Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 04:01:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779158.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_SRR1779158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779158_1.fastq.gz SRR1779158_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 04:01:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,798,892
Mapped reads	15,623,879 / 93.01%
Unmapped reads	1,175,013 / 6.99%
Mapped paired reads	15,623,879 / 93.01%
Mapped reads, first in pair	7,889,670 / 46.97%
Mapped reads, second in pair	7,734,209 / 46.04%
Mapped reads, both in pair	15,376,468 / 91.53%
Mapped reads, singletons	247,411 / 1.47%
Secondary alignments	0
Supplementary alignments	94,941 / 0.57%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	441,768 / 2.63%
Duplication rate	2.49%
Clipped reads	932,917 / 5.55%

2.2. ACGT Content

Number/percentage of A's	480,996,798 / 30.84%
Number/percentage of C's	297,195,703 / 19.06%
Number/percentage of T's	478,943,676 / 30.71%
Number/percentage of G's	301,874,972 / 19.36%
Number/percentage of N's	630,466 / 0.04%

GC Percentage	38.41%

2.3. Coverage

Mean	0.5039
Standard Deviation	1.654

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	63,031.22
Standard Deviation	2,421,518.78
P25/Median/P75	168 / 225 / 303

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	6,480,564
Insertions	128,824
Mapped reads with at least one insertion	0.81%
Deletions	158,755
Mapped reads with at least one deletion	1%
Homopolymer indels	46.82%

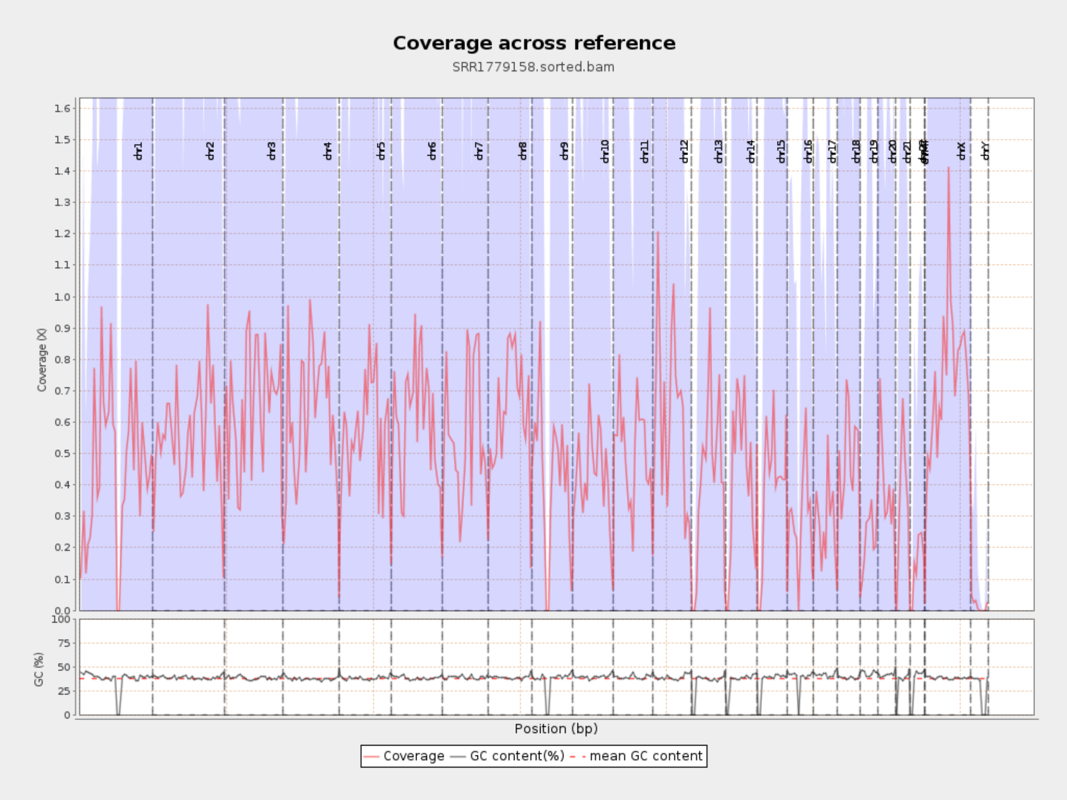
2.7. Chromosome stats

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

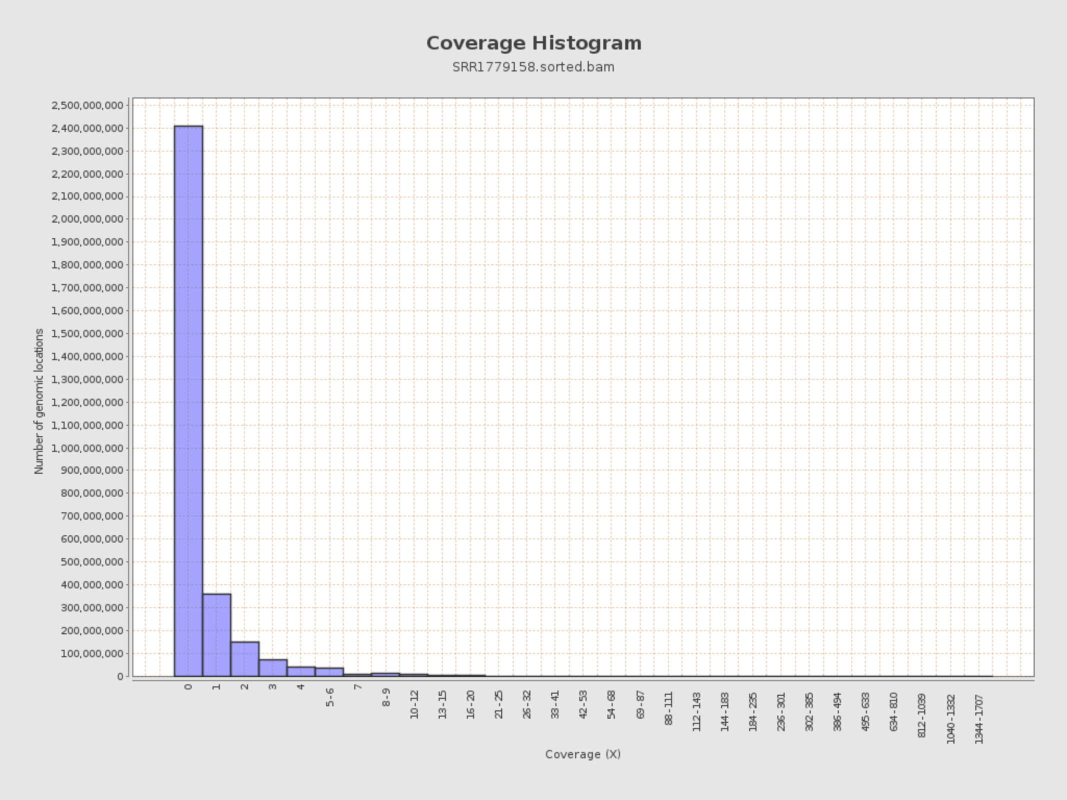
		bases	coverage	deviation
chr1	249250621	115323769	0.4627	1.7952
chr2	243199373	135667393	0.5578	1.743
chr3	198022430	130403128	0.6585	1.795
chr4	191154276	119866820	0.6271	1.6478
chr5	180915260	101369826	0.5603	1.6537
chr6	171115067	104797203	0.6124	1.6301
chr7	159138663	88600640	0.5568	1.621
chr8	146364022	93705467	0.6402	1.6374
chr9	141213431	58621630	0.4151	1.3877
chr10	135534747	58633040	0.4326	2.8474
chr11	135006516	68369622	0.5064	1.4514
chr12	133851895	82713552	0.6179	1.808
chr13	115169878	50546098	0.4389	1.2743
chr14	107349540	45274617	0.4217	1.4076
chr15	102531392	39190362	0.3822	1.3696
chr16	90354753	25256503	0.2795	0.9848
chr17	81195210	22269711	0.2743	1.1129
chr18	78077248	39186036	0.5019	1.4821
chr19	59128983	13042248	0.2206	1.1851
chr20	63025520	25229307	0.4003	1.2635
chr21	48129895	17530502	0.3642	1.1022
chr22	51304566	7314727	0.1426	0.6341
chrMT	16571	386	0.0233	0.1837
chrX	155270560	116144602	0.748	2.0176

chrY	59373566	936932	0.0158	0.2705

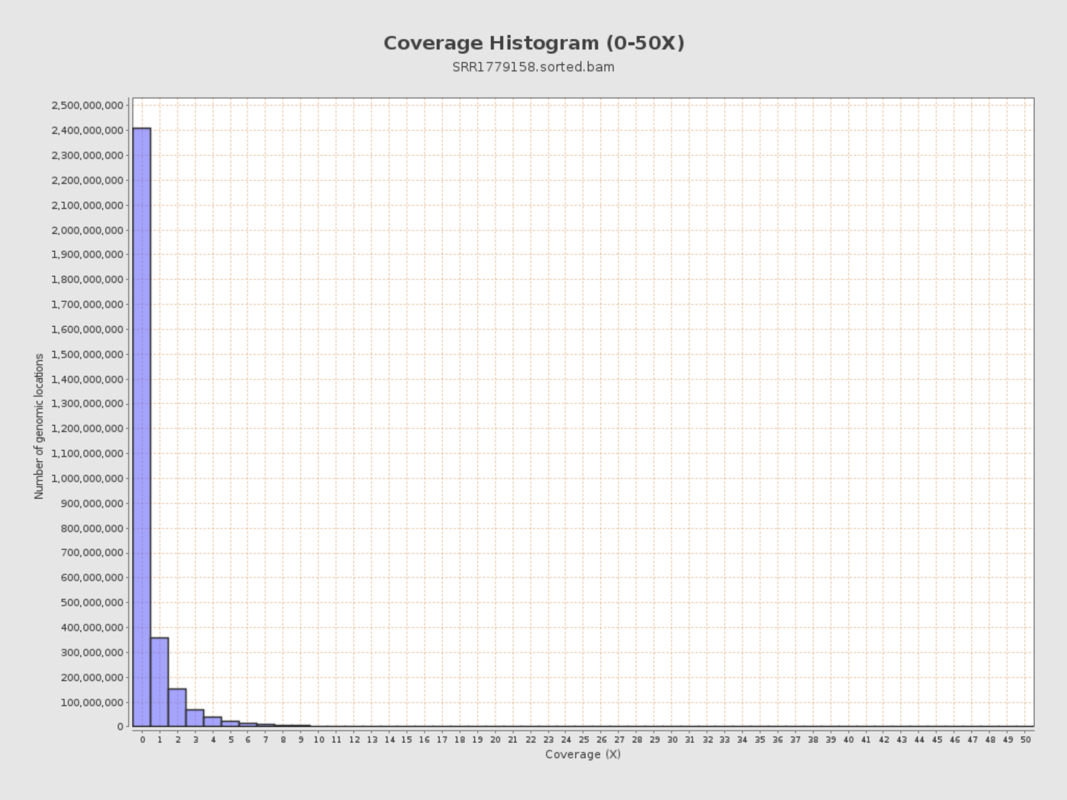
3. Results : Coverage across reference



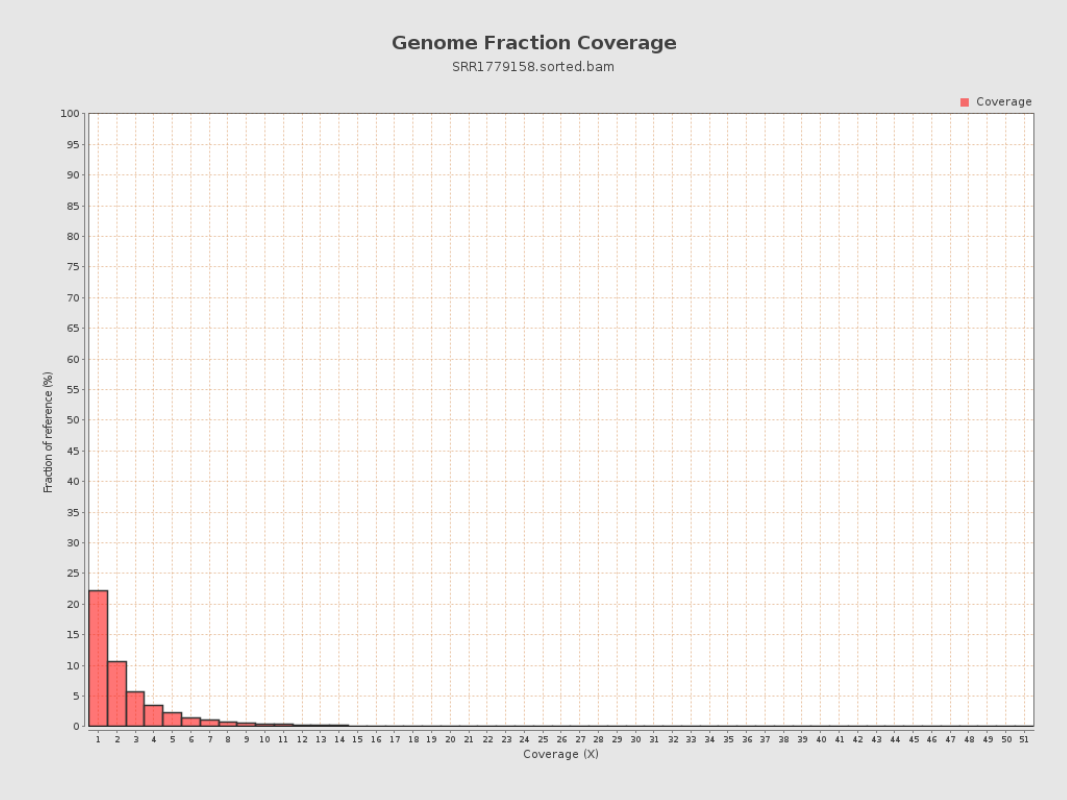
4. Results : Coverage Histogram



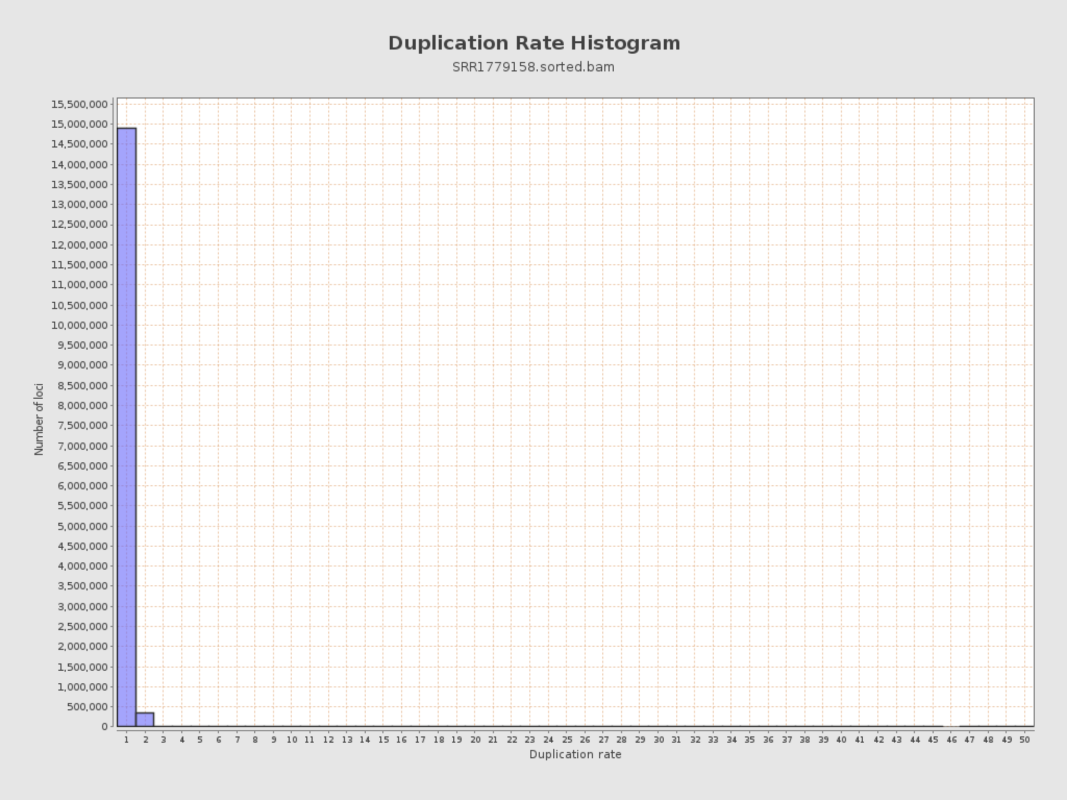
5. Results : Coverage Histogram (0-50X)



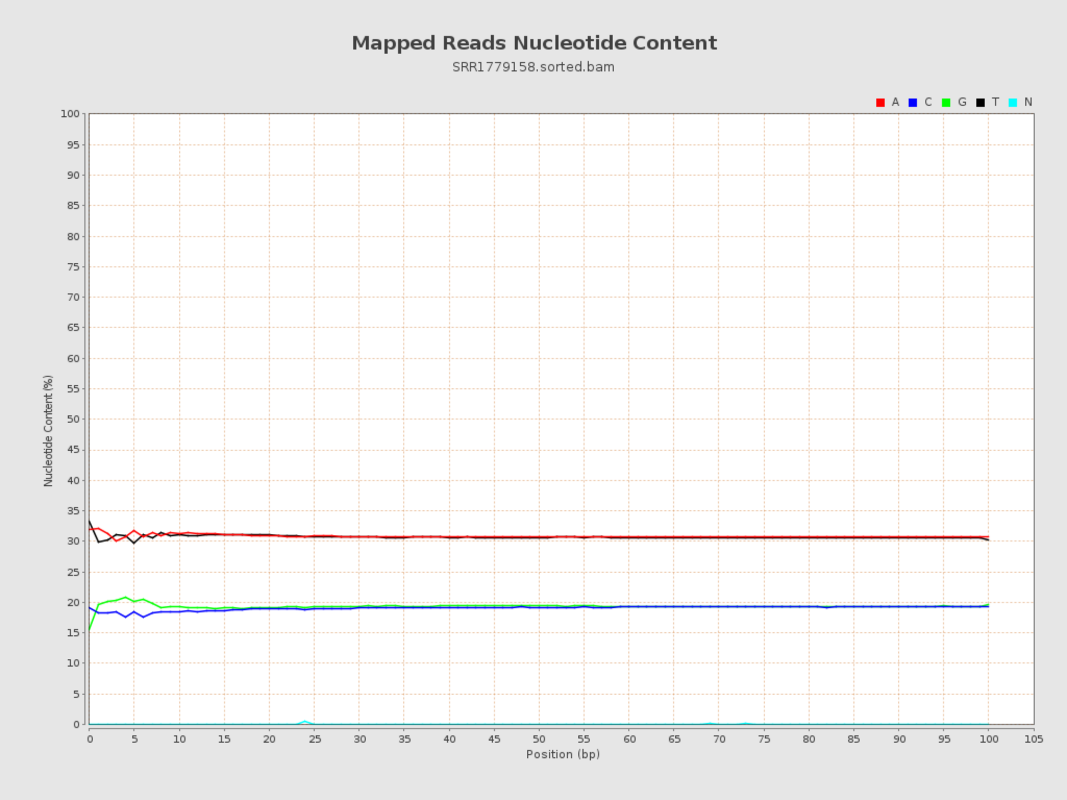
6. Results : Genome Fraction Coverage



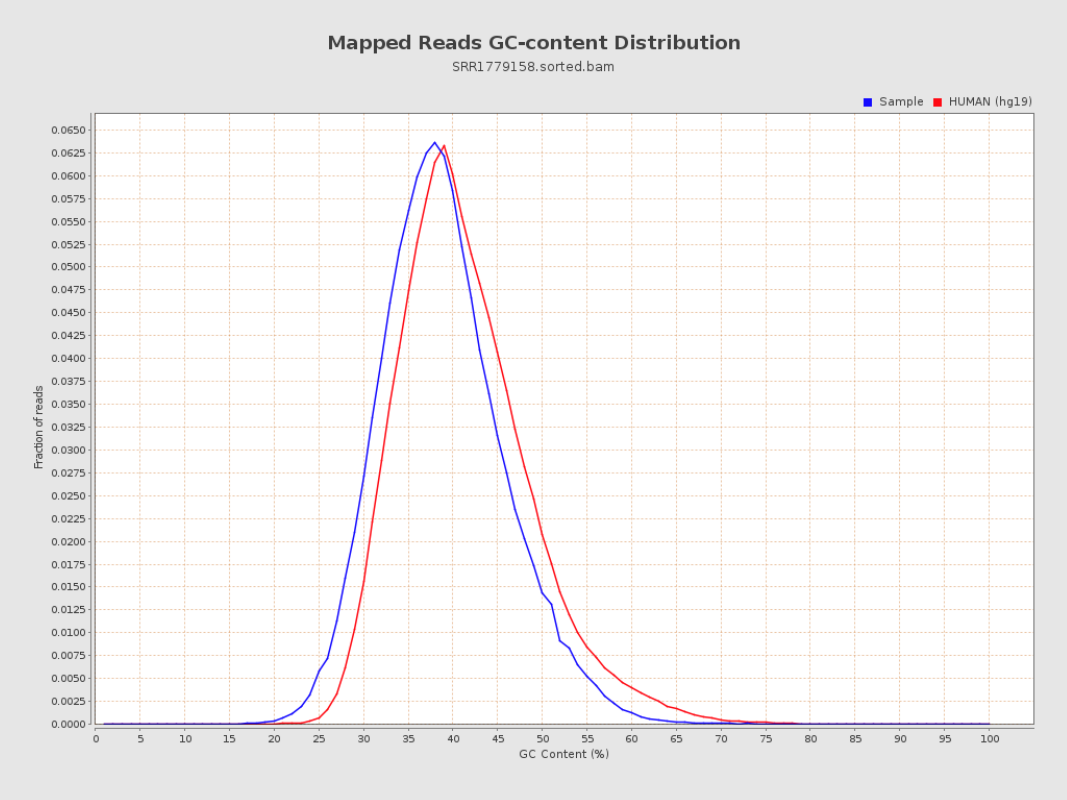
7. Results : Duplication Rate Histogram



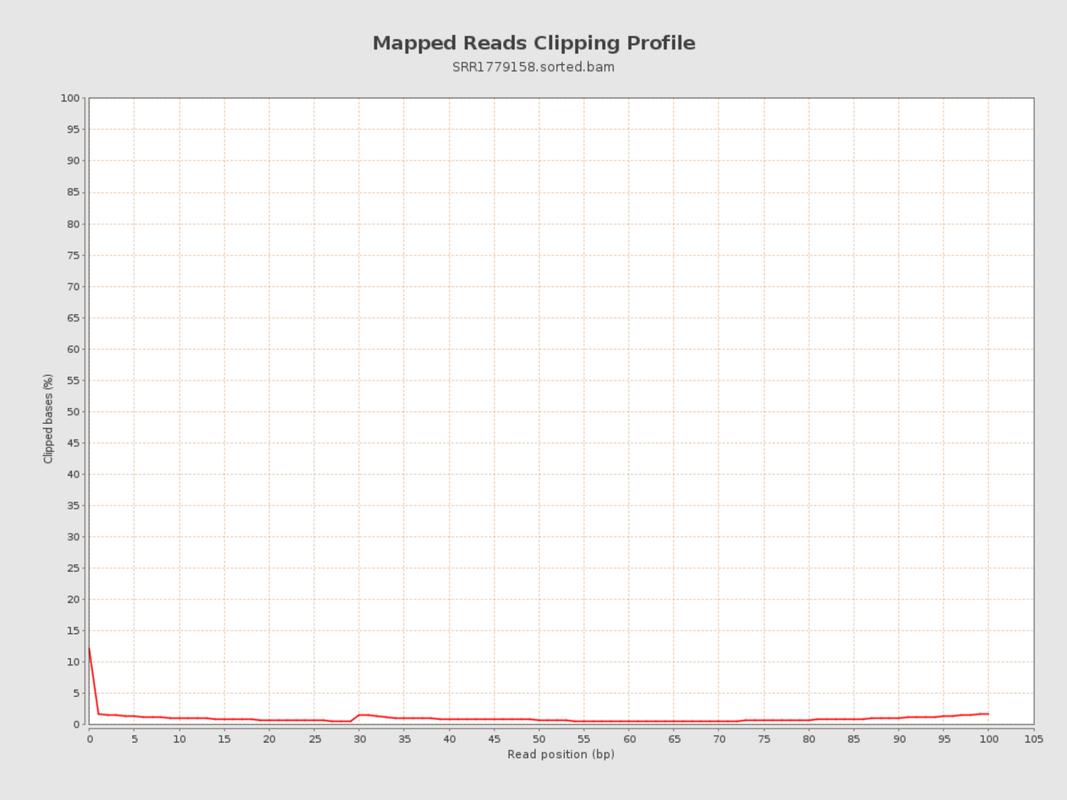
8. Results : Mapped Reads Nucleotide Content



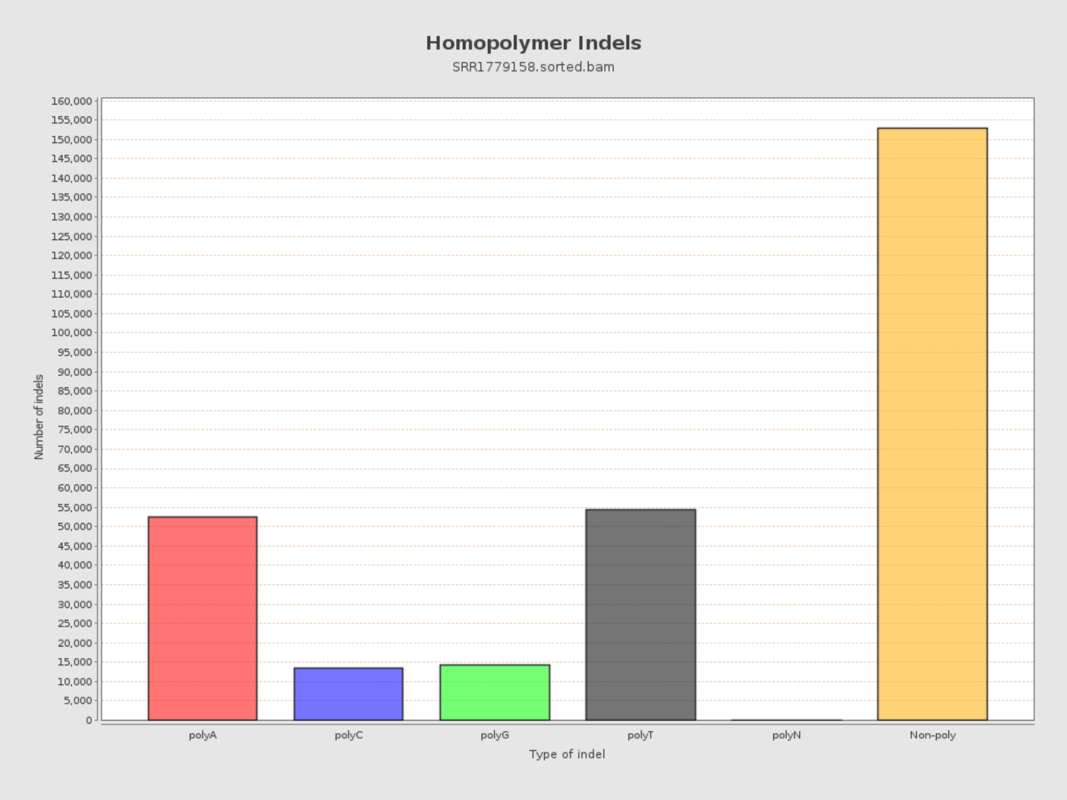
9. Results : Mapped Reads GC-content Distribution



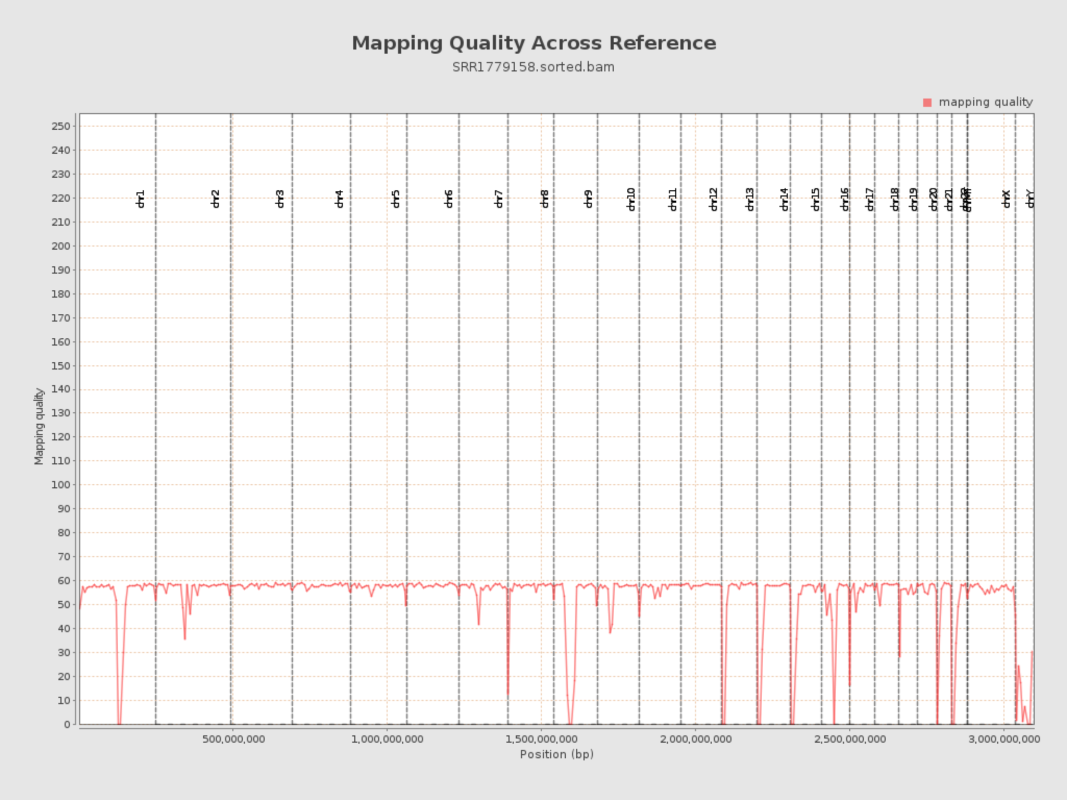
10. Results : Mapped Reads Clipping Profile



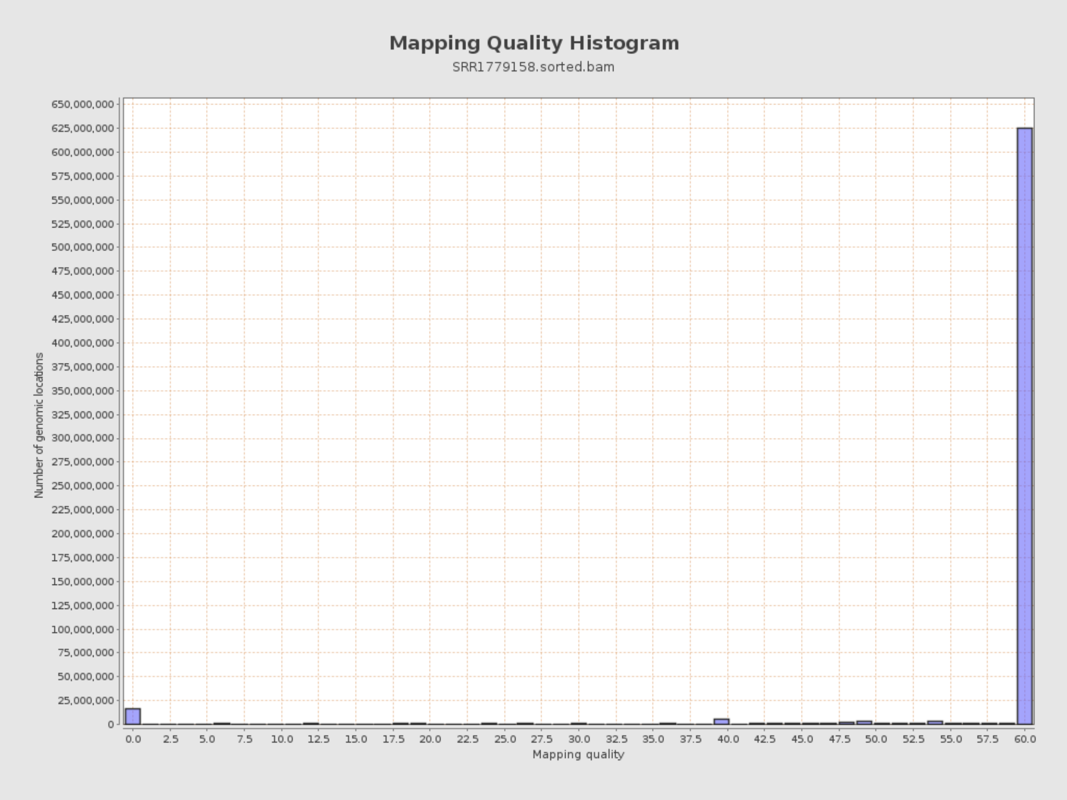
11. Results : Homopolymer Indels



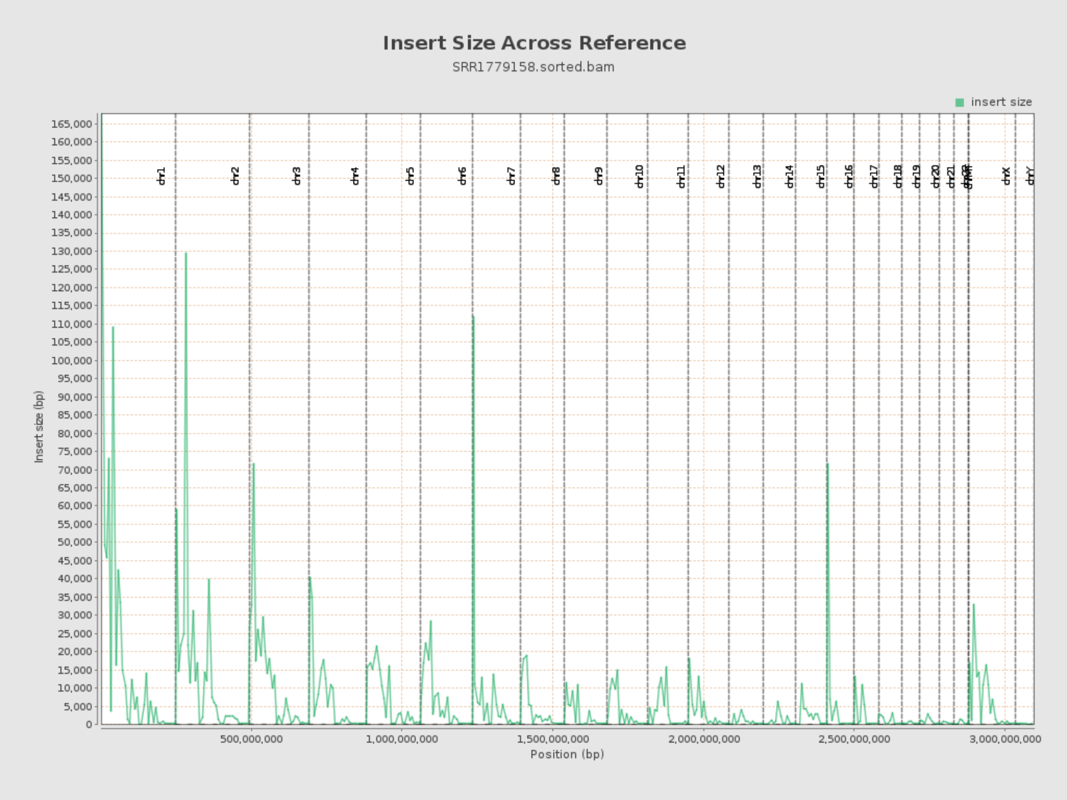
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram