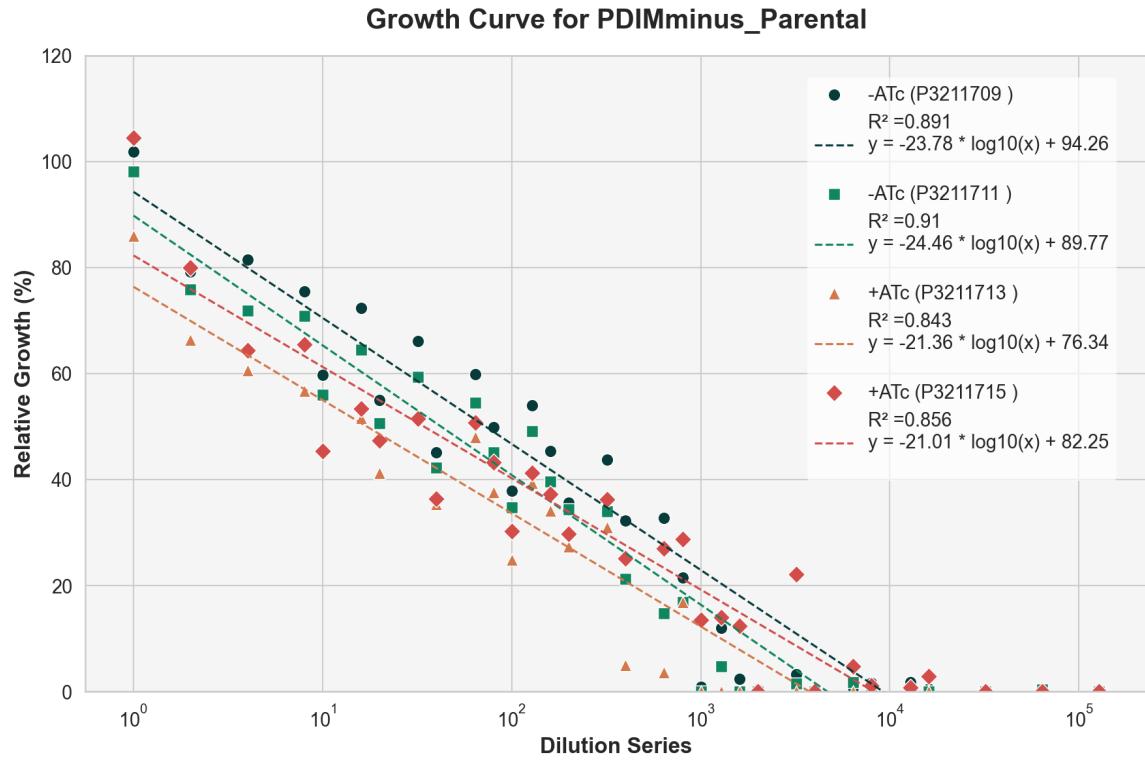
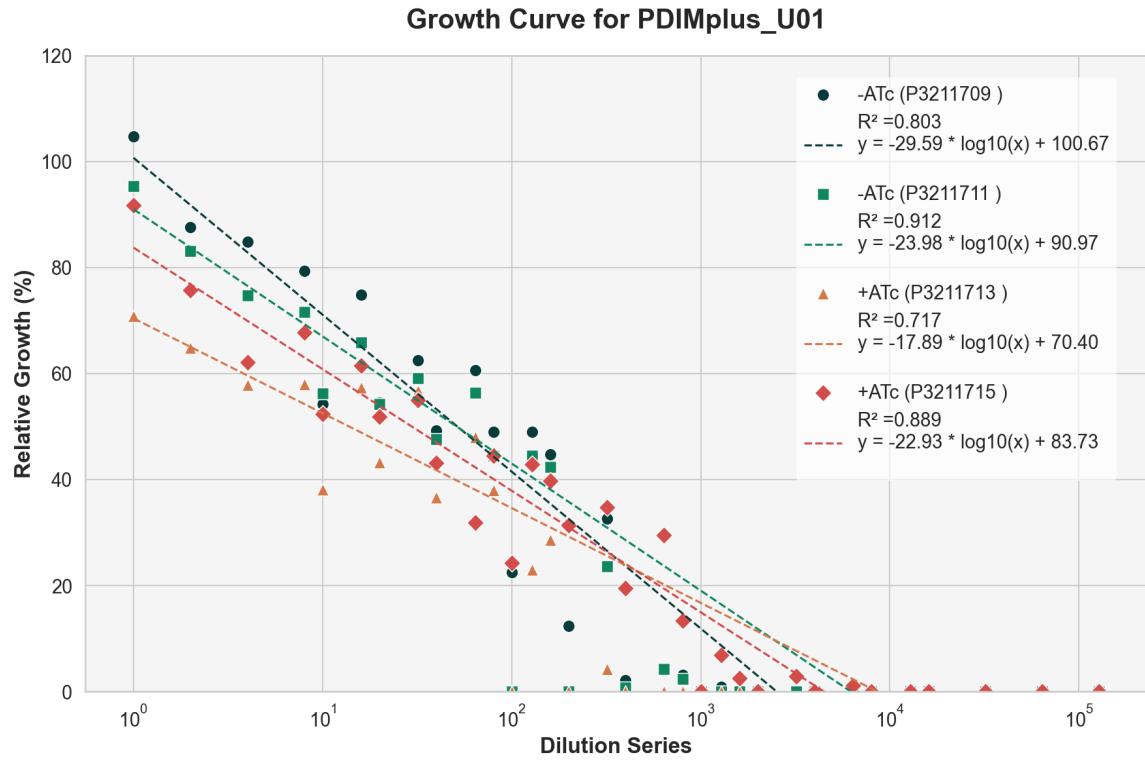


	P3211709	P3211711	P3211713	P3211715
Formula	$y = -26.73 * \log_{10}(x) + 97.69$	$y = -24.84 * \log_{10}(x) + 85.62$	$y = -29.93 * \log_{10}(x) + 52.52$	$y = -28.39 * \log_{10}(x) + 63.10$
Slope	-26.73	-24.84	-29.93	-28.39
Intercept	97.69	85.62	52.52	63.10
R-squared	0.898	0.909	0.769	0.844
Y-cut	97.69	85.62	52.52	63.10
X-cut	4508.73	2798.76	56.85	167.04
X at Y=50	60.78	27.17	1.21	2.89



	P3211709	P3211711	P3211713	P3211715
Formula	$y = -23.78 * \log_{10}(x) + 94.26$	$y = -24.46 * \log_{10}(x) + 89.77$	$y = -21.36 * \log_{10}(x) + 76.34$	$y = -21.01 * \log_{10}(x) + 82.25$
Slope	-23.78	-24.46	-21.36	-21.01
Intercept	94.26	89.77	76.34	82.25
R-squared	0.891	0.910	0.843	0.856
Y-cut	94.26	89.77	76.34	82.25
X-cut	9216.50	4673.72	3753.87	8226.08
X at Y=50	72.71	42.25	17.12	34.30



	P3211709	P3211711	P3211713	P3211715
Formula	$y = -29.59 * \log_{10}(x) + 100.67$	$y = -23.98 * \log_{10}(x) + 90.97$	$y = -17.89 * \log_{10}(x) + 70.40$	$y = -22.93 * \log_{10}(x) + 83.73$
Slope	-29.59	-23.98	-17.89	-22.93
Intercept	100.67	90.97	70.40	83.73
R-squared	0.803	0.912	0.717	0.889
Y-cut	100.67	90.97	70.40	83.73
X-cut	2521.79	6222.29	8603.98	4491.11
X at Y=50	51.55	51.14	13.80	29.61



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P3211709.JPG

Type: Control

Detergent: Tween

Treatment: None

Repeat: Repeat3

Strain A: PDIMminus_NT

Strain B: PDIMminus_Parental

Strain C: PDIMplus_U01

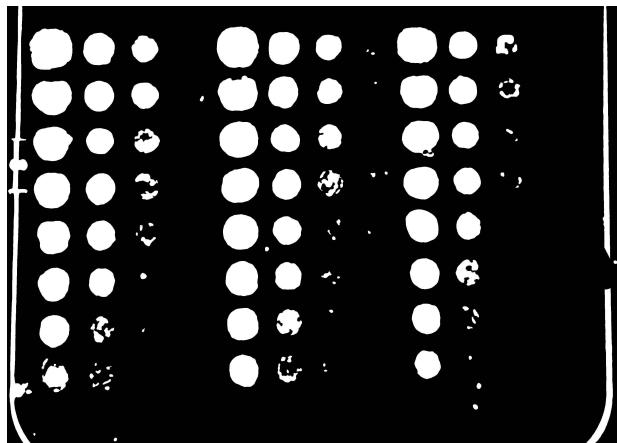
Parameters Used:

Threshold: 8.0

Minimum Area: 15



Contours Image



Binary Image

3834	2147	1102	0	3747	2195	1394	34	3207	1663	624	0
2929	1915	1482	42	2912	2020	1311	13	2581	1670	378	0
2704	1511	949	0	2997	1658	1186	0	2698	1507	66	0
2773	1911	634	0	2776	1834	754	60	2432	1502	97	0
2573	1770	268	0	2659	1667	89	18	2294	1369	0	0
2193	1269	80	0	2429	1609	118	0	1913	992	0	0
2023	433	16	0	2203	1254	26	0	1858	125	0	0
1199	139	0	0	1985	441	65	0	1500	27	0	0

Grid Image



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P3211711.JPG

Type: Control

Detergent: Tween

Treatment: None

Repeat: Repeat4

Strain A: PDIMminus_NT

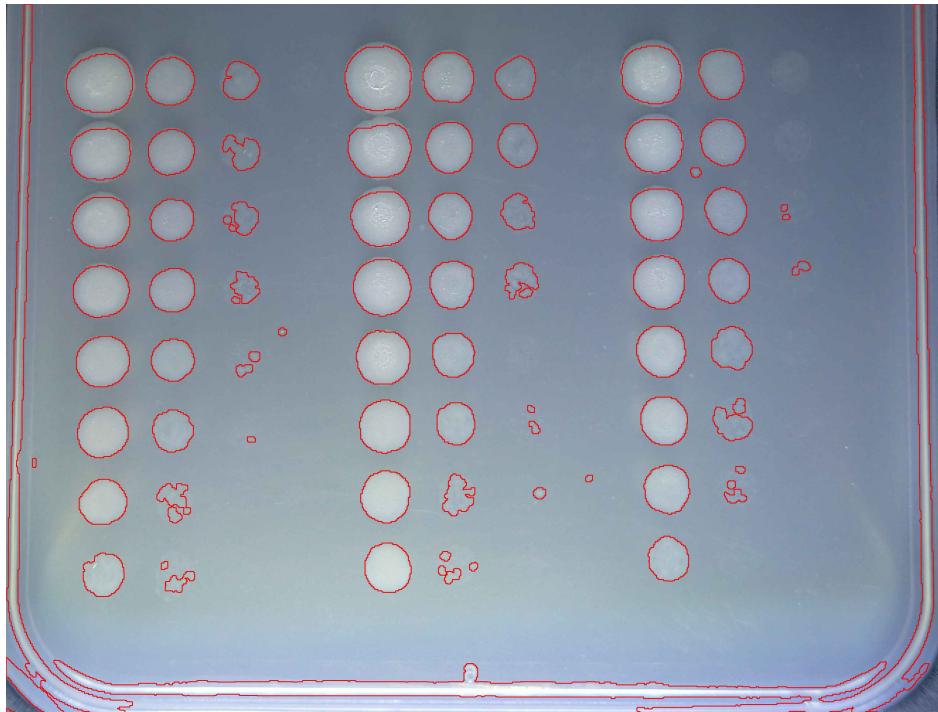
Strain B: PDIMminus_Parental

Strain C: PDIMplus_U01

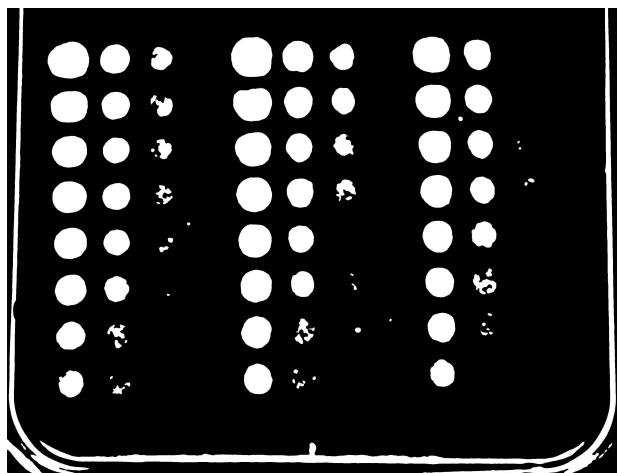
Parameters Used:

Threshold: 10.0

Minimum Area: 15



Contours Image



Binary Image

3222	1819	956	0	3608	2060	1280	0	2918	1723	0	0
2580	1640	654	0	2789	1862	1262	0	2546	1663	0	0
2357	1428	535	0	2644	1653	781	0	2287	1458	25	0
2321	1566	355	0	2606	1658	652	0	2195	1565	74	0
2168	1387	145	20	2370	1457	0	0	2016	1299	0	0
2041	1281	13	0	2181	1252	54	0	1812	745	0	0
1654	454	0	0	2006	553	66	13	1728	134	0	0
1531	209	0	0	1805	143	0	0	1362	0	0	0

Grid Image



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P3211713.JPG

Type: Control

Detergent: Tween

Treatment: ATC

Repeat: Repeat3

Strain A: PDIMminus_NT

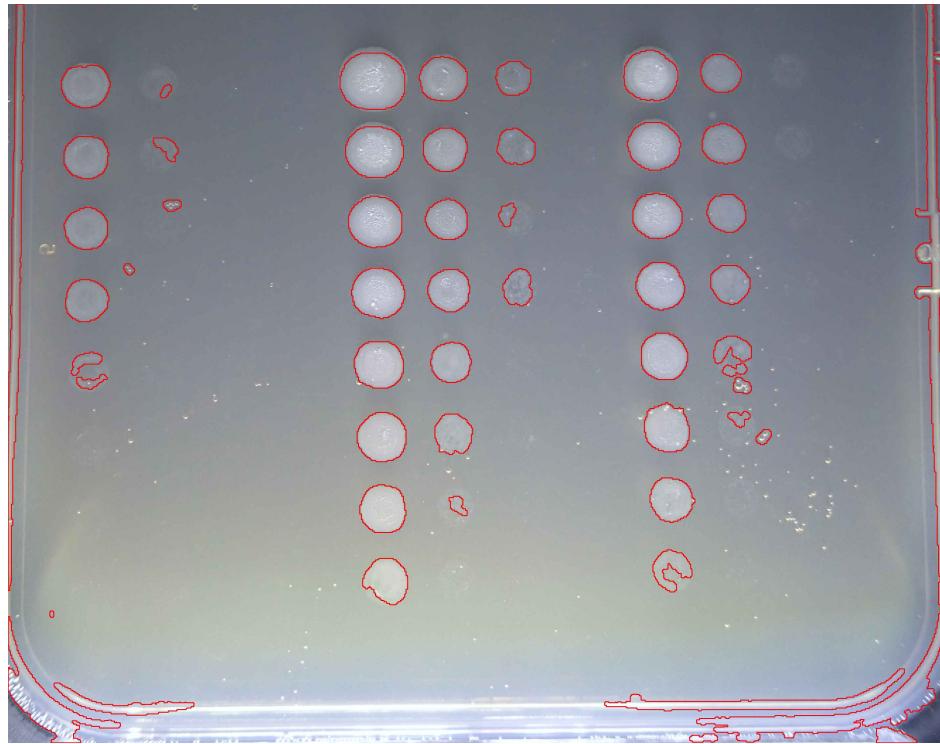
Strain B: PDIMminus_Parental

Strain C: PDIMplus_U01

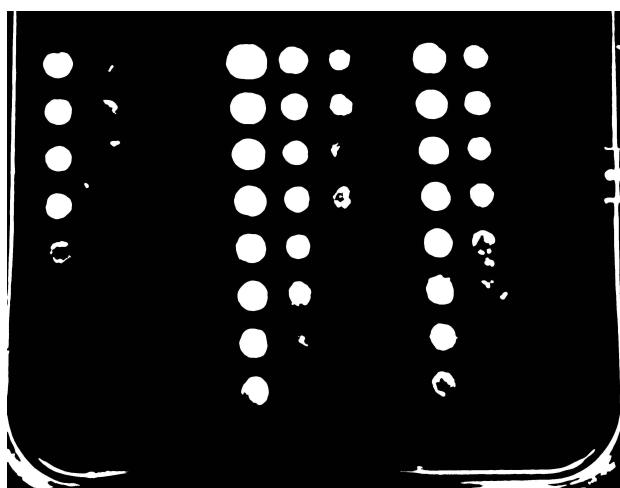
Parameters Used:

Threshold: 14.0

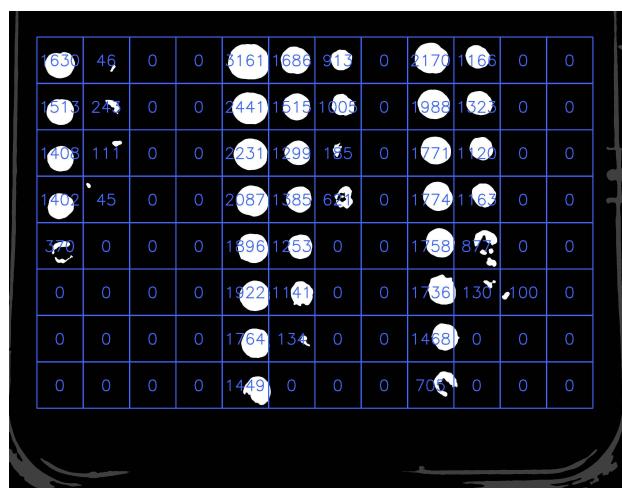
Minimum Area: 31.0



Contours Image



Binary Image



Grid Image



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P3211715.JPG

Type: Control

Detergent: Tween

Treatment: ATC

Repeat: Repeat4

Strain A: PDIMminus_NT

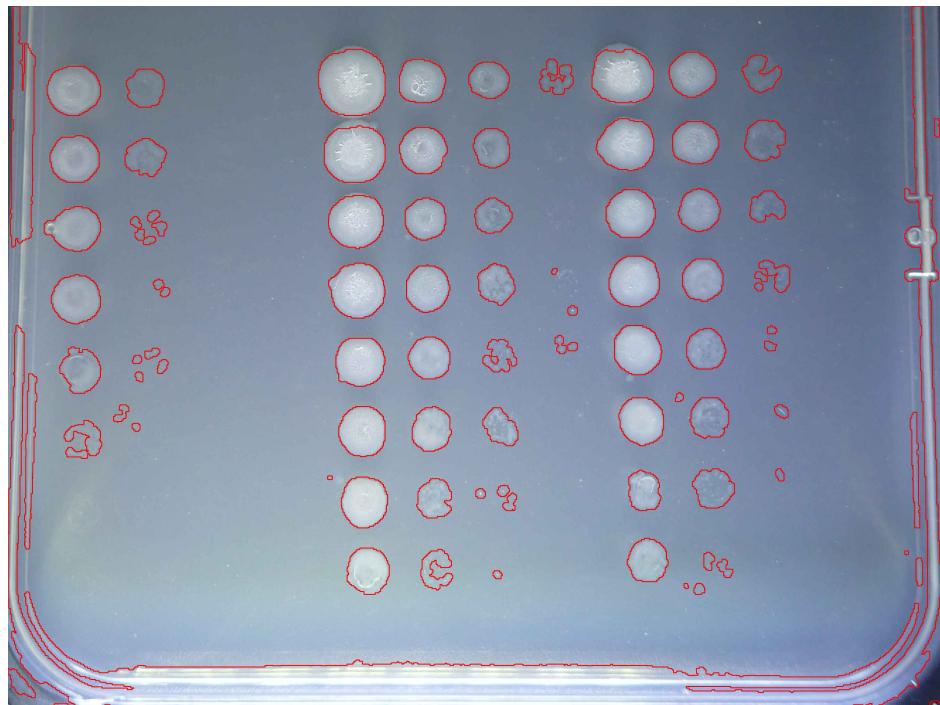
Strain B: PDIMminus_Parental

Strain C: PDIMplus_U01

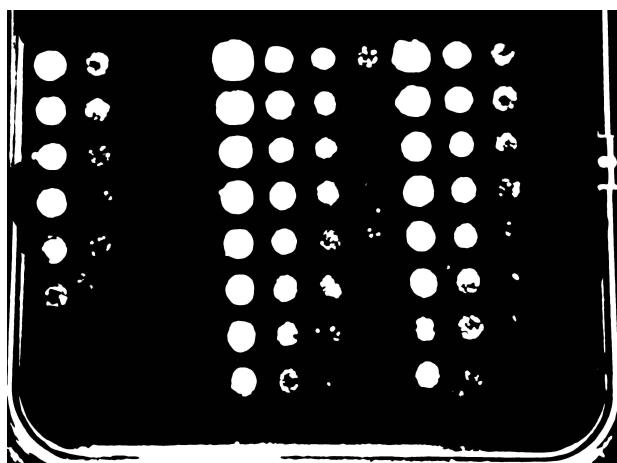
Parameters Used:

Threshold: 4

Minimum Area: 21.0



Contours Image



Binary Image

2094	86	0	0	3840	668	1112	45	2809	1604	74	0
1853	98	0	0	2940	74	1096	0	2319	588	56	0
1773	246	0	0	2366	1336	925	0	1901	1321	599	0
1849	71	0	0	2410	1591	1057	42	2074	1364	47	0
1257	179	0	0	196	167	45	106	1883	1919	76	0
514	75	0	0	1893	1531	812	0	1685	1065	88	0
0	0	0	0	1866	992	175	0	976	944	36	0
0	0	0	0	1518	510	26	0	1314	215	0	0

Grid Image



This report was generated by **Spotplotter** version **1.0** on **2024-10-11**

Spotplotter was created by **Holly Lewis** with supervision from **R Verrinder** and **Dr. M Mason** as BSc (Eng) final year project submitted in partial fulfilment of the requirements for the degree of Bachelor of Science in Electrical and Computer Engineering in the Department of Electrical Engineering at the University of Cape Town.

To read the full report please see: [GITHUB LINK](#)

Formula: The formula represents the linear regression equation that models determined using the linregress function from scipy.stats which determines the relationship between the logarithm of the dilution series and relative growth. It follows the form: $y = m \cdot \log_{10}(x) + b$

Normalization: The relative growth values were normalized to a baseline to make the results comparable across different conditions. The quantified values of each spot were divided by the average value of the first spot in the -ATP for each strain.

The slope (m): indicates the rate of change in relative growth as the dilution series increases (on a logarithmic scale). A steep slope indicated that the growth has a faster knockdown as the dilution changes. A shallow slope indicates that the growth is more stable across dilutions.

The intercept (b) and y-cut is the relative growth when the solution is not diluted.

The R-squared value measures how well the linear regression line fits the data, where 1 represents a perfect fit and 0 represents no relationship. Higher R² values indicates that the growth follows a linear relationship.

The X-cut refers to the point where the regression line crosses the x-axis, indicating the dilution value at which the relative growth would theoretically be zero (no growth).

X at Y = 50: This value represents the dilution series value when the relative growth is 50% i.e., the knockdown is 50% in comparison to the -ATP series.