Functional Annotation Clustering

Help and Manual

Current Gene List: List_1
Current Background: Homo sapiens
2998 DAVID IDs

Options **Classification Stringency** Medium

Rerun using options | Create Sublist

341 Cluster(s)

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Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	RT		525	0.0E0	5.8E0	0.0E0	0.0E0
INTERPRO	Zinc finger, C2H2-like	RT		637	0.0E0	5.2E0	0.0E0	0.0E0
INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	RT		622	0.0E0	5.4E0	0.0E0	0.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	RT		556	0.0E0	6.0E0	0.0E0	0.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	RT		519	0.0E0	6.0E0	0.0E0	0.0E0
UP_KEYWORDS	Nucleus	RT		1680	0.0E0	2.2E0	0.0E0	0.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	RT		496	0.0E0	6.1E0	0.0E0	0.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	RT		455	0.0E0	6.2E0	0.0E0	0.0E0
INTERPRO	Zinc finger, C2H2	RT		642	0.0E0	5.0E0	0.0E0	0.0E0
UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	RT		427	3.2E-315	6.3E0	3.1E-312	2.9E-312
UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	RT		473	2.6E-314	5.8E0	2.1E-311	2.0E-311
UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	RT		393	2.7E-288	6.3E0	1.9E-285	1.8E-285
SMART	ZnF_C2H2	RT		637	4.2E-283	3.4E0	2.0E-280	1.8E-280
UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	RT		355	3.2E-260	6.3E0	2.0E-257	1.9E-257
UP_KEYWORDS	Zinc-finger	RT		811	1.8E-243	3.1E0	4.3E-241	3.3E-241
UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	RT		318	2.3E-236	6.4E0	1.3E-233	1.2E-233
GOTERM_MF_DIRECT	nucleic acid binding	RT		597	2.2E-227	3.6E0	2.8E-224	2.5E-224
UP_KEYWORDS	Transcription	RT		940	2.0E-226	2.7E0	3.3E-224	2.5E-224
UP_KEYWORDS	DNA-binding	RT		854	2.8E-224	2.9E0	3.4E-222	2.6E-222
INTERPRO	Krueppel-associated box	RT		350	8.1E-222	5.4E0	4.7E-219	4.3E-219
UP_KEYWORDS	Transcription regulation	RT		917	4.4E-221	2.7E0	3.5E-219	2.7E-219
UP_SEQ_FEATURE	domain:KRAB	RT		309	7.2E-218	6.1E0	3.7E-215	3.5E-215
UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	RT		275	2.6E-197	6.2E0	1.2E-194	1.2E-194
UP_KEYWORDS	Metal-binding	RT		1153	8.1E-193	2.2E0	5.6E-191	4.3E-191
UP_KEYWORDS	Zinc	RT		877	1.9E-191	2.6E0	1.1E-189	8.7E-190
GOTERM_MF_DIRECT	metal ion binding	RT		863	2.9E-186	2.5E0	1.9E-183	1.7E-183
UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	RT		237	7.5E-173	6.3E0	3.2E-170	3.1E-170
GOTERM_BP_DIRECT	transcription, DNA-templated	RT		813	8.0E-171	2.5E0	4.8E-167	4.6E-167
SMART	KRAB	RT		345	1.2E-161	3.6E0	2.9E-159	2.7E-159
GOTERM_BP_DIRECT	regulation of transcription, DNA-templated	RT		671	2.0E-156	2.6E0	5.9E-153	5.7E-153
GOTERM_MF_DIRECT	DNA binding	RT		705	4.8E-150	2.5E0	1.5E-147	1.4E-147
UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	RT		188	1.6E-135	6.3E0	6.1E-133	5.9E-133
UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	RT		146	2.8E-107	6.4E0	1.0E-104	9.6E-105
GOTERM_CC_DIRECT	intracellular	RT		505	1.1E-93	2.4E0	3.2E-91	2.8E-91
UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	RT		122	1.0E-86	6.2E0	3.1E-84	2.9E-84
GOTERM_MF_DIRECT	transcription factor activity, sequence-specific DNA binding	RT		401	1.9E-79	2.5E0	4.9E-77	4.4E-77
UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	RT		93	2.2E-64	6.2E0	5.1E-62	4.9E-62
UP_SEQ_FEATURE	zinc finger region:C2H2-type 17	RT		74	4.8E-51	6.1E0	7.4E-49	7.1E-49
UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	RT		58	2.8E-39	6.1E0	3.9E-37	3.8E-37
UP_SEQ_FEATURE	zinc finger region:C2H2-type 19	RT		48	2.9E-32	6.1E0	3.5E-30	3.4E-30
UP_SEQ_FEATURE	zinc finger region:C2H2-type 20	RT		32	2.2E-21	6.1E0	2.2E-19	2.1E-19

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:C2H2-type 21	RT		24	1.0E-16	6.3E0	8.6E-15	8.3E-15
UP_SEQ_FEATURE	zinc finger region:C2H2-type 22	RT		23	6.2E-16	6.3E0	5.0E-14	4.8E-14
UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	RT		15	1.9E-10	6.4E0	1.2E-8	1.1E-8
UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	RT		13	6.7E-9	6.3E0	4.0E-7	3.8E-7
Annotation Cluster 2	**Enrichment Score: 92.97**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Nucleotide-binding	RT		786	2.0E-222	3.0E0	1.9E-220	1.5E-220
UP_KEYWORDS	ATP-binding	RT		640	7.5E-190	3.2E0	4.0E-188	3.1E-188
GOTERM_MF_DIRECT	ATP binding	RT		661	8.9E-153	2.6E0	3.8E-150	3.4E-150
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		472	3.3E-142	3.2E0	1.3E-139	1.3E-139
UP_SEQ_FEATURE	domain:Protein kinase	RT		267	2.4E-99	3.8E0	7.9E-97	7.6E-97
INTERPRO	Protein kinase-like domain	RT		294	7.9E-98	3.4E0	3.6E-95	3.3E-95
INTERPRO	Protein kinase, catalytic domain	RT		278	1.2E-96	3.5E0	4.4E-94	4.0E-94
UP_SEQ_FEATURE	binding site:ATP	RT		282	4.3E-91	3.4E0	1.3E-88	1.3E-88
INTERPRO	Protein kinase, ATP binding site	RT		232	2.9E-88	3.8E0	9.6E-86	8.8E-86
UP_KEYWORDS	Kinase	RT		323	3.0E-85	3.0E0	1.2E-83	9.3E-84
UP_KEYWORDS	Serine/threonine-protein kinase	RT		203	8.6E-68	3.5E0	2.8E-66	2.1E-66
UP_SEQ_FEATURE	active site:Proton acceptor	RT		272	1.3E-61	2.8E0	2.7E-59	2.6E-59
GOTERM_MF_DIRECT	protein kinase activity	RT		190	6.6E-56	3.2E0	1.2E-53	1.1E-53
GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT		193	4.6E-54	3.1E0	7.3E-52	6.5E-52
GOTERM_BP_DIRECT	protein phosphorylation	RT		215	8.3E-52	2.8E0	8.3E-49	8.0E-49
INTERPRO	Serine/threonine-protein kinase, active site	RT		166	1.6E-51	3.3E0	2.9E-49	2.6E-49
UP_KEYWORDS	Transferase	RT		469	1.1E-47	1.9E0	2.7E-46	2.1E-46
SMART	S_TKc	RT		188	2.5E-30	2.1E0	2.4E-28	2.1E-28
Annotation Cluster 3	**Enrichment Score: 57.69**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	repeat:ANK 4	RT		131	1.2E-73	5.2E0	3.3E-71	3.2E-71
UP_SEQ_FEATURE	repeat:ANK 5	RT		115	7.0E-69	5.5E0	1.8E-66	1.7E-66
UP_KEYWORDS	ANK repeat	RT		161	2.0E-67	4.2E0	6.1E-66	4.7E-66
UP_SEQ_FEATURE	repeat:ANK 3	RT		139	1.6E-65	4.6E0	3.9E-63	3.8E-63
INTERPRO	Ankyrin repeat	RT		159	2.9E-62	3.9E0	6.6E-60	6.0E-60
INTERPRO	Ankyrin repeat-containing domain	RT		162	1.1E-61	3.8E0	2.2E-59	2.1E-59
UP_SEQ_FEATURE	repeat:ANK 2	RT		146	7.5E-59	4.1E0	1.4E-56	1.4E-56
UP_SEQ_FEATURE	repeat:ANK 1	RT		145	3.2E-58	4.0E0	5.7E-56	5.5E-56
UP_SEQ_FEATURE	repeat:ANK 6	RT		83	6.8E-52	5.7E0	1.1E-49	1.0E-49
SMART	ANK	RT		157	4.9E-38	2.6E0	5.8E-36	5.2E-36
UP_SEQ_FEATURE	repeat:ANK 7	RT		55	3.8E-36	5.9E0	5.0E-34	4.8E-34
Annotation Cluster 4	**Enrichment Score: 37.87**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	rRNA processing	RT		147	3.1E-63	4.1E0	6.1E-60	5.9E-60
UP_KEYWORDS	Ribonucleoprotein	RT		160	7.0E-57	3.7E0	1.9E-55	1.5E-55
GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT		97	6.2E-53	4.8E0	7.4E-50	7.1E-50
GOTERM_BP_DIRECT	SRP-dependent cotranslational protein targeting to membrane	RT		80	2.3E-46	5.0E0	2.0E-43	1.9E-43
GOTERM_BP_DIRECT	translational initiation	RT		97	1.7E-43	4.2E0	1.3E-40	1.2E-40
KEGG_PATHWAY	Ribosome	RT		96	1.9E-38	3.7E0	2.4E-36	1.1E-36
GOTERM_BP_DIRECT	viral transcription	RT		81	2.0E-37	4.3E0	1.3E-34	1.3E-34
GOTERM_CC_DIRECT	cytosolic large ribosomal subunit	RT		58	2.5E-35	5.4E0	3.2E-33	2.8E-33
UP_KEYWORDS	Ribosomal protein	RT		98	5.8E-34	3.6E0	1.1E-32	8.4E-33
GOTERM_CC_DIRECT	ribosome	RT		93	3.6E-32	3.6E0	4.0E-30	3.5E-30

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	structural constituent of ribosome	RT		100	1.2E-22	2.7E0	1.0E-20	9.2E-21
GOTERM_BP_DIRECT	translation	RT		109	1.6E-22	2.6E0	5.7E-20	5.5E-20
GOTERM_CC_DIRECT	cytosolic small ribosomal subunit	RT		34	2.3E-16	4.5E0	1.4E-14	1.2E-14
Annotation Cluster 5	**Enrichment Score: 34.73**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Leucine-rich repeat, typical subtype	RT		141	1.0E-76	4.9E0	3.0E-74	2.7E-74
UP_SEQ_FEATURE	repeat:LRR 5	RT		147	1.2E-64	4.3E0	2.9E-62	2.8E-62
UP_SEQ_FEATURE	repeat:LRR 4	RT		153	3.0E-62	4.1E0	6.5E-60	6.3E-60
UP_SEQ_FEATURE	repeat:LRR 6	RT		136	1.5E-61	4.4E0	3.1E-59	3.0E-59
UP_SEQ_FEATURE	repeat:LRR 7	RT		123	5.4E-61	4.8E0	1.0E-58	1.0E-58
INTERPRO	Leucine-rich repeat	RT		159	1.4E-59	3.7E0	2.6E-57	2.4E-57
UP_KEYWORDS	Leucine-rich repeat	RT		167	7.8E-59	3.7E0	2.2E-57	1.7E-57
UP_SEQ_FEATURE	repeat:LRR 3	RT		161	1.1E-55	3.6E0	1.9E-53	1.8E-53
UP_SEQ_FEATURE	repeat:LRR 1	RT		164	2.2E-53	3.5E0	3.7E-51	3.6E-51
UP_SEQ_FEATURE	repeat:LRR 2	RT		164	3.8E-53	3.5E0	6.3E-51	6.1E-51
UP_SEQ_FEATURE	repeat:LRR 8	RT		105	4.7E-53	4.8E0	7.6E-51	7.3E-51
SMART	LRR_TYP	RT		141	8.3E-53	3.2E0	1.3E-50	1.2E-50
UP_SEQ_FEATURE	repeat:LRR 9	RT		95	5.9E-48	4.8E0	8.6E-46	8.2E-46
UP_SEQ_FEATURE	repeat:LRR 10	RT		81	4.0E-40	4.8E0	5.7E-38	5.5E-38
UP_SEQ_FEATURE	repeat:LRR 11	RT		72	1.3E-36	4.9E0	1.7E-34	1.7E-34
UP_SEQ_FEATURE	repeat:LRR 12	RT		65	1.3E-33	4.9E0	1.6E-31	1.6E-31
INTERPRO	Cysteine-rich flanking region, C-terminal	RT		58	1.2E-26	4.3E0	1.4E-24	1.3E-24
UP_SEQ_FEATURE	repeat:LRR 13	RT		52	1.3E-25	4.7E0	1.4E-23	1.3E-23
UP_SEQ_FEATURE	repeat:LRR 14	RT		42	5.5E-21	4.8E0	5.4E-19	5.2E-19
UP_SEQ_FEATURE	repeat:LRR 15	RT		36	3.3E-18	4.8E0	3.0E-16	2.9E-16
SMART	LRRCT	RT		58	2.1E-17	2.8E0	1.1E-15	1.0E-15
UP_SEQ_FEATURE	repeat:LRR 16	RT		31	3.1E-15	4.7E0	2.4E-13	2.3E-13
UP_SEQ_FEATURE	repeat:LRR 17	RT		27	1.1E-14	5.1E0	8.3E-13	8.0E-13
UP_SEQ_FEATURE	repeat:LRR 18	RT		20	9.4E-11	5.0E0	6.2E-9	6.0E-9
UP_SEQ_FEATURE	repeat:LRR 19	RT		19	1.6E-10	5.2E0	1.0E-8	1.0E-8
UP_SEQ_FEATURE	repeat:LRR 20	RT		18	2.7E-10	5.3E0	1.7E-8	1.6E-8
UP_SEQ_FEATURE	repeat:LRR 21	RT		14	5.9E-8	5.3E0	3.0E-6	2.9E-6
UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
UP_SEQ_FEATURE	repeat:LRR 23	RT		8	1.2E-4	5.5E0	3.5E-3	3.4E-3
UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
Annotation Cluster 6	**Enrichment Score: 29.55**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	RT		142	3.7E-55	3.8E0	5.6E-52	5.4E-52
UP_KEYWORDS	Spliceosome	RT		82	5.3E-37	4.4E0	1.1E-35	8.6E-36
KEGG_PATHWAY	Spliceosome	RT		91	9.8E-35	3.5E0	8.0E-33	3.8E-33
GOTERM_CC_DIRECT	catalytic step 2 spliceosome	RT		64	7.6E-30	4.4E0	7.6E-28	6.6E-28
UP_KEYWORDS	mRNA splicing	RT		111	7.7E-28	2.9E0	1.2E-26	9.0E-27
UP_KEYWORDS	mRNA processing	RT		128	5.9E-27	2.6E0	8.3E-26	6.4E-26
GOTERM_CC_DIRECT	spliceosomal complex	RT		59	4.6E-24	4.0E0	4.1E-22	3.6E-22
GOTERM_BP_DIRECT	RNA splicing	RT		54	1.4E-6	1.9E0	7.3E-5	7.0E-5
Annotation Cluster 7	**Enrichment Score: 27.38**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:SCAN box	RT		51	2.3E-32	5.8E0	2.9E-30	2.8E-30
INTERPRO	Transcription regulator SCAN	RT		52	8.4E-32	5.4E0	1.1E-29	1.0E-29

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Retrovirus capsid, C-terminal	RT		52	6.3E-26	4.6E0	6.6E-24	6.0E-24
SMART	SCAN	RT		51	2.5E-22	3.5E0	1.7E-20	1.5E-20
Annotation Cluster 8	**Enrichment Score: 21.42**	G		Count	P_Value	Fold Change	Benjamini	FDR
KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT		97	5.0E-39	3.7E0	1.2E-36	5.8E-37
UP_KEYWORDS	Ubl conjugation pathway	RT		213	1.8E-29	2.2E0	3.0E-28	2.3E-28
GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT		134	5.5E-25	2.4E0	5.5E-23	4.9E-23
GOTERM_MF_DIRECT	ubiquitin protein ligase activity	RT		80	1.0E-16	2.5E0	6.0E-15	5.4E-15
GOTERM_BP_DIRECT	protein ubiquitination	RT		115	2.1E-12	1.9E0	3.0E-10	2.9E-10
GOTERM_MF_DIRECT	ligase activity	RT		88	2.8E-10	1.9E0	8.7E-9	7.7E-9
Annotation Cluster 9	**Enrichment Score: 19.34**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Cell cycle	RT		211	1.5E-31	2.2E0	2.6E-30	2.0E-30
UP_KEYWORDS	Cell division	RT		133	1.7E-22	2.4E0	2.2E-21	1.7E-21
GOTERM_BP_DIRECT	cell division	RT		125	1.3E-17	2.1E0	3.2E-15	3.1E-15
UP_KEYWORDS	Mitosis	RT		92	2.4E-16	2.4E0	2.8E-15	2.2E-15
GOTERM_BP_DIRECT	mitotic nuclear division	RT		88	2.4E-12	2.1E0	3.3E-10	3.2E-10
Annotation Cluster 10	**Enrichment Score: 18.32**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Tyrosine-protein kinase	RT		83	1.5E-44	5.1E0	3.4E-43	2.6E-43
INTERPRO	Serine-threonine/tyrosine-protein kinase catalytic domain	RT		97	6.4E-44	4.3E0	1.0E-41	9.6E-42
INTERPRO	Tyrosine-protein kinase, catalytic domain	RT		69	1.2E-38	5.0E0	1.8E-36	1.6E-36
INTERPRO	Tyrosine-protein kinase, active site	RT		70	1.8E-34	4.6E0	2.6E-32	2.4E-32
SMART	TyrKc	RT		69	5.6E-27	3.3E0	4.4E-25	4.0E-25
GOTERM_MF_DIRECT	protein tyrosine kinase activity	RT		77	3.6E-26	3.4E0	3.9E-24	3.4E-24
GOTERM_BP_DIRECT	peptidyl-tyrosine phosphorylation	RT		81	7.3E-24	3.1E0	3.1E-21	3.0E-21
GOTERM_BP_DIRECT	peptidyl-tyrosine autophosphorylation	RT		32	5.2E-17	4.7E0	1.1E-14	1.1E-14
GOTERM_MF_DIRECT	non-membrane spanning protein tyrosine kinase activity	RT		34	2.1E-16	4.4E0	1.2E-14	1.1E-14
GOTERM_MF_DIRECT	transmembrane receptor protein tyrosine kinase activity	RT		26	2.1E-11	4.1E0	7.4E-10	6.6E-10
GOTERM_BP_DIRECT	transmembrane receptor protein tyrosine kinase signaling pathway	RT		43	5.8E-10	2.7E0	6.5E-8	6.2E-8
GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT		33	1.2E-9	3.1E0	4.3E-8	3.8E-8
UP_KEYWORDS	SH2 domain	RT		36	2.1E-6	2.3E0	1.5E-5	1.1E-5
INTERPRO	SH2 domain	RT		39	3.6E-6	2.1E0	8.2E-5	7.5E-5
UP_SEQ_FEATURE	domain:SH2	RT		31	2.9E-5	2.2E0	9.6E-4	9.2E-4
SMART	SH2	RT		35	3.3E-2	1.4E0	2.6E-1	2.3E-1
GOTERM_MF_DIRECT	receptor binding	RT		49	9.6E-1	8.3E-1	1.0E0	9.6E-1
Annotation Cluster 11	**Enrichment Score: 16.22**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	GTP-binding	RT		145	1.3E-35	2.9E0	2.5E-34	1.9E-34
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	RT		133	3.6E-33	2.9E0	4.5E-31	4.3E-31
GOTERM_MF_DIRECT	GTP binding	RT		155	2.7E-28	2.4E0	3.2E-26	2.8E-26
GOTERM_MF_DIRECT	GTPase activity	RT		107	8.1E-25	2.7E0	7.4E-23	6.6E-23
INTERPRO	Small GTP-binding protein domain	RT		76	1.1E-18	2.8E0	1.0E-16	9.4E-17
INTERPRO	Small GTPase superfamily, Ras type	RT		32	3.6E-18	5.1E0	3.3E-16	3.1E-16
INTERPRO	Small GTPase superfamily	RT		60	1.4E-13	2.7E0	8.9E-12	8.1E-12
GOTERM_BP_DIRECT	small GTPase mediated signal transduction	RT		83	1.9E-10	2.0E0	2.2E-8	2.1E-8
UP_SEQ_FEATURE	short sequence motif:Effector region	RT		39	1.1E-8	2.6E0	6.4E-7	6.1E-7
UP_KEYWORDS	Prenylation	RT		46	2.5E-5	1.9E0	1.5E-4	1.2E-4
UP_SEQ_FEATURE	propeptide:Removed in mature form	RT		52	2.8E-3	1.5E0	6.7E-2	6.4E-2
UP_SEQ_FEATURE	lipid moiety-binding region:S-geranylgeranyl cysteine	RT		28	3.2E-3	1.8E0	7.7E-2	7.4E-2

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 12	Enrichment Score: 16.09			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT		55	4.7E-31	5.3E0	5.6E-29	5.4E-29
UP_SEQ_FEATURE	domain:HECT	RT		23	6.6E-14	5.6E0	4.8E-12	4.7E-12
INTERPRO	HECT	RT		23	4.8E-13	5.1E0	3.0E-11	2.7E-11
SMART	HECTc	RT		23	2.8E-9	3.3E0	7.9E-8	7.2E-8
Annotation Cluster 13	**Enrichment Score: 15.77**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Helicase	RT		82	1.0E-31	3.9E0	1.8E-30	1.4E-30
INTERPRO	Helicase, superfamily 1/2, ATP-binding domain	RT		68	1.9E-26	3.8E0	2.1E-24	2.0E-24
INTERPRO	Helicase, C-terminal	RT		67	3.4E-26	3.8E0	3.7E-24	3.4E-24
UP_SEQ_FEATURE	domain:Helicase C-terminal	RT		64	8.9E-26	4.0E0	9.6E-24	9.3E-24
UP_SEQ_FEATURE	domain:Helicase ATP-binding	RT		65	6.9E-25	3.9E0	7.3E-23	7.0E-23
GOTERM_MF_DIRECT	helicase activity	RT		50	1.3E-17	3.5E0	8.6E-16	7.7E-16
SMART	DEXDc	RT		67	1.2E-15	2.5E0	5.7E-14	5.2E-14
SMART	HELICc	RT		66	1.6E-15	2.5E0	7.0E-14	6.4E-14
INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT		41	2.8E-15	3.7E0	2.1E-13	1.9E-13
GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT		38	2.4E-13	3.5E0	1.0E-11	8.9E-12
UP_SEQ_FEATURE	short sequence motif:DEAH box	RT		28	6.7E-13	4.4E0	4.6E-11	4.4E-11
GOTERM_BP_DIRECT	RNA secondary structure unwinding	RT		26	2.2E-9	3.5E0	2.1E-7	2.0E-7
INTERPRO	RNA helicase, DEAD-box type, Q motif	RT		22	2.0E-8	3.7E0	6.2E-7	5.7E-7
UP_SEQ_FEATURE	short sequence motif:Q motif	RT		21	1.4E-7	3.6E0	7.2E-6	6.9E-6
UP_SEQ_FEATURE	short sequence motif:DEAD box	RT		19	6.0E-7	3.6E0	2.6E-5	2.5E-5
INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	RT		16	3.1E-6	3.7E0	7.3E-5	6.7E-5
Annotation Cluster 14	**Enrichment Score: 15.47**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Protein phosphatase	RT		66	4.5E-21	3.4E0	5.7E-20	4.4E-20
GOTERM_BP_DIRECT	protein dephosphorylation	RT		58	9.1E-14	2.7E0	1.4E-11	1.4E-11
GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT		36	9.5E-14	3.7E0	4.4E-12	3.9E-12
Annotation Cluster 15	**Enrichment Score: 15.15**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	active site:Glycyl thioester intermediate	RT		55	4.7E-31	5.3E0	5.6E-29	5.4E-29
INTERPRO	Ubiquitin-conjugating enzyme, active site	RT		24	8.5E-16	5.7E0	6.7E-14	6.2E-14
INTERPRO	Ubiquitin-conjugating enzyme, E2	RT		31	2.1E-15	4.6E0	1.6E-13	1.5E-13
INTERPRO	Ubiquitin-conjugating enzyme/RWD-like	RT		33	2.9E-12	3.7E0	1.6E-10	1.5E-10
GOTERM_MF_DIRECT	ubiquitin conjugating enzyme activity	RT		23	3.8E-12	4.7E0	1.4E-10	1.3E-10
GOTERM_BP_DIRECT	protein K48-linked ubiquitination	RT		26	1.4E-8	3.3E0	1.2E-6	1.1E-6
Annotation Cluster 16	**Enrichment Score: 12.35**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	DNA repair	RT		98	6.9E-16	2.3E0	7.8E-15	6.0E-15
UP_KEYWORDS	DNA damage	RT		110	2.3E-15	2.1E0	2.5E-14	1.9E-14
GOTERM_BP_DIRECT	DNA repair	RT		74	5.3E-8	1.9E0	4.1E-6	4.0E-6
Annotation Cluster 17	**Enrichment Score: 12.02**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	proteasome-mediated ubiquitin-dependent protein catabolic process	RT		99	1.9E-25	2.9E0	8.9E-23	8.6E-23
GOTERM_BP_DIRECT	anaphase-promoting complex-dependent catabolic process	RT		54	3.5E-23	4.0E0	1.4E-20	1.3E-20
GOTERM_BP_DIRECT	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	RT		52	2.3E-22	4.1E0	7.5E-20	7.2E-20
GOTERM_BP_DIRECT	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		48	2.4E-20	4.0E0	6.5E-18	6.2E-18
GOTERM_BP_DIRECT	stimulatory C-type lectin receptor signaling pathway	RT		60	5.3E-20	3.4E0	1.4E-17	1.3E-17
GOTERM_BP_DIRECT	T cell receptor signaling pathway	RT		68	5.6E-16	2.7E0	1.1E-13	1.0E-13
GOTERM_BP_DIRECT	NIK/NF-kappaB signaling	RT		41	1.6E-15	3.7E0	2.9E-13	2.8E-13
GOTERM_BP_DIRECT	Fc-epsilon receptor signaling pathway	RT		73	6.3E-14	2.4E0	1.0E-11	9.8E-12

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	positive regulation of canonical Wnt signaling pathway	RT		53	8.5E-12	2.6E0	1.1E-9	1.1E-9
GOTERM_BP_DIRECT	regulation of mRNA stability	RT		46	1.5E-10	2.6E0	1.7E-8	1.7E-8
GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		18	2.5E-9	4.6E0	2.4E-7	2.3E-7
UP_KEYWORDS	Proteasome	RT		27	2.7E-9	3.5E0	2.4E-8	1.8E-8
GOTERM_CC_DIRECT	proteasome complex	RT		29	1.6E-8	3.1E0	5.0E-7	4.4E-7
GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	RT		26	1.2E-7	3.0E0	8.3E-6	8.0E-6
GOTERM_BP_DIRECT	negative regulation of canonical Wnt signaling pathway	RT		55	2.9E-7	2.0E0	1.9E-5	1.8E-5
GOTERM_BP_DIRECT	Wnt signaling pathway, planar cell polarity pathway	RT		35	3.0E-6	2.3E0	1.5E-4	1.5E-4
KEGG_PATHWAY	Proteasome	RT		23	4.1E-6	2.7E0	1.2E-5	5.8E-6
GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	RT		24	1.4E-4	2.3E0	4.3E-3	4.1E-3
GOTERM_BP_DIRECT	tumor necrosis factor-mediated signaling pathway	RT		36	4.0E-4	1.8E0	1.0E-2	1.0E-2
Annotation Cluster 18	**Enrichment Score: 11.69**	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Actin-related protein	RT		29	2.8E-17	5.3E0	2.4E-15	2.2E-15
SMART	ACTIN	RT		29	4.9E-13	3.6E0	1.8E-11	1.6E-11
INTERPRO	Actin/actin-like conserved site	RT		18	1.0E-10	5.3E0	4.3E-9	3.9E-9
INTERPRO	Actin, conserved site	RT		15	1.3E-8	5.2E0	4.2E-7	3.9E-7
Annotation Cluster 19	**Enrichment Score: 11.41**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	protein K11-linked ubiquitination	RT		25	4.5E-16	5.5E0	8.9E-14	8.6E-14
GOTERM_CC_DIRECT	anaphase-promoting complex	RT		19	5.0E-11	5.2E0	2.1E-9	1.9E-9
GOTERM_BP_DIRECT	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	RT		18	2.5E-9	4.6E0	2.4E-7	2.3E-7
Annotation Cluster 20	**Enrichment Score: 11.35**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	domain:EF-hand 3	RT		61	6.9E-27	4.3E0	7.6E-25	7.3E-25
UP_SEQ_FEATURE	domain:EF-hand 2	RT		76	5.4E-18	2.8E0	4.9E-16	4.7E-16
UP_SEQ_FEATURE	domain:EF-hand 4	RT		38	3.5E-16	4.2E0	2.9E-14	2.8E-14
UP_SEQ_FEATURE	domain:EF-hand 1	RT		72	1.7E-15	2.7E0	1.3E-13	1.3E-13
UP_SEQ_FEATURE	calcium-binding region:1	RT		55	4.0E-14	2.9E0	3.0E-12	2.9E-12
UP_SEQ_FEATURE	calcium-binding region:3	RT		27	2.2E-13	4.7E0	1.6E-11	1.5E-11
UP_SEQ_FEATURE	calcium-binding region:2	RT		51	2.8E-13	2.9E0	2.0E-11	1.9E-11
INTERPRO	EF-Hand 1, calcium-binding site	RT		67	9.0E-12	2.3E0	4.5E-10	4.1E-10
INTERPRO	EF-hand domain	RT		79	1.4E-11	2.1E0	6.7E-10	6.1E-10
INTERPRO	EF-hand-like domain	RT		90	3.9E-11	2.0E0	1.7E-9	1.6E-9
SMART	EFh	RT		72	9.8E-11	2.0E0	3.1E-9	2.8E-9
COG_ONTOLOGY	Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only	RT		31	4.9E-5	1.8E0	7.6E-4	7.6E-4
GOTERM_MF_DIRECT	calcium ion binding	RT		110	8.9E-1	9.1E-1	1.0E0	8.9E-1
UP_KEYWORDS	Calcium	RT		107	9.9E-1	8.4E-1	1.0E0	9.9E-1
Annotation Cluster 21	**Enrichment Score: 11.32**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Motor protein	RT		84	3.8E-36	4.3E0	7.7E-35	5.9E-35
UP_SEQ_FEATURE	domain:Kinesin-motor	RT		33	5.9E-18	5.1E0	5.2E-16	5.0E-16
GOTERM_CC_DIRECT	kinesin complex	RT		37	1.8E-17	4.4E0	1.2E-15	1.0E-15
INTERPRO	Kinesin, motor region, conserved site	RT		32	4.7E-17	4.8E0	4.0E-15	3.6E-15
INTERPRO	Kinesin, motor domain	RT		33	2.9E-16	4.5E0	2.4E-14	2.2E-14
GOTERM_MF_DIRECT	microtubule motor activity	RT		42	1.4E-12	3.1E0	5.4E-11	4.8E-11
GOTERM_CC_DIRECT	microtubule	RT		96	3.1E-11	2.0E0	1.4E-9	1.3E-9
SMART	KISc	RT		33	6.1E-11	3.0E0	2.1E-9	1.9E-9
GOTERM_BP_DIRECT	microtubule-based movement	RT		38	1.4E-9	2.8E0	1.4E-7	1.3E-7

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Microtubule	RT		76	6.1E-8	1.9E0	4.8E-7	3.7E-7
GOTERM_MF_DIRECT	ATP-dependent microtubule motor activity, plus-end-directed	RT		13	1.3E-6	4.6E0	2.9E-5	2.6E-5
UP_SEQ_FEATURE	region of interest:Globular	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
GOTERM_MF_DIRECT	microtubule binding	RT		61	9.1E-6	1.7E0	1.8E-4	1.6E-4
GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class II	RT		25	1.7E-2	1.6E0	2.1E-1	2.0E-1
GOTERM_BP_DIRECT	retrograde vesicle-mediated transport, Golgi to ER	RT		21	5.2E-2	1.5E0	4.8E-1	4.6E-1
Annotation Cluster 22	**Enrichment Score: 11.08**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:AGC-kinase C-terminal	RT		33	2.1E-13	4.0E0	1.5E-11	1.5E-11
INTERPRO	Protein kinase, C-terminal	RT		24	3.5E-13	5.0E0	2.2E-11	2.0E-11
INTERPRO	AGC-kinase, C-terminal	RT		33	2.9E-12	3.7E0	1.6E-10	1.5E-10
SMART	S_TK_X	RT		32	2.1E-8	2.6E0	5.3E-7	4.8E-7
Annotation Cluster 23	**Enrichment Score: 11.06**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	T cell receptor signaling pathway	RT		66	7.4E-24	3.4E0	2.0E-22	9.5E-23
KEGG_PATHWAY	Prostate cancer	RT		56	3.4E-19	3.3E0	5.9E-18	2.8E-18
KEGG_PATHWAY	Pancreatic cancer	RT		43	1.1E-15	3.4E0	1.3E-14	5.9E-15
KEGG_PATHWAY	ErbB signaling pathway	RT		51	2.2E-15	3.0E0	2.4E-14	1.1E-14
KEGG_PATHWAY	Acute myeloid leukemia	RT		39	2.3E-15	3.6E0	2.4E-14	1.1E-14
KEGG_PATHWAY	Chronic myeloid leukemia	RT		44	3.2E-14	3.2E0	3.1E-13	1.4E-13
KEGG_PATHWAY	Endometrial cancer	RT		35	3.8E-13	3.5E0	3.3E-12	1.6E-12
KEGG_PATHWAY	Glioma	RT		40	4.2E-13	3.2E0	3.5E-12	1.7E-12
KEGG_PATHWAY	B cell receptor signaling pathway	RT		41	1.0E-12	3.1E0	8.0E-12	3.8E-12
KEGG_PATHWAY	VEGF signaling pathway	RT		38	1.0E-12	3.2E0	8.1E-12	3.8E-12
KEGG_PATHWAY	Prolactin signaling pathway	RT		41	3.6E-12	3.0E0	2.7E-11	1.3E-11
KEGG_PATHWAY	Non-small cell lung cancer	RT		34	5.4E-11	3.1E0	3.5E-10	1.7E-10
KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT		38	9.4E-11	2.9E0	5.6E-10	2.7E-10
KEGG_PATHWAY	Bladder cancer	RT		27	6.4E-10	3.4E0	3.2E-9	1.5E-9
KEGG_PATHWAY	Melanoma	RT		37	2.2E-9	2.7E0	1.0E-8	4.7E-9
KEGG_PATHWAY	Sphingolipid signaling pathway	RT		52	3.3E-9	2.2E0	1.4E-8	6.6E-9
KEGG_PATHWAY	Renal cell carcinoma	RT		35	3.7E-9	2.8E0	1.5E-8	7.2E-9
KEGG_PATHWAY	Central carbon metabolism in cancer	RT		31	4.5E-7	2.5E0	1.6E-6	7.5E-7
KEGG_PATHWAY	Choline metabolism in cancer	RT		40	4.2E-6	2.1E0	1.2E-5	5.8E-6
KEGG_PATHWAY	Signaling pathways regulating pluripotency of stem cells	RT		44	7.1E-4	1.6E0	1.6E-3	7.6E-4
KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT		38	2.1E-3	1.6E0	4.5E-3	2.1E-3
Annotation Cluster 24	**Enrichment Score: 11.05**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	lipid moiety-binding region:N-myristoyl glycine	RT		57	6.6E-18	3.3E0	5.8E-16	5.5E-16
UP_KEYWORDS	Myristate	RT		72	2.6E-14	2.5E0	2.7E-13	2.1E-13
UP_KEYWORDS	Lipoprotein	RT		153	4.0E-3	1.2E0	1.9E-2	1.5E-2
Annotation Cluster 25	**Enrichment Score: 9.95**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	negative regulation of protein kinase activity	RT		53	5.0E-16	3.2E0	9.7E-14	9.3E-14
GOTERM_MF_DIRECT	protein kinase inhibitor activity	RT		32	3.9E-12	3.7E0	1.4E-10	1.3E-10
GOTERM_BP_DIRECT	negative regulation of JAK-STAT cascade	RT		25	1.0E-9	3.7E0	1.0E-7	1.0E-7
GOTERM_BP_DIRECT	cytokine-mediated signaling pathway	RT		41	7.9E-5	1.9E0	2.6E-3	2.5E-3
Annotation Cluster 26	**Enrichment Score: 9.83**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Chagas disease (American trypanosomiasis)	RT		58	4.9E-16	2.9E0	5.7E-15	2.7E-15
KEGG_PATHWAY	Toxoplasmosis	RT		58	1.3E-14	2.7E0	1.3E-13	5.9E-14
KEGG_PATHWAY	Toll-like receptor signaling pathway	RT		49	7.2E-10	2.4E0	3.4E-9	1.6E-9

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
KEGG_PATHWAY	Leishmaniasis	RT		32	2.0E-6	2.3E0	6.3E-6	3.0E-6
KEGG_PATHWAY	Pertussis	RT		32	8.0E-6	2.2E0	2.3E-5	1.1E-5
Annotation Cluster 27	**Enrichment Score: 9.7**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Motor protein	RT		84	3.8E-36	4.3E0	7.7E-35	5.9E-35
UP_KEYWORDS	Myosin	RT		44	1.5E-28	5.9E0	2.3E-27	1.8E-27
INTERPRO	Myosin head, motor domain	RT		34	3.4E-20	5.3E0	3.3E-18	3.1E-18
GOTERM_CC_DIRECT	myosin complex	RT		38	6.2E-20	4.8E0	4.2E-18	3.7E-18
UP_SEQ_FEATURE	domain:Myosin head-like	RT		31	3.0E-19	5.7E0	2.8E-17	2.7E-17
GOTERM_MF_DIRECT	motor activity	RT		41	1.3E-15	3.7E0	6.5E-14	5.8E-14
SMART	MYSc	RT		34	1.9E-14	3.5E0	7.5E-13	6.8E-13
INTERPRO	IQ motif, EF-hand binding site	RT		43	2.6E-12	3.1E0	1.5E-10	1.4E-10
GOTERM_MF_DIRECT	microfilament motor activity	RT		18	4.3E-11	5.4E0	1.5E-9	1.3E-9
UP_KEYWORDS	Muscle protein	RT		32	4.4E-11	3.5E0	4.3E-10	3.3E-10
UP_SEQ_FEATURE	region of interest:Actin-binding	RT		21	5.3E-11	4.9E0	3.6E-9	3.4E-9
UP_KEYWORDS	Calmodulin-binding	RT		55	9.2E-11	2.5E0	8.7E-10	6.8E-10
INTERPRO	Myosin, N-terminal, SH3-like	RT		15	1.0E-10	6.2E0	4.3E-9	3.9E-9
INTERPRO	Myosin-like IQ motif-containing domain	RT		17	1.2E-10	5.5E0	5.0E-9	4.6E-9
GOTERM_CC_DIRECT	muscle myosin complex	RT		15	4.8E-10	6.0E0	1.9E-8	1.6E-8
UP_SEQ_FEATURE	domain:IQ	RT		28	2.7E-8	3.1E0	1.5E-6	1.4E-6
INTERPRO	Myosin tail	RT		15	4.1E-8	4.9E0	1.3E-6	1.1E-6
GOTERM_MF_DIRECT	calmodulin binding	RT		60	6.6E-7	1.9E0	1.6E-5	1.4E-5
UP_KEYWORDS	Actin-binding	RT		71	1.1E-6	1.8E0	8.2E-6	6.3E-6
GOTERM_CC_DIRECT	myosin filament	RT		12	2.9E-6	4.8E0	6.4E-5	5.7E-5
SMART	IQ	RT		29	5.5E-6	2.3E0	9.6E-5	8.7E-5
UP_SEQ_FEATURE	domain:IQ 1	RT		16	2.3E-5	3.3E0	7.9E-4	7.6E-4
UP_SEQ_FEATURE	domain:IQ 2	RT		16	2.3E-5	3.3E0	7.9E-4	7.6E-4
UP_KEYWORDS	Thick filament	RT		11	3.1E-5	4.4E0	1.9E-4	1.4E-4
UP_SEQ_FEATURE	domain:IQ 3	RT		12	9.8E-5	3.7E0	3.0E-3	2.9E-3
GOTERM_BP_DIRECT	actin filament-based movement	RT		11	1.1E-4	3.8E0	3.5E-3	3.4E-3
UP_SEQ_FEATURE	domain:IQ 4	RT		9	5.2E-4	4.1E0	1.4E-2	1.4E-2
KEGG_PATHWAY	Tight junction	RT		30	1.3E-3	1.8E0	2.8E-3	1.3E-3
UP_SEQ_FEATURE	domain:IQ 5	RT		6	1.4E-2	3.7E0	2.7E-1	2.6E-1
GOTERM_BP_DIRECT	muscle contraction	RT		27	3.1E-2	1.5E0	3.4E-1	3.3E-1
UP_SEQ_FEATURE	domain:IQ 6	RT		3	3.3E-1	2.6E0	1.0E0	9.6E-1
Annotation Cluster 28	**Enrichment Score: 9.43**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	termination of RNA polymerase II transcription	RT		42	3.7E-17	3.9E0	8.4E-15	8.1E-15
GOTERM_BP_DIRECT	mRNA 3'-end processing	RT		35	1.3E-15	4.1E0	2.4E-13	2.3E-13
GOTERM_BP_DIRECT	RNA export from nucleus	RT		27	1.6E-7	2.9E0	1.1E-5	1.1E-5
KEGG_PATHWAY	mRNA surveillance pathway	RT		36	1.4E-5	2.1E0	3.8E-5	1.8E-5
GOTERM_BP_DIRECT	mRNA export from nucleus	RT		34	6.1E-5	2.0E0	2.1E-3	2.0E-3
Annotation Cluster 29	**Enrichment Score: 8.93**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	repeat:ANK 6	RT		83	6.8E-52	5.7E0	1.1E-49	1.0E-49
UP_SEQ_FEATURE	repeat:ANK 7	RT		55	3.8E-36	5.9E0	5.0E-34	4.8E-34
UP_SEQ_FEATURE	repeat:ANK 8	RT		41	1.3E-27	6.1E0	1.5E-25	1.5E-25
UP_SEQ_FEATURE	repeat:ANK 9	RT		36	9.9E-24	6.0E0	1.0E-21	9.8E-22
UP_SEQ_FEATURE	repeat:ANK 10	RT		26	1.7E-17	6.1E0	1.4E-15	1.4E-15

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	repeat:ANK 11	RT		23	6.2E-16	6.3E0	5.0E-14	4.8E-14
UP_SEQ_FEATURE	repeat:ANK 12	RT		16	1.6E-10	6.1E0	1.0E-8	1.0E-8
UP_SEQ_FEATURE	repeat:ANK 13	RT		13	2.9E-8	5.9E0	1.5E-6	1.5E-6
UP_SEQ_FEATURE	repeat:ANK 14	RT		13	2.9E-8	5.9E0	1.5E-6	1.5E-6
UP_SEQ_FEATURE	repeat:ANK 15	RT		13	2.9E-8	5.9E0	1.5E-6	1.5E-6
UP_SEQ_FEATURE	repeat:ANK 16	RT		11	8.5E-7	5.8E0	3.6E-5	3.5E-5
UP_SEQ_FEATURE	repeat:ANK 17	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
UP_SEQ_FEATURE	repeat:ANK 18	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
UP_SEQ_FEATURE	repeat:ANK 19	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
UP_SEQ_FEATURE	repeat:ANK 20	RT		9	2.3E-5	5.6E0	7.9E-4	7.6E-4
UP_SEQ_FEATURE	repeat:ANK 21	RT		9	2.3E-5	5.6E0	7.9E-4	7.6E-4
UP_SEQ_FEATURE	repeat:ANK 22	RT		8	1.2E-4	5.5E0	3.5E-3	3.4E-3
UP_SEQ_FEATURE	repeat:ANK 23	RT		8	1.2E-4	5.5E0	3.5E-3	3.4E-3
UP_SEQ_FEATURE	repeat:ANK 24	RT		6	2.6E-3	5.1E0	6.2E-2	6.0E-2
UP_SEQ_FEATURE	repeat:ANK 25	RT		5	1.1E-2	4.9E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	repeat:ANK 26	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:ANK 27	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
GOTERM_BP_DIRECT	protein targeting to plasma membrane	RT		9	5.9E-2	2.0E0	5.2E-1	5.0E-1
INTERPRO	ZU5	RT		4	3.0E-1	2.1E0	1.0E0	9.1E-1
SMART	DEATH	RT		9	3.4E-1	1.4E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:ZU5	RT		3	3.9E-1	2.3E0	1.0E0	9.6E-1
SMART	ZU5	RT		3	6.9E-1	1.4E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	cytoskeletal adaptor activity	RT		3	7.8E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 30	**Enrichment Score: 8.33**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:BTB	RT		58	2.1E-13	2.7E0	1.5E-11	1.5E-11
INTERPRO	BTB/POZ-like	RT		63	1.2E-9	2.2E0	4.5E-8	4.1E-8
INTERPRO	BTB/POZ fold	RT		65	1.9E-9	2.1E0	6.7E-8	6.1E-8
SMART	BTB	RT		63	9.5E-4	1.5E0	1.2E-2	1.1E-2
Annotation Cluster 31	**Enrichment Score: 8**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Estrogen signaling pathway	RT		58	1.8E-17	3.0E0	2.4E-16	1.1E-16
KEGG_PATHWAY	Chemokine signaling pathway	RT		68	4.2E-8	1.9E0	1.6E-7	7.4E-8
KEGG_PATHWAY	Melanogenesis	RT		41	1.1E-6	2.1E0	3.8E-6	1.8E-6
KEGG_PATHWAY	Cholinergic synapse	RT		42	8.8E-6	2.0E0	2.5E-5	1.2E-5
KEGG_PATHWAY	cAMP signaling pathway	RT		64	1.3E-5	1.7E0	3.5E-5	1.7E-5
Annotation Cluster 32	**Enrichment Score: 7.87**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Viral nucleoprotein	RT		20	2.2E-10	4.9E0	2.0E-9	1.5E-9
GOTERM_CC_DIRECT	viral nucleocapsid	RT		20	8.5E-10	4.5E0	3.1E-8	2.8E-8
UP_KEYWORDS	Virion	RT		20	1.4E-5	2.9E0	8.5E-5	6.6E-5
Annotation Cluster 33	**Enrichment Score: 7.86**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Chronic myeloid leukemia	RT		44	3.2E-14	3.2E0	3.1E-13	1.4E-13
KEGG_PATHWAY	Small cell lung cancer	RT		35	7.0E-6	2.1E0	2.0E-5	9.4E-6
BIOCARTA	Influence of Ras and Rho proteins on G1 to S Transition	RT		21	1.1E-5	2.4E0	5.6E-4	4.0E-4
Annotation Cluster 34	**Enrichment Score: 7.48**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Tubulin/FtsZ, C-terminal	RT		20	3.8E-12	5.4E0	2.0E-10	1.8E-10
INTERPRO	Tubulin, C-terminal	RT		20	3.8E-12	5.4E0	2.0E-10	1.8E-10
INTERPRO	Tubulin, conserved site	RT		20	3.8E-12	5.4E0	2.0E-10	1.8E-10

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Tubulin	RT		20	1.6E-11	5.2E0	7.4E-10	6.8E-10
INTERPRO	Tubulin/FtsZ, 2-layer sandwich domain	RT		19	2.0E-11	5.4E0	9.2E-10	8.4E-10
INTERPRO	Tubulin/FtsZ, GTPase domain	RT		20	5.5E-11	5.0E0	2.4E-9	2.2E-9
SMART	SM00865	RT		19	2.6E-8	3.5E0	6.3E-7	5.7E-7
SMART	SM00864	RT		20	2.9E-8	3.4E0	6.5E-7	5.9E-7
KEGG_PATHWAY	Pathogenic Escherichia coli infection	RT		27	3.4E-7	2.7E0	1.2E-6	5.7E-7
GOTERM_MF_DIRECT	structural constituent of cytoskeleton	RT		40	1.6E-6	2.2E0	3.6E-5	3.2E-5
INTERPRO	Beta tubulin	RT		9	3.5E-6	6.2E0	8.0E-5	7.3E-5
INTERPRO	Beta tubulin, autoregulation binding site	RT		9	3.5E-6	6.2E0	8.0E-5	7.3E-5
GOTERM_BP_DIRECT	microtubule-based process	RT		19	4.8E-6	3.1E0	2.4E-4	2.3E-4
INTERPRO	Alpha tubulin	RT		7	3.9E-3	3.9E0	4.3E-2	4.0E-2
KEGG_PATHWAY	Phagosome	RT		27	7.6E-1	9.3E-1	1.0E0	7.6E-1
Annotation Cluster 35	**Enrichment Score: 6.92**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	protein serine/threonine phosphatase activity	RT		36	9.5E-14	3.7E0	4.4E-12	3.9E-12
INTERPRO	Protein phosphatase 2C (PP2C)-like	RT		17	5.1E-10	5.3E0	2.1E-8	1.9E-8
UP_SEQ_FEATURE	metal ion-binding site:Manganese 1; via carbonyl oxygen	RT		13	1.1E-9	6.8E0	6.7E-8	6.4E-8
INTERPRO	Protein phosphatase 2C	RT		14	6.1E-8	5.1E0	1.8E-6	1.7E-6
INTERPRO	Protein phosphatase 2C, manganese/magnesium aspartate binding site	RT		11	1.1E-7	6.2E0	3.2E-6	3.0E-6
GOTERM_BP_DIRECT	peptidyl-threonine dephosphorylation	RT		11	1.7E-7	5.9E0	1.2E-5	1.1E-5
SMART	PP2Cc	RT		17	3.0E-7	3.5E0	5.8E-6	5.3E-6
UP_SEQ_FEATURE	metal ion-binding site:Manganese 1	RT		15	6.3E-6	3.8E0	2.4E-4	2.3E-4
UP_SEQ_FEATURE	metal ion-binding site:Manganese 2	RT		15	6.3E-6	3.8E0	2.4E-4	2.3E-4
UP_SEQ_FEATURE	domain:PP2C-like	RT		10	1.3E-5	5.2E0	4.5E-4	4.3E-4
GOTERM_MF_DIRECT	cation binding	RT		7	8.2E-3	3.5E0	6.9E-2	6.2E-2
Annotation Cluster 36	**Enrichment Score: 6.28**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Protein phosphatase	RT		66	4.5E-21	3.4E0	5.7E-20	4.4E-20
INTERPRO	Dual specificity phosphatase, catalytic domain	RT		31	6.1E-15	4.5E0	4.4E-13	4.0E-13
INTERPRO	Dual specificity phosphatase, subgroup, catalytic domain	RT		28	7.6E-15	4.8E0	5.3E-13	4.8E-13
INTERPRO	Dual specificity phosphatase	RT		24	1.2E-12	4.8E0	7.0E-11	6.4E-11
GOTERM_MF_DIRECT	protein tyrosine/serine/threonine phosphatase activity	RT		25	8.5E-11	4.0E0	2.8E-9	2.5E-9
SMART	DSPc	RT		28	2.7E-10	3.2E0	8.1E-9	7.3E-9
UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	RT		31	5.1E-10	3.4E0	3.1E-8	3.0E-8
UP_SEQ_FEATURE	domain:Rhodanese	RT		15	8.7E-8	4.9E0	4.4E-6	4.3E-6
INTERPRO	Protein-tyrosine/Dual specificity phosphatase	RT		34	1.5E-7	2.6E0	4.2E-6	3.8E-6
INTERPRO	Mitogen-activated protein (MAP) kinase phosphatase	RT		10	6.2E-7	6.2E0	1.7E-5	1.6E-5
UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	RT		32	7.2E-7	2.5E0	3.1E-5	3.0E-5
GOTERM_MF_DIRECT	protein tyrosine phosphatase activity	RT		38	9.1E-7	2.3E0	2.1E-5	1.9E-5
GOTERM_BP_DIRECT	peptidyl-tyrosine dephosphorylation	RT		37	2.4E-6	2.2E0	1.3E-4	1.2E-4
GOTERM_MF_DIRECT	MAP kinase tyrosine/serine/threonine phosphatase activity	RT		11	3.0E-6	5.0E0	6.2E-5	5.6E-5
INTERPRO	Rhodanese-like domain	RT		15	3.1E-6	3.9E0	7.2E-5	6.6E-5
GOTERM_BP_DIRECT	inactivation of MAPK activity	RT		15	1.0E-5	3.6E0	4.3E-4	4.1E-4
INTERPRO	Protein-tyrosine phosphatase, active site	RT		28	3.0E-5	2.3E0	5.5E-4	5.0E-4
SMART	RHOD	RT		15	5.5E-5	2.9E0	9.0E-4	8.2E-4
PIR_SUPERFAMILY	dual specificity protein phosphatase (MAP kinase phosphatase)	RT		7	2.2E-4	5.4E0	1.4E-2	1.4E-2
BIOCARTA	Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases	RT		9	8.3E-4	3.0E0	8.4E-3	6.0E-3
INTERPRO	Protein-tyrosine phosphatase, catalytic	RT		18	1.9E-2	1.8E0	1.6E-1	1.5E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	protein tyrosine/threonine phosphatase activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
GOTERM_BP_DIRECT	endoderm formation	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
SMART	PTPc_motif	RT		18	3.8E-1	1.2E0	1.0E0	9.1E-1
INTERPRO	Protein-tyrosine phosphatase, receptor/non-receptor type	RT		6	7.6E-1	9.8E-1	1.0E0	9.1E-1
SMART	PTPc	RT		6	9.7E-1	6.6E-1	1.0E0	9.7E-1
Annotation Cluster 37	**Enrichment Score: 6.15**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	transcription-coupled nucleotide-excision repair	RT		39	1.0E-11	3.1E0	1.3E-9	1.3E-9
GOTERM_BP_DIRECT	telomere maintenance via recombination	RT		21	9.4E-9	3.9E0	8.3E-7	7.9E-7
GOTERM_BP_DIRECT	DNA damage response, detection of DNA damage	RT		22	2.3E-8	3.6E0	1.9E-6	1.8E-6
GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex assembly	RT		19	6.1E-8	3.9E0	4.7E-6	4.5E-6
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	RT		21	2.8E-7	3.4E0	1.8E-5	1.8E-5
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	RT		21	4.9E-7	3.3E0	3.0E-5	2.9E-5
GOTERM_BP_DIRECT	error-prone translesion synthesis	RT		14	8.7E-7	4.4E0	4.9E-5	4.7E-5
KEGG_PATHWAY	Nucleotide excision repair	RT		24	4.0E-6	2.6E0	1.2E-5	5.7E-6
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA gap filling	RT		15	5.3E-6	3.7E0	2.5E-4	2.4E-4
GOTERM_BP_DIRECT	error-free translesion synthesis	RT		13	8.2E-6	4.1E0	3.6E-4	3.5E-4
GOTERM_BP_DIRECT	translesion synthesis	RT		18	2.3E-5	3.0E0	8.9E-4	8.5E-4
KEGG_PATHWAY	Mismatch repair	RT		13	4.1E-4	2.9E0	9.6E-4	4.5E-4
KEGG_PATHWAY	DNA replication	RT		17	4.8E-4	2.4E0	1.1E-3	5.3E-4
Annotation Cluster 38	**Enrichment Score: 6.12**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	ATP-dependent RNA helicase activity	RT		38	2.4E-13	3.5E0	1.0E-11	8.9E-12
INTERPRO	Domain of unknown function DUF1605	RT		13	8.4E-7	4.7E0	2.3E-5	2.1E-5
INTERPRO	Helicase-associated domain	RT		13	2.2E-6	4.5E0	5.2E-5	4.8E-5
INTERPRO	DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site	RT		14	5.7E-6	3.9E0	1.2E-4	1.1E-4
SMART	SM00847	RT		13	1.9E-4	2.9E0	2.9E-3	2.6E-3
GOTERM_MF_DIRECT	ATP-dependent helicase activity	RT		14	3.8E-4	2.9E0	4.9E-3	4.4E-3
Annotation Cluster 39	**Enrichment Score: 5.93**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:SET	RT		32	9.6E-15	4.4E0	7.4E-13	7.1E-13
INTERPRO	SET domain	RT		33	7.6E-14	4.0E0	5.1E-12	4.7E-12
GOTERM_MF_DIRECT	histone-lysine N-methyltransferase activity	RT		24	3.2E-9	3.7E0	9.6E-8	8.6E-8
SMART	SET	RT		26	9.1E-8	2.8E0	2.0E-6	1.8E-6
UP_SEQ_FEATURE	domain:Post-SET	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
INTERPRO	Post-SET domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
UP_KEYWORDS	S-adenosyl-L-methionine	RT		46	6.3E-5	1.8E0	3.6E-4	2.8E-4
UP_KEYWORDS	Methyltransferase	RT		47	4.1E-4	1.7E0	2.2E-3	1.7E-3
SMART	PostSET	RT		9	5.0E-3	2.8E0	5.1E-2	4.6E-2
KEGG_PATHWAY	Lysine degradation	RT		18	1.5E-2	1.8E0	2.8E-2	1.5E-2
GOTERM_MF_DIRECT	methyltransferase activity	RT		19	3.1E-1	1.2E0	1.0E0	8.9E-1
Annotation Cluster 40	**Enrichment Score: 5.45**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of telomere maintenance via telomerase	RT		22	1.1E-9	4.1E0	1.1E-7	1.0E-7
GOTERM_BP_DIRECT	positive regulation of telomerase activity	RT		16	1.8E-5	3.3E0	7.0E-4	6.7E-4
GOTERM_BP_DIRECT	positive regulation of telomere capping	RT		9	2.3E-3	3.3E0	4.7E-2	4.5E-2
Annotation Cluster 41	**Enrichment Score: 5.23**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	ATPase, AAA-type, conserved site	RT		19	5.6E-9	4.4E0	1.9E-7	1.8E-7
INTERPRO	ATPase, AAA-type, core	RT		24	1.0E-6	2.9E0	2.7E-5	2.5E-5
INTERPRO	AAA+ ATPase domain	RT		44	5.3E-6	2.0E0	1.1E-4	1.0E-4

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
SMART	AAA	RT		44	3.7E-2	1.3E0	2.7E-1	2.4E-1
Annotation Cluster 42	**Enrichment Score: 5.05**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:PI3K/PI4K	RT		16	1.6E-10	6.1E0	1.0E-8	1.0E-8
INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	RT		16	2.5E-9	5.2E0	9.0E-8	8.2E-8
INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	RT		14	1.7E-8	5.4E0	5.4E-7	5.0E-7
SMART	PI3Kc	RT		15	9.0E-7	3.6E0	1.7E-5	1.6E-5
UP_SEQ_FEATURE	domain:FAT	RT		6	3.6E-4	6.8E0	9.9E-3	9.5E-3
UP_SEQ_FEATURE	domain:FATC	RT		6	3.6E-4	6.8E0	9.9E-3	9.5E-3
INTERPRO	PIK-related kinase, FATC	RT		6	5.7E-4	6.2E0	7.8E-3	7.1E-3
INTERPRO	PIK-related kinase	RT		6	5.7E-4	6.2E0	7.8E-3	7.1E-3
INTERPRO	PIK-related kinase, FAT	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
SMART	SM01343	RT		6	4.3E-3	4.1E0	4.5E-2	4.1E-2
Annotation Cluster 43	**Enrichment Score: 5.01**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	nucleotide-binding oligomerization domain containing signaling pathway	RT		17	1.8E-7	4.0E0	1.2E-5	1.2E-5
GOTERM_BP_DIRECT	I-kappaB kinase/NF-kappaB signaling	RT		27	1.3E-6	2.7E0	7.3E-5	7.0E-5
GOTERM_BP_DIRECT	regulation of tumor necrosis factor-mediated signaling pathway	RT		15	1.4E-4	3.0E0	4.4E-3	4.2E-3
GOTERM_BP_DIRECT	TRIF-dependent toll-like receptor signaling pathway	RT		14	2.6E-4	3.0E0	7.3E-3	7.0E-3
Annotation Cluster 44	**Enrichment Score: 4.99**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	WD40 repeat, conserved site	RT		55	1.2E-7	2.1E0	3.6E-6	3.3E-6
UP_SEQ_FEATURE	repeat:WD 5	RT		66	2.4E-7	1.9E0	1.1E-5	1.0E-5
UP_SEQ_FEATURE	repeat:WD 4	RT		69	3.9E-7	1.8E0	1.8E-5	1.7E-5
INTERPRO	G-protein beta WD-40 repeat	RT		36	4.3E-7	2.4E0	1.2E-5	1.1E-5
UP_SEQ_FEATURE	repeat:WD 7	RT		47	5.5E-7	2.1E0	2.4E-5	2.3E-5
UP_SEQ_FEATURE	repeat:WD 6	RT		55	2.1E-6	1.9E0	8.5E-5	8.2E-5
UP_KEYWORDS	WD repeat	RT		71	3.0E-6	1.7E0	2.0E-5	1.5E-5
UP_SEQ_FEATURE	repeat:WD 3	RT		69	3.1E-6	1.7E0	1.3E-4	1.2E-4
UP_SEQ_FEATURE	repeat:WD 2	RT		69	1.0E-5	1.7E0	3.7E-4	3.5E-4
UP_SEQ_FEATURE	repeat:WD 1	RT		69	1.0E-5	1.7E0	3.7E-4	3.5E-4
INTERPRO	WD40-repeat-containing domain	RT		76	9.2E-5	1.5E0	1.6E-3	1.4E-3
INTERPRO	WD40 repeat	RT		67	2.0E-4	1.5E0	3.1E-3	2.9E-3
INTERPRO	WD40/YVTN repeat-like-containing domain	RT		74	2.7E-3	1.4E0	3.2E-2	2.9E-2
SMART	WD40	RT		67	5.1E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 45	**Enrichment Score: 4.92**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	short sequence motif:TXY	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
GOTERM_MF_DIRECT	MAP kinase activity	RT		12	6.4E-7	5.1E0	1.6E-5	1.4E-5
INTERPRO	Mitogen-activated protein (MAP) kinase, conserved site	RT		10	1.0E-5	5.2E0	2.0E-4	1.8E-4
INTERPRO	Mitogen-activated protein (MAP) kinase, p38	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
Annotation Cluster 46	**Enrichment Score: 4.88**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	cadherin binding involved in cell-cell adhesion	RT		80	4.3E-6	1.6E0	8.7E-5	7.8E-5
GOTERM_CC_DIRECT	cell-cell adherens junction	RT		82	8.2E-6	1.6E0	1.5E-4	1.3E-4
GOTERM_BP_DIRECT	cell-cell adhesion	RT		72	6.4E-5	1.6E0	2.1E-3	2.1E-3
Annotation Cluster 47	**Enrichment Score: 4.87**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Actinin-type, actin-binding, conserved site	RT		18	1.2E-9	4.9E0	4.5E-8	4.1E-8
UP_SEQ_FEATURE	domain:Actin-binding	RT		16	2.3E-9	5.5E0	1.4E-7	1.3E-7
UP_SEQ_FEATURE	repeat:Spectrin 4	RT		16	6.9E-9	5.2E0	4.0E-7	3.9E-7
UP_SEQ_FEATURE	domain:CH 1	RT		18	1.3E-8	4.5E0	7.1E-7	6.9E-7

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	domain:CH 2	RT		18	1.3E-8	4.5E0	7.1E-7	6.9E-7
UP_SEQ_FEATURE	repeat:Spectrin 3	RT		16	1.9E-8	5.0E0	1.0E-6	1.0E-6
UP_SEQ_FEATURE	repeat:Spectrin 6	RT		12	3.9E-8	6.3E0	2.0E-6	2.0E-6
UP_SEQ_FEATURE	repeat:Spectrin 7	RT		12	3.9E-8	6.3E0	2.0E-6	2.0E-6
UP_SEQ_FEATURE	repeat:Spectrin 8	RT		12	3.9E-8	6.3E0	2.0E-6	2.0E-6
UP_SEQ_FEATURE	repeat:Spectrin 9	RT		12	3.9E-8	6.3E0	2.0E-6	2.0E-6
UP_SEQ_FEATURE	repeat:Spectrin 5	RT		12	1.6E-7	5.8E0	7.9E-6	7.6E-6
UP_SEQ_FEATURE	repeat:Spectrin 10	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 11	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 12	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 13	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 14	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 15	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 16	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 17	RT		11	2.3E-7	6.2E0	1.0E-5	1.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 1	RT		16	4.7E-7	4.2E0	2.1E-5	2.0E-5
UP_SEQ_FEATURE	repeat:Spectrin 2	RT		16	4.7E-7	4.2E0	2.1E-5	2.0E-5
INTERPRO	Spectrin repeat	RT		15	5.9E-6	3.7E0	1.2E-4	1.1E-4
INTERPRO	Spectrin/alpha-actinin	RT		16	1.0E-5	3.4E0	2.0E-4	1.8E-4
UP_SEQ_FEATURE	repeat:Spectrin 18	RT		8	4.0E-5	6.1E0	1.3E-3	1.2E-3
UP_SEQ_FEATURE	repeat:Spectrin 19	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
UP_SEQ_FEATURE	repeat:Spectrin 20	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
INTERPRO	Calponin homology domain	RT		25	6.1E-4	2.0E0	8.3E-3	7.6E-3
GOTERM_CC_DIRECT	spectrin	RT		7	8.2E-4	4.9E0	8.6E-3	7.5E-3
UP_SEQ_FEATURE	repeat:Spectrin 21	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
SMART	SPEC	RT		16	1.5E-3	2.2E0	1.7E-2	1.5E-2
UP_SEQ_FEATURE	repeat:Spectrin 22	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
GOTERM_BP_DIRECT	actin filament capping	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
INTERPRO	Spectrin, beta subunit	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
PIR_SUPERFAMILY	spectrin, beta subunit	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
SMART	CH	RT		25	2.2E-2	1.5E0	1.8E-1	1.6E-1
UP_SEQ_FEATURE	repeat:Spectrin 23	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
UP_KEYWORDS	Actin capping	RT		7	4.7E-2	2.5E0	1.7E-1	1.3E-1
GOTERM_MF_DIRECT	ankyrin binding	RT		7	1.0E-1	2.1E0	5.0E-1	4.4E-1
INTERPRO	Pleckstrin homology domain, spectrin-type	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
GOTERM_MF_DIRECT	phospholipid binding	RT		11	9.3E-1	7.6E-1	1.0E0	9.3E-1
GOTERM_BP_DIRECT	ER to Golgi vesicle-mediated transport	RT		17	1.0E0	6.3E-1	1.0E0	1.0E0
Annotation Cluster 48	**Enrichment Score: 4.73**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex assembly	RT		19	6.1E-8	3.9E0	4.7E-6	4.5E-6
GOTERM_BP_DIRECT	global genome nucleotide-excision repair	RT		20	7.3E-8	3.7E0	5.4E-6	5.2E-6
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 5'-to lesion	RT		21	2.8E-7	3.4E0	1.8E-5	1.8E-5
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision	RT		21	4.9E-7	3.3E0	3.0E-5	2.9E-5
KEGG_PATHWAY	Nucleotide excision repair	RT		24	4.0E-6	2.6E0	1.2E-5	5.7E-6
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA duplex unwinding	RT		14	9.6E-6	3.8E0	4.2E-4	4.0E-4
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA damage recognition	RT		12	5.8E-4	3.1E0	1.5E-2	1.4E-2
GOTERM_BP_DIRECT	nucleotide-excision repair, preincision complex stabilization	RT		11	1.1E-3	3.1E0	2.5E-2	2.4E-2

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	nucleotide-excision repair, DNA incision, 3'-to lesion	RT		11	2.5E-3	2.8E0	5.0E-2	4.8E-2
GOTERM_BP_DIRECT	nucleotide-excision repair	RT		11	1.4E-1	1.6E0	8.3E-1	8.0E-1
Annotation Cluster 49	**Enrichment Score: 4.66**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Biological rhythms	RT		40	1.7E-6	2.2E0	1.2E-5	9.1E-6
GOTERM_BP_DIRECT	regulation of circadian rhythm	RT		21	6.3E-5	2.5E0	2.1E-3	2.0E-3
GOTERM_BP_DIRECT	rhythmic process	RT		22	9.6E-5	2.4E0	3.1E-3	3.0E-3
Annotation Cluster 50	**Enrichment Score: 4.65**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	gene expression	RT		31	1.8E-12	3.8E0	2.6E-10	2.5E-10
GOTERM_CC_DIRECT	DNA-directed RNA polymerase II, core complex	RT		14	1.4E-7	4.9E0	3.7E-6	3.3E-6
GOTERM_BP_DIRECT	7-methylguanosine mRNA capping	RT		20	1.4E-7	3.6E0	1.0E-5	9.7E-6
GOTERM_BP_DIRECT	positive regulation of viral transcription	RT		18	4.6E-7	3.7E0	2.9E-5	2.8E-5
KEGG_PATHWAY	Pyrimidine metabolism	RT		41	1.5E-6	2.1E0	4.9E-6	2.3E-6
UP_KEYWORDS	DNA-directed RNA polymerase	RT		19	2.4E-6	3.3E0	1.6E-5	1.2E-5
KEGG_PATHWAY	RNA polymerase	RT		19	3.6E-6	3.1E0	1.1E-5	5.1E-6
GOTERM_BP_DIRECT	transcription initiation from RNA polymerase I promoter	RT		18	5.3E-6	3.2E0	2.5E-4	2.4E-4
GOTERM_BP_DIRECT	transcription elongation from RNA polymerase I promoter	RT		17	5.6E-6	3.4E0	2.6E-4	2.5E-4
GOTERM_BP_DIRECT	termination of RNA polymerase I transcription	RT		17	9.7E-6	3.2E0	4.2E-4	4.0E-4
GOTERM_MF_DIRECT	DNA-directed RNA polymerase activity	RT		19	1.2E-5	3.0E0	2.2E-4	2.0E-4
GOTERM_MF_DIRECT	RNA polymerase I activity	RT		10	1.4E-5	5.0E0	2.6E-4	2.3E-4
GOTERM_BP_DIRECT	transcription elongation from RNA polymerase II promoter	RT		32	1.4E-5	2.2E0	5.8E-4	5.6E-4
GOTERM_MF_DIRECT	RNA polymerase II activity	RT		9	2.0E-5	5.4E0	3.5E-4	3.2E-4
GOTERM_CC_DIRECT	DNA-directed RNA polymerase I complex	RT		10	2.3E-5	4.9E0	3.8E-4	3.3E-4
GOTERM_BP_DIRECT	positive regulation of type I interferon production	RT		21	1.2E-4	2.4E0	3.7E-3	3.6E-3
GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	RT		44	2.9E-4	1.7E0	8.0E-3	7.7E-3
GOTERM_BP_DIRECT	snRNA transcription from RNA polymerase II promoter	RT		24	8.1E-4	2.0E0	1.9E-2	1.9E-2
GOTERM_BP_DIRECT	positive regulation of gene expression, epigenetic	RT		22	8.6E-4	2.1E0	2.0E-2	2.0E-2
GOTERM_BP_DIRECT	transcription from RNA polymerase III promoter	RT		14	1.8E-3	2.5E0	3.7E-2	3.5E-2
GOTERM_BP_DIRECT	gene silencing by RNA	RT		31	4.7E-3	1.7E0	8.3E-2	8.0E-2
GOTERM_CC_DIRECT	DNA-directed RNA polymerase III complex	RT		8	2.1E-2	2.7E0	1.3E-1	1.1E-1
GOTERM_MF_DIRECT	RNA polymerase III activity	RT		8	2.1E-2	2.6E0	1.4E-1	1.2E-1
KEGG_PATHWAY	Cytosolic DNA-sensing pathway	RT		19	5.4E-2	1.5E0	9.5E-2	5.4E-2
Annotation Cluster 51	**Enrichment Score: 4.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Purine metabolism	RT		67	8.4E-9	2.0E0	3.4E-8	1.6E-8
KEGG_PATHWAY	Pyrimidine metabolism	RT		41	1.5E-6	2.1E0	4.9E-6	2.3E-6
KEGG_PATHWAY	Metabolic pathways	RT		98	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 52	**Enrichment Score: 4.62**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	DNA synthesis involved in DNA repair	RT		20	5.1E-7	3.4E0	3.0E-5	2.9E-5
GOTERM_BP_DIRECT	strand displacement	RT		15	1.9E-5	3.4E0	7.3E-4	7.0E-4
KEGG_PATHWAY	Homologous recombination	RT		14	1.5E-3	2.5E0	3.2E-3	1.5E-3
Annotation Cluster 53	**Enrichment Score: 4.49**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Heat shock protein 70 family	RT		12	1.4E-6	5.0E0	3.5E-5	3.2E-5
INTERPRO	Heat shock protein 70, conserved site	RT		12	1.4E-6	5.0E0	3.5E-5	3.2E-5
GOTERM_BP_DIRECT	response to unfolded protein	RT		14	1.8E-2	2.0E0	2.2E-1	2.1E-1
Annotation Cluster 54	**Enrichment Score: 4.46**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Gap junction	RT		60	8.4E-23	3.5E0	1.9E-21	8.8E-22
GOTERM_MF_DIRECT	adenylate cyclase activity	RT		19	1.7E-13	6.0E0	7.5E-12	6.7E-12
INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	RT		18	4.0E-12	5.9E0	2.0E-10	1.9E-10

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	RT		17	2.2E-11	5.9E0	1.0E-9	9.4E-10
KEGG_PATHWAY	GnRH signaling pathway	RT		45	2.7E-10	2.6E0	1.5E-9	7.0E-10
KEGG_PATHWAY	Vascular smooth muscle contraction	RT		53	3.2E-10	2.4E0	1.7E-9	8.2E-10
SMART	CYCc	RT		17	1.6E-8	3.8E0	4.1E-7	3.8E-7
UP_KEYWORDS	cAMP biosynthesis	RT		10	2.5E-7	6.9E0	1.9E-6	1.5E-6
KEGG_PATHWAY	Inflammatory mediator regulation of TRP channels	RT		41	5.9E-7	2.2E0	2.1E-6	9.7E-7
KEGG_PATHWAY	Regulation of lipolysis in adipocytes	RT		28	8.5E-7	2.6E0	2.9E-6	1.4E-6
GOTERM_BP_DIRECT	cyclic nucleotide biosynthetic process	RT		11	8.8E-7	5.4E0	4.9E-5	4.7E-5
KEGG_PATHWAY	Melanogenesis	RT		41	1.1E-6	2.1E0	3.8E-6	1.8E-6
KEGG_PATHWAY	Adrenergic signaling in cardiomyocytes	RT		51	1.8E-6	1.9E0	5.8E-6	2.7E-6
GOTERM_BP_DIRECT	activation of protein kinase A activity	RT		13	3.6E-6	4.3E0	1.8E-4	1.7E-4
UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2; via carbonyl oxygen	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
KEGG_PATHWAY	Cholinergic synapse	RT		42	8.8E-6	2.0E0	2.5E-5	1.2E-5
KEGG_PATHWAY	Gastric acid secretion	RT		31	1.3E-5	2.2E0	3.5E-5	1.6E-5
GOTERM_MF_DIRECT	phosphorus-oxygen lyase activity	RT		10	1.4E-5	5.0E0	2.6E-4	2.3E-4
KEGG_PATHWAY	Dopaminergic synapse	RT		46	1.5E-5	1.9E0	3.8E-5	1.8E-5
UP_SEQ_FEATURE	metal ion-binding site:Magnesium 1	RT		18	2.9E-5	3.0E0	9.6E-4	9.2E-4
KEGG_PATHWAY	Circadian entrainment	RT		36	4.2E-5	2.0E0	1.1E-4	5.0E-5
UP_SEQ_FEATURE	metal ion-binding site:Magnesium 2	RT		17	8.3E-5	2.9E0	2.6E-3	2.5E-3
GOTERM_BP_DIRECT	cAMP biosynthetic process	RT		11	1.1E-4	3.8E0	3.5E-3	3.4E-3
GOTERM_BP_DIRECT	renal water homeostasis	RT		15	3.3E-4	2.8E0	9.0E-3	8.6E-3
GOTERM_BP_DIRECT	cellular response to glucagon stimulus	RT		17	4.4E-4	2.5E0	1.1E-2	1.1E-2
GOTERM_BP_DIRECT	cellular response to forskolin	RT		7	4.7E-4	5.2E0	1.2E-2	1.2E-2
INTERPRO	Adenylate cyclase-like	RT		6	5.7E-4	6.2E0	7.8E-3	7.1E-3
KEGG_PATHWAY	Thyroid hormone synthesis	RT		25	2.1E-3	1.9E0	4.5E-3	2.1E-3
KEGG_PATHWAY	Endocrine and other factor-regulated calcium reabsorption	RT		18	2.9E-3	2.1E0	6.1E-3	2.9E-3
KEGG_PATHWAY	Aldosterone synthesis and secretion	RT		27	3.9E-3	1.7E0	8.2E-3	3.9E-3
KEGG_PATHWAY	Salivary secretion	RT		28	4.7E-3	1.7E0	9.7E-3	4.7E-3
KEGG_PATHWAY	Retrograde endocannabinoid signaling	RT		31	7.3E-3	1.6E0	1.5E-2	7.3E-3
KEGG_PATHWAY	Glutamatergic synapse	RT		34	7.7E-3	1.5E0	1.5E-2	7.7E-3
GOTERM_BP_DIRECT	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	RT		16	8.4E-3	2.0E0	1.3E-1	1.3E-1
KEGG_PATHWAY	Ovarian steroidogenesis	RT		16	3.8E-2	1.7E0	6.8E-2	3.8E-2
GOTERM_BP_DIRECT	cAMP-mediated signaling	RT		12	4.5E-2	1.9E0	4.3E-1	4.1E-1
KEGG_PATHWAY	GABAergic synapse	RT		24	4.9E-2	1.5E0	8.7E-2	4.9E-2
GOTERM_BP_DIRECT	activation of adenylate cyclase activity	RT		12	6.3E-2	1.8E0	5.5E-1	5.2E-1
KEGG_PATHWAY	Pancreatic secretion	RT		25	7.3E-2	1.4E0	1.3E-1	7.3E-2
KEGG_PATHWAY	Insulin secretion	RT		23	8.1E-2	1.4E0	1.4E-1	8.1E-2
KEGG_PATHWAY	Calcium signaling pathway	RT		43	9.1E-2	1.2E0	1.5E-1	9.1E-2
KEGG_PATHWAY	Dilated cardiomyopathy	RT		22	1.2E-1	1.4E0	1.9E-1	1.2E-1
GOTERM_BP_DIRECT	adenylate cyclase-activating G-protein coupled receptor signaling pathway	RT		13	1.3E-1	1.5E0	8.2E-1	7.9E-1
KEGG_PATHWAY	Morphine addiction	RT		23	1.4E-1	1.3E0	2.4E-1	1.4E-1
KEGG_PATHWAY	Bile secretion	RT		17	2.4E-1	1.3E0	3.8E-1	2.4E-1
KEGG_PATHWAY	Serotonergic synapse	RT		25	3.0E-1	1.2E0	4.6E-1	3.0E-1
KEGG_PATHWAY	Taste transduction	RT		6	9.5E-1	6.9E-1	1.0E0	9.5E-1
Annotation Cluster 55	**Enrichment Score: 4.45**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	ADP-ribosylation	RT		30	2.2E-9	3.3E0	2.0E-8	1.5E-8

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	G-protein beta/gamma-subunit complex binding	RT		16	1.5E-8	4.8E0	4.2E-7	3.8E-7
INTERPRO	Guanine nucleotide binding protein (G-protein), alpha subunit	RT		14	1.7E-8	5.4E0	5.4E-7	5.0E-7
INTERPRO	G protein alpha subunit, helical insertion	RT		14	1.7E-8	5.4E0	5.4E-7	5.0E-7
SMART	SM00275	RT		14	3.0E-6	3.6E0	5.6E-5	5.0E-5
INTERPRO	G-protein alpha subunit, group I	RT		8	1.9E-5	6.2E0	3.6E-4	3.3E-4
GOTERM_MF_DIRECT	guanyl nucleotide binding	RT		8	9.8E-5	5.3E0	1.5E-3	1.3E-3
GOTERM_CC_DIRECT	heterotrimeric G-protein complex	RT		12	9.6E-3	2.3E0	7.0E-2	6.2E-2
GOTERM_BP_DIRECT	adenylate cyclase-modulating G-protein coupled receptor signaling pathway	RT		13	1.5E-2	2.1E0	2.0E-1	1.9E-1
GOTERM_MF_DIRECT	G-protein coupled serotonin receptor binding	RT		4	1.6E-2	6.0E0	1.2E-1	1.0E-1
GOTERM_MF_DIRECT	G-protein coupled receptor binding	RT		16	3.4E-2	1.7E0	2.1E-1	1.9E-1
UP_KEYWORDS	Transducer	RT		29	1.0E0	2.2E-1	1.0E0	1.0E0
Annotation Cluster 56	**Enrichment Score: 4.44**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:C2H2-type 23	RT		15	1.9E-10	6.4E0	1.2E-8	1.1E-8
UP_SEQ_FEATURE	zinc finger region:C2H2-type 24	RT		13	6.7E-9	6.3E0	4.0E-7	3.8E-7
UP_SEQ_FEATURE	zinc finger region:C2H2-type 26	RT		8	4.0E-5	6.1E0	1.3E-3	1.2E-3
UP_SEQ_FEATURE	zinc finger region:C2H2-type 25	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
UP_SEQ_FEATURE	zinc finger region:C2H2-type 27	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
UP_SEQ_FEATURE	zinc finger region:C2H2-type 28	RT		6	3.6E-4	6.8E0	9.9E-3	9.5E-3
UP_SEQ_FEATURE	zinc finger region:C2H2-type 30	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
UP_SEQ_FEATURE	zinc finger region:C2H2-type 29	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
UP_SEQ_FEATURE	zinc finger region:C2H2-type 21; degenerate	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
Annotation Cluster 57	**Enrichment Score: 4.34**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	TPR repeat	RT		53	3.7E-8	2.2E0	2.9E-7	2.3E-7
INTERPRO	Tetratricopeptide repeat-containing domain	RT		48	3.7E-8	2.3E0	1.2E-6	1.1E-6
INTERPRO	Tetratricopeptide repeat	RT		47	4.8E-7	2.1E0	1.3E-5	1.2E-5
INTERPRO	Tetratricopeptide-like helical	RT		62	6.2E-6	1.8E0	1.3E-4	1.2E-4
UP_SEQ_FEATURE	repeat:TPR 1	RT		47	6.8E-6	2.0E0	2.6E-4	2.5E-4
UP_SEQ_FEATURE	repeat:TPR 2	RT		47	6.8E-6	2.0E0	2.6E-4	2.5E-4
UP_SEQ_FEATURE	repeat:TPR 3	RT		43	1.7E-5	2.0E0	6.2E-4	6.0E-4
UP_SEQ_FEATURE	repeat:TPR 5	RT		27	2.8E-5	2.4E0	9.3E-4	9.0E-4
UP_SEQ_FEATURE	repeat:TPR 6	RT		25	3.3E-5	2.4E0	1.1E-3	1.0E-3
UP_SEQ_FEATURE	repeat:TPR 7	RT		21	2.9E-4	2.3E0	8.2E-3	7.9E-3
UP_SEQ_FEATURE	repeat:TPR 4	RT		29	4.1E-4	2.0E0	1.1E-2	1.1E-2
UP_SEQ_FEATURE	repeat:TPR 8	RT		17	1.5E-3	2.3E0	3.9E-2	3.7E-2
SMART	TPR	RT		47	4.3E-3	1.5E0	4.5E-2	4.1E-2
UP_SEQ_FEATURE	repeat:TPR 9	RT		10	3.6E-2	2.1E0	6.2E-1	6.0E-1
UP_SEQ_FEATURE	repeat:TPR 10	RT		7	9.2E-2	2.2E0	1.0E0	9.6E-1
Annotation Cluster 58	**Enrichment Score: 4.19**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Cyclin	RT		20	7.1E-7	3.4E0	5.2E-6	4.0E-6
INTERPRO	Cyclin-like	RT		22	9.7E-7	3.1E0	2.5E-5	2.3E-5
SMART	CYCLIN	RT		21	6.7E-5	2.4E0	1.1E-3	9.6E-4
INTERPRO	Cyclin, N-terminal	RT		16	1.1E-4	2.9E0	1.7E-3	1.6E-3
INTERPRO	Cyclin, C-terminal domain	RT		10	8.8E-4	3.4E0	1.2E-2	1.1E-2
SMART	SM01332	RT		10	1.7E-2	2.3E0	1.5E-1	1.4E-1
Annotation Cluster 59	**Enrichment Score: 4.18**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	DNA-binding region:Fork-head	RT		22	2.6E-6	3.0E0	1.1E-4	1.0E-4
INTERPRO	Transcription factor, fork head	RT		22	8.2E-6	2.8E0	1.7E-4	1.6E-4

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Winged helix-turn-helix DNA-binding domain	RT		65	9.8E-6	1.7E0	2.0E-4	1.8E-4
INTERPRO	Transcription factor, fork head, conserved site	RT		14	1.6E-3	2.6E0	2.0E-2	1.8E-2
SMART	FH	RT		22	3.8E-3	1.8E0	4.2E-2	3.8E-2
Annotation Cluster 60	**Enrichment Score: 4.13**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	adenylate cyclase activity	RT		19	1.7E-13	6.0E0	7.5E-12	6.7E-12
INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase	RT		18	4.0E-12	5.9E0	2.0E-10	1.9E-10
INTERPRO	Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	RT		17	2.2E-11	5.9E0	1.0E-9	9.4E-10
SMART	CYCc	RT		17	1.6E-8	3.8E0	4.1E-7	3.8E-7
UP_SEQ_FEATURE	domain:Guanylate cyclase	RT		8	1.0E-5	6.8E0	3.7E-4	3.5E-4
UP_KEYWORDS	cGMP biosynthesis	RT		8	3.8E-5	6.1E0	2.2E-4	1.7E-4
GOTERM_CC_DIRECT	guanylate cyclase complex, soluble	RT		8	6.4E-5	5.6E0	8.7E-4	7.6E-4
GOTERM_MF_DIRECT	guanylate cyclase activity	RT		8	9.8E-5	5.3E0	1.5E-3	1.3E-3
INTERPRO	Haem NO binding associated	RT		6	1.7E-3	5.3E0	2.1E-2	1.9E-2
GOTERM_BP_DIRECT	cGMP biosynthetic process	RT		8	1.1E-2	3.0E0	1.5E-1	1.5E-1
GOTERM_BP_DIRECT	receptor guanylyl cyclase signaling pathway	RT		6	1.6E-2	3.6E0	2.1E-1	2.0E-1
UP_KEYWORDS	Lyase	RT		32	2.6E-2	1.5E0	1.0E-1	8.0E-2
INTERPRO	Heme-NO binding	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
GOTERM_BP_DIRECT	positive regulation of cGMP biosynthetic process	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
INTERPRO	NO signalling/Golgi transport ligand-binding domain	RT		3	4.4E-1	2.1E0	1.0E0	9.1E-1
BIOCARTA	Ion Channels and Their Functional Role in Vascular Endothelium	RT		7	6.3E-1	1.1E0	9.5E-1	6.8E-1
INTERPRO	Extracellular ligand-binding receptor	RT		5	8.5E-1	8.6E-1	1.0E0	9.1E-1
Annotation Cluster 61	**Enrichment Score: 4.05**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	phosphatidylinositol-mediated signaling	RT		42	6.9E-8	2.3E0	5.1E-6	4.9E-6
GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphate biosynthetic process	RT		20	2.1E-4	2.4E0	6.1E-3	5.9E-3
GOTERM_BP_DIRECT	phosphatidylinositol phosphorylation	RT		31	2.5E-4	2.0E0	7.0E-3	6.7E-3
GOTERM_MF_DIRECT	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	RT		23	2.9E-4	2.2E0	3.9E-3	3.5E-3
GOTERM_BP_DIRECT	regulation of phosphatidylinositol 3-kinase signaling	RT		27	3.0E-4	2.0E0	8.0E-3	7.7E-3
GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	RT		18	3.2E-4	2.5E0	4.4E-3	3.9E-3
GOTERM_MF_DIRECT	Ras guanyl-nucleotide exchange factor activity	RT		35	4.5E-4	1.8E0	5.6E-3	5.0E-3
Annotation Cluster 62	**Enrichment Score: 4.02**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ubiquitin	RT		26	1.5E-6	2.7E0	3.8E-5	3.5E-5
INTERPRO	Ubiquitin subgroup	RT		9	2.7E-4	4.3E0	4.0E-3	3.6E-3
UP_SEQ_FEATURE	domain:Ubiquitin-like	RT		17	4.1E-4	2.6E0	1.1E-2	1.1E-2
SMART	UBQ	RT		22	4.8E-4	2.1E0	6.6E-3	6.0E-3
Annotation Cluster 63	**Enrichment Score: 4**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Alcoholism	RT		70	5.5E-10	2.1E0	2.8E-9	1.3E-9
INTERPRO	Histone core	RT		31	4.6E-8	2.8E0	1.4E-6	1.3E-6
UP_KEYWORDS	Nucleosome core	RT		32	1.4E-6	2.5E0	1.0E-5	7.9E-6
GOTERM_CC_DIRECT	nucleosome	RT		34	3.1E-6	2.3E0	6.8E-5	6.0E-5
INTERPRO	Histone-fold	RT		35	1.2E-4	1.9E0	1.9E-3	1.7E-3
GOTERM_CC_DIRECT	nuclear nucleosome	RT		18	2.0E-4	2.6E0	2.4E-3	2.1E-3
INTERPRO	Histone H2B	RT		12	6.0E-4	3.1E0	8.2E-3	7.5E-3
KEGG_PATHWAY	Systemic lupus erythematosus	RT		42	1.0E-3	1.6E0	2.3E-3	1.1E-3
INTERPRO	Histone H2A	RT		12	1.4E-3	2.9E0	1.7E-2	1.6E-2
GOTERM_BP_DIRECT	chromatin silencing	RT		16	5.4E-3	2.1E0	9.2E-2	8.8E-2
GOTERM_BP_DIRECT	nucleosome assembly	RT		31	1.3E-2	1.5E0	1.8E-1	1.7E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
SMART	H2B	RT		12	1.9E-2	2.0E0	1.6E-1	1.4E-1
SMART	H2A	RT		12	3.6E-2	1.9E0	2.6E-1	2.3E-1
Annotation Cluster 64	**Enrichment Score: 3.98**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:SOCS box	RT		20	2.9E-7	3.6E0	1.3E-5	1.3E-5
INTERPRO	SOCS protein, C-terminal	RT		20	2.1E-6	3.2E0	5.2E-5	4.8E-5
SMART	SM00969	RT		20	9.3E-4	2.1E0	1.2E-2	1.1E-2
SMART	SOCS	RT		8	2.0E-1	1.6E0	8.5E-1	7.7E-1
Annotation Cluster 65	**Enrichment Score: 3.89**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of telomere maintenance via telomerase	RT		22	1.1E-9	4.1E0	1.1E-7	1.0E-7
GOTERM_BP_DIRECT	positive regulation of telomerase RNA localization to Cajal body	RT		12	2.2E-6	4.7E0	1.2E-4	1.1E-4
INTERPRO	Chaperonin Cpn60/TCP-1	RT		12	3.7E-6	4.6E0	8.3E-5	7.6E-5
INTERPRO	GroEL-like apical domain	RT		12	3.7E-6	4.6E0	8.3E-5	7.6E-5
INTERPRO	GroEL-like equatorial domain	RT		11	1.6E-5	4.5E0	3.1E-4	2.9E-4
GOTERM_BP_DIRECT	positive regulation of protein localization to Cajal body	RT		8	2.7E-5	5.9E0	9.7E-4	9.3E-4
GOTERM_CC_DIRECT	chaperonin-containing T-complex	RT		8	6.4E-5	5.6E0	8.7E-4	7.6E-4
GOTERM_CC_DIRECT	zona pellucida receptor complex	RT		8	6.4E-5	5.6E0	8.7E-4	7.6E-4
INTERPRO	Chaperonin TCP-1, conserved site	RT		8	7.5E-5	5.5E0	1.3E-3	1.2E-3
GOTERM_BP_DIRECT	positive regulation of establishment of protein localization to telomere	RT		8	1.0E-4	5.3E0	3.2E-3	3.1E-3
INTERPRO	Chaperone tailless complex polypeptide 1 (TCP-1)	RT		9	1.2E-4	4.6E0	1.9E-3	1.7E-3
INTERPRO	TCP-1-like chaperonin intermediate domain	RT		9	1.2E-4	4.6E0	1.9E-3	1.7E-3
GOTERM_BP_DIRECT	toxin transport	RT		11	7.0E-2	1.8E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	scaRNA localization to Cajal body	RT		3	1.3E-1	4.4E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	binding of sperm to zona pellucida	RT		9	2.3E-1	1.5E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	protein binding involved in protein folding	RT		4	4.3E-1	1.7E0	1.0E0	8.9E-1
Annotation Cluster 66	**Enrichment Score: 3.85**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	precatalytic spliceosome	RT		17	6.6E-8	4.3E0	1.9E-6	1.7E-6
GOTERM_CC_DIRECT	U2 snRNP	RT		15	8.3E-8	4.8E0	2.3E-6	2.0E-6
GOTERM_CC_DIRECT	U4/U6 x U5 tri-snRNP complex	RT		15	1.1E-6	4.1E0	2.6E-5	2.3E-5
GOTERM_CC_DIRECT	U12-type spliceosomal complex	RT		16	1.2E-6	3.9E0	2.7E-5	2.4E-5
INTERPRO	Ribonucleoprotein LSM domain	RT		14	2.7E-6	4.1E0	6.5E-5	6.0E-5
GOTERM_BP_DIRECT	spliceosomal complex assembly	RT		16	3.0E-6	3.6E0	1.5E-4	1.5E-4
INTERPRO	Like-Sm (LSM) domain	RT		14	2.1E-5	3.6E0	3.9E-4	3.5E-4
GOTERM_CC_DIRECT	U5 snRNP	RT		11	6.1E-5	4.1E0	8.7E-4	7.6E-4
GOTERM_CC_DIRECT	small nuclear ribonucleoprotein complex	RT		11	6.1E-5	4.1E0	8.7E-4	7.6E-4
BIOCARTA	Spliceosomal Assembly	RT		13	6.4E-5	2.8E0	1.4E-3	1.0E-3
GOTERM_MF_DIRECT	U1 snRNP binding	RT		7	1.3E-4	6.0E0	1.9E-3	1.7E-3
GOTERM_CC_DIRECT	U1 snRNP	RT		11	2.1E-4	3.7E0	2.5E-3	2.2E-3
SMART	Sm	RT		14	3.1E-4	2.7E0	4.4E-3	4.0E-3
GOTERM_CC_DIRECT	U4 snRNP	RT		8	4.3E-4	4.6E0	4.7E-3	4.1E-3
GOTERM_CC_DIRECT	methylosome	RT		8	9.0E-4	4.2E0	9.1E-3	8.0E-3
GOTERM_BP_DIRECT	histone mRNA metabolic process	RT		8	1.4E-3	3.9E0	3.0E-2	2.9E-2
GOTERM_CC_DIRECT	spliceosomal tri-snRNP complex	RT		5	2.7E-3	6.4E0	2.5E-2	2.2E-2
GOTERM_CC_DIRECT	pICln-Sm protein complex	RT		5	7.0E-3	5.3E0	5.3E-2	4.7E-2
GOTERM_BP_DIRECT	spliceosomal snRNP assembly	RT		11	1.3E-2	2.3E0	1.8E-1	1.7E-1
GOTERM_BP_DIRECT	nuclear import	RT		7	6.9E-2	2.3E0	5.8E-1	5.5E-1
GOTERM_CC_DIRECT	U7 snRNP	RT		4	8.3E-2	3.6E0	4.0E-1	3.5E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_CC_DIRECT	SMN-Sm protein complex	RT		6	1.2E-1	2.2E0	4.9E-1	4.3E-1
Annotation Cluster 67	**Enrichment Score: 3.79**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	regulation of cellular amino acid metabolic process	RT		26	1.2E-7	3.0E0	8.3E-6	8.0E-6
GOTERM_CC_DIRECT	proteasome regulatory particle, base subcomplex	RT		11	4.4E-7	5.8E0	1.1E-5	9.9E-6
GOTERM_CC_DIRECT	proteasome accessory complex	RT		12	7.0E-6	4.5E0	1.3E-4	1.1E-4
GOTERM_CC_DIRECT	nuclear proteasome complex	RT		8	1.6E-5	6.4E0	2.7E-4	2.4E-4
GOTERM_CC_DIRECT	proteasome regulatory particle	RT		9	3.9E-5	5.2E0	6.2E-4	5.5E-4
GOTERM_BP_DIRECT	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	RT		24	1.4E-4	2.3E0	4.3E-3	4.1E-3
GOTERM_CC_DIRECT	cytosolic proteasome complex	RT		8	1.8E-4	5.1E0	2.2E-3	2.0E-3
INTERPRO	26S proteasome subunit P45	RT		6	5.7E-4	6.2E0	7.8E-3	7.1E-3
GOTERM_MF_DIRECT	proteasome-activating ATPase activity	RT		6	6.8E-4	6.0E0	7.8E-3	7.0E-3
GOTERM_MF_DIRECT	TBP-class protein binding	RT		11	1.0E-3	3.1E0	1.1E-2	9.9E-3
GOTERM_BP_DIRECT	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	RT		7	1.2E-3	4.6E0	2.8E-2	2.7E-2
GOTERM_BP_DIRECT	protein catabolic process	RT		16	1.9E-3	2.3E0	4.0E-2	3.8E-2
GOTERM_BP_DIRECT	positive regulation of proteasomal protein catabolic process	RT		8	1.1E-2	3.0E0	1.5E-1	1.5E-1
GOTERM_BP_DIRECT	ER-associated ubiquitin-dependent protein catabolic process	RT		15	1.2E-1	1.5E0	8.2E-1	7.8E-1
Annotation Cluster 68	**Enrichment Score: 3.72**	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Tyrosine-protein kinase, receptor class V, conserved site	RT		14	5.8E-10	6.2E0	2.2E-8	2.0E-8
INTERPRO	Ephrin receptor ligand binding domain	RT		14	5.8E-10	6.2E0	2.2E-8	2.0E-8
INTERPRO	Tyrosine-protein kinase, ephrin receptor	RT		14	5.8E-10	6.2E0	2.2E-8	2.0E-8
PIR_SUPERFAMILY	tyrosine-protein kinase, ephrin receptor type	RT		14	2.5E-9	5.4E0	4.9E-7	4.8E-7
SMART	EPH_lbd	RT		14	1.3E-7	4.1E0	2.6E-6	2.4E-6
GOTERM_MF_DIRECT	ephrin receptor activity	RT		11	1.6E-7	6.0E0	4.2E-6	3.7E-6
INTERPRO	Tyrosine-protein kinase ephrin type A/B receptor-like	RT		15	5.9E-6	3.7E0	1.2E-4	1.1E-4
GOTERM_BP_DIRECT	ephrin receptor signaling pathway	RT		32	1.4E-5	2.2E0	5.8E-4	5.6E-4
UP_SEQ_FEATURE	domain:SAM	RT		26	2.4E-4	2.1E0	7.0E-3	6.8E-3
INTERPRO	Sterile alpha motif domain	RT		30	2.7E-4	2.0E0	4.0E-3	3.6E-3
INTERPRO	Sterile alpha motif/pointed domain	RT		34	6.7E-4	1.8E0	9.0E-3	8.2E-3
SMART	SM01411	RT		15	7.6E-4	2.4E0	1.0E-2	9.1E-3
GOTERM_MF_DIRECT	transmembrane-ephrin receptor activity	RT		6	9.2E-3	4.0E0	7.5E-2	6.7E-2
INTERPRO	Galactose-binding domain-like	RT		23	9.2E-3	1.7E0	9.2E-2	8.4E-2
GOTERM_MF_DIRECT	GPI-linked ephrin receptor activity	RT		5	1.8E-2	4.3E0	1.2E-1	1.1E-1
UP_SEQ_FEATURE	short sequence motif:PDZ-binding	RT		19	2.8E-2	1.7E0	4.9E-1	4.8E-1
SMART	SAM	RT		28	8.1E-2	1.3E0	4.7E-1	4.3E-1
UP_SEQ_FEATURE	compositionally biased region:Cys-rich	RT		30	1.2E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 2	RT		25	1.6E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 1	RT		25	1.7E-1	1.3E0	1.0E0	9.6E-1
INTERPRO	Insulin-like growth factor binding protein, N-terminal	RT		27	2.3E-1	1.2E0	1.0E0	9.1E-1
INTERPRO	Fibronectin, type III	RT		38	2.7E-1	1.1E0	1.0E0	9.1E-1
SMART	FN3	RT		30	9.5E-1	8.1E-1	1.0E0	9.5E-1
Annotation Cluster 69	**Enrichment Score: 3.68**	G		Count	P_Value	Fold Change	Benjamini	FDR
BIOCARTA	Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	RT		18	5.8E-5	2.4E0	1.4E-3	1.0E-3
BIOCARTA	Regulation of BAD phosphorylation	RT		19	1.4E-4	2.2E0	2.4E-3	1.7E-3
BIOCARTA	Transcription factor CREB and its extracellular signals	RT		18	1.1E-3	2.0E0	1.1E-2	7.7E-3
Annotation Cluster 70	**Enrichment Score: 3.67**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	phosphoprotein phosphatase activity	RT		26	3.7E-9	3.4E0	1.1E-7	9.7E-8

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase	RT		12	1.1E-7	5.7E0	3.2E-6	2.9E-6
SMART	PP2Ac	RT		12	9.2E-6	3.8E0	1.6E-4	1.4E-4
INTERPRO	Metallophosphoesterase domain	RT		12	2.8E-3	2.7E0	3.3E-2	3.0E-2
UP_SEQ_FEATURE	metal ion-binding site:Manganese	RT		11	2.1E-2	2.2E0	3.9E-1	3.7E-1
UP_SEQ_FEATURE	metal ion-binding site:Iron	RT		12	9.5E-2	1.7E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	active site:Proton donor	RT		21	9.8E-1	7.2E-1	1.0E0	9.8E-1
Annotation Cluster 71	**Enrichment Score: 3.67**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Bromodomain	RT		20	4.3E-7	3.5E0	3.3E-6	2.5E-6
INTERPRO	Bromodomain, conserved site	RT		16	1.6E-6	3.8E0	4.0E-5	3.7E-5
INTERPRO	Bromodomain	RT		20	1.3E-5	2.9E0	2.6E-4	2.3E-4
UP_SEQ_FEATURE	domain:Bromo	RT		12	1.8E-3	2.8E0	4.5E-2	4.4E-2
SMART	BROMO	RT		20	2.8E-3	1.9E0	3.1E-2	2.8E-2
UP_SEQ_FEATURE	domain:Bromo 1	RT		7	4.1E-3	4.0E0	9.8E-2	9.4E-2
UP_SEQ_FEATURE	domain:Bromo 2	RT		7	4.1E-3	4.0E0	9.8E-2	9.4E-2
GOTERM_MF_DIRECT	lysine-acetylated histone binding	RT		9	5.5E-3	3.0E0	4.9E-2	4.4E-2
Annotation Cluster 72	**Enrichment Score: 3.41**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	extrinsic component of cytoplasmic side of plasma membrane	RT		33	1.2E-9	3.1E0	4.3E-8	3.8E-8
UP_SEQ_FEATURE	domain:SH2	RT		31	2.9E-5	2.2E0	9.6E-4	9.2E-4
UP_SEQ_FEATURE	domain:SH3	RT		44	3.6E-4	1.7E0	1.0E-2	9.7E-3
UP_KEYWORDS	SH3 domain	RT		46	7.0E-3	1.5E0	3.3E-2	2.5E-2
INTERPRO	Src homology-3 domain	RT		46	4.5E-2	1.3E0	3.3E-1	3.0E-1
SMART	SH3	RT		45	8.8E-1	8.9E-1	1.0E0	9.1E-1
Annotation Cluster 73	**Enrichment Score: 3.4**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	nucleotide binding	RT		97	2.3E-7	1.7E0	5.7E-6	5.1E-6
INTERPRO	RNA recognition motif domain	RT		64	5.1E-6	1.8E0	1.1E-4	1.0E-4
UP_SEQ_FEATURE	domain:RRM	RT		39	3.8E-5	2.0E0	1.2E-3	1.2E-3
INTERPRO	Nucleotide-binding, alpha-beta plait	RT		68	7.0E-5	1.6E0	1.2E-3	1.1E-3
UP_SEQ_FEATURE	domain:RRM 1	RT		30	7.3E-3	1.6E0	1.6E-1	1.6E-1
UP_SEQ_FEATURE	domain:RRM 2	RT		30	7.3E-3	1.6E0	1.6E-1	1.6E-1
UP_SEQ_FEATURE	domain:RRM 3	RT		15	5.6E-2	1.7E0	8.4E-1	8.1E-1
SMART	RRM	RT		63	6.8E-2	1.2E0	4.0E-1	3.6E-1
Annotation Cluster 74	**Enrichment Score: 3.24**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:PI3K/PI4K	RT		16	1.6E-10	6.1E0	1.0E-8	1.0E-8
INTERPRO	Phosphatidylinositol 3-/4-kinase, catalytic domain	RT		16	2.5E-9	5.2E0	9.0E-8	8.2E-8
INTERPRO	Phosphatidylinositol 3/4-kinase, conserved site	RT		14	1.7E-8	5.4E0	5.4E-7	5.0E-7
SMART	PI3Kc	RT		15	9.0E-7	3.6E0	1.7E-5	1.6E-5
INTERPRO	Phosphoinositide 3-kinase, accessory (PIK) domain	RT		9	1.5E-5	5.6E0	2.9E-4	2.7E-4
INTERPRO	Phosphatidylinositol 3-kinase C2 (PI3K C2) domain	RT		8	1.9E-5	6.2E0	3.6E-4	3.3E-4
SMART	PI3Ka	RT		9	9.4E-5	4.1E0	1.4E-3	1.3E-3
INTERPRO	Phosphatidylinositol 3-kinase Ras-binding (PI3K RBD) domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	Phosphatidylinositol Kinase	RT		9	1.2E-4	4.6E0	1.9E-3	1.7E-3
GOTERM_MF_DIRECT	1-phosphatidylinositol-4-phosphate 3-kinase activity	RT		7	1.3E-4	6.0E0	1.9E-3	1.7E-3
GOTERM_BP_DIRECT	phosphatidylinositol-3-phosphate biosynthetic process	RT		20	2.1E-4	2.4E0	6.1E-3	5.9E-3
GOTERM_MF_DIRECT	1-phosphatidylinositol-3-kinase activity	RT		18	3.2E-4	2.5E0	4.4E-3	3.9E-3
SMART	PI3K_C2	RT		8	3.4E-4	4.1E0	4.7E-3	4.3E-3
GOTERM_CC_DIRECT	phosphatidylinositol 3-kinase complex	RT		9	4.6E-4	4.1E0	4.9E-3	4.3E-3

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	phosphatidylinositol 3-kinase activity	RT		5	3.4E-3	6.0E0	3.2E-2	2.9E-2
SMART	PI3K_rbd	RT		6	4.3E-3	4.1E0	4.5E-2	4.1E-2
INTERPRO	Phosphatidylinositol 3-kinase adaptor-binding (PI3K ABD) domain	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
GOTERM_BP_DIRECT	phosphatidylinositol biosynthetic process	RT		17	2.8E-2	1.7E0	3.1E-1	3.0E-1
SMART	PI3K_p85B	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
KEGG_PATHWAY	Inositol phosphate metabolism	RT		14	6.3E-1	1.0E0	9.0E-1	6.3E-1
KEGG_PATHWAY	Phosphatidylinositol signaling system	RT		19	6.3E-1	1.0E0	9.0E-1	6.3E-1
UP_SEQ_FEATURE	domain:PX	RT		4	9.8E-1	5.7E-1	1.0E0	9.8E-1
INTERPRO	Phox homologous domain	RT		5	9.8E-1	5.6E-1	1.0E0	9.8E-1
GOTERM_MF_DIRECT	phosphatidylinositol binding	RT		7	1.0E0	4.9E-1	1.0E0	1.0E0
SMART	PX	RT		4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 75	**Enrichment Score: 3.19**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	receptor signaling protein tyrosine kinase activity	RT		10	8.8E-7	6.0E0	2.1E-5	1.8E-5
INTERPRO	EGF receptor, L domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	Furin-like cysteine-rich domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	Furin-like repeat	RT		10	8.8E-4	3.4E0	1.2E-2	1.1E-2
INTERPRO	Tyrosine protein kinase, EGF/ERB/XmrK receptor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
SMART	FU	RT		10	1.7E-2	2.3E0	1.5E-1	1.4E-1
PIR_SUPERFAMILY	tyrosine-protein kinase, EGF receptor type	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
Annotation Cluster 76	**Enrichment Score: 3.09**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	ligase activity	RT		88	2.8E-10	1.9E0	8.7E-9	7.7E-9
UP_KEYWORDS	Ligase	RT		91	1.7E-8	1.8E0	1.4E-7	1.1E-7
UP_SEQ_FEATURE	zinc finger region:RING-type	RT		48	1.1E-2	1.4E0	2.2E-1	2.1E-1
INTERPRO	Zinc finger, RING-type	RT		60	4.3E-2	1.3E0	3.2E-1	2.9E-1
INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT		82	1.7E-1	1.1E0	8.4E-1	7.7E-1
INTERPRO	Zinc finger, RING-type, conserved site	RT		27	6.4E-1	9.9E-1	1.0E0	9.1E-1
SMART	RING	RT		46	9.9E-1	7.7E-1	1.0E0	9.9E-1
Annotation Cluster 77	**Enrichment Score: 3.08**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Cell Cycle	RT		20	1.0E-5	2.4E0	5.6E-4	4.0E-4
BIOCARTA	cdc25 and chk1 Regulatory Pathway in response to DNA damage	RT		8	7.3E-3	2.7E0	3.7E-2	2.6E-2
BIOCARTA	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	RT		10	7.6E-3	2.3E0	3.7E-2	2.6E-2
Annotation Cluster 78	**Enrichment Score: 3.04**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	histone deacetylase activity	RT		22	1.4E-7	3.4E0	3.6E-6	3.2E-6
GOTERM_BP_DIRECT	histone deacetylation	RT		22	5.1E-6	2.8E0	2.5E-4	2.4E-4
UP_SEQ_FEATURE	region of interest:Histone deacetylase	RT		9	7.3E-6	6.1E0	2.7E-4	2.6E-4
INTERPRO	Histone deacetylase domain	RT		10	1.0E-5	5.2E0	2.0E-4	1.8E-4
GOTERM_MF_DIRECT	NAD-dependent histone deacetylase activity (H3-K14 specific)	RT		10	1.4E-5	5.0E0	2.6E-4	2.3E-4
GOTERM_MF_DIRECT	protein deacetylase activity	RT		9	2.0E-5	5.4E0	3.5E-4	3.2E-4
GOTERM_BP_DIRECT	histone H3 deacetylation	RT		13	3.4E-5	3.7E0	1.2E-3	1.2E-3
INTERPRO	Histone deacetylase superfamily	RT		10	6.7E-5	4.4E0	1.2E-3	1.1E-3
GOTERM_BP_DIRECT	protein deacetylation	RT		8	2.9E-4	4.7E0	7.9E-3	7.6E-3
GOTERM_CC_DIRECT	histone deacetylase complex	RT		15	6.7E-4	2.6E0	7.1E-3	6.2E-3
GOTERM_BP_DIRECT	histone H4 deacetylation	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
GOTERM_BP_DIRECT	peptidyl-lysine deacetylation	RT		5	1.8E-2	4.2E0	2.2E-1	2.1E-1
GOTERM_BP_DIRECT	regulation of gene expression, epigenetic	RT		7	2.0E-2	3.0E0	2.4E-1	2.3E-1
INTERPRO	Histone deacetylase class II, eukaryotic	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
GOTERM_BP_DIRECT	negative regulation of myotube differentiation	RT		7	4.0E-2	2.6E0	3.9E-1	3.8E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
PIR_SUPERFAMILY	histone deacetylase class II, eukaryotic type	RT		4	4.6E-2	4.4E0	5.6E-1	5.5E-1
COG_ONTOLOGY	Chromatin structure and dynamics / Secondary metabolites biosynthesis, transport, and catabolism	RT		7	4.7E-2	2.2E0	4.8E-1	4.8E-1
INTERPRO	Histone deacetylase, glutamine rich N-terminal domain	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	Histone deacetylase	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
PIR_SUPERFAMILY	histone deacetylase class I, eukaryotic type	RT		3	1.6E-1	4.1E0	1.0E0	1.0E0
Annotation Cluster 79	**Enrichment Score: 2.99**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	IL-2 Receptor Beta Chain in T cell Activation	RT		28	2.7E-6	2.2E0	3.9E-4	2.8E-4
BIOCARTA	Inhibition of Cellular Proliferation by Gleevec	RT		19	8.8E-6	2.5E0	5.6E-4	4.0E-4
BIOCARTA	EGF Signaling Pathway	RT		21	1.1E-5	2.4E0	5.6E-4	4.0E-4
BIOCARTA	PDGF Signaling Pathway	RT		21	2.8E-5	2.3E0	9.1E-4	6.5E-4
BIOCARTA	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling	RT		23	5.9E-5	2.1E0	1.4E-3	1.0E-3
BIOCARTA	Growth Hormone Signaling Pathway	RT		20	6.3E-5	2.3E0	1.4E-3	1.0E-3
BIOCARTA	IL 2 signaling pathway	RT		17	1.3E-4	2.4E0	2.4E-3	1.7E-3
BIOCARTA	TPO Signaling Pathway	RT		18	1.4E-4	2.3E0	2.4E-3	1.7E-3
BIOCARTA	IGF-1 Signaling Pathway	RT		16	3.0E-4	2.3E0	4.1E-3	2.9E-3
BIOCARTA	Role of ERBB2 in Signal Transduction and Oncology	RT		16	1.3E-3	2.1E0	1.2E-2	8.8E-3
BIOCARTA	IL 6 signaling pathway	RT		15	1.4E-3	2.2E0	1.2E-2	8.8E-3
BIOCARTA	Insulin Signaling Pathway	RT		15	1.4E-3	2.2E0	1.2E-2	8.8E-3
BIOCARTA	EPO Signaling Pathway	RT		14	1.5E-3	2.2E0	1.3E-2	8.9E-3
BIOCARTA	Links between Pyk2 and Map Kinases	RT		18	2.0E-3	2.0E0	1.6E-2	1.2E-2
BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT		21	3.7E-3	1.8E0	2.3E-2	1.6E-2
BIOCARTA	BCR Signaling Pathway	RT		20	4.3E-3	1.8E0	2.6E-2	1.8E-2
BIOCARTA	Fc Epsilon Receptor I Signaling in Mast Cells	RT		22	4.9E-3	1.7E0	2.9E-2	2.0E-2
BIOCARTA	T Cell Receptor Signaling Pathway	RT		24	5.3E-3	1.7E0	3.0E-2	2.1E-2
BIOCARTA	Integrin Signaling Pathway	RT		21	5.6E-3	1.7E0	3.1E-2	2.2E-2
BIOCARTA	IL 3 signaling pathway	RT		11	7.2E-3	2.2E0	3.7E-2	2.6E-2
BIOCARTA	Bioactive Peptide Induced Signaling Pathway	RT		21	8.3E-3	1.7E0	3.9E-2	2.7E-2
BIOCARTA	Nerve growth factor pathway (NGF)	RT		13	1.1E-2	2.0E0	4.9E-2	3.5E-2
BIOCARTA	fMLP induced chemokine gene expression in HMC-1 cells	RT		20	1.4E-2	1.6E0	5.9E-2	4.2E-2
BIOCARTA	Erk1/Erk2 Mapk Signaling pathway	RT		17	1.5E-2	1.7E0	6.3E-2	4.5E-2
BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		11	3.8E-2	1.9E0	1.2E-1	8.8E-2
BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		12	1.3E-1	1.5E0	3.1E-1	2.2E-1
Annotation Cluster 80	**Enrichment Score: 2.95**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	U1 snRNP binding	RT		7	1.3E-4	6.0E0	1.9E-3	1.7E-3
GOTERM_CC_DIRECT	commitment complex	RT		6	1.5E-3	5.4E0	1.5E-2	1.3E-2
GOTERM_CC_DIRECT	prespliceosome	RT		5	7.0E-3	5.3E0	5.3E-2	4.7E-2
Annotation Cluster 81	**Enrichment Score: 2.9**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	14-3-3 protein	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	14-3-3 protein, conserved site	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	14-3-3 domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
UP_SEQ_FEATURE	site:Interaction with phosphoserine on interacting protein	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
PIR_SUPERFAMILY	14-3-3 protein	RT		7	2.2E-4	5.4E0	1.4E-2	1.4E-2
SMART	14_3_3	RT		7	1.2E-3	4.1E0	1.5E-2	1.3E-2
GOTERM_BP_DIRECT	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	RT		13	2.3E-3	2.6E0	4.5E-2	4.3E-2
GOTERM_BP_DIRECT	protein targeting	RT		10	2.0E-1	1.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	membrane organization	RT		8	2.9E-1	1.5E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 82	Enrichment Score: 2.79			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	MyD88-dependent toll-like receptor signaling pathway	RT		24	2.5E-11	4.3E0	3.1E-9	2.9E-9
UP_SEQ_FEATURE	repeat:LRR 20	RT		18	2.7E-10	5.3E0	1.7E-8	1.6E-8
UP_SEQ_FEATURE	repeat:LRR 21	RT		14	5.9E-8	5.3E0	3.0E-6	2.9E-6
GOTERM_BP_DIRECT	regulation of cytokine secretion	RT		10	4.4E-6	5.4E0	2.2E-4	2.1E-4
UP_SEQ_FEATURE	repeat:LRR 22	RT		10	4.5E-6	5.7E0	1.8E-4	1.7E-4
GOTERM_BP_DIRECT	toll-like receptor signaling pathway	RT		16	5.6E-6	3.5E0	2.6E-4	2.5E-4
UP_SEQ_FEATURE	repeat:LRR 23	RT		8	1.2E-4	5.5E0	3.5E-3	3.4E-3
UP_SEQ_FEATURE	repeat:LRR 24	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
GOTERM_BP_DIRECT	I-kappaB phosphorylation	RT		8	1.4E-3	3.9E0	3.0E-2	2.9E-2
UP_SEQ_FEATURE	domain:TIR	RT		11	1.8E-3	3.0E0	4.5E-2	4.4E-2
GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		9	3.8E-3	3.1E0	6.9E-2	6.6E-2
INTERPRO	Toll/interleukin-1 receptor homology (TIR) domain	RT		11	5.1E-3	2.6E0	5.6E-2	5.1E-2
UP_SEQ_FEATURE	repeat:LRR 25	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
GOTERM_BP_DIRECT	positive regulation of interleukin-8 production	RT		11	7.2E-3	2.5E0	1.2E-1	1.1E-1
INTERPRO	Toll-like receptor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
GOTERM_BP_DIRECT	positive regulation of NF-kappaB import into nucleus	RT		9	1.7E-2	2.5E0	2.1E-1	2.0E-1
GOTERM_BP_DIRECT	positive regulation of interferon-alpha biosynthetic process	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
SMART	TIR	RT		11	1.8E-2	2.1E0	1.6E-1	1.4E-1
GOTERM_BP_DIRECT	positive regulation of interferon-beta biosynthetic process	RT		5	1.8E-2	4.2E0	2.2E-1	2.1E-1
PIR_SUPERFAMILY	toll-like receptor, 1/2/4/6/10 types [Parent=PIRSF800008]	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
UP_SEQ_FEATURE	repeat:LRR 26	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
GOTERM_BP_DIRECT	positive regulation of toll-like receptor signaling pathway	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	RT		13	6.6E-2	1.7E0	5.6E-1	5.3E-1
UP_KEYWORDS	Inflammatory response	RT		30	7.5E-2	1.4E0	2.6E-1	2.0E-1
UP_SEQ_FEATURE	repeat:LRR 27	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	positive regulation of interferon-gamma biosynthetic process	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
GOTERM_CC_DIRECT	endolysosome membrane	RT		4	2.9E-1	2.1E0	8.6E-1	7.5E-1
GOTERM_MF_DIRECT	lipopeptide binding	RT		3	4.0E-1	2.2E0	1.0E0	8.9E-1
GOTERM_CC_DIRECT	phagocytic vesicle membrane	RT		8	8.4E-1	8.6E-1	1.0E0	8.8E-1
GOTERM_MF_DIRECT	transmembrane signaling receptor activity	RT		17	1.0E0	4.7E-1	1.0E0	1.0E0
Annotation Cluster 83	Enrichment Score: 2.78			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	compositionally biased region:Ala/Asp-rich (DA-box)	RT		8	1.0E-5	6.8E0	3.7E-4	3.5E-4
UP_SEQ_FEATURE	region of interest:Flexible hinge	RT		7	6.1E-5	6.8E0	1.9E-3	1.8E-3
INTERPRO	RecF/RecN/SMC	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	Structural maintenance of chromosomes protein	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
PIR_SUPERFAMILY	structural maintenance of chromosomes protein	RT		5	4.7E-3	5.4E0	2.3E-1	2.3E-1
INTERPRO	SMCs flexible hinge	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
SMART	SM00968	RT		5	3.5E-2	3.4E0	2.6E-1	2.3E-1
GOTERM_CC_DIRECT	meiotic cohesin complex	RT		3	2.4E-1	3.2E0	8.3E-1	7.3E-1
Annotation Cluster 84	Enrichment Score: 2.76			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	SNF2-related	RT		22	4.5E-10	4.3E0	1.8E-8	1.7E-8
UP_SEQ_FEATURE	domain:Chromo 2	RT		8	4.0E-5	6.1E0	1.3E-3	1.2E-3
INTERPRO	Chromo domain-like	RT		14	8.1E-4	2.7E0	1.1E-2	9.9E-3
UP_SEQ_FEATURE	domain:Chromo 1	RT		8	1.1E-3	4.2E0	2.9E-2	2.8E-2
INTERPRO	Chromo domain/shadow	RT		14	1.1E-3	2.6E0	1.4E-2	1.3E-2

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	BRK domain	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
INTERPRO	Chromo domain	RT		10	1.7E-2	2.4E0	1.4E-1	1.3E-1
SMART	BRK	RT		5	3.5E-2	3.4E0	2.6E-1	2.3E-1
SMART	CHROMO	RT		14	4.3E-2	1.7E0	3.0E-1	2.7E-1
GOTERM_MF_DIRECT	hydrolase activity, acting on acid anhydrides	RT		3	2.7E-1	3.0E0	9.9E-1	8.8E-1
INTERPRO	Chromo domain, conserved site	RT		5	4.1E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 85	**Enrichment Score: 2.74**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	sister chromatid cohesion	RT		35	4.7E-5	2.0E0	1.7E-3	1.6E-3
GOTERM_CC_DIRECT	kinetochore	RT		28	6.8E-5	2.2E0	9.2E-4	8.0E-4
UP_KEYWORDS	Centromere	RT		35	1.0E-3	1.8E0	5.3E-3	4.1E-3
UP_KEYWORDS	Kinetochore	RT		22	4.6E-2	1.5E0	1.7E-1	1.3E-1
GOTERM_CC_DIRECT	condensed chromosome kinetochore	RT		19	1.3E-1	1.4E0	5.3E-1	4.7E-1
Annotation Cluster 86	**Enrichment Score: 2.74**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:S-adenosyl-L-methionine binding	RT		15	2.3E-4	2.9E0	6.6E-3	6.3E-3
INTERPRO	Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
INTERPRO	RNA (C5-cytosine) methyltransferase	RT		6	4.0E-3	4.6E0	4.4E-2	4.0E-2
UP_SEQ_FEATURE	binding site:S-adenosyl-L-methionine	RT		15	1.3E-2	2.0E0	2.5E-1	2.4E-1
Annotation Cluster 87	**Enrichment Score: 2.74**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Post-SET	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
INTERPRO	Post-SET domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K36 specific)	RT		5	8.9E-3	5.0E0	7.3E-2	6.5E-2
UP_SEQ_FEATURE	domain:AWS	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
INTERPRO	AWS	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
SMART	AWS	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
Annotation Cluster 88	**Enrichment Score: 2.7**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Protein kinase 1	RT		11	6.7E-6	5.0E0	2.6E-4	2.5E-4
UP_SEQ_FEATURE	domain:Protein kinase 2	RT		11	6.7E-6	5.0E0	2.6E-4	2.5E-4
INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
INTERPRO	Ribosomal protein S6 kinase II	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
PIR_SUPERFAMILY	ribosomal protein S6 kinase II	RT		4	7.9E-2	3.6E0	6.9E-1	6.8E-1
Annotation Cluster 89	**Enrichment Score: 2.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	protein peptidyl-prolyl isomerization	RT		20	2.5E-5	2.8E0	9.4E-4	9.0E-4
UP_KEYWORDS	Rotamase	RT		17	3.6E-5	3.1E0	2.1E-4	1.6E-4
GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT		20	7.2E-5	2.6E0	1.2E-3	1.0E-3
INTERPRO	Cyclophilin-like peptidyl-prolyl cis-trans isomerase domain	RT		11	2.6E-3	2.8E0	3.1E-2	2.8E-2
INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans isomerase, conserved site	RT		10	3.4E-3	3.0E0	3.8E-2	3.5E-2
UP_SEQ_FEATURE	domain:PPIase cyclophilin-type	RT		10	5.0E-3	2.8E0	1.2E-1	1.1E-1
INTERPRO	Cyclophilin-type peptidyl-prolyl cis-trans isomerase	RT		10	6.9E-3	2.7E0	7.4E-2	6.8E-2
UP_KEYWORDS	Cyclosporin	RT		5	1.1E-2	4.9E0	4.6E-2	3.6E-2
GOTERM_MF_DIRECT	cyclosporin A binding	RT		5	1.8E-2	4.3E0	1.2E-1	1.1E-1
PIR_SUPERFAMILY	peptidyl-prolyl cis-trans isomerase	RT		6	5.2E-2	2.7E0	5.9E-1	5.9E-1
INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT		7	5.7E-2	2.4E0	4.0E-1	3.7E-1
Annotation Cluster 90	**Enrichment Score: 2.61**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	protein peptidyl-prolyl isomerization	RT		20	2.5E-5	2.8E0	9.4E-4	9.0E-4
UP_KEYWORDS	Rotamase	RT		17	3.6E-5	3.1E0	2.1E-4	1.6E-4

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	peptidyl-prolyl cis-trans isomerase activity	RT		20	7.2E-5	2.6E0	1.2E-3	1.0E-3
UP_KEYWORDS	Isomerase	RT		34	2.3E-4	1.9E0	1.3E-3	1.0E-3
INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type	RT		8	3.2E-2	2.5E0	2.4E-1	2.2E-1
GOTERM_BP_DIRECT	chaperone-mediated protein folding	RT		12	3.7E-2	1.9E0	3.8E-1	3.6E-1
GOTERM_MF_DIRECT	FK506 binding	RT		8	3.8E-2	2.4E0	2.3E-1	2.0E-1
INTERPRO	Peptidyl-prolyl cis-trans isomerase, FKBP-type, domain	RT		7	5.7E-2	2.4E0	4.0E-1	3.7E-1
UP_SEQ_FEATURE	domain:PPIase FKBP-type	RT		5	8.6E-2	2.8E0	1.0E0	9.6E-1
Annotation Cluster 91	**Enrichment Score: 2.56**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	U6 snRNP	RT		7	9.1E-5	6.4E0	1.2E-3	1.0E-3
GOTERM_CC_DIRECT	Lsm1-7-Pat1 complex	RT		4	1.4E-2	6.4E0	9.3E-2	8.2E-2
GOTERM_BP_DIRECT	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	RT		11	1.7E-2	2.2E0	2.1E-1	2.0E-1
Annotation Cluster 92	**Enrichment Score: 2.55**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	compositionally biased region:Arg/Ser-rich (RS domain)	RT		11	6.4E-5	4.2E0	2.0E-3	1.9E-3
UP_SEQ_FEATURE	compositionally biased region:Gly-rich (hinge region)	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
GOTERM_BP_DIRECT	negative regulation of mRNA splicing, via spliceosome	RT		9	1.7E-2	2.5E0	2.1E-1	2.0E-1
GOTERM_BP_DIRECT	mRNA splice site selection	RT		7	5.3E-2	2.4E0	4.9E-1	4.7E-1
Annotation Cluster 93	**Enrichment Score: 2.47**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	UTP biosynthetic process	RT		9	1.7E-4	4.4E0	5.0E-3	4.8E-3
GOTERM_BP_DIRECT	CTP biosynthetic process	RT		9	1.7E-4	4.4E0	5.0E-3	4.8E-3
UP_SEQ_FEATURE	active site:Pros-phosphohistidine intermediate	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
INTERPRO	Nucleoside diphosphate kinase	RT		8	5.1E-4	4.5E0	7.3E-3	6.7E-3
GOTERM_MF_DIRECT	nucleoside diphosphate kinase activity	RT		11	6.3E-4	3.3E0	7.3E-3	6.5E-3
GOTERM_BP_DIRECT	nucleoside diphosphate phosphorylation	RT		10	1.2E-3	3.3E0	2.8E-2	2.7E-2
GOTERM_BP_DIRECT	nucleobase-containing small molecule interconversion	RT		12	1.4E-3	2.8E0	3.0E-2	2.9E-2
GOTERM_BP_DIRECT	GTP biosynthetic process	RT		8	2.6E-3	3.6E0	5.0E-2	4.8E-2
SMART	NDK	RT		8	6.8E-3	3.0E0	6.8E-2	6.1E-2
INTERPRO	Nucleoside diphosphate kinase, active site	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
GOTERM_BP_DIRECT	pyrimidine nucleotide metabolic process	RT		5	5.0E-2	3.3E0	4.7E-1	4.5E-1
GOTERM_BP_DIRECT	nucleoside triphosphate biosynthetic process	RT		6	7.2E-2	2.5E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	purine nucleotide metabolic process	RT		5	7.3E-2	3.0E0	5.8E-1	5.5E-1
UP_KEYWORDS	Nucleotide metabolism	RT		8	1.0E-1	2.0E0	3.4E-1	2.6E-1
Annotation Cluster 94	**Enrichment Score: 2.41**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	protein K6-linked ubiquitination	RT		7	4.7E-4	5.2E0	1.2E-2	1.2E-2
GOTERM_BP_DIRECT	protein K29-linked ubiquitination	RT		5	3.5E-3	5.9E0	6.6E-2	6.3E-2
GOTERM_BP_DIRECT	protein K27-linked ubiquitination	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
Annotation Cluster 95	**Enrichment Score: 2.4**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ribosomal protein S1, RNA-binding domain	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
INTERPRO	RNA-binding domain, S1	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
SMART	SM00316	RT		7	9.2E-3	3.2E0	8.7E-2	7.9E-2
UP_SEQ_FEATURE	domain:S1 motif	RT		5	3.1E-2	3.8E0	5.4E-1	5.2E-1
Annotation Cluster 96	**Enrichment Score: 2.31**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	RT		9	5.0E-6	5.9E0	2.5E-4	2.4E-4
GOTERM_BP_DIRECT	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
UP_SEQ_FEATURE	region of interest:Sufficient for nucleolar localization	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
GOTERM_CC_DIRECT	PeBoW complex	RT		3	1.2E-1	4.8E0	4.9E-1	4.3E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 97	Enrichment Score: 2.31			Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Exonuclease	RT		18	6.0E-4	2.4E0	3.2E-3	2.4E-3
GOTERM_MF_DIRECT	3'-5'-exoribonuclease activity	RT		11	6.3E-4	3.3E0	7.3E-3	6.5E-3
GOTERM_BP_DIRECT	RNA phosphodiester bond hydrolysis, exonucleolytic	RT		11	1.3E-2	2.3E0	1.8E-1	1.7E-1
GOTERM_CC_DIRECT	nuclear exosome (RNase complex)	RT		7	2.1E-2	3.0E0	1.3E-1	1.1E-1
UP_KEYWORDS	Nuclease	RT		29	2.9E-2	1.5E0	1.1E-1	8.8E-2
Annotation Cluster 98	**Enrichment Score: 2.3**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	regulation of axonogenesis	RT		13	1.1E-4	3.3E0	3.5E-3	3.4E-3
GOTERM_MF_DIRECT	Roundabout binding	RT		7	1.2E-3	4.6E0	1.3E-2	1.1E-2
GOTERM_BP_DIRECT	Roundabout signaling pathway	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
GOTERM_BP_DIRECT	axon extension involved in axon guidance	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
Annotation Cluster 99	**Enrichment Score: 2.24**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Cadmium induces DNA synthesis and proliferation in macrophages	RT		14	2.6E-4	2.5E0	4.0E-3	2.9E-3
BIOCARTA	Links between Pyk2 and Map Kinases	RT		18	2.0E-3	2.0E0	1.6E-2	1.2E-2
BIOCARTA	CXCR4 Signaling Pathway	RT		16	2.5E-3	2.0E0	1.8E-2	1.3E-2
BIOCARTA	CCR3 signaling in Eosinophils	RT		13	4.2E-2	1.7E0	1.3E-1	9.3E-2
BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	RT		11	1.1E-1	1.6E0	2.9E-1	2.0E-1
Annotation Cluster 100	**Enrichment Score: 2.19**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Cullin, N-terminal	RT		8	2.1E-4	5.0E0	3.3E-3	3.0E-3
INTERPRO	Cullin homology	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in NEDD8)	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
INTERPRO	Cullin protein, neddylation domain	RT		6	4.0E-3	4.6E0	4.4E-2	4.0E-2
SMART	CULLIN	RT		6	1.2E-2	3.5E0	1.1E-1	9.9E-2
INTERPRO	Cullin, conserved site	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
SMART	SM00884	RT		6	2.5E-2	3.0E0	2.0E-1	1.9E-1
INTERPRO	Cullin repeat-like-containing domain	RT		6	3.2E-2	3.1E0	2.4E-1	2.2E-1
GOTERM_CC_DIRECT	cullin-RING ubiquitin ligase complex	RT		4	1.6E-1	2.8E0	6.2E-1	5.4E-1
Annotation Cluster 101	**Enrichment Score: 2.16**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	guanyl nucleotide binding	RT		8	9.8E-5	5.3E0	1.5E-3	1.3E-3
INTERPRO	G-protein alpha subunit, group Q	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
GOTERM_BP_DIRECT	phospholipase C-activating dopamine receptor signaling pathway	RT		4	2.3E-1	2.4E0	1.0E0	9.6E-1
Annotation Cluster 102	**Enrichment Score: 2.14**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Thioredoxin 1	RT		9	7.3E-6	6.1E0	2.7E-4	2.6E-4
UP_SEQ_FEATURE	domain:Thioredoxin 2	RT		9	7.3E-6	6.1E0	2.7E-4	2.6E-4
GOTERM_BP_DIRECT	response to endoplasmic reticulum stress	RT		29	1.7E-5	2.3E0	6.8E-4	6.6E-4
INTERPRO	Thioredoxin domain	RT		18	9.8E-5	2.7E0	1.7E-3	1.5E-3
INTERPRO	Thioredoxin, conserved site	RT		10	5.1E-4	3.6E0	7.3E-3	6.7E-3
INTERPRO	Disulphide isomerase	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
GOTERM_BP_DIRECT	cell redox homeostasis	RT		24	3.3E-3	1.8E0	6.3E-2	6.0E-2
GOTERM_MF_DIRECT	protein disulfide isomerase activity	RT		10	6.4E-3	2.7E0	5.6E-2	5.0E-2
UP_KEYWORDS	Redox-active center	RT		15	8.4E-3	2.1E0	3.8E-2	2.9E-2
UP_SEQ_FEATURE	site:Contributes to redox potential value	RT		5	1.1E-2	4.9E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of first active site	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	site:Lowers pKa of C-terminal Cys of second active site	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
INTERPRO	Protein disulphide isomerase	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
UP_SEQ_FEATURE	domain:Thioredoxin 3	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	domain:Thioredoxin	RT		10	4.4E-2	2.1E0	7.3E-1	7.1E-1
UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT		13	1.8E-1	1.5E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	disulfide oxidoreductase activity	RT		3	2.7E-1	3.0E0	9.9E-1	8.8E-1
GOTERM_MF_DIRECT	isomerase activity	RT		6	2.7E-1	1.7E0	1.0E0	8.9E-1
GOTERM_CC_DIRECT	cell	RT		18	4.0E-1	1.1E0	1.0E0	8.8E-1
INTERPRO	Thioredoxin-like fold	RT		23	4.4E-1	1.1E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	endoplasmic reticulum lumen	RT		19	1.0E0	6.3E-1	1.0E0	1.0E0
Annotation Cluster 103	**Enrichment Score: 1.97**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ribosomal protein S5 domain 2-type fold, subgroup	RT		12	6.0E-4	3.1E0	8.2E-3	7.5E-3
INTERPRO	Translation elongation factor EFTu/EF1A, domain 2	RT		9	1.0E-3	3.7E0	1.3E-2	1.2E-2
INTERPRO	Translation elongation/initiation factor/Ribosomal, beta-barrel	RT		13	1.5E-3	2.7E0	1.9E-2	1.7E-2
INTERPRO	Elongation factor, GTP-binding domain	RT		10	2.2E-3	3.1E0	2.7E-2	2.4E-2
INTERPRO	Translation elongation factor EFG, V domain	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
INTERPRO	Elongation factor G, III-V domain	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
SMART	SM00838	RT		5	1.5E-2	4.1E0	1.3E-1	1.2E-1
INTERPRO	Translation elongation factor EFG/EF2, domain IV	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
UP_KEYWORDS	Elongation factor	RT		10	2.3E-2	2.3E0	9.3E-2	7.2E-2
SMART	SM00889	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
INTERPRO	Translation elongation factor EF1A/initiation factor IF2gamma, C-terminal	RT		4	2.6E-1	2.3E0	1.0E0	9.1E-1
INTERPRO	Translation elongation factor EFTu/EF1A, C-terminal	RT		3	3.2E-1	2.7E0	1.0E0	9.1E-1
Annotation Cluster 104	**Enrichment Score: 1.95**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:DAZ-like 14	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 15	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 2	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 3	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 4	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 5	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 6	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 7	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 8	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 9	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 1	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 2	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 3	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	chain:Deleted in azoospermia protein 4	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 1	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 10	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 11	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 12	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:DAZ-like 13	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
Annotation Cluster 105	**Enrichment Score: 1.95**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	four-way junction DNA binding	RT		10	9.2E-5	4.3E0	1.5E-3	1.3E-3
GOTERM_BP_DIRECT	mitotic recombination	RT		8	2.6E-3	3.6E0	5.0E-2	4.8E-2
GOTERM_MF_DIRECT	recombinase activity	RT		6	4.7E-3	4.5E0	4.3E-2	3.8E-2
GOTERM_BP_DIRECT	reciprocal meiotic recombination	RT		12	7.4E-3	2.4E0	1.2E-1	1.1E-1
INTERPRO	DNA recombination and repair protein, RecA-like	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
PIR_SUPERFAMILY	DNA repair and recombination protein, Rad51 type	RT		5	1.2E-2	4.5E0	2.9E-1	2.9E-1
INTERPRO	DNA recombination and repair protein Rad51, C-terminal	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
INTERPRO	DNA recombination/repair protein RecA/RadB, ATP-binding domain	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
GOTERM_BP_DIRECT	chromosome organization involved in meiotic cell cycle	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
GOTERM_BP_DIRECT	strand invasion	RT		5	1.8E-2	4.2E0	2.2E-1	2.1E-1
GOTERM_MF_DIRECT	endodeoxyribonuclease activity	RT		9	2.2E-2	2.4E0	1.4E-1	1.2E-1
GOTERM_BP_DIRECT	DNA recombinase assembly	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
INTERPRO	DNA repair Rad51/transcription factor NusA, alpha-helical	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_CC_DIRECT	Rad51B-Rad51C-Rad51D-XRCC2 complex	RT		3	1.8E-1	3.8E0	6.7E-1	5.9E-1
Annotation Cluster 106	**Enrichment Score: 1.92**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:Spectrin 18	RT		8	4.0E-5	6.1E0	1.3E-3	1.2E-3
UP_SEQ_FEATURE	repeat:Spectrin 20	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
UP_SEQ_FEATURE	repeat:Spectrin 19	RT		7	2.1E-4	6.0E0	6.2E-3	5.9E-3
UP_SEQ_FEATURE	repeat:Spectrin 21	RT		6	1.1E-3	5.8E0	2.9E-2	2.8E-2
UP_SEQ_FEATURE	repeat:Spectrin 22	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
UP_SEQ_FEATURE	repeat:Spectrin 23	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
UP_SEQ_FEATURE	repeat:Spectrin 30	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:Spectrin 31	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:Spectrin 24	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Spectrin 25	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Spectrin 26	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Spectrin 27	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Spectrin 28	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Spectrin 29	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
Annotation Cluster 107	**Enrichment Score: 1.9**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	rRNA-binding	RT		14	6.6E-6	4.0E0	4.3E-5	3.3E-5
INTERPRO	KOW	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
INTERPRO	RNA-binding S4 domain	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
UP_SEQ_FEATURE	domain:S4 RNA-binding	RT		5	2.0E-2	4.3E0	3.7E-1	3.6E-1
SMART	S4	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
INTERPRO	Ribosomal protein S4e	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ribosomal protein S4e, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ribosomal protein S4e, central region	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ribosomal protein S4e, N-terminal, conserved site	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
PIR_SUPERFAMILY	ribosomal protein S4a/S4e	RT		3	8.8E-2	5.4E0	6.9E-1	6.8E-1
Annotation Cluster 108	**Enrichment Score: 1.89**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Initiation factor	RT		19	1.1E-3	2.2E0	5.5E-3	4.3E-3
GOTERM_BP_DIRECT	regulation of translational initiation	RT		15	1.4E-3	2.5E0	3.0E-2	2.9E-2
GOTERM_MF_DIRECT	translation initiation factor activity	RT		21	1.6E-3	2.1E0	1.7E-2	1.5E-2
UP_KEYWORDS	Protein biosynthesis	RT		37	1.8E-3	1.7E0	9.1E-3	7.1E-3
GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex	RT		9	2.4E-3	3.4E0	2.2E-2	2.0E-2
GOTERM_CC_DIRECT	eukaryotic 48S preinitiation complex	RT		8	4.7E-3	3.4E0	4.0E-2	3.5E-2
GOTERM_CC_DIRECT	eukaryotic translation initiation factor 3 complex, eIF3m	RT		5	1.4E-2	4.5E0	9.4E-2	8.2E-2
GOTERM_MF_DIRECT	translation initiation factor binding	RT		9	1.6E-2	2.6E0	1.2E-1	1.0E-1
GOTERM_CC_DIRECT	eukaryotic 43S preinitiation complex	RT		7	2.1E-2	3.0E0	1.3E-1	1.1E-1
GOTERM_BP_DIRECT	formation of translation preinitiation complex	RT		9	2.9E-2	2.3E0	3.2E-1	3.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
KEGG_PATHWAY	RNA transport	RT		42	7.7E-2	1.3E0	1.3E-1	7.7E-2
INTERPRO	Proteasome component (PCI) domain	RT		6	1.3E-1	2.2E0	6.4E-1	5.8E-1
UP_SEQ_FEATURE	domain:PCI	RT		6	1.3E-1	2.2E0	1.0E0	9.6E-1
SMART	PINT	RT		6	3.6E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 109	**Enrichment Score: 1.89**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:C2 tensin-type	RT		6	5.1E-3	4.5E0	1.2E-1	1.1E-1
UP_SEQ_FEATURE	domain:Phosphatase tensin-type	RT		6	9.0E-3	4.1E0	2.0E-1	1.9E-1
INTERPRO	Tensin phosphatase, C2 domain	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
SMART	SM01326	RT		6	4.6E-2	2.7E0	3.0E-1	2.7E-1
Annotation Cluster 110	**Enrichment Score: 1.83**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Mini-chromosome maintenance, DNA-dependent ATPase	RT		7	9.4E-4	4.8E0	1.2E-2	1.1E-2
UP_SEQ_FEATURE	domain:MCM	RT		6	2.6E-3	5.1E0	6.2E-2	6.0E-2
SMART	MCM	RT		7	9.2E-3	3.2E0	8.7E-2	7.9E-2
GOTERM_CC_DIRECT	MCM complex	RT		5	4.0E-2	3.5E0	2.3E-1	2.0E-1
INTERPRO	Mini-chromosome maintenance, conserved site	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
BIOCARTA	CDK Regulation of DNA Replication	RT		9	2.1E-1	1.5E0	4.4E-1	3.1E-1
Annotation Cluster 111	**Enrichment Score: 1.8**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Post-SET	RT		12	1.4E-6	5.1E0	6.0E-5	5.8E-5
INTERPRO	Post-SET domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
SMART	PostSET	RT		9	5.0E-3	2.8E0	5.1E-2	4.6E-2
GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K4 specific)	RT		9	5.5E-3	3.0E0	4.9E-2	4.4E-2
GOTERM_CC_DIRECT	histone methyltransferase complex	RT		10	5.8E-3	2.8E0	4.8E-2	4.2E-2
GOTERM_BP_DIRECT	histone H3-K4 methylation	RT		9	1.2E-2	2.7E0	1.7E-1	1.6E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type 3	RT		5	4.7E-2	3.4E0	7.7E-1	7.4E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT		9	6.3E-2	2.0E0	9.0E-1	8.7E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT		9	1.0E-1	1.9E0	1.0E0	9.6E-1
INTERPRO	FY-rich, N-terminal	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
INTERPRO	FY-rich, C-terminal	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
SMART	FYRC	RT		3	3.6E-1	2.4E0	1.0E0	9.1E-1
SMART	FYRN	RT		3	3.6E-1	2.4E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	Set1C/COMPASS complex	RT		3	5.4E-1	1.7E0	1.0E0	8.8E-1
Annotation Cluster 112	**Enrichment Score: 1.79**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II transcription factor recruiting	RT		7	4.6E-4	5.2E0	5.6E-3	5.0E-3
UP_SEQ_FEATURE	domain:HTH myb-type 1	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
UP_SEQ_FEATURE	domain:HTH myb-type 2	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
INTERPRO	SANT/Myb domain	RT		16	2.1E-3	2.3E0	2.5E-2	2.3E-2
INTERPRO	Myb-like domain	RT		6	4.0E-3	4.6E0	4.4E-2	4.0E-2
INTERPRO	Myb domain	RT		6	7.7E-3	4.1E0	7.7E-2	7.1E-2
UP_SEQ_FEATURE	domain:HTH myb-type 3	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:Myb-like 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:Myb-like 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	C-myb, C-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
SMART	SANT	RT		16	8.5E-2	1.5E0	4.9E-1	4.4E-1
UP_SEQ_FEATURE	DNA-binding region:H-T-H motif	RT		7	1.7E-1	1.8E0	1.0E0	9.6E-1
INTERPRO	Homeodomain-like	RT		19	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 113	**Enrichment Score: 1.76**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Phototransduction	RT		13	2.4E-3	2.5E0	5.2E-3	2.5E-3

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_CC_DIRECT	photoreceptor disc membrane	RT		8	2.1E-2	2.7E0	1.3E-1	1.1E-1
GOTERM_BP_DIRECT	regulation of rhodopsin mediated signaling pathway	RT		9	1.0E-1	1.8E0	7.1E-1	6.8E-1
Annotation Cluster 114	**Enrichment Score: 1.76**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Death domain	RT		14	2.1E-3	2.5E0	2.6E-2	2.4E-2
UP_SEQ_FEATURE	domain:Death	RT		13	3.0E-3	2.5E0	7.2E-2	7.0E-2
INTERPRO	Death-like domain	RT		23	4.2E-2	1.5E0	3.1E-1	2.9E-1
SMART	DEATH	RT		9	3.4E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 115	**Enrichment Score: 1.73**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	EGF receptor, L domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
INTERPRO	Furin-like cysteine-rich domain	RT		7	1.1E-4	6.2E0	1.7E-3	1.6E-3
GOTERM_MF_DIRECT	insulin receptor substrate binding	RT		8	6.5E-4	4.3E0	7.5E-3	6.7E-3
INTERPRO	Tyrosine-protein kinase, insulin-like receptor	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
PIR_SUPERFAMILY	insulin receptor	RT		3	8.8E-2	5.4E0	6.9E-1	6.8E-1
INTERPRO	Tyrosine-protein kinase, receptor class II, conserved site	RT		3	5.5E-1	1.7E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	receptor complex	RT		20	6.3E-1	1.0E0	1.0E0	8.8E-1
UP_SEQ_FEATURE	domain:Fibronectin type-III 3	RT		6	1.0E0	4.9E-1	1.0E0	1.0E0
Annotation Cluster 116	**Enrichment Score: 1.69**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	mRNA cleavage	RT		8	1.4E-3	3.9E0	3.0E-2	2.9E-2
BIOCARTA	Polyadenylation of mRNA	RT		7	7.1E-2	2.1E0	2.0E-1	1.4E-1
GOTERM_BP_DIRECT	mRNA polyadenylation	RT		9	8.6E-2	1.9E0	6.4E-1	6.2E-1
Annotation Cluster 117	**Enrichment Score: 1.67**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Cyclins and Cell Cycle Regulation	RT		18	3.0E-4	2.2E0	4.1E-3	2.9E-3
BBID	26.cyclin-CDK_complexes	RT		11	1.6E-2	2.0E0	8.5E-1	8.5E-1
BBID	1.RBphosphoE2F	RT		9	9.2E-2	1.7E0	1.0E0	1.0E0
GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase inhibitor activity	RT		5	9.7E-2	2.7E0	4.7E-1	4.2E-1
GOTERM_BP_DIRECT	negative regulation of phosphorylation	RT		7	1.1E-1	2.1E0	7.3E-1	7.0E-1
Annotation Cluster 118	**Enrichment Score: 1.67**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	POLO box duplicated domain	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
UP_SEQ_FEATURE	domain:POLO box 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:POLO box 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
Annotation Cluster 119	**Enrichment Score: 1.66**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Glutamine amidotransferase	RT		6	5.7E-4	6.2E0	7.8E-3	7.1E-3
UP_SEQ_FEATURE	domain:Glutamine amidotransferase type-1	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
UP_KEYWORDS	Pyrimidine biosynthesis	RT		4	6.8E-2	3.9E0	2.4E-1	1.8E-1
UP_SEQ_FEATURE	active site:For GATase activity	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	glutamine metabolic process	RT		7	1.1E-1	2.1E0	7.3E-1	7.0E-1
UP_KEYWORDS	Glutamine amidotransferase	RT		4	1.3E-1	3.1E0	4.2E-1	3.3E-1
Annotation Cluster 120	**Enrichment Score: 1.65**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Protein kinase inhibitor	RT		7	1.0E-2	3.4E0	4.4E-2	3.4E-2
GOTERM_MF_DIRECT	mitogen-activated protein kinase kinase binding	RT		8	1.0E-2	3.0E0	8.2E-2	7.3E-2
INTERPRO	Pseudokinase tribbles family/serine-threonine-protein kinase 40	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
GOTERM_BP_DIRECT	regulation of MAP kinase activity	RT		5	5.0E-2	3.3E0	4.7E-1	4.5E-1
GOTERM_MF_DIRECT	ubiquitin-protein transferase regulator activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
Annotation Cluster 121	**Enrichment Score: 1.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Pre-SET	RT		5	1.1E-2	4.9E0	2.2E-1	2.1E-1
INTERPRO	Pre-SET domain	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
GOTERM_BP_DIRECT	histone H3-K9 methylation	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K9 specific)	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
SMART	PreSET	RT		5	6.7E-2	2.9E0	4.0E-1	3.6E-1
Annotation Cluster 122	**Enrichment Score: 1.63**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Shigellosis	RT		29	5.9E-6	2.4E0	1.7E-5	8.0E-6
BIOCARTA	The 4-1BB-dependent immune response	RT		14	6.7E-4	2.4E0	7.4E-3	5.3E-3
BIOCARTA	Toll-Like Receptor Pathway	RT		23	1.1E-3	1.8E0	1.1E-2	7.7E-3
BIOCARTA	Signal transduction through IL1R	RT		20	2.7E-3	1.8E0	1.8E-2	1.3E-2
KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori infection	RT		23	5.7E-3	1.8E0	1.2E-2	5.7E-3
BIOCARTA	NFkB activation by Nontypeable Hemophilus influenzae	RT		15	8.4E-3	1.9E0	3.9E-2	2.7E-2
BIOCARTA	NF-kB Signaling Pathway	RT		14	1.6E-2	1.9E0	6.4E-2	4.5E-2
BIOCARTA	CD40L Signaling Pathway	RT		10	2.7E-2	2.0E0	1.0E-1	7.1E-2
GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT		4	3.0E-2	5.1E0	1.8E-1	1.6E-1
KEGG_PATHWAY	RIG-I-like receptor signaling pathway	RT		21	3.8E-2	1.6E0	6.8E-2	3.8E-2
BIOCARTA	Activation of PKC through G protein coupled receptor	RT		6	4.2E-2	2.6E0	1.3E-1	9.3E-2
BBID	77.IkBa_Kinase_JNK_MEKK1	RT		6	6.5E-2	2.3E0	1.0E0	1.0E0
BIOCARTA	Acetylation and Deacetylation of RelA in The Nucleus	RT		9	1.2E-1	1.7E0	2.9E-1	2.1E-1
BIOCARTA	Double Stranded RNA Induced Gene Expression	RT		6	2.0E-1	1.8E0	4.3E-1	3.1E-1
BIOCARTA	TNF/Stress Related Signaling	RT		11	2.8E-1	1.3E0	5.5E-1	3.9E-1
BIOCARTA	Erythropoietin mediated neuroprotection through NF-kB	RT		7	2.9E-1	1.5E0	5.7E-1	4.0E-1
BIOCARTA	TNFR2 Signaling Pathway	RT		8	3.7E-1	1.4E0	6.8E-1	4.8E-1
BBID	90.IB_and-cat-Arm_processing_of_Ci	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	RT		6	5.8E-1	1.2E0	9.0E-1	6.4E-1
Annotation Cluster 123	**Enrichment Score: 1.6**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	RT		20	2.8E-4	2.1E0	4.0E-3	2.9E-3
BIOCARTA	Signal Dependent Regulation of Myogenesis by Corepressor MITR	RT		9	8.3E-4	3.0E0	8.4E-3	6.0E-3
UP_SEQ_FEATURE	domain:MADS-box	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
INTERPRO	Transcription factor, MADS-box	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
UP_SEQ_FEATURE	DNA-binding region:Mef2-type	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
SMART	MADS	RT		5	3.5E-2	3.4E0	2.6E-1	2.3E-1
UP_SEQ_FEATURE	region of interest:Beta domain	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	Holliday junction regulator protein family C-terminal	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
BIOCARTA	Regulation of PGC-1a	RT		12	1.3E-1	1.5E0	3.1E-1	2.2E-1
UP_SEQ_FEATURE	compositionally biased region:Lys-rich (basic)	RT		3	3.9E-1	2.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	site:Cleavage	RT		9	8.2E-1	8.8E-1	1.0E0	9.6E-1
Annotation Cluster 124	**Enrichment Score: 1.6**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	DNA-binding region:TEA	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
INTERPRO	TEA/ATTS	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	Transcriptional enhancer factor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
PIR_SUPERFAMILY	transcriptional enhancer factor	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
SMART	TEA	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
UP_SEQ_FEATURE	region of interest:Transcriptional activation	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
Annotation Cluster 125	**Enrichment Score: 1.57**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	RT		36	2.3E-5	2.1E0	7.9E-4	7.6E-4
INTERPRO	P-type ATPase, transmembrane domain	RT		11	3.7E-5	4.3E0	6.6E-4	6.0E-4
INTERPRO	Cation-transporting P-type ATPase, C-terminal	RT		11	7.6E-5	4.0E0	1.3E-3	1.2E-3
INTERPRO	Cation-transporting P-type ATPase, N-terminal	RT		11	1.5E-4	3.8E0	2.3E-3	2.1E-3
INTERPRO	P-type ATPase, A domain	RT		16	2.3E-4	2.8E0	3.5E-3	3.2E-3

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Cation-transporting P-type ATPase	RT		16	2.3E-4	2.8E0	3.5E-3	3.2E-3
INTERPRO	P-type ATPase, phosphorylation site	RT		16	2.3E-4	2.8E0	3.5E-3	3.2E-3
INTERPRO	P-type ATPase, cytoplasmic domain N	RT		16	2.3E-4	2.8E0	3.5E-3	3.2E-3
UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	RT		16	3.2E-4	2.7E0	9.1E-3	8.7E-3
INTERPRO	Sodium/potassium-transporting P-type ATPase, subfamily IIC	RT		6	5.7E-4	6.2E0	7.8E-3	7.1E-3
SMART	SM00831	RT		11	1.4E-3	2.8E0	1.7E-2	1.5E-2
GOTERM_BP_DIRECT	cellular sodium ion homeostasis	RT		10	2.0E-3	3.1E0	4.1E-2	3.9E-2
GOTERM_BP_DIRECT	establishment or maintenance of transmembrane electrochemical gradient	RT		8	2.6E-3	3.6E0	5.0E-2	4.8E-2
GOTERM_MF_DIRECT	sodium:potassium-exchanging ATPase activity	RT		6	1.6E-2	3.6E0	1.2E-1	1.0E-1
GOTERM_BP_DIRECT	sodium ion export from cell	RT		6	1.6E-2	3.6E0	2.1E-1	2.0E-1
GOTERM_MF_DIRECT	steroid hormone binding	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
GOTERM_BP_DIRECT	cellular potassium ion homeostasis	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
UP_SEQ_FEATURE	region of interest:Interaction with phosphoinositide-3 kinase	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
GOTERM_BP_DIRECT	cellular response to steroid hormone stimulus	RT		5	7.3E-2	3.0E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	response to glycoside	RT		3	7.6E-2	5.9E0	5.8E-1	5.5E-1
UP_KEYWORDS	Sodium/potassium transport	RT		4	9.8E-2	3.4E0	3.3E-1	2.5E-1
INTERPRO	HAD-like domain	RT		17	2.3E-1	1.3E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	sodium:potassium-exchanging ATPase complex	RT		4	2.4E-1	2.3E0	8.3E-1	7.3E-1
KEGG_PATHWAY	Carbohydrate digestion and absorption	RT		11	2.8E-1	1.4E0	4.4E-1	2.8E-1
GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	RT		8	2.9E-1	1.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	regulation of cardiac conduction	RT		12	3.4E-1	1.3E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cell communication by electrical coupling involved in cardiac conduction	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	potassium ion import	RT		6	5.2E-1	1.3E0	1.0E0	9.6E-1
KEGG_PATHWAY	Proximal tubule bicarbonate reclamation	RT		4	8.5E-1	9.0E-1	1.0E0	8.5E-1
GOTERM_BP_DIRECT	ion transmembrane transport	RT		30	9.0E-1	8.5E-1	1.0E0	9.6E-1
KEGG_PATHWAY	Cardiac muscle contraction	RT		11	9.3E-1	7.6E-1	1.0E0	9.3E-1
UP_KEYWORDS	Potassium	RT		12	9.9E-1	6.4E-1	1.0E0	9.9E-1
UP_KEYWORDS	Potassium transport	RT		10	9.9E-1	5.9E-1	1.0E0	9.9E-1
KEGG_PATHWAY	Mineral absorption	RT		4	9.9E-1	4.7E-1	1.0E0	9.9E-1
UP_KEYWORDS	Sodium transport	RT		4	1.0E0	2.3E-1	1.0E0	1.0E0
KEGG_PATHWAY	Protein digestion and absorption	RT		4	1.0E0	2.4E-1	1.0E0	1.0E0
UP_KEYWORDS	Sodium	RT		4	1.0E0	2.2E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	topological domain:Lumenal	RT		22	1.0E0	3.3E-1	1.0E0	1.0E0
UP_KEYWORDS	Ion transport	RT		31	1.0E0	3.3E-1	1.0E0	1.0E0
Annotation Cluster 126	**Enrichment Score: 1.51**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	single-stranded DNA-dependent ATPase activity	RT		7	2.5E-3	4.2E0	2.5E-2	2.2E-2
GOTERM_CC_DIRECT	DNA replication factor C complex	RT		5	7.0E-3	5.3E0	5.3E-2	4.7E-2
GOTERM_MF_DIRECT	DNA clamp loader activity	RT		5	3.1E-2	3.7E0	1.9E-1	1.7E-1
INTERPRO	DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
INTERPRO	Replication factor C, C-terminal domain	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_BP_DIRECT	positive regulation of DNA-directed DNA polymerase activity	RT		4	9.9E-2	3.4E0	6.9E-1	6.6E-1
GOTERM_CC_DIRECT	Ctf18 RFC-like complex	RT		4	1.2E-1	3.2E0	4.9E-1	4.3E-1
Annotation Cluster 127	**Enrichment Score: 1.49**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Bromo	RT		12	1.8E-3	2.8E0	4.5E-2	4.4E-2
INTERPRO	DDT domain superfamily	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
UP_SEQ_FEATURE	domain:DDT	RT		4	4.5E-2	4.5E0	7.4E-1	7.2E-1
SMART	DDT	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type	RT		12	1.3E-1	1.6E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 128	Enrichment Score: 1.49			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_CC_DIRECT	MLL5-L complex	RT		6	3.5E-3	4.8E0	3.1E-2	2.7E-2
GOTERM_CC_DIRECT	PTW/PP1 phosphatase complex	RT		5	1.4E-2	4.5E0	9.4E-2	8.2E-2
GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	RT		4	6.8E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 129	**Enrichment Score: 1.49**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Dynamin, GTPase domain	RT		6	1.7E-3	5.3E0	2.1E-2	1.9E-2
INTERPRO	Dynamin, GTPase region, conserved site	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
INTERPRO	Dynamin central domain	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
UP_SEQ_FEATURE	domain:GED	RT		5	1.1E-2	4.9E0	2.2E-1	2.1E-1
SMART	DYNc	RT		6	1.2E-2	3.5E0	1.1E-1	9.9E-2
INTERPRO	Dynamin GTPase effector	RT		5	1.6E-2	4.4E0	1.3E-1	1.2E-1
SMART	GED	RT		5	3.5E-2	3.4E0	2.6E-1	2.3E-1
INTERPRO	GTPase effector domain, GED	RT		5	4.3E-2	3.4E0	3.2E-1	2.9E-1
GOTERM_BP_DIRECT	dynamin polymerization involved in mitochondrial fission	RT		4	9.9E-2	3.4E0	6.9E-1	6.6E-1
INTERPRO	Dynamin	RT		6	1.3E-1	2.2E0	6.4E-1	5.8E-1
GOTERM_BP_DIRECT	mitochondrial fission	RT		5	4.0E-1	1.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	membrane fusion	RT		6	8.9E-1	8.1E-1	1.0E0	9.6E-1
Annotation Cluster 130	**Enrichment Score: 1.47**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	ubiquitin-ubiquitin ligase activity	RT		7	1.3E-2	3.2E0	9.9E-2	8.9E-2
INTERPRO	U box domain	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
UP_SEQ_FEATURE	domain:U-box	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
SMART	Ubox	RT		5	1.1E-1	2.5E0	5.6E-1	5.1E-1
Annotation Cluster 131	**Enrichment Score: 1.47**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	RNA polymerase II transcription factor binding	RT		20	1.0E-4	2.5E0	1.5E-3	1.4E-3
UP_SEQ_FEATURE	zinc finger region:GATA-type 1	RT		6	3.6E-4	6.8E0	9.9E-3	9.5E-3
UP_SEQ_FEATURE	zinc finger region:GATA-type 2	RT		6	3.6E-4	6.8E0	9.9E-3	9.5E-3
INTERPRO	Zinc finger, GATA-type	RT		7	2.4E-2	2.9E0	1.9E-1	1.7E-1
GOTERM_BP_DIRECT	anatomical structure formation involved in morphogenesis	RT		6	2.6E-2	3.2E0	2.9E-1	2.8E-1
GOTERM_MF_DIRECT	enhancer sequence-specific DNA binding	RT		8	3.8E-2	2.4E0	2.3E-1	2.0E-1
SMART	ZnF_GATA	RT		7	5.1E-2	2.4E0	3.1E-1	2.8E-1
INTERPRO	GATA-type transcription activator, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_BP_DIRECT	intestinal epithelial cell differentiation	RT		4	9.9E-2	3.4E0	6.9E-1	6.6E-1
INTERPRO	Zinc finger, NHR/GATA-type	RT		13	2.2E-1	1.4E0	1.0E0	9.1E-1
GOTERM_BP_DIRECT	tissue development	RT		4	4.8E-1	1.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cell development	RT		8	5.2E-1	1.2E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cell fate commitment	RT		9	5.2E-1	1.2E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cellular response to BMP stimulus	RT		3	9.7E-1	5.9E-1	1.0E0	9.7E-1
Annotation Cluster 132	**Enrichment Score: 1.47**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	protein kinase C activity	RT		10	2.0E-4	4.0E0	2.8E-3	2.5E-3
INTERPRO	Diacylglycerol/phorbol-ester binding	RT		11	3.7E-3	2.7E0	4.1E-2	3.8E-2
INTERPRO	Protein kinase C, delta/epsilon/eta/theta types	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
PIR_SUPERFAMILY	protein kinase C, delta/epsilon/eta/theta types	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT		8	3.3E-2	2.5E0	5.7E-1	5.5E-1
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT		8	3.3E-2	2.5E0	5.7E-1	5.5E-1
GOTERM_MF_DIRECT	calcium-independent protein kinase C activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
INTERPRO	Protein kinase C-like, phorbol ester/diacylglycerol binding	RT		15	1.7E-1	1.4E0	8.3E-1	7.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
SMART	C1	RT		15	7.6E-1	9.4E-1	1.0E0	9.1E-1
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	RT		5	9.1E-1	7.6E-1	1.0E0	9.6E-1
Annotation Cluster 133	**Enrichment Score: 1.46**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	mitotic cell cycle	RT		16	1.9E-3	2.3E0	4.0E-2	3.8E-2
GOTERM_MF_DIRECT	receptor signaling protein serine/threonine kinase activity	RT		17	1.1E-2	1.9E0	8.7E-2	7.7E-2
UP_SEQ_FEATURE	domain:CRIB	RT		7	4.9E-2	2.5E0	8.0E-1	7.7E-1
UP_SEQ_FEATURE	region of interest:GTPase-binding	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	region of interest:Autoregulatory region	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	PAK-box/P21-Rho-binding	RT		7	9.0E-2	2.2E0	5.0E-1	4.5E-1
SMART	PBD	RT		7	1.8E-1	1.8E0	7.6E-1	6.9E-1
Annotation Cluster 134	**Enrichment Score: 1.46**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	cardiac muscle contraction	RT		16	5.4E-3	2.1E0	9.2E-2	8.8E-2
GOTERM_BP_DIRECT	regulation of the force of heart contraction	RT		9	8.5E-3	2.8E0	1.3E-1	1.3E-1
KEGG_PATHWAY	Cardiac muscle contraction	RT		11	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 135	**Enrichment Score: 1.45**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	SCF ubiquitin ligase complex	RT		17	3.2E-3	2.2E0	2.8E-2	2.5E-2
UP_SEQ_FEATURE	domain:F-box	RT		18	3.3E-2	1.7E0	5.7E-1	5.5E-1
INTERPRO	F-box domain, cyclin-like	RT		19	4.4E-2	1.6E0	3.3E-1	3.0E-1
SMART	FBOX	RT		12	3.6E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 136	**Enrichment Score: 1.44**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Threonine protease	RT		9	4.9E-3	3.1E0	2.3E-2	1.8E-2
INTERPRO	Proteasome, subunit alpha/beta	RT		9	6.4E-3	2.9E0	7.0E-2	6.4E-2
GOTERM_CC_DIRECT	proteasome core complex	RT		9	1.1E-2	2.7E0	7.7E-2	6.8E-2
GOTERM_MF_DIRECT	threonine-type endopeptidase activity	RT		9	1.6E-2	2.6E0	1.2E-1	1.0E-1
GOTERM_CC_DIRECT	proteasome core complex, alpha-subunit complex	RT		5	2.5E-2	4.0E0	1.5E-1	1.3E-1
INTERPRO	Proteasome, alpha-subunit, N-terminal domain	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
INTERPRO	Proteasome A-type subunit	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
SMART	SM00948	RT		5	1.1E-1	2.5E0	5.6E-1	5.1E-1
INTERPRO	Proteasome, beta-type subunit, conserved site	RT		5	1.1E-1	2.6E0	6.3E-1	5.7E-1
INTERPRO	Proteasome B-type subunit	RT		4	2.6E-1	2.3E0	1.0E0	9.1E-1
GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	RT		10	4.2E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 137	**Enrichment Score: 1.43**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	DNA topological change	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
UP_KEYWORDS	Topoisomerase	RT		4	4.4E-2	4.6E0	1.6E-1	1.3E-1
INTERPRO	Toprim domain	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
Annotation Cluster 138	**Enrichment Score: 1.43**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	2'-5'-oligoadenylate synthase	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	2-5-oligoadenylate synthetase, conserved site	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	2'-5'-oligoadenylate synthetase 1, domain 2/C-terminal	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
GOTERM_MF_DIRECT	2'-5'-oligoadenylate synthetase activity	RT		4	1.6E-2	6.0E0	1.2E-1	1.0E-1
INTERPRO	2-5-oligoadenylate synthetase, N-terminal	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
INTERPRO	Nucleotidyl transferase domain	RT		4	2.1E-1	2.5E0	9.9E-1	9.1E-1
GOTERM_MF_DIRECT	nucleotidyltransferase activity	RT		7	2.9E-1	1.5E0	1.0E0	8.9E-1
Annotation Cluster 139	**Enrichment Score: 1.42**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	ROC GTPase	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
UP_SEQ_FEATURE	domain:Roc	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Mitochondrial Rho-like	RT		5	6.3E-2	3.1E0	4.1E-1	3.7E-1
Annotation Cluster 140	**Enrichment Score: 1.42**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of translational initiation	RT		9	1.4E-3	3.6E0	3.0E-2	2.9E-2
GOTERM_MF_DIRECT	translation activator activity	RT		5	4.9E-2	3.3E0	2.8E-1	2.5E-1
GOTERM_BP_DIRECT	3'-UTR-mediated mRNA stabilization	RT		7	5.3E-2	2.4E0	4.9E-1	4.7E-1
GOTERM_MF_DIRECT	mRNA 3'-UTR binding	RT		9	5.9E-1	1.1E0	1.0E0	8.9E-1
Annotation Cluster 141	**Enrichment Score: 1.42**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process	RT		8	2.6E-3	3.6E0	5.0E-2	4.8E-2
GOTERM_BP_DIRECT	nuclear mRNA surveillance	RT		5	5.0E-2	3.3E0	4.7E-1	4.5E-1
GOTERM_BP_DIRECT	histone mRNA catabolic process	RT		4	4.3E-1	1.7E0	1.0E0	9.6E-1
Annotation Cluster 142	**Enrichment Score: 1.42**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	DNA-binding region:A.T hook 3	RT		6	9.0E-3	4.1E0	2.0E-1	1.9E-1
UP_SEQ_FEATURE	DNA-binding region:A.T hook 1	RT		6	3.1E-2	3.1E0	5.4E-1	5.2E-1
UP_SEQ_FEATURE	DNA-binding region:A.T hook 2	RT		6	3.1E-2	3.1E0	5.4E-1	5.2E-1
INTERPRO	AT hook, DNA-binding motif	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
SMART	AT_hook	RT		4	1.6E-1	2.7E0	7.0E-1	6.4E-1
Annotation Cluster 143	**Enrichment Score: 1.4**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	RNA-processing protein, HAT helix	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
UP_SEQ_FEATURE	repeat:HAT 4	RT		6	2.2E-2	3.4E0	4.0E-1	3.9E-1
UP_SEQ_FEATURE	repeat:HAT 9	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
UP_SEQ_FEATURE	repeat:HAT 1	RT		6	3.1E-2	3.1E0	5.4E-1	5.2E-1
UP_SEQ_FEATURE	repeat:HAT 2	RT		6	3.1E-2	3.1E0	5.4E-1	5.2E-1
UP_SEQ_FEATURE	repeat:HAT 3	RT		6	3.1E-2	3.1E0	5.4E-1	5.2E-1
UP_SEQ_FEATURE	repeat:HAT 8	RT		4	4.5E-2	4.5E0	7.4E-1	7.2E-1
UP_SEQ_FEATURE	repeat:HAT 5	RT		5	6.5E-2	3.1E0	9.2E-1	8.9E-1
UP_SEQ_FEATURE	repeat:HAT 7	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
SMART	HAT	RT		6	7.3E-2	2.4E0	4.3E-1	3.9E-1
UP_SEQ_FEATURE	repeat:HAT 6	RT		4	1.3E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 144	**Enrichment Score: 1.39**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Leucine-rich repeat-containing protein 8, N-terminal	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
GOTERM_MF_DIRECT	volume-sensitive anion channel activity	RT		4	1.6E-2	6.0E0	1.2E-1	1.0E-1
GOTERM_BP_DIRECT	regulation of anion transport	RT		5	7.3E-2	3.0E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	anion transmembrane transport	RT		5	7.7E-1	9.9E-1	1.0E0	9.6E-1
Annotation Cluster 145	**Enrichment Score: 1.35**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	histone serine kinase activity	RT		5	3.4E-3	6.0E0	3.2E-2	2.9E-2
GOTERM_CC_DIRECT	chromosome passenger complex	RT		4	3.0E-2	5.1E0	1.8E-1	1.6E-1
GOTERM_CC_DIRECT	condensed nuclear chromosome, centromeric region	RT		4	2.0E-1	2.5E0	7.3E-1	6.4E-1
GOTERM_CC_DIRECT	spindle pole centrosome	RT		4	2.0E-1	2.5E0	7.3E-1	6.4E-1
Annotation Cluster 146	**Enrichment Score: 1.35**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	ESC/E(Z) complex	RT		9	1.5E-3	3.6E0	1.4E-2	1.2E-2
BIOCARTA	The PRC2 Complex Sets Long-term Gene Silencing Through Modification of Histone Tails	RT		8	1.9E-1	1.6E0	4.1E-1	2.9E-1
GOTERM_BP_DIRECT	negative regulation of gene expression, epigenetic	RT		11	3.3E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 147	**Enrichment Score: 1.34**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	HRDC domain	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	HRDC-like	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
UP_SEQ_FEATURE	domain:HRDC	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
SMART	HRDC	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
Annotation Cluster 148	**Enrichment Score: 1.33**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	fibroblast growth factor-activated receptor activity	RT		5	3.4E-3	6.0E0	3.2E-2	2.9E-2
INTERPRO	Tyrosine-protein kinase, fibroblast growth factor receptor	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
PIR_SUPERFAMILY	fibroblast growth factor receptor	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
GOTERM_BP_DIRECT	positive regulation of phospholipase activity	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
GOTERM_MF_DIRECT	fibroblast growth factor binding	RT		7	1.8E-1	1.8E0	7.5E-1	6.7E-1
UP_KEYWORDS	Craniosynostosis	RT		5	4.0E-1	1.6E0	1.0E0	7.8E-1
Annotation Cluster 149	**Enrichment Score: 1.3**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	RT		7	4.9E-3	3.8E0	8.5E-2	8.1E-2
GOTERM_MF_DIRECT	calcium sensitive guanylate cyclase activator activity	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
GOTERM_BP_DIRECT	phototransduction	RT		5	6.9E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 150	**Enrichment Score: 1.3**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ubiquitin subgroup	RT		9	2.7E-4	4.3E0	4.0E-3	3.6E-3
GOTERM_BP_DIRECT	regulation of necrotic cell death	RT		8	1.4E-3	3.9E0	3.0E-2	2.9E-2
GOTERM_BP_DIRECT	regulation of type I interferon production	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
GOTERM_BP_DIRECT	MyD88-independent toll-like receptor signaling pathway	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
INTERPRO	Ubiquitin conserved site	RT		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
GOTERM_BP_DIRECT	negative regulation of epidermal growth factor receptor signaling pathway	RT		12	3.1E-2	2.0E0	3.4E-1	3.3E-1
GOTERM_BP_DIRECT	regulation of transcription from RNA polymerase II promoter in response to hypoxia	RT		10	3.6E-2	2.1E0	3.7E-1	3.6E-1
GOTERM_BP_DIRECT	positive regulation of epidermal growth factor receptor signaling pathway	RT		9	3.8E-2	2.2E0	3.8E-1	3.6E-1
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Gly-Lys) (interchain with K-? in acceptor proteins)	RT		7	3.8E-2	2.6E0	6.4E-1	6.2E-1
GOTERM_BP_DIRECT	negative regulation of type I interferon production	RT		10	5.4E-2	2.0E0	4.9E-1	4.7E-1
GOTERM_BP_DIRECT	viral life cycle	RT		10	6.5E-2	1.9E0	5.5E-1	5.3E-1
UP_SEQ_FEATURE	chain:40S ribosomal protein S27a	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
UP_SEQ_FEATURE	site:Essential for function	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
UP_SEQ_FEATURE	compositionally biased region:Lys-rich (highly basic)	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
UP_SEQ_FEATURE	chain:Ubiquitin	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
UP_SEQ_FEATURE	binding site:Activating enzyme	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	virion assembly	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	glycogen biosynthetic process	RT		8	1.4E-1	1.8E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	interstrand cross-link repair	RT		12	1.9E-1	1.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	intracellular transport of virus	RT		11	3.6E-1	1.3E0	1.0E0	9.6E-1
GOTERM_CC_DIRECT	endocytic vesicle membrane	RT		8	9.1E-1	7.7E-1	1.0E0	9.1E-1
GOTERM_BP_DIRECT	endosomal transport	RT		5	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 151	**Enrichment Score: 1.27**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	dendritic spine development	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
GOTERM_BP_DIRECT	central nervous system projection neuron axonogenesis	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
GOTERM_MF_DIRECT	axon guidance receptor activity	RT		4	9.7E-2	3.4E0	4.7E-1	4.2E-1
GOTERM_BP_DIRECT	retinal ganglion cell axon guidance	RT		6	2.1E-1	1.9E0	1.0E0	9.6E-1
Annotation Cluster 152	**Enrichment Score: 1.26**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
OMIM_DISEASE	Schimmelpenning-Feuerstein-Mims syndrome, somatic mosaic	RT		3	4.5E-2	7.8E0	1.0E0	1.0E0
UP_SEQ_FEATURE	region of interest:Hypervariable region	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
BBID	65.Integrin_affinity_modulation	RT		5	6.2E-2	2.7E0	1.0E0	1.0E0
Annotation Cluster 153	**Enrichment Score: 1.26**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:I-domain	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
INTERPRO	5'-3' exonuclease, C-terminal domain	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Helix-hairpin-helix motif, class 2	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
INTERPRO	XPG/Rad2 endonuclease	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
INTERPRO	XPG-I domain	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
UP_SEQ_FEATURE	region of interest:N-domain	RT		4	4.5E-2	4.5E0	7.4E-1	7.2E-1
INTERPRO	XPG N-terminal	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
SMART	HhH2	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
SMART	XPGI	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
SMART	XPGN	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1
INTERPRO	XPG conserved site	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
GOTERM_MF_DIRECT	nuclease activity	RT		7	1.8E-1	1.8E0	7.5E-1	6.7E-1
Annotation Cluster 154	**Enrichment Score: 1.26**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	peptidyl-lysine monomethylation	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
GOTERM_BP_DIRECT	peptidyl-lysine dimethylation	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT		6	1.4E-1	2.1E0	6.1E-1	5.5E-1
Annotation Cluster 155	**Enrichment Score: 1.25**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	rRNA catabolic process	RT		8	6.8E-4	4.3E0	1.7E-2	1.6E-2
INTERPRO	Ribonuclease II/R, conserved site	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
GOTERM_CC_DIRECT	nuclear exosome (RNase complex)	RT		7	2.1E-2	3.0E0	1.3E-1	1.1E-1
UP_KEYWORDS	Exosome	RT		6	3.0E-2	3.2E0	1.2E-1	9.2E-2
GOTERM_CC_DIRECT	cytoplasmic exosome (RNase complex)	RT		6	4.1E-2	2.9E0	2.3E-1	2.0E-1
GOTERM_BP_DIRECT	nuclear mRNA surveillance	RT		5	5.0E-2	3.3E0	4.7E-1	4.5E-1
INTERPRO	Exoribonuclease, phosphorolytic domain 1	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
GOTERM_CC_DIRECT	exosome (RNase complex)	RT		6	9.3E-2	2.4E0	4.3E-1	3.8E-1
INTERPRO	Exoribonuclease, phosphorolytic domain 2	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
GOTERM_BP_DIRECT	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	exoribonuclease activity	RT		5	2.0E-1	2.1E0	7.8E-1	7.0E-1
INTERPRO	PNPase/RNase PH domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
GOTERM_BP_DIRECT	U4 snRNA 3'-end processing	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 156	**Enrichment Score: 1.25**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Heat shock factor (HSF)-type, DNA-binding	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-A/B	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	region of interest:Hydrophobic repeat HR-C	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
SMART	HSF	RT		5	1.1E-1	2.5E0	5.6E-1	5.1E-1
Annotation Cluster 157	**Enrichment Score: 1.25**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Guanylate kinase, conserved site	RT		9	1.7E-3	3.5E0	2.1E-2	1.9E-2
GOTERM_CC_DIRECT	ionotropic glutamate receptor complex	RT		6	3.5E-3	4.8E0	3.1E-2	2.7E-2
GOTERM_MF_DIRECT	ionotropic glutamate receptor binding	RT		10	4.4E-3	2.8E0	4.1E-2	3.7E-2
INTERPRO	Guanylate kinase	RT		10	4.9E-3	2.8E0	5.3E-2	4.9E-2
UP_SEQ_FEATURE	domain:Guanylate kinase-like	RT		10	5.0E-3	2.8E0	1.2E-1	1.1E-1
GOTERM_BP_DIRECT	GMP metabolic process	RT		8	7.1E-3	3.2E0	1.2E-1	1.1E-1
GOTERM_MF_DIRECT	guanylate kinase activity	RT		7	8.2E-3	3.5E0	6.9E-2	6.2E-2
GOTERM_BP_DIRECT	establishment or maintenance of epithelial cell apical/basal polarity	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
INTERPRO	PDZ-associated domain of NMDA receptors	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	Membrane-associated guanylate kinase (MAGUK), PEST domain, N-terminal	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	Membrane-associated guanylate kinase (MAGUK) scaffold protein	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	Guanylate kinase/L-type calcium channel	RT		10	1.7E-2	2.4E0	1.4E-1	1.3E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	GDP metabolic process	RT		6	2.6E-2	3.2E0	2.9E-1	2.8E-1
SMART	SM01277	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
PIR_SUPERFAMILY	membrane-associated guanylate kinase (MAGUK) scaffold protein	RT		3	8.8E-2	5.4E0	6.9E-1	6.8E-1
SMART	GuKc	RT		10	1.4E-1	1.6E0	6.9E-1	6.2E-1
INTERPRO	Variant SH3	RT		14	1.7E-1	1.4E0	8.6E-1	7.9E-1
INTERPRO	L27	RT		5	1.8E-1	2.2E0	8.7E-1	8.0E-1
GOTERM_BP_DIRECT	receptor localization to synapse	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
BIOCARTA	Synaptic Proteins at the Synaptic Junction	RT		9	2.1E-1	1.5E0	4.4E-1	3.1E-1
GOTERM_BP_DIRECT	receptor clustering	RT		6	2.4E-1	1.8E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:L27 1	RT		3	2.7E-1	2.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:L27 2	RT		3	2.7E-1	2.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:PDZ 3	RT		6	4.6E-1	1.4E0	1.0E0	9.6E-1
INTERPRO	L27, C-terminal	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
SMART	L27	RT		4	6.0E-1	1.4E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:PDZ 1	RT		6	7.6E-1	9.7E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:PDZ 2	RT		6	7.6E-1	9.7E-1	1.0E0	9.6E-1
GOTERM_MF_DIRECT	ligand-gated ion channel activity	RT		4	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 158	**Enrichment Score: 1.25**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Tyrosine-protein kinase, receptor class III, conserved site	RT		8	1.9E-5	6.2E0	3.6E-4	3.3E-4
GOTERM_BP_DIRECT	positive regulation of phospholipase C activity	RT		8	1.0E-4	5.3E0	3.2E-3	3.1E-3
GOTERM_MF_DIRECT	vascular endothelial growth factor-activated receptor activity	RT		5	1.8E-2	4.3E0	1.2E-1	1.1E-1
INTERPRO	Tyrosine-protein kinase, CSF-1/PDGF receptor	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
PIR_SUPERFAMILY	tyrosine-protein kinase, CSF-1/PDGF receptor type	RT		4	4.6E-2	4.4E0	5.6E-1	5.5E-1
GOTERM_MF_DIRECT	growth factor binding	RT		7	2.9E-1	1.5E0	1.0E0	8.9E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 7	RT		5	4.1E-1	1.5E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 5	RT		10	4.2E-1	1.2E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		18	7.1E-1	9.6E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 4	RT		10	8.0E-1	9.0E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 6	RT		5	8.1E-1	9.2E-1	1.0E0	9.6E-1
INTERPRO	Immunoglobulin	RT		10	9.3E-1	7.6E-1	1.0E0	9.3E-1
Annotation Cluster 159	**Enrichment Score: 1.25**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	vagina development	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
GOTERM_BP_DIRECT	natural killer cell differentiation	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
GOTERM_BP_DIRECT	negative regulation of lymphocyte activation	RT		3	7.6E-2	5.9E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	apoptotic cell clearance	RT		6	9.4E-2	2.4E0	6.8E-1	6.5E-1
GOTERM_BP_DIRECT	secretion by cell	RT		4	2.3E-1	2.4E0	1.0E0	9.6E-1
Annotation Cluster 160	**Enrichment Score: 1.23**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:PC 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:PC 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:PC 3	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:PC 4	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
Annotation Cluster 161	**Enrichment Score: 1.22**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	nucleotide-activated protein kinase complex	RT		6	1.9E-2	3.5E0	1.2E-1	1.1E-1
GOTERM_MF_DIRECT	cAMP-dependent protein kinase regulator activity	RT		4	9.7E-2	3.4E0	4.7E-1	4.2E-1
BIOCARTA	ChREBP regulation by carbohydrates and cAMP	RT		11	1.1E-1	1.6E0	2.9E-1	2.0E-1
Annotation Cluster 162	**Enrichment Score: 1.22**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
KEGG_PATHWAY	Apoptosis	RT		28	9.7E-6	2.3E0	2.7E-5	1.2E-5
GOTERM_BP_DIRECT	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
GOTERM_BP_DIRECT	glial cell apoptotic process	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
BIOCARTA	HIV-I Nef	RT		28	3.8E-2	1.4E0	1.2E-1	8.8E-2
BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT		12	7.0E-2	1.7E0	2.0E-1	1.4E-1
BIOCARTA	D4-GDI Signaling Pathway	RT		8	9.5E-2	1.9E0	2.5E-1	1.8E-1
BIOCARTA	Induction of apoptosis through DR3 and DR4/5 Death Receptors	RT		15	1.6E-1	1.4E0	3.6E-1	2.6E-1
BBID	86.Apoptosis_Nematode&_Vert	RT		6	2.0E-1	1.8E0	1.0E0	1.0E0
BIOCARTA	Caspase Cascade in Apoptosis	RT		10	3.8E-1	1.3E0	7.0E-1	4.9E-1
BBID	127.Mito-stress	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
BIOCARTA	Stress Induction of HSP Regulation	RT		6	6.4E-1	1.1E0	9.6E-1	6.8E-1
BBID	46.P13K_PTEN	RT		4	8.8E-1	9.0E-1	1.0E0	1.0E0
Annotation Cluster 163	**Enrichment Score: 1.22**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Signaling of Hepatocyte Growth Factor Receptor	RT		21	3.7E-3	1.8E0	2.3E-2	1.6E-2
BIOCARTA	Role of MAL in Rho-Mediated Activation of SRF	RT		13	6.1E-3	2.1E0	3.3E-2	2.3E-2
GOTERM_BP_DIRECT	Bergmann glial cell differentiation	RT		6	9.4E-3	3.9E0	1.4E-1	1.3E-1
GOTERM_BP_DIRECT	regulation of Golgi inheritance	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
BIOCARTA	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	RT		9	3.1E-2	2.1E0	1.1E-1	7.8E-2
GOTERM_BP_DIRECT	regulation of early endosome to late endosome transport	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
BIOCARTA	Sprouty regulation of tyrosine kinase signals	RT		11	3.8E-2	1.9E0	1.2E-1	8.8E-2
GOTERM_BP_DIRECT	trachea formation	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
BIOCARTA	Roles of ?-arrestin-dependent Recruitment of Src Kinases in GPCR Signaling	RT		11	8.2E-2	1.7E0	2.2E-1	1.6E-1
BIOCARTA	Aspirin Blocks Signaling Pathway Involved in Platelet Activation	RT		11	1.1E-1	1.6E0	2.9E-1	2.0E-1
GOTERM_BP_DIRECT	thyroid gland development	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
BIOCARTA	Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia	RT		12	1.3E-1	1.5E0	3.1E-1	2.2E-1
GOTERM_BP_DIRECT	regulation of stress-activated MAPK cascade	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
BIOCARTA	Regulation of Splicing through Sam68	RT		5	1.6E-1	2.2E0	3.7E-1	2.6E-1
GOTERM_BP_DIRECT	ERK1 and ERK2 cascade	RT		6	3.8E-1	1.5E0	1.0E0	9.6E-1
BIOCARTA	Pelp1 Modulation of Estrogen Receptor Activity	RT		4	4.2E-1	1.7E0	7.3E-1	5.2E-1
BIOCARTA	Role of ?-arrestins in the activation and targeting of MAP kinases	RT		7	4.3E-1	1.3E0	7.3E-1	5.2E-1
Annotation Cluster 164	**Enrichment Score: 1.21**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Xeroderma pigmentosum	RT		5	3.1E-2	3.8E0	1.2E-1	9.2E-2
UP_KEYWORDS	Cockayne syndrome	RT		4	4.4E-2	4.6E0	1.6E-1	1.3E-1
GOTERM_CC_DIRECT	holo TFIIH complex	RT		5	8.0E-2	2.9E0	3.9E-1	3.4E-1
GOTERM_BP_DIRECT	UV protection	RT		5	1.3E-1	2.5E0	8.2E-1	7.9E-1
Annotation Cluster 165	**Enrichment Score: 1.2**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of chemokine production	RT		9	3.8E-3	3.1E0	6.9E-2	6.6E-2
GOTERM_BP_DIRECT	positive regulation of interferon-beta production	RT		10	2.8E-2	2.2E0	3.2E-1	3.0E-1
GOTERM_BP_DIRECT	positive regulation of interleukin-6 production	RT		13	6.6E-2	1.7E0	5.6E-1	5.3E-1
GOTERM_BP_DIRECT	positive regulation of interleukin-12 production	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
GOTERM_BP_DIRECT	positive regulation of tumor necrosis factor production	RT		12	1.6E-1	1.5E0	9.1E-1	8.7E-1
GOTERM_BP_DIRECT	cellular response to lipoteichoic acid	RT		3	4.6E-1	2.0E0	1.0E0	9.6E-1
Annotation Cluster 166	**Enrichment Score: 1.2**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:Rho-like	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:BTB 1	RT		5	6.5E-2	3.1E0	9.2E-1	8.9E-1
UP_SEQ_FEATURE	domain:BTB 2	RT		5	6.5E-2	3.1E0	9.2E-1	8.9E-1
Annotation Cluster 167	**Enrichment Score: 1.2**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
BIOCARTA	Regulation of cell cycle progression by Plk3	RT		7	1.8E-2	2.7E0	7.0E-2	5.0E-2
GOTERM_BP_DIRECT	replicative senescence	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
GOTERM_BP_DIRECT	DNA damage checkpoint	RT		10	5.4E-2	2.0E0	4.9E-1	4.7E-1
BIOCARTA	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility	RT		9	4.4E-1	1.2E0	7.3E-1	5.2E-1
Annotation Cluster 168	**Enrichment Score: 1.18**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:WW 4	RT		5	2.0E-3	6.8E0	5.0E-2	4.8E-2
UP_SEQ_FEATURE	domain:WW 3	RT		6	2.6E-3	5.1E0	6.2E-2	6.0E-2
INTERPRO	WW domain	RT		16	1.8E-2	1.9E0	1.5E-1	1.3E-1
UP_SEQ_FEATURE	domain:WW 1	RT		10	1.9E-2	2.3E0	3.7E-1	3.5E-1
UP_SEQ_FEATURE	domain:WW 2	RT		10	1.9E-2	2.3E0	3.7E-1	3.5E-1
GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transporter activity	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
SMART	WW	RT		16	2.1E-1	1.3E0	8.6E-1	7.8E-1
UP_SEQ_FEATURE	domain:WW	RT		6	2.1E-1	1.9E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	regulation of membrane potential	RT		8	9.8E-1	6.3E-1	1.0E0	9.8E-1
SMART	C2	RT		18	1.0E0	5.8E-1	1.0E0	1.0E0
GOTERM_BP_DIRECT	regulation of ion transmembrane transport	RT		3	1.0E0	1.6E-1	1.0E0	1.0E0
Annotation Cluster 169	**Enrichment Score: 1.17**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	histone H3-K27 methylation	RT		4	1.7E-2	5.9E0	2.1E-1	2.0E-1
GOTERM_MF_DIRECT	histone methyltransferase activity (H3-K27 specific)	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
GOTERM_BP_DIRECT	DNA methylation	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
GOTERM_MF_DIRECT	protein-lysine N-methyltransferase activity	RT		6	1.4E-1	2.1E0	6.1E-1	5.5E-1
Annotation Cluster 170	**Enrichment Score: 1.16**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	UBA/THIF-type NAD/FAD binding fold	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
GOTERM_MF_DIRECT	ubiquitin activating enzyme activity	RT		4	3.6E-2	4.8E0	2.2E-1	1.9E-1
INTERPRO	Ubiquitin-activating enzyme e1, C-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ubiquitin-activating enzyme, E1	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_MF_DIRECT	small protein activating enzyme activity	RT		4	9.7E-2	3.4E0	4.7E-1	4.2E-1
INTERPRO	Ubiquitin-activating enzyme	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	Ubiquitin/SUMO-activating enzyme E1	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
SMART	SM00985	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
Annotation Cluster 171	**Enrichment Score: 1.16**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ribosomal protein L1, 2-layer alpha/beta-sandwich	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ribosomal protein L1, 3-layer alpha/beta-sandwich	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ribosomal protein L1, superfamily	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
Annotation Cluster 172	**Enrichment Score: 1.16**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Pseudouridine synthase, RsuA/RluB/C/D/E/F	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	Pseudouridine synthase, catalytic domain	RT		6	4.5E-2	2.9E0	3.3E-1	3.0E-1
GOTERM_MF_DIRECT	pseudouridine synthase activity	RT		6	5.2E-2	2.8E0	3.0E-1	2.7E-1
GOTERM_BP_DIRECT	tRNA pseudouridine synthesis	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
GOTERM_MF_DIRECT	deaminase activity	RT		4	1.4E-1	3.0E0	5.9E-1	5.3E-1
GOTERM_BP_DIRECT	pseudouridine synthesis	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 173	**Enrichment Score: 1.15**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	RNA polymerase Rpb2, domain 3	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	DNA-directed RNA polymerase, subunit 2	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	DNA-directed RNA polymerase, subunit 2, domain 6	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase, beta subunit, conserved site	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase Rpb2, OB-fold	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	RNA polymerase Rpb2, domain 7	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase Rpb2, domain 2	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase, beta subunit, protrusion	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_MF_DIRECT	ribonucleoside binding	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
Annotation Cluster 174	**Enrichment Score: 1.14**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:C2HC-type	RT		6	2.6E-3	5.1E0	6.2E-2	6.0E-2
INTERPRO	MOZ/SAS-like protein	RT		5	2.9E-3	6.2E0	3.3E-2	3.1E-2
GOTERM_BP_DIRECT	histone acetylation	RT		11	4.9E-2	1.9E0	4.7E-1	4.5E-1
GOTERM_MF_DIRECT	histone acetyltransferase activity	RT		13	9.5E-2	1.6E0	4.7E-1	4.2E-1
GOTERM_MF_DIRECT	acetyltransferase activity	RT		4	3.8E-1	1.8E0	1.0E0	8.9E-1
INTERPRO	Acyl-CoA N-acyltransferase	RT		7	7.7E-1	9.4E-1	1.0E0	9.1E-1
UP_KEYWORDS	Acyltransferase	RT		12	1.0E0	4.8E-1	1.0E0	1.0E0
Annotation Cluster 175	**Enrichment Score: 1.13**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	extrinsic apoptotic signaling pathway in absence of ligand	RT		15	7.0E-4	2.6E0	1.7E-2	1.7E-2
GOTERM_MF_DIRECT	BH3 domain binding	RT		4	1.6E-2	6.0E0	1.2E-1	1.0E-1
INTERPRO	Apoptosis regulator, Bcl-2, BH1 motif, conserved site	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
INTERPRO	Apoptosis regulator, Bcl-2, BH2 motif, conserved site	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
INTERPRO	Apoptosis regulator, Bcl-2, BH3 motif, conserved site	RT		5	2.7E-2	3.9E0	2.2E-1	2.0E-1
GOTERM_BP_DIRECT	regulation of protein heterodimerization activity	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
GOTERM_BP_DIRECT	regulation of mitochondrial membrane potential	RT		10	3.6E-2	2.1E0	3.7E-1	3.6E-1
GOTERM_BP_DIRECT	negative regulation of anoikis	RT		7	5.3E-2	2.4E0	4.9E-1	4.7E-1
UP_SEQ_FEATURE	short sequence motif:BH1	RT		5	6.5E-2	3.1E0	9.2E-1	8.9E-1
GOTERM_CC_DIRECT	Bcl-2 family protein complex	RT		3	6.6E-2	6.4E0	3.3E-1	2.9E-1
GOTERM_BP_DIRECT	regulation of mitochondrial membrane permeability	RT		5	7.3E-2	3.0E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	release of cytochrome c from mitochondria	RT		8	7.9E-2	2.1E0	6.0E-1	5.7E-1
INTERPRO	Blc2 family	RT		5	8.7E-2	2.8E0	4.9E-1	4.5E-1
INTERPRO	Bcl2-like	RT		5	8.7E-2	2.8E0	4.9E-1	4.5E-1
UP_SEQ_FEATURE	short sequence motif:BH2	RT		5	1.1E-1	2.6E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	short sequence motif:BH3	RT		5	2.3E-1	2.0E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	endoplasmic reticulum calcium ion homeostasis	RT		5	2.4E-1	2.0E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	positive regulation of intrinsic apoptotic signaling pathway	RT		8	3.2E-1	1.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	regulation of protein homodimerization activity	RT		3	3.4E-1	2.5E0	1.0E0	9.6E-1
BBID	127.Mito-stress	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
BBID	152.altered_synaptic_signalling-neurodegenerative_disorders	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
GOTERM_CC_DIRECT	pore complex	RT		3	4.3E-1	2.1E0	1.0E0	8.8E-1
Annotation Cluster 176	**Enrichment Score: 1.13**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	eukaryotic translation initiation factor 4F complex	RT		5	4.0E-2	3.5E0	2.3E-1	2.0E-1
BIOCARTA	Eukaryotic protein translation	RT		10	4.4E-2	1.9E0	1.4E-1	9.7E-2
GOTERM_BP_DIRECT	nuclear-transcribed mRNA poly(A) tail shortening	RT		9	1.0E-1	1.8E0	7.1E-1	6.8E-1
BIOCARTA	Internal Ribosome entry pathway	RT		5	1.6E-1	2.2E0	3.7E-1	2.6E-1
Annotation Cluster 177	**Enrichment Score: 1.13**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:IQ 5	RT		6	1.4E-2	3.7E0	2.7E-1	2.6E-1
INTERPRO	Dilute	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
UP_SEQ_FEATURE	domain:Dilute	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
SMART	SM01132	RT		4	2.4E-1	2.3E0	9.5E-1	8.6E-1
Annotation Cluster 178	**Enrichment Score: 1.12**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:Bridging helix	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	RNA polymerase Rpb1, domain 1	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase Rpb1, domain 5	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase Rpb1, domain 4	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase, alpha subunit	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	RNA polymerase Rpb1, domain 3	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
SMART	RPOLA_N	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
Annotation Cluster 179	**Enrichment Score: 1.12**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Proprotein convertase, P	RT		6	1.7E-3	5.3E0	2.1E-2	1.9E-2
INTERPRO	Peptidase S8, subtilisin, Asp-active site	RT		5	7.7E-3	5.2E0	7.7E-2	7.1E-2
INTERPRO	Peptidase S8, subtilisin, Ser-active site	RT		6	7.7E-3	4.1E0	7.7E-2	7.1E-2
INTERPRO	Peptidase S8, subtilisin, His-active site	RT		6	7.7E-3	4.1E0	7.7E-2	7.1E-2
INTERPRO	Peptidase S8, subtilisin-related	RT		6	1.3E-2	3.7E0	1.3E-1	1.1E-1
INTERPRO	Peptidase S8/S53 domain	RT		6	2.1E-2	3.4E0	1.7E-1	1.6E-1
GOTERM_BP_DIRECT	peptide biosynthetic process	RT		4	3.7E-2	4.7E0	3.7E-1	3.6E-1
INTERPRO	Proteinase inhibitor, propeptide	RT		6	1.3E-1	2.2E0	6.4E-1	5.8E-1
GOTERM_BP_DIRECT	peptide hormone processing	RT		5	2.8E-1	1.9E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	protein processing	RT		11	8.0E-1	9.0E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	signal peptide processing	RT		4	8.2E-1	9.5E-1	1.0E0	9.6E-1
UP_KEYWORDS	Serine protease	RT		8	1.0E0	3.9E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	active site:Charge relay system	RT		8	1.0E0	2.7E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	serine-type endopeptidase activity	RT		10	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 180	**Enrichment Score: 1.11**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	MAP kinase kinase activity	RT		7	8.2E-3	3.5E0	6.9E-2	6.2E-2
UP_SEQ_FEATURE	site:Cleavage; by anthrax lethal factor	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	proteolysis in other organism	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 181	**Enrichment Score: 1.1**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:TFIIB-type	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	Transcription factor TFIIB	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Zinc finger, TFIIB-type	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
Annotation Cluster 182	**Enrichment Score: 1.07**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	rRNA methylation	RT		7	2.9E-2	2.8E0	3.2E-1	3.1E-1
INTERPRO	Ribosomal RNA adenine methylase transferase	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Ribosomal RNA adenine methylase transferase, N-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
SMART	rADc	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
GOTERM_MF_DIRECT	rRNA (adenine-N6,N6-)-dimethyltransferase activity	RT		3	2.0E-1	3.6E0	7.8E-1	7.0E-1
Annotation Cluster 183	**Enrichment Score: 1.07**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	RT		15	7.4E-3	2.1E0	7.7E-2	7.1E-2
UP_SEQ_FEATURE	domain:UBA	RT		13	1.0E-2	2.2E0	2.2E-1	2.1E-1
GOTERM_BP_DIRECT	regulation of proteasomal ubiquitin-dependent protein catabolic process	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
INTERPRO	Ubiquilin	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
INTERPRO	Heat shock chaperonin-binding	RT		5	6.3E-2	3.1E0	4.1E-1	3.7E-1
GOTERM_MF_DIRECT	polyubiquitin binding	RT		8	7.7E-2	2.1E0	3.9E-1	3.5E-1
SMART	STI1	RT		5	2.1E-1	2.0E0	8.9E-1	8.1E-1
SMART	UBA	RT		10	2.7E-1	1.4E0	1.0E0	9.1E-1
INTERPRO	UBA-like	RT		11	4.9E-1	1.2E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	autophagosome	RT		7	9.5E-1	6.9E-1	1.0E0	9.5E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 184	Enrichment Score: 1.06			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_CC_DIRECT	actomyosin	RT		7	5.9E-3	3.7E0	4.8E-2	4.2E-2
GOTERM_CC_DIRECT	myosin II filament	RT		3	6.6E-2	6.4E0	3.3E-1	2.9E-1
GOTERM_CC_DIRECT	myosin II complex	RT		4	8.3E-2	3.6E0	4.0E-1	3.5E-1
GOTERM_BP_DIRECT	actomyosin structure organization	RT		7	3.0E-1	1.5E0	1.0E0	9.6E-1
UP_KEYWORDS	Cell shape	RT		5	5.0E-1	1.4E0	1.0E0	7.8E-1
Annotation Cluster 185	**Enrichment Score: 1.06**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	histone H2A monoubiquitination	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
GOTERM_BP_DIRECT	UV-damage excision repair	RT		5	9.9E-2	2.7E0	6.9E-1	6.6E-1
GOTERM_CC_DIRECT	Cul4B-RING E3 ubiquitin ligase complex	RT		3	1.8E-1	3.8E0	6.7E-1	5.9E-1
Annotation Cluster 186	**Enrichment Score: 1.05**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	activation of JNKK activity	RT		4	6.4E-2	3.9E0	5.5E-1	5.2E-1
INTERPRO	Mitogen-activated protein (MAP) kinase kinase kinase, 9/10/11	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_MF_DIRECT	JUN kinase kinase kinase activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
PIR_SUPERFAMILY	mitogen-activated protein kinase kinase kinase, types 9/10/11	RT		3	8.8E-2	5.4E0	6.9E-1	6.8E-1
UP_SEQ_FEATURE	domain:Leucine-zipper 1	RT		4	1.3E-1	3.0E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Leucine-zipper 2	RT		4	1.3E-1	3.0E0	1.0E0	9.6E-1
Annotation Cluster 187	**Enrichment Score: 1.03**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	regulation of interferon-gamma-mediated signaling pathway	RT		9	3.8E-4	4.1E0	1.0E-2	9.6E-3
GOTERM_BP_DIRECT	JAK-STAT cascade involved in growth hormone signaling pathway	RT		9	1.4E-3	3.6E0	3.0E-2	2.9E-2
BIOCARTA	Stat3 Signaling Pathway	RT		8	2.3E-3	3.0E0	1.7E-2	1.2E-2
UP_SEQ_FEATURE	domain:SH2; atypical	RT		5	5.4E-3	5.7E0	1.2E-1	1.2E-1
INTERPRO	Tyrosine-protein kinase, non-receptor Jak/Tyk2	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
PIR_SUPERFAMILY	tyrosine-protein kinase, Jak/Tyk2 type	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT		9	3.1E-2	2.1E0	1.1E-1	7.8E-2
INTERPRO	MyTH4 domain	RT		5	4.3E-2	3.4E0	3.2E-1	2.9E-1
UP_SEQ_FEATURE	domain:MyTH4 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:MyTH4 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
BBID	48.mice_minus_JAKs_and_STATs	RT		8	6.1E-2	2.0E0	1.0E0	1.0E0
BBID	75.Stats_activators_of_Apoptosis	RT		4	1.4E-1	2.7E0	1.0E0	1.0E0
SMART	MyTH4	RT		5	1.6E-1	2.3E0	7.0E-1	6.4E-1
GOTERM_MF_DIRECT	growth hormone receptor binding	RT		3	2.0E-1	3.6E0	7.8E-1	7.0E-1
BIOCARTA	IL-10 Anti-inflammatory Signaling Pathway	RT		7	2.3E-1	1.6E0	4.7E-1	3.4E-1
BIOCARTA	IFN gamma signaling pathway	RT		4	3.1E-1	2.0E0	5.9E-1	4.2E-1
GOTERM_MF_DIRECT	CCR5 chemokine receptor binding	RT		3	4.0E-1	2.2E0	1.0E0	8.9E-1
INTERPRO	FERM domain	RT		10	4.4E-1	1.2E0	1.0E0	9.1E-1
INTERPRO	Band 4.1 domain	RT		10	4.4E-1	1.2E0	1.0E0	9.1E-1
BBID	12.IL-6_type_cytok-signal-transduct	RT		8	5.1E-1	1.2E0	1.0E0	1.0E0
INTERPRO	FERM central domain	RT		9	5.9E-1	1.1E0	1.0E0	9.1E-1
BBID	11.IL-6_gp130-Jak-STAT	RT		3	6.0E-1	1.6E0	1.0E0	1.0E0
UP_SEQ_FEATURE	domain:FERM	RT		7	7.4E-1	9.7E-1	1.0E0	9.6E-1
BIOCARTA	IFN alpha signaling pathway	RT		3	8.5E-1	1.0E0	1.0E0	8.5E-1
SMART	B41	RT		10	9.1E-1	8.0E-1	1.0E0	9.1E-1
INTERPRO	FERM/acyl-CoA-binding protein, 3-helical bundle	RT		5	9.7E-1	6.2E-1	1.0E0	9.7E-1
Annotation Cluster 188	**Enrichment Score: 1.03**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Non-homologous end-joining	RT		7	2.5E-2	2.8E0	4.6E-2	2.5E-2
GOTERM_CC_DIRECT	nonhomologous end joining complex	RT		4	1.2E-1	3.2E0	4.9E-1	4.3E-1
GOTERM_BP_DIRECT	establishment of integrated proviral latency	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	regulation of smooth muscle cell proliferation	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
Annotation Cluster 189	**Enrichment Score: 1.03**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Elongation factor	RT		10	2.3E-2	2.3E0	9.3E-2	7.2E-2
GOTERM_BP_DIRECT	translational elongation	RT		6	1.7E-1	2.0E0	9.8E-1	9.4E-1
GOTERM_MF_DIRECT	translation elongation factor activity	RT		9	2.0E-1	1.6E0	7.9E-1	7.0E-1
Annotation Cluster 190	**Enrichment Score: 1.01**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Innate immunity	RT		53	1.1E-2	1.4E0	4.6E-2	3.6E-2
GOTERM_BP_DIRECT	innate immune response	RT		82	1.5E-1	1.1E0	8.8E-1	8.4E-1
UP_KEYWORDS	Immunity	RT		73	5.6E-1	1.0E0	1.0E0	7.8E-1
Annotation Cluster 191	**Enrichment Score: 1.01**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	E2F1 Destruction Pathway	RT		7	7.1E-2	2.1E0	2.0E-1	1.4E-1
BIOCARTA	Regulation of p27 Phosphorylation during Cell Cycle Progression	RT		8	9.5E-2	1.9E0	2.5E-1	1.8E-1
BIOCARTA	Cyclin E Destruction Pathway	RT		6	1.4E-1	2.0E0	3.3E-1	2.4E-1
Annotation Cluster 192	**Enrichment Score: 1**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:C2	RT		21	1.4E-2	1.7E0	2.6E-1	2.5E-1
INTERPRO	C2 calcium-dependent membrane targeting	RT		35	7.5E-2	1.3E0	4.3E-1	4.0E-1
SMART	C2	RT		18	1.0E0	5.8E-1	1.0E0	1.0E0
Annotation Cluster 193	**Enrichment Score: 0.98**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	IL22 Soluble Receptor Signaling Pathway	RT		9	3.1E-2	2.1E0	1.1E-1	7.8E-2
BBID	48.mice_minus_JAKs_and_STATs	RT		8	6.1E-2	2.0E0	1.0E0	1.0E0
GOTERM_BP_DIRECT	JAK-STAT cascade	RT		10	7.8E-2	1.9E0	5.9E-1	5.6E-1
INTERPRO	STAT transcription factor, coiled coil	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
INTERPRO	STAT transcription factor, protein interaction	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
INTERPRO	STAT transcription factor, DNA-binding, subdomain	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
INTERPRO	STAT transcription factor, all-alpha	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
INTERPRO	STAT transcription factor, DNA-binding	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
INTERPRO	STAT transcription factor, core	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
BIOCARTA	IL-10 Anti-inflammatory Signaling Pathway	RT		7	2.3E-1	1.6E0	4.7E-1	3.4E-1
SMART	SM00964	RT		4	2.4E-1	2.3E0	9.5E-1	8.6E-1
INTERPRO	p53-like transcription factor, DNA-binding	RT		9	4.2E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 194	**Enrichment Score: 0.98**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of protein metabolic process	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
GOTERM_BP_DIRECT	cellular response to laminar fluid shear stress	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	negative regulation of heterotypic cell-cell adhesion	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	negative regulation of response to cytokine stimulus	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
Annotation Cluster 195	**Enrichment Score: 0.97**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	Swr1 complex	RT		5	4.0E-2	3.5E0	2.3E-1	2.0E-1
GOTERM_CC_DIRECT	NuA4 histone acetyltransferase complex	RT		7	5.1E-2	2.5E0	2.8E-1	2.5E-1
GOTERM_BP_DIRECT	histone H2A acetylation	RT		5	2.4E-1	2.0E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	histone H4 acetylation	RT		8	2.6E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 196	**Enrichment Score: 0.97**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:REM 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:REM 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	repeat:REM 3	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	HR1 rho-binding repeat	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
SMART	Hr1	RT		4	2.4E-1	2.3E0	9.5E-1	8.6E-1
GOTERM_BP_DIRECT	epithelial cell migration	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 197	Enrichment Score: 0.95			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Zinc finger, PHD-finger	RT		21	2.4E-2	1.6E0	1.9E-1	1.7E-1
INTERPRO	Zinc finger, PHD-type	RT		23	2.4E-2	1.6E0	1.9E-1	1.7E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type 2	RT		9	6.3E-2	2.0E0	9.0E-1	8.7E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type 1	RT		9	1.0E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	zinc finger region:PHD-type	RT		12	1.3E-1	1.6E0	1.0E0	9.6E-1
INTERPRO	Zinc finger, FYVE/PHD-type	RT		27	2.6E-1	1.2E0	1.0E0	9.1E-1
INTERPRO	Zinc finger, PHD-type, conserved site	RT		13	3.9E-1	1.2E0	1.0E0	9.1E-1
SMART	PHD	RT		23	5.3E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 198	**Enrichment Score: 0.95**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Histone H2B	RT		12	6.0E-4	3.1E0	8.2E-3	7.5E-3
SMART	H2B	RT		12	1.9E-2	2.0E0	1.6E-1	1.4E-1
GOTERM_BP_DIRECT	innate immune response in mucosa	RT		7	2.4E-1	1.7E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	antibacterial humoral response	RT		7	7.8E-1	9.4E-1	1.0E0	9.6E-1
UP_KEYWORDS	Antibiotic	RT		4	1.0E0	2.9E-1	1.0E0	1.0E0
UP_KEYWORDS	Antimicrobial	RT		4	1.0E0	2.5E-1	1.0E0	1.0E0
Annotation Cluster 199	**Enrichment Score: 0.95**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:Domain A	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	region of interest:Domain B	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	Domain of unknown function DUF3452, retinoblastoma-associated	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Retinoblastoma-associated protein, B-box	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Retinoblastoma-associated protein, A-box	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Rb C-terminal	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
SMART	SM01367	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
SMART	SM01368	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
SMART	SM01369	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
GOTERM_BP_DIRECT	regulation of lipid kinase activity	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	region of interest:Spacer	RT		4	7.1E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 200	**Enrichment Score: 0.94**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	nucleosomal DNA binding	RT		15	1.6E-2	1.9E0	1.2E-1	1.0E-1
INTERPRO	Histone H3	RT		6	1.8E-1	2.0E0	8.8E-1	8.0E-1
SMART	H3	RT		6	5.2E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 201	**Enrichment Score: 0.92**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	regulation of actin polymerization or depolymerization	RT		4	9.9E-2	3.4E0	6.9E-1	6.6E-1
INTERPRO	DEK, C-terminal	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
GOTERM_BP_DIRECT	regulation of lamellipodium assembly	RT		4	1.4E-1	3.0E0	8.2E-1	7.9E-1
Annotation Cluster 202	**Enrichment Score: 0.91**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	RT		9	2.8E-2	2.3E0	1.8E-1	1.6E-1
GOTERM_BP_DIRECT	regulation of nucleotide-binding oligomerization domain containing signaling pathway	RT		3	7.6E-2	5.9E0	5.8E-1	5.5E-1
UP_SEQ_FEATURE	repeat:BIR 1	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:BIR 2	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:BIR 3	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
INTERPRO	Baculoviral inhibition of apoptosis protein repeat	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
GOTERM_BP_DIRECT	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
SMART	BIR	RT		4	3.1E-1	2.0E0	1.0E0	9.1E-1
GOTERM_BP_DIRECT	regulation of innate immune response	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 203	**Enrichment Score: 0.9**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	Rap protein signal transduction	RT		6	1.6E-2	3.6E0	2.1E-1	2.0E-1
GOTERM_BP_DIRECT	microvillus assembly	RT		6	1.5E-1	2.1E0	8.5E-1	8.1E-1
GOTERM_CC_DIRECT	recycling endosome membrane	RT		6	8.4E-1	8.7E-1	1.0E0	8.8E-1
Annotation Cluster 204	**Enrichment Score: 0.9**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Brix domain	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
UP_SEQ_FEATURE	domain:Brix	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
SMART	SM00879	RT		4	1.6E-1	2.7E0	7.0E-1	6.4E-1
INTERPRO	Anticodon-binding	RT		4	4.0E-1	1.8E0	1.0E0	9.1E-1
Annotation Cluster 205	**Enrichment Score: 0.89**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:PDZ	RT		26	2.1E-2	1.6E0	4.0E-1	3.9E-1
INTERPRO	PDZ domain	RT		32	1.2E-1	1.3E0	6.3E-1	5.8E-1
SMART	PDZ	RT		32	8.8E-1	8.7E-1	1.0E0	9.1E-1
Annotation Cluster 206	**Enrichment Score: 0.88**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	endoplasmic reticulum chaperone complex	RT		5	8.0E-2	2.9E0	3.9E-1	3.4E-1
GOTERM_BP_DIRECT	protein folding in endoplasmic reticulum	RT		5	1.6E-1	2.3E0	9.3E-1	8.9E-1
UP_SEQ_FEATURE	short sequence motif:Prevents secretion from ER	RT		13	1.8E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 207	**Enrichment Score: 0.88**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:Autoinhibitory domain	RT		4	4.5E-2	4.5E0	7.4E-1	7.2E-1
GOTERM_MF_DIRECT	calmodulin-dependent protein kinase activity	RT		8	6.2E-2	2.2E0	3.5E-1	3.1E-1
BIOCARTA	Ca++/ Calmodulin-dependent Protein Kinase Activation	RT		4	8.5E-1	9.4E-1	1.0E0	8.5E-1
Annotation Cluster 208	**Enrichment Score: 0.86**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	ubiquitin conjugating enzyme binding	RT		10	6.3E-2	1.9E0	3.5E-1	3.1E-1
INTERPRO	Zinc finger, C6HC-type	RT		6	8.0E-2	2.5E0	4.6E-1	4.2E-1
UP_SEQ_FEATURE	zinc finger region:RING-type 1; atypical	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	zinc finger region:IBR-type	RT		5	1.1E-1	2.6E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	zinc finger region:RING-type 2	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
SMART	IBR	RT		5	4.6E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 209	**Enrichment Score: 0.86**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:KEN	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	KEN domain	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	PUB domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
SMART	PUG	RT		3	3.6E-1	2.4E0	1.0E0	9.1E-1
Annotation Cluster 210	**Enrichment Score: 0.85**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	spectrin-associated cytoskeleton	RT		5	2.5E-2	4.0E0	1.5E-1	1.3E-1
UP_KEYWORDS	Elliptocytosis	RT		3	3.3E-1	2.6E0	9.1E-1	7.1E-1
UP_KEYWORDS	Hereditary hemolytic anemia	RT		7	3.5E-1	1.5E0	9.5E-1	7.3E-1
Annotation Cluster 211	**Enrichment Score: 0.84**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Glycolysis	RT		11	1.0E-2	2.4E0	4.4E-2	3.4E-2
INTERPRO	Enolase, C-terminal	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
GOTERM_CC_DIRECT	phosphopyruvate hydratase complex	RT		4	5.4E-2	4.2E0	2.9E-1	2.5E-1
INTERPRO	Enolase	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
INTERPRO	Enolase, N-terminal	RT		4	5.7E-2	4.1E0	4.0E-1	3.7E-1
GOTERM_BP_DIRECT	canonical glycolysis	RT		9	5.9E-2	2.0E0	5.2E-1	5.0E-1
GOTERM_MF_DIRECT	phosphopyruvate hydratase activity	RT		4	6.3E-2	4.0E0	3.5E-1	3.1E-1
INTERPRO	Enolase, conserved site	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
SMART	SM01192	RT		4	9.9E-2	3.3E0	5.3E-1	4.8E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	glycolytic process	RT		10	1.1E-1	1.7E0	7.3E-1	7.0E-1
PIR_SUPERFAMILY	enolase	RT		3	1.6E-1	4.1E0	1.0E0	1.0E0
SMART	SM01193	RT		4	1.6E-1	2.7E0	7.0E-1	6.4E-1
BIOCARTA	Glycolysis Pathway	RT		5	4.3E-1	1.5E0	7.3E-1	5.2E-1
GOTERM_BP_DIRECT	gluconeogenesis	RT		8	6.3E-1	1.1E0	1.0E0	9.6E-1
KEGG_PATHWAY	Biosynthesis of amino acids	RT		12	8.4E-1	8.6E-1	1.0E0	8.4E-1
KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		11	8.6E-1	8.5E-1	1.0E0	8.6E-1
KEGG_PATHWAY	Carbon metabolism	RT		15	9.8E-1	6.9E-1	1.0E0	9.8E-1
UP_SEQ_FEATURE	binding site:Substrate	RT		20	1.0E0	4.5E-1	1.0E0	1.0E0
Annotation Cluster 212	**Enrichment Score: 0.83**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:CXXC-type	RT		5	4.7E-2	3.4E0	7.7E-1	7.4E-1
INTERPRO	Zinc finger, CXXC-type	RT		5	1.1E-1	2.6E0	6.3E-1	5.7E-1
INTERPRO	Leucine-rich repeat, cysteine-containing subtype	RT		6	1.8E-1	2.0E0	8.8E-1	8.0E-1
SMART	LRR_CC	RT		6	5.2E-1	1.3E0	1.0E0	9.1E-1
Annotation Cluster 213	**Enrichment Score: 0.83**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:HSA	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
INTERPRO	Helicase/SANT-associated, DNA binding	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
SMART	HSA	RT		3	2.5E-1	3.0E0	9.9E-1	9.0E-1
Annotation Cluster 214	**Enrichment Score: 0.82**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	JAB1/Mov34/MPN/PAD-1	RT		7	6.7E-3	3.6E0	7.2E-2	6.6E-2
UP_SEQ_FEATURE	domain:MPN	RT		6	2.2E-2	3.4E0	4.0E-1	3.9E-1
SMART	JAB_MPN	RT		7	3.2E-2	2.6E0	2.5E-1	2.3E-1
UP_SEQ_FEATURE	short sequence motif:JAMM motif	RT		4	7.0E-2	3.9E0	9.7E-1	9.3E-1
INTERPRO	Rpn11/EIF3F C-terminal domain	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
GOTERM_MF_DIRECT	metallopeptidase activity	RT		6	1.0E0	4.4E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	thiol-dependent ubiquitin-specific protease activity	RT		5	1.0E0	3.7E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	RT		4	1.0E0	2.1E-1	1.0E0	1.0E0
UP_KEYWORDS	Metalloprotease	RT		5	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 215	**Enrichment Score: 0.82**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of cyclin-dependent protein serine/threonine kinase activity	RT		9	3.8E-2	2.2E0	3.8E-1	3.6E-1
GOTERM_MF_DIRECT	cyclin-dependent protein serine/threonine kinase regulator activity	RT		5	2.4E-1	2.0E0	9.0E-1	8.1E-1
GOTERM_BP_DIRECT	positive regulation of phosphorylation of RNA polymerase II C-terminal domain	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 216	**Enrichment Score: 0.81**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Adenylate kinase, active site lid domain	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	Adenylate kinase	RT		4	1.7E-1	2.8E0	8.2E-1	7.5E-1
GOTERM_MF_DIRECT	adenylate kinase activity	RT		4	1.8E-1	2.6E0	7.5E-1	6.7E-1
Annotation Cluster 217	**Enrichment Score: 0.8**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of cell adhesion mediated by integrin	RT		7	1.3E-2	3.2E0	1.8E-1	1.7E-1
UP_SEQ_FEATURE	domain:SH2 1	RT		3	5.4E-1	1.7E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:SH2 2	RT		3	5.4E-1	1.7E0	1.0E0	9.6E-1
Annotation Cluster 218	**Enrichment Score: 0.8**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A2	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A3	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	chain:Putative uncharacterized protein C21orf81	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	chain:Ankyrin repeat domain-containing protein 20A1	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
Annotation Cluster 219	**Enrichment Score: 0.8**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	active site:Phosphoserine intermediate	RT		6	9.0E-3	4.1E0	2.0E-1	1.9E-1
INTERPRO	Alkaline phosphatase, active site	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Alkaline phosphatase	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
SMART	alkPPc	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
GOTERM_MF_DIRECT	alkaline phosphatase activity	RT		4	6.3E-2	4.0E0	3.5E-1	3.1E-1
UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated aspartate	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
KEGG_PATHWAY	Folate biosynthesis	RT		5	2.8E-1	1.9E0	4.3E-1	2.8E-1
INTERPRO	Alkaline phosphatase-like, alpha/beta/alpha	RT		4	9.0E-1	8.0E-1	1.0E0	9.1E-1
INTERPRO	Alkaline-phosphatase-like, core domain	RT		4	9.1E-1	7.7E-1	1.0E0	9.1E-1
UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	RT		4	9.9E-1	5.0E-1	1.0E0	9.9E-1
UP_KEYWORDS	GPI-anchor	RT		8	1.0E0	4.0E-1	1.0E0	1.0E0
GOTERM_CC_DIRECT	anchored component of membrane	RT		6	1.0E0	3.4E-1	1.0E0	1.0E0
Annotation Cluster 220	**Enrichment Score: 0.79**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	regulation of establishment of endothelial barrier	RT		5	1.8E-2	4.2E0	2.2E-1	2.1E-1
GOTERM_BP_DIRECT	negative regulation of bicellular tight junction assembly	RT		3	1.3E-1	4.4E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	negative regulation of myosin-light-chain-phosphatase activity	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cortical actin cytoskeleton organization	RT		6	3.8E-1	1.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	establishment of protein localization to plasma membrane	RT		8	5.8E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 221	**Enrichment Score: 0.79**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	isotype switching	RT		7	2.9E-2	2.8E0	3.2E-1	3.1E-1
OMIM_DISEASE	Mismatch repair cancer syndrome	RT		3	8.2E-2	5.9E0	1.0E0	1.0E0
GOTERM_MF_DIRECT	guanine/thymine mispair binding	RT		3	1.3E-1	4.5E0	5.9E-1	5.3E-1
GOTERM_BP_DIRECT	somatic hypermutation of immunoglobulin genes	RT		5	2.8E-1	1.9E0	1.0E0	9.6E-1
UP_KEYWORDS	Hereditary nonpolyposis colorectal cancer	RT		3	3.9E-1	2.3E0	1.0E0	7.8E-1
GOTERM_MF_DIRECT	mismatched DNA binding	RT		3	5.7E-1	1.6E0	1.0E0	8.9E-1
Annotation Cluster 222	**Enrichment Score: 0.78**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:WD 8	RT		15	4.9E-2	1.7E0	8.1E-1	7.8E-1
INTERPRO	Quinonprotein alcohol dehydrogenase-like superfamily	RT		13	7.5E-2	1.7E0	4.4E-1	4.0E-1
UP_SEQ_FEATURE	repeat:WD 9	RT		11	1.0E-1	1.7E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:WD 11	RT		8	1.4E-1	1.8E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:WD 10	RT		8	1.6E-1	1.8E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:WD 13	RT		5	2.7E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:WD 12	RT		5	4.1E-1	1.5E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:WD 14	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 223	**Enrichment Score: 0.78**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	sulfate assimilation	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
GOTERM_MF_DIRECT	oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	RT		4	1.4E-1	3.0E0	5.9E-1	5.3E-1
INTERPRO	Thioredoxin	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
GOTERM_BP_DIRECT	glycerol ether metabolic process	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	protein disulfide oxidoreductase activity	RT		4	7.9E-1	9.9E-1	1.0E0	8.9E-1
Annotation Cluster 224	**Enrichment Score: 0.76**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT		7	1.5E-1	1.9E0	8.9E-1	8.5E-1
GOTERM_CC_DIRECT	beta-catenin destruction complex	RT		5	1.7E-1	2.3E0	6.5E-1	5.7E-1
GOTERM_BP_DIRECT	beta-catenin destruction complex assembly	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
Annotation Cluster 225	**Enrichment Score: 0.76**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
PIR_SUPERFAMILY	heat shock protein, HSP90/HTPG types	RT		4	2.1E-2	5.4E0	2.9E-1	2.9E-1
INTERPRO	Heat shock protein Hsp90, conserved site	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	Heat shock protein Hsp90, N-terminal	RT		4	1.7E-1	2.8E0	8.2E-1	7.5E-1
INTERPRO	Heat shock protein Hsp90	RT		4	2.6E-1	2.3E0	1.0E0	9.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Histidine kinase-like ATPase, ATP-binding domain	RT		7	4.5E-1	1.3E0	1.0E0	9.1E-1
SMART	HATPase_c	RT		4	5.3E-1	1.5E0	1.0E0	9.1E-1
Annotation Cluster 226	**Enrichment Score: 0.76**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:RCC1 7	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
INTERPRO	Regulator of chromosome condensation, RCC1	RT		7	1.1E-1	2.1E0	6.0E-1	5.5E-1
UP_SEQ_FEATURE	repeat:RCC1 5	RT		6	1.1E-1	2.3E0	1.0E0	9.6E-1
INTERPRO	Regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II	RT		7	1.3E-1	2.0E0	6.6E-1	6.0E-1
UP_SEQ_FEATURE	repeat:RCC1 4	RT		6	1.3E-1	2.2E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:RCC1 1	RT		6	1.6E-1	2.0E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:RCC1 2	RT		6	1.6E-1	2.0E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:RCC1 3	RT		6	1.6E-1	2.0E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:RCC1 6	RT		4	3.0E-1	2.1E0	1.0E0	9.6E-1
COG_ONTOLOGY	Cell division and chromosome partitioning / Cytoskeleton	RT		5	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 227	**Enrichment Score: 0.74**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
INTERPRO	ATP-grasp fold, subdomain 2	RT		7	9.0E-2	2.2E0	5.0E-1	4.5E-1
INTERPRO	ATP-grasp fold	RT		5	1.4E-1	2.4E0	7.3E-1	6.7E-1
INTERPRO	Pre-ATP-grasp domain	RT		5	1.8E-1	2.2E0	8.7E-1	8.0E-1
INTERPRO	ATP-grasp fold, subdomain 1	RT		5	2.1E-1	2.1E0	1.0E0	9.1E-1
INTERPRO	Rudiment single hybrid motif	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:ATP-grasp	RT		3	5.9E-1	1.6E0	1.0E0	9.6E-1
Annotation Cluster 228	**Enrichment Score: 0.74**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Hedgehog signaling pathway	RT		12	8.1E-3	2.3E0	1.6E-2	8.1E-3
BIOCARTA	Repression of Pain Sensation by the Transcriptional Regulator DREAM	RT		10	1.5E-2	2.2E0	6.3E-2	4.5E-2
BIOCARTA	Sonic Hedgehog (Shh) Pathway	RT		10	4.4E-2	1.9E0	1.4E-1	9.7E-2
GOTERM_CC_DIRECT	ciliary base	RT		8	1.2E-1	1.9E0	4.9E-1	4.3E-1
BIOCARTA	Regulation of ck1/cdk5 by type 1 glutamate receptors	RT		9	1.6E-1	1.6E0	3.6E-1	2.6E-1
UP_KEYWORDS	cAMP	RT		8	2.6E-1	1.5E0	7.6E-1	5.9E-1
GOTERM_CC_DIRECT	cAMP-dependent protein kinase complex	RT		3	3.0E-1	2.7E0	8.8E-1	7.7E-1
BIOCARTA	Transcription Regulation by Methyltransferase of CARM1	RT		6	3.5E-1	1.5E0	6.5E-1	4.6E-1
BIOCARTA	Cystic fibrosis transmembrane conductance regulator (CFTR) and beta 2 adrenergic receptor (b2AR) pathway	RT		6	3.5E-1	1.5E0	6.5E-1	4.6E-1
BIOCARTA	Phospholipase C-epsilon pathway	RT		6	3.5E-1	1.5E0	6.5E-1	4.6E-1
BIOCARTA	Attenuation of GPCR Signaling	RT		6	4.3E-1	1.4E0	7.3E-1	5.2E-1
BIOCARTA	GATA3 participate in activating the Th2 cytokine genes expression	RT		7	4.3E-1	1.3E0	7.3E-1	5.2E-1
BIOCARTA	mCalpain and friends in Cell motility	RT		9	4.4E-1	1.2E0	7.3E-1	5.2E-1
BIOCARTA	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor	RT		9	4.4E-1	1.2E0	7.3E-1	5.2E-1
BIOCARTA	Stathmin and breast cancer resistance to antimicrotubule agents	RT		9	6.1E-1	1.1E0	9.4E-1	6.7E-1
Annotation Cluster 229	**Enrichment Score: 0.72**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Presenilin action in Notch and Wnt signaling	RT		8	1.4E-1	1.7E0	3.3E-1	2.4E-1
GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT		7	1.5E-1	1.9E0	8.9E-1	8.5E-1
GOTERM_CC_DIRECT	Wnt signalosome	RT		4	2.4E-1	2.3E0	8.3E-1	7.3E-1
BIOCARTA	Multi-step Regulation of Transcription by Pitx2	RT		8	2.5E-1	1.5E0	5.0E-1	3.6E-1
Annotation Cluster 230	**Enrichment Score: 0.72**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	TATA-box binding protein	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Beta2-adaptin/TBP, C-terminal domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	DNA-templated transcription, initiation	RT		8	4.1E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 231	**Enrichment Score: 0.71**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 1	RT		8	3.3E-2	2.5E0	5.7E-1	5.5E-1
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type 2	RT		8	3.3E-2	2.5E0	5.7E-1	5.5E-1
GOTERM_MF_DIRECT	calcium-transporting ATPase activity	RT		5	4.9E-2	3.3E0	2.8E-1	2.5E-1
INTERPRO	Protein kinase C, alpha/beta/gamma types	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
PIR_SUPERFAMILY	protein kinase C, alpha/beta/gamma types	RT		3	8.8E-2	5.4E0	6.9E-1	6.8E-1
GOTERM_BP_DIRECT	negative regulation of glial cell apoptotic process	RT		4	9.9E-2	3.4E0	6.9E-1	6.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT		10	1.1E-1	1.7E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	calcium-dependent protein kinase C activity	RT		3	1.3E-1	4.5E0	5.9E-1	5.3E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	RT		11	3.2E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	RT		9	3.8E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	RT		4	6.1E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1; via carbonyl oxygen	RT		4	8.7E-1	8.5E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	RT		4	8.7E-1	8.5E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cellular calcium ion homeostasis	RT		11	9.6E-1	7.0E-1	1.0E0	9.6E-1
UP_KEYWORDS	Calcium transport	RT		5	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 232	**Enrichment Score: 0.7**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_CC_DIRECT	rDNA heterochromatin	RT		3	1.2E-1	4.8E0	4.9E-1	4.3E-1
GOTERM_CC_DIRECT	chromatin silencing complex	RT		4	1.6E-1	2.8E0	6.2E-1	5.4E-1
GOTERM_BP_DIRECT	chromatin silencing at rDNA	RT		8	4.4E-1	1.3E0	1.0E0	9.6E-1
Annotation Cluster 233	**Enrichment Score: 0.69**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:Btk-type	RT		4	1.3E-1	3.0E0	1.0E0	9.6E-1
INTERPRO	Zinc finger, Btk motif	RT		4	1.7E-1	2.8E0	8.2E-1	7.5E-1
SMART	BTK	RT		4	3.9E-1	1.8E0	1.0E0	9.1E-1
Annotation Cluster 234	**Enrichment Score: 0.69**	G		Count	P_Value	Fold Change	Benjamini	FDR
BIOCARTA	AKAP95 role in mitosis and chromosome dynamics	RT		8	6.1E-2	2.0E0	1.8E-1	1.3E-1
BIOCARTA	Protein Kinase A at the Centrosome	RT		8	1.9E-1	1.6E0	4.1E-1	2.9E-1
BIOCARTA	Rho-Selective Guanine Exchange Factor AKAP13 Mediates Stress Fiber Formation	RT		4	7.6E-1	1.1E0	1.0E0	7.6E-1
Annotation Cluster 235	**Enrichment Score: 0.69**	G		Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	positive regulation of chemokine biosynthetic process	RT		7	2.6E-3	4.1E0	5.0E-2	4.8E-2
GOTERM_BP_DIRECT	positive regulation of calcidiol 1-monooxygenase activity	RT		3	7.6E-2	5.9E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	positive regulation of membrane protein ectodomain proteolysis	RT		4	4.8E-1	1.6E0	1.0E0	9.6E-1
KEGG_PATHWAY	Graft-versus-host disease	RT		5	9.0E-1	7.9E-1	1.0E0	9.0E-1
KEGG_PATHWAY	Type I diabetes mellitus	RT		6	9.3E-1	7.4E-1	1.0E0	9.3E-1
GOTERM_BP_DIRECT	regulation of insulin secretion	RT		8	9.5E-1	7.1E-1	1.0E0	9.6E-1
Annotation Cluster 236	**Enrichment Score: 0.67**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	repeat:1-2	RT		10	4.4E-2	2.1E0	7.3E-1	7.1E-1
UP_SEQ_FEATURE	repeat:1-1	RT		10	5.2E-2	2.0E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	region of interest:2 X 16 AA Gly-rich approximate repeats	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	region of interest:2 X 19 AA perfect repeats	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:2-1	RT		7	3.3E-1	1.5E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:2-2	RT		7	3.8E-1	1.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:1-4	RT		4	5.4E-1	1.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:1-3	RT		4	5.8E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 237	**Enrichment Score: 0.67**	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Aspartic peptidase, DDI1-type	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_MF_DIRECT	aspartic-type endopeptidase activity	RT		10	8.9E-2	1.8E0	4.5E-1	4.0E-1
INTERPRO	Aspartic peptidase	RT		8	1.3E-1	1.8E0	6.7E-1	6.1E-1
INTERPRO	Peptidase A1	RT		4	2.1E-1	2.5E0	9.9E-1	9.1E-1
INTERPRO	Propeptide, peptidase A1	RT		3	3.2E-1	2.7E0	1.0E0	9.1E-1
UP_KEYWORDS	Aspartyl protease	RT		4	6.1E-1	1.3E0	1.0E0	7.8E-1
INTERPRO	Peptidase aspartic, active site	RT		4	6.8E-1	1.2E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	propeptide:Activation peptide	RT		4	1.0E0	3.6E-1	1.0E0	1.0E0
Annotation Cluster 238	**Enrichment Score: 0.66**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Purine biosynthesis	RT		5	1.1E-1	2.6E0	3.6E-1	2.8E-1
GOTERM_BP_DIRECT	purine nucleobase biosynthetic process	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	'de novo' IMP biosynthetic process	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	purine ribonucleoside monophosphate biosynthetic process	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 239	**Enrichment Score: 0.66**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:PDZ	RT		26	2.1E-2	1.6E0	4.0E-1	3.9E-1
UP_SEQ_FEATURE	short sequence motif:LD motif 1	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	short sequence motif:LD motif 2	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	short sequence motif:LD motif 3	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:LIM zinc-binding 3	RT		6	3.0E-1	1.6E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:LIM zinc-binding	RT		5	3.0E-1	1.8E0	1.0E0	9.6E-1
UP_KEYWORDS	LIM domain	RT		13	3.5E-1	1.2E0	9.6E-1	7.4E-1
UP_SEQ_FEATURE	domain:LIM zinc-binding 4	RT		3	5.0E-1	1.9E0	1.0E0	9.6E-1
INTERPRO	Zinc finger, LIM-type	RT		13	5.0E-1	1.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:LIM zinc-binding 1	RT		8	6.1E-1	1.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:LIM zinc-binding 2	RT		8	6.1E-1	1.1E0	1.0E0	9.6E-1
SMART	LIM	RT		13	9.6E-1	7.3E-1	1.0E0	9.6E-1
Annotation Cluster 240	**Enrichment Score: 0.65**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:PUA	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
INTERPRO	Pseudouridine synthase/archaeosine transglycosylase	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
INTERPRO	PUA-like domain	RT		5	3.7E-1	1.6E0	1.0E0	9.1E-1
Annotation Cluster 241	**Enrichment Score: 0.65**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	calcineurin complex	RT		3	1.2E-1	4.8E0	4.9E-1	4.3E-1
GOTERM_BP_DIRECT	positive regulation of NFAT protein import into nucleus	RT		4	2.3E-1	2.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	calcineurin-NFAT signaling cascade	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
Annotation Cluster 242	**Enrichment Score: 0.65**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Small Leucine-rich Proteoglycan (SLRP) molecules	RT		6	1.6E-2	3.0E0	6.6E-2	4.7E-2
GOTERM_BP_DIRECT	keratan sulfate catabolic process	RT		6	3.8E-2	3.0E0	3.8E-1	3.6E-1
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...) (keratan sulfate)	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_KEYWORDS	Proteoglycan	RT		11	1.7E-1	1.5E0	5.2E-1	4.0E-1
GOTERM_BP_DIRECT	keratan sulfate biosynthetic process	RT		6	5.2E-1	1.3E0	1.0E0	9.6E-1
GOTERM_CC_DIRECT	lysosomal lumen	RT		13	7.0E-1	9.7E-1	1.0E0	8.8E-1
GOTERM_CC_DIRECT	Golgi lumen	RT		14	7.6E-1	9.3E-1	1.0E0	8.8E-1
UP_KEYWORDS	Sulfation	RT		6	8.8E-1	8.1E-1	1.0E0	8.8E-1
UP_KEYWORDS	Extracellular matrix	RT		19	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 243	**Enrichment Score: 0.64**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of transporter activity	RT		4	9.9E-2	3.4E0	6.9E-1	6.6E-1
GOTERM_MF_DIRECT	calcium channel regulator activity	RT		8	1.5E-1	1.8E0	6.6E-1	5.9E-1
GOTERM_MF_DIRECT	chloride channel regulator activity	RT		4	2.3E-1	2.4E0	8.8E-1	7.8E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
GOTERM_BP_DIRECT	positive regulation of sodium ion transport	RT		5	4.0E-1	1.6E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	sodium channel regulator activity	RT		7	4.5E-1	1.3E0	1.0E0	8.9E-1
Annotation Cluster 244	**Enrichment Score: 0.64**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	GKAP/Homer scaffold activity	RT		3	1.3E-1	4.5E0	5.9E-1	5.3E-1
GOTERM_BP_DIRECT	vocalization behavior	RT		5	2.0E-1	2.1E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	adult behavior	RT		6	4.5E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 245	**Enrichment Score: 0.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	type I interferon signaling pathway	RT		15	1.8E-1	1.4E0	1.0E0	9.6E-1
UP_KEYWORDS	Antiviral defense	RT		21	2.4E-1	1.2E0	7.1E-1	5.5E-1
GOTERM_BP_DIRECT	defense response to virus	RT		32	2.9E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 246	**Enrichment Score: 0.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	lung-associated mesenchyme development	RT		5	7.3E-2	3.0E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	branching involved in salivary gland morphogenesis	RT		4	2.8E-1	2.2E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	midbrain development	RT		6	6.2E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 247	**Enrichment Score: 0.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Circadian rhythm	RT		13	9.3E-3	2.2E0	1.8E-2	9.3E-3
GOTERM_MF_DIRECT	AMP-activated protein kinase activity	RT		5	1.8E-2	4.3E0	1.2E-1	1.1E-1
GOTERM_CC_DIRECT	nucleotide-activated protein kinase complex	RT		6	1.9E-2	3.5E0	1.2E-1	1.1E-1
UP_SEQ_FEATURE	domain:CBS 3	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:CBS 4	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
BIOCARTA	Reversal of Insulin Resistance by Leptin	RT		7	1.1E-1	1.9E0	2.9E-1	2.0E-1
GOTERM_BP_DIRECT	carnitine shuttle	RT		4	1.8E-1	2.6E0	1.0E0	9.6E-1
UP_KEYWORDS	Fatty acid biosynthesis	RT		10	3.4E-1	1.3E0	9.4E-1	7.3E-1
GOTERM_BP_DIRECT	fatty acid biosynthetic process	RT		9	6.7E-1	1.0E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:CBS 1	RT		3	7.6E-1	1.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:CBS 2	RT		3	7.6E-1	1.1E0	1.0E0	9.6E-1
UP_KEYWORDS	CBS domain	RT		3	8.1E-1	1.0E0	1.0E0	8.1E-1
INTERPRO	Cystathionine beta-synthase, core	RT		3	8.6E-1	9.3E-1	1.0E0	9.1E-1
SMART	CBS	RT		3	8.9E-1	8.7E-1	1.0E0	9.1E-1
UP_KEYWORDS	Fatty acid metabolism	RT		13	9.6E-1	7.2E-1	1.0E0	9.6E-1
UP_KEYWORDS	Lipid biosynthesis	RT		11	1.0E0	4.8E-1	1.0E0	1.0E0
UP_KEYWORDS	Lipid metabolism	RT		19	1.0E0	3.0E-1	1.0E0	1.0E0
Annotation Cluster 248	**Enrichment Score: 0.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of interleukin-12 production	RT		8	1.2E-1	1.9E0	7.7E-1	7.4E-1
GOTERM_BP_DIRECT	positive regulation of interleukin-10 production	RT		7	1.8E-1	1.8E0	1.0E0	9.6E-1
BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	RT		8	6.2E-1	1.1E0	9.5E-1	6.7E-1
Annotation Cluster 249	**Enrichment Score: 0.63**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	Dorso-ventral axis formation	RT		12	8.1E-3	2.3E0	1.6E-2	8.1E-3
UP_SEQ_FEATURE	repeat:LNR 3	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
INTERPRO	Notch, NOD domain	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
INTERPRO	Notch, NODP domain	RT		4	1.5E-2	6.2E0	1.3E-1	1.1E-1
UP_SEQ_FEATURE	repeat:LNR 1	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
UP_SEQ_FEATURE	repeat:LNR 2	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
UP_SEQ_FEATURE	domain:EGF-like 28	RT		4	2.5E-2	5.5E0	4.4E-1	4.3E-1
SMART	SM01338	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
SMART	SM01339	RT		4	4.9E-2	4.1E0	3.0E-1	2.7E-1
UP_SEQ_FEATURE	domain:EGF-like 29	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	domain:EGF-like 33	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
UP_SEQ_FEATURE	domain:EGF-like 34	RT		3	5.8E-2	6.8E0	8.4E-1	8.1E-1
INTERPRO	Domain of unknown function DUF3454, notch	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
INTERPRO	Notch domain	RT		4	8.8E-2	3.5E0	4.9E-1	4.5E-1
SMART	SM01334	RT		3	1.5E-1	4.1E0	6.9E-1	6.2E-1
UP_SEQ_FEATURE	domain:EGF-like 20	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 24	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 26	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 27	RT		3	1.6E-1	4.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 13; calcium-binding	RT		4	2.1E-1	2.5E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 17; calcium-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 21; calcium-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 22	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 23; calcium-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
SMART	NL	RT		4	2.4E-1	2.3E0	9.5E-1	8.6E-1
UP_SEQ_FEATURE	domain:EGF-like 14; calcium-binding	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 15; calcium-binding	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
KEGG_PATHWAY	Notch signaling pathway	RT		12	3.1E-1	1.3E0	4.8E-1	3.1E-1
UP_SEQ_FEATURE	domain:EGF-like 19	RT		3	3.3E-1	2.6E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 11; calcium-binding	RT		4	3.4E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 12; calcium-binding	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
UP_KEYWORDS	Notch signaling pathway	RT		9	4.7E-1	1.2E0	1.0E0	7.8E-1
UP_SEQ_FEATURE	domain:EGF-like 8; calcium-binding	RT		5	4.8E-1	1.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 16; calcium-binding	RT		3	5.0E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 9; calcium-binding	RT		3	7.0E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 9	RT		4	7.1E-1	1.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 10	RT		3	7.4E-1	1.2E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 6	RT		6	7.9E-1	9.3E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 7; calcium-binding	RT		4	8.0E-1	9.7E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 3	RT		9	8.9E-1	8.1E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 7	RT		3	9.3E-1	7.3E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 4	RT		6	9.5E-1	6.9E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 5	RT		4	9.6E-1	6.5E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:EGF-like 5; calcium-binding	RT		3	9.8E-1	5.4E-1	1.0E0	9.8E-1
UP_SEQ_FEATURE	domain:EGF-like 2	RT		8	9.8E-1	6.1E-1	1.0E0	9.8E-1
UP_SEQ_FEATURE	domain:EGF-like 1	RT		9	1.0E0	5.1E-1	1.0E0	1.0E0
INTERPRO	EGF-like calcium-binding, conserved site	RT		7	1.0E0	4.3E-1	1.0E0	1.0E0
INTERPRO	EGF-type aspartate/asparagine hydroxylation site	RT		7	1.0E0	4.1E-1	1.0E0	1.0E0
INTERPRO	EGF-like calcium-binding	RT		7	1.0E0	3.4E-1	1.0E0	1.0E0
INTERPRO	EGF-like, conserved site	RT		10	1.0E0	3.1E-1	1.0E0	1.0E0
INTERPRO	Epidermal growth factor-like domain	RT		12	1.0E0	3.2E-1	1.0E0	1.0E0
UP_KEYWORDS	EGF-like domain	RT		10	1.0E0	2.9E-1	1.0E0	1.0E0
SMART	EGF_CA	RT		7	1.0E0	2.2E-1	1.0E0	1.0E0
SMART	EGF	RT		11	1.0E0	2.4E-1	1.0E0	1.0E0
Annotation Cluster 250	**Enrichment Score: 0.61**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	High mobility group (HMG) box domain	RT		15	6.6E-2	1.6E0	4.1E-1	3.7E-1
UP_SEQ_FEATURE	DNA-binding region:HMG box 1	RT		5	2.7E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	DNA-binding region:HMG box 2	RT		5	2.7E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	DNA-binding region:HMG box	RT		9	3.1E-1	1.4E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
SMART	HMG	RT		14	5.9E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 251	**Enrichment Score: 0.61**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Actin-related protein 3 (Arp3)	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_CC_DIRECT	Arp2/3 protein complex	RT		4	2.9E-1	2.1E0	8.6E-1	7.5E-1
GOTERM_BP_DIRECT	Arp2/3 complex-mediated actin nucleation	RT		4	7.4E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 252	**Enrichment Score: 0.6**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Natriuretic peptide receptor	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_MF_DIRECT	natriuretic peptide receptor activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
GOTERM_MF_DIRECT	hormone binding	RT		4	2.8E-1	2.2E0	1.0E0	8.9E-1
INTERPRO	Extracellular ligand-binding receptor	RT		5	8.5E-1	8.6E-1	1.0E0	9.1E-1
GOTERM_MF_DIRECT	peptide hormone binding	RT		4	8.5E-1	8.8E-1	1.0E0	8.9E-1
Annotation Cluster 253	**Enrichment Score: 0.59**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BBID	108.Regulating_glucose_transport	RT		7	1.1E-1	1.9E0	1.0E0	1.0E0
BBID	104.Insulin_signaling	RT		9	2.5E-1	1.4E0	1.0E0	1.0E0
BBID	105.Signaling_glucose_uptake	RT		6	2.8E-1	1.6E0	1.0E0	1.0E0
BBID	106.Glycogen_synthase-synthesis	RT		5	3.3E-1	1.7E0	1.0E0	1.0E0
BBID	107.mRNA_translation-protein_synthesis	RT		7	4.1E-1	1.4E0	1.0E0	1.0E0
Annotation Cluster 254	**Enrichment Score: 0.58**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	execution phase of apoptosis	RT		7	4.0E-2	2.6E0	3.9E-1	3.8E-1
BIOCARTA	Role of Mitochondria in Apoptotic Signaling	RT		12	7.0E-2	1.7E0	2.0E-1	1.4E-1
BIOCARTA	D4-GDI Signaling Pathway	RT		8	9.5E-2	1.9E0	2.5E-1	1.8E-1
GOTERM_MF_DIRECT	death receptor binding	RT		6	1.2E-1	2.2E0	5.5E-1	4.9E-1
INTERPRO	Peptidase C14, caspase precursor p45, core	RT		5	1.8E-1	2.2E0	8.7E-1	8.0E-1
BBID	86.Apoptosis_Nematode&_Vert	RT		6	2.0E-1	1.8E0	1.0E0	1.0E0
INTERPRO	Peptidase C14, ICE, catalytic subunit p20, active site	RT		4	2.1E-1	2.5E0	9.9E-1	9.1E-1
INTERPRO	Peptidase C14, ICE, catalytic subunit p20	RT		5	2.1E-1	2.1E0	1.0E0	9.1E-1
GOTERM_BP_DIRECT	response to cobalt ion	RT		3	2.7E-1	3.0E0	1.0E0	9.6E-1
INTERPRO	Peptidase C14, caspase non-catalytic subunit p10	RT		4	3.0E-1	2.1E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	death-inducing signaling complex	RT		3	3.0E-1	2.7E0	8.8E-1	7.7E-1
GOTERM_MF_DIRECT	cysteine-type endopeptidase activity involved in apoptotic process	RT		4	3.8E-1	1.8E0	1.0E0	8.9E-1
BIOCARTA	Caspase Cascade in Apoptosis	RT		10	3.8E-1	1.3E0	7.0E-1	4.9E-1
SMART	CASc	RT		5	4.0E-1	1.6E0	1.0E0	9.1E-1
BBID	72.IAP_interaction_with_cell_death_pathways	RT		6	7.0E-1	1.1E0	1.0E0	1.0E0
BBID	150.caspase_and_NFKB_activation	RT		6	8.1E-1	9.6E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	cysteine-type endopeptidase activity	RT		9	8.3E-1	8.8E-1	1.0E0	8.9E-1
UP_KEYWORDS	Thiol protease	RT		9	1.0E0	4.0E-1	1.0E0	1.0E0
Annotation Cluster 255	**Enrichment Score: 0.58**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	beta-catenin destruction complex disassembly	RT		7	1.5E-1	1.9E0	8.9E-1	8.5E-1
INTERPRO	DIX domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:DIX	RT		3	2.7E-1	2.9E0	1.0E0	9.6E-1
SMART	DAX	RT		3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 256	**Enrichment Score: 0.57**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, TBP-class protein binding, involved in preinitiation complex assembly	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
GOTERM_CC_DIRECT	transcription factor TFIID complex	RT		9	2.0E-1	1.6E0	7.3E-1	6.4E-1
GOTERM_MF_DIRECT	transcription factor activity, RNA polymerase II core promoter sequence-specific binding involved in preinitiation complex assembly	RT		3	4.6E-1	2.0E0	1.0E0	8.9E-1
GOTERM_BP_DIRECT	RNA polymerase II transcriptional preinitiation complex assembly	RT		3	7.5E-1	1.2E0	1.0E0	9.6E-1
Annotation Cluster 257	**Enrichment Score: 0.57**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:CR-type	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:CXXCXGXG motif	RT		3	1.1E-1	5.1E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Chaperone DnaJ	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	HSP40/DnaJ peptide-binding	RT		4	1.7E-1	2.8E0	8.2E-1	7.5E-1
INTERPRO	Chaperone DnaJ, C-terminal	RT		4	1.7E-1	2.8E0	8.2E-1	7.5E-1
INTERPRO	Heat shock protein DnaJ, cysteine-rich domain	RT		3	1.9E-1	3.7E0	8.9E-1	8.1E-1
INTERPRO	DnaJ domain, conserved site	RT		5	6.5E-1	1.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:J	RT		8	6.6E-1	1.0E0	1.0E0	9.6E-1
INTERPRO	DnaJ domain	RT		8	7.4E-1	9.7E-1	1.0E0	9.1E-1
SMART	DnaJ	RT		8	9.7E-1	6.8E-1	1.0E0	9.7E-1
Annotation Cluster 258	**Enrichment Score: 0.56**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	embryonic skeletal limb joint morphogenesis	RT		3	7.6E-2	5.9E0	5.8E-1	5.5E-1
GOTERM_BP_DIRECT	embryonic hindlimb morphogenesis	RT		7	3.3E-1	1.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	embryonic forelimb morphogenesis	RT		5	8.1E-1	9.3E-1	1.0E0	9.6E-1
Annotation Cluster 259	**Enrichment Score: 0.56**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	telomerase RNA binding	RT		6	1.2E-1	2.2E0	5.5E-1	4.9E-1
GOTERM_BP_DIRECT	telomere maintenance via telomerase	RT		5	3.6E-1	1.6E0	1.0E0	9.6E-1
UP_KEYWORDS	Dyskeratosis congenita	RT		3	4.9E-1	1.9E0	1.0E0	7.8E-1
Annotation Cluster 260	**Enrichment Score: 0.56**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	BRCT domain	RT		8	1.5E-1	1.8E0	7.7E-1	7.0E-1
UP_SEQ_FEATURE	domain:BRCT 1	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:BRCT 2	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
SMART	BRCT	RT		7	2.7E-1	1.6E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:BRCT	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 261	**Enrichment Score: 0.56**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	DNA-directed DNA polymerase, family B, exonuclease domain	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	DNA-directed DNA polymerase, family B, multifunctional domain	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
INTERPRO	DNA-directed DNA polymerase, family B	RT		3	1.2E-1	4.6E0	6.4E-1	5.8E-1
GOTERM_MF_DIRECT	3'-5' exonuclease activity	RT		6	2.0E-1	1.9E0	7.9E-1	7.1E-1
SMART	POLBc	RT		3	2.5E-1	3.0E0	9.9E-1	9.0E-1
UP_KEYWORDS	DNA-directed DNA polymerase	RT		6	2.7E-1	1.7E0	7.6E-1	5.9E-1
GOTERM_MF_DIRECT	DNA-directed DNA polymerase activity	RT		7	3.6E-1	1.4E0	1.0E0	8.9E-1
UP_KEYWORDS	4Fe-4S	RT		7	4.6E-1	1.3E0	1.0E0	7.8E-1
GOTERM_MF_DIRECT	4 iron, 4 sulfur cluster binding	RT		7	7.3E-1	9.9E-1	1.0E0	8.9E-1
UP_KEYWORDS	Iron-sulfur	RT		7	8.9E-1	8.0E-1	1.0E0	8.9E-1
Annotation Cluster 262	**Enrichment Score: 0.55**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Nitric Oxide Signaling Pathway	RT		11	1.5E-1	1.5E0	3.5E-1	2.5E-1
BIOCARTA	Effects of calcineurin in Keratinocyte Differentiation	RT		9	2.6E-1	1.4E0	5.2E-1	3.7E-1
BIOCARTA	Role of MEF2D in T-cell Apoptosis	RT		7	5.7E-1	1.2E0	8.9E-1	6.3E-1
Annotation Cluster 263	**Enrichment Score: 0.55**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	I-kappaB/NF-kappaB complex	RT		4	3.0E-2	5.1E0	1.8E-1	1.6E-1
INTERPRO	NF-kappa-B/Rel/Dorsal	RT		4	3.2E-2	5.0E0	2.4E-1	2.2E-1
INTERPRO	Rel homology domain	RT		4	2.1E-1	2.5E0	9.9E-1	9.1E-1
UP_SEQ_FEATURE	domain:RHD	RT		3	3.9E-1	2.3E0	1.0E0	9.6E-1
INTERPRO	p53-like transcription factor, DNA-binding	RT		9	4.2E-1	1.3E0	1.0E0	9.1E-1
INTERPRO	Cell surface receptor IPT/TIG	RT		6	5.8E-1	1.2E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding	RT		5	6.2E-1	1.2E0	1.0E0	8.9E-1
SMART	IPT	RT		5	9.3E-1	7.5E-1	1.0E0	9.3E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Immunoglobulin E-set	RT		12	9.7E-1	7.0E-1	1.0E0	9.7E-1
Annotation Cluster 264	**Enrichment Score: 0.54**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:BRO1	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
INTERPRO	BRO1 domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
SMART	SM01041	RT		3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 265	**Enrichment Score: 0.51**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Glycogen metabolism	RT		8	7.3E-2	2.1E0	2.5E-1	2.0E-1
GOTERM_BP_DIRECT	glycogen metabolic process	RT		8	2.1E-1	1.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	entrainment of circadian clock by photoperiod	RT		4	6.8E-1	1.2E0	1.0E0	9.6E-1
UP_KEYWORDS	Carbohydrate metabolism	RT		11	8.9E-1	8.0E-1	1.0E0	8.9E-1
Annotation Cluster 266	**Enrichment Score: 0.5**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Zinc finger, TFIIS-type	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	zinc finger region:TFIIS-type	RT		3	2.7E-1	2.9E0	1.0E0	9.6E-1
SMART	ZnF_C2C2	RT		3	4.6E-1	2.0E0	1.0E0	9.1E-1
Annotation Cluster 267	**Enrichment Score: 0.48**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	social behavior	RT		12	1.8E-1	1.5E0	9.8E-1	9.4E-1
GOTERM_BP_DIRECT	positive regulation of excitatory postsynaptic potential	RT		5	4.4E-1	1.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	adult behavior	RT		6	4.5E-1	1.4E0	1.0E0	9.6E-1
Annotation Cluster 268	**Enrichment Score: 0.46**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:KH	RT		6	7.3E-2	2.6E0	1.0E0	9.6E-1
INTERPRO	K Homology domain	RT		10	1.5E-1	1.6E0	7.4E-1	6.8E-1
INTERPRO	K Homology domain, type 1	RT		10	2.7E-1	1.4E0	1.0E0	9.1E-1
SMART	KH	RT		10	6.1E-1	1.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:KH 3	RT		3	6.7E-1	1.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:KH 1	RT		4	7.1E-1	1.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:KH 2	RT		4	7.1E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 269	**Enrichment Score: 0.44**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:MATH	RT		4	2.5E-1	2.3E0	1.0E0	9.6E-1
INTERPRO	MATH	RT		4	3.0E-1	2.1E0	1.0E0	9.1E-1
INTERPRO	TRAF-like	RT		6	3.8E-1	1.5E0	1.0E0	9.1E-1
SMART	MATH	RT		4	6.0E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 270	**Enrichment Score: 0.44**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:SWIRM	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
INTERPRO	SWIRM domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
INTERPRO	SANT domain	RT		6	4.1E-1	1.4E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:SANT	RT		3	7.9E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 271	**Enrichment Score: 0.42**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of guanylate cyclase activity	RT		7	4.9E-3	3.8E0	8.5E-2	8.1E-2
INTERPRO	Nitric oxide synthase, oxygenase domain	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
GOTERM_MF_DIRECT	nitric-oxide synthase activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
UP_SEQ_FEATURE	domain:Flavodoxin-like	RT		4	1.0E-1	3.4E0	1.0E0	9.6E-1
INTERPRO	Flavodoxin/nitric oxide synthase	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
INTERPRO	Flavodoxin	RT		4	1.2E-1	3.1E0	6.4E-1	5.8E-1
GOTERM_MF_DIRECT	tetrahydrobiopterin binding	RT		3	1.3E-1	4.5E0	5.9E-1	5.3E-1
GOTERM_MF_DIRECT	NADP binding	RT		9	2.2E-1	1.5E0	8.7E-1	7.8E-1
INTERPRO	FAD-binding, type 1	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	NADPH-cytochrome p450 reductase, FAD-binding, alpha-helical domain-3	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FMN	RT		4	3.0E-1	2.1E0	1.0E0	9.6E-1
INTERPRO	Oxidoreductase FAD/NAD(P)-binding	RT		4	3.0E-1	2.1E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	arginine binding	RT		3	3.3E-1	2.6E0	1.0E0	8.9E-1
GOTERM_BP_DIRECT	positive regulation of vasodilation	RT		7	3.6E-1	1.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	nitric oxide biosynthetic process	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	arginine catabolic process	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	nitric oxide mediated signal transduction	RT		5	4.0E-1	1.6E0	1.0E0	9.6E-1
INTERPRO	Flavoprotein pyridine nucleotide cytochrome reductase	RT		3	4.4E-1	2.1E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	FMN binding	RT		4	4.7E-1	1.6E0	1.0E0	8.9E-1
UP_SEQ_FEATURE	domain:FAD-binding FR-type	RT		4	5.4E-1	1.4E0	1.0E0	9.6E-1
KEGG_PATHWAY	Arginine biosynthesis	RT		5	5.6E-1	1.3E0	8.3E-1	5.6E-1
UP_KEYWORDS	FMN	RT		4	6.1E-1	1.3E0	1.0E0	7.8E-1
INTERPRO	Ferredoxin reductase-type FAD-binding domain	RT		4	6.1E-1	1.3E0	1.0E0	9.1E-1
INTERPRO	Riboflavin synthase-like beta-barrel	RT		4	6.1E-1	1.3E0	1.0E0	9.1E-1
GOTERM_BP_DIRECT	negative regulation of blood pressure	RT		4	9.0E-1	7.9E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	RT		7	9.1E-1	7.7E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	RT		8	9.3E-1	7.4E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT		8	9.9E-1	5.5E-1	1.0E0	9.9E-1
GOTERM_MF_DIRECT	heme binding	RT		13	1.0E0	5.7E-1	1.0E0	1.0E0
KEGG_PATHWAY	Arginine and proline metabolism	RT		4	1.0E0	4.2E-1	1.0E0	1.0E0
COG_ONTOLOGY	Inorganic ion transport and metabolism	RT		5	1.0E0	4.7E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	flavin adenine dinucleotide binding	RT		4	1.0E0	3.7E-1	1.0E0	1.0E0
UP_KEYWORDS	Heme	RT		9	1.0E0	4.7E-1	1.0E0	1.0E0
UP_KEYWORDS	FAD	RT		6	1.0E0	3.7E-1	1.0E0	1.0E0
UP_KEYWORDS	Flavoprotein	RT		6	1.0E0	3.4E-1	1.0E0	1.0E0
UP_KEYWORDS	NADP	RT		10	1.0E0	3.7E-1	1.0E0	1.0E0
Annotation Cluster 272	**Enrichment Score: 0.42**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	calcium-transporting ATPase activity	RT		5	4.9E-2	3.3E0	2.8E-1	2.5E-1
INTERPRO	Calcium-transporting P-type ATPase, subfamily IIA, SERCA-type	RT		3	7.0E-2	6.2E0	4.1E-1	3.7E-1
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	RT		10	1.1E-1	1.7E0	1.0E0	9.6E-1
GOTERM_CC_DIRECT	platelet dense tubular network membrane	RT		3	4.3E-1	2.1E0	1.0E0	8.8E-1
GOTERM_CC_DIRECT	sarcoplasmic reticulum membrane	RT		7	4.5E-1	1.3E0	1.0E0	8.8E-1
GOTERM_CC_DIRECT	sarcoplasmic reticulum	RT		7	4.5E-1	1.3E0	1.0E0	8.8E-1
UP_KEYWORDS	Sarcoplasmic reticulum	RT		6	7.1E-1	1.0E0	1.0E0	7.8E-1
GOTERM_BP_DIRECT	cellular calcium ion homeostasis	RT		11	9.6E-1	7.0E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	calcium ion transport	RT		6	1.0E0	4.7E-1	1.0E0	1.0E0
GOTERM_BP_DIRECT	calcium ion transmembrane transport	RT		10	1.0E0	5.0E-1	1.0E0	1.0E0
UP_KEYWORDS	Calcium transport	RT		5	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 273	**Enrichment Score: 0.41**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	actin crosslink formation	RT		4	2.8E-1	2.2E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	actin filament bundle assembly	RT		7	4.0E-1	1.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	actin filament network formation	RT		3	5.2E-1	1.8E0	1.0E0	9.6E-1
Annotation Cluster 274	**Enrichment Score: 0.4**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:SANT 1	RT		3	3.9E-1	2.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:SANT 2	RT		3	3.9E-1	2.3E0	1.0E0	9.6E-1
INTERPRO	SANT domain	RT		6	4.1E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 275	**Enrichment Score: 0.4**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Postsynaptic cell membrane	RT		33	1.3E-1	1.3E0	4.1E-1	3.1E-1
GOTERM_CC_DIRECT	postsynaptic membrane	RT		39	2.0E-1	1.2E0	7.4E-1	6.5E-1
GOTERM_CC_DIRECT	postsynaptic density	RT		34	2.3E-1	1.2E0	8.2E-1	7.2E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Synapse	RT		48	8.0E-1	9.2E-1	1.0E0	8.0E-1
UP_KEYWORDS	Cell junction	RT		88	9.1E-1	8.9E-1	1.0E0	9.1E-1
GOTERM_CC_DIRECT	cell junction	RT		62	9.4E-1	8.6E-1	1.0E0	9.4E-1
Annotation Cluster 276	**Enrichment Score: 0.4**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BBID	68.Mitogen_signaling_in_growth_control	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
BBID	2.Cytokine_Receptors	RT		4	3.8E-1	1.8E0	1.0E0	1.0E0
BBID	54.T-cell_anergy	RT		8	4.3E-1	1.3E0	1.0E0	1.0E0
Annotation Cluster 277	**Enrichment Score: 0.39**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Sirtuin family, catalytic core small domain	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:Deacetylase sirtuin-type	RT		3	2.7E-1	2.9E0	1.0E0	9.6E-1
INTERPRO	Sirtuin family, catalytic core domain	RT		3	3.2E-1	2.7E0	1.0E0	9.1E-1
INTERPRO	Sirtuin family	RT		3	3.2E-1	2.7E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	NAD+ binding	RT		3	6.7E-1	1.4E0	1.0E0	8.9E-1
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	RT		7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 278	**Enrichment Score: 0.39**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	RISC complex	RT		4	2.4E-1	2.3E0	8.3E-1	7.3E-1
GOTERM_CC_DIRECT	RISC-loading complex	RT		3	3.0E-1	2.7E0	8.8E-1	7.7E-1
GOTERM_BP_DIRECT	miRNA loading onto RISC involved in gene silencing by miRNA	RT		3	3.4E-1	2.5E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	pre-miRNA processing	RT		4	3.8E-1	1.8E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	production of miRNAs involved in gene silencing by miRNA	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:PAZ	RT		3	4.4E-1	2.0E0	1.0E0	9.6E-1
INTERPRO	Argonaute/Dicer protein, PAZ	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
BIOCARTA	Dicer Pathway	RT		3	5.3E-1	1.8E0	8.4E-1	6.0E-1
SMART	SM00949	RT		3	6.9E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 279	**Enrichment Score: 0.39**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:DOC	RT		3	3.3E-1	2.6E0	1.0E0	9.6E-1
INTERPRO	Anaphase-promoting complex, subunit 10/DOC domain	RT		3	3.8E-1	2.3E0	1.0E0	9.1E-1
SMART	SM01337	RT		3	5.5E-1	1.7E0	1.0E0	9.1E-1
Annotation Cluster 280	**Enrichment Score: 0.39**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	protein ADP-ribosylation	RT		7	1.3E-1	2.0E0	8.2E-1	7.9E-1
GOTERM_BP_DIRECT	negative regulation of telomere maintenance via telomere lengthening	RT		3	2.0E-1	3.6E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	NAD+ ADP-ribosyltransferase activity	RT		7	3.3E-1	1.5E0	1.0E0	8.9E-1
UP_SEQ_FEATURE	domain:PARP catalytic	RT		3	7.4E-1	1.2E0	1.0E0	9.6E-1
INTERPRO	Poly(ADP-ribose) polymerase, catalytic domain	RT		3	7.9E-1	1.1E0	1.0E0	9.1E-1
UP_KEYWORDS	Glycosyltransferase	RT		5	1.0E0	1.5E-1	1.0E0	1.0E0
Annotation Cluster 281	**Enrichment Score: 0.37**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:RanBP2-type	RT		5	2.7E-1	1.9E0	1.0E0	9.6E-1
INTERPRO	Zinc finger, RanBP2-type	RT		6	3.8E-1	1.5E0	1.0E0	9.1E-1
SMART	ZnF_RBZ	RT		5	7.6E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 282	**Enrichment Score: 0.37**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Bernard Soulier syndrome	RT		3	5.7E-2	6.9E0	2.1E-1	1.6E-1
GOTERM_BP_DIRECT	blood coagulation, intrinsic pathway	RT		5	3.6E-1	1.6E0	1.0E0	9.6E-1
UP_KEYWORDS	Blood coagulation	RT		6	8.5E-1	8.6E-1	1.0E0	8.5E-1
UP_KEYWORDS	Hemostasis	RT		6	8.5E-1	8.6E-1	1.0E0	8.5E-1
KEGG_PATHWAY	ECM-receptor interaction	RT		7	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 283	**Enrichment Score: 0.36**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:HEAT 9	RT		5	1.7E-1	2.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 10	RT		5	1.7E-1	2.3E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	repeat:HEAT 7	RT		6	2.7E-1	1.7E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 8	RT		5	3.0E-1	1.8E0	1.0E0	9.6E-1
INTERPRO	HEAT, type 2	RT		5	3.7E-1	1.6E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	repeat:HEAT 6	RT		6	4.6E-1	1.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 11	RT		3	5.0E-1	1.9E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 5	RT		6	6.0E-1	1.2E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 1	RT		8	7.7E-1	9.4E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 2	RT		8	7.7E-1	9.4E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 4	RT		6	7.8E-1	9.5E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:HEAT 3	RT		6	8.8E-1	8.2E-1	1.0E0	9.6E-1
Annotation Cluster 284	**Enrichment Score: 0.36**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	region of interest:Interaction with KCND2	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
UP_SEQ_FEATURE	domain:EF-hand 1; degenerate	RT		4	1.1E-2	6.8E0	2.2E-1	2.1E-1
GOTERM_BP_DIRECT	regulation of potassium ion transmembrane transport	RT		4	4.8E-1	1.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cardiac conduction	RT		6	9.0E-1	7.9E-1	1.0E0	9.6E-1
GOTERM_MF_DIRECT	voltage-gated ion channel activity	RT		3	9.8E-1	5.6E-1	1.0E0	9.8E-1
UP_KEYWORDS	Potassium	RT		12	9.9E-1	6.4E-1	1.0E0	9.9E-1
GOTERM_CC_DIRECT	voltage-gated potassium channel complex	RT		8	9.9E-1	5.8E-1	1.0E0	9.9E-1
GOTERM_MF_DIRECT	potassium channel activity	RT		3	9.9E-1	4.8E-1	1.0E0	9.9E-1
UP_KEYWORDS	Potassium transport	RT		10	9.9E-1	5.9E-1	1.0E0	9.9E-1
UP_KEYWORDS	Potassium channel	RT		4	1.0E0	3.7E-1	1.0E0	1.0E0
GOTERM_BP_DIRECT	potassium ion transmembrane transport	RT		5	1.0E0	2.4E-1	1.0E0	1.0E0
UP_KEYWORDS	Voltage-gated channel	RT		4	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 285	**Enrichment Score: 0.34**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	positive regulation of chemokine biosynthetic process	RT		7	2.6E-3	4.1E0	5.0E-2	4.8E-2
GOTERM_BP_DIRECT	positive regulation of MHC class II biosynthetic process	RT		5	3.2E-2	3.7E0	3.4E-1	3.3E-1
KEGG_PATHWAY	African trypanosomiasis	RT		12	4.0E-2	1.9E0	7.0E-2	4.0E-2
KEGG_PATHWAY	Malaria	RT		15	7.4E-2	1.6E0	1.3E-1	7.4E-2
GOTERM_BP_DIRECT	defense response to protozoan	RT		7	8.7E-2	2.2E0	6.4E-1	6.2E-1
KEGG_PATHWAY	Inflammatory bowel disease (IBD)	RT		18	9.5E-2	1.5E0	1.6E-1	9.5E-2
BBID	111.Stress_influences_immunity	RT		5	1.3E-1	2.3E0	1.0E0	1.0E0
BBID	112.StressandCRHinfluence	RT		5	1.3E-1	2.3E0	1.0E0	1.0E0
BBID	19.Cytokine_microglia	RT		7	1.7E-1	1.7E0	1.0E0	1.0E0
BBID	18.Cytokine_astocytes	RT		9	1.9E-1	1.5E0	1.0E0	1.0E0
BBID	56.Macrophage_regulation_of_CD4+T_cells	RT		6	2.8E-1	1.6E0	1.0E0	1.0E0
BBID	58.(CD40L)_immnosurveillance	RT		8	3.6E-1	1.4E0	1.0E0	1.0E0
GOTERM_BP_DIRECT	positive regulation of isotype switching to IgG isotypes	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
BBID	22.Cytokine-chemokine_CNS	RT		6	4.6E-1	1.4E0	1.0E0	1.0E0
BBID	20.Cytokine_oligodendrocytes	RT		3	4.7E-1	2.0E0	1.0E0	1.0E0
BBID	21.Cytokine_neurons	RT		3	4.7E-1	2.0E0	1.0E0	1.0E0
BBID	113.Th1andTh2cells	RT		4	5.0E-1	1.6E0	1.0E0	1.0E0
GOTERM_BP_DIRECT	negative regulation of growth of symbiont in host	RT		4	5.2E-1	1.5E0	1.0E0	9.6E-1
BBID	80.T_cell_Activation	RT		10	6.0E-1	1.1E0	1.0E0	1.0E0
BBID	35.Chemokines_EAE_Autoreactive_T_Cells	RT		4	6.1E-1	1.4E0	1.0E0	1.0E0
BIOCARTA	Dendritic cells in regulating TH1 and TH2 Development	RT		8	6.2E-1	1.1E0	9.5E-1	6.7E-1
BBID	88.Alternatively_Activated_APC	RT		5	6.2E-1	1.2E0	1.0E0	1.0E0
KEGG_PATHWAY	Rheumatoid arthritis	RT		17	6.4E-1	1.0E0	9.2E-1	6.4E-1
INTERPRO	Four-helical cytokine, core	RT		8	7.4E-1	9.7E-1	1.0E0	9.1E-1
BIOCARTA	Regulation of hematopoiesis by cytokines	RT		5	7.8E-1	1.0E0	1.0E0	7.8E-1
BIOCARTA	Cytokine Network	RT		7	7.8E-1	9.7E-1	1.0E0	7.8E-1
BIOCARTA	Cytokines and Inflammatory Response	RT		9	7.9E-1	9.4E-1	1.0E0	7.9E-1
INTERPRO	Four-helical cytokine-like, core	RT		8	7.9E-1	9.2E-1	1.0E0	9.1E-1
BBID	76.Sig_trans_Ca2_Calcineurin_NF-AT	RT		3	7.9E-1	1.2E0	1.0E0	1.0E0

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
KEGG_PATHWAY	Intestinal immune network for IgA production	RT		8	8.3E-1	8.8E-1	1.0E0	8.3E-1
BIOCARTA	Antigen Dependent B Cell Activation	RT		4	8.5E-1	9.4E-1	1.0E0	8.5E-1
BBID	59.L-type_Ca2+_Tat_immune_cells	RT		3	8.6E-1	1.0E0	1.0E0	1.0E0
KEGG_PATHWAY	Allograft rejection	RT		6	8.7E-1	8.4E-1	1.0E0	8.7E-1
BBID	97.Immune_injury_MS-lesions_MS_antigen	RT		5	9.0E-1	8.5E-1	1.0E0	1.0E0
KEGG_PATHWAY	Graft-versus-host disease	RT		5	9.0E-1	7.9E-1	1.0E0	9.0E-1
BIOCARTA	Adhesion and Diapedesis of Granulocytes	RT		4	9.2E-1	8.1E-1	1.0E0	9.2E-1
UP_KEYWORDS	Growth factor	RT		15	9.2E-1	7.9E-1	1.0E0	9.2E-1
BBID	15.T-cell_polarization-chemokine_receptors	RT		5	9.2E-1	8.0E-1	1.0E0	1.0E0
BIOCARTA	Selective expression of chemokine receptors during T-cell polarization	RT		7	9.4E-1	7.6E-1	1.0E0	9.4E-1
KEGG_PATHWAY	Asthma	RT		4	9.5E-1	6.9E-1	1.0E0	9.5E-1
BIOCARTA	Cells and Molecules involved in local acute inflammatory response	RT		4	9.5E-1	7.2E-1	1.0E0	9.5E-1
BBID	5.B7_CD40_B-cell_activa	RT		3	9.7E-1	6.8E-1	1.0E0	1.0E0
BIOCARTA	Role of Tob in T-cell activation	RT		4	9.7E-1	6.4E-1	1.0E0	9.7E-1
BIOCARTA	Th1/Th2 Differentiation	RT		4	9.8E-1	6.1E-1	1.0E0	9.8E-1
GOTERM_MF_DIRECT	growth factor activity	RT		19	9.8E-1	7.0E-1	1.0E0	9.8E-1
KEGG_PATHWAY	Autoimmune thyroid disease	RT		4	1.0E0	4.0E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	cytokine activity	RT		14	1.0E0	4.7E-1	1.0E0	1.0E0
UP_KEYWORDS	Cytokine	RT		12	1.0E0	4.3E-1	1.0E0	1.0E0
KEGG_PATHWAY	Cytokine-cytokine receptor interaction	RT		16	1.0E0	3.4E-1	1.0E0	1.0E0
GOTERM_BP_DIRECT	immune response	RT		31	1.0E0	4.4E-1	1.0E0	1.0E0
Annotation Cluster 286	**Enrichment Score: 0.33**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Caspase Cascade in Apoptosis	RT		10	3.8E-1	1.3E0	7.0E-1	4.9E-1
UP_SEQ_FEATURE	domain:CARD	RT		6	4.2E-1	1.4E0	1.0E0	9.6E-1
INTERPRO	Caspase Recruitment	RT		6	5.1E-1	1.3E0	1.0E0	9.1E-1
SMART	CARD	RT		4	6.0E-1	1.4E0	1.0E0	9.1E-1
Annotation Cluster 287	**Enrichment Score: 0.32**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Exportin-1/Importin-beta-like	RT		3	2.5E-1	3.1E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	Ran GTPase binding	RT		7	3.9E-1	1.4E0	1.0E0	8.9E-1
INTERPRO	Importin-beta, N-terminal	RT		4	5.3E-1	1.5E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:Importin N-terminal	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
SMART	SM00913	RT		4	7.9E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 288	**Enrichment Score: 0.32**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Filamin/ABP280 repeat-like	RT		4	3.0E-1	2.1E0	1.0E0	9.1E-1
INTERPRO	Filamin/ABP280 repeat	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
SMART	IG_FLMN	RT		3	7.5E-1	1.2E0	1.0E0	9.1E-1
Annotation Cluster 289	**Enrichment Score: 0.28**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Immunoglobulin I-set	RT		37	2.7E-3	1.6E0	3.2E-2	2.9E-2
INTERPRO	Immunoglobulin subtype 2	RT		42	4.8E-1	1.0E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	RT		18	7.1E-1	9.6E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	RT		24	9.3E-1	8.1E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	RT		24	9.3E-1	8.1E-1	1.0E0	9.6E-1
SMART	IGc2	RT		42	1.0E0	6.8E-1	1.0E0	1.0E0
UP_KEYWORDS	Immunoglobulin domain	RT		49	1.0E0	6.2E-1	1.0E0	1.0E0
INTERPRO	Immunoglobulin subtype	RT		47	1.0E0	5.9E-1	1.0E0	1.0E0
INTERPRO	Immunoglobulin-like fold	RT		85	1.0E0	5.5E-1	1.0E0	1.0E0
INTERPRO	Immunoglobulin-like domain	RT		51	1.0E0	4.1E-1	1.0E0	1.0E0
SMART	IG	RT		47	1.0E0	3.8E-1	1.0E0	1.0E0
Annotation Cluster 290	**Enrichment Score: 0.27**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	SMAD protein complex assembly	RT		3	4.0E-1	2.2E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	type I transforming growth factor beta receptor binding	RT		3	4.6E-1	2.0E0	1.0E0	8.9E-1
GOTERM_MF_DIRECT	transforming growth factor beta receptor binding	RT		6	8.6E-1	8.5E-1	1.0E0	8.9E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
Annotation Cluster 291	Enrichment Score: 0.24			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	short sequence motif:"KMSKS" region	RT		5	2.0E-1	2.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	short sequence motif:"HIGH" region	RT		5	2.7E-1	1.9E0	1.0E0	9.6E-1
INTERPRO	Aminoacyl-tRNA synthetase, class I, conserved site	RT		4	4.4E-1	1.7E0	1.0E0	9.1E-1
INTERPRO	Glutathione S-transferase, C-terminal	RT		5	5.2E-1	1.3E0	1.0E0	9.1E-1
INTERPRO	Rossmann-like alpha/beta/alpha sandwich fold	RT		8	5.3E-1	1.2E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	aminoacyl-tRNA ligase activity	RT		4	5.6E-1	1.4E0	1.0E0	8.9E-1
INTERPRO	Aminoacyl-tRNA synthetase, class 1a, anticodon-binding	RT		3	6.4E-1	1.4E0	1.0E0	9.1E-1
UP_KEYWORDS	Aminoacyl-tRNA synthetase	RT		5	8.2E-1	9.0E-1	1.0E0	8.2E-1
INTERPRO	Glutathione S-transferase, C-terminal-like	RT		5	9.2E-1	7.6E-1	1.0E0	9.2E-1
UP_SEQ_FEATURE	domain:GST C-terminal	RT		4	9.2E-1	7.4E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	tRNA aminoacylation for protein translation	RT		5	9.2E-1	7.4E-1	1.0E0	9.6E-1
KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT		5	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 292	Enrichment Score: 0.23			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	domain:MIF4G	RT		3	4.4E-1	2.0E0	1.0E0	9.6E-1
INTERPRO	MIF4G-like, type 3	RT		3	5.0E-1	1.9E0	1.0E0	9.1E-1
INTERPRO	MIF4-like, type 1/2/3	RT		3	7.2E-1	1.2E0	1.0E0	9.1E-1
SMART	MIF4G	RT		3	7.5E-1	1.2E0	1.0E0	9.1E-1
Annotation Cluster 293	Enrichment Score: 0.23			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	domain:MBD	RT		3	5.0E-1	1.9E0	1.0E0	9.6E-1
INTERPRO	Methyl-CpG DNA binding	RT		3	5.5E-1	1.7E0	1.0E0	9.1E-1
INTERPRO	DNA-binding, integrase-type	RT		3	5.5E-1	1.7E0	1.0E0	9.1E-1
SMART	MBD	RT		3	7.9E-1	1.1E0	1.0E0	9.1E-1
Annotation Cluster 294	Enrichment Score: 0.23			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	region of interest:Heparin-binding	RT		5	3.4E-1	1.7E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	organ induction	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
UP_KEYWORDS	Heparin-binding	RT		8	9.8E-1	6.2E-1	1.0E0	9.8E-1
Annotation Cluster 295	Enrichment Score: 0.23			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Importin subunit alpha	RT		3	3.2E-1	2.7E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:IBB	RT		3	3.3E-1	2.6E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	NLS-bearing protein import into nucleus	RT		6	3.5E-1	1.5E0	1.0E0	9.6E-1
PIR_SUPERFAMILY	importin subunit alpha	RT		3	3.8E-1	2.3E0	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:ARM 8	RT		5	4.1E-1	1.5E0	1.0E0	9.6E-1
INTERPRO	Importin-alpha, importin-beta-binding domain	RT		3	4.4E-1	2.1E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	repeat:ARM 7	RT		5	4.8E-1	1.4E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:ARM 6	RT		5	5.4E-1	1.3E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:ARM 5	RT		5	6.3E-1	1.2E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:ARM 4	RT		5	6.9E-1	1.1E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	nuclear localization sequence binding	RT		5	7.1E-1	1.1E0	1.0E0	8.9E-1
UP_SEQ_FEATURE	repeat:ARM 9	RT		3	7.6E-1	1.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:ARM 3	RT		5	7.9E-1	9.5E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:ARM 2	RT		5	8.1E-1	9.2E-1	1.0E0	9.6E-1
INTERPRO	Armadillo	RT		5	9.3E-1	7.2E-1	1.0E0	9.3E-1
UP_SEQ_FEATURE	repeat:ARM 1	RT		3	9.5E-1	6.6E-1	1.0E0	9.6E-1
SMART	ARM	RT		5	9.9E-1	5.2E-1	1.0E0	9.9E-1
GOTERM_MF_DIRECT	protein transporter activity	RT		6	1.0E0	5.0E-1	1.0E0	1.0E0
Annotation Cluster 296	Enrichment Score: 0.23			Count	P_Value	Fold Change	Benjamini	FDR

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:ZZ-type	RT		4	4.6E-1	1.6E0	1.0E0	9.6E-1
INTERPRO	Zinc finger, ZZ-type	RT		4	5.7E-1	1.4E0	1.0E0	9.1E-1
SMART	ZnF_ZZ	RT		4	7.9E-1	1.0E0	1.0E0	9.1E-1
Annotation Cluster 297	**Enrichment Score: 0.23**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	protein-hormone receptor activity	RT		3	7.5E-2	6.0E0	3.9E-1	3.4E-1
INTERPRO	G protein-coupled receptor, rhodopsin-like	RT		7	1.0E0	6.0E-2	1.0E0	1.0E0
INTERPRO	GPCR, rhodopsin-like, 7TM	RT		7	1.0E0	5.9E-2	1.0E0	1.0E0
GOTERM_MF_DIRECT	G-protein coupled receptor activity	RT		10	1.0E0	8.4E-2	1.0E0	1.0E0
UP_KEYWORDS	G-protein coupled receptor	RT		11	1.0E0	9.0E-2	1.0E0	1.0E0
Annotation Cluster 298	**Enrichment Score: 0.22**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Cyclic nucleotide-binding, conserved site	RT		5	2.5E-1	1.9E0	1.0E0	9.1E-1
INTERPRO	Cyclic nucleotide-binding domain	RT		7	5.1E-1	1.2E0	1.0E0	9.1E-1
INTERPRO	Cyclic nucleotide-binding-like	RT		7	5.9E-1	1.1E0	1.0E0	9.1E-1
UP_KEYWORDS	cAMP-binding	RT		3	7.3E-1	1.2E0	1.0E0	7.8E-1
INTERPRO	RmlC-like jelly roll fold	RT		7	7.9E-1	9.2E-1	1.0E0	9.1E-1
GOTERM_MF_DIRECT	cAMP binding	RT		4	7.9E-1	9.9E-1	1.0E0	8.9E-1
SMART	cNMP	RT		7	8.1E-1	9.2E-1	1.0E0	9.1E-1
Annotation Cluster 299	**Enrichment Score: 0.21**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	nuclear pore	RT		14	3.4E-1	1.2E0	9.5E-1	8.3E-1
UP_KEYWORDS	Nuclear pore complex	RT		7	7.6E-1	9.6E-1	1.0E0	7.8E-1
UP_KEYWORDS	Translocation	RT		9	9.4E-1	7.4E-1	1.0E0	9.4E-1
Annotation Cluster 300	**Enrichment Score: 0.2**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	chain:Histone H2A type 1-D	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	chain:Histone H3.1	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	chain:Histone H3.2	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
Annotation Cluster 301	**Enrichment Score: 0.19**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Vision	RT		20	3.1E-1	1.2E0	8.8E-1	6.8E-1
GOTERM_BP_DIRECT	visual perception	RT		29	8.9E-1	8.5E-1	1.0E0	9.6E-1
UP_KEYWORDS	Sensory transduction	RT		22	1.0E0	2.5E-1	1.0E0	1.0E0
Annotation Cluster 302	**Enrichment Score: 0.18**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Forkhead-associated (FHA) domain	RT		7	5.6E-1	1.2E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	domain:FHA	RT		6	6.0E-1	1.2E0	1.0E0	9.6E-1
INTERPRO	SMAD/FHA domain	RT		9	6.4E-1	1.1E0	1.0E0	9.1E-1
SMART	FHA	RT		5	8.5E-1	8.8E-1	1.0E0	9.1E-1
Annotation Cluster 303	**Enrichment Score: 0.18**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	binding site:NAD; via carbonyl oxygen	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	NAD binding	RT		5	9.0E-1	7.8E-1	1.0E0	9.0E-1
UP_SEQ_FEATURE	binding site:NAD	RT		5	9.7E-1	6.3E-1	1.0E0	9.7E-1
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NAD	RT		7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 304	**Enrichment Score: 0.18**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	ATP hydrolysis coupled proton transport	RT		8	2.9E-1	1.5E0	1.0E0	9.6E-1
UP_KEYWORDS	Hydrogen ion transport	RT		4	9.8E-1	5.6E-1	1.0E0	9.8E-1
KEGG_PATHWAY	Oxidative phosphorylation	RT		5	1.0E0	2.0E-1	1.0E0	1.0E0
Annotation Cluster 305	**Enrichment Score: 0.17**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	TACI and BCMA stimulation of B cell immune responses.	RT		6	5.8E-1	1.2E0	9.0E-1	6.4E-1
GOTERM_BP_DIRECT	membrane protein intracellular domain proteolysis	RT		4	6.1E-1	1.3E0	1.0E0	9.6E-1
BIOCARTA	Bone Remodelling	RT		5	7.3E-1	1.1E0	1.0E0	7.3E-1
BBID	99.NF-kB_activation	RT		6	8.1E-1	9.6E-1	1.0E0	1.0E0
Annotation Cluster 306	**Enrichment Score: 0.17**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Steroid-binding	RT		5	1.9E-1	2.1E0	5.9E-1	4.6E-1
UP_SEQ_FEATURE	region of interest:Steroid-binding	RT		3	2.2E-1	3.4E0	1.0E0	9.6E-1
INTERPRO	Zinc finger, NHR/GATA-type	RT		13	2.2E-1	1.4E0	1.0E0	9.1E-1
UP_SEQ_FEATURE	region of interest:Modulating	RT		3	6.3E-1	1.5E0	1.0E0	9.6E-1
GOTERM_MF_DIRECT	steroid binding	RT		5	6.9E-1	1.1E0	1.0E0	8.9E-1
UP_SEQ_FEATURE	zinc finger region:NR C4-type	RT		6	8.1E-1	9.1E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	RT		6	8.1E-1	9.1E-1	1.0E0	9.6E-1
INTERPRO	Zinc finger, nuclear hormone receptor-type	RT		6	8.8E-1	8.1E-1	1.0E0	9.1E-1
INTERPRO	Steroid hormone receptor	RT		6	9.0E-1	7.9E-1	1.0E0	9.1E-1
INTERPRO	Nuclear hormone receptor, ligand-binding, core	RT		6	9.1E-1	7.7E-1	1.0E0	9.1E-1
UP_SEQ_FEATURE	region of interest:Hinge	RT		3	9.3E-1	7.3E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	region of interest:Ligand-binding	RT		3	9.5E-1	6.8E-1	1.0E0	9.6E-1
GOTERM_MF_DIRECT	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	RT		4	9.5E-1	6.6E-1	1.0E0	9.5E-1
GOTERM_MF_DIRECT	steroid hormone receptor activity	RT		6	9.7E-1	6.4E-1	1.0E0	9.7E-1
GOTERM_BP_DIRECT	steroid hormone mediated signaling pathway	RT		5	9.9E-1	5.2E-1	1.0E0	9.9E-1
SMART	ZnF_C4	RT		6	9.9E-1	5.3E-1	1.0E0	9.9E-1
SMART	HOLI	RT		6	1.0E0	5.1E-1	1.0E0	1.0E0
Annotation Cluster 307	**Enrichment Score: 0.16**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:OPR	RT		3	5.4E-1	1.7E0	1.0E0	9.6E-1
INTERPRO	Phox/Bem1p	RT		3	6.9E-1	1.3E0	1.0E0	9.1E-1
SMART	PB1	RT		3	8.9E-1	8.7E-1	1.0E0	9.1E-1
Annotation Cluster 308	**Enrichment Score: 0.15**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	mitochondrial small ribosomal subunit	RT		5	5.7E-1	1.3E0	1.0E0	8.8E-1
GOTERM_BP_DIRECT	mitochondrial translational elongation	RT		14	7.0E-1	9.8E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	mitochondrial translation	RT		6	7.5E-1	9.9E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	mitochondrial translational termination	RT		13	8.1E-1	9.0E-1	1.0E0	9.6E-1
Annotation Cluster 309	**Enrichment Score: 0.15**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Patatin/Phospholipase A2-related	RT		3	4.4E-1	2.1E0	1.0E0	9.1E-1
INTERPRO	Acyl transferase/acyl hydrolase/lysophospholipase	RT		3	8.1E-1	1.0E0	1.0E0	9.1E-1
KEGG_PATHWAY	Glycerophospholipid metabolism	RT		5	1.0E0	2.7E-1	1.0E0	1.0E0
Annotation Cluster 310	**Enrichment Score: 0.14**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
BIOCARTA	Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration	RT		7	4.3E-1	1.3E0	7.3E-1	5.2E-1
BIOCARTA	How does salmonella hijack a cell	RT		4	8.5E-1	9.4E-1	1.0E0	8.5E-1
BIOCARTA	Y branching of actin filaments	RT		3	1.0E0	4.3E-1	1.0E0	1.0E0
Annotation Cluster 311	**Enrichment Score: 0.13**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	histone H4-K16 acetylation	RT		4	6.8E-1	1.2E0	1.0E0	9.6E-1
GOTERM_CC_DIRECT	histone acetyltransferase complex	RT		4	7.2E-1	1.1E0	1.0E0	8.8E-1
GOTERM_BP_DIRECT	histone H4-K5 acetylation	RT		3	7.8E-1	1.1E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	histone H4-K8 acetylation	RT		3	7.8E-1	1.1E0	1.0E0	9.6E-1
Annotation Cluster 312	**Enrichment Score: 0.12**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
KEGG_PATHWAY	One carbon pool by folate	RT		5	5.6E-1	1.3E0	8.3E-1	5.6E-1
UP_KEYWORDS	One-carbon metabolism	RT		3	7.3E-1	1.2E0	1.0E0	7.8E-1
GOTERM_BP_DIRECT	folic acid metabolic process	RT		3	8.3E-1	9.9E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	one-carbon metabolic process	RT		3	9.7E-1	5.9E-1	1.0E0	9.7E-1
Annotation Cluster 313	**Enrichment Score: 0.11**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_BP_DIRECT	negative regulation of viral transcription	RT		3	6.7E-1	1.4E0	1.0E0	9.6E-1
GOTERM_BP_DIRECT	negative regulation of viral release from host cell	RT		3	7.8E-1	1.1E0	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:B box-type	RT		8	8.9E-1	8.0E-1	1.0E0	9.6E-1
Annotation Cluster 314	**Enrichment Score: 0.11**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Phospholipid-transporting P-type ATPase, subfamily IV	RT		3	6.9E-1	1.3E0	1.0E0	9.1E-1
GOTERM_MF_DIRECT	phospholipid-translocating ATPase activity	RT		3	7.1E-1	1.3E0	1.0E0	8.9E-1
GOTERM_BP_DIRECT	phospholipid translocation	RT		4	7.4E-1	1.1E0	1.0E0	9.6E-1
UP_KEYWORDS	Lipid transport	RT		4	1.0E0	2.9E-1	1.0E0	1.0E0
Annotation Cluster 315	**Enrichment Score: 0.11**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	cAMP response element binding	RT		4	3.8E-1	1.8E0	1.0E0	8.9E-1
INTERPRO	Basic-leucine zipper domain	RT		5	9.8E-1	5.7E-1	1.0E0	9.8E-1
SMART	BRLZ	RT		5	1.0E0	4.0E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		10	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 316	**Enrichment Score: 0.1**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:SAP	RT		4	7.1E-1	1.1E0	1.0E0	9.6E-1
INTERPRO	SAP domain	RT		4	7.7E-1	1.0E0	1.0E0	9.1E-1
SMART	SAP	RT		4	9.5E-1	7.1E-1	1.0E0	9.5E-1
Annotation Cluster 317	**Enrichment Score: 0.09**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:CS	RT		3	7.0E-1	1.3E0	1.0E0	9.6E-1
INTERPRO	CS-like domain	RT		3	7.9E-1	1.1E0	1.0E0	9.1E-1
INTERPRO	HSP20-like chaperone	RT		3	9.5E-1	6.6E-1	1.0E0	9.5E-1
Annotation Cluster 318	**Enrichment Score: 0.06**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Nuclear pore complex	RT		7	7.6E-1	9.6E-1	1.0E0	7.8E-1
GOTERM_BP_DIRECT	tRNA export from nucleus	RT		4	9.2E-1	7.4E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	regulation of glucose transport	RT		4	9.3E-1	7.2E-1	1.0E0	9.6E-1
Annotation Cluster 319	**Enrichment Score: 0.05**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Ig-like 3	RT		3	7.9E-1	1.1E0	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like 1	RT		3	9.4E-1	7.0E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:Ig-like 2	RT		3	9.4E-1	7.0E-1	1.0E0	9.6E-1
Annotation Cluster 320	**Enrichment Score: 0.05**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	3',5'-cyclic-nucleotide phosphodiesterase activity	RT		4	7.7E-1	1.0E0	1.0E0	8.9E-1
INTERPRO	3'5'-cyclic nucleotide phosphodiesterase	RT		3	8.4E-1	9.8E-1	1.0E0	9.1E-1
INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, conserved site	RT		3	8.7E-1	8.9E-1	1.0E0	9.1E-1
INTERPRO	3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	RT		3	8.9E-1	8.5E-1	1.0E0	9.1E-1
INTERPRO	HD/PDEase domain	RT		3	9.1E-1	8.1E-1	1.0E0	9.1E-1
UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	RT		3	9.3E-1	7.3E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	RT		3	9.3E-1	7.3E-1	1.0E0	9.6E-1
SMART	HDc	RT		3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 321	**Enrichment Score: 0.05**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:DEP	RT		3	7.9E-1	1.1E0	1.0E0	9.6E-1
INTERPRO	DEP domain	RT		3	9.1E-1	8.1E-1	1.0E0	9.1E-1
SMART	DEP	RT		3	9.8E-1	5.5E-1	1.0E0	9.8E-1
Annotation Cluster 322	**Enrichment Score: 0.04**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Kelch-like protein, gigaxonin	RT		7	6.9E-1	1.0E0	1.0E0	9.1E-1
GOTERM_CC_DIRECT	Cul3-RING ubiquitin ligase complex	RT		10	7.5E-1	9.5E-1	1.0E0	8.8E-1
PIR_SUPERFAMILY	kelch-like protein, gigaxonin type	RT		7	8.1E-1	9.1E-1	1.0E0	1.0E0
INTERPRO	Galactose oxidase, beta-propeller	RT		4	8.7E-1	8.5E-1	1.0E0	9.1E-1
UP_SEQ_FEATURE	repeat:Kelch 6	RT		6	9.0E-1	7.9E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Kelch 5	RT		7	9.4E-1	7.2E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:BACK	RT		3	9.5E-1	6.8E-1	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?			Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	BTB/Kelch-associated	RT		7	9.5E-1	7.0E-1	1.0E0	9.5E-1
UP_SEQ_FEATURE	repeat:Kelch 4	RT		7	9.6E-1	6.8E-1	1.0E0	9.6E-1
INTERPRO	Kelch repeat type 1	RT		7	9.6E-1	6.8E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Kelch 1	RT		7	9.6E-1	6.7E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Kelch 2	RT		7	9.6E-1	6.7E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:Kelch 3	RT		7	9.6E-1	6.7E-1	1.0E0	9.6E-1
UP_KEYWORDS	Kelch repeat	RT		7	9.6E-1	6.7E-1	1.0E0	9.6E-1
INTERPRO	Kelch-type beta propeller	RT		4	9.9E-1	4.7E-1	1.0E0	9.9E-1
SMART	Kelch	RT		7	1.0E0	4.9E-1	1.0E0	1.0E0
SMART	SM00875	RT		7	1.0E0	4.7E-1	1.0E0	1.0E0
Annotation Cluster 323	**Enrichment Score: 0.03**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Heparin-binding growth factor/Fibroblast growth factor	RT		3	8.9E-1	8.5E-1	1.0E0	9.1E-1
INTERPRO	Cytokine, IL-1-like	RT		4	9.2E-1	7.5E-1	1.0E0	9.2E-1
SMART	FGF	RT		3	9.8E-1	5.5E-1	1.0E0	9.8E-1
Annotation Cluster 324	**Enrichment Score: 0.02**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:G-patch	RT		3	8.7E-1	8.9E-1	1.0E0	9.6E-1
INTERPRO	G-patch domain	RT		3	9.7E-1	5.8E-1	1.0E0	9.7E-1
SMART	G_patch	RT		3	1.0E0	3.9E-1	1.0E0	1.0E0
Annotation Cluster 325	**Enrichment Score: 0.02**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Host cell receptor for virus entry	RT		7	9.2E-1	7.5E-1	1.0E0	9.2E-1
GOTERM_BP_DIRECT	viral entry into host cell	RT		10	9.4E-1	7.4E-1	1.0E0	9.6E-1
GOTERM_MF_DIRECT	virus receptor activity	RT		7	9.8E-1	6.0E-1	1.0E0	9.8E-1
Annotation Cluster 326	**Enrichment Score: 0.02**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_KEYWORDS	Cilium biogenesis/degradation	RT		17	9.3E-1	7.9E-1	1.0E0	9.3E-1
GOTERM_BP_DIRECT	cilium morphogenesis	RT		18	9.4E-1	7.8E-1	1.0E0	9.6E-1
GOTERM_BP_DIRECT	cilium assembly	RT		14	9.8E-1	6.7E-1	1.0E0	9.8E-1
Annotation Cluster 327	**Enrichment Score: 0.02**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:LisH	RT		3	9.3E-1	7.3E-1	1.0E0	9.6E-1
INTERPRO	LisH dimerisation motif	RT		3	9.5E-1	6.6E-1	1.0E0	9.5E-1
SMART	LisH	RT		3	9.9E-1	5.3E-1	1.0E0	9.9E-1
Annotation Cluster 328	**Enrichment Score: 0.01**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Zinc finger, B-box	RT		11	8.7E-1	8.3E-1	1.0E0	9.1E-1
UP_SEQ_FEATURE	zinc finger region:B box-type	RT		8	8.9E-1	8.0E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	domain:B30.2/SPRY	RT		10	9.6E-1	7.0E-1	1.0E0	9.6E-1
INTERPRO	SPla/RYanodine receptor SPRY	RT		10	9.8E-1	6.6E-1	1.0E0	9.8E-1
INTERPRO	B30.2/SPRY domain	RT		10	9.9E-1	6.3E-1	1.0E0	9.9E-1
INTERPRO	SPRY-associated	RT		4	9.9E-1	5.0E-1	1.0E0	9.9E-1
SMART	BBOX	RT		10	1.0E0	5.5E-1	1.0E0	1.0E0
INTERPRO	Butyrophylin-like	RT		5	1.0E0	4.3E-1	1.0E0	1.0E0
SMART	PRY	RT		4	1.0E0	3.3E-1	1.0E0	1.0E0
SMART	SPRY	RT		10	1.0E0	4.4E-1	1.0E0	1.0E0
INTERPRO	Concanavalin A-like lectin/glucanase, subgroup	RT		13	1.0E0	3.5E-1	1.0E0	1.0E0
Annotation Cluster 329	**Enrichment Score: 0.01**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	zinc finger region:FYVE-type	RT		4	9.4E-1	7.0E-1	1.0E0	9.6E-1
INTERPRO	Zinc finger, FYVE-type	RT		3	9.6E-1	6.4E-1	1.0E0	9.6E-1
INTERPRO	Zinc finger, FYVE-related	RT		3	9.8E-1	5.5E-1	1.0E0	9.8E-1
SMART	FYVE	RT		3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 330	**Enrichment Score: 0.01**			**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_MF_DIRECT	histone demethylase activity	RT		3	9.2E-1	7.8E-1	1.0E0	9.2E-1
UP_SEQ_FEATURE	domain:JmjC	RT		3	9.6E-1	6.4E-1	1.0E0	9.6E-1

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	JmjC domain	RT		3	9.8E-1	5.6E-1	1.0E0	9.8E-1
SMART	JmjC	RT		3	1.0E0	4.2E-1	1.0E0	1.0E0
UP_KEYWORDS	Dioxygenase	RT		5	1.0E0	4.1E-1	1.0E0	1.0E0
Annotation Cluster 331	**Enrichment Score: 0.01**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Ras-association	RT		4	9.7E-1	6.2E-1	1.0E0	9.7E-1
UP_SEQ_FEATURE	domain:Ras-associating	RT		3	9.7E-1	6.0E-1	1.0E0	9.7E-1
SMART	RA	RT		3	1.0E0	4.2E-1	1.0E0	1.0E0
Annotation Cluster 332	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	repeat:22	RT		4	9.5E-1	6.6E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:21	RT		4	9.6E-1	6.3E-1	1.0E0	9.6E-1
UP_SEQ_FEATURE	repeat:24	RT		3	9.7E-1	6.0E-1	1.0E0	9.7E-1
UP_SEQ_FEATURE	repeat:20	RT		4	9.7E-1	5.9E-1	1.0E0	9.7E-1
UP_SEQ_FEATURE	repeat:19	RT		4	9.8E-1	5.7E-1	1.0E0	9.8E-1
UP_SEQ_FEATURE	repeat:18	RT		4	9.8E-1	5.6E-1	1.0E0	9.8E-1
UP_SEQ_FEATURE	repeat:1	RT		27	9.9E-1	7.2E-1	1.0E0	9.9E-1
UP_SEQ_FEATURE	repeat:2	RT		27	9.9E-1	7.1E-1	1.0E0	9.9E-1
UP_SEQ_FEATURE	repeat:17	RT		4	9.9E-1	4.9E-1	1.0E0	9.9E-1
UP_SEQ_FEATURE	repeat:16	RT		4	1.0E0	4.5E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:8	RT		10	1.0E0	5.5E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:9	RT		8	1.0E0	5.1E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:6	RT		12	1.0E0	5.6E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:10	RT		7	1.0E0	4.9E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:11	RT		6	1.0E0	4.6E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:7	RT		10	1.0E0	5.1E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:3	RT		19	1.0E0	5.8E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:12	RT		5	1.0E0	4.0E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:15	RT		4	1.0E0	3.7E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:4	RT		15	1.0E0	5.3E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:14	RT		4	1.0E0	3.4E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:5	RT		11	1.0E0	4.7E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	repeat:13	RT		4	1.0E0	3.2E-1	1.0E0	1.0E0
Annotation Cluster 333	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:PH	RT		25	9.9E-1	7.0E-1	1.0E0	9.9E-1
INTERPRO	Pleckstrin homology domain	RT		25	1.0E0	5.7E-1	1.0E0	1.0E0
INTERPRO	Pleckstrin homology-like domain	RT		40	1.0E0	5.8E-1	1.0E0	1.0E0
SMART	PH	RT		24	1.0E0	3.7E-1	1.0E0	1.0E0
Annotation Cluster 334	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	peroxisome	RT		9	1.0E0	5.5E-1	1.0E0	1.0E0
UP_KEYWORDS	Peroxisome	RT		6	1.0E0	4.2E-1	1.0E0	1.0E0
KEGG_PATHWAY	Peroxisome	RT		6	1.0E0	3.8E-1	1.0E0	1.0E0
Annotation Cluster 335	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
GOTERM_CC_DIRECT	mitochondrial matrix	RT		37	9.9E-1	7.2E-1	1.0E0	9.9E-1
UP_SEQ_FEATURE	transit peptide:Mitochondrion	RT		39	1.0E0	5.5E-1	1.0E0	1.0E0
GOTERM_CC_DIRECT	mitochondrial inner membrane	RT		37	1.0E0	5.3E-1	1.0E0	1.0E0
UP_KEYWORDS	Transit peptide	RT		43	1.0E0	5.5E-1	1.0E0	1.0E0
UP_KEYWORDS	Mitochondrion	RT		109	1.0E0	6.7E-1	1.0E0	1.0E0
Annotation Cluster 336	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
INTERPRO	Chemokine interleukin-8-like domain	RT		3	1.0E0	4.0E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	chemokine activity	RT		3	1.0E0	3.6E-1	1.0E0	1.0E0
GOTERM_BP_DIRECT	chemokine-mediated signaling pathway	RT		4	1.0E0	3.3E-1	1.0E0	1.0E0
SMART	SCY	RT		3	1.0E0	2.8E-1	1.0E0	1.0E0
BBID	109.Chemokine_families	RT		3	1.0E0	3.0E-1	1.0E0	1.0E0
Annotation Cluster 337	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:DH	RT		4	1.0E0	4.0E-1	1.0E0	1.0E0
GOTERM_BP_DIRECT	regulation of Rho protein signal transduction	RT		6	1.0E0	4.4E-1	1.0E0	1.0E0
INTERPRO	Dbl homology (DH) domain	RT		4	1.0E0	3.5E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	Rho guanyl-nucleotide exchange factor activity	RT		4	1.0E0	3.1E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	guanyl-nucleotide exchange factor activity	RT		6	1.0E0	3.0E-1	1.0E0	1.0E0
SMART	RhoGEF	RT		4	1.0E0	2.4E-1	1.0E0	1.0E0
UP_KEYWORDS	Guanine-nucleotide releasing factor	RT		5	1.0E0	2.3E-1	1.0E0	1.0E0
Annotation Cluster 338	**Enrichment Score: 0**	G		**Count**	**P_Value**	**Fold Change**	**Benjamini**	**FDR**
UP_SEQ_FEATURE	domain:Rho-GAP	RT		3	1.0E0	3.0E-1	1.0E0	1.0E0
INTERPRO	Rho GTPase activation protein	RT		5	1.0E0	3.4E-1	1.0E0	1.0E0

Annotation Cluster 1	Enrichment Score: ?	G		Count	P_Value	Fold Change	Benjamini	FDR
INTERPRO	Rho GTPase-activating protein domain	RT		3	1.0E0	2.8E-1	1.0E0	1.0E0
UP_KEYWORDS	GTPase activation	RT		9	1.0E0	3.1E-1	1.0E0	1.0E0
SMART	RhoGAP	RT		3	1.0E0	1.9E-1	1.0E0	1.0E0
GOTERM_MF_DIRECT	GTPase activator activity	RT		15	1.0E0	3.2E-1	1.0E0	1.0E0
Annotation Cluster 339	**Enrichment Score: 0**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_SEQ_FEATURE	DNA-binding region:Basic motif	RT		10	1.0E0	4.2E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	RT		5	1.0E0	3.0E-1	1.0E0	1.0E0
INTERPRO	Myc-type, basic helix-loop-helix (bHLH) domain	RT		5	1.0E0	2.7E-1	1.0E0	1.0E0
SMART	HLH	RT		5	1.0E0	1.8E-1	1.0E0	1.0E0
Annotation Cluster 340	**Enrichment Score: -0**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Cell membrane	RT		320	1.0E0	6.9E-1	1.0E0	1.0E0
GOTERM_CC_DIRECT	plasma membrane	RT		457	1.0E0	7.0E-1	1.0E0	1.0E0
UP_KEYWORDS	Membrane	RT		612	1.0E0	5.6E-1	1.0E0	1.0E0
Annotation Cluster 341	**Enrichment Score: -0**	G		Count	P_Value	Fold Change	Benjamini	FDR
UP_KEYWORDS	Glycoprotein	RT		276	1.0E0	4.2E-1	1.0E0	1.0E0
UP_KEYWORDS	Signal	RT		267	1.0E0	4.4E-1	1.0E0	1.0E0
GOTERM_CC_DIRECT	integral component of membrane	RT		288	1.0E0	3.5E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	signal peptide	RT		219	1.0E0	4.5E-1	1.0E0	1.0E0
UP_KEYWORDS	Receptor	RT		108	1.0E0	4.5E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		217	1.0E0	3.5E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	disulfide bond	RT		161	1.0E0	3.8E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	topological domain:Cytoplasmic	RT		175	1.0E0	3.4E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	topological domain:Extracellular	RT		145	1.0E0	3.5E-1	1.0E0	1.0E0
UP_SEQ_FEATURE	transmembrane region	RT		226	1.0E0	3.0E-1	1.0E0	1.0E0
GOTERM_CC_DIRECT	integral component of plasma membrane	RT		100	1.0E0	4.5E-1	1.0E0	1.0E0
UP_KEYWORDS	Disulfide bond	RT		204	1.0E0	4.1E-1	1.0E0	1.0E0
UP_KEYWORDS	Transmembrane	RT		312	1.0E0	3.8E-1	1.0E0	1.0E0
UP_KEYWORDS	Transmembrane helix	RT		309	1.0E0	3.8E-1	1.0E0	1.0E0
UP_KEYWORDS	Membrane	RT		612	1.0E0	5.6E-1	1.0E0	1.0E0

3237 terms were not clustered.