Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 21:32:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779093.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_SRR1779093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779093_1.fastq.gz SRR1779093_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 21:32:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,792,926
Mapped reads	24,897,478 / 96.53%
Unmapped reads	895,448 / 3.47%
Mapped paired reads	24,897,478 / 96.53%
Mapped reads, first in pair	12,590,688 / 48.81%
Mapped reads, second in pair	12,306,790 / 47.71%
Mapped reads, both in pair	24,528,112 / 95.1%
Mapped reads, singletons	369,366 / 1.43%
Secondary alignments	0
Supplementary alignments	130,053 / 0.5%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	682,362 / 2.65%
Duplication rate	2.47%
Clipped reads	1,367,214 / 5.3%

2.2. ACGT Content

Number/percentage of A's	766,823,014 / 30.82%
Number/percentage of C's	474,167,676 / 19.06%
Number/percentage of T's	764,275,760 / 30.72%
Number/percentage of G's	481,693,192 / 19.36%
Number/percentage of N's	843,926 / 0.03%

GC Percentage	38.42%

2.3. Coverage

Mean	0.8038
Standard Deviation	1.9794

2.4. Mapping Quality

Mean Mapping Quality	53.32

2.5. Insert size

Mean	71,763.45
Standard Deviation	2,567,813.58
P25/Median/P75	218 / 285 / 359

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	11,990,073
Insertions	216,892
Mapped reads with at least one insertion	0.86%
Deletions	266,542
Mapped reads with at least one deletion	1.05%
Homopolymer indels	47.21%

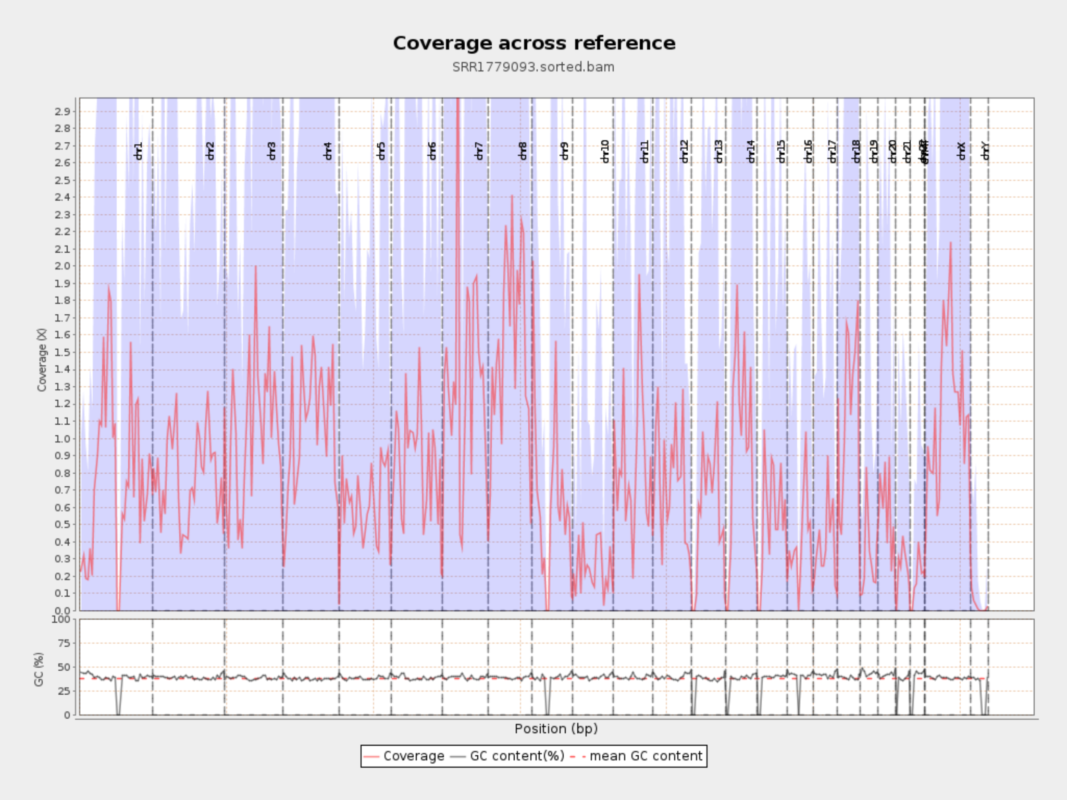
2.7. Chromosome stats

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

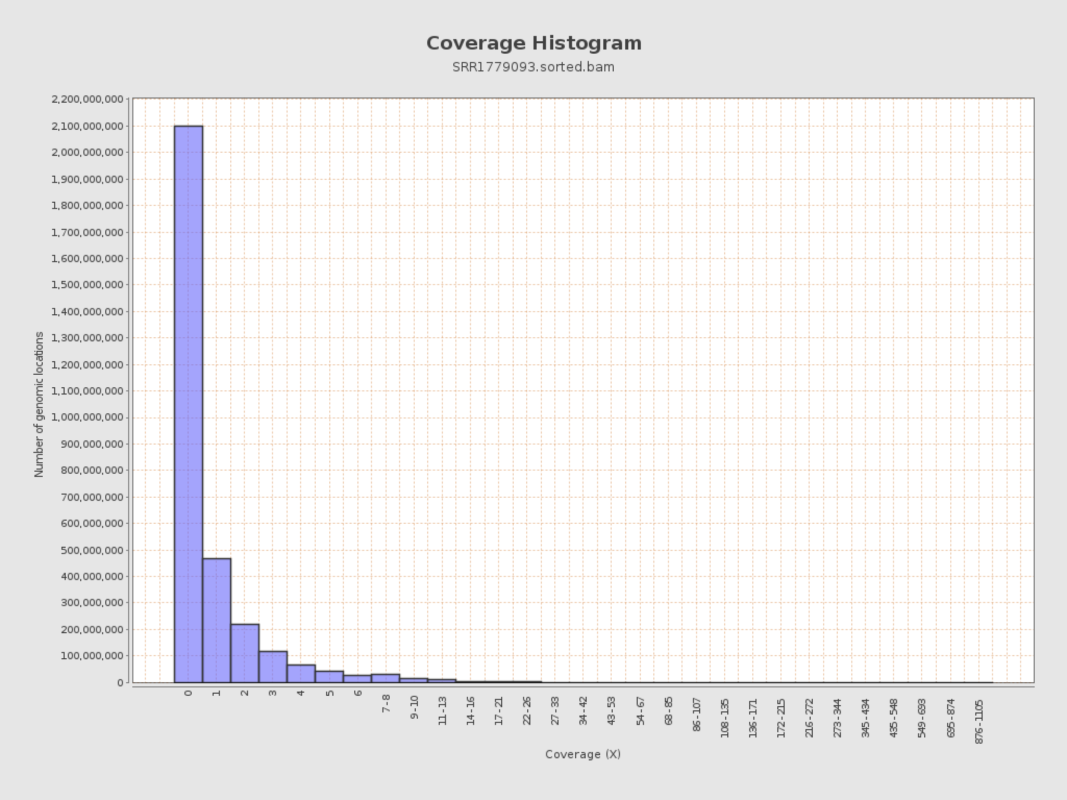
		bases	**coverage**	**deviation**
chr1	249250621	194937444	0.7821	2.1162
chr2	243199373	190742034	0.7843	1.8945
chr3	198022430	205549134	1.038	2.0233
chr4	191154276	205268864	1.0738	2.0311
chr5	180915260	111638758	0.6171	1.4716
chr6	171115067	151162268	0.8834	1.8753
chr7	159138663	216266287	1.359	3.4759
chr8	146364022	230017801	1.5715	2.5388
chr9	141213431	91275841	0.6464	1.7527
chr10	135534747	34845472	0.2571	1.3256
chr11	135006516	114044809	0.8447	1.8768
chr12	133851895	100592371	0.7515	1.8062
chr13	115169878	68129383	0.5916	1.4833
chr14	107349540	100881915	0.9398	2.0354
chr15	102531392	55145862	0.5378	1.5618
chr16	90354753	34420686	0.381	1.1445
chr17	81195210	31128564	0.3834	1.3062
chr18	78077248	92191703	1.1808	2.096
chr19	59128983	16968119	0.287	1.1778
chr20	63025520	36372953	0.5771	1.5161
chr21	48129895	12704080	0.264	0.915
chr22	51304566	9160905	0.1786	0.6793
chrMT	16571	4975	0.3002	0.6341
chrX	155270560	183306030	1.1806	2.3647

chrY	59373566	1645175	0.0277	0.4186

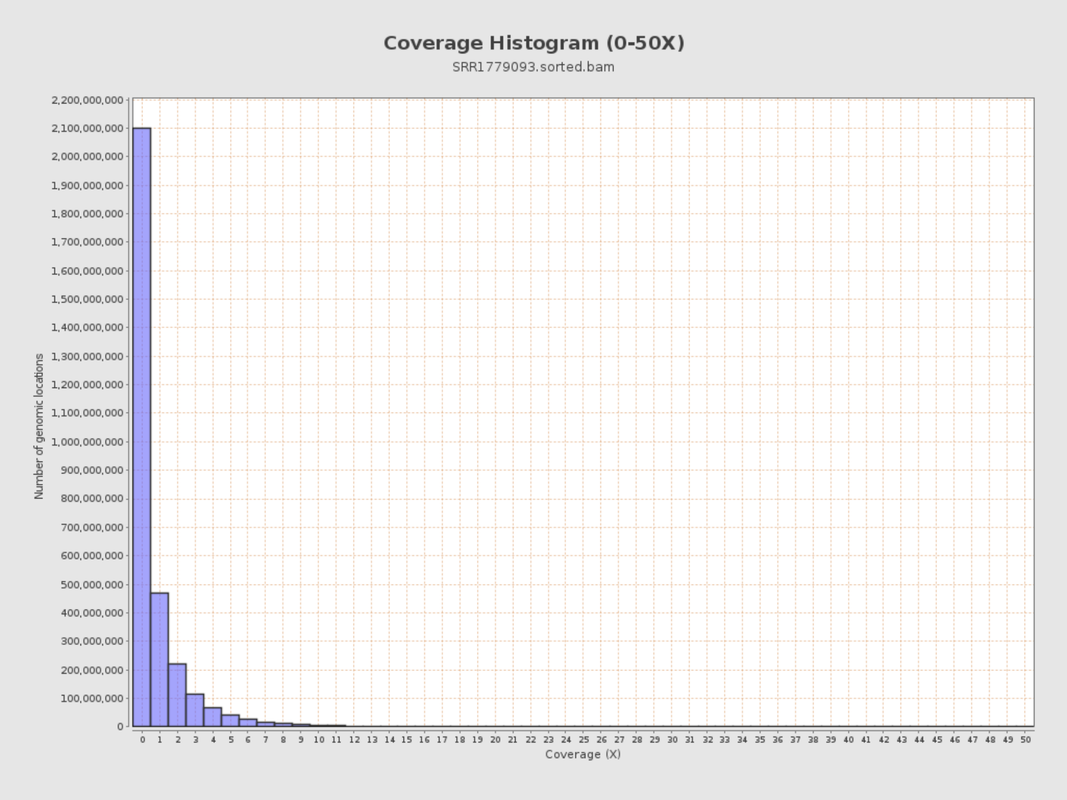
3. Results : Coverage across reference



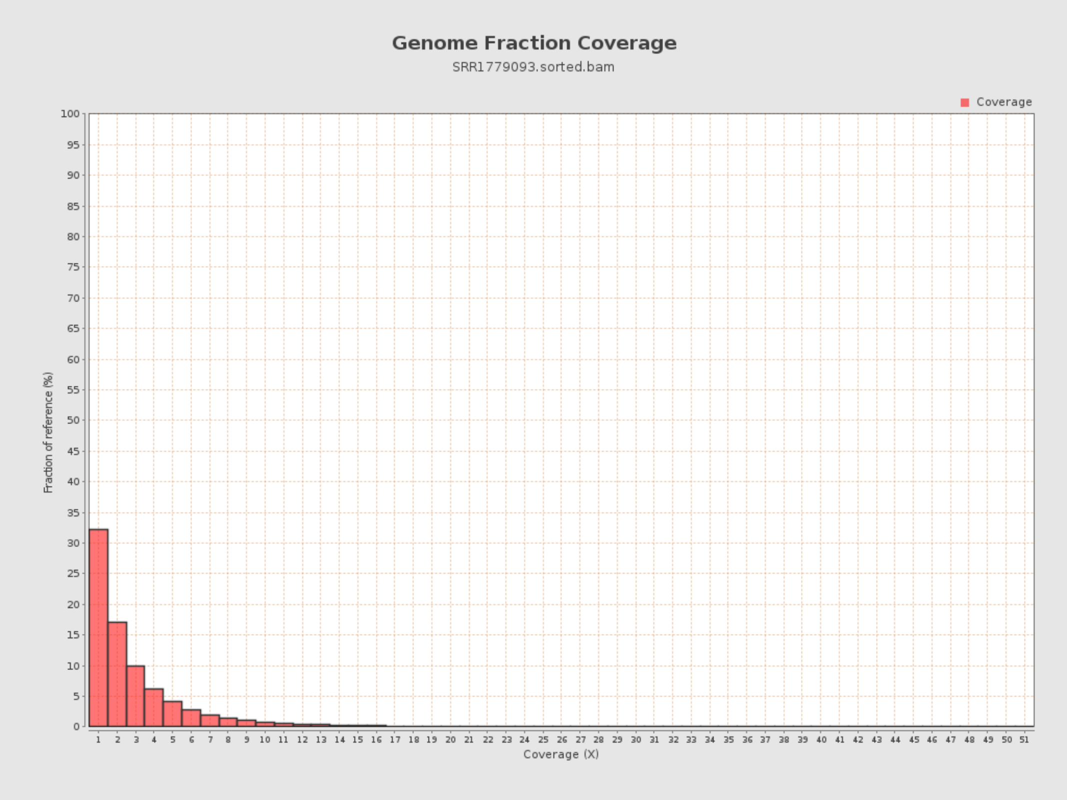
4. Results : Coverage Histogram



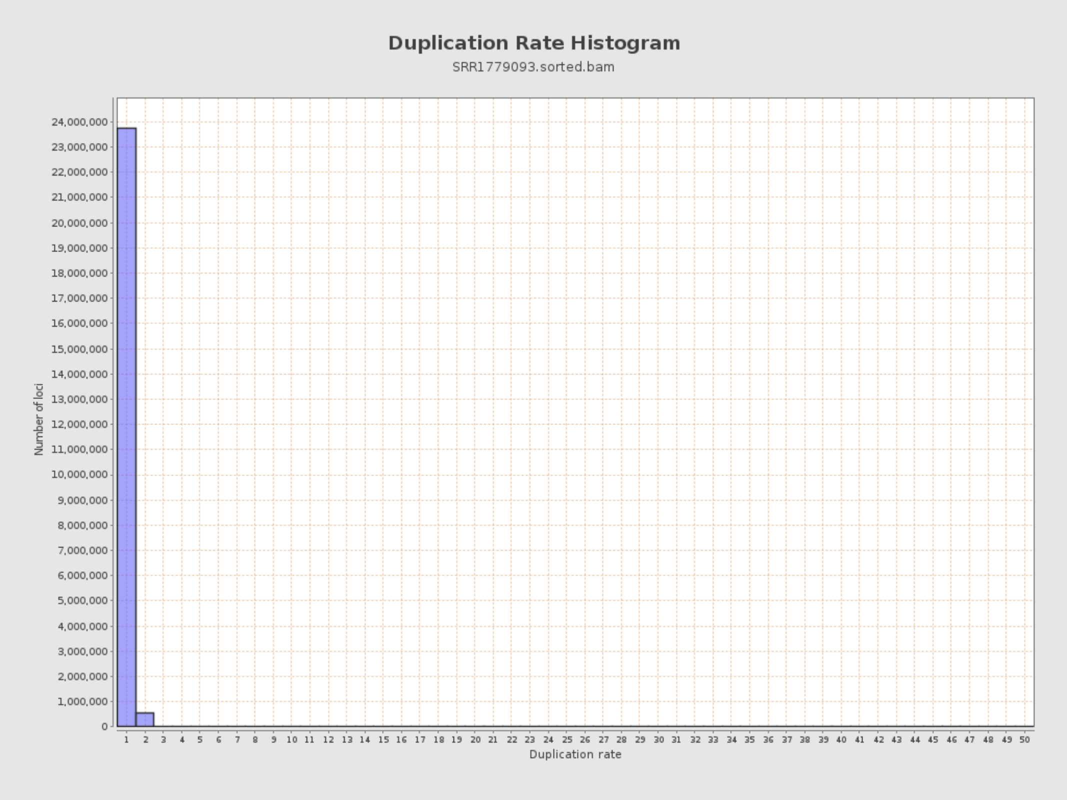
5. Results : Coverage Histogram (0-50X)



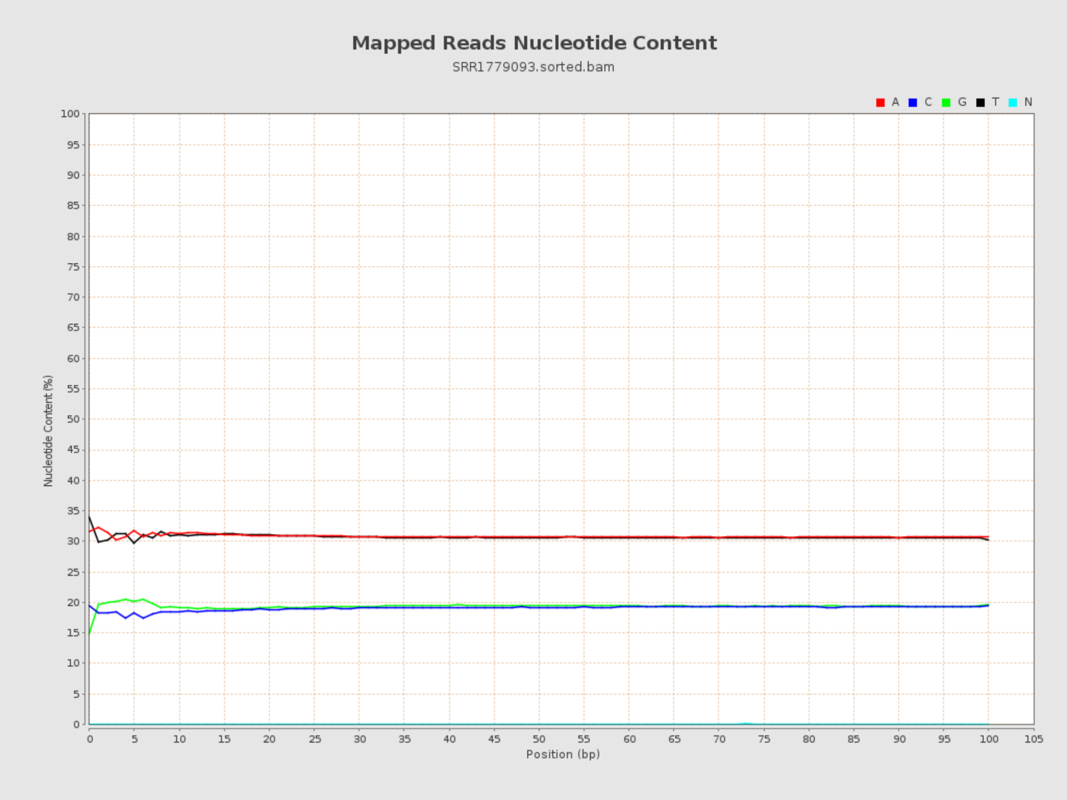
6. Results : Genome Fraction Coverage



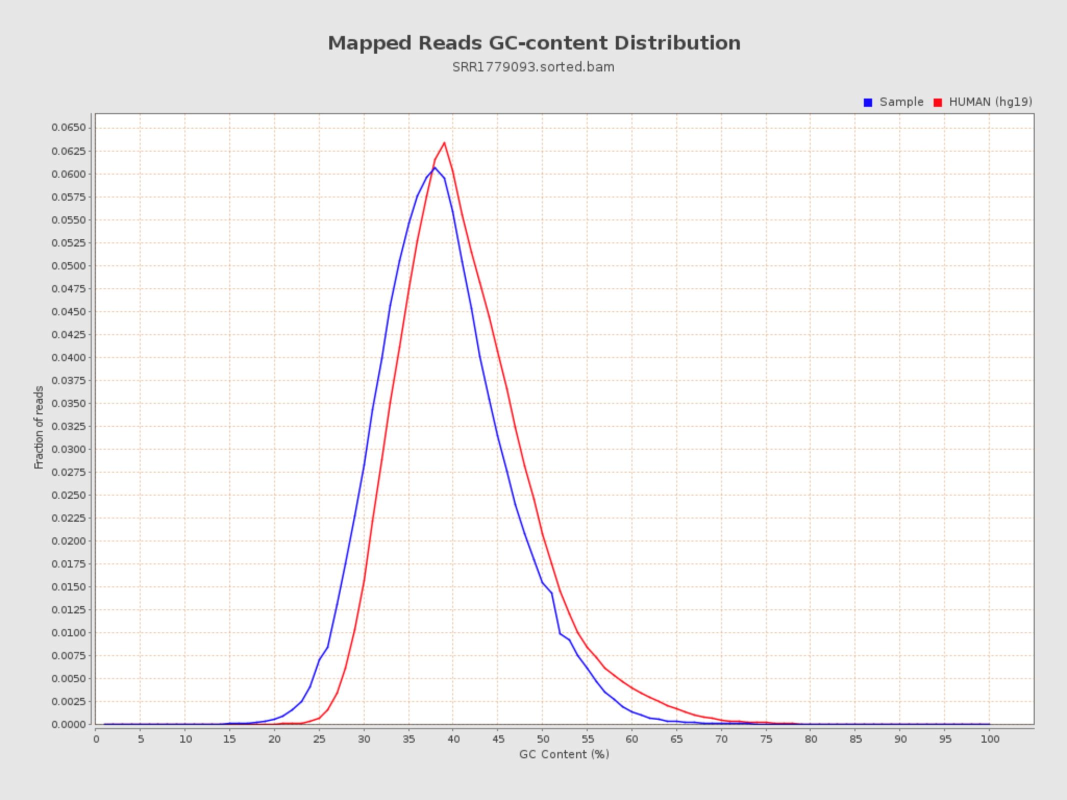
7. Results : Duplication Rate Histogram



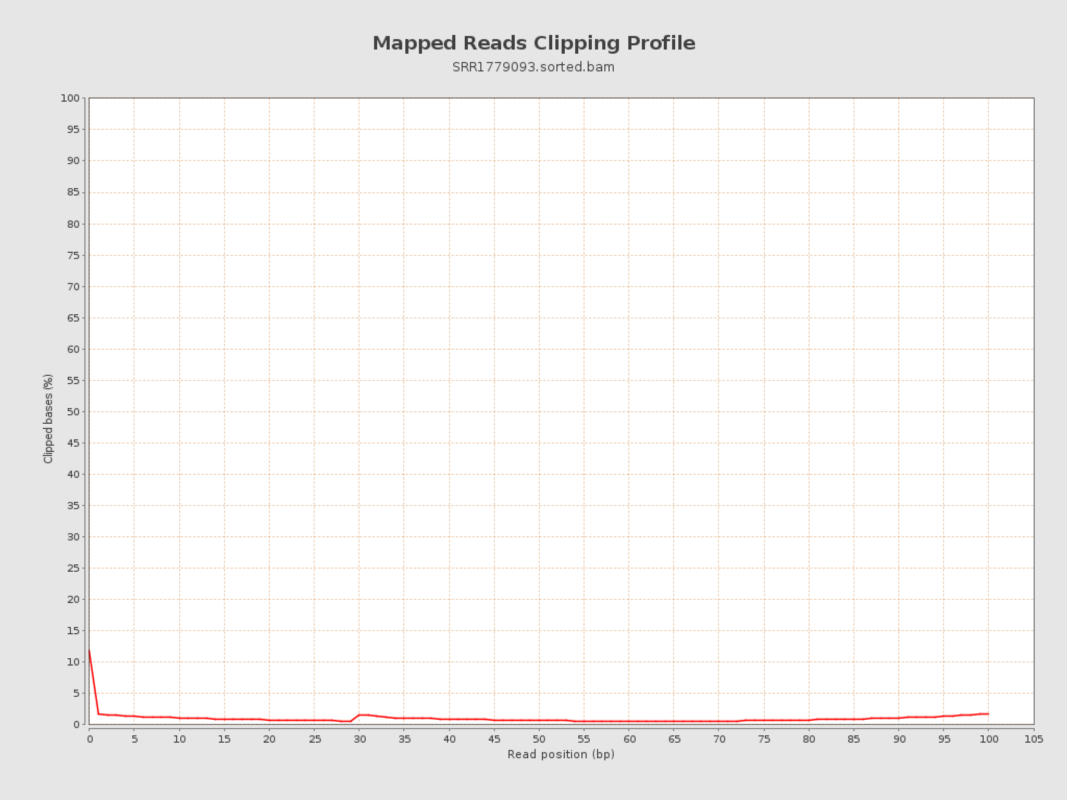
8. Results : Mapped Reads Nucleotide Content



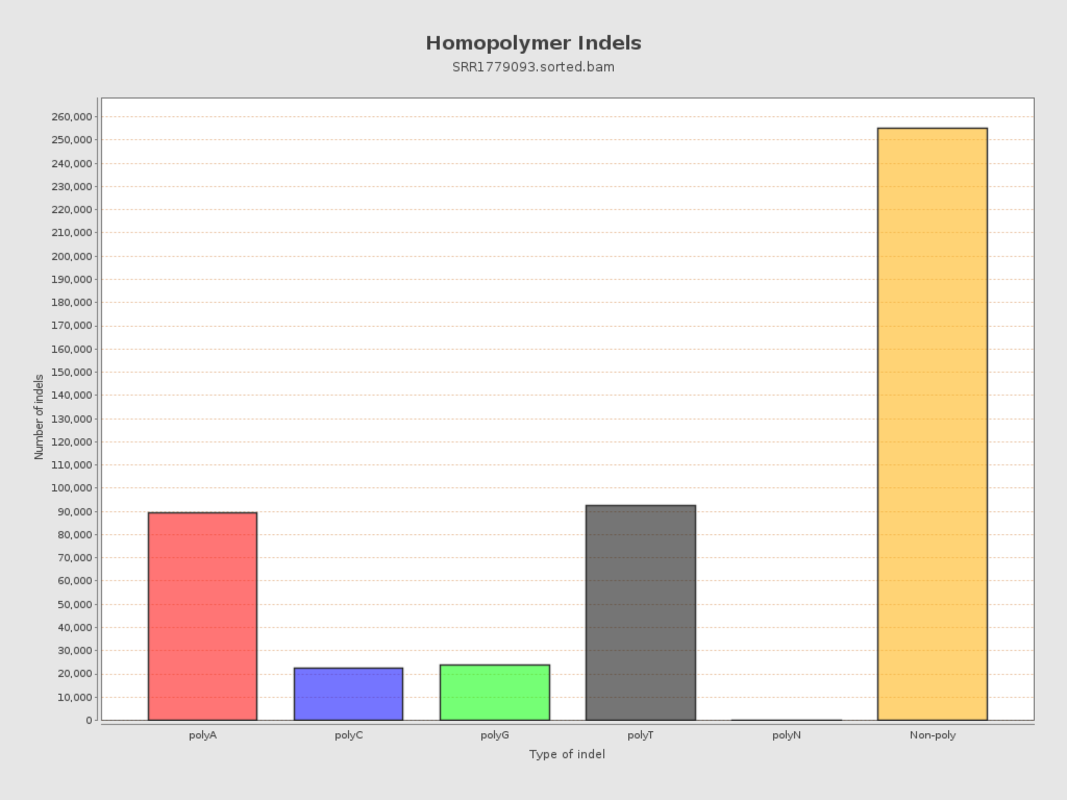
9. Results : Mapped Reads GC-content Distribution



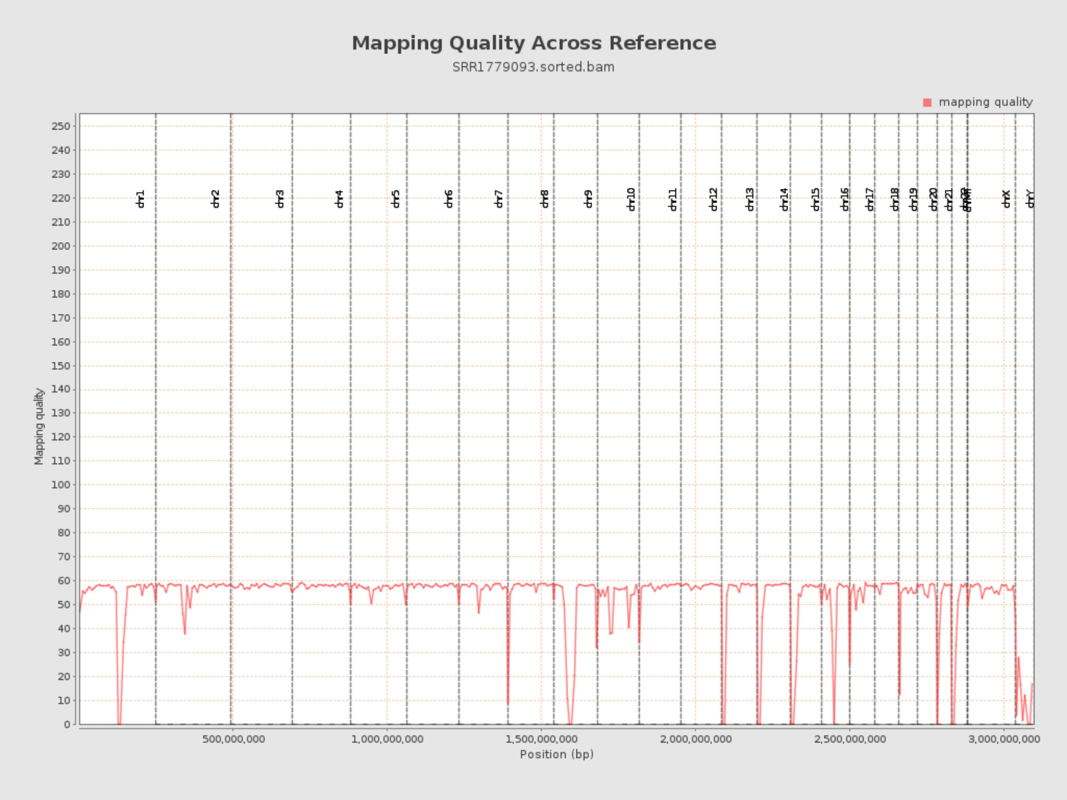
10. Results : Mapped Reads Clipping Profile



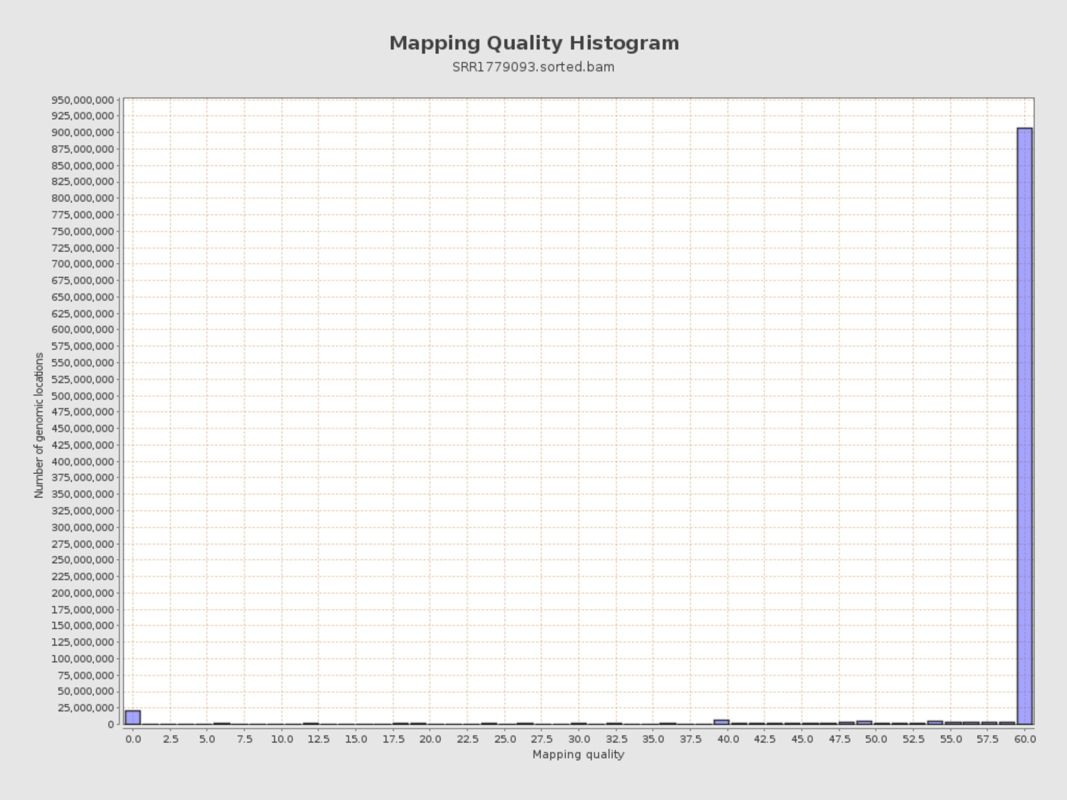
11. Results : Homopolymer Indels



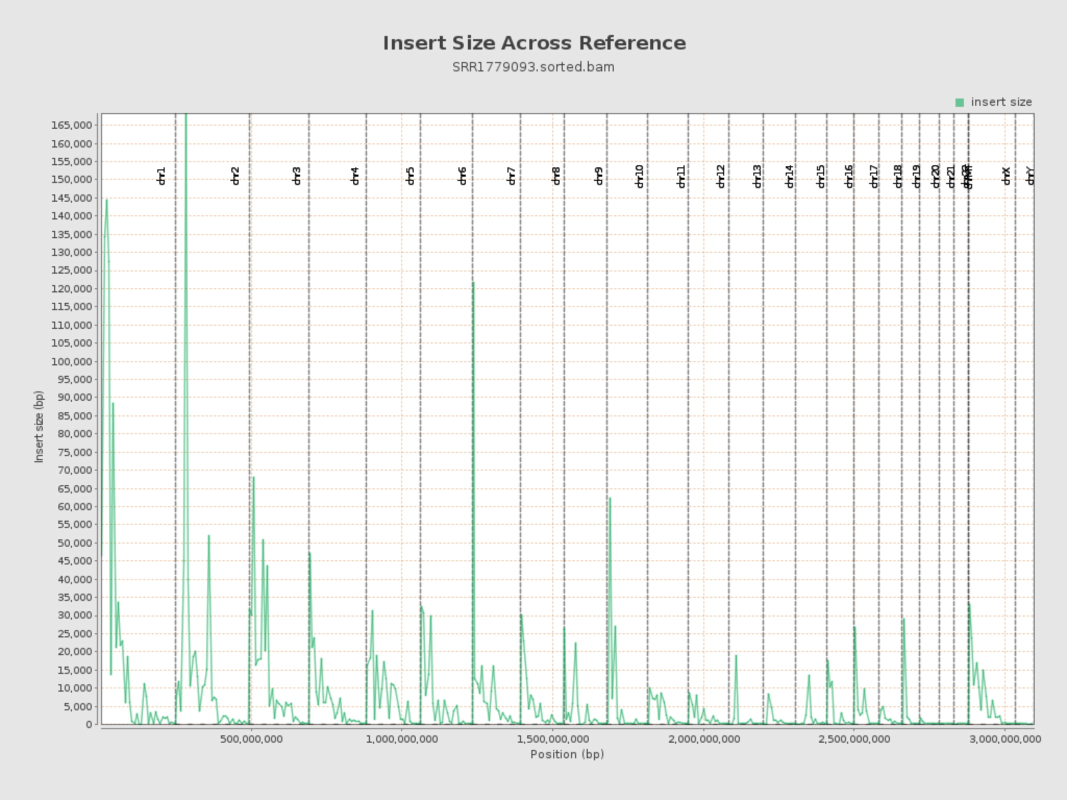
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram