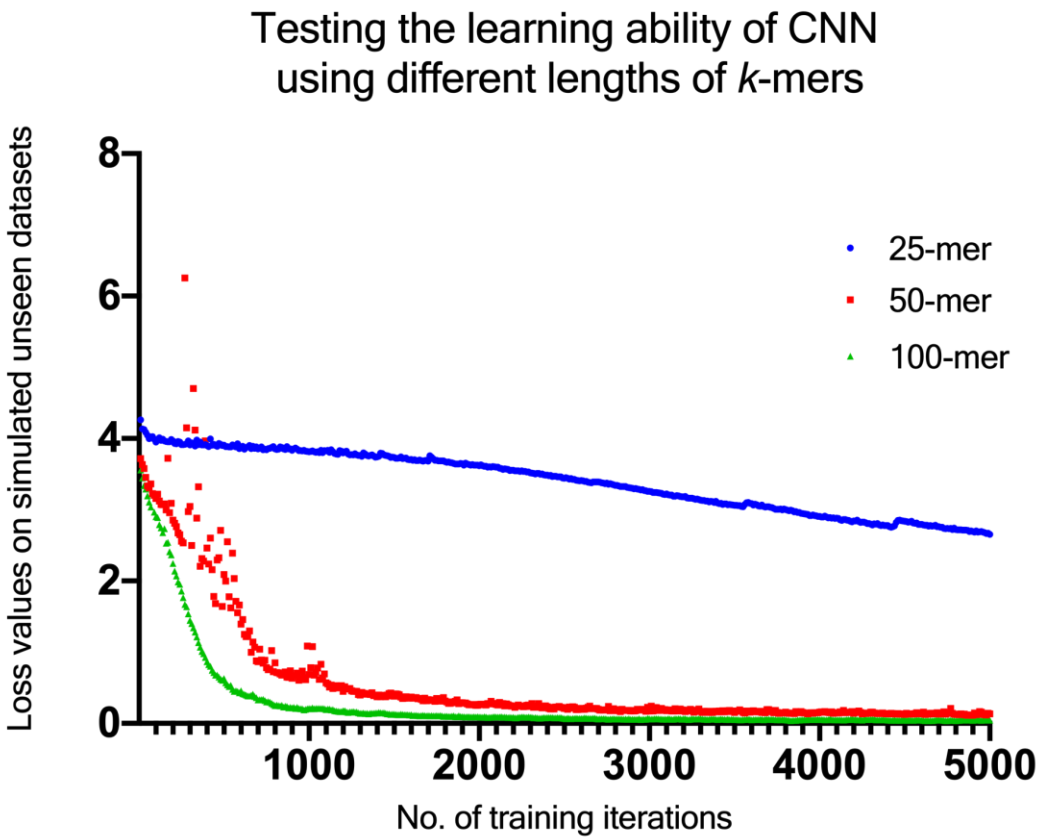
Additional file 1 of A Multi-task CNN Learning Model for Taxonomic Assignment of Human Viruses



Additional file 1 figure S1. Testing the learning ability of MT-CNN using different lengths of *k*-mers. Three datasets were generated from 434 human viral genomes in ICTV as 25-mers, 50-mers and 100-mers, respectively. The datasets were split into training and test datasets. Three CNN models were trained using the same architecture and parameters for 5000 iterations (batch size equals to 512). The loss values on test datasets were recorded.

Additional file 1 table S1. Transformation of percentage of assigned reads to discrete variables [a] for the naive Bayesian network.

The percentage of assigned reads	Transformed discrete variables
<1%	0
[1%, 3%)	1
[3%, 5%)	2
[5%, 10%)	3

[10%, 20%)	4
[20%, 30%)	5
[30%, 50%)	6
>=50%	7

[a] The percentage of assigned reads was transformed to 8 discrete variables.

Additional file 1 table S2. The insertion, deletion, and mismatch rates for simulating 50-mers using Mason2.

	Insertion rate	Deletion rate	Mismatch rate
Dataset 1	0.001	0.001	0.004
Dataset 2	0.00125	0.00125	0.005
Dataset 3	0.0015	0.0015	0.006
Dataset 4	0.00175	0.00175	0.007
Dataset 5	0.002	0.002	0.008
Dataset 6	0.00225	0.00225	0.009
Dataset 7	0.0025	0.0025	0.01
Dataset 8	0.00275	0.00275	0.011
Dataset 9	0.003	0.003	0.012