Supplementary files for

Development and Validation of a Deep Learning Model for Histopathological Slide Analysis in Lung Cancer Diagnosis

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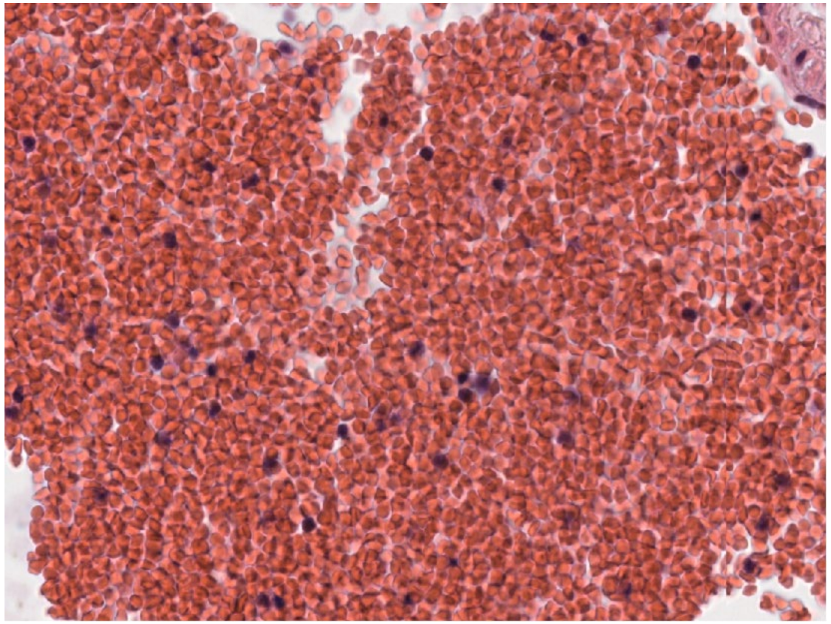
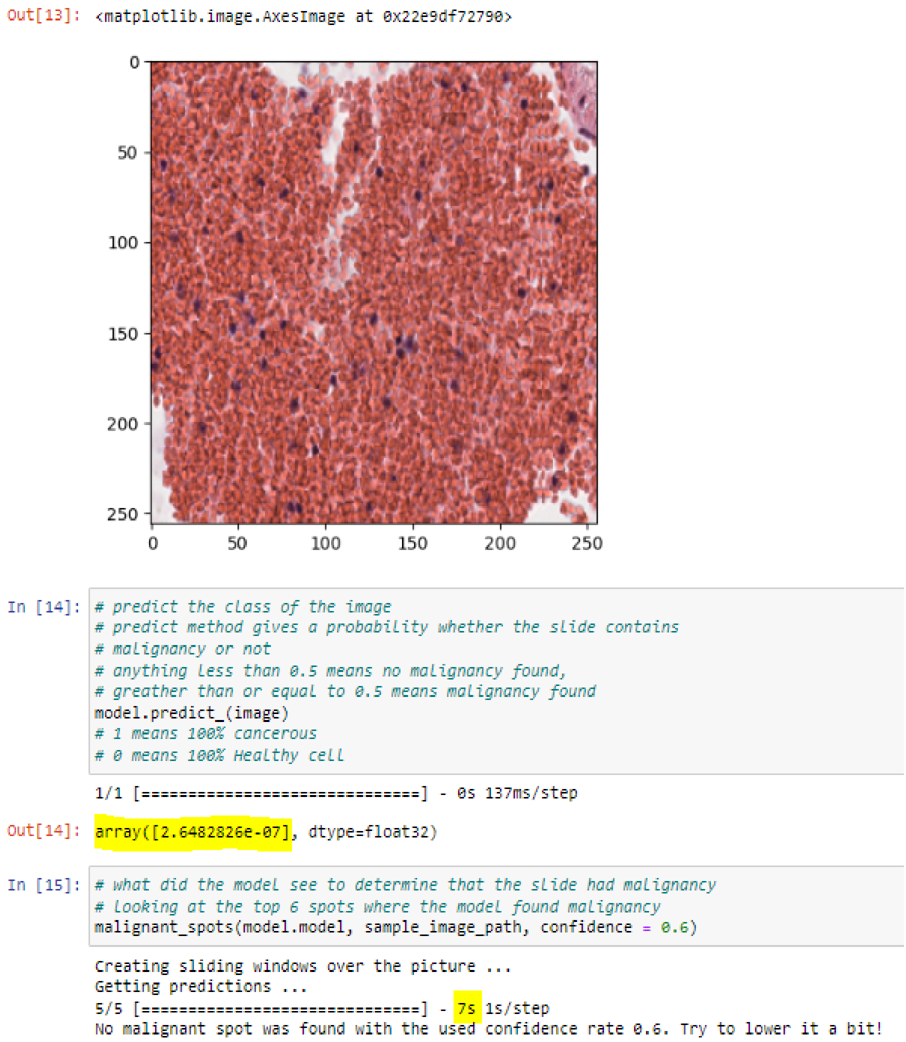
Image nr	AI decision	Array	Accuracy	Pathologist 1	Pathologist 2	Pathologist 3	Pathologist 4	Pathologist 5	Pathologist 6	Pathologist 7	Pathologist 8	Pathologist 9	Pathologist 10	Ref page	Path Accuracy
1	Healthy	<0.001	100%	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	**'1'!A1**	100%
2	Healthy	<0.001	100%	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	**'2'!A1**	100%
3	Healthy	<0.001	100%	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	**'3'!A1**	100%
4	Healthy	0.05	100%	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	**'4'!A1**	100%
5	Healthy	0.004	100%	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	**'5'!A1**	100%
6	Healthy	<0.001	100%	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Healthy	Cancer	**'6'!A1**	90%
7	Cancer	1	100%	Not Certain	Not Certain	Not Certain	Not Certain	Not Certain	Not Certain	Not Certain	Not Certain	Not Certain	Not Certain	**'7'!A1**	0%
8	Cancer	1	100%	Not Certain	Not Certain	Cancer	Not Certain	Not Certain	Cancer	Not Certain	Not Certain	Not Certain	Not Certain	**'8'!A1**	20%
9	Cancer	1	100%	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	**'9'!A1**	100%
10	Cancer	1	100%	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	**'10'!A1**	100%
11	Cancer	1	100%	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Not Certain	**'11'!A1**	90%
12	Cancer	1	100%	Not Certain	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Not Certain	Cancer	Not Certain	**'12'!A1**	70%
13	Cancer	1	100%	Cancer	Not Certain	Cancer	Not Certain	Not Certain	Cancer	Not Certain	Not Certain	Cancer	Not Certain	**'13'!A1**	40%
14	Cancer	1	100%	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	**'14'!A1**	100%
15	Cancer	1	100%	Not Certain	Not Certain	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	Cancer	**'15'!A1**	80%
Years of experience				**3**	**2**	**20**	**10**	**6**	**33**	**18**	**18**	**7**	**2**	**Average**	**79%**

Intrpretation: 1 = Cancer 100%; and < 0.5 = Healthy

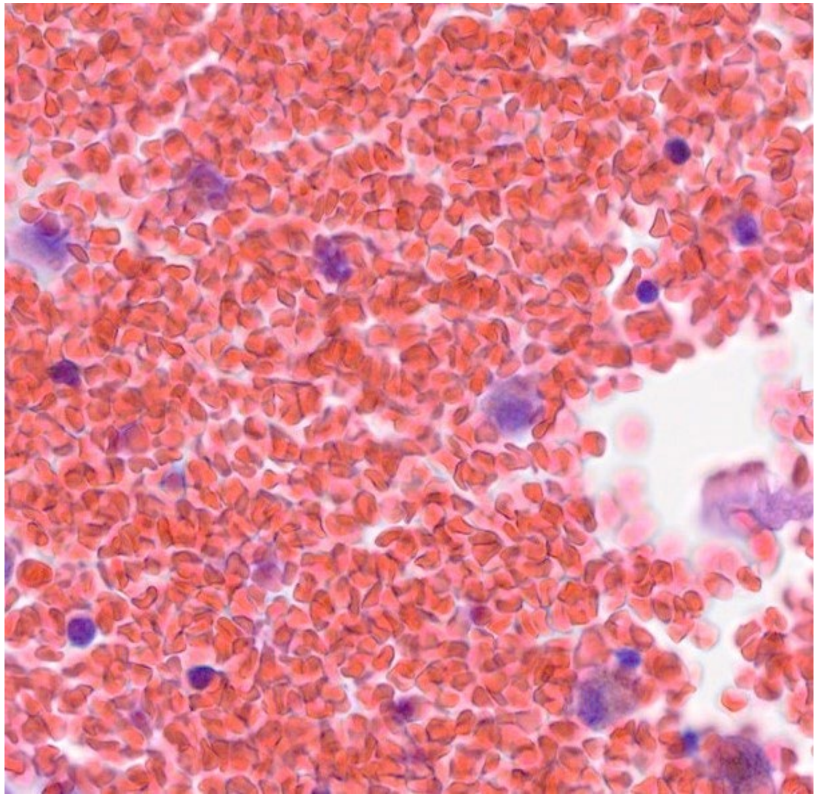


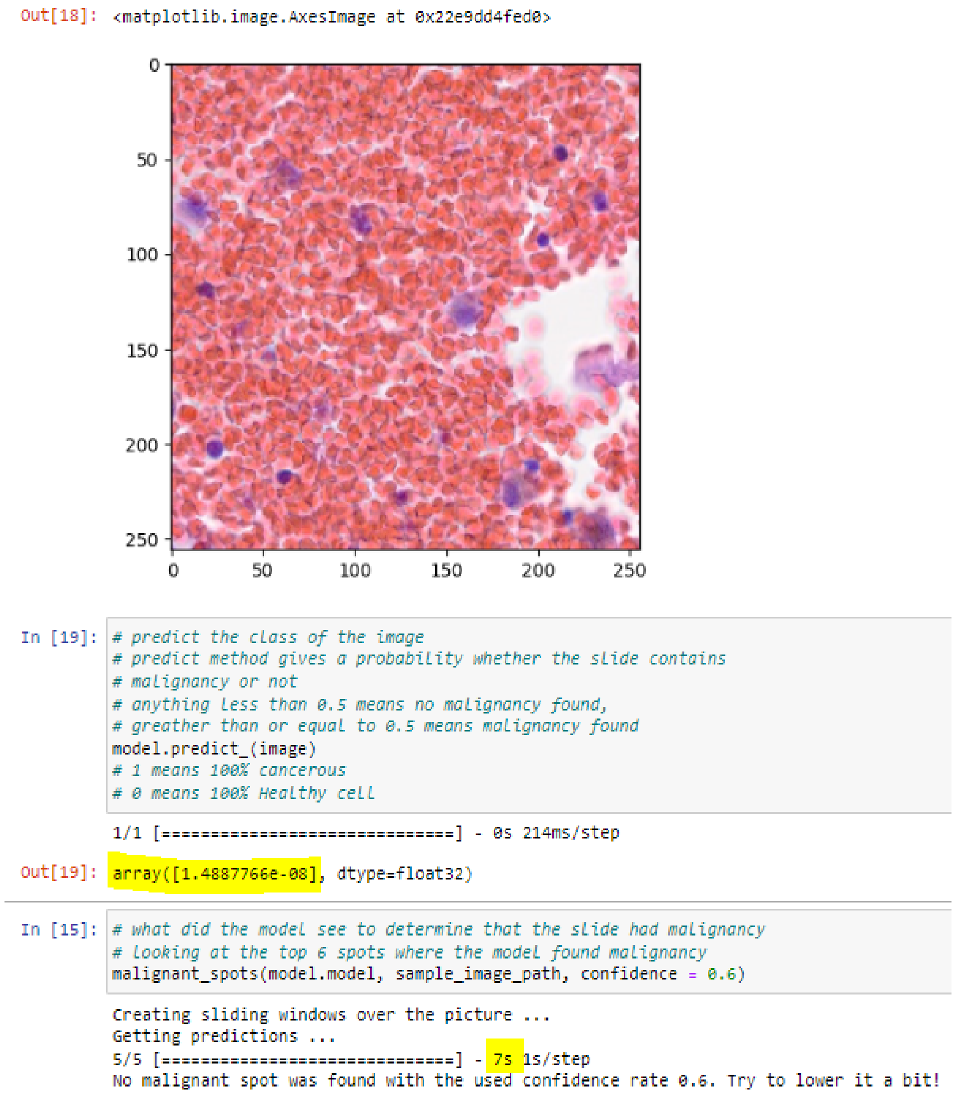


```
Out[13]: <matplotlib.image.AxesImage at 0x22e9df72790>
```

```
In [14]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 137ms/step

Out[14]: array([2.6482826e-07], dtype=float32)
```

```
In [15]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         No malignant spot was found with the used confidence rate 0.6. Try to lower it a bit!
```





```
<matplotlib.image.AxesImage at 0x22e9dd4fed0>
```

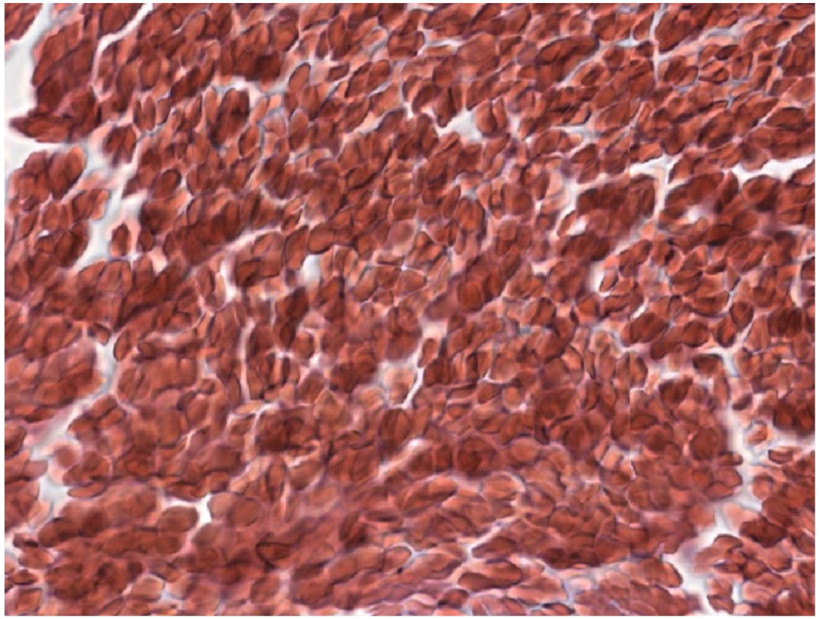
```
# predict the class of the image
# predict method gives a probability whether the slide contains
# malignancy or not
# anything less than 0.5 means no malignancy found,
# greather than or equal to 0.5 means malignancy found
model.predict_(image)
# 1 means 100% cancerous
# 0 means 100% Healthy cell
```

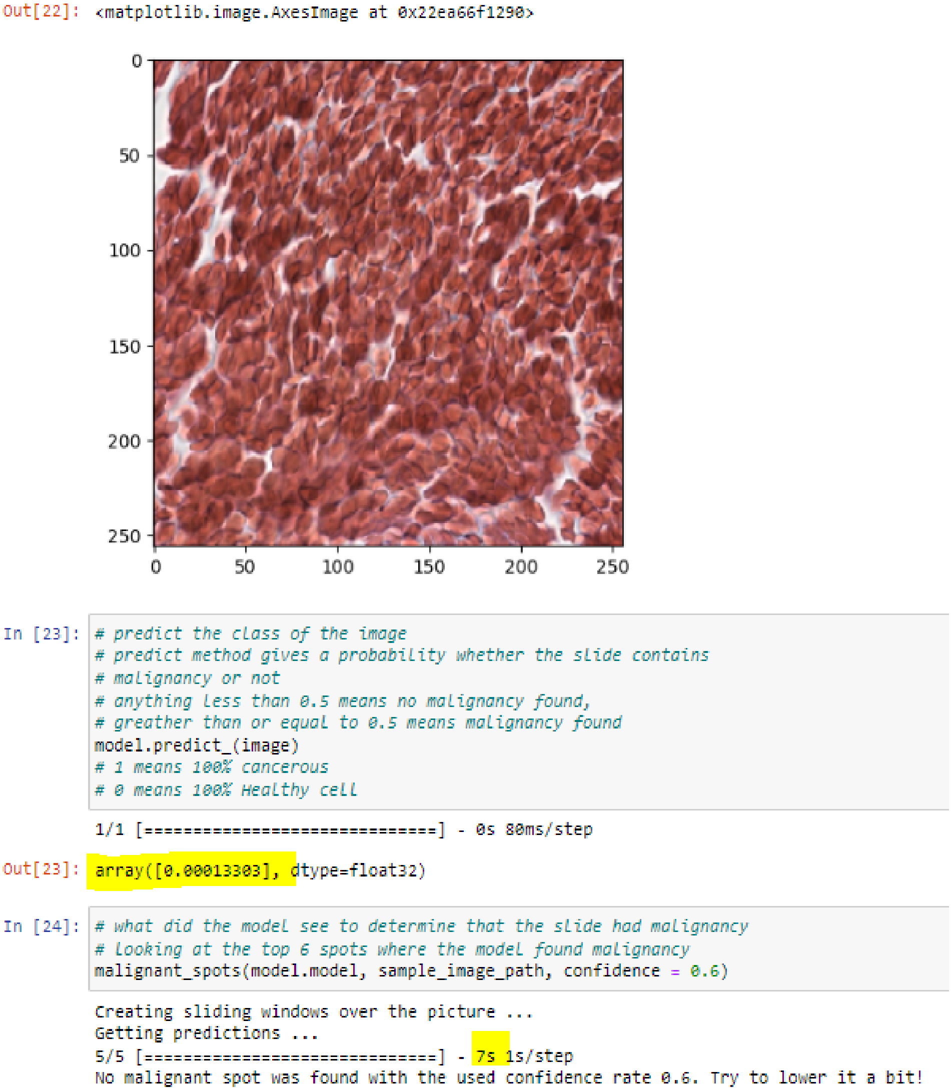
```
1/1 [==============================] - 0s 214ms/step
```

```
array([1.4887766e-08], dtype=float32)
```

```
# what did the model see to determine that the slide had malignancy
# looking at the top 6 spots where the model found malignancy
malignant_spots(model.model, sample_image_path, confidence = 0.6)
```

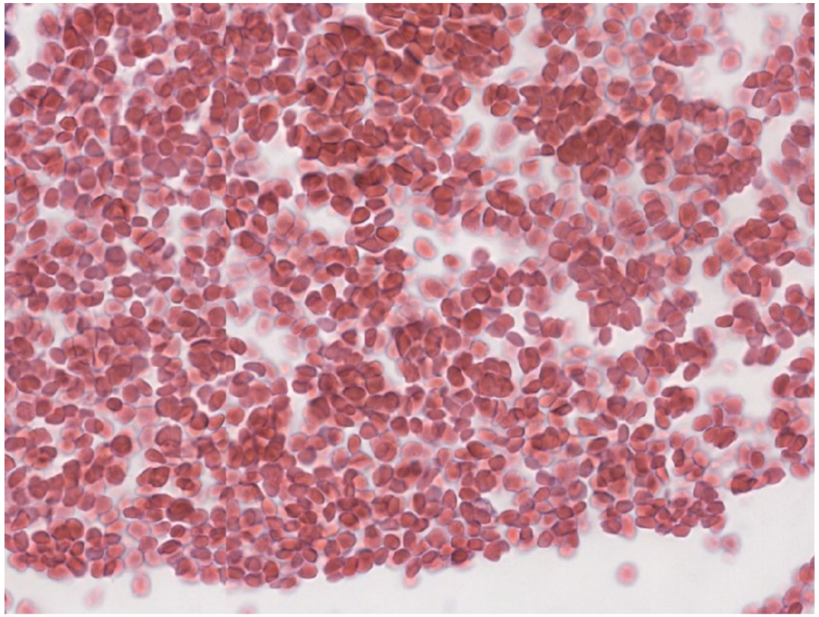
```
Creating sliding windows over the picture ...
Getting predictions ...
5/5 [==============================] - 7s 1s/step
No malignant spot was found with the used confidence rate 0.6. Try to lower it a bit!
```

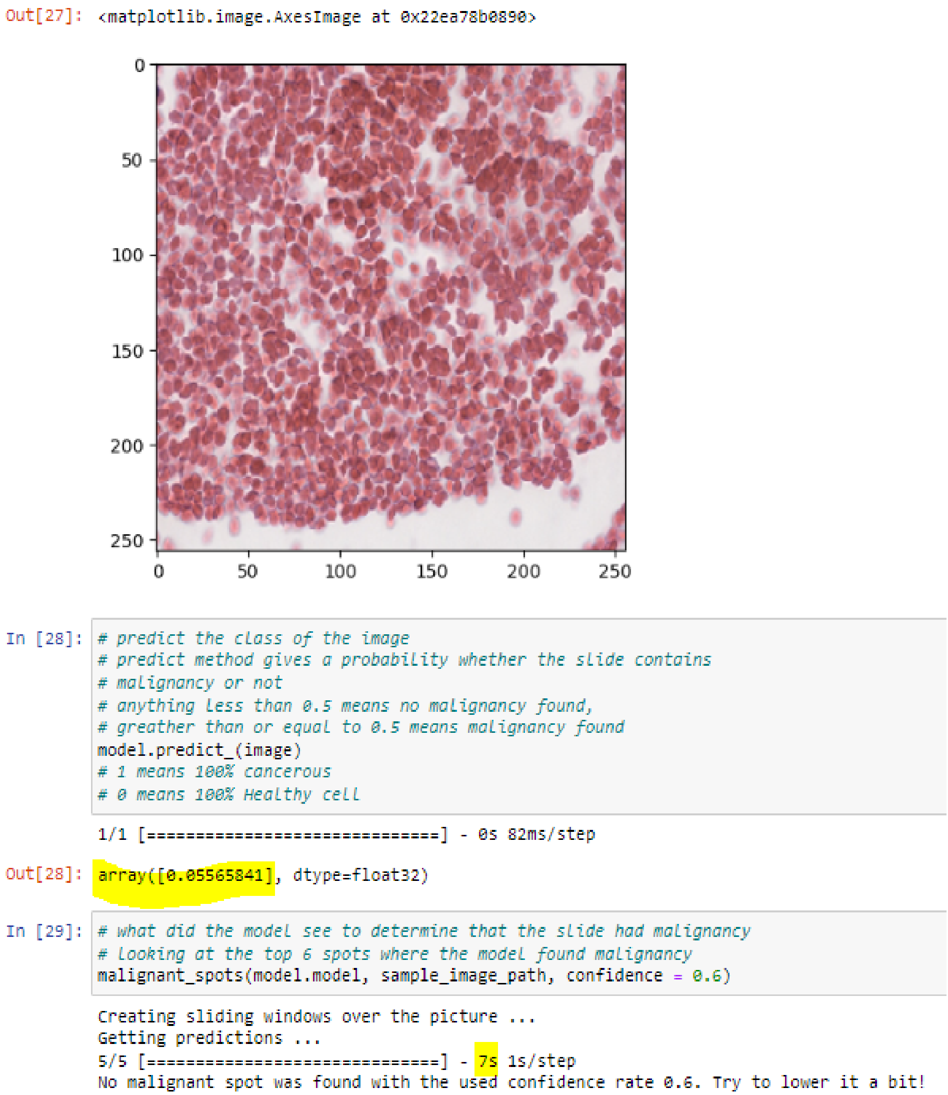




```
Out[22]: <matplotlib.image.AxesImage at 0x22ea66f1290>
```

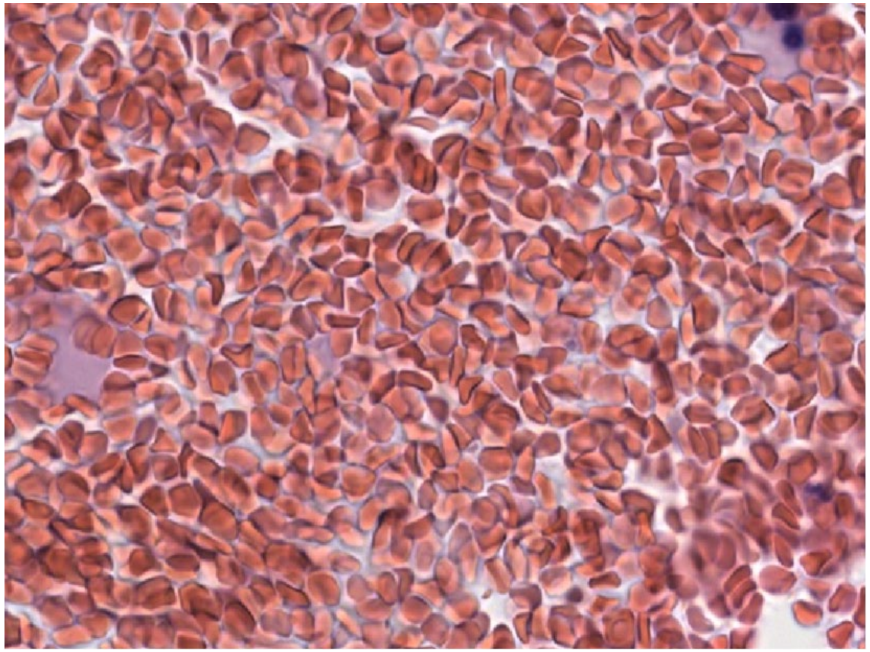
```
In [23]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 80ms/step

Out[23]: array([0.00013303], dtype=float32)

In [24]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         No malignant spot was found with the used confidence rate 0.6. Try to lower it a bit!
```

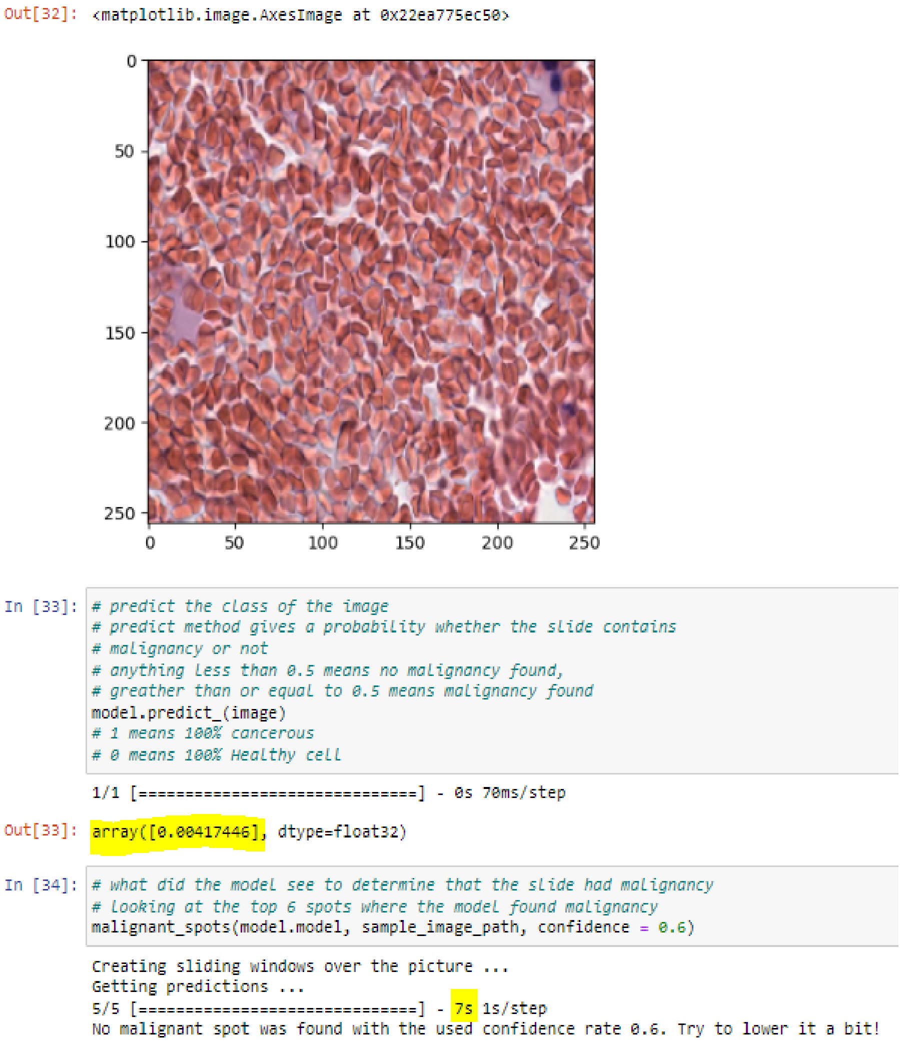




```
Out[27]: <matplotlib.image.AxesImage at 0x22ea78b0890>
```

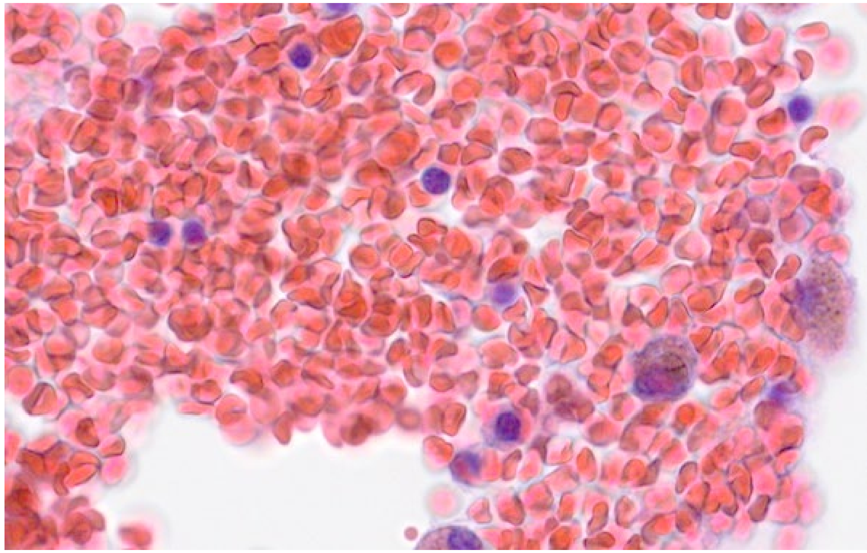
```
In [28]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 82ms/step

Out[28]: array([0.05565841], dtype=float32)

In [29]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         No malignant spot was found with the used confidence rate 0.6. Try to lower it a bit!
```

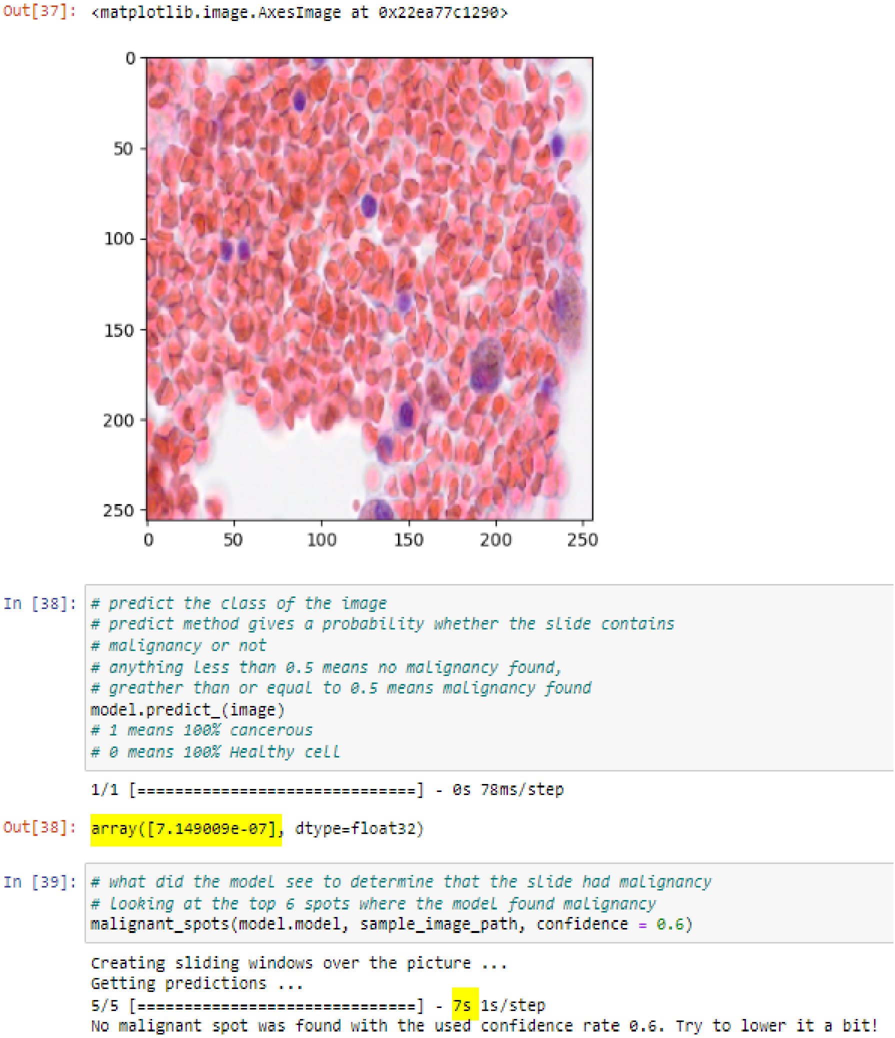




```
Out[32]: <matplotlib.image.AxesImage at 0x22ea775ec50>
```

```
In [33]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 70ms/step

Out[33]: array([0.00417446], dtype=float32)

In [34]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         No malignant spot was found with the used confidence rate 0.6. Try to lower it a bit!
```

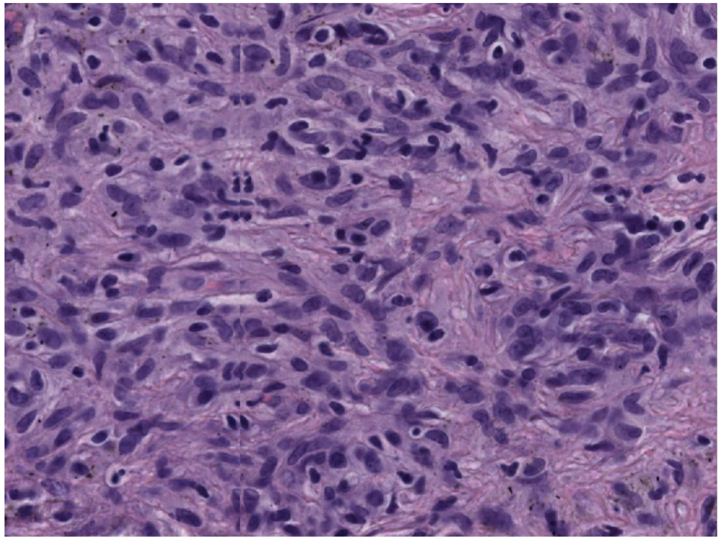


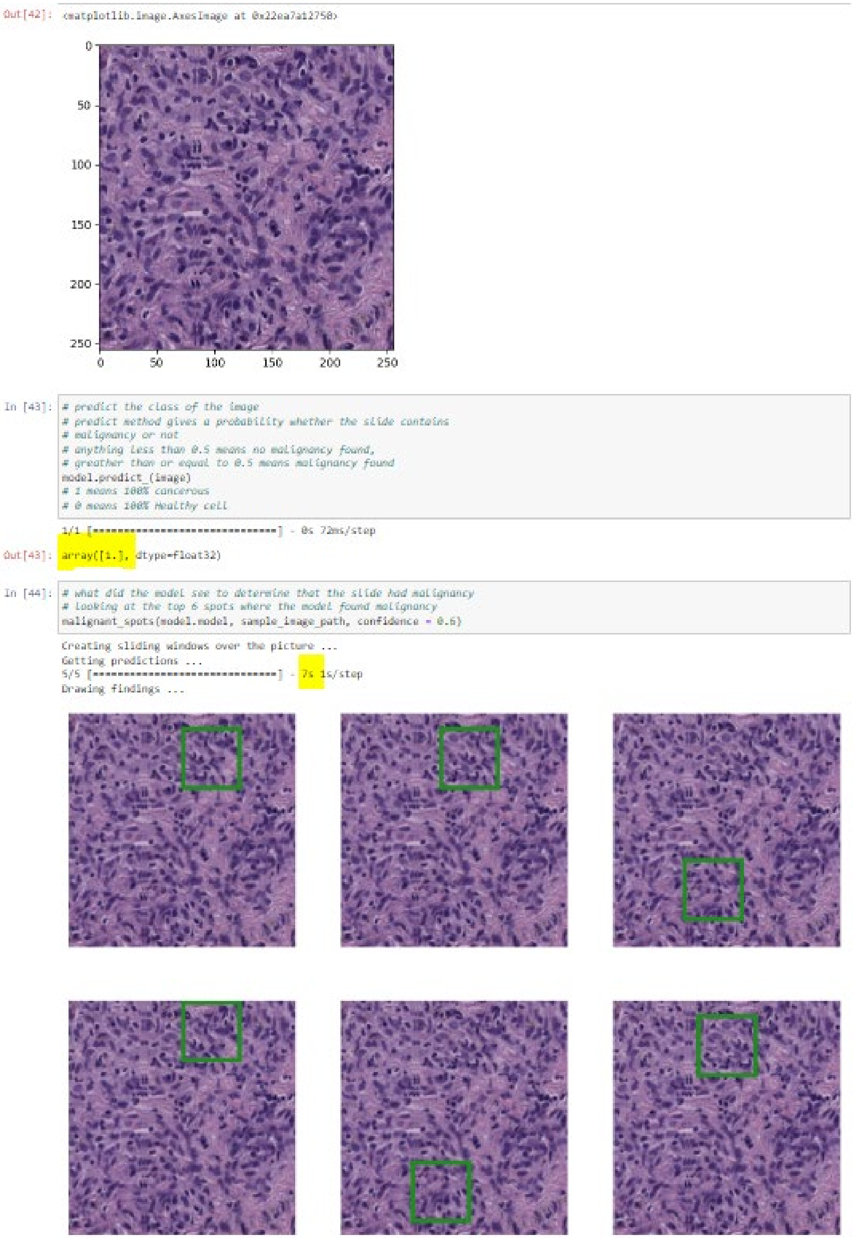


```
Out[37]: <matplotlib.image.AxesImage at 0x22ea77c1290>
```

```
In [38]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 78ms/step

Out[38]: array([7.149009e-07], dtype=float32)
```

```
In [39]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         No malignant spot was found with the used confidence rate 0.6. Try to lower it a bit!
```

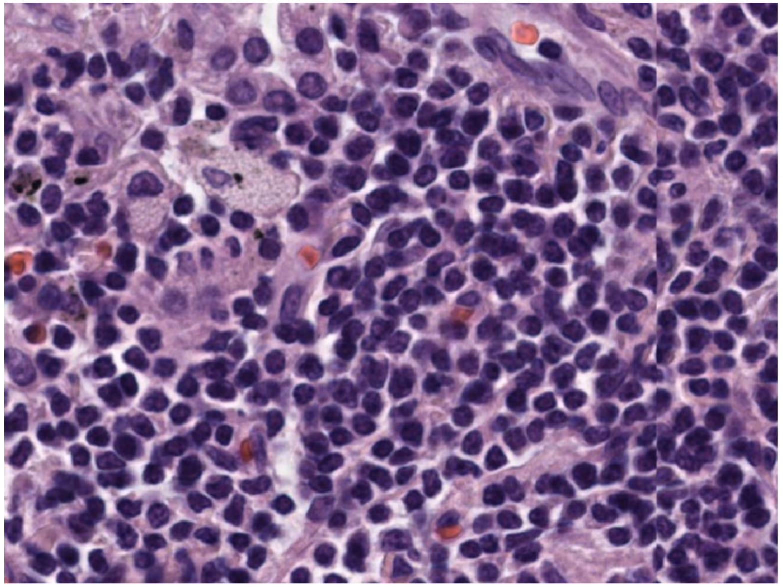


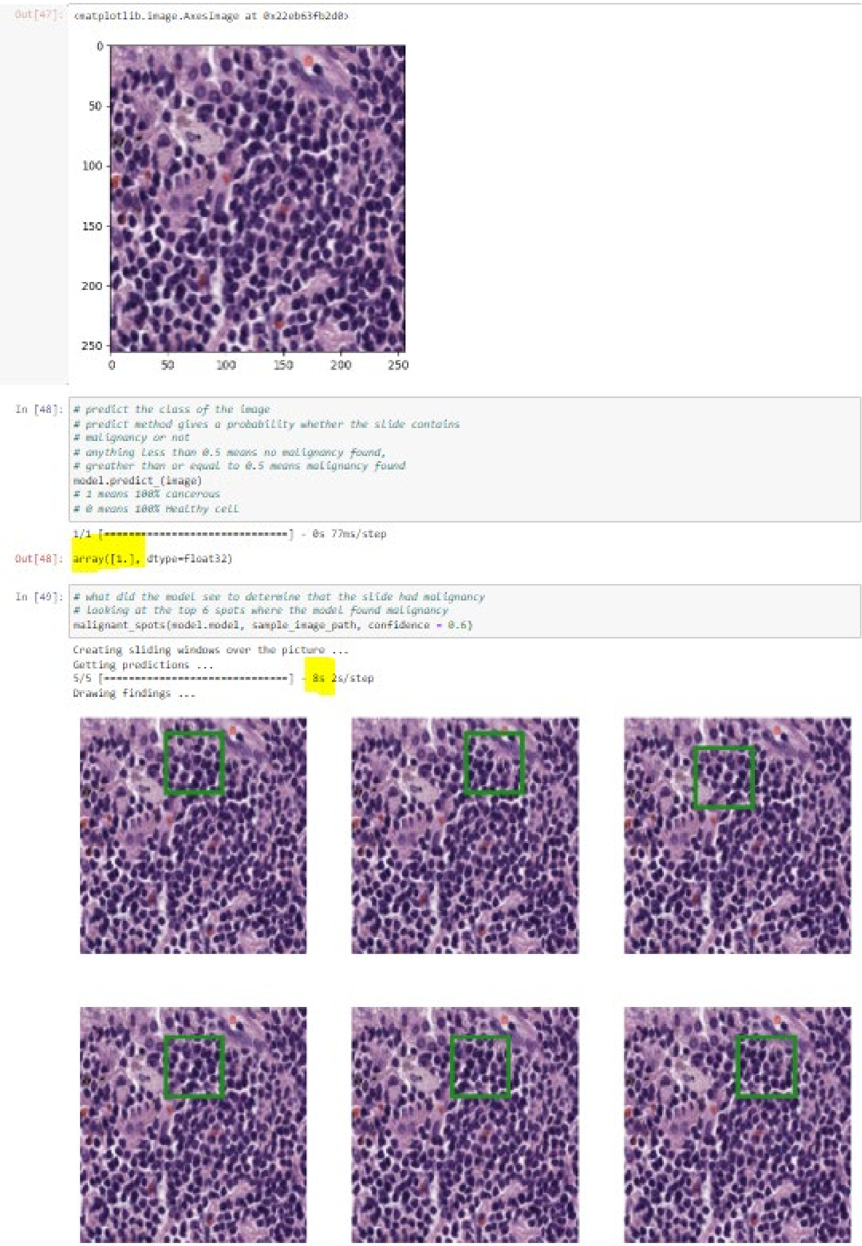


```
Out[42]: <matplotlib.image.AxesImage at 0x22ea7a12750>
```

```
In [43]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 72ms/step

Out[43]: array([1.], dtype=float32)
```

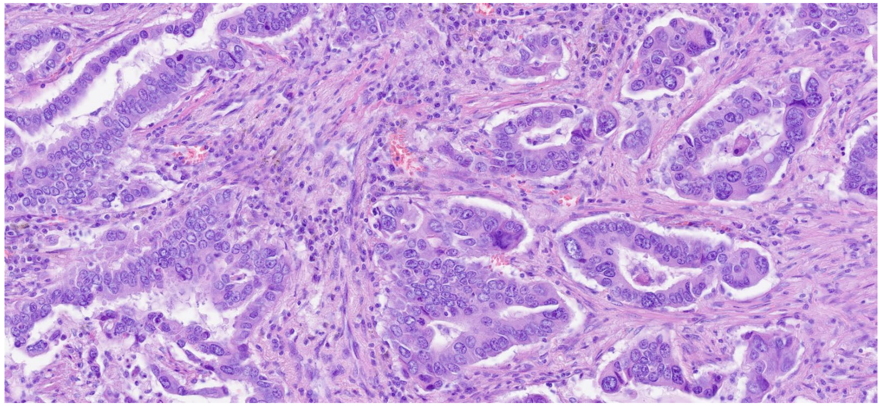
```
In [44]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

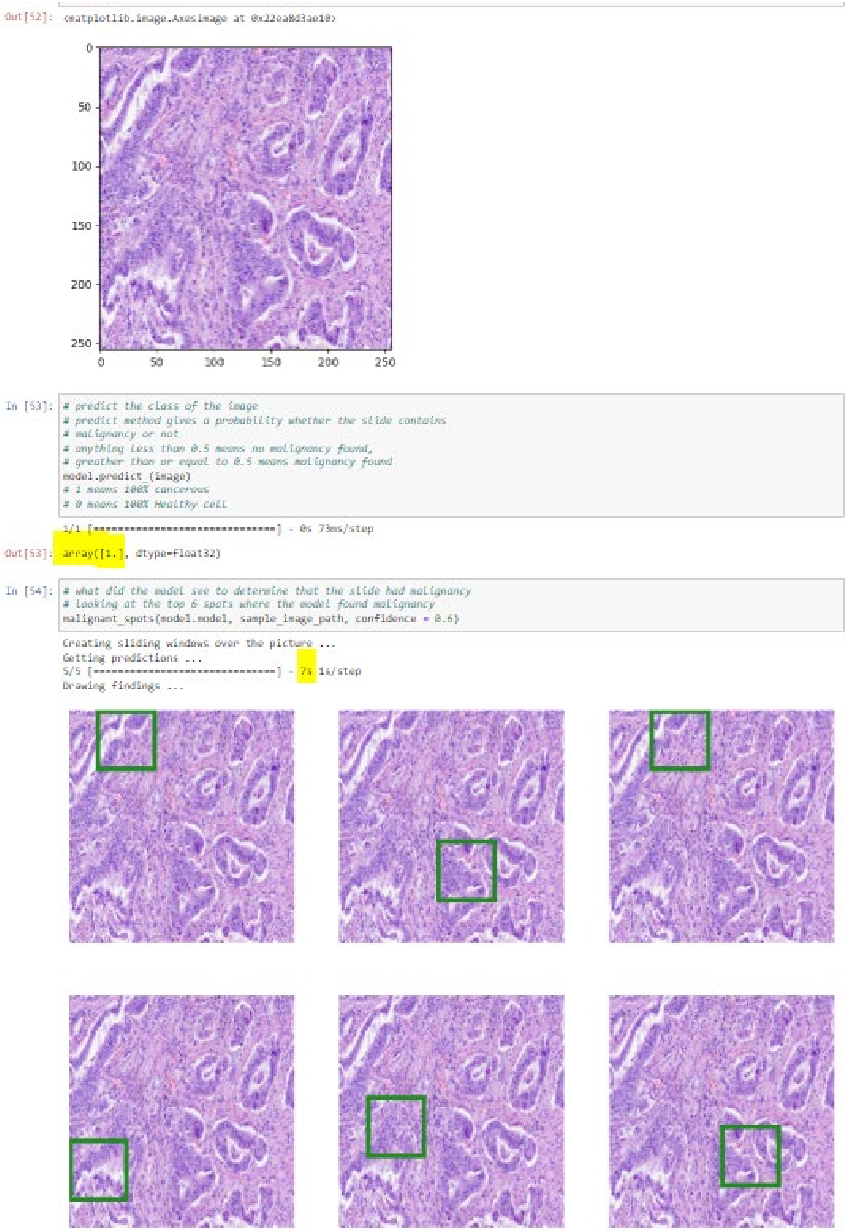




```
Out[47]: <matplotlib.image.AxesImage at 0x22eb63fb2d0>
```

```
In [48]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 77ms/step

Out[48]: array([1.], dtype=float32)

In [49]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 8s 2s/step
         Drawing findings ...
```

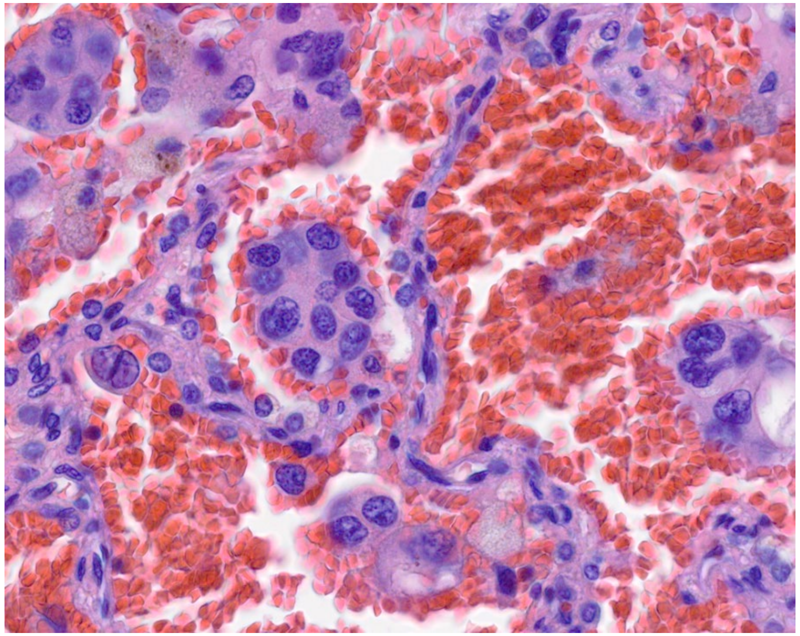


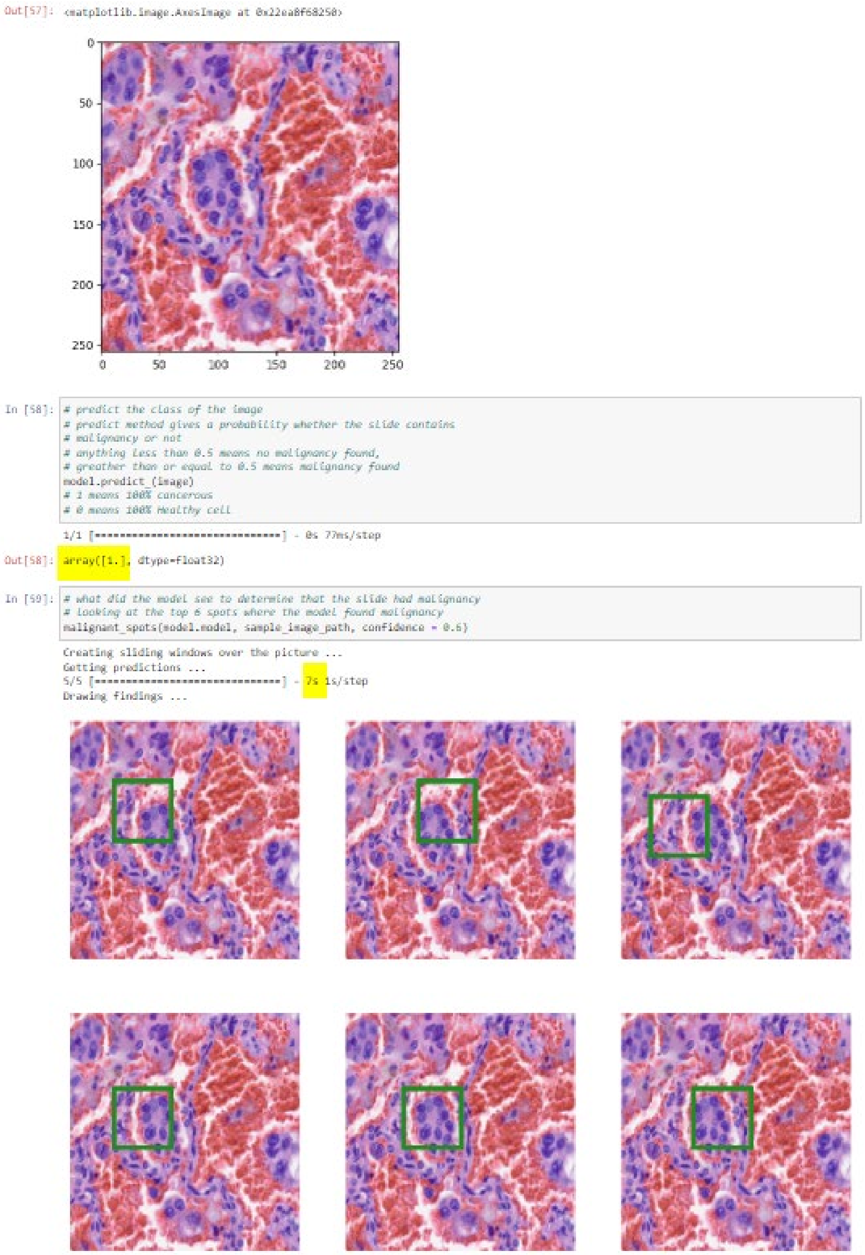


```
Out[52]: <matplotlib.image.AxesImage at 0x22ea8d3ae10>
```

```
In [53]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 73ms/step

Out[53]: array([1.], dtype=float32)
```

```
In [54]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

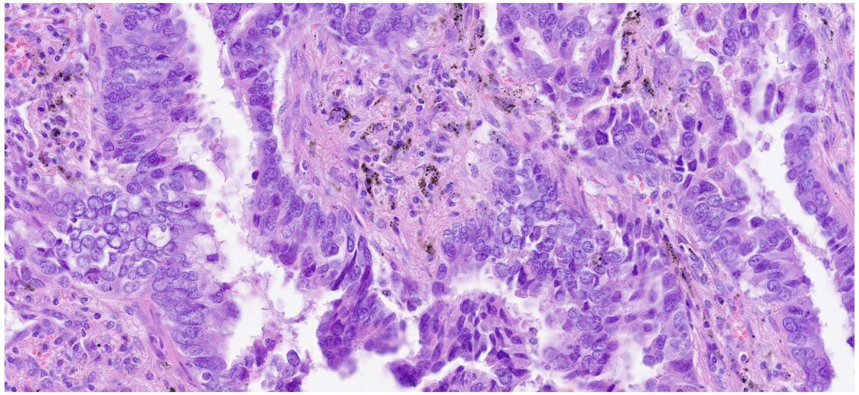


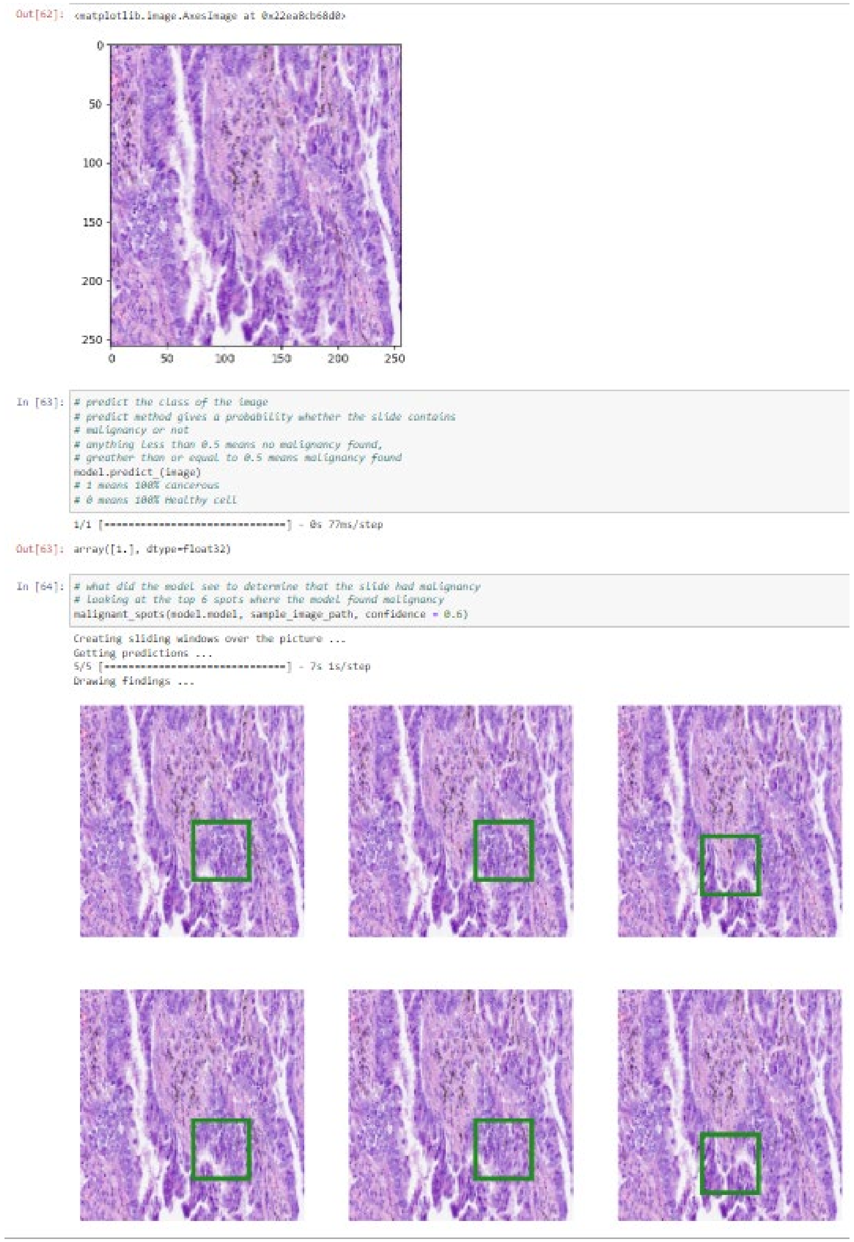


```
Out[57]: <matplotlib.image.AxesImage at 0x22ea8f68250>
```

```
In [58]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 77ms/step

Out[58]: array([1.], dtype=float32)
```

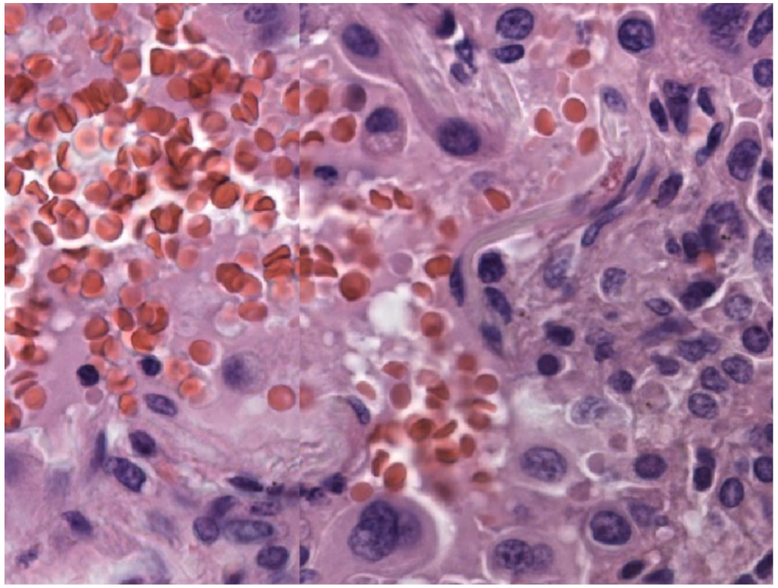
```
In [59]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

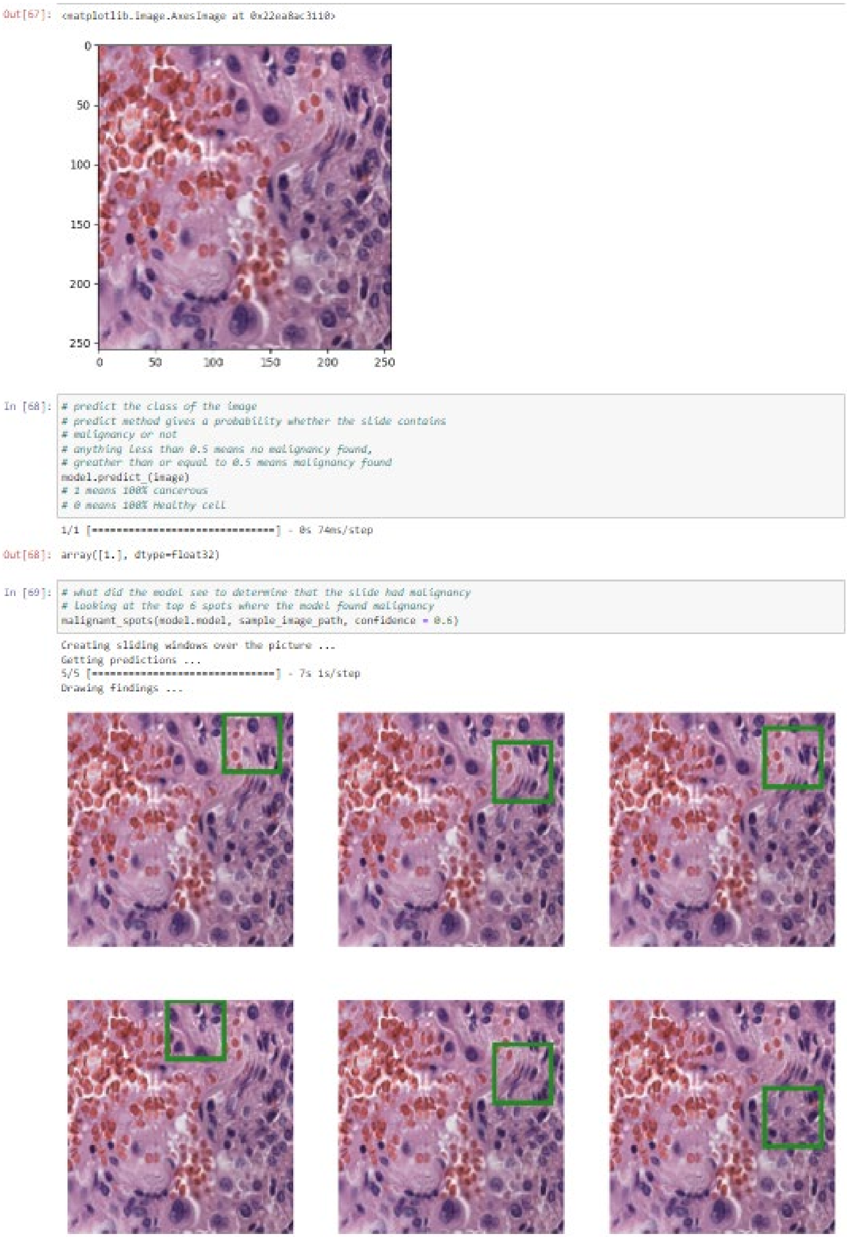




```
Out[62]: <matplotlib.image.AxesImage at 0x22ea8cb68d0>
```

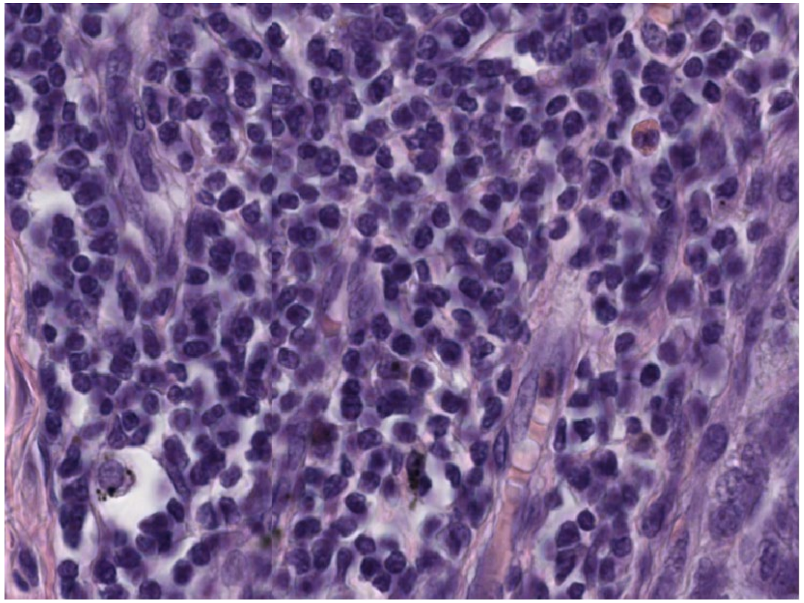
```
In [63]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 77ms/step

Out[63]: array([1.], dtype=float32)

In [64]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

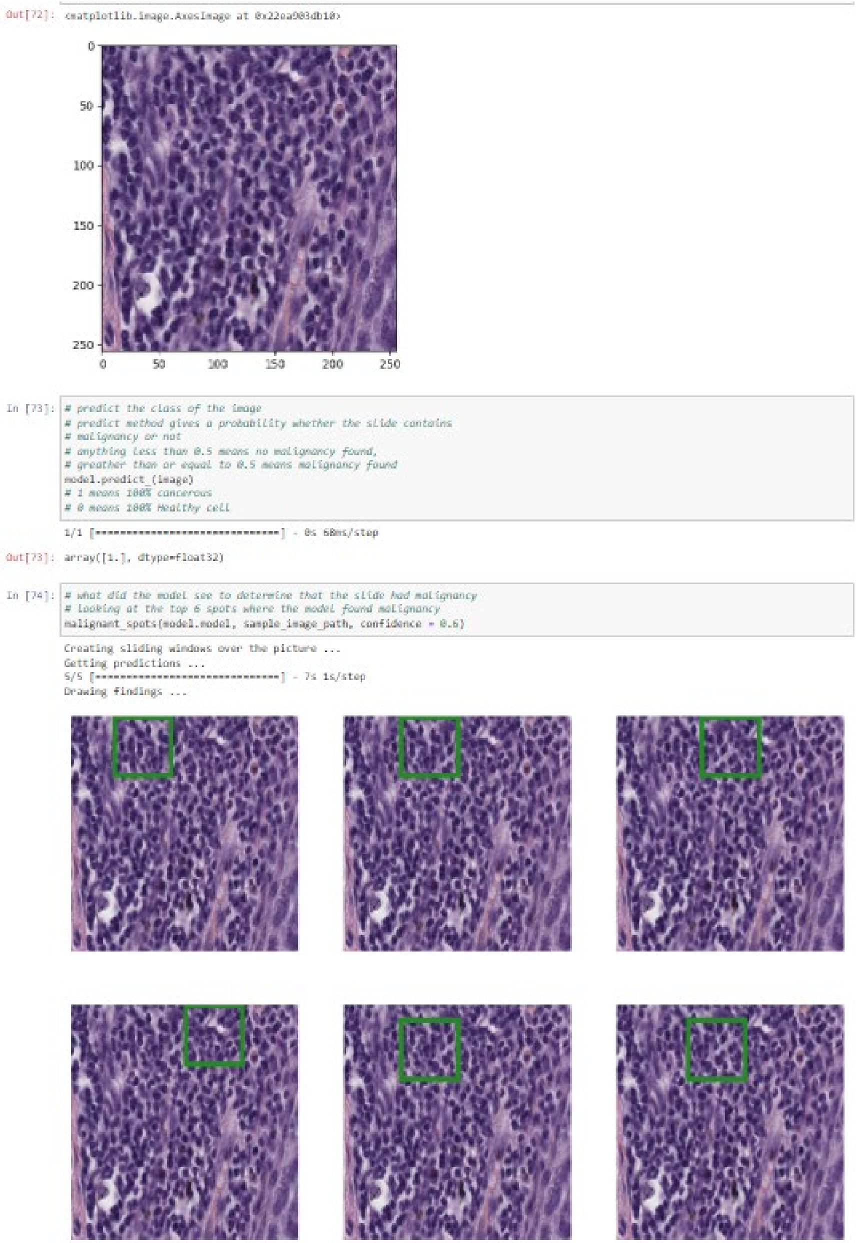




```
Out[67]: <matplotlib.image.AxesImage at 0x22ea8ac3118>
```

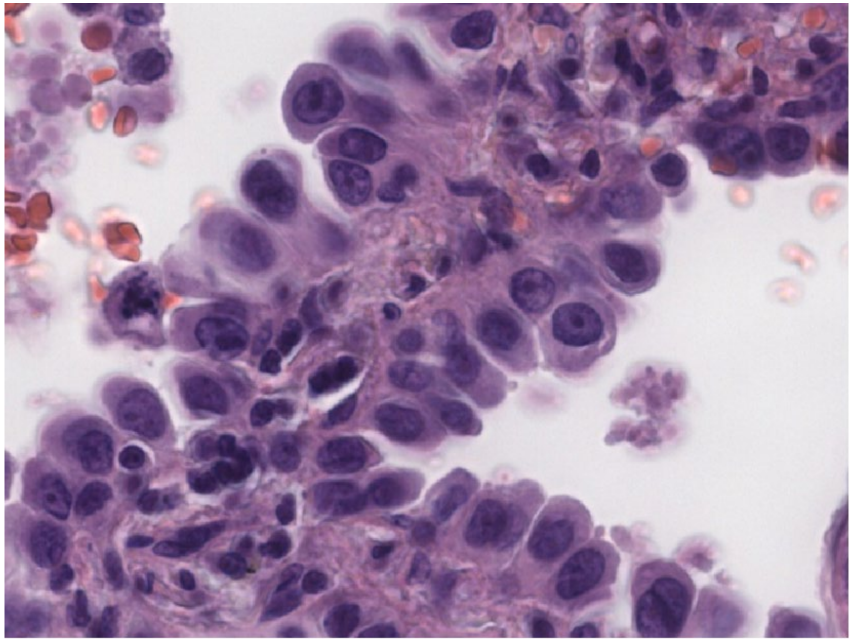
```
In [68]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 74ms/step

Out[68]: array([1.], dtype=float32)

In [69]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

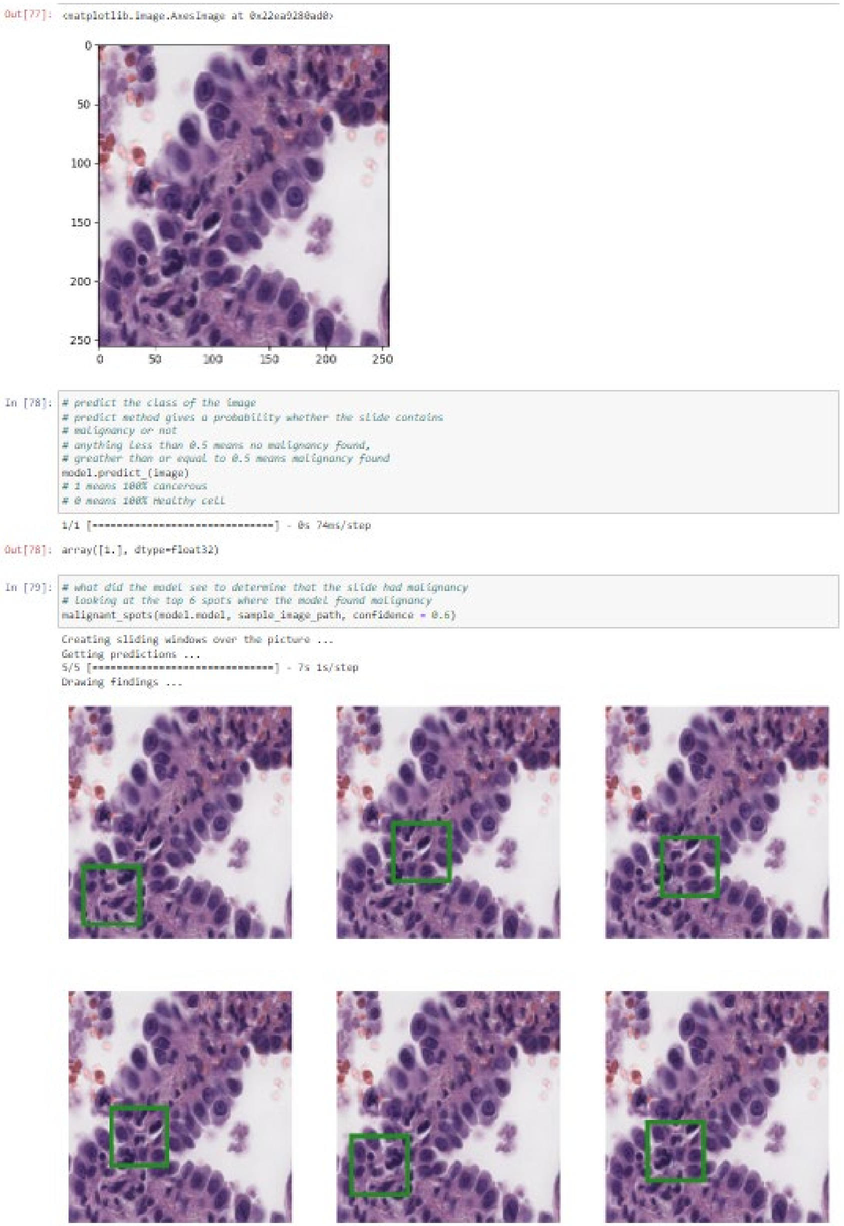




```
Out[72]: <matplotlib.image.AxesImage at 0x22ea903db10>
```

```
In [73]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 68ms/step

Out[73]: array([1.], dtype=float32)

In [74]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

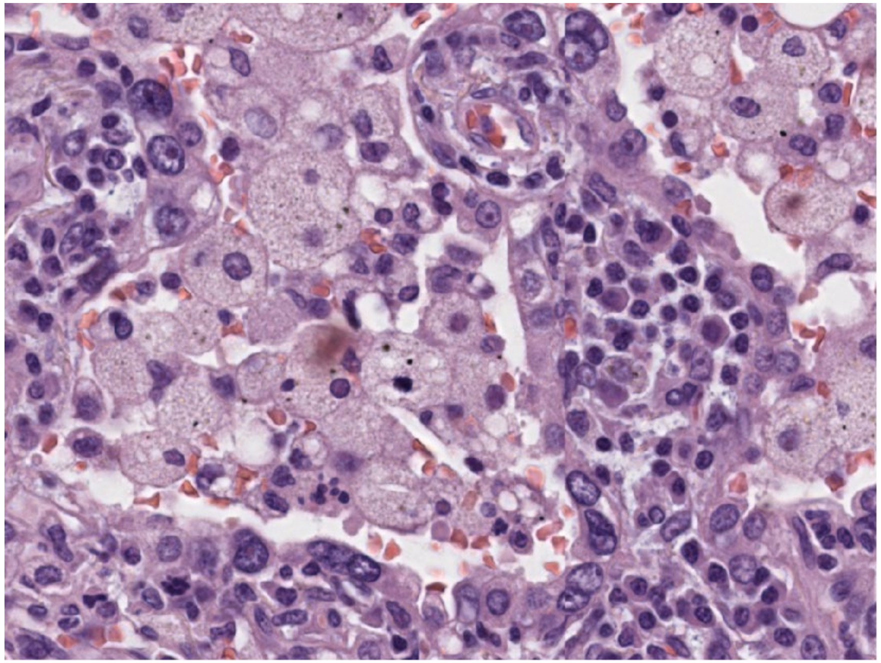


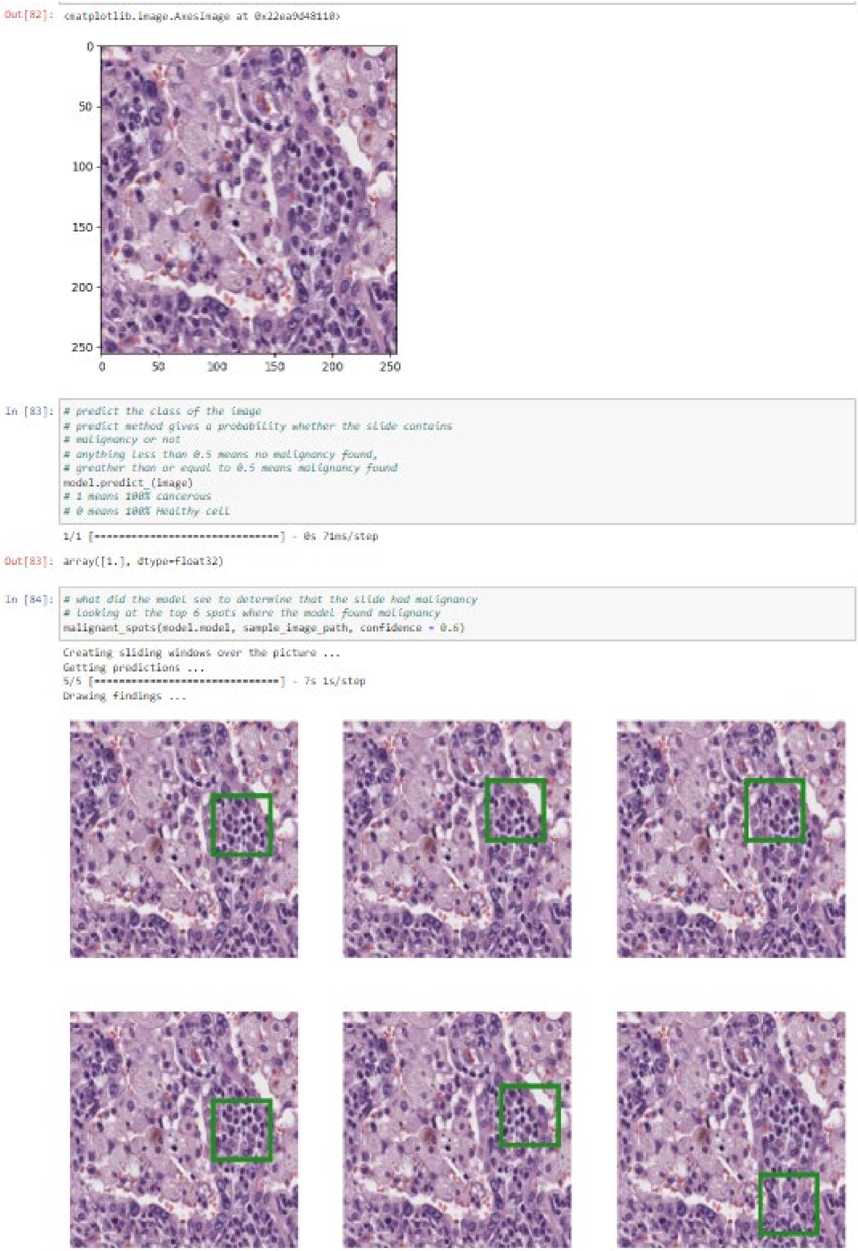


```
Out[77]: <matplotlib.image.AxesImage at 0x22ea9280ad0>
```

```
In [78]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 74ms/step

Out[78]: array([1.], dtype=float32)
```

```
In [79]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```



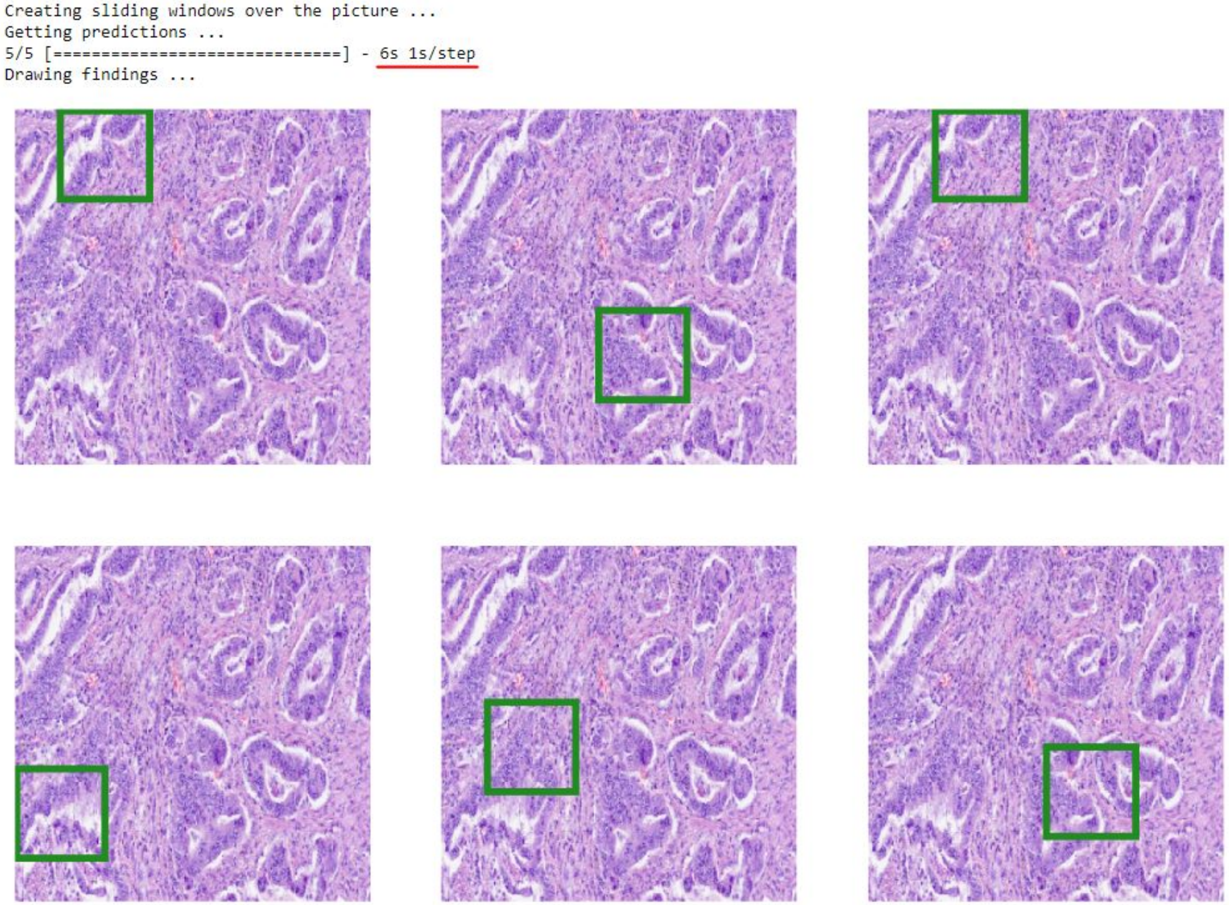


```
Out[82]: <matplotlib.image.AxesImage at 0x22ea9d48110>
```

```
In [83]: # predict the class of the image
         # predict method gives a probability whether the slide contains
         # malignancy or not
         # anything less than 0.5 means no malignancy found,
         # greather than or equal to 0.5 means malignancy found
         model.predict_(image)
         # 1 means 100% cancerous
         # 0 means 100% Healthy cell

         1/1 [==============================] - 0s 71ms/step

Out[83]: array([1.], dtype=float32)
```

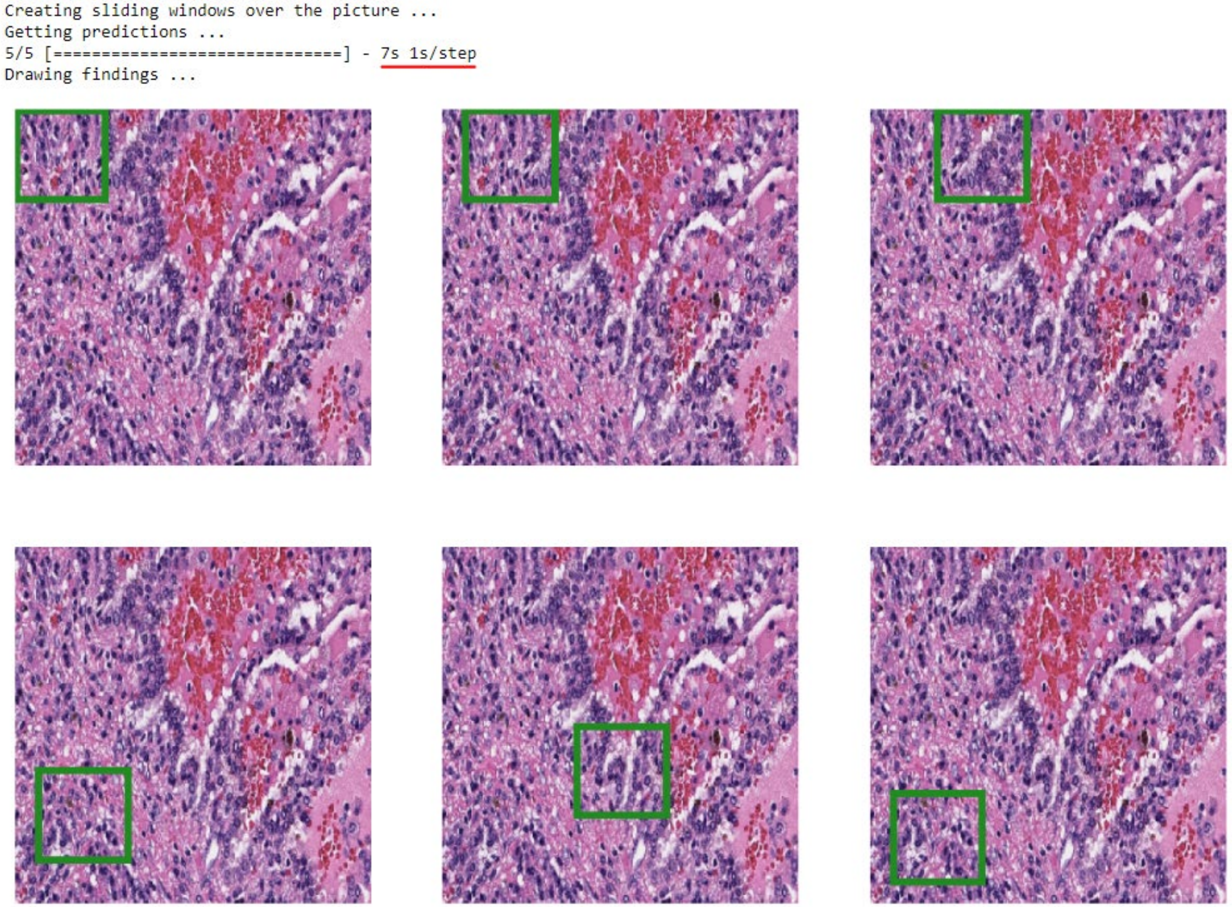
```
In [84]: # what did the model see to determine that the slide had malignancy
         # looking at the top 6 spots where the model found malignancy
         malignant_spots(model.model, sample_image_path, confidence = 0.6)

         Creating sliding windows over the picture ...
         Getting predictions ...
         5/5 [==============================] - 7s 1s/step
         Drawing findings ...
```

input_1 input: [(None, 256, 256, 3)]
InputLayer output: [(None, 256, 256, 3)]
rescaling input: (None, 256, 256, 3)
Rescaling output: (None, 256, 256, 3)
first_conv input: (None, 256, 256, 3)
Conv2D output: (None, 252, 252, 32)
batch_normalization input: (None, 252, 252, 32)
BatchNormalization output: (None, 252, 252, 32)
activation input: (None, 252, 252, 32)
Activation output: (None, 252, 252, 32)
last_conv32 input: (None, 252, 252, 32)
Conv2D output: (None, 126, 126, 32)
sep_conv32 input: (None, 252, 252, 32)
SeparableConv2D output: (None, 252, 252, 32)
batch_normalization_1 input: (None, 252, 252, 32)
BatchNormalization output: (None, 252, 252, 32)
activation_1 input: (None, 252, 252, 32)
Activation output: (None, 252, 252, 32)
sep_conv232 input: (None, 252, 252, 32)
SeparableConv2D output: (None, 252, 252, 32)
max_pooling2d input: (None, 252, 252, 32)
MaxPooling2D output: (None, 126, 126, 32)
add input: [(None, 126, 126, 32), (None, 126, 126, 32)]
Add output: (None, 126, 126, 32)
batch_normalization_2 input: (None, 126, 126, 32)
BatchNormalization output: (None, 126, 126, 32)
activation_2 input: (None, 126, 126, 32)
Activation output: (None, 126, 126, 32)
last_conv64 input: (None, 126, 126, 32)
Conv2D output: (None, 63, 63, 64)
sep_conv64 input: (None, 126, 126, 32)
SeparableConv2D output: (None, 126, 126, 64)
batch_normalization_3 input: (None, 126, 126, 64)
BatchNormalization output: (None, 126, 126, 64)
activation_3 input: (None, 126, 126, 64)
Activation output: (None, 126, 126, 64)
sep_conv264 input: (None, 126, 126, 64)
SeparableConv2D output: (None, 126, 126, 64)
max_pooling2d_1 input: (None, 126, 126, 64)
MaxPooling2D output: (None, 63, 63, 64)
add_1 input: [(None, 63, 63, 64), (None, 63, 63, 64)]
Add output: (None, 63, 63, 64)
batch_normalization_4 input: (None, 63, 63, 64)
BatchNormalization output: (None, 63, 63, 64)
activation_4 input: (None, 63, 63, 64)
Activation output: (None, 63, 63, 64)
last_conv128 input: (None, 63, 63, 64)
Conv2D output: (None, 32, 32, 128)
sep_conv128 input: (None, 63, 63, 64)
SeparableConv2D output: (None, 63, 63, 128)
batch_normalization_5 input: (None, 63, 63, 128)
BatchNormalization output: (None, 63, 63, 128)
activation_5 input: (None, 63, 63, 128)
Activation output: (None, 63, 63, 128)
sep_conv2128 input: (None, 63, 63, 128)
SeparableConv2D output: (None, 63, 63, 128)
max_pooling2d_2 input: (None, 63, 63, 128)
MaxPooling2D output: (None, 32, 32, 128)
add_2 input: [(None, 32, 32, 128), (None, 32, 32, 128)]
Add output: (None, 32, 32, 128)
batch_normalization_6 input: (None, 32, 32, 128)
BatchNormalization output: (None, 32, 32, 128)
activation_6 input: (None, 32, 32, 128)
Activation output: (None, 32, 32, 128)
last_conv256 input: (None, 32, 32, 128)
Conv2D output: (None, 16, 16, 256)
sep_conv256 input: (None, 32, 32, 128)
SeparableConv2D output: (None, 32, 32, 256)
batch_normalization_7 input: (None, 32, 32, 256)
BatchNormalization output: (None, 32, 32, 256)
activation_7 input: (None, 32, 32, 256)
Activation output: (None, 32, 32, 256)
sep_conv2256 input: (None, 32, 32, 256)
SeparableConv2D output: (None, 32, 32, 256)
max_pooling2d_3 input: (None, 32, 32, 256)
MaxPooling2D output: (None, 16, 16, 256)
add_3 input: [(None, 16, 16, 256), (None, 16, 16, 256)]
Add output: (None, 16, 16, 256)
batch_normalization_8 input: (None, 16, 16, 256)
BatchNormalization output: (None, 16, 16, 256)
activation_8 input: (None, 16, 16, 256)
Activation output: (None, 16, 16, 256)
last_conv512 input: (None, 16, 16, 256)
Conv2D output: (None, 8, 8, 512)
sep_conv512 input: (None, 16, 16, 256)
SeparableConv2D output: (None, 16, 16, 512)
batch_normalization_9 input: (None, 16, 16, 512)
BatchNormalization output: (None, 16, 16, 512)
activation_9 input: (None, 16, 16, 512)
Activation output: (None, 16, 16, 512)
sep_conv2512 input: (None, 16, 16, 512)
SeparableConv2D output: (None, 16, 16, 512)
max_pooling2d_4 input: (None, 16, 16, 512)
MaxPooling2D output: (None, 8, 8, 512)
add_4 input: [(None, 8, 8, 512), (None, 8, 8, 512)]
Add output: (None, 8, 8, 512)
global_avg_pool input: (None, 8, 8, 512)
GlobalAveragePooling2D output: (None, 512)
dropout input: (None, 512)
Dropout output: (None, 512)
dense_out input: (None, 512)
Dense output: (None, 1)



```
Creating sliding windows over the picture ...
Getting predictions ...
5/5 [==============================] - 6s 1s/step
Drawing findings ...
```

Image from our collected slides after running through the model



```
Creating sliding windows over the picture ...
Getting predictions ...
5/5 [==============================] - 7s 1s/step
Drawing findings ...
```

Image from external source after running through the model

Table S1. Comparing the results of the model by images from Department of Pathology and Laboratory Medicine at Dartmouth-Hitchcock Medical Center (DHMC) [1].

Image nr	Dartmouth-Hitchcock MC	Our model
1	solid	1
2	solid	1
3	solid	1
4	solid	1
5	lepidic	1
6	acinar	1
7	acinar	1
8	solid	1
9	acinar	1
10	acinar	1
11	acinar	1
12	solid	1
13	solid	1
14	acinar	1
15	acinar	1
16	acinar	1
17	solid	1
18	lepidic	1
19	lepidic	1
20	micropapillary	1
21	solid	1
22	solid	1
23	acinar	1
24	papillary	1
25	solid	1
26	acinar	1
27	acinar	1
28	solid	1
29	solid	1
30	solid	1
31	micropapillary	1
32	micropapillary	1
33	lepidic	1
34	acinar	1
35	lepidic	1
36	acinar	1
37	solid	1
38	lepidic	1

39	solid	1
40	solid	1
41	solid	1
42	acinar	1
43	solid	1
44	solid	1
45	solid	1
46	solid	1
47	solid	1
48	acinar	1
49	micropapillary	1
50	acinar	1
51	papillary	1
52	lepidic	1
53	micropapillary	1
54	acinar	1
55	solid	1
56	acinar	1
57	acinar	1
58	acinar	1
59	acinar	1
60	micropapillary	1
61	acinar	1
62	solid	1
63	lepidic	1
64	acinar	1
65	solid	1
66	acinar	1
67	acinar	1
68	acinar	1
69	solid	1
70	solid	1
71	solid	1
72	solid	1
73	solid	1
74	acinar	1
75	solid	1
76	solid	1
77	solid	1
78	acinar	1
79	acinar	1
80	acinar	1
81	lepidic	1

82	acinar	1
83	acinar	1
84	acinar	1
85	acinar	1
86	lepidic	1
87	lepidic	1
88	acinar	1
89	acinar	1
90	acinar	1
91	solid	1
92	acinar	1
93	lepidic	1
94	acinar	1
95	solid	1
96	papillary	1
97	acinar	1
98	acinar	1
99	acinar	1
100	acinar	1
101	lepidic	1
102	lepidic	1
103	acinar	1
104	acinar	1
105	acinar	1

Refrences

1. Wei, J.W.; Tafe, L.J.; Linnik, Y.A.; Vaickus, L.J.; Tomita, N.; Hassanpour, S. Pathologist-Level Classification of Histologic Patterns on Resected Lung Adenocarcinoma Slides with Deep Neural Networks. *Sci Rep* **2019**, *9*, 3358, doi:10.1038/s41598-019-40041-7.