Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 01:09:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779295.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_SRR1779295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779295_1.fastq.gz SRR1779295_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 01:09:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,468,708
Mapped reads	20,939,664 / 97.54%
Unmapped reads	529,044 / 2.46%
Mapped paired reads	20,939,664 / 97.54%
Mapped reads, first in pair	10,536,235 / 49.08%
Mapped reads, second in pair	10,403,429 / 48.46%
Mapped reads, both in pair	20,774,348 / 96.77%
Mapped reads, singletons	165,316 / 0.77%
Secondary alignments	0
Supplementary alignments	54,895 / 0.26%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	918,307 / 4.28%
Duplication rate	3.84%
Clipped reads	646,397 / 3.01%

2.2. ACGT Content

Number/percentage of A's	513,365,495 / 30.8%
Number/percentage of C's	318,845,741 / 19.13%
Number/percentage of T's	509,169,146 / 30.54%
Number/percentage of G's	325,159,846 / 19.51%
Number/percentage of N's	442,329 / 0.03%

GC Percentage	38.63%

2.3. Coverage

Mean	0.5386
Standard Deviation	2.1868

2.4. Mapping Quality

Mean Mapping Quality	52.99

2.5. Insert size

Mean	45,817.98
Standard Deviation	2,006,293.36
P25/Median/P75	152 / 201 / 269

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	5,597,924
Insertions	118,530
Mapped reads with at least one insertion	0.56%
Deletions	153,208
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.68%

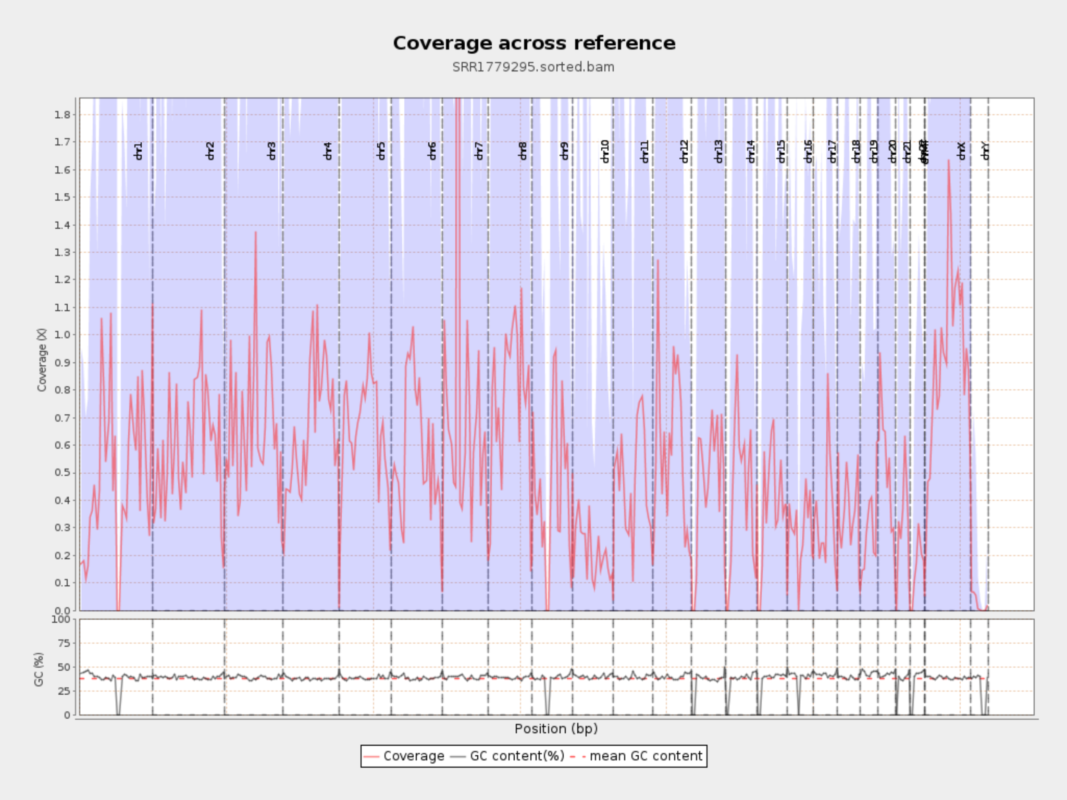
2.7. Chromosome stats

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

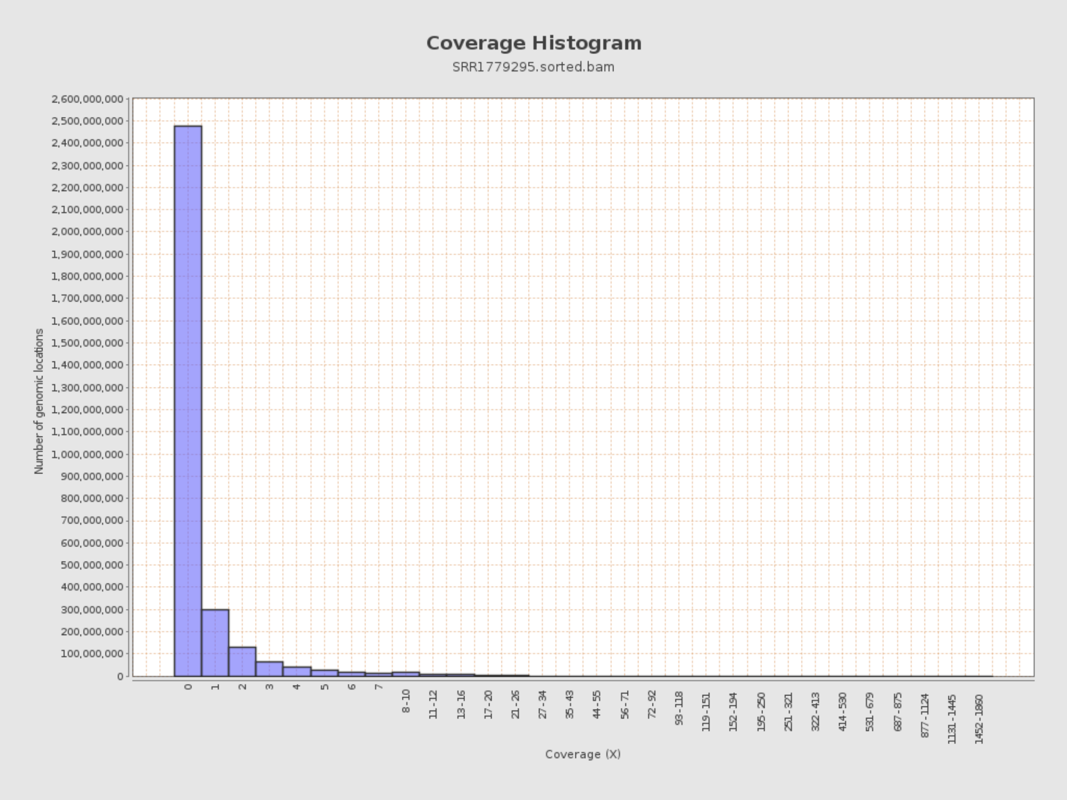
		bases	coverage	deviation
chr1	249250621	123208209	0.4943	2.495
chr2	243199373	145103995	0.5966	1.8603
chr3	198022430	133775946	0.6756	1.9136
chr4	191154276	127020276	0.6645	1.9117
chr5	180915260	116941899	0.6464	1.8006
chr6	171115067	101702894	0.5944	1.8654
chr7	159138663	135617704	0.8522	5.4776
chr8	146364022	115566040	0.7896	2.1224
chr9	141213431	59717118	0.4229	1.5988
chr10	135534747	28606597	0.2111	2.2152
chr11	135006516	63298357	0.4689	1.5429
chr12	133851895	78179877	0.5841	1.8347
chr13	115169878	53931406	0.4683	1.4814
chr14	107349540	45588358	0.4247	1.4131
chr15	102531392	38656471	0.377	1.2795
chr16	90354753	25284898	0.2798	1.0488
chr17	81195210	27632239	0.3403	1.3612
chr18	78077248	28467431	0.3646	1.1987
chr19	59128983	15413398	0.2607	1.3812
chr20	63025520	33333583	0.5289	1.758
chr21	48129895	15260583	0.3171	1.3474
chr22	51304566	7700148	0.1501	0.729
chrMT	16571	2055	0.124	0.3695
chrX	155270560	145789580	0.9389	2.5671

chrY	59373566	1504051	0.0253	0.3334

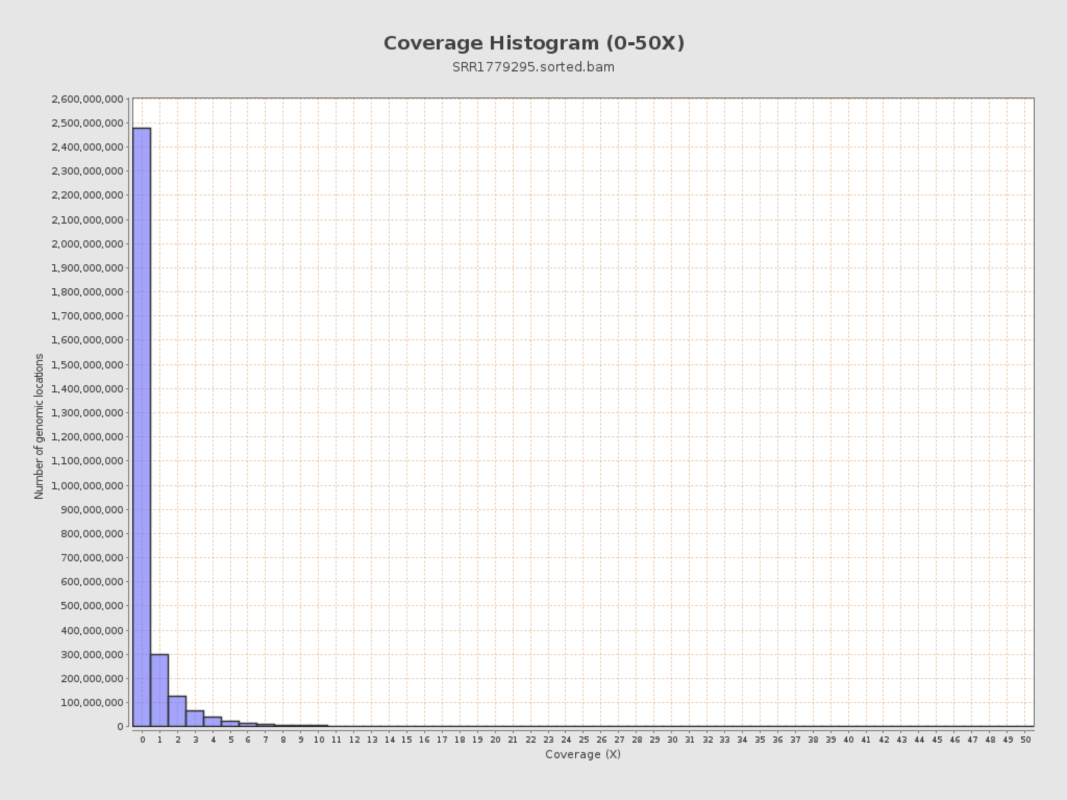
3. Results : Coverage across reference



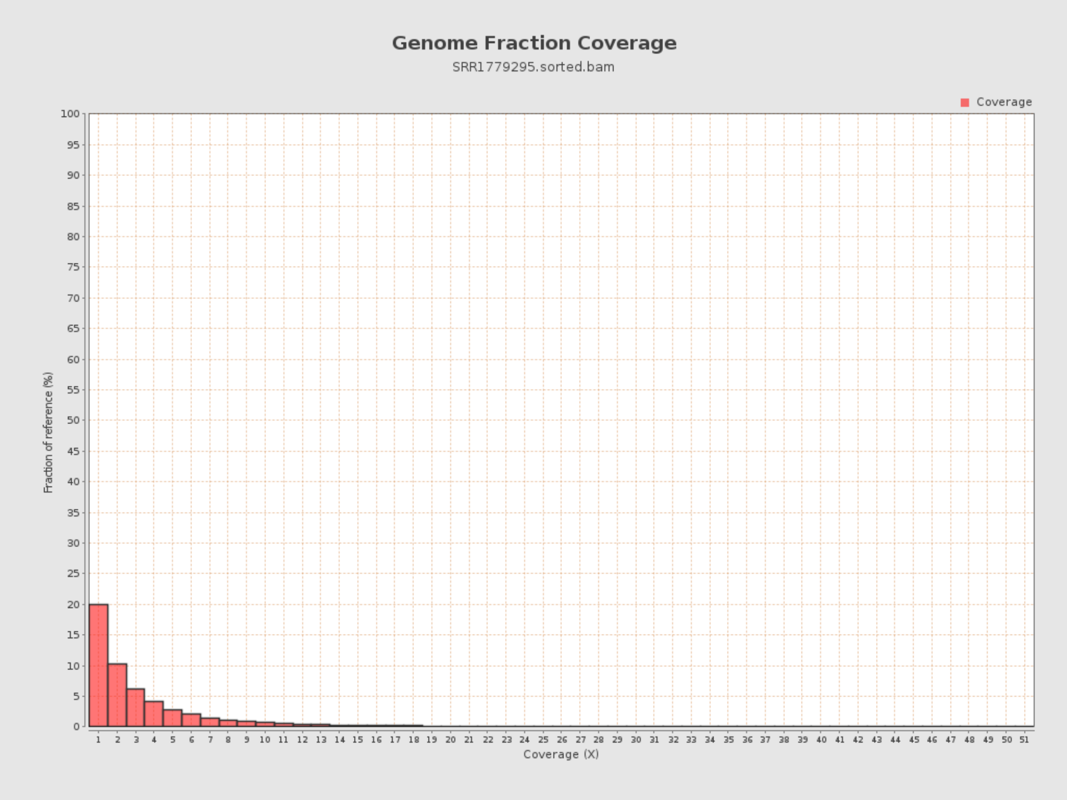
4. Results : Coverage Histogram



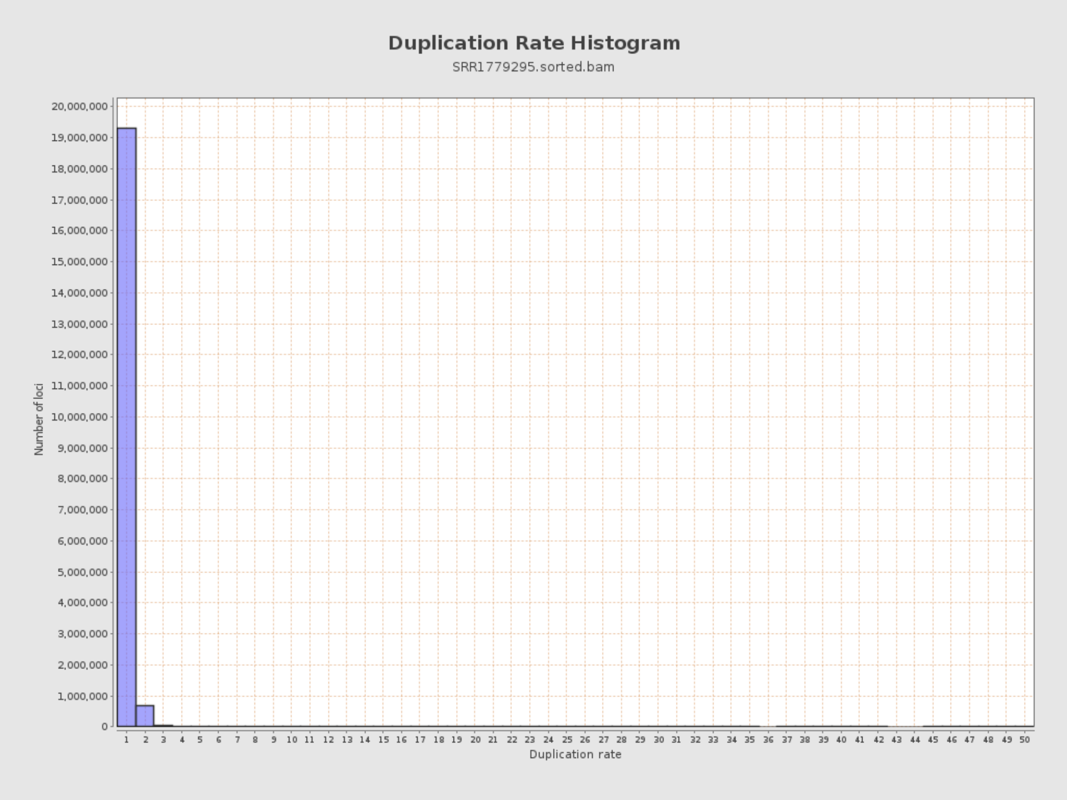
5. Results : Coverage Histogram (0-50X)



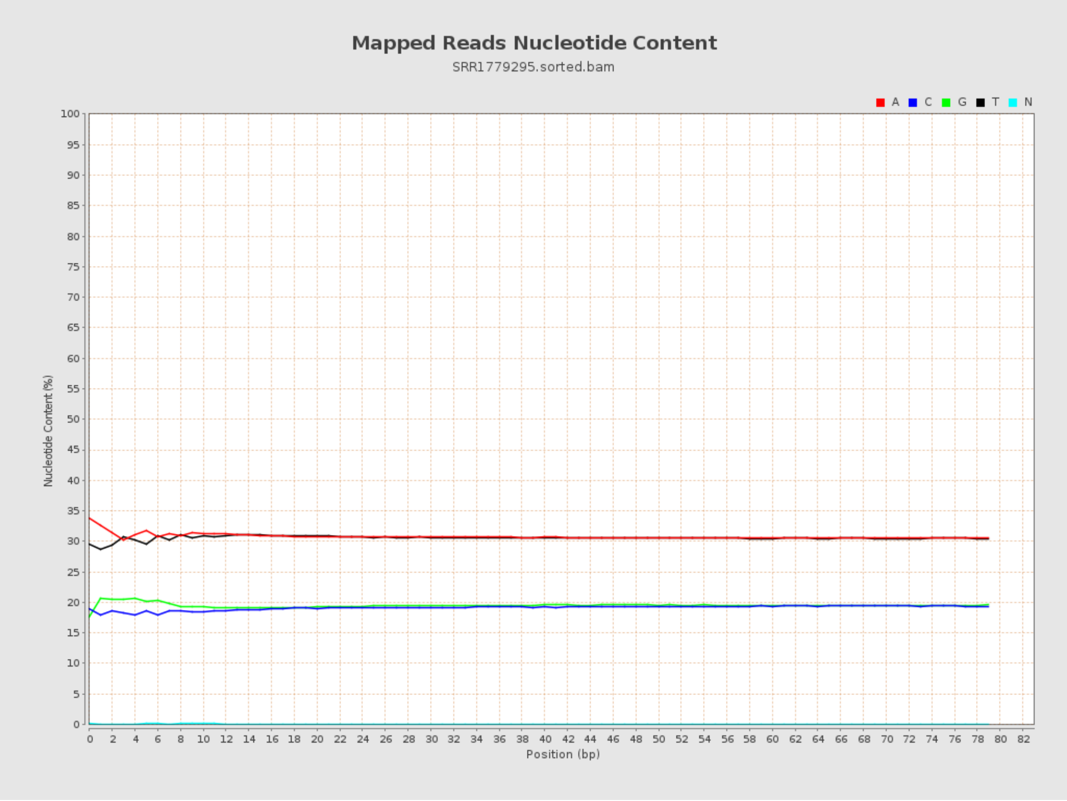
6. Results : Genome Fraction Coverage



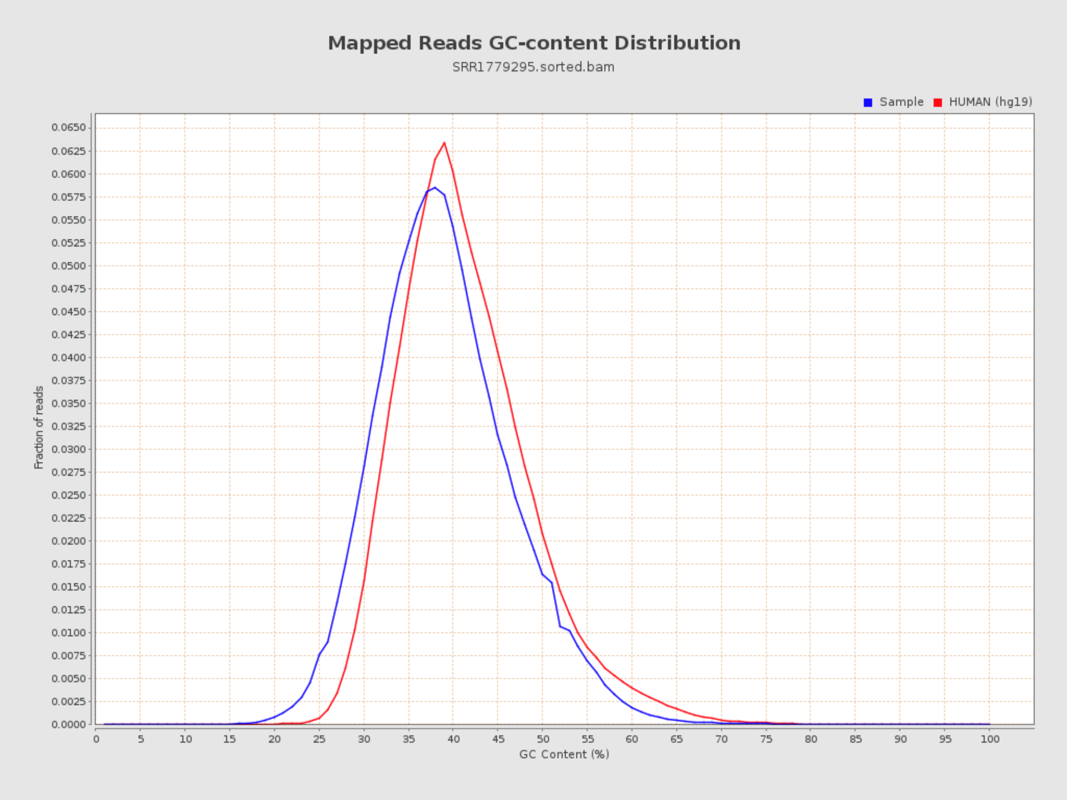
7. Results : Duplication Rate Histogram



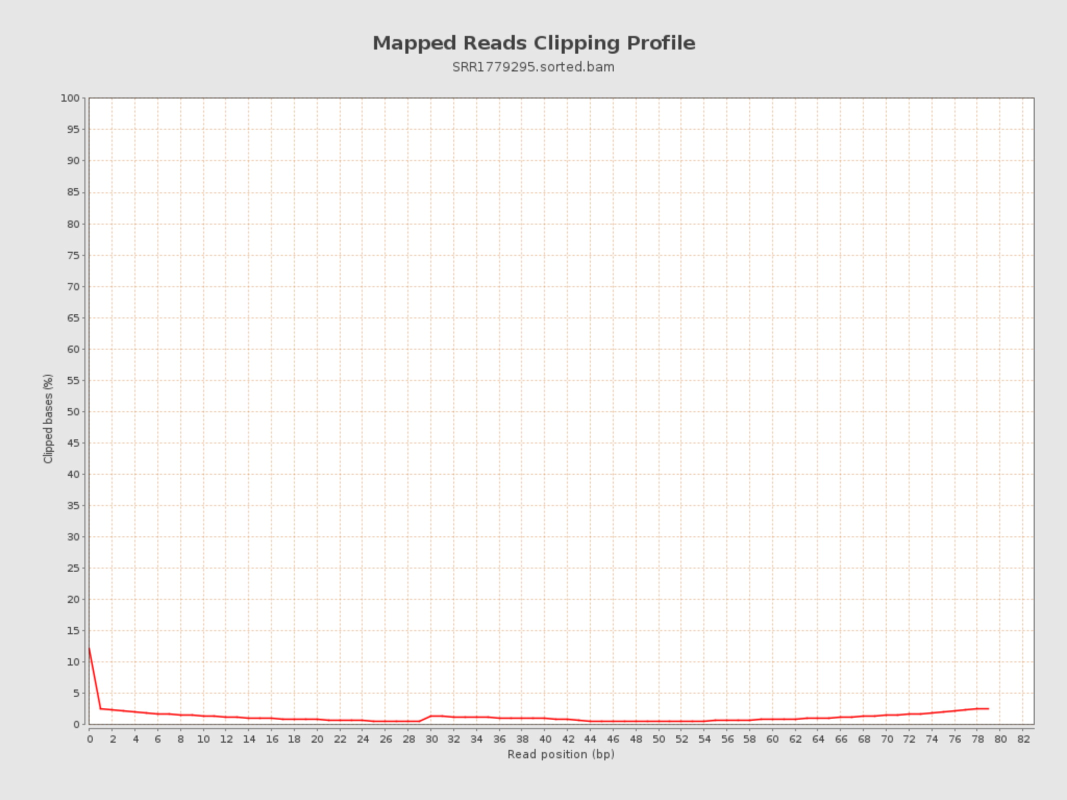
8. Results : Mapped Reads Nucleotide Content



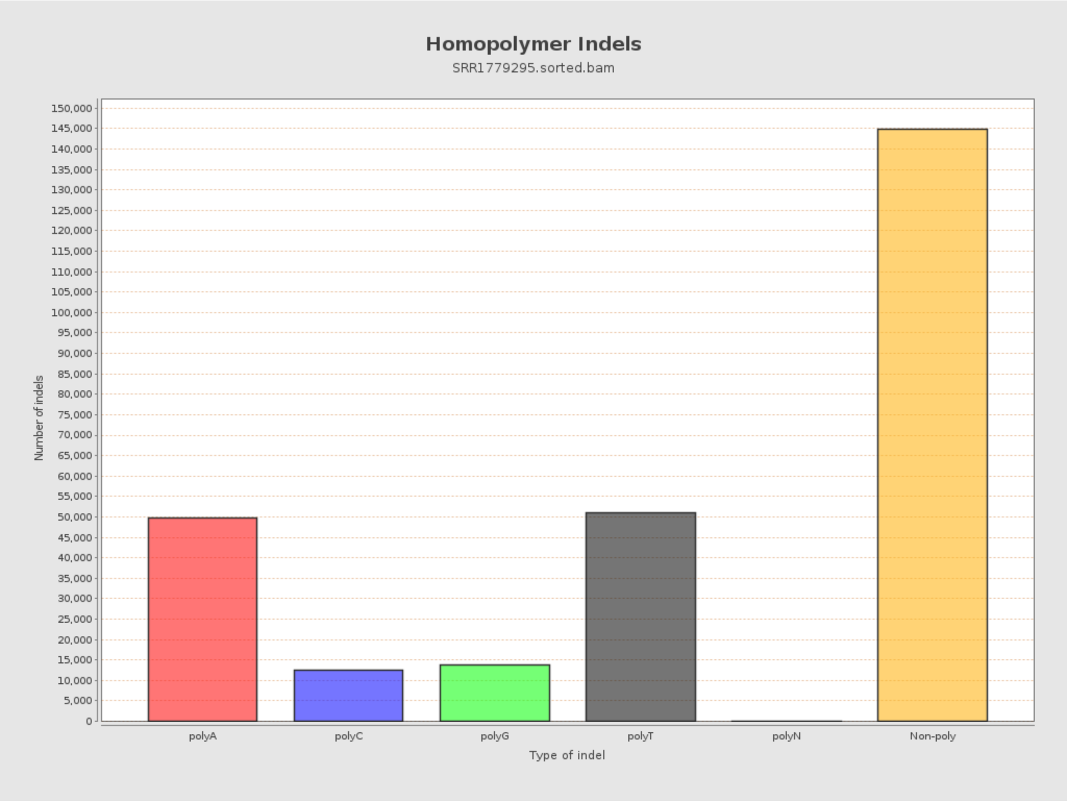
9. Results : Mapped Reads GC-content Distribution



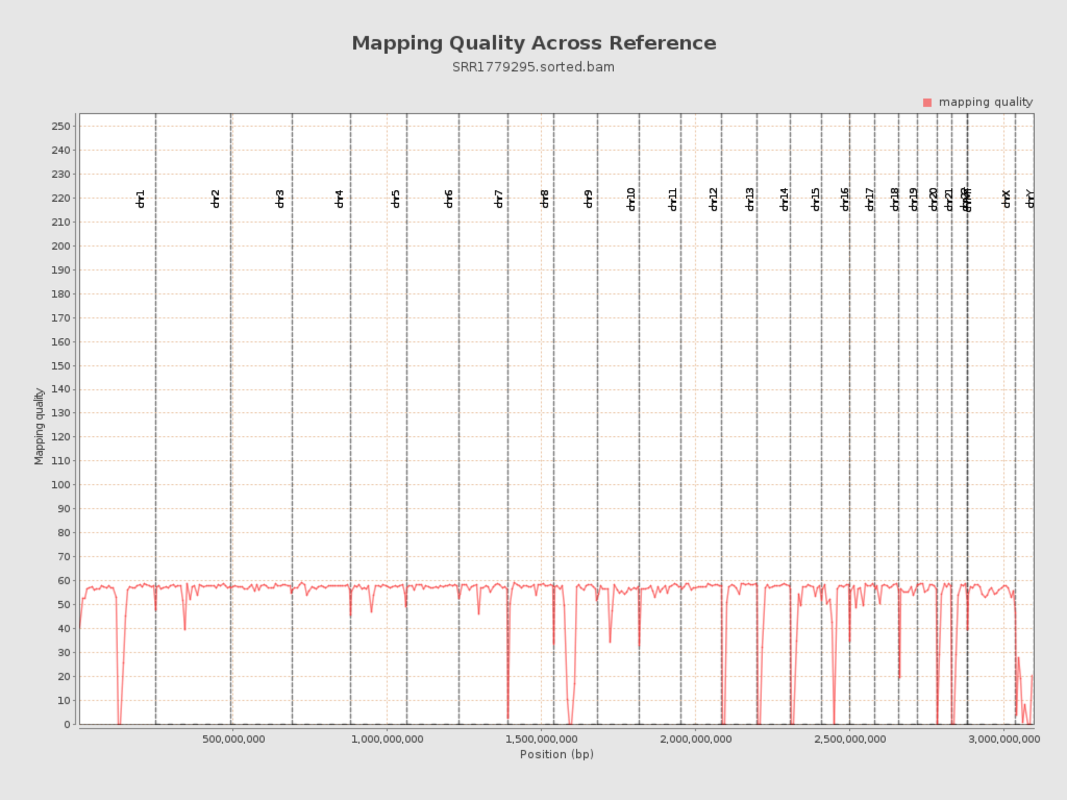
10. Results : Mapped Reads Clipping Profile



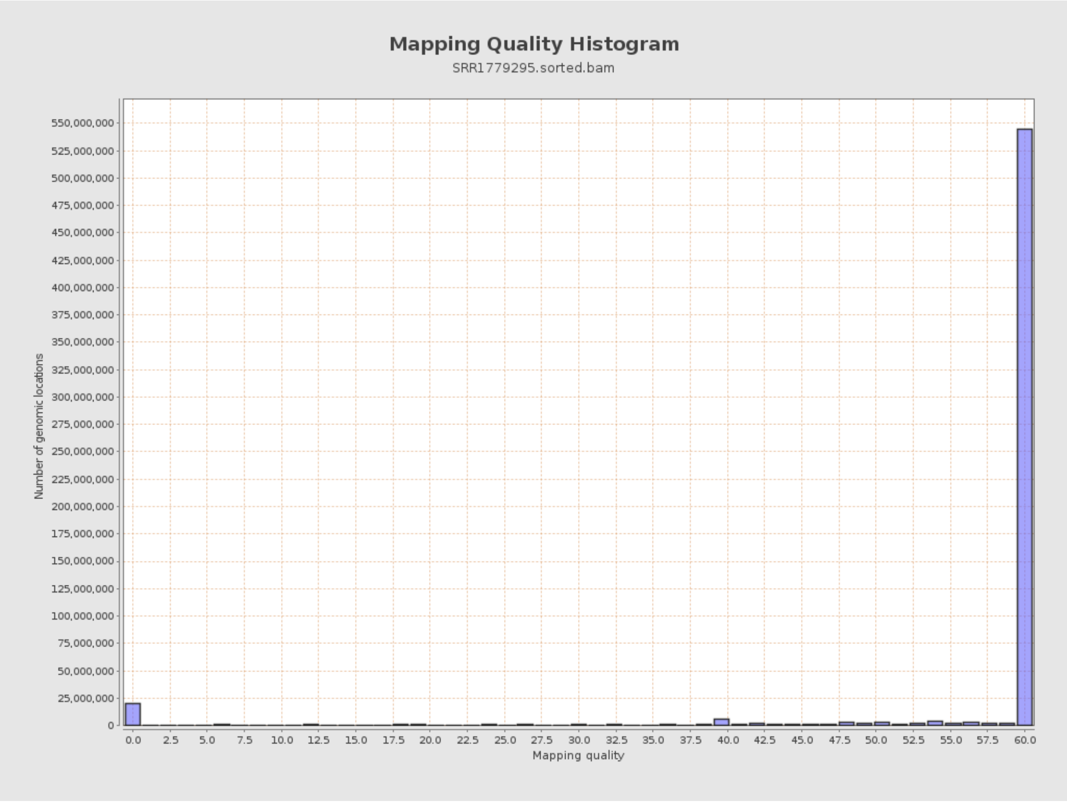
11. Results : Homopolymer Indels



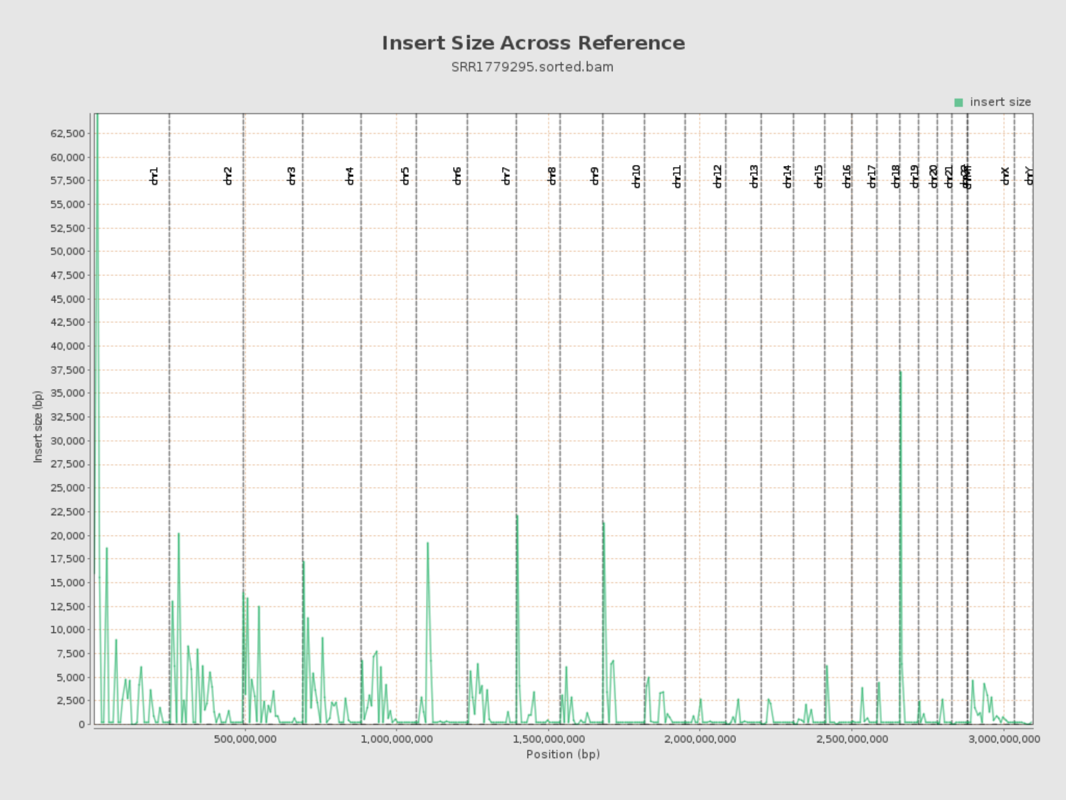
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram