Supplementary Fig. 1. New putative regulatory elements within the 5' flanking region of the PAI-1 gene. (A) The seventeen Alu elements, containing putative c-jun/ATF binding sites, have been identified using the software available on the Internet. The sequences of binding sites are bolded and underlined; the location of the binding sites (relatively to the transcription start site) is indicated. (B) Alu element were cloned in front of the 115 bp long PAI-1 promoter, whereas the putative c-jun/ATF elements were cloned in the front of the *tk* minimal promoter. A172 cells were nucleofected with the indicated reporter constructs, stimulated with EGF, and analyzed as described in the legend Fig. 2C. (Insert) Binding to the putative c-jun/ATF element was analyzed by EMSA as described in the legend to Fig. 2B.

Supplementary Figure 1

| Δ | |
|---|--|
| ~ | |

| SINE | LOCATION | STRAND | SEQUENCE |
|-------|------------------|--------|--|
| AluSx | -14,091 - 14,057 | - | GTCTCAAACTCC TG G CCTCA ACTGATCTGCCTGC |
| AluSx | -13,586 - 13,619 | - | CTCTTGAACTCC TGACCTCA GGTGATCCACCTGC |
| AluSx | -13,260 - 13,294 | - | GTCTCGAACTCT TGACCTCA AGTGATCCACCTGC |
| AluSx | -11,977 - 11,943 | + | GTCTTGAACTCC TG G CCTCA GGAGATCCACCTGC |
| AluSx | -11,114 - 11,080 | + | GTCTCGAACTCC TGACCTCA TGTAGTCCGCCCAT |
| AluSc | -10,810 - 10,778 | + | GTCTCCGTCTCC TGACCTCA TGATCTGCCCGC |
| AluSx | -10,234 - 10,268 | - | GTCTCGAACTCC TGA T CTCA AGTGATCTGCCCGC |
| AluSg | -9,007 - 8,975 | + | GTCTTGAACTCC TGACCTC GTGATCCGCCCGC |
| AluJo | -8,187 - 8,153 | + | GTCTCGAACTCC TG G CCTCA AGCAATCCTGCCAC |
| AluSx | -7,671 - 7,705 | - | GTCTCAAACTCC TGAGCTCA ACTGATCTTCCCAC |
| AluJb | -6,456 - 6,490 | - | TTCTTGAACTCC TGAGCTCA AGTGACCGACCTGC |
| AluSq | -6,130 - 6,164 | - | GTCTTGAACTCC TGACCTCA AGTGATCCGCCTTC |
| AluSg | -5,435 - 5,457 | - | GTCTCGATCTCC TGACCTCA TGATCCACCCAC |
| AluJo | -3,598 - 3,564 | + | GCCTTGAGCTCC T AG GCTCA AGCGATCCTCCTAC |
| AluSx | -2,835 - 2,801 | + | GTCTTGAACTCC TG G CCTCA AGTGATCCACCTGC |
| AluJo | -2,530 - 2,556 | - | GACTTGAACTCC TG G GCTCA AGCAAG |
| AluSg | -1,837 - 1,869 | - | GTCTCGAACTCC TGAC T TC GTG—ATCCGGCTGC |

