

Table 1 Suppl. Primer pairs used in reverse transcription quantitative PCR. *Actin* (*ACT*) was used as an internal control.

Gene	Primer pairs (5 - 3')
<i>CRE1-1</i>	forward: GTCTGGGGTATGGATCCTCG reverse: AGCTGCTTTCTGTTTTCGGG
<i>CRE1-2</i>	forward: GCTGGCCTACACATGGTTCT reverse: GTACCGGAGCCACCCATAAC
<i>CRE1-3</i>	forward: CTCGTCCGTGAACCCAATCA reverse: GGCCTAAGCCGTTACCAACT
<i>CRE1-4</i>	forward: TGATGGAAACTTGCAGAAGAC reverse: TGCAATGTGCTTTAACAGTG
<i>GID1-1</i>	forward: CAGCTTGTGACGATGGCTAC reverse: GGGTGGATAGGGATAGCACC
<i>GID1-2</i>	forward: GCCACAAAGTACAACCCCAG reverse: GGCCAGCCTGTAATCAATCG
<i>GID1-3</i>	forward: CGAGAGACTCCGGCAAATTG reverse: GCCGTGGATGTAGATGAGGA
<i>PYR</i>	forward: GGGCAGCTTCATGTGGATTT reverse: AAGACGAACAGATCCAGGGG
<i>PR-1</i>	forward: CAGCTCCACCATCAATGCTG reverse: GTGGTTTGTGTCAGGTTTGCGA
<i>CKX</i>	forward: TCCACTGTCTTGCAGTCCAC reverse: ACCTCCGCTACGTACTCTCA
<i>UGT76C1</i>	forward: GGCCAGATTCCGTGATTGGA reverse: AAAGTTGAGTTCCACCCGCT
<i>GA20ox</i>	forward: CTTGCGAGACCTACGTTTGT reverse: AACGGGACCTCAACCAGTTC
<i>GA3ox1</i>	forward: GGCTTGGAGCAATGGGAGAT reverse: AGCCGAGGATGTTGGTCATC
<i>ST5A_B_C</i>	forward: TGGGTCAACTTCCTTCGTCG reverse: GTCCCGGCAGATGTAAACGA
<i>UBE1</i>	forward: CTATGGCCACTGGTCTCGTC reverse: CATCGGTCCCAAACAGTCCA
<i>UBE2DE</i>	forward: TGGAAATGTGCACCGGGTTA reverse: TACAAGGCCCACACCATGTC
<i>UBE2G1</i>	forward: ATGGGTTCTCGGCTGGATTG reverse: CTGTTGGAGGGCTGTTTGGA
<i>ACT</i>	forward: ATCCTCCGTCTTGACCTTG reverse: TGTCCGTCAGGCAACTCAT

Table 2 Suppl. Identified differentially accumulated proteins in a pathway potentially associated with dwarfism in LH-1 compared with LA-1. The red color-codes are differentially-expressed proteins with a high biological relevance discussed in the paper.

Accession	KEGG(ko_id and definition)	Unique peptide	Ratio
Cotton_D_gene_10017980	K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]	3	1.827
Cotton_D_gene_10007513	K01792 glucose-6-phosphate-1-epimerase [EC:5.1.3.15]	2	1.472
Cotton_D_gene_10032788	K00134 glyceraldehyde-3-phosphate dehydrogenase [EC:1.2.1.12]	3	1.3265
Cotton_D_gene_10026040	K00011 alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	7	2.0215
Cotton_D_gene_10036518	K00850 6-phosphofructokinase [EC:2.7.1.11]	3	1.526
Cotton_D_gene_10004251	K03841 fructose-1,6-bisphosphatase I [EC:3.1.3.11]	6	1.6125
Cotton_D_gene_10005016	K00873 pyruvate kinase [EC:2.7.1.40]	6	1.657
Cotton_D_gene_10014113	K00134 glyceraldehyde-3-phosphate dehydrogenase [EC:1.2.1.12]	3	3.989
Cotton_D_gene_10013278	K00121 S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC: 1.1.1.1]	6	1.886
Cotton_D_gene_10009509	K00627 pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	7	2.64
Cotton_D_gene_10011074	K00001 alcohol dehydrogenase [EC:1.1.1.1]	1	3.388
Cotton_D_gene_10022268	K01895 acetyl-CoA synthetase [EC:6.2.1.1]	6	1.638
Cotton_D_gene_10028686	K00134 glyceraldehyde-3-phosphate dehydrogenase [EC:1.2.1.12]	1	1.6805
Cotton_D_gene_10027572	K00134 glyceraldehyde-3-phosphate dehydrogenase [EC:1.2.1.12]	4	1.4805
Cotton_D_gene_10029740	K00873 pyruvate kinase [EC:2.7.1.40]	3	1.956
Cotton_D_gene_10006630	K13993 HSP20 family protein	2	1.4
Cotton_D_gene_10033427	K09580 protein disulfide-isomerase A1 [EC:5.3.4.1]	5	3.2995
Cotton_D_gene_10029521	K12670 oligosaccharyltransferase complex subunit beta	2	2.259
Cotton_D_gene_10017746	K09490 heat shock 70 kDa protein 5	1	1.9145
Cotton_D_gene_10007690	K09580 protein disulfide-isomerase A1 [EC:5.3.4.1]	7	2.6375
Cotton_D_gene_10025567	K14016 ubiquitin fusion degradation protein 1	1	2.1025
Cotton_D_gene_10028022	K12667 oligosaccharyltransferase complex subunit delta (ribophorin II)	7	1.707
Cotton_D_gene_10021424	K08054 calnexin	4	2
Cotton_D_gene_10038223	K04043 molecular chaperone DnaK	15	3.1825
Cotton_D_gene_10025340	K03283 heat shock 70 kDa protein 1/8	4	2.8055
Cotton_D_gene_10029674	K13993 HSP20 family protein	6	2.1165
Cotton_D_gene_10002643	K09487 heat shock protein 90 kDa beta	1	2.062
Cotton_D_gene_10001601	K09503 DnaJ homologue subfamily A member 2	2	2.07
Cotton_D_gene_10032487	K03283 heat shock 70 kDa protein 1/8	4	3.184
Cotton_D_gene_10027653	K12666 oligosaccharyltransferase complex subunit alpha (ribophorin I)	7	1.3835
Cotton_D_gene_10006598	K09580 protein disulfide-isomerase A1 [EC:5.3.4.1]	7	2.605
Cotton_D_gene_10022065	K04079 molecular chaperone HtpG	5	2.7125
Cotton_D_gene_10033869	K14012 UBX domain-containing protein 1	4	1.528
Cotton_D_gene_10037518	K09490 heat shock 70 kDa protein 5	2	2.247
Cotton_D_gene_10013822	K09487 heat shock protein 90 kDa beta	1	2.982
Cotton_D_gene_10006411	K13525 transitional endoplasmic reticulum ATPase	2	2.7235
Cotton_D_gene_10032208	K03283 heat shock 70 kDa protein 1/8	4	2.377
Cotton_D_gene_10020948	K09503 DnaJ homolog subfamily A member 2	3	2.5765
Cotton_D_gene_10012471	K09490 heat shock 70 kDa protein 5	4	1.79
Cotton_D_gene_10006705	K13993 HSP20 family protein	1	3.513
Cotton_D_gene_10023691	K04079 molecular chaperone HtpG	5	2.7835
Cotton_D_gene_10015425	K03237 translation initiation factor 2 subunit 1	5	2.5265
Cotton_D_gene_10025541	K11718 UDP-glucose:glycoprotein glucosyltransferase [EC:2.4.1.-]	6	2.542
Cotton_D_gene_10024474	K13993 HSP20 family protein	1	2.92
Cotton_D_gene_10020670	K10839 UV excision repair protein RAD23	3	1.5365
Cotton_D_gene_10009349	K08054 calnexin	7	2.374
Cotton_D_gene_10025013	K04079 molecular chaperone HtpG	3	2.6365
Cotton_D_gene_10031848	K09580 protein disulfide-isomerase A1 [EC:5.3.4.1]	7	3.014
Cotton_D_gene_10024858	K08057 calreticulin	4	1.9295
Cotton_D_gene_10017255	K03283 heat shock 70 kDa protein 1/8	2	2.3895
Cotton_D_gene_10013627	K14004 protein transport protein SEC13	7	1.5515
Cotton_D_gene_10025488	K12670 oligosaccharyltransferase complex subunit beta	5	1.4545

Cotton_D_gene_10023096	K03283 heat shock 70 kDa protein 1/8	2	3.2855
Cotton_D_gene_10004229	K03283 heat shock 70 kDa protein 1/8	1	2.3025
Cotton_D_gene_10025558	K13249 translocon-associated protein subunit alpha	1	2.225
Cotton_D_gene_10018465	K04523 ubiquilin	2	0.6965
Cotton_D_gene_10004953	K10575 ubiquitin-conjugating enzyme E2 G1 [EC:6.3.2.19]	2	0.6915
Cotton_D_gene_10027217	K07953 GTP-binding protein SAR1 [EC:3.6.5.-]	2	0.668
Cotton_D_gene_10036283	K06689 ubiquitin-conjugating enzyme E2 D/E [EC:6.3.2.19]	1	0.603
Cotton_D_gene_10003255	K13719 ubiquitin thioesterase OTU1 [EC:3.1.2.-]	2	0.638
Cotton_D_gene_10035082	K14009 B-cell receptor-associated protein 31	2	0.5645
Cotton_D_gene_10038978	K14489 arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3]	3	2.8525
Cotton_D_gene_10005437	K14493 gibberellin receptor GID1 [EC:3.-.-.]	10	2.259
Cotton_D_gene_10004615	K13449 pathogenesis-related protein 1	3	0.515
Cotton_D_gene_10009055	K14496 abscisic acid receptor PYR/PYL family	8	0.3805
Cotton_D_gene_10016489	K13258 2-hydroxyisoflavanone dehydratase/gibberellin receptor GID1 [EC:3.-.-.]	2	0.638
Cotton_D_gene_10025048	K06892 gibberellin 3-beta-dioxygenase [EC:1.14.11.15]	5	0.378
Cotton_D_gene_10001937	K06892 gibberellin 20-oxidase [EC:1.14.11.12]	1	0.4725
Cotton_D_gene_10036506	K11821 desulfoglucosinolate sulfotransferase /aryl sulfotransferase [EC:2.8.2.1]	5	0.6815
Cotton_D_gene_10021604	K13030 cyanohydrin beta-glucosyltransferase/cytokinin-N-glucosyltransferase/pathogen-in- ducible salicylic acid glucosyltransferase [EC:2.4.1.-]	2	1.5405
Cotton_D_gene_10031171	K00102 D-lactate dehydrogenase /cytokinin dehydrogenase [EC:1.5.99.12]	5	3.3755
Cotton_D_gene_10025336	K03178 ubiquitin-activating enzyme E1 [EC:6.3.2.19]	5	1.6845
Cotton_D_gene_10004953	K10575 ubiquitin-conjugating enzyme E2 G1 [EC:6.3.2.19]	2	0.6915
Cotton_D_gene_10036283	K06689 ubiquitin-conjugating enzyme E2 D/E [EC:6.3.2.19]	1	0.603

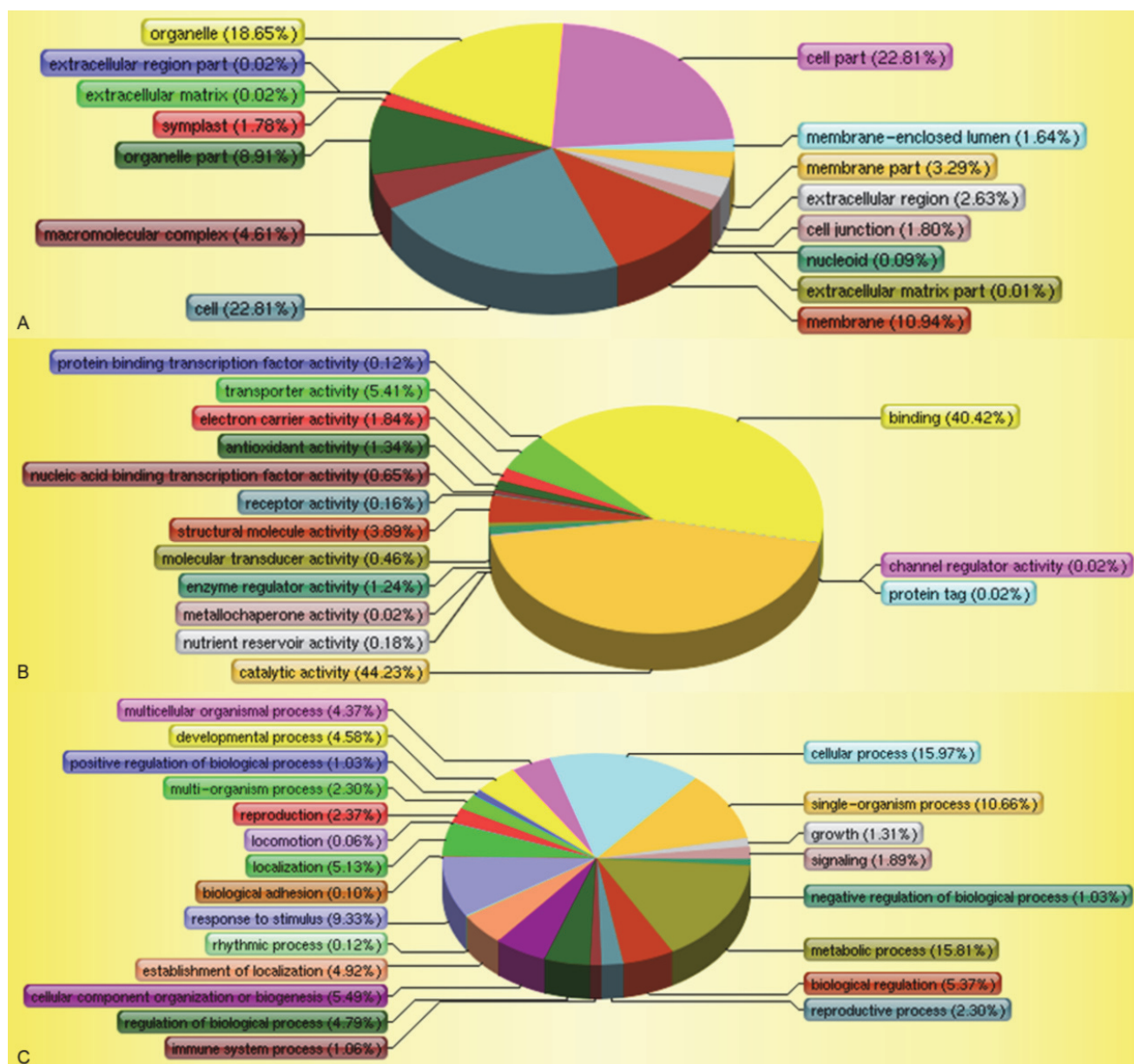


Fig. 1 Suppl. Gene ontology classification of distribution of differentially-expressed proteins. The gene ontology terms used for categorisation are cellular components (A), molecular functions (B), and biological processes (C).

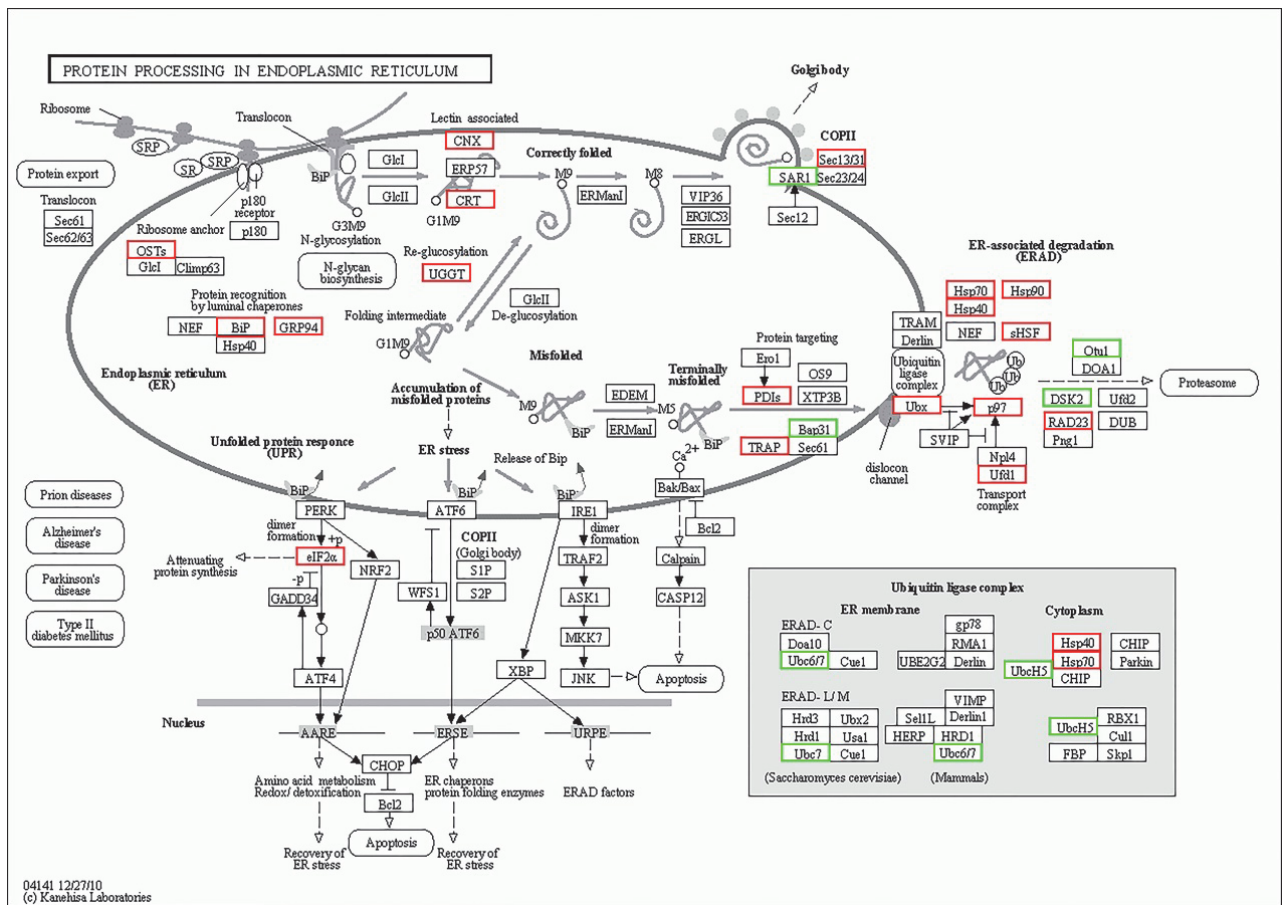


Fig. 3 Suppl. Protein processing in endoplasmic reticulum derived from KEGG. The numbers in the red boxes represent proteins whose expression changed significantly. The numbers in the green boxes represent proteins whose expression decreased significantly.

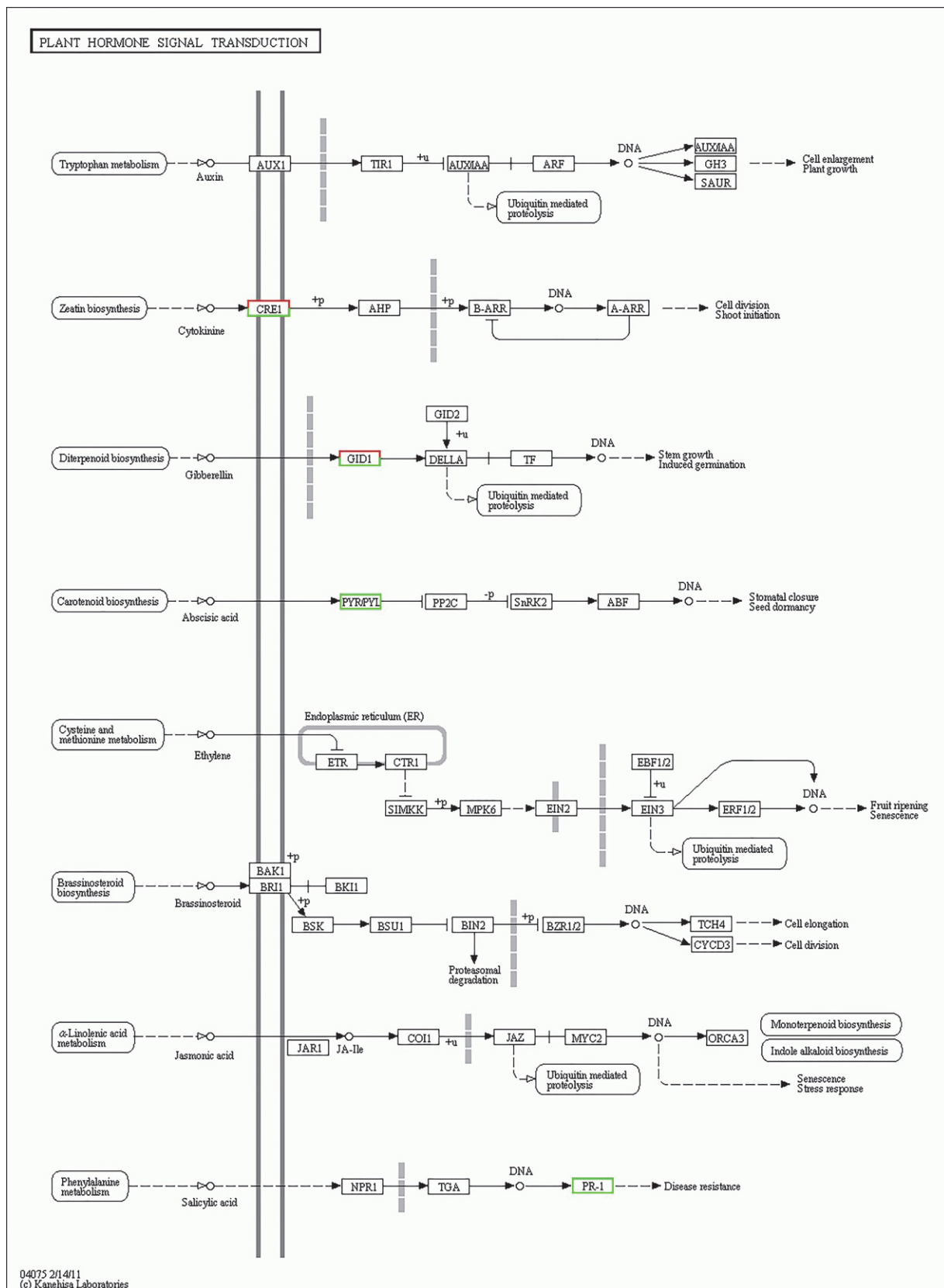
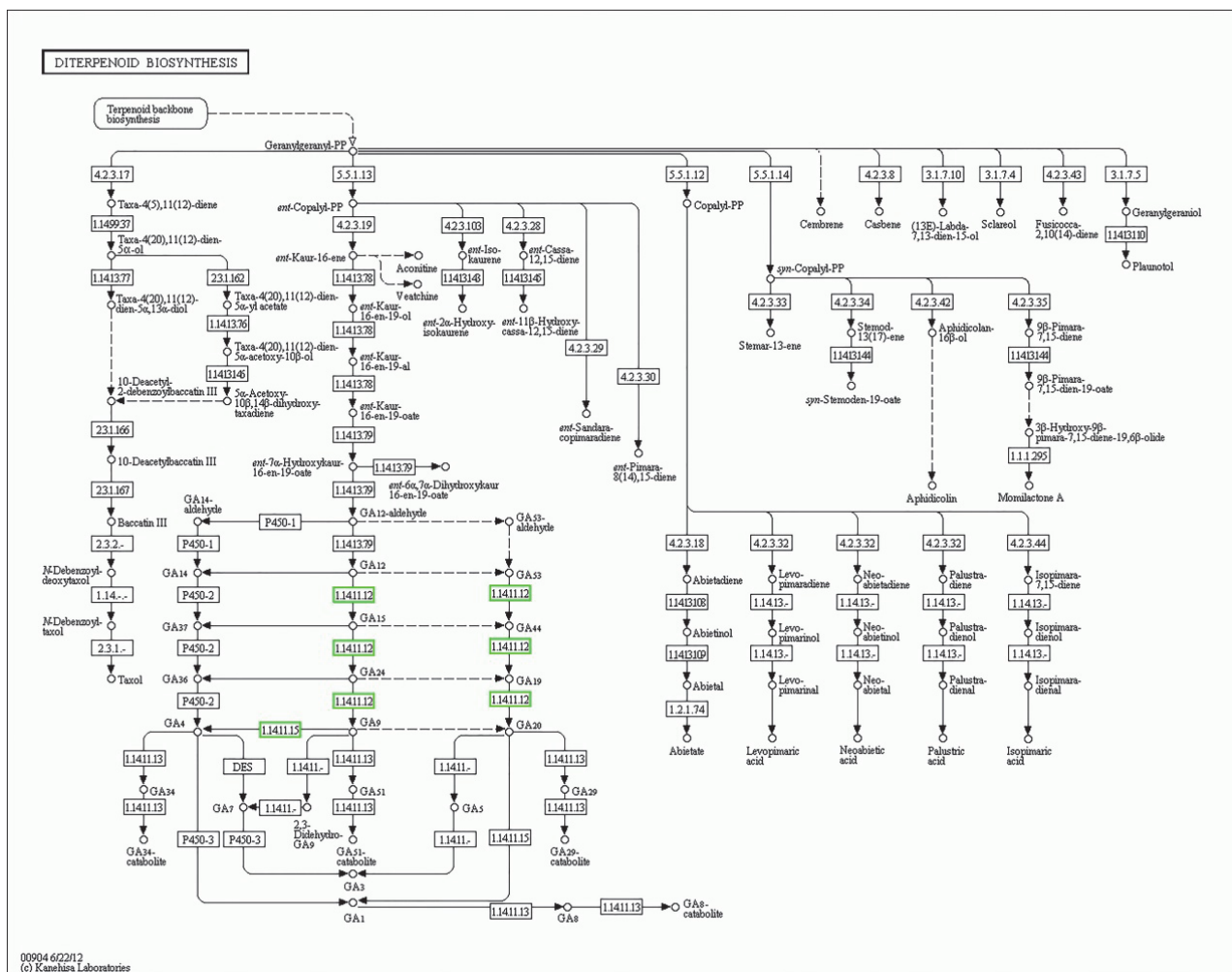


Fig. 4 Suppl. The plant hormone signal transduction derived from KEGG. The numbers in the red boxes represent proteins whose expression changed significantly, the numbers in the green boxes represent proteins whose expression decreased significantly.



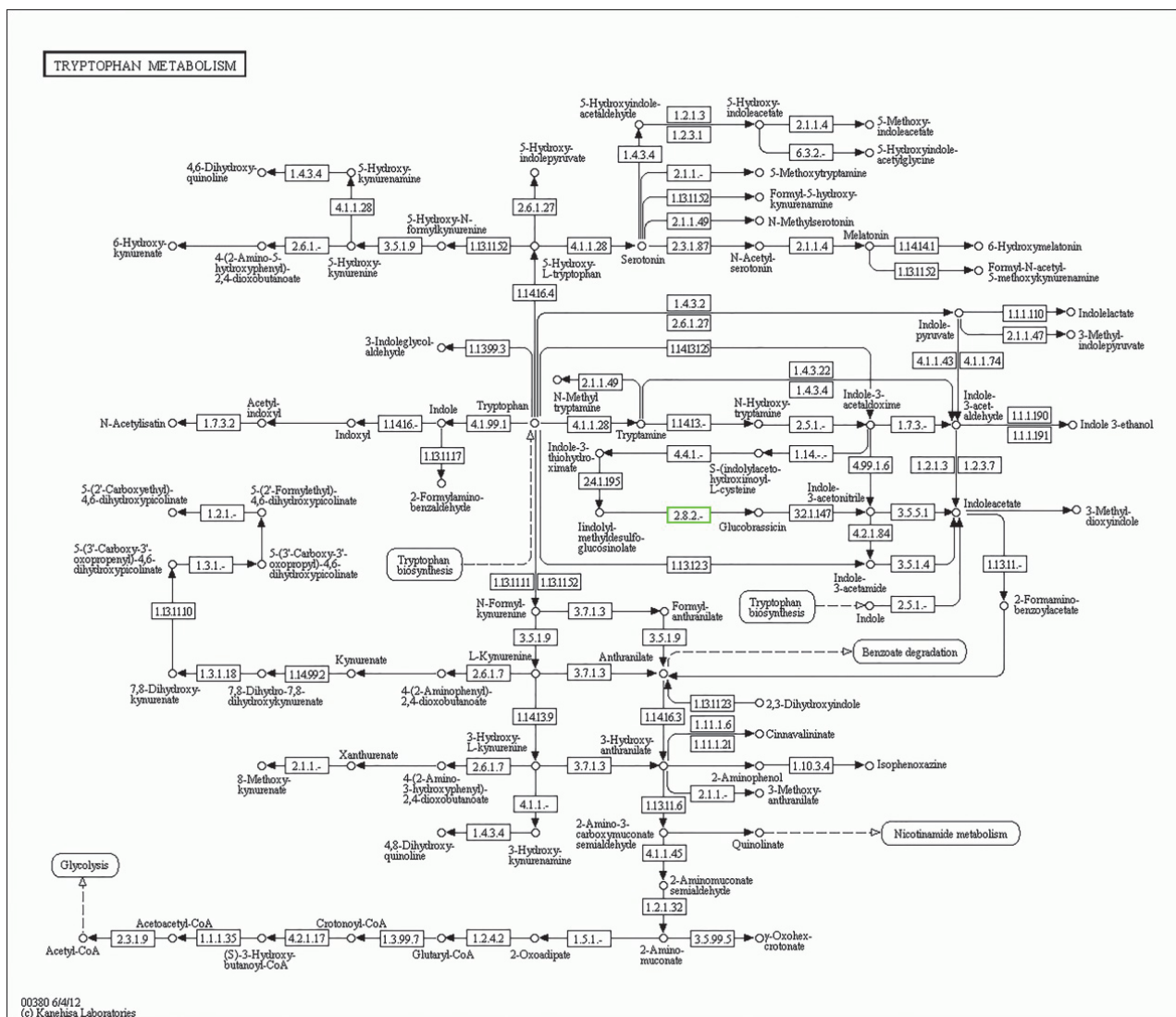


Fig. 6 Suppl. The tryptophan metabolism derived from *KEGG*. The numbers in the *green boxes* represent proteins whose expression decreased significantly.

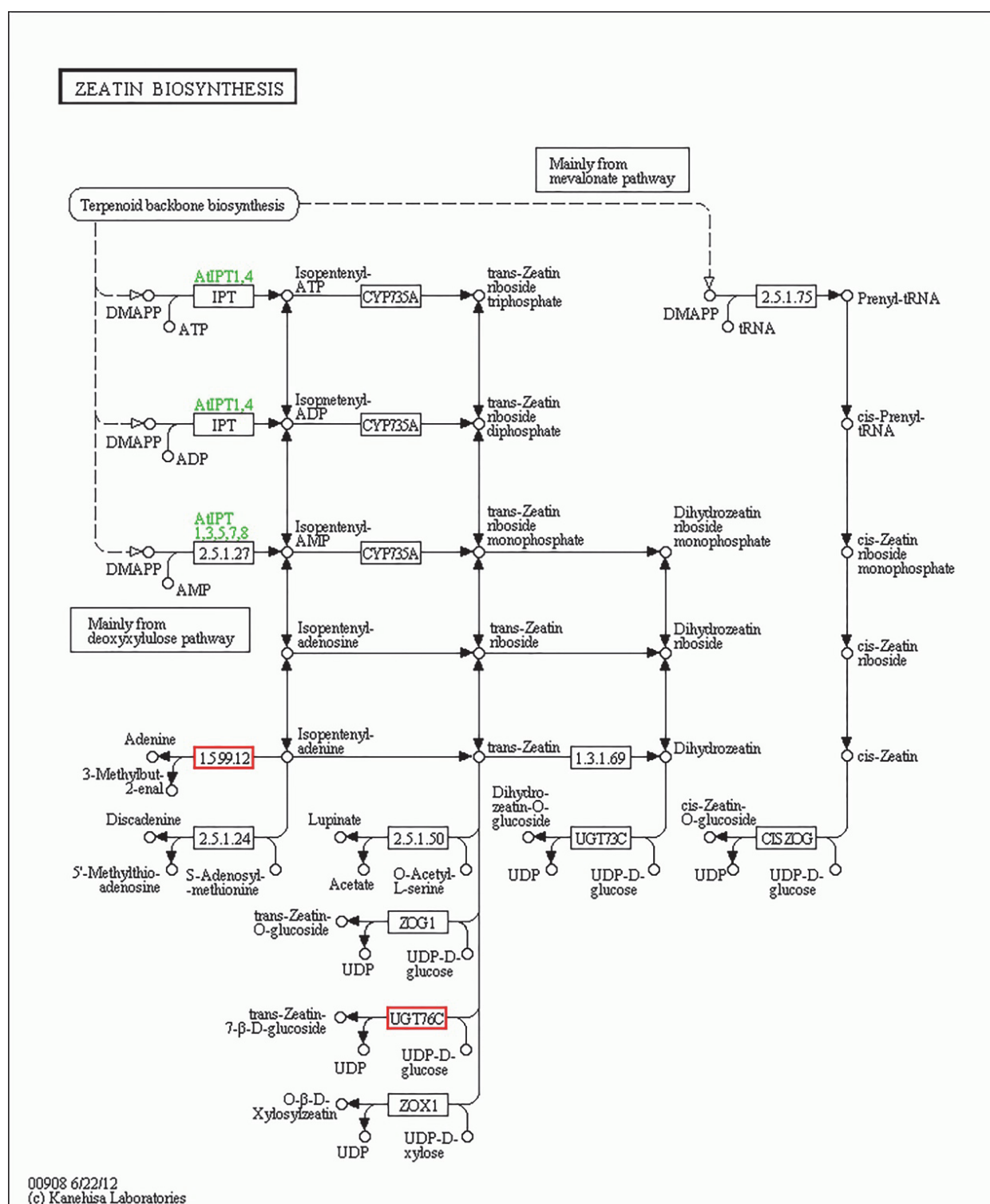


Fig. 7 Suppl. The zeatin biosynthesis pathway derived from *KEGG*. The numbers in the *red boxes* represent proteins whose expression increased significantly. The numbers in the *green boxes* represent proteins whose expression decreased significantly.

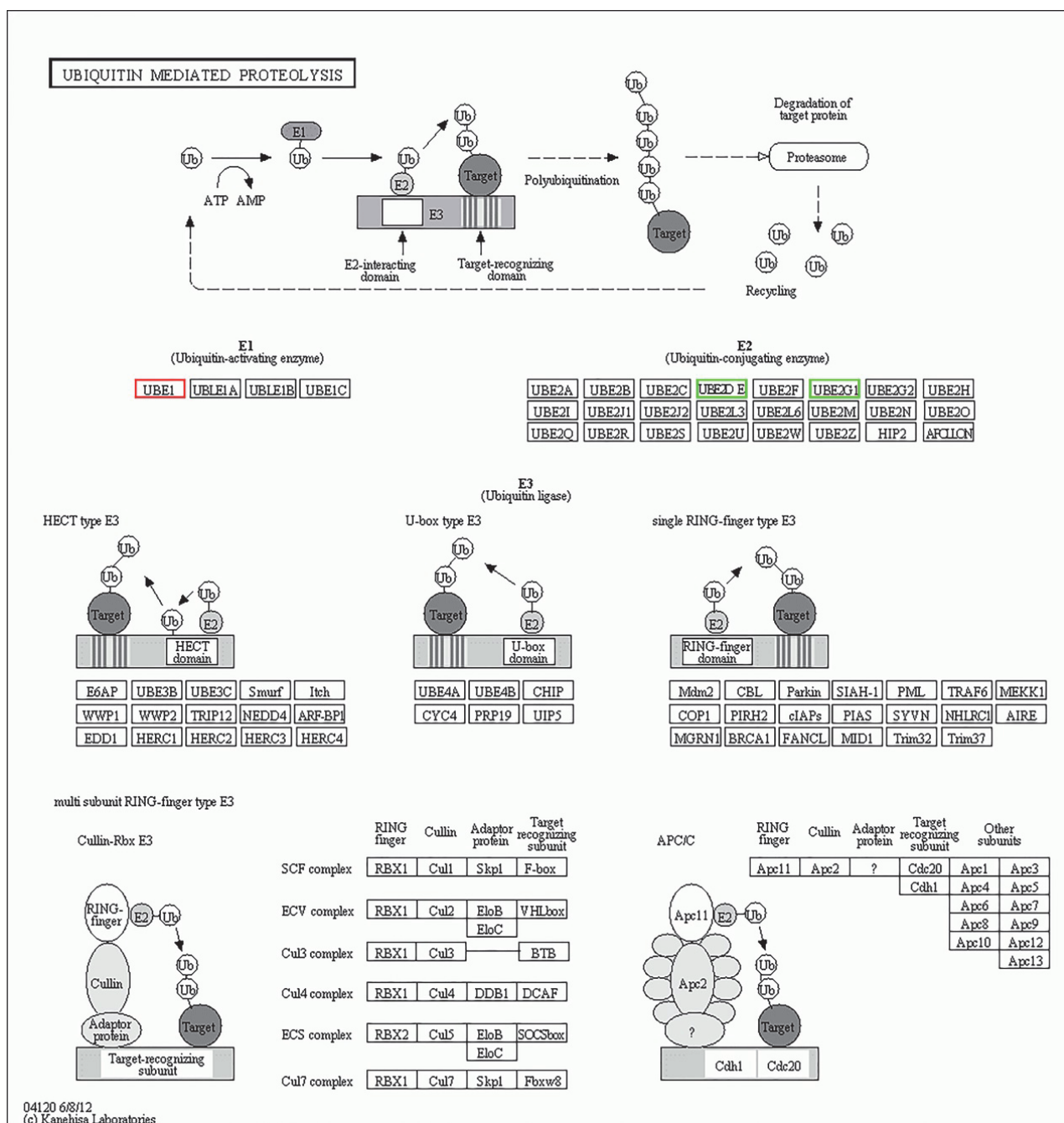


Fig. 8 Suppl. The ubiquitin mediated proteolysis system derived from KEGG. The numbers in the red boxes represent proteins whose expression increased significantly. The numbers in the green boxes represent proteins whose expression decreased significantly.