Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 21:50:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617379.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_SRR617379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617379_1.fastq.gz SRR617379_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 21:50:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	28,984,323 / 90.58%
Unmapped reads	3,015,677 / 9.42%
Mapped paired reads	28,984,323 / 90.58%
Mapped reads, first in pair	14,678,052 / 45.87%
Mapped reads, second in pair	14,306,271 / 44.71%
Mapped reads, both in pair	28,199,702 / 88.12%
Mapped reads, singletons	784,621 / 2.45%
Secondary alignments	0
Supplementary alignments	62,760 / 0.2%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,453,049 / 4.54%
Duplication rate	1.47%
Clipped reads	2,930,504 / 9.16%

2.2. ACGT Content

Number/percentage of A's	860,224,369 / 30.38%
Number/percentage of C's	559,972,241 / 19.78%
Number/percentage of T's	846,749,249 / 29.91%
Number/percentage of G's	563,224,331 / 19.89%
Number/percentage of N's	1,279,073 / 0.05%

GC Percentage	39.67%

2.3. Coverage

Mean	0.9149
Standard Deviation	9.1073

2.4. Mapping Quality

Mean Mapping Quality	53.31

2.5. Insert size

Mean	51,123.66
Standard Deviation	2,162,706.21
P25/Median/P75	170 / 209 / 270

2.6. Mismatches and indels

General error rate	1.57%
Mismatches	43,783,197
Insertions	286,317
Mapped reads with at least one insertion	0.96%
Deletions	341,231
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.74%

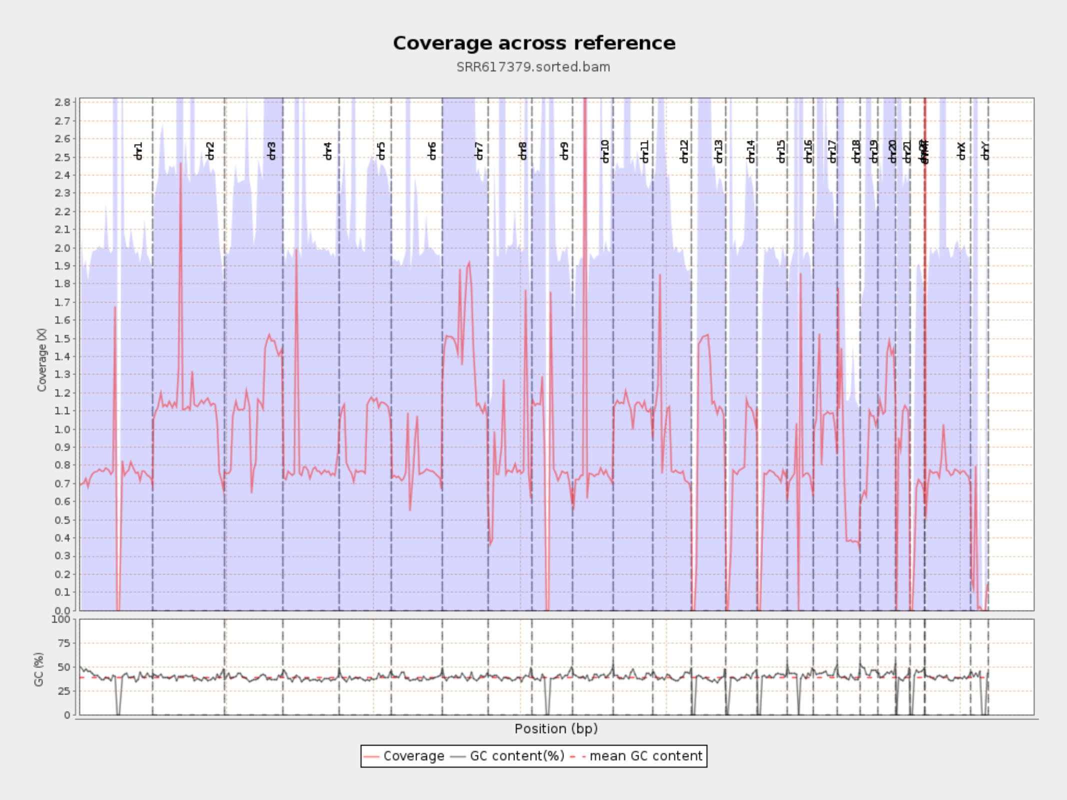
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

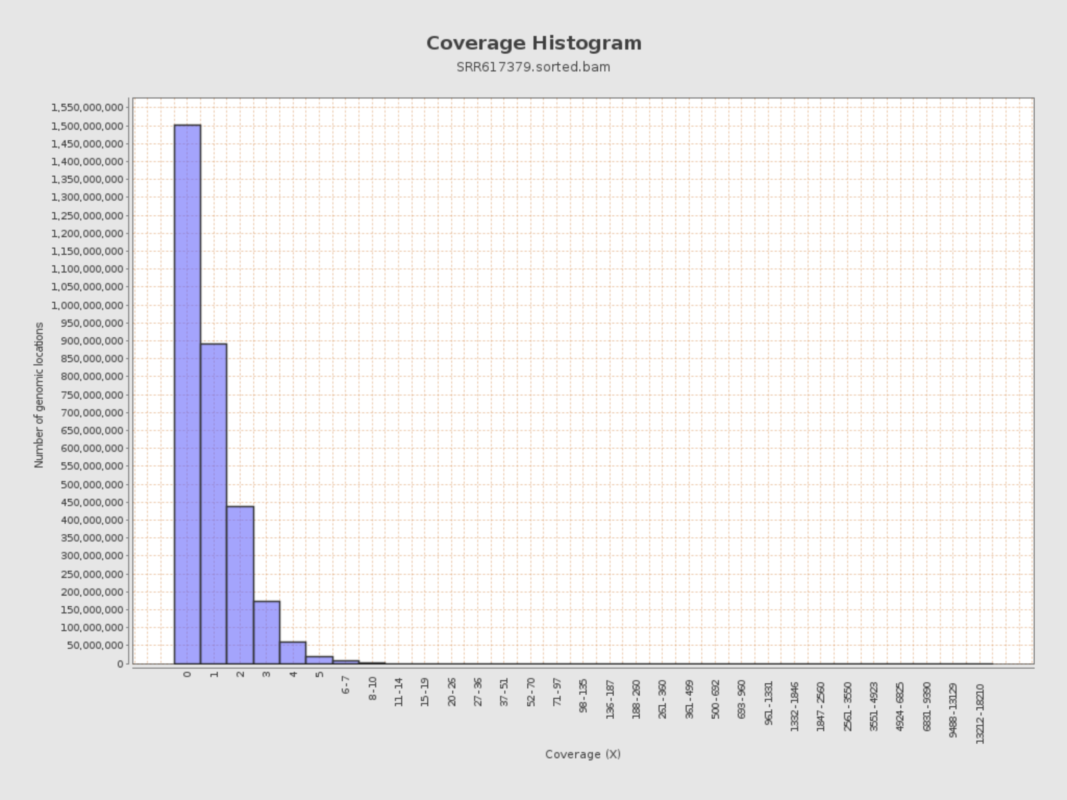
		bases	coverage	deviation
chr1	249250621	183544327	0.7364	18.6411
chr2	243199373	279642996	1.1499	8.0725
chr3	198022430	226344696	1.143	1.444
chr4	191154276	155880836	0.8155	8.1769
chr5	180915260	178807310	0.9883	1.4078
chr6	171115067	133300660	0.779	3.4916
chr7	159138663	230246475	1.4468	10.4396
chr8	146364022	119566602	0.8169	7.0764
chr9	141213431	118837066	0.8415	13.5061
chr10	135534747	119213316	0.8796	19.0798
chr11	135006516	151619596	1.1231	5.0733
chr12	133851895	125019971	0.934	1.292
chr13	115169878	124306682	1.0793	1.2646
chr14	107349540	82134491	0.7651	1.3378
chr15	102531392	63504361	0.6194	0.9517
chr16	90354753	70878672	0.7844	7.7157
chr17	81195210	87050708	1.0721	6.5791
chr18	78077248	51031444	0.6536	14.0048
chr19	59128983	51760617	0.8754	9.0847
chr20	63025520	80327588	1.2745	2.2602
chr21	48129895	44910337	0.9331	3.0148
chr22	51304566	24644116	0.4803	0.878
chrMT	16571	1913720	115.4861	23.3797
chrX	155270560	118409838	0.7626	2.7798

chrY	59373566	9366613	0.1578	7.3905

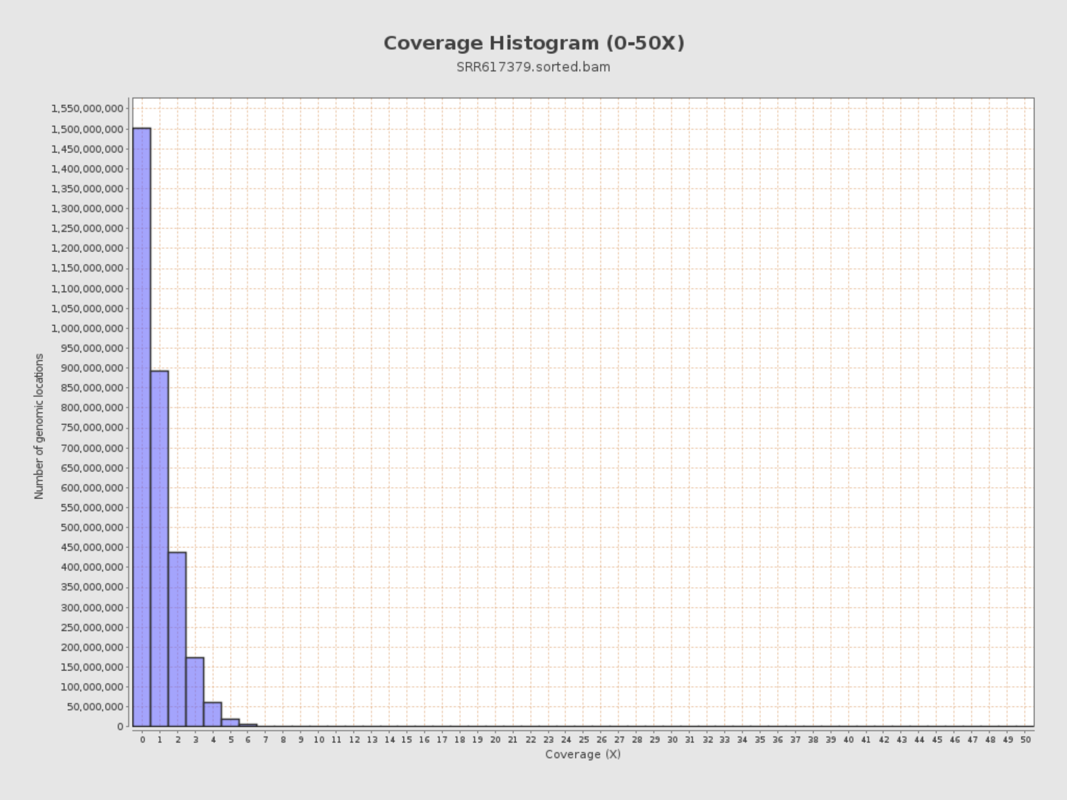
3. Results : Coverage across reference



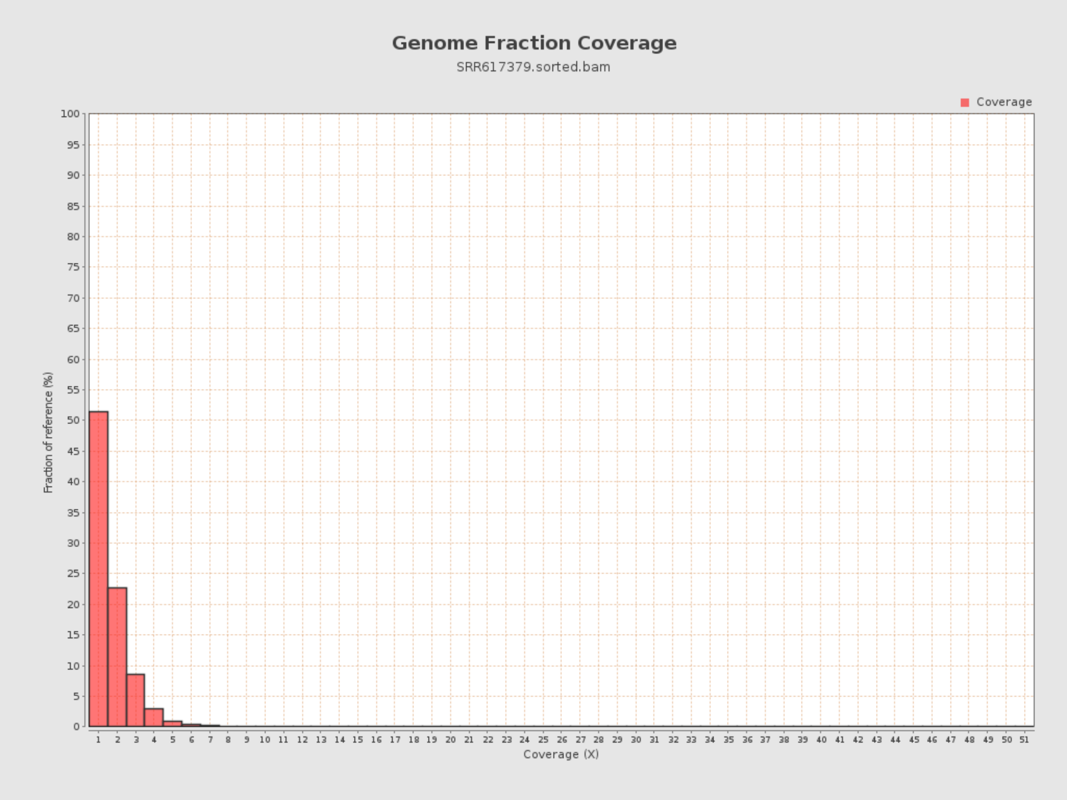
4. Results : Coverage Histogram



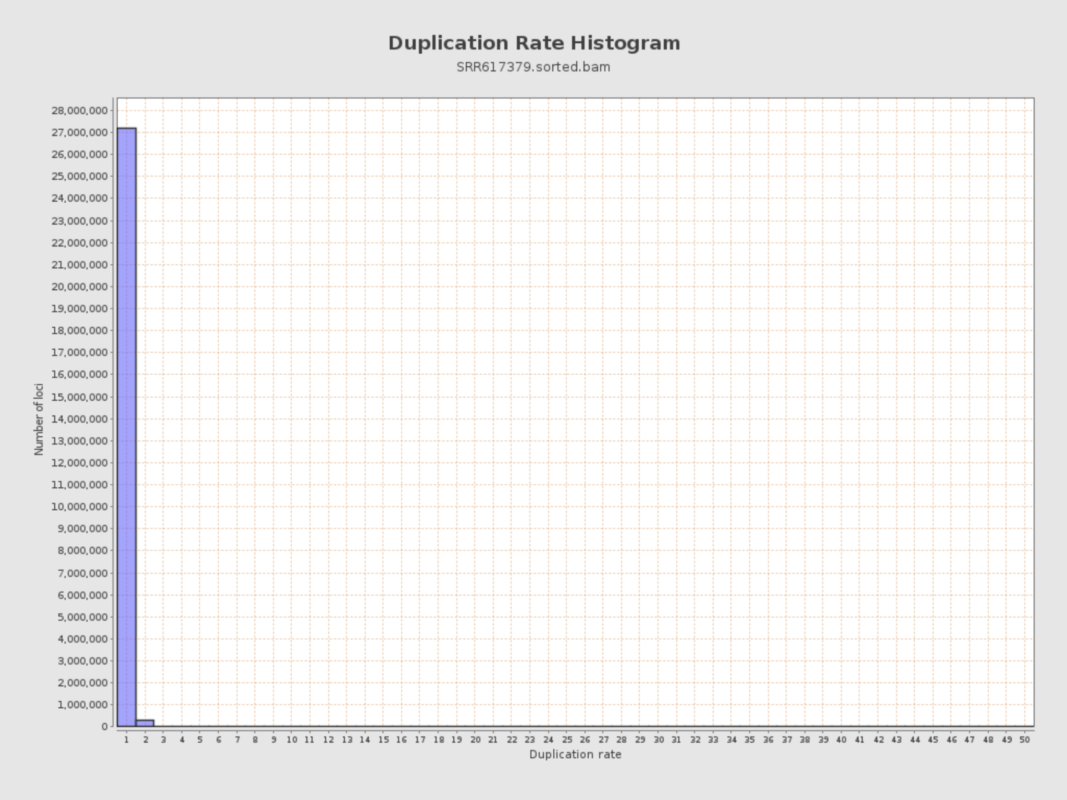
5. Results : Coverage Histogram (0-50X)



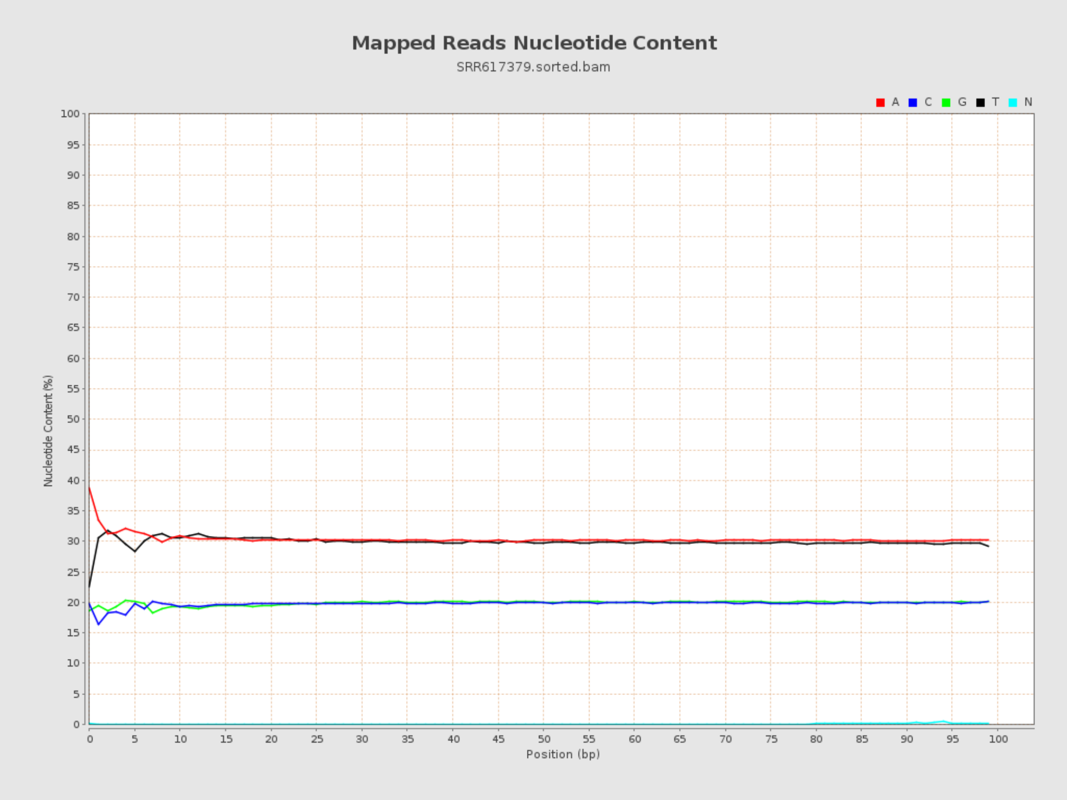
6. Results : Genome Fraction Coverage



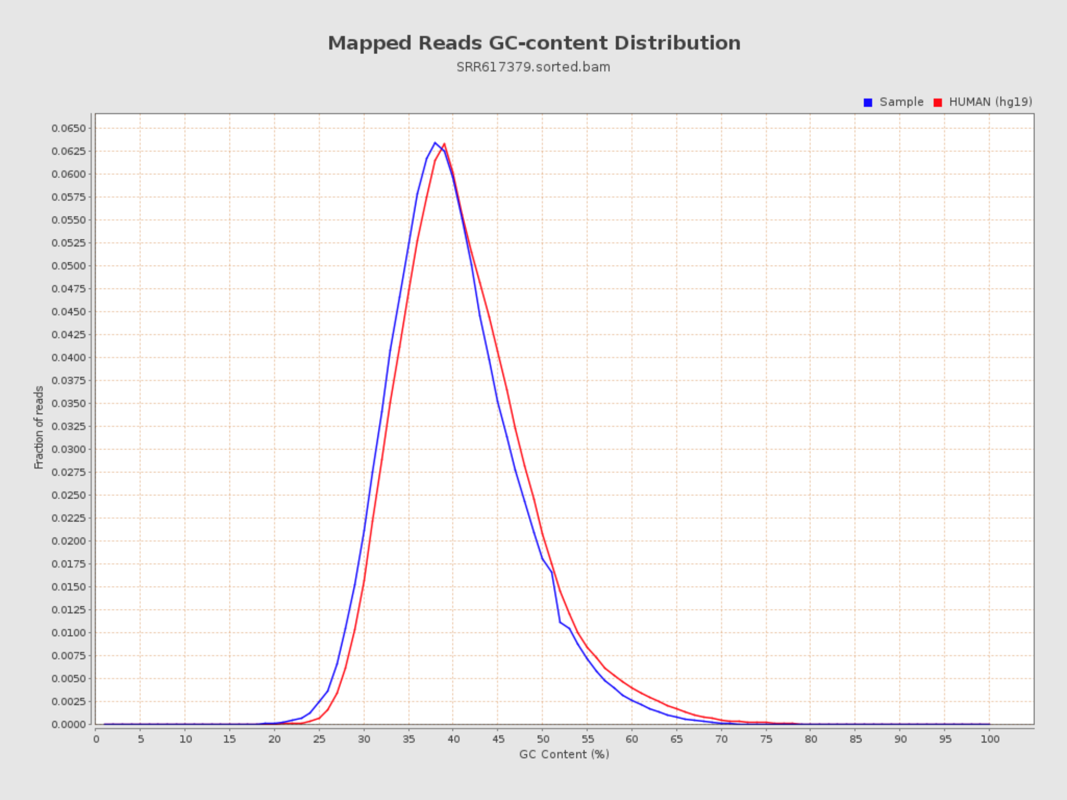
7. Results : Duplication Rate Histogram



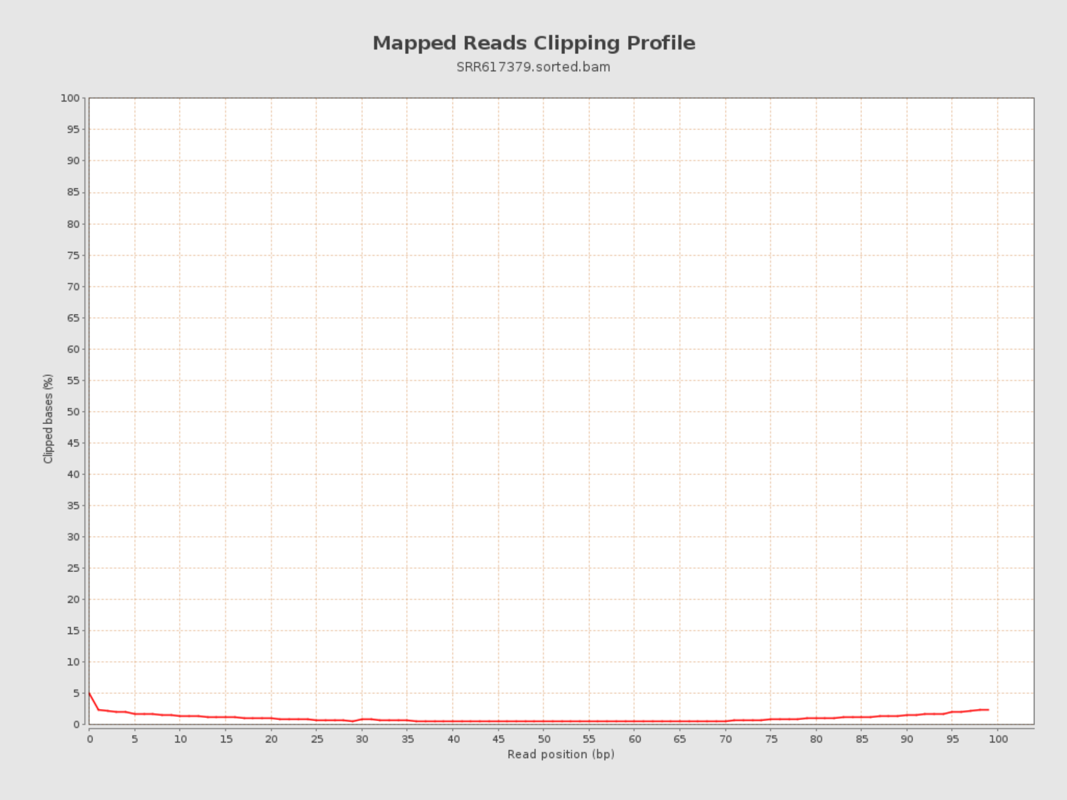
8. Results : Mapped Reads Nucleotide Content



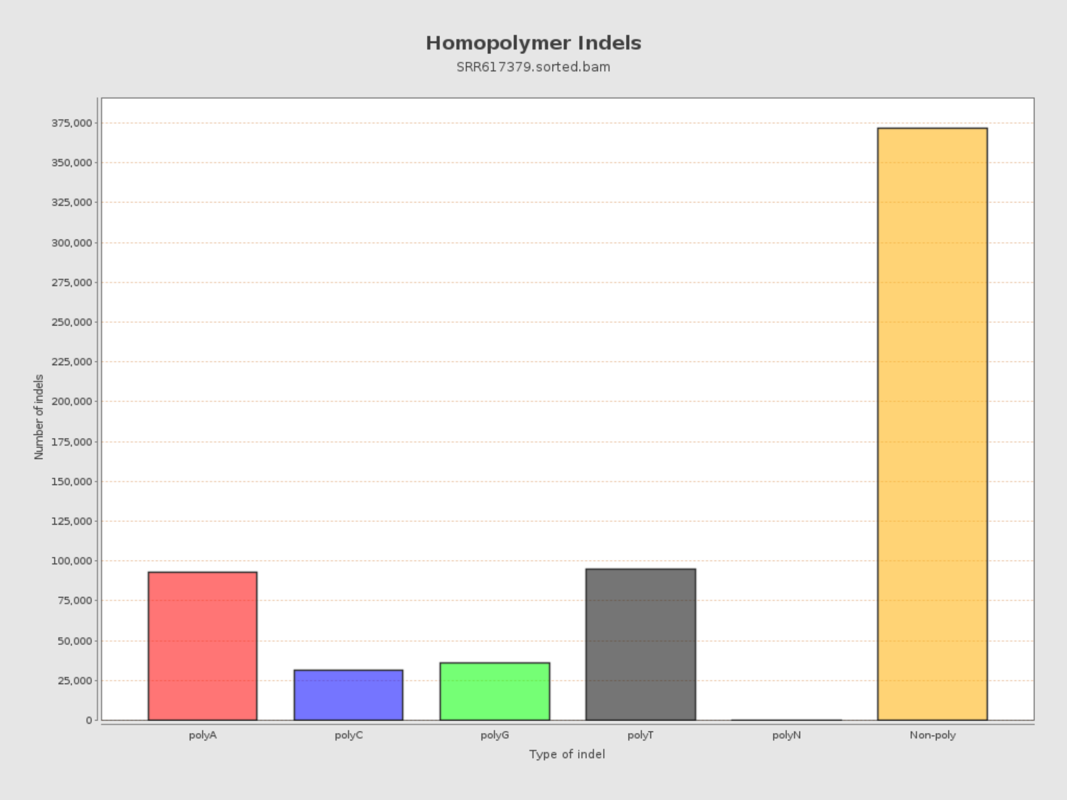
9. Results : Mapped Reads GC-content Distribution



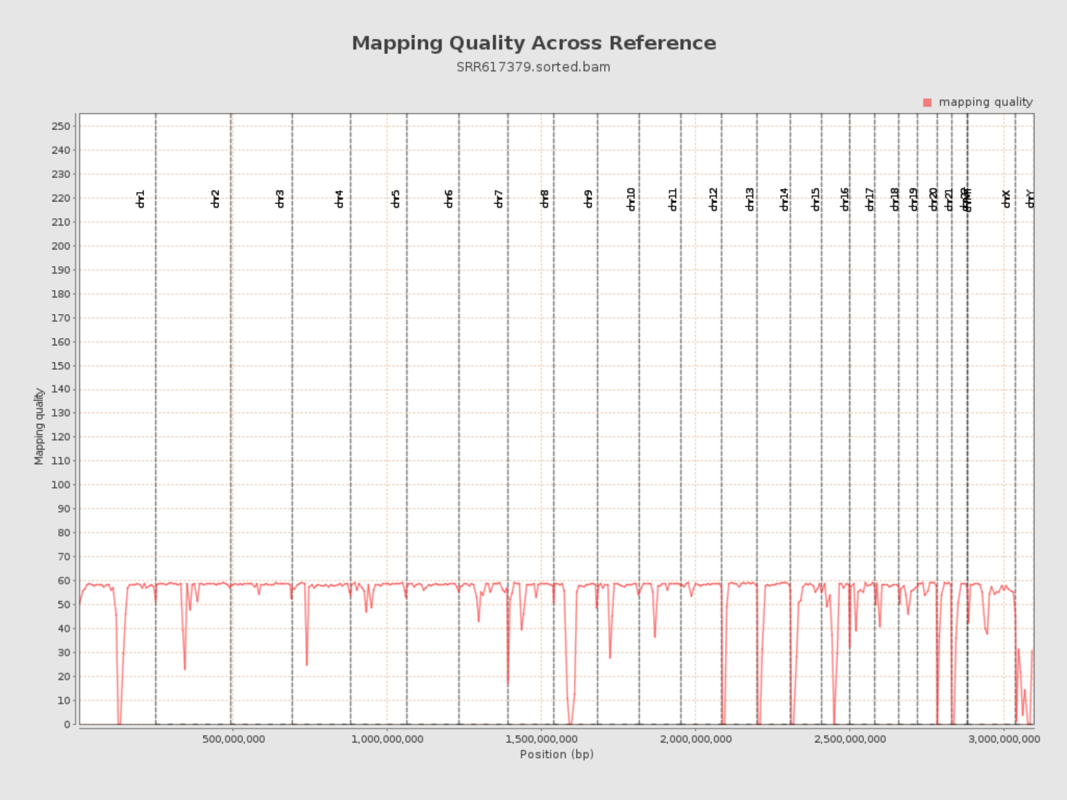
10. Results : Mapped Reads Clipping Profile



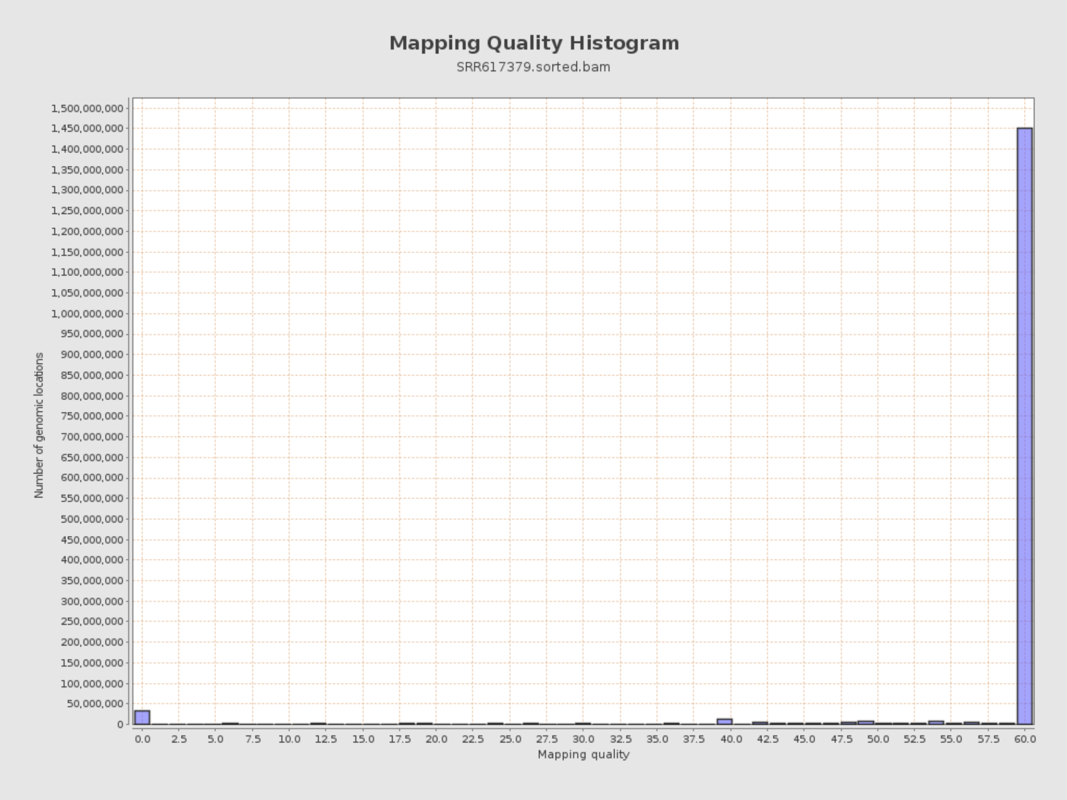
11. Results : Homopolymer Indels



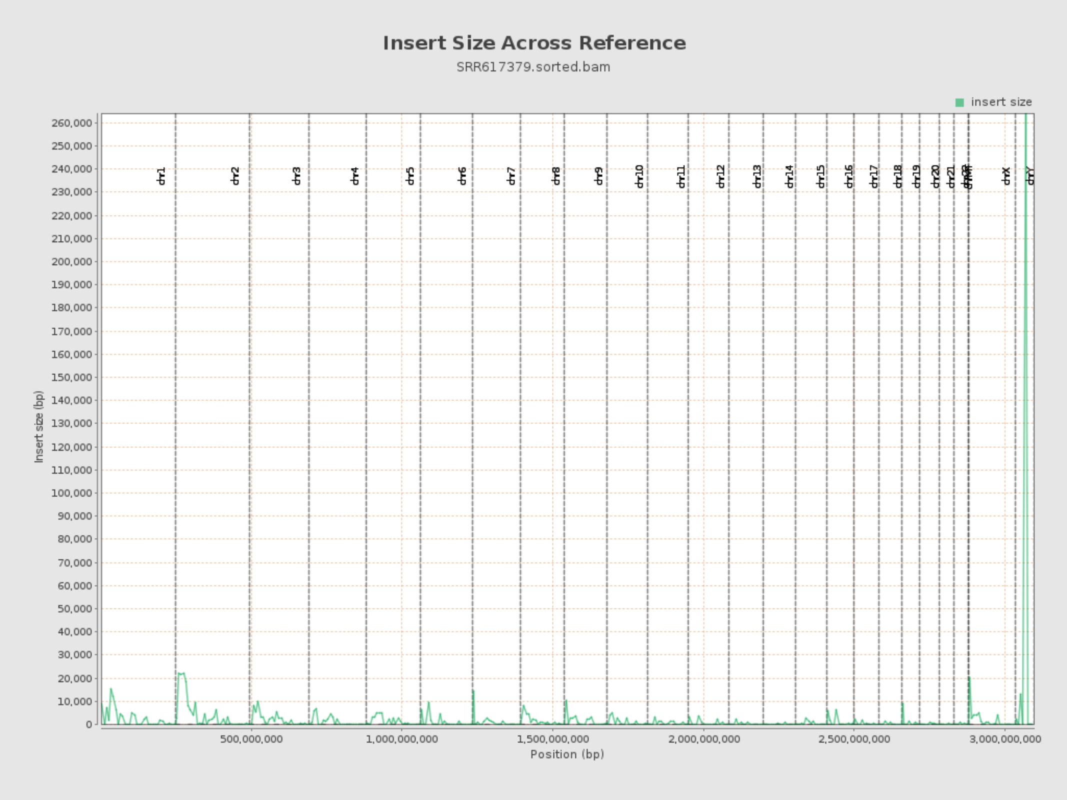
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram