Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 13:13:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006015.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_SRR1006015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006015_1.fastq.gz SRR1006015_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 13:13:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,544,380
Mapped reads	6,058,973 / 70.91%
Unmapped reads	2,485,407 / 29.09%
Mapped paired reads	6,058,973 / 70.91%
Mapped reads, first in pair	3,050,272 / 35.7%
Mapped reads, second in pair	3,008,701 / 35.21%
Mapped reads, both in pair	5,375,120 / 62.91%
Mapped reads, singletons	683,853 / 8%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	187,226 / 2.19%
Duplication rate	2.48%
Clipped reads	508,043 / 5.95%

2.2. ACGT Content

Number/percentage of A's	68,076,918 / 29.09%
Number/percentage of C's	48,705,189 / 20.81%
Number/percentage of T's	67,661,667 / 28.91%
Number/percentage of G's	49,386,701 / 21.1%
Number/percentage of N's	180,015 / 0.08%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0756
Standard Deviation	0.4936

2.4. Mapping Quality

Mean Mapping Quality	47.35

2.5. Insert size

Mean	63,815.55
Standard Deviation	2,422,813.08
P25/Median/P75	68 / 98 / 143

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	1,583,058
Insertions	6,740
Mapped reads with at least one insertion	0.11%
Deletions	21,238
Mapped reads with at least one deletion	0.35%
Homopolymer indels	44.26%

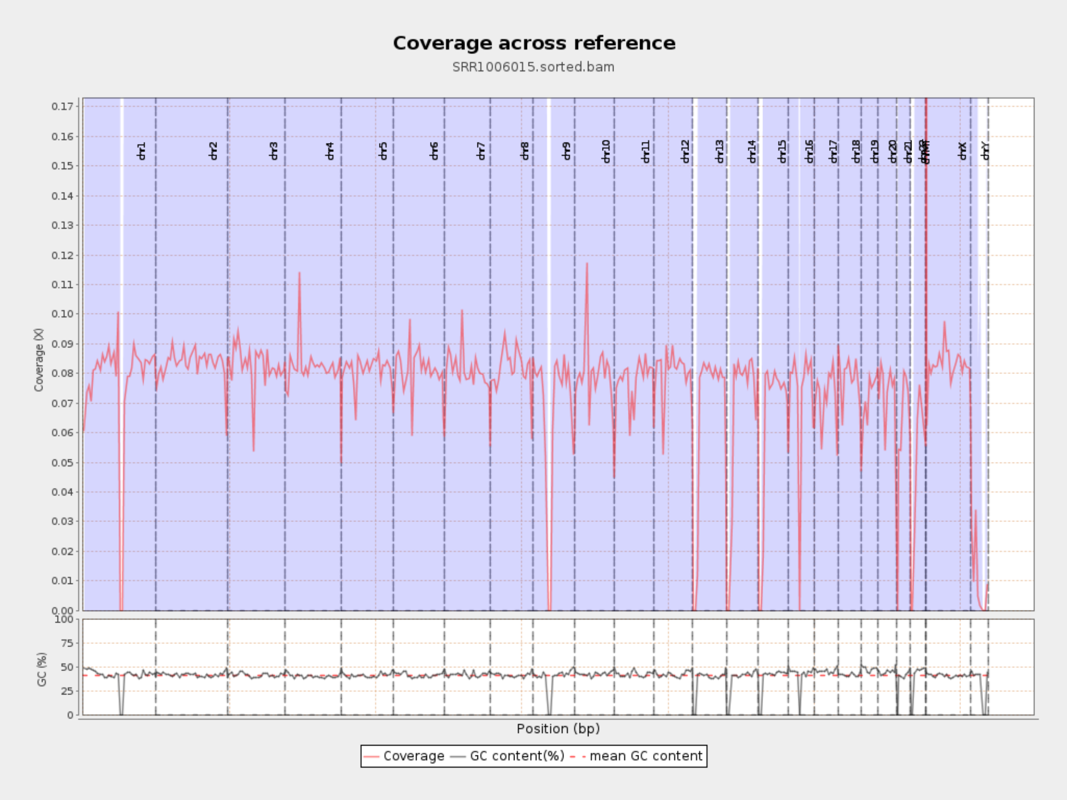
2.7. Chromosome stats

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

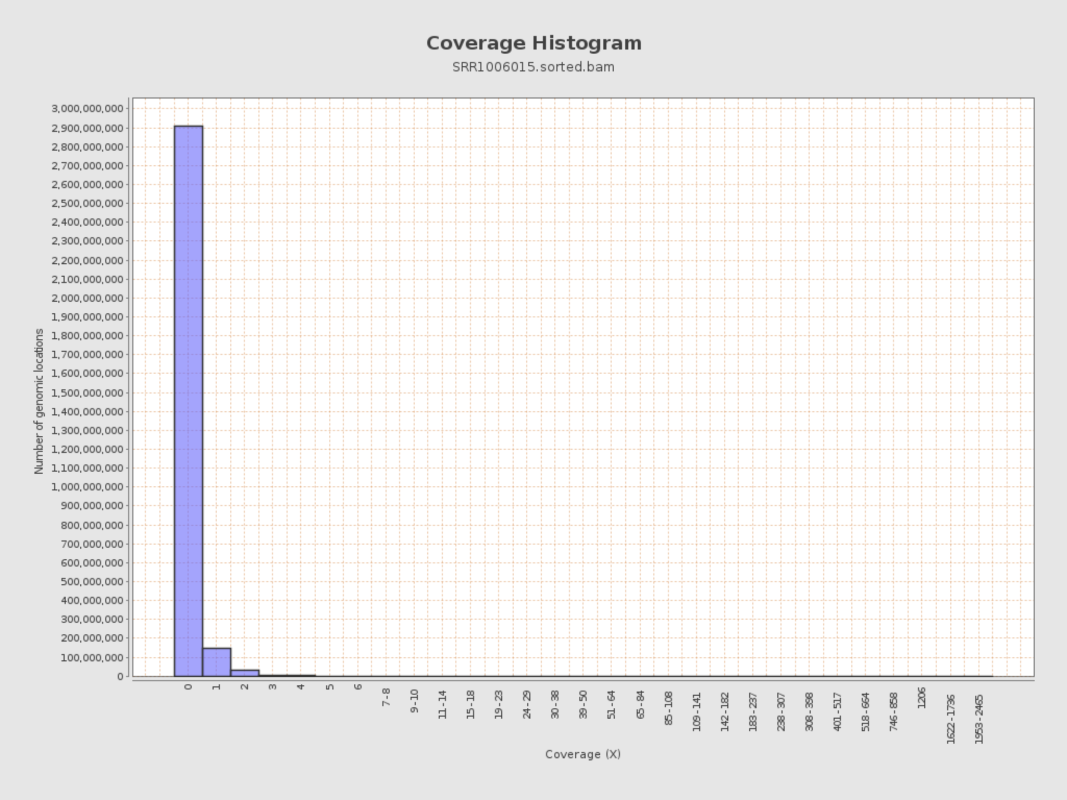
chr1	249250621	19180777	0.077	0.6904
chr2	243199373	20338101	0.0836	0.4179
chr3	198022430	16412217	0.0829	0.3436
chr4	191154276	15835608	0.0828	0.3818
chr5	180915260	14673253	0.0811	0.3405
chr6	171115067	13917373	0.0813	0.4182
chr7	159138663	12890526	0.081	0.5409
chr8	146364022	11956537	0.0817	1.2455
chr9	141213431	9455791	0.067	0.354
chr10	135534747	10904533	0.0805	0.4865
chr11	135006516	10420872	0.0772	0.3769
chr12	133851895	10796998	0.0807	0.3407
chr13	115169878	7674546	0.0666	0.3072
chr14	107349540	7092137	0.0661	0.3236
chr15	102531392	6340731	0.0618	0.2959
chr16	90354753	6392588	0.0707	0.3584
chr17	81195210	5904667	0.0727	0.3344
chr18	78077248	6132874	0.0785	0.5195
chr19	59128983	4235829	0.0716	0.5641
chr20	63025520	4635555	0.0736	0.3338
chr21	48129895	2941873	0.0611	0.3314
chr22	51304566	2399431	0.0468	0.2683
chrMT	16571	33958	2.0492	1.9483
chrX	155270560	12870556	0.0829	0.3694

chrY	59373566	601054	0.0101	0.2352

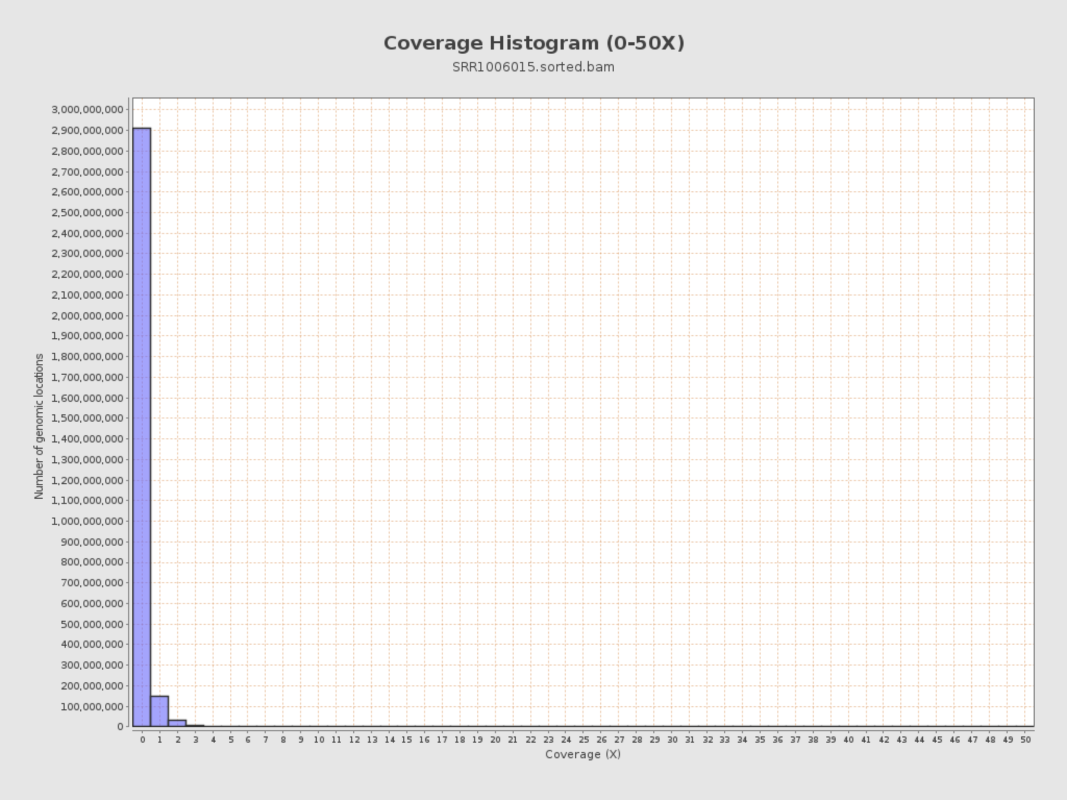
3. Results : Coverage across reference



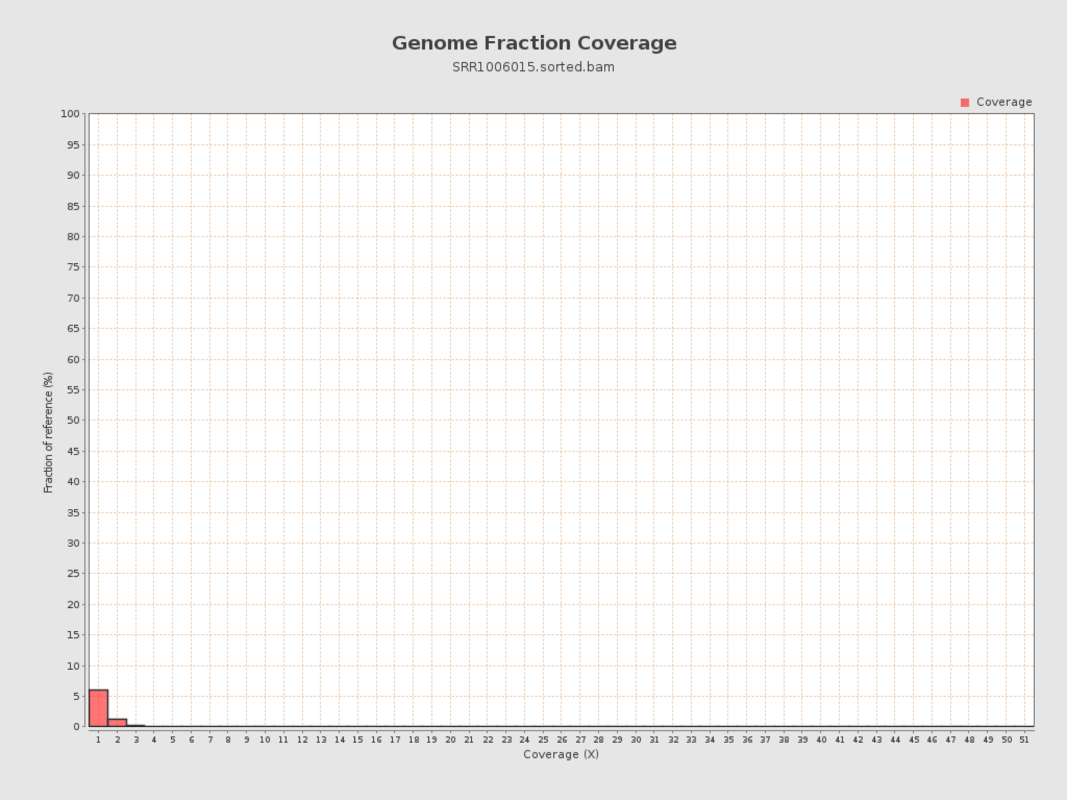
4. Results : Coverage Histogram



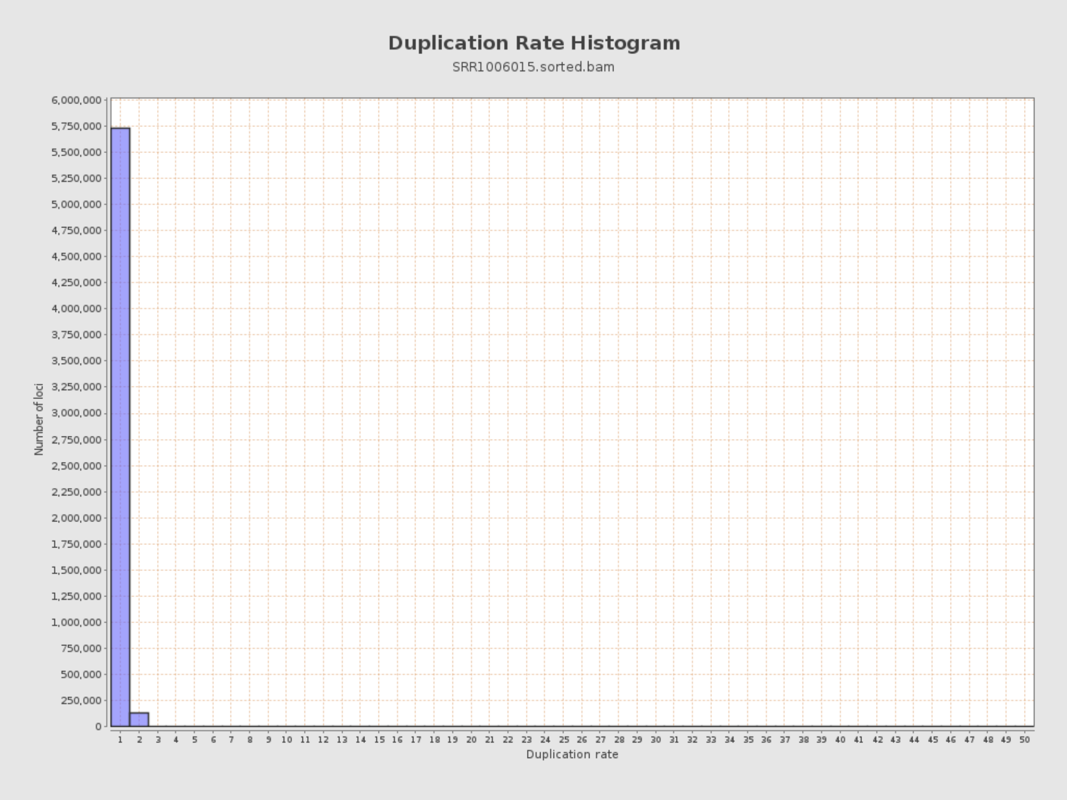
5. Results : Coverage Histogram (0-50X)



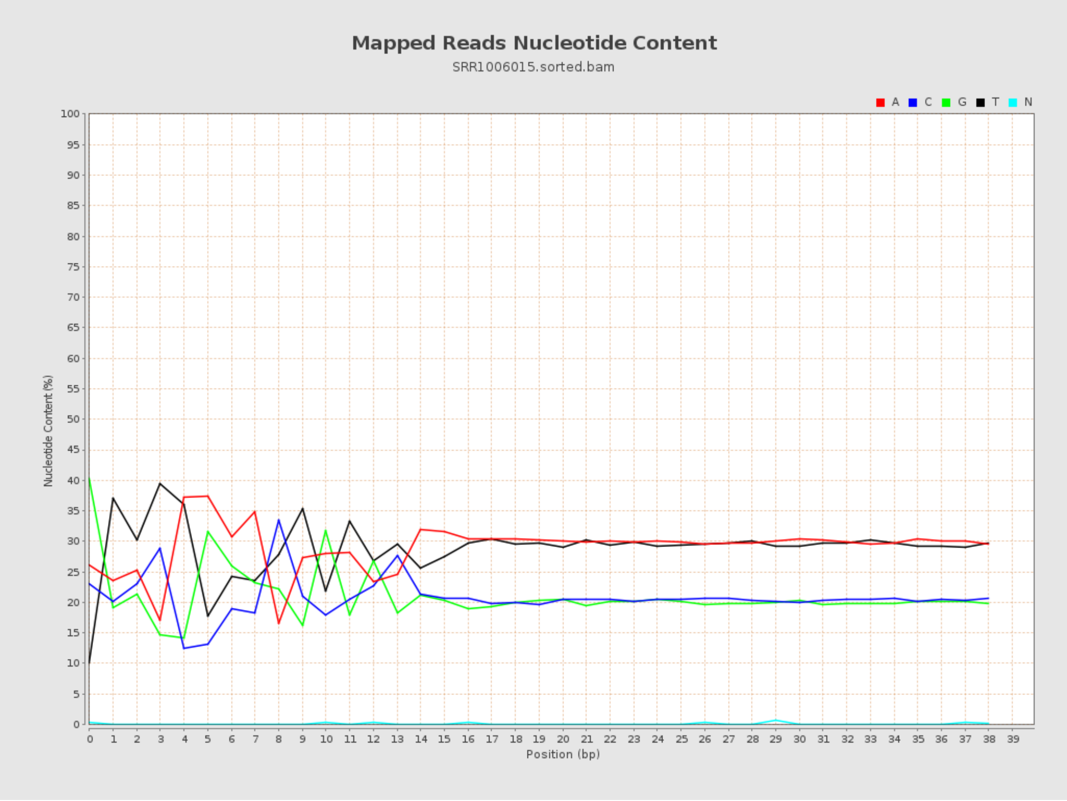
6. Results : Genome Fraction Coverage



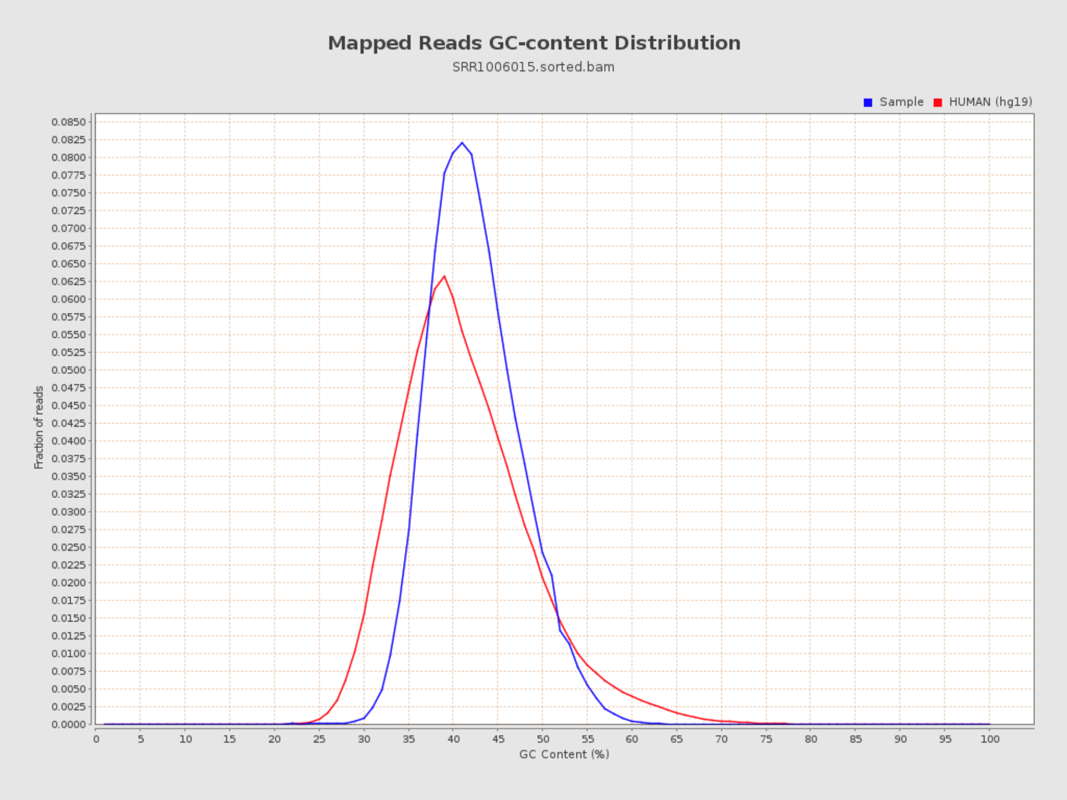
7. Results : Duplication Rate Histogram



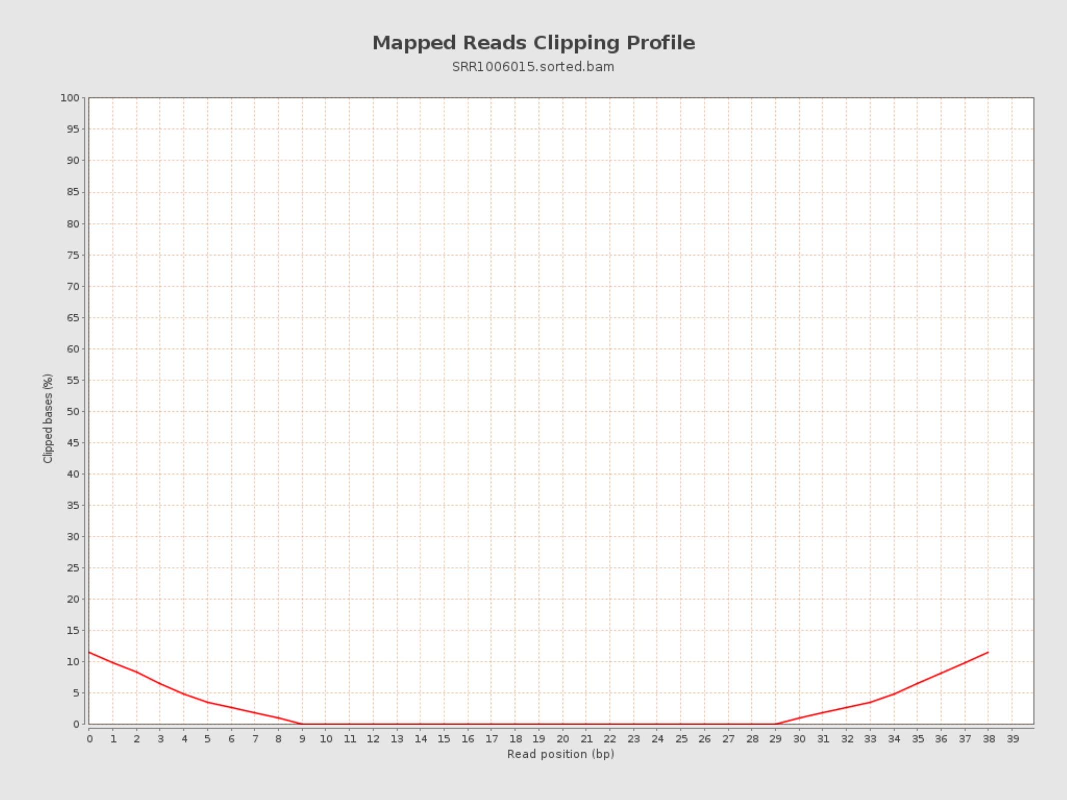
8. Results : Mapped Reads Nucleotide Content



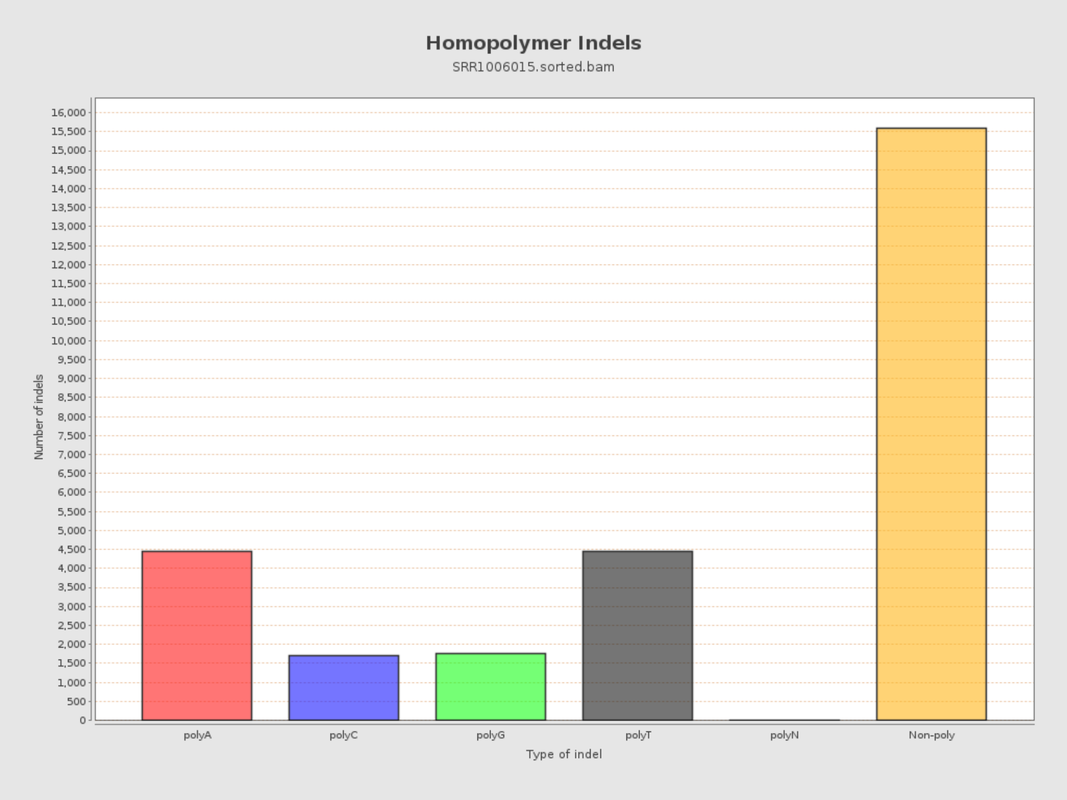
9. Results : Mapped Reads GC-content Distribution



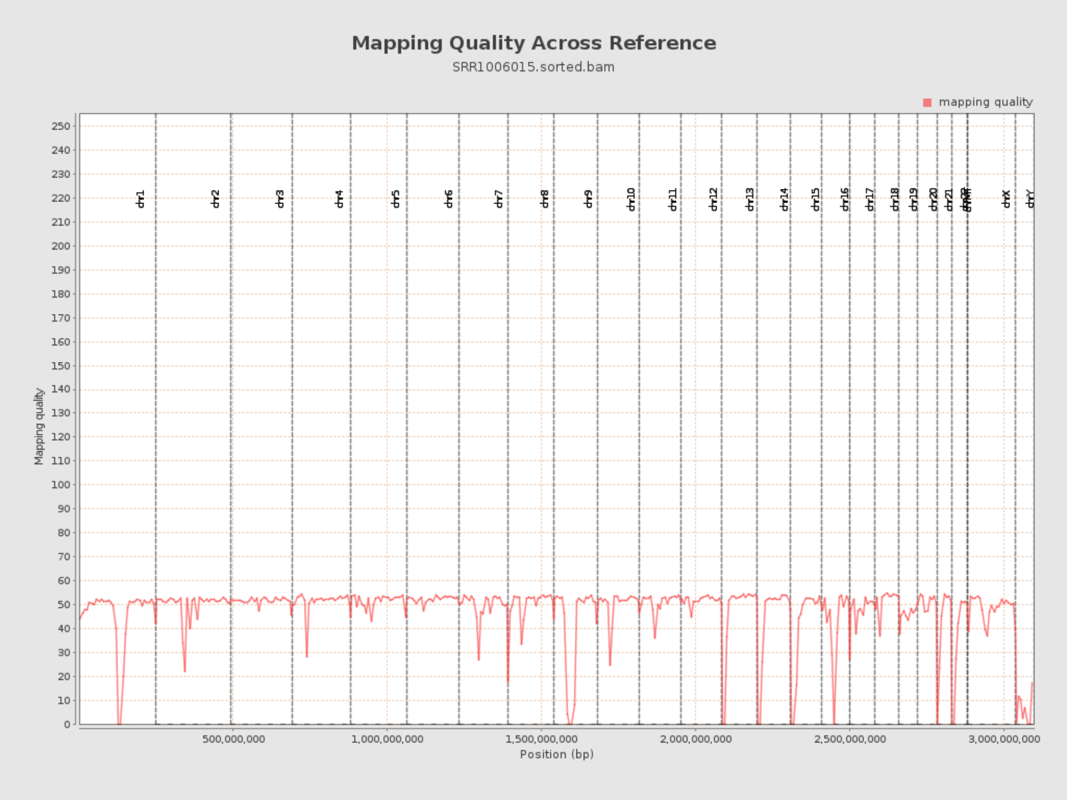
10. Results : Mapped Reads Clipping Profile



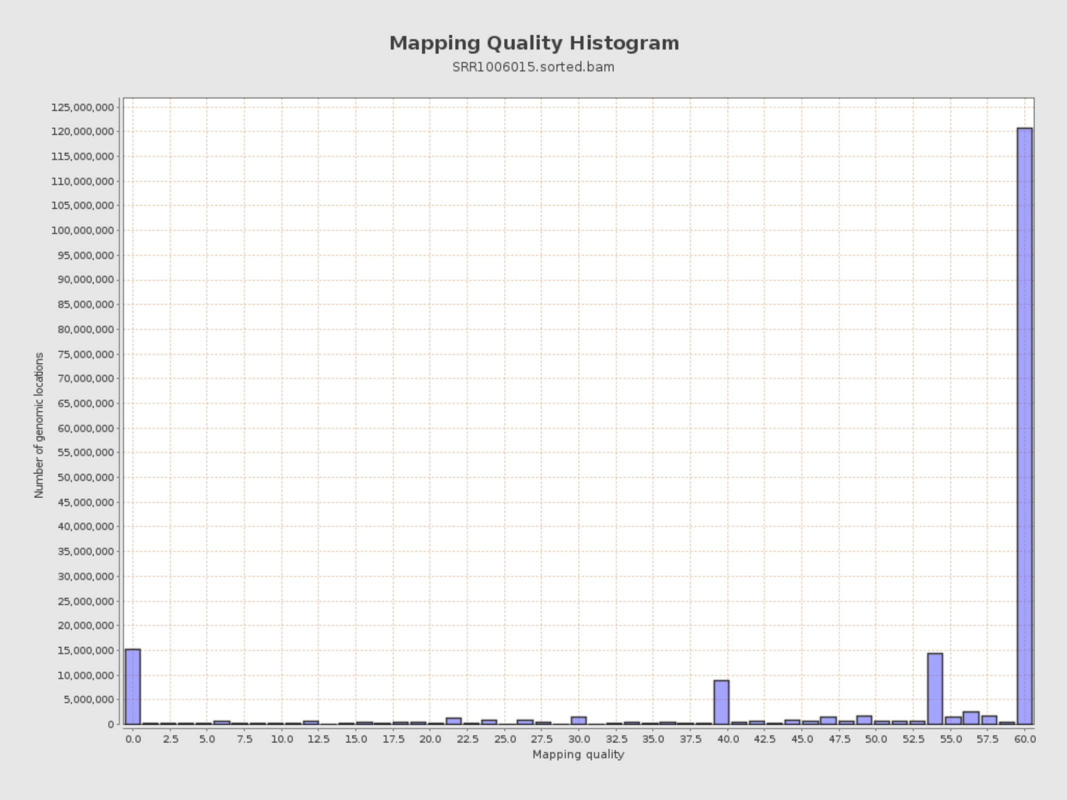
11. Results : Homopolymer Indels



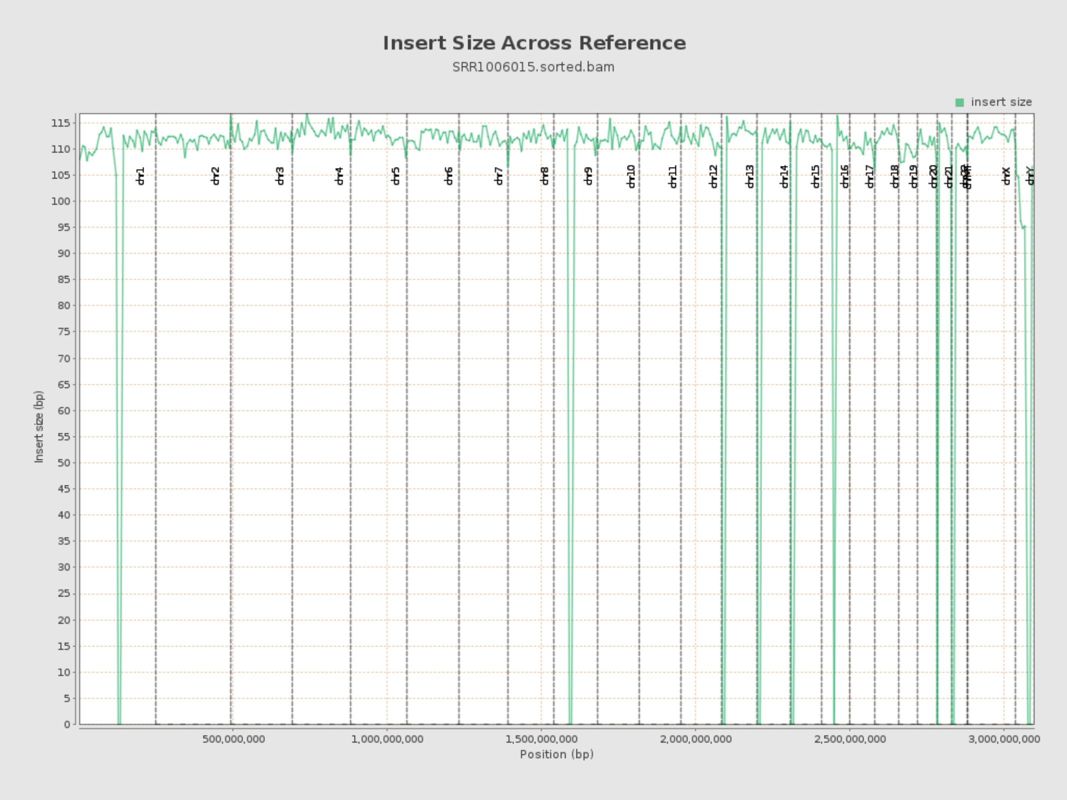
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram