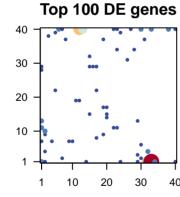
Tocai_acclim

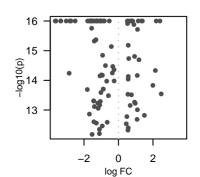
Global Summary

%DE = NA # genes with fdr < 0.2 = 5398 (3068 + /2330 -) # genes with fdr < 0.1 = 3799 (2179 + /1620 -) # genes with fdr < 0.05 = 2547 (1458 + /1089 -) # genes with fdr < 0.01 = 1693 (944 + /749 -)

<FC> = 0<p-value> = 0.04<fdr> = 0.48

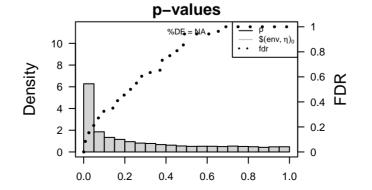
Portrait 40 30 20 10 1 10 20 30 40





Differentially expressed genes

Rank			log(FC) fdr		Description		
		ID		p-va	lue	Meta	gene
	Over	expressed					-
	1	Vitvi03g00932	1.39	1e-16	1e-13	12 x 19	Binding to an RNA molecule or a portion thereof.
		Vitvi05g02096	1.34	1e-16	1e-13	1 x 29	Binding to a protein.
	2	Vitvi07g00890	2.19	1e-16	1e-13	20 x 15	Binding to ADP, adenosine 5'-diphosphate.
	4	Vitvi09g00691	0.82	1e-16	1e-13	22 x 40	Binding to ATP, adenosine 5'-triphosphate, a universally impo
	4 5	Vitvi11g01455	0.74	1e-16	1e-13	16 x 29	
	6 7	Vitvi14g01460	1.14	1e-16	1e-13	3 x 38	
	7	Vitvi15g01388	2.41	1e-16	1e-13	33 x 40	The component of a membrane consisting of the gene produc
	8	Vitvi17g00714	0.63	1e-16	1e-13	15 x 32	Binding to a protein.
	9	Vitvi18g00112	0.52	1e-16	1e-13	23 x 34	Binding to a protein.
	10	Vitvi18g01103	0.76	1e-16	1e-13	24 x 39	The process in which a methyl group is covalently attached to
	11	Vitvi07g00545	0.53	1e-16	1e-13	8 x 37	The contents of a cell excluding the plasma membrane and n
	12	Vitvi16g00860	0.9	1e-16	3e-13	30 x 40	The component of a membrane consisting of the gene produc
	13	Vitvi04g00365	1.1	2e-16	8e-13	26 x 31	The component of a membrane consisting of the gene produc
	14	Vitvi11g00484	0.57	7e-16	1e-12	6 x 40	A membrane-bounded organelle of eukaryotic cells in which
	15	Vitvi18g00840	0.94	2e-15	3e-12	11 x 19	Catalysis of the hydrolysis of peptide bonds in a polypeptide c
	16	Vitvi03g00361	0.59	2e-15	3e-12	17 x 29	Binding to a protein.
	17	Vitvi10g01162	1.19	2e-15	4e-12	1 x 28	Binding to ATP, adenosine 5'-triphosphate, a universally impo
	18	Vitvi15g00947	2.14	5e-15	4e-12	38 x 40	A membrane-bounded organelle of eukaryotic cells in which
	19	Vitvi14g02630	1.09	7e-15	4e-12	19 x 17	
	20	Vitvi16g00519	0.57	7e-15	1e-11	6 x 40	A lipid bilayer along with all the proteins and protein complexe
	Unde	erexpressed					
	1	Vitvi07g02606	-2.81	1e-16	1e-13	34 x 1	
	ż	Vitvi00g01651	-3.35	1e-16	1e-13	13 x 40	
	3	Vitvi10g02090	-3.35	1e-16	1e-13	13 x 40	
	2 3 4 5 6 7	Vitvi00g02302	-1.26	1e-16	1e-13	33 x 1	
	5	Vitvi18g03400	-1.26	1e-16	1e-13	33 x 1	
	6	Vitvi02g00304	-1.56	1e-16	1e-13	12 x 40	The component of a membrane consisting of the gene produc
	7	Vitvi03g01127	-3.66	1e-16	1e-13	33 x 1	The component of a membrane consisting of the gene produc
	8	Vitvi04g02022	-0.81	1e-16	1e-13	29 x 3	Catalysis of the transfer of a phosphate group, usually from A
	9	Vitvi05g02097	-1.23	1e-16	1e-13	13 x 40	A lipid bilayer along with all the proteins and protein complexe
	10	Vitvi06g00712	-1.25	1e-16	1e-13	1 x 13	
	11 12	Vitvi07g01586	-3.03	1e-16	1e-13	33 x 1	Pinding to ATD adenosine Et triphosphote a universally impo
	13	Vitvi08g01351 Vitvi09g01930	-1.1 -1.79	1e-16 1e-16	1e-13 1e-13	29 x 1 32 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impo
	14	Vitvi11g01156	-1.75	1e-16	1e-13	14 x 1	The component of a membrane consisting of the gene produc
	15	Vitvi11g01692	-2.75	1e-16	1e-13	22 x 11	A lipid bilayer along with all the proteins and protein complexe
	16	Vitvi11g01488	-1.37	1e-16	1e-13	12 x 40	The space external to the outermost structure of a cell. For ce
	17	Vitvi12g01816		1e-16	1e-13	32 x 4	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (
	18	Vitvi12g02726	-2.81	1e-16	1e-13	12 x 40	
	19	Vitvi12g02153	-1.61	1e-16	1e-13	33 x 1	
	20	Vitvi12g02157	-1.06	1e-16	1e-13	32 x 4	Catalysis of the transfer of a group, e.g. a methyl group, glyco



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset

	Overe.	xpressed			
	1	8.92	0e+00	18	Energy mētadorgljsmetalBobistors yn Placisios symtheres as paroteims a proteins
	2	8.75	0e+00	18	Photosyn Pleasissy rathlesis a-paroteims a proteins
	3	7.11	0e+00	47	Transporterazatatorge-catalogo-tTeterasportoalerideron carriers
impc	4	4.51	0e+00	10	Photosyn Priessis symutreissis Princeteissys Pelmoto(\$9750@nchl (\$77600ydhalo) rophyll
	5	3.84	0e+00	217	Cell motilitiell metjulgation enjulation vytosktile trynoskeleton
	6	3.77	0e+00	30	Glycan bi Ostycatmetsios symuthemsita bobismetallylei Ostrycan Net Cylractertide grada
roduc	7	3.5	5e-04	41	Porphyrin Poetalyolismetabolism
	8	3.49	6e-04	28	Transcription Matters- MTERF
	9	3.09	3e-03	38	Photosyn tPlassis synthesis
ed to	10	3.06	3e-03	41	Replication
nd n	11	2.95	4e-03	75	Mitochon dilliad charredorigitaren societares la tipo francia de la companya del companya de la companya de la companya del companya de la co
roduc	12	2.82	6e-03	18	Transcription faction for ARF
roduc	13	2.73	8e-03	31	Chromos@heoarrobassevainatealspacetriated-p@eeiassile@eing silencing
hich	14	2.7	8e-03	22	Fatty acidFettyn questionelongation
tide (15	2.67	8e-03	80	Cytoskele@ntoslMeletotubulleisrotubules
	16	2.58	1e-02	78	Energy m EtæbralismetaBbüsons yn Pleasis synthesis
impc	17	2.54	1e-02	13	Cutin sub ©uitie suble wiane Laino dywathelsies synthesis
hich	18	2.48	2e-02	90	Lipid met alipidismetaGblisenoe)விலுற்குற்குற்கு வக்கிறும் காetabolism
	19	2.47	2e-02	11	Transcription faction faction and a story
plexe	20	2.47	2e-02	36	DNA replication
pronc	20	2.47	20-02	50	510 (10phbattonic photator)
	Under	expressed	d		
	1	-7.83	0e+00	48	Transcription taleton taleton WRKY
	2	-6.36	0e+00	73	Transcription faction ARCOEREBP2 EREBP
	2 3 4 5 6	-5.65	0e+00	140	Hormonelskigmating signaling signaling
	4	-5.02	0e+00	49	Transcription field resemble Transcription field as NAC
	5	-4.52	0e+00	64	TranscriptToanfactipitison CaltherstranCathreptionanfactipitison factors
roduc		-4.52	0e+00	45	Galactos@alatatbotismetabolism
roduc	7	-3.82	0e+00	15	Chaperor@haphes@n7@ ≠ DNS.RR0 / DNAK
om A	8	-3.68	2e-04	144	RibosomeRib EsukarreyoteEsukaryotes
plexe	9_	-3.58	4e-04	26	Flavonoid Hidavsynttildelsies synthesis
	10	-3.56	5e-04	162	Plant spe@liansigmedifig signalingpatRagenpathageiminteraction
	11	-3.49	6e-04	42	Tryptopha Tryptxtpbelism etabolism
impc	12	-3.2	2e-03	17	Proteasor Prote Asseme blings sautubring factors
	13	-3.07	3e-03	40	SLC47: MSLIGCHTIG Mouti Toxignalizet Toxion E, MATSTO rfa (MIA)TE) family
roduc	14	-3.03	3e-03	38	Protein – Polotepieren Ghapediateed naetolipteed paul (Coloffe) (CMA)
plexe	15	-2.98	4e-03	10	Valine leuk/antienenheluisionle auridestailesuorintheelsiesynthesis
or ce	16	-2.93	4e-03	71	Exosome Exosomeias formula imsrfmante imsonase exosomes
–N, (17	-2.93	4e-03	111 11	Hormonelskigmating sight Bulling signaling
	18 19	-2.77 -2.76	7e-03 7e-03	11 12	BiosyntheBiosyntheesisdafryenetatarljsmetahBlAstriosynthesis Endoplastriidoetastriin metanbramenenbrantesahd cytosol

