

Supplementary Table 4: Results of the pathway analysis by the David tool on the proteins modulated in response to PCL beads						
Annotation Cluster 1	Enrichment Score: 22.30396913455931					
Category	Term	Count	PValue	Genes	FDR	
GOTERM_MF_DIRECT	GO:0005524~ATP binding	138	1.39147E-32	Q9JMH9, P07901, Q9CWX03, P10630, P70268, Q9DBL7, Q61035, P12382, O55098, Q9EPU0, Q01768, Q9JLV6, P62196, P25206, P09411, Q8BU30, P56480, Q569Z5, Q99JTI, Q9CQ37, Q9CWX9, Q6NZL6, E9QAM5, Q8VDN2, Q6PDO2, P15532, Q9R008, Q6FL6, Q4FZF3, O88685, Q9JHU4, E9Q555, Q8CDM1, Q61655, Q91VR5, Q60967, Q5SUR0, Q9DCL9, Q3U186, Q6A028, Q9J178, P23249, Q6PGC1, Q921N6, B1ARD6, Q9CZ30, Q61024, Q9D2R0, O35379, P35991, P33175, Q61390, Q04447, Q99LE6, Q8BH69, Q9D0M1, Q8C0C7, Q8K4L0, Q61879, O70172, P37913, Q9CS42, Q9ER41, P70227, Q9DBP5, B2RX12, P51829, Q9Z1F9, Q3THS6, Q810A7, P52480, P41216, P49615, P97310, Q64518, P46460, Q3TRM8, Q9ER38, O35286, P11499, Q9ESV0, P70698, P54823, O35280, Q9JIK5, Q920A7, Q5SUA5, P42932, Q9Z219, P09581, P28741, Q8VCW8, O89051, Q61699, P54276, Q3UMC0, Q9R0N0, P11983, P50516, Q9CU62, Q922D8, P36371, P49718, Q3TL44, O8CFE4, O54984, Q04899, P62334, Q9D7H3, O88351, Q99JF5, P80315, P80314, Q9Z1O9, Q9CQNI, P80313, Q60930, E9Q4Z2, Q8R5F7, Q9JHG7, P62192, Q99M31, Q3THK7, Q61102, Q9WUA2, P47809, O09110, P21958, Q8BHK9, P25911, Q9WUA3, P63038, Q922S8, P80317, Q6P542, Q8BGQ7, Q9D019, P80316	5.4545665096E-30	
				P07901, Q9QXZ0, Q8K4L0, Q9CWX03, P10630, Q9ER41, B2RX12, Q9EPU0, P62196, P25206, Q810A7, P56480, Q569Z5, P97310, Q64518, P46460, Q9CWX9, Q9ER38, O35286, P11499, E9QAM5, Q8VDN2, Q6PDO2, Q9ESV0, P54823, Q9JIK5, Q920A7, Q4FZF3, P42932, O88685, Q9JHU4, Q9DB20, E9Q555, P28741, Q8CDM1, Q61655, Q91VR5, Q3UMC0, P11983, P50516, Q9CU62, P36371, P49718, O54984, Q99J3D9, P23249, Q6PGC1, P62334, Q921N6, P80315, P80314, Q9CQNI, P80313, B1ARD6, Q9CZ30, Q8R5F7, P62192, Q99M31, Q61102, O35379, P33175, Q61390, P21958, Q8BHK9, Q99LE6, P80317, Q922S8, Q6P542, P80316	1.1652308956E-28	
GOTERM_MF_DIRECT	GO:0016887~ATP hydrolysis activity	69	3.96337E-31			

UP_KW_LIGAND	KW-0547~Nucleotide-binding	170	1.30864E-19	Q9JMH9, P07901, Q9CW03, P10630, P16858, P70268, Q9DBL7, Q61035, P12382, O55131, O55098, Q9EPU0, Q01768, Q9JLV6, P62196, P61021, P25206, P61028, P09411, Q8BU30, P62631, P56480, P47758, Q56925, Q99J11, Q9CQ37, Q9DBC7, Q9CWX9, P10126, Q3UX10, E9QAM5, Q8VDN2, Q6PDQ2, P15532, Q9R008, Q68FL6, Q4FEZ3, O88685, Q9JHU4, E9Q555, Q8CDM1, Q61655, Q91VR5, Q8BG51, Q60967, Q91YH5, Q5SUR0, Q9DCL9, Q3UI186, Q9JH78, P23249, Q6PGC1, Q921N6, BIARD6, P62827, Q9CZ30, P68372, Q9WUM5, P32233, Q61024, Q9D2R0, O35379, P61211, P35991, P33175, Q61390, Q04447, Q99LE6, Q8BH69, P60766, P62821, O8C0C7, Q8K4L0, Q922F4, Q61879, O70172, O08749, P63094, P37913, Q9CS42, Q9ER41, P70227, Q9DBP5, B2RX12, P51829, Q9ZJF9, Q3TH56, Q810A7, P52480, P41216, P49615, P97310, Q9JMF9, Q9K70, E9Q4Z2, Q8R5F7, Q9JHG7, P62192, Q99M31, P36916, P80315, P80314, Q9Z1Q9, Q9CQNI, P80313, Q60930, Q60931, Q99K70, E9Q4Z2, Q8R5F7, Q9JHG7, P62192, Q99M31, Q3THK7, Q61102, Q9WUA2, P47809, P58252, O09110, P21958, Q8BHK9, Q91V41, P62746, P25911, Q9WUA3, P63038, Q922S8, P08752, P21279, P80317, Q6P542, Q8BGQ7, Q9D019, P21278, P80316
UP_KW_LIGAND	KW-0067~ATP-binding	133	1.37069E-14	Q9JMH9, P07901, Q9CW03, P10630, P70268, Q9DBL7, Q61035, P12382, O55098, Q9EPU0, Q01768, Q9JLV6, P62196, P61021, P25206, Q810A7, P56480, P62631, P47758, Q56925, Q9Z0U1, P97310, P46460, Q9CWX9, Q9ER38, O35286, Q9Z0E6, P10126, E9QAM5, Q6PDQ2, Q9ESV0, P54823, P70698, Q9JIK5, Q920A7, Q5SUA5, Q4FEZ3, P61750, O88685, Q9JHU4, E9Q555, Q8CDM1, Q61655, Q91VR5, Q60967, Q5SUR0, Q9DCL9, Q3UI186, Q9JH78, P23249, Q6PGC1, Q921N6, BIARD6, Q9CZ30, Q61024, Q9D2R0, O35379, P35991, P33175, Q61390, Q04447, Q99LE6, Q8BH69, Q8C0C7, Q8K4L0, Q61879, O70172, P37913, Q9CS42, Q9ER41, P70227, Q9DBP5, B2RX12, P51829, Q9ZJF9, Q3TH56, Q810A7, P52480, P41216, P49615, P97310, Q64518, P46460, Q3TRM8, Q9ER38, O35286, P11499, Q9Z0E6, Q9ESV0, P70698, P54823, O35280, Q9JIK5, Q920A7, Q5SUA5, P42932, P61750, Q9Z219, P09581, P35290, P28741, Q8VCW8, Q61699, P54276, Q3UMC0, Q9R0N0, P11983, P50516, P59325, Q9CUI62, Q922D8, P35283, P62331, P36371, P49718, Q3TL44, O54984, Q04899, Q9D6F9, P62334, Q9D7H3, O88351, Q99JF5, P36916, P80315, P80314, Q9Z1Q9, Q9CQNI, P80313, Q60930, Q60931, Q99K70, E9Q4Z2, Q8R5F7, Q9JHG7, P62192, Q99M31, Q3THK7, Q61102, Q9WUA2, P47809, P58252, O09110, P21958, Q8BHK9, Q91V41, P62746, P25911, Q9WUA3, P63038, Q922S8, P08752, P21279, P80317, Q6P542, Q8BGQ7, Q9D019, P21278, P80316
INTERPRO	IPR027417:P-loop_NTPase	94	3.05391E-17	Q9JMH9, Q8K4L0, Q9CW03, Q9BDB7, Q61879, P10630, Q9DBL7, P63094, Q9ER41, Q9DBP5, B2RX12, O55131, Q9EPU0, Q9JLV6, P62196, P61021, P61028, P25206, Q810A7, P56480, P62631, P47758, Q56925, Q9Z0U1, P97310, P46460, Q9CWX9, Q9ER38, O35286, Q9Z0E6, P10126, E9QAM5, Q6PDQ2, Q9ESV0, P54823, P70698, Q9JIK5, Q920A7, Q5SUA5, Q4FEZ3, P61750, O88685, Q9JHU4, Q9JIK5, Q920A7, Q5SUA5, Q4FEZ3, P61750, O88685, Q9JHU4, Q922D8, P35283, P62331, P36371, P49718, Q3TL44, O54984, P23249, Q6PGC1, P62334, Q921N6, P36916, BIARD6, Q99K70, P62827, Q9CZ30, Q8R5F7, P32233, P62192, Q61102, O35379, P58252, P61211, P33175, P21958, Q8BHK9, Q8BVA6, Q91V41, P62746, Q99LE6, Q922S8, P08752, P21279, Q6P542, P60766, P21278, P62821
				8.0745350241E-14
UP_KW_LIGAND	KW-0067~ATP-binding	133	1.37069E-14	Q9JMH9, P07901, Q9CW03, P10630, P70268, Q9DBL7, Q61035, P12382, O55098, Q9EPU0, Q01768, Q9JLV6, P62196, P61021, P25206, Q810A7, P56480, P62631, P47758, Q56925, Q9Z0U1, P97310, P46460, Q9CWX9, Q9ER38, O35286, Q9Z0E6, P10126, E9QAM5, Q6PDQ2, Q9ESV0, P54823, P70698, Q9JIK5, Q920A7, Q5SUA5, Q4FEZ3, P61750, O88685, Q9JHU4, E9Q555, Q8CDM1, Q61655, Q91VR5, Q60967, Q5SUR0, Q9DCL9, Q3UI186, Q9JH78, P23249, Q6PGC1, Q921N6, BIARD6, Q9CZ30, Q61024, Q9D2R0, O35379, P35991, P33175, Q61390, Q04447, Q99LE6, Q8BH69, Q8C0C7, Q8K4L0, Q61879, O70172, P37913, Q9CS42, Q9ER41, P70227, Q9DBP5, B2RX12, P51829, Q9ZJF9, Q3TH56, Q810A7, P52480, P41216, P49615, P97310, Q64518, P46460, Q3TRM8, Q9ER38, O35286, P11499, Q9Z0E6, Q9ESV0, P70698, P54823, O35280, Q9JIK5, Q920A7, Q5SUA5, P42932, Q9Z219, P09581, P28741, Q8VCW8, Q61699, P54276, Q3UMC0, Q9R0N0, P11983, P50516, Q922D8, P36371, Q3UMC0, Q9R0N0, P11983, P50516, Q9CUI62, Q922D8, P36371, P49718, Q3TL44, O54984, Q04899, P62334, Q9D7H3, O88351, Q99JF5, Q99JF5, P80315, P80314, Q9Z1Q9, Q9CQNI, P80313, Q60930, E9Q4Z2, Q8R5F7, Q9JHG7, P62192, Q99M31, Q3THK7, Q61102, Q9WUA2, P47809, O09110, P21958, Q8BHK9, P25911, Q9WUA3, P63038, Q922S8, P80317, Q6P542, Q8BGQ7, Q9D019, P80316
				2.0560355812E-13

Annotation Cluster 2	Enrichment Score: 21.32238308001226			
Category	Term	Count	PValue	FDR
UP_SEQ_FEATURE	CROSSLINK:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO2)	125	6.94883E-31	1.7323436979E-27
			Genes P52431, Q8BT18, P16858, P18760, Q61550, Q61033, Q9JHH2, P62751, Q8VDF2, Q8R3Y8, P60335, Q9JHX8, P62911, P47911, P62754, Q569Z5, Q8VH51, Q9CQ37, Q80U70, P61957, Q88291, Q9ESZ8, Q62376, Q6PDO2, Q9D3E6, Q8R2N2, Q5SS16, Q9D903, Q88286, E9Q555, Q921F2, Q8CDM1, P83917, Q7TPV4, Q78PY7, Q3TLH4, P70288, Q99K48, Q8VDM6, Q62187, Q9Z2N8, Q8CGC6, P40142, Q9J178, Q8C854, P28659, P61979, Q61029, P62827, Q3UYV9, Q91WK2, Q9D6Z1, Q3UKJ7, Q8BGD9, P62267, Q8C2O3, P62702, Q55128, Q9D0E1, B1AXP6, Q8BIQ5, P41105, Q9EOK5, Q62448, P23198, P19096, Q60668, P12970, Q9DBP5, P35980, Q9Z1F9, Q3THS6, Q810A7, P52480, P62317, Q9C RB2, Q8K310, C0HKD8, Q99PL5, Q5PSV9, P97310, Q9CPN8, P62849, Q9CX56, P50580, Q6PDM2, Q35286, P70333, Q9ESV0, P42932, P62960, P21619, Q922U1, P17918, Q8CH18, Q9C WK3, Q8K019, Q3UMC0, P57784, P59325, Q8V1I6, P84089, Q6A068, Q8K4Z5, Q9DBE9, P62908, P80314, E9Q5K9, Q80U93, P80313, E9Q7G0, Q62318, Q91VM5, P97379, Q99020, Q7TMK9, P35700, Q497V5, Q8CGF7, Q61191, Q88466, P27659, Q35737, P63038, P80317, P80316	
UP_KW_PTM	KW-1017-Isopeptide bond	181	1.79077E-19	1.134151779E-18
			Genes Q9D0E1, B1AXP6, Q8BIQ5, P41105, P62821, Q61510, Q9EOK5, Q62448, P23198, P10711, P19099, Q922F4, Q60668, P63094, P12970, Q9QY76, Q9DBP5, P35980, Q9Z1F9, Q3THS6, Q810A7, Q35609, P52480, P62317, Q9C RB2, Q8K310, C0HKD8, Q99PL5, Q5PSV9, P97310, Q9CPN8, P62849, Q9CX56, P50580, Q6PDM2, Q35286, P70333, Q9ESV0, Q35280, P42932, P62960, P21619, Q61093, Q922U1, P17918, P62962, Q8CH18, Q9C WK3, Q8K019, Q3UMC0, P57784, Q9R1P4, P59325, Q8V1I6, Q6PDI5, P84089, Q9D6F9, Q9J1I3, Q5SUF2, Q6A068, Q9JKV1, Q8K4Z5, Q88351, Q9DBE9, P62908, P80314, E9Q5K9, Q80U93, P80313, Q60930, Q9CQV8, Q60931, E9Q7G0, Q62318, Q9CX34, Q91VM5, P97379, Q8R5F7, P62192, Q99020, Q7TMK9, Q61462, Q9D2V7, P35700, P17742, Q497V5, Q8CGF7, Q9Z0X1, P58252, Q61191, P17183, Q88466, P27659, Q35737, P63038, P80317, P80316	

UP_KW_PTM	KW-0832~Ubl conjugation	232	8.66763E-16	4.1171221815E-15
Q3KXN2, P52431, Q8BL97, Q8BT18, Q9CWX0, P56477, P18760, Q61550, Q8R3Y8, P62911, Q569Z5, Q8VH51, Q9CQ37, P61957, Q60591, P10126, Q5DQK4, Q9D3E6, Q5SS16, Q9DP90, Q9DBZ0, Q921FE, Q61655, Q91VR5, Q9D7M1, P48036, Q7TPV4, Q78PY7, Q99K48, Q8VDM6, Q62187, P47738, P01899, P28659, P62259, P61979, P62827, Q3UYV9, P68254, Q9DD6Z1, P32233, Q3UK17, P62267, Q8C2Q3, P14152, Q3UUV1, P47962, P62702, B1AXH6, Q8BIO5, P62821, O70456, Q62448, Q91VH2, P10711, P19096, P63094, Q9QY76, Q8BZZ3, Q9DBH0, P62317, O88895, P84228, Q8K310, Q61249, Q5PSV9, P97310, Q9CX56, P50580, Q6PDM2, P11499, Q9ESV0, P54823, Q08509, P21619, P17918, Q9DIE6, Q8CH18, O89053, Q3UMC0, P57784, Q8VJ16, Q6PD15, P68433, Q9J113, Q9JKV1, P02301, P80314, Q9DBE9, P62908, P80313, Q9CQV8, Q60930, P28352, Q60931, E9Q7G0, Q62318, Q9CX34, Q99020, Q9D2V7, Q61462, P83940, P80317, Q8BGQ7, P80316, Q9D8Y7, P07901, Q60864, Q9WTX6, P16858, Q9WVL2, Q61033, Q80U87, Q9J1H2, P42225, P62751, Q9EQ61, Q8VDF2, P60335, Q9J1X8, P07356, P47911, Q99MB1, P25322, P62754, Q80U70, O88291, Q9ESZ8, P14206, Q62376, Q6PDC2, Q6WVKZ8, P15532, Q8BMB3, Q9D071, Q8R2N2, E9Q555, O88286, Q8CDM1, Q9D8W5, P83917, Q8BG51, Q3TLH4, P70288, Q9Z2N8, Q8CGC6, P40142, Q9J178, Q8C854, Q9EPB4, P23249, Q9D1H7, Q61029, Q91WK2, Q8BGD9, Q04207, Q04447, O55128, Q9D0E1, P41105, Q61510, Q9EOK5, P23198, Q60668, P12970, Q9DBP5, P35980, Q3THS6, Q9Z1F9, Q810A7, O35609, P52480, Q3UCV8, Q9CGRB2, COHKD8, Q99PL5, Q9CPN8, P62849, O35286, P70333, O35282, Q42932, P62960, Q61093, Q922U1, P09581, P62962, Q9CWX3, Q8K019, Q9R1P4, P59325, P52019, Q9CU62, Q91XB0, P84089, P09671, Q5SUE2, Q6A068, Q8K4Z5, Q80UK7, O88351, E9Q5K9, Q80U93, Q91VM5, P97379, Q8R5F7, P62192, Q7TMK9, P35700, P17742, Q497V5, Q8CGF7, Q9Z0X1, P58252, Q61191, P17183, P25911, P27659, O88466, O35737, P63038, Q922S8				

Annotation Cluster 3 Enrichment Score: 14.766911850964359				
Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0002181~cytoplasmic translation	34	1.51802E-23	5.1005412555E-20
GOTERM_CC_DIRECT	GO:0005840~ribosome	38	9.32718E-23	6.7052043105E-21
UP_KW_MOLECULAR_FUNCTION	KW-0687~Ribonucleoprotein CTION	63	3.30529E-22	2.3798081109E-20
GOTERM_BP_DIRECT	GO:0140242~translation at postsynapse	25	8.249E-21	1.385831718E-17
GOTERM_BP_DIRECT	GO:0140236~translation at presynapse	24	1.0916E-19	1.2225872484E-16

GOTERM_BP_DIRECT	GO:0006412~translation	39	1.54195E-19	Q91KE7, P31230, P19253, P63323, P62751, P35980, P62911, Q9D7N3, P62858, Q924T2, P47911, P62631, P62830, P62754, P62908, P62849, Q991C8, P10126, Q6NZL6, P14206, Q99N96, Q497V5, P14131, P62267, Q8BWW4, P47962, P62702, P27659, P41105	1.2952369858E-16
GOTERM_CC_DIRECT	GO:0045202~synapse	73	1.54326E-18	Q60668, P19253, Q5SOX6, P12970, Q8K1A6, O55131, P63323, P62751, Q7TMB8, P35980, Q8CDG3, P62911, Q8QZV1, P61982, P47911, P62631, P62830, P98086, Q9DBCF, P62849, P29341, Q9ES97, P14206, P67778, Q08509, O55142, P14131, O55022, P62960, O89053, P70280, Q70435, Q91KJB, Q70194, P59325, Q8VDM6, P68510, P62855, P62858, Q8C052, P62259, P62908, P06800, Q9EQH3, Q60931, Q91MA1, O08539, P68254, Q0VGY8, Q9J1I6, O35382, Q04207, P62267, P58252, P47962, P62702, P62746, Q9D0E1, P27659, P21279, P41105, P21278, P62821	9.9848697934E-17
GOTERM_CC_DIRECT	GO:0098793~presynapse	48	2.45902E-18	Q91VH2, Q61735, P19253, O08529, P12970, A2A5R2, P17426, Q64324, P70227, P62331, P63323, P62751, P68510, P62855, P61028, P62911, P61982, P62858, P47911, P62830, P62754, P49615, P60904, Q8BG67, Q9EQH3, P61957, P62849, Q62418, Q9ES97, O08539, O35711, O55142, P14131, P47962, P62962, Q922S8, P41105, P62821	1.4463511044E-16
GOTERM_MF_DIRECT	GO:0003735~structural constituent of ribosome	39	5.45224E-18	Q9CXW2, Q61733, Q91KE7, P19253, P12970, P63323, P62751, P35980, P62855, P62911, Q9D7N3, Q9D1N9, P62858, Q924T2, P47911, P62858, P62754, P62908, P62849, P14206, Q99N96, Q497V5, O55142, P14131, P62267, P47962, P62702, P27659, P41105	9.159760917E-16
GOTERM_CC_DIRECT	GO:0098794~postsynapse	51	1.07492E-17	P28741, P70460, O08529, P19253, P12970, A2A5R2, P62331, P63323, P62751, Q7TMB8, Q6A028, P62196, Q9QYJ3, Q9DB96, P62855, P62911, P62858, P47911, P62830, P49615, P98086, P62908, P61979, P61957, Q9EQH3, P62849, Q62418, O08539, Q6NZL6, P14206, Q99020, O55142, P14131, P62267, P58252, P47962, Q8BPV7, P62962, Q922S8, P41105, P60766	5.7956211094E-16
GOTERM_BP_DIRECT	GO:0042274~ribosomal small subunit biogenesis	25	3.39733E-17	P62849, P70279, Q9D6Z1, Q8BU03, P14131, P63323, P62267, Q8BW10, Q9J1I3, Q8R2N2, Q9DB96, P62702, Q5SSI6, P62858, P62754	2.2830064864E-14
GOTERM_CC_DIRECT	GO:0022627~cytosolic small ribosomal subunit	22	3.9412E-17	P62908, P14131, P63323, P62267, Q8BWW4, P62849, P62855, P62702, P62858, P14206, Q6PGC1, P62754	1.9615070045E-15
GOTERM_BP_DIRECT	GO:1990145~maintenance of translational fidelity	12	7.28308E-16	P63323, P62267	3.4958803753E-13
GOTERM_CC_DIRECT	GO:0032040~small-subunit processome	23	4.57341E-15	P62849, Q9D6Z1, Q8BU03, P14131, P63323, P62267, Q9J1I3, Q9DB96, Q8R2N2, P62702, P62858, Q5SSI6, P62754	1.6438874701E-13
INTERPRO	IPR000530:Ribosomal_eS12	11	7.95552E-14	P63323	5.2586010722E-11
INTERPRO	IPR047860:Ribosomal_eS12_CS	11	7.95552E-14	P63323	5.2586010722E-11
UP_KW_MOLECULAR_FUNCTION	KW:0689~Ribosomal protein	39	1.81854E-13	Q9CXW2, Q61733, Q91KE7, Q8BK72, P19253, P12970, P63323, P62751, P35980, P62855, P62911, Q9D7N3, Q9D1N9, P62858, Q924T2, P47911, P62830, P62754, P62908, P62849, P14206, Q99N96, O55142, P14131, P62267, P47962, P62702, P27659, P41105	4.3644854566E-12
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	22	2.6552E-11	O55142, P63323, P62751, P35980, P19253, P47962, P62911, P27659, P12970, P47911, P62830, P41105	7.808696186E-10
INTERPRO	IPR004038:Ribosomal_eL8/eL30/eS12/Gad45	13	1.11989E-10	P63323, P12970, Q9CRB2	4.9349923858E-08
GOTERM_CC_DIRECT	GO:0022626~cytosolic ribosome	21	1.67654E-10	P62908, P62849, P19253, Q8CCP0, P10126, P14206, P12970, O55142, P14131, P62751, P62267, P63323, P35980, P47962, P62702, P62911, P27659, P47911, P62830, P41105, P62754	4.519669566E-09
UP_SEQ_FEATURE	DOMAIN:Ribosomal protein eL8/eL30/eS12/Gad45	12	3.07371E-10	P63323, P12970	1.5325508788E-07

INTERPRO	IPR029064:Ribosomal_eL30-like_sf	13	7.87408E-10	P63323, P12970, Q9CRB2	2.3132294929E-07
KEGG_PATHWAY	mmu03010:Ribosome	35	4.66595E-06	P19253, P12970, P63323, P62751, P35980, P62855, P62911, Q9D7N3, Q9DIN9, P62858, Q92472, P47911, P62830, P62754, P62908, P62849, P14206, Q99N96, O55142, P14131, P62267, P47962, P62702, P27659, P41105	0.00012513236066
KEGG_PATHWAY	mmu05171:Coronavirus disease - COVID-19	40	9.40421E-06	P19253, Q9WVU2, P12970, P42225, P63323, P62751, P35980, P62855, P62911, P62858, P47911, Q99MB1, P62830, P62754, O88351, P98086, P62908, P62849, Q8RSF7, P14206, P30993, Q04207, O55142, P14131, P62267, Q61093, P47962, P62702, P27659, P41105	0.00021340330196
Annotation Cluster 4	Enrichment Score: 9.880026172995398				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	55	2.11077E-15	Q8CAQ8, Q9CXW2, Q9CWU6, Q8BK72, Q9CR62, Q9CZB0, Q9DCZ4, Q9CQH3, Q9D7N3, Q9DIN9, P56480, Q8RI11, Q8BH59, Q9D7J4, P03911, Q9WTO8, P19783, Q9CQX2, Q920A7, P67778, O35435, P54071, Q9DB20, Q8R216, Q62425, Q61733, Q9JKF7, Q78IK2, P03921, P56135, P99028, Q91WD5, P42125, P09671, Q9DB84, Q9D3D9, Q9DCX2, Q92472, Q9D616, P62908, Q9CON1, Q60930, Q60931, Q9QZD8, Q9CQN6, Q791V5, Q9CQZ6, Q9WUM5, Q99N96, Q61102, Q91VD9, Q9Z0X1, O88986, Q78IK4, P63038	8.0333547665E-14
UP_KW_DOMAIN	KW-0809~Transit peptide	49	1.0392E-09	Q8CAQ8, Q8BH95, Q8BK72, Q9EP89, O08749, Q9CZB0, Q9CQH3, Q9D7N3, Q9DIN9, P56480, Q991T1, P19783, Q920A7, Q99KE1, O35435, Q9Z219, Q99K10, P54071, Q9DB20, Q8R216, Q8VCW8, Q8K411, Q61733, P99028, Q9CQ62, Q91WD5, Q91VA6, P42125, Q3UI86, P47738, Q3TL44, P09671, Q9D3D9, Q9D616, P97493, Q6PB66, Q9CQN1, E9Q4Z2, Q9WUM5, Q91WK5, Q99N96, Q61102, P20108, Q91VD9, Q9Z0X1, O88986, Q78IK4, P63038, Q9JK81	2.3901712123E-08
UP_KW_CELLULAR_COMPO	KW-0496~Mitochondrion	104	1.72134E-09	Q3KNN2, Q8CAQ8, P07901, Q8BH95, Q8BK72, Q9CR62, Q9DBL7, Q9D7N3, P56480, Q991T1, Q9WTO8, Q9DIK1, Q99KE1, P67778, O55022, P54071, Q9DB20, Q921F2, Q91VR5, Q8BG51, Q78IK2, P03921, P56135, Q91WD5, Q62465, Q91VA6, Q3UI86, Q9CQB5, P47738, Q9D3D9, Q920L1, Q9EPB4, Q92472, Q9D616, P62897, Q9CQZ6, Q9WUM5, Q91WK5, Q99N96, O08734, Q04447, Q78IK4, Q8BHG1, Q9JK81, B1AXRP6, Q9CXW2, Q9CWU6, Q9EP89, O08749, Q9CZB0, Q9DCZ4, Q9CQH3, Q9DIN9, P41216, Q8RI11, Q8BH59, Q9D7J4, Q9DOL7, P03911, Q9D7A8, P19783, Q9CQX2, Q9JK5, Q920A7, O35435, Q9Z219, Q99K10, Q9D8S9, Q8R216, Q8VCW8, Q8K411, Q62425, Q61733, Q9JKF7, P99028, Q3UMC0, Q9CQ62, Q9CPU4, P42125, Q3TL44, P09671, Q9D8B4, P49710, Q9DCX2, Q9JN90, P97493, P62908, Q6PB66, Q9CQN1, Q60930, P28352, Q60931, Q9QZD8, Q9CQN6, Q791V5, E9Q4Z2, Q8RSF7, Q61102, Q91VD9, P20108, Q9Z0X1, O88986, Q8VB10, P63038	1.6352717621E-08
UP_SEQ_FEATURE	TRANSIT:Mitochondrion	48	7.99625E-08	Q8K411, Q8VCW8, Q8CAQ8, Q61733, Q8BH95, Q8BK72, P99028, O08749, Q9EP89, Q9CQ62, Q91WD5, Q91VA6, P42125, Q3UI86, P47738, Q3TL44, P09671, Q9CZB0, Q9D3D9, Q9CQH3, Q9D7N3, E9Q4Z2, Q9WUM5, P19783, Q91WK5, Q99N96, Q920A7, Q61102, Q99KE1, P20108, Q91VD9, Q9Z0X1, Q9Z219, O88986, Q99K10, Q78IK4, P63038, Q9JK81, P54071, Q9DB20, Q8R216	1.8122403949E-05
Annotation Cluster 5	Enrichment Score: 9.224259191443705				
Category	Term	Count	PValue	Genes	FDR

GOTERM_MF_DIRECT	GO:0016887~ATP hydrolysis activity	69	3.96337E-31	P07901, Q9OXXZ, Q8K4L0, Q9CW03, P10630, Q9ER41, B2RX12, Q9EPU0, P62196, P25206, Q810A7, P56480, Q569Z5, P97310, Q64518, P46460, Q9CWXX9, Q9ER38, O35286, P11499, E9QAM5, Q8VDN2, Q6PDQ2, Q9ESV0, P54823, Q9IJK5, Q920A7, Q4FZF3, P42932, O88685, Q9IHU4, Q9DB20, E9Q555, P28741, Q8CDM1, Q61655, Q91VR5, Q3UMC0, P11983, P50516, Q9CU62, P36371, P49718, O54984, Q9D3D9, P23249, Q6PGC1, P62334, Q921N6, P80315, P80314, Q9CQNI, P80313, B1ARD6, Q9CZ30, Q8RSF7, P62192, Q99M31, Q61102, O35379, P33175, Q61390, P21938, Q8BHK9, Q99LE6, P80317, Q922S8, Q6P542, P80316	1.16523085956E-28
GOTERM_BP_DIRECT	GO:0140588~chromatin looping	30	1.36109E-16	Q8CDM1, Q61655, Q91VR5, Q8K4L0, Q3UMC0, P10630, Q61550, Q9ER41, P49718, Q9EPU0, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5, P97310, P46460, Q9CWXX9, Q8RSF7, O35286, E9QAM5, Q9ESV0, Q6PDQ2, P54823, Q9IJK5, Q920A7, Q4FZF3, Q8BHK9, E9Q555	7.622093903E-14
GOTERM_MF_DIRECT	GO:0061775~cohesin loader activity	30	1.38485E-16	Q8CDM1, Q61655, Q91VR5, Q9CW03, Q8K4L0, Q3UMC0, P10630, Q9ER41, P49718, Q9EPU0, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5, P97310, P46460, Q9CWXX9, Q8RSF7, O35286, E9QAM5, Q9ESV0, Q6PDQ2, P54823, Q9IJK5, Q920A7, Q4FZF3, Q8BHK9, E9Q555	1.8095396088E-14
GOTERM_MF_DIRECT	GO:0140665~ATP-dependent H3-H4 histone complex chaperrone activity	29	7.88537E-16	Q8CDM1, Q61655, Q91VR5, Q8K4L0, Q3UMC0, P10630, Q9ER41, P49718, Q9EPU0, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5, P97310, P46460, Q9CWXX9, Q8RSF7, O35286, E9QAM5, Q9ESV0, Q6PDQ2, P54823, Q9IJK5, Q920A7, Q4FZF3, Q8BHK9, E9Q555	7.7276610138E-14
GOTERM_MF_DIRECT	GO:0140584~chromatin extrusion motor activity	29	7.88537E-16	Q8CDM1, Q61655, Q91VR5, Q8K4L0, Q3UMC0, P10630, Q9ER41, P49718, Q9EPU0, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5, P97310, P46460, Q9CWXX9, Q8RSF7, O35286, E9QAM5, Q9ESV0, Q6PDQ2, P54823, Q9IJK5, Q920A7, Q4FZF3, Q8BHK9, E9Q555	7.7276610138E-14
GOTERM_MF_DIRECT	GO:0140849~ATP-dependent H2AZ histone chaperrone activity	29	1.09904E-15	Q8CDM1, Q61655, Q91VR5, Q8K4L0, Q3UMC0, P10630, Q9ER41, P49718, Q9EPU0, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5, P97310, P46460, Q9CWXX9, Q8RSF7, O35286, E9QAM5, Q9ESV0, Q6PDQ2, P54823, Q9IJK5, Q920A7, Q4FZF3, Q8BHK9, E9Q555	9.9421065413E-14
GOTERM_MF_DIRECT	GO:0003689~DNA clamp loader activity	29	3.9599E-15	Q8CDM1, Q61655, Q91VR5, Q8K4L0, Q3UMC0, P10630, Q9ER41, P49718, Q9EPU0, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5, P97310, P46460, Q9CWXX9, Q8RSF7, O35286, E9QAM5, Q9ESV0, Q6PDQ2, P54823, Q9IJK5, Q920A7, Q4FZF3, Q8BHK9, E9Q555	3.3263177054E-13
GOTERM_MF_DIRECT	GO:0003724~RNA helicase activity	17	1.16187E-10	Q61655, Q91VR5, Q8K4L0, Q9CWXX9, Q8RSF7, P10630, O35286, E9QAM5, Q9ESV0, P54823, Q9IJK5, Q4FZF3, Q9EPU0, Q810A7, Q6PGC1, Q921N6, Q569Z5	8.0374275203E-09
UP_SEQ_FEATURE	MOTIF:DEAD box	12	1.20664E-08	Q61655, Q4FZF3, Q91VR5, Q8K4L0, Q9CWXX9, P10630, Q810A7, Q9ESV0, Q921N6, P54823, Q569Z5, Q9IJK5	5.0135910325E-06
UP_SEQ_FEATURE	MOTIF:Q motif	12	1.64283E-07	Q61655, Q4FZF3, Q91VR5, Q8K4L0, Q9CWXX9, P10630, Q810A7, Q9ESV0, Q921N6, P54823, Q569Z5, Q9IJK5	3.412977376E-05
INTERPRO	IPR050079:DEAD_box_RNA_helicase	8	1.82983E-07	Q4FZF3, Q8K4L0, Q9CWXX9, Q810A7, Q9ESV0, Q921N6, Q569Z5, Q9IJK5	2.1991262892E-05
INTERPRO	IPR014014:RNA_helicase_DEAD_Q_motif	11	5.66756E-07	Q61655, Q4FZF3, Q91VR5, Q8K4L0, Q9CWXX9, P10630, Q810A7, Q9ESV0, Q921N6, P54823, Q569Z5	5.9940085276E-05

GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling	54	6.40886E-07	Q8K4L0, Q9D967, P10630, P70268, Q9ER41, O55098, Q9EP10, P25206, Q810A7, P52480, O569Z5, P49615, Q6PB44, P46460, Q9CWX9, O35286, E9QAM5, Q6PDO2, Q9ESV0, P54823, Q91JK5, Q920A7, O35280, Q4FZF3, P09581, E9O555, O8CDM1, Q922H1, Q61655, Q91VRS, Q7TPV4, P70288, Q3UMC0, Q9WUP7, Q62187, Q922N8, P49718, Q8V1J6, Q91J78, Q6PGC1, Q921N6, O88351, Q9D853, P06800, Q8R5F7, Q9JHG7, Q9CPCP0, P47809, P35991, O09110, Q61191, Q8BHK9, P60762, P25911	8.9724108736E-05
UP_KW_MOLECULAR_FUNCTION	KW-0347~Helicase	23	8.07084E-07	Q61655, Q91VRS, P97310, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, E9QAM5, Q9ESV0, Q6PDO2, P54823, Q91JK5, P49718, Q4FZF3, Q9EP10, Q8BHK9, Q810A7, P25206, P23249, Q6PGC1, Q921N6, Q569Z5	9.6850119352E-06
UP_SEQ_FEATURE	DOMAIN:Helicase C-terminal	17	3.85335E-06	Q61655, Q91VRS, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, Q9ESV0, Q6PDO2, P54823, Q91JK5, Q4FZF3, Q8BHK9, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00050560001585
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	25	3.86289E-06	Q99JW2, Q91VRS, P19096, P10630, P51569, P18242, Q8BLF1, P49718, Q91LV6, Q921N6, Q569Z5, P23780, P27046, Q9CWX9, Q8R5F7, O35286, P17439, Q3UX10, Q9ESV0, Q6PDO2, P12265, Q91JK5, Q4FZF3, Q9DTE3, P48999	0.00014196131885
INTERPRO	IPR011545:DEAD/DEAH_box_helicase_dom	14	4.20759E-06	Q61655, Q91VRS, Q8K4L0, Q9CWX9, P10630, O35286, Q9ESV0, P54823, Q91JK5, Q4FZF3, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00041203173871
INTERPRO	IPR001650:Helicase_C-like	17	6.09549E-06	Q61655, Q91VRS, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, Q9ESV0, Q6PDO2, P54823, Q91JK5, Q4FZF3, Q8BHK9, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00057558795795
UP_SEQ_FEATURE	DOMAIN:Helicase ATP-binding	17	7.71455E-06	Q61655, Q91VRS, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, Q9ESV0, Q6PDO2, P54823, Q91JK5, Q4FZF3, Q8BHK9, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00091582749241
SMART	SM00490:HELICc	17	8.60543E-06	Q61655, Q91VRS, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, Q9ESV0, Q6PDO2, P54823, Q91JK5, Q4FZF3, Q8BHK9, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00050944161435
INTERPRO	IPR014001:Helicase_ATP-bd	17	8.64566E-06	Q61655, Q91VRS, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, Q9ESV0, Q6PDO2, P54823, Q91JK5, Q4FZF3, Q8BHK9, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00078824602707
SMART	SM00487:DEXDc	17	1.08631E-05	Q61655, Q91VRS, Q8K4L0, Q9CWX9, Q8R5F7, P10630, O35286, Q9ESV0, Q6PDO2, P54823, Q91JK5, Q4FZF3, Q8BHK9, Q810A7, Q6PGC1, Q921N6, Q569Z5	0.00053591186472
INTERPRO	IPR000629:RNA-helicase_DEAD-box_CS	9	1.37852E-05	Q4FZF3, Q8K4L0, Q9CWX9, P10630, Q810A7, Q9ESV0, Q921N6, P54823, Q569Z5	0.00117574015557
UP_SEQ_FEATURE	DOMAIN:DEAD-box RNA helicase Q	7	0.000506066	Q4FZF3, Q91VRS, Q8K4L0, Q9CWX9, P10630, Q9ESV0, Q921N6	0.04350425671469
Annotation Cluster 6	Enrichment Score: 8.891782974625919				
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	33	4.16117E-13	Q921F2, Q8BNV1, Q8BL97, Q91VRS, Q99K48, Q9EP14, Q8V1J6, Q8CGC6, Q6NVF9, P84104, P60335, Q91IX8, P28659, Q8K4Z5, Q9DBR1, Q8VH51, P61979, O88291, Q91VM5, Q9CWX9, P29341, O35286, Q7TNMK9, Q9DBC3, Q8CGF7, P62960, Q3U0V1, Q922U1, O55128, O35737, Q91K81, Q91VU7, Q9CWK3	1.7476904975E-10
UP_KW_BIOLOGICAL_PROCESS	KW-0507~mRNA processing	54	7.99017E-13	Q8BNV1, Q8BL97, Q8BT18, Q9D883, Q9EP14, Q91KP5, P62311, P84104, Q91IX8, P62317, O569Z5, C0HKD8, Q8VH51, O88291, Q9CWX9, P29341, Q6PDM2, O35286, Q9DBC3, P62320, P62960, Q7TNK4, Q922U1, Q9CWK3, Q921F2, Q91VRS, Q99K48, P57784, Q6ZWM4, Q8CGC6, Q8V1J6, Q6NVF9, Q5SUF2, Q6A068, P28659, Q8K4Z5, Q9DBR1, E9O5K9, P61979, Q3UYV9, Q91VM5, Q3UKJ7, Q7TNK9, Q64213, Q99PV0, Q3U0V1, P62305, O55128, Q9D0E1, O35737, Q91VU7, Q8BIQ5, Q921M3, Q9DAW6	7.5121424055E-11

UP_KW_BIOLOGICAL_PROC	KW-0508~mRNA splicing	47	1.40414E-12	E9Q5K9, P61979, O88291, Q91VM5, Q3UYV9, Q9CWX9, P29341, Q6PDM2, O35286, Q3UKJ7, Q7TMK9, Q64213, Q99PV0, P62320, P62960, Q3U0V1, Q7TNC4, Q922U1, P62305, O55128, Q9DOE1, O35737, Q91VU7, Q921M3, Q9CWK3, Q9DAW6	7.5121424055E-11
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	28	4.56822E-12	Q921F2, Q8BL97, Q99K48, P57784, Q9IKP5, Q8VJL6, Q8CGC6, P84104, QSSUE2, Q9JIX8, P28659, Q8VH51, P61979, O88291, Q91VM5, Q9CWX9, P29341, Q6PDM2, O35286, Q3UKJ7, Q7TMK9, Q8CGF7, P62960, Q3U0V1, O55128, O35737, Q91VU7, Q9CWK3	1.7054674025E-09
GOTERM_BP_DIRECT	GO:0000398~mRNA splicing, via spliceosome	25	2.63494E-10	Q8BL97, Q8BT18, P57784, Q9D883, Q6ZWM4, P62311, P84104, Q6A068, P62317, Q8K4Z5, C0HKD8, Q569Z5, E9Q5K9, Q3UYV9, Q9EPV8, Q3UKJ7, Q64213, Q62376, Q99PV0, P62320, Q8C2Q3, Q922U1, P62305, Q921M3, Q9DAW6	8.0485530753E-08
GOTERM_CC_DIRECT	GO:0071005~U2-type precatalytic spliceosome	14	1.21966E-08	Q8BT18, P57784, Q3UKJ7, Q99PV0, P62320, Q6ZWM4, P62311, Q922U1, P62305, P62317, Q8K4Z5, C0HKD8, Q921M3, Q9DAW6	2.4659981382E-07
GOTERM_CC_DIRECT	GO:0005681~spliceosomal complex	20	4.82354E-08	P61979, Q91VM5, P29341, Q6PDM2, O35286, P57784, Q7TMK9, Q64213, Q9D883, Q62376, Q99PV0, P62320, Q8CGC6, Q922U1, P62305, P62317, Q6A068, Q8K4Z5, Q9DOE1, O35737	8.916666781E-07
UP_KW_CELLULAR_COMPO	KW-0747~Spliceosome	25	5.57054E-08	Q8BT18, P57784, Q9D883, Q6ZWM4, P62311, Q8CGC6, Q6A068, P62317, Q8K4Z5, C0HKD8, Q569Z5, P61979, P29341, Q6PDM2, Q3UKJ7, Q7TMK9, Q64213, Q99PV0, P62320, Q922U1, P62305, Q9DOE1, O35737, Q921M3, Q9DAW6	4.2336096132E-07
GOTERM_CC_DIRECT	GO:0071013~catalytic step 2 spliceosome	18	9.0247E-08	P61979, Q8BT18, Q91VM5, P29341, Q6PDM2, P57784, Q7TMK9, Q9D883, Q99PV0, P62311, P62305, P62317, Q6A068, Q8K4Z5, Q9DOE1, O35737, Q921M3	1.5781037762E-06
KEGG_PATHWAY	mmu03040:Spliceosome	26	0.007270026	Q8BL97, P57784, Q9D883, Q6ZWM4, P62311, P84104, Q810A7, P60335, Q6A068, Q9JIX8, P62317, Q8K4Z5, Q569Z5, P61979, Q3UYV9, Q6PDM2, O35286, Q62376, Q99PV0, P62320, Q8CGF7, Q922U1, P62305, Q9DOE1, Q921M3, Q9DAW6	0.06702055016645
Annotation Cluster 7 Enrichment Score: 8.490985769601545					
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0000502~proteasome complex	19	7.81184E-15	Q9D8W5, O70435, Q9CX56, Q9JMA1, O35593, P54728, Q9R1P4, P62192, Q9R1P3, Q60692, Q99JL4, Q6PDI5, Q8BHL8, P62196, O88685, Q9IKV1, P62334, Q8CDN6, Q922X2	2.6601363579E-13
UP_KW_CELLULAR_COMPO	KW-0647~Proteasome	21	1.62903E-14	P97372, Q9D8W5, O70435, Q9CX56, Q9JMA1, O35593, Q9WUP7, P54728, Q9R1P4, P62192, Q9R1P3, Q60692, Q99JL4, Q6PDI5, Q8BHL8, P62196, O88685, Q9IKV1, P62334, Q8CDN6, O35955	2.0634430096E-13
KEGG_PATHWAY	mmu03050:Proteasome	16	1.94773E-08	Q9D8W5, O70435, Q9CX56, O35593, Q9R1P4, P62192, Q9R1P3, Q60692, Q99JL4, Q8BHL8, P62196, O88685, Q9IKV1, P62334, O35955	8.2082939241E-07
GOTERM_CC_DIRECT	GO:0022624~proteasome accessory complex	8	2.37002E-07	Q9D8W5, Q99JL4, Q9CX56, P62196, O35593, P62192, O88685, P62334	3.9318017393E-06
KEGG_PATHWAY	mmu05017:Spinocerebellar ataxia	22	3.51197E-05	Q9D8W5, P51432, O70435, Q60930, Q64518, Q60931, Q9CX56, O35593, Q9R1P4, P62192, Q9D6Z1, Q9R1P3, Q60692, Q920A7, P70227, Q99JL4, P62196, O88685, Q9IKV1, P62334, P62897, P21279	0.00064751966528
GOTERM_BP_DIRECT	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	25	5.48997E-05	O70435, Q9D7M1, Q9WIX6, P70362, O35593, Q9R1P4, Q9R1P3, Q9DBH0, Q8BHL8, Q8BZZ2, P62196, Q9J78, P62334, Q9CX56, Q9JMA1, Q62318, P54728, P62192, P17439, Q60692, Q6WKZ8, Q99JL4, Q78IE5, O88685, O35955	0.0042898396482

Annotation Cluster 8 Enrichment Score: 6.889986260078688

Category	Term	Count	PValue	Genes	FDR
INTERPRO	IPR035979:RBD_domain_sf	33	2.04804E-08	Q921F2, Q8BNV1, Q8BL97, Q60668, Q99K48, Q9Z1D1, Q9D883, Q8VU6, Q8CGC6, Q6NVF9, Q8C854, P84104, Q9JIX8, P28659, Q8K310, Q8VH51, Q9CPN8, Q91VM5, P97379, P29341, Q6PDM2, P70333, Q7TMK9, Q99020, Q62376, Q8BGD9, Q9JIK5, Q8C203, Q8BWW4, Q91V81, Q9D0E1, Q35737, Q8BIQ5	4.2107430859E-06
UP_SEQ_FEATURE	DOMAIN:RRM	30	2.09889E-08	Q921F2, Q8BNV1, Q8BL97, Q60668, Q99K48, Q9Z1D1, Q9D883, Q8VU6, Q8CGC6, Q6NVF9, Q8C854, P84104, P28659, Q8K310, Q8VH51, Q91VM5, P97379, P29341, Q6PDM2, P70333, Q7TMK9, Q99020, Q62376, Q8BGD9, Q8C203, Q8BWW4, Q91V81, Q9D0E1, Q35737, Q8BIQ5	6.5406625252E-06
UP_SEQ_FEATURE	DOMAIN:RRM 1	18	3.47664E-08	Q8VH51, Q921F2, Q9CPN8, Q60668, P29341, Q99K48, Q6PDM2, P70333, Q7TMK9, Q99020, Q8CGC6, Q8VU6, Q8C203, Q8C854, P28659, Q9D0E1, Q35737, Q8K310	8.6672724212E-06
UP_SEQ_FEATURE	DOMAIN:RRM 2	18	3.47664E-08	Q8VH51, Q921F2, Q9CPN8, Q60668, P29341, Q99K48, Q6PDM2, P70333, Q7TMK9, Q99020, Q8CGC6, Q8VU6, Q8C203, Q8C854, P28659, Q9D0E1, Q35737, Q8K310	8.6672724212E-06
INTERPRO	IPR012677:Nucleotide-bd_a/b_plait_sf	33	3.78317E-08	Q921F2, Q8BNV1, Q8BL97, Q60668, Q99K48, Q9Z1D1, Q9D883, Q8VU6, P62751, Q8CGC6, Q6NVF9, Q8C854, P84104, Q9JIX8, P28659, Q8K310, Q8VH51, Q9CPN8, Q91VM5, P97379, P29341, Q6PDM2, P70333, Q7TMK9, Q99020, Q62376, Q8BGD9, Q8C203, Q91V81, Q9D8C4, Q9D0E1, Q35737, Q8BIQ5	5.8839481508E-06
SMART	SM00360:RRM	29	1.05692E-07	Q921F2, Q8BL97, Q60668, Q99K48, Q9Z1D1, Q9D883, Q8VU6, Q8CGC6, Q6NVF9, Q8C854, P84104, P28659, Q8K310, Q8VH51, Q9CPN8, Q91VM5, P97379, P29341, Q6PDM2, P70333, Q7TMK9, Q99020, Q62376, Q8BGD9, Q8C203, Q91V81, Q9D0E1, Q35737, Q8BIQ5	1.0535889212E-05
INTERPRO	IPR000504:RRM_dom	29	2.14199E-07	Q921F2, Q8BL97, Q60668, Q99K48, Q9Z1D1, Q9D883, Q8VU6, Q8CGC6, Q6NVF9, Q8C854, P84104, P28659, Q8K310, Q8VH51, Q9CPN8, Q91VM5, P97379, P29341, Q6PDM2, P70333, Q7TMK9, Q99020, Q62376, Q8BGD9, Q8C203, Q91V81, Q9D0E1, Q35737, Q8BIQ5	2.462531114E-05
UP_SEQ_FEATURE	DOMAIN:RRM 3	9	0.000170508	Q8VH51, Q8CGC6, Q8C854, P29341, P28659, P70333, Q7TMK9, Q9D0E1, Q35737	0.0177115584347
Annotation Cluster 9					
Category	Enrichment Score: 6.860901537799974	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0140662~ ATP-dependent protein folding chaperone	14	6.67948E-13	P80315, P80314, Q9CQNI, Q61699, P80313, P07901, P11983, P11499, Q99M31, P42932, Q61390, P63038, P80317, P80316	5.2367084477E-11
GOTERM_BP_DIRECT	GO:0061077~chaperone-mediated protein folding	13	3.81256E-10	P60904, P80315, P80314, P45878, P80313, P42932, P24369, P11983, P11499, Q99KID5, P80317, P80316	1.0675178138E-07
INTERPRO	IPR017998:Chaperone_TCP-1	9	7.50882E-10	P80315, P80314, P80313, P42932, Q61390, P11983, P63038, P80317, P80316	2.3132294929E-07
GOTERM_CC_DIRECT	GO:0005832~chaperonin-containing T-complex	8	1.74418E-09	P80315, P80314, P80313, P42932, Q61390, P11983, P80317, P80316	4.0302923659E-08
GOTERM_BP_DIRECT	GO:0006457~protein folding	20	4.55446E-09	Q8BYA0, P80315, P80314, Q9CQNI, Q61699, P80313, P07901, P11983, P11499, Q99M31, Q8R180, P17742, P42932, Q35685, Q61390, Q9QYJ3, P24369, P63038, P80317, P80316	1.0201981043E-06
GOTERM_MF_DIRECT	GO:0044183~protein folding chaperone	14	5.27088E-09	P80315, P80314, P80313, P07901, Q9R233, P11983, P11499, Q99M31, P42932, Q310V1, Q61390, Q9QYJ3, P80317, P80316	2.951690964E-07
INTERPRO	IPR027413:GROEL-like_equatorial_sf	9	1.23117E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P63038, P80317, P80316	3.2552223982E-06
INTERPRO	IPR002194:Chaperonin_TCP-1_CS	8	1.41811E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P80317, P80316	3.4086135535E-06

INTERPRO	IPR027410:TCP-1-like_intermed_sf	9	2.5481E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P63038, P80317, P80316	4.2107430859E-06
INTERPRO	IPR002423:Cpn60/GroEL/TCP-1	9	2.5481E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P63038, P80317, P80316	4.2107430859E-06
INTERPRO	IPR027409:GroEL-like_apical_dom_sf	9	2.5481E-08	P80315, P80314, P80313, P42932, Q61390, P11983, P63038, P80317, P80316	4.2107430859E-06
INTERPRO	IPR053374:TCP-1_chaperonin	7	8.88067E-08	P80315, P80314, P80313, Q61390, P11983, P80317, P80316	1.1181185028E-05
GOTERM_BP_DIRECT	GO:1904851~positive regulation of establishment of protein localization to telomere	7	1.02682E-07	P80315, P80314, P80313, P42932, P11983, P80317, P80316	1.8158518446E-05
UP_KW_MOLECULAR_FUNCTION	KW-0143~Chaperone	30	3.3421E-07	Q8BYA0, P07901, Q99L47, Q3UMC0, P11983, Q9ER41, Q9DAP7, Q9QYJ3, Q9QKD5, P60904, P80315, P80314, Q9CON1, P80313, Q61249, Q78Z47, P11499, Q99M31, Q9CYP0, Q9DIR1, P42932, Q61390, Q9CQI6, P63038, Q9DIE6, P80317, Q9Z2X2, Q9W7Z0, P80316, Q91YW3	4.812620085E-06
GOTERM_BP_DIRECT	GO:0051086~chaperone mediated protein folding independent of cofactor	6	3.79632E-07	P80315, P80314, P80313, P42932, P11983, P80316	6.0741150416E-05
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	15	3.90479E-07	P80315, P80314, Q9CON1, P80313, P07901, Q99L47, P11983, P11499, Q8BQM4, P42932, O35683, Q61390, Q9QYJ3, P80317, P80316	1.766168271E-05
GOTERM_CC_DIRECT	GO:0044297~cell body	17	5.58465E-07	Q9WTR1, P80315, Q3UHQ3, P80314, P80313, P11983, P42932, Q61160, P09581, O09131, P41105, P62754, P80317, P08752, P21279, P80316	8.8128475686E-06
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	23	5.69851E-07	P80315, P80314, P80313, P07901, P11438, P16858, P11983, Q9JMD0, P11499, Q91XBO, P67778, P42932, Q61191, Q80UM3, P47962, P24369, P63038, P62962, P62830, P80317, P21279, O88286, P80316	8.3247856544E-05
GOTERM_BP_DIRECT	GO:0032212~positive regulation of telomere maintenance via telomerase	9	9.93244E-06	P80315, P80314, P80313, P42932, Q9JLV6, Q60668, P11983, P80317, P80316	0.00095351382745
GOTERM_BP_DIRECT	GO:0007339~binding of sperm to zona pellucida	9	6.93906E-05	P80315, P80314, P80313, P42932, Q60930, P11983, P80317, Q80X50, P80316	0.00485734324259
GOTERM_CC_DIRECT	GO:0002199~zona pellucida receptor complex	5	0.000189341	P80315, P80314, P42932, P11983, P80317	0.00170143862985
Annotation Cluster 10	Enrichment Score: 5.467196327923353				
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0005764~lysosome	35	1.676E-10	Q9D8Y7, P31996, O70172, Q68FD5, O08529, P51569, P18242, P50516, P70665, P35283, O54782, Q9CQF9, P45377, O70439, O89023, P10605, P57716, P23780, Q9EQH3, Q9Z0M5, P11438, Q99K70, P17439, P12265, P16675, O35657, Q9CWK8, O35114, P50429, O88668, O89017, Q91V41, P29416, O70404, P06797	4.519669566E-09
KEGG_PATHWAY	mmu04142:Lysosome	21	5.79903E-05	P10605, P31996, P23780, Q9Z0M5, P11438, Q8BVE3, Q68FD5, P18242, P51569, P17439, P51863, P12265, P16675, O35657, P50429, O35114, O89017, P24668, P29416, P06797, O89023	0.00100603289647
UP_KW_CELLULAR_COMPONENT	KW-0458~Lysosome	31	0.004081132	P70280, P09528, Q9D8Y7, P31996, O70172, P51569, P18242, P29391, P50516, P51863, P70665, P35283, Q9CQF9, O89023, P10605, P23780, Q9Z0M5, P11438, Q99K70, P17439, P12265, P16675, O35657, Q58A65, O35114, P50429, O89017, P24668, P29416, O70404, P06797	0.0134783776351
Annotation Cluster 11	Enrichment Score: 5.17867379906589				
Category	Term	Count	PValue	Genes	FDR
UP_SEQ_FEATURE	LIPID:N6-decanoyllysine	12	6.32129E-14	P68433, P84228	5.2529878514E-11
INTERPRO	IPR000164:Histone_H3CENP-A	13	2.34965E-12	P68433, P84228, P02301	1.2424944041E-09

SMART	SM00428.H3	13	3.25595E-12	P68433, P84228, P02301	9.6376260297E-10
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	36	3.10927E-09	Q9WV55, Q9RUT2, Q9CWC03, Q9CU62, Q9QY76, P68433, P68510, Q8BHL8, Q9Z1F9, Q6ZOM8, P84228, P02301, O88351, P62259, Q99K70, P63827, P70353, Q61462, Q8VDN2, O08734, Q8VE37, P67778, Q9CWK8, Q61093, Q8BH69, P29416	1.8282521871E-07
GOTERM_BP_DIRECT	GO:0040029~epigenetic regulation of gene expression	13	6.04636E-08	P67778, Q80W54, O88895, P84228, Q8BZM1, Q8R216	1.1286537925E-05
UP_KW_PTM	KW-0164~Citullination	22	4.16216E-07	Q9DBE9, Q61029, Q8K019, Q62318, Q7TPV4, P19253, P70279, Q61033, P62751, P68433, Q9J113, P84228, P02301	1.3180180378E-06
GOTERM_BP_DIRECT	GO:0006325~chromatin organization	24	2.54139E-06	Q80U70, P23198, Q5PSV9, Q62318, P70288, Q80W54, Q04207, P68433, O54962, Q61191, Q9J113, P60762, O88895, P84228	0.00029445108842
UP_SEQ_FEATURE	DOMAIN:Histone H2A/H2B/H3	14	3.31966E-06	P68433, P70353, P84228, P02301	0.00045977283886
INTERPRO	IPR007125:Histone_H2A/H2B/H3	14	8.99065E-06	P68433, P70353, P84228, P02301	0.00079237620857
UP_KW_PTM	KW-0013~ADP-ribosylation	20	5.14003E-05	P42225, P68433, E9Q7G0, Q62318, P16858, P63094, P70168, P84228, P02301, P62754	0.00013951501979
GOTERM_MF_DIRECT	GO:0030527~structural constituent of chromatin	13	8.14985E-05	P68433, P84228, P02301	0.00212982752363
GOTERM_CC_DIRECT	GO:0000786~nucleosome	15	0.000105156	P68433, P60762, P84228, P02301, Q9Z2N8	0.00106306140355
UP_KW_PTM	KW-0379~Hydroxylation	24	0.000461544	Q920E5, P32233, P62267, P68433, Q7TNC4, P01899, P17183, P52480, P09411, P84228, P02301, P98086, P62754, O88351	0.00097436977617
UP_KW_CELLULAR_COMPO	KW-0544~Nucleosome core	13	0.000851417	P68433, P84228, P02301	0.00404423187835
INTERPRO	IPR009072:Histone-fold	14	0.001008698	P68433, P70353, P84228, P02301	0.06667494888463
KEGG_PATHWAY	mmu04613:Neutrophil extracellular trap formation	24	0.001439134	P51432, Q60930, Q60931, O70145, P11835, P70288, Q61462, P30993, Q04207, P68433, Q61093, O88895, P84228, P02301	0.01463946845733
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	17	0.009686565	P62320, Q7TPR4, P68433, P57780, P84228, P02301, P98086	0.07723072179048

Annotation Cluster 12	Enrichment Score: 4.9088340501212695	Count	PValue	Genes	FDR
Category	Term				
UP_KW_BIOLOGICAL_PROC	KW-0648~Protein biosynthesis	29	5.50726E-11	Q62448, P10711, Q8C0C7, O70194, P31230, P10630, Q9Z1D1, P59325, Q61035, Q3U186, Q9DBZ5, Q8QZY1, Q8BU30, Q6PGC1, P62631, Q99J11, Q9Z1Q9, Q99LC8, Q91WK2, P10126, Q6NZJ6, Q8BGD9, Q8BMB3, Q68FL6, Q9WUA2, Q8BWW4, P58252, Q8BGQ7, Q9D019	1.9642549676E-09
GOTERM_BP_DIRECT	GO:0006413~translational initiation	13	1.94912E-07	Q62448, Q91WK2, Q99LC8, O70194, P10630, Q9Z1D1, Q6NZJ6, P59325, Q8BGD9, Q8BMB3, Q9DBZ5, Q8QZY1, Q6P542	3.2745152862E-05
GOTERM_MF_DIRECT	GO:0003743~translation initiation factor activity	13	5.0928E-07	Q62448, Q91WK2, Q99LC8, O70194, P10630, Q9Z1D1, Q6NZJ6, P59325, Q8BGD9, Q8BMB3, Q9DBZ5, Q8QZY1, Q6PGC1	2.2181994364E-05
UP_KW_MOLECULAR_FUNC	KW-0396~Initiation factor	13	6.61032E-06	Q62448, Q91WK2, Q99LC8, O70194, P10630, Q9Z1D1, Q6NZJ6, P59325, Q8BGD9, Q8BMB3, Q9DBZ5, Q8QZY1, Q6PGC1	6.7991828847E-05
GOTERM_BP_DIRECT	GO:0001732~formation of cytoplasmic translation initiation complex	6	6.36829E-05	Q91WK2, O70194, Q9Z1D1, Q9DBZ5, Q8QZY1, P59325	0.00455264774411
GOTERM_CC_DIRECT	GO:0016282~eukaryotic 43S preinitiation complex	6	0.000267266	Q91WK2, O70194, Q9Z1D1, Q9DBZ5, Q8QZY1, Q6PGC1	0.00230561165088
GOTERM_CC_DIRECT	GO:0005852~eukaryotic translation initiation factor 3 complex	5	0.000931171	Q91WK2, O70194, Q9Z1D1, Q9DBZ5, Q8QZY1	0.00669408663311
GOTERM_CC_DIRECT	GO:0033290~eukaryotic 48S preinitiation complex	5	0.00149569	Q91WK2, O70194, Q9Z1D1, Q9DBZ5, Q8QZY1	0.01003347410037

Annotation Cluster 13
Enrichment Score: 4.858592099342454

Count PValue Genes FDR

GOTERM_MF_DIRECT	GO:0051015~actin filament binding	24	2.25256E-07	O89053, Q91MH9, Q7TPR4, Q9WV32, Q9QXZ0, Q61879, Q62418, O08539, P18760, P59999, Q5SUA5, Q9J128, Q9L126, Q3U044, P13020, Q7TMB8, P58252, P57780, Q9CQI6, Q8BRT1, P49710, Q8C052, P26645, P26039	1.0596060853E-05
GOTERM_MF_DIRECT	GO:0003779~actin binding	29	1.31311E-06	O89053, Q91MH9, Q7TPR4, Q9WV32, Q9QXZ0, P26041, P70460, Q8RI16, P18760, P68510, Q9ERD8, P61982, Q9ERL7, Q8C052, P26039, Q8BQ30, Q62418, Q9Z0E6, Q9ET54, Q9D2V7, Q5SUA5, Q9J128, Q9L126, Q08509, P13020, P57780, Q9CQI6, P62962	5.3248840099E-05
GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	21	2.58844E-05	Q91VR8, O89053, Q7TPR4, Q9QXZ0, P70460, P62827, Q61879, Q8RI16, Q9ET54, Q5SXY1, Q9J128, Q9L126, Q08509, P13020, Q9ERD8, P57780, Q8BPU7, P62962, Q9WVE8, P60766, P26039	0.00217429256726
UP_KW_MOLECULAR_FUNCTION	KW-0009~Actin-binding	24	0.004804132	O89053, Q91MH9, Q7TPR4, Q9WV32, Q9QXZ0, P70460, P26043, Q61879, Q62418, Q9ET54, P18760, Q9D2V7, P59999, Q5SUA5, Q9J128, Q08509, P13020, Q7TMB8, Q9ERD8, P57780, Q9CQI6, P62962, P26645, Q8BQ30	0.02660750133382
Annotation Cluster 14	Enrichment Score: 4.7121522107111815	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0005525~GTP binding	38	2.92753E-10	P07901, Q8BG51, Q922F4, P63094, P59325, Q91YH5, P35283, P62331, O55131, Q9D6F9, P61021, P61028, P62631, P47758, P36916, Q99K70, P62827, Q99IC8, Q9CZ30, P11499, P14824, Q9Z0E6, P68372, P32233, P10126, Q3UX10, P15532, P61750, P61211, P58252, Q91V41, P62746, P35290, P08752, P21279, P60766, P21278, P62821	1.8119888799E-08
GOTERM_MF_DIRECT	GO:0003924~GTPase activity	30	5.03803E-08	Q61599, Q8BG51, Q922F4, P63094, Q91YH5, P35283, P62331, O55131, Q9D6F9, P61021, P61028, P62631, P36916, Q99K70, Q9Z0E6, P68372, P32233, P10126, P61750, P61211, P58252, Q91V41, P62746, P35290, P08752, P21279, P60766, P21278, P62821	2.4686345114E-06
UP_KW_LIGAND	KW-0342~GTP-binding	32	0.001740058	Q8BG51, Q922F4, P63094, P59325, Q91YH5, P35283, P62331, O55131, Q9D6F9, P61021, P61028, P62631, P47758, P36916, Q99K70, P62827, Q9Z0E6, P68372, P32233, P10126, Q3UX10, P61750, P61211, P58252, Q91V41, P62746, P35290, P08752, P21279, P60766, P21278, P62821	0.01305043130108
INTERPRO	IPR005225~Small_GTP-bd_dom	15	0.0005749843	Q8BG51, P62827, P32233, P35283, P62331, P61750, P61211, P58252, P61021, P61028, Q91V41, P62746, P35290, P60766, P62821	0.28152934050316
SMART	SM00175~RAB	13	0.018631887	Q8BG51, P62827, P35283, P62331, P61750, P61211, P61021, P61028, Q91V41, P62746, P35290, P60766, P62821	0.42423374309977
Annotation Cluster 15	Enrichment Score: 4.6930645198225385	Count	PValue	Genes	FDR
KEGG_PATHWAY	mmu05020~Prion disease	44	4.98175E-10	Q9D8W5, O70435, Q60864, Q62425, Q922F4, P03921, P99028, O35593, Q9R1P4, Q9R1P3, Q91WD5, P70227, Q9D8B4, Q9CZB0, Q9D6F9, P62196, Q9D3D9, Q9IKV1, Q9DCX2, Q9CQH3, P62334, Q9P616, Q9P616, Q8RI11, P62897, P98086, Q60930, Q60931, Q9CX56, O70145, P03911, Q9CQZ6, P68372, P62192, P19783, Q3UX10, Q61462, Q60692, Q91VD9, Q99J14, P33175, Q61093, O88685, Q9DB20	5.5165935117E-08

KEGG_PATHWAY	mmu05012:Parkinson disease	44	5.6101E-10	P10639, Q9D8W5, O70435, Q62425, Q922F4, P03921, P99028, O35593, Q9R1P4, P63094, Q9R1P3, Q91WD5, P70227, Q9D8B4, Q9CZB0, Q9D6F9, P62196, Q9D3D9, Q9JKV1, Q9DCX2, Q9CQH3, P62334, P56480, Q9D616, Q8R111, P62897, P97493, Q9CQNI, Q60930, Q60931, Q9CX56, P03911, Q9CQZ6, P68372, P62192, P19783, Q3UX10, Q60692, Q91VD9, Q99J14, P33175, O88685, P08752, Q9DB20
KEGG_PATHWAY	mmu05014:Amyotrophic lateral sclerosis	52	2.41524E-09	Q8B197, Q922F4, F6ZDS4, Q9QY76, P70227, Q9JIH2, Q9CZB0, P62196, P84104, Q9CQH3, P56480, Q8R111, Q8K310, Q9CX56, P03911, P59235, P19783, Q3UX10, Q8R332, O88685, P62962, Q9DB20, Q921F2, Q9D8W5, O70435, Q62425, P03921, P99028, O35593, Q9R1P4, Q9R1P3, Q91WD5, Q9D8B4, Q9D6F9, Q9D3D9, Q9JKV1, Q9DCX2, P62334, Q9D616, P62897, Q9Z0W3, Q80U93, Q3UYV9, Q9CQZ6, P68372, P62192, Q60692, Q91VD9, Q99J14, O09110, P33175, P62821
UP_KW_BIOLOGICAL_PROCESS	KW-0249-Electron transport	23	6.51669E-09	P97493, P10639, Q62425, P03921, P03911, P99028, Q8R2E9, Q9CQZ6, Q9CQX2, Q61462, Q91WD5, Q8R180, Q91VD9, Q9D8B4, Q61093, Q9CZB0, Q920L1, Q8VBT0, Q9CQH3, Q9D616, Q8CDN6, Q8R111, P62897
KEGG_PATHWAY	mmu05016:Huntington disease	45	7.14168E-09	Q9D8W5, O70435, Q62425, Q922F4, P03921, P99028, P70288, O35593, Q68FED5, Q9R1P4, Q9R1P3, Q91WD5, P17426, P96671, Q9D8B4, Q9CZB0, Q9D6F9, P62196, Q9D3D9, Q9JKV1, Q9DCX2, P62334, P56480, Q9D616, Q8R111, P62897, P51432, Q60930, Q60931, Q9CX56, P03911, Q9CQZ6, P68372, P62192, P19783, Q3UX10, Q60692, Q91VD9, Q99J14, P33175, P42859, O88685, P21279, Q9DB20
KEGG_PATHWAY	mmu05010:Alzheimer disease	52	8.61086E-09	Q91ZX7, Q922F4, P16858, P70227, Q9CZB0, P62196, Q61160, Q9CQH3, P56480, Q8R111, P49615, P51432, Q64518, Q9CX56, P03911, Q9ES97, P19783, Q3UX10, Q61093, O88685, Q9DB20, Q9D8W5, O70435, Q62425, P03921, P99028, O35593, O08529, Q9R1P4, Q9R1P3, Q91WD5, Q9D8B4, Q9D6F9, Q9D3D9, Q9JKV1, Q9DCX2, P62334, Q9D616, P62897, O88331, P57716, Q60930, Q60931, Q9CQZ6, P68372, P62192, Q60692, Q04207, Q91VD9, Q99J14, P33175, P21279
GOTERM_BP_DIRECT	GO:0042776-proton motive force-driven mitochondrial ATP synthesis	14	2.68846E-08	P56135, P03921, P03911, Q9CQZ6, Q91WD5, Q91VD9, Q9D8B4, Q9CZB0, Q9D3D9, Q9DCX2, Q9CQH3, P56480, Q9DB20
KEGG_PATHWAY	mmu05022:Pathways of neurodegeneration - multiple diseases	54	1.36015E-06	Q922F4, Q9QY76, P70227, Q9CZB0, P62196, Q61160, Q9CQH3, P56480, Q8R111, P49615, P51432, Q64518, Q9CX56, P03911, P19783, Q3UX10, Q61093, P42859, O88685, Q9DB20, Q921F2, Q9D8W5, O70435, Q62425, P03921, P99028, O35593, O08529, Q9R1P4, Q9R1P3, Q91WD5, Q9D8B4, Q9D6F9, Q9D3D9, Q9JKV1, Q9DCX2, P62334, Q9D616, P62897, Q9CQNI, Q60930, Q60931, Q9CQZ6, P68372, P62192, Q60692, O08734, Q04207, Q91VD9, Q99J14, O09110, P33175, P21279, P62821
UP_KW_CELLULAR_COMPONENT	KW-0999-Mitochondrion inner membrane	34	1.0096E-05	Q8CAO8, Q62425, P56135, P03921, Q9CWU6, P99028, Q9CR62, Q91WD5, Q9D8B4, Q9CZB0, Q9D3D9, Q9DCZ4, Q9DCX2, Q9CQH3, P56480, Q9D616, Q8R111, Q8BH59, Q9D714, P62908, Q9CQNI, Q9QZD8, P03911, Q9WTO8, Q9CQZ6, P19783, Q920A7, Q61102, P67778, Q91VD9, Q9Z0X1, O35435, Q78IK4, Q9DB20
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	23	1.082E-05	Q62425, P56135, Q8BVE3, P03921, P03911, P99028, Q9CQZ6, P19783, P50516, P51863, Q91WD5, Q91VD9, Q9D8B4, Q9CZB0, Q9D3D9, Q9DCX2, Q9CQH3, P56480, Q9D616, Q8R111, P62897, Q9DB20, Q9D819

KEGG_PATHWAY	mmu05208:Chemical carcinogenesis - reactive oxygen species	31	1.11843E-05	Q62425, P03921, P99028, Q91WD5, Q9CPI4, P09671, Q9D8B4, Q9CZB0, Q9D3D9, Q9DCX2, Q9CQH3, P56480, Q9D616, Q8RI11, Q60930, Q60931, Q70145, P03911, Q9CQZ6, P19783, Q91I16, Q61462, Q04207, Q91VD9, P47809, P48774, Q09131, P48758, Q91WU5, Q9DB20	0.000219955879274
KEGG_PATHWAY	mmu05017:Spinocerebellar ataxia	22	3.51197E-05	Q9D8W5, P51432, Q70435, Q60930, Q64518, Q60931, Q9CX56, Q35593, Q9R1P4, P62192, Q9D6Z1, Q9R1P3, Q60692, Q920A7, P70227, Q99J14, P62196, Q88685, Q91KVL, P62334, P62897, P21279	0.00064751966528
KEGG_PATHWAY	mmu05415:Diabetic cardiomyopathy	28	7.61224E-05	Q62425, P03921, P99028, P16858, P18242, Q91WD5, Q00612, Q9D8B4, Q9CZB0, Q9D3D9, Q9DCX2, Q9CQH3, P56480, Q9D616, Q8RI11, P51432, Q60930, Q64518, Q60931, Q70145, P03911, Q9CQZ6, P19783, Q61462, Q04207, Q91VD9, Q61093, Q9DB20	0.00118190080306
GOTERM_BP_DIRECT	GO:1902600~proton transmembrane transport	14	8.07964E-05	P56135, P03921, P03911, P99028, P50516, Q91WD5, Q8VDN2, Q91VD9, Q9D3D9, Q9DCX2, P56480, Q9D616, Q8BH59, Q9DB20	0.00532305680693
GOTERM_CC_DIRECT	GO:0045271~respiratory chain complex I	9	0.000164581	Q91VD9, Q62425, Q9D8B4, P03921, P03911, Q9CQZ6, Q9CQH3, Q91WD5, Q9D616	0.00149977053554
GOTERM_MF_DIRECT	GO:0003954~NADH dehydrogenase activity	5	0.000193189	Q9Z0X1, P03921, P03911, Q91WD5, Q9D616	0.00463652530138
UP_KW_BIOLOGICAL_PROCESS	KW-0679-Respiratory chain	12	0.000201497	Q91VD9, Q62425, Q9D8B4, P03921, P03911, P99028, Q9CQZ6, Q9CQH3, Q91WD5, Q9D616, Q8RI11, P62897	0.00269501854507
GOTERM_BP_DIRECT	GO:0032981~mitochondrial respiratory chain complex I assembly	9	0.000705984	Q91VD9, Q9Z0X1, Q9D8B4, P03921, P03911, Q9CQZ6, Q9CQH3, Q91WD5, Q9DIR1	0.03002664847944
GOTERM_BP_DIRECT	GO:0006120~mitochondrial electron transport, NADH to ubiquinone	6	0.00090663	Q91VD9, P03921, P03911, Q08749, Q91WD5, Q9D616	0.03626520448394
GOTERM_BP_DIRECT	GO:0009060~aerobic respiration	9	0.001133055	Q91VD9, Q9D8B4, P03921, P03911, Q9D3D9, Q9CQZ6, Q9CQH3, Q91WD5, Q9D616	0.04250380911998
GOTERM_MF_DIRECT	GO:0008137~NADH dehydrogenase (ubiquinone) activity	5	0.001524812	Q91VD9, P03921, P03911, Q91WD5, Q9D616	0.02758736846244
KEGG_PATHWAY	mmu04714:Thermogenesis	26	0.001772352	Q62425, P56135, P03921, P54310, P99028, P63094, Q91WD5, Q9Z2N8, Q9D8B4, Q9CZB0, P51829, Q9D3D9, Q9DCX2, Q9CQH3, P56480, P41216, Q9D616, Q8RI11, P62754, Q9D714, P03911, Q9CQZ6, P19783, Q91VD9, Q09110, Q9DB20	0.01742813028317
UP_KW_MOLECULAR_FUNCTION	KW-1278-Translocase	13	0.00326068	Q64518, P03921, P03911, P50516, Q91WD5, Q8VDN2, B2RX12, P36371, Q91VD9, Q35379, P21958, P56480, Q9D616	0.01956407885924
UP_KW_LIGAND	KW-0830-Ubiquinone	5	0.019084939	Q91VD9, P03921, P03911, Q91WD5, Q9D616	0.0929053264314
Annotation Cluster 16					
Category	Enrichment Score: 4.328685675177518	Count	PValue	Genes	FDR
UP_SEQ_FEATURE	Term SITE:Interaction with phosphoserine on interacting protein	7	1.84836E-08	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	6.5406625252E-06
INTERPRO	IPR023409:14-3-3_CS	7	2.29611E-08	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	4.2107430859E-06
INTERPRO	IPR02410:14-3-3_domain	7	8.88067E-08	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	1.1181185028E-05
INTERPRO	IPR000308:14-3-3	7	8.88067E-08	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	1.1181185028E-05
SMART	SM00101:14_3_3	7	1.06783E-07	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	1.0535889212E-05
INTERPRO	IPR036815:14-3-3_dom_sf	7	2.57615E-07	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	2.8380538127E-05
PIR_SUPERFAMILY	PIRSF000868:14-3-3	7	5.49971E-07	P63101, Q70456, Q9CQV8, P68510, P68254, P61982, P62259	6.5446508287E-05
UP_SEQ_FEATURE	DOMAIN:14-3-3	6	1.44288E-06	P63101, Q70456, Q9CQV8, P68254, P61982, P62259	0.00021159465292
GOTERM_MF_DIRECT	GO:0050815~phosphoserine residue binding	5	4.39243E-05	P63101, Q70456, Q9CQV8, P61982, P62259	0.00121995637503
GOTERM_BP_DIRECT	GO:0045184~establishment of protein localization	9	0.000161092	P63101, Q70456, Q9CQV8, P26043, P68254, P61982, Q8BT07, P62259, Q91XBO	0.00966549762041
GOTERM_BP_DIRECT	GO:0008104~protein localization	16	0.00135181	Q70456, Q9CQV8, P61957, Q9QXZ0, P62827, P68254, Q8C547, P63101, Q55131, Q9R0E1, P68510, Q810A7, P61982, Q88653, P62259, P60766	0.04731335221595
GOTERM_BP_DIRECT	GO:0006605~protein targeting	7	0.001696242	P63101, Q9CQV8, Q3UVL4, P68254, Q9Z0E6, P61982, P62259	0.05719670944977

Annotation Cluster 17		Enrichment Score: 4.083991194399335			
Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0022624~proteasome accessory complex	8	2.37002E-07	Q9D8W5, Q99J14, Q9CXS6, P62196, O35593, P62192, O88685, P62334	3.9318017393E-06
INTERPRO	IPR003593:AAA+_ATPase	21	9.96852E-07	Q8CDM1, P46460, Q3UMC0, P62192, E9QAM5, Q9ER41, Q61102, Q920A7, B2RX12, P36371, O35379, P21958, P62196, P25206, O88685, Q99LE6, Q9JHU4, P56480, P62334, Q6P542, E9Q555	0.00010137221586
SMART	SM00382:AAA	21	1.48572E-06	Q8CDM1, P46460, Q3UMC0, P62192, E9QAM5, Q9ER41, Q61102, Q920A7, B2RX12, P36371, O35379, P21958, P62196, P25206, O88685, Q99LE6, Q9JHU4, P56480, P62334, Q6P542, E9Q555	0.00010994359325
INTERPRO	IPR041569:AAA_lid_3	8	4.50229E-05	Q8CDM1, P46460, P62196, Q3UMC0, P62192, O88685, P62334, Q920A7	0.00350119229476
INTERPRO	IPR003960:ATPase_AAA_CS	8	7.572E-05	Q8CDM1, P46460, P62196, Q3UMC0, P62192, O88685, P62334, Q920A7	0.00572010859772
GOTERM_CC_DIRECT	GO:0008540~proteasome regulatory particle, base subcomplex	5	0.000277563	P62196, P62192, O88685, P62334, Q9Z2X2	0.00233224827684
GOTERM_MF_DIRECT	GO:0036402~proteasome-activating activity	4	0.000448609	P62196, P62192, O88685, P62334	0.00925551657269
INTERPRO	IPR032501:Prot_ATP_ID_OB_2nd	4	0.000551883	P62196, P62192, O88685, P62334	0.03839945107864
INTERPRO	IPR050221:26S_Proteasome_ATPase	4	0.001071821	P62196, P62192, O88685, P62334	0.06767528909676
Annotation Cluster 18		Enrichment Score: 3.8497950239646213			
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0051301~cell division	31	4.22482E-07	Q9CW03, Q8R3C0, Q68FD5, Q9JMD0, P37913, Q61550, F6ZDS4, Q9CU62, O55131, O35685, Q9J111, Q8K2Z4, Q8BRT1, Q3UA16, P53995, P62908, Q60875, E9Q7G0, P62827, P59235, Q8VE37, Q9D3E6, Q8BHK9, Q3UMY5, Q9JHU4, O35638, Q922S8, P08752, P60766	6.4677246455E-05
UP_KW_BIOLOGICAL_PROC	KW-0498-Mitosis	28	0.000398344	Q9CW03, Q91VH2, Q8R3C0, Q68FD5, Q9JMD0, Q61550, Q8BRT07, F6ZDS4, Q9CU62, O55131, O35685, Q9J111, Q8K2Z4, Q8BRT1, Q3UA16, P53995, P62908, Q60875, E9Q7G0, P62827, P59235, Q8VE37, Q9D3E6, Q8BHK9, Q3UMY5, Q9JHU4, O35638, Q922S8	0.00426228416357
UP_KW_BIOLOGICAL_PROC	KW-0132-Cell division	34	0.000929177	Q8K2Z4, Q8BRT1, Q3UA16, P25322, P49615, P53995, P62908, Q60875, E9Q7G0, P62827, P59235, Q8VE37, Q9D3E6, Q8BHK9, Q3UMY5, Q9JHU4, O35638, Q922S8, P08752, P60766	0.00828516165288
UP_KW_BIOLOGICAL_PROC	KW-0131-Cell cycle	48	0.002544649	Q9CW03, Q91VH2, Q8R3C0, Q68FD5, Q9JMD0, P37913, Q61550, Q8BRT07, F6ZDS4, Q9CU62, Q80U87, P62331, P49718, O55131, O35098, Q8VDF2, O35685, P84089, Q9J111, Q8K2Z4, Q8BRT1, P53995, P62908, Q6A068, Q80U87, Q3UA16, P25322, O35207, P49615, P53995, P62908, Q5PSV9, Q60875, P97310, E9Q7G0, P62827, P59235, O35280, Q8VE37, Q9D3E6, Q61191, Q8BHK9, Q3UMY5, Q9JHU4, O35638, Q922S8, P08752, Q8CH18, P60766	0.01701754078631
Annotation Cluster 19		Enrichment Score: 3.1992983018385517			
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:2000767~positive regulation of cytoplasmic translation	6	6.36829E-05	P62960, P58252, Q60668, P29341, P52480, Q7TMK9	0.00455264774411
GOTERM_BP_DIRECT	GO:0070934-CRD-mediated mRNA stabilization	5	0.000187075	P62960, Q9CPN8, Q60668, P29341, Q7TMK9	0.0103628554871
GOTERM_BP_DIRECT	GO:1900152~negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	4	0.001723555	P62960, Q60668, P29341, Q7TMK9	0.05719670944977

GOTERM_CC_DIRECT	GO:0106002~mCRD-mediated mRNA stability complex	3	0.007768596	Q60668, P29341, Q7TMK9	0.03989112250616
Annotation Cluster 20					
Category	Enrichment Score: 3.172033911386319	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006281~DNA repair	26	1.00541E-06	P52431, Q9CWX03, P54276, Q99K48, Q9WUP7, P37913, Q61550, Q9CU62, Q9Z2N8, Q9EPU0, Q8VDF2, Q9JLV6, Q6A068, Q9DBR1, Q9CPR8, P62908, Q9CQ37, Q5PSV9, P28352, P33609, Q62318, Q80W54, Q35280, Q9D071, Q8BHK9	0.00013512704381
UP_KW_BIOLOGICAL_PROC	KW-0234~DNA repair	27	0.012379576	P52431, Q9CWX03, P54276, Q35593, Q99K48, Q9WUP7, P37913, Q61550, Q9CU62, Q9Z2N8, Q91VA6, Q8VJL6, Q8VDF2, Q9JLV6, Q8CDG3, Q6A068, Q9CPR8, P62908, Q9CQ37, Q5PSV9, P28352, P54728, Q35280, Q9D071, P60762, P17918	0.0602097518378
Annotation Cluster 21					
Category	Enrichment Score: 3.091610362497161	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006913~nucleocytoplasmic transport	12	1.56482E-06	Q80U93, Q78JE5, Q9ERK4, Q8R332, P34022, P59235, Q6PF9, Q35381, F6ZDS4, P49615, Q9Z0W3, Q9JIH2	0.00019473365787
GOTERM_CC_DIRECT	GO:0005643~nuclear pore	11	3.4165E-05	Q9CRT8, Q80U93, Q9CT10, Q8R332, P62827, P34022, P59235, P70168, F6ZDS4, Q9Z0W3, Q9JIH2	0.00037465664727
UP_KW_BIOLOGICAL_PROC	KW-0509~mRNA transport	15	0.000106441	Q6FPB6, Q80U93, Q8BL97, Q9CPN8, Q3UYV9, P97379, Q6PDM2, P59235, Q6PF9, F6ZDS4, Q9JIH2, Q8R332, Q3U0V1, P84104, Q9Z0W3	0.00162702159637
UP_KW_CELLULAR_COMPO	KW-0906~Nuclear pore complex	6	0.02891587	Q80U93, Q8R332, P59235, F6ZDS4, Q9Z0W3, Q9JIH2	0.0732535380079
Annotation Cluster 22					
Category	Enrichment Score: 3.0578974896594064	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0071005~U2-type precatalytic spliceosome	14	1.21966E-08	Q8BTI8, P57784, Q3UKJ7, Q9PPV0, P62320, Q6ZWM4, P62311, Q922U1, P62305, P62317, Q8K4Z5, C0HKD8, Q921M3, Q9DAW6	2.4659981382E-07
GOTERM_CC_DIRECT	GO:0046540~U4/U6 x U5 tri-snRNP complex	9	8.22835E-06	P62320, Q6ZWM4, P62311, Q91V81, Q922U1, P62305, P62317, Q9DAW6, Q9PPV0	0.00010844120473
GOTERM_CC_DIRECT	GO:0071011~precatalytic spliceosome	8	1.095E-05	P62320, Q6ZWM4, P62311, P62305, Q9JIH8, P62317, Q3UKJ7, Q62376	0.00013119691705
GOTERM_CC_DIRECT	GO:0005684~U2-type spliceosomal complex	8	1.79083E-05	P62320, P62305, P57784, P62317, Q8K4Z5, Q569Z5, Q921M3, C0HKD8	0.00021066628104
GOTERM_MF_DIRECT	GO:1990446~U1 snRNP binding	5	0.000125812	Q8VH51, P62320, P62305, P62317, Q62376	0.00314798622087
GOTERM_CC_DIRECT	GO:0005683~U1 snRNP	6	0.000160178	P62320, Q7TNC4, P62305, Q5SUF2, P62317, Q62376	0.00148049889024
GOTERM_CC_DIRECT	GO:0005686~U2 snRNP	6	0.000267266	P62320, P62305, P57784, P62317, Q8K4Z5, Q921M3	0.00230561165088
GOTERM_CC_DIRECT	GO:0005682~U5 snRNP	5	0.000931171	P62320, P62305, P62317, Q9CWX3, Q9PPV0	0.00669408663311
GOTERM_CC_DIRECT	GO:0005689~U12-type spliceosomal complex	6	0.001289951	P62320, P62960, P62305, Q35286, P62317, Q921M3	0.00878524628831
GOTERM_CC_DIRECT	GO:0071007~U2-type catalytic step 2 spliceosome	7	0.0002164522	P62320, Q8BTI8, P62305, P57784, Q6A068, P62317, Q9PPV0	0.01346582556423
GOTERM_CC_DIRECT	GO:0034709~methylosome	4	0.006770357	P62320, P84089, P62305, P62317	0.03561317804537
GOTERM_CC_DIRECT	GO:0034715~pICln-Sm protein complex	3	0.015702213	P62320, P62305, P62317	0.06857557412866
Annotation Cluster 25					
Category	Enrichment Score: 2.7145668857765197	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006098~pentose-phosphate shunt	6	2.01552E-05	Q8VEE0, P40142, Q00612, E9Q4Z2, Q93092, Q9CS42	0.00178089025291
KEGG_PATHWAY	mmu00030.Pentose phosphate pathway	9	0.000455506	P12382, Q8VEE0, Q7TSV4, P40142, Q00612, Q9WUA3, Q9D0F9, Q93092, Q9CS42	0.00516823800669

GOTERM_MF_DIRECT	GO:0048029~monosaccharide binding	5	0.001524812	P12382, Q8VEE0, P40142, Q9WUA3, Q93092	0.02758736846244
Annotation Cluster 26					
Category	Enrichment Score: 2.703726159584193				
GOTERM_BP_DIRECT	GO:0090307~mitotic spindle assembly	Count	PValue	Genes	FDR
		10	4.33516E-06	Q91VA6, Q9D3E6, Q8VDF2, Q9CW03, Q8BRT1, Q68FD5, Q9JMD0, P70168, Q35638, Q9CU62	0.00046852311364
GOTERM_CC_DIRECT	GO:0008278~cohesin complex	5	2.20189E-05	Q9D3E6, Q9CW03, Q35638, Q61550, Q9CU62	0.0002543968756
GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	6	6.36829E-05	Q9D3E6, Q9CW03, Q8R3C0, Q35638, Q61550, Q9CU62	0.00455264774411
GOTERM_CC_DIRECT	GO:0030892~mitotic cohesin complex	4	0.000225701	Q9CW03, Q35638, Q61550, Q9CU62	0.00200059346443
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	9	0.000875179	P23198, Q9D3E6, P83917, Q9CW03, Q9DB96, Q35638, Q61550, F6ZDS4, Q922S8	0.00643455704289
GOTERM_CC_DIRECT	GO:0030893~meiotic cohesin complex	3	0.015702213	Q9CW03, Q61550, Q9CU62	0.06857557412866
Annotation Cluster 27					
Category	Enrichment Score: 2.618803134862678				
INTERPRO	IPR014729~Rossmann-like_a/b/a_fold	Count	PValue	Genes	FDR
		10	3.33403E-05	Q68FL6, Q9Z1Q9, Q3U186, Q3U308, Q60967, Q9DBL7, Q8BU30, Q3THK7, Q61024, Q9D019	0.00267126460139
GOTERM_CC_DIRECT	GO:0017101~aminoacyl-tRNA synthetase multienzyme complex	5	0.000277563	Q68FL6, P31230, P47962, Q8BU30, Q9D019	0.00233224827684
UP_KW_MOLECULAR_FUNCTION	KW-0030~Aminoacyl-tRNA synthetase	9	0.00041725	Q68FL6, Q9Z1Q9, Q3U186, Q9WUA2, Q8C0C7, Q8BU30, Q61035, Q8BGQ7, Q9D019	0.00300419817434
INTERPRO	IPR009080:tRNAAsynth_La_anticonodon-bd	5	0.0001223642	Q68FL6, Q9Z1Q9, Q3U186, Q8BU30, Q9D019	0.07523977711402
KEGG_PATHWAY	mmu00970:Aminoacyl-tRNA biosynthesis	10	0.010795981	Q99JTI, Q68FL6, Q9Z1Q9, Q3U186, Q9WUA2, Q8C0C7, Q8BU30, Q61035, Q8BGQ7, Q9D019	0.07865117107896
Annotation Cluster 28					
Category	Enrichment Score: 2.5946836060263765				
GOTERM_CC_DIRECT	GO:0005838~proteasome regulatory particle	Count	PValue	Genes	FDR
INTERPRO	IPR000717:PC1_dom	5	0.000123292	Q9D8W5, Q99J14, Q9CX56, P62196, P62192	0.00119059450982
		6	0.001645928	Q9D8W5, Q99J14, Q9CX56, Q88544, Q9DBZ5, Q8QZY1	0.0989052873406
Annotation Cluster 29					
Category	Enrichment Score: 2.506062188746895				
GOTERM_BP_DIRECT	GO:1902600~proton transmembrane transport	Count	PValue	Genes	FDR
		14	8.07964E-05	P56135, P03921, P03911, P99028, P50516, Q91WD5, Q8VDN2, Q91VD9, Q9D3D9, Q9DCX2, P56480, Q9D616, Q8BH59, Q9DBB20	0.00352305680693
GOTERM_MF_DIRECT	GO:0046933~proton-transporting ATP synthase activity, rotational mechanism	6	9.16379E-05	P56135, Q9D3D9, P50516, Q9DCX2, P56480, Q9DBB20	0.00234274304815
GOTERM_CC_DIRECT	GO:0045259~proton-transporting ATP synthase complex	6	0.000160178	Q78IK2, P56135, Q9D3D9, Q9DCX2, P56480, Q9DBB20	0.00148049889024
UP_KW_BIOLOGICAL_PROCESS	KW-0375~Hydrogen ion transport	8	0.011618602	Q8BVE3, P56135, Q9D3D9, P50516, Q9DCX2, P51863, P56480, Q9DBB20	0.05919954563962
Annotation Cluster 30					
Category	Enrichment Score: 2.434268523934506				
GOTERM_BP_DIRECT	GO:0045087~innate immune response	Count	PValue	Genes	FDR
		35	7.33156E-06	Q61510, Q9D8Y7, Q91VR5, Q91YN5, P56477, Q6R5N8, Q91VJ1, Q99K48, P16858, Q91XB0, Q8VJ16, Q3TL44, Q61160, Q9EPB4, Q99NH8, Q3UCV8, Q99MB1, Q8K310, P98086, Q60875, Q9JMA1, Q62318, P97379, Q8R5F7, Q91R02, Q61462, Q9JIK5, Q04207, P35991, Q8C2Q3, Q61093, Q9D8C4, P09581, Q62084, P25911, Q61510, Q9D8Y7, Q91VR5, Q91YN5, P56477, Q6R5N8, Q91VJ1, Q99K48, P16858, Q8VJ16, Q3TL44, Q61160, Q9EPB4, Q3UCV8, Q99MB1, Q8K310, P98086, Q60875, Q9JMA1, P97379, Q8R5F7, Q35286, Q9R002, Q9Z0E6, Q9JIK5, P35991, Q8C2Q3, Q9D8C4, P09581, P25911	0.0007369752793
UP_KW_BIOLOGICAL_PROCESS	KW-0399~Innate immunity	30	0.010854198	Q99MB1, Q8K310, P98086, Q60875, Q9JMA1, P97379, Q8R5F7, Q35286, Q9R002, Q9Z0E6, Q9JIK5, P35991, Q8C2Q3, Q9D8C4, P09581, P25911	0.0580699593324

Annotation Cluster 31			Enrichment Score: 2.312745338426355		
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0045454~cell redox homeostasis	9	4.08037E-06	P97493, P10639, P20108, P28352, O08807, Q8R2E9, Q9CQM9, Q8R180, P35700	0.00045700094967
Annotation Cluster 32			Enrichment Score: 2.289077721324972		
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0006099~tricarboxylic acid cycle	6	0.00264972	Q9Z219, P14152, Q9CZB0, Q99KI0, Q9WUM5, P54071	0.07609451533303
UP_KW_BIOLOGICAL_PROC	KW-0816~Tricarboxylic acid cycle	6	0.006568201	Q9Z219, P14152, Q9CZB0, Q99KI0, Q9WUM5, P54071	0.03904430709019
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	7	0.007800464	Q9Z219, P14152, Q9CZB0, Q99KI0, O08749, Q9WUM5, P54071	0.06973142256804
Annotation Cluster 33			Enrichment Score: 2.2832510930129604		
Category	Term	Count	PValue	Genes	FDR
KEGG_PATHWAY	mmu00010:Glycolysis / Gluconeogenesis	14	7.14681E-05	Q7TSV4, Q3TRM8, P28474, O08749, Q8VDL4, P16858, Q9J1I6, P12382, P47738, P17183, P52480, P09411, Q9WUA3, Q9D0F9	0.00117128223415
GOTERM_BP_DIRECT	GO:0006096~glycolytic process	9	8.05534E-05	P12382, Q9Z0M5, Q3TRM8, Q8VDL4, P16858, P52480, P09411, P17183, Q9WUA3	0.00352305680693
GOTERM_BP_DIRECT	GO:0061621~canonical glycolysis	6	0.000119109	P12382, P16858, P52480, P09411, P17183, Q9WUA3	0.00731363234816
UP_KW_BIOLOGICAL_PROC	KW-0324~Glycolysis	8	0.000593967	P12382, Q3TRM8, Q8VDL4, P16858, P52480, P09411, P17183, Q9WUA3	0.00577768056685
Annotation Cluster 34			Enrichment Score: 2.1654149799774167		
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0045454~cell redox homeostasis	9	4.08037E-06	P97493, P10639, P20108, P28352, O08807, Q8R2E9, Q9CQM9, Q8R180, P35700	0.00045700094967
UP_KW_DOMAIN	KW-0676~Redox-active center	10	3.87193E-05	P97493, P10639, P20108, O08807, Q8R2E9, O08749, Q8VBT0, Q8CDN6, Q8R180, P35700	0.00029684803551
GOTERM_MF_DIRECT	GO:0015035~protein-disulfide reductase activity	6	0.00034595	P97493, P10639, Q8R2E9, Q8VBT0, Q8CDN6, Q8R180	0.00753401343143
INTERPRO	IPR013766:Thioredoxin_domain	8	0.001075024	P97493, P10639, P20108, O08807, Q9CQM9, Q8VBT0, Q8CDN6, P35700	0.06767528909676
Annotation Cluster 35			Enrichment Score: 2.035270644847366		
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0030833~regulation of actin filament polymerization	7	0.000587566	O89053, Q7TMB8, Q62418, Q9CQI6, Q5SQX6, P49710, P62962	0.02686016113668
GOTERM_CC_DIRECT	GO:0030427~site of polarized growth	3	0.015702213	Q62418, Q9CQI6, P49710	0.06857557412866
Annotation Cluster 36			Enrichment Score: 2.024542972323167		
Category	Term	Count	PValue	Genes	FDR
UP_KW_MOLECULAR_FUNCTION	KW-0030~Aminoacyl-tRNA synthetase	9	0.00041725	Q68FL6, Q9Z1O9, Q3U1I86, Q9WUA2, Q8C0C7, Q8BU30, Q61035, Q8BGQ7, Q9D019	0.00300419817434
Annotation Cluster 37			Enrichment Score: 1.9276323650831986		
Category	Term	Count	PValue	Genes	FDR
GOTERM_BP_DIRECT	GO:0051603~proteolysis involved in protein catabolic process	9	0.000375259	P10605, O70435, O89017, O08529, Q9R1P4, Q60692, O35955, P06797, Q91YW3	0.01939802288615
GOTERM_CC_DIRECT	GO:0005839~proteasome core complex	5	0.001851827	O70435, Q9R1P4, Q9R1P3, Q60692, O35955	0.01174638991867
Annotation Cluster 38			Enrichment Score: 1.9206766777740807		

Category	Term	Count	PValue	Genes	FDR
GOTERM_CC_DIRECT	GO:0030687~peribosome, large subunit precursor	4	0.013938837	Q9DBE9, P97452, Q9EQ61, Q9DP903	0.06396047878619
Annotation Cluster 39	Enrichment Score: 1.9068496446976821	Count	PValue	Genes	FDR
Category	Term	6	0.00041541	Q3THK7, P70698, Q5SUR0, Q61024, Q9JHW2, Q8R216	0.02052614551488
GOTERM_BP_DIRECT	GO:0006541~glutamine metabolic process	4	0.006322249	Q3THK7, P70698, Q5SUR0, Q61024	0.02423528959312
UP_KW_DOMAIN	KW-0315~Glutamine amidotransferase				
Annotation Cluster 40	Enrichment Score: 1.8736854041527398	Count	PValue	Genes	FDR
Category	Term	7	0.000250054	Q9J28, P13020, Q62418, Q9CQI6, P18760, Q9ERL7, Q9DP62	0.01836508774736
INTERPRO	IPR029006:ADF-H/Gelsolin-like_dom_sf				
Annotation Cluster 41	Enrichment Score: 1.8651667635666245	Count	PValue	Genes	FDR
Category	Term	5	0.003935627	Q91VD9, Q99K10, Q9CQM9, Q9CZX0, Q9D6I6	0.05933713804259
GOTERM_MF_DIRECT	GO:0051536~iron-sulfur cluster binding	9	0.023476717	Q91VD9, Q9CQB5, P52431, Q99K10, Q9CQM9, Q9CZX0, Q91WD5, Q9D6I6, P33610	0.0929053264314
UP_KW_LIGAND	KW-0411~Iron-sulfur				
Annotation Cluster 42	Enrichment Score: 1.8036867715347773	Count	PValue	Genes	FDR
Category	Term	4	0.006322249	P48036, P14824, P07356, P97429	0.02423528959312
UP_KW_DOMAIN	KW-0041~Annexin	8	0.006799641	P48036, O35114, P14824, Q99NH8, P07356, P97429, P26645, P26039	0.08877356042325
GOTERM_MF_DIRECT	GO:0001786~phosphatidyserine binding	5	0.021018954	P48036, P14824, Q9Z0E6, P07356, P97429	0.08717476501973
GOTERM_CC_DIRECT	GO:0012506~vesicle membrane				
Annotation Cluster 43	Enrichment Score: 1.8000891164985555	Count	PValue	Genes	FDR
Category	Term	14	0.000941743	Q9CX34, Q9JMD0, P59235, Q8K2L8, Q6P5F9, F6ZDS4, Q9CU62, Q9Z2N8, O55131, Q8BHK9, Q8BRT1, Q3UA16, Q9Z2S8, Q9Z0W3	0.00669568592256
GOTERM_CC_DIRECT	GO:0000776~kinetochore	13	0.025999084	Q9CWX3, Q9JMD0, P59235, Q61550, F6ZDS4, Q9CU62, O55131, Q8BHK9, Q9DPB96, Q8BRT1, O35638, Q3UA16, Q9Z2S8	0.07056894136038
UP_KW_CELLULAR_COMPO	KW-0137~Centromere				
NENT					
Annotation Cluster 44	Enrichment Score: 1.7754171395292937	Count	PValue	Genes	FDR
Category	Term	8	0.004358482	Q8K4I1, Q8C129, O35864, Q91WK2, O35593, Q8BHG1, Q9Z2W0, Q99PV0	0.06327869445747
GOTERM_MF_DIRECT	GO:0008237~metallopeptidase activity				
Annotation Cluster 45	Enrichment Score: 1.7548118009245322	Count	PValue	Genes	FDR
Category	Term	6	0.000625568	Q60862, P49718, P97310, P33609, P25206, P33610	0.02729750400464
GOTERM_BP_DIRECT	GO:0006270~DNA replication initiation	9	0.000687676	Q9CWX8, P49718, P52431, P97310, P33609, P25206, P17918, P37913, P33610	0.00751349733221
KEGG_PATHWAY	mmu03030:DNA replication	4	0.003272468	P49718, P97310, Q8R3C0, P25206	0.0185726900351
GOTERM_CC_DIRECT	GO:0042555~MCM complex	8	0.003548794	P49718, Q9EPU0, Q91VR5, P97310, Q8BHK9, P25206, Q6PDQ2, Q91XB0	0.09539156965913
GOTERM_BP_DIRECT	GO:0032508~DNA duplex unwinding				
Annotation Cluster 46	Enrichment Score: 1.6890784636083607	Count	PValue	Genes	FDR
Category	Term	4	0.00486866	Q9DBP5, O35435, P13439, P70698	0.03064391988519
UP_KW_BIOLOGICAL_PROC	KW-0665~Pyrimidine biosynthesis				
ESS					

Annotation Cluster 47	Enrichment Score: 1.6624610754165863								
Category	Term	Count	PValue	Genes				FDR	
GOTERM_CC_DIRECT	GO:0030136~clathrin-coated vesicle	9	0.001504246	Q8CS47, Q61335, Q91ZX7, P98078, Q91VH2, Q8CFE4, P42859, Q68FD5, P17426				0.01003347410037	
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	8	0.00300407	Q91ZX7, P98078, Q91VH2, O35114, P11835, Q68FD5, P56480, P15379				0.08341880861737	
Annotation Cluster 48	Enrichment Score: 1.6324465617392088								
Category	Term	Count	PValue	Genes				FDR	
GOTERM_MF_DIRECT	GO:0008017~microtubule binding	17	0.006058676	P28741, P62908, Q60875, Q9WVV5, Q9QXZ0, E9Q7G0, P16858, Q91MD0, Q8BUK6, P32233, Q9QY76, Q4QRL3, P33175, Q8BR11, Q3UMY5, Q8C052, Q922S8				0.08189658285665	
Annotation Cluster 49	Enrichment Score: 1.5937598339134724								
Category	Term	Count	PValue	Genes				FDR	
KEGG_PATHWAY	mmu00030:Pentose phosphate pathway	9	0.000455506	P12382, Q8VEE0, Q7TSV4, P40142, Q00612, Q9WUA3, Q9D0F9, Q93092, Q9CS42				0.00516823800669	
Annotation Cluster 50	Enrichment Score: 1.499197454844517								
Category	Term	Count	PValue	Genes				FDR	
GOTERM_MF_DIRECT	GO:0019003~GDP binding	13	5.87785E-06	P62827, Q99K70, Q99LC8, Q9WUM5, Q9Z0E6, Q9CS42, P35283, P62331, Q01768, P61021, P61028, Q91V41, P62746				0.00020946528011	
Annotation Cluster 51	Enrichment Score: 1.495355445622655								
Category	Term	Count	PValue	Genes				FDR	
GOTERM_CC_DIRECT	GO:0043202~lysosomal lumen	7	0.000120567	O54782, O35657, O35114, O89017, P17439, P29416, P12265				0.00118192105973	
Annotation Cluster 52	Enrichment Score: 1.4152142407433403								
Category	Term	Count	PValue	Genes				FDR	
GOTERM_MF_DIRECT	GO:0005200~structural constituent of cytoskeleton	9	0.001554274	Q9WV32, P21619, P57780, Q922F4, Q9D6F9, P68372, Q3UX10, P59999, P26039				0.02769434079002	
Annotation Cluster 53	Enrichment Score: 1.3498030367767189								
Category	Term	Count	PValue	Genes				FDR	
GOTERM_MF_DIRECT	GO:0042288~MHC class I protein binding	6	0.006952288	Q61335, P36371, P21958, P01899, P01897, P56480				0.08886837292876	
Annotation Cluster 54	Enrichment Score: 1.0626319009099847								
Category	Term	Count	PValue	Genes				FDR	
UP_KW_BIOLOGICAL_PROCESS	KW-0375~Hydrogen ion transport	8	0.011618602	Q8BVE3, P56135, Q9D3D9, P50516, Q9DCX2, P51863, P56480, Q9DB20				0.05919954563962	
GOTERM_CC_DIRECT	GO:0030665~clathrin-coated vesicle membrane	5	0.012801167	P98078, Q8BVE3, Q62418, P50516, P51863				0.06001706549546	
Annotation Cluster 55	Enrichment Score: 0.9312861621893955								
Category	Term	Count	PValue	Genes				FDR	
UP_KW_LIGAND	KW-0411~Iron-sulfur	9	0.023476717	Q91VD9, Q9CQB5, P52431, Q99KI0, Q9CQM9, Q9CZX0, Q91WD5, Q9D6f6, P33610				0.0929053264314	