Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:28:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006379.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_SRR1006379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006379_1.fastq.gz SRR1006379_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:28:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,845,598
Mapped reads	4,007,222 / 45.3%
Unmapped reads	4,838,376 / 54.7%
Mapped paired reads	4,007,222 / 45.3%
Mapped reads, first in pair	2,033,063 / 22.98%
Mapped reads, second in pair	1,974,159 / 22.32%
Mapped reads, both in pair	3,586,656 / 40.55%
Mapped reads, singletons	420,566 / 4.75%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	191,485 / 2.16%
Duplication rate	4.18%
Clipped reads	236,070 / 2.67%

2.2. ACGT Content

Number/percentage of A's	43,564,462 / 28.1%
Number/percentage of C's	33,317,145 / 21.49%
Number/percentage of T's	44,040,066 / 28.41%
Number/percentage of G's	34,105,008 / 22%
Number/percentage of N's	6,427 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0501
Standard Deviation	0.4155

2.4. Mapping Quality

Mean Mapping Quality	47.93

2.5. Insert size

Mean	89,079.05
Standard Deviation	2,900,663.11
P25/Median/P75	123 / 161 / 222

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	580,399
Insertions	4,431
Mapped reads with at least one insertion	0.11%
Deletions	14,841
Mapped reads with at least one deletion	0.37%
Homopolymer indels	42.37%

