Table S3 Top 20 significantly enriched KEGG pathways of DEGs in pituitary tissues.

Term	*p*-value	Enrichment_score	Genes
Neuroactive ligand-receptor interaction	1.02E-12	4.271579355	ADRA1B;APELA;BDKRB2;CHRNB4;DRD3;GABRA2;GABRE;GH;GRIA3;GRIN2C;HTR7L;LOC101751902;LOC107054855;LOC771308;LPAR1;MC3R;MC5R;MLNR;NPW;NPY;NPY7R;OPRD1;OXTR;P2RX1;PGR2;3;PPY;PTGER2;RLN3;RXFP3;SST1;TACR3
Calcium signaling pathway	0.002060331	2.591995842	ADRA1B;BDKRB2;CAMK4;FGF18;GRIN2C;HTR7L;MCOLN2;OXTR;P2RX1;PGR2;3;RYR2;TACR3
Nitrogen metabolism	0.004843334	8.462104072	CA3A;CA3B;CA8
Amino sugar and nucleotide sugar metabolism	0.017198868	3.99599359	CHIA;CHIA-M31;GCK;LOC768786
Cytokine-cytokine receptor interaction	0.021597039	2.179632867	BMP15;CRLF2;CXCL13L3;GH;IL10;IL20RA;INHBB;INHBE;RELT
Steroid hormone biosynthesis	0.041013739	3.887993763	CYP11A1;CYP2C18;RP11-400G3.5
One carbon pool by folate	0.047792011	5.641402715	FTCD;MTHFD2
Arachidonic acid metabolism	0.085432275	2.877115385	CYP2C18;PTGS1;RP11-400G3.5
Caffeine metabolism	0.100050332	9.590384615	LOC101747367
Neomycin, kanamycin and gentamicin biosynthesis	0.100050332	9.590384615	GCK
Linoleic acid metabolism	0.12166932	3.307029178	CYP2C18;RP11-400G3.5
Intestinal immune network for IgA production	0.157484377	2.820701357	AICDA;IL10
Retinol metabolism	0.194973224	2.459072978	CYP2C18;RP11-400G3.5
Apelin signaling pathway	0.258758965	1.546836228	APELA;CAMK4;MYL3;RYR2
C-type lectin receptor signaling pathway	0.266488891	1.672741503	EGR3;IL10;LOC101748577
NOD-like receptor signaling pathway	0.272678812	1.51029679	CATH1;CATH2;CATH3;DEFB4A
Drug metabolism - other enzymes	0.342010144	1.653514589	CES1L2;LPO
Histidine metabolism	0.344468172	2.397596154	FTCD
Glycerolipid metabolism	0.349648662	1.625488918	DGKK;MOGAT2
Wnt signaling pathway	0.377316601	1.287299948	MMP7;RSPO4;WNT6;WNT9A