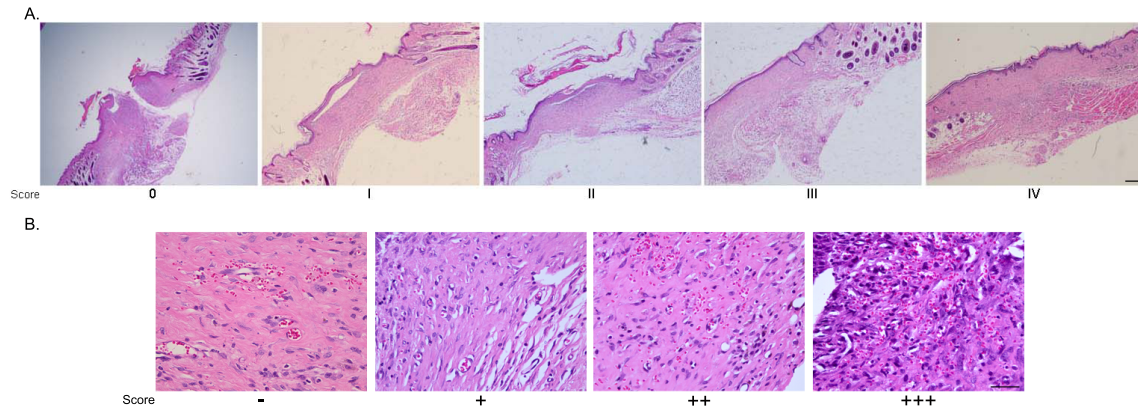


## Supporting Information Legends



### Supplementary figure 1. (A) Dermo-epidermal junction histological scores.

Haematoxylin-eosin stained that represents the dermo-epidermal junction. Image J analysis software was used for estimating unbound area size.

0: > 2,801 area per pixels represents an incomplete junction

I: 1,201-2,800 area per pixels

II: 751-1,200 area per pixels

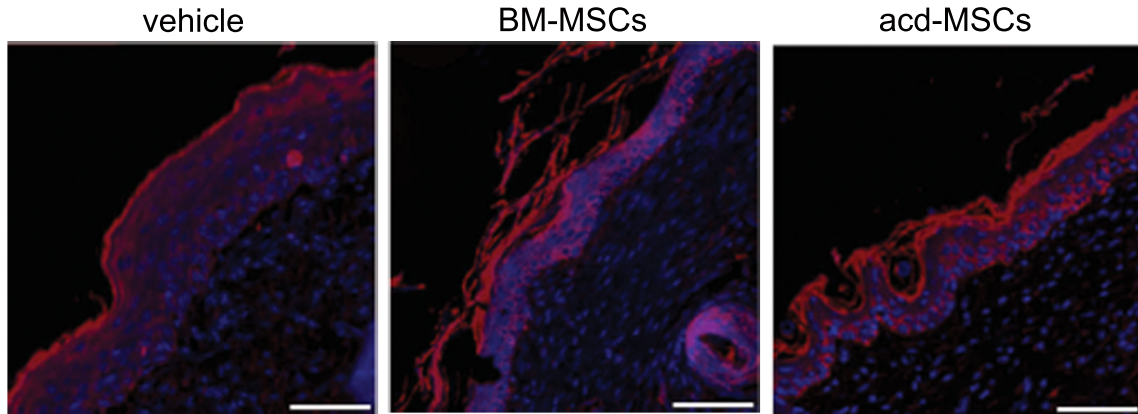
III: 401-750 area per pixels

IV: 0.1-400 area per pixels represents a complete junction

Scale bar 100  $\mu\text{m}$ .

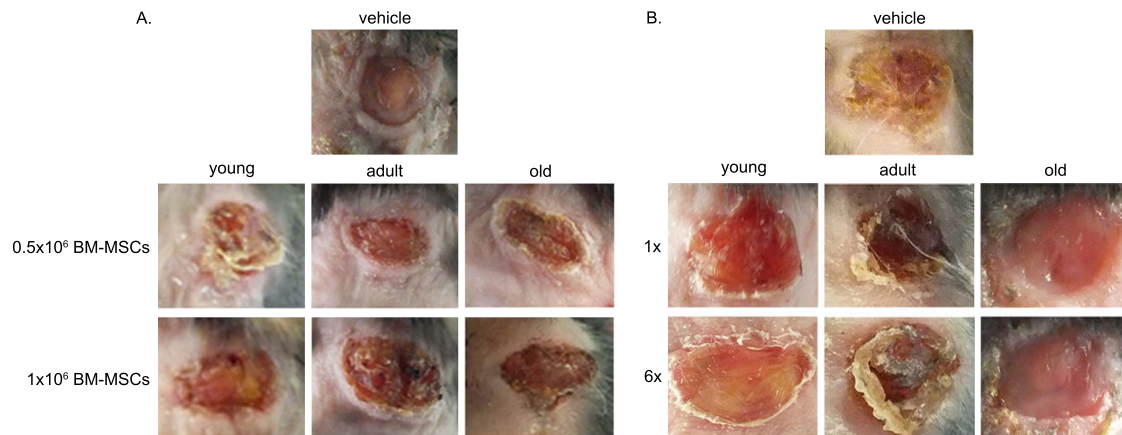
**(B) Histological scores regarding leukocyte infiltration level.** (-) absent, (+)

mild, (++) moderate, (+++) severe. Scale bar 50  $\mu\text{m}$



**Supplementary figure 2. Pan-cytokeratin expression 12 days after treatment.**

Keratinocytes were stained with a monoclonal antibody against epidermal keratin subunits and visualized with a secondary antibody: Alexa Fluor 647. DAPI was used for nuclear staining. The representative results of 5-15 animals per experimental group. Scale bar 50  $\mu\text{m}$ .



**Supplementary figure 3. Granulation tissue formation (A)** After 4 days the bed

of a wound treated with bmMSCs isolated from young, adult and old female C57BL/6 donors and **(B)** the bed of a wound treated with acd-MSCs.

## Tables

### Supplementary table 1. Statistical data of flow cytometry.

Percentage of cells positive for the marker

Age	CD90.2	Sca-1	ASMA
Young	65.2	75.7	95.4
Adult	63.8	77.3	96.1
Old	60.2	93.7	88.3

Mean fluorescence intensity (isotype / marker)

Age	CD90.2		Sca-1		ASMA		CD45.2		CD11b	
Young	21.5	73.6	7.8	126.5	6.8	387.5	5.3	10.9	5.1	7.8
Adult	16.1	49.4	4.2	59.2	6.8	922.0	4.2	4.6	5.1	6.8
Old	16.8	46.0	2.8	162.8	5.3	57.1	4.2	5.9	7.0	11.3

### Supplementary table 2. Primer and amplicon characteristics.

Gene	GenBank	Sequences 5'→3'	Amplicon Tm size (°C) (bp)		Reference
KGF (FGF-7)	NM_008008 .4	F- TGAGTCCGGAGCAAACG GCT R- TGAGTCCGGAGCAAACG GCT	86	131	[1]
IGF-1	NM_010512 .3	F- TGGATGCTCTCAGTTCG TG R- GCTTTGGGCATGTCAGTG TG	88	220	[2]
HGF	NM_001289 458.1	F- TCTGCTCGAACTGCAAG CATGA R- TCCTGATACACCTGTTGG CACACT	86	250	<a href="http://pga.mgh.harvard.edu/primerbank/">http://pga.mgh.harvard.edu/primerbank/</a> PRIMER BANK
VEGF alpha	NM_001025 257.3	F- AGGAGAGCAGAAGTCCC ATGAAGT R- GGTGAGGTTTGATCCGC ATGATCT	88	242	[3]
VEGF delta	NM_010216 .1	F- CCGGTTGAAGCTCAAAA GTCTTGC R- CCTCCACACCGGAAGAC ATTTACA	86	231	[3]
ANG 1	XM_006520 323.1	F- TGCACTAAAGAAGGTGT TTTGCT R- CCTCCCCATTACATCC ATATT	83	176	<a href="http://pga.mgh.harvard.edu/primerbank/">http://pga.mgh.harvard.edu/primerbank/</a> PRIMER BANK
ANG 2	NM_007426 .4	F- CCTCGACTACGACGACT CAGT R- TCTGCACCACATTCTGTT GGA	84	148	<a href="http://pga.mgh.harvard.edu/primerbank/">http://pga.mgh.harvard.edu/primerbank/</a> PRIMER BANK
Collagen type1	NM_007742 .3	F- AGAACATCACCTATCAC TGCAAGA R- GTGGTTTTGTATTGATG ACTGTCT	89 <sup>a</sup>	205	[4]
MMP1	NM_008607 .2	F- GAACATCCATCCCCTGA CCTT R- AAGAGGGTCTTCCCCTG CTT	85	173	our design PRIMER PREMIER 5.0
MMP3	NM_010809 .1	F- ACATGGAGACTTTGTCCC TTTTG R- TTGGCTGAGTGGTAGAG TCCC	86	192	<a href="http://pga.mgh.harvard.edu/primerbank/">http://pga.mgh.harvard.edu/primerbank/</a> PRIMER BANK
GAPDH	NM_001289 726.1	F- ACTCCACTACGGCAA TTC R- TCTCCATGGTGGTGAAG ACA	86	171	[5]