Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 07:06:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779311.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_SRR1779311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779311_1.fastq.gz SRR1779311_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 07:06:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,827,198
Mapped reads	13,637,220 / 91.97%
Unmapped reads	1,189,978 / 8.03%
Mapped paired reads	13,637,220 / 91.97%
Mapped reads, first in pair	6,903,976 / 46.56%
Mapped reads, second in pair	6,733,244 / 45.41%
Mapped reads, both in pair	13,435,632 / 90.61%
Mapped reads, singletons	201,588 / 1.36%
Secondary alignments	0
Supplementary alignments	34,554 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	464,791 / 3.13%
Duplication rate	3.14%
Clipped reads	426,013 / 2.87%

2.2. ACGT Content

Number/percentage of A's	333,241,242 / 30.71%
Number/percentage of C's	207,589,995 / 19.13%
Number/percentage of T's	332,767,119 / 30.67%
Number/percentage of G's	211,252,892 / 19.47%
Number/percentage of N's	282,214 / 0.03%

GC Percentage	38.6%

2.3. Coverage

Mean	0.3506
Standard Deviation	1.486

2.4. Mapping Quality

Mean Mapping Quality	53.32

2.5. Insert size

Mean	35,562.27
Standard Deviation	1,771,479.1
P25/Median/P75	167 / 223 / 300

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	3,891,364
Insertions	79,531
Mapped reads with at least one insertion	0.58%
Deletions	101,530
Mapped reads with at least one deletion	0.74%
Homopolymer indels	46.98%

