Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 13:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779193.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_SRR1779193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779193_1.fastq.gz SRR1779193_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 13:24:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,877,842
Mapped reads	8,610,575 / 96.99%
Unmapped reads	267,267 / 3.01%
Mapped paired reads	8,610,575 / 96.99%
Mapped reads, first in pair	4,334,482 / 48.82%
Mapped reads, second in pair	4,276,093 / 48.17%
Mapped reads, both in pair	8,540,812 / 96.2%
Mapped reads, singletons	69,763 / 0.79%
Secondary alignments	0
Supplementary alignments	21,206 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	105,581 / 1.19%
Duplication rate	1.15%
Clipped reads	279,558 / 3.15%

2.2. ACGT Content

Number/percentage of A's	210,391,013 / 30.7%
Number/percentage of C's	131,360,580 / 19.17%
Number/percentage of T's	210,063,482 / 30.66%
Number/percentage of G's	133,302,709 / 19.45%
Number/percentage of N's	130,438 / 0.02%

GC Percentage	38.62%

2.3. Coverage

Mean	0.2214
Standard Deviation	0.7556

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	44,109.73
Standard Deviation	1,996,046.59
P25/Median/P75	154 / 202 / 270

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	2,605,358
Insertions	50,756
Mapped reads with at least one insertion	0.58%
Deletions	62,912
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.99%

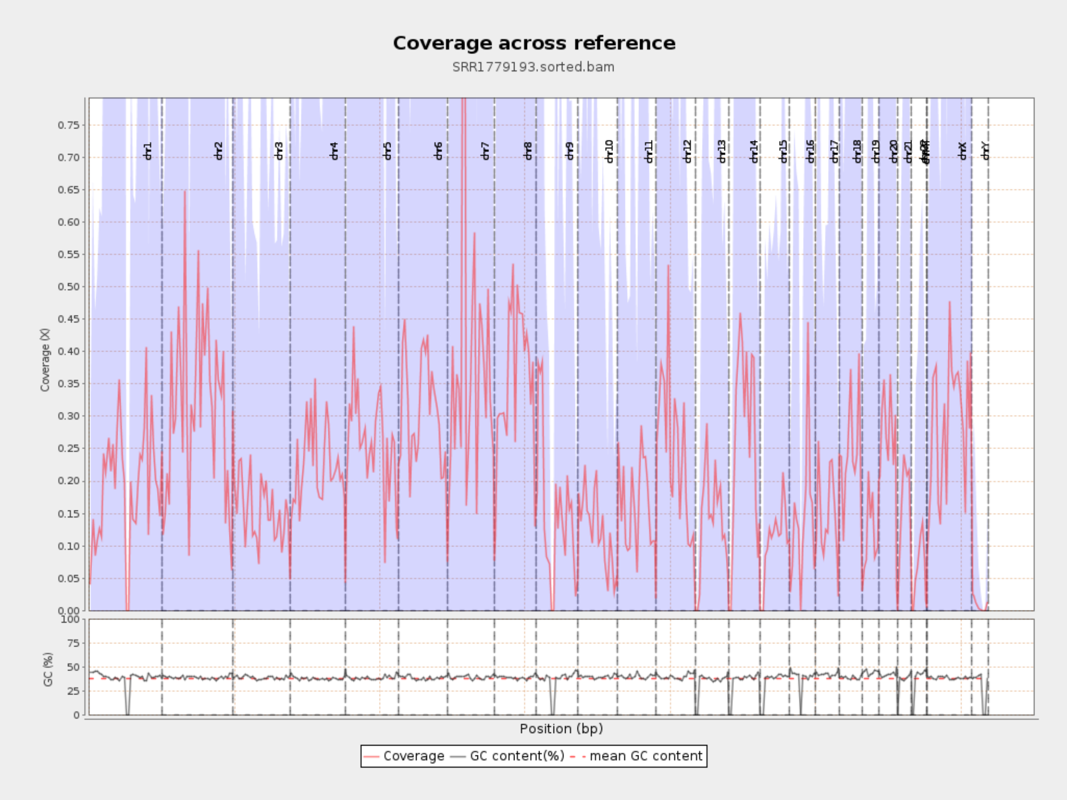
2.7. Chromosome stats

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

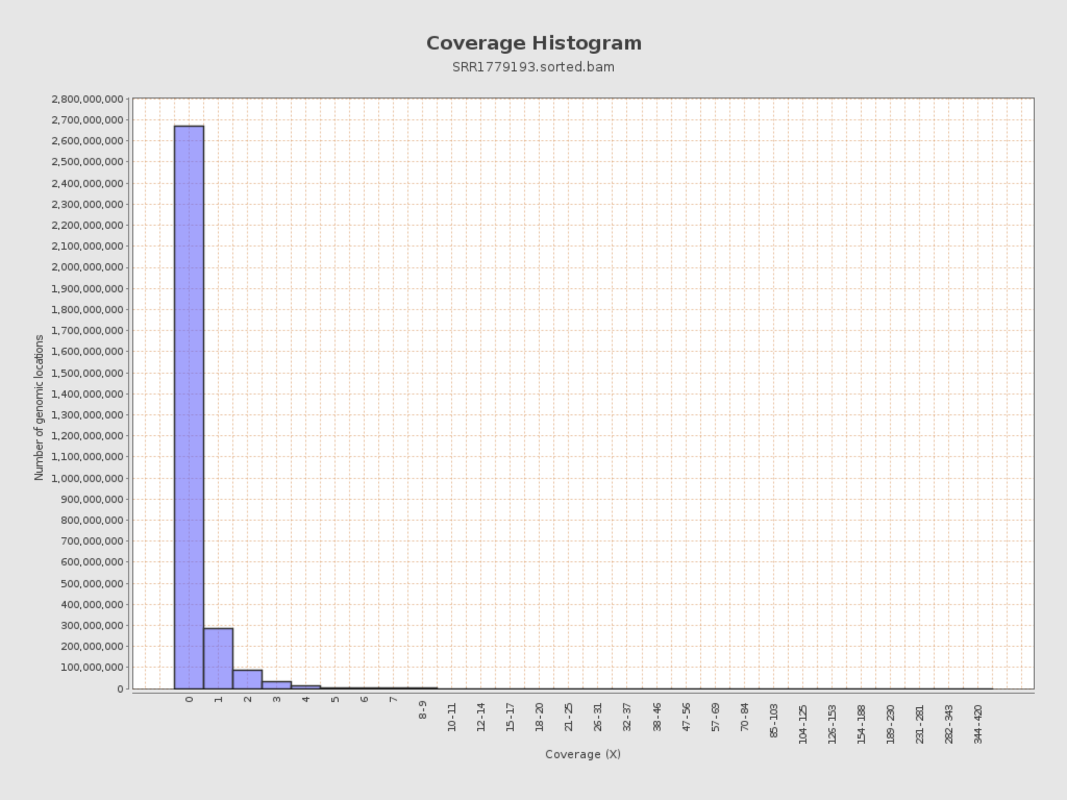
		bases	coverage	deviation
chr1	249250621	47984432	0.1925	0.7482
chr2	243199373	76176310	0.3132	0.8383
chr3	198022430	30961314	0.1564	0.5528
chr4	191154276	43225950	0.2261	0.6869
chr5	180915260	46873117	0.2591	0.7214
chr6	171115067	52222910	0.3052	0.7994
chr7	159138663	62703287	0.394	1.4178
chr8	146364022	52621356	0.3595	0.8961
chr9	141213431	21892461	0.155	0.6239
chr10	135534747	17289791	0.1276	0.7541
chr11	135006516	21824188	0.1617	0.5989
chr12	133851895	32943950	0.2461	0.7327
chr13	115169878	15552875	0.135	0.5144
chr14	107349540	28747587	0.2678	0.7879
chr15	102531392	11158018	0.1088	0.4561
chr16	90354753	12967208	0.1435	0.5227
chr17	81195210	11613445	0.143	0.5229
chr18	78077248	18969413	0.243	0.6934
chr19	59128983	7208844	0.1219	0.5731
chr20	63025520	17215489	0.2732	0.8121
chr21	48129895	7499054	0.1558	0.5661
chr22	51304566	3453631	0.0673	0.3379
chrMT	16571	69	0.0042	0.0644
chrX	155270560	43741317	0.2817	0.8156

chrY	59373566	530781	0.0089	0.137

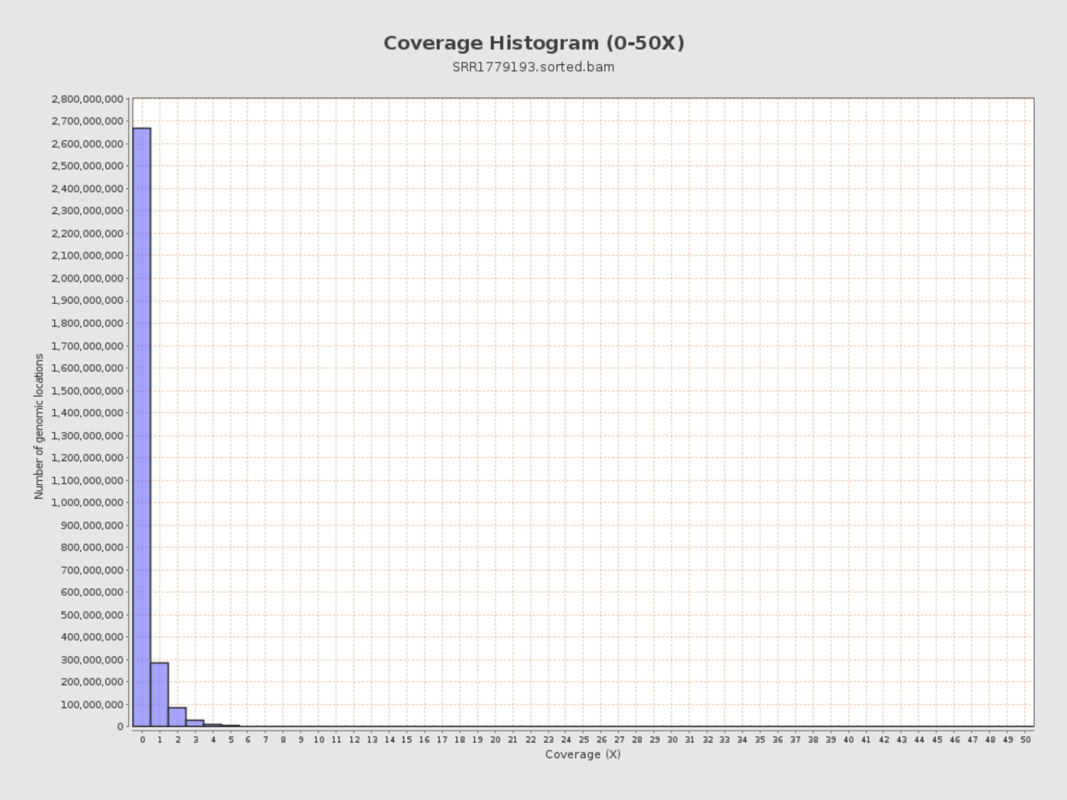
3. Results : Coverage across reference



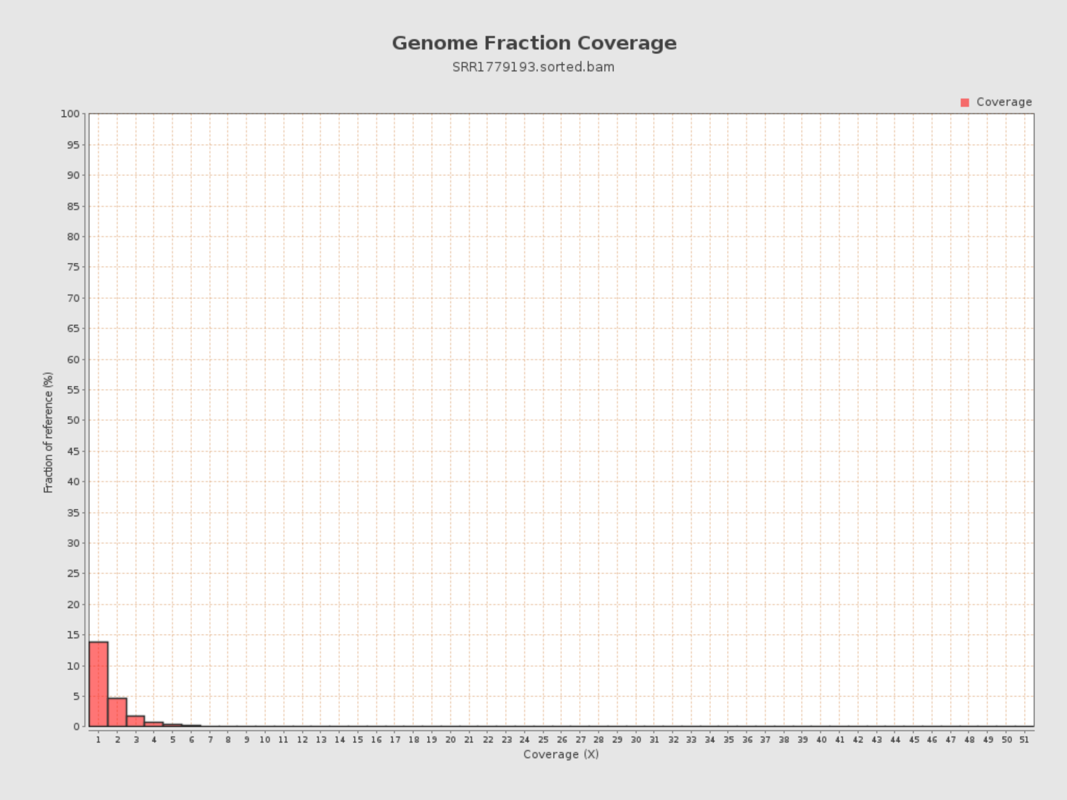
4. Results : Coverage Histogram



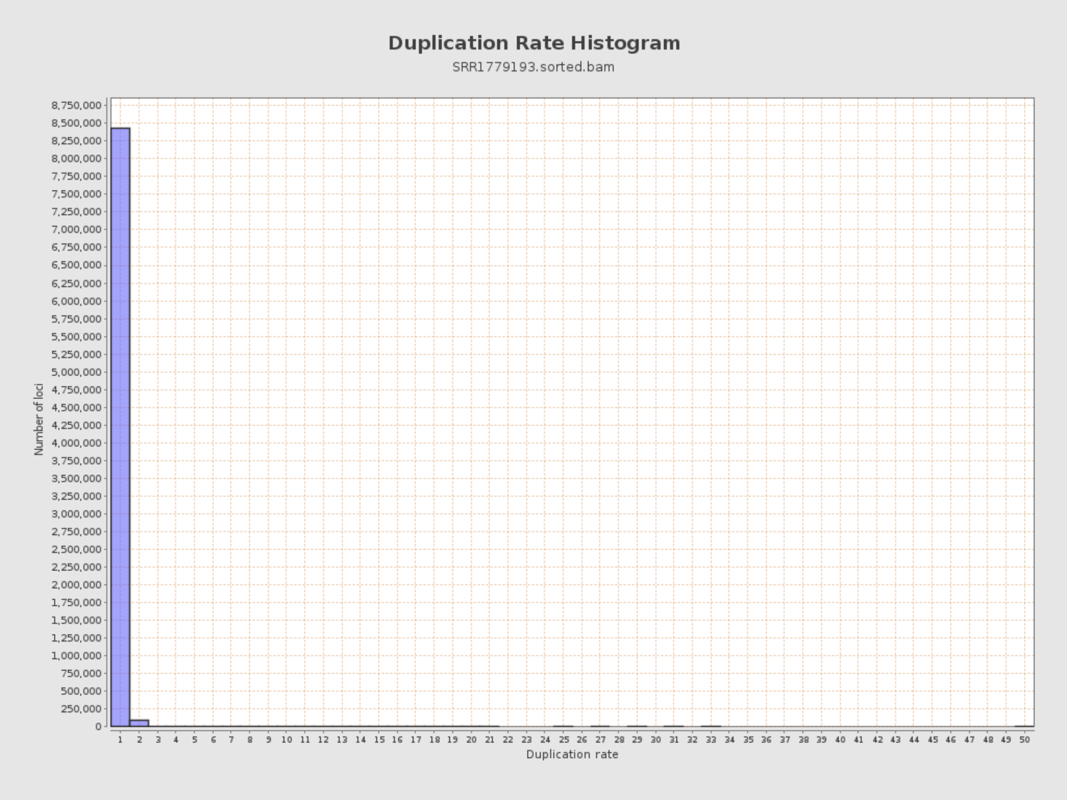
5. Results : Coverage Histogram (0-50X)



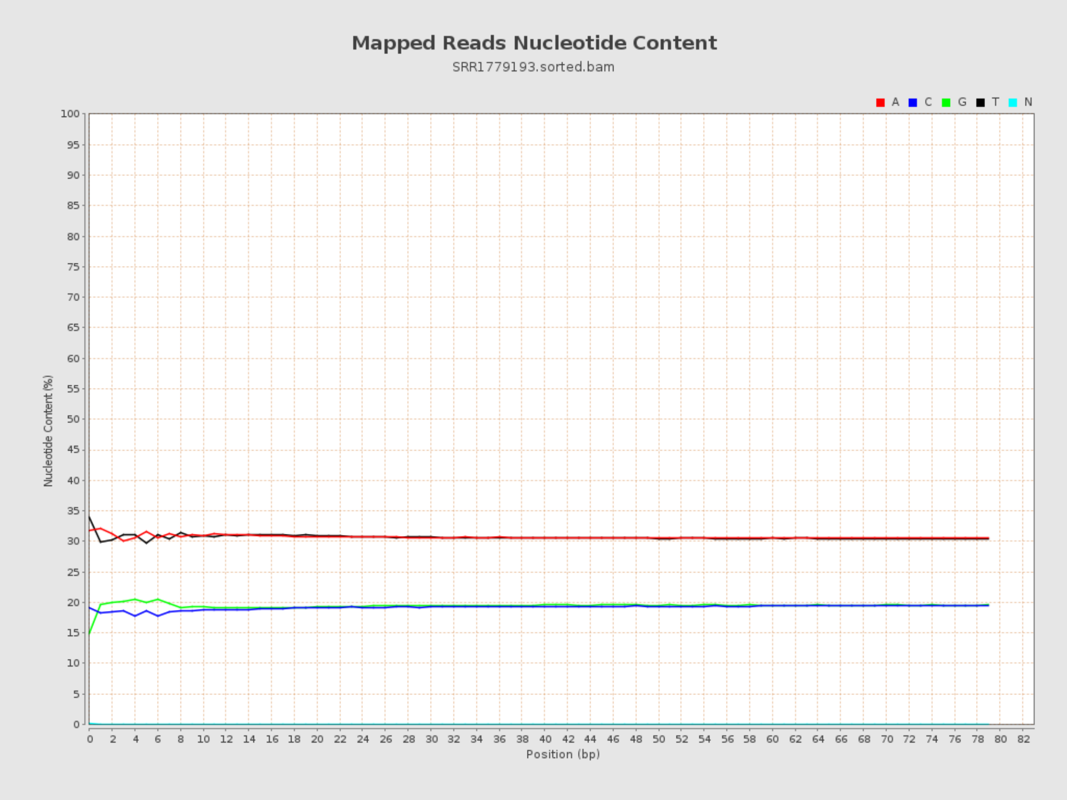
6. Results : Genome Fraction Coverage



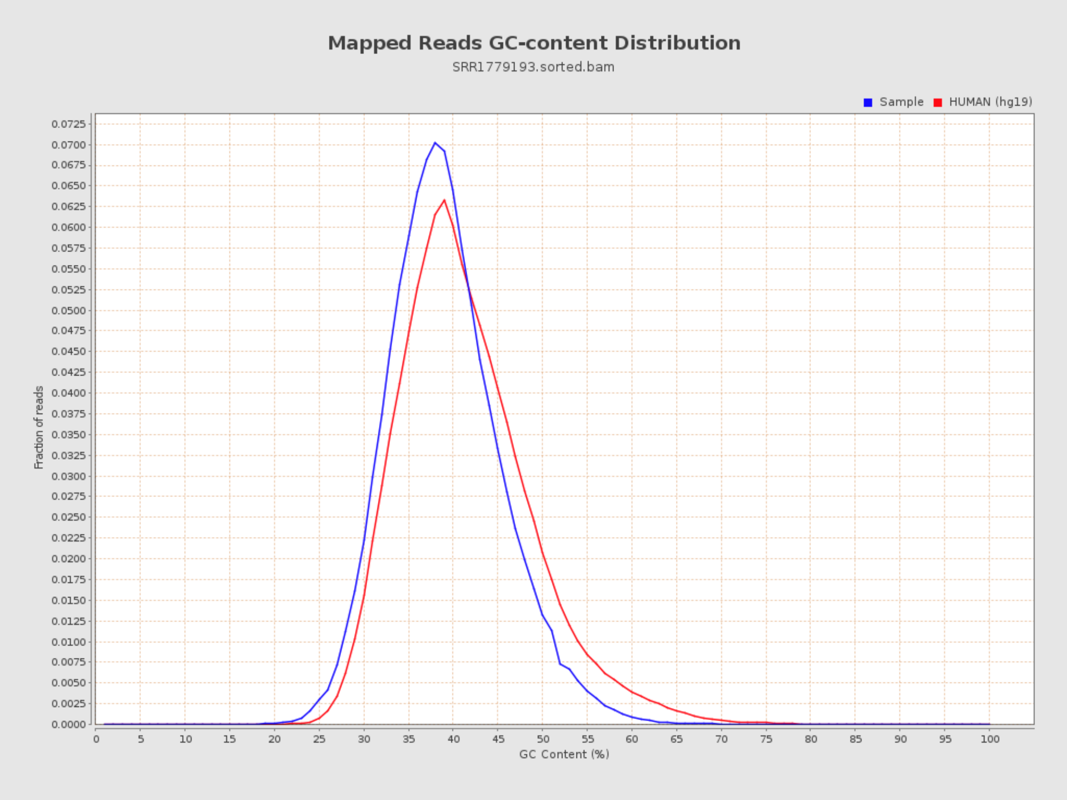
7. Results : Duplication Rate Histogram



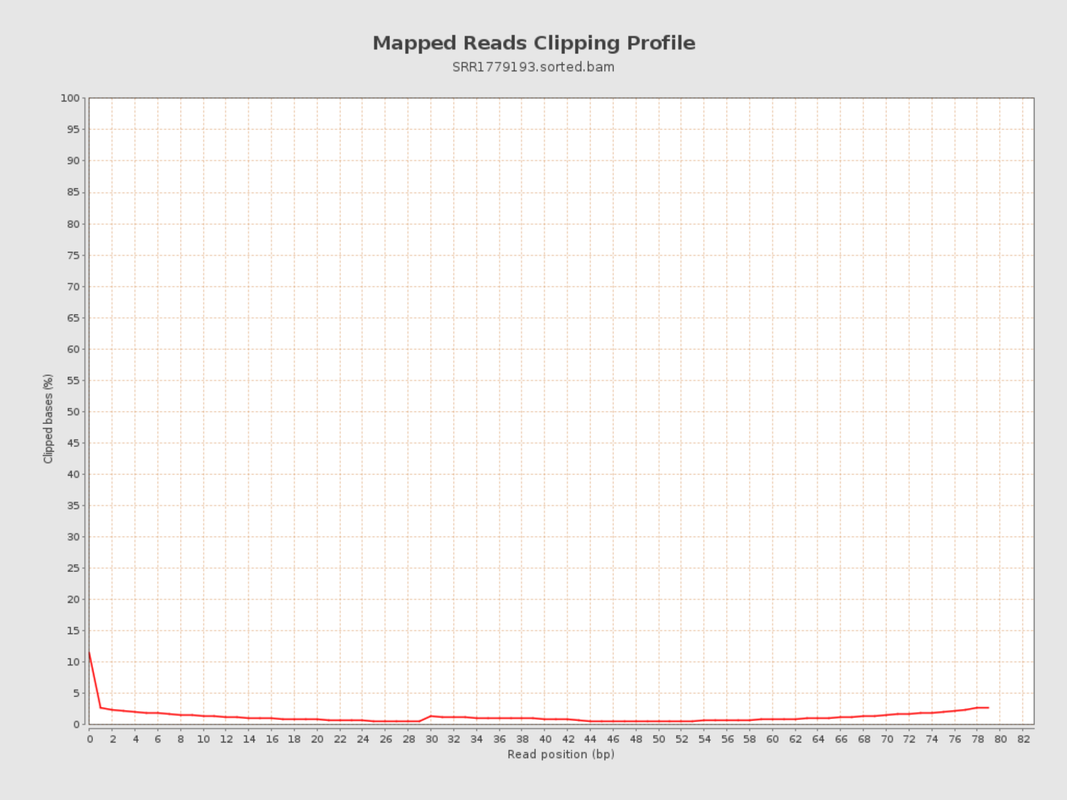
8. Results : Mapped Reads Nucleotide Content



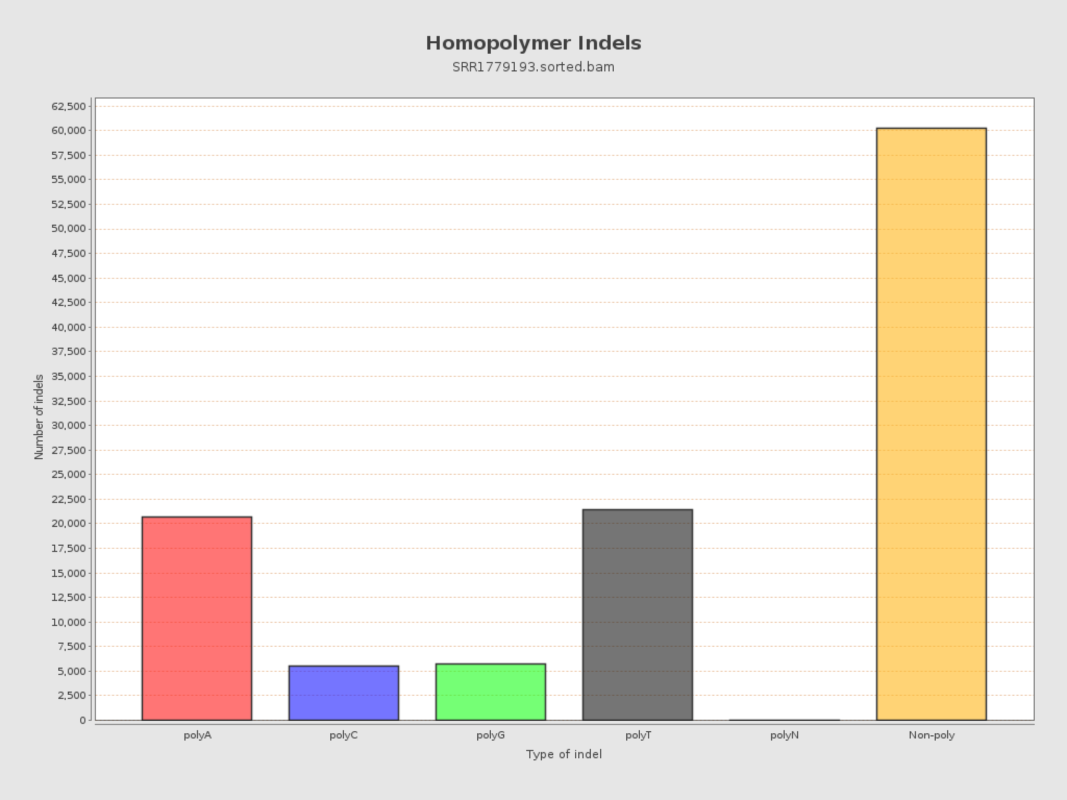
9. Results : Mapped Reads GC-content Distribution



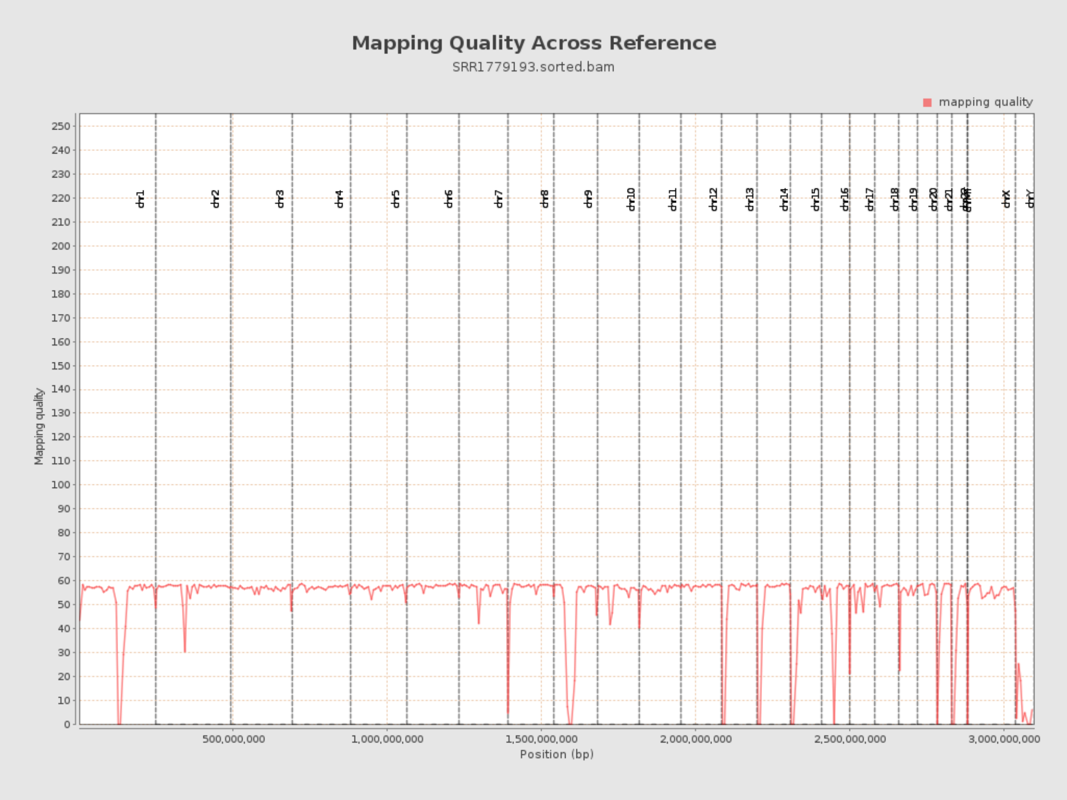
10. Results : Mapped Reads Clipping Profile



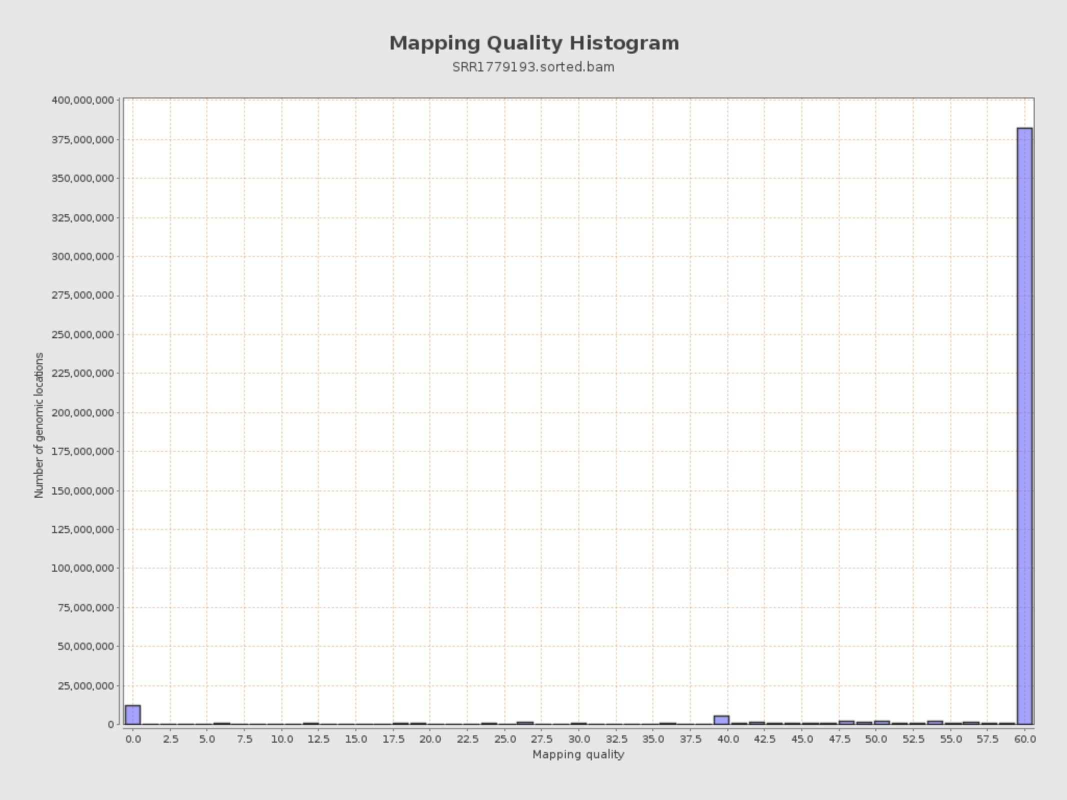
11. Results : Homopolymer Indels



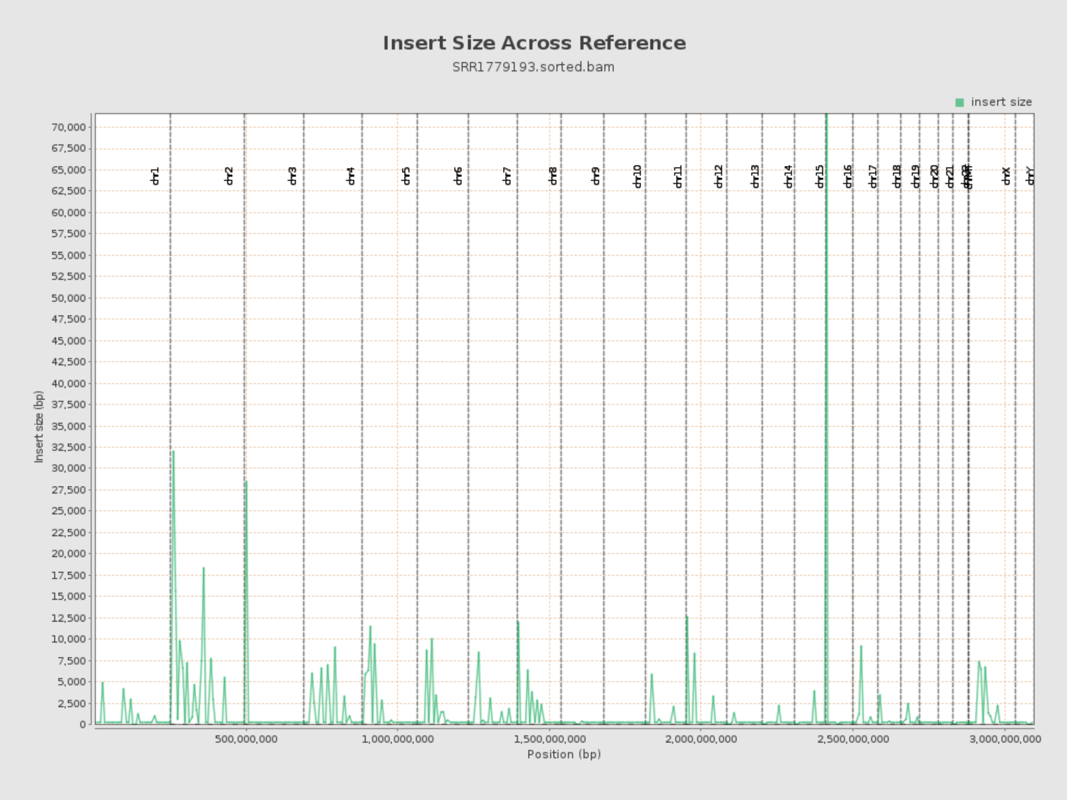
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram