Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 19:51:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779402.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_SRR1779402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779402_1.fastq.gz SRR1779402_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 19:51:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,499,320
Mapped reads	14,888,106 / 96.06%
Unmapped reads	611,214 / 3.94%
Mapped paired reads	14,888,106 / 96.06%
Mapped reads, first in pair	7,487,294 / 48.31%
Mapped reads, second in pair	7,400,812 / 47.75%
Mapped reads, both in pair	14,765,620 / 95.27%
Mapped reads, singletons	122,486 / 0.79%
Secondary alignments	0
Supplementary alignments	49,405 / 0.32%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	522,742 / 3.37%
Duplication rate	3.26%
Clipped reads	672,471 / 4.34%

2.2. ACGT Content

Number/percentage of A's	356,800,243 / 30.17%
Number/percentage of C's	235,334,428 / 19.9%
Number/percentage of T's	349,502,846 / 29.56%
Number/percentage of G's	240,565,283 / 20.34%
Number/percentage of N's	264,139 / 0.02%

GC Percentage	40.25%

2.3. Coverage

Mean	0.3821
Standard Deviation	1.2956

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Insert size

Mean	248,463.89
Standard Deviation	4,749,466.43
P25/Median/P75	139 / 182 / 230

2.6. Mismatches and indels

General error rate	0.33%
Mismatches	3,672,992
Insertions	108,997
Mapped reads with at least one insertion	0.72%
Deletions	131,461
Mapped reads with at least one deletion	0.87%
Homopolymer indels	47.04%

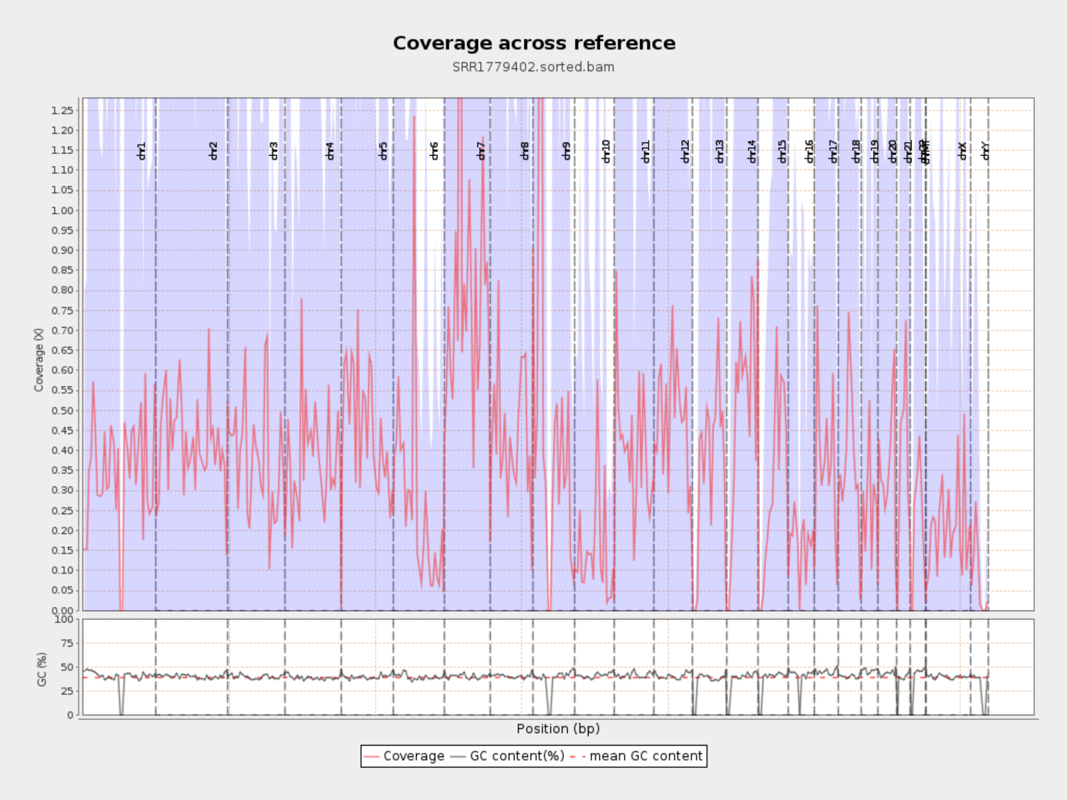
2.7. Chromosome stats

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

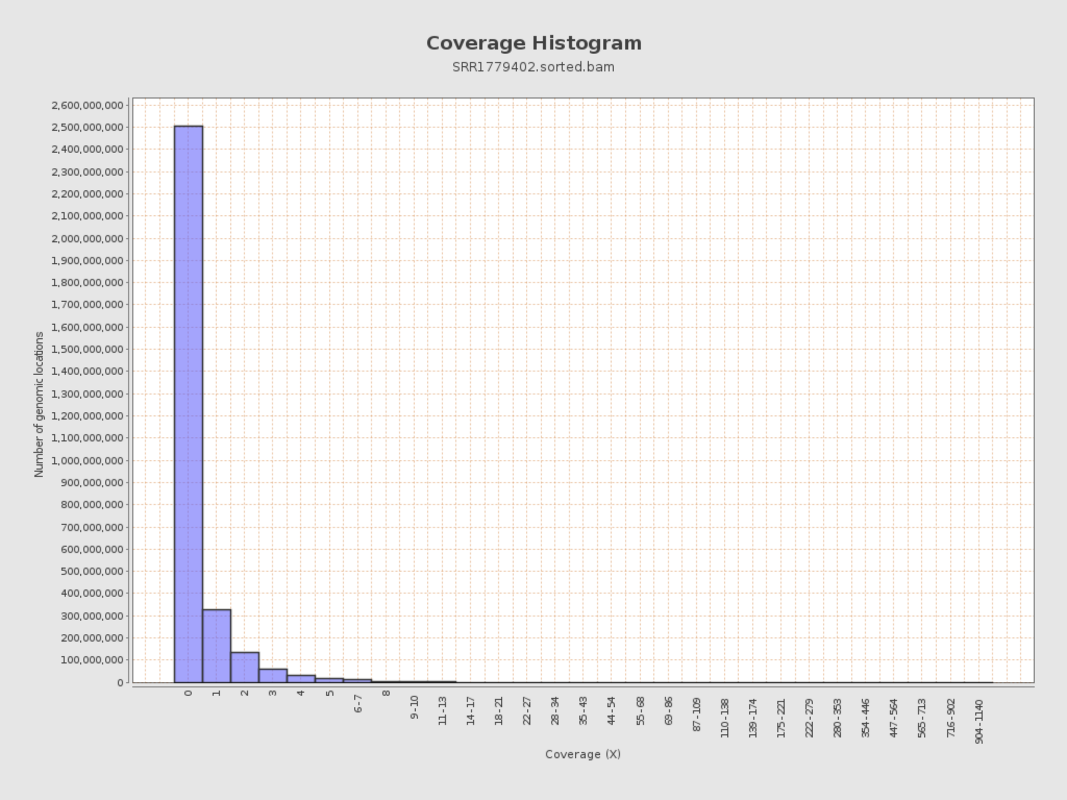
		bases	coverage	deviation
chr1	249250621	86097711	0.3454	1.5161
chr2	243199373	102257864	0.4205	1.0763
chr3	198022430	75426411	0.3809	1.0342
chr4	191154276	73384524	0.3839	0.9735
chr5	180915260	82461423	0.4558	1.1211
chr6	171115067	45708731	0.2671	1.0465
chr7	159138663	139082670	0.874	3.0161
chr8	146364022	63733391	0.4354	1.0928
chr9	141213431	67743448	0.4797	1.5639
chr10	135534747	20225398	0.1492	1.3007
chr11	135006516	54474047	0.4035	1.0688
chr12	133851895	64092546	0.4788	1.1401
chr13	115169878	41752513	0.3625	0.9593
chr14	107349540	52000966	0.4844	1.1906
chr15	102531392	31774706	0.3099	0.9783
chr16	90354753	14968362	0.1657	0.6567
chr17	81195210	31375155	0.3864	1.278
chr18	78077248	29452743	0.3772	1.0555
chr19	59128983	15526420	0.2626	1.0762
chr20	63025520	24483268	0.3885	1.0629
chr21	48129895	17600564	0.3657	0.9873
chr22	51304566	11623621	0.2266	0.8302
chrMT	16571	1114	0.0672	0.4878
chrX	155270560	32524326	0.2095	0.7631

chrY	59373566	4973052	0.0838	0.4158

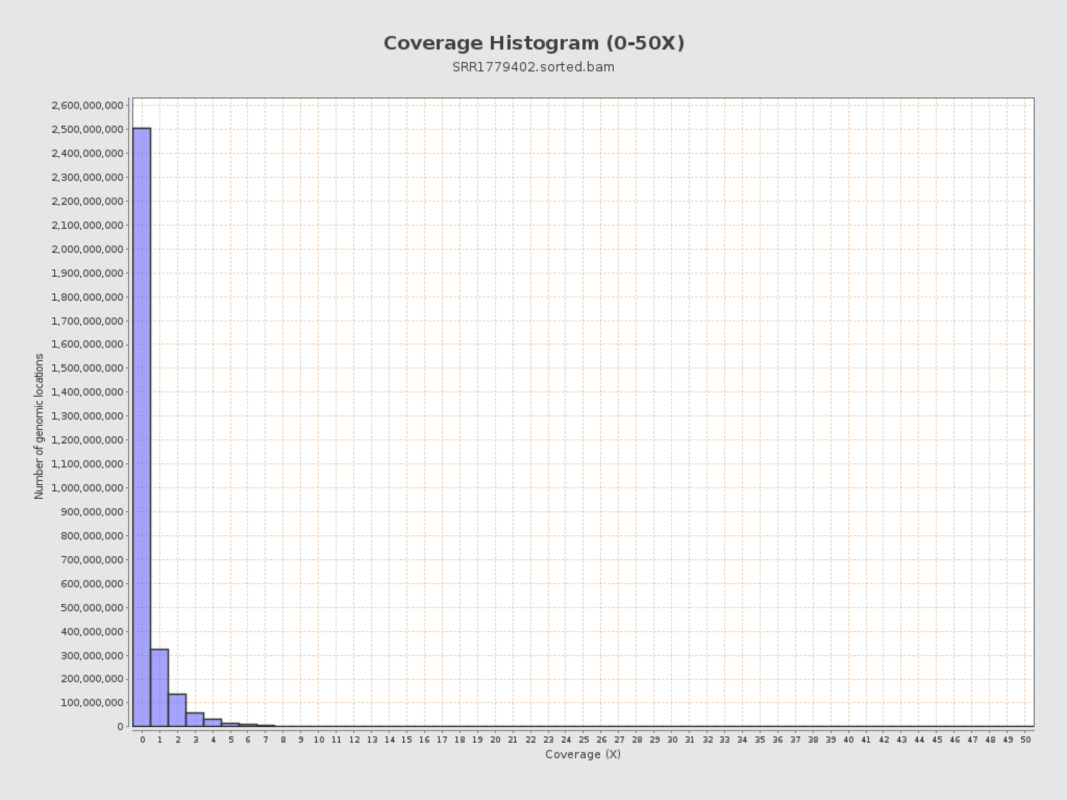
3. Results : Coverage across reference



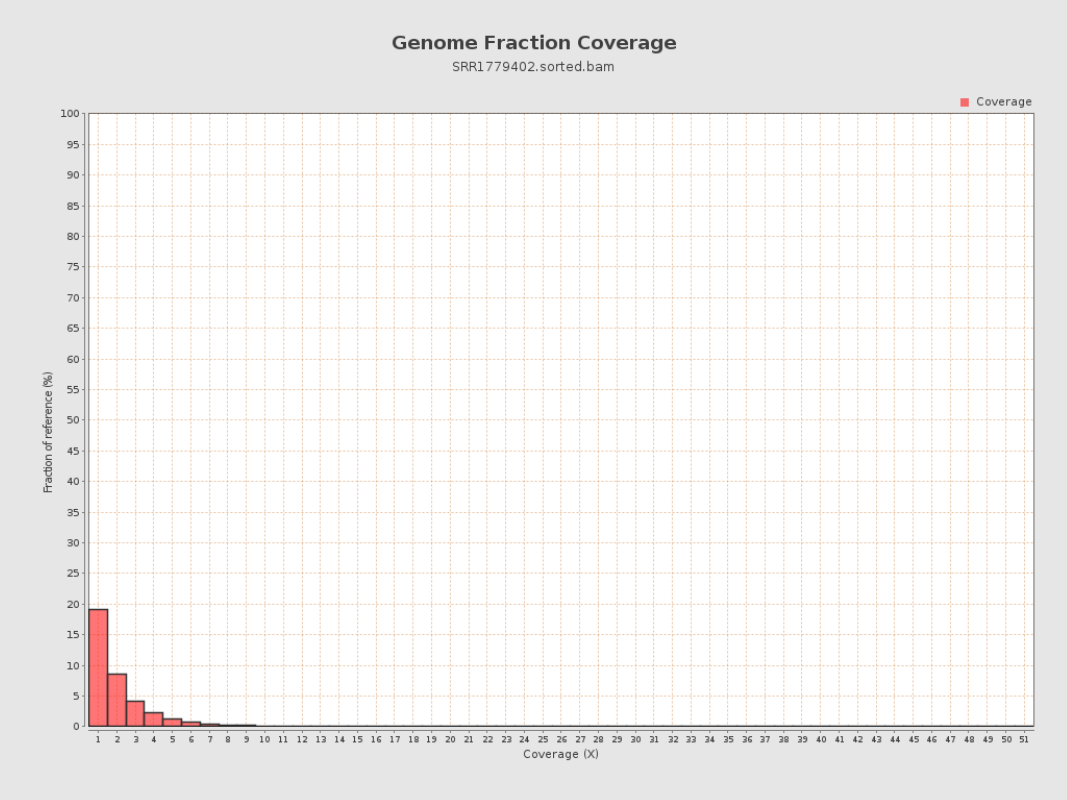
4. Results : Coverage Histogram



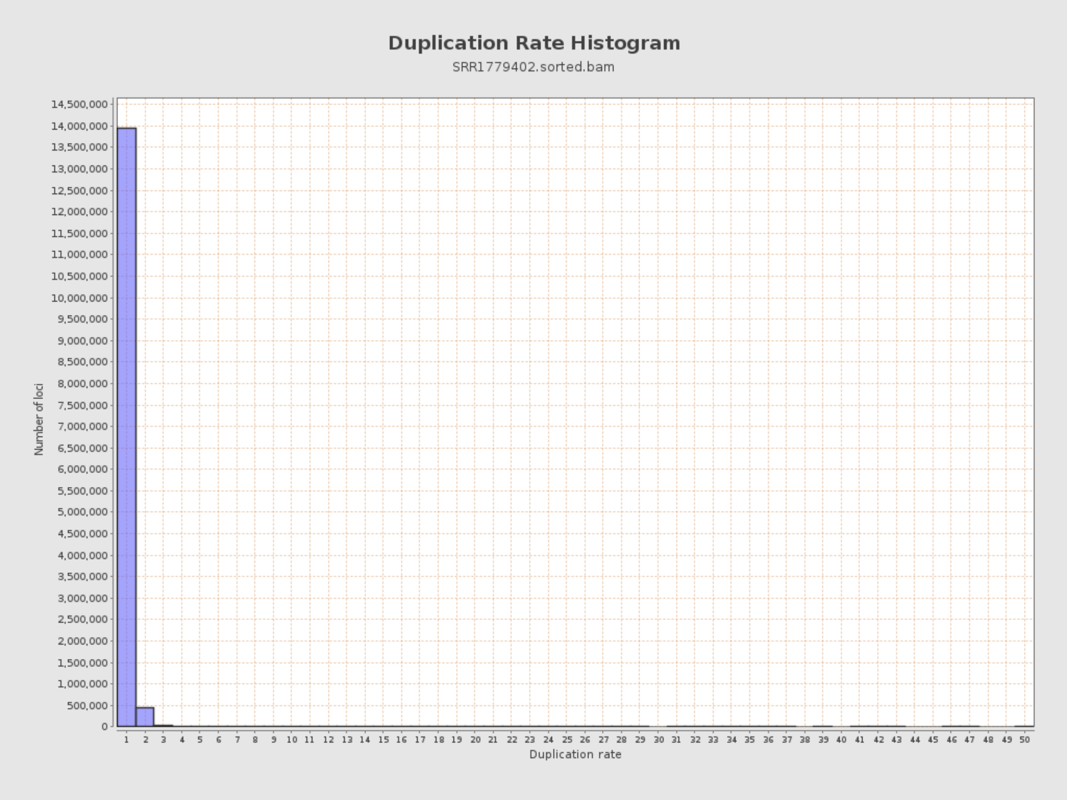
5. Results : Coverage Histogram (0-50X)



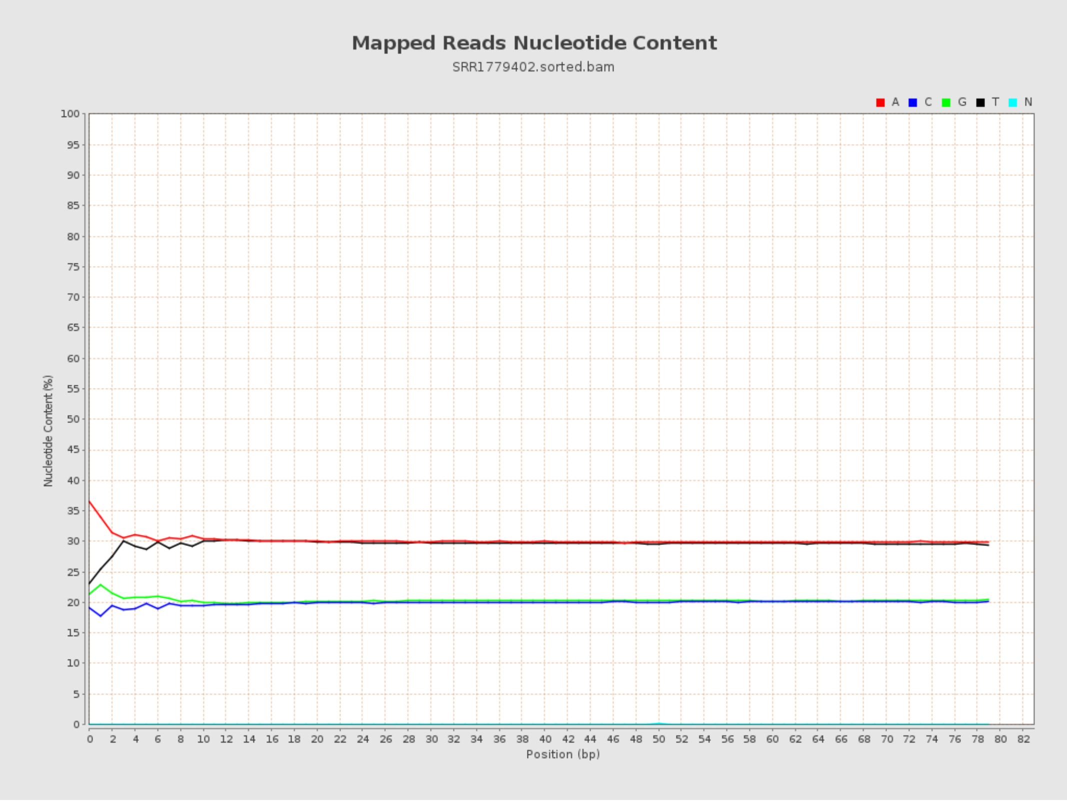
6. Results : Genome Fraction Coverage



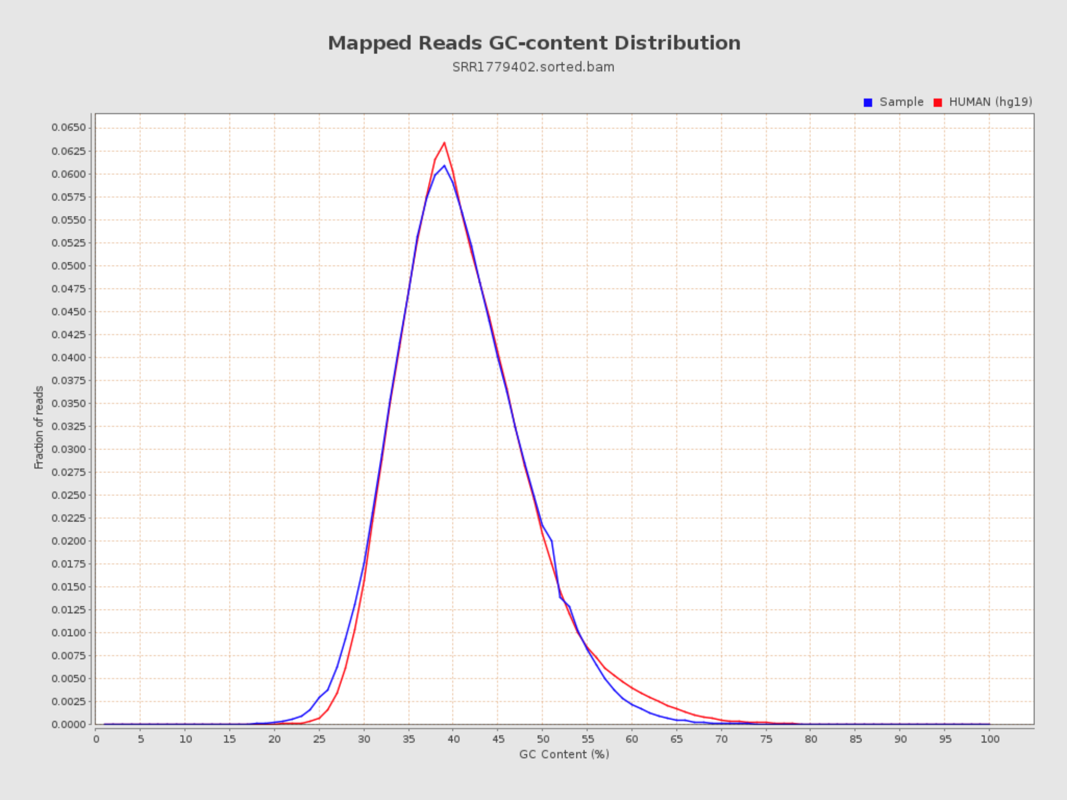
7. Results : Duplication Rate Histogram



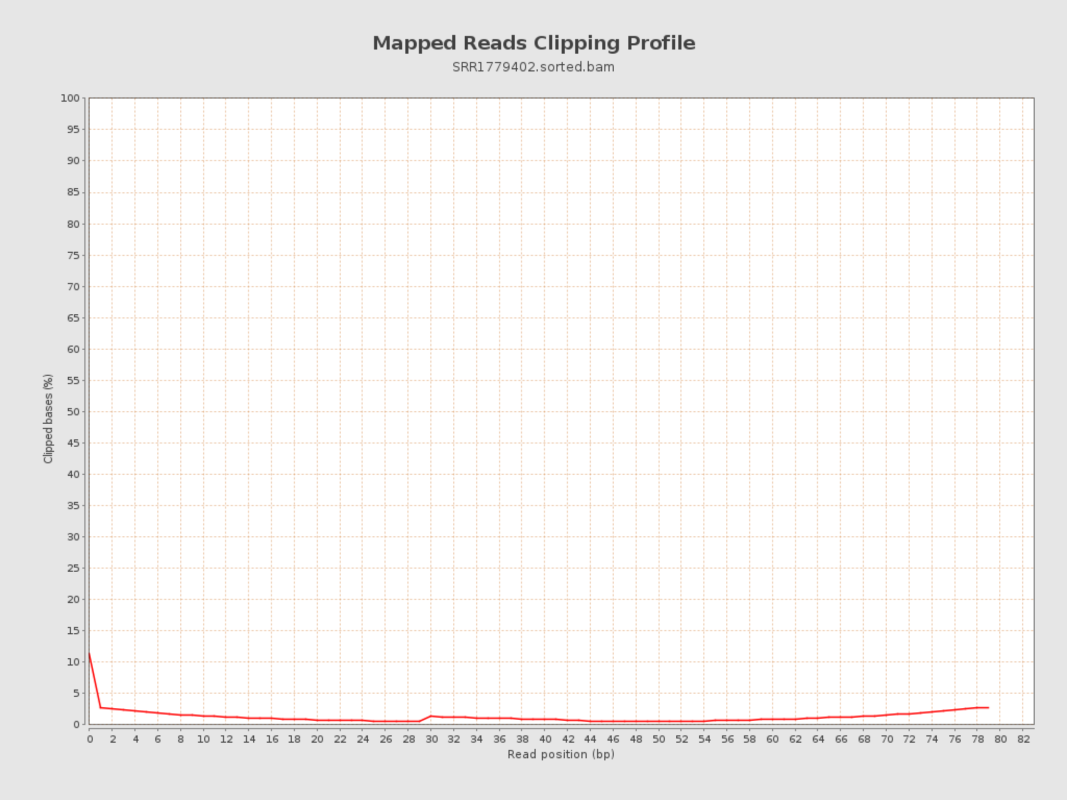
8. Results : Mapped Reads Nucleotide Content



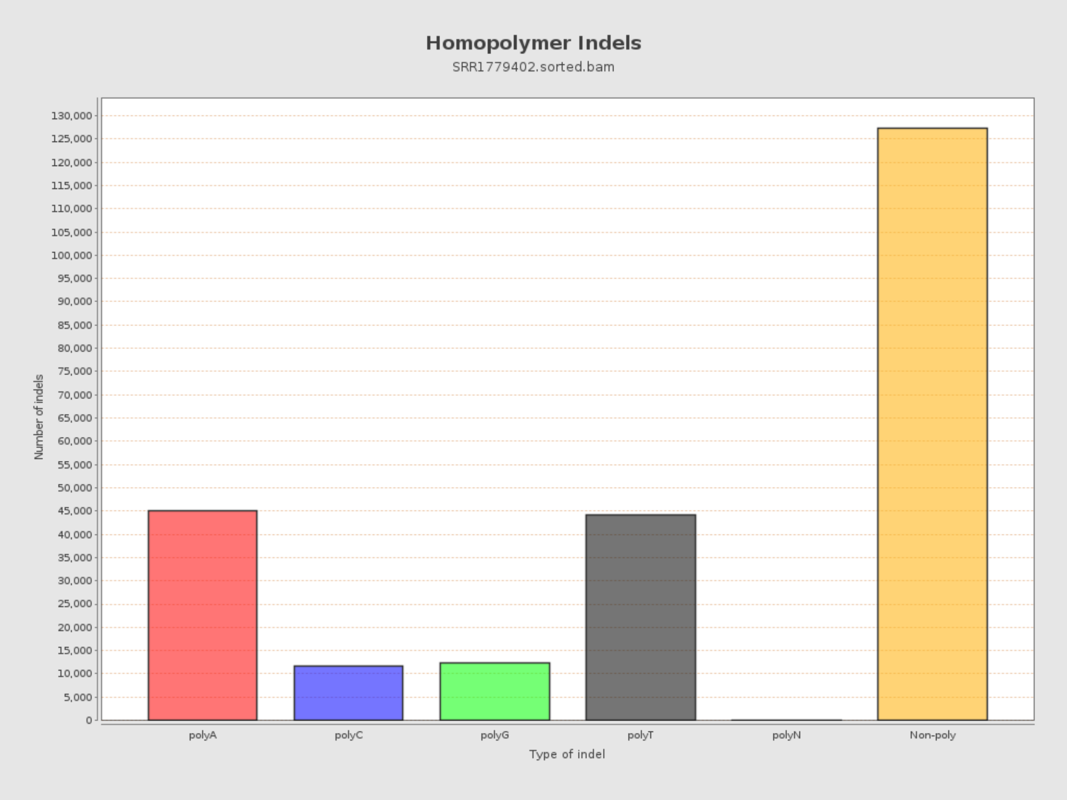
9. Results : Mapped Reads GC-content Distribution



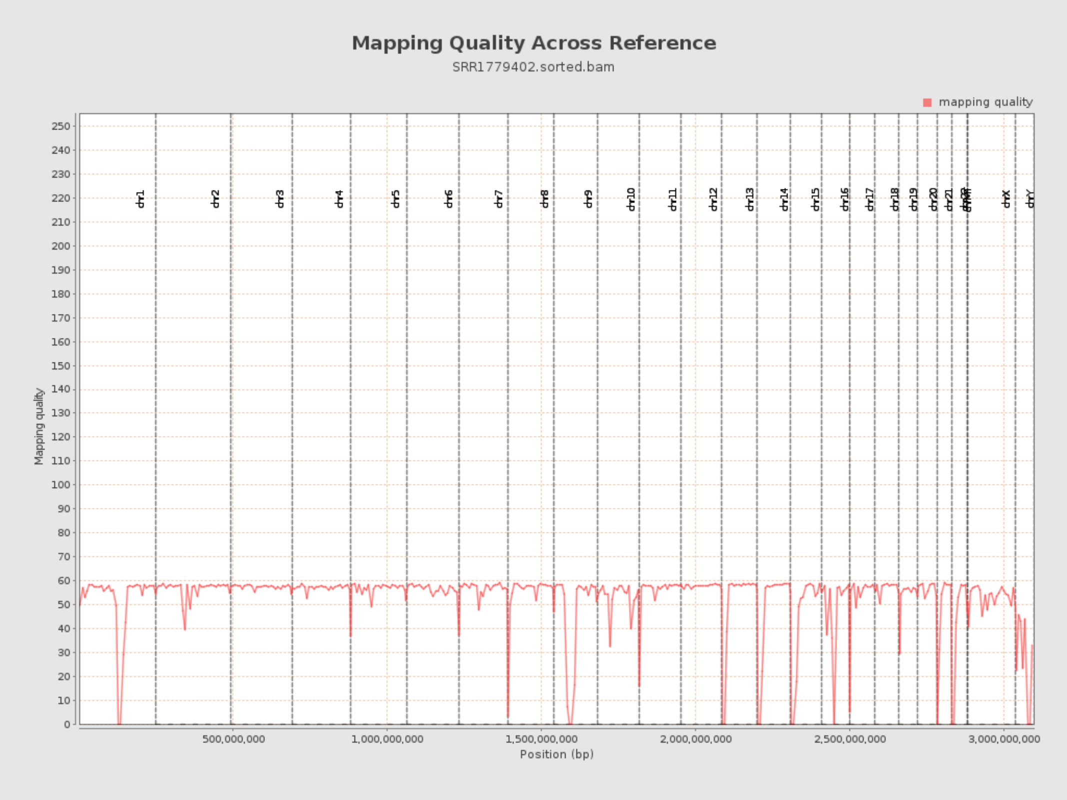
10. Results : Mapped Reads Clipping Profile



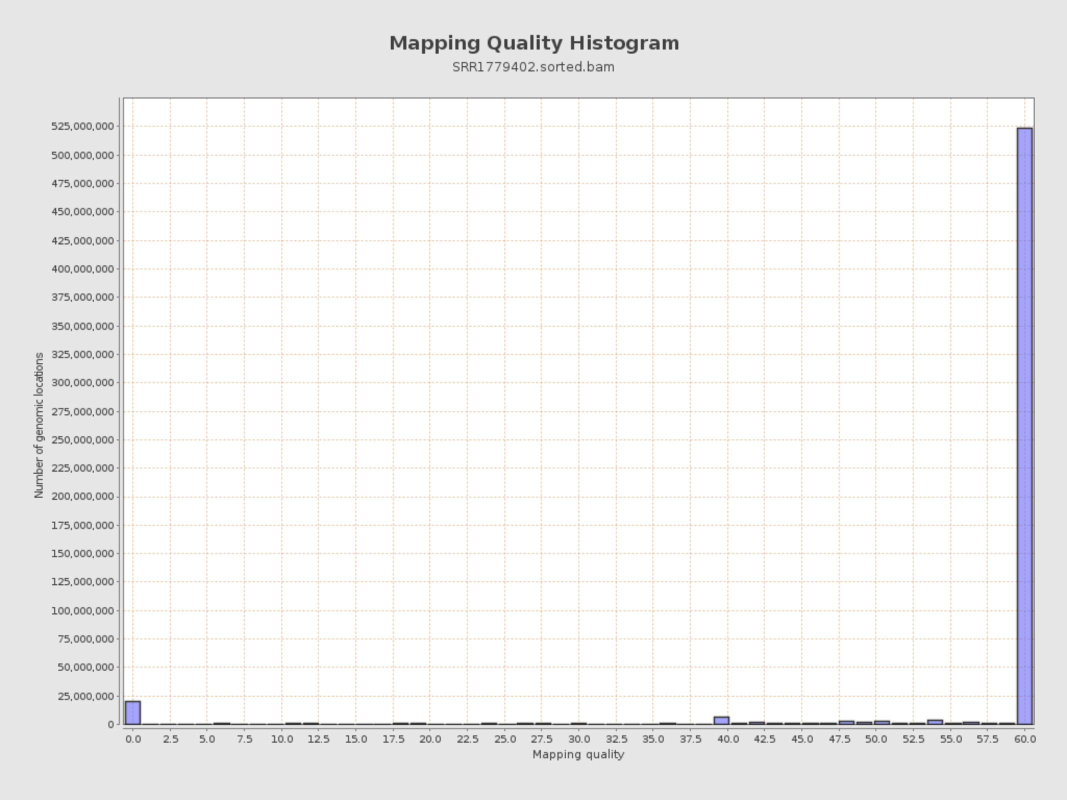
11. Results : Homopolymer Indels



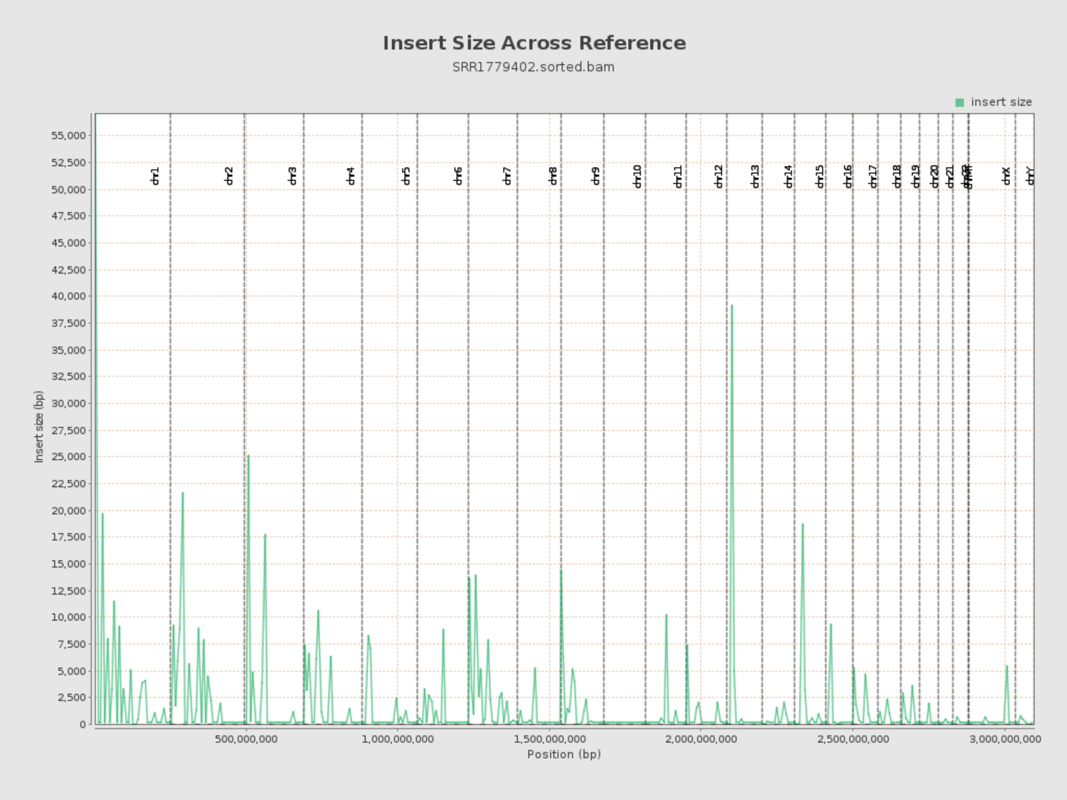
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram