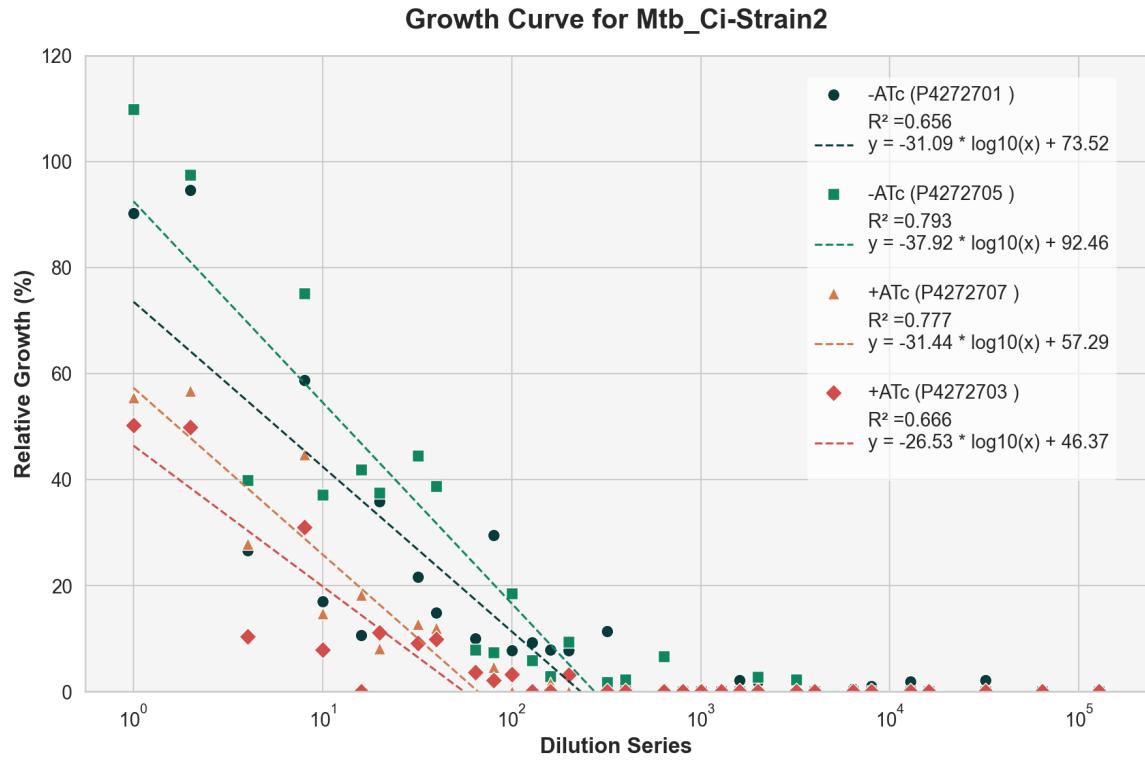
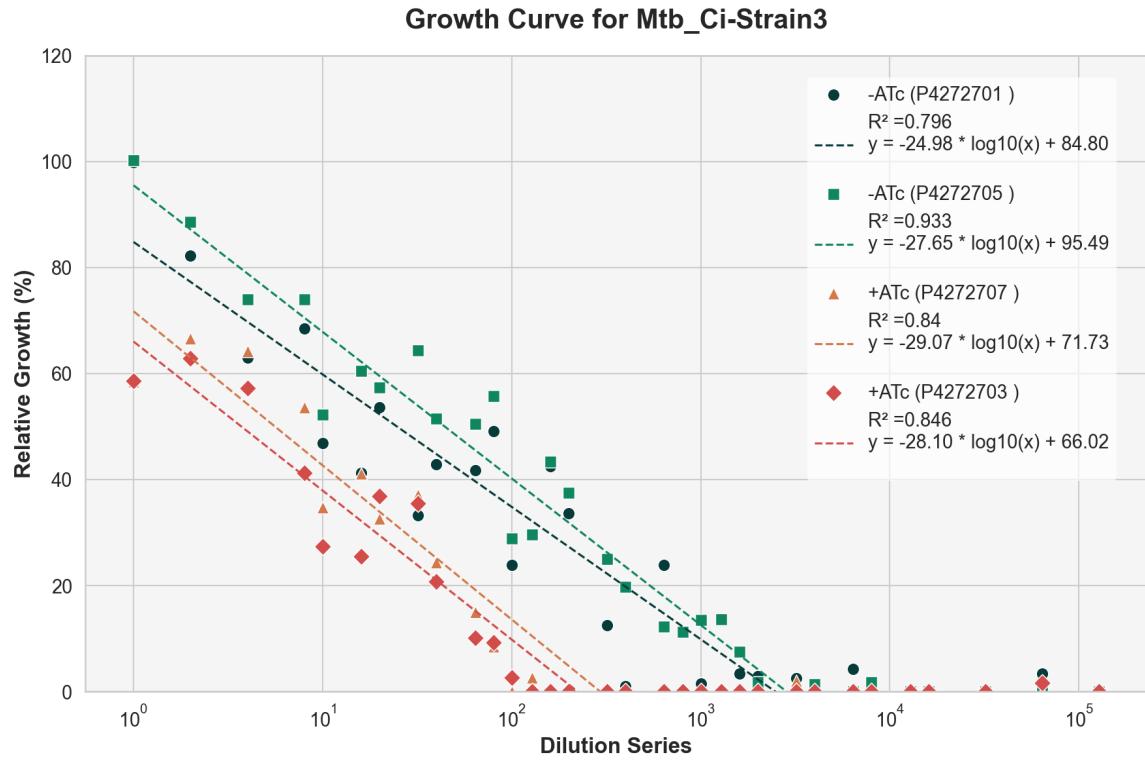


	P4272701	P4272705	P4272707	P4272703
Formula	$y = -23.17 * \log_{10}(x) + 78.60$	$y = -27.23 * \log_{10}(x) + 98.02$	$y = -27.01 * \log_{10}(x) + 70.47$	$y = -25.30 * \log_{10}(x) + 56.94$
Slope	-23.17	-27.23	-27.01	-25.30
Intercept	78.60	98.02	70.47	56.94
R-squared	0.850	0.875	0.840	0.827
Y-cut	78.60	98.02	70.47	56.94
X-cut	2471.52	3978.95	406.83	177.97
X at Y=50	17.17	58.03	5.73	1.88



	P4272701	P4272705	P4272707	P4272703
Formula	$y = -31.09 * \log_{10}(x) + 73.52$	$y = -37.92 * \log_{10}(x) + 92.46$	$y = -31.44 * \log_{10}(x) + 57.29$	$y = -26.53 * \log_{10}(x) + 46.37$
Slope	-31.09	-37.92	-31.44	-26.53
Intercept	73.52	92.46	57.29	46.37
R-squared	0.656	0.793	0.777	0.666
Y-cut	73.52	92.46	57.29	46.37
X-cut	231.66	274.33	66.41	55.95
X at Y=50	5.71	13.17	1.71	0.73



	P4272701	P4272705	P4272707	P4272703
Formula	$y = -24.98 * \log_{10}(x) + 84.80$	$y = -27.65 * \log_{10}(x) + 95.49$	$y = -29.07 * \log_{10}(x) + 71.73$	$y = -28.10 * \log_{10}(x) + 66.02$
Slope	-24.98	-27.65	-29.07	-28.10
Intercept	84.80	95.49	71.73	66.02
R-squared	0.796	0.933	0.840	0.846
Y-cut	84.80	95.49	71.73	66.02
X-cut	2480.80	2845.26	293.65	223.46
X at Y=50	24.72	44.21	5.59	3.72



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P4272701.JPG

Type: Hypomorph

Detergent: NA

Treatment: None

Repeat: Repeat 1

Strain A: Mtb_Ci-Strain1

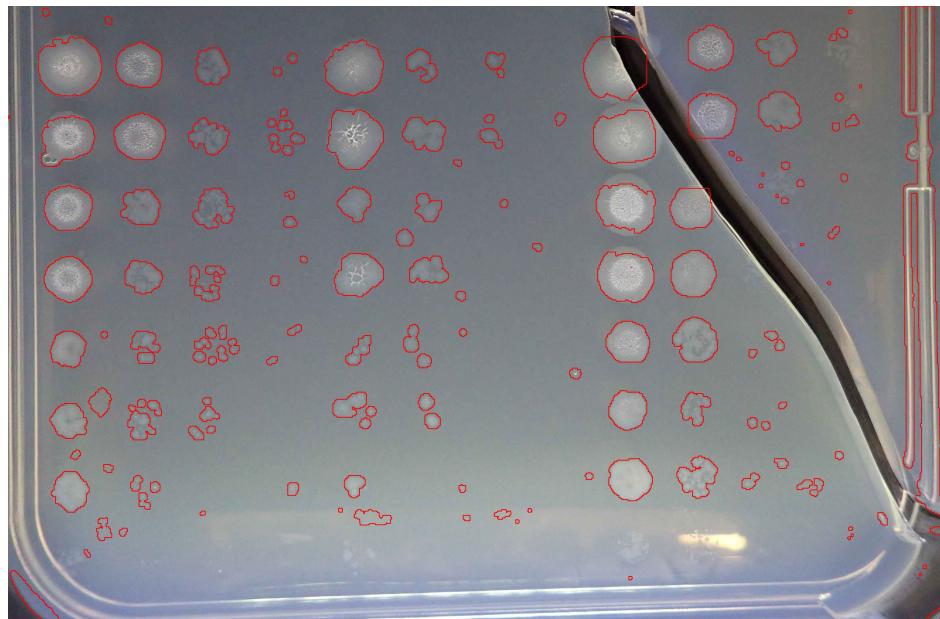
Strain B: Mtb_Ci-Strain2

Strain C: Mtb_Ci-Strain3

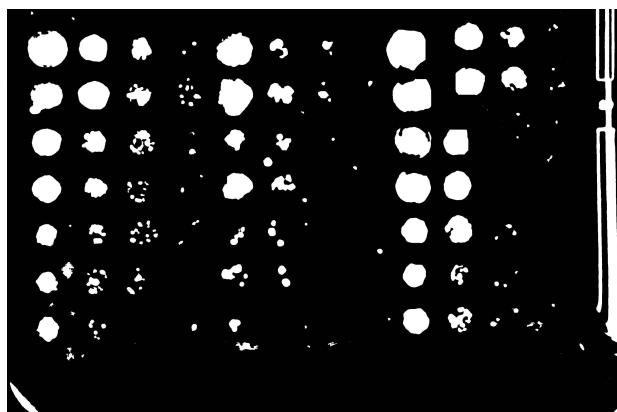
Parameters Used:

Threshold: 2

Minimum Area: 15



Contours Image



Binary Image

2975	1639	864	69	2409	454	206	0	3365	1578	844	51
1866	1853	782	285	2524	958	206	40	2770	1808	1132	98
1696	1004	697	15	710	396	32	0	2124	1445	35	30
1584	856	176	129	1567	780	0	28	2310	1857	0	33
917	458	437	44	285	210	57	0	1692	1453	116	0
1175	331	165	0	579	304	0	58	1121	421	86	0
1042	306	93	81	267	0	13	0	1405	805	143	116
0	41	1	0	249	0	49	0	0	0	0	1

Grid Image



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P4272705.JPG

Type: Hypomorph

Detergent: NA

Treatment: None

Repeat: Repeat 2

Strain A: Mtb_Ci-Strain1

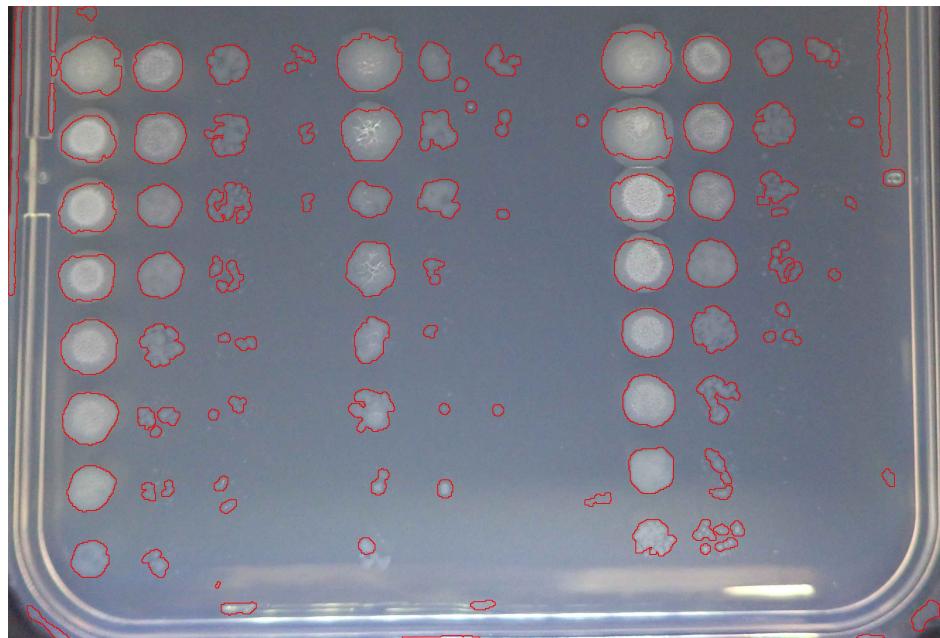
Strain B: Mtb_Ci-Strain2

Strain C: Mtb_Ci-Strain3

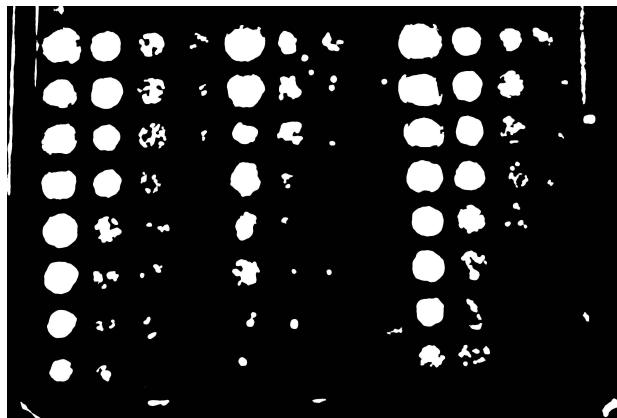
Parameters Used:

Threshold: 6.0

Minimum Area: 32.0



Contours Image



Binary Image

2784	933	1050	287	2931	99	44	0	3376	759	976	455
925	2128	1450	112	2604	1000	250	73	2985	1932	1285	61
2246	1476	1014	91	1063	1174	60	0	2495	1734	605	42
2198	1600	745	0	2004	118	0	0	2493	1879	370	58
2486	1024	240	0	116	77	0	0	2038	1460	255	0
2281	507	185	0	134	48	61	0	2168	84	0	0
1643	206	196	0	21	176	0	0	1701	413	0	0
1047	318	0	0	157	0	0	0	957	46	0	0

Grid Image



SPOTPLOTTER

AUTOMATED SPOTTING ASSAY QUANTIFICATION

Filename: P4272707.JPG

Type: Hypomorph

Detergent: NA

Treatment: ATC

Repeat: Repeat 2

Strain A: Mtb_Ci-Strain1

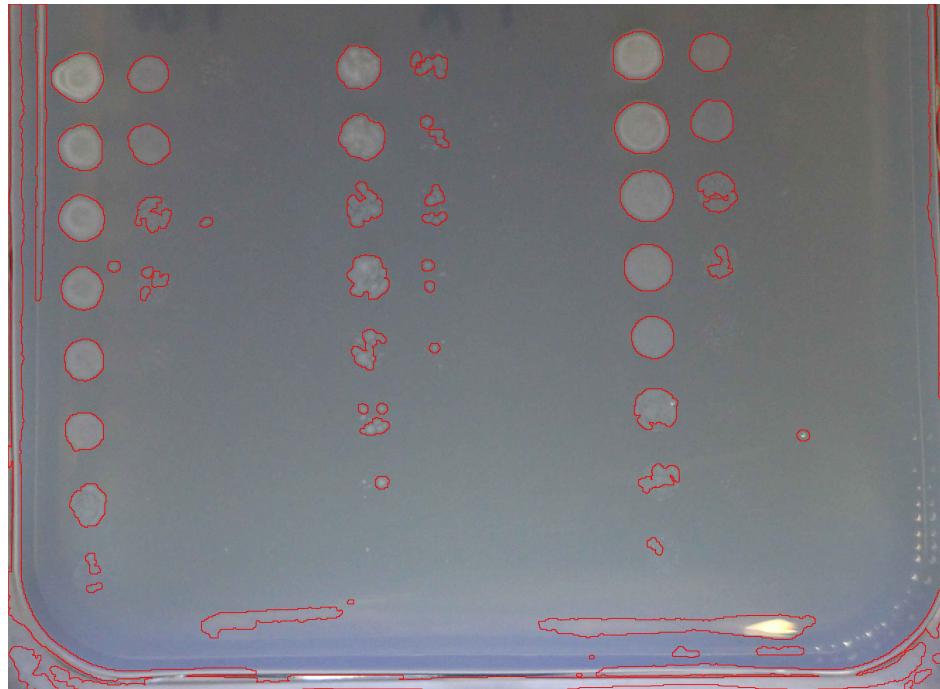
Strain B: Mtb_Ci-Strain2

Strain C: Mtb_Ci-Strain3

Parameters Used:

Threshold: 14

Minimum Area: 32.0



Contours Image



Binary Image

1946	1125	0	0	1483	515	0	0	1972	170	0	0
1619	1240	0	0	514	247	0	0	2245	101	0	0
1823	518	54	0	515	32	0	0	2165	830	0	0
1426	256	0	0	1195	123	0	0	1808	288	0	0
1239	0	0	0	438	44	0	0	1387	0	0	0
1141	0	0	0	32	0	0	0	1254	0	70	0
956	0	0	0	109	0	0	0	505	0	0	0
152	0	0	0	0	0	0	0	89	0	0	0

Grid Image



Filename: P4272703.JPG

Type: Hypomorph

Detergent: NA

Treatment: ATC

Repeat: Repeat 1

Strain A: Mtb_Ci-Strain1

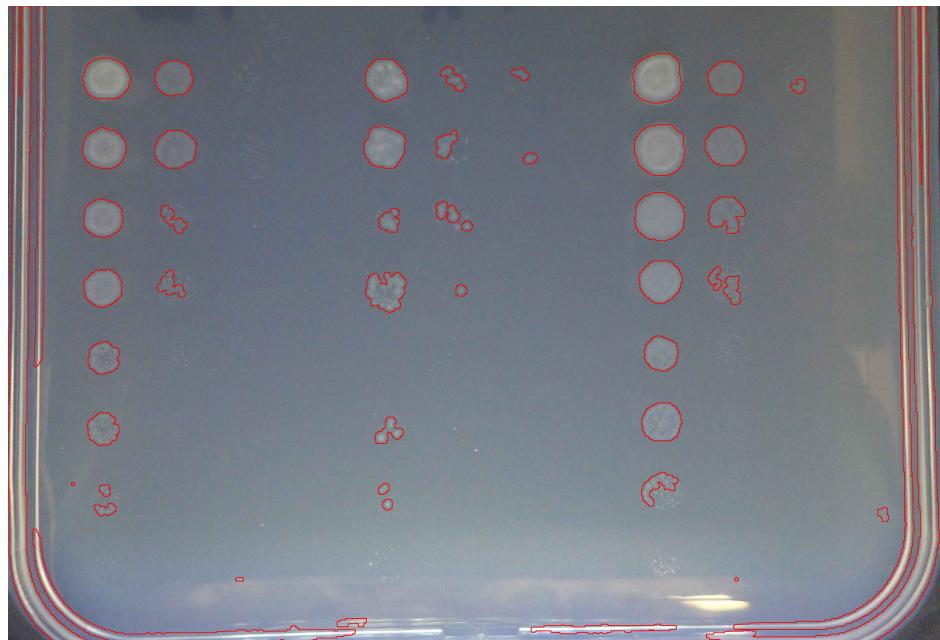
Strain B: Mtb_Ci-Strain2

Strain C: Mtb_Ci-Strain3

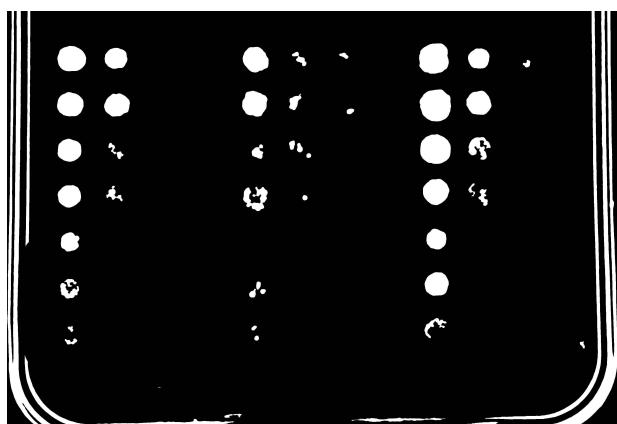
Parameters Used:

Threshold: 12

Minimum Area: 32.0



Contours Image



Binary Image

154	1002	0	0	640	261	85	0	975	921	9	0
154	1215	0	0	1532	267	85	0	1120	1243	0	0
149	137	0	0	278	233	0	0	193	69	0	0
180	241	0	0	58	58	0	0	1790	54	0	0
130	0	0	0	0	0	0	0	855	0	0	0
51	0	0	0	246	0	0	0	1198	0	0	0
153	0	0	0	95	0	0	0	511	0	0	54
0	0	3	0	0	0	0	0	0	0	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.