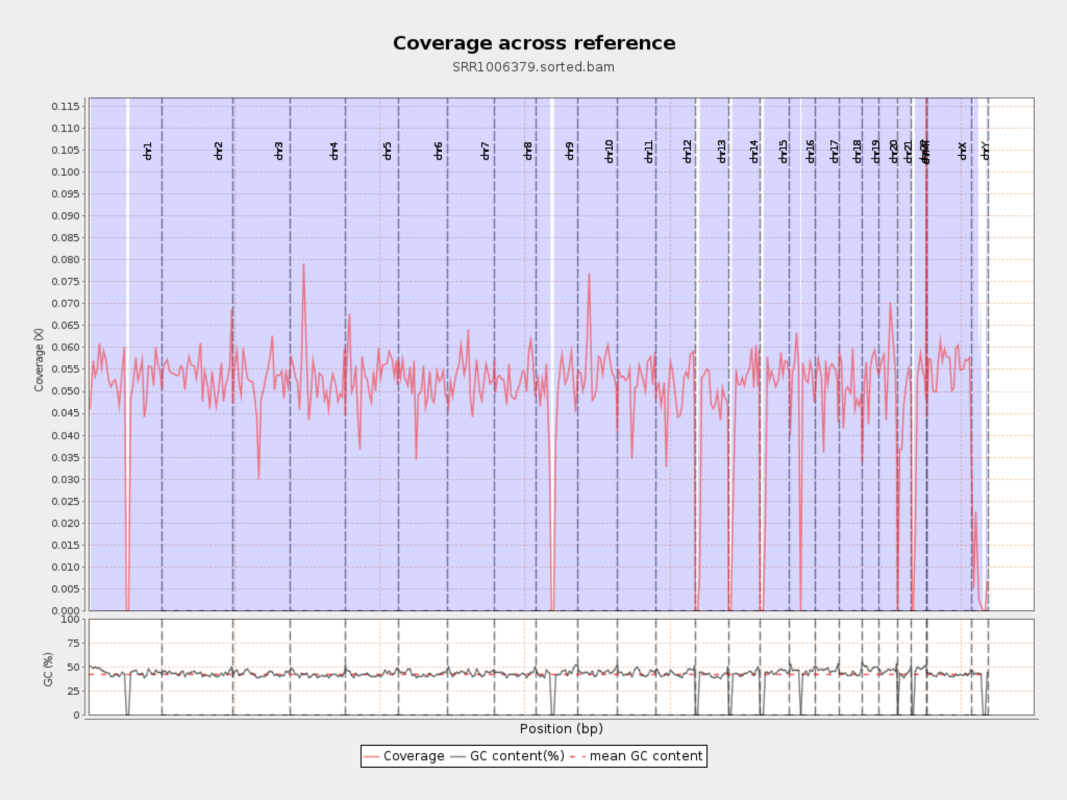
2.7. Chromosome stats

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

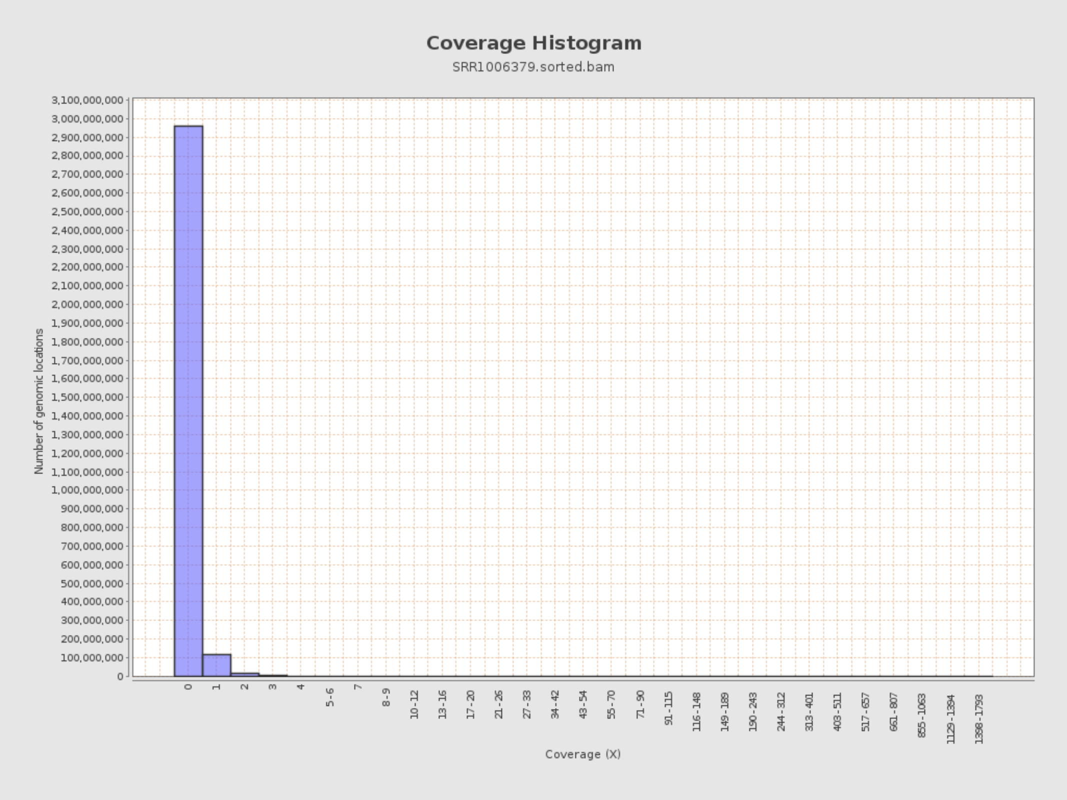
chr1	249250621	12562279	0.0504	0.4132
chr2	243199373	13110129	0.0539	0.6361
chr3	198022430	10347562	0.0523	0.2536
chr4	191154276	10105133	0.0529	0.2826
chr5	180915260	9707279	0.0537	0.8419
chr6	171115067	8787373	0.0514	0.3782
chr7	159138663	8448858	0.0531	0.3309
chr8	146364022	7697628	0.0526	0.7105
chr9	141213431	6386965	0.0452	0.2579
chr10	135534747	7550271	0.0557	0.3473
chr11	135006516	7084075	0.0525	0.3005
chr12	133851895	6762449	0.0505	0.2503
chr13	115169878	4777351	0.0415	0.2265
chr14	107349540	4834815	0.045	0.2616
chr15	102531392	4552168	0.0444	0.235
chr16	90354753	4470697	0.0495	0.2808
chr17	81195210	4253087	0.0524	0.2835
chr18	78077248	3933867	0.0504	0.3775
chr19	59128983	3143114	0.0532	0.3299
chr20	63025520	3538347	0.0561	0.2736
chr21	48129895	2017657	0.0419	0.2967
chr22	51304566	1938793	0.0378	0.2227
chrMT	16571	2473	0.1492	0.6956
chrX	155270560	8639891	0.0556	0.2741

chrY	59373566	400596	0.0067	0.1718

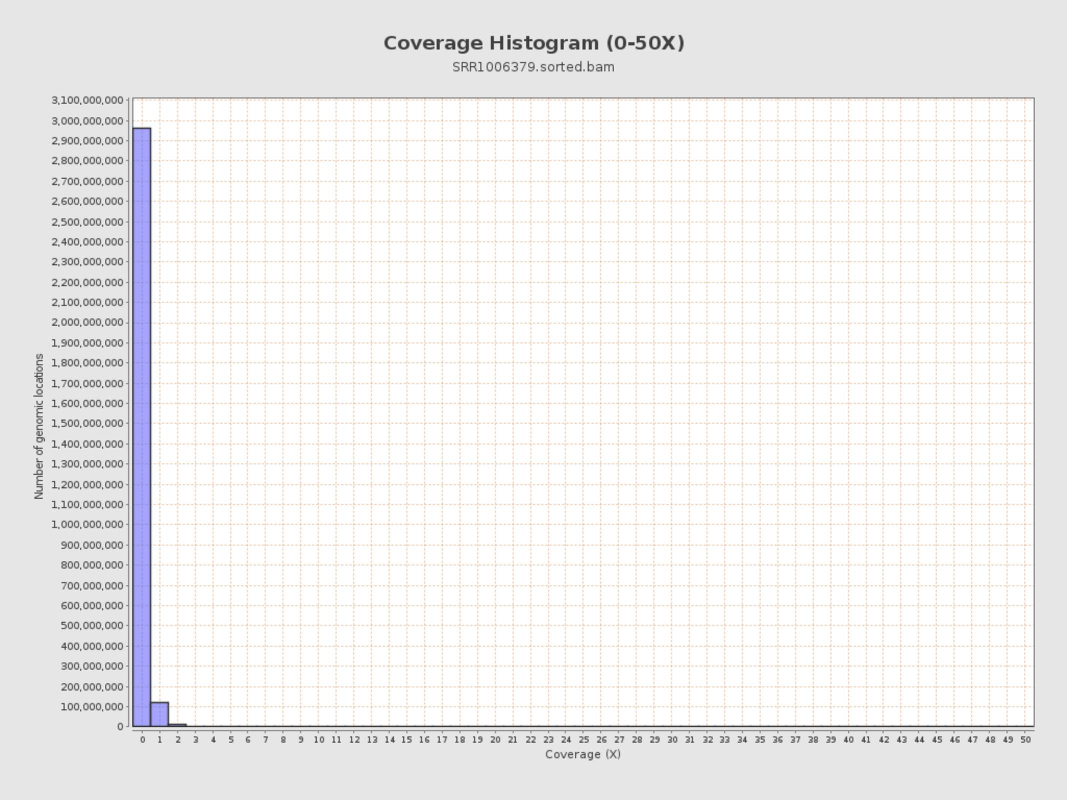
3. Results : Coverage across reference



