0.2003

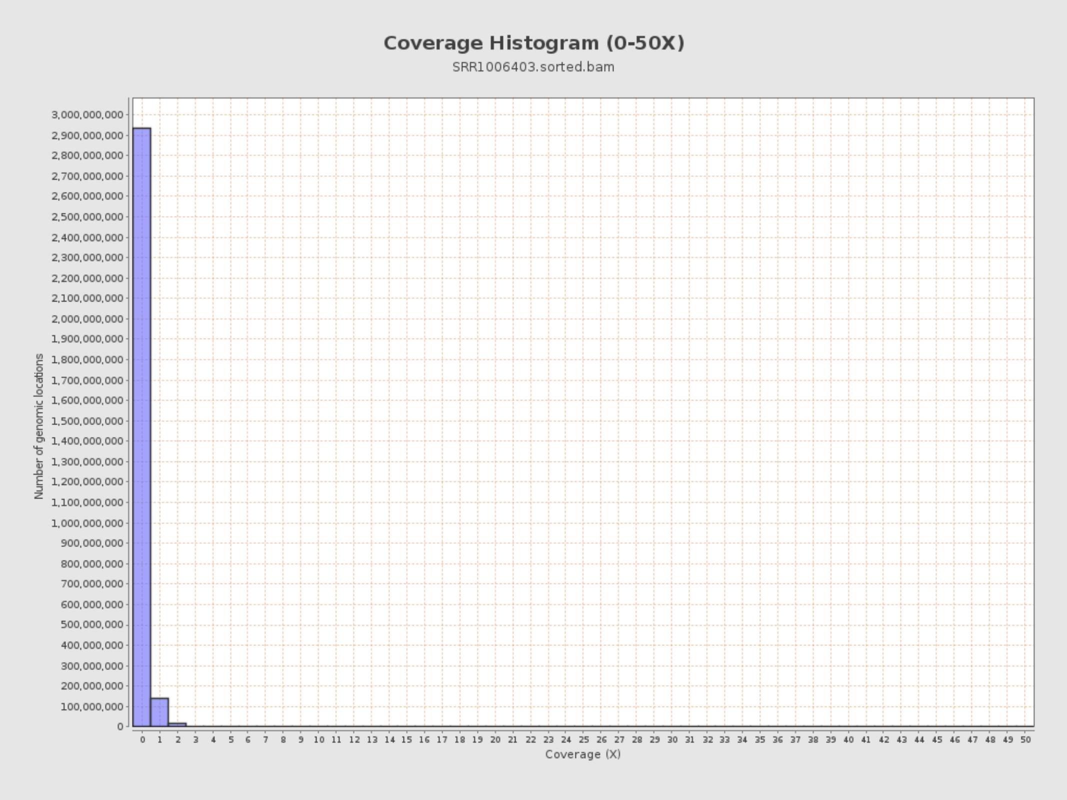
3. Results : Coverage across reference



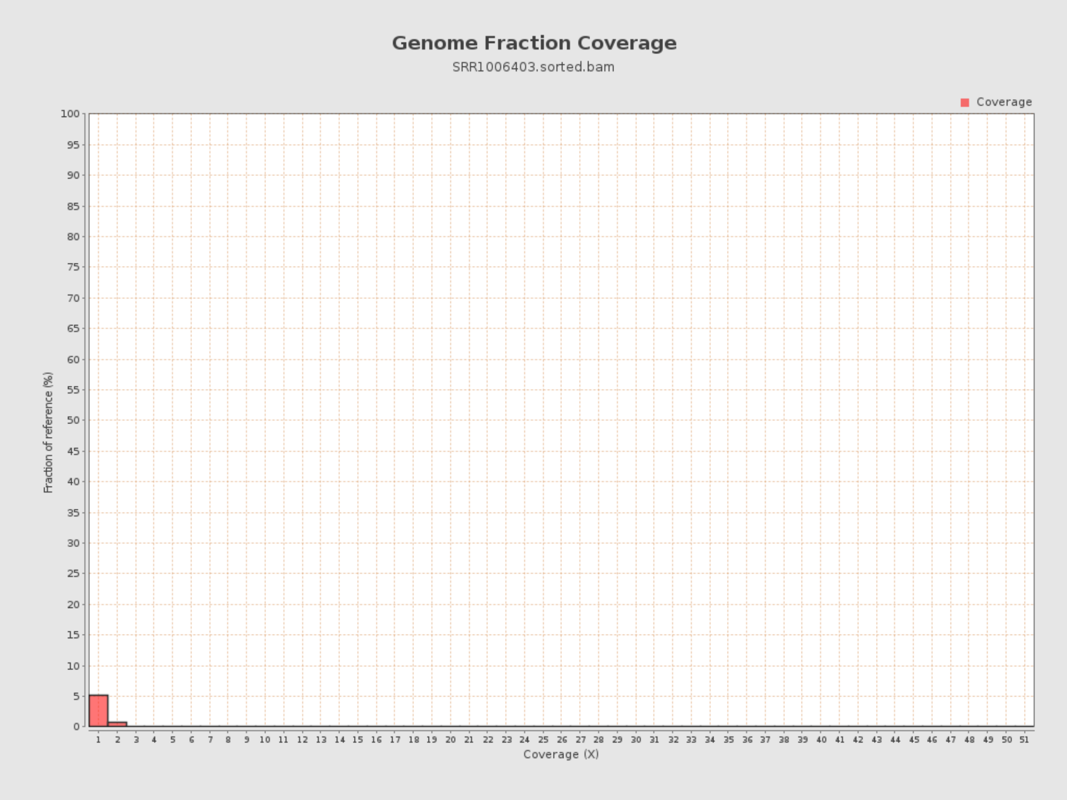
4. Results : Coverage Histogram



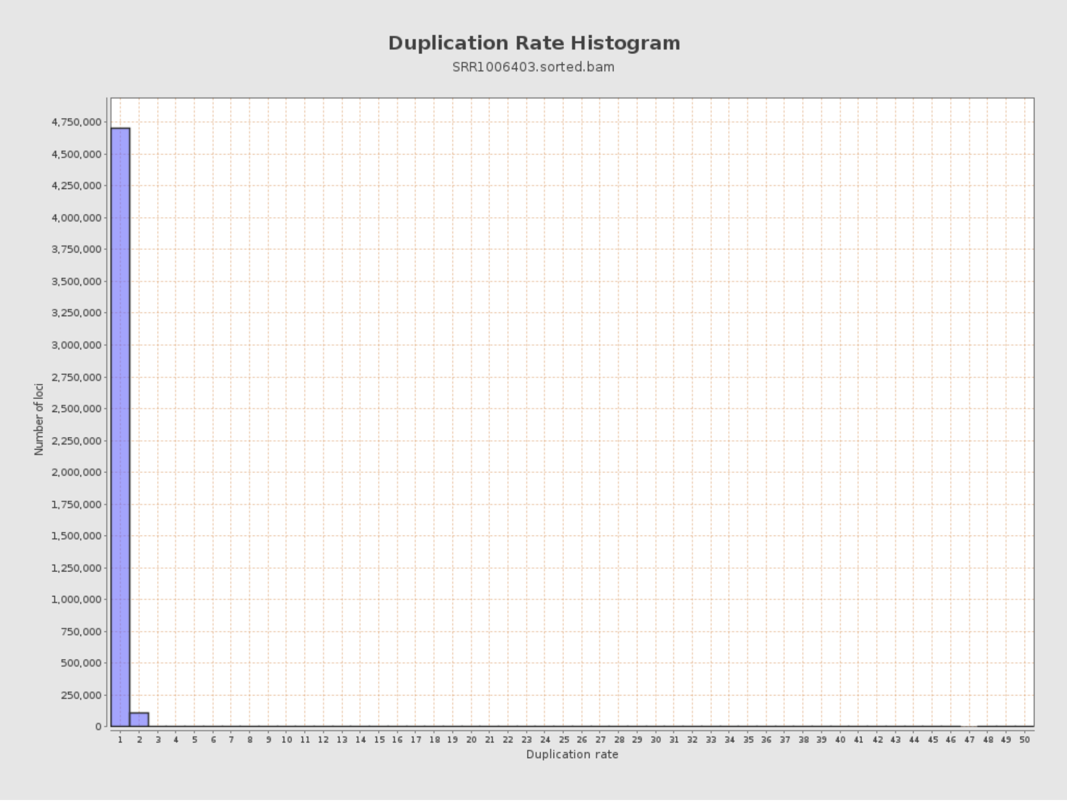
5. Results : Coverage Histogram (0-50X)



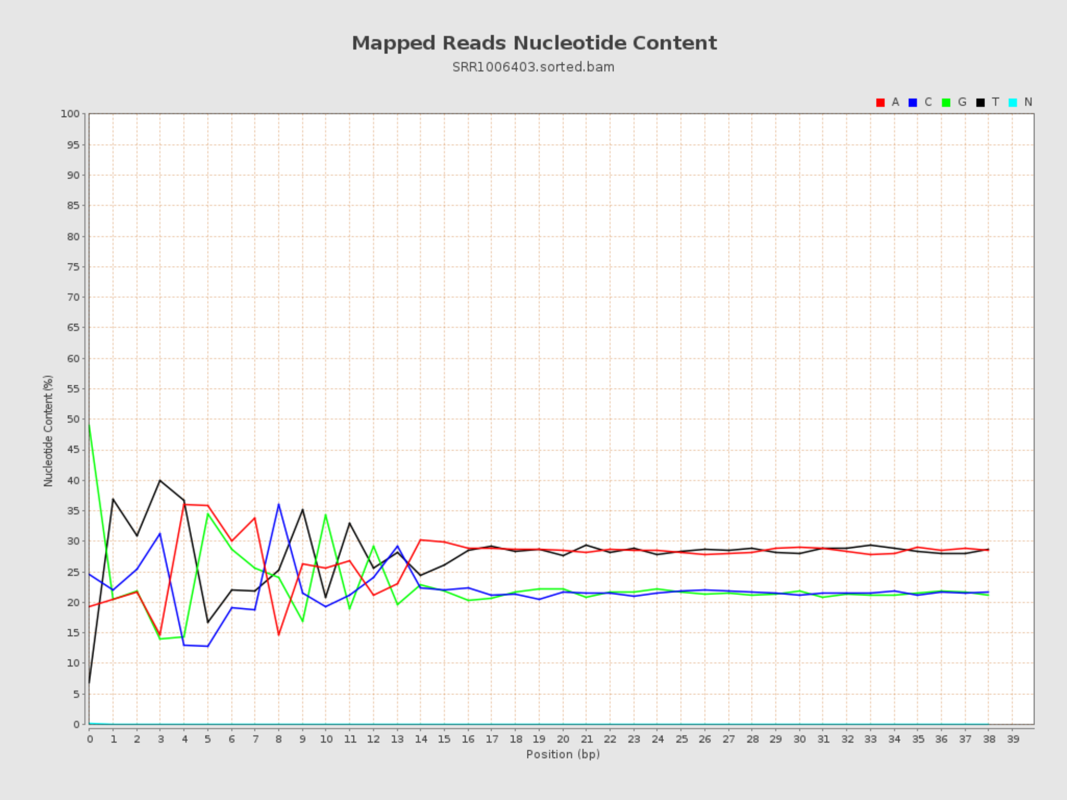
6. Results : Genome Fraction Coverage



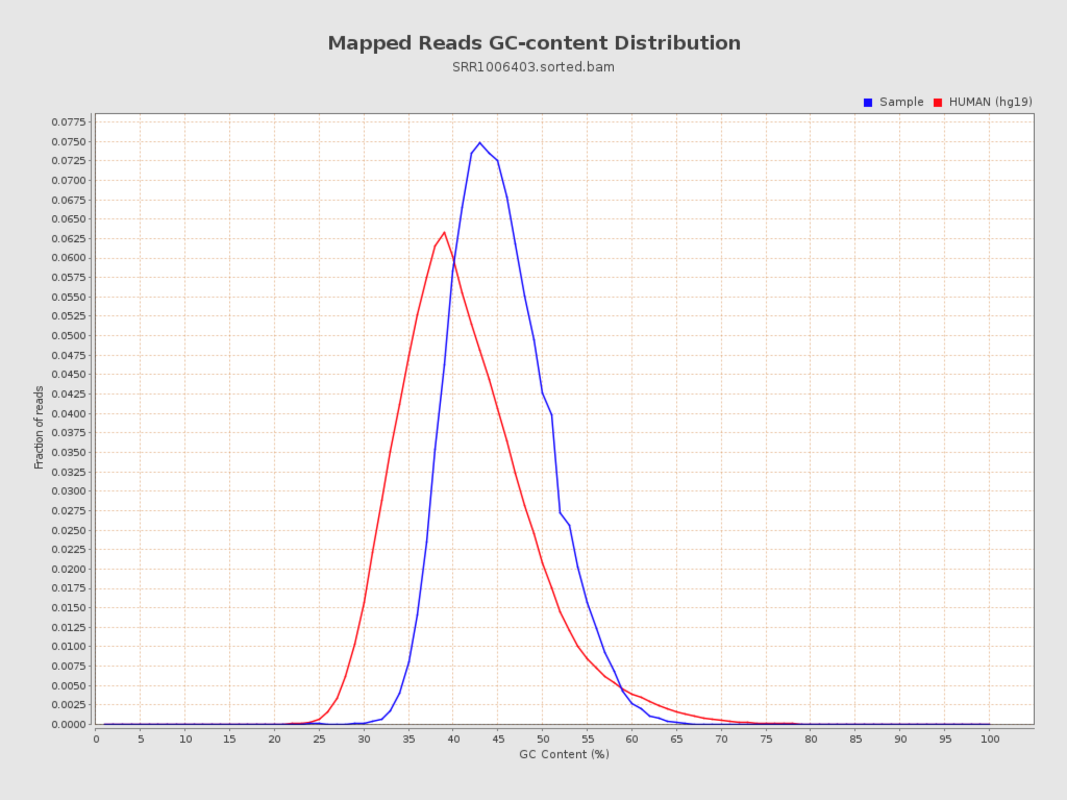
