

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 15:33:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779385.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_SRR1779385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779385_1.fastq.gz SRR1779385_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 15:33:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,652,806
Mapped reads	11,421,495 / 90.27%
Unmapped reads	1,231,311 / 9.73%
Mapped paired reads	11,421,495 / 90.27%
Mapped reads, first in pair	5,783,516 / 45.71%
Mapped reads, second in pair	5,637,979 / 44.56%
Mapped reads, both in pair	11,233,702 / 88.78%
Mapped reads, singletons	187,793 / 1.48%
Secondary alignments	0
Supplementary alignments	175,547 / 1.39%
Read min/max/mean length	30 / 80 / 80.49
Duplicated reads (estimated)	6,896,958 / 54.51%
Duplication rate	12.17%
Clipped reads	1,136,081 / 8.98%

2.2. ACGT Content

Number/percentage of A's	272,209,658 / 30.19%
Number/percentage of C's	176,615,472 / 19.59%
Number/percentage of T's	271,427,692 / 30.1%
Number/percentage of G's	181,164,683 / 20.09%
Number/percentage of N's	198,917 / 0.02%

GC Percentage	39.68%
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2.3. Coverage

Mean	0.2913
Standard Deviation	62.2281

2.4. Mapping Quality

Mean Mapping Quality	50.92
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2.5. Insert size

Mean	49,931.7
Standard Deviation	2,038,796.56
P25/Median/P75	167 / 221 / 285

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	3,670,513
Insertions	71,482
Mapped reads with at least one insertion	0.62%
Deletions	102,648
Mapped reads with at least one deletion	0.89%
Homopolymer indels	48%

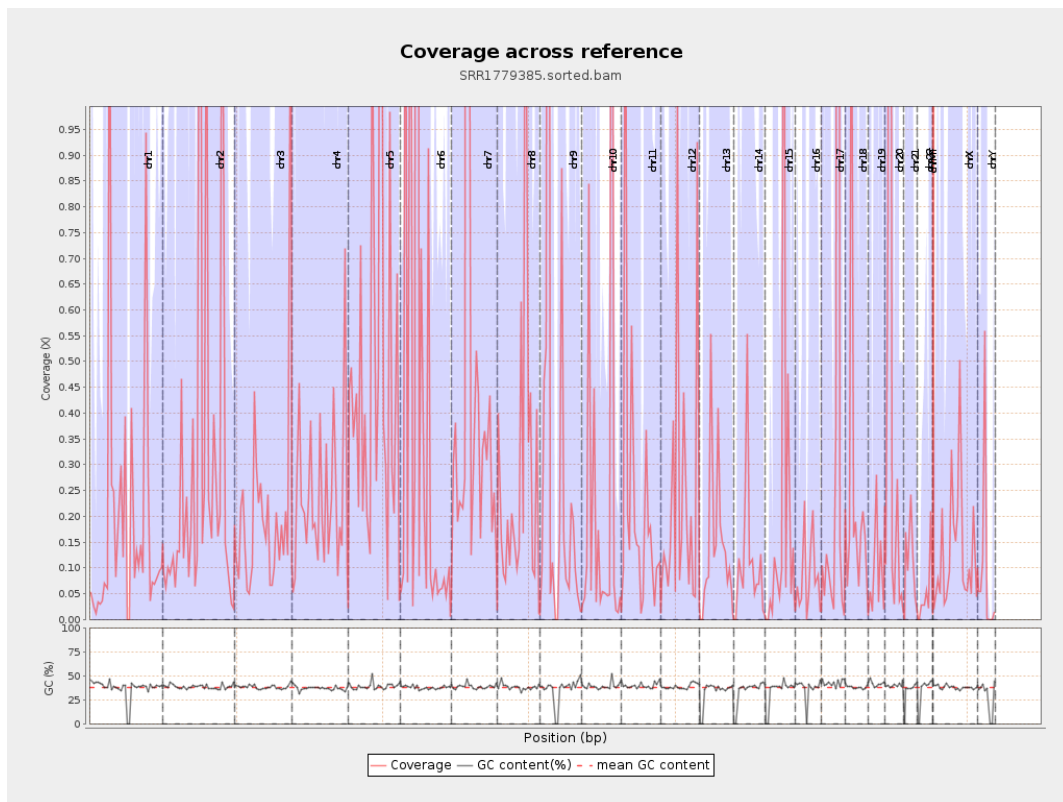
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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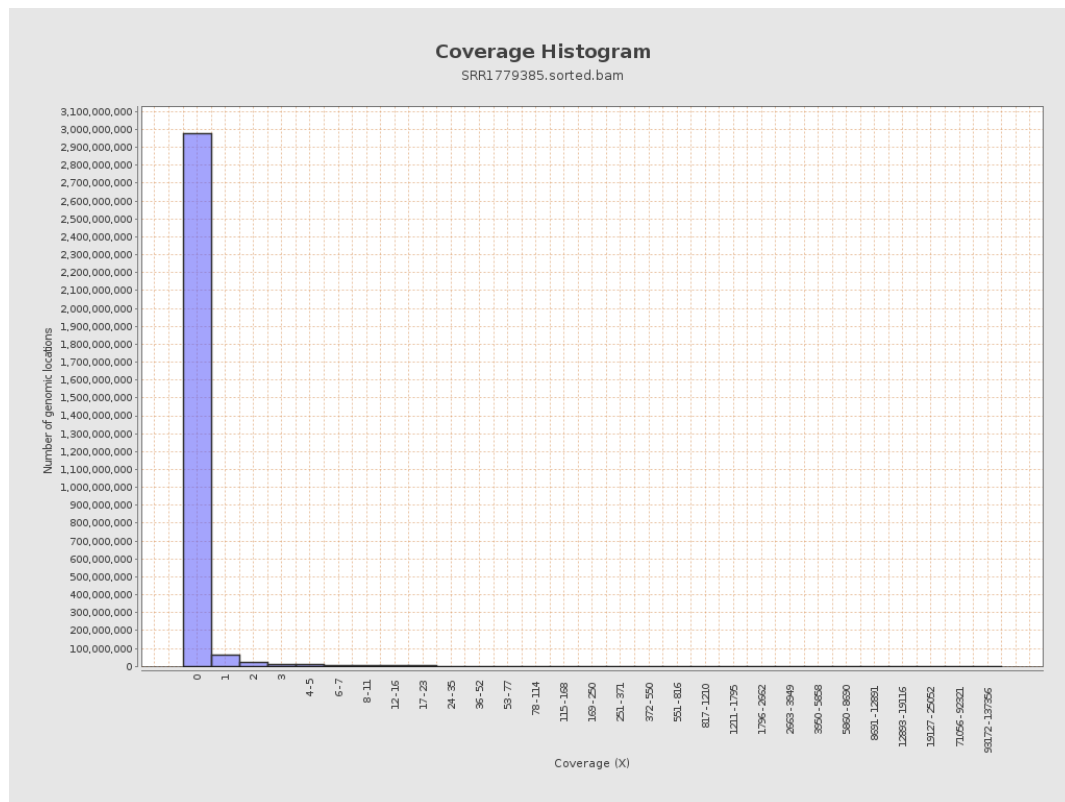
		bases	coverage	deviation
chr1	249250621	46397076	0.1861	20.9444
chr2	243199373	73826870	0.3036	31.2044
chr3	198022430	42816304	0.2162	14.3659
chr4	191154276	45578489	0.2384	12.0996
chr5	180915260	87768350	0.4851	41.063
chr6	171115067	122468528	0.7157	228.5616
chr7	159138663	103184975	0.6484	75.0084
chr8	146364022	40565506	0.2772	13.165
chr9	141213431	52482958	0.3717	22.8449
chr10	135534747	34550548	0.2549	56.2001
chr11	135006516	31082209	0.2302	22.2303
chr12	133851895	31678269	0.2367	19.3052
chr13	115169878	16593133	0.1441	16.3594
chr14	107349540	12552328	0.1169	5.3983
chr15	102531392	22326038	0.2177	27.974
chr16	90354753	7346832	0.0813	2.142
chr17	81195210	36179511	0.4456	61.9402
chr18	78077248	21205581	0.2716	36.6382
chr19	59128983	5788132	0.0979	3.9998
chr20	63025520	32841809	0.5211	59.1587
chr21	48129895	5275204	0.1096	0.9962
chr22	51304566	2681283	0.0523	12.8547
chrMT	16571	551112	33.2576	15.3976
chrX	155270560	20032301	0.129	13.3955

chrY	59373566	6039197	0.1017	2.4531
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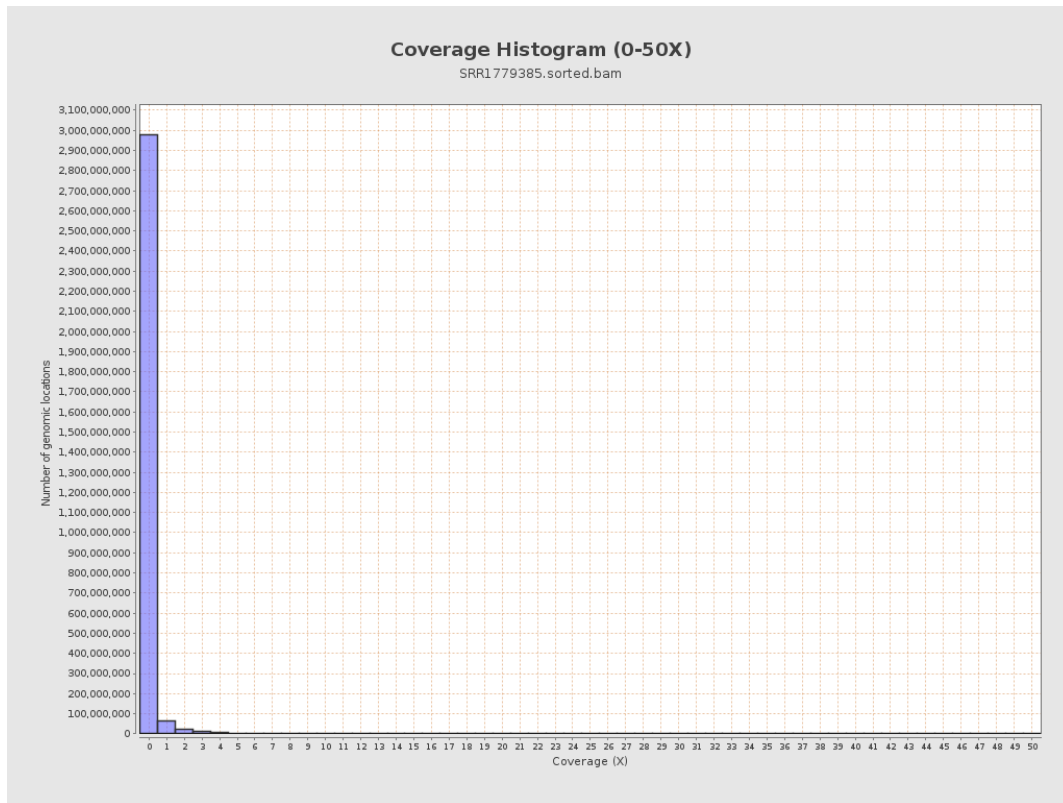
3. Results : Coverage across reference



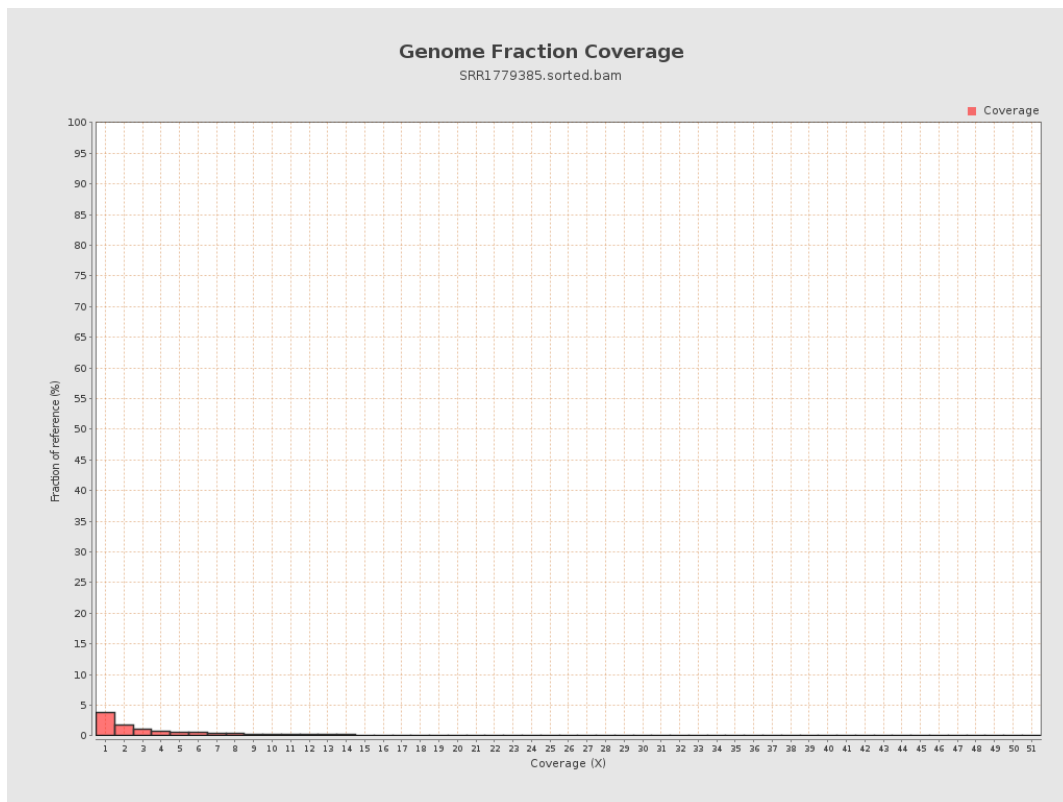
4. Results : Coverage Histogram



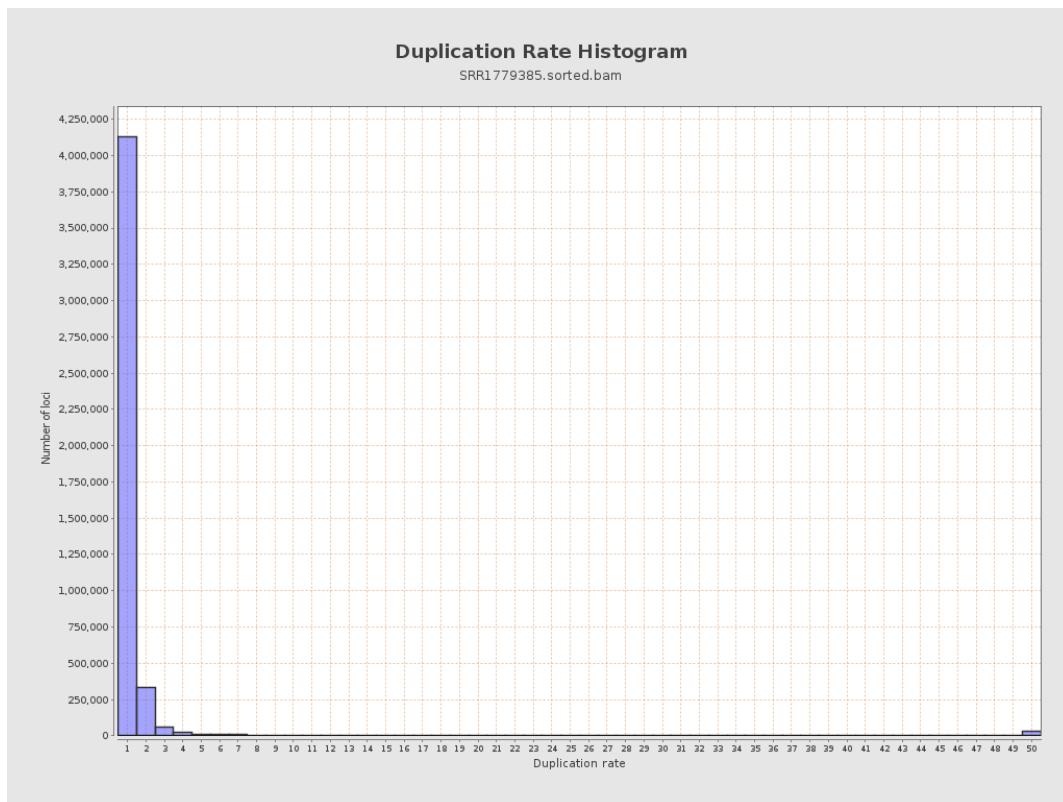
5. Results : Coverage Histogram (0-50X)



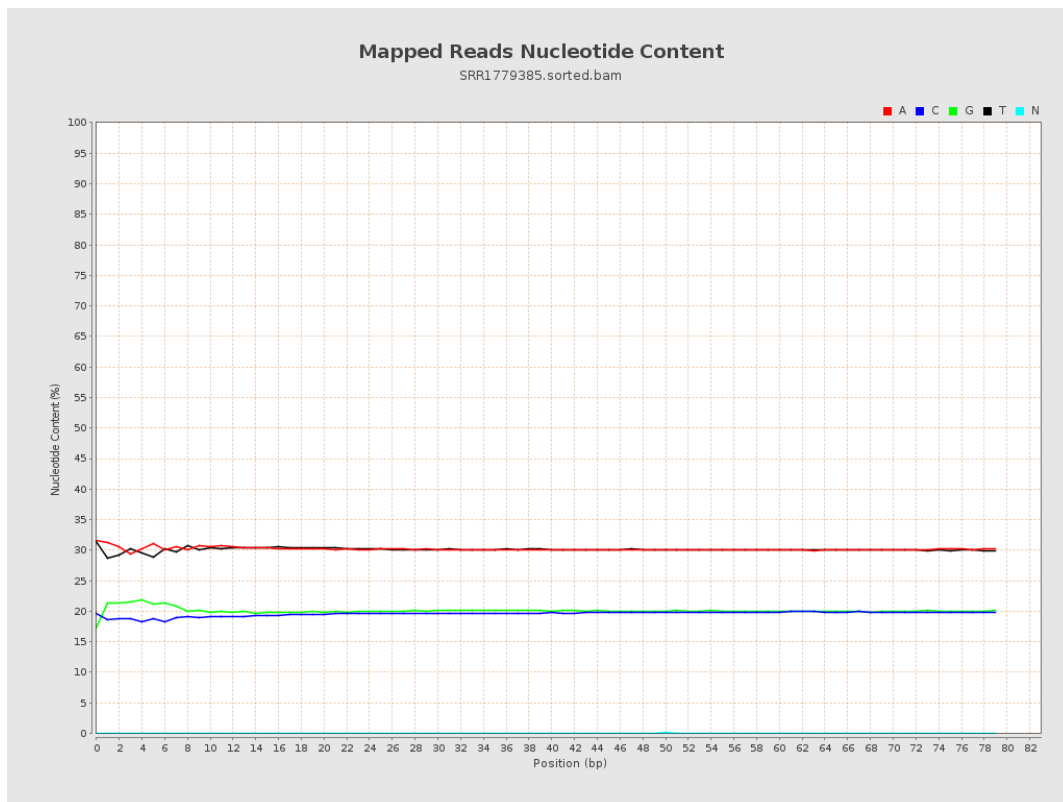
6. Results : Genome Fraction Coverage



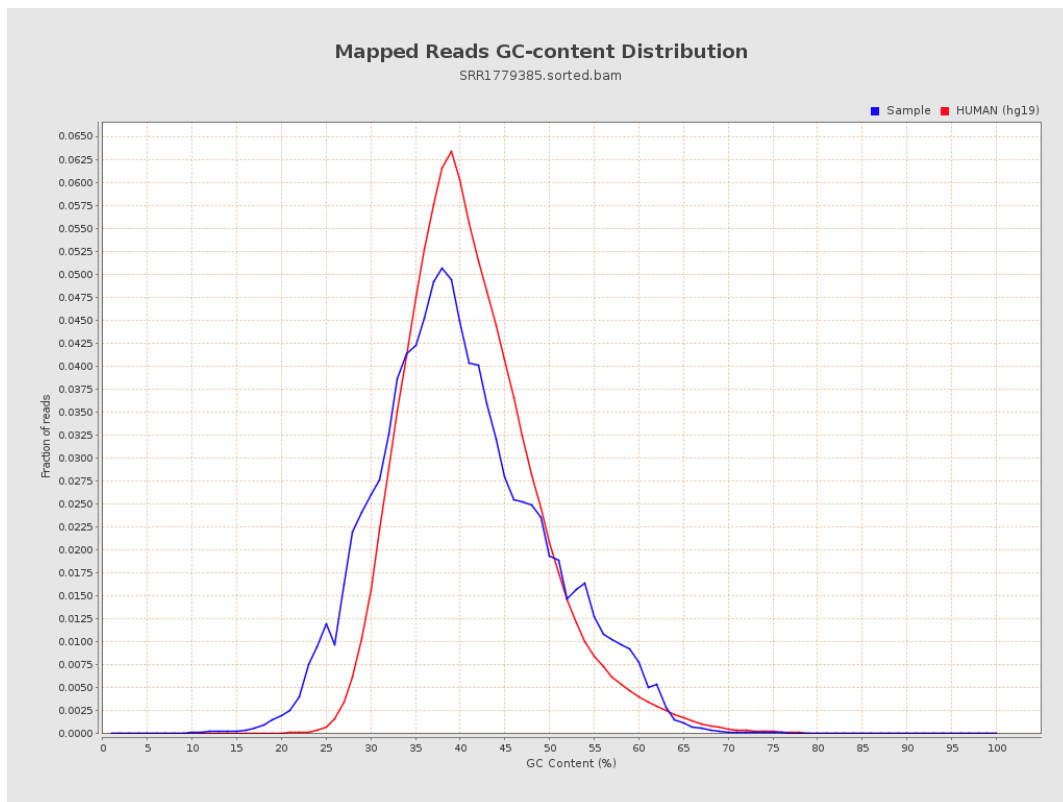
7. Results : Duplication Rate Histogram



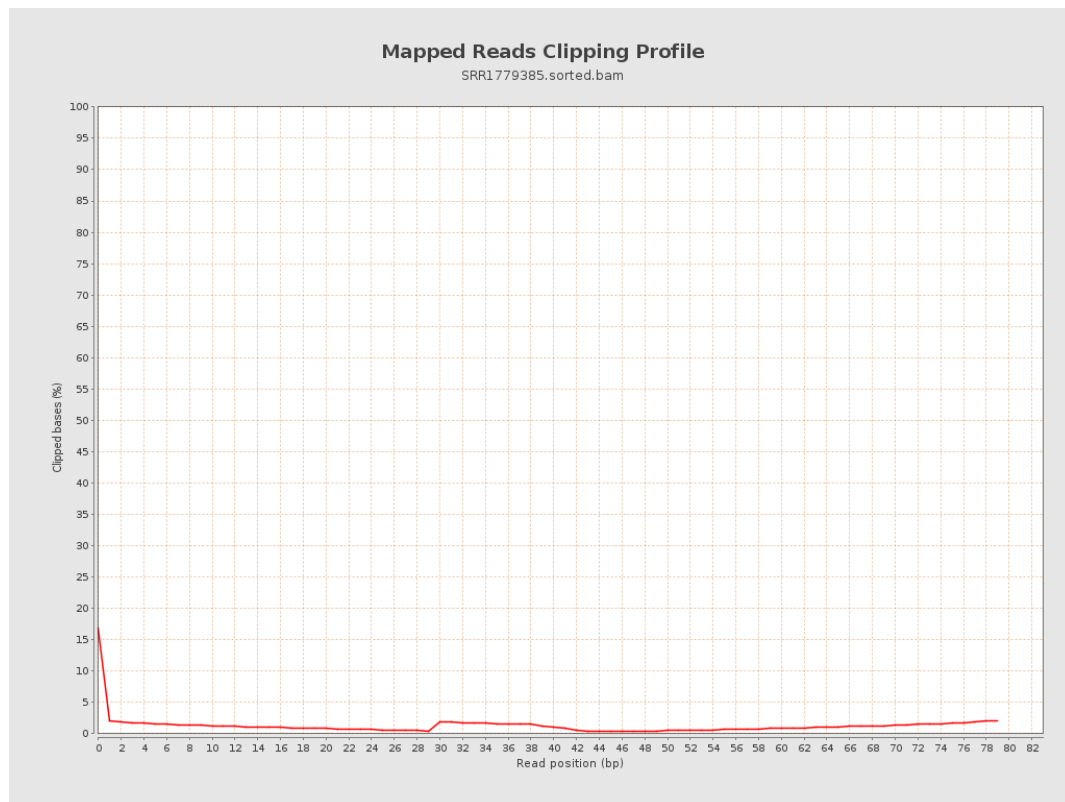
8. Results : Mapped Reads Nucleotide Content



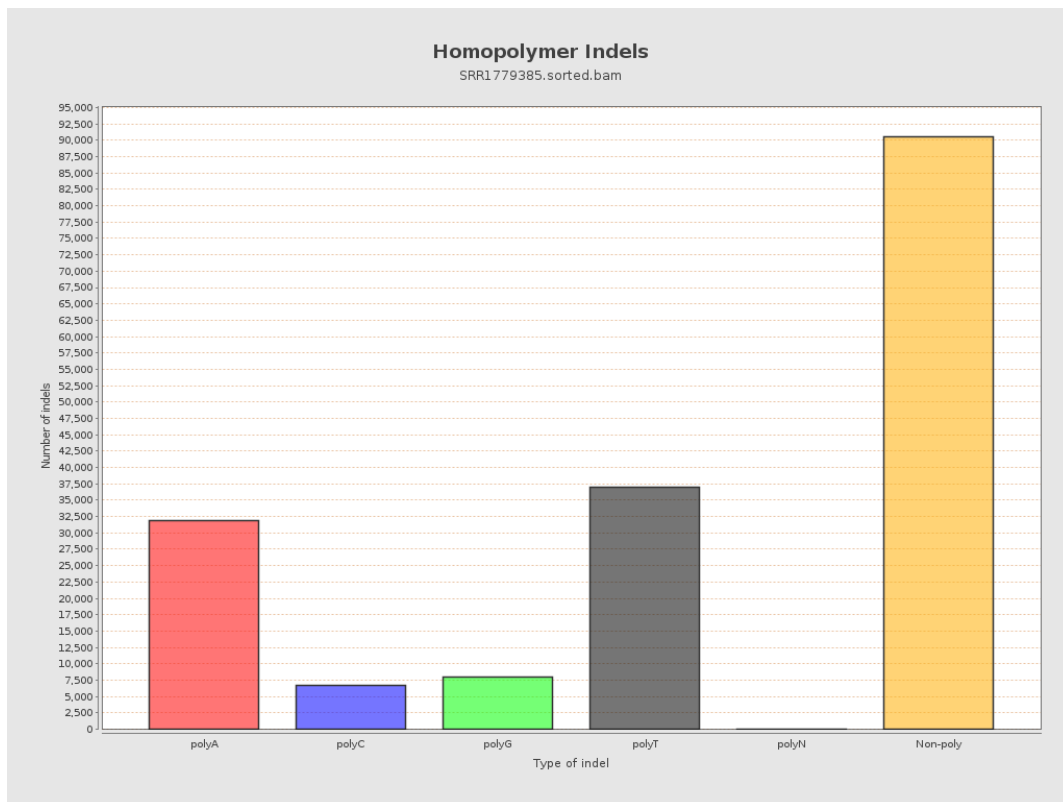
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



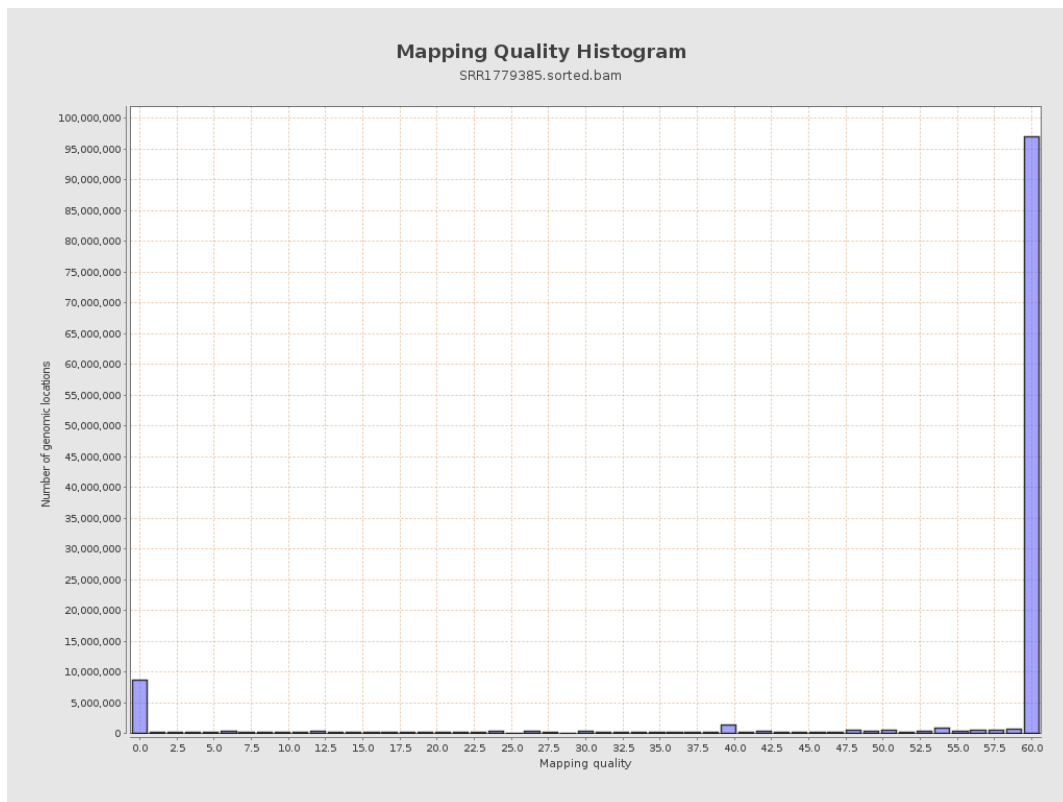
11. Results : Homopolymer Indels



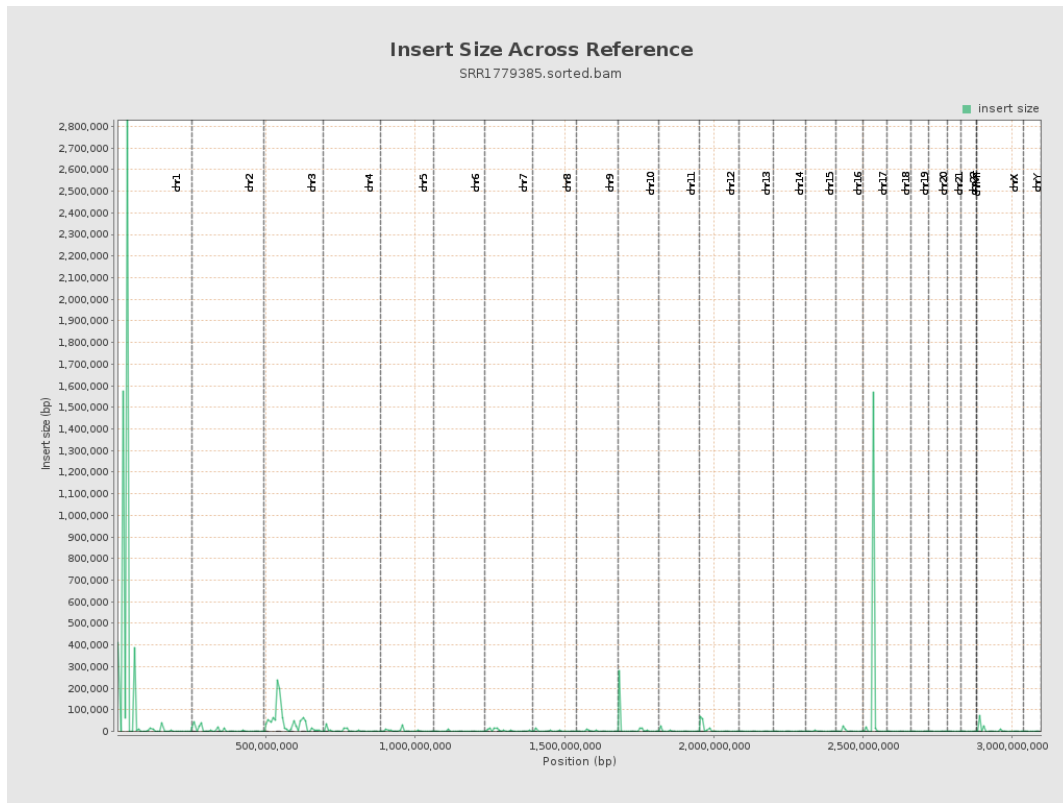
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

