

**Supplemental Information for: “A Nanomule Peptide Carrier Delivers siRNA Across the Blood-Brain Barrier to Attenuate Neuroinflammation in Ischemic Stroke”**

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**Supplemental Table 1. Fluorescence associated with the localization of siRNA and MTfp-siRNA to brain tissues.**

Legend:

TTV - Total Tissue Volume

- Sum of voxels in entire reconstructed 3D field

BCV - Brain Capillary Volume

- Total FITC voxels

BPV - Brain Parenchyma Volume

- TTV minus BCV

TTAV - Total Test Article Volume

- Total voxels of AF680 fluorescence

TAV<sub>BC</sub> – Volume of fluorescence in Brain Capillaries

- Voxels of AF680 Co-localized with FITC voxels

TAV<sub>BP</sub> - Volume of fluorescence in Parenchyma

- TTAV minus TAV<sub>BC</sub>

VTA<sub>BC</sub> - Volume fraction of Test Article in Brain Capillaries

- TAV<sub>BC</sub> / TTV

VTA<sub>BP</sub> - Volume fraction of Test Article in Brain Parenchyma

- TAV<sub>BP</sub> / TTV

VTA<sub>TOT</sub> – Volume fraction of Test Article in the Brain Capillaries and Parenchyma

- TTAV / TTV 66



**Supplemental Table 2. Quantitation of stroke infarct size by TTC assay**

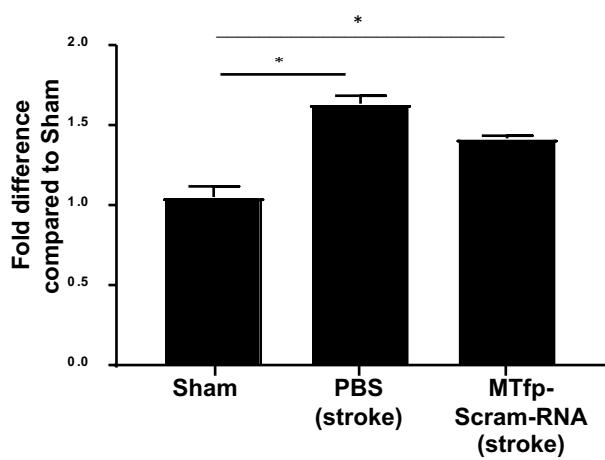
**Trial #1**

| Treatment           | Animal # | Absorb,<br>Ischemic | Absorb,<br>Contralateral | Infarct Volume (% loss) |
|---------------------|----------|---------------------|--------------------------|-------------------------|
| Sham                | 1        | 0.163               | 0.162                    | -0.23                   |
|                     | 2        | 0.161               | 0.161                    | 0.02                    |
|                     | Mean     |                     |                          | <b>-0.10</b>            |
|                     | SEM      |                     |                          | <b>0.12</b>             |
| PBS                 | 3        | 0.093               | 0.173                    | 46.34                   |
|                     | 4        | 0.042               | 0.085                    | 50.41                   |
|                     | 5        | 0.122               | 0.218                    | 44.04                   |
|                     | Mean     |                     |                          | <b>46.93</b>            |
| NOX4 siRNA<br>Alone | SEM      |                     |                          | <b>1.86</b>             |
|                     | 7        | 0.068               | 0.150                    | 54.76                   |
|                     | 8        | 0.068               | 0.121                    | 43.39                   |
|                     | 9        | 0.098               | 0.205                    | 52.36                   |
| MTfp-NOX4<br>siRNA  | 10       | 0.097               | 0.162                    | 39.81                   |
|                     | Mean     |                     |                          | <b>47.58</b>            |
|                     | SEM      |                     |                          | <b>3.56</b>             |
|                     | 11       | 0.105               | 0.167                    | 37.32                   |
| MTfp-NOX4<br>siRNA  | 12       | <u>0.072</u>        | <u>0.111</u>             | <u>35.14</u>            |
|                     | 13       | <u>0.146</u>        | <u>0.207</u>             | <u>29.31</u>            |
|                     | Mean     |                     |                          | <b>33.92</b>            |
|                     | SEM      |                     |                          | <b>2.39</b>             |

**Trial #2**

| Treatment         | Animal # | Absorb,<br>Ischemic | Absorb,<br>Contralateral | Infarct Volume (% loss) |
|-------------------|----------|---------------------|--------------------------|-------------------------|
| Sham              | 50       | 2.615               | 2.907                    | 10.04                   |
|                   | 51       | 1.904               | 2.077                    | 8.33                    |
|                   | 53       | <u>1.788</u>        | <u>1.581</u>             | <u>-13.09</u>           |
|                   | Mean     |                     |                          | <b>1.76</b>             |
| PBS               | SEM      |                     |                          | <b>7.44</b>             |
|                   | 46       | 0.630               | 1.117                    | 43.60                   |
|                   | 47       | 0.578               | 1.260                    | 54.13                   |
|                   | 55       | <u>0.356</u>        | <u>0.862</u>             | <u>58.70</u>            |
| MTfp-<br>scramRNA | Mean     |                     |                          | <b>52.14</b>            |
|                   | SEM      |                     |                          | <b>4.47</b>             |
|                   | 59       | 0.571               | 1.550                    | 63.16                   |
|                   | 60       | <u>0.902</u>        | <u>1.301</u>             | <u>30.67</u>            |
| MTfp-<br>scramRNA | 65       | <u>0.577</u>        | <u>0.956</u>             | <u>39.64</u>            |
|                   | Mean     |                     |                          | <b>44.49</b>            |
|                   | SEM      |                     |                          | <b>9.69</b>             |

**Supplemental Table 3: Raw data and calculations for Figure 3.** The qPCR values were compared using the method described by Huggett et al. (2005)



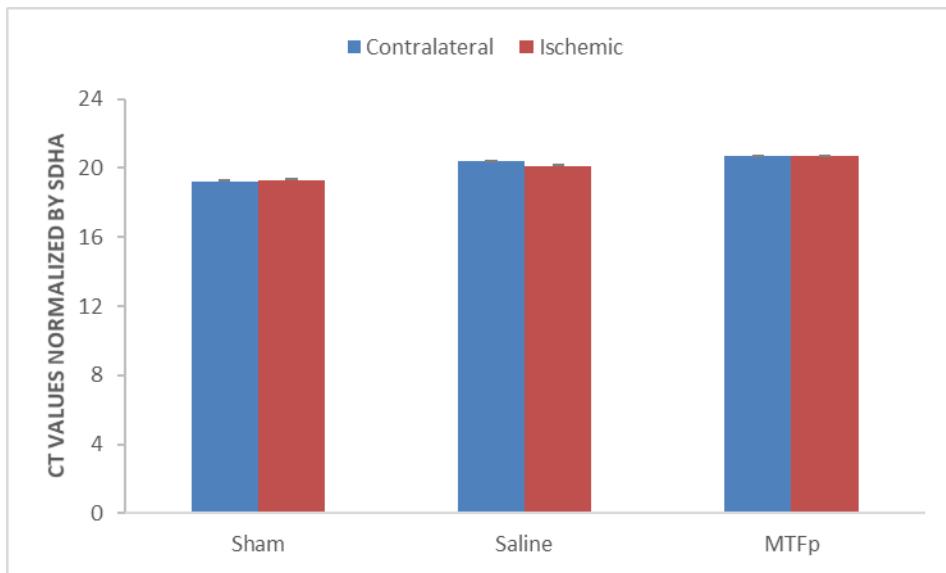
**Supplemental Figure 1. NOX4 mRNA expression in the brain after MTfp-scrambled RNA treatment and stroke induction.** Relative gene expression of *Nox4* in the mouse brain hemispheres by RT-PCR following treatment and 24 hours post-stroke (GAPDH as a reference gene). For each treatment group, the *Nox4* expression in the left hemisphere (stroke) is normalized against the right hemisphere (contralateral) of the same animal. Data are shown as mean  $\pm$  SEM; \* P-value  $<0.05$ .

**Supplemental Table 4: Raw data for Supplemental Figure 2:**

|                      | Target Name | Ct       |
|----------------------|-------------|----------|
| Sham Contralateral   | SDHA        | 22.74603 |
|                      | SDHA        | 22.73561 |
|                      | GAPDH       | 19.22237 |
|                      | GAPDH       | 19.26666 |
| Sham Ischemic        | SDHA        | 24.31267 |
|                      | SDHA        | 24.29483 |
|                      | GAPDH       | 20.93466 |
|                      | GAPDH       | 20.82387 |
| Saline Contralateral | SDHA        | 23.56614 |
|                      | SDHA        | 23.58747 |
|                      | GAPDH       | 20.34948 |
|                      | GAPDH       | 20.4035  |
| Saline Ischemic      | SDHA        | 23.91395 |
|                      | SDHA        | 23.89643 |
|                      | GAPDH       | 20.30284 |
|                      | GAPDH       | 20.26963 |
| MTFp Contralateral   | SDHA        | 24.45157 |
|                      | SDHA        | 24.46888 |
|                      | GAPDH       | 20.6589  |
|                      | GAPDH       | 20.6973  |
| MTFp Ischemic        | SDHA        | 24.92251 |
|                      | SDHA        | 24.9525  |
|                      | GAPDH       | 21.22842 |
|                      | GAPDH       | 21.28262 |

Average

|        |       | Contralateral | Ischemic |
|--------|-------|---------------|----------|
| Sham   | SDHA  | 22.74         | 24.3     |
|        | GAPDH | 19.23         | 20.87    |
| Saline | SDHA  | 23.57         | 23.9     |
|        | GAPDH | 20.37         | 20.28    |
| MTFp   | SDHA  | 24.46         | 24.93    |
|        | GAPDH | 20.67         | 21.25    |



**Supplemental Figure 2. GAPDH as a reliable reference gene to evaluate NOX4 mRNA expression.** GAPDH expression was normalized to succinate dehydrogenase complex flavoprotein subunit A (SDHA) expression, a gene known to be a reliable reference gene in brain ischemia. Sham = surgical control (no hypoxia). Saline = surgical hypoxia induction with saline injection. MTFp = surgical hypoxia induction with MTF peptide injection. Error bars represent standard error of mean (SEM) of duplicate values. GAPDH gene expression does not significantly change after induction of ischemia in the brain, making it a reliable reference gene to evaluate NOX4 mRNA expression.

#### Methodology for Supplemental Figure 2:

Frozen brain tissue samples were first processed with 70 µm cell strainer to disintegrate them and immediately transferred to lysis buffer (Qiagen) and then homogenised using an 18G needles and syringes. RNA was isolated using the RNeasy® plus Mini Kit (Qiagen) in accordance with the manufacturer's instructions. Subsequently RNA was quantified spectrophotometrically (NanoDrop, ThermoFisher Scientific) at 260 nm ( $A_{260}$ ) and purity was estimated by an  $A_{260}/A_{280}$  ratio  $> 1.8$ . The integrity, purity, and amount of RNA were verified by visualization of total RNAs after electrophoresis on 1% agarose gel. 2 µg of RNAs were reverse transcribed using a SuperScript II Reverse Transcriptase (Thermofisher Scientific) according to the manufacturer's instructions.

RT-Q-PCR reactions were carried out for GAPDH and SDHA in each sample using GeneAmp 9600 Fast Instrument (ThermoFisher Scientific). Each reaction was performed in a final volume of 20 µL containing 2µL cDNA diluted with H<sub>2</sub>O, 10 µl of iTaq Universal SYBR® Green Supermix (Bio-Rad) and 1 µl of each gene specific primers (SDHA Fwd primer: 5'-GGAACACTCCAAAACAGACCT 3' and Rev primer" 5'-ACCACTGGTATTGAGTAGAA-3', GAPDH Fwd primer:5'-AACTTGGCATTGTGGAAGG-3' and Rev primer 5'-ACACATTGGGGTAGGAACA-3'. All samples were run in triplicate and average values were calculated. Two independent reverse transcriptions were tested for each gene.