SUPPLEMENTAL FIGURE LEGENDS

- **Supplemental Figure A1** –Schematic of the rat MEK-1 promoter and sequence. Numbers indicate the positions from the transcriptional start site. There are one potential CREB binding site, two GATA-1 sites, three Sp1 sites, and many other regulatory elements within the fragment of MEK-1 promoter.
- **Supplemental Figure A2** –Effect of polyamine depletion on MEK-1 protein stability. *A*: representative immunoblots of MEK-1 in cells exposed to DFMO alone or DFMO plus putrescine. After cells were cultured in control medium and medium containing DFMO alone or DFMO plus Put for 6 days, cycloheximide (CHX) at the concentration of 25 μ g/ml was added to cultures and whole cell lysates were harvested at the indicated times. Levels of MEK-1 protein were assayed using Western blot analysis, and equal loading of peoteins was monitored using actin. *B*: quantitative densitometric Western blot analysis of cells described in *A*. Value are means \pm SE of data from three separate experiments, and relative levels of MEK-1 protein were corrected for protein loading as measured using densitometry of actin.
- **Supplemental Figure 3** Effect of increasing cellular poyamines by ectopic ODC expression on MEK-1 protein stability. *A*: representative immunoblots of MEK-1: *a*, cells transfected with the Null (control); and *b* stable ODC-IEC-C1 cells; and *c*, stable ODC-IEC-C2 cells. After cycloheximide (CHX) was added to cultures, whole cell lysates were harvested at the indicated times. *B*: quantitative densitometric Western blot analysis of cells described in *A*. Value are means \pm SE of data from three separate experiments, and relative levels of MEK-1 protein were corrected for protein loading as measured using densitometry of actin.



MEK-1 promoter sequence

CGATAGGTAC	CGAACCTGCG	TGCAGAACCT	CCTACAGCAT	TCACCTGGCC	-545
ACCGATTGGT	CAGCAGAGGG	CGCCTGGAAA	GCCTCCTTTT	AACCCCGCCC	-495
CAGGCCAGCG	CGCCGCGCCT	CCCGTGACGT	ATTTCCGCGT	CATCTGCCGC	-445
TGAGGCTAGT	CCCCATTGGC	TGTCGGCAAA	GCTACAGGGC	GGAGTCAGGC	-395
GGGCGTGAGG	GAAGCTCTGC	AGCTCCCCGT	GGGGGGGGGG	CTTGCCTATT	-345
TCCCCGCCCC	TCCCTCGCCC	TCCAGTCCCT	CTCTGGGACG	TCTGTACGCC	-295
GCGTCTCTGA	GTGCGGTGGC	CGCGGTGGCC	GCACTTTCTC	CGGGTGGTGC	-245
TGTAGCCGAG	CTGTGGGGAG	TGCGCAGAAG	GGCCGCCCGA	GCCCAAGGAA	-195
AGCGTGCGCT	GAGGCGAGAG	TCCCGGGCCG	GCGAGCGCGC	GCAGCTAGTT	-145
CTCCGCGTGG	GTTGGGCGGA	GGGTCCCAGG	AGCGTGGCGC	TGAGAGAGAG	-95
AGAGGGAGAG	AGAGAGAGAG	AGCGGCCCCG	ACTCTGGGCA	GAGCCGAGGG	-45
AGGAAGCGAG	AAGCGGCCGC	GCGCTCCCTG	CTGAGTTGCA	GGCTG <u>TTTCC</u>	+5
				└→ + 1	
CGGCTGCAAG	ATGCCCAAGA	AGAAGCCGAC	GCCCATCCAG	CTGAACCCGG	+55
CTGAACCCGG	CCCCCGATGG	CTCCGCGGTT	AACGGGACCA	GCTCGGCCGA	+95
GTGAGTACCG	GGAGTGGCCG	GG			

undersored sequence: coding region of MEK-1



