**Supplementary File 1**

1. **Synthesis of complementary DNA**
   1. Prepare a master mix in a sterile microcentrifuge tube adequate to the number of RNA samples. For a single sample, add 1 µL of dNTPs mix (1,000 µM) to 1 µL of random hexamer primes (25 µM) as shown in **Table 1**.
   2. Add 0.1–1 µg/µL of extracted RNA sample to the master mix and then add RNAse-free water to a final volume to 10 µL in a PCR tube.
   3. Vortex the tubes to mix and spin down using a table-top microfuge.
   4. Denature the RNA and primer mixture at 65 ˚C for 5 min.
   5. Following incubation, place the tube on ice for 1 min.
   6. In a sterile PCR tube, prepare a 2x reaction mix by adding RT buffer to MgCl2, DTT, and RNAse inhibitor as shown in **Table 2**. Pipette 9 µL of 2x reaction mix and add it to the incubated RNA/primer mix in the PCR tube followed by incubation at room temperature for 2 min.
   7. Pipette 1 µL of Superscript III reverse transcriptase to each sample in the microcentrifuge tube.
   8. Mix the content by pipetting followed by incubation at 42 ˚C for 50 min. Terminate the enzymatic activity by incubation at 70 ˚C for 15 min followed by immediate cooling on ice.
   9. Pipette 1 µL of RNase H to each sample with subsequent incubation at 37 ˚C for 20 min.
   10. Finally, use the cDNA at 1–100 dilutions for qPCR assay or store at – 20 ˚C.
2. **Real-time quantitative polymerase chain reaction (qPCR)**

NOTE: For qPCR, cDNA samples are run in triplicates. Bovine mRNA transcript levels for *Ki-67* and *IFN-γ* are quantified using specific primer sets in reference to the *YWHAZ* gene as shown in **Table 3**.

* 1. Prepare a master mix for all samples in a sterile microcentrifuge tube by mixing SYBR Green supermix, specific primer sets, and nuclease-free water for a final reaction volume of 10 µL per sample as shown in **Table 4**.
  2. In a 96-well plate, pipette 8 µL of master mix. Add 2 µL of cDNA (1:10–1:100 diluted) sample and mix via pipetting as shown in **Table 4**.
  3. Vortex the plate for 30 s followed by a short spin.

NOTE: Seal the plate before vortexing and spinning to avoid spillage and contaminating samples.

* 1. Perform the qPCR with an initial denaturation step of 3 min at 95 °C, followed by 40 cycles of 10 s at 95 °C, 20 s at 59 °C, and 20 s at 72 °C with a fluorescence read at the end of extension.

* 1. Analyze the melting curves (Tm) of amplicons at 65–95 °C with 0.5 °C increments every 5 s. Run no template controls (NTC) without cDNA template in parallel with samples and run controls in triplicate.
  2. Use the Cq values for determining relative gene expression in the MoDC-lymphocyte co-culture using the comparative Ct (ΔΔCt) method, and overall fold change of targeted genes against untreated controls (naïve lymphocytes) calculated as 2–ΔΔCt 34.

NOTE: Relative fold changes are graphically presented using GraphPad prism software.

1. **Enzyme-linked immunosorbent assay (ELISA)**
   1. Collect supernatants rich in secretory proteins when processing sample cell pellets for flow cytometry and qPCR.
   2. Prepare a working solution of coating buffer in a 1:5 dilution. For example, make a total volume of 10 mL by diluting 2 mL of concentrated coating buffer in 8 mL of distilled water.
   3. Prepare 1:200 dilution of coating antibody (i.e., 50 µL of coating antibody in 10 mL of working solution of coating buffer prepared in protocol step 7.2) and mix thoroughly using a pipette.
   4. Add 100 µL of diluted coating antibody to each well in a sterile 96-well plate.
   5. Seal the wells with a lid or adhesive plastic cover and incubate for 1 h at room temperature or 2–8 ˚C overnight.
   6. After incubation, remove the cover and wash the wells 3x with wash buffer (PBS plus 0.05% Tween 20).
   7. Gently tap the plate upside down on a paper towel.
   8. Add 200 µL of blocking buffer (PBS + BSA + Tween 20) immediately before the wells dry out. Cover the wells and incubate 1 h at room temperature.
   9. Resuspend 625 µL of distilled water to the IFN-γ standard. Pipette gently for 5 min. Afterward prepare 1 to 9 serial dilutions of IFN-γ standard as shown in **Table 5**.
   10. After completion of incubation in protocol step 10, wash the wells 3x with wash buffer and aspirate the wells by tapping gently on a paper towel.
   11. Now add 100 µL of each serially diluted IFN-γ standard to designated wells (as positive controls).
   12. Add 100 µL of MoDCs–lymphocyte culture supernatant and 100 µL of lymphocyte culture supernatant (as negative control) to their respective designated wells.

NOTE: Each sample should be run in duplicates at least.

* 1. Seal the wells and incubate the plate for 1 h at room temperature.
  2. After incubation, wash the wells 3x and aspirate by tapping on paper towel.
  3. Pipette 100 µL of prediluted detection antibody to all wells.

NOTE: Dilute the detection antibody at a 1:500 dilution, that is, 20 µL of detection antibody with 10 mL of PBS.

* 1. Seal the wells and incubate for 1 h at room temperature.
  2. Wash the wells 3x with wash buffer and discard the supernatant by gently tapping on a paper towel.
  3. Pipette 100 µL of prediluted Streptavidin-HRP conjugate to all wells.

NOTE: Dilute the Streptavidin-HRP conjugate at a 1:1,000 dilution (i.e., 50 µL of conjugate with 50 mL of PBS).

* 1. Seal the wells and incubate for 1 h at room temperature in the dark.
  2. Wash the wells 3x with wash buffer and aspirate by gently tapping on a paper towel.
  3. Pipette 100 µL of HRP substrate into all wells followed by incubation for 10 min in the dark.
  4. After 10 min, immediately stop the reaction by adding 100 µL of stop solution to all wells.
  5. Measure the absorbance at 450 nm using a microplate reader.