

Additional file 1

Table S1. Significant enrichment of differential genes in GO terms and KEGG pathways.

Category	Term	Describe	Count	PValue
GOTERM_BP	GO:0060749	mammary gland alveolus development	4	5.34E-05
GOTERM_BP	GO:0006366	transcription from RNA polymerase II promoter	10	4.09E-04
GOTERM_BP	GO:0045893	positive regulation of transcription, DNA-templated	10	4.21E-04
GOTERM_BP	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	13	0.001129762
GOTERM_BP	GO:0008283	cell proliferation	8	0.001133991
GOTERM_BP	GO:0048485	sympathetic nervous system development	3	0.001938348
GOTERM_BP	GO:0008284	positive regulation of cell proliferation	8	0.004397438
GOTERM_BP	GO:0006338	chromatin remodeling	4	0.006471285
GOTERM_BP	GO:0032355	response to estradiol	4	0.007562598
GOTERM_BP	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	9	0.013700033
GOTERM_BP	GO:0060750	epithelial cell proliferation involved in mammary gland duct elongation	2	0.017512815
GOTERM_BP	GO:0010629	negative regulation of gene expression	4	0.022613062
GOTERM_BP	GO:0060548	negative regulation of cell death	3	0.024476563

GOTERM_BP	GO:0008285	negative regulation of cell proliferation	6	0.030438403
GOTERM_BP	GO:0060740	prostate gland epithelium morphogenesis	2	0.030448545
GOTERM_BP	GO:0014009	glial cell proliferation	2	0.030448545
GOTERM_BP	GO:0043627	response to estrogen	3	0.033333732
GOTERM_BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	3	0.04016646
GOTERM_BP	GO:0033148	positive regulation of intracellular estrogen receptor signaling pathway	2	0.04321623
GOTERM_BP	GO:0048646	anatomical structure formation involved in morphogenesis	2	0.047435155
GOTERM_BP	GO:0055078	sodium ion homeostasis	2	0.047435155
GOTERM_BP	GO:0001701	in utero embryonic development	4	0.049577503
GOTERM_CC	GO:0070062	extracellular exosome	22	0.004528379
GOTERM_MF	GO:0001077	transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	9	8.83E-06
GOTERM_MF	GO:0001158	enhancer sequence-specific DNA binding	4	8.74E-05
GOTERM_MF	GO:0005154	epidermal growth factor receptor binding	4	3.33E-04
GOTERM_MF	GO:0000981	RNA polymerase II transcription factor activity, sequence-specific DNA binding	6	9.22E-04
GOTERM_MF	GO:0044212	transcription regulatory region DNA binding	6	0.002427076
GOTERM_MF	GO:0005496	steroid-binding	3	0.00619852

GOTERM_MF	GO:0043565	sequence-specific DNA binding	8	0.007522255
GOTERM_MF	GO:0003700	transcription factor activity, sequence-specific DNA binding	11	0.00893077
GOTERM_MF	GO:0034056	estrogen response element binding	2	0.017421084
GOTERM_MF	GO:0001085	RNA polymerase II transcription factor binding	3	0.018044359
GOTERM_MF	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	6	0.019753363
GOTERM_MF	GO:0003707	steroid hormone receptor activity	3	0.025065675
GOTERM_MF	GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	3	0.025904554
GOTERM_MF	GO:0008134	transcription factor binding	5	0.036070234
GOTERM_MF	GO:0002162	dystroglycan binding	2	0.038776915
GOTERM_MF	GO:0042803	protein homodimerization activity	8	0.040532128
GOTERM_MF	GO:0051117	ATPase binding	3	0.041808786
KEGG_PATHWAY	hsa04917	Prolactin signaling pathway	3	0.03793765
