

Lab_Notebook_2024

Callum Malcolm

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January 2024

Tuesday 16-01-2024

WILDseq - Mouse Experiment 1: PCR 1 Samples 1-8 / PCR 2 Sample 5

Overview:

- PCR tests to see if PCR would work for WS-ME1 cDNA previously made
- Started with samples 1-8 so as not to waste sample/reagents if PCR 1 did not work

Sample List

Sample ID	Treatment/Sample	ng/uL	i7 index	i5 index
1	Cyclophosphamide	773.7	N701	S502
2	Cyclophosphamide	545.3	N702	S502
3	Cyclophosphamide	903.6	N703	S502
4	Cyclophosphamide	1056.1	N704	S502
5	Cyclophosphamide	959.1	N705	S502
6	Combination	730.1	N706	S502
7	Combination	602.3	N707	S502
8	Combination	449.6	N710	S502
9	Combination	1002.1	N701	S503
10	Combination	1929.2	N702	S503
11	Methotrexate	861.5	N703	S503
12	Methotrexate	1110.4	N704	S503
13	Methotrexate	1171.0	N705	S503
14	Methotrexate	1347.8	N706	S503
15	Methotrexate	891.4	N707	S503
16	Vehicle	374.5	N710	S503
17	Vehicle	911.2	N701	S505
18	Vehicle	829.8	N702	S505
19	Vehicle	600.1	N703	S505
20	Vehicle	750.3	N704	S505
21	Baseline	401.5	N705	S505
22	Baseline	443.3	N706	S505
23	Baseline	373.4	N707	S505
24	Baseline	444.5	N710	S505
25	Baseline	267.6	N701	S506
26	BLLW 14K	378.7	N702	S506
27	BLLW 2K	362.7	N703	S506
28	BLLW 1K	563.8	N704	S506
29	Methotrexate (outlier)	348.1	N705	S506
30	Combo	380.8	N706	S506
31	RBL2P 2K	173.3	N707	S506
32	RBL2P 7K	2708.0	N7010	S506
33	RBL2P 250K	1418.5	N701	S507
34	Mock_direct_1	-	N702	S507
35	Mock_direct_2	-	N703	S507
36	Mock_direct_3	-	N704	S507
37	Mock_culture_1	-	N705	S507
38	Mock_culture_2	-	N706	S507
39	Mock_culture_3	-	N707	S507

PCR 1: Samples 1-8

- Checked [cDNA] on NanoDrop of sample 8 to make sure samples were still intact
 - Sample 8 $\text{ng}/\mu\text{L} = 1042.3$
 - It is assumed all other cDNA is of similar quality

1. Made a master mix of PCR1 reagents

- Made enough for 31 samples
- Primer mix was made earlier

Component	Volume	Master Mix
10uM WS PCR1 Primer Mix	3 μL	93 μL
DNase/RNase H20	12 μL	372 μL
Kapa Hifi HotStart Ready Mix (2X)	25 μL	775 μL

2. Add following components to tubes

Component	Volume
PCR1 MasterMix	40 μL
cDNA	10 μL

3. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Bead Clean Up

Overview

- Clean PCR reaction by removing leftover primers
- This prevents false reads, cleaner indexing in later steps, and higher quality samples

Materials

- For 40 samples

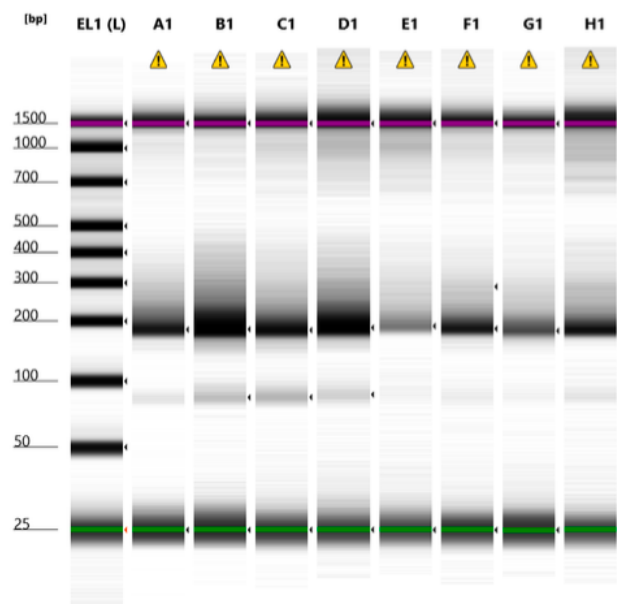
Component	Expected Volume/experiment	Material ID
Ampure Bead Kit	200 μL	

Protocol

1. Equilibrate Ampure beads to room temp (available from supplies cold room)
2. Mix well and vortex for 30sec to ensure uniform distribution.
3. Add 90ul (1.8X volume) to PCR reaction and mix thoroughly by pipetting.

4. Incubate 5min, room temp
 5. Place on magnet for 2 min and keep on magnet until final elution
 6. Remove supernatant and add 200ul 70% ethanol (make fresh)
 7. Incubate 30sec and remove
 8. Repeat 70% ethanol wash
 9. Air dry beads 5-10min room temp. Once dry the beads will go from shiny to matt in appearance. Avoid over drying (cracked appearance).
 10. Add 15 ul EB buffer and resuspend beads by pipetting
 11. Incubate 2min room temp
 12. Place on magnet and remove eluate
 13. Assess PCR product size, contamination and concentration on tapestation.
- Expected size = 165-172bp**

Tapestation PCR 1 - Samples 1-8



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Sample Info

Well	Conc. [pg/ul]	Sample Description	Alert	Observations
EL1	2350	Electronic Ladder		Ladder
A1	310	1 PCR1	⚠	Caution! Expired ScreenTape device
B1	631	2 PCR1	⚠	Caution! Expired ScreenTape device
C1	333	3 PCR1	⚠	Caution! Expired ScreenTape device
D1	369	4 PCR1	⚠	Caution! Expired ScreenTape device
E1	90.0	5 PCR1	⚠	Caution! Expired ScreenTape device
F1	266	6 PCR1	⚠	Caution! Expired ScreenTape device
G1	181	7 PCR1	⚠	Caution! Expired ScreenTape device
H1	206	8 PCR1	⚠	Caution! Expired ScreenTape device

Initial Test PCR 1

PCR 2: Samples 5

Overview

- Yield from PCR1 is low (.09 - .631 ng/ μ L)
- Sample with lowest concentration was taken ahead to PCR 2 (E1 - Sample 5)
- PCR to index samples for sequencing by attaching UMI

Materials

Component	Expected Volume/experiment	Material ID
10uM Nxxx Nextera i7 adapter	-	-
10uM Sxxx Nextera i5 adapter	-	-
DNase/RNase H20	1000 μ L	
Kapa Hifi HotStart Ready Mix (2X)	1200 μ L	KK2601

Protocol

1. Prepared samples according to the following table:

- Sample - Adaptor pairs in table above

Component	Volume
10uM N705 Nextera i7 adapter	1.5 μ L
10uM S502 Nextera i5 adapter	1.5 μ L
DNase/RNase H20	21 μ L
Kapa Hifi HotStart Ready Mix (2X)	25 μ L
10ng/ μ L PCR1	1 μ L

2. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 55C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	2 min
Hold Step	Step 6: 12C	Hold

8 cycles of steps 2-4

3. Performed Ampure bead clean up as above with 90ul beads per 50ul PCR reaction

4. Checked size and concentration on tapestation

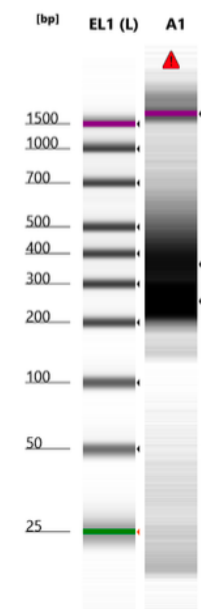
Tapestation PCR 2

Review

- Contamination/PCR bubble?
- Yield is adequate (assuming it is representative of the correct peak)
- Chris wants to repeat PCR1 for remaining samples, take PCR2 ahead, and re-run same with D1000 tape (non High-Sensitivity)

Plan for tomorrow

- PCR 1 samples 9-30
- Bead Clean Up
- Tape Station



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Sample Info

Well	Conc. [pg/ul]	Sample Description	Alert	Observations
EL1	2350	Electronic Ladder		Ladder
A1	3180	5 PCR2	▲	Marker(s) not detected: Caution! Expired ScreenTape device

Figure 1: 2024-01-16 Tapestation PCR 2 Test Samples 5

Wednesday 17-01-2024

WILDseq - Mouse Experiment 1: PCR 1 Samples 9-30

Overview:

- Completed PCR 1 for Samples 9-30

PCR 1: Samples 9-30

- Used master mix of PCR1 reagents made 2024-01-16
- Add following components to tubes |Component |Volume| |:————|—| | PCR1 MasterMix | 40 μ L |
| cDNA | 10 μ L |
- Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Bead Clean Up

Overview

- Clean PCR reaction by removing leftover primers
- This prevents false reads, cleaner indexing in later steps, and higher quality samples

Materials

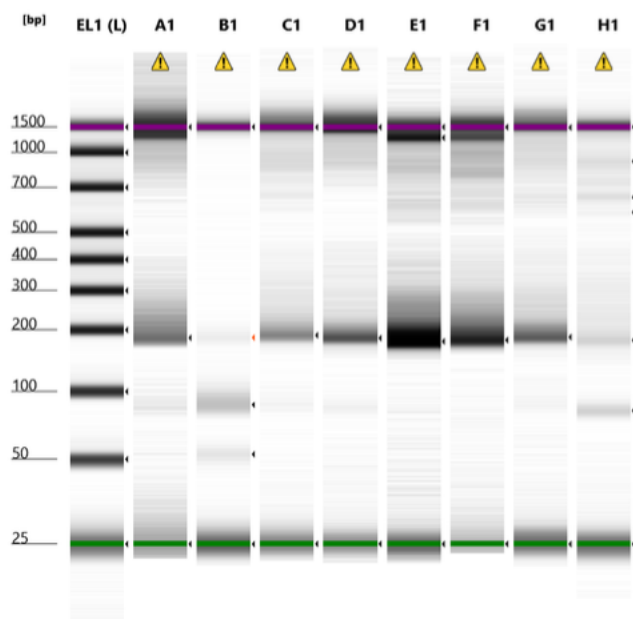
- For 40 samples

Component	Expected Volume/experiment	Material ID
Ampure Bead Kit	200 μ L	

Protocol

- Equilibrate Ampure beads to room temp (available from supplies cold room)
- Mix well and vortex for 30sec to ensure uniform distribution.
- Add 90ul (1.8X volume) to PCR reaction and mix thoroughly by pipetting.
- Incubate 5min, room temp
- Place on magnet for 2 min and keep on magnet until final elution
- Remove supernatant and add 200ul 70% ethanol (make fresh)
- Incubate 30sec and remove
- Repeat 70% ethanol wash
- Air dry beads 5-10min room temp. Once dry the beads will go from shiny to matt in appearance.
Avoid over drying (cracked appearance).
- Add 15 ul EB buffer and resuspend beads by pipetting
- Incubate 2min room temp

12. Place on magnet and remove eluate
13. Assess PCR product size, contamination and concentration on tapestation.
Expected size = 165-172bp



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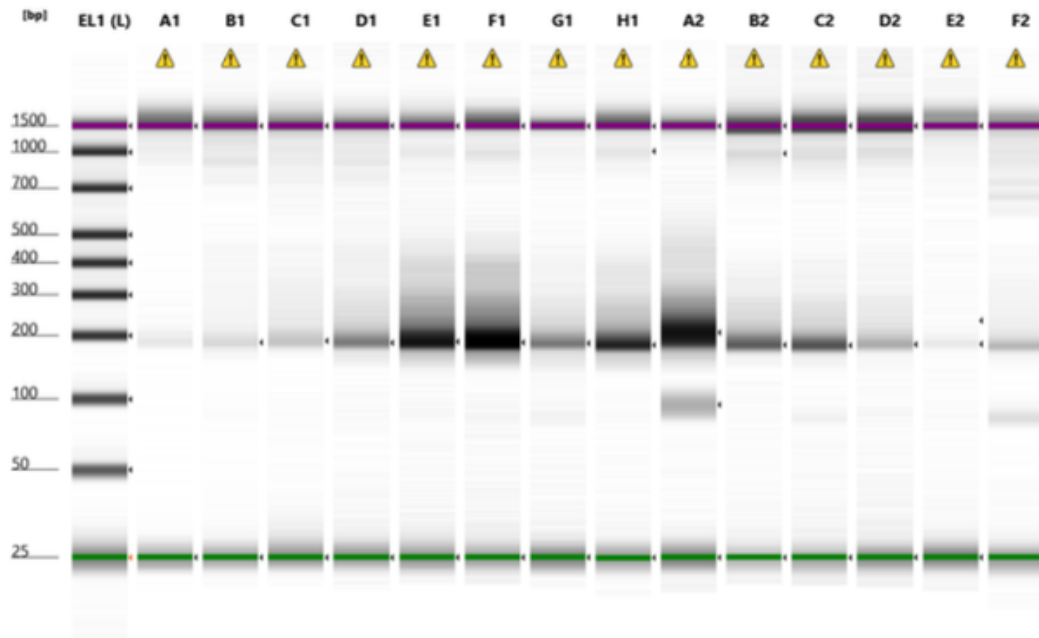
Sample Info

Well	Conc. [pg/μl]	Sample Description	Alert	Observations
EL1	2350	Electronic Ladder		Ladder
A1	88.4	9 PCR 1	⚠	Caution! Expired ScreenTape device
B1	164	10 PCR 1	⚠	Caution! Expired ScreenTape device
C1	142	11 PCR 1	⚠	Caution! Expired ScreenTape device
D1	140	12 PCR 1	⚠	Caution! Expired ScreenTape device
E1	1070	13 PCR 1	⚠	Caution! Expired ScreenTape device
F1	354	14 PCR 1	⚠	Caution! Expired ScreenTape device
G1	203	15 PCR 1	⚠	Caution! Expired ScreenTape device
H1	203	16 PCR 1	⚠	Caution! Expired ScreenTape device

Figure 2: 2024-01-17 Tapestation PCR 1 Samples 9-16

Tapestation PCR 1

Tapestation PCR 1



Default image (Contrast 100%)

Sample Info

Well	Conc. [pg/ul]	Sample Description	Alert	Observations
EL1	2350	Electronic Ladder		Ladder
A1		17 PCR 1	⚠	Caution! Expired ScreenTape device
B1	40.7	18 PCR 1	⚠	Caution! Expired ScreenTape device
C1	84.0	19 PCR 1	⚠	Caution! Expired ScreenTape device
D1	226	20 PCR 1	⚠	Caution! Expired ScreenTape device
E1	665	21 PCR 1	⚠	Caution! Expired ScreenTape device
F1	820	22 PCR 1	⚠	Caution! Expired ScreenTape device
G1	270	23 PCR 1	⚠	Caution! Expired ScreenTape device
H1	423	24 PCR 1	⚠	Caution! Expired ScreenTape device
A2	1290	25 PCR 1	⚠	Caution! Expired ScreenTape device
B2	223	26 PCR 1	⚠	Caution! Expired ScreenTape device
C2	170	27 PCR 1	⚠	Caution! Expired ScreenTape device
D2	71.5	28 PCR 1	⚠	Caution! Expired ScreenTape device
E2	30.5	29 PCR 1	⚠	Caution! Expired ScreenTape device
F2	157	30 PCR 1	⚠	Caution! Expired ScreenTape device

Review

- Samples 10/17/18/29 don't have adequate yield
 - Will need to redo PCR 1
 - Sample 10 has acceptable PCR1 sample from previous run
- Yield is adequate for the rest to move ahead

Plan for tomorrow

- PCR 1 samples 17/18/29
 - Bead Clean Up
 - Tape Station
- PCR 2 for all samples
 - Double check reagents amounts
 - Running low on KAPA (re-ordered) and Nextera Primers

- Chris wants to add 2 additional samples
 - To Do - RNA Extraction / RT / PCR 1 / PCR 2
 - Wait until majority of samples have acceptable PCR 2 product

Thursday 18-01-2024

WILDseq - Mouse Experiment 1: PCR 1 Samples 17/18/29

Overview:

- Repeated PCR 1 for Samples 17/18/29

PCR 1: Samples 17/18/29

1. Used master mix of PCR1 reagents made 2024-01-16
2. Add following components to tubes |Component |Volume| |:—————:|:|—————:| | PCR1 MasterMix | 40 μ L | | cDNA | 10 μ L |
3. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Bead Clean Up

Overview

- Clean PCR reaction by removing leftover primers
- This prevents false reads, cleaner indexing in later steps, and higher quality samples

Materials

- For 40 samples

Component	Expected Volume/experiment	Material ID
Ampure Bead Kit	200 μ L	

Protocol

1. Equilibrate Ampure beads to room temp (available from supplies cold room)
2. Mix well and vortex for 30sec to ensure uniform distribution.
3. Add 90ul (1.8X volume) to PCR reaction and mix thoroughly by pipetting.
4. Incubate 5min, room temp
5. Place on magnet for 2 min and keep on magnet until final elution
6. Remove supernatant and add 200ul 70% ethanol (make fresh)
7. Incubate 30sec and remove
8. Repeat 70% ethanol wash

9. Air dry beads 5-10min room temp. Once dry the beads will go from shiny to matt in appearance.
Avoid over drying (cracked appearance).
10. Add 15 ul EB buffer and resuspend beads by pipetting
11. Incubate 2min room temp
12. Place on magnet and remove eluate
13. Assess PCR product size, contamination and concentration on tapestation.
Expected size = 165-172bp

Tapestation PCR 1

Review

- Samples 10/17/18/29 don't have adequate yield
 - Will need to redo PCR 1
 - Sample 10 has acceptable PCR1 sample from previous run
- Yield is adequate for the rest to move ahead

Plan for tomorrow

- PCR 1 samples 17/18/29
 - Bead Clean Up
 - Tape Station
- PCR 2 for all samples
 - Double check reagents amounts
 - Running low on KAPA (re-ordered) and Nextera Primers
- Chris wants to add 2 additional samples
 - To Do - RNA Extraction / RT / PCR 1 / PCR 2
 - Wait until majority of samples have acceptable PCR 2 product

Friday 19-01-2024

WILDseq - Mouse Experiment 1: RNA Extraction/RT Samples 31-33

Overview: Extra samples given by Chris for whitelist

RNA extraction Samples 31-33

- Performed RNA extraction of tissue/cell samples according to the following kit:

RT Protocol Samples 31-33

1. In PCR strip tubes, prepared 5 μ g of RNA in a total volume of 10 μ l of RNase/DNAase-free water.
2. Add 1 μ l of WS_RT_UMI_NexteraR2 primer (2 μ M stock)
3. Add 1 μ l dNTPs (10 mM each).
4. Denature at 65 C for 5 mins in the PCR machine, then straight onto ice for at least 2 mins, spin briefly to get liquid to the bottom of the tube.
5. Used Master Mix previously made
6. Add 7 μ l of RT MM prepared above to each sample and mix, spin briefly to get liquid to the bottom of the tube.
 - Spin briefly to get liquid to bottom of the tube
7. In the PCR machine incubate at 53 C for 10 mins followed by 80 C for 10 mins.
8. Add 1 μ l Themolabile Exonuclease I (NEB M0568) to remove excess RT primer.

Component	Volume	MM volume
Thermolabile Exonuclease I	1 μ L	
NEBuffer r3.1*	2 μ L	

Most PCR buffers are compatible

9. In PCR Machine: heat at 37C for 4 mins followed by 80C for 1 min
 - Spin briefly to get liquid to bottom of the tube
10. Add 1 μ l of RNase H and incubate at 37 C for 20 mins.
11. Checked [cDNA] on NanoDrop
 - Added to Sample List

Monday 22-01-2024

PCR 1: Samples 31-33

- Included negative control (MM + H2O)
1. Used master mix of PCR1 reagents made 2024-01-16
 2. Add following components to tubes

Component	Volume
PCR1 MasterMix	40 μ L
cDNA	10 μ L

3. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Bead Clean Up

Overview

- Clean PCR reaction by removing leftover primers
- This prevents false reads, cleaner indexing in later steps, and higher quality samples

Materials

- For 40 samples

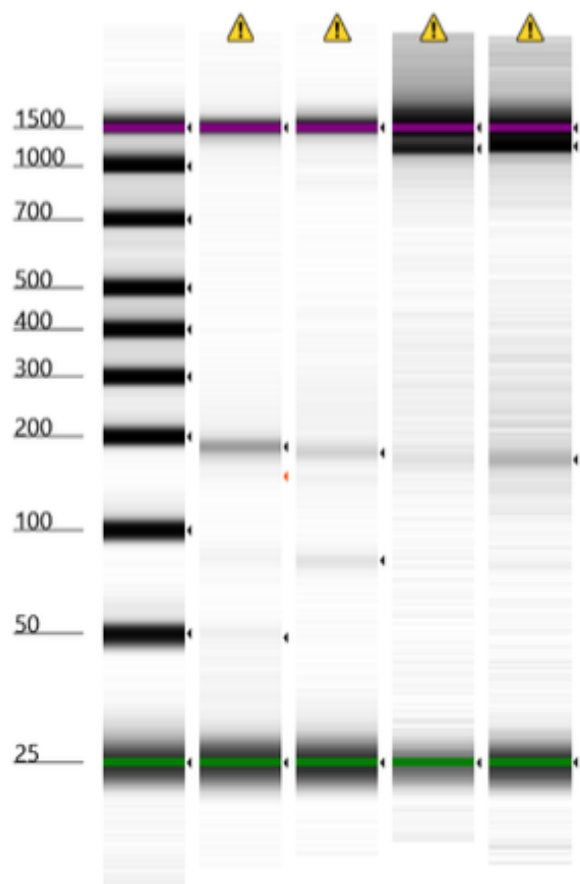
Component	Expected Volume/experiment	Material ID
Ampure Bead Kit	200 μ L	

Protocol

1. Equilibrate Ampure beads to room temp (available from supplies cold room)
2. Mix well and vortex for 30sec to ensure uniform distribution.
3. Add 90ul (1.8X volume) to PCR reaction and mix thoroughly by pipetting.
4. Incubate 5min, room temp
5. Place on magnet for 2 min and keep on magnet until final elution
6. Remove supernatant and add 200ul 70% ethanol (make fresh)
7. Incubate 30sec and remove
8. Repeat 70% ethanol wash
9. Air dry beads 5-10min room temp. Once dry the beads will go from shiny to matt in appearance.
Avoid over drying (cracked appearance).
10. Add 15 ul EB buffer and resuspend beads by pipetting
11. Incubate 2min room temp
12. Place on magnet and remove eluate
13. Assess PCR product size, contamination and concentration on tapestation.
Expected size = 165-172bp

Tapestation PCR 1 31-33

Tapestation PCR 1



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Sample Info

Well	Conc. [pg/μl]	Sample Description
EL1	2350	Electronic Ladder
A1	89.4	-RT Control
B1	46.1	31 PCR 1
C1	87.3	32 PCR 1
D1	195	33 PCR 1

!!!! Band present in - Control lane !!!!

PCR 1: Negative Control

- Remade negative control (MM + H2O)
1. Used master mix of PCR1 reagents made 2024-01-16
 2. Add following components to tubes

Component	Volume
PCR1 MasterMix	40 μ L
cDNA	10 μ L

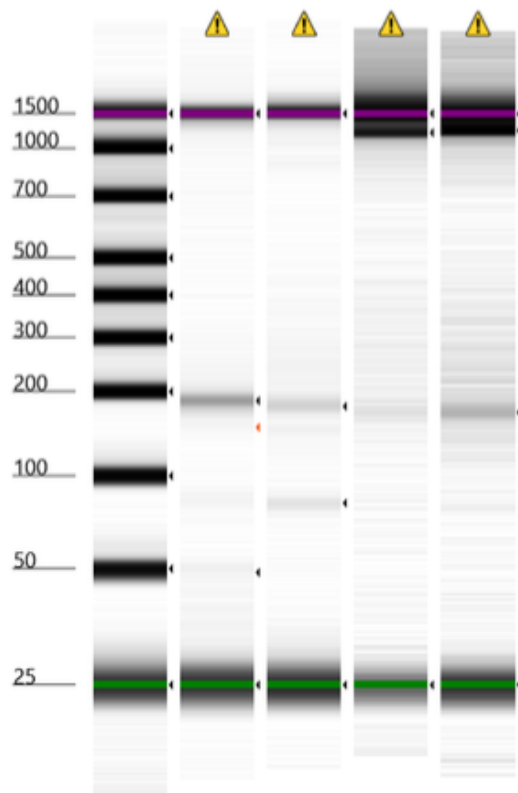
3. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Tapestation Control Test 1

- Compared New -Control to old
 - Wanted to determine if this was a pipetting error



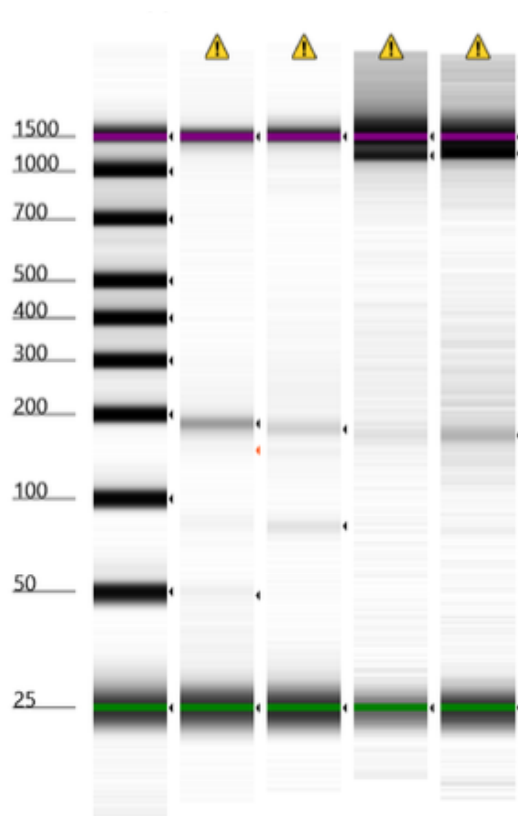
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Sample Info

Well	Conc. [pg/μl]	Sample Description
EL1	2350	Electronic Ladder
A1	89.4	-RT Control
B1	46.1	31 PCR 1
C1	87.3	32 PCR 1
D1	195	33 PCR 1

Tapestation Control Test 2

- Compared New -Control to H2O
 - Wanted to determine if water was contaminated



Default image (Contrast 100%)

Sample Info

Well	Conc. [pg/μl]	Sample Description
EL1	2350	Electronic Ladder
A1	89.4	-RT Control
B1	46.1	31 PCR 1
C1	87.3	32 PCR 1
D1	195	33 PCR 1

Tuesday 23-01-2024

Made New Media: AR-5

1. Made new media: AR-5

Solution	ID code	Volume	% Total volume
Advanced RMPI	—	500 mL	78%
Glutamax	—	6.5 mL	20%
Pen-Strep	—	6.5 mL	1%
FBS	—	128 mL	1%

Cell Culture

A20

- Thawed A20 and seeded in T25
- Spun down CS to remove DMSO, cell pellet small
- Cells didn't look super healthy
- Monitor tomorrow

HEK

- Got T75 flask from Chris
- 70% confluent
- Added 10mL of trypsin and tapped flask until cells were dislodged
- Added 10mL of DMEM (20% FBS) and added to 50mL tube
- Added 25mL of DMEM to 5 T75 flasks
- Mixed CS to get single cell suspension and remove clumps
- Transferred 4mL of CS to each flask
- Will grow up for 1-2 days and freeze down 4 T75 flasks
 - Other flask will be used to grow WILDseq library virus for A20's

WS-ME1 Library Prep: Control Test 3

Overview: question around contaminated primers - Ran PCR1 with new primer/PCR 1 mix

PCR 1: Negative Control

- Remade negative control (MM + H2O)
- Remade Primer mix and PCR1 MM

PCR1 Primer Mix

- WILDseq protocol from Kirsty dictates 8 fwd primers mixed in equal amounts with equivalent amount of rev primer
- Primers were reconstituted at 100 μ M so needed to be diluted to 10 μ

Component	Volume
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	16 μ L
DNase/RNase H2O	320 μ L

PCR1 MM

Component	Volume	Master Mix
10uM WS PCR1 Primer Mix	3 μ L	
DNase/RNase H2O	12 μ L	
Kapa Hifi HotStart Ready Mix (2X)	25 μ L	

1. Add following components to tubes

Component	Volume
PCR1 MasterMix	40 μ L
H2O	10 μ L

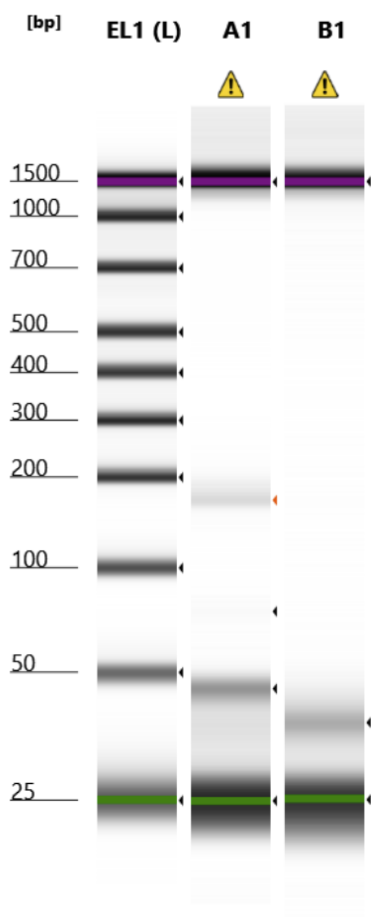
2. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Tapestation Control Test 3

- Compared New -Control to old -control
 - Wanted to determine if water was contaminated



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Sample Info

Well	Conc. [ng/μl]	Sample Description
EL1	20.3	Electronic Ladder
A1	2.13	Control 1
B1	2.01	Control 2

Wednesday 24-01-2024

Cell Culture

A20

- Checked cells ~10% confluent
- Cells looked healthy but sparse
- Grow up for injection
- Ask Chris about cell numbers needed for injecting into 12 mice

HEK

- 20% confluent
- Check tomorrow and split on Friday

WILDseq - Mouse Experiment 1: Library Prep Attempt 5 - RT

- Decided to repeat the entire library prep process using RNA extracted previously
- Everything done in PCR room RNA hood

RT Protocol

1. In PCR strip tubes, prepared 5 μg of RNA in a total volume of 10 μl of RNase/DNAase-free water.
2. Add 1 μl of WS_RT_UMI_NexteraR2 primer (2 μM)
 - Diluted primer from stock (100 μM)
 - Added 1 μL RT-Primer stock into 49 μL water
3. Add 1 μl dNTPs (10 mM each).
4. Denature at 65 C for 5 mins in the PCR machine, then straight onto ice for at least 2 mins, spin briefly to get liquid to the bottom of the tube.
5. Prepare mastermix of RT enzyme and buffers. 1.1x the number of samples.

Component	Volume	MM volume
5x SSIV Buffer	4 μL	134 μL
SSIV RT	1 μL	33.5 μL
100 mM DTT	1 μL	33.5 μL
RNase Out	1 μL	33.5 μL

6. Add 7 μl of RT MM prepared above to each sample and mix, spin briefly to get liquid to the bottom of the tube.
 - Spin briefly to get liquid to bottom of the tube
7. In the PCR machine incubate at 53 C for 10 mins followed by 80 C for 10 mins.
8. Add 1 μl Themolabile Exonuclease I (NEB M0568) to remove excess RT primer.

Component	Volume	MM volume
Themolabile Exonuclease I	1 μL	33.5 μL
NEBuffer r3.1*	2 μL	67 μL

Most PCR buffers are compatible

9. In PCR Machine: heat at 37C for 4 mins followed by 80C for 1 min
 - Spin briefly to get liquid to bottom of the tube
10. Add 1 μl of RNase H and incubate at 37 C for 20 mins.
 - Stored at -4C

Plan for tomorrow

- PCR 1 (check for KAPA HIFI amount)
 - Bead Clean Up
 - Tape Station
- Check on cells
- Plan cell numbers needed for A20 mouse injections

Thursday 25-01-2024

Cell Culture

A20

- Checked cells ~50% confluent
- Cells looked healthy but sparse
- Added 10ml of AR-5
- Grow up for injection
- Ask Chris about cell numbers needed for injecting into 12 mice

HEK

- Collected all T175 and froze down
- Left one flask going at 20% confluency

WS-ME1 Library Prep - Attempt 5 PCR 1

Ran PCR1 for attempt 5

PCR 1: Negative Control

- Remade negative control (MM + H2O)
- Remade Primer mix and PCR1 MM

PCR1 Primer Mix

- WILDseq protocol from Kirsty dictates 8 fwd primers mixed in equal amounts with equivalent amount of rev primer
- Primers were reconstituted at 100 μ M so needed to be diluted to 10 μ M

Component	Volume
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	2 μ L
100uM WS PCR1 Primer Mix	16 μ L
DNase/RNase H2O	144 μ L

PCR1 MM

Component	Volume	Master Mix
10uM WS PCR1 Primer Mix	3 μ L	
DNase/RNase H2O	12 μ L	
Q5 Master Mix	25 μ L	

- Used Q5 instead of KAPA
1. Add following components to tubes

Component	Volume
PCR1 MasterMix	40 μ L
H2O	10 μ L

2. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Bead Clean Up

Overview

- Clean PCR reaction by removing leftover primers
- This prevents false reads, cleaner indexing in later steps, and higher quality samples

Materials

- For 40 samples

Component	Expected Volume/experiment	Material ID
Ampure Bead Kit	200 μ L	

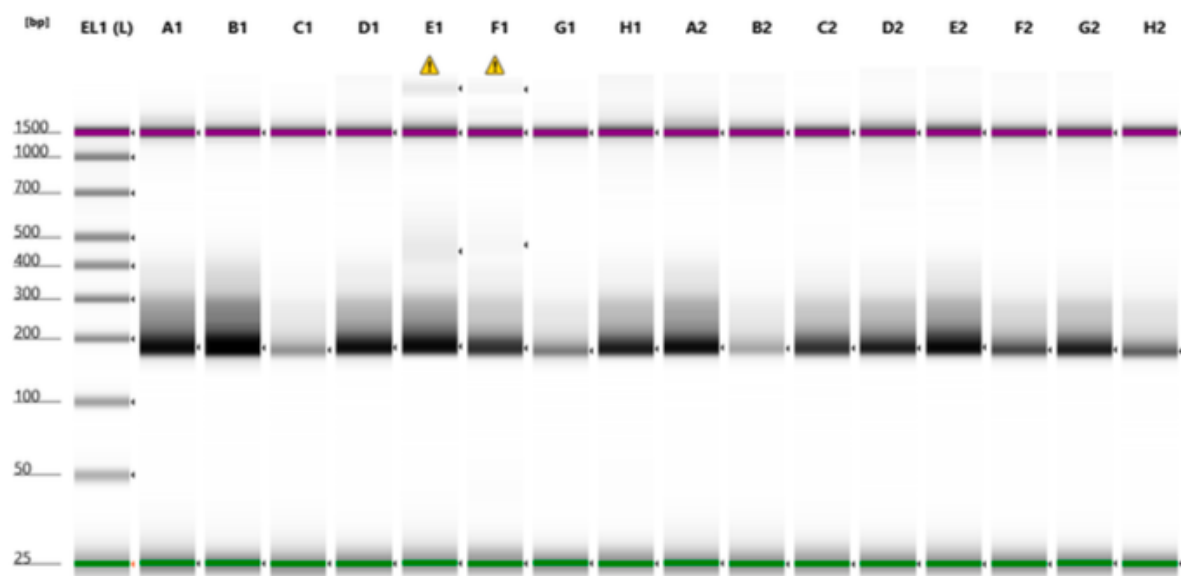
Protocol

1. Equilibrate Ampure beads to room temp (available from supplies cold room)
2. Mix well and vortex for 30sec to ensure uniform distribution.
3. Add 90ul (1.8X volume) to PCR reaction and mix thoroughly by pipetting.
4. Incubate 5min, room temp
5. Place on magnet for 2 min and keep on magnet until final elution
6. Remove supernatant and add 200ul 70% ethanol (make fresh)
7. Incubate 30sec and remove
8. Repeat 70% ethanol wash
9. Air dry beads 5-10min room temp. Once dry the beads will go from shiny to matt in appearance. Avoid over drying (cracked appearance).
10. Add 15 ul EB buffer and resuspend beads by pipetting
11. Incubate 2min room temp
12. Place on magnet and remove eluate
13. Assess PCR product size, contamination and concentration on tapestation.
Expected size = 165-172bp

Tapestation PCR 1 Samples 1-33

Tapestation PCR 1 1-16

Tapestation PCR 1



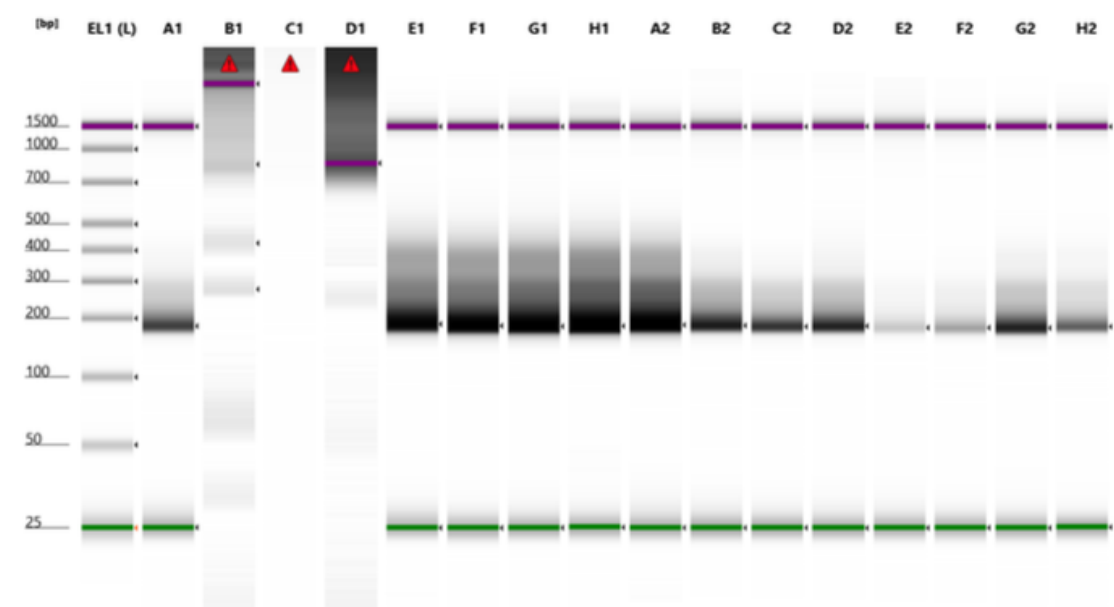
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Sample Info

Well	Conc. [ng/ul]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1	18.8	1 PCR 1		
B1	28.9	2 PCR 1		
C1	4.49	3 PCR 1		
D1	17.5	4 PCR 1		
E1	19.4	5 PCR 1	⚠	Peak out of Sizing Range
F1	12.7	6 PCR 1	⚠	Peak out of Sizing Range
G1	5.42	7 PCR 1		
H1	13.6	8 PCR 1		
A2	15.8	9 PCR 1		
B2	3.52	10 PCR 1		
C2	12.2	11 PCR 1		
D2	13.0	12 PCR 1		
E2	18.8	13 PCR 1		
F2	8.74	14 PCR 1		
G2	13.2	15 PCR 1		
H2	6.68	16 PCR 1		

Figure 3: 2024-01-25 Tapestation PCR 1 Samples 1-16

Tapestation PCR 1 1-32



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Sample Info

Well	Conc. [ng/ul]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1	15.5	17 PCR 1		
B1	2.76	18 PCR 1	▲	Marker(s) not detected
C1		19 PCR 1	▲	Marker(s) not detected
D1		20 PCR 1	▲	Marker(s) not detected
E1	39.1	21 PCR 1		
F1	43.3	22 PCR 1		
G1	46.2	23 PCR 1		
H1	49.7	24 PCR 1		
A2	47.3	25 PCR 1		
B2	20.2	26 PCR 1		
C2	15.7	27 PCR 1		
D2	18.5	28 PCR 1		
E2	2.85	29 PCR 1		
F2	5.29	30 PCR 1		
G2	20.4	31 PCR 1		
H2	10.8	32 PCR 1		

Figure 4: 2024-01-25 TapeStation PCR 1 Samples 17-32

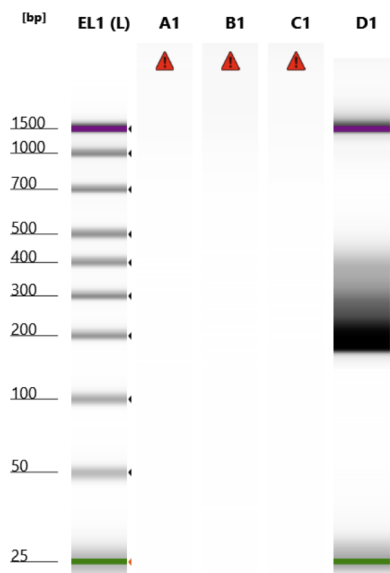
Tapestation PCR 1

- Samples 18, 19, and 20 DNW

Tapestation PCR 1 18-20, 33

Tapestation PCR 1

- Samples 18, 19, and 20 DNW again



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Sample Info

Well	Conc. [ng/μl]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1		17 PCR 1 v2	▲	Marker(s) not detected
B1		18 PCR 1 v2	▲	Marker(s) not detected
C1		20 PCR 1 v2	▲	Marker(s) not detected
D1	36.1	33 PCR 1		

Figure 5: 2024-01-25 Tapestation PCR 1 Samples 33 and redo 18-20

Friday 26-01-2024

Cell Culture

A20

- Expanded to T175
- Grow up for injection
- Ask Chris about cell numbers needed for injecting into 12 mice

HEK

- Split 1/2
- DMEM

WS-ME1 Library Prep - Attempt 5 PCR 1 repeat and PCR 2 prep

- Reran PCR1 for samples 18,19,20
- Prepped PCR2 primers

PCR2 Prep

- Reconstituted PCR2 primers bought by Chris
 - Used DNase/RNase Free H2O and diluted to 100 μ M
- Diluted into strip tubes working stock (10 μ M)
 - 90 μ L H2O + 10 μ L primer stock

PCR1 Samples 18-20

PCR1 Protocol

- Used Primer Mix previously made on 25-01-2024

Component	Volume	Master Mix
10uM WS PCR1 Primer Mix	3 μ L	
DNase/RNase H2O	12 μ L	
Q5 Master Mix	25 μ L	

- Used Q5 instead of KAPA

1. Add following components to tubes

Component	Volume
PCR1 MasterMix	40 μ L
H2O	10 μ L

2. Performed PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 60C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	1 min

Step Name	Steps	Time
Hold Step	Step 6: 12C	Hold

10-25 cycles of steps 2-4

Bead Clean Up

Overview

- Clean PCR reaction by removing leftover primers
- This prevents false reads, cleaner indexing in later steps, and higher quality samples

Materials

- For 40 samples

Component	Expected Volume/experiment	Material ID
Ampure Bead Kit	200 μ L	

Protocol

1. Equilibrate Ampure beads to room temp (available from supplies cold room)
2. Mix well and vortex for 30sec to ensure uniform distribution.
3. Add 90ul (1.8X volume) to PCR reaction and mix thoroughly by pipetting.
4. Incubate 5min, room temp
5. Place on magnet for 2 min and keep on magnet until final elution
6. Remove supernatant and add 200ul 70% ethanol (make fresh)
7. Incubate 30sec and remove
8. Repeat 70% ethanol wash
9. Air dry beads 5-10min room temp. Once dry the beads will go from shiny to matt in appearance. Avoid over drying (cracked appearance).
10. Add 15 ul EB buffer and resuspend beads by pipetting
11. Incubate 2min room temp
12. Place on magnet and remove eluate
13. Assess PCR product size, contamination and concentration on tapestation.
Expected size = 165-172bp

Tapestation PCR 1 Samples 18-20

Tapestation PCR 1 18-20

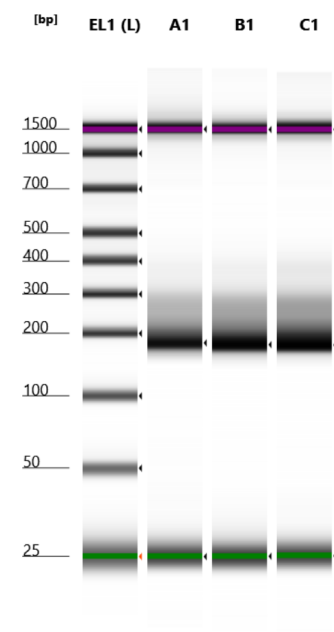
Tapestation PCR 1

Monday 29-01-2024

Cell Culture

A20

- Split 1:6
- AR-5
- Ask Chris about cell numbers needed for injecting into 12 mice



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Sample Info

Well	Conc. [ng/ul]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1	8.30	18 PCR 1		
B1	9.76	19 PCR 1		
C1	10.3	20 PCR 1		

Figure 6: 2024-01-26 Tapestation PCR 1 Samples 18-20

HEK

- Split 1/6
- DMEM

PCR Step 2 - Samples 1-24

Overview

- PCR to index samples for sequencing by attaching UMI
- Didn't have enough Q5 to complete all the samples

PCR2 Protocol

1. Prepare samples according to the following table:
 - Keep careful note of which adaptors are added to which sample

Component	Volume
10uM Nxxx Nextera i7 adapter	1.5 μ L
10uM Sxxx Nextera i5 adapter	1.5 μ L
DNase/RNase H20	21 μ L
Q5	25 μ L
10ng/ μ L PCR1	1 μ L

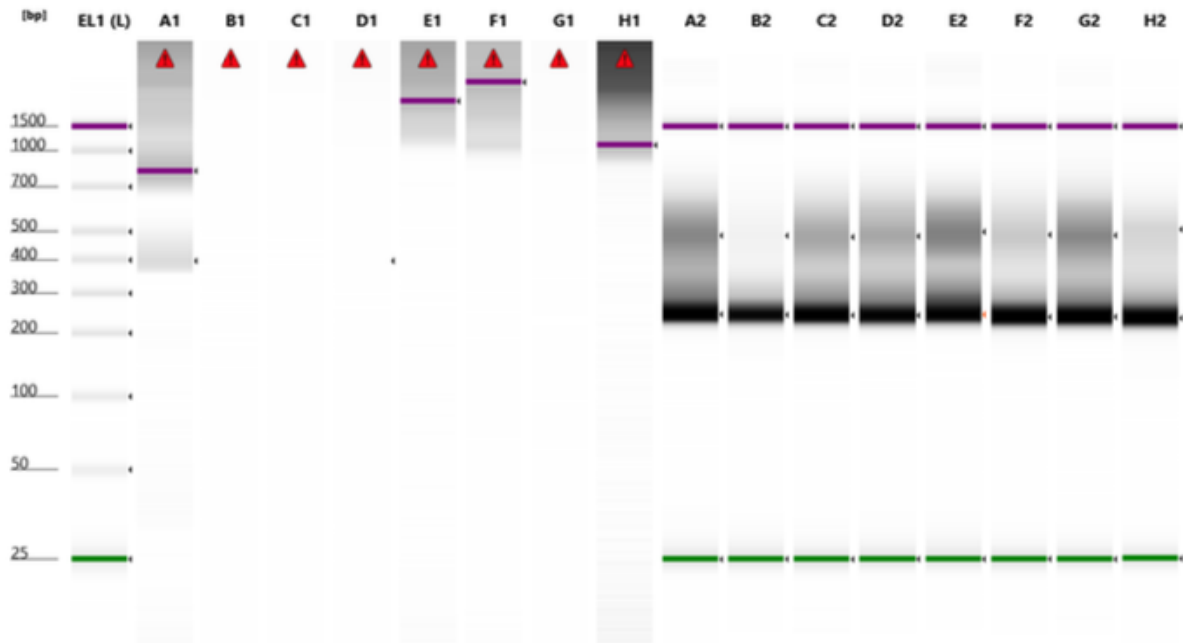
2. Perform PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 55C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	2 min
Hold Step	Step 6: 12C	Hold

8 cycles of steps 2-4

3. Perform Ampure bead clean up as above with 90ul beads per 50ul PCR reaction.
 - If you don't have a crazy number of samples you might also want to consider doing up to 4 PCR2 reactions per sample and pooling them afterwards just to make sure all your sequences are captured.
4. Check size and concentration on tapestation. Dilute and pool samples for sequencing.

Tapestation

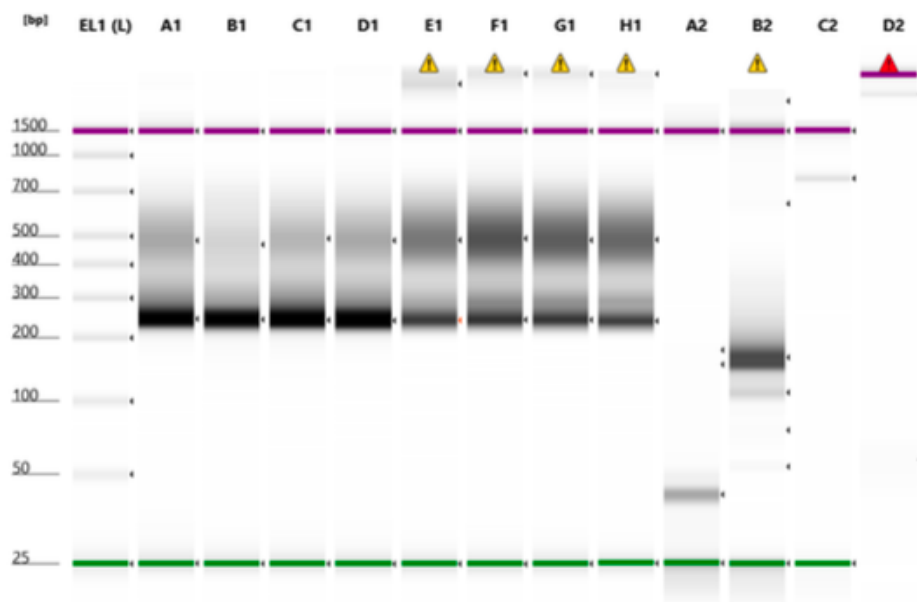


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Sample Info

Well	Conc. [ng/ul]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1	2.72	1 PCR 2	▲	Marker(s) not detected
B1		2 PCR 2	▲	Marker(s) not detected
C1		3 PCR 2	▲	Marker(s) not detected
D1		4 PCR 2	▲	Marker(s) not detected
E1		5 PCR 2	▲	Marker(s) not detected
F1		6 PCR 2	▲	Marker(s) not detected
G1		7 PCR 2	▲	Marker(s) not detected
H1		8 PCR 2	▲	Marker(s) not detected
A2	206	9 PCR 2		
B2	88.9	10 PCR 2		
C2	173	11 PCR 2		
D2	159	12 PCR 2		
E2	160	13 PCR 2		
F2	164	14 PCR 2		
G2	214	15 PCR 2		
H2	149	16 PCR 2		

- 1-8 PCR DNW (suspected issue with bead clean-up)



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Sample Info

Well	Conc. [ng/ul]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1	167	17 PCR 2		
B1	155	18 PCR 2		
C1	186	19 PCR 2		
D1	200	20 PCR 2		
E1	177	21 PCR 2	⚠	Peak out of Sizing Range
F1	224	22 PCR 2	⚠	Peak out of Sizing Range
G1	210	23 PCR 2	⚠	Peak out of Sizing Range
H1	184	24 PCR 2	⚠	Peak out of Sizing Range
A2	13.5			
B2	37.3		⚠	Peak out of Sizing Range
C2	2.29			
D2	3.24		⚠	Marker(s) not detected

- Last 4 samples are from Chris (seperate experiment)

Tuesday 30-01-2024

Cell Culture

HEK

- Unhealthy
- Discarded

A20

- Split 1/6

February 2024

Thursday 01-02-2024

PCR Step 2 - Samples 1-8, 25-39

- Repeated PCR2 for samples 1-8

Overview

- PCR to index samples for sequencing by attaching UMI
- Didn't have enough Q5 to complete all the samples

PCR2 Protocol

1. Prepare samples according to the following table:
 - Keep careful note of which adaptors are added to which sample

Component	Volume
10uM Nxxx Nextera i7 adapter	1.5 μ L
10uM Sxxx Nextera i5 adapter	1.5 μ L
DNase/RNase H20	21 μ L
Q5	25 μ L
10ng/ μ L PCR1	1 μ L

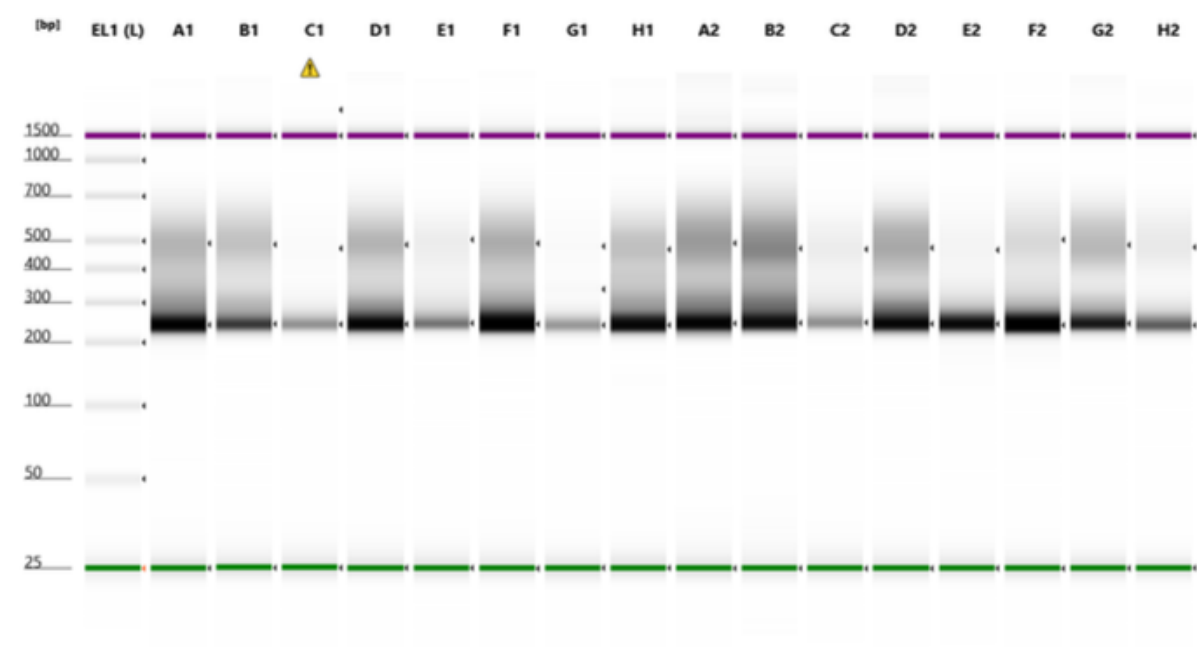
2. Perform PCR using the following parameters:

Step Name	Steps	Time
Initial Denaturation	Step 1: 95C	3mins
Denaturation	Step 2: 98C	20s
Annealing	Step 3: 55C	15s
Extension	Step 4: 72C	15s
Final Extension	Step 5: 72C	2 min
Hold Step	Step 6: 12C	Hold

8 cycles of steps 2-4

3. Perform Ampure bead clean up as above with 90ul beads per 50ul PCR reaction.
 - If you don't have a crazy number of samples you might also want to consider doing up to 4 PCR2 reactions per sample and pooling them afterwards just to make sure all your sequences are captured.
4. Check size and concentration on tapestation. Dilute and pool samples for sequencing.

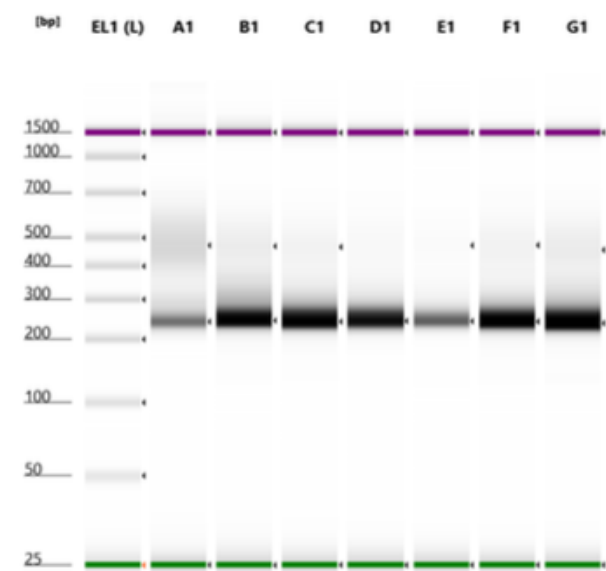
Tapestation



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Sample Info

Well	Conc. [ng/ul]	Sample Description	Alert	Observations
EL1	20.3	Electronic Ladder		Ladder
A1	133	1 PCR 2		
B1	83.8	2 PCR 2		
C1	20.0	3 PCR 2	⚠	Peak out of Sizing Range
D1	130	4 PCR 2		
E1	34.0	5 PCR 2		
F1	166	6 PCR 2		
G1	21.2	7 PCR 2		
H1	94.9	8 PCR 2		
A2	153	25 PCR 2		
B2	147	26 PCR 2		
C2	29.1	27 PCR 2		
D2	149	28 PCR 2		
E2	81.6	29 PCR 2		
F2	141	30 PCR 2		
G2	104	31 PCR 2		
H2	45.9	32 PCR 2		



Monday 05-02-2024

Cell Culture

Made DMEM

Solution	ID code	Volume	% Total volume
DMEM	—	500 mL	78%
Pen-Strep	—	5.5 mL	1%
FBS	—	55 mL	10%

HEK - Seeded

- Seeded New HEK
 - HEK stock are in CM Box 1 -80
1. Thawed vial
 2. Added 1mL DMEM to vial
 3. Transferred to 15mL falcon tube
 4. Slowly added 5mL DMEM
 5. Spun down at 650rpm for 4min
 6. Removed supernant and resuspended vial flicking
 7. Added 1mL DMEM and pipetted multiple times to create single cell suspension
 8. Added to T25 flask
 9. Added 14mL of DMEM
 10. Placed in incubator

A20 - Split

- Split 1/6
- Split T25 vial for Emily James (EJ)

Tuesday 06-02-2024

WS-ME1 Pooling for Submission

- Genomics core indicated that library should be submitted at 5nM-10nM in a volume of 20-30uL
- Cubit PCR2 Samples to determine concentration

Sample ID	Submission ID	Nextera Adaptor Indices	Desired ng/uL	Base Pair	[Final] nM	Sample Volume (uL)	H2O (uL)
1	1_Cyclophosphamidei701-i502		1.5	241	9.43	1	29.60
2	2_Cyclophosphamidei702-i502		1.5	241	9.43	1	19.20
3	3_Cyclophosphamidei703-i502		1.5	241	9.43	1	4.52
4	4_Cyclophosphamidei704-i502		1.5	241	9.43	1	25.90
5	5_Cyclophosphamidei705-i502		1.5	241	9.43	1	6.40
6	6_Combination	i706-i502	1.5	241	9.43	1	31.90
7	7_Combination	i707-i502	1.5	241	9.43	1	4.50
8	8_Combination	i710-i502	1.5	241	9.43	1	24.70
9	9_Combination	i701-i503	1.5	241	9.43	1	45.70
10	10_Combination	i702-i503	1.5	241	9.43	1	22.30
11	11_Methotrexate	i703-i503	1.5	241	9.43	1	43.90
12	12_Methotrexate	i704-i503	1.5	241	9.43	1	32.70

Sample ID	Submission ID	Nextera Adaptor Indices	Desired ng/uL	Base Pair	[Final] nM	Sample Volume (uL)	H2O (uL)
13	13_Methotrexate	i705-i503	1.5	241	9.43	1	41.20
14	14_Methotrexate	i706-i503	1.5	241	9.43	1	34.80
15	15_Methotrexate	i707-i503	1.5	241	9.43	1	46.10
16	16_Vehicle	i710-i503	1.5	241	9.43	1	28.30
17	17_Vehicle	i701-i505	1.5	241	9.43	1	39.70
18	18_Vehicle	i702-i505	1.5	241	9.43	1	32.00
19	19_Vehicle	i703-i505	1.5	241	9.43	1	34.90
20	20_Vehicle	i704-i505	1.5	241	9.43	1	34.00
21	21_Baseline	i705-i505	1.5	241	9.43	1	34.10
22	22_Baseline	i706-i505	1.5	241	9.43	1	34.30
23	23_Baseline	i707-i505	1.5	241	9.43	1	28.90
24	24_Baseline	i710-i505	1.5	241	9.43	1	31.60
25	25_Baseline	i701-i506	1.5	241	9.43	1	27.60
26	26_BLLW 14K	i702-i506	1.5	241	9.43	1	24.10
27	27_BLLW 2K	i703-i506	1.5	241	9.43	1	5.20
28	28_BLLW 1K	i704-i506	1.5	241	9.43	1	30.50
29	29_Methotrexate (outlier)	i705-i506	1.5	241	9.43	1	14.00
30	30_Combo	i706-i506	1.5	241	9.43	1	28.10
31	31_RBL2P_2K	i707-i506	1.5	241	9.43	1	15.10
32	32_RBL2P_7K	i710-i506	1.5	241	9.43	1	49.40
33	33_RBL2P_250K	i701-i507	1.5	241	9.43	1	41.50
34	34_Mock_direct_1	i702-i507	1.5	241	9.43	1	15.30
35	35_Mock_direct_2	i703-i507	1.5	241	9.43	1	15.90
36	36_Mock_direct_3	i704-i507	1.5	241	9.43	1	10.90
37	37_Mock_culture_1	i705-i507	1.5	241	9.43	1	4.48
38	38_Mock_culture_2	i706-i507	1.5	241	9.43	1	18.00
39	39_Mock_culture_3	i707-i507	1.5	241	9.43	1	17.70

- Used IDT Library Concentration Conversion Calculator
 - Link: <https://eu.idtdna.com/Calc/library-concentration-conversion>

Wednesday 07-02-2024

Cell Culture

HEK

- Decided to wait till Monday to start making virus
- Discarded HEK
- Will reseed HEK Sunday

A20

- Split 1/6
- Keeping going for NSG/BALBc injection
 - Issue with procedure room in AMB, waiting for that to be resolved
- Also plan to incorporate WILDseq

Friday 09-02-2024

Cell Culture

A20

- Split 1/6
- Keeping going for NSG/BALBc injection
 - Issue with procedure room in AMB, waiting for that to be resolved
- Also plan to incorporate WILDseq

Monday 12-02-2024

Cell Culture

Made DMEM-V1

- DMEM for virus production
- Does not have Pen/Strep

Solution	ID code	Volume	% Total volume
DMEM	—	500 mL	78%
FBS	—	128 mL	20%
Glutamax	—	6.5 mL	1%

Thawed HEK

A20

- Split 1/6
- Keeping going for NSG/BALBc injection
 - Planning to inject with Chris tomorrow
- Also plan to incorporate WILDseq once virus is made

Processing scRNAseq

Tuesday 13-02-2024

Cell Culture

HEK

- Morphology looked weird
- 20% FBS is probably too high
- Threw away will start next week

Processing scRNAseq

Wednesday 14-02-2024

Cell Culture

A20

- Split 1/6
- Keeping going for NSG/BALBc injection

- Planning to inject with Chris tomorrow
- Also plan to incorporate WILDseq once virus is made

Processing scRNAseq

Friday 16-02-2024

A20 Xenograft EXP 1

Cell Prep

1. Thawed 2.5mL of Matrigel on ice ~3hours before
2. Transferred 12×10^6 cells to a 15mL eppendorf
3. Pelleted CS
4. Resuspended in 2.5mL of PBS
5. Transferred 400 μ L CS to 6 different 1mL eppendorfs
6. Added 400 μ L of Matrigel, mixed gently and placed back on ice
7. Brought materials over to the AMB for injection

Injection

- Chris Injected
- Study Plan: SP140164

Mouse ID	Earmark	Genotype	Injection Location
TUAD36.2h	NM	NSG	IP
TUAD36.2i	1R	NSG	IP
TUAD36.2k	2R	NSG	IP
TUAD36.2a	NM	NSG	SC
TUAD36.2b	1L	NSG	SC
TUAD36.2c	1R	NSG	SC
TUAP3.1e	1L	BALB/c	IP
TUAP3.1a	NM	BALB/c	IP
TUAP4.1a	2L	BALB/c	IP
TUAP3.1b	1L	BALB/c	SC
TUAP4.1b	2R	BALB/c	SC
TUAP3.1c	1R	BALB/c	SC

- Each mouse received $\sim 1 \times 10^6$ cells
- Mice will be monitored over the coming weeks for tumour development

Monday 19-02-2024

Cell Culture

A20

- Split 1/6
- Used AR-5

Wednesday 21-02-2024

Cell Culture

A20

- Split 1/6
- Used AR-5

HEK

- Seeded New HEK
 - HEK stock are in CM Box 1 -80
 - Used DMEM-V1
1. Thawed vial
 2. Added 1mL DMEM to vial
 3. Transferred to 15mL falcon tube
 4. Slowly added 5mL DMEM
 5. Spun down at 650rpm for 4min
 6. Removed supernant and resuspended vial flicking
 7. Added 1mL DMEM and pipetted multiple times to create single cell suspension
 8. Added to T25 flask
 9. Added 14mL of DMEM
 10. Placed in incubator

Friday 23-02-2024

Cell Culture

A20

- Split 1/6
- Used AR-5

HEK

- Split 1/6
- Used DMEM-V1

Monday 26-02-2024

Cell Culture

A20

- Split into T25
- Froze down 4 vials
- 4×10^6 cells per vial
- Used AR-5

HEK

- Froze down 7 vials
- 6×10^6 cells per vial

WILDseq Virus Production Day 1

- Seeded 2 10cm dishes of HEK cells
 - Coated with Poly-D-Lysine (covered plate, removed liquid, let sit for 10 min, washed with PBS)
 - 4.5×10^6 cells seeded per dish (seeded at 13:00)

Wednesday 06-03-2024

- Collected SC tumours
- HEK infection
 - binned A20/HEK

Wednesday 13-03-2024

- Made media
- Seeded in N2-BC4
- Froze down A20
- Collected 3 IP NSG tumours

Thursday 14-03-2024

- Changed media (N2-BC4)

Friday 15-03-2024

Cell Culture

N2-BC4 RTX CDC Assay - version 1

Monday 18-03-2024

Cell Culture - N2 -C4

- Split: seeded 5×10^6 cells

N2-BC4 RTX CDC Assay - version 2

Overview: Trying to optimise RTX CDC assay - Using 0% serum, since there are no complement factors in the media the cell live/dead reading should not change - Next step: add varying amounts of human serum

Friday 22-03-2024

Cell Culture

N2-BC4

- Cells look healthy
- Feeders in flask are also healthy
- Split 5×10^6 back into T175 with 30mL of AR-6

EC50 RTX N2-BC4 22324 - Seeding

- Seeded 96-well plate with N2-BC4 and treated with RTX concentration range with or without 10% Human Serum (HS)

- Plate seeding protocol:
 1. Diluted cell suspension to seed 20000 cells/well in 50 μ L amounts

Well Number	Cells total	Volume total	CS cells/mL	Flask cell count	Flask Volume	Media Volume
60 wells	1.2x10 ⁶ cells	3 mL	4x10 ⁵	3.06x10 ⁶	400 μ L	2.6 mL

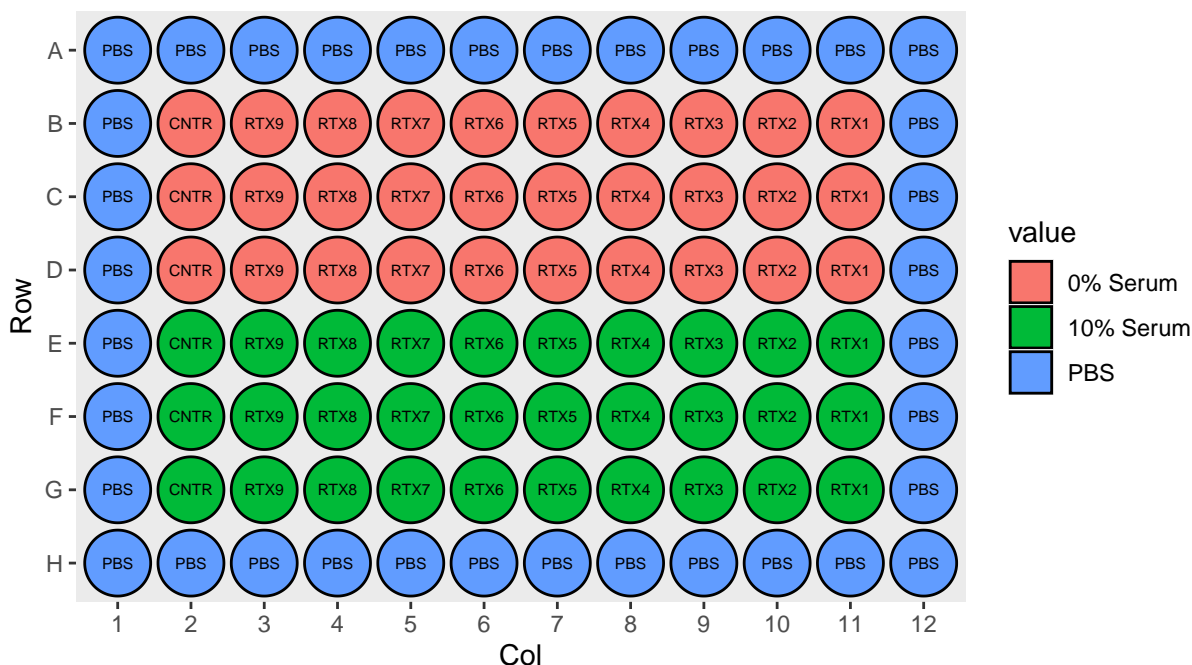
2. Made RTX dilutions and added to respective wells in 50 μ L
 - [RTX stock] = 10.3 mg/mL - Drug volumes are added in triplicate - Drug volumes are being added constitute 1/4 of well volume: [RTX working] needs to be 4x [RTX well]
 - 6 wells per condition, 50 μ L per well ~ minimum of 300 μ L per condition needed (recommend 500 μ L)

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 1	100 μ g/mL	1 mL	50 μ L stock	400 μ g/mL
RTX 2	50 μ g/mL	500 mL	500 μ L RTX 1	200 μ g/mL
RTX 3	25 μ g/mL	500 mL	500 μ L RTX 2	100 μ g/mL
RTX 4	12.5 μ g/mL	500 mL	500 μ L RTX 3	50 μ g/mL
RTX 5	6.25 μ g/mL	500 mL	500 μ L RTX 4	25 μ g/mL
RTX 6	3.125 μ g/mL	500 mL	500 μ L RTX 5	12.5 μ g/mL
RTX 7	1.56 μ g/mL	500 mL	500 μ L RTX 6	6.25 μ g/mL
RTX 8	.78 μ g/mL	500 mL	500 μ L RTX 7	3.125 μ g/mL
RTX 9	.39 μ g/mL	500 mL	500 μ L RTX 8	1.56 μ g/mL
CNTR	0 μ g/mL	500 mL	-	0 μ g/mL

3. Added 10% serum or media control
 - This provides complement factors to bind BL-bound RTX and initiate CDC
 - Serum/media amounts added at 100 μ L/well
 - Serum volume is added in 1:4 ratio (20 μ L serum in 200 μ L final well volume)
 - Serum stock mix is 1.2mL HS : 2.4 mL media / plate
4. Plate is incubated for 72 hrs at 37C

96 Well Plate Map

EC50_RTX_N2-BC4_22324



Monday 25-03-2024

EC50 RTX N2-BC4 22324 - Collection

- Collected plate seeded on 22-03-2025
- EC Plate collection protocol:
 - Added 40 μ L Cell Titre Blue (CTB) to each conditioned well
 - 20 μ L CTB/100 μ L of conditioned well recommended by manufacturer
 - Incubated for 1hr at 37C
 - Read on plate reader according to Cell Titre Blue Protocol
- Results:

EC50 RTX N2-BC4 25324 - Seeding (DNW)

- Seeded an EC50 experiment comparing the effects of RTX on N2-BC4 with or without 10% serum
- Decreased overall well volume to reduce CTB being used
- Used RTX provided by Jamie
- Plate seeding protocol:
 - Diluted cell suspension to seed 20000 cells/well in 25 μ L amounts

Well Number	Cells total	Volume total	CS cells/mL	Flask cell count	Flask Volume	Media Volume
60 wells	1.2x10 ⁶ cells	1.5 mL	8x10 ⁵	2.92x10 ⁶	410 μ L	1.1 mL

- Made RTX dilutions and added to respective wells in 50 μ L
 - [RTX stock] = 10.3 mg/mL - Drug volumes are added in triplicate - Drug volumes are being added constitute 1/4 of well volume: [RTX working] needs to be 4x [RTX well]

- 6 wells per condition, 25 μ L per well ~ minimum of 150 μ L per condition needed (recommend 200 μ L)

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 1	100 μ g/mL	400 μ L	15.5 μ L stock	400 μ g/mL
RTX 2	50 μ g/mL	200 mL	200 μ L RTX 1	200 μ g/mL
RTX 3	25 μ g/mL	200 mL	200 μ L RTX 2	100 μ g/mL
RTX 4	12.5 μ g/mL	200 mL	200 μ L RTX 3	50 μ g/mL
RTX 5	6.25 μ g/mL	200 mL	200 μ L RTX 4	25 μ g/mL
RTX 6	3.125 μ g/mL	200 mL	200 μ L RTX 5	12.5 μ g/mL
RTX 7	1.56 μ g/mL	200 mL	200 μ L RTX 6	6.25 μ g/mL
RTX 8	.78 μ g/mL	200 mL	200 μ L RTX 7	3.125 μ g/mL
RTX 9	.39 μ g/mL	200 mL	200 μ L RTX 8	1.56 μ g/mL
CNTR	0 μ g/mL	500 mL	-	0 μ g/mL

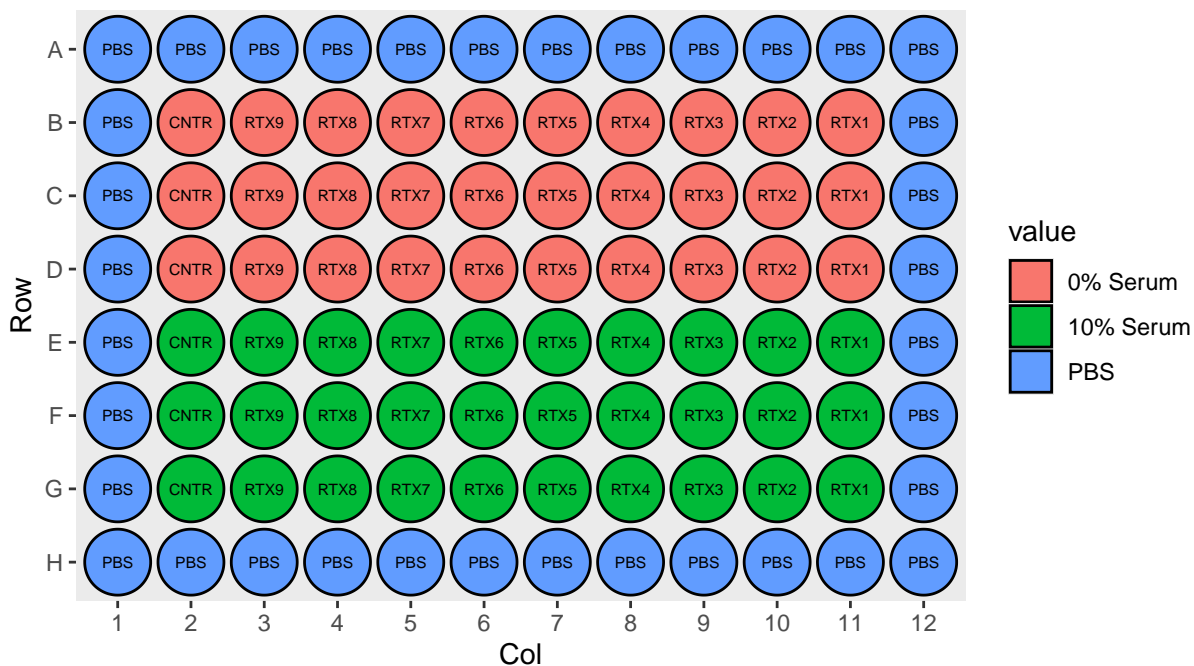
3. Added 10% serum or media control

- This provides complement factors to bind BL-bound RTX and initiate CDC
- Serum/media amounts added at 50 μ L/well
- Serum volume is added in 1:4 ratio (10 μ L serum in 100 μ L final well volume)
- Serum stock mix is 600 μ L HS : 1.2 mL media / plate

4. Plate is incubated for 72 hrs at 37C

96 Well Plate Map

EC50_RTX_N2-BC4_25324



Cell Culture

N2-BC4

- Cells look healthy
- Feeders in flask are also healthy
- Split 5x10⁶ back into T175 with 30mL of AR-6

Wednesday 27-03-2024

Thursday 28-03-2024

Friday 29-03-2024

EC50 RTX N2-BC4/RAMOS-BC5 25324 - Seeding (DNW)

- Seeded an EC50 experiment comparing the effects of RTX on N2-BC4 and RAMOS-BC5 with or without 10% serum
- Decreased overall well volume to reduce CTB being used
- Used RTX provided by Jamie
- Plate seeding protocol:
 1. Diluted cell suspension to seed 20000 cells/well in 25 μ L amounts

Cell Line	Well Number	Cells total	Volume total	CS cells/mL	Flask cell count	Flask Volume
N2-BC4	60 wells	1.2x10 ⁶ cells	1.5 mL	8x10 ⁵	2.92x10 ⁶	410 μ L
RAMOS-BC5	60 wells	1.2x10 ⁶ cells	1.5 mL	8x10 ⁵	2.92x10 ⁶	410 μ L

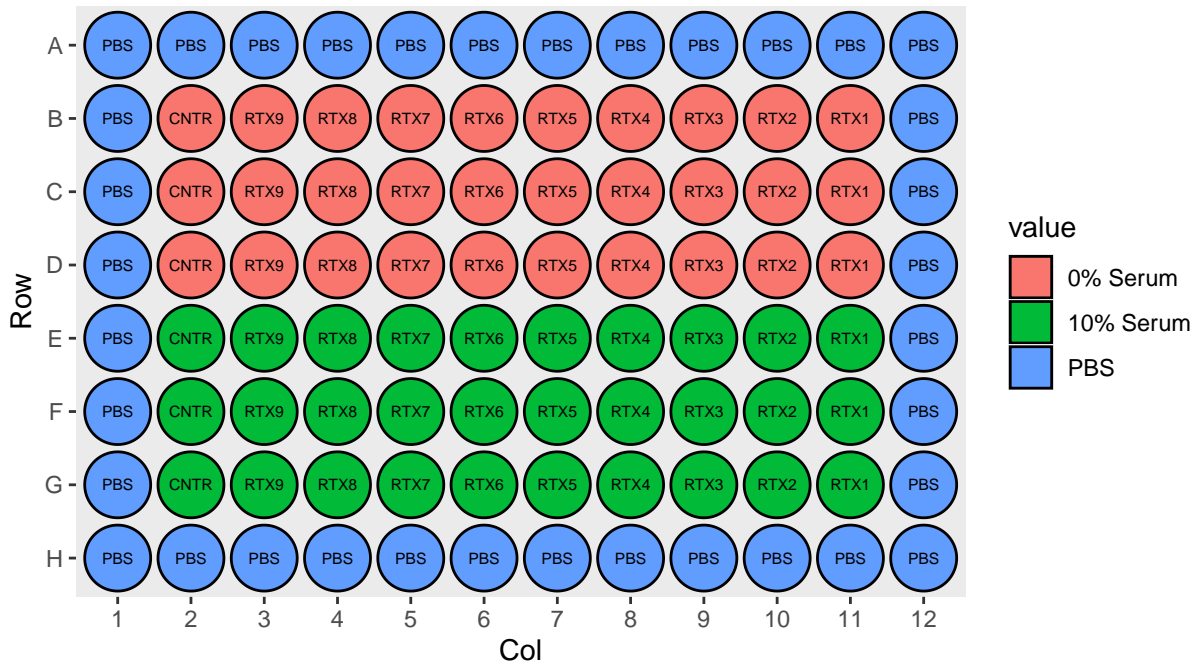
2. Made RTX dilutions and added to respective wells in 50 μ L
 - [RTX stock] = 10.3 mg/mL - Drug volumes are added in triplicate - Drug volumes are being added constitute 1/4 of well volume: [RTX working] needs to be 4x [RTX well]
 - 6 wells per condition, 25 μ L per well ~ minimum of 150 μ L per condition needed (recommend 200 μ L)

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 1	100 μ g/mL	400 μ L	15.5 μ L stock	400 μ g/mL
RTX 2	50 μ g/mL	200 mL	200 μ L RTX 1	200 μ g/mL
RTX 3	25 μ g/mL	200 mL	200 μ L RTX 2	100 μ g/mL
RTX 4	12.5 μ g/mL	200 mL	200 μ L RTX 3	50 μ g/mL
RTX 5	6.25 μ g/mL	200 mL	200 μ L RTX 4	25 μ g/mL
RTX 6	3.125 μ g/mL	200 mL	200 μ L RTX 5	12.5 μ g/mL
RTX 7	1.56 μ g/mL	200 mL	200 μ L RTX 6	6.25 μ g/mL
RTX 8	.78 μ g/mL	200 mL	200 μ L RTX 7	3.125 μ g/mL
RTX 9	.39 μ g/mL	200 mL	200 μ L RTX 8	1.56 μ g/mL
CNTR	0 μ g/mL	500 mL	-	0 μ g/mL

3. Added 10% serum or media control
 - This provides complement factors to bind BL-bound RTX and initiate CDC
 - Serum/media amounts added at 50 μ L/well
 - Serum volume is added in 1:4 ratio (10 μ L serum in 100 μ L final well volume)
 - Serum stock mix is 600 μ L HS : 1.2 mL media / plate
4. Plate is incubated for 72 hrs at 37C

96 Well Plate Map

EC50_RTX_N2-BC4_25324



Sunday 31-03-2024

Cell Culture

N2-BC4

- Healthy, split
- Changed FDC:
 1. Thawed vial
 2. Added 1mL DMEM to vial
 3. Transferred to 15mL falcon tube
 4. Slowly added 5mL DMEM
 5. Spun down at 650rpm for 4min
 6. Removed supernant and resuspended vial flicking
 7. Added 1mL DMEM and pipetted multiple times to create single cell suspension
 8. Added to T175 flask
 9. Added 30mL of DMEM
 10. Added 5×10^5 N2 cells from previous flask
 11. Placed in incubator

Ramos-BC5

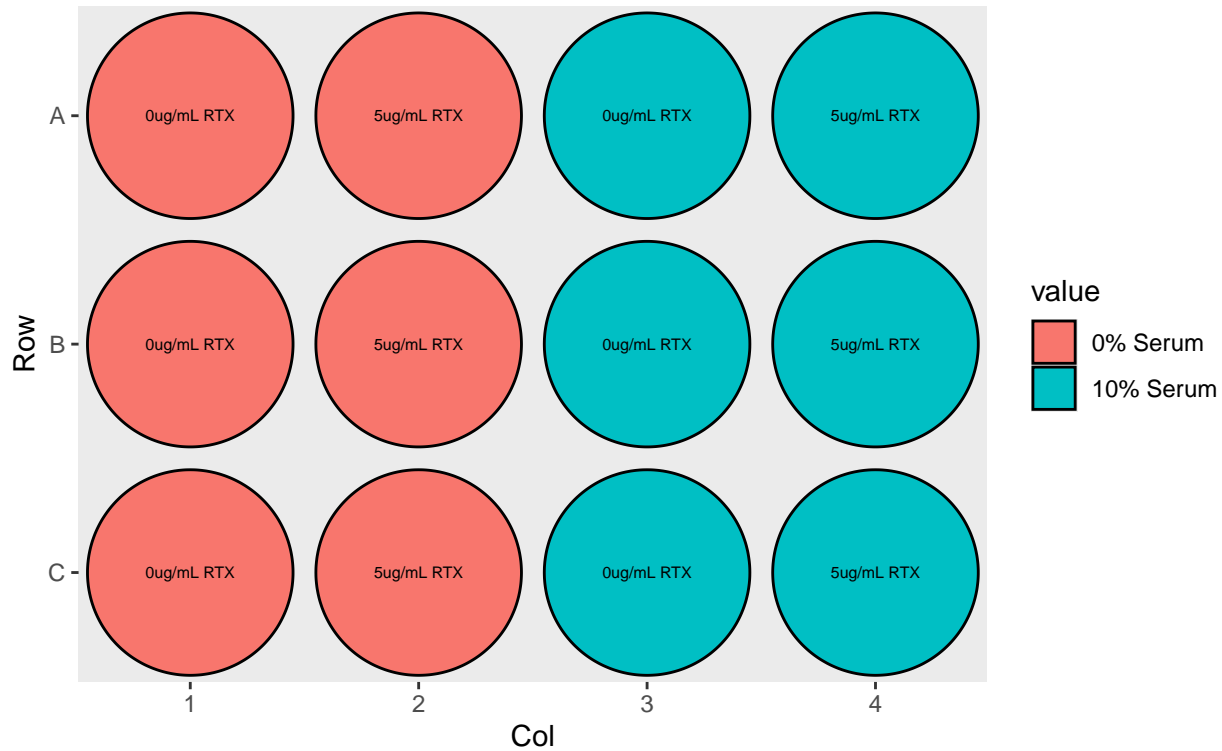
- Healthy, split
- Count: 2.18×10^6 cells/mL
- Split: 7×10^5 cells in 15 mL

Ramos CDC Testing

- Tested CDC assay adapted from [Ge et al., 2019](#)

- CDC protocol
1. Seed 250k cells 500uL volumes per well of a 12-well plate
 2. Add RTX or media in 250uL volumes per well
- [RTX] working needs to be 4x final desired well volume
3. Add Serum or media in 250uL volumes per well
- Serum amount should be 4x final % desired

CDC_24331_Ramos



EC50 RTX N2-BC4/RAMOS-BC5 24331 - Seeding (DNW)

- Seeded an EC50 experiment comparing the effects of RTX on N2-BC4 and RAMOS-BC5 with or without 10% serum
- Decreased overall well volume to reduce CTB being used
- Used RTX provided by Jamie
- Only incubated for 24hr
- Plate seeding protocol:
 1. Diluted cell suspension to seed 20000 cells/well in 25μL amounts

Cell Line	Well Number	Cells total	Volume total	CS cells/mL	Flask cell count	Flask Volume
N2-BC4	60 wells	1.2x10 ⁶ cells	1.5 mL	8x10 ⁵	2.92x10 ⁶	410μL
RAMOS-BC5	60 wells	1.2x10 ⁶ cells	1.5 mL	8x10 ⁵	2.92x10 ⁶	410μL

2. Made RTX dilutions and added to respective wells in 50μL

- [RTX stock] = 10.3 mg/mL - Drug volumes are added in triplicate - Drug volumes are being added constitute 1/4 of well volume: [RTX working] needs to be 4x [RTX well]
- 6 wells per condition, 25 μ L per well ~ minimum of 150 μ L per condition needed (recommend 200 μ L)

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 1	100 μ g/mL	400 μ L	15.5 μ L stock	400 μ g/mL
RTX 2	50 μ g/mL	200 mL	200 μ L RTX 1	200 μ g/mL
RTX 3	25 μ g/mL	200 mL	200 μ L RTX 2	100 μ g/mL
RTX 4	12.5 μ g/mL	200 mL	200 μ L RTX 3	50 μ g/mL
RTX 5	6.25 μ g/mL	200 mL	200 μ L RTX 4	25 μ g/mL
RTX 6	3.125 μ g/mL	200 mL	200 μ L RTX 5	12.5 μ g/mL
RTX 7	1.56 μ g/mL	200 mL	200 μ L RTX 6	6.25 μ g/mL
RTX 8	.78 μ g/mL	200 mL	200 μ L RTX 7	3.125 μ g/mL
RTX 9	.39 μ g/mL	200 mL	200 μ L RTX 8	1.56 μ g/mL
CNTR	0 μ g/mL	500 mL	-	0 μ g/mL

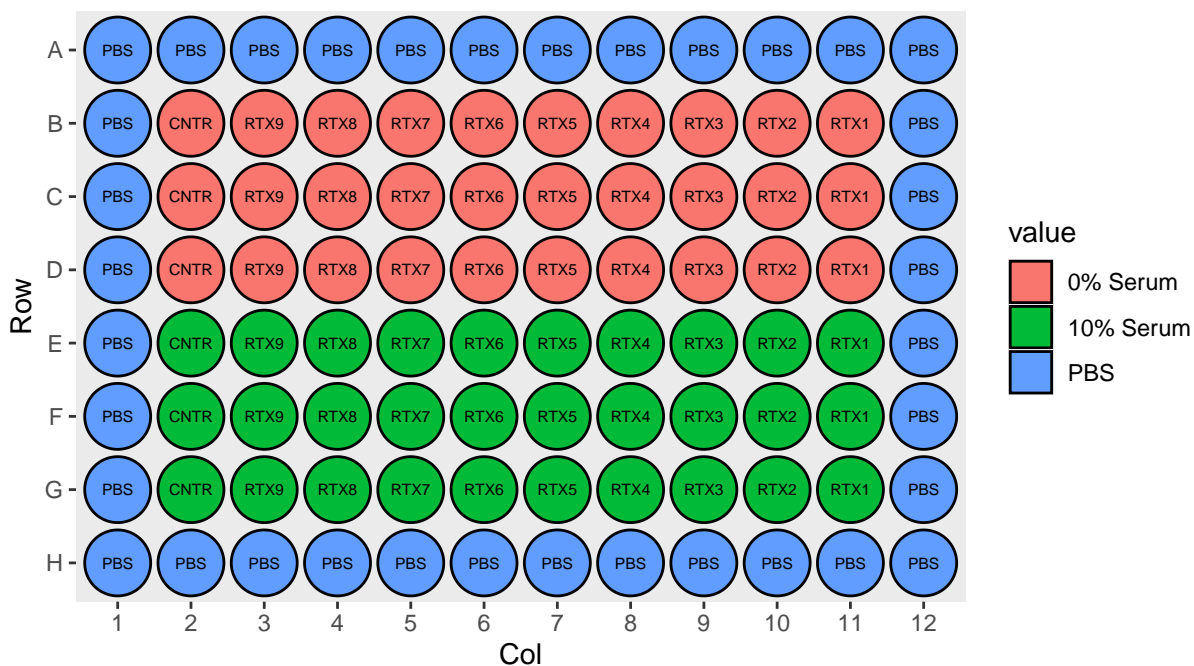
3. Added 10% serum or media control

- This provides complement factors to bind BL-bound RTX and initiate CDC
- Serum/media amounts added at 50 μ L/well
- Serum volume is added in 1:4 ratio (10 μ L serum in 100 μ L final well volume)
- Serum stock mix is 600 μ L HS : 1.2 mL media / plate

4. Plate is incubated for 72 hrs at 37C

96 Well Plate Map

EC50_RTX_N2-BC4_2431



Monday 01-04-2024

Cell Culture

N2

- Not ready to split
- Added 5mL media

Ramos

- Count: 1.6×10^6 cells/mL
- Seeded: 5×10^5 cells in 15mL

EC50 Collection: 24329/24331

- Collected plates seeded on 24-03-2024 and 31-3-2024
- EC Plate collection protocol:
 1. Added 40 μ L Cell Titre Blue (CTB) to each conditioned well
 - 20 μ L CTB/100 μ L of conditioned well recommended by manufacturer
 2. Incubated for 1hr at 37C
 3. Read on plate reader according to Cell Titre Blue Protocol
- Results:

EC50 RTX N2-BC4/RAMOS-BC5 24401 - Seeding (DNW)

- Seeded an EC50 experiment comparing the effects of RTX on N2-BC4 and RAMOS-BC5 with or without 10% serum
- Increased [RTX] to 1mg/mL (closer to Sorcha EC50)
- Used RTX provided by Jamie
- Plate seeding protocol:
 1. Diluted cell suspension to seed 20000 cells/well in 25 μ L amounts

Cell Line	Well Number	Cells total	Volume total	CS cells/mL	Flask cell count	Flask Volume
N2-BC4	60 wells	1.2×10^6 cells	1.5 mL	8×10^5	2.92×10^6	410 μ L
RAMOS-BC5	60 wells	1.2×10^6 cells	1.5 mL	8×10^5	2.92×10^6	410 μ L

2. Made RTX dilutions and added to respective wells in 50 μ L
 - [RTX stock] = 10.3 mg/mL - Drug volumes are added in triplicate - Drug volumes are being added constitute 1/4 of well volume: [RTX working] needs to be 4x [RTX well]
 - 6 wells per condition, 25 μ L per well ~ minimum of 150 μ L per condition needed (recommend 200 μ L)

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 1	1 mg/mL	400 μ L	15.5 μ L stock	4 mg/mL
RTX 2	500 μ g/mL	200 mL	200 μ L RTX 1	2 μ g/mL
RTX 3	250 μ g/mL	200 mL	200 μ L RTX 2	1 μ g/mL
RTX 4	125 μ g/mL	200 mL	200 μ L RTX 3	5 μ g/mL
RTX 5	62.5 μ g/mL	200 mL	200 μ L RTX 4	2.5 μ g/mL
RTX 6	31.25 μ g/mL	200 mL	200 μ L RTX 5	1.25 μ g/mL
RTX 7	15.6 μ g/mL	200 mL	200 μ L RTX 6	.625 μ g/mL
RTX 8	7.8 μ g/mL	200 mL	200 μ L RTX 7	.3125 μ g/mL

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 9	3.9 $\mu\text{g/mL}$	200 mL	200 μL RTX 8	.156 $\mu\text{g/mL}$
CNTR	0 $\mu\text{g/mL}$	500 mL	-	0 $\mu\text{g/mL}$

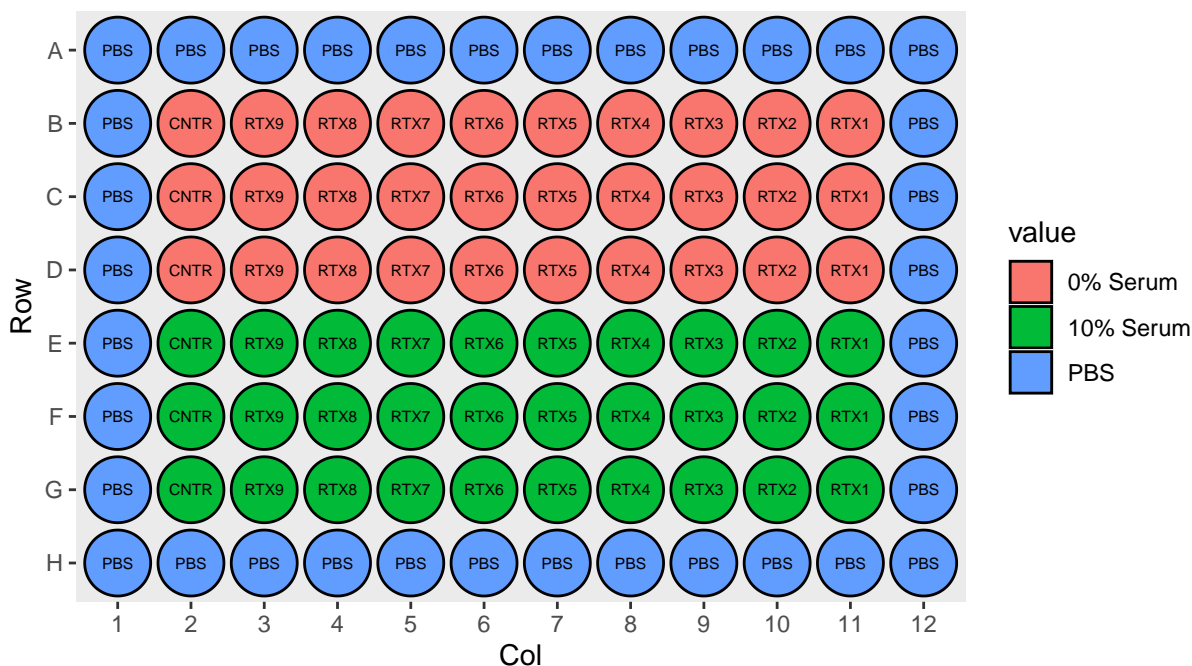
3. Added 10% serum or media control

- This provides complement factors to bind BL-bound RTX and initiate CDC
- Serum/media amounts added at 50 μL /well
- Serum volume is added in 1:4 ratio (10 μL serum in 100 μL final well volume)
- Serum stock mix is 600 μL HS : 1.2 mL media / plate

4. Plate is incubated for 72 hrs at 37C

96 Well Plate Map

EC50_RTX_N2-BC4_2431



Tuesday 02-04-2024

N2/Ramos CD20 Flow Cytometry

- Got antibody from Chris for CD20
- Cat#: 562873

Cell Stain Protocol: 1. Resuspend cells to 1×10^6 cells in 1mL 2. Distribute CS into 3 wells of a 96-well plate 3. Spin down @ 1500g for 2min 4. Flick media out 5. Make Cell Stain: - 500uL PBS + 2uL Stain -Make this while cells are spinning down 6. Resuspend w/ 100uL in the first well and then resuspend the next 2 wells in the same stain volume - Consolidate into 1 well/sample 7. incubate in the fridge for 20min 8. Spin down @ 1500g for 2 min 9. Transfer to FACS tube and run

- Results:

Thursday 04-04-2024

Cell Culture

N2

- Count: 2.1×10^6 cells/mL
- Seeded: 5×10^5 cells in 15mL

Ramos

- Count: 1.9×10^6 cells/mL
- Seeded: 5×10^5 cells in 15mL

EC50 Collection: 24401

- Collected plate seeded on 01-04-2024
- EC Plate collection protocol:
 1. Added 40 μ L Cell Titre Blue (CTB) to each conditioned well
 - 20 μ L CTB/100 μ L of conditioned well recommended by manufacturer
 2. Incubated for 1hr at 37C
 3. Read on plate reader according to Cell Titre Blue Protocol
- Results:DNW

Monday 08-04-2024

Cell Culture

N2

- Count: 1.4×10^6 cells/mL
- Seeded: 3×10^5 cells in 15mL

Ramos

- Count: 2.9×10^6 cells/mL
- Seeded: 3×10^5 cells in 15mL

Tuesday 09-04-2024

Perla Drug Randomizer

- Randomized drugs for Perla Pucci mouse experiment

Drug	Identification
Vehicle	B
Beta 30	F
Beta 10	D
Plo 30	A
Plo 10	E
TESA 4	C
TESA0,4	G

Saturday 14-04-2024

Cell Culture

N2-BC4

- Count: 6.7×10^5 cells/mL
- Seeded: 3×10^5 cells in 15mL

Ramos-BC5

- Count: 6.0×10^5 cells/mL
- Seeded: 3×10^5 cells in 15mL

EC50 RTX N2-BC4/RAMOS-BC5 24414 - Seeding (DNW)

- Seeded an EC50 experiment comparing the effects of RTX on N2-BC4 and RAMOS-BC5 with or without 10% serum
- Increased [RTX] to 1mg/mL (closer to Sorcha EC50)
- Used RTX provided by Jamie
- Looked at cell-intrinsic effects of RTX (no serum)
- Plate seeding protocol:
 1. Diluted cell suspension to seed 20000 cells/well in 25 μ L amounts

Cell Line	Well Number	Cells total	Volume total	CS cells/mL	Flask cell count	Flask Volume
N2-BC4	60 wells	1.2×10^6 cells	1.5 mL	8×10^5	2.92×10^6	410 μ L
RAMOS-BC5	60 wells	1.2×10^6 cells	1.5 mL	8×10^5	2.92×10^6	410 μ L

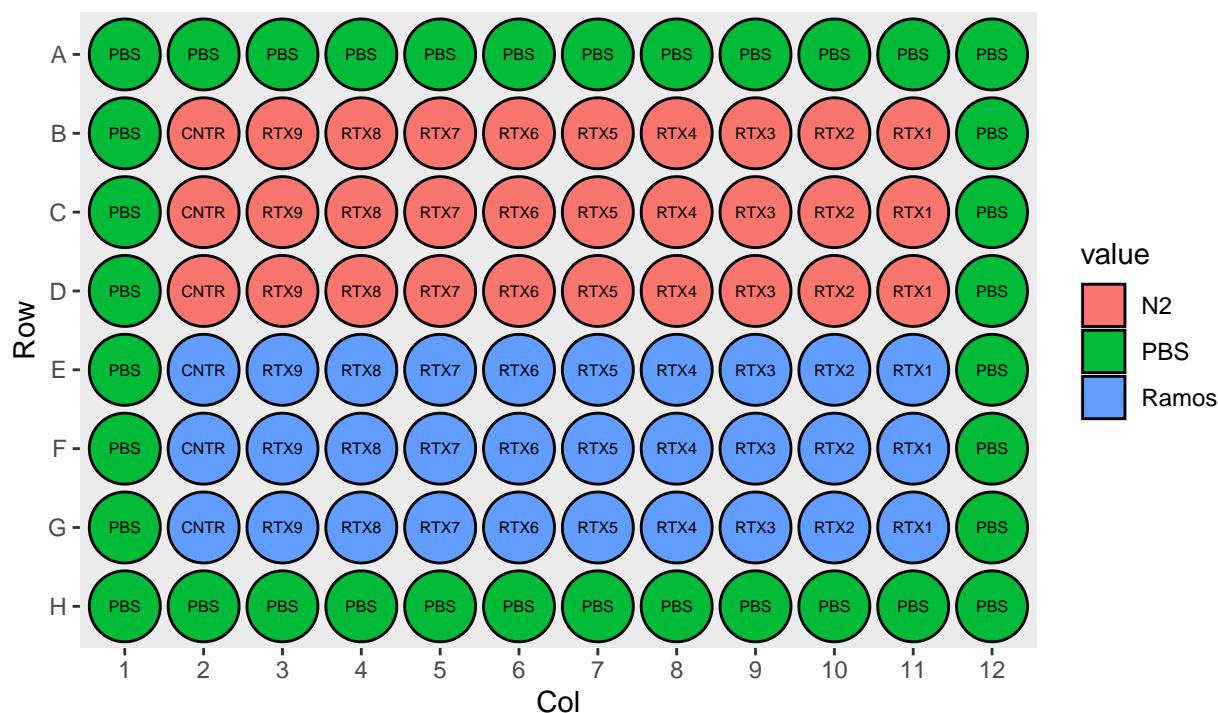
2. Made RTX dilutions and added to respective wells in 50 μ L
 - [RTX stock] = 10.3 mg/mL - Drug volumes are added in triplicate - Drug volumes are being added constitute 1/4 of well volume: [RTX working] needs to be 4x [RTX well]
 - 6 wells per condition, 25 μ L per well ~ minimum of 150 μ L per condition needed (recommend 200 μ L)

Dilution ID	[RTX Well]	Media Volume	Source	[RTX WS]
RTX 1	1 mg/mL	400 μ L	15.5 μ L stock	4 mg/mL
RTX 2	500 μ g/mL	200 mL	200 μ L RTX 1	2 μ g/mL
RTX 3	250 μ g/mL	200 mL	200 μ L RTX 2	1 μ g/mL
RTX 4	125 μ g/mL	200 mL	200 μ L RTX 3	5 μ g/mL
RTX 5	62.5 μ g/mL	200 mL	200 μ L RTX 4	2.5 μ g/mL
RTX 6	31.25 μ g/mL	200 mL	200 μ L RTX 5	1.25 μ g/mL
RTX 7	15.6 μ g/mL	200 mL	200 μ L RTX 6	.625 μ g/mL
RTX 8	7.8 μ g/mL	200 mL	200 μ L RTX 7	.3125 μ g/mL
RTX 9	3.9 μ g/mL	200 mL	200 μ L RTX 8	.156 μ g/mL
CNTR	0 μ g/mL	500 mL	-	0 μ g/mL

3. Plate is incubated for 72 hrs at 37C

96 Well Plate Map

EC50_RTX_N2-BC4_2431



Wednesday 17-04-2024

EC50 Collection: 24414

- Collected plate seeded on 14-04-2024
- EC Plate collection protocol:
 - Added 40 μ L Cell Titre Blue (CTB) to each conditioned well
 - 20 μ L CTB/100 μ L of conditioned well recommended by manufacturer
 - Incubated for 1hr at 37C
 - Read on plate reader according to Cell Titre Blue Protocol
- Results:DNW

Monday 22-04-2024

Cell Culture

N2-BC4

- Seeded: 3x10⁵ cells in 15mL

Ramos-BC5

- Seeded: 3x10⁵ cells in 15mL

Thawed NK-92

- Obtained from Chris Steele
- Cultured in Advanced RPMI

- Added 200u/mL of IL-2 (#78036.1)
 - Obtained from Emily
 - Product listed as 4.1×10^4 IU/ug
 - Stock diluted to 10ug/mL
 - Added .48 uL stock/mL of media

Wednesday 24-04-2024

Cell Culture

N2-BC4

- Seeded: 3×10^5 cells in 15mL

Ramos-BC5

- Seeded: 3×10^5 cells in 15mL

NK-92

- Looked very unhealthy
- Lots of dead cells/debris in the media
- Spun down, resuspended in 1mL of media
- Split into 4 wells of a 48 well plate with increasing amounts of IL-2

Friday 26-04-2024

Cell Culture

N2-BC4

- Seeded: 3×10^5 cells in 15mL

Ramos-BC5

- Seeded: 3×10^5 cells in 15mL

NK-92

- Cells still look unhealthy
- Tried to consolidate in single well of 24 well plate
- Spun down in eppendorf and resuspended in 1mL of media

Monday 29-04-2024

Cell Culture

N2-BC4

- Seeded: 3×10^5 cells in 15mL

Ramos-BC5

- Seeded: 3×10^5 cells in 15mL