Station A: MagMAX Viral/Pathogen Nucleic Acid Isolation (v2)

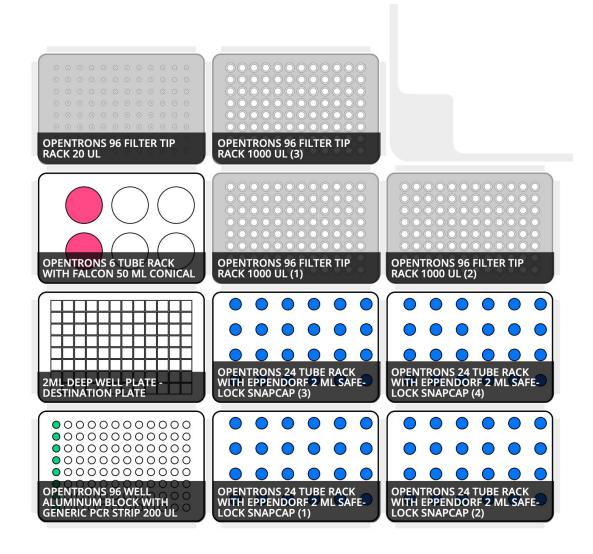
Code parameters:

- Change the sample number on line 14 (default is 8, max is 96)
- Change the sample volume (μL) on line 15 (default is 400μL)
- Tip rack tracking can be changed to from False to True on line 16 (default is False)

Pipettes:

- P1000 single-channel on the right mount
- P20 multi-channel on the left mount

Deck Layout:



Labware and module requirements:

- \leq 96 x 1.5 2mL tubes [input samples]
- 4 x 24-Position Tube Rack [holds 1.5/2mL sample tubes]
- 3 x 1000µL Filter Tip Racks
- 1 x 6-Position Tube Rack [holds 50mL tube with Binding Bead Mix]
- 2 x 50mL Falcon Tube [1 tube per 48 samples]
- 1 x 2mL Deep Well Plate [output destination plate]
- 1 x 20µL Filter Tip Racks
- 1 x 96-Well Aluminum Block [holds 1 PCR strip tube in column 1]
- 1 x 200µL PCR strip tube [holds Proteinase K]

Volume requirements:

Note ~ the below volumes account for a dead volume; the dead volume can be adjusted depending on the calibration of the pipette to the labware, but we've found it's best to have a dead volume of at least 10%

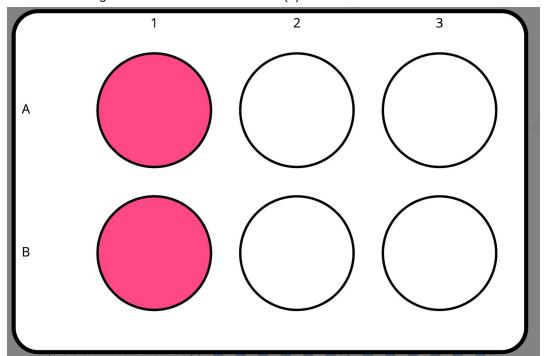
Reagent	Volume per sample	Volume for 8 samples	Volume for 48 samples	Volume for 96 samples
Binding Bead Mix	550µL	4.84mL	29mL	58.1mL
Proteinase K	10μL	90μL	530µL	1060µL

Before you begin:

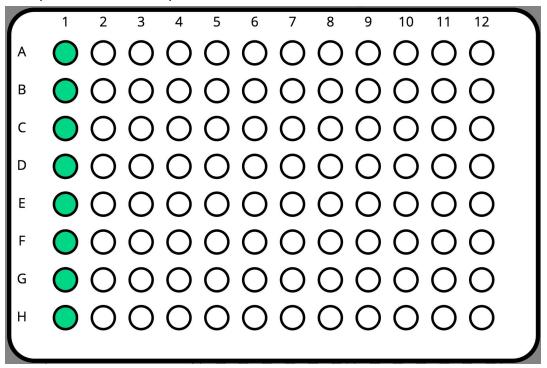
- 1. Load the samples onto the tube racks, starting with slot 2, then slot 3, slot5, and slot 6
- 2. Create the **Binding Bead Mix for slot 7**

Reagent	Volume per sample	Volume for 8 samples	Volume for 48 samples	Volume for 96 samples
Binding Solution	530µL	4.66mL	28mL	56mL
Total Nucleic Acid Magnetic Beads	20μL	176µL	1050µL	2100µL

3. Add the binding bead mix in the 50mL tube(s) to the rack in Slot 7



4. Divide the total volume of the Proteinase K mix by 8 and add it to a 200µL PCR strip tube to be place in **Slot 1** on top of a 96-well Aluminum Block in column1



The final destination will be the deep well plate in slot 4. Once the run is finished, move the deep well plate to Station B to complete the remainder of the extraction protocol.