Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006050.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_SRR1006050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006050_1.fastq.gz SRR1006050_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:30:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,978,850
Mapped reads	5,183,570 / 86.7%
Unmapped reads	795,280 / 13.3%
Mapped paired reads	5,183,570 / 86.7%
Mapped reads, first in pair	2,651,420 / 44.35%
Mapped reads, second in pair	2,532,150 / 42.35%
Mapped reads, both in pair	4,751,442 / 79.47%
Mapped reads, singletons	432,128 / 7.23%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	208,039 / 3.48%
Duplication rate	3.58%
Clipped reads	397,309 / 6.65%

2.2. ACGT Content

Number/percentage of A's	54,368,011 / 27.14%
Number/percentage of C's	44,438,128 / 22.19%
Number/percentage of T's	55,636,275 / 27.78%
Number/percentage of G's	45,768,047 / 22.85%
Number/percentage of N's	79,795 / 0.04%
GC Percentage	45.04%

2.3. Coverage

Mean	0.0647
Standard Deviation	0.3839

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Insert size

Mean	55,388.92
Standard Deviation	2,332,846.85
P25/Median/P75	63 / 90 / 130

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	1,116,804
Insertions	6,152
Mapped reads with at least one insertion	0.12%
Deletions	15,692
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.76%

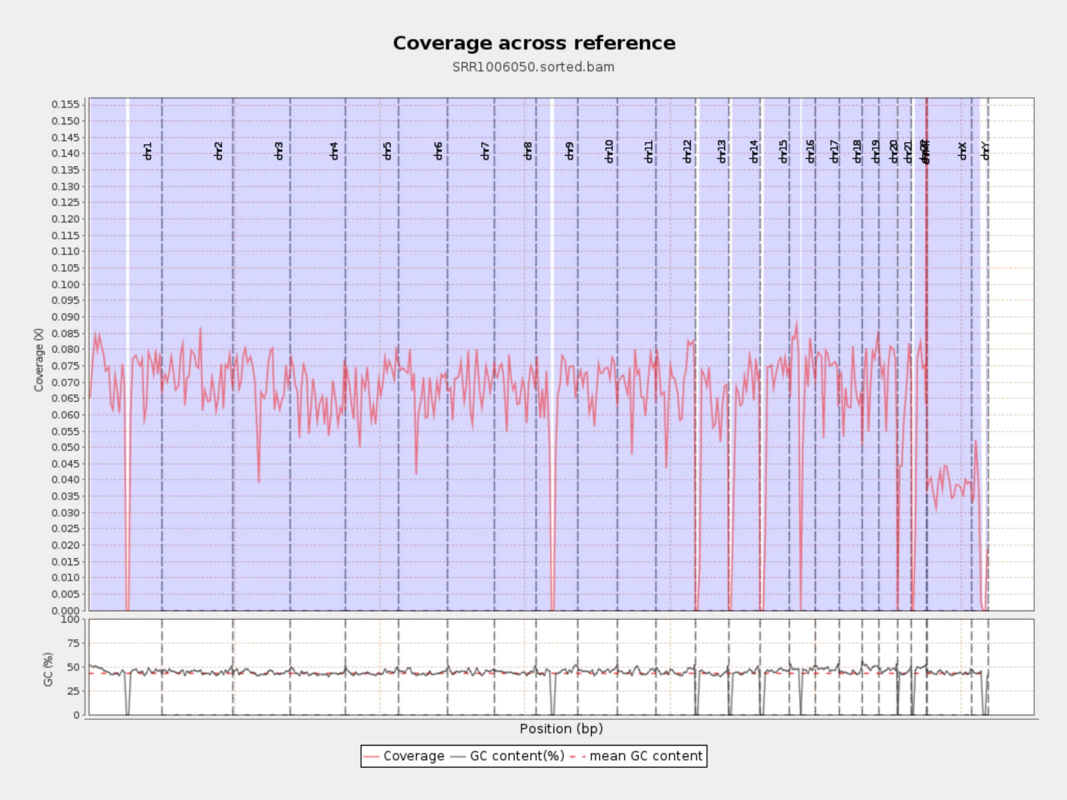
2.7. Chromosome stats

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

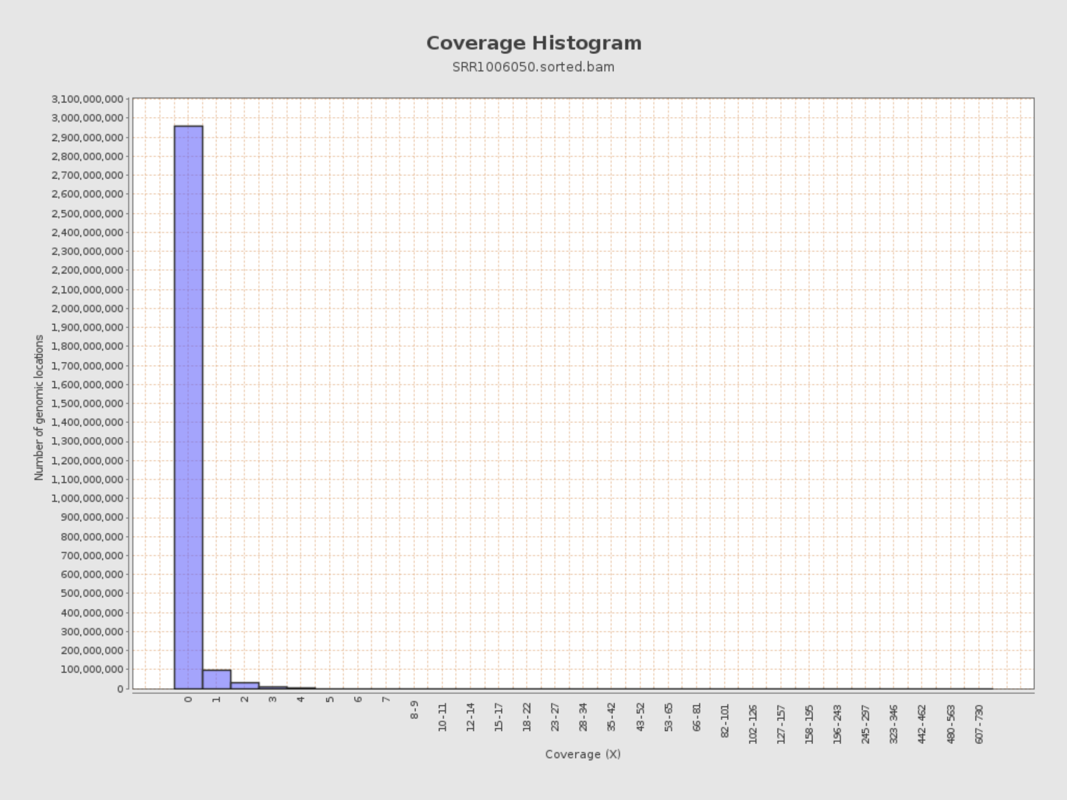
chr1	249250621	17085818	0.0685	0.4039
chr2	243199373	17432835	0.0717	0.4288
chr3	198022430	13814256	0.0698	0.353
chr4	191154276	12387936	0.0648	0.3534
chr5	180915260	12336678	0.0682	0.351
chr6	171115067	11619108	0.0679	0.3812
chr7	159138663	10990697	0.0691	0.4629
chr8	146364022	10140804	0.0693	0.4114
chr9	141213431	8485669	0.0601	0.3596
chr10	135534747	9576139	0.0707	0.3763
chr11	135006516	9389408	0.0695	0.5204
chr12	133851895	9356390	0.0699	0.3565
chr13	115169878	6284133	0.0546	0.3148
chr14	107349540	6193395	0.0577	0.3316
chr15	102531392	6138506	0.0599	0.3323
chr16	90354753	6250995	0.0692	0.3935
chr17	81195210	6008747	0.074	0.4017
chr18	78077248	5217896	0.0668	0.4568
chr19	59128983	4342259	0.0734	0.4483
chr20	63025520	4601078	0.073	0.3695
chr21	48129895	2669384	0.0555	0.3497
chr22	51304566	2702949	0.0527	0.3387
chrMT	16571	3999	0.2413	0.6634
chrX	155270560	5986996	0.0386	0.2751

chrY	59373566	1294339	0.0218	0.2284

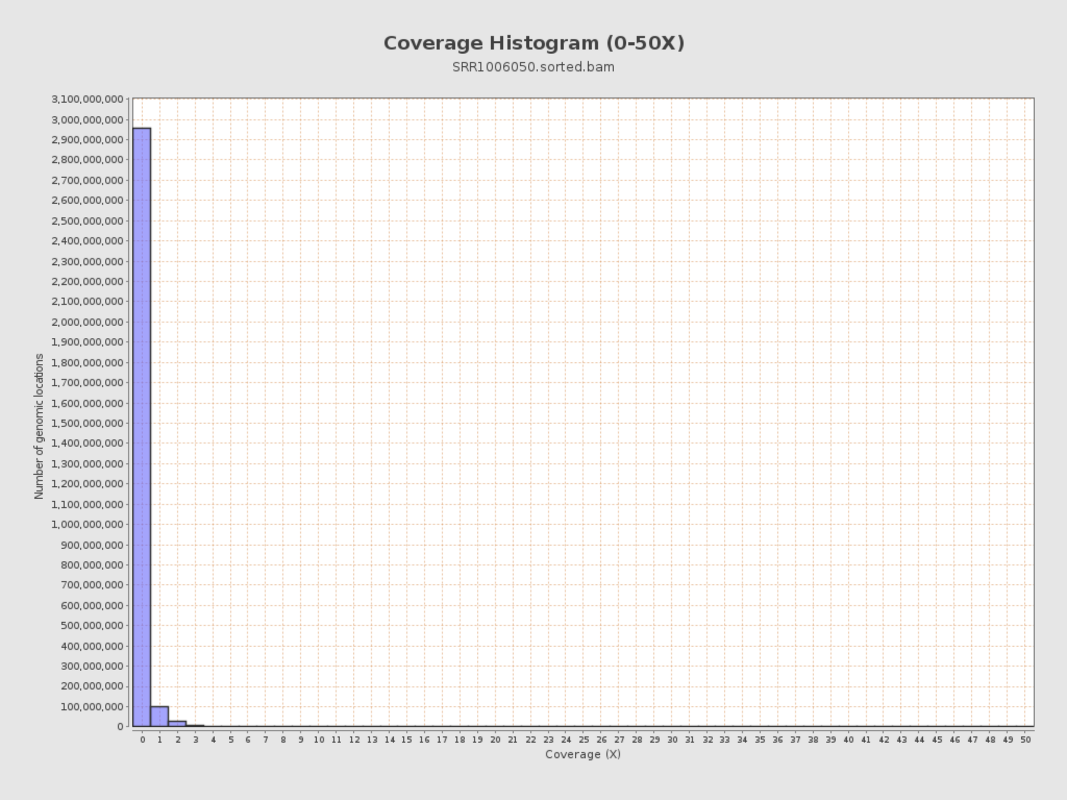
3. Results : Coverage across reference



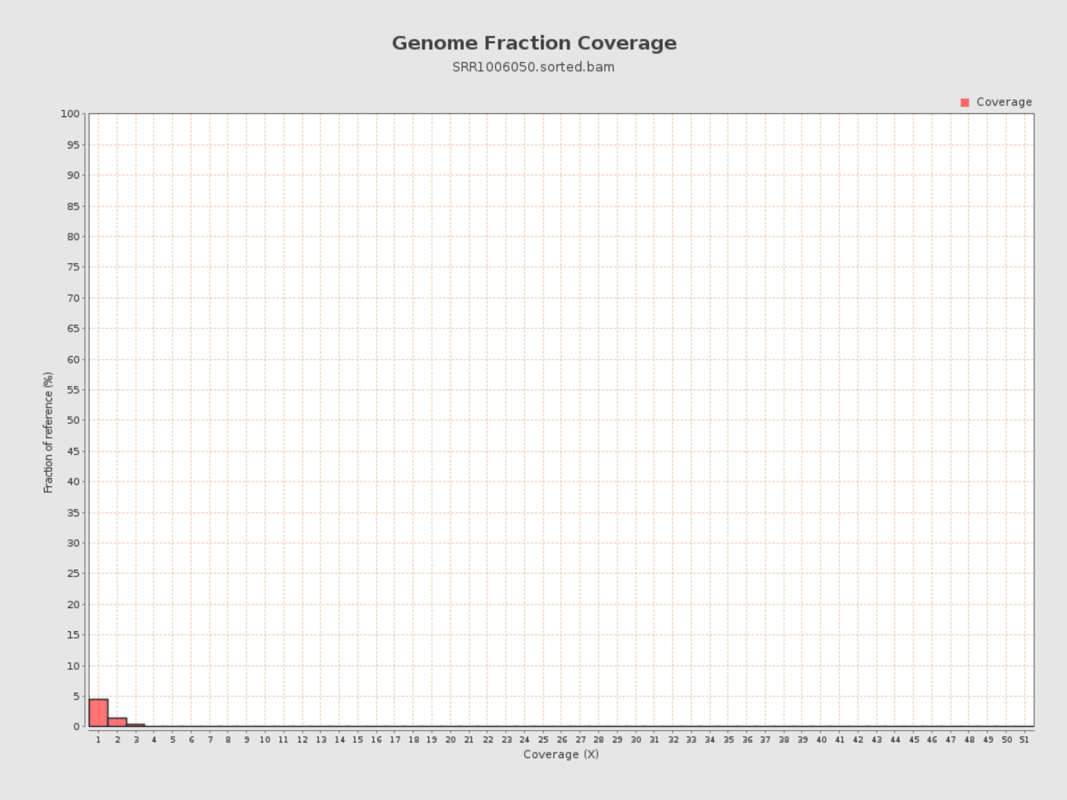
4. Results : Coverage Histogram



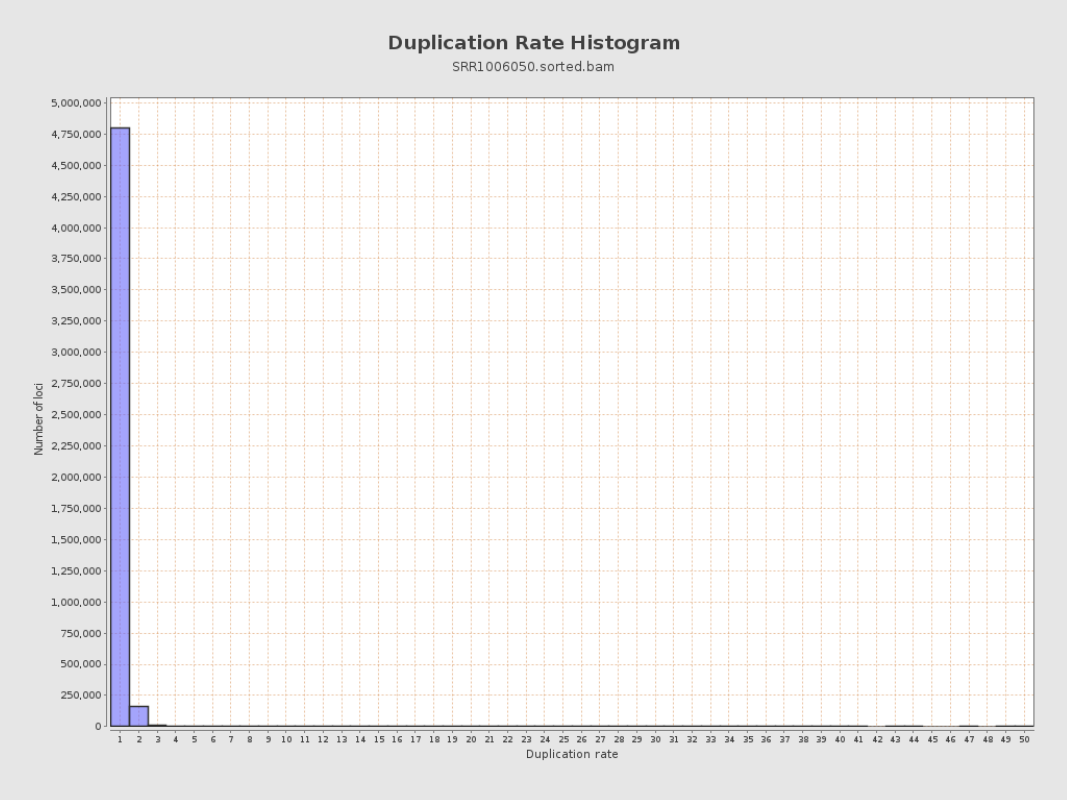
5. Results : Coverage Histogram (0-50X)



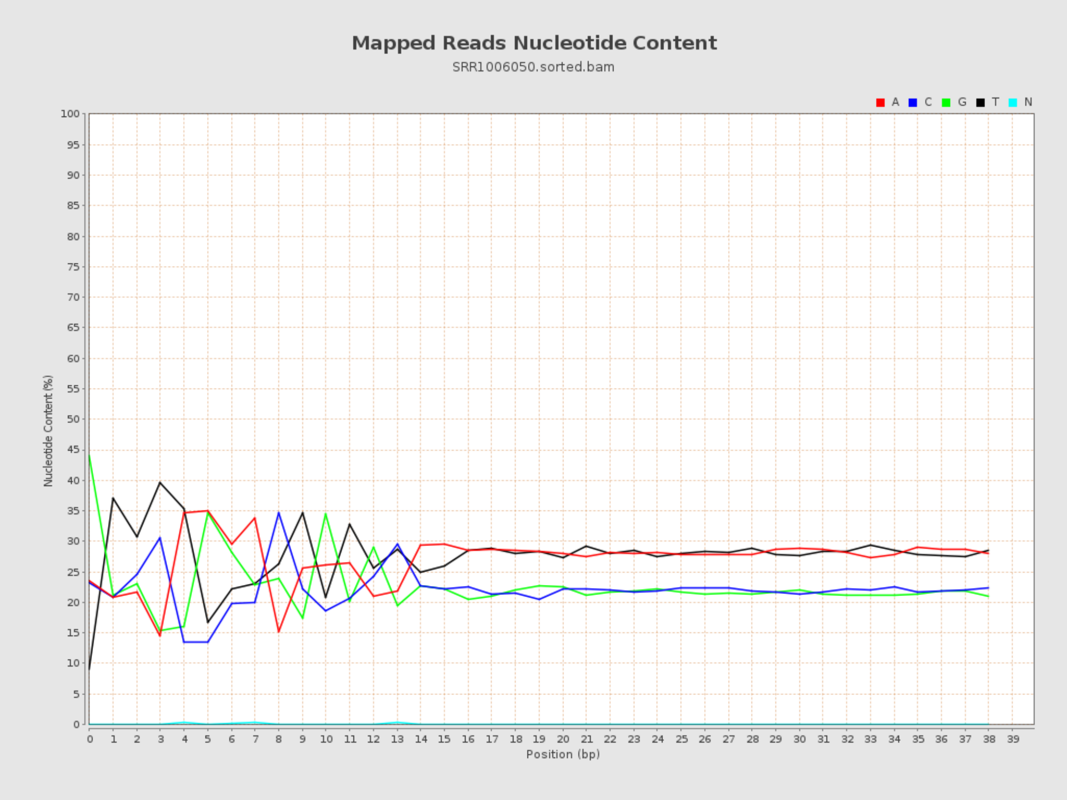
6. Results : Genome Fraction Coverage



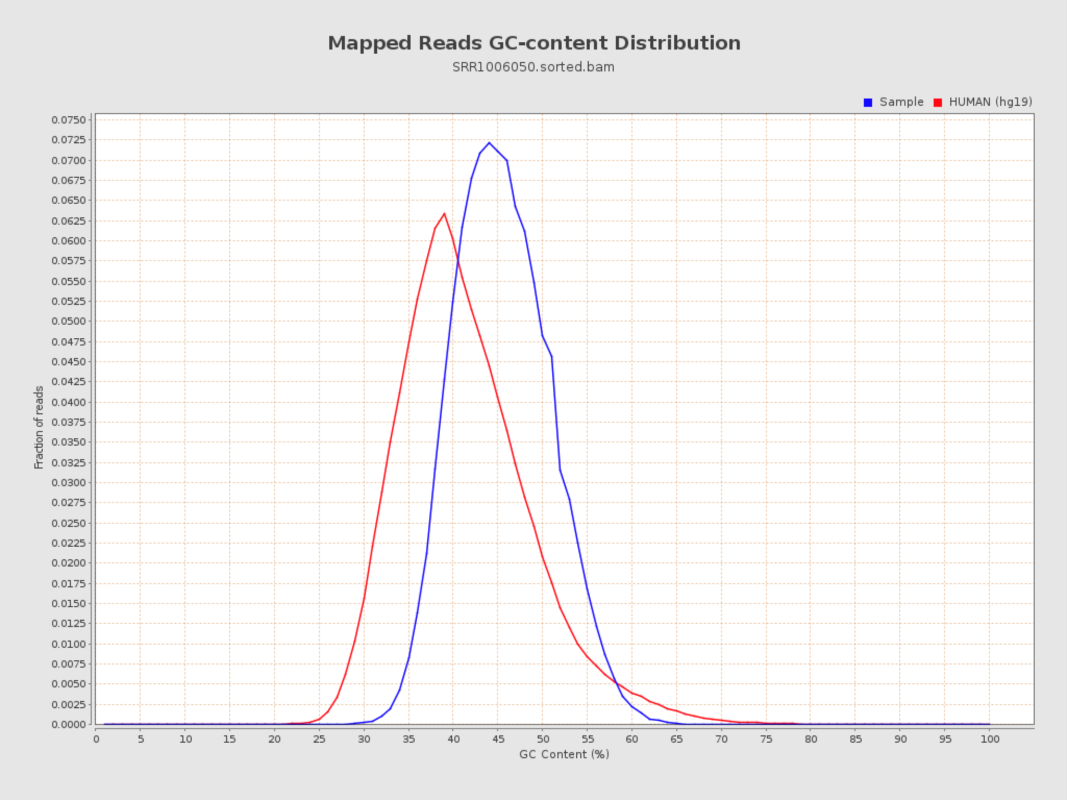
7. Results : Duplication Rate Histogram