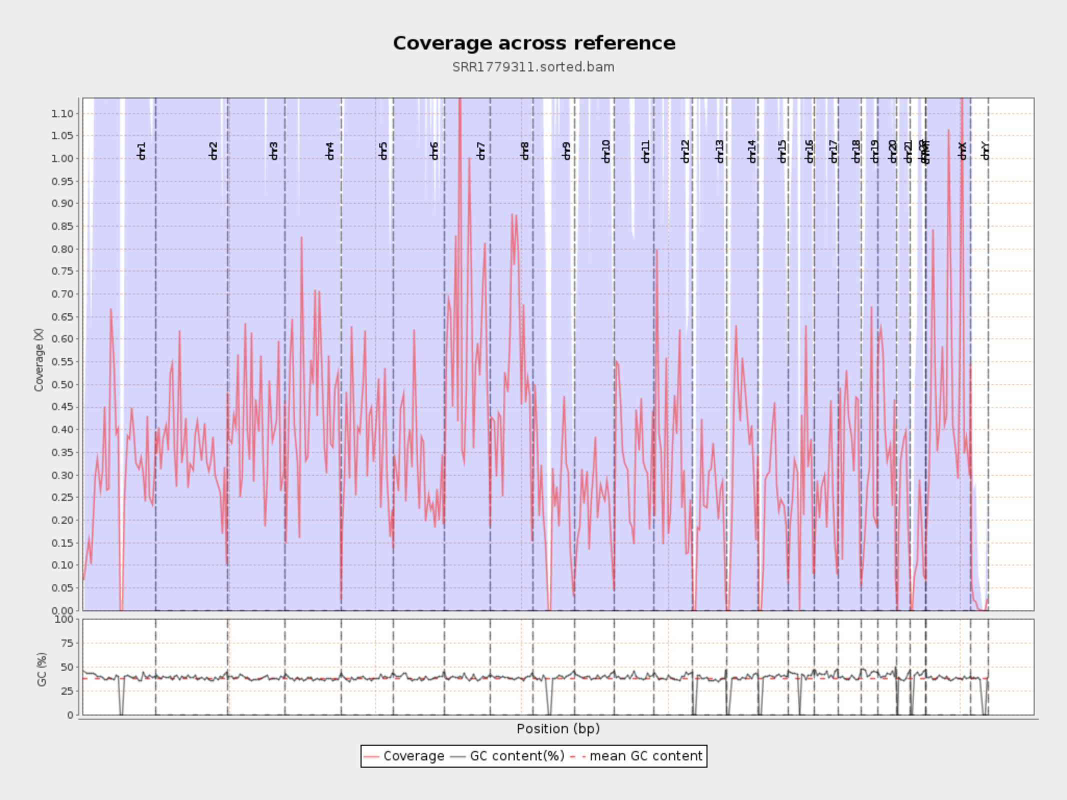
2.7. Chromosome stats

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

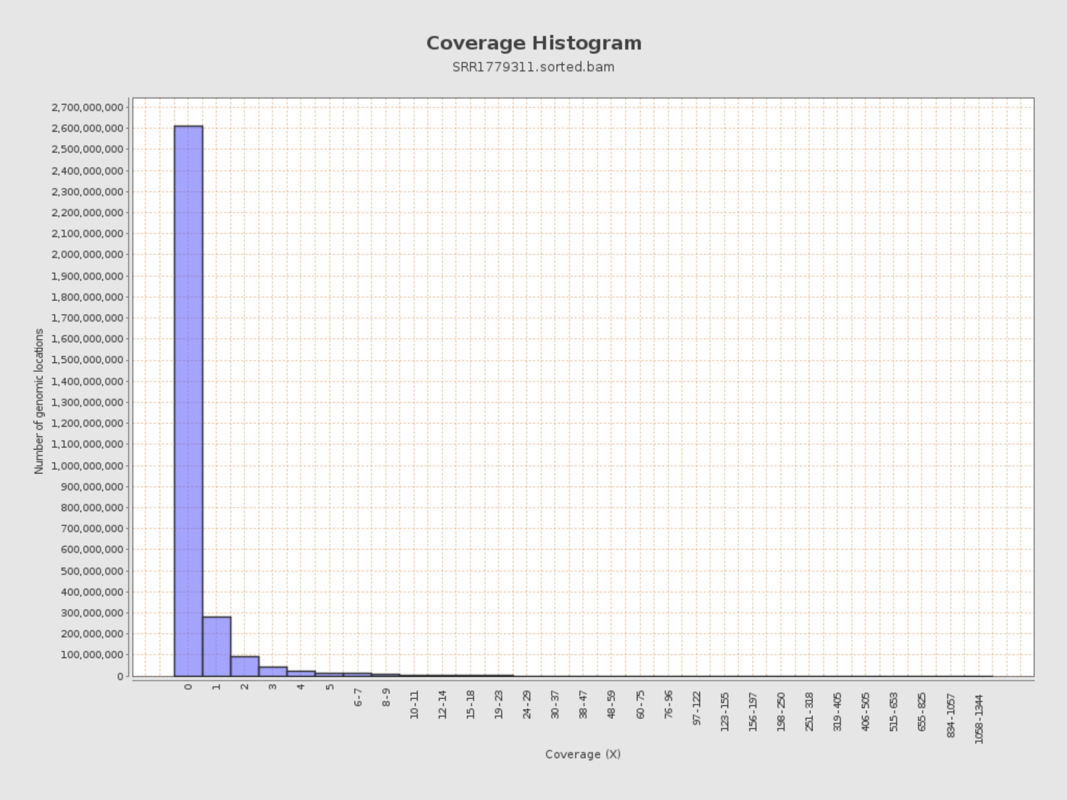
		bases	coverage	deviation
chr1	249250621	73807529	0.2961	1.7536
chr2	243199373	86266226	0.3547	1.3439
chr3	198022430	80287240	0.4054	1.4419
chr4	191154276	87359603	0.457	1.7765
chr5	180915260	68005337	0.3759	1.3928
chr6	171115067	54122538	0.3163	1.1799
chr7	159138663	96634298	0.6072	1.9968
chr8	146364022	76706163	0.5241	1.5643
chr9	141213431	34573677	0.2448	1.1629
chr10	135534747	31559075	0.2328	1.3935
chr11	135006516	46101290	0.3415	1.358
chr12	133851895	44597442	0.3332	1.7335
chr13	115169878	26508224	0.2302	0.9901
chr14	107349540	38371075	0.3574	1.451
chr15	102531392	23706611	0.2312	0.8948
chr16	90354753	24560346	0.2718	1.1878
chr17	81195210	20360808	0.2508	1.1039
chr18	78077248	30034629	0.3847	1.7659
chr19	59128983	16455368	0.2783	1.3337
chr20	63025520	26716122	0.4239	1.4788
chr21	48129895	11723135	0.2436	1.0038
chr22	51304566	5953721	0.116	0.6738
chrMT	16571	2559	0.1544	0.8011
chrX	155270560	80059592	0.5156	2.0903

