Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/06 19:42:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778457.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_SRR1778457 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778457_1.fastq.gz SRR1778457_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 06 19:42:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778457.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	436,478,520
Mapped reads	423,668,252 / 97.07%
Unmapped reads	12,810,268 / 2.93%
Mapped paired reads	423,668,252 / 97.07%
Mapped reads, first in pair	213,075,550 / 48.82%
Mapped reads, second in pair	210,592,702 / 48.25%
Mapped reads, both in pair	418,184,404 / 95.81%
Mapped reads, singletons	5,483,848 / 1.26%
Secondary alignments	0
Supplementary alignments	1,587,887 / 0.36%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	60,929,043 / 13.96%
Duplication rate	9.64%
Clipped reads	27,863,162 / 6.38%

2.2. ACGT Content

Number/percentage of A's	9,492,629,845 / 28.38%
Number/percentage of C's	7,224,056,699 / 21.59%
Number/percentage of T's	9,450,348,073 / 28.25%
Number/percentage of G's	7,276,972,227 / 21.75%
Number/percentage of N's	9,385,672 / 0.03%

GC Percentage	43.35%

2.3. Coverage

Mean	10.8094
Standard Deviation	117.1384

2.4. Mapping Quality

Mean Mapping Quality	52.58

2.5. Insert size

Mean	123,485.62
Standard Deviation	3,382,158.79
P25/Median/P75	132 / 165 / 205

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	172,829,395
Insertions	3,389,190
Mapped reads with at least one insertion	0.78%
Deletions	4,138,757
Mapped reads with at least one deletion	0.96%
Homopolymer indels	42.26%

2.7. Chromosome stats

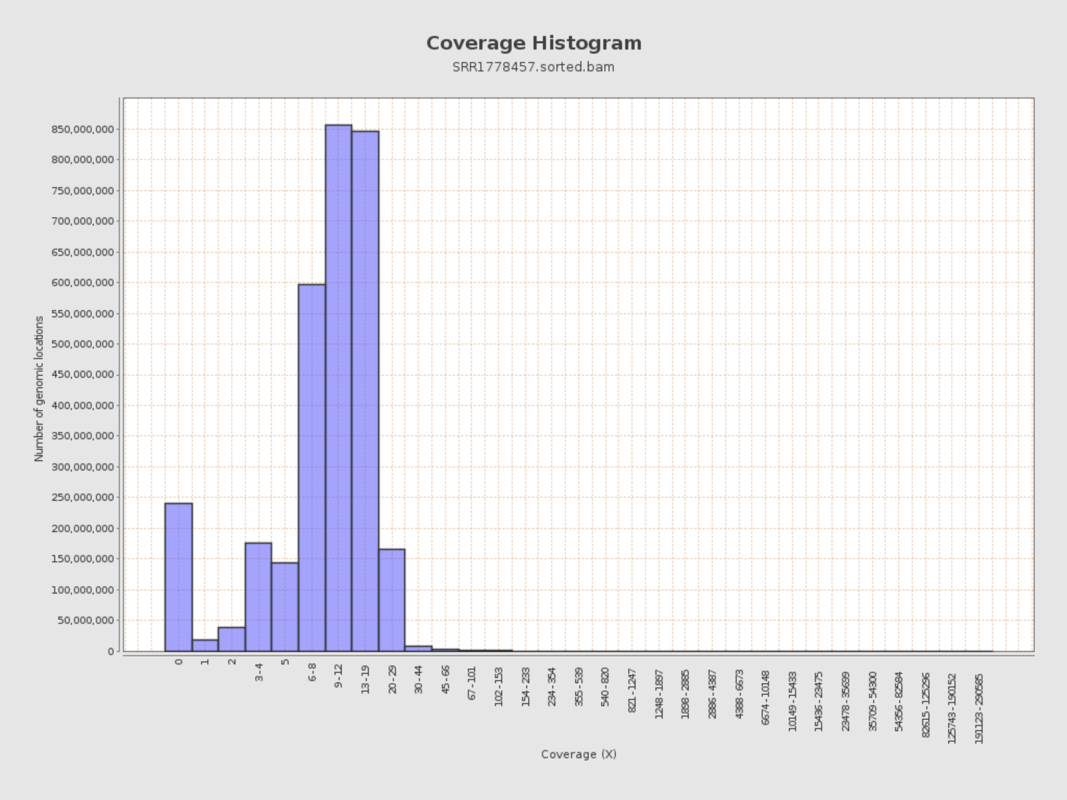
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	**coverage**	**deviation**
chr1	249250621	2831843139	11.3614	288.1651
chr2	243199373	2863394326	11.7739	79.135
chr3	198022430	2151702037	10.866	20.734
chr4	191154276	2106610956	11.0205	70.7098
chr5	180915260	1958305320	10.8244	13.0508
chr6	171115067	1877262667	10.9708	49.4999
chr7	159138663	1844946630	11.5933	107.24
chr8	146364022	1665309098	11.3779	107.2616
chr9	141213431	1440343228	10.1998	94.8962
chr10	135534747	1820031167	13.4285	257.7758
chr11	135006516	1558401060	11.5432	57.4258
chr12	133851895	1492218475	11.1483	13.092
chr13	115169878	1008486515	8.7565	8.5724
chr14	107349540	1014949168	9.4546	14.3855
chr15	102531392	977941629	9.538	7.6769
chr16	90354753	1117788772	12.3711	56.4407
chr17	81195210	1044653245	12.8659	50.4852
chr18	78077248	899114856	11.5157	137.74
chr19	59128983	823956622	13.9349	159.2945
chr20	63025520	757210005	12.0143	22.998
chr21	48129895	474801514	9.865	55.4899
chr22	51304566	487249846	9.4972	36.8241
chrMT	16571	10942517	660.3414	114.1566
chrX	155270560	883733797	5.6916	25.7929

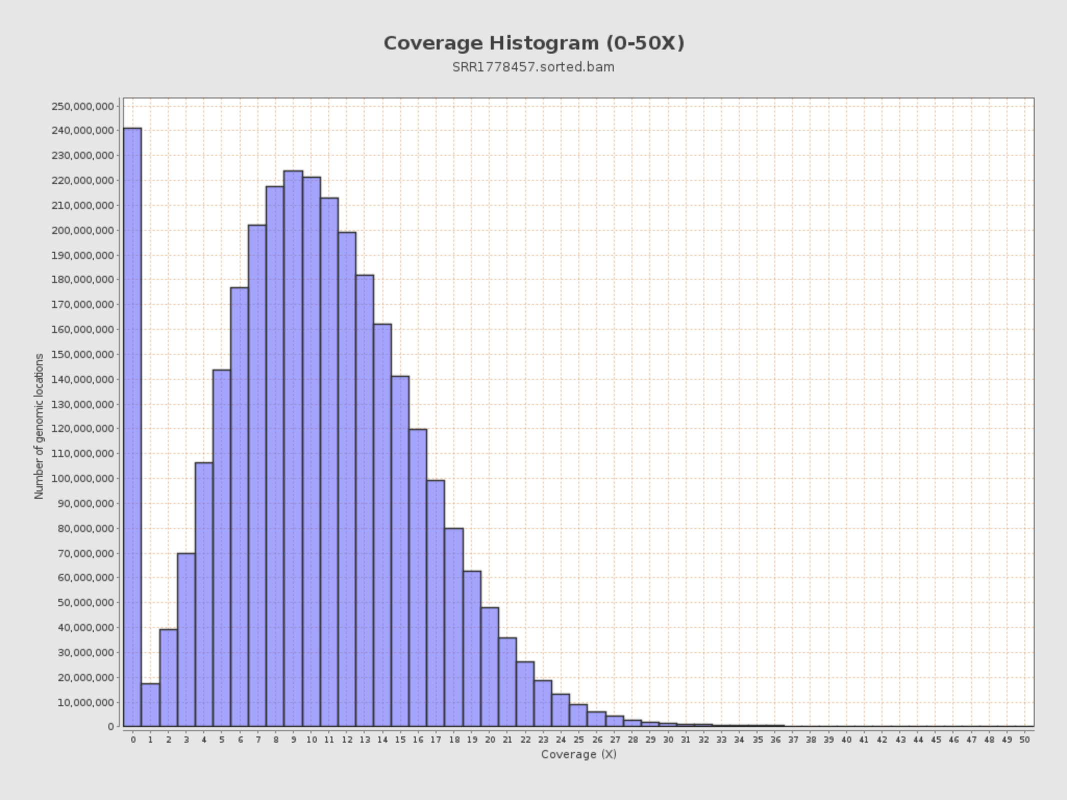
chrY	59373566	351469494	5.9196	102.3288

3. Results : Coverage across reference

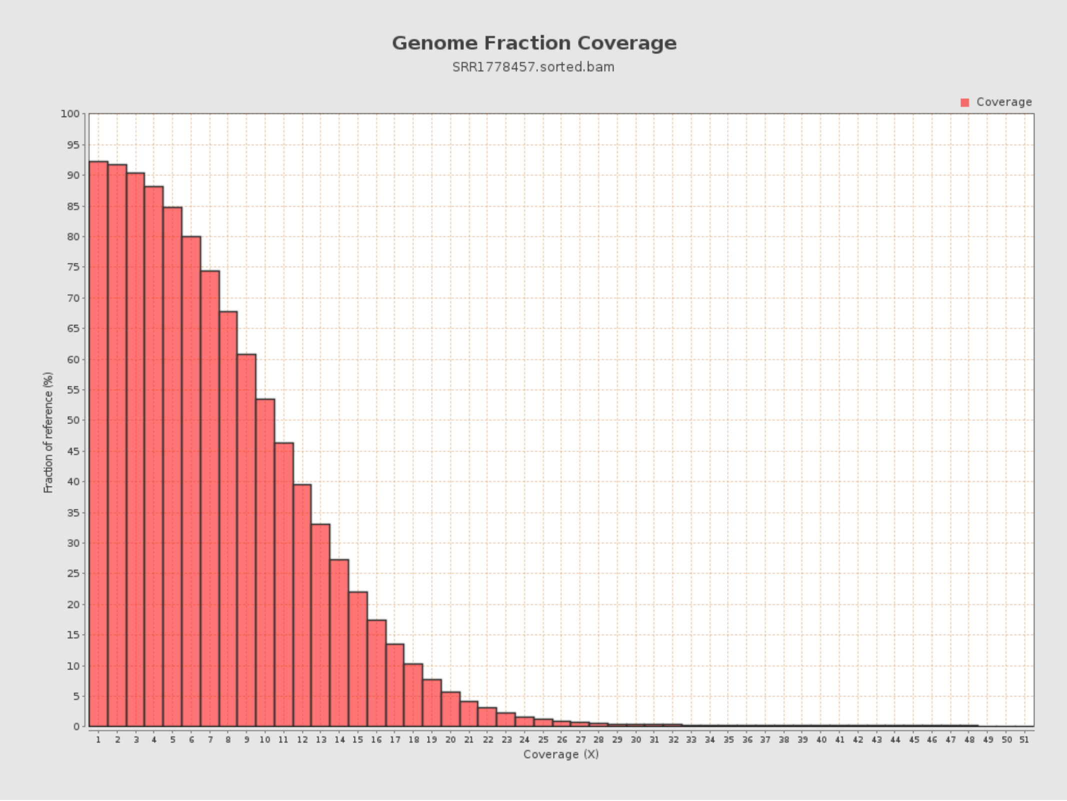
4. Results : Coverage Histogram



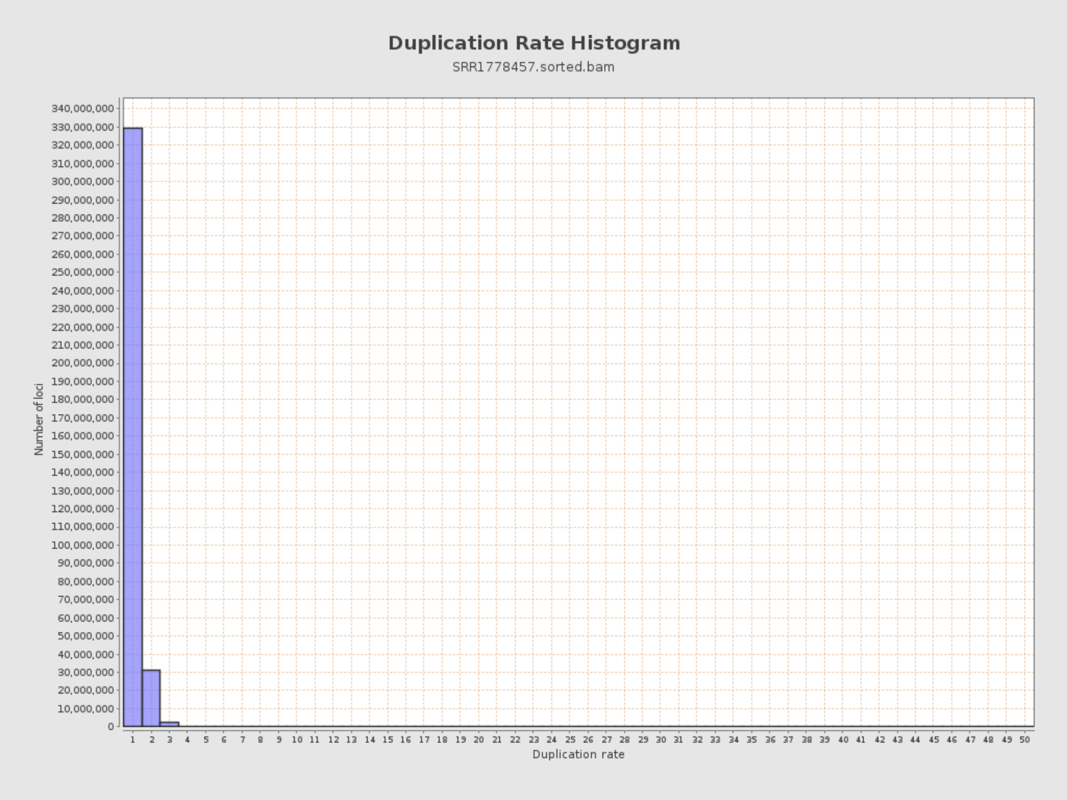
5. Results : Coverage Histogram (0-50X)



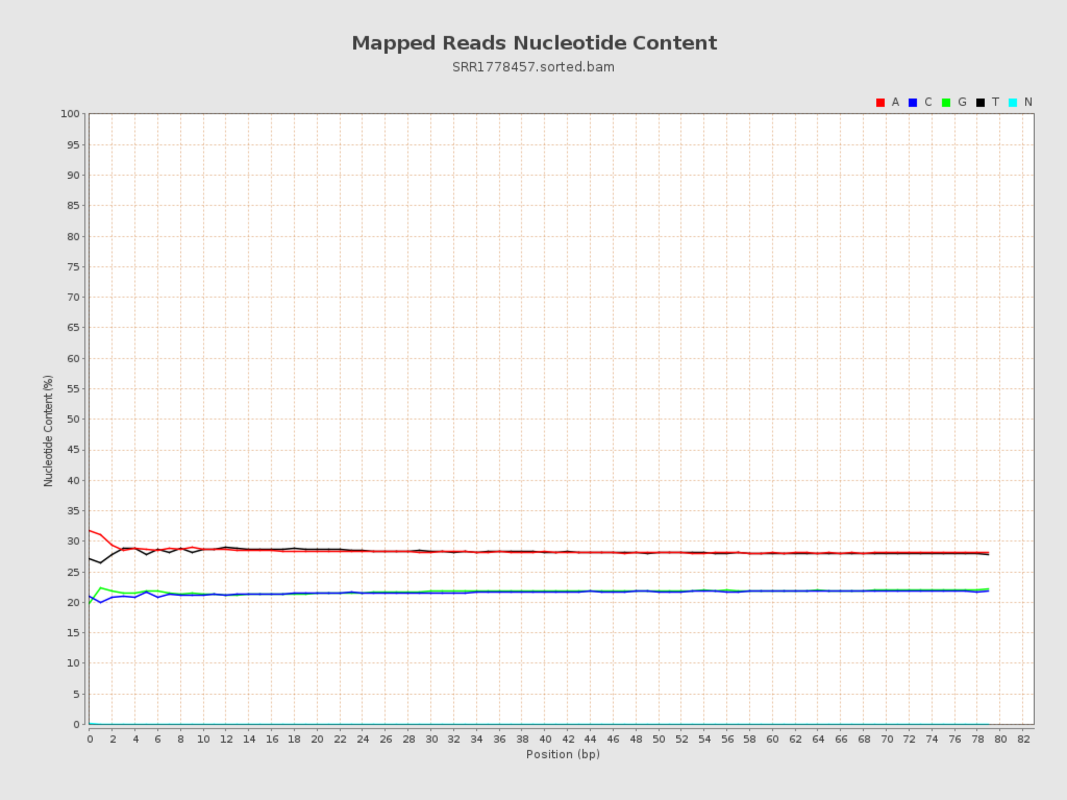
6. Results : Genome Fraction Coverage



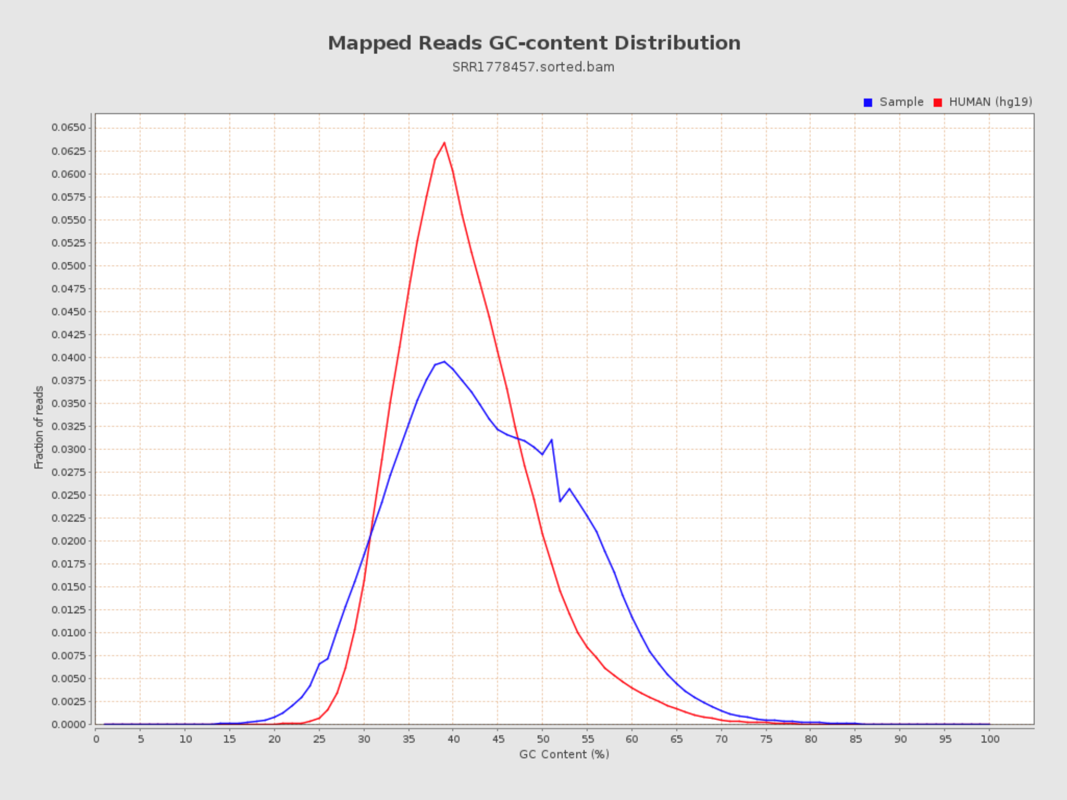
7. Results : Duplication Rate Histogram



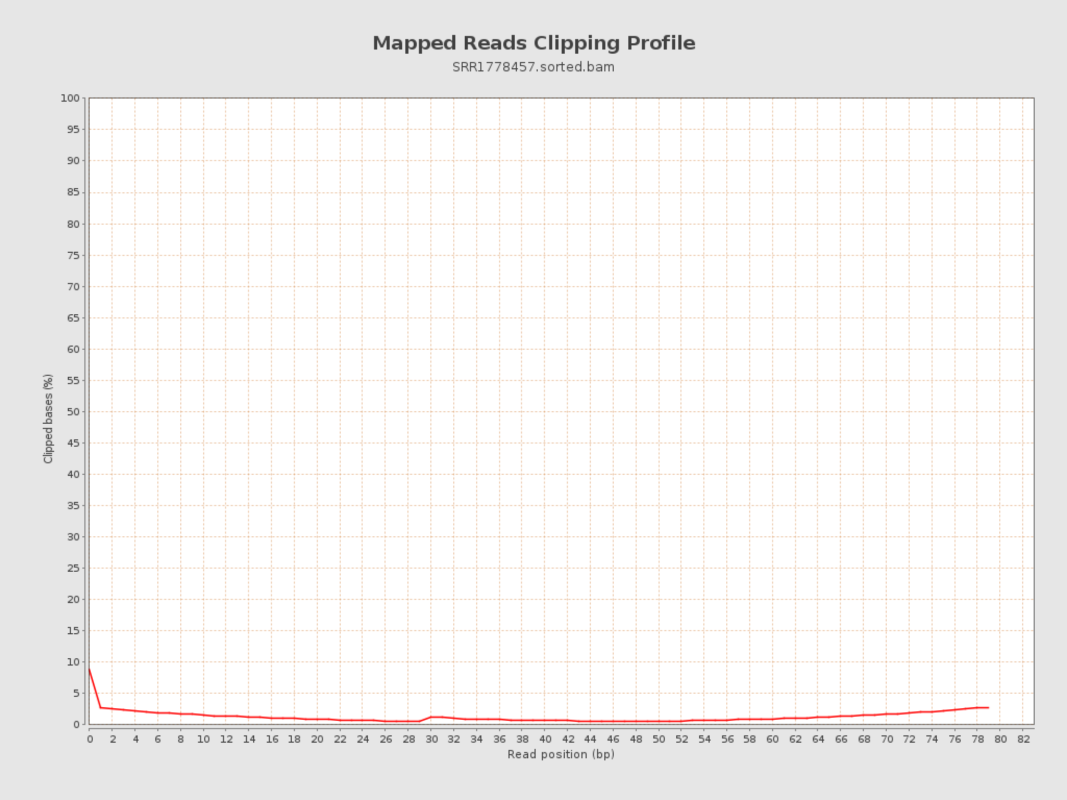
8. Results : Mapped Reads Nucleotide Content



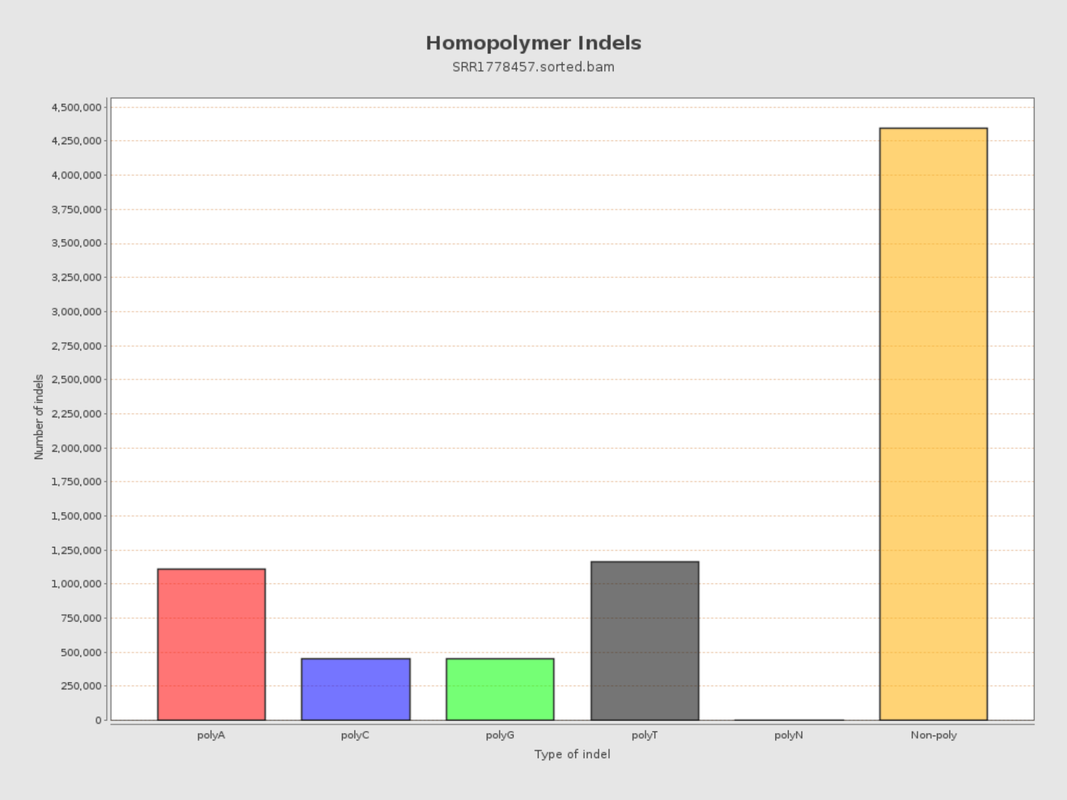
9. Results : Mapped Reads GC-content Distribution



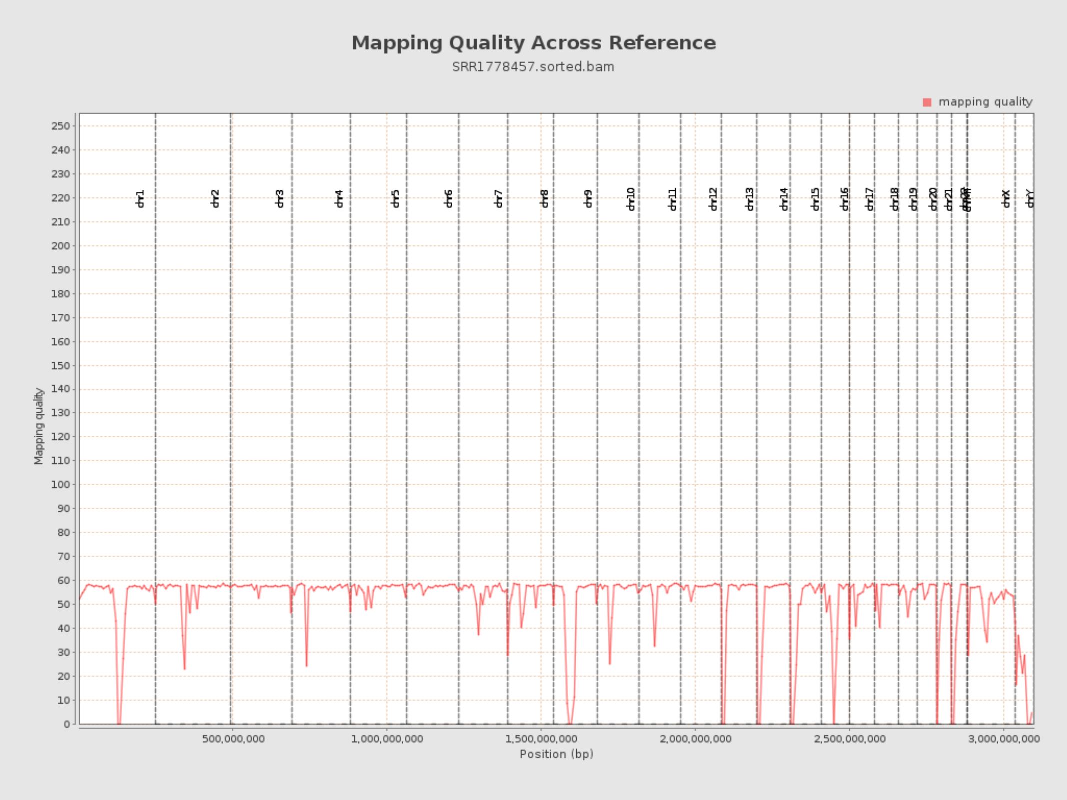
10. Results : Mapped Reads Clipping Profile



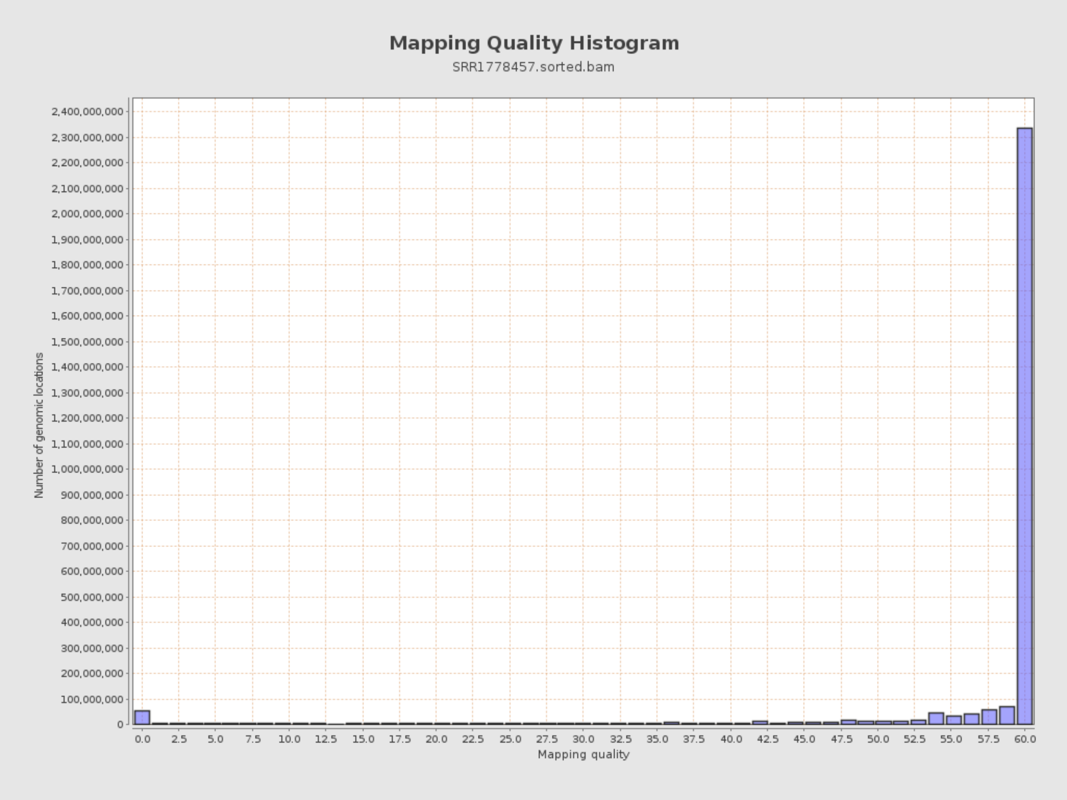
11. Results : Homopolymer Indels



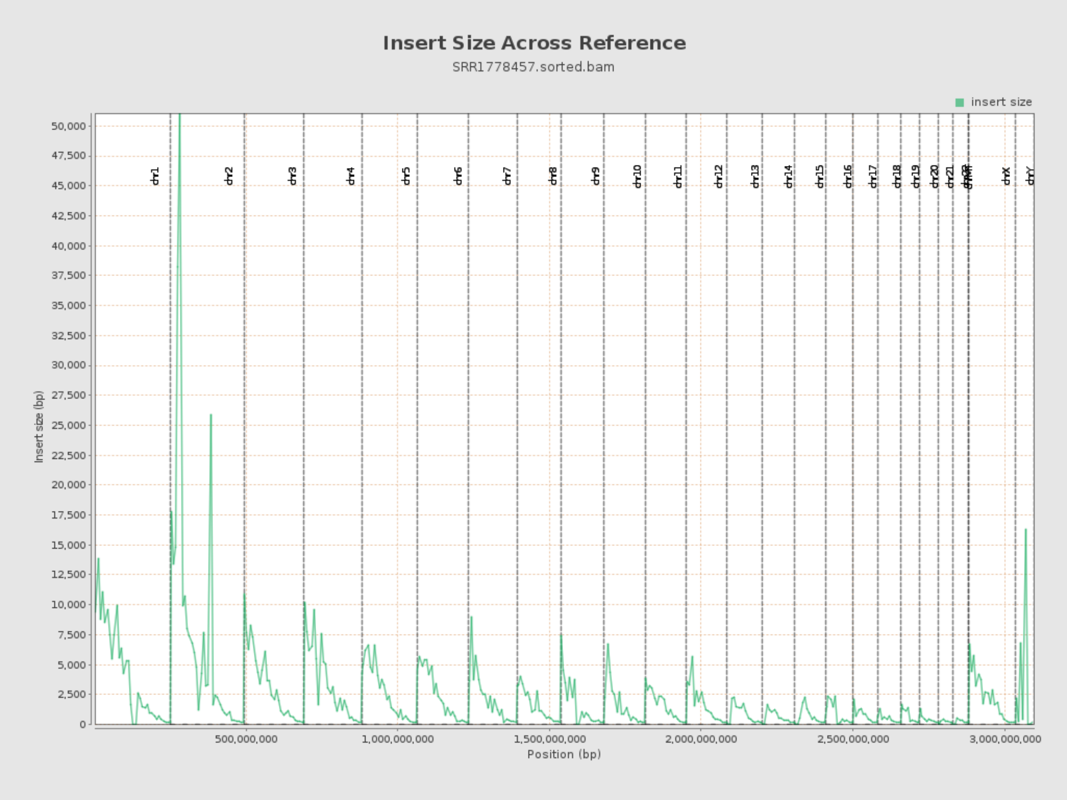
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram