

Additional Table 8. Gene ontologies enriched for differentially expressed genes comparing TFA+MSG to TFA diet in males and females.

Term ID	Category	No. of genes	P Value
Ratio > 1.5 (upregulated in TFA+ MSG males vs TFA)			
Biological Process			
GO:0009987	cellular process	61	0.02
GO:0008152	metabolic process	51	0.008
GO:0006807	nitrogen compound metabolic process	30	0.002
GO:0009058	biosynthetic process	30	0.001
GO:0019222	regulation of metabolic process	27	0.007
GO:0006350	transcription	24	<.0001
GO:0043687	post-translational protein modification	12	0.03
GO:0032774	RNA biosynthetic process	5	0.005
GO:0006468	protein amino acid phosphorylation	9	0.02
GO:0032583	regulation of gene-specific transcription	3	0.05
BP00031	Nucleoside, nucleotide and nucleic acid metabolism	28	0.004
BP00040	mRNA transcription	22	<.001
Cellular Component			
GO:0005576	extracellular region	11	0.05
GO:0005622	intracellular	77	0.001
GO:0019898	extrinsic to membrane	10	0.002
Molecular Function			
GO:0005488	binding	78	0.007
GO:0046914	transition metal ion binding	25	0.01
GO:0003677	DNA binding	21	0.002
GO:0008270	zinc ion binding	21	0.01
GO:0016740	transferase activity	17	0.04
GO:0030528	transcription regulator activity	16	0.004
Pathway			
P00040	Metabotropic glutamate receptor group II pathway	3	0.04
Ratio ≤ -1.5 (downregulated in TFA+ MSG males vs TFA)			
Biological Process			
GO:0032502	developmental process	17	0.03
GO:0009308	amine metabolic process	5	0.03
GO:0051049	regulation of transport	5	0.02
GO:0022898	regulation of transmembrane transporter activity	2	0.04
Molecular Function			
GO:0016740	transferase activity	12	0.04
GO:0004857	enzyme inhibitor activity	7	<.001
GO:0004866	endopeptidase inhibitor activity	4	0.02
GO:0030594	neurotransmitter receptor activity	3	0.03
MF00016	Signaling molecule	8	0.01
MF00250	Serine protease inhibitor	4	0.007

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Term ID	Category	No. of genes	P Value
Ratio >1.5 (upregulated in TFA+ MSG females vs TFA)			
Biological Process			
GO:0008152	metabolic process	29	0.02
GO:0006807	nitrogen compound metabolic process	19	0.003
GO:0080090	regulation of primary metabolic process	14	0.04
GO:0045449	regulation of transcription	13	0.02
GO:0009791	post-embryonic development	3	0.02
GO:0048265	response to pain	2	0.05
BP00040	mRNA transcription	11	0.04
Cellular Compartment			
GO:0005634	nucleus	20	0.042
Molecular Function			
GO:0030528	transcription regulator activity	10	0.016
GO:0005516	calmodulin binding	3	0.05
GO:0004806	triacylglycerol lipase activity	2	0.04
MF00139	Acyltransferase	3	0.03
Ratio ≤ -1.5 (downregulated in TFA+ MSG females vs TFA)			
Biological Process			
GO:0007275	multicellular organismal development	15	0.05
GO:0006082	organic acid metabolic process	8	0.001
GO:0042180	cellular ketone metabolic process	8	0.001
GO:0006811	ion transport	7	0.04
GO:0009308	amine metabolic process	6	0.006
GO:0042981	regulation of apoptosis	6	0.04
BP00102	Signal transduction	21	0.02
BP00013	Amino acid metabolism	5	0.006
Molecular function			
GO:0004857	enzyme inhibitor activity	5	0.01
GO:0048037	cofactor binding	5	0.01
GO:0019842	vitamin binding	4	0.01
GO:0016597	amino acid binding	3	0.008
GO:0070279	vitamin B6 binding	3	0.02
GO:0010851	cyclase regulator activity	2	0.01
GO:0016841	ammonia-lyase activity	2	0.01
GO:0030249	guanylate cyclase regulator activity	2	0.01
MF00141	Hydrolase	7	0.04
MF00108	Protein kinase	6	0.04