Supplemental Material

TABLE S1 Primers used for amplification of gene fragments based on peptide sequences, inverse PCR, sequencing of obtained PCR products and subcloning of selected genes

Primer	Sequence (5' → 3')[a]	Position[b]
Amplification of gene fragments		
DR4F	ACSAACGCSGARGGCGARGG	2101 – 2120
DR3R	GCYTCSGGGTCGTTGTTSAC	2395 – 2414
DR3F	GTSAACAACGACCCSGARGC	2395 – 2414
DR1R	CTTSGCCTTSAGYTCGTCSGCGTA	4382 – 4405
Inverse PCR		
DR8F	CAGCGTTTGAAGGGCAAGAAG	4250 – 4270
DR7R	TGAGAGCGAGGTTTTCCTTCG	2177 – 2197
DR10sF	ACGGCGCGAACATTATTATC	4644 – 4663
DR9sR	GCCAAAGGAATGCCATAGAA	3796 – 3815
1745sF	TGAAAGCGTGACCTGGTATG	1728 – 1747
1745R	GGTGATAATTGCCCATACGC	1595 – 1614
1745bF	GATGCGTTGGTCGTGACTC	1286 – 1304
1745bR	CGATAACAACCGCGTCCAC	1172 – 1190
DR15fbF	CCTTGACCATCGACGAGATT	6108 – 6127
DR16fR	TCATAATTTCGGGAAGAACTGC	6059 – 6080
Eco-F	GCATGATTCGCAAAGACAAC	8779 – 8798
Eco-R	GCATTGGCCCTGATTCAC	8652 – 8669
Sequencing		
DR6F	TGGCGGCAAGGCAGTGATTCTG	3138 – 3159
DR14F	GATTGGCGTTCAGTTCGTTACC	5251 – 5272
DR18F	GTCAACTCCTCGGTGGAATC	7974 – 7993
DR21F	CGTTGAACTGCTCACCAAGA	1310 – 1329
Subcloning of genes		
1642F	AAGGACCTCATGGCGCGTAG	4086 – 4105
1642R	GTCGACGCAGGCGCTTTAG	5023 – 5041
1015F	CGCGGTTTAGGCATACCAAGG	2543 – 2563
DR19F	CTTATTTTCCTCAAGCCTGTGC	5564 – 5585
DR20R	AACCCGTTTGTTTTCCCTTC	7770 – 7789
F-DAI	AGCGGCTCTTCAATGCAGCACGCGAAATACCCCC	5693 – 5711
R-DAI	AGCGGCTCTTCTCCCCACCATGCGCGCTACGGC	7604 – 7621
F-DHD	AGCGGCTCTTCAATGGCACAAGAGGTTAAGGCTCC	4172 – 4191
R-DHD	AGCGGCTCTTCTCCCGGCGATTTCGCCCTGCATA	5005 – 5023
F-THD	AGCGGCTCTTCAATGGCAGAATTCGACGTTGAATAC	2575 – 2595
R-THD	AGCGGCTCTTCTCCCCATGTTTGCAATCGCGTGGC	4010 – 4029

[a] Underlined sequences indicate enzyme recognition regions and combinatorial sites for directed insertion of PCR products into the vectors used for expression of tagged proteins.

[b] Positions correspond to the nucleotide sequence deposited in the GenBank database (accession no. JQ358709; primer DR21F, accession no. KC143072).

TABLE S2 Proteins clearly upregulated in the presence of daidzein compared to growth without daidzein (2D-DIGE analysis) and corresponding peptide sequences determined by MS analysis and matching the amino acid sequence deduced from the identified gene

Protein spot	Encoding gene	-fold upregulated	Peptide sequences (amino acid position)[a]
1	*ifcA*	142	LQTEGEGVSGIAVR (69 – 82) VDDFEeaR (83 – 90)
2	*ifcB*	210	TTIAIFK (2 – 8) EGDALVVTR (139 – 147) QDVQVDSPAVIAVAAR (154 – 169) KLPVEK (186 – 191)
3	*ifcC*	26	ALVFGSSGLagR (30 – 41) TLPEAmagtiAK (58 – 69) VDGDAATVER (111 – 120) VLSTNAEGEGGAGLQQAER (169 – 187) VVGVGLGIGAK (188 – 198) VVGTSTQK (233 – 240) VIAAVNNDPEASIFR (266 – 280) ecTYGIVGDVQK (281 – 292) ILPAFIQALK (293 – 302)
4	*tdr*	179	nvVVIEK (32 – 38) imGYSHQR (83 – 90) ANYEVAR (91 – 97) AFVENSAETIDIYR (98 – 111) ELIIEDGR (167 – 174) VVGVVAESDGEPLR (175 – 188) AVILATGGMGSSPDR (193 – 207) GVDEAYFK (389 – 396) KPQYLR (397 – 402)
5	*ddr*	83	AQEVKAPK (2 – 9) ISGAPEFGK (10 – 18) WISPEESVGQR (19 – 29) KILLTGTTK (34 – 42) TPGAAAAYADELK (65 – 77) AAGFDCDLADYEAVK (83 – 97) QLAAEGGPFGIR (195 – 206) EMASGLVAAQTTQR (226 – 239)

CONTINUED TABLE S2

Protein spot	Encoding gene	-fold upregulated	Peptide sequences (amino acid position)[a]
6	*ifcE*	24	AKLSVEPR (2 – 9) FGSFVEEYER (16 – 25) TLIDAPVNIR (192 – 201) saVDQLAADK (206 – 215) ATPAPAAATGK (216 – 227) YGIPAYR (267 – 273) ERLDEDVR (277 – 284) IGDNECPDFTGK (347 – 358) NVVVIGGGnvamdcar (359 – 374) AGAASVTVAYR (379 – 389) TYFEADDGLK (486 – 495) TVIIAIGAGK (515 – 524) VNIVERPAR (560 – 568)

[a] Lower case letters indicate amino acids, the sequence of which was not clearly identified in the MS analysis.