Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 03:03:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779426.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_SRR1779426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779426_1.fastq.gz SRR1779426_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 03:03:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779426.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,767,828
Mapped reads	12,024,161 / 94.18%
Unmapped reads	743,667 / 5.82%
Mapped paired reads	12,024,161 / 94.18%
Mapped reads, first in pair	6,069,494 / 47.54%
Mapped reads, second in pair	5,954,667 / 46.64%
Mapped reads, both in pair	11,861,516 / 92.9%
Mapped reads, singletons	162,645 / 1.27%
Secondary alignments	0
Supplementary alignments	105,812 / 0.83%
Read min/max/mean length	30 / 80 / 80.3
Duplicated reads (estimated)	3,471,168 / 27.19%
Duplication rate	12.16%
Clipped reads	777,568 / 6.09%

2.2. ACGT Content

Number/percentage of A's	298,982,751 / 31.37%
Number/percentage of C's	178,154,394 / 18.69%
Number/percentage of T's	292,995,558 / 30.74%
Number/percentage of G's	182,880,189 / 19.19%
Number/percentage of N's	207,949 / 0.02%

GC Percentage	37.88%

2.3. Coverage

Mean	0.308
Standard Deviation	12.6824

2.4. Mapping Quality

Mean Mapping Quality	51.98

2.5. Insert size

Mean	157,538.39
Standard Deviation	3,778,482.32
P25/Median/P75	162 / 203 / 254

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	3,842,573
Insertions	95,857
Mapped reads with at least one insertion	0.79%
Deletions	106,591
Mapped reads with at least one deletion	0.88%
Homopolymer indels	45.67%

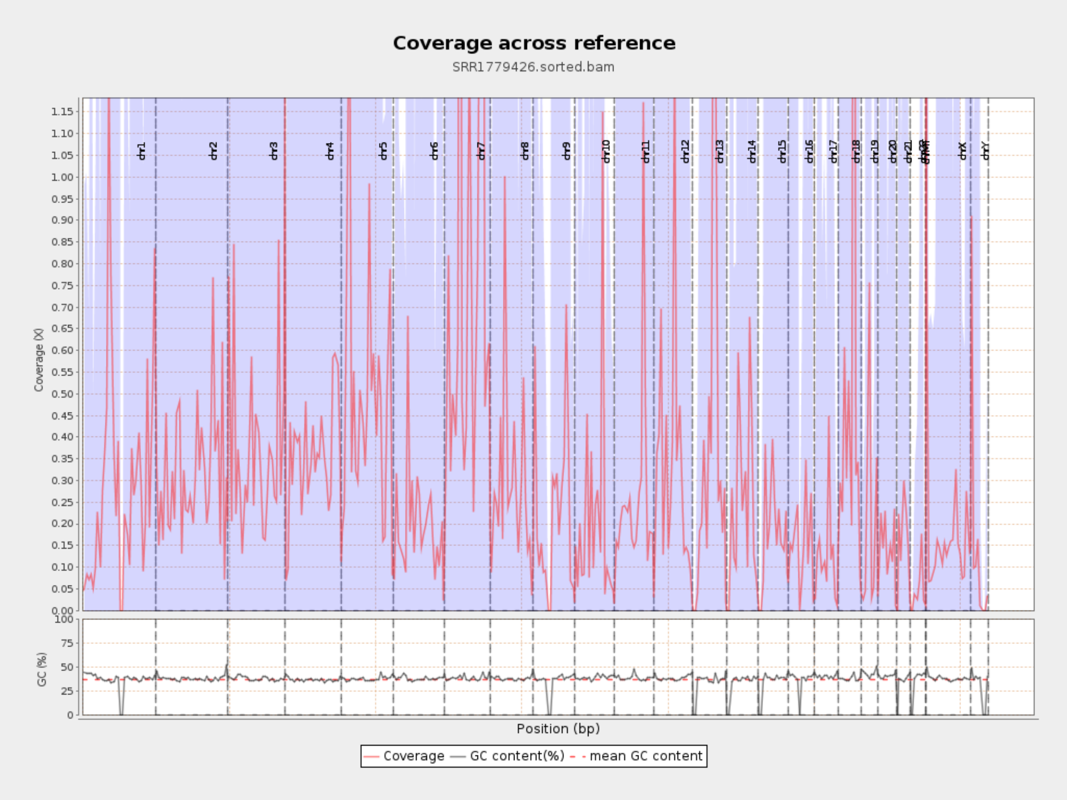
2.7. Chromosome stats

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

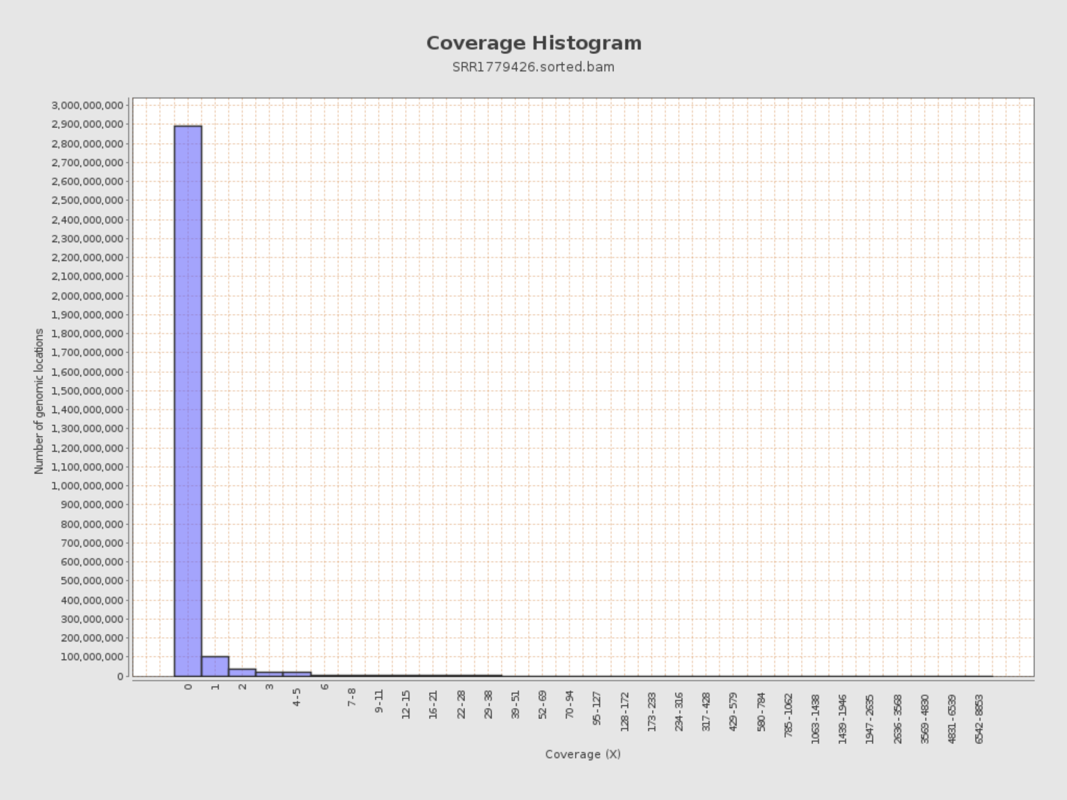
		bases	coverage	deviation
chr1	249250621	73592306	0.2953	14.8321
chr2	243199373	76613211	0.315	6.4705
chr3	198022430	74009256	0.3737	10.2466
chr4	191154276	68404360	0.3578	4.2263
chr5	180915260	87041490	0.4811	10.4743
chr6	171115067	34667727	0.2026	3.9247
chr7	159138663	128537277	0.8077	27.1212
chr8	146364022	42241695	0.2886	5.1338
chr9	141213431	32524028	0.2303	3.5325
chr10	135534747	28315821	0.2089	6.8064
chr11	135006516	36033691	0.2669	11.7747
chr12	133851895	45509098	0.34	10.6016
chr13	115169878	45254869	0.3929	27.5719
chr14	107349540	27439288	0.2556	9.8796
chr15	102531392	18359518	0.1791	3.0109
chr16	90354753	13429049	0.1486	3.2099
chr17	81195210	10454022	0.1288	1.6414
chr18	78077248	44255377	0.5668	24.005
chr19	59128983	12835019	0.2171	18.1941
chr20	63025520	9687131	0.1537	1.379
chr21	48129895	8051370	0.1673	1.3288
chr22	51304566	2601674	0.0507	0.8956
chrMT	16571	72511	4.3758	2.8341
chrX	155270560	25594563	0.1648	13.7262

chrY	59373566	7903597	0.1331	22.1949

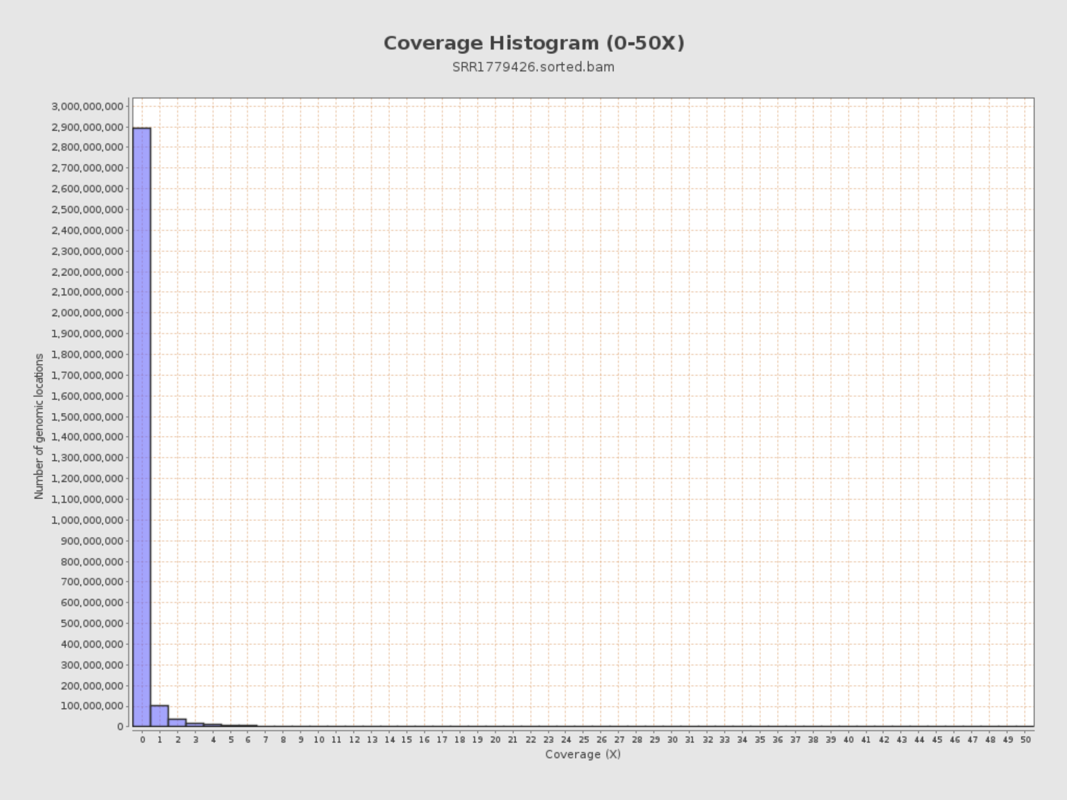
3. Results : Coverage across reference



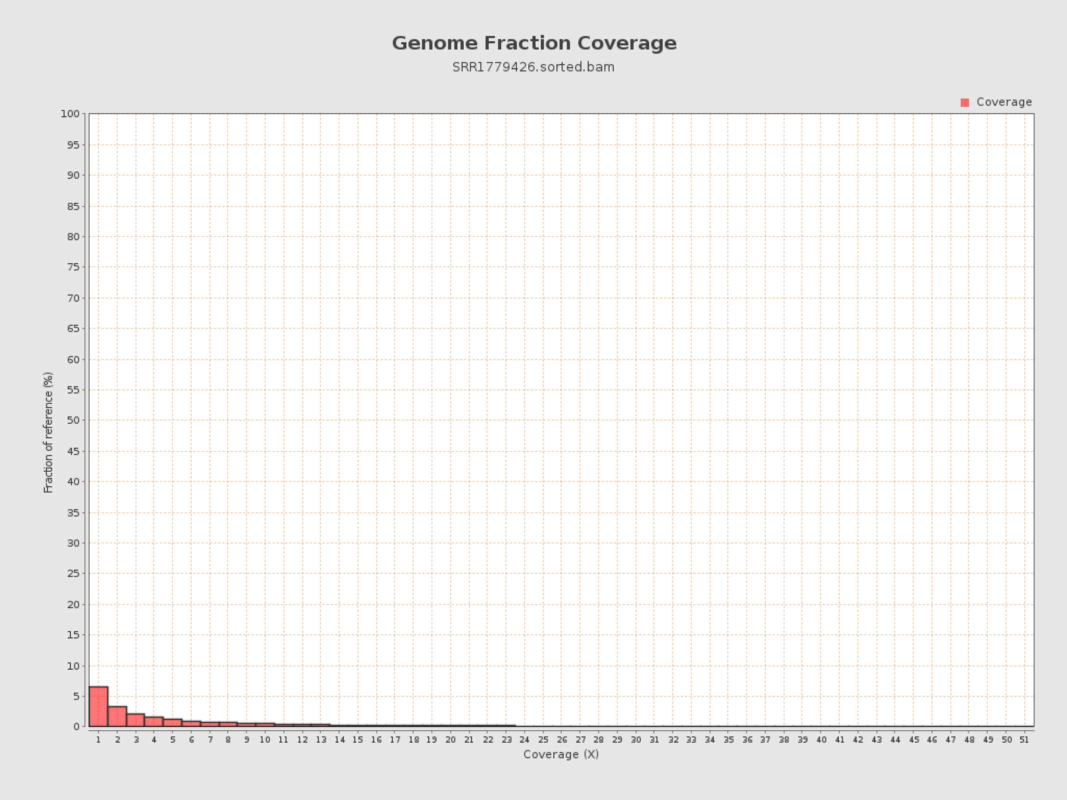
4. Results : Coverage Histogram



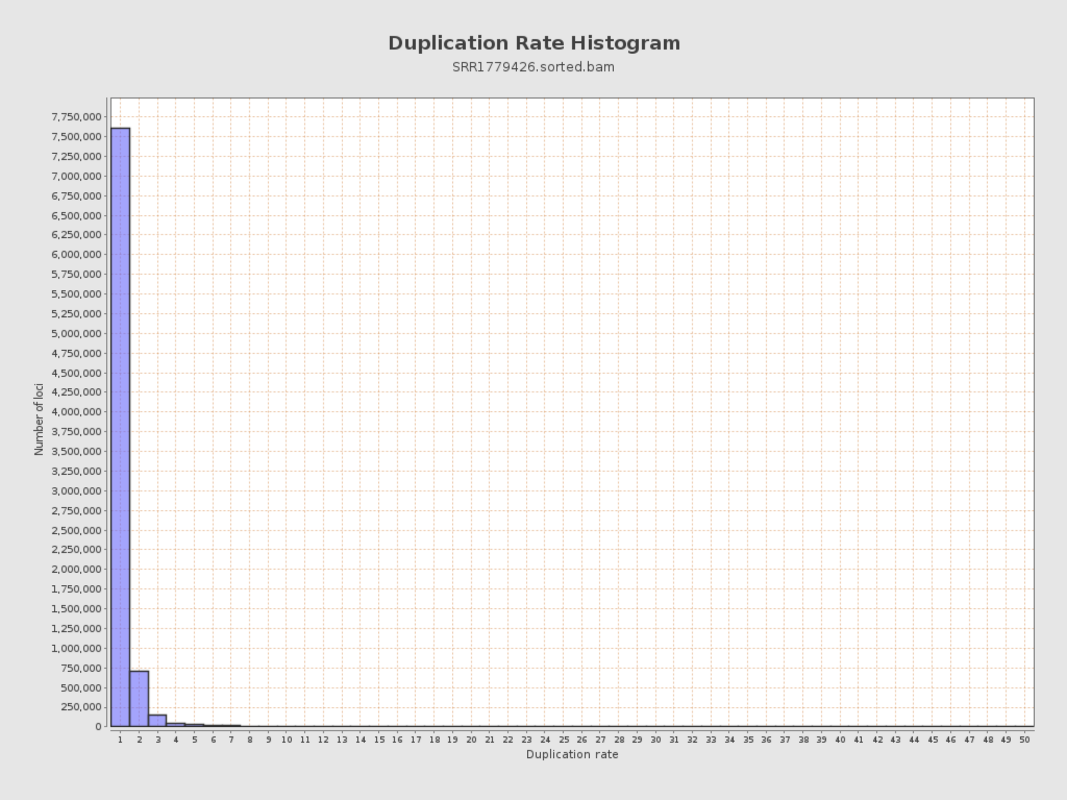
5. Results : Coverage Histogram (0-50X)



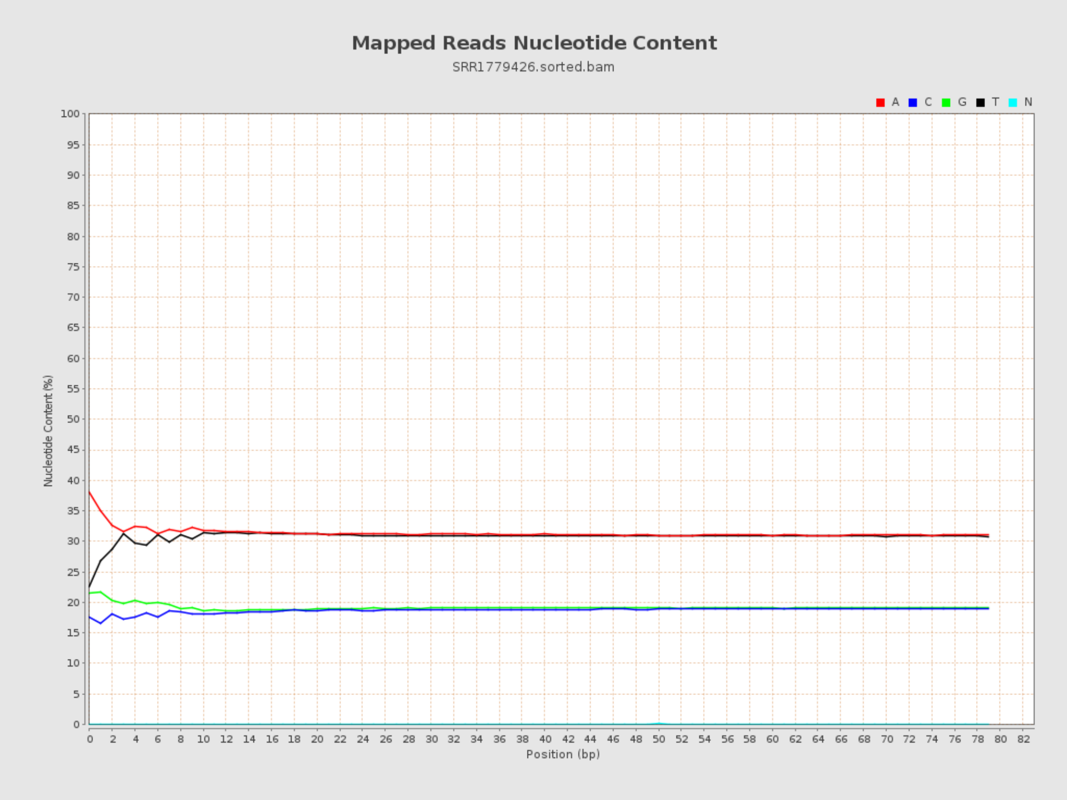
6. Results : Genome Fraction Coverage



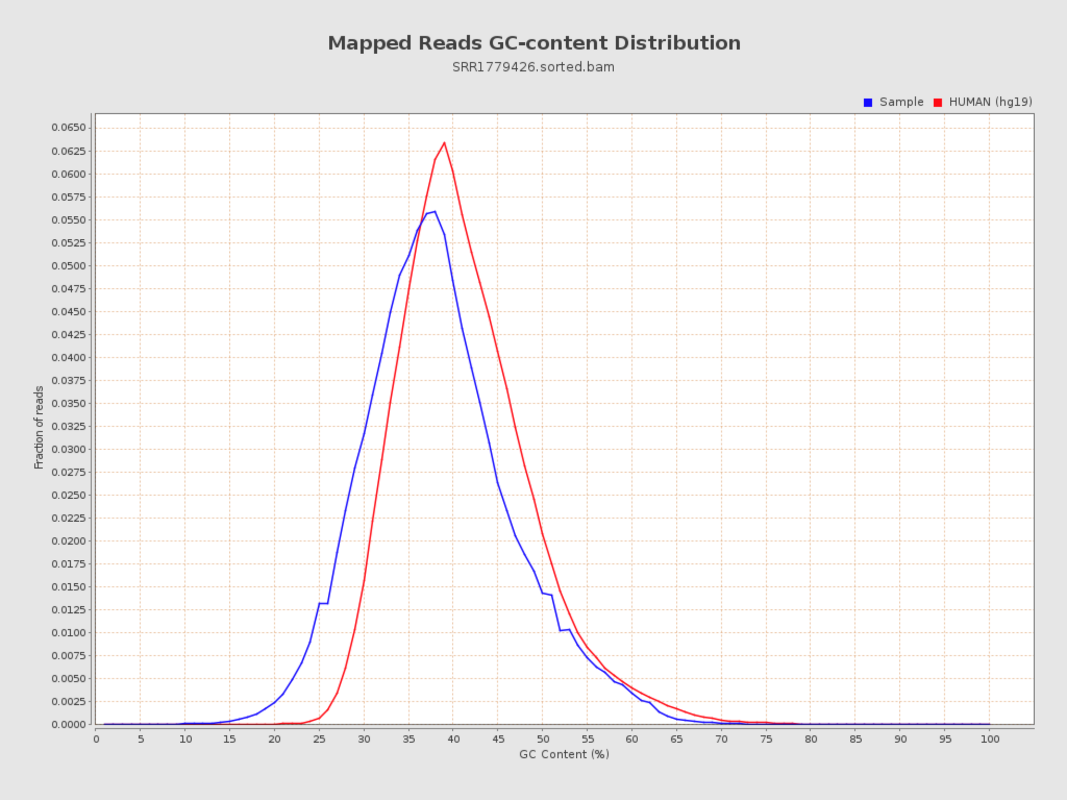
7. Results : Duplication Rate Histogram



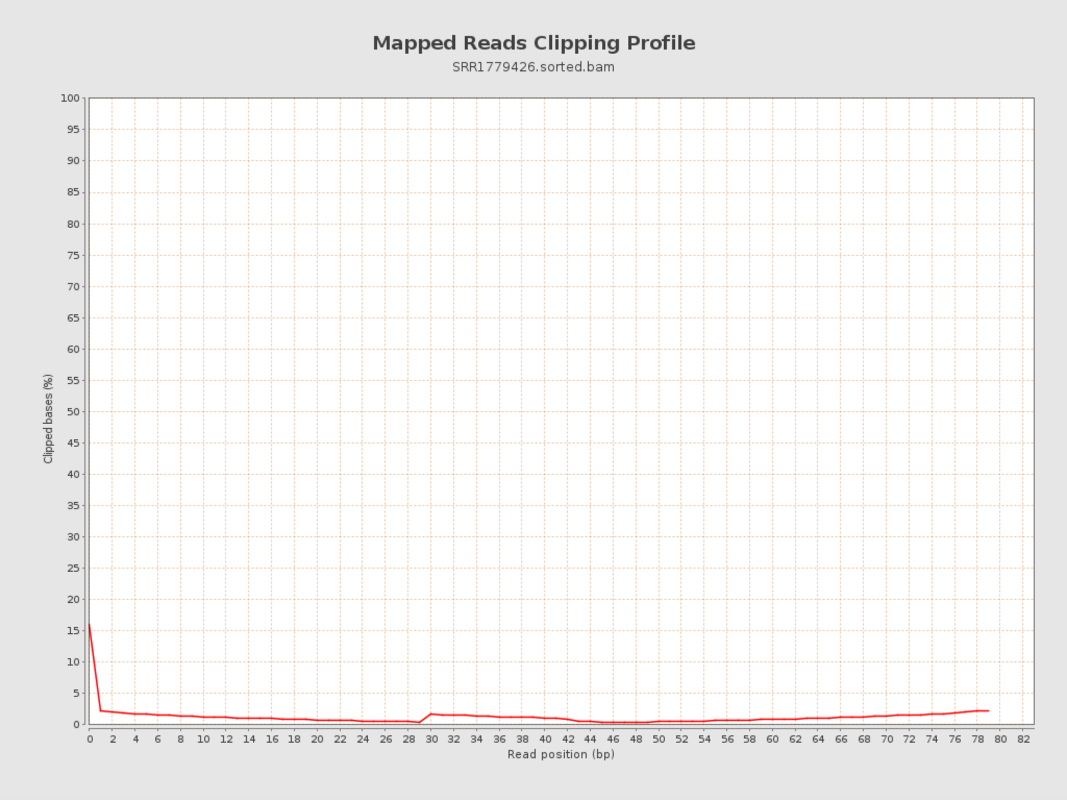
8. Results : Mapped Reads Nucleotide Content



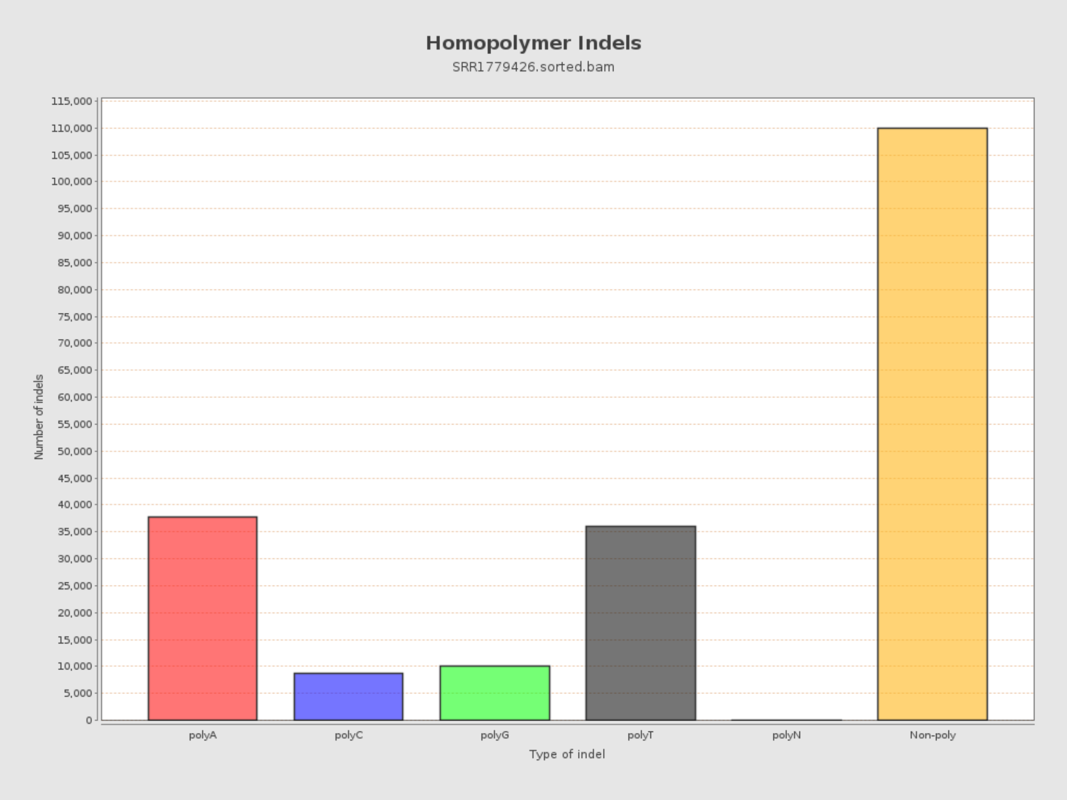
9. Results : Mapped Reads GC-content Distribution



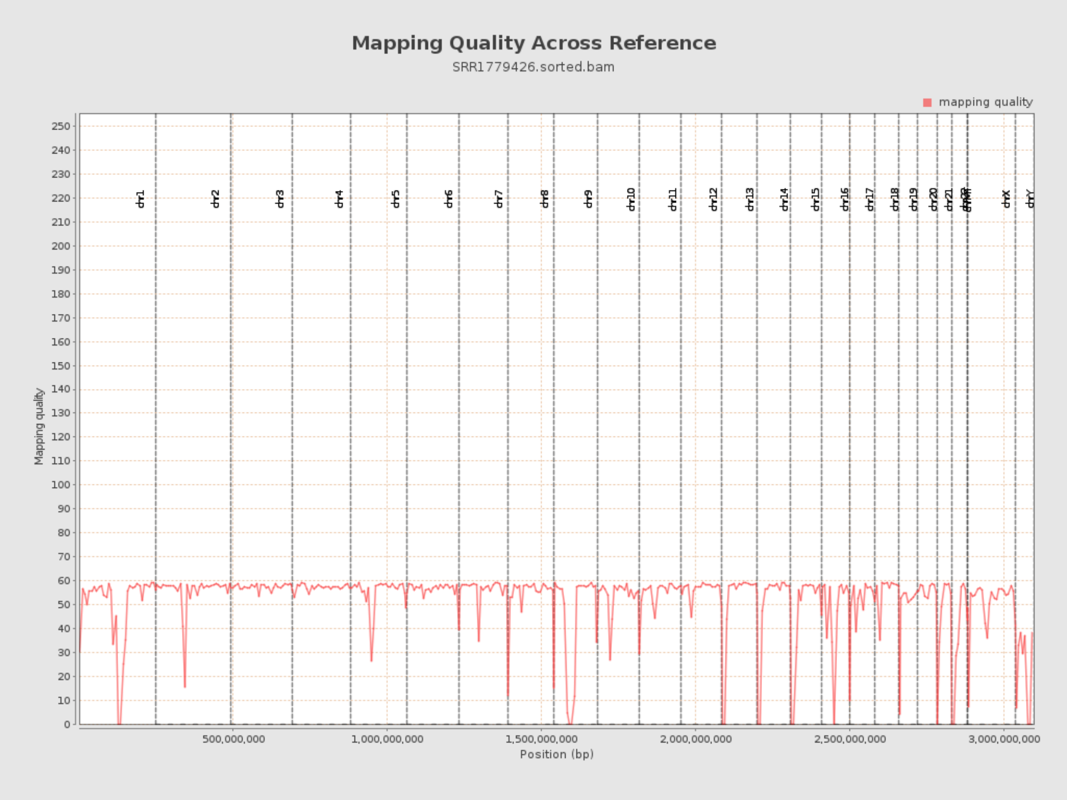
10. Results : Mapped Reads Clipping Profile



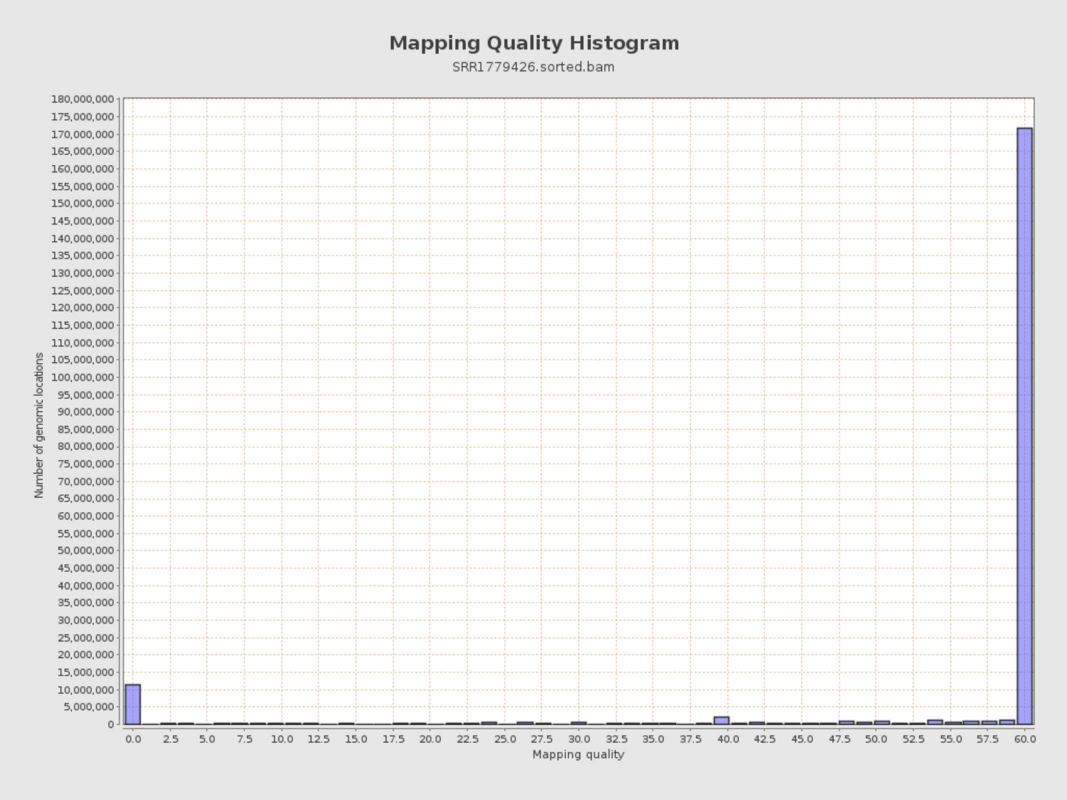
11. Results : Homopolymer Indels



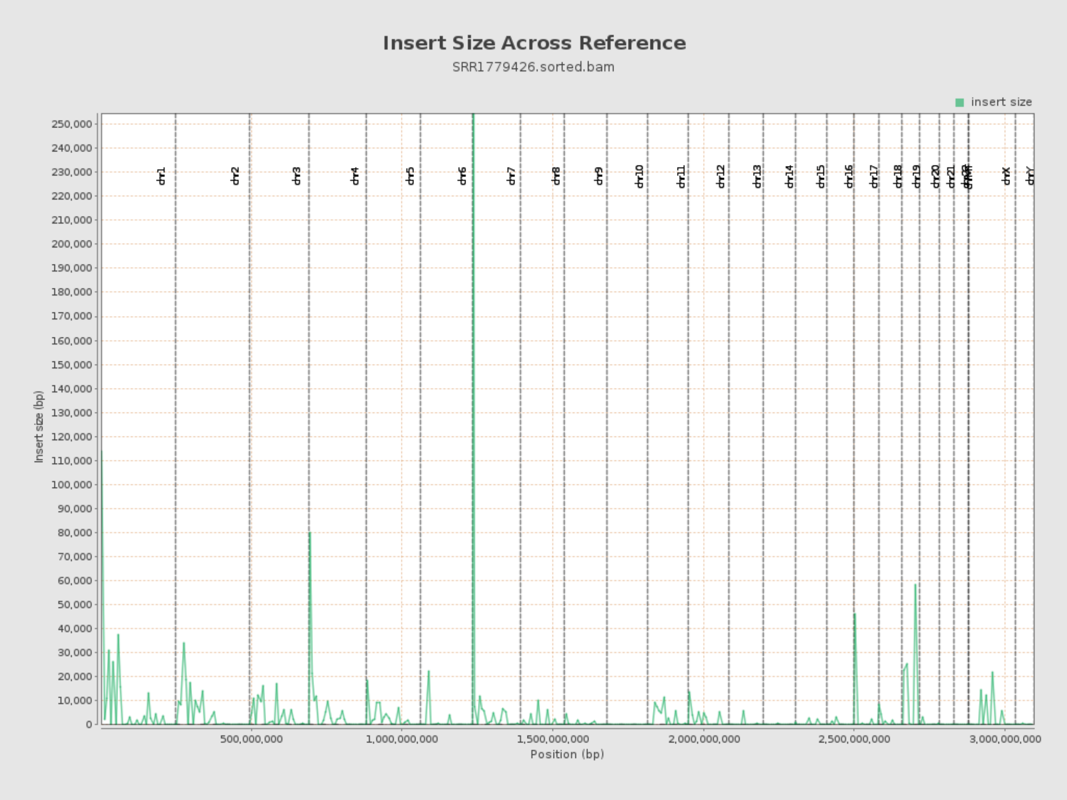
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram