Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 21:51:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006159.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_SRR1006159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006159_1.fastq.gz SRR1006159_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 21:51:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,902,882
Mapped reads	14,552,968 / 86.1%
Unmapped reads	2,349,914 / 13.9%
Mapped paired reads	14,552,968 / 86.1%
Mapped reads, first in pair	7,347,178 / 43.47%
Mapped reads, second in pair	7,205,790 / 42.63%
Mapped reads, both in pair	13,516,212 / 79.96%
Mapped reads, singletons	1,036,756 / 6.13%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	842,748 / 4.99%
Duplication rate	4.64%
Clipped reads	1,048,663 / 6.2%

2.2. ACGT Content

Number/percentage of A's	158,813,456 / 28.23%
Number/percentage of C's	119,530,829 / 21.25%
Number/percentage of T's	161,510,902 / 28.71%
Number/percentage of G's	122,693,226 / 21.81%
Number/percentage of N's	22,583 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.1817
Standard Deviation	1.2008

2.4. Mapping Quality

Mean Mapping Quality	47.91

2.5. Insert size

Mean	57,928.08
Standard Deviation	2,312,456.07
P25/Median/P75	70 / 96 / 129

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	2,759,516
Insertions	17,245
Mapped reads with at least one insertion	0.12%
Deletions	47,651
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.45%

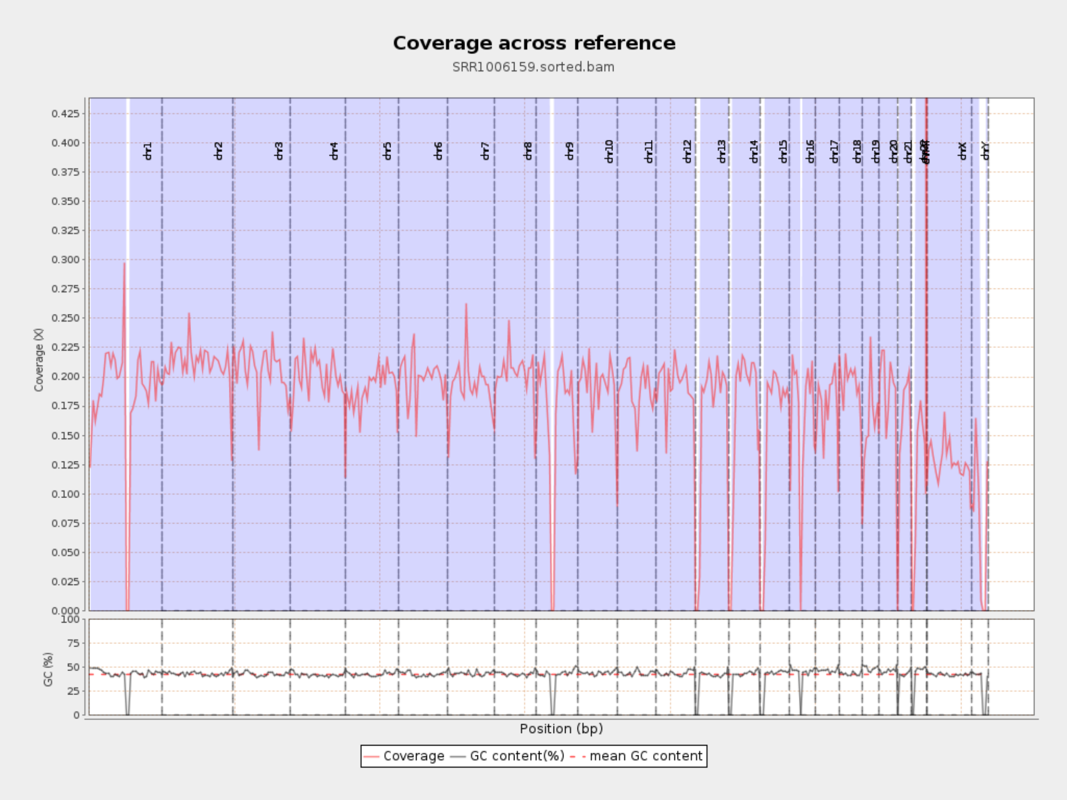
2.7. Chromosome stats

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

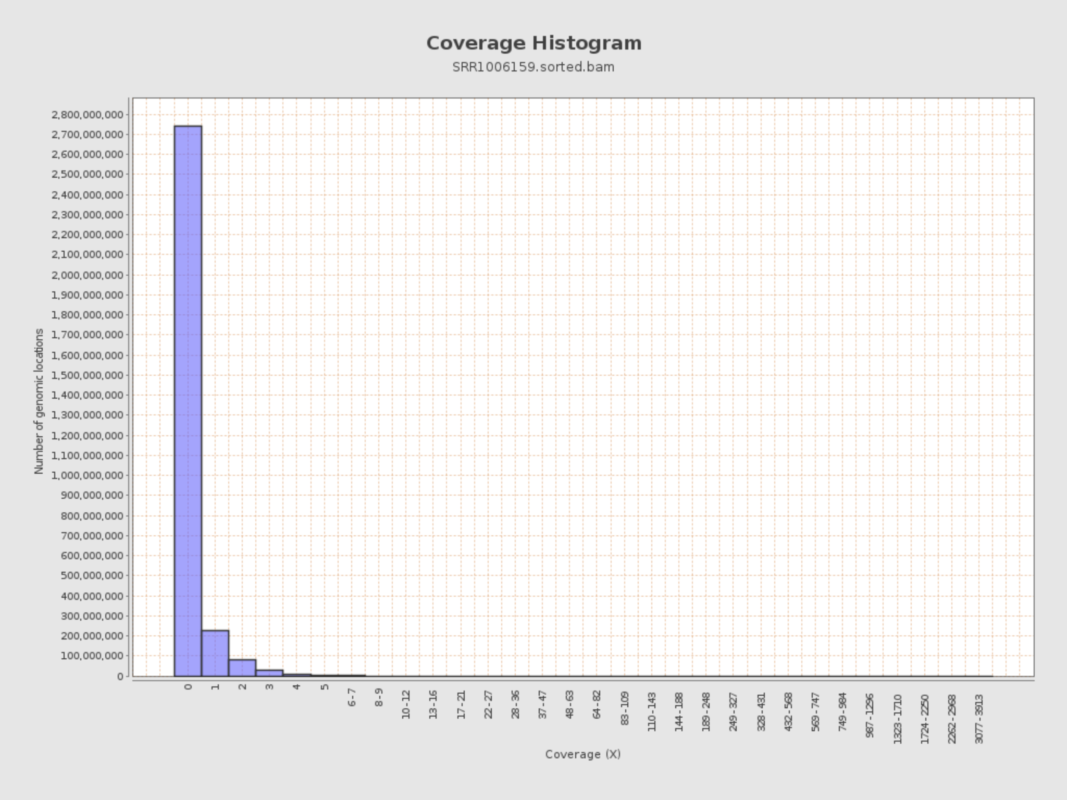
chr1	249250621	46121953	0.185	2.5421
chr2	243199373	51523264	0.2119	0.9932
chr3	198022430	40974140	0.2069	0.6567
chr4	191154276	38376311	0.2008	0.7023
chr5	180915260	34578127	0.1911	0.6357
chr6	171115067	34062776	0.1991	0.7989
chr7	159138663	30911496	0.1942	1.5847
chr8	146364022	29716081	0.203	2.0619
chr9	141213431	23451563	0.1661	0.8549
chr10	135534747	26351178	0.1944	0.8531
chr11	135006516	25503766	0.1889	1.3224
chr12	133851895	25799116	0.1927	0.6485
chr13	115169878	18639393	0.1618	0.5707
chr14	107349540	17793124	0.1657	0.6491
chr15	102531392	15755162	0.1537	0.5647
chr16	90354753	14982268	0.1658	0.6432
chr17	81195210	14067749	0.1733	0.8174
chr18	78077248	15262956	0.1955	1.4648
chr19	59128983	9598050	0.1623	1.7609
chr20	63025520	11939838	0.1894	0.6556
chr21	48129895	7434863	0.1545	0.6798
chr22	51304566	5563397	0.1084	0.6869
chrMT	16571	175996	10.6207	6.3765
chrX	155270560	19825916	0.1277	0.6691

chrY	59373566	4223794	0.0711	0.6984

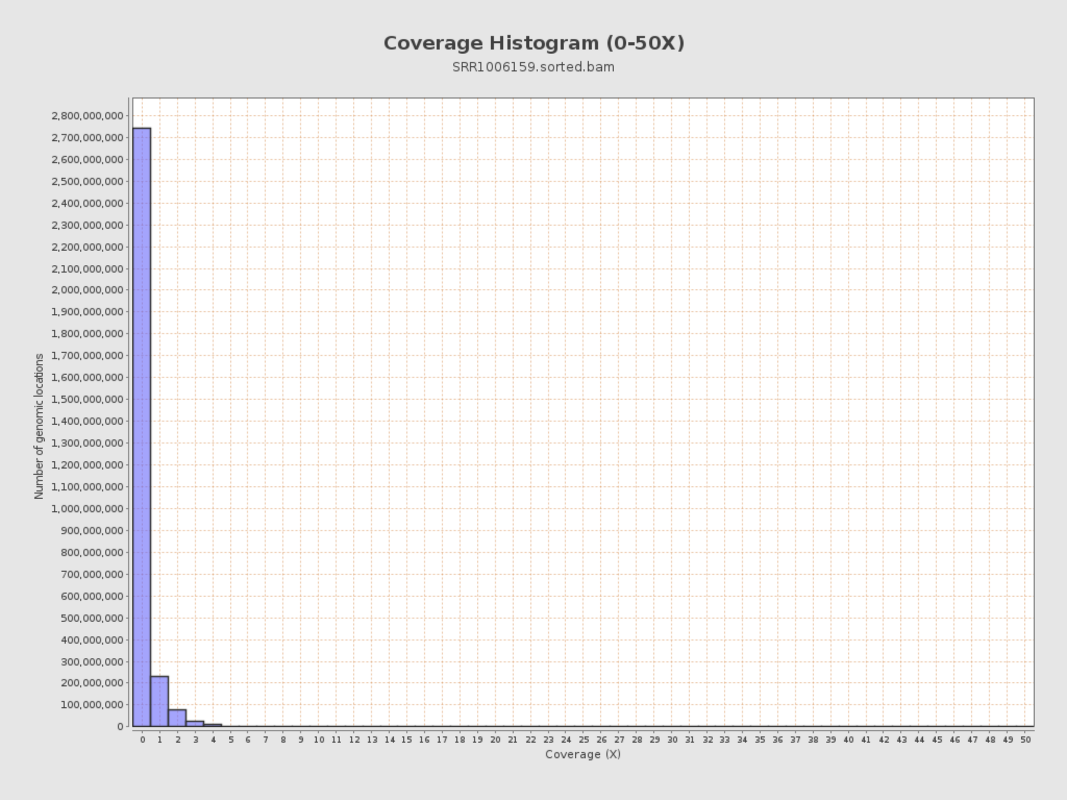
3. Results : Coverage across reference



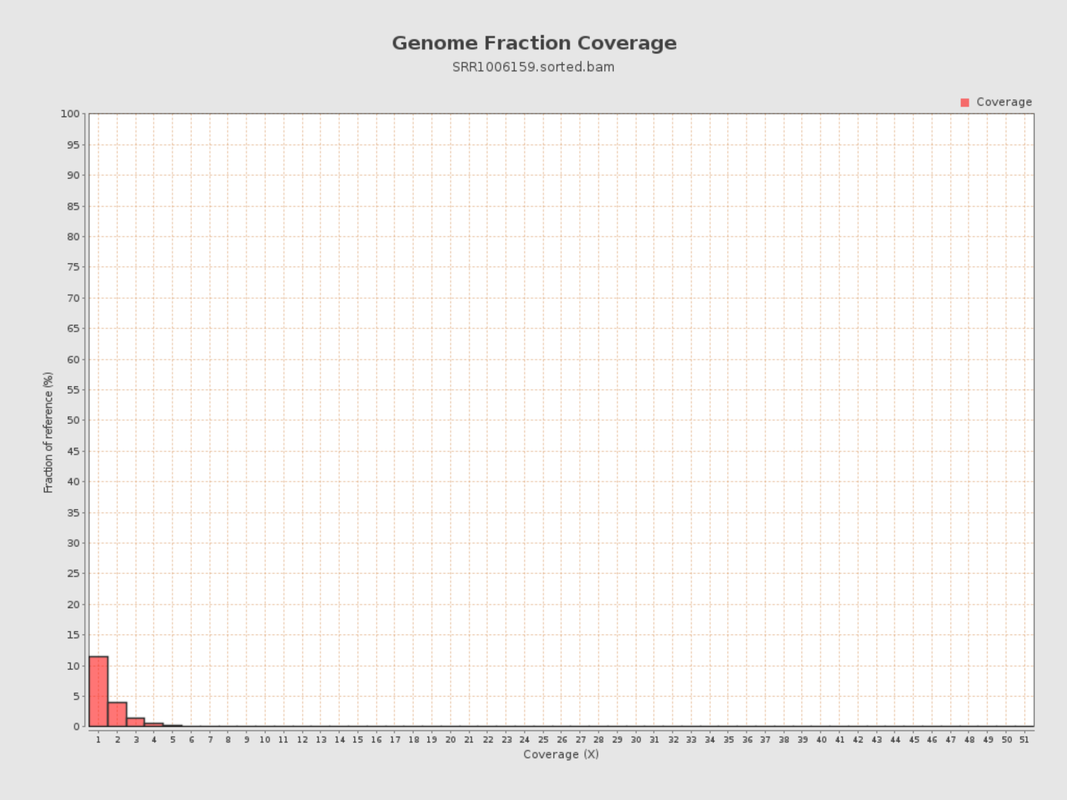
4. Results : Coverage Histogram



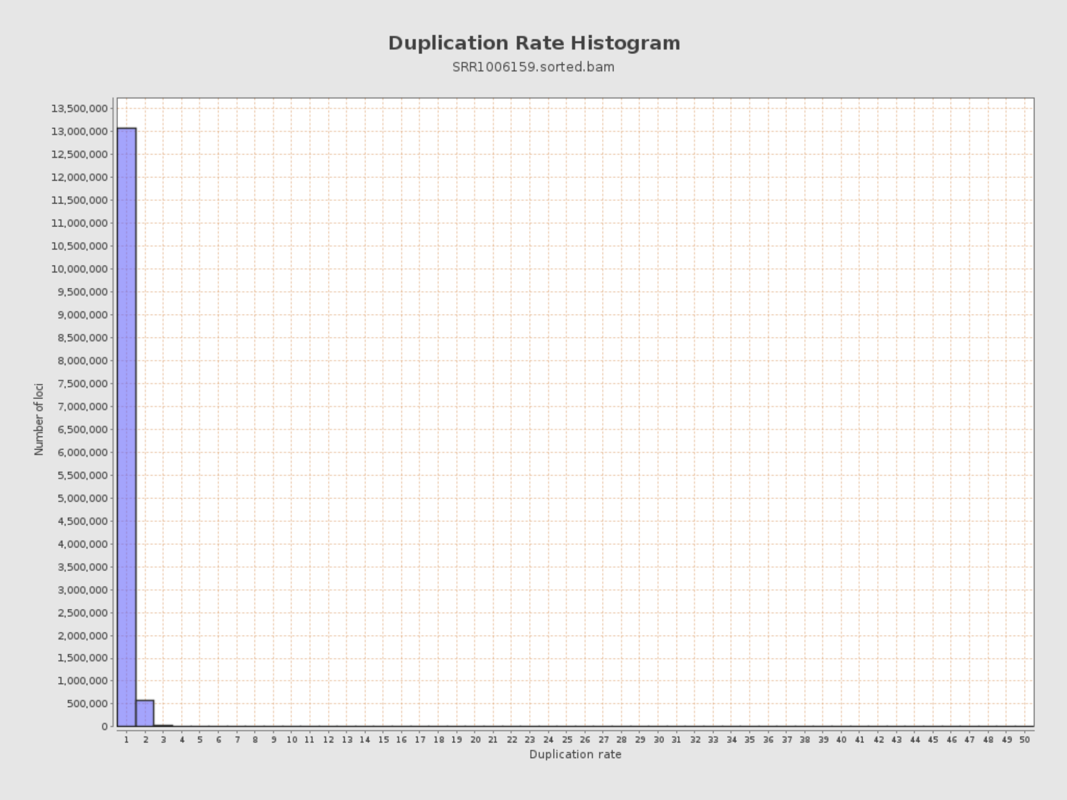
5. Results : Coverage Histogram (0-50X)



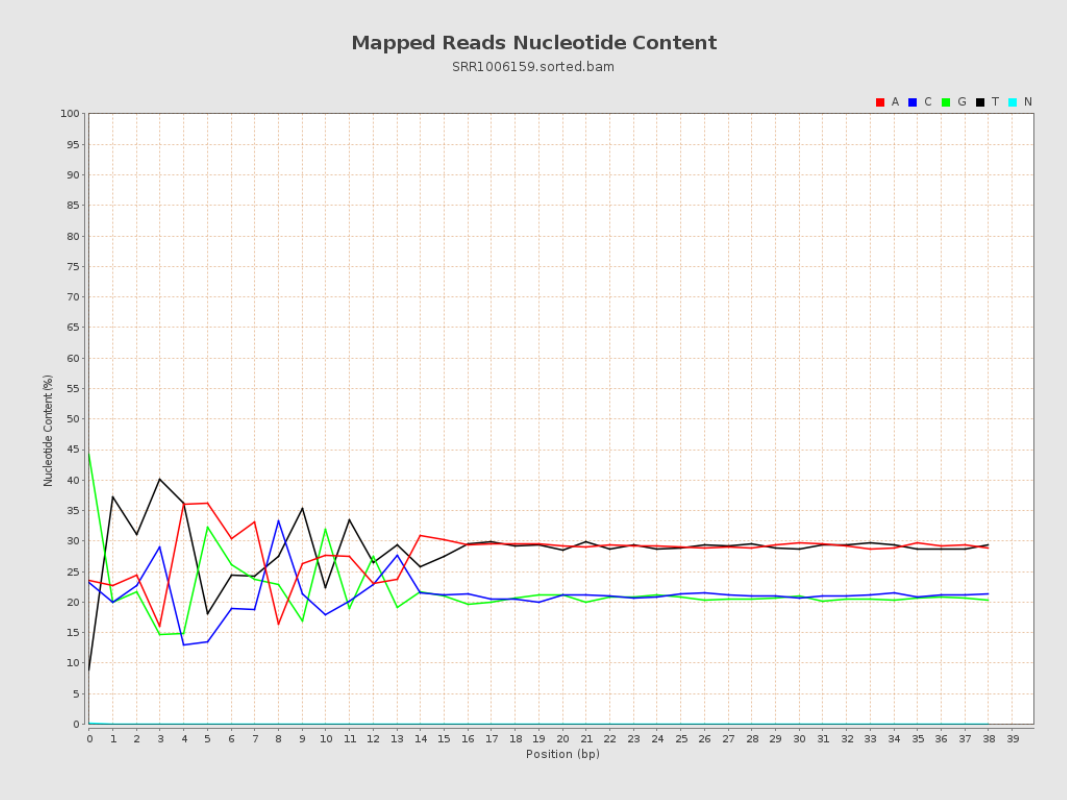
6. Results : Genome Fraction Coverage



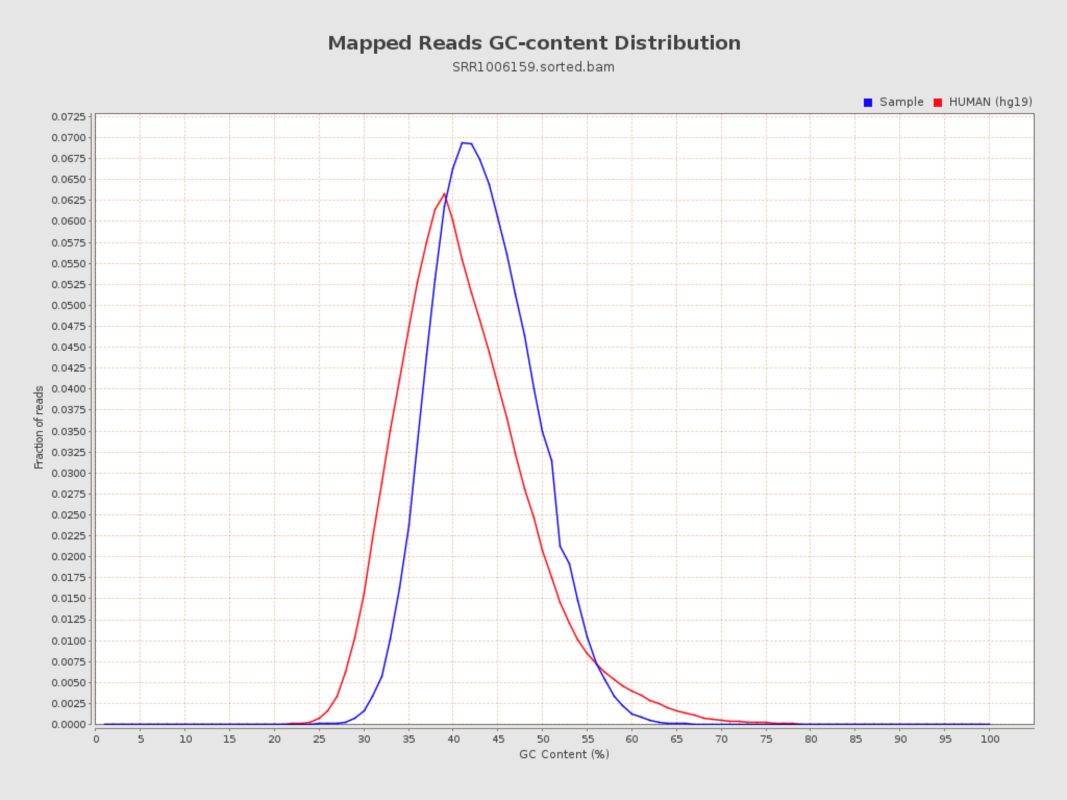
7. Results : Duplication Rate Histogram



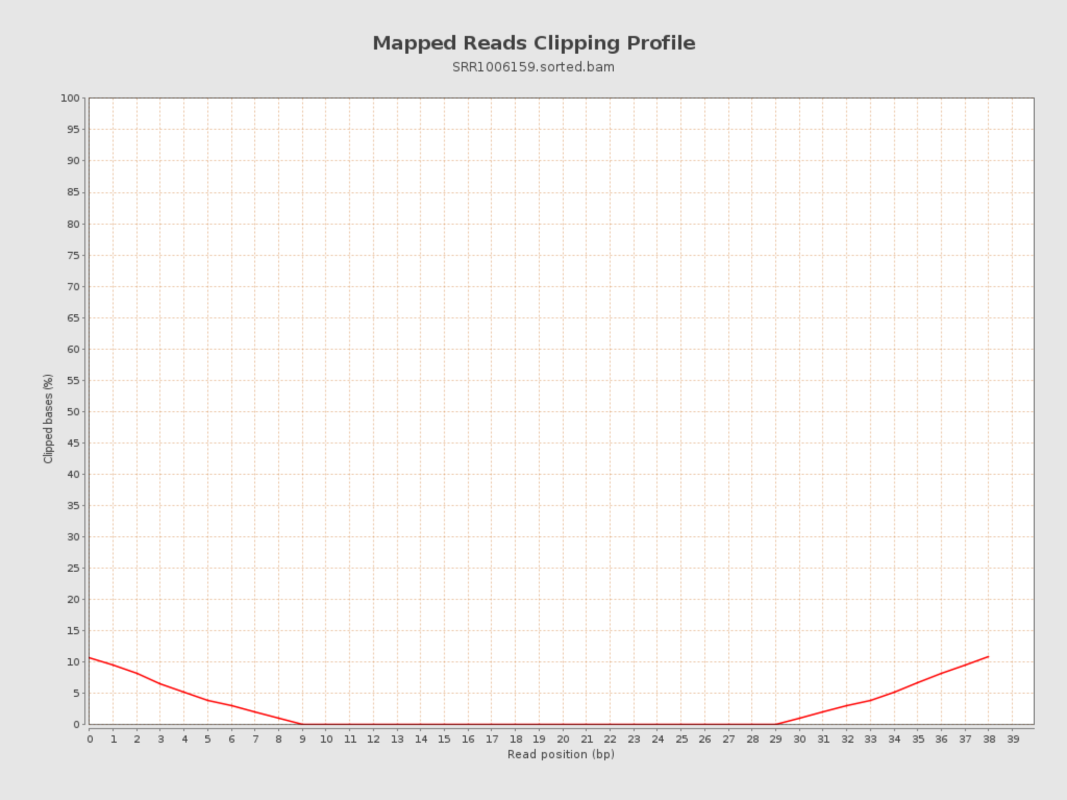
8. Results : Mapped Reads Nucleotide Content



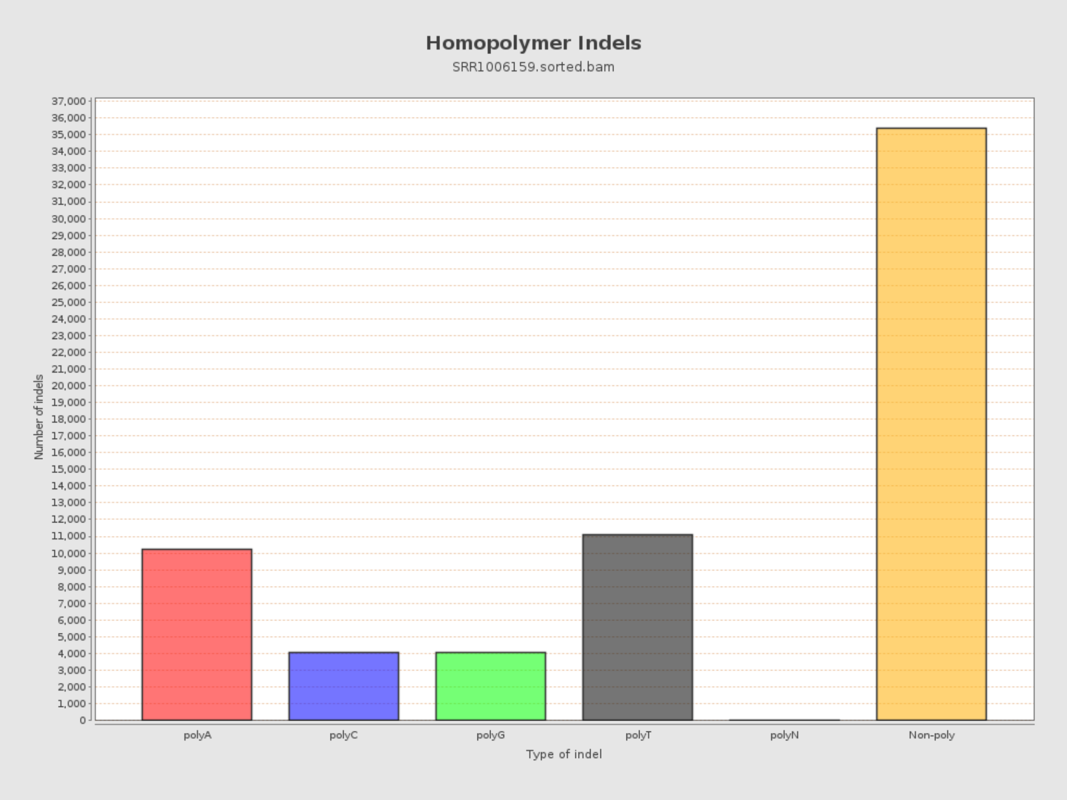
9. Results : Mapped Reads GC-content Distribution



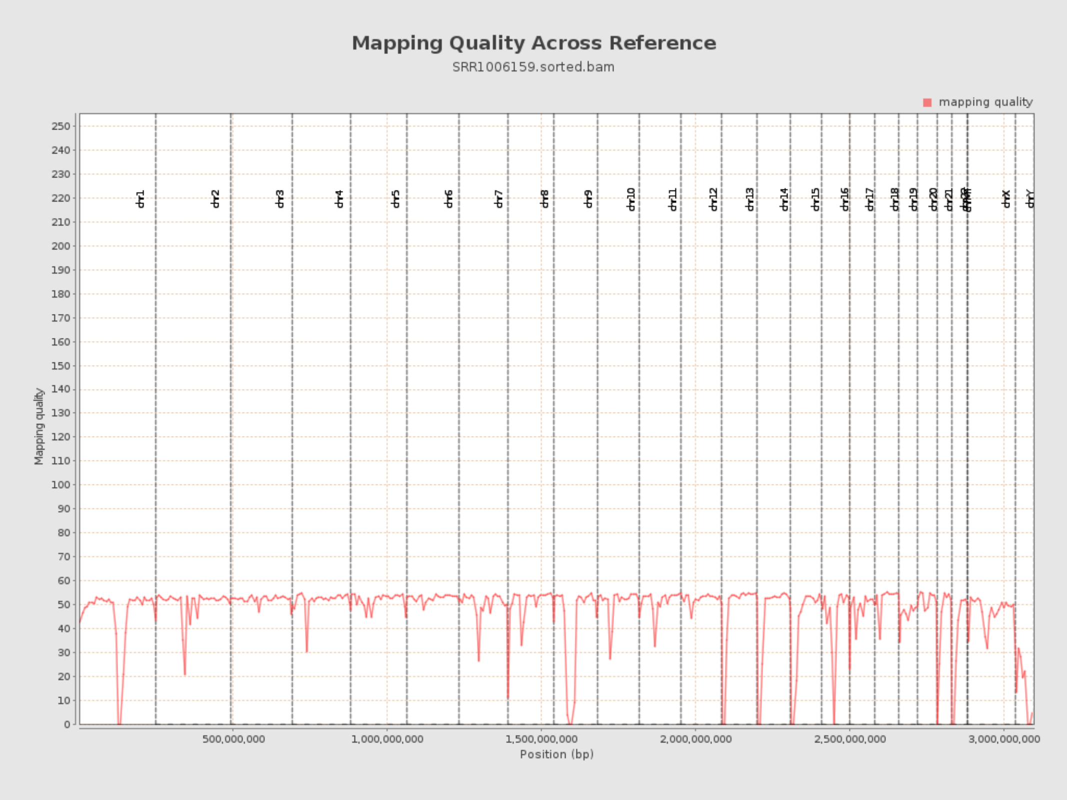
10. Results : Mapped Reads Clipping Profile



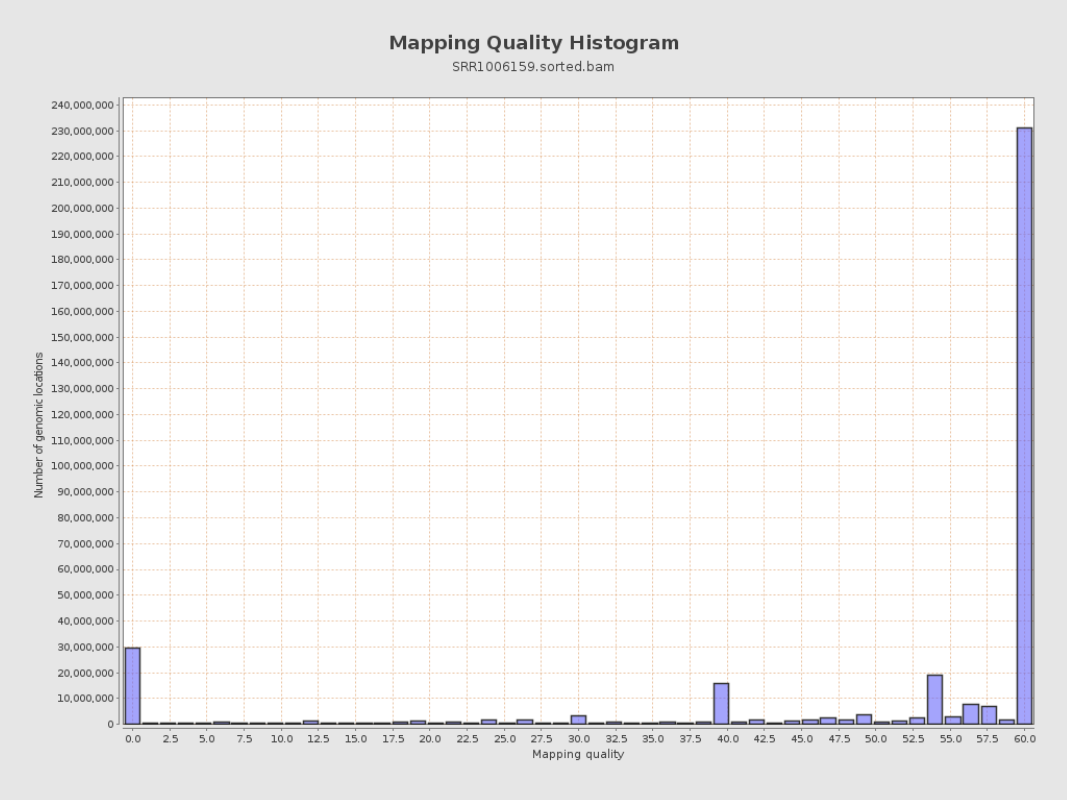
11. Results : Homopolymer Indels



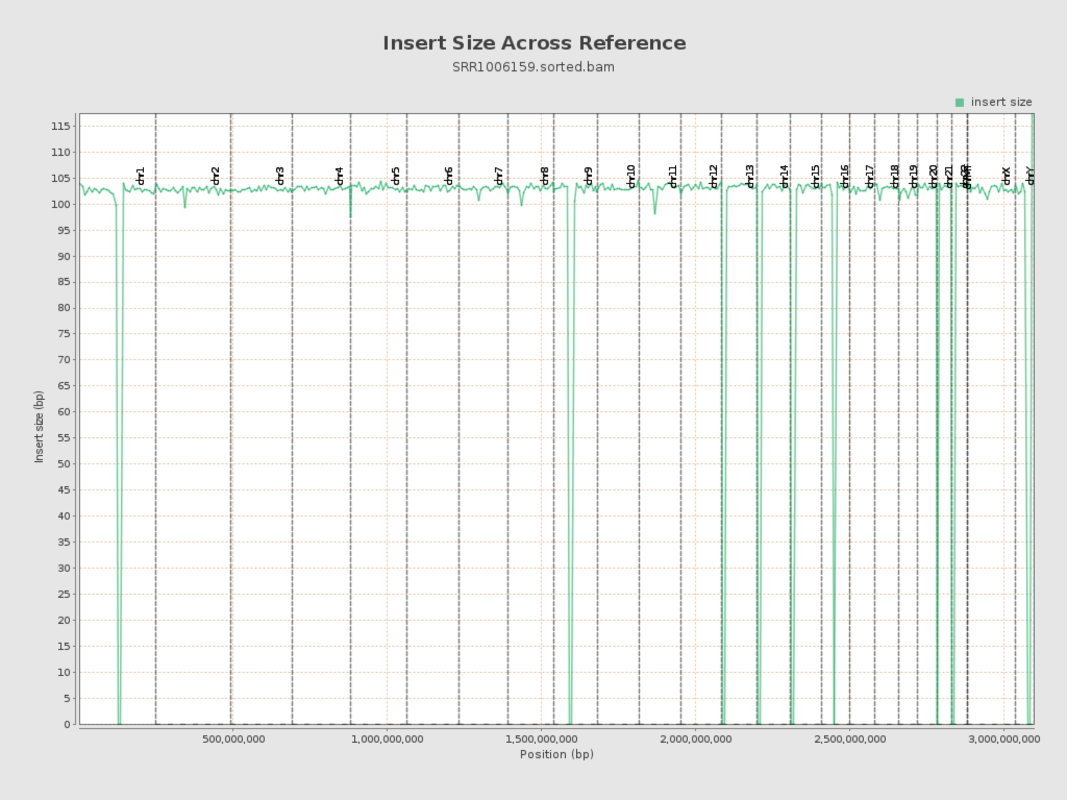
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram