

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 14:52:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779382.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_SRR1779382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779382_1.fastq.gz SRR1779382_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 14:52:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,215,850
Mapped reads	15,561,641 / 95.97%
Unmapped reads	654,209 / 4.03%
Mapped paired reads	15,561,641 / 95.97%
Mapped reads, first in pair	7,824,623 / 48.25%
Mapped reads, second in pair	7,737,018 / 47.71%
Mapped reads, both in pair	15,444,398 / 95.24%
Mapped reads, singletons	117,243 / 0.72%
Secondary alignments	0
Supplementary alignments	64,305 / 0.4%
Read min/max/mean length	30 / 80 / 80.14
Duplicated reads (estimated)	746,282 / 4.6%
Duplication rate	4.49%
Clipped reads	729,380 / 4.5%

2.2. ACGT Content

Number/percentage of A's	373,484,944 / 30.21%
Number/percentage of C's	244,493,891 / 19.77%
Number/percentage of T's	368,949,521 / 29.84%
Number/percentage of G's	249,263,496 / 20.16%
Number/percentage of N's	271,740 / 0.02%

GC Percentage	39.93%
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2.3. Coverage

Mean	0.3995
Standard Deviation	1.6941

2.4. Mapping Quality

Mean Mapping Quality	46.22
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2.5. Insert size

Mean	123,389.51
Standard Deviation	3,244,387.34
P25/Median/P75	136 / 180 / 233

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,975,479
Insertions	110,657
Mapped reads with at least one insertion	0.7%
Deletions	129,637
Mapped reads with at least one deletion	0.82%
Homopolymer indels	47.24%

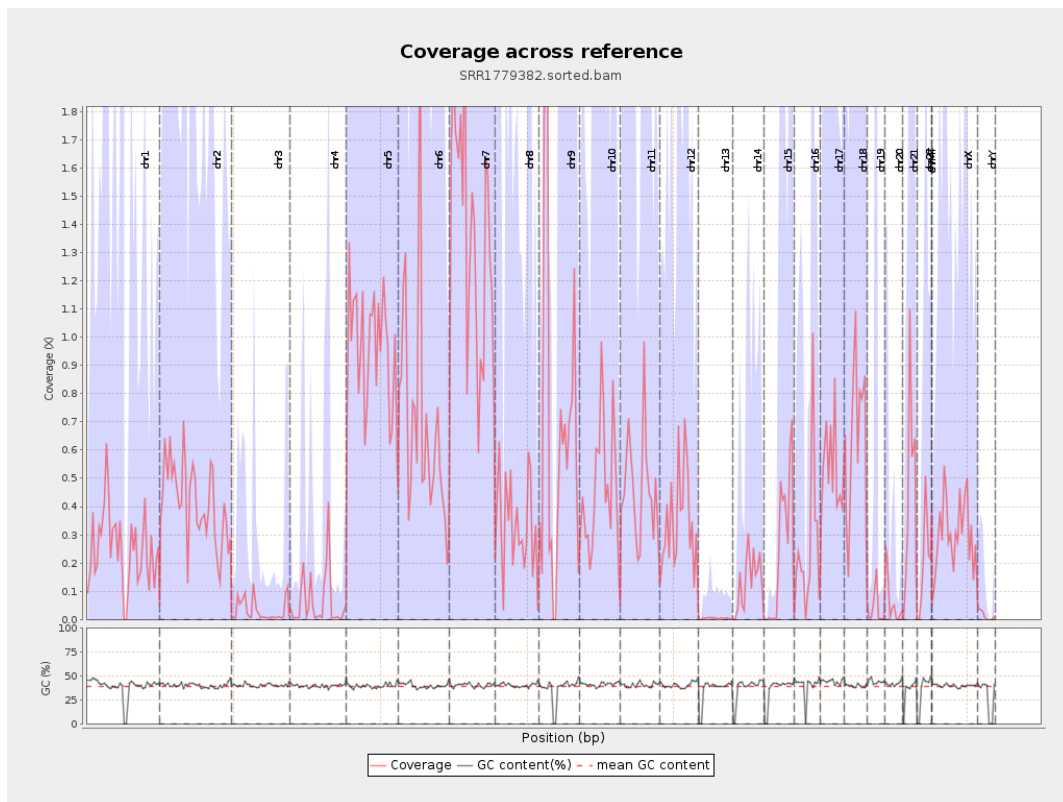
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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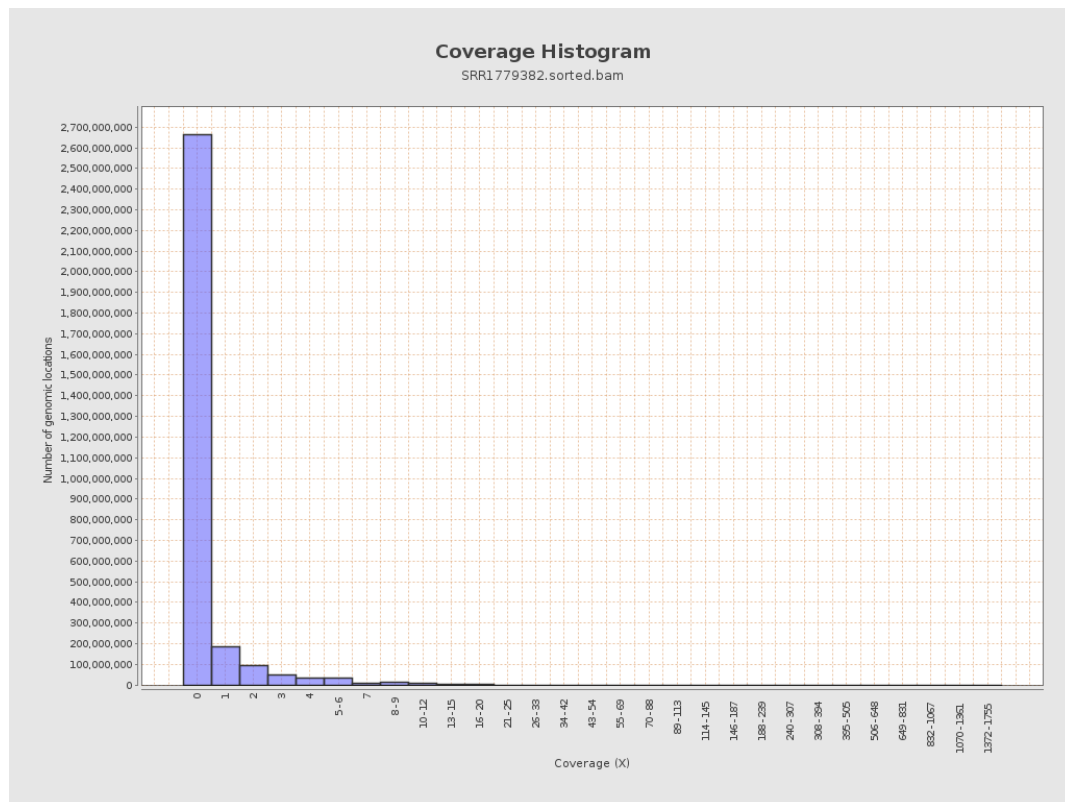
		bases	coverage	deviation
chr1	249250621	62651524	0.2514	2.1821
chr2	243199373	100534916	0.4134	1.405
chr3	198022430	6542078	0.033	0.4106
chr4	191154276	11641975	0.0609	0.5382
chr5	180915260	170536814	0.9426	2.0863
chr6	171115067	118082917	0.6901	2.1797
chr7	159138663	213132739	1.3393	3.3363
chr8	146364022	49009033	0.3348	1.3565
chr9	141213431	89789229	0.6358	2.0991
chr10	135534747	63484558	0.4684	1.6257
chr11	135006516	62526034	0.4631	1.6523
chr12	133851895	45746370	0.3418	1.2857
chr13	115169878	493206	0.0043	0.1013
chr14	107349540	14003342	0.1304	0.7013
chr15	102531392	25078346	0.2446	1.1865
chr16	90354753	21572386	0.2388	1.0662
chr17	81195210	43531268	0.5361	2.3675
chr18	78077248	51360951	0.6578	1.948
chr19	59128983	2171639	0.0367	1.5744
chr20	63025520	4259437	0.0676	0.5775
chr21	48129895	22163187	0.4605	1.5137
chr22	51304566	10361190	0.202	0.9591
chrMT	16571	823	0.0497	0.2946
chrX	155270560	47234456	0.3042	1.1369

chrY	59373566	825360	0.0139	0.2019
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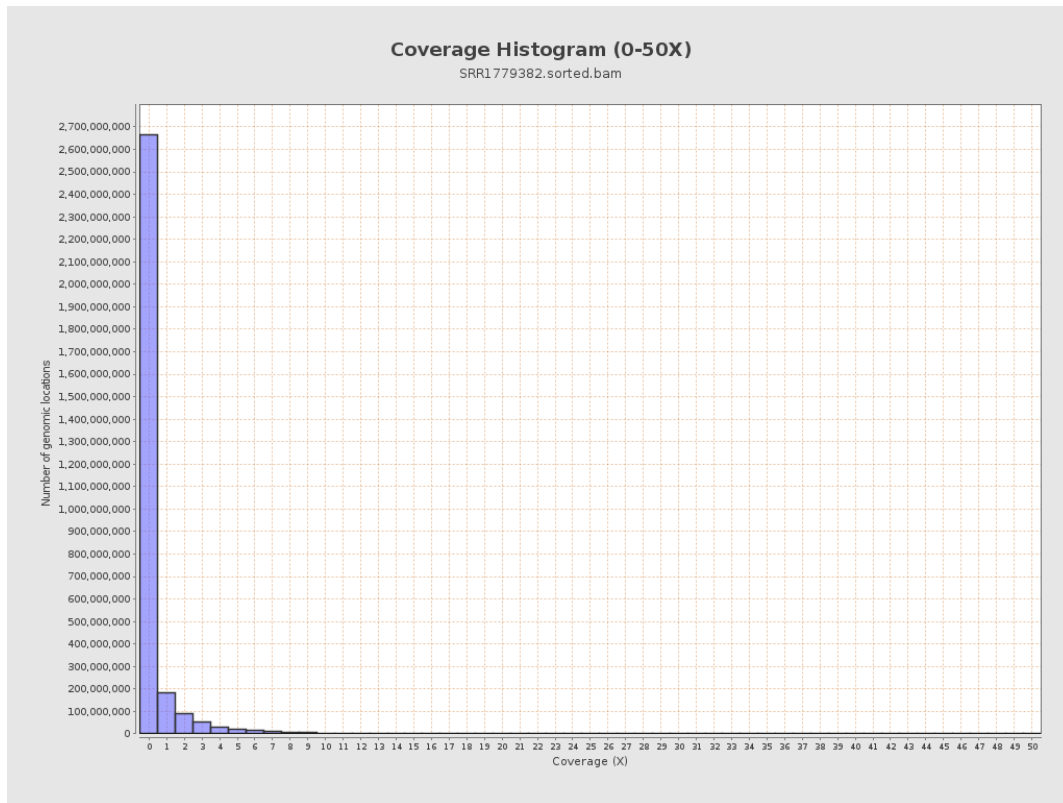
3. Results : Coverage across reference



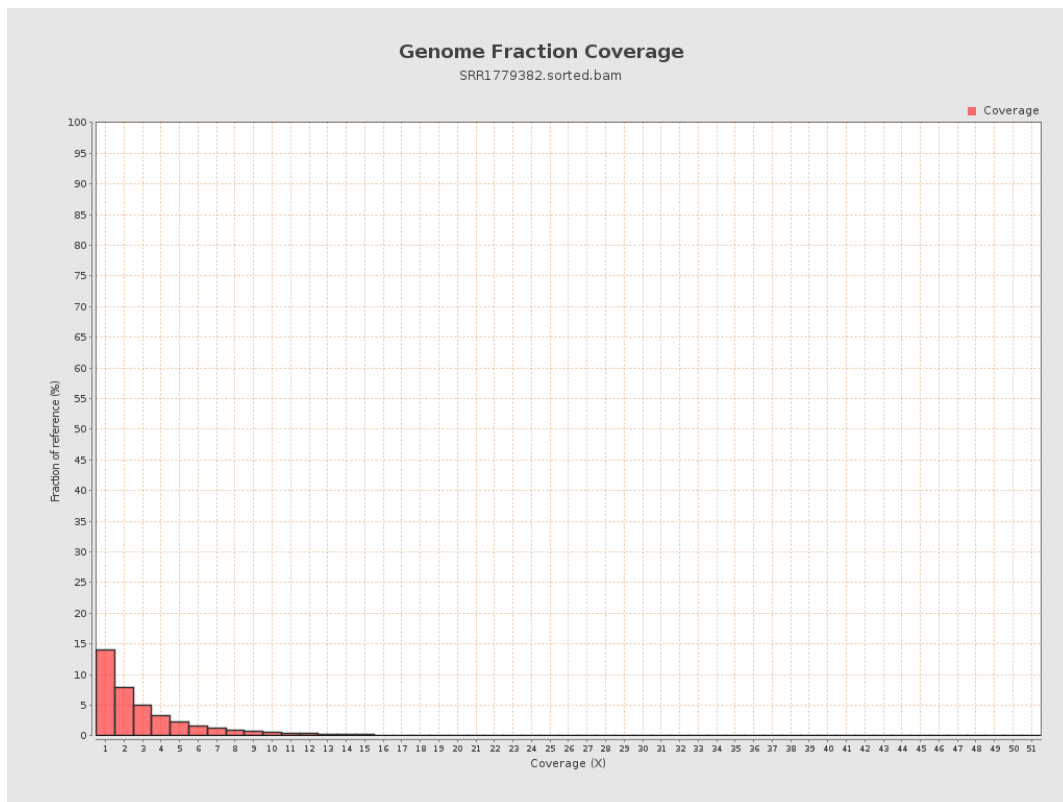
4. Results : Coverage Histogram



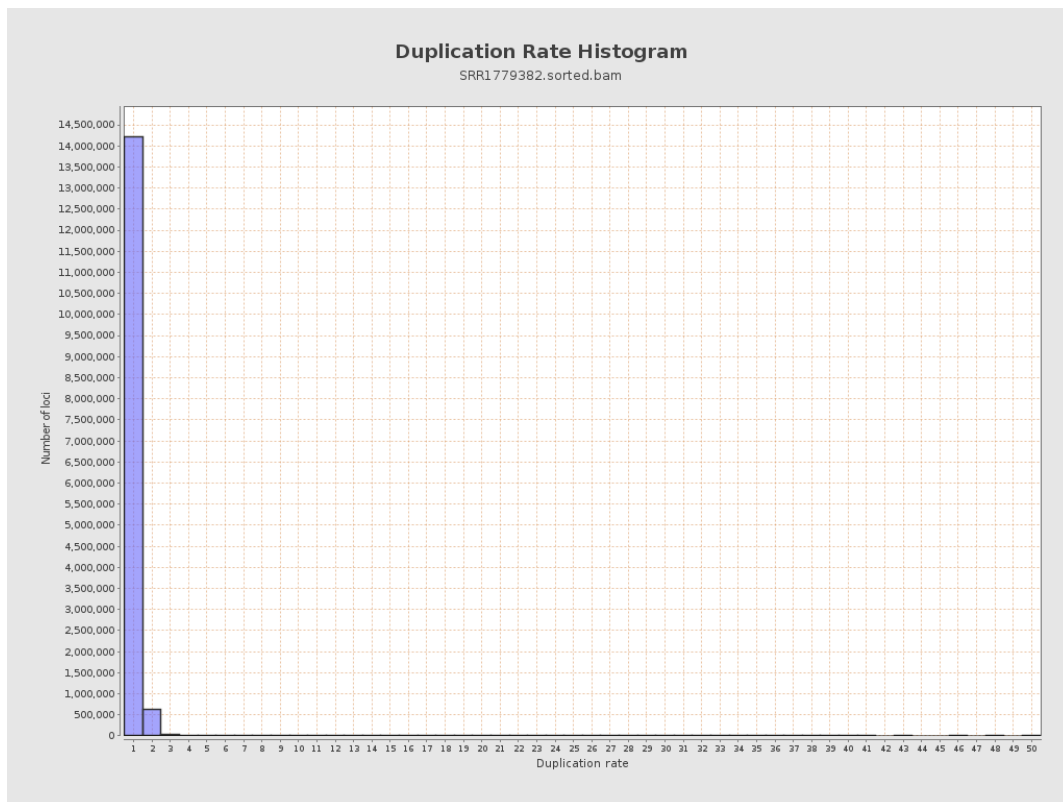
5. Results : Coverage Histogram (0-50X)



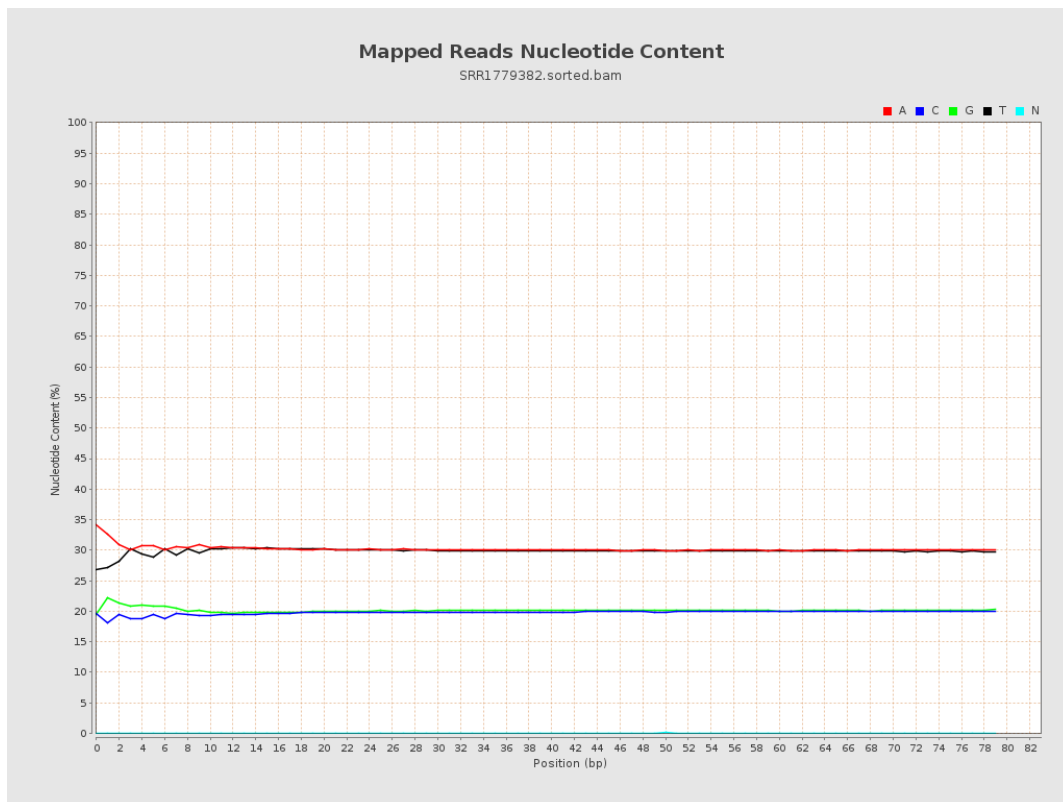
6. Results : Genome Fraction Coverage



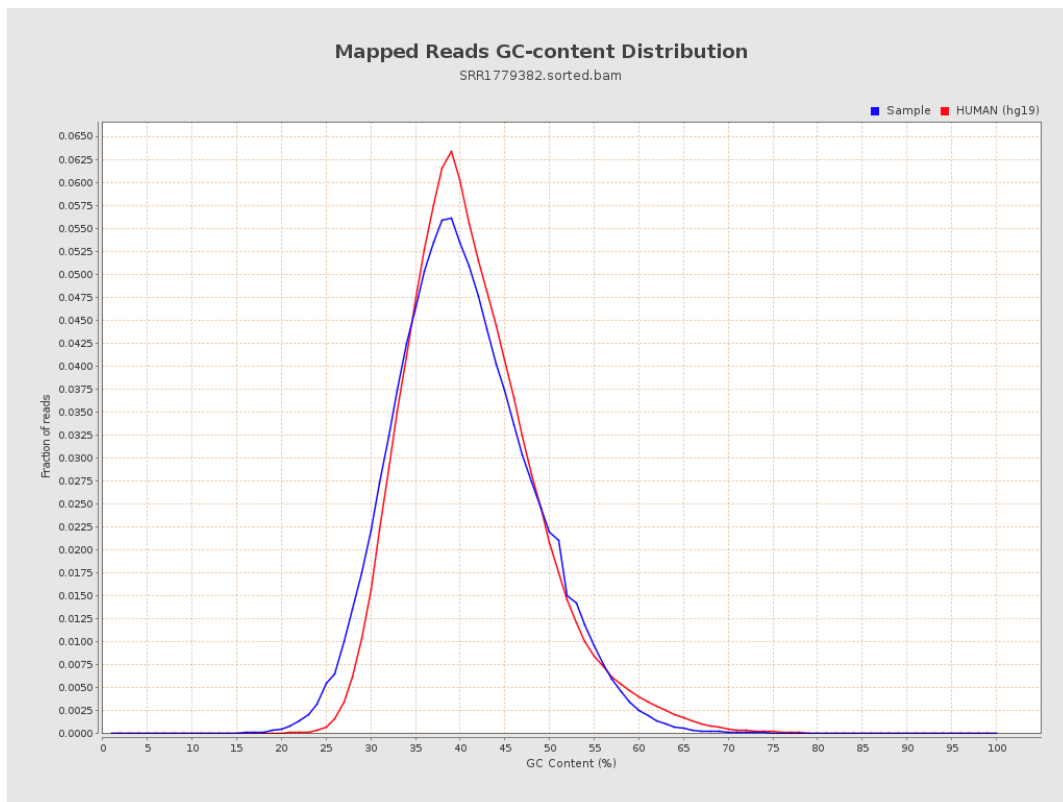
7. Results : Duplication Rate Histogram



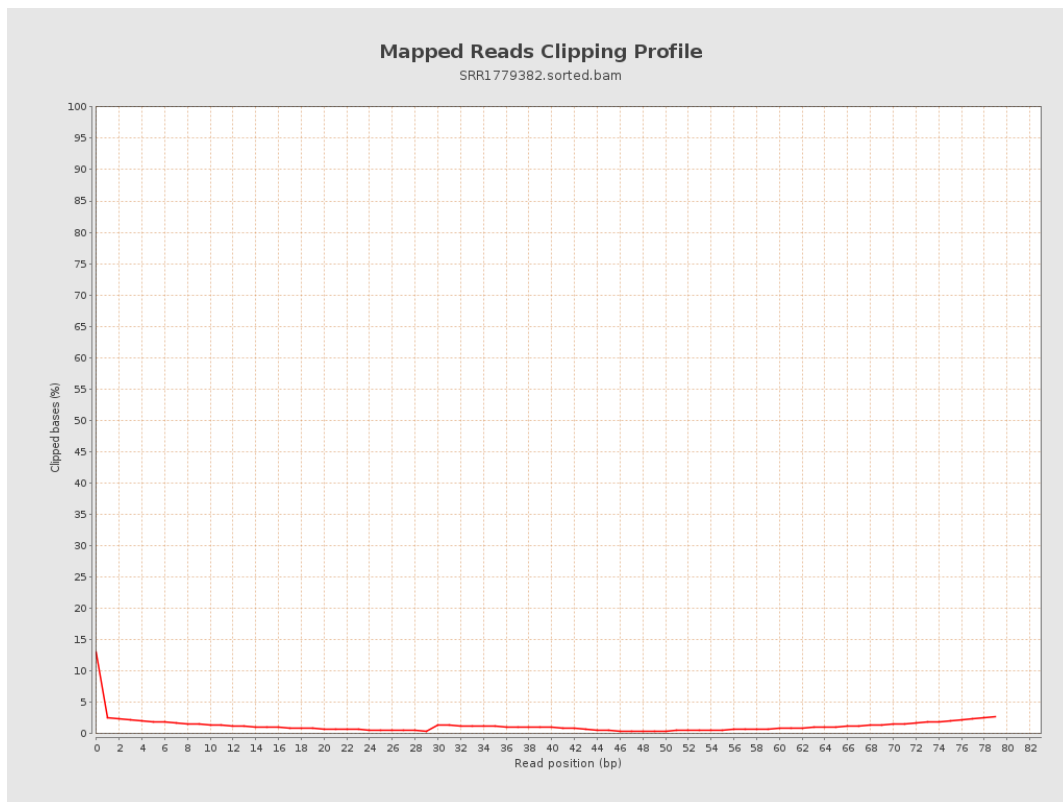
8. Results : Mapped Reads Nucleotide Content



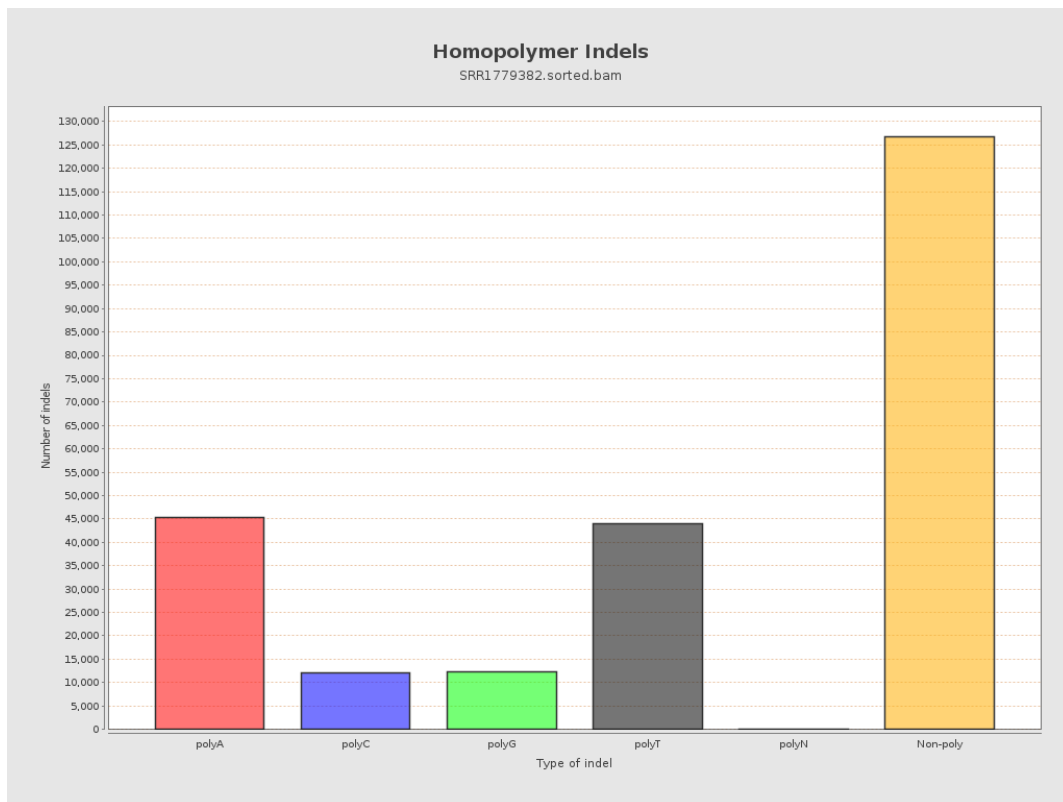
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



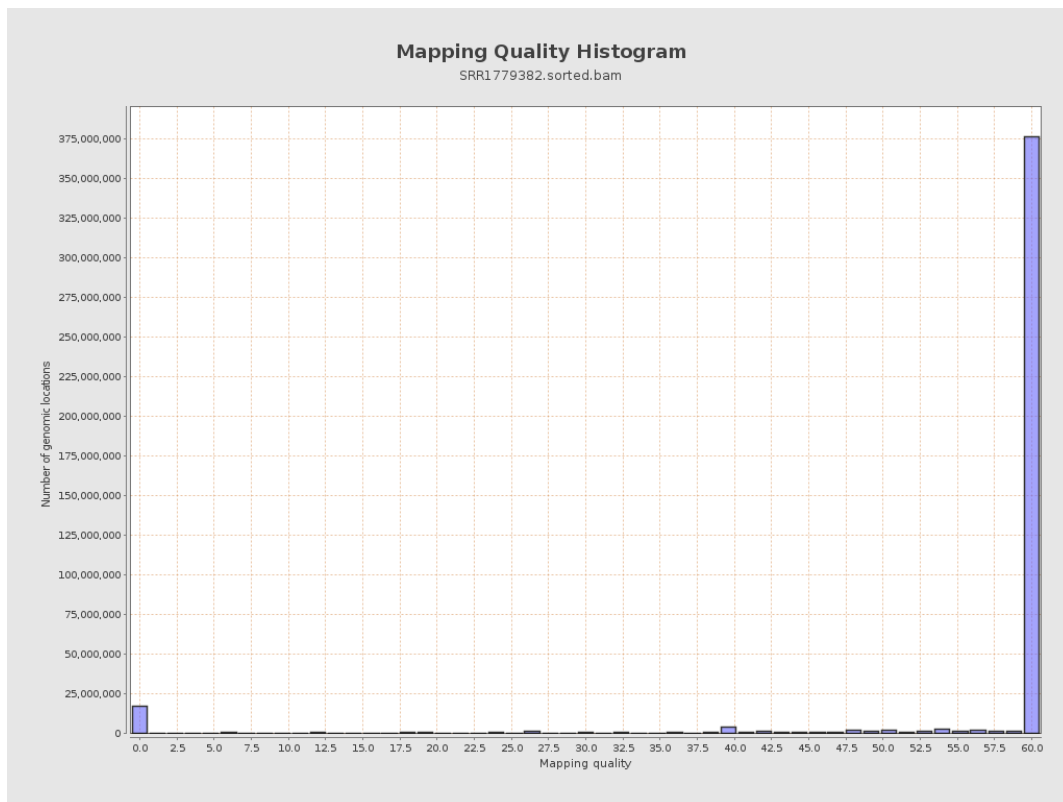
11. Results : Homopolymer Indels



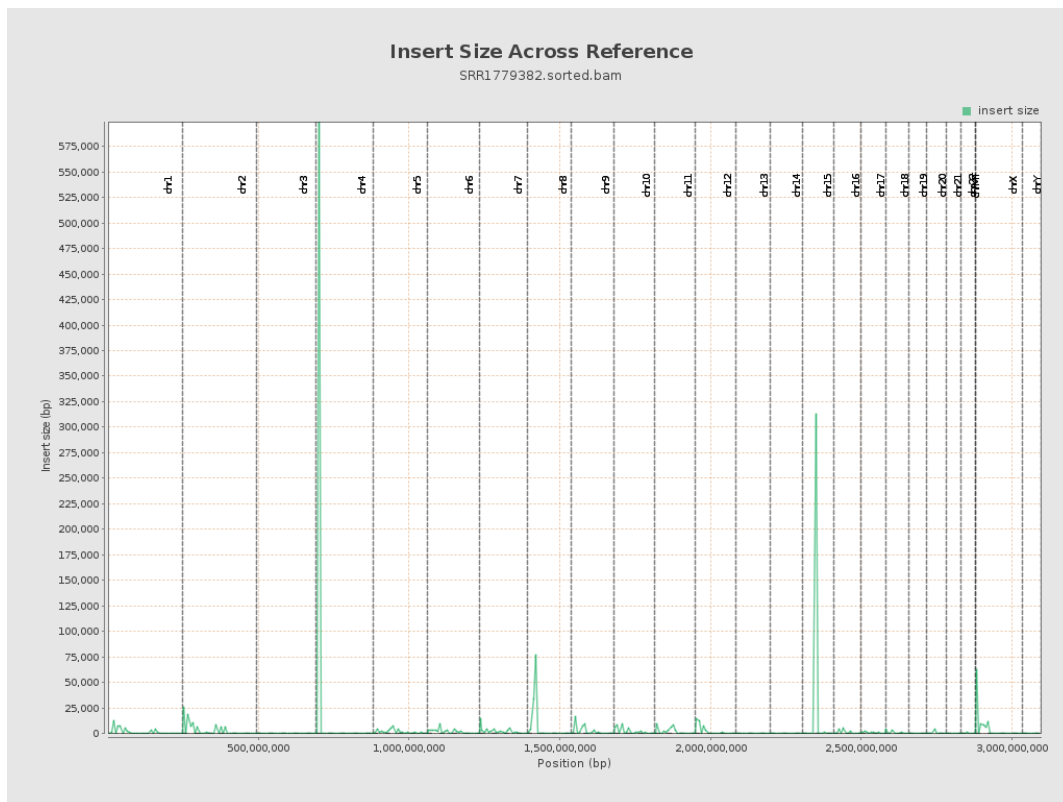
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

