Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 03:47:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779348.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_SRR1779348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779348_1.fastq.gz SRR1779348_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 03:47:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	318,062,820
Mapped reads	302,201,094 / 95.01%
Unmapped reads	15,861,726 / 4.99%
Mapped paired reads	302,201,094 / 95.01%
Mapped reads, first in pair	152,205,722 / 47.85%
Mapped reads, second in pair	149,995,372 / 47.16%
Mapped reads, both in pair	297,426,882 / 93.51%
Mapped reads, singletons	4,774,212 / 1.5%
Secondary alignments	0
Supplementary alignments	1,437,907 / 0.45%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	59,547,344 / 18.72%
Duplication rate	16.88%
Clipped reads	18,442,369 / 5.8%

2.2. ACGT Content

Number/percentage of A's	9,156,522,219 / 30.27%
Number/percentage of C's	5,957,664,330 / 19.69%
Number/percentage of T's	9,083,696,927 / 30.03%
Number/percentage of G's	6,043,603,051 / 19.98%
Number/percentage of N's	8,872,988 / 0.03%

GC Percentage	39.67%

2.3. Coverage

Mean	9.7741
Standard Deviation	27.021

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	63,773.99
Standard Deviation	2,448,604.78
P25/Median/P75	151 / 205 / 284

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	102,731,174
Insertions	2,538,928
Mapped reads with at least one insertion	0.83%
Deletions	3,242,054
Mapped reads with at least one deletion	1.05%
Homopolymer indels	47.02%

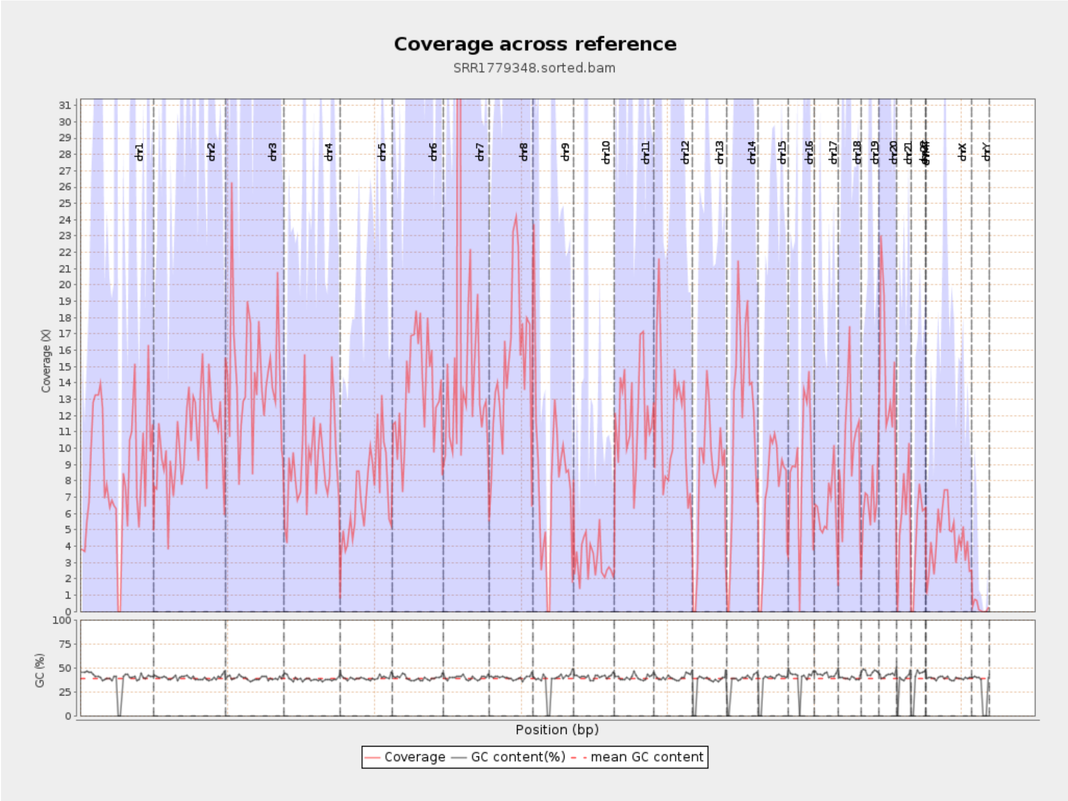
2.7. Chromosome stats

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

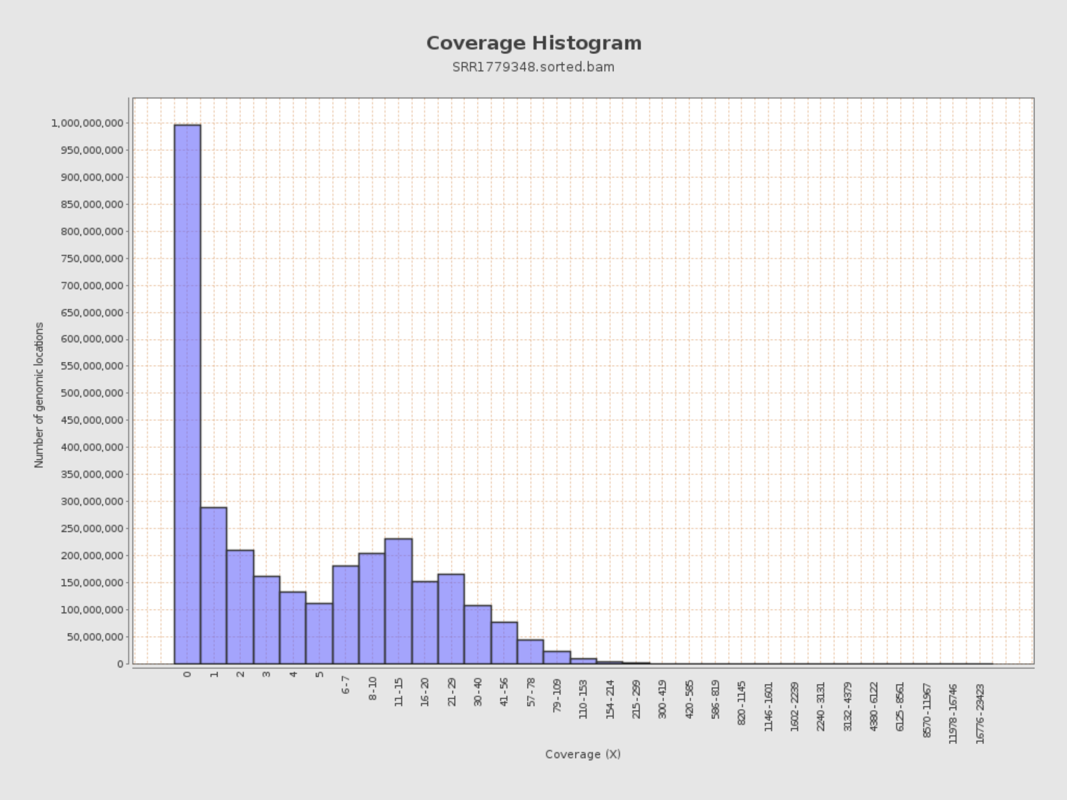
		bases	coverage	deviation
chr1	249250621	2092958440	8.397	21.8793
chr2	243199373	2544909929	10.4643	20.73
chr3	198022430	2845623745	14.3702	22.3555
chr4	191154276	1759144355	9.2027	16.7912
chr5	180915260	1313811396	7.262	14.0792
chr6	171115067	2334188480	13.641	22.2471
chr7	159138663	2791902705	17.5438	79.6522
chr8	146364022	2242191497	15.3193	22.8837
chr9	141213431	1133639997	8.0278	20.3248
chr10	135534747	428995450	3.1652	35.8722
chr11	135006516	1596938486	11.8286	20.8685
chr12	133851895	1532673432	11.4505	22.2373
chr13	115169878	970250297	8.4245	14.9039
chr14	107349540	1310985800	12.2123	20.7621
chr15	102531392	736143062	7.1797	15.0407
chr16	90354753	790632602	8.7503	16.8944
chr17	81195210	496990927	6.1209	14.3584
chr18	78077248	797632604	10.2159	20.1287
chr19	59128983	385890444	6.5262	19.8823
chr20	63025520	904135827	14.3456	24.8775
chr21	48129895	301526861	6.2649	14.1392
chr22	51304566	244257507	4.7609	10.6185
chrMT	16571	58896	3.5542	5.5988
chrX	155270560	686148446	4.4191	12.5922

chrY	59373566	16020611	0.2698	4.3028

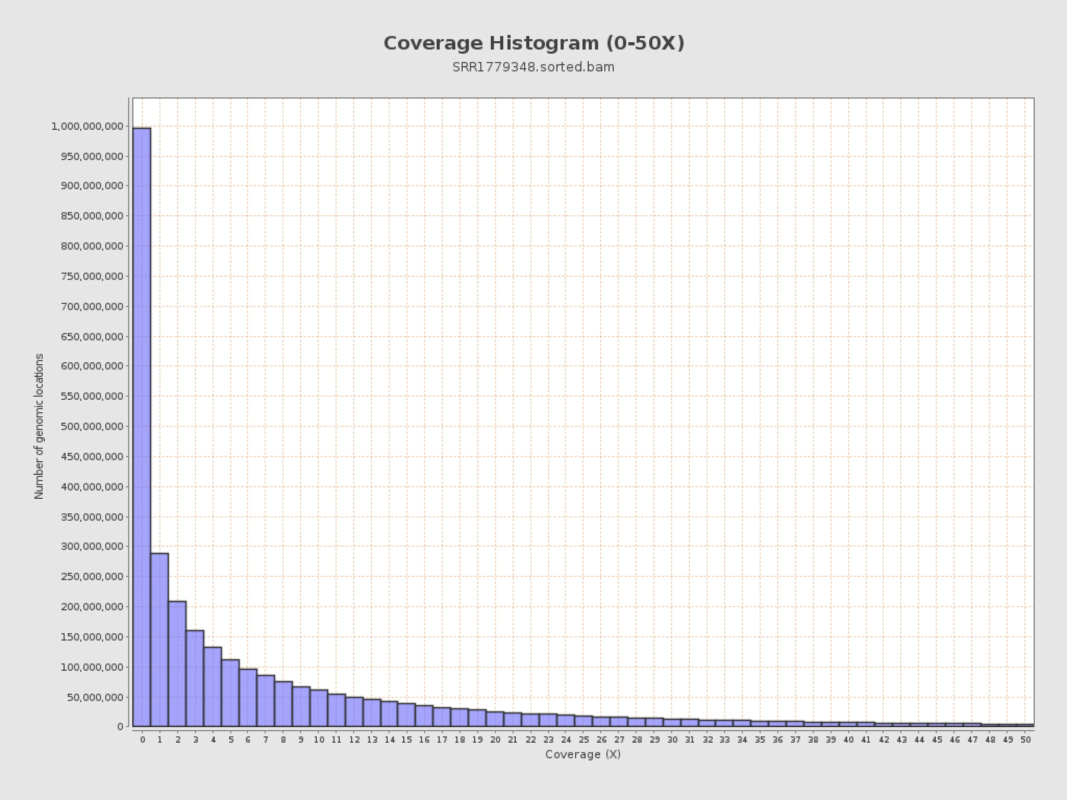
3. Results : Coverage across reference



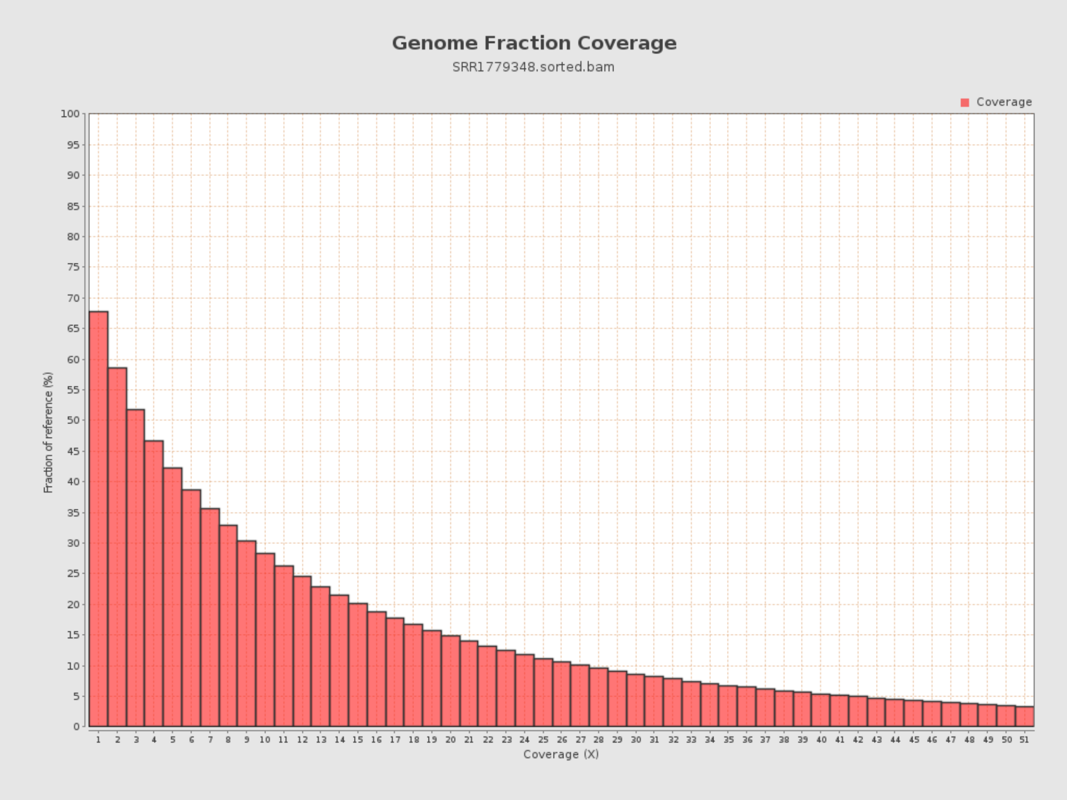
4. Results : Coverage Histogram



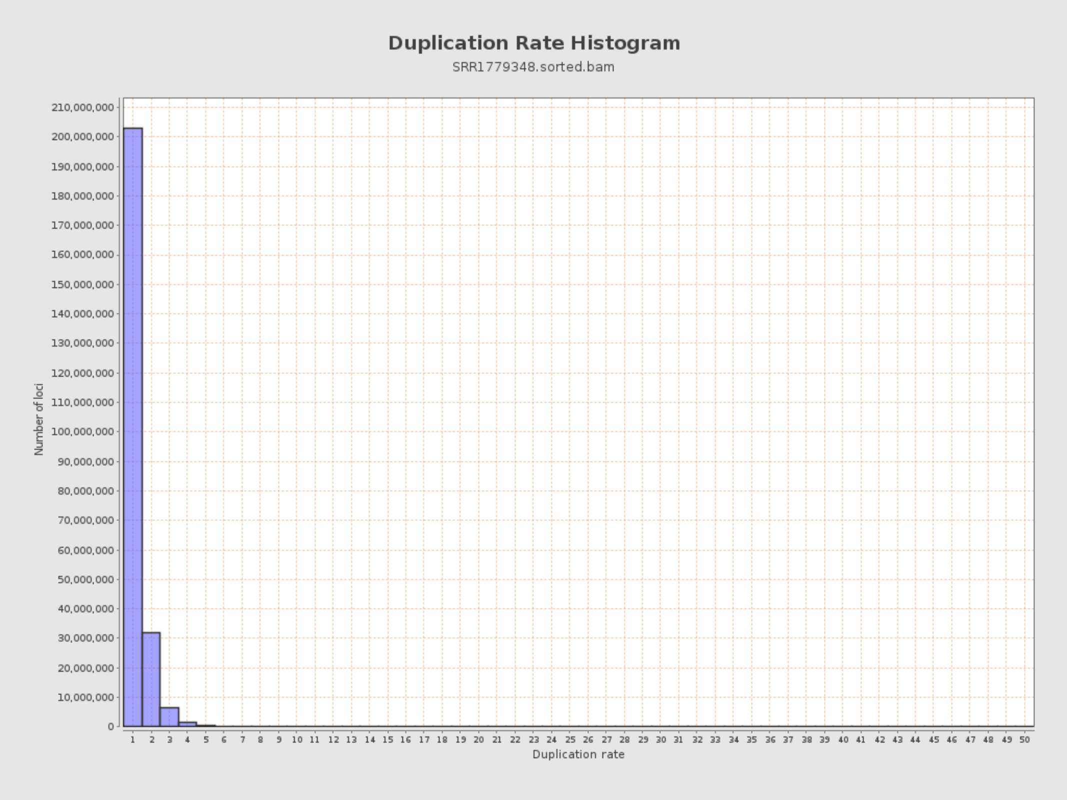
5. Results : Coverage Histogram (0-50X)



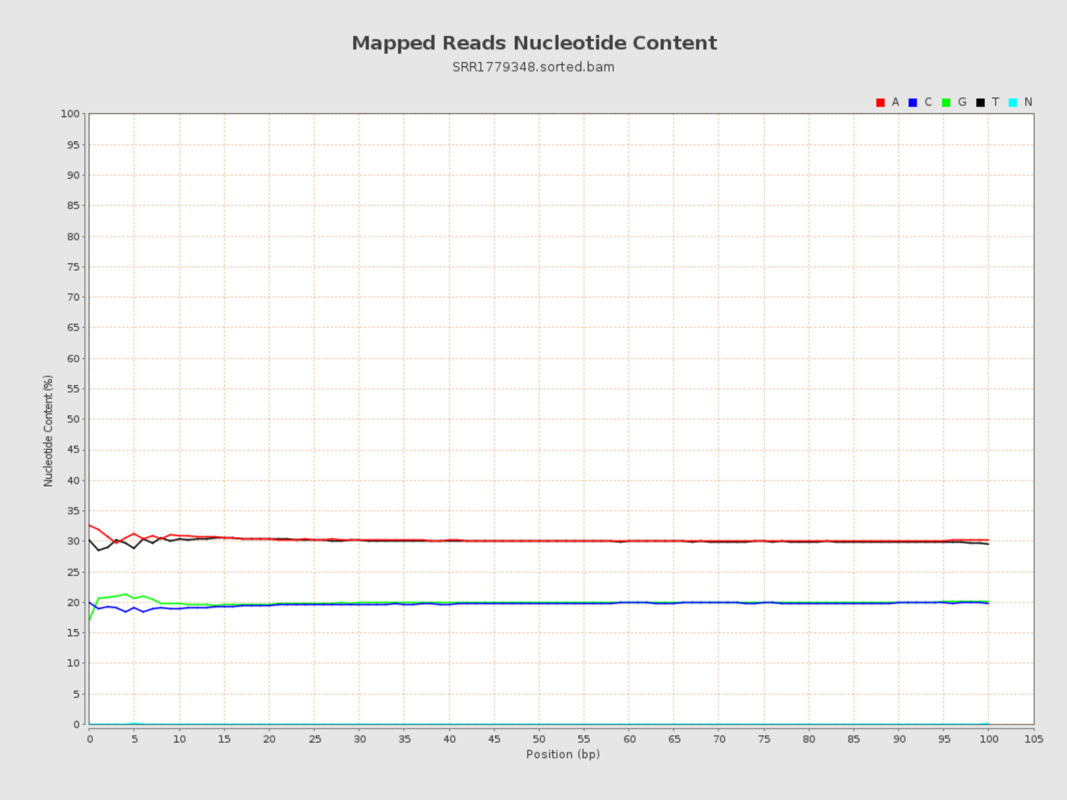
6. Results : Genome Fraction Coverage



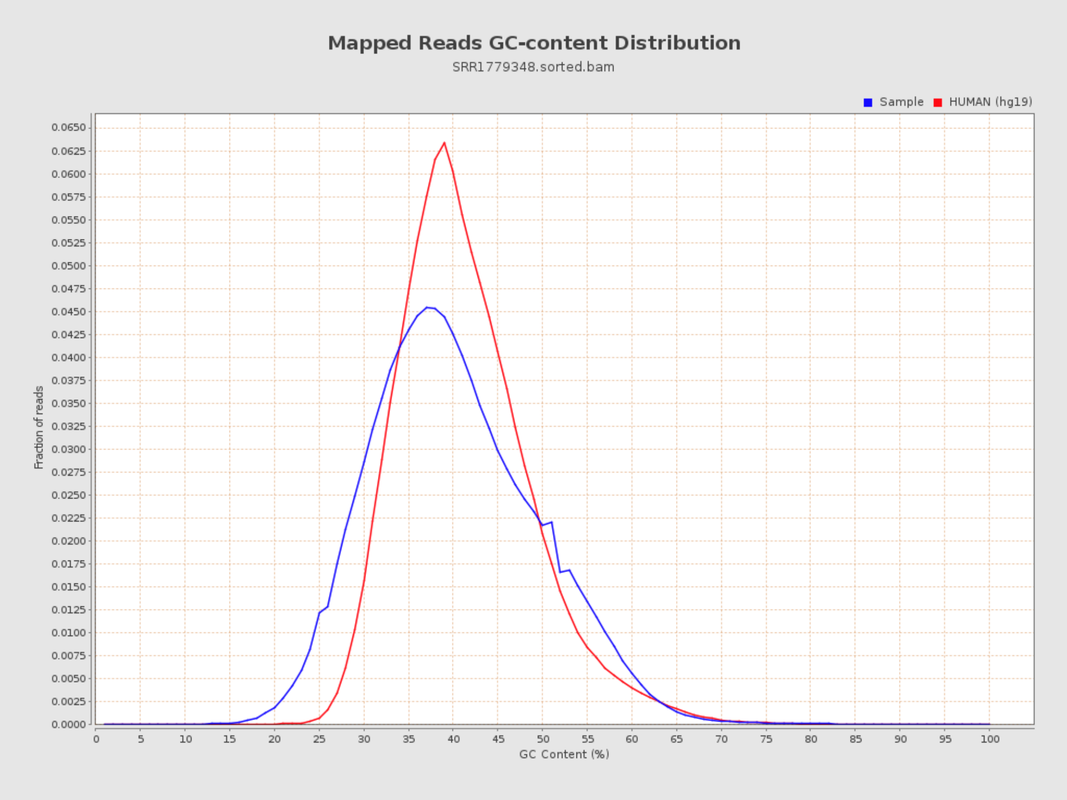
7. Results : Duplication Rate Histogram



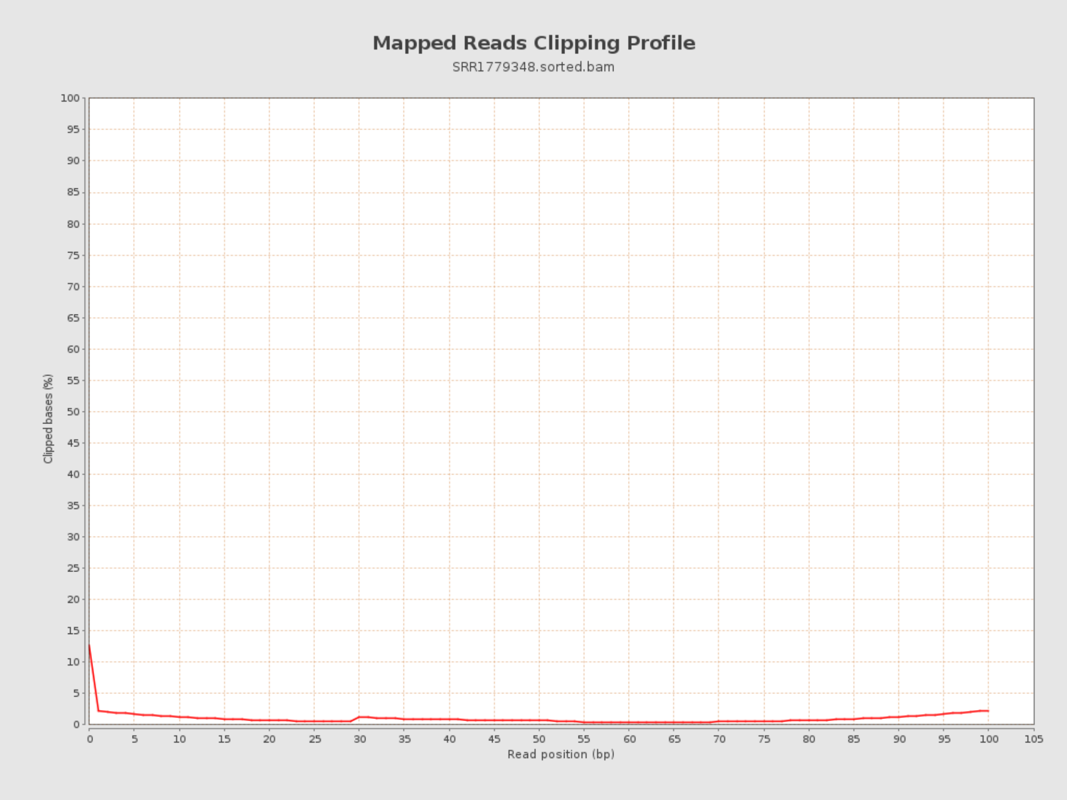
8. Results : Mapped Reads Nucleotide Content



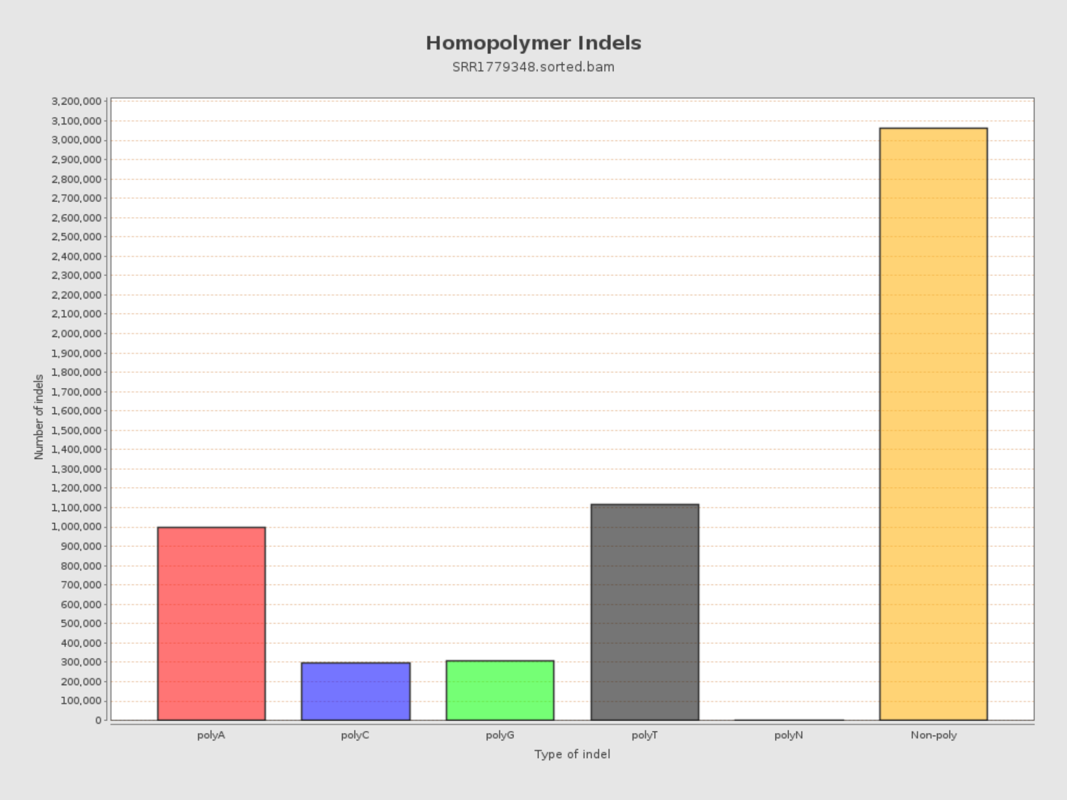
9. Results : Mapped Reads GC-content Distribution



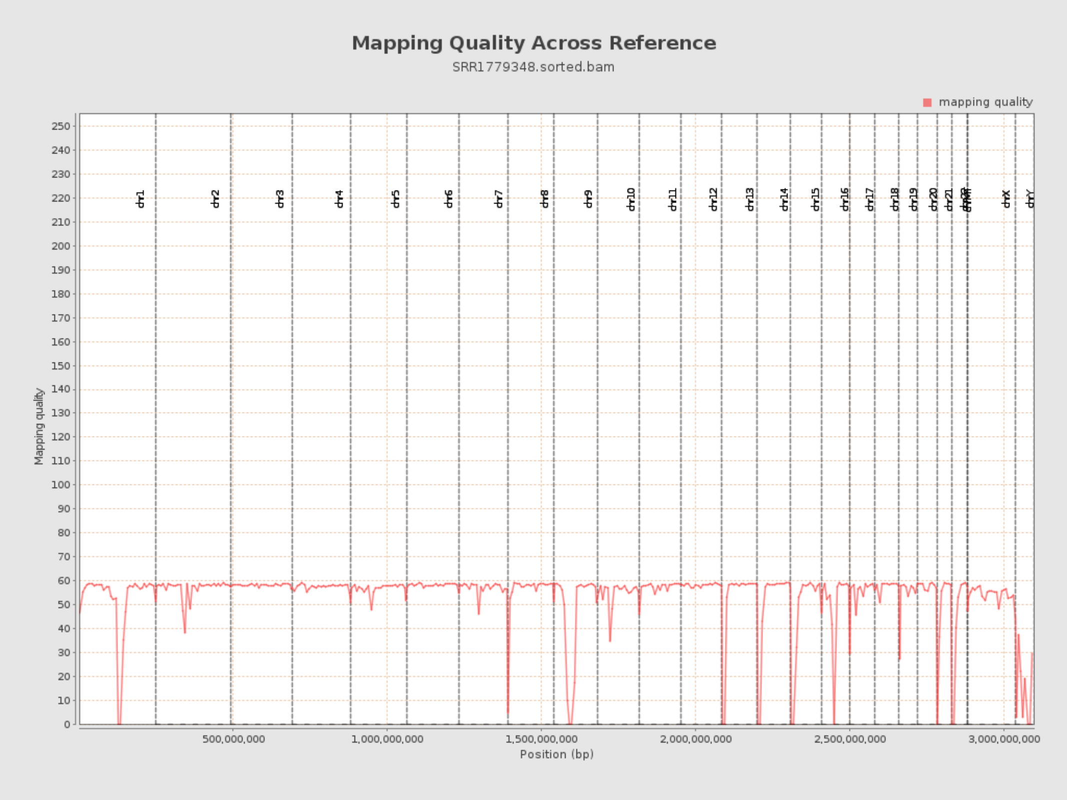
10. Results : Mapped Reads Clipping Profile



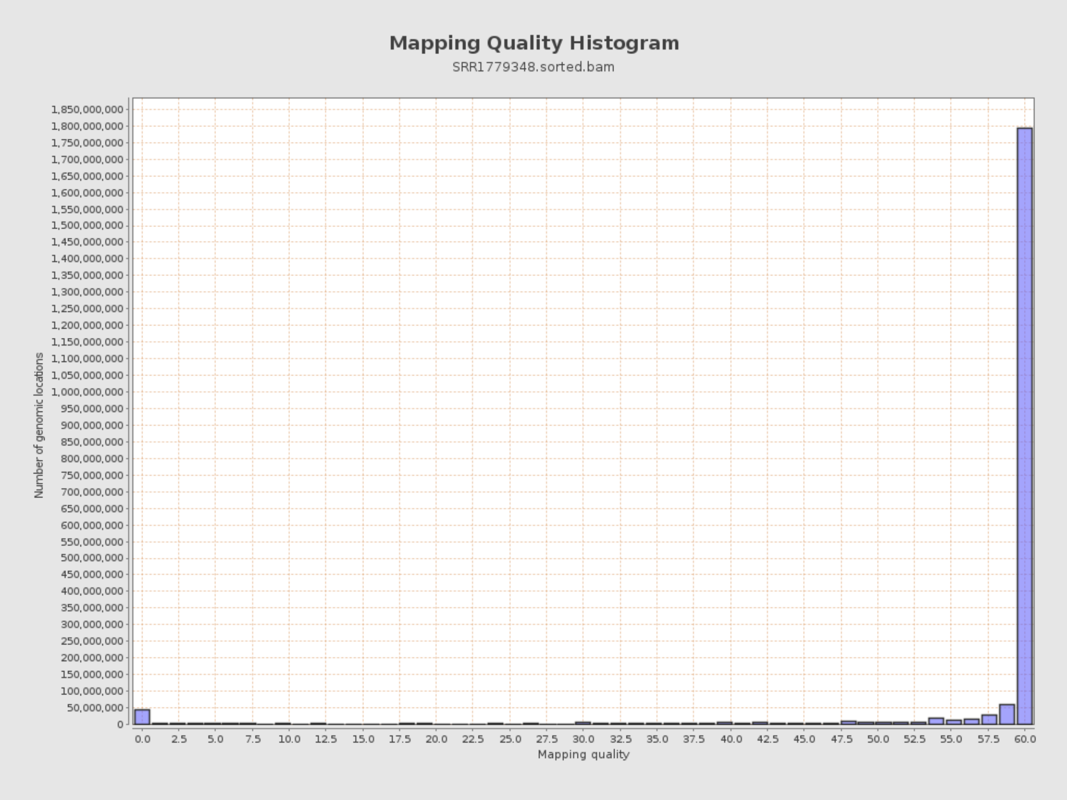
11. Results : Homopolymer Indels



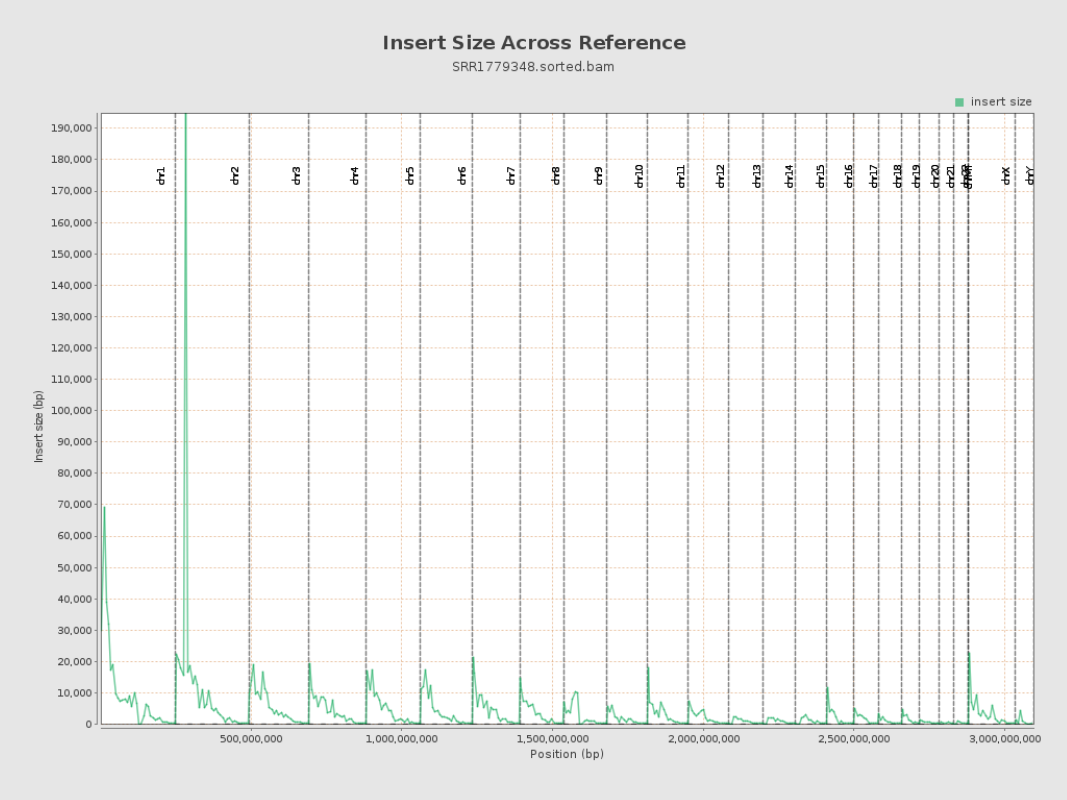
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram