Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 18:12:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779397.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_SRR1779397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779397_1.fastq.gz SRR1779397_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 18:12:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,741,952
Mapped reads	14,035,053 / 95.2%
Unmapped reads	706,899 / 4.8%
Mapped paired reads	14,035,053 / 95.2%
Mapped reads, first in pair	7,063,503 / 47.91%
Mapped reads, second in pair	6,971,550 / 47.29%
Mapped reads, both in pair	13,909,158 / 94.35%
Mapped reads, singletons	125,895 / 0.85%
Secondary alignments	0
Supplementary alignments	48,819 / 0.33%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	418,716 / 2.84%
Duplication rate	2.64%
Clipped reads	677,209 / 4.59%

2.2. ACGT Content

Number/percentage of A's	335,260,420 / 30.09%
Number/percentage of C's	222,247,706 / 19.95%
Number/percentage of T's	328,993,327 / 29.53%
Number/percentage of G's	227,455,153 / 20.41%
Number/percentage of N's	240,649 / 0.02%

GC Percentage	40.36%

2.3. Coverage

Mean	0.36
Standard Deviation	1.3954

2.4. Mapping Quality

Mean Mapping Quality	53.18

2.5. Insert size

Mean	238,026.42
Standard Deviation	4,752,577.05
P25/Median/P75	140 / 185 / 237

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,716,811
Insertions	103,721
Mapped reads with at least one insertion	0.73%
Deletions	123,849
Mapped reads with at least one deletion	0.87%
Homopolymer indels	47.25%

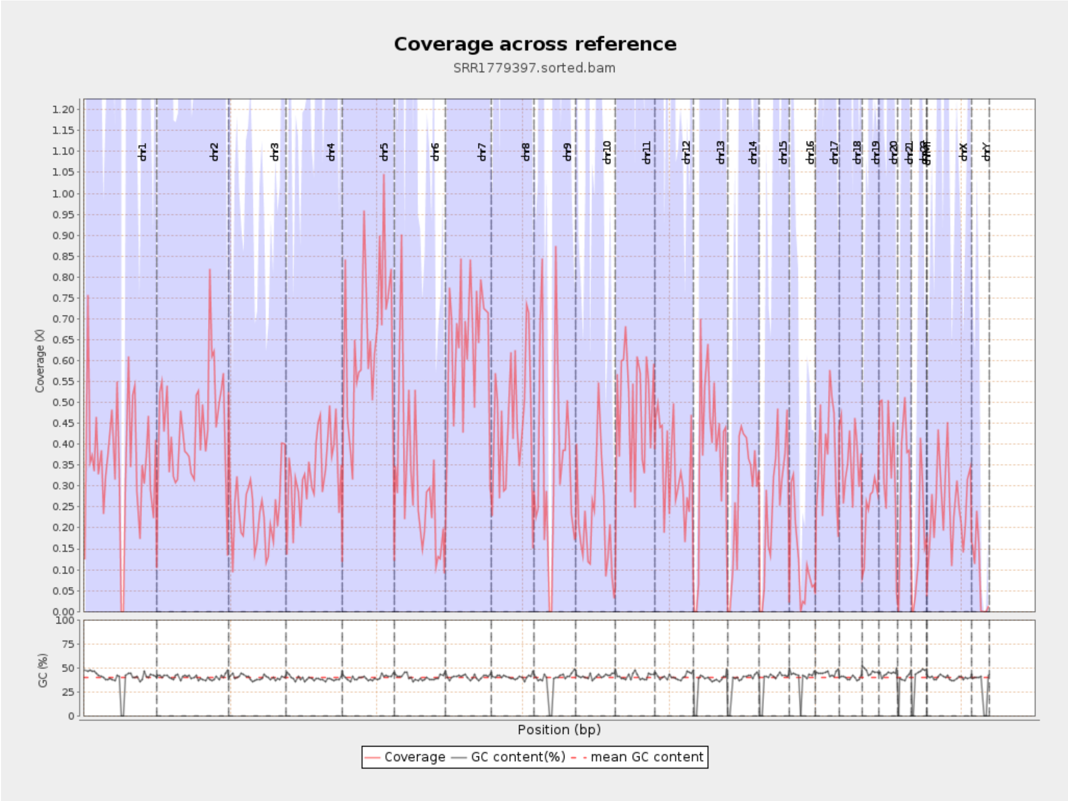
2.7. Chromosome stats

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

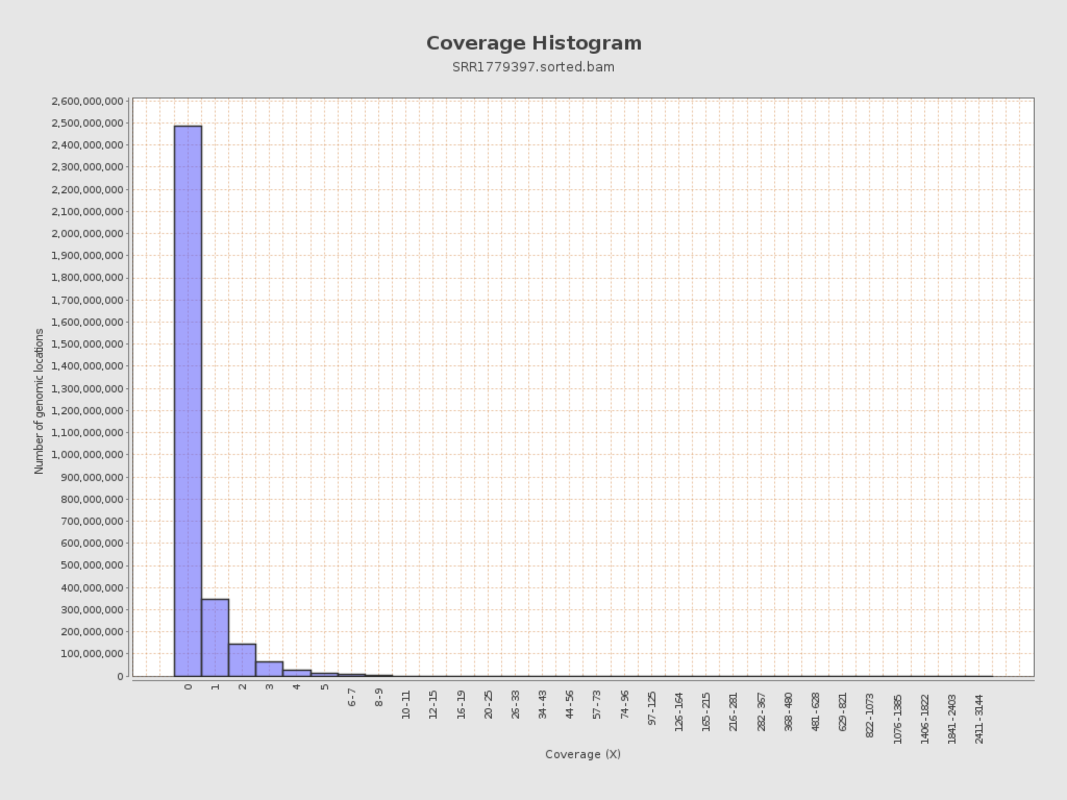
		bases	coverage	deviation
chr1	249250621	88193374	0.3538	3.2802
chr2	243199373	107883266	0.4436	1.0797
chr3	198022430	48162968	0.2432	0.743
chr4	191154276	64075782	0.3352	0.8479
chr5	180915260	115513802	0.6385	1.2201
chr6	171115067	52915581	0.3092	0.9996
chr7	159138663	100634381	0.6324	1.6443
chr8	146364022	66752062	0.4561	1.0521
chr9	141213431	51590444	0.3653	1.1756
chr10	135534747	30448591	0.2247	1.3183
chr11	135006516	65859603	0.4878	1.188
chr12	133851895	45776146	0.342	0.9015
chr13	115169878	44387163	0.3854	0.9639
chr14	107349540	30275604	0.282	0.7995
chr15	102531392	25950674	0.2531	0.7741
chr16	90354753	10541351	0.1167	0.5555
chr17	81195210	31192024	0.3842	1.4897
chr18	78077248	28518288	0.3653	1.2675
chr19	59128983	14868884	0.2515	1.8854
chr20	63025520	23034010	0.3655	0.9567
chr21	48129895	14759947	0.3067	0.853
chr22	51304566	8368607	0.1631	0.6421
chrMT	16571	598	0.0361	0.2279
chrX	155270560	39827245	0.2565	0.7788

chrY	59373566	4927672	0.083	0.4295

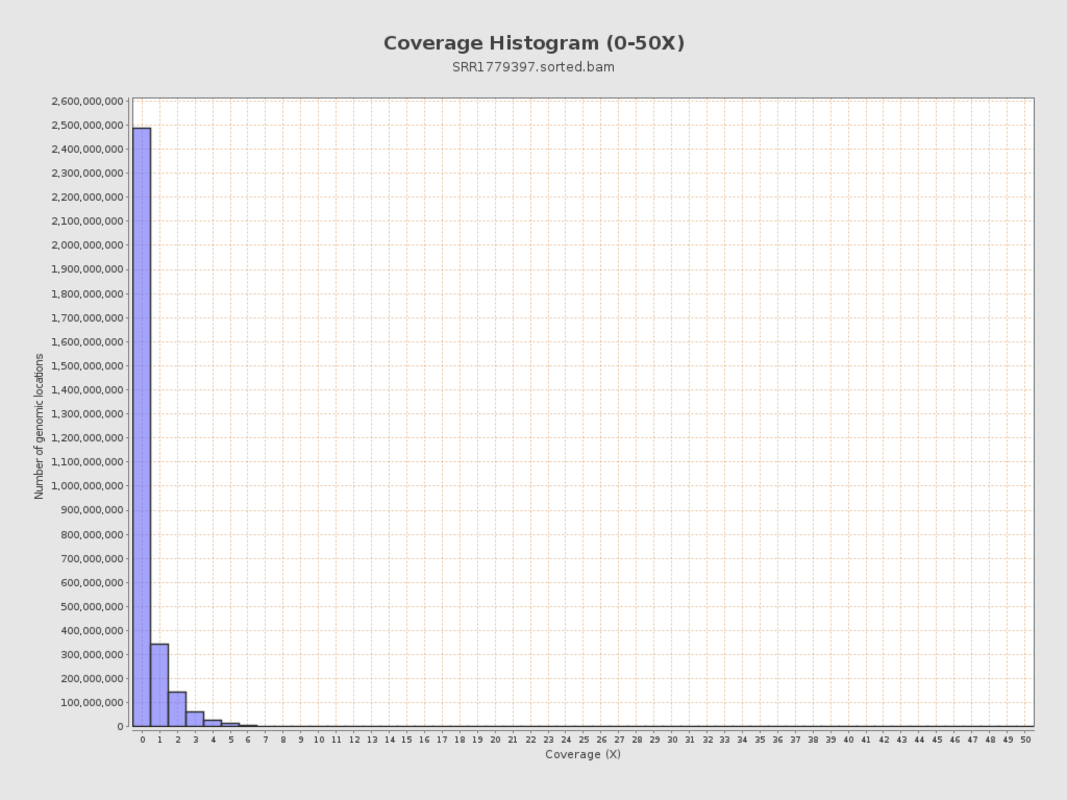
3. Results : Coverage across reference



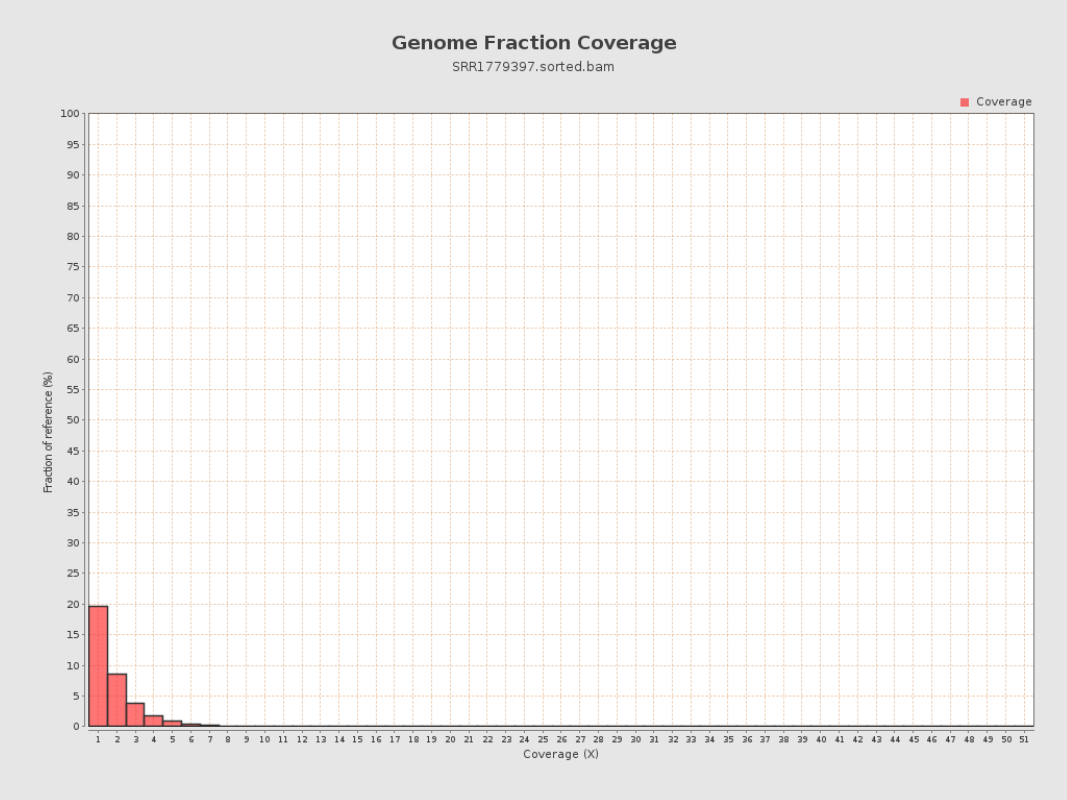
4. Results : Coverage Histogram



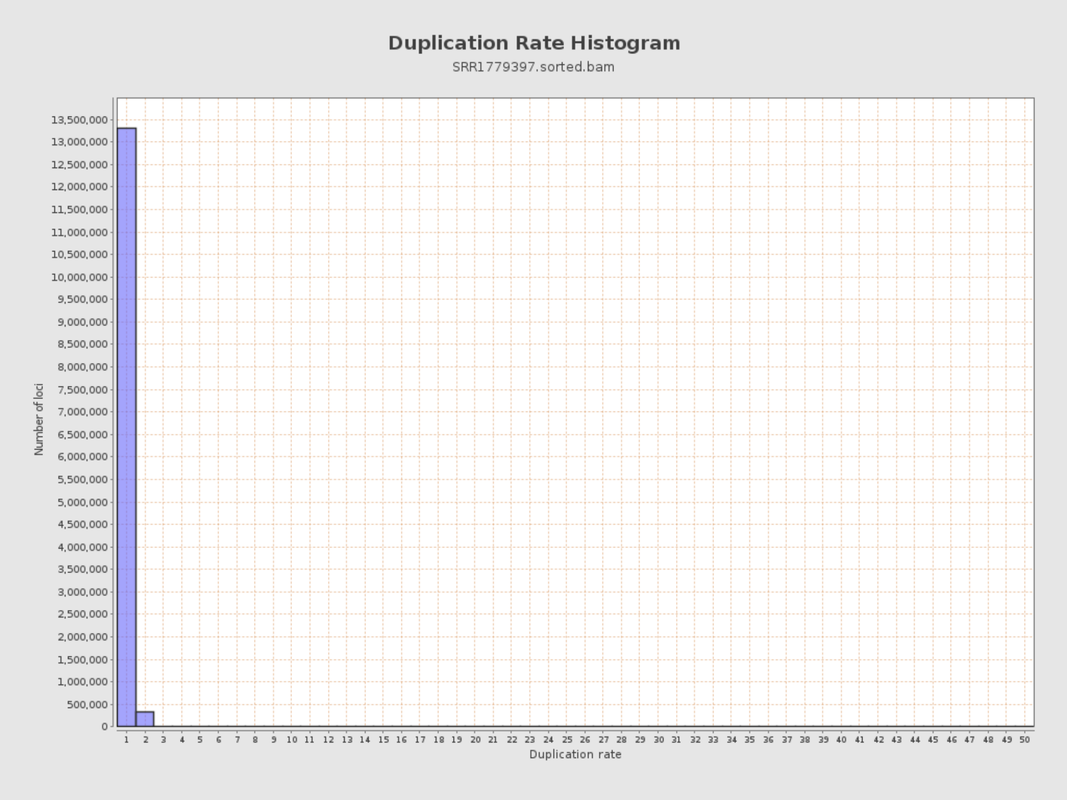
5. Results : Coverage Histogram (0-50X)



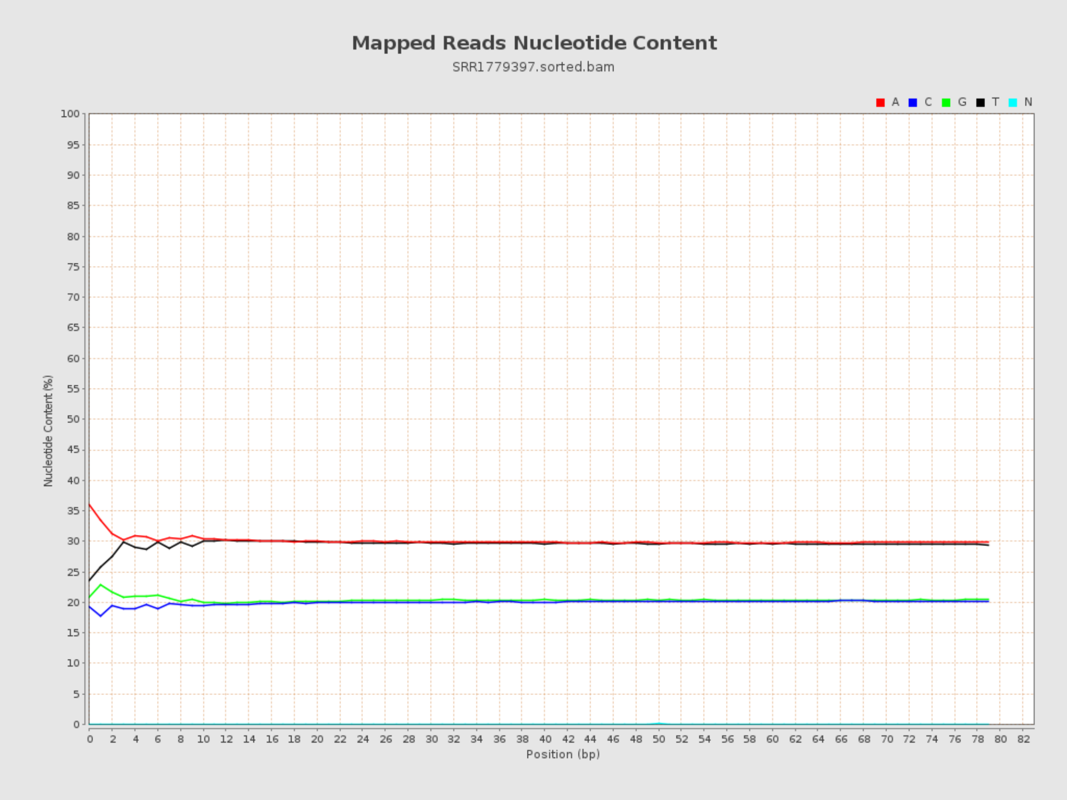
6. Results : Genome Fraction Coverage



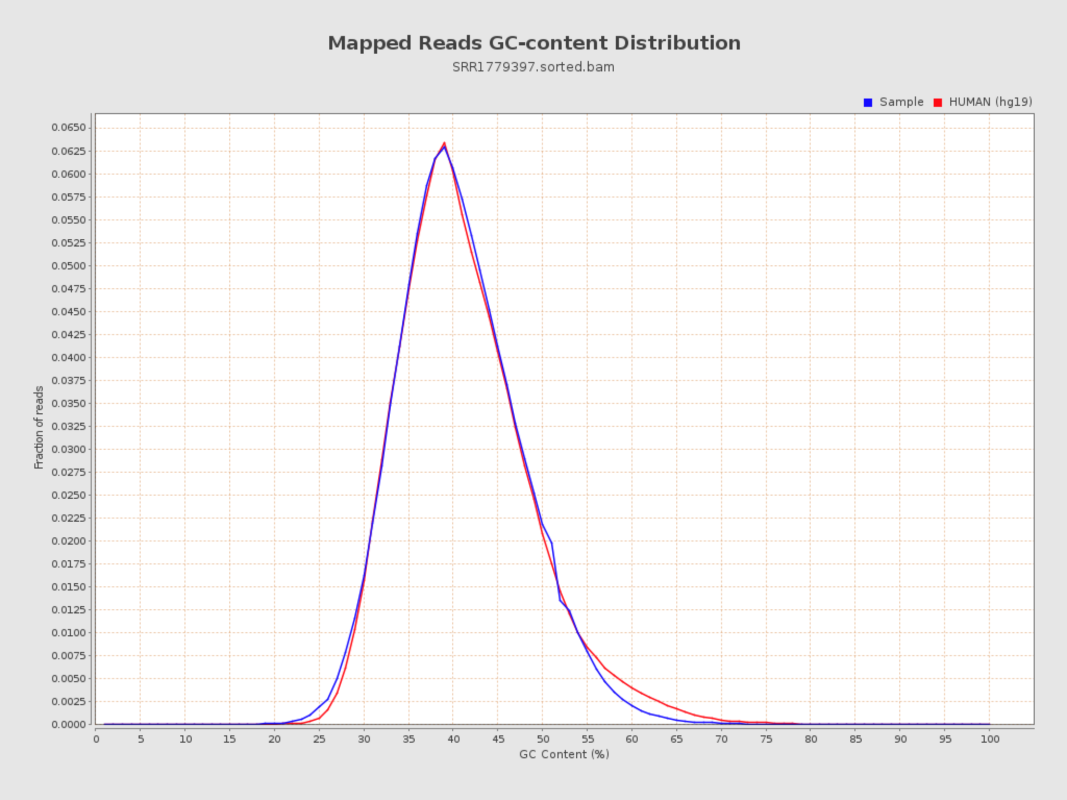
7. Results : Duplication Rate Histogram



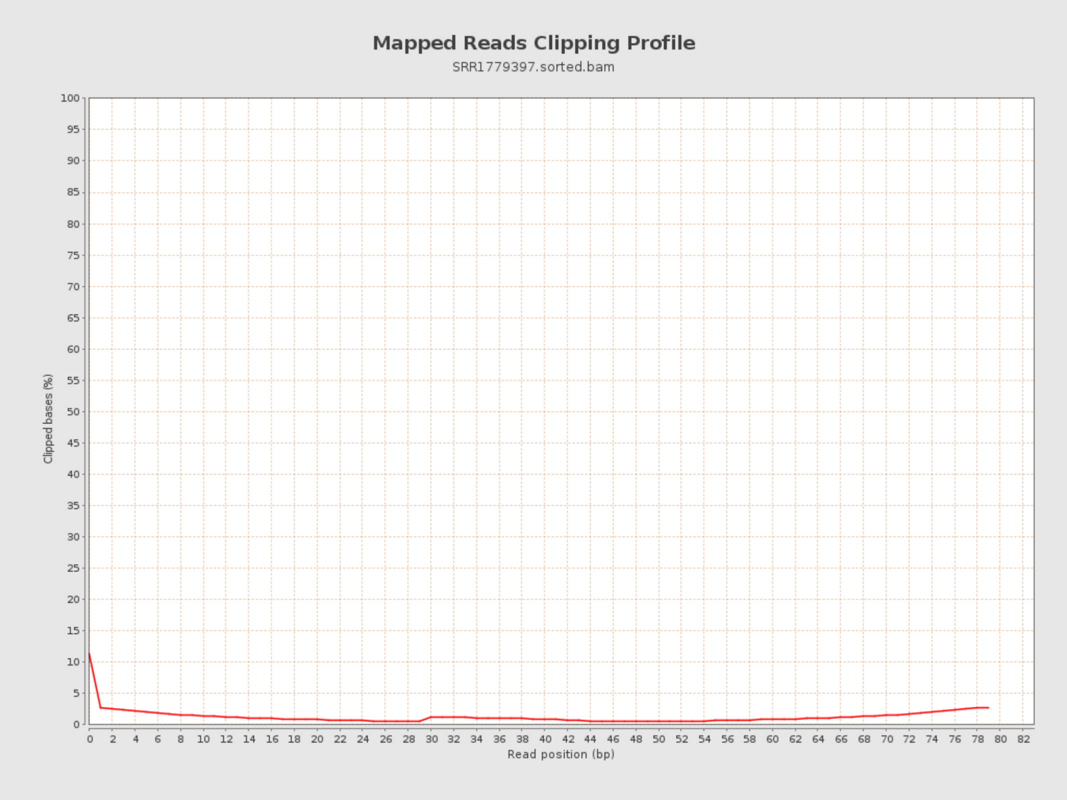
8. Results : Mapped Reads Nucleotide Content



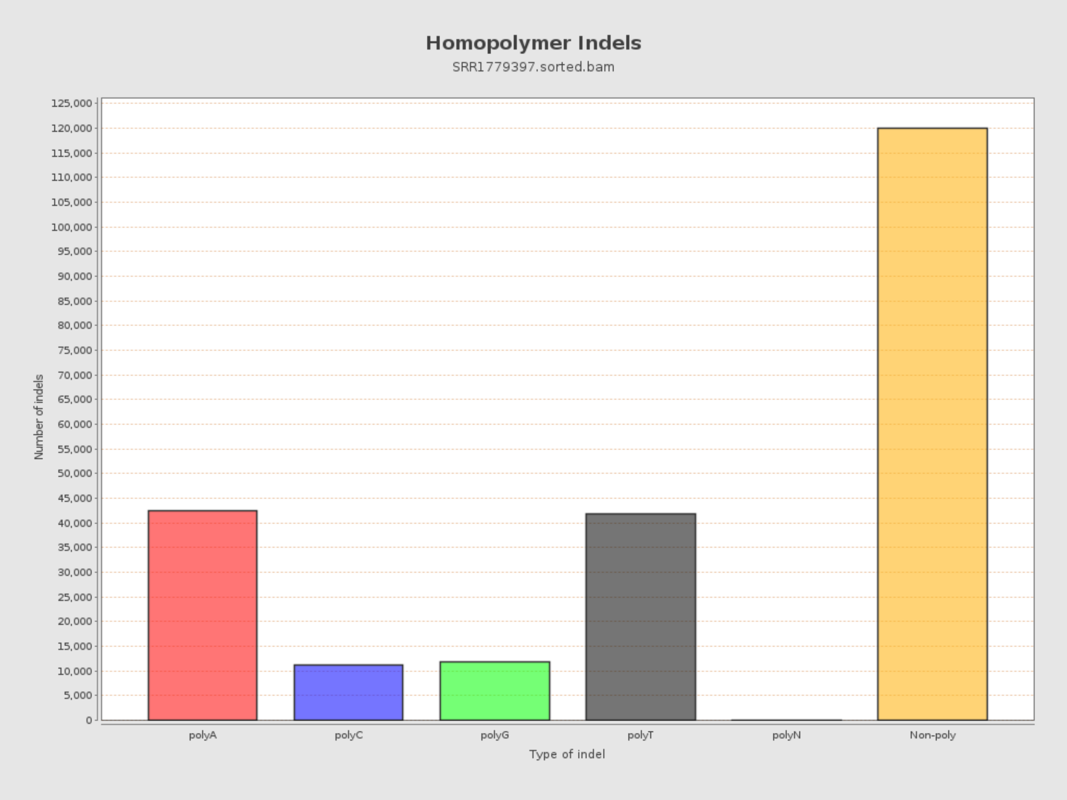
9. Results : Mapped Reads GC-content Distribution



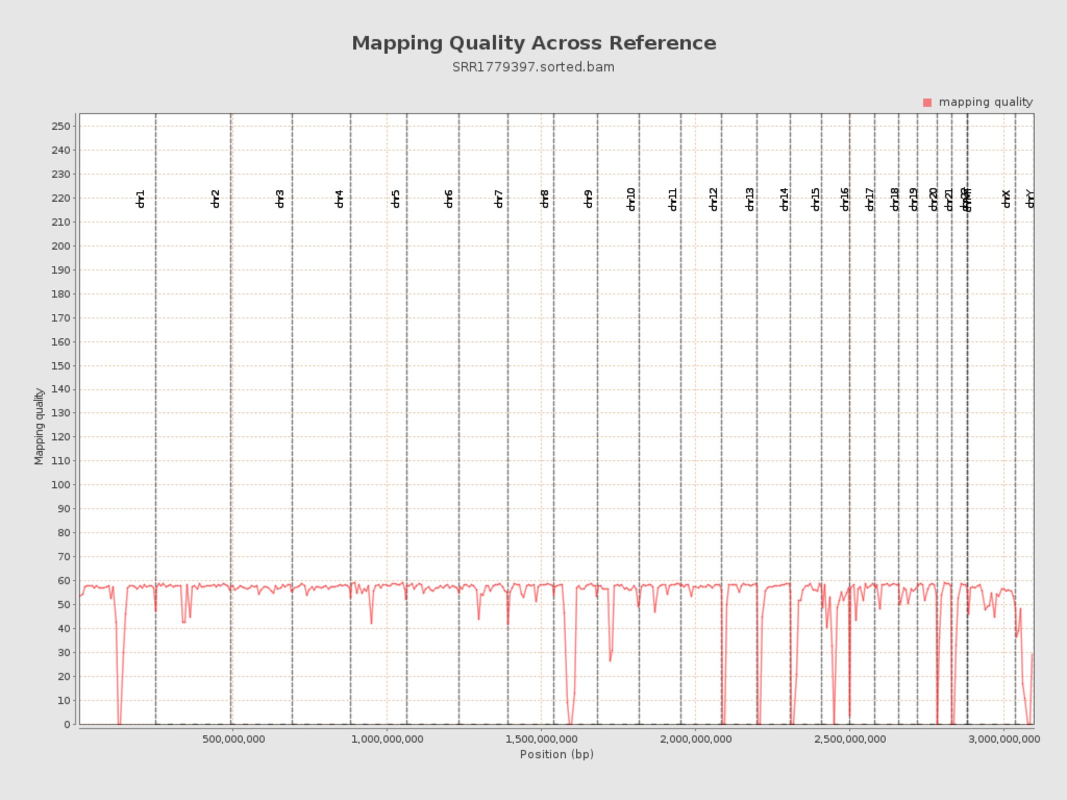
10. Results : Mapped Reads Clipping Profile



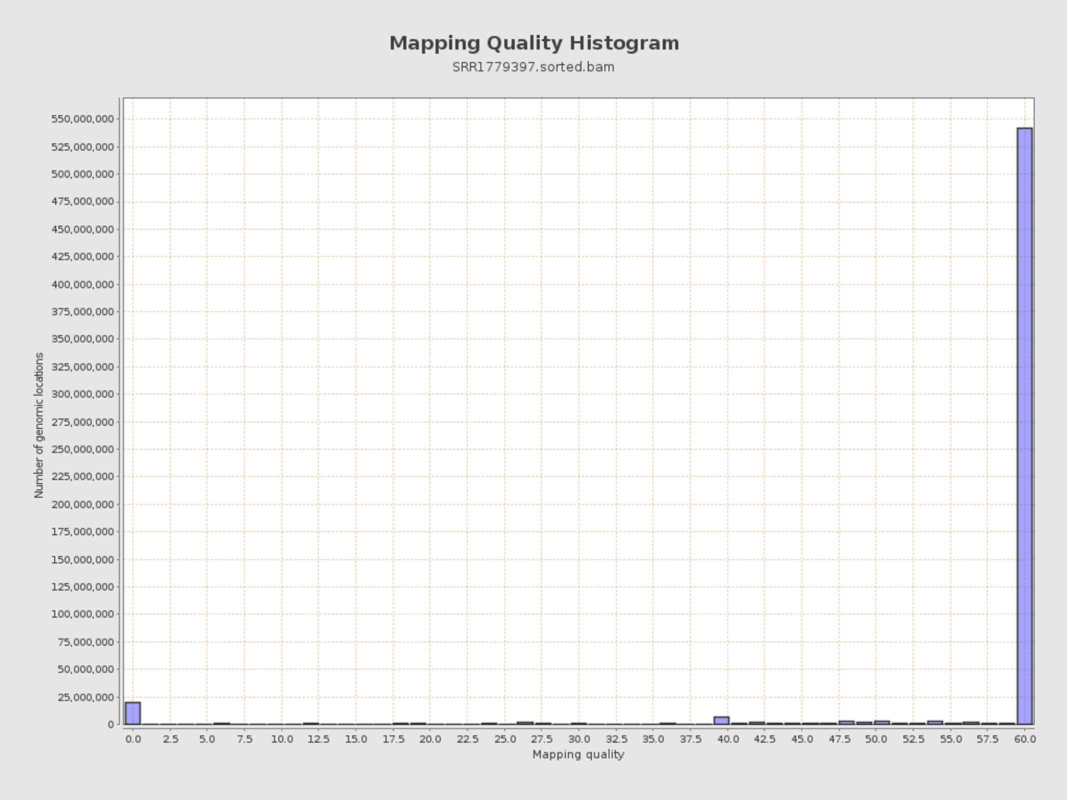
11. Results : Homopolymer Indels



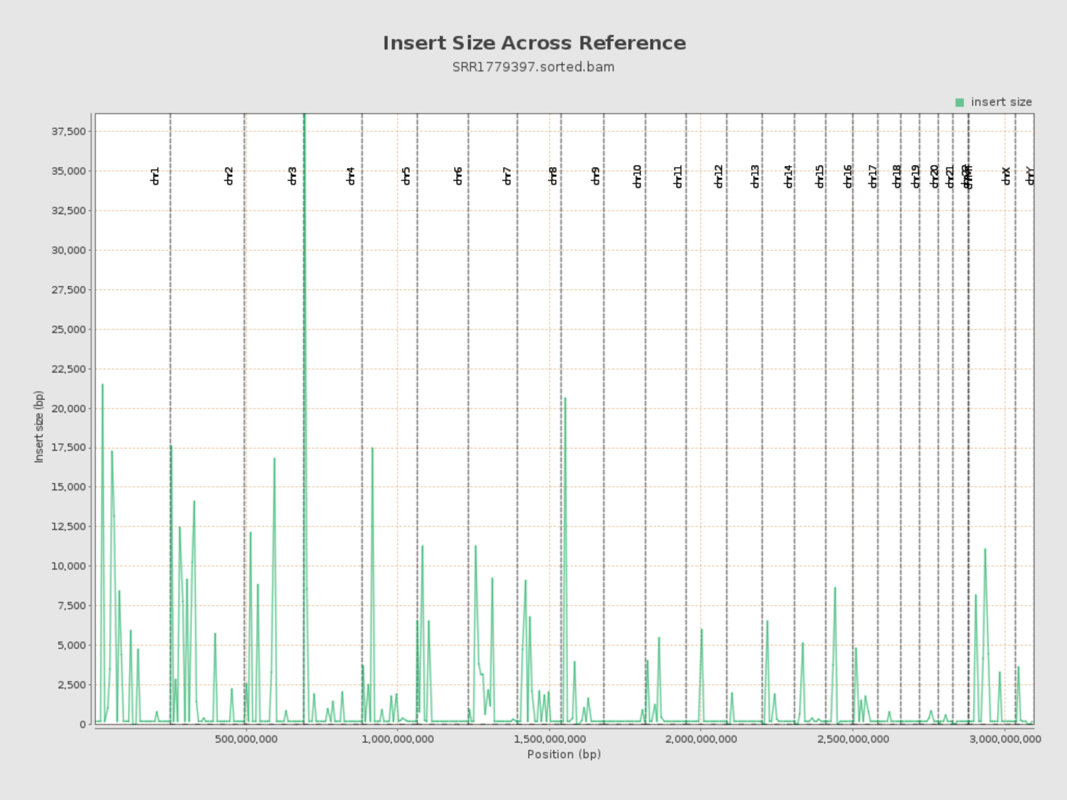
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram