

Table S2. Functional annotation clustering of the ChREBP ChIP-seq dataset.

Annotation Cluster 1		Enrichment Score: 2.62			
Category	Term	Number	%	p-Value	FDR
GOTERM_MF_ALL	GO:0046983~protein dimerization activity	41	5.5	2.4E-04	0.4
GOTERM_MF_ALL	GO:0042803~protein homodimerization activity	26	3.5	2.8E-03	4.3
GOTERM_MF_ALL	GO:0046982~protein heterodimerization activity	18	2.4	5.4E-03	8.1
Annotation Cluster 2		Enrichment Score: 2.54			
Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0006066~alcohol metabolic process	39	5.2	2.5E-05	0.0
GOTERM_BP_ALL	GO:0044262~cellular carbohydrate metabolic process	34	4.5	1.8E-04	0.3
GOTERM_BP_ALL	GO:0005975~carbohydrate metabolic process	41	5.5	4.8E-04	0.9
GOTERM_BP_ALL	GO:0005996~monosaccharide metabolic process	22	2.9	7.0E-04	1.2
GOTERM_BP_ALL	GO:0006006~glucose metabolic process	16	2.1	2.7E-03	4.8
GOTERM_BP_ALL	GO:0044275~cellular carbohydrate catabolic process	11	1.5	3.7E-03	6.5
GOTERM_BP_ALL	GO:0019318~hexose metabolic process	18	2.4	4.3E-03	7.5
Annotation Cluster 3		Enrichment Score: 2.52			
Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0009790~embryonic development	42	5.6	1.0E-03	1.8
GOTERM_BP_ALL	GO:0043009~chordate embryonic development	27	3.6	2.7E-03	4.7
GOTERM_BP_ALL	GO:0009792~embryonic development ending in birth or egg hatching	27	3.6	3.0E-03	5.3
Annotation Cluster 4		Enrichment Score: 2.16			
Category	Term	Number	%	p-Value	FDR
PANTHER_BP_ALL	BP00019:Lipid, fatty acid and steroid metabolism	51	6.8	2.3E-04	0.3
GOTERM_BP_ALL	GO:0046486~glycerolipid metabolic process	18	2.4	6.9E-04	1.2
Annotation Cluster 5		Enrichment Score: 2.07			
Category	Term	Number	%	p-Value	FDR
GOTERM_MF_ALL	GO:0030234~enzyme regulator activity	58	7.8	1.2E-04	0.2
PANTHER_MF_ALL	MF00100:G-protein modulator	30	4.0	5.5E-04	0.7
GOTERM_MF_ALL	GO:0030695~GTPase regulator activity	30	4.0	2.5E-03	3.8
GOTERM_MF_ALL	GO:0008047~enzyme activator activity	26	3.5	2.9E-03	4.5
GOTERM_MF_ALL	GO:0060589~nucleoside-triphosphatase regulator activity	30	4.0	3.5E-03	5.3
GOTERM_MF_ALL	GO:0005083~small GTPase regulator activity	22	2.9	4.5E-03	6.8
GOTERM_BP_ALL	GO:0046578~regulation of Ras protein signal transduction	19	2.5	4.7E-03	8.2
Annotation Cluster 6		Enrichment Score: 1.96			
Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0006639~acylglycerol metabolic process	13	1.7	8.7E-07	0.0
GOTERM_BP_ALL	GO:0006638~neutral lipid metabolic process	13	1.7	1.1E-06	0.0
GOTERM_BP_ALL	GO:0006662~glycerol ether metabolic process	13	1.7	1.4E-06	0.0
GOTERM_BP_ALL	GO:0018904~organic ether metabolic process	13	1.7	2.1E-06	0.0
GOTERM_BP_ALL	GO:0033700~phospholipid efflux	6	0.8	3.2E-05	0.1
GOTERM_BP_ALL	GO:0034381~lipoprotein particle clearance	7	0.9	3.6E-05	0.1
GOTERM_BP_ALL	GO:0006641~triglyceride metabolic process	10	1.3	7.9E-05	0.1
GOTERM_BP_ALL	GO:0065005~protein-lipid complex assembly	6	0.8	9.4E-05	0.2
GOTERM_BP_ALL	GO:0034377~plasma lipoprotein particle assembly	6	0.8	9.4E-05	0.2
GOTERM_BP_ALL	GO:0044269~glycerol ether catabolic process	5	0.7	3.7E-04	0.7
GOTERM_BP_ALL	GO:0046464~acylglycerol catabolic process	5	0.7	3.7E-04	0.7
GOTERM_BP_ALL	GO:0046461~neutral lipid catabolic process	5	0.7	3.7E-04	0.7
GOTERM_BP_ALL	GO:0015914~phospholipid transport	8	1.1	4.5E-04	0.8
GOTERM_BP_ALL	GO:0046339~diacylglycerol metabolic process	5	0.7	6.0E-04	1.1
GOTERM_BP_ALL	GO:0046486~glycerolipid metabolic process	18	2.4	6.9E-04	1.2
GOTERM_BP_ALL	GO:0046503~glycerolipid catabolic process	5	0.7	1.3E-03	2.3
GOTERM_BP_ALL	GO:0046463~acylglycerol biosynthetic process	5	0.7	1.3E-03	2.3
GOTERM_BP_ALL	GO:0046460~neutral lipid biosynthetic process	5	0.7	1.3E-03	2.3
GOTERM_BP_ALL	GO:0034367~macromolecular complex remodeling	6	0.8	1.4E-03	2.4
GOTERM_BP_ALL	GO:0034368~protein-lipid complex remodeling	6	0.8	1.4E-03	2.4
GOTERM_BP_ALL	GO:0034369~plasma lipoprotein particle remodeling	6	0.8	1.4E-03	2.4

GOTERM_BP_ALL	GO:0046504~glycerol ether biosynthetic process	5	0.7	1.9E-03	3.3
GOTERM_BP_ALL	GO:0010873~positive regulation of cholesterol esterification	4	0.5	2.5E-03	4.4
GOTERM_MF_ALL	GO:0005543~phospholipid binding	17	2.3	2.6E-03	3.9
GOTERM_BP_ALL	GO:0019433~triglyceride catabolic process	4	0.5	3.9E-03	6.7
GOTERM_BP_ALL	GO:0010872~regulation of cholesterol esterification	4	0.5	3.9E-03	6.7
GOTERM_BP_ALL	GO:0043691~reverse cholesterol transport	5	0.7	4.2E-03	7.3
GOTERM_BP_ALL	GO:0006869~lipid transport	15	2.0	4.3E-03	7.4
GOTERM_BP_ALL	GO:0030301~cholesterol transport	7	0.9	4.9E-03	8.3
GOTERM_BP_ALL	GO:0015918~sterol transport	7	0.9	4.9E-03	8.3
GOTERM_MF_ALL	GO:0070653~high-density lipoprotein receptor binding	3	0.4	4.9E-03	7.4
GOTERM_BP_ALL	GO:0010903~negative regulation of very-low-density lipoprotein particle remodeling	3	0.4	5.5E-03	9.4
GOTERM_BP_ALL	GO:0042632~cholesterol homeostasis	7	0.9	5.6E-03	9.5
GOTERM_BP_ALL	GO:0055092~sterol homeostasis	7	0.9	5.6E-03	9.5
GOTERM_BP_ALL	GO:0034374~low-density lipoprotein particle remodeling	4	0.5	5.7E-03	9.6

Annotation Cluster 7 Enrichment Score: 1.77

Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0032502~developmental process	167	22.3	2.7E-03	4.7
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	73	9.8	2.9E-03	5.0
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	152	20.3	4.6E-03	8.0
GOTERM_BP_ALL	GO:0048856~anatomical structure development	136	18.2	4.7E-03	8.1

Annotation Cluster 8 Enrichment Score: 1.70

Category	Term	Number	%	p-Value	FDR
GOTERM_MF_ALL	GO:0008092~cytoskeletal protein binding	36	4.8	1.7E-03	2.6

Annotation Cluster 9 Enrichment Score: 1.61

Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0005996~monosaccharide metabolic process	22	2.9	7.0E-04	1.2
GOTERM_BP_ALL	GO:0044275~cellular carbohydrate catabolic process	11	1.5	3.7E-03	6.5
GOTERM_BP_ALL	GO:0019318~hexose metabolic process	18	2.4	4.3E-03	7.5

Annotation Cluster 10 Enrichment Score: 1.57

Category	Term	Number	%	p-Value	FDR
GOTERM_MF_ALL	GO:0043169~cation binding	203	27.1	3.2E-03	4.9
GOTERM_MF_ALL	GO:0043167~ion binding	205	27.4	3.9E-03	5.9
GOTERM_MF_ALL	GO:0046872~metal ion binding	199	26.6	6.0E-03	8.9

Annotation Cluster 11 Enrichment Score: 1.56

Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0016043~cellular component organization	138	18.4	1.7E-03	3.0

Annotation Cluster 12 Enrichment Score: 1.56

Category	Term	Number	%	p-Value	FDR
GOTERM_MF_ALL	GO:0015291~secondary active transmembrane transporter activity	19	2.5	2.2E-03	3.4
GOTERM_MF_ALL	GO:0015171~amino acid transmembrane transporter activity	9	1.2	2.7E-03	4.1
GOTERM_MF_ALL	GO:0015179~L-amino acid transmembrane transporter activity	7	0.9	4.2E-03	6.3
GOTERM_MF_ALL	GO:0022804~active transmembrane transporter activity	27	3.6	4.2E-03	6.4
GOTERM_BP_ALL	GO:0046942~carboxylic acid transport	15	2.0	4.9E-03	8.3
GOTERM_BP_ALL	GO:0015849~organic acid transport	15	2.0	5.2E-03	8.8

Annotation Cluster 13 Enrichment Score: 1.44

Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0030201~heparan sulfate proteoglycan metabolic process	6	0.8	2.2E-04	0.4
GOTERM_BP_ALL	GO:0015012~heparan sulfate proteoglycan biosynthetic process	5	0.7	9.2E-04	1.6

Annotation Cluster 14 Enrichment Score: 1.40

Category	Term	Number	%	p-Value	FDR
GOTERM_BP_ALL	GO:0034637~cellular carbohydrate biosynthetic process	10	1.3	2.9E-03	5.1