

TDF	
Dulc unigene	Best dulc hit ($E < 1E-10$) (assembly4-1)
Tom locus	Annotation of the dulc hit, or of the best BLAST hit from tomato in case E value ($E < 1E-10$) was lower than from BLAST to dulc (ITAG2.3 cDNAs)
Ath locus	Idem (TAIR10 cDNAs)
Functional description Tom	Annotation of the Tom hit
Functional description Ath	Annotation of the Ath hit
GO annotation	Annotation of the dulc hit, or of the best BLAST hit from tomato ($E < 1E-10$) if no dulc hit available
KEGG pathway	Annotation of the dulc hit, or of the best BLAST hit from tomato ($E < 1E-10$) if no dulc hit available
Functional description	Integrated description data from Tom and Ath hits
Category (manual)	Integrated description data from Tom and Ath hits and GO and KEGG data from Dulc unigene

Up-regulated TDFs

TDF	Dulc unigene	Length	Functional description (manual)	Category Functional
11_1	comp131_c0_seq1	162	Phosphoglycerate kinase	
20_5	comp279_c0_seq1	136	Diphosphate--fructose-6-phosphate 1-phosphotransferase	Carbohydrate metabolism/ glycolysis
24_2	comp112_c0_seq1	265	Phosphoenolpyruvate carboxykinase	
11_9	comp5145_c0_seq1	177	Myb-related transcription factor	
16_1	comp3023_c0_seq1	75	Ethylene responsive transcription factor 1a	
2_2	comp414_c0_seq1	82	Ethylene responsive transcription factor 2b	
21_10	comp663_c0_seq1	148	LOB domain protein 42	Transcription regulation
21_8	comp4698_c0_seq1	273	Ethylene responsive transcription factor 1a	
25_2	comp16211_c0_seq1	344	Homeodomain-like superfamily protein	
3_5	comp6283_c0_seq1	129	BHLH transcription factor	
18_12	comp2971_c0_seq1	122	phototropin 2	
2_9	comp2332_c0_seq1	155	Protein phosphatase 2C	
21_1	comp8146_c0_seq1	60	Calmodulin	Signalling
21_11	comp19305_c0_seq1	189	Serine/threonine protein kinase	
22_2	comp1434_c0_seq3	190	Calmodulin	
2_4	comp203_c0_seq1	98	60S ribosomal protein L35	
21_7	comp270_c0_seq1	109	Ribosomal L9-like protein	Protein synthesis & metabolism
24_3	comp2277_c0_seq1	233	Ribosomal protein S6 kinase 2 alpha	
18_1	comp130_c0_seq1	287	Peroxidase 4	
18_5	comp160_c0_seq1	107	Unknown Protein	
20_2	comp2820_c0_seq1	155	WD-40 repeat family protein	
22_4	comp4682_c0_seq1	204	Calcium-transporting ATPase 1	
23_2	comp3924_c0_seq1	104	Unknown Protein	
3_2	comp2249_c0_seq1	91	Unknown Protein	Miscellaneous
4_1	comp4622_c0_seq1	116	Nodal modulator 3	
5_1	comp1799_c0_seq1	131	Cysteine proteinase inhibitor	
9_2	comp4585_c0_seq1	95	High affinity copper uptake protein	
9_6	comp278_c0_seq1	219	Farnesyl pyrophosphate synthase	
5_6	n.a.	112	Wound induced protein	
19_1	n.a.	222	Unknown Protein	
19_7	n.a.	197	Unknown Protein	
22_4	comp4682_c0_seq1	216	n.a.	
14_4	n.a.	67	n.a.	Not available
15_1	n.a.	91	n.a.	
18_7	n.a.	91	n.a.	
22_3	n.a.	34	n.a.	
22_5	n.a.	197	n.a.	

Down regulated TDFs

TDF	Dulc unigene	Length	Functional description (manual)	Category (manual)
15_9	comp7317_c0_seq1	167	Laccase-13	
11_10	n.a.	182	Laccase	
11_6	comp138_c0_seq1	187	Pectinesterase	Cell wall
12_4	comp274_c0_seq1	164	Expansin protein	
9_3	comp312_c0_seq1	262	Pectinesterase	
5_5	comp3717_c0_seq1	81	BHLH transcription factor	
9_5	comp603_c0_seq1	199	Histone H2A	Transcription regulation
18_10	comp15317_c0_seq1	141	Histone-lysine N-methyltransferase	
18_14	comp2153_c0_seq1	244	Auxin response factor 4	
21_3	comp3196_c0_seq1	66	Thioredoxin y	
12_3	comp6249_c0_seq1	156	Calcium-dependent protein kinase 2	
13_10	comp7381_c0_seq2	79	Protein kinase-like protein	Signalling
16_8	comp26171_c0_seq1	72	Protein serine/threonine kinase	
17_4	comp5360_c0_seq5	158	RLK, Receptor like protein	
17_6	comp2671_c0_seq1	264	Calcium-dependent protein kinase 2	
11_7	comp7186_c0_seq2	137	Peptidyl-prolyl cis-trans isomerase	
2_3	comp63_c0_seq2	322	DNAJ chaperone	
20_1	comp3962_c0_seq1	407	Ribosomal protein S6 kinase alpha-3	Protein synthesis & metabolism
20_3	comp343_c0_seq1	68	60S ribosomal protein L7	
22_1	comp953_c0_seq1	187	40S ribosomal protein S24	
10_2	comp47_c0_seq1	241	Aminotransferase-like protein	
11_2	comp709_c0_seq1	92	Unknown Protein	
15_2	comp8620_c0_seq1	127	Unknown Protein	
17_1	comp2181_c0_seq1	177	Protein transport protein sec31	
16_2	comp262_c0_seq1	160	Cortical cell-delineating protein	
18_3	comp16247_c0_seq1	192	Uncharacterized plant-specific domain 01589	
18_8	comp4199_c0_seq1	366	Cysteine protease inhibitor 8	
19_2	comp125_c0_seq1	582	2-oxoglutarate-dependent dioxygenase	
19_4	comp11040_c0_seq1	101	Glucose transporter 8	
19_6	comp4249_c0_seq1	231	Unknown Protein	Miscellaneous
2_1	comp489_c0_seq1	91	F1F0-ATPase inhibitor protein	
2_5	comp859_c0_seq1	250	Unknown Protein	
2_7	comp233_c0_seq1	185	Photosystem I reaction center subunit VI, chloroplastic	
2_8	comp1713_c0_seq1	179	Phosphomethylpyrimidine synthase	
20_4	comp12224_c0_seq1	118	EXS (ERD1/XPR1/SYG1) family protein	
22_6	comp5303_c0_seq1	89	1-aminocyclopropane-1-carboxylate oxidase-like protein	
23_1	comp2630_c0_seq1	200	Polyphenol oxidase	
24_1	comp2476_c0_seq1	230	Indole-3-glycerol phosphate synthase-like	
4_6	comp34_c0_seq1	126	cold, circadian rhythm, and rna binding 2	
9_4	comp33_c0_seq1	336	Metallothionein-like protein	
22_7	n.a.	133	n.a.	
3_4	n.a.	70	n.a.	Not available
4_3	n.a.	63	n.a.	
13_3	n.a.	140	n.a.	