Supplementary Material

1  Cellular uptake of siRNA analogue.

Supplementary Figure 1. Uptake of siRNA analogue was evident in BMSCs. BMSCs were transfected with 10 nM fluorescently-labeled siRNA analogue Trilencer-27 (Origene) in siTRAN2.0 for 18 hours. Cells were then imaged with EVOS M5000 Imaging System (Invitrogen, USA) to check siRNA delivery to the cells. Panel A shows BMSCs with a phase-contrast imaging. Red color on panel B indicates transfected cells. Overlay image shown in panel C confirms cellular uptake of siRNA analogue. Magnification 100x.
### Supplementary Table 1: Primer Sequences

| Symbol | Gene   | Primer Sequences (5’-3’)                                             | Length (bp) | Product (bp) | Tm (°C) |
|--------|--------|------------------------------------------------------------------------|-------------|--------------|---------|
| Alpl   | NM_013059.1 | F-TGCAGGATCGGAACGTCAAT<br>R-GGGTCTTTTCTTTCCTCTGGCA                      | 20          | 170          | 60      |
|        |        |                                                                        |             |              |         |
| Bglap  | NM_013414.1 | F-TGAGTCTGACAAAGCCTTCATGT<br>R-GAAGCCAATGTGGTGGTCCGCTA                  | 23          | 178          | 61      |
|        |        |                                                                        |             |              |         |
| Ppib   | NM_022536.1 | F-ACCTGTAGGAGCAGTGAGCTT<br>R-GCTCTTTCTCTCTGCGCAT                          | 20          | 187          | 60      |
|        |        |                                                                        |             |              |         |
| Runx2  | NM_053470.2 | F-CGGCTACACAAACTAACCACAG<br>R-TGCAGCCTAATATTACTGCATG                    | 20          | 173          | 60      |
|        |        |                                                                        |             |              |         |
| slc2a1 | NM_138827.1 | F-GCCGCTTCATCATATTGGAGTG<br>R-GAGTCTAAGCCGAGAACCCTGG                    | 20          | 160          | 58      |
|        |        |                                                                        |             |              |         |
| slc2a2 | NM_012879.2 | F-CGGGCACATGCTCTCATCAT<br>R-CTGAGCCAGCAATCTAGCTA                        | 20          | 182          | 58      |
|        |        |                                                                        |             |              |         |
| slc2a3 | NM_017102.2 | F-GATCCTTTGGCTGGCTTCTT<br>R-ATCTCCGCTGCTGGTCCTT                        | 20          | 180          | 58      |
|        |        |                                                                        |             |              |         |
| slc2a4 | NM_012751.1 | F-CGCGGCCTCCTCATATGAGTAC<br>R-ATCTCAACCCCAACACCTGG                     | 20          | 188          | 58      |
3 Results of RNA-seq analysis

Supplementary Figure 2 Top 10 most significantly changed pathways due to silencing of either GLUT1 (A), GLUT3 (B) and GLUT4 (C). DE genes were used for common pathway enrichment analysis utilizing the Gene Ontology annotations. Enriched pathways are categorized by biological processes (BPs), cellular components (CCs), and molecular functions (MFs).
Supplementary Material

4 Transcriptome of GLUT family when silencing class I glucose transporters

Supplementary Figure 3. Silencing of GLUT1 (dark grey), GLUT3 (grey) and GLUT4 (white) was specific and resulted in minor changes in transcription of other members of GLUT-family. Data is presented as fragments per kilobase of transcript per millions reads mapped (FPKM).