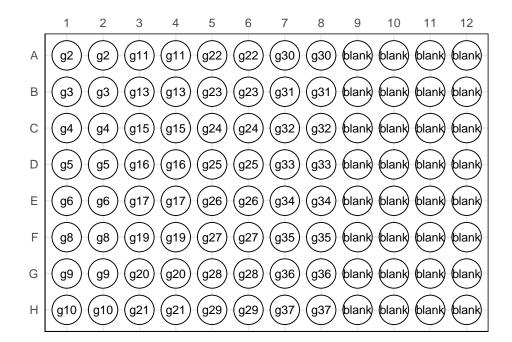# growth curve batch 3 at 35C

Growth curve of 32 strains

	genome_id	exp_id		genome_id	exp_id		genome_id	exp_id		genome_id	exp_id
1	g2	H2M3R1	9	g11	L2M4R1	17	g22	fp1-2	25	g30	gp1-3
2	g3	H2M3R2	10	g13	L3M5R1	18	g23	fp1-3	26	g31	bg-2
3	g4	H3M1R1	11	g15	L4M2R2	19	g24	fp2-2	27	g32	bg-3
4	g5	H3M3R2	12	g16	L4M3R3	20	g25	crp1-2	28	g33	pms-1
5	g6	H3M4R1	13	g17	L4M4R1	21	g26	crp1-3	29	g34	pms-2
6	g8	H4M5R1	14	g19	L4M7R1	22	g27	crp2-2	30	g35	pms-3
7	g9	L1M2R2	15	g20	L3M1R1	23	g28	gp1-1	31	g36	ppf-1
8	g10	L2M2R1	16	g21	src-2	24	g29	gp1-2	32	g37	40th-1

- revive glycerol stock of rhizobia on TY agar

  - prepare labelled plates
  - use a sterilized inoculation loop to streak the glycerol stock on TY agar
  - incubate the petri plates at 30C for 2-3 days until the colony is identifiably large

- prepare ensifer inoculum

  - prepare a DW96 filled with 300uL of PBS
  - pick colonies from the petri plate and dissolve the colonies in the PBS. Use wells in column 1, 5, and 9
  - dispense 100 uL of the dissolved colony to a NUNC96 and measure od at 600 nm
  - standardize the OD600 to 0.1. For target od = 0.1 `od_target` and target inoculum volume = 100 uL `volume_target`, and given the measured od of dissolved colonies `od_dissolved`, use the code below to calculate the needed volume of the dissolved colonies `volume_dissolved` and the pbs volume `volume_pbs`
  - prepare another NUNC96, follow the table to add required volume of dissolved colonies and pbs to make 100 uL of standardized inoculum
  - measure the od of the standardized inoculum as `od_inoculum`

- prepare 100 uL of TY medium in NUNC96

  - inoculate 2 uL of the standardized inoculum to each well

	1	2	3	4	5	6	7	8	9	10	11	12
A	g2	g2	g11	g11	g22	g22	g30	g30	blank	blank	blank	blank
B	g3	g3	g13	g13	g23	g23	g31	g31	blank	blank	blank	blank
C	g4	g4	g15	g15	g24	g24	g32	g32	blank	blank	blank	blank
D	g5	g5	g16	g16	g25	g25	g33	g33	blank	blank	blank	blank
E	g6	g6	g17	g17	g26	g26	g34	g34	blank	blank	blank	blank
F	g8	g8	g19	g19	g27	g27	g35	g35	blank	blank	blank	blank
G	g9	g9	g20	g20	g28	g28	g36	g36	blank	blank	blank	blank
H	g10	g10	g21	g21	g29	g29	g37	g37	blank	blank	blank	blank

genome_id	well	od_dissolved	od_target	volume_target	volume_dissolved	volume_pbs
g2	A01	0.449125	0.1	100	22.27	77.73
g3	B01	0.844125	0.1	100	11.85	88.15
g4	C01	0.340125	0.1	100	29.40	70.60
g5	D01	0.221125	0.1	100	45.22	54.78
g6	E01	0.227125	0.1	100	44.03	55.97
g8	F01	0.330125	0.1	100	30.29	69.71
g9	G01	0.214125	0.1	100	46.70	53.30
g10	H01	0.398125	0.1	100	25.12	74.88
g11	A03	0.245125	0.1	100	40.80	59.20
g13	B03	0.115125	0.1	100	86.86	13.14
g15	C03	0.817125	0.1	100	12.24	87.76
g16	D03	0.190125	0.1	100	52.60	47.40
g17	E03	0.209125	0.1	100	47.82	52.18
g19	F03	0.104125	0.1	100	96.04	3.96
g20	G03	0.169125	0.1	100	59.13	40.87
g21	H03	0.196125	0.1	100	50.99	49.01
g22	A05	0.474125	0.1	100	21.09	78.91
g23	B05	0.384125	0.1	100	26.03	73.97
g24	C05	0.302125	0.1	100	33.10	66.90
g25	D05	0.141125	0.1	100	70.86	29.14
g26	E05	0.304125	0.1	100	32.88	67.12
g27	F05	0.319125	0.1	100	31.34	68.66
g28	G05	0.178125	0.1	100	56.14	43.86
g29	H05	0.194125	0.1	100	51.51	48.49
g30	A07	0.318125	0.1	100	31.43	68.57
g31	B07	0.255125	0.1	100	39.20	60.80
g32	C07	0.557125	0.1	100	17.95	82.05
g33	D07	0.317125	0.1	100	31.53	68.47
g34	E07	0.292125	0.1	100	34.23	65.77
g35	F07	0.336125	0.1	100	29.75	70.25
g36	G07	0.174125	0.1	100	57.43	42.57
g37	H07	0.403125	0.1	100	24.81	75.19