Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 14:57:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779204.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_SRR1779204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779204_1.fastq.gz SRR1779204_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 14:57:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,968,802
Mapped reads	8,672,507 / 96.7%
Unmapped reads	296,295 / 3.3%
Mapped paired reads	8,672,507 / 96.7%
Mapped reads, first in pair	4,390,202 / 48.95%
Mapped reads, second in pair	4,282,305 / 47.75%
Mapped reads, both in pair	8,550,016 / 95.33%
Mapped reads, singletons	122,491 / 1.37%
Secondary alignments	0
Supplementary alignments	30,065 / 0.34%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	88,122 / 0.98%
Duplication rate	0.76%
Clipped reads	386,828 / 4.31%

2.2. ACGT Content

Number/percentage of A's	206,451,817 / 29.97%
Number/percentage of C's	136,574,661 / 19.82%
Number/percentage of T's	206,080,032 / 29.91%
Number/percentage of G's	139,681,446 / 20.28%
Number/percentage of N's	126,608 / 0.02%

GC Percentage	40.1%

2.3. Coverage

Mean	0.2226
Standard Deviation	0.8514

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	55,419.8
Standard Deviation	2,283,533.27
P25/Median/P75	207 / 276 / 348

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	3,388,844
Insertions	59,127
Mapped reads with at least one insertion	0.68%
Deletions	69,871
Mapped reads with at least one deletion	0.79%
Homopolymer indels	47.46%

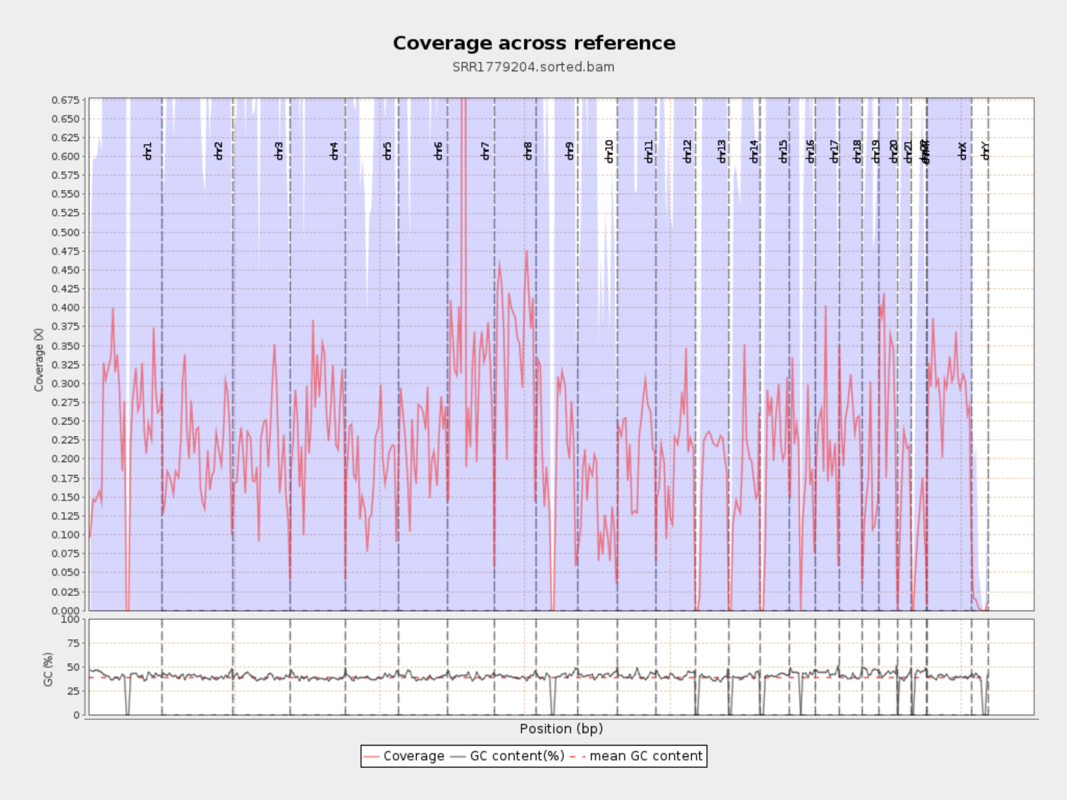
2.7. Chromosome stats

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

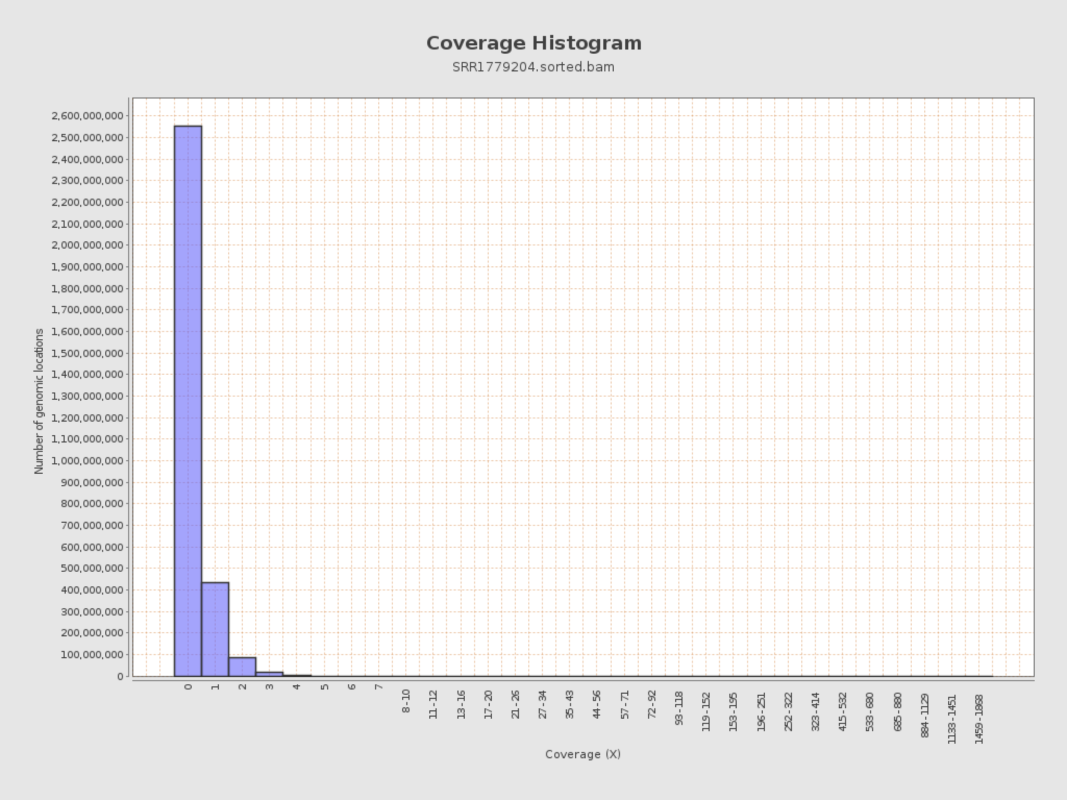
		bases	**coverage**	**deviation**
chr1	249250621	60430403	0.2424	1.9319
chr2	243199373	50376265	0.2071	0.566
chr3	198022430	40738852	0.2057	0.5026
chr4	191154276	49835595	0.2607	0.5699
chr5	180915260	32830361	0.1815	0.4688
chr6	171115067	38381361	0.2243	0.6085
chr7	159138663	60563585	0.3806	1.3311
chr8	146364022	53840671	0.3679	0.694
chr9	141213431	28762853	0.2037	0.6227
chr10	135534747	17871302	0.1319	0.9398
chr11	135006516	29523734	0.2187	0.5465
chr12	133851895	26924130	0.2011	0.505
chr13	115169878	20364084	0.1768	0.4666
chr14	107349540	17098792	0.1593	0.4511
chr15	102531392	20524372	0.2002	0.51
chr16	90354753	16629671	0.184	0.49
chr17	81195210	17440882	0.2148	0.7881
chr18	78077248	19831050	0.254	0.73
chr19	59128983	9046184	0.153	1.3917
chr20	63025520	19512233	0.3096	0.6397
chr21	48129895	7668717	0.1593	0.4539
chr22	51304566	4500575	0.0877	0.3337
chrMT	16571	96	0.0058	0.0993
chrX	155270560	45818442	0.2951	0.6179

