Supplementary Table 5. Biological process analysis of differentially upregulated genes.

GO.ID	Term	Ontology	Count	Pop.Hits	List.Total	Pop.Total	Fold.Enrichment	Pvalue	FDR	Enrichment.Score	GENES
GO:0048856	anatomical structure development	Biological process	22	3218	76	23448	2.10925386804488	0.000406333936266738	0.436844883173175	3.3911169046785	SH3PXD2B//EFNA1//CCL12//C1GALT1//ADCYAP1//MEIS2//PRM2//YBX2//SYCP2//FOXK2//FNBP1//SEMA6B//ATOH8//MYH7//PPARA//PBX3//HOOK3//CDK13//POU2F1//LMO2//ITGB2//RCAN1
GO:0009987	cellular process	Biological process	57	13121	76	23448	1.34029418489444	0.000454073907314605	0.436844883173175	3.342873453472	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//HOOK3//CDK13//PUS3//RPUSD1//RASGRP4//ITGB2//CCL12//LMO2//RBL2//DNAJA1//ACTN4//STEAP3//SYCP2//MRAS//OLFR954//OLFR912//OLFR652//OLFR1390//SRGAP3//TAS2R134//HK3//MYH7//2310003H01RIK//PBX3//POU2F1//ZFP318//THAP7//ATOH8//MEIS2//YBX2//SMOK2B//UBE2W//HPD//SMPD4//GGT5//SH3PXD2B//FNBP1//PRM2//EPDR1//ADCYAP1//NPFF//RCAN1//RAB32//AGPAT4//C1GALT1//IFT81//SEMA6B//DCUN1D3//TBC1D15//SFXN3//SLC43A3//SLC5A9
GO:0032502	developmental process	Biological process	24	3757	76	23448	1.97088942745472	0.00055859303093856	0.436844883173175	3.25290448690177	SH3PXD2B//EFNA1//CCL12//C1GALT1//ADCYAP1//MEIS2//IFT81//ITGB2//PRM2//SEMA6B//ATOH8//YBX2//FOXK2//SYCP2//FNBP1//MYH7//PPARA//PBX3//HOOK3//CDK13//RASGRP4//POU2F1//LMO2//RCAN1
GO:0032099	negative regulation of appetite	Biological process	2	11	76	23448	56.0956937799043	0.000559524550052075	0.436844883173175	3.25218085333896	PPARA//NPFF
GO:0032096	negative regulation of response to food	Biological process	2	12	76	23448	51.4210526315789	0.000670019640561262	0.436844883173175	3.17391246645983	PPARA//NPFF
GO:0007275	multicellular organismal development	Biological process	22	3369	76	23448	2.01471622064958	0.000768301481410888	0.436844883173175	3.11446832942032	SH3PXD2B//EFNA1//CCL12//C1GALT1//ADCYAP1//MEIS2//FOXK2//SYCP2//FNBP1//SEMA6B//ATOH8//MYH7//PPARA//PBX3//HOOK3//CDK13//POU2F1//LMO2//ITGB2//RCAN1//IFT81//PRM2
GO:0001522	pseudouridine synthesis	Biological process	2	14	76	23448	44.0751879699248	0.000919940866831686	0.436844883173175	3.03624008790886	PUS3//RPUSD1
GO:0032105	negative regulation of response to extracellular stimulus	Biological process	2	16	76	23448	38.5657894736842	0.00120802394272032	0.436844883173175	2.91792445802592	PPARA//NPFF
GO:0032108	negative regulation of response to nutrient levels	Biological process	2	16	76	23448	38.5657894736842	0.00120802394272032	0.436844883173175	2.91792445802592	PPARA//NPFF
GO:0045596	negative regulation of cell differentiation	Biological process	6	368	76	23448	5.03032036613272	0.00124509673069586	0.436844883173175	2.90479690722242	EFNA1//PPARA//LMO2//HOOK3//RCAN1//ADCYAP1
GO:0032098	regulation of appetite	Biological process	2	17	76	23448	36.297213622291	0.00136622243631705	0.436844883173175	2.86447858689121	PPARA//NPFF
GO:0048731	system development	Biological process	19	2835	76	23448	2.06772486772487	0.00143625972197625	0.436844883173175	2.84276701857426	SH3PXD2B//EFNA1//CCL12//C1GALT1//ADCYAP1//MEIS2//SYCP2//FNBP1//SEMA6B//ATOH8//MYH7//PPARA//PBX3//HOOK3//CDK13//POU2F1//LMO2//ITGB2//RCAN1

GO:0034641	cellular nitrogen compound metabolic process	Biological process	27	4760	76	23448	1.7500442282176	0.00145961175812755	0.436844883173175	2.83576264676714	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//MRAS//MYH7//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//HPD//GGT5//ADCYAP1//PRM2//TBC1D15//SRGAP3//ITGB2
GO:0032095	regulation of response to food	Biological process	2	18	76	23448	34.280701754386	0.00153377748532786	0.436844883173175	2.81423764162809	PPARA//NPFF
GO:0032501	multicellular organismal process	Biological process	30	5558	76	23448	1.66530936914074	0.0015778168185884	0.436844883173175	2.80194341893023	SH3PXD2B//EFNA1//CCL12//C1GALT1//ADCYAP1//TAS2R134//MEIS2//MYH7//PBX3//IFT81//ITGB2//PRM2//SEMA6B//ATOH8//DNAJA1//YBX2//FOXK2//SYCP2//FNBP1//OLFR954//OLFR912//OLFR652//OLFR1390//PPARA//NPFF//HOOK3//CDK13//POU2F1//LMO2//RCAN1
GO:0006807	nitrogen compound metabolic process	Biological process	27	4850	76	23448	1.71756918068367	0.00194535788467433	0.504941955940781	2.71100049046091	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//MRAS//MYH7//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//HPD//GGT5//ADCYAP1//PRM2//TBC1D15//SRGAP3//ITGB2
GO:0032094	response to food	Biological process	2	22	76	23448	28.0478468899522	0.00229635348634977	0.560985648753564	2.63896125854114	PPARA//NPFF
GO:0006139	nucleobase-containing compound metabolic process	Biological process	25	4427	76	23448	1.74229905008738	0.00253319372953153	0.584464086596914	2.59633159566178	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//MRAS//MYH7//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//ADCYAP1//PRM2//TBC1D15//SRGAP3//ITGB2
GO:0030154	cell differentiation	Biological process	16	2336	76	23448	2.11319394376352	0.00296031556338369	0.647062659722761	2.52866199159934	EFNA1//PRM2//YBX2//PPARA//ADCYAP1//SH3PXD2B//LMO2//PBX3//RCAN1//HOOK3//POU2F1//IFT81//SEMA6B//ATOH8//C1GALT1//RASGRP4
GO:0032104	regulation of response to extracellular stimulus	Biological process	2	27	76	23448	22.8538011695906	0.00345289603295307	0.682851296421624	2.46181649810422	PPARA//NPFF
GO:0032107	regulation of response to nutrient levels	Biological process	2	27	76	23448	22.8538011695906	0.00345289603295307	0.682851296421624	2.46181649810422	PPARA//NPFF
GO:0010721	negative regulation of cell development	Biological process	3	96	76	23448	9.64144736842105	0.00376643743036249	0.71100066583161	2.42406924285346	EFNA1//HOOK3//ADCYAP1
GO:0051093	negative regulation of developmental process	Biological process	6	466	76	23448	3.97244183419923	0.00403806856990294	0.729134729165518	2.39382631063318	EFNA1//PPARA//LMO2//HOOK3//RCAN1//ADCYAP1
GO:0044237	cellular metabolic process	Biological process	36	7615	76	23448	1.45856170300999	0.00479301965919554	0.829392110193295	2.31939078968907	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//DNAJA1//HK3//MRAS//MYH7//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//SMOK2B//UBE2W//HPD//SMPD4//GGT5//SH3PXD2B//ADCYAP1//AGPAT4//C1GALT1//PRM2//TBC1D15

											//SRGAP3//RCAN1//ITGB2
GO:0032102	negative regulation of response to external stimulus	Biological process	3	107	76	23448	8.65027053615347	0.00510102190878276	0.847381759486992	2.29234281117906	ADCYAP1//PPARA//NPFF
GO:0048869	cellular developmental process	Biological process	16	2484	76	23448	1.98728705822527	0.0054165980689124	0.865197376161277	2.26627338943212	EFNA1//PRM2//YBX2//PPARA//ADCYAP1//IFT81//SEMA6B//ATOH8//C1GALT1//RASGRP4//SH3PXD2B//LMO2//PBX3//RCAN1//HOOK3//POU2F1
GO:0006954	inflammatory response	Biological process	5	356	76	23448	4.33323477232407	0.0060093662020203	0.870971150452339	2.22117132990742	ITGB2//ADCYAP1//SAA3//CCL12//GGT5
GO:0044238	primary metabolic process	Biological process	36	7712	76	23448	1.44021620441144	0.00602071546699589	0.870971150452339	2.22035189663166	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//DNAJA1//HK3//MRAS//MYH7//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//SMOK2B//2010106G01RIK//UBE2W//HPD//SMPD4//GGT5//ADCYAP1//AGPAT4//PLD3//C1GALT1//PRM2//TBC1D15//SRGAP3//ITGB2
GO:0002027	regulation of heart rate	Biological process	2	36	76	23448	17.140350877193	0.0060819078649453	0.870971150452339	2.21596016328576	NPFF//MYH7
GO:0090304	nucleic acid metabolic process	Biological process	20	3540	76	23448	1.74308652988403	0.00779005582993255	1	2.10845942980565	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//PRM2//ITGB2
GO:0060078	regulation of postsynaptic membrane potential	Biological process	2	42	76	23448	14.6917293233083	0.00820844286419564	1	2.08573922042331	NPFF//ADCYAP1
GO:0009611	response to wounding	Biological process	6	569	76	23448	3.25335306632134	0.0103740348946621	1	1.98405229552368	ITGB2//ADCYAP1//SAA3//CCL12//GGT5//PPARA
GO:0019219	regulation of nucleobase-containing compound metabolic process	Biological process	17	2977	76	23448	1.7618230999063	0.0132869156238483	1	1.87657582289529	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//ADCYAP1//TBC1D15//SRGAP3//LMO2//ITGB2//CDK13
GO:0009451	RNA modification	Biological process	2	54	76	23448	11.4269005847953	0.0133056914820755	1	1.87596255072204	PUS3//RPUSD1
GO:0006096	glycolysis	Biological process	2	55	76	23448	11.2191387559809	0.0137790953362318	1	1.86077929501038	PPARA//HK3
GO:0055072	iron ion homeostasis	Biological process	2	55	76	23448	11.2191387559809	0.0137790953362318	1	1.86077929501038	STEAP3//SFXN3
GO:0008152	metabolic process	Biological process	40	9272	76	23448	1.33100222514872	0.0139662166036513	1	1.85492122671996	PAPD7//EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//DNAJA1//HK3//HPD//STEAP3//MRAS//MYH7//2310003H01RIK//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//SMOK2B//2010106G01RIK//UBE2W//SMPD4//GGT5//SH3PXD2B//ADCYAP1//AGPAT4//PLD3//C1GALT1//PRM2//TBC1D15//SRGAP3//RCAN1//ITGB2//RASGRP4
GO:0008015	blood circulation	Biological process	4	286	76	23448	4.31505336768495	0.0139985144766555	1	1.85391804923762	MYH7//ADCYAP1//NPFF//PPARA
GO:0003013	circulatory system process	Biological process	4	287	76	23448	4.30001833852925	0.0141622558208482	1	1.84886756497126	MYH7//ADCYAP1//NPFF//PPARA

GO:0051171	regulation of nitrogen compound metabolic process	Biological process	17	3009	76	23448	1.74308652988403	0.0146739674323446	1	1.83345244914081	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//ADCYAP1//TBC1D15//SRGAP3//ITGB2//LMO2//CDK13
GO:0019953	sexual reproduction	Biological process	5	449	76	23448	3.43570507560661	0.0153164834145943	1	1.81484093502625	IFT81//DNAJA1//PRM2//YBX2//SYCP2
GO:0044249	cellular biosynthetic process	Biological process	21	4041	76	23448	1.60332903528309	0.0158865133569857	1	1.79897140776271	PAPD7//EFNA1//PPARA//FOXK2//LMO2//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//GGT5//ADCYAP1//AGPAT4//UPF3B//C1GALT1//ITGB2//SMPD4//CDK13
GO:0007283	spermatogenesis	Biological process	4	298	76	23448	4.14129282938891	0.0160442438581288	1	1.79468074575329	PRM2//YBX2//IFT81//DNAJA1
GO:0048232	male gamete generation	Biological process	4	298	76	23448	4.14129282938891	0.0160442438581288	1	1.79468074575329	IFT81//DNAJA1//PRM2//YBX2
GO:0016070	RNA metabolic process	Biological process	17	3049	76	23448	1.72021888108267	0.0165669165624862	1	1.78075831502716	EFNA1//PPARA//FOXK2//UPF3B//CDK13//PUS3//RPUSD1//LMO2//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//ITGB2
GO:0048513	organ development	Biological process	13	2099	76	23448	1.91083473333166	0.0167928838122577	1	1.7748747168336	ADCYAP1//MEIS2//SH3PXD2B//C1GALT1//EFNA1//SYCP2//MYH7//PPARA//HOOK3//CDK13//POU2F1//LMO2//RCAN1
GO:0051100	negative regulation of binding	Biological process	2	65	76	23448	9.49311740890688	0.0189031429153361	1	1.72346598221247	PPARA//YBX2
GO:0031326	regulation of cellular biosynthetic process	Biological process	16	2848	76	23448	1.73329390892963	0.0189145556902807	1	1.72320385598507	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//ADCYAP1//UPF3B//ITGB2//LMO2//CDK13
GO:0001525	angiogenesis	Biological process	4	315	76	23448	3.91779448621554	0.0192504000823291	1	1.71556024009095	EFNA1//ITGB2//CCL12//C1GALT1
GO:2000112	regulation of cellular macromolecule biosynthetic process	Biological process	15	2628	76	23448	1.76099495313627	0.0202932022278477	1	1.69264941673439	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//UPF3B//LMO2//ITGB2//CDK13
GO:0006007	glucose catabolic process	Biological process	2	68	76	23448	9.07430340557276	0.0205741368688245	1	1.68667837536087	HK3//PPARA
GO:0031589	cell-substrate adhesion	Biological process	3	180	76	23448	5.14210526315789	0.0207752955897441	1	1.68245278838229	ITGB2//EPDR1//EFNA1
GO:0009889	regulation of biosynthetic process	Biological process	16	2883	76	23448	1.7122514924147	0.0210062268023227	1	1.67765194978794	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//ADCYAP1//UPF3B//ITGB2//LMO2//CDK13
GO:0009058	biosynthetic process	Biological process	21	4158	76	23448	1.55821371610845	0.0214369193961027	1	1.66883762501471	PAPD7//EFNA1//PPARA//FOXK2//LMO2//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//GGT5//ADCYAP1//AGPAT4//UPF3B//C1GALT1//ITGB2//SMPD4//CDK13
GO:0006355	regulation of transcription, DNA-dependent	Biological process	14	2414	76	23448	1.78929926307068	0.0220538978710086	1	1.6565146409234	EFNA1//PPARA//FOXK2//POU2F1//THAP7//LMO2//MEIS2//ITGB2//CDK13//PBX3//RBL2//YBX2//ZFP318//ATOH8
GO:0019320	hexose catabolic process	Biological process	2	71	76	23448	8.69088213491475	0.0223045521542609	1	1.65160649239035	HK3//PPARA
GO:0007264	small GTPase mediated signal transduction	Biological process	5	499	76	23448	3.09144604999473	0.0230021176078838	1	1.63823218037003	RASGRP4//MRAS//RAB32

GO:2001141	regulation of RNA biosynthetic process	Biological process	14	2431	76	23448	1.77678668081145	0.023282198819494	1	1.63297600640709	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//LMO2//ITGB2//CDK13
GO:0072358	cardiovascular system development	Biological process	6	684	76	23448	2.70637119113573	0.0235383653088266	1	1.62822370130599	EFNA1//CCL12//C1GALT1//SH3PXD2B//MYH7//ITGB2
GO:0072359	circulatory system development	Biological process	6	684	76	23448	2.70637119113573	0.0235383653088266	1	1.62822370130599	EFNA1//CCL12//C1GALT1//SH3PXD2B//MYH7//ITGB2
GO:0022414	reproductive process	Biological process	7	879	76	23448	2.45697862403449	0.0237093515876742	1	1.62508032310936	ADCYAP1//ZFP318//SYCP2//IFT81//DNAJA1//PRM2//YBX2
GO:0032504	multicellular organism reproduction	Biological process	5	505	76	23448	3.05471599791558	0.0240658359536342	1	1.61859904802174	ADCYAP1//IFT81//DNAJA1//PRM2//YBX2
GO:0048609	multicellular organismal reproductive process	Biological process	5	505	76	23448	3.05471599791558	0.0240658359536342	1	1.61859904802174	ADCYAP1//IFT81//DNAJA1//PRM2//YBX2
GO:0046365	monosaccharide catabolic process	Biological process	2	74	76	23448	8.33854907539118	0.0240931120004325	1	1.61810710048623	HK3//PPARA
GO:0000003	reproduction	Biological process	7	882	76	23448	2.44862155388471	0.0240990138540236	1	1.61800072864996	ADCYAP1//ZFP318//SYCP2//IFT81//DNAJA1//PRM2//YBX2
GO:0010556	regulation of macromolecule biosynthetic process	Biological process	15	2694	76	23448	1.71785253780331	0.0248129933596661	1	1.60532084067869	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//UPF3B//LMO2//ITGB2//CDK13
GO:0007049	cell cycle	Biological process	8	1095	76	23448	2.25407354001442	0.0251981878403825	1	1.59863069093357	RBL2//PAPD7//ZFP318//SYCP2//DCUN1D3//ADCYAP1//STEAP3//CDK13
GO:0007286	spermatid development	Biological process	2	77	76	23448	8.01367053998633	0.025938558231869	1	1.586054167394	PRM2//YBX2
GO:0045595	regulation of cell differentiation	Biological process	7	902	76	23448	2.3943283930447	0.0268108833178415	1	1.57168887741045	EFNA1//PPARA//ADCYAP1//SH3PXD2B//LMO2//HOOK3//RCAN1
GO:0009056	catabolic process	Biological process	11	1776	76	23448	1.91091749644381	0.0275186260058141	1	1.56037325404807	UPF3B//HK3//MRAS//MYH7//HPD//SMPD4//PLD3//TBC1D15//ADCYAP1//SRGAP3//PPARA
GO:0006351	transcription, DNA-dependent	Biological process	14	2485	76	23448	1.73817642698295	0.0275302107020263	1	1.56019046472809	EFNA1//PPARA//FOXK2//LMO2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//ITGB2//CDK13
GO:0034645	cellular macromolecule biosynthetic process	Biological process	17	3232	76	23448	1.62281787389265	0.0278027297127386	1	1.55591256232003	PAPD7//EFNA1//PPARA//FOXK2//LMO2//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//UPF3B//C1GALT1//ITGB2//CDK13
GO:0050768	negative regulation of neurogenesis	Biological process	2	80	76	23448	7.71315789473684	0.0278396510360596	1	1.55533621281376	ADCYAP1//HOOK3
GO:0051252	regulation of RNA metabolic process	Biological process	14	2497	76	23448	1.7298231562085	0.0285485111783677	1	1.54441653553999	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//LMO2//ITGB2//CDK13
GO:0032774	RNA biosynthetic process	Biological process	14	2503	76	23448	1.72567655655319	0.0290681145633826	1	1.53658313683206	EFNA1//PPARA//FOXK2//LMO2//PBX3//POU2F1//RBL2//ZFP318//THAP7//ATOH8//MEIS2//YBX2//ITGB2//CDK13
GO:0048515	spermatid differentiation	Biological process	2	82	76	23448	7.52503209242619	0.0291373569635716	1	1.53554984543478	PRM2//YBX2
GO:0048610	cellular process involved in reproduction	Biological process	4	369	76	23448	3.34445870774497	0.0319436100166995	1	1.49561600486197	ZFP318//SYCP2//PRM2//YBX2
GO:0001821	histamine secretion	Biological process	1	10	76	23448	30.8526315789474	0.0319495055956742	1	1.49553585796667	ADCYAP1
GO:0003188	heart valve formation	Biological process	1	10	76	23448	30.8526315789474	0.0319495055956742	1	1.49553585796667	EFNA1

GO:0006570	tyrosine metabolic process	Biological process	1	10	76	23448	30.8526315789474	0.0319495055956742	1	1.49553585796667	HPD
GO:0010719	negative regulation of epithelial to mesenchymal transition	Biological process	1	10	76	23448	30.8526315789474	0.0319495055956742	1	1.49553585796667	EFNA1
GO:0003006	developmental process involved in reproduction	Biological process	4	370	76	23448	3.33541963015647	0.0322157164028976	1	1.49193220650712	ADCYAP1//PRM2 //YBX2//SYCP2
GO:0008016	regulation of heart contraction	Biological process	2	88	76	23448	7.01196172248804	0.0331720476022552	1	1.47922772007188	MYH7//NPFF
GO:0031323	regulation of cellular metabolic process	Biological process	19	3822	76	23448	1.53375196232339	0.0336724592310317	1	1.47272516423369	EFNA1//PPARA //FOXK2//MEIS2 //PBX3//POU2F1 //RBL2//YBX2 //ZFP318//THAP7 //ATOH8//ADCYAP1 //UPF3B//TBC1D15 //SRGAP3//RCAN1 //ITGB2//LMO2 //CDK13
GO:0009059	macromolecule biosynthetic process	Biological process	17	3316	76	23448	1.58170909783506	0.0345888980780474	1	1.46106327337871	PAPD7//EFNA1 //PPARA//FOXK2 //LMO2//PBX3 //POU2F1//RBL2 //ZFP318//THAP7 //ATOH8//MEIS2 //YBX2//UPF3B //C1GALT1//ITGB2 //CDK13
GO:0009991	response to extracellular stimulus	Biological process	3	220	76	23448	4.20717703349282	0.0347350769885942	1	1.45923173419614	PPARA//NPFF //RASGRP4
GO:0055080	cation homeostasis	Biological process	4	380	76	23448	3.24764542936288	0.035012166220668	1	1.45578101838153	ADCYAP1//NPFF //STEAP3//SFXN3
GO:0002674	negative regulation of acute inflammatory response	Biological process	1	11	76	23448	28.0478468899522	0.0350885037002363	1	1.45483515126553	ADCYAP1
GO:0010885	regulation of cholesterol storage	Biological process	1	11	76	23448	28.0478468899522	0.0350885037002363	1	1.45483515126553	PPARA
GO:0022617	extracellular matrix disassembly	Biological process	1	11	76	23448	28.0478468899522	0.0350885037002363	1	1.45483515126553	SH3PXD2B
GO:0030730	sequestering of triglyceride	Biological process	1	11	76	23448	28.0478468899522	0.0350885037002363	1	1.45483515126553	PPARA
GO:0046321	positive regulation of fatty acid oxidation	Biological process	1	11	76	23448	28.0478468899522	0.0350885037002363	1	1.45483515126553	PPARA
GO:0070252	actin-mediated cell contraction	Biological process	1	11	76	23448	28.0478468899522	0.0350885037002363	1	1.45483515126553	MYH7
GO:0019233	sensory perception of pain	Biological process	2	92	76	23448	6.7070938215103	0.0359763216214746	1	1.44398324291267	NPFF//ADCYAP1
GO:0046164	alcohol catabolic process	Biological process	2	92	76	23448	6.7070938215103	0.0359763216214746	1	1.44398324291267	HK3//PPARA
GO:0043542	endothelial cell migration	Biological process	2	93	76	23448	6.63497453310696	0.0366913058412884	1	1.43543683145545	EFNA1//ITGB2
GO:0050794	regulation of cellular process	Biological process	34	8027	76	23448	1.30682630333152	0.0368159394190156	1	1.43396411331061	EFNA1//PPARA //FOXK2//RBL2 //MRAS//OLFR954 //OLFR912//OLFR652 //OLFR1390 //SRGAP3 //TAS2R134 //RASGRP4//MEIS2 //PBX3//POU2F1 //YBX2//ZFP318 //THAP7//ATOH8 //STEAP3//ADCYAP1 //NPFF//ITGB2 //RCAN1//RAB32 //UPF3B//ACTN4 //DCUN1D3 //DNAJA1//TBC1D15 //SH3PXD2B//LMO2 //HOOK3//CDK13
GO:0002526	acute inflammatory response	Biological process	2	94	76	23448	6.56438969764838	0.037411771586822	1	1.42699172585248	ADCYAP1//SAA3
GO:0061351	neural precursor cell proliferation	Biological process	2	94	76	23448	6.56438969764838	0.037411771586822	1	1.42699172585248	HOOK3//ADCYAP1
GO:0065009	regulation of molecular function	Biological process	11	1871	76	23448	1.81389068609525	0.0381970087233191	1	1.41797064614123	EFNA1//ADCYAP1 //PPARA//TBC1D15 //SRGAP3//RBL2 //RCAN1//RASGRP4 //FOXK2//ITGB2 //YBX2

GO:0002087	regulation of respiratory gaseous exchange by neurological system process	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	PBX3
GO:0002862	negative regulation of inflammatory response to antigenic stimulus	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	ADCYAP1
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	EFNA1
GO:0010878	cholesterol storage	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	PPARA
GO:0010888	negative regulation of lipid storage	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	PPARA
GO:0034260	negative regulation of GTPase activity	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	ADCYAP1
GO:0043267	negative regulation of potassium ion transport	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	ADCYAP1
GO:0051608	histamine transport	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	ADCYAP1
GO:0060123	regulation of growth hormone secretion	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	ADCYAP1
GO:0061001	regulation of dendritic spine morphogenesis	Biological process	1	12	76	23448	25.7105263157895	0.0382174567965705	1	1.41773821670447	EFNA1
GO:0007276	gamete generation	Biological process	4	391	76	23448	3.15627944541661	0.0382470983532805	1	1.41740150735897	IFT81//DNAJA1//PRM2//YBX2
GO:0010468	regulation of gene expression	Biological process	15	2859	76	23448	1.6187109957475	0.0394406566584796	1	1.40405586298082	EFNA1//PPARA//FOXK2//MEIS2//PBX3//POU2F1//RBL2//YBX2//ZFP318//THAP7//ATOH8//UPF3B//LMO2//ITGB2//CDK13
GO:0030595	leukocyte chemotaxis	Biological process	2	97	76	23448	6.36136733586544	0.0396056388884611	1	1.4022429766048	CCL12//ITGB2
GO:0048514	blood vessel morphogenesis	Biological process	4	396	76	23448	3.11642743221691	0.039772691286642	1	1.40041502074668	EFNA1//CCL12//C1GALT1//ITGB2
GO:0044275	cellular carbohydrate catabolic process	Biological process	2	98	76	23448	6.29645542427497	0.0403476126859075	1	1.39418215680336	HK3//PPARA
GO:0044282	small molecule catabolic process	Biological process	3	234	76	23448	3.95546558704453	0.0405242831059754	1	1.39228465928939	HK3//HPD//PPARA
GO:0006684	sphingomyelin metabolic process	Biological process	1	13	76	23448	23.7327935222672	0.0413363966021454	1	1.38366738460307	SMPD4
GO:0007512	adult heart development	Biological process	1	13	76	23448	23.7327935222672	0.0413363966021454	1	1.38366738460307	MYH7
GO:0009074	aromatic amino acid family catabolic process	Biological process	1	13	76	23448	23.7327935222672	0.0413363966021454	1	1.38366738460307	HPD
GO:0044065	regulation of respiratory system process	Biological process	1	13	76	23448	23.7327935222672	0.0413363966021454	1	1.38366738460307	PBX3
GO:0006184	GTP catabolic process	Biological process	4	406	76	23448	3.03966813585688	0.0429274857437193	1	1.36726454733713	TBC1D15//ADCYAP1//SRGAP3//MRAS
GO:0007218	neuropeptide signaling pathway	Biological process	2	102	76	23448	6.04953560371517	0.0433678344500723	1	1.36283226357558	ADCYAP1//NPFF
GO:0009725	response to hormone stimulus	Biological process	4	409	76	23448	3.01737228155964	0.0439008730866716	1	1.35752684256077	PPARA//SERPINA3I//RCAN1//LMO2
GO:0030252	growth hormone secretion	Biological process	1	14	76	23448	22.0375939849624	0.0444453547356313	1	1.35217362317757	ADCYAP1
GO:0031122	cytoplasmic microtubule organization	Biological process	1	14	76	23448	22.0375939849624	0.0444453547356313	1	1.35217362317757	HOOK3
GO:0035112	genitalia morphogenesis	Biological process	1	14	76	23448	22.0375939849624	0.0444453547356313	1	1.35217362317757	SYCP2
GO:0043584	nose development	Biological process	1	14	76	23448	22.0375939849624	0.0444453547356313	1	1.35217362317757	POU2F1
GO:0045022	early endosome to late endosome transport	Biological process	1	14	76	23448	22.0375939849624	0.0444453547356313	1	1.35217362317757	HOOK3

GO:0060251	regulation of glial cell proliferation	Biological process	1	14	76	23448	22.0375939849624	0.0444453547356313	1	1.35217362317757	ADCYAP1
GO:0046039	GTP metabolic process	Biological process	4	414	76	23448	2.98093058733791	0.0455508210984407	1	1.34150379003439	MRAS//TBC1D15//ADCYAP1//SRGAP3
GO:0002548	monocyte chemotaxis	Biological process	1	15	76	23448	20.5684210526316	0.0475443627172003	1	1.32290096949312	CCL12
GO:0010869	regulation of receptor biosynthetic process	Biological process	1	15	76	23448	20.5684210526316	0.0475443627172003	1	1.32290096949312	PPARA
GO:0043043	peptide biosynthetic process	Biological process	1	15	76	23448	20.5684210526316	0.0475443627172003	1	1.32290096949312	GGT5
GO:2000677	regulation of transcription regulatory region DNA binding	Biological process	1	15	76	23448	20.5684210526316	0.0475443627172003	1	1.32290096949312	PPARA
GO:0003015	heart process	Biological process	2	109	76	23448	5.66103331723805	0.048848462508365	1	1.31114910102691	MYH7//NPFF
GO:0060047	heart contraction	Biological process	2	109	76	23448	5.66103331723805	0.048848462508365	1	1.31114910102691	MYH7//NPFF
GO:0090276	regulation of peptide hormone secretion	Biological process	2	110	76	23448	5.60956937799043	0.0496510585097658	1	1.30407148835591	NPFF//ADCYAP1