

Table 1 Suppl. The primer sequences of the detected genes in real-time qPCR experiments (unigene sequence database downloaded on 14 August 2017).

Gene ID	Forward (5'→3')	Reverse (3'→5')
DN67964_c2_g1	GAAACCGCCTCATCATCCCTCC	CAGGGCACTTGCTGGTTGTAGT
DN72984_c1_g4	ACCCGATCAACAATCCCAACAGG	TCAAACGTGTAAGTCCGCAGCA
DN74092_c1_g1	CCATGGCTGGATTCGGGTTTCAT	CATGCTCATGTCTTCCCGGGAG
DN64299_c0_g1	TCTCTCTCCTCCATCACCGCTC	GTGTCGGAGGTTTGCTTGCCTA
DN71697_c0_g1	CCAAGTCCGAAGTGGTGGCTAA	TGGCTAGTCCCTACACTTGTGGT
DN68990_c4_g2	GCGGCGTTGATGATGATTGTGG	GGCACGATCTCCTGCAAATTGC
DN82214_c1_g1	GTCGTCGGGATCTACGTTACAGC	AGTTCCAAAGACGACCTGCGAC
DN73071_c0_g1	AGGCCTCTGAAGGGATTGCCTA	AAGAACCAGCGACACACTCGTC
DN64753_c3_g4	TTGGGCCTCGTCACCAACATAT	ATCAAATGGCTGACGGTGAGGA

Table 2 Suppl. Growth conditions of two ecotypes of *Portulaca oleracea*.

<i>Purslane</i> ecotypes	Mean annual temperature [°C]	Mean annual precipitation [mm]	Mean irradiance [$\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$]	Original conditions	Soil moisture content [%]
Red-stem	17	1386.2	336.3	dry and sunny	18
Green-stem	17	1386.2	1150	moist and shady	14

Table 3 Suppl. Green-stem vs. red stem down-regulated differentially expressed genes (DEGs).

Gene ID	log2FC	Description
TRINITY_DN68203_c6_g2	-4.5	inorganic ion transport and metabolism
TRINITY_DN74354_c0_g1	-4.6	protein VITISV_008909
TRINITY_DN74735_c0_g2	-6.3	probable cytochrome P450 313a4
TRINITY_DN74768_c4_g2	-6.0	zinc finger BED domain-containing protein RICESLEEPER 2-like
TRINITY_DN63239_c0_g1	-9.0	DNA integration
TRINITY_DN64915_c0_g2	-5.1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9
TRINITY_DN82508_c10_g2	-9.4	uncharacterized protein LOC104905603
TRINITY_DN63933_c0_g2	-8.1	ADP binding
TRINITY_DN74090_c3_g1	-5.4	sulfotransferase activity
TRINITY_DN64347_c0_g2	-4.4	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5-like
TRINITY_DN79843_c1_g3	-4.6	uncharacterized protein LOC104905271

TRINITY_DN60140_c0_g1	-4.1	M1-alkyl-2-acetyl-glycerophosphocholine esterase activity; chlorophyll catabolic process; lipid catabolic process; chlorophyllase activity
TRINITY_DN78264_c2_g2	-3.7	posttranslational modification, protein turnover, chaperones
TRINITY_DN80888_c2_g2	-4.5	zinc finger BED domain-containing protein RICESLEEPER 2-like
TRINITY_DN79849_c0_g6	-9.8	predicted protein [<i>Physcomitrella patens</i>]
TRINITY_DN66625_c0_g1	-3.6	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process
TRINITY_DN71227_c2_g1	-8.1	ty3-gypsy retrotransposon protein
TRINITY_DN82170_c1_g1	-7.4	cell cycle control, cell division, chromosome partitioning
TRINITY_DN67931_c13_g1	-3.9	DNA-directed RNA polymerase III subunit RPC5
TRINITY_DN77144_c1_g1	-3.6	<i>O</i> -glucosyltransferase rumi homolog isoform X2
TRINITY_DN71587_c0_g3	-8.5	uncharacterized protein LOC104899254 isoform X3
TRINITY_DN82234_c2_g3	-5.6	polyprotein [<i>Oryza sativa japonica</i> group]
TRINITY_DN81532_c0_g1	-5.5	nucleic acid binding; RNA-DNA hybrid ribonuclease activity; DNA integration
TRINITY_DN80577_c2_g1	-4.6	protein MTR_7g077880
TRINITY_DN68424_c2_g3	-4.1	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN77590_c2_g3	-3.9	protein EUTSA_v10002214mg, partial
TRINITY_DN82521_c4_g2	-8.2	uncharacterized protein LOC102583312
TRINITY_DN82073_c3_g1	-6.3	protein MIMGU_mgv1a013758mg
TRINITY_DN73071_c0_g1	-3.5	PI-PLC X domain-containing protein At5g67130-like
TRINITY_DN79726_c1_g1	-8.5	unnamed protein product [<i>Coffea canephora</i>]
TRINITY_DN73560_c0_g1	-8.9	THUMP domain-containing protein 1 homolog
TRINITY_DN72191_c2_g1	-5.1	dual specificity tyrosine-phosphorylation-regulated kinase 3
TRINITY_DN80958_c1_g2	-10.9	protein PRUPE_ppa023217mg
TRINITY_DN70768_c0_g3	-5.3	translation, ribosomal structure and biogenesis
TRINITY_DN68620_c0_g1	-3.8	copper ion binding; oxidoreductase activity; oxidation-reduction process
TRINITY_DN71276_c2_g1	-4.4	nucleic acid binding; cellulase activity; cellulose catabolic process
TRINITY_DN70629_c0_g2	-7.5	disease resistance protein RGA2-like
TRINITY_DN82474_c4_g1	-4.1	DNA integration
TRINITY_DN68158_c1_g1	-4.4	HVA22-like protein a
TRINITY_DN77567_c0_g3	-11.5	uncharacterized protein LOC104882879
TRINITY_DN74117_c6_g1	-3.7	uncharacterized protein LOC104894399
TRINITY_DN73422_c0_g5	-6.3	tetraspanin-20
TRINITY_DN79260_c0_g1	-8.5	protein binding
TRINITY_DN68719_c0_g1	-6.1	pre-mRNA-processing factor 39-like isoform X2
TRINITY_DN79956_c5_g1	-6.4	RAB GTPaseC isoform 4
TRINITY_DN69684_c0_g1	-6.5	pleiotropic drug resistance protein TUR2-like
TRINITY_DN66142_c2_g2	-6.8	amino acid transport and metabolism
TRINITY_DN81737_c0_g1	-4.6	uncharacterized protein LOC104905833
TRINITY_DN64617_c0_g2	-8.5	protein JCGZ_02634
TRINITY_DN82515_c2_g1	-4.6	uncharacterized protein LOC104886284

TRINITY_DN73549_c2_g1	-5.4	uncharacterized protein LOC104884611
TRINITY_DN75233_c1_g3	-8.6	protein PHYLLO, chloroplastic
TRINITY_DN79851_c0_g1	-4.9	uncharacterized protein LOC102581500
TRINITY_DN73197_c2_g4	-8.9	FAR1-related protein
TRINITY_DN77363_c1_g1	-4.5	disease resistance protein RGA3
TRINITY_DN69585_c0_g5	-3.8	uncharacterized protein LOC104888756 isoform X2
TRINITY_DN78032_c0_g2	-4.5	uncharacterized protein LOC104900266
TRINITY_DN66557_c1_g1	-8.8	uncharacterized protein LOC104893306
TRINITY_DN76516_c4_g1	-5.6	stromal 70 kDa heat shock-related protein, chloroplastic-like
TRINITY_DN75258_c0_g1	-3.6	uncharacterized protein LOC104896579
TRINITY_DN77587_c3_g1	-4.5	conserved hypothetical protein
TRINITY_DN82164_c2_g1	-4.5	50S ribosomal protein L18, chloroplastic
TRINITY_DN80828_c4_g2	-5.8	integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN82386_c5_g1	-5.6	probable disease resistance protein At1g12280
TRINITY_DN71648_c0_g1	-3.6	thioredoxin-like 3-3-like
TRINITY_DN72051_c0_g2	-4.2	catalytic activity; 3-hydroxyisobutyryl-CoA hydrolase activity; metabolic process
TRINITY_DN71711_c4_g1	-4.0	uncharacterized protein LOC103629576 isoform X1
TRINITY_DN74374_c3_g2	-6.8	unnamed protein product [<i>Vitis vinifera</i>]
TRINITY_DN76439_c0_g3	-4.0	xyloglucan endotransglucosylase/hydrolase protein 33
TRINITY_DN82386_c5_g2	-6.7	Signal transduction mechanisms
TRINITY_DN72395_c0_g2	-8.7	protein POPTR_0001s38670g
TRINITY_DN64341_c0_g1	-3.8	protein BOBBER 1
TRINITY_DN75928_c2_g1	-3.8	protein M569_05560
TRINITY_DN68861_c1_g3	-4.3	protein EUGRSUZ_J02069
TRINITY_DN64189_c1_g1	-9.9	uncharacterized protein LOC104896455
TRINITY_DN67845_c0_g1	-7.6	uncharacterized protein LOC104907210
TRINITY_DN72243_c0_g2	-4.2	protein JCGZ_07190
TRINITY_DN64743_c2_g1	-6.7	transporter activity; transport; membrane
TRINITY_DN81865_c3_g1	-3.6	microtubule cytoskeleton organization; spindle pole; microtubule organizing center; microtubule nucleation; gamma-tubulin binding
TRINITY_DN81615_c7_g1	-3.9	protein VITISV_041904
TRINITY_DN68301_c2_g1	-3.7	uncharacterized protein LOC104907384
TRINITY_DN66246_c1_g2	-7.8	chloroplast RF1
TRINITY_DN81209_c0_g3	-7.9	retroelement pol polyprotein
TRINITY_DN81635_c0_g1	-4.3	phosphatidylinositol 4-kinase gamma
TRINITY_DN75498_c3_g2	-6.4	uncharacterized protein LOC100245099
TRINITY_DN71594_c2_g1	-6.6	uncharacterized protein LOC104885420
TRINITY_DN63279_c0_g1	-3.9	piezo-type mechanosensitive ion channel homolog isoform X3
TRINITY_DN75641_c1_g1	-6.1	disease resistance protein RGA2-like
TRINITY_DN65911_c1_g2	-6.6	transcription factor PosF21
TRINITY_DN74137_c0_g1	-4.8	uncharacterized protein LOC104888873

TRINITY_DN78223_c0_g6	-8.8	xyloglucan endotransglucosylase/hydrolase protein 23
TRINITY_DN79375_c1_g2	-4.2	auxin-induced protein X15-like
TRINITY_DN76032_c0_g2	-3.5	F-box protein SKIP23-like
TRINITY_DN66264_c3_g1	-6.3	nucleic acid binding; zinc ion binding
TRINITY_DN77177_c0_g2	-4.4	nucleic acid binding; mRNA processing
TRINITY_DN78380_c0_g1	-3.8	ATP binding; transferase activity, transferring phosphorus-containing groups
TRINITY_DN70503_c0_g1	-7.5	uncharacterized protein LOC104908276
TRINITY_DN72680_c0_g2	-8.2	replication, recombination and repair
TRINITY_DN81507_c1_g1	-3.1	transmembrane 9 superfamily member 3-like
TRINITY_DN78003_c0_g1	-3.2	transcription factor VIP1-like
TRINITY_DN81896_c1_g1	-3.2	unnamed protein product [<i>Coffea canephora</i>]
TRINITY_DN77975_c0_g4	-3.2	uncharacterized protein LOC104895697
TRINITY_DN66262_c0_g3	-3.2	posttranslational modification, protein turnover, chaperones
TRINITY_DN73838_c0_g2	-3.1	acid phosphatase-like
TRINITY_DN68735_c0_g3	-3.0	U-box domain-containing protein 35
TRINITY_DN67114_c1_g2	-3.4	LOB domain-containing protein 12-like
TRINITY_DN71566_c0_g2	-3.1	uncharacterized protein LOC101489594
TRINITY_DN75706_c0_g1	-3.2	metal-nicotianamine transporter YSL1-like
TRINITY_DN71251_c1_g2	-3.0	B3 domain-containing protein Os01g0723500-like
TRINITY_DN79179_c1_g3	-3.2	uncharacterized protein At1g04910
TRINITY_DN64946_c0_g1	-3.3	GRF zinc finger
TRINITY_DN75529_c0_g1	-3.2	replication, recombination and repair
TRINITY_DN76631_c0_g2	-3.3	uncharacterized protein LOC104891150 isoform X3
TRINITY_DN71402_c0_g1	-3.2	signal transduction mechanisms
TRINITY_DN70874_c0_g1	-3.4	carbohydrate transport and metabolism
TRINITY_DN81759_c3_g2	-3.0	scopoletin glucosyltransferase-like
TRINITY_DN82515_c1_g1	-3.2	putative polyprotein
TRINITY_DN79682_c2_g2	-3.2	pentatricopeptide repeat-containing protein At1g17630
TRINITY_DN70075_c0_g1	-3.3	uncharacterized protein LOC104901211
TRINITY_DN73266_c1_g1	-3.1	hypothetical protein [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
TRINITY_DN75363_c5_g2	-3.0	cytosolic sulfotransferase 5-like
TRINITY_DN74786_c0_g1	-3.0	uncharacterized protein LOC104884364
TRINITY_DN75902_c0_g2	-3.1	protein EUGRSUZ_L00405
TRINITY_DN77654_c0_g1	-3.2	uncharacterized protein LOC104883398
TRINITY_DN80689_c2_g1	-3.3	protein MTR_4g091430
TRINITY_DN75318_c0_g3	-3.1	uncharacterized protein LOC104895761

Table 4 Suppl. Green-stem vs. red stem up-regulated DEGs.

Gene ID	log2FC	Description
TRINITY_DN76790_c2_g1	1.9	GDSL esterase/lipase 5-like
TRINITY_DN81337_c1_g2	4.5	casein kinase I isoform delta-like isoform X4
TRINITY_DN68225_c3_g3	2.6	serine/threonine-protein phosphatase 7 long form homolog
TRINITY_DN66887_c0_g1	1.8	phospholipid-transporting ATPase 1
TRINITY_DN79921_c1_g3	3.7	protein PRUPE_ppa022115mg
TRINITY_DN68614_c0_g1	3.9	EC protein homolog 2-like
TRINITY_DN78051_c0_g3	3.7	phospholipid-transporting ATPase 1
TRINITY_DN71442_c2_g4	6.0	uncharacterized protein LOC104900511 isoform X1
TRINITY_DN82437_c6_g1	2.7	ribonuclease H protein At1g65750-like
TRINITY_DN77900_c4_g1	6.7	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process
TRINITY_DN69717_c0_g1	2.2	protein P21-like
TRINITY_DN74615_c3_g1	7.9	protein VITISV_012031
TRINITY_DN82141_c10_g1	2.0	fatty acid biosynthetic process; membrane; transferase activity, transferring acyl groups other than amino-acyl groups
TRINITY_DN68233_c0_g4	6.0	uncharacterized protein LOC104908415
TRINITY_DN70624_c1_g3	4.4	protein kinase activity; ATP binding; protein phosphorylation; recognition of pollen
TRINITY_DN65635_c1_g2	2.5	protein kinase activity; protein phosphorylation
TRINITY_DN67673_c1_g3	7.7	chlorophyll catabolic process; chlorophyllase activity
TRINITY_DN68967_c0_g1	5.3	telomere maintenance; DNA helicase activity; DNA repair
TRINITY_DN82408_c4_g8	3.2	ribonuclease H protein At1g65750-like
TRINITY_DN65678_c2_g1	3.3	polyadenylate-binding protein 7-like
TRINITY_DN80901_c1_g3	5.9	GAI-like protein 1
TRINITY_DN72756_c0_g1	2.2	ATP binding; ATPase activity
TRINITY_DN70495_c0_g2	5.1	uncharacterized protein LOC104907384
TRINITY_DN71155_c1_g2	2.9	polygalacturonase inhibitor 1-like
TRINITY_DN74566_c0_g1	2.6	catechol oxidase activity; metabolic process; oxidoreductase activity; oxidation-reduction process
TRINITY_DN77350_c0_g1	2.9	squalene monooxygenase activity; integral component of membrane; oxidoreductase activity; flavin adenine dinucleotide binding; oxidation-reduction process; FAD binding
TRINITY_DN67004_c0_g1	6.7	intracellular protein transport
TRINITY_DN73328_c1_g4	4.1	uncharacterized protein LOC105169149
TRINITY_DN77144_c2_g1	2.1	<i>O</i> -glucosyltransferase rumi homolog
TRINITY_DN79413_c4_g2	1.9	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process

TRINITY_DN81834_c2_g1	1.8	ankyrin-3-like
TRINITY_DN72210_c1_g3	3.8	serine-type carboxypeptidase activity; proteolysis
TRINITY_DN77057_c4_g1	5.1	transcription, DNA-templated; sequence-specific DNA binding
TRINITY_DN70194_c0_g1	4.8	uncharacterized protein LOC104584197
TRINITY_DN82066_c1_g1	2.3	protein kinase activity; ATP binding; Biological Process: protein phosphorylation; carbohydrate binding
TRINITY_DN63201_c0_g3	3.2	uncharacterized protein LOC104905544
TRINITY_DN66739_c1_g1	4.8	disease resistance protein RGA2-like
TRINITY_DN74385_c0_g2	1.8	hydrogen ion transmembrane transporter activity; ATP hydrolysis coupled proton transport; proton-transporting two-sector ATPase complex, proton-transporting domain
TRINITY_DN67648_c9_g1	3.0	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process
TRINITY_DN73748_c0_g1	2.5	amino acid transport and metabolism
TRINITY_DN66344_c0_g1	4.1	intracellular trafficking, secretion, and vesicular transport
TRINITY_DN66793_c1_g1	5.0	uncharacterized protein LOC104893474
TRINITY_DN82482_c3_g2	2.3	intracellular trafficking, secretion, and vesicular transport
TRINITY_DN68352_c3_g2	2.6	calcium ion binding; calcium-dependent phospholipid binding
TRINITY_DN75951_c1_g1	3.3	protein binding; ADP binding
TRINITY_DN70494_c0_g1	2.5	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN65078_c1_g1	2.4	ADP binding
TRINITY_DN79172_c0_g4	4.5	G-type lectin S-receptor-like serine/threonine-protein kinase At1g67520
TRINITY_DN74106_c2_g2	4.0	tetrahydroxychalcone glucosyltransferase
TRINITY_DN60860_c0_g1	6.8	signal transduction mechanisms
TRINITY_DN71697_c0_g1	1.7	myb-related protein Myb4-like
TRINITY_DN66812_c0_g1	2.5	electron carrier activity; protein disulfide oxidoreductase activity; cell redox homeostasis
TRINITY_DN73794_c1_g6	2.8	uncharacterized protein LOC102621413
TRINITY_DN62348_c0_g1	3.1	uncharacterized protein LOC104591601
TRINITY_DN71402_c0_g2	2.8	protein binding; ADP binding
TRINITY_DN81996_c2_g4	3.9	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process
TRINITY_DN66869_c3_g1	8.9	uncharacterized protein LOC104886511
TRINITY_DN81843_c2_g3	4.1	calcium ion binding
TRINITY_DN78043_c2_g1	2.2	secondary metabolites biosynthesis, transport and catabolism
TRINITY_DN78102_c3_g1	2.4	integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN64793_c0_g1	5.2	protein VITISV_000588
TRINITY_DN77379_c2_g1	2.3	cysteine-rich receptor-like protein kinase 10
TRINITY_DN81305_c1_g4	4.6	pentatricopeptide repeat-containing protein At2g35130
TRINITY_DN75104_c1_g1	3.6	uncharacterized protein LOC104904467
TRINITY_DN62770_c1_g1	7.5	uncharacterized protein LOC104893557

TRINITY_DN80969_c1_g3	6.9	DNA integration
TRINITY_DN65781_c1_g2	4.4	WRKY transcription factor 46
TRINITY_DN67477_c2_g3	6.9	uncharacterized protein LOC104891516
TRINITY_DN72741_c2_g2	2.5	uncharacterized protein LOC105160070
TRINITY_DN65900_c0_g1	2.7	oxidoreductase activity; oxidation-reduction process
TRINITY_DN76879_c0_g1	2.2	integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN67954_c3_g3	3.1	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN77835_c0_g1	6.3	hypothetical protein [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
TRINITY_DN79402_c3_g5	3.3	energy production and conversion
TRINITY_DN70574_c0_g1	4.4	RHO guanyl-nucleotide exchange factor activity
TRINITY_DN69501_c2_g2	1.9	molybdate ion transmembrane transporter activity; molybdate ion transport; integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN70733_c5_g2	3.3	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN73697_c0_g1	2.3	uncharacterized protein PB18E9.04c
TRINITY_DN82185_c2_g2	2.2	phospholipid-transporting ATPase 1
TRINITY_DN76727_c0_g2	2.1	energy production and conversion
TRINITY_DN64869_c0_g2	5.6	60S ribosomal protein L39
TRINITY_DN63556_c0_g1	4.5	endopeptidase inhibitor activity
TRINITY_DN80464_c5_g1	2.3	receptor-like protein 12
TRINITY_DN82411_c1_g1	3.2	disease resistance protein RGA3
TRINITY_DN77033_c1_g1	4.6	protein VITISV_020252
TRINITY_DN66120_c1_g1	4.1	posttranslational modification, protein turnover, chaperones
TRINITY_DN66135_c0_g1	2.6	ribonuclease H protein At1g65750-like
TRINITY_DN67867_c1_g3	2.1	metal ion transport; metal ion binding
TRINITY_DN81759_c3_g3	3.3	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN69748_c2_g2	5.5	metabolic process; oxidoreductase activity; oxidation-reduction process
TRINITY_DN73682_c3_g1	2.7	gag-pol polyprotein
TRINITY_DN47612_c0_g1	10.1	protein PRUPE_ppa016553mg
TRINITY_DN65405_c0_g1	2.5	FK506-binding protein 4-like isoform X2
TRINITY_DN74178_c0_g1	2.8	lanC-like protein GCR2
TRINITY_DN74204_c4_g3	3.1	F-box protein PP2-B12
TRINITY_DN72046_c0_g1	1.7	cation/H(+) antiporter 18-like
TRINITY_DN76842_c1_g2	2.3	protein MTR_7g017090
TRINITY_DN72522_c1_g1	5.2	enzyme inhibitor activity; cell wall; pectinesterase activity; cell wall modification
TRINITY_DN68990_c4_g2	2.0	sequence-specific DNA binding transcription factor activity; regulation of transcription, DNA-templated; sequence-specific DNA binding
TRINITY_DN78097_c0_g2	3.6	protein VITISV_018870
TRINITY_DN63984_c0_g1	6.2	V-type proton ATPase subunit a3
TRINITY_DN66664_c0_g1	2.7	uncharacterized protein isoform 4 [<i>Theobroma cacao</i>]
TRINITY_DN67843_c2_g4	1.9	methylthioribose kinase

TRINITY_DN76646_c1_g2	3.4	hypothetical protein [Beta vulgaris]
TRINITY_DN68386_c0_g1	3.9	F-box/RNI/FBD-like domains-containing protein, putative
TRINITY_DN81620_c3_g2	3.7	uncharacterized protein LOC104597156
TRINITY_DN78130_c4_g2	3.1	F-box/kelch-repeat protein At1g23390
TRINITY_DN75089_c1_g1	2.2	ammonium transmembrane transporter activity; ammonium transport; membrane
TRINITY_DN72363_c0_g2	2.5	uncharacterized protein DDB_G0271670
TRINITY_DN79902_c0_g1	3.6	uncharacterized protein LOC104896251
TRINITY_DN70199_c0_g1	2.1	phosphate transporter
TRINITY_DN67642_c0_g2	3.0	polygalacturonase inhibitor-like
TRINITY_DN60500_c0_g1	3.6	F-box/FBD/LRR-repeat protein At1g13570-like
TRINITY_DN79825_c1_g1	6.8	response to metal ion; glutathione gamma-glutamylcysteinyltransferase activity; metal ion binding; phytochelatin biosynthetic process
TRINITY_DN68494_c10_g1	2.6	posttranslational modification, protein turnover, chaperones
TRINITY_DN78601_c1_g3	6.8	uncharacterized protein LOC101232512
TRINITY_DN69456_c3_g3	6.2	replication, recombination and repair
TRINITY_DN70096_c2_g1	3.2	transferase activity, transferring acyl groups other than amino-acyl groups
TRINITY_DN68030_c2_g2	4.0	tobamovirus multiplication protein 3
TRINITY_DN68845_c2_g6	1.9	uncharacterized protein LOC104897758
TRINITY_DN81042_c1_g1	2.9	protein phosphatase 2
TRINITY_DN67735_c0_g3	6.8	protein JCGZ_12090
TRINITY_DN66013_c0_g1	2.9	protein CISIN_1g018026mg
TRINITY_DN66509_c0_g1	2.2	probable WRKY transcription factor 40
TRINITY_DN79128_c2_g3	3.3	uncharacterized protein LOC104883940
TRINITY_DN82187_c3_g3	4.4	serine/threonine protein phosphatase 2a regulatory subunit A, partial
TRINITY_DN68697_c1_g1	1.8	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN75569_c3_g10	9.3	nucleic acid binding
TRINITY_DN67166_c2_g1	5.6	inactive receptor-like protein kinase At1g65250
TRINITY_DN68083_c3_g1	2.6	F-box protein family, AtFBL4
TRINITY_DN80207_c0_g1	2.7	receptor-like protein 12
TRINITY_DN72685_c1_g2	3.0	disease resistance protein RGA4
TRINITY_DN70286_c1_g2	1.9	uncharacterized protein LOC103333523
TRINITY_DN67251_c5_g1	5.5	protein CISIN_1g0088402mg
TRINITY_DN67642_c0_g4	3.0	polygalacturonase inhibitor-like
TRINITY_DN77132_c1_g1	1.8	ATP binding; kinase activity
TRINITY_DN68271_c0_g1	8.0	cellular aromatic compound metabolic process; ferrous iron binding; oxidoreductase activity
TRINITY_DN68368_c2_g3	9.0	protein CISIN_1g014942mg
TRINITY_DN73211_c2_g1	3.8	uncharacterized protein LOC104894089
TRINITY_DN71734_c0_g1	2.6	protein FAR1-RELATED SEQUENCE 11-like
TRINITY_DN70495_c0_g3	2.7	uncharacterized protein LOC104888880
TRINITY_DN69804_c4_g2	2.4	heat shock protein 70
TRINITY_DN67483_c0_g1	3.5	metabolic process; transferase activity, transferring hexosyl groups

TRINITY_DN80894_c0_g1	2.4	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN74049_c0_g3	7.4	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN68615_c0_g2	2.4	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN69546_c2_g2	2.8	transferase activity, transferring acyl groups other than amino-acyl groups
TRINITY_DN66794_c4_g1	9.9	uncharacterized protein LOC104891166
TRINITY_DN79098_c0_g4	3.9	uncharacterized protein LOC104892012
TRINITY_DN67756_c2_g1	3.6	uncharacterized protein LOC104895893
TRINITY_DN64327_c0_g1	3.8	zinc ion binding
TRINITY_DN68329_c0_g2	2.5	uncharacterized protein LOC104899180
TRINITY_DN66364_c1_g3	2.6	protein phosphatase 2C 29-like
TRINITY_DN71387_c3_g1	3.7	uncharacterized protein LOC104899180
TRINITY_DN76562_c2_g1	2.4	profilin-like protein
TRINITY_DN79802_c1_g1	1.8	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN64700_c0_g1	2.8	endopeptidase inhibitor activity
TRINITY_DN72998_c0_g5	2.9	L3 ribosomal protein
TRINITY_DN73223_c0_g1	3.6	protein phosphatase 2C 37
TRINITY_DN65700_c3_g2	5.0	nucleic acid binding; zinc ion binding
TRINITY_DN65042_c2_g1	2.1	cell morphogenesis
TRINITY_DN74809_c1_g1	2.5	DNA binding; protein dimerization activity
TRINITY_DN65476_c0_g2	3.2	uncharacterized protein LOC103428728
TRINITY_DN67983_c4_g3	6.8	protein VITISV_036909
TRINITY_DN70360_c3_g1	2.7	oxidoreductase activity; oxidation-reduction process
TRINITY_DN71372_c0_g1	2.8	70 kDa peptidyl-prolyl isomerase-like isoform X2
TRINITY_DN79503_c1_g1	2.4	molybdate ion transmembrane transporter activity; molybdate ion transport; integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN71086_c0_g1	2.7	protein binding; ADP binding
TRINITY_DN66850_c0_g4	4.2	long-chain-alcohol O-fatty-acyltransferase-like
TRINITY_DN74783_c0_g3	3.3	UDP-N-acetylglucosamine transferase subunit ALG14 homolog
TRINITY_DN80663_c5_g1	4.8	uncharacterized protein LOC103449768
TRINITY_DN78238_c1_g1	2.2	catalytic activity; 3-beta-hydroxy-delta5-steroid dehydrogenase activity; steroid biosynthetic process; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; coenzyme binding; oxidation-reduction process
TRINITY_DN80888_c2_g1	3.0	zinc finger BED domain-containing protein RICESLEEPER 2-like
TRINITY_DN80718_c5_g2	2.1	DNA binding; protein dimerization activity
TRINITY_DN73521_c4_g1	3.5	basic 7S globulin-like
TRINITY_DN68588_c0_g1	2.2	signal transduction mechanisms
TRINITY_DN72977_c0_g1	2.5	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN79912_c1_g2	1.9	remorin-like
TRINITY_DN82204_c3_g1	7.9	eukaryotic translation initiation factor 3 subunit B-like

TRINITY_DN69501_c0_g1	2.6	molybdate ion transmembrane transporter activity; molybdate ion transport; integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN78679_c4_g1	4.4	ankyrin repeat-containing protein At5g02620-like
TRINITY_DN67964_c2_g1	2.9	NAC domain-containing protein 21/22-like isoform X3
TRINITY_DN70591_c2_g2	6.3	palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic-like
TRINITY_DN73977_c0_g2	2.6	1-aminocyclopropane-1-carboxylate synthase
TRINITY_DN68785_c0_g1	6.8	nucleic acid binding; zinc ion binding
TRINITY_DN78681_c0_g1	1.9	cytochrome P450 94B3
TRINITY_DN79503_c1_g2	2.3	integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN66013_c0_g3	2.7	cucumber peeling cupredoxin-like
TRINITY_DN81916_c1_g2	2.5	peroxidase activity; response to oxidative stress; heme binding; oxidation-reduction process
TRINITY_DN72303_c0_g1	3.1	uncharacterized protein At1g08160-like
TRINITY_DN82496_c8_g1	2.4	disease resistance protein RGA1
TRINITY_DN69839_c1_g4	2.1	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN82037_c2_g1	2.4	uncharacterized protein LOC104902677
TRINITY_DN66320_c2_g1	3.1	acyl-activating enzyme 17, peroxisomal
TRINITY_DN71031_c0_g2	2.3	magnesium ion binding; metabolic process; terpene synthase activity; lyase activity
TRINITY_DN70904_c0_g1	2.6	indole-3-acetic acid-amido synthetase GH3.1
TRINITY_DN63733_c0_g1	4.3	mechanosensitive ion channel protein 4-like isoform X2
TRINITY_DN72893_c1_g1	7.2	iron ion binding; lipid biosynthetic process; oxidoreductase activity; oxidation-reduction process
TRINITY_DN70020_c2_g2	1.7	3-ketoacyl-CoA thiolase 2, peroxisomal
TRINITY_DN76518_c4_g4	2.7	energy production and conversion
TRINITY_DN66452_c2_g1	2.0	uncharacterized protein LOC104908415
TRINITY_DN78547_c0_g1	3.8	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN73460_c0_g1	2.0	LRR receptor-like serine/threonine-protein kinase At1g53430
TRINITY_DN73741_c2_g2	4.9	carbohydrate transport and metabolism
TRINITY_DN75298_c0_g1	2.7	secondary metabolites biosynthesis, transport and catabolism
TRINITY_DN74472_c0_g1	2.1	amino acid transport and metabolism
TRINITY_DN72185_c0_g3	3.4	DNA integration
TRINITY_DN63443_c0_g1	5.7	protein NDR1-like
TRINITY_DN65522_c0_g2	2.8	receptor-like protein 12
TRINITY_DN71446_c2_g3	2.1	pathogenesis-related protein 1
TRINITY_DN75908_c0_g1	2.2	copper ion binding; oxidoreductase activity; oxidation-reduction process
TRINITY_DN67920_c0_g2	1.8	protein kinase activity ; ATP binding;protein phosphorylation; polysaccharide binding
TRINITY_DN67663_c0_g1	2.9	DNA binding; transposase activity; transposition, DNA-mediated; hydrolase activity, acting on ester bonds
TRINITY_DN74450_c0_g1	2.2	regulator of chromosome condensation family protein

TRINITY_DN79443_c3_g2	2.2	translation, ribosomal structure and biogenesis
TRINITY_DN69318_c2_g2	3.7	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN70910_c1_g2	4.8	TBP-class protein binding
TRINITY_DN70746_c1_g1	3.3	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN70229_c0_g1	2.3	protein MIMGU_mgv1a022871mg
TRINITY_DN82451_c0_g1	2.3	M-phase inducer phosphatase
TRINITY_DN70672_c0_g1	2.1	defense response to bacterium; defense response to fungus
TRINITY_DN72984_c1_g4	2.3	dirigent protein 22-like
TRINITY_DN73653_c0_g1	1.8	intracellular; zinc ion binding
TRINITY_DN71738_c2_g1	2.7	integral component of membrane; transmembrane transporter activity; transmembrane transport
TRINITY_DN71837_c0_g2	2.0	oxidoreductase activity; flavin adenine dinucleotide binding; oxidation-reduction process
TRINITY_DN80444_c2_g1	2.1	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN74726_c1_g7	4.4	uncharacterized protein LOC104885412
TRINITY_DN61883_c0_g1	2.9	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN71422_c3_g2	6.0	ankyrin repeat-containing protein At3g12360-like
TRINITY_DN59326_c0_g1	8.6	uncharacterized protein LOC104897672
TRINITY_DN81937_c3_g3	4.0	nucleic acid binding; zinc ion binding
TRINITY_DN78667_c2_g6	5.0	UPF0481 protein At3g47200-like
TRINITY_DN67642_c0_g1	1.9	polygalacturonase inhibitor-like
TRINITY_DN76861_c2_g3	2.4	enzyme inhibitor activity; cell wall; pectinesterase activity; cell wall modification
TRINITY_DN71402_c1_g1	2.6	ADP binding
TRINITY_DN67287_c0_g4	4.6	eukaryotic translation initiation factor 4E-1-like
TRINITY_DN78838_c0_g3	1.9	coenzyme transport and metabolism
TRINITY_DN68773_c4_g1	4.8	uncharacterized protein LOC105120398 isoform X2
TRINITY_DN78244_c1_g2	4.9	protein dimerization activity
TRINITY_DN76264_c0_g1	6.9	protein PAIR1
TRINITY_DN71841_c1_g1	2.1	phosphatidylinositol kinase
TRINITY_DN72528_c2_g1	3.4	disease resistance protein RGA1
TRINITY_DN62081_c0_g1	8.0	uncharacterized protein LOC104883796
TRINITY_DN73458_c0_g2	2.7	uncharacterized protein LOC104904039
TRINITY_DN70122_c6_g1	5.4	nucleic acid binding
TRINITY_DN72445_c1_g1	2.5	MADS-box transcription factor ANR1
TRINITY_DN65396_c2_g1	3.1	uncharacterized protein LOC104900698
TRINITY_DN68266_c1_g3	4.1	replication, recombination and repair
TRINITY_DN63687_c0_g1	4.0	basic endochitinase C
TRINITY_DN81644_c2_g4	4.3	uncharacterized protein LOC102623579
TRINITY_DN66789_c1_g1	6.5	unnamed protein product [Vitis vinifera]
TRINITY_DN80089_c1_g2	3.1	energy production and conversion
TRINITY_DN74702_c1_g5	3.5	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN69405_c0_g3	4.4	secondary metabolites biosynthesis, transport and catabolism

TRINITY_DN67065_c0_g2	7.1	replication, recombination and repair
TRINITY_DN76791_c1_g1	2.8	protein kinase activity; protein phosphorylation
TRINITY_DN68539_c0_g2	3.8	--
TRINITY_DN82388_c2_g3	7.5	low quality protein: MND1-interacting protein 1-like
TRINITY_DN77401_c4_g3	2.0	transferase activity, transferring acyl groups other than amino-acyl groups
TRINITY_DN79503_c0_g1	2.5	polyol transporter 5 isoform X2
TRINITY_DN68385_c0_g1	3.5	uncharacterized protein LOC104899180
TRINITY_DN82343_c2_g1	9.5	zinc finger BED domain-containing protein RICESLEEPER 1-like
TRINITY_DN78433_c0_g1	2.7	uncharacterized protein LOC105046754 isoform X2
TRINITY_DN68116_c0_g1	3.1	transport; integral component of membrane; transmembrane transport
TRINITY_DN77356_c2_g1	4.7	vesicle transport v-SNARE 13-like
TRINITY_DN81414_c0_g3	2.9	intracellular trafficking, secretion, and vesicular transport
TRINITY_DN68708_c2_g1	3.7	amino acid transport and metabolism
TRINITY_DN76712_c0_g1	3.2	posttranslational modification, protein turnover, chaperones
TRINITY_DN70788_c1_g2	2.0	protein kinase activity; protein phosphorylation
TRINITY_DN67602_c1_g3	5.2	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN72191_c1_g2	7.7	extracellular region; lipid transport; lipid binding; lipoprotein metabolic process
TRINITY_DN77594_c0_g3	3.4	electron carrier activity
TRINITY_DN66238_c0_g2	2.2	GTPase-activating protein gyp7
TRINITY_DN80835_c1_g3	7.5	auxilin-related protein 2-like
TRINITY_DN70614_c1_g1	2.1	umecyanin
TRINITY_DN64964_c4_g2	2.7	uncharacterized protein LOC104887816
TRINITY_DN80910_c2_g1	1.7	3-deoxy-7-phosphoheptulonate synthase activity; aromatic amino acid family biosynthetic process
TRINITY_DN74178_c0_g2	3.8	defense mechanisms
TRINITY_DN80601_c1_g1	3.5	amino acid transport and metabolism
TRINITY_DN78005_c0_g1	3.1	secondary metabolites biosynthesis, transport and catabolism
TRINITY_DN68611_c3_g1	3.6	ASR5 protein
TRINITY_DN72167_c2_g2	3.5	nucleic acid binding; transcription, DNA-templated; zinc ion binding
TRINITY_DN72950_c5_g3	3.8	coenzyme transport and metabolism
TRINITY_DN64549_c0_g2	3.1	ripening-related protein 1
TRINITY_DN71375_c0_g1	3.3	F-box protein At4g22030
TRINITY_DN80765_c1_g1	2.3	signal transduction mechanisms
TRINITY_DN78199_c1_g1	2.8	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN77401_c2_g1	3.7	transferase activity, transferring acyl groups other than amino-acyl groups
TRINITY_DN77595_c0_g1	2.3	phosphatidate cytidyltransferase activity; cardiolipin biosynthetic process
TRINITY_DN69368_c0_g1	2.7	integral component of membrane; transmembrane transport
TRINITY_DN68506_c0_g2	3.6	putative quinone-oxidoreductase homolog, chloroplastic
TRINITY_DN81014_c1_g1	1.8	retinol dehydrogenase
TRINITY_DN76096_c1_g3	1.9	posttranslational modification, protein turnover, chaperones
TRINITY_DN73890_c1_g1	2.8	lipid transport and metabolism
TRINITY_DN73215_c1_g1	1.8	cell number regulator 1

TRINITY_DN71348_c0_g4	7.9	uncharacterized protein LOC104884358
TRINITY_DN69544_c1_g1	9.6	biological process: DNA integration (GO:0015074);;
TRINITY_DN78732_c0_g1	4.8	gag-pol polyprotein
TRINITY_DN66865_c2_g3	2.5	7-deoxyloganetin glucosyltransferase-like
TRINITY_DN77915_c1_g1	3.2	integral component of membrane; transmembrane transport
TRINITY_DN80738_c1_g3	2.2	putative F-box protein PP2-B12
TRINITY_DN70927_c0_g5	2.0	hypothetical protein [Beta vulgaris subsp. vulgaris]
TRINITY_DN72937_c1_g1	4.2	disease resistance protein RGA1
TRINITY_DN80941_c2_g6	3.2	defense mechanisms
TRINITY_DN65345_c1_g1	3.3	cytochrome P450 CYP82D47-like
TRINITY_DN65468_c2_g1	5.6	uncharacterized protein LOC104893808
TRINITY_DN70590_c2_g4	7.0	AP2 4, putative
TRINITY_DN65553_c0_g1	2.8	uncharacterized protein LOC104890085
TRINITY_DN81615_c6_g1	4.4	protein JCGZ_19660
TRINITY_DN65455_c0_g1	2.4	F-box/kelch-repeat protein At3g06240-like
TRINITY_DN72460_c0_g1	2.5	serine/threonine-protein kinase BRI1-like 2
TRINITY_DN76043_c0_g1	2.2	benzyl alcohol O-benzoyltransferase-like
TRINITY_DN76952_c0_g2	7.7	uncharacterized protein LOC104908415
TRINITY_DN74572_c3_g7	3.5	protein F383_29180
TRINITY_DN67277_c0_g1	3.5	crossover junction endodeoxyribonuclease
TRINITY_DN64299_c0_g2	2.6	protein EXORDIUM-like 2
TRINITY_DN79129_c0_g1	3.3	nucleic acid binding; zinc ion binding; DNA integration
TRINITY_DN77595_c0_g2	2.7	phosphatidate cytidyltransferase, mitochondrial isoform X3
TRINITY_DN70786_c0_g1	3.3	polygalacturonase inhibitor 1-like
TRINITY_DN64216_c0_g1	2.7	polygalacturonase inhibitor 2-like
TRINITY_DN65333_c0_g1	4.5	Replication, recombination and repair
TRINITY_DN80044_c2_g1	2.2	uncharacterized protein LOC103710465 isoform X1
TRINITY_DN71372_c0_g2	2.8	uncharacterized protein LOC104906294
TRINITY_DN80910_c1_g1	3.2	polypeptide with reverse transcriptase and RNaseH domains
TRINITY_DN76732_c0_g3	5.2	uncharacterized protein LOC104900511 isoform X1
TRINITY_DN80914_c0_g1	1.9	uncharacterized protein LOC104901900
TRINITY_DN67266_c0_g2	2.0	uncharacterized protein LOC104891532
TRINITY_DN72233_c2_g1	7.7	NADH--cytochrome b5 reductase 1-like
TRINITY_DN71168_c0_g1	2.4	UDP-glycosyltransferase 89A2-like
TRINITY_DN76010_c2_g2	2.6	serine/threonine-protein kinase UCNL
TRINITY_DN71085_c0_g1	2.3	glucosyltransferase
TRINITY_DN67609_c0_g3	1.8	inorganic ion transport and metabolism
TRINITY_DN67858_c2_g1	5.7	translation, ribosomal structure and biogenesis
TRINITY_DN69302_c2_g1	2.0	secondary metabolites biosynthesis, transport and catabolism
TRINITY_DN63783_c0_g1	4.9	uncharacterized protein LOC104888389
TRINITY_DN70216_c0_g1	8.5	protein glysoja_043802
TRINITY_DN81496_c1_g3	9.3	uncharacterized protein LOC104893474

TRINITY_DN75962_c4_g2	3.6	signal transduction mechanisms
TRINITY_DN68523_c1_g3	2.9	RNA processing and modification
TRINITY_DN63468_c0_g4	8.3	general function prediction only
TRINITY_DN63426_c0_g1	3.1	signal transduction mechanisms
TRINITY_DN77394_c0_g3	2.6	receptor-like protein kinase HSL1
TRINITY_DN75635_c0_g2	4.3	uncharacterized protein LOC104803157
TRINITY_DN77226_c0_g3	2.9	uncharacterized protein LOC104904165
TRINITY_DN80794_c3_g1	2.4	posttranslational modification, protein turnover, chaperones
TRINITY_DN70173_c1_g4	7.4	uncharacterized protein LOC104892720
TRINITY_DN64301_c0_g1	4.9	hypothetical protein [Beta vulgaris subsp. vulgaris]
TRINITY_DN75151_c0_g3	2.3	putative membrane protein [Glycine soja]
TRINITY_DN66018_c2_g3	2.4	translation, ribosomal structure and biogenesis
TRINITY_DN72403_c4_g3	3.0	GDSL esterase/lipase At5g45670
TRINITY_DN76979_c1_g2	4.0	leucine-rich repeat receptor-like protein kinase At5g49770
TRINITY_DN63711_c0_g1	2.9	uncharacterized protein LOC104896545
TRINITY_DN70636_c0_g2	2.5	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process
TRINITY_DN72023_c2_g3	3.0	thaumatin-like protein 1b
TRINITY_DN67839_c0_g2	4.6	protein PRUPE_ppa006928mg
TRINITY_DN76669_c0_g2	4.3	hypothetical protein [Beta vulgaris subsp. vulgaris]
TRINITY_DN77278_c0_g1	2.5	protein ECERIFERUM 3-like
TRINITY_DN71667_c2_g2	1.8	inorganic ion transport and metabolism
TRINITY_DN80904_c3_g1	2.0	lipid transport and metabolism
TRINITY_DN65344_c0_g1	3.2	signal transduction mechanisms
TRINITY_DN77603_c1_g1	2.3	protein JCGZ_10207
TRINITY_DN66865_c2_g7	4.2	7-deoxyloganetin glucosyltransferase-like
TRINITY_DN79843_c1_g6	2.8	low quality protein: UDP-sugar-dependent glycosyltransferase 52-like
TRINITY_DN73259_c0_g1	3.0	protein kinase activity; protein binding; ATP binding; protein phosphorylation
TRINITY_DN60721_c0_g1	3.2	uncharacterized protein LOC104613516
TRINITY_DN73062_c3_g3	3.5	protein VITISV_035665
TRINITY_DN71935_c1_g2	2.7	general function prediction only
TRINITY_DN72453_c2_g2	4.5	dynamamin-related protein 1E
TRINITY_DN64034_c0_g1	2.7	protein kinase activity; ATP binding; protein phosphorylation
TRINITY_DN63110_c0_g1	5.4	uncharacterized protein LOC104902499
TRINITY_DN67585_c1_g2	3.2	protein AALP_AA2G236900
TRINITY_DN71728_c1_g7	2.7	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding; oxidation-reduction process
TRINITY_DN72493_c2_g3	3.9	transcription
TRINITY_DN74092_c1_g1	1.7	dirigent protein 23-like
TRINITY_DN65933_c0_g3	2.0	uncharacterized protein LOC104649587
TRINITY_DN75575_c2_g2	2.8	lipid transport and metabolism
TRINITY_DN68588_c0_g2	1.9	signal transduction mechanisms

TRINITY_DN78966_c2_g2	4.4	intracellular trafficking, secretion, and vesicular transport
TRINITY_DN82415_c6_g1	2.0	reticuline oxidase-like protein
TRINITY_DN62758_c0_g1	2.7	cystathionine beta-synthase family protein
TRINITY_DN61977_c0_g1	3.2	protein POPTR_0001s38530g
TRINITY_DN80015_c2_g2	3.0	ABC transporter G family member 11-like
TRINITY_DN69033_c0_g1	2.5	ubiquitin-protein transferase activity; protein ubiquitination
TRINITY_DN65858_c0_g2	9.1	nephrocystin-3
TRINITY_DN77184_c0_g1	2.6	glucosyltransferase
TRINITY_DN68886_c0_g3	3.1	chitinase activity; chitin catabolic process; chitin binding; cell wall macromolecule catabolic process
TRINITY_DN72153_c0_g1	2.7	receptor like protein 33
TRINITY_DN69598_c0_g3	1.9	protein VITISV_002984
TRINITY_DN73242_c2_g3	3.7	uncharacterized protein LOC104102190
TRINITY_DN71763_c0_g3	5.1	uncharacterized protein LOC100795315 isoform X1
TRINITY_DN72328_c3_g5	4.1	uncharacterized protein LOC101219957
TRINITY_DN72210_c1_g2	4.0	serine carboxypeptidase-like 10 isoform X2
TRINITY_DN63761_c1_g1	3.0	UMP-CMP kinase 3-like isoform X2
TRINITY_DN66163_c2_g1	2.1	cysteine-rich receptor-like protein kinase 10
TRINITY_DN74307_c3_g1	2.7	protein trichome birefringence-like 25
TRINITY_DN82388_c2_g8	2.6	protein M569_06424
TRINITY_DN78009_c4_g1	4.6	protein VITISV_044445
TRINITY_DN72820_c1_g1	2.6	peroxidase activity; response to oxidative stress; heme binding; oxidation-reduction process
TRINITY_DN76109_c0_g3	4.9	uncharacterized protein LOC104890491 isoform X2
TRINITY_DN75440_c0_g2	2.3	protein FAR-RED ELONGATED HYPOCOTYL 3-like
TRINITY_DN80879_c2_g3	5.6	receptor-like protein 12
TRINITY_DN73771_c1_g5	3.8	polypeptide with reverse transcriptase and RNaseH domains
TRINITY_DN74805_c0_g1	10.9	putative polyprotein [Solanum lycopersicum]
TRINITY_DN67995_c2_g1	3.9	iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; heme binding ; oxidation-reduction process
TRINITY_DN67483_c0_g2	4.0	metabolic process; transferase activity, transferring hexosyl groups
TRINITY_DN64299_c0_g1	1.8	protein EXORDIUM-like 2
TRINITY_DN46332_c0_g1	6.2	serine-type carboxypeptidase activity; proteolysis
TRINITY_DN67876_c3_g1	2.2	pyruvate dehydrogenase E1 component subunit beta-like isoform X2
TRINITY_DN72997_c1_g1	6.0	receptor-like protein 12
TRINITY_DN74352_c4_g2	2.5	protein VITISV_009833
TRINITY_DN82363_c0_g1	2.0	low quality protein: probable LRR receptor-like serine/threonine-protein kinase At1g53430
TRINITY_DN75739_c1_g1	4.4	unnamed protein product [Coffea canephora]
TRINITY_DN62363_c0_g1	3.7	conserved hypothetical protein [Ricinus communis]
TRINITY_DN61664_c0_g1	4.5	uncharacterized protein LOC104905603
TRINITY_DN64215_c0_g1	3.0	uncharacterized protein LOC104884184

TRINITY_DN69108_c2_g2	2.6	general function prediction only
TRINITY_DN70286_c1_g3	1.9	gag-pol polyprotein
TRINITY_DN82214_c1_g1	2.0	WRKY transcription factor 22
TRINITY_DN67229_c2_g1	7.2	catalytic activity; 3-beta-hydroxy-delta5-steroid dehydrogenase activity; steroid biosynthetic process; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; coenzyme binding; oxidation-reduction process
TRINITY_DN74752_c1_g1	1.8	carbohydrate transport and metabolism
TRINITY_DN68404_c4_g1	3.4	indole-3-acetic acid-amido synthetase GH3.1
TRINITY_DN70456_c2_g1	5.0	uncharacterized protein TCM_044860
TRINITY_DN71155_c0_g1	3.8	polygalacturonase inhibitor 1-like
TRINITY_DN74615_c3_g2	4.8	uncharacterized protein LOC101513325
TRINITY_DN68679_c0_g2	4.6	<i>O</i> -acyltransferase WSD1
TRINITY_DN81508_c2_g3	2.4	uncharacterized protein LOC104906101
TRINITY_DN70078_c0_g1	10.4	adenylosuccinate lyase-like
TRINITY_DN70497_c2_g2	3.1	linoleate 9S-lipoxygenase 5
TRINITY_DN76059_c1_g1	1.7	L-ascorbate peroxidase 2, cytosolic-like
TRINITY_DN64555_c0_g1	5.2	uncharacterized protein LOC104898724
TRINITY_DN71672_c1_g2	2.7	cysteine-rich receptor-like protein kinase 10
TRINITY_DN67483_c0_g4	4.0	7-deoxyloganetin glucosyltransferase-like
TRINITY_DN79345_c2_g1	2.5	uncharacterized protein LOC104907750
TRINITY_DN73351_c0_g1	1.7	REF/SRPP-like protein At3g05500
TRINITY_DN66462_c0_g1	2.9	basic 7S globulin 2-like
TRINITY_DN70559_c1_g3	1.8	DNA-directed RNA polymerase I subunit RPA12-like
TRINITY_DN72859_c0_g1	3.2	glucosyltransferase
TRINITY_DN65965_c0_g1	2.1	uncharacterized protein LOC104889847
TRINITY_DN81061_c2_g2	1.7	ribonuclease II, chloroplastic/mitochondrial
TRINITY_DN76607_c1_g1	2.0	ATP-dependent DNA helicase DDM1
TRINITY_DN68475_c0_g4	3.8	protein tesmin/TSO1-like CXC 5
TRINITY_DN68921_c1_g5	7.2	hydrolase activity, acting on ester bonds
TRINITY_DN81473_c4_g6	5.5	disease resistance protein RGA2-like
TRINITY_DN81620_c4_g2	3.2	cysteine-rich receptor-like protein kinase 15
TRINITY_DN80115_c2_g2	3.5	aspartic-type endopeptidase activity; proteolysis
TRINITY_DN80061_c1_g2	4.5	calcium-dependent protein kinase 26-like
TRINITY_DN81536_c0_g1	1.7	WAX2 C-terminal domain
TRINITY_DN76558_c1_g4	1.6	long-chain-alcohol <i>O</i> -fatty-acyltransferase 5
TRINITY_DN70419_c0_g2	1.6	protein EXORDIUM-like 2
TRINITY_DN80216_c0_g2	1.7	nucleotide transport and metabolism
TRINITY_DN66394_c2_g3	1.6	protein VITISV_041548
TRINITY_DN67750_c0_g1	1.5	uncharacterized protein LOC104906207
TRINITY_DN79449_c0_g3	1.7	LRR receptor-like serine/threonine-protein kinase At1g53430
TRINITY_DN79205_c3_g1	1.6	uncharacterized protein LOC104904575
TRINITY_DN71427_c1_g3	1.7	1-aminocyclopropane-1-carboxylate oxidase 5

TRINITY_DN71869_c1_g3	1.7	lipid binding protein
TRINITY_DN72552_c0_g1	1.5	protein phosphatase 2C 2
TRINITY_DN80182_c3_g1	1.6	Glucan endo-1 3-beta-d-glucosidase
TRINITY_DN68135_c5_g1	1.7	elicitor-responsive protein 1
TRINITY_DN79825_c1_g2	1.7	polygalacturonase inhibitor
TRINITY_DN78734_c0_g1	1.7	phosphatidylinositol/phosphatidylcholine transfer protein SFH12-like
TRINITY_DN78913_c3_g1	1.6	miraculin-like
TRINITY_DN80182_c3_g5	1.7	glucan endo-1,3-beta-glucosidase-like
TRINITY_DN80493_c1_g1	1.5	LRR receptor-like serine/threonine-protein kinase At1g74360
TRINITY_DN74008_c1_g1	1.7	uncharacterized protein LOC104898355
TRINITY_DN66516_c4_g4	1.6	MLO-like protein 1
TRINITY_DN77506_c3_g1	1.7	acidic mammalian chitinase-like
TRINITY_DN68191_c0_g1	1.5	protein EXORDIUM-like
TRINITY_DN80182_c3_g4	1.6	glucan endo-1,3-beta-glucosidase-like
TRINITY_DN66931_c5_g2	1.5	protein MIMGU_mgv1a022871mg
TRINITY_DN79033_c2_g1	1.6	thioredoxin H-type 1
TRINITY_DN81149_c1_g1	1.7	receptor-like protein kinase HSL1
TRINITY_DN72829_c1_g1	1.5	peroxisomal fatty acid beta-oxidation multifunctional protein AIM1-like
TRINITY_DN80947_c0_g1	1.6	autophagy-related protein 11 isoform X1
TRINITY_DN82406_c2_g1	1.6	uncharacterized protein LOC104890338
TRINITY_DN75424_c0_g1	1.7	U-box domain-containing protein 20-like
TRINITY_DN73668_c1_g1	1.7	ankyrin repeat-containing protein At5g02620-like
TRINITY_DN74040_c0_g2	1.7	phospholipase A1-IIdelta-like
TRINITY_DN72890_c0_g1	1.7	protein Csa_3G820480
TRINITY_DN80047_c1_g1	1.5	GABA transporter 2 isoform X2
TRINITY_DN72051_c0_g3	1.7	short-chain type dehydrogenase/reductase

Table 5 Suppl. Analysis of transcriptome sequencing expression multiples and RT-qPCR validation expression multiples.

Family/subfamily	Gene ID	Transcriptome sequencing expression multiples	RT-qPCR validation expression multiples
NAC	DN67964_c2_g1	7.4	7.3
NAC	DN72984_c1_g4	5.0	1.4
NAC	DN74092_c1_g1	3.3	2.9
MYB	DN64299_c0_g1	3.5	5.6
MYB	DN71697_c0_g1	3.3	4.8
WRKY	DN68990_c4_g2	4.0	2.5
WRKY	DN82214_c1_g1	4.1	3.6
bZIP	DN73071_c0_g1	-0.1	-0.8

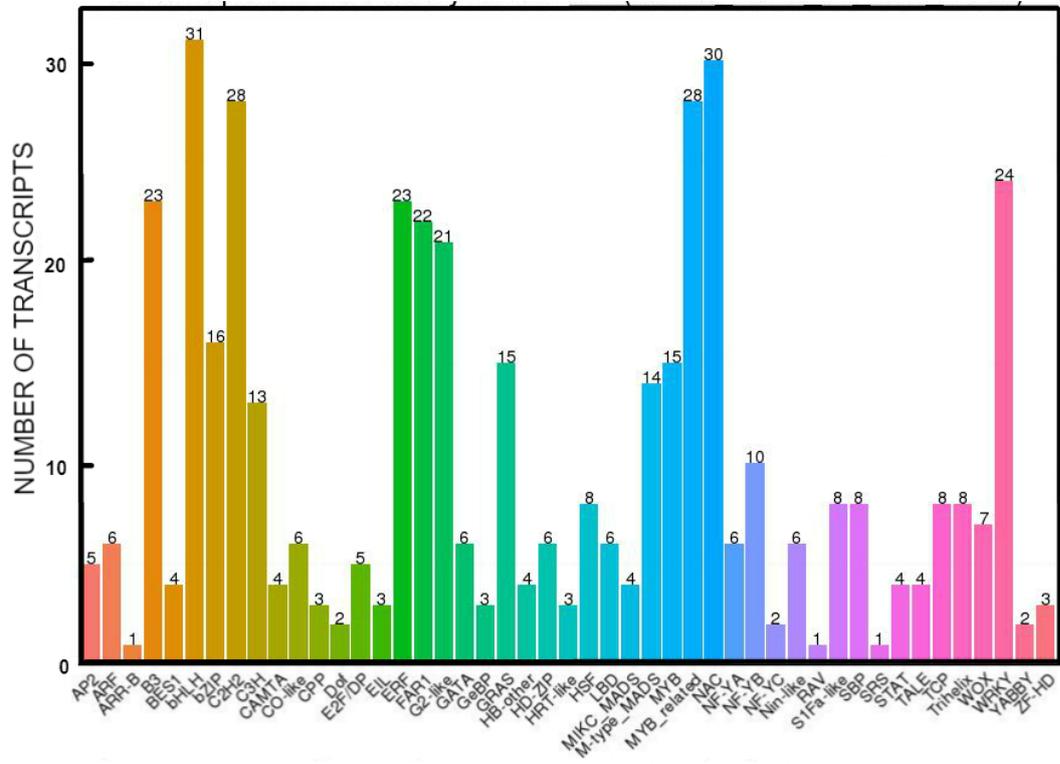


Fig. 1 Suppl. Number of DEGs of green-stem vs. red-stem purslane in transcription factors (TF) families.

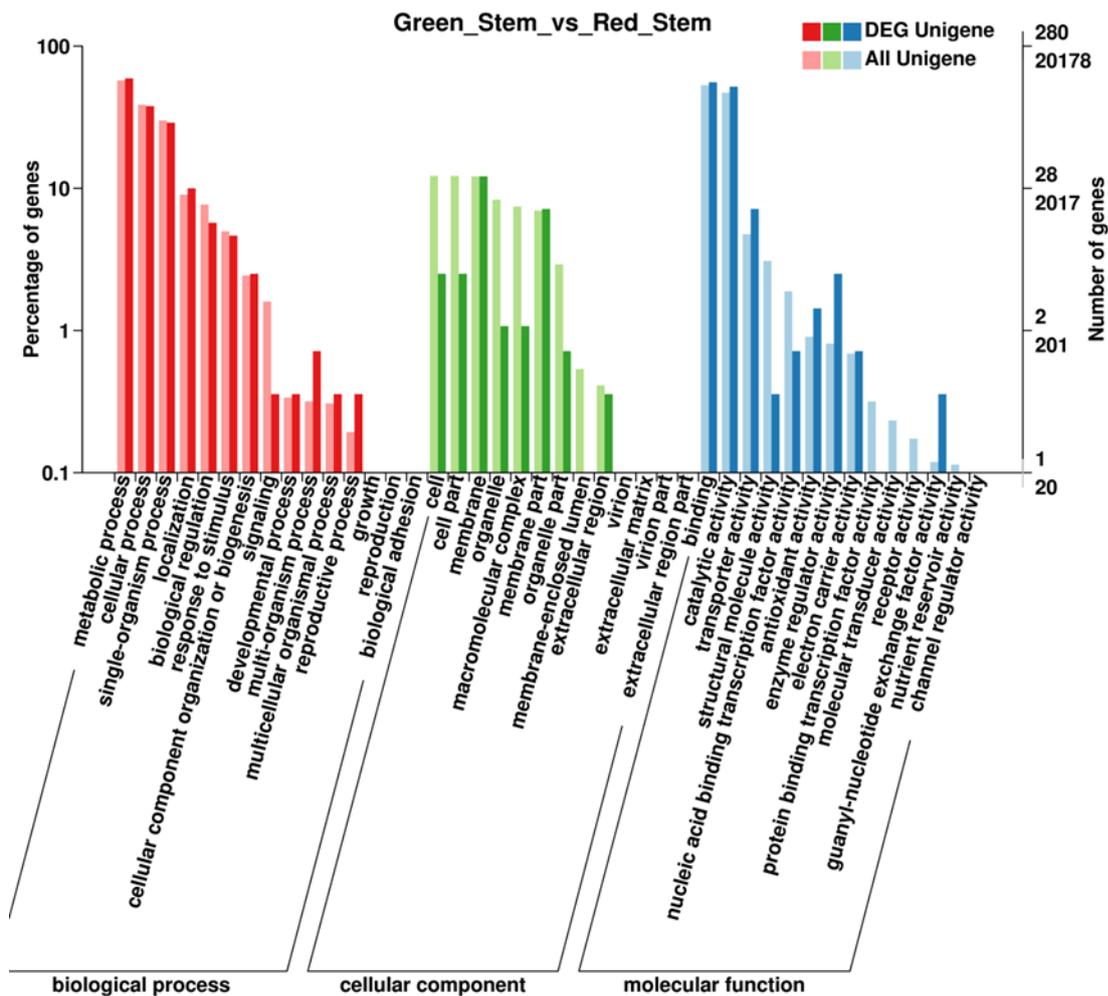


Fig. 2 Suppl. Gene ontology terms and numbers of the predicted target genes for differentially expressed miRNAs at the single nuclear pollen and bi-cellular pollen stage. The *GO* term and number of target genes were summarized under three main *GO* categories: biological process, cellular component, and molecular function. The left y-axis indicates the percentage of a specific category of genes corresponding to the *GO* term. The right y-axis indicates the number of target genes corresponding to the *GO* term.

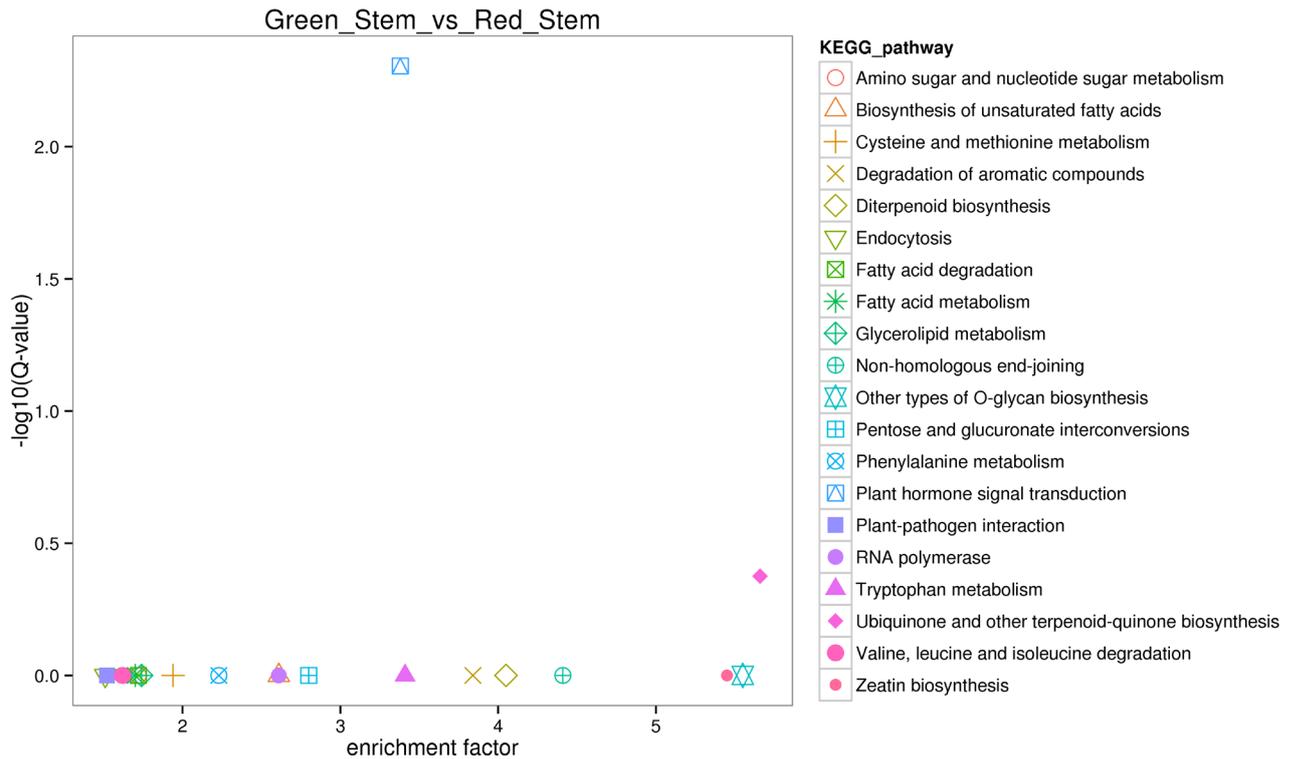


Fig. 3 Suppl. Each point in the figure represents a *KEGG* path. The x-axis shows the enrichment factor, which represents the ratio of the proportion of genes annotated to a certain pathway in DEGs (green-stem vs. red-stem ecotype) to the proportion of genes annotated to that pathway in all genes. The larger the enrichment factor, the more significant the enrichment of differentially expressed genes in this pathway. The y-axis is $\log_{10}(Q\text{-value})$, where $Q\text{-value}$ is the $P\text{-value}$ after multiple hypothesis test correction. Therefore, the larger the ordinate, the more reliable the enrichment significance of differentially expressed genes in this pathway.

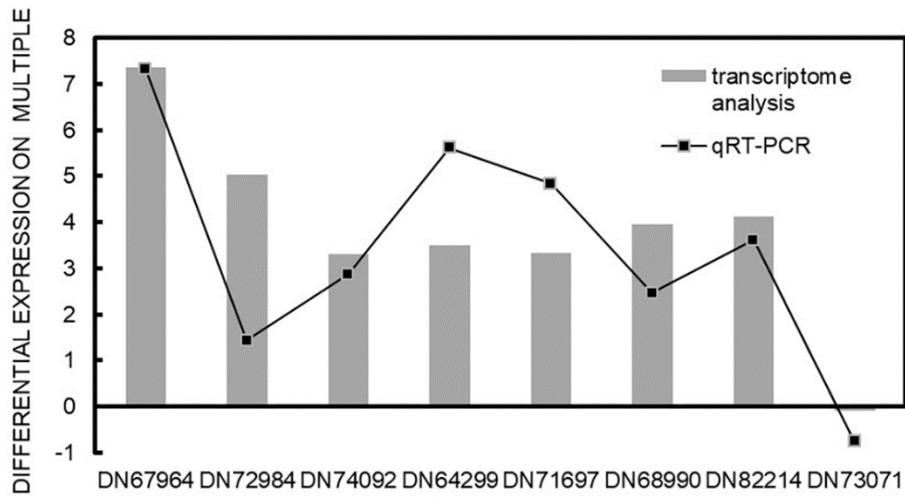


Fig. 4 Suppl. The correlation between the result of real-time qPCR and transcriptome analysis (x-axis indicates various transcription factor families as coded in *Unigene* sequence database; y-axis represents relative differential expression for both transcriptome analysis and qPCR).