

**Table S1 Gene functional annotation for up-regulated transcripts by EA
(profile B-a, b and c in Fig. 3)**

EA-Targeted Function	Name of sub-category	p-value	Number of transcripts	
Cortex	Protein of unknown function DUF622	6.33E-05	4	
Protein function and Modification	Ligase activity, forming carbon-nitrogen bonds	2.58E-04	10	
	Small conjugating protein ligase activity (2)	0.003215	7	
	Phosphoprotein	3.99E-04	64	
	Acetylation	0.003203	32	
	GTP binding (3)	2.77E-04	13	
	GTPase activity	0.005642	6	
	Nucleotide	Small GTP-binding protein	0.008774	7
	and	Nucleotide binding	0.004805	36
	Nucleotide	DNA recombination and DNA repair	0.007939	5
	metabolism	Purine nucleotide metabolic process	0.012207	8
	Purine nucleotide biosynthetic process	0.013449	7	
	Cytosol	0.001331	26	
	Intracellular transport	0.003014	15	
	Synaptic vesicle	0.014385	5	
Cellular transport	Establishment of protein localization	0.008444	15	
	Endomembrane system	0.00868	16	
	Integral to endoplasmic reticulum membrane	0.010956	4	
	Zymogen granule	0.013286	3	
STR	Repeat:TPR 10	0.011438	2	
Cell signal	Glycoprotein	0.012100	14	
	Signal	0.012629	12	
	Negative regulation of appetite or response to nutrient levels	0.014925	2	

Table S2 Gene functional annotation for down-regulated transcripts by EA (profile C-a, b and c in Fig. 3)

EA-Targeted Function	Name of sub-category	p-value	Number of transcripts	
Cortex	Regulation of growth	3.15E-04	14	
	Regulation of cell proliferation	4.53E-04	22	
	Regulation of organ growth	9.02E-04	5	
	Organ regeneration	0.001334	6	
	Regeneration	0.001347	8	
	Growth and Proliferation	Negative regulation of smooth muscle cell proliferation	0.001359	4
		Regulation of smooth muscle cell proliferation	0.001801	6
		Positive regulation of cell proliferation	0.009080	13
		Regulation of cardiac muscle growth or regulation of heart growth	0.011956	3
		Mitotic cell cycle	0.014662	9
Development	Tissue morphogenesis	0.001449	11	
	Tube development	0.008710	10	
	Positive regulation of multicellular organismal process	0.008933	10	
	Tyrosine protein kinase	0.001435	7	
	Tyrosine protein kinase, active site	0.003738	6	
Kinase	Protein tyrosine kinase activity	0.006982	7	
	Kinase	0.006915	15	
	Protein kinase, core	0.007412	12	
	Cyclin-dependent protein kinase holoenzyme complex	0.008807	3	
	Positive regulation of immune system process	0.001700	11	
Immune system	Regulation of leukocyte activation	0.002042	9	
	Positive regulation of lymphocyte activation	0.002505	7	
	Positive regulation of alpha-beta T cell	0.002654	4	

	differentiation		
	Positive regulation of T cell activation	0.003691	6
	Positive regulation of immune response	0.003872	8
	Regulation of lymphocyte activation	0.004346	8
	Regulation of T cell activation	0.005101	7
	Positive regulation of CD4-positive, alpha beta T cell differentiation	0.010056	3
	Regulation of adaptive immune response	0.012039	5
	Positive regulation of B cell activation	0.012058	4
	Immunoglobulin-like fold	0.012693	11
	Immunoglobulin subtype	0.013768	8
	T cell differentiation	0.014101	5
	Plasma membrane	0.008638	42
Cell adhesion	Cell adhesion	8.72E-04	17
	Extracellular region	0.002518	28
	Protein complex binding	0.004429	10
	Intracellular signaling cascade	0.005626	24
	Extracellular region part	0.009106	17
	Variant SH3	0.009152	4
Cell signal and Transport	Lipid transport	0.007389	7
	Lipid transporter activity	0.005452	5
	DNA binding	0.008310	31
	Src homology-3 domain	0.013131	7
	Transcription factor activity	0.010139	18
	Protein amino acid phosphorylation	0.014200	17
STR			
Response to stimulus	Response to endogenous stimulus	0.005533	7
	Response to hormone stimulus	0.014925	6
Proteinase	Proteinase inhibitor or bait region or alpha-2-macroglobulin	0.013300	2

**Table S3 Gene functional annotation for regulated transcripts by EA
($p \leq 1$, profile E-a in Fig. 3)**

EA-Targeted Function	Name of sub-category	p-value	Number of transcripts
Cortex			
	Structural constituent of ribosome	1.01E-17	30
	Ribosome	1.10E-17	31
	Ribonucleoprotein complex	6.56E-16	35
RNA and Ribosome	Ribosomal subunit	6.65E-04	7
	Cytosolic ribosome	0.004038	5
	Large ribosomal subunit	0.010777	4
	Ribosomal small subunit biogenesis	0.012186	3
	RNA processing	0.020564	11
	Cytoplasm	0.007598	29
	Translation	8.09E-17	34
Protein and protein processing	Protein biosynthesis	5.87E-07	12
	Translational elongation	3.46E-05	9
	Acetylation	4.06E-06	34
	Phosphoprotein	0.003938	49
	UBL conjugation	0.015003	9
	Glyceraldehyde-3-phosphate dehydrogenase activity	or 4.43E-05	6
	Oxidoreductase activity		
Metabolism	Glucose metabolic process	1.09E-04	11
	Generation of precursor metabolites and energy	0.004210	10
	NAD or NADH binding	0.001092	7
	Structural molecule activity	1.88E-12	33
Structure	Intracellular non-membrane-bounded organelle	2.52E-07	49
STR			
	Neuropeptide signaling pathway	1.69E-05	7
Cell Signal	Neuropeptide	1.74E-04	5
	Signal	1.77E-04	28
Secretion	Extracellular region	8.98E-04	22

	Secreted	9.94E-04	17
	Regulation of secretion	0.011457	7
	Glycoprotein	0.002002	30
Protein	Compositionally biased region:Ser-rich	0.006704	6
	Glycosylation site:N-linked (GlcNAc...)	0.008202	28
	Epidermis or Ectoderm development	0.008123	5
	Regulation of system process	0.011394	8
Development	Regulation of cellular localization	0.005438	8
	Regulation of muscle contraction	0.014215	4
	Regulation of neurological system process	0.014887	6

**Table S4 Gene functional annotation for regulated transcripts by EA
($p \leq 1$, profile E-b in Fig. 3)**

EA-Targeted Function	Name of sub-category	p-value	Number of transcripts	
Cortex				
Protein	Basic leucine zipper	1.25E-04	4	
	Basic-leucine zipper (bZIP) transcription factor	2.08E-04	5	
	CCAAT/enhancer-binding	3.06E-04	3	
	Protein dimerization activity	0.005100	10	
	Transcription factor activity	5.44E-04	13	
	Transcription regulator activity	5.74E-04	17	
	Sequence-specific DNA binding	9.94E-04	11	
	Regulation of transcription from RNA polymerase II promoter	0.002696	12	
	Transcription	Regulation of transcription, DNA-dependent or RNA metabolic process	0.003510	18
	Development	DNA binding	0.007374	17
Transcription activator activity		0.007890	7	
Transcription regulation		0.009472	11	
Transcription repressor activity		0.013137	6	
Positive regulation of developmental process		0.001294	9	
Regulation of cell development		0.005380	7	
Embryonic placenta development		0.006989	4	
Cytoskeleton		0.008597	3	
Positive regulation of cell differentiation		0.007651	7	
Positive regulation of macromolecule metabolic process		0.010296	13	
Signal	Positive regulation of JAK-STAT cascade	0.011649	3	
	Plasma membrane	0.006914	24	
	Extracellular region	0.014396	15	
	Immune response	0.007403	9	
STR				
Cell Signal	Response to hormone or endogenous stimulus	0.001222	10	

	Cellular response to hormone stimulus	0.006199	5
	Plasma membrane	0.001697	23
	Plasma membrane part	0.005853	15
	Phospholipid transport or lipid transporter activity	0.011272	3
	Response to organic substance	0.007872	12
Development	Regulation of ossification	0.008328	4
	Positive regulation of macromolecule metabolic process	0.009762	11

Table S5 Primers used in real-time PCR

Gene name	GenBank_ID	PCR fragment	Sequence of primers
GRIA2	NM_017261.2	nt2687-2768	5'-TACGGCATCGCCACACCTAA -3' 5'-AGACGCCTTGCTCACTGAGTTTC -3'
NOS3	NM_021838.2	nt1064-1157	5'-GCGGCTGGTACATGAGTTCAGA-3' 5'-AGATCCATGCAGACAGCCACA-3'
HRH4	NM_131909.1	nt325-504	5'-TGTGCACAGCATCCGTCTACAG-3' 5'-AAGAATCCGAAGCCAGAATCATTG-3'
PRL	NM_012629.1	nt399-538	5'-CCAAGATCGTGAGTTTATTGCCAAG-3' 5'-TCCAGGAGTGCACCAAACCTGAG-3'
OPRK1	NM_017167.2	nt609-704	5'-TCTGCATTTGGCTACTGGCATC-3' 5'-AGGAGCATTCAATGACATCCACA-3'
OLR1078	NM_207597.1	nt281-382	5'-ATGCAGGATGCATTACCCAGA-3' 5'-GACAGATGGCTACGTAACGGTCATA-3'
OLR1523	NM_001000713.1	nt803-896	5'-ACAAAGCCGTGTCCATCAGCTAC-3' 5'-TTCATGGCTGCCTGCATCTC-3'
PLA2G10	NM_017176.1	nt173-344	5'-CTCGATCGCCGATGGCTTA-3' 5'-TCCATGCACTTCCACGGGTA-3'

Figure Legends for Supplementary Materials

Figure S1 Dynamic Gene Network for genes in profile Aa-Af of Fig.3. The Dynamic Gene Network of the cortex is presented in S1A and S1B. The blue dots indicate the differentially regulated genes. The lines show the relationships between genes. The solid line denotes positive regulation, and the dashed line denotes negative regulation. The size of the dots indicates the capability of the gene to interact with others. This capability was quantified by “degree” (refer to “Materials and Methods”). The larger the degree, the more genes interacted with the corresponding gene were and the more important this gene was in the network.

Figure S1B

