

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 06:23:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779165.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_SRR1779165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779165_1.fastq.gz SRR1779165_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 06:23:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,696
Mapped reads	8,170 / 76.38%
Unmapped reads	2,526 / 23.62%
Mapped paired reads	8,170 / 76.38%
Mapped reads, first in pair	4,922 / 46.02%
Mapped reads, second in pair	3,248 / 30.37%
Mapped reads, both in pair	6,416 / 59.99%
Mapped reads, singletons	1,754 / 16.4%
Secondary alignments	0
Supplementary alignments	40 / 0.37%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	37 / 0.35%
Duplication rate	0.45%
Clipped reads	562 / 5.25%

2.2. ACGT Content

Number/percentage of A's	248,648 / 30.59%
Number/percentage of C's	155,796 / 19.17%
Number/percentage of T's	248,408 / 30.56%
Number/percentage of G's	159,733 / 19.65%
Number/percentage of N's	218 / 0.03%

GC Percentage	38.82%
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2.3. Coverage

Mean	0.0003
Standard Deviation	0.0175

2.4. Mapping Quality

Mean Mapping Quality	51.73
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2.5. Insert size

Mean	236,378.95
Standard Deviation	4,525,510.92
P25/Median/P75	160 / 218 / 299

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	3,978
Insertions	60
Mapped reads with at least one insertion	0.73%
Deletions	83
Mapped reads with at least one deletion	0.99%
Homopolymer indels	43.36%

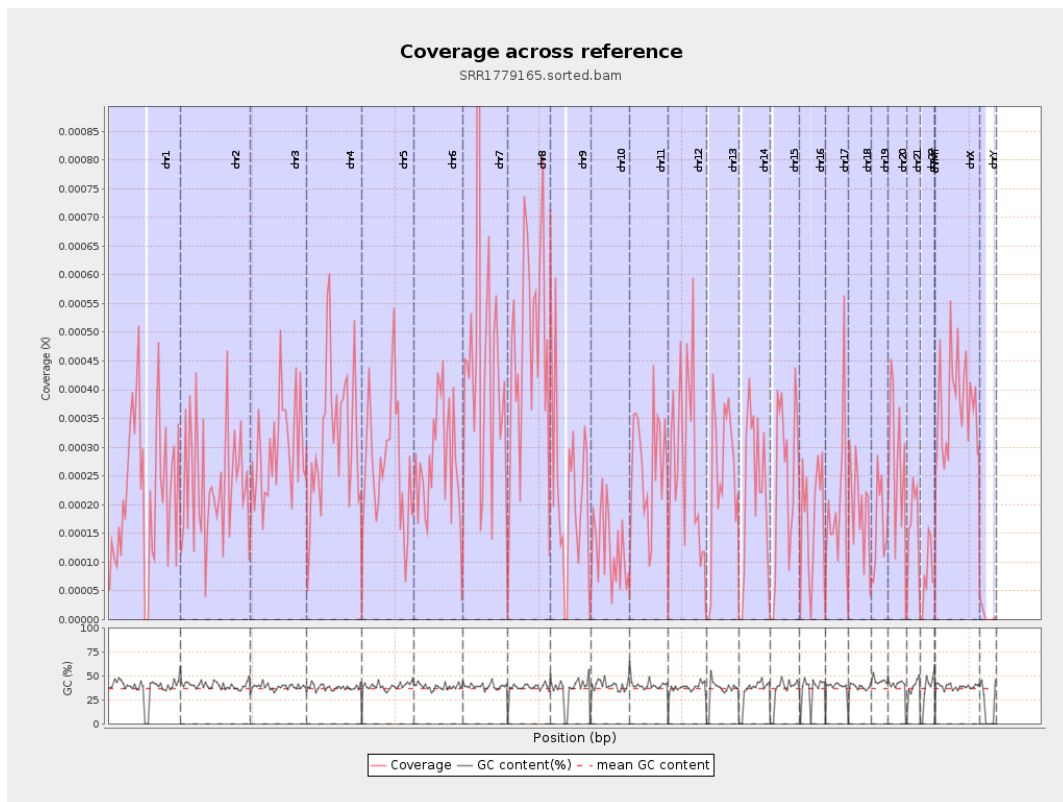
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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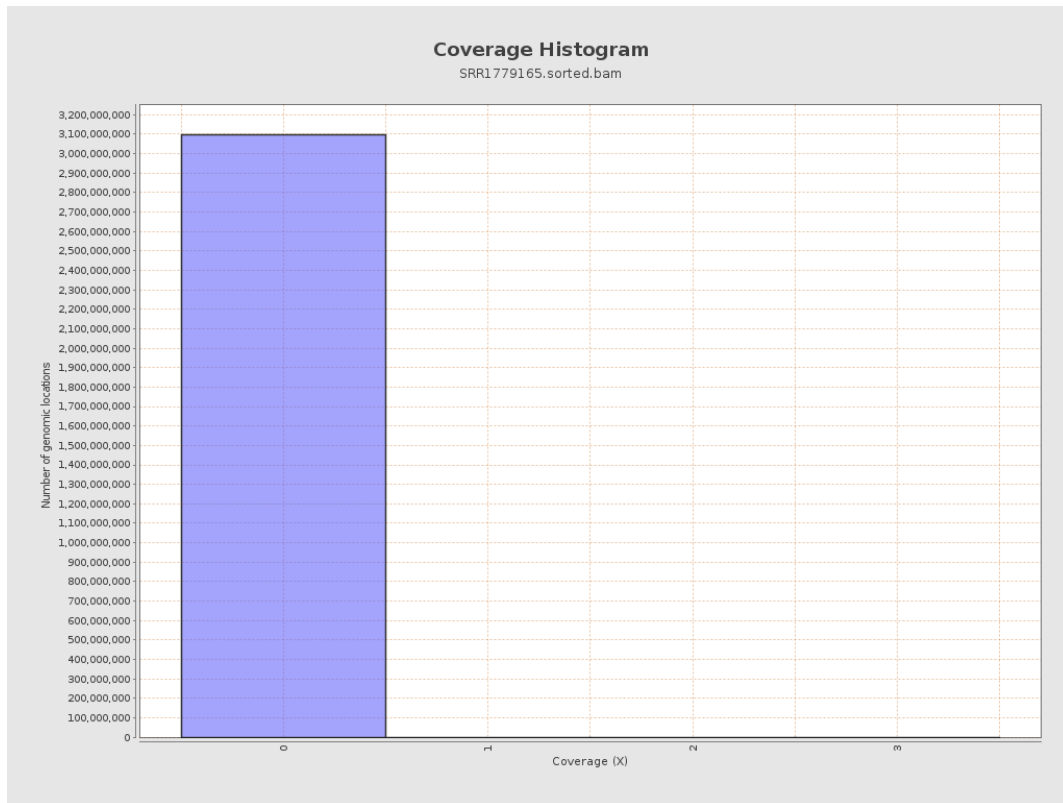
		bases	coverage	deviation
chr1	249250621	55698	0.0002	0.0162
chr2	243199373	57244	0.0002	0.0165
chr3	198022430	58235	0.0003	0.0184
chr4	191154276	61163	0.0003	0.0193
chr5	180915260	48760	0.0003	0.0176
chr6	171115067	46931	0.0003	0.0176
chr7	159138663	73006	0.0005	0.0229
chr8	146364022	69792	0.0005	0.0235
chr9	141213431	32475	0.0002	0.0166
chr10	135534747	17144	0.0001	0.0122
chr11	135006516	36370	0.0003	0.0177
chr12	133851895	36615	0.0003	0.018
chr13	115169878	27512	0.0002	0.0168
chr14	107349540	23009	0.0002	0.0158
chr15	102531392	24209	0.0002	0.0168
chr16	90354753	15284	0.0002	0.0142
chr17	81195210	16034	0.0002	0.0152
chr18	78077248	15698	0.0002	0.0153
chr19	59128983	9710	0.0002	0.0136
chr20	63025520	17563	0.0003	0.0179
chr21	48129895	8127	0.0002	0.0141
chr22	51304566	3999	0.0001	0.01
chrMT	16571	0	0	0
chrX	155270560	57860	0.0004	0.0208

chrY	59373566	547	0	0.003
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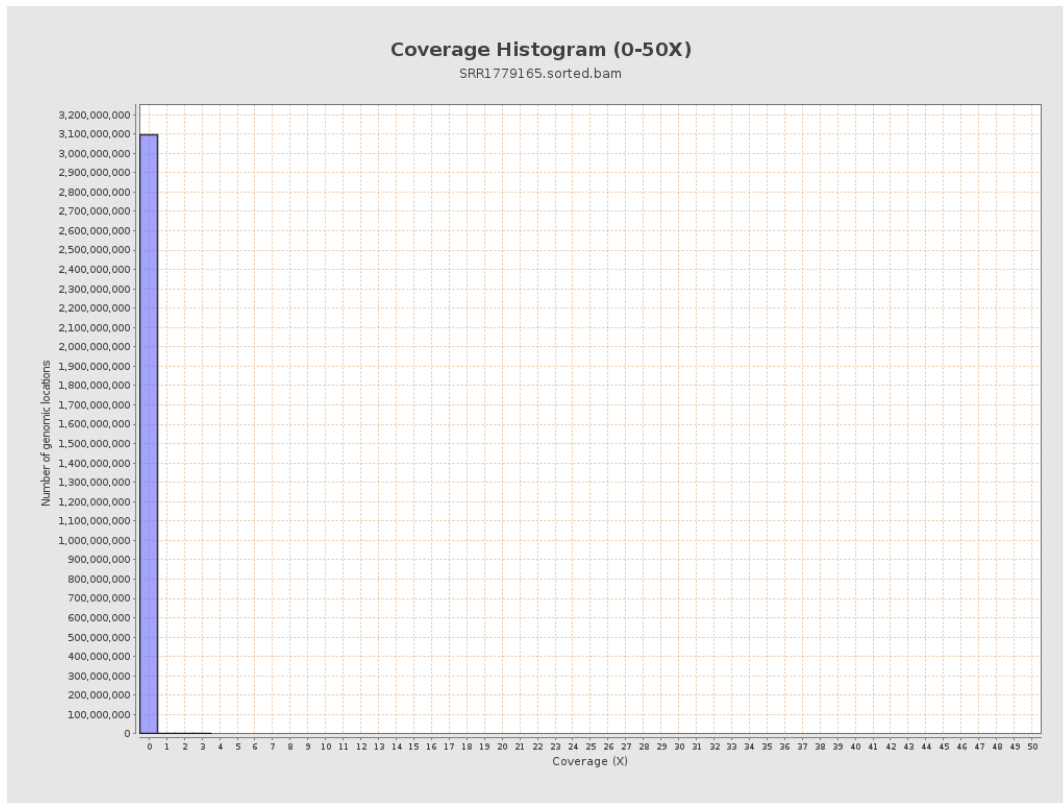
3. Results : Coverage across reference



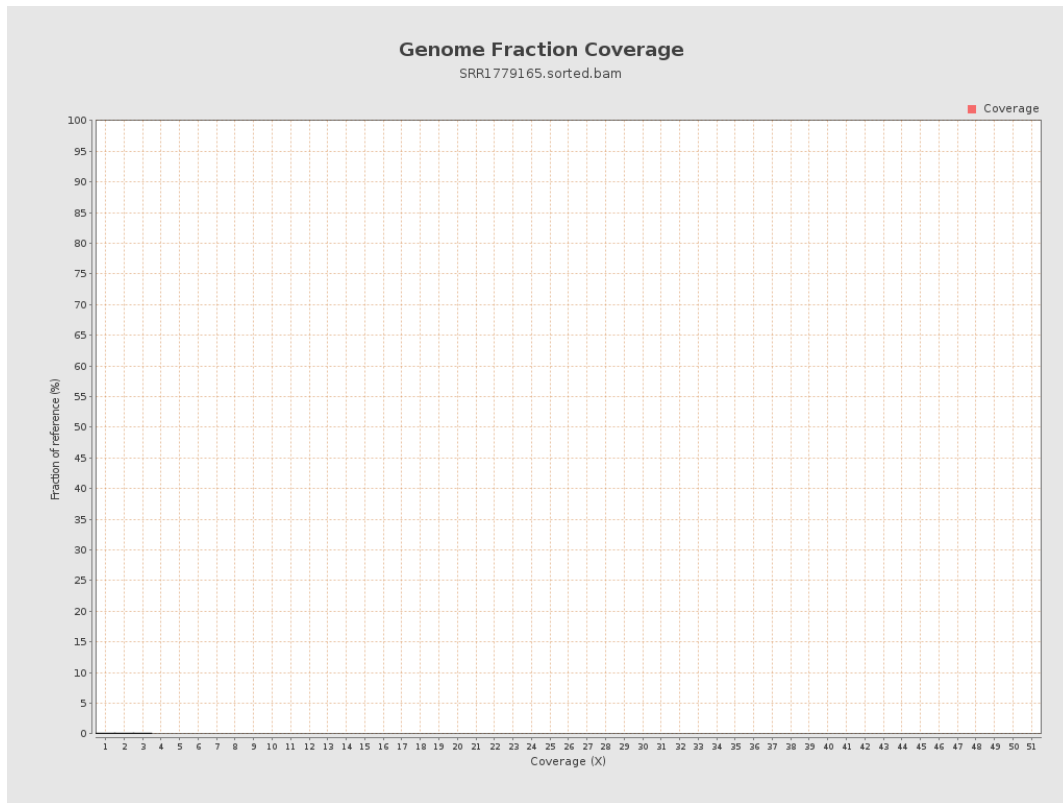
4. Results : Coverage Histogram



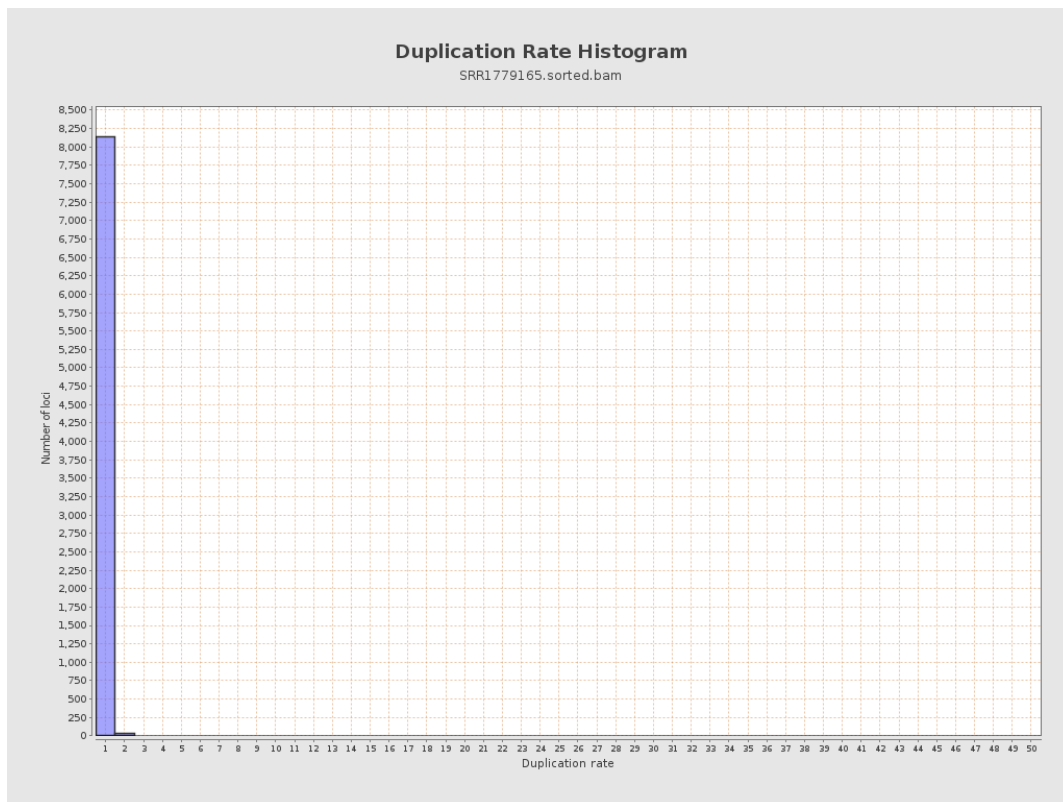
5. Results : Coverage Histogram (0-50X)



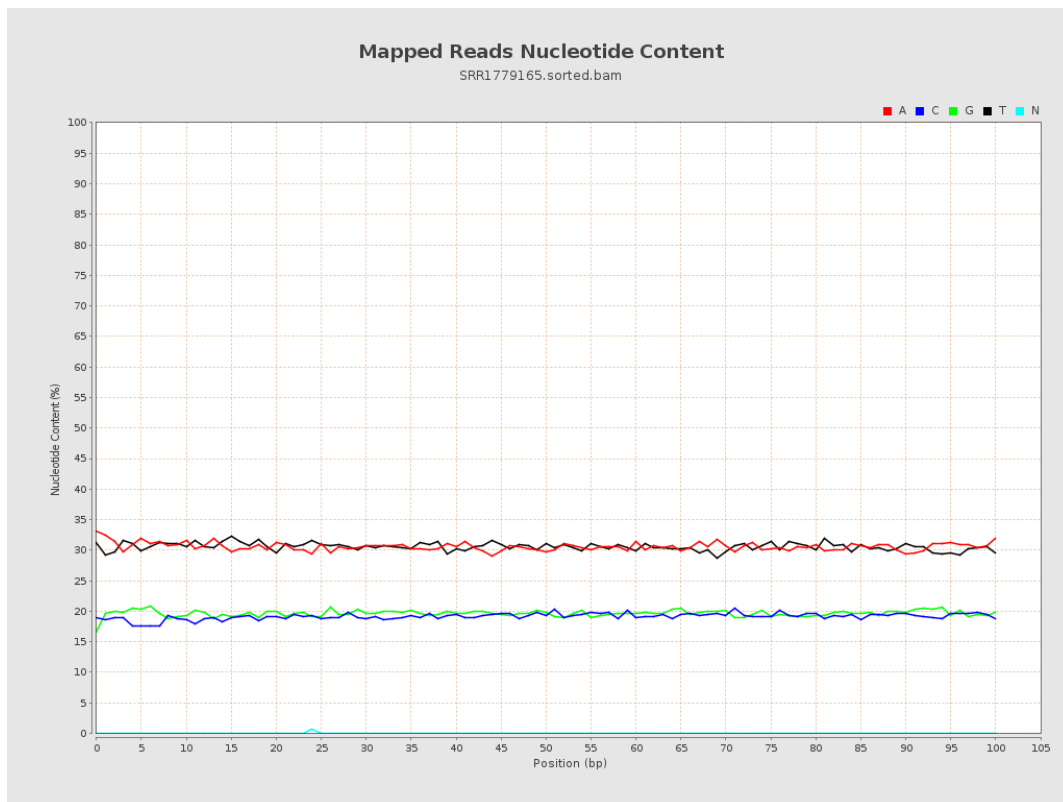
6. Results : Genome Fraction Coverage



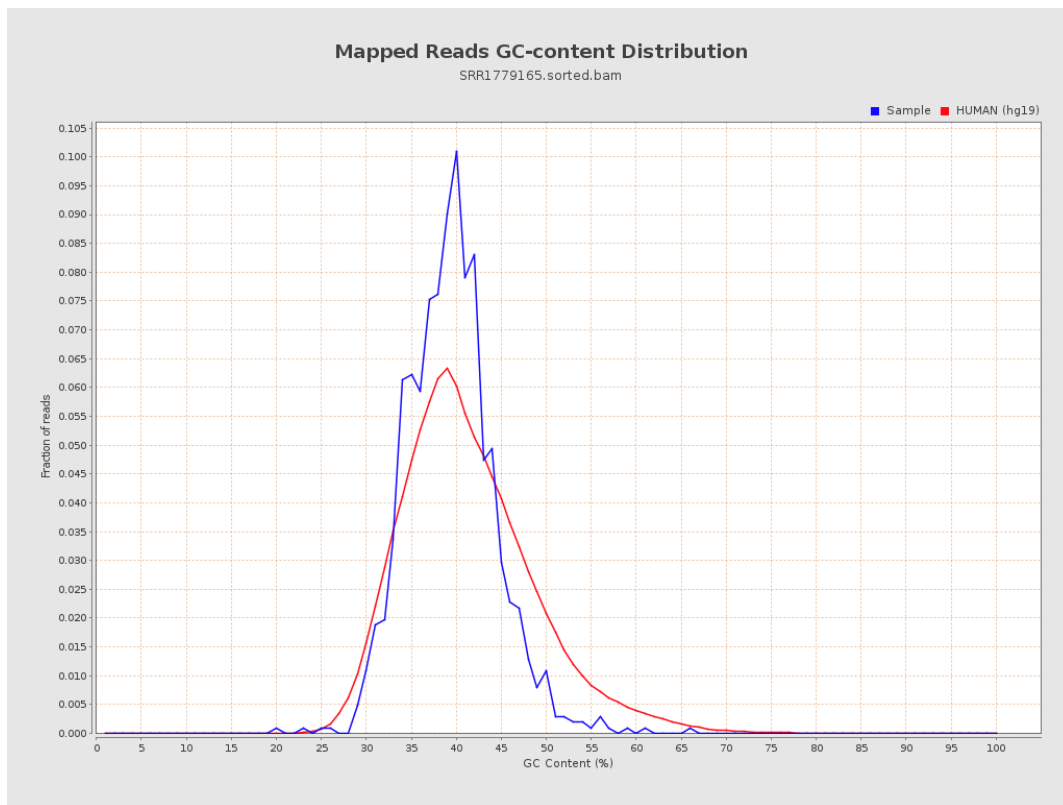
7. Results : Duplication Rate Histogram



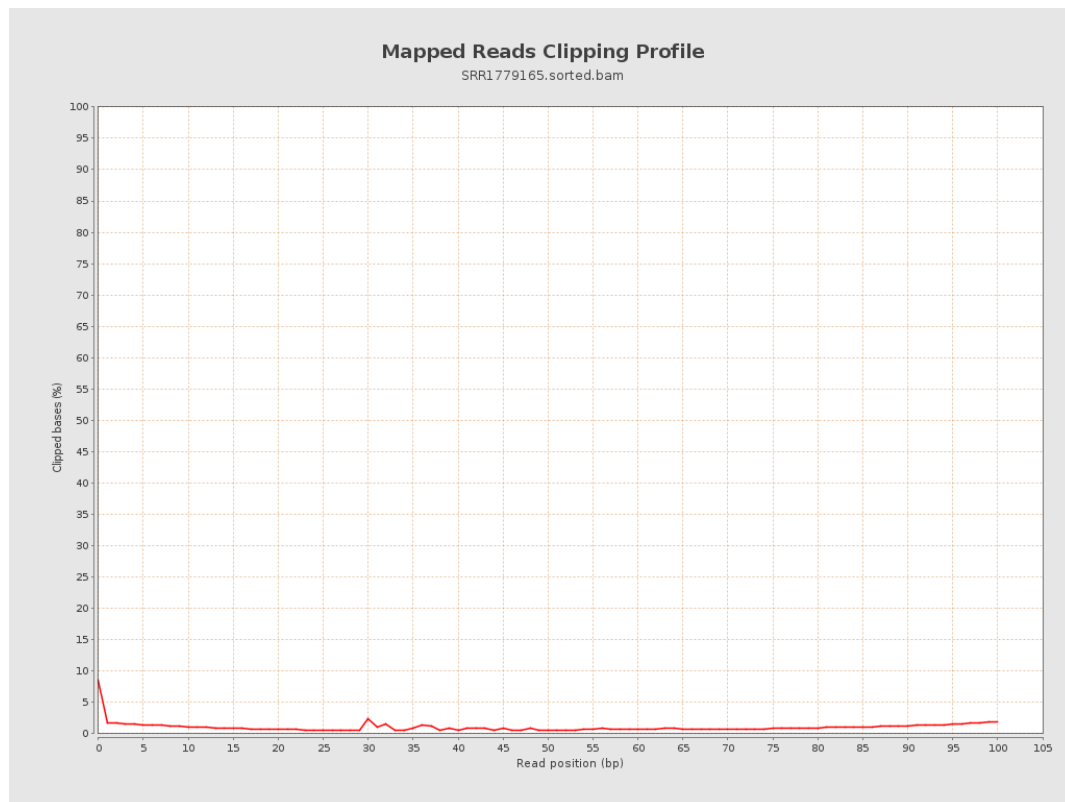
8. Results : Mapped Reads Nucleotide Content



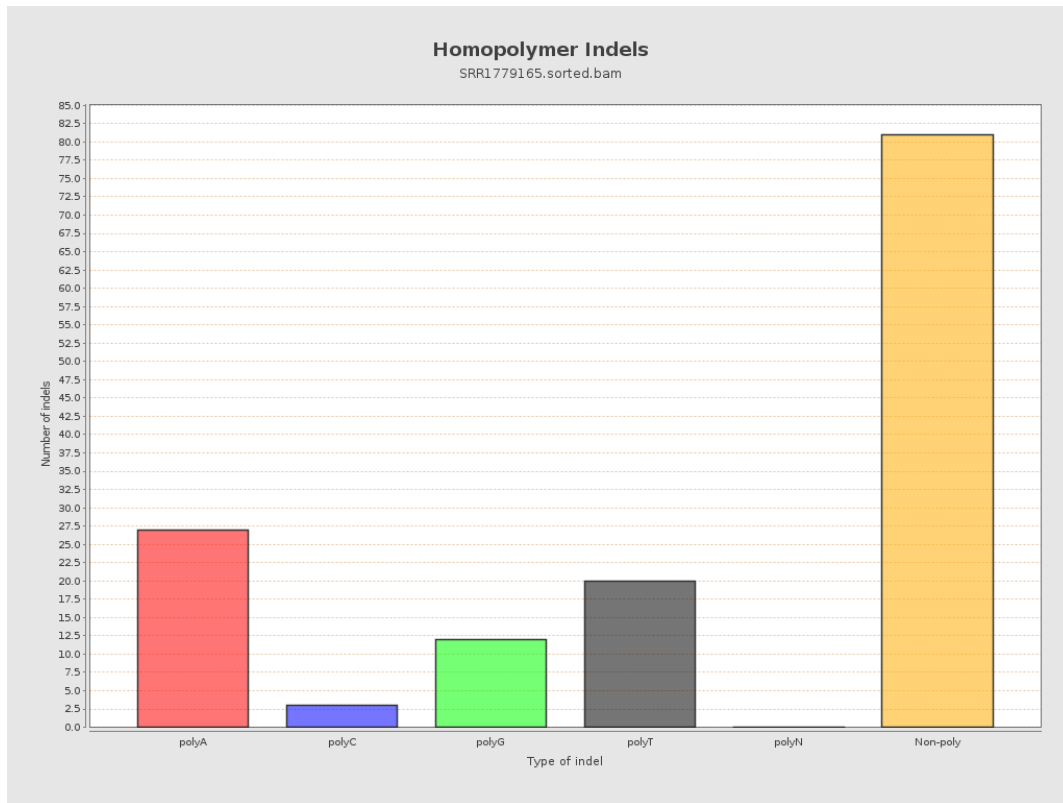
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



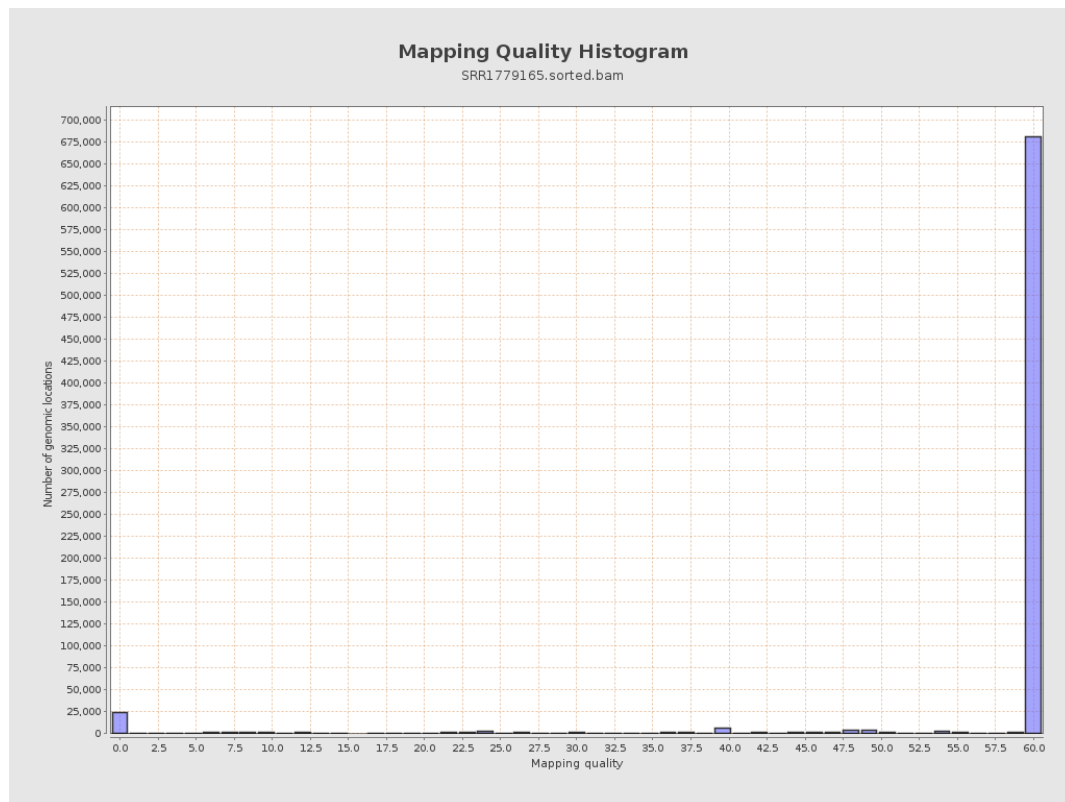
11. Results : Homopolymer Indels



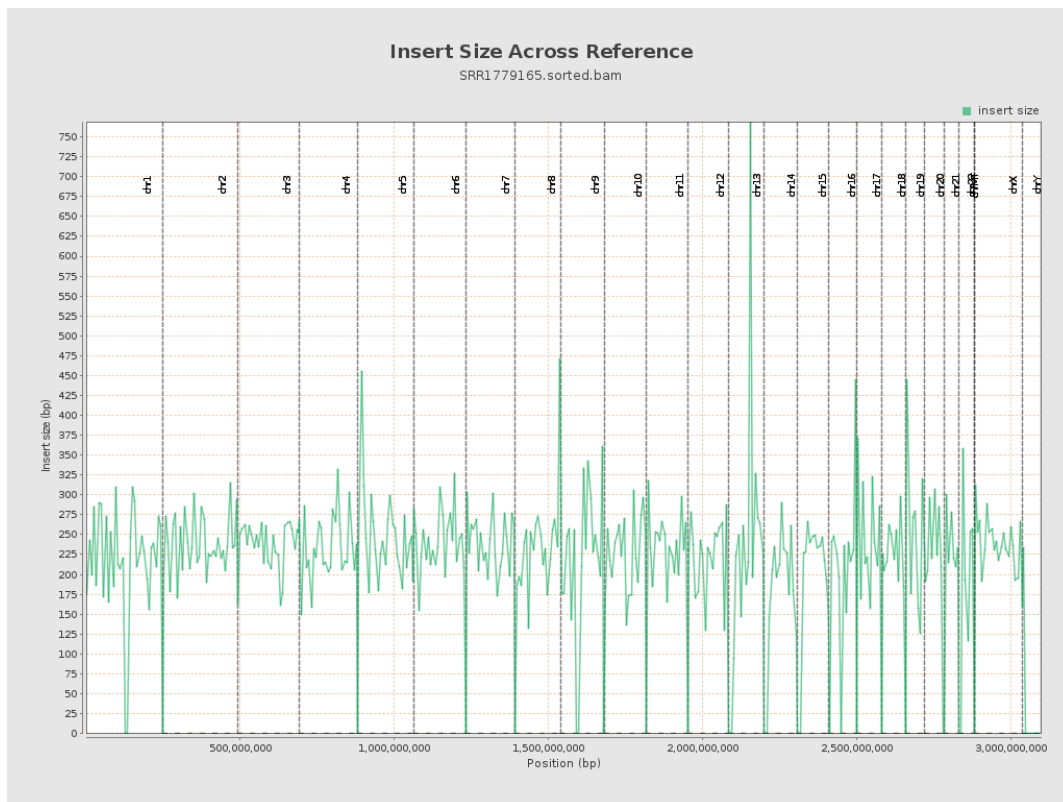
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