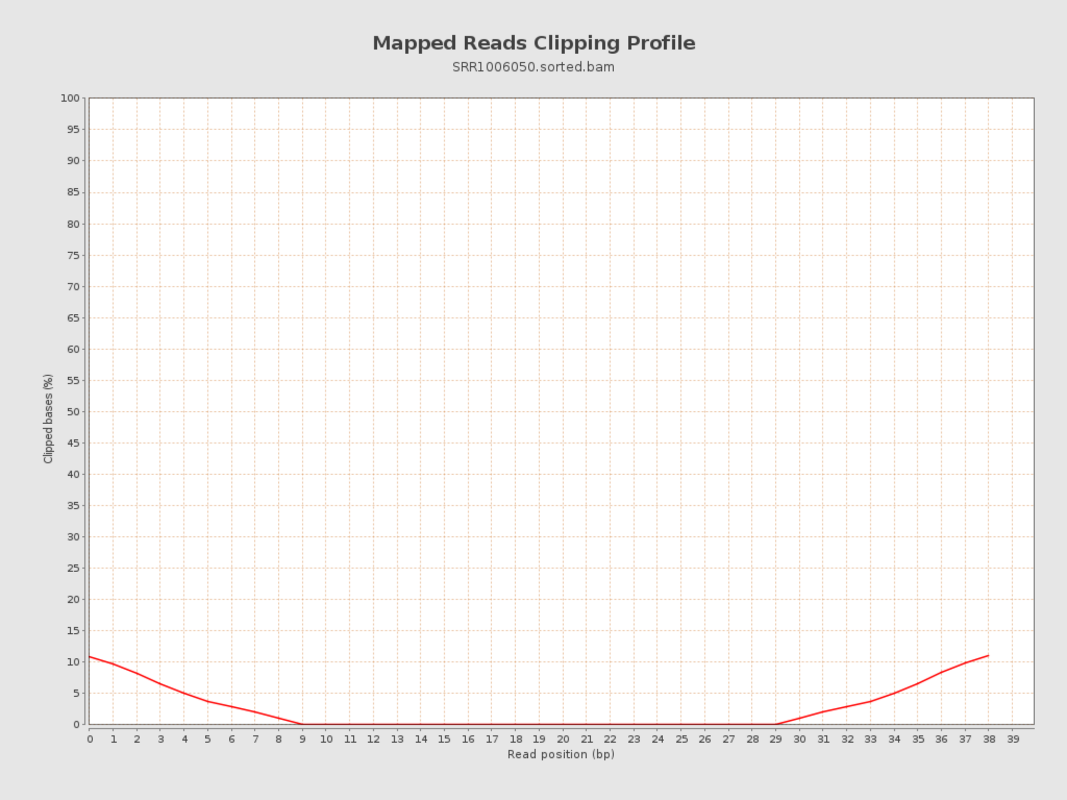
8. Results : Mapped Reads Nucleotide Content



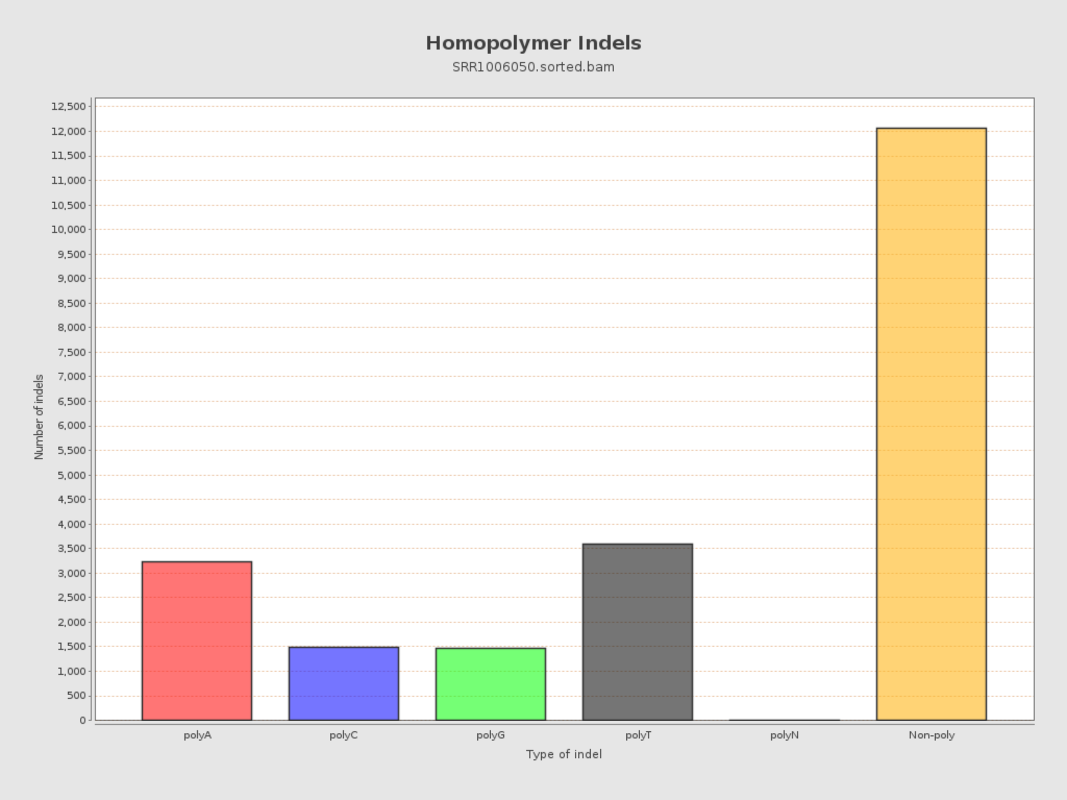
9. Results : Mapped Reads GC-content Distribution



