

## **Similar Colors Analysis based on Deep Learning (SCAD) for Multiplex Digital PCR *via* Single Fluorescent Channel**

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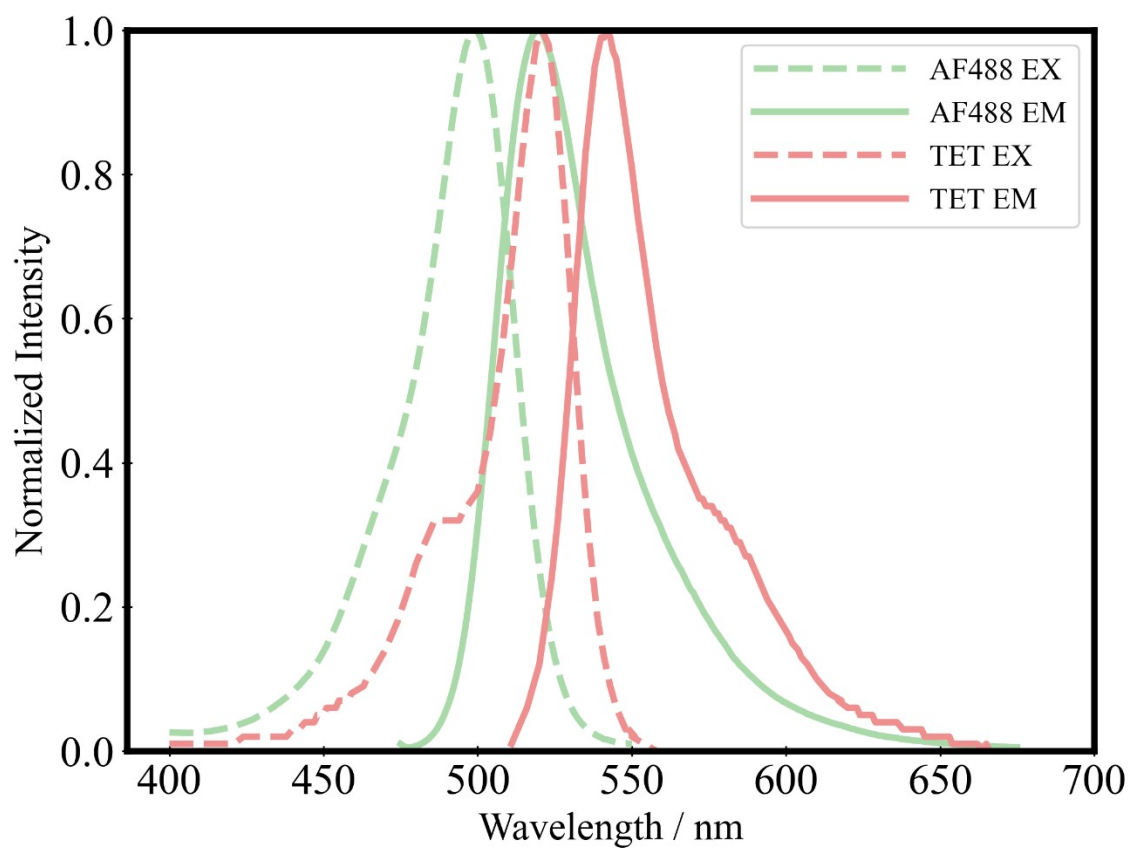
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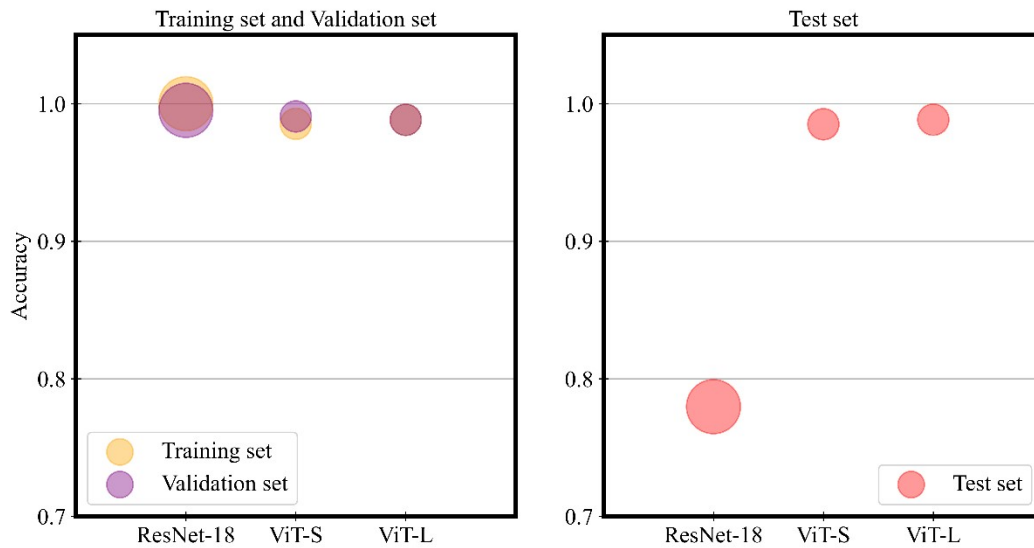


**Figure S1. Excitation (EX) and emission (EM) spectrums of AF488 and TET.**

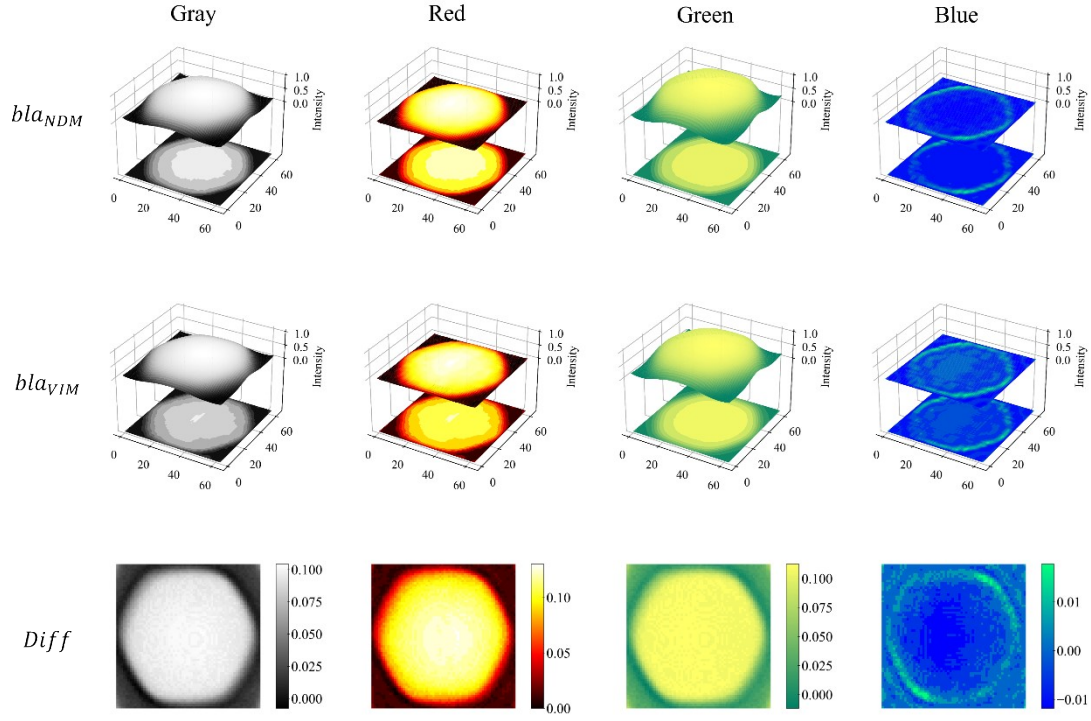
**Table S1. dPCR reaction system design**

