

Putative Id	Uniprot Accession	Score	Description	Fold change (6, 24, 72, 120 h)
Set 1 (21 genes): Early up-regulation				
Histone H3-K4 methyltransferase	Q8WTS6	1E-161	Transcription	1.40, 2.06, 1.37, 1.55
LINE-1 reverse transcriptase homolog	P08548	3E-15	Reverse transcriptase	1.23, 1.78, 1.25, 1.13
<i>Cell death-inducing DFFA-like effector protein C</i>	<i>Q96AQ7</i>	<i>9E-54</i>	<i>Apoptosis/cytoplasm</i>	<i>3.03, 5.39, 3.90, 1.10</i>
<i>Ecto-ADP-ribosyltransferase 4</i>	<i>Q95NE0</i>	<i>3E-16</i>	<i>Apoptosis/membrane</i>	<i>1.83, 3.26, 1.96, 2.75</i>
<i>Protein phosphatase 2C homolog 1</i>	<i>P35182</i>	<i>1E-11</i>	<i>Reset stress response</i>	<i>2.48, 1.67, 2.15, 1.17</i>
<i>Meiotic recombination protein REC8-like 1</i>	<i>O95072</i>	<i>3E-11</i>	<i>Meiosis</i>	<i>1.85, 1.42, 1.16, 1.18</i>
<i>Bola-like protein 2</i>	<i>Q8BGS2</i>	<i>2E-28</i>	<i>Cell proliferation</i>	<i>2.05, 3.16, 1.81, -1.12</i>
<i>Interferon-related developmental regulator 1</i>	<i>Q5S1U6</i>	<i>1E-21</i>	<i>Cell proliferation</i>	<i>1.55, 1.67, 1.06, 1.71</i>
<i>Pescadillo</i>	<i>P79741</i>	<i>1E-114</i>	<i>Cell proliferation</i>	<i>1.77, 1.98, 1.02, 1.01</i>
Collagen α -2 (VIII) chain	P25067	2E-10	Cell adhesion/structural constituent	1.38, 1.57, 1.24, 1.07
CD209 antigen-like protein D	Q91ZW8	5E-21	Probable pathogen-recognition/endocytosis	1.05, 2.17, 1.81, 1.50
Gamma-aminobutyric acid receptor-associated protein-like 1	Q8R3R8	3E-31	Microtubule/intracellular/autophagic vacuole	1.25, 2.09, 1.31, -1.33
<i>Cystathionine β-synthase</i>	<i>P35520</i>	<i>4E-97</i>	<i>Cysteine synthesis</i>	<i>2.42, 2.54, 1.18, 1.26</i>
<i>Cysteine dioxygenase type 1</i>	<i>Q6NWZ9</i>	<i>1E-100</i>	<i>Cysteine oxidation</i>	<i>2.17, 2.62, 1.42, 1.80</i>
<i>L-2-hydroxyglutarate dehydrogenase</i>	<i>Q9H9P8</i>	<i>3E-35</i>	<i>Oxidoreductase activity</i>	<i>1.91, 1.56, 1.69, 1.62</i>
<i>Metalloreductase STEAP2</i>	<i>Q8BWB6</i>	<i>2E-34</i>	<i>Oxidoreductase activity</i>	<i>1.84, 2.69, 3.99, 2.32</i>
Acid cholesteryl ester hydrolase	P38571	6E-78	Lipase activity/receptor mediated endocytosis/lysosome	1.50, 1.78, 1.83, 1.56
Lipoprotein lipase	P11602	1E-172	Lipase activity/plasma membrane	2.07, 1.72, 1.08, 1.72
Heart-type fatty acid-binding protein	O13008	3E-56	Intracellular fatty acid transport	1.24, 1.99, 2.36, 1.38
<i>Cytochrome P450 3A10</i>	<i>Q64148</i>	<i>5E-8</i>	<i>Hydroxylation of steroids</i>	<i>1.47, 1.65, 1.67, 1.44</i>
<i>Estradiol 17-β-dehydrogenase 1</i>	<i>P14061</i>	<i>2E-37</i>	<i>Estrogen biosynthesis</i>	<i>1.48, 2.10, 1.46, 1.25</i>
Set 2 (51 genes): Delayed and strong up-regulation				
<i>Transcription factor Sp1</i>	<i>P08047</i>	<i>2E-22</i>	<i>Transcription</i>	<i>-1.07, 3.07, 1.19, 1.68</i>
<i>Transcription initiation factor IIE subunit β</i>	<i>P29540</i>	<i>3E-84</i>	<i>Transcription</i>	<i>1.11, 1.40, 1.03, 1.02</i>
<i>Zinc finger protein 330</i>	<i>Q9Y3S2</i>	<i>1E-105</i>	<i>Transcription</i>	<i>1.07, 1.59, 1.11, -1.33</i>
<i>Zinc finger protein 479</i>	<i>Q96JC4</i>	<i>5E-31</i>	<i>Transcription</i>	<i>1.14, 1.80, 1.05, 1.20</i>
<i>Zinc finger protein 9</i>	<i>Q3T0Q6</i>	<i>1E-65</i>	<i>Transcription/sterol mediated repression</i>	<i>1.14, 1.74, 1.13, -1.32</i>
<i>ATP-dependent RNA helicase DDX39</i>	<i>Q8VDW0</i>	<i>1E-108</i>	<i>mRNA processing</i>	<i>-1.14, 2.84, 1.38, 1.11</i>
<i>Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15</i>	<i>O35286</i>	<i>3E-60</i>	<i>mRNA processing</i>	<i>1.04, 3.75, 2.89, 1.61</i>
<i>Splicing factor, arginine/serine-rich 3</i>	<i>P84104</i>	<i>3E-50</i>	<i>mRNA processing</i>	<i>1.16, 2.47, 1.22, -1.24</i>
<i>Eukaryotic peptide chain release factor subunit 1</i>	<i>P62498</i>	<i>6E-22</i>	<i>Translation</i>	<i>1.87, 3.80, 1.64, 1.21</i>
<i>Protein pelota homolog</i>	<i>Q7ZWC4</i>	<i>1E-100</i>	<i>Translation</i>	<i>1.17, 3.08, 1.67, 1.15</i>
<i>Threonyl-tRNA synthetase</i>	<i>Q3ZBV8</i>	<i>4E-49</i>	<i>Translation</i>	<i>-1.05, 2.51, 1.29, 1.41</i>
Developmentally-regulated GTP-binding protein 2	P55039	2E-52	Signal transduction	-1.20, 2.41, 1.28, -1.39

Protein separation anxiety	Q9NHD5	1E-68	Cell proliferation/DNA replication	1.00, 2.94, 1.29, 1.12
Sestrin-2	P58004	6E-31	Cell cycle arrest/nucleus	1.13, 1.73, 1.92, -1.58
Nucleolar protein family A member 2-like protein	Q6PBV6	4E-49	Ribosome biogenesis	1.15, 1.98, 1.37, -1.33
<i>cAMP-regulated phosphoprotein 19</i>	<i>Q712U5</i>	<i>2E-46</i>	<i>Post-translational modification/protein catabolism</i>	<i>-1.01, 2.41, 1.40, 1.33</i>
<i>Trypsin-1</i>	<i>P35031</i>	<i>1E-122</i>	<i>Proteolysis</i>	<i>1.45, 3.82, 1.88, 1.11</i>
<i>Dipeptidyl aminopeptidase-like protein 6</i>	<i>Q9Z218</i>	<i>3E-97</i>	<i>Proteolysis/integral to membrane</i>	<i>-1.11, 3.59, 1.11, 2.67</i>
<i>Hyaluronan-binding protein 1</i>	<i>Q3T0B6</i>	<i>2E-36</i>	<i>Proteolysis/secreted/tissue repair and remodeling</i>	<i>1.66, 3.25, 1.80, -1.08</i>
Protein transport protein Sec61 subunit β	Q5RB31	5E-22	Protein translocation in the ER	-1.21, 3.06, 1.10, -1.30
Transmembrane emp24 domain-containing protein 9	Q3T133	7E-52	Protein translocation in the ER	-1.02, 4.08, 1.22, 1.37
Signal recognition particle 14 kDa protein	P37108	7E-39	Protein translocation and targeting of secretory proteins to ER	1.30, 2.83, 1.49, -1.37
Derlin-1	Q5R9W3	3E-17	ER-associated protein degradation	-1.23, 2.29, 1.10, -1.04
ER-associated Hsp40 co-chaperone	Q9UBS4	2E-93	ER-associated protein degradation	-1.04, 8.70, 1.80, 1.79
RING finger protein 175	Q8N4F7	5E-26	ER-associated protein degradation	-1.37, 1.97, 1.44, -1.83
Ubiquitin-conjugating enzyme E2 N	Q9EQX9	1E-77	ER-associated protein degradation	1.12, 1.91, 1.15, 1.03
Ubiquitin-protein ligase	P61078	4E-80	ER-associated protein degradation	1.57, 3.07, 1.37, 1.50
UBX domain-containing protein 2	Q92575	4E-69	ER-associated protein degradation	1.19, 2.78, 2.06, 1.48
170 kDa glucose-regulated protein	Q60432	5E-98	Unfolded protein response/ER	-1.04, 3.36, 1.45, 1.86
94 kDa glucose-regulated protein	Q29092	1E-132	Unfolded protein response/ER	-1.10, 4.87, 1.81, 1.71
Glucosidase 2 subunit beta	P14314	2E-79	Unfolded protein response/ER	-1.05, 2.30, 1.40, 1.24
Protein disulfide-isomerase 4/rearrangement of -S-S- bonds	P13667	1E-156	Unfolded protein response/ER	-1.25, 7.08, 1.60, 2.79
UDP-glucose ceramide glucosyltransferase-like 1	Q6P5E4	2E-7	Unfolded protein response/ER	1.12, 3.84, 1.39, 2.05
Hsp90 co-chaperone	Q15185	3E-40	Unfolded protein/Cytoplasm	1.01, 2.95, 1.14, -1.34
Fukutin	Q8R507	4E-29	Protein modification/Golgi	1.09, 2.59, 1.25, 1.65
Glutaminy-peptide cyclotransferase	Q16769	3E-22	Protein modification/acyltransferase	-1.04, 1.82, 1.28, 1.38
Protein Chibby (PKD2 interactor)	Q9Y3M2	1E-33	Intracellular protein transport	1.04, 2.07, 1.68, 1.0
SEC13-like protein 1	Q9D1M0	1E-135	Intracellular protein transport	1.15, 4.08, 1.81, 1.43
Endoplasmic reticulum-Golgi intermediate compartment protein 1	Q4V8Y6	3E-65	Vesicle-mediated transport	-1.33, 3.18, 1.22, 1.64
KDEL endoplasmic reticulum protein retention receptor 2	Q6PEH1	2E-87	Vesicle-mediated transport	-1.11, 3.10, 1.66, -1.25
Vesicular integral-membrane protein VIP36	Q12907	6E-12	Vesicle-mediated transport	-1.23, 2.51, 1.30, 1.04
<i>Arachidonate lipoxygenase 3</i>	<i>Q9BYJ1</i>	<i>2E-47</i>	<i>Cholesterol & sterol biosyntheses</i>	<i>-1.21, 2.36, 2.00, -1.05</i>
<i>Δ (14)-sterol reductase</i>	<i>Q8WMV1</i>	<i>1E-115</i>	<i>Cholesterol & sterol biosyntheses</i>	<i>-1.34, 2.73, 2.19, 1.14</i>
<i>Diphosphomevalonate decarboxylase</i>	<i>Q62967</i>	<i>5E-66</i>	<i>Cholesterol & sterol biosyntheses</i>	<i>-1.41, 4.62, 1.82, -1.68</i>
<i>Farnesyl diphosphate synthetase</i>	<i>P08836</i>	<i>1E-106</i>	<i>Cholesterol & sterol biosyntheses</i>	<i>-1.57, 5.00, 1.84, -1.65</i>
<i>Probable ergosterol biosynthetic protein 28</i>	<i>Q5R589</i>	<i>1E-57</i>	<i>Sterol biosynthesis</i>	<i>-1.89, 3.39, 1.74, -1.37</i>
<i>Long-chain-fatty-acid--CoA ligase 1</i>	<i>P33121</i>	<i>1E-81</i>	<i>Fatty acid metabolism</i>	<i>1.14, 2.01, 1.48, 1.18</i>
Acidic mammalian chitinase	Q91XA9	4E-58	Carbohydrate hydrolysis	-1.49, 2.25, 1.42, 1.21
Arsenical pump-driving ATPase	O54984	2E-99	Anion transport/membrane	-1.13, 1.83, 1.16, 1.15
ATP-binding cassette sub-family F member 2	Q9UG63	1E-98	Nucleotide transporter/mitochondria	1.44, 3.27, 1.35, 1.01
Gluconate kinase 1	P39208	1E-8	Carbohydrate metabolism	1.37, 3.12, 1.83, 1.15

Set 3 (57 genes): Delayed and persistent up-regulation

<i>Cyclic AMP response element-binding protein 2</i>	<i>P18848</i>	<i>4E-23</i>	<i>Transcription activation</i>	<i>1.21, 2.15, 1.66, 1.45</i>
<i>Probable ATP-dependent RNA helicase DDX5</i>	<i>Q5R4I9</i>	<i>1E-111</i>	<i>mRNA processing/nucleus</i>	<i>1.20, 2.24, 1.25, 1.83</i>
<i>Vigilin</i>	<i>P81021</i>	<i>4E-85</i>	<i>mRNA stabilization/cytoplasm</i>	<i>1.14, 1.82, 1.20, 1.96</i>
<i>Elongation factor 1-alpha</i>	<i>Q9YIC0</i>	<i>2E-82</i>	<i>Translation</i>	<i>1.21, 1.56, 1.45, 1.93</i>
<i>Nucleolar phosphoprotein p130</i>	<i>P41777</i>	<i>8E-35</i>	<i>Translation</i>	<i>1.13, 2.58, 1.37, 1.44</i>
Phospholipase C- γ -2	P16885	8E-17	Signal transduction	-1.19, 2.22, 1.86, 1.93
Phospholipase A-2-activating protein	Q9Y263	1E-95	Signal transduction	1.04, 2.22, 1.86, 1.15
Mitogen-activated protein kinase 6	Q5F3W3	9E-8	Apoptosis inhibition/cytoplasm	1.46, 2.68, 1.31, 2.11
Nucleolysin TIAR	Q01085	3E-32	Apoptosis induction/nucleolysis	-1.38, 2.69, 3.20, 1.59
<i>Cathepsin B</i>	<i>P07858</i>	<i>9E-13</i>	<i>Proteolysis/lysosome</i>	<i>-1.10, 1.75, 1.36, 1.81</i>
<i>Hyaluronan-binding protein 2</i>	<i>Q6L711</i>	<i>2E-36</i>	<i>Proteolysis/secreted</i>	<i>-1.66, 1.81, 3.02, 4.71</i>
<i>α-1-microglobulin/bikunin precursor</i>	<i>P00978</i>	<i>3E-16</i>	<i>Protease inhibitor/secreted</i>	<i>-1.25, 1.94, 1.08, -1.64</i>
<i>α-2-macroglobulin</i>	<i>P01023</i>	<i>1E-130</i>	<i>Protease inhibitor/secreted</i>	<i>1.06, 1.22, 1.12, 2.19</i>
<i>Hsp70-binding protein 1</i>	<i>Q6IMX7</i>	<i>4E-29</i>	<i>Proteasome inhibitor</i>	<i>1.1, 1.94, 1.91, 1.73</i>
<i>RWD domain-containing protein 1</i>	<i>Q99ND9</i>	<i>8E-77</i>	<i>Proteasome inhibitor</i>	<i>1.21, 1.69, 1.18, 2.11</i>
Signal recognition particle 54 kDa protein	Q6AYB5	1E-107	Targeting of secretory and membrane proteins to ER	-1.15, 1.84, 1.37, 1.28
Signal recognition particle receptor subunit beta	P47758	3E-17	Targeting of secretory and membrane proteins to ER	-1.0, 4.20, 1.41, 2.08
Glycoprotein-processing glucosidase I	Q80UM7	1E-91	Protein glycosylation/ER	1.21, 2.67, 1.53, 1.66
Ribophorin I	P04843	3E-65	Protein glycosylation/ER	-1.04, 3.33, 2.24, 2.54
Clathrin assembly protein assembly protein complex 1	Q9BXS5	6E-75	Vesicle-mediated transport	-1.1, 2.31, 1.56, 1.29
Clathrin heavy chain 1	P49951	7E-48	Vesicle-mediated transport	1.03, 2.17, 1.45, 1.42
Coatomer subunit β	P23514	1E-126	Vesicle-mediated transport	1.43, 2.79, 1.77, 1.78
Protein transport protein Sec23B	Q9D662	1E-74	Vesicle-mediated transport	1.85, 2.52, 1.17, 1.52
Ras-related protein Rab-10	P61027	1E-61	Vesicle-mediated transport	1.10, 1.80, 1.28, 1.18
Ras-related protein Rab-1A	Q05974	1E-106	Vesicle-mediated transport	1.34, 3.77, 1.93, 1.76
Ras-related protein Rab-6A	Q5RAV6	1E-102	Vesicle-mediated transport	1.71, 2.71, 1.65, 1.63
TBC1 domain family member 10A	P58802	5E-66	Vesicle-mediated transport	-1.29, 2.14, 1.74, 2.23
<i>Apolipoprotein Eb</i>	<i>O42364</i>	<i>5E-93</i>	<i>Lipid transport</i>	<i>1.18, 5.97, 7.03, 7.79</i>
<i>ATP-binding cassette sub-family A member 1</i>	<i>P41233</i>	<i>3E-80</i>	<i>Cholesterol homeostasis/assembly of HDL</i>	<i>1.12, 1.68, 1.49, 1.93</i>
<i>Hydroxymethylglutaryl-CoA synthase</i>	<i>P23228</i>	<i>4E-93</i>	<i>Cholesterol and sterol biosyntheses</i>	<i>-1.08, 2.93, 1.99, 1.81</i>
Cystathionine γ -lyase	P32929	1E-58	Cysteine synthesis/antioxidant defence	-1.01, 2.89, 2.35, 1.91
Glycine N-methyltransferase	P13255	3E-65	Cysteine synthesis/antioxidant defence	-1.07, 1.70, 1.83, 1.49
GDH/6PGL endoplasmic bifunctional protein	Q8CFX1	9E-42	Pentose-phosphate shunt/NADPH/antioxidant defence	1.06, 2.07, 1.58, 1.73
Ferroxidase/ceruloplasmin	P13635	2E-69	Iron storage/antioxidant defence	-1.05, 1.93, 1.48, 2.34
Hemoglobin subunit β	Q6Y239	2E-34	Oxygen transport/antioxidant defence	-1.22, 1.98, 2.58, 3.95
Isocitrate dehydrogenase [NADP] cytoplasmic	Q9Z2K8	1E-174	NADPH /antioxidant defence	1.25, 2.51, 2.20, 1.60
<i>Complement C1s subcomponent (classical pathway)</i>	<i>Q69DK8</i>	<i>3E-7</i>	<i>Complement activation</i>	<i>-1.04, 2.86, 3.31, 3.73</i>

<i>Complement component C7 (classical & alternative pathways)</i>	<i>Q9TUQ3</i>	<i>2E-54</i>	<i>Complement activation</i>	<i>1.79, 7.53, 7.06, 9.13</i>
<i>Complement component C9 (classical & alternative pathways)</i>	<i>P79755</i>	<i>1E-43</i>	<i>Complement activation</i>	<i>1.15, 2.45, 2.06, 3.13</i>
<i>Complement factor B (alternative pathway)</i>	<i>P04186</i>	<i>2E-25</i>	<i>Complement activation</i>	<i>-1.18, 2.24, 1.66, 1.31</i>
<i>Complement factor H (alternative pathway)</i>	<i>P08603</i>	<i>2E-25</i>	<i>Complement inactivation</i>	<i>1.18, 1.91, 1.14, 1.65</i>
<i>Complement factor I (classical & alternative pathways)</i>	<i>Q9WUW3</i>	<i>4E-24</i>	<i>Complement inactivation</i>	<i>1.72, 3.16, 2.30, 4.17</i>
<i>C-type lectin domain family 4 member D</i>	<i>Q8WXI8</i>	<i>7E-19</i>	<i>Immune response/endocytic receptor</i>	<i>-1.32, 1.35, 1.53, 1.15</i>
<i>Cyclosporin A-binding protein</i>	<i>P54985</i>	<i>9E-66</i>	<i>Immune suppressive activity</i>	<i>-1.06, 2.63, 1.84, 1.35</i>
<i>Hepcidin</i>	<i>P82951</i>	<i>7E-34</i>	<i>Anemia of inflammation</i>	<i>-1.07, 4.14, 5.39, 8.57</i>
<i>Leukocyte cell-derived chemotaxin 2</i>	<i>O62644</i>	<i>1E-9</i>	<i>Chemotaxis/cell differentiation and repair</i>	<i>-1.18, 2.82, 3.15, 3.36</i>
<i>Coronin-1C</i>	<i>Q9ULV4</i>	<i>1E-97</i>	<i>Actin cytoskeleton /cytokinesis/motility</i>	<i>1.02, 2.17, 1.23, 1.52</i>
<i>Extracellular matrix protein 2</i>	<i>O94769</i>	<i>2E-16</i>	<i>Cell-matrix adhesion</i>	<i>1.45, 2.96, 2.20, 1.52</i>
<i>Gap junction Cx32.2 protein</i>	<i>P51915</i>	<i>8E-38</i>	<i>Cell communication</i>	<i>1.39, 4.50, 3.86, 3.94</i>
<i>Tubulin α chain</i>	<i>P30436</i>	<i>0</i>	<i>Microtubule-based movement</i>	<i>1.00, 1.45, 1.13, 1.45</i>
<i>6-Pyruvoyl tetrahydrobiopterin synthase</i>	<i>Q90W95</i>	<i>1E-66</i>	<i>Zinc ion binding</i>	<i>1.42, 5.29, 3.22, 2.73</i>
<i>Ancient ubiquitous protein 1</i>	<i>Q9Y679</i>	<i>1E-21</i>	<i>Acytransferase activity</i>	<i>-1.22, 1.31, 1.58, 1.28</i>
<i>Cation transport regulator-like protein 1</i>	<i>Q5SPB6</i>	<i>1E-43</i>	<i>Protein binding</i>	<i>-1.60, 4.70, 3.40, 7.13</i>
<i>Proteoglycan-4 precursor (Megakaryocyte-stimulating factor)</i>	<i>Q9JM99</i>	<i>9E-60</i>	<i>Catalytic activity/extracellular</i>	<i>1.06, 1.61, 1.15, 1.52</i>
<i>Rhamnose-binding lectin</i>	<i>Q9PVW8</i>	<i>2E-37</i>	<i>Sugar binding/secreted</i>	<i>-1.24, 2.11, 2.26, 2.18</i>
<i>Type II antifreeze protein</i>	<i>P05140</i>	<i>9E-29</i>	<i>Response to freezing/sugar binding</i>	<i>-1.40, 2.94, 1.80, 2.37</i>
<i>Xylulose kinase</i>	<i>Q3MIF4</i>	<i>1E-31</i>	<i>D-xylose metabolism</i>	<i>-1.61, 2.12, 3.51, 5.40</i>