

Supplementary Table 3-6. Gene Ontology terms and numbers of clones expressing changes in the accumulated mRNA levels in OLNDR-e3 cells cultured at 15°C during 3 days

GO term	All				P<0.05									
	All		> 0.5 in log ₂ ratio on day 3		> 0.5 in log ₂ ratio on day 3		< -0.5 in log ₂ ratio on day 3							
	Number of clones in GO term	Number of clones in Expectation	P	Number of clones GO term	Number of clones in Expectation	P	Number of clones GO term	Number of clones in Expectation	P					
All	1118	625	277	143	154.9	0.230	66	33	36.90	0.388	113	64	63.17	0.840
Molecular function	564	130	139.7	2	1.2	0.346	2	2	0.30	0.500	1	1	0.51	0.966
Signal transducer activity	44	8	10.9	2	1.0	0.300	2	2	0.24	0.436	1	1	0.40	0.876
Receptor activity	21	3	5.2	2	0.5	0.090	2	2	0.12	0.213	3	3	0.20	0.507
Receptor binding	14	3	3.5	1	1.7	0.105	1	1	0.41	0.565	3	3	0.71	0.033
Receptor signaling protein activity	361	81	89.4	6	4.2	0.268	6	6	0.06	0.058	4	4	1.72	0.174
Binding	2	2	0.5	17	16.4	0.361	17	17	3.90	0.552	20	20	14.76	0.217
Amino acid binding	5	4	1.0	66	36.2	0.358	35	35	8.62	0.499	20	20	14.76	0.217
Calcium oxalate binding	4	2	0.5	23	24.5	0.349	23	23	5.84	0.534	8	8	10.01	0.633
Carbohydrate binding	2	2	0.5	1	0.2	0.297	1	1	0.06	0.058	1	1	0.51	0.966
Cofactor binding	7	4	1.7	6	4.2	0.268	6	6	0.30	0.500	10	10	9.10	0.889
Drug binding	17	17	17.0	1	0.2	0.297	1	1	0.06	0.058	5	5	1.42	0.009
Glycosaminoglycan binding	66	66	66.0	1	0.2	0.297	1	1	0.06	0.058	5	5	1.42	0.009
Isoprenoid binding	146	146	146.0	2	1.2	0.346	2	2	0.83	0.506	5	5	1.42	0.009
Lipid binding	99	99	99.0	5	3.5	0.286	5	5	0.83	0.506	5	5	1.42	0.009
Metal ion binding	1	1	1.0	14	14.0	0.286	14	14	0.83	0.506	5	5	1.42	0.009
Nucleic acid binding	5	5	5.0	1	0.2	0.297	1	1	0.06	0.058	1	1	0.51	0.966
Nucleotide binding	90	90	90.0	2	1.2	0.346	2	2	0.30	0.500	10	10	9.10	0.889
Oxygen binding	1	1	1.0	22	22.3	0.361	22	22	5.31	0.136	10	10	9.10	0.889
Peptide binding	14	14	14.0	5	3.5	0.286	5	5	0.83	0.506	5	5	1.42	0.009
Protein binding	1	1	1.0	2	2.0	0.297	2	2	0.06	0.058	1	1	0.51	0.966
Pyridoxal phosphate binding	2	2	2.0	2	2.0	0.362	2	2	0.12	0.213	5	5	4.25	0.896
Receptor binding	3	3	3.0	7	7.0	0.340	7	7	0.18	0.342	5	5	4.25	0.896
Ribonucleoprotein binding	229	229	229.0	56	56.7	0.361	56	56	13.52	0.536	20	20	23.15	0.581
Selenium binding	4	4	4.0	19	19.0	0.300	19	19	0.24	0.436	7	7	8.59	0.708
Steroid binding	85	85	85.0	4	3.7	0.358	4	4	0.89	0.488	2	2	1.52	0.965
Tetrapyrrole binding	19	19	19.0	7	7.0	0.218	7	7	1.12	0.418	2	2	1.92	0.759
Vitamin binding	19	19	19.0	8	8.0	0.115	8	8	1.12	0.021	2	2	1.92	0.759
Catalytic activity	13	13	13.0	3	3.2	0.355	3	3	0.77	0.524	1	1	1.31	0.867
Helicase activity	66	66	66.0	13	16.4	0.249	13	13	3.90	0.552	4	4	6.67	0.400
Hydrolase activity	1	1	1.0	13	16.4	0.249	13	13	3.90	0.552	4	4	6.67	0.400
Isomerase activity	6	6	6.0	4	4.0	0.297	4	4	0.06	0.058	4	4	6.67	0.400
Kinase activity	42	42	42.0	4	4.0	0.297	4	4	0.06	0.058	4	4	6.67	0.400
Ligase activity	19	19	19.0	4	4.0	0.297	4	4	0.06	0.058	4	4	6.67	0.400
Oxidoreductase activity	19	19	19.0	7	7.0	0.218	7	7	1.12	0.418	2	2	1.92	0.759
Polyketide synthase activity	6	6	6.0	4	4.0	0.297	4	4	0.06	0.058	4	4	6.67	0.400
Small protein conjugating enzyme activity	42	42	42.0	13	16.4	0.249	13	13	3.90	0.552	4	4	6.67	0.400
Transferase activity	19	19	19.0	7	7.0	0.218	7	7	1.12	0.418	2	2	1.92	0.759
Enzyme regulator activity	6	6	6.0	3	3.0	0.509	3	3	0.35	0.000	5	5	4.25	0.896
Caspase regulator activity	11	11	11.0	4	4.0	0.263	4	4	2.48	0.403	5	5	4.25	0.896
Enzyme activator activity	4	4	4.0	1	1.0	0.300	1	1	1.12	0.418	5	5	4.25	0.896
Enzyme inhibitor activity	2	2	2.0	2	2.0	0.090	2	2	0.12	0.213	1	1	0.20	0.507
GTPase regulator activity	1	1	1.0	2	2.0	0.297	2	2	0.06	0.058	1	1	0.20	0.507
Nitric-oxide synthase regulator activity	1	1	1.0	1	1.0	0.300	1	1	0.24	0.436	3	3	1.11	0.188
Kinase regulator activity	2	2	2.0	2	2.0	0.090	2	2	0.12	0.213	1	1	0.20	0.507
Ornithine decarboxylase regulator activity	1	1	1.0	1	1.0	0.297	1	1	0.06	0.058	1	1	0.10	0.209
Phosphatase regulator activity	1	1	1.0	1	1.0	0.297	1	1	0.06	0.058	1	1	0.10	0.209

P and P values were obtained by Kruskal-Wallis ANOVA and χ^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 3-6. continued

GO term	P < 0.05													
	All					> 0.5 in log ₂ ratio on day 3			< -0.5 in log ₂ ratio on day 3					
	Number of clones in GO term	Number of clones in Expectation	P	Number of clones GO term	Number of clones in Expectation	P	Number of clones GO term	Number of clones in Expectation	P	Number of clones GO term	P			
All	1118	625	277	143	154.9	0.230	66	33	36.90	0.388	113	64	63.17	0.840
Molecular function	564	130	139.7	19	20.3	0.352	29	4	4.84	0.562	59	57.01	8.29	0.534
Transporter activity	82	1	0.2	0.297					0.06	0.058	6	0.10	0.209	
Amine/polyamine transporter activity														
Auxiliary transport protein activity														
Carbohydrate transporter activity														
Carrier activity	31	6	7.7	0.314			2	1.83	0.542		1	3.13	0.356	
Channel/pore class transporter activity	7	4	1.7	0.105				0.41	0.565		2	0.71	0.346	
Drug transporter activity														
Electron transporter activity	27	6	6.7	0.360			2	1.59	0.573		1	2.73	0.456	
Intracellular transporter activity	3	1	0.7	0.340				0.18	0.342			0.30	0.719	
Ion transporter activity	30	6	7.4	0.330			2	1.77	0.552		1	3.03	0.378	
Lipid transporter activity	3	0.7	0.340					0.18	0.342			0.30	0.719	
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	2	1	0.5	0.362				0.12	0.213			0.20	0.507	
Organic acid transporter activity	1	0.2	0.297					0.06	0.058			0.10	0.209	
Oxygen transporter activity	2	0.5	0.362					0.12	0.213			0.20	0.507	
Protein transporter activity	7	1	1.7	0.353				0.41	0.565			0.71	0.802	
Vitamin/cofactor transporter activity														
Transcription regulator activity	36	11	8.9	0.292			5	2.13	0.085		4	3.64	0.933	
RNA polymerase II transcription factor activity	10	2	2.5	0.362			1	0.59	0.568		1	1.01	0.625	
RNA polymerase III transcription factor activity														
Transcription cofactor activity	5	4	1.2	0.026			4	0.30	0.000			0.51	0.966	
Transcription factor activity	22	8	5.5	0.206			3	1.30	0.233		3	2.22	0.849	
Transcriptional activator activity	4	1.0	0.300					0.24	0.436			0.40	0.876	
Transcriptional repressor activity	4	1	1.0	0.300				0.24	0.436			0.40	0.876	
Transcription initiation factor activity														
Transcription termination factor activity														
Structural molecule activity	91	22	22.5	0.362			5	5.37	0.574		11	9.20	0.666	
Extracellular matrix structural constituent	5	4	1.2	0.026			1	0.30	0.500		2	0.51	0.162	
Structural constituent of bone	2	2	0.5	0.090				0.12	0.213		1	0.20	0.507	
Structural constituent of cytoskeleton	9	4	2.2	0.212			1	0.53	0.575		3	0.91	0.095	
Structural constituent of muscle	1	0.2	0.297					0.06	0.058			0.10	0.209	
Structural constituent of ribosome	66	9	16.4	0.054				3.90	0.070		6	6.67	0.938	
Translational regulator activity	26	8	6.4	0.316			1	1.53	0.576		6	2.63	0.076	
Translation factor activity, nucleic acid binding	26	8	6.4	0.316			1	1.53	0.576		6	2.63	0.076	
Chaperone regulator activity														
Antioxidant activity	6	1.5	0.223					0.35	0.542			0.61	0.886	
Peroxisome activity	6	1.5	0.223					0.35	0.542			0.61	0.886	
Molecular function unknown	10	2.5	0.121					0.59	0.568			1.01	0.610	
Motor activity	7	4	1.7	0.105			1	0.41	0.565		2	0.71	0.346	
Microtubule motor activity	3	2	0.7	0.206				0.18	0.342		1	0.30	0.719	

Supplementary Table 3-6. 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	1118	277	143	154.9	33	36.90	113	64	63.17
Biological process	625	143	154.9	36.90	33	36.90	113	64	63.17
Cellular process	547	136	135.5	0.362	29	32.29	62	55.29	0.403
Cell communication	236	59	58.5	0.362	11	13.93	27	23.85	0.587
Cell differentiation	73	19	18.1	0.359	3	4.31	12	7.38	0.129
Cellular physiological process	9	2	2.2	0.352	1	0.53	1	0.91	0.666
Membrane fusion	195	52	48.3	0.307	10	11.51	22	19.71	0.685
Regulation of cellular process	4	1	1.0	0.300	0	0.24	0	0.40	0.876
Physiological process	29	6	7.2	0.343	2	1.71	3	2.93	0.799
Cellular physiological process	511	124	126.6	0.352	27	30.17	54	51.65	0.794
Cellular physiological process	195	52	48.3	0.307	10	11.51	22	19.71	0.685
Coagulation	5	1	1.2	0.346	0	0.30	0	0.51	0.966
Death	9	2	2.2	0.140	0	0.53	0	0.91	0.666
Homeostasis	3	0	0.7	0.340	0	0.18	0	0.30	0.719
Metabolism	412	93	102.1	0.213	18	24.32	42	41.64	0.963
Organismal physiological process	37	12	9.2	0.232	3	2.18	6	3.74	0.362
Pathogenesis	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Regulation of physiological process	74	21	18.3	0.297	5	4.37	9	7.48	0.707
Response to stimulus	54	23	13.4	0.168	6	3.19	11	5.46	0.051
Secretion	7	2	1.7	0.353	0	0.41	2	0.71	0.346
Biological process unknown	59	20	14.6	0.117	6	3.48	11	5.96	0.063
Development	9	2	2.2	0.352	1	0.53	1	0.91	0.666
Cell differentiation	1	1	0.2	0.297	0	0.06	0	0.10	0.209
Embryonic development	9	4	2.2	0.212	2	0.53	2	0.91	0.535
Genetic transfer	2	1	0.5	0.362	0	0.12	1	0.20	0.507
Growth	46	15	11.4	0.195	4	2.72	9	4.65	0.074
Mesoderm development	1	1	0.2	0.297	0	0.06	0	0.10	0.209
Morphogenesis	2	2	1.2	0.346	0	0.12	0	0.20	0.507
Pattern specification	5	2	1.2	0.346	0	0.30	0	0.51	0.966
Pigmentation	8	2	2.0	0.330	0	0.47	1	0.81	0.730
Regulation of gene expression, epigenetic	96	26	23.8	0.328	7	5.67	11	9.70	0.795
Reproduction	29	6	7.2	0.343	2	1.71	3	2.93	0.799
Sex determination	5	2	1.2	0.346	1	0.30	1	0.51	0.966
Sex differentiation	3	0	0.7	0.340	0	0.18	0	0.30	0.719
Regulation of biological process	74	21	18.3	0.297	5	4.37	9	7.48	0.707
Regulation of cellular process	2	2	0.5	0.090	0	0.12	2	0.20	0.004
Regulation of development	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Regulation of enzyme activity	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Regulation of gene expression, epigenetic	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Regulation of physiological process	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Behavior	74	21	18.3	0.297	5	4.37	9	7.48	0.707
Feeding behavior	2	2	0.5	0.090	0	0.12	2	0.20	0.004
Learning and/or memory	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Mechanosensory behavior	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Viral life cycle	1	1	0.2	0.297	0	0.06	1	0.10	0.209
Viral infectious cycle	1	1	0.2	0.297	0	0.06	1	0.10	0.209

Supplementary Table 3-6. continued

GO term	All				P < 0.05				P				
	Number of clones		Number of clones in GO term		> 0.5 in log ₂ ratio on day 3		< -0.5 in log ₂ ratio on day 3						
	of clones	GO term	Expectation	P	Number of clones	Expectation	P	Number of clones					
All	1118	625	277	143	154.9	0.221	66	33	36.90	113	64	63.17	0.950
Cellular component		503		115	124.6	0.165		29	29.69		51	50.84	0.770
Cell		480		107	118.9	0.351		27	28.34		46	48.52	0.933
Cell fraction		36		10	8.9	0.320		3	2.13		4	3.64	0.937
Cell projection		426		101	105.5	0.117		26	25.15		43	43.06	0.396
Intracellular		146		28	36.2	0.080		4	8.62		11	14.76	0.080
Membrane		30		12	7.4	0.362		3	1.77		8	3.03	0.209
Extracellular		14		7	3.5	0.297		2	0.83		4	1.42	0.058
Extracellular matrix		6		2	1.5				0.35		2	0.61	
Extracellular space		1			0.2				0.06			0.10	
Unlocalized		1			0.2				0.06			0.10	
cAMP-dependent protein kinase complex		1			0.2				0.06			0.10	
Ferritin complex													
Glycerol-3-phosphate dehydrogenase complex													
Protein kinase CK2 complex													
Protein serine/threonine phosphatase complex													
Ribonucleoside-diphosphate reductase complex													
Cellular component unknown		12		3	3.0	0.341			0.71		2	1.21	0.792

Supplementary Table 3-7. Gene Ontology terms and numbers of clones the accumulated mRNA levels of which were different between OLHNI-e1 and OLHdirR-e3 cells during culture at 15°C for 3 days

GO term	All						$P < 0.05$			$P < 0.05$			
	All		All		All		> 0.5 in log ₂ ratio on day 3 in OLHdirR-e3		< -0.5 in log ₂ ratio on day 3 in OLHdirR-e3		Expectation	P	
	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Number of clones	Number of clones in GO term			
All	952	537	127	71	71.6	0.862	30	17	16.9	57	25	32.2	
Molecular function	488	37	4.9	0.518	65.1	0.862	67	15	15.4	0.915	23	29.2	0.114
Signal transducer activity	15	14	1.9	0.643	2.0	0.289	3	3	0.5	0.912	2	1.2	0.235
Receptor activity	2	2	0.3	0.651	0.3	0.651	3	3	0.4	0.892	2	0.9	0.213
Receptor binding	317	317	42.3	0.339	42.3	0.339	49	10	10.0	0.881	18	0.8	0.168
Receptor signaling protein activity													0.1
Binding													190
Amino acid binding													0.239
Calcium oxalate binding	4	4	0.5	0.961	0.5	0.961	1	1	0.1	0.290	2	0.2	0.198
Carbohydrate binding	3	3	0.4	0.874	0.4	0.874	1	1	0.1	0.186	2	0.2	0.163
Cofactor binding	2	2	0.3	0.017	0.3	0.017	2	2	0.1	0.081	1	0.1	0.108
Drug binding	6	6	0.8	0.057	0.8	0.057	3	3	0.2	0.470	2	0.4	0.025
Glycosaminoglycan binding	1	1	0.1	0.315	0.1	0.315	1	1	0.0	0.008	1	0.1	0.032
Isonrenoid binding	16	16	2.1	0.664	2.1	0.664	1	1	0.5	0.918	1	1.0	0.207
Lipid binding	55	55	7.3	0.425	7.3	0.425	10	2	1.7	0.838	7	3.3	0.034
Metal ion binding	134	134	17.9	0.882	17.9	0.882	19	3	4.2	0.398	9	8.0	0.236
Nucleic acid binding	88	88	11.7	0.643	11.7	0.643	19	3	2.8	0.847	4	5.3	0.222
Nucleotide binding	1	1	0.1	0.315	0.1	0.315	1	1	0.0	0.008	1	0.1	0.032
Oxygen binding	3	3	0.4	0.874	0.4	0.874	1	1	0.1	0.186	2	0.2	0.163
Peptide binding	78	78	10.4	0.973	10.4	0.973	11	4	2.5	0.501	3	4.7	0.196
Protein binding													
Pyridoxal phosphate binding	14	14	1.9	0.643	1.9	0.643	3	3	0.4	0.892	2	0.8	0.168
Receptor binding													
Ribonucleoprotein binding	1	1	0.1	0.315	0.1	0.315	1	1	0.0	0.008	1	0.1	0.032
Selenium binding	1	1	0.1	0.315	0.1	0.315	1	1	0.0	0.008	1	0.1	0.032
Steroid binding	3	3	0.4	0.882	0.4	0.882	2	2	0.1	0.186	1	0.2	0.163
Tetrapyrrole binding													
Vitamin binding													
Catalytic activity	184	184	24.5	0.229	24.5	0.229	31	9	5.8	0.260	7	11.0	0.114
Helicase activity	4	4	0.5	0.961	0.5	0.961	1	1	0.1	0.290	2	0.2	0.198
Hydrolase activity	70	70	9.3	0.956	9.3	0.956	10	3	2.2	0.823	2	4.2	0.151
Isomerase activity	11	11	1.5	0.975	1.5	0.975	2	2	0.3	0.779	2	0.7	0.234
Kinase activity	15	15	2.0	0.289	2.0	0.289	4	3	0.5	0.912	3	0.9	0.040
Ligase activity	15	15	2.0	0.724	2.0	0.724	2	2	0.5	0.134	3	0.9	0.213
Lyase activity	9	9	1.2	0.784	1.2	0.784	2	2	0.3	0.675	2	0.5	0.079
Oxidoreductase activity	54	54	7.2	0.219	7.2	0.219	11	3	1.7	0.535	1	3.2	0.129
Polyketide synthase activity	1	1	0.1	0.315	0.1	0.315	1	2	0.0	0.008	1	0.1	0.032
Small protein conjugating enzyme activity	4	4	0.5	0.186	0.5	0.186	2	2	0.1	0.000	2	0.2	0.198
Transferase activity	33	33	4.4	0.961	4.4	0.961	4	3	1.0	0.590	3	2.0	0.218
Enzyme regulator activity	17	17	2.3	0.413	2.3	0.413	4	2	0.5	0.910	2	1.0	0.205
Caspase regulator activity	6	6	0.8	0.737	0.8	0.737	1	1	0.2	0.470	1	0.4	0.232
Enzyme activator activity	9	9	1.2	0.236	1.2	0.236	3	1	0.3	0.675	1	0.5	0.240
Enzyme inhibitor activity	4	4	0.5	0.961	0.5	0.961	4	1	0.1	0.290	2	0.2	0.198
GTPase regulator activity													
Nitric-oxide synthase regulator activity	2	2	0.3	0.017	0.3	0.017	2	1	0.1	0.081	1	0.1	0.108
Kinase regulator activity	1	1	0.1	0.315	0.1	0.315	1	1	0.0	0.008	1	0.1	0.032
Ornithine decarboxylase regulator activity	1	1	0.1	0.315	0.1	0.315	1	1	0.0	0.008	1	0.1	0.032
Phosphatase regulator activity													

P and P values were obtained by Mann-Whitney test and χ^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 3-7. continued

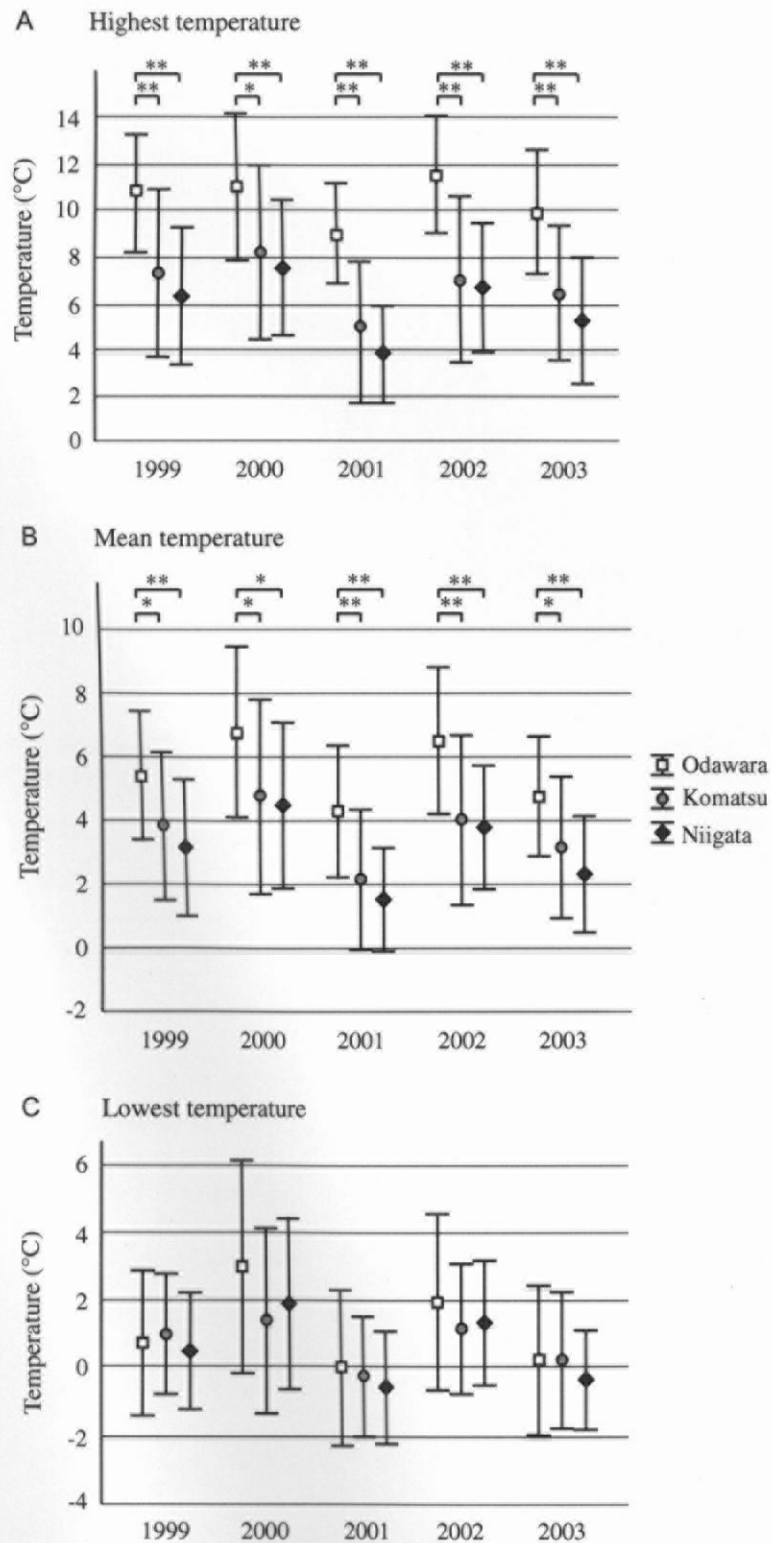
GO term	All						P < 0.05			> 0.5 in log ₂ ratio on day 3 in OI.HdrR-e3			< -0.5 in log ₂ ratio on day 3 in OI.HdrR-e3			
	Number of clones in GO term		Number of clones in GO term		Expectation		P	Number of clones in GO term	Expectation	P	Number of clones in GO term	Expectation	P	Number of clones in GO term	Expectation	P
	952	537	127	71	71.6	30										
Molecular function	488	67	11	65.1	0.862	15	15.4	0.915	23	29.2	0.114					
Transporter activity	71	1		9.5	0.738	4	2.2	0.395	1	4.3	0.076					
Amine/polyamine transporter activity				0.1	0.315		0.0	0.008		0.1	0.032					
Auxiliary transport protein activity																
Carrier activity	28	7		3.7	0.692	2	0.9	0.506		1.7	0.138					
Channel/pore class transporter activity	7			0.9	0.653		0.2	0.546		0.4	0.238					
Drug transporter activity																
Electron transporter activity	22	3		2.9	0.637	2	0.7	0.330		1.3	0.170					
Intracellular transporter activity	3			0.4	0.874		0.1	0.186		0.2	0.163					
Ion transporter activity	27	3		3.6	0.636	2	0.9	0.477		1.6	0.143					
Lipid transporter activity	3			0.4	0.874		0.1	0.186		0.2	0.163					
Nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	2			0.3	0.651		0.1	0.081		0.1	0.108					
Organic acid transporter activity	1			0.1	0.315		0.0	0.008		0.1	0.032					
Oxygen transporter activity	2			0.3	0.651		0.1	0.081		0.1	0.108					
Protein transporter activity	5			0.7	0.837		0.2	0.385		0.3	0.219					
Vitamin/cofactor transporter activity																
Transcription regulator activity	33	9		4.4	0.961	2	1.0	0.644		2.0	0.222					
RNA polymerase II transcription factor activity	9	1		1.2	0.784	1	0.3	0.675		0.5	0.240					
RNA polymerase III transcription factor activity																
Transcription cofactor activity	5	2		0.7	0.308	2	0.2	0.001		0.3	0.219					
Transcription factor activity	19	2		2.5	0.978	2	0.6	0.870		1.1	0.222					
Transcriptional activator activity	4			0.5	0.961		0.1	0.290		0.2	0.198					
Transcriptional repressor activity	4			0.5	0.961		0.1	0.290		0.2	0.198					
Transcription initiation factor activity																
Transcription termination factor activity																
Structural molecule activity	86	4		11.5	0.040	1	2.7	0.458		5.1	0.018					
Extracellular matrix structural constituent	4			0.5	0.961		0.1	0.290		0.2	0.198					
Structural constituent of bone	1			0.1	0.315		0.0	0.008		0.1	0.032					
Structural constituent of cytoskeleton	7	1		0.9	0.653		0.2	0.546		0.4	0.238					
Structural constituent of muscle	1			0.1	0.315		0.0	0.008		0.1	0.032					
Structural constituent of ribosome	65	1		8.7	0.015	1	2.0	0.277		3.9	0.037					
Translation regulator activity	24	4		3.2	0.867	2	0.8	0.755		1.4	0.240					
Translation factor activity, nucleic acid binding	24	4		3.2	0.867	4	0.8	0.755		1.4	0.240					
Chaperone regulator activity																
Antioxidant activity	4	3		0.5	0.007	1	0.1	0.290		0.2	0.198					
Peroxidase activity	4	3		0.5	0.007	1	0.1	0.290		0.2	0.198					
Molecular function unknown	8	1		1.1	0.675		0.3	0.614		0.5	0.241					
Motor activity	5			0.7	0.837		0.2	0.385		0.3	0.219					
Microtubule motor activity	2			0.3	0.651		0.1	0.081		0.12	0.108					

Supplementary Table 3-7. continued

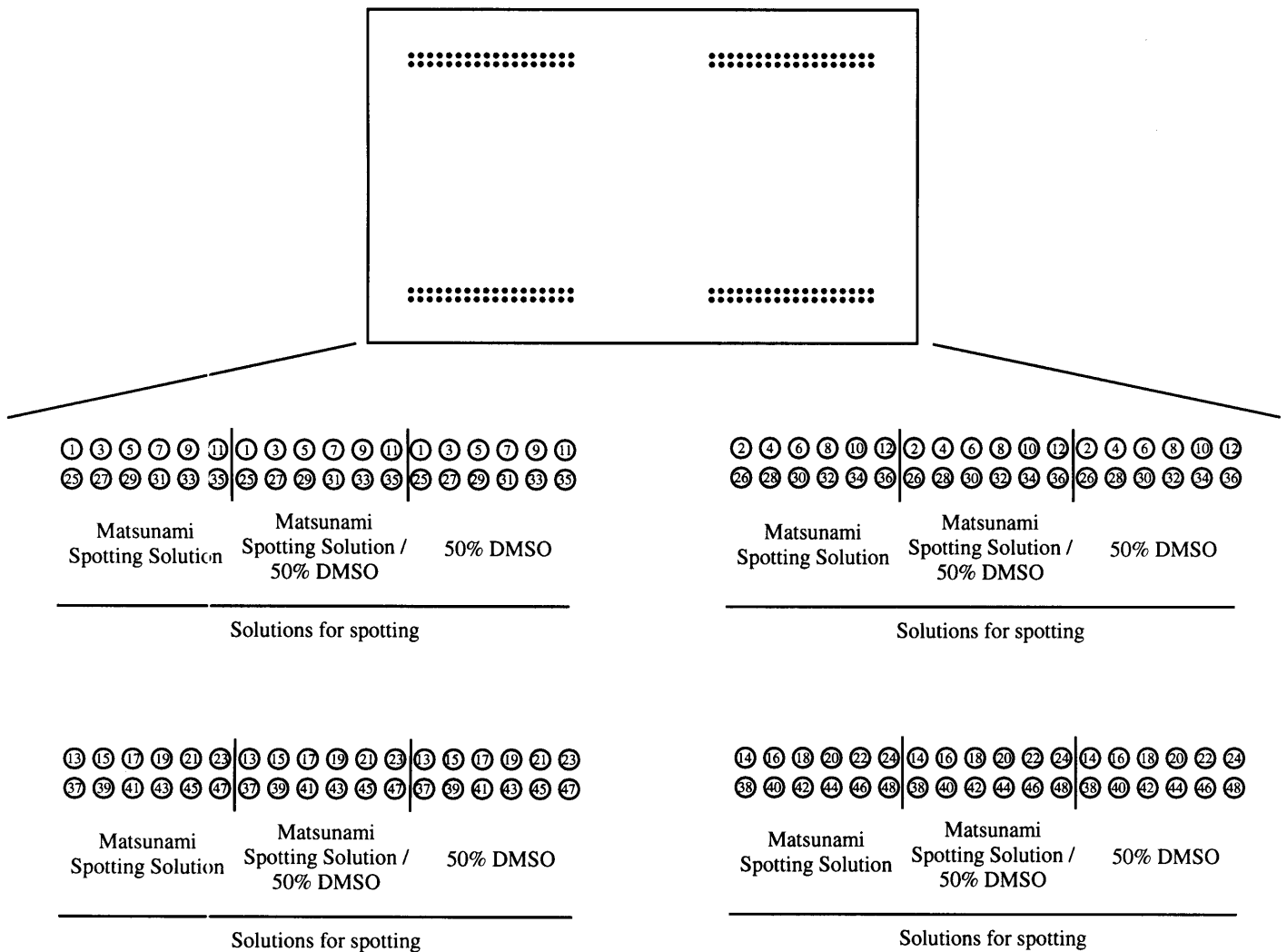
GO term	P < 0.05											
	All					P < 0.05					P	
	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	952	127	71.6	0.846	30	17	16.9	0.848	57	25	32.2	0.140
Biological process	537	71	63.0	0.846	16	14.9	14.9	0.848	23	23	28.3	0.072
Cellular process	472	65	27.3	0.825	29	27.3	27.3	0.917	7	7	12.3	0.237
Cell communication	205	29	8.4	0.971	8	8.4	8.4	0.971	3	3	3.8	0.240
Cell differentiation	63	3	1.2	0.236	3	1.2	1.2	0.236	1	1	0.5	0.065
Cellular physiological process	9	26	22.3	0.495	7	22.3	22.3	0.583	5	5	10.0	0.198
Membrane fusion	167	1	0.5	0.961	1	0.5	0.5	0.961	1	1	1.4	0.159
Regulation of cellular process	4	2	3.2	0.695	2	3.2	3.2	0.695	2	2	1.4	0.065
Physiological process	24	56	58.6	0.787	15	58.6	58.6	0.836	18	18	26.3	0.055
Cellular physiological process	439	26	22.3	0.495	7	22.3	22.3	0.583	5	5	10.0	0.065
Coagulation	167	2	0.7	0.308	2	0.7	0.7	0.308	2	2	0.3	0.219
Death	5	2	0.9	0.558	2	0.9	0.9	0.558	2	2	0.4	0.238
Homeostasis	7	2	0.3	0.651	2	0.3	0.3	0.651	2	2	0.1	0.108
Metabolism	2	42	47.4	0.480	10	47.4	47.4	0.818	14	14	21.3	0.061
Organismal physiological process	355	8	4.0	0.080	3	4.0	4.0	0.109	5	5	1.8	0.020
Pathogenesis	30	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Regulation of physiological process	1	9	8.4	0.971	2	8.4	8.4	0.971	4	4	3.8	0.237
Response to stimulus	63	9	5.7	0.248	5	5.7	5.7	0.248	1	1	2.6	0.177
Secretion	43	9	5.7	0.248	5	5.7	5.7	0.248	1	1	2.6	0.177
Biological process unknown	7	3	0.9	0.105	3	0.9	0.9	0.105	2	2	0.4	0.041
Development	50	10	6.7	0.273	4	6.7	6.7	0.273	3	3	3.0	0.227
Ageing	9	3	1.2	0.236	1	1.2	1.2	0.236	1	1	0.5	0.240
Cell differentiation	1	3	0.1	0.315	3	0.1	0.1	0.315	2	2	0.0	0.008
Embryonic development	9	3	1.1	0.165	3	1.1	1.1	0.165	2	2	0.1	0.032
Genetic transfer	1	1	0.3	0.651	1	0.3	0.3	0.651	1	1	0.5	0.241
Growth	8	3	1.1	0.165	3	1.1	1.1	0.165	2	2	0.1	0.032
Mesoderm development	2	1	0.3	0.651	1	0.3	0.3	0.651	1	1	0.1	0.108
Morphogenesis	38	8	5.1	0.280	2	5.1	5.1	0.280	3	3	2.3	0.237
Pattern specification	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Pigmentation	2	2	0.3	0.651	2	0.3	0.3	0.651	1	1	0.1	0.108
Regulation of development	4	1	0.5	0.961	1	0.5	0.5	0.961	1	1	0.2	0.198
Regulation of gene expression, epigenetic	8	1	1.1	0.675	1	1.1	1.1	0.675	0.3	0.3	0.5	0.241
Reproduction	8	1	1.1	0.675	1	1.1	1.1	0.675	0.3	0.3	0.5	0.241
Sex determination	8	1	1.1	0.675	1	1.1	1.1	0.675	0.3	0.3	0.5	0.241
Sex differentiation	8	1	1.1	0.675	1	1.1	1.1	0.675	0.3	0.3	0.5	0.241
Regulation of biological process	81	11	10.8	0.925	4	10.8	10.8	0.925	4	4	4.8	0.236
Regulation of cellular process	24	2	3.2	0.695	2	3.2	3.2	0.695	2	2	1.4	0.159
Regulation of development	4	1	0.5	0.961	1	0.5	0.5	0.961	1	1	0.2	0.198
Regulation of enzyme activity	3	3	0.4	0.874	1	0.4	0.4	0.874	0.1	0.1	0.2	0.163
Regulation of gene expression, epigenetic	63	9	8.4	0.971	2	8.4	8.4	0.971	2	2	3.8	0.237
Regulation of physiological process	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Behavior	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Feeding behavior	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Learning and/or memory	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Mechanosensory behavior	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Viral life cycle	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032
Viral infectious cycle	1	1	0.1	0.315	1	0.1	0.1	0.315	1	1	0.1	0.032

Supplementary Table 3-7. continued

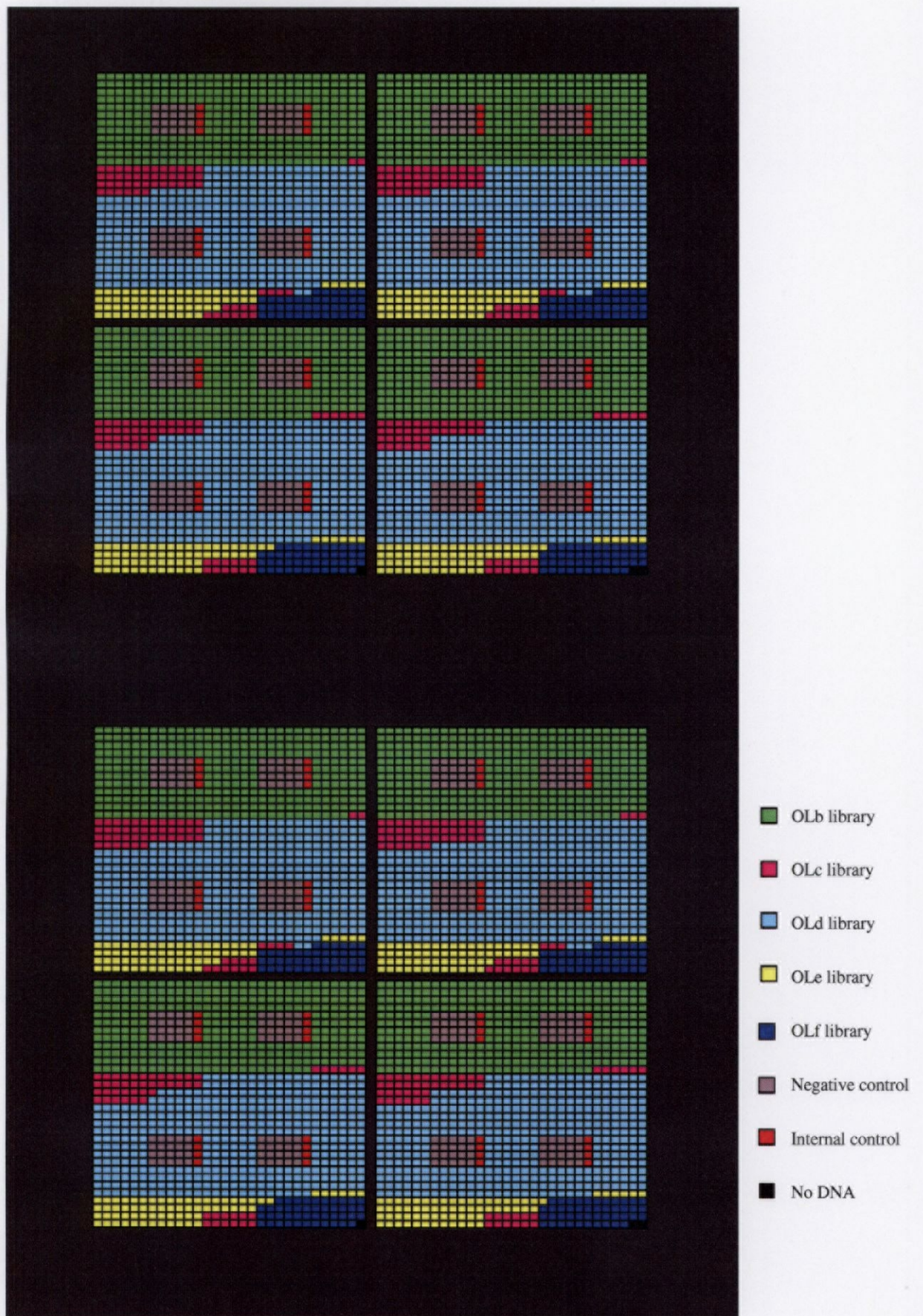
GO term	All			$P < 0.05$			> 0.5 in \log_2 ratio on day 3 in OL.HdrR-e3			< -0.5 in \log_2 ratio on day 3 in OL.HdrR-e3			
	Number of clones in GO term	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P	Number of clones	Number of clones in GO term	Expectation	P
All	952	127	71	71.6		30	17	16.9		57	25	32.2	
Cellular component	537		71	71.6									
Cell	443		54	59.1	0.550		15	14.0	0.859		17	26.5	0.035
Cell fraction	421		46	56.2	0.197		13	13.3	0.904		12	25.2	0.005
Intracellular	28		1	3.7	0.247		1	0.9	0.675			1.7	0.138
Membrane													
Extracellular	377		45	50.3	0.499		13	11.9	0.836		12	22.6	0.015
Extracellular matrix	122		12	16.3	0.349		2	3.8	0.488		2	7.3	0.033
Extracellular space	26		6	3.5	0.275		1	0.8	0.448		4	1.6	0.051
Unlocalized	11		2	1.5	0.975		1	0.3	0.779		1	0.7	0.234
cAMP-dependent protein kinase complex	4		1	0.5	0.961			0.1	0.290		1	0.2	0.198
Ferritin complex	1			0.1	0.315			0.0	0.008			0.1	0.032
Glycerol-3-phosphate dehydrogenase complex				0.1	0.315			0.0	0.008			0.1	0.032
Protein kinase CK2 complex													
Protein serine/threonine phosphatase complex													
Ribonucleoside-diphosphate reductase complex													
Cellular component unknown	11		3	1.5	0.394			0.3	0.779		2	0.7	0.117



Supplementary Fig. 1-1. The differences in the daily highest (A), mean (B) and lowest (C) temperatures in January for 5 years in Odawara, Niigata and Komatsu. The data of Odawara, Komatsu and Niigata, where fish for HdrR inbred strain of the Southern Japanese population, and Kaga and HNI inbred strains of the Northern Japanese population were collected, respectively, were cited from the databases of Japan Meteorological Agency (http://www.jma.go.jp/JMA_HP/jma/index.html). The vertical lines represent SD. Student's *t* test was employed for statistical comparison among the temperatures in the three places for each year (* $P < 0.005$, ** $P < 0.0005$).



Supplementary Figure 2-1. Spot placement diagram. The box represent one of the images in panel A in Fig. 2-2. The numbers correspond to those of genes shown in Supplementary Table 2-2. DNAs of the clones were mixed with indicated solutions for spotting.



Supplementary Fig. 2-2. Spot placement diagram for cDNA microarray containing 7,680 spots (see Fig. 2-4A). Clones from the OL libraries were located as well as artificial genes and clones encoding EF-1 α as negative controls and internal controls, respectively. Spots containing no DNA were also indicated. Upper 4 blocks contained the same DNA sets as in the other 4 blocks.