Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 20:27:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006142.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_SRR1006142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006142_1.fastq.gz SRR1006142_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 20:27:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,062,110
Mapped reads	6,110,781 / 86.53%
Unmapped reads	951,329 / 13.47%
Mapped paired reads	6,110,781 / 86.53%
Mapped reads, first in pair	3,114,216 / 44.1%
Mapped reads, second in pair	2,996,565 / 42.43%
Mapped reads, both in pair	5,518,914 / 78.15%
Mapped reads, singletons	591,867 / 8.38%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	246,976 / 3.5%
Duplication rate	3.57%
Clipped reads	484,407 / 6.86%

2.2. ACGT Content

Number/percentage of A's	63,235,108 / 26.8%
Number/percentage of C's	52,069,947 / 22.07%
Number/percentage of T's	65,366,297 / 27.7%
Number/percentage of G's	55,287,578 / 23.43%
Number/percentage of N's	9,874 / 0%
GC Percentage	45.5%

2.3. Coverage

Mean	0.0762
Standard Deviation	0.4137

2.4. Mapping Quality

Mean Mapping Quality	47.09

2.5. Insert size

Mean	69,287.54
Standard Deviation	2,585,940.2
P25/Median/P75	80 / 112 / 147

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	1,165,554
Insertions	7,423
Mapped reads with at least one insertion	0.12%
Deletions	19,894
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.44%

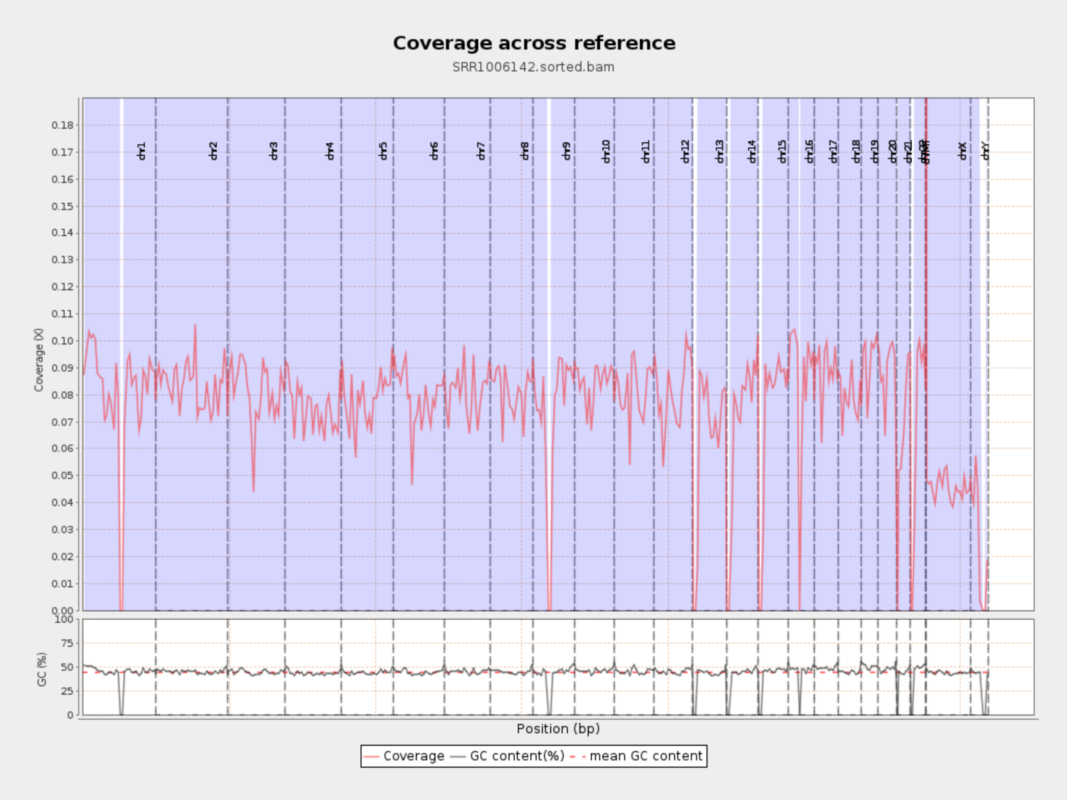
2.7. Chromosome stats

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

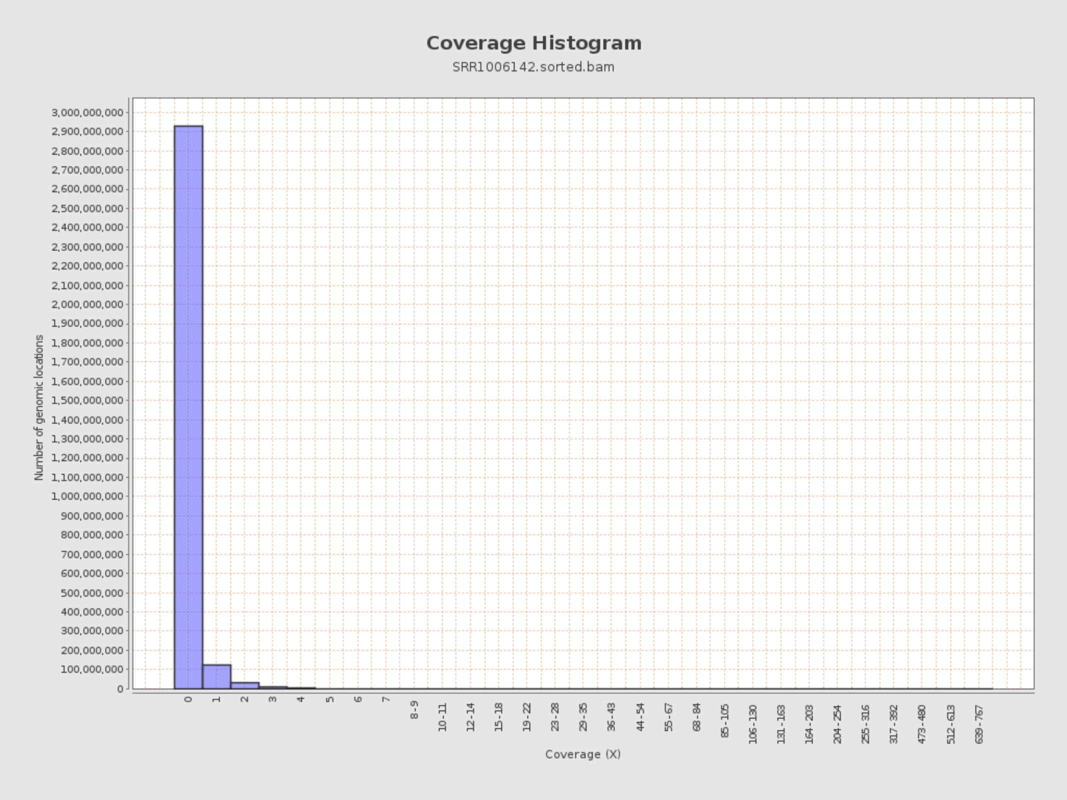
chr1	249250621	20033499	0.0804	0.4427
chr2	243199373	20356720	0.0837	0.4662
chr3	198022430	16017072	0.0809	0.3718
chr4	191154276	14388328	0.0753	0.3723
chr5	180915260	14247022	0.0787	0.3672
chr6	171115067	13499368	0.0789	0.4034
chr7	159138663	12935081	0.0813	0.5417
chr8	146364022	11848413	0.081	0.4353
chr9	141213431	10144243	0.0718	0.3799
chr10	135534747	11430538	0.0843	0.3954
chr11	135006516	10965337	0.0812	0.5605
chr12	133851895	10903814	0.0815	0.375
chr13	115169878	7311695	0.0635	0.3349
chr14	107349540	7313881	0.0681	0.3523
chr15	102531392	7235021	0.0706	0.3531
chr16	90354753	7614910	0.0843	0.4356
chr17	81195210	7300166	0.0899	0.43
chr18	78077248	6165271	0.079	0.4813
chr19	59128983	5473253	0.0926	0.4745
chr20	63025520	5614889	0.0891	0.4007
chr21	48129895	3173104	0.0659	0.3758
chr22	51304566	3372245	0.0657	0.3678
chrMT	16571	64349	3.8832	5.2522
chrX	155270560	7094308	0.0457	0.2969

chrY	59373566	1491616	0.0251	0.2408

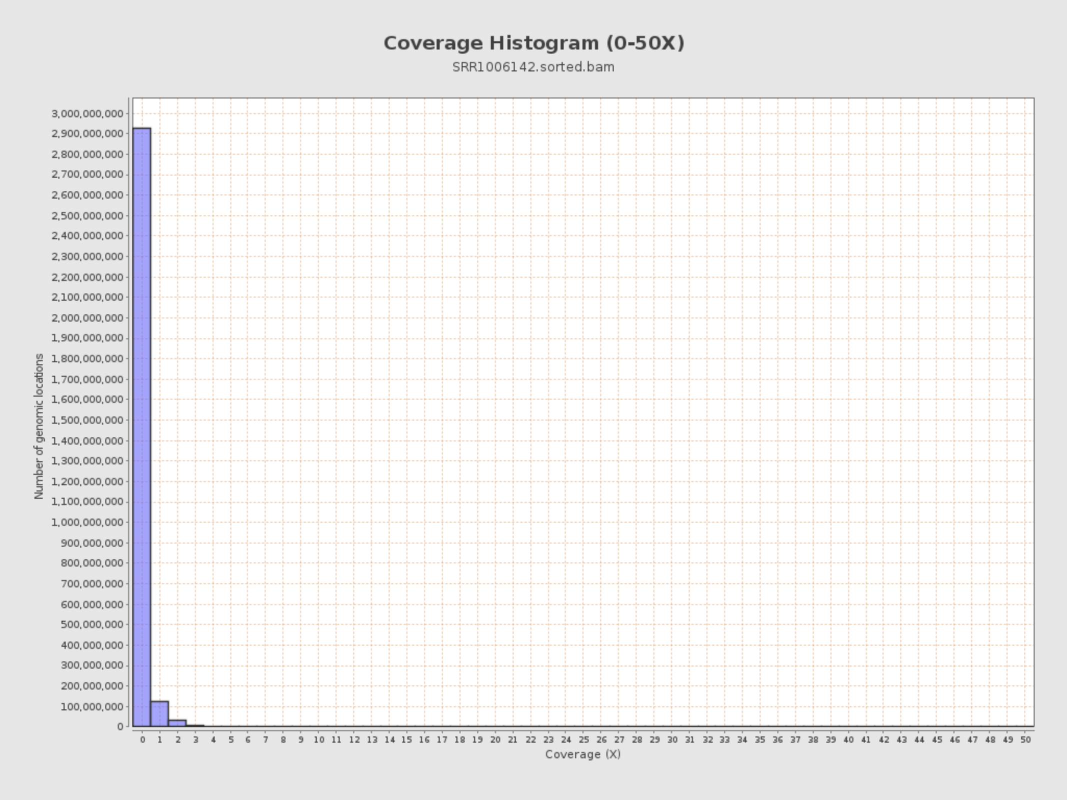
3. Results : Coverage across reference



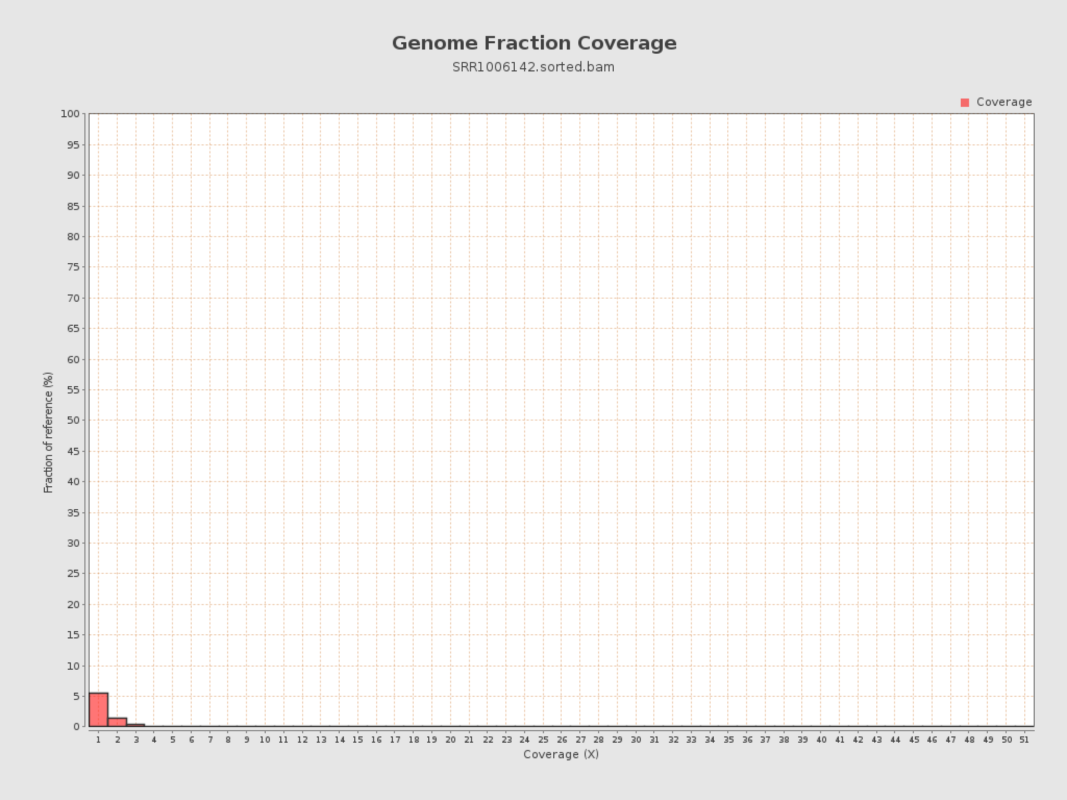
4. Results : Coverage Histogram



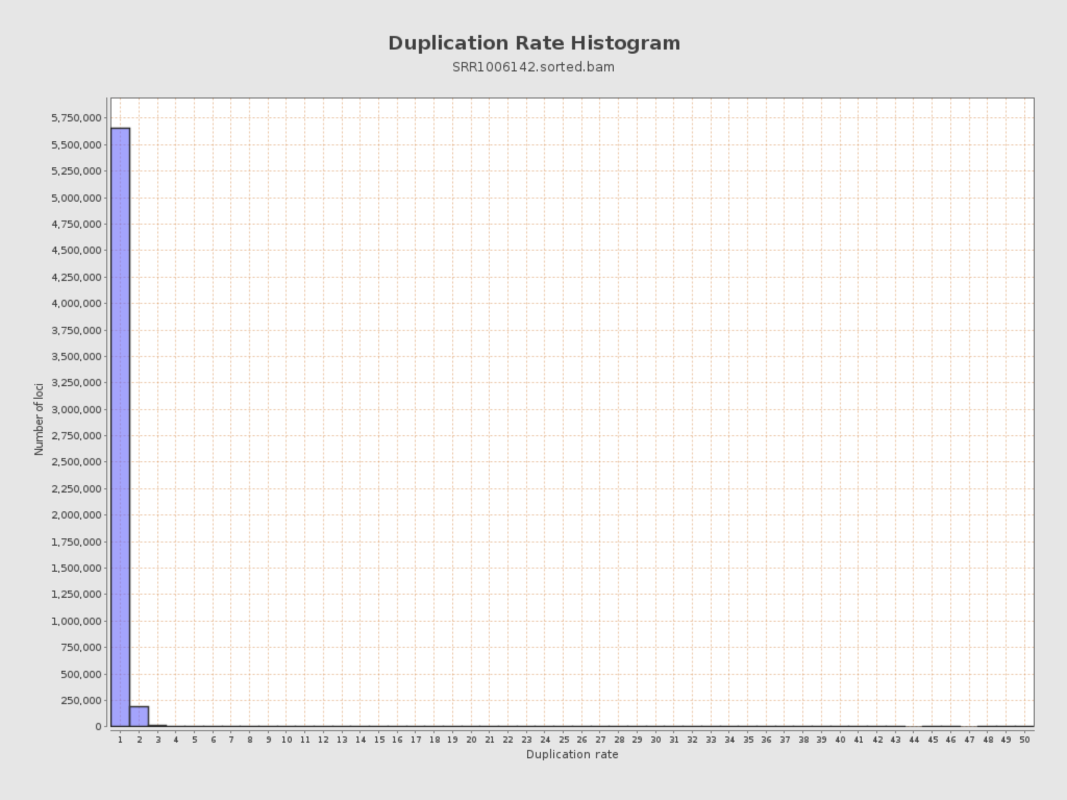
5. Results : Coverage Histogram (0-50X)



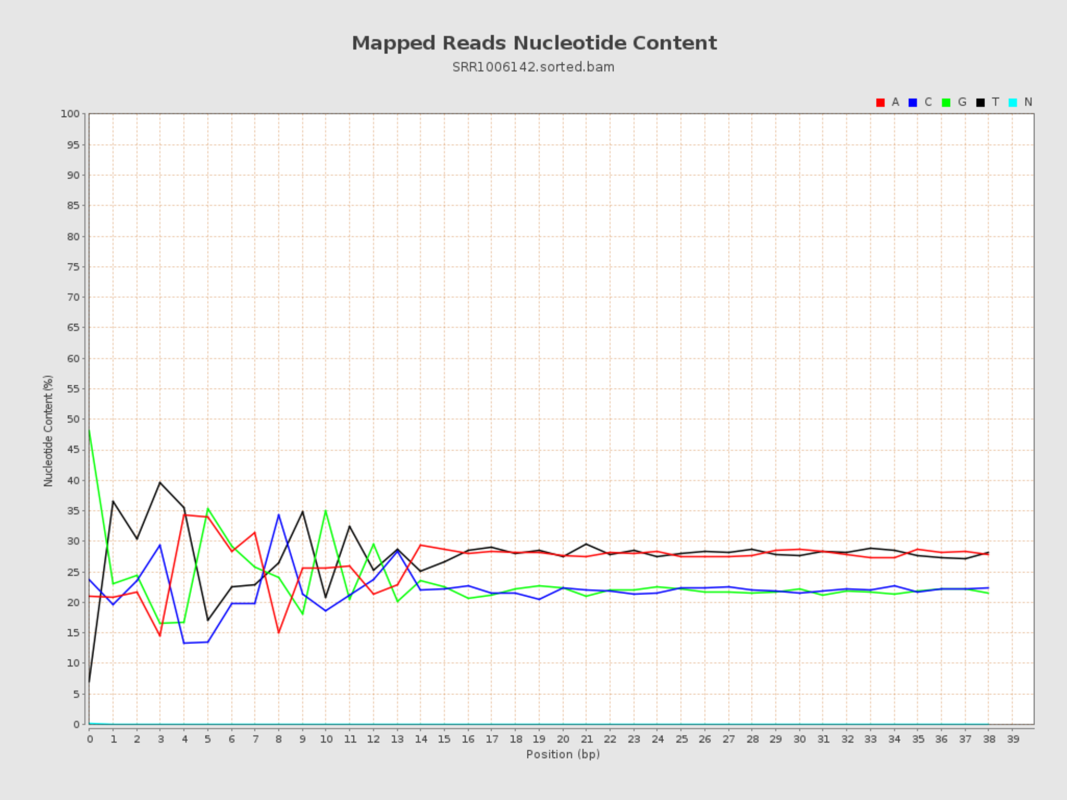
6. Results : Genome Fraction Coverage



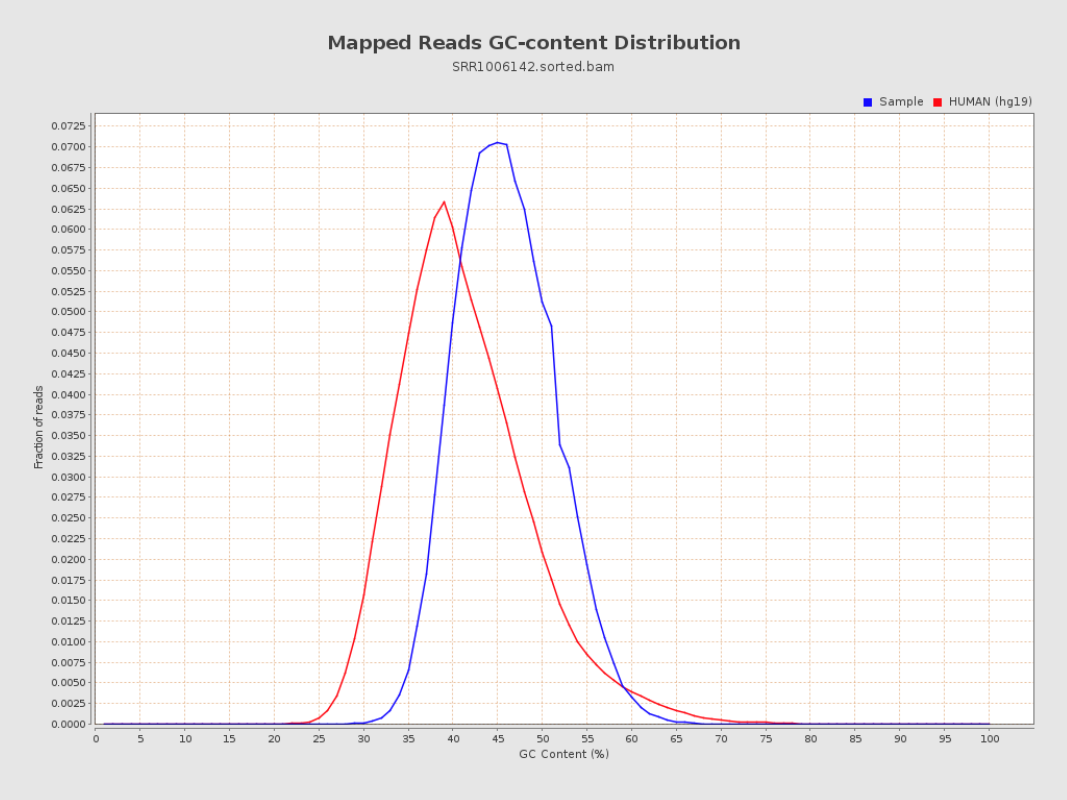
7. Results : Duplication Rate Histogram



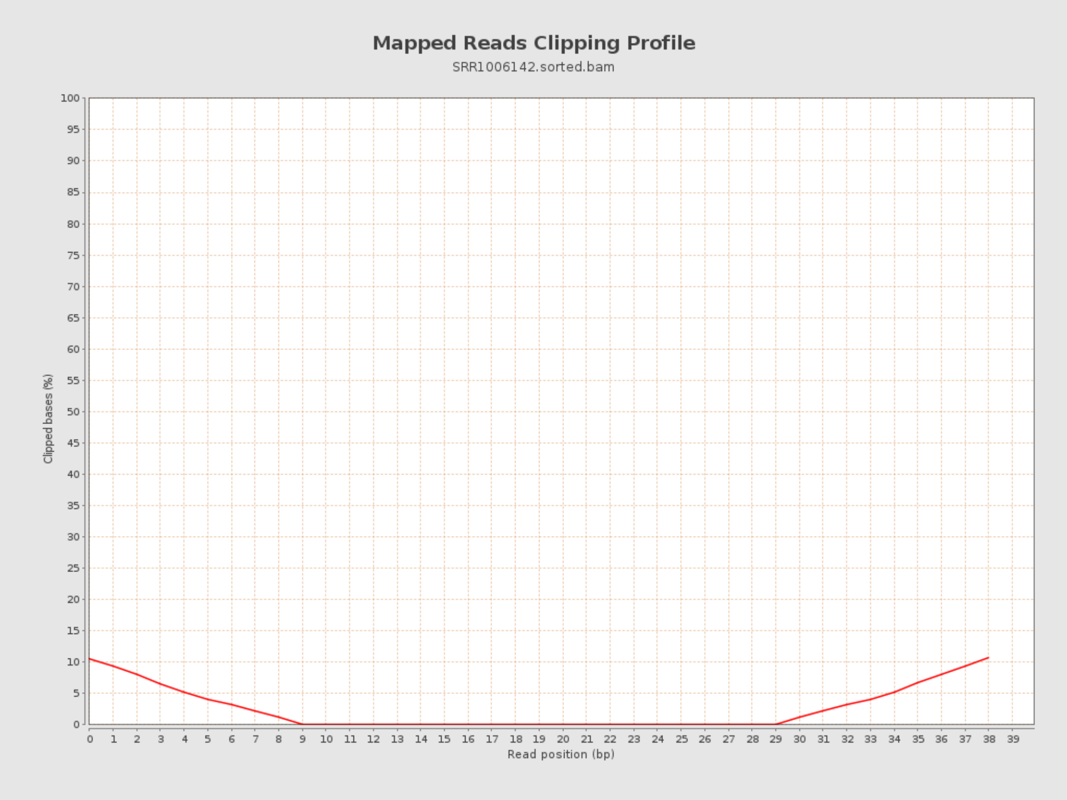
8. Results : Mapped Reads Nucleotide Content



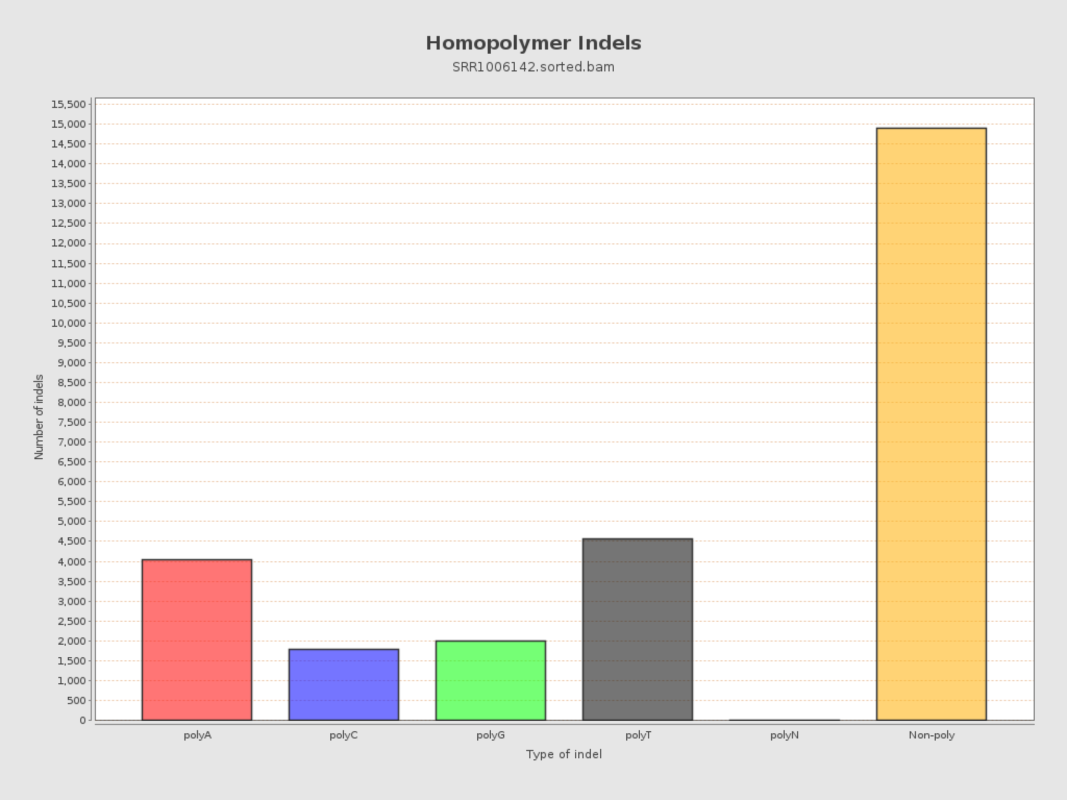
9. Results : Mapped Reads GC-content Distribution



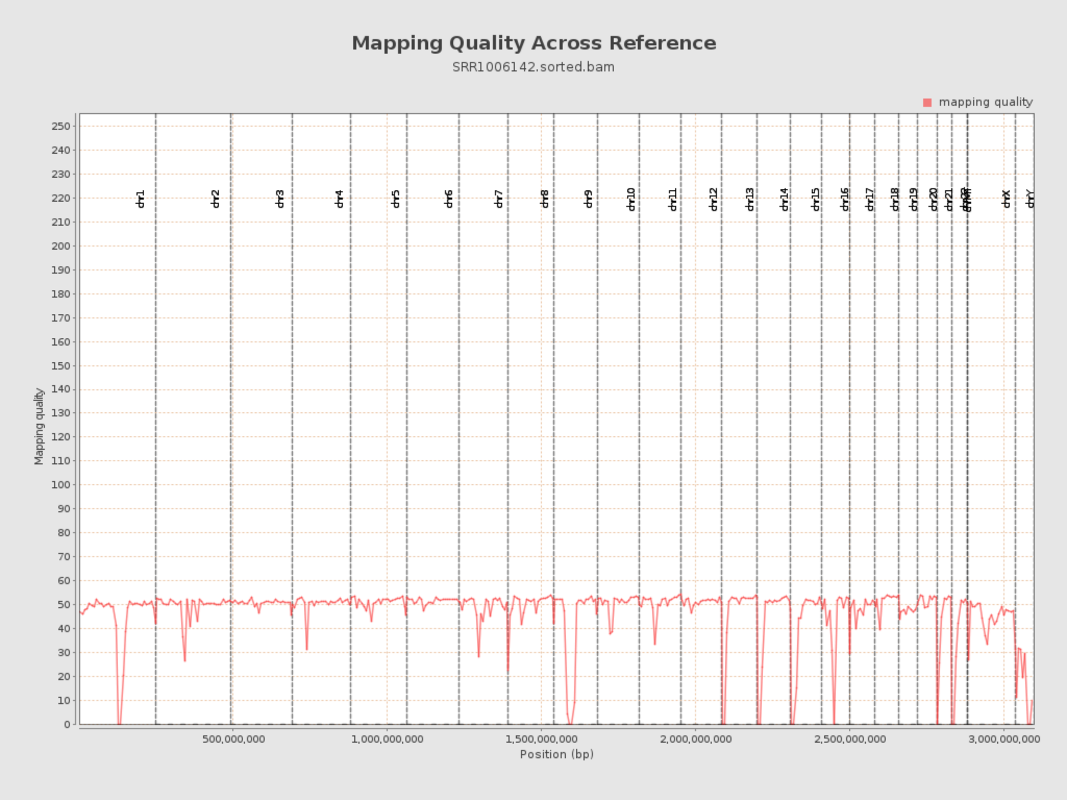
10. Results : Mapped Reads Clipping Profile



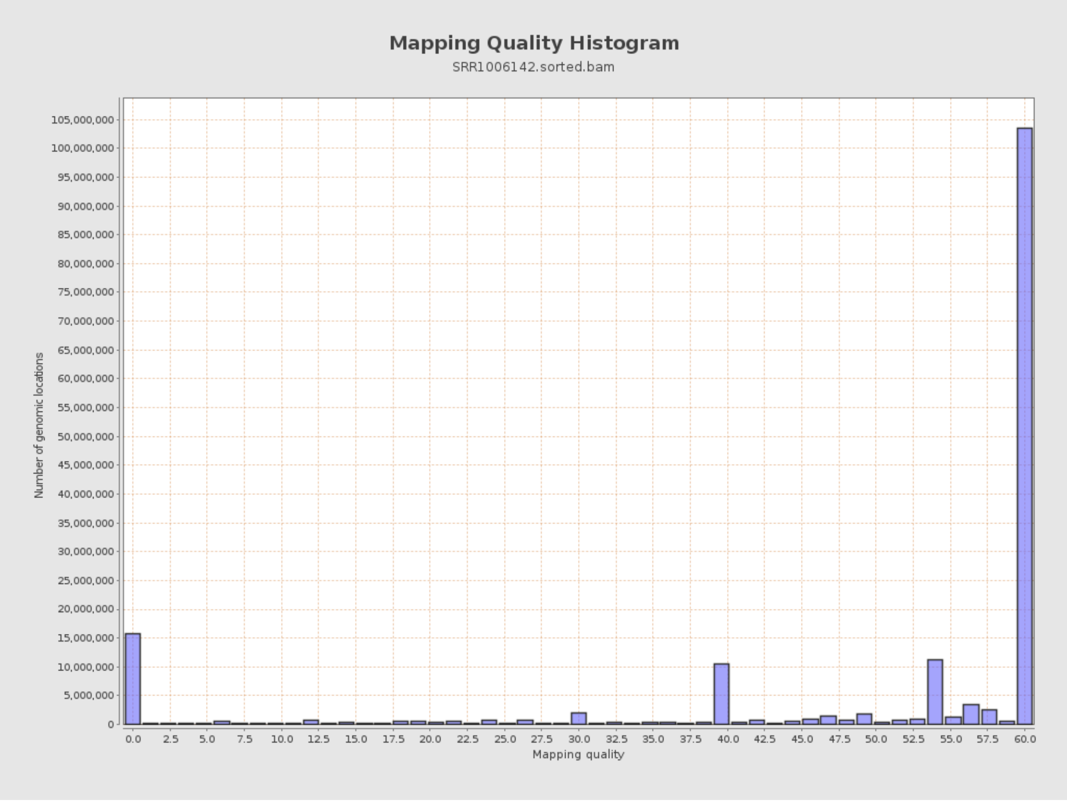
11. Results : Homopolymer Indels



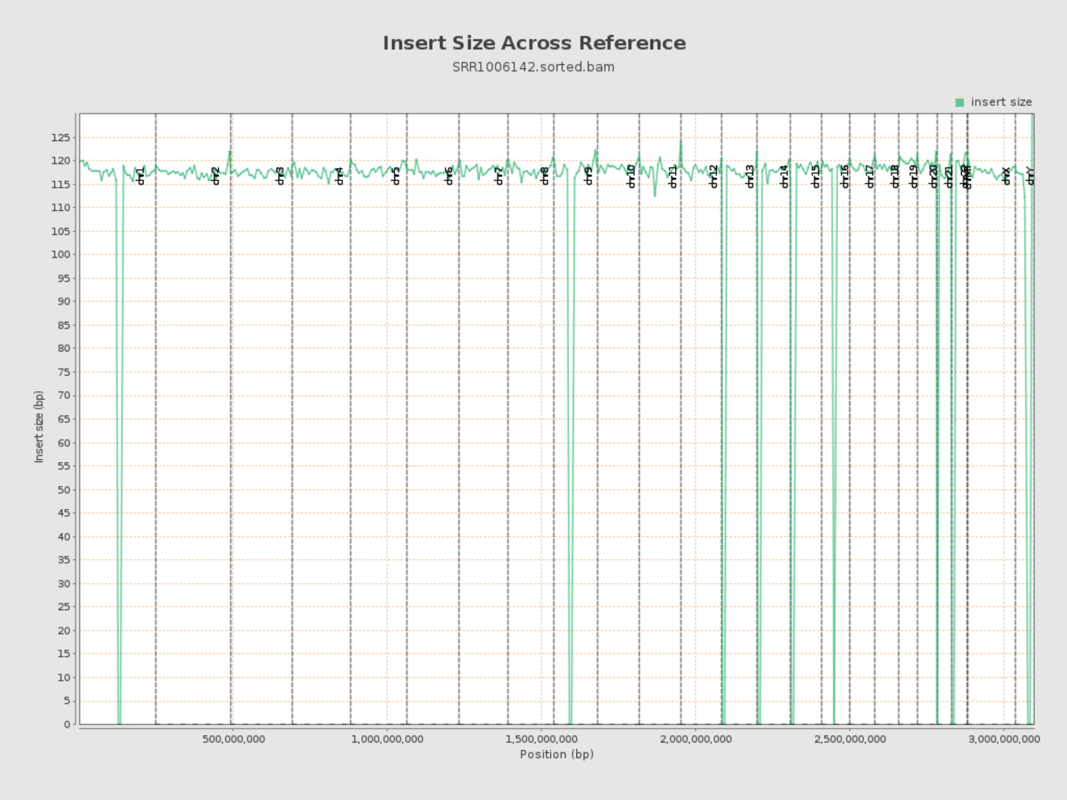
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram