

# Biosensing Analysis

This notebook walks through the biosensing analysis: segmenting the image, calculating intensity and plotting against refractive index

```
In [1]: import os
import json
import torch
from sam2.build_sam import build_sam2
from sam2.automatic_mask_generator import SAM2AutomaticMaskGenerator
import numpy as np
import cv2
from PIL import Image
import pandas as pd
import matplotlib.pyplot as plt
from scipy.stats import linregress
```

## Extract NaCl percentage and images

```
In [2]: data_dir = "C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Ch

def extract_params(filename):
    """
    Extracts the NaCl percentage from the filename.

    Args:
        filename (str): The name of the image file.

    Returns:
        dict: A dictionary with the file path and NaCl percentage.
    """
    if filename.endswith(".jpg"):
        name = filename.replace(".", ".")
        parts = name.split("-")
        prefix = "-".join(parts[:3])
        nacl_percentage = float(parts[3].strip("_"))
        chip_part = parts[4]
        return {
            "nacl_percentage": nacl_percentage,
            "group": "-".join([prefix, chip_part])
        }

def data_preprocessing(path):
    data = {}
    for filename in os.listdir(path):
        if filename.endswith(".jpg"):
            params = extract_params(filename)
            if params["group"] not in data.keys():
                data[params["group"]] = []
            data[params["group"]].append({
                "file_path": os.path.join(path, filename),
                "nacl_percentage": params["nacl_percentage"]
            })
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    })  
    for group in data.keys():  
        data[group] = sorted(data[group], key=lambda x: x["nac1_percentage"])  
    return data  
  
data = data_preprocessing(data_dir)  
print(json.dumps(data, indent=4))
```

```

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```

## Initialize SAM2

```

In [3]: # use bfloat16 for the entire notebook
# from Meta notebook
torch.autocast("cuda", dtype=torch.bfloat16).__enter__()
if torch.cuda.get_device_properties(0).major >= 8:
    torch.backends.cuda.matmul.allow_tf32 = True
    torch.backends.cudnn.allow_tf32 = True

model_cfg = "C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/sam2/s
checkpoint_base = "C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/
sam2_base = build_sam2(model_cfg, checkpoint_base, device="cuda")
generator = SAM2AutomaticMaskGenerator(
    sam2_base,
    points_per_side=96
)

```

## Helper Functions

```

In [4]: # Mask visualization for AMG masks
def show_anns(anns, ax=None, color_mask=np.array([0.0, 1.0, 0.0, 0.5])):
    if len(anns) == 0:
        return
    sorted_anns = sorted(anns, key=(lambda x: x['area']), reverse=True)
    if ax is None:
        ax = plt.gca()
    ax.set_autoscale_on(False)

    img = np.ones((sorted_anns[0]['segmentation'].shape[0], sorted_anns[0]['segm
    img[:, :, 3] = 0
    for ann in sorted_anns:
        m = ann['segmentation']
        img[m] = color_mask
        contours, _ = cv2.findContours(m.astype(np.uint8), cv2.RETR_EXTERNAL, cv
        # Try to smooth contours
        contours = [cv2.approxPolyDP(contour, epsilon=0.01, closed=True) for con
        cv2.drawContours(img, contours, -1, (0, 0, 1, 0.4), thickness=1)

    ax.imshow(img)

# Function to calculate circularity of a contour
def compute_circularity(mask):
    mask_uint8 = mask.astype(np.uint8)
    contours, _ = cv2.findContours(mask_uint8, cv2.RETR_EXTERNAL, cv2.CHAIN_APPR
    if not contours:
        return 0 # No valid contour found

    contour = max(contours, key=cv2.contourArea) # Get the largest contour
    area = cv2.contourArea(contour)
    perimeter = cv2.arcLength(contour, True)

    if perimeter == 0: # Avoid division by zero

```

```

        return 0

    circularity = (4 * np.pi * area) / (perimeter ** 2)
    return circularity

```

## Perform Segmentation

```

In [5]: def segment_image(image_path, generator):
    image = np.array(Image.open(image_path).convert("RGB"))
    masks = generator.generate(image)

    height, width = image.shape[:2]
    area = height * width

    masks = [mask for mask in masks if 0.00015 < mask['area'] / area < 0.005]
    masks = [mask for mask in masks if compute_circularity(mask['segmentation'])

    #print(f"Image size: {area}")
    #print(f"Max mask area: {max(mask['area'] for mask in masks) / area}")
    #print(f"Min mask area: {min(mask['area'] for mask in masks) / area}")

    # Group masks by well size
    masks_large = [mask for mask in masks if mask['area'] / area > 0.003]
    masks_medium = [mask for mask in masks if 0.0005 < mask['area'] / area < 0.003]
    masks_small = [mask for mask in masks if mask['area'] / area <= 0.0005]

    return masks, masks_large, masks_medium, masks_small

def calculate_intensity(gray_image, masks):
    circle_masks = []
    for mask in masks:
        m = mask["segmentation"].astype(np.uint8)
        contours, _ = cv2.findContours(m, cv2.RETR_EXTERNAL, cv2.CHAIN_APPROX_NONE)
        M = cv2.moments(m)
        if M["m00"] != 0:
            cx = int(M["m10"] / M["m00"])
            cy = int(M["m01"] / M["m00"])
        else:
            cx, cy = 0, 0 # fallback if mask is empty
        (_, _), radius = cv2.minEnclosingCircle(contours[0])
        reduced_radius = int(radius * 0.75)
        circle_mask = np.zeros(m.shape[:2], dtype=np.uint8)
        cv2.circle(circle_mask, (cx, cy), reduced_radius, 255, -1)
        circle_masks.append(circle_mask)

    intensities = [np.mean(gray_image[circle_mask]) for circle_mask in circle_masks]
    return intensities

for group, items in data.items():
    calibration_data = []
    for item in items:
        image_path = item["file_path"]
        masks, masks_large, masks_medium, masks_small = segment_image(image_path, generator)

        # Create grayscale version for intensity measurement
        gray_image = np.array(Image.open(image_path).convert("L"))

```

```

# Compute mean intensity for each filtered mask
#intensities = [np.mean(gray_image[mask['segmentation']])] for mask in ma
intensities_large = [np.mean(gray_image[mask['segmentation']])] for mask
intensities_medium = [np.mean(gray_image[mask['segmentation']])] for mask
intensities_small = [np.mean(gray_image[mask['segmentation']])] for mask
intensities_all = [np.mean(gray_image[mask['segmentation']])] for mask in

# Remove outliers using a 2σ filter
#mean_val = np.mean(intensities)
#std_val = np.std(intensities)
#lower_thresh = mean_val - 2 * std_val
#upper_thresh = mean_val + 2 * std_val
#valid_indices = [i for i, intensity in enumerate(intensities)
                  #if lower_thresh <= intensity <= upper_thresh]
#intensities = [intensities[i] for i in valid_indices]
#masks = [masks[i] for i in valid_indices]

mean_intensity_large = np.mean(intensities_large)
std_intensity_large = np.std(intensities_large)
mean_intensity_medium = np.mean(intensities_medium)
std_intensity_medium = np.std(intensities_medium)
mean_intensity_small = np.mean(intensities_small)
std_intensity_small = np.std(intensities_small)
mean_intensity_all = np.mean(intensities_all)
std_intensity_all = np.std(intensities_all)

calibration_data.append({
    'NaCl_percentage': item["nacl_percentage"],
    'mean_intensity_large': mean_intensity_large,
    'std_intensity_large': std_intensity_large,
    'mean_intensity_medium': mean_intensity_medium,
    'std_intensity_medium': std_intensity_medium,
    'mean_intensity_small': mean_intensity_small,
    'std_intensity_small': std_intensity_small,
    'mean_intensity_all': mean_intensity_all,
    'std_intensity_all': std_intensity_all,
    'num_wells': len(masks),
    'image_path': image_path,
    'image_name': os.path.basename(image_path),
    'masks': masks,
    'masks_large': masks_large,
    'masks_medium': masks_medium,
    'masks_small': masks_small
})

# Create DataFrame and sort by NaCl percentage
df_data = pd.DataFrame(calibration_data).sort_values('NaCl_percentage')
df_data = df_data.drop(columns=['masks', 'masks_large', 'masks_medium', 'mas

# Fill NaN values with 0 if the entire column is NaN
df_data.loc[:, df_data.isna().all()] = 0

# Compute refractive index (RI) using a simplified linear model
df_data['RI'] = 1.3330 + 0.0018 * df_data['NaCl_percentage']
# Drop rows with NaN values
df_calibration = df_data.dropna()

# Draw 9 plots visualizing the detected masks filtered by large, medium, sma
fig, axes = plt.subplots(3, 3, figsize=(10, 10))

```

```

for i in range(3):
    for j in range(3):
        idx = i * 3 + j
        ax = axes[i, j]
        masks_large = calibration_data[idx]["masks_large"]
        masks_medium = calibration_data[idx]["masks_medium"]
        masks_small = calibration_data[idx]["masks_small"]
        masks = calibration_data[idx]["masks"]

        if len(masks) == len(masks_large) + len(masks_medium) + len(masks_small):
            print(f"Image {idx} - {calibration_data[idx]['image_name']} has {len(masks)} masks")

        image_path = calibration_data[idx]["image_path"]

        ax.imshow(np.array(Image.open(image_path)))
        ax.set_title(f"{os.path.basename(image_path)} - {calibration_data[idx]['image_name']}")
        if masks_large:
            show_anns(masks_large, ax=ax, color_mask=np.array([1.0, 0.0, 0.0]))
        if masks_medium:
            show_anns(masks_medium, ax=ax, color_mask=np.array([0.0, 1.0, 0.0]))
        if masks_small:
            show_anns(masks_small, ax=ax, color_mask=np.array([0.0, 0.0, 1.0]))
        ax.axis("off")

plt.tight_layout()
plt.show()

# Draw 3 plots visualizing the average intensity vs RI by well size
# Plot the calibration curve - Large
fig, axes = plt.subplots(1, 4, figsize=(20, 5))
axes[0].errorbar(df_calibration['RI'], df_calibration['mean_intensity_large'],
                 yerr=df_calibration['std_intensity_large'], fmt='o', capsize=5,
                 color='blue', markersize=8, label='Measured Data')

# Perform Linear regression - Large
slope, intercept, r_value, p_value, std_err = linregress(
    df_calibration['RI'], df_calibration['mean_intensity_large']
)
r_squared = r_value**2
x_fit = np.linspace(df_calibration['RI'].min(), df_calibration['RI'].max(), 100)
y_fit = slope * x_fit + intercept
axes[0].plot(x_fit, y_fit, '--', color='red',
             label=f'Linear Fit\ny = {slope:.2f}x + {intercept:.2f}\nR² = {r_squared:.2f}')

# Annotate points with NaCl percentages - Large
for i, row in df_calibration.iterrows():
    axes[0].annotate(f"{row['NaCl_percentage']}%",
                    (row['RI'], row['mean_intensity_large']),
                    xytext=(5, 5), textcoords='offset points')

axes[0].set_title(f'Calibration Curve - Large Wells')
axes[0].set_xlabel('Refractive Index (RI)')
axes[0].set_ylabel('Mean Intensity (AU/pixel)')
axes[0].grid(True)
axes[0].legend()

# Plot the calibration curve - medium
axes[1].errorbar(df_calibration['RI'], df_calibration['mean_intensity_medium'],
                 yerr=df_calibration['std_intensity_medium'], fmt='o', capsize=5,
                 color='blue', markersize=8, label='Measured Data')

```

```

# Perform Linear regression - medium
slope, intercept, r_value, p_value, std_err = linregress(
    df_calibration['RI'], df_calibration['mean_intensity_medium']
)
r_squared = r_value**2
x_fit = np.linspace(df_calibration['RI'].min(), df_calibration['RI'].max(),
y_fit = slope * x_fit + intercept
axes[1].plot(x_fit, y_fit, '--', color='red',
    label=f'Linear Fit\ny = {slope:.2f}x + {intercept:.2f}\nR² = {r_squ

# Annotate points with NaCl percentages - medium
for i, row in df_calibration.iterrows():
    axes[1].annotate(f"{row['NaCl_percentage']}%",
        (row['RI'], row['mean_intensity_medium']),
        xytext=(5, 5), textcoords='offset points')

axes[1].set_title(f'Calibration Curve - Medium Wells')
axes[1].set_xlabel('Refractive Index (RI)')
axes[1].set_ylabel('Mean Intensity (AU/pixel)')
axes[1].grid(True)
axes[1].legend()

# Plot the calibration curve - small
axes[2].errorbar(df_calibration['RI'], df_calibration['mean_intensity_small'],
    yerr=df_calibration['std_intensity_small'], fmt='o', capsize=5,
    color='blue', markersize=8, label='Measured Data')

# Perform Linear regression - small
slope, intercept, r_value, p_value, std_err = linregress(
    df_calibration['RI'], df_calibration['mean_intensity_small']
)
r_squared = r_value**2
x_fit = np.linspace(df_calibration['RI'].min(), df_calibration['RI'].max(),
y_fit = slope * x_fit + intercept
axes[2].plot(x_fit, y_fit, '--', color='red',
    label=f'Linear Fit\ny = {slope:.2f}x + {intercept:.2f}\nR² = {r_squ

# Annotate points with NaCl percentages - small
for i, row in df_calibration.iterrows():
    axes[2].annotate(f"{row['NaCl_percentage']}%",
        (row['RI'], row['mean_intensity_small']),
        xytext=(5, 5), textcoords='offset points')

axes[2].set_title(f'Calibration Curve - Small Wells')
axes[2].set_xlabel('Refractive Index (RI)')
axes[2].set_ylabel('Mean Intensity (AU/pixel)')
axes[2].grid(True)
axes[2].legend()

# Plot the calibration curve - all
axes[3].errorbar(df_calibration['RI'], df_calibration['mean_intensity_all'],
    yerr=df_calibration['std_intensity_all'], fmt='o', capsize=5,
    color='blue', markersize=8, label='Measured Data')

# Perform Linear regression - all
slope, intercept, r_value, p_value, std_err = linregress(
    df_calibration['RI'], df_calibration['mean_intensity_all']
)
r_squared = r_value**2

```

```

x_fit = np.linspace(df_calibration['RI'].min(), df_calibration['RI'].max(),
y_fit = slope * x_fit + intercept
axes[3].plot(x_fit, y_fit, '--', color='red',
              label=f'Linear Fit\ny = {slope:.2f}x + {intercept:.2f}\nR² = {r_squ

# Annotate points with NaCl percentages - all
for i, row in df_calibration.iterrows():
    axes[3].annotate(f"{row['NaCl_percentage']}%",
                    (row['RI'], row['mean_intensity_all']),
                    xytext=(5, 5), textcoords='offset points')

axes[3].set_title(f'Calibration Curve - All Wells')
axes[3].set_xlabel('Refractive Index (RI)')
axes[3].set_ylabel('Mean Intensity (AU/pixel)')
axes[3].grid(True)
axes[3].legend()

plt.tight_layout()
plt.show()

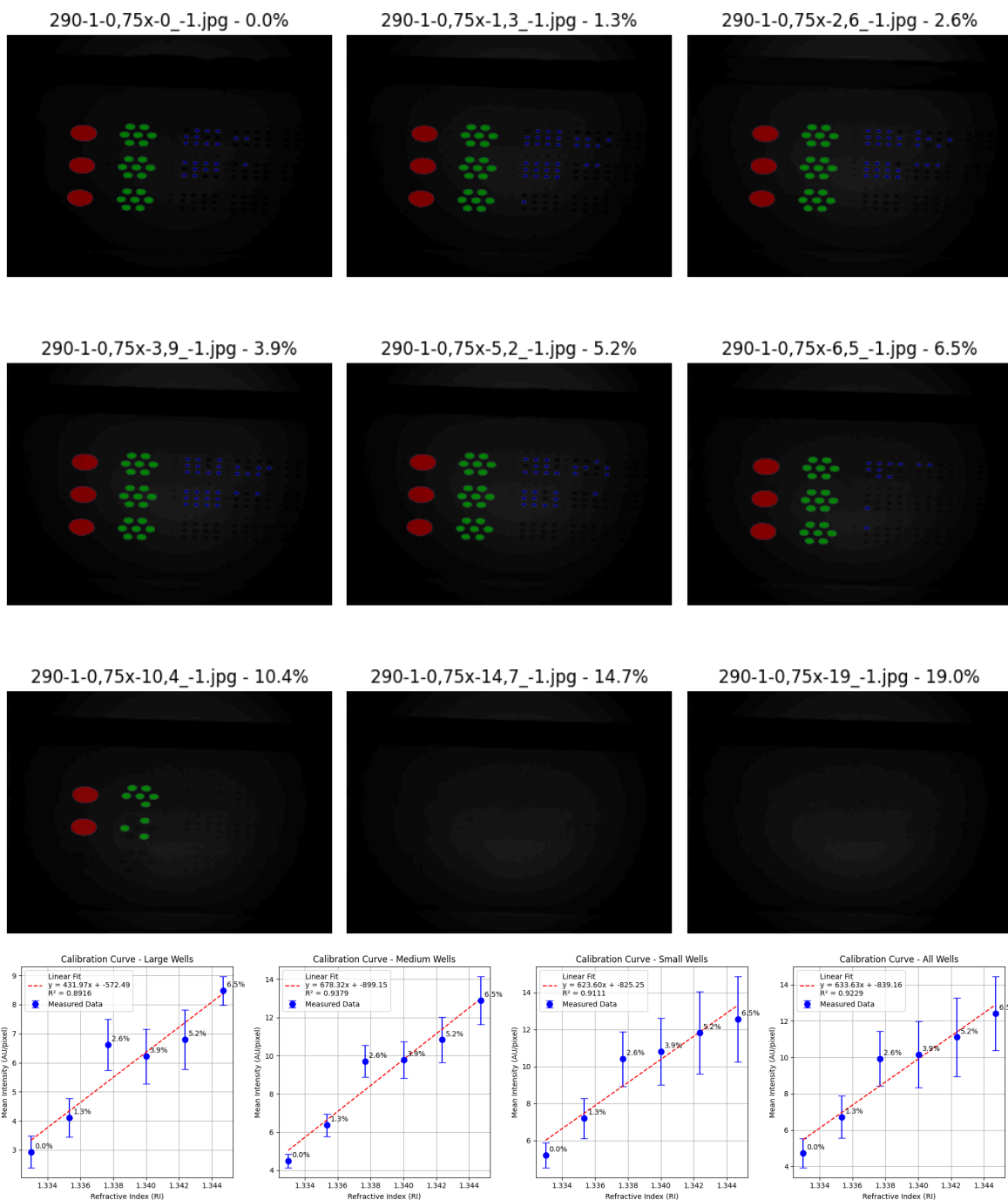
# Output calibration data and regression results
print("\n==== Calibration Data =====")
print(df_data.to_string(index=False))

```

```

c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\fromnumeric.py:3860: RuntimeWarning: Mean of empty slice.
    return _methods._mean(a, axis=axis, dtype=dtype,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:145: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:223: RuntimeWarning: Degrees of freedom <= 0 for slic
e
    ret = _var(a, axis=axis, dtype=dtype, out=out, ddof=ddof,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:181: RuntimeWarning: invalid value encountered in div
ide
    arrmean = um.true_divide(arrmean, div, out=arrmean,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:215: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
Image 0 - 290-1-0,75x-0_-1.jpg has all masks
Image 1 - 290-1-0,75x-1,3_-1.jpg has all masks
Image 2 - 290-1-0,75x-2,6_-1.jpg has all masks
Image 3 - 290-1-0,75x-3,9_-1.jpg has all masks
Image 4 - 290-1-0,75x-5,2_-1.jpg has all masks
Image 5 - 290-1-0,75x-6,5_-1.jpg has all masks
Image 6 - 290-1-0,75x-10,4_-1.jpg has all masks
Image 7 - 290-1-0,75x-14,7_-1.jpg has all masks
Image 8 - 290-1-0,75x-19_-1.jpg has all masks

```





==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI	
3	0.0	0.360004	0.548564	0.681705	4.7	0.802929	45	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-0_-1.jpg	290-1-0,75x-0_-1.jpg	1.33300	2.932525	0.548564	4.48695
8	1.3	0.578902	0.663795	1.078060	6.7	1.162909	56	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-1,3_-1.jpg	290-1-0,75x-1,3_-1.jpg	1.33534	4.116211	0.663795	6.36453
5	2.6	0.834715	0.881224	1.469010	9.9	1.505651	55	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-2,6_-1.jpg	290-1-0,75x-2,6_-1.jpg	1.33768	6.619399	0.881224	9.70823
0	3.9	0.963379	0.939964	1.792511	10.1	1.828182	54	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-3,9_-1.jpg	290-1-0,75x-3,9_-1.jpg	1.34002	6.223832	0.939964	9.78514
9	5.2	1.181527	1.021439	2.229968	11.1	2.156241	50	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-5,2_-1.jpg	290-1-0,75x-5,2_-1.jpg	1.34236	6.797808	1.021439	10.83357
8	6.5	1.253227	0.493453	2.311463	12.4	2.037976	36	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-6,5_-1.jpg	290-1-0,75x-6,5_-1.jpg	1.34470	8.478402	0.493453	12.90095
5	10.4	1.717897	0.048926	NaN	15.47118	2.313074	11	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-10,4_-1.jpg	290-1-0,75x-10,4_-1.jpg	1.35172	11.029154	0.048926	15.47118
N	14.7	NaN	NaN	NaN	NaN	NaN	0	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-14,7_-1.jpg	290-1-0,75x-14,7_-1.jpg	1.35946	NaN	NaN	NaN
N	19.0	NaN	NaN	NaN	NaN	NaN	0	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_\290-1-0,75x-19_-1.jpg	290-1-0,75x-19_-1.jpg	1.36720	NaN	NaN	NaN

```

c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\fromnumeric.py:3860: RuntimeWarning: Mean of empty slice.
    return _methods._mean(a, axis=axis, dtype=dtype,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:145: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:223: RuntimeWarning: Degrees of freedom <= 0 for slic
e
    ret = _var(a, axis=axis, dtype=dtype, out=out, ddof=ddof,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:181: RuntimeWarning: invalid value encountered in div
ide
    arrmean = um.true_divide(arrmean, div, out=arrmean,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:215: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)

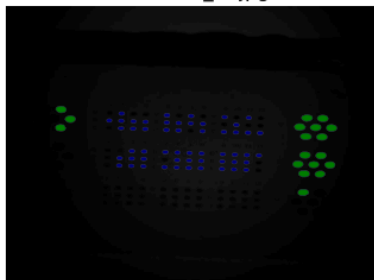
```

Image 0 - 290-1-0,75x-0\_-2.jpg has all masks  
Image 1 - 290-1-0,75x-1,3\_-2.jpg has all masks  
Image 2 - 290-1-0,75x-2,6\_-2.jpg has all masks  
Image 3 - 290-1-0,75x-3,9\_-2.jpg has all masks  
Image 4 - 290-1-0,75x-5,2\_-2.jpg has all masks  
Image 5 - 290-1-0,75x-6,5\_-2.jpg has all masks  
Image 6 - 290-1-0,75x-10,4\_-2.jpg has all masks  
Image 7 - 290-1-0,75x-14,7\_-2.jpg has all masks  
Image 8 - 290-1-0,75x-19\_-2.jpg has all masks

290-1-0,75x-0\_-2.jpg - 0.0%



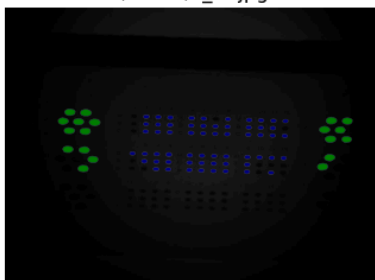
290-1-0,75x-1,3\_-2.jpg - 1.3%



290-1-0,75x-2,6\_-2.jpg - 2.6%



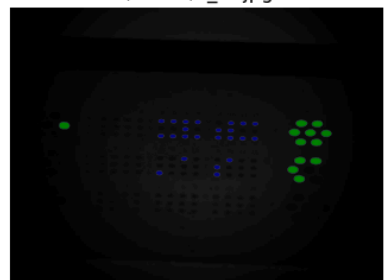
290-1-0,75x-3,9\_-2.jpg - 3.9%



290-1-0,75x-5,2\_-2.jpg - 5.2%



290-1-0,75x-6,5\_-2.jpg - 6.5%



290-1-0,75x-10,4\_-2.jpg - 10.4%

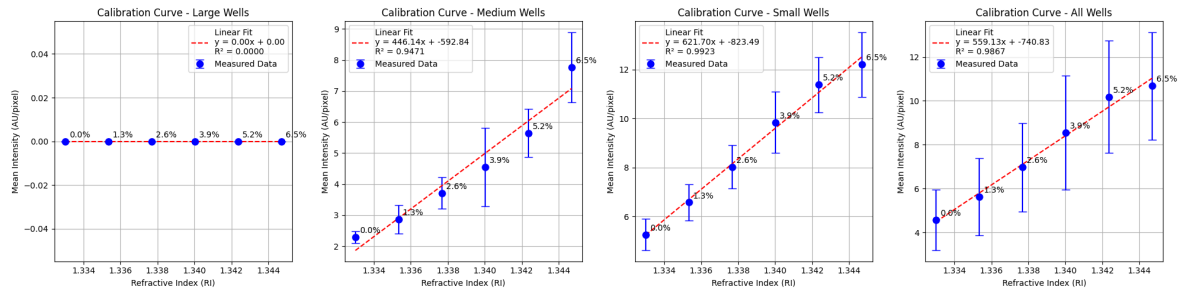


290-1-0,75x-14,7\_-2.jpg - 14.7%



290-1-0,75x-19\_-2.jpg - 19.0%





==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.29343					
3	0.192377		5.260525	0.646457		4.5							
65113	1.381444	64	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-0_-2.jpg	290-1-0,75x-0_-2.jpg	1.33300								
	1.3	0.0	0.0	2.86335									
2	0.457338		6.574073	0.745653		5.6							
33327	1.753257	71	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-1,3_-2.jpg	290-1-0,75x-1,3_-2.jpg	1.33534								
	2.6	0.0	0.0	3.70891									
3	0.510834		8.021173	0.880778		6.9							
72245	2.018302	74	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-2,6_-2.jpg	290-1-0,75x-2,6_-2.jpg	1.33768								
	3.9	0.0	0.0	4.54847									
0	1.260153		9.843510	1.248060		8.5							
53692	2.594426	78	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-3,9_-2.jpg	290-1-0,75x-3,9_-2.jpg	1.34002								
	5.2	0.0	0.0	5.64402									
1	0.773367		11.374764	1.132572		10.1							
80859	2.560594	72	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-5,2_-2.jpg	290-1-0,75x-5,2_-2.jpg	1.34236								
	6.5	0.0	0.0	7.76490									
1	1.133128		12.199160	1.325328		10.6							
78842	2.454507	35	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-6,5_-2.jpg	290-1-0,75x-6,5_-2.jpg	1.34470								
	10.4	0.0	0.0	Na									
N	NaN	NaN	NaN	NaN									
NaN	NaN	0	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-10,4_-2.jpg	290-1-0,75x-10,4_-2.jpg	1.35172								
	14.7	0.0	0.0	Na									
N	NaN	NaN	NaN	NaN									
NaN	NaN	0	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-14,7_-2.jpg	290-1-0,75x-14,7_-2.jpg	1.35946								
	19.0	0.0	0.0	Na									
N	NaN	NaN	NaN	NaN									
NaN	NaN	0	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-19_-2.jpg	290-1-0,75x-19_-2.jpg	1.36720								

```

c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\fromnumeric.py:3860: RuntimeWarning: Mean of empty slice.
    return _methods._mean(a, axis=axis, dtype=dtype,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:145: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:223: RuntimeWarning: Degrees of freedom <= 0 for slic
e
    ret = _var(a, axis=axis, dtype=dtype, out=out, ddof=ddof,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:181: RuntimeWarning: invalid value encountered in div
ide
    arrmean = um.true_divide(arrmean, div, out=arrmean,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:215: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)

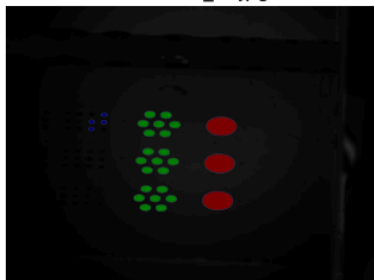
```

Image 0 - 290-1-0,75x-0\_-3.jpg has all masks  
 Image 1 - 290-1-0,75x-1,3\_-3.jpg has all masks  
 Image 2 - 290-1-0,75x-2,6\_-3.jpg has all masks  
 Image 3 - 290-1-0,75x-3,9\_-3.jpg has all masks  
 Image 4 - 290-1-0,75x-5,2\_-3.jpg has all masks  
 Image 5 - 290-1-0,75x-6,5\_-3.jpg has all masks  
 Image 6 - 290-1-0,75x-10,4\_-3.jpg has all masks  
 Image 7 - 290-1-0,75x-14,7\_-3.jpg has all masks  
 Image 8 - 290-1-0,75x-19\_-3.jpg has all masks

290-1-0,75x-0\_-3.jpg - 0.0%



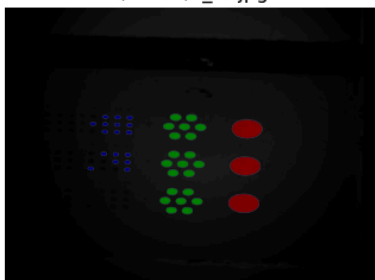
290-1-0,75x-1,3\_-3.jpg - 1.3%



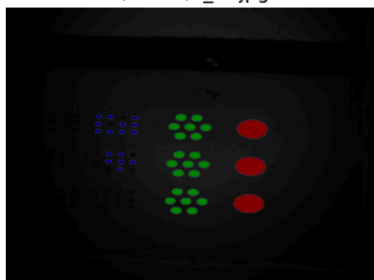
290-1-0,75x-2,6\_-3.jpg - 2.6%



290-1-0,75x-3,9\_-3.jpg - 3.9%



290-1-0,75x-5,2\_-3.jpg - 5.2%



290-1-0,75x-6,5\_-3.jpg - 6.5%



290-1-0,75x-10,4\_-3.jpg - 10.4%

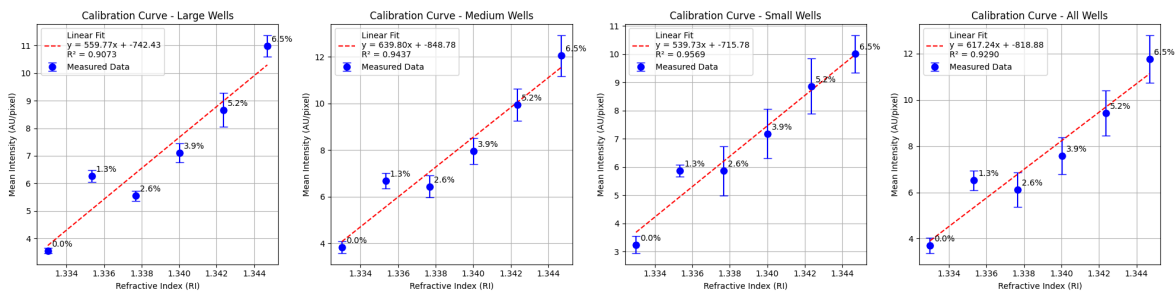


290-1-0,75x-14,7\_-3.jpg - 14.7%



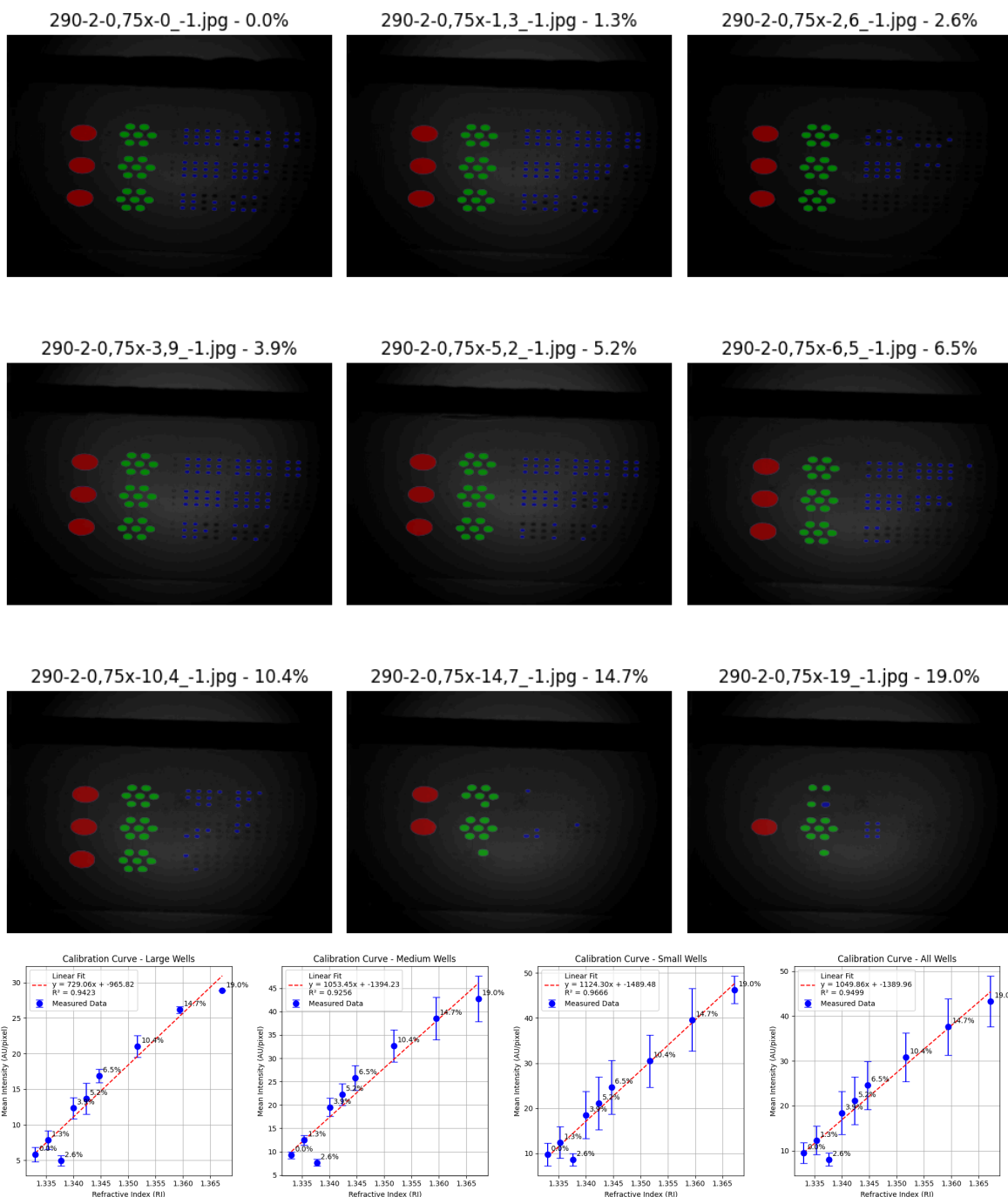
290-1-0,75x-19\_-3.jpg - 19.0%





==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
0	0.0	3.563477	0.103248	3.82733									
1	0.262321	3.241290	0.309914	3.6									
98762	0.336970	31	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-0_-3.jpg	290-1-0,75x-0_-3.jpg	1.33300								
0	1.3	6.268437	0.222021	6.68655									
20891	0.325229	5.862215	0.207828	6.5									
20891	0.419963	30	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-1,3_-3.jpg	290-1-0,75x-1,3_-3.jpg	1.33534								
6	2.6	5.550845	0.181660	6.43958									
19022	0.460976	5.864361	0.876892	6.1									
19022	0.744732	46	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-2,6_-3.jpg	290-1-0,75x-2,6_-3.jpg	1.33768								
6	3.9	7.105982	0.338247	7.94849									
76083	0.563133	7.177095	0.873162	7.5									
76083	0.797337	42	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-3,9_-3.jpg	290-1-0,75x-3,9_-3.jpg	1.34002								
7	5.2	8.664396	0.612565	9.94099									
29225	0.685450	8.868943	0.983780	9.4									
29225	0.981375	41	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-5,2_-3.jpg	290-1-0,75x-5,2_-3.jpg	1.34236								
4	6.5	10.983926	0.393353	12.05284									
72786	0.883909	10.015471	0.663244	11.7									
72786	1.027347	26	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-6,5_-3.jpg	290-1-0,75x-6,5_-3.jpg	1.34470								
3	10.4	15.374262	0.860400	16.37305									
23234	1.543124	NaN	NaN	16.2									
23234	1.504088	20	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-10,4_-3.jpg	290-1-0,75x-10,4_-3.jpg	1.35172								
N	14.7	20.678398	0.000000	NaN									
78398	NaN	NaN	NaN	20.6									
78398	0.000000	1	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-14,7_-3.jpg	290-1-0,75x-14,7_-3.jpg	1.35946								
N	19.0	NaN	NaN	NaN									
NaN	NaN	NaN	NaN	NaN									
NaN	NaN	0	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-1-0,75x-19_-3.jpg	290-1-0,75x-19_-3.jpg	1.36720								
Image 0 - 290-2-0,75x-0_-1.jpg has all masks													
Image 1 - 290-2-0,75x-1,3_-1.jpg has all masks													
Image 2 - 290-2-0,75x-2,6_-1.jpg has all masks													
Image 3 - 290-2-0,75x-3,9_-1.jpg has all masks													
Image 4 - 290-2-0,75x-5,2_-1.jpg has all masks													
Image 5 - 290-2-0,75x-6,5_-1.jpg has all masks													
Image 6 - 290-2-0,75x-10,4_-1.jpg has all masks													
Image 7 - 290-2-0,75x-14,7_-1.jpg has all masks													
Image 8 - 290-2-0,75x-19_-1.jpg has all masks													



==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
0	0.0	5.816510	0.996627	9.24992									
7	0.738406	9.749811	2.541925	9.4									
93518	2.317952	87	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-0_-1.jpg	290-2-0,75x-0_-1.jpg	1.33300								
1.3	7.877655	1.299227	12.46115										
6	1.075049	12.449116	3.457241	12.3									
02795	3.132635	92	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-1,3_-1.jpg	290-2-0,75x-1,3_-1.jpg	1.33534								
2.6	4.948489	0.748481	7.66675										
0	0.738471	8.630635	1.387462	8.0									
04875	1.440767	50	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-2,6_-1.jpg	290-2-0,75x-2,6_-1.jpg	1.33768								
3.9	12.351756	1.506091	19.53178										
2	1.912867	18.531145	5.207390	18.4									
23715	4.764893	92	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-3,9_-1.jpg	290-2-0,75x-3,9_-1.jpg	1.34002								
5.2	13.679728	2.172478	22.23356										
6	2.319041	21.159634	5.857591	21.1									
61027	5.299559	81	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-5,2_-1.jpg	290-2-0,75x-5,2_-1.jpg	1.34236								
6.5	16.853365	0.948158	25.77210										
8	2.642172	24.671232	5.924230	24.5									
61056	5.376319	74	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-6,5_-1.jpg	290-2-0,75x-6,5_-1.jpg	1.34470								
10.4	21.034698	1.560333	32.63615										
4	3.402287	30.491062	5.766301	30.8									
38517	5.415063	48	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-10,4_-1.jpg	290-2-0,75x-10,4_-1.jpg	1.35172								
14.7	26.178101	0.477937	38.50334										
1	4.566178	39.641862	6.981992	37.6									
00585	6.284097	21	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-14,7_-1.jpg	290-2-0,75x-14,7_-1.jpg	1.35946								
19.0	28.854130	0.000000	42.74849										
8	4.892191	46.297724	3.074410	43.3									
24825	5.639870	19	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-19_-1.jpg	290-2-0,75x-19_-1.jpg	1.36720								



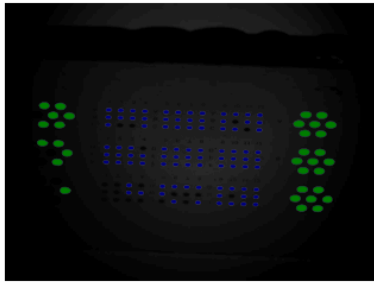
```

c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\fromnumeric.py:3860: RuntimeWarning: Mean of empty slice.
    return _methods._mean(a, axis=axis, dtype=dtype,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:145: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:223: RuntimeWarning: Degrees of freedom <= 0 for slic
e
    ret = _var(a, axis=axis, dtype=dtype, out=out, ddof=ddof,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:181: RuntimeWarning: invalid value encountered in div
ide
    arrmean = um.true_divide(arrmean, div, out=arrmean,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:215: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)

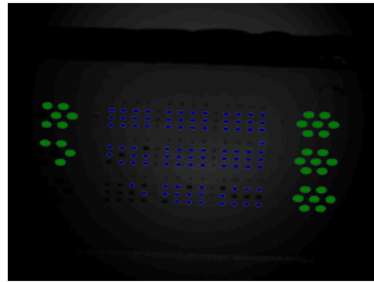
```

Image 0 - 290-2-0,75x-0\_-2.jpg has all masks  
 Image 1 - 290-2-0,75x-1,3\_-2.jpg has all masks  
 Image 2 - 290-2-0,75x-2,6\_-2.jpg has all masks  
 Image 3 - 290-2-0,75x-3,9\_-2.jpg has all masks  
 Image 5 - 290-2-0,75x-6,5\_-2.jpg has all masks  
 Image 6 - 290-2-0,75x-10,4\_-2.jpg has all masks  
 Image 7 - 290-2-0,75x-14,7\_-2.jpg has all masks  
 Image 8 - 290-2-0,75x-19\_-2.jpg has all masks

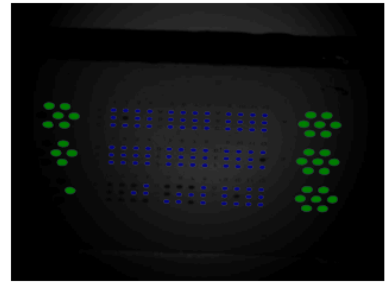
290-2-0,75x-0\_-2.jpg - 0.0%



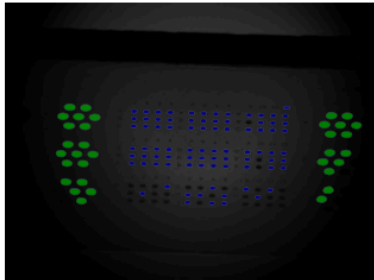
290-2-0,75x-1,3\_-2.jpg - 1.3%



290-2-0,75x-2,6\_-2.jpg - 2.6%



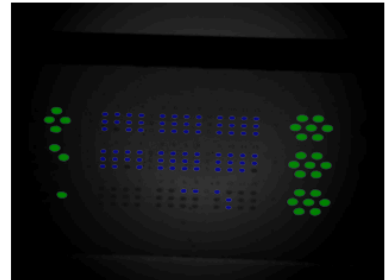
290-2-0,75x-3,9\_-2.jpg - 3.9%



290-2-0,75x-5,2\_-2.jpg - 5.2%



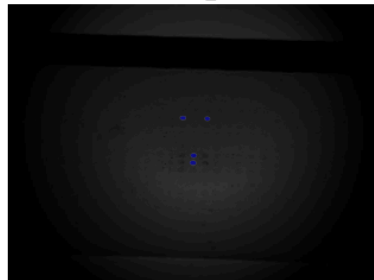
290-2-0,75x-6,5\_-2.jpg - 6.5%



290-2-0,75x-10,4\_-2.jpg - 10.4%

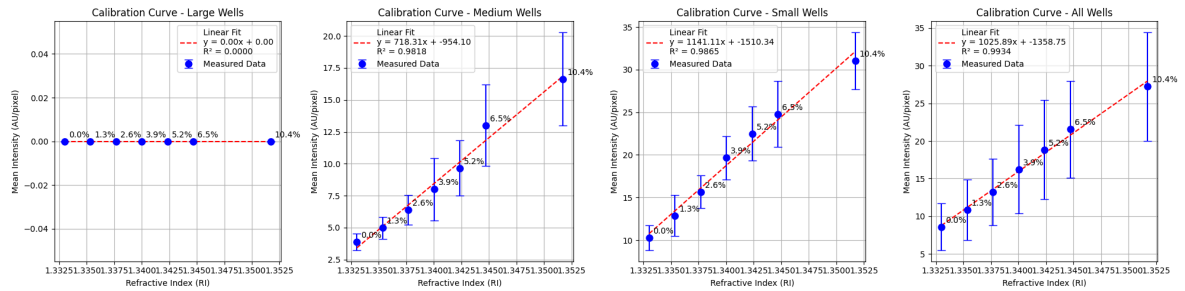


290-2-0,75x-14,7\_-2.jpg - 14.7%



290-2-0,75x-19\_-2.jpg - 19.0%





==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.87961					
8	0.669568	10.273323	1.477157	8.5									
68335	3.116711	120	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-0_-2.jpg	290-2-0,75x-0_-2.jpg	1.33300							
	1.3	0.0	0.0	0.0	4.98192								
4	0.859163	12.870703	2.407647	10.8									
49611	4.044737	121	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-1,3_-2.jpg	290-2-0,75x-1,3_-2.jpg	1.33534							
	2.6	0.0	0.0	0.0	6.39849								
5	1.169837	15.656260	1.913059	13.2									
47736	4.422698	123	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-2,6_-2.jpg	290-2-0,75x-2,6_-2.jpg	1.33768							
	3.9	0.0	0.0	0.0	7.99779								
2	2.452127	19.652003	2.571891	16.2									
36113	5.880430	116	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-3,9_-2.jpg	290-2-0,75x-3,9_-2.jpg	1.34002							
	5.2	0.0	0.0	0.0	9.66215								
1	2.156059	22.487412	3.149504	18.8									
52037	6.571562	115	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-5,2_-2.jpg	290-2-0,75x-5,2_-2.jpg	1.34236							
	6.5	0.0	0.0	0.0	13.01058								
1	3.195065	24.774933	3.867623	21.5									
45503	6.420086	102	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-6,5_-2.jpg	290-2-0,75x-6,5_-2.jpg	1.34470							
	10.4	0.0	0.0	0.0	16.63837								
5	3.663104	31.043435	3.351967	27.2									
52630	7.214336	57	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-10,4_-2.jpg	290-2-0,75x-10,4_-2.jpg	1.35172							
	14.7	0.0	0.0	0.0	Na								
N	NaN	31.937047	1.934941	31.9									
37047	1.934941	4	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-14,7_-2.jpg	290-2-0,75x-14,7_-2.jpg	1.35946							
	19.0	0.0	0.0	0.0	Na								
N	NaN	43.283843	0.000000	43.2									
83843	0.000000	1	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl	0-19_290-2-0,75x-19_-2.jpg	290-2-0,75x-19_-2.jpg	1.36720							

```

c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\fromnumeric.py:3860: RuntimeWarning: Mean of empty slice.
    return _methods._mean(a, axis=axis, dtype=dtype,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:145: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:223: RuntimeWarning: Degrees of freedom <= 0 for slic
e
    ret = _var(a, axis=axis, dtype=dtype, out=out, ddof=ddof,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:181: RuntimeWarning: invalid value encountered in div
ide
    arrmean = um.true_divide(arrmean, div, out=arrmean,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:215: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)

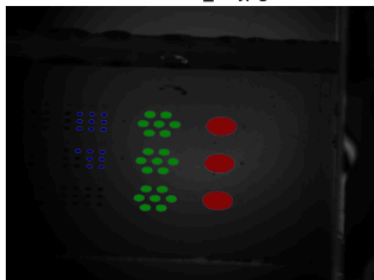
```

Image 0 - 290-2-0,75x-0\_-3.jpg has all masks  
 Image 1 - 290-2-0,75x-1,3\_-3.jpg has all masks  
 Image 2 - 290-2-0,75x-2,6\_-3.jpg has all masks  
 Image 3 - 290-2-0,75x-3,9\_-3.jpg has all masks  
 Image 4 - 290-2-0,75x-5,2\_-3.jpg has all masks  
 Image 5 - 290-2-0,75x-6,5\_-3.jpg has all masks  
 Image 6 - 290-2-0,75x-10,4\_-3.jpg has all masks  
 Image 7 - 290-2-0,75x-14,7\_-3.jpg has all masks  
 Image 8 - 290-2-0,75x-19\_-3.jpg has all masks

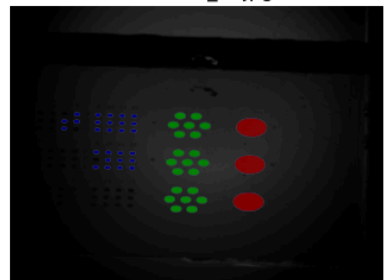
290-2-0,75x-0\_-3.jpg - 0.0%



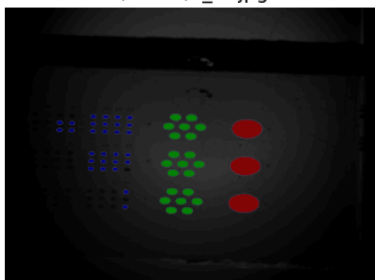
290-2-0,75x-1,3\_-3.jpg - 1.3%



290-2-0,75x-2,6\_-3.jpg - 2.6%



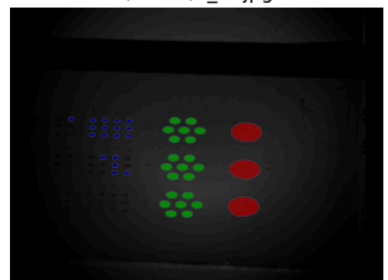
290-2-0,75x-3,9\_-3.jpg - 3.9%



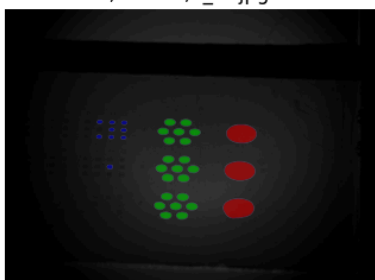
290-2-0,75x-5,2\_-3.jpg - 5.2%



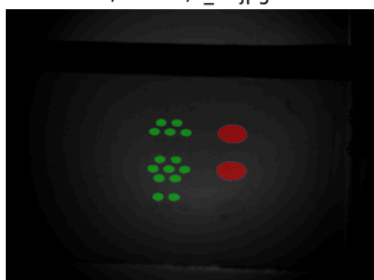
290-2-0,75x-6,5\_-3.jpg - 6.5%



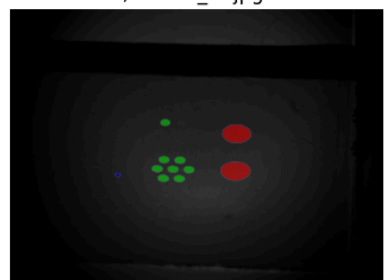
290-2-0,75x-10,4\_-3.jpg - 10.4%

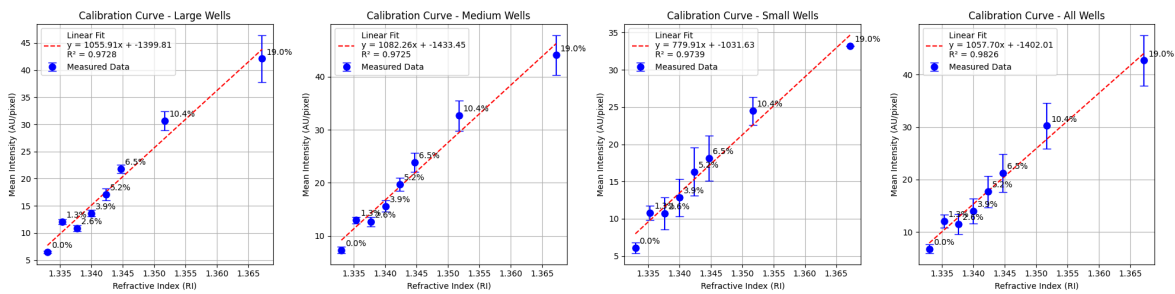


290-2-0,75x-14,7\_-3.jpg - 14.7%



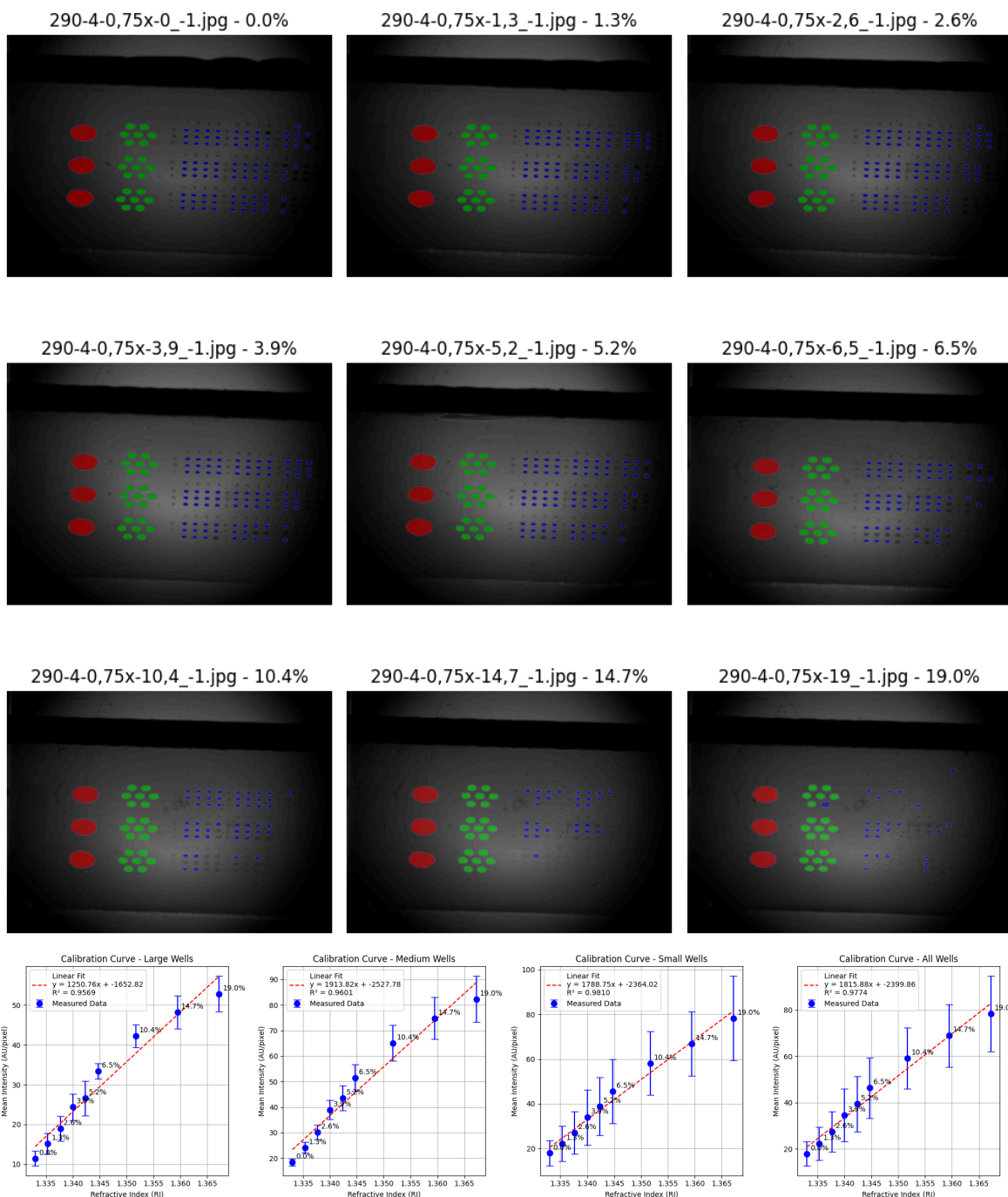
290-2-0,75x-19\_-3.jpg - 19.0%





==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
	0.0	6.482269	0.251758	7.34133									
4	0.641489	6.056168	0.713812	6.7									
87340	0.884736	41	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-0_-3.jpg	290-2-0,75x-0_-3.jpg	1.33300								
	1.3	12.109639	0.438318	12.95934									
8	0.610224	10.805045	0.966673	12.0									
58943	1.249272	43	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-1,3_-3.jpg	290-2-0,75x-1,3_-3.jpg	1.33534								
	2.6	10.875608	0.507892	12.63871									
9	0.911118	10.703126	2.127041	11.5									
10281	1.909227	51	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-2,6_-3.jpg	290-2-0,75x-2,6_-3.jpg	1.33768								
	3.9	13.641611	0.623828	15.61904									
6	1.088691	12.837036	2.494733	14.0									
15146	2.376559	54	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-3,9_-3.jpg	290-2-0,75x-3,9_-3.jpg	1.34002								
	5.2	17.084518	1.118730	19.72648									
1	1.252949	16.326259	3.196800	17.7									
02682	3.003217	56	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-5,2_-3.jpg	290-2-0,75x-5,2_-3.jpg	1.34236								
	6.5	21.764319	0.768184	23.89309									
4	1.777125	18.136046	3.031718	21.2									
73732	3.636950	42	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-6,5_-3.jpg	290-2-0,75x-6,5_-3.jpg	1.34470								
	10.4	30.615244	1.738703	32.65998									
5	2.867015	24.470614	1.901553	30.2									
40634	4.394229	33	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-10,4_-3.jpg	290-2-0,75x-10,4_-3.jpg	1.35172								
	14.7	37.304731	3.463495	37.59886									
4	3.878987	NaN	NaN	37.5									
62097	3.830752	16	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-14,7_-3.jpg	290-2-0,75x-14,7_-3.jpg	1.35946								
	19.0	42.090304	4.345833	44.04679									
6	3.776029	33.169173	0.000000	42.7									
02195	4.842338	11	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-2-0,75x-19_-3.jpg	290-2-0,75x-19_-3.jpg	1.36720								
Image 0 - 290-4-0,75x-0_-1.jpg has all masks													
Image 1 - 290-4-0,75x-1,3_-1.jpg has all masks													
Image 2 - 290-4-0,75x-2,6_-1.jpg has all masks													
Image 3 - 290-4-0,75x-3,9_-1.jpg has all masks													
Image 4 - 290-4-0,75x-5,2_-1.jpg has all masks													
Image 5 - 290-4-0,75x-6,5_-1.jpg has all masks													
Image 6 - 290-4-0,75x-10,4_-1.jpg has all masks													
Image 7 - 290-4-0,75x-14,7_-1.jpg has all masks													
Image 8 - 290-4-0,75x-19_-1.jpg has all masks													



==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
	0.0	11.482585	1.921116	18.39110									
4	1.435389	17.863227	5.762957	17.7									
89314	5.250361	109	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-0_-1.jpg	290-4-0,75x-0_-1.jpg	1.33300								
	1.3	15.182646	2.601475	24.21363									
8	2.079530	22.070864	7.835862	22.2									
90085	7.157438	111	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-1,3_-1.jpg	290-4-0,75x-1,3_-1.jpg	1.33534								
	2.6	18.909638	3.116150	30.20710									
9	2.798817	26.945902	9.477567	27.3									
42121	8.710459	112	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-2,6_-1.jpg	290-4-0,75x-2,6_-1.jpg	1.33768								
	3.9	24.371042	3.331327	39.00257									
5	3.839395	33.853436	12.450055	34.5									
26217	11.414000	112	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-3,9_-1.jpg	290-4-0,75x-3,9_-1.jpg	1.34002								
	5.2	26.574030	4.306974	43.62373									
9	4.816853	38.787008	12.959905	39.3									
88234	11.999678	108	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-5,2_-1.jpg	290-4-0,75x-5,2_-1.jpg	1.34236								
	6.5	33.426994	1.962524	51.45126									
4	5.299251	45.480619	14.394073	46.3									
19413	13.084950	92	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-6,5_-1.jpg	290-4-0,75x-6,5_-1.jpg	1.34470								
	10.4	42.242018	2.836362	65.09715									
4	6.965307	58.077664	14.263956	59.2									
13701	13.235330	74	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-10,4_-1.jpg	290-4-0,75x-10,4_-1.jpg	1.35172								
	14.7	48.224731	4.152224	74.82929									
5	8.205459	66.802700	14.412175	68.9									
31466	13.484759	53	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-14,7_-1.jpg	290-4-0,75x-14,7_-1.jpg	1.35946								
	19.0	52.803503	4.522682	82.37151									
6	9.081784	78.288963	18.957088	78.4									
78295	16.334813	49	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-19_-1.jpg	290-4-0,75x-19_-1.jpg	1.36720								

```

c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\fromnumeric.py:3860: RuntimeWarning: Mean of empty slice.
    return _methods._mean(a, axis=axis, dtype=dtype,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:145: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:223: RuntimeWarning: Degrees of freedom <= 0 for slic
e
    ret = _var(a, axis=axis, dtype=dtype, out=out, ddof=ddof,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:181: RuntimeWarning: invalid value encountered in div
ide
    arrmean = um.true_divide(arrmean, div, out=arrmean,
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packa
ges\numpy\_core\_methods.py:215: RuntimeWarning: invalid value encountered in sca
lar divide
    ret = ret.dtype.type(ret / rcount)

```

Image 3 - 290-4-0,75x-3,9\_-2.jpg has all masks

Image 5 - 290-4-0,75x-6,5\_-2.jpg has all masks

Image 6 - 290-4-0,75x-10,4\_-2.jpg has all masks

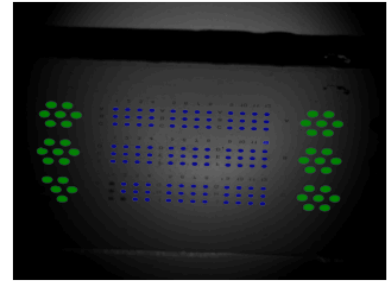
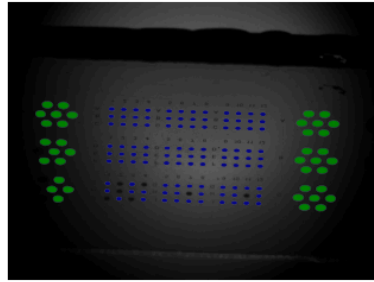
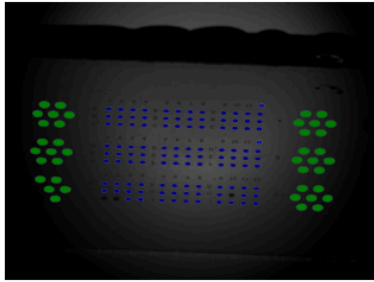
Image 7 - 290-4-0,75x-14,7\_-2.jpg has all masks

Image 8 - 290-4-0,75x-19\_-2.jpg has all masks

290-4-0,75x-0\_-2.jpg - 0.0%

290-4-0,75x-1,3\_-2.jpg - 1.3%

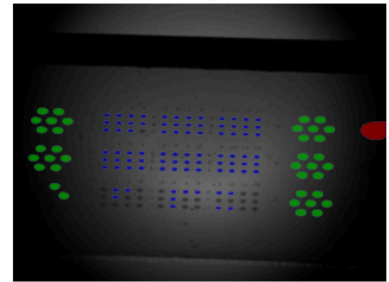
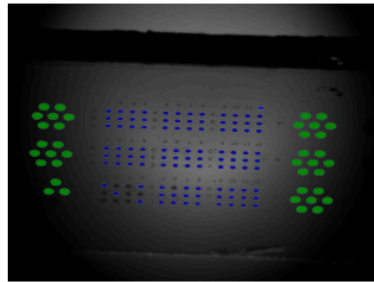
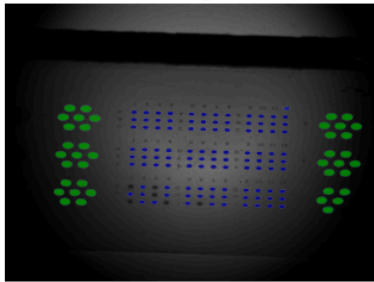
290-4-0,75x-2,6\_-2.jpg - 2.6%



290-4-0,75x-3,9\_-2.jpg - 3.9%

290-4-0,75x-5,2\_-2.jpg - 5.2%

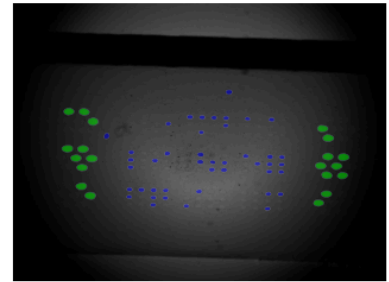
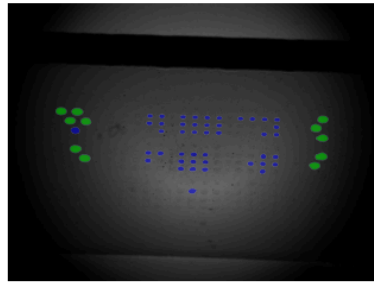
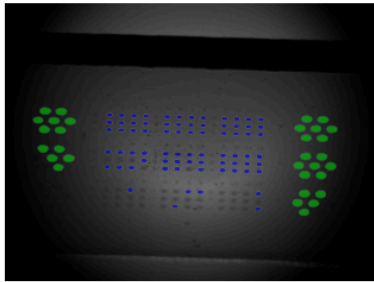
290-4-0,75x-6,5\_-2.jpg - 6.5%



290-4-0,75x-10,4\_-2.jpg - 10.4%

290-4-0,75x-14,7\_-2.jpg - 14.7%

290-4-0,75x-19\_-2.jpg - 19.0%





```
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packages\scipy\stats\_stats_py.py:10730: RuntimeWarning: invalid value encountered in scalar divide
```

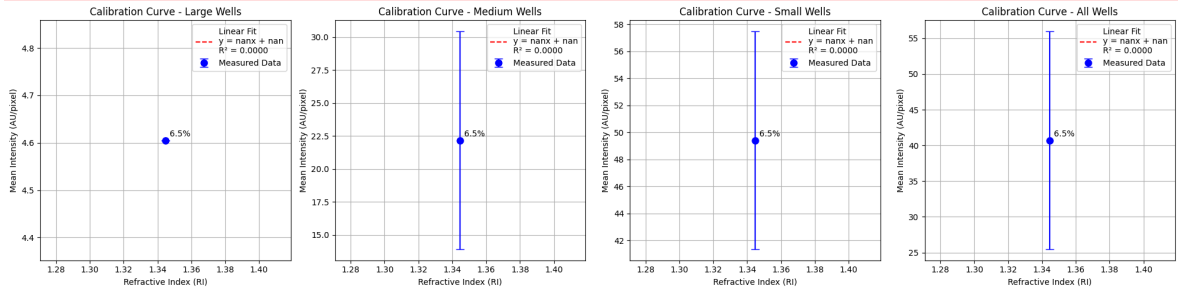
```
slope = ssxym / ssxm
```

```
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packages\scipy\stats\_stats_py.py:10744: RuntimeWarning: invalid value encountered in sqrt
```

```
t = r * np.sqrt(df / ((1.0 - r + TINY)*(1.0 + r + TINY)))
```

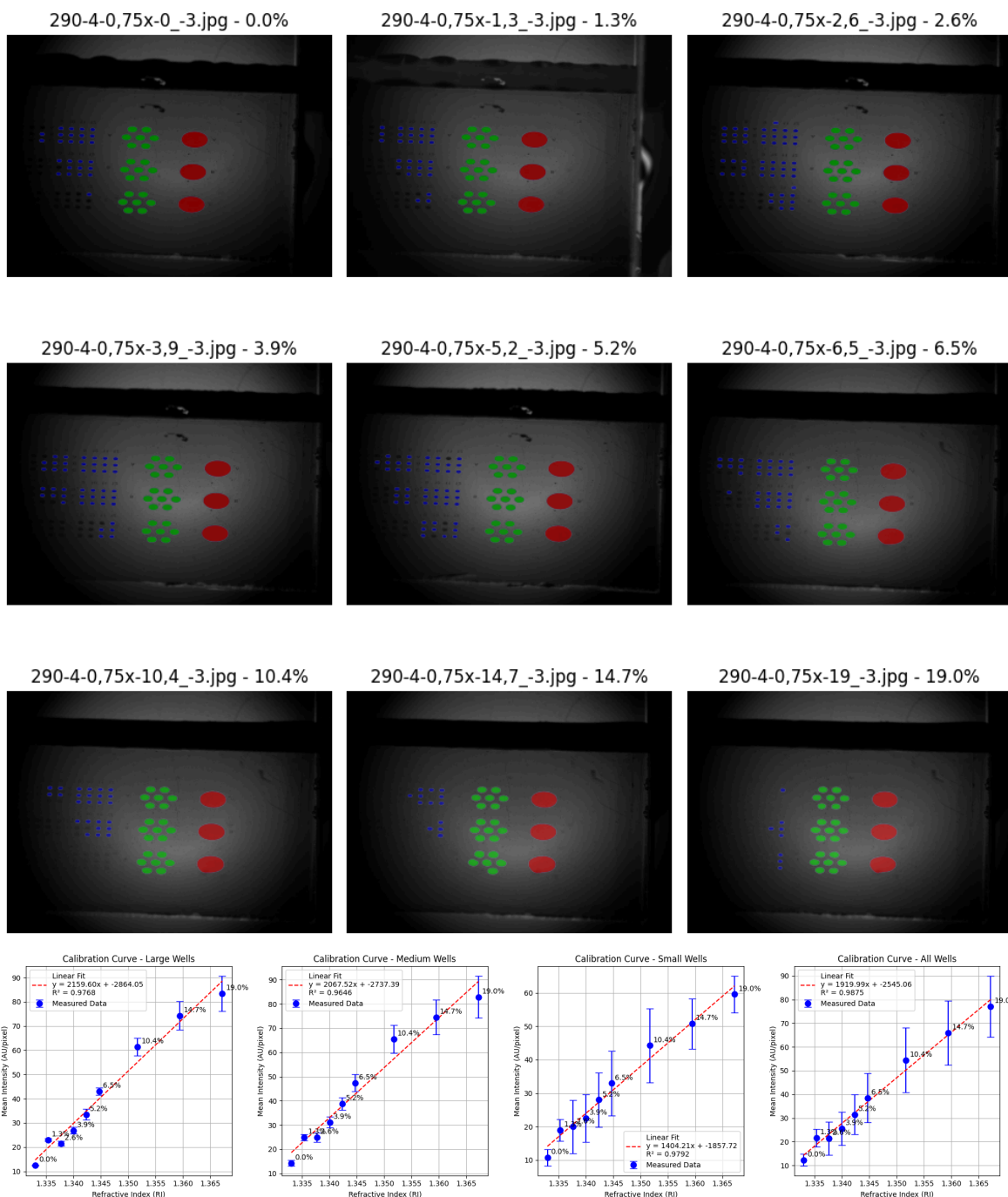
```
c:\Users\Micha\Desktop\BachelorProject\AI-Powered-Biosensing\.venv\Lib\site-packages\scipy\stats\_stats_py.py:10750: RuntimeWarning: invalid value encountered in scalar divide
```

```
slope_stderr = np.sqrt((1 - r**2) * ssym / ssxm / df)
```



==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
0.0													
9	1.625984	20.497450	4.983980	16.5									
88199	7.607735	149	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-0_-2.jpg	290-4-0,75x-0_-2.jpg	1.33300								
1.3													
1	2.042656	24.952741	3.290911	20.3									
88827	7.888988	141	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-1,3_-2.jpg	290-4-0,75x-1,3_-2.jpg	1.33534								
2.6													
7	3.108314	31.289251	5.196065	25.4									
78008	10.366115	147	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-2,6_-2.jpg	290-4-0,75x-2,6_-2.jpg	1.33768								
3.9													
2	5.463716	38.150123	5.362285	31.0									
09787	12.296460	146	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-3,9_-2.jpg	290-4-0,75x-3,9_-2.jpg	1.34002								
5.2													
3	5.313784	43.635961	5.767362	36.0									
30775	13.325176	140	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-5,2_-2.jpg	290-4-0,75x-5,2_-2.jpg	1.34236								
6.5													
5	8.278749	49.417475	8.070427	40.7									
18215	15.277931	121	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-6,5_-2.jpg	290-4-0,75x-6,5_-2.jpg	1.34470								
10.4													
6	6.993356	61.464508	7.929996	51.8									
60445	16.610962	104	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-10,4_-2.jpg	290-4-0,75x-10,4_-2.jpg	1.35172								
14.7													
4	4.466965	68.103039	8.971727	62.0									
23826	14.704135	55	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-14,7_-2.jpg	290-4-0,75x-14,7_-2.jpg	1.35946								
19.0													
3	6.198696	76.317965	11.122529	64.1									
66364	20.349631	63	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-19_-2.jpg	290-4-0,75x-19_-2.jpg	1.36720								
Image 0 - 290-4-0,75x-0_-3.jpg has all masks													
Image 1 - 290-4-0,75x-1,3_-3.jpg has all masks													
Image 2 - 290-4-0,75x-2,6_-3.jpg has all masks													
Image 3 - 290-4-0,75x-3,9_-3.jpg has all masks													
Image 4 - 290-4-0,75x-5,2_-3.jpg has all masks													
Image 5 - 290-4-0,75x-6,5_-3.jpg has all masks													
Image 6 - 290-4-0,75x-10,4_-3.jpg has all masks													
Image 7 - 290-4-0,75x-14,7_-3.jpg has all masks													
Image 8 - 290-4-0,75x-19_-3.jpg has all masks													



==== Calibration Data =====

	NaCl_percentage	mean_intensity_large	std_intensity_large	mean_intensity_medium	std_intensity_medium	mean_intensity_small	std_intensity_small	mean_intensity_all	std_intensity_all	num_wells	image_path	image_name	RI
0	0.0	12.479941	0.294931	14.29077									
4	1.242790	10.654606	2.470220	12.3									
36160	2.572493	53	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-0_-3.jpg	290-4-0,75x-0_-3.jpg	1.33300								
0	1.3	23.042132	0.515625	24.87915									
0	1.218596	18.888191	3.272346	21.6									
12669	3.790857	56	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-1,3_-3.jpg	290-4-0,75x-1,3_-3.jpg	1.33534								
2	2.6	21.526760	1.028428	24.83064									
2	1.867259	19.935647	8.034255	21.3									
91105	6.985073	75	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-2,6_-3.jpg	290-4-0,75x-2,6_-3.jpg	1.33768								
8	3.9	26.879532	1.381286	31.16070									
8	2.284745	22.525829	7.107821	25.5									
86534	6.959925	72	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-3,9_-3.jpg	290-4-0,75x-3,9_-3.jpg	1.34002								
6	5.2	33.477093	2.288102	38.76246									
6	2.560646	27.991044	8.202504	31.5									
10897	8.393898	72	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-5,2_-3.jpg	290-4-0,75x-5,2_-3.jpg	1.34236								
7	6.5	43.016907	1.555308	47.38177									
7	3.575875	32.947821	9.684056	38.5									
03160	10.391879	60	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-6,5_-3.jpg	290-4-0,75x-6,5_-3.jpg	1.34470								
8	10.4	61.404046	3.668797	65.47757									
8	5.821945	44.255588	11.116775	54.4									
00632	13.656581	49	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-10,4_-3.jpg	290-4-0,75x-10,4_-3.jpg	1.35172								
2	14.7	74.243446	5.854417	74.53801									
2	7.147354	50.801638	7.531433	65.9									
41996	13.464435	36	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-14,7_-3.jpg	290-4-0,75x-14,7_-3.jpg	1.35946								
0	19.0	83.445588	7.268460	82.92000									
0	8.729733	59.595533	5.537637	77.1									
38157	12.854367	32	C:/Users/Micha/Desktop/BachelorProject/AI-Powered-Biosensing/data/Chip2-NaCl 0-19_\290-4-0,75x-19_-3.jpg	290-4-0,75x-19_-3.jpg	1.36720								