

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 17:13:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779394.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_SRR1779394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779394_1.fastq.gz SRR1779394_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 17:13:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,039,106
Mapped reads	14,336,535 / 95.33%
Unmapped reads	702,571 / 4.67%
Mapped paired reads	14,336,535 / 95.33%
Mapped reads, first in pair	7,208,626 / 47.93%
Mapped reads, second in pair	7,127,909 / 47.4%
Mapped reads, both in pair	14,215,646 / 94.52%
Mapped reads, singletons	120,889 / 0.8%
Secondary alignments	0
Supplementary alignments	54,813 / 0.36%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	530,297 / 3.53%
Duplication rate	3.41%
Clipped reads	737,127 / 4.9%

2.2. ACGT Content

Number/percentage of A's	342,962,969 / 30.14%
Number/percentage of C's	225,688,154 / 19.84%
Number/percentage of T's	338,872,313 / 29.78%
Number/percentage of G's	230,051,674 / 20.22%
Number/percentage of N's	250,911 / 0.02%

GC Percentage	40.05%
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2.3. Coverage

Mean	0.3676
Standard Deviation	1.3363

2.4. Mapping Quality

Mean Mapping Quality	53.14
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2.5. Insert size

Mean	149,206.41
Standard Deviation	3,743,204.83
P25/Median/P75	134 / 176 / 222

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,803,939
Insertions	109,105
Mapped reads with at least one insertion	0.75%
Deletions	128,876
Mapped reads with at least one deletion	0.89%
Homopolymer indels	46.99%

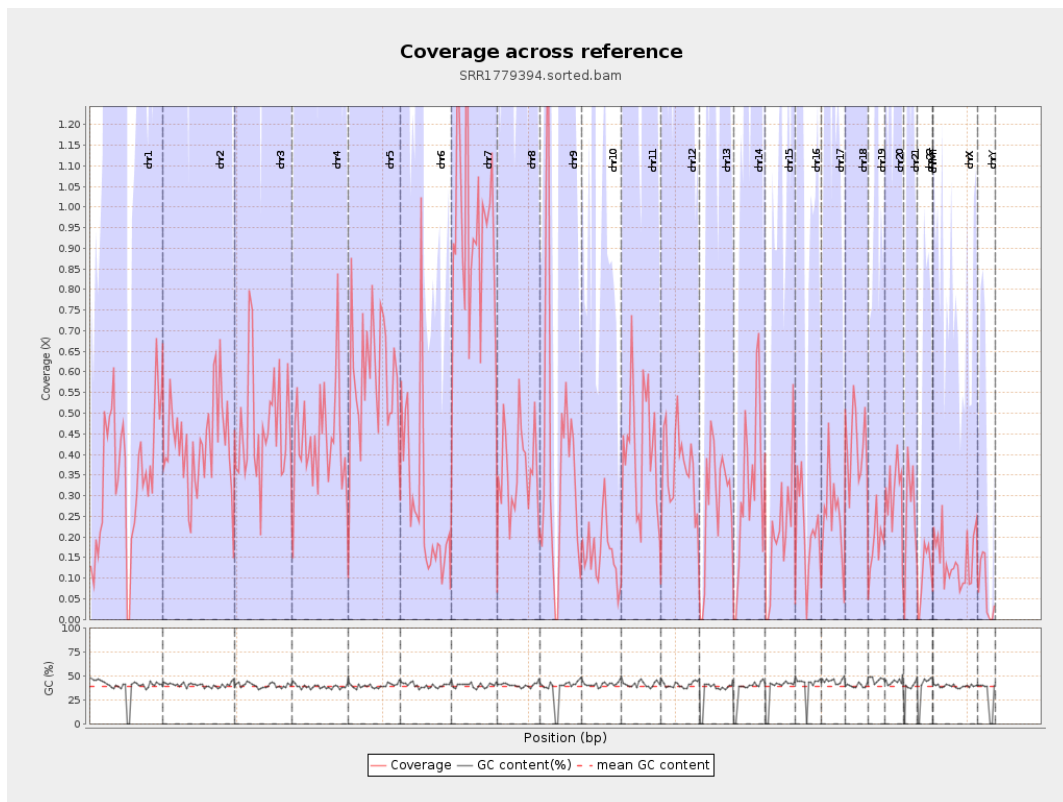
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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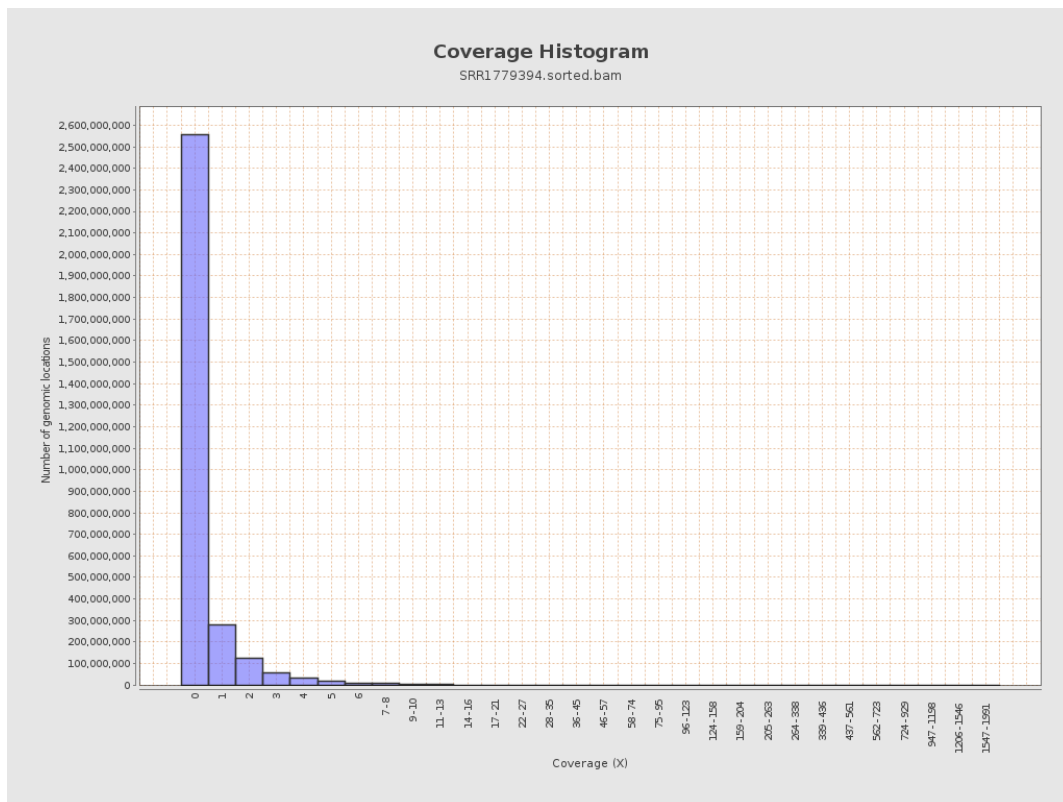
		bases	coverage	deviation
chr1	249250621	85806308	0.3443	2.2153
chr2	243199373	103376170	0.4251	1.2391
chr3	198022430	90964586	0.4594	1.2167
chr4	191154276	83921147	0.439	1.1392
chr5	180915260	104741216	0.579	1.3446
chr6	171115067	46748577	0.2732	1.1153
chr7	159138663	150560359	0.9461	2.2208
chr8	146364022	53882025	0.3681	1.0499
chr9	141213431	55883939	0.3957	1.4451
chr10	135534747	22059050	0.1628	1.4422
chr11	135006516	54645364	0.4048	1.2101
chr12	133851895	49107297	0.3669	1.0308
chr13	115169878	32680337	0.2838	0.908
chr14	107349540	34384145	0.3203	1.0027
chr15	102531392	21911941	0.2137	0.7922
chr16	90354753	18645645	0.2064	0.8226
chr17	81195210	20672930	0.2546	1.0588
chr18	78077248	33075949	0.4236	1.4566
chr19	59128983	11028513	0.1865	1.3555
chr20	63025520	19647000	0.3117	1.0073
chr21	48129895	11897343	0.2472	0.8886
chr22	51304566	5741808	0.1119	0.5735
chrMT	16571	1493	0.0901	0.344
chrX	155270560	22349719	0.1439	0.6476

chrY	59373566	4366105	0.0735	0.4373
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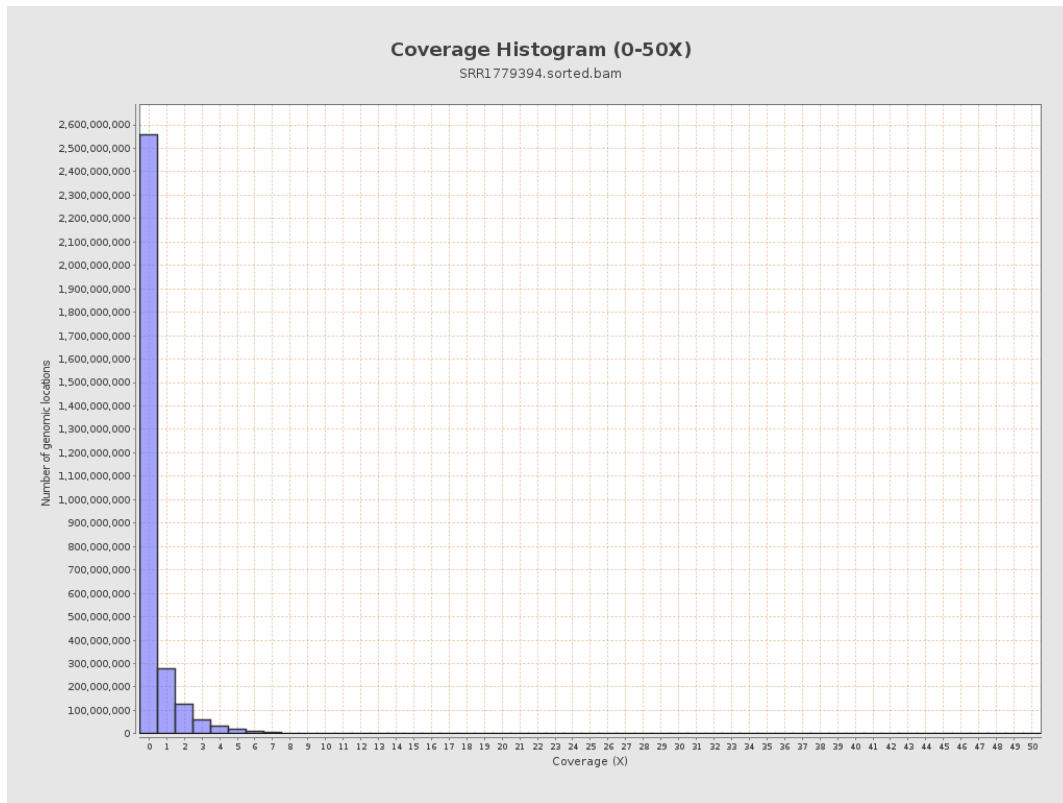
3. Results : Coverage across reference



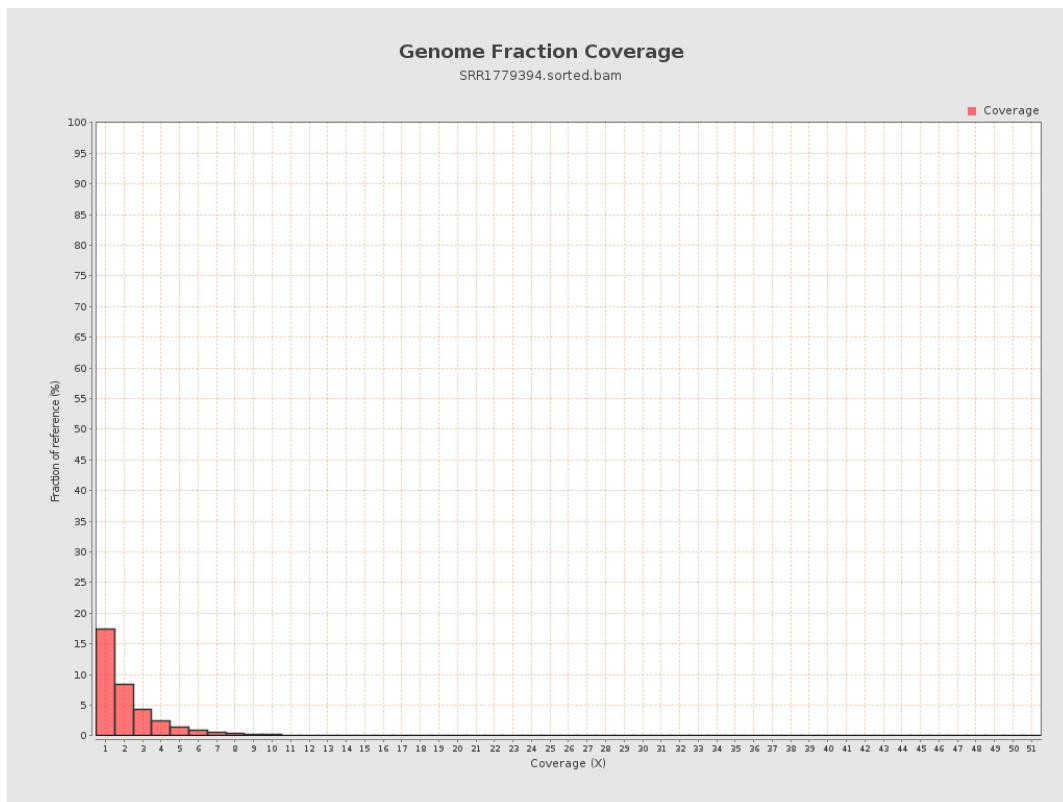
4. Results : Coverage Histogram



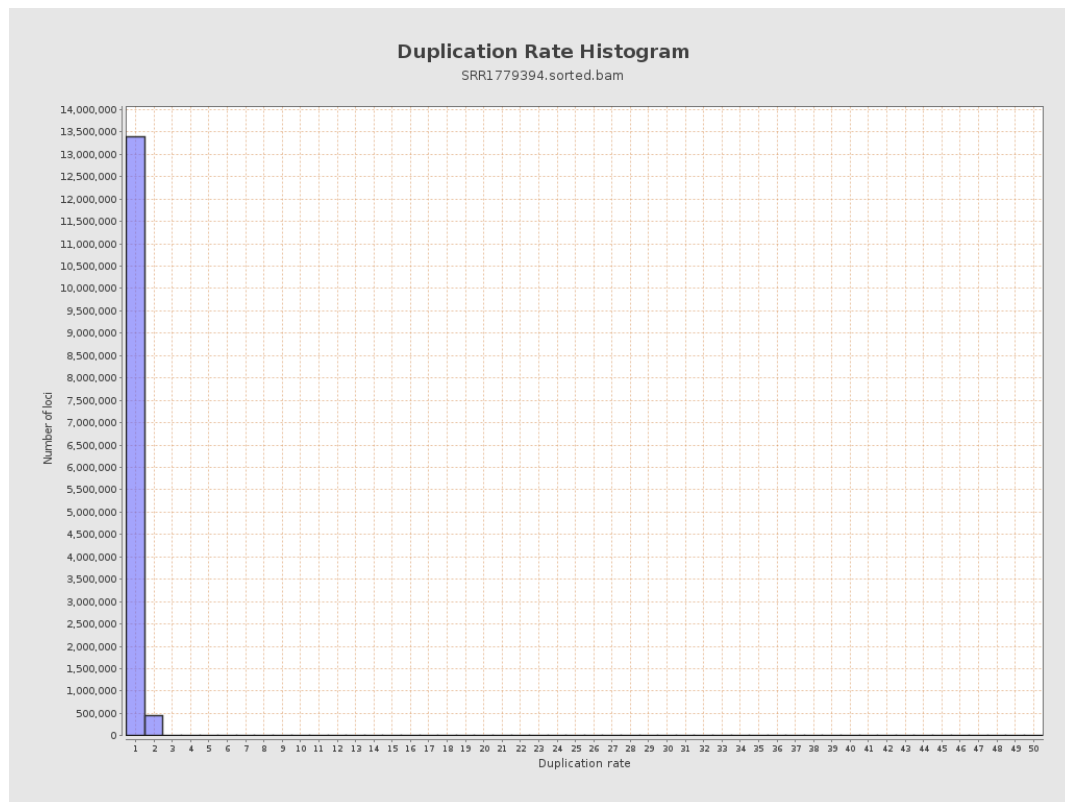
5. Results : Coverage Histogram (0-50X)



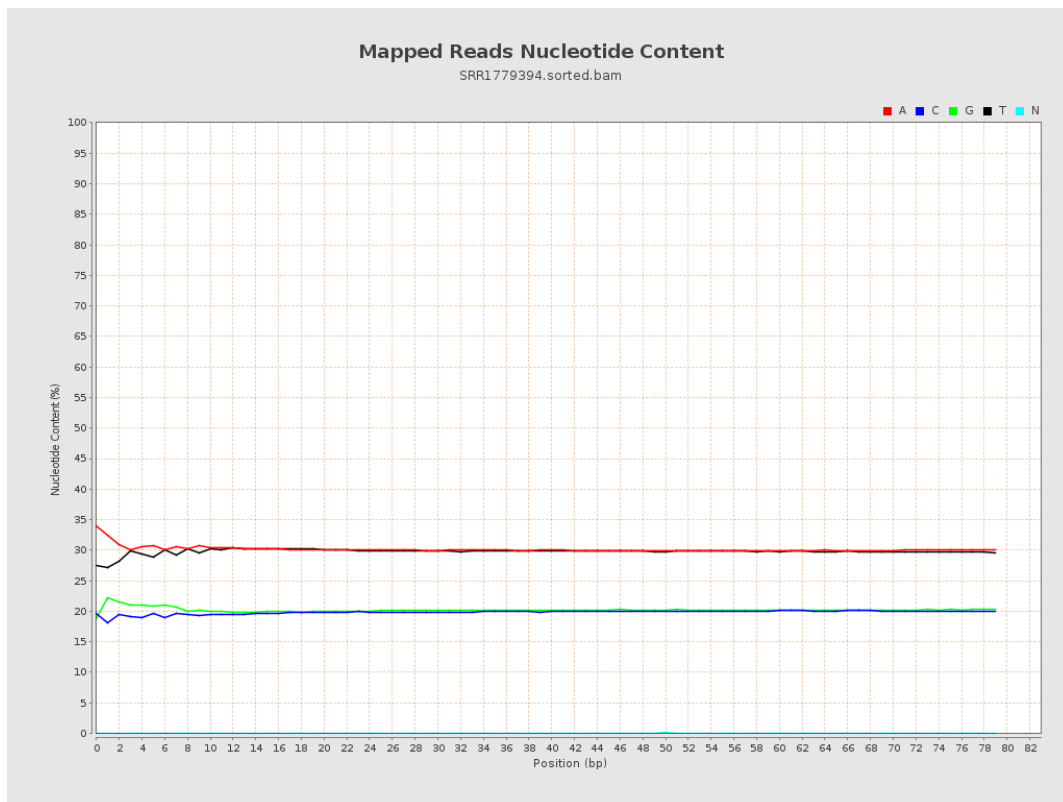
6. Results : Genome Fraction Coverage



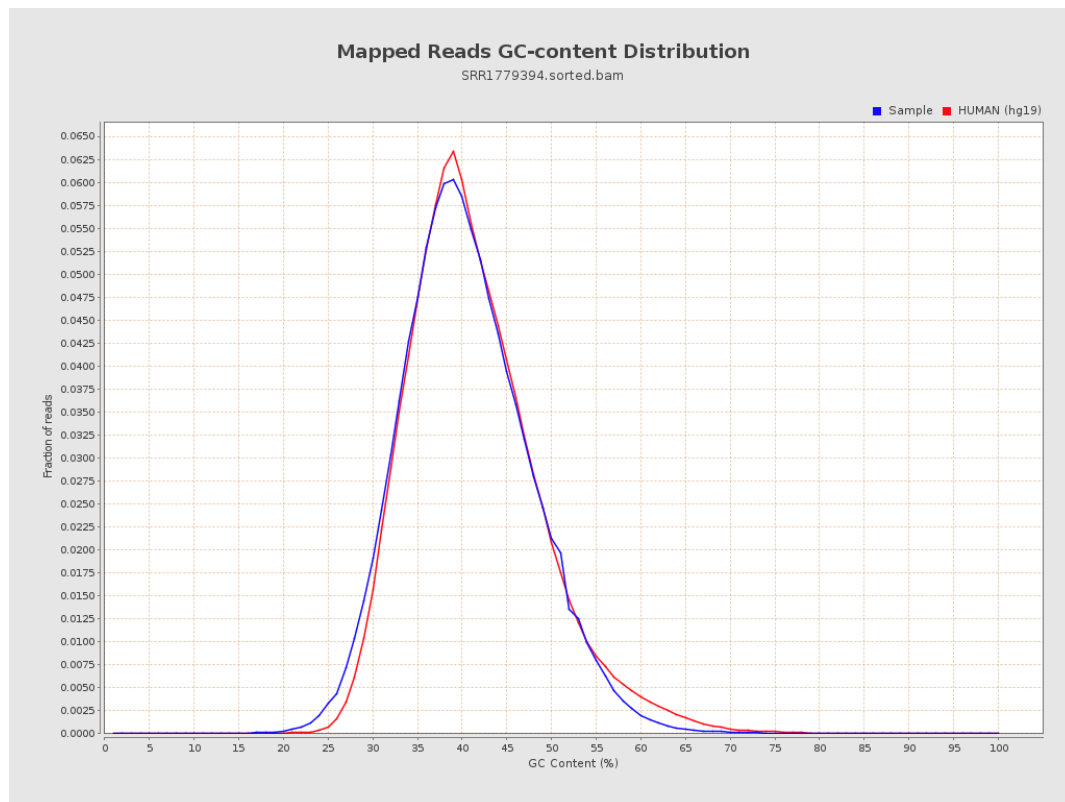
7. Results : Duplication Rate Histogram



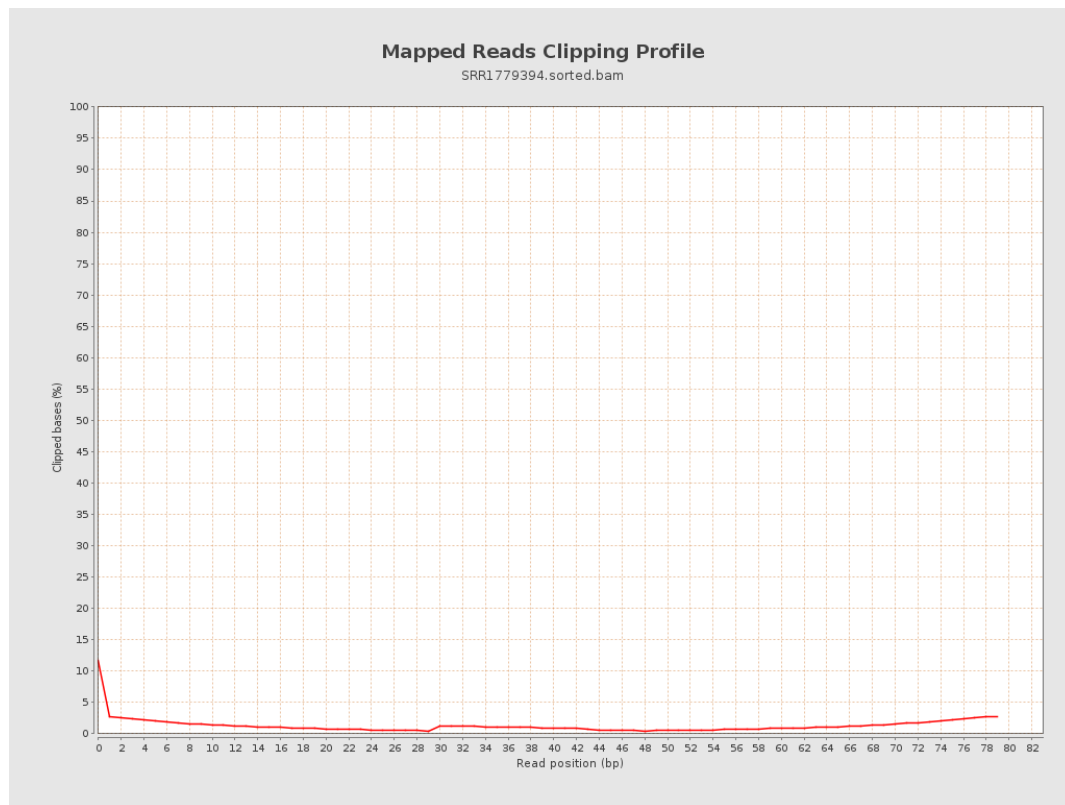
8. Results : Mapped Reads Nucleotide Content



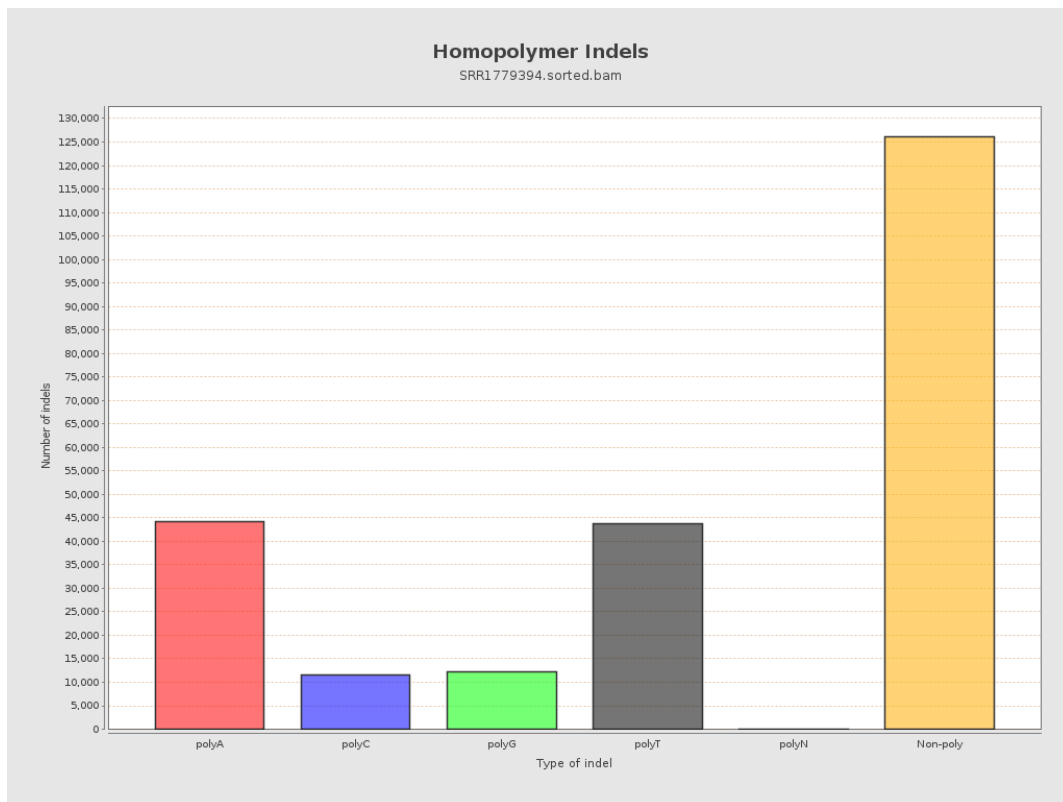
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



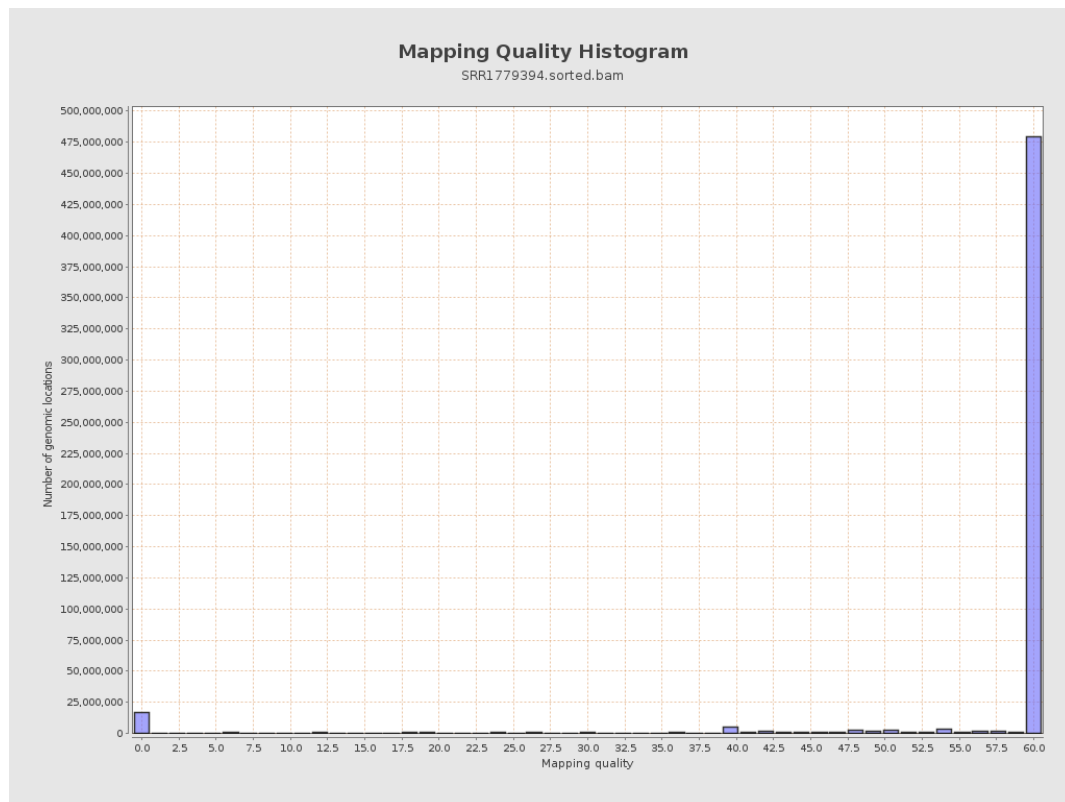
11. Results : Homopolymer Indels



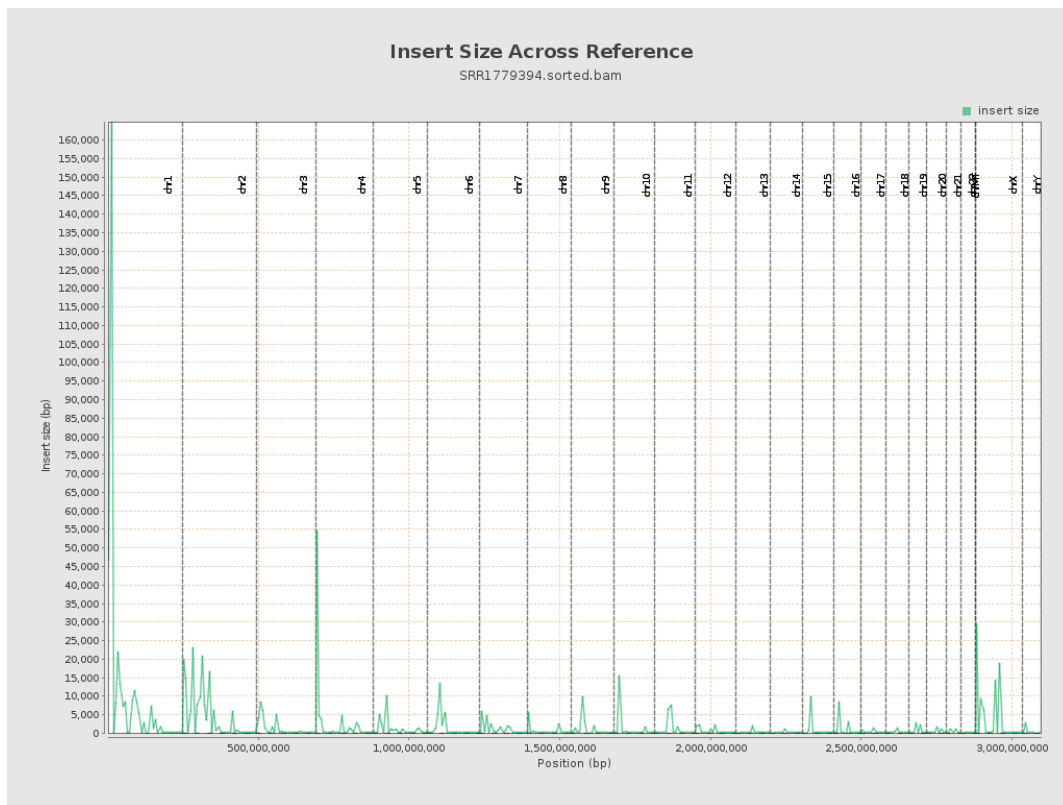
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