<i>bla<sub>NDM</sub></i>	<b>Gene (85)</b>	CACACCAGTGACAATATCACCGTTGGGATCGACGGCACCGAC ATCGCTTTTGGTGGCTGCCTGATCAAGGACAGCAAGGCCAAGT
	<b>NDM-F</b>	CACACCAGTGACAATATCACCGTTG
	<b>NDM-R</b>	ACTTGGCCTTGCTGTCCTTGAT
	<b>Probe</b>	TCGACGGCACCGACATCGCTT

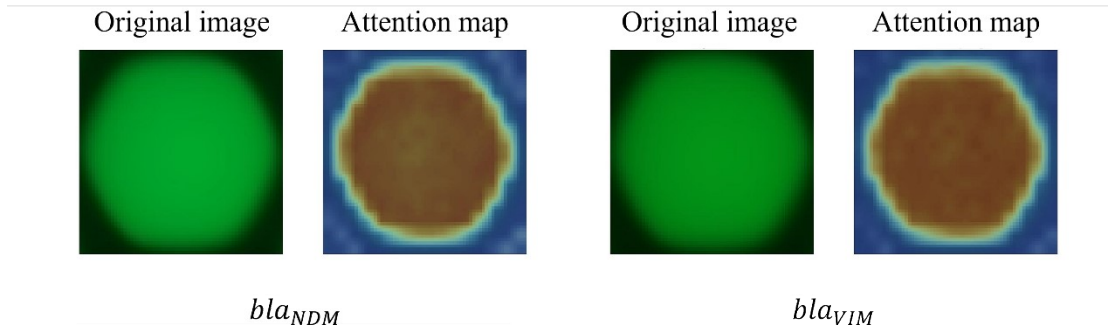
<i>bla<sub>VIM</sub></i>	<b>Gene</b>	CTTCGGTCCAGTAGAACTCTTCTATCCTGGTGCTGCGCATTCG ACCGACAACCTTAGTTGTGTACGTCCCGTCTGCGAGTGTGCTCT ATGGTGGTTGTGCGATTTATGAGTTGTCACGCACGTCTGCGGG GAACGTGGCCGATGCCGATCTGGCTGAATGGCCCACCTCCATT GAGCGGATTCAACAACACTACCCGGAAGCACAGTTCGTCATTC CGGGGCACGGCCTGCCGGGCGGTCTAGACTTGCTCAAGCACA C
	<b>VIM-F</b>	CTTCGGTCCAGTAGAACTCT
	<b>VIM-R</b>	GTGTGCTTGAGCAAGTCT
	<b>Probe</b>	ATGCCGATCTGGCTGAATGGCCCAC



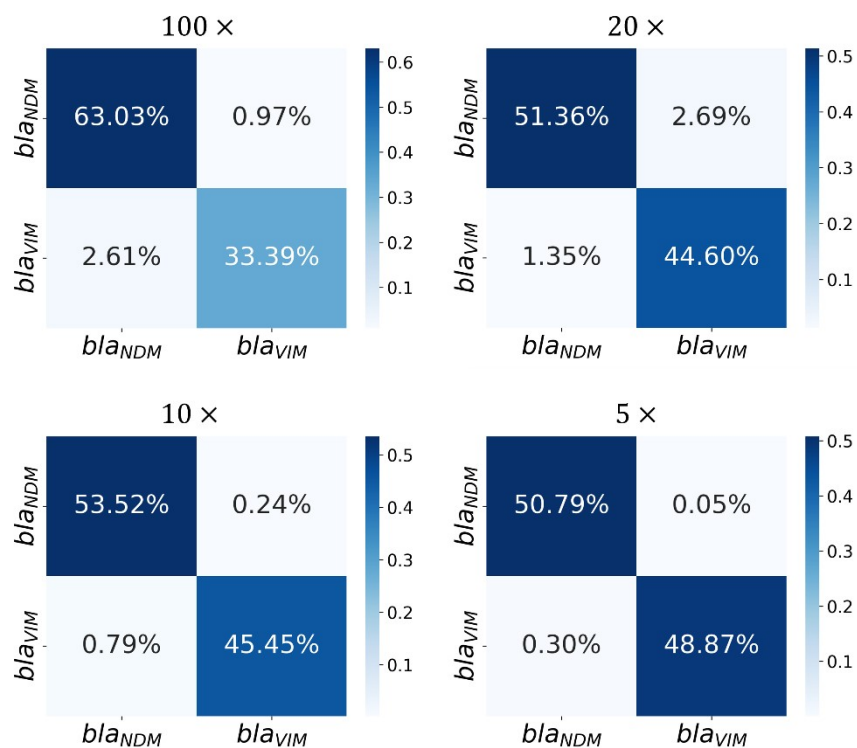
**Figure S2. Performance comparison of ResNet-18 and ViT.** Performances of ResNet-18, ViT model on small dataset (ViT-S) (7000 images in training set and 3000 images in test set) and ViT model on larger dataset (ViT-L) (70000 images in training set and 30000 images in test set) are compared. Radius of the scatters indicates MACs (1.49G for ResNet-18 and 0.86G for ViT).



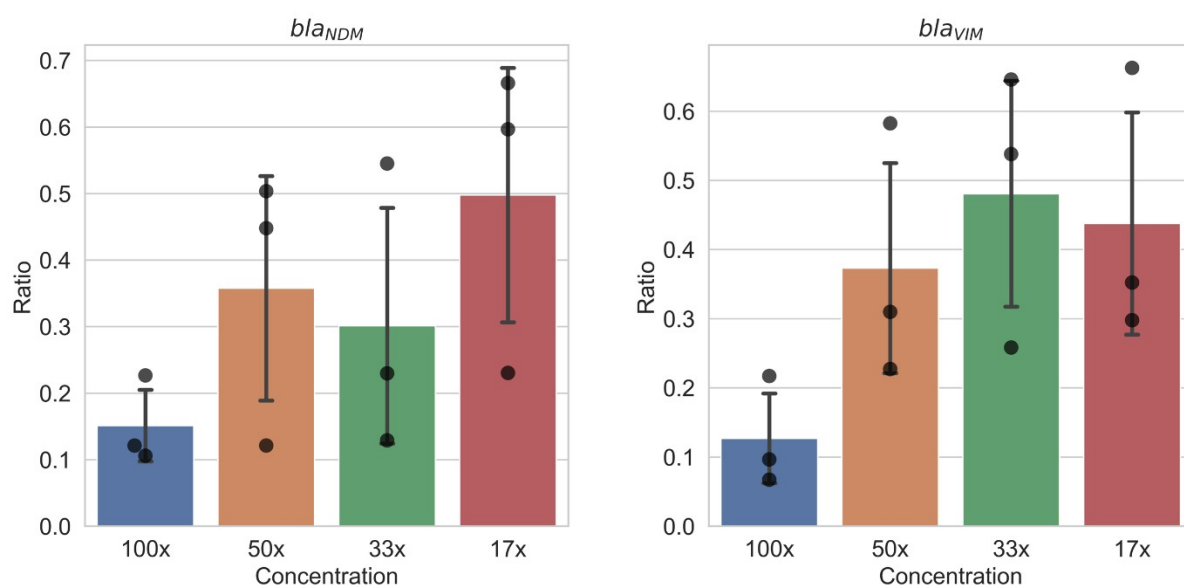
**Figure S3.** The intensities spatial distribution of gray and RGB values within  $bla_{NDM}$  and  $bla_{VIM}$  microwells (the first and the second rows) and their difference (the third row). Gray intensities in the figure were normalized by the maximum value in the gray intensities of  $bla_{NDM}$  and  $bla_{VIM}$  merged images. RGB values are normalized by the maximum value in all three channels for  $bla_{NDM}$  and  $bla_{VIM}$  merged images.



**Figure S4.** Attention map for the last layer of ViT.



**Figure S5. Confusion matrix for test set on different concentration.**



**Figure S6. Quantification results for *bla<sub>NDM</sub>* and *bla<sub>VIM</sub>* dual target samples by intensity-based method (Gaussian multi-peak fitting on intensity distribution histogram). Both gene have unstable performance on quantification.**