Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779391.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_SRR1779391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779391_1.fastq.gz SRR1779391_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:32:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,758,082
Mapped reads	5,605,233 / 64%
Unmapped reads	3,152,849 / 36%
Mapped paired reads	5,605,233 / 64%
Mapped reads, first in pair	2,836,732 / 32.39%
Mapped reads, second in pair	2,768,501 / 31.61%
Mapped reads, both in pair	5,461,518 / 62.36%
Mapped reads, singletons	143,715 / 1.64%
Secondary alignments	0
Supplementary alignments	47,301 / 0.54%
Read min/max/mean length	30 / 80 / 80.2
Duplicated reads (estimated)	1,252,088 / 14.3%
Duplication rate	10%
Clipped reads	703,515 / 8.03%

2.2. ACGT Content

Number/percentage of A's	139,027,132 / 31.46%
Number/percentage of C's	77,976,336 / 17.64%
Number/percentage of T's	131,242,533 / 29.69%
Number/percentage of G's	93,641,716 / 21.19%
Number/percentage of N's	89,950 / 0.02%

GC Percentage	38.83%

2.3. Coverage

Mean	0.1428
Standard Deviation	4.4221

2.4. Mapping Quality

Mean Mapping Quality	51.26

2.5. Insert size

Mean	89,563.99
Standard Deviation	2,727,486.53
P25/Median/P75	214 / 327 / 509

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	3,415,498
Insertions	46,718
Mapped reads with at least one insertion	0.83%
Deletions	49,433
Mapped reads with at least one deletion	0.87%
Homopolymer indels	46.78%

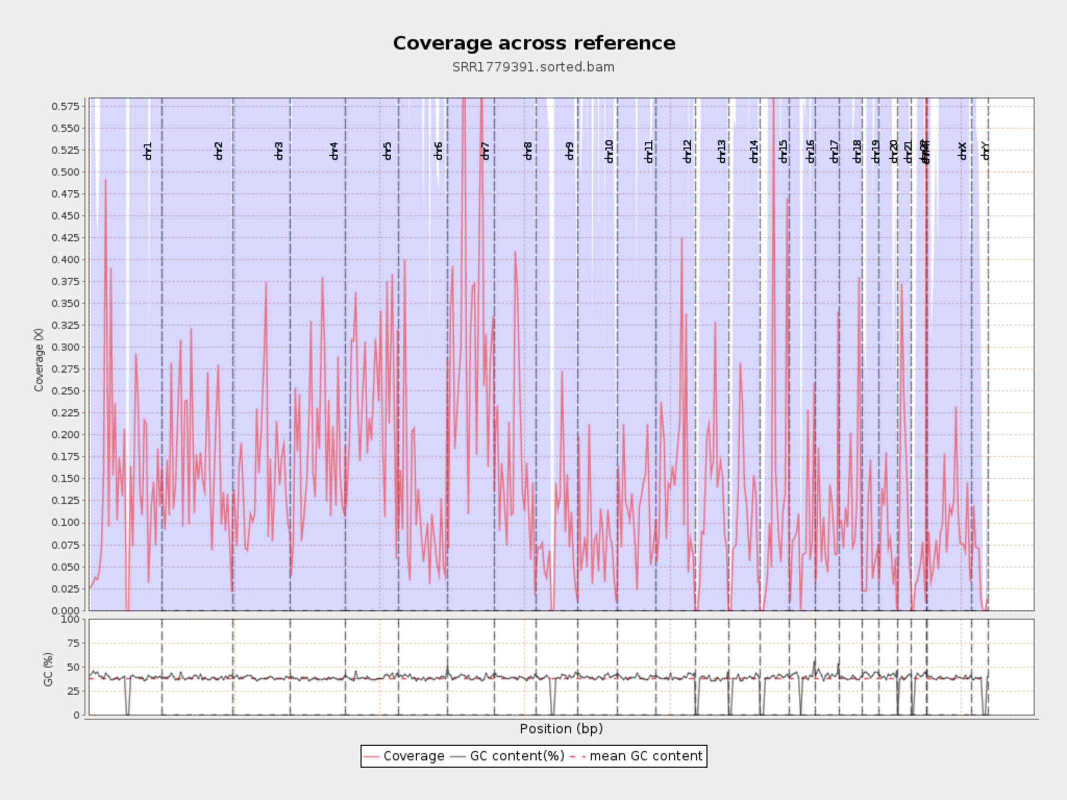
2.7. Chromosome stats

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

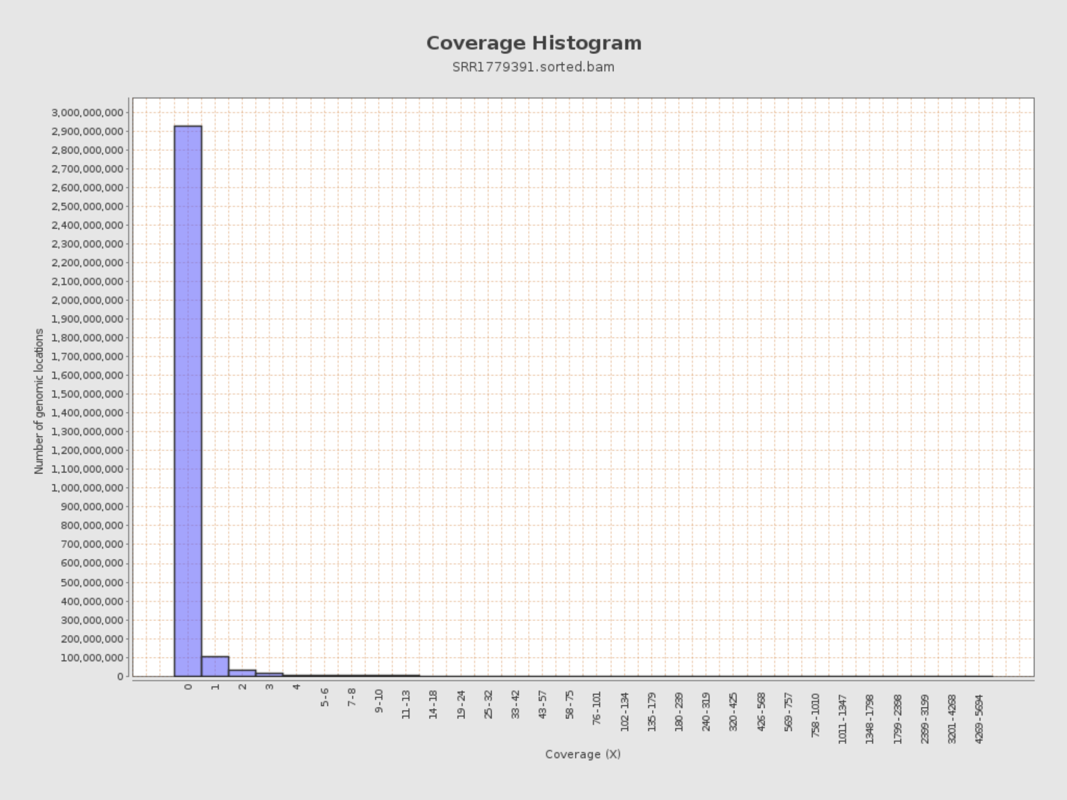
		bases	coverage	deviation
chr1	249250621	35200089	0.1412	5.073
chr2	243199373	39965978	0.1643	5.0949
chr3	198022430	30175491	0.1524	2.4425
chr4	191154276	34963378	0.1829	3.2737
chr5	180915260	43521884	0.2406	6.386
chr6	171115067	18852607	0.1102	3.8036
chr7	159138663	51172724	0.3216	7.7407
chr8	146364022	24361747	0.1664	4.1161
chr9	141213431	12018772	0.0851	3.2963
chr10	135534747	11037343	0.0814	2.8682
chr11	135006516	15587976	0.1155	1.2704
chr12	133851895	20883025	0.156	4.8124
chr13	115169878	14675874	0.1274	1.5596
chr14	107349540	12016712	0.1119	2.3176
chr15	102531392	14166968	0.1382	8.7514
chr16	90354753	8683923	0.0961	5.8013
chr17	81195210	8299781	0.1022	4.9796
chr18	78077248	10402748	0.1332	2.6662
chr19	59128983	4090087	0.0692	2.136
chr20	63025520	5582784	0.0886	2.3919
chr21	48129895	7447280	0.1547	4.0062
chr22	51304566	1751097	0.0341	0.5209
chrMT	16571	98636	5.9523	4.5086
chrX	155270560	14543081	0.0937	2.513

chrY	59373566	2573073	0.0433	0.5209

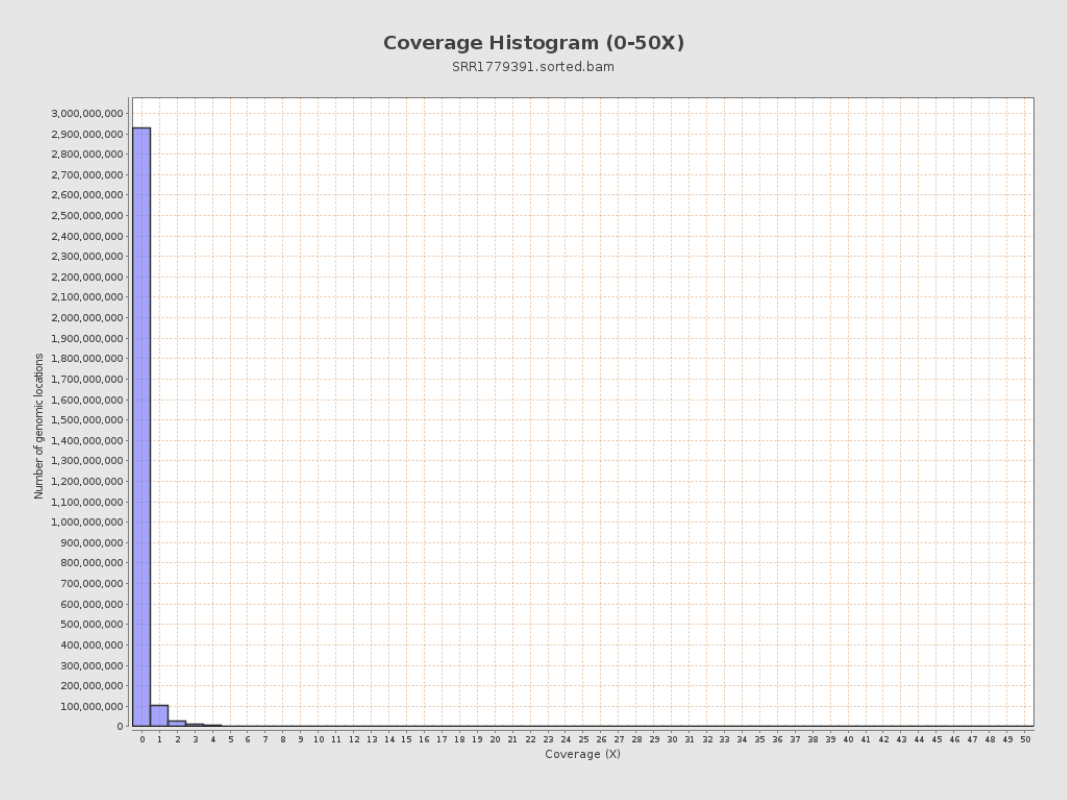
3. Results : Coverage across reference



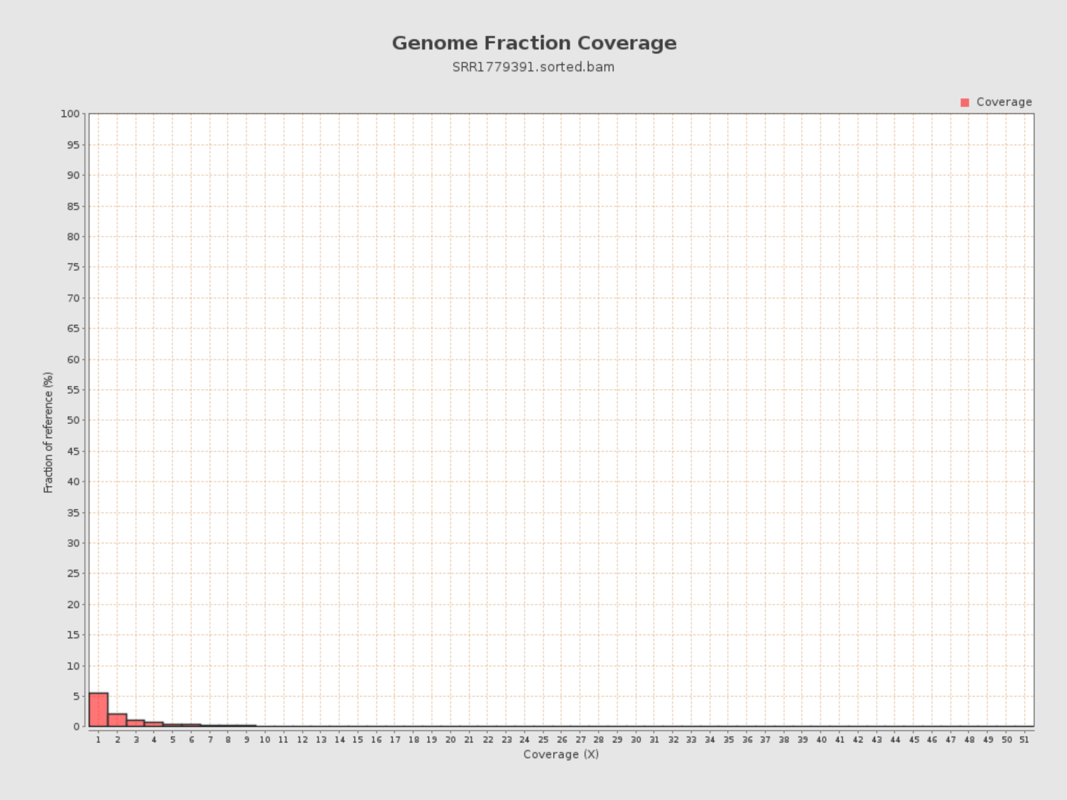
4. Results : Coverage Histogram



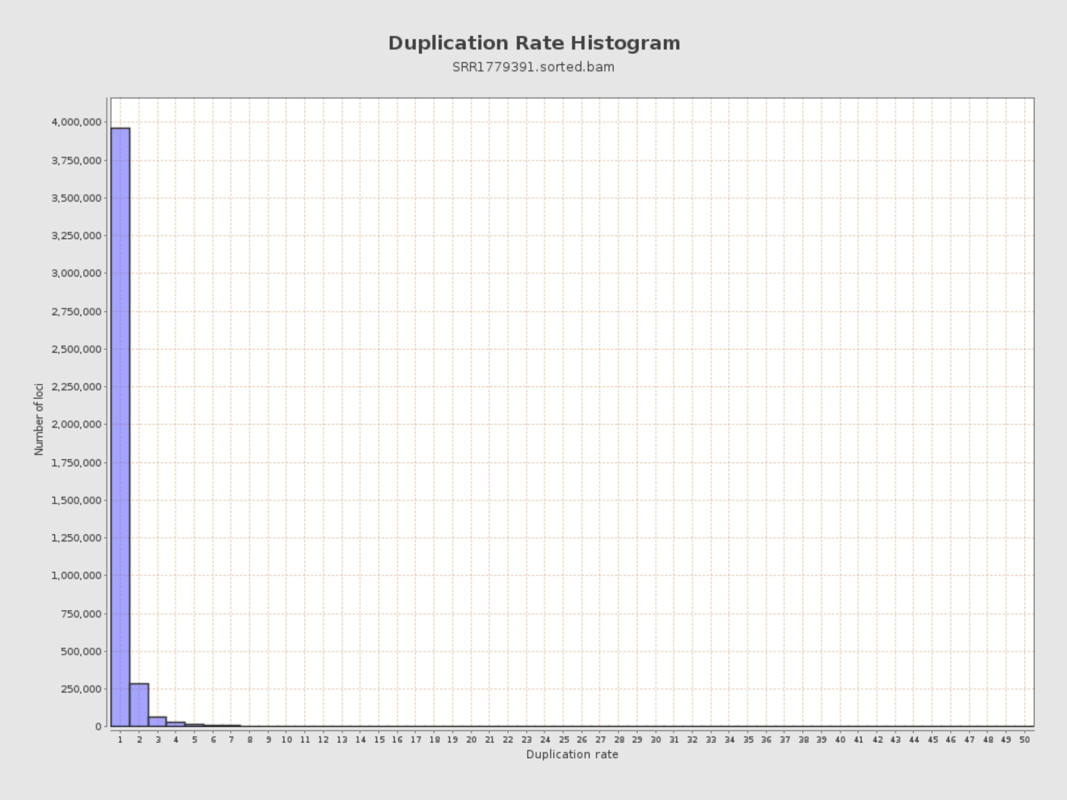
5. Results : Coverage Histogram (0-50X)



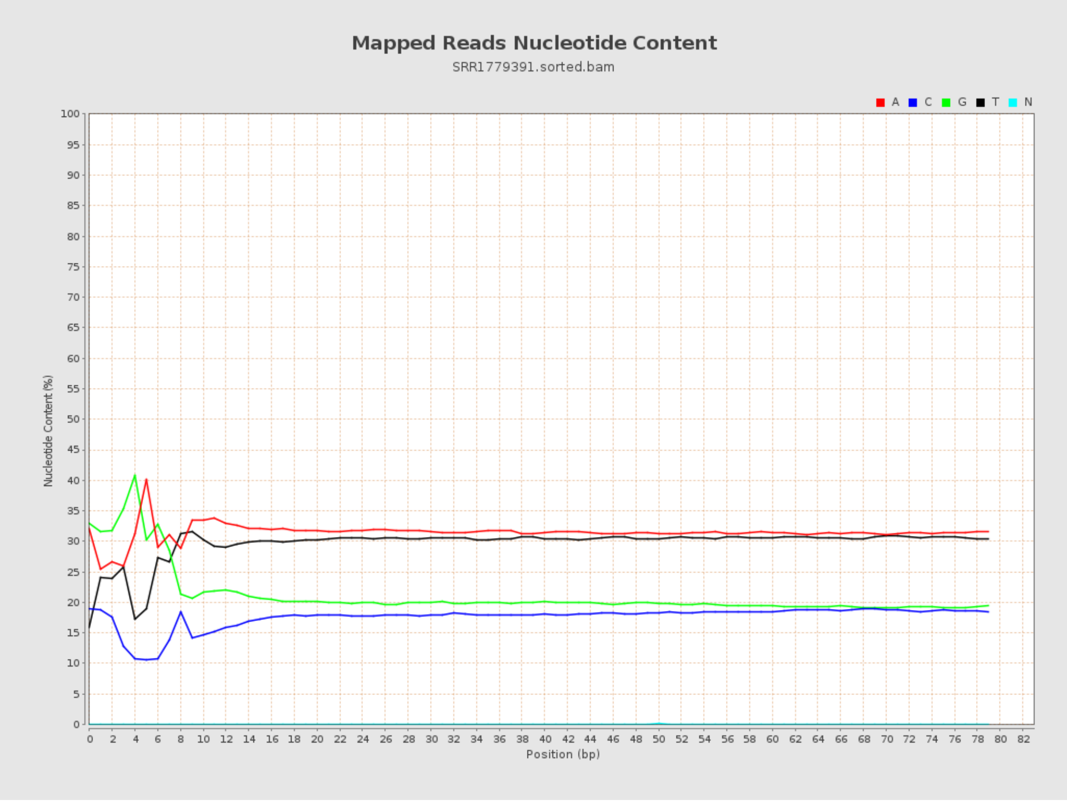
6. Results : Genome Fraction Coverage



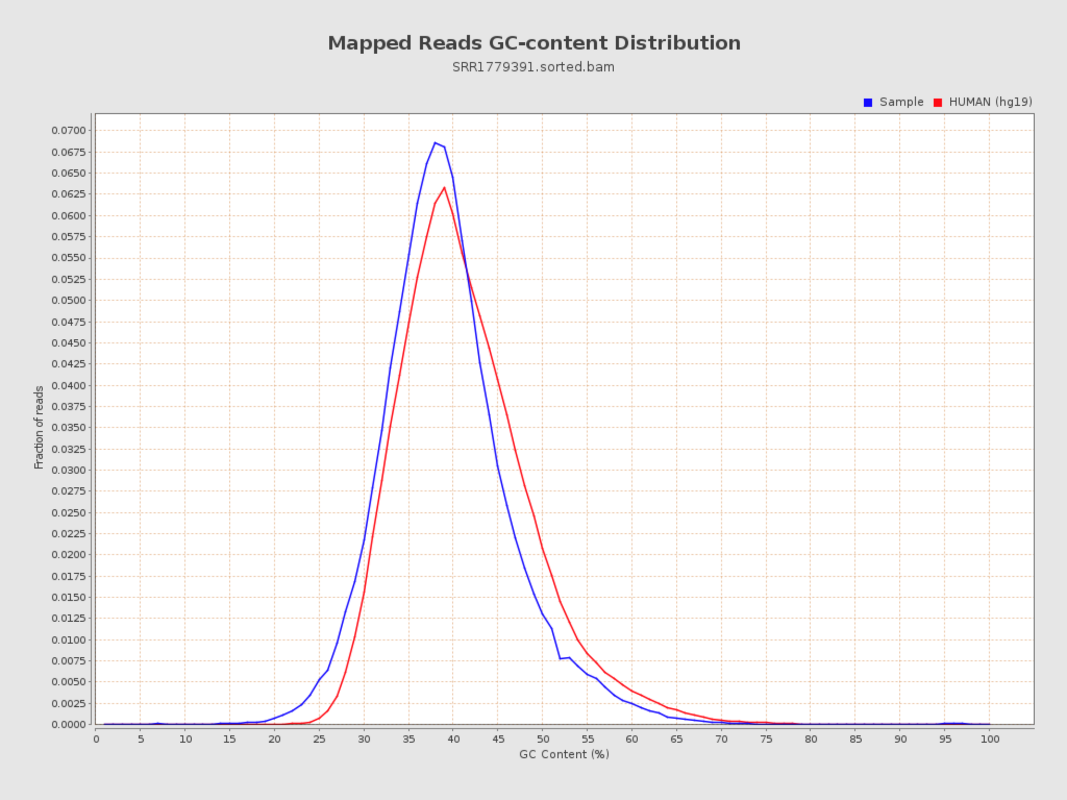
7. Results : Duplication Rate Histogram



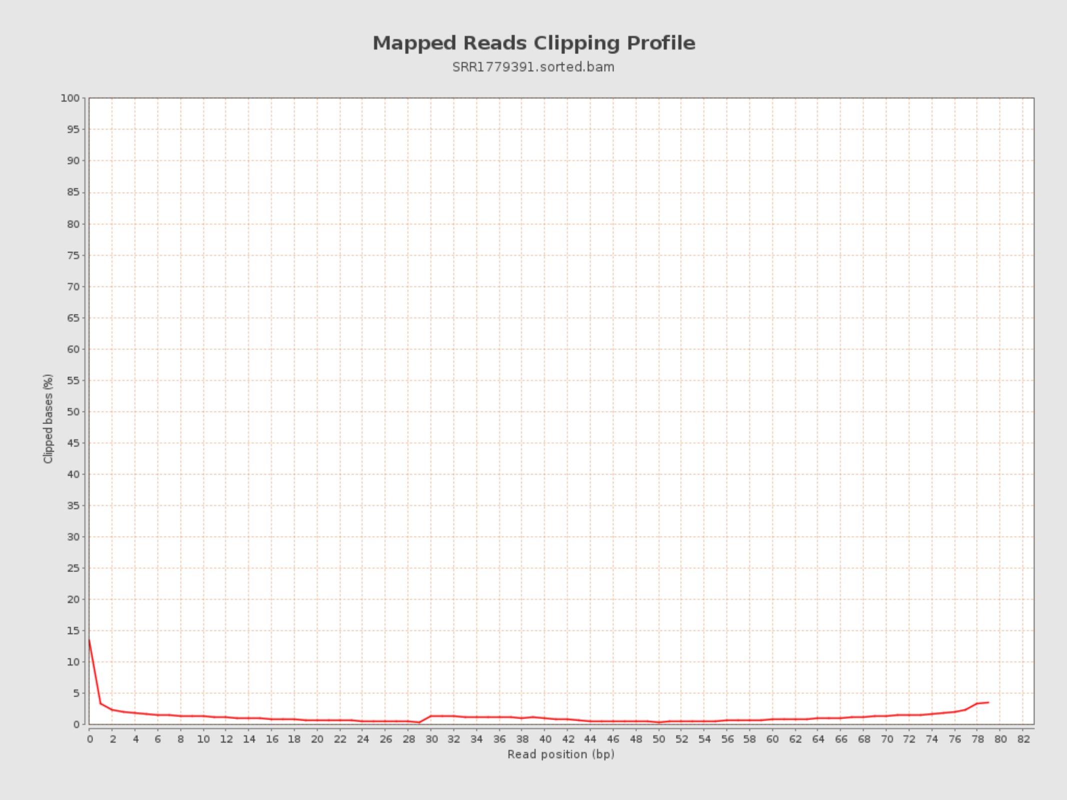
8. Results : Mapped Reads Nucleotide Content



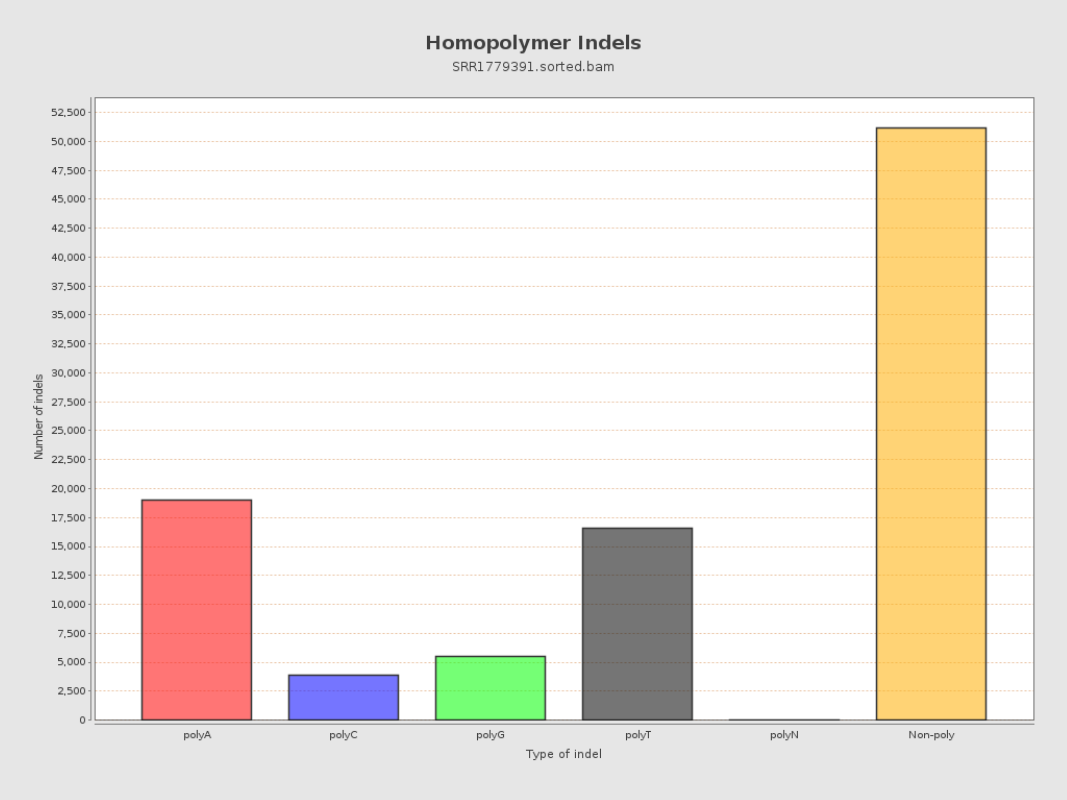
9. Results : Mapped Reads GC-content Distribution



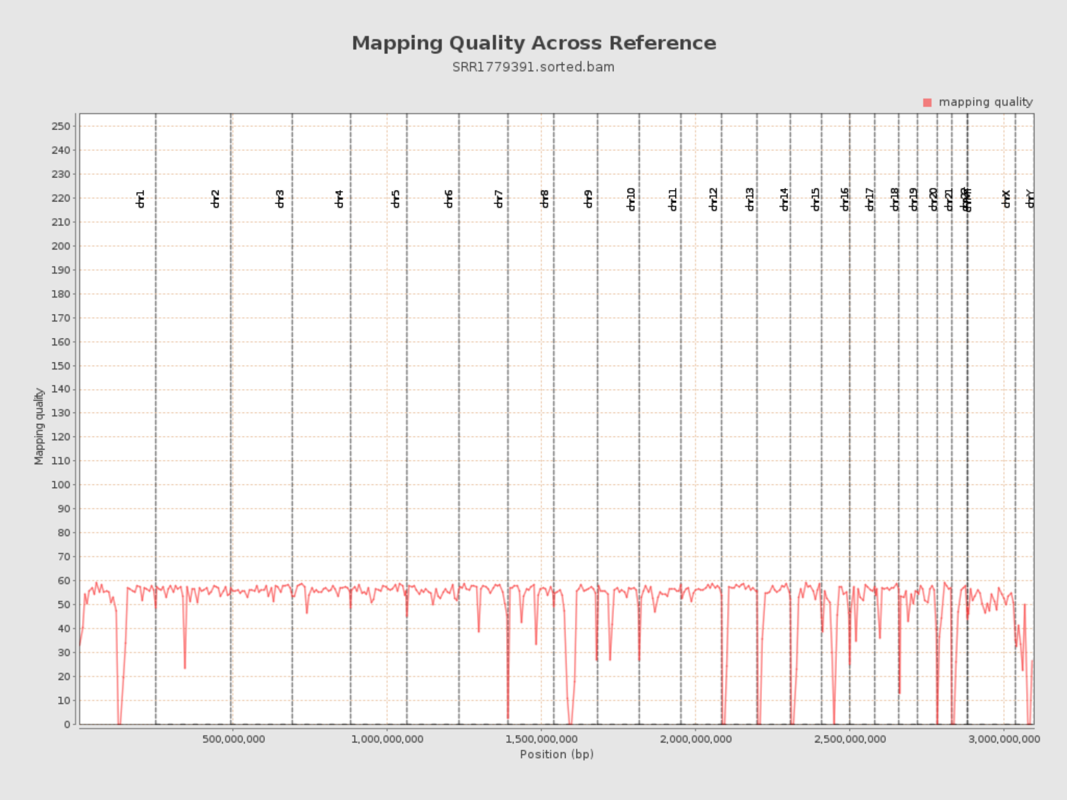
10. Results : Mapped Reads Clipping Profile



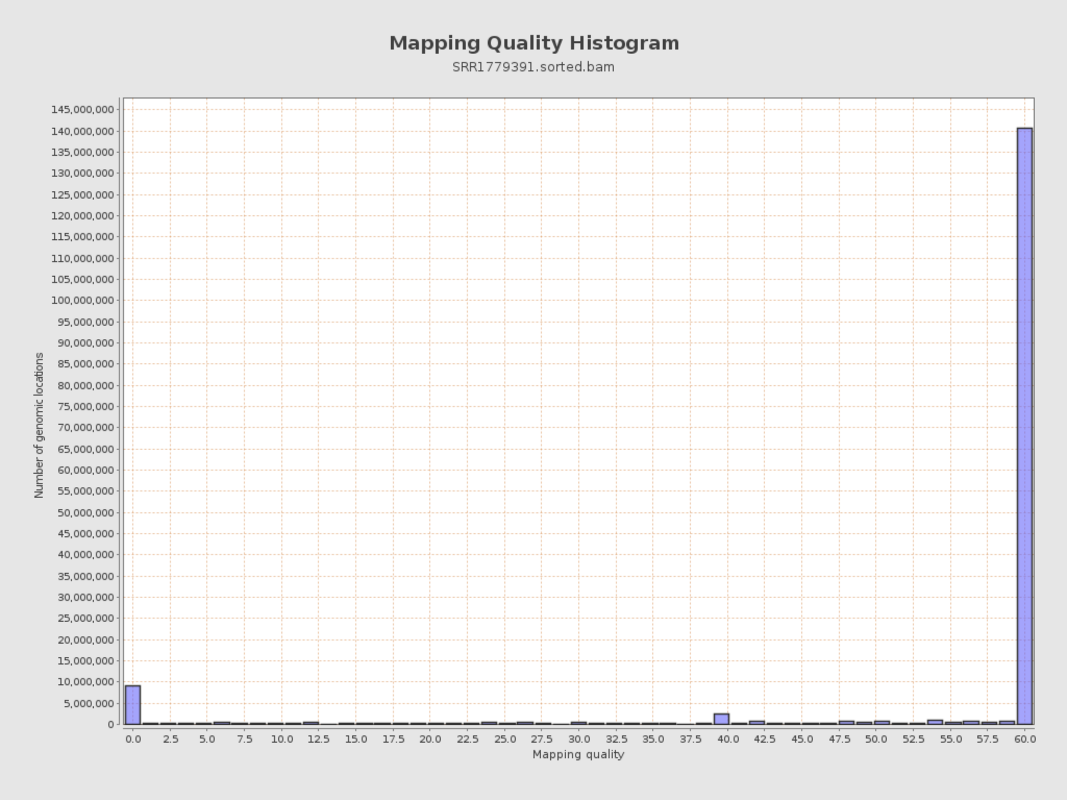
11. Results : Homopolymer Indels



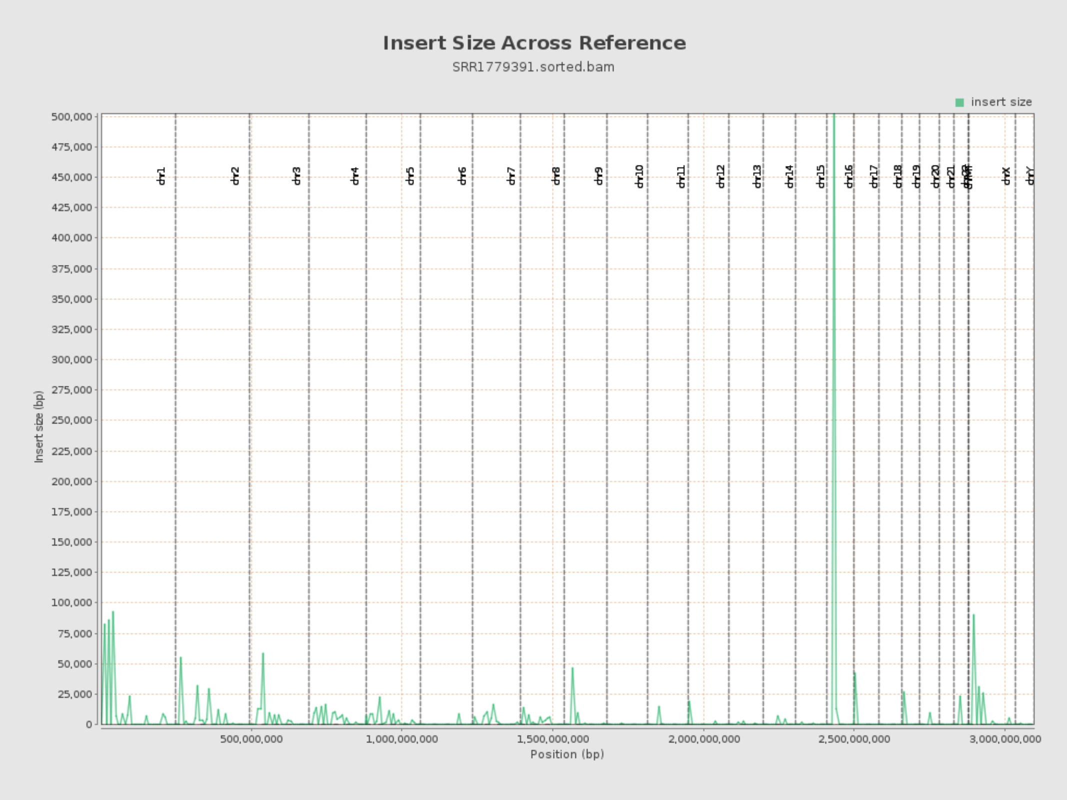
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram