Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:41:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779286.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_SRR1779286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779286_1.fastq.gz SRR1779286_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:40:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,775,538
Mapped reads	9,523,375 / 97.42%
Unmapped reads	252,163 / 2.58%
Mapped paired reads	9,523,375 / 97.42%
Mapped reads, first in pair	4,805,663 / 49.16%
Mapped reads, second in pair	4,717,712 / 48.26%
Mapped reads, both in pair	9,422,466 / 96.39%
Mapped reads, singletons	100,909 / 1.03%
Secondary alignments	0
Supplementary alignments	24,104 / 0.25%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	127,240 / 1.3%
Duplication rate	1.26%
Clipped reads	320,105 / 3.27%

2.2. ACGT Content

Number/percentage of A's	232,155,782 / 30.64%
Number/percentage of C's	145,840,652 / 19.25%
Number/percentage of T's	231,249,476 / 30.52%
Number/percentage of G's	148,373,848 / 19.58%
Number/percentage of N's	143,378 / 0.02%

GC Percentage	38.83%

2.3. Coverage

Mean	0.2448
Standard Deviation	0.8107

2.4. Mapping Quality

Mean Mapping Quality	53.12

2.5. Insert size

Mean	47,347.29
Standard Deviation	2,050,979.33
P25/Median/P75	164 / 212 / 277

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	3,017,075
Insertions	55,238
Mapped reads with at least one insertion	0.57%
Deletions	70,216
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.83%

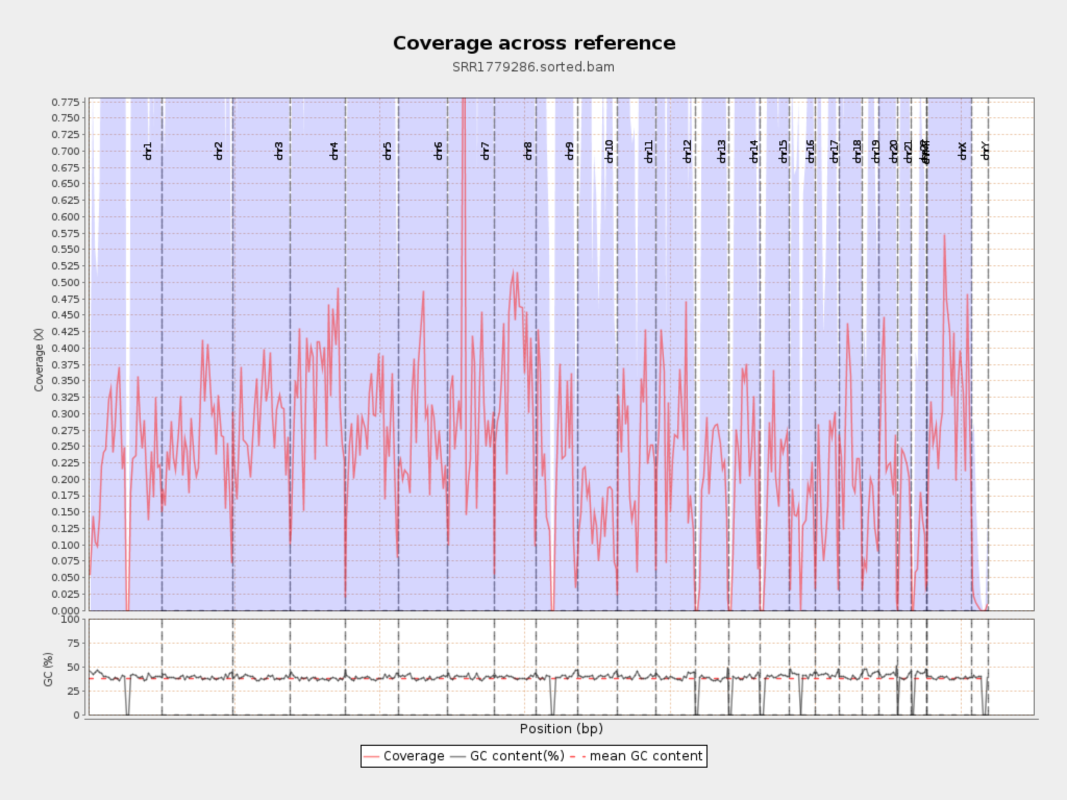
2.7. Chromosome stats

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

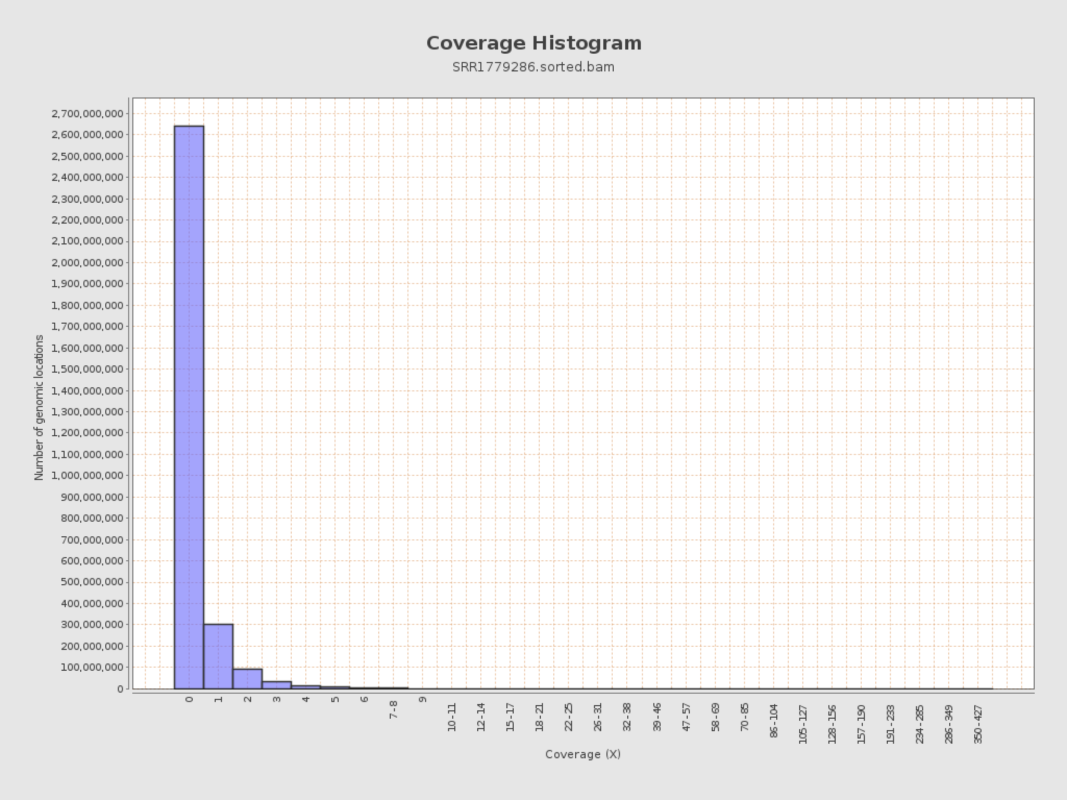
		bases	coverage	deviation
chr1	249250621	54196188	0.2174	0.8155
chr2	243199373	62689428	0.2578	0.7655
chr3	198022430	56860256	0.2871	0.8068
chr4	191154276	65360174	0.3419	0.8916
chr5	180915260	48434715	0.2677	0.7968
chr6	171115067	46728773	0.2731	0.8113
chr7	159138663	52581926	0.3304	1.1793
chr8	146364022	55122959	0.3766	0.9656
chr9	141213431	30455376	0.2157	0.7736
chr10	135534747	19937266	0.1471	0.8911
chr11	135006516	33528241	0.2483	0.7646
chr12	133851895	34106160	0.2548	0.7638
chr13	115169878	21793804	0.1892	0.6634
chr14	107349540	22664866	0.2111	0.7005
chr15	102531392	19711441	0.1922	0.667
chr16	90354753	12524620	0.1386	0.5323
chr17	81195210	14117320	0.1739	0.6422
chr18	78077248	19409447	0.2486	0.7588
chr19	59128983	7444831	0.1259	0.5946
chr20	63025520	16502270	0.2618	0.7937
chr21	48129895	8493563	0.1765	0.621
chr22	51304566	4374906	0.0853	0.427
chrMT	16571	720	0.0434	0.2388
chrX	155270560	50324800	0.3241	0.9883

chrY	59373566	544710	0.0092	0.1397

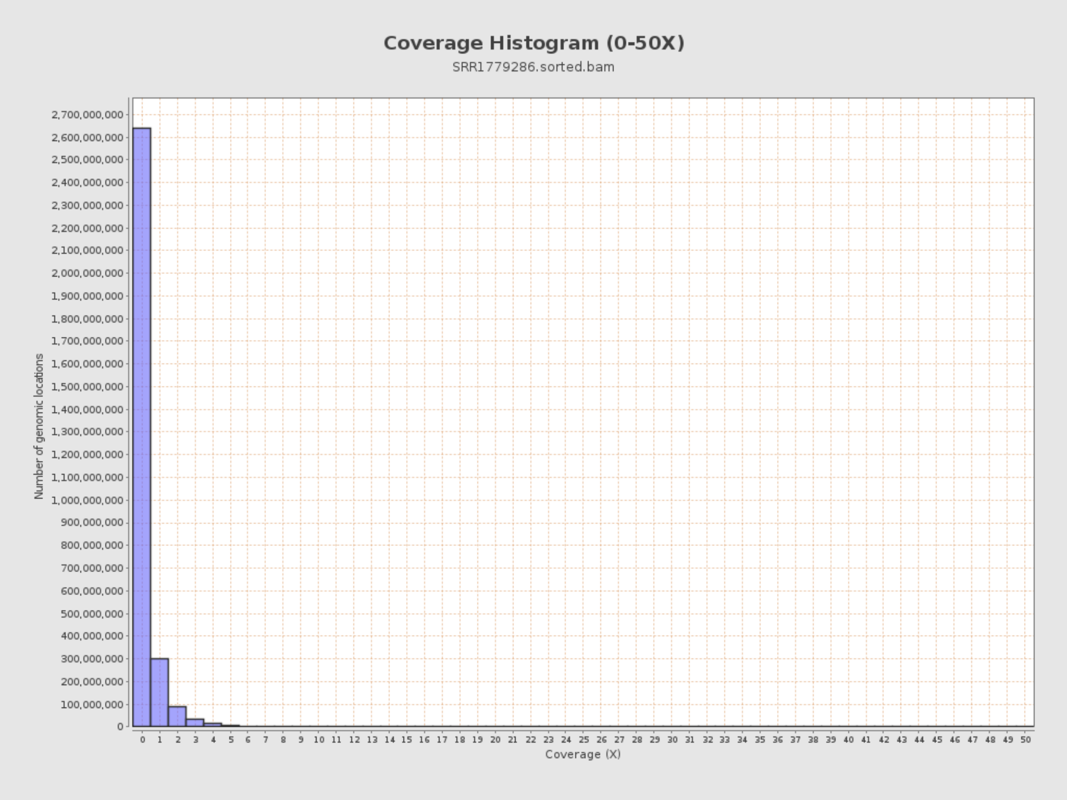
3. Results : Coverage across reference



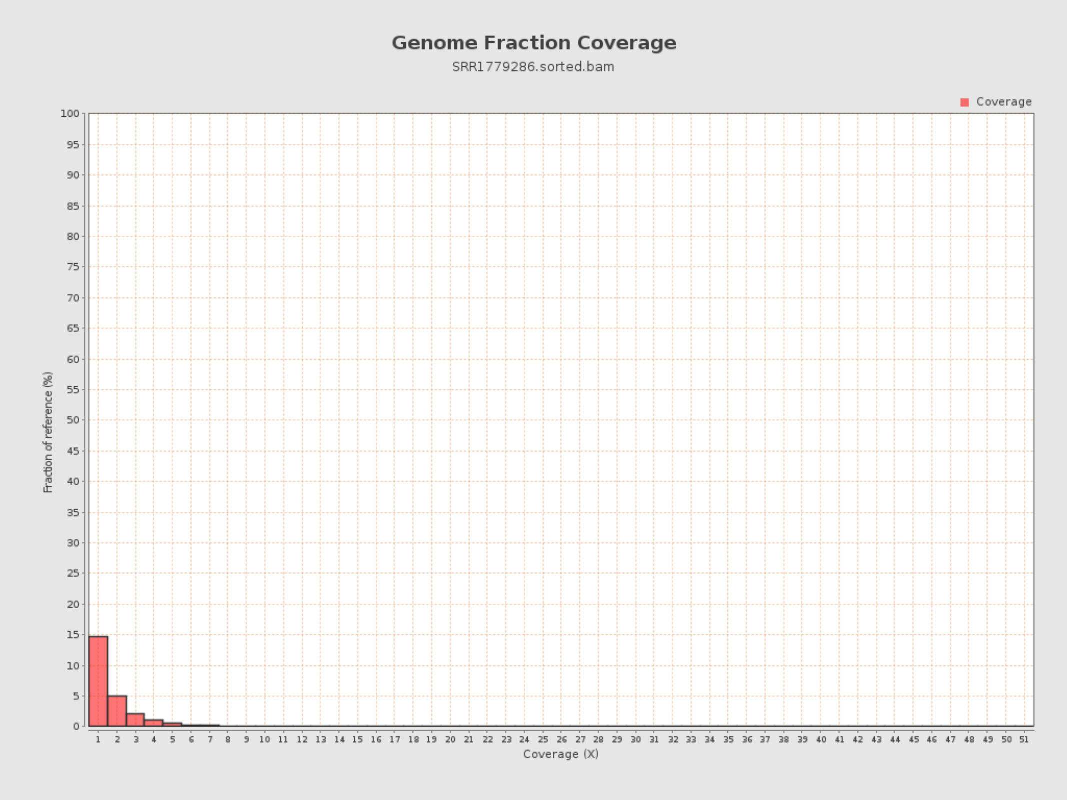
4. Results : Coverage Histogram



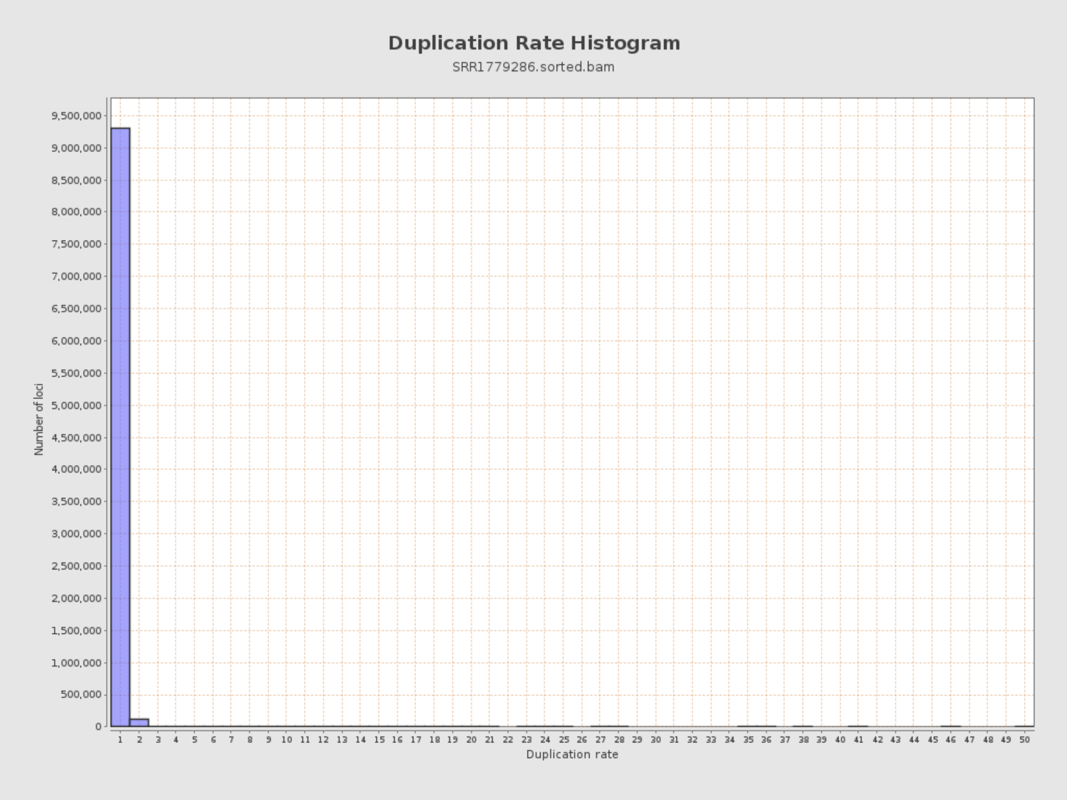
5. Results : Coverage Histogram (0-50X)



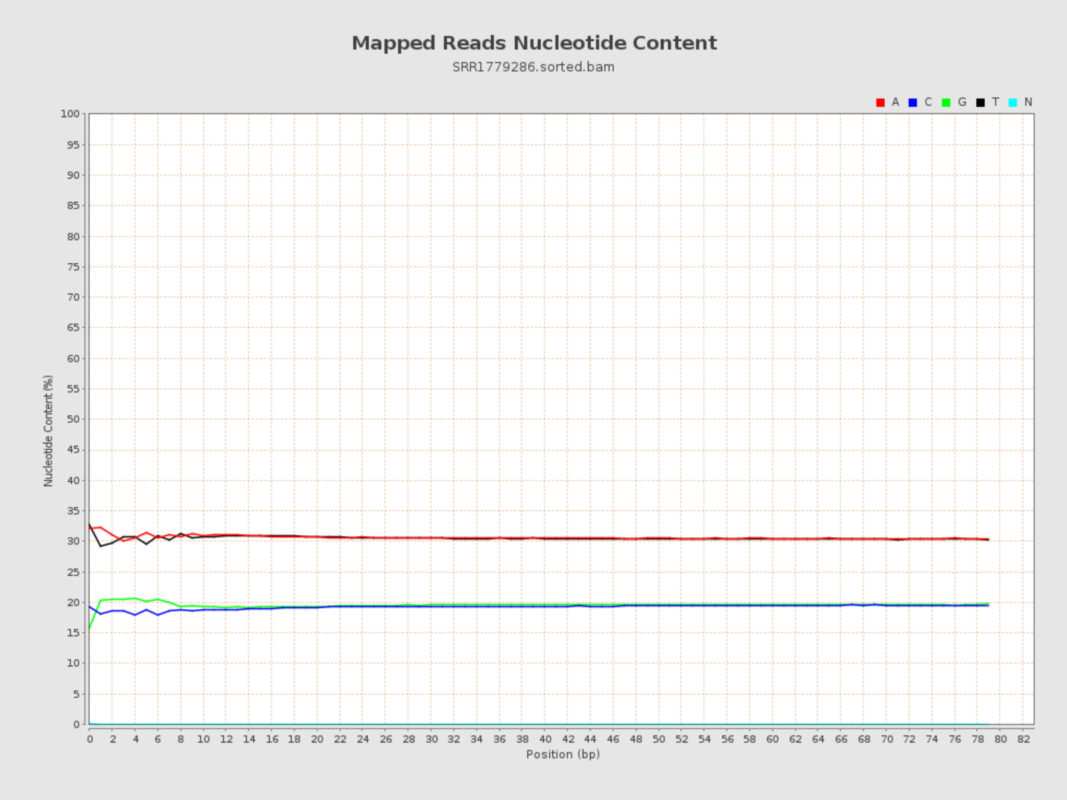
6. Results : Genome Fraction Coverage



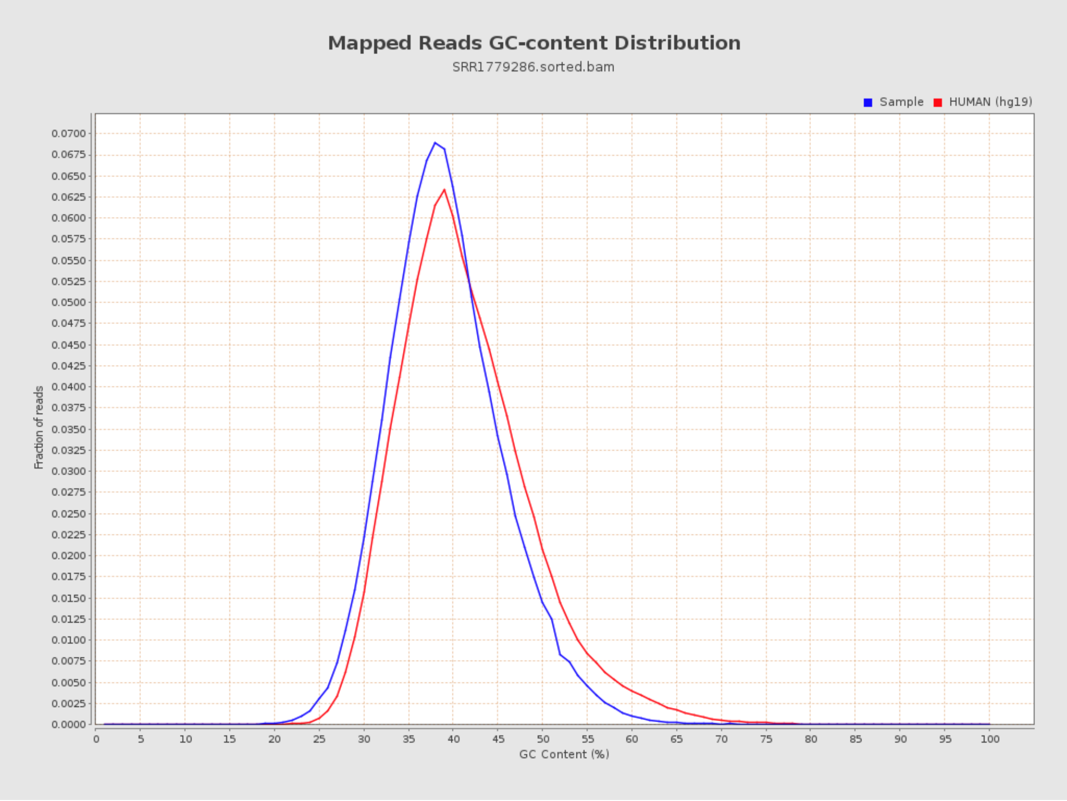
7. Results : Duplication Rate Histogram



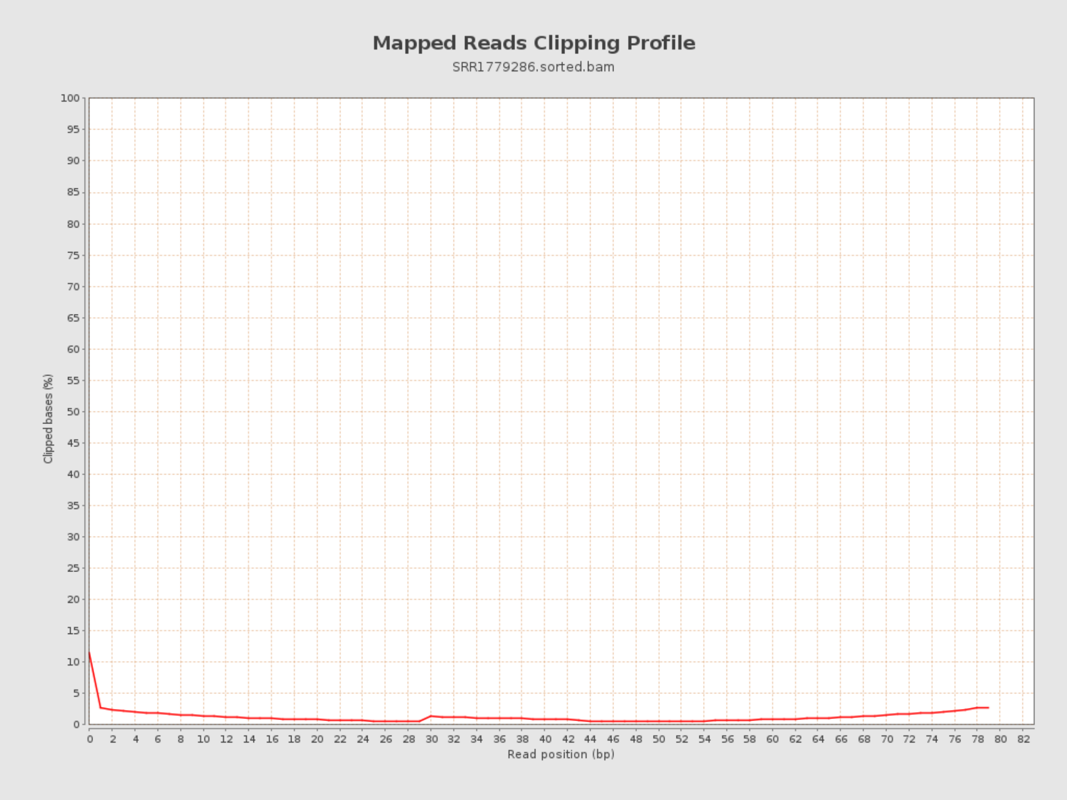
8. Results : Mapped Reads Nucleotide Content



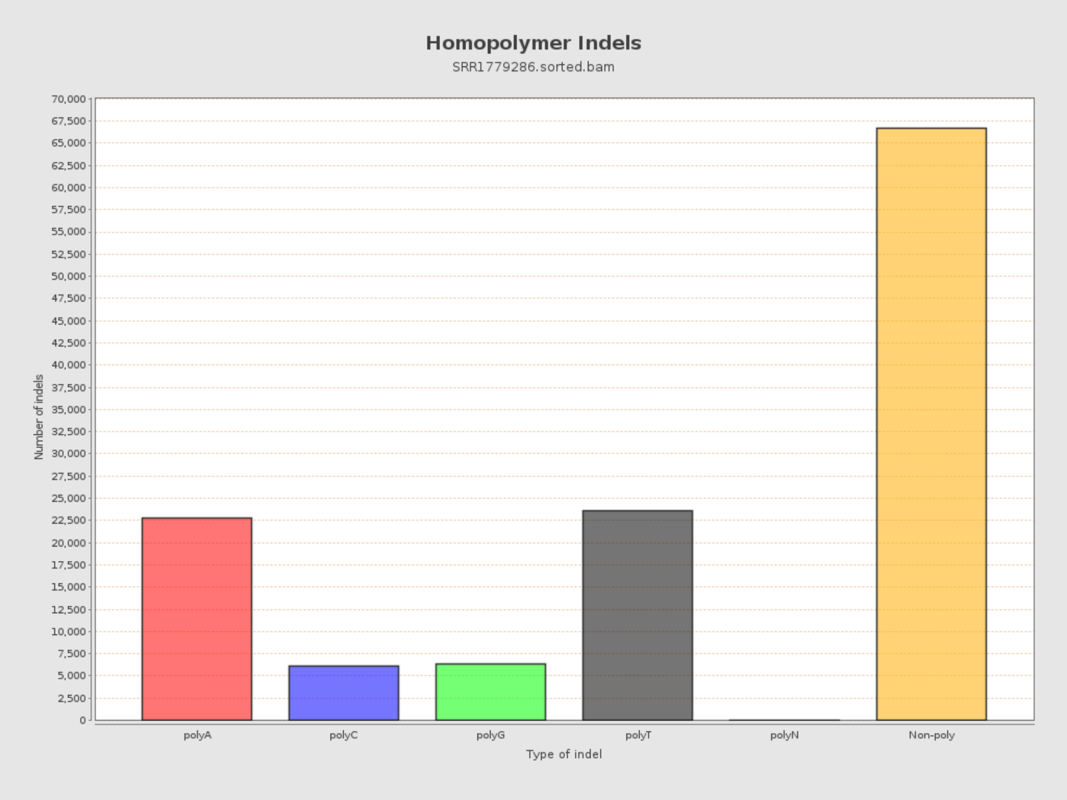
9. Results : Mapped Reads GC-content Distribution



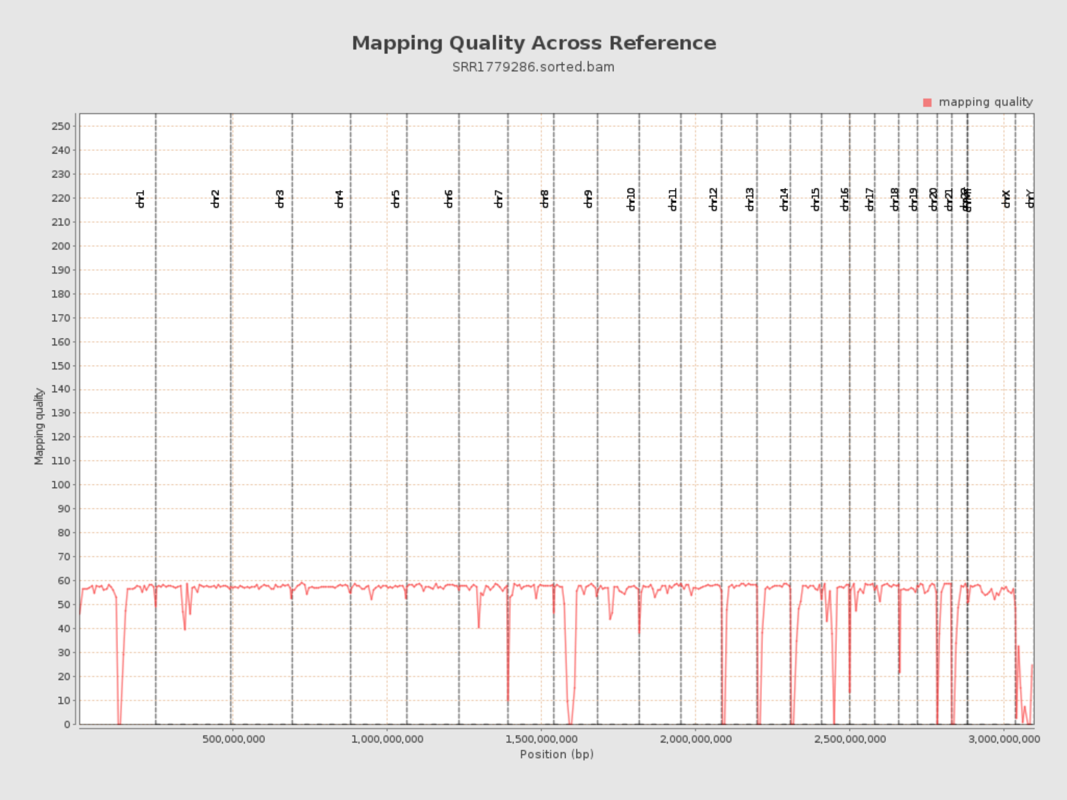
10. Results : Mapped Reads Clipping Profile



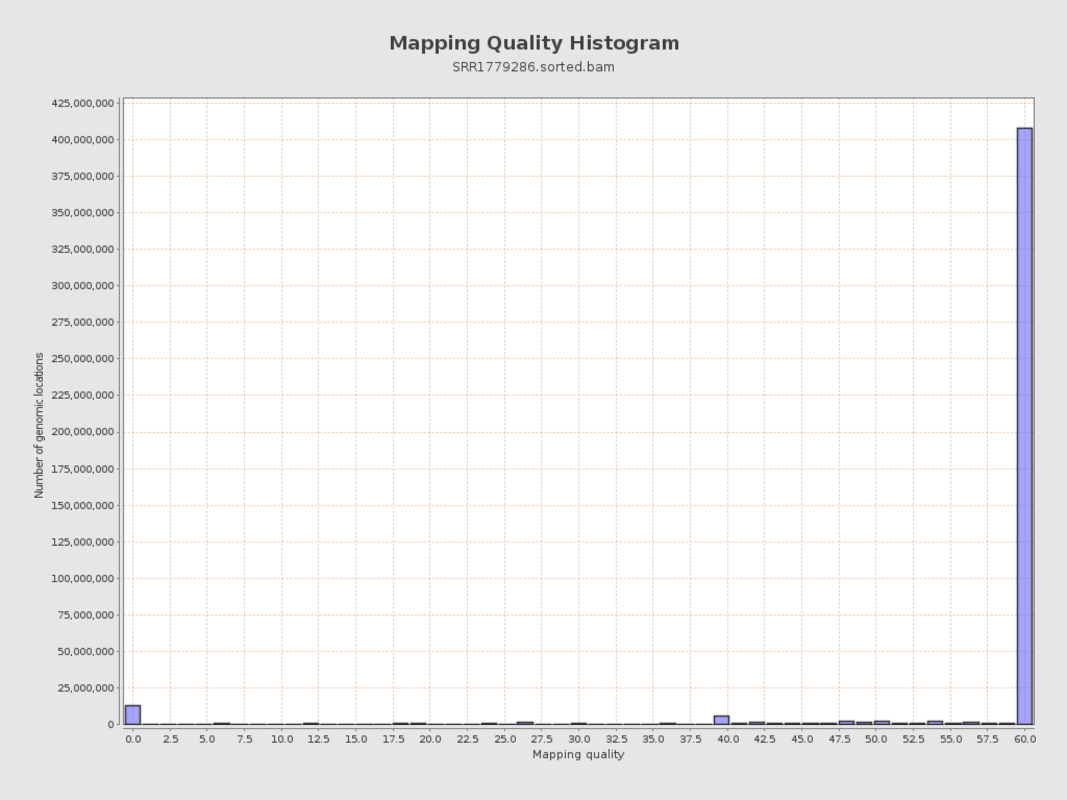
11. Results : Homopolymer Indels



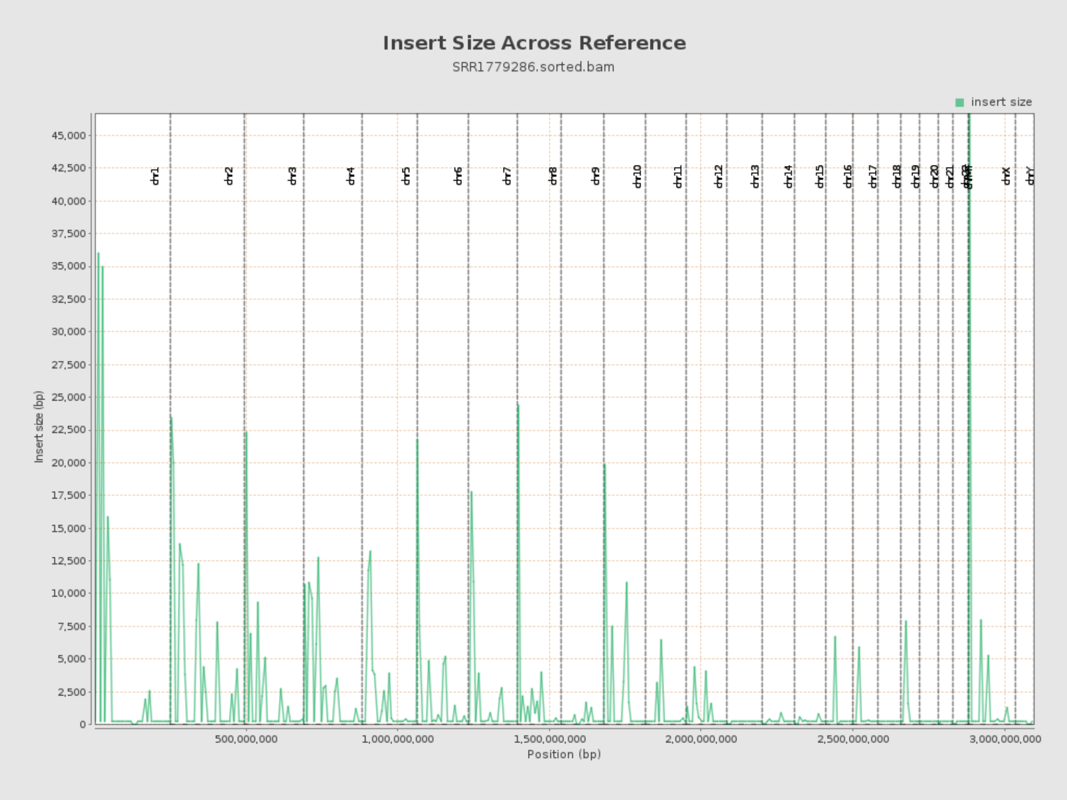
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram