Table S1. Primer sequences and shRNA used in this study

Gene	Primer (5'-3')	
mCD206	Forward	ACGCAGTGGTTGGCAGTGGG
	Reverse	TTGCCAGGTCCCCACCCTCC
mArg1	Forward	CAGTCTGGCAGTTGGAAGC
	Reverse	TTGGCAGATATGCAGGGAG
mCCL22	Forward	CAGGCAGGTCTGGGTGAA
	Reverse	TAAAGGTGGCGTCGTTGG
mIL10	Forward	CAACATACTGCTAACCGACTC
	Reverse	CATGGCCTTGTAGACACCT
mTNFα	Forward	CCTCTTCTCATTCCTGCTTG
	Reverse	CACTTGGTGGTTTGCTACG
mIL1β	Forward	ATCCAGCTTCAAATCTCGC
	Reverse	ATCTCGGAGCCTGTAGTGC
hCD206	Forward	GGGTTGCTATCACTCTCTATGC
	Reverse	TTTCTTGTCTGTTGCCGTAGTT
hMMP9	Forward	ATGCGTGGAGAGTCGAAATC
	Reverse	TACACGCGAGTGAAGGTGAG
hIL10	Forward	GGTTGCCAAGCCTTGTCTGA
	Reverse	GGGAGTTCACATGCGCCT
hArg1	Forward	ACCATAGGGATTATTGGAGC
	Reverse	TGTCATTAGGGATGTCAGCA
hCCL22	Forward	AGCCAATGAAGAGCCTAC
	Reverse	GCAGAGGATGGGTTAGAG
hTNFα	Forward	CGAGTGACAAGCCTGTAGCC
	Reverse	TGAAGAGGACCTGGGAGTAGAT
hIL1β	Forward	GCTTATTACAGTGGCAATGAGGAT
	Reverse	CCTCGTTATCCCATGTGTCG
mCxcl1	Forward	GCACCCAAACCGAAGTCA
	Reverse	AAGCCAGCGTTCACCAGA
hCxcl1	Forward	CCAAACCGAAGTCATAGCC
	Reverse	TTCCTCCTCCCTTCTGGTC
mIFNγ	Forward	AGCAACAACATAAGCGTCAT
	Reverse	CCTCAAACTTGGCAATACTC
GAPDH	Forward	GGAGCGAGATCCCTCCAAAAT
	Reverse	GGCTGTTGTCATACTTCTCATGG
hCxcl1-E_2box1	Forward	GGGGTAGAAACGGAGAGGCT
	Reverse	GCCCAGCTCAATAGGTAAGA
hCxcl1-E_2box2	Forward	CCTTCTCCGTTCCCAGCCCC
	Reverse	CGCCTTCTGCCCCAGATCCC
shZeb1-1	CGGCGCAATAACGTTACAAAT	
shZeb1-2	GGCGCAATAACGTTACAAA	

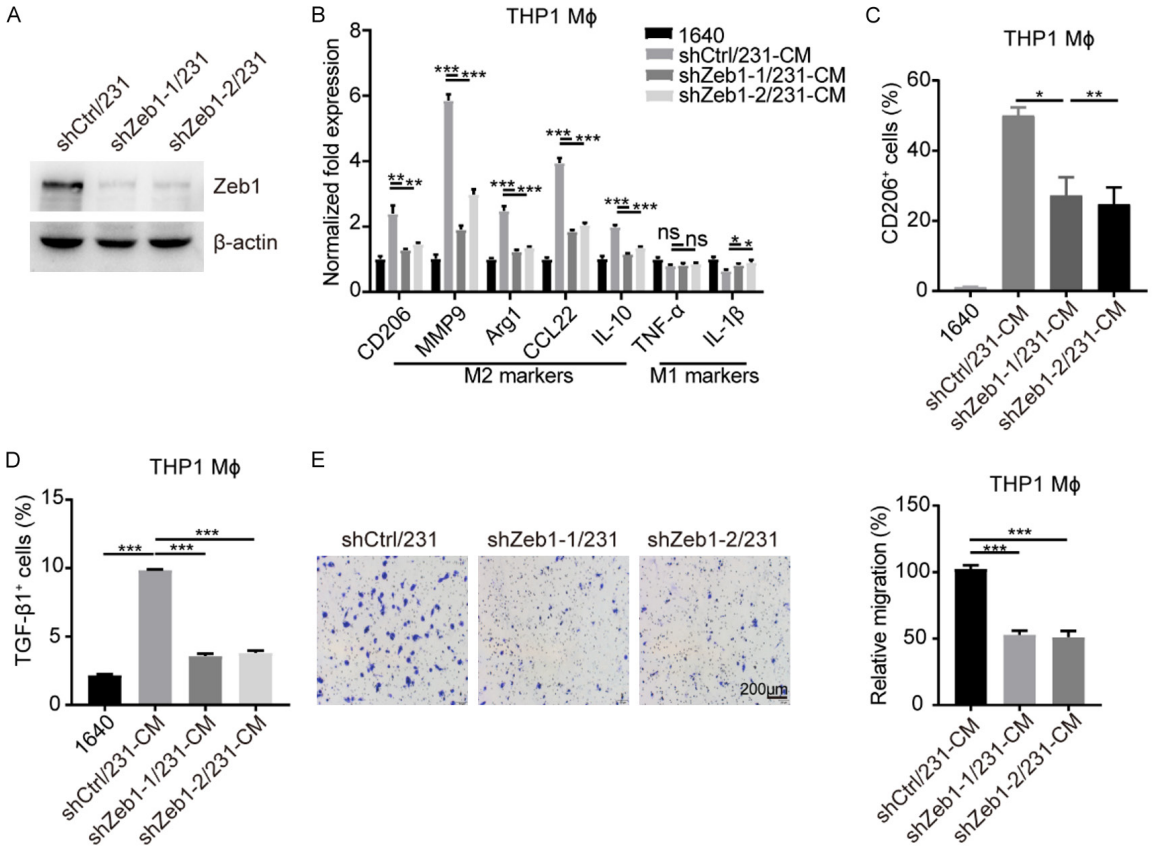

Figure S1. (A) Western blotting of Zeb1 expression in Zeb1-interfered MDA-MB-231 cells. (B) Relative mRNA levels of M1- and M2-TAM markers in THP1 macrophages treated with CM from Zeb1-interfered MDA-MB-231 cells. (C, D) Flow cytometry analysis of $CD206^+$ (C) and TGF-$\beta1^+$ (D) cells in THP1 macrophages treated with CM from Zeb1-interfered MDA-MB-231 cells. (E) Transwell migration assay in THP1 macrophages treated with CM from Zeb1-interfered MDA-MB-231 cells. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A-E). Data are representative of three (A-E) independent experiments. Source data are provided as a Source Data file.

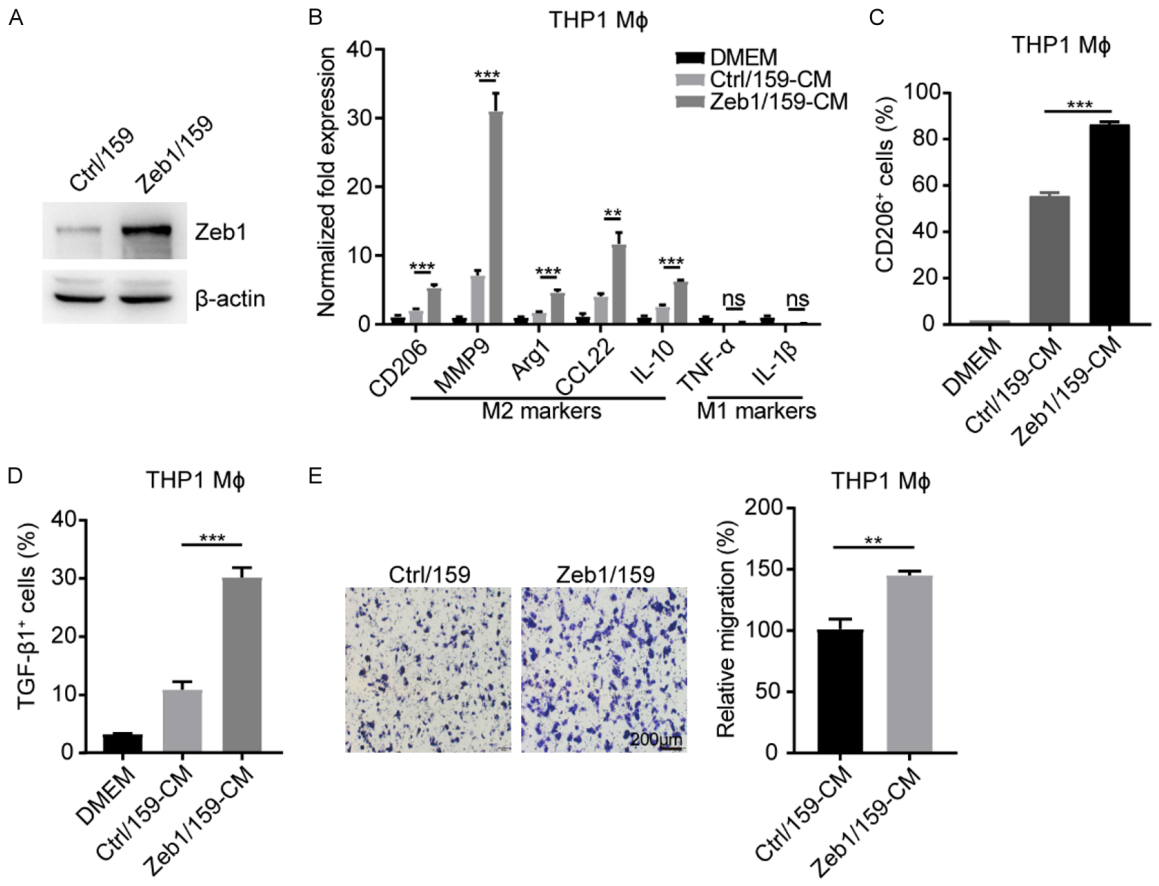

Figure S2. (A) Western blotting of Zeb1 expression in Zeb1-expressing SUM-159 cells. (B) Relative mRNA levels of M1- and M2-TAM markers in THP1 macrophages treated with CM from Zeb1-expressing SUM-159 cells. (C, D) Flow cytometry analysis of (C) CD206$^+$ and (D) TGF-β1$^+$ cells in THP1 macrophages treated with CM from Zeb1-expressing SUM-159 cells. (E) Transwell migration assay in THP1 macrophages treated with CM from Zeb1-expressing SUM-159 cells. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A-E). Data are representative of three (A-E) independent experiments. Source data are provided as a Source Data file.

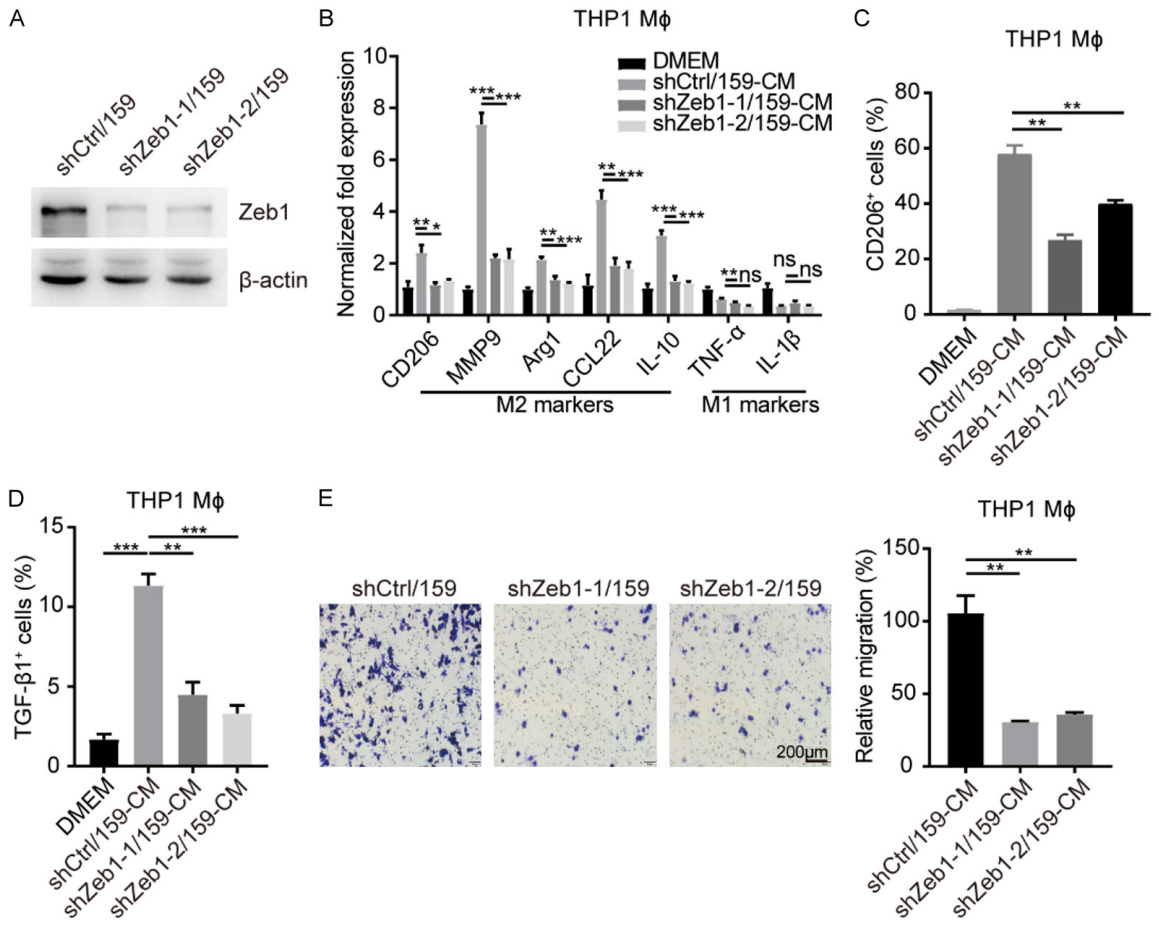

Figure S3. (A) Western blotting of Zeb1 expression in Zeb1-interfered SUM-159 cells. (B) Relative mRNA levels of M1- and M2-TAM markers in THP1 macrophages treated with CM from Zeb1-interfered SUM-159 cells. (C, D) Flow cytometry analysis of (C) CD206⁺ and (D) TGF-β1⁺ cells in THP1 macrophages treated with CM from Zeb1-interfered SUM-159 cells. (E) Transwell migration assay in THP1 macrophages treated with CM from Zeb1-interfered SUM-159 cells. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A-E). Data are representative of three (A-E) independent experiments. Source data are provided as a Source Data file.

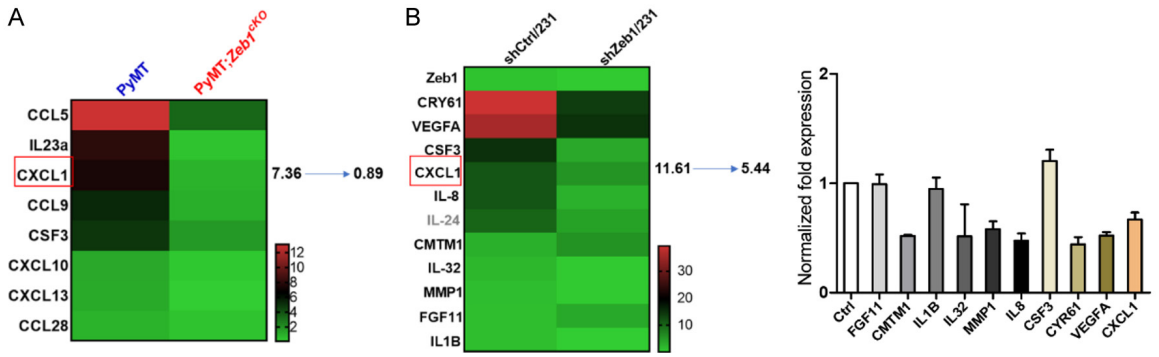

Figure S4. (A, B) RNA sequencing analysis of paracrine factors expressed in the indicated breast cancer tissues (A) and Zeb1-interfered MDA-MB-231 cells (B). Source data are provided as a Source Data file.

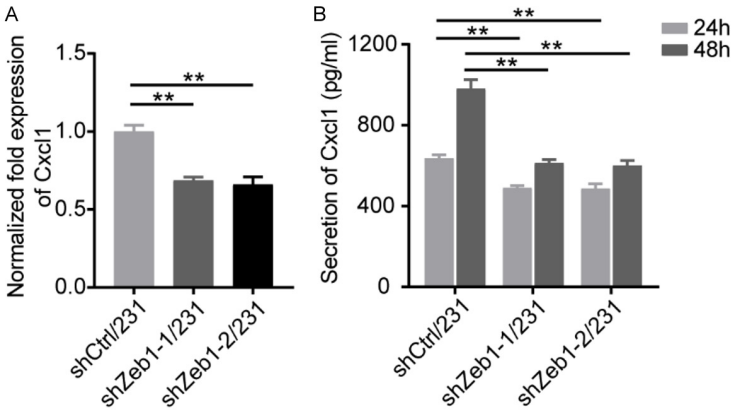

Figure S5. (A) Relative mRNA levels of Cxcl1 in Zeb1-interfered MDA-MB-231 cells. (B) ELISA analysis of Cxcl1 concentration in CM from Zeb1-interfered MDA-MB-231 cells. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A, B). Data are representative of three (A, B) independent experiments. Source data are provided as a Source Data file.

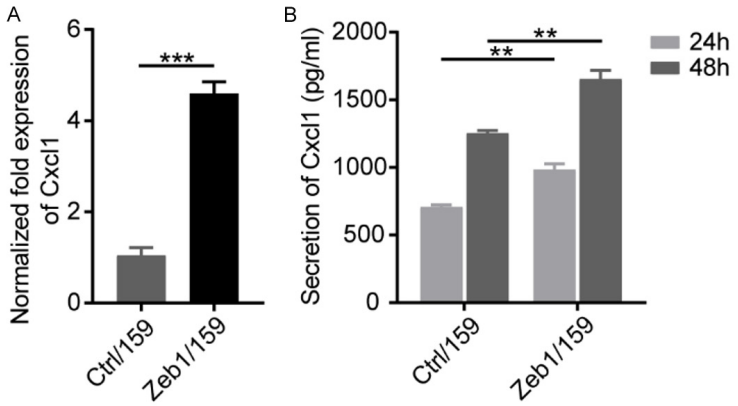

Figure S6. (A) Relative mRNA levels of Cxcl1 in Zeb1-expressing SUM-159 cells. (B) ELISA analysis of Cxcl1 concentration in CM from Zeb1-expressing SUM-159 cells. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A, B). Data are representative of three (A, B) independent experiments. Source data are provided as a Source Data file.

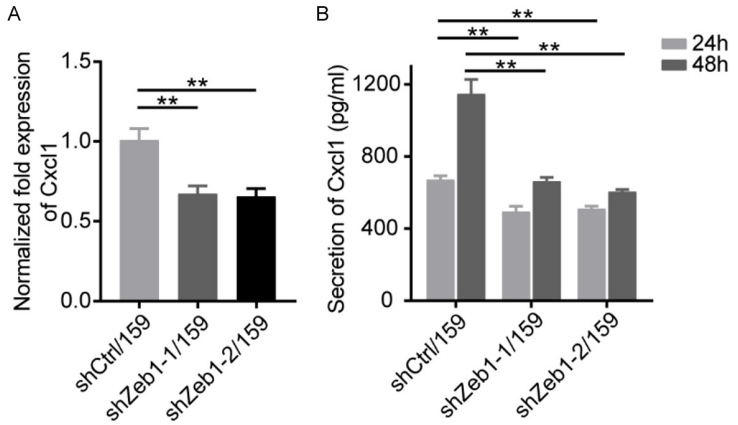

Figure S7. (A) Relative mRNA levels of Cxcl1 in Zeb1-interfered SUM-159 cells. (B) ELISA analysis of Cxcl1 concentration in CM from Zeb1-interfered SUM-159 cells. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A, B). Data are representative of three (A, B) independent experiments. Source data are provided as a Source Data file.

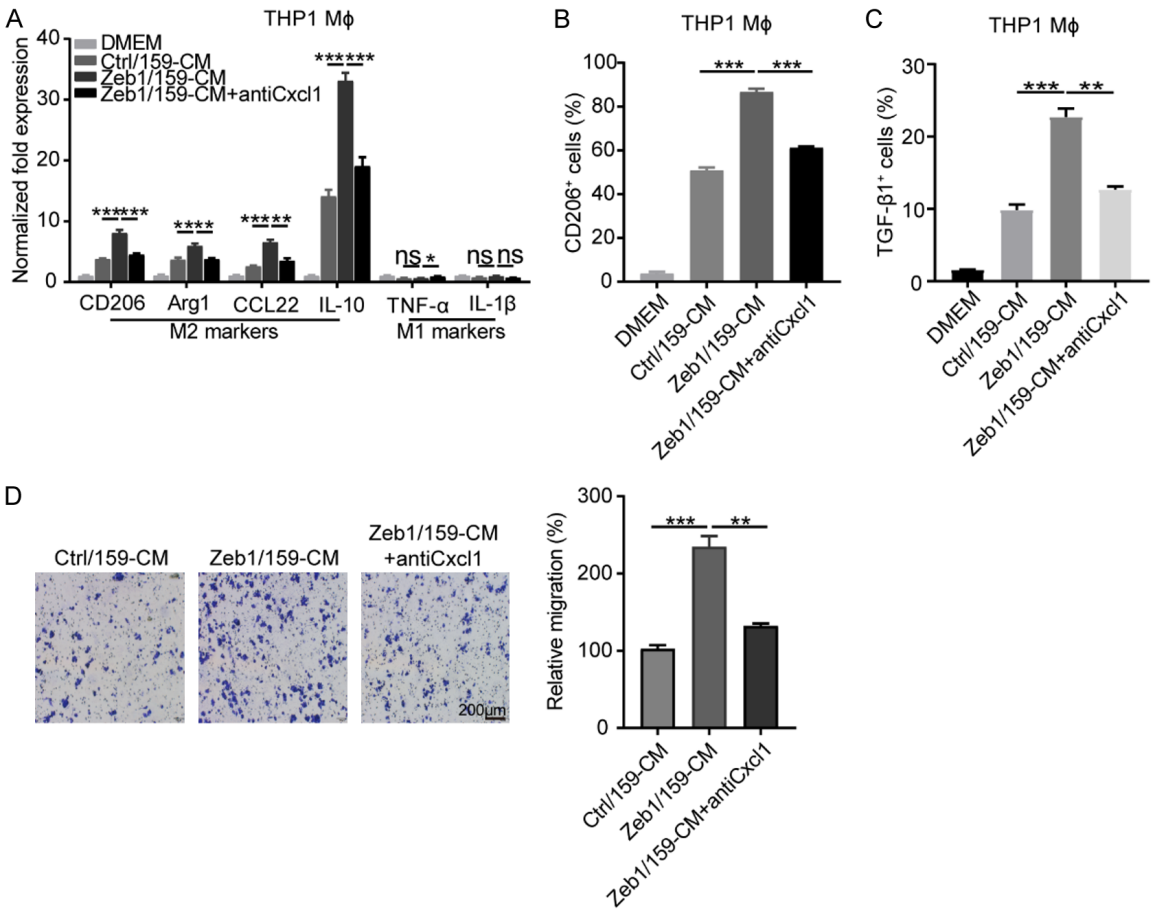

Figure S8. (A) Relative mRNA levels of M1- and M2-TAM markers in THP1 macrophages treated with CM from Zeb1-expressing SUM-159 cells in the presence of a Cxcl1 neutralizing antibody. (B, C) Flow cytometry analysis of $CD206^+$ (B) and TGF-$\beta1^+$ (C) cells in THP1 macrophages treated with CM from Zeb1-expressing SUM-159 cells in the presence of a Cxcl1 neutralizing antibody. (D) Transwell migration assay in THP1 macrophages treated with CM from Zeb1-expressing SUM-159 cells in the presence of a Cxcl1 neutralizing antibody. Indicated *P*-values were calculated using two-tailed unpaired Student's *t*-test. Data are presented as mean ± SEM in (A-D). Data are representative of three (A-D) independent experiments. Source data are provided as a Source Data file.