Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:38:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006195.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_SRR1006195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006195_1.fastq.gz SRR1006195_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:38:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,526,788
Mapped reads	1,606,389 / 45.55%
Unmapped reads	1,920,399 / 54.45%
Mapped paired reads	1,606,389 / 45.55%
Mapped reads, first in pair	804,488 / 22.81%
Mapped reads, second in pair	801,901 / 22.74%
Mapped reads, both in pair	1,452,580 / 41.19%
Mapped reads, singletons	153,809 / 4.36%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	45,740 / 1.3%
Duplication rate	2.35%
Clipped reads	109,921 / 3.12%

2.2. ACGT Content

Number/percentage of A's	17,040,858 / 27.45%
Number/percentage of C's	13,612,392 / 21.93%
Number/percentage of T's	17,370,045 / 27.98%
Number/percentage of G's	14,053,981 / 22.64%
Number/percentage of N's	3,022 / 0%
GC Percentage	44.57%

2.3. Coverage

Mean	0.0201
Standard Deviation	0.2137

2.4. Mapping Quality

Mean Mapping Quality	47.36

2.5. Insert size

Mean	46,510.55
Standard Deviation	2,062,954.28
P25/Median/P75	63 / 95 / 148

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	184,773
Insertions	2,090
Mapped reads with at least one insertion	0.13%
Deletions	6,517
Mapped reads with at least one deletion	0.41%
Homopolymer indels	41.21%

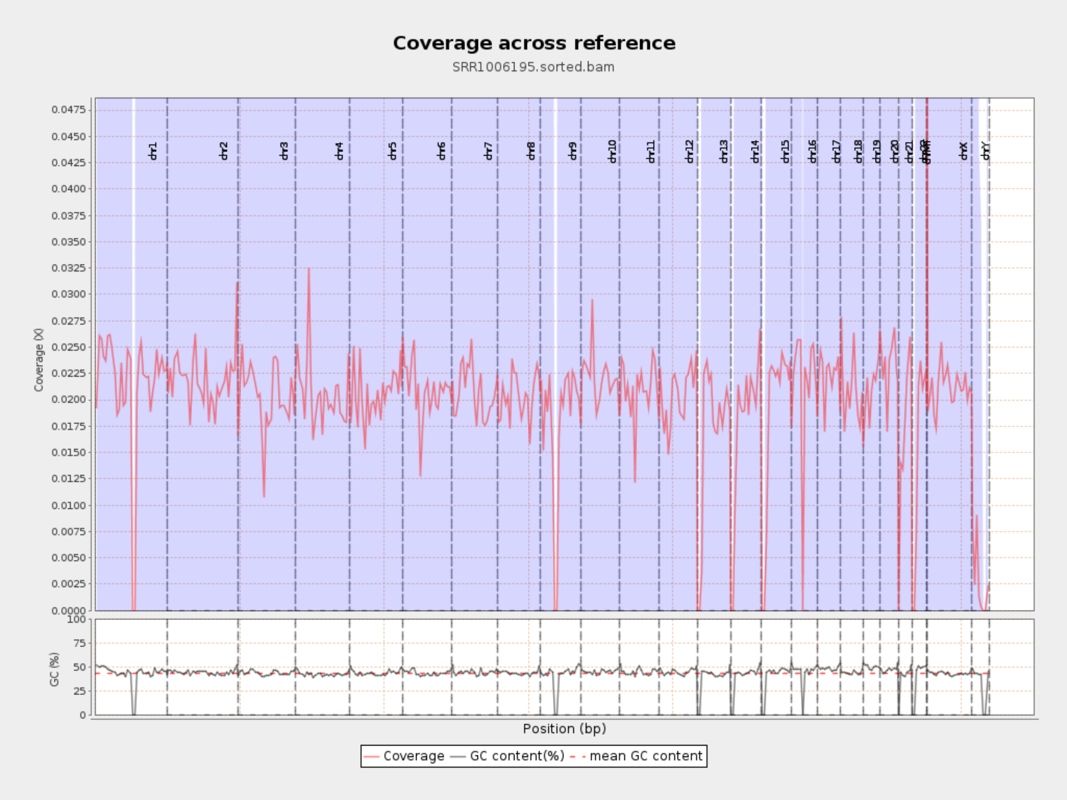
2.7. Chromosome stats

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

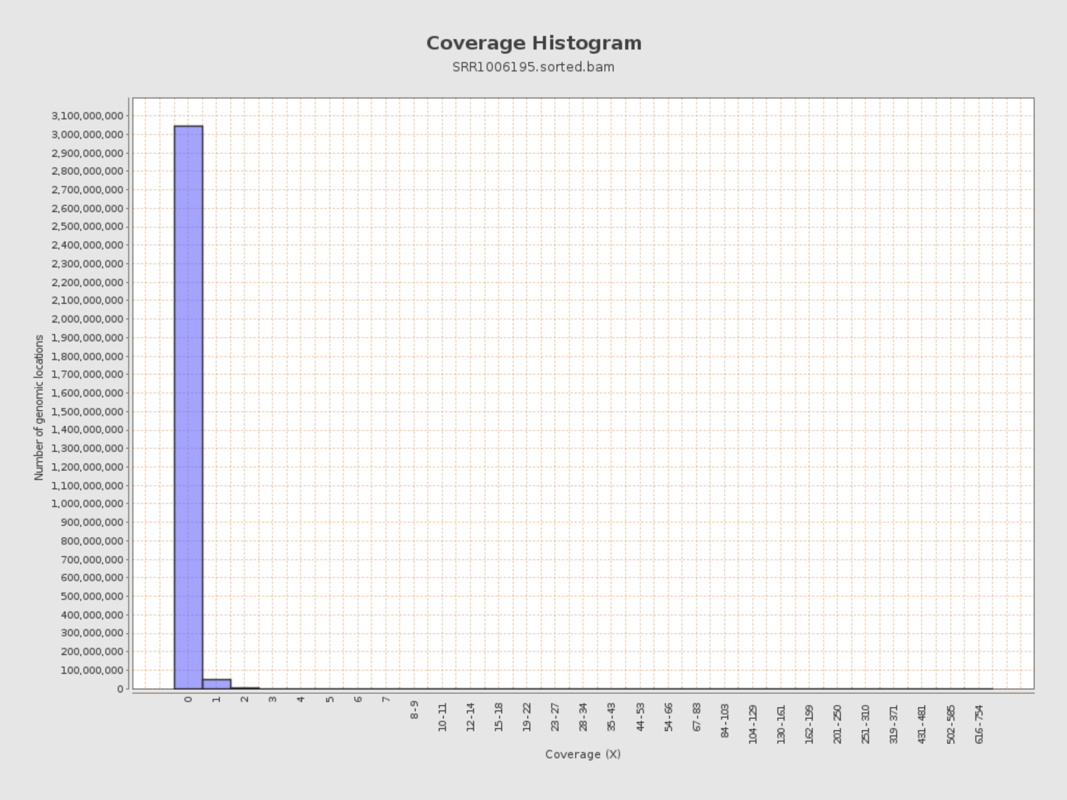
chr1	249250621	5323907	0.0214	0.2078
chr2	243199373	5321525	0.0219	0.342
chr3	198022430	4040479	0.0204	0.1599
chr4	191154276	3955047	0.0207	0.17
chr5	180915260	3716994	0.0205	0.3723
chr6	171115067	3570204	0.0209	0.1987
chr7	159138663	3291373	0.0207	0.1861
chr8	146364022	2966536	0.0203	0.1962
chr9	141213431	2507262	0.0178	0.158
chr10	135534747	3015600	0.0222	0.1905
chr11	135006516	2842189	0.0211	0.1753
chr12	133851895	2720708	0.0203	0.1611
chr13	115169878	1919398	0.0167	0.1445
chr14	107349540	1890350	0.0176	0.2632
chr15	102531392	1883609	0.0184	0.1521
chr16	90354753	1903729	0.0211	0.1725
chr17	81195210	1810498	0.0223	0.1761
chr18	78077248	1639268	0.021	0.2006
chr19	59128983	1247790	0.0211	0.1885
chr20	63025520	1459474	0.0232	0.1743
chr21	48129895	837718	0.0174	0.2005
chr22	51304566	781117	0.0152	0.1581
chrMT	16571	1248	0.0753	0.3186
chrX	155270560	3280669	0.0211	0.1676

chrY	59373566	162235	0.0027	0.0814

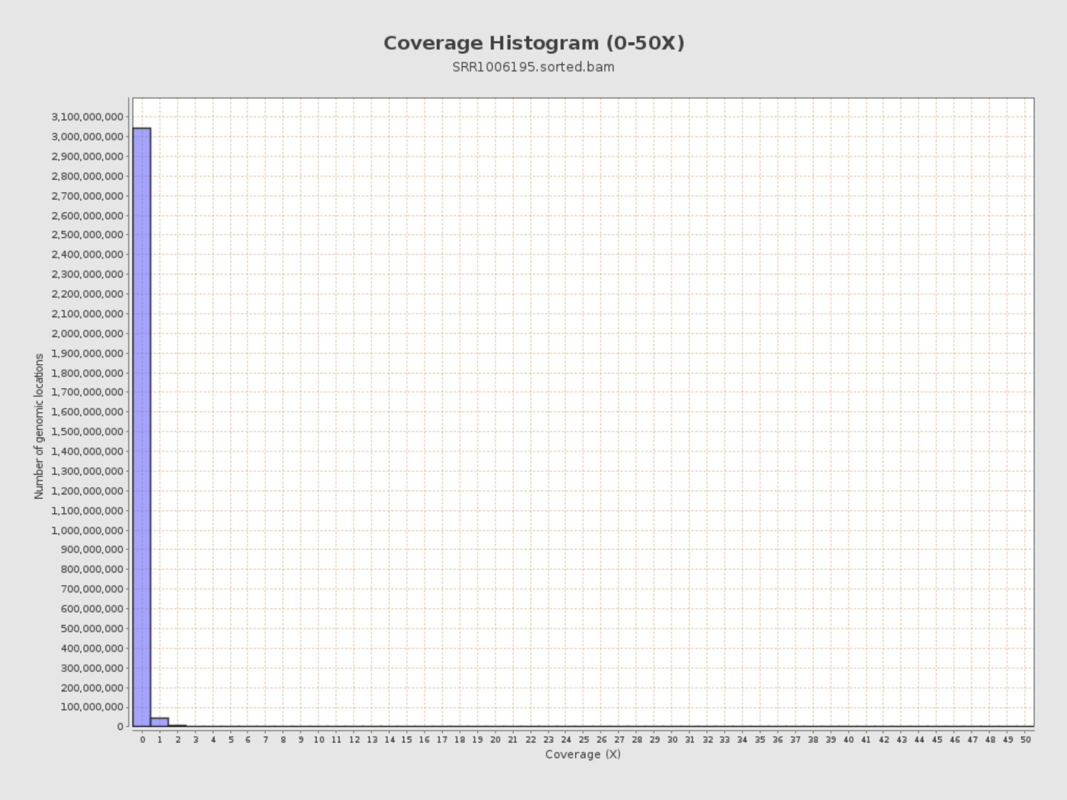
3. Results : Coverage across reference



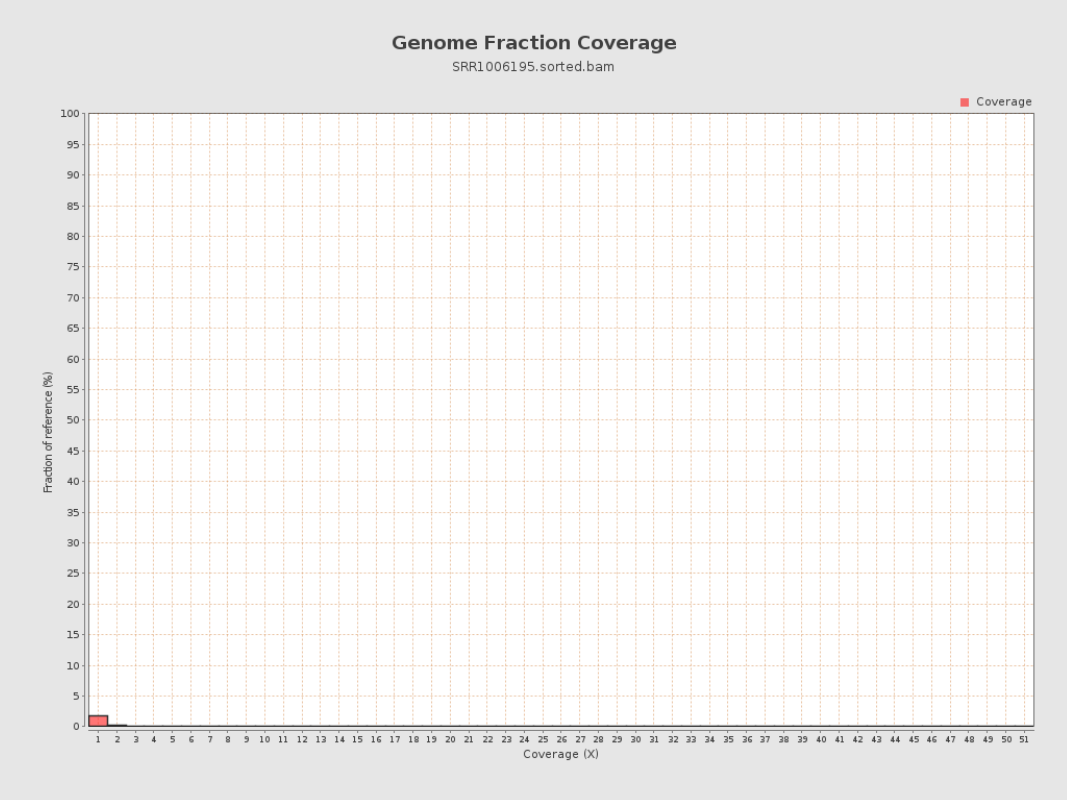
4. Results : Coverage Histogram



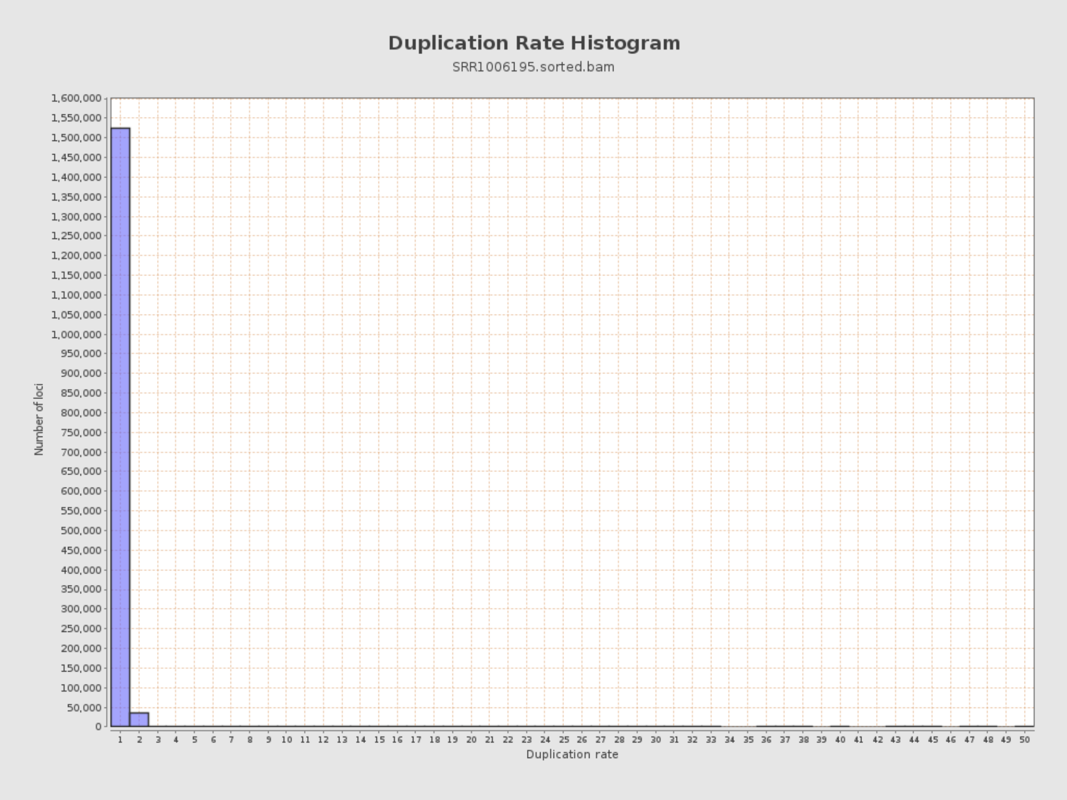
5. Results : Coverage Histogram (0-50X)



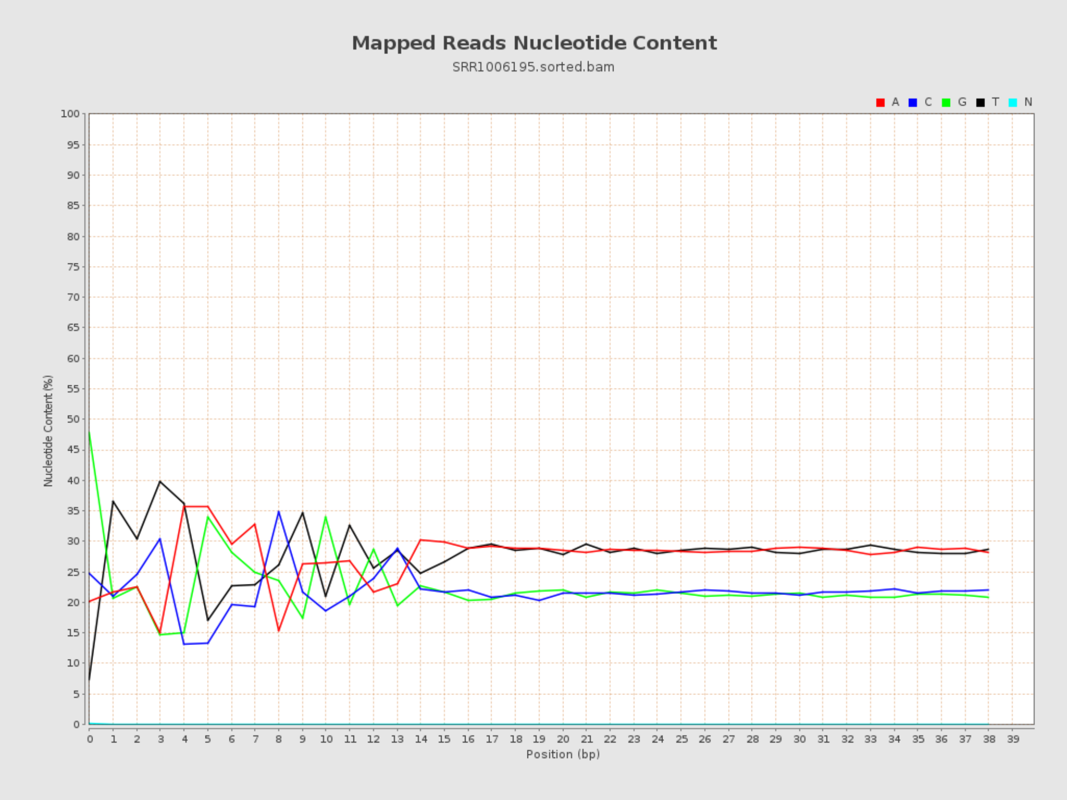
6. Results : Genome Fraction Coverage



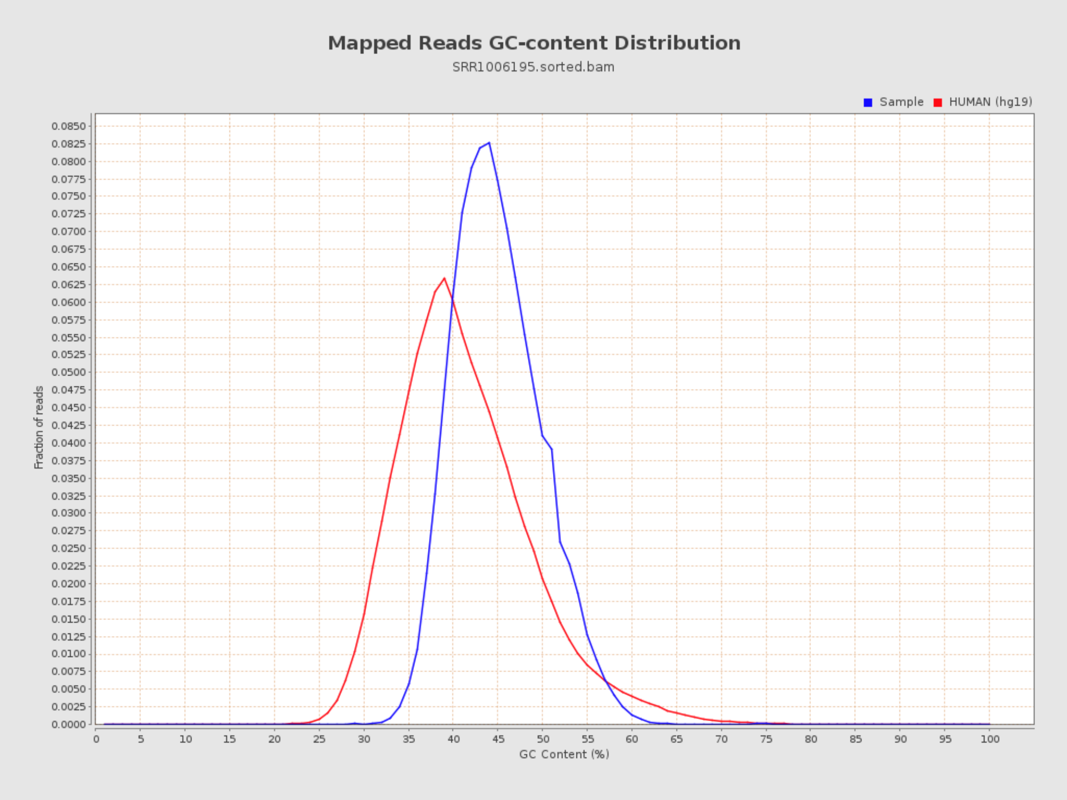
7. Results : Duplication Rate Histogram



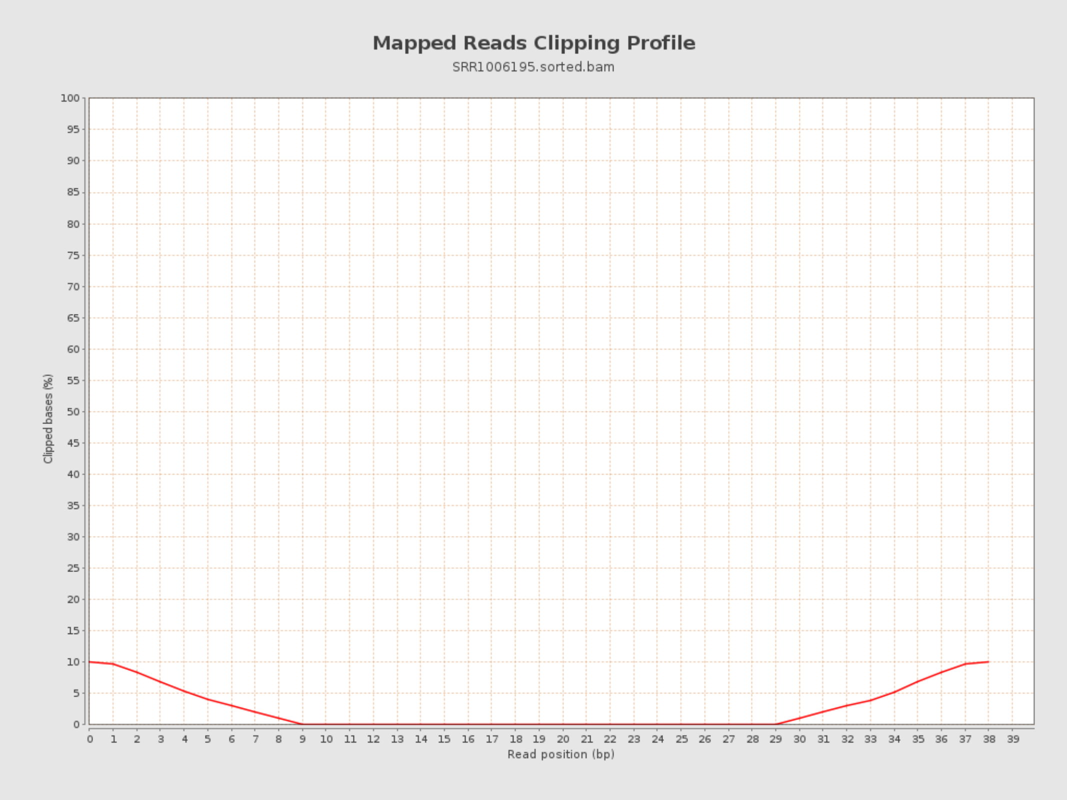
8. Results : Mapped Reads Nucleotide Content



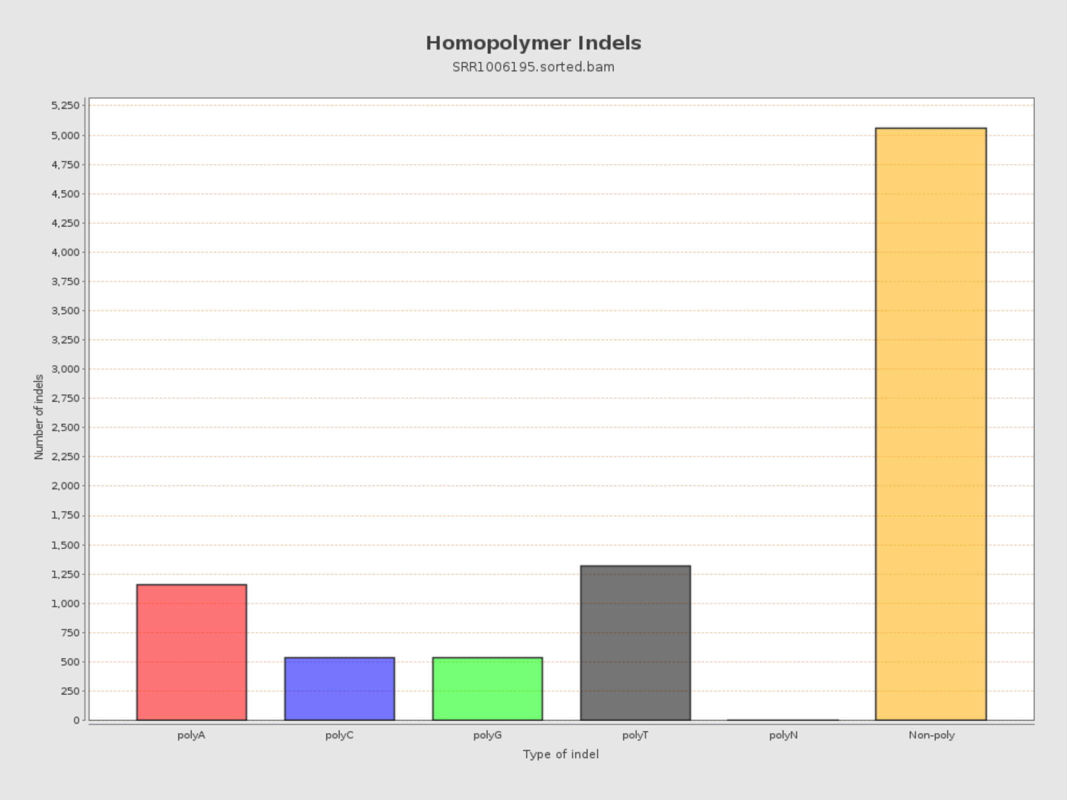
9. Results : Mapped Reads GC-content Distribution



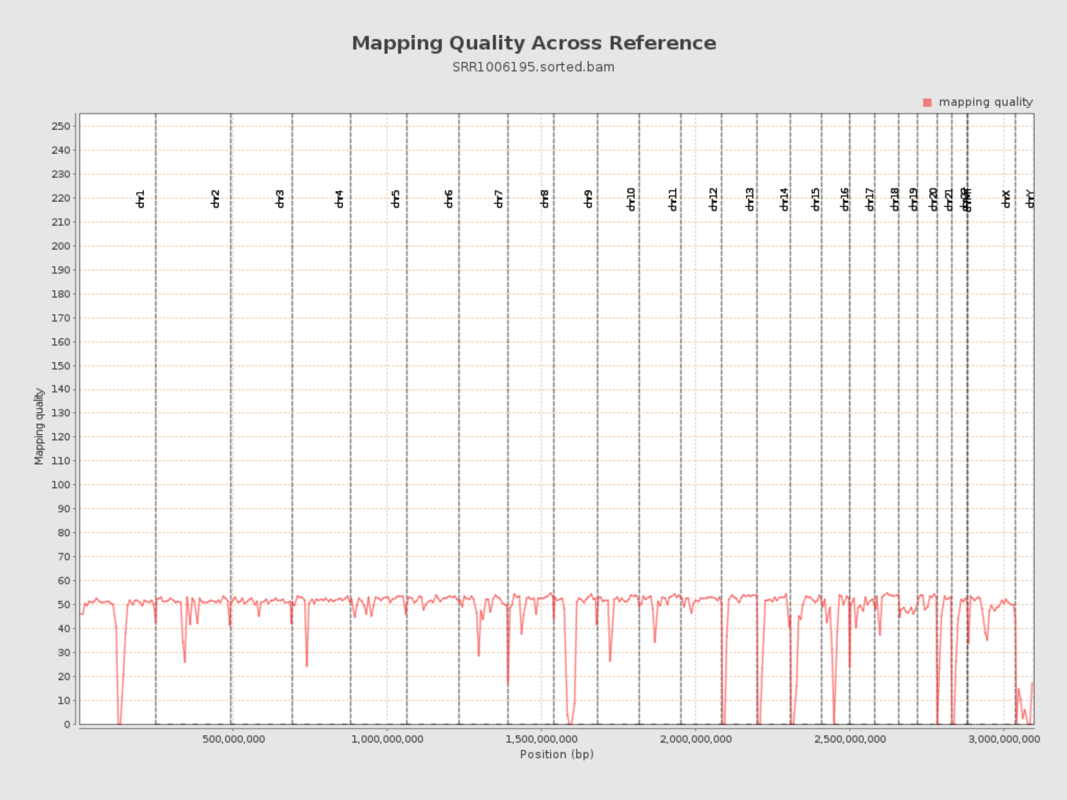
10. Results : Mapped Reads Clipping Profile



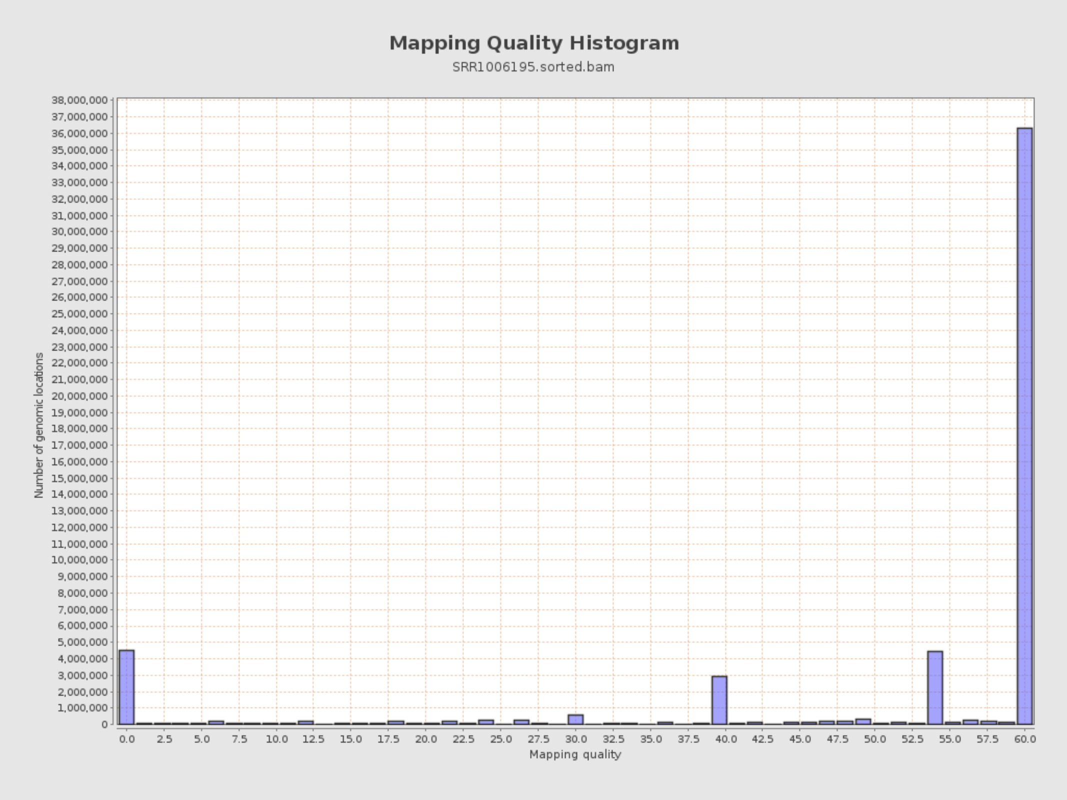
11. Results : Homopolymer Indels



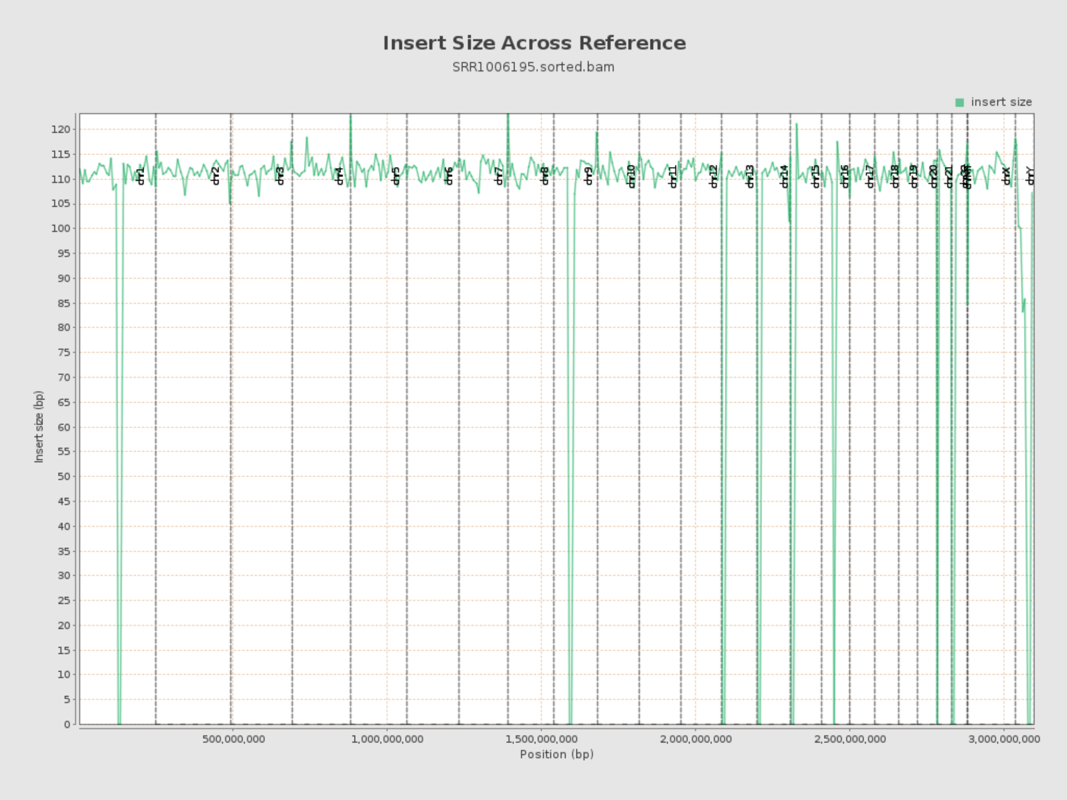
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram