Figure S1. Effect of the NBD peptide and the control CBD peptide on the expression and the localization of NF-kB p65. (A) Localization of NF-kB p65. (B) Western blot analysis of p-IkB-α activation. The images of p-IkB-α and IkB-α were produced from the different blots. β-actin was used as a loading control. Full size images of the western blots are shown in Fig. S7.

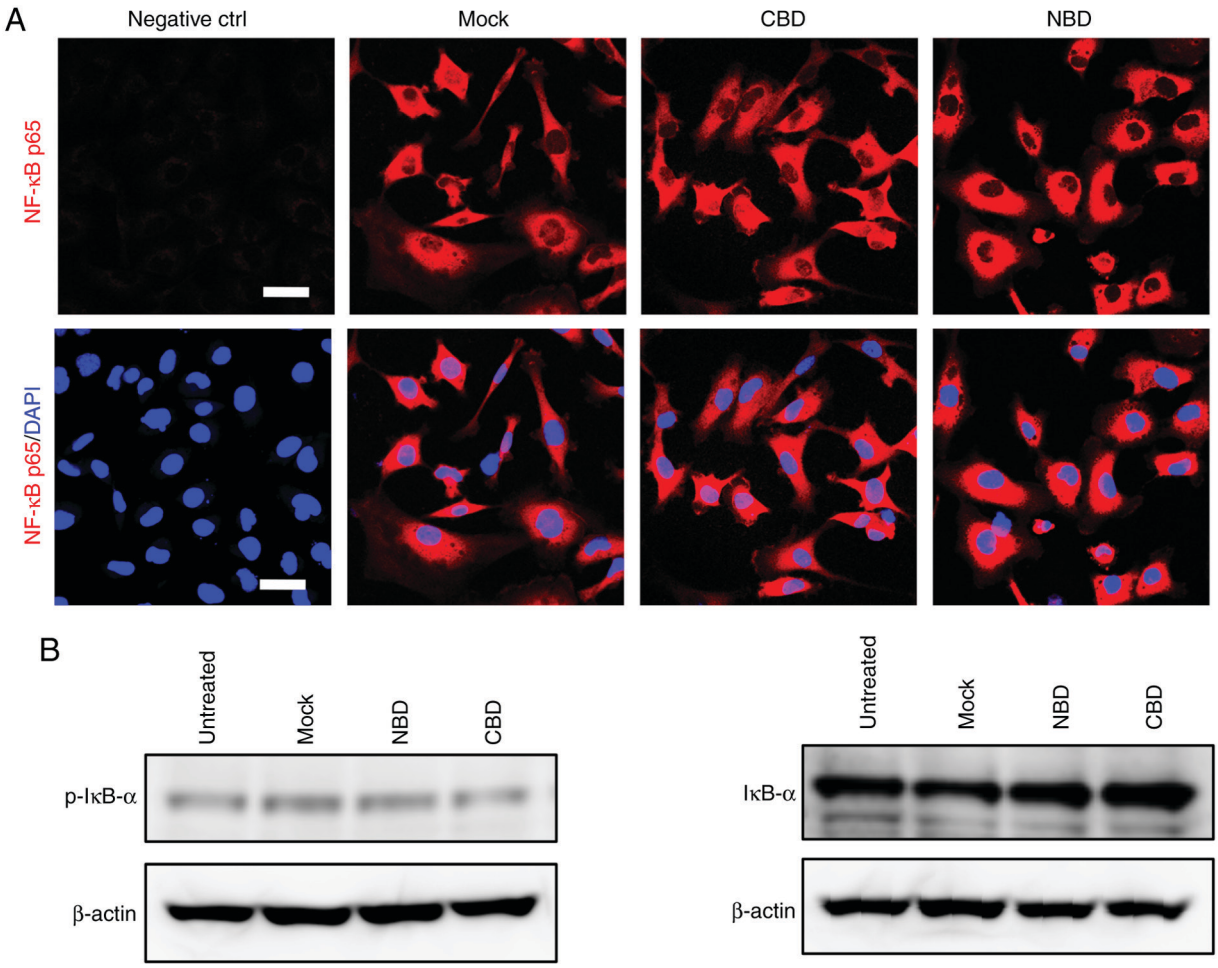

Figure S2. Effect of the NBD peptide and the control CBD peptide on the expression and the localization of EGR1 and ELK3. (A) Immunofluorescence of EGR1. (B) Fluorescence intensity of EGR1 per cell analyzed by ImageJ software; n=35, 35 and 32 cells for the Mock, CBD and NBD-treated samples, respectively. (C) Immunofluorescence staining of ELK3. (D) Fluorescence intensity of ELK3 per cell analyzed by ImageJ software; n=31, 42 and 38 cells for the Mock, CBD and NBD-treated samples, respectively. Nuclei were stained with DAPI. Scale bars, 50 μm; ns, not significant.

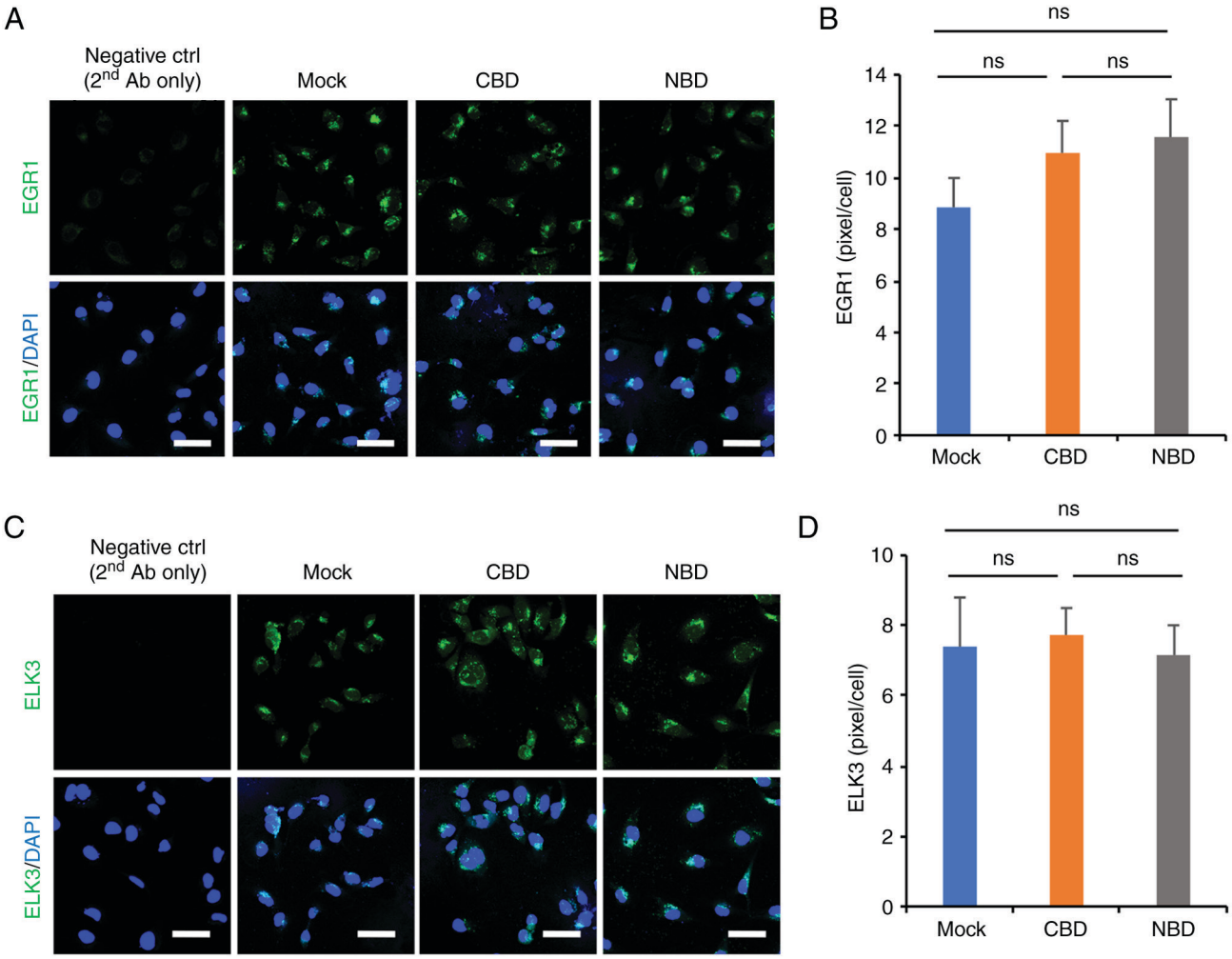

Figure S3. Inhibition of MMP-14 expression by mithramycin A1. MDA-MB-231-D3H2LN cells were treated with 50 nM mithramycin A1 for 2 days. β-actin was used as a loading control. Full size images of the western blots are shown in Fig. S7.

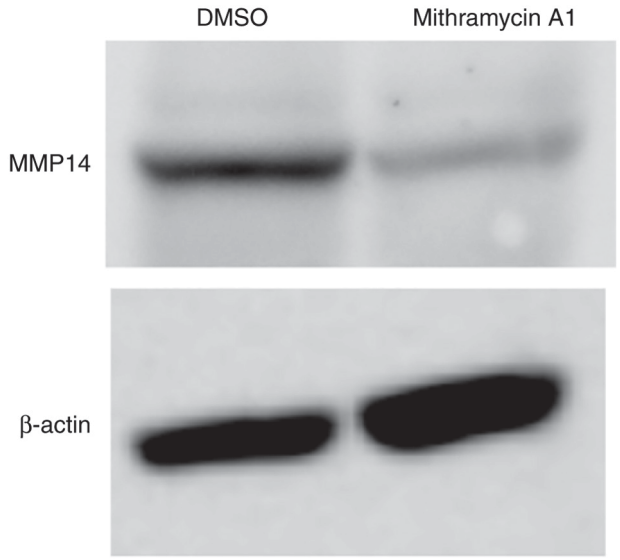

Figure S4. RT-qPCR analysis of the effect of fumagillin on the expression of MMP-14 mRNA. MDA-MB-231-D3H2LN cells were treated with the indicated concentrations of fumagillin for 2 days; ns, not significant.

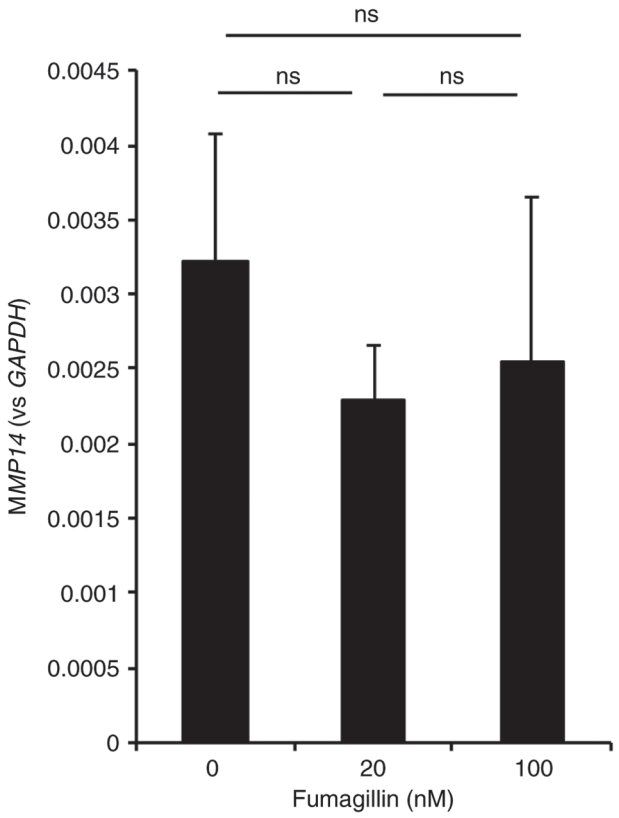

Figure S5. Tumor angiogenesis in primary tumor tissues. (A) CD31 staining. (B) Vessel density. Scale bars, 50 μm; PBS, n=10 fields; Empty-GlycoLipos, n=11 fields; NBD-GlycoLipos, n=10 fields; ns, not significant.

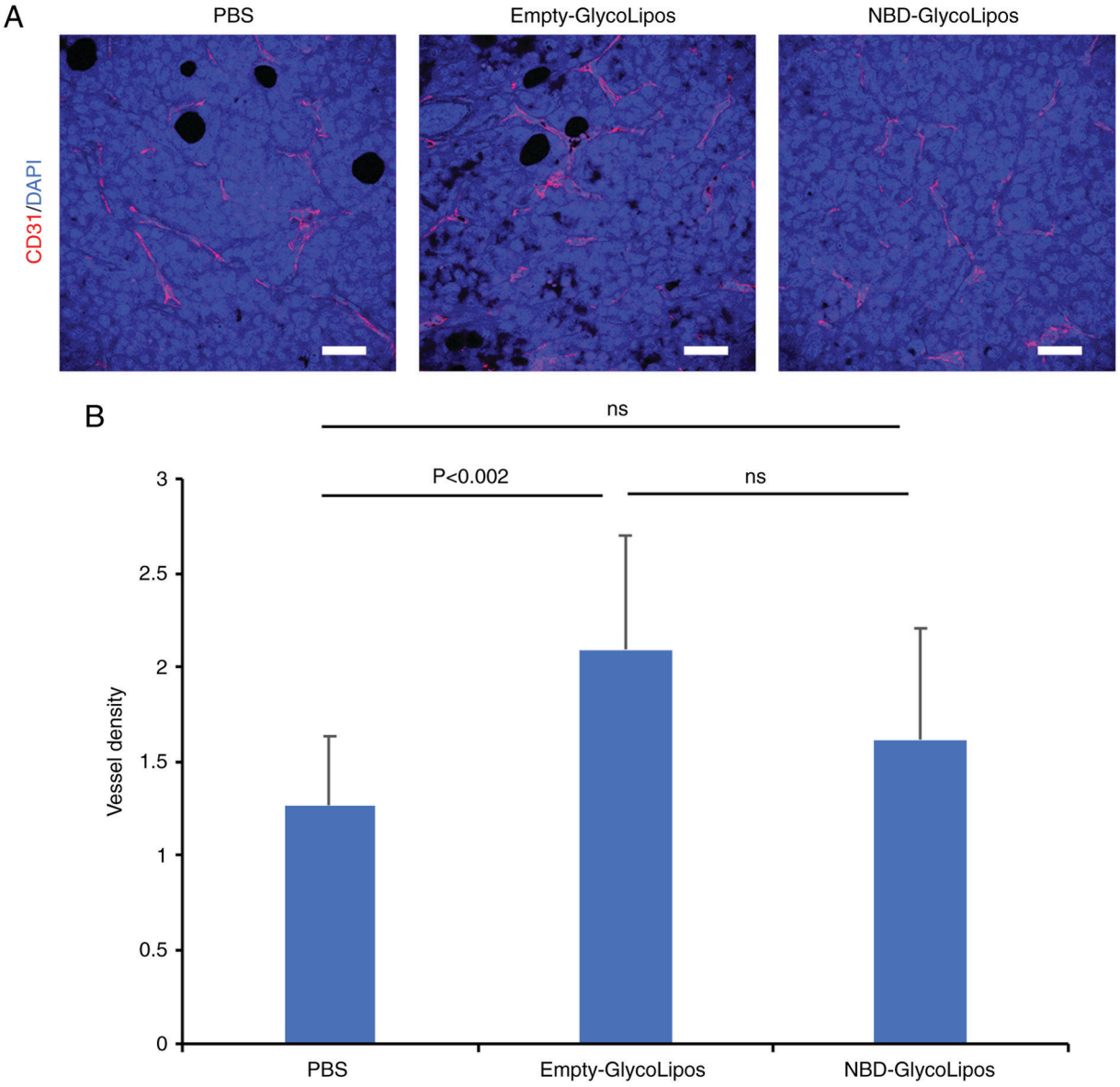

Figure S6. Full size images of the western blots shown in Figs. 1A, 2C, 3A, and 4A and D.

Fig. 1A

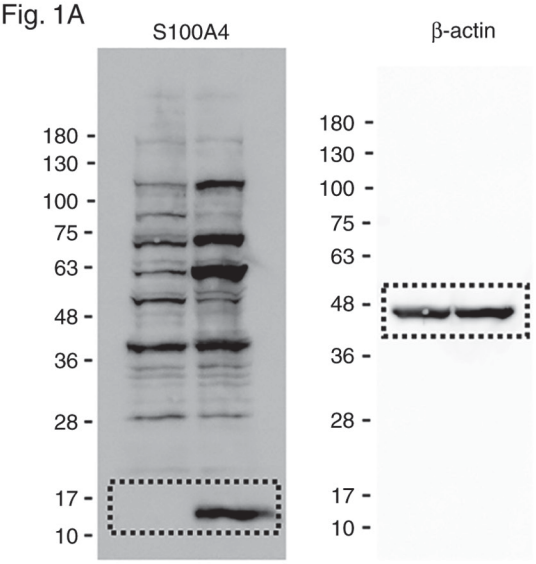

Fig. 2C

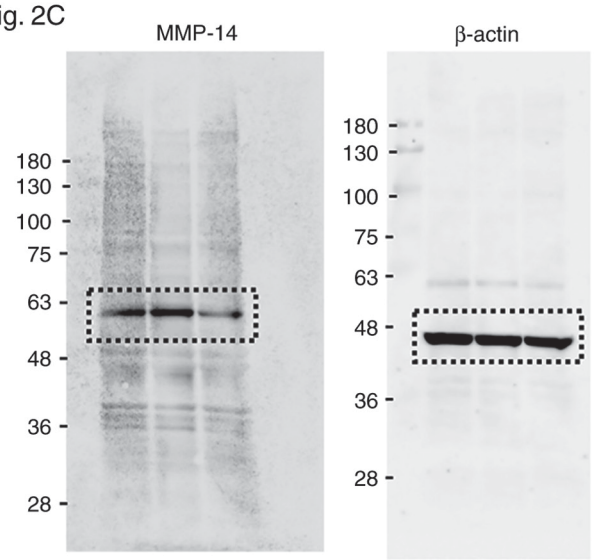

Fig. 3A

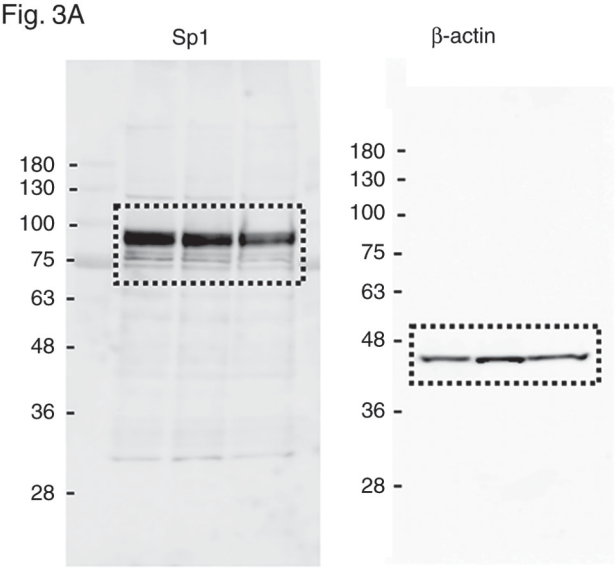

Fig. 4A

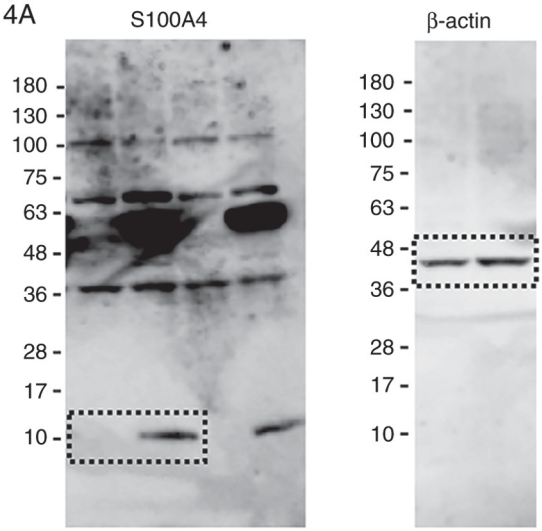

Fig. 4D

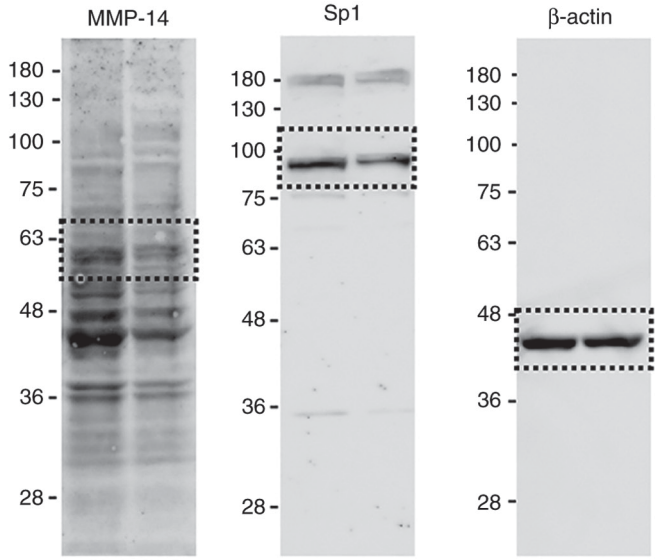

Figure S7. Full size images of the western blots shown in Figs. S1B and S3.

Fig. S1B

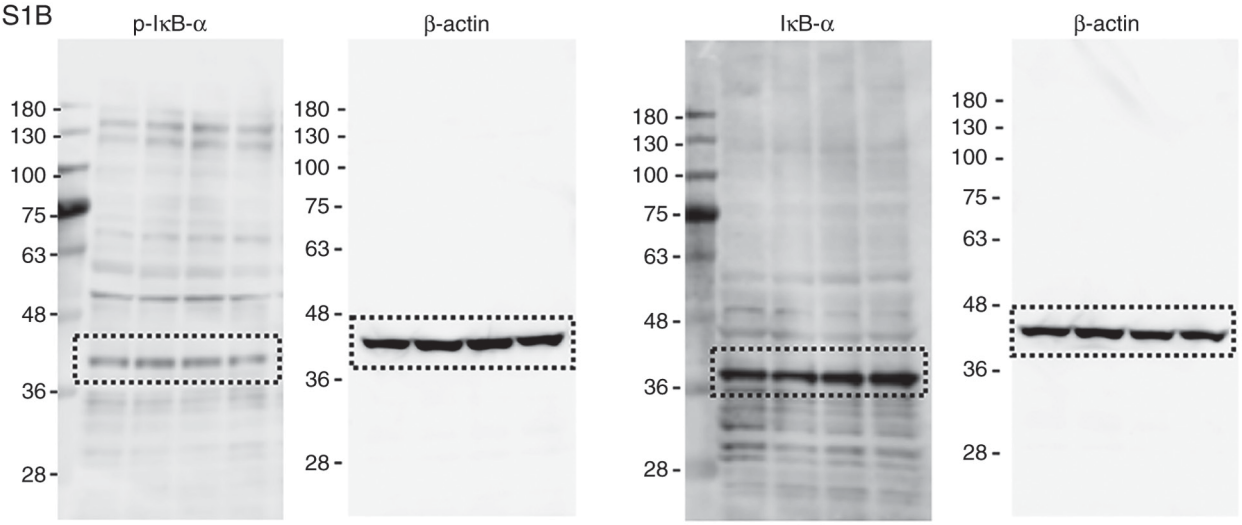

Fig. S3

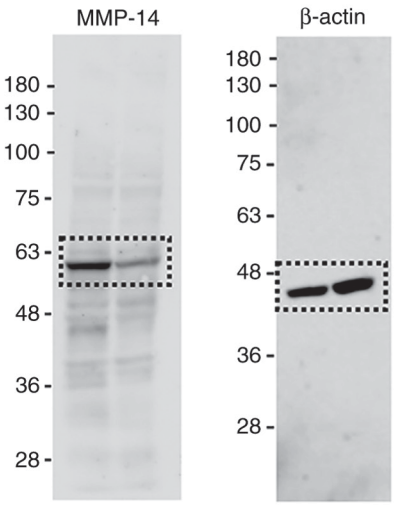

Table SI. Sequences of primers used for RT-qPCR.

Gene	Forward/reverse	Sequence (5'-3')	Accession no.
MMP-1	Forward	ACTCTGGAGTAATGTCACACCT	NM_002421.3
	Reverse	GTTGGTCCACCTTTCATCTTCA	
MMP-2	Forward	GACATACATCTTTGCTGGAGAC	NM_004530.5
	Reverse	TTCAGGTAATAGGCACCCTT	
MMP-7	Forward	ATGTGGAGTGCCAGATGTTGC	NM_002423.3
	Reverse	AGCAGTTCCCCATACAACTTTC	
MMP-9	Forward	CTTCACTTTCCTGGGTAAGG	NM_004994.2
	Reverse	CACTTCTTGTCGCTGTCAAA	
MMP-13	Forward	AAATTATGGAGGAGATGCCCATT	NM_002427.3
	Reverse	TCCTTGGAGTGGTCAAGACCTAA	
MMP-14	Forward	CCTTGGACTGTCAGGAATGAGG	NM_004995.3
	Reverse	TTCTCCGTGTCCATCCACTGGT	
TIMP-1	Forward	GGAGAGTGTCTGCGGATACTTC	NM_003254.2
	Reverse	GCAGGTAGTGATGTGCAAGAGTC	
TIMP-2	Forward	ACCCTCTGTGACTTCATCGTGC	NM_003255.4
	Reverse	GGAGATGTAGCACGGGATCATG	
GAPDH	Forward	CGCTCTCTGCTCCTCCTGTT	NM_002046.6
	Reverse	CCATGGTGTCTGAGCGATGT	
ACTB	Forward	ACTCTTCCAGCCTTCCTTCC	NM_007393.5
	Reverse	AGCACTGTGTTGGCGTACAG	

MMP, matrix metalloproteinase; TIMP, tissue inhibitor of metalloproteinases.