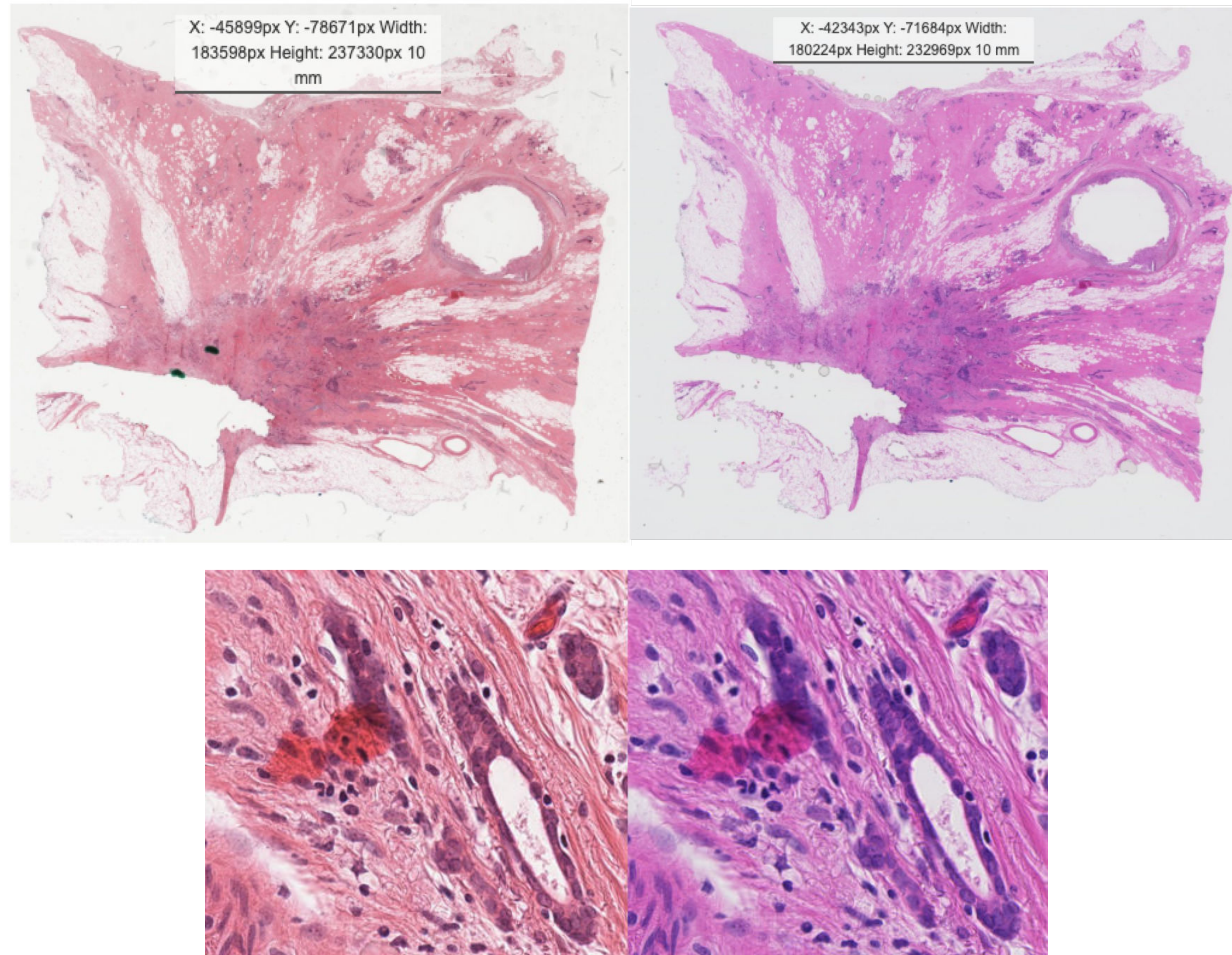
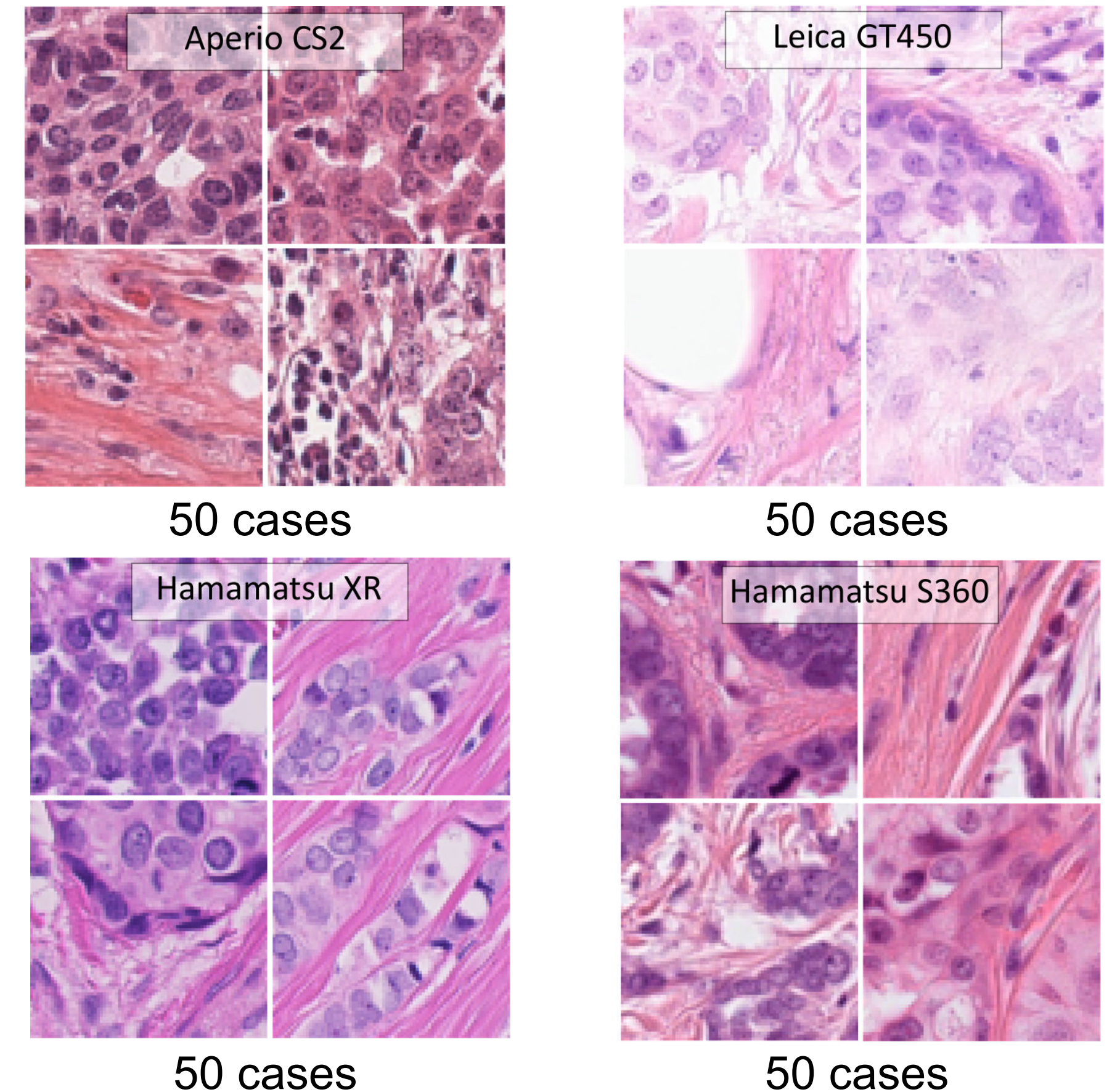


Motivation



Digital representation of a microscopy slide **varies strongly** with the scanner used to digitize the image.

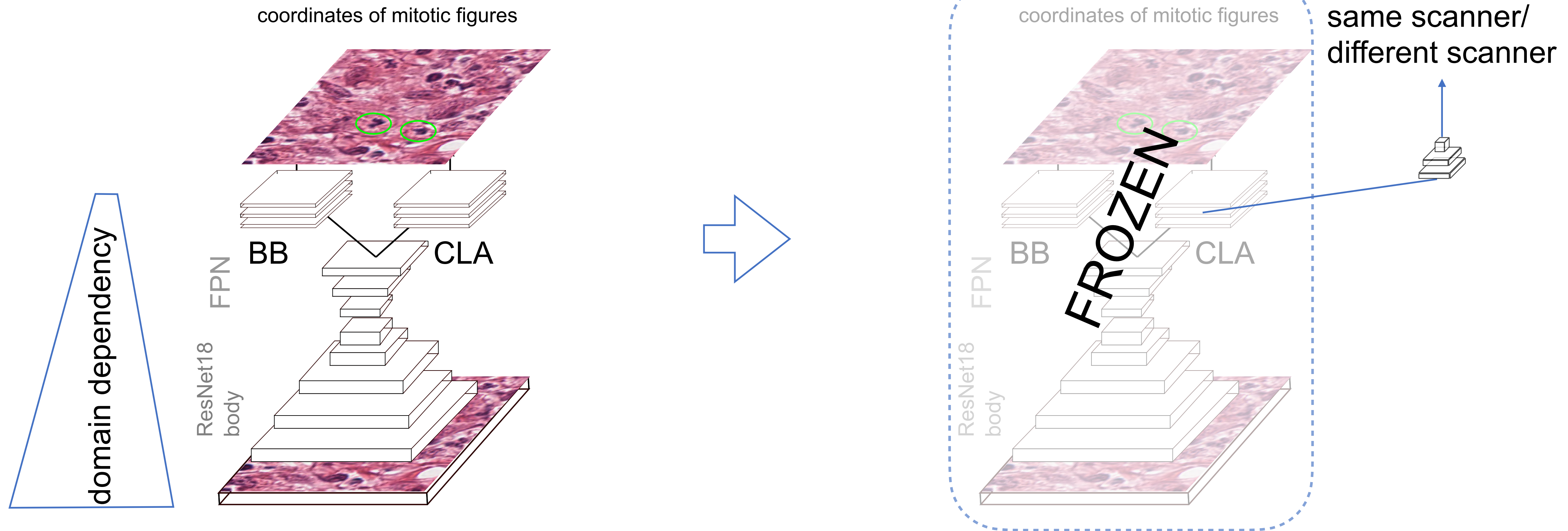
MIDOG Challenge Training Set



Cases **randomly assigned** from a consecutive selection of the diagnostic archive of UMC Utrecht Hospital.

1. RetinaNet Object Detection

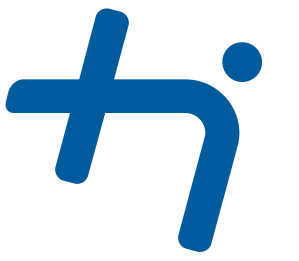
2. Proxy \mathcal{A} distance (PAD*, Elsahar/Gallé 2019)



code available: <https://github.com/DeepPathology/MIDOG/tree/main/DomainShiftQuantification>

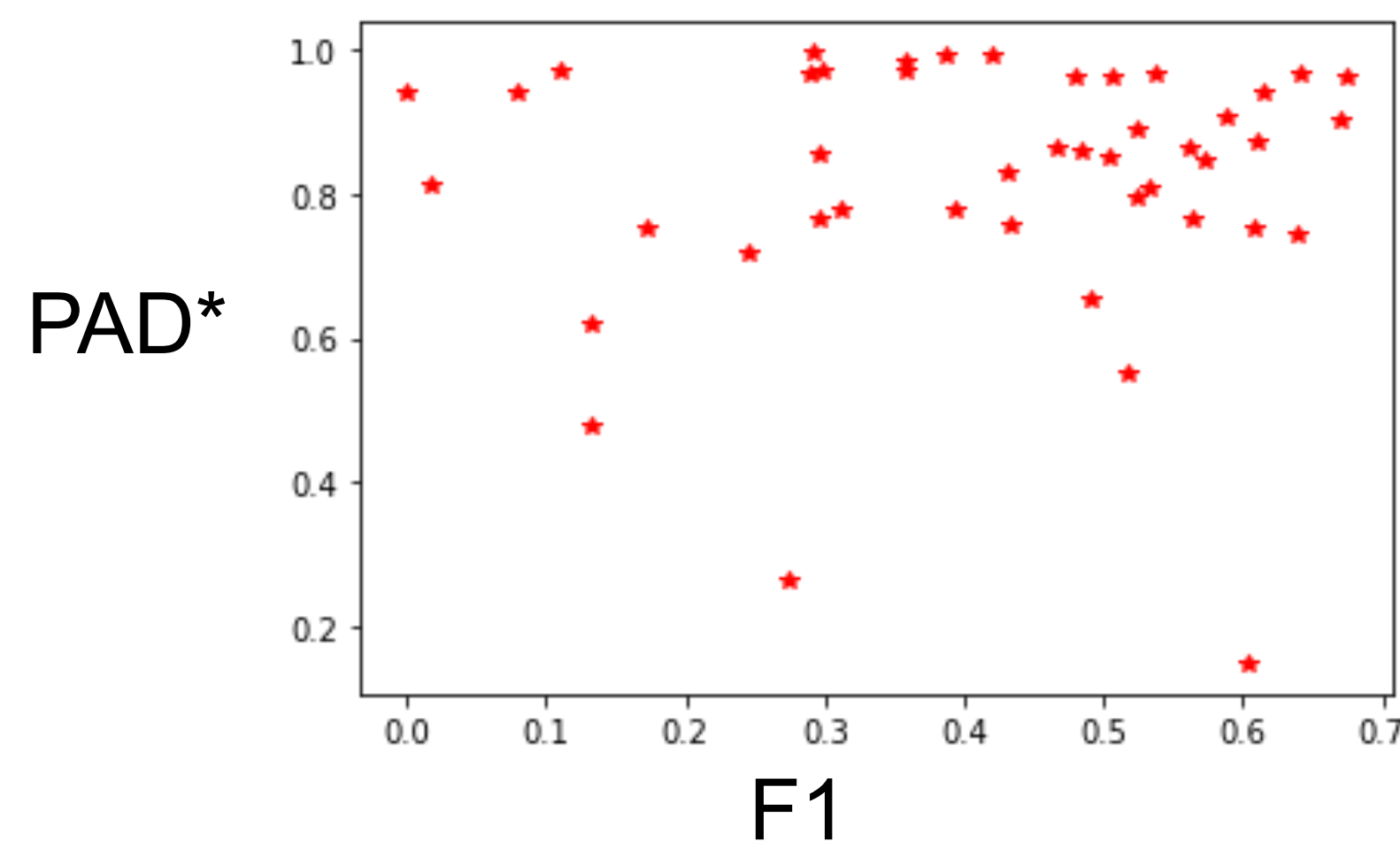
Quantifying the Scanner-Induced Domain Gap in Mitosis Detection (3): Results

Mean +/- std of 5 complete runs



Training set	F1 score on test set			PAD* score on test set		
	Hamamatsu XR	Aperio CS2	Hamamatsu S360	Hamamatsu XR	Aperio CS2	Hamamatsu S360
TUPAC	0.553 ± 0.04	0.613 ± 0.05	0.404 ± 0.09	0.719 ± 0.28	0.906 ± 0.07	0.945 ± 0.09
XR	0.578 ± 0.03	0.138 ± 0.13	0.190 ± 0.06	-	0.861 ± 0.07	0.567 ± 0.18
CS2	0.390 ± 0.10	0.751 ± 0.02	0.433 ± 0.17	0.946 ± 0.04	-	0.931 ± 0.04
S360	0.432 ± 0.08	0.574 ± 0.09	0.721 ± 0.03	0.769 ± 0.06	0.741 ± 0.11	-

- Strong difference in performance between in-domain and out-of-domain results.
- Consistent differences in PAD* metric, yet not correlated to the drop in F1 score.



Pearson's correlation coefficient = 0.04