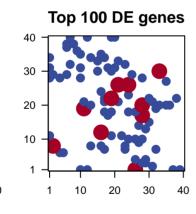
# Tocai\_acclim\_r2

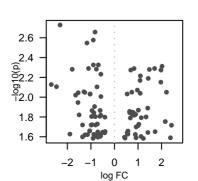
### **Global Summary**

%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> = 0.47 <fdr> = 1

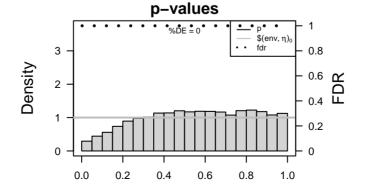
## 





### Differentially expressed genes

Rank ID		log(F	C) p–va	fdr alue	Meta	Description gene	Rank	GS	
	Over	Overexpressed							resse
	1	Vitvi09g01860	2.02	0.005	1	1 x 28		1	7.83
	ż	Vitvi00q02072	1.7	0.005	1	11 x 19		ż	7.72
	3	Vitvi06g00764	0.83	0.005	1	28 x 28	A membrane-bounded organelle of eukaryotic cells in which	3	5.82
	4	Vitvi12g02239	1.48	0.005	1	6 x 37	Binding to ATP, adenosine 5'-triphosphate, a universally impo	4	3.83
	5	Vitvi06q00425	0.69	0.005	1	21 x 26	Binding to a protein.	5	3.49
	6	Vitvi06g01629	1.97	0.005	1	1 x 34	•	6	3.2
	7	Vitvi06g01901	1.1	0.006	1	7 x 32		7	2.94
	8	Vitvi16g01543	1.43	0.006	1	20 x 31		8	2.63
	9	-	1.09	0.007	1	24 x 25	A membrane-bounded organelle of eukaryotic cells in which	9	2.63
	10	Vitvi19g02100	1.97	0.007	1	38 x 22	Binding to a metal ion.	Ĭ0	2.59
	11	Vitvi12g02003	0.97	0.008	1	21 x 33	Binding to ATP, adenosine 5'-triphosphate, a universally impo	11	2.55
	12	Vitvi01g01738	0.74	0.009	1	13 x 34	A ubiquitin ligase complex in which a cullin from the Cul1 sub	12	2.33
	13	Vitvi16g01475	2.21	0.009	1	2 x 8		13	2.33
	14	Vitvi11g00859	1.09	0.009	1	13 x 20		14	2.29
	15	Vitvi04g01472	0.54	0.009	1	19 x 30	A membrane-bounded organelle of eukaryotic cells in which	15	2.28
	16	Vitvi14g00012	1.41	0.013	1	25 x 29	•	16	2.27
	17	Vitvi13g01214	1.01	0.014	1	19 x 18		17	2.23
	18	Vitvi18q00641		0.014	1	4 x 28	The contents of a cell excluding the plasma membrane and n	18	2.23
	19	Vitvi06g01974	0.77	0.014	1	17 x 34	Binding to a nucleic acid.	19	2.2
	20	Vitvi04g00265	0.64	0.014	1	9 x 36	The contents of a cell excluding the plasma membrane and n	20	2.2
	_							-	
		erexpressed						Underex	
	1	Vitvi13g00161	-2.31	0.002	1	12 x 1		1	-6.72
	2	Vitvi16g01280	-0.82	0.002	1	28 x 3	A semiautonomous, self replicating organelle that occurs in v	2	-6.67
	3	Vitvi04g01192	-0.9	0.003	1	16 x 8	A small, dense body one or more of which are present in the	3	-6.26
	4	Vitvi07g01646	-1.17	0.003	1	31 x 21	Binding to a zinc ion (Zn).	4	-4.87
	5	Vitvi10g00382 Vitvi14g00992	-0.68	0.005	1	28 x 17	Binding to an RNA molecule or a portion thereof.  The formation of a tri–snRNP complex containing U4 and U6	5	-4.68
	6 7	Vitvi14g00992 Vitvi16g02082	-0.9 -1.1	0.005	1 1	26 x 10 18 x 22	The formation of a til-strking complex containing 04 and 06	6 7	-3.83 -3.59
	8	Vitvi04g00447	-0.77	0.005	1	24 x 23	Organized structure of distinctive morphology and function, by	8	-3.58
	9	Vitvi09q00146	-1.79	0.005	1	35 x 27	The directed movement of proteins in a cell, including the mo	9	-3.3
	10	Vitvi04g01142	-0.58	0.006	1	29 x 13	Binding to ATP, adenosine 5'-triphosphate, a universally impo	10	-3.27
	11	Vitvi11g01692	-2.68	0.007	1	22 x 11	A lipid bilayer along with all the proteins and protein complexe	11	-3.08
	12	Vitvi19g00566	-2.46	0.008	1	1 x 11	The component of a membrane consisting of the gene produc	12	-3.05
	13	Vitvi10g01751	-0.74	0.008	1	19 x 22	Binding to a protein.	13	-2.99
	14	Vitvi07g01888	-1.3	0.009	1	19 x 11	The action of a molecule that contributes to the structural inte	14	-2.98
	15	Vitvi08g02357	-1.26	0.009	1	26 x 18	The cell membranes and intracellular regions in a plant are co	15	-2.84
	16	Vitvi08g01525	-1.54	0.009	1	27 x 14	A membrane-bounded organelle of eukaryotic cells in which	16	-2.8
	17	Vitvi00g00990	-1.03	0.009	1	16 x 12		17	-2.74
	18	Vitvi11g01709	-1.03	0.009	1	16 x 12		18	-2.63
	19	Vitvi05g01256	-1.65	0.010	1	31 x 2	The cell cycle process in which double-strand breaks are ger	19	-2.62
	20	Vitvi19g00114	-0.58	0.010	1	21 x 26	The component of a membrane consisting of the gene produc	20	-2.5



#### Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset
	Overexp	ressed			
	1	7.83	0e+00	18	Photosyn Pleasissy rathlesisa-paroteimsa proteins
	2	7.72	0e+00	18	Energy m <b>EtabrgljsmetalBblistorsynPlassissaymteresasparoteims</b> a proteins
which	3	5.82	0e+00	47	Transporterarestatorige - datalogo - t Televispoort celevisiron carriers
ly impo	4	3.83	8e-05	10	Photosyn Priessis spreuteissis Priesteissys Pelmoto(sP/SDenoth(P70/DD) ythato) rophy
		3.49	7e-04	51	Plant spe <b>Pliansispredifig</b> si@Ciatiandian@Involution rhythm
	5 6 7	3.2	1e-03	17	Kinase – KRAdséamíRAK family
	7	2.94	4e-03	18	TranscriptToarrfsactipition fallsfors - ARF
	8	2.63	1e-02	30	Glycan bi@dycatmetsics.symuthressitsabolitsmetaltde/@dycarNde@frectertide.grad
which	9	2.63	1e-02	28	TranscriptToanfactipition McToRF- MTERF
	10	2.59	1e-02	38	Lipid metalipoidismetalistriismlipidEthetalipoidismetabolism
ly impc	11	2.55	1e-02	90	Lipid metalipoidismmeta@bylisenopl@lyphodipliobspetalipoidismmetabolism
ıl1 sub	12	2.33	2e-02	32	Circadian Chrytholian phythm - plant
	13	2.33	2e-02	89	MAPK sightlahlPkg spighthankang-patlannkay – plant
	14	2.29	2e-02	409	Enzyme -E2bz7ymTeans2le7rinTgapbafæsrpihgrpbesphtærinnisn-grogmtaupisng group
which	15	2.28	2e-02	35	Lipid metalipoidismeta Sphisingeli Siphinegtalipoidismetabolism
	16	2.27	3e-02	13	Cutin sub Crutie and enime lained youthelsies yn the sis
	17	2.23	3e-02	56	Hormone Higmating sightalingnatesignaling signaling
and n	18	2.23	3e-02	110	Ubiquitin sylateinsub white sub-white sub-whit
	19	2.2	3e-02	31	Chromos@heoarrosasseciatealspacoteiteal-p@eeiesile@eing silencing
and n	20	2.2	3e-02	33	Glycan bi <b>Glycatmelsissayındhessisabolismetalsle/GlycanNeiGlycatmelsis</b> synt
	Underex	pressed	1		
	1	-6.72	0e+00	211	RibosomeRibosome
rs in va	2	-6.67	0e+00	247	TranslatioTranStatisomeRibosome
in the	3	-6.26	0e+00	144	RibosomeRib EstatamyoteEsukaryotes
	4	-4.87	0e+00	73	Transcription faction factors Relation factors and Transcription facto
	5	-4.68	0e+00	97	RibosomeRib Aschaea Archaea
nd U6	4 5 6 7	-3.83	8e-05	26	Flavonoid Flavos ynddelsie synthesis
		-3.59	4e-04	72	RibosomeRibleStoroleondMiteddDblodoipalaShloroplast
tion, b	8	-3.58	4e-04	15	Chaperon@hapts@nn@≠DNS.Rnt0/DNAK
he mo	9	-3.3	1e-03	140	Hormone Higmating signaling signaling
ly impc	10	-3.27	1e-03	45	Galactos@alatabsesmetabolism
mplexe	11	-3.08	2e-03	11	Zeatin biozsyatimelsissynthesis
produc	12	-3.05	2e-03	40	SLC47: Mishirida Maduli di
	13	-2.99	3e-03	67	RibosomeRibBauteeia-Bacteria

3e-03 5e-03

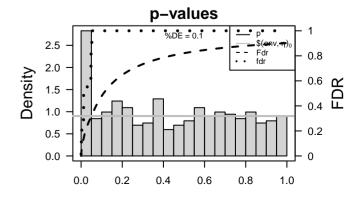
6e-03

7e-03

1e-02 1e-02 10

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Valine leukärlien enheluisionle varideskoilessyorintheelsissynthesis

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