

Supplementary table 1: List of annotation clusters and GO terms of abundance-altered proteins

Annotation Cluster 1		Cytoskeletal protein binding		
Enrichment Score: 3.08				
Term	%	p-value	Fold Enrichment	
GO:0003779~actin binding	9.2	3.09E-06	8.1	
GO:0030833~regulation of actin filament polymerization	4.6	6.35E-05	22.2	
GO:0008064~regulation of actin polymerization or depolymerization	4.6	7.41E-05	21.4	
GO:0030832~regulation of actin filament length	4.6	7.41E-05	21.4	
GO:0032271~regulation of protein polymerization	4.6	1.29E-04	18.6	
GO:0032956~regulation of actin cytoskeleton organization	4.6	1.29E-04	18.6	
GO:0008092~cytoskeletal protein binding	9.2	1.30E-04	5.1	
GO:0032970~regulation of actin filament-based process	4.6	1.47E-04	18.1	
GO:0043254~regulation of protein complex assembly	4.6	1.87E-04	17.0	
GO:0051129~negative regulation of cellular component organization	4.6	5.60E-04	12.8	
GO:0044087~regulation of cellular component biogenesis	4.6	7.76E-04	11.8	
GO:0051493~regulation of cytoskeleton organization	4.6	8.38E-04	11.6	
GO:0030837~negative regulation of actin filament polymerization	2.8	3.76E-03	31.5	
GO:0033043~regulation of organelle organization	4.6	3.95E-03	7.6	
GO:0032272~negative regulation of protein polymerization	2.8	4.49E-03	28.9	
GO:0031333~negative regulation of protein complex assembly	2.8	4.49E-03	28.9	
GO:0032535~regulation of cellular component size	4.6	4.54E-03	7.3	
GO:0051494~negative regulation of cytoskeleton organization	2.8	1.49E-02	15.8	
GO:0010639~negative regulation of organelle organization	2.8	2.52E-02	12.0	
bta04810:Regulation of actin cytoskeleton	5.5	3.05E-02	3.3	
bta04666:Fc gamma R-mediated phagocytosis	3.7	4.52E-02	4.9	
Annotation Cluster 2		Actin binding		
Enrichment Score: 2.71				
Term	%	p-value	Fold Enrichment	
GO:0003779~actin binding	9.2	3.09E-06	8.1	
GO:0008092~cytoskeletal protein binding	9.2	1.30E-04	5.1	
GO:0030036~actin cytoskeleton organization	3.7	3.48E-02	5.5	
GO:0030029~actin filament-based process	3.7	3.69E-02	5.4	
GO:0007010~cytoskeleton organization	4.6	5.41E-02	3.5	
Annotation Cluster 3		Translation		
Enrichment Score: 2.47				
Term	%	p-value	Fold Enrichment	
GO:0006412~translation	9.2	6.40E-04	4.1	
bta03010:Ribosome	5.5	1.00E-03	7.5	
GO:0003735~structural constituent of ribosome	6.4	4.02E-03	4.6	
GO:0005198~structural molecule activity	7.3	5.22E-02	2.3	
Annotation Cluster 4		Identical protein binding		
Enrichment Score: 1.90				
Term	%	p-value	Fold Enrichment	
GO:0042802~identical protein binding	7.3	6.44E-03	3.6	
GO:0042803~protein homodimerization activity	5.5	7.05E-03	4.9	
GO:0046983~protein dimerization activity	5.5	4.47E-02	3.1	
Annotation Cluster 5		Lipid binding		
Enrichment Score: 1.69				
Term	%	p-value	Fold Enrichment	
GO:0033700~phospholipid efflux	2.8	1.47E-03	49.5	
GO:0034367~macromolecular complex remodeling	2.8	2.49E-03	38.5	
GO:0034368~protein-lipid complex remodeling	2.8	2.49E-03	38.5	

GO:0034369~plasma lipoprotein particle remodeling	2.8	2.49E-03	38.5
GO:0008289~lipid binding	7.3	2.67E-03	4.2
GO:0050994~regulation of lipid catabolic process	2.8	3.10E-03	34.7
GO:0032371~regulation of sterol transport	2.8	5.28E-03	26.7
GO:0032374~regulation of cholesterol transport	2.8	5.28E-03	26.7
GO:0033344~cholesterol efflux	2.8	5.28E-03	26.7
GO:0005543~phospholipid binding	4.6	5.94E-03	6.8
GO:0032368~regulation of lipid transport	2.8	7.99E-03	21.7
GO:0042632~cholesterol homeostasis	2.8	1.36E-02	16.5
GO:0055092~sterol homeostasis	2.8	1.36E-02	16.5
GO:0015918~sterol transport	2.8	1.36E-02	16.5
GO:0030301~cholesterol transport	2.8	1.36E-02	16.5
GO:0060191~regulation of lipase activity	2.8	1.49E-02	15.8
GO:0015914~phospholipid transport	2.8	1.49E-02	15.8
GO:0043933~macromolecular complex subunit organization	7.3	1.57E-02	3.0
GO:0006639~acylglycerol metabolic process	2.8	1.90E-02	13.9
GO:0006638~neutral lipid metabolic process	2.8	2.20E-02	12.8
GO:0006662~glycerol ether metabolic process	2.8	2.20E-02	12.8
GO:0018904~organic ether metabolic process	2.8	2.36E-02	12.4
GO:0055088~lipid homeostasis	2.8	2.52E-02	12.0
GO:0009894~regulation of catabolic process	2.8	3.57E-02	9.9
GO:0016042~lipid catabolic process	3.7	3.69E-02	5.4
GO:0019216~regulation of lipid metabolic process	2.8	4.15E-02	9.1
GO:0042157~lipoprotein metabolic process	2.8	5.19E-02	8.1
GO:0008203~cholesterol metabolic process	2.8	5.19E-02	8.1
GO:0016125~sterol metabolic process	2.8	6.08E-02	7.4
GO:0046486~glycerolipid metabolic process	2.8	1.29E-01	4.8
GO:0006869~lipid transport	2.8	1.40E-01	4.5
GO:0008202~steroid metabolic process	2.8	1.61E-01	4.1
GO:0010876~lipid localization	2.8	1.70E-01	4.0
GO:0048878~chemical homeostasis	3.7	2.85E-01	2.1
GO:0051336~regulation of hydrolase activity	2.8	3.36E-01	2.5
GO:0042592~homeostatic process	4.6	3.56E-01	1.6
Annotation Cluster 6			
Enrichment Score: 1.67		Enzyme inhibitor activity	
<i>Term</i>	<i>%</i>	<i>p-value</i>	<i>Fold Enrichment</i>
GO:0004857~enzyme inhibitor activity	6.4	3.27E-03	4.8
GO:0004866~endopeptidase inhibitor activity	4.6	1.73E-02	5.0
GO:0030414~peptidase inhibitor activity	4.6	2.35E-02	4.5
GO:0004867~serine-type endopeptidase inhibitor activity	2.8	1.58E-01	4.2
Annotation Cluster 7			
Enrichment Score: 1.39		Immune response	
<i>Term</i>	<i>%</i>	<i>p-value</i>	<i>Fold Enrichment</i>
GO:0045087~innate immune response	3.7	1.51E-02	7.6
GO:0006955~immune response	6.4	3.86E-02	2.8
GO:0006952~defense response	5.5	4.15E-02	3.1
GO:0002526~acute inflammatory response	2.8	5.19E-02	8.1
GO:0006954~inflammatory response	3.7	5.90E-02	4.4
GO:0009611~response to wounding	4.6	6.22E-02	3.3