Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 23:39:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779414.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_SRR1779414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779414_1.fastq.gz SRR1779414_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 23:39:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,158,556
Mapped reads	13,828,915 / 97.67%
Unmapped reads	329,641 / 2.33%
Mapped paired reads	13,828,915 / 97.67%
Mapped reads, first in pair	6,958,228 / 49.15%
Mapped reads, second in pair	6,870,687 / 48.53%
Mapped reads, both in pair	13,716,288 / 96.88%
Mapped reads, singletons	112,627 / 0.8%
Secondary alignments	0
Supplementary alignments	56,744 / 0.4%
Read min/max/mean length	30 / 80 / 80.15
Duplicated reads (estimated)	490,296 / 3.46%
Duplication rate	3.24%
Clipped reads	553,471 / 3.91%

2.2. ACGT Content

Number/percentage of A's	332,710,414 / 30.26%
Number/percentage of C's	216,781,670 / 19.71%
Number/percentage of T's	328,775,220 / 29.9%
Number/percentage of G's	221,119,020 / 20.11%
Number/percentage of N's	243,534 / 0.02%

GC Percentage	39.82%

2.3. Coverage

Mean	0.3553
Standard Deviation	1.3898

2.4. Mapping Quality

Mean Mapping Quality	52.69

2.5. Insert size

Mean	83,387.43
Standard Deviation	2,790,553.75
P25/Median/P75	150 / 191 / 242

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,669,601
Insertions	97,705
Mapped reads with at least one insertion	0.7%
Deletions	111,133
Mapped reads with at least one deletion	0.79%
Homopolymer indels	47.36%

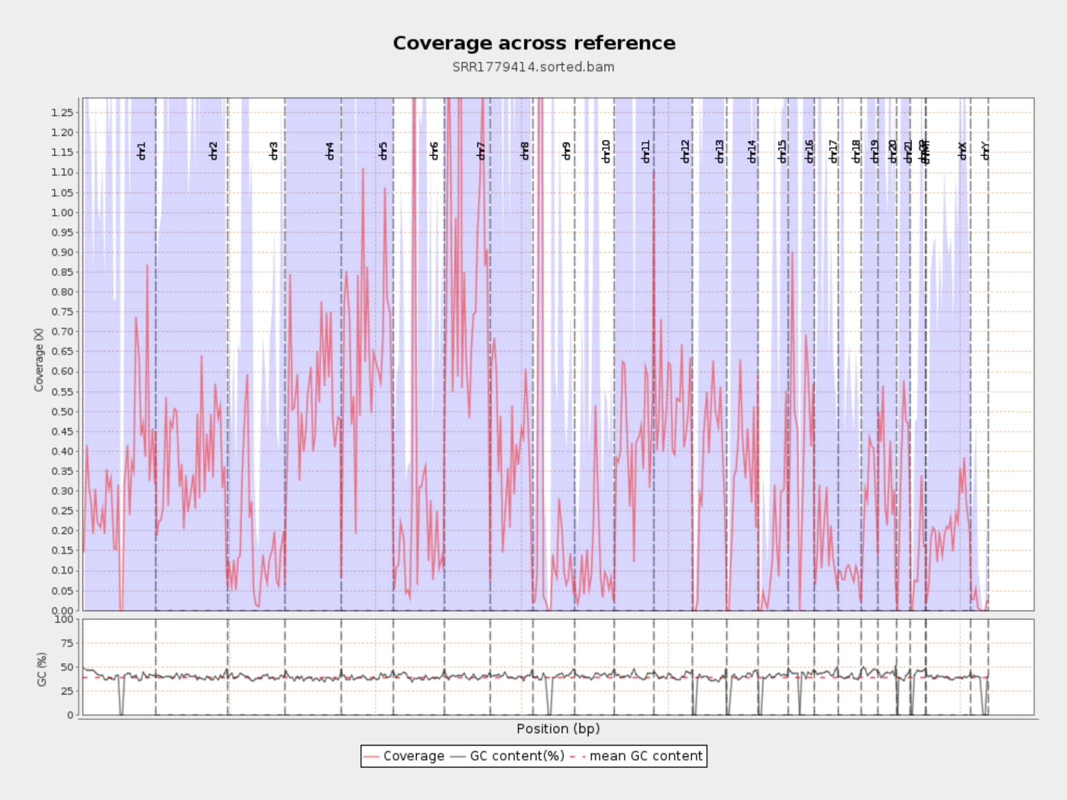
2.7. Chromosome stats

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

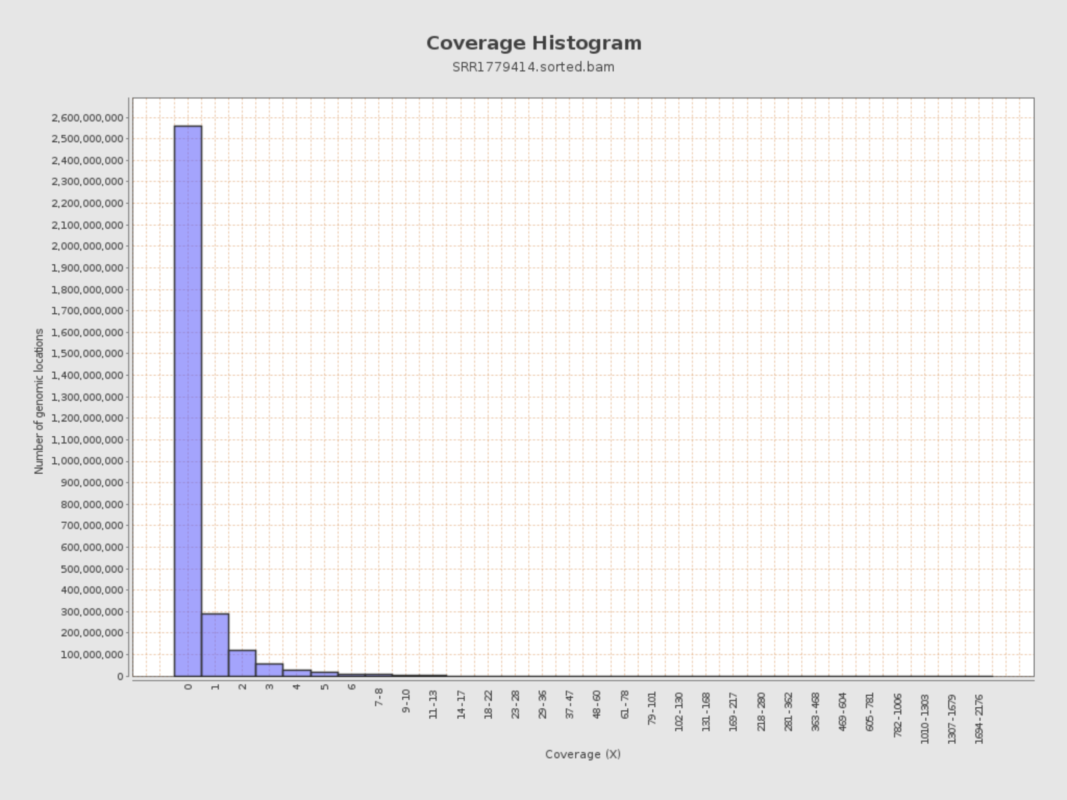
		bases	coverage	deviation
chr1	249250621	81865162	0.3284	2.4347
chr2	243199373	89719467	0.3689	1.0193
chr3	198022430	31372835	0.1584	0.6952
chr4	191154276	102134926	0.5343	1.1937
chr5	180915260	116854336	0.6459	1.3674
chr6	171115067	39931815	0.2334	1.0369
chr7	159138663	140824510	0.8849	2.4444
chr8	146364022	59618083	0.4073	1.1479
chr9	141213431	43712979	0.3096	1.6513
chr10	135534747	16177818	0.1194	1.8393
chr11	135006516	57553086	0.4263	1.1558
chr12	133851895	69332276	0.518	1.1814
chr13	115169878	41542826	0.3607	1.0069
chr14	107349540	35574163	0.3314	0.9898
chr15	102531392	16254081	0.1585	0.6723
chr16	90354753	40839672	0.452	1.1953
chr17	81195210	13684527	0.1685	0.969
chr18	78077248	6991721	0.0895	0.8437
chr19	59128983	17596320	0.2976	1.6059
chr20	63025520	21875477	0.3471	0.9613
chr21	48129895	16549297	0.3438	1.0327
chr22	51304566	6820471	0.1329	0.5893
chrMT	16571	282	0.017	0.1293
chrX	155270560	31989852	0.206	0.705

chrY	59373566	1042996	0.0176	0.2209

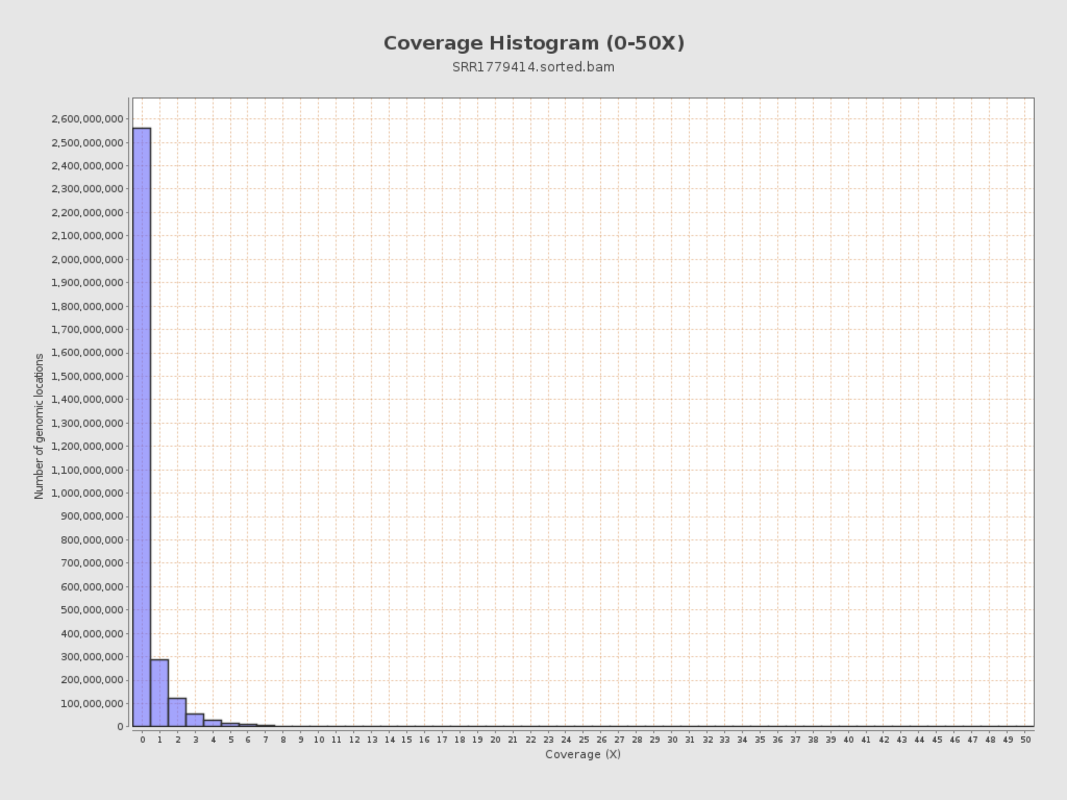
3. Results : Coverage across reference



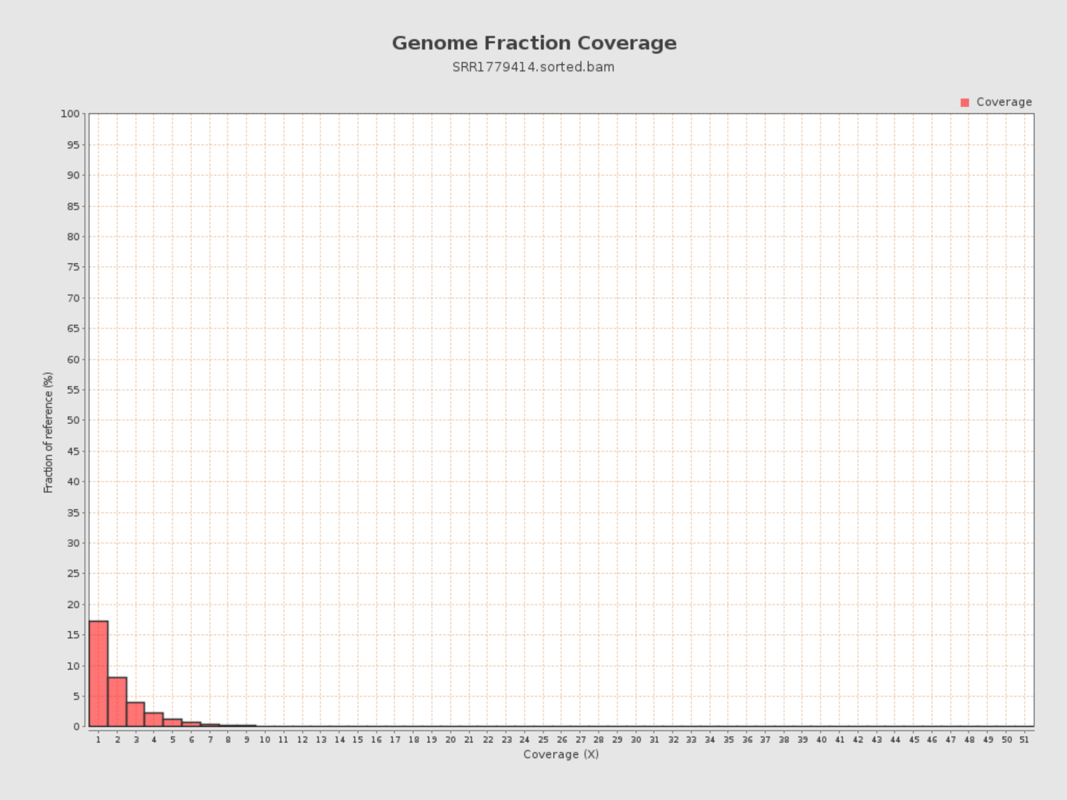
4. Results : Coverage Histogram



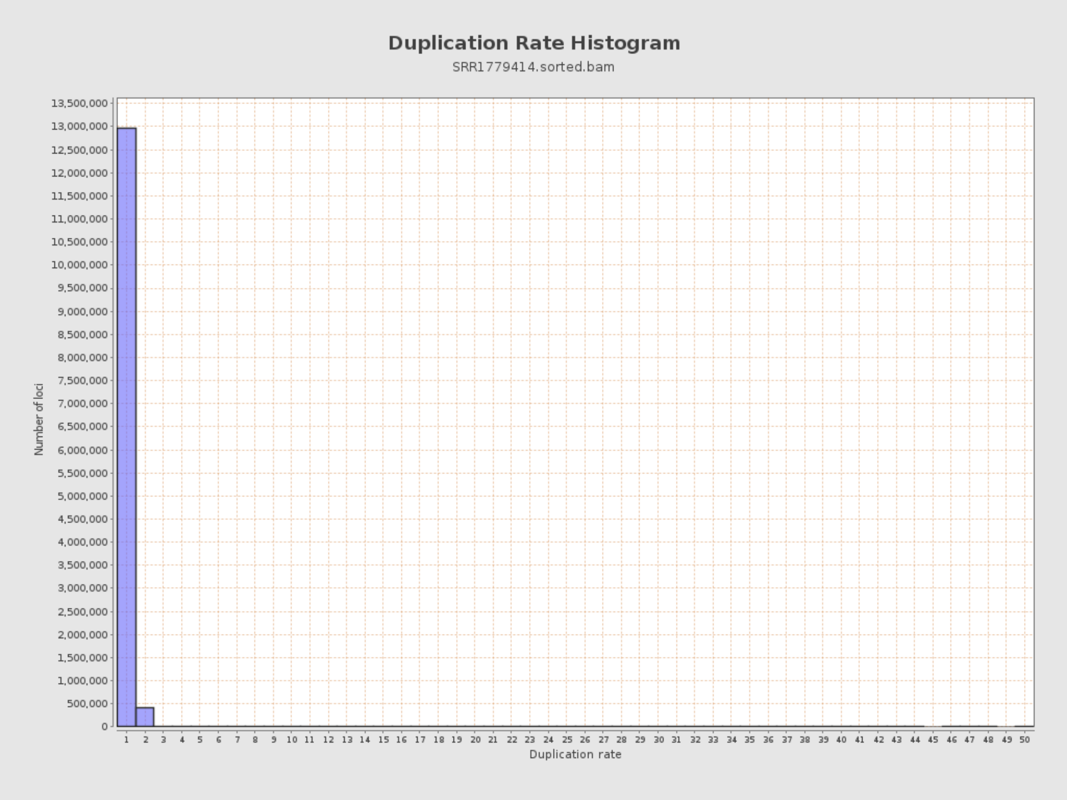
5. Results : Coverage Histogram (0-50X)



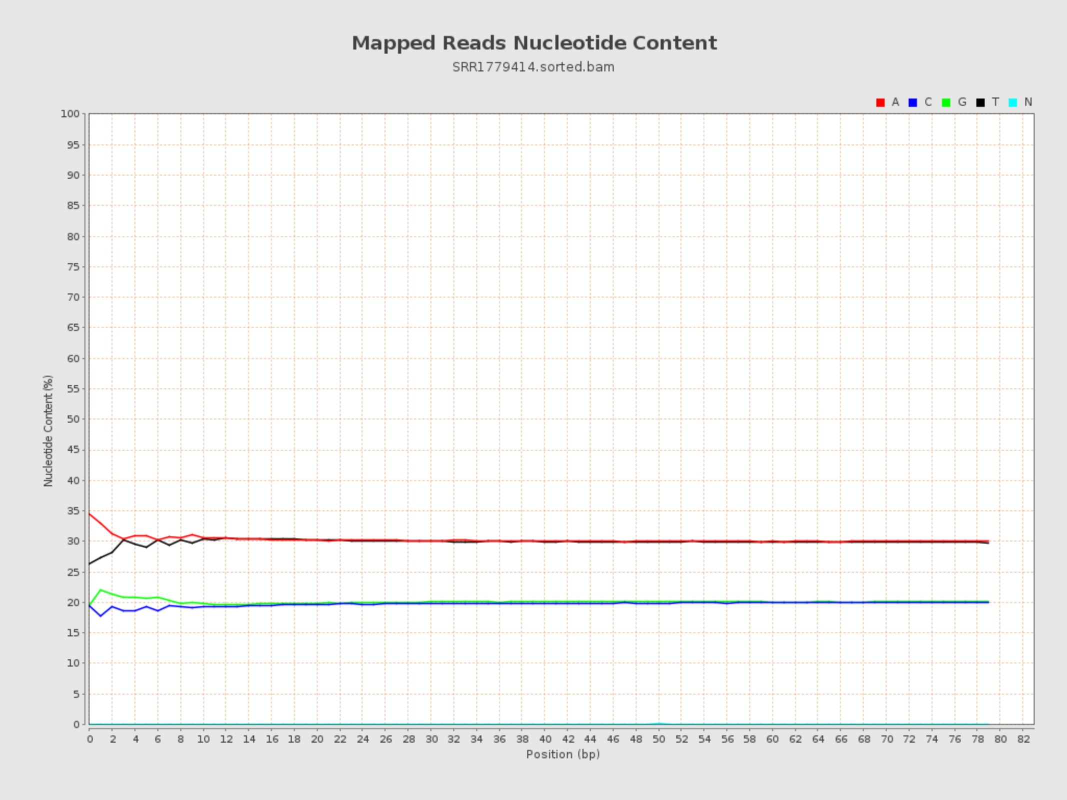
6. Results : Genome Fraction Coverage



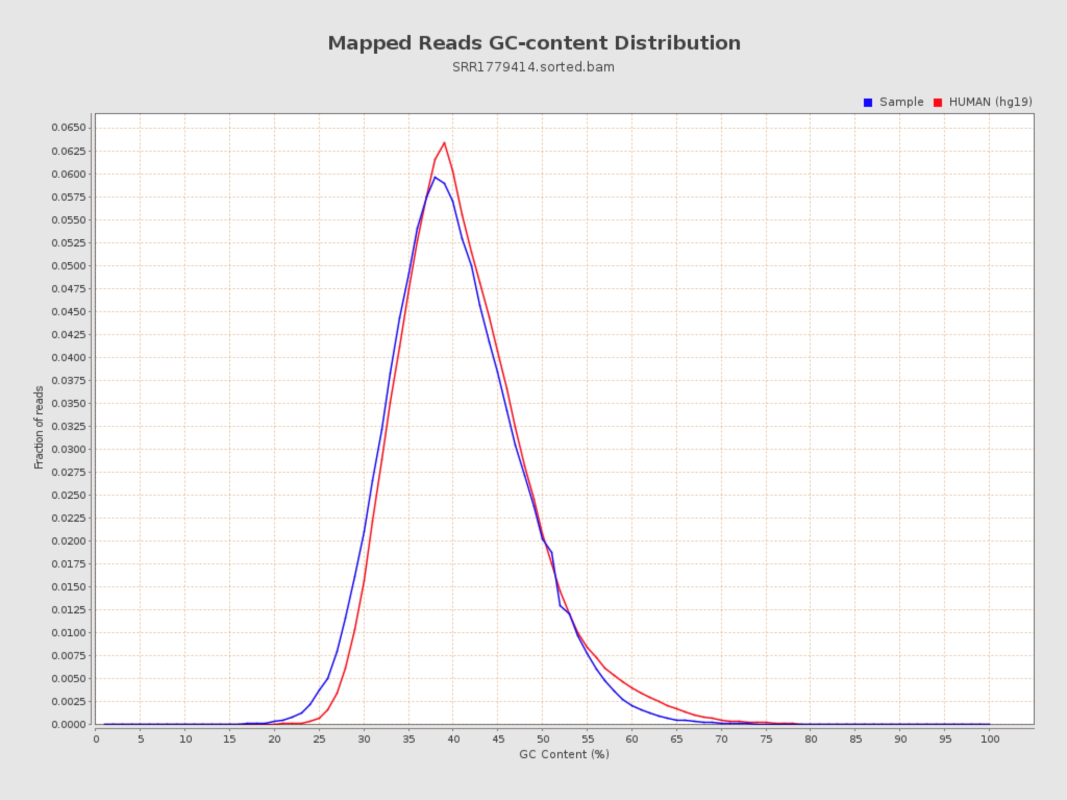
7. Results : Duplication Rate Histogram



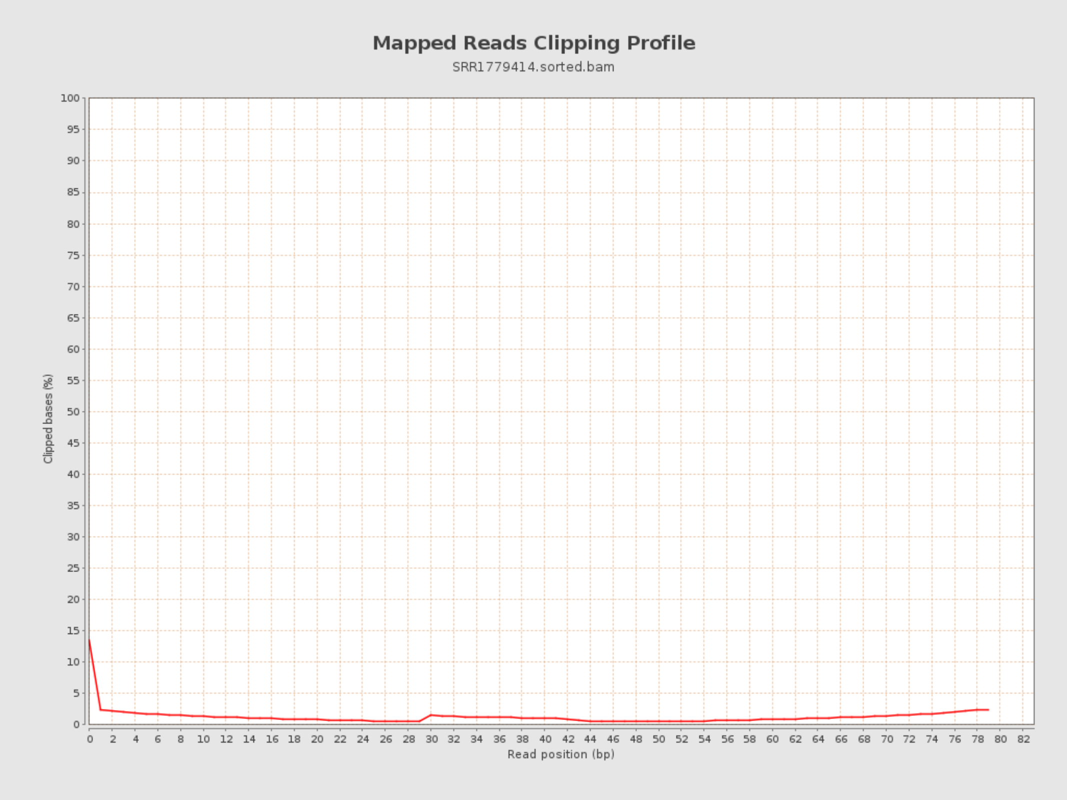
8. Results : Mapped Reads Nucleotide Content



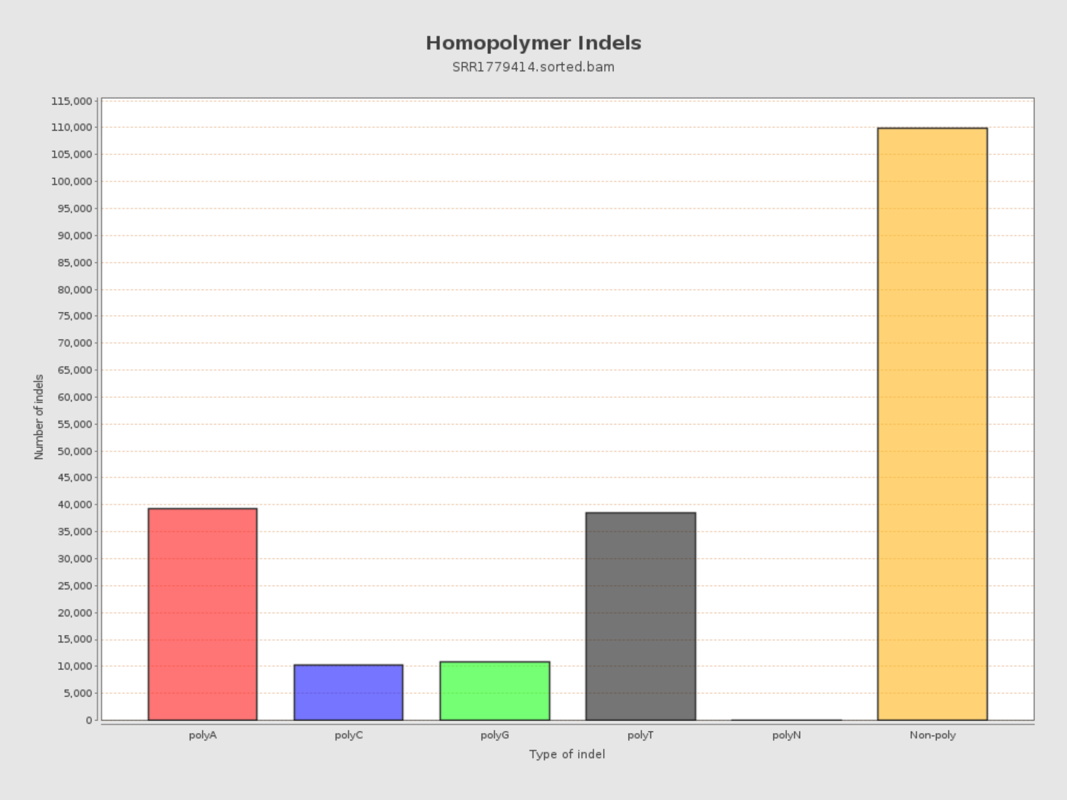
9. Results : Mapped Reads GC-content Distribution



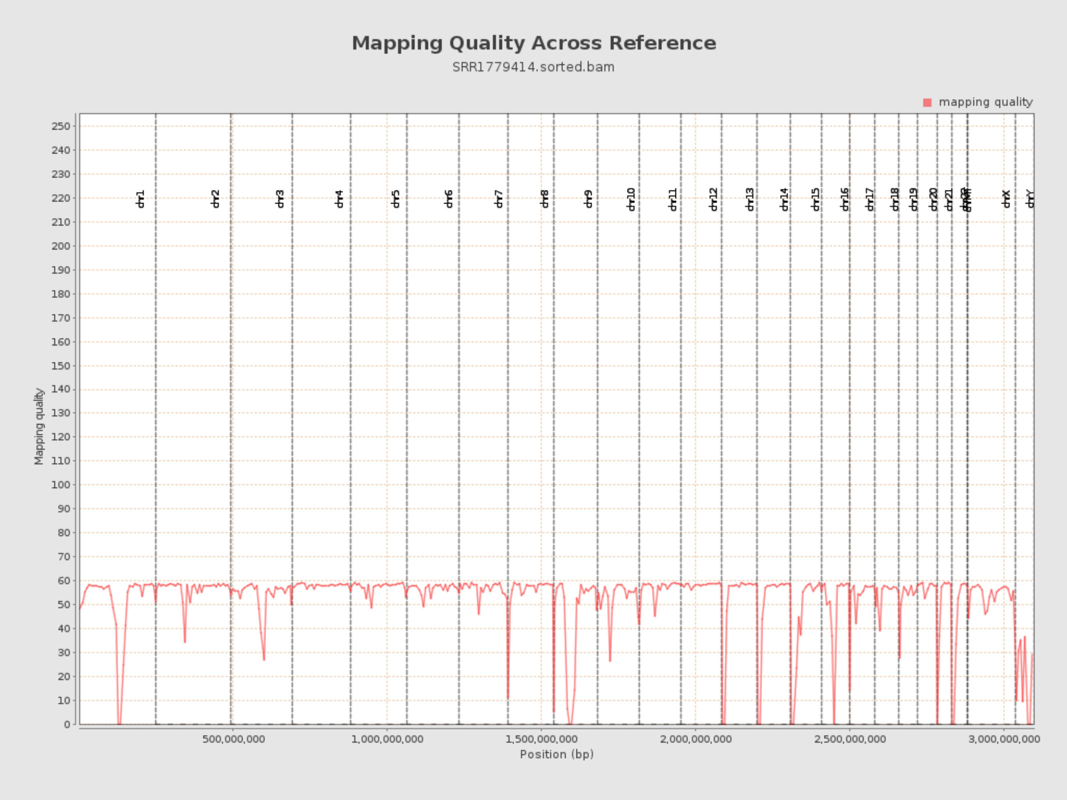
10. Results : Mapped Reads Clipping Profile



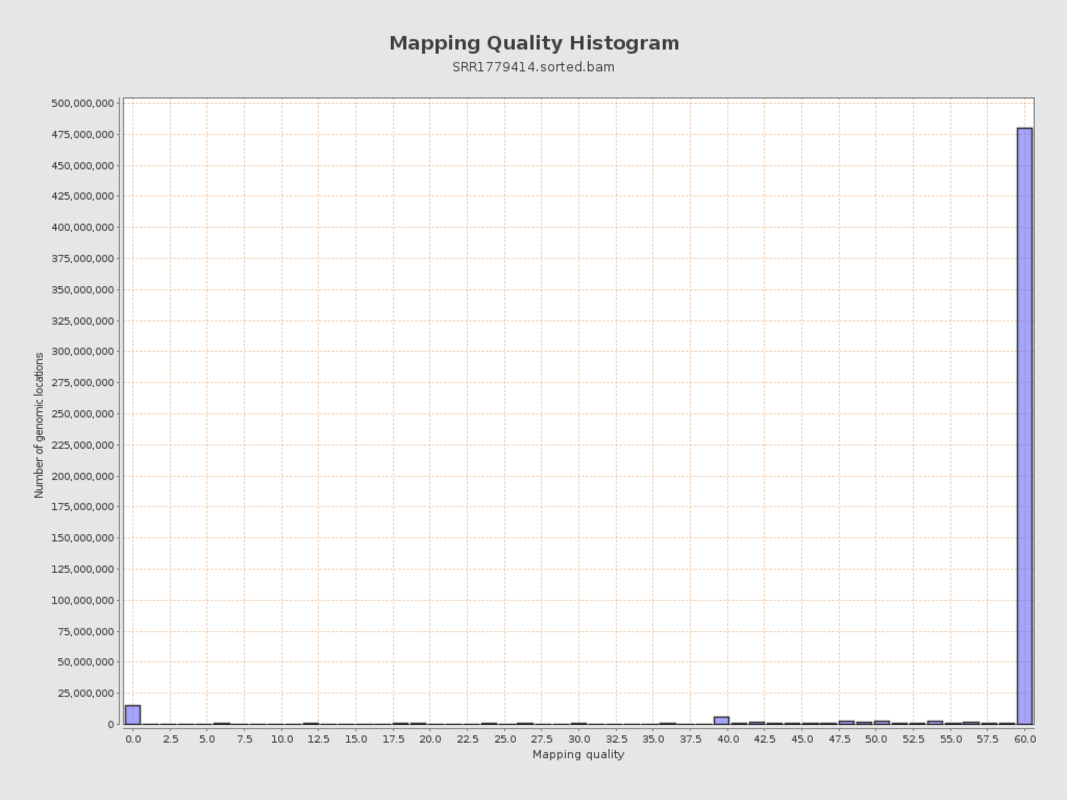
11. Results : Homopolymer Indels



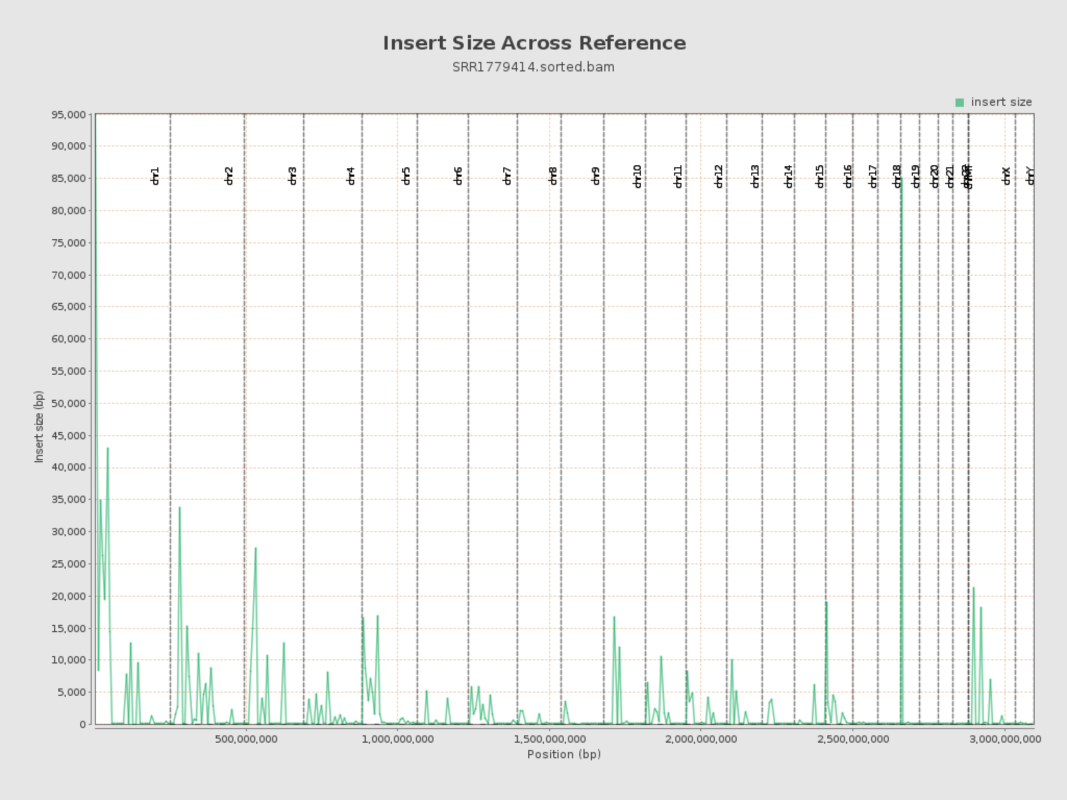
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram