

Supplementary Table 3-2. Gene Ontology terms and numbers of cDNA clones expressing changes in the accumulated mRNA levels in OLHNI-e1 cells cultured at 15°C during 7 days

GO term	All				P<0.05							
	Number of clones in GO term	Number of clones	Number of clones in GO term	P	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	1244	632	348	199	176.8	87	39	44.2	95	57	48.3	
Molecular function	568	184	158.9	0.011	39.7	0.330	53	43.4	0.068			
Signal transducer activity	48	11	13.4	0.086	3	3.4	1	3.7	0.101			
Receptor activity	19	4	5.3	0.095	1	1.3	0.470	1.5	0.236			
Receptor binding	18	4	5.0	0.099	1	1.3	0.328	1.4	0.161			
Receptor signaling protein activity	5	2	1.4	0.102	0.3	0.453	0.3	0.4	0.230			
Binding	365	132	102.1	0.001	25.5	0.462	24	27.9	0.144			
Amino acid binding												
Calcium oxalate binding	5	2	1.4	0.102	0.3	0.453	2	0.4	0.031			
Carbohydrate binding	3	1	0.8	0.094	0.2	0.343	0.2	0.2	0.189			
Cofactor binding	2	1	0.6	0.102	0.1	0.232	0.1	0.2	0.138			
Drug binding	7	5	2.0	0.015	0.5	0.108	2	0.5	0.235			
Glycosaminoglycan binding	2	2	0.6	0.102	0.1	0.232	0.1	0.2	0.138			
Isoprenoid binding	17	3	4.8	0.083	1	1.2	0.446	1.3	0.231			
Lipid binding	67	22	18.7	0.080	5	4.7	0.476	5.1	0.182			
Metal ion binding	150	56	42.0	0.008	9	10.5	0.441	11.5	0.137			
Nucleic acid binding	99	35	27.7	0.057	3	6.9	0.139	7.6	0.081			
Nucleotide binding	1	1	0.3	0.092	0.1	0.076	0.1	0.1	0.053			
Oxygen binding	3	2	0.8	0.074	0.2	0.343	0.2	0.2	0.004			
Peptide binding	91	38	25.5	0.004	6.4	0.270	7	6.9	0.231			
Protein binding												
Pyridoxal phosphate binding	18	4	5.0	0.099	1	1.3	0.460	1.4	0.161			
Receptor binding	1	1	0.3	0.092	0.1	0.076	0.1	0.1	0.053			
Ribonucleoprotein binding	2	2	0.6	0.102	0.1	0.232	0.1	0.2	0.138			
Selenium binding	1	1	0.3	0.092	0.1	0.076	0.1	0.1	0.053			
Steroid binding	3	1	0.8	0.094	0.2	0.343	0.2	0.2	0.189			
Tetrapyrrole binding												
Vitamin binding												
Catalytic activity	214	71	59.9	0.053	15.0	0.176	10	16.3	0.001			
Helicase activity	4	2	1.1	0.095	0.3	0.412	2	0.3	0.014			
Hydrolase activity	84	28	23.5	0.067	7	5.9	0.452	6.4	0.020			
Isomerase activity	11	4	3.1	0.099	0.8	0.441	4	0.8	0.002			
Kinase activity	18	10	5.0	0.019	1	1.3	0.460	1.4	0.234			
Ligase activity	19	5	5.3	0.102	1.3	0.313	4	1.5	0.038			
Lyase activity	9	4	2.5	0.081	0.6	0.468	2	0.7	0.124			
Oxidoreductase activity	58	16	16.2	0.102	4.1	0.057	6	4.4	0.197			
Polyketide synthase activity	1	1	0.3	0.092	0.1	0.076	0.1	0.1	0.053			
Small protein conjugating enzyme activity	5	1	1.4	0.102	0.3	0.453	1	0.4	0.230			
Transferase activity	42	18	11.7	0.019	2.9	0.452	2	3.2	0.165			
Enzyme regulator activity	21	9	5.9	0.050	1.5	0.269	2	1.6	0.235			
Caspase regulator activity												
Enzyme activator activity	7	4	2.0	0.046	0.5	0.480	1	0.5	0.235			
Enzyme inhibitor activity	11	4	3.1	0.099	0.8	0.275	2	0.8	0.214			
GTPase regulator activity	5	1	1.4	0.102	0.3	0.453	0.4	0.4	0.230			
Nitric-oxide synthase regulator activity												
Kinase regulator activity	4	4	1.1	0.005	0.3	0.412	1	0.3	0.216			
Ornithine decarboxylase regulator activity	1	1	0.3	0.092	0.1	0.076	0.1	0.1	0.053			
Phosphatase regulator activity	2	1	0.6	0.102	0.1	0.232	1	0.2	0.138			

P and P values were obtained by Kruskal-Wallis ANOVA and  $\chi^2$  test, respectively. Red color boxes represent the GO terms the clone numbers of which were significantly more than the expectation values ( $P<0.05$ ).

Supplementary Table 3-2, continued

GO term	All				P<0.05			
	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	1244	632	176.8	0.011	87	39	44.2	95
Molecular function	568	184	158.9	0.102	87	39	44.2	95
Transporter activity	83	24	23.2	0.102	87	39	44.2	95
Amine/polyamine transporter activity	1	0.3	0.092		1	0.3	0.092	
Auxiliary transport protein activity	3	0.8	0.094		3	0.8	0.094	
Carbohydrate transporter activity	1	0.3	0.092		1	0.3	0.092	
Carrier activity	31	8.7	0.073		1	1	0.401	
Channel/pore class transporter activity	9	2.5	0.081		4	0.6	0.468	
Drug transporter activity	22	6.2	0.101		7	1.5	0.273	
Electron transporter activity	3	0.8	0.094		1	0.2	0.343	
Intracellular transporter activity	29	8.1	0.101		2	2.0	0.435	
Ion transporter activity	3	0.8	0.094		1	0.2	0.343	
Lipid transporter activity	2	0.6	0.102		1	0.1	0.232	
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	1	0.3	0.092		1	0.1	0.076	
Organic acid transporter activity	2	0.6	0.102		2	0.5	0.480	
Oxygen transporter activity	7	2.0	0.096		4	0.1	0.076	
Protein transporter activity	1	0.3	0.092		2	0.5	0.480	
Vitamin/cofactor transporter activity	42	11.7	0.094		4	2.9	0.436	
Transcription factor activity	11	3.1	0.096		2	0.8	0.441	
RNA polymerase II transcription factor activity	1	0.3	0.092		2	0.1	0.076	
RNA polymerase III transcription factor activity	7	2.0	0.092		2	0.5	0.108	
Transcription cofactor activity	26	7.3	0.102		3	1.8	0.385	
Transcription factor activity	4	1.1	0.095		1	0.3	0.412	
Transcriptional activator activity	4	1.1	0.095		1	0.3	0.412	
Transcriptional repressor activity	4	1.1	0.083		1	0.3	0.412	
Transcription initiation factor activity	95	26.6	0.100		4	6.6	0.275	
Transcription termination factor activity	4	1.1	0.005		2	0.3	0.016	
Structural molecule activity	8	2.2	0.101		3	0.6	0.477	
Extracellular matrix structural constituent	1	0.3	0.092		1	0.1	0.076	
Structural constituent of bone	8	2.2	0.101		3	0.6	0.477	
Structural constituent of cytoskeleton	1	0.3	0.092		1	0.1	0.076	
Structural constituent of muscle	68	19.0	0.069		15	4.8	0.099	
Structural constituent of ribosome	25	7.0	0.084		9	1.7	0.465	
Translation regulator activity	25	7.0	0.084		2	1.7	0.465	
Translation factor activity, nucleic acid binding	25	7.0	0.084		2	1.7	0.465	
Chaperone regulator activity	4	1.1	0.095		2	0.3	0.412	
Antioxidant activity	4	1.1	0.095		2	0.3	0.412	
Peroxidase activity	8	2.2	0.101		3	0.6	0.477	
Molecular function unknown	6	1.7	0.080		3	0.4	0.473	
Motor activity	2	0.6	0.102		1	0.1	0.232	
Microtubule motor activity	2	0.6	0.102		1	0.1	0.232	

Supplementary Table 3-2. continued

GO term	All				P < 0.05			
	Number of clones in GO term	Number of clones in GO term	Expectation	P	Number of clones in GO term	Number of clones in GO term	Expectation	P
All	1244	348	176.8		87	95	44.2	
Biological process	632	199	176.8		39	57	44.2	48.3
Cellular process	562	181	157.2	0.013	36	52	39.3	0.403
Cell communication	252	91	70.5	0.004	16	29	17.6	0.450
Cell differentiation	83	34	23.2	0.007	9	4	5.8	0.186
Cellular physiological process	10	4	2.8	0.092		1	0.7	0.456
Membrane fusion	205	78	57.3	0.002	13	28	14.3	0.459
Regulation of cellular process	4	1	1.1	0.095		0.3	0.412	0.216
Physiological process	32	11	9.0	0.087	3	3	2.2	0.466
Cellular physiological process	522	162	146.0	0.038	28	50	36.5	0.133
Coagulation	205	78	57.3	0.002	13	28	14.3	0.459
Death	5	3	1.4	0.060		1	0.4	0.230
Homeostasis	9	4	2.5	0.081	2	1	0.6	0.192
Metabolism	5	1	1.4	0.102		0.3	0.453	0.230
Organismal physiological process	411	123	115.0	0.076	20	39	28.7	0.091
Pathogenesis	37	14	10.4	0.057	4	2	2.6	0.365
Regulation of physiological process	1	1	0.3	0.092		0.1	0.076	0.1053
Response to stimulus	78	23	21.8	0.101	4	5	5.5	0.414
Secretion	56	26	15.7	0.0003	5	7	3.9	0.444
Biological process unknown	7	5	2.0	0.115	1	1	0.5	0.480
Development	61	27	17.1	0.005	12	5	4.3	0.009
Aging	1		0.3	0.092		0.1	0.076	0.1053
Cell differentiation	10	4	2.8	0.092		0.7	0.456	0.221
Embryonic development	1		0.3	0.092		0.1	0.076	0.1053
Genetic transfer								
Growth	9	4	2.5	0.081		0.6	0.468	0.227
Mesoderm development	2	1	0.6	0.102		0.1	0.232	0.138
Morphogenesis	48	24	13.4	0.001	11	4	3.4	0.006
Pattern specification	1		0.3	0.092		0.1	0.076	0.1053
Pigmentation	2		0.6	0.102		0.1	0.232	0.138
Regulation of development	5	2	1.4	0.102		0.3	0.453	0.230
Regulation of gene expression, epigenetic								
Reproduction	8	2	2.2	0.101		0.6	0.477	0.232
Sex determination								
Sex differentiation								
Regulation of biological process	103	32	28.8	0.088	7	7	7.2	0.474
Regulation of cellular process	32	11	9.0	0.087	3	3	2.2	0.466
Regulation of development	5	2	1.4	0.102		0.3	0.453	0.230
Regulation of enzyme activity	3		0.8	0.094		0.2	0.343	0.189
Regulation of gene expression, epigenetic								
Regulation of physiological process	78	23	21.8	0.101	4	5	5.5	0.414
Behavior	2	1	0.6	0.102		0.1	0.232	0.138
Feeding behavior	1	1	0.3	0.092		0.1	0.076	0.1053
Learning and/or memory	1	1	0.3	0.092		0.1	0.076	0.1053
Mechanosensory behavior	1	1	0.3	0.092		0.1	0.076	0.1053
Viral life cycle								
Viral infectious cycle								

Supplementary Table 3-2. continued

GO term	All			P < 0.05			> 0.5 in log <sub>2</sub> ratio on day 7			< -0.5 in log <sub>2</sub> ratio on day 7		
	Number of clones in GO term	Number of clones in GO term	Expectation	Number of clones in GO term	Number of clones in GO term	Expectation	Number of clones in GO term	Number of clones in GO term	Expectation	Number of clones in GO term	Number of clones in GO term	Expectation
All	1244	632	176.8	87	39	44.2	95	57	48.3	48.3	0.149	
Cellular component	515	164	144.1	87	32	36.0	95	45	39.3	39.3	0.141	
Cell	487	153	136.2	87	30	34.1	95	43	37.2	37.2	0.234	
Cell fraction	35	9	9.8	87	1	2.4	95	2	2.7	2.7	0.053	
Cell projection	1	0.3	0.092	87	0	0.1	95	0	0.1	0.1	0.058	
Intracellular	432	140	120.8	87	23	30.2	95	42	33.0	33.0	0.235	
Membrane	147	40	41.1	87	13	10.3	95	11	11.2	11.2	0.086	
Extracellular	32	12	9.0	87	7	2.2	95	7	2.4	2.4	0.191	
Extracellular matrix	14	6	3.9	87	3	1.0	95	3	1.1	1.1	0.232	
Extracellular space	8	2	2.2	87	2	0.6	95	2	0.6	0.6	0.189	
Unilocalized	3	2	0.8	87	2	0.2	95	2	0.2	0.2	0.138	
cAMP-dependent protein kinase complex				87	1	0.1	95	1	0.1	0.1	0.053	
Ferritin complex	2	1	0.6	87	1	0.1	95	1	0.1	0.1	0.076	
Glycerol-3-phosphate dehydrogenase complex				87	1	0.3	95	1	0.1	0.1	0.076	
Protein kinase CK2 complex	1	1	0.3	87	1	0.3	95	1	0.1	0.1	0.076	
Protein serine/threonine phosphatase complex				87	1	0.3	95	1	0.1	0.1	0.076	
Ribonucleoside-diphosphate reductase complex				87	1	0.3	95	1	0.1	0.1	0.076	
Cellular component unknown	12	7	3.4	87	7	3.4	95	2	0.9	0.9	0.182	

Supplementary Table 3-3. Gene Ontology terms and numbers of cDNA clones expressing changes in the accumulated mRNA levels in OLNHI-e1 cells cultured at 33°C for during 7 days

GO term	All				P<0.05						
	All		> 0.5 in log <sub>2</sub> ratio on day 7		P<0.05		< -0.5 in log <sub>2</sub> ratio on day 7				
	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P			
All	1100	579	133	84	32	19	16.8	25	12	13.2	0.818
Molecular function		525		79		17	15.3		12	11.9	0.603
Signal transducer activity		43		5		3	1.3		3	1.0	0.234
Receptor activity		16		2		2	2.2		2	0.4	0.703
Receptor binding		17		2		1	2.4		1	0.4	0.791
Receptor signaling protein activity		4					0.6			0.1	0.231
Binding		436		53		11	60.6		7	9.9	0.430
Amino acid binding											
Calcium oxalate binding		5		1		1	0.7		1	0.1	0.309
Carbohydrate binding		4					0.6			0.1	0.231
Cofactor binding		1		1		1	0.1			0.0	0.005
Drug binding		7		1		1	1.0			0.2	0.437
Glycosaminoglycan binding		1					0.1			0.0	0.005
Isoprenoid binding		16		1		1	2.2			0.5	0.676
Lipid binding		62		7		2	8.6		3	1.8	0.348
Metal ion binding		144		23		4	20.0		2	4.2	0.659
Nucleic acid binding		97		21		6	13.5		2	2.8	0.099
Nucleotide binding		1		1		1	0.1			0.0	0.005
Oxygen binding		4		1		1	0.6			0.1	0.231
Peptide binding		88		12		2	12.2		2	2.6	0.677
Protein binding		17		2		1	2.4			0.5	0.678
Pyridoxal phosphate binding											
Receptor binding		2					0.3			0.1	0.060
Ribonucleoprotein binding		1					0.1			0.0	0.005
Selenium binding		3					0.4			0.1	0.145
Steroid binding											
Tetrapyrrole binding											
Vitamin binding		193		35		9	26.8		8	5.6	0.198
Catalytic activity		4		1		1	0.6			0.1	0.231
Helicase activity		71		16		6	9.9		2	2.1	0.014
Hydrolase activity		12		2		2	1.7			0.3	0.626
Isomerase activity		21		2		2	2.9		1	0.6	0.661
Kinase activity		16		3		1	2.2		1	0.5	0.676
Ligase activity		8		1		1	1.1			0.2	0.489
Lyase activity		50		10		2	7.0		4	1.5	0.677
Oxidoreductase activity		1		1		1	0.1			0.0	0.005
Polyketide synthase activity		4		1		1	0.6			0.1	0.171
Small protein conjugating enzyme activity		40		6		1	5.6		1	1.2	0.604
Transferase activity		21		6		2	2.9		1	0.6	0.226
Enzyme regulator activity											
Caspase regulator activity		6		1		1	0.8			0.2	0.377
Enzyme activator activity		11		4		1	1.5		1	0.3	0.601
Enzyme inhibitor activity		4					0.6			0.1	0.231
GTPase regulator activity											
Nitric-oxide synthase regulator activity		5		3		1	0.7		1	0.1	0.309
Kinase regulator activity		1					0.1			0.0	0.005
Ornithine decarboxylase regulator activity		2		1		1	0.3			0.1	0.060
Phosphatase regulator activity											

P and P values were obtained by Kruskal-Wallis ANOVA and  $\chi^2$  test, respectively.

Red color box represents the GO term the clone number of which was significantly more than the expectation value (P<0.05).

Supplementary Table 3-3. continued

GO term	P<0.05											
	All					> 0.5 in log <sub>2</sub> ratio on day 7					< -0.5 in log <sub>2</sub> ratio on day 7	
	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	1100	579	80.5	84	32	19	16.8	25	12	13.2		
Molecular function		525	73.0	79		17	15.3	603		11.9	0.818	
Transporter activity		71	9.9	8		1	2.1	0.568		1.6	0.369	
Amine/polyamine transporter activity		1	0.1	0.306			0.0	0.005		0.0	0.002	
Auxiliary transport protein activity		2	0.3	0.591			0.1	0.060		0.0	0.032	
Carbohydrate transporter activity												
Carrier activity		26	3.6	0.245			0.8	0.611		0.6	0.821	
Channel/pore class transporter activity		8	1.1	0.503			0.2	0.489		0.2	0.441	
Drug transporter activity												
Electron transporter activity		20	2.8	0.279		1	0.6	0.668		0.5	0.838	
Intracellular transporter activity		3	0.4	0.720			0.1	0.145		0.1	0.096	
Ion transporter activity		25	3.5	0.266			0.7	0.622		0.6	0.831	
Lipid transporter activity		3	0.4	0.720			0.1	0.145		0.1	0.096	
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity		2	0.3	0.591			0.1	0.060		0.0	0.032	
Organic acid transporter activity		1	0.1	0.306			0.0	0.005		0.0	0.002	
Oxygen transporter activity		2	0.3	0.591			0.1	0.060		0.0	0.032	
Protein transporter activity		4	0.6	0.732		1	0.1	0.231		0.1	0.171	
Vitamin/cofactor transporter activity		1	0.1	0.306			0.0	0.005		0.0	0.002	
Transcription regulator activity		41	5.7	0.410		8	1.2	0.449		0.9	0.626	
RNA polymerase II transcription factor activity		12	1.7	0.720		2	0.3	0.626		0.3	0.634	
RNA polymerase III transcription factor activity		1	0.1	0.306			0.0	0.005		0.0	0.002	
Transcription cofactor activity		7	1.0	0.114		3	0.2	0.437		0.2	0.381	
Transcription factor activity		25	3.5	0.521		5	0.7	0.622		0.6	0.831	
Transcriptional activator activity		4	0.6	0.732			0.1	0.231		0.1	0.171	
Transcriptional repressor activity		4	0.6	0.732		1	0.1	0.231		0.1	0.171	
Transcription initiation factor activity												
Transcription termination factor activity												
Structural molecule activity		93	12.9	0.450		4	2.7	0.524		2.1	0.260	
Extracellular matrix structural constituent		4	0.6	0.732			0.1	0.231		0.1	0.171	
Structural constituent of bone		1	0.1	0.306			0.0	0.005		0.0	0.002	
Structural constituent of cytoskeleton		9	1.3	0.453			0.3	0.533		0.2	0.496	
Structural constituent of muscle		1	0.1	0.306			0.0	0.005		0.0	0.002	
Structural constituent of ribosome		68	9.5	0.100		4	2.0	0.259		1.5	0.388	
Translation regulator activity		24	3.3	0.473		5	0.7	0.633		0.5	0.840	
Translation factor activity, nucleic acid binding		24	3.3	0.473		5	0.7	0.633		0.5	0.840	
Chaperone regulator activity												
Antioxidant activity		4	0.6	0.732		1	0.1	0.231		0.1	0.171	
Peroxidase activity		4	0.6	0.732		1	0.1	0.231		0.1	0.171	
Molecular function unknown		7	1.0	0.559			0.2	0.437		0.2	0.381	
Motor activity		6	0.8	0.620			0.2	0.377		0.1	0.316	
Microtubule motor activity		2	0.3	0.591			0.1	0.060		0.0	0.032	

Supplementary Table 3-3. continued

GO term	P < 0.05													
	All			> 0.5 in log <sub>2</sub> ratio on day 7			< -0.5 in log <sub>2</sub> ratio on day 7			P				
	Number of clones in GO term	Number of clones in Expectation	P	Number of clones in GO term	Number of clones in Expectation	P	Number of clones in GO term	Number of clones in Expectation	P					
All	1100	579	153	84	80.5	0.450	32	19	16.8	0.545	25	12	13.2	0.846
Biological process		509		77	70.8	0.450		17	14.8	0.545		12	11.6	0.846
Cellular process		220		27	30.6	0.514		10	6.4	0.196		3	5.0	0.485
Cell communication		79		13	11.0	0.572		4	2.3	0.371		1	1.8	0.770
Cell differentiation		7			1.0	0.559			0.2	0.437			0.2	0.381
Cellular physiological process		174		21	24.2	0.520		8	5.1	0.246		3	4.0	0.765
Membrane fusion		3			0.4	0.720			0.1	0.145			0.1	0.096
Regulation of cellular process		26										1		
Physiological process		472		67	65.7	0.726		14	13.7	0.675		11	10.7	0.838
Cellular physiological process		174		21	24.2	0.520		8	5.1	0.246		3	4.0	0.765
Coagulation		4			0.6	0.732			0.1	0.231			0.1	0.171
Death		6			0.8	0.620			0.2	0.377			0.1	0.316
Homeostasis		4			0.6	0.732			0.2	0.377			0.1	0.171
Metabolism		380		52	52.9	0.735		7	11.1	0.251		11	8.6	0.507
Organismal physiological process		39		7	5.4	0.569		3	1.1	0.178		1	0.9	0.650
Pathogenesis		1			0.1	0.306			0.0	0.005			0.0	0.002
Regulation of physiological process		75		12	10.4	0.638		1	2.2	0.535		3	1.7	0.523
Response to stimulus		54		12	7.5	0.135		3	1.6	0.396		3	1.2	0.244
Secretion														
Biological process unknown		6		3	0.8	0.064		1	0.2	0.377		1	0.1	0.316
Development		58		12	8.1	0.210		4	1.7	0.145		2	1.3	0.803
Aging														
Cell differentiation		7												
Embryonic development		1			0.1	0.306			0.0	0.005			0.0	0.002
Genetic transfer		1			0.1	0.306			0.0	0.005			0.0	0.002
Growth		5			0.7	0.683			0.1	0.309			0.1	0.245
Mesoderm development		1			0.1	0.306			0.0	0.005			0.0	0.002
Morphogenesis		46		11	6.4	0.098		4	1.3	0.056		2	1.0	0.628
Pattern specification		1			0.1	0.306			0.0	0.005			0.0	0.002
Pigmentation		2			0.3	0.591			0.1	0.060			0.0	0.032
Regulation of development		4			0.6	0.732			0.1	0.231			0.1	0.171
Regulation of gene expression , epigenetic														
Reproduction		8		2	1.1	0.620			0.2	0.489		2	0.2	0.002
Sex determination														
Sex differentiation														
Regulation of biological process		95		14	13.2	0.731		1	2.8	0.387		3	2.2	0.763
Regulation of cellular process		26		3	3.6	0.734			0.8	0.611		1	0.6	0.821
Regulation of development		4			0.6	0.732			0.1	0.231			0.1	0.171
Regulation of enzyme activity		3			0.4	0.720			0.1	0.145			0.1	0.096
Regulation of gene expression , epigenetic														
Regulation of physiological process		75		12	10.4	0.638		1	2.2	0.535		3	1.7	0.523
Behavior		2		1	0.3	0.591			0.1	0.060			0.0	0.032
Feeding behavior		1			0.1	0.306			0.0	0.005			0.0	0.002
Learning and/or memory		1			0.1	0.306			0.0	0.005			0.0	0.002
Mechanosensory behavior		1		1	0.1	0.306			0.0	0.005			0.0	0.002
Viral life cycle														
Viral infectious cycle														

Supplementary Table 3-3. continued

GO term	All						P < 0.05							
	All			> 0.5 in log <sub>2</sub> ratio on day 7			< -0.5 in log <sub>2</sub> ratio on day 7							
	Number of clones	Number of clones in GO term	Expectation	Number of clones	Number of clones in GO term	P	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	1100	579	153	84	80.5	0.738	32	16	16.8	0.519	25	12	13.2	0.841
Cellular component		470		66	65.4	0.738		16	13.7	0.519		11	10.7	0.841
Cell		443		59	61.6	0.668		13	12.9	0.668		10	10.1	0.814
Cell fraction		34		6	4.7	0.626		1	1.0	0.520		3	0.8	0.048
Cell projection		1		1	0.1	0.306		1	0.0	0.005		10	0.0	0.002
Intracellular		398		54	55.4	0.724		11	11.6	0.678		10	9.0	0.807
Membrane		132		16	18.4	0.584		3	3.8	0.653		4	3.0	0.729
Extracellular		32		6	4.5	0.549		4	0.9	0.007		1	0.7	0.742
Extracellular matrix		13		4	1.8	0.193		3	0.4	0.001		1	0.3	0.672
Extracellular space		7		1	1.0	0.559		1	0.2	0.437		1	0.2	0.381
Unlocalized		3		1	0.4	0.720		1	0.1	0.145		1	0.1	0.096
cAMP-dependent protein kinase complex		1		1	0.1	0.306		1	0.0	0.005		1	0.0	0.002
Ferritin complex		1		1	0.1	0.306		1	0.0	0.005		1	0.0	0.002
Glycerol-3-phosphate dehydrogenase complex		1		1	0.1	0.306		1	0.0	0.005		1	0.0	0.002
Protein kinase CK2 complex		1		1	0.1	0.306		1	0.0	0.005		1	0.0	0.002
Protein serine/threonine phosphatase complex		1		1	0.1	0.306		1	0.0	0.005		1	0.0	0.002
Ribonucleoside-diphosphate reductase complex		1		1	0.1	0.306		1	0.0	0.005		1	0.0	0.002
Cellular component unknown		9		1.3	0.453				0.3	0.533		1	0.2	0.496