

SUPPLEMENTARY TABLE S5. RNA SEQUENCING DATA CONFIRMED BY QUANTITATIVE POLYMERASE CHAIN REACTION AND TRANSLATION EFFICIENCY DETERMINED AS THE RATIO OF THE LEVELS OF SPECIFIC TRANSCRIPTS IN THE POLYSOMAL VERSUS THE NONPOLYSOMAL FRACTION

<i>Gene ID</i>	<i>Specificity</i>	<i>LogFC</i> ^a		<i>Translation efficiency</i> ^b (<i>qPCR</i>)		
		<i>RNA-seq</i>	<i>qPCR</i>	<i>Fibroblast (A)</i>	<i>ADSC (B)</i>	<i>A/B</i>
<i>CAMK2N1</i>	Fibroblasts	5.27	5.14	1.00	0.22	4.55
<i>RPL10A</i>	Equal	0.02	0.20	1.36	1.12	1.21
<i>TMSB10</i>	Equal	-0.07	-0.11	1.94	1.91	1.02
<i>ARPC2</i>	Equal	-0.07	-0.30	1.89	1.62	1.17
<i>SCRG1</i>	ADSCs	-6.51	-5.97	1.12	0.23	4.87

^aLog-fold change of fibroblasts/ADSCs obtained by RNA-seq and qPCR using the polysomal fraction.

^bThe translation efficiency of the five selected transcripts was calculated as the ratio of the normalized qPCR data obtained from the polysomal versus the nonpolysomal fraction.

qPCR, quantitative polymerase chain reaction.