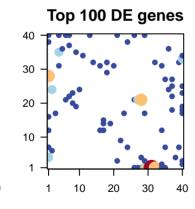
Sangio_accfreeze

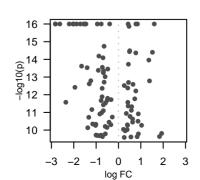
Global Summary

%DE = NA # genes with fdr < 0.2 = 1940 (1085 + /855 -) # genes with fdr < 0.1 = 1181 (625 + /556 -) # genes with fdr < 0.05 = 962 (490 + /472 -) # genes with fdr < 0.01 = 598 (273 + /325 -)

<FC> = 0<p-value> = 0.12<fdr> = 0.59

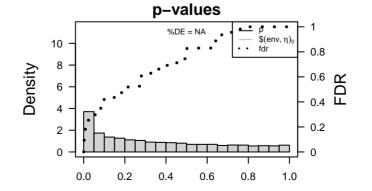
Portrait 40 30 20 1 1 10 20 30 40





Differentially expressed genes

Rank ID		log(F	C) p–va	fdr lue	Meta	Description gene	F
Overexpressed							(
1	Vitvi07g01231	0.78	1e-16	4e-13	7 x 37	A process that is carried out at the cellular level which results	1
2	Vitvi05g00464	0.43	1e-16	4e-13	8 x 23	A lipid bilayer along with all the proteins and protein complexe	
3	Vitvi09g00546	0.85	1e-16	4e-13	34 x 2	Binding to ADP, adenosine 5'-diphosphate.	2
4	Vitvi13g01200	1.6	1e-16	4e-13	13 x 40	Catalysis of an oxidation–reduction (redox) reaction in which:	2
5	Vitvi06q00473	0.47	1e-16	9e-12	4 x 31	Binding to ATP, adenosine 5'-triphosphate, a universally impo	5
6	Vitvi10g01607	0.5	3e-15	9e-12	6 x 21	The contents of a cell excluding the plasma membrane and n	ě
7	Vitvi04g01234	0.49	4e-15	9e-12	14 x 32	A transcription regulator activity that modulates transcription c	7
8	Vitvi04g00282	1.52	4e-15	9e-12	8 x 20	The membrane surrounding a cell that separates the cell from	έ
9	Vitvi08g01683	0.77	4e-15	2e-11	1 x 16	Binding to a calcium ion (Ca2+).	ć
10	Vitvi03g00017	1.36	1e-14	5e-11	9 x 19	Binding to a metal ion.	1
11	Vitvi14g01820	0.44	2e-14	5e-11	18 x 32	The component of a membrane consisting of the gene produc	
12	Vitvi03g01260	1.39	2e-14 2e-13	3e-10	1 x 7	The component of a membrane consisting of the gene produc	- 1
13	Vitvi06g00681	0.45	2e-13	3e-10	5 x 36	A membrane-bounded organelle of eukaryotic cells in which	- 1
14	Vitvi08g01583	0.45	3e-13	5e-10	4 x 40	The contents of a cell excluding the plasma membrane and n	,
	Vitvi07g01806	0.05	3e-13	5e-10 5e-10	4 x 40 20 x 31	The component of a membrane consisting of the gene produc	
15	Vitvi07g01806 Vitvi09g01349					The irregular network of unit membranes, visible only by elect	
16	-	0.41	4e-13	5e-10	23 x 17		
17	Vitvi08g00950	0.78	6e-13	3e-09	1 x 12	The component of a membrane consisting of the gene produc	
18	Vitvi01g00511	0.73	2e-12	3e-09	1 x 38	A membrane–bounded organelle of eukaryotic cells in which	1
19	Vitvi05g01537	0.42	3e-12	3e-09	24 x 38	A membrane–bounded organelle of eukaryotic cells in which	1
20	Vitvi15g01063	0.43	4e-12	6e-09	7 x 22	The component of a membrane consisting of the gene produc	2
Unde	erexpressed						L
1	Vitvi05g02250	-2.62	1e-16	4e-13	37 x 25		4
	Vitvi07g02390	-2.04	1e-16	4e-13	17 x 15		Ġ
2	Vitvi11g01385	-1.45	1e-16	4e-13	40 x 17	The component of a membrane consisting of the gene produc	2
4	Vitvi12g02160	-1.71	1e-16	4e-13	27 x 21	A membrane-bounded organelle of eukaryotic cells in which	2
5	Vitvi12g02179	-1.87	1e-16	4e-13	29 x 40	The component of a membrane consisting of the gene produc	5
4 5 6 7	Vitvi12g02545	-0.95	1e-16	4e-13	28 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impo	
7	Vitvi13g01997	-1.51	1e-16	4e-13	36 x 24	Catalysis of an oxidation-reduction (redox) reaction, a reversi	7
8	Vitvi13g00521	-0.77	1e-16	4e-13	27 x 1	The component of a membrane consisting of the gene produc	Š
9	Vitvi14g00297	-2.82	1e-16	4e-13	30 x 1		ç
10	Vitvi15g01136	-2.01	1e-16	4e-13	28 x 21	Binding to ADP, adenosine 5'-diphosphate.	1
11	Vitvi16g01449	-2.2	1e-16	4e-13	1 x 28		1
12	Vitvi18g02715	-2.83	1e-16	4e-13	31 x 1	Binding to a heme, a compound composed of iron complexed	1
13	Vitvi18g02371	-1.56	1e-16	4e-13	34 x 31		1
14	Vitvi19g00446	-0.39	1e-16	4e-13	34 x 12	The component of a membrane consisting of the gene produc	1
15	Vitvi14g02627	-0.64	2e-15	9e-12	26 x 21		1
16	Vitvi15g01552	-0.88	7e-15	2e-11	16 x 12		- 1
17	Vitvi14g01474	-0.69	8e-15	3e-11	37 x 22	Catalysis of an oxidation-reduction (redox) reaction, a reversi	- 1
18	Vitvi19g00423	-1.65	2e-14	5e-11	32 x 1	Binding to a protein.	1
19	Vitvi14g01647	-0.72	3e-14	5e-11	28 x 21		1
20	Vitvi16g00160	-1.4	3e-14	5e-11	19 x 14	A lipid bilayer along with all the proteins and protein complexe	2



Differentially expressed gene sets

Rank G	SZ p-val	ue #all	Geneset
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	Overe	xpressed			
s	1	7.23	0e+00	48	Transcription taketintion taketint - WRKY
κE	2	6.33	0e+00	49	Transcription faction factors - NAC
	3	5.75	0e+00	64	Transcription factors
1;	4	5.66	0e+00	73	Transcription AREDEREBP2 EREBP
OC	5	5.64	0e+00	162	Plant spe@liansispredifig.sig@lahit-gpatPlagetapatboogetionnteraction
n	6	5.22	0e+00	140	Hormone Istignating signaturing signaturing signaturing
	7	5.05	0e+00	153	Plant-pathappahpathappahopinteraction
n	8	4.81	0e+00	62	RibosomeRitiosenesisiec@@@siartid@s particles
	9	4.07	0e+00	116	RibosomeRibiosenesisiedenesisOS PaetidleS particles
	10	3.64	2e-04	89	MAPK sightAliPks sightwiliang-patlaway – plant
J(11	3.49	6e-04	151	RNA polyRNeAspellyrsestase II system
	12	3.47	6e-04	86	Signal tra6ispheditioensoCeditioum-sQarleiling sighthaliang pathway
1	13	3.42	1e-03	75	Translatio Translatiosome Ribiose mesision Endesis/ortes
n	14	3.39	1e-03	64	Ribosome Ribiosemes is iong en easisy in tessukaryotes
JC	15	3.26	2e-03	128	Ubiquitin bilosteritin sõistelen Rinõinglen Rintropen Teor type E3
ct	16	2.93	4e-03	67	Replication Replication Replication
J(17	2.93	7e-03	51	Plant spe Elfantsisprædifig sigCiediandian Chytholian rhythm
1	18	2.68	7e-03 8e-03	110	Ubiquitin systeming systems white state of the state of t
1	19		9e-03	110	Channel -Clayotielnu-Ogotidenuptetetidehagateb(CNMB)nel (CNG)
		2.64 2.55		33	Carbohyd Catebore tabadës me ta Andisors e carminos tabadës me tabadës me
1(20	2.55	1e-02	33	Carbonyo cateore, caratesimie taleonisios e generio e tagaos inile tabonism
	Under	expressed	d		
	1	-8.87	0e+00	47	Transporterarasplutger-datalogo-tTeterasportoalerieron carriers
	2	-8.42	0e+00	78	Energy metaebolismsynPleosiesynthesis
J(2 3	-8.38	0e+00	18	Energy mētadogljsmeta@bbistosyn@lecsissymtthresissparoteimsa proteins
1	4	-7.73	0e+00	18	Photosyn Phessios synathlessis a-paroteims a proteins
J(5 6 7	-7.58	0e+00	38	Photosyn Pleasis synthesis
C	6	-5.45	0e+00	10	Photosyn Priessis sproute is is Priodetic ys Petro to (\$750 and hit (\$750 by that) rophyll
si		-4.85	0e+00	67	RibosomeRibBanteeia-Bacteria
10	8	-4.67	0e+00	26	Flavonoid Flavos yn the sis synthesis
	9_	-4.35	0e+00	40	Transport Torgasteprort Stylsytenkoid Ttaydyektionid pearthentiang pathway
	10	-4.23	0e+00	24	Replication phytheine phytheinephythiation Factors
	11	-4.17	0e+00	41	Transporterarastaturger-derinangy-aletineanna asspireterarastplonter cat D1
d	12	-4.11	0e+00	72	RibosomeRibosomolatomolaticodolatomo
	13	-4.01	0e+00	80	Cytoskele@ytoskeletotubulkisrotubules
1(14	-3.87	0e+00	25	Nitrogen Niëtalgelismetabolism
	15	-3.87	0e+00	79 105	Transporterandurger-eatellers-catcificits 64t 30 to 64
si	16 17	-3.79 -3.5	0e+00 5e-04	105 26	Energy mētæbrgljsmeta@alidantive@kiadaphverplætisphorylation Glycosylt@hysfesaytæanshfavdasaphadbiydnopleobile molecule
ol .	17	-3.5 -3.38	5e-04 1e-03	26 81	Enzyme -E4:2/r0ærber2-00-adæmilyassesen lyases
	19	-3.38	1e-03	57	Glyoxylat Ehroxydiatar hoxlythio a mexaftatili smetabolism
	19	-3.38	16-03	31	O 1 y O A y 1 C 1 to O G 1 to

