Supplement

Table S1: Nucleotide sequence of codon-optimized HMGB2

Codon-optimized HMGB2
ATGGGGAAAGGCGACCCGAACAAACCGCGCGGTAAAATGTCGTCCTACGCGTTCT TTGTCCAAACGTGTCGTGAGGAACACAAAAAAAAACACCCGGACTCTTCGGTGAACT TTGCGGAATTTAGCAAAAAGTGCTCTGAACGCTGGAAAACCATGAGTGCAAAGAG AAAAGCAAATTTGAAGATATGGCGAAAGCGATAAAGCCCGTTATGATCGCGAAAT GAAGAACTACGTTCCACCGAAAGGGGACAAGAAAGGCAAAAAAAAAGACCCGAAT GCTCCCAAACGTCCTCCATCAGCCTTCTTCCTGTTTTGCAGTGAACATCGCCCGAAAA TCAAAAGCGAACATCCGGGCTTATCGATTGGCGATACTGCCAAGAAATTGGGAGAA ATGTGGTCAGAACAGAGTGCTAAGGACAAACAGCCCTATGAACAGAAAGCGGCCAA ACTGAAAGAGAAGTACGAGAAAGATATTGCGGCTTATCGCGCAAAAGGCAAAGC GAAGCAGGAAAGAAAGGTCCTGGTCGGCCAACCGGTTCCAAAAAGAAGAATGAA CCGGAGGATGAAGAAGAAGAAGAGGAAGAAGAGGATGAGGATGAGGAAGAAG AAGATGAGGACGAAGAATAA

Table S2: Forward and reverse primers used for quantitative real-time PCR and recombinant
protein expression

	Forward (5'-3`)	Reverse (5'-3`)
HMGB2 real-time PCR	TTACGTTCCTCCCAAAGGTG	TCTTTGGCTGACTGCTCAGA
rec. expression HMGB2	ATGGGGAAAGGCGACC	TTATTCTTCGTCCTCATCTTCTTCT
rec. expression A-Box	ATGGGGAAAGGCGACCCG	TTAGTCCCCTTTCGGTGGAA
rec. expression B-Box	GGGGACAAGAAAGGCAAAA	TTACCGACCAGGACCTTTCTT
rec. expression Acidic-tail	GCAGGAAAGAAAGGTCCTG	AGTAACGGCCGCCAGTGT (binds in vector sequence)

Table S3: Calculated molecular weight and extinction coefficient of fusion-proteins and full-
length HMGB2 (ExPASy Protparam tool)

	MW (kDa)	Extinction coefficient
HMGB2 (fusion-protein)	37.43	21555
HMGB2 (full-length)	24.03	20065

A-Box (fusion-protein)	23.21	11585
B-Box (fusion-protein)	23.97	11460
Acidic-tail (fusion-protein)	18.01	1490*

* Peptide contains no Tryptophan residues, this could result in more than 10 % error in computed

ext. coefficient

Table S4: Amino acid sequences of recombinant expressed proteins/peptides

Name	Amino acid sequence
HMGB2	MGKGDPNKPR GKMSSYAFFV QTCREEHKKK HPDSSVNFAE FSKKCSERWK TMSAKEKSKF EDMAKSDKAR YDREMKNYVP PKGDKKGKKK DPNAPKRPPS AFFLFCSEHR PKIKSEHPGL SIGDTAKKLG EMWSEQSAKD KQPYEQKAAK LKEKYEKDIA AYRAKGKSEA GKKGPGRPTG SKKKNEPEDE EEEEEEEDED EEEEDEDEE
A-Box	MGKGDPNKPR GKMSSYAFFV QTCREEHKKK HPDSSVNFAE FSKKCSERWK TMSAKEKSKF EDMAKSDKAR YDREMKNYVP PKGD
B-Box	GDKKGKKKDP NAPKRPPSAF FLFCSEHRPK IKSEHPGLSI GDTAKKLGEM WSEQSAKDKQ PYEQKAAKLK EKYEKDIAAY RAKGKSEAGK KGPGR
Acidic-tail	AGKKGPGRPT GSKKKNEPED EEEEEEEEDE DEEEEDEDEE