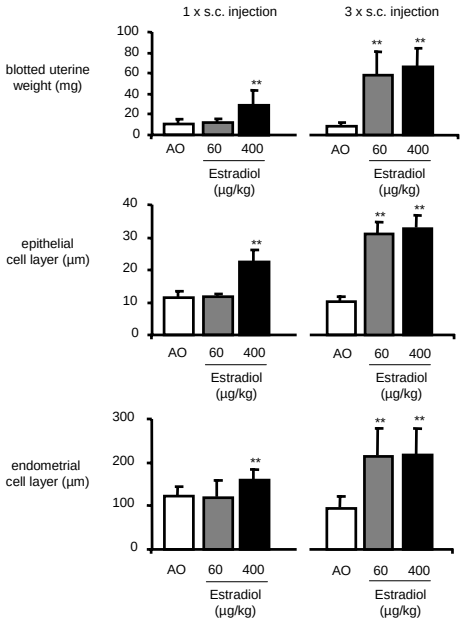
Supplementary Figure 1



Supplementary Figure 1.
Comparison of single and multiple doses of E_2 (60 µg/kg versus 400 µg/kg) in the uterotrophic assay. A single s.c. dose of E_2 (400 µg/kg) was required to induce an increase in uterine wet weight after 72 hr compared to the lower dose (e.g. 60 µg/kg) required in standard uterotrophic assay exposure regime (i.e. repeated administration on 3 consecutive days). Data shown are mean + SD from 10 immature female mice in each treatment group. $P<0.01$ (**).

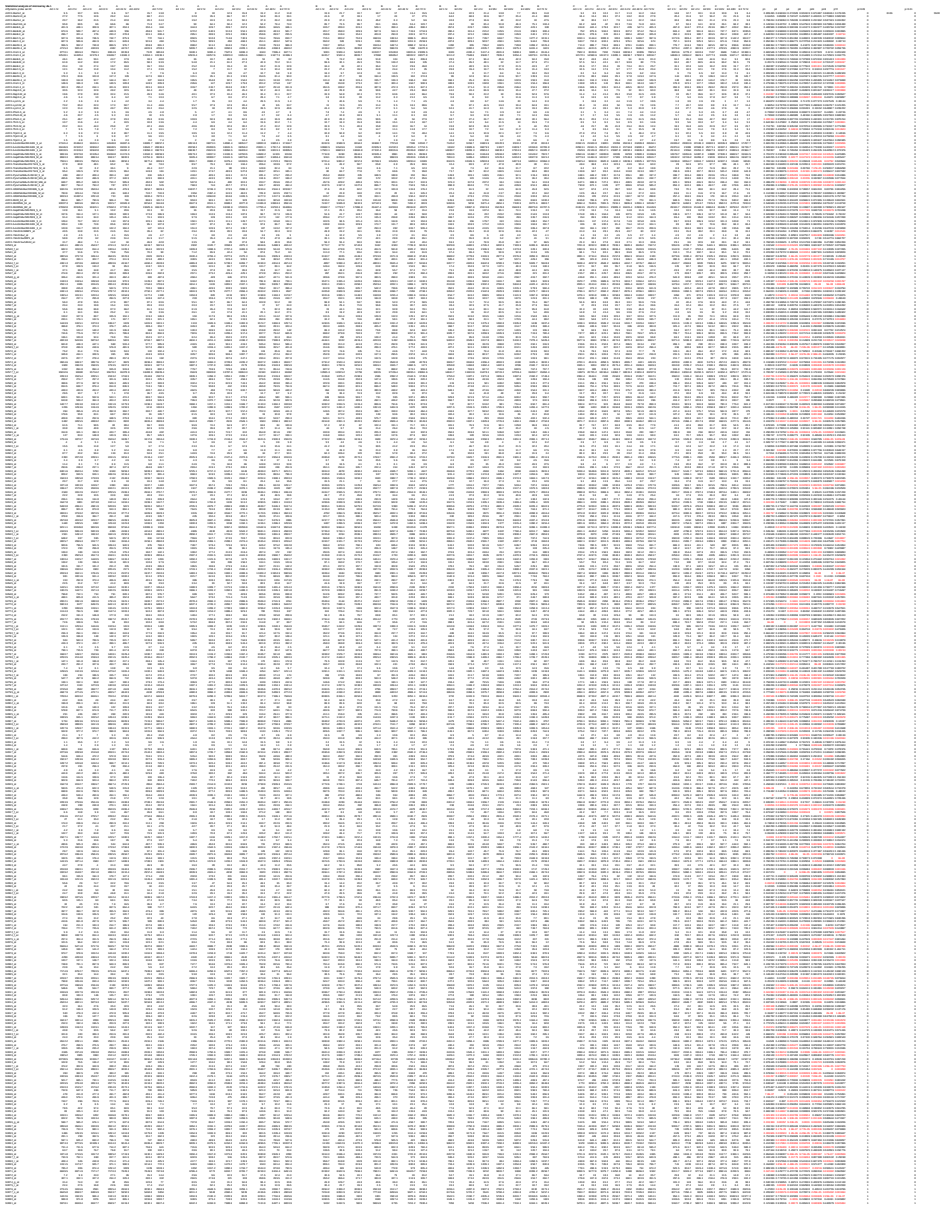
Supplementary Table 2. Major Gene Ontology associations of 3,538 E2-responsive genes*.

GO IDs	GO Annotation	Significant children in branch	Count	Total	P-Value
GO:0043170	Macromolecule metabolism		486	2428	3.04e-20
GO:0019538		-Protein metabolism	410	2047	4.87e-17
GO:0043039		-tRNA aminoacylation	18	39	7.9e-07
GO:0006418		-tRNA aminoacylation for protein translation	18	39	7.9e-07
GO:0043038		-Amino acid activation	18	39	7.9e-07
GO:0006400		-tRNA modification	18	41	3.04e-06
GO:0009059		-macromolecule biosynthesis	126	602	6.61e-06
GO:0043037		-translation	42	149	1.62e-05
GO:0009057		-macromolecule catabolism	116	564	5.34e-05
GO:0006412		-protein biosynthesis	94	436	5.34e-05
GO:0016126		-sterol biosynthesis	11	17	6e-05
GO:0007049	Cell Cycle		143	514	1.31e-18
GO:0008283		-cell proliferation	168	658	4.87e-17
GO:0000067		-DNA replication and chromosome cycle	40	102	2.21e-11

GO:0006260		-DNA replication	33	82	9.28e-10
GO:0000074		-regulation of cell cycle	70	262	8.51e-08
GO:0019752	Carboxylic acid metabolism		83	278	7.28e-13
GO:0006082		-organic acid metabolism	83	278	7.28e-13
GO:0006520		-amino acid metabolism	43	127	8.58e-09
GO:0006631		-fatty acid metabolism	31	103	7.35e-05
GO:0009308	Amine metabolism		57	191	1.26e-08
GO:0016125	Sterol metabolism		20	42	5.95e-08
GO:0008203		-cholesterol metabolism	18	39	7.9e-07
GO:0019219	Regulation of nucleic acid metabolism		262	1400	6.73e-07
GO:0045449		-regulation of transcription	261	1395	6.73e-07
GO:0006355		-regulation of transcription, DNA-dependent	253	1366	2.44e-06
GO:0009451	RNA modification		21	49	6.73e-07
GO:0016070		-RNA metabolism	61	242	9.23e-06
GO:0006350	Transcription		269	1455	1.08e-06
GO:0006351		-transcription, DNA-dependent	258	1396	2.26e-06
GO:0016049	Cell Growth		21	53	4.89e-06
GO:0008361		-regulation of cell size	21	56	2.06e-05

GO:0001568	Blood vessel development	25	72	1.77e-05
GO:0006259	DNA metabolism	80	358	6.15e-05

*GO analysis was performed using GOStat (http://gostat.wehi.edu.au; Beissbarth and Speed, Bioinformatics (2004) 20(9):1464-1465). Shown are GO terms that are significantly over-represented ($p<0.0001$, using the Benjamini and Hochberg false discovery rate multiple testing correction) in the 3538 probesets altered by oestrogen when compared to the MGI database. GO terms were clustered so that terms with the same set of genes were grouped and then ranked by p-value.



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