

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 14:28:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779200.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_SRR1779200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779200_1.fastq.gz SRR1779200_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 14:28:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,043,210
Mapped reads	7,782,477 / 96.76%
Unmapped reads	260,733 / 3.24%
Mapped paired reads	7,782,477 / 96.76%
Mapped reads, first in pair	3,939,159 / 48.97%
Mapped reads, second in pair	3,843,318 / 47.78%
Mapped reads, both in pair	7,670,736 / 95.37%
Mapped reads, singletons	111,741 / 1.39%
Secondary alignments	0
Supplementary alignments	25,384 / 0.32%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	76,320 / 0.95%
Duplication rate	0.64%
Clipped reads	343,885 / 4.28%

2.2. ACGT Content

Number/percentage of A's	185,747,260 / 30.05%
Number/percentage of C's	122,136,018 / 19.76%
Number/percentage of T's	185,246,829 / 29.96%
Number/percentage of G's	124,977,847 / 20.22%
Number/percentage of N's	111,874 / 0.02%

GC Percentage	39.97%
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2.3. Coverage

Mean	0.1997
Standard Deviation	0.8712

2.4. Mapping Quality

Mean Mapping Quality	53.23
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2.5. Insert size

Mean	49,020.5
Standard Deviation	2,136,783.3
P25/Median/P75	205 / 268 / 340

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	3,062,542
Insertions	52,728
Mapped reads with at least one insertion	0.67%
Deletions	63,684
Mapped reads with at least one deletion	0.81%
Homopolymer indels	47.2%

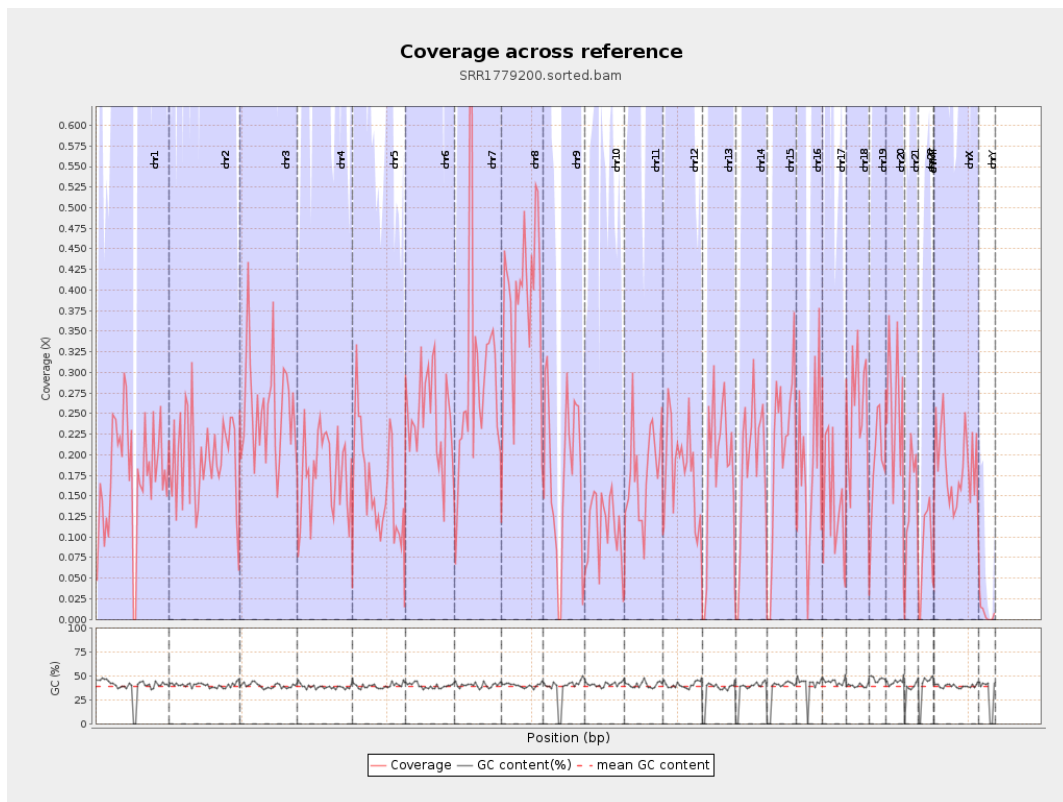
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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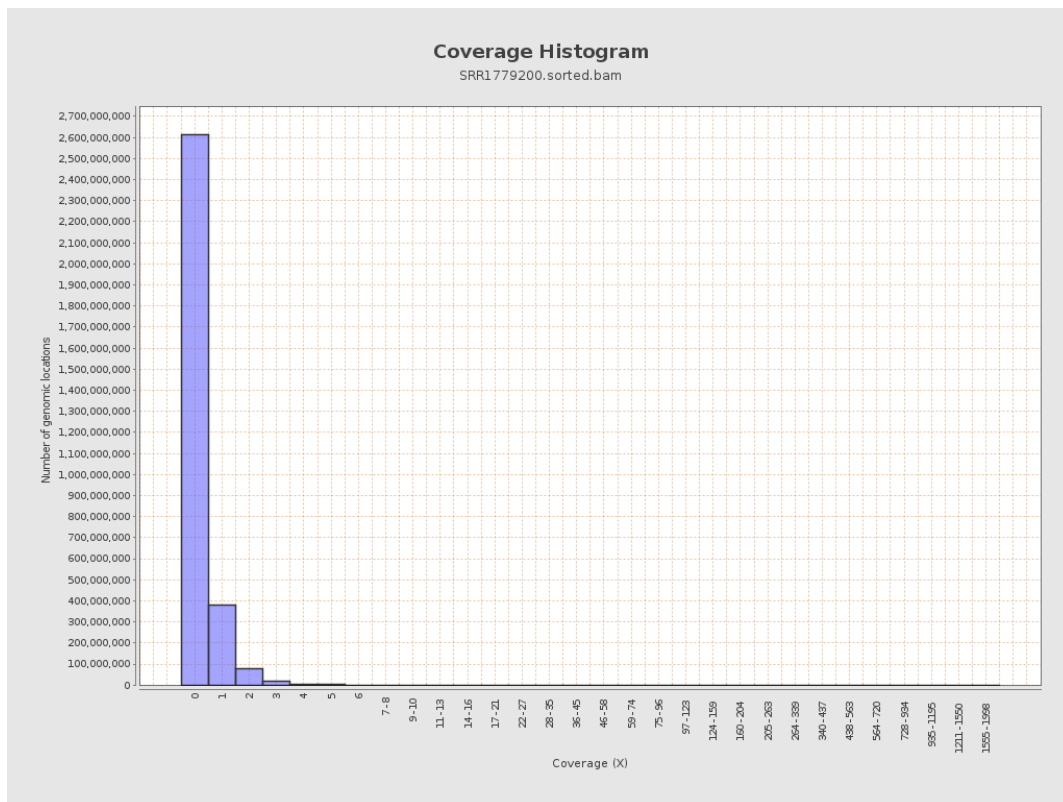
		bases	coverage	deviation
chr1	249250621	43516154	0.1746	1.9977
chr2	243199373	47672303	0.196	0.5557
chr3	198022430	50736822	0.2562	0.5783
chr4	191154276	34164844	0.1787	0.4948
chr5	180915260	29141814	0.1611	0.455
chr6	171115067	42246896	0.2469	0.6441
chr7	159138663	46737919	0.2937	0.9778
chr8	146364022	57423244	0.3923	0.7424
chr9	141213431	25374712	0.1797	0.6412
chr10	135534747	15370755	0.1134	1.54
chr11	135006516	24342260	0.1803	0.5075
chr12	133851895	24291675	0.1815	0.4942
chr13	115169878	20898916	0.1815	0.4896
chr14	107349540	20011243	0.1864	0.5043
chr15	102531392	21105660	0.2058	0.5329
chr16	90354753	16881952	0.1868	0.5146
chr17	81195210	10833682	0.1334	0.7065
chr18	78077248	19829443	0.254	0.7529
chr19	59128983	11456523	0.1938	1.2714
chr20	63025520	15895094	0.2522	0.5964
chr21	48129895	6737764	0.14	0.4436
chr22	51304566	4447220	0.0867	0.3456
chrMT	16571	657	0.0396	0.1951
chrX	155270560	28765755	0.1853	0.4953

chrY	59373566	466564	0.0079	0.1163
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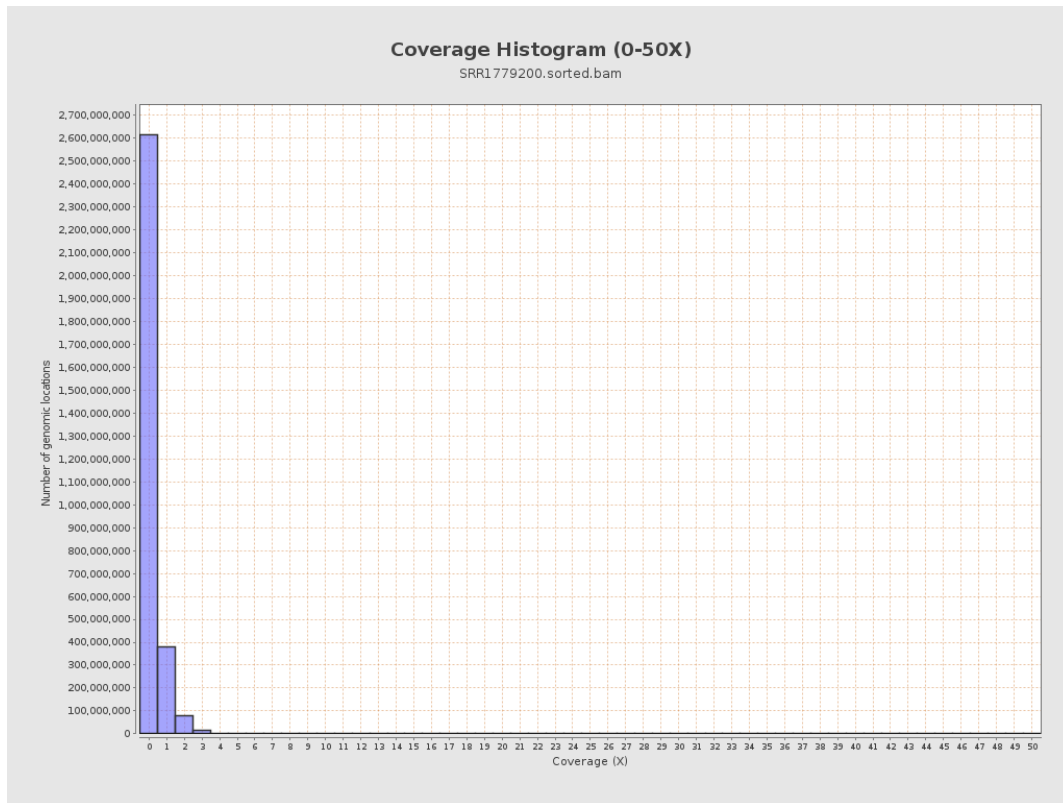
3. Results : Coverage across reference



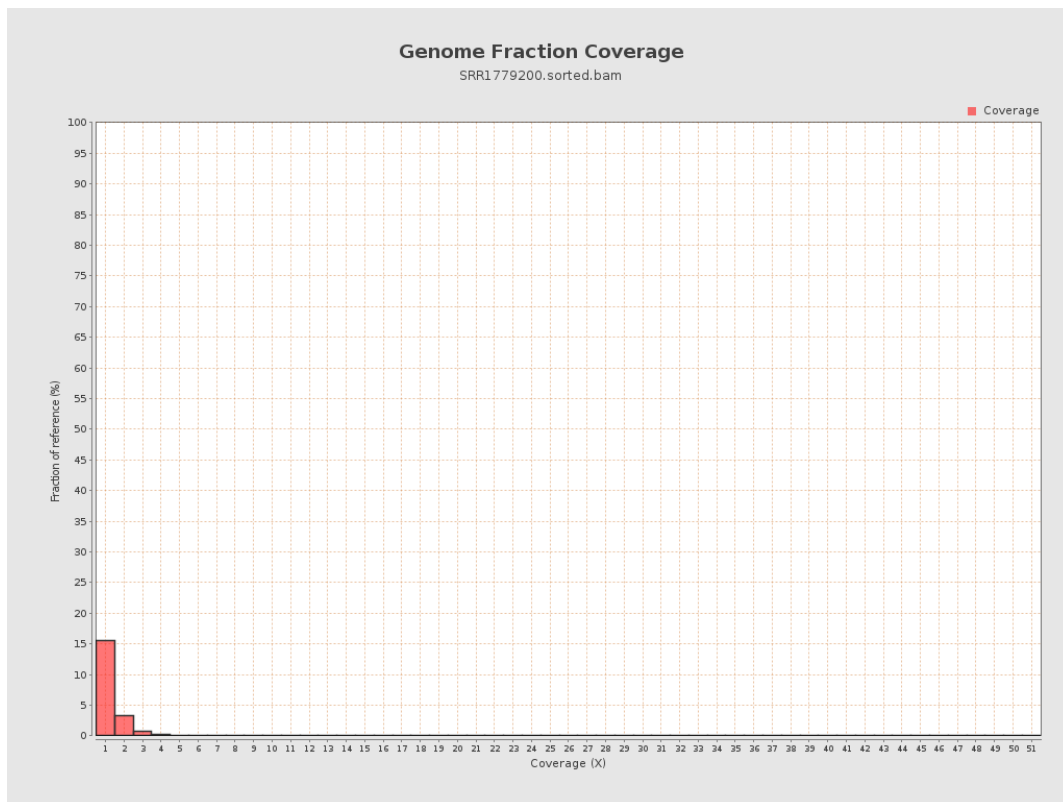
4. Results : Coverage Histogram



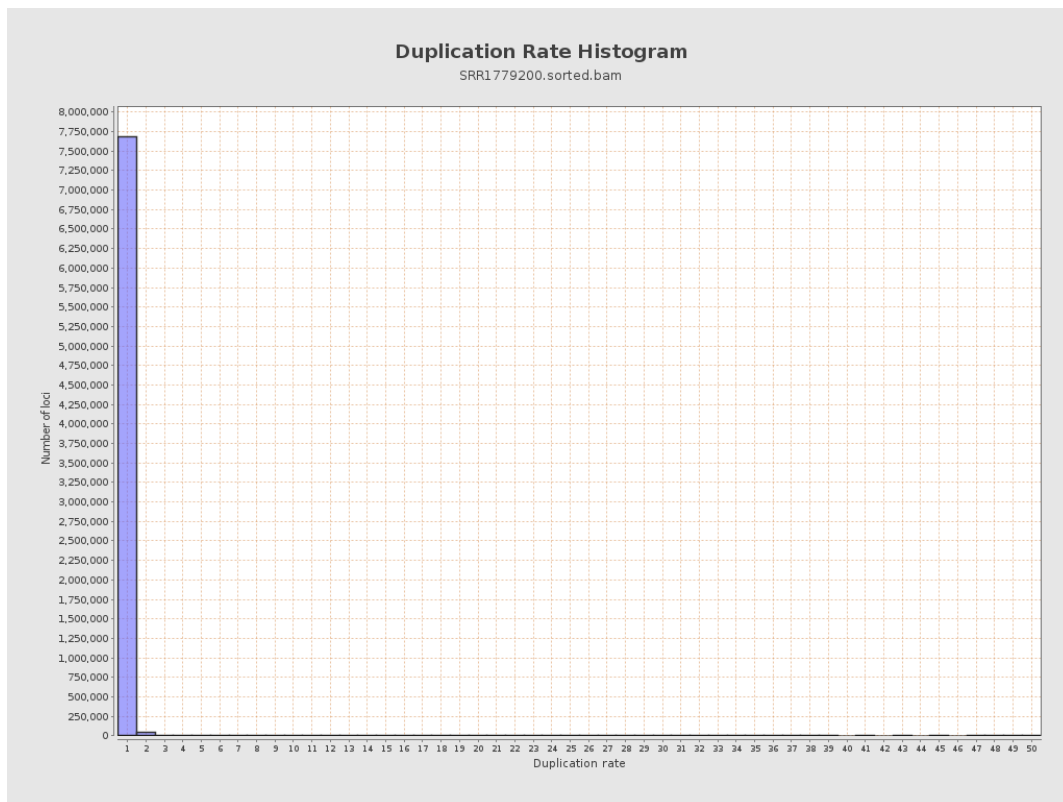
5. Results : Coverage Histogram (0-50X)



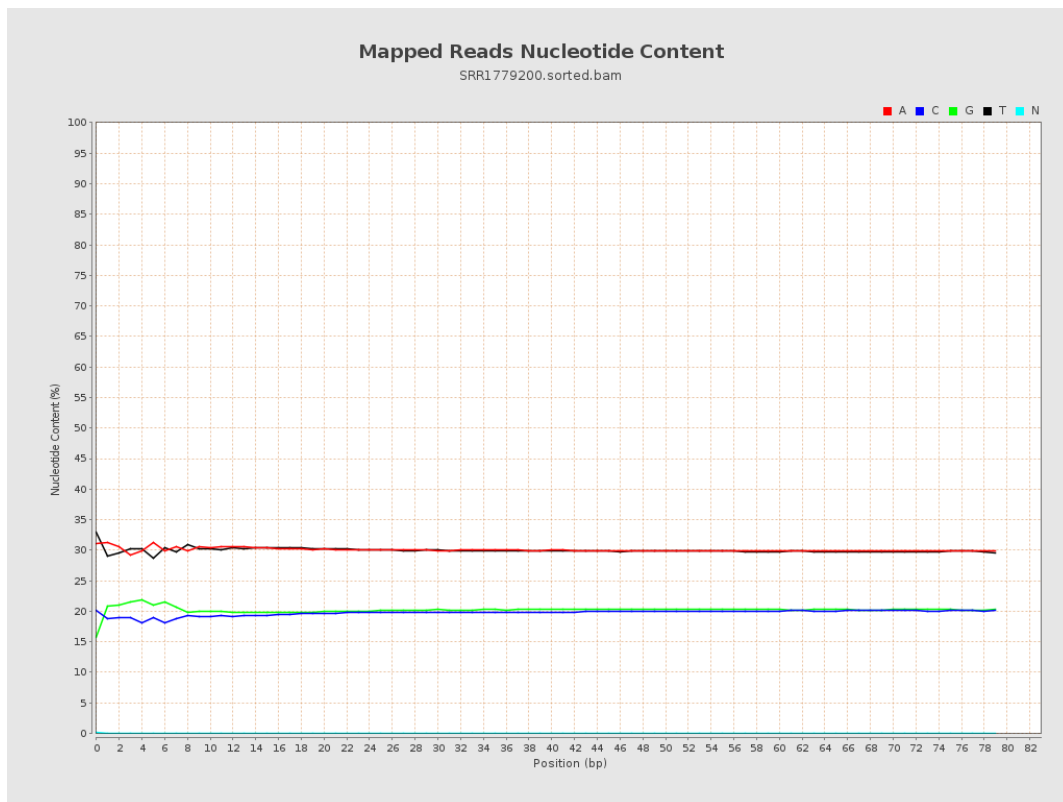
6. Results : Genome Fraction Coverage



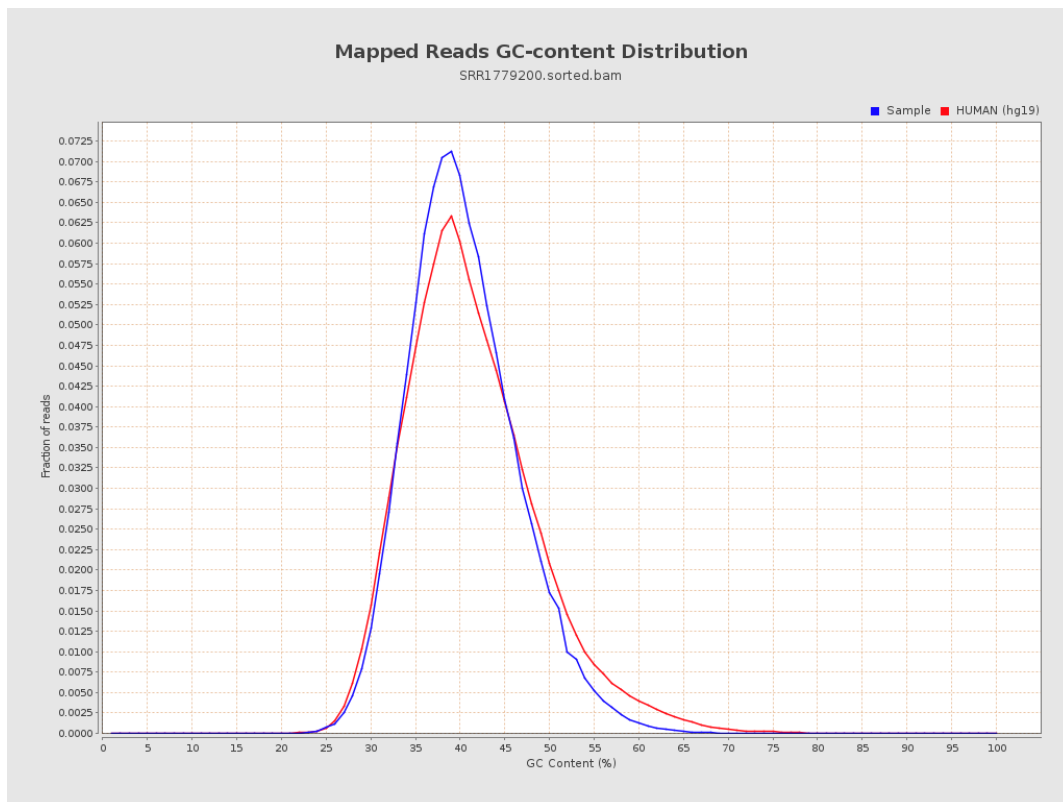
7. Results : Duplication Rate Histogram



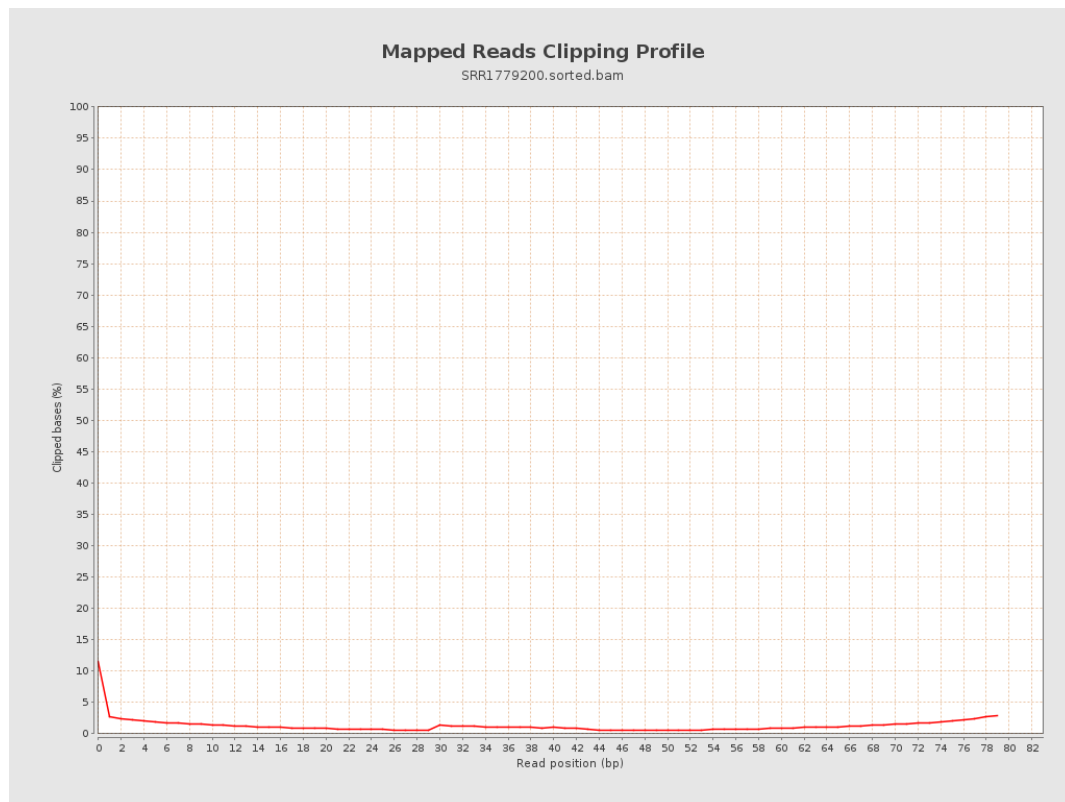
8. Results : Mapped Reads Nucleotide Content



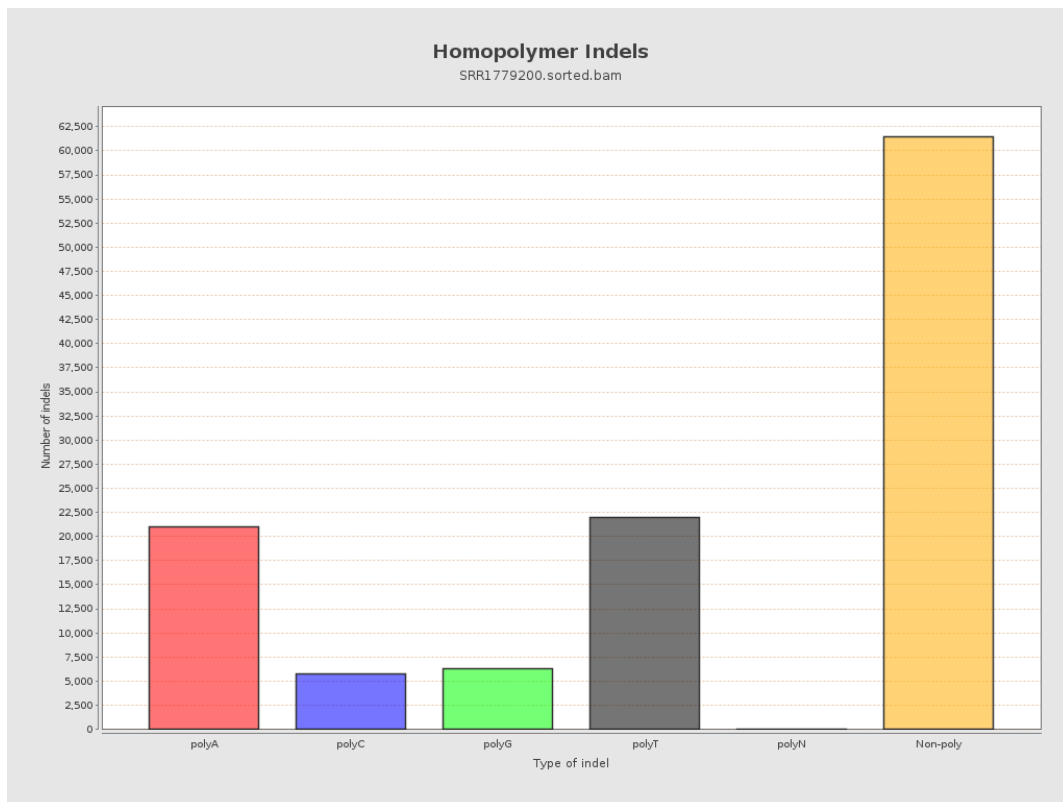
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



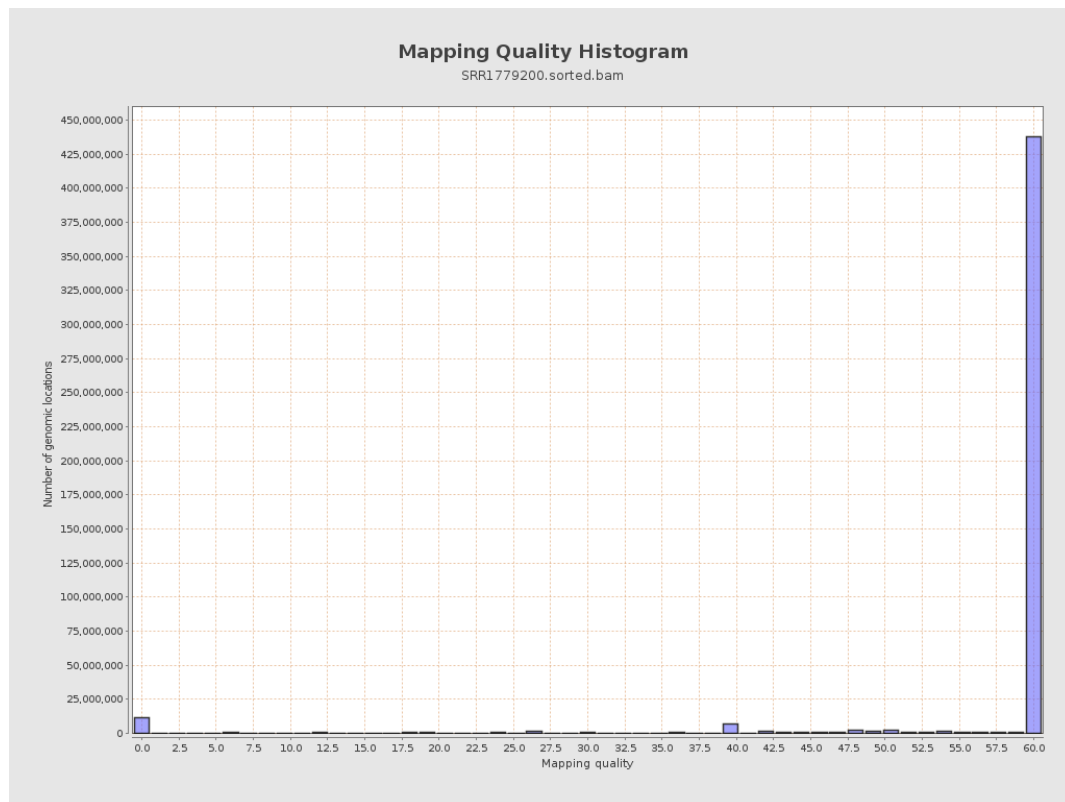
11. Results : Homopolymer Indels



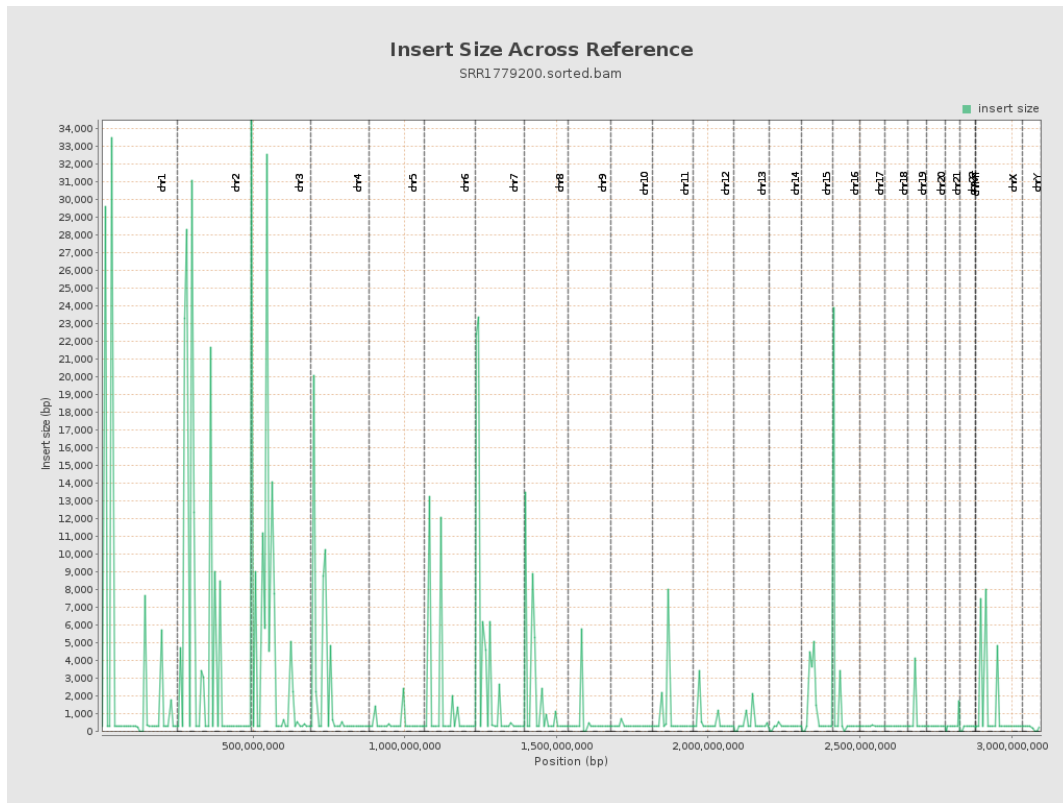
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