chrY	59373566	872360	0.0147	0.1941

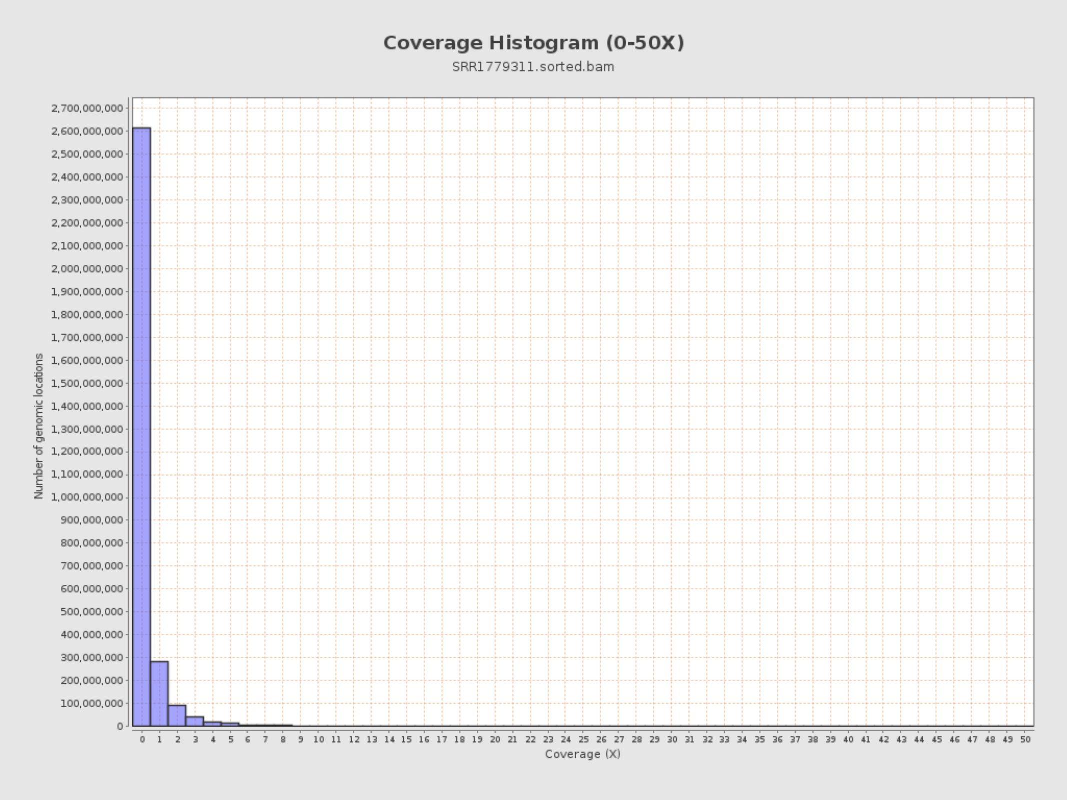
3. Results : Coverage across reference



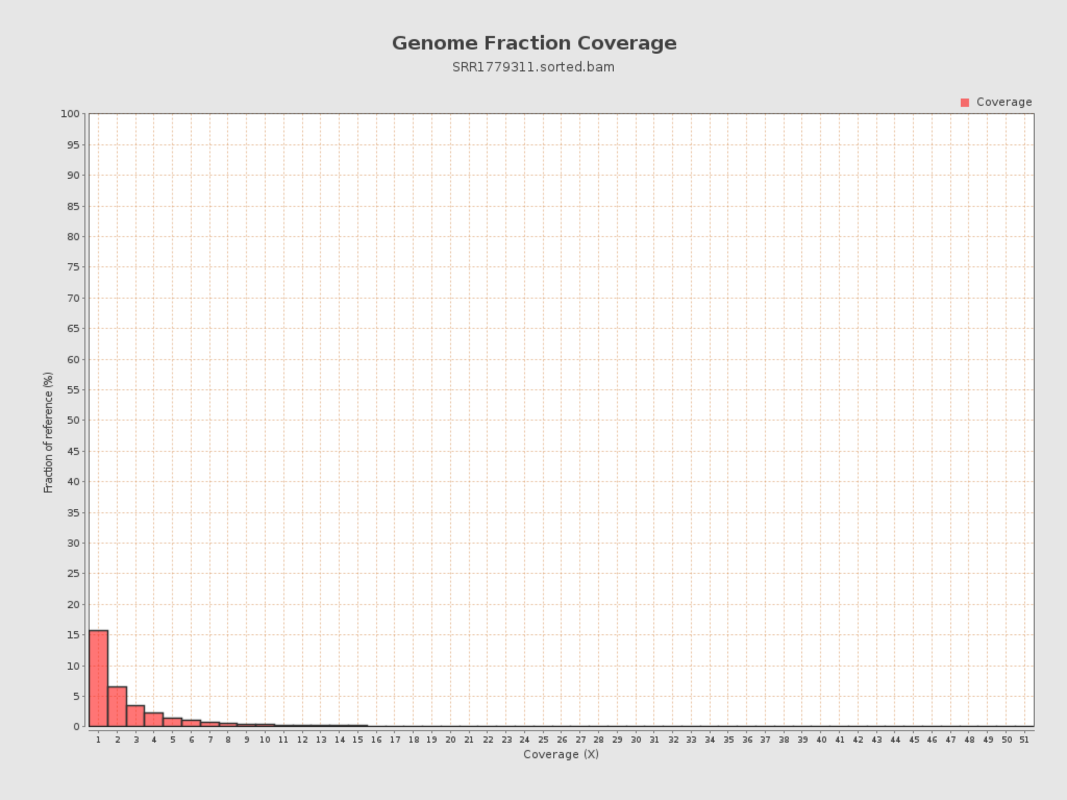
4. Results : Coverage Histogram



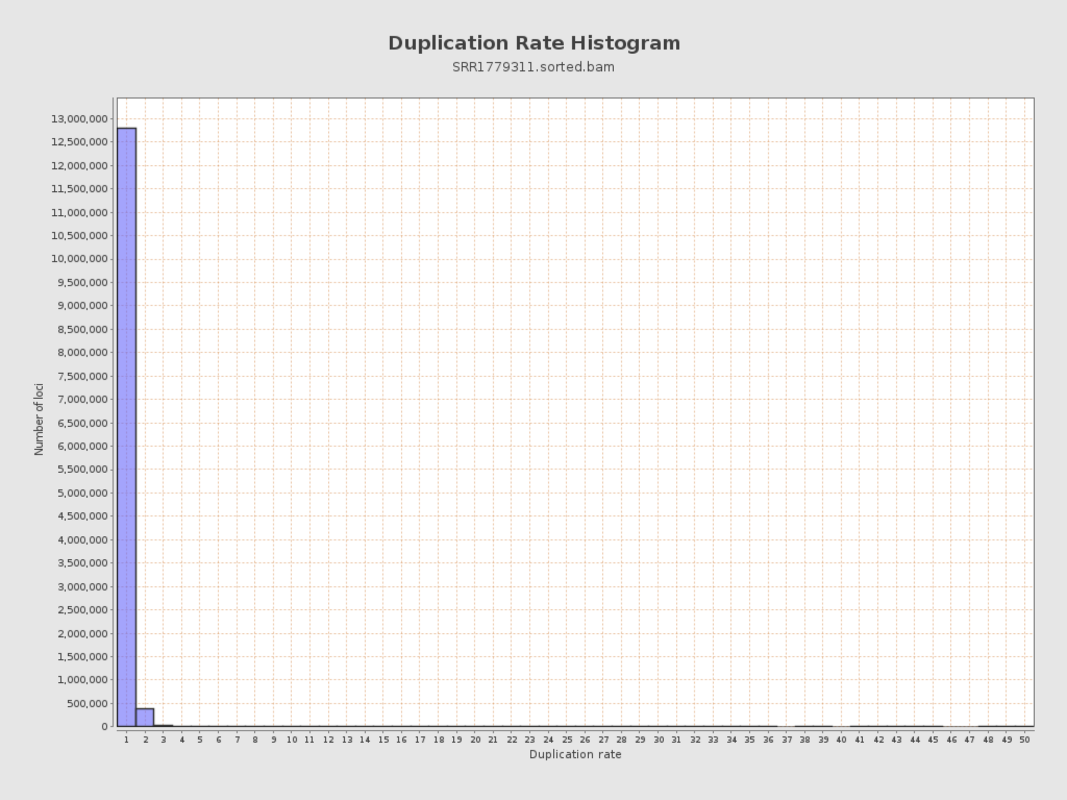
5. Results : Coverage Histogram (0-50X)



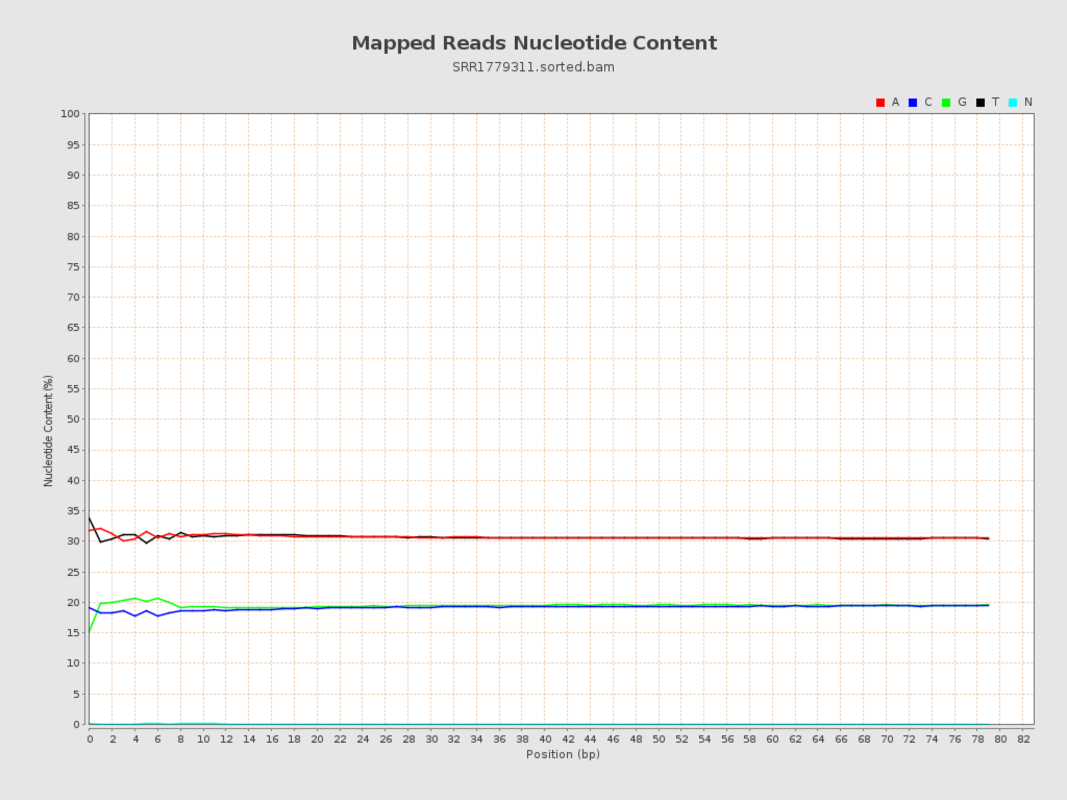
6. Results : Genome Fraction Coverage



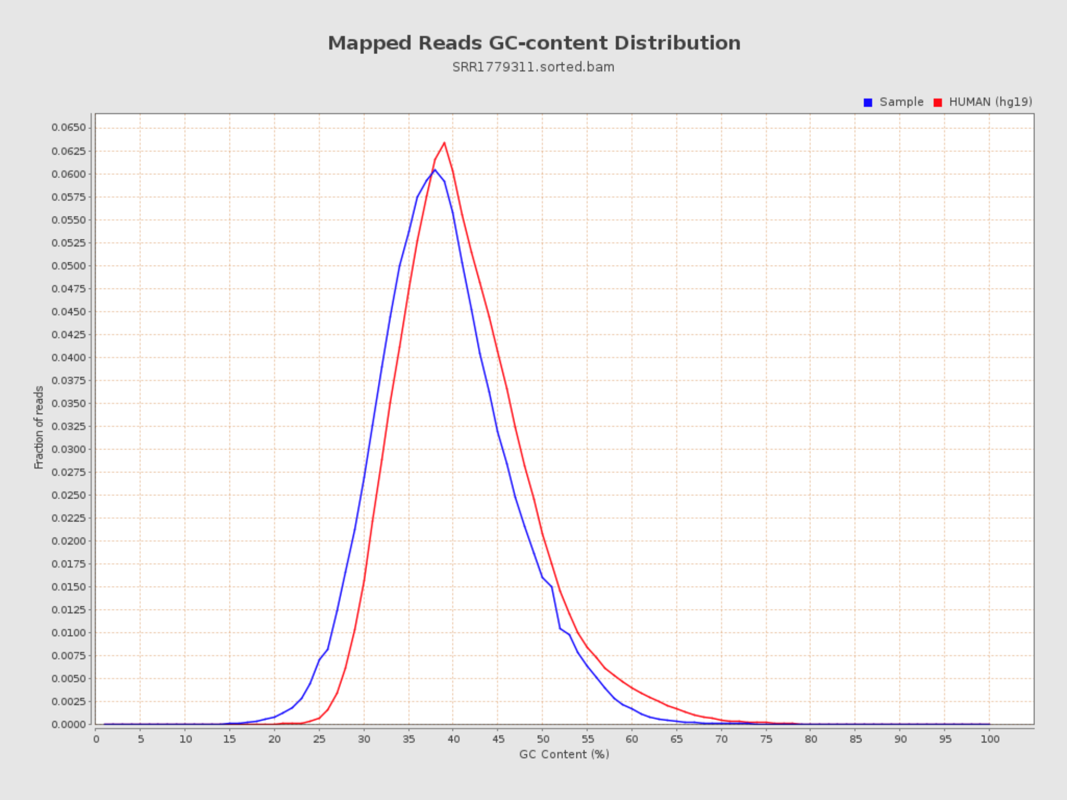
7. Results : Duplication Rate Histogram



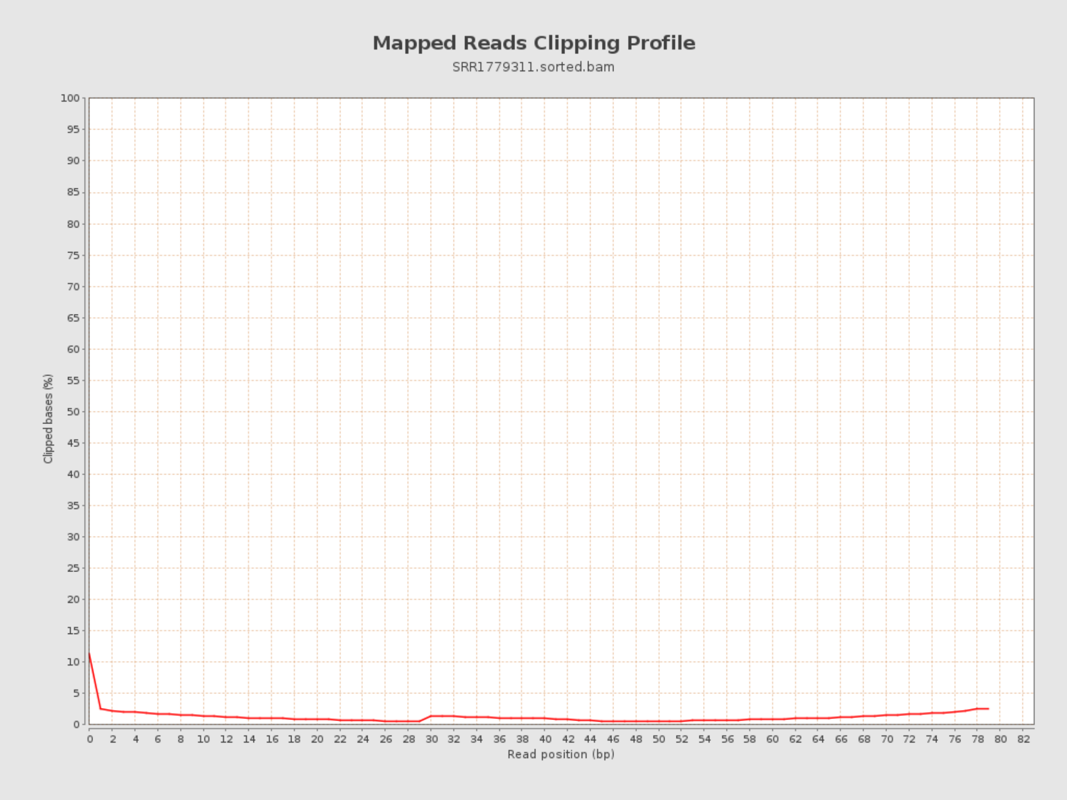
8. Results : Mapped Reads Nucleotide Content



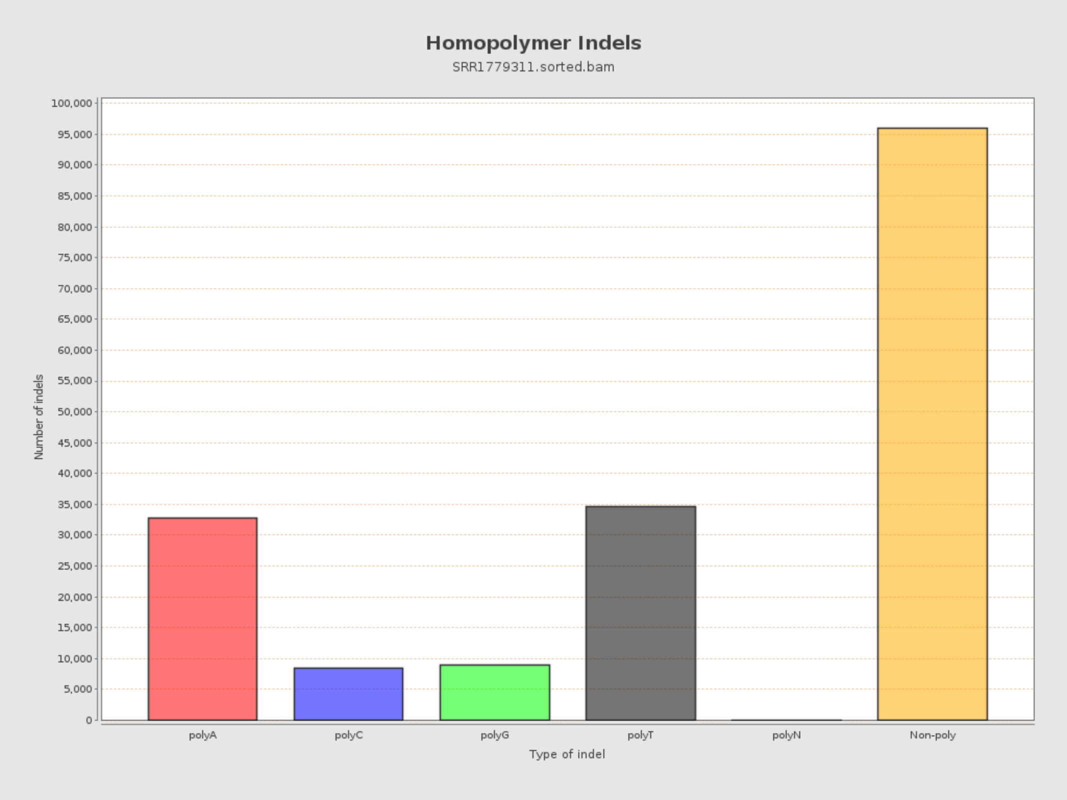
9. Results : Mapped Reads GC-content Distribution



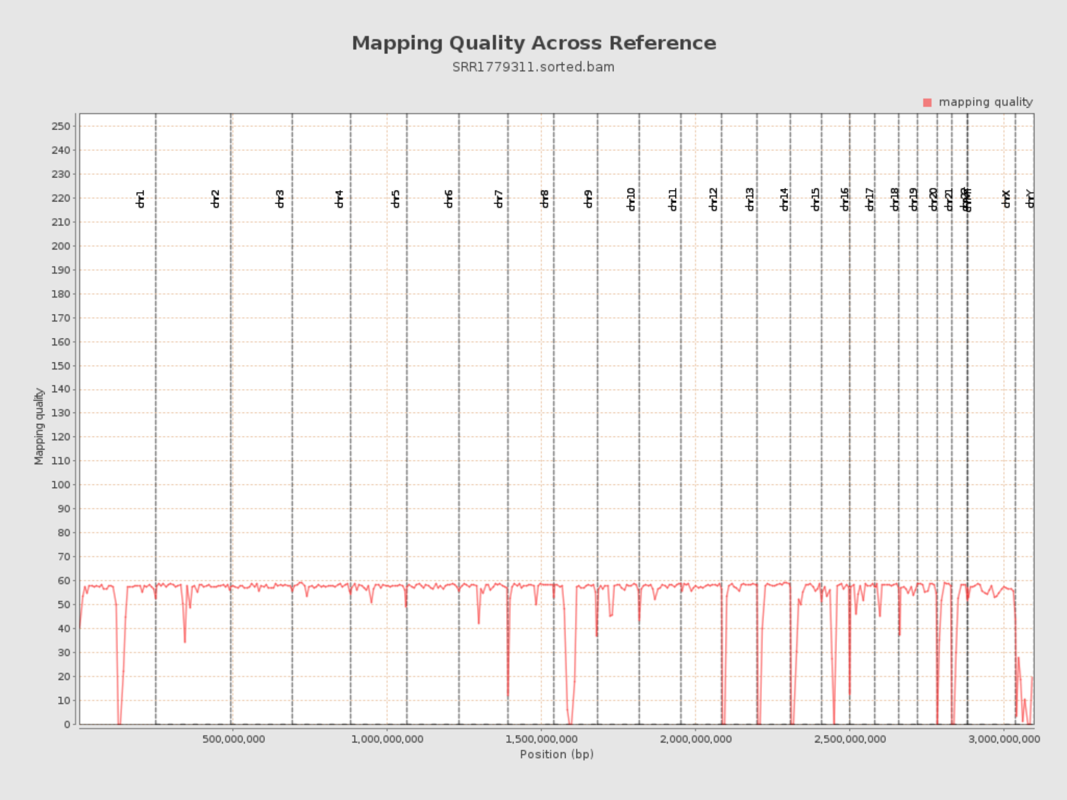
10. Results : Mapped Reads Clipping Profile



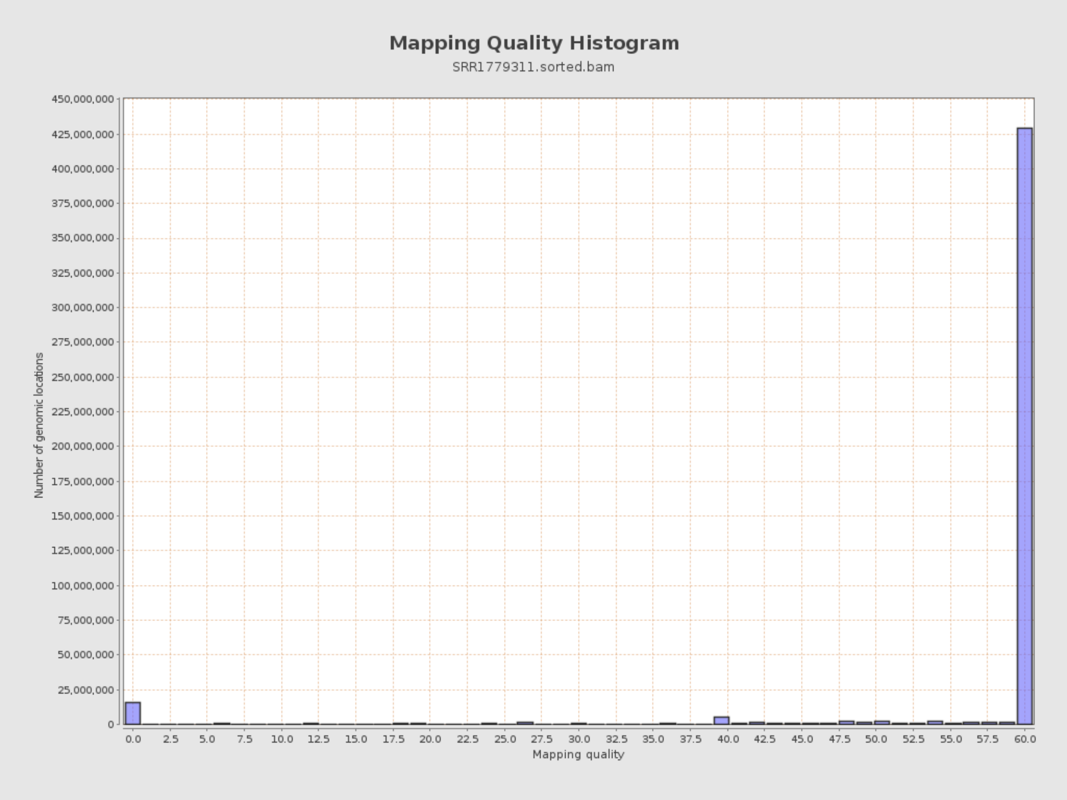
11. Results : Homopolymer Indels



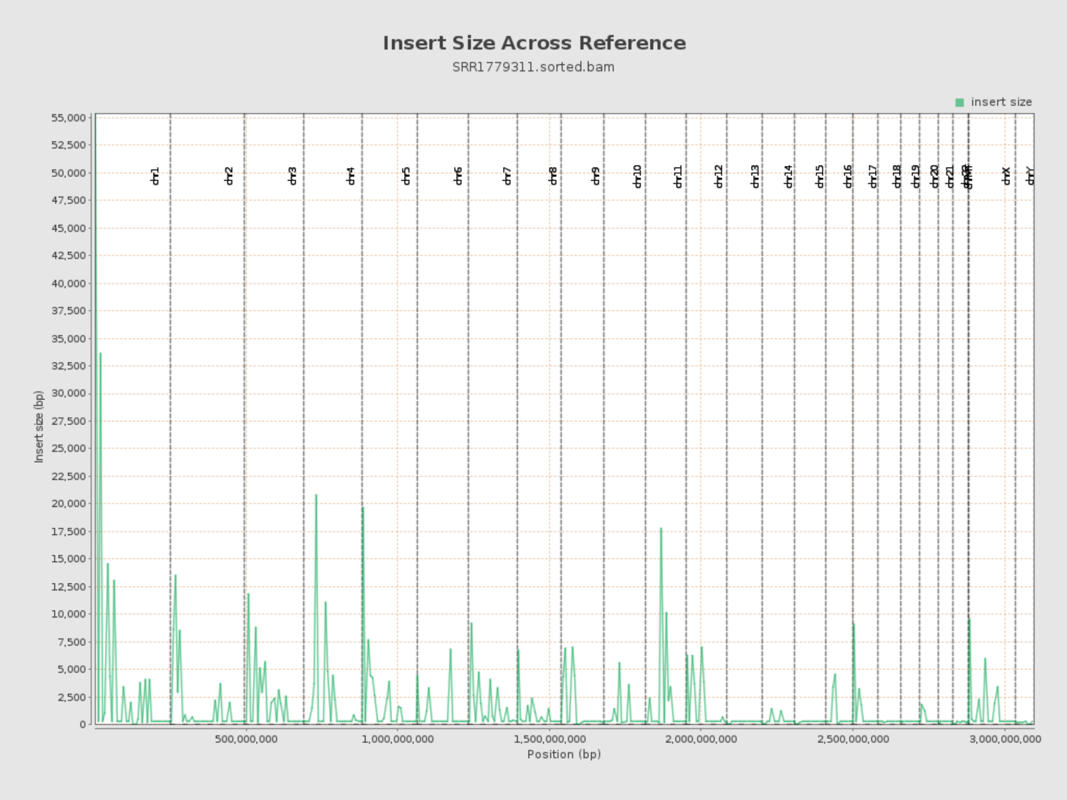
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram