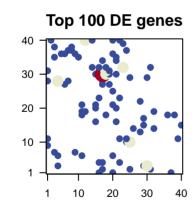
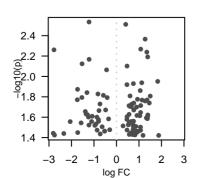
Tocai_acclim_r1

Global Summary

%DE = 0 # genes with fdr < 0.2 = 0 (0+/0 -) # genes with fdr < 0.1 = 0 (0+/0 -) # genes with fdr < 0.05 = 0 (0+/0 -) # genes with fdr < 0.01 = 0 (0+/0 -)

<FC> = 0 <p-value> = 0.46 <fdr> = 1





Differentially expressed genes

fdr

Description

log(FC)

Vitvi11g01035 -0.73

Vitvi16g0002C -0.48

Vitvi09g00358 -0.78

Vitvi05g02231 -1.38

Vitvi12g02632 -1.35

Vitvi11g01205 -1.28

Vitvi18g03218 -1.08

Vitvi10g01663 -1.24

0.019

0.022

0.023

0.025

Rank

itai	ÏD	.09(.	p-va	lue	Meta	gene	rtanit	002	p	"an	Concoct
Overexpressed							Overexpressed				
1	Vitvi03g00243	0.41	0.003	1	15 x 21	Binding to a calcium ion (Ca2+).	1	8.29	0e+00	18	Energy militatorgijsmmetalib bijstoos yn tiPleosijo sayımtibressias paroteimsa proteins
2	Vitvi07g01075	1.27	0.004	1	18 x 30	Binding to a zinc ion (Zn).	2	8.11	0e+00	18	Photosyn Plessissy rathlesis a-paroteims a proteins
3	Vitvi04g00186	1.08	0.005	1	17 x 27	Binding to ATP, adenosine 5'-triphosphate, a universally impo	3	6.29	0e+00	47	Transporterareatatorer-dated sport Televispoort celevièren carriers
4	Vitvi06g00325	1.35	0.006	1	23 x 32	Catalysis of the sequential cleavage of nucleotides (such as r	4	4.23	0e+00	10	Photosyn Priessis symutreis is Priodeins ys Pelmoto (\$730@noth) (\$730@noth) (\$730@noth) (\$730@noth)
5	Vitvi04g01532	1.39	0.006	1	5 x 36		5	3.44	8e-04	30	Glycan bi@slycatnelsisssymuthensitaaboblsmetalsle@slycanNel@glycodartide.gradation
6	Vitvi06g00389	0.47	0.008	1	17 x 34	Any process that modulates the frequency, rate or extent of co	6	3.4	9e-04	28	Transcriptioanfactipition Mactions - MTERF
7	Vitvi09g01860	1.83	0.011	1	1 x 28		7	3.35	1e-03	51	Plant spellian signedifig signiadian dinytholian rhythm
8	Vitvi02g00377	1.12	0.012	1	21 x 16	Binding to a heme, a compound composed of iron complexed	8	3.21	1e-03	18	TranscriptToanfactipition ARTors - ARF
9	Vitvi14g01820	0.75	0.012	1	18 x 32	The component of a membrane consisting of the gene produc	9	3.06	2e-03	11	Transcriptioanfactipition faltifiers - GRF
10	Vitvi17g00929	0.47	0.012	1	15 x 20	Binding to ATP, adenosine 5'-triphosphate, a universally impo	10	3.01	3e-03	75	Mitochon dulitad otheomeschi itali toennasood pitteomesteniab tratemestlantison factors
11	Vitvi07g01816	1.06	0.014	1	17 x 30	Organized structure of distinctive morphology and function, be	11	2.91	4e-03	110	Ubiquitin skriterit in- skriters ub- uh utlfRindp-tinigRintgp-Entiger type E3
12	Vitvi17g00875	0.6	0.016	1	6 x 27	A lipid bilayer along with all the proteins and protein complexe	12	2.83	5e-03	32	Circadian Chytholian phythm - plant
13	Vitvi12g02238	1.5	0.016	1	20 x 40		13	2.76	7e-03	41	Porphyrin Poeptalyolismetabolism
14	Vitvi07g00222	0.93	0.017	1	15 x 30		14	2.62	1e-02	101	Starch an Stauchcasedraetabolism
15	Vitvi14g00012	1.36	0.017	1	25 x 29		15	2.61	1e-02	38	Photosyn Plassics synthesis
16	Vitvi14g00311	1.14	0.017	1	30 x 29	The component of a membrane consisting of the gene produc	16	2.49	1e-02	90	Lipid metalopidismeta@b/isenopl@dyphodipirobspetalopidismetabolism
17	Vitvi07g01380	1.27	0.017	1	39 x 11	Binding to a protein.	17	2.44	2e-02	217	Cell motilitigell integritidation and antion of the control of the
18	Vitvi03g00932	1.46	0.018	1	12 x 19	Binding to an RNA molecule or a portion thereof.	18	2.43	2e-02	100	Plant spe@liansigmedifig.sigifialiveg.devielwpemdentelopment
19	Vitvi09g00063	0.77	0.018	1	23 x 39	Binding to a nucleic acid.	19	2.4	2e-02	19	Hormonelstigmating signialingelli@itsigeralling signaling
20	Vitvi18g01219	0.68	0.019	1	18 x 18	The network of interconnected tubular and cisternal structures	20	2.29	2e-02	41	TranscriptTomnsdRitsHopo+yRitsHapelymerase
Underexpressed							Underexpressed				
1	Vitvi05g00228	-1.22	0.003	1	25 x 10		1	-8.58	0e+00	48	Transcription faction to the WRKY
2	Vitvi11g01692	-2.78	0.005	1	22 x 11	A lipid bilayer along with all the proteins and protein complexe	2	-8.04	0e+00	144	RibosomeRib EstkarreyeteEsukaryotes
3	Vitvi19g01870	-1.22	0.007	1	11 x 6		3	-7	0e+00	247	TranslatioTranStatisnomeRibosome
4	Vitvi07g02644		0.008	1	16 x 4	The component of a membrane consisting of the gene produc	4	-6.98	0e+00	211	RibosomeRibosome
5	Vitvi17g00626		0.009	1	21 x 20		5	-4.92	0e+00	162	Plant spe@lfansispredifig signahingpatPlagetopatbougetointeraction
6	Vitvi05g02085		0.013	1	14 x 40	Binding to a protein.	6	-4.83	0e+00	97	RibosomeRib Aschaea - Archaea
7			0.014	1	25 x 10		7	-4.65	0e+00	49	Transcription faction factoris - NAC
8	-	-0.82	0.015	1	25 x 2	The transfer of electrons from ubiquinol to cytochrome c that	8	-4.57	0e+00	73	Transcription faction factoriscon factoris
9	Vitvi12g02402		0.015	1	29 x 17	The component of a membrane consisting of the gene produc	9	-4.36	0e+00	45	Galactos@aletatbsesmetabolism
10	Vitvi05g01256		0.016	1	31 x 2	The cell cycle process in which double-strand breaks are ger	10	-3.95	4e-05	140	Hormone Holognading sightlaling sightland signaling
11	Vitvi17g01421		0.016	1		A membrane-bounded organelle of eukaryotic cells in which	11	-3.67	3e-04	42	TryptophaTryptetabelismetabolism
12	Vitvi02g01464	-1.74	0.017	1	20 x 1		12	-3.34	1e-03	15	Chaperon@hapts@n7@ ≠ DNS.R7K0 / DNAK

28 x 13 A spliceosomal complex that is formed following the release c

24 x 11 The part of the cytoplasm that does not contain organelles bu

The component of a membrane consisting of the gene produc

13

15

16 17

18

19

-3.25

-3.07

-3.02

-2.82

-2.78

-2.74

-2.65

-2.6

1e-03

2e-03

3e-03

6e-03

6e-03

8e-03

9e-03

1e-02

77

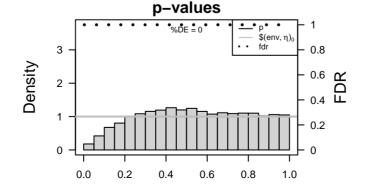
71

77

58

17

71



20 x 25 Binding to a protein.

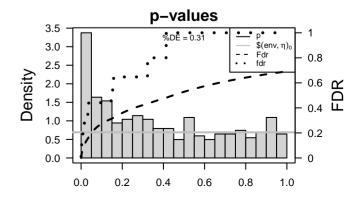
37 x 1

17 x 2

9 x 7

12 x 40

24 x 10



Plant-pathagenpiatecageiointeraction

Pores ion Robrassriels (Ti@nth]els [TC:1]

Glutathior@dutættabolismetabolism

ExosomeEx**Psoteins**-fProteinsrfmstrehimsnrseexosomes

Other am@ther.inlenterindisameta@hikathie@kutathinbeametabolism

StilbenoicStillaenloethtaiaoithaptagirigenothtjörsgentolesiasynthesis

Cysteine Orysteriethiamidne ethicitarbio esmetabolism

Proteason Prote Assertabling start during factors

Differentially expressed gene sets

Rank GSZ p-value #all Geneset