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Protocol status: Working
 We use this protocol and it's working

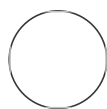
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DNA extraction v9.0 (modified BOMB)

Forked from [DNA extraction \(BOMB\)](#)

Guan Jie Phang¹, Yin-Tse Tsu-Chun Hung², Huang²

¹Kaohsiung Medical University; ²KMU



Guan Jie Phang

Kaohsiung Medical University, National Taiwan University, Bi...

ABSTRACT

DNA extraction using yttria-stabilized zirconia beads lysing and automated magnetic bead-based extraction.

MATERIALS

1. Lysis master mix 870 ml (870 µl/sample)

Chemical	Volume
TE buffer	225 µl
Lysis buffer	375 µl
10M Ammonium acetate	270 µl

2. TE buffer stocks 225 ml

Chemical	Volume	Notes
1M Tris-HCl pH8.0	2.25 ml	10mM
1M EDTA	0.225 ml	1mM
ddH2O	adjust the volume with water to 225 ml	

Note

Prepare 1M Tris-HCl and 1M EDTA first.

Chemical	Mass	Total volume
Tris-HCl	7.88 g	50 ml
EDTA	14.61	50 ml

Note

adjust the pH of EDTA with solid NaOH or 1M NaOH to 8.0. The undissolved EDTA will be dissolved entirely when the pH reaches 8.0.

3. Lysis buffer stocks 375 ml

Chemical	Volume/Mass	Notes
Guanidine thiocyanate (GTC)	177.3 g	4M
1M Tris HCl pH8.0	18.75 ml	50mM
Sodium Lauryl Sulfate	3.75 g	0.5 g
1M EDTA	7.5 ml	20mM
ddH2O	adjust the pH with HCl to 7.6–8.0 and the volume with water to 375 ml	

4. 10M Ammonium acetate 270 ml

Chemical	Volume/Mass
Ammonium acetate	208.116 g
ddH2O	adjust the volume with water to 270 ml

Note

Ammonium acetate is hygroscopic. Do not add more than half of the water needed to dissolve it.

Sample Collection

3m

- 1 Add  200 μL of **0.5 mm beads** to a 2mL screw tube.


30s



- 2 Add  200 μL of **1 mm beads** to a 2mL screw tube.

30s



- 3 Add  870 μL Lysis master mix to 2mL screw tube. The final look:

30s



Note

In 11F, 4°C fridge

Lysis master mix: **225 μ L** of TE buffer + **375 μ L** of lysis buffer + **270 μ L** of 10M ammonium acetate

- 4 Collect  20-50 mg of **sample** to 2mL screw tube


1m

Note

You can collect up to 100 mg of sample if you can until you bump into the low DNA quality or PCR success rate; by then it means too many inhibitors in the sample and you have to lower the input.

Sample lysis

4m

- 5 Put the 2mL screw tube on vortex for sample lysis, at 3200 rpm  00:04:00

4m

Note

Remember to balance if you have odd number of samples

Centrifugation

3m

- 6 Put 2mL screw tube in centrifuge for centrifugation, at this condition:  10 x g, 25°C, 00:03:00

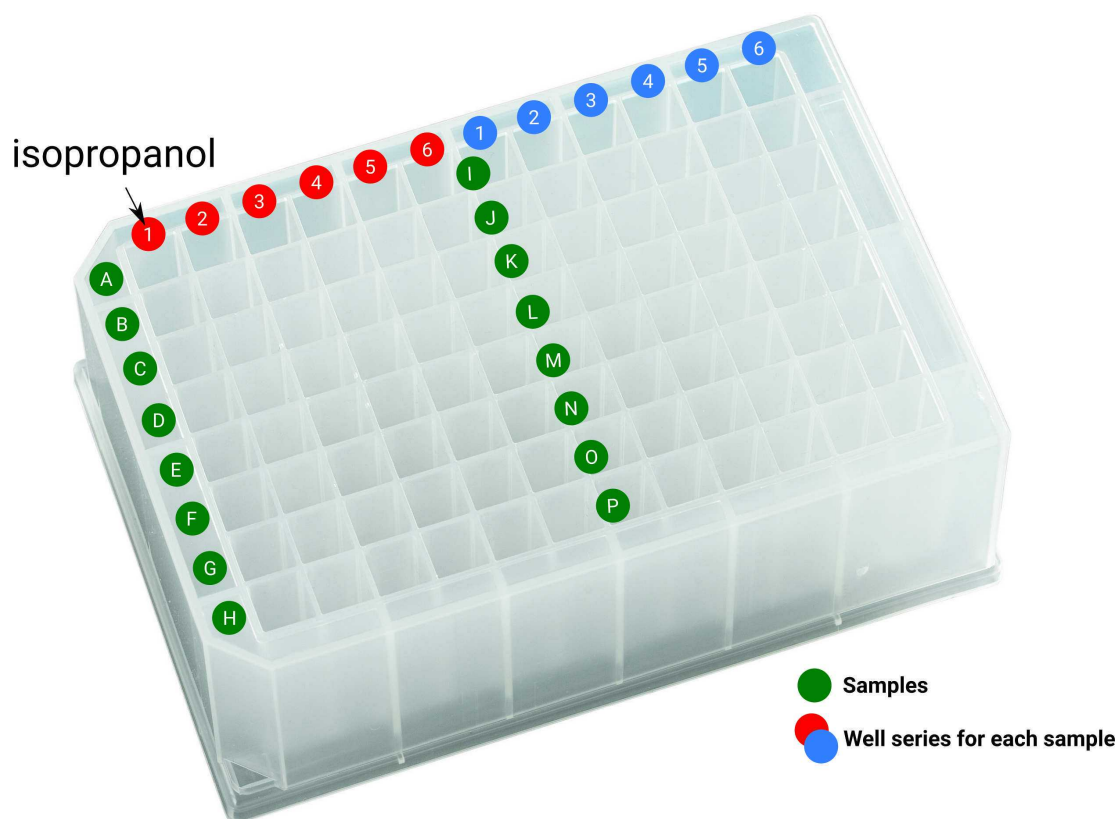
3m


DNA extraction

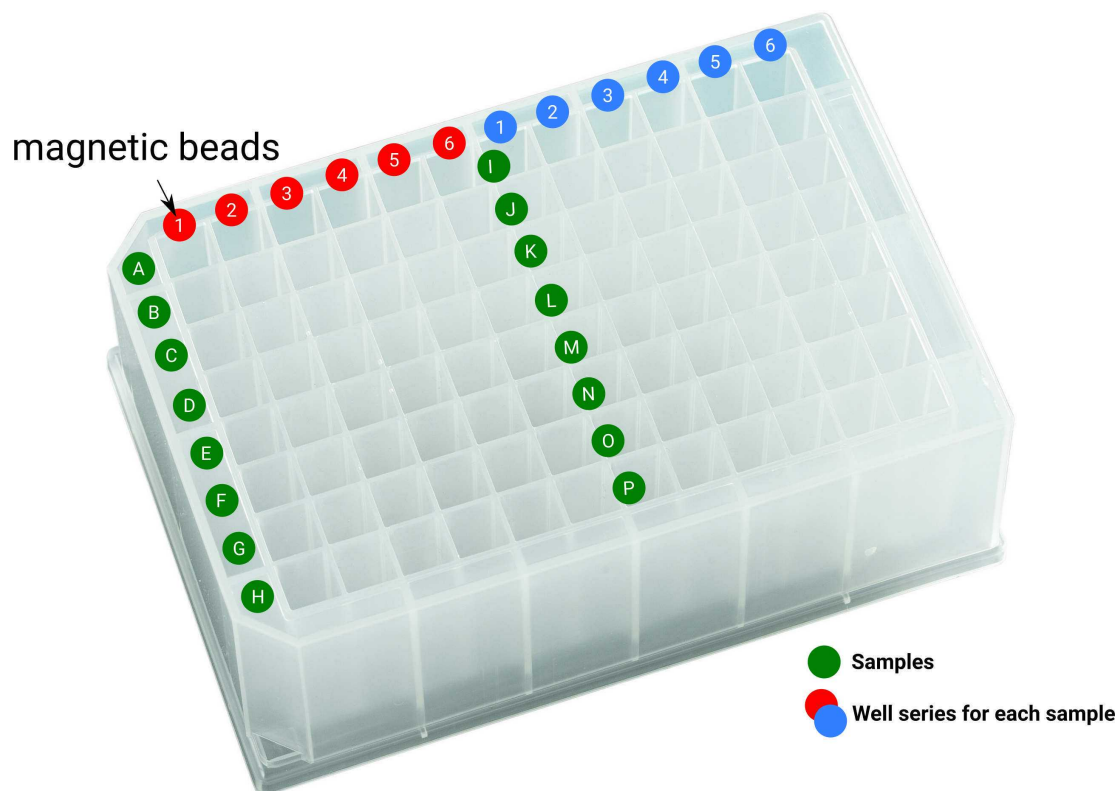
37m 30s

- 7 Add  350 μ L of **isopropanol** to the 1st well of 96 well plate

30s

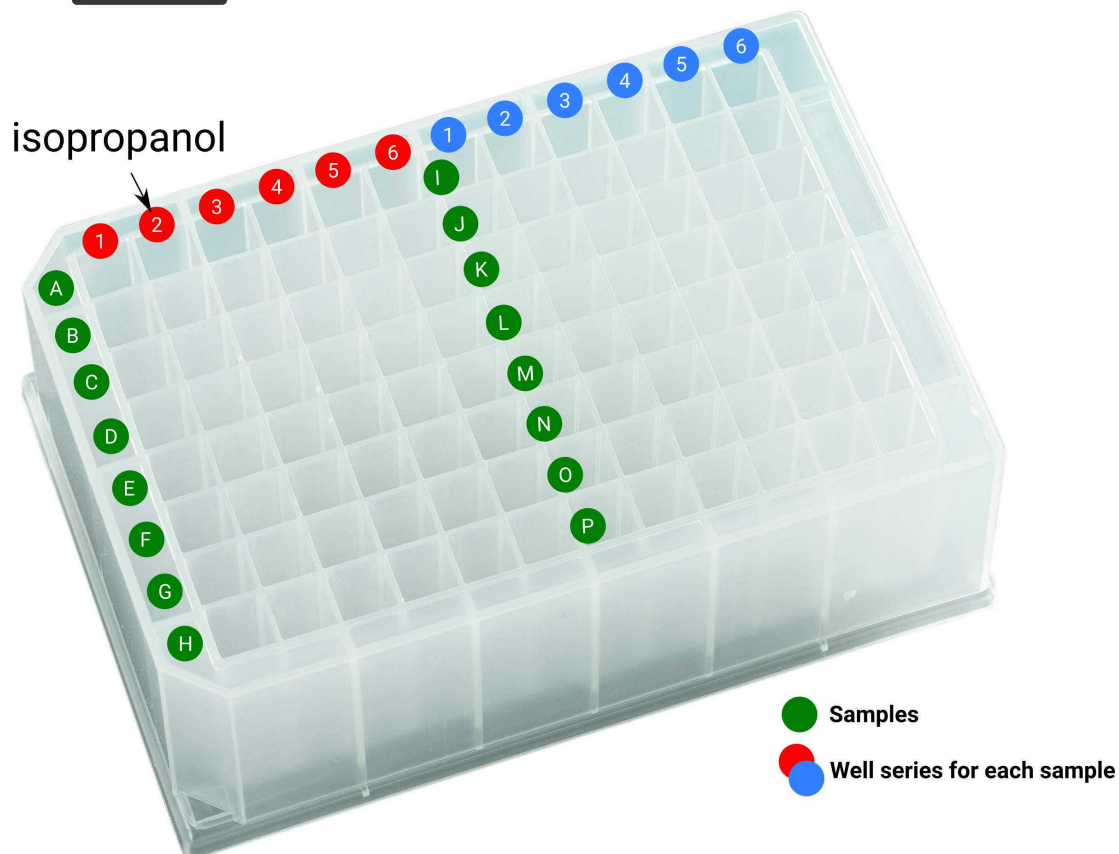


- 8 Add  50 μ L of **magnetic beads (10mg/ml)** to the 1st well of 96 deep well plate



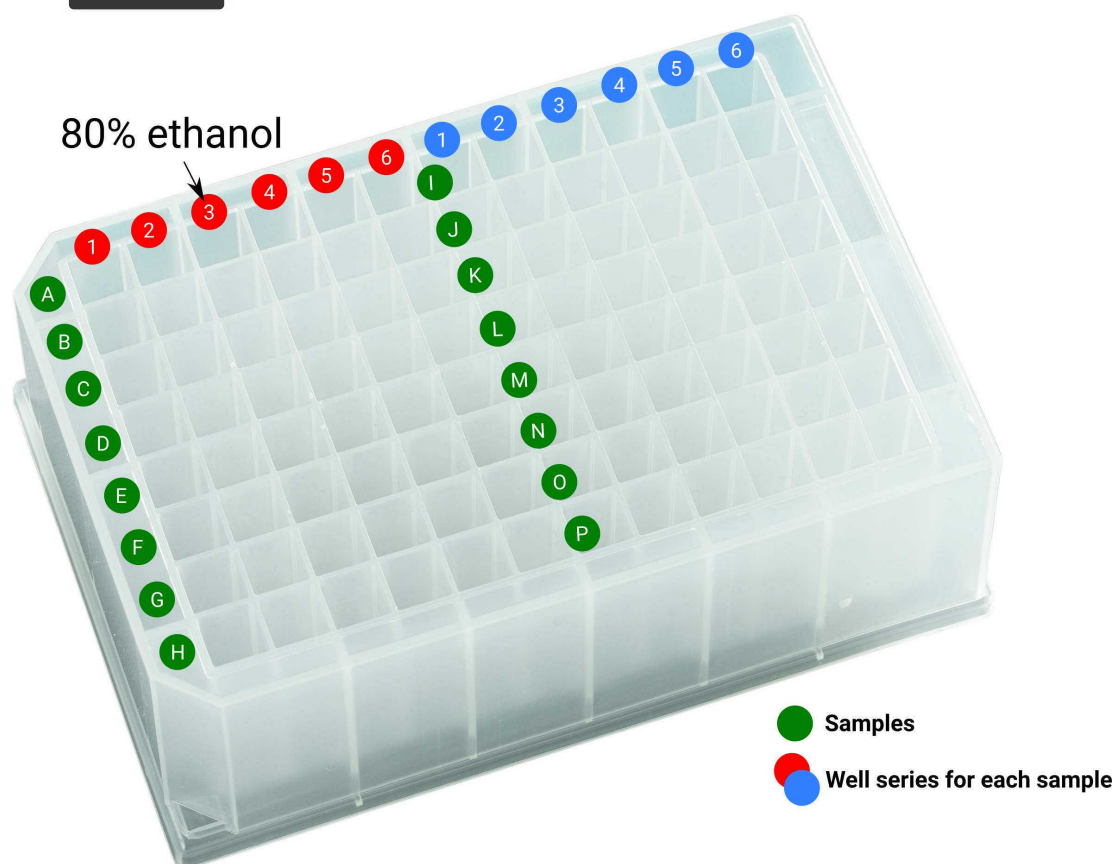
9 Add  400 μL of **isopropanol** to the 2nd well of 96 deep well plate

30s



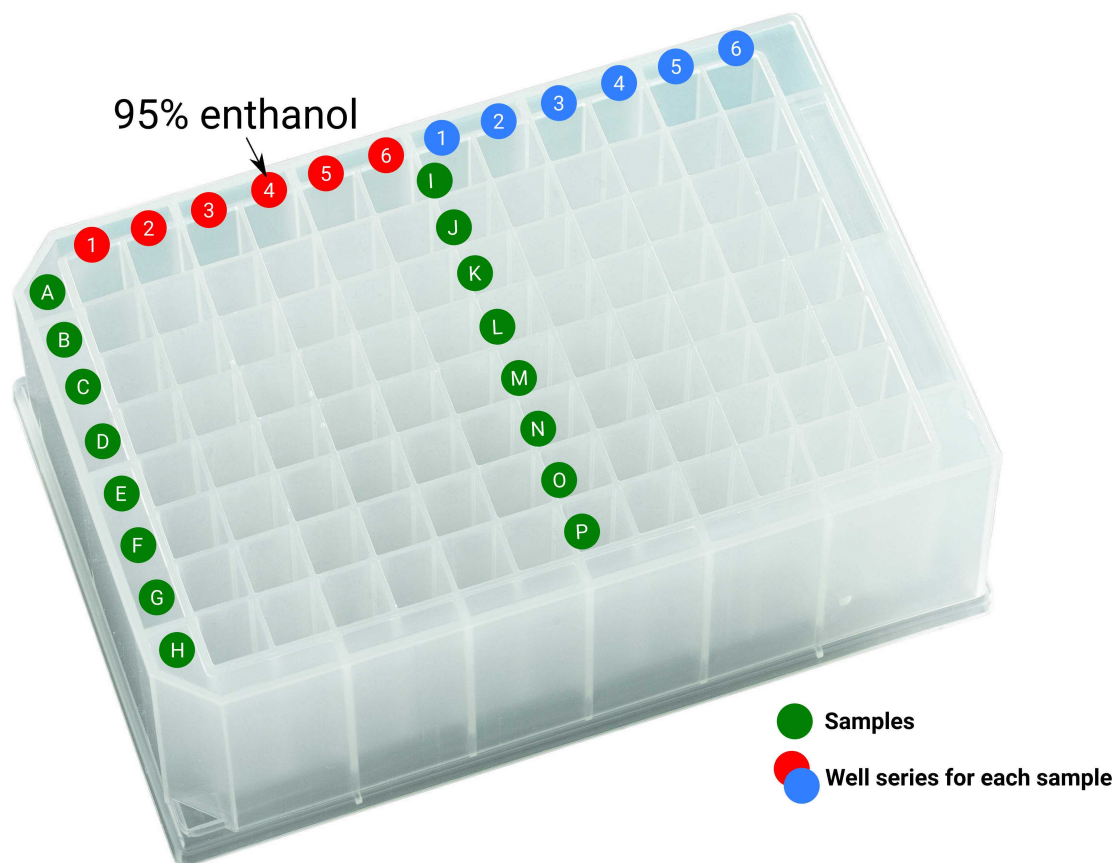
10 Add  300 μL of **80% ethanol** to the 3rd well of 96 deep well plate


30s

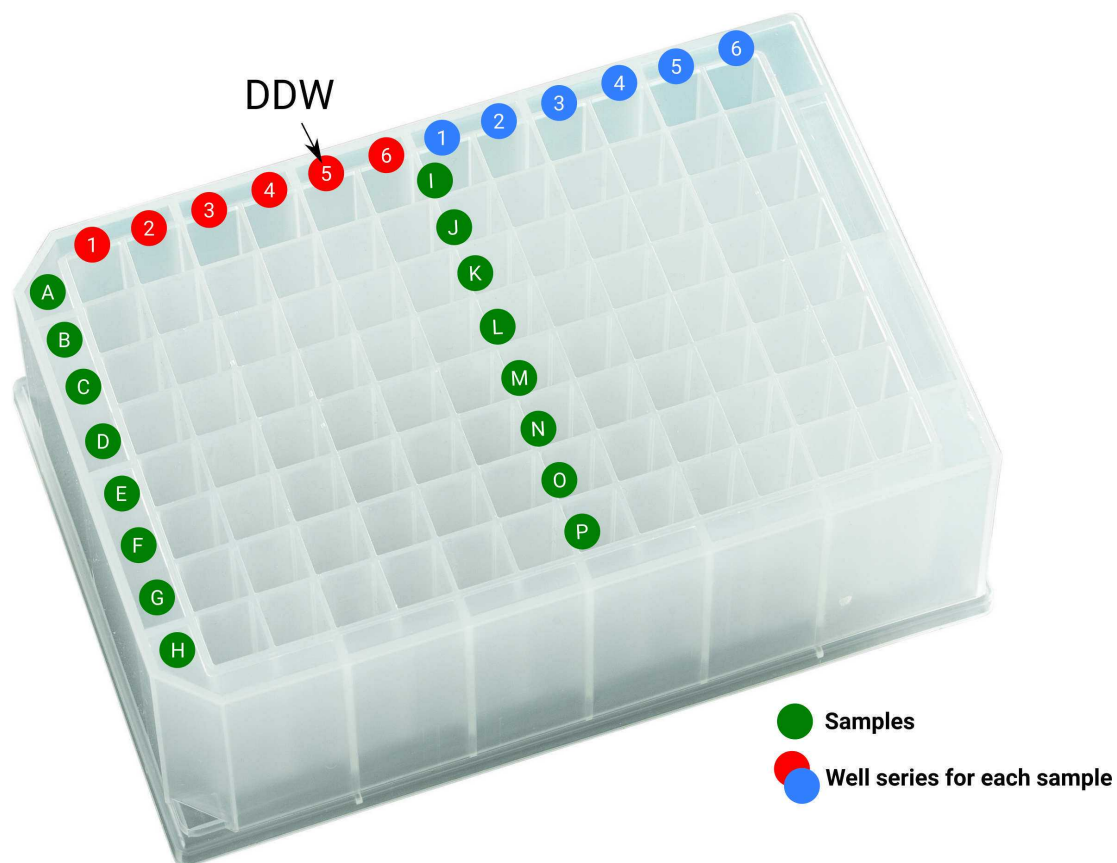


11 Add  300 μL of **95% ethanol** to the 4th well of 96 deep well plate

30s

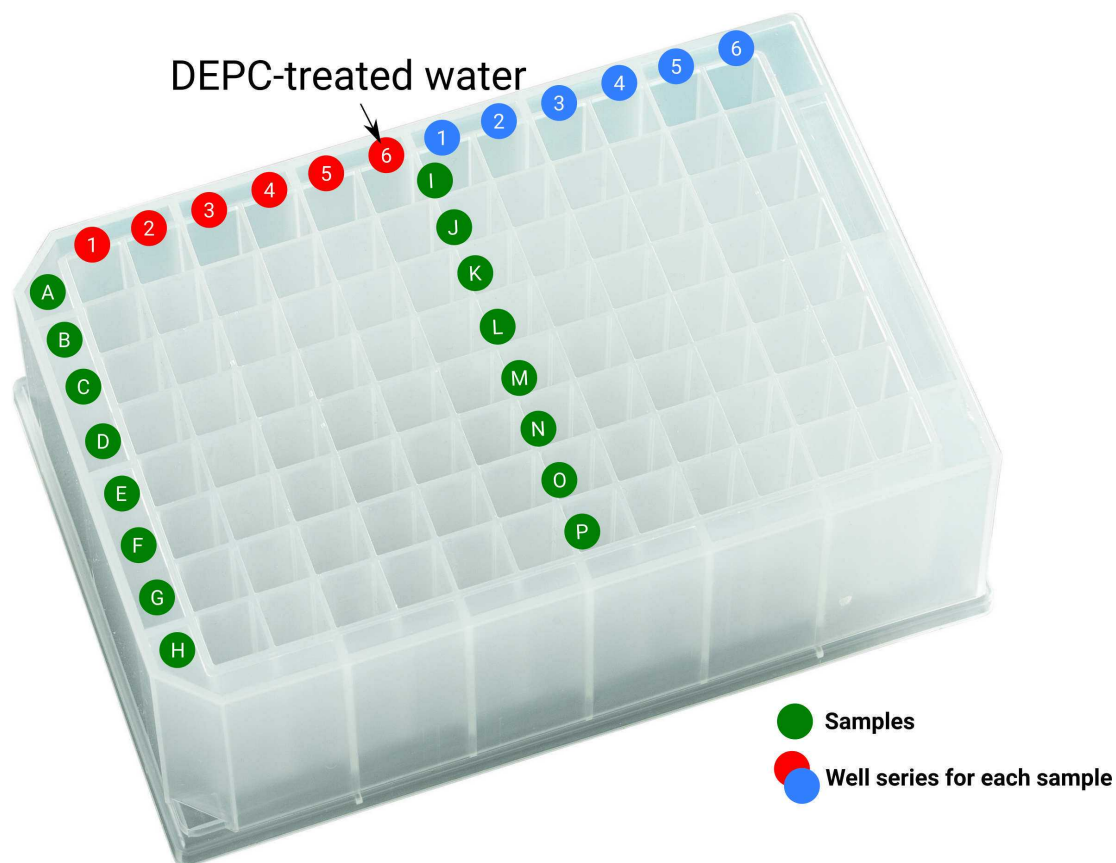



12 Add  300 μL of **DDW** to the 5th well of 96 deep well plate

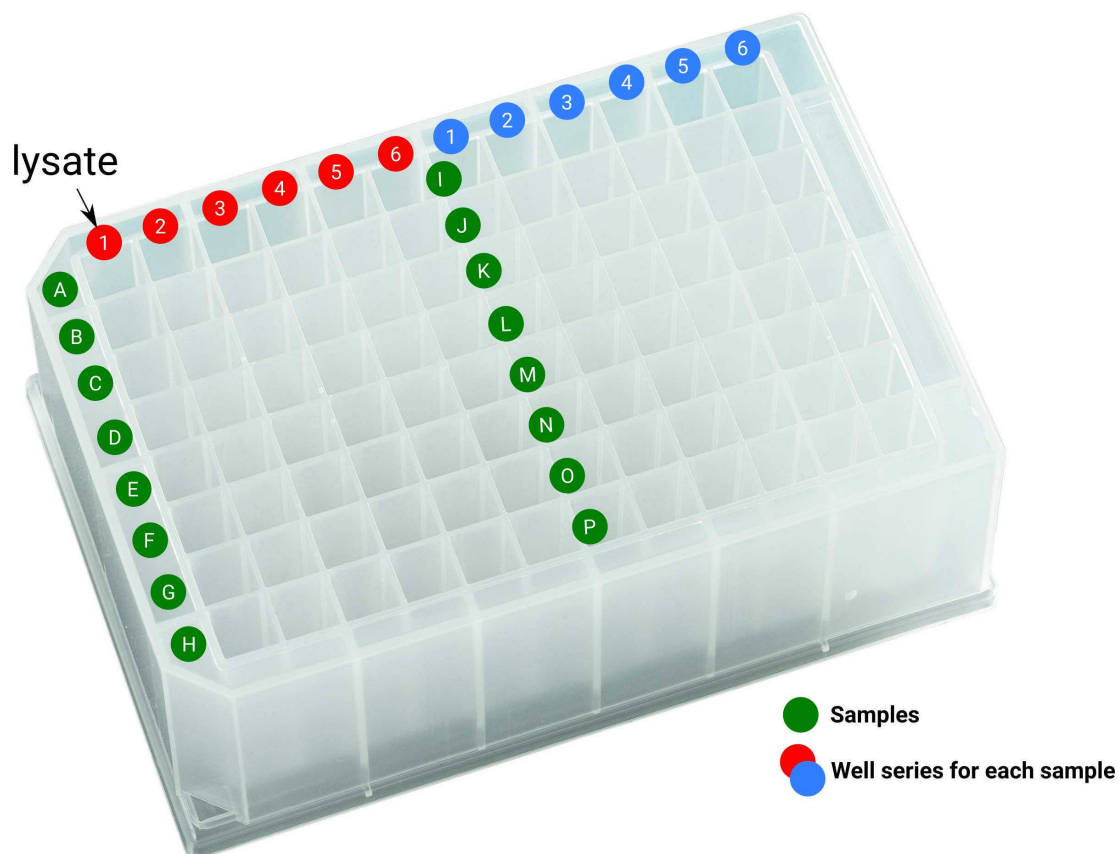


13 Add  100 μL of **DEPC-treated water** to the 6th well of 96 deep well plate

30s



- 14 Add  300-500 μL of the **sample (lysate)** from the 1.5mL centrifuged tube to the 1st well of 96 deep well plate 30s



Note

Pipetting **as many lysate as you can**, as long as it's free of any cell debris (no solids in your tip)

- 15 Put the prepared 96-deep well plate in the automated DNA extraction machine (ZiXpress 32) and set up the settings as below. 34m

Program settings

37m 30s

- 16 The automated extraction program settings for ZiXpress 32.

Well no.	Standby(mins)	Mix(mins)	Volume(μ l)	Mix speed	Mag(s)	Temp.($^{\circ}$ C)
1	0	10	1000	3	120	0

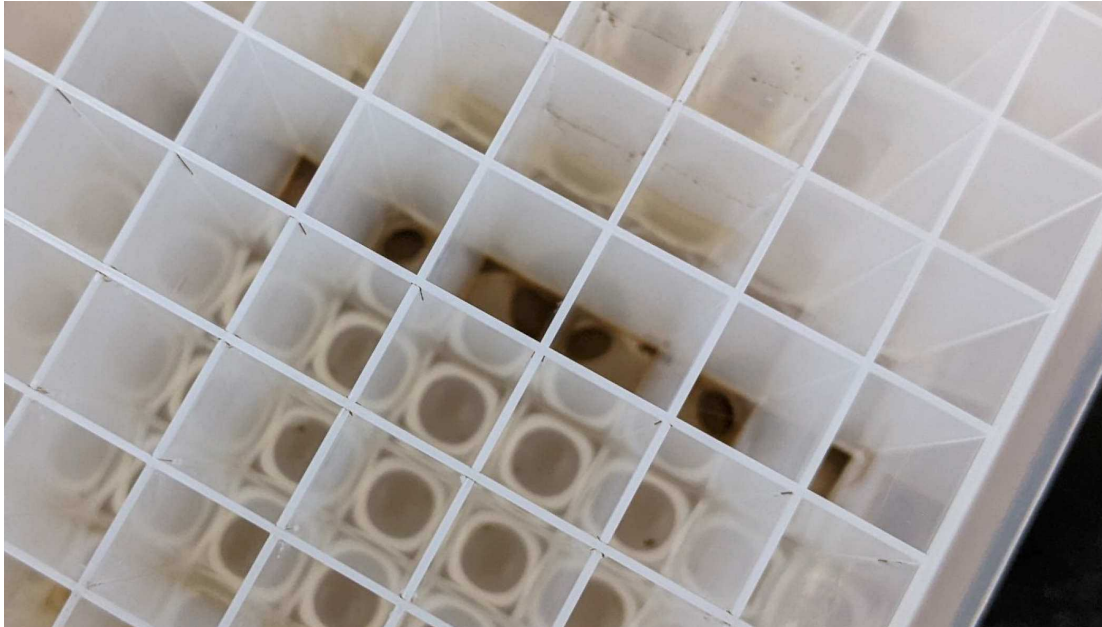
Well no.	Standby(mins)	Mix(mins)	Volume(μ l)	Mix speed	Mag(s)	Temp.(°C)
2	0	2	400	3	60	0
3	0	2	300	3	60	0
4	15	0	0	0	0	0
4	0	2	300	3	60	0
5	0	1	300	3	0	0
6	0	5	100	3	120	55


gDNA collection

37m 30s

- 17 After the extraction is done, put on the 96 magnetic plate to pellet the magnetic bead residues.





- 18 Collect  100 μL of the **eluted sample** (avoid getting magnetic bead) as the DNA template for downstream experiments



