Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 19:50:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779341.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_SRR1779341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779341_1.fastq.gz SRR1779341_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 19:50:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	127,455,246
Mapped reads	123,965,328 / 97.26%
Unmapped reads	3,489,918 / 2.74%
Mapped paired reads	123,965,328 / 97.26%
Mapped reads, first in pair	62,518,130 / 49.05%
Mapped reads, second in pair	61,447,198 / 48.21%
Mapped reads, both in pair	122,333,340 / 95.98%
Mapped reads, singletons	1,631,988 / 1.28%
Secondary alignments	0
Supplementary alignments	434,745 / 0.34%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	6,778,134 / 5.32%
Duplication rate	5.22%
Clipped reads	7,025,538 / 5.51%

2.2. ACGT Content

Number/percentage of A's	3,637,962,010 / 29.62%
Number/percentage of C's	2,493,524,270 / 20.3%
Number/percentage of T's	3,621,161,372 / 29.48%
Number/percentage of G's	2,528,472,642 / 20.59%
Number/percentage of N's	799,432 / 0.01%

GC Percentage	40.89%

2.3. Coverage

Mean	3.9683
Standard Deviation	5.7129

2.4. Mapping Quality

Mean Mapping Quality	53.94

2.5. Insert size

Mean	49,516.69
Standard Deviation	2,199,584.72
P25/Median/P75	153 / 201 / 266

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	44,731,747
Insertions	1,214,149
Mapped reads with at least one insertion	0.96%
Deletions	1,264,638
Mapped reads with at least one deletion	1%
Homopolymer indels	47.31%

2.7. Chromosome stats

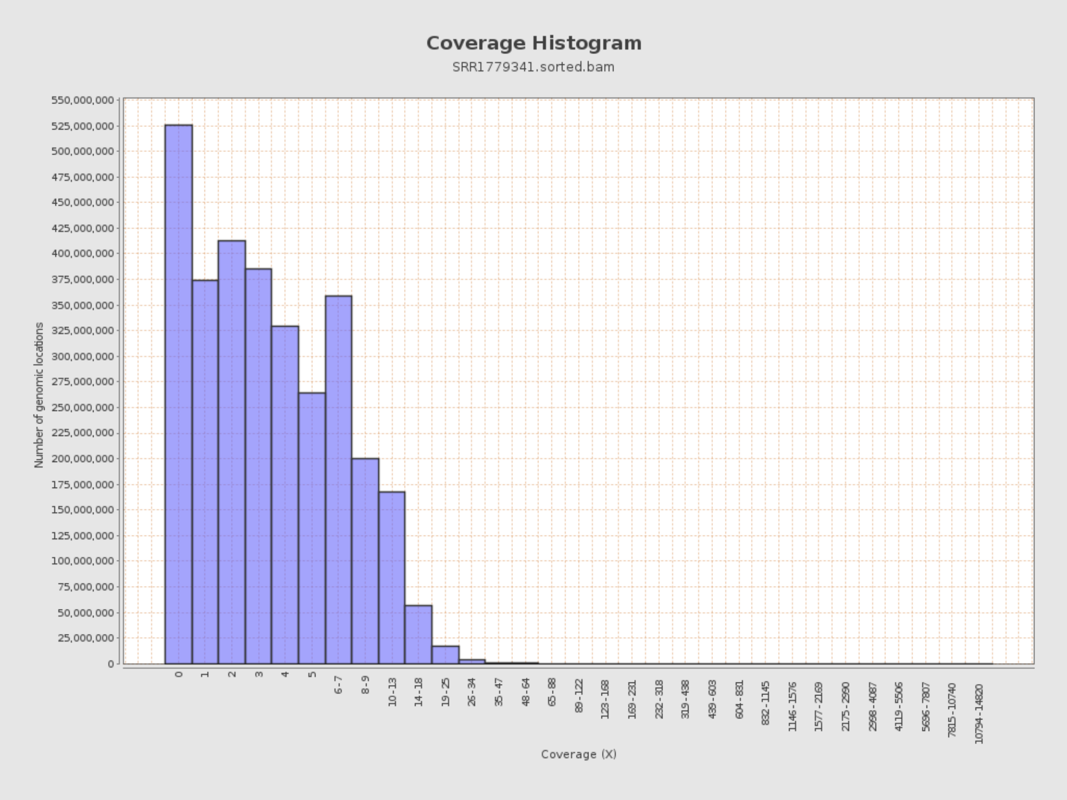
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	989798860	3.9711	7.1713
chr2	243199373	1022049202	4.2025	12.3573
chr3	198022430	844677910	4.2656	3.688
chr4	191154276	779668927	4.0787	4.1516
chr5	180915260	748575192	4.1377	3.5521
chr6	171115067	722271899	4.221	4.2956
chr7	159138663	634707701	3.9884	4.2652
chr8	146364022	611282461	4.1765	3.7579
chr9	141213431	503374858	3.5646	4.8301
chr10	135534747	693540060	5.1171	7.1251
chr11	135006516	562421089	4.1659	3.9246
chr12	133851895	650880338	4.8627	4.8139
chr13	115169878	384099271	3.3351	3.443
chr14	107349540	369589471	3.4429	3.6763
chr15	102531392	351285002	3.4261	3.7831
chr16	90354753	304772892	3.3731	3.7633
chr17	81195210	285388637	3.5148	4.2623
chr18	78077248	314521841	4.0283	5.0823
chr19	59128983	189546575	3.2056	5.0119
chr20	63025520	247190266	3.9221	4.2813
chr21	48129895	146856686	3.0513	5.7473
chr22	51304566	119216422	2.3237	3.2685
chrMT	16571	2202282	132.8998	33.3172
chrX	155270560	794848199	5.1191	4.4755

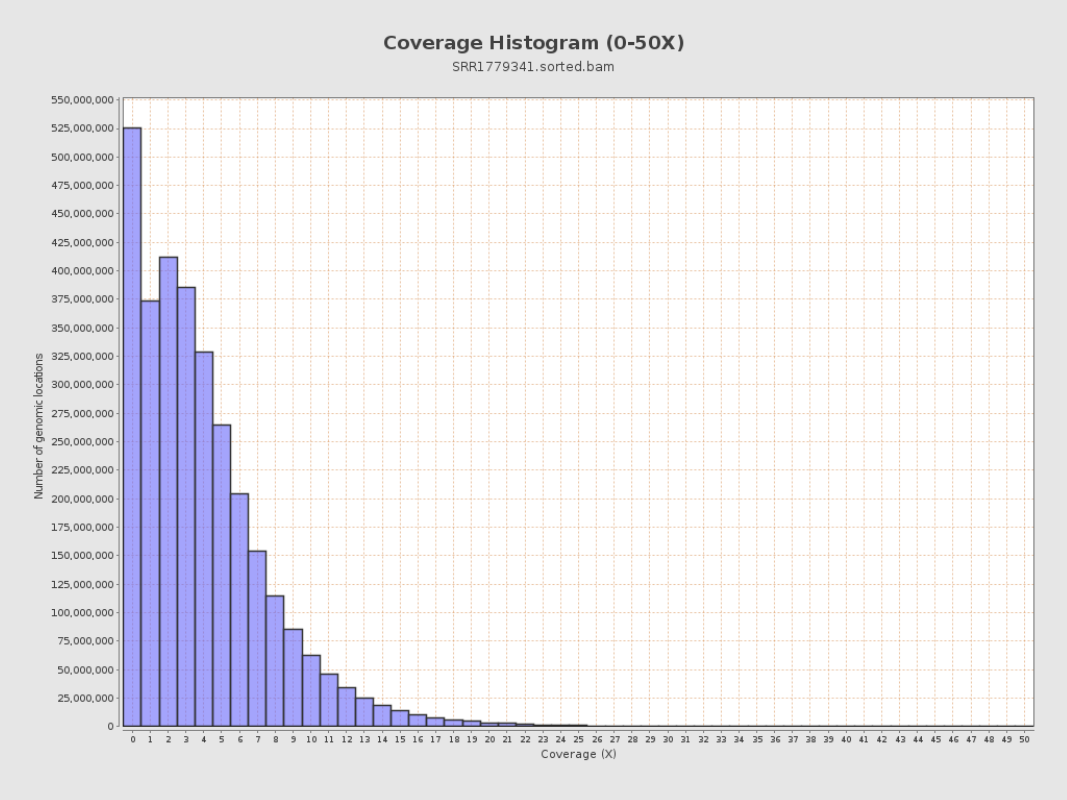
chrY	59373566	11943301	0.2012	2.2846

3. Results : Coverage across reference

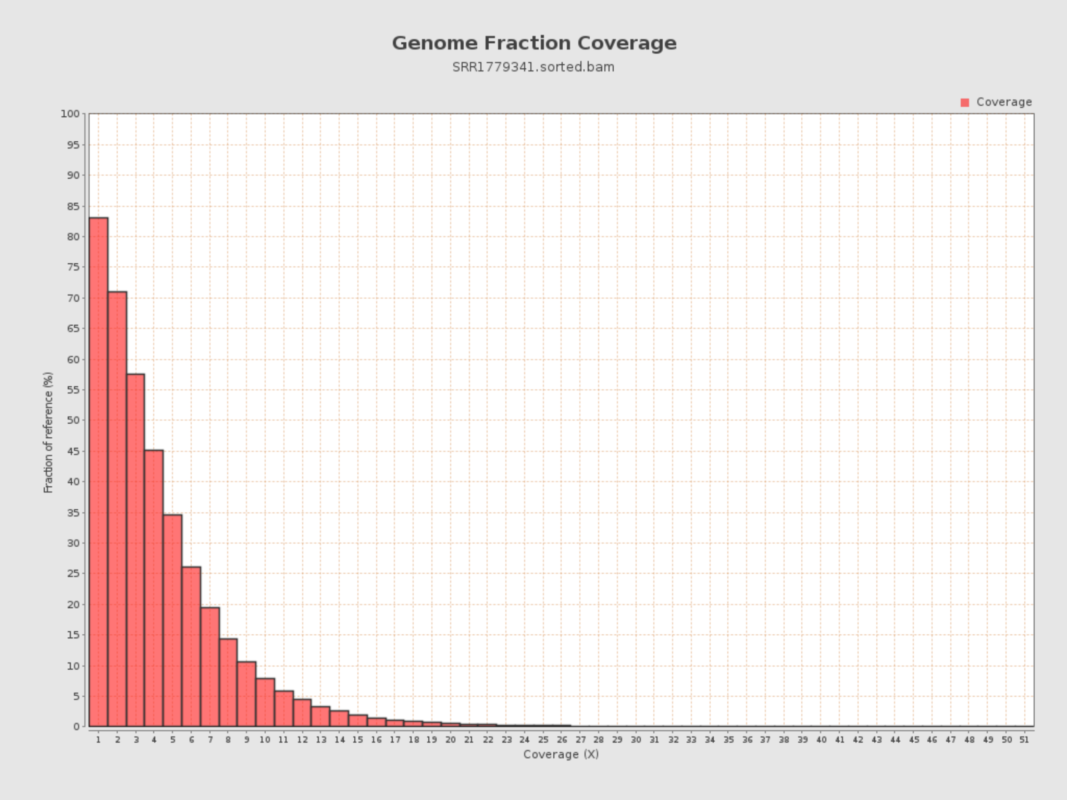
4. Results : Coverage Histogram



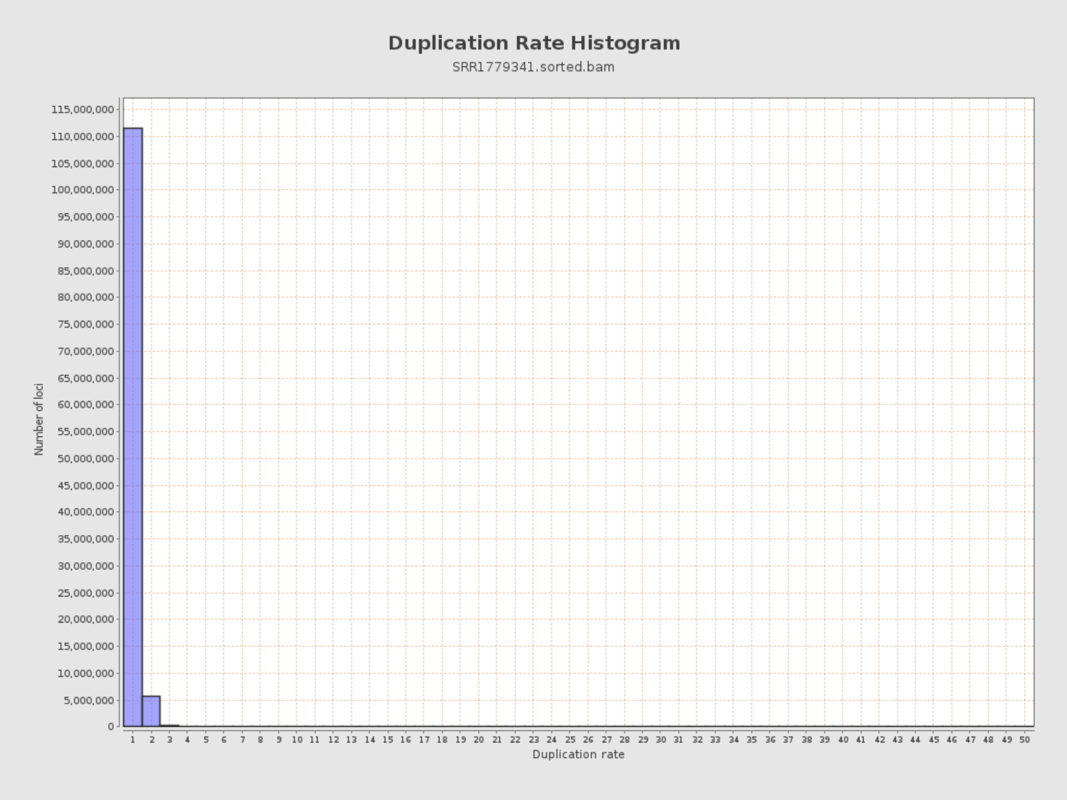
5. Results : Coverage Histogram (0-50X)



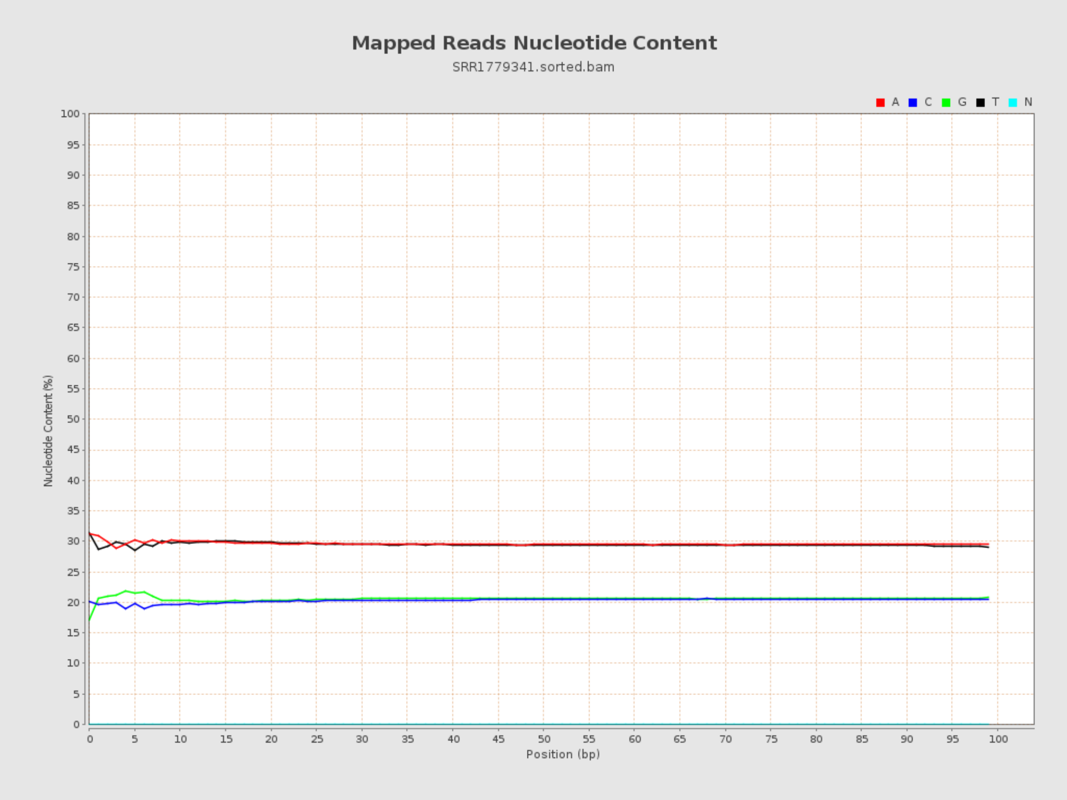
6. Results : Genome Fraction Coverage



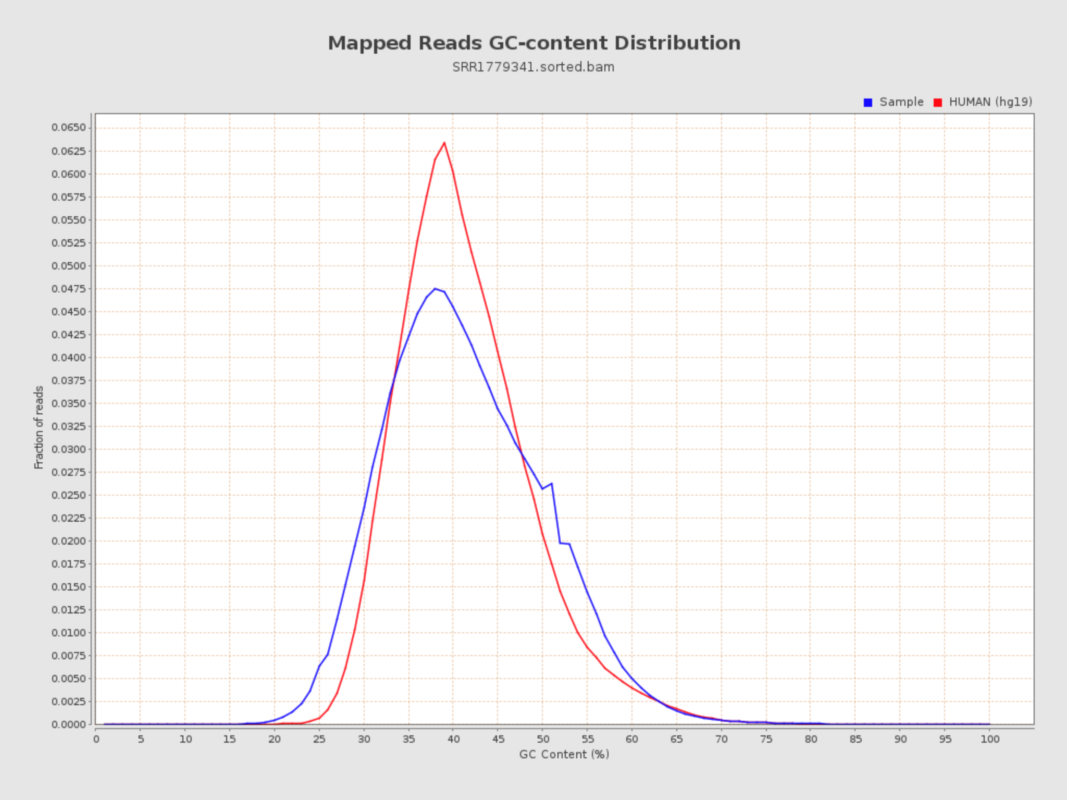
7. Results : Duplication Rate Histogram



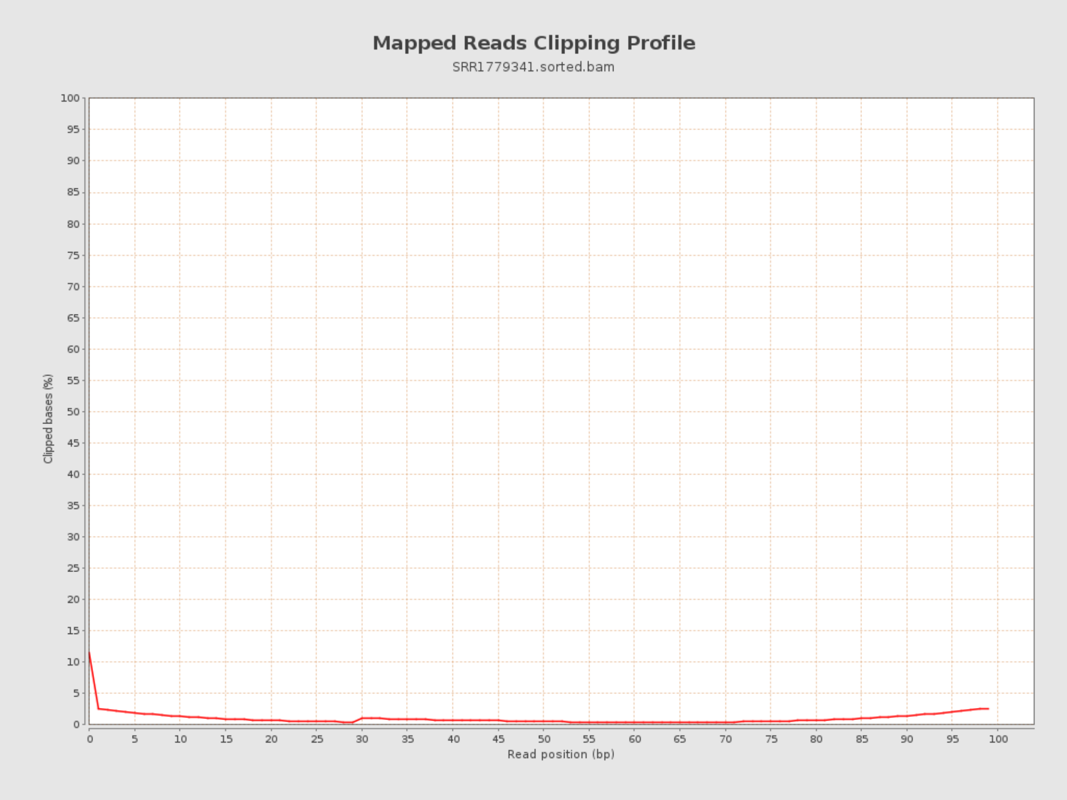
8. Results : Mapped Reads Nucleotide Content



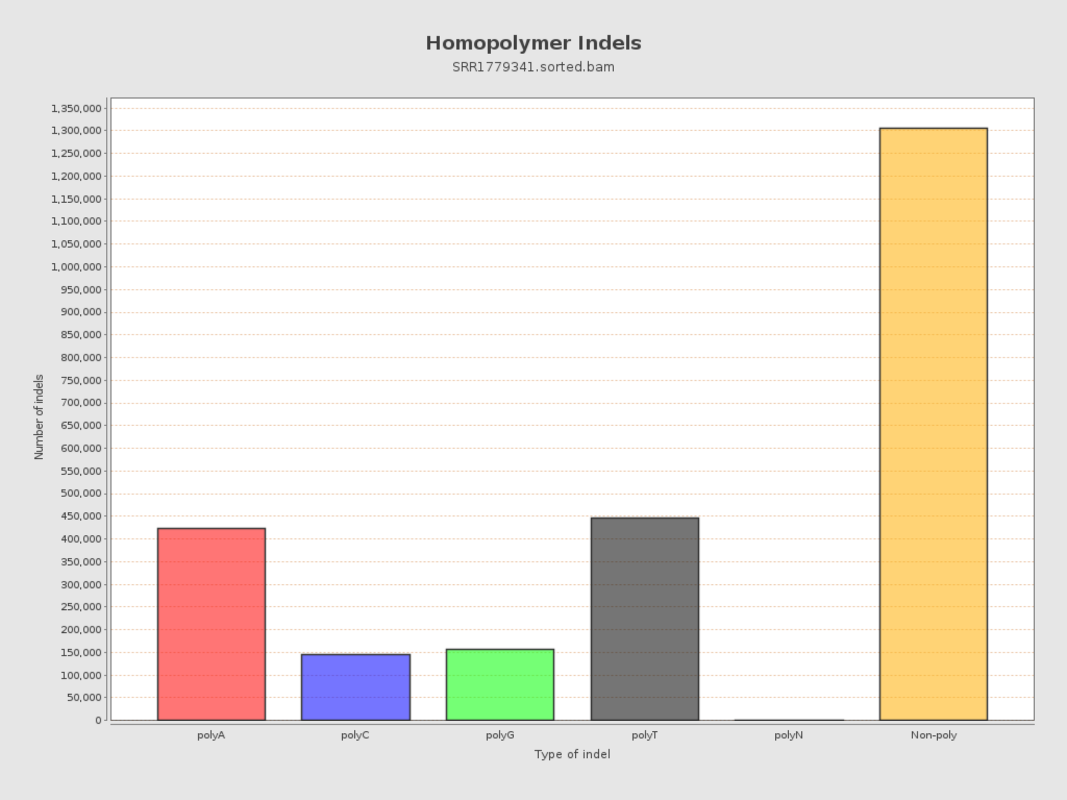
9. Results : Mapped Reads GC-content Distribution



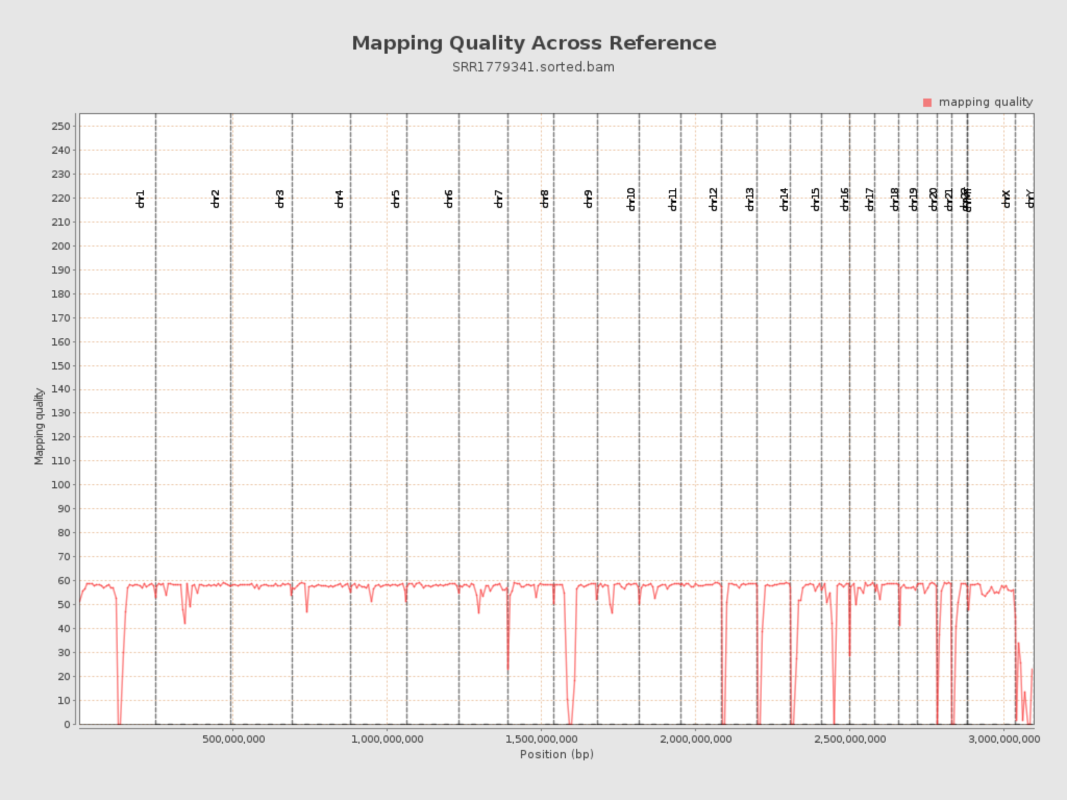
10. Results : Mapped Reads Clipping Profile



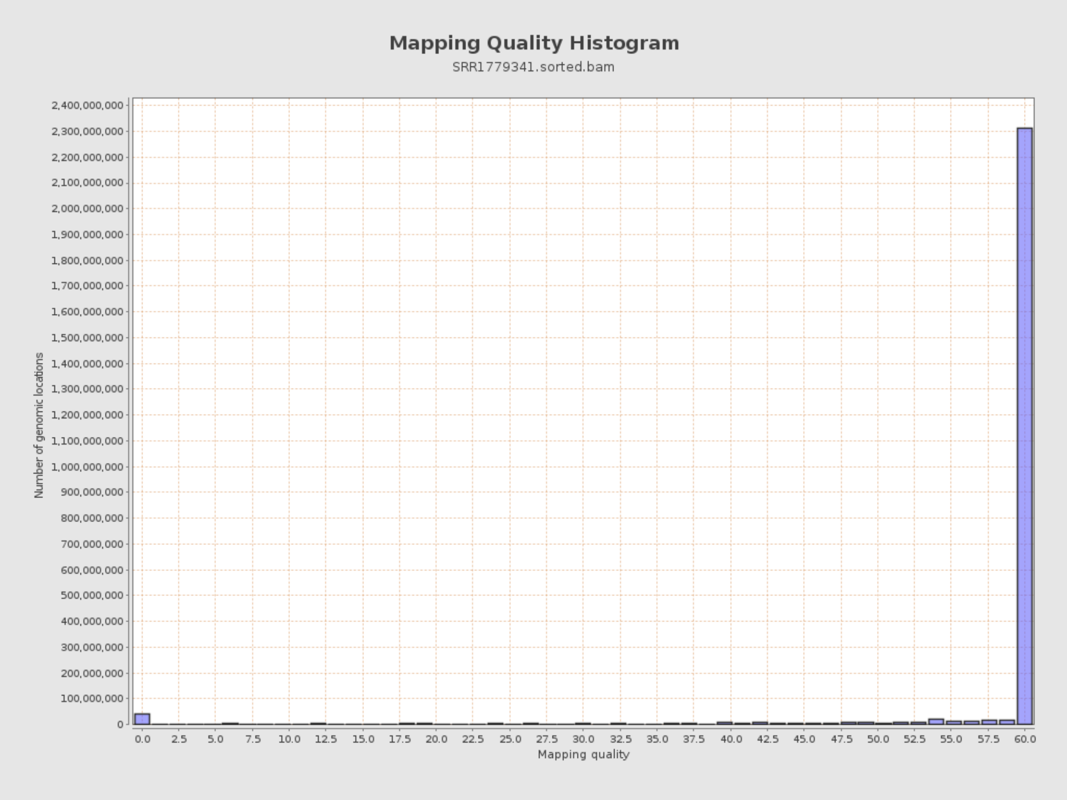
11. Results : Homopolymer Indels



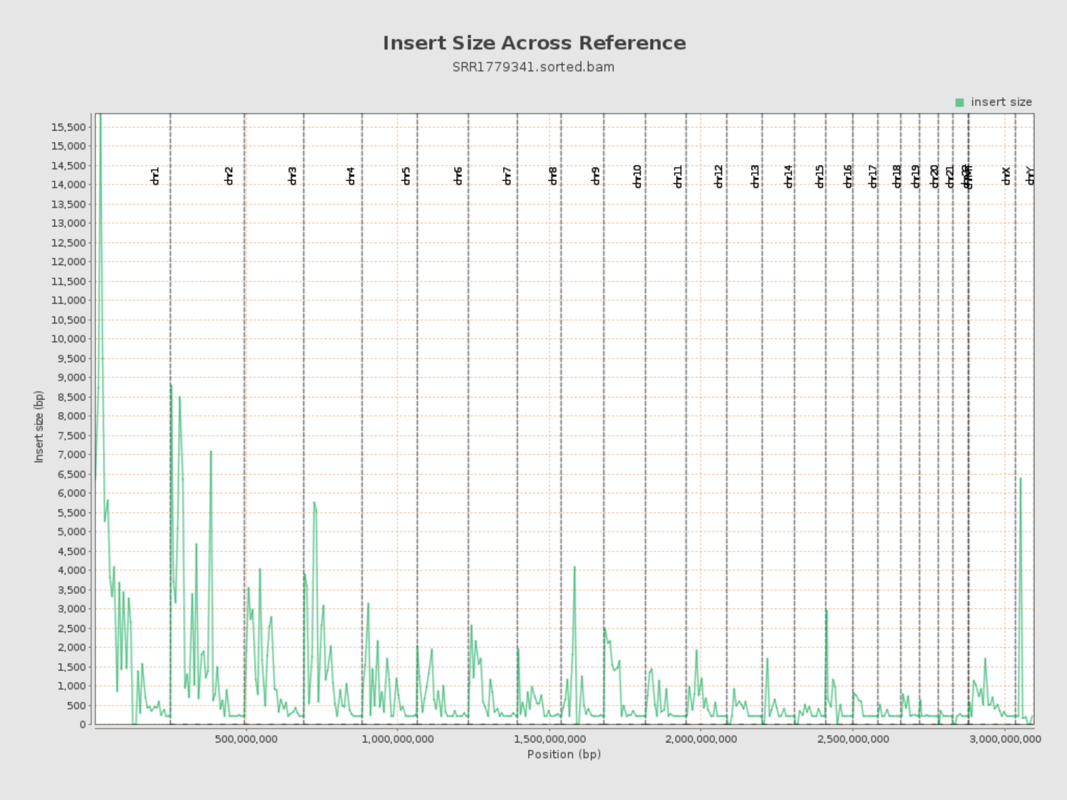
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram