## **Supplementary Materials**

## For article:

Incorporating label correlations into deep neural networks to classify protein subcellular location patterns in immunohistochemistry images

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Immunofluorescence subcellular location	Mapped to major subcellular location		
Aggresome			
Cytoplasmic bodies			
Cytosol	Cytoplasm		
Rods & rings			
Cell junctions			
Plasma membrane	Plasma membrane		
Golgi apparatus	Golgi apparatus		
Mitochondria	Mitochondria		
Nuclear bodies			
Nuclear membrane			
Nuclear speckles			
Nucleoli	Nucleus		
Nucleoli fibrillar center			
Nucleoplasm			
Nucleus			

**Table S1**Mapping subcellular locations of immunofluorescence images in the human protein atlasto five major subcellular locations.

Beam size	Subset accuracy	Accuracy	Precision	Recall	F1-score
1	0.575	0.665	0.751	0.667	0.694
2	0.580	0.670	0.757	0.675	0.701
3	0.581	0.671	0.757	0.675	0.701

**Table S2**Experimental results of using different beam sizes.

Iteration number	Subset accuracy	Accuracy	Precision	Recall	F1-score
<i>M</i> =0 *	0.553	0.652	0.719	0.684	0.686
<i>M</i> =1	0.575	0.673	0.741	0.703	0.707
<i>M</i> =2	0.585	0.676	0.743	0.699	0.707
<i>M</i> =3 *	0.594	0.682	0.748	0.705	0.713
<i>M</i> =4	0.582	0.675	0.742	0.704	0.709

**Table S3** Experimental results of screening the dataset.

\* M=0: CNN without data screening; M=3: deep model used as encoder in laceDNN.

Method <sup>†</sup>	Subset	Accuracy	Precision	Recall	F1-score
	accuracy				
CNN	0.554	0.652	0.719	0.684	0.686
CNN <sup>S</sup>	0.594	0.682	0.749	0.705	0.713
CNN+LSTM <sup>WP</sup>	0.563	0.654	0.744	0.654	0.684
CNN+LSTM <sup>p</sup>	0.581	0.671	0.758	0.676	0.701
Liu et al. (CNN+LSTM)	0.398	0.422	0.445	0.422	0.429
Islam et al. (CNN+LSTM)	0.447	0.504	0.572	0.506	0.527
Wang et al. (CNN+LSTM)	0.559	0.653	0.744	0.652	0.683
laceDNN (CNN <sup>S</sup> +LSTM)	0.614	0.707	0.798	0.709	0.738

**Table S4**Experimental results of whether incorporating label correlations. The results areobtained by five-fold cross validation.

<sup>†</sup> CNN: CNN trained on the initial dataset. CNN<sup>S</sup>: CNN fine-tuned with screened dataset. LSTM<sup>WP</sup>: LST M without using the predicted probabilities. LSTM<sup>P</sup>: LSTM incorporating the label correlations (predicted probabilities). laceCNN: our final proposed method.