

Additional Table 6. Gene ontologies enriched for differentially expressed genes comparing MSG to Control diet in males and females.

Term ID	Category	No. of genes	P Value
Ratio ≥ 1.5 (upregulated in MSG males vs Control)			
Biological Process			
GO:0009987	cellular process	61	0.006
GO:0008152	metabolic process	49	0.01
GO:0034641	cellular nitrogen compound metabolic process	30	<.001
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	25	0.01
GO:0009058	biosynthetic process	25	0.02
GO:0044249	cellular biosynthetic process	24	0.03
GO:0032502	developmental process	23	0.02
GO:0007275	multicellular organismal development	21	0.03
GO:0045449	regulation of transcription	19	0.04
GO:0051716	cellular response to stimulus	10	0.002
GO:0051726	regulation of cell cycle	5	0.02
GO:0051270	regulation of cell motion	4	0.01
Cellular Component			
GO:0005634	nucleus	31	0.01
Molecular Function			
GO:0005488	binding	70	0.01
GO:0043167	ion binding	38	<.0001
GO:0043169	Select calcium binding protein	38	<.0001
GO:0046872	metal ion binding	38	<.0001
Ratio < - 1.5 (downregulated in MSG Males vs Control)			
Biological Process			
GO:0006796	phosphate metabolic process	7	0.03
GO:0016310	phosphorylation	6	0.05
Molecular Function			
GO:0030234	enzyme regulator activity	8	0.003
GO:0030249	guanylate cyclase regulator activity	2	0.008
GO:0005515	protein binding	23	0.04
MF00188	Select calcium binding protein	4	0.03

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Ratio ≥ 1.5 (upregulated in MSG females vs Control)			
Biological Process			
GO:0032502	developmental process	26	0.002
GO:0032879	regulation of localization	8	0.005
GO:0043065	positive regulation of apoptosis	6	0.009
GO:0006816	calcium ion transport	4	0.02
GO:0006909	phagocytosis	3	0.02
GO:0048856	anatomical structure development	19	0.02
GO:0009308	amine metabolic process	6	0.03
GO:0006811	ion transport	9	0.03
GO:0019752	carboxylic acid metabolic process	7	0.03
GO:0048513	organ development	15	0.04
Cellular Component			
GO:0031226	intrinsic to plasma membrane	8	0.02
GO:0045177	apical part of cell	4	0.03
Molecular Function			
GO:0004857	enzyme inhibitor activity	7	0.002
GO:0005488	binding	75	0.003
GO:0030234	enzyme regulator activity	11	0.006
GO:0016841	ammonia-lyase activity	2	0.02
GO:0000287	magnesium ion binding	7	0.02
GO:0043167	ion binding	31	0.02
GO:0048037	cofactor binding	5	0.03
GO:0016840	carbon-nitrogen lyase activity	2	0.04
GO:0005262	calcium channel activity	3	0.05
Ratio $< - 1.5$ (downregulated in MSG females vs Control)			
Cellular Component			
GO:0031012	extracellular matrix	6	0.001
GO:0005783	endoplasmic reticulum	9	0.002
GO:0005576	extracellular region	12	0.007
Molecular Function			
MF00180	Extracellular matrix glycoprotein	4	0.002
MF00178	Extracellular matrix	6	0.003