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# PBMCs Processing for Single Cell Multiome ATAC + Gene Expression Sequencing

Weiyan Jia<sup>1</sup>, Etiena Basner-Tschakarjan<sup>1</sup>, William Beggs<sup>1</sup>, Derek Kelly<sup>1</sup>, Ning Xie<sup>1</sup>, Yuanqing Feng<sup>1</sup>, Sarah Tishkoff<sup>1</sup>

<sup>1</sup>University of Pennsylvania



Weiyan Jia University of Pennsylvania

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#### **ABSTRACT**

This protocol was designed for the workflow of the Multiome assay on 16 PBMC samples using the 10X Next GEM Single Cell Multiome ATAC + Gene Expression Kit. We adapted Jimmy Ye Lab's pooling and demultiplexing strategy, overloading cells in each well. For the demultiplexing step using this protocol, you may need genotyping information of your samples.

#### BEFORE START INSTRUCTIONS

1. This protocol is designed for sample pooling and overloading strategy and needs sample genotyping information.

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2.Double-check if your samples have neutrophil contamination; if so, you should consider removing them to get good quality of your ATAC libraries.



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

working

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snRNA

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# 1. Thawing PBMCs( ~ 2 hrs, Benzonase treatment)

| 1 | 1 Domovo orvoviolo fra | sm liquid nitrogon otorogo   | and place them on dry ice. |
|---|------------------------|------------------------------|----------------------------|
|   | remove divoviais in    | iii ilaala ilitroaen storaae | and blace them on dry ice. |

- Warm The medium to **37°C** in a water bath and prepare the washing Medium.
- Thaw frozen vials in the water bath at **37°C** for **1-2** min.
- 4 Pour the thawed cells gently into a **15 mL conical tube** containing 10 mL pre-warmed **Complete medium**.

| 5  | Rinse the         | cryovial with <b>1 mL</b> pre-warmed <b>Complete medium</b> and add the rinse to the 15 mL tube.                                     |
|----|-------------------|--|
| 6  | Centrifug         | e at <b>300g</b> for <b>5 min</b> at room temperature and aspirate the supernatant.  |
| 7  | Resuspen<br>tube. | nd cells with <b>1 mL</b> pre-warmed <b>Washing medium</b> and add 9 mL more <b>Washing medium</b> to each                           |
| 8  | Incubate 1        | for <b>10 min</b> at room temperature to ensure the free-floating DNA is depleted.   |
| 9  | Centrifug         | e at <b>300g</b> for <b>5 min</b> at room temperature and aspirate the supernatant.  |
| 10 | Prepare s         | amples for Cell counting.  |
|    | 10.1              | Resuspend thecell pellet in <b>1 mL</b> of pre-warmed Complete medium (dropped slowly along the side of the tube) by gently tapping. |
|    | 10.2              | Add <b>4 mL</b> of pre-warmed Complete medium.   |
|    |                   |  |

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Resuspend cell pellet in **1 mL** of pre-warmed Complete medium by gently tapping. Add another **9 mL** of pre-warmed Complete medium. Briefly vortex (optional). Centrifuge at **350g** for **5 min** at **room temperature**.

#### Note

Using Complete medium from now on is to wash away benzonase.

- Resuspend cells in Complete medium and adjust to 1 x 10<sup>6</sup> cells per mL. Gently tap tubes.
- Seed cells into a 24-well plate (low attachment plate) at 1 x 10<sup>6</sup> cells per well in 1 mL Complete medium, using a wide-bore 1 mL pipet tip.

Note

# Tips:

- 1. If there are more than 4 million cells per individual, seed four wells (1 million cells per well): two for the control (Ctr) and the other two for lipopolysaccharide (LPS).
- 2. Pellet, wash once with PBS, and freeze all the leftover cells at -80°C.
- 15 Transfer the cell culture plate to the incubator (37°C, 5% CO<sub>2</sub>) for 16-24 hrs, and leave the cells for recovery.

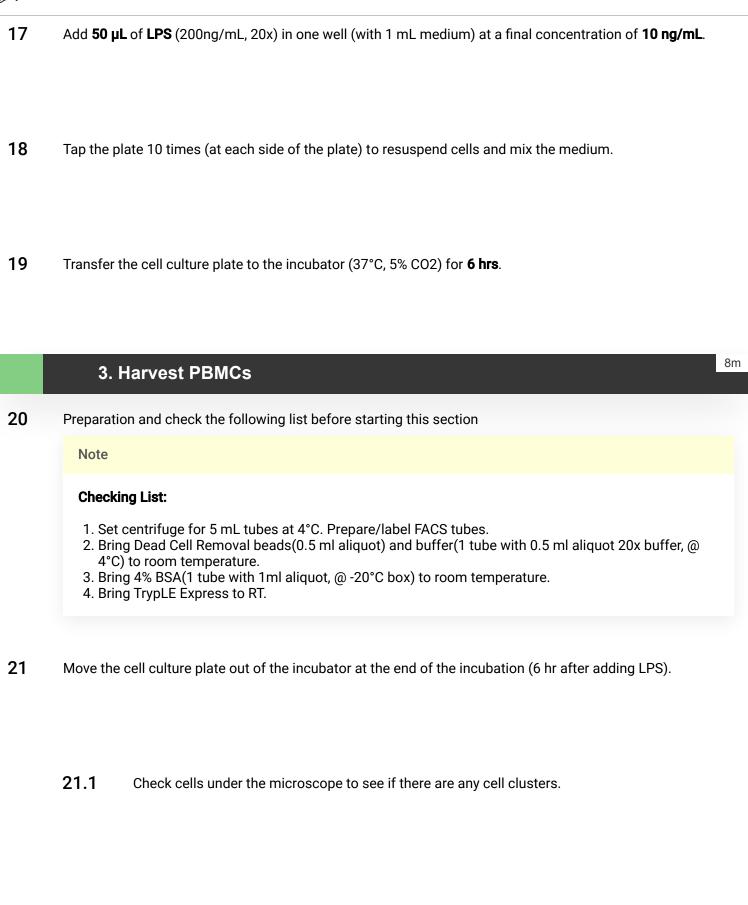
# 2. Stimulation of the PBMCs with ligands

Prepare LPS (200ng/mL, 20x) in Complete medium.

Note

## Tips:

- Prepare these 20x solutions in Complete medium and can be stored in 4°C overnight.
- To prepare 1000 μL of 200 ng/mL LPS, add 10 μL of 20 μg/mL LPS (-80°C stock) into 990 μL Complete medium.



- 21.2 Transfer cells with medium into a 5 mL FACS tube using a 1 mL wide-bore pipette. Rinse the well with 1 mL PBS and add the rinse to the FACS tube.
- 21.3 Check the cell plate under a microscope to see if any cells are left over.
- 21.4 Add 200 μL Tryple E, incubate at 37°C for 5 min, and rinse with another 1 mL PBS.
- 21.5 Pipette a few times and transfer all the cells to the FACS tubes by wide-bore pipette.

8m

- 22.1 Pour off the supernatant into the sink (usually will have 50 uL liquid leftover).
- 22.2 Invert the tube and dry the tube top with a Kim wipe.
- Wash cells with Staining Buffer (from BioLegend)

# Note

# **Examples:**

- we thawed PBMCs from 8 individuals, and each received 2 treatments (Ctrl, LPS); thus we had 16 cell samples;
- We pool the Ctr and LPS treated samples into two separated tubes and label them as P1(Ctr) and P2(LPS).
- If we do 16 individuals and we plate the samples to two groups and each group has 8 individuals and we pool samples the same as 8 individuals, but pool the other group to P3(Ctr) and P4(LPS).
- For each cell sample, we collect as many cells as possible and pool the same amount of cells from each sample.
- 27 Place extra cells at 4°C (in case).

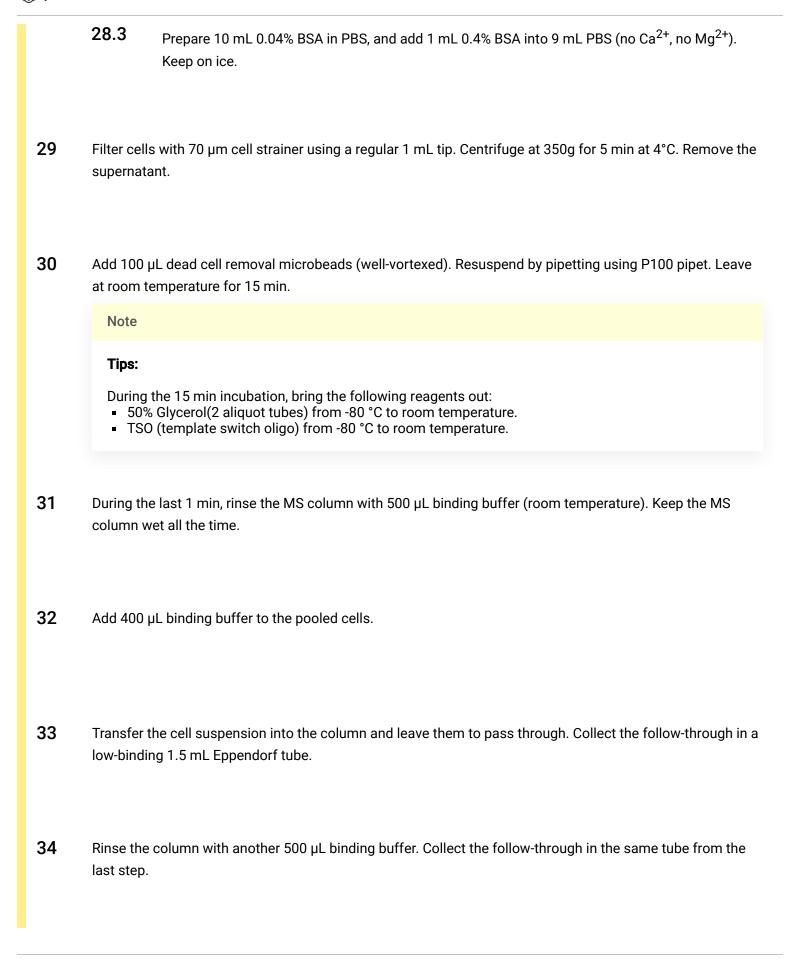
#### Note

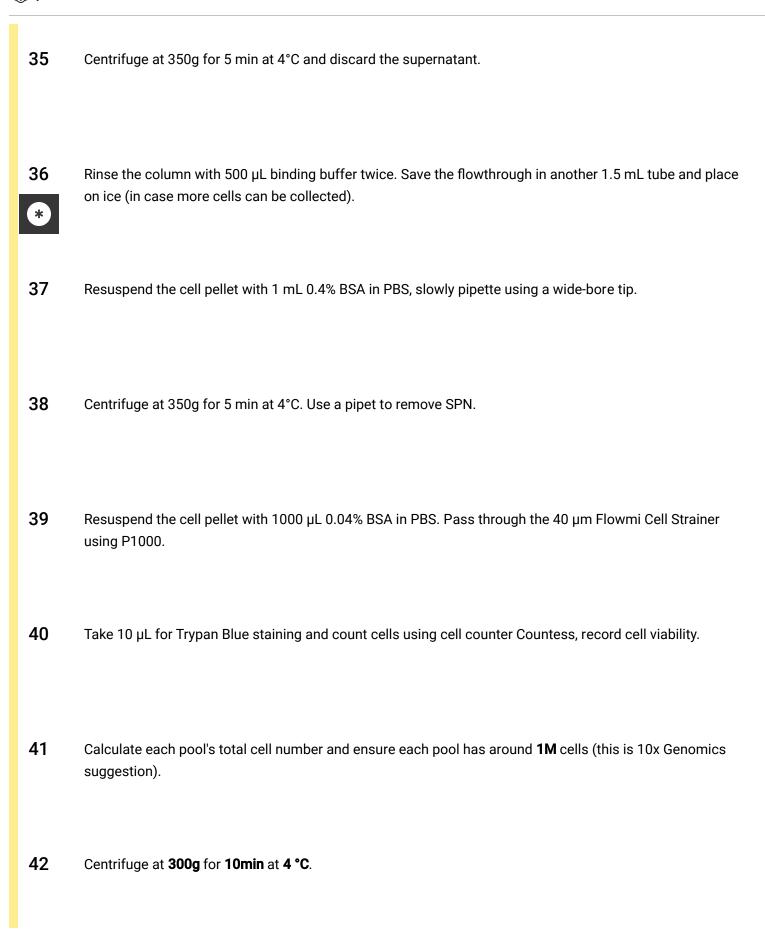
#### Caution:

- Total cell number after pooling should be better higher than 2 million, at least higher than 1 million;
- If less than 2 million, the cell number after dead cell removal and filtration will be too low due to cell loss in each step.
- Use low-binding Eppendorf tubes for all steps below.

# 4. Dead cell removal(~1.5 hrs)

- 28 Check the list below before this section:
  - **28.1** Prepare Binding buffer (from Dead cell removal kit, 4°C), and add 0.5 mL Binding buffer into 9.5 mL distilled water. Bring to RT before use.
  - Prepare 10 mL 0.4% BSA in PBS, add 400  $\mu$ L 10% BSA (-20°C aliquots) into 9.6 mL PBS (no Ca<sup>2+</sup>, no Mg<sup>2+</sup>). Keep on ice.





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Remove **ALL** the supernatant without disrupting the cell pellet and put cells **ON ICE**.



Note

## **CRITICAL STEP:**

- Get rid of all the supernatant.
- Make sure to avoid the visible cell pellet when pipetting. Optimal removal of supernatant and minimal disruption of the cell pellet is attained when the final 100 μl is removed in a consistent and fluid motion without starting and stopping.
- Two pipetting steps:
  - 1. Aspirate down to 100 µl with a p1000 pipette.
  - 2. Then, remove the final 100 µl with a p200 pipette.

# 5. Neutrophils depletion(Optional, CD66abce MicroBead Kit, human)

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#### Note

## Attention:

- There is no need for the overnight recovered PBMCs since most of the neutrophils will be broken.
- Kit: CD66abce MicroBead Kit
  - Miltenyi Biotec: Order no. 130-092-393
- Column:
  - Miltenyi Biotec: MS(Order no. 130-042-201)

# 6 Nuclei isolation(pool cells, ~ 70 min)

45



Add 100  $\mu$ L of chilled Lysis Buffer for every 1 million cells. You need to scale up or down the volume of the lysis Buffer based on the cell numbers of each sample. Pipette mix 10 times and incubate for 3 min on ice.

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#### Note

## Tips:

- Use an **interval timer** for this step.
- For 2 pools, set a **75-second** timer for each pool and a **30-second** break at the end. The total time will be 180 seconds(3min).
- For 3 pools, set a **50-second** timer for each pool and a **30-second** break at the end. The total time will be 180 seconds(3min).
- For 4 pools, set a **40-second** timer for each pool and a **20-second** break at the end. The total time will be 180 seconds(3min).
- Run the Interval timer script in the terminal: swift IntervalTimergTTS4FourSamples.swift
- Start timer, add LSB to sample 1, and pipet mix 10x. Follow the timer to add LSB to sample 2, and pipet mix 10x. Continue the step to add LSB to all samples.

#### Command

# Interval Timer by Swift language (MacOS 14.3.1)

```
import Foundation
import AVFoundation
func intervalTimer(intervals: [(TimeInterval, () -> Void, String)]) {
    for interval in intervals {
        let (duration, action, intervalName) = interval
        print("Interval name: \(intervalName)")
        // Convert the interval name to an AVSpeechUtterance
        let utterance = AVSpeechUtterance(string: intervalName)
        utterance.voice = AVSpeechSynthesisVoice(language: "en")
        // Use AVSpeechSynthesizer to speak the utterance
        let synthesizer = AVSpeechSynthesizer()
        synthesizer.speak(utterance)
        // Wait for the specified duration
        Thread.sleep(forTimeInterval: duration)
        // Perform the action
        action()
    }
}
// Define the intervals and corresponding actions
let intervals: [(TimeInterval, () -> Void, String)] = [
    (10, { print("Interval 0 action") }, "Be ready for nuclei isolation"),
    (40, { print("Interval 1 action") }, "Sample 1"),
    (40, { print("Interval 2 action") }, "Sample 2"),
    (40, { print("Interval 3 action") }, "Sample 3"),
    (40, { print("Interval 4 action") }, "Sample 4"),
    (20, { print("Interval 5 action") }, "Break time and prepare for adding
washing buffer"),
    (40, { print("Interval 6 action") }, "Sample 1"),
    (40, { print("Interval 7 action") }, "Sample 2"),
```

```
(40, { print("Interval 8 action") }, "Sample 3"),
  (40, { print("Interval 9 action") }, "Sample 4"),
  (10, { print("Interval 10 action") }, "Nuclei isolation is done")
]

// Run the interval timer with the specified intervals
intervalTimer(intervals: intervals)
```

Add 500 µL chilled Wash Buffer(WSB) for every 1 million cells to the lysed cells. Invert the tube 5 times to mix. You need to scale up or down the volume of the lysis Buffer based on the cell numbers of each sample.

Note

## Tips:

- Use the same **interval timer** used in the lysis step(Step 45) for this step.
- Add 500 μl of WSB for every 1 M cells.
- 47 Centrifuge at **500g** for **5 min** at **4 °C**.
- Remove the supernatant without disrupting the nuclei pellet.
- Resuspend nuclei pellet with 1000 µl **chilled Wash Buffer(WSB)** and pipette **5 times** to mix. There is no need for an interval timer for washing.(If the volume is more than 1.5 ml, transfer the nuclei to a 2-ml microcentrifuge tube)
- Centrifuge at 500g for 5 min at 4 °C.

Pass nuclei suspension through a **40 μm Flowmi Cell Strainer**.

## Note

#### Attention:

- 1. Use the Flowmi to remove cell nuclei aggregates and cellular debris.
- 2. Since the recommendation for samples having a maximum concentration of 2 million cells/ml(40 μm), I moved the filter step here from step 55.
- 3. The Dead volume of Flowmi is around 20 to 30 μL(for 50μl to 1000μl in total).
- Centrifuge at **500g** for **5 min** at **4 °C**.
- Remove ALL supernatant, taking care not to disturb the pellet.
- Resuspend pooled nuclei in ~50μL chilled **Diluted Nuclei Buffer (DNB)** to reach the target **15M/ml** concentration. Maintain on ice.



#### Note

## Critical:

The resuspension in Diluted Nuclei Buffer is critical for optimal Single Cell ATAC assay performance.

Take **2µL** of nuclei suspension for counting, and record counts in the attached template.





## Critical:

Note

Prepare sample slides one by one for counting because the nuclei will be broken in Trypan blue buffer for a short time.

- 56.1 Make 1:5 dilution by adding 8µL DNB to 2µL nuclei.
- 56.2 Count on a Countess II in duplicates.
- 56.3 The desired concentration is 2.5-4M/mL for diluted nuclei and 12-20M/mL for nuclei in Transposition.
- 56.4 If observe a clump of nuclei, filter through a 40µm strainer and count again.
- 57 Proceed immediately to Chromium Next GEM Single Cell Multiome ATAC + Gene Expression User Guide(CG000338).

# 7. Transposition( ~ 75 min)

58 During Cell count in **Step 56**, bring out the transposition reagents.

# 58.1

| Action            | Item              | 10x PN          | Storage |
|-------------------|-------------------|-----------------|---------|
| Equilibrate to RT | ATAC Buffer B     | 2000193         | -20 °C  |
| Equilibrate to RT | 20X Nuclei Buffer | 2000207         | -20 °C  |
| Place on Ice      | ATAC Enzyme B     | 2000265/2000272 | -20 °C  |
| Place on Ice      | Nuclei            | -               | Ice     |

- Based on the nuclei count from **step 6.15**, calculate the volume of nuclei resuspension and DNB needed to load **50k single nuclei/well** to **4 wells**(for 16 samples) or 6 wells (for 24 samples) using the attached template.
- Refer to Single Cell Multiome User Guide for Transposition Mix and Isothermal Incubation(Page 30).

# 8. GEM Generation & Barcoding(~ 130 min, Move forward to 10X Single Ce...

- Prepare single-cell master mix.
- **62** Bring following items to the Room 540

# Note Checking list: Transposed Nuclei Master Mixture Ice box PCR stripe(8-well) Kit Box(Chip J and Gasket) ■ 50% Glycerol Partition oil Gel Beads 100 μl pipet tips 100 µl pipet 200 μl multi-channel pipet PCR tube rack Gloves 10X Single Cell Multiome user guide 63 Load chromium next GEM Chip J (cells are used in this step). 64 Run the chromium controller. 65 Transfer GEMs. 66 GEM incubation.

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# 67 Quenching Reaction.

# 9. Buffers

Preparation before the assay:

#### Note

## Caution:

- Add DTT to each buffer during cell counting at the end of Part 1 because the DTT is unstable in the solution.
- For Digitonin in **LYB**, incubate at 65 °C to dissolve it entirely and cool down to RT before using. Otherwise, the Digitonin solution shows a backflow in the P10 tip.
- **68.1** Prepare the following buffers and keep all at 4 °C.
- 68.2 Cool down the centrifuge at 4 °C.
- **68.3** Prepare a total of 550  $\mu$ l(11 vials) of RNase inhibitor.
- **69** DNB(Diluted Nuclei Buffer)

69.1

| 1X Nuclei Buffer    | Stock  | Final | 975µL    |
|---------------------|--------|-------|----------|
| Nuclei Buffer (20X) | 20X    | 1X    | 50µL     |
| DTT                 | 1000mM |       | <u> </u> |

| 1X Nuclei Buffer    | Stock | Final | 975µL |
|---------------------|-------|-------|-------|
| Nuclease-free Water | -     | -     | 924µL |

# 69.2

| DNB              | Stock  | Final | 400µL |
|------------------|--------|-------|-------|
|                  |        |       |       |
| 1X Nuclei Buffer | 1X     | 1X    | 390µL |
| RNase inhibitor  | 40U/μL | 1U/μL | 10µL  |

# **70** WSB(Wash Buffer)

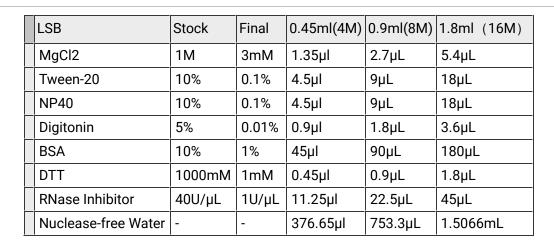
# 70.1

| WSB                 | Stock  | Final | 2.5mL(1M) | 10mL(4M) | 15mL(6M) | 20mL(8M) |
|---------------------|--------|-------|-----------|----------|----------|----------|
|                     |        |       |           |          |          |          |
| Tris-HCl (pH 7.4)   | 1M     | 10mM  | 25µL      | 100µL    | 150µL    | 200µL    |
| NaCl                | 5M     | 10mM  | 5µL       | 20µL     | 30µL     | 40µL     |
| MgCl2               | 1M     | 3mM   | 7.5µL     | 30µL     | 45µL     | 60µL     |
| BSA                 | 10%    | 1%    | 250µL     | 1000µL   | 1.5mL    | 2.0mL    |
| Tween-20            | 10%    | 0.1%  | 25µL      | 100µL    | 150µL    | 200µL    |
| DTT                 | 1000mM | 1mM   | 2.5µL     | 10μL     | 15µL     | 20μL     |
| RNase Inhibitor     | 40U/μL | 1U/μL | 62.5µL    | 250µL    | 375µL    | 500µL    |
| Nuclease-free Water | -      | -     | 2.1225mL  | 8.49mL   | 12.735mL | 16.98mL  |

# 71 LSB(Lysis Buffer)

# 71.1

| LSB               | Stock | Final | 0.45ml(4M) | 0.9ml(8M) | 1.8ml (16M) |
|-------------------|-------|-------|------------|-----------|-------------|
|                   |       |       |            |           |             |
| Tris-HCl (pH 7.4) | 1M    | 10mM  | 4.5µl      | 9µL       | 18µL        |
| NaCl              | 5M    | 10mM  | 0.9µl      | 1.8µL     | 3.6µL       |



# 10. Reagents Details

72 Complete medium (for PBMC culture)

Note

## Recipe:

RPMI-1640 + 10% FBS + 100 U/mL penicillin + 100 U/mL streptomycin + 1 mM sodium pyruvate + 2 mM L-glutamine

**73** Washing medium

Note

## Recipe:

50% Complete medium + 50% X-vivo 15 medium + 25 U/mL benzonase (3.1 uL of 400 U/mL benzonzase into 50 mL Washing medium)

- **74** Benzonase (Millipore, Cat: 71205-3)
- The Table 1 Lipopolysaccharide (LPS). Ultrapure lipopolysaccharide from E. coli K12 (InvivoGen, Cat. tlrl-peklps)

