

Supplementary Table S12. Biological processes enriched for Differentially expressed genes (n = 213 genes) between Peanut baseline and Peanut 4 hrs.

Term	Count	%	Pathways	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR	Term
GO:0002544	5	2.56410256	chronic inflammatory response	1.35E-06	VNN1, THBS1	175	9	16792	53.3079365	0.00158899	0.00107272	0.0010709	GO:0002544
GO:0006954	17	8.71794872	inflammatory response	2.14E-06	ORM1, CEBPE	175	379	16792	4.30401809	0.00252326	0.00107272	0.0010709	GO:0006954
GO:0042742	11	5.64102564	defense response to bacterium	2.73E-06	CEBPB, CLEC4	175	145	16792	7.27929064	0.003213	0.00107272	0.0010709	GO:0042742
GO:0045087	17	8.71794872	innate immune response	1.06E-05	CRISP3, HMG	175	430	16792	3.79354153	0.01245182	0.00313248	0.00312717	GO:0045087
GO:0051591	6	3.07692308	response to cAMP	1.10E-04	THBD, PER1, I	175	46	16792	12.5157764	0.12133222	0.02586826	0.02582442	GO:0051591
GO:0032496	9	4.61538462	response to lipopolysaccharide	3.14E-04	THBD, GIB6, I	175	164	16792	5.26578397	0.30984934	0.06179785	0.06169311	GO:0032496
GO:0015939	3	1.53846154	pantothenate metabolic process	0.00286915	VNN1, VNN2,	175	8	16792	35.9828571	0.96630712	0.48365749	0.48283773	GO:0015939
GO:0006955	12	6.15384615	immune response	0.00451462	CEBPB, IL18R,	175	421	16792	2.73503902	0.99520083	0.66018742	0.65906845	GO:0006955
GO:0071222	6	3.07692308	cellular response to lipopolysaccharide	0.00543921	CEBPB, ARG1,	175	113	16792	5.09491783	0.99951085	0.66018742	0.65906845	GO:0071222
GO:0045444	5	2.56410256	fat cell differentiation	0.00695772	NR4A2, SOCS	175	73	16792	6.57221135	0.9997358	0.66018742	0.65906845	GO:0045444
GO:0006953	4	2.05128205	acute-phase response	0.00760164	CEBPB, ORM1,	175	39	16792	9.8414652	0.99987711	0.66018742	0.65906845	GO:0006953
GO:0030890	4	2.05128205	positive regulation of B cell proliferation	0.00760164	BST1, PELL1, I	175	39	16792	9.8414652	0.99987711	0.66018742	0.65906845	GO:0030890
GO:0002526	3	1.53846154	acute inflammatory response	0.00772516	VNN1, S100A,	175	13	16792	22.1432967	0.9998939	0.66018742	0.65906845	GO:0002526
GO:0050900	6	3.07692308	leukocyte migration	0.00883137	THBD, FPR1, I	175	122	16792	4.71906323	0.99997155	0.66018742	0.65906845	GO:0050900
GO:0006768	3	1.53846154	biotin metabolic process	0.00895169	VNN1, VNN2,	175	14	16792	20.5616327	0.99997535	0.66018742	0.65906845	GO:0006768
GO:0006807	3	1.53846154	nitrogen compound metabolic process	0.00895169	VNN1, VNN2,	175	14	16792	20.5616327	0.99997535	0.66018742	0.65906845	GO:0006807
GO:0014002	3	1.53846154	astrocyte development	0.01164539	S100A9, TLR4	175	16	16792	17.9914286	0.99999901	0.79326347	0.79191896	GO:0014002
GO:0006928	5	2.56410256	movement of cell or subcellular component	0.01224339	VNN1, VNN2,	175	86	16792	5.57873754	0.99999951	0.79326347	0.79191896	GO:0006928
GO:0009416	3	1.53846154	response to light stimulus	0.01310902	DUSP1, SLC11,	175	17	16792	16.9331092	0.99999983	0.79326347	0.79191896	GO:0009416
GO:0006909	4	2.05128205	phagocytosis	0.01344514	ANXA3, SLC11,	175	48	16792	7.99619048	0.99999988	0.79326347	0.79191896	GO:0006909
GO:0042542	4	2.05128205	response to hydrogen peroxide	0.01582548	NR4A3, DUSP	175	51	16792	7.52582633	0.99999999	0.8894096	0.88790213	GO:0042542
GO:0050829	4	2.05128205	defense response to Gram-negative bacterium	0.01935255	SLC11A1, HMG	175	55	16792	6.97849351	1	0.99915182	GO:0050829	
GO:0071345	3	1.53846154	cellular response to cytokine stimulus	0.02152643	NFKBIA, IL18F	175	22	16792	13.0846753	1	0.99915182	GO:0071345	
GO:0048661	4	2.05128205	positive regulation of smooth muscle cell proliferat	0.02431812	NR4A3, NAM	175	60	16792	6.39695238	1	0.99915182	GO:0048661	
GO:0001819	3	1.53846154	positive regulation of cytokine production	0.0253757	SLC11A1, PEL	175	24	16792	11.9942857	1	0.99915182	GO:0001819	
GO:0042327	3	1.53846154	positive regulation of phosphorylation	0.02739735	THBS1, AREG,	175	25	16792	11.5145143	1	0.99915182	GO:0042327	
GO:0060326	4	2.05128205	cell chemotaxis	0.02990673	NOV, FPR1, I	175	65	16792	5.90487912	1	0.99915182	GO:0060326	
GO:0030593	4	2.05128205	neutrophil chemotaxis	0.03109889	S100A12, TRE	175	66	16792	5.81541126	1	0.99915182	GO:0030593	
GO:0007200	4	2.05128205	phospholipase C-activating G-protein coupled rece	0.03109889	FPR1, FPR2, C	175	66	16792	5.81541126	1	0.99915182	GO:0007200	
GO:0050832	3	1.53846154	defense response to fungus	0.03162704	S100A12, S10	175	27	16792	10.6615873	1	0.99915182	GO:0050832	
GO:0006952	4	2.05128205	defense response	0.03231573	CRISP3, HP, IF	175	67	16792	5.72861407	1	0.99915182	GO:0006952	
GO:0043388	3	1.53846154	positive regulation of DNA binding	0.03383211	PLAUR, HMG1,	175	28	16792	10.2808163	1	0.99915182	GO:0043388	
GO:0016339	3	1.53846154	calcium-dependent cell-cell adhesion via plasma m	0.03383211	CDH2, NRXN1,	175	28	16792	10.2808163	1	0.99915182	GO:0016339	
GO:0006935	5	2.56410256	chemotaxis	0.03814758	PLAUR, FPR1,	175	122	16792	3.93255269	1	0.99915182	GO:0006935	
GO:0050729	4	2.05128205	positive regulation of inflammatory response	0.04013087	S100A12, S10	175	73	16792	5.25776908	1	0.99915182	GO:0050729	
GO:0050873	3	1.53846154	brown fat cell differentiation	0.0432203	CEBPB, RGS2,	175	32	16792	8.99571429	1	0.99915182	GO:0050873	
GO:0014066	4	2.05128205	regulation of phosphatidylinositol 3-kinase signalin	0.04730592	KL, IRS2, ERE	175	78	16792	4.9207326	1	0.99915182	GO:0014066	
GO:0051092	5	2.56410256	positive regulation of NF-kappaB transcription fact	0.04965678	NFKBIA, LIOX	175	133	16792	3.60730397	1	0.99915182	GO:0051092	
GO:0007605	5	2.56410256	sensory perception of sound	0.04965678	NFKBIA, LIOX	175	133	16792	3.60730397	1	0.99915182	GO:0007605	
GO:0007155	10	5.12820513	cell adhesion	0.04991136	CNTNAP3, CD	175	459	16792	2.09050731	1	0.99915182	GO:0007155	
GO:0048013	4	2.05128205	ephrin receptor signaling pathway	0.05999703	SDC2, MMP9,	175	86	16792	4.46299003	1	0.99915182	GO:0048013	
GO:0001541	3	1.53846154	ovarian follicle development	0.07019563	FOXCl, CEBP1	175	42	16792	6.85387755	1	0.99915182	GO:0001541	
GO:0045892	10	5.12820513	negative regulation of transcription, DNA-templated	0.07568225	ZMYND15, PE	175	499	16792	1.92293158	1	0.99915182	GO:0045892	
GO:0043434	3	1.53846154	response to peptide hormone	0.0761113	AREG, CD55,	175	44	16792	6.54233766	1	0.99915182	GO:0043434	
GO:0015701	3	1.53846154	bicarbonate transport	0.0761113	CA4, SLC26A	175	44	16792	6.54233766	1	0.99915182	GO:0015701	
GO:0050885	3	1.53846154	neuromuscular process controlling balance	0.0821788	NR4A3, NRXN	175	46	16792	6.2578882	1	0.99915182	GO:0050885	
GO:0032729	3	1.53846154	positive regulation of interferon-gamma production	0.0821788	SLC11A1, TLR	175	46	16792	6.2578882	1	0.99915182	GO:0032729	
GO:0014070	3	1.53846154	response to organic cyclic compound	0.09154579	ACSL1, NAMF	175	49	16792	5.87475219	1	0.99915182	GO:0014070	
GO:0002576	4	2.05128205	platelet degranulation	0.09156261	SRGN, ORM1,	175	103	16792	3.72638003	1	0.99915182	GO:0002576	
GO:0007568	5	2.56410256	aging	0.09305958	KL, BCL2A1, A	175	165	16792	2.90770563	1	0.99915182	GO:0007568	
GO:0007165	18	9.23076923	signal transduction	0.09402788	GPR27, TNFA	175	1161	16792	1.48766334	1	0.99915182	GO:0007165	
GO:0000187	4	2.05128205	activation of MAPK activity	0.09981993	FPR1, PROK2,	175	107	16792	3.5870761	1	0.99915182	GO:0000187	
GO:0021766	3	1.53846154	hippocampus development	0.11449955	NR4A3, ANXA	175	56	16792	5.14040816	1	0.99915182	GO:0021766	
GO:0045766	4	2.05128205	positive regulation of angiogenesis	0.1171841	LRG1, ANXA3	175	115	16792	3.33754037	1	0.99915182	GO:0045766	
GO:0032922	3	1.53846154	circadian regulation of gene expression	0.11788993	PER1, NAMP1	175	57	16792	5.05022556	1	0.99915182	GO:0032922	
GO:0051592	3	1.53846154	response to calcium ion	0.12130539	DUSP1, THBS	175	58	16792	4.96315271	1	0.99915182	GO:0051592	
GO:0007267	6	3.07692308	cell-cell signaling	0.123801	NOV, TNFAIP1	175	254	16792	2.26663667	1	0.99915182	GO:0007267	
GO:0007417	4	2.05128205	central nervous system development	0.1285704	VNN1, VNN2,	175	120	16792	3.19847619	1	0.99915182	GO:0007417	
GO:0051384	3	1.53846154	response to glucocorticoid	0.14584404	ANXA3, DUSP	175	65	16792	4.42865934	1	0.99915182	GO:0051384	
GO:0019221	4	2.05128205	cytokine-mediated signaling pathway	0.15490366	SOCS1, IL1R2,	175	131	16792	2.92990185	1	0.99915182	GO:0019221	
GO:0009749	3	1.53846154	response to glucose	0.15665382	PKFNB2, IRS2,	175	68	16792	4.23327731	1	0.99915182	GO:0009749	
GO:0006914	4	2.05128205	autophagy	0.1598631	GABARAPL1,	175	133	16792	2.88584318	1	0.99915182	GO:0006914	
GO:0001938	3	1.53846154	positive regulation of endothelial cell proliferation	0.16029056	LRG1, ARG1, I	175	69	16792	4.17192547	1	0.99915182	GO:0001938	
GO:0007204	4	2.05128205	positive regulation of cytosolic calcium ion concent	0.162361	FPR1, PROK2,	175	134	16792	2.86430704	1	0.99915182	GO:0007204	
GO:0071347	3	1.53846154	cellular response to interleukin-1	0.1676099	CEBPB, USP1I	175	71	16792	4.05440644	1	0.99915182	GO:0071347	
GO:0008283	7	3.58974359	cell proliferation	0.18041413	FOXCl, DDIT4	175	366	16792	1.83519126	1	0.99915182	GO:0008283	
GO:0007623	3	1.53846154	circadian rhythm	0.18241275	PER1, NAMP1	175	75	16792	3.83817143	1	0.99915182	GO:0007623	
GO:0008286	3	1.53846154	insulin receptor signaling pathway	0.19363775	KL, NAMPT, IF	175	78	16792	3.69054945	1	0.99915182	GO:0008286	
GO:0043066	8	4.1025641	negative regulation of apoptotic process	0.1940277	NFKBIA, BCL2	175	455	16792	1.68710832	1	0.99915182	GO:0043066	
GO:0050728	3	1.53846154	negative regulation of inflammatory response	0.19739947	NOV, TNFAIP1	175							

GO:0042060	3	1.53846154	wound healing	0.2011702	SLC11A1, S10	175	80	16792	3.59828571	1	1	0.99915182	GO:0042060	wound healing
GO:0042493	6	3.07692308	response to drug	0.20929539	ACSL1, ARG1,	175	304	16792	1.89383459	1	1	0.99915182	GO:0042493	response to drug
GO:0008284	8	4.1025641	positive regulation of cell proliferation	0.20999257	HLX, NAMPT,	175	466	16792	1.64728387	1	1	0.99915182	GO:0008284	positive regulation of cell proliferation
GO:0007283	7	3.58974359	spermatogenesis	0.2105234	PHC2, RGS2, I	175	385	16792	1.74462338	1	1	0.99915182	GO:0007283	spermatogenesis
GO:0045944	14	7.17948718	positive regulation of transcription from RNA polym	0.21787787	FOXCl, CEBPI	175	981	16792	1.36937819	1	1	0.99915182	GO:0045944	positive regulation of transcription from RNA polymerase II promoter
GO:0050830	3	1.53846154	defense response to Gram-positive bacterium	0.22013898	HMGB2, PGLI	175	85	16792	3.38662185	1	1	0.99915182	GO:0050830	defense response to Gram-positive bacterium
GO:0007565	3	1.53846154	female pregnancy	0.23541939	THBD, NAMP	175	89	16792	3.23441413	1	1	0.99915182	GO:0007565	female pregnancy
GO:0046854	3	1.53846154	phosphatidylinositol phosphorylation	0.25459832	KL, IRS2, EREC	175	94	16792	3.06237082	1	1	0.99915182	GO:0046854	phosphatidylinositol phosphorylation
GO:0030182	3	1.53846154	neuron differentiation	0.25843985	CEBPB, DDI74	175	95	16792	3.03013534	1	1	0.99915182	GO:0030182	neuron differentiation
GO:0016477	4	2.05128205	cell migration	0.26505435	FOXC1, CDH2	175	172	16792	2.23149502	1	1	0.99915182	GO:0016477	cell migration
GO:0035335	3	1.53846154	peptidyl-tyrosine dephosphorylation	0.27381046	PTPRN2, DUS	175	99	16792	2.90770563	1	1	0.99915182	GO:0035335	peptidyl-tyrosine dephosphorylation
GO:0007218	3	1.53846154	neuropeptide signaling pathway	0.28149269	PROK2, GPR8	175	101	16792	2.8501273	1	1	0.99915182	GO:0007218	neuropeptide signaling pathway
GO:0002223	3	1.53846154	stimulatory C-type lectin receptor signaling pathwa	0.29683537	NFKBIA, CLEC	175	105	16792	2.74155102	1	1	0.99915182	GO:0002223	stimulatory C-type lectin receptor signaling pathway
GO:0001764	3	1.53846154	neuron migration	0.29683537	NR4A2, DDI7	175	105	16792	2.74155102	1	1	0.99915182	GO:0001764	neuron migration
GO:0006464	3	1.53846154	cellular protein modification process	0.29683537	QPCT, PADI4,	175	105	16792	2.74155102	1	1	0.99915182	GO:0006464	cellular protein modification process
GO:0048015	3	1.53846154	phosphatidylinositol-mediated signaling	0.30066436	KL, IRS2, EREC	175	106	16792	2.71568733	1	1	0.99915182	GO:0048015	phosphatidylinositol-mediated signaling
GO:0007420	4	2.05128205	brain development	0.31430964	FOXC1, DDI74	175	190	16792	2.02009023	1	1	0.99915182	GO:0007420	brain development
GO:0006979	3	1.53846154	response to oxidative stress	0.31594316	VNN1, DUSP1	175	110	16792	2.61693506	1	1	0.99915182	GO:0006979	response to oxidative stress
GO:0070588	3	1.53846154	calcium ion transmembrane transport	0.35001722	LOXHD1, TRP	175	119	16792	2.41901561	1	1	0.99915182	GO:0070588	calcium ion transmembrane transport
GO:0001934	3	1.53846154	positive regulation of protein phosphorylation	0.37982029	PLAUR, MMP	175	127	16792	2.26663667	1	1	0.99915182	GO:0001934	positive regulation of protein phosphorylation
GO:0008285	6	3.07692308	negative regulation of cell proliferation	0.39116544	GJB6, ZBTB16	175	396	16792	1.45385281	1	1	0.99915182	GO:0008285	negative regulation of cell proliferation
GO:0043524	3	1.53846154	negative regulation of neuron apoptotic process	0.3981585	NR4A2, CEBP	175	132	16792	2.18077922	1	1	0.99915182	GO:0043524	negative regulation of neuron apoptotic process
GO:0001501	3	1.53846154	skeletal system development	0.41624438	FOXC1, ZBTB:	175	137	16792	2.10118874	1	1	0.99915182	GO:0001501	skeletal system development
GO:0002250	3	1.53846154	adaptive immune response	0.46034668	BTNL8, CLEC4	175	148	16792	1.94501931	1	1	0.99915182	GO:0002250	adaptive immune response
GO:0018108	3	1.53846154	peptidyl-tyrosine phosphorylation	0.47512102	IL5RA, EPHB4	175	153	16792	1.88145658	1	1	0.99915182	GO:0018108	peptidyl-tyrosine phosphorylation
GO:0006629	3	1.53846154	lipid metabolic process	0.49006513	PTPRN2, ABH	175	157	16792	1.83352138	1	1	0.99915182	GO:0006629	lipid metabolic process
GO:0007411	3	1.53846154	axon guidance	0.4954797	NR4A3, NRXN	175	159	16792	1.81045822	1	1	0.99915182	GO:0007411	axon guidance
GO:0043123	3	1.53846154	positive regulation of I-kappaB kinase/NF-kappaB s	0.50166207	C18ORF32, PI	175	161	16792	1.78796806	1	1	0.99915182	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0000165	4	2.05128205	MAPK cascade	0.51242738	KL, IL5RA, IRS	175	262	16792	1.46495093	1	1	0.99915182	GO:0000165	MAPK cascade
GO:0043547	7	3.58974359	positive regulation of GTPase activity	0.5338096	KL, FGD4, RG:	175	565	16792	1.18881416	1	1	0.99915182	GO:0043547	positive regulation of GTPase activity
GO:0001666	3	1.53846154	response to hypoxia	0.53693726	NR4A2, DDI7	175	172	16792	1.67362126	1	1	0.99915182	GO:0001666	response to hypoxia
GO:0006915	7	3.58974359	apoptotic process	0.53728547	NFKBIA, GJB6	175	567	16792	1.18462081	1	1	0.99915182	GO:0006915	apoptotic process
GO:0005975	3	1.53846154	carbohydrate metabolic process	0.54426148	KL, MGAM, SI	175	174	16792	1.65438424	1	1	0.99915182	GO:0005975	carbohydrate metabolic process
GO:0030335	3	1.53846154	positive regulation of cell migration	0.5651459	TNFAIP6, IRS:	175	184	16792	1.56447205	1	1	0.99915182	GO:0030335	positive regulation of cell migration
GO:0007596	3	1.53846154	blood coagulation	0.5651459	THBD, PLAUR	175	184	16792	1.56447205	1	1	0.99915182	GO:0007596	blood coagulation
GO:0042127	3	1.53846154	regulation of cell proliferation	0.58775566	NFKBIA, GUC:	175	185	16792	1.55601544	1	1	0.99915182	GO:0042127	regulation of cell proliferation
GO:0043065	4	2.05128205	positive regulation of apoptotic process	0.60409484	FGD4, BCL2A:	175	300	16792	1.27939048	1	1	0.99915182	GO:0043065	positive regulation of apoptotic process
GO:0030198	3	1.53846154	extracellular matrix organization	0.60534669	CRISPLD2, NIL	175	196	16792	1.46868805	1	1	0.99915182	GO:0030198	extracellular matrix organization
GO:0007275	6	3.07692308	multicellular organism development	0.63116271	BST1, PHC2, I	175	521	16792	1.10503976	1	1	0.99915182	GO:0007275	multicellular organism development
GO:0034220	3	1.53846154	ion transmembrane transport	0.64288192	TSC2D3, ATF	175	210	16792	1.37077551	1	1	0.99915182	GO:0034220	ion transmembrane transport
GO:0030154	5	2.56410256	cell differentiation	0.70904562	HLX, INSC, CR	175	462	16792	1.0384663	1	1	0.99915182	GO:0030154	cell differentiation
GO:0000122	7	3.58974359	negative regulation of transcription from RNA polyr	0.76161452	NR4A2, PER1,	175	720	16792	0.93288889	1	1	0.99915182	GO:0000122	negative regulation of transcription from RNA polymerase II promoter
GO:0006366	5	2.56410256	transcription from RNA polymerase II promoter	0.78241438	FOXC1, CEBPI	175	513	16792	0.93522696	1	1	0.99915182	GO:0006366	transcription from RNA polymerase II promoter
GO:0035556	4	2.05128205	intracellular signal transduction	0.79159278	GUCY2C, DUS	175	403	16792	0.95239986	1	1	0.99915182	GO:0035556	intracellular signal transduction
GO:0007399	3	1.53846154	nervous system development	0.80105121	INSC, FOS, SC	175	287	16792	1.00300647	1	1	0.99915182	GO:0007399	nervous system development
GO:0007186	8	4.1025641	G-protein coupled receptor signaling pathway	0.82926674	GPR27, GPR1	175	899	16792	0.85387573	1	1	0.99915182	GO:0007186	G-protein coupled receptor signaling pathway
GO:0055114	5	2.56410256	oxidation-reduction process	0.86638077	CBS, CYP4F3,	175	592	16792	0.81042471	1	1	0.99915182	GO:0055114	oxidation-reduction process
GO:0045893	4	2.05128205	positive regulation of transcription, DNA-templated	0.90566391	FOXC1, ZBTB:	175	515	16792	0.74527601	1	1	0.99915182	GO:0045893	positive regulation of transcription, DNA-templated
GO:0006357	3	1.53846154	regulation of transcription from RNA polymerase II	0.94536592	HMGB2, FOS,	175	441	16792	0.65275024	1	1	0.99915182	GO:0006357	regulation of transcription from RNA polymerase II promoter
GO:0006351	13	6.66666667	transcription, DNA-templated	0.98639658	ZMYND15, CE	175	1955	16792	0.63805919	1	1	0.99915182	GO:0006351	transcription, DNA-templated
GO:0006355	9	4.61538462	regulation of transcription, DNA-templated	0.99025165	FOXC1, CEBPI	175	1504	16792	0.57419453	1	1	0.99915182	GO:0006355	regulation of transcription, DNA-templated