7. Results : Duplication Rate Histogram



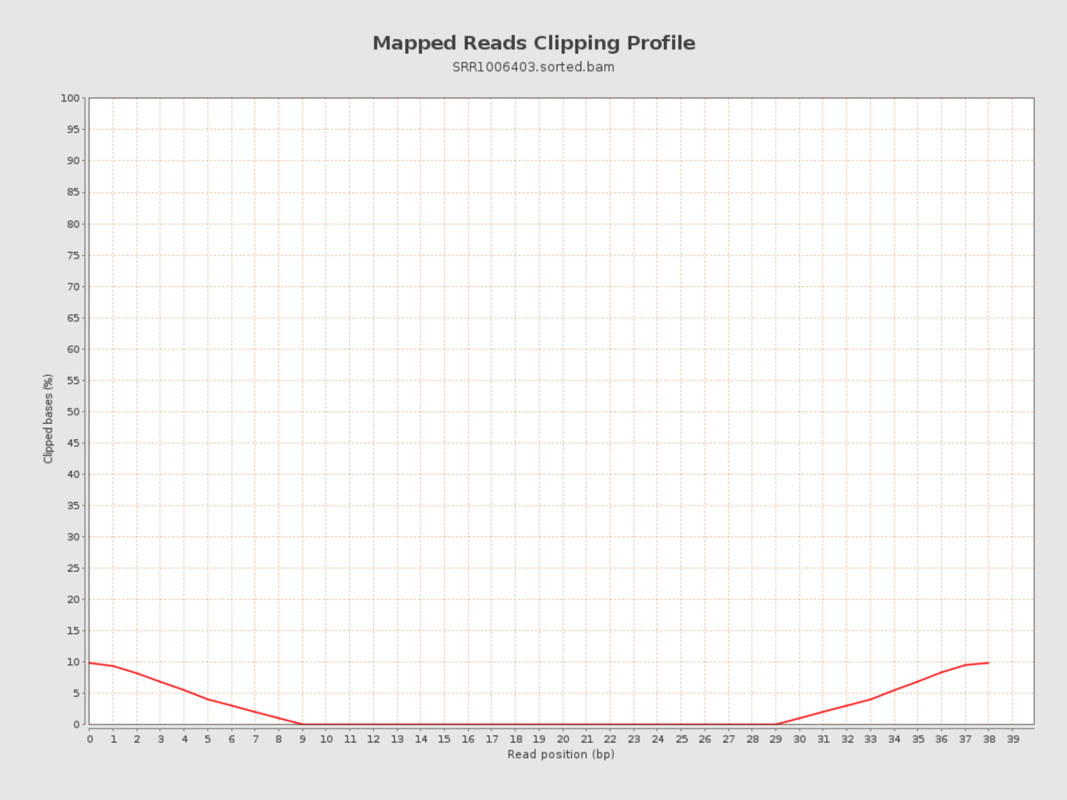
8. Results : Mapped Reads Nucleotide Content



