

Table S2 Top 30 GO terms of DEGs in pituitary tissues.

Category	GO Term	p-value	Enrichment_score	Genes
BP	defense response to bacterium	6.18E-07	8.865968009	AvBD1;AvBD12;AvBD6;AvBD7;DEFB4A;EXFABP;IL10;LYG2;PGR2;3
BP	antimicrobial humoral immune response mediated by antimicrobial peptide	5.72E-05	11.49292149	CATH1;CATH2;CATH3;CXCL13L3;S100A12
BP	response to fungus	8.53E-05	28.96216216	CHIA;CHIA-M31;LOC768786
BP	positive regulation of chemokine secretion	0.00016807	24.13513514	CHIA;CHIA-M31;LOC768786
BP	defense response to Gram-negative bacterium	0.000245145	8.61969112	AvBD4;AvBD7;CATH1;CATH2;CATH3
BP	neuropeptide signaling pathway	0.000312749	5.363363363	ECEL1;LOC101751902;NPW;NPY;OPRD1;PPY;RXFP3
BP	cell-cell signaling	0.000345027	5.279560811	BHLHA15;EREG;FGF18;FGFBP1;PCDH1;SHH;WNT6
BP	homophilic cell adhesion via plasma membrane adhesion molecules	0.000447688	3.629343629	CDH7;LOC100857119;LOC107049499;LOC107056913;LOC121106477;LOC124416950;MYOT;PCDH1;PCDH10;PTPRT
BP	G protein-coupled receptor signaling pathway	0.000678805	2.613913553	ADGRB2;APOC3;BHLHA15;DRD3;LOC112531260;LOC431250;LPAR1;MC3R;MLNR;NPW;OPRD1;RAPGEFL1;RLN3;RXFP3;TACR3
BP	circadian regulation of gene expression	0.00071931	6.895752896	BHLHE41;CIART;DRD3;MC3R;NR1D1
CC	extracellular space	6.46E-11	2.808452088	APELA;AvBD1;AvBD6;AvBD7;BMP15;BMPEP;BPIFCB;C1QTNF8;CATH1;CATH2;CATH3;CHIA;CHIA-M31;CHRDL2;COL12A1;CPB2;CXCL13L3;DEFB4A;EREG;EXFABP;FETUB;FGF18;FGFBP1;GH;HEPHL1;IGFALS;IL10;INHBB;INHBE;KMO;LECT2;LOC107054855;LOC112530909;LOC768786;LY86;NPY;PPY;RSPO4;SEMA3D;SEMA3DL;SERPINB10B;SHH;SPINK5;SST1;SULF1;VIT;WNT6;WNT9A
CC	extracellular region	1.97E-06	2.329396421	APELA;AvBD12;AvBD4;BMPEP;BPIFB3;C1QL3;C7H2ORF66;CHIA;CHIA-M31;CLEC19A;CRLF2;EREG;FAM150B;FAM166A;FBLN7;FETUB;FGF18;IL10;ITIH2;KERA;LOC101750367;LOC121108602;LOC768786;LYG2;NPTX2;NPW;NTNG1;OVCH1;PCSK9;PROK2;REG1A;RLN3;SHH;SPINK5;STC2;VSTM2A
CC	integral component of plasma membrane	5.61E-06	2.165608347	ADGRB2;AQP3;AQP8;C1QTNF8;CALHM3;CHRNA4;DRD3;ECEL1;EPHA6;EREG;GABRE;GRIN2C;HTR7L;INSRR;LOC100857119;LOC101751902;LOC107049499;LOC107056913;LOC112531260;LOC121106477;LOC124416950;LOC431250;LPAR1;MC3R;OPRD1;PCDH1;PCDH10;PLXNC1;PTPRT;RHAG;ROS1;RXFP3;SEMA3D;SEMA3DL;SLC6A12;SYT13;TACR3;TRPC7
CC	nucleosome	0.000166124	5.927927928	HIST1H11L;HIST1H2B7L4;HIST1H2BO;HIST1H3A;HIST1H4D;HIST2H3A;LOC769852

CC	receptor complex	0.000534161	3.549284579	CRLF2;EPHA6;GFRA2;INSRR;KCTD8;LOC107055115;LOC771308;MTTPL;PKD2L1;ROS1
CC	specific granule	0.00067394	16.09009009	CATH1;CATH2;CATH3
CC	anchored component of presynaptic active zone membrane	0.004104241	19.30810811	CPLX3;NTNG1
CC	chylomicron	0.006072327	16.09009009	APOC3;APOV1
CC	dendrite membrane	0.01012523	6.582309582	GABRE;OPRD1;TACR3
CC	plasma membrane	0.010166196	1.306679291	ADGRB2;ADRA1B;AMER3;AQP3;AQP8;BDKRB2;CALN1;CDH7;CLDN25;CPNE4;CRLF2;CSMD2;DGKK;DNAJC5B;DRD3;DUOXA2;EPB42;EPHA6;FGFBP1;GH;GPA33;GPIHBP1;GRIN2C;GSG1L;IL20RA;KCNG1;KCNK15;KLB;LOC100859420;LOC101751902;LOC107055115;LOC121106436;LOC121106940;LOC431250;LOC771308;LPAR1;MC3R;MC5R;MCOLN2;MLNR;MYO16;MYOT;NOX3;NPTX2;NPY7R;NTNG1;OPRD1;PCDH1;PKD2L1;PLP1;PLXNC1;PTGER2;PTPRT;RELT;RHAG;RXFP3;SH2D2A;SHH;SLC6A12;SLC6A5;STEAP4;SYT13;TACR3;TMEFF1;TRPC7;TRPM3;VEPH1;ZP2
MF	lysozyme activity	2.62E-06	32.18018018	CHIA;CHIA-M31;LOC768786;LYG2
MF	CCR6 chemokine receptor binding	1.18E-05	24.13513514	AvBD1;AvBD6;AvBD7;DEFB4A
MF	chitin binding	0.00016807	24.13513514	CHIA;CHIA-M31;LOC768786
MF	hormone activity	0.000230164	5.631531532	APELA;GH;INHBB;INHBE;RLN3;SST1;STC2
MF	carbohydrate binding	0.000684562	4.152281314	CHIA;CHIA-M31;CLEC19A;LOC121106940;LOC768786;NPTX2;PGR2;3;VCAN
MF	calcium ion binding	0.000706028	2.090802667	107056913;LOC112530909;LOC121106477;LOC124416950;MGP;MMP13;MYL3;PCDH1;PCDH10;PKD2L1;S100A12;SHH;SULF1;SYT13;TGM3;VCAN
MF	chemoattractant activity	0.001382499	8.045045045	AvBD1;AvBD6;AvBD7;DEFB4A
MF	lipopolysaccharide binding	0.001619271	7.723243243	BPIFCB;CATH1;CATH2;CATH3
MF	carbonate dehydratase activity	0.002704275	10.34362934	CA3A;CA3B;CA8
MF	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	0.002704275	10.34362934	EREG;FGF18;KLB
