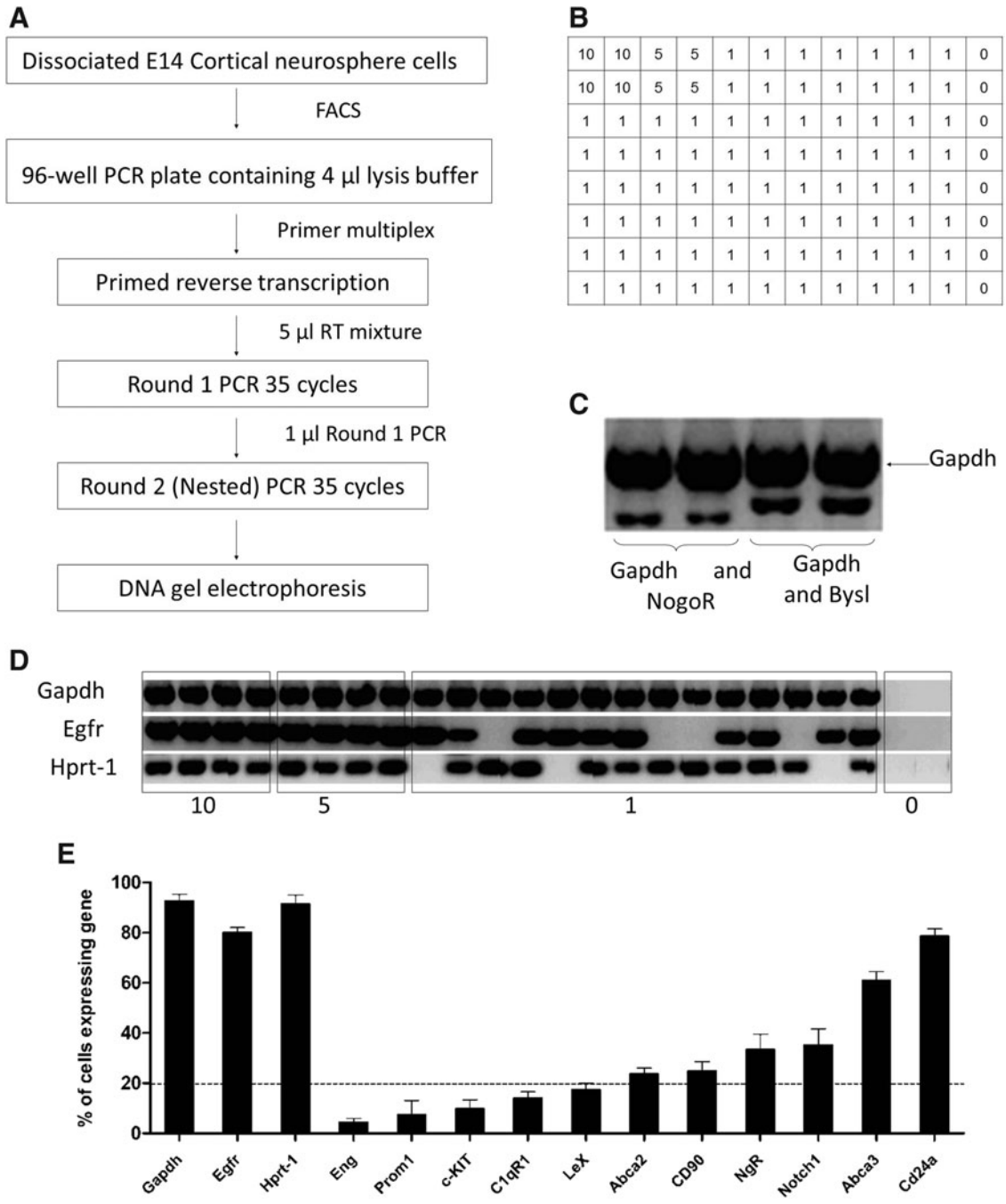
Supplementary Data



SUPPLEMENTARY FIG. S1. Single-cell reverse transcription polymerase chain reaction (RT_PCR) methodology. **(A)** The flow diagram represents the various steps in the single-cell RT-PCR procedure. Dissociated E14 cortical neurospheres were fluorescence-activated cell sorting (FACS)-sorted into 96-well polymerase chain reaction (PCR) plates containing neural progenitor (NP)-40 lysis buffer. Gene-specific reverse transcription was performed, followed by one round of PCR with the primer multiplex, and then a second round of single-gene PCR with nested primers. PCR products were analyzed on 2% agarose gels and sequenced. **(B)** The layout of the 96-well PCR plates. Individual plates contained wells with 10, 5, 1, and 0 cells. **(C)** DNA bands from derived sets of primers have to show up to indicate compatibility of primers for used in the multiplex. This is illustrated by Gapdh/NogoR and Gapdh/Bsyl. **(D)** DNA bands for control messenger RNAs (mRNAs)—Gapdh, Egfr, and Hprt-1—are shown. These genes are used as reference genes to assess the consistency of this assay. For each single-cell RT-PCR, lanes containing 10, 5, 1, and 0 cells are shown. Repeats of any single plate yield highly consistent results with $P < 0.001$. **(E)** Histogram showing the percentage of cells expressing genes encoding a variety of cell surface receptors. Genes with percentage expression of below 20% are considered possible neural stem cell markers. Data are presented as mean ± SEM from five experiments.