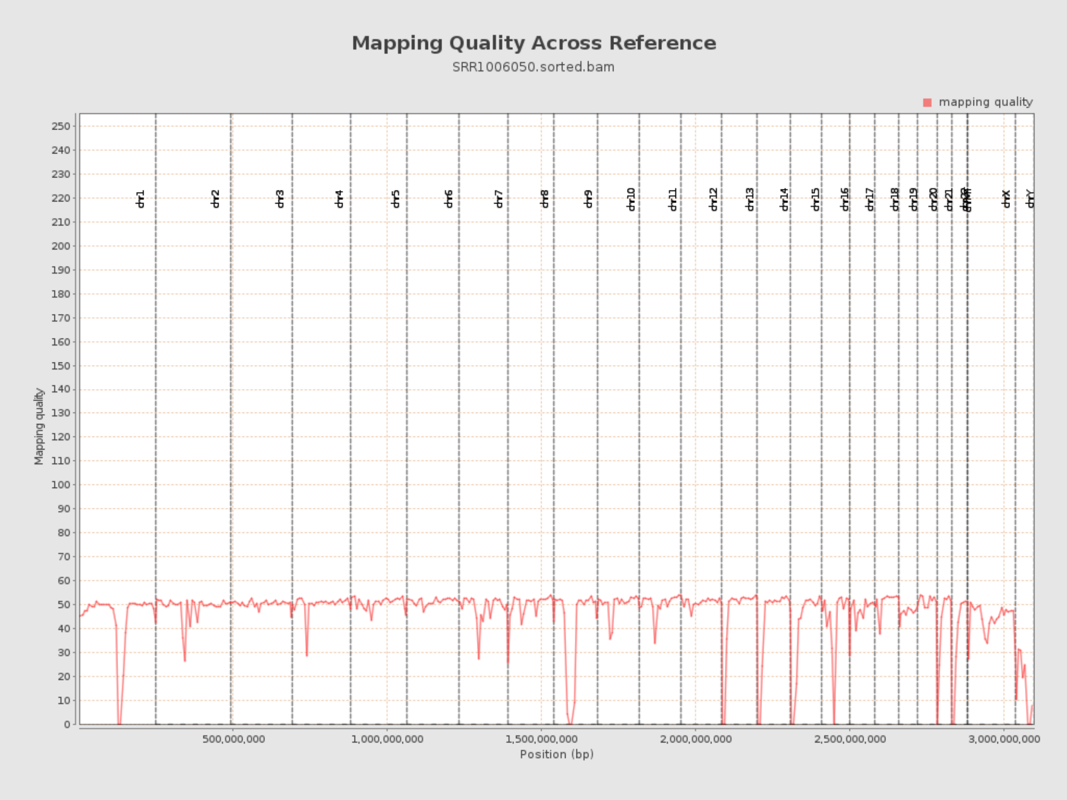
10. Results : Mapped Reads Clipping Profile



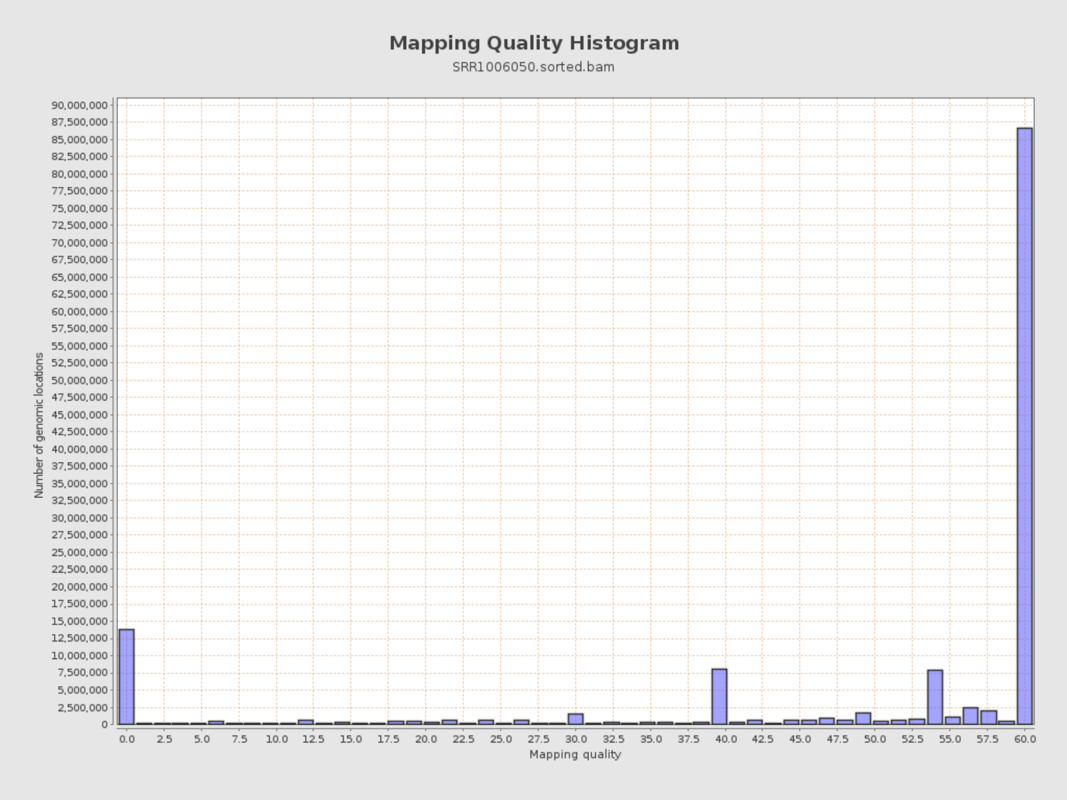
11. Results : Homopolymer Indels



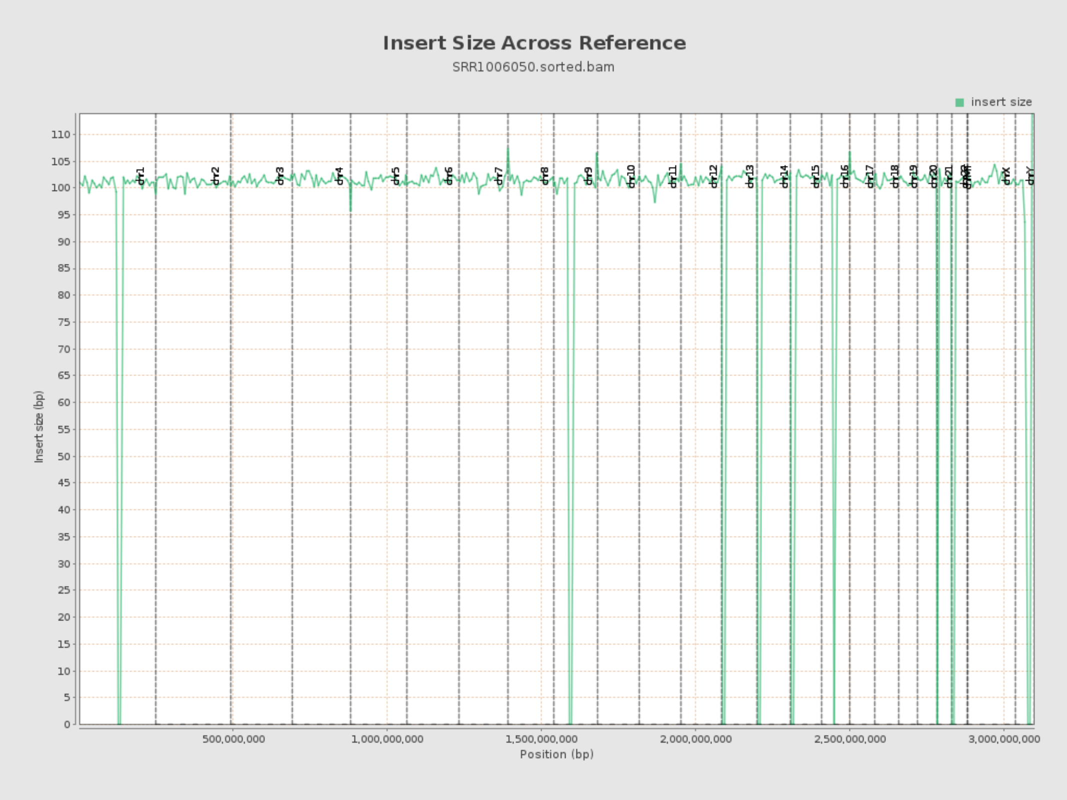
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram