Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 02:09:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779422.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_SRR1779422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779422_1.fastq.gz SRR1779422_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 02:09:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,913,238
Mapped reads	13,224,381 / 95.05%
Unmapped reads	688,857 / 4.95%
Mapped paired reads	13,224,381 / 95.05%
Mapped reads, first in pair	6,672,364 / 47.96%
Mapped reads, second in pair	6,552,017 / 47.09%
Mapped reads, both in pair	13,068,694 / 93.93%
Mapped reads, singletons	155,687 / 1.12%
Secondary alignments	0
Supplementary alignments	59,109 / 0.42%
Read min/max/mean length	30 / 80 / 80.15
Duplicated reads (estimated)	692,335 / 4.98%
Duplication rate	4.35%
Clipped reads	599,470 / 4.31%

2.2. ACGT Content

Number/percentage of A's	326,881,982 / 31.11%
Number/percentage of C's	198,126,281 / 18.85%
Number/percentage of T's	321,692,941 / 30.61%
Number/percentage of G's	203,960,986 / 19.41%
Number/percentage of N's	231,841 / 0.02%

GC Percentage	38.26%

2.3. Coverage

Mean	0.3395
Standard Deviation	2.375

2.4. Mapping Quality

Mean Mapping Quality	52.94

2.5. Insert size

Mean	61,881.27
Standard Deviation	2,309,479.1
P25/Median/P75	159 / 201 / 254

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,989,787
Insertions	98,168
Mapped reads with at least one insertion	0.74%
Deletions	110,356
Mapped reads with at least one deletion	0.82%
Homopolymer indels	46.93%

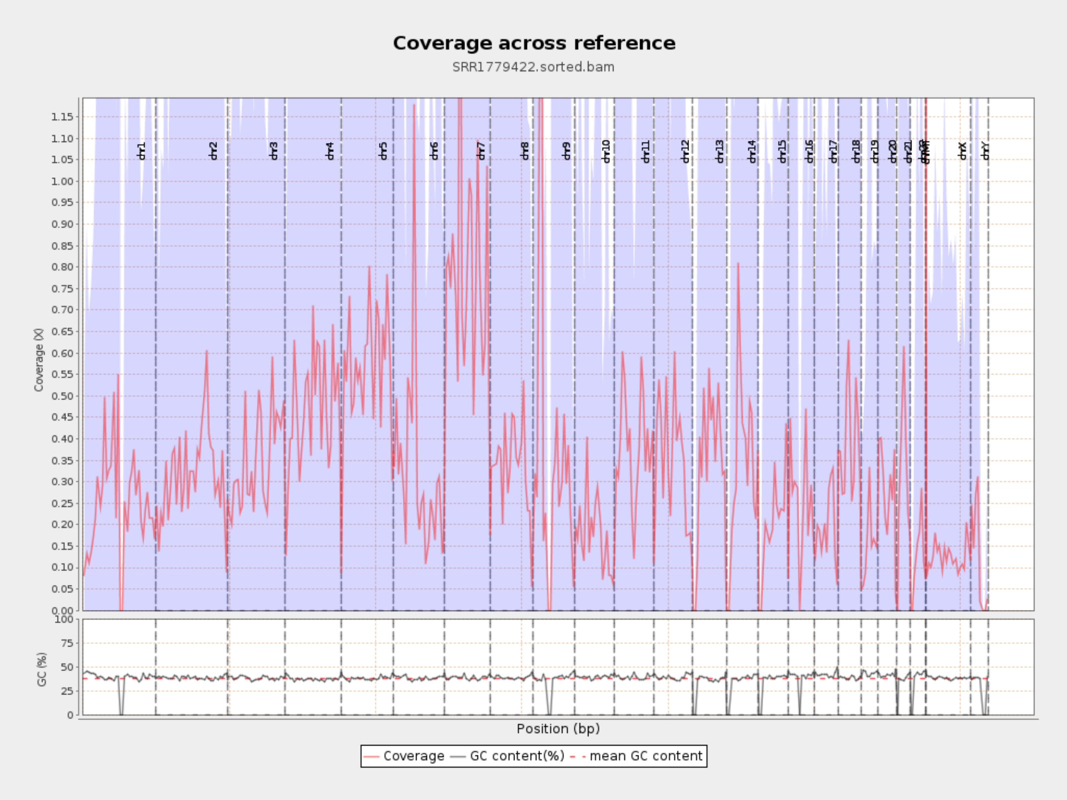
2.7. Chromosome stats

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

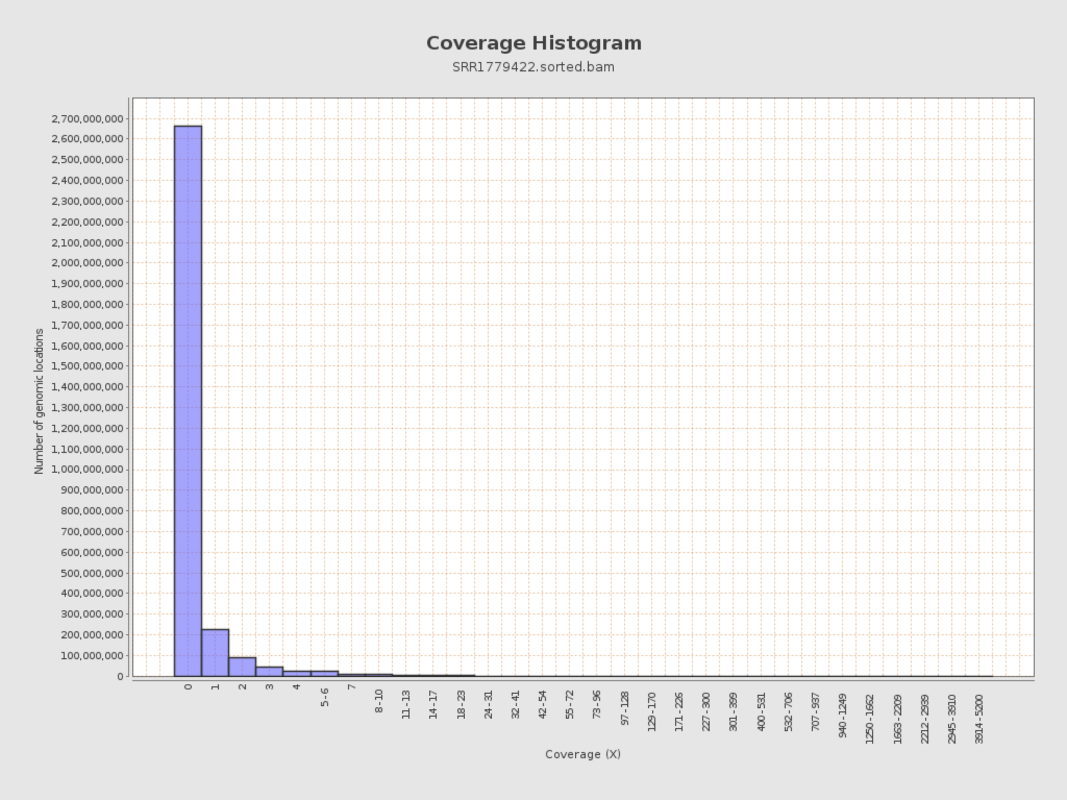
		bases	coverage	deviation
chr1	249250621	61823735	0.248	5.4198
chr2	243199373	77300009	0.3178	1.325
chr3	198022430	68228734	0.3446	1.4168
chr4	191154276	89175161	0.4665	1.6213
chr5	180915260	102259877	0.5652	1.6427
chr6	171115067	55745326	0.3258	1.5191
chr7	159138663	125235600	0.787	3.6739
chr8	146364022	49474889	0.338	1.2997
chr9	141213431	57233312	0.4053	1.9691
chr10	135534747	24021129	0.1772	4.1479
chr11	135006516	51150133	0.3789	1.451
chr12	133851895	47268073	0.3531	1.3316
chr13	115169878	39647874	0.3443	1.2561
chr14	107349540	36594754	0.3409	1.3776
chr15	102531392	20904365	0.2039	0.9165
chr16	90354753	22326928	0.2471	1.0949
chr17	81195210	16007329	0.1971	1.2434
chr18	78077248	30775610	0.3942	1.8892
chr19	59128983	9369661	0.1585	3.5659
chr20	63025520	18413048	0.2922	1.1757
chr21	48129895	14940860	0.3104	1.4563
chr22	51304566	6527035	0.1272	0.7929
chrMT	16571	27199	1.6414	1.5428
chrX	155270560	19375873	0.1248	0.714

chrY	59373566	7290190	0.1228	0.6803

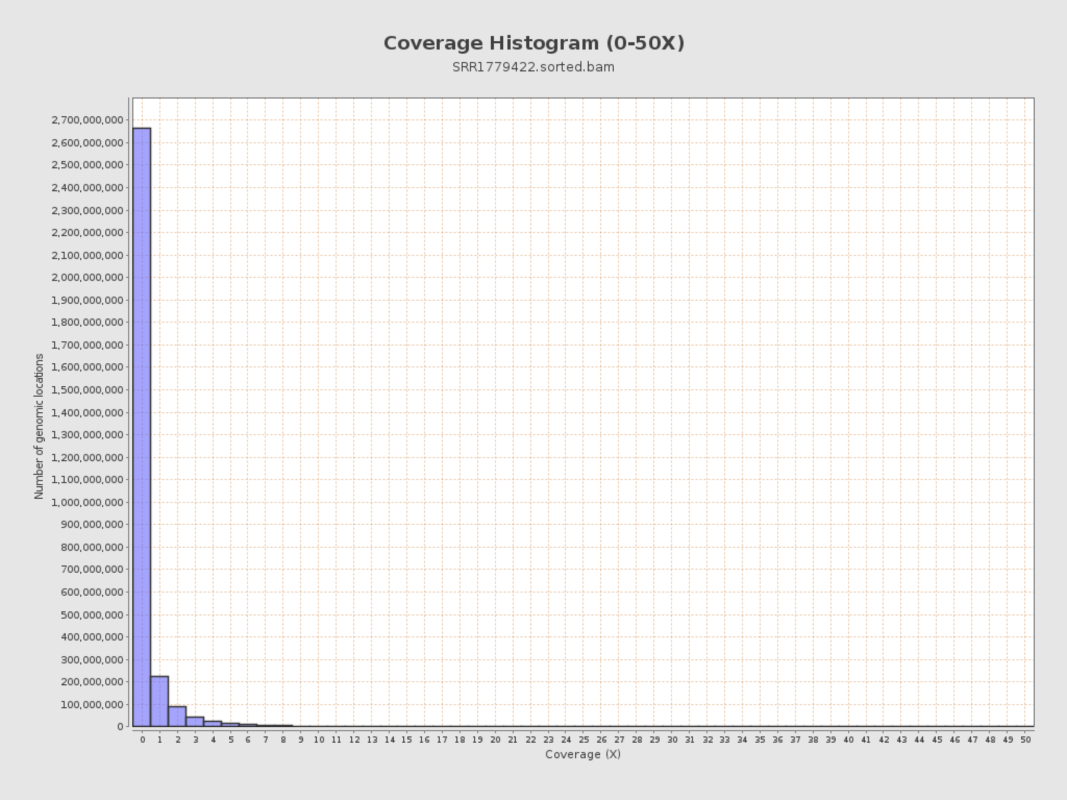
3. Results : Coverage across reference



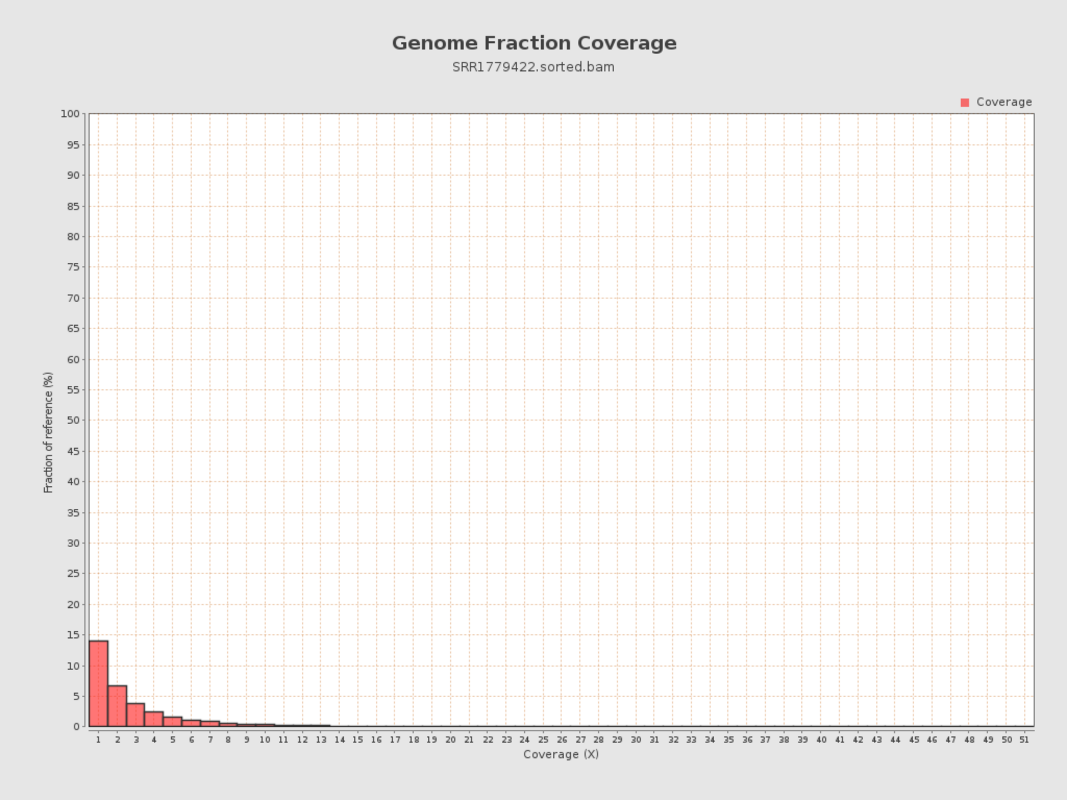
4. Results : Coverage Histogram



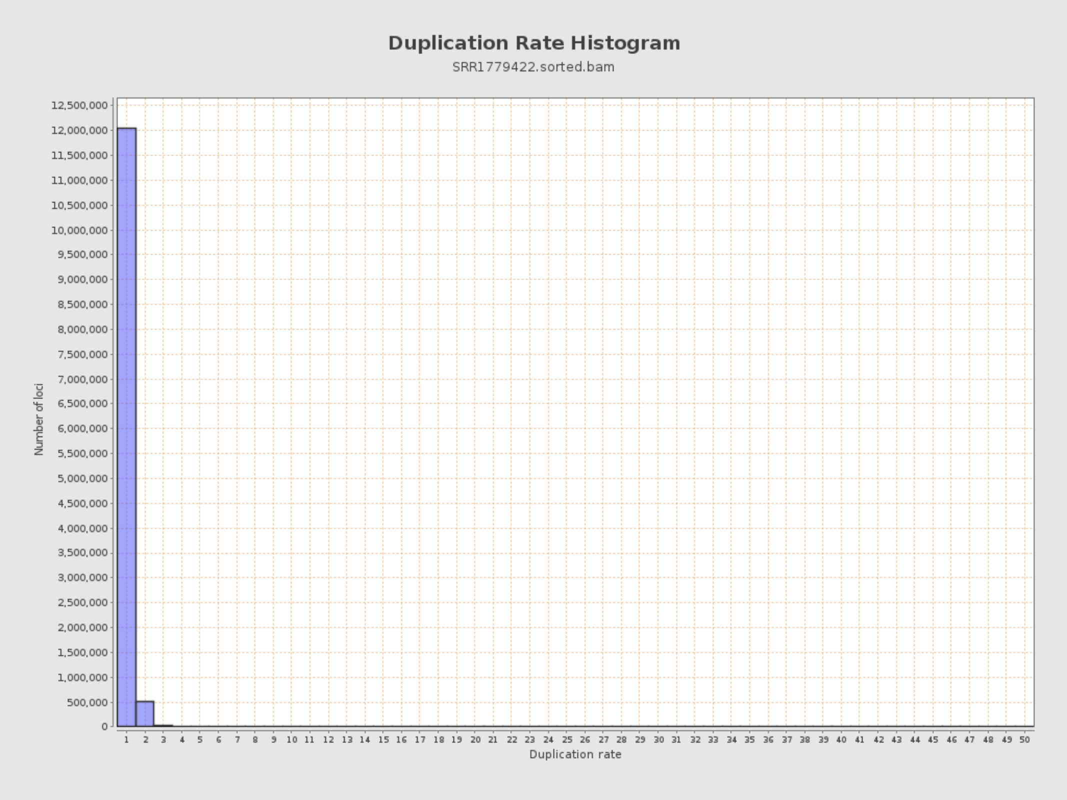
5. Results : Coverage Histogram (0-50X)



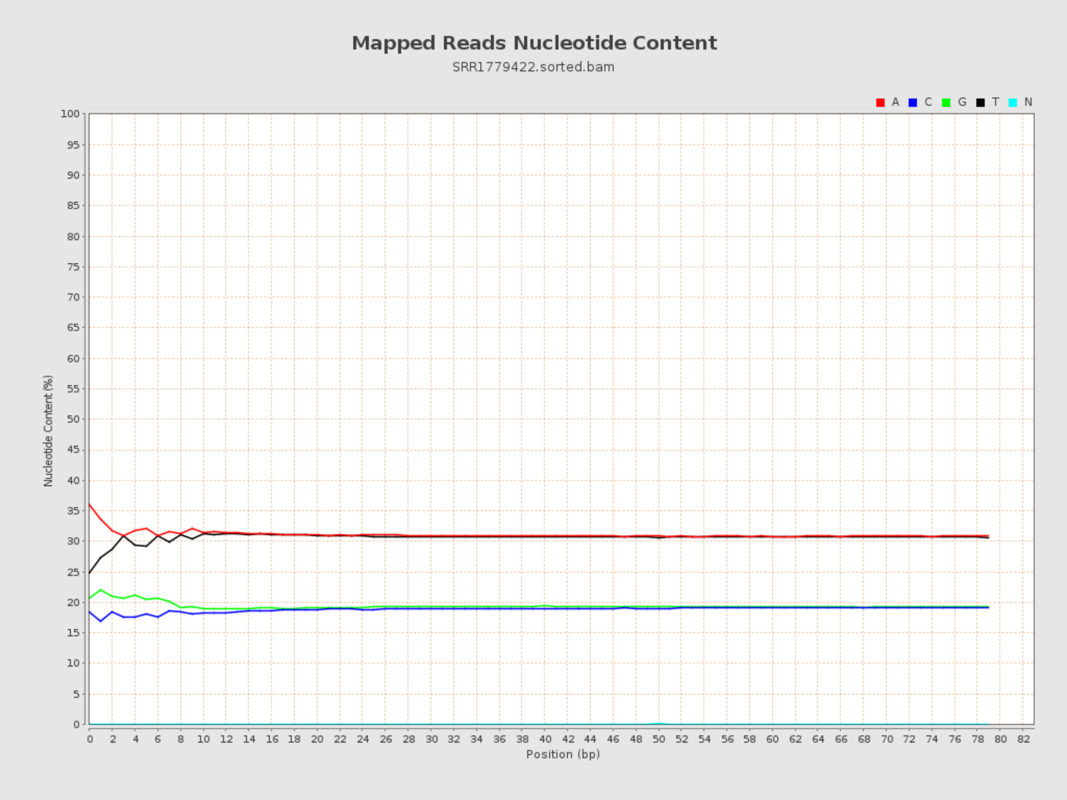
6. Results : Genome Fraction Coverage



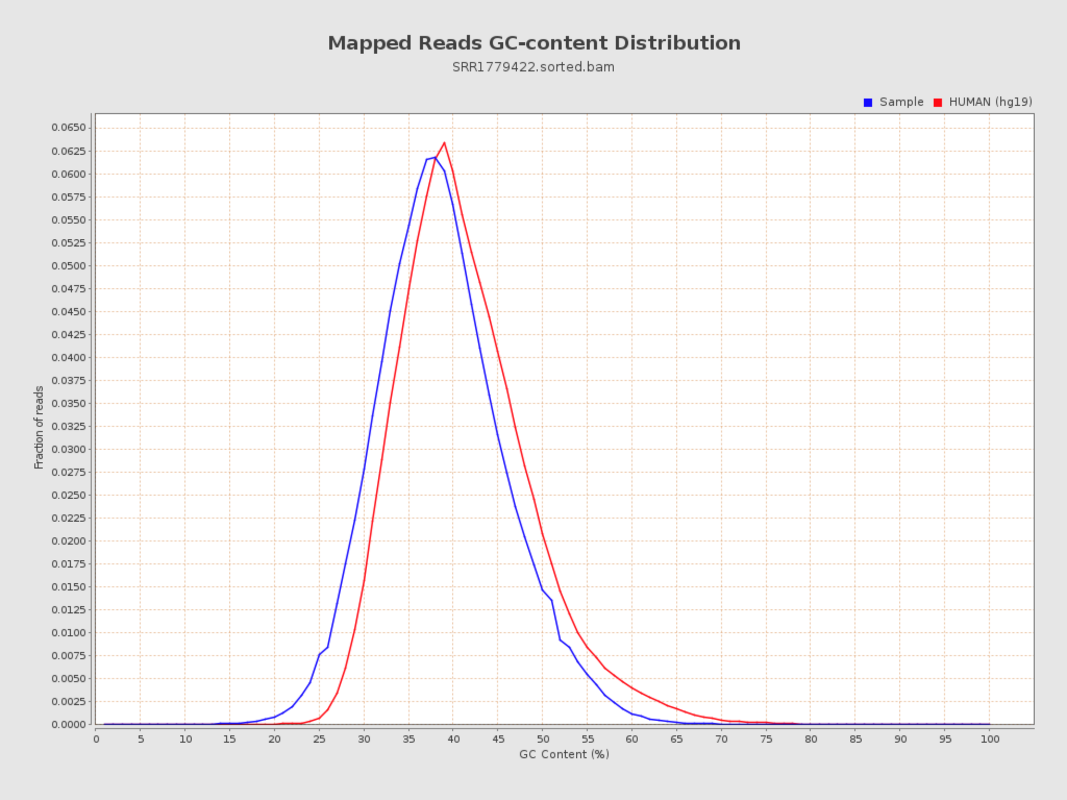
7. Results : Duplication Rate Histogram



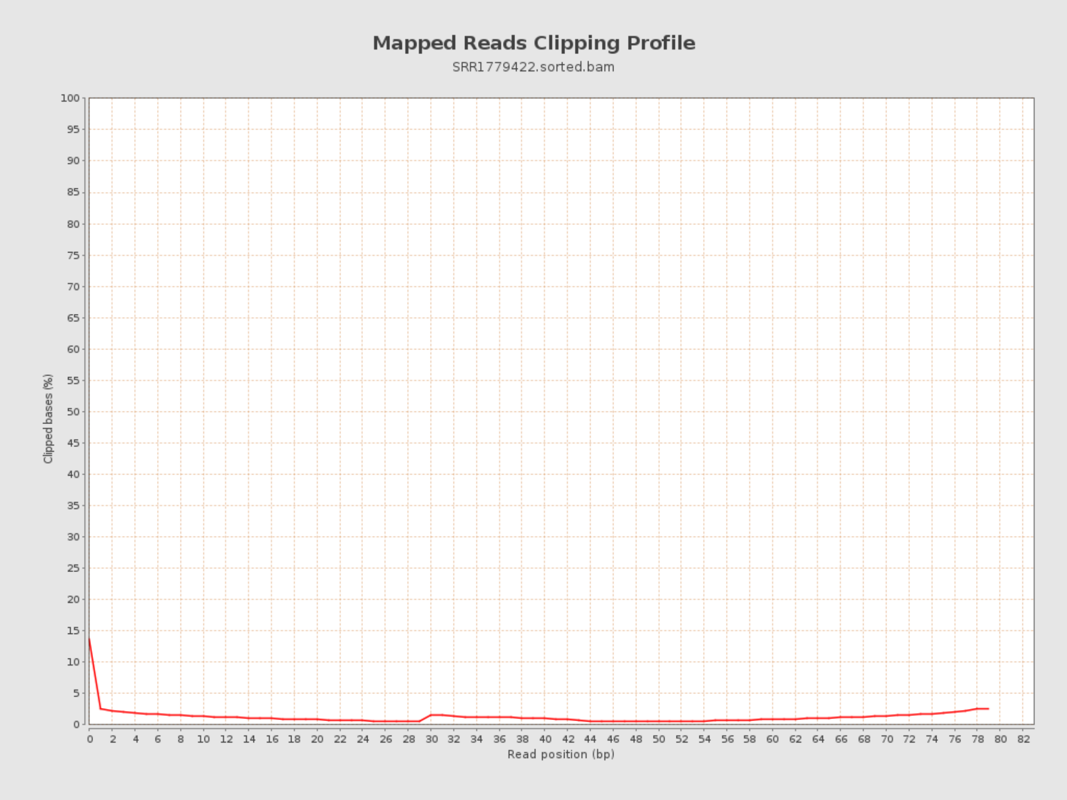
8. Results : Mapped Reads Nucleotide Content



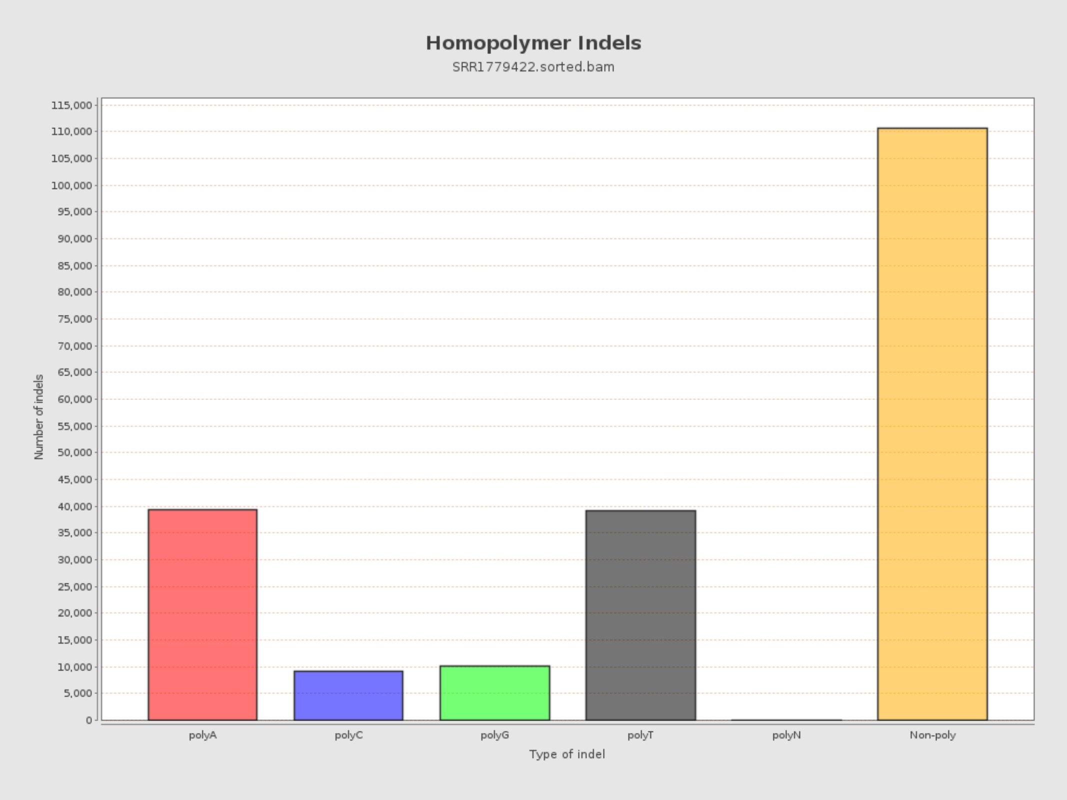
9. Results : Mapped Reads GC-content Distribution



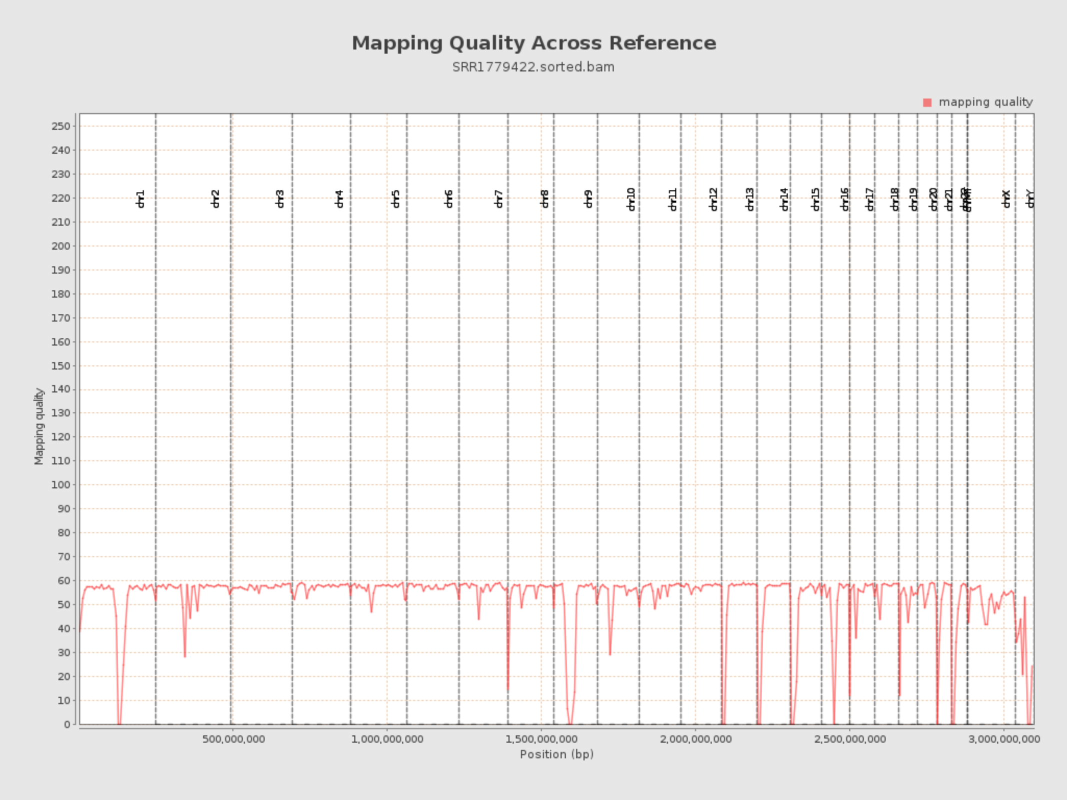
10. Results : Mapped Reads Clipping Profile



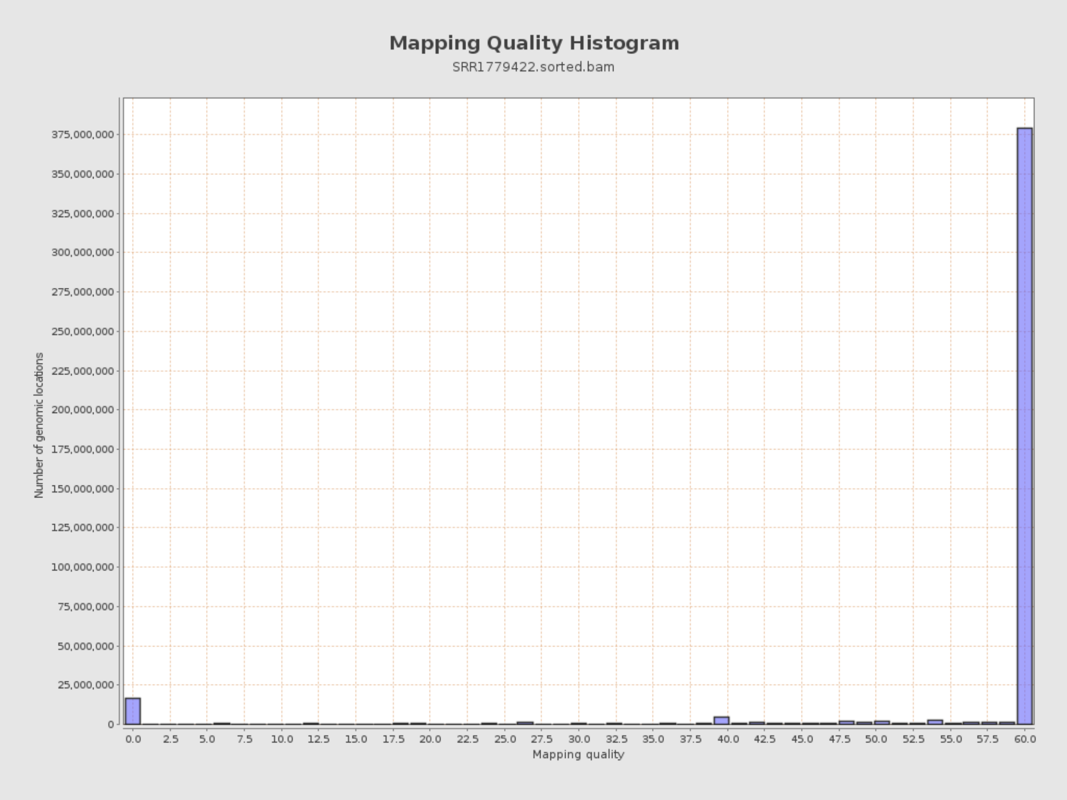
11. Results : Homopolymer Indels



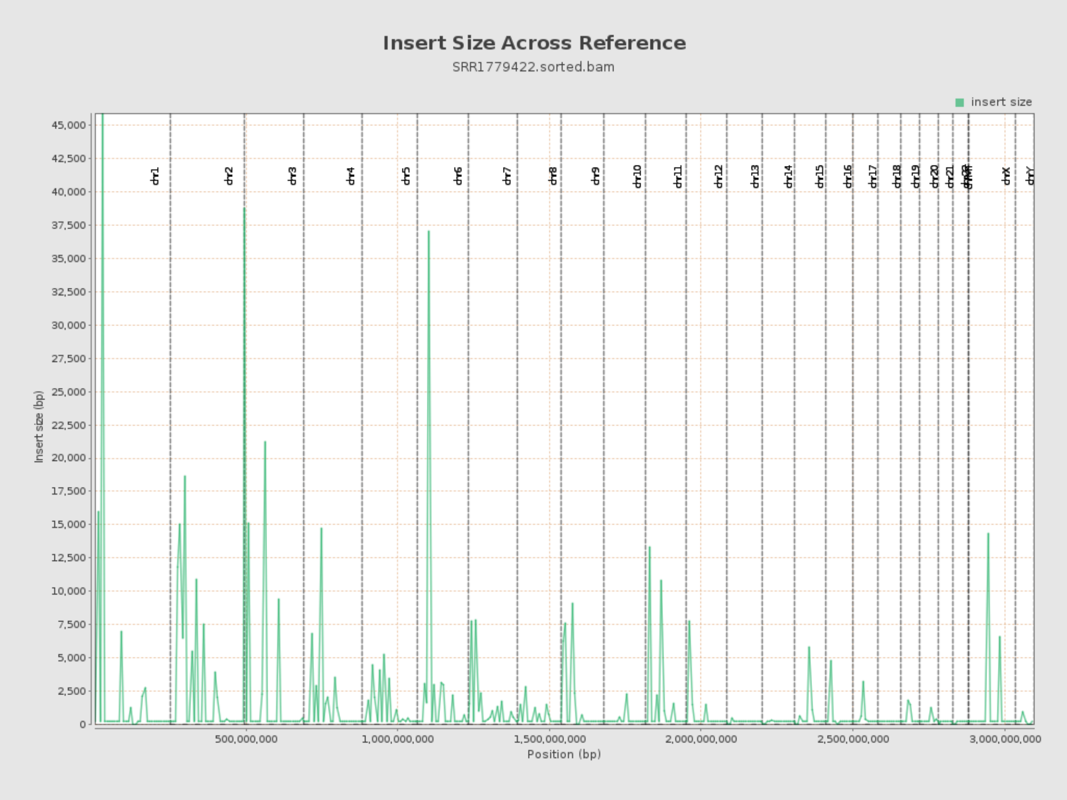
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram