

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 21:27:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779278.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_SRR1779278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779278_1.fastq.gz SRR1779278_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 21:27:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,226,620
Mapped reads	13,710,031 / 96.37%
Unmapped reads	516,589 / 3.63%
Mapped paired reads	13,710,031 / 96.37%
Mapped reads, first in pair	6,913,920 / 48.6%
Mapped reads, second in pair	6,796,111 / 47.77%
Mapped reads, both in pair	13,568,362 / 95.37%
Mapped reads, singletons	141,669 / 1%
Secondary alignments	0
Supplementary alignments	31,171 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	276,185 / 1.94%
Duplication rate	1.73%
Clipped reads	467,988 / 3.29%

2.2. ACGT Content

Number/percentage of A's	332,517,030 / 30.49%
Number/percentage of C's	211,551,850 / 19.4%
Number/percentage of T's	331,256,658 / 30.37%
Number/percentage of G's	215,216,531 / 19.73%
Number/percentage of N's	208,344 / 0.02%

GC Percentage	39.13%
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2.3. Coverage

Mean	0.3524
Standard Deviation	1.26

2.4. Mapping Quality

Mean Mapping Quality	52.97
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2.5. Insert size

Mean	40,387.4
Standard Deviation	1,869,907.94
P25/Median/P75	144 / 193 / 261

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	4,172,959
Insertions	79,570
Mapped reads with at least one insertion	0.57%
Deletions	100,746
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.19%

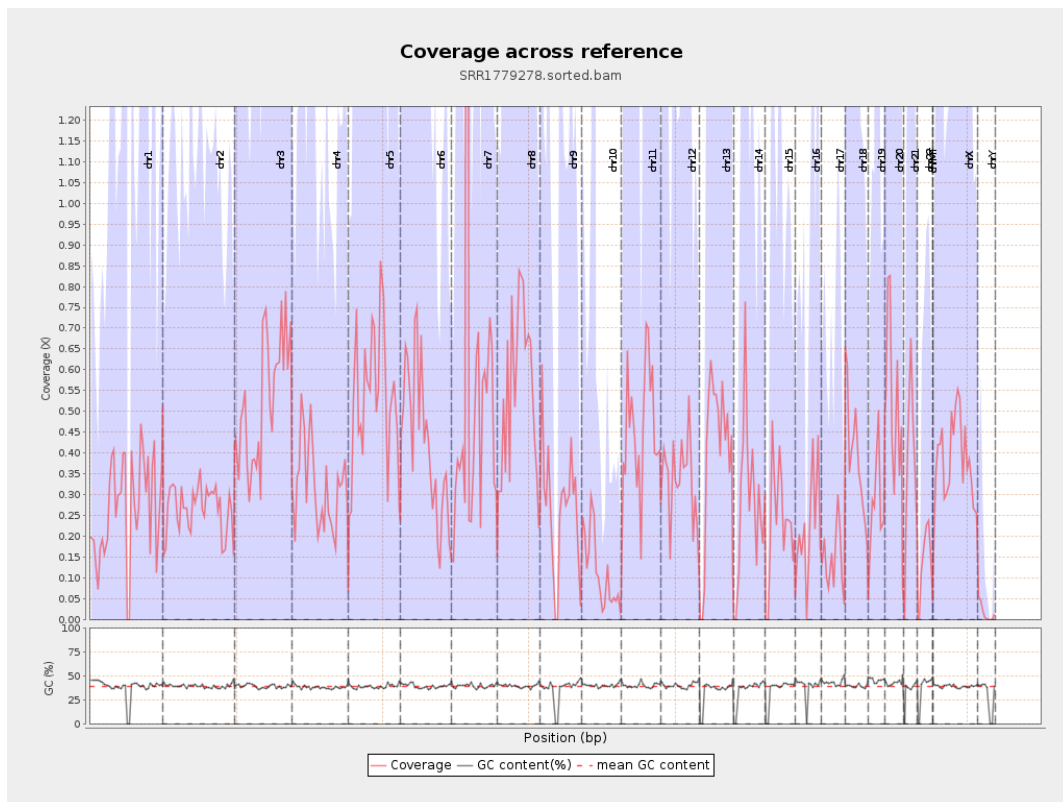
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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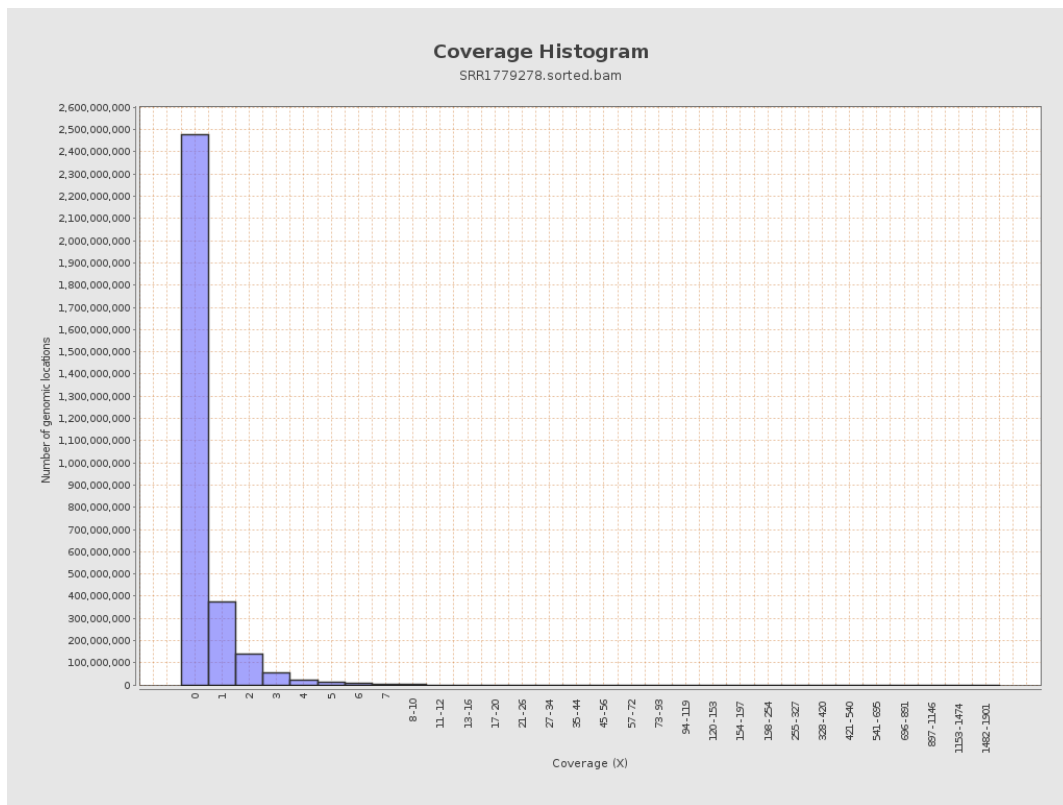
		bases	coverage	deviation
chr1	249250621	66709357	0.2676	2.0092
chr2	243199373	64719182	0.2661	0.7679
chr3	198022430	103758384	0.524	1.093
chr4	191154276	60516269	0.3166	0.8198
chr5	180915260	94689132	0.5234	1.0852
chr6	171115067	72491661	0.4236	1.0383
chr7	159138663	90406851	0.5681	2.8368
chr8	146364022	80932465	0.553	1.1505
chr9	141213431	37563898	0.266	0.8259
chr10	135534747	15318961	0.113	1.6464
chr11	135006516	61411611	0.4549	1.0255
chr12	133851895	45222492	0.3379	0.8707
chr13	115169878	46154458	0.4008	0.9735
chr14	107349540	30454352	0.2837	0.8042
chr15	102531392	23643396	0.2306	0.7167
chr16	90354753	19383567	0.2145	0.6861
chr17	81195210	12201992	0.1503	0.5384
chr18	78077248	30243678	0.3874	0.9834
chr19	59128983	17269778	0.2921	1.3398
chr20	63025520	32704354	0.5189	1.1373
chr21	48129895	17339550	0.3603	0.9411
chr22	51304566	7245500	0.1412	0.5296
chrMT	16571	1225	0.0739	0.342
chrX	155270560	59614321	0.3839	0.9582

chrY	59373566	963040	0.0162	0.2413
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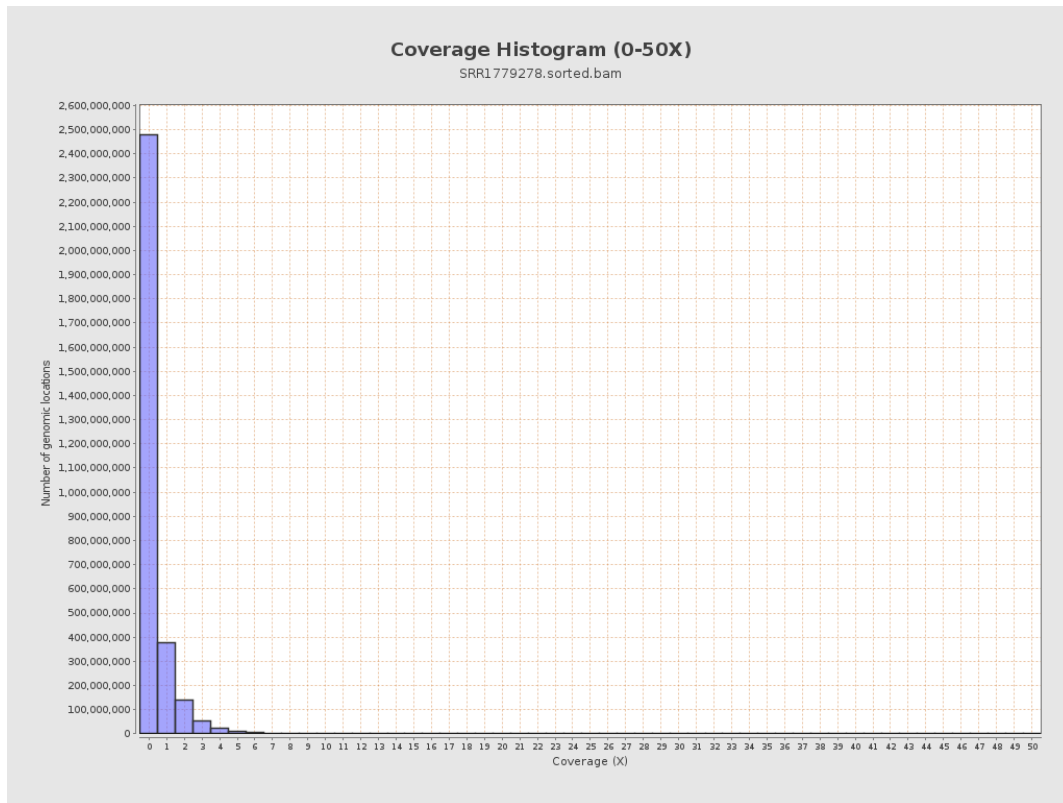
3. Results : Coverage across reference



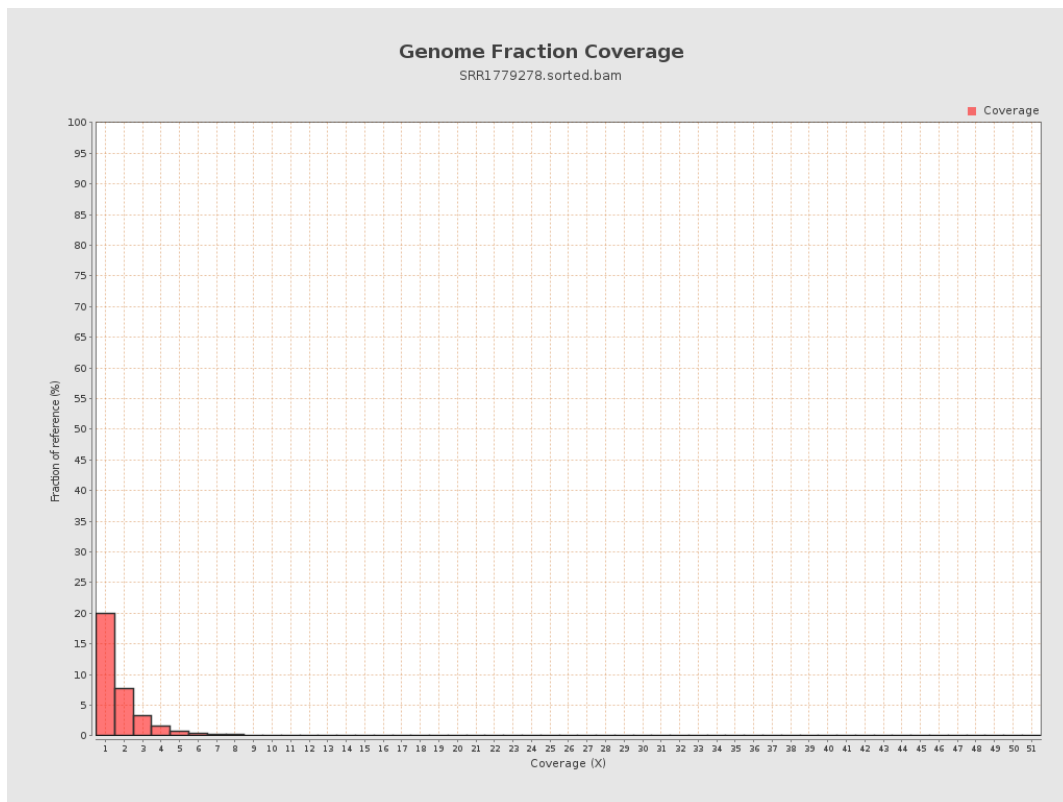
4. Results : Coverage Histogram



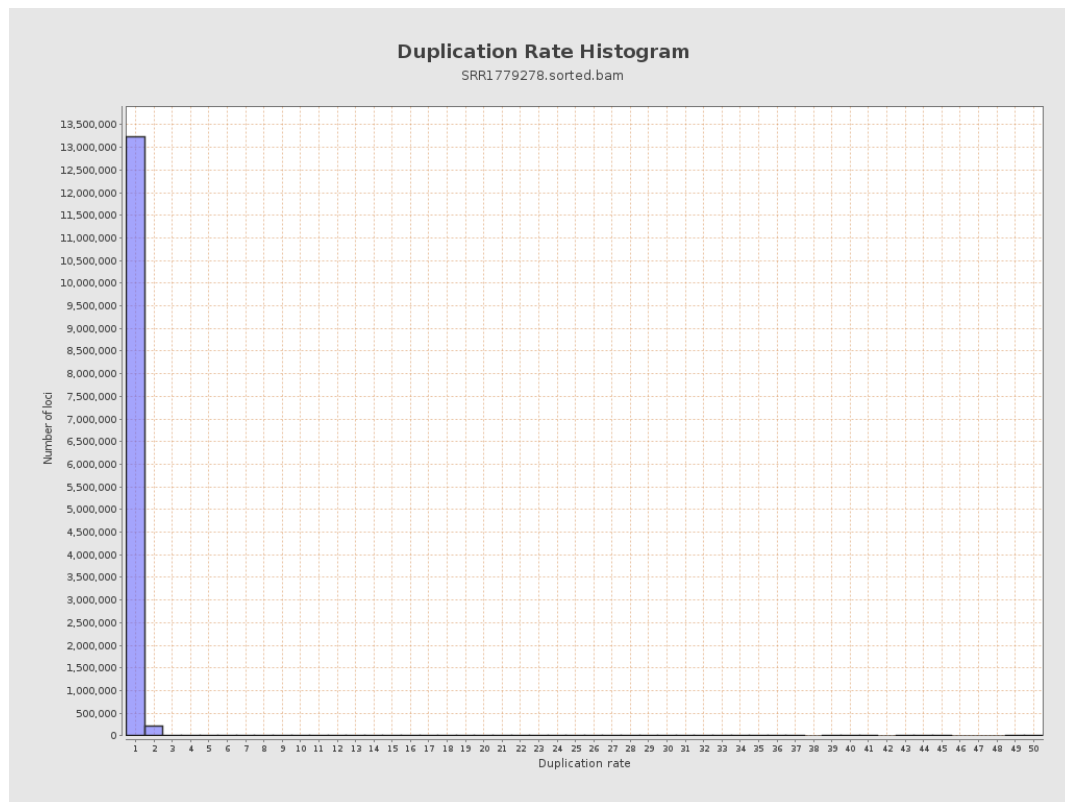
5. Results : Coverage Histogram (0-50X)



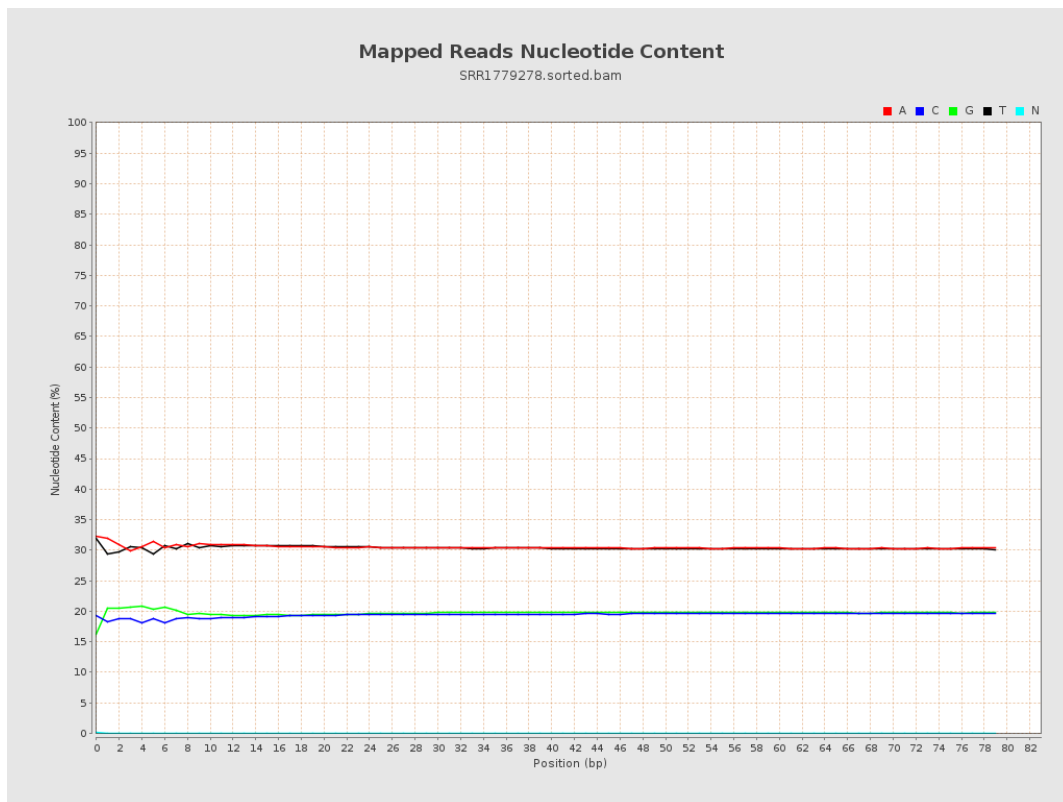
6. Results : Genome Fraction Coverage



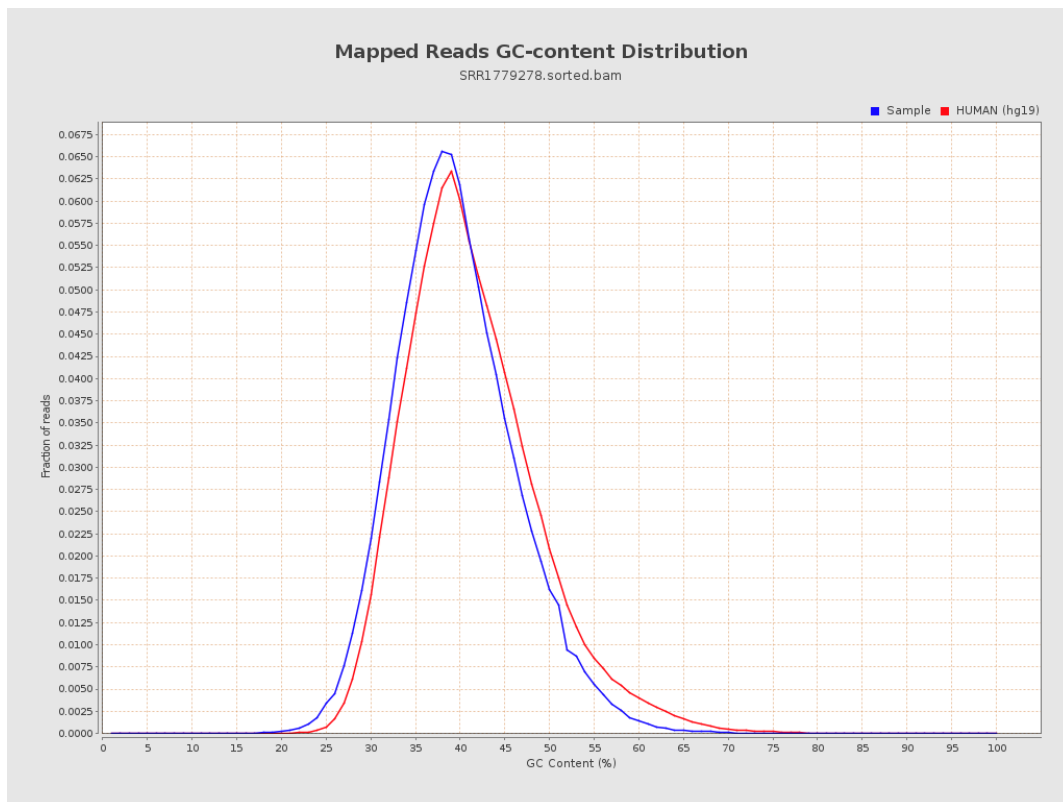
7. Results : Duplication Rate Histogram



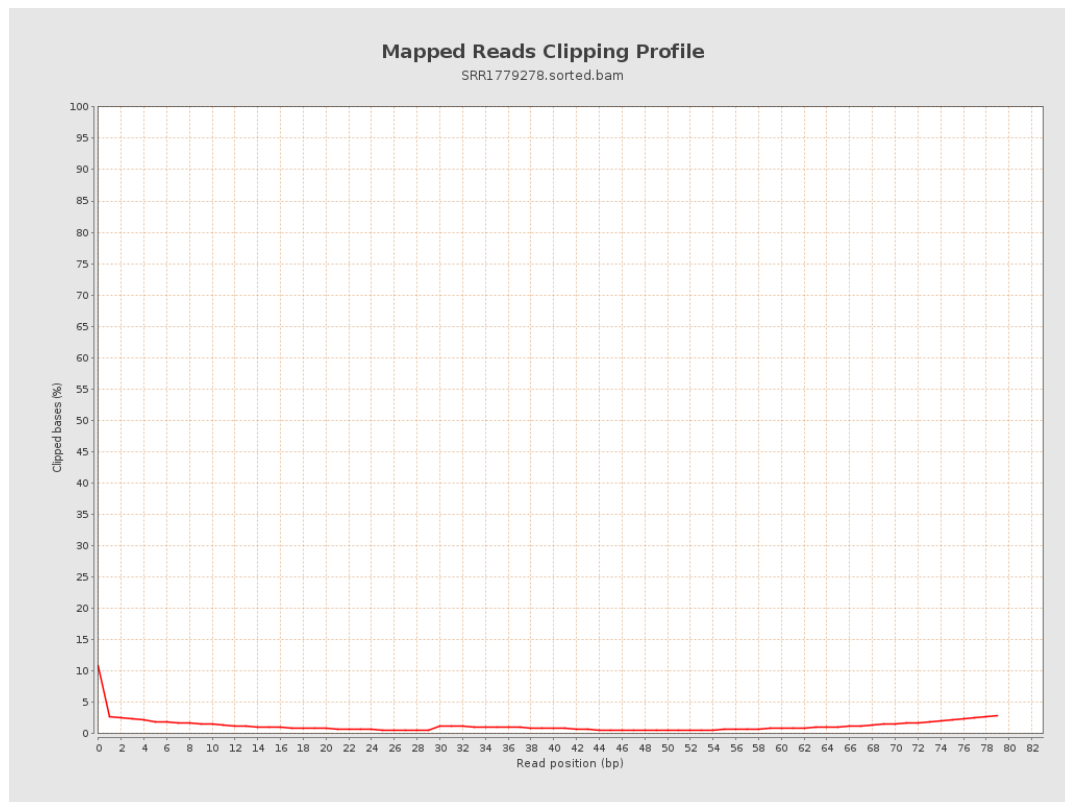
8. Results : Mapped Reads Nucleotide Content



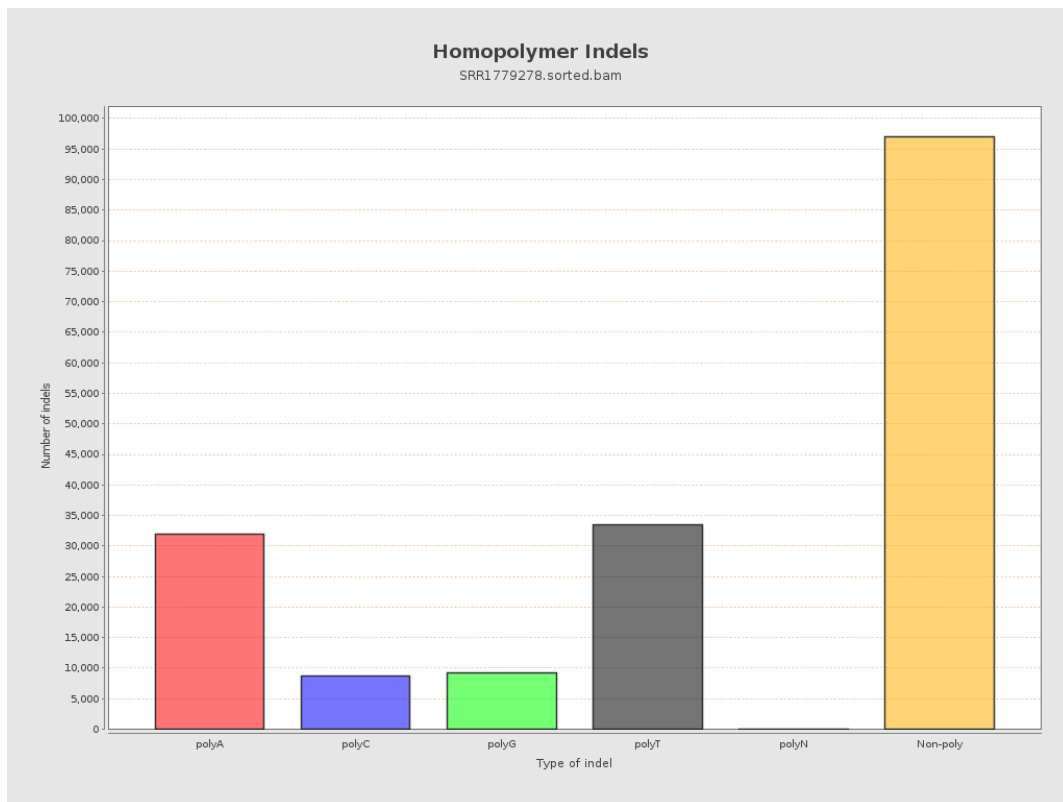
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



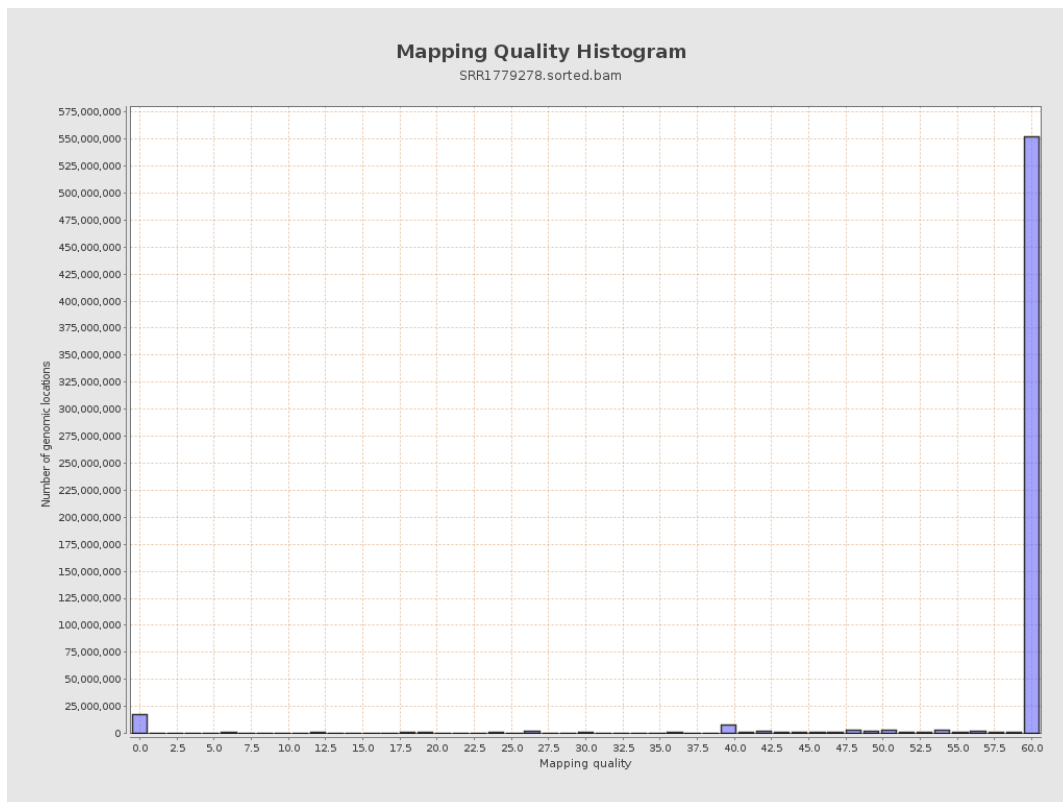
11. Results : Homopolymer Indels



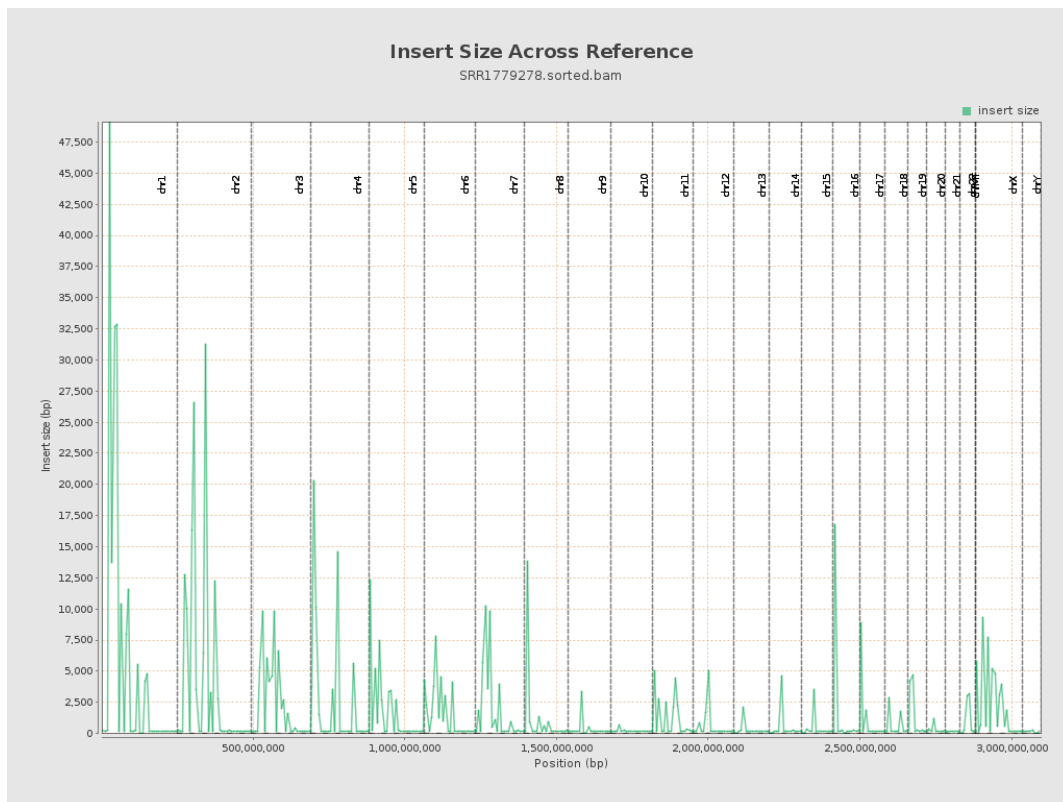
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

