Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:16:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006397.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_SRR1006397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006397_1.fastq.gz SRR1006397_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:16:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,187,564
Mapped reads	3,731,560 / 89.11%
Unmapped reads	456,004 / 10.89%
Mapped paired reads	3,731,560 / 89.11%
Mapped reads, first in pair	1,877,786 / 44.84%
Mapped reads, second in pair	1,853,774 / 44.27%
Mapped reads, both in pair	3,452,278 / 82.44%
Mapped reads, singletons	279,282 / 6.67%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	87,632 / 2.09%
Duplication rate	1.95%
Clipped reads	202,666 / 4.84%

2.2. ACGT Content

Number/percentage of A's	39,395,230 / 27.27%
Number/percentage of C's	31,888,322 / 22.07%
Number/percentage of T's	40,166,624 / 27.8%
Number/percentage of G's	33,008,125 / 22.85%
Number/percentage of N's	6,442 / 0%
GC Percentage	44.92%

2.3. Coverage

Mean	0.0467
Standard Deviation	0.2863

2.4. Mapping Quality

Mean Mapping Quality	48.01

2.5. Insert size

Mean	72,517.11
Standard Deviation	2,593,067.36
P25/Median/P75	93 / 130 / 179

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	433,644
Insertions	3,958
Mapped reads with at least one insertion	0.11%
Deletions	13,137
Mapped reads with at least one deletion	0.35%
Homopolymer indels	43.88%

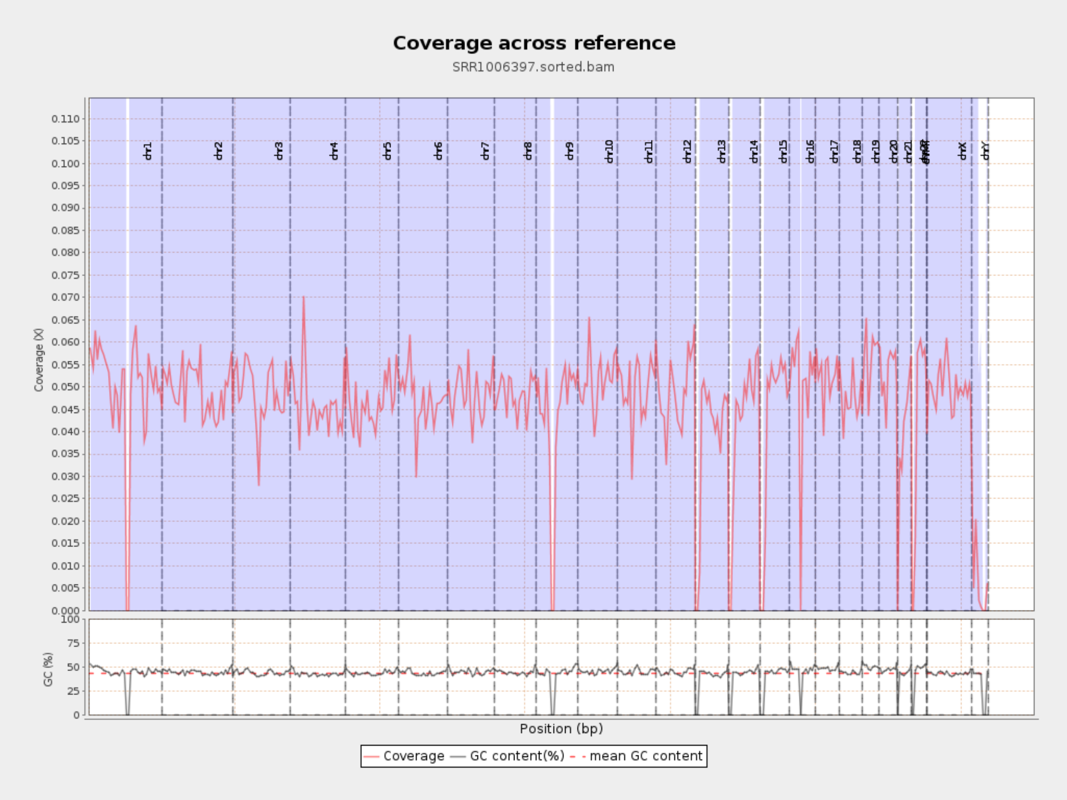
2.7. Chromosome stats

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

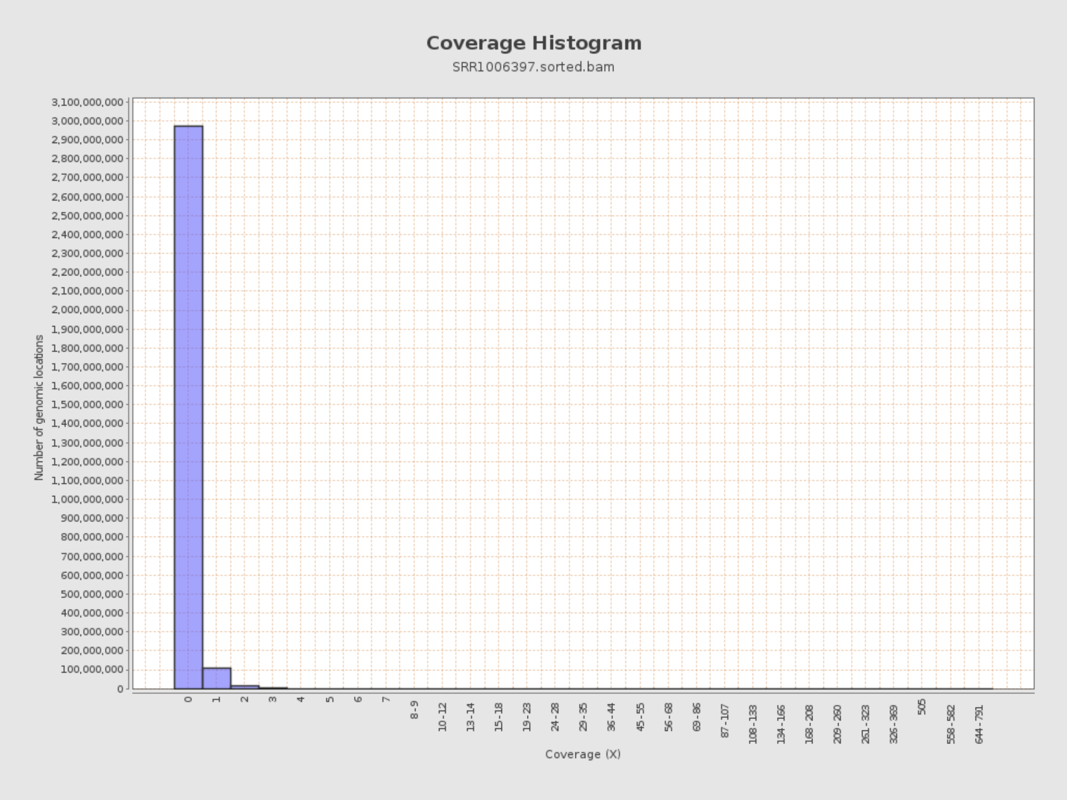
chr1	249250621	12211193	0.049	0.358
chr2	243199373	12084177	0.0497	0.2884
chr3	198022430	9647595	0.0487	0.2444
chr4	191154276	8818562	0.0461	0.2639
chr5	180915260	8417852	0.0465	0.2397
chr6	171115067	8105669	0.0474	0.2542
chr7	159138663	7704600	0.0484	0.3034
chr8	146364022	7058719	0.0482	0.458
chr9	141213431	5976022	0.0423	0.2482
chr10	135534747	6923660	0.0511	0.3173
chr11	135006516	6686374	0.0495	0.2698
chr12	133851895	6537069	0.0488	0.2509
chr13	115169878	4355661	0.0378	0.2185
chr14	107349540	4439469	0.0414	0.2616
chr15	102531392	4331155	0.0422	0.2291
chr16	90354753	4525459	0.0501	0.2799
chr17	81195210	4251028	0.0524	0.2627
chr18	78077248	3705450	0.0475	0.3486
chr19	59128983	3347148	0.0566	0.3256
chr20	63025520	3343332	0.053	0.2664
chr21	48129895	1875827	0.039	0.2525
chr22	51304566	2042725	0.0398	0.2288
chrMT	16571	754	0.0455	0.3388
chrX	155270560	7730572	0.0498	0.259

chrY	59373566	362300	0.0061	0.1659

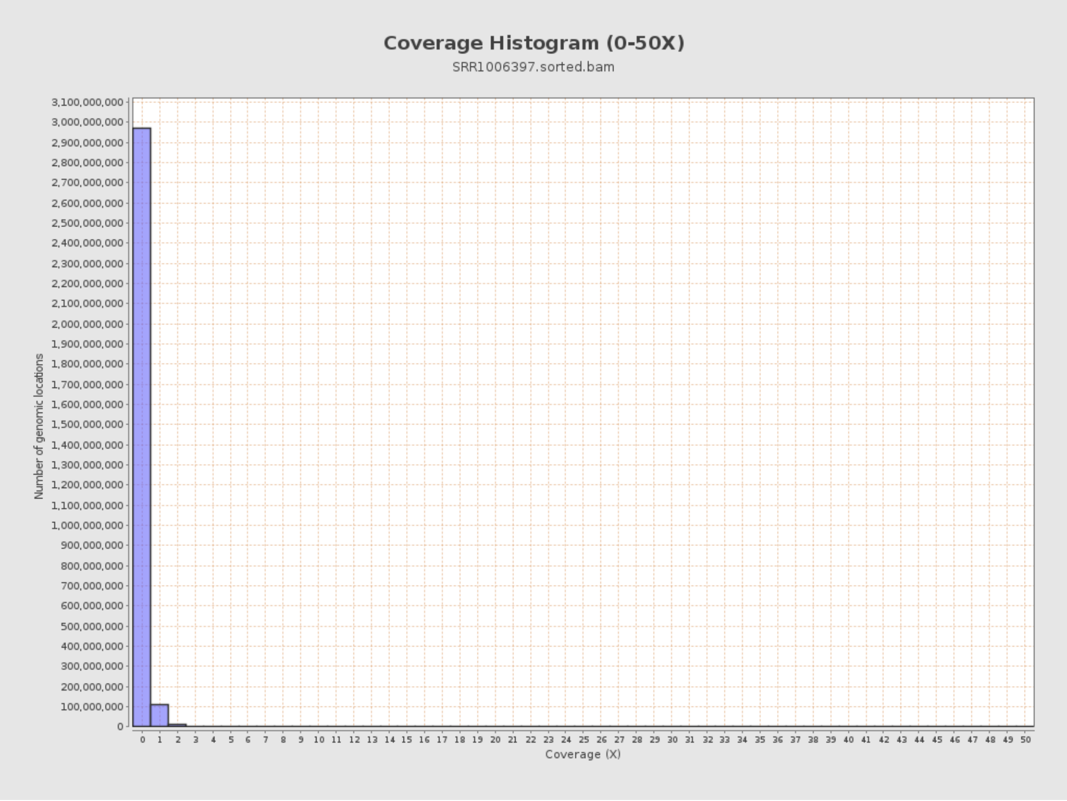
3. Results : Coverage across reference



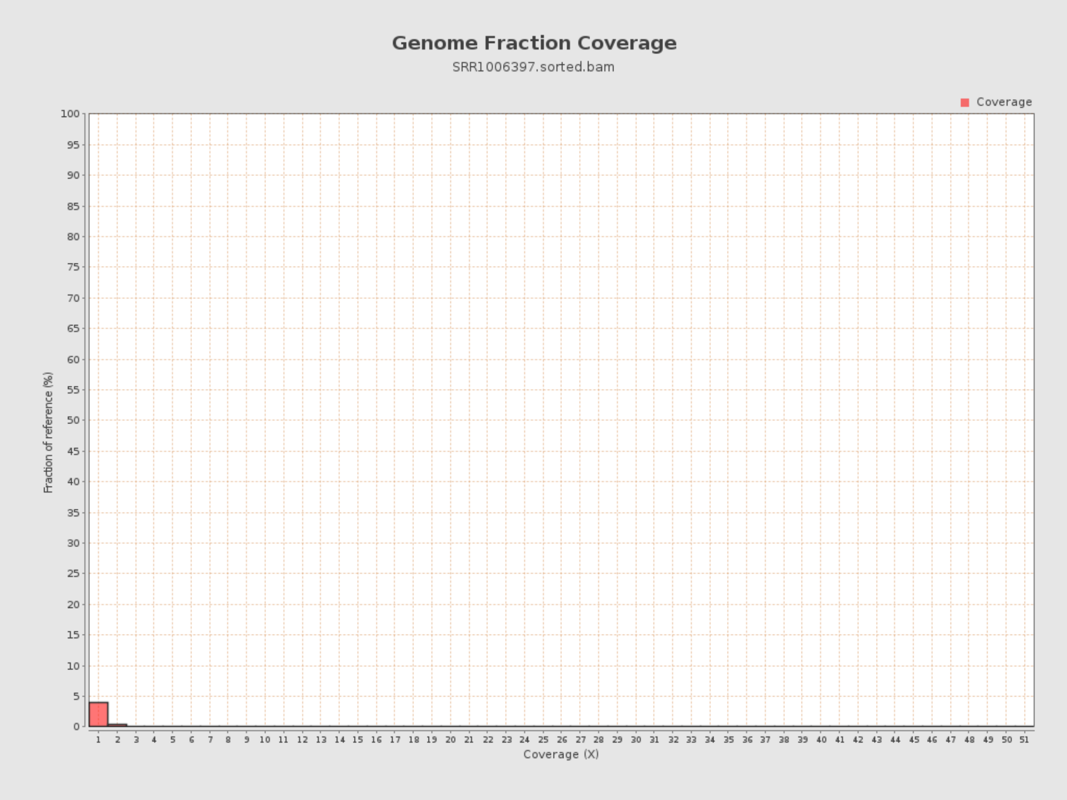
4. Results : Coverage Histogram



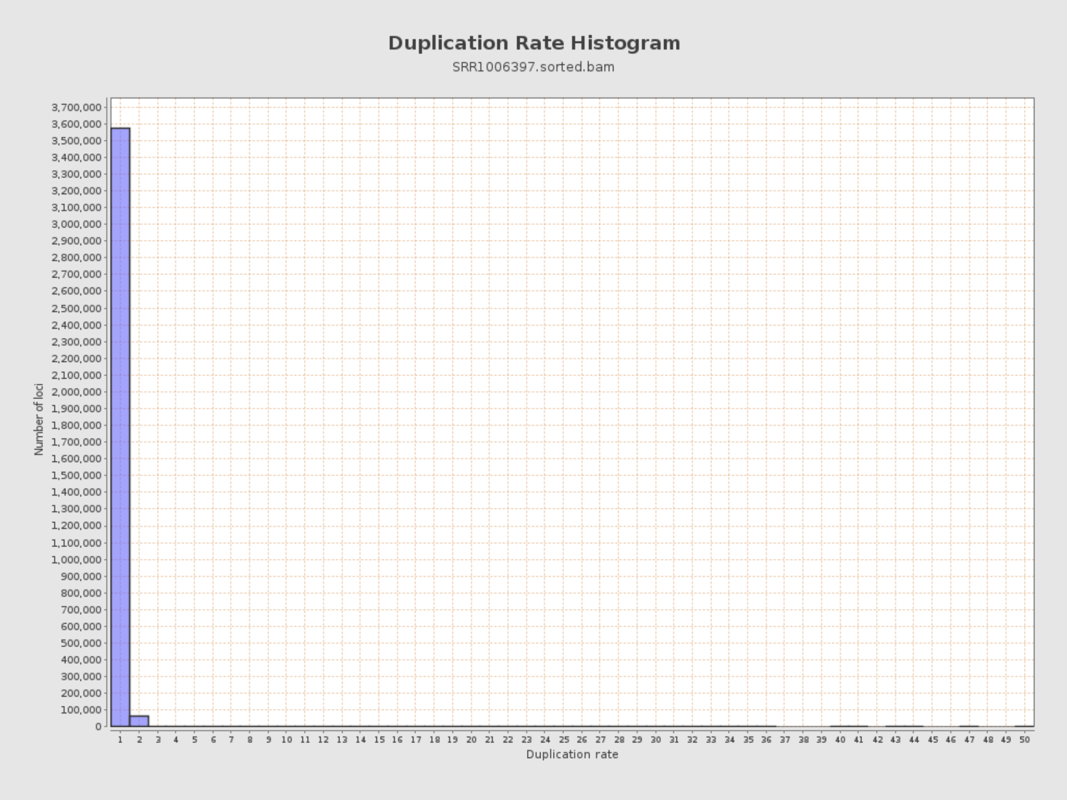
5. Results : Coverage Histogram (0-50X)



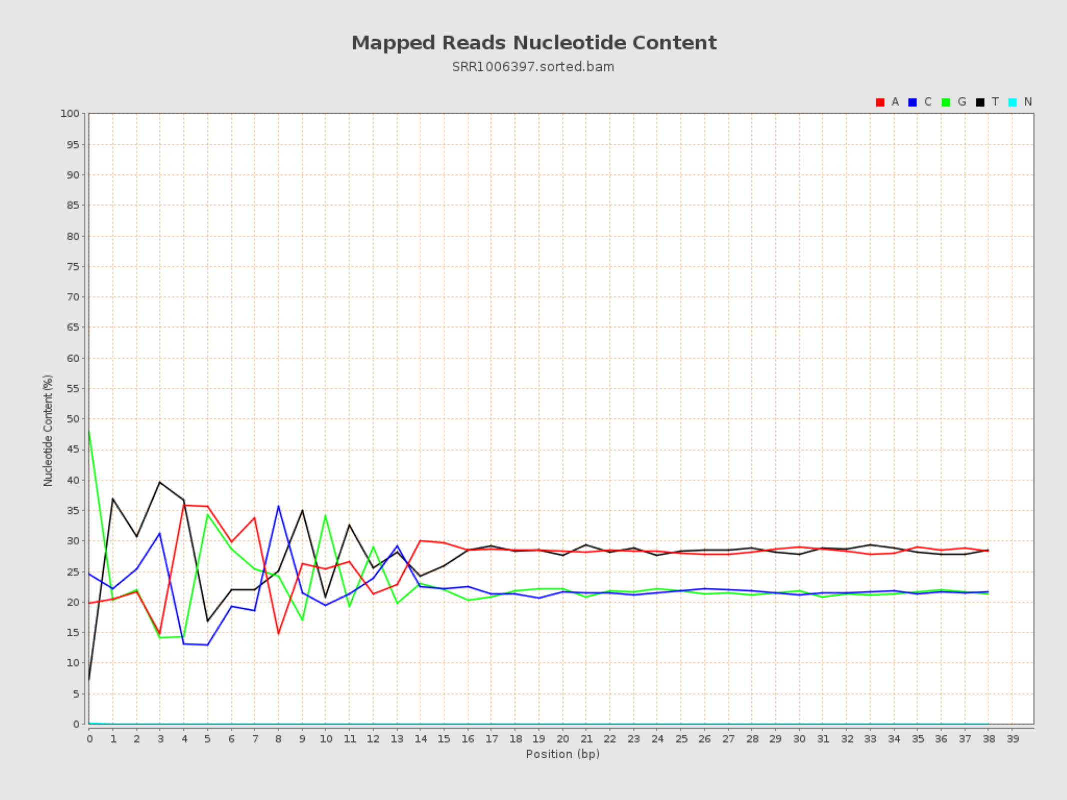
6. Results : Genome Fraction Coverage



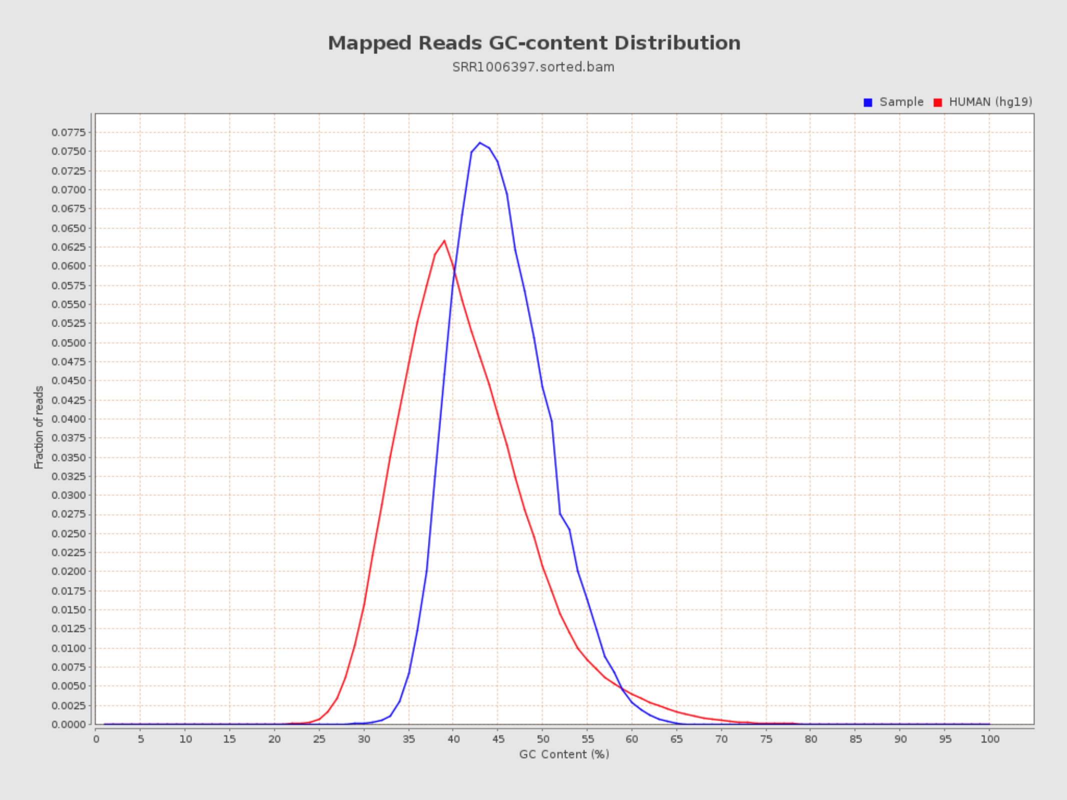
7. Results : Duplication Rate Histogram



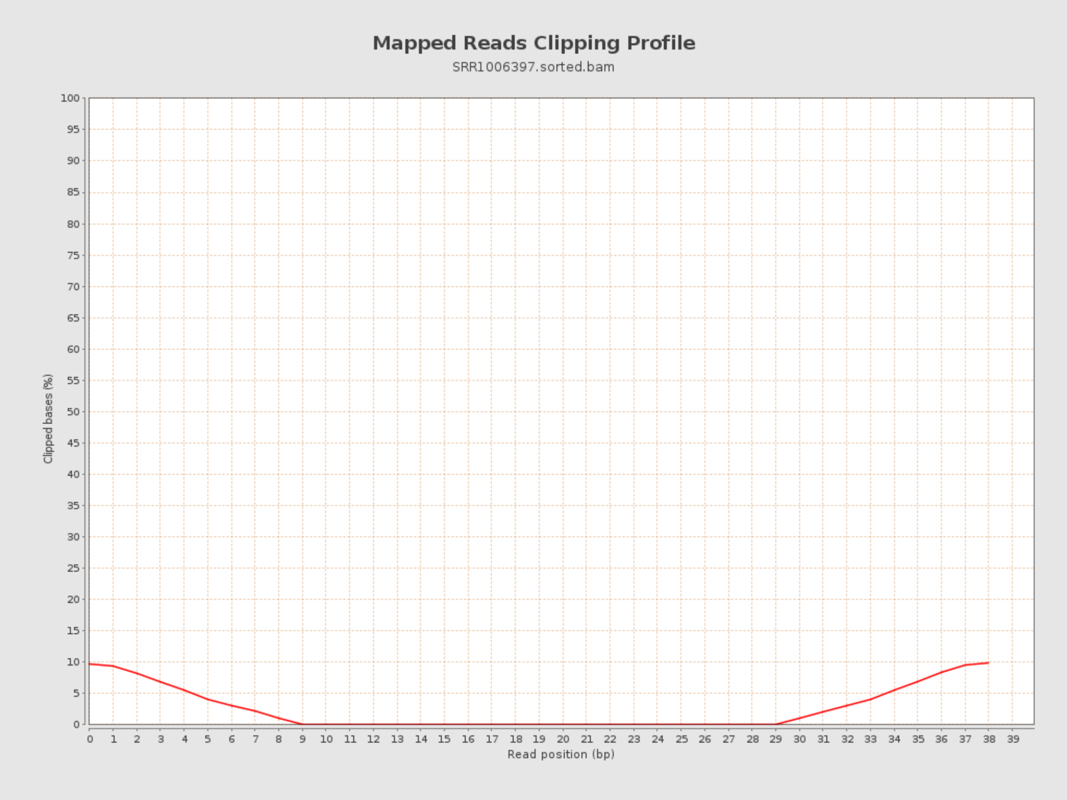
8. Results : Mapped Reads Nucleotide Content



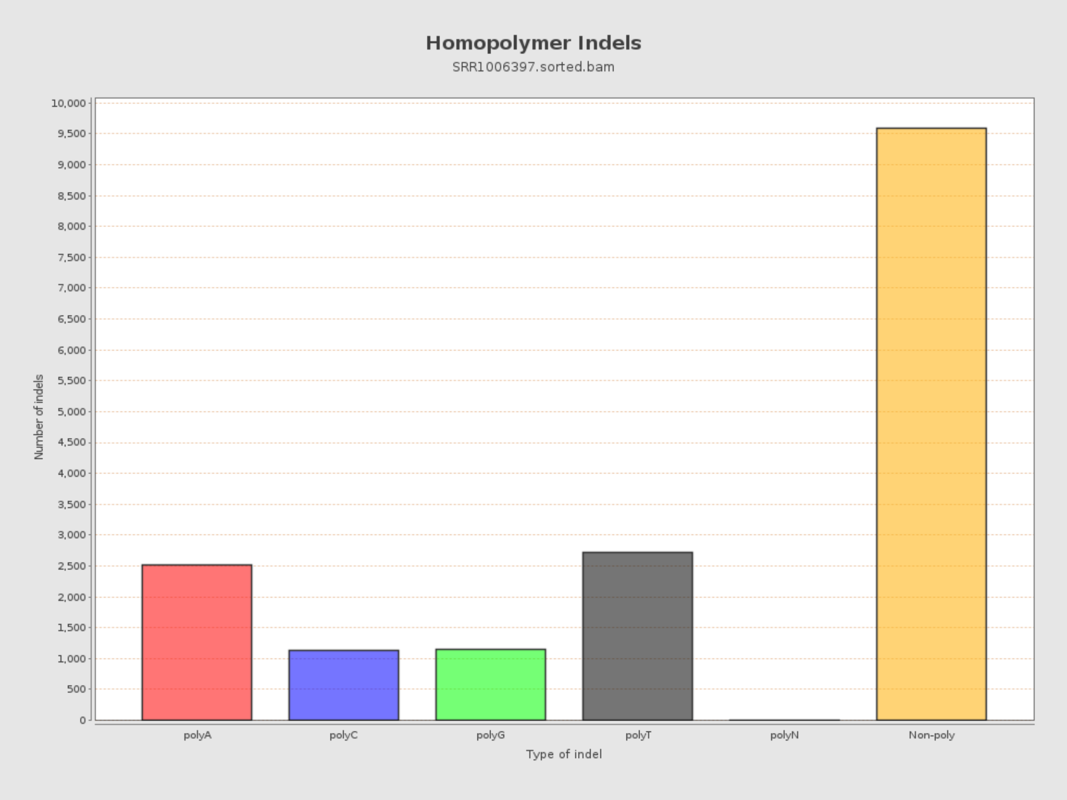
9. Results : Mapped Reads GC-content Distribution



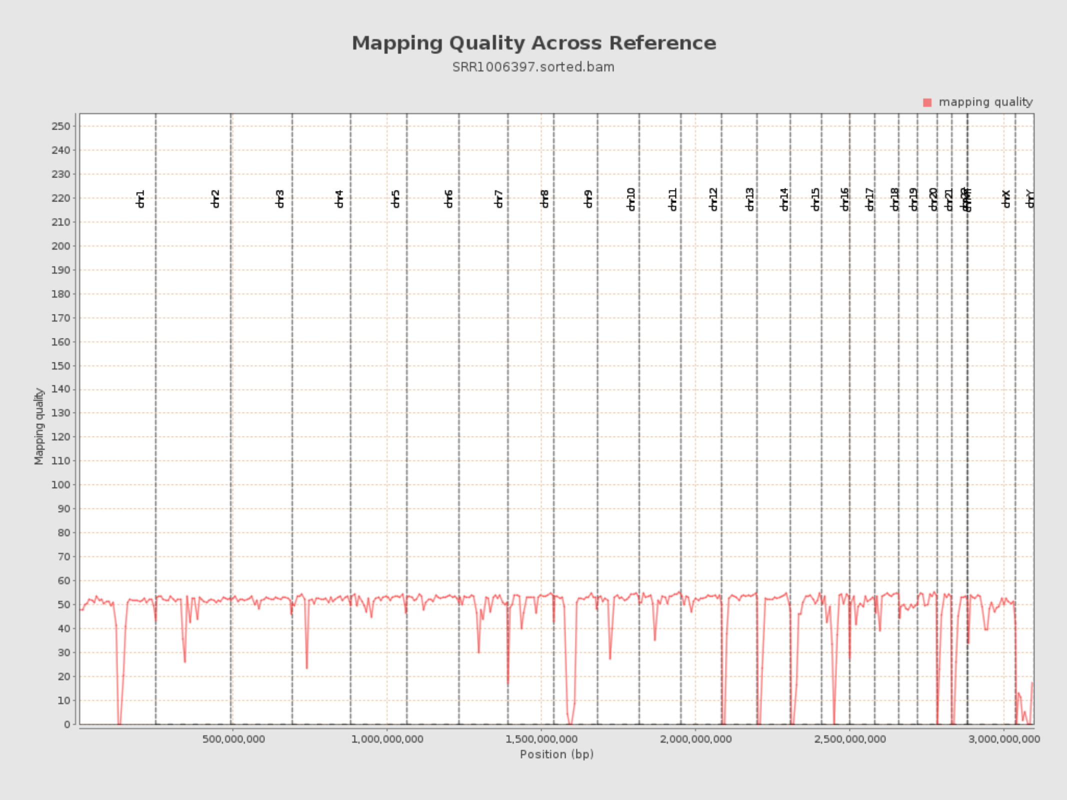
10. Results : Mapped Reads Clipping Profile



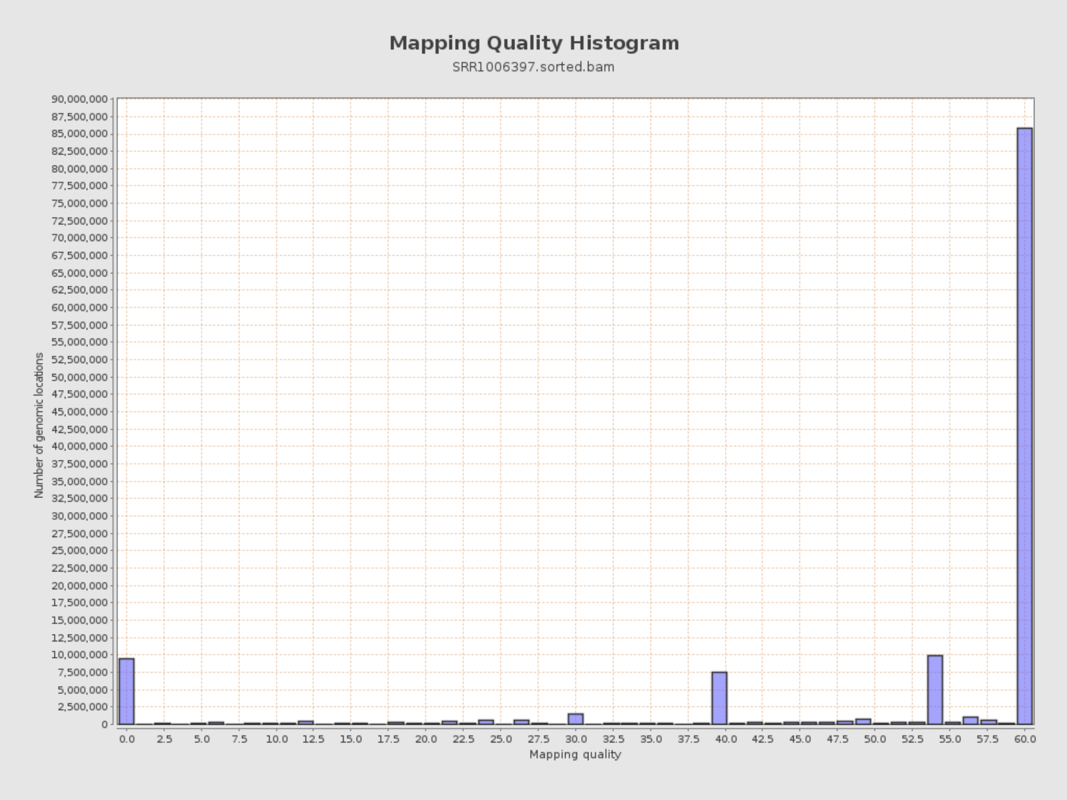
11. Results : Homopolymer Indels



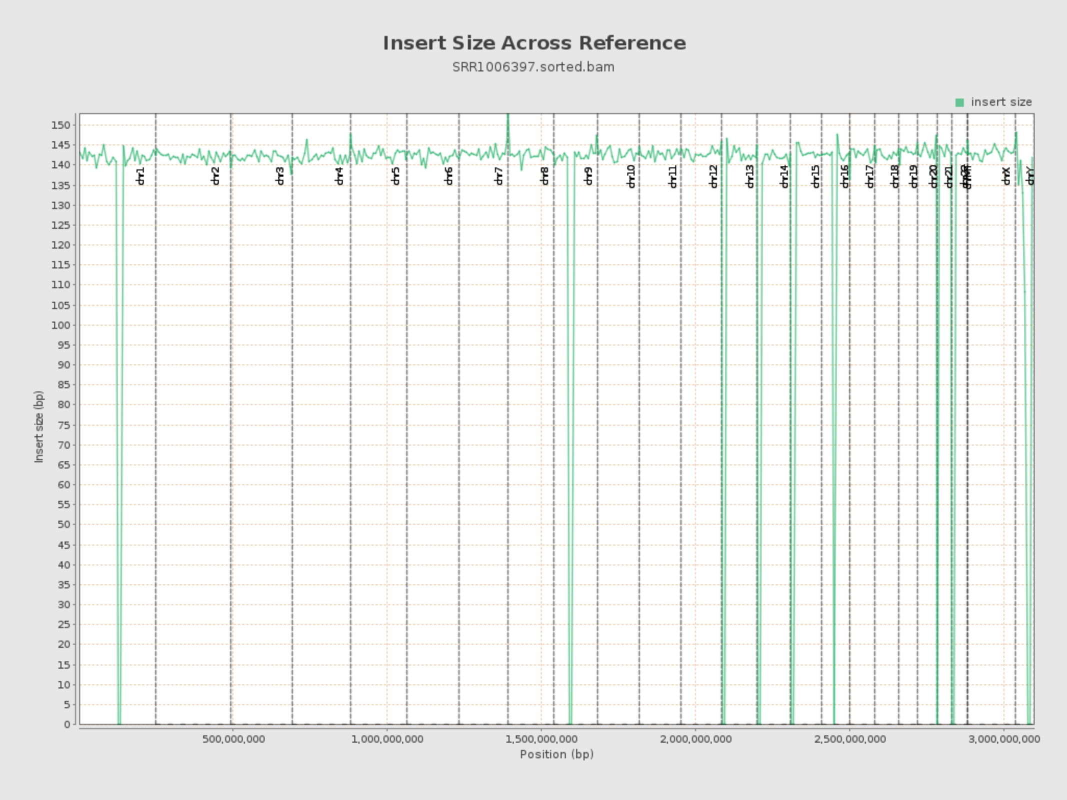
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram