Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:50:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006220.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_SRR1006220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006220_1.fastq.gz SRR1006220_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:50:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,765,066
Mapped reads	1,553,561 / 88.02%
Unmapped reads	211,505 / 11.98%
Mapped paired reads	1,553,561 / 88.02%
Mapped reads, first in pair	777,928 / 44.07%
Mapped reads, second in pair	775,633 / 43.94%
Mapped reads, both in pair	1,433,516 / 81.22%
Mapped reads, singletons	120,045 / 6.8%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	30,323 / 1.72%
Duplication rate	1.69%
Clipped reads	86,501 / 4.9%

2.2. ACGT Content

Number/percentage of A's	16,540,065 / 27.5%
Number/percentage of C's	13,058,566 / 21.71%
Number/percentage of T's	16,931,513 / 28.16%
Number/percentage of G's	13,603,550 / 22.62%
Number/percentage of N's	3,086 / 0.01%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0194
Standard Deviation	0.1647

2.4. Mapping Quality

Mean Mapping Quality	47.96

2.5. Insert size

Mean	66,426.68
Standard Deviation	2,492,739.14
P25/Median/P75	108 / 151 / 189

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	176,547
Insertions	1,794
Mapped reads with at least one insertion	0.12%
Deletions	6,048
Mapped reads with at least one deletion	0.39%
Homopolymer indels	45.45%

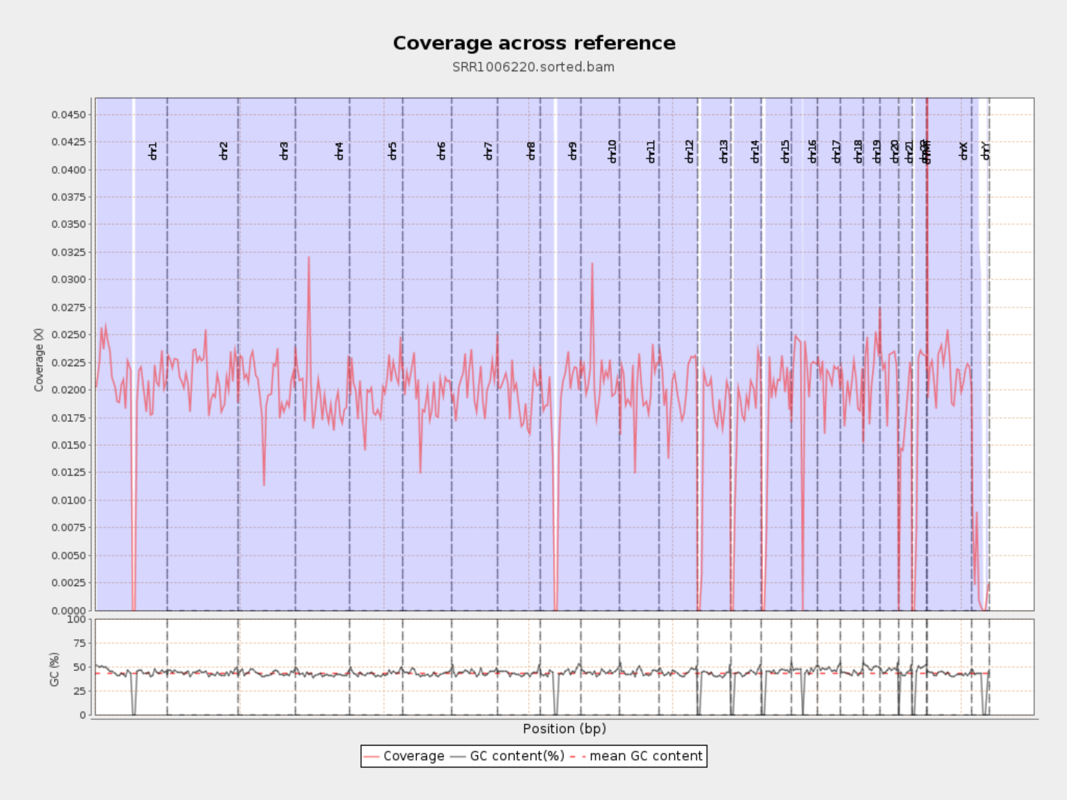
2.7. Chromosome stats

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

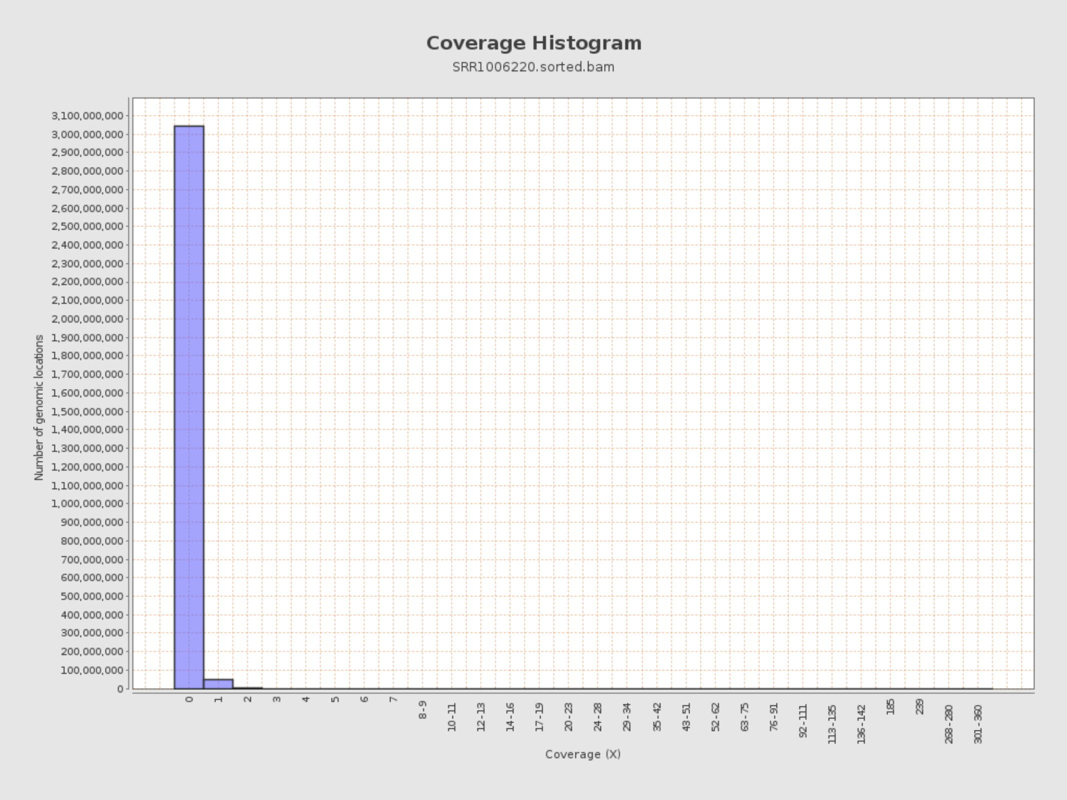
chr1	249250621	4949689	0.0199	0.1838
chr2	243199373	5204911	0.0214	0.1697
chr3	198022430	4009245	0.0202	0.1525
chr4	191154276	3767642	0.0197	0.1607
chr5	180915260	3622005	0.02	0.1517
chr6	171115067	3363448	0.0197	0.1539
chr7	159138663	3258711	0.0205	0.1787
chr8	146364022	2846251	0.0194	0.2313
chr9	141213431	2501290	0.0177	0.1482
chr10	135534747	2890456	0.0213	0.1837
chr11	135006516	2707263	0.0201	0.1595
chr12	133851895	2700448	0.0202	0.153
chr13	115169878	1848738	0.0161	0.136
chr14	107349540	1783613	0.0166	0.1538
chr15	102531392	1722028	0.0168	0.1386
chr16	90354753	1868025	0.0207	0.1662
chr17	81195210	1721621	0.0212	0.1581
chr18	78077248	1570365	0.0201	0.1846
chr19	59128983	1306533	0.0221	0.1705
chr20	63025520	1378082	0.0219	0.161
chr21	48129895	781091	0.0162	0.1474
chr22	51304566	818437	0.016	0.1379
chrMT	16571	1596	0.0963	0.3683
chrX	155270560	3360670	0.0216	0.1609

chrY	59373566	162597	0.0027	0.0842

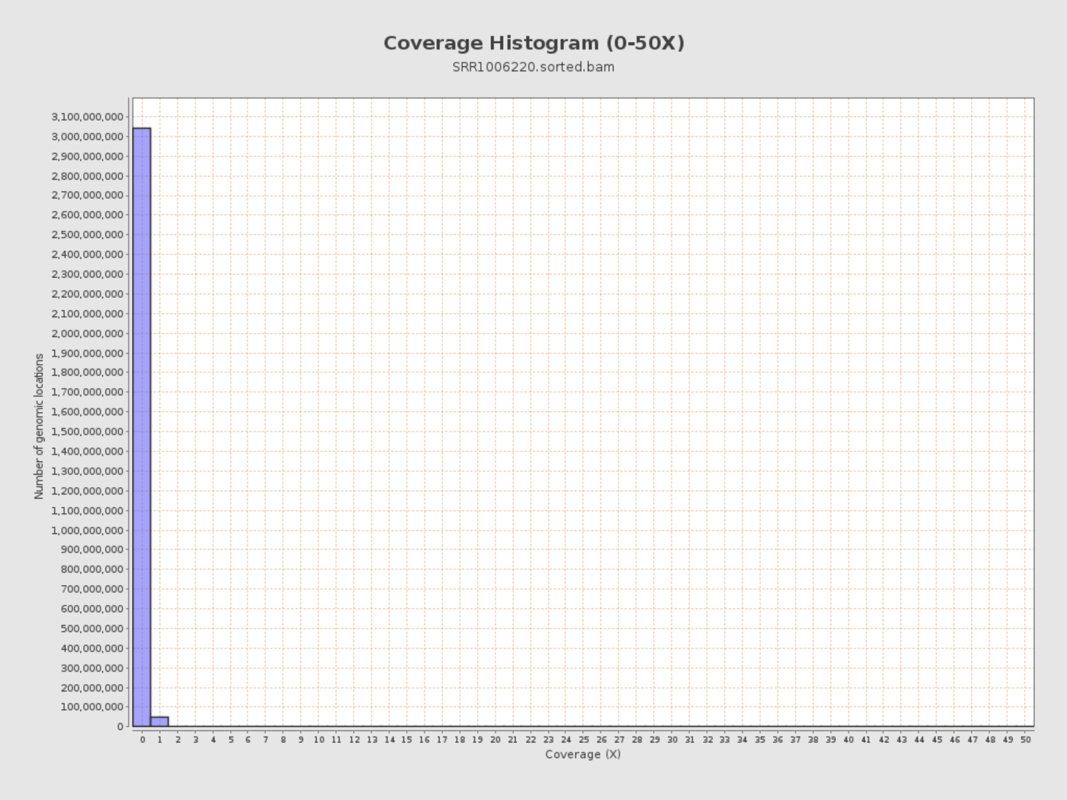
3. Results : Coverage across reference



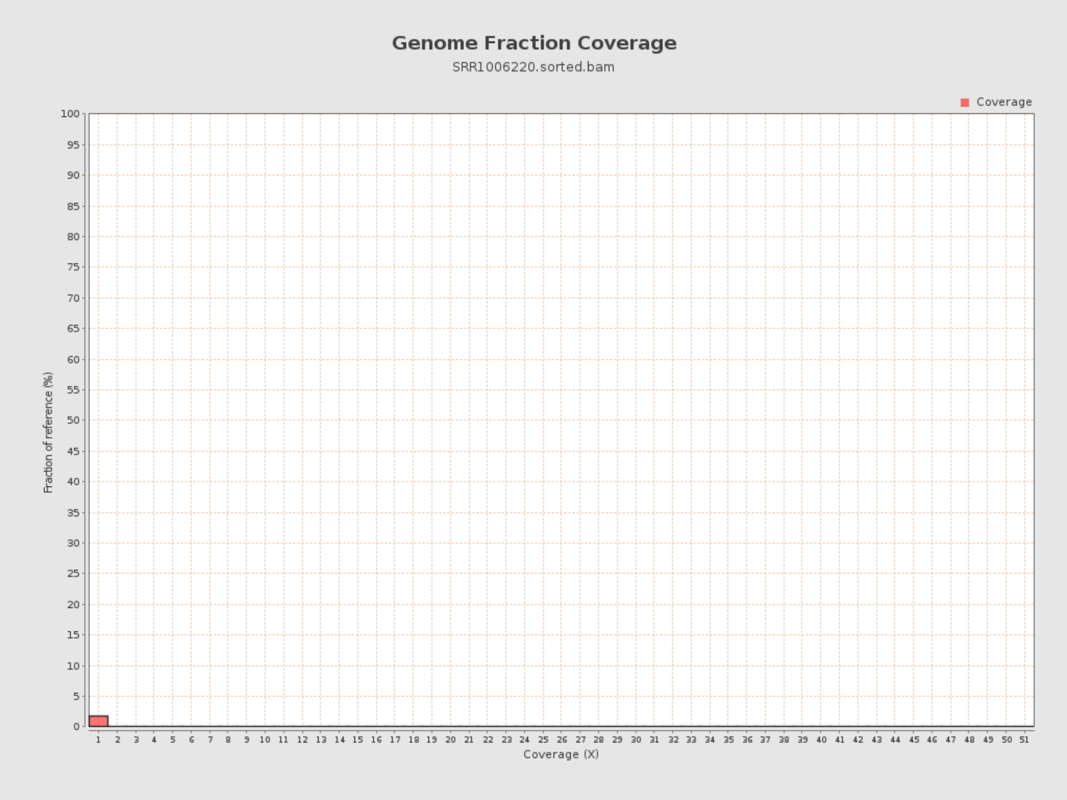
4. Results : Coverage Histogram



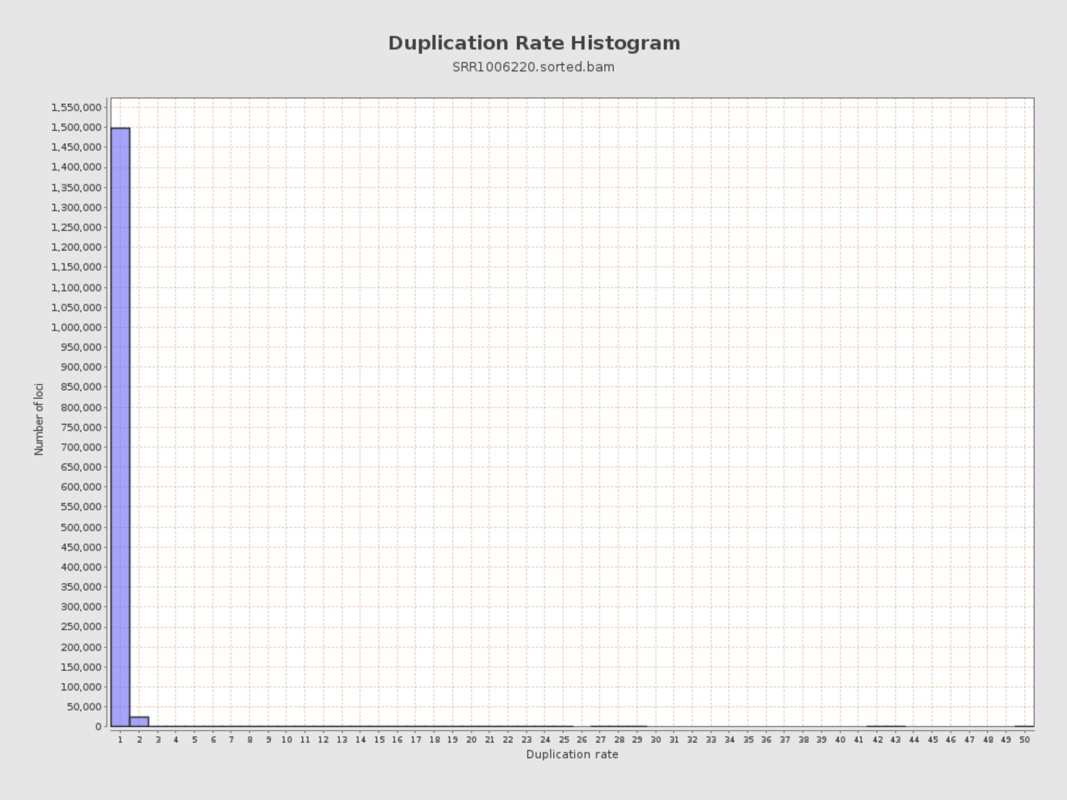
5. Results : Coverage Histogram (0-50X)



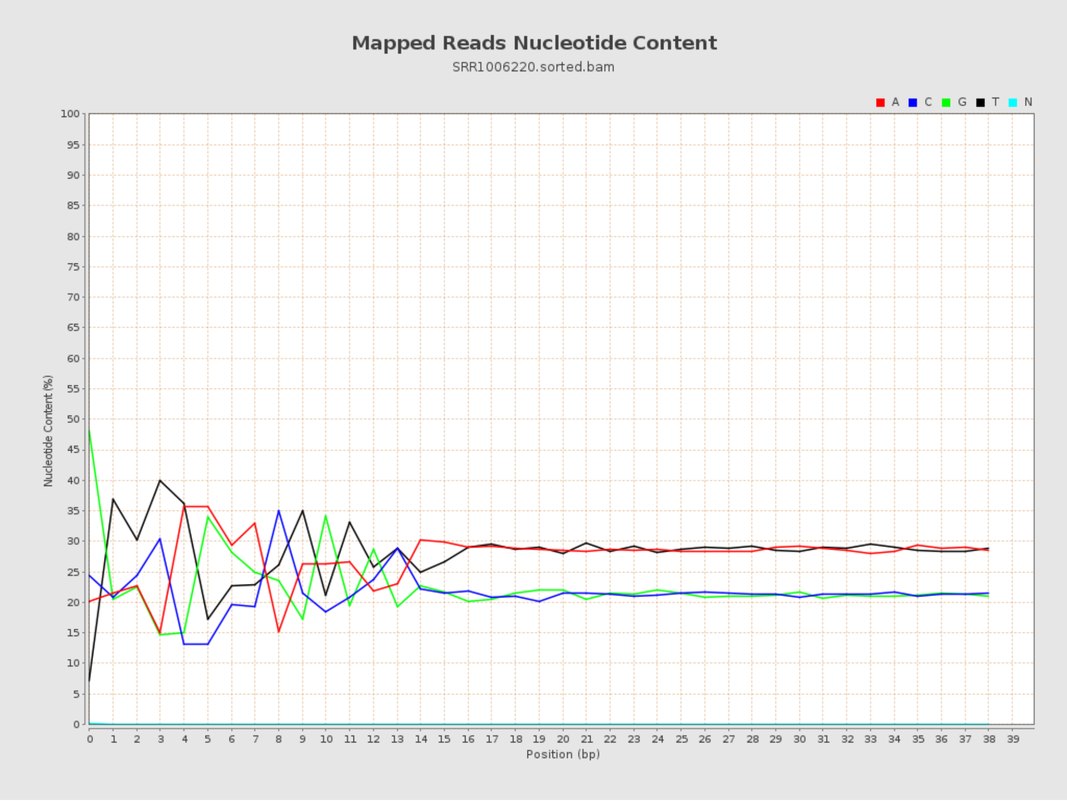
6. Results : Genome Fraction Coverage



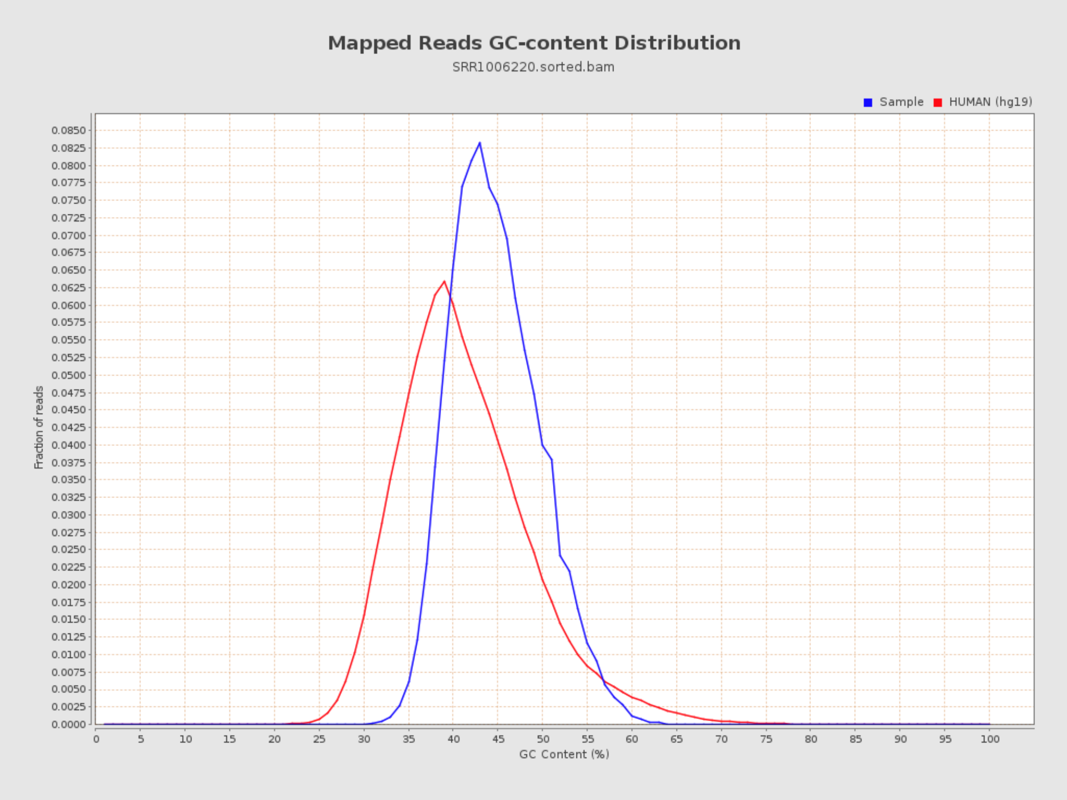
7. Results : Duplication Rate Histogram



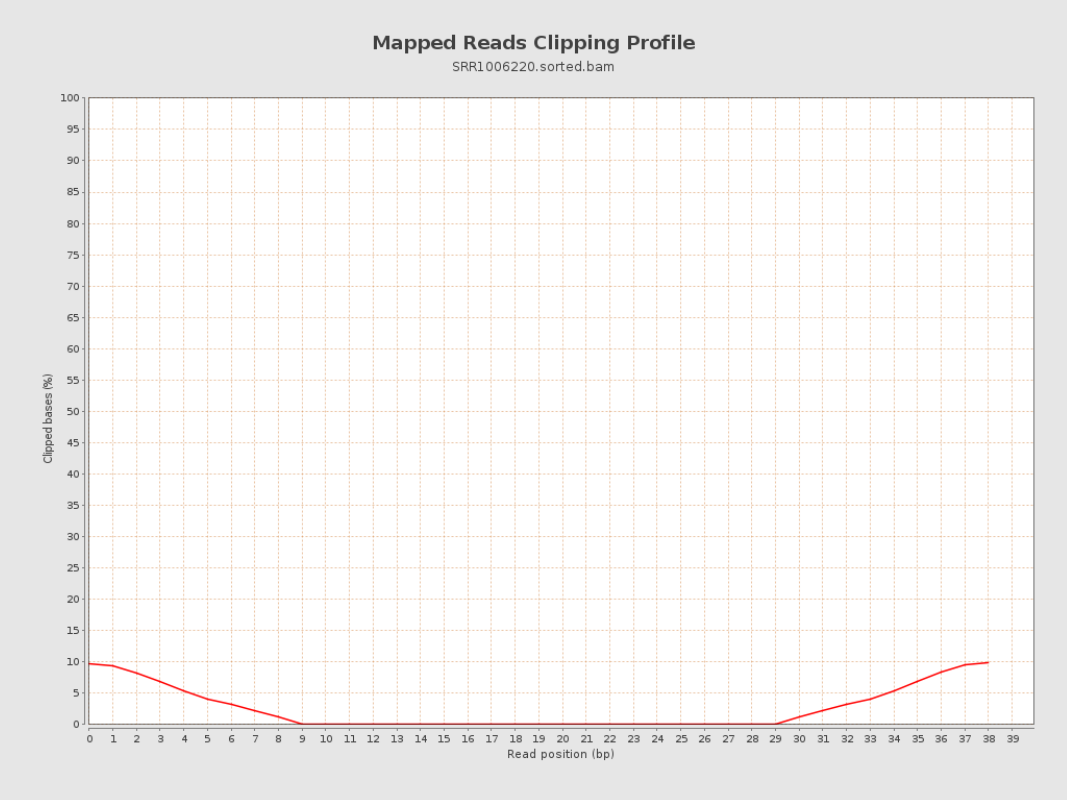
8. Results : Mapped Reads Nucleotide Content



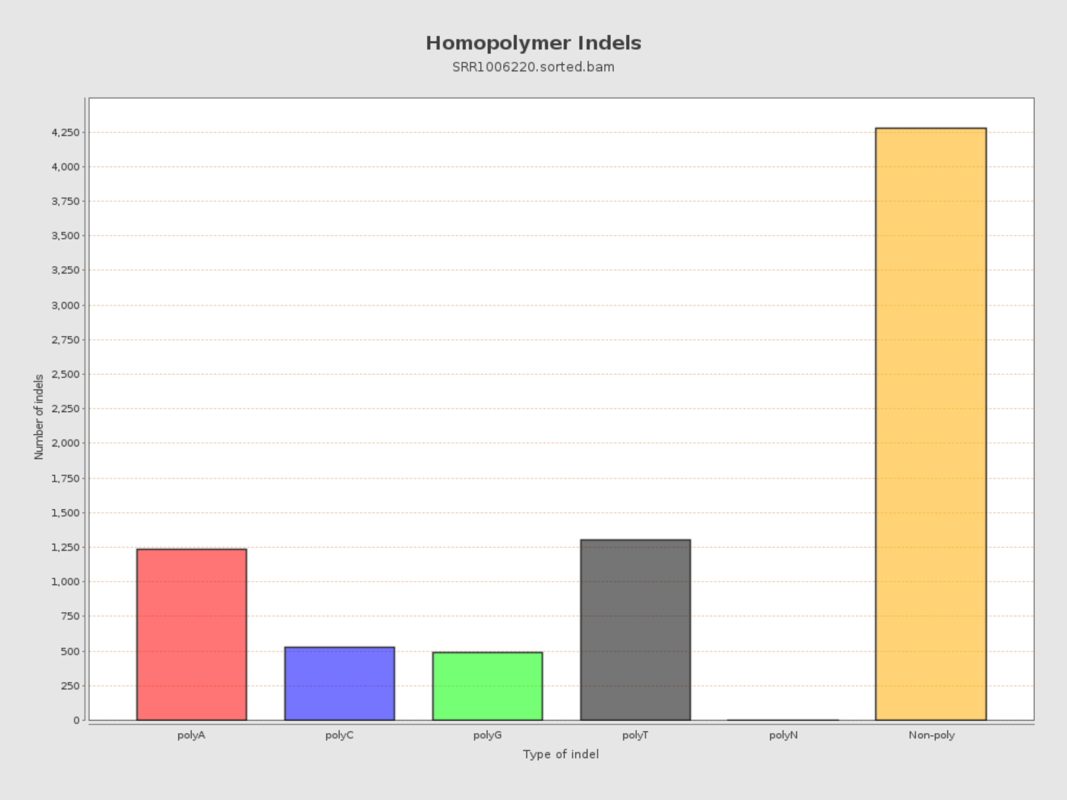
9. Results : Mapped Reads GC-content Distribution



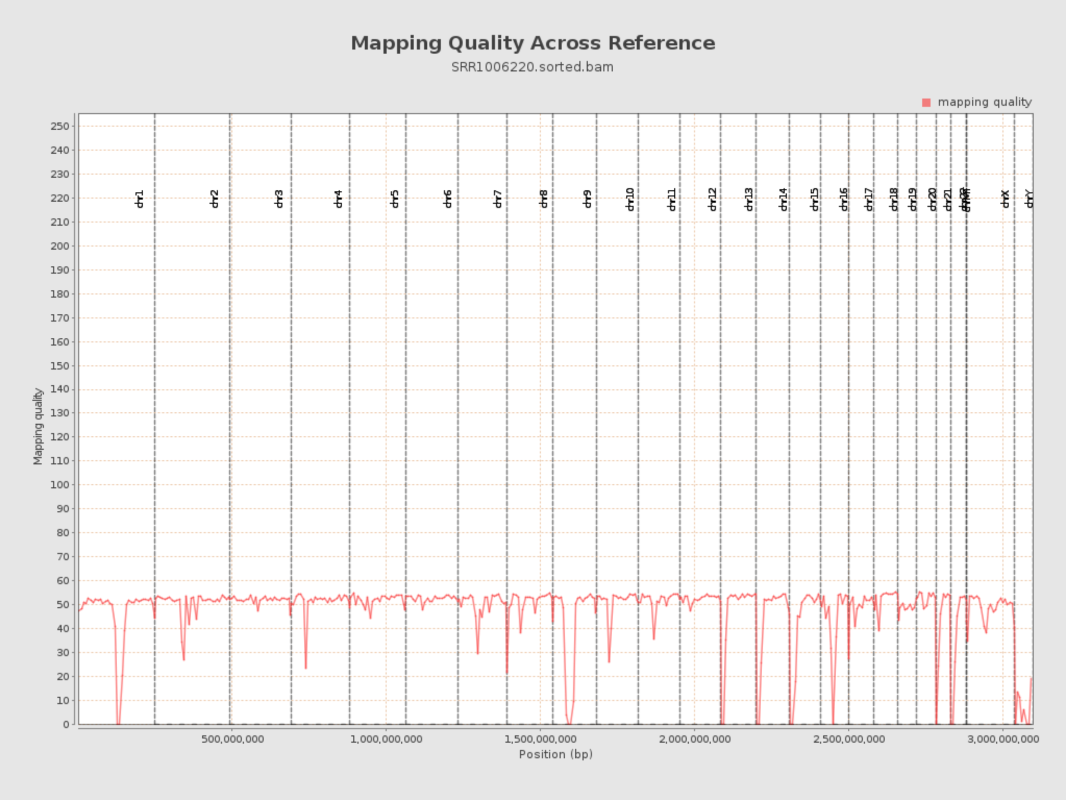
10. Results : Mapped Reads Clipping Profile



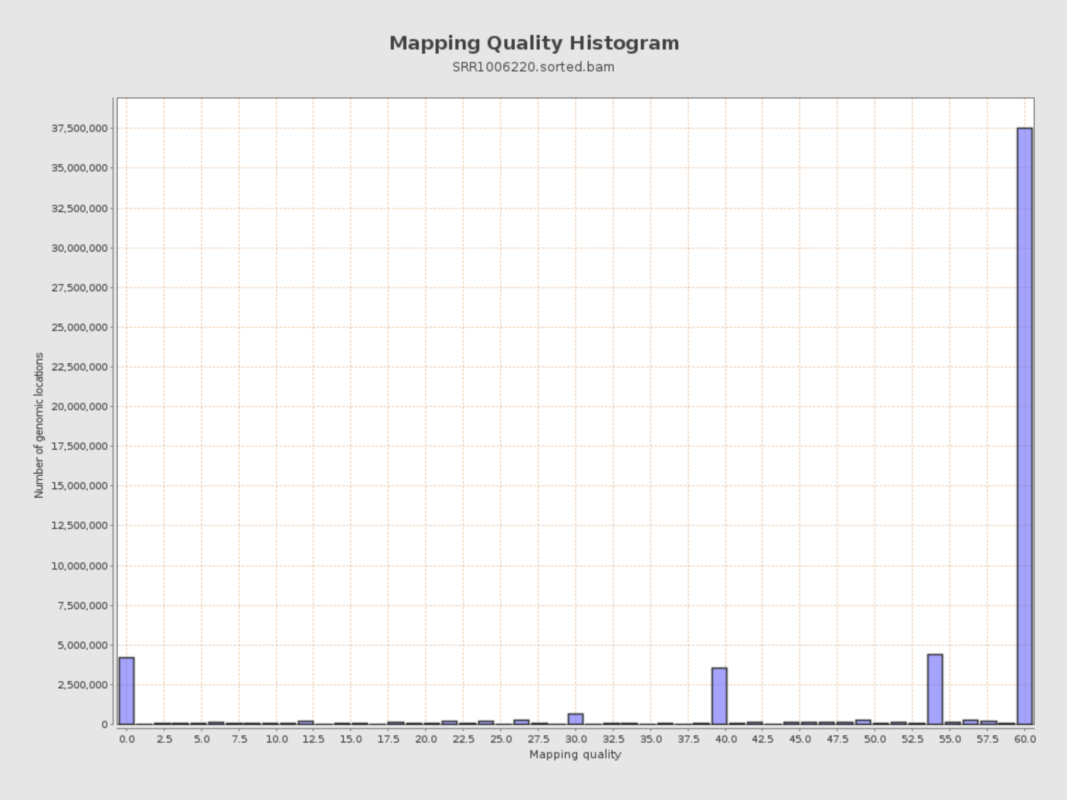
11. Results : Homopolymer Indels



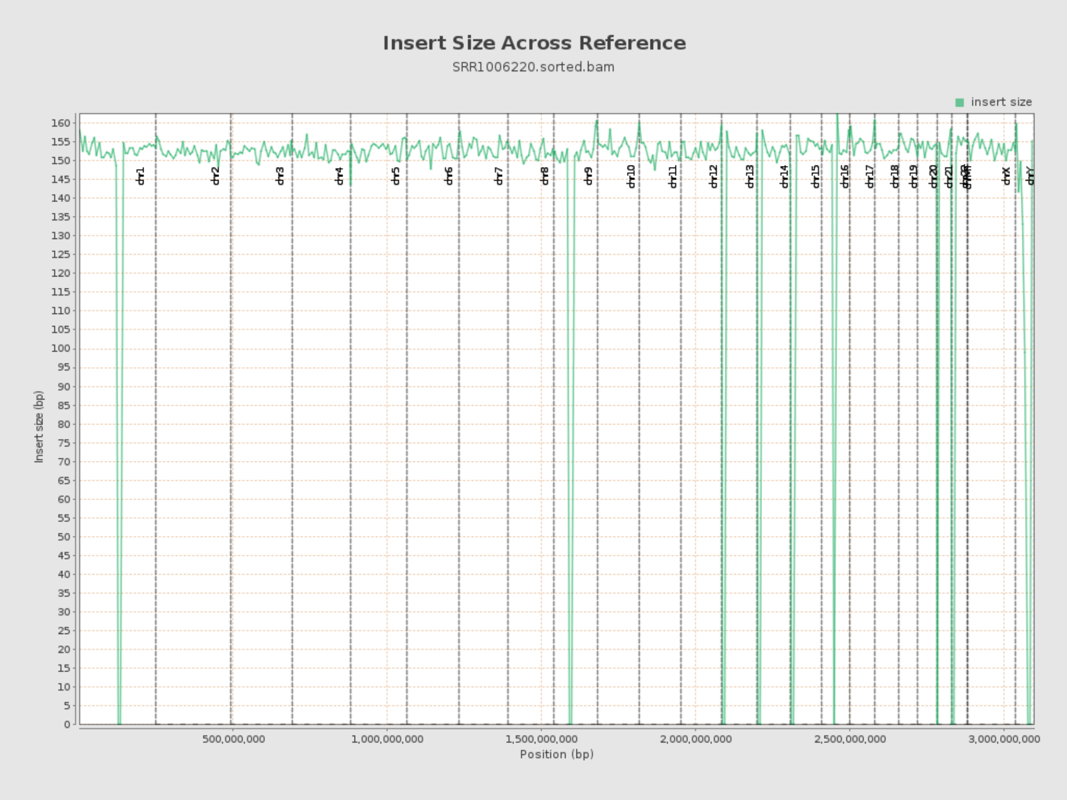
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram