

**Supplementary Table S21.** List of primary and secondary antibodies used in this study.

Antibody		Provider	Cat. Nb.	Dilution ICC	Dilution WB	Host
<b>Primary antibodies</b>						
<b>Albumin</b>		Santa Cruz		1:100	-	Goat
<b>BEST1</b>	Bestrophin 1 Antibody (E6-6)	Novus Biologicals	NB300-164	1:250	-	Mouse
<b>H3F3A</b>	Anti-Histone H3 Antibody, CT, pan	Sigma-Aldrich	07-690	-	1:5000	Rabbit
<b>MERTK</b>	Anti-MERTK antibody [Y323]	Abcam	ab52968	1:100	-	Rabbit
<b>NR3C1</b>	Glucocorticoid Receptor (D6H2L) XP® Rabbit mAb	Cell Signaling	12041	1:100	1:1000	Rabbit
<b>NR3C2</b>	Anti-Mineralocorticoid Receptor Antibody, clone 6G1	MERCK	MABS496	1:100	1:50	Mouse
<b>OCLN</b>	Occludin Polyclonal Antibody	Thermo Fisher SCIENTIFIC	71-1500	1:200	-	Rabbit
<b>Phalloidin</b>	Rhodamine Phalloidin	Thermo Fisher SCIENTIFIC	R415	1:100	-	N/A
<b>PTGER2</b>	Recombinant Anti-Prostaglandin E Receptor EP2/PTGER2 antibody [EPR8030(B)]	Abcam	ab167171	-	1:2000	Rabbit
<b>RLBP1</b>	Anti-CRALBP antibody [B2]	Abcam	ab15051	1:200	-	Mouse
<b>RPE65</b>	N/A	Provided by Christian Grimm (Wenzel <i>et al</i> , 2005)		1:200	-	Rabbit
<b>S100A2</b>	S100A2 Polyclonal Antibody	Thermo Fisher SCIENTIFIC	PA5-31861	1:100	1:1000	Rabbit
<b>SCNN1A</b>	alpha-ENaC Polyclonal Antibody	Thermo Fisher SCIENTIFIC	PA1-920A	1:100	1:250	Rabbit
<b>TJP1</b>	ZO-1 Polyclonal Antibody	Thermo Fisher SCIENTIFIC	40-2200	1:250	-	Rabbit
<b>TUBA1A</b>	Anti-alpha Tubulin antibody [DM1A]	Abcam	ab7291	-	1:2000	Mouse
<b>Secondary antibodies</b>						
<b>GAR</b>	F(ab')2-Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 488	Thermo Fisher SCIENTIFIC	A-11070	1:1000	-	Goat
<b>GAM</b>	F(ab')2-Goat anti-Mouse IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 633	Thermo Fisher SCIENTIFIC	A-21053	1:1000	-	Goat
<b>DAG</b>	Alexa Fluor 596-coupled donkey anti-goat IgG			1:200	-	Donkey
<b>AR</b>	Rabbit IgG HRP Linked Whole Ab	Sigma-Aldrich	GENA934	-	1:5000	Rabbit
<b>AM</b>	Mouse IgG HRP Linked Whole Ab	Sigma-Aldrich	GENA931	-	1:5000	Mouse

ICC, immunocytochemistry; WB, western blot; GAR, goat anti-rabbit; GAM, goat anti-mouse; DAG, donkey anti-goat; AR, anti-rabbit; AM, anti-mouse.

**Supplementary Table S20.** List of PCR and qPCR primers used in this study.

Gene		Primers sequence	Amplicon length	Design
Human qPCR Primers				
<b>ABCC3</b>	Forward Reverse	5'-GAGAAGGGCATTAACCTGTC-3' 5'-CGTGGTCAAAGATGTGCTTG-3'	<b>142</b>	NM_003786.4 / Exon 17 - Exon 18 junction NM_003786.4 / Exon 18
<b>BEST1</b>	Forward Reverse	5'-CCTTGGAACAGGGATGAAGC-3' 5'-AGCTGTATGGCTGTGACTGG-3'	<b>120</b>	NM_004183.3 / Exon 10 - Exon 11 junction NM_004183.3 / Exon 11
<b>FKBP5</b>	Forward Reverse	5'-CGGCGACAGGTTCTCTACTT-3' 5'-ATCGGCGTTTCCTCACCATT-3'	<b>171</b>	NM_004117.3 / Exon 1 - Exon 2 junction NM_004117.3 / Exon 3
<b>GAPDH</b>	Forward Reverse	5'-CTCTGCTCCTCTGTTTCGAC-3' 5'-ACCAAATCCGTTGACTCCGA-3'	<b>109</b>	NM_002046.5 / Exon 1 NM_002046.5 / Exon 1 - Exon 2 junction
<b>HMGA1</b>	Forward Reverse	5'-CTCCAAGAAGGCCATCCCAG-3' 5'-TCTCAGTGCCGTCTTTTCC-3'	<b>123</b>	NM_145903.2 / Exon 1 - Exon 2 junction NM_145903.2 / Exon 2
<b>HSD11B1</b>	Forward Reverse	5'-CTGCCTGCTTAGGAGGTTGT-3' 5'-TCCTTGGAGCATCTCTGGT-3'	<b>184</b>	NM_005525.4 / Exon 1 NM_005525.4 / Exon 1 - Exon 2 junction
<b>HSD11B2</b>	Forward Reverse	5'-CTCATCACCGGCTGTGACTC-3' 5'-CTCCTGGTTTGGTCAGGTCC-3'	<b>175</b>	NM_000196.4 / Exon 1 - Exon 2 junction NM_000196.4 / Exon 2
<b>LCN2</b>	Forward Reverse	5'-ACAATGTCACCTCCGTCCTG-3' 5'-AGCTCCTTGGTTCTCCCGTA-3'	<b>241</b>	NM_005564.4 / Exon 2 NM_005564.4 / Exon 4 - Exon 5 junction
<b>LRAT</b>	Forward Reverse	5'-TACTGCAGATATGGCACCCC-3' 5'-CCAAGACTGCTGAAGCAAGA-3'	<b>106</b>	NM_004744.4 / Exon 2 NM_004744.4 / Exon 3
<b>MERTK</b>	Forward Reverse	5'-AAGGCCGCATTGCTAAGAT-3' 5'-CGCGTAGCTATTCCCACAT-3'	<b>121</b>	NM_006343.2 / Exon 17 NM_006343.2 / Exon 18
<b>NR3C1</b> GR	Forward Reverse	5'-AAGAGCAGTGAAGGACAGC-3' 5'-CCAGGTTCATTCCAGCCTGA-3'	<b>128</b>	NM_000176.3 / Exon 3 - Exon 4 junction NM_000176.3 / Exon 4
<b>NR3C2</b> MR	Forward Reverse	5'-AGTGAAGGGCAACAACT-3' 5'-ACTTCTTGACTTTCGTGCTCC-3'	<b>143</b>	NM_000901.5 / Exon 3 - Exon 4 junction NM_000901.5 / Exon 4 - Exon 5 junction
<b>PER1</b>	Forward Reverse	5'-TCATGATGACCTACCAGGTG-3' 5'-ACACAGGCCATCACATCAAG-3'	<b>187</b>	NM_002616.2 / Exon NM_002616.2 / Exon - Exon junction
<b>PLAUR</b>	Forward Reverse	5'-TGTGGGAAGAAGGAGAAGAG-3' 5'-CCTGGTTGCACAAGTCTAAC-3'	<b>144</b>	NM_002659.3 / Exon 2 - Exon 3 junction NM_002659.3 / Exon 3
<b>PMEL</b>	Forward Reverse	5'-GCCTGGCAGTGGTCAGCACC-3' 5'-CGGGGTAGACGCAGCCAGTGA-3'	<b>199</b>	NM_006928.4 / Exon 7 NM_006928.4 / Exon 7
<b>PTGER2</b>	Forward Reverse	5'-ACAGATGTGCTGACAAGGCACT-3' 5'-TGCAGCCGATTGTTCTCCAAA-3'	<b>103</b>	NM_000956.3 / Exon 2 NM_000956.3 / Exon 2
<b>PTX3</b>	Forward Reverse	5'-CCGGCAGGTTGTGAAACAG-3' 5'-CTCCACCCACCACAAACT-3'	<b>229</b>	NM_002852.3 / Exon 2 - Exon 3 junction NM_002852.3 / Exon 3
<b>RDH5</b>	Forward Reverse	5'-GGAGGCCTTCTCTGACAGC-3' 5'-CCAGACTCTCCAGTTGGTC-3'	<b>110</b>	NM_002905.3 / Exon 3 NM_002905.3 / Exon 4
<b>RLBP1</b>	Forward Reverse	5'-AGATCTCAGGAAGATGGTGGAC-3' 5'-GAAGTGGATGGCTTTGAACC-3'	<b>67</b>	NM_000326.4 / Exon 7 NM_000326.4 / Exon 8
<b>RPE65</b>	Forward Reverse	5'-CAATGGGTTTCTGATTGTGGA-3' 5'-CCAGTTCTCACGTAAATTGGCTA-3'	<b>91</b>	NM_000329.2 / Exon 9 NM_000329.2 / Exon 10
<b>S100A2</b>	Forward Reverse	5'-AAGAGGGCGACAAGTTCAAG-3' 5'-ACTGTTCTCATCCAGGCTGC-3'	<b>134</b>	NM_005978.3 / Exon 2 NM_005978.3 / Exon 3
<b>SCNN1A</b> αENaC	Forward Reverse	5'-CTCTGTACGATGGTCACCC-3' 5'-GACCAGCAGGTCAAAGACGA-3'	<b>115</b>	NM_001159576.1 / Exon 11 - Exon 12 junction NM_001159576.1 / Exon 12
<b>SERPINA3</b>	Forward Reverse	5'-AAGGACCTTGACTCGCAGAC-3' 5'-ATGGGCACCATTAACCACT-3'	<b>140</b>	NM_001085.4 / Exon 2 NM_001085.4 / Exon 3
<b>SGK1</b>	Forward Reverse	5'-CGGAGAAGGACCAGCTGAAG-3' 5'-CCCAACAAGCACGTTGGAAG-3'	<b>108</b>	NM_5627.3 / Exon 8 - Exon 9 junction NM_5627.3 / Exon 9 - Exon 10 junction

<b>TSC22D3</b> GILZ	Forward Reverse	5'-TGGTGGCCATAGACAACAAG-3' 5'-CACGCTCTAGCTGGGAGTTC-3'	<b>138</b>	NM_004089.3 / Exon 2 NM_004089.3 / Exon 3
<b>TYR</b>	Forward Reverse	5'-ACTTACTCAGCCCAGCATC-3' 5'-GGTTTCCAGGATTACGCC-3'	<b>129</b>	NM_000372.4 / Exon 1 NM_000372.4 / Exon 2
<b>TYRP1</b>	Forward Reverse	5'-CCGAAACACAGTGGAGGTT-3' 5'-TCTGTGAAGGTGTGCAGGA-3'	<b>159</b>	NM_000550.2 / Exon 5 - Exon 6 junction NM_000550.2 / Exon 6

#### Rat qPCR Primers

<b>Plaur</b>	Forward Reverse	5'-CTGAAGTGCTGCAACTTCAC-3' 5'-AGCACATCTAAGCCTGTAGC-3'	<b>188</b>	NM_017350.1 / Exon 5 NM_017350.1 / Exon 8 - Exon 9 junction
<b>Ptger2</b>	Forward Reverse	5'-TGC GGATTGTCTGGCAGTAG-3' 5'-AGCAAAGATTGTGAAAGGCAGG-3'	<b>150</b>	NM_031088.1 NM_031088.1 / Exon 1 - Exon 2 junction
<b>Ptx3</b>	Forward Reverse	5'-TACCCGCAGGCTGTGAAAC-3' 5'-GGGTTCCACTTGGTGCCATA-3'	<b>175</b>	NM_001109536.1 / Exon 2 - Exon 3 junction NM_001109536.1 / Exon 3
<b>Rpl8</b>	Forward Reverse	5'-TGCTAACCGAGCTGTTGTTG-3' 5'-CTCCACAGGATTCATGGCAA-3'	<b>145</b>	NM_001034916.2 / Exon 3 NM_001034916.2 / Exon 4 - Exon 5 junction
<b>Scnn1a</b> αENaC	Forward Reverse	5'-TGCTAACCGAGCTGTTGTTG-3' 5'-CTCCACAGGATTCATGGCAA-3'	<b>145</b>	NM_001034916.2 / Exon 3 NM_001034916.2 / Exon 4 - Exon 5 junction

#### Mouse qPCR Primers

<b>β-Actin</b>	Forward Reverse	5'-AAGTACCCCATTTGAACATGGCA-3' 5'-CATCTTTTCACGTTGGCCTTA-3'	<b>156</b>	NM_007393.5 / Exon 3 NM_007393.5 / Exon 3
<b>Nr3c1</b> GR	Forward Reverse	<b>Canonica, Jeremie</b> Could you please provide me with the primers sequence you used to quantify mouse <i>Nr3c1</i> mRNA transcripts relative expression? Many thanks in advance.		
<b>Nr3c2</b> MR	Forward Reverse	5'-ATGGAAACCACACGGTGACCT-3' 5'-GCCTCATCTCCACACACCAAG-3'	<b>153</b>	NM_001083906.2 / Exon 2 NM_001083906.2 / Exon 3
<b>Human Nr3c2</b> hMR	Forward Reverse	5'-CCCTCTGAACATGACATCTTCG-3' 5'-CTGGAGCCTCGATTTTCAAC-3'	<b>153</b>	NM_000901.5 / Exon 2 NM_000901.5 / Exon 2

**Supplementary Table S8.** Specific aldosterone-regulated enriched REACTOME pathways as predicted by bioinformatic enrichment analysis.

**REACTOME pathway analysis on DEGs**

**Aldosterone 10<sup>-7</sup> M versus Control**

REACTOME Pathway Description	Link to REACTOME	Gene name	Description	Regulation	FC	P-value
<b>ECM proteoglycans</b>	R-HSA-3000178	<b>ITGB3</b>	EF-hand calcium binding domain 13 // integrin subunit beta 3	up	<b>1.71</b>	3.11E-02
		<b>ITGAX</b>	Integrin subunit alpha X	up	<b>1.51</b>	1.27E-02
		<b>FMOD</b>	Fibromodulin	down	<b>-2.09</b>	3.28E-02
		<b>BGN</b>	Biglycan	down	<b>-1.57</b>	3.68E-03
		<b>COL2A1</b>	Collagen type II alpha 1 chain	down	<b>-1.52</b>	2.59E-03
<b>Integrin cell surface interactions</b>	R-HSA-216083	<b>ITGB3</b>	EF-hand calcium binding domain 13 // integrin subunit beta 3	up	<b>1.71</b>	3.11E-02
		<b>ITGA4</b>	integrin subunit alpha 4	up	<b>1.53</b>	2.06E-03
		<b>ITGAX</b>	Integrin subunit alpha X	up	<b>1.51</b>	1.27E-02
		<b>COL2A1</b>	Collagen type II alpha 1 chain	down	<b>-1.52</b>	2.59E-03
<b>Dissolution of Fibrin Clot</b>	R-HSA-75205	<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.16</b>	6.77E-03
		<b>PLAT</b>	Plasminogen activator, tissue type	up	<b>1.60</b>	1.38E-02

Up, up-regulated genes in the REACTOME pathway; down, down-regulated genes in the REACTOME pathway; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S9.** Specific cortisol-regulated enriched REACTOME pathways as predicted by bioinformatic enrichment analysis.

**REACTOME pathway analysis on DEGs**

**Cortisol 10<sup>-7</sup> M versus Control**

REACTOME Pathway Description	Link to REACTOME	Gene name	Description	Regulation	FC	P-value
Regulation of Insulin-like Growth Factor transport and uptake by Insulin-like Growth Factor Binding Proteins	R-HSA-381426	IGF1	Insulin like growth factor 1	down	-1.85	1.51E-18
		PAPPA	Pappalysin 1	down	-1.66	1.58E-02
		IGFBP3	Insulin like growth factor binding protein 3	down	-1.64	1.77E-03
Integrin cell surface interactions	R-HSA-216083	SPP1	Secreted phosphoprotein 1	down	-2.25	5.38E-05
		ITGA11	Integrin subunit alpha 11	down	-2.24	3.58E-07
		COL1A1	Collagen type I alpha 1 chain	down	-1.68	3.34E-03
O-glycosylation of TSR domain-containing proteins	R-HSA-5173214	ADAMTSL1	ADAMTS like 1	up	1.53	3.58E-05
		ADAMTSL4	ADAMTS like 4	up	1.53	4.94E-18
		ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif 1	down	-1.57	8.90E-12

Up, up-regulated genes in the REACTOME pathway; down, down-regulated genes in the REACTOME pathway; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S10.** Specific cortisol + RU-486-regulated enriched REACTOME pathways as predicted by bioinformatic enrichment analysis.

**REACTOME pathway analysis on DEGs**

**Cortisol  $10^{-7}$  M + RU-486  $10^{-5}$  M versus Control**

REACTOME Pathway Description	Link to REACTOME	Gene name	Description	Regulation	FC	P-value
Cyclin A/B1/B2 associated events during G2/M transition	R-HSA-69273	CCNA1	Cyclin A1	down	-1.92	1.29E-07
		PLK1	Polo like kinase 1	down	-1.72	2.43E-04
		CCNA2	Cyclin A2	down	-1.72	1.60E-07
		FOXM1	Forkhead box M1	down	-1.62	3.17E-03
		CDK1	Cyclin dependent kinase 1	down	-1.62	4.47E-10
G0 and Early G1	R-HSA-1538133	CCNA1	Cyclin A1	down	-1.92	1.29E-07
		CCNA2	Cyclin A2	down	-1.72	1.60E-07
		CDK1	Cyclin dependent kinase 1	down	-1.62	4.47E-10
		TOP2A	Topoisomerase (DNA) II alpha	down	-1.56	2.82E-06
		MYBL2	MYB proto-oncogene like 2	down	-1.56	8.14E-06
Resolution of Sister Chromatid Cohesion	R-HSA-2500257	SPC24	SPC24, NDC80 kinetochore complex component	down	-1.84	4.74E-07
		BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	down	-1.81	2.76E-11
		PLK1	Polo like kinase 1	down	-1.72	2.43E-04
		CENPF	Centromere protein F	down	-1.63	2.37E-05
		CDK1	Cyclin dependent kinase 1	down	-1.62	4.47E-10
		CENPM	Centromere protein M	down	-1.58	5.36E-03
		SPC25	SPC25, NDC80 kinetochore complex component	down	-1.54	3.80E-02
CDC20	Cell division cycle 20	down	-1.52	1.12E-03		
RHO GTPases Activate Formins	R-HSA-5663220	SPC24	SPC24, NDC80 kinetochore complex component	down	-1.84	4.74E-07

		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CENPM</b>	Centromere protein M	down	<b>-1.58</b>	5.36E-03
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
		<b>DIAPH3</b>	Diaphanous related formin 3	down	<b>-1.53</b>	1.22E-08
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
Phosphorylation of proteins involved in the G2/M transition by Cyclin A:Cdc2 complexes	R-HSA-170145	<b>CCNA1</b>	Cyclin A1	down	<b>-1.92</b>	1.29E-07
		<b>CCNA2</b>	Cyclin A2	down	<b>-1.72</b>	1.60E-07
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
Polo-like kinase mediated events	R-HSA-156711	<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>FOXM1</b>	Forkhead box M1	down	<b>-1.62</b>	3.17E-03
		<b>MYBL2</b>	MYB proto-oncogene like 2	down	<b>-1.56</b>	8.14E-06
Mitotic Prometaphase	R-HSA-68877	<b>SPC24</b>	SPC24, NDC80 kinetochore complex component	down	<b>-1.84</b>	4.74E-07
		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CENPM</b>	Centromere protein M	down	<b>-1.58</b>	5.36E-03
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
Phosphorylation of Emi1	R-HSA-176417	<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03

<b>Regulation of APC/C activators between G1/S and early anaphase</b>	R-HSA-176408	<b>CCNA1</b>	Cyclin A1	down	<b>-1.92</b>	1.29E-07
		<b>CCNA2</b>	Cyclin A2	down	<b>-1.72</b>	1.60E-07
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
<b>Cdc20:Phospho-APC/C mediated degradation of Cyclin A</b>	R-HSA-174184	<b>CCNA1</b>	Cyclin A1	down	<b>-1.92</b>	1.29E-07
		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B // p21 (RAC1) activated kinase 6	down	<b>-1.81</b>	2.76E-11
		<b>CCNA2</b>	Cyclin A2	down	<b>-1.72</b>	1.60E-07
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
<b>Dissolution of Fibrin Clot</b>	R-HSA-75205	<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.38</b>	1.14E-10
		<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
<b>Separation of Sister Chromatids</b>	R-HSA-2467813	<b>SPC24</b>	SPC24, NDC80 kinetochore complex component	down	<b>-1.84</b>	4.74E-07
		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CENPM</b>	Centromere protein M	down	<b>-1.58</b>	5.36E-03
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
<b>Degradation of the extracellular matrix</b>	R-HSA-1474228	<b>MMP1</b>	Matrix metalloproteinase 1	up	<b>6.06</b>	2.25E-08
		<b>LAMC2</b>	Laminin subunit gamma 2	up	<b>1.76</b>	5.04E-12
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09





Platelet degranulation	R-HSA-114608	RAB27B	RAB27B, member RAS oncogene family	up	2.05	2.46E-14
		EFCAB13	EF-hand calcium binding domain 13	up	1.94	2.60E-06
		ECM1	Extracellular matrix protein 1	up	1.82	3.16E-06
		SERPINA3	Serpin family A member 3	up	1.62	3.90E-07
		SERPINE1	Serpin family E member 1	up	1.54	2.46E-03
Antagonism of Activin by Follistatin	R-HSA-2473224	INHBA	Inhibin beta A subunit	down	-1.96	6.23E-03
		INHBB	Inhibin beta B subunit	down	-1.68	4.33E-13
Mitotic Telophase/Cytokinesis	R-HSA-68884	KIF20A	Kinesin family member 20A	down	-2.04	5.94E-08
		PLK1	Polo like kinase 1	down	-1.72	2.43E-04
G2 Phase	R-HSA-68911	CCNA1	Cyclin A1	down	-1.92	1.29E-07
		CCNA2	Cyclin A2	down	-1.72	1.60E-07
ECM proteoglycans	R-HSA-3000178	EFCAB13	EF-hand calcium binding domain 13	up	1.94	2.60E-06
		SERPINE1	Serpin family E member 1	up	1.54	2.46E-03
		LUM	Lumican	down	-1.72	6.80E-05
		COL1A1	Collagen type I alpha 1 chain	down	-1.64	4.98E-03
		COL3A1	Collagen type III alpha 1 chain	down	-1.52	1.44E-13
O-glycosylation of TSR domain-containing proteins	R-HSA-5173214	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif 5	down	-2.24	3.58E-08
		ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif 15	down	-1.67	1.10E-04
		THBS2	Thrombospondin 2	down	-1.53	2.41E-06

Up, up-regulated genes in the REACTOME pathway; down, down-regulated genes in the REACTOME pathway; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S11.** Specific aldosterone-regulated enriched biological process gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Biological Process** analysis on DEGs

**Aldosterone 10<sup>-7</sup> M versus Control**

GO cellular components term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Chemical synaptic transmission</b>	GO:0007268	<b>OPRD1</b>	Opioid receptor delta 1	up	<b>1.55</b>	2,95E-03
		<b>DOC2A</b>	Double C2 domain alpha	down	<b>-2.31</b>	3,39E-03
		<b>PLP1</b>	Proteolipid protein 1	down	<b>-1.87</b>	3,19E-02
		<b>SST</b>	Somatostatin	down	<b>-1.81</b>	1,02E-04
		<b>GJD2</b>	Gap junction protein delta 2	down	<b>-1.67</b>	1,70E-02
		<b>TPGS1</b>	Tubulin polyglutamylase complex subunit 1	down	<b>-1.59</b>	1,70E-03
		<b>KCNMB2</b>	Potassium calcium-activated channel subfamily M regulatory beta subunit 2	down	<b>-1.56</b>	1,09E-02
		<b>SLC12A5</b>	Solute carrier family 12 member 5	down	<b>-1.52</b>	2,40E-03
		<b>HTR1D</b>	5-hydroxytryptamine receptor 1D	down	<b>-1.51</b>	4,09E-02
<b>Axonogenesis</b>	GO:0007409	<b>OMD</b>	Osteomodulin	up	<b>1.87</b>	2,87E-03
		<b>DSCAML1</b>	DS cell adhesion molecule like 1	up	<b>1.57</b>	7,08E-03
		<b>S100A6</b>	S100 calcium binding protein A6	up	<b>1.55</b>	2,27E-03
		<b>FMOD</b>	Fibromodulin	down	<b>-2.09</b>	3,28E-02
		<b>CTNNA2</b>	Catenin alpha 2	down	<b>-1.79</b>	1,23E-02
		<b>OMG</b>	Oligodendrocyte myelin glycoprotein	down	<b>-1.58</b>	3,84E-03
<b>Cell adhesion</b>	GO:0007155	<b>MYBPC2</b>	Myosin binding protein C, fast type	up	<b>1.95</b>	4,04E-02
		<b>OMD</b>	Osteomodulin	up	<b>1.87</b>	2,87E-03
		<b>SVEP1</b>	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	up	<b>1.73</b>	1,08E-02
		<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>EPHA8</b>	EPH receptor A8	up	<b>1,70</b>	2,77E-02
		<b>DSCAML1</b>	DS cell adhesion molecule like 1	up	<b>1.57</b>	7,08E-03
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03

		<b>ITGAX</b>	Integrin subunit alpha X	up	<b>1.51</b>	1,27E-02
		<b>CTNNA2</b>	Catenin alpha 2	down	<b>-1.79</b>	1,23E-02
		<b>OMG</b>	Oligodendrocyte myelin glycoprotein	down	<b>-1.58</b>	3,84E-03
<b>Heterotypic cell-cell adhesion</b>	GO:0034113	<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03
		<b>ITGAX</b>	Integrin subunit alpha X	up	<b>1.51</b>	1,27E-02
<b>Epithelial cell differentiation</b>	GO:0030855	<b>EHF</b>	ETS homologous factor	up	<b>3.55</b>	2,68E-04
		<b>GDF7</b>	Growth differentiation factor 7	down	<b>-2.01</b>	2,21E-03
		<b>SIX1</b>	SIX homeobox 1	down	<b>-1.95</b>	4,58E-03
		<b>KRT4</b>	Keratin 4	down	<b>-1.55</b>	4,15E-03
<b>Response to progesterone</b>	GO:0032570	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>1.89</b>	3,69E-03
		<b>PTGER2</b>	Prostaglandin E receptor 2	up	<b>1.57</b>	7,18E-06
		<b>RAMP2</b>	Receptor activity modifying protein 2	down	<b>-1.57</b>	1,23E-02
<b>Negative regulation of JAK-STAT cascade</b>	GO:0046426	<b>RTN4RL2</b>	Reticulon 4 receptor-like 2	down	<b>-1.67</b>	3,22E-04
		<b>BGN</b>	Biglycan	down	<b>-1.57</b>	3,68E-03
		<b>SOCS1</b>	Suppressor of cytokine signaling 1	down	<b>-1.51</b>	3,26E-02
<b>Integrin-mediated signaling pathway</b>	GO:0007229	<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03
		<b>ITGAX</b>	Integrin subunit alpha X	up	<b>1.51</b>	1,27E-02
		<b>PLP1</b>	Proteolipid protein 1	down	<b>-1.87</b>	3,19E-02
<b>Negative regulation of protein kinase activity</b>	GO:0006469	<b>RTN4RL2</b>	Reticulon 4 receptor-like 2	down	<b>-1.67</b>	3,22E-04
		<b>PTPRC</b>	Protein tyrosine phosphatase, receptor type C	down	<b>-1.64</b>	2,25E-02
		<b>BGN</b>	Biglycan	down	<b>-1.57</b>	3,68E-03

		<b>SOCS1</b>	Suppressor of cytokine signaling 1	down	<b>-1.51</b>	3,26E-02
<b>Otic vesicle development</b>	GO:0071599	<b>SIX1</b>	SIX homeobox 1	down	<b>-1.95</b>	4,58E-03
		<b>COL2A1</b>	Collagen type II alpha 1 chain	down	<b>-1.52</b>	2,59E-03
<b>Response to cAMP</b>	GO:0051591	<b>AGXT</b>	Alanine-glyoxylate aminotransferase	up	<b>2.13</b>	4,53E-02
		<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>1.89</b>	3,69E-03
		<b>PER1</b>	MicroRNA 6883 // period circadian clock 1	up	<b>1.51</b>	3,53E-06

GO, gene ontology; up, up-regulated genes in the biological process gene ontology term; down, down-regulated genes in the biological process gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S12.** Specific cortisol-regulated enriched biological process gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Biological Process** analysis on DEGs

**Cortisol 10<sup>-7</sup> M versus Control**

GO biological process term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Negative regulation of skeletal muscle tissue development</b>	GO:0048642	<b>TSC22D3</b>	TSC22 domain family member 3	up	<b>1.83</b>	2.58E-107
		<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	<b>1.76</b>	5.76E-04
		<b>USP2</b>	Ubiquitin specific peptidase 2	up	<b>1.57</b>	4.64E-09
<b>Positive regulation of apoptotic process</b>	GO:0043065	<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>1.82</b>	2.93E-03
		<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.79</b>	4.35E-45
		<b>WNT11</b>	Wnt family member 11	up	<b>1.61</b>	3.74E-04
		<b>ADAMTSL4</b>	ADAMTS like 4	up	<b>1.53</b>	4.94E-18
		<b>TGM2</b>	Transglutaminase 2	down	<b>-2.40</b>	1.64E-04
		<b>ANKRD1</b>	Ankyrin repeat domain 1	down	<b>-1.79</b>	1.02E-02
		<b>SFRP2</b>	Secreted frizzled related protein 2	down	<b>-1.78</b>	2.39E-03
		<b>IGFBP3</b>	Insulin like growth factor binding protein 3	down	<b>-1.64</b>	1.77E-03
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.61</b>	4.88E-04
<b>Response to drug</b>	GO:0042493	<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>1.82</b>	2.93E-03
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.69</b>	1.35E-18
		<b>TGFBR2</b>	Transforming growth factor beta receptor 2	up	<b>1.64</b>	2.09E-18
		<b>PLIN2</b>	Perilipin 2	up	<b>1.60</b>	3.19E-14
		<b>INHBA</b>	Inhibin beta A subunit	down	<b>-2.07</b>	3.31E-03
		<b>SFRP2</b>	Secreted frizzled related protein 2	down	<b>-1.78</b>	2.39E-03
		<b>SST</b>	Somatostatin	down	<b>-1.69</b>	3.85E-03
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.68</b>	3.34E-03
<b>Response to hyperoxia</b>	GO:0055093	<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.69</b>	1.35E-18
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.57</b>	6.84E-17

		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.68</b>	3.34E-03
<b>Action potential</b>	GO:0001508	<b>USP53</b>	Ubiquitin specific peptidase 53	up	<b>1.73</b>	1.71E-40
		<b>KCND2</b>	Potassium voltage-gated channel subfamily D member 2	down	<b>-1.74</b>	8.81E-05
		<b>GJD2</b>	Gap junction protein delta 2	down	<b>-1.70</b>	8.95E-05
<b>Osteoblast differentiation</b>	GO:0001649	<b>WNT11</b>	Wnt family member 11	up	<b>1.61</b>	3.74E-04
		<b>ITGA11</b>	Integrin subunit alpha 11	down	<b>-2.24</b>	3.58E-07
		<b>SPP1</b>	Secreted phosphoprotein 1	down	<b>-2.25</b>	5.38E-05
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.68</b>	3.34E-03
		<b>IGFBP3</b>	Insulin like growth factor binding protein 3	down	<b>-1.64</b>	1.77E-03
<b>Ganglioside biosynthetic process</b>	GO:0001574	<b>ST6GALNA C2</b>	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	up	<b>2.24</b>	8.46E-132
		<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	up	<b>1.72</b>	1.01E-12
		<b>B4GALNT1</b>	Beta-1,4-N-acetyl-galactosaminyltransferase 1	up	<b>1.51</b>	1.60E-02
<b>Activation of MAPK activity</b>	GO:0000187	<b>DUSP5</b>	Dual specificity phosphatase 5	up	<b>1.84</b>	3.95E-03
		<b>CXCR4</b>	C-X-C motif chemokine receptor 4	up	<b>1.81</b>	5.67E-15
		<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>1.82</b>	2.93E-03
		<b>IGF1</b>	Insulin like growth factor 1	down	<b>-1.85</b>	1.51E-18
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.61</b>	4.88E-04
<b>Cellular response to tumor necrosis factor</b>	GO:0071356	<b>ZFP36</b>	ZFP36 ring finger protein	up	<b>1.58</b>	1.58E-04
		<b>INPP5K</b>	Inositol polyphosphate-5-phosphatase K	up	<b>1.57</b>	3.18E-28
		<b>CD58</b>	CD58 molecule	up	<b>1.51</b>	1.09E-05
		<b>ANKRD1</b>	Ankyrin repeat domain 1	down	<b>-1.79</b>	1.02E-02

		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	-1.68	3.34E-03
Response to steroid hormone	GO:0048545	<b>TGFBR2</b>	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		<b>SPP1</b>	Secreted phosphoprotein 1	down	-2.25	5.38E-05
		<b>SST</b>	Somatostatin	down	-1.69	3.85E-03
Positive regulation of smooth muscle cell proliferation	GO:0048661	<b>SERPINF2</b>	Serpin family F member 2	up	1.70	2.01E-40
		<b>TGFBR2</b>	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		<b>TGM2</b>	Transglutaminase 2	down	-2.40	1.64E-04
		<b>IGF1</b>	Insulin like growth factor 1	down	-1.85	1.51E-18
Peptidyl-serine phosphorylation	GO:0018105	<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	1.79	4.35E-45
		<b>TGFBR2</b>	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		<b>SGK1</b>	Serum/glucocorticoid regulated kinase 1	up	1.57	8.43E-35
		<b>STK32B</b>	Serine/threonine kinase 32B	down	-1.55	1.49E-02
		<b>TTK</b>	TTK protein kinase	down	-1.54	3.29E-03
Cell adhesion	GO:0007155	<b>EPHA8</b>	EPH receptor A8	up	2.38	4.21E-20
		<b>ITGB4</b>	Integrin subunit beta 4	up	1.60	8.17E-52
		<b>CD58</b>	CD58 molecule	up	1.51	1.09E-05
		<b>SPP1</b>	Secreted phosphoprotein 1	down	-2.25	5.38E-05
		<b>ITGA11</b>	Integrin subunit alpha 11	down	-2.24	3.58E-07
		<b>AMTN</b>	Amelotin	down	-2.08	1.63E-06
		<b>OMG</b>	Oligodendrocyte myelin glycoprotein	down	-2.02	2.94E-05
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	-1.68	3.34E-03
Regulation of endodermal cell fate specification	GO:0042663	<b>ROBO2</b>	Roundabout guidance receptor 2	down	-1.61	1.18E-10
		<b>DUSP6</b>	Dual specificity phosphatase 6	up	1.82	2.93E-03
		<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	1.76	5.76E-04



Cellular response to epidermal growth factor stimulus	GO:0071364	<b>ZFP36</b>	ZFP36 ring finger protein	up	<b>1.58</b>	1.58E-04
		<b>INPP5K</b>	Inositol polyphosphate-5-phosphatase K	up	<b>1.57</b>	3.18E-28
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.68</b>	3.34E-03
Oxidation-reduction process	GO:0055114	<b>MAOA</b>	Monoamine oxidase A	up	<b>1.94</b>	3.65E-09
		<b>KIAA1456</b>	KIAA1456	up	<b>1.92</b>	2.89E-22
		<b>HPD</b>	4-hydroxyphenylpyruvate dioxygenase	up	<b>1.91</b>	1.93E-34
		<b>SH3PXD2B</b>	SH3 and PX domains 2B	up	<b>1.88</b>	1.13E-22
		<b>ALDH1L1</b>	Aldehyde dehydrogenase 1 family member L1	up	<b>1.73</b>	1.10E-11
		<b>CP</b>	Ceruloplasmin	up	<b>1.70</b>	8.53E-12
		<b>PRODH</b>	Proline dehydrogenase 1	up	<b>1.69</b>	6.92E-91
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.69</b>	1.35E-18
		<b>CRYZ</b>	Crystallin zeta	up	<b>1.64</b>	3.83E-80
		<b>RRM2</b>	Ribonucleotide reductase regulatory subunit M2	down	<b>-1.55</b>	1.46E-08
Negative regulation of mesodermal cell fate specification	GO:0042662	<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	<b>1.76</b>	5.76E-04
		<b>SFRP2</b>	secreted frizzled related protein 2	down	<b>-1.78</b>	2.39E-03
Transmembrane transport	GO:0055085	<b>SLC13A4</b>	Solute carrier family 13 member 4	up	<b>2.03</b>	3.40E-95
		<b>SLC16A12</b>	Solute carrier family 16 member 12	up	<b>1.96</b>	6.25E-39
		<b>ABCC5</b>	ATP binding cassette subfamily C member 5	up	<b>1.75</b>	3.28E-22
		<b>ABCA4</b>	ATP binding cassette subfamily A member 4	up	<b>1.69</b>	4.72E-11
		<b>SLC16A10</b>	Solute carrier family 16 member 10	up	<b>1.57</b>	1.76E-30
		<b>GJD2</b>	Gap junction protein delta 2	down	<b>-1.70</b>	8.95E-05
Collagen fibril organization	GO:0030199	<b>SERPINF2</b>	Serpin family F member 2	up	<b>1.70</b>	2.01E-40
		<b>SFRP2</b>	Secreted frizzled related protein 2	down	<b>-1.78</b>	2.39E-03
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.68</b>	3.34E-03

Embryo implantation	GO:0007566	PRLR	Prolactin receptor	up	2.01	9.89E-34
		TGFBR2	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		SPP1	Secreted phosphoprotein 1	down	-2.25	5.38E-05
Regulation of cell adhesion	GO:0030155	EPHA8	EPH receptor A8	up	2.38	4.21E-20
		PRLR	Prolactin receptor	up	2.01	9.89E-34
		CYTIP	Cytohesin 1 interacting protein	up	1.53	2.87E-03
Convergent extension involved in axis elongation	GO:0060028	WNT11	Wnt family member 11	up	1.61	3.74E-04
		SFRP2	Secreted frizzled related protein 2	down	-1.78	2.39E-03
Substrate-dependent cell migration	GO:0006929	EPHA8	EPH receptor A8	up	2.38	4.21E-20
		ITGA11	Integrin subunit alpha 11	down	-2.24	3.58E-07
Outflow tract morphogenesis	GO:0003151	TGFBR2	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		WNT11	Wnt family member 11	up	1.61	3.74E-04
		SFRP2	Secreted frizzled related protein 2	down	-1.78	2.39E-03
Heart development	GO:0007507	SH3PXD2B	SH3 and PX domains 2B	up	1.88	1.13E-22
		RPS6KA2	Ribosomal protein S6 kinase A2	up	1.79	4.35E-45
		SOD2	Superoxide dismutase 2, mitochondrial	up	1.69	1.35E-18
		TGFBR2	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		NTRK3	Neurotrophic receptor tyrosine kinase 3	down	-1.61	4.88E-04
Regulation of cell proliferation	GO:0042127	PTGER2	Prostaglandin E receptor 2	up	2.62	5.28E-54
		TGFBR2	Transforming growth factor beta receptor 2	up	1.64	2.09E-18
		SGK1	Serum/glucocorticoid regulated kinase 1	up	1.57	8.43E-35
		CHST11	Carbohydrate sulfotransferase 11	up	1.55	1.45E-25

		<b>CDCA7</b>	Cell division cycle associated 7	down	<b>-1.71</b>	2.48E-04
<b>Positive regulation of fat cell differentiation</b>	GO:0045600	<b>SH3PXD2B</b>	SH3 and PX domains 2B	up	<b>1.88</b>	1.13E-22
		<b>ZFP36</b>	ZFP36 ring finger protein	up	<b>1.58</b>	1.58E-04
		<b>SFRP2</b>	Secreted frizzled related protein 2	down	<b>-1.78</b>	2.39E-03
<b>Proton transport</b>	GO:0015992	<b>HVCN1</b>	Hydrogen voltage gated channel 1	up	<b>4.15</b>	4.71E-32
		<b>SLC2A12</b>	Solute carrier family 2 member 12	up	<b>1.58</b>	2.58E-42
		<b>ATP6V0A4</b>	ATPase H <sup>+</sup> transporting V0 subunit a4	up	<b>1.58</b>	1.75E-05

GO, gene ontology; up, up-regulated genes in the biological process gene ontology term; down, down-regulated genes in the biological process gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S13.** Specific cortisol + RU-486-regulated enriched biological process gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Biological Process** analysis on DEGs

**Cortisol  $10^{-7}$  M + RU-486  $10^{-5}$  M versus Control**

GO biological process term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Mitotic nuclear division</b>	GO:0007067	<b>CCNA1</b>	Cyclin A1	down	<b>-1.92</b>	1.29E-07
		<b>SPC24</b>	SPC24, NDC80 kinetochore complex component	down	<b>-1.84</b>	4.74E-07
		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CCNA2</b>	Cyclin A2	down	<b>-1.72</b>	1.60E-07
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
		<b>CDCA3</b>	Cell division cycle associated 3	down	<b>-1.59</b>	4.27E-03
		<b>ASPM</b>	Abnormal spindle microtubule assembly	down	<b>-1.58</b>	1.97E-06
		<b>ANLN</b>	Anillin actin binding protein	down	<b>-1.58</b>	1.99E-06
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
<b>Response to drug</b>	GO:0042493	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>2.85</b>	1.83E-07
		<b>PLIN2</b>	Perilipin 2	up	<b>2.83</b>	3.52E-64
		<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>CPT1A</b>	Carnitine palmitoyltransferase 1A	up	<b>1.67</b>	3.98E-52
		<b>MGST1</b>	Microsomal glutathione S-transferase 1	up	<b>1.57</b>	3.47E-18
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.52</b>	2.06E-12
		<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03

		<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>SST</b>	Somatostatin	down	<b>-1.60</b>	8.94E-03
		<b>CA9</b>	Carbonic anhydrase 9	down	<b>-1.50</b>	7.90E-24
Positive regulation of apoptotic process	GO:0043065	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>DUSP6</b>	dual specificity phosphatase 6	up	<b>2.85</b>	1.83E-07
		<b>KCNMA1</b>	Potassium calcium-activated channel subfamily M alpha 1	up	<b>1.92</b>	6.93E-10
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>OSGIN1</b>	Oxidative stress induced growth inhibitor 1	up	<b>1.74</b>	1.43E-08
		<b>PMAIP1</b>	Phorbol-12-myristate-13-acetate-induced protein 1	up	<b>1.61</b>	1.21E-06
		<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
		<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
		<b>FGD3</b>	FYVE, RhoGEF and PH domain containing 3	down	<b>-2.16</b>	4.81E-09
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.97</b>	1.20E-06
		<b>ANKRD1</b>	Ankyrin repeat domain 1	down	<b>-1.85</b>	6.52E-03
		<b>BMF</b>	Bcl2 modifying factor	down	<b>-1.69</b>	8.82E-13
		<b>TOP2A</b>	Topoisomerase (DNA) II alpha	down	<b>-1.56</b>	2.82E-06
Response to organic cyclic compound	GO:0014070	<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>2.85</b>	1.83E-07
		<b>PLIN2</b>	Perilipin 2	up	<b>2.83</b>	3.52E-64
		<b>CPT1A</b>	Carnitine palmitoyltransferase 1A	up	<b>1.67</b>	3.98E-52
		<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
		<b>MKI67</b>	Marker of proliferation Ki-67	down	<b>-1.69</b>	6.36E-05
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
	GO:0043066	<b>ANGPTL4</b>	Angiopoietin like 4	up	<b>3.56</b>	2.07E-31

Negative regulation of apoptotic process		PLAUR	Plasminogen activator, urokinase receptor	up	2.38	1.14E-10
		ANXA1	Annexin A1	up	1.93	1.17E-08
		SPRY2	Sprouty RTK signaling antagonist 2	up	1.77	3.61E-07
		IL6	Interleukin 6	up	1.76	3.15E-05
		NQO1	NAD(P)H quinone dehydrogenase 1	up	1.72	9.60E-09
		PRLR	Prolactin receptor	up	1.66	1.57E-18
		TNFSF18	Tumor necrosis factor superfamily member 18	up	1.59	8.30E-04
		CD44	CD44 molecule (Indian blood group)	up	1.54	2.73E-09
		SOD2	Superoxide dismutase 2, mitochondrial	up	1.52	2.06E-12
		CHST11	Carbohydrate sulfotransferase 11	up	1.50	2.25E-22
		TGM2	Transglutaminase 2	down	-2.86	6.47E-06
		SOX8	SRY-box 8	down	-1.97	1.41E-07
		PLK1	Polo like kinase 1	down	-1.72	2.43E-04
		CDK1	Cyclin dependent kinase 1	down	-1.62	4.47E-10
		CCND2	Cyclin D2	down	-1.54	2.85E-17
Collagen fibril organization	GO:0030199	CYP1B1	Cytochrome P450 family 1 subfamily B member 1	up	1.55	3.67E-05
		MMP11	Matrix metallopeptidase 11	down	-1.76	9.27E-23
		LUM	Lumican	down	-1.72	6.80E-05
		COL1A1	Collagen type I alpha 1 chain	down	-1.64	4.98E-03
		COL3A1	Collagen type III alpha 1 chain	down	-1.52	1.44E-13
Negative regulation of fat cell differentiation	GO:0045599	IL6	Interleukin 6	up	1.76	3.15E-05
		TRIB3	Tribbles pseudokinase 3	up	1.71	2.94E-06
		SOD2	Superoxide dismutase 2, mitochondrial	up	1.52	2.06E-12
		RUNX1T1	RUNX1 translocation partner 1	down	-1.93	1.02E-05
		MMP11	Matrix metallopeptidase 11	down	-1.76	9.27E-23
Sister chromatid cohesion	GO:0007062	SPC24	SPC24, NDC80 kinetochore complex component	down	-1.84	4.74E-07
		BUB1B	BUB1 mitotic checkpoint serine/threonine Kinase B	down	-1.81	2.76E-11

		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CENPM</b>	Centromere protein M	down	<b>-1.58</b>	5.36E-03
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
Cell division	GO:0051301	<b>CCNA1</b>	Cyclin A1	down	<b>-1.92</b>	1.29E-07
		<b>SPC24</b>	SPC24, NDC80 kinetochore complex component	down	<b>-1.84</b>	4.74E-07
		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>CCNA2</b>	Cyclin A2	down	<b>-1.72</b>	1.60E-07
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
		<b>CDCA3</b>	Cell division cycle associated 3	down	<b>-1.59</b>	4.27E-03
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
		<b>CCND2</b>	Cyclin D2	down	<b>-1.54</b>	2.85E-17
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
		<b>KIFC1</b>	Kinesin family member C1	down	<b>-1.50</b>	4.13E-05
Response to cAMP	GO:0051591	<b>AGXT</b>	Alanine-glyoxylate aminotransferase	up	<b>5.02</b>	6.09E-05
		<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>PTPRN</b>	protein tyrosine phosphatase, receptor type N	up	<b>1.73</b>	2.71E-05
		<b>PER1</b>	Period circadian clock 1	up	<b>1.51</b>	1.76E-11
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
Microtubule bundle formation	GO:0001578	<b>KIF20A</b>	Kinesin family member 20A	down	<b>-2.04</b>	5.94E-08
		<b>TPPP3</b>	Tubulin polymerization promoting protein family member 3	down	<b>-1.73</b>	5.85E-04
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04

		<b>CAPN6</b>	Calpain 6	down	<b>-1.67</b>	3.35E-12
<b>Cell adhesion</b>	GO:0007155	<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
		<b>LAMC2</b>	Laminin subunit gamma 2	up	<b>1.76</b>	5.04E-12
		<b>ATP1B2</b>	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 2	up	<b>1.57</b>	1.62E-10
		<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
		<b>EPHA8</b>	EPH receptor A8	up	<b>1.50</b>	2.43E-05
		<b>OMG</b>	Oligodendrocyte myelin glycoprotein	down	<b>-2.80</b>	1.53E-09
		<b>AMTN</b>	Amelotin	down	<b>-2.37</b>	1.93E-08
		<b>ITGA11</b>	Integrin subunit alpha 11	down	<b>-2.19</b>	7.41E-07
		<b>HAPLN3</b>	Hyaluronan and proteoglycan link protein 3	down	<b>-2.00</b>	8.82E-05
		<b>MOG</b>	Myelin oligodendrocyte glycoprotein	down	<b>-1.73</b>	2.64E-02
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
		<b>MFAP4</b>	Microfibrillar associated protein 4	down	<b>-1.55</b>	2.66E-07
		<b>THBS2</b>	Thrombospondin 2	down	<b>-1.53</b>	2.41E-06
		<b>MFGE8</b>	Milk fat globule-EGF factor 8 protein	down	<b>-1.52</b>	9.70E-30
<b>Negative regulation of cell adhesion mediated by integrin</b>	GO:0033629	<b>ACER2</b>	Alkaline ceramidase 2	up	<b>1.67</b>	2.27E-02
		<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
<b>Extracellular matrix organization</b>	GO:0030198	<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
		<b>LAMC2</b>	Laminin subunit gamma 2	up	<b>1.76</b>	5.04E-12
		<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
		<b>ELF3</b>	E74 like ETS transcription factor 3	down	<b>-2.34</b>	1.44E-08
		<b>ITGA11</b>	Integrin subunit alpha 11	down	<b>-2.19</b>	7.41E-07
		<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
		<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13



<b>Positive regulation of ubiquitin protein ligase activity</b>	GO:1904668	<b>CDC20B</b>	Cell division cycle 20B	down	<b>-1.85</b>	3.55E-03
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
<b>Negative regulation of platelet aggregation</b>	GO:0090331	<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
		<b>UBASH3B</b>	Ubiquitin associated and SH3 domain containing B	up	<b>1.51</b>	1.04E-03
<b>Mitotic cytokinesis</b>	GO:0000281	<b>KIF20A</b>	Kinesin family member 20A	down	<b>-2.04</b>	5.94E-08
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>KIF4A</b>	Kinesin family member 4A	down	<b>-1.71</b>	6.57E-05
		<b>ANLN</b>	Anillin actin binding protein	down	<b>-1.58</b>	1.99E-06
<b>Negative regulation of cell proliferation</b>	GO:0008285	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>HMGA1</b>	High mobility group AT-hook 1	up	<b>1.97</b>	7.42E-07
		<b>SPRY2</b>	Sprouty RTK signaling antagonist 2	up	<b>1.77</b>	3.61E-07
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>TESC</b>	Tescalcin	up	<b>1.69</b>	7.70E-06
		<b>IFITM1</b>	Interferon induced transmembrane protein 1	up	<b>1.59</b>	2.00E-05
		<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.52</b>	2.06E-12
		<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03
		<b>SST</b>	Somatostatin	down	<b>-1.60</b>	8.94E-03
		<b>CDKN2C</b>	Cyclin dependent kinase inhibitor 2C	down	<b>-1.57</b>	1.97E-04
<b>Positive regulation of gene expression</b>	GO:0010628	<b>IL7R</b>	Interleukin 7 receptor	up	<b>3.40</b>	3.11E-08

		<b>SPRY2</b>	Sprouty RTK signaling antagonist 2	up	<b>1.77</b>	3.61E-07
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>TESC</b>	Tescalcin	up	<b>1.69</b>	7.70E-06
		<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
		<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
		<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta	down	<b>-2.13</b>	4.92E-19
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.97</b>	1.20E-06
		<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
<b>Protein homooligomerization</b>	GO:0051260	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1	up	<b>16.20</b>	8.08E-17
		<b>ANGPTL4</b>	Angiopoietin like 4	up	<b>3.56</b>	2.07E-31
		<b>CPT1A</b>	Carnitine palmitoyltransferase 1A	up	<b>1.67</b>	3.98E-52
		<b>SLC22A6</b>	Solute carrier family 22 member 6	up	<b>1.63</b>	1.17E-05
		<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.52</b>	2.06E-12
		<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
<b>Positive regulation of cell proliferation</b>	GO:0008284	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>HILPDA</b>	Hypoxia inducible lipid droplet associated	up	<b>1.76</b>	2.88E-09
		<b>LAMC2</b>	Laminin subunit gamma 2	up	<b>1.76</b>	5.04E-12
		<b>ACER2</b>	Alkaline ceramidase 2	up	<b>1.67</b>	2.27E-02
		<b>OSMR</b>	Oncostatin M receptor	up	<b>1.53</b>	4.39E-10
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.97</b>	1.20E-06
		<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
		<b>FOXO1</b>	Forkhead box M1	down	<b>-1.62</b>	3.17E-03
		<b>MLXIPL</b>	MLX interacting protein like	down	<b>-1.56</b>	3.07E-04
		<b>EDN2</b>	Endothelin 2	down	<b>-1.54</b>	4.96E-12

		<b>CCND2</b>	Cyclin D2	down	<b>-1.54</b>	2.85E-17
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
		<b>NTN1</b>	Netrin 1	down	<b>-1.51</b>	3.14E-06
<b>Mitotic spindle assembly</b>	GO:0090307	<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
		<b>MYBL2</b>	MYB proto-oncogene like 2	down	<b>-1.56</b>	8.14E-06
		<b>KIFC1</b>	Kinesin family member C1	down	<b>-1.50</b>	4.13E-05
<b>Epithelial cell differentiation</b>	GO:0030855	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1	up	<b>16.20</b>	8.08E-17
		<b>CPT1A</b>	Carnitine palmitoyltransferase 1A	up	<b>1.67</b>	3.98E-52
		<b>TAGLN</b>	Transgelin	down	<b>-2.35</b>	7.00E-33
		<b>ELF3</b>	E74 like ETS transcription factor 3	down	<b>-2.34</b>	1.44E-08
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
<b>Response to virus</b>	GO:0009615	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>HMGA1</b>	High mobility group AT-hook 1	up	<b>1.97</b>	7.42E-07
		<b>RSAD2</b>	Radical S-adenosyl methionine domain containing 2	up	<b>1.74</b>	3.08E-17
		<b>CXCR4</b>	C-X-C motif chemokine receptor 4	up	<b>1.64</b>	1.05E-10
		<b>IFITM1</b>	Interferon induced transmembrane protein 1	up	<b>1.59</b>	2.00E-05
		<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta	down	<b>-2.13</b>	4.92E-19
<b>Regulation of cell migration</b>	GO:0030334	<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
		<b>CXCR4</b>	C-X-C motif chemokine receptor 4	up	<b>1.64</b>	1.05E-10
		<b>SST</b>	Somatostatin	down	<b>-1.60</b>	8.94E-03
		<b>NTN1</b>	Netrin 1	down	<b>-1.51</b>	3.14E-06
<b>Regulation of pH</b>	GO:0006885	<b>PDK4</b>	Pyruvate dehydrogenase kinase 4	up	<b>2.21</b>	1.14E-10
		<b>SLC9A9</b>	Solute carrier family 9 member A9	up	<b>1.61</b>	3.20E-07

		ATP6V1B1	ATPase H <sup>+</sup> transporting V1 subunit B1	down	-1.85	5.46E-07
Extracellular matrix disassembly	GO:0022617	MMP1	Matrix metalloproteinase 1	up	6.06	2.25E-08
		LAMC2	Laminin subunit gamma 2	up	1.76	5.04E-12
		CD44	CD44 molecule (Indian blood group)	up	1.54	2.73E-09
		ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif 5	down	-2.24	3.58E-08
		MMP11	Matrix metalloproteinase 11	down	-1.76	9.27E-23
Platelet activation	GO:0030168	EFCAB13	EF-hand calcium binding domain 13	up	1.94	2.60E-06
		IL6	Interleukin 6	up	1.76	3.15E-05
		GNG2	G protein subunit gamma 2	up	1.54	5.57E-13
		ADRA2C	Adrenoceptor alpha 2C	down	-1.67	3.79E-20
		COL1A1	Collagen type I alpha 1 chain	down	-1.64	4.98E-03
		COL3A1	Collagen type III alpha 1 chain	down	-1.52	1.44E-13
Visual perception	GO:0007601	PRCD	Progressive rod-cone degeneration	up	1.99	4.97E-04
		RLBP1	Retinaldehyde binding protein 1	up	1.57	6.70E-10
		CYP1B1	Cytochrome P450 family 1 subfamily B member 1	up	1.55	3.67E-05
		ABCA4	ATP binding cassette subfamily A member 4	up	1.54	5.36E-08
		GJD2	Gap junction protein delta 2	down	-3.92	6.10E-20
		RGS9	Regulator of G-protein signaling 9	down	-1.74	3.78E-06
		LUM	Lumican	down	-1.72	6.80E-05
		COL1A1	Collagen type I alpha 1 chain	down	-1.64	4.98E-03
Response to hyperoxia	GO:0055093	KCNA5	Potassium voltage-gated channel subfamily A member 5	up	1.53	3.15E-15
		SOD2	Superoxide dismutase 2, mitochondrial	up	1.52	2.06E-12
		COL1A1	Collagen type I alpha 1 chain	down	-1.64	4.98E-03

<b>Xenobiotic metabolic process</b>	GO:0006805	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1	up	<b>16.20</b>	8.08E-17
		<b>NQO1</b>	NAD(P)H quinone dehydrogenase 1	up	<b>1.72</b>	9.60E-09
		<b>MGST1</b>	Microsomal glutathione S-transferase 1	up	<b>1.57</b>	3.47E-18
		<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>CYP2W1</b>	Cytochrome P450 family 2 subfamily W member 1	down	<b>-1.94</b>	1.98E-11
<b>Ganglioside biosynthetic process</b>	GO:0001574	<b>B4GALNT1</b>	Beta-1,4-N-acetyl-galactosaminyltransferase 1	up	<b>2.46</b>	3.94E-08
		<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	up	<b>1.75</b>	1.86E-13
		<b>ST3GAL4</b>	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	down	<b>-1.54</b>	1.14E-17
<b>Positive regulation of MAPK cascade</b>	GO:0043410	<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
		<b>EPHA8</b>	EPH receptor A8	up	<b>1.50</b>	2.43E-05
		<b>GPR37L1</b>	G protein-coupled receptor 37 like 1	down	<b>-2.01</b>	2.81E-06
		<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
<b>Potassium ion transport</b>	GO:0006813	<b>SLC24A4</b>	Solute carrier family 24 member 4	up	<b>2.12</b>	1.61E-05
		<b>KCNMA1</b>	Potassium calcium-activated channel subfamily M alpha 1	up	<b>1.92</b>	6.93E-10
		<b>ATP1B2</b>	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 2	up	<b>1.57</b>	1.62E-10
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
		<b>KCNAB1</b>	Potassium voltage-gated channel subfamily A member regulatory beta subunit 1	down	<b>-2.41</b>	3.67E-12

<b>Positive regulation of ovulation</b>	GO:0060279	<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03
		<b>INHBB</b>	Inhibin beta B subunit	down	<b>-1.68</b>	4.33E-13
<b>Leukocyte migration</b>	GO:0050900	<b>MMP1</b>	Matrix metalloproteinase 1	up	<b>6.06</b>	2.25E-08
		<b>EFCAB13</b>	EF-hand calcium binding domain 13 // integrin subunit beta 3	up	<b>1.94</b>	2.60E-06
		<b>ATP1B2</b>	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 2	up	<b>1.57</b>	1.62E-10
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
		<b>SLC7A11</b>	Solute carrier family 7 member 11	up	<b>1.52</b>	6.66E-14
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
<b>Defense response to virus</b>	GO:0051607	<b>ISG15</b>	ISG15 ubiquitin-like modifier	up	<b>1.88</b>	3.91E-04
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>RSAD2</b>	Radical S-adenosyl methionine domain containing 2	up	<b>1.74</b>	3.08E-17
		<b>IL33</b>	Interleukin 33	up	<b>1.62</b>	2.89E-15
		<b>PMAIP1</b>	Phorbol-12-myristate-13-acetate-induced protein 1	up	<b>1.61</b>	1.21E-06
		<b>IFITM1</b>	Interferon induced transmembrane protein 1	up	<b>1.59</b>	2.00E-05
		<b>UNC13D</b>	Unc-13 homolog D	down	<b>-1.55</b>	1.57E-12
<b>Cell differentiation</b>	GO:0030154	<b>ANGPTL4</b>	Angiopoietin like 4	up	<b>3.56</b>	2.07E-31
		<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>2.85</b>	1.83E-07
		<b>NDRG4</b>	NDRG family member 4	up	<b>2.71</b>	1.93E-12
		<b>OSGIN1</b>	Oxidative stress induced growth inhibitor 1	up	<b>1.74</b>	1.43E-08
		<b>ETV5</b>	ETS variant 5	up	<b>1.55</b>	4.11E-10
		<b>MGP</b>	Matrix Gla protein	down	<b>-2.21</b>	5.47E-07
		<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03
		<b>ERF</b>	ETS2 repressor factor	down	<b>-1.88</b>	1.18E-23
		<b>INHBB</b>	Inhibin beta B subunit	down	<b>-1.68</b>	4.33E-13
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>ABCB5</b>	ATP binding cassette subfamily B member 5	down	<b>-1.59</b>	3.70E-08

		<b>MYBL2</b>	MYB proto-oncogene like 2	down	<b>-1.56</b>	8.14E-06
		<b>PLXNB3</b>	Plexin B3	down	<b>-1.52</b>	4.18E-11
<b>Regulation of vasoconstriction</b>	GO:0019229	<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
		<b>ADRA2C</b>	Adrenoceptor alpha 2C	down	<b>-1.67</b>	3.79E-20
		<b>EDN2</b>	Endothelin 2	down	<b>-1.54</b>	4.96E-12
<b>Mitotic spindle assembly checkpoint</b>	GO:0007094	<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
<b>Response to hydrogen peroxide</b>	GO:0042542	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.52</b>	2.06E-12
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
<b>Positive regulation of protein localization to nucleus</b>	GO:1900182	<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>GTSE1</b>	G2 and S-phase expressed 1	down	<b>-1.51</b>	6.60E-05
<b>Response to cytokine</b>	GO:0034097	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>OSMR</b>	Oncostatin M receptor	up	<b>1.53</b>	4.39E-10
		<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
		<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13
	GO:1900087	<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08

Positive regulation of G1/S transition of mitotic cell cycle		KCNA5	Potassium voltage-gated channel subfamily A member 5	up	1.53	3.15E-15
		CCND2	Cyclin D2	down	-1.54	2.85E-17
Cell surface receptor signaling pathway	GO:0007166	IL7R	Interleukin 7 receptor	up	3.40	3.11E-08
		ANXA1	Annexin A1	up	1.93	1.17E-08
		PRLR	Prolactin receptor	up	1.66	1.57E-18
		IFITM1	Interferon induced transmembrane protein 1	up	1.59	2.00E-05
		TSPAN1	Tetraspanin 1	up	1.52	1.87E-02
		INHBA	Inhibin beta A subunit	down	-1.96	6.23E-03
		OXTR	Oxytocin receptor	down	-1.85	1.73E-15
		SST	Somatostatin	down	-1.60	8.94E-03
		EDN2	Endothelin 2	down	-1.54	4.96E-12
Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	GO:0051439	PLK1	Polo like kinase 1	down	-1.72	2.43E-04
		CDK1	Cyclin dependent kinase 1	down	-1.62	4.47E-10
		CDC20	Cell division cycle 20	down	-1.52	1.12E-03
Negative regulation of follicle-stimulating hormone secretion	GO:0046882	INHBA	Inhibin beta A subunit	down	-1.96	6.23E-03
		INHBB	Inhibin beta B subunit	down	-1.68	4.33E-13
Regulation of endodermal cell fate specification	GO:0042663	DUSP6	Dual specificity phosphatase 6	up	2.85	1.83E-07
		DKK1	Dickkopf WNT signaling pathway inhibitor 1	up	2.47	3.24E-08
Tooth eruption	GO:0044691	ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif 5	down	-2.24	3.58E-08
		COL1A1	Collagen type I alpha 1 chain	down	-1.64	4.98E-03
Male gonad development	GO:0008584	TESC	Tescalcin	up	1.69	7.70E-06
		SOX8	SRY-box 8	down	-1.97	1.41E-07



		<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03
		<b>WNT2B</b>	Wnt family member 2B	down	<b>-1.74</b>	2.06E-06
		<b>ASPM</b>	Abnormal spindle microtubule assembly	down	<b>-1.58</b>	1.97E-06
<b>G2/M transition of mitotic cell cycle</b>	GO:0000086	<b>PHLDA1</b>	Pleckstrin homology like domain family A member 1	up	<b>1.88</b>	1.08E-07
		<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>FOXM1</b>	Forkhead box M1	down	<b>-1.62</b>	3.17E-03
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
<b>Heart development</b>	GO:0007507	<b>FGF12</b>	Fibroblast growth factor 12	up	<b>2.03</b>	3.17E-08
		<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
		<b>SOD2</b>	Superoxide dismutase 2, mitochondrial	up	<b>1.52</b>	2.06E-12
		<b>KCNAB1</b>	Potassium voltage-gated channel subfamily A member regulatory beta subunit 1	down	<b>-2.41</b>	3.67E-12
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.97</b>	1.20E-06
		<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
		<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13
<b>Cell growth</b>	GO:0016049	<b>IL7R</b>	Interleukin 7 receptor	up	<b>3.40</b>	3.11E-08
		<b>NDRG4</b>	NDRG family member 4	up	<b>2.71</b>	1.93E-12
		<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
<b>Cellular response to hydrogen peroxide</b>	GO:0070301	<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10

<b>Regulation of cell shape</b>	GO:0008360	<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>FGD3</b>	FYVE, RhoGEF and PH domain containing 3	down	<b>-2.16</b>	4.81E-09
		<b>CDC42EP1</b>	CDC42 effector protein 1	down	<b>-1.60</b>	1.93E-31
		<b>CDC42EP2</b>	CDC42 effector protein 2	down	<b>-1.55</b>	3.78E-12
		<b>PLXNB3</b>	Plexin B3	down	<b>-1.52</b>	4.18E-11
<b>Response to calcium ion</b>	GO:0051592	<b>KCNMA1</b>	Potassium calcium-activated channel subfamily M alpha 1	up	<b>1.92</b>	<b>6.93E-10</b>
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	<b>3.15E-05</b>
		<b>TNNT2</b>	Troponin T2, cardiac type	down	<b>-2.09</b>	<b>5.81E-11</b>
		<b>AQP3</b>	Aquaporin 3 (Gill blood group)	down	<b>-1.54</b>	<b>1.97E-02</b>
<b>Mitotic sister chromatid segregation</b>	GO:0000070	<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>KIFC1</b>	Kinesin family member C1	down	<b>-1.50</b>	4.13E-05
<b>Response to mechanical stimulus</b>	GO:0009612	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
		<b>INHBB</b>	Inhibin beta B subunit	down	<b>-1.68</b>	4.33E-13
		<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13

GO, gene ontology; up, up-regulated genes in the biological process gene ontology term; down, down-regulated genes in the biological process gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S14.** Specific aldosterone-regulated enriched molecular function gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Molecular Function** analysis on DEGs

**Aldosterone 10<sup>-7</sup> M versus Control**

GO molecular function term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Coreceptor activity</b>	GO:0015026	<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03
		<b>CXCR4</b>	C-X-C motif chemokine receptor 4	up	<b>1.52</b>	2,33E-03
		<b>RAMP2</b>	Receptor activity modifying protein 2	down	<b>-1.57</b>	1,23E-02
<b>Calcium ion binding</b>	GO:0005509	<b>PCDH1</b>	Protocadherin 1	up	<b>2.13</b>	6,84E-04
		<b>S100A2</b>	S100 calcium binding protein A2	up	<b>1.81</b>	2,50E-04
		<b>SVEP1</b>	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	up	<b>1.73</b>	1,08E-02
		<b>S100A3</b>	S100 calcium binding protein A3	up	<b>1.67</b>	3,26E-03
		<b>MCTP2</b>	Multiple C2 and transmembrane domain containing 2	up	<b>1.61</b>	1,81E-06
		<b>S100A6</b>	S100 calcium binding protein A6	up	<b>1.55</b>	2,27E-03
		<b>DOC2A</b>	Double C2 domain alpha	down	<b>-2.31</b>	3,39E-03
		<b>MGP</b>	Matrix Gla protein	down	<b>-2.16</b>	5,66E-03
		<b>MYL3</b>	Myosin light chain 3	down	<b>-1.78</b>	3,41E-02
		<b>EFCAB5</b>	EF-hand calcium binding domain 5	down	<b>-1.61</b>	9,46E-03
		<b>KCNIP1</b>	Potassium voltage-gated channel interacting protein 1	down	<b>-1.58</b>	4,02E-04
		<b>AHRR</b>	Aryl-hydrocarbon receptor repressor	down	<b>-1.52</b>	1,57E-02
<b>Fibronectin binding</b>	GO:0001968	<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03
		<b>IGFBP3</b>	Insulin like growth factor binding protein 3	down	<b>-1.70</b>	3,37E-05

Receptor activity	GO:0004872	PLAUR	Plasminogen activator, urokinase receptor	up	2.16	6,77E-03
		ITGB3	Integrin subunit beta 3	up	1.71	3,11E-02
		ITGAX	Integrin subunit alpha X	up	1.51	1,27E-02
		RTN4RL2	Reticulon 4 receptor-like 2	down	-1.67	3,22E-04
		GFRA2	GDNF family receptor alpha 2	down	-1.61	6,54E-04
		CADM3	Cell adhesion molecule 3	down	-1.59	1,70E-03
Transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	GO:0001077	EHF	ETS homologous factor	up	3.55	2,68E-04
		FOSL1	FOS like 1, AP-1 transcription factor subunit	up	1.89	3,69E-03
		SIX1	SIX homeobox 1	down	-1.95	4,58E-03
		EGR1	Early growth response 1	down	-1.85	3,76E-04
		MAFA	MAF bZIP transcription factor A	down	-1.80	7,75E-04
		EGR2	Early growth response 2	down	-1.69	4,72E-02
Transcription factor activity, sequence-specific DNA binding	GO:0003700	EHF	ETS homologous factor	up	3.55	2,68E-04
		ZBTB16	Zinc finger and BTB domain containing 16	up	3.35	2,87E-06
		POU5F1	POU class 5 homeobox 1	up	2.97	1,80E-05
		FOSL1	FOS like 1, AP-1 transcription factor subunit	up	1.89	3,69E-03
		RXRG	Retinoid X receptor gamma	up	1.71	2,61E-03
		HMGA1	High mobility group AT-hook 1	up	1.53	7,70E-03
		SIX1	SIX homeobox 1	down	-1.95	4,58E-03
		EGR1	Early growth response 1	down	-1.85	3,76E-04
		SOX3	SRY-box 3	down	-1.80	3,61E-03
		MAFA	MAF bZIP transcription factor A	down	-1.80	7,75E-04
		EGR2	Early growth response 2	down	-1.69	4,72E-02
		TBX6	T-box 6	down	-1.56	4,27E-02
		ZNF837	Zinc finger protein 837	down	-1.51	6,00E-04
C-X3-C chemokine binding	GO:0019960	ITGB3	Integrin subunit beta 3	up	1.71	3,11E-02
		ITGA4	integrin subunit alpha 4	up	1.53	2,06E-03

Receptor binding	GO:0005102	PLAUR	Plasminogen activator, urokinase receptor	up	2.16	6,77E-03
		AGXT	Alanine-glyoxylate aminotransferase	up	2.13	4,53E-02
		TNFSF18	Tumor necrosis factor superfamily member 18	up	2.00	2,57E-02
		TAC4	Tachykinin 4 (hemokinin)	up	2.00	3,64E-02
		PLAT	Plasminogen activator, tissue type	up	1.60	1,38E-02
		PCSK1N	Proprotein convertase subtilisin/kexin type 1 inhibitor	down	-1.86	1,03E-03
		CADM3	Cell adhesion molecule 3	down	-1.59	1,70E-03
RNA polymerase II core promoter proximal region sequence-specific DNA binding	GO:0000978	EHF	ETS homologous factor	up	3.55	2,68E-04
		FOSL1	FOS like 1, AP-1 transcription factor subunit	up	1.89	3,69E-03
		ZNF114	Zinc finger protein 114	up	1.57	1,64E-02
		PER1	Period circadian clock 1	up	1.51	3,53E-06
		SIX1	SIX homeobox 1	down	-1.95	4,58E-03
		MAFA	MAF bZIP transcription factor A	down	-1.80	7,75E-04
		EGR2	Early growth response 2	down	-1.69	4,72E-02
Ubiquitin protein ligase binding	GO:0031625	POU5F1	POU class 5 homeobox 1	up	2.97	1,80E-05
		LTBR	Lymphotoxin beta receptor	up	2.71	2,30E-04
		GPR75	G protein-coupled receptor 75	up	1.58	7,16E-03
		CXCR4	C-X-C motif chemokine receptor 4	up	1.52	2,33E-03
		PER1	Period circadian clock 1	up	1.51	3,53E-06
		EGR2	Early growth response 2	down	-1.69	4,72E-02
Protein kinase inhibitor activity	GO:0004860	RTN4RL2	Reticulon 4 receptor-like 2	down	-1.67	3,22E-04
		BGN	Biglycan	down	-1.57	3,68E-03
		SOCS1	Suppressor of cytokine signaling 1	down	-1.51	3,26E-02

GO, gene ontology; up, up-regulated genes in the molecular function gene ontology term; down, down-regulated genes in the molecular function gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplemental Table S15.** Specific cortisol-regulated enriched molecular function gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Molecular Function** analysis on DEGs

**Cortisol 10<sup>-7</sup> M versus Control**

GO molecular function term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Protein serine/threonine/tyrosine kinase activity</b>	GO:0004712	<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.79</b>	4.35E-45
		<b>SGK1</b>	Serum/glucocorticoid regulated kinase 1	up	<b>1.57</b>	8.43E-35
		<b>TTK</b>	TTK protein kinase	down	<b>-1.54</b>	3.29E-03
<b>Thyroid hormone transmembrane transporter activity</b>	GO:0015349	<b>SLC16A10</b>	Solute carrier family 16 member 10	up	<b>1.57</b>	1.76E-30
		<b>SLCO4A1</b>	Solute carrier organic anion transporter family member 4A1	up	<b>1.53</b>	9.95E-16
<b>Metalloendopeptidase activity</b>	GO:0004222	<b>PAPLN</b>	Papilin, proteoglycan like sulfated glycoprotein	up	<b>1.75</b>	4.18E-05
		<b>ADAMTSL4</b>	ADAMTS like 4	up	<b>1.53</b>	4.94E-18
		<b>PAPPA</b>	Pappalysin 1	down	<b>-1.66</b>	1.58E-02
		<b>ADAMTS1</b>	ADAM metalloproteinase with thrombospondin type 1 motif 1	down	<b>-1.57</b>	8.90E-12
<b>GPI-linked ephrin receptor activity</b>	GO:0005004	<b>EPHA8</b>	EPH receptor A8	up	<b>2.38</b>	4.21E-20
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.61</b>	4.88E-04

GO, gene ontology; up, up-regulated genes in the molecular function gene ontology term; down, down-regulated genes in the molecular function gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplemental Table S16.** Specific cortisol + RU-486-regulated enriched molecular function gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Molecular Function** analysis on DEGs

**Cortisol  $10^{-7}$  M + RU-486  $10^{-5}$  M versus Control**

GO molecular function term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Carbonate dehydratase activity</b>	GO:0004089	<b>CA12</b>	Carbonic anhydrase 12	up	<b>2.28</b>	1.56E-06
		<b>CA2</b>	Carbonic anhydrase 2	down	<b>-1.55</b>	2.48E-06
		<b>CA11</b>	Carbonic anhydrase 11	down	<b>-1.51</b>	8.23E-15
		<b>CA9</b>	Carbonic anhydrase 9	down	<b>-1.50</b>	7.90E-24
<b>Anaphase-promoting complex binding</b>	GO:0010997	<b>CDC20B</b>	Cell division cycle 20B	down	<b>-1.85</b>	3.55E-03
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
<b>Extracellular matrix binding</b>	GO:0050840	<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
		<b>SPARCL1</b>	SPARC like 1	up	<b>1.53</b>	2.85E-08
		<b>ADAMTS5</b>	ADAM metalloproteinase with thrombospondin type 1 motif 5	down	<b>-2.24</b>	3.58E-08
		<b>ADAMTS15</b>	ADAM metalloproteinase with thrombospondin type 1 motif 15	down	<b>-1.67</b>	1.10E-04
<b>Collagen binding</b>	GO:0005518	<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
		<b>SPARCL1</b>	SPARC like 1	up	<b>1.53</b>	2.85E-08
		<b>ITGA11</b>	Integrin subunit alpha 11	down	<b>-2.19</b>	7.41E-07
		<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05

<b>Extracellular matrix structural constituent</b>	GO:0005201	<b>MGP</b>	Matrix Gla protein	down	<b>-2.21</b>	5.47E-07
		<b>HAPLN3</b>	Hyaluronan and proteoglycan link protein 3	down	<b>-2.00</b>	8.82E-05
		<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
		<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13
<b>Aldo-keto reductase (NADP) activity</b>	GO:0004033	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1	up	<b>16.20</b>	8.08E-17
		<b>AKR1B10</b>	Aldo-keto reductase family 1 member B10	up	<b>7.56</b>	1.07E-12
		<b>KCNAB1</b>	Potassium voltage-gated channel subfamily A member regulatory beta subunit 1	down	<b>-2.41</b>	3.67E-12
<b>Symporter activity</b>	GO:0015293	<b>SLC24A4</b>	Solute carrier family 24 member 4	up	<b>2.12</b>	1.61E-05
		<b>SLC1A7</b>	Solute carrier family 1 member 7	up	<b>1.84</b>	6.79E-11
		<b>SLC16A6</b>	Solute carrier family 16 member 6	up	<b>1.53</b>	4.76E-05
		<b>MFSD2A</b>	Major facilitator superfamily domain containing 2A	down	<b>-1.69</b>	2.54E-11
<b>Protein kinase binding</b>	GO:0019901	<b>SPRY2</b>	Sprouty RTK signaling antagonist 2	up	<b>1.77</b>	3.61E-07
		<b>TRIB3</b>	Tribbles pseudokinase 3	up	<b>1.71</b>	2.94E-06
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
		<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta	down	<b>-2.13</b>	4.92E-19
		<b>KIF20A</b>	Kinesin family member 20A	down	<b>-2.04</b>	5.94E-08
		<b>CCNA2</b>	Cyclin A2	down	<b>-1.72</b>	1.60E-07
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>FOXM1</b>	Forkhead box M1	down	<b>-1.62</b>	3.17E-03
		<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
		<b>CDKN2C</b>	Cyclin dependent kinase inhibitor 2C	down	<b>-1.57</b>	1.97E-04
		<b>CCND2</b>	Cyclin D2	down	<b>-1.54</b>	2.85E-17
<b>ATP binding</b>	GO:0005524	<b>HSPA6</b>	Heat shock protein family A member 6	up	<b>13.96</b>	9.08E-12
		<b>ABCC3</b>	ATP binding cassette subfamily C member 3	up	<b>2.60</b>	6.14E-08



<b>PDK4</b>	Pyruvate dehydrogenase kinase 4	up	<b>2.21</b>	1.14E-10
<b>ACSL5</b>	Acyl-CoA synthetase long-chain family member 5	up	<b>1.74</b>	6.15E-04
<b>TRIB3</b>	Tribbles pseudokinase 3	up	<b>1.71</b>	2.94E-06
<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
<b>ABCA4</b>	ATP binding cassette subfamily A member 4	up	<b>1.54</b>	5.36E-08
<b>EPHA8</b>	EPH receptor A8	up	<b>1.50</b>	2.43E-05
<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta	down	<b>-2.13</b>	4.92E-19
<b>KIF20A</b>	Kinesin family member 20A	down	<b>-2.04</b>	5.94E-08
<b>CARNS1</b>	Carnosine synthase 1	down	<b>-2.02</b>	5.05E-16
<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.97</b>	1.20E-06
<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
<b>ATP6V1B1</b>	ATPase H <sup>+</sup> transporting V1 subunit B1	down	<b>-1.85</b>	5.46E-07
<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
<b>KIF4A</b>	Kinesin family member 4A	down	<b>-1.71</b>	6.57E-05
<b>MKI67</b>	Marker of proliferation Ki-67	down	<b>-1.69</b>	6.36E-05
<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
<b>UBE2T</b>	Ubiquitin conjugating enzyme E2 T	down	<b>-1.61</b>	1.75E-04
<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
<b>ABCB5</b>	ATP binding cassette subfamily B member 5	down	<b>-1.59</b>	3.70E-08
<b>ENTPD8</b>	Ectonucleoside triphosphate diphosphohydrolase 8	down	<b>-1.57</b>	4.41E-10
<b>TOP2A</b>	Topoisomerase (DNA) II alpha	down	<b>-1.56</b>	2.82E-06
<b>PLXNB3</b>	Plexin B3	down	<b>-1.52</b>	4.18E-11
<b>ABCG1</b>	ATP binding cassette subfamily G member 1	down	<b>-1.52</b>	5.50E-18
<b>KIFC1</b>	Kinesin family member C1	down	<b>-1.50</b>	4.13E-05

<b>Hyaluronic acid binding</b>	GO:0005540	<b>LAYN</b>	Layilin	up	<b>1.55</b>	4.50E-10
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
		<b>HAPLN3</b>	Hyaluronan and proteoglycan link protein 3	down	<b>-2.00</b>	8.82E-05

<b>Indanol dehydrogenase activity</b>	GO:0047718	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1	up	<b>16.20</b>	8.08E-17
		<b>AKR1B10</b>	Aldo-keto reductase family 1 member B10	up	<b>7.56</b>	1.07E-12
<b>Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen</b>	GO:0016705	<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1	up	<b>1.55</b>	3.67E-05
		<b>CYP2W1</b>	Cytochrome P450 family 2 subfamily W member 1	down	<b>-1.94</b>	1.98E-11
		<b>CYP19A1</b>	Cytochrome P450 family 19 subfamily A member 1	down	<b>-1.89</b>	5.27E-06
		<b>CYP2S1</b>	Cytochrome P450 family 2 subfamily S member 1	down	<b>-1.67</b>	1.31E-04
<b>Peptide binding</b>	GO:0042277	<b>MME</b>	Membrane metallo-endoropeptidase	up	<b>1.79</b>	8.51E-07
		<b>TMEM158</b>	Transmembrane protein 158	up	<b>1.63</b>	3.83E-20
		<b>GPR37L1</b>	G protein-coupled receptor 37 like 1	down	<b>-2.01</b>	2.81E-06
		<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
<b>Steroid hydroxylase activity</b>	GO:0008395	<b>CYP2W1</b>	Cytochrome P450 family 2 subfamily W member 1	down	<b>-1.94</b>	1.98E-11
		<b>CYP19A1</b>	Cytochrome P450 family 19 subfamily A member 1	down	<b>-1.89</b>	5.27E-06
		<b>CYP2S1</b>	Cytochrome P450 family 2 subfamily S member 1	down	<b>-1.67</b>	1.31E-04

GO, gene ontology; up, up-regulated genes in the molecular function gene ontology term; down, down-regulated genes in the molecular function gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplemental Table S17.** Specific aldosterone-regulated enriched cellular component gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Cellular Component** analysis on DEGs

**Aldosterone 10<sup>-7</sup> M versus Control**

GO cellular components term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Cell surface</b>	GO:0009986	<b>OPRD1</b>	Opioid receptor delta 1	up	<b>1.55</b>	2,95E-03
		<b>DOC2A</b>	Double C2 domain alpha	down	<b>-2.31</b>	3,39E-03
		<b>PLP1</b>	Proteolipid protein 1	down	<b>-1.87</b>	3,19E-02
		<b>SST</b>	Somatostatin	down	<b>-1.81</b>	1,02E-04
		<b>GJD2</b>	Gap junction protein delta 2	down	<b>-1.67</b>	1,70E-02
		<b>TPGS1</b>	Tubulin polyglutamylase complex subunit 1	down	<b>-1.59</b>	1,70E-03
		<b>KCNMB2</b>	Potassium calcium-activated channel subfamily M regulatory beta subunit 2	down	<b>-1.56</b>	1,09E-02
		<b>SLC12A5</b>	Solute carrier family 12 member 5	down	<b>-1.52</b>	2,40E-03
		<b>HTR1D</b>	5-hydroxytryptamine receptor 1D	down	<b>-1.51</b>	4,09E-02
<b>Integral component of plasma membrane</b>	GO:0005887	<b>LTBR</b>	Lymphotoxin beta receptor	up	<b>2.71</b>	2,30E-04
		<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit	up	<b>2.22</b>	1,02E-06
		<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.16</b>	6,77E-03
		<b>PCDH1</b>	Protocadherin 1	up	<b>2.13</b>	6,84E-04
		<b>GRID2</b>	Glutamate ionotropic receptor delta type subunit 2	up	<b>2.02</b>	1,15E-02
		<b>HVCN1</b>	Hydrogen voltage gated channel 1	up	<b>1.87</b>	4,26E-03
		<b>SLC3A1</b>	Solute carrier family 3 member 1	up	<b>1.87</b>	4,91E-04
		<b>P2RY6</b>	Pyrimidinergic receptor P2Y6	up	<b>1.71</b>	4,23E-02
		<b>ITGB3</b>	EF-hand calcium binding domain 13 // integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>EPHA8</b>	EPH receptor A8	up	<b>1.70</b>	2,77E-02
		<b>GPR75</b>	G protein-coupled receptor 75	up	<b>1.58</b>	7,16E-03
		<b>PTGER2</b>	Prostaglandin E receptor 2	up	<b>1.57</b>	7,18E-06
		<b>ABCC3</b>	ATP binding cassette subfamily C member 3	up	<b>1.55</b>	2,40E-02
		<b>OPRD1</b>	Opioid receptor delta 1	up	<b>1.55</b>	2,95E-03

		<b>PLPPR3</b>	Phospholipid phosphatase related 3	down	<b>-1.64</b>	1,00E-03
		<b>PTPRC</b>	Protein tyrosine phosphatase, receptor type C	down	<b>-1.64</b>	2,25E-02
		<b>CADM3</b>	Cell adhesion molecule 3	down	<b>-1.59</b>	1,70E-03
		<b>RAMP2</b>	Receptor activity modifying protein 2	down	<b>-1.57</b>	1,23E-02
		<b>KCNMB2</b>	Potassium calcium-activated channel subfamily M regulatory beta subunit 2	down	<b>-1.56</b>	1,09E-02
		<b>SLC12A5</b>	Solute carrier family 12 member 5	down	<b>-1.52</b>	2,40E-03
		<b>HTR1D</b>	5-hydroxytryptamine receptor 1D	down	<b>-1.51</b>	4,09E-02
Integrin complex	GO:0008305	<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03
		<b>ITGAX</b>	Integrin subunit alpha X	up	<b>1.51</b>	1,27E-02
Focal adhesion	GO:0005925	<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.16</b>	6,77E-03
		<b>SPRY4</b>	Sprouty RTK signaling antagonist 4	up	<b>1.82</b>	4,71E-03
		<b>ITGB3</b>	Integrin subunit beta 3	up	<b>1.71</b>	3,11E-02
		<b>ITGA4</b>	Integrin subunit alpha 4	up	<b>1.53</b>	2,06E-03
		<b>HMGA1</b>	High mobility group AT-hook 1	up	<b>1.53</b>	7,70E-03
		<b>CNN1</b>	Calponin 1	down	<b>-1.72</b>	1,02E-02
		<b>RPL13AP5</b>	Ribosomal protein L13a pseudogene 5	down	<b>-1.72</b>	2,24E-04
		<b>PTPRC</b>	Protein tyrosine phosphatase, receptor type C	down	<b>-1.64</b>	2,25E-02
Extracellular space	GO:0005615	<b>SERPINA3</b>	Serpin family A member 3	up	<b>2.99</b>	1,86E-03
		<b>TNFSF18</b>	Tumor necrosis factor superfamily member 18	up	<b>2.00</b>	2,57E-02
		<b>TAC4</b>	Tachykinin 4 (hemokinin)	up	<b>2.00</b>	3,64E-02
		<b>OMD</b>	Osteomodulin	up	<b>1.87</b>	2,87E-03
		<b>PLAT</b>	Plasminogen activator, tissue type	up	<b>1.60</b>	1,38E-02
		<b>DSCAML1</b>	DS cell adhesion molecule like 1	up	<b>1.57</b>	7,08E-03
		<b>PTX3</b>	Pentraxin 3	up	<b>1.54</b>	2,66E-02
		<b>HIST1H2BC</b>	Histone cluster 1, H2bc	up	<b>1.54</b>	7,46E-03
		<b>FMOD</b>	Fibromodulin	down	<b>-2.09</b>	3,28E-02
		<b>GDF7</b>	Growth differentiation factor 7	down	<b>-2.01</b>	2,21E-03

<b>PCSK1N</b>	Proprotein convertase subtilisin/kexin type 1 inhibitor	down	<b>-1.86</b>	1,03E-03
<b>SST</b>	Somatostatin	down	<b>-1.81</b>	1,02E-04
<b>ACTG2</b>	Actin, gamma 2, smooth muscle, enteric	down	<b>-1.73</b>	3,72E-02
<b>IGFBP3</b>	Insulin like growth factor binding protein 3	down	<b>-1.70</b>	3,37E-05
<b>CLEC11A</b>	C-type lectin domain family 11 member A	down	<b>-1.54</b>	4,83E-03
<b>COL2A1</b>	Collagen type II alpha 1 chain	down	<b>-1.52</b>	2,59E-03
<b>CFD</b>	Complement factor D	down	<b>-1.52</b>	4,62E-03

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GO, gene ontology; up, up-regulated genes in the cellular component gene ontology term; down, down-regulated genes in the cellular component gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplemental Table S18.** Specific cortisol-regulated enriched cellular component gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Cellular Component** analysis on DEGs

**Cortisol 10<sup>-7</sup> M versus Control**

GO cellular components term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
<b>Integral component of plasma membrane</b>	GO:0005887	<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit	up	<b>6.48</b>	1.80E-152
		<b>HVCN1</b>	Hydrogen voltage gated channel 1	up	<b>4.15</b>	4.71E-32
		<b>SLC28A3</b>	Solute carrier family 28 member 3	up	<b>2.66</b>	2.79E-12
		<b>PTGER2</b>	Prostaglandin E receptor 2	up	<b>2.62</b>	5.28E-54
		<b>EPHA8</b>	EPH receptor A8	up	<b>2.38</b>	4.21E-20
		<b>SLC13A4</b>	Solute carrier family 13 member 4	up	<b>2.03</b>	3.40E-95
		<b>SLC16A12</b>	Solute carrier family 16 member 12	up	<b>1.96</b>	6.25E-39
		<b>ABCC5</b>	ATP binding cassette subfamily C member 5	up	<b>1.75</b>	3.28E-22
		<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	up	<b>1.72</b>	1.01E-12
		<b>ABCA4</b>	ATP binding cassette subfamily A member 4	up	<b>1.69</b>	4.72E-11
		<b>TGFB2</b>	Transforming growth factor beta receptor 2	up	<b>1.64</b>	2.09E-18
		<b>SLC2A12</b>	Solute carrier family 2 member 12	up	<b>1.58</b>	2.58E-42
		<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.57</b>	6.84E-17
		<b>SLC16A10</b>	Solute carrier family 16 member 10	up	<b>1.57</b>	1.76E-30
		<b>SLCO4A1</b>	Solute carrier organic anion transporter family member 4A1	up	<b>1.53</b>	9.95E-16
		<b>CD58</b>	CD58 molecule	up	<b>1.51</b>	1.09E-05
<b>Insulin-like growth factor binding protein complex</b>	GO:0016942	<b>KCND2</b>	Potassium voltage-gated channel subfamily D member 2	down	<b>-1.74</b>	8.81E-05
		<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.61</b>	4.88E-04
		<b>IGF1</b>	Insulin like growth factor 1	down	<b>-1.85</b>	1.51E-18
<b>Insulin-like growth factor binding protein complex</b>	GO:0016942	<b>IGFBP3</b>	Insulin like growth factor binding protein 3	down	<b>-1.64</b>	1.77E-03
		<b>IGF1</b>	Insulin like growth fact	down	<b>-1.85</b>	1.51E-18

<b>Insulin-like growth factor ternary complex</b>		<b>IGFBP3</b>	Insulin like growth fact	down	<b>-1.64</b>	1.77E-03
<b>Proteinaceous extracellular matrix</b>	GO:0005578	<b>PAPLN</b>	Papilin, proteoglycan like sulfated glycoprotein	up	<b>1.75</b>	4.18E-05
		<b>WNT11</b>	Wnt family member 11	up	<b>1.61</b>	3.74E-04
		<b>ADAMTSL1</b>	ADAMTS like 1	up	<b>1.53</b>	3.58E-05
		<b>AMTN</b>	Amelotin	down	<b>-2.08</b>	1.63E-06
		<b>SMOC1</b>	SPARC related modular calcium binding 1	down	<b>-1.63</b>	1.12E-04
		<b>ADAMTS1</b>	ADAM metalloproteinase with thrombospondin type 1 motif 1	down	<b>-1.57</b>	8.90E-12
<b>Extracellular space</b>	GO:0005615	<b>SERPINA3</b>	Serpin family A member 3	up	<b>2.53</b>	1.29E-22
		<b>CES4A</b>	Carboxylesterase 4A	up	<b>2.06</b>	7.08E-08
		<b>TLE2</b>	Transducin like enhancer of split 2	up	<b>2.31</b>	2.98E-22
		<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	<b>1.76</b>	5.76E-04
		<b>CP</b>	Ceruloplasmin	up	<b>1.70</b>	8.53E-12
		<b>SERPINF2</b>	Serpin family F member 2	up	<b>1.70</b>	2.01E-40
		<b>SCGB1D2</b>	Secretoglobin family 1D member 2	up	<b>1.68</b>	2.03E-04
		<b>WNT11</b>	Wnt family member 11	up	<b>1.61</b>	3.74E-04
		<b>KRT81</b>	Keratin 81	down	<b>-2.35</b>	9.24E-04
		<b>SPP1</b>	Secreted phosphoprotein 1	down	<b>-2.25</b>	5.38E-05
		<b>IGF1</b>	Insulin like growth factor 1	down	<b>-1.85</b>	1.51E-18
		<b>SFRP2</b>	Secreted frizzled related protein 2	down	<b>-1.78</b>	2.39E-03
		<b>SST</b>	Somatostatin	down	<b>-1.69</b>	3.85E-03
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.68</b>	3.34E-03
		<b>PAPPA</b>	Pappalysin 1	down	<b>-1.66</b>	1.58E-02
		<b>IGFBP3</b>	Insulin like growth factor binding protein 3	down	<b>-1.64</b>	1.77E-03

GO, gene ontology; up, up-regulated genes in the cellular component gene ontology term; down, down-regulated genes in the cellular component gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplemental Table S19.** Specific cortisol + RU-486-regulated enriched cellular component gene ontology terms as predicted by bioinformatic enrichment analysis.

**GO Cellular Component** analysis on DEGs

**Cortisol  $10^{-7}$  M + RU-486  $10^{-5}$  M versus Control**

GO cellular component term	Link to GO ID	Gene name	Description	Regulation	FC	P-value
Extracellular matrix	GO:0031012	<b>MMP1</b>	Matrix metalloproteinase 1	up	<b>6.06</b>	2.25E-08
		<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>ECM1</b>	Extracellular matrix protein 1	up	<b>1.82</b>	3.16E-06
		<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
		<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
		<b>MGP</b>	Matrix Gla protein	down	<b>-2.21</b>	5.47E-07
		<b>MMP11</b>	Matrix metalloproteinase 11	down	<b>-1.76</b>	9.27E-23
		<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
		<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
		<b>MFAP4</b>	Microfibrillar associated protein 4	down	<b>-1.55</b>	2.66E-07
		<b>THBS2</b>	Thrombospondin 2	down	<b>-1.53</b>	2.41E-06
		<b>MFGE8</b>	Milk fat globule-EGF factor 8 protein	down	<b>-1.52</b>	9.70E-30
		<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13
Plasma membrane	GO:0005886	<b>IL7R</b>	Interleukin 7 receptor	up	<b>3.40</b>	3.11E-08
		<b>PLIN2</b>	Perilipin 2	up	<b>2.83</b>	3.52E-64
		<b>ABCC3</b>	ATP binding cassette subfamily C member 3	up	<b>2.60</b>	6.14E-08
		<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	<b>2.47</b>	3.24E-08
		<b>B4GALNT1</b>	Beta-1,4-N-acetyl-galactosaminyltransferase 1	up	<b>2.46</b>	3.94E-08
		<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.38</b>	1.14E-10
		<b>CA12</b>	Carbonic anhydrase 12	up	<b>2.28</b>	1.56E-06
		<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit	up	<b>2.21</b>	3.92E-26
		<b>CLMP</b>	CXADR like membrane protein	up	<b>2.17</b>	1.94E-07
		<b>SLC24A4</b>	Solute carrier family 24 member 4	up	<b>2.12</b>	1.61E-05
		<b>HVCN1</b>	Hydrogen voltage gated channel 1	up	<b>1.97</b>	7.60E-08
		<b>PTGER2</b>	Prostaglandin E receptor 2	up	<b>1.95</b>	1.63E-26



<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
<b>KCNMA1</b>	Potassium calcium-activated channel subfamily M alpha 1	up	<b>1.92</b>	6.93E-10
<b>CDCP1</b>	CUB domain containing protein 1	up	<b>1.84</b>	3.65E-12
<b>SLC1A7</b>	Solute carrier family 1 member 7	up	<b>1.84</b>	6.79E-11
<b>MME</b>	Membrane metallo-endopeptidase	up	<b>1.79</b>	8.51E-07
<b>SPRY2</b>	Sprouty RTK signaling antagonist 2	up	<b>1.77</b>	3.61E-07
<b>PTPRN</b>	Protein tyrosine phosphatase, receptor type N	up	<b>1.73</b>	2.71E-05
<b>SLC3A1</b>	Solute carrier family 3 member 1	up	<b>1.72</b>	1.76E-03
<b>TRIB3</b>	Tribbles pseudokinase 3	up	<b>1.71</b>	2.94E-06
<b>TESC</b>	Tescalcin	up	<b>1.69</b>	7.70E-06
<b>PRLR</b>	Prolactin receptor	up	<b>1.66</b>	1.57E-18
<b>ANO4</b>	Anoctamin 4	up	<b>1.65</b>	1.28E-03
<b>CXCR4</b>	C-X-C motif chemokine receptor 4	up	<b>1.64</b>	1.05E-10
<b>SLC22A6</b>	Solute carrier family 22 member 6	up	<b>1.63</b>	1.17E-05
<b>SLC9A9</b>	Solute carrier family 9 member A9	up	<b>1.61</b>	3.20E-07
<b>RAET1G</b>	Retinoic acid early transcript 1G	up	<b>1.60</b>	1.87E-02
<b>TNFSF18</b>	Tumor necrosis factor superfamily member 18	up	<b>1.59</b>	8.30E-04
<b>IFITM1</b>	Interferon induced transmembrane protein 1	up	<b>1.59</b>	2.00E-05
<b>ATP1B2</b>	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 2	up	<b>1.57</b>	1.62E-10
<b>SLC18A3</b>	Solute carrier family 18 member A3	up	<b>1.55</b>	1.33E-26
<b>ETV5</b>	ETS variant 5	up	<b>1.55</b>	4.11E-10
<b>GNG2</b>	G protein subunit gamma 2	up	<b>1.54</b>	5.57E-13
<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
<b>RIN1</b>	Ras and Rab interactor 1	up	<b>1.54</b>	5.00E-04
<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
<b>OSMR</b>	Oncostatin M receptor	up	<b>1.53</b>	4.39E-10
<b>TSPAN1</b>	Tetraspanin 1	up	<b>1.52</b>	1.87E-02
<b>MGLL</b>	Monoglyceride lipase	up	<b>1.52</b>	5.27E-09
<b>SLC7A11</b>	Solute carrier family 7 member 11	up	<b>1.52</b>	6.66E-14
<b>GABBR2</b>	Gamma-aminobutyric acid type B receptor subunit 2	up	<b>1.51</b>	2.82E-07
<b>EPHA8</b>	EPH receptor A8	up	<b>1.50</b>	2.43E-05

<b>GJD2</b>	Gap junction protein delta 2	down	<b>-3.92</b>	6.10E-20
<b>C14orf180</b>	Chromosome 14 open reading frame 180	down	<b>-3.24</b>	8.78E-16
<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
<b>OMG</b>	Oligodendrocyte myelin glycoprotein	down	<b>-2.80</b>	1.53E-09
<b>KCNAB1</b>	Potassium voltage-gated channel subfamily A member regulatory beta subunit 1	down	<b>-2.41</b>	3.67E-12
<b>ITGA11</b>	Integrin subunit alpha 11	down	<b>-2.19</b>	7.41E-07
<b>GFRA2</b>	GDNF family receptor alpha 2	down	<b>-2.01</b>	4.14E-07
<b>GPR37L1</b>	G protein-coupled receptor 37 like 1	down	<b>-2.01</b>	2.81E-06
<b>CYP2W1</b>	Cytochrome P450 family 2 subfamily W member 1	down	<b>-1.94</b>	1.98E-11
<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
<b>RHBDL2</b>	Rhomboid like 2	down	<b>-1.84</b>	2.52E-08
<b>C10orf54</b>	Chromosome 10 open reading frame 54	down	<b>-1.80</b>	1.02E-13
<b>SYT10</b>	Synaptotagmin 10	down	<b>-1.75</b>	3.49E-04
<b>PRSS12</b>	Protease, serine 12	down	<b>-1.74</b>	4.60E-28
<b>RGS9</b>	Regulator of G-protein signaling 9	down	<b>-1.74</b>	3.78E-06
<b>MOG</b>	Myelin oligodendrocyte glycoprotein	down	<b>-1.73</b>	2.64E-02
<b>BMF</b>	Bcl2 modifying factor	down	<b>-1.69</b>	8.82E-13
<b>MFSD2A</b>	Major facilitator superfamily domain containing 2A	down	<b>-1.69</b>	2.54E-11
<b>ADRA2C</b>	Adrenoceptor alpha 2C	down	<b>-1.67</b>	3.79E-20
<b>CDC42EP1</b>	CDC42 effector protein 1	down	<b>-1.60</b>	1.93E-31
<b>PHLDB2</b>	Pleckstrin homology like domain family B member 2	down	<b>-1.59</b>	2.92E-05
<b>ABCB5</b>	ATP binding cassette subfamily B member 5	down	<b>-1.59</b>	3.70E-08
<b>ENTPD8</b>	Ectonucleoside triphosphate diphosphohydrolase 8	down	<b>-1.57</b>	4.41E-10
<b>RGS6</b>	Regulator of G-protein signaling 6	down	<b>-1.57</b>	5.04E-03
<b>UNC5B</b>	Unc-5 netrin receptor B	down	<b>-1.56</b>	4.34E-19
<b>CDC42EP2</b>	CDC42 effector protein 2	down	<b>-1.55</b>	3.78E-12
<b>CA2</b>	Carbonic anhydrase 2	down	<b>-1.55</b>	2.48E-06
<b>AQP3</b>	Aquaporin 3 (Gill blood group)	down	<b>-1.54</b>	1.97E-02
<b>SMPD3</b>	Sphingomyelin phosphodiesterase 3	down	<b>-1.53</b>	8.77E-03
<b>PLXNB3</b>	Plexin B3	down	<b>-1.52</b>	4.18E-11
<b>ABCG1</b>	ATP binding cassette subfamily G member 1	down	<b>-1.52</b>	5.50E-18

		<b>GRIK3</b>	Glutamate ionotropic receptor kainate type subunit 3	down	<b>-1.51</b>	9.06E-06
		<b>CA9</b>	Carbonic anhydrase 9	down	<b>-1.50</b>	7.90E-24
Proteinaceous extracellular matrix	GO:0005578	<b>MMP1</b>	Matrix metalloproteinase 1	up	<b>6.06</b>	2.25E-08
		<b>ANGPTL4</b>	Angiopoietin like 4	up	<b>3.56</b>	2.07E-31
		<b>ECM1</b>	Extracellular matrix protein 1	up	<b>1.82</b>	3.16E-06
		<b>SPARCL1</b>	SPARC like 1	up	<b>1.53</b>	2.85E-08
		<b>AMTN</b>	Amelotin	down	<b>-2.37</b>	1.93E-08
		<b>ADAMTS5</b>	ADAM metalloproteinase with thrombospondin type 1 motif 5	down	<b>-2.24</b>	3.58E-08
		<b>MGP</b>	Matrix Gla protein	down	<b>-2.21</b>	5.47E-07
		<b>HAPLN3</b>	Hyaluronan and proteoglycan link protein 3	down	<b>-2.00</b>	8.82E-05
		<b>MMP11</b>	Matrix metalloproteinase 11	down	<b>-1.76</b>	9.27E-23
		<b>WNT2B</b>	Wnt family member 2B	down	<b>-1.74</b>	2.06E-06
		<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
		<b>ADAMTS15</b>	ADAM metalloproteinase with thrombospondin type 1 motif 15	down	<b>-1.67</b>	1.10E-04
Spindle	GO:0005819	<b>KBTBD8</b>	Kelch repeat and BTB domain containing 8	up	<b>1.67</b>	1.62E-06
		<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
		<b>KIF20A</b>	Kinesin family member 20A	down	<b>-2.04</b>	5.94E-08
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
		<b>CDC20</b>	Cell division cycle 20	down	<b>-1.52</b>	1.12E-03
		<b>KIFC1</b>	Kinesin family member C1	down	<b>-1.50</b>	4.13E-05
Extracellular space	GO:0005615	<b>ANGPTL4</b>	Angiopoietin like 4	up	<b>3.56</b>	2.07E-31
		<b>SRPX2</b>	Sushi repeat containing protein, X-linked 2	up	<b>3.54</b>	1.92E-11
		<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	<b>2.47</b>	3.24E-08
		<b>PTX3</b>	Pentraxin 3	up	<b>2.14</b>	3.89E-05
		<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09

<b>FGF12</b>	Fibroblast growth factor 12	up	<b>2.03</b>	3.17E-08
<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
<b>ECM1</b>	Extracellular matrix protein 1	up	<b>1.82</b>	3.16E-06
<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
<b>LAMC2</b>	Laminin subunit gamma 2	up	<b>1.76</b>	5.04E-12
<b>HILPDA</b>	Hypoxia inducible lipid droplet associated	up	<b>1.76</b>	2.88E-09
<b>SERPINA3</b>	Serpin family A member 3	up	<b>1.62</b>	3.90E-07
<b>IL33</b>	Interleukin 33	up	<b>1.62</b>	2.89E-15
<b>TNFSF18</b>	Tumor necrosis factor superfamily member 18	up	<b>1.59</b>	8.30E-04
<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
<b>SPARCL1</b>	SPARC like 1	up	<b>1.53</b>	2.85E-08
<b>ADAMTS5</b>	ADAM metalloproteinase with thrombospondin type 1 motif 5	down	<b>-2.24</b>	3.58E-08
<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta	down	<b>-2.13</b>	4.92E-19
<b>KRT81</b>	Keratin 81	down	<b>-2.06</b>	4.57E-03
<b>HAPLN3</b>	Hyaluronan and proteoglycan link protein 3	down	<b>-2.00</b>	8.82E-05
<b>WNT2B</b>	Wnt family member 2B	down	<b>-1.74</b>	2.06E-06
<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
<b>INHBB</b>	Inhibin beta B subunit	down	<b>-1.68</b>	4.33E-13
<b>ADAMTS15</b>	ADAM metalloproteinase with thrombospondin type 1 motif 15	down	<b>-1.67</b>	1.10E-04
<b>SEMA3D</b>	Semaphorin 3D	down	<b>-1.65</b>	6.47E-07
<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
<b>SST</b>	Somatostatin	down	<b>-1.60</b>	8.94E-03
<b>CA2</b>	Carbonic anhydrase 2	down	<b>-1.55</b>	2.48E-06
<b>EDN2</b>	Endothelin 2	down	<b>-1.54</b>	4.96E-12
<b>MFGE8</b>	Milk fat globule-EGF factor 8 protein	down	<b>-1.52</b>	9.70E-30
<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13
<b>PCSK2</b>	Proprotein convertase subtilisin/kexin type 2	down	<b>-1.51</b>	2.35E-03

Cell surface

GO:0009986

<b>SRPX2</b>	Sushi repeat containing protein, X-linked 2	up	<b>3.54</b>	1.92E-11
<b>CLMP</b>	CXADR like membrane protein	up	<b>2.17</b>	1.94E-07
<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06

<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
<b>HILPDA</b>	Hypoxia inducible lipid droplet associated	up	<b>1.76</b>	2.88E-09
<b>PRLR</b>	Prolactin receptor	up	<b>1.66</b>	1.57E-18
<b>CXCR4</b>	C-X-C motif chemokine receptor 4	up	<b>1.64</b>	1.05E-10
<b>TNFSF18</b>	Tumor necrosis factor superfamily member 18	up	<b>1.59</b>	8.30E-04
<b>LAYN</b>	Layilin	up	<b>1.55</b>	4.50E-10
<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
<b>IQGAP2</b>	IQ motif containing GTPase activating protein 2	up	<b>1.52</b>	1.10E-24
<b>SLC7A11</b>	Solute carrier family 7 member 11	up	<b>1.52</b>	6.66E-14
<b>CYP2W1</b>	Cytochrome P450 family 2 subfamily W member 1	down	<b>-1.94</b>	1.98E-11
<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
<b>C10orf54</b>	Chromosome 10 open reading frame 54	down	<b>-1.80</b>	1.02E-13
<b>ADAMTS15</b>	ADAM metalloproteinase with thrombospondin type 1 motif 15	down	<b>-1.67</b>	1.10E-04
<b>PLXNB3</b>	Plexin B3	down	<b>-1.52</b>	4.18E-11

<b>Extracellular region</b>	GO:0005576	<b>MMP1</b>	Matrix metalloproteinase 1	up	<b>6.06</b>	2.25E-08
		<b>ANGPTL4</b>	Angiopoietin like 4	up	<b>3.56</b>	2.07E-31
		<b>IL7R</b>	Interleukin 7 receptor	up	<b>3.40</b>	3.11E-08
		<b>PLIN2</b>	Perilipin 2	up	<b>2.83</b>	3.52E-64
		<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1	up	<b>2.47</b>	3.24E-08
		<b>PTX3</b>	Pentraxin 3	up	<b>2.14</b>	3.89E-05
		<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
		<b>ISM2</b>	Isthmin 2	up	<b>1.89</b>	4.09E-05
		<b>ISG15</b>	ISG15 ubiquitin-like modifier	up	<b>1.88</b>	3.91E-04
		<b>CDCP1</b>	CUB domain containing protein 1	up	<b>1.84</b>	3.65E-12
		<b>ECM1</b>	Extracellular matrix protein 1	up	<b>1.82</b>	3.16E-06
		<b>IL6</b>	Interleukin 6	up	<b>1.76</b>	3.15E-05
		<b>LAMC2</b>	Laminin subunit gamma 2	up	<b>1.76</b>	5.04E-12
		<b>PRLR</b>	Prolactin receptor	up	<b>1.66</b>	1.57E-18
		<b>IL33</b>	Interleukin 33	up	<b>1.62</b>	2.89E-15
		<b>SERPINA3</b>	Serpin family A member 3	up	<b>1.62</b>	3.90E-07

<b>RAET1G</b>	Retinoic acid early transcript 1G	up	<b>1.60</b>	1.87E-02
<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
<b>SERPINE1</b>	Serpin family E member 1	up	<b>1.54</b>	2.46E-03
<b>ADAMTS5</b>	ADAM metalloproteinase with thrombospondin type 1 motif 5	down	<b>-2.24</b>	3.58E-08
<b>INHBA</b>	Inhibin beta A subunit	down	<b>-1.96</b>	6.23E-03
<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
<b>MMP11</b>	Matrix metalloproteinase 11	down	<b>-1.76</b>	9.27E-23
<b>WNT2B</b>	Wnt family member 2B	down	<b>-1.74</b>	2.06E-06
<b>LUM</b>	Lumican	down	<b>-1.72</b>	6.80E-05
<b>INHBB</b>	Inhibin beta B subunit	down	<b>-1.68</b>	4.33E-13
<b>COL1A1</b>	Collagen type I alpha 1 chain	down	<b>-1.64</b>	4.98E-03
<b>SST</b>	Somatostatin	down	<b>-1.60</b>	8.94E-03
<b>MFAP4</b>	Microfibrillar associated protein 4	down	<b>-1.55</b>	2.66E-07
<b>EDN2</b>	Endothelin 2	down	<b>-1.54</b>	4.96E-12
<b>THBS2</b>	Thrombospondin 2	down	<b>-1.53</b>	2.41E-06
<b>MFGE8</b>	Milk fat globule-EGF factor 8 protein	down	<b>-1.52</b>	9.70E-30
<b>COL3A1</b>	Collagen type III alpha 1 chain	down	<b>-1.52</b>	1.44E-13
<b>CA11</b>	Carbonic anhydrase 11	down	<b>-1.51</b>	8.23E-15
<b>NTN1</b>	Netrin 1	down	<b>-1.51</b>	3.14E-06
<b>MMP1</b>	Matrix metalloproteinase 1	down	<b>-6.06</b>	2.25E-08

Integral component of plasma  
membrane

GO:0005887

<b>ABCC3</b>	ATP binding cassette subfamily C member 3	up	<b>2.60</b>	6.14E-08
<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.38</b>	1.14E-10
<b>TM4SF1</b>	Transmembrane 4 L six family member 1	up	<b>2.30</b>	1.04E-05
<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit	up	<b>2.21</b>	3.92E-26
<b>SLC24A4</b>	Solute carrier family 24 member 4	up	<b>2.12</b>	1.61E-05
<b>HVCN1</b>	Hydrogen voltage gated channel 1	up	<b>1.97</b>	7.60E-08
<b>PTGER2</b>	Prostaglandin E receptor 2	up	<b>1.95</b>	1.63E-26
<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
<b>MME</b>	Membrane metallo-endopeptidase	up	<b>1.79</b>	8.51E-07
<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2,3-Sialyltransferase 5	up	<b>1.75</b>	1.86E-13
<b>SLC3A1</b>	Solute carrier family 3 member 1	up	<b>1.72</b>	1.76E-03

<b>SLC22A6</b>	Solute carrier family 22 member 6	up	<b>1.63</b>	1.17E-05
<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1	up	<b>1.56</b>	9.15E-14
<b>SLC18A3</b>	Solute carrier family 18 member A3	up	<b>1.55</b>	1.33E-26
<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
<b>ABCA4</b>	ATP binding cassette subfamily A member 4	up	<b>1.54</b>	5.36E-08
<b>SLC16A6</b>	Solute carrier family 16 member 6	up	<b>1.53</b>	4.76E-05
<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5	up	<b>1.53</b>	3.15E-15
<b>SLC7A11</b>	Solute carrier family 7 member 11	up	<b>1.52</b>	6.66E-14
<b>TSPAN1</b>	Tetraspanin 1	up	<b>1.52</b>	1.87E-02
<b>GABBR2</b>	Gamma-aminobutyric acid type B receptor subunit 2	up	<b>1.51</b>	2.82E-07
<b>EPHA8</b>	EPH receptor A8	up	<b>1.50</b>	2.43E-05
<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3	down	<b>-1.97</b>	1.20E-06
<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
<b>MFSD2A</b>	Major facilitator superfamily domain containing 2A	down	<b>-1.69</b>	2.54E-11
<b>ADRA2C</b>	Adrenoceptor alpha 2C	down	<b>-1.67</b>	3.79E-20
<b>ABCB5</b>	ATP binding cassette subfamily B member 5	down	<b>-1.59</b>	3.70E-08
<b>AQP3</b>	Aquaporin 3 (Gill blood group)	down	<b>-1.54</b>	1.97E-02
<b>PLXNB3</b>	Plexin B3	down	<b>-1.52</b>	4.18E-11
<b>ABCG1</b>	ATP binding cassette subfamily G member 1	down	<b>-1.52</b>	5.50E-18
<b>GRIK3</b>	Glutamate ionotropic receptor kainate type subunit 3	down	<b>-1.51</b>	9.06E-06

<b>Focal adhesion</b>	GO:0005925	<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	<b>2.38</b>	1.14E-10
		<b>HMGA1</b>	High mobility group AT-hook 1	up	<b>1.97</b>	7.42E-07
		<b>EFCAB13</b>	EF-hand calcium binding domain 13	up	<b>1.94</b>	2.60E-06
		<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
		<b>MME</b>	Membrane metallo-endopeptidase	up	<b>1.79</b>	8.51E-07
		<b>LAYN</b>	Layilin	up	<b>1.55</b>	4.50E-10
		<b>CD44</b>	CD44 molecule (Indian blood group)	up	<b>1.54</b>	2.73E-09
		<b>CNN1</b>	Calponin 1	down	<b>-4.32</b>	6.93E-06

		<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
		<b>ITGA11</b>	Integrin subunit alpha 11	down	<b>-2.19</b>	7.41E-07
		<b>FGFR3</b>	Fibroblast growth factor receptor 3	down	<b>-1.91</b>	5.84E-19
		<b>CDC42EP1</b>	CDC42 effector protein 1	down	<b>-1.60</b>	1.93E-31
		<b>PHLDB2</b>	Pleckstrin homology like domain family B member 2	down	<b>-1.59</b>	2.92E-05
Midbody	GO:0030496	<b>KIF20A</b>	Kinesin family member 20A	down	<b>-2.04</b>	5.94E-08
		<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
		<b>KIF4A</b>	Kinesin family member 4A	down	<b>-1.71</b>	6.57E-05
		<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
		<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
		<b>ASPM</b>	Abnormal spindle microtubule assembly	down	<b>-1.58</b>	1.97E-06
Cytosol	GO:0005829	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1	up	<b>16.20</b>	8.08E-17
		<b>HSPA6</b>	Heat shock protein family A member 6	up	<b>13.96</b>	9.08E-12
		<b>AKR1B10</b>	Aldo-keto reductase family 1 member B10	up	<b>7.56</b>	1.07E-12
		<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit	up	<b>3.81</b>	3.16E-08
		<b>DUSP6</b>	Dual specificity phosphatase 6	up	<b>2.85</b>	1.83E-07
		<b>PLIN2</b>	Perilipin 2	up	<b>2.83</b>	3.52E-64
		<b>NDRG4</b>	NDRG family member 4	up	<b>2.71</b>	1.93E-12
		<b>SERPINE2</b>	Serpin family E member 2	up	<b>2.12</b>	3.52E-09
		<b>HMGA1</b>	High mobility group AT-hook 1	up	<b>1.97</b>	7.42E-07
		<b>CALB2</b>	Calbindin 2	up	<b>1.96</b>	7.57E-03
		<b>PHLDA1</b>	Pleckstrin homology like domain family A member 1	up	<b>1.88</b>	1.08E-07
		<b>MT2A</b>	Metallothionein 2A	up	<b>1.88</b>	4.02E-11
		<b>ISG15</b>	ISG15 ubiquitin-like modifier	up	<b>1.88</b>	3.91E-04
		<b>SPRY2</b>	Sprouty RTK signaling antagonist 2	up	<b>1.77</b>	3.61E-07
		<b>NQO1</b>	NAD(P)H quinone dehydrogenase 1	up	<b>1.72</b>	9.60E-09
		<b>TRIB3</b>	Tribbles pseudokinase 3	up	<b>1.71</b>	2.94E-06
		<b>PMAIP1</b>	Phorbol-12-myristate-13-acetate-induced protein 1	up	<b>1.61</b>	1.21E-06
		<b>RLBP1</b>	Retinaldehyde binding protein 1	up	<b>1.57</b>	6.70E-10



<b>UPP1</b>	Uridine phosphorylase 1	up	<b>1.57</b>	1.64E-04
<b>PCP4</b>	Purkinje cell protein 4	up	<b>1.55</b>	2.98E-38
<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2	up	<b>1.54</b>	6.36E-26
<b>CHAT</b>	Choline O-acetyltransferase	up	<b>1.53</b>	2.92E-04
<b>IQGAP2</b>	IQ motif containing GTPase activating protein 2	up	<b>1.52</b>	1.10E-24
<b>MGLL</b>	Monoglyceride lipase	up	<b>1.52</b>	5.27E-09
<b>TGM2</b>	Transglutaminase 2	down	<b>-2.86</b>	6.47E-06
<b>RPL3L</b>	Ribosomal protein L3 like	down	<b>-2.55</b>	1.32E-10
<b>KCNAB1</b>	Potassium voltage-gated channel subfamily A member regulatory beta subunit 1	down	<b>-2.41</b>	3.67E-12
<b>FGD3</b>	FYVE, RhoGEF and PH domain containing 3	down	<b>-2.16</b>	4.81E-09
<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta	down	<b>-2.13</b>	4.92E-19
<b>TNNT2</b>	Troponin T2, cardiac type	down	<b>-2.09</b>	5.81E-11
<b>CARNS1</b>	Carnosine synthase 1	down	<b>-2.02</b>	5.05E-16
<b>CCNA1</b>	Cyclin A1	down	<b>-1.92</b>	1.29E-07
<b>AP1M2</b>	Adaptor related protein complex 1 mu 2 subunit	down	<b>-1.91</b>	2.49E-11
<b>PPP1R14A</b>	Protein phosphatase 1 regulatory inhibitor subunit 14A	down	<b>-1.88</b>	3.09E-07
<b>ERF</b>	ETS2 repressor factor	down	<b>-1.88</b>	1.18E-23
<b>ATP6V1B1</b>	ATPase H <sup>+</sup> transporting V1 subunit B1	down	<b>-1.85</b>	5.46E-07
<b>ANKRD1</b>	Ankyrin repeat domain 1	down	<b>-1.85</b>	6.52E-03
<b>SPC24</b>	SPC24, NDC80 kinetochore complex component	down	<b>-1.84</b>	4.74E-07
<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
<b>PLK1</b>	Polo like kinase 1	down	<b>-1.72</b>	2.43E-04
<b>KIF4A</b>	Kinesin family member 4A	down	<b>-1.71</b>	6.57E-05
<b>BMF</b>	Bcl2 modifying factor	down	<b>-1.69</b>	8.82E-13
<b>DEPDC1B</b>	DEP domain containing 1B	down	<b>-1.65</b>	1.03E-04
<b>CENPF</b>	Centromere protein F	down	<b>-1.63</b>	2.37E-05
<b>CDK1</b>	Cyclin dependent kinase 1	down	<b>-1.62</b>	4.47E-10
<b>TPX2</b>	TPX2, microtubule nucleation factor	down	<b>-1.60</b>	1.84E-10
<b>CDCA3</b>	Cell division cycle associated 3	down	<b>-1.59</b>	4.27E-03

		<b>CENPM</b>	Centromere protein M	down	-1.58	5.36E-03
		<b>CDKN2C</b>	Cyclin dependent kinase inhibitor 2C	down	-1.57	1.97E-04
		<b>RGS6</b>	Regulator of G-protein signaling 6	down	-1.57	5.04E-03
		<b>MLXIPL</b>	MLX interacting protein like	down	-1.56	3.07E-04
		<b>CDC42EP2</b>	CDC42 effector protein 2	down	-1.55	3.78E-12
		<b>CA2</b>	Carbonic anhydrase 2	down	-1.55	2.48E-06
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	-1.54	3.80E-02
		<b>CCND2</b>	Cyclin D2	down	-1.54	2.85E-17
		<b>DIAPH3</b>	Diaphanous related formin 3	down	-1.53	1.22E-08
		<b>CDC20</b>	Cell division cycle 20	down	-1.52	1.12E-03
		<b>PYGM</b>	Phosphorylase, glycogen, muscle	down	-1.51	1.45E-24
		<b>GTSE1</b>	G2 and S-phase expressed 1	down	-1.51	6.60E-05
Basolateral plasma membrane	GO:0016323	<b>NDRG4</b>	NDRG family member 4	up	2.71	1.93E-12
		<b>ANXA1</b>	Annexin A1	up	1.93	1.17E-08
		<b>SLC22A6</b>	Solute carrier family 22 member 6	up	1.63	1.17E-05
		<b>ATP6V1B1</b>	ATPase H <sup>+</sup> transporting V1 subunit B1	down	-1.85	5.46E-07
		<b>CA2</b>	Carbonic anhydrase 2	down	-1.55	2.48E-06
		<b>AQP3</b>	Aquaporin 3 (Gill blood group)	down	-1.54	1.97E-02
		<b>CA11</b>	Carbonic anhydrase 11	down	-1.51	8.23E-15
		<b>CA9</b>	Carbonic anhydrase 9	down	-1.50	7.90E-24
Spindle microtubule	GO:0005876	<b>PLK1</b>	Polo like kinase 1	down	-1.72	2.43E-04
		<b>KIF4A</b>	Kinesin family member 4A	down	-1.71	6.57E-05
		<b>CAPN6</b>	Calpain 6	down	-1.67	3.35E-12
		<b>CDK1</b>	Cyclin dependent kinase 1	down	-1.62	4.47E-10
Extrinsic component of membrane	GO:0019898	<b>PLAUR</b>	Plasminogen activator, urokinase receptor	up	2.38	1.14E-10
		<b>ANXA1</b>	Annexin A1	up	1.93	1.17E-08
		<b>MGLL</b>	Monoglyceride lipase	up	1.52	5.27E-09
		<b>GFRA2</b>	GDNF family receptor alpha 2	down	-2.01	4.14E-07
		<b>RGS6</b>	Regulator of G-protein signaling 6	down	-1.57	5.04E-03

<b>Condensed chromosome kinetochore</b>	GO:0000777	<b>SPC24</b>	SPC24, NDC80 kinetochore complex component	down	<b>-1.84</b>	4.74E-07
		<b>BUB1B</b>	BUB1 mitotic checkpoint serine/threonine kinase B	down	<b>-1.81</b>	2.76E-11
		<b>NEK2</b>	NIMA related kinase 2	down	<b>-1.77</b>	2.50E-03
		<b>CENPM</b>	Centromere protein M	down	<b>-1.58</b>	5.36E-03
		<b>SPC25</b>	SPC25, NDC80 kinetochore complex component	down	<b>-1.54</b>	3.80E-02
<b>Microvillus</b>	GO:0005902	<b>IQGAP2</b>	IQ motif containing GTPase activating protein 2	up	<b>1.52</b>	1.10E-24
		<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15
		<b>ATP6V1B1</b>	ATPase H <sup>+</sup> transporting V1 subunit B1	down	<b>-1.85</b>	5.46E-07
		<b>CA2</b>	Carbonic anhydrase 2	down	<b>-1.55</b>	2.48E-06
<b>Integral component of Golgi membrane</b>	GO:0030173	<b>B4GALNT1</b>	Beta-1,4-N-acetyl-galactosaminyltransferase 1	up	<b>2.46</b>	3.94E-08
		<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	up	<b>1.75</b>	1.86E-13
		<b>ACER2</b>	Alkaline ceramidase 2	up	<b>1.67</b>	2.27E-02
		<b>ST3GAL4</b>	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	down	<b>-1.54</b>	1.14E-17
<b>Apical plasma membrane</b>	GO:0016324	<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit	up	<b>2.21</b>	3.92E-26
		<b>RAB27B</b>	RAB27B, member RAS oncogene family	up	<b>2.05</b>	2.46E-14
		<b>ANXA1</b>	Annexin A1	up	<b>1.93</b>	1.17E-08
		<b>KCNMA1</b>	Potassium calcium-activated channel subfamily M alpha 1	up	<b>1.92</b>	6.93E-10
		<b>ATP1B2</b>	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 2	up	<b>1.57</b>	1.62E-10
		<b>OSMR</b>	Oncostatin M receptor	up	<b>1.53</b>	4.39E-10
		<b>OXTR</b>	Oxytocin receptor	down	<b>-1.85</b>	1.73E-15

<b>ATP6V1B1</b>	ATPase H <sup>+</sup> transporting V1 subunit B1	down	<b>-1.85</b>	5.46E-07
<b>TMEM235</b>	Transmembrane protein 235	down	<b>-1.52</b>	3.22E-04

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GO, gene ontology; up, up-regulated genes in the cellular component gene ontology term; down, down-regulated genes in the cellular component gene ontology term; DEG, differentially expressed gene; FC, fold-change.

**Supplementary Table S2** RNA-Seq transcriptomic analysis predicted aldosterone up-regulated genes. Aldosterone-treated samples compared to untreated control samples.

Aldosterone 10 <sup>-7</sup> M			Up-regulated genes
P-value	FC	Gene name	Description
2.68E-04	3.55	EHF	ETS homologous factor
2.87E-06	3.35	ZBTB16	Zinc finger and BTB domain containing 16
1.87E-03	2.99	SERPINA3	Serpin family A member 3
1.80E-05	2.97	POU5F1	POU class 5 homeobox 1
2.30E-04	2.71	LTBR	Lymphotoxin beta receptor
7.89E-03	2.53	LINC01844	<i>Long intergenic non-protein coding RNA 1844 (LOC101926975)</i>
4.88E-03	2.48	AL021395.1	<i>Long intergenic non-coding RNA</i>
3.10E-03	2.46	ARMC12	Armadillo repeat containing 12
4.73E-03	2.45	AC112206.2	<i>Long intergenic non-protein coding RNA (LOC101928858)</i>
1.40E-03	2.41	LINC01603	<i>Long intergenic non-protein coding RNA 1603</i>
1.02E-06	2.22	SCNN1A	Sodium channel epithelial 1 alpha subunit
4.69E-03	2.18	RP11-1024P17.1	<i>Long non-protein coding RNA</i>
6.77E-03	2.16	PLAUR	Plasminogen activator, urokinase receptor
2.86E-02	2.15	GCK	Glucokinase
2.70E-02	2.14	TMPRSS15	Transmembrane protease, serine 15
6.85E-04	2.13	PCDH1	Protocadherin 1
4.54E-02	2.13	AGXT	Alanine-glyoxylate aminotransferase
2.06E-02	2.10	LINC00176	<i>Long intergenic non-protein coding RNA 176</i>
1.15E-02	2.02	GRID2	Glutamate ionotropic receptor delta type subunit 2
2.57E-02	2.00	TNFSF18	Tumor necrosis factor superfamily member 18
2.70E-03	2.00	LRRC37A17P	Leucine rich repeat containing 37 member A17, pseudogene
3.65E-02	2.00	TAC4	Tachykinin 4 (hemokinin)
7.27E-03	1.99	AC132938.5	<i>Long non-protein coding RNA</i>
1.93E-02	1.95	MPP4	Membrane palmitoylated protein 4
4.04E-02	1.95	MYBPC2	Myosin binding protein C, fast type
2.24E-02	1.94	RNU6ATAC18P	RNA, U6atac small nuclear 18, pseudogene
8.17E-03	1.93	SEZ6L	Seizure related 6 homolog like
1.56E-03	1.92	AC009542.2	<i>Transcribed unprocessed pseudogene</i>
1.58E-03	1.90	FKBP5	FK506 binding protein 5
3.69E-03	1.89	FOSL1	FOS like 1, AP-1 transcription factor subunit
3.93E-02	1.88	AL390066.1	<i>Long intergenic non-protein coding RNA</i>
2.87E-03	1.87	OMD	Osteomodulin
4.26E-03	1.87	HVCN1	Hydrogen voltage gated channel 1
4.91E-04	1.87	SLC3A1	Solute carrier family 3 member 1
2.85E-04	1.86	DUSP8P5	Dual specificity phosphatase 8 pseudogene 5
3.34E-03	1.85	DRGX	Dorsal root ganglia homeobox
3.48E-05	1.84	AP001596.1	<i>Antisense RNA</i>
4.72E-03	1.82	SPRY4	Sprouty RTK signaling antagonist 4
2.50E-04	1.81	S100A2	S100 calcium binding protein A2
4.40E-03	1.81	AC005162.3	<i>Antisense RNA</i>
8.65E-03	1.80	AC124312.5	<i>Long non-protein coding RNA</i>
4.34E-03	1.74	CYYR1-AS1	Cysteine and tyrosine rich 1 antisense RNA 1
2.64E-02	1.74	ADH1B	Alcohol dehydrogenase 1B (class I), beta polypeptide
1.09E-02	1.73	SVEP1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1

2.61E-03	1.71	<b>RXRG</b>	Retinoid X receptor gamma
3.12E-02	1.71	<b>ITGB3</b>	Integrin subunit beta 3
3.97E-06	1.71	<b>TMEM72</b>	Transmembrane protein 72
4.23E-02	1.71	<b>P2RY6</b>	Pyrimidinergic receptor P2Y6
1.81E-02	1.70	<b>SNORD109A</b>	Small nucleolar RNA, C/D box 109A
2.87E-02	1.70	<b>LINC01443</b>	<i>Long intergenic non-protein coding RNA 1443</i>
2.10E-02	1.70	<b>AL353801.1</b>	<i>Long intergenic non-protein coding RNA</i>
2.77E-02	1.70	<b>EPHA8</b>	EPH receptor A8
6.41E-04	1.69	<b>TMEM72-AS1</b>	TMEM72 antisense RNA 1
2.60E-02	1.68	<b>NLRC3</b>	NLR family CARD domain containing 3
1.65E-02	1.68	<b>RFTN2</b>	Raftlin family member 2
1.94E-02	1.68	<b>PNMT</b>	Phenylethanolamine N-methyltransferase
3.27E-03	1.67	<b>S100A3</b>	S100 calcium binding protein A3
8.81E-03	1.67	<b>AC128688.2</b>	<i>Antisense RNA</i>
3.01E-03	1.66	<b>VWA5B2</b>	Von Willebrand factor A domain containing 5B2
1.54E-02	1.64	<b>LINC00930</b>	<i>Long intergenic non-protein coding RNA 930</i>
3.89E-02	1.63	<b>AC025263.1</b>	<i>Antisense RNA (LOC101928002)</i>
9.51E-04	1.62	<b>GPRIN1</b>	G protein regulated inducer of neurite outgrowth 1
1.81E-06	1.61	<b>MCTP2</b>	Multiple C2 and transmembrane domain containing 2
3.30E-02	1.60	<b>AC024075.1</b>	<i>Sense intronic RNA</i>
1.39E-02	1.60	<b>PLAT</b>	Plasminogen activator, tissue type
7.17E-03	1.58	<b>GPR75</b>	G protein-coupled receptor 75
1.27E-04	1.58	<b>AC083843.3</b>	<i>Long intergenic non-protein coding RNA</i>
7.08E-03	1.57	<b>DSCAML1</b>	DS cell adhesion molecule like 1
1.37E-05	1.57	<b>DUSP6</b>	Dual specificity phosphatase 6
7.18E-06	1.57	<b>PTGER2</b>	Prostaglandin E receptor 2
1.44E-02	1.57	<b>AC245060.4</b>	<i>Transcribed unprocessed pseudogene</i>
1.64E-02	1.57	<b>ZNF114</b>	Zinc finger protein 114
8.84E-04	1.55	<b>ATP6V0A4</b>	ATPase H <sup>+</sup> transporting V0 subunit a4
2.95E-03	1.55	<b>OPRD1</b>	Opioid receptor delta 1
2.28E-03	1.55	<b>S100A6</b>	S100 calcium binding protein A6
5.61E-03	1.55	<b>ANKRD23</b>	Ankyrin repeat domain 23
2.41E-02	1.55	<b>ABCC3</b>	ATP binding cassette subfamily C member 3
2.66E-02	1.54	<b>PTX3</b>	Pentraxin 3
2.43E-03	1.54	<b>FAM196B</b>	Family with sequence similarity 196 member B
2.82E-03	1.54	<b>LINC01238</b>	<i>Long intergenic non-protein coding RNA 1238</i>
7.46E-03	1.54	<b>HIST1H2BC</b>	Histone cluster 1, H2bc
7.70E-03	1.53	<b>HMGA1</b>	High mobility group AT-hook 1
2.06E-03	1.53	<b>ITGA4</b>	Integrin subunit alpha 4
2.34E-03	1.52	<b>CXCR4</b>	C-X-C motif chemokine receptor 4
1.27E-02	1.51	<b>ITGAX</b>	Integrin subunit alpha X
3.53E-06	1.51	<b>PER1</b>	Period circadian clock 1
4.01E-02	1.51	<b>C19orf71</b>	<i>Chromosome 19 open reading frame 71</i>
1.47E-03	1.51	<b>GNL3L</b>	G protein nucleolar 3 like
5.68E-03	1.51	<b>MGAM2</b>	Maltase-glucoamylase 2 (putative)
6.91E-03	1.50	<b>GHRLOS</b>	Ghrelin opposite strand/antisense RNA

Genes are classified according to the fold change with a *P*-value and fold-change cut-off of *P* < 0.05 and FC > 1.5, respectively. FC, fold-change.

Supplementary Table S3 RNA-Seq transcriptomic analysis predicted aldosterone down-regulated genes. Aldosterone-treated samples compared to untreated control samples.

Aldosterone 10 <sup>-7</sup> M			Down-regulated genes
P-value	FC	Gene name	Description
2.06E-04	-2.70	SOCS2-AS1	SOCS2 antisense RNA 1
1.20E-03	-2.53	SERPINB9P1	Serpin family B member 9 pseudogene 1
1.36E-04	-2.48	LINC01164	<i>Long intergenic non-protein coding RNA 1164</i>
3.39E-03	-2.31	DOC2A	Double C2 domain alpha
4.78E-03	-2.30	STK32A	Serine/threonine kinase 32A
2.16E-03	-2.19	MPPED1	Metallophosphoesterase domain containing 1
5.66E-03	-2.16	MGP	Matrix Gla protein
8.28E-04	-2.15	AL589740.1	<i>Long intergenic non-protein coding RNA (LOC101927314)</i>
2.31E-02	-2.11	LINC00844	<i>Long intergenic non-protein coding RNA 844</i>
3.29E-02	-2.09	FMOD	Fibromodulin
4.51E-04	-2.05	ABCB1	ATP binding cassette subfamily B member 1
1.38E-03	-2.04	IL5RA	Interleukin 5 receptor subunit alpha
4.87E-04	-2.02	RPRML	Reprimo like
2.21E-03	-2.01	GDF7	Growth differentiation factor 7
1.32E-03	-1.97	TMEM160	Transmembrane protein 160
7.25E-03	-1.96	C19orf81	<i>Chromosome 19 open reading frame 81</i>
3.10E-03	-1.96	PCOLCE-AS1	PCOLCE antisense RNA 1
4.59E-03	-1.95	SIX1	SIX homeobox 1
3.45E-02	-1.95	LINC00639	<i>Long intergenic non-protein coding RNA 639</i>
9.35E-04	-1.94	CDC20P1	Cell division cycle 20 pseudogene 1
1.28E-02	-1.93	AL603840.1	<i>Long intergenic non-protein coding RNA</i>
4.99E-03	-1.92	EVC2	EvC ciliary complex subunit 2
2.06E-02	-1.92	RBFOX3	RNA binding protein, fox-1 homolog 3
1.90E-03	-1.92	MAP3K7CL	MAP3K7 C-terminal like
3.72E-02	-1.89	LINC01719	<i>Long intergenic non-protein coding RNA 1719</i>
2.77E-03	-1.88	NYAP2	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2
3.57E-03	-1.88	NPW	Neuropeptide W
1.10E-03	-1.88	C4orf48	<i>Chromosome 4 open reading frame 48</i>
3.20E-02	-1.87	PLP1	Proteolipid protein 1
1.04E-03	-1.86	PCSK1N	Proprotein convertase subtilisin/kexin type 1 inhibitor
3.76E-04	-1.85	EGR1	Early growth response 1
1.80E-02	-1.82	LMX1A	LIM homeobox transcription factor 1 alpha
1.66E-02	-1.82	FIGNL2	Fidgetin like 2
1.03E-04	-1.81	SST	Somatostatin
3.33E-02	-1.81	AL731563.3	<i>Long intergenic non-protein coding RNA</i>
3.62E-03	-1.80	SOX3	SRY-box 3
1.66E-02	-1.80	GRIN3B	Glutamate ionotropic receptor NMDA type subunit 3B
7.76E-04	-1.80	MAFA	MAF bZIP transcription factor A
2.31E-03	-1.80	AC087741.3	<i>Uncategorized gene</i>
7.77E-03	-1.79	PNMA8C	PNMA family member 8C
9.00E-03	-1.79	CCDC3	Coiled-coil domain containing 3
9.23E-03	-1.79	MORN5	MORN repeat containing 5
1.23E-02	-1.79	CTNNA2	Catenin alpha 2
3.42E-02	-1.78	MYL3	Myosin light chain 3
1.79E-02	-1.78	AC110285.7	<i>Long non-protein coding RNA</i>
5.10E-04	-1.78	CDC37L1-AS1	CDC37L1 antisense RNA 1 (head to head)

1.56E-02	-1.76	UNC5B-AS1	UNC5B antisense RNA 1
3.21E-02	-1.76	AC100814.1	<i>Long intergenic non-protein coding RNA</i>
2.52E-02	-1.75	AC120053.1	<i>Antisense RNA</i>
3.56E-03	-1.74	AL441883.1	<i>Antisense RNA</i>
3.73E-02	-1.73	ACTG2	Actin, gamma 2, smooth muscle, enteric
1.03E-02	-1.72	CNN1	Calponin 1
3.69E-02	-1.72	AC024681.1	<i>Long non-protein coding RNA</i>
2.25E-04	-1.72	RPL13AP5	Ribosomal protein L13a pseudogene 5
1.86E-03	-1.72	PRKAG2-AS1	PRKAG2 antisense RNA 1
3.19E-02	-1.71	AP000473.2	<i>Long intergenic non-protein coding RNA</i>
1.71E-02	-1.70	ADARB2	Adenosine deaminase, RNA specific B2 (inactive)
3.40E-05	-1.70	IGFBP3	Insulin like growth factor binding protein 3
2.25E-03	-1.70	RASL12	RAS like family 12
4.72E-02	-1.69	EGR2	Early growth response 2
3.22E-04	-1.67	RTN4RL2	Reticulon 4 receptor-like 2
1.70E-02	-1.67	GJD2	Gap junction protein delta 2
5.39E-03	-1.67	SCGB1B2P	Secretoglobin family 1B member 2, pseudogene
2.59E-03	-1.66	EEF1A1P6	Eukaryotic translation elongation factor 1 alpha 1 pseudogene 6
4.60E-03	-1.66	ADAT3	Adenosine deaminase, tRNA specific 3
1.38E-04	-1.65	LIX1	Limb and CNS expressed 1
1.36E-02	-1.65	MXRA5Y	Matrix remodeling associated 5, Y-linked (pseudogene)
1.01E-03	-1.64	PLPPR3	Phospholipid phosphatase related 3
2.25E-02	-1.64	PTPRC	Protein tyrosine phosphatase, receptor type C
7.16E-04	-1.63	AC004540.2	<i>Antisense RNA (LOC105375304)</i>
3.09E-02	-1.62	PGM5P4	Phosphoglucomutase 5 pseudogene 4
6.55E-04	-1.61	GFRA2	GDNF family receptor alpha 2
9.47E-03	-1.61	EFCAB5	EF-hand calcium binding domain 5
6.71E-04	-1.61	TESMIN	Testis expressed metallothionein like protein
1.13E-02	-1.61	RPS2P7	Ribosomal protein S2 pseudogene 7
1.79E-02	-1.60	DRC1	Dynein regulatory complex subunit 1
1.74E-02	-1.60	LINC02256	<i>Long intergenic non-protein coding RNA 2256</i>
2.24E-03	-1.60	GPR158	G protein-coupled receptor 158
1.65E-03	-1.59	AP000892.3	<i>Uncategorized gene</i>
2.69E-02	-1.59	EPS8L1	EPS8 like 1
1.71E-03	-1.59	TPGS1	Tubulin polyglutamylase complex subunit 1
1.70E-03	-1.59	CADM3	Cell adhesion molecule 3
3.34E-02	-1.59	AL138963.3	<i>Antisense RNA</i>
3.88E-03	-1.58	HES4	Hes family bHLH transcription factor 4
4.02E-04	-1.58	KCNIP1	Potassium voltage-gated channel interacting protein 1
3.85E-03	-1.58	OMG	Oligodendrocyte myelin glycoprotein
1.11E-03	-1.58	DPY19L2P3	DPY19L2 pseudogene 3
5.77E-03	-1.58	SOX21-AS1	SOX21 antisense RNA 1 (head to head)
5.62E-03	-1.58	CCDC85B	Coiled-coil domain containing 85B
2.66E-02	-1.57	AL391261.2	<i>Long intergenic non-protein coding RNA</i>
7.69E-03	-1.57	RPS15P4	Ribosomal Protein S15 Pseudogene 4
3.69E-03	-1.57	BGN	Biglycan
1.24E-02	-1.57	RAMP2	Receptor activity modifying protein 2
4.28E-02	-1.56	TBX6	T-box 6
1.10E-02	-1.56	KCNMB2	Potassium calcium-activated channel subfamily M regulatory beta subunit 2
7.45E-03	-1.56	JSRP1	Junctional sarcoplasmic reticulum protein 1
1.18E-03	-1.55	STUM	Stum, mechanosensory transduction mediator homolog
4.73E-03	-1.55	AC084824.4	<i>Sense intronic RNA</i>
4.16E-03	-1.55	KRT4	Keratin 4
1.93E-03	-1.55	AL391650.1	<i>Protein coding gene</i>
4.84E-03	-1.54	CLEC11A	C-type lectin domain family 11 member A



1.61E-02	-1.54	CR2	Complement component 3d receptor 2
6.37E-03	-1.54	MIR503HG	MIR503 host gene
5.83E-03	-1.54	FAM69C	Family with sequence similarity 69 member C
2.60E-02	-1.53	FAM19A4	Family with sequence similarity 19 member A4, C-C motif chemokine like
9.35E-03	-1.53	LINC01024	<i>Long intergenic non-protein coding RNA 1024</i>
1.58E-02	-1.52	AHRR	Aryl-hydrocarbon receptor repressor
4.63E-03	-1.52	CFD	Complement factor D
2.40E-03	-1.52	SLC12A5	Solute carrier family 12 member 5
2.60E-03	-1.52	COL2A1	Collagen type II alpha 1 chain
1.77E-02	-1.51	LINC00862	<i>Long intergenic non-protein coding RNA 862</i>
6.00E-04	-1.51	ZNF837	Zinc finger protein 837
3.26E-02	-1.51	SOCS1	Suppressor of cytokine signaling 1
4.10E-02	-1.51	HTR1D	5-hydroxytryptamine receptor 1D
1.47E-03	-1.51	ERICH6-AS1	ERICH6 antisense RNA 1
3.29E-03	-1.51	FAM81B	Family with sequence similarity 81 member B
2.60E-02	-1.51	AC016723.1	<i>Antisense RNA</i>
2.32E-02	-1.51	STX17-AS1	STX17 antisense RNA 1
2.71E-03	-1.50	EVA1B	Eva-1 homolog B
8.12E-03	-1.50	CTU1	Cytosolic thiouridylase subunit 1
2.56E-02	-1.50	AL117332.1	<i>Antisense RNA</i>
3.63E-02	-1.50	ID2-AS1	ID2 antisense RNA 1 (head to head)

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Genes are classified according to the fold change with a *P*-value and fold-change cut-off of  $P < 0.05$  and  $FC < -1.5$ , respectively. FC, fold-change.

**Supplementary Table S4** RNA-Seq transcriptomic analysis predicted cortisol up-regulated genes. Cortisol-treated samples compared to untreated control samples.

Cortisol 10 <sup>-7</sup> M			Up-regulated genes
P-value	FC	Gene name	Description
1.81E-152	<b>6.48</b>	<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit
1.88E-202	<b>5.36</b>	<b>FKBP5</b>	FK506 binding protein 5
4.71E-32	<b>4.15</b>	<b>HVCN1</b>	Hydrogen voltage gated channel 1
5.41E-49	<b>3.13</b>	<b>POU5F1</b>	POU class 5 homeobox 1
1.10E-07	<b>3.06</b>	<b>ADH1B</b>	Alcohol dehydrogenase 1B (class I), beta polypeptide
5.32E-77	<b>3.00</b>	<b>MIR6883 / PER1</b>	MicroRNA 6883 / Period circadian clock 1
4.19E-40	<b>2.97</b>	<b>HIF3A</b>	Hypoxia inducible factor 3 alpha subunit
1.44E-82	<b>2.68</b>	<b>ACSS1</b>	Acyl-CoA synthetase short-chain family member 1
2.79E-12	<b>2.66</b>	<b>SLC28A3</b>	Solute carrier family 28 member 3
5.28E-54	<b>2.62</b>	<b>PTGER2</b>	Prostaglandin E receptor 2
1.93E-36	<b>2.56</b>	<b>MAP7D2</b>	MAP7 domain containing 2
1.29E-22	<b>2.53</b>	<b>SERPINA3</b>	Serpin family A member 3
4.21E-20	<b>2.38</b>	<b>EPHA8</b>	EPH receptor A8
2.99E-22	<b>2.31</b>	<b>TLE2</b>	Transducin like enhancer of split 2
8.46E-132	<b>2.24</b>	<b>ST6GALNAC2</b>	ST6 N-acetylgalactosaminide alpha-2, 6-sialyltransferase 2
1.57E-03	<b>2.18</b>	<b>APCDD1L</b>	APC down-regulated 1 like
8.35E-04	<b>2.15</b>	<b>MIR7-1</b>	MicroRNA 7-1
4.57E-51	<b>2.12</b>	<b>REPS2</b>	RALBP1 associated Eps domain containing 2
7.08E-08	<b>2.06</b>	<b>CES4A</b>	Carboxylesterase 4A
3.41E-95	<b>2.03</b>	<b>SLC13A4</b>	Solute carrier family 13 member 4
9.89E-34	<b>2.01</b>	<b>PRLR</b>	Prolactin receptor
1.82E-08	<b>1.96</b>	<b>CDH20</b>	Cadherin 20
6.25E-39	<b>1.96</b>	<b>SLC16A12</b>	Solute carrier family 16 member 12
1.16E-24	<b>1.95</b>	<b>FAM196B</b>	Family with sequence similarity 196 member B
3.65E-09	<b>1.94</b>	<b>MAOA</b>	Monoamine oxidase A
4.56E-05	<b>1.93</b>	<b>STAC2</b>	SH3 and cysteine rich domain 2
9.77E-16	<b>1.92</b>	<b>SYTL3</b>	Synaptotagmin like 3
2.90E-22	<b>1.92</b>	<b>TRMT9B</b>	TRNA Methyltransferase 9B
3.25E-09	<b>1.92</b>	<b>H19 / MIR675</b>	H19, imprinted maternally expressed transcript / MicroRNA 675
1.94E-34	<b>1.91</b>	<b>HPD</b>	4-hydroxyphenylpyruvate dioxygenase
1.13E-22	<b>1.88</b>	<b>SH3PXD2B</b>	SH3 and PX domains 2B
7.99E-71	<b>1.87</b>	<b>TCEAL4</b>	Transcription elongation factor A like 4
4.28E-21	<b>1.85</b>	<b>RND2</b>	Rho family GTPase 2
3.95E-03	<b>1.84</b>	<b>DUSP5</b>	Dual specificity phosphatase 5
6.57E-17	<b>1.83</b>	<b>TMEM72</b>	Transmembrane protein 72
2.59E-107	<b>1.83</b>	<b>TSC22D3</b>	TSC22 domain family member 3
2.93E-03	<b>1.82</b>	<b>DUSP6</b>	Dual specificity phosphatase 6
5.67E-15	<b>1.81</b>	<b>CXCR4</b>	C-X-C motif chemokine receptor 4
2.08E-50	<b>1.80</b>	<b>IQSEC3</b>	IQ motif and Sec7 domain 3
2.86E-13	<b>1.79</b>	<b>TMEM229B</b>	Transmembrane protein 229B
4.35E-45	<b>1.79</b>	<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2
3.40E-40	<b>1.77</b>	<b>KLF15</b>	Kruppel like factor 15
5.28E-12	<b>1.77</b>	<b>METTL7A</b>	Methyltransferase like 7A
5.77E-04	<b>1.76</b>	<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1

3.59E-22	<b>1.75</b>	<b>AIM1</b>	Absent in melanoma 1
1.03E-30	<b>1.75</b>	<b>MIOS</b>	Meiosis regulator for oocyte development
3.29E-22	<b>1.75</b>	<b>ABCC5</b>	ATP binding cassette subfamily C member 5
4.18E-05	<b>1.75</b>	<b>PAPLN</b>	Papilin, proteoglycan like sulfated glycoprotein
1.71E-40	<b>1.73</b>	<b>USP53</b>	Ubiquitin specific peptidase 53
1.01E-05	<b>1.73</b>	<b>GRAMD1C</b>	GRAM domain containing 1C
1.10E-11	<b>1.73</b>	<b>ALDH1L1</b>	Aldehyde dehydrogenase 1 family member L1
1.02E-12	<b>1.72</b>	<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2, 3-sialyltransferase 5
4.31E-07	<b>1.72</b>	<b>KBTBD8</b>	Kelch repeat and BTB domain containing 8
5.22E-05	<b>1.71</b>	<b>KRT5</b>	Keratin 5
2.01E-40	<b>1.70</b>	<b>SERPINF2</b>	Serpin family F member 2
8.53E-12	<b>1.70</b>	<b>CP</b>	Ceruloplasmin
1.36E-18	<b>1.69</b>	<b>SOD2</b>	Superoxide dismutase 2, mitochondrial
6.93E-91	<b>1.69</b>	<b>PRODH</b>	Proline dehydrogenase 1
4.73E-11	<b>1.69</b>	<b>ABCA4</b>	ATP binding cassette subfamily A member 4
2.04E-04	<b>1.68</b>	<b>SCGB1D2</b>	Secretoglobin family 1D member 2
3.04E-03	<b>1.66</b>	<b>S100A2</b>	S100 calcium binding protein A2
2.10E-18	<b>1.64</b>	<b>TGFR2</b>	Transforming growth factor beta receptor 2
2.21E-09	<b>1.64</b>	<b>BICDL1</b>	BICD family like cargo adaptor 1
3.83E-80	<b>1.64</b>	<b>CRYZ</b>	Crystallin zeta
1.05E-14	<b>1.63</b>	<b>MT1X</b>	Metallothionein 1X
1.57E-33	<b>1.63</b>	<b>IQGAP2</b>	IQ motif containing GTPase activating protein 2
1.47E-16	<b>1.62</b>	<b>MCTP2</b>	Multiple C2 and transmembrane domain containing 2
3.75E-04	<b>1.61</b>	<b>WNT11</b>	Wnt family member 11
1.69E-03	<b>1.61</b>	<b>LINC01088</b>	<i>Long intergenic non-protein coding RNA 1088</i>
2.05E-44	<b>1.61</b>	<b>PCP4</b>	Purkinje cell protein 4
4.79E-07	<b>1.60</b>	<b>SLC1A7</b>	Solute carrier family 1 member 7
3.19E-14	<b>1.60</b>	<b>PLIN2</b>	Perilipin 2
8.18E-52	<b>1.60</b>	<b>ITGB4</b>	Integrin subunit beta 4
4.87E-12	<b>1.60</b>	<b>FHIT</b>	Fragile histidine triad
1.75E-05	<b>1.58</b>	<b>ATP6V0A4</b>	ATPase H <sup>+</sup> transporting V0 subunit a4
1.58E-04	<b>1.58</b>	<b>ZFP36</b>	ZFP36 ring finger protein
2.75E-04	<b>1.58</b>	<b>FAM167A-AS1</b>	FAM167A antisense RNA 1
3.72E-02	<b>1.58</b>	<b>MIR641</b>	MicroRNA 641
2.58E-42	<b>1.58</b>	<b>SLC2A12</b>	Solute carrier family 2 member 12
2.97E-14	<b>1.57</b>	<b>CEBPD</b>	CCAAT/enhancer binding protein delta
2.25E-03	<b>1.57</b>	<b>NDRG4</b>	NDRG family member 4
4.65E-09	<b>1.57</b>	<b>USP2</b>	Ubiquitin specific peptidase 2
6.84E-17	<b>1.57</b>	<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5
8.43E-35	<b>1.57</b>	<b>SGK1</b>	Serum/glucocorticoid regulated kinase 1
3.19E-28	<b>1.57</b>	<b>INPP5K</b>	Inositol polyphosphate-5-phosphatase K
1.77E-30	<b>1.57</b>	<b>SLC16A10</b>	Solute carrier family 16 member 10
2.80E-20	<b>1.56</b>	<b>PPM1K</b>	Protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent 1K
3.76E-07	<b>1.56</b>	<b>XYLB</b>	Xylulokinase
1.45E-25	<b>1.55</b>	<b>CHST11</b>	Carbohydrate sulfotransferase 11
2.78E-03	<b>1.54</b>	<b>EEPD1</b>	Endonuclease/exonuclease/phosphatase family domain containing 1
2.87E-03	<b>1.53</b>	<b>CYTIP</b>	Cytohesin 1 interacting protein
3.65E-13	<b>1.53</b>	<b>AADACL4</b>	Arylacetamide deacetylase like 4
9.96E-16	<b>1.53</b>	<b>SLCO4A1</b>	Solute carrier organic anion transporter family member 4A1
3.59E-05	<b>1.53</b>	<b>ADAMTSL1</b>	ADAMTS like 1
4.94E-18	<b>1.53</b>	<b>ADAMTSL4</b>	ADAMTS like 4
1.72E-07	<b>1.52</b>	<b>LINC00330</b>	<i>Long intergenic non-protein coding RNA 330</i>
1.61E-02	<b>1.51</b>	<b>B4GALNT1</b>	Beta-1, 4-N-acetyl-galactosaminyltransferase 1
1.09E-05	<b>1.51</b>	<b>CD58</b>	CD58 molecule
3.95E-06	<b>1.50</b>	<b>MAFF</b>	MAF bZIP transcription factor F

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Genes are classified according to the fold change with a  $P$ -value and fold-change cut-off of  $P < 0.05$  and  $FC > 1.5$ , respectively. FC, fold-change.

**Supplementary Table S5** RNA-Seq transcriptomic analysis predicted cortisol down-regulated genes. Cortisol-treated samples compared to untreated control samples.

**Cortisol 10<sup>-7</sup> M**

**Down-regulated genes**

<i>P</i> -value	FC	Gene name	Description
1.64E-04	<b>-2.40</b>	<b>TGM2</b>	Transglutaminase 2
9.25E-04	<b>-2.35</b>	<b>KRT81</b>	Keratin 81
8.37E-03	<b>-2.26</b>	<b>CNN1</b>	Calponin 1
5.39E-05	<b>-2.25</b>	<b>SPP1</b>	Secreted phosphoprotein 1
3.59E-07	<b>-2.24</b>	<b>ITGA11</b>	Integrin subunit alpha 11
1.63E-06	<b>-2.08</b>	<b>AMTN</b>	Amelotin
3.31E-03	<b>-2.07</b>	<b>INHBA</b>	Inhibin beta A subunit
2.95E-05	<b>-2.02</b>	<b>OMG</b>	Oligodendrocyte myelin glycoprotein
6.84E-04	<b>-1.95</b>	<b>C1orf61 / MIR9-1</b>	<i>Chromosome 1 open reading frame 61 /</i> MicroRNA 9-1
1.81E-05	<b>-1.95</b>	<b>TK1</b>	Thymidine kinase 1
1.52E-18	<b>-1.85</b>	<b>IGF1</b>	Insulin like growth factor 1
8.35E-04	<b>-1.83</b>	<b>CYS1</b>	Cystin 1
2.47E-08	<b>-1.81</b>	<b>DTL</b>	Denticleless E3 ubiquitin protein ligase homolog
1.02E-02	<b>-1.79</b>	<b>ANKRD1</b>	Ankyrin repeat domain 1
2.40E-03	<b>-1.78</b>	<b>SFRP2</b>	Secreted frizzled related protein 2
8.82E-05	<b>-1.74</b>	<b>KCND2</b>	Potassium voltage-gated channel subfamily D member 2
2.48E-04	<b>-1.71</b>	<b>CDCA7</b>	Cell division cycle associated 7
8.96E-05	<b>-1.70</b>	<b>GJD2</b>	Gap junction protein delta 2
4.81E-05	<b>-1.69</b>	<b>DEPDC1B</b>	DEP domain containing 1B
3.85E-03	<b>-1.69</b>	<b>SST</b>	Somatostatin
3.35E-03	<b>-1.68</b>	<b>COL1A1</b>	Collagen type I alpha 1 chain
1.58E-02	<b>-1.66</b>	<b>PAPPA</b>	Pappalysin 1
1.77E-03	<b>-1.64</b>	<b>IGFBP3</b>	Insulin like growth factor binding protein 3
1.13E-04	<b>-1.63</b>	<b>SMOC1</b>	SPARC related modular calcium binding 1
4.88E-04	<b>-1.61</b>	<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3
3.67E-03	<b>-1.61</b>	<b>ZNF367</b>	Zinc finger protein 367
1.18E-10	<b>-1.61</b>	<b>ROBO2</b>	Roundabout guidance receptor 2
3.80E-05	<b>-1.60</b>	<b>FAM111B</b>	Family with sequence similarity 111 member B
1.79E-04	<b>-1.60</b>	<b>ASF1B</b>	Anti-silencing function 1B histone chaperone
6.15E-04	<b>-1.58</b>	<b>TCF19</b>	Transcription factor 19
1.44E-03	<b>-1.58</b>	<b>CDCA5</b>	Cell division cycle associated 5
3.00E-02	<b>-1.58</b>	<b>CDC20B</b>	Cell division cycle 20B
8.91E-12	<b>-1.57</b>	<b>ADAMTS1</b>	ADAM metalloproteinase with thrombospondin type 1 motif 1
1.46E-08	<b>-1.55</b>	<b>RRM2</b>	Ribonucleotide reductase regulatory subunit M2
3.77E-02	<b>-1.55</b>	<b>NACAD</b>	NAC alpha domain containing
1.50E-02	<b>-1.55</b>	<b>STK32B</b>	Serine/threonine kinase 32B
8.99E-05	<b>-1.54</b>	<b>NDST3</b>	N-deacetylase and N-sulfotransferase 3
3.30E-03	<b>-1.54</b>	<b>TTK</b>	TTK protein kinase
8.85E-03	<b>-1.54</b>	<b>CENPK</b>	Centromere protein K
1.36E-08	<b>-1.52</b>	<b>IGSF9</b>	Immunoglobulin superfamily member 9
2.11E-03	<b>-1.52</b>	<b>SHCBP1</b>	SHC binding and spindle associated 1

Genes are classified according to the fold change with a *P*-value and fold-change cut-off of *P* < 0.05 and FC < -1.5, respectively. FC, fold-change.

**Supplementary Table S6** RNA-Seq transcriptomic analysis predicted cortisol + RU-486 up-regulated genes. Cortisol + RU-486-treated samples compared to untreated control samples.

**Cortisol 10<sup>-7</sup> M + RU-486 10<sup>-5</sup> M**

**Up-regulated genes**

<i>P</i> -value	FC	Gene name	Description
8.09E-17	<b>16.20</b>	<b>AKR1C1</b>	Aldo-keto reductase family 1 member C1
9.08E-12	<b>13.96</b>	<b>HSPA6</b>	Heat shock protein family A (Hsp70) member 6
1.08E-12	<b>7.56</b>	<b>AKR1B10</b>	Aldo-keto reductase family 1 member B10
2.25E-08	<b>6.06</b>	<b>MMP1</b>	Matrix metalloproteinase 1
6.09E-05	<b>5.02</b>	<b>AGXT</b>	Alanine-glyoxylate aminotransferase
5.65E-14	<b>4.82</b>	<b>DUSP5</b>	Dual specificity phosphatase 5
3.17E-08	<b>3.81</b>	<b>FOSL1</b>	FOS like 1, AP-1 transcription factor subunit
2.08E-31	<b>3.56</b>	<b>ANGPTL4</b>	Angiopoietin like 4
1.92E-11	<b>3.54</b>	<b>SRPX2</b>	Sushi repeat containing protein, X-linked 2
3.12E-08	<b>3.40</b>	<b>IL7R</b>	Interleukin 7 receptor
5.36E-54	<b>2.96</b>	<b>HMGCS2</b>	3-hydroxy-3-methylglutaryl-CoA synthase 2
1.83E-07	<b>2.85</b>	<b>DUSP6</b>	Dual specificity phosphatase 6
3.52E-64	<b>2.83</b>	<b>PLIN2</b>	Perilipin 2
1.94E-12	<b>2.71</b>	<b>NDRG4</b>	NDRG family member 4
6.14E-08	<b>2.60</b>	<b>ABCC3</b>	ATP binding cassette subfamily C member 3
3.25E-08	<b>2.47</b>	<b>DKK1</b>	Dickkopf WNT signaling pathway inhibitor 1
3.94E-08	<b>2.46</b>	<b>B4GALNT1</b>	Beta-1, 4-N-acetyl-galactosaminyltransferase 1
1.15E-10	<b>2.38</b>	<b>PLAUR</b>	Plasminogen activator, urokinase receptor
1.05E-05	<b>2.30</b>	<b>TM4SF1</b>	Transmembrane 4 L six family member 1
1.56E-06	<b>2.28</b>	<b>CA12</b>	Carbonic anhydrase 12
3.93E-26	<b>2.21</b>	<b>SCNN1A</b>	Sodium channel epithelial 1 alpha subunit
1.15E-10	<b>2.21</b>	<b>PDK4</b>	Pyruvate dehydrogenase kinase 4
1.95E-07	<b>2.17</b>	<b>CLMP</b>	CXADR like membrane protein
3.89E-05	<b>2.14</b>	<b>PTX3</b>	Pentraxin 3
1.62E-05	<b>2.12</b>	<b>SLC24A4</b>	Solute carrier family 24 member 4
3.52E-09	<b>2.12</b>	<b>SERPINE2</b>	Serpin family E member 2
6.41E-05	<b>2.08</b>	<b>MARCH4</b>	Membrane associated ring-CH-type finger 4
2.47E-14	<b>2.05</b>	<b>RAB27B</b>	RAB27B, member RAS oncogene family
3.18E-08	<b>2.03</b>	<b>FGF12</b>	Fibroblast growth factor 12
5.61E-34	<b>2.02</b>	<b>FKBP5</b>	FK506 binding protein 5
4.98E-04	<b>1.99</b>	<b>PRCD</b>	Progressive rod-cone degeneration
7.60E-08	<b>1.97</b>	<b>HVCN1</b>	Hydrogen voltage gated channel 1
7.43E-07	<b>1.97</b>	<b>HMGA1 / MIR6835</b>	High mobility group AT-hook 1 / MicroRNA 6835
7.58E-03	<b>1.96</b>	<b>CALB2</b>	Calbindin 2
1.63E-26	<b>1.95</b>	<b>PTGER2</b>	Prostaglandin E receptor 2
2.60E-06	<b>1.94</b>	<b>EFCAB13 / ITGB3</b>	EF-hand calcium binding domain 13 / Integrin subunit beta 3
1.18E-08	<b>1.93</b>	<b>ANXA1</b>	Annexin A1
6.93E-10	<b>1.92</b>	<b>KCNMA1</b>	Potassium calcium-activated channel subfamily M alpha 1
4.91E-06	<b>1.91</b>	<b>METTL7B</b>	Methyltransferase like 7B
7.22E-08	<b>1.90</b>	<b>DLGAP1-AS2</b>	DLGAP1 antisense RNA 2
4.09E-05	<b>1.89</b>	<b>ISM2</b>	Isthmin 2

1.08E-07	<b>1.88</b>	<b>PHLDA1</b>	Pleckstrin homology like domain family A member 1
3.92E-04	<b>1.88</b>	<b>ISG15</b>	ISG15 ubiquitin-like modifier
4.02E-11	<b>1.88</b>	<b>MT2A</b>	Metallothionein 2A
8.34E-13	<b>1.87</b>	<b>MAFF</b>	MAF bZIP transcription factor F
6.79E-11	<b>1.84</b>	<b>SLC1A7</b>	Solute carrier family 1 member 7
3.66E-12	<b>1.84</b>	<b>CDCP1</b>	CUB domain containing protein 1
3.17E-06	<b>1.82</b>	<b>ECM1</b>	Extracellular matrix protein 1
1.24E-20	<b>1.80</b>	<b>DBI</b>	Diazepam binding inhibitor, acyl-CoA binding protein
8.51E-07	<b>1.79</b>	<b>MME</b>	Membrane metallo-endopeptidase
3.61E-07	<b>1.77</b>	<b>SPRY2</b>	Sprouty RTK signaling antagonist 2
5.04E-12	<b>1.76</b>	<b>LAMC2</b>	Laminin subunit gamma 2
5.49E-15	<b>1.76</b>	<b>TMEM72</b>	Transmembrane protein 72
2.88E-09	<b>1.76</b>	<b>HILPDA</b>	Hypoxia inducible lipid droplet associated
3.15E-05	<b>1.76</b>	<b>IL6</b>	Interleukin 6
1.87E-13	<b>1.75</b>	<b>ST3GAL5</b>	ST3 beta-galactoside alpha-2, 3-sialyltransferase 5
6.16E-04	<b>1.74</b>	<b>ACSL5</b>	Acyl-CoA synthetase long-chain family member 5
3.09E-17	<b>1.74</b>	<b>RSAD2</b>	Radical S-adenosyl methionine domain containing 2
1.43E-08	<b>1.74</b>	<b>OSGIN1</b>	Oxidative stress induced growth inhibitor 1
2.72E-05	<b>1.73</b>	<b>PTPRN</b>	Protein tyrosine phosphatase, receptor type N
2.71E-02	<b>1.73</b>	<b>VMO1</b>	Vitelline membrane outer layer 1 homolog
1.76E-03	<b>1.72</b>	<b>SLC3A1</b>	Solute carrier family 3 member 1
9.60E-09	<b>1.72</b>	<b>NQO1</b>	NAD(P)H quinone dehydrogenase 1
2.94E-06	<b>1.71</b>	<b>TRIB3</b>	Tribbles pseudokinase 3
1.66E-03	<b>1.71</b>	<b>S100A2</b>	S100 calcium binding protein A2
2.37E-02	<b>1.69</b>	<b>MIR7-1</b>	MicroRNA 7-1
7.71E-06	<b>1.69</b>	<b>TESC</b>	Tescalcin
3.99E-52	<b>1.67</b>	<b>CPT1A</b>	Carnitine palmitoyltransferase 1A
1.62E-06	<b>1.67</b>	<b>KBTBD8</b>	Kelch repeat and BTB domain containing 8
2.28E-02	<b>1.67</b>	<b>ACER2</b>	Alkaline ceramidase 2
1.58E-18	<b>1.66</b>	<b>PRLR</b>	Prolactin receptor
3.29E-03	<b>1.66</b>	<b>WSCD2</b>	WSC domain containing 2
2.09E-28	<b>1.66</b>	<b>RMI1</b>	RecQ mediated genome instability 1
1.29E-03	<b>1.65</b>	<b>ANO4</b>	Anoctamin 4
3.38E-15	<b>1.65</b>	<b>FRMPD3</b>	FERM and PDZ domain containing 3
1.05E-10	<b>1.64</b>	<b>CXCR4</b>	C-X-C motif chemokine receptor 4
6.53E-04	<b>1.64</b>	<b>DRGX</b>	Dorsal root ganglia homeobox
1.18E-05	<b>1.63</b>	<b>SLC22A6</b>	Solute carrier family 22 member 6
3.84E-20	<b>1.63</b>	<b>TMEM158</b>	Transmembrane protein 158 (gene/pseudogene)
3.90E-07	<b>1.62</b>	<b>SERPINA3</b>	Serpin family A member 3
2.90E-15	<b>1.62</b>	<b>IL33</b>	Interleukin 33
3.20E-07	<b>1.61</b>	<b>SLC9A9</b>	Solute carrier family 9 member A9
1.21E-06	<b>1.61</b>	<b>PMAIP1</b>	Phorbol-12-myristate-13-acetate-induced protein 1
1.87E-02	<b>1.60</b>	<b>RAET1G</b>	Retinoic acid early transcript 1G
1.52E-06	<b>1.60</b>	<b>BSPRY</b>	B-box and SPRY domain containing
2.00E-05	<b>1.59</b>	<b>IFITM1</b>	Interferon induced transmembrane protein 1
8.30E-04	<b>1.59</b>	<b>TNFSF18</b>	Tumor necrosis factor superfamily member 18
5.00E-03	<b>1.59</b>	<b>BTBD11</b>	BTB domain containing 11
3.47E-18	<b>1.57</b>	<b>MGST1</b>	Microsomal glutathione S-transferase 1
6.71E-10	<b>1.57</b>	<b>RLBP1</b>	Retinaldehyde binding protein 1
1.63E-10	<b>1.57</b>	<b>ATP1B2</b>	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 2
1.65E-04	<b>1.57</b>	<b>UPP1</b>	Uridine phosphorylase 1
9.15E-14	<b>1.56</b>	<b>C1QTNF1</b>	C1q and tumor necrosis factor related protein 1
3.68E-05	<b>1.55</b>	<b>CYP1B1</b>	Cytochrome P450 family 1 subfamily B member 1
2.99E-38	<b>1.55</b>	<b>PCP4</b>	Purkinje cell protein 4
1.34E-26	<b>1.55</b>	<b>SLC18A3</b>	Solute carrier family 18 member A3
1.10E-07	<b>1.55</b>	<b>BICDL1</b>	BICD family like cargo adaptor 1
2.16E-02	<b>1.55</b>	<b>FAM196A</b>	Family with sequence similarity 196 member A

4.12E-10	<b>1.55</b>	<b>ETV5</b>	ETS variant 5
4.50E-10	<b>1.55</b>	<b>LAYN</b>	Layilin
6.36E-26	<b>1.54</b>	<b>RPS6KA2</b>	Ribosomal protein S6 kinase A2
5.36E-08	<b>1.54</b>	<b>ABCA4</b>	ATP binding cassette subfamily A member 4
5.01E-04	<b>1.54</b>	<b>RIN1</b>	Ras and Rab interactor 1
2.47E-03	<b>1.54</b>	<b>SERPINE1</b>	Serpin family E member 1
2.73E-09	<b>1.54</b>	<b>CD44</b>	CD44 molecule (Indian blood group)
5.57E-13	<b>1.54</b>	<b>GNG2</b>	G protein subunit gamma 2
6.35E-11	<b>1.54</b>	<b>FAM196B</b>	Family with sequence similarity 196 member B
2.85E-08	<b>1.53</b>	<b>SPARCL1</b>	SPARC like 1
4.39E-10	<b>1.53</b>	<b>OSMR</b>	Oncostatin M receptor
3.15E-15	<b>1.53</b>	<b>KCNA5</b>	Potassium voltage-gated channel subfamily A member 5
4.76E-05	<b>1.53</b>	<b>SLC16A6</b>	Solute carrier family 16 member 6
2.93E-04	<b>1.53</b>	<b>C10orf53 /</b> <b>CHAT</b>	<i>Chromosome 10 open reading frame 53 /</i> Choline O-acetyltransferase
5.28E-09	<b>1.52</b>	<b>MGLL</b>	Monoglyceride lipase
2.07E-12	<b>1.52</b>	<b>SOD2</b>	Superoxide dismutase 2, mitochondrial
1.88E-02	<b>1.52</b>	<b>TSPAN1</b>	Tetraspanin 1
1.10E-24	<b>1.52</b>	<b>IQGAP2</b>	IQ motif containing GTPase activating protein 2
6.66E-14	<b>1.52</b>	<b>SLC7A11</b>	Solute carrier family 7 member 11
3.03E-10	<b>1.51</b>	<b>RND2</b>	Rho family GTPase 2
1.76E-11	<b>1.51</b>	<b>MIR6883 /</b> <b>PER1</b>	MicroRNA 6883 / Period circadian clock 1
2.83E-07	<b>1.51</b>	<b>GABBR2</b>	Gamma-aminobutyric acid type B receptor subunit 2
1.04E-03	<b>1.51</b>	<b>UBASH3B</b>	Ubiquitin associated and SH3 domain containing B
2.43E-05	<b>1.50</b>	<b>EPHA8</b>	EPH receptor A8
2.26E-22	<b>1.50</b>	<b>CHST11</b>	Carbohydrate sulfotransferase 11

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Genes are classified according to the fold change with a *P*-value and fold-change cut-off of  $P < 0.05$  and  $FC > 1.5$ , respectively. FC, fold-change.



**Supplementary Table S7** RNA-Seq transcriptomic analysis predicted cortisol + RU-486 down-regulated genes. Cortisol + RU-486-treated samples compared to untreated control samples.

**Cortisol 10<sup>-7</sup> M + RU-486 10<sup>-5</sup> M**

**Down-regulated genes**

P-value	FC	Gene name	Description
6.94E-06	<b>-4.32</b>	<b>CNN1</b>	Calponin 1
6.10E-20	<b>-3.92</b>	<b>GJD2</b>	Gap junction protein delta 2
8.79E-16	<b>-3.24</b>	<b>C14orf180</b>	<i>Chromosome 14 open reading frame 180</i>
6.48E-06	<b>-2.86</b>	<b>TGM2</b>	Transglutaminase 2
1.54E-09	<b>-2.80</b>	<b>OMG</b>	Oligodendrocyte myelin glycoprotein
1.32E-10	<b>-2.55</b>	<b>RPL3L</b>	Ribosomal protein L3 like
3.67E-12	<b>-2.41</b>	<b>KCNAB1</b>	Potassium voltage-gated channel subfamily A member regulatory beta subunit 1
1.93E-08	<b>-2.37</b>	<b>AMTN</b>	Amelotin
7.01E-33	<b>-2.35</b>	<b>TAGLN</b>	Transgelin
1.45E-08	<b>-2.34</b>	<b>ELF3</b>	E74 like ETS transcription factor 3
6.16E-29	<b>-2.27</b>	<b>GAS2L1P2</b>	Growth arrest specific 2 like 1 pseudogene 2
3.59E-08	<b>-2.24</b>	<b>ADAMTS5</b>	ADAM metalloproteinase with thrombospondin type 1 motif 5
5.48E-07	<b>-2.21</b>	<b>MGP</b>	Matrix Gla protein
3.49E-07	<b>-2.20</b>	<b>HHATL</b>	Hedgehog acyltransferase-like
7.42E-07	<b>-2.19</b>	<b>ITGA11</b>	Integrin subunit alpha 11
4.81E-09	<b>-2.16</b>	<b>FGD3</b>	FYVE, RhoGEF and PH domain containing 3
4.92E-19	<b>-2.13</b>	<b>ACTA2</b>	Actin, alpha 2, smooth muscle, aorta
5.82E-11	<b>-2.09</b>	<b>TNNT2</b>	Troponin T2, cardiac type
4.58E-03	<b>-2.06</b>	<b>KRT81</b>	Keratin 81
5.94E-08	<b>-2.04</b>	<b>KIF20A</b>	Kinesin family member 20A
5.05E-16	<b>-2.02</b>	<b>CARNS1</b>	Carnosine synthase 1
4.15E-07	<b>-2.01</b>	<b>GFRA2</b>	GDNF family receptor alpha 2
2.81E-06	<b>-2.01</b>	<b>GPR37L1</b>	G protein-coupled receptor 37 like 1
8.82E-05	<b>-2.00</b>	<b>HAPLN3</b>	Hyaluronan and proteoglycan link protein 3
1.42E-07	<b>-1.97</b>	<b>SOX8</b>	SRY-box 8
1.21E-06	<b>-1.97</b>	<b>NTRK3</b>	Neurotrophic receptor tyrosine kinase 3
5.82E-03	<b>-1.96</b>	<b>SEMA3B-AS1</b>	SEMA3B antisense RNA 1 (head to head)
6.23E-03	<b>-1.96</b>	<b>INHBA</b>	Inhibin beta A subunit
1.99E-11	<b>-1.94</b>	<b>CYP2W1</b>	Cytochrome P450 family 2 subfamily W member 1
1.03E-05	<b>-1.93</b>	<b>RUNX1T1</b>	RUNX1 translocation partner 1
1.30E-07	<b>-1.92</b>	<b>CCNA1</b>	Cyclin A1
5.84E-19	<b>-1.91</b>	<b>FGFR3</b>	Fibroblast growth factor receptor 3
2.49E-11	<b>-1.91</b>	<b>AP1M2</b>	Adaptor related protein complex 1 mu 2 subunit
5.27E-06	<b>-1.89</b>	<b>CYP19A1</b>	Cytochrome P450 family 19 subfamily A member 1
1.19E-23	<b>-1.88</b>	<b>ERF</b>	ETS2 repressor factor
3.09E-07	<b>-1.88</b>	<b>PPP1R14A</b>	Protein phosphatase 1 regulatory inhibitor subunit 14A
5.47E-07	<b>-1.85</b>	<b>ATP6V1B1</b>	ATPase H <sup>+</sup> transporting V1 subunit B1
1.74E-15	<b>-1.85</b>	<b>OXTR</b>	Oxytocin receptor
6.52E-03	<b>-1.85</b>	<b>ANKRD1</b>	Ankyrin repeat domain 1
3.55E-03	<b>-1.85</b>	<b>CDC20B</b>	Cell division cycle 20B
4.51E-03	<b>-1.84</b>	<b>NACAD</b>	NAC alpha domain containing
4.74E-07	<b>-1.84</b>	<b>SPC24</b>	SPC24, NDC80 kinetochore complex component
2.53E-08	<b>-1.84</b>	<b>RHBDL2</b>	Rhomboid like 2
1.67E-10	<b>-1.81</b>	<b>C5orf46</b>	Chromosome 5 open reading frame 46
2.77E-11	<b>-1.81</b>	<b>BUB1B /</b>	BUB1 mitotic checkpoint serine/threonine kinase B /

		<b>PAK6</b>	p21 (RAC1) activated kinase 6
1.02E-13	<b>-1.80</b>	<b>C10orf54</b>	<i>Chromosome 10 open reading frame 54</i>
7.86E-08	<b>-1.79</b>	<b>GAS6-AS1</b>	GAS6 antisense RNA 1
4.00E-08	<b>-1.79</b>	<b>DLGAP5</b>	DLG associated protein 5
2.51E-03	<b>-1.77</b>	<b>NEK2</b>	NIMA related kinase 2
9.27E-23	<b>-1.76</b>	<b>MMP11</b>	Matrix metalloproteinase 11
3.50E-04	<b>-1.75</b>	<b>SYT10</b>	Synaptotagmin 10
3.78E-06	<b>-1.74</b>	<b>RGS9</b>	Regulator of G-protein signaling 9
4.60E-28	<b>-1.74</b>	<b>PRSS12</b>	Protease, serine 12
2.06E-06	<b>-1.74</b>	<b>WNT2B</b>	Wnt family member 2B
7.83E-04	<b>-1.74</b>	<b>C21orf58</b>	<i>Chromosome 21 open reading frame 58</i>
2.64E-02	<b>-1.73</b>	<b>MOG</b>	Myelin oligodendrocyte glycoprotein
5.86E-04	<b>-1.73</b>	<b>TPPP3</b>	Tubulin polymerization promoting protein family member 3
2.44E-04	<b>-1.72</b>	<b>PLK1</b>	Polo like kinase 1
6.81E-05	<b>-1.72</b>	<b>LUM</b>	Lumican
1.61E-07	<b>-1.72</b>	<b>CCNA2</b>	Cyclin A2
6.57E-05	<b>-1.71</b>	<b>KIF4A</b>	Kinesin family member 4A
2.54E-11	<b>-1.69</b>	<b>MFSD2A</b>	Major facilitator superfamily domain containing 2A
2.68E-06	<b>-1.69</b>	<b>NDST3</b>	N-deacetylase and N-sulfotransferase 3
8.82E-13	<b>-1.69</b>	<b>BMF</b>	Bcl2 modifying factor
6.37E-05	<b>-1.69</b>	<b>MKI67</b>	Marker of proliferation Ki-67
3.07E-07	<b>-1.69</b>	<b>VGLL3</b>	Vestigial like family member 3
4.34E-13	<b>-1.68</b>	<b>INHBB</b>	Inhibin beta B subunit
1.89E-12	<b>-1.68</b>	<b>ERC2</b>	ELKS/RAB6-interacting/CAST family member 2
3.78E-09	<b>-1.68</b>	<b>HSPB7</b>	Heat shock protein family B (small) member 7
1.31E-04	<b>-1.67</b>	<b>CYP2S1</b>	Cytochrome P450 family 2 subfamily S member 1
1.11E-04	<b>-1.67</b>	<b>ADAMTS15</b>	ADAM metalloproteinase with thrombospondin type 1 motif 15
3.35E-12	<b>-1.67</b>	<b>CAPN6</b>	Calpain 6
3.80E-20	<b>-1.67</b>	<b>ADRA2C</b>	Adrenoceptor alpha 2C
1.33E-07	<b>-1.66</b>	<b>PLEKHG4B</b>	Pleckstrin homology and RhoGEF domain containing G4B
1.04E-04	<b>-1.65</b>	<b>DEPDC1B</b>	DEP domain containing 1B
6.47E-07	<b>-1.65</b>	<b>SEMA3D</b>	Semaphorin 3D
2.79E-03	<b>-1.64</b>	<b>SH3PXD2A</b>	SH3 and PX domains 2A
4.98E-03	<b>-1.64</b>	<b>COL1A1</b>	Collagen type I alpha 1 chain
1.16E-02	<b>-1.63</b>	<b>C1orf61 / MIR9-1</b>	<i>Chromosome 1 open reading frame 61 /</i> MicroRNA 9-1
2.38E-05	<b>-1.63</b>	<b>CENPF</b>	Centromere protein F
5.25E-09	<b>-1.63</b>	<b>FBXO15</b>	F-box protein 15
4.47E-10	<b>-1.62</b>	<b>CDK1</b>	Cyclin dependent kinase 1
3.18E-03	<b>-1.62</b>	<b>FOXM1</b>	Forkhead box M1
3.18E-03	<b>-1.62</b>	<b>ZNF367</b>	Zinc finger protein 367
5.85E-03	<b>-1.61</b>	<b>FAM81B</b>	Family with sequence similarity 81 member B
1.75E-04	<b>-1.61</b>	<b>UBE2T</b>	Ubiquitin conjugating enzyme E2 T
1.55E-04	<b>-1.60</b>	<b>CASC15</b>	Cancer susceptibility candidate 15 (non-protein coding)
8.94E-03	<b>-1.60</b>	<b>SST</b>	Somatostatin
1.94E-31	<b>-1.60</b>	<b>CDC42EP1</b>	CDC42 effector protein 1
1.85E-10	<b>-1.60</b>	<b>TPX2</b>	TPX2, microtubule nucleation factor
7.98E-09	<b>-1.59</b>	<b>NANOS1</b>	Nanos C2HC-type zinc finger 1
4.27E-03	<b>-1.59</b>	<b>CDC43</b>	Cell division cycle associated 3
3.71E-08	<b>-1.59</b>	<b>ABCB5</b>	ATP binding cassette subfamily B member 5
2.92E-05	<b>-1.59</b>	<b>PHLDB2 / PLCXD2</b>	Pleckstrin homology like domain family B member 2 / Phosphatidylinositol specific phospholipase C X domain containing 2
5.36E-03	<b>-1.58</b>	<b>CENPM</b>	Centromere protein M
1.97E-06	<b>-1.58</b>	<b>ASPM</b>	Abnormal spindle microtubule assembly
1.99E-06	<b>-1.58</b>	<b>ANLN</b>	Anillin actin binding protein
5.04E-03	<b>-1.57</b>	<b>RGS6</b>	Regulator of G-protein signaling 6

1.97E-04	-1.57	<b>CDKN2C</b>	Cyclin dependent kinase inhibitor 2C
1.09E-04	-1.57	<b>FILIP1</b>	Filamin A interacting protein 1
4.42E-10	-1.57	<b>ENTPD8</b>	Ectonucleoside triphosphate diphosphohydrolase 8
3.07E-04	-1.56	<b>MLXIPL</b>	MLX interacting protein like
4.35E-19	-1.56	<b>UNC5B</b>	Unc-5 netrin receptor B
8.15E-06	-1.56	<b>MYBL2</b>	MYB proto-oncogene like 2
2.82E-06	-1.56	<b>TOP2A</b>	Topoisomerase (DNA) II alpha
2.66E-07	-1.55	<b>MFAP4</b>	Microfibrillar associated protein 4
1.58E-12	-1.55	<b>UNC13D</b>	Unc-13 homolog D
3.79E-12	-1.55	<b>CDC42EP2</b>	CDC42 effector protein 2
2.48E-06	-1.55	<b>CA2</b>	Carbonic anhydrase 2
3.81E-02	-1.54	<b>SPC25</b>	SPC25, NDC80 kinetochore complex component
2.85E-17	-1.54	<b>CCND2</b>	Cyclin D2
4.96E-12	-1.54	<b>EDN2</b>	Endothelin 2
1.57E-05	-1.54	<b>SERTAD4</b>	SERTA domain containing 4
1.97E-02	-1.54	<b>AQP3</b>	Aquaporin 3 (Gill blood group)
1.15E-17	-1.54	<b>ST3GAL4</b>	ST3 beta-galactoside alpha-2, 3-sialyltransferase 4
8.78E-03	-1.53	<b>SMPD3</b>	Sphingomyelin phosphodiesterase 3
1.23E-08	-1.53	<b>DIAPH3</b>	Diaphanous related formin 3
7.64E-03	-1.53	<b>USP43</b>	Ubiquitin specific peptidase 43
2.42E-06	-1.53	<b>THBS2</b>	Thrombospondin 2
1.45E-13	-1.52	<b>COL3A1 / MIR3606</b>	Collagen type III alpha 1 chain / MicroRNA 3606
3.23E-04	-1.52	<b>TMEM235</b>	Transmembrane protein 235
5.51E-18	-1.52	<b>ABCG1</b>	ATP binding cassette subfamily G member 1
4.18E-11	-1.52	<b>PLXNB3 / SRPK3</b>	Plexin B3 / SRSF protein kinase 3
3.25E-03	-1.52	<b>ZNF467</b>	Zinc finger protein 467
1.13E-03	-1.52	<b>CDC20</b>	Cell division cycle 20
9.70E-30	-1.52	<b>MFGE8</b>	Milk fat globule-EGF factor 8 protein
1.01E-03	-1.51	<b>C14orf80</b>	<i>Chromosome 14 open reading frame 80</i>
8.23E-15	-1.51	<b>CA11</b>	Carbonic anhydrase 11
6.61E-05	-1.51	<b>GTSE1</b>	G2 and S-phase expressed 1
9.06E-06	-1.51	<b>GRIK3</b>	Glutamate ionotropic receptor kainate type subunit 3
3.14E-06	-1.51	<b>NTN1</b>	Netrin 1
1.46E-24	-1.51	<b>PYGM</b>	Phosphorylase, glycogen, muscle
2.35E-03	-1.51	<b>PCSK2</b>	Proprotein convertase subtilisin/kexin type 2
4.14E-05	-1.50	<b>KIFC1</b>	Kinesin family member C1
4.13E-04	-1.50	<b>SLC25A35</b>	Solute carrier family 25 member 35
2.54E-02	-1.50	<b>LINC01186</b>	<i>Long intergenic non-protein coding RNA 1186</i>
7.91E-24	-1.50	<b>CA9</b>	Carbonic anhydrase 9

Genes are classified according to the fold change with a  $P$ -value and fold-change cut-off of  $P < 0.05$  and  $FC < -1.5$ , respectively. FC, fold-change.

**Supplementary Table S1.** Glucocorticoids hormones levels in iRPE cell culture media, basement membrane matrices. Green rectangles indicate cell culture conditions at which corticosteroids were added to iRPE cells. Red rectangle indicates presence of corticosteroids.

Cell culture medium		F (nM)	B (nM)
A	<b>RDMw/oA (<i>n</i> = 5)</b>	0,00	12,88
B	<b>ECFM (<i>n</i> = 5)</b>	0,00	0,00

Cell culture media constituent		F (nM)	B (nM)
A	<b>DMEM GlutaMAX (<i>n</i> = 1)</b>	0,00	0,00
A	<b>Ham's F-12 (<i>n</i> = 1)</b>	0,00	0,00
B	<b>DMEM no phenol red (<i>n</i> = 5)</b>	0,00	0,00
B	<b>Charcoal FBS (<i>n</i> = 1)</b>	0,00	0,00

Basement membrane matrix		F (nM)	B (nM)
N/A	<b>Matrigel (<i>n</i> = 1)</b>	0,00	0,00

F, cortisol; B, corticosterone; S, 11-deoxycortisol; DOC, Deoxycorticosterone; nM, nanomolar; RDMw/oA, differentiation medium without vitamin A; ECFM, experimental corticosteroid-free medium; GlutaMAX™, GlutaMAX™ Supplement, HEPES medium; Ham's F-12, Ham's F-12 Nutrient Supplement; DMEM, high glucose, HEPES, no phenol red; Charcoal FBS, Fetal Bovine Serum, charcoal-treated; B, ECFM-related.

, cell culture media constituents and  
e time exogenous experimental  
sterone in the RDMw/oA medium.

S (nM)	DOC (nM)
0,00	0,00
0,00	0,00

S (nM)	DOC (nM)
0,00	0,00
0,00	0,00
0,00	0,00
0,00	0,00

S (nM)	DOC (nM)
0,00	0,00

omolar; RDMw/oA, retinal  
um;DMEM GlutaMAX, DMEM, high  
Mix medium; DMEM no phenol red,  
ircoal stripped; A, RDMw/oA-related;