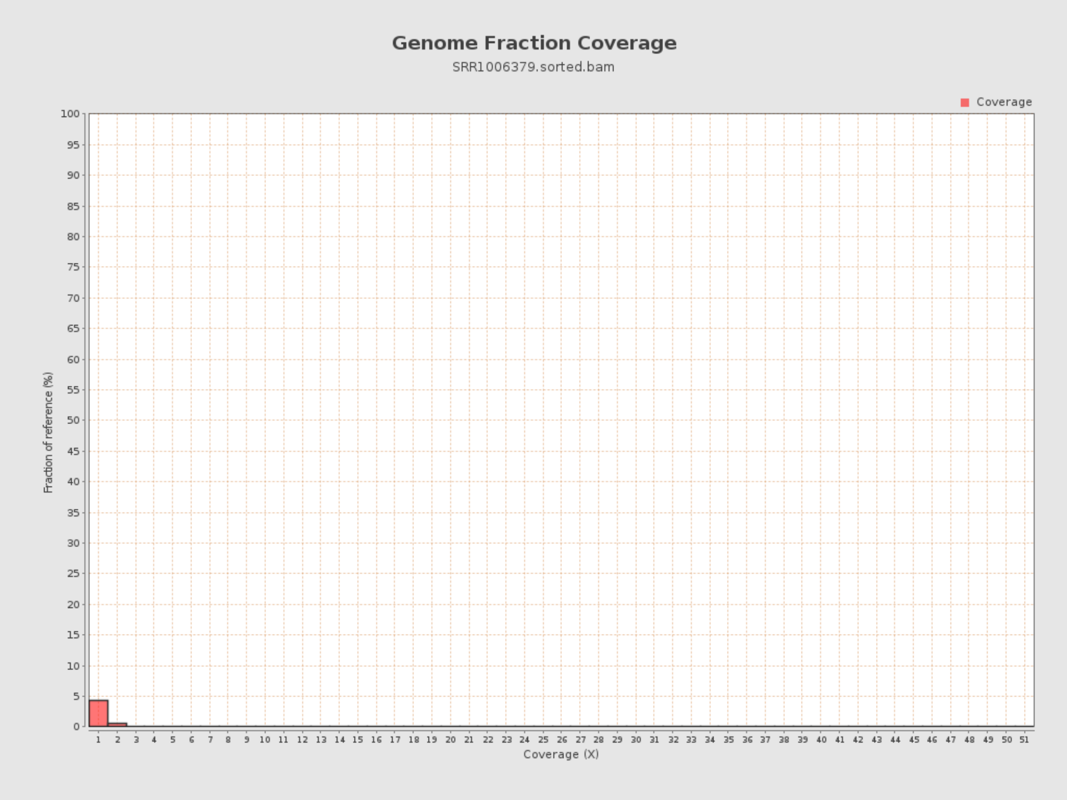
4. Results : Coverage Histogram



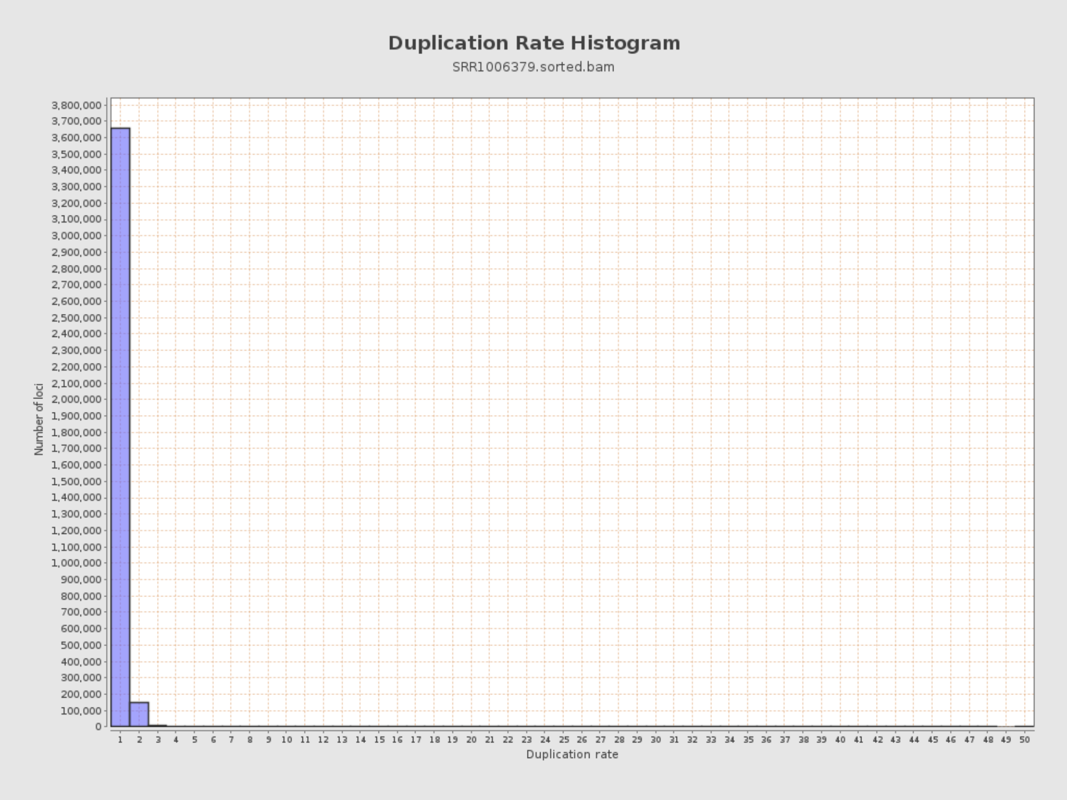
5. Results : Coverage Histogram (0-50X)



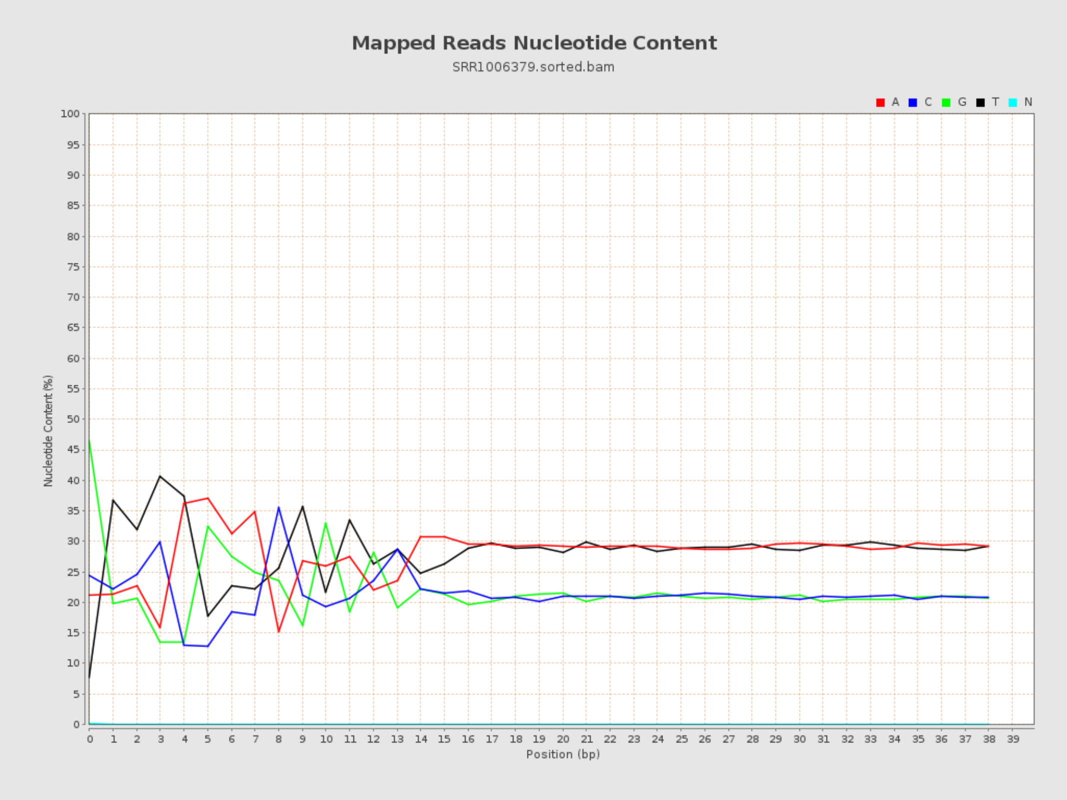
6. Results : Genome Fraction Coverage



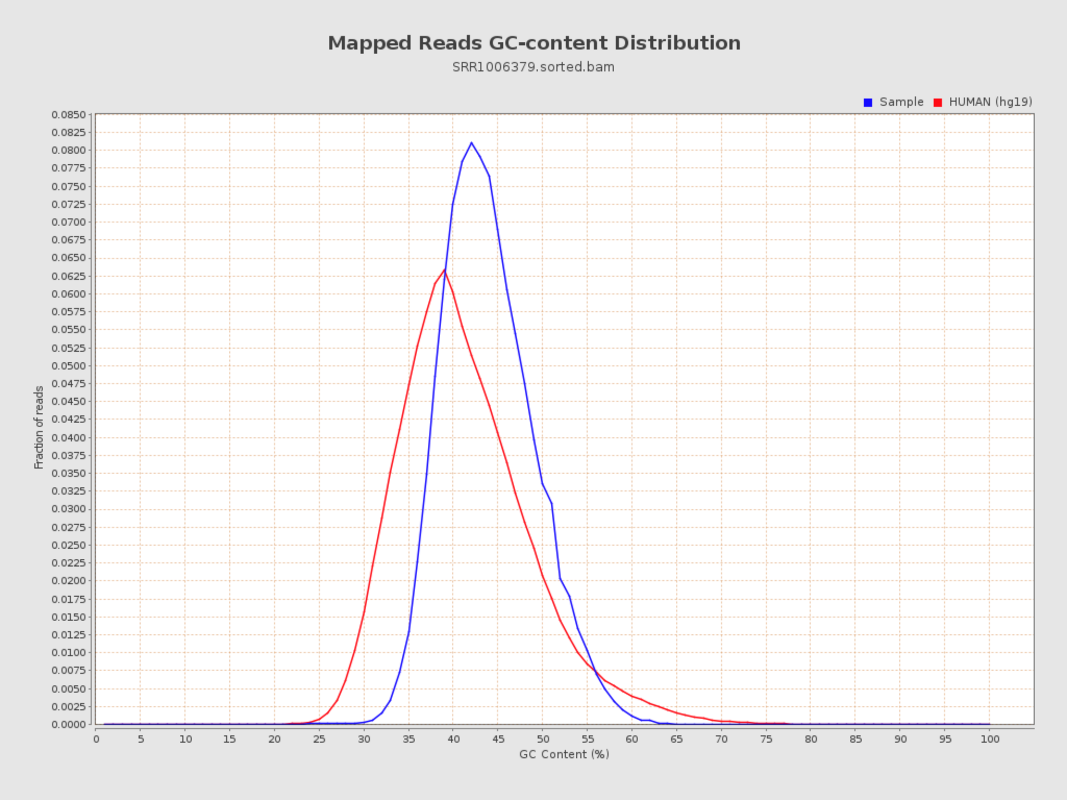
7. Results : Duplication Rate Histogram



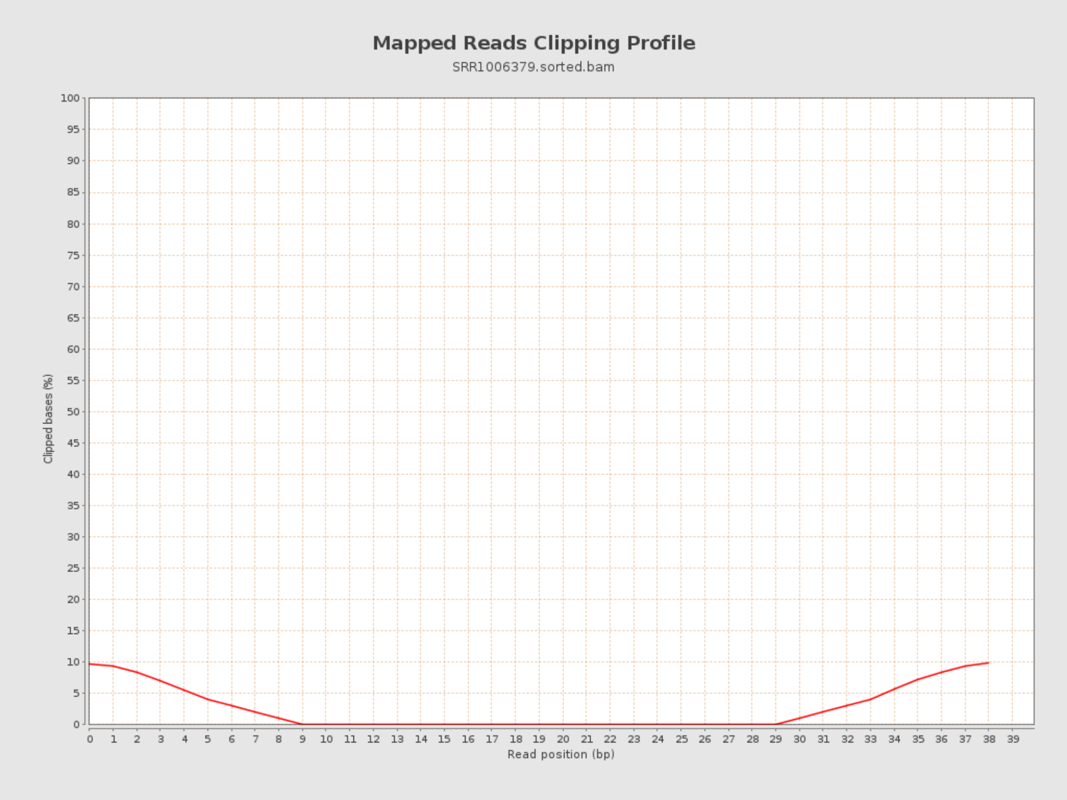
8. Results : Mapped Reads Nucleotide Content



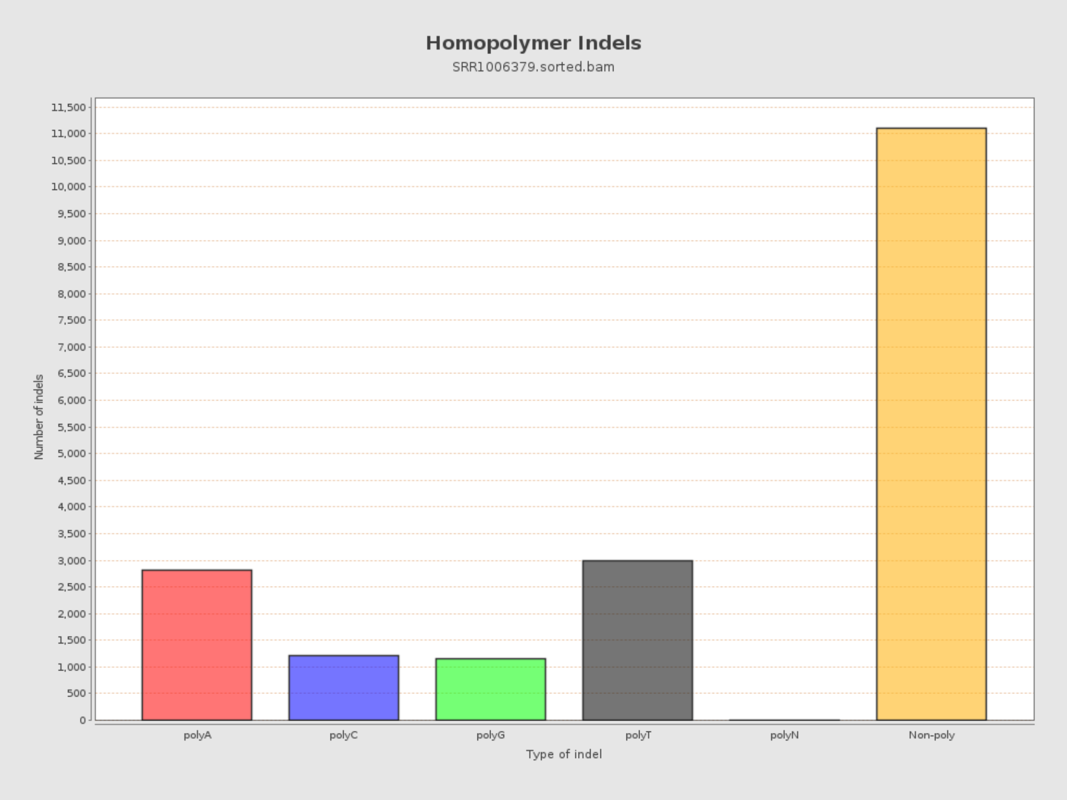
9. Results : Mapped Reads GC-content Distribution



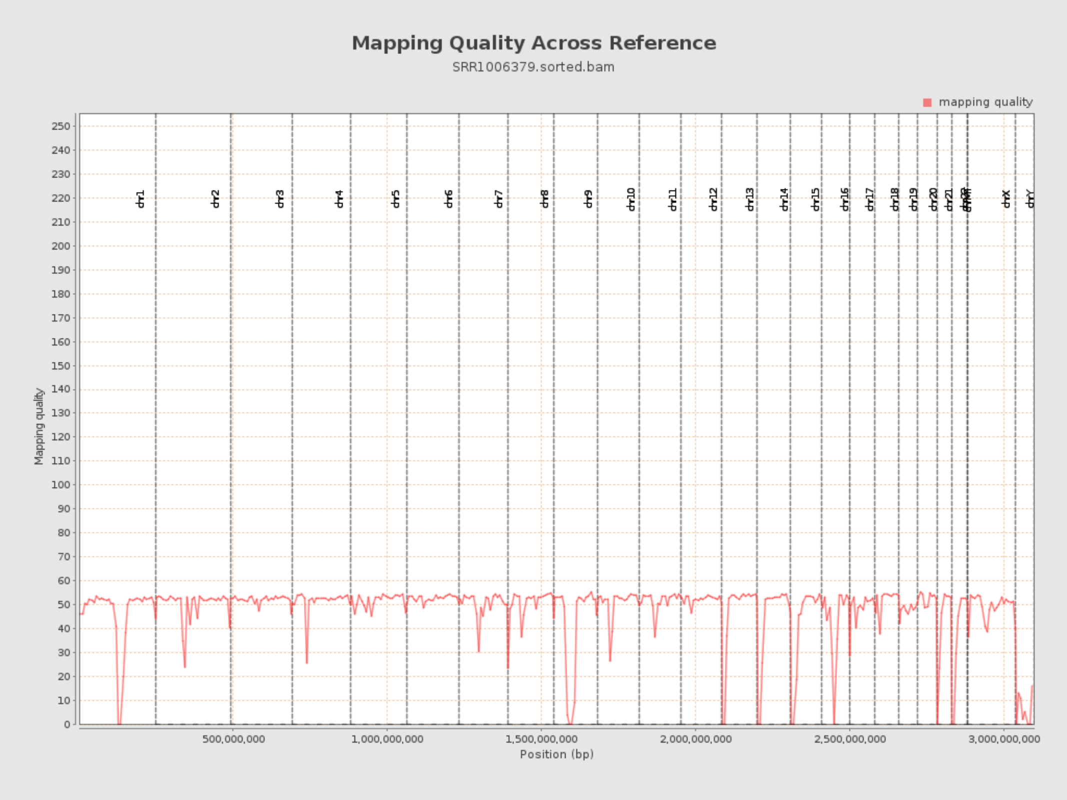
10. Results : Mapped Reads Clipping Profile



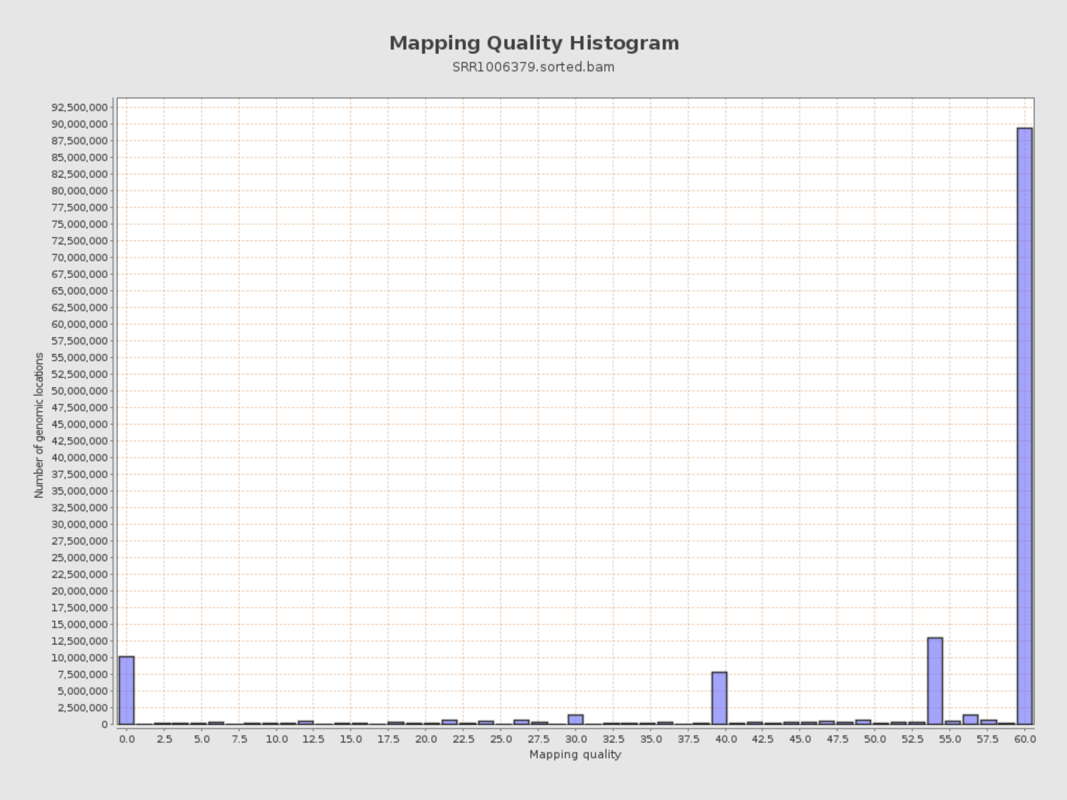
11. Results : Homopolymer Indels



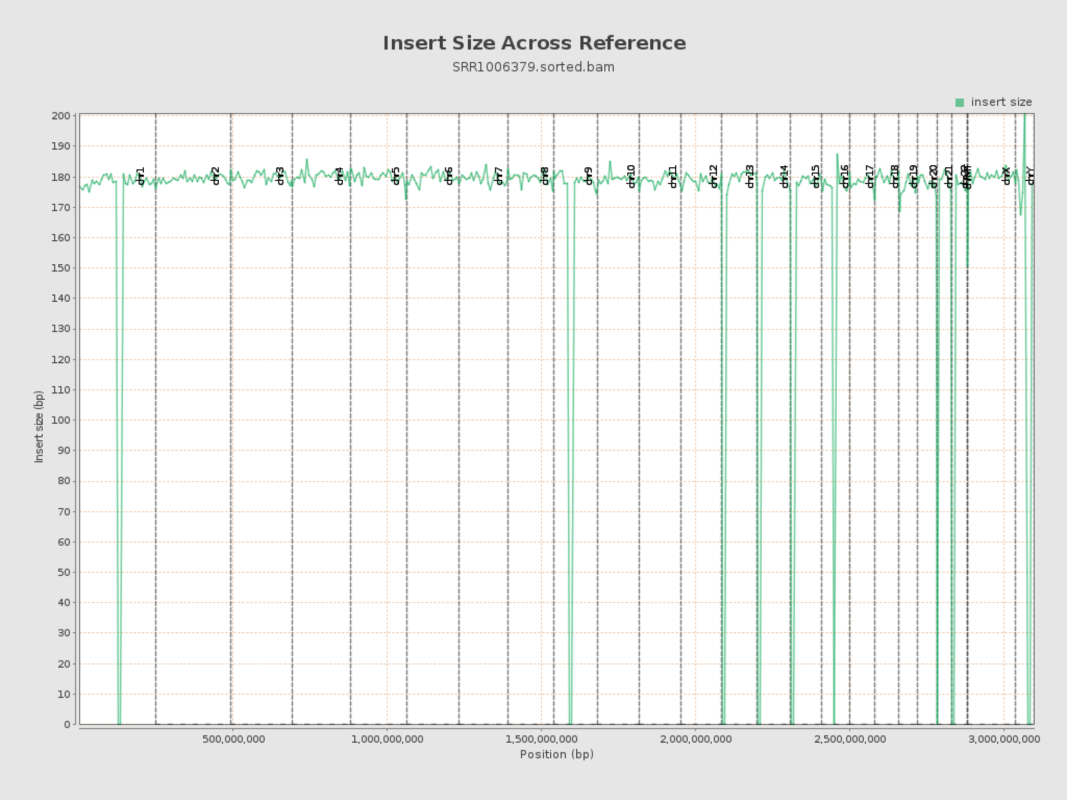
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram