

Supplementary Table 3: Results of the pathway analysis by the David tool on the proteins modulated in response to PCL beads

Annotation Cluster 1 Category	Enrichment Score: 21.94533929185782 Term	Count	P-Value	Genes	FDR
UP_SEQ_FEATURE	CROSSLINK:Glycyl Lysine Isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2)	62	6.7828565E-37	P23198, Q60864, Q9Z277, Q8BTM8, P62082, P13864, P63166, P42225, D3YXK2, Q9Z1F9, Q9JIX8, P20152, O88532, Q9CRB2, Q569Z6, P46061, P61957, P56960, Q99ME9, Q61164, P21619, P48678, P62889, P17918, P62962, O88286, Q9D8W5, Q8IZX4, P10854, P48036, Q501J6, Q9K48, P11103, P14733, P10853, Q80X82, Q8VJL6, Q9J1I3, P17095, Q9CQV8, E9Q7G0, P62827, P14869, P63280, P68254, Q64012, Q91VE6, Q8C2Q3, Q3U0V1, P67871, P47962, Q9QZQ8, P17182, Q9D0E1, Q9R190, Q9CQI7, E9PVX6	1.13070217303663E-33
UP_SEQ_FEATURE	CROSSLINK:Glycyl Lysine Isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2)	87	5.0671786E-24	Q8K114, P23198, Q9Z277, Q9CZW5, Q99L45, P62082, P13864, P56959, Q61550, Q61990, P63166, Q9Z2D8, Q8BHB4, P35980, D3YXK2, Q9Z1F9, P60335, Q9JIX8, P20152, O88532, Q9CRB2, P47713, Q6Y7W8, Q569Z6, Q61686, P46061, Q9CQ37, P61957, Q60710, Q9CX56, P56960, Q99ME9, P97315, Q61164, Q64511, P21619, P48678, P17918, Q9WVA4, O88286, Q9CWX3, Q9CX86, Q60520, Q9CXV6, Q8IZX4, Q8BHX3, Q6ZQ58, P83917, Q9CZU3, Q501J6, Q99K48, P11103, P14733, Q80X82, Q9D1Q1, Q8VJL6, Q8C854, Q9QYJ0, Q3UA37, Q8R2M2, Q91XV3, O88271, E9Q7G0, Q3TEA8, P62827, Q9D8N0, Q91WK2, Q9Z2K7, P97379, P63280, Q64012, Q8BGD9, Q91VE6, Q3UEB3, Q3V300, Q8C2Q3, Q9D8E6, P62702, Q9QZQ8, Q9D0E1, O88466, P63038, B1AXP6, Q8BIQ5, P41105, Q9R190, E9PVX6	4.22349336785982E-21
UP_KW_PTM	KW-1017~Isopeptide bond	132	2.0542606E-18	Q8K114, Q60864, P56477, Q9CZW5, P13864, P62082, Q9Z2D3, Q61550, P42225, P63166, Q9Z2D8, Q8BHB4, P60335, Q9JIX8, P20152, Q569Z6, Q61686, Q9CQ37, P61957, Q99LX0, Q61164, P48678, P62889, O88286, Q9CX86, Q9D8W5, Q9CXV6, P97287, Q8BHX3, P83917, P10854, P48036, Q9CZU3, Q99K48, P10853, Q9D1Q1, Q8C854, P17095, Q8R2M2, Q91XV3, O88271, Q3TEA8, Q9D8N0, P62827, Q91WK2, P68254, Q9WTK5, Q64012, Q8BGD9, Q3V300, Q8C2Q3, Q9D8E6, Q3U0V1, P47962, Q9QZQ8, P62702, Q9D0E1, B1AXP6, Q8BIQ5, Q99L45, A2A432, P56959, Q61990, P17751, P40124, P35980, Q9Z1F9, D3YXK2, Q35609, O88532, Q9CRB2, P47713, Q6Y7W8, P46061, Q80X90, Q60710, Q9CX56, P56960, Q99ME9, P97315, Q64511, P21619, Q61093, P17918, Q9WVA3, P62962, Q9WVA4, Q9CWX3, Q60520, Q8IZX4, Q6ZQ58, Q501J6, P11103, P14733, Q80X82, P31750, Q8VJL6, Q9QYJ0, Q9J1I3, Q3UA37, O88351, Q9CQV8, Q60931, E9Q7G0, P14869, Q9Z2K7, P97379, Q8R5F7, P63280, Q8VCF0, Q61462, Q91VE6, Q3UEB3, P67871, P17182, O88466, P63038, Q9R190, E9PVX6	1.84883454990359E-17

UP_KW_PTM	KW-0832~Ub1 conjugation	153	2.3431951E-11	Q99KW3, Q8K114, Q9D8Y7, Q60864, P56477, Q9CZW5, Q9JMH6, Q9WVL2, P13864, P62082, Q9Z2D3, Q61550, P42225, P63166, Q9Z2D8, Q8BHB4, P60335, Q9IIX8, A11314, P20152, Q9IIZ4, Q56926, Q61686, Q9CQ37, P61957, Q99LX0, Q61164, Q9D071, P52293, P48678, P62889, O88286, Q9CX86, Q9D8W5, Q9CXV6, P97287, Q8BHX3, P83917, P10854, P48036, Q9CZU3, Q99K48, P10853, Q9DIQ1, Q8C854, P17095, Q8R2M2, Q91XV3, O88271, Q3TEA8, Q9D8N0, P62827, Q91WK2, P68254, P32233, Q9WTK5, Q64012, Q64378, Q8BGD9, Q3V300, Q8C2Q3, Q9D8E6, Q3U0V1, P47962, Q9QZQ8, P62702, Q9D0E1, B1AXP6, Q8BIQ5, Q8CIN4, P57080, P41105, Q9CQ17, Q70456, P23198, P10711, Q9Z277, Q8BTM8, Q99145, A2A432, P56959, Q61990, P17751, P40124, P35980, Q9Z1F9, D3YXK2, Q35609, O88332, Q3UCV8, Q9CRB2, P47713, Q6Y7W8, P46061, Q80X90, Q60710, Q9CX56, P56960, Q99ME9, P97315, P54823, Q64511, P21619, Q61093, P17918, Q9WVA3, P62962, Q9WVA4, Q9CWK3, O89053, Q60520, Q8IZX4, Q6ZQ58, Q50116, P11103, P14733, Q80X82, P31750, Q9CUE2, Q8VJ16, P09671, P57791, Q9QY10, Q9J113, Q3UA37, O88351, Q9CQV8, Q60931, E9Q7G0, P14869, Q922K7, P97379, Q8R5F7, P63280, Q8VCF0, Q61462, Q91VE6, Q3UEB3, Q9D0R2, P67871, P17182, P83940, O88466, P25911, P63038, Q9R190, E9PVX6	1.40591707217304E-10
-----------	-------------------------	-----	---------------	---	----------------------

Annotation Cluster 2	Enrichment Score: 14.715355384679746				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0002181~cytoplasmic translation	30	2.8878557E-24	P51410, P99027, P14869, P62082, P32223, P62281, P14115, P14148, P62892, P63323, P35980, Q9D8E6, P62274, P47962, P62702, P62889, P26638, P62852, P62830, P41105	7.41890138930357E-21
GOTERM_BP_DIRECT	GO:0006412~translation	44	8.298166E-24	Q9JKE7, O70194, Q9Z1D1, Q99145, P62082, P62281, P14115, P31750, P62892, P63323, Q8BML9, P35980, P62274, P26638, Q8QZY1, Q6PGC1, P62830, Q99JT1, P51410, Q9D8N0, Q99LC8, Q91WK2, Q9ER72, P14148, P57776, Q8BCG9, Q8IZQ9, Q9D0R2, Q9D8E6, P47962, P62702, P60229, P41105, Q9D019	1.06589941989972E-20
GOTERM_CC_DIRECT	GO:1990904~ribonucleoprotein complex	44	1.7577874E-20	Q9CX86, Q9CXV6, Q61733, Q9JKE7, P99027, Q9CQQ8, Q8BK72, Q50116, P62082, Q80WS3, Q9JKE1, P62281, P52912, P14115, Q61990, Q62189, P62892, P63323, P62311, P35980, Q8C854, P62274, P60335, Q9CRB2, P62852, P62830, Q61686, Q8VE97, P51410, P14869, P97379, Q64012, P14148, Q3UEB3, Q9CQV5, Q64511, Q8K2F8, Q9D8E6, P47962, P62702, P62889, Q9D0E1, P41105, Q9CQ17	1.27565144683596E-18
GOTERM_CC_DIRECT	GO:0005840~ribosome	34	2.1759868E-20	P11928, P51410, Q61733, Q9JKE7, P99027, P14869, Q8BK72, P62082, P62281, P14115, P14148, Q9CQV5, Q9JKE5, P62892, P63323, P35980, Q9D8E6, P62274, P47962, P62702, P62889, P62852, P62830, P41105	1.3817516135234E-18
GOTERM_BP_DIRECT	GO:0140236~translation at presynapse	20	2.7977969E-18	P51410, P63323, P99027, Q9D8E6, P47962, P62281, P14115, P14148, P62830, P41105	2.39584672438355E-15
GOTERM_BP_DIRECT	GO:0140242~translation at postsynapse	20	3.8833945E-18	P51410, P63323, P99027, Q9D8E6, P47962, P62281, P14115, P14148, P62830, P41105	2.4941101493982E-15
UP_KW_MOLECULAR_FUNCTION	KW-0687~Ribonucleoprotein	45	4.2960098E-18	Q9CX86, Q61733, Q9JKE7, P99027, Q9CQQ8, Q8BK72, P62082, Q80WS3, P62281, P14115, Q61990, Q62189, P62892, P63323, P62311, P35980, P62274, P60335, Q9CRB2, P62852, P62830, P51410, P14869, Q64012, P14148, Q3UEB3, Q9CQV5, Q8K2F8, Q9D8E6, P47962, P62702, P62889, Q9D0E1, P41105, Q9CQ17	2.9212866530764E-16
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	31	1.5010747E-16	P51410, Q61733, Q9JKE7, P99027, P14869, P62082, P62281, P14115, P14148, Q9CQV5, P62892, P63323, P35980, Q9D8E6, P62274, P47962, P62702, P62889, P62852, P62830, P41105	2.10400634199175E-14
INTERPRO	IPR000530:Ribosomal_eS12	11	8.8765682E-16	P63323	7.76255887293619E-13
INTERPRO	IPR047860:Ribosomal_eS12_CS	11	8.8765682E-16	P63323	7.76255887293619E-13

GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	24	9.2626355E-16	P51410, P99027, P14869, P14115, P14148, P62892, P63323, P35980, Q9D8E6, P47962, P62889, Q9CRB2, P62830, P41105	4.27765347218431E-14
GOTERM_CC_DIRECT	GO:0032040~small-subunit processome	20	1.9555234E-15	Q8R5K4, P63323, Q8BBH4, P56960, Q91113, P62702, Q80W53, P62082, P62281, Q8R2M2	8.27838232896555E-14
GOTERM_BP_DIRECT	GO:0042274~ribosomal small subunit biogenesis	20	1.9726394E-15	Q8R5K4, P63323, Q8BBH4, P56960, Q91113, P62702, P62082, P62281, P62852, Q8R2M2	8.44618441031934E-13
UP_KW_MOLECULAR_FUNCTION	KW-0689~Ribosomal protein	32	2.9297568E-14	P51410, Q61733, Q91KF7, P99027, P14869, Q8BK72, P62082, P62281, P14115, P14148, Q9CQV5, P62892, P63323, P35980, Q9D8E6, P62274, P47962, P62702, P62889, P62852, P62830, P41105	6.64078209305209E-13
GOTERM_CC_DIRECT	GO:0098793~presynapse	33	4.7320975E-14	P51410, Q9EQH3, P61957, P99027, Q99LX0, Q62418, P62281, P14115, P14148, Q64324, P40124, P62331, O08553, P63323, Q9CVB6, P68510, Q9D8E6, P47962, P22892, P61982, P62962, P62830, P41105	1.84915808939598E-12
GOTERM_CC_DIRECT	GO:0045202~synapse	58	2.230734E-13	O89053, Q9CX86, Q80UY2, O70435, P99027, P97300, O70194, Q8BFZ3, Q99L45, P62082, P62281, P14115, O08553, P63323, O35864, Q9CVB6, P35980, P68510, G5E829, Q8QZY1, P61982, P62852, P62830, Q8BH43, P51410, Q9EQH3, P14869, Q62418, P68254, O35382, Q6WVG3, P14148, P57776, Q81ZQ9, Q99199, Q76MZ3, O55100, O55101, P67778, P84078, Q9D8E6, P47962, P62702, P62746, P62889, Q9D0E1, P41105, P21278	6.66595798948274E-12
GOTERM_CC_DIRECT	GO:0098794~postsynapse	34	2.4801003E-13	P51410, Q9EQH3, P61957, P99027, P14869, Q62418, Q8BTM8, P62082, P62281, P14115, P14148, P17426, P40124, P62331, P63323, Q9CVB6, Q8VDC3, Q9D8E6, P47962, P62889, P27601, P62962, P62830, P41105	6.99939415536949E-12
INTERPRO	IPR004038:Ribosomal_eL8/eL30/eS12/Gad45	13	6.082703E-13	P63323, P62889, Q9CRB2	3.54621585582084E-10
INTERPRO	IPR029064:Ribosomal_eL30-like_sf	13	4.5099243E-12	P63323, P62889, Q9CRB2	1.9719644103581E-09
GOTERM_CC_DIRECT	GO:0022626~cytosolic ribosome	17	3.5922927E-10	P51410, P14869, P62082, P62281, P14115, P14148, P62892, P63323, P35980, Q9D8E6, Q80YR4, P47962, P62702, P62889, P62852, P62830, P41105	8.68992714377449E-09
KEGG_PATHWAY	mmu05171:Coronavirus disease - COVID-19	38	1.7360083E-09	P11928, P99027, Q9WVL2, P62082, P62281, P14115, P42225, P62892, P63323, P35980, Q920F8, P62274, P62852, P62830, O88351, Q8V193, P51410, P14869, P08508, Q8R5F7, Q8VCF0, P14148, Q61093, Q9D8E6, P47962, P62702, P62889, P41105	4.68722234315802E-07
KEGG_PATHWAY	mmu03010:Ribosome	28	1.6063061E-06	P51410, P99027, P14869, P62082, P62281, P14115, P14148, P62892, P63323, P35980, Q9D8E6, P62274, P47962, P62702, P62889, P62852, P62830, P41105	0.000120456334736
Annotation Cluster 3 Category	Enrichment Score: 13.10698403192111 Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	110	7.1650835E-27	Q8CAQ8, P10639, Q9CR68, O08709, Q9CZW5, Q9JMH6, Q8BK72, P38647, O08553, Q9CZM7, P16460, Q8BGH2, Q99T11, Q61207, Q99LX0, P54987, Q9D1R1, Q99KE1, P67778, Q9CZU6, P54071, Q8R5K4, P97287, Q91WD5, Q8K2B3, P47738, Q9D3D9, P17095, P26638, Q6PGC1, P62897, Q91VR2, Q9D6R2, P53395, Q9D051, Q991R1, Q99199, Q9CQA3, Q04447, P38060, P29758, B1AXP6, P05202, P07742, P11928, O70579, Q81ZRO, P37913, Q91LJ2, Q64105, P36552, Q9CRB9, Q91HR7, Q9CZ13, Q9DCZ4, P45377, P41216, P08249, P10605, Q64516, Q81ZQ2, P19783, Q9CQX2, O08756, Q9JIK5, P16675, Q9Z219, Q61093, Q9Z0V7, Q99LC5, Q8QZT1, Q8K411, P26443, Q62425, Q61733, Q91KF7, P11103, P50516, P50637, P31750, Q9CPR4, Q9CWI9, P97807, Q3TL44, P09671, Q9QUJ7, Q9DCX2, Q91M90, P21300, Q9CQNI, P08228, Q9EQH3, Q60931, P51174, Q791V5, Q8R5F7, P39749, Q8VCF0, Q61462, Q9CQV5, Q991V5, O88986, Q80Y14, Q9Z110, P63038, P28867, Q91Y5, Q9D019, Q9DCW4	7.27972488165232E-25

GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	41	1.1090957E-13	Q8CAQ8, P26443, Q9CR68, Q62425, Q61733, Q9JKE7, Q8IZR0, Q8BK72, Q91WD5, Q8K2B3, Q9CZNT, P36552, Q9CRB9, P09671, Q9D3D9, Q9CZ13, Q9DCZ4, Q8BGH2, Q9DCX2, P08249, Q91VR2, Q9CQNI, Q60931, Q791V5, Q8IZQ2, P19783, Q9CQX2, Q08756, Q9CQV5, Q99JRI, Q99J99, P67778, Q9CQA3, Q88986, P38060, Q9Z0V7, Q9Z110, P63038, P54071, Q8QZT1, P05202	4.02443281914598E-12
UP_KW_DOMAIN	KW-0809~Transit peptide	42	1.0487526E-12	Q8K411, Q8CAQ8, P26443, Q9CR68, Q61733, Q8BK72, P38647, Q91WD5, Q8K2B3, P97807, Q9CZNT, P47738, Q3TL44, P36552, P09671, Q9D3D9, Q9CZ13, P08249, Q91VR2, Q99JTI, Q9D6R2, Q9CQNI, P51174, P53395, Q8IZQ2, P19783, Q9D051, Q9CQV5, Q99KE1, Q9CQA3, Q9Z219, Q88986, Q80Y14, P38060, Q9CZU6, Q99LC5, P29758, P63038, Q9JIV5, P54071, Q8QZT1, P05202	1.99262989688746E-11
UP_KW_CELLULAR_COM PONENT	KW-0496~Mitochondrion	79	1.4206966E-10	Q8CAQ8, Q9CR68, P11928, Q8IZR0, Q9CZW5, Q8BK72, P38647, Q9CZNT, P36552, Q9CRB9, Q9CZ13, Q8BGH2, Q9DCZ4, P41216, P08249, Q99JTI, Q64516, Q99LX0, Q8IZQ2, P19783, Q9CQX2, Q08756, P54987, Q9JIK5, Q9D1R1, Q99KE1, P67778, Q9Z219, Q9Z0V7, Q9CZU6, Q99LC5, P54071, Q8QZT1, Q8K411, P26443, P97287, Q62425, Q61733, Q9JKE7, P50637, Q91WD5, Q8K2B3, Q9CPI4, P97807, P47738, Q3TL44, P09671, Q9D3D9, Q9QUI7, Q9DCX2, Q9JM90, P62897, Q91VR2, Q9D6R2, Q9CQNI, Q60931, P51174, Q791V5, P53395, Q8R5F7, Q9D051, P39749, Q8VCF0, Q9CQV5, Q99JRI, Q99J99, Q9CQA3, Q88986, Q04447, Q80Y14, P38060, Q9Z110, P63038, P29758, B1AXP6, Q9JIV5, P28867, Q9DCW4, P05202	1.4206966392078E-09
UP_SEQ_FEATURE	TRANSIT:Mitochondrion	41	2.4088302E-10	Q8K411, Q8CAQ8, P26443, Q61733, Q8BK72, P38647, Q91WD5, Q8K2B3, P97807, Q9CZNT, P47738, Q3TL44, P36552, P09671, Q9D3D9, Q9CZ13, P08249, Q91VR2, Q99JTI, Q9D6R2, Q9CQNI, P51174, P53395, Q8IZQ2, P19783, Q9D051, Q9CQV5, Q99KE1, Q9CQA3, Q9Z219, Q88986, Q80Y14, P38060, Q9CZU6, Q99LC5, P29758, P63038, Q9JIV5, P54071, Q8QZT1, P05202	8.03103977960622E-08
GOTERM_CC_DIRECT	GO:0005759~mitochondrial matrix	22	7.9969608E-09	Q8K411, P26443, Q9CQNI, Q99LX0, P51174, P53395, P38647, Q99KE1, P97807, Q9CZNT, P47738, P09671, Q80Y14, P38060, Q9CZU6, Q99LC5, P29758, P63038, P08249, Q8QZT1, Q9DCW4, P05202	1.84657095461216E-07
Annotation Cluster 4 Category	Enrichment Score: 11.648105357022203 Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	97	2.214163E-22	Q8CG47, P38647, Q8BML9, P16460, P61021, P43274, P25206, Q9CQDI, Q6P9R2, Q9JIZ4, Q569Z6, Q99JTI, Q9CQ37, Q9ER72, Q8VDN2, Q9R008, P84096, Q9JIV9, Q88685, Q9CZU3, P26638, Q6PGCI, P27601, P62827, P32233, Q3V300, P61211, Q04447, Q8BHG9, Q8CIN4, P07742, Q8IZR0, Q9Z2F4, Q9Z277, Q8BFEZ, P37913, Q9JHR7, Q9Z1F9, P41216, Q64516, Q60710, P56960, Q99ME9, Q8IZQ2, Q9Z0E6, P54823, Q9JIK5, Q64511, P61750, Q9Z219, Q3UH66, P83887, E90634, P26443, Q9JKE7, Q9JIB3, Q50116, P50516, Q99KQ4, P31750, Q9CUI2, P62331, P36371, P49718, Q3TL44, Q9QUI7, G5E829, P62334, Q88351, Q9R061, Q62159, Q8V193, Q9ESTL4, Q9CQNI, Q60931, Q61107, Q64737, Q99K70, Q8R5F7, P63280, Q9EQP2, Q9DOR4, Q3UMI8, Q9DOR2, P84078, Q8BHK9, P08113, P62746, Q9Z110, P25911, Q9WUA3, P63038, P28867, Q9D019, P21278, E9PVX6, Q9DCW4	6.20703707954007E-20

GOTERM_MF_DIRECT	GO:0005524~ATP binding	76	1.8808007E-14	P11928, Q9D0M1, Q8CG47, Q8IZR0, Q9Z277, Q8BFEZ3, P38647, P37913, Q8BML9, Q9IHR7, P16460, Q9Z1F9, P43274, P25206, Q6P9R2, Q9IJZ4, P41216, Q569Z6, Q99JT1, Q9CQ37, Q64516, Q8IZQ2, Q9ER72, Q8VDN2, P54823, Q9IJK5, Q9R008, Q64511, Q9Z219, Q88685, Q3UH66, E9Q634, Q89051, P26443, Q9CZU3, Q9IIB3, Q50116, P50516, Q9E500, P31750, Q9CU62, P36371, P49718, Q3TL44, Q8CFE4, Q9QY10, Q9QUJ7, P26638, G5E829, Q6PGC1, P62334, Q88351, Q9R061, Q8V193, Q9ESL4, Q9CQNI, Q64737, Q8R5F7, P63280, Q9EQP2, Q9D0R4, Q9D0R2, Q3V300, Q8BHK9, Q04447, P08113, Q9Z110, P25911, P63038, Q8BH69, Q9WUA3, P28867, Q8CIN4, Q9D0I9, P07742, E9PVX6	2.25964773159815E-12
UP_KW_LIGAND	KW-0547~Nucleotide-binding	94	1.2196495E-07	P11928, Q8CG47, Q8IZR0, Q9Z277, Q8BFEZ3, P38647, P37913, Q8BML9, Q9IHR7, P16460, P61021, Q9Z1F9, P25206, Q6P9R2, Q9CQD1, Q9IJZ4, P41216, Q569Z6, Q99JT1, Q9CQ37, Q64516, Q60710, Q99ME9, Q8IZQ2, Q9Z0E6, Q9ER72, Q8VDN2, P54823, Q9IJK5, Q9R008, Q64511, P84096, P61750, Q9Z219, Q9IIV9, Q88685, Q3UH66, P83887, E9Q634, P26443, Q9CZU3, Q9IIB3, Q50116, P50516, P31750, Q9CU62, P62331, P36371, P49718, Q3TL44, Q9QUJ7, P26638, G5E829, Q6PGC1, P62334, P27601, Q88351, Q9R061, Q62159, Q8V193, Q9ESL4, Q9CQNI, Q60931, Q61107, Q99K70, P62827, Q64737, Q8R5F7, P63280, P32233, Q9EQP2, Q9D0R4, Q3UM18, Q9D0R2, Q3V300, P84078, P61211, Q8BHK9, Q04447, P08113, P62746, Q9Z110, P25911, P63038, Q8BH69, Q9WUA3, P28867, Q8CIN4, Q9D0I9, P07742, E9PVX6, P21278, Q9DCW4	3.65894854480029E-06
UP_KW_LIGAND	KW-0067~ATP-binding	70	5.0325853E-05	P11928, Q8CG47, Q8IZR0, Q9Z277, Q8BFEZ3, P38647, P37913, Q8BML9, Q9IHR7, P16460, Q9Z1F9, P25206, Q6P9R2, Q9IJZ4, P41216, Q569Z6, Q99JT1, Q9CQ37, Q64516, Q8IZQ2, Q9ER72, Q8VDN2, P54823, Q9IJK5, Q9R008, Q64511, Q9Z219, Q88685, Q3UH66, E9Q634, P26443, Q9CZU3, Q9IIB3, Q50116, P50516, P31750, Q9CU62, P36371, P49718, Q3TL44, Q9QUJ7, P26638, G5E829, Q6PGC1, P62334, Q88351, Q9R061, Q8V193, Q9ESL4, Q9CQNI, Q64737, Q8R5F7, P63280, Q9EQP2, Q9D0R4, Q9D0R2, Q3V300, Q8BHK9, Q04447, P08113, Q9Z110, P25911, P63038, Q8BH69, Q9WUA3, P28867, Q8CIN4, Q9D0I9, P07742, E9PVX6	0.000754887789642
Annotation Cluster 5 Category	Enrichment Score: 7.932871907538455 Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005694~chromosome	47	5.9440261E-16	Q8R5K4, Q8CG47, P10854, Q8BHX3, Q8BH74, Q99K48, Q9JMD0, P11103, Q61550, P15864, Q9CU62, Q9Z2D8, P97807, P49718, Q8K2Z4, P43274, Q3UHX9, P25206, P43275, Q8CFE2, P43276, Q88532, P43277, Q3UA16, Q35207, Q8R2M2, Q61686, P46061, Q88271, Q60710, E9Q7G0, Q3TEA8, P10922, Q9WU62, Q6RPD03, Q61164, Q9Z1E6, Q91VE6, Q6WKZ8, Q9IJK5, Q76MZ3, Q8VE37, Q8BHK9, Q9QZQ8, Q9WVA3, Q8BK67, E9PVX6	3.01956524689137E-14
UP_KW_CELLULAR_COM PONENT	KW-0158~Chromosome	51	1.6627328E-11	Q8R5K4, Q8CG47, Q8BHX3, P10854, Q8BH74, Q99K48, Q9JMD0, P11103, P10853, Q61550, P15864, Q9CU62, Q9Z2D8, P97807, P49718, P43274, P25206, Q8K2Z4, Q3UHX9, P17095, P43275, Q8CFE2, P43276, Q88532, P43277, Q3UA16, Q35207, Q61686, P46061, Q88271, Q60710, E9Q7G0, Q3TEA8, Q9WU62, P10922, Q6RPD03, Q9Z1E6, Q61164, Q6WKZ8, Q91VE6, Q76MZ3, Q8VE37, Q8BHK9, Q9QZQ8, Q9WVA3, Q8BK67, E9PVX6	2.21697712128473E-10
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	21	1.686596E-11	Q61686, P46061, P23198, Q8CG47, Q88271, Q8BHX3, P83917, Q8BH74, Q9WU62, Q9JMD0, Q6RPD03, Q61164, Q61550, Q9CU62, Q76MZ3, Q8BHK9, Q3UHX9, Q3UA16, Q9WVA3, Q8BK67, E9PVX6	4.50942505417899E-10

UP_KW_CELLULAR_COM PONENT	KW-0137~Centromere	17	3.9925526E-06	Q61686, P46061, O88271, Q8BHX3, Q8BH74, Q9WU62, Q9JMD0, Q6PD03, Q61164, Q61550, Q9CU62, Q76MZ3, Q8BHK9, Q3UHX9, Q3UA16, Q9WVA3, Q8BK67	3.19404211532792E-05
GOTERM_CC_DIRECT	GO:0000776~kinetochore	12	0.00040296966	Q60520, Q61686, P46061, O88271, Q8BH74, Q9WU62, Q8BHK9, Q3UHX9, Q9JMD0, Q3UA16, Q9CU62, Q9WVA3	0.003790899774262
UP_KW_CELLULAR_COM PONENT	KW-0995~Kinetochore	9	0.00942608411	P46061, O88271, Q8BH74, Q9WU62, Q8BHK9, Q3UHX9, Q9JMD0, Q3UA16, Q9WVA3	0.041893707151487
Annotation Cluster 6 Category	Enrichment Score: 6.796997709640492 Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0003723~RNA binding	81	2.0599842E-29	Q9CQ08, Q8BK72, P97789, P13864, P56959, P62281, P52912, Q61990, Q8K2D3, O35326, Q8BML9, P62311, P35980, Q62093, D3YXK2, P60335, Q9JIX8, P20152, O88532, Q9CRB2, P46061, Q9D554, Q3UPF5, Q60710, P56960, Q9LX0, Q99ME9, P54823, Q9JIK5, Q8IZQ9, Q8K2F8, P62889, P62488, Q8RSK4, Q9CX86, Q60520, Q8IZX4, Q9JKF7, Q6ZQ58, Q6R5N8, Q9CZU3, Q70194, Q50116, Q99K48, Q9Z1D1, Q80WS3, Q62189, Q9D1Q1, Q8VJI6, P17095, Q6PGC1, Q8R2M2, Q8VI94, Q8VI93, Q8VE97, Q9ESL4, Q9CQV1, Q922K7, P97379, Q8R5F7, Q64012, P14148, Q9D0R4, Q8BGD9, Q91VE6, Q3UEB3, O08583, Q8C2Q3, Q8VDG3, Q3U0V1, Q9D8E6, P47962, P62702, P08113, P17182, Q9D0E1, O88466, Q8BIQ5, Q9CQI7	8.66223376680121E-27
UP_KW_MOLECULAR_FUNCTION	KW-0694~RNA-binding	62	1.6341286E-14	P11928, Q9CQ08, Q8BK72, P97789, P56959, P62281, P52912, Q61990, Q8K2D3, O35326, P62311, Q62093, D3YXK2, P60335, O88532, Q9CRB2, Q569Z6, Q3UPF5, P56960, Q9LX0, P54823, Q9JIK5, Q8IZQ9, P62488, Q8R5K4, Q9CX86, Q8IZX4, Q6ZQ58, Q6R5N8, Q70194, Q50116, Q9JIX8, Q9Z1D1, Q80WS3, Q62189, Q9D1Q1, Q8VJI6, Q8C854, Q5SW19, Q8VI94, Q8VI93, Q8VE97, Q9ESL4, Q922K7, P97379, Q8R5F7, Q64012, P14148, Q9D0R4, Q8BGD9, Q91VE6, Q3UEB3, O08583, Q8C2Q3, Q8VDG3, Q3U0V1, P47962, P62702, Q9D0E1, O88466, Q8BIQ5, Q9CQI7	5.55603726987392E-13
GOTERM_MF_DIRECT	GO:0003676~nucleic acid binding	42	1.1583378E-13	Q9CX86, Q8IZX4, P10711, Q9CZU3, Q50116, Q99K48, Q9Z1D1, P97789, P52912, Q61990, Q62189, O35326, Q8VJI6, Q62093, D3YXK2, P60335, Q9JIX8, O88532, Q6PGC1, Q8VE97, Q60710, Q9D554, P03975, P56960, P97379, Q64012, P54823, Q9D0R4, Q91VE6, Q3UEB3, Q8BGD9, Q9JIK5, Q8IZQ9, Q8C2Q3, O08583, Q8VDG3, Q3U0V1, Q9D0E1, P62488, Q8BIQ5, Q9CQI7	1.08240235144362E-11
INTERPRO	IPR035979:RBD_domain_sf	27	4.0699586E-09	Q9CX86, Q8IZX4, Q99K48, Q9Z1D1, P52912, P56959, Q62189, O35326, Q8VJI6, Q62093, D3YXK2, Q8C854, Q9JIX8, Q8VE97, P97379, Q64012, Q91VE6, Q3UEB3, Q8BGD9, Q9JIK5, Q8IZQ9, Q8C2Q3, O08583, Q8VDG3, Q9D0E1, Q8BIQ5, Q9CQI7	1.4236715240408E-06
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	24	8.5434236E-09	Q8VE97, Q8IZX4, Q9D554, Q9CZU3, Q9CQ08, Q50116, Q99K48, P52912, P56959, Q64012, Q62189, Q3UEB3, O35326, Q8VJI6, P62311, O08583, Q62093, Q3U0V1, Q9JIX8, Q9D0E1, Q569Z6, Q9DAW6, Q9CWX3, Q9CQI7	2.19480553480762E-06
INTERPRO	IPR012677:Nucleotide-bd_a/b_plait_sf	26	2.9749945E-08	Q9CX86, Q8IZX4, Q99K48, Q9Z1D1, P52912, P56959, Q62189, O35326, Q8VJI6, Q62093, D3YXK2, Q8C854, Q9JIX8, Q8VE97, P97379, Q64012, Q91VE6, Q3UEB3, Q8BGD9, Q8IZQ9, Q8C2Q3, O08583, Q8VDG3, Q9D0E1, Q8BIQ5, Q9CQI7	6.50408174959034E-06
INTERPRO	IPR000504:RRM_dom	24	3.4556251E-08	Q9CX86, Q8VE97, Q8IZX4, P97379, Q99K48, Q9Z1D1, P52912, P56959, Q64012, Q62189, Q91VE6, Q3UEB3, Q8BGD9, Q8IZQ9, O35326, Q8VJI6, O08583, Q8C2Q3, Q62093, D3YXK2, Q8C854, Q9D0E1, Q8BIQ5, Q9CQI7	6.7154314062252E-06
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	26	4.1939221E-08	Q8IZX4, Q9CZU3, Q9CQ08, Q50116, Q99K48, P52912, Q80X82, Q62189, O35326, Q8VJI6, P62311, Q62093, P60335, Q9JIX8, Q569Z6, Q8VE97, Q9D554, Q64012, Q3UEB3, O08583, Q3U0V1, Q9D0E1, Q8BIQ5, Q9CWX3, Q9CQI7, Q9DAW6	8.97848830257558E-06

UP_SEQ_FEATURE	DOMAIN:RRM	23	6.5565514E-08	Q8VE97, Q8IZX4, P97379, Q99K48, Q9Z1D1, P52912, P56959, Q64012, Q62189, Q91VE6, Q3UEB3, Q8BGD9, Q8IZQ9, Q35326, Q8VJL6, Q08583, Q8C2Q3, Q62093, D3YXK2, Q8C854, Q9D0E1, Q8BIQ5, Q9CQI7	1.82162852818736E-05
SMART	SM00360:RRM	23	1.7339076E-07	Q9CX86, Q8VE97, P97379, Q99K48, Q9Z1D1, P52912, P56959, Q64012, Q62189, Q91VE6, Q3UEB3, Q8BGD9, Q8IZQ9, Q35326, Q8VJL6, Q08583, Q8C2Q3, Q62093, D3YXK2, Q8C854, Q9D0E1, Q8BIQ5, Q9CQI7	4.19605630330958E-05
UP_SEQ_FEATURE	DOMAIN:RRM 1	12	1.0225846E-05	Q35326, Q9CX86, Q8VE97, Q8VJL6, Q8C2Q3, Q8C854, Q99K48, P52912, Q9D0E1, Q3UEB3, Q62189, Q9CQI7	0.001636978860794
UP_SEQ_FEATURE	DOMAIN:RRM 2	12	1.0225846E-05	Q35326, Q9CX86, Q8VE97, Q8VJL6, Q8C2Q3, Q8C854, Q99K48, P52912, Q9D0E1, Q3UEB3, Q62189, Q9CQI7	0.001636978860794
UP_KW_BIOLOGICAL_PROCESS	KW-0508~mRNA splicing	24	1.9964469E-05	Q8VE97, Q8IZX4, Q9D554, Q9CZU3, Q9CQ08, Q501I6, Q99K48, P52912, Q64012, Q62189, Q3UEB3, Q35326, Q8VJL6, P62311, Q08583, Q62093, Q3U0V1, Q7TNC4, Q9JIX8, Q9D0E1, Q569Z6, Q9DAW6, Q9CWK3, Q9CQI7	0.000391303592433
UP_KW_BIOLOGICAL_PROCESS	KW-0507~mRNA processing	26	9.8625554E-05	Q8IZX4, Q9CZU3, Q9CQ08, Q501I6, Q99K48, P52912, Q80X82, Q62189, Q35326, Q8VJL6, P62311, Q62093, Q9JIX8, Q569Z6, Q8VE97, Q9D554, Q64012, Q3UEB3, Q08583, Q3U0V1, Q7TNC4, Q9D0E1, Q8BIQ5, Q9CWK3, Q9CQI7, Q9DAW6	0.001380757749008
GOTERM_CC_DIRECT	GO:0071013~catalytic step 2 spliceosome	11	0.0001277505	Q9CX86, Q9CXY6, Q9D554, P62311, Q08583, Q9CZU3, Q9CQ08, Q64012, Q9D0E1, Q3UEB3, Q9CQI7	0.001410809832401
GOTERM_CC_DIRECT	GO:0005681~spliceosomal complex	12	0.00107552079	Q9D554, Q8IZX4, P62311, Q08583, Q62093, Q9CZU3, Q9CQ08, Q64012, Q9D0E1, Q62189, Q9DAW6, Q9CQI7	0.000812331599874
GOTERM_BP_DIRECT	GO:0000398~mRNA splicing, via spliceosome	11	0.00186525205	Q35326, Q9CX86, Q9D554, P62311, Q8C2Q3, Q62093, Q9CQ08, Q9EPV8, Q62189, Q9DAW6, Q9CQI7	0.065577353622348
UP_KW_CELLULAR_COMPONENT	KW-0747~Spliceosome	11	0.01244172384	Q9D554, Q8IZX4, P62311, Q08583, Q9CZU3, Q9CQ08, Q64012, Q9D0E1, Q62189, Q9DAW6, Q9CQI7	0.049766895349914
Annotation Cluster 7	Enrichment Score: 6.355008447305392				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0051015~actin filament binding	22	3.7725223E-09	Q8R5K4, Q99KW3, Q89053, Q99K51, Q80X90, Q3V0K9, Q62418, Q6P9Q4, Q8BTM8, P58774, Q9JKE1, Q61233, Q9QZQ1, P13020, P21107, Q9CVB6, Q3UZAI, P47753, P47754, E9Q634, Q9WVA4, P26039	2.88426474047919E-07
GOTERM_MF_DIRECT	GO:0003779~actin binding	28	5.823644E-09	Q8R5K4, Q99KW3, Q89053, Q9ES46, Q3V0K9, Q8BTM8, P58774, P19973, Q61233, P07091, P40124, P21107, Q9CVB6, P68510, P47753, P47754, P61982, Q9ERL7, P26039, Q99K51, Q8BH43, Q80X90, Q62418, Q6P9Q4, Q9Z0E6, P13020, P62962, E9Q634	4.08140381761863E-07
GOTERM_CC_DIRECT	GO:0015629~actin cytoskeleton	18	1.272382E-05	Q99KW3, Q89053, Q9ES46, P10922, Q8BFZ3, Q8BTM8, P97315, P58774, Q9Z0E6, Q9JKE1, Q61233, P13020, P21107, Q9CVB6, Q9Z0F8, Q9CQD1, E9Q634, Q9WVA4	0.000184677157553
UP_KW_MOLECULAR_FUNCTION	KW-0009~Actin-binding	21	0.00013599473	Q8R5K4, Q99KW3, Q89053, Q99K51, Q8BH43, Q80X90, Q9ES46, Q3V0K9, Q62418, Q6P9Q4, Q8BTM8, P58774, Q61233, P40124, P13020, P21107, Q9CVB6, P47753, P47754, P62962, E9Q634	0.001849528290733
Annotation Cluster 8	Enrichment Score: 6.027783878053076				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0045087~innate immune response	34	2.617781E-09	Q9D8Y7, P11928, B2RRE7, P56477, P10810, Q6R5N8, Q99K48, P11103, Q61990, P0DOV2, Q8VJL6, Q3T144, AIL314, Q3UCV8, Q8V194, Q8V193, Q60710, Q3UPF5, P26151, Q61107, P97379, Q8R5F7, Q9R002, Q9Z0E6, Q9WTK5, Q8VCF0, Q61462, Q9R007, P54987, Q9JIK5, Q8C2Q3, Q61093, Q62084, P25911	9.60725628243336E-07

GOTERM_BP_DIRECT	GO:0002376~immune system process	34	4.0390785E-09	Q9D8Y7, B2RRE7, P56477, P10810, Q6R5N8, Q501J6, Q99K48, P11103, Q61990, PDOOV2, P36371, Q8VJL6, Q3TL44, AIL314, Q3UCV8, P04441, Q8V194, Q8V193, Q60710, Q3UPF5, P26151, Q61107, P97379, Q62418, Q8R5F7, Q9Z0E6, Q8VCF0, Q9R007, P54987, Q9IJK5, Q8C2Q3, Q64281, P01902, P25911	1.29704908718478E-06
UP_KW_BIOLOGICAL_PROCESS	KW-0339~Innate Immunity	30	3.4885145E-06	Q9D8Y7, P11928, B2RRE7, P56477, P10810, Q6R5N8, Q99K48, P11103, Q61990, PDOOV2, Q8VJL6, Q3TL44, AIL314, Q3UCV8, Q8V194, Q8V193, Q60710, Q3UPF5, P26151, Q61107, P97379, Q8R5F7, Q9R002, Q9Z0E6, Q8VCF0, Q9R007, P54987, Q9IJK5, Q8C2Q3, P25911	0.000113958140315
Annotation Cluster 9	Enrichment Score: 5.262412358372292				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0003824~catalytic activity	23	5.4809324E-08	Q99IT1, Q60710, O08709, Q64737, P51569, P11103, P13864, Q9D051, P39749, Q9C065, Q9CWI9, Q99KE1, P97807, Q9Z219, Q9JHR7, Q04447, P38060, Q9Z110, Q9WUA3, P08249, Q8CIN4, P07742, P05202	2.7114494877902E-06
GOTERM_BP_DIRECT	GO:0008152~metabolic process	17	2.6965417E-06	Q60710, O08709, Q64737, P51569, P11103, P13864, Q9CWI9, Q99KE1, Q9QWR8, Q9JHR7, Q8R0X7, Q8BX80, Q9Z110, Q9WUA3, E9Q634, Q8CIN4, P07742	0.000329876940077
UP_KW_MOLECULAR_FUNCTION	KW-0021~Allosteric enzyme	8	0.00110433626	Q99KE1, Q60710, Q9JHR7, P11103, P13864, Q9WUA3, Q8CIN4, P07742	0.009386858232293
Annotation Cluster 10	Enrichment Score: 5.180975467421494				
Category	Term	Count	PValue	Genes	FDR
UP_KW_BIOLOGICAL_PROCESS	KW-0648~Protein biosynthesis	19	1.1015429E-07	Q99IT1, P10711, Q9D8N0, Q91WK2, Q99LC8, O70194, Q9Z1D1, Q99L45, P57776, Q9ER72, Q8BGD9, Q8IZQ9, Q9D0R2, Q8BML9, P26638, Q8QZY1, Q6PGC1, P60229, Q9D019	1.07951199490176E-05
GOTERM_BP_DIRECT	GO:0001732~formation of cytoplasmic translation initiation complex	7	2.5104675E-07	Q91WK2, O70194, Q9Z1D1, Q99L45, Q8QZY1, P60229, Q8IZQ9	4.29959401404992E-05
GOTERM_BP_DIRECT	GO:0006413~translational initiation	11	5.7754393E-07	Q6ZQ58, Q91WK2, Q99LC8, O70194, Q9Z1D1, Q99L45, Q8QZY1, P60229, Q6PGC1, Q8BGD9, Q8IZQ9	8.24283530360492E-05
GOTERM_CC_DIRECT	GO:0016282~eukaryotic 43S preinitiation complex	7	1.5683464E-06	Q91WK2, O70194, Q9Z1D1, Q8QZY1, P60229, Q6PGC1, Q8IZQ9	2.95081462749062E-05
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	10	4.4867376E-06	Q91WK2, Q99LC8, O70194, Q9Z1D1, Q99L45, Q8QZY1, P60229, Q6PGC1, Q8BGD9, Q8IZQ9	0.000142192411821
GOTERM_CC_DIRECT	GO:0005852~eukaryotic translation initiation factor 3 complex	6	7.4436996E-06	Q91WK2, O70194, Q9Z1D1, Q8QZY1, P60229, Q8IZQ9	0.000121980625547
GOTERM_CC_DIRECT	GO:0033290~eukaryotic 48S preinitiation complex	6	1.4165243E-05	Q91WK2, O70194, Q9Z1D1, Q8QZY1, P60229, Q8IZQ9	0.000194484963944
UP_KW_MOLECULAR_FUNCTION	KW-0396~Initiation factor	10	2.5322458E-05	Q91WK2, Q99LC8, O70194, Q9Z1D1, Q99L45, Q8QZY1, P60229, Q6PGC1, Q8BGD9, Q8IZQ9	0.000430481782785
GOTERM_BP_DIRECT	GO:0075525~viral translational termination-reinitiation	4	5.9378185E-05	O70194, Q9Z1D1, Q8QZY1, Q8IZQ9	0.00435835878511
GOTERM_CC_DIRECT	GO:0071541~eukaryotic translation initiation factor 3 complex, eIF3m	3	0.00869733091	Q91WK2, O70194, Q8IZQ9	0.046023376065817
Annotation Cluster 11	Enrichment Score: 5.078640238792538				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006886~intracellular protein transport	23	6.2772206E-09	Q9CQ58, Q9QZ55, Q9EQH3, Q61207, P70168, P17426, Q8BKCS, Q64324, P62331, Q91YE6, O35643, Q8CIE6, P84078, P61750, P68510, P61211, P61021, Q9CQD1, O35609, P62746, P22892, P04441, O70439	1.79179774420037E-06

GOTERM_BP_DIRECT	GO:0015031~protein transport	34	1.3016249E-07	Q9QZE5, Q9CQS8, Q9D620, Q8BH74, Q9DBH5, Q99P88, Q9CR60, P70168, P17426, Q8BKC5, Q64324, P62331, P36371, Q91YE6, O35643, Q8CIE6, O35344, P61021, Q9CQD1, O35609, P22892, Q9EQH3, P62827, Q9CR16, Q64310, Q8R519, O35382, Q99156, Q3UM18, P84078, P61750, P62746, Q9Z0V7, B1AXP6		2.57221112043282E-05
UP_KW_BIOLOGICAL_PR OCESS	KW-0653~Protein transport	34	0.00040146494	Q9QZE5, Q9CQS8, Q9D620, Q8BH74, Q9DBH5, Q99P88, Q9CR60, P70168, P17426, Q8BKC5, Q64324, P62331, P36371, Q91YE6, O35643, Q8CIE6, O35344, P61021, Q9CQD1, O35609, P22892, Q9EQH3, P62827, Q9CR16, Q64310, Q35382, Q99156, Q3UM18, P84078, P61750, P52293, P62746, Q9Z0V7, B1AXP6		0.004917945496581
UP_KW_BIOLOGICAL_PR OCESS	KW-0813~Transport	76	0.01477536343	Q9QZE5, P10639, Q9CR68, O70579, Q8BVE3, Q9DBH5, Q99P88, Q9CR60, P17426, Q8BKC5, Q91YE6, O35643, Q8CIE6, Q9DAV9, P61021, Q9CQD1, O35609, Q9CZ13, P22892, Q56926, Q148V7, Q9CR16, Q62418, Q64310, Q9CQX2, Q8VDN2, Q9R0Q9, P61750, Q61093, Q63829, P52293, Q9Z0V7, Q991C5, Q9CQS8, Q9Z0I0, Q62425, Q9D620, Q8BH74, P50516, P50637, P70168, Q91WDS, P31750, Q8K2B3, Q64324, P57746, P62331, P36371, O35344, Q9D3D9, Q9DCX2, G5E829, P62897, Q91VR2, Q9EQH3, Q60931, P62827, P97379, Q791V5, O35382, Q61462, Q99156, Q991V5, Q3UM18, Q99JR1, Q9CQA3, O08583, P84078, Q3U0V1, P62746, B9E186, Q92111, Q9CXK4, B1AXP6, Q9DCW4, P05202		0.0590499101001564
Annotation Cluster 12	Enrichment Score: 4.7910108074782745					
Category	Term	Count	PValue	Genes	FDR	
GOTERM_MF_DIRECT	GO:0009055~electron transfer activity	8	4.6364268E-07	Q9CQA3, P37040, Q61093, Q991C5, Q61462, P62897, Q8K2B3, Q9DCW4		1.94961747575344E-05
UP_KW_BIOLOGICAL_PR OCESS	KW-0249~Electron transport	13	7.8217325E-05	P10639, Q9CR68, Q62425, Q9CQX2, Q61462, Q91WDS, Q8K2B3, Q9CQA3, Q61093, Q9CZ13, Q991C5, P62897, Q9DCW4		0.001277549635122
GOTERM_BP_DIRECT	GO:0022904~respiratory electron transport chain	6	0.00011681032	Q9CR68, Q9CQA3, P09671, Q991C5, Q8K2B3, Q9DCW4		0.007694505402451
Annotation Cluster 13	Enrichment Score: 4.73450428367765					
Category	Term	Count	PValue	Genes	FDR	
GOTERM_BP_DIRECT	GO:0006099~tricarboxylic acid cycle	9	2.3114374E-07	P97807, Q9D6R2, Q9CQA3, Q9Z219, Q9D051, Q9CZU6, P08249, P54071, Q8K2B3		4.2414877178154E-05
UP_KW_BIOLOGICAL_PR OCESS	KW-0816~Tricarboxylic acid cycle	9	4.4840501E-07	P97807, Q9D6R2, Q9CQA3, Q9Z219, Q9D051, Q9CZU6, P08249, P54071, Q8K2B3		2.19718453269616E-05
KEGG_PATHWAY	mmu01200:Carbon metabolism	19	4.7904865E-07	Q9D6R2, P26443, Q8VDL4, Q9D051, P17751, Q8K2B3, Q99KE1, P97807, Q9CQA3, Q9CZN7, Q9Z219, P17182, Q9CZU6, Q9WUA3, P08249, P54071, Q8QZT1, P05202		6.46715681161028E-05
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	9	1.5494278E-05	P97807, Q9D6R2, Q9CQA3, Q9Z219, Q9D051, Q9CZU6, P08249, P54071, Q8K2B3		0.000836691036885
KEGG_PATHWAY	mmu01210:2-Oxocarboxylic acid metabolism	6	0.00770280325	Q9D6R2, P53395, Q9D051, Q9CZU6, P54071, P05202		0.069325229276194
Annotation Cluster 14	Enrichment Score: 4.7229373432786215					
Category	Term	Count	PValue	Genes	FDR	
INTERPRO	IPR005819:H1/H5	7	1.8047636E-08	Q3TEA8, P10922, P43274, P43275, P43276, P43277, P15864		4.50933084030273E-06
GOTERM_MF_DIRECT	GO:0030527~structural constituent of chromatin	15	2.7220382E-08	Q3TEA8, P10854, P10922, P43274, P17095, Q9QZQ8, P43275, P43276, P10853, P43277, P15864		1.52615607374113E-06
GOTERM_BP_DIRECT	GO:0030261~chromosome condensation	8	3.2271351E-07	Q8CG47, P10922, P43274, Q8K2Z4, P43275, P43276, P43277, P15864		5.18156885089032E-05
UP_SEQ_FEATURE SMART	DOMAIN:H15	7	4.7118494E-07	Q3TEA8, P10922, P43274, P43275, P43276, P43277, P15864		0.000112209327456
SMART	SM00526:H15	7	5.2331517E-07	Q3TEA8, P10922, P43274, P43275, P43276, P43277, P15864		6.33211353550737E-05
INTERPRO	IPR005818:Histone_H1/H5_H15	7	5.8016637E-07	Q3TEA8, P10922, P43274, P43275, P43276, P43277, P15864		9.22464536068527E-05