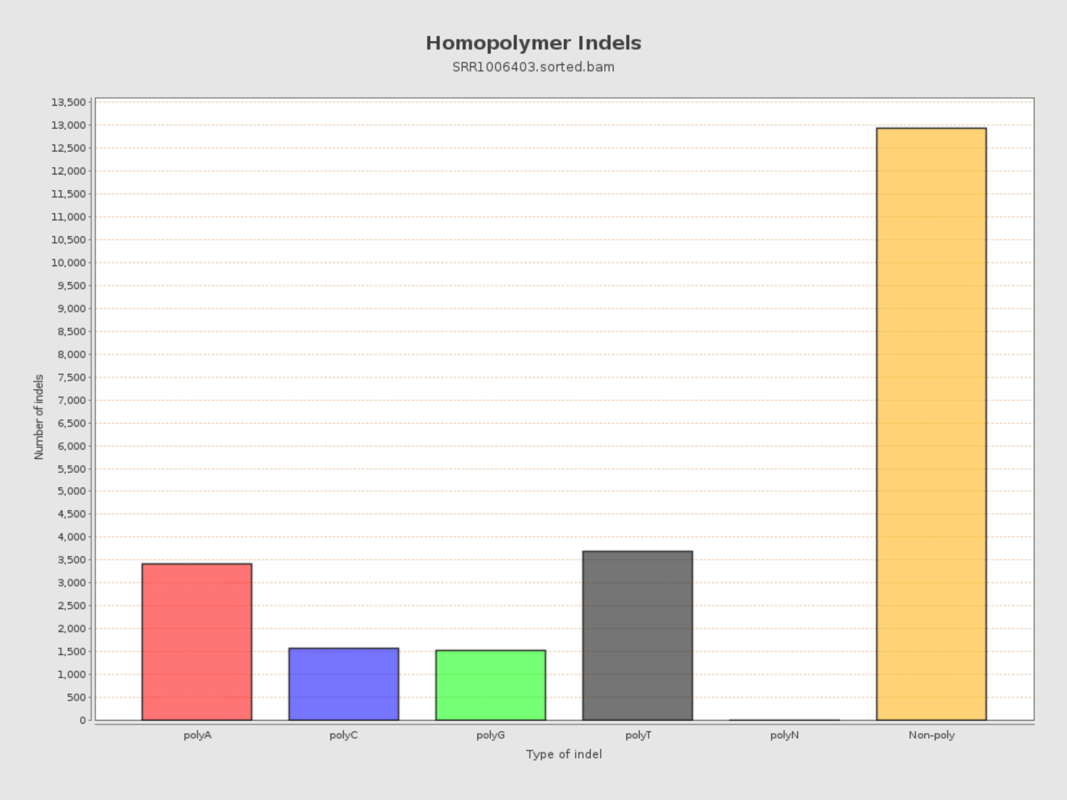
9. Results : Mapped Reads GC-content Distribution



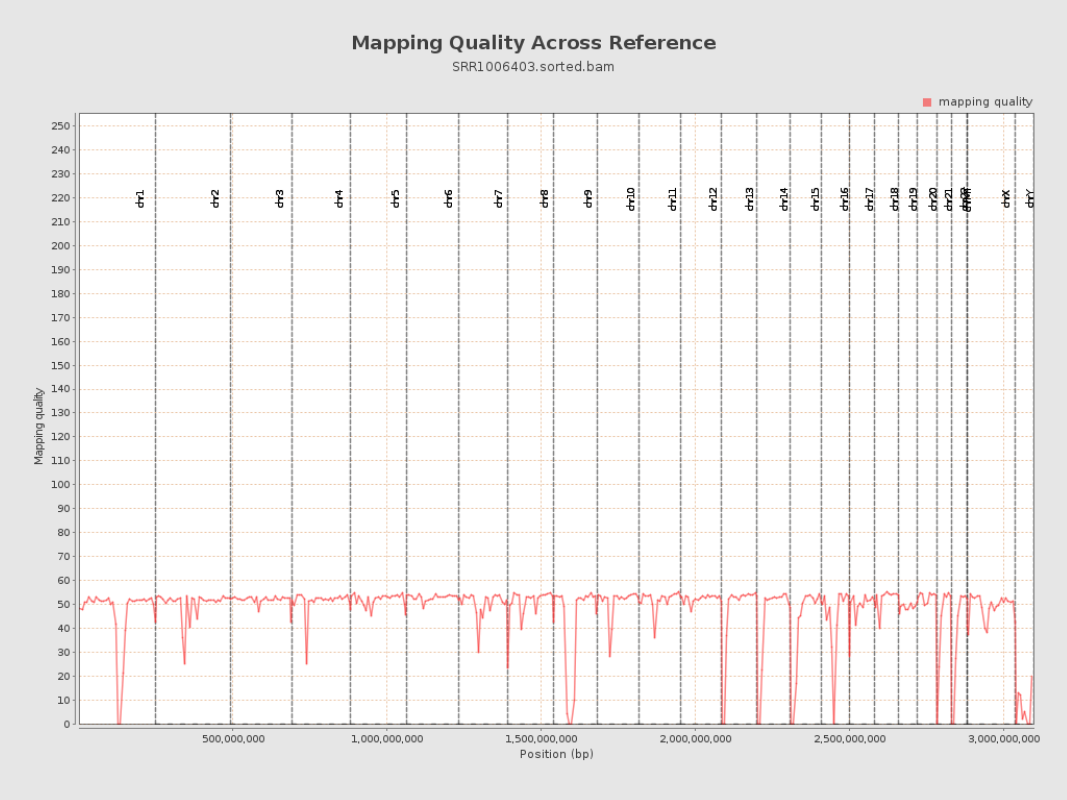
10. Results : Mapped Reads Clipping Profile



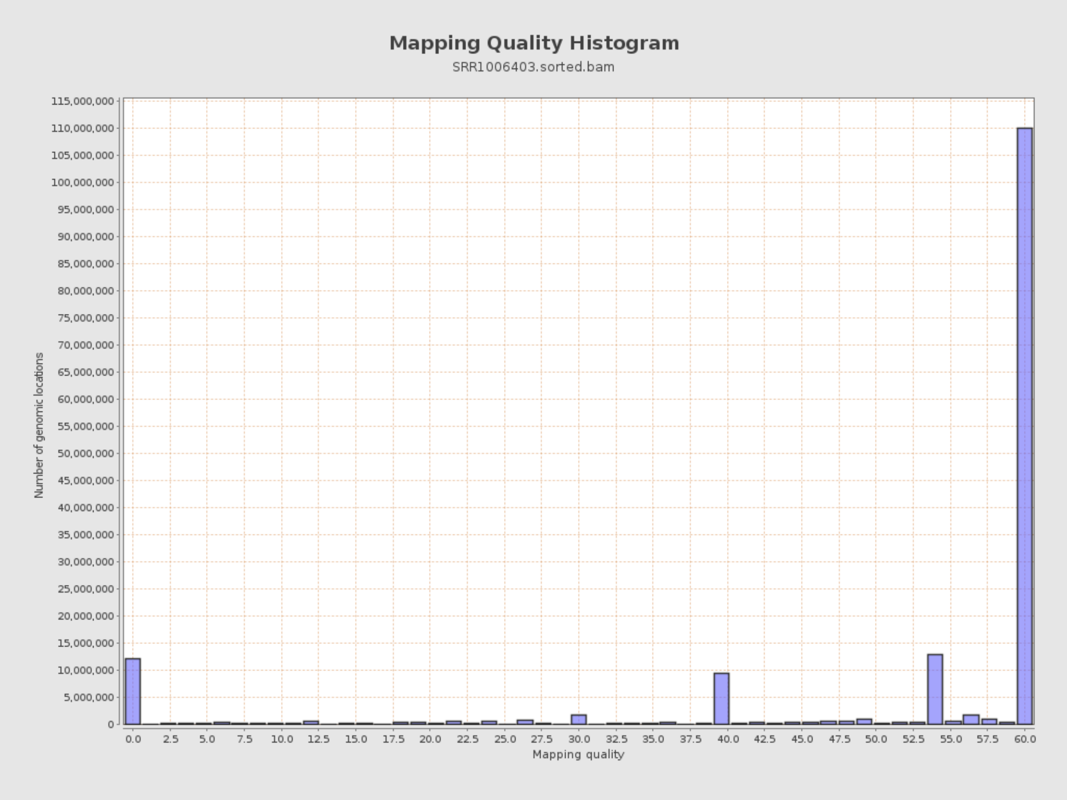
11. Results : Homopolymer Indels



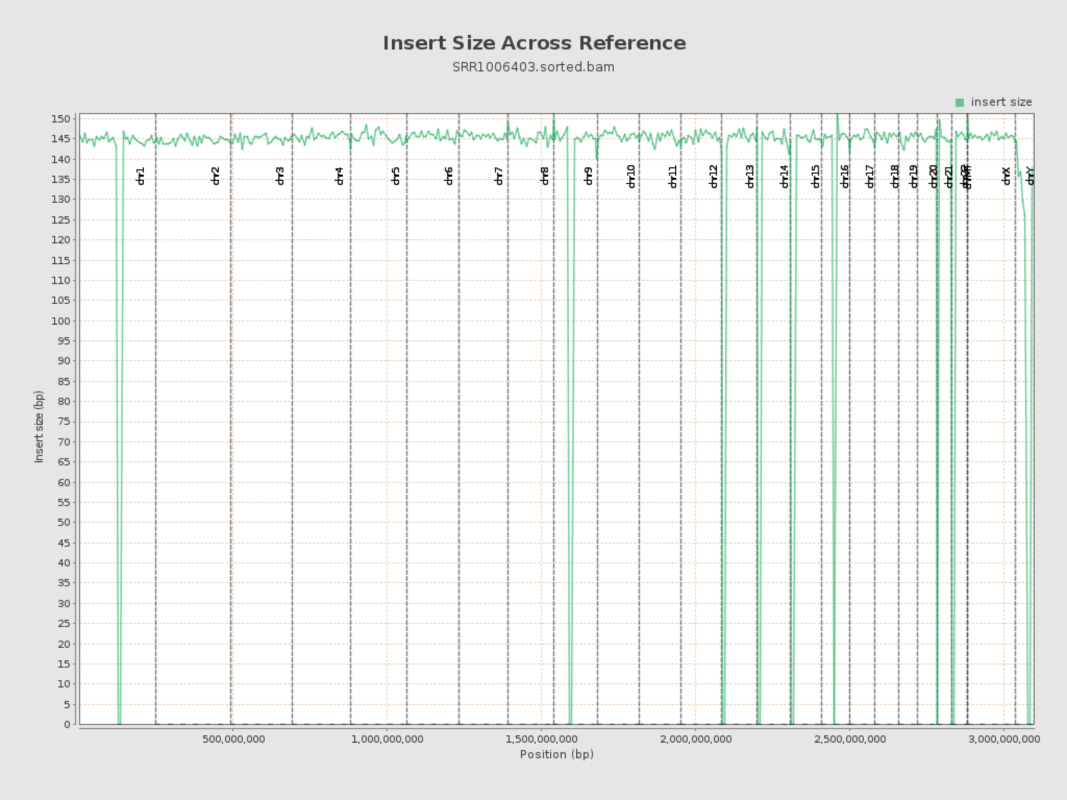
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram