**SUPPLEMENTARY METHODS**

**Methods for determining neural stem cell (NSC) identity and viability.**

Nestin expression for cell identity testing was determined using anti- human nestin- FITC conjugated primary antibody (IC59F; R&D systems) and gated against cells that were stained with mouse IgG1 Isotype control –FITC conjugated primary antibody. For assessing transgene expression of bacterial (b) CD, CD-NSCs were stained with either anti-bCD primary antibody (623412; BD Pharmanigen) or mouse IgG1 kappa isotype control antibody (555746; BD Pharmanigen) and subjected to secondary incubation with goat anti-mouse FITC conjugated antibody (555988; BD Pharmanigen). All stained cells were run on Guava Easy Cyte under Express Plus software. Cell viability was evaluated using the Viacount software on flow cytometer, Guava Easy Cyte (EMD Millipore).

**High performance liquid chromatography-electrospray ionization tandem mass spectrometry(HPLC-ESI-MS/MS) analysis of 5-fluorocytosine (5-FC) and 5-fluorouracil (5-FU) in plasma and dialysate samples.**

HPLC grade ethyl acetate and acetonitrile were purchased from Fisher Scientific. American Chemical Society (ACS) grade formic acid (FA), glacial acetic acid and 2-propanol were purchased from J.T.Baker. Water was purified using the Millipore Milli-Q system. 5-FU and 5-FC were obtained from Sigma. 5-Fluorouracil-15N2 was purchased from C/D/N Isotopes, Inc. and used as an internal standard (IS). HPLCseparation was achieved using a Synergi hydro-RP 4μ 150 x 2.00 mm analytical column (Phenomenex). The auto-injector temperature was maintained at 5oC and the column temperature at 25oC. An isocratic mobile phase of 0.1% FA in water was used to elute the analytes from the column at a flow rate of 0.2 ml/min. Total run time was 7 min. The electrospray ionization source of the mass spectrometer was operated in positive ion mode with a cone gas flow of 50 L/h and a desolvation gas flow of 750 L/h. The capillary voltage was set to 3.5 kV. The cone voltage was optimized at 45 V for 5-FC and 37 V for 5-FU and the IS. The collision cell energy was 20 eV for 5-FC and 17 eV for 5-FU and the IS. The source temperature was 125oC and the desolvation temperature was 450oC. A solvent delay program was used from 0 to 2 min and from 6 to 7 min to minimize the mobile phase flow to the source. MassLynx version 4.1 software was used for data acquisition and processing.

Positive electrospray ionization of 5-FU, 5-FC,and the IS produced abundant protonated molecular ions (MH+). The fragmentation of these compounds was induced under collision-induced dissociation conditions and acidic mobile phase. The precursor→product ion combinations at m/z 131.1→114.12 for 5-FU**,** 130.1→113.25 for5-FC and 133.0→115.20 for the IS were used in multiple reaction monitoring (MRM) mode to determinate these compounds. The use of MRM provided sufficient specificity and sensitivity. MS/MS experimental conditions, such as collision energy and collision cell pressure, were optimized from continuous flow injection sample introduction of standard solutions. Under optimized assay conditions, the retention time was 3.14 min for 5-FCand5.28 min for 5-FUand the IS, and the lower limits of quantitation were 6 nM and 0.25 nM, respectively.

**Serum antibody binding assay**

Aliquots of cultured NSCs were incubated at 4⁰C for 20 min with cryopreserved patient serum samples that had been heat-treated to inactivate complement. After incubation, the NSCs were washed twice with 1 mL of FACS buffer (PBS with 5 g/L of BSA and 0.06 g/L of sodium azide). After each wash, NSCs were pelleted by centrifugation (1000 × g, 5 min). After the second wash and spin, the NSCs were resuspended in FACS buffer and analyzed using flow cytometry for bound antibodies detected using a secondary goat anti-human Fc antibody conjugated to fluorescein isothiocyanate. Binding of human antibodies to the NSCs was detected as a shift in the mean fluorescence intensity (MFI) compared to NSCs not treated with human serum. All samples obtained from individual study participants before and after therapy were analyzed in parallel to assess for possible development of humoral anti-NSC responses over time. The statistical significance of any detected MFI shifts was evaluated by comparison with data from the NSC binding of a reference panel of normal human sera using a two-tailed student’s t-test. The assay included the parental NSCs (not transduced with the CD gene) as a control to evaluate whether possible antibody responses were directed against the CD gene product.

**Supplementary Table S1.** Dose escalation schema.

**Supplementary Table S2.** Characteristics of study patients.