Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 00:25:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779416.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_SRR1779416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779416_1.fastq.gz SRR1779416_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 00:25:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,797,054
Mapped reads	16,148,023 / 96.14%
Unmapped reads	649,031 / 3.86%
Mapped paired reads	16,148,023 / 96.14%
Mapped reads, first in pair	8,132,470 / 48.42%
Mapped reads, second in pair	8,015,553 / 47.72%
Mapped reads, both in pair	15,970,686 / 95.08%
Mapped reads, singletons	177,337 / 1.06%
Secondary alignments	0
Supplementary alignments	108,544 / 0.65%
Read min/max/mean length	30 / 80 / 80.24
Duplicated reads (estimated)	3,047,156 / 18.14%
Duplication rate	9.89%
Clipped reads	980,345 / 5.84%

2.2. ACGT Content

Number/percentage of A's	400,723,387 / 31.29%
Number/percentage of C's	239,364,654 / 18.69%
Number/percentage of T's	395,673,870 / 30.89%
Number/percentage of G's	244,686,847 / 19.11%
Number/percentage of N's	285,533 / 0.02%

GC Percentage	37.79%

2.3. Coverage

Mean	0.4138
Standard Deviation	9.924

2.4. Mapping Quality

Mean Mapping Quality	52.18

2.5. Insert size

Mean	60,364.53
Standard Deviation	2,291,817.74
P25/Median/P75	146 / 189 / 246

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	5,675,764
Insertions	124,481
Mapped reads with at least one insertion	0.76%
Deletions	142,593
Mapped reads with at least one deletion	0.87%
Homopolymer indels	45.05%

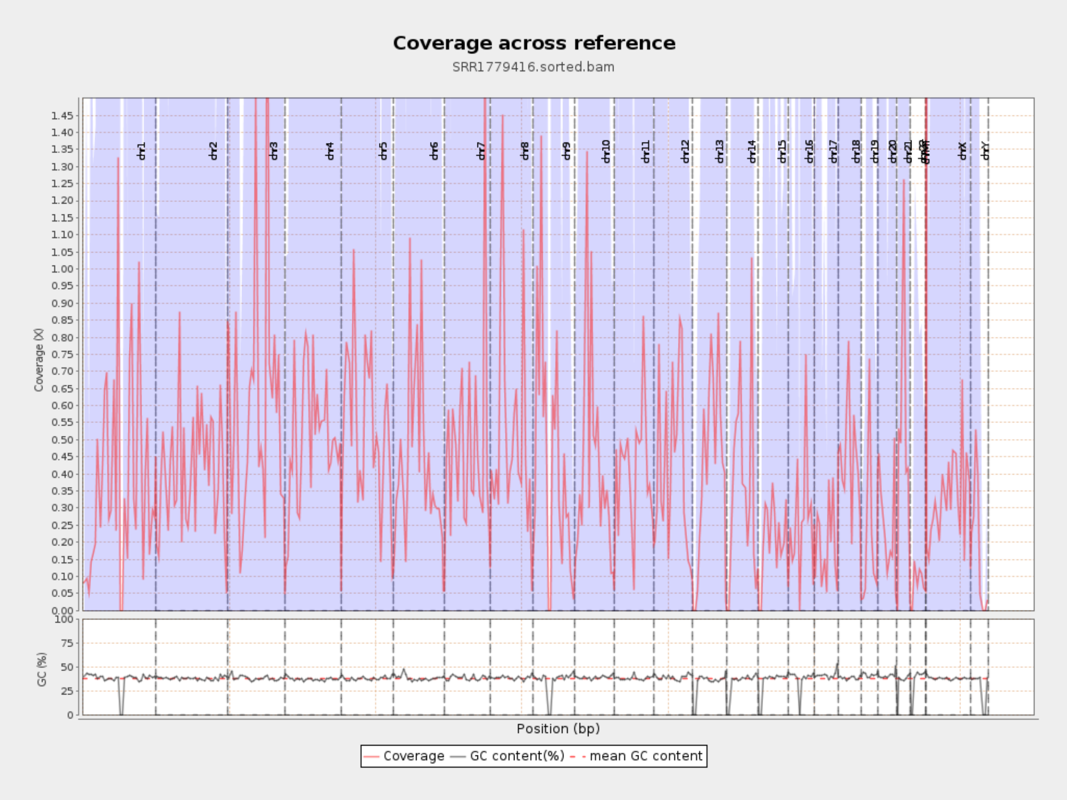
2.7. Chromosome stats

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

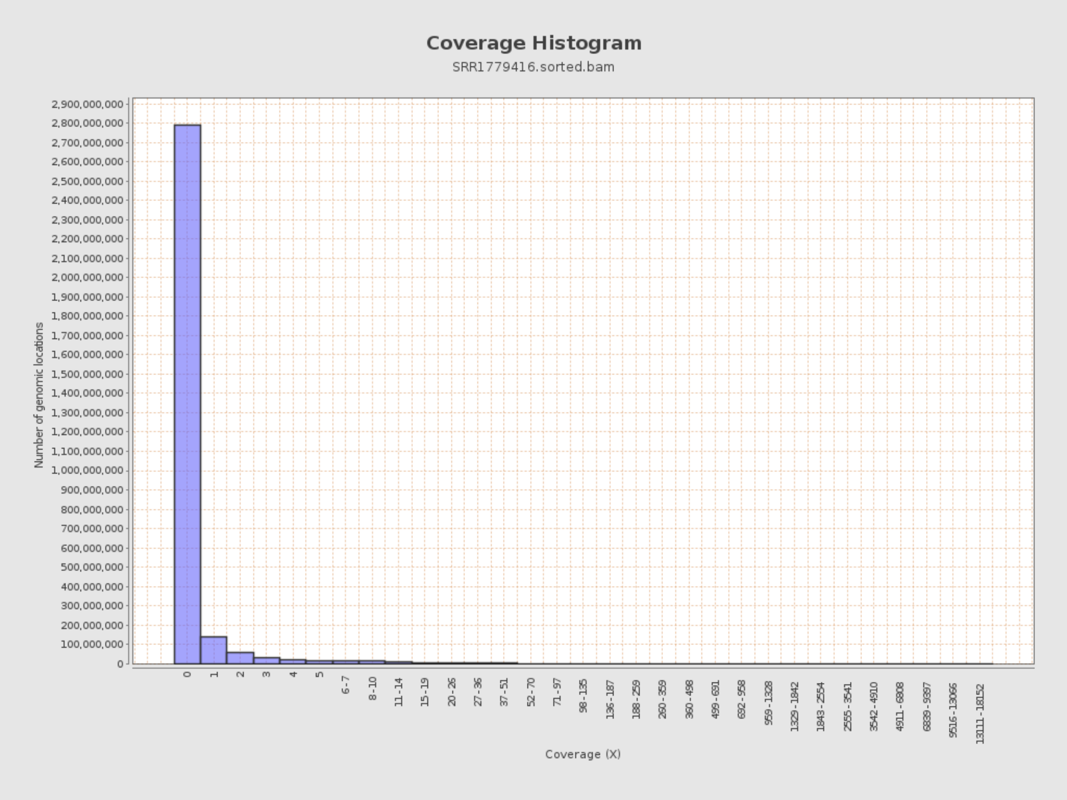
		bases	coverage	deviation
chr1	249250621	94142391	0.3777	19.4156
chr2	243199373	99506125	0.4092	4.4694
chr3	198022430	122189120	0.617	19.8943
chr4	191154276	97937258	0.5123	3.3781
chr5	180915260	97087124	0.5366	5.5572
chr6	171115067	75585361	0.4417	4.4843
chr7	159138663	77264409	0.4855	12.9235
chr8	146364022	77165084	0.5272	14.8199
chr9	141213431	63751413	0.4515	6.465
chr10	135534747	58566498	0.4321	12.8212
chr11	135006516	56204741	0.4163	6.0328
chr12	133851895	55533720	0.4149	6.227
chr13	115169878	49636830	0.431	2.4239
chr14	107349540	40104463	0.3736	3.9847
chr15	102531392	21307626	0.2078	2.6697
chr16	90354753	23139613	0.2561	3.1322
chr17	81195210	15771040	0.1942	3.503
chr18	78077248	35932417	0.4602	6.8594
chr19	59128983	13461102	0.2277	11.4697
chr20	63025520	16494813	0.2617	4.1666
chr21	48129895	24135103	0.5015	2.9918
chr22	51304566	4098823	0.0799	0.7275
chrMT	16571	534505	32.2554	12.8619
chrX	155270560	50363636	0.3244	2.7135

chrY	59373566	11104450	0.187	2.1313

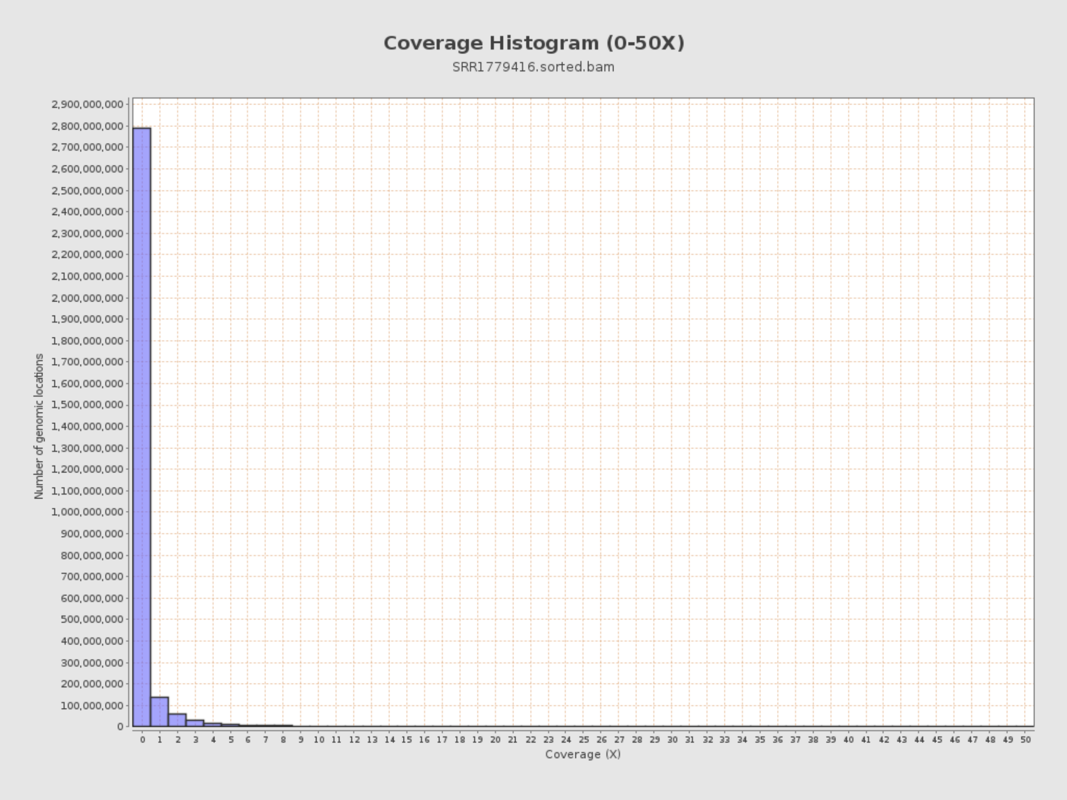
3. Results : Coverage across reference



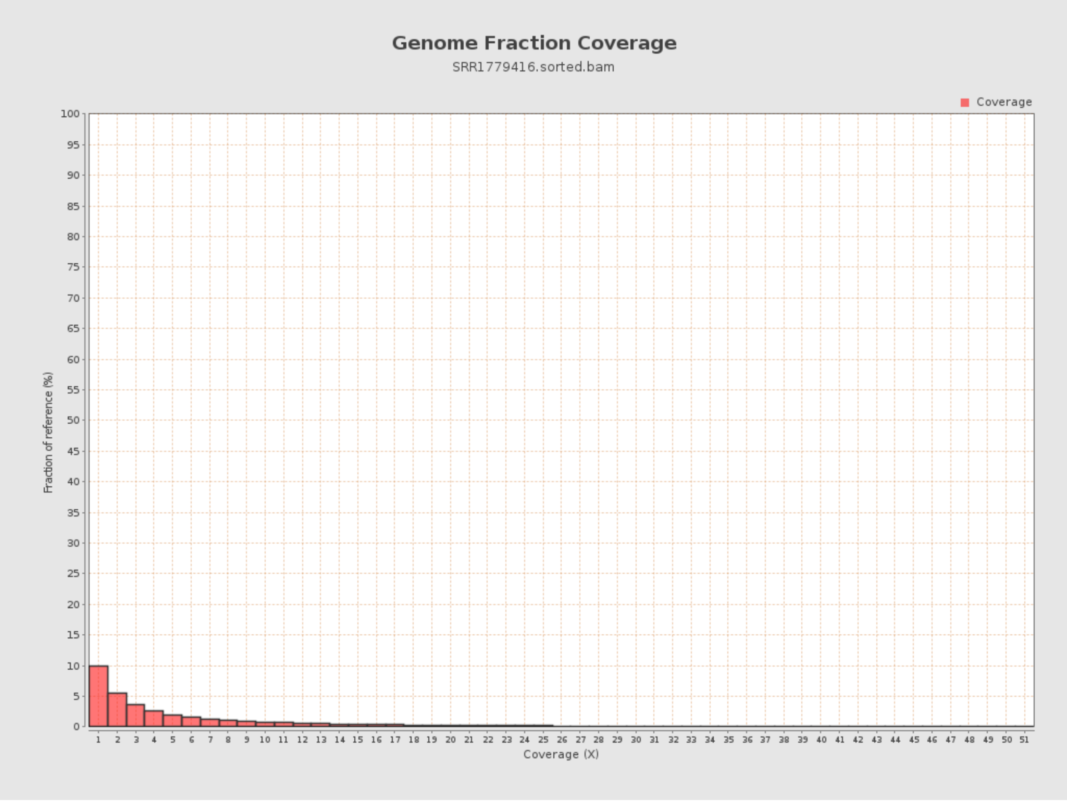
4. Results : Coverage Histogram



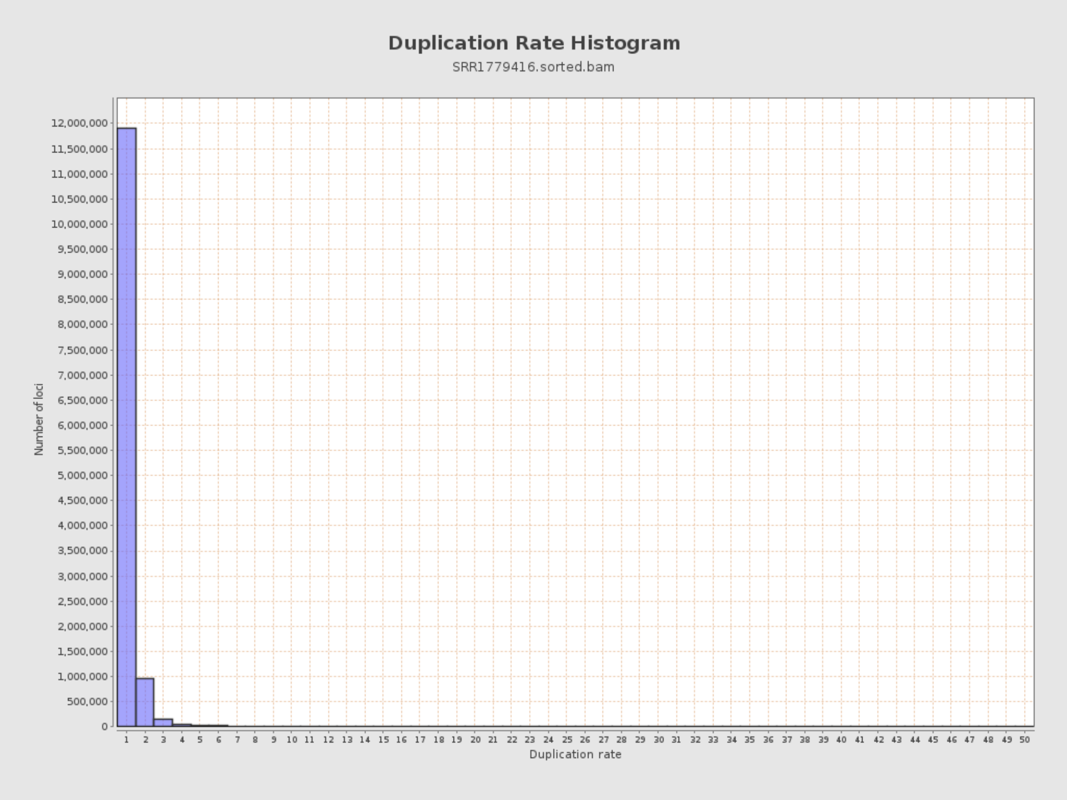
5. Results : Coverage Histogram (0-50X)



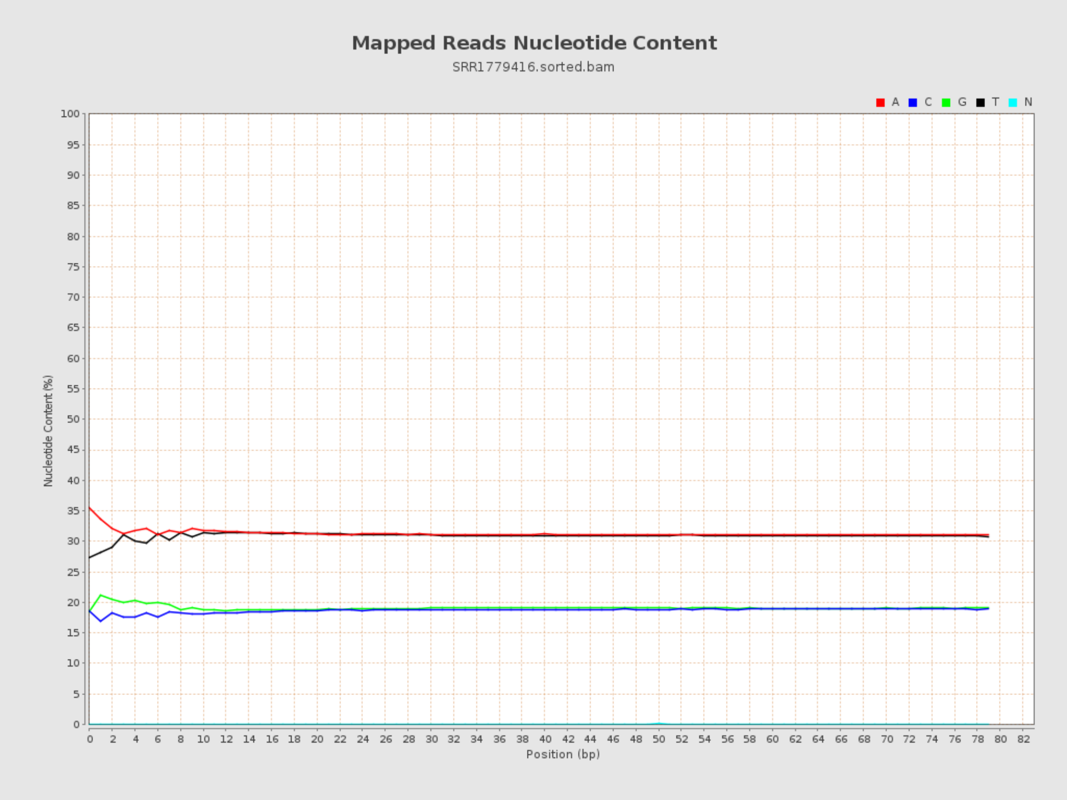
6. Results : Genome Fraction Coverage



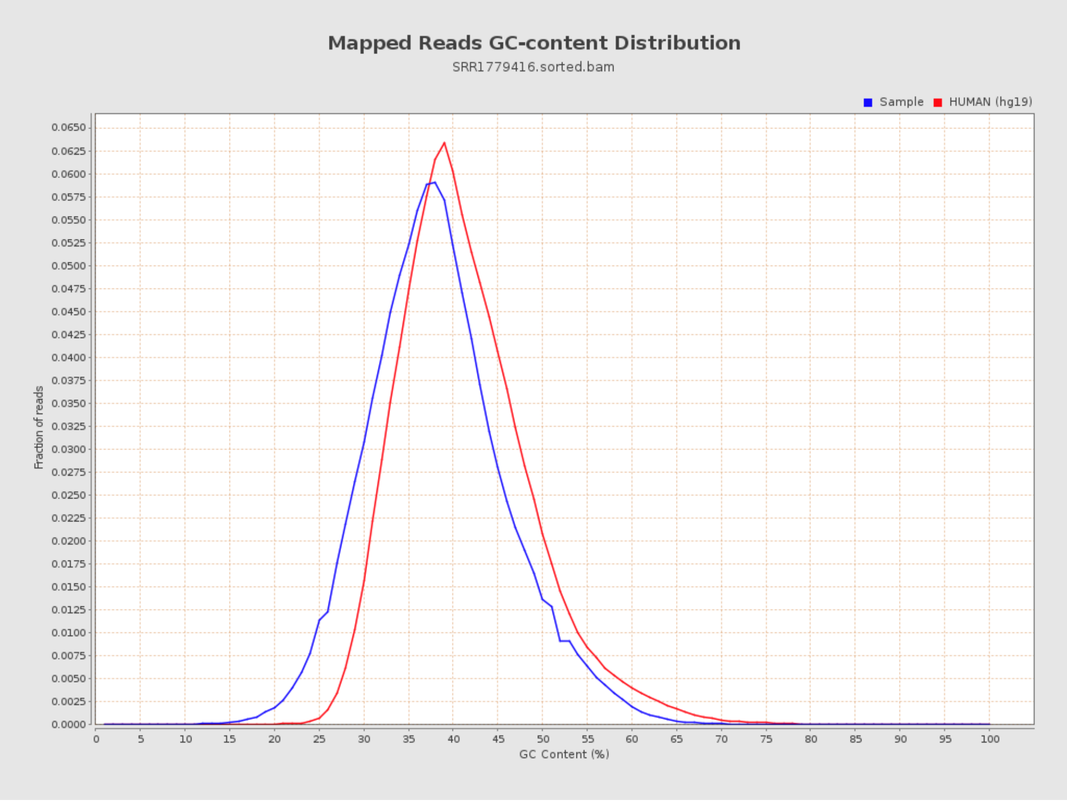
7. Results : Duplication Rate Histogram



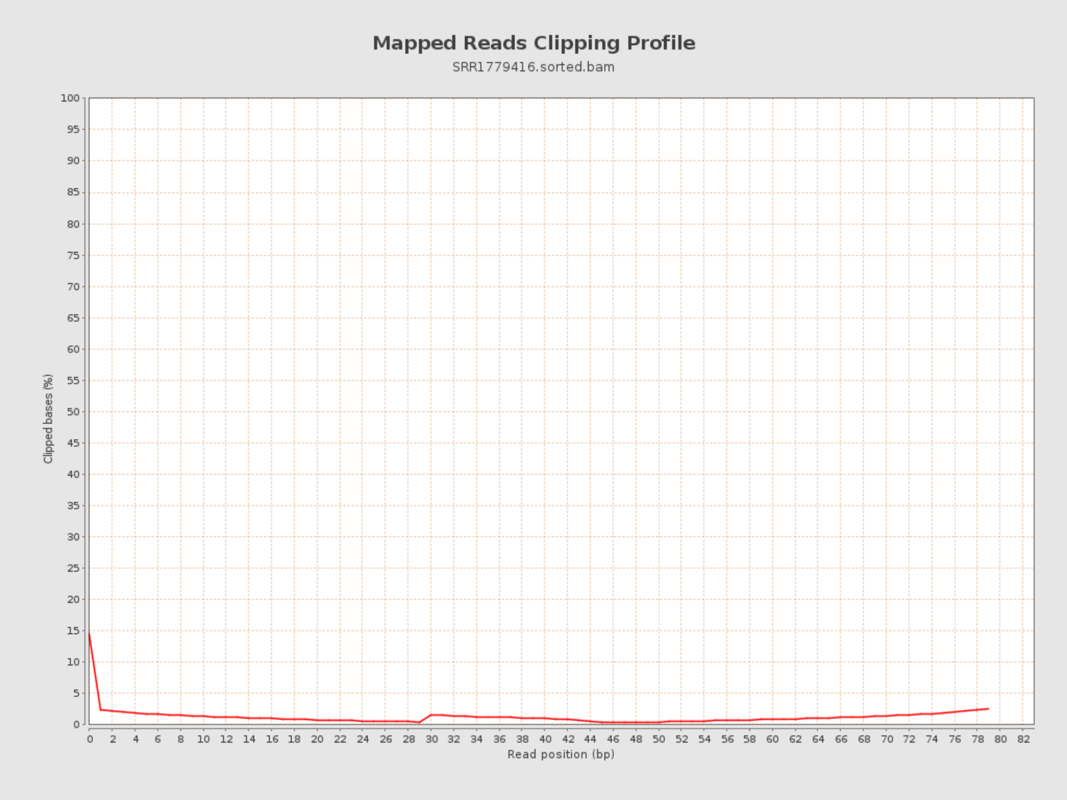
8. Results : Mapped Reads Nucleotide Content



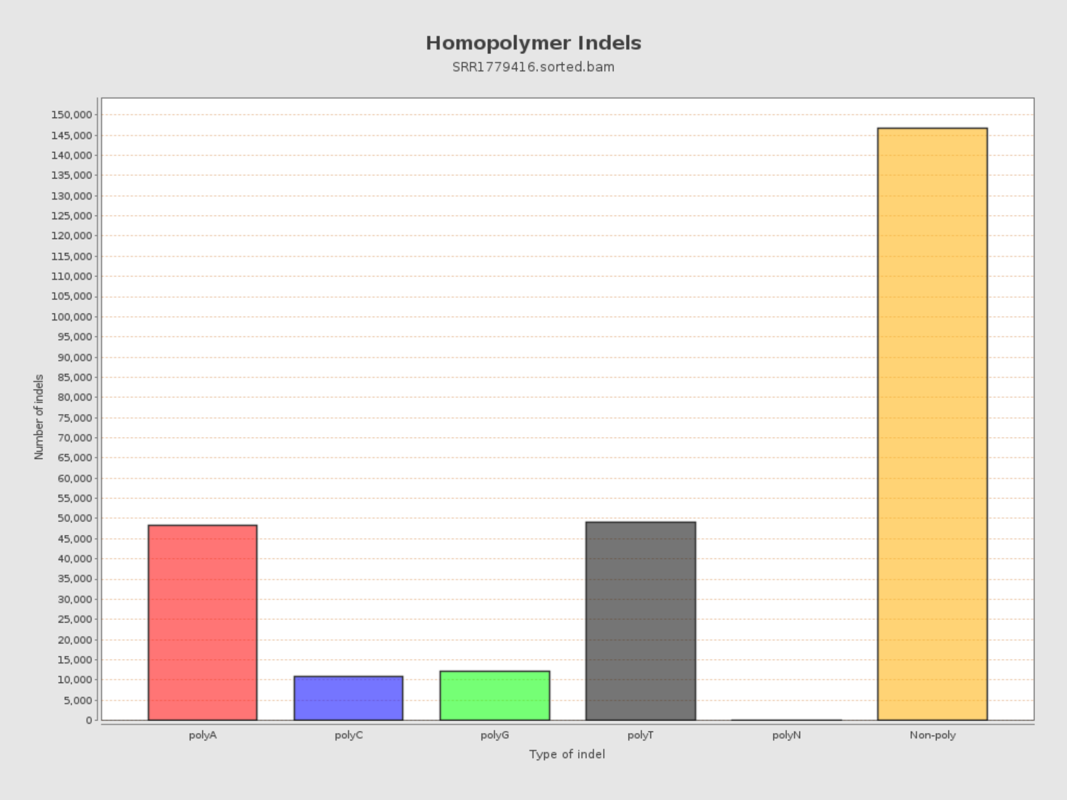
9. Results : Mapped Reads GC-content Distribution



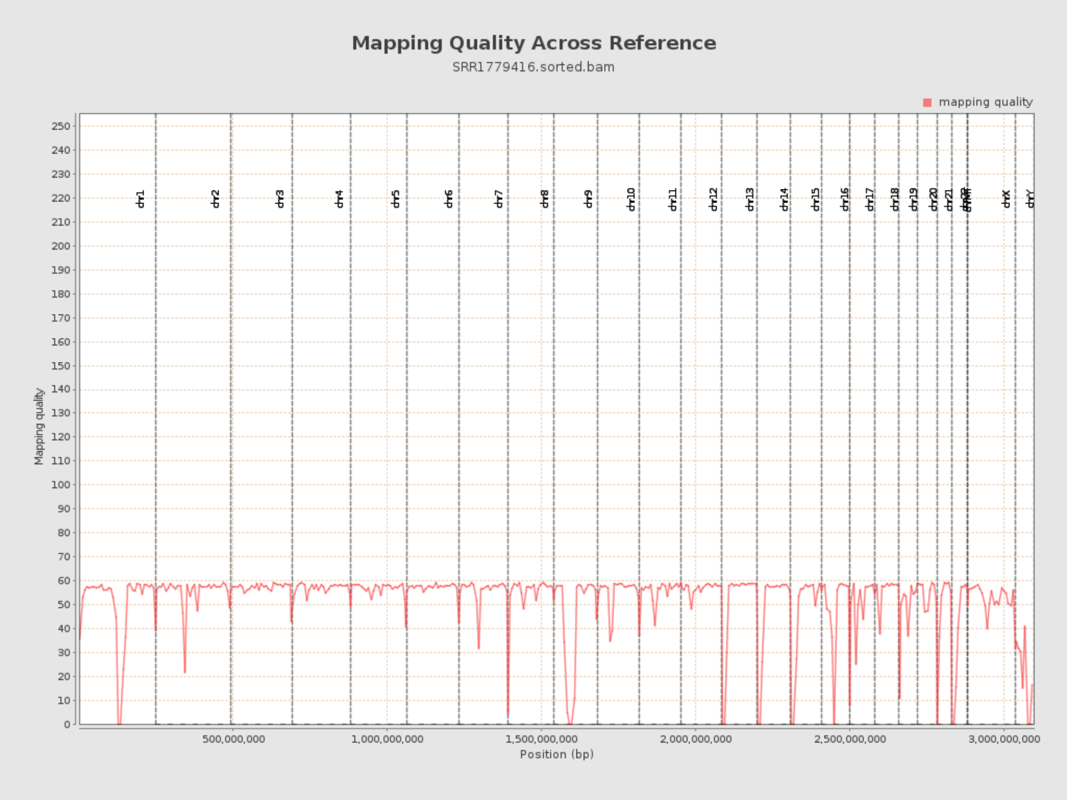
10. Results : Mapped Reads Clipping Profile



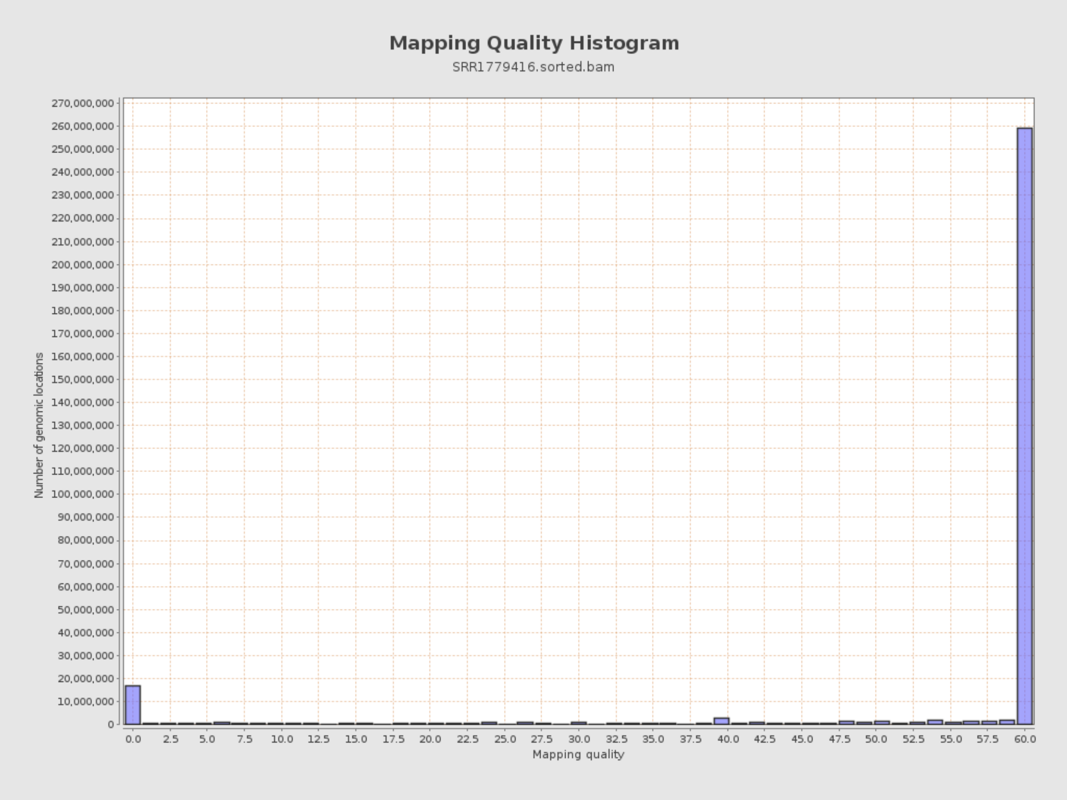
11. Results : Homopolymer Indels



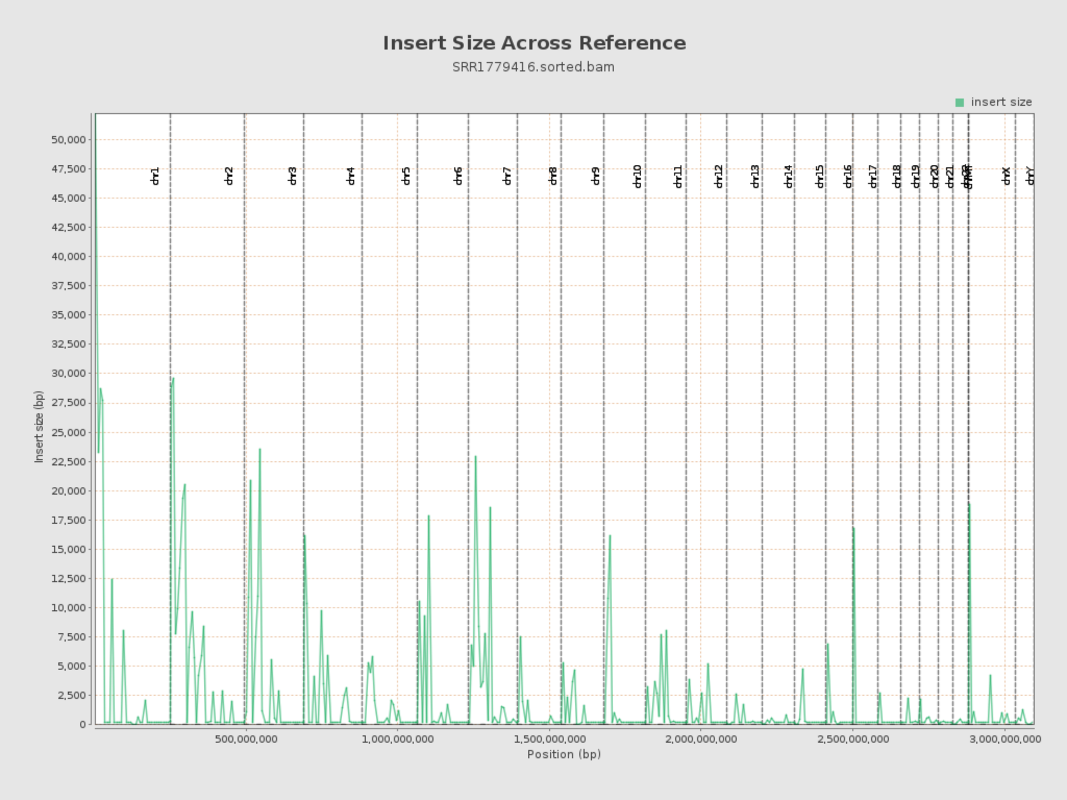
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram