

Figure S1. Alkali-burn mouse model set-up and MRI assessment of corneal damage over time. 7T MRI T_{2w} -images of corneal damage following alkali treatment at Days 0, 1, 3, 7 and 14. Red arrow indicates the injured eye of animal models with application of NaOH paper disc for 30 sec. Inset shows visible corneal damage at Day 14 post alkali-burn.

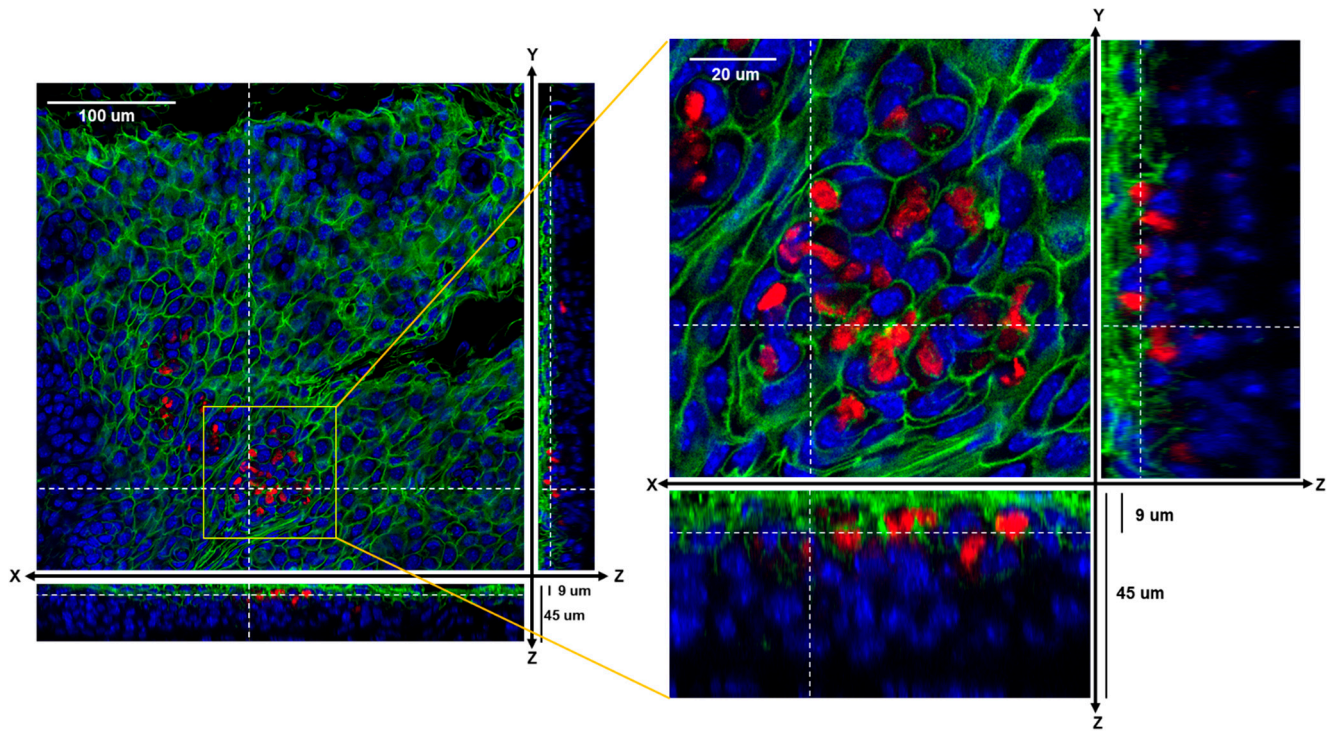
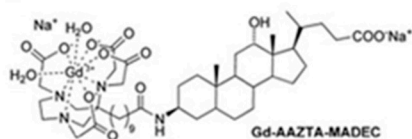
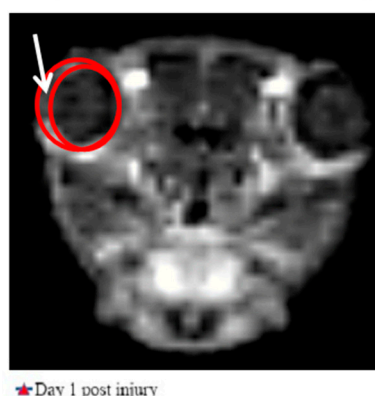


Figure S2: Confocal microscopy (Leica Sp5) images of corneal whole mounts, following treatment of the injured corneas with PKH26-labelled (Red) MSC-EVs at 40× magnification (scale bar: 100nm). A zoomed insert is shown for detail (scale bar: 20nm). F-actin and nuclei were stained with phalloidin-FITC (green) and DAPI (blue), respectively. The axes represent 3D corneal structure.

A Gd-AAZTA-MADEC chemical structure



B Region Of Interest for MRI quantification



C MRI Signal enhancement before Gd-AAZTA-MADEC injection

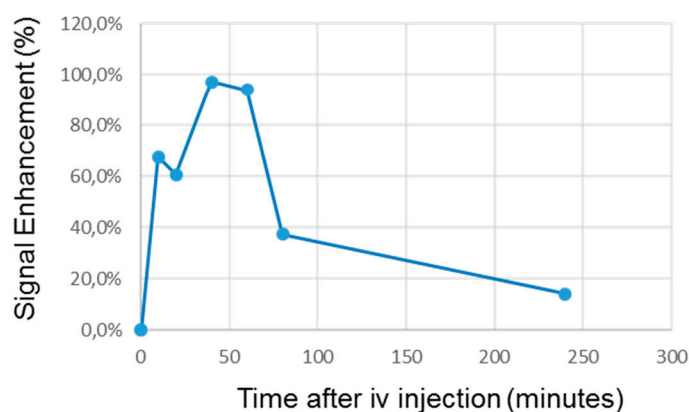


Figure S3: MRI-based corneal angiogenesis evaluation with Gd-AAZTA-MADEC set-up (A) Chemical structure of Gd-AAZTA-MADEC. (B) Representative Region of Interest (ROI) drawn on a 1T MRI image of cornea. Arrow indicates quantified region. (C) Representative MRI signal enhancement between injured and uninjured contralateral eyes followed for 4 h after injection of Gd-AAZTA-MADEC at Day 3, where Signal Intensities post-Gd-AAZTA-MADEC injection were normalized against signal intensities measured in the same regions before the injection (time=0).

Table S1: qPCR primer sequences using SYBR Green® technology for *Mus musculus* (Mm) and *Homo sapiens* (Hs).

<u>Mm PRIMER</u>	Forward Sequence	Reverse Sequence
<i>Inflammation gene</i>		
Tnfa	ACTTCTGCTCTAGGGTGAGTGC	GGCCAGGGGGGTATTCTTG
Il1b	AGTTGACGGACCCCAAAG	AGCTGGATGCTCTCATCAGG
Il1r2	GCAAGAAGCAGCAAGGTACA	CCGCACCAACTTCCTGAG
Il6	GCTACCAAAGTGGATATAATCAGGA	CCAGGTAGCTATGGTACTCCAGAA
Spp1 (Opn)	GGAAACCAGCCAAGGTAAGC	TGCCAATCTCATGGTCGTAG
Tgfβ	TGGAGCAACATGTGGAAGTC	GTCAGCAGCCGGTTACCA
<i>Angiogenic gene</i>		
Vegfa	AAAAACGAAAGCGCAAGAAA	TTTCTCCGCTCTGAACAAGG
Vegfd	GCAACTTTCTATGACACTGAAACAC	TCTCTCTAGGGCTGCATTGG
Flt1	GGCCCGGGATATTTATAAGA	CCATCCATTTTAGGGGAAGT
Flt4	TGTCACCTTCGACTGGGATT	TGCTGGAGAGTTCTGTGTGG
Kdr(Flk1)	GGGGTATGGAGACGAGCTG	GCACAGATCTGACTAAATTGCTG
<i>Housekeeping</i>		
Gapdh	AGCCCAATCGCTCAG	GCCCAATACGACCAA

<u>Hs PRIMER</u>	Forward Sequence	Reverse Sequence
<i>Inflammation gene</i>		
TNFA	AGAACCGGCAAGAAATCAAG	CTGGTAGGAGTCCTTCTTGTC
PTGS2 (COX2)	GCTTTATGCTGAAGCCCTATGA	TCCAAGTCTGCTAGACATTTCC
IL1B	TACCTGTCCTGCGTGTTGAA	TCTTTGGGTAATTTTGGGATCT
<i>Housekeeping</i>		
GAPDH	AGCCACATCGCTCAGACAC	GCCCAATACGACCAAATCC