

Immunoverse[™]-HS TCR Workflow Overview

Follow the instructions and incubations for each step. All mixing steps should be performed on ice. Pipette up and down 8 times or vortex to mix after re-suspending each lyosphere and spin down prior to incubations and transfers. For incubations, use a lid heated $\geq 100^{\circ}$ C except where specified otherwise.

| TCR Specific RT Priming | Add optimal amount (see Appendix) of RNA input to TCR Specific RT Priming reagent for a total volume of 20 μL. | Step | Incubation Temperature 65°C | Incubation Time 5 min |
|----------------------------|--|---------|-----------------------------------|-----------------------------|
| | Incubate as indicated 🖆 | 2 | 4°C | Hold |
| | Transfer 20 μL TCR Specific RT Priming mixture to First Strand cDNA Synthesis reagent. | Step | Incubation Temperature | Incubation Time |
| First Strong | | 1 | 50°C | 30 min |
| | Incubate as indicated 🥌 | 2 | 80°C | 20 min |
| CDNA Synthesis | | 3 | 4°C | Hold |
| Synthesis | | | - | |
| | Add 20 μ L ultrapure water to 20 μ L First Strand cDNA Synthesis mixture and then transfer to | Step | Incubation Temperature | Incubation Time |
| | Second Strand cDNA Synthesis reagent. | 1 | 16°C | 60 min |
| Second | Incubate as indicated 🗲 | 2 | 75°C | 20 min |
| | _ | 3 | 4°C | Hold |
| Synthesis | STOP Optional stopping point after this step. Store at -10°C to -30°C. | | | |
| | Transfer 40 μL Second Strand cDNA Synthesis mixture to End Repair reagent. | Step | Incubation Temperature | Incubation Time |
| | | 1 | 25°C | 30 min |
| End | Incubate as indicated with <u>unneated lid</u> | 2 | 4°C | Hold |
| Repair | | | ¹ XP clean-up (100 μL |). Elute in 20 μL |
| | Transfer 20 μL End Repair mixture to Ligation Step 1 reagent. | Step | Incubation Temperature | Incubation Time |
| | Incubate as indicated 🗲 | 1 | 37°C | 15 min |
| Ligation | After insubation add 20 ul of 10 mM Tris UCL all | 2 | 4°C | Hold |
| Step 1 | 8.0 and mix. | | | |
| МВС | Transfer 40 μL Ligation Step 1 mixture to the MBC add | apters. | | |

| | Transfer the entire volume of the MBC adapters to Ligation Step 2 reagent | Step | Incubation Temperature | Incubation Time | |
|--------------------|---|--|---------------------------|--------------------|--|
| Ligation Step 2 | Incubate as indicated with <u>unheated lid</u> | 1 | 25°C | 15 min | |
| | | 2 | 4°C | Hold | |
| | STOP Optional stopping point before purification. Store at -10°C to -30°C. | Ligation clean-up beads (50 μL). Elute in 36 μL 5mM NaOH, 75°C 10 min | | | |
| First PCR | Add 4 μL GSP1 primers to the First PCR HS reagent. Then add 36 μL of purified Adapter Ligation mixture and mix. | Incubation Temperature | Incubation Time | # of cycle | |
| | | 95°C | 3 min | 1 | |
| | | 95°C | 30 sec | | |
| | | 65°C | 3 min (ramp rate 100%) | 24 | |
| | | 72°C | 3 min | 1 | |
| | Optional stopping point after this | 4°C | Hold | 1 | |
| | step. Store at -10°C to -30°C. | AMPure TM XP clean-up (48 μ L). Elute in 44 | | | |
| | Transfer 40 μL of purified First PCR mixture and mix. | Incubation Temperature | Incubation Time | # of cycle | |
| | | 95°C | 3 min | 1 | |
| Second PCR | Incubate as indicated 🛩 | 95°C | 30 sec | | |
| | | 65°C | 3 min (ramp rate 100%) | 8 | |
| | | 72°C | 3 min | 1 | |
| | | 4°C | Hold | 1 | |
| | STOP Optional stopping point after this step. Store at -10°C to -30°C. | AMPure TM XP clean-up (48 μL). Elute in 20 μl | | | |

Appendix: RNA Input Recommendations and Sequencing Read Depth

| Panel | Application | RNA Input Recommendations* | Sequencing Read Depth |
|----------------|--|----------------------------|-----------------------|
| TCR B/G | Clonality or Dominant Clones | 25-400 ng | 250,000 |
| TCR A/D | Clonality or Dominant Clones | 25-400 ng | 250,000 |
| TCR All Chains | Clonality or Dominant Clones | 25-400 ng | 500,000 |
| TCR B/G | Thorough Characterization of Repertoire or Rare Clonotype Identification | 400-2000 ng | 1.5 M |
| TCR A/D | Thorough Characterization of Repertoire or Rare Clonotype Identification | 400-2000 ng | 1.5 M |
| TCR All Chains | Thorough Characterization of Repertoire or Rare Clonotype Identification | 400-2000 ng | 3 M |

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