Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 20:32:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779405.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_SRR1779405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779405_1.fastq.gz SRR1779405_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 20:32:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779405.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,632,936
Mapped reads	20,281,028 / 89.61%
Unmapped reads	2,351,908 / 10.39%
Mapped paired reads	20,281,028 / 89.61%
Mapped reads, first in pair	10,200,932 / 45.07%
Mapped reads, second in pair	10,080,096 / 44.54%
Mapped reads, both in pair	20,090,006 / 88.76%
Mapped reads, singletons	191,022 / 0.84%
Secondary alignments	0
Supplementary alignments	428,928 / 1.9%
Read min/max/mean length	30 / 80 / 80.67
Duplicated reads (estimated)	17,076,780 / 75.45%
Duplication rate	28.94%
Clipped reads	2,292,440 / 10.13%

2.2. ACGT Content

Number/percentage of A's	480,461,525 / 29.96%
Number/percentage of C's	319,681,620 / 19.94%
Number/percentage of T's	475,265,338 / 29.64%
Number/percentage of G's	327,739,411 / 20.44%
Number/percentage of N's	352,520 / 0.02%

GC Percentage	40.38%

2.3. Coverage

Mean	0.518
Standard Deviation	227.8537

2.4. Mapping Quality

Mean Mapping Quality	49.5

2.5. Insert size

Mean	105,494.37
Standard Deviation	3,440,203.76
P25/Median/P75	158 / 208 / 267

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	5,541,237
Insertions	87,077
Mapped reads with at least one insertion	0.43%
Deletions	89,489
Mapped reads with at least one deletion	0.44%
Homopolymer indels	48.28%

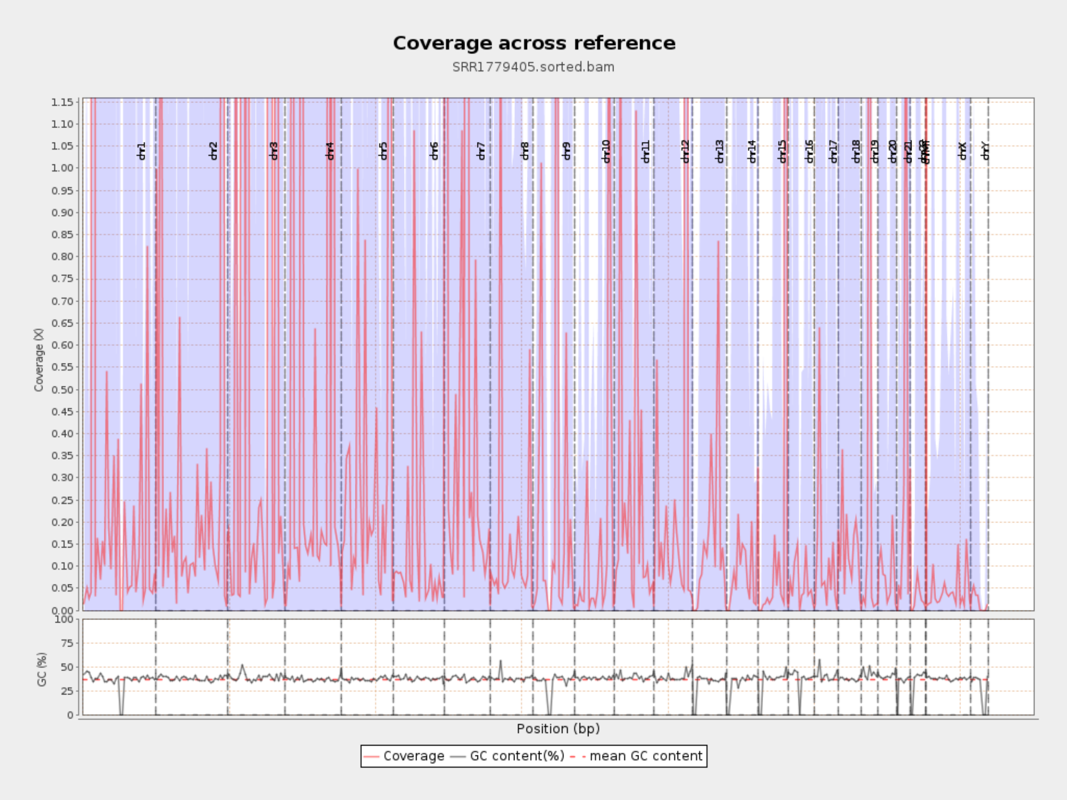
2.7. Chromosome stats

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

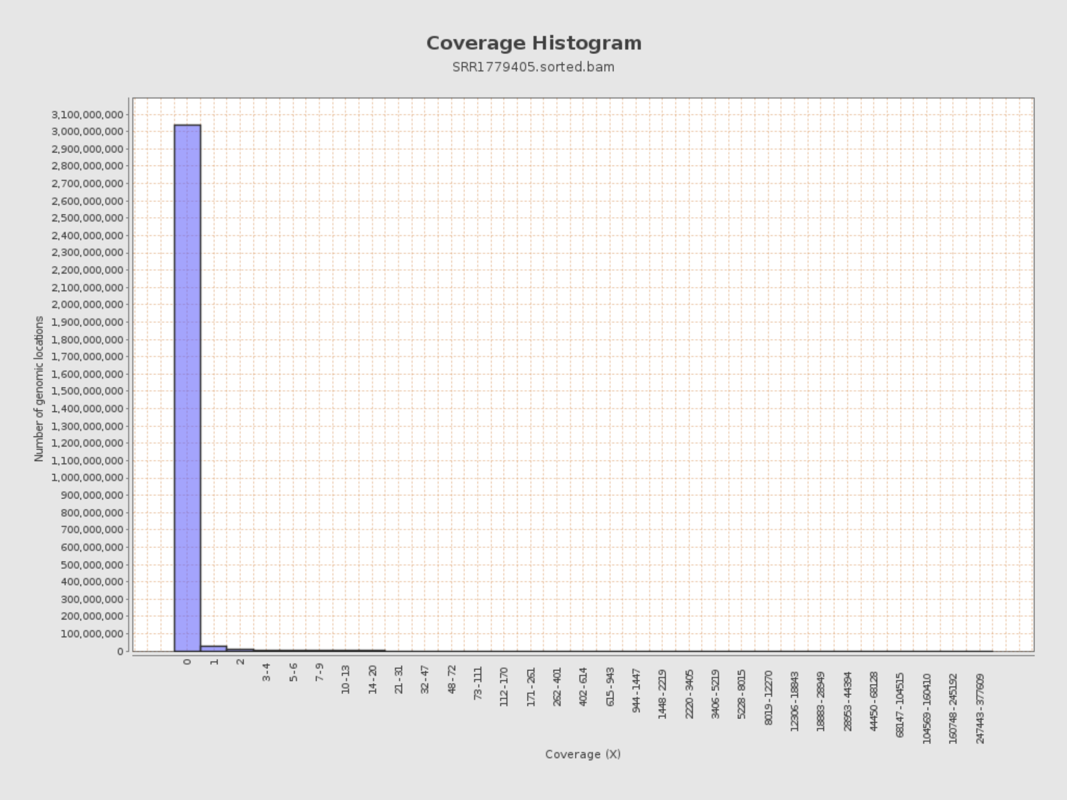
		bases	coverage	deviation
chr1	249250621	191693385	0.7691	246.2979
chr2	243199373	161541351	0.6642	271.7481
chr3	198022430	470952447	2.3783	723.3702
chr4	191154276	143761701	0.7521	124.7504
chr5	180915260	63503101	0.351	21.912
chr6	171115067	26899078	0.1572	5.8738
chr7	159138663	113475564	0.7131	91.3184
chr8	146364022	26334360	0.1799	63.3069
chr9	141213431	42292863	0.2995	17.1056
chr10	135534747	23992692	0.177	53.7668
chr11	135006516	36357964	0.2693	24.4595
chr12	133851895	70918198	0.5298	104.885
chr13	115169878	19387901	0.1683	5.8767
chr14	107349540	8926811	0.0832	5.6053
chr15	102531392	122340516	1.1932	406.4511
chr16	90354753	5264377	0.0583	2.2243
chr17	81195210	10094647	0.1243	22.6903
chr18	78077248	11796695	0.1511	9.5396
chr19	59128983	21019735	0.3555	28.8695
chr20	63025520	5710287	0.0906	4.2767
chr21	48129895	17503000	0.3637	12.3961
chr22	51304566	1465270	0.0286	1.2633
chrMT	16571	346906	20.9345	10.4615
chrX	155270560	6806785	0.0438	1.861

chrY	59373566	1273901	0.0215	0.5374

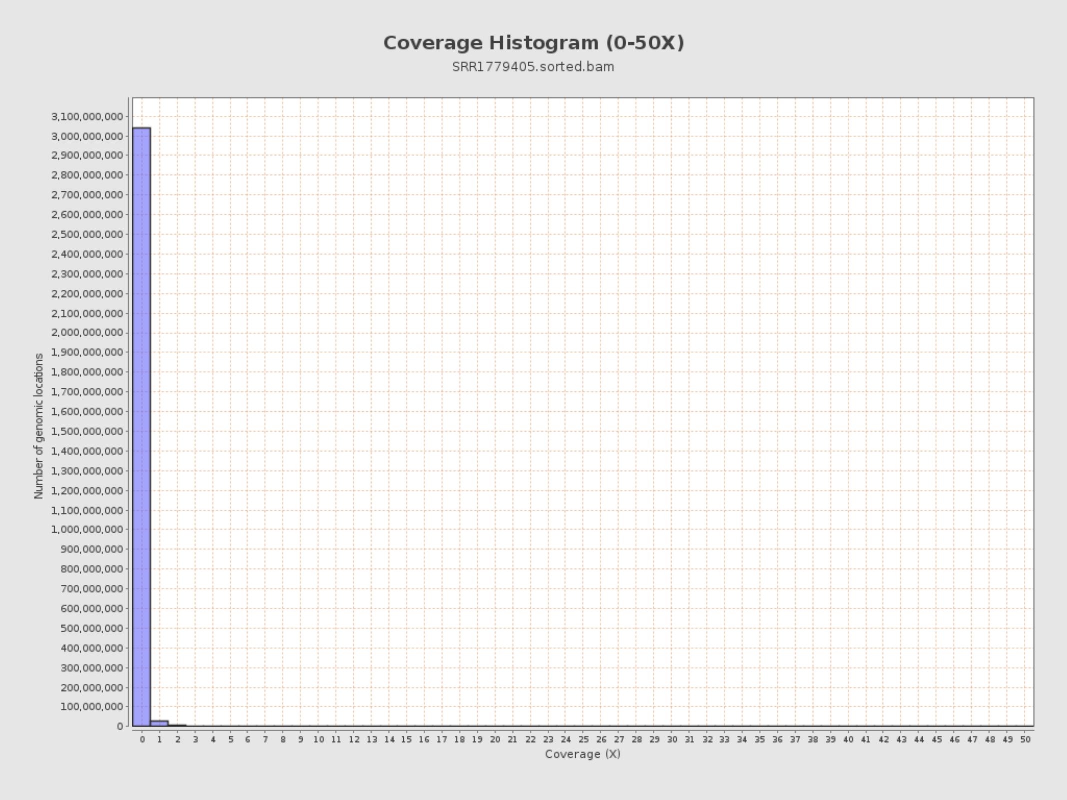
3. Results : Coverage across reference



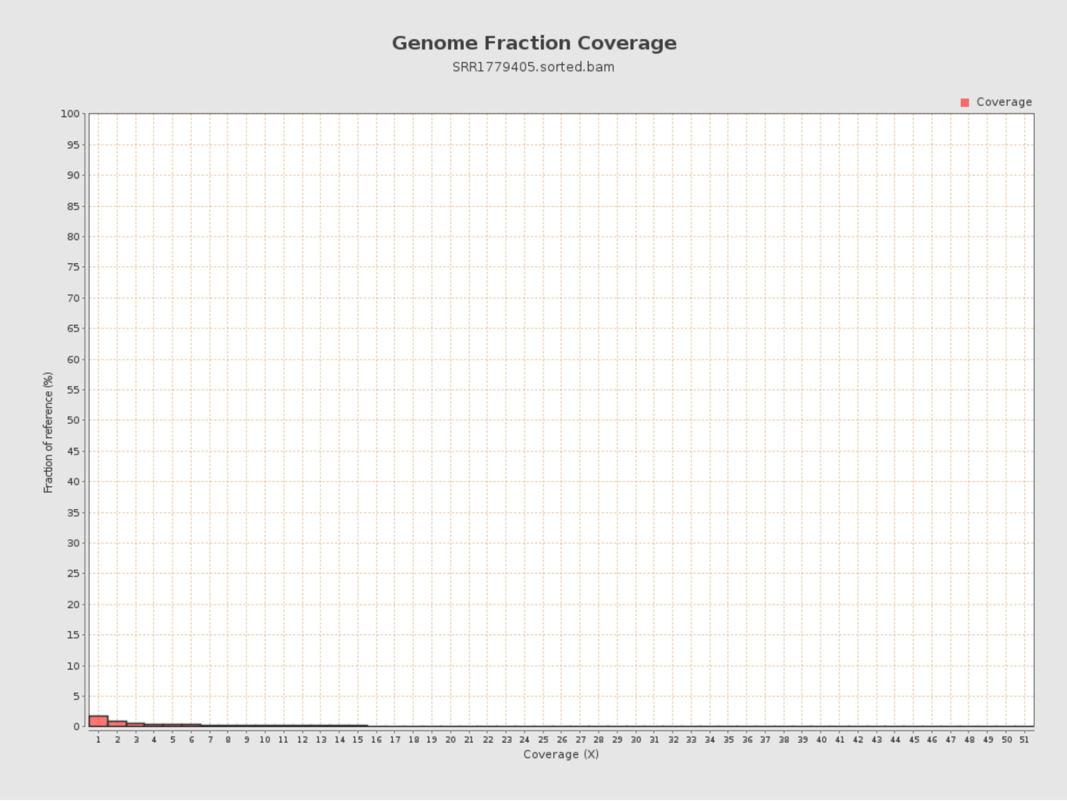
4. Results : Coverage Histogram



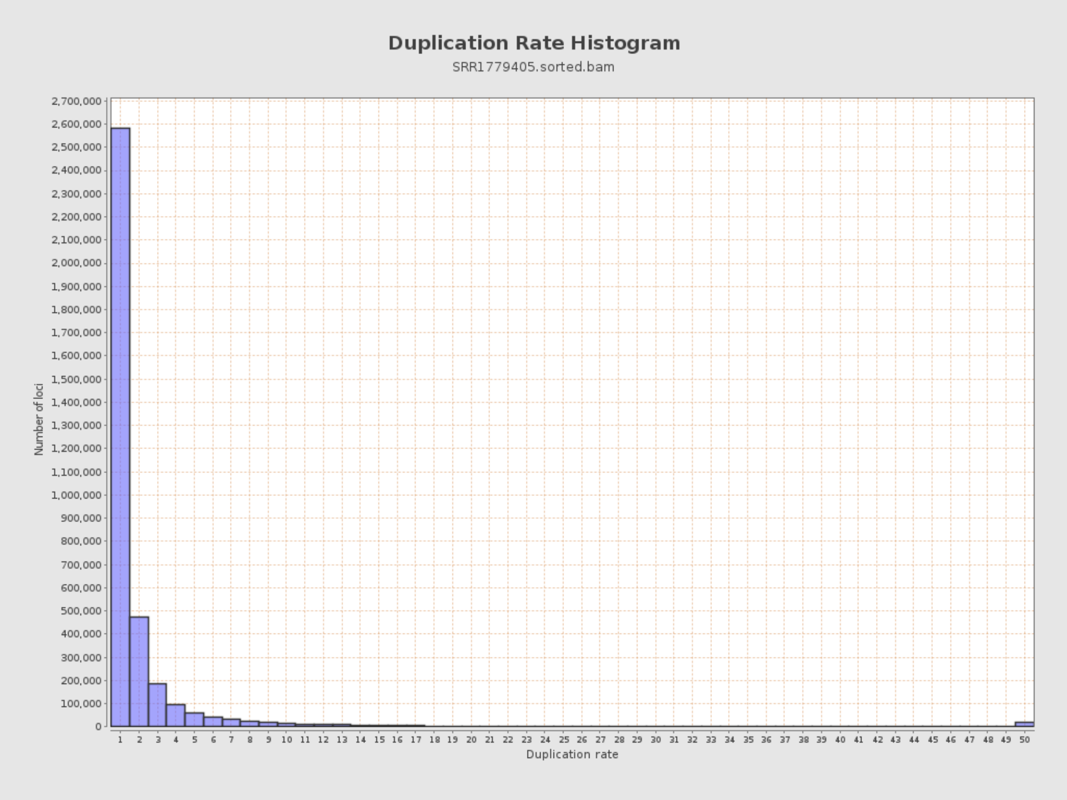
5. Results : Coverage Histogram (0-50X)



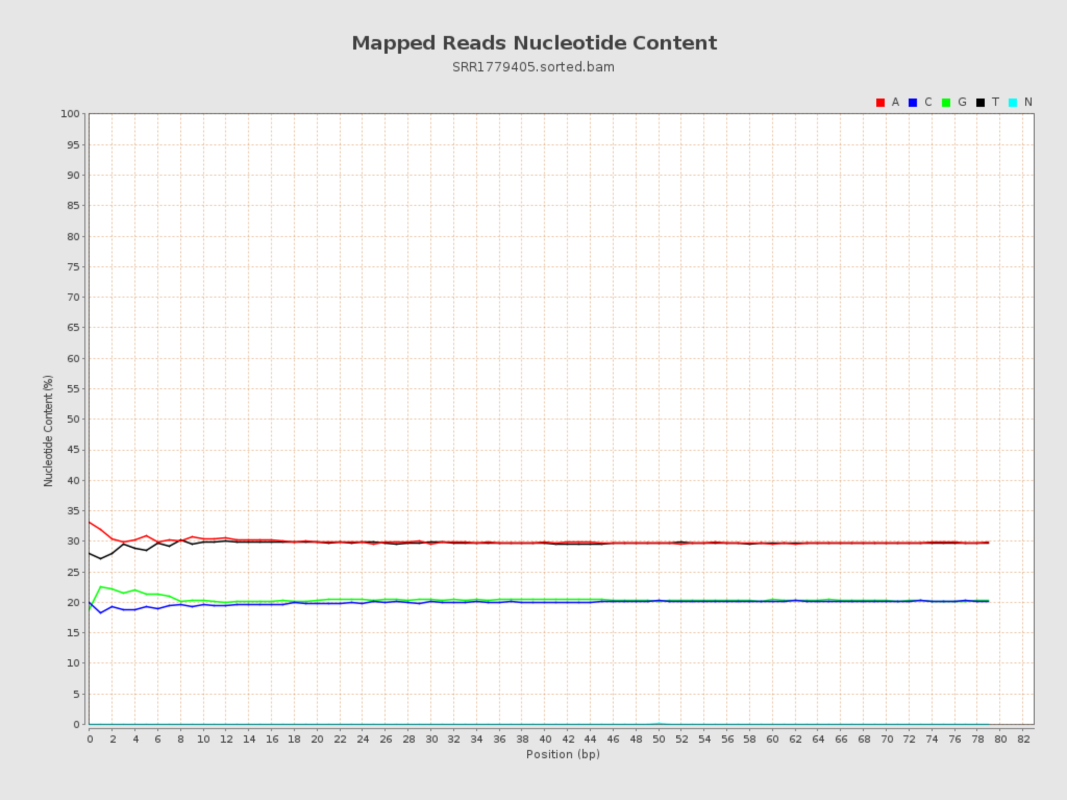
6. Results : Genome Fraction Coverage



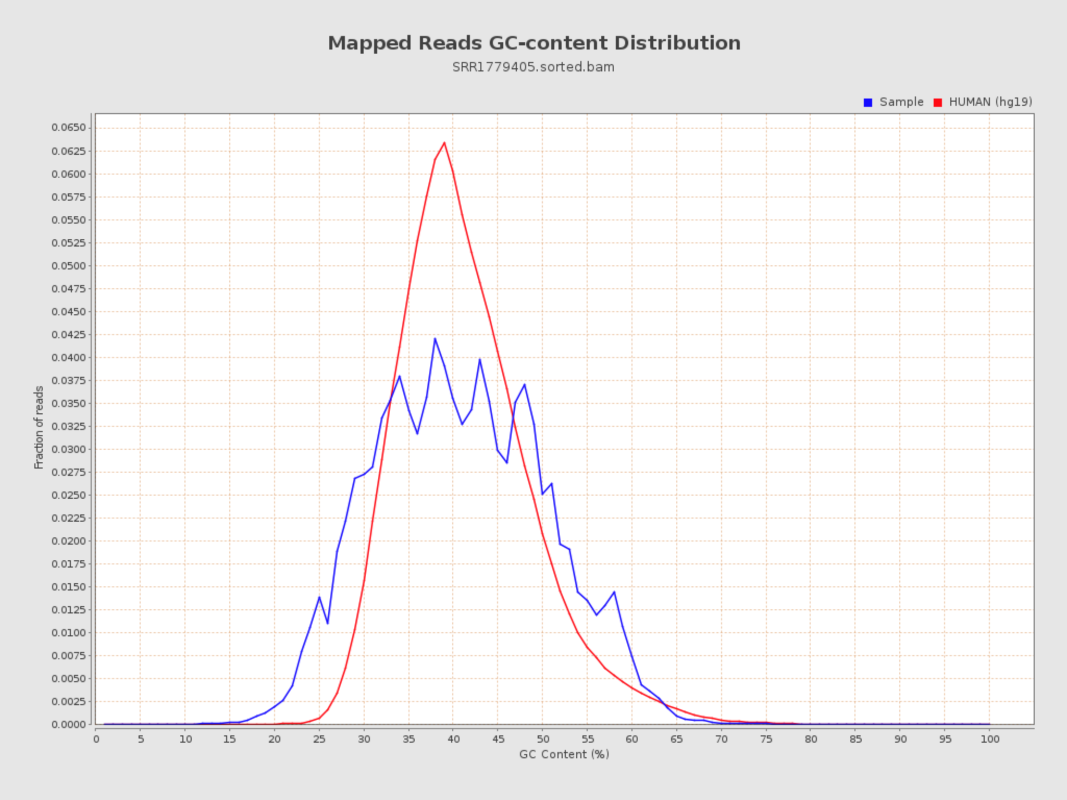
7. Results : Duplication Rate Histogram



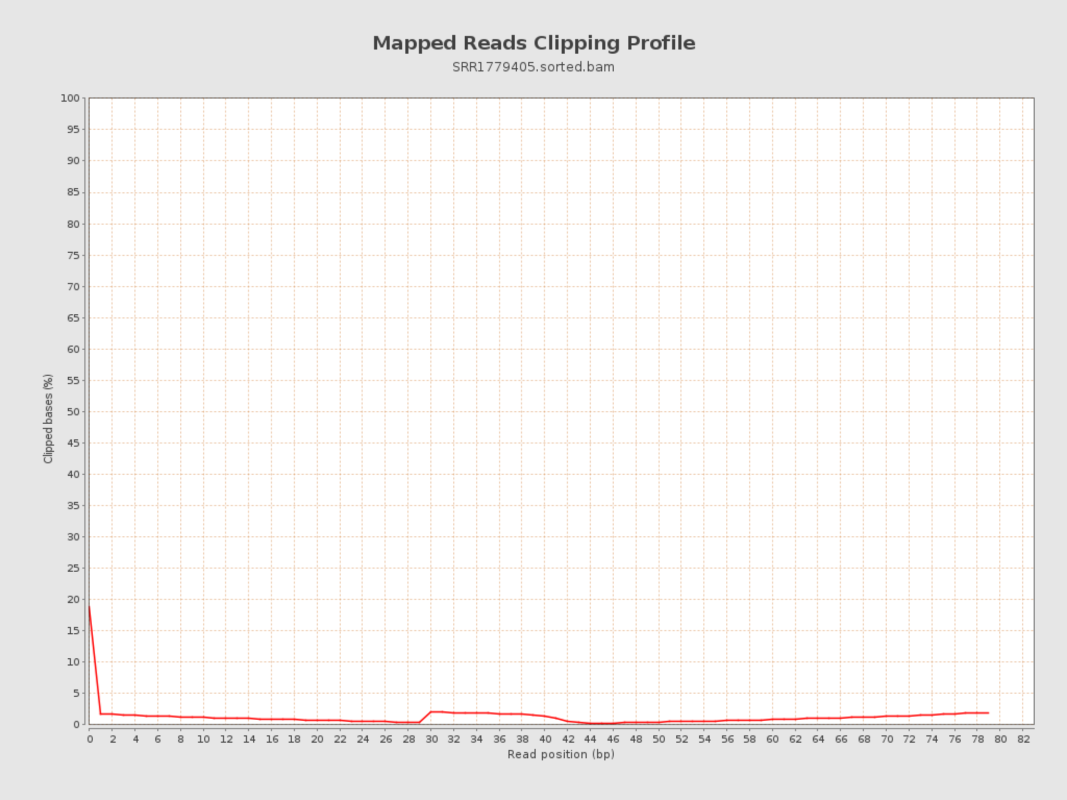
8. Results : Mapped Reads Nucleotide Content



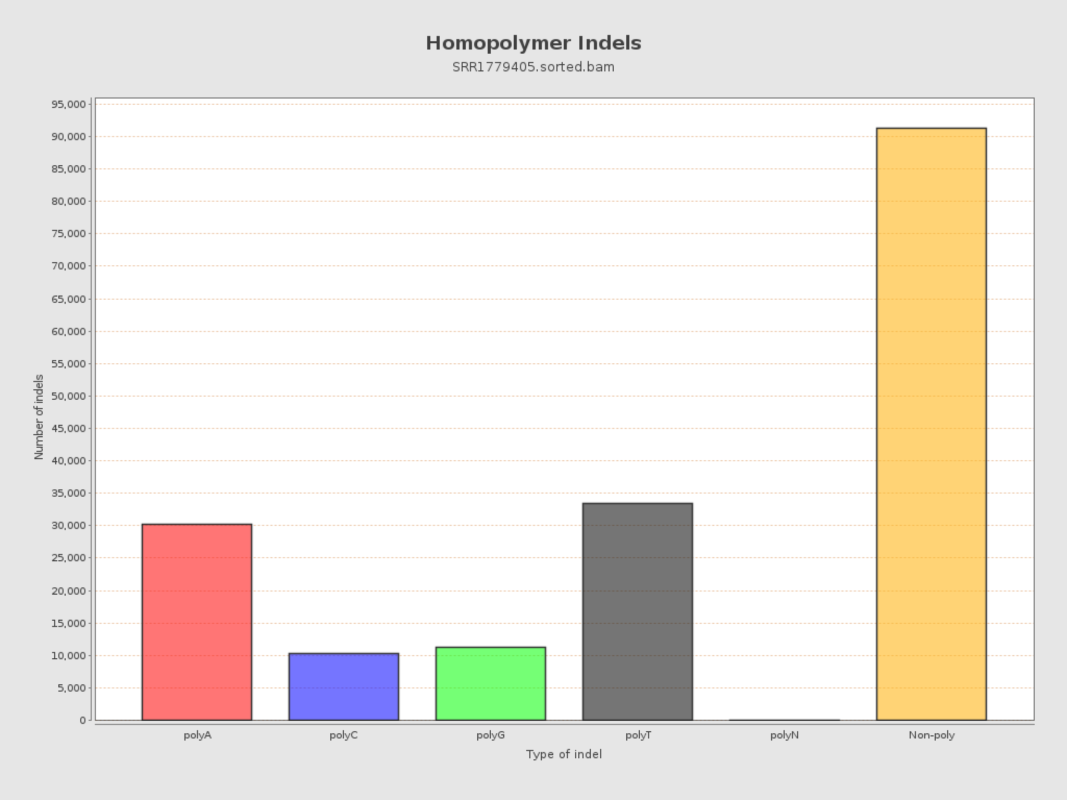
9. Results : Mapped Reads GC-content Distribution



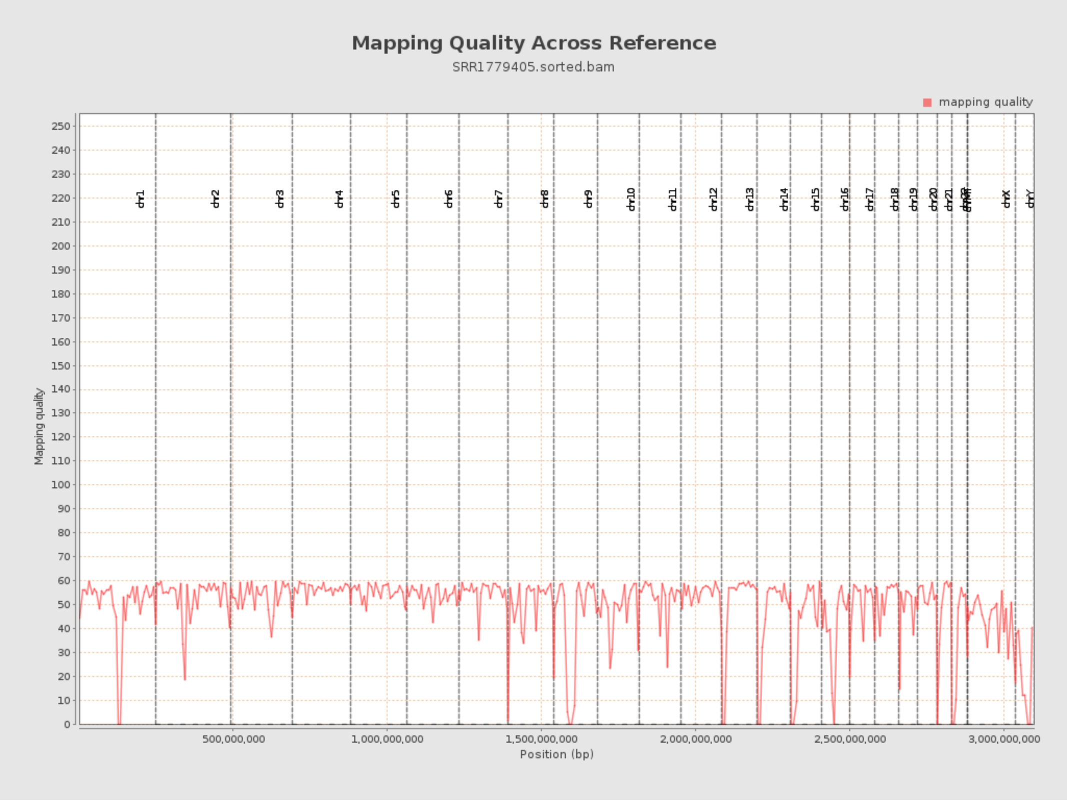
10. Results : Mapped Reads Clipping Profile



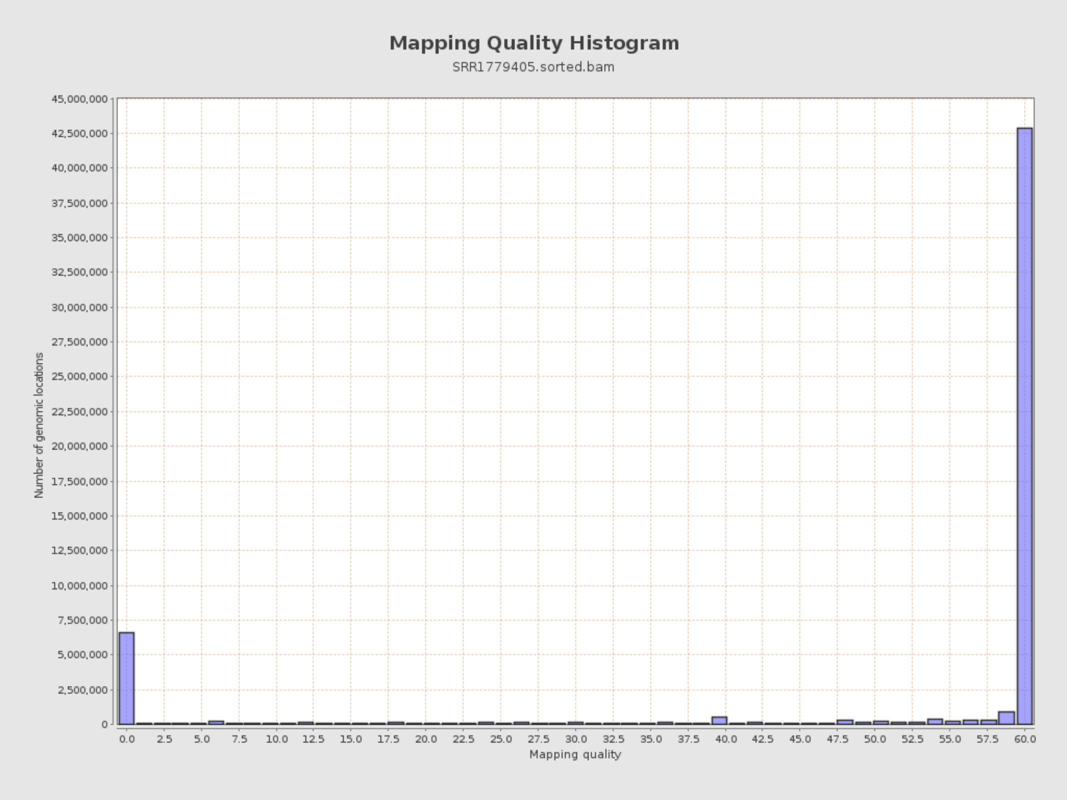
11. Results : Homopolymer Indels



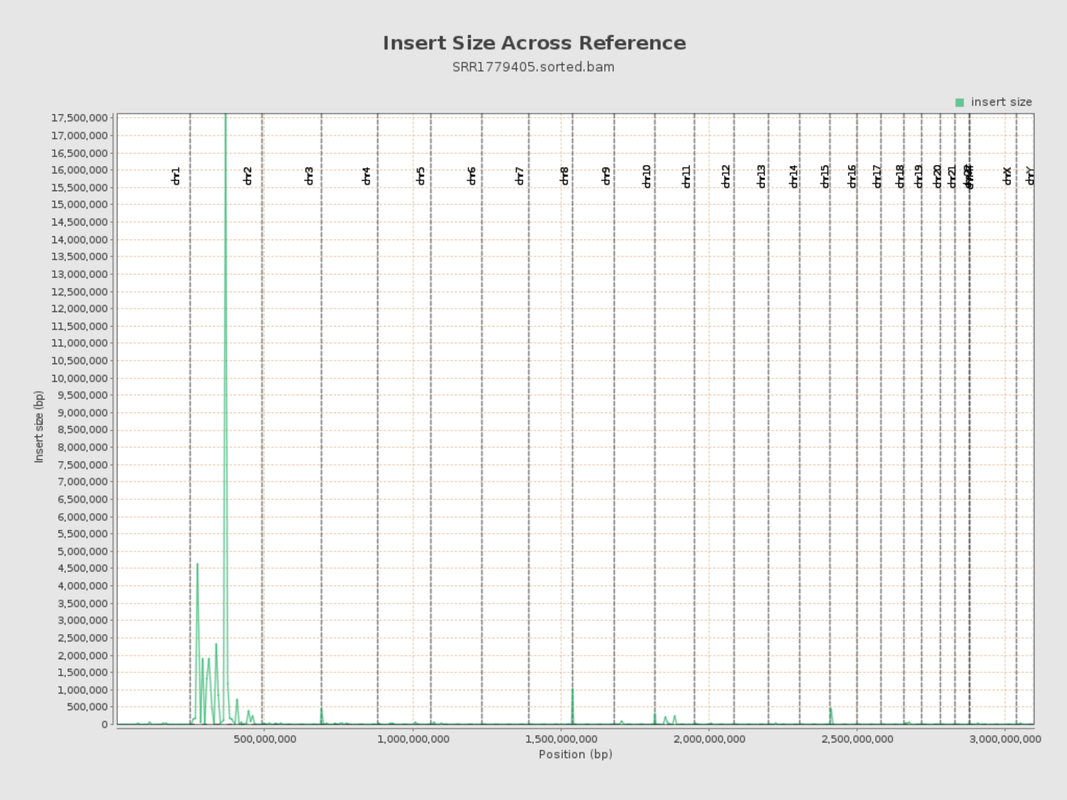
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram