

Potency of umbilical cord blood- and Wharton's jelly-derived mesenchymal stem cells for scarless wound healing

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Supplemental table 1. The primer sequences used to quantify gene expression levels.

gene	Sequence (5'->3')	
	Forward primer	Reverse primer
<i>HGF</i>	GCCCTATTTCCCGTTGTGAAGG	CCCGCAGTTGTTTTGTTTTGGC
<i>MMP2</i>	CTGGTCGCAGTGATGGCTTC	GTCCATCTGCATTGCCACCC
<i>PLAU</i>	AACAGATTCCTGCAAGGGCGA	CCCAGCTCACAATCCCCTCA
<i>TGFBI</i>	CGTCACTGGAGTTGTACGGC	TTGGGGCTGATCCCGTTGA
<i>IL-1A</i>	GTCGGCAAAGAAATCAAGATGGC	TCAGAGAGAGATGGTCAATGGCA
<i>IL-1B</i>	TGCCACCTTTTGACAGTGATGAG	TGTTGATGTGCTGCTGCGAG
<i>IL-10</i>	AGGCGCTGTCATCGATTTCTC	CATGGCCTTGTAGACACCTTGG
<i>VEGFA</i>	CTCCACCATGCCAAGTGGTC	ACCAGGGTCTCAATCGGACG
<i>18S ribosomal RNA</i>	TTCTGGCCAACGGTCTAGACAAC	CCAGTGGTCTTGGTGTGCTGA
<i>COL1A2</i>	GGATACGCGGACTCTGTTGC	CCTTTCGTA CTGATCCCGATTGC
<i>COL3A1</i>	TGGACTGAAGGGTGAAAATGGTCT	CCGAGCACCATCATTGCCTC
<i>TGFBI3</i>	CGAGTGGCTGTTGAGGAGAG	TCATCTTCATTGTCCACTCCTTGA
<i>MMP1B</i>	AGCTTCCTGCCAGAACCTTTGA	AGCCCATACTTTGCTGCCTTTG

Supplemental table 2. Information about the isolation and ex vivo expansion of mesenchymal stem cells from umbilical cord blood (UCB-MSCs) and Wharton’s jelly (WJ-MSCs)

Donor number	WJ-MSCs	UCB-MSCs
#1	○	×
#2	○	×
#3	○	×
#4	○	×
#5	○	○
#6	△	×
#7	○	-
#8	○	×
#9	-	×
#10	-	×
#11	-	×
#12	-	○
#13	-	×
#14	-	×

○: successfully expanded a sufficient number of cells (>1,000,000)

×: failed to expand a sufficient number of cells.

△: the most of tissues (explants) failed to attach to dishes due to technical error.

-: no procedure was performed.

Supplemental table 3. Results of RT² Profiler PCR array. The fold regulation represents the expression levels in umbilical cord blood-derived mesenchymal stem cells (UCB-MSCs) when compared to Wharton's jelly-derived mesenchymal stem cells (WJ-MSCs). The data are presented as the means from three separate experiments. Bolded p-value shows significant difference (P<0.05).

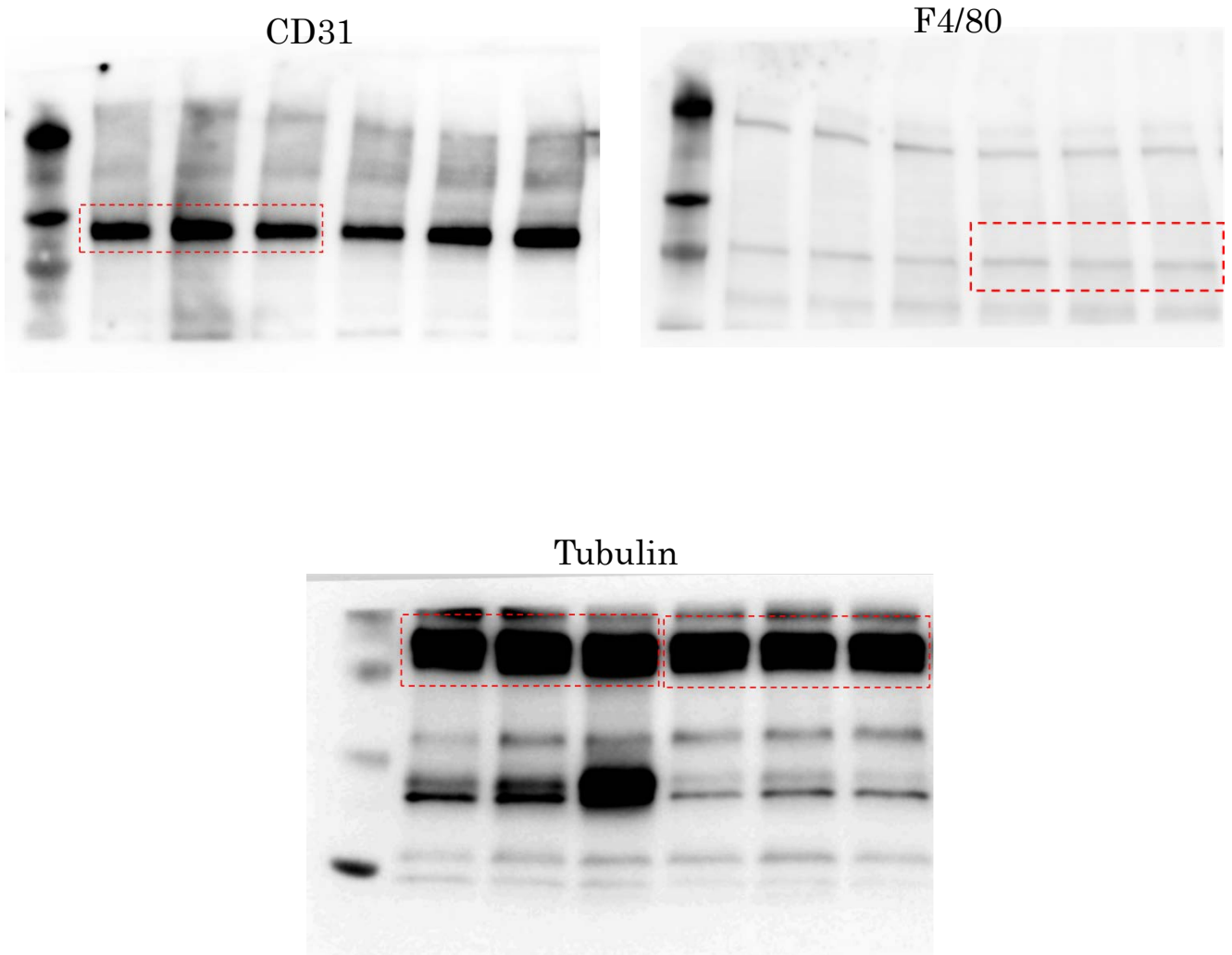
Inflammatory cytokines & chemokines		
Gene symbol	Fold Regulation	p-value
<i>CCL11</i>	-1.19	0.197
<i>CCL2</i>	-11.83	0.009
<i>CCL3</i>	-1.19	0.197
<i>CCR2</i>	-1.31	0.007
<i>CXCR4</i>	-3.80	0.168
<i>IFNG</i>	-1.19	0.197
<i>IL10</i>	1.01	0.859
<i>IL13</i>	2.12	0.239
<i>IL13RA2</i>	-1.11	0.653
<i>IL1A</i>	-52.02	0.005
<i>IL1B</i>	-183.26	0.026
<i>IL4</i>	1.15	0.551
<i>IL5</i>	-1.06	0.974
<i>ILK</i>	1.27	0.448
<i>TNF</i>	-3.48	0.097
TGF-beta superfamily members		
Gene symbol	Fold Regulation	p-value
<i>BMP7</i>	-1.19	0.197
<i>CAV1</i>	5.49	0.102
<i>DCN</i>	-3.16	0.026
<i>ENG</i>	1.18	0.759
<i>GREM1</i>	1.48	0.191
<i>LTBP1</i>	2.13	0.007
<i>SMAD2</i>	1.26	0.099
<i>SMAD3</i>	1.05	0.836
<i>SMAD4</i>	1.42	0.009
<i>SMAD6</i>	1.34	0.400
<i>SMAD7</i>	-2.25	0.062
<i>TGFB1</i>	1.20	0.626
<i>TGFB2</i>	-11.51	0.048
<i>TGFB3</i>	-2.05	0.210
<i>TGFBR1</i>	-1.17	0.485
<i>TGFBR2</i>	-1.40	0.311
<i>TGIF1</i>	-1.01	0.751
<i>THBS1</i>	1.19	0.749
<i>THBS2</i>	-7.23	0.029

ECM structural constituents & remodeling enzyme		
Gene symbol	Fold Regulation	p-value
<i>COL1A2</i>	-4.01	0.000
<i>COL3A1</i>	-97.53	0.003
<i>LOX</i>	-9.37	0.019
<i>MMP1</i>	184.68	0.000
<i>MMP13</i>	2.07	0.262
<i>MMP14</i>	1.05	0.683
<i>MMP2</i>	-5.73	0.024
<i>MMP3</i>	8.37	0.237
<i>MMP8</i>	2.37	0.214
<i>MMP9</i>	1.76	0.301
<i>PLAT</i>	1.29	0.534
<i>PLAU</i>	27.39	0.007
<i>PLG</i>	1.00	0.819
<i>SERPINA1</i>	-4.88	0.013
<i>SERPINE1</i>	-3.68	0.106
<i>SERPINH1</i>	-1.98	0.001
<i>TIMP1</i>	-2.41	0.056
<i>TIMP2</i>	1.64	0.061
<i>TIMP3</i>	-8.06	0.063
<i>TIMP4</i>	2.17	0.060
Growth factors		
Gene symbol	Fold Regulation	p-value
<i>AGT</i>	2.83	0.381
<i>CTGF</i>	-1.88	0.103
<i>EDNI</i>	-2.16	0.155
<i>EGF</i>	-5.11	0.013
<i>HGF</i>	4.70	0.013
<i>PDGFA</i>	-1.74	0.022
<i>PDGFB</i>	-1.19	0.197
<i>VEGFA</i>	-3.79	0.259

Cell adhesion molecules		
Gene symbol	Fold Regulation	p-value
<i>ITGA1</i>	-3.71	0.117
<i>ITGA2</i>	2.18	0.106
<i>ITGA3</i>	3.21	0.031
<i>ITGAV</i>	-2.30	0.008
<i>ITGB1</i>	1.07	0.787
<i>ITGB3</i>	-1.27	0.158
<i>ITGB5</i>	-2.62	0.016
<i>ITGB6</i>	2.24	0.381
<i>ITGB8</i>	1.39	0.506
Transcription factors		
Gene symbol	Fold Regulation	p-value
<i>CEBPB</i>	1.47	0.368
<i>JUN</i>	2.02	0.275
<i>MYC</i>	1.61	0.159
<i>NFKB1</i>	1.01	0.890
<i>SPI1</i>	1.50	0.048
<i>STAT1</i>	-1.66	0.124
<i>STAT6</i>	1.75	0.294
Other fibrosis factors		
Gene symbol	Fold Regulation	p-value
<i>ACTA2</i>	-11.09	0.022
<i>AKT1</i>	1.47	0.244
<i>BCL2</i>	10.74	0.053
<i>FASLG</i>	2.42	0.175
<i>SNAI1</i>	-2.68	0.080

Supplementary Figure 1.

Original images of blots for Figure 7-B and D. Squared frame with redline indicates the cropped area.



Right square frame indicates internal control of CD31
Left square frame indicates internal control of F4/80