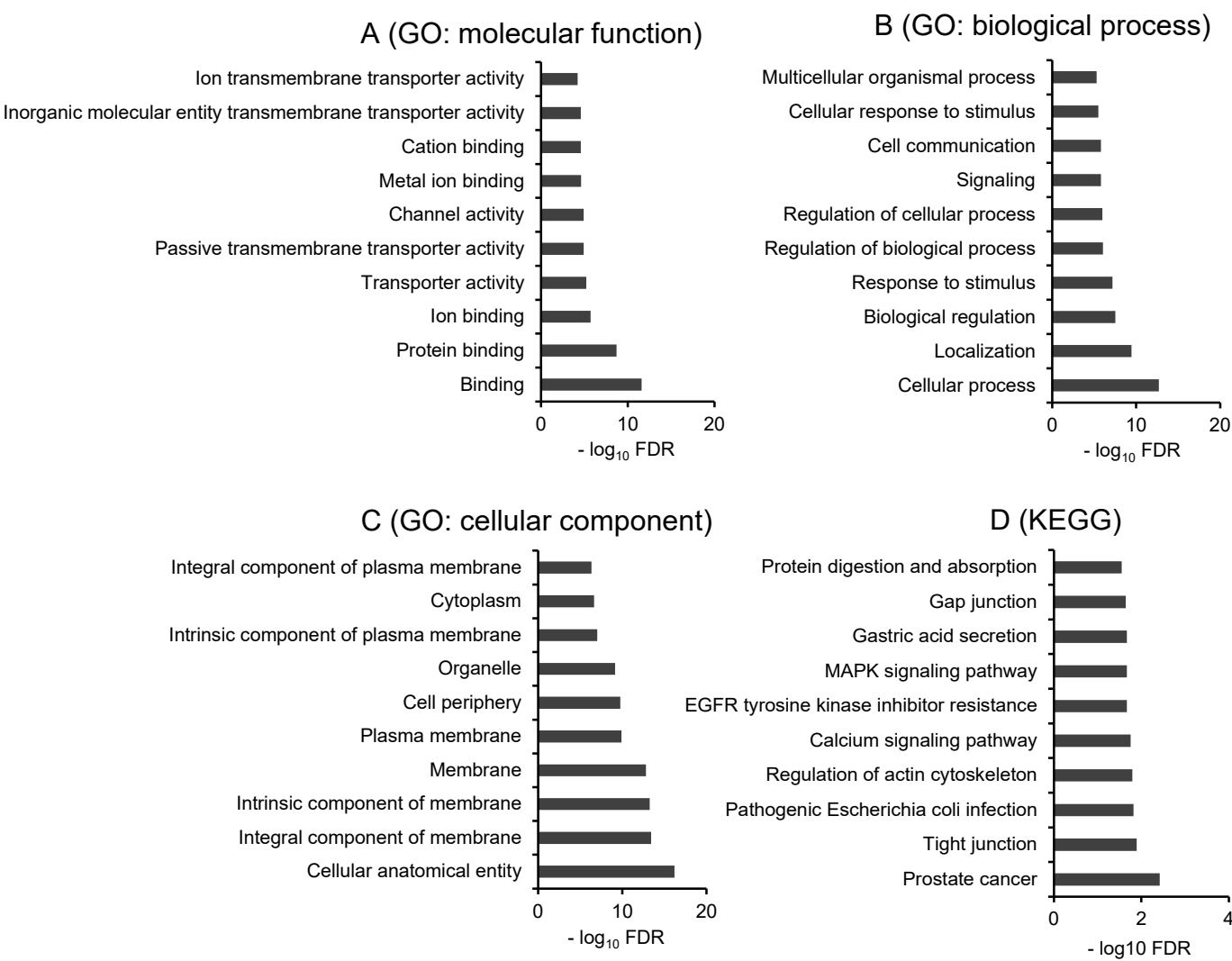




Supplementary figure 1. Functional enrichment of down-regulated genes by oxytocin in human retinal pigment epithelial cells

Supplementary table 1. Up-regulated genes by oxytocin in human retinal pigment epithelial cells

Ensembl ID	Gene Symbol	log ₂ FC	FDR
ENSG00000235884	LINC00941	9.9874e-01	0.0085577
ENSG00000131016	AKAP12	9.9072e-01	4.7574E-10
ENSG00000261604	AC114947.2	9.8529e-01	0.00046132
ENSG00000144583	MARCH4	9.8285e-01	0.00021487
ENSG00000115221	ITGB6	9.7972e-01	0.00028073
ENSG00000175832	ETV4	9.7904e-01	0.0060646
ENSG00000170006	TMEM154	9.7645e-01	0.0088871
ENSG00000011347	SYT7	9.4652e-01	0.00016535
ENSG00000164761	TNFRSF11B	9.3943e-01	0.026331
ENSG00000163661	PTX3	9.3293e-01	1.3167E-07
ENSG00000132639	SNAP25	9.3207e-01	0.020979
ENSG00000154678	PDE1C	9.3115e-01	1.4579E-06
ENSG00000083454	P2RX5	9.2218e-01	0.034284
ENSG00000013619	MAMLD1	9.2131e-01	0.0016644
ENSG00000172995	ARPP21	9.0396e-01	0.0029819
ENSG00000186480	INSIG1	9.0344e-01	2.0107E-08
ENSG00000163814	CDCP1	8.9604e-01	0.00027441
ENSG00000120437	ACAT2	8.9117e-01	0.000015716
ENSG00000112972	HMGCS1	8.7442e-01	1.1636E-07
ENSG00000273003	ARL2-SNX15	8.6471e+00	0.0002681
ENSG00000235770	LINC00607	8.6234e-01	0.047836
ENSG00000170356	OR2A20P	8.6146e-01	0.041885
ENSG00000118523	CTGF	8.6138e-01	1.2935E-07
ENSG00000156453	PCDH1	8.5384e-01	0.00016025
ENSG00000146592	CREB5	8.5140e-01	0.00079619
ENSG00000079841	RIMS1	8.4668e-01	2.4127E-06
ENSG00000145777	TSLP	8.4435e-01	1.7158E-07
ENSG00000130164	LDLR	8.4252e-01	9.9415E-06
ENSG00000132196	HSD17B7	8.3677e-01	1.8703E-06
ENSG00000117525	F3	8.2777e-01	1.1636E-07
ENSG00000138131	LOXL4	8.1973e-01	0.0022693
ENSG00000052802	MSMO1	8.1591e-01	7.2748E-06
ENSG00000173166	RAPH1	8.0129e-01	1.3905E-06
ENSG00000185022	MAFF	7.9092e-01	0.00028073
ENSG00000138675	FGF5	7.9060e-01	1.1636E-07
ENSG00000134516	DOCK2	7.9023e-01	1.2257E-07
ENSG00000176697	BDNF	7.8490e-01	0.000014501
ENSG00000154127	UBASH3B	7.8304e-01	0.000009147
ENSG00000143882	ATP6V1C2	7.8115e-01	0.010691
ENSG00000276851	AC002401.4	7.5965e-01	0.042486

Supplementary table 1. continue

ENSG00000103489	XYLT1	7.5564e-01	0.0017505
ENSG00000113578	FGF1	7.5557e-01	1.1337E-06
ENSG00000127824	TUBA4A	7.5243e-01	0.000013058
ENSG00000166923	GREM1	7.5027e-01	5.0485E-06
ENSG00000115339	GALNT3	7.4989e-01	2.6357E-06
ENSG00000099194	SCD	7.4771e-01	0.000025046
ENSG00000273301	AC016717.2	7.4745e-01	0.00013312
ENSG00000185697	MYBL1	7.4244e-01	0.0038158
ENSG00000139278	GLIPR1	7.2974e-01	0.00037718
ENSG00000179546	HTR1D	7.2626e-01	0.0090134
ENSG00000166401	SERPINB8	7.1819e-01	0.0023816
ENSG00000180914	OXTR	7.1597e-01	0.00025137
ENSG00000052795	FNIP2	7.0345e-01	1.6316E-10
ENSG00000073008	PVR	7.0254e-01	0.000017323
ENSG00000011422	PLAUR	6.9753e-01	0.0017917
ENSG00000138623	SEMA7A	6.9516e-01	0.0038263
ENSG00000259207	ITGB3	6.9405e-01	0.026188
ENSG00000079459	FDFT1	6.9278e-01	2.0899E-06
ENSG00000164211	STARD4	6.9272e-01	0.00007148
ENSG00000067064	IDI1	6.9098e-01	0.000043641
ENSG00000178726	THBD	6.8303e-01	0.010133
ENSG00000148154	UGCG	6.8132e-01	0.00011878
ENSG00000197646	PDCD1LG2	6.7681e-01	0.010879
ENSG00000001630	CYP51A1	6.7115e-01	0.00019915
ENSG00000113361	CDH6	6.6963e-01	0.00028231
ENSG00000162772	ATF3	6.6728e-01	0.0037086
ENSG00000147155	EBP	6.6700e-01	5.0574E-06
ENSG00000104549	SQLE	6.6535e-01	6.2281E-06
ENSG00000150556	LYPD6B	6.6212e-01	0.0019245
ENSG00000106366	SERPINE1	6.6131e-01	0.03359
ENSG00000166073	GPR176	6.5765e-01	0.002558
ENSG00000157680	DGKI	6.5485e-01	0.00054169
ENSG00000133107	TRPC4	6.5194e-01	0.000047689
ENSG00000258757	AL133453.1	6.4960e-01	0.0054557
ENSG00000113389	NPR3	6.4681e-01	0.0001597
ENSG00000164741	DLC1	6.4614e-01	6.5209E-06
ENSG00000112414	ADGRG6	6.4320e-01	3.198E-08
ENSG00000113161	HMGCR	6.4188e-01	7.2444E-06
ENSG00000139211	AMIGO2	6.4073e-01	9.1401E-06
ENSG00000128606	LRRC17	6.3778e-01	0.000094192
ENSG00000187720	THSD4	6.3753e-01	0.0083723
ENSG00000182667	NTM	6.3404e-01	0.00017566

Supplementary table 1. continue

ENSG00000149218	ENDOD1	6.3329e-01	0.0014156
ENSG00000148082	SHC3	6.3277e-01	0.0010887
ENSG00000187123	LYPD6	6.3268e-01	0.0019363
ENSG00000135318	NT5E	6.2617e-01	0.022907
ENSG00000135074	ADAM19	6.2534e-01	0.00034974
ENSG00000128342	LIF	6.2320e-01	0.0094931
ENSG00000272414	FAM47E-STBD1	6.1607e-01	0.00039305
ENSG00000153976	HS3ST3A1	6.1241e-01	0.026188
ENSG00000067082	KLF6	6.1221e-01	0.0046697
ENSG00000166598	HSP90B1	6.1065e-01	0.0029358
ENSG00000096696	DSP	6.0948e-01	0.0010573
ENSG00000198108	CHSY3	6.0934e-01	0.026895
ENSG00000079931	MOXD1	6.0744e-01	5.0485E-06
ENSG00000184164	CRELD2	6.0545e-01	0.000094192
ENSG00000204516	MICB	6.0530e-01	0.026758
ENSG00000157193	LRP8	6.0137e-01	0.0077528
ENSG00000152495	CAMK4	6.0102e-01	0.0035023
ENSG00000152422	XRCC4	5.9997e-01	0.0070222
ENSG00000161791	FMNL3	5.9804e-01	0.0019363
ENSG00000044574	HSPA5	5.9592e-01	0.0045139
ENSG00000160752	FDPS	5.9524e-01	0.0021102
ENSG00000131473	ACLY	5.9318e-01	0.00014877
ENSG00000142871	CYR61	5.9192e-01	0.000088465
ENSG00000178922	HYI	5.8829e-01	0.022895
ENSG00000094804	CDC6	5.8647e-01	0.032069
ENSG00000136158	SPRY2	5.8634e-01	0.00065644
ENSG00000026508	CD44	5.8500e-01	0.0094931
ENSG00000168334	XIRP1	2.5915e+00	0.00015109
ENSG00000170498	KISS1	2.2393e+00	0.0011553
ENSG00000196611	MMP1	2.1173e+00	0.042855
ENSG00000168685	IL7R	1.6825e+00	8.2077E-11
ENSG00000157335	CLEC18C	1.6260e+00	0.018993
ENSG00000136928	GABBR2	1.5753e+00	0.000043641
ENSG00000164283	ESM1	1.5731e+00	0.00011844
ENSG00000148677	ANKRD1	1.4344e+00	1.1769E-09
ENSG00000183644	C11orf88	1.3815e+00	0.041232
ENSG00000203721	LINC00862	1.3754e+00	7.6586E-16
ENSG00000277247	AC083809.1	1.3567e+00	0.0016644
ENSG00000153233	PTPRR	1.3126e+00	0.00054169
ENSG00000198959	TGM2	1.2762e+00	1.2257E-07
ENSG00000144063	MALL	1.2370e+00	0.00000202
ENSG00000277954	AC092376.2	1.1967e+00	0.00016025

Supplementary table 1. continue

ENSG00000182261	NLRP10	1.1866e+00	0.01898
ENSG00000273221	AL355816.2	1.1816e+00	0.009184
ENSG00000171631	P2RY6	1.1743e+00	0.0013076
ENSG00000081181	ARG2	1.1610e+00	2.4127E-06
ENSG00000113070	HBEGF	1.1470e+00	8.1801E-11
ENSG00000100311	PDGFB	1.1378e+00	0.00019915
ENSG00000164171	ITGA2	1.1341e+00	2.3901E-10
ENSG00000282849	AL359834.1	1.1251e+00	0.015453
ENSG00000166292	TMEM100	1.1166e+00	0.017594
ENSG00000233117	LINC00702	1.1045e+00	6.3417E-07
ENSG00000110427	KIAA1549L	1.1036e+00	2.0693E-06
ENSG00000127329	PTPRB	1.0745e+00	2.535E-12
ENSG00000130477	UNC13A	1.0648e+00	0.00090217
ENSG00000170323	FABP4	1.0256e+00	0.049653
ENSG00000147573	TRIM55	1.0173e+00	5.8148E-06
ENSG00000125148	MT2A	1.0050e+00	0.00045592

log₂FC, log₂(fold change); FDR, false discovery rate that is a corrected p-value by the Benjamini-Hochberg procedure.

Supplementary table 2. Down-regulated genes by oxytocin in human retinal pigment epithelial cells

Ensembl ID	Gene Symbol	log ₂ FC	FDR
ENSG00000170959	DCDC1	-0.58536	0.0094931
ENSG00000104081	BMF	-0.58937	0.032069
ENSG00000081803	CADPS2	-0.60147	0.030761
ENSG00000108924	HLF	-0.60503	0.0012464
ENSG00000110900	TSPAN11	-0.60611	0.0023816
ENSG00000188467	SLC24A5	-0.61796	0.0080078
ENSG00000136732	GYPC	-0.64646	0.043296
ENSG00000162989	KCNJ3	-0.64791	0.04329
ENSG00000187672	ERC2	-0.65153	0.011338
ENSG00000141401	IMPA2	-0.65429	0.033489
ENSG00000183785	TUBA8	-0.66125	0.00089273
ENSG00000269881	AC004754.1	-0.66568	0.040273
ENSG00000008277	ADAM22	-0.66839	0.012999
ENSG00000134765	DSC1	-0.67116	0.00033049
ENSG00000073282	TP63	-0.67705	0.0083723
ENSG00000180447	GAS1	-0.69446	0.00016025
ENSG00000066468	FGFR2	-0.70139	0.000014501
ENSG00000125872	LRRN4	-0.71109	0.040273
ENSG00000170962	PDGFD	-0.71569	6.7054E-06
ENSG00000114698	PLSCR4	-0.72874	0.0012101
ENSG00000100033	PRODH	-0.73521	0.026188
ENSG00000118322	ATP10B	-0.73955	0.0035734
ENSG00000130600	H19	-0.74064	1.8703E-06
ENSG00000166265	CYYR1	-0.74232	0.027541
ENSG00000169083	AR	-0.7485	0.039203
ENSG00000168453	HR	-0.77106	0.00044861
ENSG00000138080	EMILIN1	-0.80757	0.0026043
ENSG00000184408	KCND2	-0.81626	0.0023847
ENSG00000184809	B3GALT5-AS1	-0.82381	0.027178
ENSG00000180730	SHISA2	-0.83115	0.035136
ENSG00000205336	ADGRG1	-0.83663	0.049653
ENSG00000106333	PCOLCE	-0.84051	0.03096
ENSG00000171219	CDC42BPG	-0.84597	0.020581
ENSG00000279592	AC010653.2	-0.87347	0.040371
ENSG00000105409	ATP1A3	-0.877	0.0005431
ENSG00000156097	GPR61	-0.88474	0.036032
ENSG00000162267	ITIH3	-0.88815	0.0094715
ENSG00000174807	CD248	-0.92117	0.0030099
ENSG00000013297	CLDN11	-0.92291	0.0044293
ENSG00000145721	LIX1	-0.9469	1.1636E-07

Supplementary table 2. continue

ENSG00000182612	TSPAN10	-0.95958	0.000060343
ENSG00000253417	LINC02159	-0.96665	0.00011793
ENSG00000251491	OR7E28P	-1.0046	0.02013
ENSG00000166473	PKD1L2	-1.0268	0.0045139
ENSG00000198732	SMOC1	-1.0392	0.00023707
ENSG00000163331	DAPL1	-1.0674	2.7152E-09
ENSG00000147606	SLC26A7	-1.1516	1.8703E-06
ENSG00000124749	COL21A1	-1.1622	0.0054557
ENSG00000168874	ATOH8	-1.164	0.026188
ENSG00000198216	CACNA1E	-1.1999	0.032069
ENSG00000133392	MYH11	-1.2755	0.014687
ENSG00000126778	SIX1	-1.3333	0.0099313
ENSG00000010932	FMO1	-1.6798	0.00171
ENSG00000166825	ANPEP	-2.36	0.00072974
ENSG00000141469	SLC14A1	-2.362	0.00034974
ENSG00000206585	RNVU1-7	-4.1166	0.0088871

log₂FC, log₂(fold change); FDR, false discovery rate that is a corrected p-value by the Benjamini-Hochberg procedure. The minus sign with the fold change data denotes downregulation.

Supplementary table 3. Enriched KEGG terms from up-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})
Metabolic pathways	KEGG:01100	5.493×10 ⁻¹¹	10.260208757933059
Steroid biosynthesis	KEGG:00100	2.965×10 ⁻¹⁰	9.52802338202263
Terpenoid backbone biosynthesis	KEGG:00900	6.749×10 ⁻⁸	7.1707924079289524
PI3K-Akt signaling pathway	KEGG:04151	4.012×10 ⁻⁷	6.396613015701344
Calcium signaling pathway	KEGG:04020	4.500×10 ⁻⁵	4.346772353328488
cAMP signaling pathway	KEGG:04024	2.673×10 ⁻⁴	3.5730327987922217
Regulation of actin cytoskeleton	KEGG:04810	2.673×10 ⁻⁴	3.5730327987922217
Estrogen signaling pathway	KEGG:04915	3.438×10 ⁻⁴	3.4636350946754777
PPAR signaling pathway	KEGG:03320	4.908×10 ⁻⁴	3.309058986245986
Arrhythmogenic right ventricular cardiomyopathy	KEGG:05412	4.908×10 ⁻⁴	3.309058986245986
Synaptic vesicle cycle	KEGG:04721	4.908×10 ⁻⁴	3.309058986245986
Complement and coagulation cascades	KEGG:04610	6.351×10 ⁻⁴	3.197126706631979
ECM-receptor interaction	KEGG:04512	6.756×10 ⁻⁴	3.1703110339129124
Hematopoietic cell lineage	KEGG:04640	8.855×10 ⁻⁴	3.0527958208281993
Focal adhesion	KEGG:04510	1.169×10 ⁻³	2.932283209403435
Proteoglycans in cancer	KEGG:05205	1.235×10 ⁻³	2.9084565471529005
Neuroactive ligand-receptor interaction	KEGG:04080	1.407×10 ⁻³	2.8515698299418273
Ras signaling pathway	KEGG:04014	1.924×10 ⁻³	2.715845331753448
Pathways in cancer	KEGG:05200	1.997×10 ⁻³	2.6995775865716922
Synthesis and degradation of ketone bodies	KEGG:00072	1.997×10 ⁻³	2.6995775865716922
Fluid shear stress and atherosclerosis	KEGG:05418	2.372×10 ⁻³	2.6247995971678524
Phagosome	KEGG:04145	3.041×10 ⁻³	2.5170105348989837
GnRH secretion	KEGG:04929	3.266×10 ⁻³	2.4859330642671384
JAK-STAT signaling pathway	KEGG:04630	3.931×10 ⁻³	2.4054834929764155
Melanoma	KEGG:05218	4.100×10 ⁻³	2.38716491246505
MAPK signaling pathway	KEGG:04010	4.100×10 ⁻³	2.38716491246505
Thyroid hormone synthesis	KEGG:04918	4.301×10 ⁻³	2.3664669300702172
Glioma	KEGG:05214	4.301×10 ⁻³	2.3664669300702172
Alcoholism	KEGG:05034	5.465×10 ⁻³	2.2624426785498937
Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	KEGG:00532	5.465×10 ⁻³	2.2624426785498937
Taste transduction	KEGG:04742	5.606×10 ⁻³	2.2513692862277073
Human papillomavirus infection	KEGG:05165	5.643×10 ⁻³	2.2485244171773244
Hypertrophic cardiomyopathy	KEGG:05410	6.223×10 ⁻³	2.206011883646719
Dilated cardiomyopathy	KEGG:05414	6.866×10 ⁻³	2.1632668677376152
Glycosaminoglycan biosynthesis - heparan sulfate / heparin	KEGG:00534	6.866×10 ⁻³	2.1632668677376152
Rap1 signaling pathway	KEGG:04015	6.906×10 ⁻³	2.1607755067291463
Prostate cancer	KEGG:05215	6.906×10 ⁻³	2.1607755067291463
Aldosterone synthesis and secretion	KEGG:04925	6.930×10 ⁻³	2.159283785119226
AGE-RAGE signaling pathway in diabetic complications	KEGG:04933	7.159×10 ⁻³	2.145146187185454
Butanoate metabolism	KEGG:00650	8.121×10 ⁻³	2.090383777319861
Glyoxylate and dicarboxylate metabolism	KEGG:00630	9.096×10 ⁻³	2.041164854412673

Supplementary table 3. continue

AMPK signaling pathway	KEGG:04152	1.067×10^{-2}	1.9716326771139658
Neurotrophin signaling pathway	KEGG:04722	1.067×10^{-2}	1.9716326771139658
Osteoclast differentiation	KEGG:04380	1.199×10^{-2}	1.9211375490562366
Relaxin signaling pathway	KEGG:04926	1.254×10^{-2}	1.9017178921910014
Apelin signaling pathway	KEGG:04371	1.455×10^{-2}	1.8372810995351536
Bladder cancer	KEGG:05219	1.476×10^{-2}	1.8310457768869457
Gastric cancer	KEGG:05226	1.664×10^{-2}	1.7789473430994798
Breast cancer	KEGG:05224	1.664×10^{-2}	1.7789473430994798
Cytokine-cytokine receptor interaction	KEGG:04060	1.664×10^{-2}	1.7789473430994798
Phospholipase D signaling pathway	KEGG:04072	1.664×10^{-2}	1.7789473430994798
MicroRNAs in cancer	KEGG:05206	1.811×10^{-2}	1.7419994522905842
Huntington disease	KEGG:05016	1.811×10^{-2}	1.7419994522905842
Valine, leucine and isoleucine degradation	KEGG:00280	1.811×10^{-2}	1.7419994522905842
Hippo signaling pathway	KEGG:04390	1.811×10^{-2}	1.7419994522905842
Cocaine addiction	KEGG:05030	1.811×10^{-2}	1.7419994522905842
Ovarian steroidogenesis	KEGG:04913	1.870×10^{-2}	1.7280815004429235
Fatty acid metabolism	KEGG:01212	2.281×10^{-2}	1.6419042662967722
Cortisol synthesis and secretion	KEGG:04927	2.803×10^{-2}	1.552315442450255
Amphetamine addiction	KEGG:05031	3.185×10^{-2}	1.496916932204297
Epithelial cell signaling in Helicobacter pylori infection	KEGG:05120	3.221×10^{-2}	1.4920413759104951
EGFR tyrosine kinase inhibitor resistance	KEGG:01521	3.990×10^{-2}	1.399075703999735
ErbB signaling pathway	KEGG:04012	4.410×10^{-2}	1.3555307958725178
Insulin secretion	KEGG:04911	4.539×10^{-2}	1.343003874863852
Longevity regulating pathway	KEGG:04211	4.561×10^{-2}	1.3409329420229636
Gap junction	KEGG:04540	4.561×10^{-2}	1.3409329420229636
Morphine addiction	KEGG:05032	4.561×10^{-2}	1.3409329420229636
Rheumatoid arthritis	KEGG:05323	4.561×10^{-2}	1.3409329420229636
Bile secretion	KEGG:04976	4.591×10^{-2}	1.3380713568369411
TGF-beta signaling pathway	KEGG:04350	4.813×10^{-2}	1.3175405871726733
IL-17 signaling pathway	KEGG:04657	4.843×10^{-2}	1.3149235266239303
Endocrine resistance	KEGG:01522	4.968×10^{-2}	1.3038271261311332

KEGG, Kyoto Encyclopedia of Genes and Genomes database; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 4. Enriched GO molecular function terms from up-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})
Binding	GO:0005488	3.626×10^{-41}	40.440518247687415
Protein binding	GO:0005515	3.289×10^{-33}	32.48291927768249
Ion binding	GO:0043167	1.445×10^{-13}	12.840083774670706
Cation binding	GO:0043169	4.711×10^{-11}	10.326890329108851
Signaling receptor binding	GO:0005102	8.569×10^{-11}	10.067069982211294
Metal ion binding	GO:0046872	8.860×10^{-11}	10.052586057685692
Signaling receptor activity	GO:0038023	2.449×10^{-10}	9.610979860507184
Molecular transducer activity	GO:0060089	2.449×10^{-10}	9.610979860507184
Catalytic activity	GO:0003824	7.523×10^{-10}	9.123601479679202
Cell adhesion molecule binding	GO:0050839	2.074×10^{-9}	8.683195852407941
Receptor regulator activity	GO:0030545	2.069×10^{-8}	7.684206759449206
Protein-containing complex binding	GO:0044877	4.420×10^{-8}	7.354624021820886
Growth factor receptor binding	GO:0070851	6.198×10^{-8}	7.207747275039933
Integrin binding	GO:0005178	7.594×10^{-8}	7.119531622247917
Transmembrane signaling receptor activity	GO:0004888	1.974×10^{-7}	6.704700081904414
Molecular function regulator	GO:0098772	6.315×10^{-7}	6.199600105304236
Receptor ligand activity	GO:0048018	6.632×10^{-7}	6.178362933480093
Signaling receptor activator activity	GO:0030546	7.101×10^{-7}	6.148672299588162
Growth factor activity	GO:0008083	2.852×10^{-6}	5.544902072205491
Intramolecular oxidoreductase activity	GO:0016860	3.669×10^{-6}	5.435419744142716
Insulin-like growth factor binding	GO:0005520	1.350×10^{-5}	4.869555505777967
Exogenous protein binding	GO:0140272	2.060×10^{-5}	4.68607660216971
Virus receptor activity	GO:0001618	2.060×10^{-5}	4.68607660216971
Calcium ion binding	GO:0005509	2.060×10^{-5}	4.68607660216971
Enzyme binding	GO:0019899	3.000×10^{-5}	4.522827401559904
Isomerase activity	GO:0016853	5.261×10^{-5}	4.278900087351218
Carbohydrate derivative binding	GO:0097367	1.024×10^{-4}	3.9896415865497645
Organic cyclic compound binding	GO:0097159	1.201×10^{-4}	3.920525482965963
Calmodulin binding	GO:0005516	1.348×10^{-4}	3.8703834532888903

Supplementary table 4. continue

Extracellular matrix binding	GO:0050840	1.348×10^{-4}	3.8703834532888903
Transition metal ion binding	GO:0046914	1.715×10^{-4}	3.7656889837818985
Growth factor binding	GO:0019838	2.602×10^{-4}	3.5847113908672483
Small molecule binding	GO:0036094	2.876×10^{-4}	3.541241900880014
Collagen binding	GO:0005518	2.876×10^{-4}	3.541241900880014
Identical protein binding	GO:0042802	3.608×10^{-4}	3.4427681780723143
Very-low-density lipoprotein particle receptor activity	GO:0030229	4.110×10^{-4}	3.3861530136859206
Heterocyclic compound binding	GO:1901363	4.838×10^{-4}	3.315298818111507
Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0016705	5.682×10^{-4}	3.2455325091436
Anion binding	GO:0043168	5.702×10^{-4}	3.24400608539834
Transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0046912	6.172×10^{-4}	3.2095458355430253
Catalytic activity, acting on a protein	GO:0140096	1.250×10^{-3}	2.9030161104831858
Monooxygenase activity	GO:0004497	1.259×10^{-3}	2.8999731520120386
Nucleotide binding	GO:0000166	1.722×10^{-3}	2.763914284782142
Nucleoside phosphate binding	GO:1901265	1.722×10^{-3}	2.763914284782142
Vascular endothelial growth factor receptor 2 binding	GO:0043184	1.969×10^{-3}	2.705853890866936
Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	GO:0016709	1.974×10^{-3}	2.7047132697360006
Glycosaminoglycan binding	GO:0005539	2.378×10^{-3}	2.6237687082737255
Protease binding	GO:0002020	3.123×10^{-3}	2.505469850559008

Supplementary table 4. continue

Low-density lipoprotein particle receptor activity	GO:0005041	3.679×10^{-3}	2.4342145271774376
Transferase activity	GO:0016740	3.679×10^{-3}	2.4342145271774376
Sulfur compound binding	GO:1901681	3.679×10^{-3}	2.4342145271774376
UDP-glycosyltransferase activity	GO:0008194	3.679×10^{-3}	2.4342145271774376
Neurotransmitter receptor regulator activity	GO:0099602	3.925×10^{-3}	2.4061652807426404
Vascular endothelial growth factor receptor binding	GO:0005172	3.925×10^{-3}	2.4061652807426404
Manganese ion binding	GO:0030145	3.925×10^{-3}	2.4061652807426404
Oxidoreductase activity	GO:0016491	3.925×10^{-3}	2.4061652807426404
Acetylcholine receptor regulator activity	GO:0030548	3.925×10^{-3}	2.4061652807426404
Cytokine receptor binding	GO:0005126	3.945×10^{-3}	2.4039770996612853
Platelet-derived growth factor receptor binding	GO:0005161	4.362×10^{-3}	2.3603118555296807
Enzyme regulator activity	GO:0030234	4.729×10^{-3}	2.325187205921824
Lipoprotein particle receptor activity	GO:0030228	4.741×10^{-3}	2.3241673528864473
Intramolecular oxidoreductase activity, transposing C=C bonds	GO:0016863	4.741×10^{-3}	2.3241673528864473
Heparin binding	GO:0008201	4.882×10^{-3}	2.31140208016566
Transmembrane receptor protein tyrosine phosphatase activity	GO:0005001	5.121×10^{-3}	2.2906711040499843
Transmembrane receptor protein phosphatase activity	GO:0019198	5.121×10^{-3}	2.2906711040499843
Cargo receptor activity	GO:0038024	5.576×10^{-3}	2.25366164251801
Prenyltransferase activity	GO:0004659	5.583×10^{-3}	2.253141468253114
Syntaxin binding	GO:0019905	5.622×10^{-3}	2.2501338663515127
Protein disulfide isomerase activity	GO:0003756	5.967×10^{-3}	2.224244016220836
Intramolecular oxidoreductase activity, transposing S-S bonds	GO:0016864	5.967×10^{-3}	2.224244016220836
Hydrolase activity	GO:0016787	6.620×10^{-3}	2.1791431595203967

Supplementary table 4. continue

Purinergic nucleotide receptor activity	GO:0001614	7.010×10^{-3}	2.1543094318997986
Nucleotide receptor activity	GO:0016502	7.010×10^{-3}	2.1543094318997986
Cytokine receptor activity	GO:0004896	1.029×10^{-2}	1.9874510068388644
Fibroblast growth factor receptor binding	GO:0005104	1.035×10^{-2}	1.985190376229314
Polysaccharide binding	GO:0030247	1.035×10^{-2}	1.985190376229314
Purine ribonucleotide binding	GO:0032555	1.069×10^{-2}	1.9710975656270313
Urokinase plasminogen activator receptor activity	GO:0030377	1.071×10^{-2}	1.970037984407178
Kisspeptin receptor binding	GO:0031773	1.071×10^{-2}	1.970037984407178
Ribonucleotide binding	GO:0032553	1.071×10^{-2}	1.970037984407178
C-8 sterol isomerase activity	GO:0000247	1.071×10^{-2}	1.970037984407178
Syntaxin-1 binding	GO:0017075	1.071×10^{-2}	1.970037984407178
Phosphoric ester hydrolase activity	GO:0042578	1.071×10^{-2}	1.970037984407178
Hydroxymethylglutaryl-CoA reductase activity	GO:0042282	1.071×10^{-2}	1.970037984407178
Purine nucleotide binding	GO:0017076	1.071×10^{-2}	1.970037984407178
Palmitoyl-CoA 9-desaturase activity	GO:0032896	1.071×10^{-2}	1.970037984407178
Laminin binding	GO:0043236	1.071×10^{-2}	1.970037984407178
fibronectin binding	GO:0001968	1.071×10^{-2}	1.970037984407178
Hydroxypyruvate isomerase activity	GO:0008903	1.071×10^{-2}	1.970037984407178
Cytokine activity	GO:0005125	1.071×10^{-2}	1.970037984407178
Dihydroceramide glucosyltransferase activity	GO:0102769	1.071×10^{-2}	1.970037984407178
Farnesyl-diphosphate farnesyltransferase activity	GO:0004310	1.071×10^{-2}	1.970037984407178
Metalloendopeptidase activity	GO:0004222	1.071×10^{-2}	1.970037984407178
Enzyme Inhibitor activity	GO:0004857	1.071×10^{-2}	1.970037984407178
Squalene synthase activity	GO:0051996	1.071×10^{-2}	1.970037984407178
Ceramide glucosyltransferase activity	GO:0008120	1.071×10^{-2}	1.970037984407178

Supplementary table 4. continue

Squalene monooxygenase activity	GO:0004506	1.071×10^{-2}	1.970037984407178
Protein tyrosine phosphatase activity	GO:0004725	1.071×10^{-2}	1.970037984407178
Hydroxymethylglutaryl-CoA reductase (NADPH) activity	GO:0004420	1.071×10^{-2}	1.970037984407178

GO, gene ontology; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 5. Enriched GO biological process terms from up-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})
Cellular process	GO:0009987	5.636×10^{-40}	39.248994299366224
Biological regulation	GO:0065007	3.728×10^{-39}	38.42857151509331
Regulation of biological process	GO:0050789	1.707×10^{-35}	34.767653521538634
Response to stimulus	GO:0050896	3.598×10^{-31}	30.443973111463524
Multicellular organismal process	GO:0032501	5.435×10^{-31}	30.264794794662446
Regulation of cellular process	GO:0050794	3.278×10^{-29}	28.484395353658087
System development	GO:0048731	2.174×10^{-28}	27.662695436054065
Multicellular organism development	GO:0007275	1.012×10^{-27}	26.99499130719817
Metabolic process	GO:0008152	1.315×10^{-26}	25.88100783083141
Developmental process	GO:0032502	2.626×10^{-26}	25.580679879145805
Anatomical structure development	GO:0048856	9.588×10^{-26}	25.01828889857453
Signaling	GO:0023052	1.081×10^{-25}	24.96626082530698
Cellular response to stimulus	GO:0051716	1.081×10^{-25}	24.96626082530698
Organic substance metabolic process	GO:0071704	1.081×10^{-25}	24.96626082530698
Cell communication	GO:0007154	1.081×10^{-25}	24.96626082530698
Signal transduction	GO:0007165	3.250×10^{-24}	23.488178969634866
Positive regulation of biological process	GO:0048518	3.539×10^{-23}	22.45107705833425
Cholesterol biosynthetic process	GO:0006695	3.644×10^{-23}	22.438474911968157
Secondary alcohol biosynthetic process	GO:1902653	3.644×10^{-23}	22.438474911968157
Sterol biosynthetic process	GO:0016126	1.248×10^{-22}	21.903840594726393
Alcohol biosynthetic process	GO:0046165	1.800×10^{-21}	20.744825309864176
Positive regulation of cellular process	GO:0048522	2.452×10^{-21}	20.610401304046007
Cell surface receptor signaling pathway	GO:0007166	3.011×10^{-21}	20.52132205521476
Regulation of biological quality	GO:0065008	3.134×10^{-21}	20.503893177312552

Supplementary table 5. continue

Primary metabolic process	GO:0044238	8.999×10^{-21}	20.04579526166116
Regulation of metabolic process	GO:0019222	1.194×10^{-20}	19.923155494113104
Localization	GO:0051179	1.194×10^{-20}	19.923155494113104
Regulation of multicellular organismal process	GO:0051239	1.914×10^{-20}	19.71796061522868
Response to organic substance	GO:0010033	2.758×10^{-20}	19.55936762523311
Response to chemical	GO:0042221	3.053×10^{-20}	19.51521347751633
Cholesterol metabolic process	GO:0008203	4.723×10^{-20}	19.325791016186304
Positive regulation of response to stimulus	GO:0048584	9.248×10^{-20}	19.033931522909782
Organic hydroxy compound biosynthetic process	GO:1901617	1.174×10^{-19}	18.930422232475166
Secondary alcohol metabolic process	GO:1902652	1.219×10^{-19}	18.91383894314866
Cellular metabolic process	GO:0044237	1.886×10^{-19}	18.724427730336227
Sterol metabolic process	GO:0016125	2.293×10^{-19}	18.639533977867355
Regulation of response to stimulus	GO:0048583	4.973×10^{-19}	18.303424306790642
Regulation of cell communication	GO:0010646	7.247×10^{-19}	18.139815405786862
Regulation of signaling	GO:0023051	1.031×10^{-18}	17.9867353851213
Steroid biosynthetic process	GO:0006694	1.924×10^{-18}	17.71569718060544
Cellular response to organic substance	GO:0071310	2.784×10^{-18}	17.55528468034964
Cellular response to chemical stimulus	GO:0070887	7.229×10^{-18}	17.140926264877212
Positive regulation of metabolic process	GO:0009893	7.881×10^{-18}	17.10342608903777
Positive regulation of cell communication	GO:0010647	9.341×10^{-18}	17.02959860468892
Positive regulation of signaling	GO:0023056	9.917×10^{-18}	17.00360438629913
Animal organ development	GO:0048513	1.693×10^{-17}	16.77142208827361
Response to external stimulus	GO:0009605	1.839×10^{-17}	16.73532298368638
Response to stress	GO:0006950	4.316×10^{-17}	16.36490572042233

Supplementary table 5. continue

Alcohol metabolic process	GO:0006066	1.194×10^{-16}	15.923086366411141
Macromolecule metabolic process	GO:0043170	1.491×10^{-16}	15.826481917472732
Cellular developmental process	GO:0048869	4.023×10^{-16}	15.395465924793236
Steroid metabolic process	GO:0008202	4.215×10^{-16}	15.37520702771085
Positive regulation of signal transduction	GO:0009967	4.215×10^{-16}	15.37520702771085
Regulation of primary metabolic process	GO:0080090	5.354×10^{-16}	15.271294265068038
Anatomical structure morphogenesis	GO:0009653	1.262×10^{-15}	14.898829963537477
Regulation of signal transduction	GO:0009966	1.284×10^{-15}	14.891505550054227
Organonitrogen compound metabolic process	GO:1901564	2.672×10^{-15}	14.573094086895612
Locomotion	GO:0040011	2.798×10^{-15}	14.553151583938968
Cellular component organization	GO:0016043	3.036×10^{-15}	14.51769686476687
Lipid biosynthetic process	GO:0008610	3.409×10^{-15}	14.467358179079826
Phosphate-containing compound metabolic process	GO:0006796	3.633×10^{-15}	14.439758543848697
Phosphorus metabolic process	GO:0006793	4.717×10^{-15}	14.326303728362836
Cell differentiation	GO:0030154	5.999×10^{-15}	14.221903672632495
Organic hydroxy compound metabolic process	GO:1901615	5.999×10^{-15}	14.221903672632495
Regulation of lipid biosynthetic process	GO:0046890	7.411×10^{-15}	14.130106062957951
Cellular component organization or biogenesis	GO:0071840	9.434×10^{-15}	14.025287543010602
Nitrogen compound metabolic process	GO:0006807	1.041×10^{-14}	13.982678383814232
Biosynthetic process	GO:0009058	1.546×10^{-14}	13.810871427644898
Regulation of steroid metabolic process	GO:0019218	1.591×10^{-14}	13.79840313558002
Small molecule biosynthetic process	GO:0044283	1.664×10^{-14}	13.77875728137286

Supplementary table 5. continue

Regulation of cholesterol metabolic process	GO:0090181	2.017×10^{-14}	13.695367303186883
Regulation of steroid biosynthetic process	GO:0050810	2.632×10^{-14}	13.579695758112212
Organic substance biosynthetic process	GO:1901576	3.948×10^{-14}	13.403622154794121
Wound healing	GO:0042060	4.479×10^{-14}	13.34880515467915
Cell adhesion	GO:0007155	4.838×10^{-14}	13.3153780764793
Biological adhesion	GO:0022610	5.231×10^{-14}	13.281433850929368
Regulation of phosphate metabolic process	GO:0019220	5.231×10^{-14}	13.281433850929368
Regulation of phosphorus metabolic process	GO:0051174	5.231×10^{-14}	13.281433850929368
Secretion	GO:0046903	5.292×10^{-14}	13.276400743537067
Regulation of molecular function	GO:0065009	6.898×10^{-14}	13.161271308181187
Response to wounding	GO:0009611	9.559×10^{-14}	13.019569009479138
Positive regulation of cellular metabolic process	GO:0031325	1.107×10^{-13}	12.955689339517685
Positive regulation of macromolecule metabolic process	GO:0010604	1.200×10^{-13}	12.920766267512949
Regulation of sterol biosynthetic process	GO:0106118	1.312×10^{-13}	12.882070241507579
Regulation of cholesterol biosynthetic process	GO:0045540	1.312×10^{-13}	12.882070241507579
Regulation of catalytic activity	GO:0050790	1.312×10^{-13}	12.882070241507579
Regulation of alcohol biosynthetic process	GO:1902930	1.334×10^{-13}	12.874932257230519
Regulation of lipid metabolic process	GO:0019216	1.538×10^{-13}	12.812916621875905
Regulation of response to stress	GO:0080134	1.764×10^{-13}	12.753622989540558
Lipid metabolic process	GO:0006629	2.168×10^{-13}	12.664028904386821
Protein metabolic process	GO:0019538	2.179×10^{-13}	12.661732666356976
Regulation of developmental process	GO:0050793	2.333×10^{-13}	12.632000908070724

Supplementary table 5. continue

Establishment of localization	GO:0051234	2.894×10^{-13}	12.53853007389822
Cell activation	GO:0001775	3.702×10^{-13}	12.431594024922713
Secretion by cell	GO:0032940	4.427×10^{-13}	12.353879106544463
Transport	GO:0006810	5.019×10^{-13}	12.29937481238874
Regulation of localization	GO:0032879	5.019×10^{-13}	12.29937481238874
Enzyme linked receptor protein signaling pathway	GO:0007167	5.019×10^{-13}	12.29937481238874
Immune system process	GO:0002376	5.812×10^{-13}	12.23563833898486

GO, gene ontology; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 6. Enriched GO cellular component terms from up-regulated genes by oxytocin in human retinal pigment epithelial cells

Cellular anatomical entity	GO:0110165	1.515×10^{-43}	42.819572188537826
Intracellular anatomical structure	GO:0005622	1.220×10^{-29}	28.91369418460477
Cytoplasm	GO:0005737	1.220×10^{-29}	28.91369418460477
Membrane	GO:0016020	5.202×10^{-29}	28.283864626213326
Extracellular region	GO:0005576	1.294×10^{-28}	27.88793902783956
Cell periphery	GO:0071944	3.294×10^{-25}	24.482286349175936
Organelle	GO:0043226	3.294×10^{-25}	24.482286349175936
Plasma membrane	GO:0005886	7.030×10^{-25}	24.153046059535388
Intrinsic component of membrane	GO:0031224	3.796×10^{-24}	23.42072612254043
Membrane-bounded organelle	GO:0043227	1.243×10^{-22}	21.905393248674198
Extracellular space	GO:0005615	8.893×10^{-22}	21.05093193503294
Integral component of membrane	GO:0016021	1.199×10^{-20}	19.921340617599647
Intracellular organelle	GO:0043229	2.871×10^{-19}	18.54203198238773
Endomembrane system	GO:0012505	3.308×10^{-18}	17.48045807250561
Intracellular membrane-bounded organelle	GO:0043231	3.999×10^{-17}	16.398102242858975
Cell junction	GO:0030054	4.576×10^{-16}	15.339549695996844
Vesicle	GO:0031982	4.165×10^{-14}	13.380363919453353
Extracellular matrix	GO:0031012	4.490×10^{-13}	12.347712903052374
Organelle membrane	GO:0031090	8.863×10^{-13}	12.052396653880603
Cell surface	GO:0009986	8.863×10^{-13}	12.052396653880603
Intrinsic component of plasma membrane	GO:0031226	3.941×10^{-12}	11.404384353001076
Integral component of plasma membrane	GO:0005887	7.528×10^{-11}	10.123297639856489
Anchoring junction	GO:0070161	2.086×10^{-10}	9.680589448525316
Cytosol	GO:0005829	4.060×10^{-10}	9.391424685362086
Bounding membrane of organelle	GO:0098588	4.071×10^{-10}	9.390247183878573
Intracellular vesicle	GO:0097708	8.780×10^{-10}	9.056488735985784
Cytoplasmic vesicle	GO:0031410	8.780×10^{-10}	9.056488735985784
Plasma membrane region	GO:0098590	1.336×10^{-9}	8.874170852158798
Organelle subcompartment	GO:0031984	1.676×10^{-9}	8.775816160868322
Secretory vesicle	GO:0099503	3.391×10^{-9}	8.469620425256482
Focal adhesion	GO:0005925	3.459×10^{-9}	8.461049568415156
Collagen-containing extracellular matrix	GO:0062023	3.942×10^{-9}	8.404241592879071
Cell-substrate junction	GO:0030055	4.036×10^{-9}	8.3940555727671
Extracellular exosome	GO:0070062	1.211×10^{-8}	7.916771079957095
Secretory granule	GO:0030141	1.558×10^{-8}	7.807520727114773
Extracellular organelle	GO:0043230	2.356×10^{-8}	7.627915850781699
Extracellular vesicle	GO:1903561	2.356×10^{-8}	7.627915850781699
Synapse	GO:0045202	2.149×10^{-7}	6.667831131603802
Endoplasmic reticulum	GO:0005783	2.792×10^{-7}	6.554015759188535
Cytoplasmic vesicle membrane	GO:0030659	3.600×10^{-7}	6.443654583078667
Vesicle membrane	GO:0012506	4.829×10^{-7}	6.31614818683838
Cell projection	GO:0042995	9.466×10^{-7}	6.023811345722025
Golgi apparatus	GO:0005794	1.721×10^{-6}	5.7641212993258835
Plasma membrane bounded cell projection	GO:0120025	2.075×10^{-6}	5.6830365321725385
Secretory granule membrane	GO:0030667	4.655×10^{-6}	5.332095204455005
External side of plasma membrane	GO:0009897	4.812×10^{-6}	5.317663170789771

Supplementary table 6. continue

Intracellular non-membrane-bounded organelle	GO:0043232	1.404×10^{-5}	4.852768866448239
Non-membrane-bounded organelle	GO:0043228	1.417×10^{-5}	4.848493561642155
Endoplasmic reticulum membrane	GO:0005789	1.448×10^{-5}	4.8392796782825425
Endoplasmic reticulum subcompartment	GO:0098827	1.490×10^{-5}	4.826706240805956
Side of membrane	GO:0098552	1.577×10^{-5}	4.802217721163005
Nuclear outer membrane-endoplasmic reticulum membrane network	GO:0042175	1.706×10^{-5}	4.768123449567282
Anchored component of membrane	GO:0031225	2.205×10^{-5}	4.656686060539318
Receptor complex	GO:0043235	2.282×10^{-5}	4.641706011487204
Nucleus	GO:0005634	3.710×10^{-5}	4.430587986287493
Organelle lumen	GO:0043233	3.839×10^{-5}	4.4157570496069445
Membrane-enclosed lumen	GO:0031974	3.839×10^{-5}	4.4157570496069445
Cell cortex	GO:0005938	5.837×10^{-5}	4.233828487048155
Cytoskeleton	GO:0005856	1.416×10^{-4}	3.8488828833308752
Basolateral plasma membrane	GO:0016323	1.494×10^{-4}	3.8256812427066538
Specific granule	GO:0042581	1.914×10^{-4}	3.7181620003952127
Presynaptic membrane	GO:0042734	1.914×10^{-4}	3.7181620003952127
Synaptic membrane	GO:0097060	2.113×10^{-4}	3.675107628338128
Somatodendritic compartment	GO:0036477	2.458×10^{-4}	3.6093512182823715
Integrin complex	GO:0008305	2.933×10^{-4}	3.5326398094089515
Perinuclear region of cytoplasm	GO:0048471	3.083×10^{-4}	3.5110789601413055
Intracellular organelle lumen	GO:0070013	3.798×10^{-4}	3.4204052707114188
Protein complex involved in cell adhesion	GO:0098636	4.358×10^{-4}	3.360678266713334
Postsynapse	GO:0098794	6.815×10^{-4}	3.1665046068516953
Synaptic vesicle	GO:0008021	7.099×10^{-4}	3.1488298339862415
Cell-cell junction	GO:0005911	8.847×10^{-4}	3.0532155571211215
Exocytic vesicle	GO:0070382	1.044×10^{-3}	2.981115792865395
Endoplasmic reticulum chaperone complex	GO:0034663	1.067×10^{-3}	2.971668481420264
Golgi apparatus subcompartment	GO:0098791	1.067×10^{-3}	2.971668481420264
Glutamatergic synapse	GO:0098978	1.095×10^{-3}	2.9605860081398006
Axon terminus	GO:0043679	1.225×10^{-3}	2.912009856517894
Presynapse	GO:0098793	1.251×10^{-3}	2.9027703033856866
Nucleolus	GO:0005730	1.521×10^{-3}	2.817742645739028
Golgi stack	GO:0005795	1.762×10^{-3}	2.7538947190871568
Neuron projection	GO:0043005	1.804×10^{-3}	2.7437482758655345
Neuron projection terminus	GO:0044306	1.877×10^{-3}	2.726489710002695
Golgi membrane	GO:0000139	1.877×10^{-3}	2.726489710002695
Vacuolar membrane	GO:0005774	2.313×10^{-3}	2.6357781831247826
Tertiary granule	GO:0070820	2.325×10^{-3}	2.633511503522435
Presynaptic active zone cytoplasmic component	GO:0098831	2.460×10^{-3}	2.6090875750097653
Endoplasmic reticulum lumen	GO:0005788	3.010×10^{-3}	2.521476223164561
Extrinsic component of plasma membrane	GO:0019897	3.053×10^{-3}	2.5152896053869145
Leading edge membrane	GO:0031256	3.053×10^{-3}	2.5152896053869145
Presynaptic active zone	GO:0048786	3.053×10^{-3}	2.5152896053869145
Extrinsic component of membrane	GO:0019898	3.137×10^{-3}	2.5034728246572864
Nucleoplasm	GO:0005654	3.265×10^{-3}	2.486058072754075

Supplementary table 6. continue

Distal axon	GO:0150034	3.294×10^{-3}	2.482260925888621
Secretory granule lumen	GO:0034774	3.351×10^{-3}	2.474797394708258
Axon	GO:0030424	3.420×10^{-3}	2.466005784765486
Cytoplasmic vesicle lumen	GO:0060205	3.468×10^{-3}	2.459980078731775
Caveola	GO:0005901	3.491×10^{-3}	2.457080540781166
Vesicle lumen	GO:0031983	3.491×10^{-3}	2.457080540781166
Nuclear lumen	GO:0031981	3.516×10^{-3}	2.453935055384948
Clathrin-coated vesicle	GO:0030136	3.705×10^{-3}	2.431242846835

GO, gene ontology; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 7. Enriched KEGG terms from down-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P_{adj}	$-\log_{10}(P_{adj})$
Prostate cancer	KEGG:05215	3.826×10^{-3}	2.417266909954961
Tight junction	KEGG:04530	1.283×10^{-2}	1.8917596936726857
Pathogenic Escherichia coli infection	KEGG:05130	1.505×10^{-2}	1.822523978398466
Regulation of actin cytoskeleton	KEGG:04810	1.614×10^{-2}	1.7920080352569085
Calcium signaling pathway	KEGG:04020	1.774×10^{-2}	1.7509252104799957
EGFR tyrosine kinase inhibitor resistance	KEGG:01521	2.131×10^{-2}	1.6713909714973918
MAPK signaling pathway	KEGG:04010	2.131×10^{-2}	1.6713909714973918
Gastric acid secretion	KEGG:04971	2.131×10^{-2}	1.6713909714973918
Gap junction	KEGG:04540	2.296×10^{-2}	1.639066183265045
Protein digestion and absorption	KEGG:04974	2.839×10^{-2}	1.54680031659501
Serotonergic synapse	KEGG:04726	3.117×10^{-2}	1.5062457987655398

KEGG, Kyoto Encyclopedia of Genes and Genomes database; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 8. Enriched GO molecular function terms from down-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})
Binding	GO:0005488	2.566×10 ⁻¹²	11.590671341724613
Protein binding	GO:0005515	1.962×10 ⁻⁹	8.707385658108226
Ion binding	GO:0043167	1.861×10 ⁻⁶	5.730169202035372
Transporter activity	GO:0005215	5.916×10 ⁻⁶	5.228002258015082
Passive transmembrane transporter activity	GO:0022803	1.232×10 ⁻⁵	4.909235415114469
Channel activity	GO:0015267	1.232×10 ⁻⁵	4.909235415114469
Metal ion binding	GO:0046872	2.463×10 ⁻⁵	4.608462491848632
Cation binding	GO:0043169	2.594×10 ⁻⁵	4.586075836210209
Inorganic molecular entity transmembrane transporter activity	GO:0015318	2.594×10 ⁻⁵	4.586075836210209
Ion transmembrane transporter activity	GO:0015075	6.154×10 ⁻⁵	4.2108226479476
Metal ion transmembrane transporter activity	GO:0046873	6.430×10 ⁻⁵	4.191795586454621
Structural molecule activity	GO:0005198	6.430×10 ⁻⁵	4.191795586454621
Ion channel activity	GO:0005216	6.430×10 ⁻⁵	4.191795586454621
Transmembrane transporter activity	GO:0022857	1.060×10 ⁻⁴	3.974755464217867
Cation channel activity	GO:0005261	2.514×10 ⁻⁴	3.5996476814475318
Potassium ion transmembrane transporter activity	GO:0015079	2.514×10 ⁻⁴	3.5996476814475318
Heparin binding	GO:0008201	2.515×10 ⁻⁴	3.599466554816906
Extracellular matrix binding	GO:0050840	2.515×10 ⁻⁴	3.599466554816906
Inorganic cation transmembrane transporter activity	GO:0022890	2.515×10 ⁻⁴	3.599466554816906
Cation transmembrane transporter activity	GO:0008324	3.610×10 ⁻⁴	3.4424707186681403
Calcium ion binding	GO:0005509	6.172×10 ⁻⁴	3.2095883466761026
Antipporter activity	GO:0015297	7.613×10 ⁻⁴	3.1184372568243215
Glycosaminoglycan binding	GO:0005539	7.613×10 ⁻⁴	3.1184372568243215
Sulfur compound binding	GO:1901681	1.108×10 ⁻³	2.955475225534366
Calcium channel activity	GO:0005262	1.900×10 ⁻³	2.721254096921713
Carbohydrate derivative binding	GO:0097367	2.050×10 ⁻³	2.6882749155556227
Calcium ion transmembrane transporter activity	GO:0015085	2.557×10 ⁻³	2.5922191082320407
Transcription coactivator binding	GO:0001223	2.652×10 ⁻³	2.576495372671437
Voltage-gated cation channel activity	GO:0022843	2.884×10 ⁻³	2.539991029546977
Intramembrane lipid transporter activity	GO:0140303	3.882×10 ⁻³	2.410897808823162
Monovalent inorganic cation transmembrane transporter activity	GO:0015077	3.882×10 ⁻³	2.410897808823162
Divalent inorganic cation transmembrane transporter activity	GO:0072509	3.882×10 ⁻³	2.410897808823162
Extracellular matrix structural constituent	GO:0005201	4.061×10 ⁻³	2.3913787704699696
Nucleoside phosphate binding	GO:1901265	5.583×10 ⁻³	2.253121344238904
Nucleotide binding	GO:0000166	5.583×10 ⁻³	2.253121344238904
Voltage-gated ion channel activity	GO:0005244	6.006×10 ⁻³	2.2214120744015844
Voltage-gated channel activity	GO:0022832	6.006×10 ⁻³	2.2214120744015844
POU domain binding	GO:0070974	6.238×10 ⁻³	2.2049518822448873

Supplementary table 8. continue

Ion antiporter activity involved in regulation of presynaptic membrane potential	GO:0099520	6.238×10^{-3}	2.2049518822448873
DNA-binding transcription activator activity, RNA polymerase II-specific	GO:0001228	7.503×10^{-3}	2.124776903063652
DNA-binding transcription activator activity	GO:0001216	7.542×10^{-3}	2.1225192258739995
Heterocyclic compound binding	GO:1901363	7.634×10^{-3}	2.1172224359110583
Secondary active transmembrane transporter activity	GO:0015291	8.307×10^{-3}	2.0805554957669234
Organic cyclic compound binding	GO:0097159	8.307×10^{-3}	2.0805554957669234
Anion binding	GO:0043168	8.807×10^{-3}	2.055165204199345
Transcription coregulator binding	GO:0001221	9.197×10^{-3}	2.0363569818122755
Active ion transmembrane transporter activity	GO:0022853	9.288×10^{-3}	2.0320766363566283
Proline dehydrogenase activity	GO:0004657	9.288×10^{-3}	2.0320766363566283
Integrin binding involved in cell-matrix adhesion	GO:0098640	9.288×10^{-3}	2.0320766363566283
Small molecule binding	GO:0036094	9.288×10^{-3}	2.0320766363566283
Collagen binding	GO:0005518	9.288×10^{-3}	2.0320766363566283
Voltage-gated ion channel activity involved in regulation of postsynaptic membrane potential	GO:1905030	9.288×10^{-3}	2.0320766363566283
Urea channel activity	GO:0015265	9.288×10^{-3}	2.0320766363566283
Carbohydrate binding	GO:0030246	1.050×10^{-2}	1.9790039098179584
Chromatin binding	GO:0003682	1.094×10^{-2}	1.9611604678591745
Inositol monophosphate 3-phosphatase activity	GO:0052832	1.226×10^{-2}	1.9114874300974793
Inositol monophosphate 1-phosphatase activity	GO:0008934	1.226×10^{-2}	1.9114874300974793
Inositol monophosphate phosphatase activity	GO:0052834	1.226×10^{-2}	1.9114874300974793
Flavin adenine dinucleotide binding	GO:0050660	1.226×10^{-2}	1.9114874300974793
Inositol monophosphate 4-phosphatase activity	GO:0052833	1.226×10^{-2}	1.9114874300974793
Hormone binding	GO:0042562	1.248×10^{-2}	1.903800474635782
Voltage-gated potassium channel activity	GO:0005249	1.343×10^{-2}	1.8720418426500274
Voltage-gated potassium channel activity involved in atrial cardiac muscle cell action potential repolarization	GO:0086089	1.466×10^{-2}	1.8339212106965441
G-protein activated inward rectifier potassium channel activity	GO:0015467	1.466×10^{-2}	1.8339212106965441
A-type (transient outward) potassium channel activity	GO:0005250	1.466×10^{-2}	1.8339212106965441
Structural constituent of presynaptic active zone	GO:0098882	1.466×10^{-2}	1.8339212106965441
Androgen binding	GO:0005497	1.466×10^{-2}	1.8339212106965441
Gated channel activity	GO:0022836	1.523×10^{-2}	1.8173177457309369
Active transmembrane transporter activity	GO:0022804	1.575×10^{-2}	1.8026318163435948

Supplementary table 8. continue

Protein domain specific binding	GO:0019904	1.588×10^{-2}	1.7992201183217094
Steroid binding	GO:0005496	1.588×10^{-2}	1.7992201183217094
Calcium, potassium:sodium antiporter activity	GO:0008273	1.639×10^{-2}	1.7855092901512022
Extracellular matrix protein binding	GO:1990430	1.639×10^{-2}	1.7855092901512022
N,N-dimethylaniline monooxygenase activity	GO:0004499	1.639×10^{-2}	1.7855092901512022
Fibroblast growth factor-activated receptor activity	GO:0005007	1.639×10^{-2}	1.7855092901512022
Steroid hormone binding	GO:1990239	1.915×10^{-2}	1.7178024407764152
RNA polymerase II transcription coactivator binding	GO:0001225	1.915×10^{-2}	1.7178024407764152
Potassium channel activity	GO:0005267	2.030×10^{-2}	1.6924354397769297
Protein-containing complex binding	GO:0044877	2.095×10^{-2}	1.6787760643993546
Urea transmembrane transporter activity	GO:0015204	2.124×10^{-2}	1.6727682604757277
Cell-matrix adhesion mediator activity	GO:0098634	2.124×10^{-2}	1.6727682604757277
Purine ribonucleoside triphosphate binding	GO:0035639	2.150×10^{-2}	1.6676605291301845
Transcription regulator activity	GO:0140110	2.381×10^{-2}	1.6233244316554363
RNA polymerase II transcription regulatory region sequence-specific DNA binding	GO:0000977	2.381×10^{-2}	1.6233244316554363
DNA-binding transcription factor activity, RNA polymerase II-specific	GO:0000981	2.381×10^{-2}	1.6233244316554363
Extracellular matrix constituent conferring elasticity	GO:0030023	2.381×10^{-2}	1.6233244316554363
Oxalate transmembrane transporter activity	GO:0019531	2.381×10^{-2}	1.6233244316554363
Purine ribonucleotide binding	GO:0032555	2.381×10^{-2}	1.6233244316554363
Integrin binding	GO:0005178	2.381×10^{-2}	1.6233244316554363
CD4 receptor binding	GO:0042609	2.381×10^{-2}	1.6233244316554363
MDM2/MDM4 family protein binding	GO:0097371	2.381×10^{-2}	1.6233244316554363
Purine nucleotide binding	GO:0017076	2.381×10^{-2}	1.6233244316554363
Ribonucleotide binding	GO:0032553	2.381×10^{-2}	1.6233244316554363
Anion transmembrane transporter activity	GO:0008509	2.462×10^{-2}	1.6086531924204024
Calcium:sodium antiporter activity	GO:0005432	2.513×10^{-2}	1.5997855599937763
Sodium ion transmembrane transporter activity	GO:0015081	2.513×10^{-2}	1.5997855599937763
Phospholipid scramblase activity	GO:0017128	2.513×10^{-2}	1.5997855599937763
Arrestin family protein binding	GO:1990763	2.513×10^{-2}	1.5997855599937763
DNA-binding transcription factor activity	GO:0003700	2.578×10^{-2}	1.5887388004684426

GO, gene ontology; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 9. Enriched GO biological process terms from down-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})
Cellular process	GO:0009987	2.029×10^{-13}	12.692740963917366
Localization	GO:0051179	3.789×10^{-10}	9.421469627408213
Biological regulation	GO:0065007	3.050×10^{-8}	7.5156901087564245
Response to stimulus	GO:0050896	6.891×10^{-8}	7.161738440881226
Regulation of biological process	GO:0050789	8.820×10^{-7}	6.054507407700432
Regulation of cellular process	GO:0050794	1.083×10^{-6}	5.965332792525254
Signaling	GO:0023052	1.593×10^{-6}	5.797679023051116
Cell communication	GO:0007154	1.593×10^{-6}	5.797679023051116
Cellular response to stimulus	GO:0051716	3.258×10^{-6}	5.487063626841329
Multicellular organismal process	GO:0032501	5.158×10^{-6}	5.287506475986964
Epithelial cell differentiation involved in prostate gland development	GO:0060742	2.148×10^{-5}	4.668046413383457
Developmental process	GO:0032502	2.237×10^{-5}	4.650405361169093
Lateral sprouting from an epithelium	GO:0060601	2.392×10^{-5}	4.621329302252169
Morphogenesis of an epithelial bud	GO:0060572	4.362×10^{-5}	4.360308836374909
Transport	GO:0006810	4.583×10^{-5}	4.338820207530083
Animal organ formation	GO:0048645	4.583×10^{-5}	4.338820207530083
Regulation of biological quality	GO:0065008	5.475×10^{-5}	4.261578620421884
Establishment of localization	GO:0051234	6.018×10^{-5}	4.220519552269339
Squamous basal epithelial stem cell differentiation involved in prostate gland acinus development	GO:0060529	6.737×10^{-5}	4.171505330258466
Multicellular organism development	GO:0007275	1.204×10^{-4}	3.919335523169756
Cellular response to chemical stimulus	GO:0070887	1.204×10^{-4}	3.919335523169756
Anatomical structure formation involved in morphogenesis	GO:0048646	1.204×10^{-4}	3.919335523169756
Prostate gland epithelium morphogenesis	GO:0060740	1.207×10^{-4}	3.9181660712366178
Morphogenesis of an epithelial fold	GO:0060571	1.207×10^{-4}	3.9181660712366178
Prostate gland morphogenesis	GO:0060512	1.461×10^{-4}	3.8353875263554764
Tube morphogenesis	GO:0035239	1.618×10^{-4}	3.7910933489236402
Cellular component organization	GO:0016043	1.618×10^{-4}	3.7910933489236402
Cell-cell signaling	GO:0007267	1.998×10^{-4}	3.6994061466065733
Cellular component organization or biogenesis	GO:0071840	2.257×10^{-4}	3.646378312125121
Anatomical structure development	GO:0048856	2.770×10^{-4}	3.557510055805106
Specification of animal organ identity	GO:0010092	3.037×10^{-4}	3.5175642808302214
Negative regulation of cellular metabolic process	GO:0031324	3.130×10^{-4}	3.5044050698894
Cell differentiation	GO:0030154	3.192×10^{-4}	3.4958939777555242
Cellular developmental process	GO:0048869	3.828×10^{-4}	3.417060893591739
System development	GO:0048731	3.981×10^{-4}	3.400047137198232
Regulation of localization	GO:0032879	4.109×10^{-4}	3.386243743478247
Tube development	GO:0035295	4.725×10^{-4}	3.325584853713102
Prostate gland development	GO:0030850	5.076×10^{-4}	3.2944617666896305
Morphogenesis of embryonic epithelium	GO:0016331	5.280×10^{-4}	3.277328227290312

Supplementary table 9. continue

Inorganic Ion Transmembrane Transport	GO:0098660	6.063×10^{-4}	3.2173365934184135
Urogenital system development	GO:0001655	6.830×10^{-4}	3.165553002486967
Response to chemical	GO:0042221	6.830×10^{-4}	3.165553002486967
Regulation of morphogenesis of a branching structure	GO:0060688	6.830×10^{-4}	3.165553002486967
Regionalization	GO:0003002	6.880×10^{-4}	3.1624368830456815
Ion transport	GO:0006811	7.060×10^{-4}	3.1511652868662043
Regulation of cell division	GO:0051302	7.060×10^{-4}	3.1511652868662043
Programmed cell death	GO:0012501	7.955×10^{-4}	3.099360454992931
Morphogenesis of a branching epithelium	GO:0061138	9.575×10^{-4}	3.018846728994864
Signal transduction	GO:0007165	9.817×10^{-4}	3.00803682522394
Positive regulation of cell population proliferation	GO:0008284	1.064×10^{-3}	2.973049899717762
Regulation of epithelial cell proliferation	GO:0050678	1.083×10^{-3}	2.965213011404578
Prostatic bud formation	GO:0060513	1.083×10^{-3}	2.965213011404578
Elastic fiber assembly	GO:0048251	1.083×10^{-3}	2.965213011404578
Ion transmembrane transport	GO:0034220	1.083×10^{-3}	2.965213011404578
Cranial skeletal system development	GO:1904888	1.083×10^{-3}	2.965213011404578
Morphogenesis of a branching structure	GO:0001763	1.086×10^{-3}	2.9641491286177657
Cellular response to organic substance	GO:0071310	1.091×10^{-3}	2.9623480711067907
Cell death	GO:0008219	1.140×10^{-3}	2.943212185477096
System process	GO:0003008	1.141×10^{-3}	2.942647424769794
Prostate gland growth	GO:0060736	1.152×10^{-3}	2.93857117577472
Prostate glandular acinus development	GO:0060525	1.152×10^{-3}	2.93857117577472
Negative regulation of cellular process	GO:0048523	1.152×10^{-3}	2.93857117577472
Cellular response to endogenous stimulus	GO:0071495	1.152×10^{-3}	2.93857117577472
Intracellular signal transduction	GO:0035556	1.164×10^{-3}	2.9341104487827736
Response to organic substance	GO:0010033	1.299×10^{-3}	2.8864499325752964
Potassium ion transmembrane transport	GO:0071805	1.329×10^{-3}	2.8765550324857125
Pattern specification process	GO:0007389	1.490×10^{-3}	2.826773889867346
Seminiferous tubule development	GO:0072520	1.492×10^{-3}	2.8262635056603322
Genitalia morphogenesis	GO:0035112	1.492×10^{-3}	2.8262635056603322
Negative regulation of metabolic process	GO:0009892	1.505×10^{-3}	2.8224442395262654
Cellular localization	GO:0051641	1.579×10^{-3}	2.8015020951343077
Epithelial cell proliferation	GO:0050673	1.600×10^{-3}	2.7959488967786035
Apoptotic process	GO:0006915	1.774×10^{-3}	2.7511143820715493
Regulation of signaling	GO:0023051	1.798×10^{-3}	2.745213475538878
Inorganic cation transmembrane transport	GO:0098662	1.798×10^{-3}	2.745213475538878
Potassium ion transport	GO:0006813	1.798×10^{-3}	2.745213475538878
Blood vessel development	GO:0001568	1.984×10^{-3}	2.7024571495993657
Otic vesicle development	GO:0071599	2.027×10^{-3}	2.693066575209626
Epithelial cell differentiation	GO:0030855	2.027×10^{-3}	2.693066575209626
Transmembrane transport	GO:0055085	2.275×10^{-3}	2.6429770472428764
Cell fate commitment	GO:0045165	2.322×10^{-3}	2.634166856049344
Vasculature development	GO:0001944	2.322×10^{-3}	2.634166856049344
Animal organ development	GO:0048513	2.322×10^{-3}	2.634166856049344
Circulatory system development	GO:0072359	2.322×10^{-3}	2.634166856049344
Cell migration	GO:0016477	2.551×10^{-3}	2.5932968284905797

Supplementary table 9. continue

Tissue Development	GO:0009888	2.551×10^{-3}	2.5932968284905797
Hematopoietic stem cell homeostasis	GO:0061484	2.593×10^{-3}	2.586264792353666
Response to endogenous stimulus	GO:0009719	2.639×10^{-3}	2.578571382286883
Branch elongation of an epithelium	GO:0060602	2.784×10^{-3}	2.5553189951766417
Synaptic vesicle priming	GO:0016082	2.784×10^{-3}	2.5553189951766417
Metabolic process	GO:0008152	2.802×10^{-3}	2.55255594358548
Negative regulation of biological process	GO:0048519	2.802×10^{-3}	2.55255594358548
Blood circulation	GO:0008015	2.833×10^{-3}	2.547762280994588
Positive regulation of cellular process	GO:0048522	2.904×10^{-3}	2.537020949786287
Cation transmembrane transport	GO:0098655	3.035×10^{-3}	2.517848535396592
Regulation of cell death	GO:0010941	3.035×10^{-3}	2.517848535396592
Metal ion transport	GO:0030001	3.318×10^{-3}	2.47915839131816
Regulation of cell population proliferation	GO:0042127	3.432×10^{-3}	2.4644399020943166
Response to lipid	GO:0033993	3.432×10^{-3}	2.464

GO, gene ontology; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 10. Enriched GO cellular component terms from down-regulated genes by oxytocin in human retinal pigment epithelial cells

Term name	Term ID	P _{adj}	-log ₁₀ (P _{adj})
Cellular anatomical entity	GO:0110165	6.633×10 ⁻¹⁷	16.178318914163697
Integral component of membrane	GO:0016021	3.682×10 ⁻¹⁴	13.433948231296466
Intrinsic component of membrane	GO:0031224	5.611×10 ⁻¹⁴	13.250923220785452
Membrane	GO:0016020	1.528×10 ⁻¹³	12.815934162281662
Plasma membrane	GO:0005886	1.239×10 ⁻¹⁰	9.906948349899338
Cell periphery	GO:0071944	1.706×10 ⁻¹⁰	9.76793023730715
Organelle	GO:0043226	7.271×10 ⁻¹⁰	9.138422052525831
Intrinsic component of plasma membrane	GO:0031226	9.511×10 ⁻⁸	7.021762554878594
Cytoplasm	GO:0005737	2.187×10 ⁻⁷	6.660086184039969
Integral component of plasma membrane	GO:0005887	4.761×10 ⁻⁷	6.322337578536363
Vesicle	GO:0031982	1.228×10 ⁻⁶	5.910642647228262
Intracellular anatomical structure	GO:0005622	1.591×10 ⁻⁶	5.798247416596149
Membrane-bounded organelle	GO:0043227	1.762×10 ⁻⁵	4.754015462000814
Cytoplasmic vesicle	GO:0031410	1.464×10 ⁻⁴	3.8343259384736417
Endomembrane system	GO:0012505	1.464×10 ⁻⁴	3.8343259384736417
Intracellular vesicle	GO:0097708	1.464×10 ⁻⁴	3.8343259384736417
Extracellular matrix	GO:0031012	1.583×10 ⁻⁴	3.80048642046554
Organelle membrane	GO:0031090	1.851×10 ⁻⁴	3.7327074125133506
Plasma membrane region	GO:0098590	1.851×10 ⁻⁴	3.7327074125133506
Excitatory synapse	GO:0060076	1.851×10 ⁻⁴	3.7327074125133506
Cell junction	GO:0030054	2.026×10 ⁻⁴	3.6933299902954584
Intracellular organelle	GO:0043229	2.753×10 ⁻⁴	3.560225163038242
Synaptic membrane	GO:0097060	2.855×10 ⁻⁴	3.5443425758353158
Extracellular organelle	GO:0043230	2.855×10 ⁻⁴	3.5443425758353158
Extracellular vesicle	GO:1903561	2.855×10 ⁻⁴	3.5443425758353158
Synapse	GO:0045202	2.855×10 ⁻⁴	3.5443425758353158
Collagen-containing extracellular matrix	GO:0062023	3.490×10 ⁻⁴	3.4571911684217698
Extracellular region	GO:0005576	3.617×10 ⁻⁴	3.4415944458088643
Extracellular space	GO:0005615	5.734×10 ⁻⁴	3.2415441624470644
Parallel fiber to Purkinje cell synapse	GO:0098688	8.050×10 ⁻⁴	3.0941951409693274
Extracellular exosome	GO:0070062	1.010×10 ⁻³	2.9955233864806647
Transmembrane transporter complex	GO:1902495	1.603×10 ⁻³	2.795158523425778
Transporter complex	GO:1990351	1.763×10 ⁻³	2.753761127717098
Neuronal cell body membrane	GO:0032809	2.114×10 ⁻³	2.674949398119247
Protein-containing complex	GO:0032991	2.154×10 ⁻³	2.666824484339111
Glutamatergic synapse	GO:0098978	2.325×10 ⁻³	2.633631364421265
Cell body membrane	GO:0044298	2.374×10 ⁻³	2.6244677187634733
Presynaptic membrane	GO:0042734	2.423×10 ⁻³	2.615632968985932
Integral component of synaptic membrane	GO:0099699	2.479×10 ⁻³	2.605685467748823
Plasma membrane protein complex	GO:0098797	2.479×10 ⁻³	2.605685467748823
Intrinsic component of synaptic membrane	GO:0099240	3.080×10 ⁻³	2.511405459244796
EMILIN complex	GO:1990971	4.722×10 ⁻³	2.325841778893487
Protein complex involved in cell-matrix adhesion	GO:0098637	4.722×10 ⁻³	2.325841778893487
Cytoskeleton	GO:0005856	5.397×10 ⁻³	2.2678787114778376

Supplementary table 9. continue

Cation channel complex	GO:0034703	6.013×10^{-3}	2.220942466437225
Myosin complex	GO:0016459	6.088×10^{-3}	2.2155454562677623
Neuron projection	GO:0043005	7.883×10^{-3}	2.1033237371541493
Endoplasmic reticulum	GO:0005783	9.322×10^{-3}	2.030495246190832
Postsynaptic membrane	GO:0045211	1.062×10^{-2}	1.9736727517435635
Integral component of postsynaptic specialization membrane	GO:0099060	1.096×10^{-2}	1.960164532784744
GABA-ergic synapse	GO:0098982	1.102×10^{-2}	1.9579918014657907
Integrin alpha4-beta1 complex	GO:0034668	1.115×10^{-2}	1.9526239189683925
Intrinsic component of postsynaptic specialization membrane	GO:0098948	1.115×10^{-2}	1.9526239189683925
Ion channel complex	GO:0034702	1.115×10^{-2}	1.9526239189683925
Glial limiting end-foot	GO:0097451	1.115×10^{-2}	1.9526239189683925
Endoplasmic reticulum lumen	GO:0005788	1.116×10^{-2}	1.9523209600457108
Cell cortex	GO:0005938	1.174×10^{-2}	1.9304725682554735
Organelle lumen	GO:0043233	1.174×10^{-2}	1.9304725682554735
Voltage-gated potassium channel complex	GO:0008076	1.174×10^{-2}	1.9304725682554735
Axon	GO:0030424	1.174×10^{-2}	1.9304725682554735
Membrane-enclosed lumen	GO:0031974	1.174×10^{-2}	1.9304725682554735
Bounding membrane of organelle	GO:0098588	1.194×10^{-2}	1.922909846974657
Collagen trimer	GO:0005581	1.223×10^{-2}	1.9124187436153208
Photoreceptor inner segment membrane	GO:0060342	1.277×10^{-2}	1.8938228661235381
Potassium channel complex	GO:0034705	1.311×10^{-2}	1.8822577865880155
Melanosome	GO:0042470	1.380×10^{-2}	1.8600778646911527
Plasma membrane bounded cell projection	GO:0120025	1.380×10^{-2}	1.8600778646911527
Pigment granule	GO:0048770	1.380×10^{-2}	1.8600778646911527
Neuron to neuron synapse	GO:0098984	1.577×10^{-2}	1.8021117381507983
Intracellular non-membrane-bounded organelle	GO:0043232	1.638×10^{-2}	1.7856363524331225
Cell projection	GO:0042995	1.638×10^{-2}	1.7856363524331225
Non-membrane-bounded organelle	GO:0043228	1.638×10^{-2}	1.7856363524331225
Cytoplasmic vesicle membrane	GO:0030659	1.770×10^{-2}	1.751932941268313
Integral component of postsynaptic membrane	GO:0099055	1.781×10^{-2}	1.749366823368563
Postsynaptic specialization membrane	GO:0099634	1.785×10^{-2}	1.7484216167797098
Vesicle membrane	GO:0012506	1.872×10^{-2}	1.7276150843194438
Intrinsic component of postsynaptic membrane	GO:0098936	1.875×10^{-2}	1.727024923842619
External side of plasma membrane	GO:0009897	1.924×10^{-2}	1.7158236531643538
Membrane protein complex	GO:0098796	2.005×10^{-2}	1.6978845260852014
Astrocyte end-foot	GO:0097450	2.046×10^{-2}	1.6891380244923226
Intracellular organelle lumen	GO:0070013	2.054×10^{-2}	1.6873615844986976
Secretory granule	GO:0030141	2.094×10^{-2}	1.679085205401438
Intracellular membrane-bounded organelle	GO:0043231	2.324×10^{-2}	1.633762103133748
Cell surface	GO:0009986	2.646×10^{-2}	1.57744445514638604
Neurofilament	GO:0005883	2.646×10^{-2}	1.5774285979376148
Sodium:potassium-exchanging atpase complex	GO:0005890	2.852×10^{-2}	1.54485406490759
Receptor complex	GO:0043235	3.049×10^{-2}	1.5158372303841654

Supplementary table 9. continue

Platelet dense granule lumen	GO:0031089	3.250×10^{-2}	1.4881644023670602
Presynapse	GO:0098793	3.331×10^{-2}	1.4774819142121358
Supramolecular fiber	GO:0099512	3.331×10^{-2}	1.4774819142121358
Muscle myosin complex	GO:0005859	3.331×10^{-2}	1.4774819142121358
Supramolecular polymer	GO:0099081	3.331×10^{-2}	1.4774819142121358
Secretory vesicle	GO:0099503	3.449×10^{-2}	1.462292987183275
Presynaptic active zone cytoplasmic component	GO:0098831	3.476×10^{-2}	1.4588923205483098
Cation-transporting atpase complex	GO:0090533	4.080×10^{-2}	1.3893855299723292
Myosin II complex	GO:0016460	4.205×10^{-2}	1.376256991284904
Astrocyte projection	GO:0097449	4.205×10^{-2}	1.376256991284904
Platelet dense granule	GO:0042827	4.368×10^{-2}	1.3596697978456322
Side of membrane	GO:0098552	4.494×10^{-2}	1.3473376982199676

GO, gene ontology; P_{adj} or FDR (false discovery rate), a corrected p-value.

Supplementary table 11. Top 50 differentially expressed genes (DEGs) in human retinal pigment epithelial cells treated with oxytocin

Ensembl ID	Gene Symbol	logFC	FDR
ENSG00000203721	LINC00862	1.38E+00	7.66E-16
ENSG00000127329	PTPRB	1.07E+00	2.54E-12
ENSG00000113070	HBEGF	1.15E+00	8.18E-11
ENSG00000168685	IL7R	1.68E+00	8.21E-11
ENSG00000052795	FNIP2	7.03E-01	1.63E-10
ENSG00000164171	ITGA2	1.13E+00	2.39E-10
ENSG00000131016	AKAP12	9.91E-01	4.76E-10
ENSG00000148677	ANKRD1	1.43E+00	1.18E-09
ENSG00000163331	DAPL1	-1.07E+00	2.72E-09
ENSG00000186480	INSIG1	9.03E-01	2.01E-08
ENSG00000112414	ADGRG6	6.43E-01	3.20E-08
ENSG00000112972	HMGCS1	8.74E-01	1.16E-07
ENSG00000117525	F3	8.28E-01	1.16E-07
ENSG00000138675	FGF5	7.91E-01	1.16E-07
ENSG00000145721	LIX1	-9.47E-01	1.16E-07
ENSG00000134516	DOCK2	7.90E-01	1.23E-07
ENSG00000198959	TGM2	1.28E+00	1.23E-07
ENSG00000118523	CTGF	8.61E-01	1.29E-07
ENSG00000163661	PTX3	9.33E-01	1.32E-07
ENSG00000145777	TSLP	8.44E-01	1.72E-07
ENSG00000233117	LINC00702	1.10E+00	6.34E-07
ENSG00000113578	FGF1	7.56E-01	1.13E-06
ENSG00000173166	RAPH1	8.01E-01	1.39E-06
ENSG00000154678	PDE1C	9.31E-01	1.46E-06
ENSG00000130600	H19	-7.41E-01	1.87E-06
ENSG00000132196	HSD17B7	8.37E-01	1.87E-06
ENSG00000147606	SLC26A7	-1.15E+00	1.87E-06
ENSG00000144063	MALL	1.24E+00	2.02E-06
ENSG00000110427	KIAA1549L	1.10E+00	2.07E-06
ENSG00000079459	FDFT1	6.93E-01	2.09E-06
ENSG00000079841	RIMS1	8.47E-01	2.41E-06
ENSG00000081181	ARG2	1.16E+00	2.41E-06
ENSG00000115339	GALNT3	7.50E-01	2.64E-06
ENSG00000079931	MOXD1	6.07E-01	5.05E-06
ENSG00000166923	GREM1	7.50E-01	5.05E-06
ENSG00000147155	EBP	6.67E-01	5.06E-06

Supplementary table 11. continue

ENSG00000147573	TRIM55	1.02E+00	5.81E-06
ENSG00000104549	SQLE	6.65E-01	6.23E-06
ENSG00000164741	DLC1	6.46E-01	6.52E-06
ENSG00000170962	PDGFD	-7.16E-01	6.71E-06
ENSG00000113161	HMGCR	6.42E-01	7.24E-06
ENSG00000052802	MSMO1	8.16E-01	7.27E-06
ENSG00000139211	AMIGO2	6.41E-01	9.14E-06
ENSG00000154127	UBASH3B	7.83E-01	9.15E-06
ENSG00000130164	LDLR	8.43E-01	9.94E-06
ENSG00000127824	TUBA4A	7.52E-01	1.31E-05
ENSG00000066468	FGFR2	-7.01E-01	1.45E-05
ENSG00000176697	BDNF	7.85E-01	1.45E-05
ENSG00000120437	ACAT2	8.91E-01	1.57E-05
ENSG00000073008	PVR	7.03E-01	1.73E-05

log₂FC, log₂(fold change); FDR, false discovery rate that is a corrected p-value by the Benjamini-Hochberg procedure; Fold change data without a minus sign denote up-regulation; Fold change data with a minus sign denote down-regulation.