

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 07:01:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779167.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_SRR1779167 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779167_1.fastq.gz SRR1779167_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 07:01:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,209,704
Mapped reads	33,413,851 / 97.67%
Unmapped reads	795,853 / 2.33%
Mapped paired reads	33,413,851 / 97.67%
Mapped reads, first in pair	16,783,082 / 49.06%
Mapped reads, second in pair	16,630,769 / 48.61%
Mapped reads, both in pair	33,147,766 / 96.9%
Mapped reads, singletons	266,085 / 0.78%
Secondary alignments	0
Supplementary alignments	203,955 / 0.6%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	1,136,894 / 3.32%
Duplication rate	3.09%
Clipped reads	2,313,483 / 6.76%

2.2. ACGT Content

Number/percentage of A's	1,020,889,155 / 30.6%
Number/percentage of C's	645,629,877 / 19.35%
Number/percentage of T's	1,011,339,805 / 30.32%
Number/percentage of G's	656,558,046 / 19.68%
Number/percentage of N's	1,360,564 / 0.04%

GC Percentage	39.04%
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2.3. Coverage

Mean	1.0778
Standard Deviation	2.3907

2.4. Mapping Quality

Mean Mapping Quality	53.53
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2.5. Insert size

Mean	79,531.86
Standard Deviation	2,663,841.49
P25/Median/P75	149 / 200 / 273

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	13,491,652
Insertions	273,011
Mapped reads with at least one insertion	0.81%
Deletions	335,088
Mapped reads with at least one deletion	0.98%
Homopolymer indels	46.49%

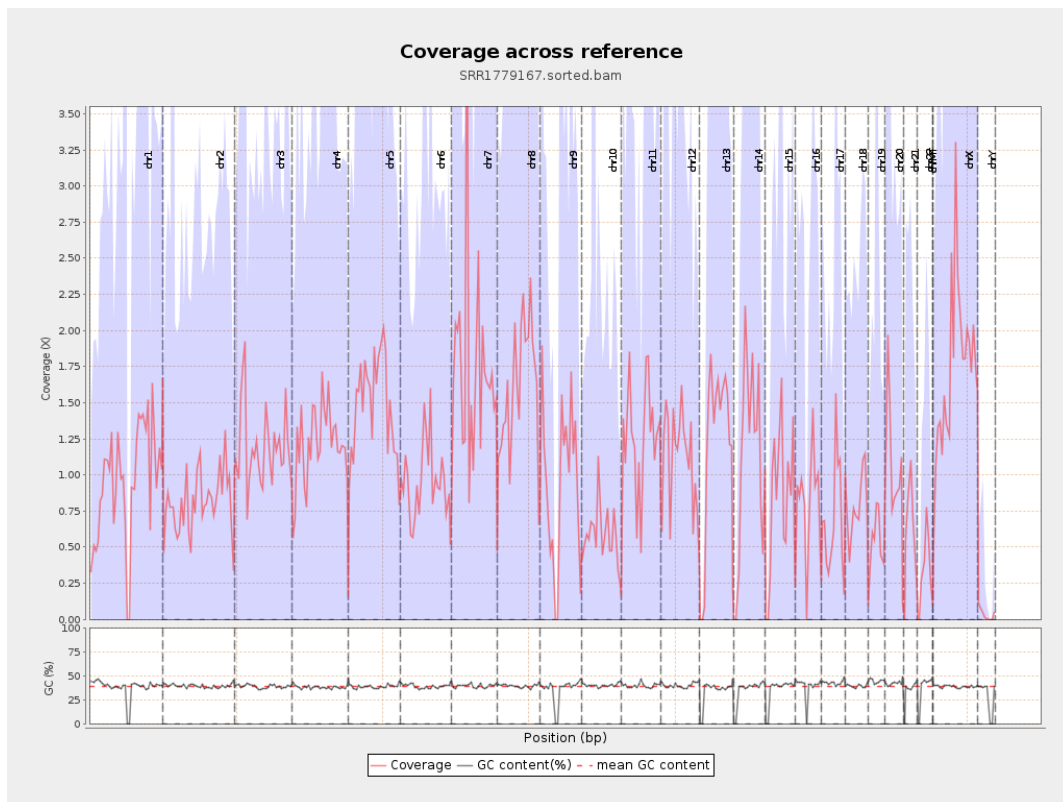
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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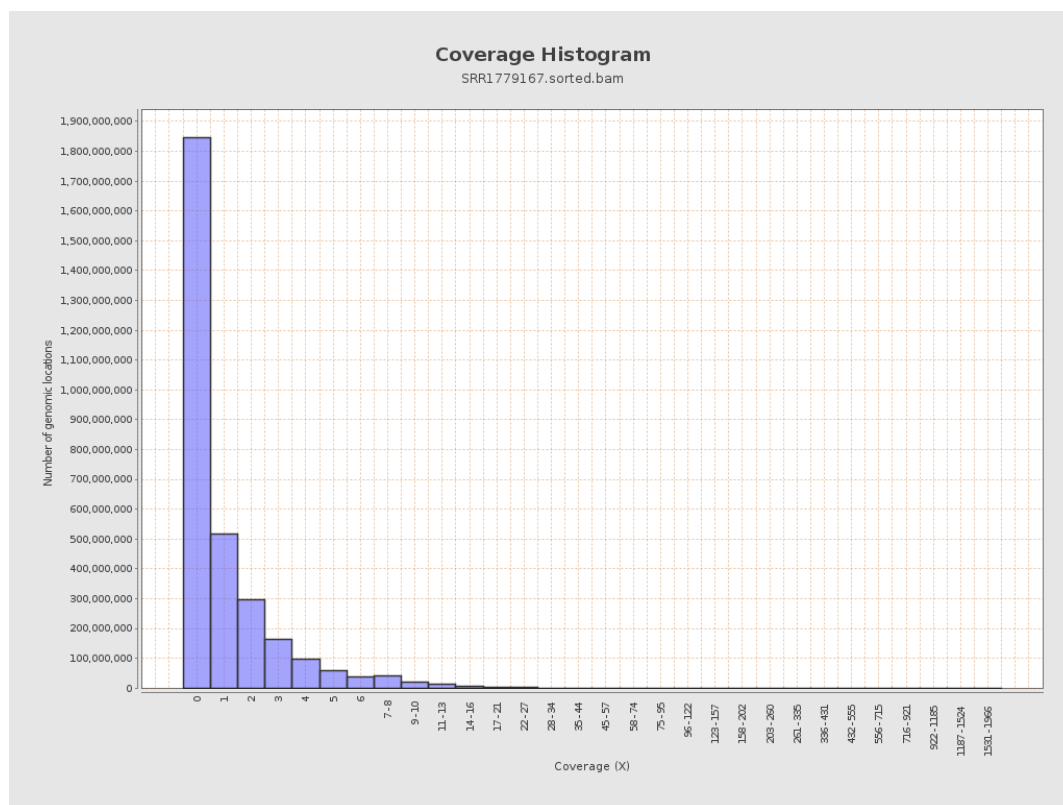
		bases	coverage	deviation
chr1	249250621	237300987	0.9521	2.7854
chr2	243199373	196226901	0.8069	2.0811
chr3	198022430	236604983	1.1948	2.0697
chr4	191154276	231746283	1.2124	2.0896
chr5	180915260	265986399	1.4702	2.3006
chr6	171115067	163676587	0.9565	1.8853
chr7	159138663	279034461	1.7534	4.0508
chr8	146364022	236240630	1.6141	2.6101
chr9	141213431	132606246	0.939	2.0028
chr10	135534747	80284605	0.5924	3.2603
chr11	135006516	168948115	1.2514	2.1723
chr12	133851895	150087256	1.1213	2.076
chr13	115169878	138678542	1.2041	2.1832
chr14	107349540	121267461	1.1297	2.1297
chr15	102531392	85965883	0.8384	1.8718
chr16	90354753	71129554	0.7872	1.7053
chr17	81195210	57337959	0.7062	1.7393
chr18	78077248	61643064	0.7895	1.6376
chr19	59128983	32696723	0.553	1.9212
chr20	63025520	67973446	1.0785	2.1069
chr21	48129895	28887264	0.6002	1.5248
chr22	51304566	17723186	0.3455	1.0673
chrMT	16571	1671	0.1008	0.4047
chrX	155270560	272341004	1.754	2.999

chrY	59373566	2136175	0.036	0.4855
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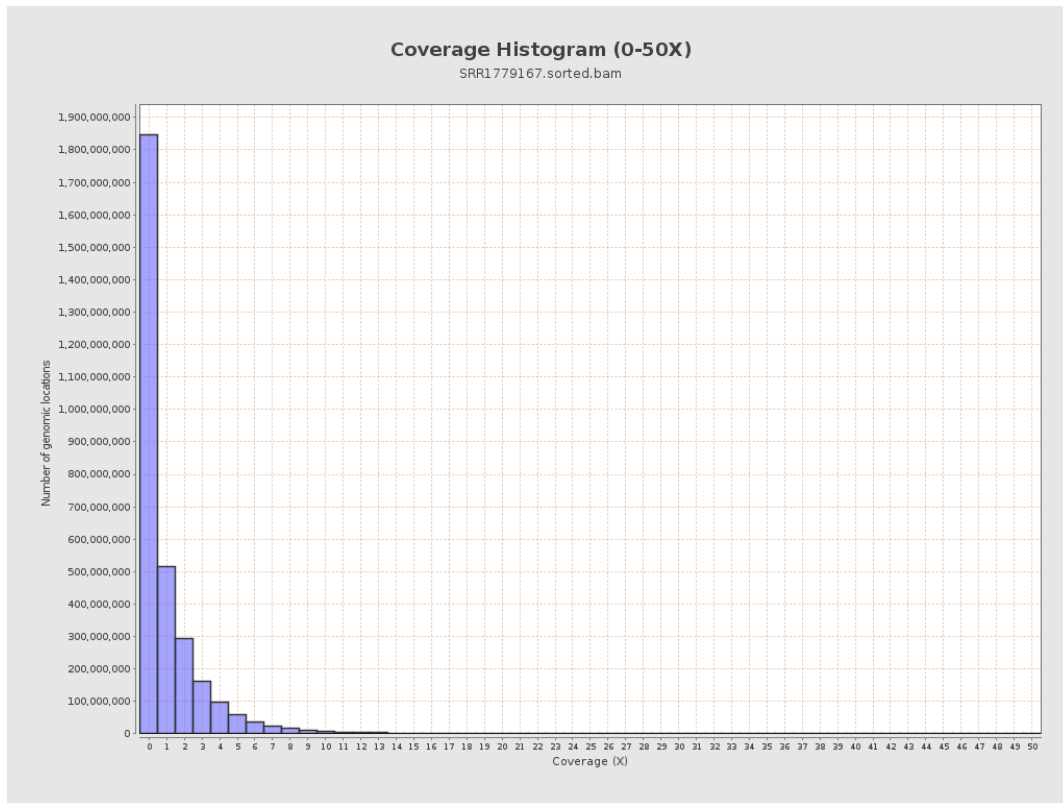
3. Results : Coverage across reference



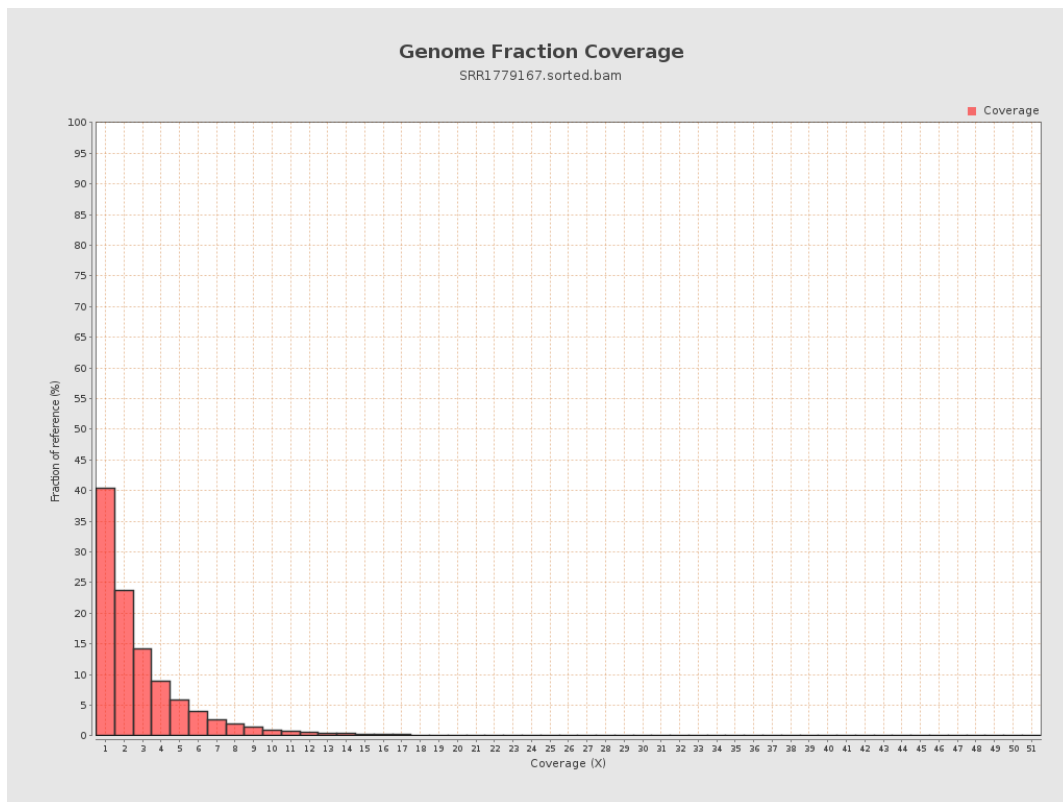
4. Results : Coverage Histogram



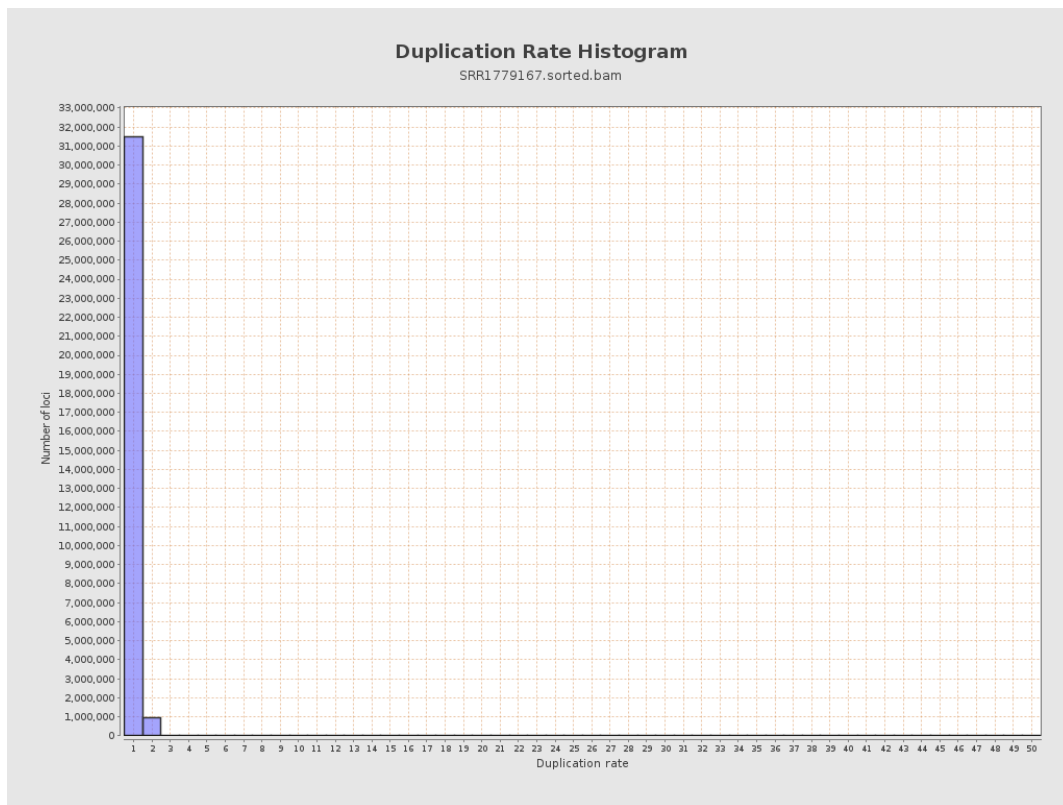
5. Results : Coverage Histogram (0-50X)



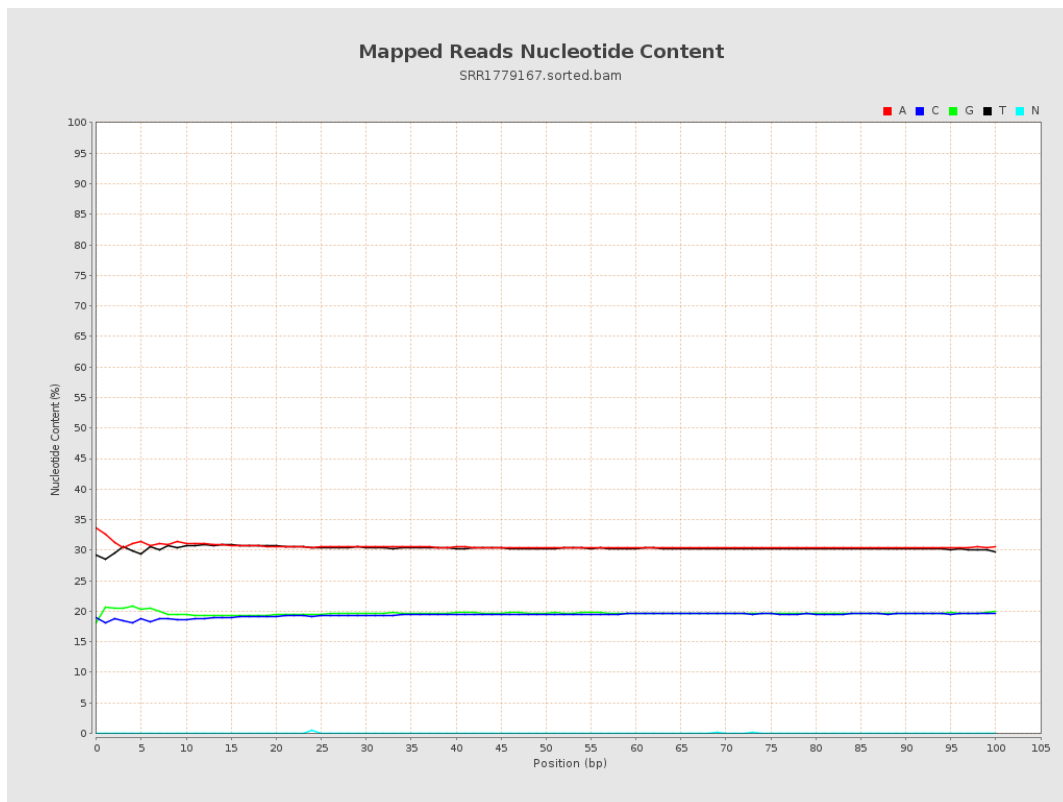
6. Results : Genome Fraction Coverage



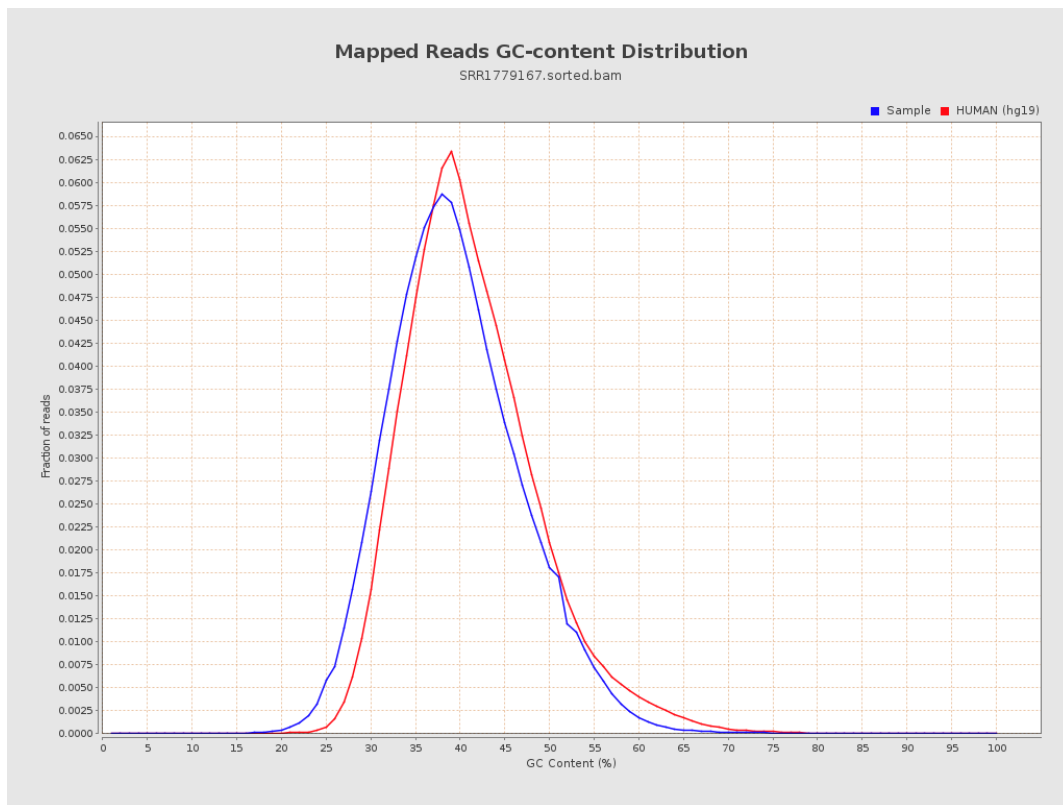
7. Results : Duplication Rate Histogram



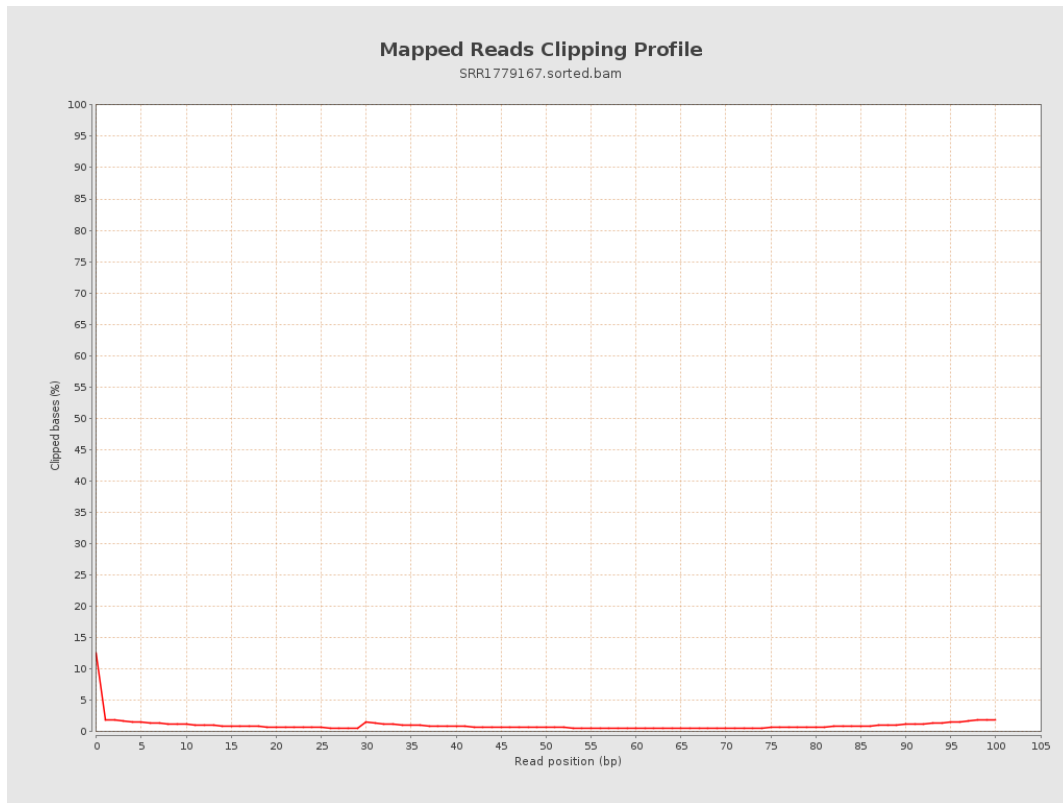
8. Results : Mapped Reads Nucleotide Content



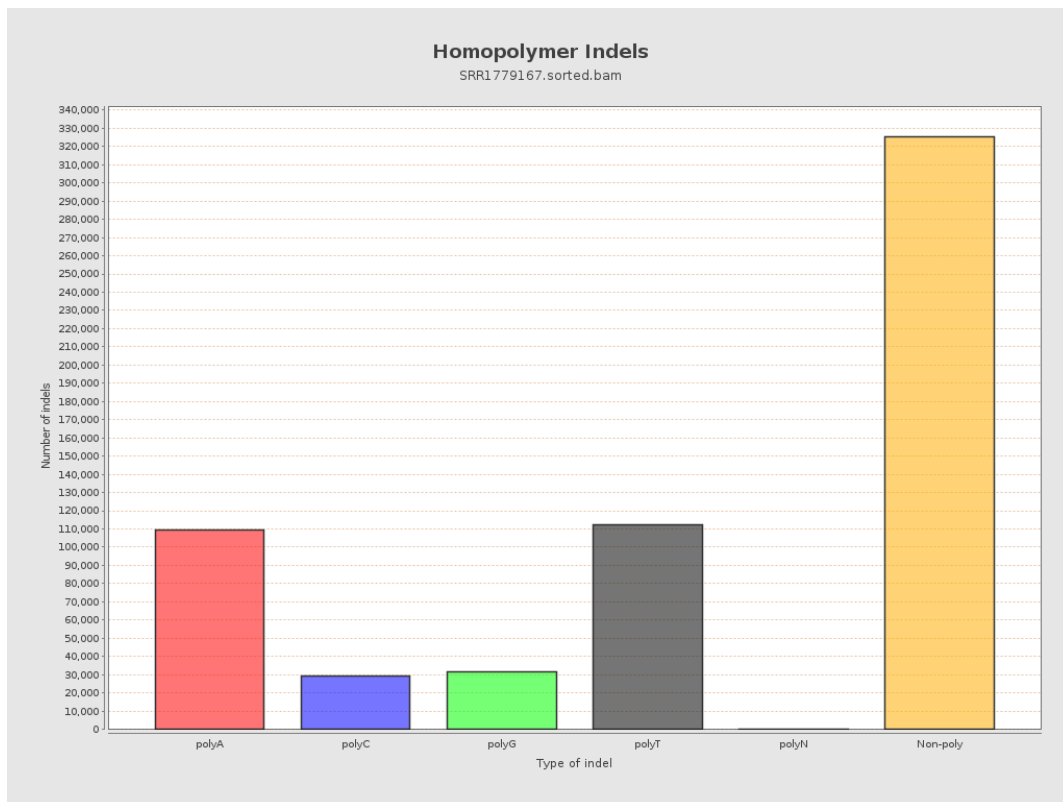
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



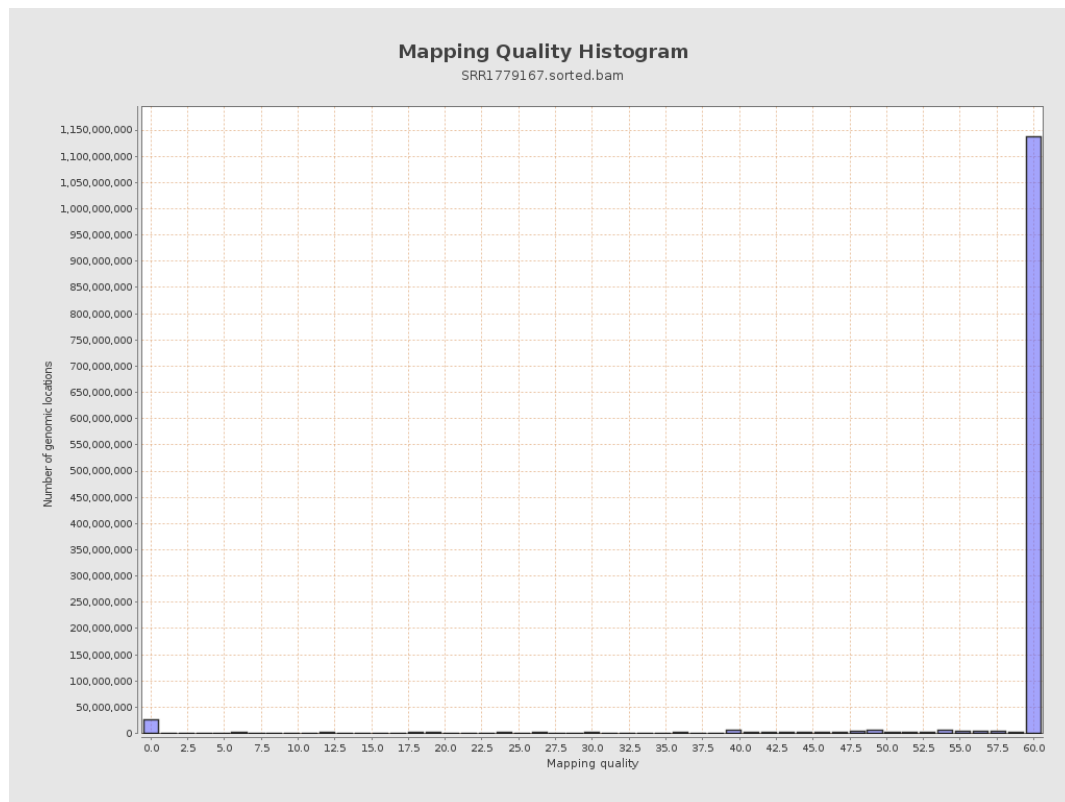
11. Results : Homopolymer Indels



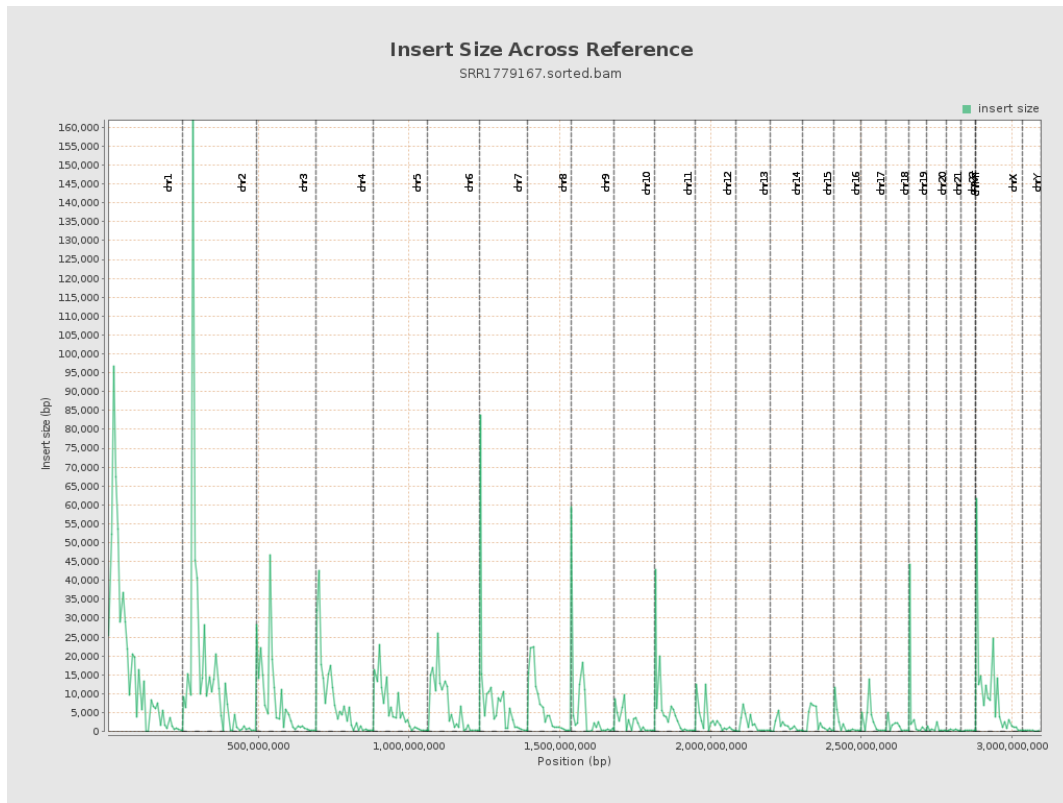
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