GOTERM_CC_DIRECT	GO:0000786~nucleosome	14	5.5868411E-06	Q3TEA8, P10854, P10922, P43274, Q9QZQ8, P43275, P60762, P43276, P10853, P43277, P15864	9.46038426662765E-05
GOTERM_CC_DIRECT	GO:0000791~euchromatin	10	8.2757239E-06	Q3UZ18, P23198, P56960, P10922, P43274, P43275, P43276, P43277, P15864, Q9ERF3	0.000127395992705
UP_KW_PTM	KW-0013~ADP-ribosylation	17	1.1052863E-05	P26443, E9Q7G0, P10854, P10922, P11103, P10853, P70168, P15864, P42225, P43274, P17095, Q8CFE2, Q9WVA3	3.31585896727081E-05
GOTERM_BP_DIRECT	GO:0045910~negative regulation of DNA recombination	6	1.4205089E-05	P10922, P43274, P43275, P43276, P43277, P15864	0.001216429159782
INTERPRO	IPR036390:WH_DNA-bd_sf	17	6.0991222E-05	Q9D8W5, Q6ZQ58, P56477, Q3TEA8, P10922, A2A432, Q61550, P15864, Q6WKZ8, Q91HK5, O08663, P43274, P43275, P43276, O88543, P43277, P60229	0.0006274920466302
GOTERM_BP_DIRECT	GO:0006325~chromatin organization	21	6.3785621E-05	Q64701, Q61686, P23198, P83917, Q9Z277, P13864, P10853, Q921E6, Q61164, P15864, Q91113, P43274, P17095, Q9QZQ8, P60762, P43276, P43277	0.004551812768967
GOTERM_MF_DIRECT	GO:0031492~nucleosomal DNA binding	8	0.00019804786	P10922, P43274, Q9QZQ8, P43275, P43276, P43277, P15864, Q8VE37	0.0003785414869411
UP_KW_PTM	KW-0379~Hydroxylation	19	0.00025815841	P26443, P10854, P32233, P10853, P14115, P15864, P50247, Q7TNC4, P43274, P43275, P08113, P17182, P43276, P43277, O88351	0.000580856429345
GOTERM_BP_DIRECT	GO:0006334~nucleosome assembly	9	0.00031259211	Q3TEA8, P10922, P43274, Q9QZQ8, P43275, P43276, Q9EST5, P43277, P15864	0.018631983465267
GOTERM_MF_DIRECT	GO:0003690~double-stranded DNA binding	12	0.00036663301	P42225, Q8K2F8, P10922, P43274, Q9R002, P43275, P14733, P43276, P43277, P15864, P0DOV1, P0DOV2	0.0006703007868622
UP_KW_PTM	KW-0164~Circullination	13	0.00057646723	Q8BHX3, P10922, Q922K7, P6281, Q91VE6, P15864, O08583, Q9D8E6, Q91113, P43274, P43275, P43276, P43277	0.001152934457135
INTERPRO	IPR036388:WH-like_DNA-bd_sf	16	0.00058823392	Q9D8W5, Q3UPF5, Q6ZQ58, P56477, Q3TEA8, P10922, A2A432, P15864, Q91HK5, O08663, P43274, P43275, P43276, O88543, P43277, P62852	0.048991481918605
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding	8	0.00247322369	P10922, Q50116, P43274, Q9QZQ8, P43275, P43276, P43277, P15864	0.036153756897203
UP_SEQ_FEATURE	COMPBIA5:Basic residues	27	0.01104787756	Q8VE97, Q3UPF5, P10854, Q8BHX3, P10922, P10853, Q61164, P14115, P15864, O35326, P35980, Q62093, Q7TNC4, Q91113, P43274, P43275, Q91IX8, Q9QZQ8, B9E186, P43276, Q3UH66, P43277, Q56926, P29788	0.472225946022053
Enrichment Cluster 15					
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0007049~cell cycle	33	5.2591312E-07	Q64701, Q99KW3, P97384, Q8CG47, Q8BHX3, Q8R3C0, Q9JMD0, A2A432, P37913, Q61550, Q8BT07, P61290, Q9CU62, P62331, P49718, Q8K2Z4, Q3UHX9, P25206, Q3UA16, Q35207, Q9ESI4, E9Q7G0, P62827, Q9WU62, Q80YV2, P63280, Q8VE37, Q8BHK9, Q91IW9, P28867, Q9WVA3, Q8BK67, E9PVX6	7.94747537622062E-05
GOTERM_BP_DIRECT	GO:0051301~cell division	24	2.3233345E-06	Q99KW3, P97384, Q8CG47, E9Q7G0, Q8BHX3, P62827, Q8R3C0, Q9WU62, Q80YV2, P63280, Q9JMD0, P37913, Q8BT07, Q61550, Q9CU62, Q8VE37, P62331, Q8BHK9, Q91IW9, Q8K2Z4, Q3UHX9, Q3UA16, Q9WVA3, Q8BK67	0.000298432314103
GOTERM_CC_DIRECT	GO:0030496~midbody	14	0.00027247166	Q99KW3, P97384, Q8BHX3, P62827, Q9WU62, Q9JKE1, Q8BT07, Q61550, P62331, D3YXK2, Q91IW9, P08113, Q8BK67, O88286	0.002714031440782
UP_KW_BIOLOGICAL_PR	KW-0498~Mitosis	20	0.00060318623	Q99KW3, Q8CG47, E9Q7G0, Q8BHX3, P62827, Q8R3C0, Q9WU62, Q80YV2, P63280, Q9JMD0, Q8BT07, Q61550, Q9CU62, Q8VE37, Q8BHK9, Q8K2Z4, Q3UHX9, Q3UA16, Q9WVA3, Q8BK67	0.00656802781749
UP_KW_BIOLOGICAL_PR	KW-0132~Cell division	24	0.00111567872	Q99KW3, P97384, Q8CG47, E9Q7G0, Q8BHX3, P62827, Q8R3C0, Q9WU62, Q80YV2, P63280, Q9JMD0, P37913, Q8BT07, Q61550, Q9CU62, Q8VE37, P62331, Q8BHK9, Q91IW9, Q8K2Z4, Q3UHX9, Q3UA16, Q9WVA3, Q8BK67	0.0009939683123319

UP_KW_BIOLOGICAL_PR OCESS	KW-0131~Cell cycle	33	0.00258740194	Q64701, Q99KW3, P97384, Q8CG47, Q8BHX3, Q8R3C0, Q9JMD0, A2A432, P37913, Q61550, Q8BT07, P61290, Q9CU62, P62331, P49718, Q8K2Z4, Q3UHX9, P25206, Q3UA16, O35207, Q9ESL4, E9Q7G0, P62827, Q9WU62, Q80YV2, P63280, Q8VE37, Q8BHK9, Q9JW9, P28867, Q9WVA3, Q8BK67, E9PVX6	0.021130449147654
------------------------------	--------------------	----	---------------	---	-------------------

Annotation Cluster 16	Enrichment Score: 3.9749583254644514	Count	PValue	Genes	FDR
Category	Term				
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	34	3.9752966E-08	P26443, Q9CR68, O08709, Q9JMH6, Q91WD5, Q91LJ2, Q8BKE6, Q64105, Q8K2B3, Q9CPU4, P47738, P36552, P37040, P09671, P45377, Q91Z53, P08249, P21300, Q8CD15, Q8R0F3, Q9D6R2, P08228, Q9CXRL, P51174, Q9D051, Q61462, O08756, Q99KE1, Q9CQA3, Q61093, Q9Z110, Q99LC5, P54071, P07742	2.08951527192151E-06
UP_KW_MOLECULAR_FU NCTION	KW-0560~Oxidoreductase	34	0.0010293794	P26443, O08709, Q9JMH6, Q91WD5, Q91LJ2, Q8BKE6, Q64105, Q8K2B3, Q9CPU4, P47738, P36552, P37040, P09671, P45377, Q91Z53, P08249, P21300, Q8CD15, Q8R0F3, Q9D6R2, P08228, Q9CQV8, Q9CXRL, P51174, P68254, Q9D051, Q61462, O08756, Q99KE1, Q9CQA3, Q61093, Q9Z110, P54071, P07742	0.009386858232293

Annotation Cluster 17	Enrichment Score: 3.45342854333704	Count	PValue	Genes	FDR
Category	Term				
GOTERM_BP_DIRECT	GO:0006974~DNA damage response	28	3.2911284E-06	P23198, P97287, P83917, Q9Z277, Q9CZU3, Q99K48, P11103, A2A432, P37913, Q61550, P31750, Q9CU62, Q3V300, P97807, Q8VU6, Q9QZN4, Q8CFE2, Q61686, Q9CQ37, Q60710, P56960, Q99LX0, P39749, Q9D071, P08113, P60762, P17918, P25911, P28867	0.000384314034877
GOTERM_BP_DIRECT	GO:0006281~DNA repair	22	1.9984456E-05	Q9CQ37, Q60710, P56960, Q99LX0, Q99K48, P11103, A2A432, P39749, P37913, Q61550, Q9CU62, Q3V300, P97807, Q8VU6, Q9D071, Q9QZN4, Q9QZQ8, P60762, Q8CFE2, P17918, P07742	0.001604377092513
UP_KW_BIOLOGICAL_PR OCESS	KW-0234~DNA repair	19	0.01225416347	Q9CQ37, Q60710, P56960, Q99LX0, Q99K48, P11103, A2A432, P39749, P37913, Q61550, Q9CU62, P97807, Q8VU6, Q9D071, Q9QZN4, P60762, Q8CFE2, P17918	0.085464117591821

Annotation Cluster 18	Enrichment Score: 3.0979456076239535	Count	PValue	Genes	FDR
Category	Term				
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	65	4.0442624E-08	Q9QZE5, P11928, Q8UZR0, Q8BFEZ9, P62082, Q9CR60, P14115, Q9DAV9, P37040, P35980, Q8BLN5, P62274, Q9DCZ4, Q9JUZ4, P47713, P41216, P04441, Q6Y7W8, Q8R0F3, Q99LX0, Q9CXRL, P18572, Q64310, Q99P31, O08756, Q8VDN2, P57776, P01902, Q9DCQ7, Q8BCS7, Q8QZT1, Q9CQ88, Q9Z0U0, P26443, P61804, Q9WV55, Q8BYI6, P50637, Q9CPU4, P36371, Q8BHL8, P57791, Q9QUJ7, Q9CYN2, P29788, Q9D8N0, P14869, Q8VDL4, Q9EQP2, Q8R5I9, Q9Z2C6, Q99I56, O35381, Q9D8V0, Q99IV5, Q3UM18, Q6P5E4, P50247, Q8R0X7, P47962, P08113, B9E186, Q9ERE7, P28867, P57080	8.93254479961126E-07

Annotation Cluster 19	Enrichment Score: 3.0732261742056894	Count	PValue	Genes	FDR
Category	Term				
UP_SEQ_FEATURE	SITE:Interaction with phosphoserine on interacting protein	5	1.08019E-05	O70456, Q9CQV8, P68510, P68254, P61982	0.001636978860794
INTERPRO	IPR023409:14-3-3_CS	5	1.242982E-05	O70456, Q9CQV8, P68510, P68254, P61982	0.001811646300963
INTERPRO	IPR023410:14-3-3_domain	5	2.4370215E-05	O70456, Q9CQV8, P68510, P68254, P61982	0.0002841567027238
INTERPRO	IPR000308:14-3-3	5	2.4370215E-05	O70456, Q9CQV8, P68510, P68254, P61982	0.0002841567027238
SMART	SM00101:14_3_3	5	3.2816251E-05	O70456, Q9CQV8, P68510, P68254, P61982	0.002647177606505
INTERPRO	IPR036815:14-3-3_dom_sf	5	4.3003467E-05	O70456, Q9CQV8, P68510, P68254, P61982	0.0004700816536274
PIR_SUPERFAMIL Y	PIRSF000868:14-3-3	5	0.00017009416	O70456, Q9CQV8, P68510, P68254, P61982	0.015478568809322

GOTERM_BP_DIRECT	GO:0045184~establishment of protein localization	7	0.00036518036	O70456, Q9CQV8, Q8BTM8, P68254, P61982, Q8BT07, Q8BK67	0.019960602872561
UP_SEQ_FEATURE	DOMAIN:14-3-3	4	0.00044649783	O70456, Q9CQV8, P68254, P61982	0.03544342626369
Annotation Cluster 20	Enrichment Score: 2.633441123537235				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0000502~proteasome complex	8	0.00013610863	Q9D8W5, O70435, Q9CX56, Q8BHL8, O88685, P62334, P61290, P57080	0.00147113153103
UP_KW_CELLULAR_COM PONENT	KW-0647~Proteasome	8	0.00062315347	P97372, Q9D8W5, O70435, Q9CX56, Q8BHL8, O88685, P62334, P61290	0.004154356480084
KEGG_PATHWAY	mmu03050:Proteasome	8	0.00155567691	P97372, Q9D8W5, O70435, Q9CX56, Q8BHL8, O88685, P62334, P61290	0.028002184406709
GOTERM_CC_DIRECT	GO:0022624~proteasome accessory complex	4	0.00342166736	Q9D8W5, Q9CX56, O88685, P62334	0.022284705399362
Annotation Cluster 21	Enrichment Score: 2.6052655980457478				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0010494~cytoplasmic stress granule	10	7.9986904E-05	Q8K2F8, Q6ZQ58, Q3U0V1, P97379, P52293, P52912, P70168, P54823, Q6Y7W8, Q8IZQ9	0.000923485166099
Annotation Cluster 22	Enrichment Score: 2.5645200647505657				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0050665~hydrogen peroxide biosynthetic process	4	0.0006535992	P08228, P09671, Q61093, Q61462	0.03351587496756
Annotation Cluster 23	Enrichment Score: 2.493032830330887				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0005525~GTP binding	26	9.5197081E-08	P26443, Q922F4, P62331, P61021, P43274, Q9CQD1, P27601, Q62159, Q60710, Q61107, Q99K70, P62827, Q99LC8, Q99ME9, Q9Z0E6, P32233, Q9EQP2, Q3UM18, P84096, P84078, P61750, P61211, Q9JIW9, P62746, P83887, P21278	4.44781916949646E-06
GOTERM_MF_DIRECT	GO:0003924~GTPase activity	20	9.8438359E-06	Q62159, Q61107, Q922F4, P62827, Q99K70, Q99ME9, Q9Z0E6, P32233, Q3UM18, P84096, P62331, P84078, P61750, P61211, Q9JIW9, P61021, Q9CQD1, P62746, P27601, P21278	0.000285471241821
INTERPRO	IPR027417:P-loop_NTPase	46	1.7041544E-05	Q8CG47, Q9BDB7, Q9CZU3, Q9JIB3, Q50116, Q9IKF1, P50516, Q9CUG2, P62331, P36371, P49718, Q3TL44, P61021, Q9CQD1, P25206, Q6PGC1, P62334, P27601, Q62159, Q9R061, P70290, Q61107, Q99K70, P62827, Q99ME9, Q8IZQ2, Q8R5F7, Q9Z0E6, P32233, Q9EQP2, P54823, Q9D0R4, Q3UM18, Q9JIK5, Q3V300, P84096, P84078, P61750, P61211, Q8BHK9, Q9JIW9, Q8BV66, P62746, O88685, E9Q634, P21278	0.002292743126586
GOTERM_MF_DIRECT	GO:0019003~GDP binding	10	2.8382743E-05	P62331, P84078, P62827, Q99K70, Q99LC8, P61021, Q9JIW9, Q9CQD1, P62746, Q9Z0E6	0.000702055498682
GOTERM_MF_DIRECT	GO:0003925~G. protein activity	8	9.5612861E-05	P62331, P84078, P62827, P61021, Q9JIW9, Q9CQD1, Q9Z0E6, P21278	0.001961229651715
UP_KW_LIGAND	KW-0342~GTP-binding	23	0.00180435104	Q62159, P26443, Q60710, Q61107, Q922F4, P62827, Q99K70, Q99ME9, Q9Z0E6, P32233, Q3UM18, P84096, P62331, P84078, P61750, P61211, Q9JIW9, P61021, Q9CQD1, P62746, P27601, P83887, P21278	0.018043510397199
UP_KW_PTM	KW-0636~Prenylation	12	0.0515541017	P84096, Q62159, P11928, P21619, P61021, Q9QY10, Q9JIW9, Q9CQD1, P48678, P62746, Q9Z0E6, P14733	0.092797383053347
Annotation Cluster 24	Enrichment Score: 2.4799545746358067				
Category	Term	Count	PValue	Genes	FDR

GOTERM_BP_DIRECT	GO:0032760~positive regulation of tumor necrosis factor production	9	0.00159431373	Q8V193, P11928, P10810, Q61093, P08508, Q8R5F7, Q8VCF0, Q61462, P63038	0.062086553628903
GOTERM_BP_DIRECT	GO:0032727~positive regulation of interferon-alpha production	5	0.00160498048	P42225, Q3UPF5, Q8R5F7, Q8VCF0, P63038	0.062086553628903
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	6	0.00164339651	Q8V194, Q8V193, P11928, Q3UPF5, Q8R5F7, Q8VCF0	0.062086553628903
GOTERM_BP_DIRECT	GO:0032728~positive regulation of interferon-beta production	6	0.00258403725	Q8V193, P11928, Q3UPF5, Q9CZW5, Q8R5F7, Q8VCF0	0.081331023415676

Annotation Cluster 25	Enrichment Score: 2.4680636865320373	Count	PValue	Genes	FDR
Category	Term				
GOTERM_MF_DIRECT	GO:0044388~small protein activating enzyme binding	4	6.1485517E-05	P63166, Q99LX0, Q9Z1F9, P63280	0.001360771580284
GOTERM_BP_DIRECT	GO:0016925~protein sumoylation	6	0.00036230468	P63166, P46061, P61957, Q9Z1F9, Q8R5F7, P63280	0.0119960602872561
GOTERM_CC_DIRECT	GO:0016605~PML body	8	0.00555865545	Q61686, P63166, P61957, Q99LX0, P67871, P63280, P60229, Q91XV3	0.032088601938759
GOTERM_CC_DIRECT	GO:0099524~postsynaptic cytosol	5	0.00913177279	P63166, P61957, P63280, P56959, P28867	0.047632234123654
GOTERM_CC_DIRECT	GO:0099523~presynaptic cytosol	5	0.01062457302	P63166, P61957, P63280, Q8R5I9, P56959	0.053972830934312

Annotation Cluster 26	Enrichment Score: 2.4628499026360995	Count	PValue	Genes	FDR
Category	Term				
KEGG_PATHWAY	mmu05020:Prion disease	24	0.00019010292	Q9D8W5, Q9CR68, P08228, O70435, Q60864, Q62425, Q60931, Q922F4, Q9CX56, P19783, Q61462, Q91WD5, Q8K2B3, Q9CQA3, Q61093, P67871, Q9D3D9, Q9CZ13, O88685, Q9DCX2, P62334, P28867, P62897, Q91VR2	0.006827179746218
KEGG_PATHWAY	mmu05012:Parkinson disease	24	0.00020228681	Q9D8W5, P10639, Q9CR68, Q9CQNI, P08228, O70435, Q62425, Q60931, Q99LX0, Q922F4, Q9CX56, P19783, Q91WD5, Q8K2B3, Q9CQA3, Q9D3D9, Q9CZ13, O88685, Q9DCX2, Q9IIZ4, P62334, Q91Y5, P62897, Q91VR2	0.006827179746218
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	15	0.00070165452	Q9CR68, Q62425, Q8BVE3, P19783, P50516, Q91WD5, Q8K2B3, P57746, Q9CQA3, Q9D3D9, Q9CZ13, Q9DCX2, P62897, Q91VR2, Q9D8I9	0.01578722668429
KEGG_PATHWAY	mmu05208:Chemical carcinogenesis - reactive oxygen species	19	0.00205089308	P10649, Q9CR68, P08228, Q62425, Q60931, P19783, Q61462, Q91WD5, P31750, Q8K2B3, Q9CPU4, Q9CQA3, P09671, Q9D3D9, Q9CZ13, Q9DCX2, P28867, Q91VR2, O88351	0.030763396244561
KEGG_PATHWAY	mmu05016:Huntington disease	23	0.00233765232	Q60520, Q9D8W5, Q9CR68, P08228, O70435, Q62425, Q60931, Q922F4, Q9CX56, P19783, Q91WD5, P17426, Q8K2B3, Q9CQA3, P09671, Q9D3D9, Q9CZ13, O88685, Q9DCX2, P62334, P62488, P62897, Q91VR2	0.031796001030497
KEGG_PATHWAY	mmu05010:Alzheimer disease	27	0.0024730223	Q9D8W5, Q9CR68, O70435, Q62425, Q91ZX7, Q922F4, Q91WD5, P31750, Q8K2B3, Q9Z0F8, Q9JHR7, Q9D3D9, Q9CZ13, Q9DCX2, P62334, P62897, O88351, Q91VR2, Q60931, Q9CX56, Q9CR16, P19783, O08756, Q9CQA3, Q61093, P67871, O88685	0.031796001030497
UP_KW_CELLULAR_COM PONENT	KW-0999~Mitochondrion inner membrane	20	0.00277464872	Q8CAQ8, Q9CR68, Q9CQNI, Q62425, Q8IZQ2, P19783, Q91WD5, Q99R1, Q8K2B3, P67783, Q9CQD1, Q9CZNT, Q9CRB9, Q9D3D9, Q9CZ13, Q9DCX2, Q9Z0V7, Q9Z1I0, Q91VR2	0.013873243622639
KEGG_PATHWAY	mmu05014:Anyotrophic lateral sclerosis	26	0.00308438714	P97384, Q9D8W5, Q9CR68, O70435, Q62425, Q922F4, Q8BH74, Q99R88, P56959, Q91WD5, Q8K2B3, Q9D3D9, Q9CQD1, Q9CZ13, Q9DCX2, P62334, P62897, Q91VR2, P08228, Q9CX56, P19783, Q99J56, Q9CQA3, O08583, O88685, P62962	0.0346939355322594
KEGG_PATHWAY	mmu05022:Pathways of neurodegeneration - multiple diseases	30	0.00625992676	Q9D8W5, Q9CR68, O70435, Q62425, Q922F4, P56959, Q91WD5, Q8K2B3, Q9D3D9, Q9CQD1, Q9CZ13, Q9DCX2, P62334, Q9IIZ4, P62897, Q91VR2, Q9CQNI, P08228, Q60931, Q9CX56, Q99LX0, Q9CR16, P19783, O08756, Q99J56, Q9CQA3, Q61093, P67871, O88685, Q91Y5	0.062599267647556

KEGG_PATHWAY	mmu05415:Diabetic cardiomyopathy	17	0.00657413894	Q9C868, Q62425, Q60931, P11103, P19783, Q9D051, Q61462, Q91WDS, P31750, Q8K2B3, Q9CQA3, Q61093, Q9D3D9, Q9CZ13, Q9DCX2, P28867, Q91VR2	0.063393482678638
Annotation Cluster 27	Enrichment Score: 2.438885852463351				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	59	1.5656845E-06	Q6P1B1, B2RRE7, O08709, P97789, O08553, P37040, Q9JHR7, P61021, P25206, Q9CQD1, Q3UCV8, P47713, P10605, Q60710, P56960, Q99LX0, Q8VCT3, Q8IZQ2, Q9Z0E6, P54823, Q9JHK5, P16675, Q91W9, Q8BX80, Q8IZQ2, Q8K411, Q9WTV6, Q9WV54, Q9CZU3, P29351, Q501J6, P51569, Q9CWX9, Q9CQUR6, P62331, P49718, O35864, Q9QWR8, P57791, Q9Z0F8, Q6PGC1, Q9D819, Q61107, Q99KK70, P62827, Q8R5F7, P32233, P39749, Q9D0R4, Q9D8V0, Q3UM18, Q99KK7, O08663, Q8C9W3, P84078, Q8VDC3, Q8BHK9, Q9JIV5, P57080	5.26696265864823E-05
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	25	4.8530399E-05	Q8K411, Q9WTV6, Q6P1B1, B2RRE7, P61290, Q9QUR6, O35864, P57791, Q9Z0F8, Q9JHR7, Q9CYN2, Q3UCV8, P10605, Q99LX0, Q91WK2, Q8VCT3, Q8IZQ2, Q9D8V0, P16675, Q99KK7, O08663, Q8C9W3, Q9JIV5, Q9D1A2, P57080	0.001166116147362
GOTERM_MF_DIRECT	GO:0008237~metallopeptidase activity	11	0.00101117242	Q8K411, Q99KK7, O35864, Q6P1B1, Q8C9W3, Q9Z0F8, Q9JHR7, Q91WK2, Q8VCT3, Q8IZQ2, Q9D1A2	0.01610481925153
GOTERM_BP_DIRECT	GO:0006508~proteolysis	24	0.00194643042	P10605, Q8K411, Q9WTV6, Q6P1B1, B2RRE7, Q99LX0, Q9CX56, Q8VCT3, Q8IZQ2, Q9D8V0, P61290, P16675, Q99KK7, Q9QUR6, O08663, O35864, Q8C9W3, Q9Z0F8, Q9JHR7, P57791, Q3UCV8, Q9JIV5, Q9D1A2, P57080	0.065577353622348
Annotation Cluster 28	Enrichment Score: 2.3441699309569133				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0016874~ligase activity	13	1.0630804E-05	Q99JTI, Q8IZR0, Q64737, P37913, Q9ER72, Q9D0R2, Q8BML9, Q9Z219, P16460, Q9QJ17, P26638, P41216, Q9D019	0.00029801686835
UP_KW_MOLECULAR_FUNCTION	KW-0436~Ligase	13	0.00095211069	Q99JTI, Q8IZR0, Q64737, P37913, Q9ER72, Q9D0R2, Q8BML9, Q9Z219, P16460, Q9QJ17, P26638, P41216, Q9D019	0.0009386858232293
GOTERM_BP_DIRECT	GO:0006418~RNA aminoacylation for protein translation	5	0.00333422685	Q8BML9, P26638, Q9ER72, Q9D0R2, Q9D019	0.093104660632503
GOTERM_MF_DIRECT	GO:0004812~aminoacyl-tRNA ligase activity	5	0.00685826298	Q8BML9, P26638, Q9ER72, Q9D0R2, Q9D019	0.084820575926634
Annotation Cluster 29	Enrichment Score: 2.267167959297744				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0009055~electron transfer activity	8	4.6364268E-07	Q9CQA3, P37040, Q61093, Q99LC5, Q61462, P62897, Q8K2B3, Q9DCW4	1.9496174757344E-05
Annotation Cluster 30	Enrichment Score: 2.261577509452456				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0009615~response to virus	9	0.00051107808	Q8VI94, Q8VI93, Q9Z010, P11928, Q3UPF5, Q6R5N8, Q9D8N0, Q8R5F7, Q9JHK5	0.026795093411321
UP_KW_BIOLOGICAL_PROCESS	KW-0051~Antiviral defense	11	0.00078262488	Q8VI94, Q8VI93, P11928, Q3UPF5, Q60710, P56477, Q501J6, Q8R5F7, Q8VCF0, Q61990, Q9JHK5	0.007669723836873
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	6	0.00164339651	Q8VI94, Q8VI93, P11928, Q3UPF5, Q8R5F7, Q8VCF0	0.062086553628903
GOTERM_BP_DIRECT	GO:0032728~positive regulation of interferon-beta production	6	0.00258403725	Q8VI93, P11928, Q3UPF5, Q9CZW5, Q8R5F7, Q8VCF0	0.081331023415676
Annotation Cluster 31	Enrichment Score: 2.247033225531146				
Category	Term	Count	PValue	Genes	FDR

INTERPRO	IPR011989:ARM-like	25	7.0340084E-09	Q9QZE5, Q8BYA0, P19182, Q8BVE3, Q148V7, Q6P9Q4, Q61151, Q06138, Q6PD03, Q99P21, P70168, Q80X82, P17426, Q8BKC5, Q76MZ3, Q91YE6, Q35643, Q35344, Q8CFE4, Q9D071, Q8K2Z4, P52293, P22892, Q9DBR3	2.05041345967359E-06
UP_SEQ_FEATURE	REPEAT:HEAT 3	9	2.2948482E-05	Q9QZE5, Q8BYA0, Q9D071, Q148V7, P70168, Q80X82, Q8BKC5, Q76MZ3	0.002942701480501
UP_SEQ_FEATURE	REPEAT:HEAT 1	9	7.8477318E-05	Q9QZE5, Q8BYA0, Q9D071, Q148V7, P70168, Q80X82, Q8BKC5, Q76MZ3	0.008721445939867
UP_SEQ_FEATURE	REPEAT:HEAT 2	9	7.8477318E-05	Q9QZE5, Q8BYA0, Q9D071, Q148V7, P70168, Q80X82, Q8BKC5, Q76MZ3	0.008721445939867
UP_SEQ_FEATURE	REPEAT:HEAT 4	8	0.00010425278	Q9QZE5, Q8BYA0, Q9D071, P70168, Q80X82, Q8BKC5, Q76MZ3	0.010861836182407
Annotation Cluster 32	Enrichment Score: 2.2429478555121594				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006606~protein import into nucleus	10	0.00031057477	Q91YE6, Q35344, P62827, Q8BHT4, P52293, Q99P88, P48678, P70168, P31750, Q8BKC5	0.018631983465267
KEGG_PATHWAY	mmu03013:Nucleocytoplasmic transport	14	0.00039986455	P46061, P61957, P62827, Q8BHT4, Q99P88, P63280, P70168, Q8BKC5, P63166, Q91YE6, Q35344, Q08583, P52293, Q91IX8	0.0111529705348809
GOTERM_MF_DIRECT	GO:0061608~nuclear import signal receptor activity	5	0.00044565431	Q91YE6, Q35344, P52293, P70168, Q8BKC5	0.007974367514811
GOTERM_BP_DIRECT	GO:0006607~NLS-bearing protein import into nucleus	4	0.00118695924	Q35344, P52293, P70168, Q8BKC5	0.052988079653068
GOTERM_CC_DIRECT	GO:0042564~NLS-dependent protein nuclear import complex	3	0.01364346169	O35344, P52293, P70168	0.063007986728696
Annotation Cluster 33	Enrichment Score: 2.1947246474952875				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0000786~nucleosome	14	5.5868411E-06	Q3TEA8, P10854, P10922, P43274, Q9QZQ8, P43275, P60762, P43276, P10853, P43277, P15864	9.46038426662765E-05
UP_SEQ_FEATURE	CARBOHYD:O-linked (GlcNAc) serine	10	2.0879657E-05	P10854, Q99P88, P48678, P10853, Q9WUA3, P41216, P08249	0.002290053240141
GOTERM_CC_DIRECT	GO:0043505~CENP-A containing nucleosome	4	0.01420948539	P10853	0.065030798007281
Annotation Cluster 34	Enrichment Score: 2.0850382773326834				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030117~membrane coat	5	0.00208264192	Q9QZE5, Q35643, Q8CIE6, P22892, P17426	0.015333307381046
Annotation Cluster 35	Enrichment Score: 2.0600025605999748				
Category	Term	Count	PValue	Genes	FDR
SMART	SM00033:CH	10	6.2276762E-05	Q99K51, P27870, Q80X90, Q9ES46, Q3V0K9, Q99MS7, Q8BTM8, Q91KF1, Q9WVA4, Q61233	0.0003767744128275
UP_SEQ_FEATURE	DOMAIN:Calponin-homology (CH) 1	6	0.00018300583	Q99K51, Q80X90, Q9ES46, Q3V0K9, Q8BTM8, Q61233	0.016948373561098
UP_SEQ_FEATURE	DOMAIN:Calponin-homology (CH) 2	6	0.00018300583	Q99K51, Q80X90, Q9ES46, Q3V0K9, Q8BTM8, Q61233	0.016948373561098
INTERPRO	IPR001715:CH_dom	10	0.00019778498	Q99K51, P27870, Q80X90, Q9ES46, Q3V0K9, Q99MS7, Q8BTM8, Q91KF1, Q9WVA4, Q61233	0.019218106921324
INTERPRO	IPR036872:CH_dom_sf	10	0.00023781853	Q99K51, P27870, Q80X90, Q9ES46, Q3V0K9, Q99MS7, Q8BTM8, Q91KF1, Q9WVA4, Q61233	0.021891821541386
UP_SEQ_FEATURE	DOMAIN:Calponin-homology (CH)	9	0.00051125259	Q99K51, P27870, Q9ES46, Q3V0K9, Q99MS7, Q8BTM8, Q91KF1, Q9WVA4, Q61233	0.038379003344089
GOTERM_CC_DIRECT	GO:0005884~actin filament	9	0.00070474632	O89053, Q99K51, P21107, Q3V0K9, Q62418, Q8BTM8, Q8BFZ3, P58774, Q61233	0.00617260568204
GOTERM_CC_DIRECT	GO:0032432~actin filament bundle	4	0.00235255722	Q99K51, Q3V0K9, Q8BTM8, Q61233	0.016676858359476
Annotation Cluster 36	Enrichment Score: 2.036568307114623				

Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0030170~pyridoxal phosphate binding	6	0.00295540973	Q9CZLN7, O88986, Q8R0X7, P29758, Q8VCN5, P05202	0.040745894778717
Annotation Cluster 37	Enrichment Score: 2.0321637763825593				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0016887~ATP hydrolysis activity	27	1.263843E-07	Q8CG47, Q9CZU3, Q501J6, P38647, P50516, Q9CU62, P36371, P49718, Q9JHR7, Q9D3D9, P25206, G5E829, Q6PGC1, P62334, Q91VR2, Q9CQN1, Q8IZQ2, Q8R5F7, Q8VDN2, P54823, Q9D0R4, Q9JIK5, Q3V300, Q8BHK9, P08113, O88685, E9Q634	5.59416837195884E-06
GOTERM_MF_DIRECT	GO:0004386~helicase activity	10	0.00085921191	P49718, Q9CZU3, Q8BHK9, Q501J6, Q8R5F7, P25206, Q6PGC1, Q9D0R4, P54823, Q9JIK5	0.014451944323225
GOTERM_MF_DIRECT	GO:0003724~RNA helicase activity	7	0.00327406749	Q9CZU3, Q501J6, Q8R5F7, Q6PGC1, Q9D0R4, P54823, Q9JIK5	0.044411141249332
Annotation Cluster 38	Enrichment Score: 2.023726381007481				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0046166~glyceraldehyde-3-phosphate biosynthetic process	4	0.00152214601	P17182, P17751, P08249	0.062069731669738
GOTERM_BP_DIRECT	GO:0061621~canonical glycolysis	4	0.00342738968	P17182, Q9WUA3, P17751	0.094677033144059
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	8	0.01148054954	P47738, Q8VDL4, P17182, Q9D051, Q9JLJ2, Q9WUA3, P17751	0.099898153532957
UP_KW_BIOLOGICAL_PR	KW-0324~Glycolysis	5	0.01308124249	Q8VDL4, P17182, Q9WUA3, P17751	0.085464117591821
OCESS					
Annotation Cluster 39	Enrichment Score: 1.990458135663206				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006457~protein folding	9	0.00143081603	Q8BYA0, Q9CQN1, Q9CRL6, Q9QYI0, P38647, P08113, Q9ES00, Q9ERE7, P63038	0.059286554326917
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	7	0.00771293398	Q9CQN1, Q9QYI0, P38647, P08113, Q9ES00, P63038, Q6P5E4	0.09266539257601
Annotation Cluster 40	Enrichment Score: 1.9545491605843281				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005764~lysosome	20	0.00131593169	P10605, Q9D8Y7, Q9Z0J0, Q9WV54, P08228, Q9EQH3, O08709, Q61207, Q99K70, P51569, P50516, P16675, P17047, O35114, Q9QWR8, Q9D1L9, P45377, P04441, O70439, P21300	0.010445207805163
KEGG_PATHWAY	mmu04142:Lysosome	13	0.00418701314	P10605, Q9Z0J0, Q8R0F3, Q9WV54, Q61207, Q8BVE3, P51569, P16675, P17047, O35643, O35114, Q9QWR8, P22892	0.043480521030504
Annotation Cluster 41	Enrichment Score: 1.9342897882549515				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:1902600~proton transmembrane transport	7	0.00309189708	Q8BVE3, Q9D3D9, P50516, Q9DCX2, Q8VDN2, Q91VR2, P57746	0.090321501970174
GOTERM_MF_DIRECT	GO:0046933~proton-transporting ATP synthase activity, rotational mechanism	4	0.00354219327	Q9D3D9, P50516, Q9DCX2, Q91VR2	0.047285468946754
Annotation Cluster 42	Enrichment Score: 1.9189519595849882				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0000139~Golgi membrane	24	0.00056278628	Q9QZE5, Q61543, O89051, Q9WV55, Q61107, Q8BYI6, Q62418, Q9DBH5, Q64310, Q9Z0E6, Q9CRL6, Q9D8V0, Q9CRL4, O09200, Q8CIE6, P84078, P61750, P61211, P01902, Q91VW5, O35609, Q9DCZ4, P47713, Q9CXK4	0.005015709279076

GOTERM_CC_DIRECT	GO:0005794~Golgi apparatus	40	0.00767958525	Q9QZE5, O89051, Q91ZX7, P10810, Q8BY16, Q9DBH5, P51569, Q9CR60, Q9CR64, Q8BKC5, P62331, O35643, P63323, Q8CIE6, Q8CFE4, P61021, Q8BWZ3, Q9CQD1, Q9DCZ4, P22892, P47713, P04441, Q6Y7W8, Q61543, Q61107, P10922, Q148V7, Q62418, Q64310, Q9Z0E6, Q8VDN2, Q09200, P84078, P61750, P61211, P01902, Q91VW5, P25911, Q8BG57, Q9CXB4	0.041502439455816
Annotation Cluster 43	Enrichment Score: 1.9150968793029055				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0061608~nuclear import signal receptor activity	5	0.00044565431	Q91YE6, O35344, P52293, P70168, Q8BKC5	0.007974367514811
Annotation Cluster 44	Enrichment Score: 1.8928827903719694				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005777~peroxisome	10	0.00138191547	P08228, O70579, Q9JHR7, Q9QUJ7, P38060, P20152, Q8VCF0, P41216, P54071, Q9R008	0.010800200874806
GOTERM_BP_DIRECT	GO:0015908~fatty acid transport	5	0.00298458895	O70579, Q8IZR0, Q9QUJ7, P41216, P05202	0.089155918701791
Annotation Cluster 45	Enrichment Score: 1.8659865751617364				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005721~pericentric heterochromatin	7	6.1282183E-05	Q61686, P23198, P83917, Q9Z277, Q9WU62, Q9QZQ8, P13864	0.000741222591597
GOTERM_CC_DIRECT	GO:0010369~chromocenter	5	0.00021830082	Q61686, P23198, Q8BHX3, P83917, Q9WU62	0.002217936370305
GOTERM_CC_DIRECT	GO:0090734~site of DNA damage	6	0.00097965981	Q61686, P23198, P83917, Q9QZQ8, P11103, Q8CFE2	0.008158478410019
Annotation Cluster 46	Enrichment Score: 1.8117884683758254				
Category	Term	Count	PValue	Genes	FDR
UP_KW_BIOLOGICAL_PROCESS	KW-0249~Electron transport	13	7.8217325E-05	P10639, Q9CR68, Q62425, Q9CQX2, Q61462, Q91WD5, Q8K2B3, Q9CQA3, Q61093, Q9CZ13, Q991C5, P62897, Q9DCW4	0.001277549635122
Annotation Cluster 47	Enrichment Score: 1.78476793415105				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0035985~senescence-associated heterochromatin focus	3	0.00322153738	P23198, P17095	0.021820546525291
Annotation Cluster 48	Enrichment Score: 1.7820845824722988				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	108	4.5650358E-06	Q80UY2, P27870, Q9CR68, Q6P1B1, P13864, Q6P9R2, A6H5X4, Q99K51, Q8VCT3, Q80WC7, Q61164, Q9ER72, Q8VDN2, Q9Z1K5, Q6WKZ8, Q9R008, Q99KE1, Q9D1A2, P54071, O88286, Q8R5K4, Q3V0K9, Q8BY16, Q91WD5, Q8BKE6, P27601, P62897, Q9D6R2, Q924K8, P62827, Q8VLD4, Q80YV2, P32233, Q3TBD2, Q99KK7, Q9CQA3, P61211, Q8C9W3, P38060, Q8BH69, O89112, P11928, Q91ZX7, P10711, Q9Z2F4, Q9Z277, Q9DBH5, Q9JMD0, Q99L45, P56959, P37913, Q61233, Q9JHR7, Q9Z1F9, P62274, Q9CZ13, P47713, Q8R0F3, Q8CD15, Q64516, Q9D554, Q3UPF5, Q60710, P56960, Q8IZQ2, P97315, Q9CQX2, Q64511, Q9Z219, Q61093, Q99N69, Q8BG57, Q8QZT1, Q8K411, Q505B7, Q9JIB3, P11103, P07091, P36371, O35864, P09671, Q9Z0F8, Q9QXY0, P00920, G5E829, Q9D819, Q9R061, Q8V193, Q9ESL4, P08228, P03975, Q64737, Q8R5F7, Q9EQP2, P39749, Q61462, O08663, P13020, Q8VDC3, Q80YR4, Q80Y14, P67871, O88466, Q92111, Q9WUA3, P28867, P21278, Q9R190	0.000142192411821
Annotation Cluster 49	Enrichment Score: 1.7381297480930578				

Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0033962~P-body assembly	4	0.00235652827	Q8K2F8, P62311, Q8K2D3, P54823	0.075674014027588
GOTERM_CC_DIRECT	GO:0000932~P-body	7	0.01122699196	Q8K2F8, P62311, O88685, P97789, P62488, Q8K2D3, P54823	0.055371960324666
Annotation Cluster 50	Enrichment Score: 1.6515760216432305				
Category	Term	Count	PValue	Genes	FDR
UP_KW_BIOLOGICAL_PROCESS	KW-0698~rRNA processing	9	0.00744673151	P56960, Q9CZU3, Q922K7, Q501J6, Q80WS3, Q9CRB2, Q9D0R4, Q9D1Q1, Q91IK5	0.056136899069274
Annotation Cluster 51	Enrichment Score: 1.6291836213518598				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0005200~structural constituent of cytoskeleton	9	8.2249918E-05	Q9CVB6, P21619, Q922F4, P58774, P48678, P20152, P14733, P83887, P26039	0.001729304521021
GOTERM_CC_DIRECT	GO:0005652~nuclear lamina	4	0.00190782494	P21619, P48678, P17918, P14733	0.014325721295462
GOTERM_BP_DIRECT	GO:0051664~nuclear pore localization	3	0.00322532712	P21619, P48678, P14733	0.09112503583389
GOTERM_CC_DIRECT	GO:0005638~lamin filament	3	0.00477384018	P21619, P48678, P14733	0.028530715439378
Annotation Cluster 52	Enrichment Score: 1.5938275948493417				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006260~DNA replication	9	0.00121080465	Q60520, P49718, Q60710, Q8R3C0, P25206, P17918, P37913, P39749, P07742	0.052988079653068
GOTERM_CC_DIRECT	GO:0042555~MCM complex	3	0.01647514078	P49718, Q8R3C0, P25206	0.073415539601173
Annotation Cluster 53	Enrichment Score: 1.4621875416380643				
Category	Term	Count	PValue	Genes	FDR
UP_KW_DOMAIN	KW-0041~Annexin	3	0.02469836107	P97384, P48036, P97429	0.093853772066733
Annotation Cluster 54	Enrichment Score: 1.438093832299798				
Category	Term	Count	PValue	Genes	FDR
UP_KW_CELLULAR_COMPONENT	KW-0995~Kinetochore	9	0.00942608411	P46061, O88271, Q8BHZ4, Q9WU62, Q8BHK9, Q3UHX9, Q9IMD0, Q3UAI6, Q9WVA3	0.041893707151487
Annotation Cluster 55	Enrichment Score: 1.3247061843244519				
Category	Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:1990583~phospholipase D activator activity	3	0.00101492916	P84078, P61750, P61211	0.01610481925153
INTERPRO	IPR006689:Small_GTPase_ARF/SAR	4	0.03768923702	P62331, P84078, P61750, P61211	0.98981324278438
SMART	SM00178:SAR	4	0.04191542879	P62331, P84078, P61750, P61211	0.676235584493744
SMART	SM00177:ARF	4	0.11387686599	P62331, P84078, P61750, P61211	0.991803278688525
UP_SEQ_FEATURE	LIPID:N-myristoyl glycine	8	0.14572629211	P62331, Q8R1F1, P61750, P61211, Q9CRB9, P25911, Q3UW53, Q91XV3	0.98814463544754
UP_KW_PTM	KW-0519~Myristate	9	0.42341133976	P62331, Q8R1F1, P84078, P61750, P61211, Q9CRB9, P25911, Q3UW53, Q91XV3	0.586261855047425
Annotation Cluster 56	Enrichment Score: 1.314273509450554				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0016581~NuRD complex	4	0.00405067578	Q9Z2D8, Q924K8, O35207, Q9R190	0.025404238241229
Annotation Cluster 57	Enrichment Score: 1.3092998616003875				
Category	Term	Count	PValue	Genes	FDR
KEGG_PATHWAY	mmu04216:Ferroptosis	8	0.00067239331	Q60931, Q8IZR0, Q61093, Q9QUJ7, P60335, Q61990, Q92111, P41216	0.01578722668429
KEGG_PATHWAY	mmu00071:Fatty acid degradation	7	0.01183978116	P47738, Q8IZR0, P51174, Q9QUJ7, Q9ILJ2, P41216, Q8QZT1	0.099898153532957

Annotation Cluster 58 Category GOTERM_MF_DIRECT	Enrichment Score: 1.266495273839511 Term GO:0015485~cholesterol binding	Count 6	PValue 0.00271728603	Genes Q9Z0U0, O35114, Q8BFEZ9, B9E1B6, P50637, Q991V5	FDR 0.038732839915642
Annotation Cluster 59 Category GOTERM_BP_DIRECT	Enrichment Score: 1.1762996135901642 Term GO:1902600~proton transmembrane transport	Count 7	PValue 0.00309189708	Genes Q8BVE3, Q9D3D9, P50516, Q9DCX2, Q8VDN2, Q91VR2, P57746	FDR 0.090321501970174
GOTERM_CC_DIRECT	GO:0033180~proton-transporting V-type ATPase, V1 domain	3	0.01104761189	Q8BVE3, P50516, P57746	0.055021439624112
GOTERM_CC_DIRECT	GO:0030665~clathrin-coated vesicle membrane	4	0.01714387704	Q8BVE3, Q62418, P50516, P57746	0.075731213341704
GOTERM_CC_DIRECT	GO:0000221~vacuolar proton-transporting V-type ATPase, V1 domain	3	0.01953318268	Q8BVE3, P50516, P57746	0.08481074188534
GOTERM_CC_DIRECT	GO:0033176~proton-transporting V-type ATPase complex	3	0.0228083873	Q8BVE3, P50516, P57746	0.097366897038186
Annotation Cluster 60 Category KEGG_PATHWAY	Enrichment Score: 1.1533706248925886 Term mmu00620:Pyruvate metabolism	Count 8	PValue 0.00104220932	Genes Q99KE1, P97807, P47738, Q9D051, Q9JLJ2, Q91Z53, P08249, Q8QZT1	FDR 0.020205357885108
Annotation Cluster 61 Category GOTERM_BP_DIRECT	Enrichment Score: 1.1276240581322439 Term GO:0002774~Fc receptor mediated inhibitory signaling pathway	Count 3	PValue 0.00099151369	Genes Q64281, P25911	FDR 0.046312703161397
Annotation Cluster 62 Category GOTERM_BP_DIRECT	Enrichment Score: 1.0091543053038265 Term GO:0002485~antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-dependent	Count 3	PValue 0.00195894755	Genes P36371, P01902	FDR 0.065577353622348
Annotation Cluster 63 Category KEGG_PATHWAY	Enrichment Score: 0.8464377517853936 Term mmu05169:Epstein-Barr virus infection	Count 19	PValue 0.00195176748	Genes Q60520, Q8VI93, Q9D8W5, P11928, Q9CX56, Q9WVL2, Q9WTK5, Q8VCF0, P31750, P42225, P36371, P01902, O88685, P20152, P25911, P62334, P62897, O88351	FDR 0.0330763396244561
KEGG_PATHWAY	mmu05160:Hepatitis C	15	0.00352072128	Q8VI93, P11928, Q9CQV8, P68254, Q9WVL2, Q8VCF0, P31750, P61290, Q76MZ3, P42225, P68510, P61982, P60229, P62897, O88351	0.038023789774442
Annotation Cluster 64 Category GOTERM_MF_DIRECT	Enrichment Score: 0.8168601533279145 Term GO:0019888~protein phosphatase regulator activity	Count 5	PValue 0.00277532225	Genes Q62084, Q61151, Q6PD03, Q922D4, Q76MZ3	FDR 0.03890076680934
Annotation Cluster 65 Category GOTERM_BP_DIRECT	Enrichment Score: 0.4156025014959683 Term GO:0042590~antigen processing and presentation of exogenous peptide antigen via MHC class I	Count 5	PValue 2.1377831E-05	Genes P26151, P01902, P08508, A1L314	FDR 0.001664231778309

Annotation Cluster 66 Category	Enrichment Score: 0.3772147206763222 Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0016020~membrane	189	0.00545433842	Q9QZE5, Q8CAQ8, Q9CR68, Q8BVE3, Q9CZW5, Q99P88, Q9CR60, Q9Z2D3, P19973, P17426, Q9CR64, Q8BH20, P63166, O08553, O35643, Q9CZLN7, P37040, P61021, P47753, Q9CQD1, P47754, Q8BGH2, A11314, P20152, Q9JIZ4, P26151, Q99LX0, Q80WC7, Q9CXR1, Q62418, Q9ET30, Q6WVG3, Q64310, Q9R007, Q8VDN2, Q9R0Q9, Q9DIR1, P84096, P67778, P17047, P01902, Q64281, O35114, Q9JW9, Q8BK67, Q8BYA0, Q9CQ58, P97287, Q9WV55, Q9D620, Q8BYI6, Q8BH74, Q91WD5, Q8BKE6, P57746, Q8K2B3, Q9D3D9, P27601, Q91VR2, Q91XV3, Q61543, Q8R5I9, Q9Z2G6, Q9D8V0, Q99IR1, Q9EQ32, Q76MZ3, Q3TBD2, Q9CQA3, P61211, Q04447, Q8R0X7, Q62084, Q8BH69, O89112, B1AXP6, Q8CIN4, P05202, P11928, O70579, Q91ZX7, P97300, Q81ZR0, Q8BFZ9, Q8BFZ3, Q9DBH5, P56959, P97429, Q61233, P40124, Q8CIE6, Q9DAV9, Q8BLN5, P36552, Q9CRB9, Q9JHR7, P40240, O35609, Q9CZ13, Q9DCZ4, P22892, P47713, P41216, P04441, P08249, Q6Y7W8, P10605, Q8BH43, P70290, Q64516, Q99LC8, Q81ZQ2, P18572, P19783, Q9Z0E6, Q9CQX2, Q09200, O55100, O55101, P61750, Q61093, Q99N69, Q91VW5, Q9Z0V7, Q3UH66, Q8BGS7, E9Q634, O89053, O89051, P61804, Q62425, P10810, Q9ES46, Q6R5N8, Q9IKF1, P50516, P50637, Q80X82, P31750, Q9CPI4, P62331, P36371, Q3T144, Q8CFE4, P57791, Q9Z0F8, Q9QYI0, Q9QU17, P00920, Q9CYN2, Q9DCX2, G5E829, Q3UA37, O88351, O70439, P26039, Q62159, Q8VI94, Q8VI93, Q8RI1F1, Q9CON1, Q9EQH3, Q60931, E9Q7G0, Q61107, Q99K70, P08508, Q791V5, Q9EQP2, Q8VCF0, Q61462, Q99I56, Q3UW53, P84078, P62746, B9E186, P17182, Q9Z110, O88466, P25911, Q92111, Q9WUA3, P63038, Q9CXA4, P28867, Q9J1Y5, P21278	0.031848320873929