Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 14:03:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006020.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_SRR1006020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006020_1.fastq.gz SRR1006020_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 14:03:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,400,944
Mapped reads	14,962,746 / 69.92%
Unmapped reads	6,438,198 / 30.08%
Mapped paired reads	14,962,746 / 69.92%
Mapped reads, first in pair	7,538,499 / 35.23%
Mapped reads, second in pair	7,424,247 / 34.69%
Mapped reads, both in pair	13,418,298 / 62.7%
Mapped reads, singletons	1,544,448 / 7.22%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	709,188 / 3.31%
Duplication rate	3.89%
Clipped reads	1,203,460 / 5.62%

2.2. ACGT Content

Number/percentage of A's	165,900,205 / 28.72%
Number/percentage of C's	120,941,150 / 20.93%
Number/percentage of T's	167,859,490 / 29.06%
Number/percentage of G's	122,936,632 / 21.28%
Number/percentage of N's	72,586 / 0.01%
GC Percentage	42.21%

2.3. Coverage

Mean	0.1866
Standard Deviation	0.9333

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Insert size

Mean	64,905.54
Standard Deviation	2,479,270.58
P25/Median/P75	56 / 74 / 103

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	3,096,963
Insertions	17,756
Mapped reads with at least one insertion	0.12%
Deletions	52,449
Mapped reads with at least one deletion	0.35%
Homopolymer indels	45.06%

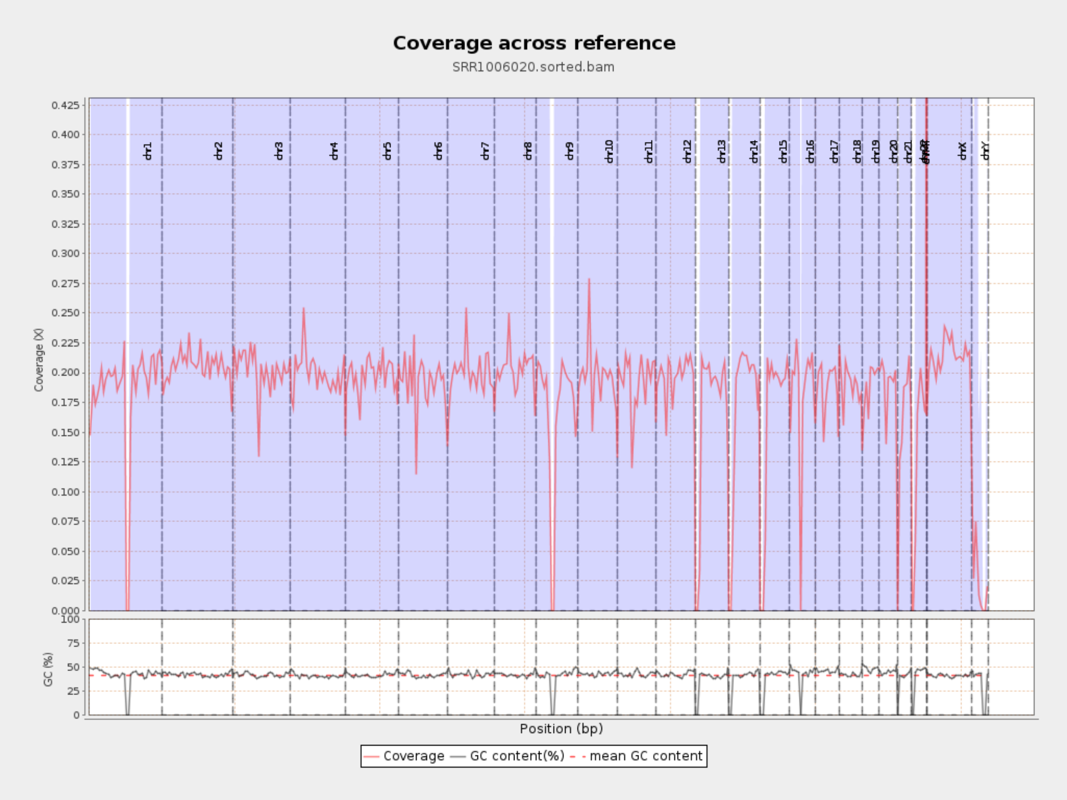
2.7. Chromosome stats

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

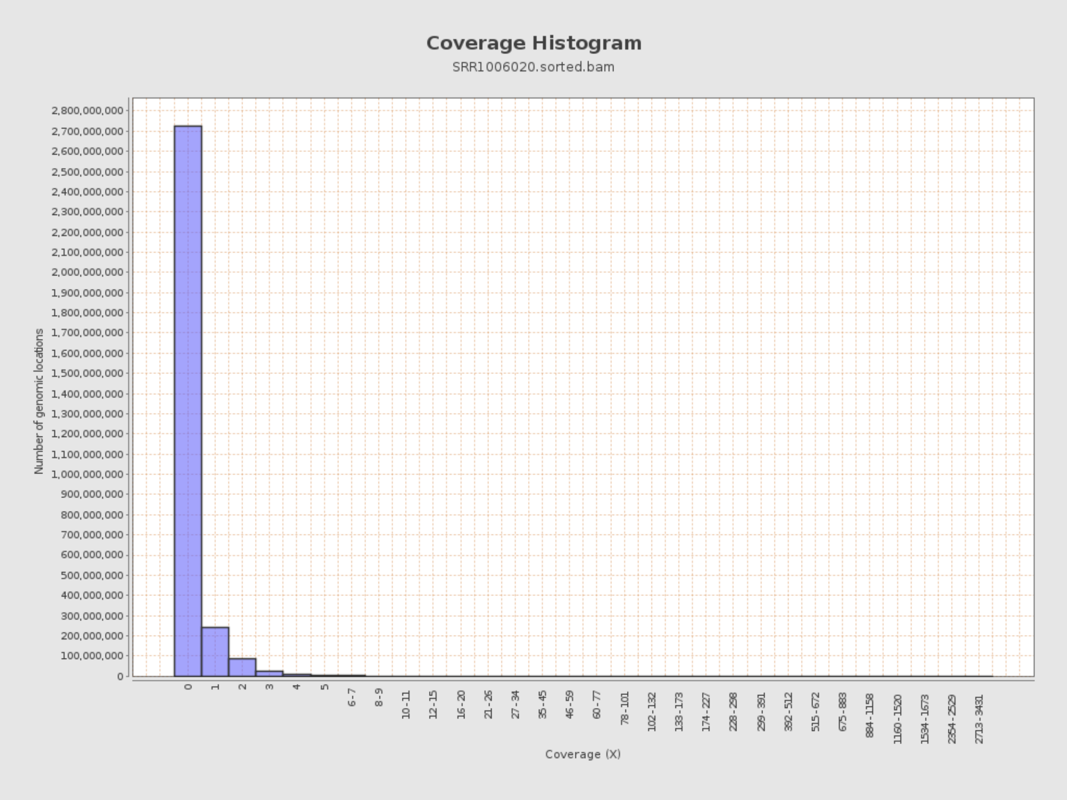
chr1	249250621	45798133	0.1837	1.3563
chr2	243199373	50097801	0.206	0.88
chr3	198022430	39932921	0.2017	0.6333
chr4	191154276	38130159	0.1995	0.7088
chr5	180915260	35822098	0.198	0.6252
chr6	171115067	32808672	0.1917	1.0544
chr7	159138663	31894492	0.2004	1.1655
chr8	146364022	29744095	0.2032	1.8092
chr9	141213431	23204404	0.1643	0.7454
chr10	135534747	26846397	0.1981	1.0582
chr11	135006516	26007104	0.1926	0.7263
chr12	133851895	26279810	0.1963	0.633
chr13	115169878	18803926	0.1633	0.5635
chr14	107349540	18101321	0.1686	0.6506
chr15	102531392	16467985	0.1606	0.5666
chr16	90354753	16347348	0.1809	0.7395
chr17	81195210	15111714	0.1861	0.6531
chr18	78077248	14831659	0.19	1.2219
chr19	59128983	11148556	0.1885	1.2389
chr20	63025520	11903080	0.1889	0.6511
chr21	48129895	7480057	0.1554	0.6456
chr22	51304566	6381386	0.1244	0.5572
chrMT	16571	26392	1.5927	1.6616
chrX	155270560	33143291	0.2135	0.7141

