Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 14:44:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779202.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_SRR1779202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779202_1.fastq.gz SRR1779202_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 14:44:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,587,008
Mapped reads	8,871,184 / 92.53%
Unmapped reads	715,824 / 7.47%
Mapped paired reads	8,871,184 / 92.53%
Mapped reads, first in pair	4,513,464 / 47.08%
Mapped reads, second in pair	4,357,720 / 45.45%
Mapped reads, both in pair	8,691,132 / 90.66%
Mapped reads, singletons	180,052 / 1.88%
Secondary alignments	0
Supplementary alignments	27,536 / 0.29%
Read min/max/mean length	30 / 80 / 80.1
Duplicated reads (estimated)	120,567 / 1.26%
Duplication rate	1.05%
Clipped reads	393,509 / 4.1%

2.2. ACGT Content

Number/percentage of A's	213,246,214 / 30.26%
Number/percentage of C's	137,572,323 / 19.52%
Number/percentage of T's	212,000,056 / 30.08%
Number/percentage of G's	141,819,108 / 20.12%
Number/percentage of N's	128,251 / 0.02%

GC Percentage	39.64%

2.3. Coverage

Mean	0.2277
Standard Deviation	0.9035

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	41,973.57
Standard Deviation	1,991,479.14
P25/Median/P75	230 / 292 / 363

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	3,660,804
Insertions	60,566
Mapped reads with at least one insertion	0.68%
Deletions	71,792
Mapped reads with at least one deletion	0.8%
Homopolymer indels	47.56%

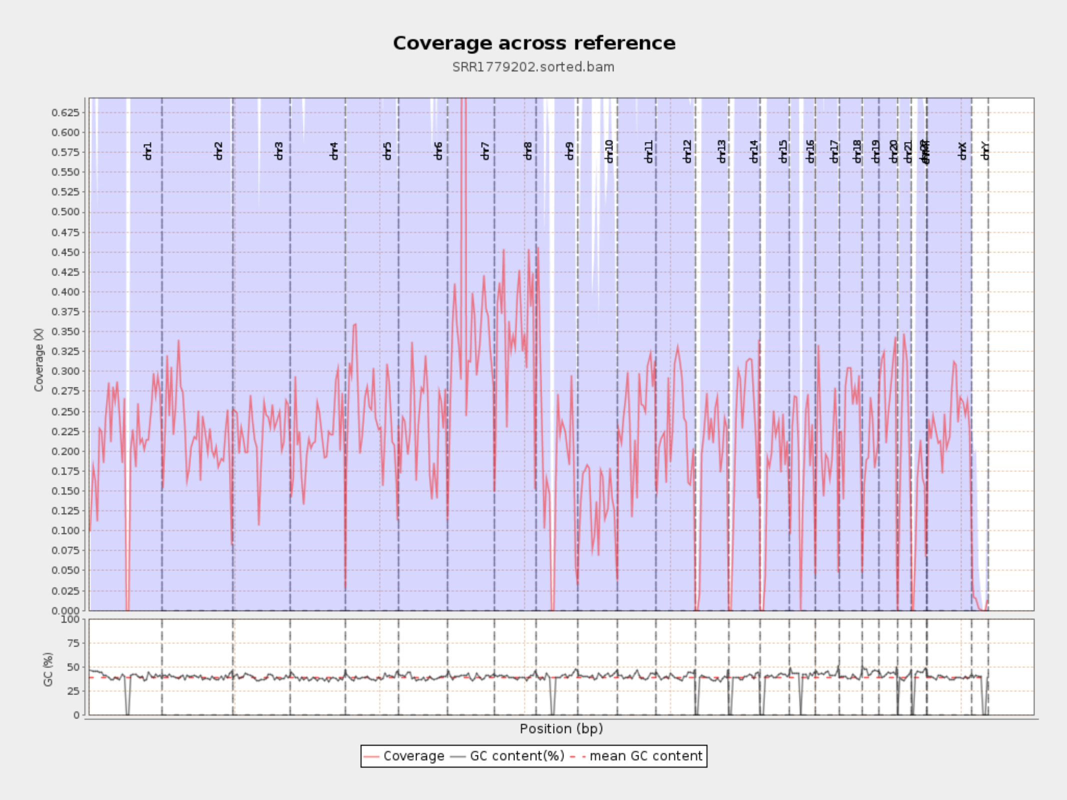
2.7. Chromosome stats

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

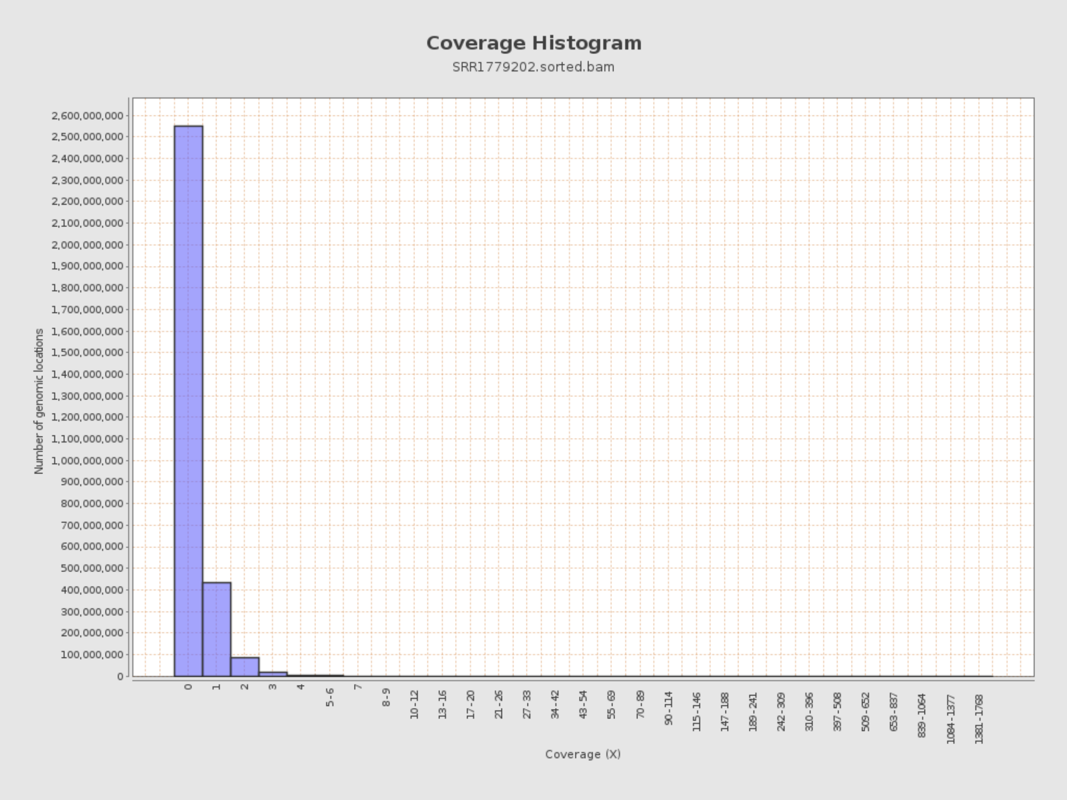
		bases	coverage	deviation
chr1	249250621	52861265	0.2121	1.8549
chr2	243199373	54020009	0.2221	0.573
chr3	198022430	44725140	0.2259	0.5331
chr4	191154276	41538275	0.2173	0.5303
chr5	180915260	45261293	0.2502	0.5629
chr6	171115067	39622072	0.2316	0.5899
chr7	159138663	68750522	0.432	1.7716
chr8	146364022	51159501	0.3495	0.6961
chr9	141213431	27238245	0.1929	0.5989
chr10	135534747	18319194	0.1352	1.3811
chr11	135006516	33046868	0.2448	0.576
chr12	133851895	30439094	0.2274	0.5428
chr13	115169878	21424601	0.186	0.4885
chr14	107349540	23529116	0.2192	0.5404
chr15	102531392	16924229	0.1651	0.4696
chr16	90354753	17313226	0.1916	0.5057
chr17	81195210	16135288	0.1987	0.6678
chr18	78077248	19737409	0.2528	0.7356
chr19	59128983	11816430	0.1998	1.3252
chr20	63025520	17605398	0.2793	0.6138
chr21	48129895	10209491	0.2121	0.5493
chr22	51304566	6119884	0.1193	0.4003
chrMT	16571	2080	0.1255	0.4057
chrX	155270560	36577273	0.2356	0.5653

chrY	59373566	537049	0.009	0.1296

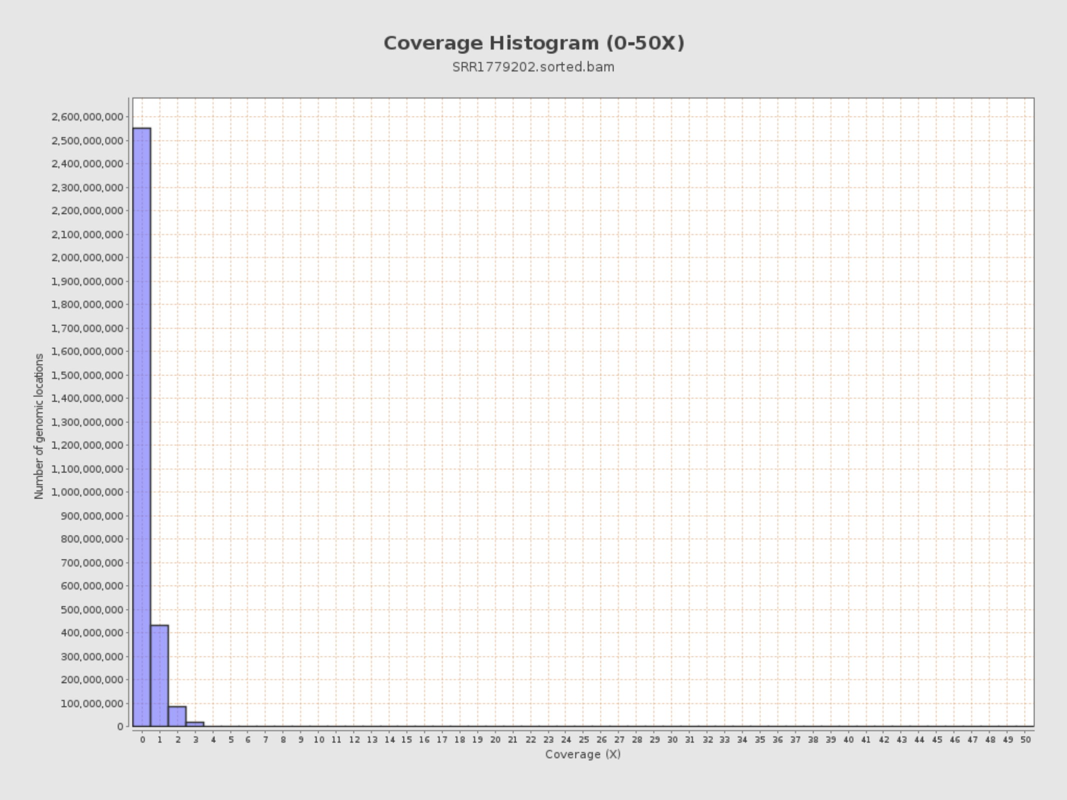
3. Results : Coverage across reference



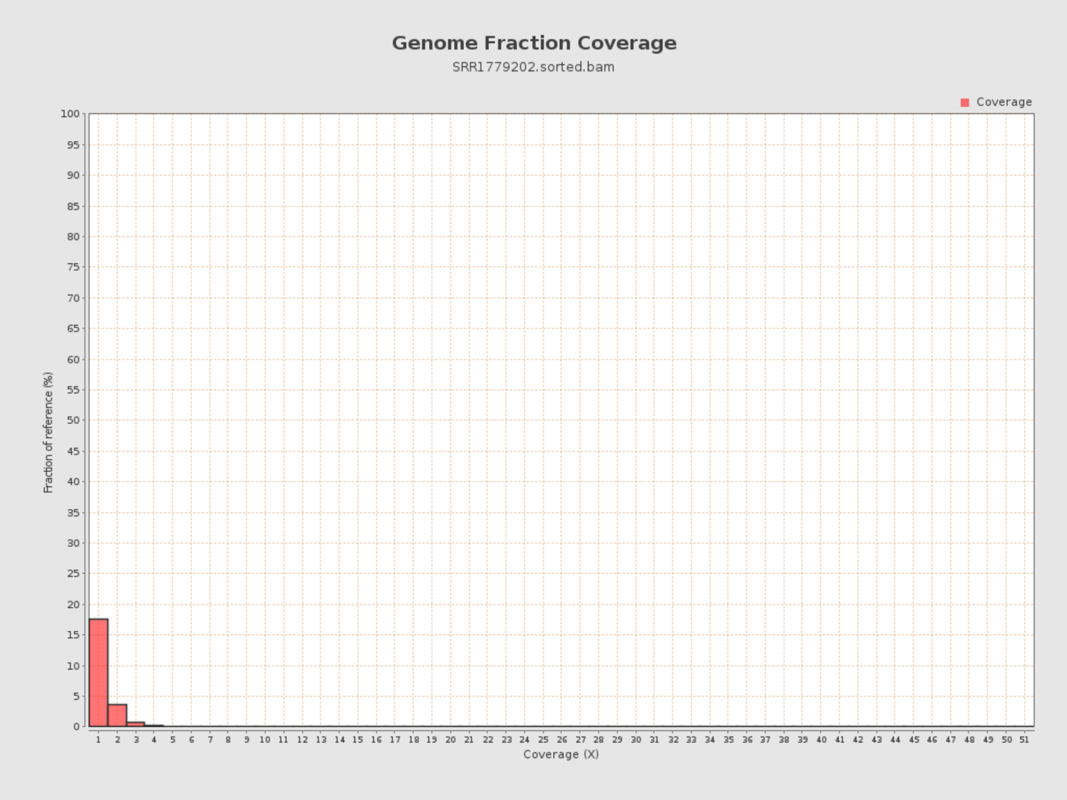
4. Results : Coverage Histogram



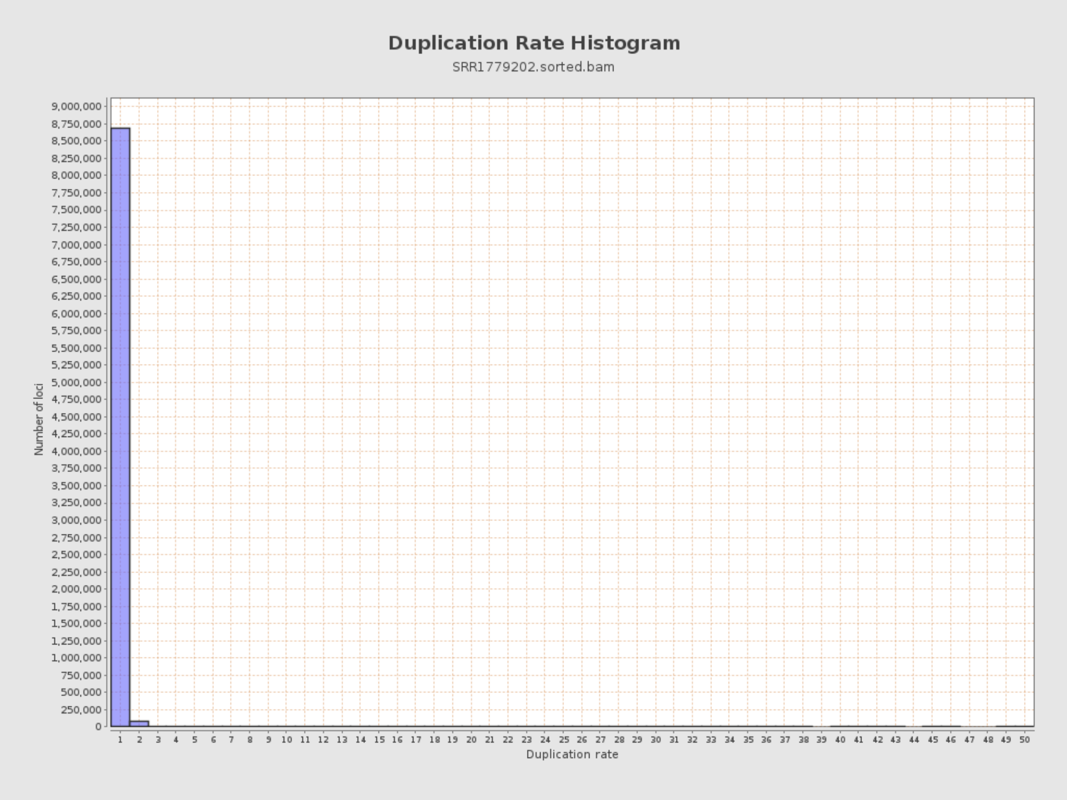
5. Results : Coverage Histogram (0-50X)



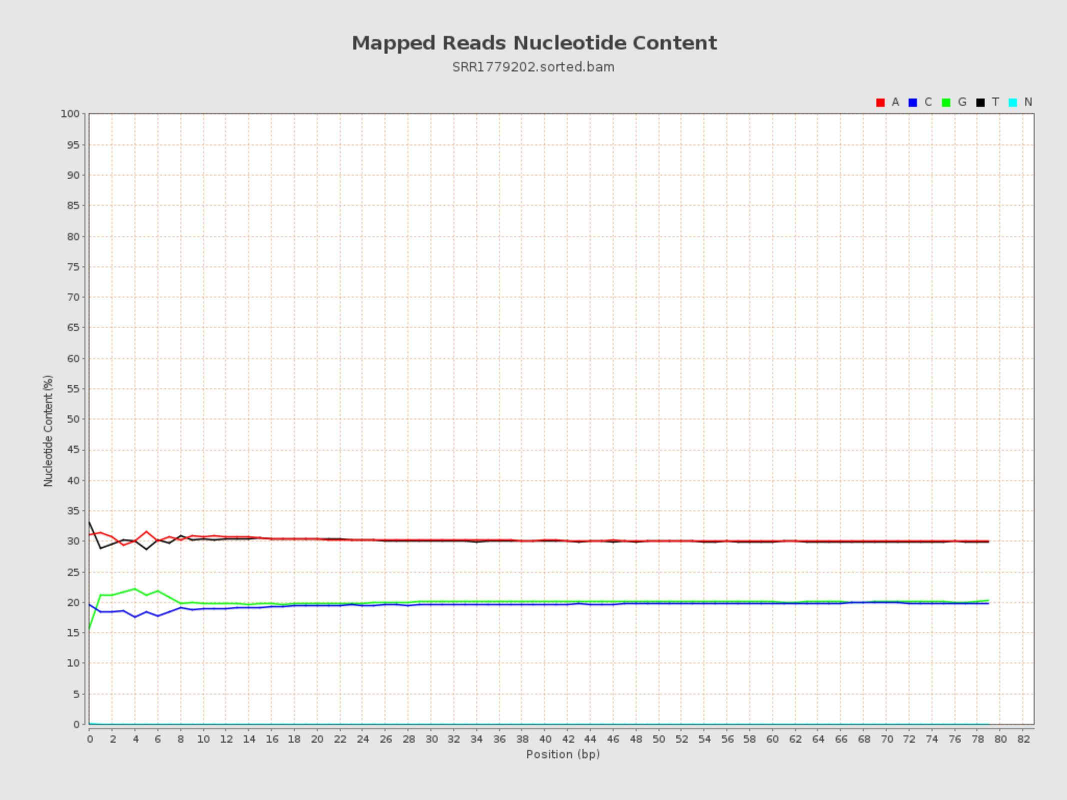
6. Results : Genome Fraction Coverage



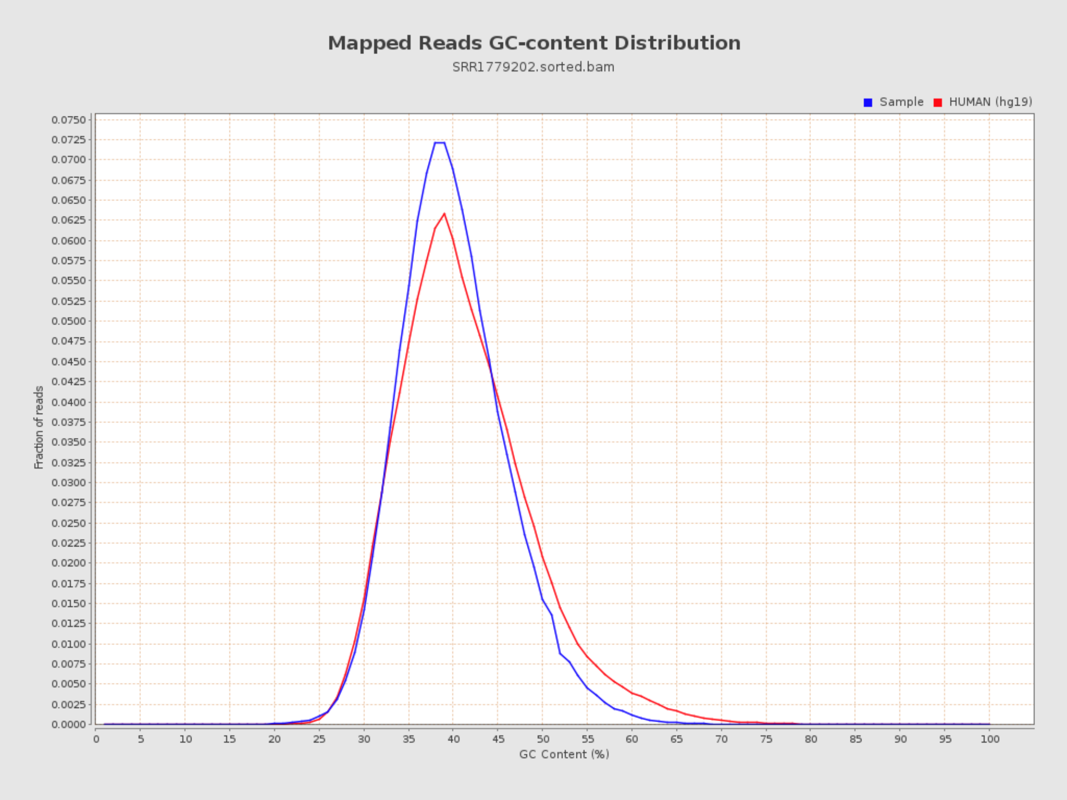
7. Results : Duplication Rate Histogram



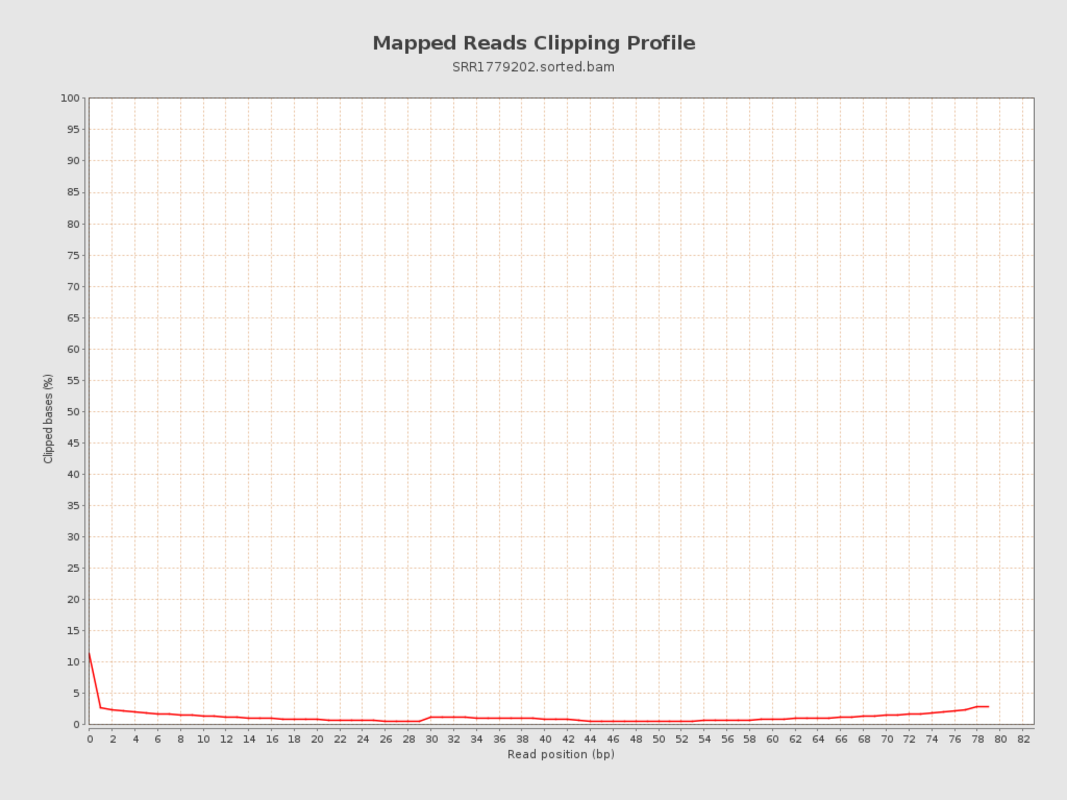
8. Results : Mapped Reads Nucleotide Content



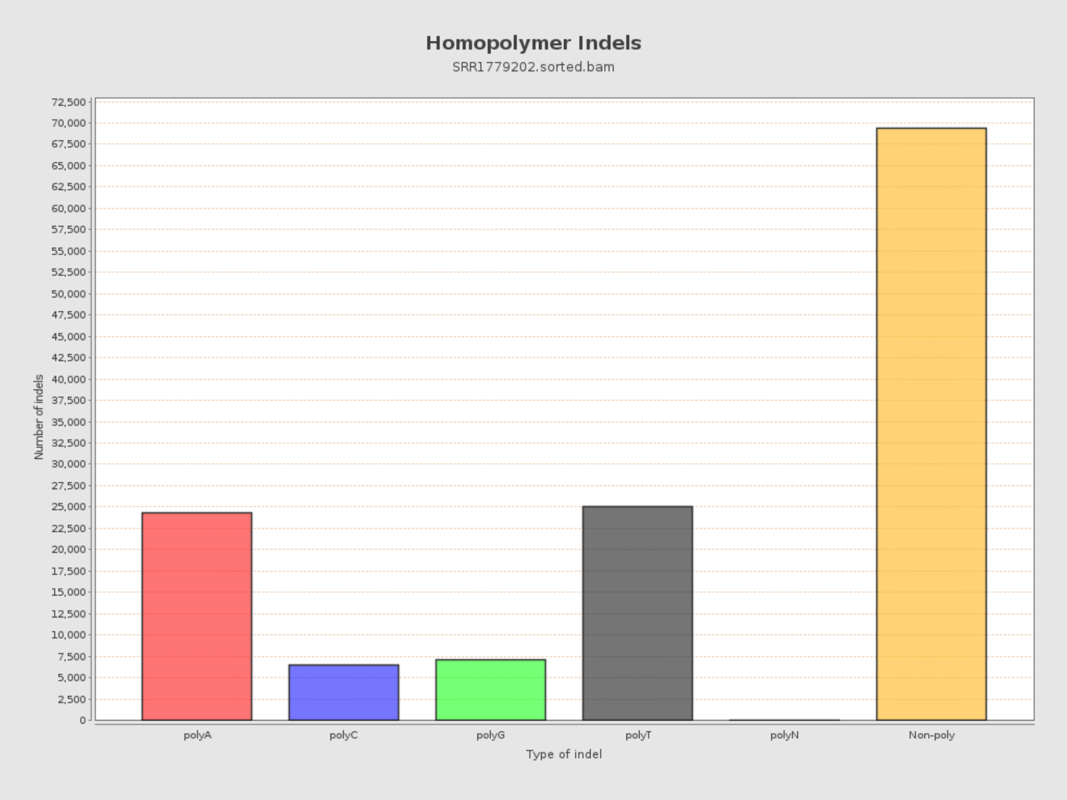
9. Results : Mapped Reads GC-content Distribution



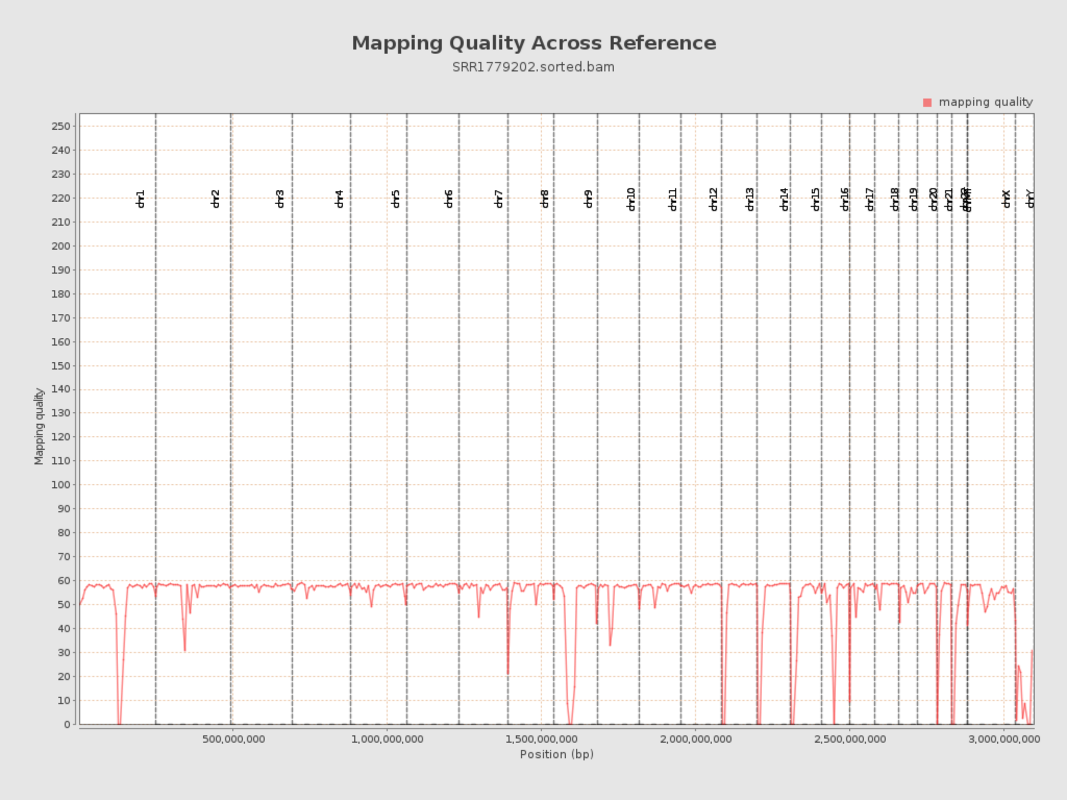
10. Results : Mapped Reads Clipping Profile



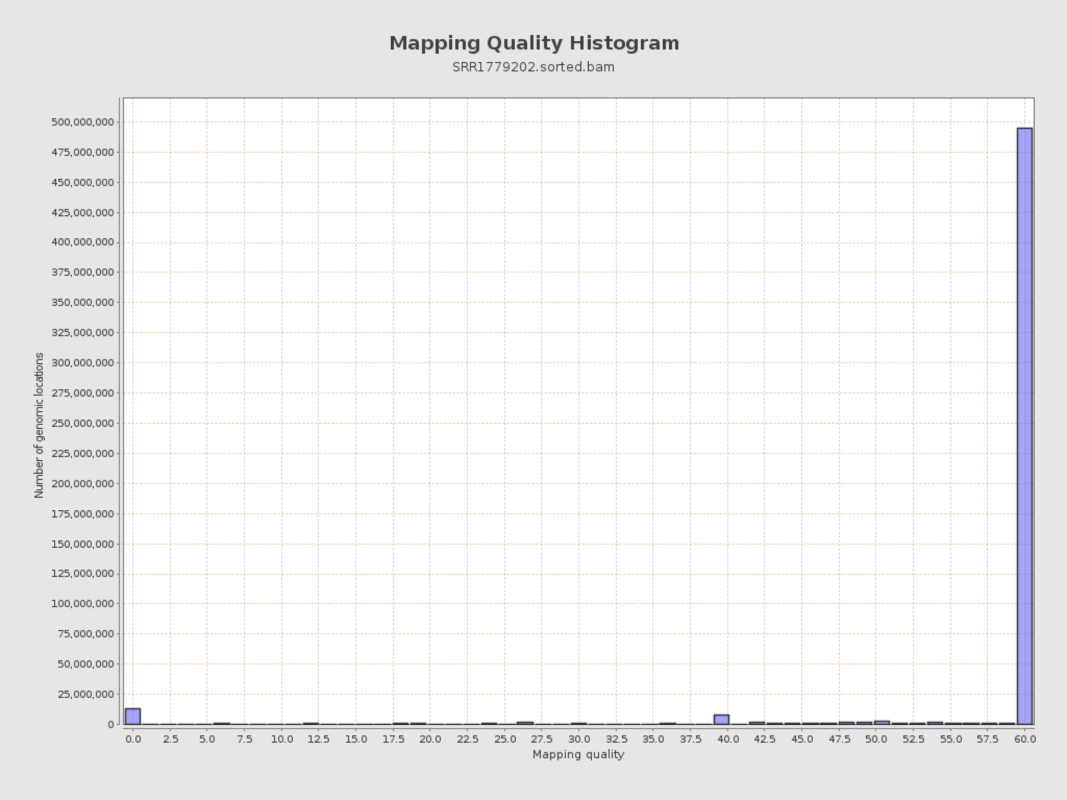
11. Results : Homopolymer Indels



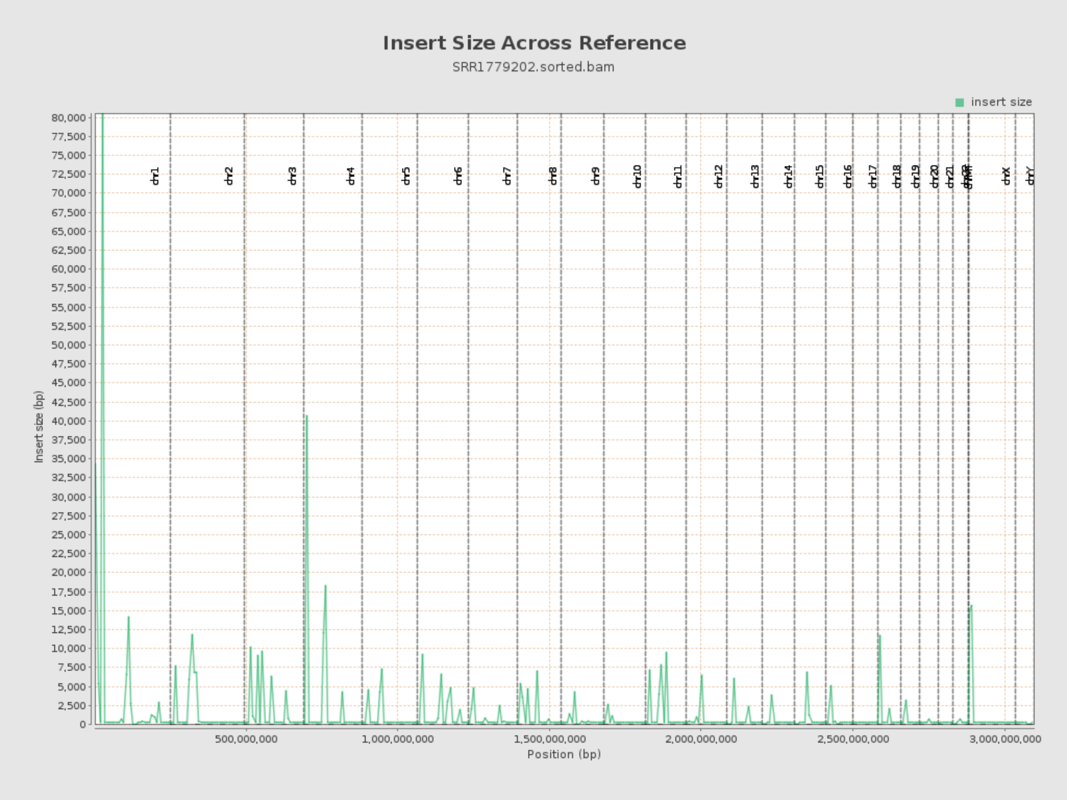
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram