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Table 1. ERα-mediated gene expression in response to E2

Gene Name	Symbol	Process	Relative Change[a]
V-abl Abelson murine leukemia viral oncogene homolog 1	*ABL1*	Signal transduction, transcription	0.61
Actin binding LIM protein family, member 3	*ABLIM3*	Cytoskeleton biogenesis	2.395
Acyl-coa synthetase long-chain family member 5	*ACSL5*	Metabolic processes	1.626
Adrenomedullin	*ADM*	Signal transduction	0.75
Adenosine A2b receptor	*ADORA2B*	Signal transduction	0.398
Angiotensinogen	*AGT*	Signal transduction	0.775
Aldehyde dehydrogenase 3 family, member B1	*ALDH3B1*	Metabolic processes	2.78
Adhesion molecule with Ig-like domain 2	*AMIGO2*	Cell adhesion	0.447
Ankyrin repeat domain 1 (cardiac muscle)	*ANKRD1*	Signal transduction	1.461
Annexin A11	*ANXA11*	Immune processes	2.45
Aquaporin 3	*AQP3*	Excretion, transport	2.99
Rho gtpase activating protein 18	*ARHGAP18*	Signal transduction	0.54
Rho gtpase activating protein 26	*ARHGAP26*	Signal transduction	3.91
Rho/rac guanine nucleotide exchange factor (GEF) 2	*ARHGEF2*	Signal transduction	0.73
AT rich interactive domain 4A (RBP1-like)	*ARID4A*	Transcription	2.29
ADP-ribosylation factor-like 3	*ARL3*	Signal transduction	1.78
Aryl hydrocarbon receptor nuclear translocator-like	*ARNTL*	Signal transduction	1.53
Adipocyte-specific adhesion molecule	*ASAM*	Cell adhesion	8.17
Ankyrin repeat and SOCS box-containing 13	*ASB13*	Protein degradation in cell	4.09
Brain abundant, membrane attached signal protein 1	*BASP1*	Unclear	0.8
Bridging integrator 1	*BIN1*	Cellular proliferation, differentiation	2.01
Baculoviral IAP repeat-containing 2	*BIRC2*	Signal transduction, apoptosis	0.625
Brain protein 44-like	*BRP44L*	Unclear	3.27
Complement component 3	*C3*	Signal transduction	2.65
Cdk5 and Abl enzyme substrate 2	*CABLES2*	Cell cycle regulation	6.63
Centrosome-associated protein 350	*CAP350*	Microtubule anchoring	1.46
Caspase recruitment domain family, member 10	*CARD10*	Apoptosis regulation	2.65
Caspase recruitment domain family, member 6	*CARD6*	Apoptosis regulation	1.659
Caspase 7, apoptosis-related cysteine peptidase	*CASP7*	Apoptosis regulation	2.07
Carbonyl reductase 3	*CBR3*	Metabolic processes	0.498
Cyclin A1	*CCNA1*	Cell cycle regulation	5.128
CD44 antigen	*CD44*	Cell adhesion, signal transduction	0.508
CD83 antigen	*CD83*	Signal transduction	2.27
Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	*CDKN1A*	Cell cycle regulation	2.936
Cdon homolog (mouse)	*CDON*	Cell adhesion	1.6
CCAAT/enhancer binding protein (C/EBP), delta	*CEBPD*	Transcription	1.393
Creatine kinase, brain	*CKB*	Metabolic processes	1.67
Cysteine-rich secretory protein LCCL domain containing 2	*CRISPLD2*	Signal transduction	8.754
Connective tissue growth factor	*CTGF*	Proliferation, adhesion, motility	0.68
Cathepsin D (Lysosomal aspartyl peptidase)	*CTSD*	Proteolysis	1.758
DAB2 interacting protein	*DAB2IP*	Signal transduction	1.449
Development and differentiation enhancing factor 1	*DDEF1*	Regulation of GTPase ARF	0.669
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	*DDX47*	RNA metabolic process	0.73

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[a] Gene expression regulated by E2-ERα compared to those mediated by the parent Ad5 in the presence of E2. The SEM, which was less then 10% of the mean, is not shown for simplicity.

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Dickkopf homolog 1 (Xenopus laevis)	*DKK1*	Signal transduction	0.455
Desmuslin	*DMN*	Protein binding	1.3
Dnaj (Hsp40) homolog, subfamily B, member 1	*DNAJB1*	Protein folding	0.645
Dual specificity phosphatase 5	*DUSP5*	Protein dephosphorylation	0.448
Ectodermal-neural cortex (with BTB-like domain)	*ENC1*	System development	0.529
Epiplakin 1	*EPPK1*	Biological process	1.26
Family with sequence similarity 46, member A	*FAM46A*	Unclear	3.19
Family with sequence similarity 8, member A1	*FAM8A1*	Unclear	1.85
FK506 binding protein 4, 59kda	*FKBP4*	Protein folding	1.35
FOS-like antigen 1	*FOSL1*	Cellular defense response	0.52
Forkhead box O1A (rhabdomyosarcoma)	*FOXO1A*	Transcription	2.26
Follicular lymphoma variant translocation 1	*FVT1*	Metabolic processes	0.68
Galnac-Transferase 1	*GALNT1*	Protein glycosylation	1.7
GTP cyclohydrolase 1 (dopa-responsive dystonia)	*GCH1*	Metabolic and catabolic processes	2.28
Gap junction protein, beta 2, 26kda (connexin 26)	*GJB2*	Cell-to-cell signaling	0.391
G protein-coupled receptor, family C, group 5, member A	*GPRC5A*	Signal transduction	0.64
General transcription factor IIF, polypeptide 2, 30kda	*GTF2F2*	Transcription	0.679
H19, imprinted maternally expressed untranslated mrna	*H19*	Unclear	1.28
Hyaluronan synthase 2	*HAS2*	Matrix formation	0.346
Heparin-binding EGF-like growth factor	*HBEGF*	Signal transduction	0.379
HEG homolog 1 (zebrafish)	*HEG*	Unclear	1.68
Hexokinase 1	*HK1*	Glycolysis	2.03
Heat shock 22kda protein 8	*HSPB8*	Stress responses	1.29
Paraneoplastic antigen	*HUMPPA*	Unclear	3.109
Immediate early response 2	*IER2*	Unclear	0.623
Immediate early response 5	*IER5*	Unclear	0.652
Immediate early response 5-like	*IER5L*	Unclear	2.4
Insulin-like growth factor binding protein 3	*IGFBP3*	Cell growth and apoptosis	2.04
Insulin-like growth factor binding protein 4	*IGFBP4*	Signal Transduction, Cellular growth	1.559
Interleukin 18 (interferon-gamma-inducing factor)	*IL18*	Signal transduction	0.533
Inhibin, beta A (activin A, activin AB alpha polypeptide)	*INHBA*	Multifunctional signaling processes	2.74
Juxtaposed with another zinc finger gene 1	*JAZF1*	Transcription	5.47
Jumonji domain containing 2B	*JMJD2B*	Transcription	5.42
Kiaa0247	*KIAA0247*	Unclear	2.14
KIAA0830 protein	*KIAA0830*	Unclear	1.76
Kiaa1553	*KIAA1553*	Unclear	0.687
KIAA1609 protein	*KIAA1609*	Unclear	0.49
KIAA1799 protein	*KIAA1799*	Unclear	1.33
Kinesin family member 21A	*KIF21A*	Microtubule based motility	1.8
Kruppel-like factor 10	*KLF10*	Cell-to-cell signaling	2.26
Lysosomal associated multispanning membrane protein 5	*LAPTM5*	Transport	6.59
Leukemia inhibitory factor receptor	*LIFR*	Cellular proliferation	2.08
Lipase, endothelial	*LIPG*	Lipid catabolism	3.53
Hypothetical protein LOC149832	*LOC149832*	Unclear	1.47
Hypothetical LOC201484	*LOC201484*	Unclear	1.47
Hypothetical protein LOC283551	*LOC283551*	Unclear	44.93
Lysyl oxidase	*LOX*	Protein modification	3.3
Lysyl oxidase-like 4	*LOXL4*	Ion binding	139.4
Mitogen-activated protein kinase kinase 3	*MAP2K3*	Signal transduction	0.614

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Mitogen-activated protein kinase kinase 5	*MAP2K5*	Signal transduction	4.39
MARCKS-like 1	*MARCKSL1*	Unclear	2.9
MADS box transcription enhancer factor 2, polypeptide A	*MEF2A*	Transcription	2.24
Likely ortholog of mouse schlafen 5	*MGC19764*	Cellular differentiation	2.48
Microphthalmia-associated transcription factor	*MITF*	Transcription	5.47
MAP kinase interacting serine/threonine kinase 2	*MKNK2*	Signal Transduction, phosphorylation	1.96
Matrix metallopeptidase 1 (interstitial collagenase)	*MMP1*	Collagen catabolism, Proteolysis	0.22
Matrix metallopeptidase 3 (stromelysin 1, progelatinase)	*MMP3*	Collagen catabolism, Proteolysis	0.47
Metallothionein 1X	*MT1X*	Responses to metal ions	2.02
MAX dimerization protein 1	*MXD1*	Transcription	2.06
Myeloid-associated differentiation marker	*MYADM*	Unclear	0.591
Nanos homolog 1	*NANOS1*	Regulation of translation	4.9
Neuron navigator 2	*NAV2*	Neural growth	1.85
Nuclear receptor coactivator 1	*NCOA1*	Transcription	3.13
Neural precursor expr, develop down-reg 4-like	*NEDD4L*	Protein modification	0.51
Normal mucosa of esophagus specific 1	*NMES1*	Unclear	1.79
Noggin	*NOG*	Tissue and organ development	0.72
Neighbor of Punc E11	*NOPE*	Unclear	0.65
Neuregulin 1	*NRG1*	Cellular differentiation	0.5
O-acyltransferase domain containing 1	*OACT1*	Protein modification	1.627
Ornithine decarboxylase 1	*ODC1*	Polyamine biosynthetic process	0.649
Olfactomedin-like 3	*OLFML3*	Matrix related function	8.62
Oxysterol binding protein-like 3	*OSBPL3*	Lipid transport, steroid metabolism	2.04
OTU domain, ubiquitin aldehyde binding 2	*OTUB2*	Amino acid metabolism	7.39
3'-phosphoadenosine 5'-phosphosulfate synthase 2	*PAPSS2*	Nucleic acid metabolism	2.82
Pim-1 oncogene /// pim-1 oncogene	*PIM1*	Cellular proliferation and apoptosis	2.33
Phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	*PIP5K1C*	Phosphatidylinositol metabolism	3.2
Plasminogen activator, tissue	*PLAT*	Proteolysis	0.639
Plasminogen activator, urokinase	*PLAU*	Proteolysis	0.28
Plasminogen activator, urokinase receptor	*PLAUR*	Signal trans, motility, proteolysis	0.405
POU domain, class 3, transcription factor 2	*POU3F2*	Transcription	1.89
Protein phosphatase 1, regulatory (inhibitor) subunit 13B	*PPP1R13B*	Apoptosis regulation	1.9
Prostaglandin-endoperoxide synthase 2	*PTGS2*	Fatty acid biosynthetic process	9.67
Ral GEF with PH domain and SH3 binding motif 2	*RALGPS2*	Signal transduction	2.72
RNA binding motif protein 24	*RBM24*	Type I hypersensitivity	1.68
REST corepressor 3	*RCOR3*	Transcription	1.74
Radixin	*RDX*	Cytoskeletal anchoring	1.77
Regulator of nonsense transcripts 1	*RENT1*	DNA and RNA processing	2.75
RGM domain family, member B	*RGMB*	Signal transduction	0.66
Regulator of G-protein signalling 10	*RGS10*	Signal transduction	1.73
Regulator of G-protein signalling 19	*RGS19*	Signal transduction	3.63
Rho-related BTB domain containing 3	*RHOBTB3*	Biological process	2.17
Rhophilin, Rho gtpase binding protein 2	*RHPN2*	Signal transduction	0.599
Ras and Rab interactor 2	*RIN2*	Signal transduction	0.597
RNA-binding region (RNP1, RRM) containing 1	*RNPC1*	DNA damage response	0.614
Ribonucleotide reductase M2 B (TP53 inducible)	*RRM2B*	DNA Repair and replication	1.49
Retinoid X receptor, alpha	*RXRA*	Signal transduction	1.47
Spermidine/spermine N1-acetyltransferase 2	*SAT2*	Metabolic processes	1.82
Sema domain, immunoglobulin domain,(semaphorin) 3B	*SEMA3B*	Cell-to-cell signaling	1.45

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Sema domain (semaphorin) 6B	*SEMA6B*	Cellular differentiation	2.21
Serpin peptidase inhibitor, clade B, member 2	*SERPINB2*	Apoptosis regulation	0.154
Serpin peptidase inhibitor, clade B, member 6	*SERPINB6*	Endopeptidase inhibitor activity	1.54
Serpin peptidase inhibitor, clade B, member 9	*SERPINB9*	Apoptosis regulation	17.92
SERTA domain containing 2	*SERTAD2*	Transcription	0.72
SERTA domain containing	*SERTAD4*	Unclear	0.48
SH3-domain binding protein 5 (BTK-associated)	*SH3BP5*	Intracellular signaling cascade	1.77
Solute carrier family 9, member 3 regulator 1	*SLC9A3R1*	Protein complex assembly	2.64
Slit-like 2 (Drosophila)	*SLITL2*	Unclear	1.67
Cbl-interacting protein Sts-1	*STS-1*	Endocytosis inhibition	0.436
TBC1 domain family, member 4	*TBC1D4*	Unclear	0.685
Thromboxane A2 receptor	*TBXA2R*	Signal transduction	5.65
T-cell, immune regulator 1, atpase, H+ transporting	*TCIRG1*	Ion and proton transport	3.02
Transforming growth factor, alpha	*TGFA*	Cellular proliferation	2
Transforming growth factor, beta 2	*TGFB2*	Cellular proliferation, apoptosis	0.39
Transmembrane protein 2	*TMEM2*	Unclear	2.61
Tumor necrosis factor receptor superfamily, member 21	*TNFRSF21*	Signal transduction	0.66
TNFAIP3 interacting protein 1	*TNIP1*	Glycoprotein anabolism	2.02
Transducer of ERBB2, 1	*TOB1*	Cellular proliferation	3.298
Tumor protein p53 inducible protein 3	*TP53I3*	Apoptosis regulation	2.05
Trophoblast glycoprotein	*TPBG*	Cell adhesion and motility	1.88
Tumor protein D52-like 1	*TPD52L1*	Apoptosis regulation	12.549
Translocation associated membrane protein 2	*TRAM2*	Protein transport	0.53
Tripartite motif-containing 47	*TRIM47*	Ion binding	1.67
Twisted gastrulation homolog 1 (Drosophila)	*TWSG1*	Multicellular organismal development	1.71
Ubiquitin-conjugating enzyme E2Q (putative) 2	*UBE2Q2*	Regulation of protein metabolism	0.74
UDP-glucose ceramide glucosyltransferase	*UGCG*	Glucosylceramide anabolism	0.64
UDP-glucuronate decarboxylase 1	*UXS1*	Metabolic processes	1.71
Vascular endothelial growth factor C	*VEGFC*	Signaling, proliferation	0.52
Wiskott-Aldrich syndrome protein interacting protein	*WASPIP*	Protein complex assembly	1.38
Wingless-type MMTV integration site family, member 16	*WNT16*	Cell-to-cell signaling	151.1
Wilms tumor	*WT1*	Transcription	0.38
Yippee-like 2 (Drosophila)	*YPEL2*	Unclear	44.73
Zinc finger and BTB domain containing 38	*ZBTB38*	Transcription	1.97
Zinc finger protein 336	*ZNF336*	Transcription	2.46

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Table 2. ERα_{EBD}-mediated gene expression in response to E2

Gene Name	Symbol	Function	Relative Change[a]
Ankyrin repeat domain 1 (cardiac muscle)	*ANKRD1*	Signal transduction	1.556
Cysteine-rich secretory protein LCCL domain containing 2	*CRISPLD2*	Signal transduction	1.47
Connective tissue growth factor	*CTGF*	DNA replication, cell growth	0.595
Dual specificity phosphatase 5	*DUSP5*	Protein dephosphorylation	1.436
Follistatin	*FST*	Signal transduction	3.67
Gap junction protein, beta 2	*GJB2*	Cell-cell signaling	1.797
G protein-coupled receptor, family C, group 5, member A	*GPRC5A*	Signal transduction	1.489
Hyaluronan synthase 2	*HAS2*	Matrix formation	0.695
Heparin-binding EGF-like growth factor	*HBEGF*	Signal transduction	0.786
Insulin-like growth factor binding protein 4	*IGFBP4*	Signal transduction	1.262
Matrix metallopeptidase 1	*MMP1*	Collagen catabolism	0.791
Matrix metallopeptidase 3	*MMP3*	Collagen catabolism	3.83
Neuregulin 1	*NRG1*	Cellular differentiation	1.87
Plasminogen activator, tissue	*PLAT*	Proteolysis	2.211
Plasminogen activator, urokinase	*PLAU*	Proteolysis	2.404
Serpin peptidase inhibitor, clade B, member 2	*SERPINB2*	Anti-apoptosis	2.686

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[a] Gene expression regulated by E2-ERα_{EBD} compared to those mediated by the parent Ad5 in the presence of E2. The SEM, which was less then 10% of the mean, is not shown for simplicity.