

Table S4: Effect of cell storage on transcript abundance of TGFb-signaling target genes in ADSC cultures

| Genes | Fold difference (Stored cells :Primary cells) | |
|---------------------------|--|-----------------------------|
| | DSL D Paso 24h ¹ | NA Paso 24h ¹ |
| <i>PTK2B</i> ⁴ | 1.42 | -1.68 |
| <i>ATF3</i> | 2.36 | -2.11 |
| <i>MAPK14</i> | -1.49 | -2.17 |
| <i>ME2</i> | 2.39 | -1.39 |
| <i>ACVRL1</i> | 2.07 | 1.36 |
| <i>NFIB</i> | 1.48 | -1.89 |
| <i>EPHB2</i> | 1.37 | -2.13 |
| <i>HMOX1</i> | -1.42 | -3.92 |
| <i>SMAD6</i> | 1.48 | 1.06 |
| <i>FOS</i> | -1.43 | -3.66 |
| <i>GLI2</i> | 1.17 | -1.12 |
| <i>STC2</i> | 2.02 | -3.62 |
| <i>ID2</i> | -1.06 | -1.56 |
| <i>PPARA</i> | 1.67 | 1.18 |
| <i>ENG</i> | 1.34 | -1.76 |
| <i>CREBBP</i> | 1.21 | -1.40 |
| <i>NFKBIA</i> | -1.04 | -2.05 |
| <i>BRD2</i> | 1.60 | -1.36 |
| <i>TGFBR2</i> | -1.15 | -1.31 |
| <i>MMP2</i> | -1.24 | -2.68 |
| <i>CDKN1B</i> | 1.45 | -1.51 |
| <i>EP300</i> | 1.23 | -1.52 |
| <i>FURIN</i> | -1.36 | -2.41 |
| <i>MBD1</i> | 2.16 | 1.11 |
| <i>IFRD1</i> | 1.22 | -1.73 |
| <i>SMAD3</i> | 1.02 | 1.06 |
| <i>BCL2L1</i> | 1.40 | -1.54 |
| <i>MAPK8</i> | 1.07 | -1.36 |
| <i>SMAD1</i> | 1.17 | -1.15 |
| <i>RHOA</i> | 1.88 | -1.01 |
| <i>BACH1</i> | 1.10 | -1.56 |
| <i>MYC</i> | 1.12 | -1.43 |
| <i>PAI-1</i> | 2.58 | 1.24 |
| <i>ID3</i> | 1.23 | 1.01 |
| <i>SNAI1</i> | -1.23 | -1.34 |

¹Fold difference in transcript abundance in stored cells vs primary cultures. (see Methods section on isolation and storage of adipose-derived stromal fibroblasts (ADSCs) for details). Mean transcript abundance in stored cells was calculated from triplicate cultures of 2 DSLD-Paso and 2 NA-Paso horses (see Table S1 for animal details). ⁴Genes are listed in the same order as in Table 1.