chrY	59373566	1464473	0.0247	0.4563

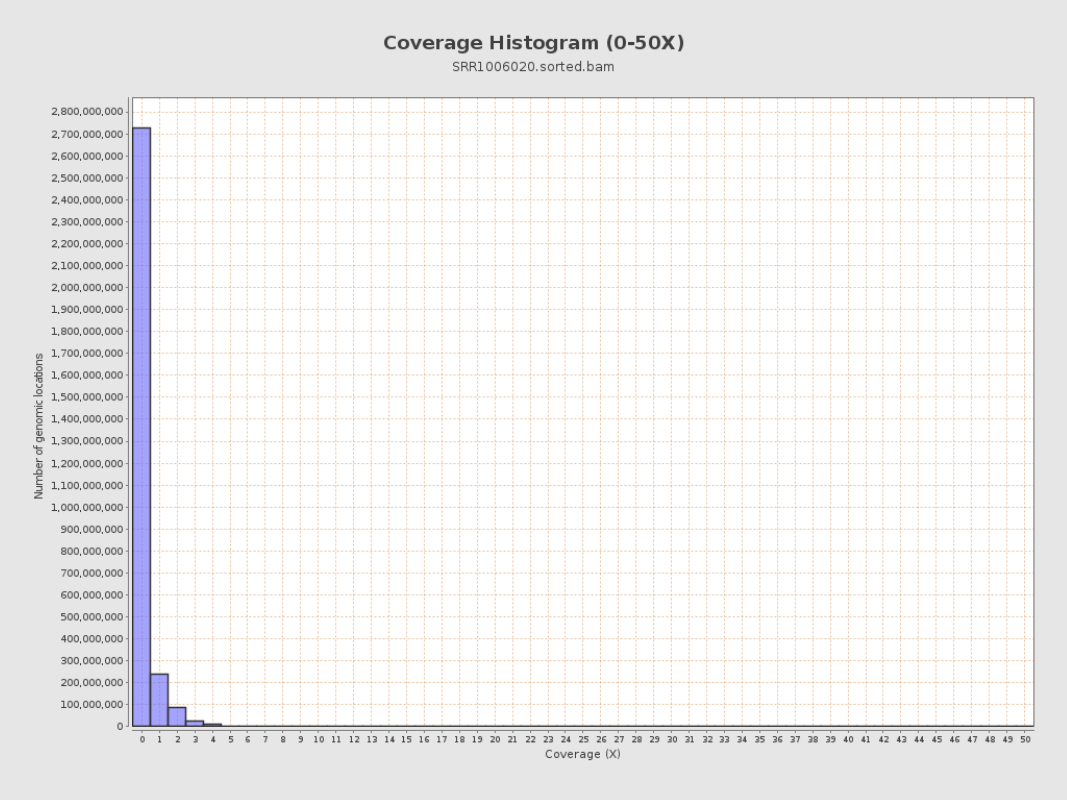
3. Results : Coverage across reference



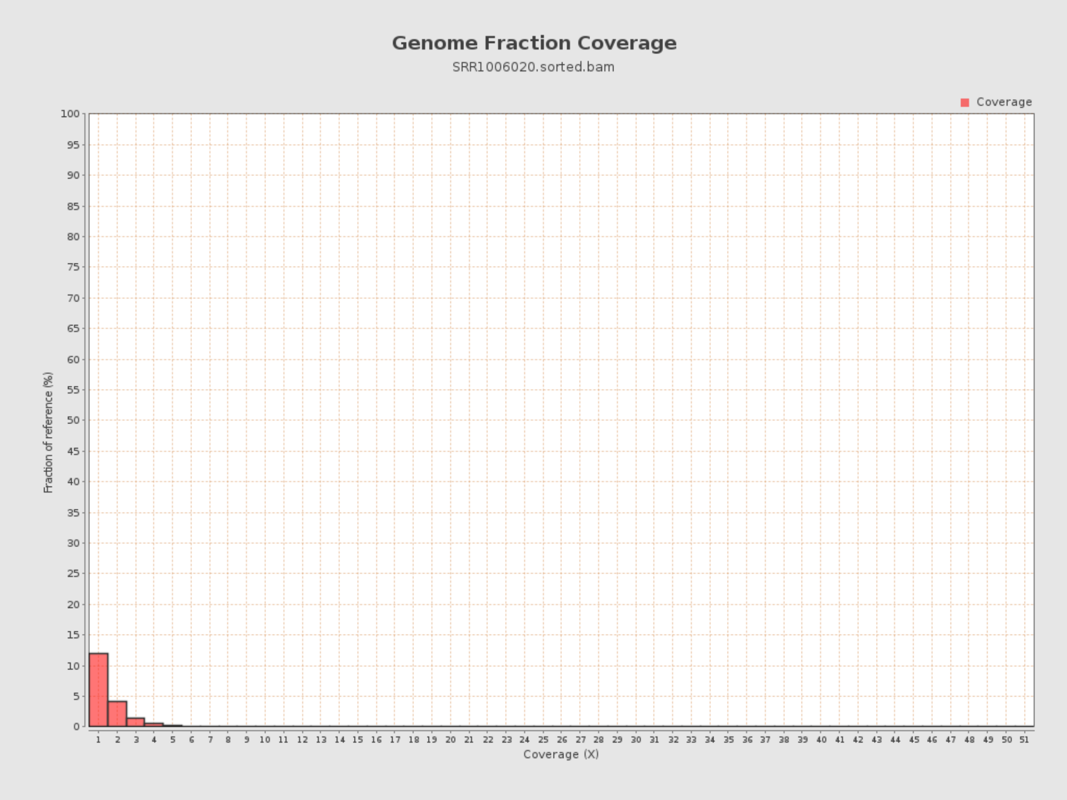
4. Results : Coverage Histogram



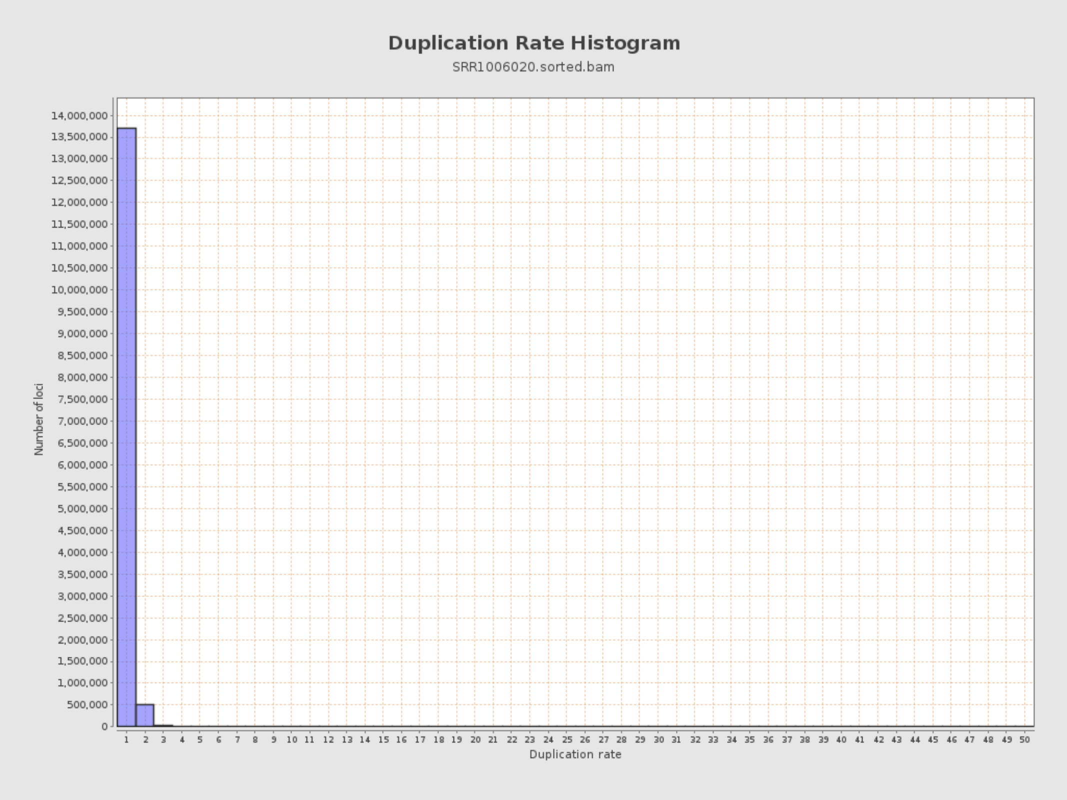
5. Results : Coverage Histogram (0-50X)



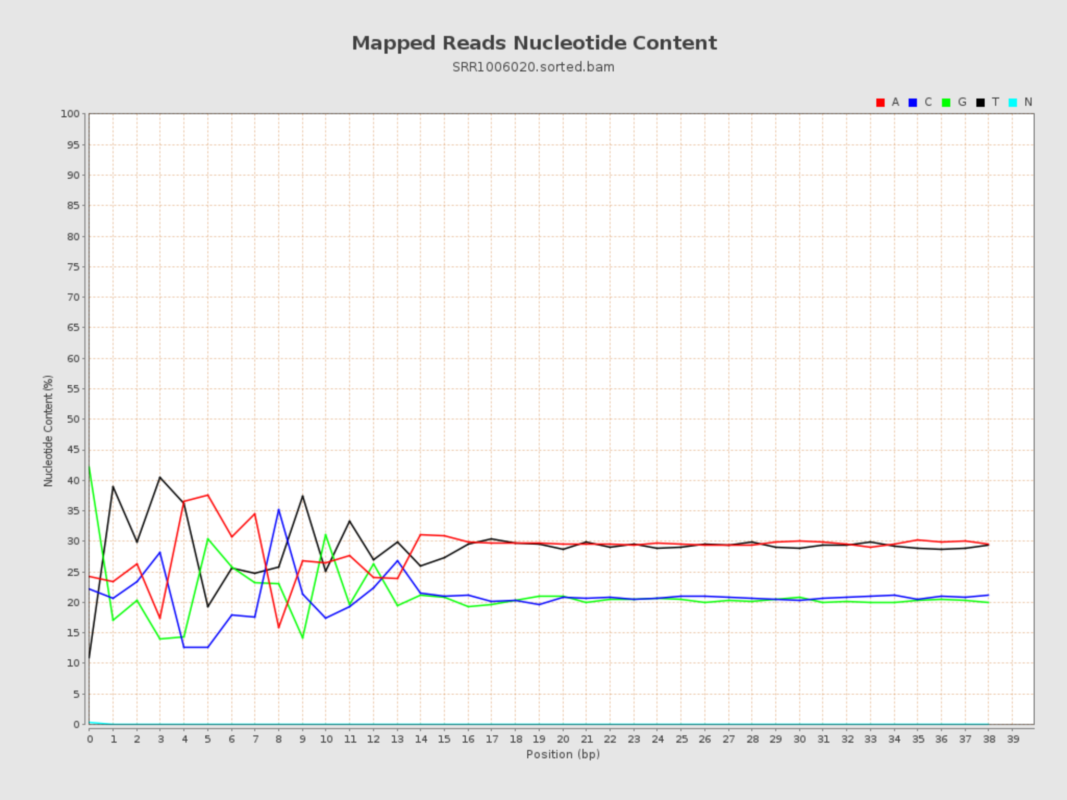
6. Results : Genome Fraction Coverage



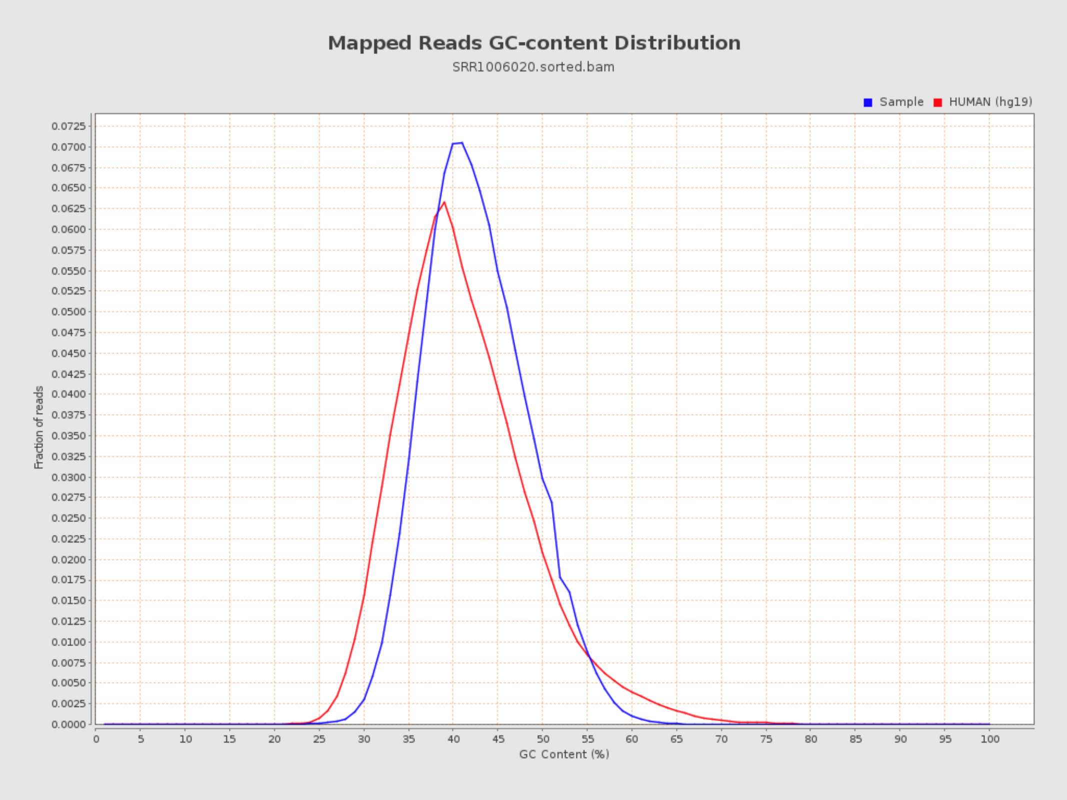
7. Results : Duplication Rate Histogram



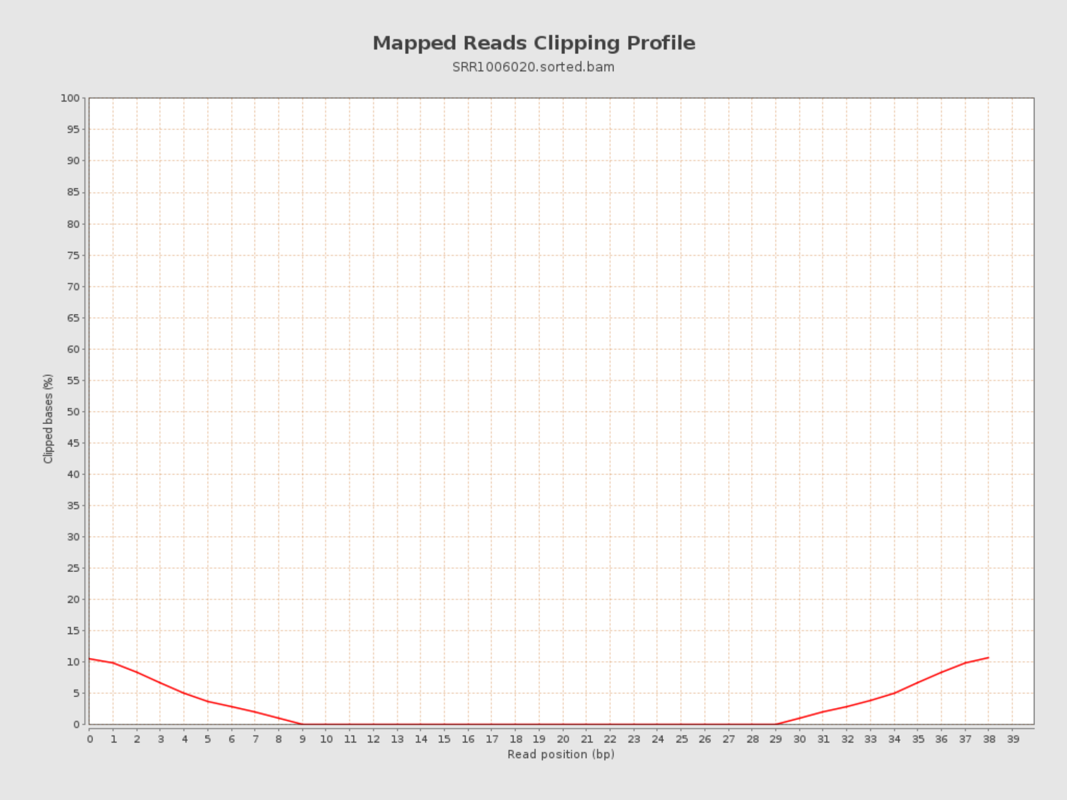
8. Results : Mapped Reads Nucleotide Content



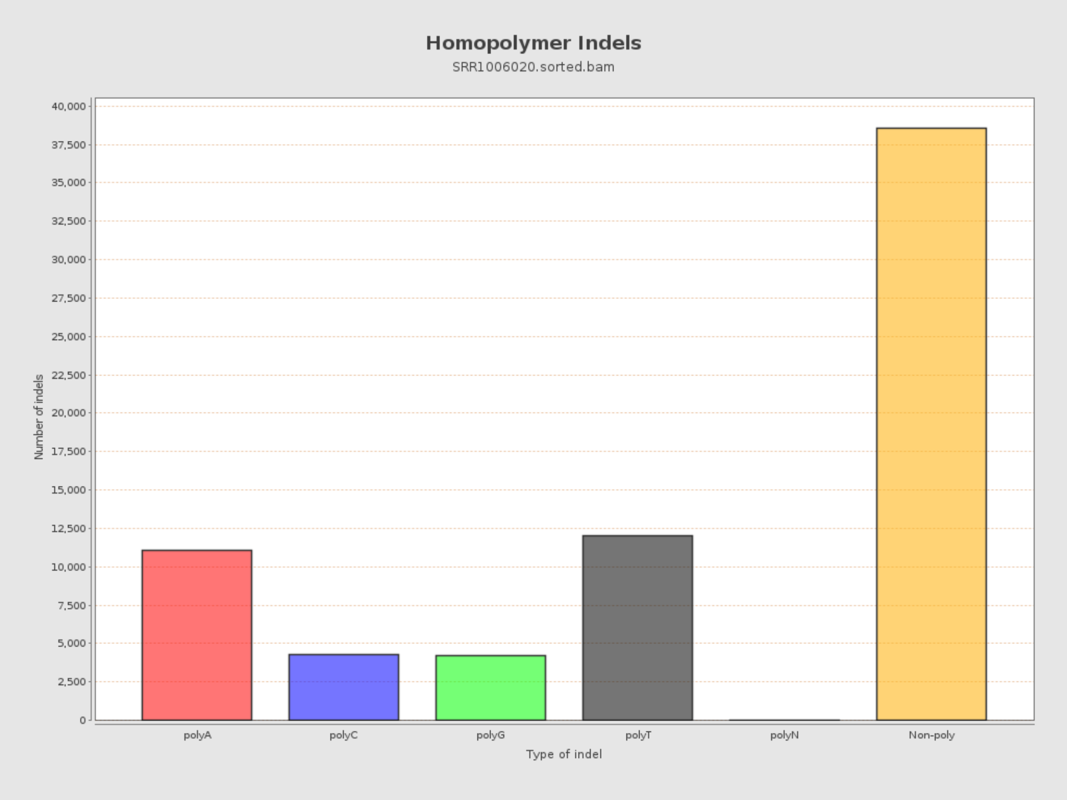
9. Results : Mapped Reads GC-content Distribution



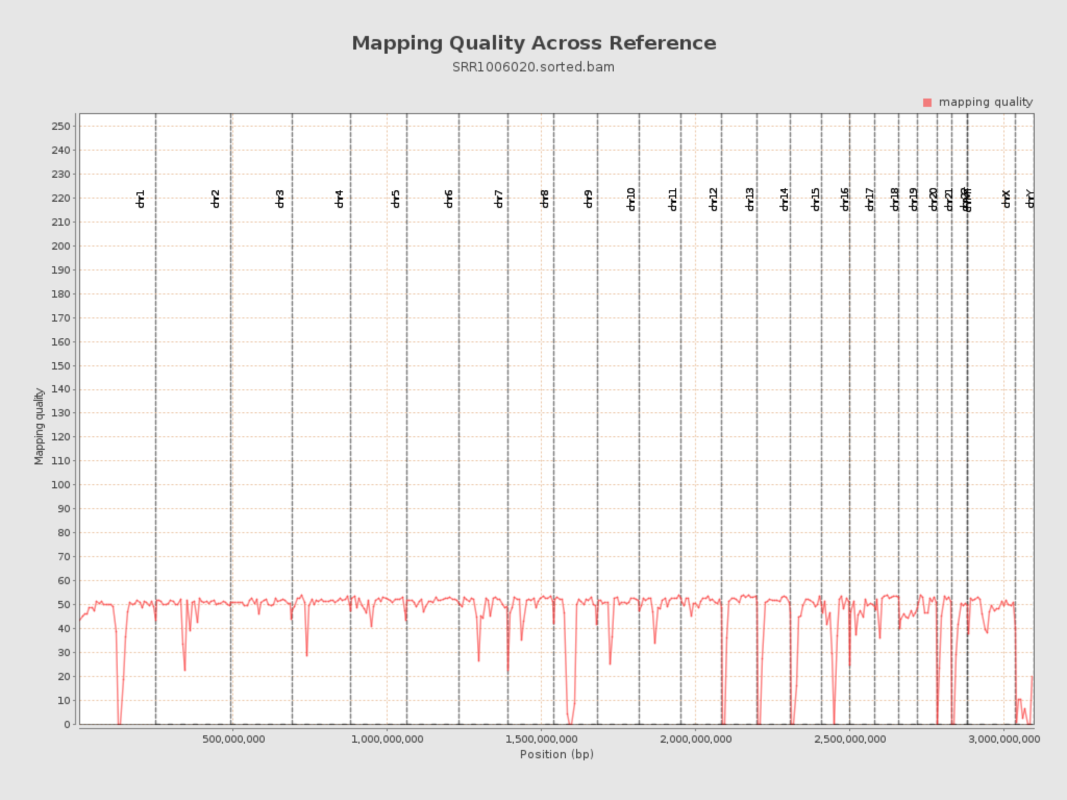
10. Results : Mapped Reads Clipping Profile



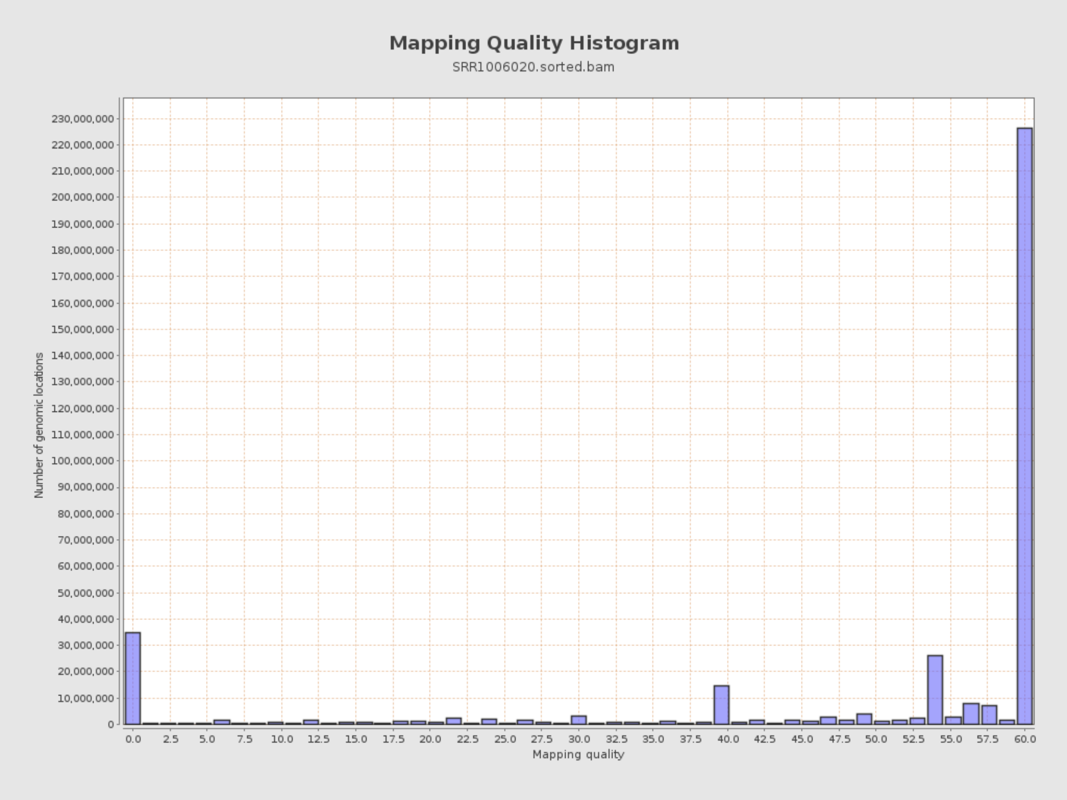
11. Results : Homopolymer Indels



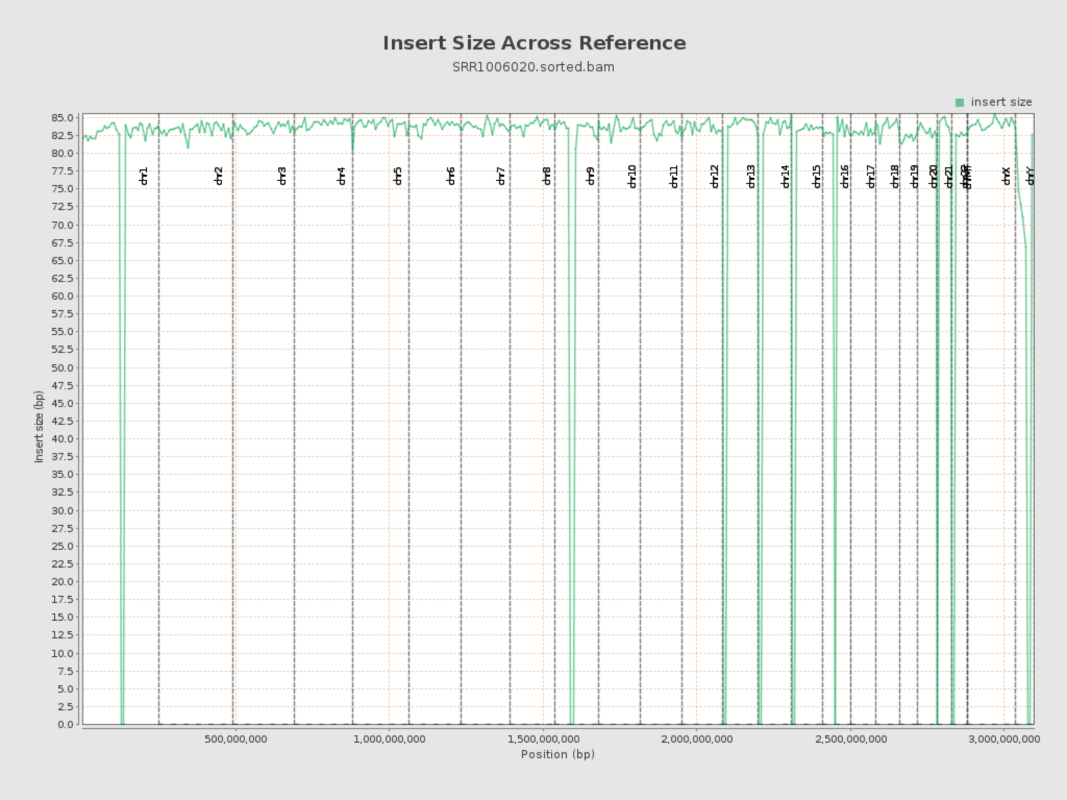
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram