

Supplementary Table 3-4. Gene Ontology terms and numbers of clones the accumulated mRNA levels of which were different between at 15 and 25°C for 7 days in OLHNJ-e1 cells

GO term	All						P < 0.05						
	All			> 0.5 in log <sub>2</sub> ratio on day 7 at 15°C			All			< -0.5 in log <sub>2</sub> ratio on day 7 at 15°C			
	Number of clones GO term	Number of clones GO term	Expectation	Number of clones GO term	Number of clones GO term	P	Number of clones GO term	Number of clones GO term	Expectation	Number of clones GO term	Number of clones GO term	Expectation	P
All	1209	621	159	89	81.7	0.372	60	26	30.8	57	38	29.3	
Molecular function	558	78	73.4	78	73.4	0.372	60	26	30.8	57	38	29.3	
Signal transducer activity	48	5	6.3	5	6.3	0.413		2	2.4		2	2.3	0.128
Receptor activity	19	1	2.5	1	2.5	0.326		1	0.9		1	0.9	0.116
Receptor binding	18	2	2.4	2	2.4	0.449		1	0.9		1	0.8	0.118
Receptor signaling protein activity	5	1	0.7	1	0.7	0.437		1	0.2		1	0.2	0.107
Binding	359	54	47.2	54	47.2	0.236		15	17.8		26	16.9	0.010
Amino acid binding													
Calcium oxalate binding	5	2	0.7	2	0.7	0.200			0.2		2	0.2	0.003
Carbohydrate binding	3	1	0.4	1	0.4	0.441			0.1		1	0.1	0.073
Cofactor binding	2		0.3		0.3	0.377			0.1		1	0.1	0.044
Drug binding	7		0.9		0.9	0.384			0.3		1	0.3	0.123
Glycosaminoglycan binding	2		0.3		0.3	0.377			0.1		1	0.1	0.044
Isoprenoid binding	17		2.2		2.2	0.369		1	0.8		1	0.8	0.121
Lipid binding	64		8.4		8.4	0.111		4	3.2		5	3.0	0.082
Metal ion binding	147		19.3		19.3	0.451		4	7.3		9	6.9	0.104
Nucleic acid binding	98		12.9		12.9	0.447		2	4.9		8	4.6	0.043
Nucleotide binding	1		0.1		0.1	0.206			0.0		1	0.0	0.010
Oxygen binding	3		0.4		0.4	0.441			0.1		1	0.1	0.073
Peptide binding	91		12.0		12.0	0.205		7	4.5		5	4.3	0.129
Protein binding	18		2.4		2.4	0.449		1	0.9		1	0.8	0.118
Pyridoxal phosphate binding	1		0.1		0.1	0.206			0.0		1	0.0	0.010
Receptor binding	2		0.3		0.3	0.377			0.1		1	0.1	0.044
Ribonucleoprotein binding	1		0.1		0.1	0.206			0.0		1	0.0	0.010
Selenium binding	1		0.1		0.1	0.206			0.0		1	0.0	0.010
Steroid binding	3		0.4		0.4	0.441			0.1		1	0.1	0.073
Tetrapyrrole binding													
Vitamin binding	208		27.4		27.4	0.163		5	10.3		21	9.8	0.000
Catalytic activity	4		0.5		0.5	0.451			0.2		4	0.2	0.094
Helicase activity	82		10.8		10.8	0.174		4	4.1		8	3.9	0.017
Hydrolase activity	11		1.4		1.4	0.248			0.5		3	0.5	0.002
Isomerase activity	18		2.4		2.4	0.449		1	0.9		1	0.8	0.118
Kinase activity	18		2.4		2.4	0.449			0.9		5	0.8	0.000
Ligase activity	8		1.1		1.1	0.384			0.4		1	0.4	0.127
Lyase activity	56		7.4		7.4	0.451			2.8		4	2.6	0.109
Oxidoreductase activity	1		0.1		0.1	0.206			0.0		1	0.0	0.010
Polyketide synthase activity	5		0.7		0.7	0.437			0.2		1	0.2	0.107
Small protein conjugating enzyme activity	41		5.4		5.4	0.267		1	2.0		1	1.9	0.122
Transferase activity	21		2.8		2.8	0.603		2	1.0		1	1.0	0.111
Enzyme regulator activity	7		0.9		0.9	0.000		1	0.3		1	0.3	0.123
Caspase regulator activity	11		1.4		1.4	0.451		1	0.5		1	0.5	0.130
Enzyme activator activity	5		0.7		0.7	0.200			0.2		2	0.2	0.107
Enzyme inhibitor activity													
GTPase regulator activity	4		0.5		0.5	0.451			0.2		1	0.2	0.094
Nitric-oxide synthase regulator activity	1		0.1		0.1	0.206			0.0		1	0.0	0.010
Kinase regulator activity	2		0.3		0.3	0.377			0.1		1	0.1	0.044
Ornithine decarboxylase regulator activity													
Phosphatase regulator activity													

P and P values were obtained by Mann-Whitney test and  $\chi^2$  test, respectively.

Red and blue color boxes represent the clone numbers of which were significantly more and less than the expectation values, respectively (P < 0.05).

Supplementary Table 3-4. 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	1209	159	81.7	0.372	60	26	30.8	0.116
Molecular function	621	159	81.7	0.372	60	26	30.8	0.116
Transporter activity	558	78	73.4	0.1041	20	20	27.7	0.053
Amine/polyamine transporter activity	1	1	0.1	0.206	0	0	0.0	0.030
Auxiliary transport protein activity	3	3	0.4	0.441	0	0	0.0	0.232
Carbohydrate transporter activity	1	1	0.1	0.206	0	0	0.0	0.030
Carrier activity	31	31	4.1	0.054	1	1	1.5	0.254
Channel/pore class transporter activity	9	9	1.2	0.327	0	0	0.4	0.436
Drug transporter activity	21	21	2.8	0.442	1	1	1.0	0.348
Electron transporter activity	3	3	0.4	0.441	0	0	0.1	0.232
Intracellular transporter activity	29	29	3.8	0.063	1	1	1.4	0.271
Ion transporter activity	3	3	0.4	0.441	0	0	0.1	0.232
Lipid transporter activity	2	2	0.3	0.377	0	0	0.1	0.136
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	1	1	0.1	0.206	0	0	0.0	0.030
Organic acid transporter activity	2	2	0.3	0.377	0	0	0.1	0.136
Oxygen transporter activity	7	7	0.9	0.384	0	0	0.3	0.414
Protein transporter activity	1	1	0.1	0.206	0	0	0.0	0.030
Vitamin/cofactor transporter activity	40	40	5.3	0.448	2	2	2.0	0.397
Transcription regulator activity	11	11	1.4	0.276	0	0	0.5	0.437
RNA polymerase II transcription factor activity	1	1	0.1	0.206	0	0	0.0	0.030
RNA polymerase III transcription factor activity	7	7	0.9	0.005	2	2	0.3	0.035
Transcription cofactor activity	24	24	3.2	0.437	1	1	1.2	0.409
Transcription factor activity	4	4	0.5	0.451	0	0	0.2	0.304
Transcriptional activator activity	4	4	0.5	0.451	0	0	0.2	0.304
Transcriptional repressor activity	4	4	0.5	0.451	0	0	0.2	0.304
Transcription initiation factor activity	95	95	12.5	0.034	1	1	4.7	0.095
Transcription termination factor activity	4	4	0.5	0.451	1	1	0.2	0.304
Structural molecule activity	1	1	0.1	0.206	0	0	0.0	0.030
Extracellular matrix structural constituent	8	8	1.1	0.355	0	0	0.4	0.428
Structural constituent of bone	1	1	0.1	0.206	0	0	0.0	0.030
Structural constituent of cytoskeleton	1	1	0.1	0.206	0	0	0.0	0.030
Structural constituent of muscle	68	68	8.9	0.049	3	3	3.4	0.081
Structural constituent of ribosome	25	25	3.3	0.446	1	1	1.2	0.419
Translation regulator activity	25	25	3.3	0.446	1	1	1.2	0.419
Translation factor activity, nucleic acid binding	4	4	0.5	0.451	0	0	0.2	0.304
Chaperone regulator activity	4	4	0.5	0.451	0	0	0.2	0.304
Antioxidant activity	8	8	1.1	0.384	1	1	0.4	0.428
Peroxidase activity	6	6	0.8	0.412	1	1	0.3	0.390
Molecular function unknown	2	2	0.3	0.377	0	0	0.1	0.136
Motor activity	2	2	0.3	0.377	0	0	0.1	0.136
Microtubule motor activity	2	2	0.3	0.377	0	0	0.1	0.136

Supplementary Table 3-4. continued

GO term	All			P < 0.05			P < 0.05		
	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	1209	159	81.7	60	26	30.8	57	38	29.3
Biological process	621	159	81.7	60	26	30.8	57	38	29.3
Cellular process	552	79	72.6	0	21	27.4	0	34	26.0
Cell communication	247	34	32.5	0	9	12.3	0	18	11.6
Cell differentiation	81	15	10.7	0	6	4.0	0	4	3.8
Cellular physiological process	9	2	1.2	0	6	0.4	0	1	0.4
Membrane fusion	201	28	26.4	0	6	10.0	0	16	9.5
Regulation of cellular process	4	1	0.5	0	1	0.2	0	2	0.2
Physiological process	31	3	4.1	0	1	1.5	0	2	1.5
Cellular physiological process	513	67	67.5	0	13	25.5	0	33	24.2
Cellular physiological process	201	28	26.4	0	6	10.0	0	16	9.5
Coagulation	5	2	0.7	0	1	0.2	0	1	0.2
Death	9	2	1.2	0	1	0.4	0	1	0.4
Homeostasis	5	2	0.7	0	1	0.2	0	1	0.2
Metabolism	403	53	53.0	0	9	20.0	0	29	19.0
Organismal physiological process	36	6	4.7	0	2	1.8	0	2	1.7
Pathogenesis	1	0	0.1	0	1	0.0	0	1	0.0
Regulation of physiological process	75	7	9.9	0	1	3.7	0	2	3.5
Response to stimulus	56	11	7.4	0	3	2.8	0	4	2.6
Secretion	7	2	0.9	0	1	0.3	0	1	0.3
Biological process unknown	60	11	7.9	0	6	3.0	0	2	2.8
Development	1	0	0.1	0	1	0.0	0	1	0.0
Aging	9	2	1.2	0	1	0.4	0	1	0.4
Cell differentiation	1	0	0.1	0	1	0.0	0	1	0.0
Embryonic development	8	1	1.1	0	1	0.4	0	1	0.4
Genetic transfer	2	0	0.3	0	1	0.1	0	1	0.1
Growth	47	10	6.2	0	5	2.3	0	2	2.2
Mesoderm development	1	0	0.1	0	1	0.0	0	1	0.0
Morphogenesis	2	0	0.2	0	1	0.0	0	1	0.0
Pattern specification	1	0	0.1	0	1	0.0	0	1	0.0
Pigmentation	2	0	0.3	0	1	0.1	0	1	0.1
Regulation of development	5	0	0.7	0	1	0.2	0	1	0.2
Regulation of gene expression, epigenetic	8	2	1.1	0	1	0.4	0	1	0.4
Reproduction	99	11	13.0	0	2	4.9	0	3	4.7
Sex determination	31	3	4.1	0	1	1.5	0	2	1.5
Sex differentiation	5	0	0.7	0	1	0.2	0	1	0.2
Regulation of biological process	3	2	0.4	0	1	0.1	0	1	0.1
Regulation of cellular process	3	2	0.4	0	1	0.1	0	1	0.1
Regulation of development	3	2	0.4	0	1	0.1	0	1	0.1
Regulation of enzyme activity	75	7	9.9	0	1	3.7	0	2	3.5
Regulation of gene expression, epigenetic	2	0	0.3	0	1	0.1	0	1	0.1
Regulation of physiological process	1	0	0.1	0	1	0.0	0	1	0.0
Behavior	1	0	0.1	0	1	0.0	0	1	0.0
Feeding behavior	1	0	0.1	0	1	0.0	0	1	0.0
Learning and/or memory	1	0	0.1	0	1	0.0	0	1	0.0
Mechanosensory behavior	1	0	0.1	0	1	0.0	0	1	0.0
Viral life cycle	1	0	0.1	0	1	0.0	0	1	0.0
Viral infectious cycle	1	0	0.1	0	1	0.0	0	1	0.0

Supplementary Table 3-4. continued

GO term	All						P < 0.05			P < 0.05				
	Number of clones		Number of clones in		Expectation		P		Number of clones		Expectation		P	
	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term	GO term
All	1209	621	159	89	81.7	60	26	30.8	57	38	29.3			
Cellular component	506	206	71	66.5	0.371	21	25.1	0.290	31	23.9	0.042			
Cell	478	145	64	62.9	0.449	20	23.7	0.308	29	22.5	0.046			
Cell fraction	35	1	6	4.6	0.389	2	1.7	0.426	4	1.7	0.037			
Cell projection	1	0	0	0.1	0.206	0	0.0	0.030	0	0.0	0.010			
Intracellular	424	145	55	55.8	0.451	14	21.0	0.105	28	20.0	0.054			
Membrane	145	32	20	19.1	0.448	8	7.2	0.434	8	6.8	0.125			
Extracellular	32	14	8	4.2	0.076	5	1.6	0.015	1	1.5	0.130			
Extracellular matrix	14	8	5	1.8	0.036	2	0.7	0.216	1	0.7	0.127			
Extracellular space	8	2	2	1.1	0.384	2	0.4	0.056	0	0.4	0.127			
Unlocalized	3	0	1	0.4	0.441	0	0.1	0.232	0	0.1	0.073			
cAMP-dependent protein kinase complex	2	0	0	0.3	0.377	0	0.1	0.136	0	0.1	0.044			
Ferritin complex	2	0	0	0.3	0.377	0	0.1	0.136	0	0.1	0.044			
Glycerol-3-phosphate dehydrogenase complex	1	0	0	0.1	0.206	0	0.0	0.030	0	0.0	0.010			
Protein kinase CK2 complex	1	0	0	0.1	0.206	0	0.0	0.030	0	0.0	0.010			
Protein serine/threonine phosphatase complex	1	0	0	0.1	0.206	0	0.0	0.030	0	0.0	0.010			
Ribonucleoside-diphosphate reductase complex	1	0	0	0.1	0.206	0	0.0	0.030	0	0.0	0.010			
Cellular component unknown	12	3	3	1.6	0.293	1	0.6	0.433	1	0.6	0.129			

Supplementary Table 3-5. Gene Ontology terms and numbers of clones expressing changes in the accumulated mRNA levels in OLHdrR-e3 cells cultured at 25°C during 7 days

GO term	All			P<0.05		
	Number of clones in GO term	Number of clones in Expectation	P	Number of clones in GO term	Expectation	P
All	1296	103	110.9	84	45.4	27
Molecular function	701	205	99.5	37	17	14.6
Signal transducer activity	629	92	8.1	34	40.8	14
Receptor activity	51	3	3.3	1	3.3	0.053
Receptor binding	21	1	3.3	1	1.4	0.166
Receptor signaling protein activity	17	1	2.7	1	1.1	0.192
Binding	5	1	0.8	21	0.3	0.225
Receptor signaling protein activity	403	61	63.7	2	26.1	0.139
Amino acid binding	2	2	0.3	2	0.1	0.000
Calcium oxalate binding	5	1	0.8	1	0.3	0.225
Carbohydrate binding	4	4	0.6	1	0.3	0.206
Cofactor binding	2	1	0.3	1	0.1	0.119
Drug binding	7	1	1.1	1	0.5	0.240
Glycosaminoglycan binding	1	1	0.2	1	0.1	0.038
Isoprenoid binding	17	3	2.7	2	1.1	0.218
Lipid binding	80	16	12.7	8	5.2	0.121
Metal ion binding	159	20	25.2	6	10.3	0.095
Nucleic acid binding	113	17	17.9	3	7.3	0.066
Nucleotide binding	1	1	0.2	1	0.1	0.038
Oxygen binding	4	4	0.6	7	0.3	0.206
Peptide binding	104	16	16.5	7	6.7	0.240
Protein binding	17	1	2.7	1	1.1	0.192
Pyridoxal phosphate binding	3	3	0.5	1	0.2	0.173
Receptor binding	2	1	0.3	1	0.1	0.119
Ribonucleoprotein binding	3	1	0.5	1	0.2	0.173
Selenium binding	2	1	0.3	1	0.1	0.119
Steroid binding	3	1	0.5	1	0.2	0.173
Tetrapyrrole binding	3	1	0.5	1	0.2	0.173
Vitamin binding	3	1	0.5	1	0.2	0.173
Catalytic activity	254	41	40.2	18	16.5	0.230
Helicase activity	4	4	0.6	18	0.3	0.206
Hydrolase activity	93	15	14.7	6	6.0	0.235
Isomerase activity	17	3	2.7	6	1.1	0.192
Kinase activity	25	4	4.0	1	1.6	0.143
Ligase activity	21	4	3.3	1	1.4	0.166
Lyase activity	15	1	2.4	1	1.0	0.205
Oxidoreductase activity	69	14	10.9	11	4.5	0.065
Polyketide synthase activity	1	1	0.2	1	0.1	0.038
Small protein conjugating enzyme activity	6	1	0.9	1	0.4	0.236
Transferase activity	50	6	7.9	2	3.2	0.214
Enzyme regulator activity	24	3	3.8	1	1.6	0.241
Caspase regulator activity	8	2	1.3	1	0.5	0.241
Enzyme activator activity	12	1	1.9	1	0.8	0.225
Enzyme inhibitor activity	5	5	0.8	1	0.3	0.225
GTPase regulator activity	4	1	0.6	1	0.3	0.206
Nitric-oxide synthase regulator activity	1	1	0.2	1	0.1	0.038
Kinase regulator activity	1	1	0.2	1	0.1	0.038
Ornithine decarboxylase regulator activity	1	1	0.2	1	0.1	0.038
Phosphatase regulator activity	1	1	0.2	1	0.1	0.038

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

Red and blue color boxes represent the clone numbers of which were significantly more and less than the expectation values, respectively (P<0.05).

Supplementary Table 3-5. continued

GO term	All			P < 0.05			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	Number of clones in GO term	Number of clones in GO term	Expectation P
All	1296	701	110.9	84	37	45.4	27	17	14.6
Molecular function	629	92	99.5	34	34	40.8	14	14	13.1
Transporter activity	90	15	14.2	6	6	5.8	3	3	1.9
Amine/polyamine transporter activity	1		0.1			0.1			0.0
Auxiliary transport protein activity	3		0.5			0.2			0.1
Carbohydrate transporter activity	31	2	4.9			2.0		1	0.6
Carrier activity	8	2	1.3			0.5			0.2
Channel/pore class transporter activity	28	3	4.4			1.8			0.6
Electron transporter activity	3	1	0.5			0.2			0.1
Intracellular transporter activity	30	4	4.7			1.9		2	0.6
Ion transporter activity	4		0.6			0.3			0.1
Lipid transporter activity	2	1	0.3			0.1			0.0
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	1		0.2			0.1			0.0
Organic acid transporter activity	2	1	0.3			0.1			0.0
Oxygen transporter activity	8	1	1.3			0.5		1	0.2
Protein transporter activity	46	7	7.3			3.0			1.0
Vitamin/cofactor transporter activity	14	1	2.2			0.9			0.3
Transcription regulator activity	9	4	1.4			0.6			0.2
RNA polymerase II transcription factor activity	28	2	4.4			1.8			0.6
RNA polymerase III transcription factor activity	5	1	0.8			0.3			0.1
Transcription cofactor activity	4		0.6			0.3			0.1
Transcription factor activity	2		0.3			0.1			0.0
Transcriptional activator activity	95	7	15.0			6.2		1	2.0
Transcriptional repressor activity	5	1	0.8			0.3			0.1
Transcription initiation factor activity	2		0.3			0.1			0.0
Transcription termination factor activity	2		0.3			0.1			0.0
Structural molecule activity	95	7	15.0			6.2		1	2.0
Extracellular matrix structural constituent	5	1	0.8			0.3			0.1
Structural constituent of bone	2		0.3			0.1			0.0
Structural constituent of cytoskeleton	11	2	1.7			0.7		1	0.2
Structural constituent of muscle	2		0.3			0.1			0.0
Structural constituent of ribosome	66	4	10.4			4.3			1.4
Translation regulator activity	28	8	4.4			1.8		2	0.6
Translation factor activity, nucleic acid binding	28	8	4.4			1.8		2	0.6
Chaperone regulator activity	1	1	0.2			0.1			0.0
Antioxidant activity	6	4	0.9			0.4			0.1
Peroxidase activity	6	4	0.9			0.4			0.1
Molecular function unknown	14	1	2.2			0.9			0.3
Motor activity	10	1	1.6			0.6			0.2
Microtubule motor activity	4		0.6			0.3			0.1

Supplementary Table 3-5. 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		< -0.5 in log <sub>2</sub> ratio on day 7	
	Number of clones in clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	1296	701	110.9	0.482	84	37	45.4	0.143
Biological process	618	97	97.8	0.482			17	14.6
Cellular process	273	36	43.2	0.216			17	12.9
Cell differentiation	87	11	13.8	0.352			7	5.7
Cellular physiological process	223	4	1.4	0.480			1	1.8
Membrane fusion	4	1	0.6	0.470			7	4.6
Regulation of cellular process	31	3	4.9	0.344				0.1
Physiological process	570	85	90.2	0.391			15	11.9
Cellular physiological process	223	32	35.3	0.399			7	4.6
Coagulation	5	1	0.8	0.438				0.1
Death	8	1	1.3	0.464				0.6
Homeostasis	5	1	0.8	0.438				0.6
Metabolism	452	68	71.5	0.431			10	9.4
Organismal physiological process	43	8	6.8	0.452				0.9
Pathogenesis	1	1	0.2	0.267				0.0
Regulation of physiological process	85	11	13.4	0.379			1	1.8
Response to stimulus	63	15	10.0	0.110			6	1.3
Secretion								0.2
Biological process unknown	11	4	1.7	0.132			1	0.2
Development	67	14	10.6	0.256			8	1.4
Aging								0.6
Cell differentiation	9	2	1.4	0.480				0.0
Embryonic development	1	1	0.2	0.267				0.0
Genetic transfer	1	1	0.2	0.267				0.0
Growth	8	3	1.3	0.193				0.2
Mesoderm development	2	1	0.3	0.438			6	0.0
Morphogenesis	53	11	8.4	0.311				1.1
Pattern specification	1	1	0.2	0.267				0.0
Pigmentation	2		0.3	0.438				0.0
Regulation of development	5	1	0.8	0.438				0.1
Regulation of gene expression, epigenetic								0.2
Reproduction	9	2	1.4	0.480			1	0.2
Sex determination								0.6
Sex differentiation								0.3
Regulation of biological process	110	12	17.4	0.171			3	7.1
Regulation of cellular process	31	3	4.9	0.344				2.0
Regulation of development	5	1	0.8	0.438				0.3
Regulation of enzyme activity	3		0.5	0.482				0.2
Regulation of gene expression, epigenetic								0.1
Regulation of physiological process	85	11	13.4	0.379			3	5.5
Behavior	2	1	0.3	0.438				0.1
Feeding behavior	1	1	0.2	0.267				0.1
Learning and/or memory	1	1	0.2	0.267				0.1
Mechanosensory behavior	1	1	0.2	0.267				0.1
Viral life cycle	1	1	0.2	0.267				0.0
Viral infectious cycle	1	1	0.2	0.267				0.1

Supplementary Table 3-5. 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 Expectation	P	
	Number of clones in clones GO term	Number of clones in clones GO term	Number of clones in clones GO term	Number of clones in clones GO term	Number of clones in clones GO term	Number of clones in clones GO term				
All	1296	701	205	103	110.9	84	34	45.4	17	14.6
Cellular component	563	80	89.1	0.251	27	36.5	0.058	16	11.7	0.227
Cell	531	72	84.0	0.151	22	34.4	0.019	16	11.1	0.154
Cell fraction	37	6	5.9	0.473	1	2.4	0.191	1	0.8	0.558
Cell projection	474	65	75.0	0.193	19	30.7	0.019	15	9.9	0.120
Intracellular	157	19	24.8	0.200	8	10.2	0.199	5	3.3	0.400
Membrane	31	5	4.9	0.468	5	2.0	0.055	5	0.6	0.597
Extracellular	15	4	2.4	0.310	4	1.0	0.005	4	0.3	0.549
Extracellular matrix	6	0.9	0.4	0.401	0.4	0.4	0.236	0.1	0.1	0.241
Extracellular space	5	0.8	0.438		0.3	0.225		0.1	0.186	
Unlocalized	1	0.2	0.267		0.1	0.038		0.0	0.001	
cAMP-dependent protein kinase complex	2	0.3	0.438		0.1	0.119		0.0	0.021	
Ferritin complex	1	0.2	0.267		0.1	0.038		0.0	0.001	
Glycerol.3-phosphate dehydrogenase complex	1	0.2	0.267		0.1	0.038		0.0	0.001	
Protein kinase CK2 complex	1	0.2	0.267		0.1	0.038		0.0	0.001	
Protein serine/threonine phosphatase complex	1	0.2	0.267		0.1	0.038		0.0	0.001	
Ribonucleoside-diphosphate reductase complex	1	0.2	0.267		0.1	0.038		0.0	0.001	
Cellular component unknown	17	4	2.7	0.390	1	1.1	0.218	1	0.4	0.579