Supplementary Figure S1. (A) ESE1/ELF3 is overexpressed in primary prostate tumors. Level of ESE1/ELF3 in primary tumors versus normal prostate gland in the indicated microarray datasets. Statistical significance was computed using TTest. (B) Level and distribution (lower) of ESE1/ELF3 and ERG mRNA determined by qRT-PCR in primary prostate tumours. (C) Immunohistochemical determination of ESE1/ELF3 and ERG protein in prostate tumors. Left, distribution based on IHC score of ERG and ESE1/ELF3 in prostate tumors. Right, representative images of two prostate tumors.
**Supplementary Figure S2.** Generation of stable ESE-1/ELF3 over-expressing prostate cancer cell lines. (A) ESE1/ELF3 protein levels in a panel of prostate cancer cell lines. (B) ESE1/ELF3 level in 22RV1 and LNCaP cells stably expressing ESE1/ELF3 determined by qRT-PCR and immunoblotting. (C) Immunofluorescence microscopy of ESE1/ELF3 (green) showing both cytoplasmic and intranuclear localization of ESE1/ELF3 in control (pcDNA) and ESE1/ELF3 overexpressing (pESE-1) LNCaP and 22RV1 cells. (D) Level of ESE1/ELF3 in prostate tumors from the Biella dataset and in cell lines determined by qRT-PCR (P values were determined using t-test. **, P<0.01.
Supplementary Figure S3. Level of ESE1/ELF3 in prostate tumor xenografts. (A) Level of ESE1/ELF3 was evaluated by IHC in xenografts derived from 22RV1-pcDNA and 22RV1pESE1 and in human prostate tumors with high level of ESE1/ELF3 (ESE1-H).
**Supplementary Figure S4.** Network interactions between ESE1/ELF3-induced genes and ETS transcription factors. ESE1/ELF3-induced genes (red colors) and ETS transcription factors (grey colors, highlighted in pink). Intensity of red color of genes depends on degree of overexpression of ESE1-induced genes. The color and pattern of lines connecting the genes and the shape of gene products is explained aside the network. The analysis was performed using Pathway Studio® software from Ariadne Genomics using a curated database of gene relationships based on scientific publications. Red lines, direct inhibition between gene products. Green lines, direct activation between gene products.
Supplementary Figure S5. Left, Position of ETS binding sites identified by computational analysis using Motiviz and validated by ChIP in the promoter of ESE1/ELF3 target genes. Right, Chromosomal location of the selected promoter regions.
**Supplementary Figure S6.** Convergence between the transcriptional program induced in IL-1β transgenic mice and ESE1/ELF3 overexpressing 22RV1 cells. Venn diagram shows overlapping between the genes induced in adenocarcinoma (top left), Intestinal Metaplasia (top right), Bile acidic induced metaplasia (bottom center) in IL-1β transgenic mice vs normal tissue from wild type mice and genes induced in 22RV1-pESE1 vs 22RV1-pcDNA cells. Overlapping significance was computed using Fisher’s Exact Test.
Supplementary Figure S7. Reciprocal regulatory loops between ESE1/ELF3 and NFkB. (A) ESE1/ELF3 target genes are involved in NF-kB regulation (green lines from ESE1/ELF3 genes to NF-kB). (B) NF-kB regulates ESE1/ELF3 induced genes (green lines from NF-kB to ESE1 target genes). Intensity of red color depends on degree of overexpression of ESE1-regulated genes. Red lines, direct inhibition between gene products. Green lines, direct activation between gene products. Dashed lines, regulation not demonstrated to be direct. Analysis performed using Pathway Studio® software from Ariadne Genomics using a curated database of gene relationships based on scientific publications.
Supplementary Figure S8. Immunofluorescence microscopy for detection of ESE1/ELF3 (green), p50 (red, left), p65 (red, right) and nuclei (blue) in 22RV1 cells transfected with control (siGL3) or ESE1/ELF3 targeting (siESE1) siRNA and exposed to IL-1β for 4 h.
**Supplementary Figure S9.** (A) ESE1/ELF3, nuclear p50 and p65 positivity is associated with poor prognosis. Kaplan-Meyer analysis of overall survival of prostate cancer patients from the TMA cohort subdivided according to ESE1/ELF3 and p50/p65 nuclear expression status. Log rank test (Mantel-Cox): $p=0.06$. Number of patients is indicated in parenthesis. N⁺=nuclear positive. (B) Kaplan-Meier analysis of biochemical relapse-free survival of patients from the Biella cohort divided according to ELF3/ESE1, p65/RELA and p50/NFKB1 level. For details see Supplementary Methods.