chrY	59373566	544058	0.0092	0.1307

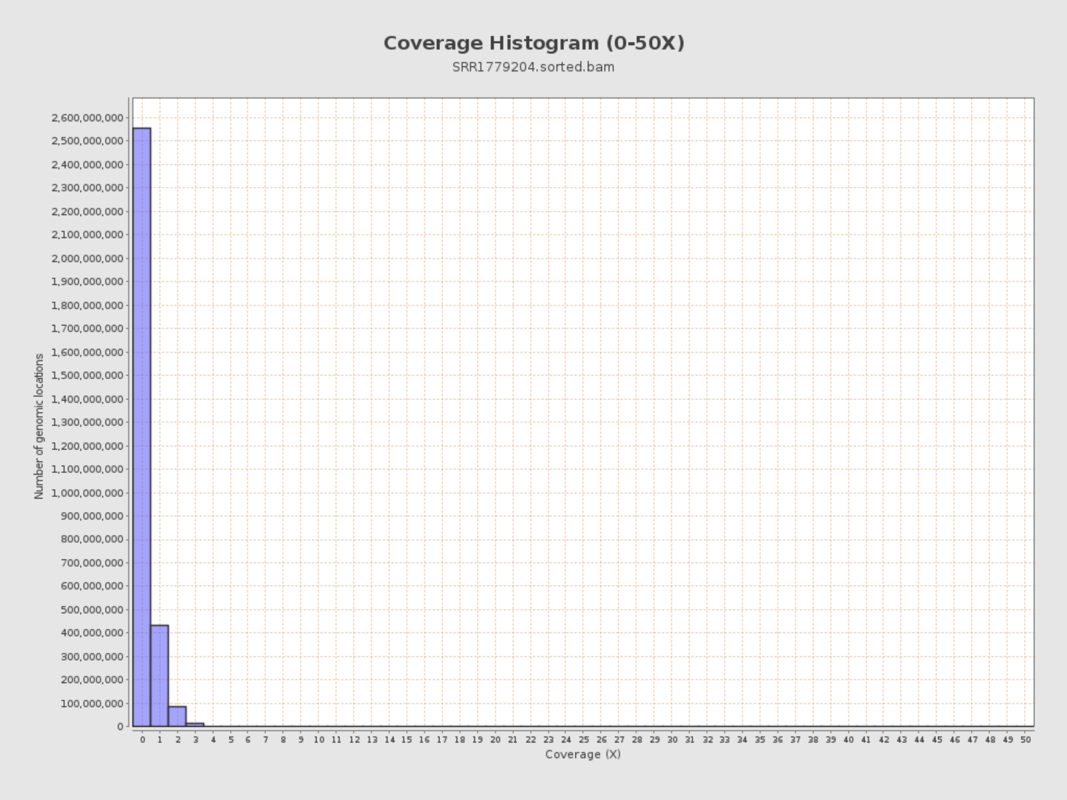
3. Results : Coverage across reference



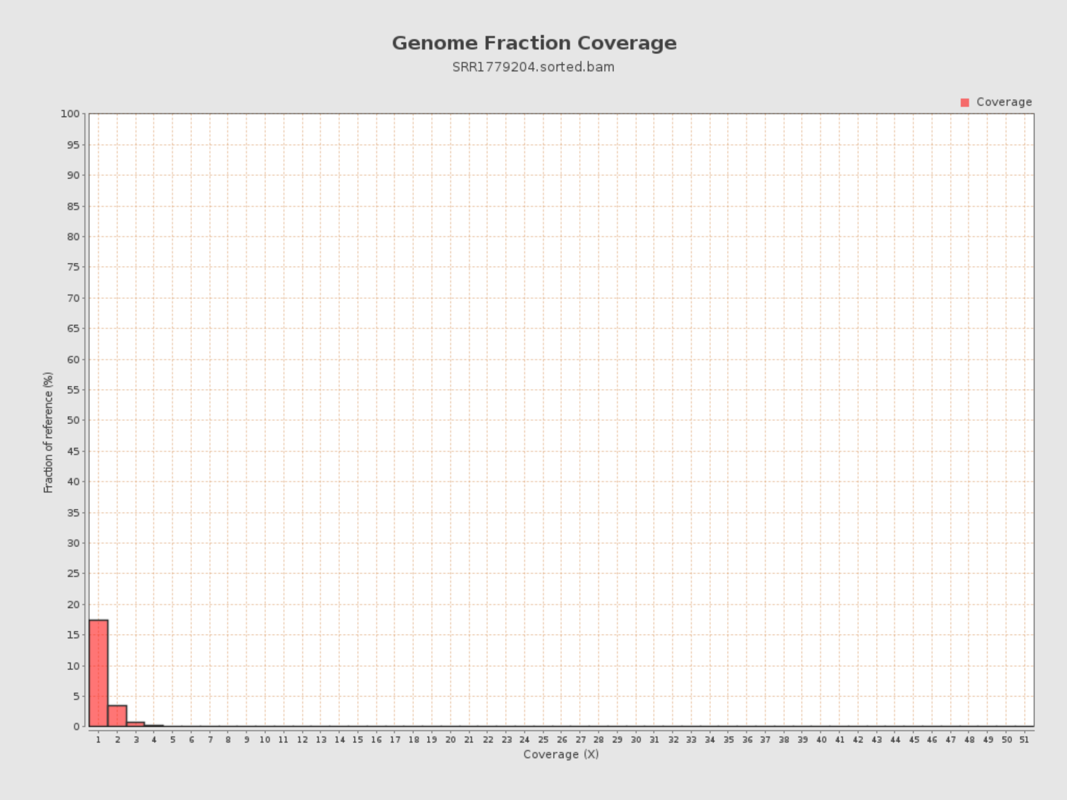
4. Results : Coverage Histogram



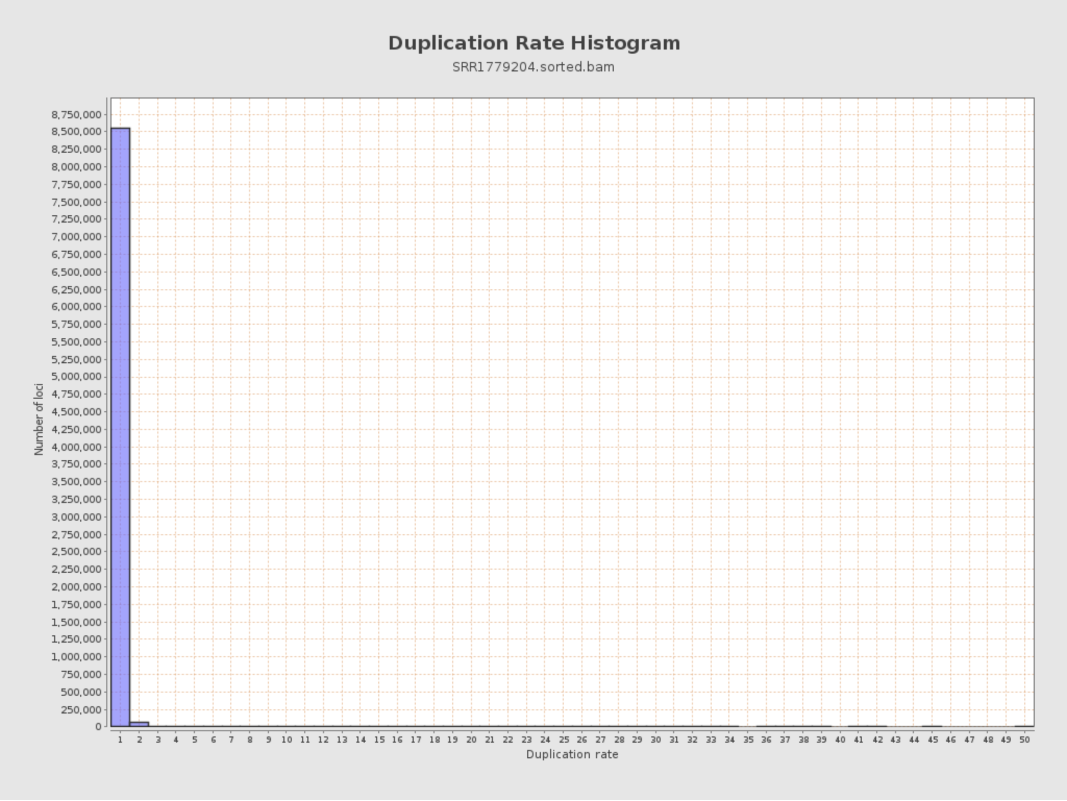
5. Results : Coverage Histogram (0-50X)



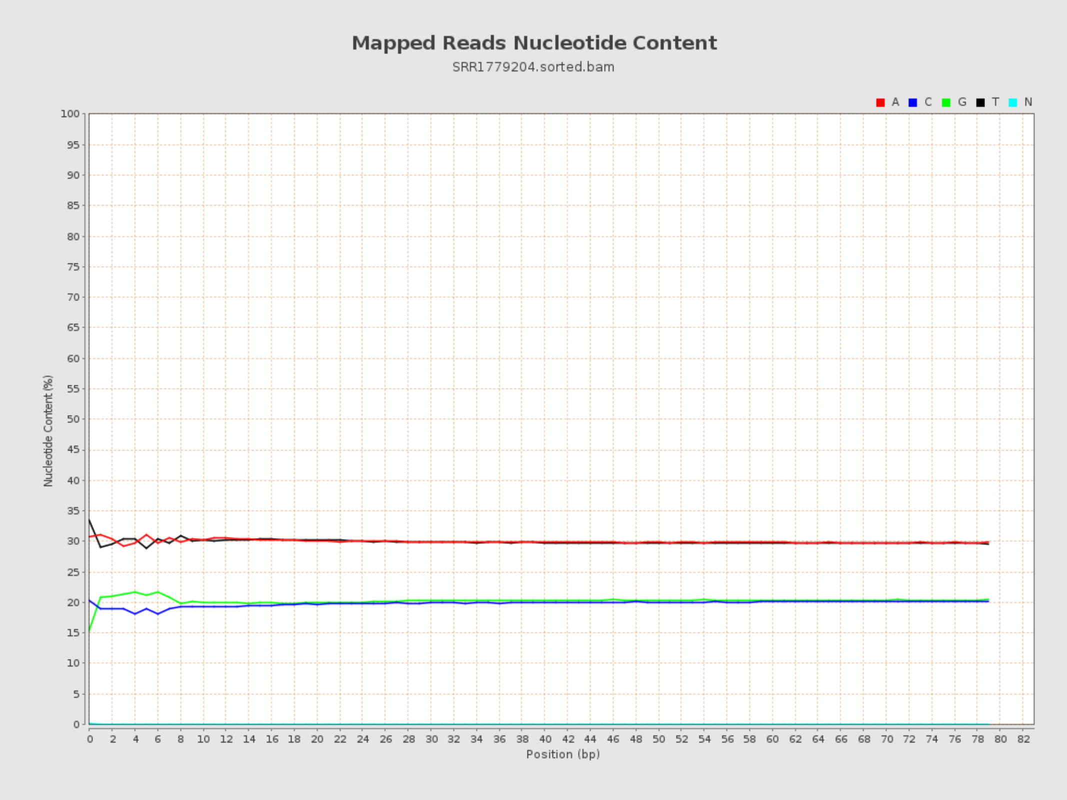
6. Results : Genome Fraction Coverage



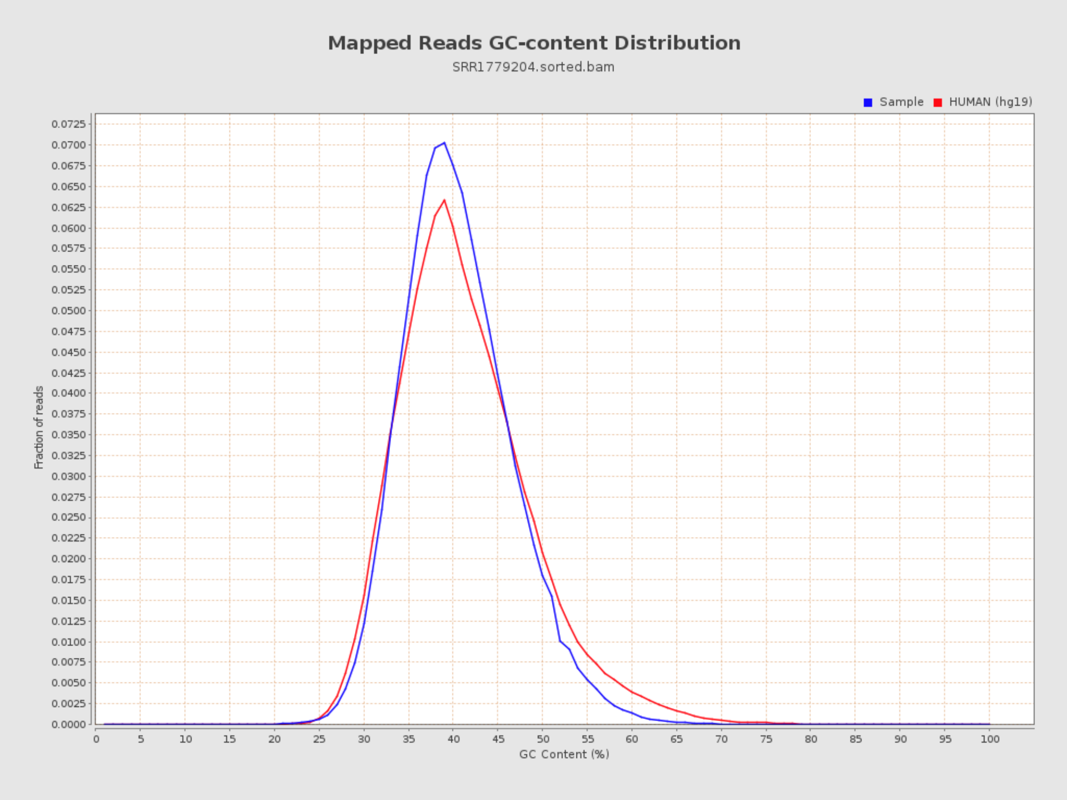
7. Results : Duplication Rate Histogram



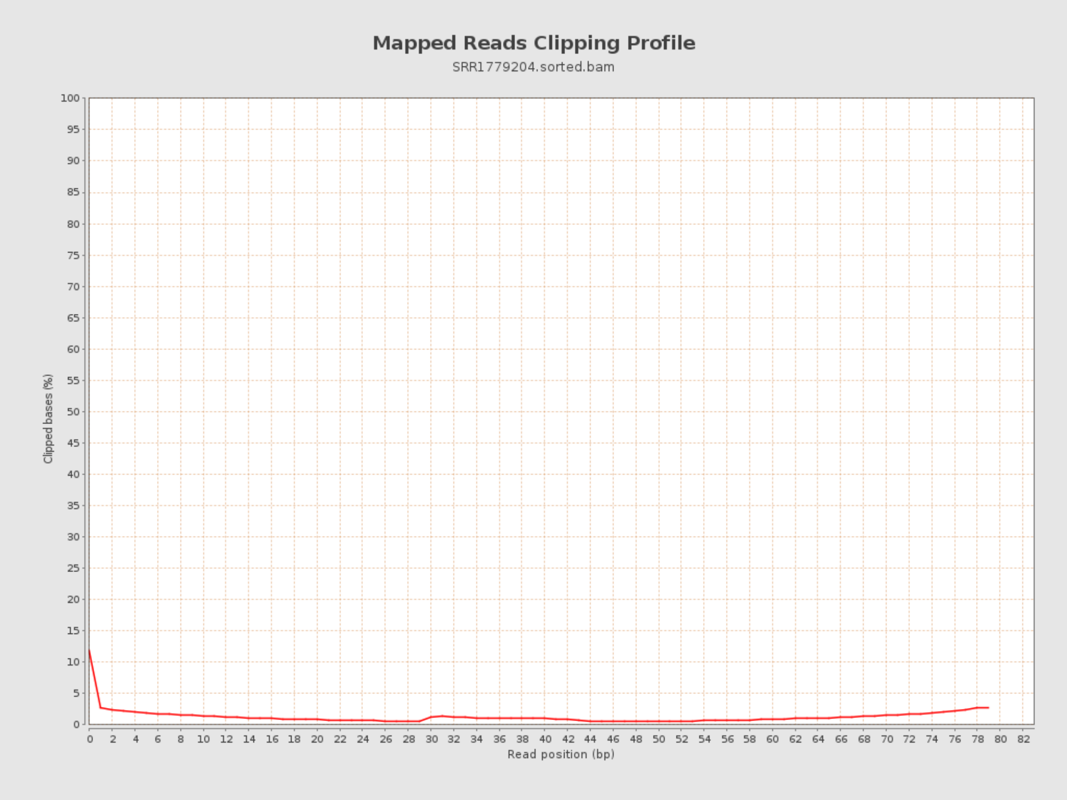
8. Results : Mapped Reads Nucleotide Content



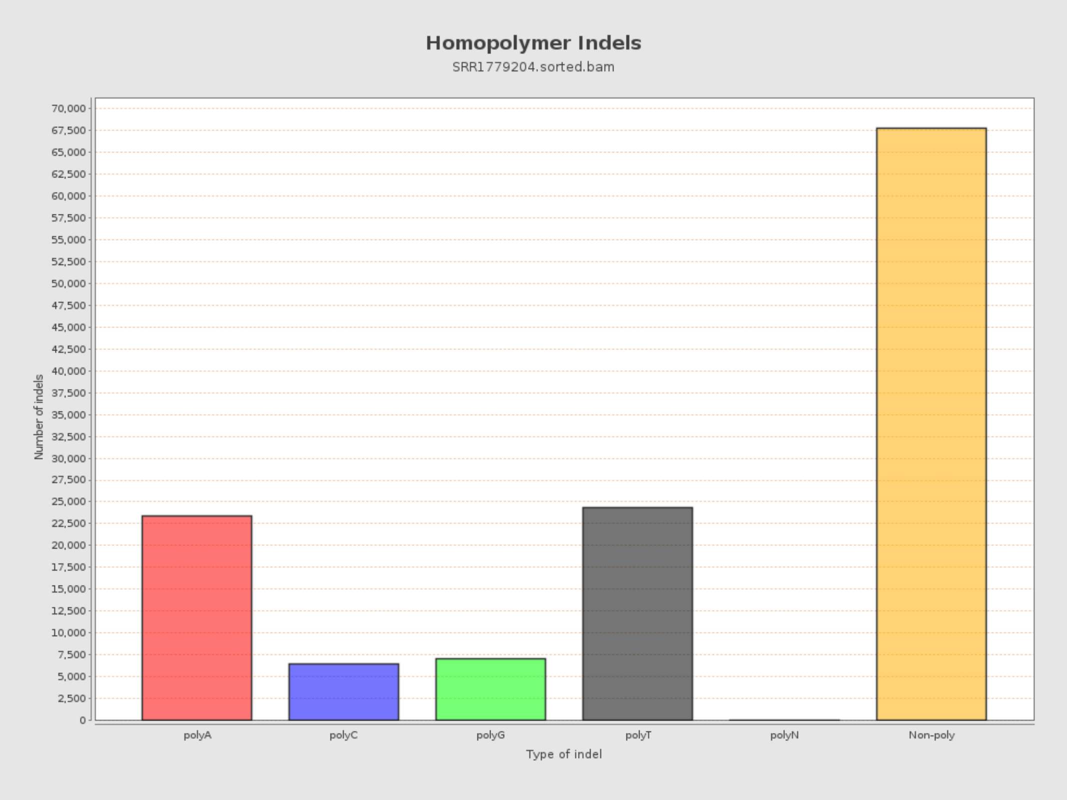
9. Results : Mapped Reads GC-content Distribution



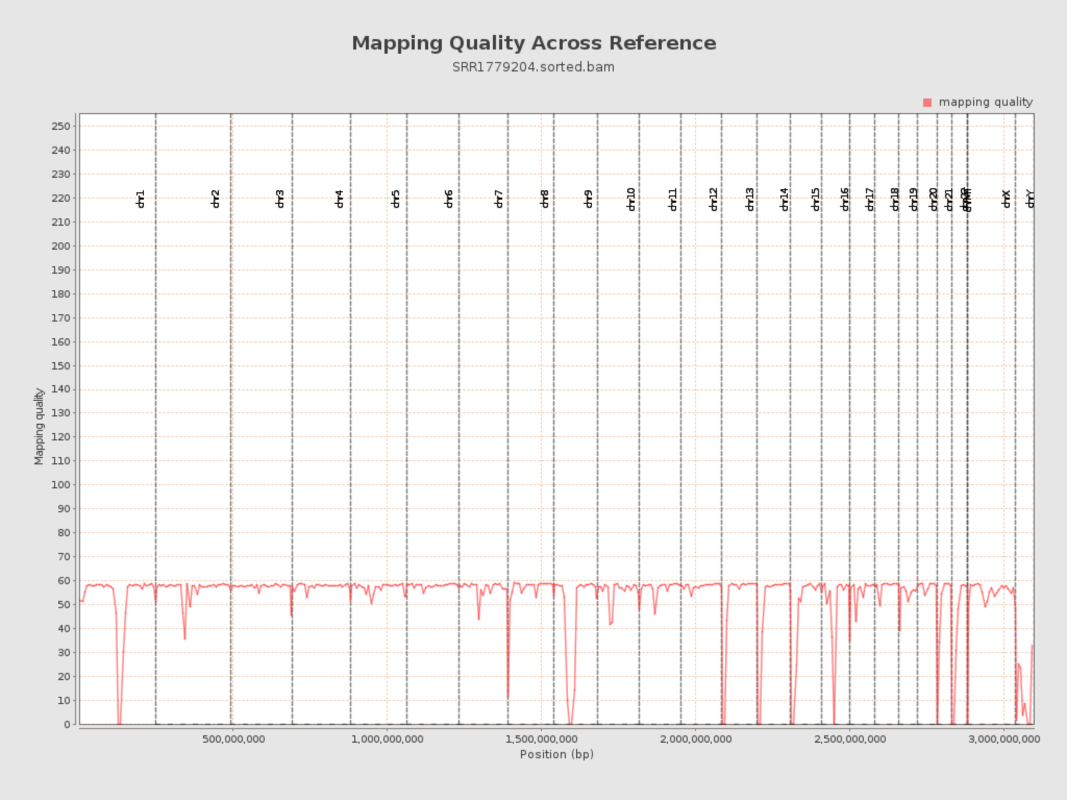
10. Results : Mapped Reads Clipping Profile



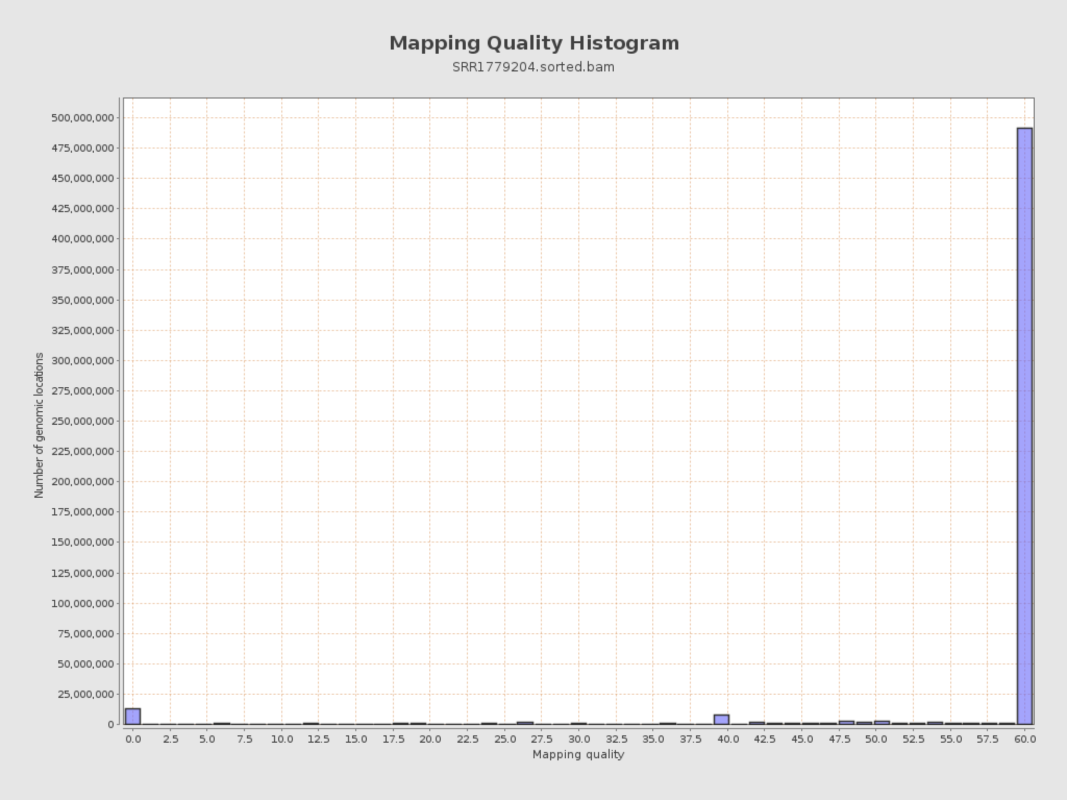
11. Results : Homopolymer Indels



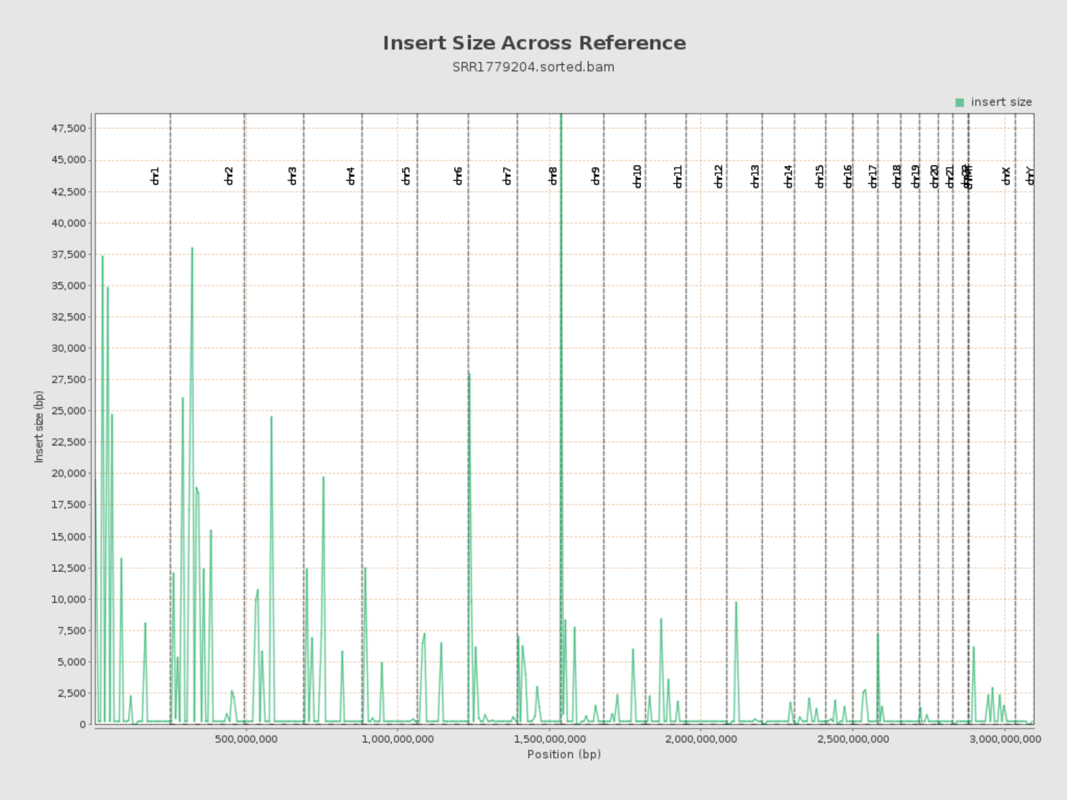
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram