Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:46:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006053.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_SRR1006053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006053_1.fastq.gz SRR1006053_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:46:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,271,448
Mapped reads	5,502,993 / 87.75%
Unmapped reads	768,455 / 12.25%
Mapped paired reads	5,502,993 / 87.75%
Mapped reads, first in pair	2,795,295 / 44.57%
Mapped reads, second in pair	2,707,698 / 43.18%
Mapped reads, both in pair	5,065,218 / 80.77%
Mapped reads, singletons	437,775 / 6.98%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	247,127 / 3.94%
Duplication rate	4.05%
Clipped reads	437,870 / 6.98%

2.2. ACGT Content

Number/percentage of A's	56,270,870 / 26.48%
Number/percentage of C's	47,786,680 / 22.49%
Number/percentage of T's	58,205,448 / 27.39%
Number/percentage of G's	50,235,169 / 23.64%
Number/percentage of N's	10,079 / 0%
GC Percentage	46.13%

2.3. Coverage

Mean	0.0687
Standard Deviation	0.4014

2.4. Mapping Quality

Mean Mapping Quality	46.86

2.5. Insert size

Mean	56,052.04
Standard Deviation	2,316,082.36
P25/Median/P75	66 / 94 / 135

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	983,786
Insertions	6,965
Mapped reads with at least one insertion	0.13%
Deletions	18,055
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.36%

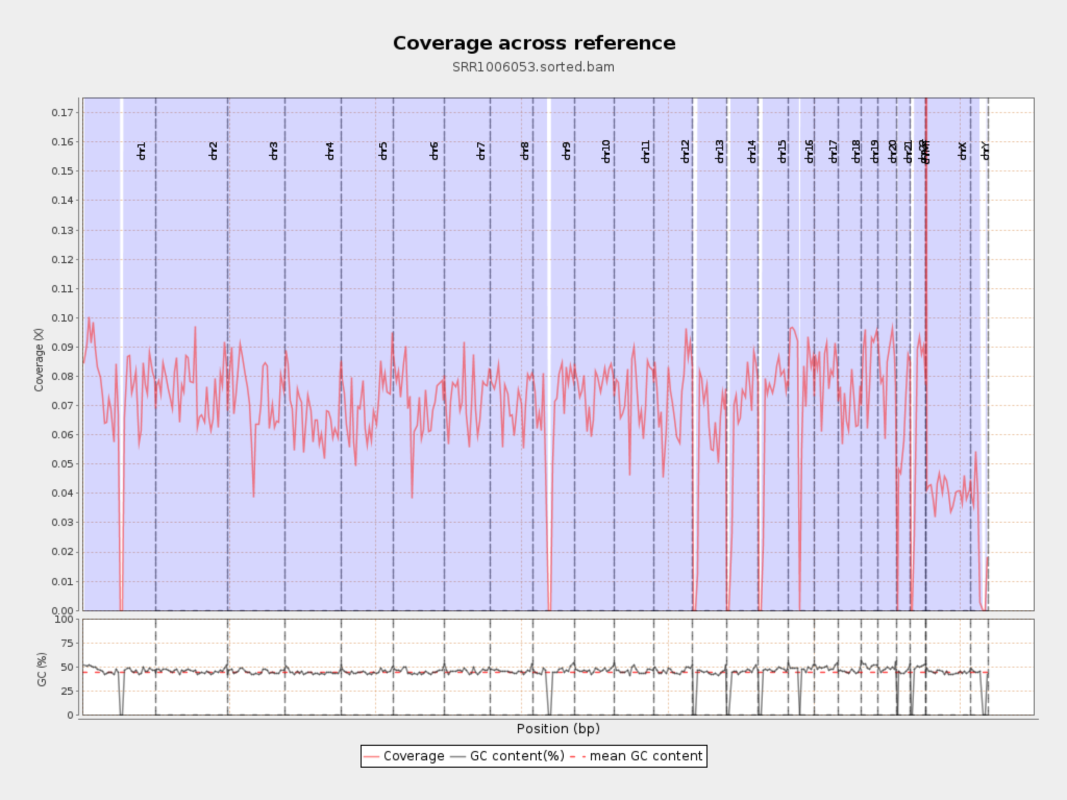
2.7. Chromosome stats

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

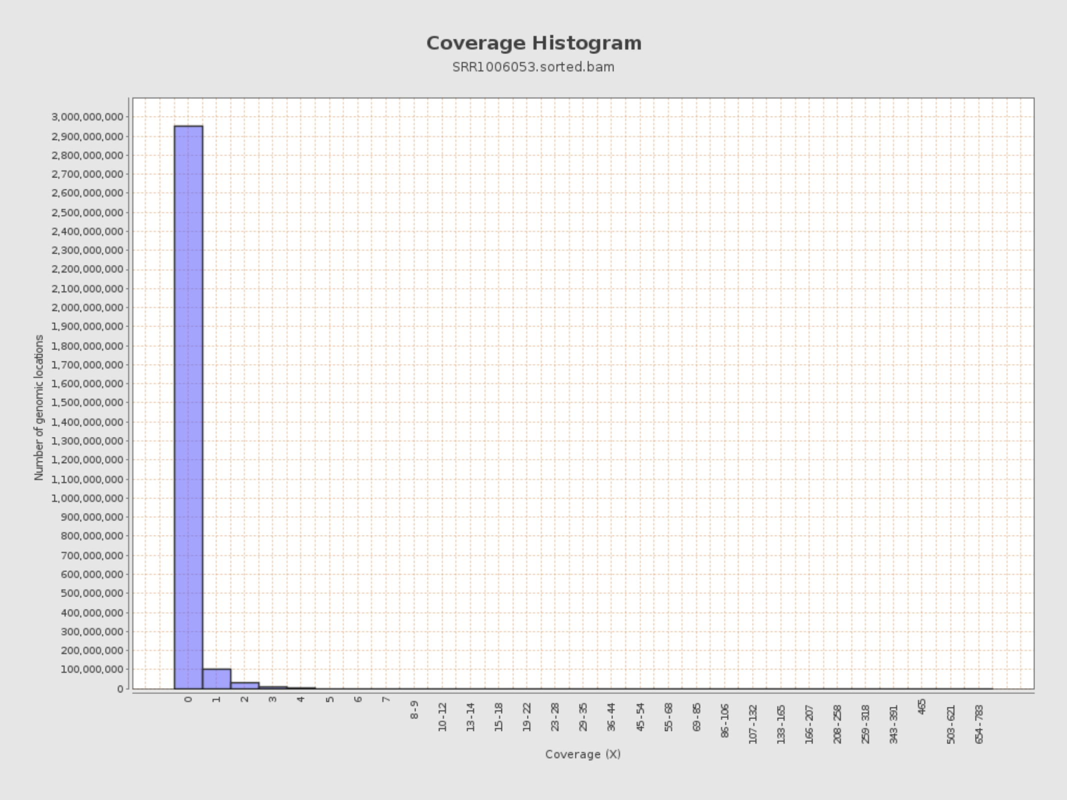
chr1	249250621	18274632	0.0733	0.425
chr2	243199373	18410628	0.0757	0.4539
chr3	198022430	14426337	0.0729	0.3676
chr4	191154276	12708357	0.0665	0.3648
chr5	180915260	12680713	0.0701	0.3608
chr6	171115067	12118080	0.0708	0.3957
chr7	159138663	11542896	0.0725	0.4788
chr8	146364022	10543427	0.072	0.4142
chr9	141213431	9038145	0.064	0.3688
chr10	135534747	10275957	0.0758	0.3919
chr11	135006516	9968480	0.0738	0.5529
chr12	133851895	9785536	0.0731	0.3704
chr13	115169878	6485227	0.0563	0.3259
chr14	107349540	6668280	0.0621	0.3482
chr15	102531392	6512287	0.0635	0.3483
chr16	90354753	7001598	0.0775	0.4391
chr17	81195210	6733386	0.0829	0.4304
chr18	78077248	5389805	0.069	0.4392
chr19	59128983	5070528	0.0858	0.4853
chr20	63025520	5203536	0.0826	0.4059
chr21	48129895	2851495	0.0592	0.3804
chr22	51304566	3143046	0.0613	0.384
chrMT	16571	24104	1.4546	2.2083
chrX	155270560	6305504	0.0406	0.2792

chrY	59373566	1369378	0.0231	0.2376

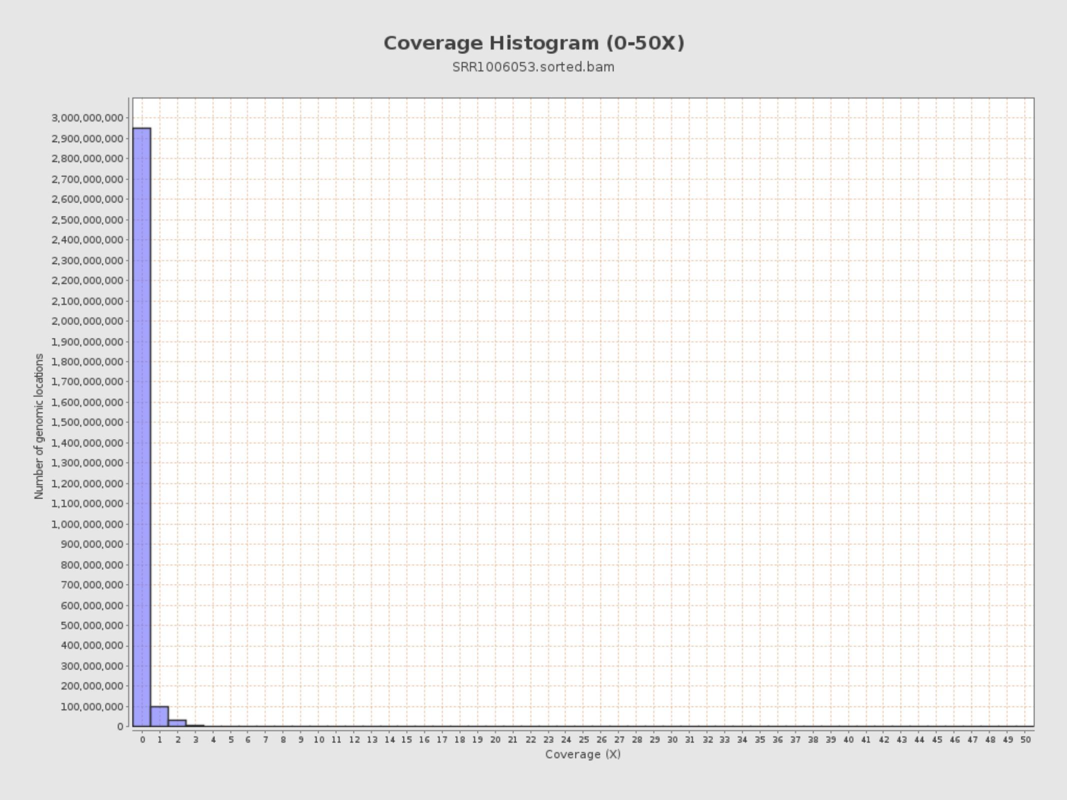
3. Results : Coverage across reference



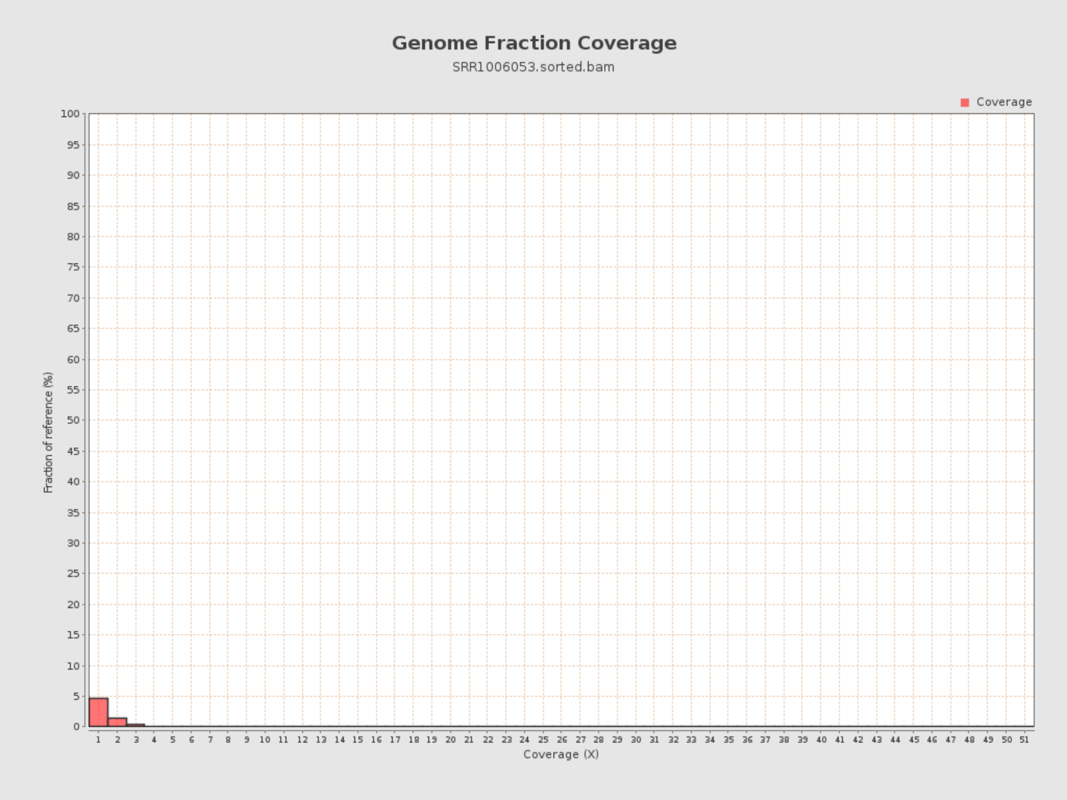
4. Results : Coverage Histogram



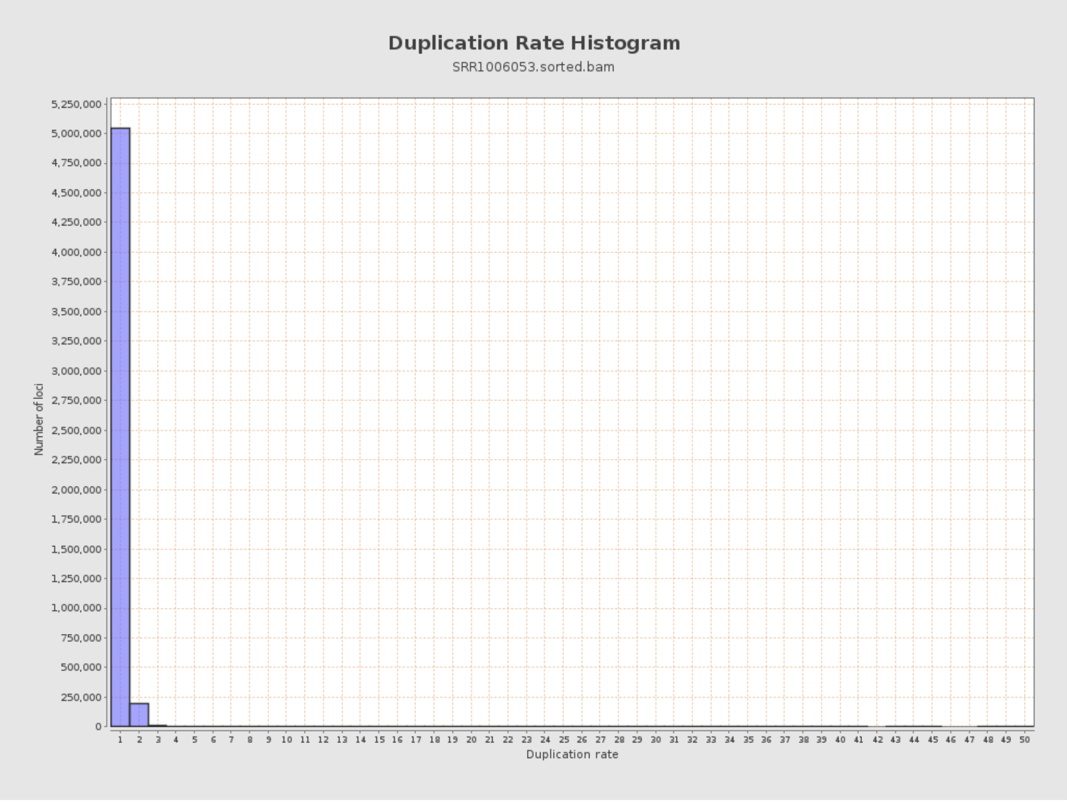
5. Results : Coverage Histogram (0-50X)



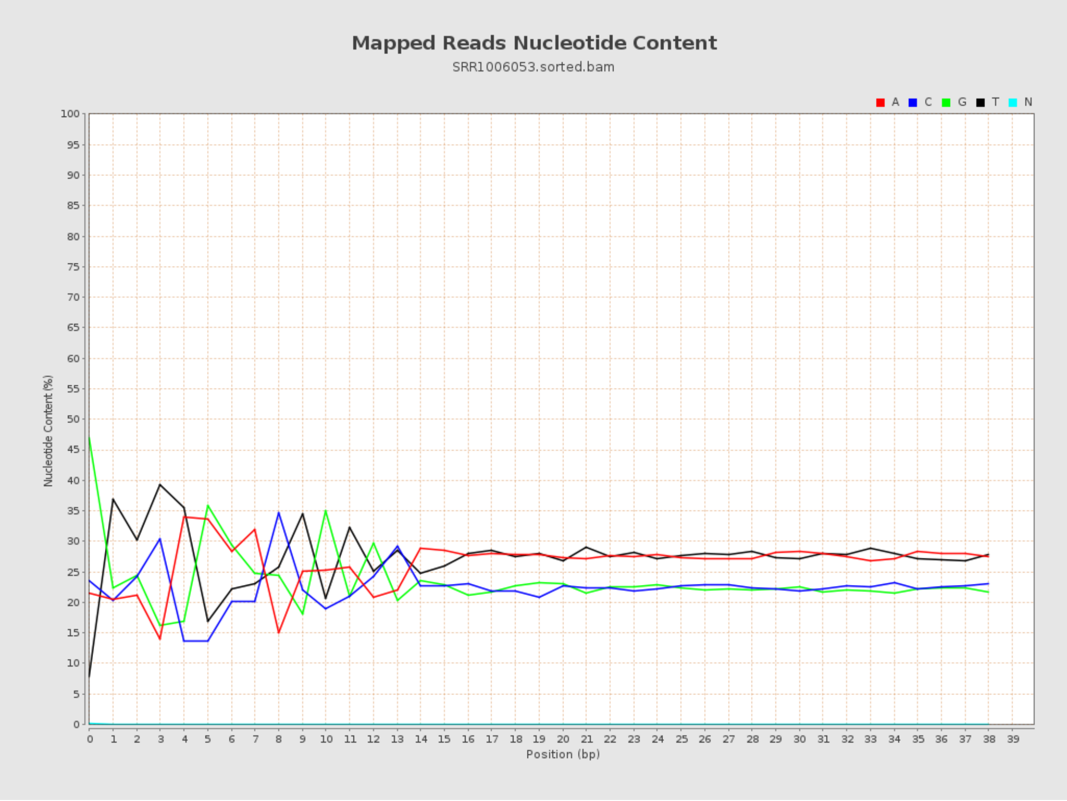
6. Results : Genome Fraction Coverage



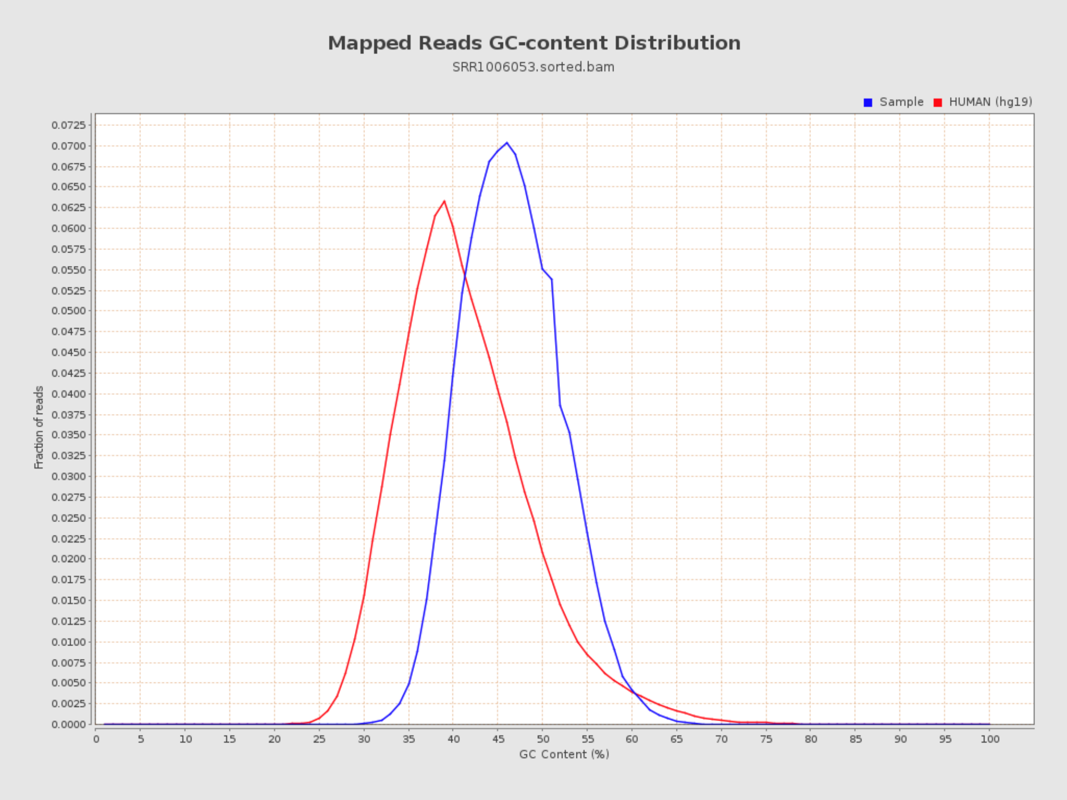
7. Results : Duplication Rate Histogram



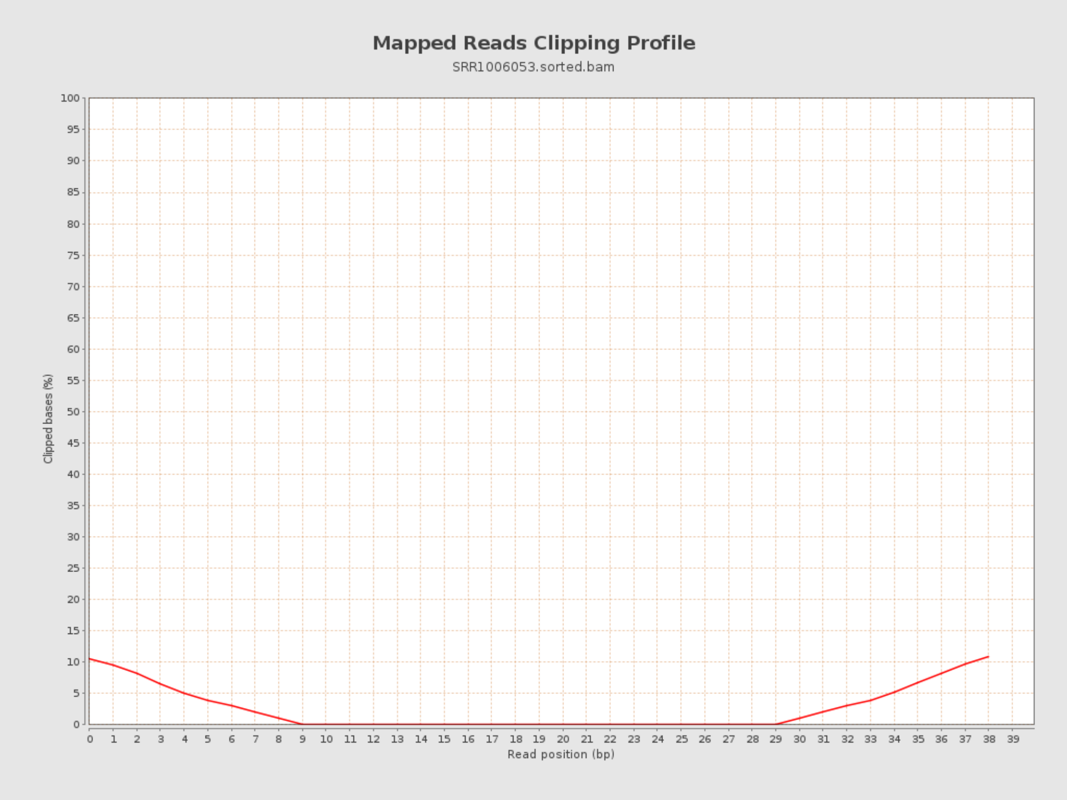
8. Results : Mapped Reads Nucleotide Content



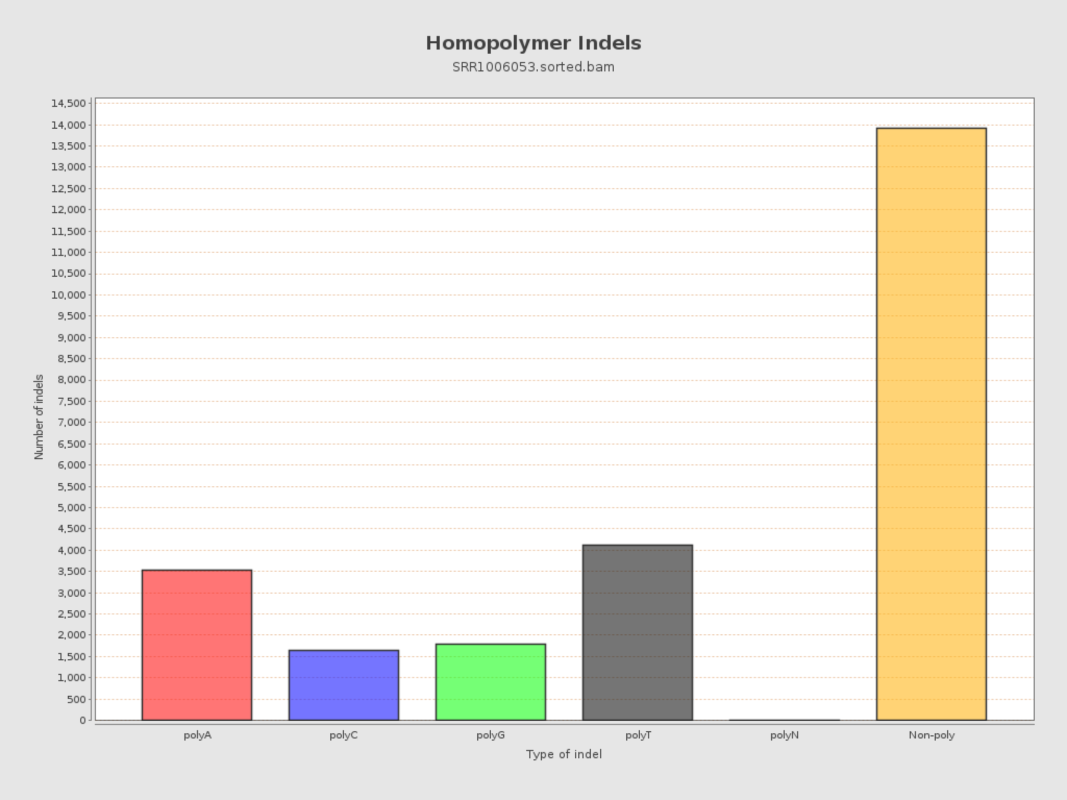
9. Results : Mapped Reads GC-content Distribution



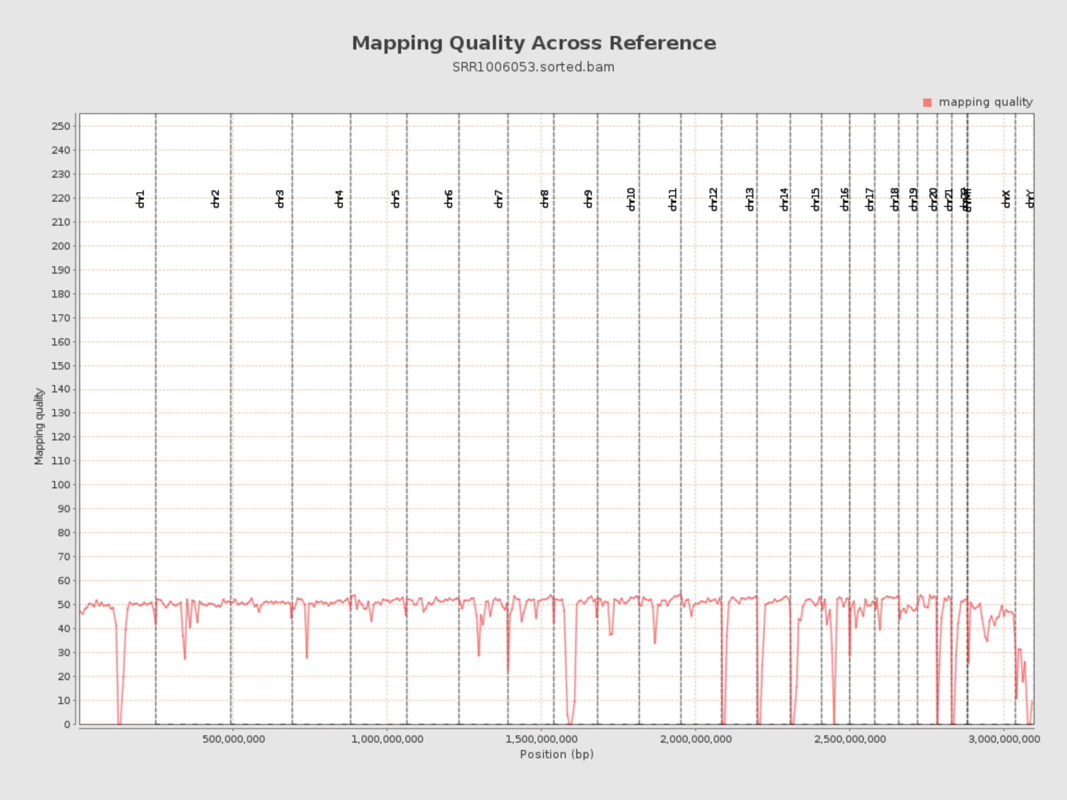
10. Results : Mapped Reads Clipping Profile



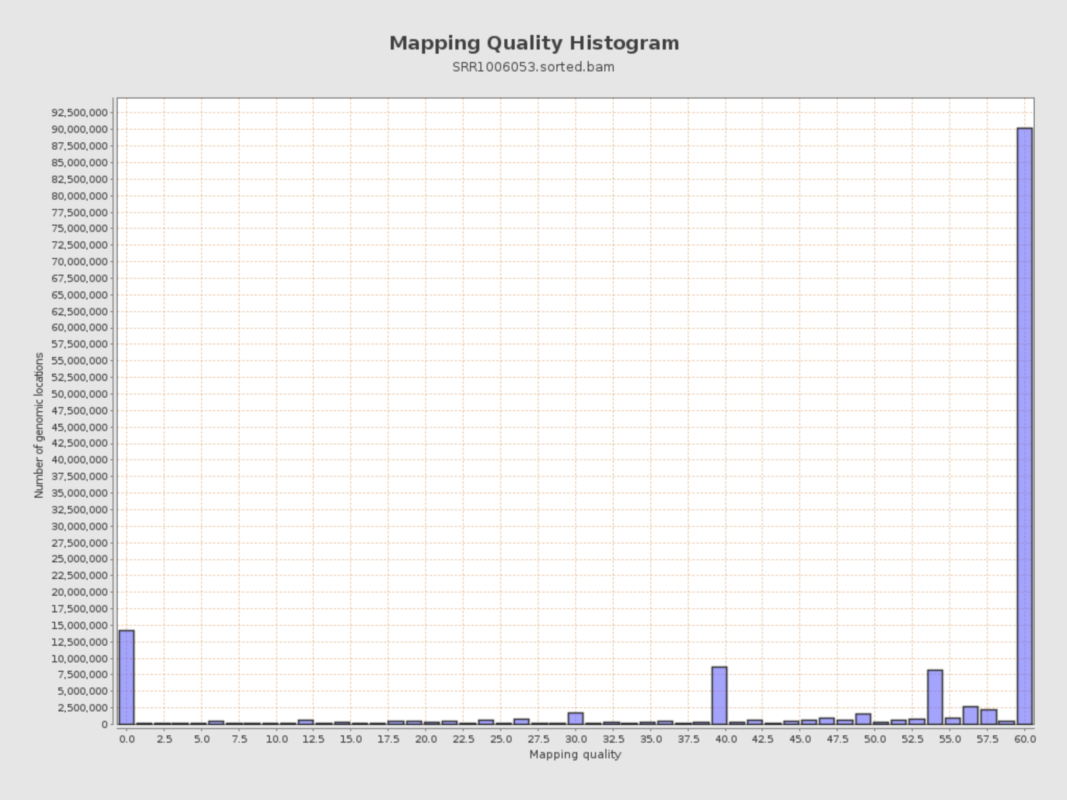
11. Results : Homopolymer Indels



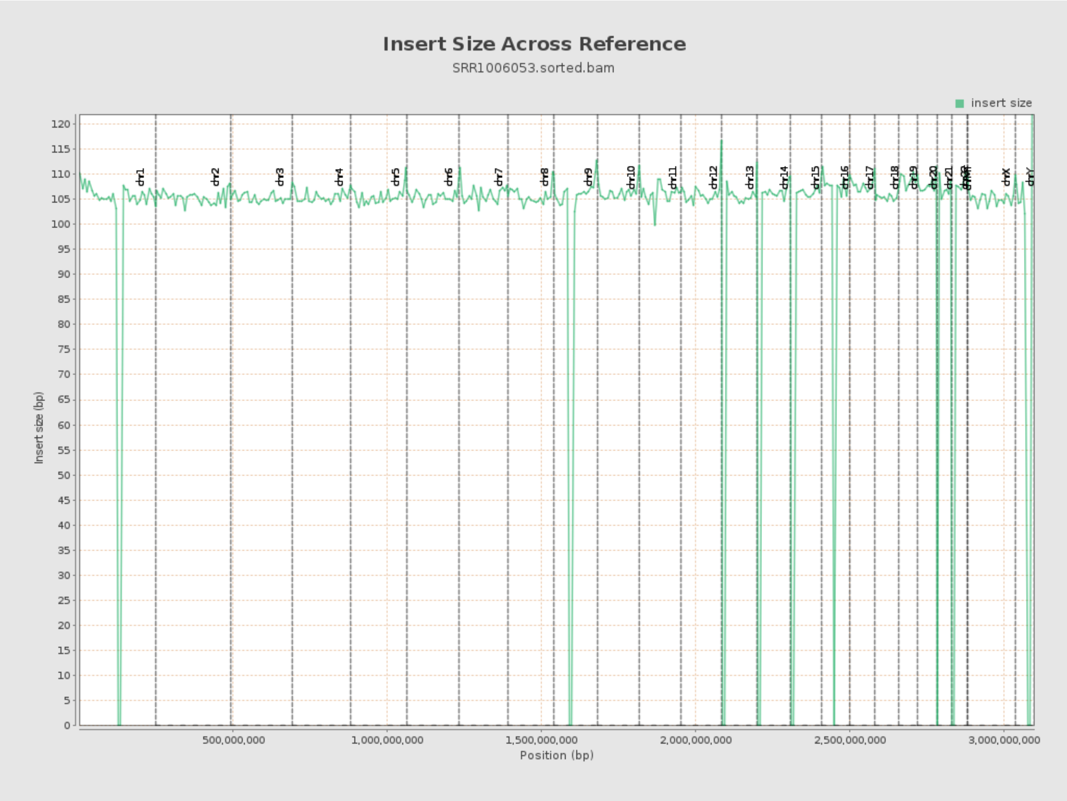
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram