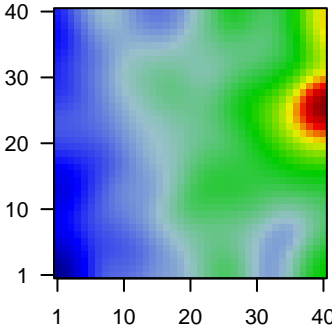


Tocai\_warm\_r3

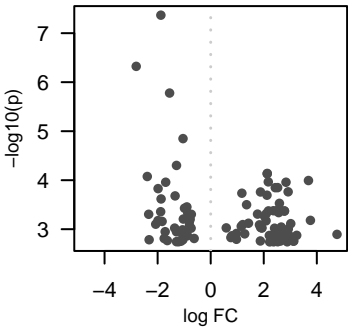
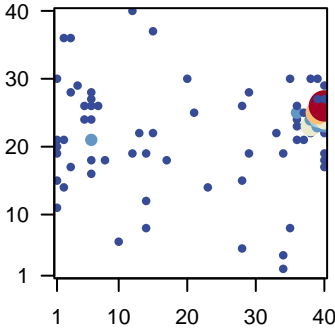
Global Summary

%DE = 0.22  
# genes with fdr < 0.2 = 19 ( 11 + / 8 - )  
# genes with fdr < 0.1 = 2 ( 0 + / 2 - )  
# genes with fdr < 0.05 = 2 ( 0 + / 2 - )  
# genes with fdr < 0.01 = 1 ( 0 + / 1 - )  
  
<FC> = 0  
<p-value> = 0.27  
<fdr> = 0.78

Portrait



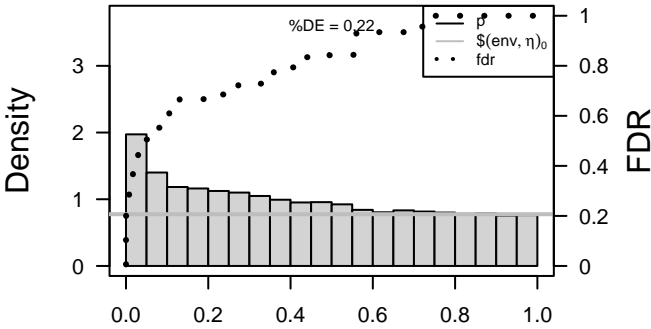
Top 100 DE genes



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
Overexpressed					
1	Vitv100g00967	2.13	7e-05	0.2	38 x 23
2	Vitv110g0219E	2.13	7e-05	0.2	38 x 23
3	Vitv110g0138E	3.68	1e-04	0.2	40 x 26
4	Vitv103g0069Z	2.17	1e-04	0.2	40 x 19 Catalysis of the transfer of an acyl group, other than amino-a
5	Vitv107g0129E	2.84	1e-04	0.2	40 x 23 A membrane-bounded organelle of eukaryotic cells in which
6	Vitv105g0147E	2.52	1e-04	0.2	35 x 30 A lipid bilayer along with all the proteins and protein complex
7	Vitv115g0071C	2.43	1e-04	0.2	37 x 25 Binding to a zinc ion (Zn).
8	Vitv116g0205E	2.92	2e-04	0.2	40 x 22 Binding to a metal ion.
9	Vitv101g0102E	1.88	2e-04	0.2	38 x 22 A membrane-bounded organelle of eukaryotic cells in which
10	Vitv114g0005Z	1.18	2e-04	0.2	23 x 14 Binding to a metal ion.
11	Vitv102g0005I	2.12	2e-04	0.2	36 x 25 A lipid bilayer along with all the proteins and protein complex
12	Vitv105g0008A	2.59	3e-04	0.2	39 x 23 A membrane-bounded organelle of eukaryotic cells in which
13	Vitv107g0054Z	1.35	3e-04	0.2	29 x 28
14	Vitv110g0189A	2.58	4e-04	0.2	40 x 24 Any process that results in a change in state or activity of a cr
15	Vitv114g0192E	2.36	4e-04	0.2	39 x 30 The formation of a protein dimer, a macromolecular structure
16	Vitv107g0261Z	2.18	4e-04	0.2	36 x 25 The formation of a protein dimer, a macromolecular structure
17	Vitv110g0013I	2.49	4e-04	0.2	39 x 24 Binding to a protein.
18	Vitv100g0076I	2.78	4e-04	0.2	39 x 25
19	Vitv110g0225E	2.78	4e-04	0.2	39 x 25 The part of a cell encompassing the cell cortex, the plasma m
20	Vitv111g0002E	2.56	5e-04	0.2	39 x 24 Binding to ATP, adenosine 5'-triphosphate, a universally impo
Underexpressed					
1	Vitv113g0125I	-1.88	4e-08	0.006	28 x 5 Any process that modulates the frequency, rate or extent of cr
2	Vitv114g0029I	-2.81	5e-07	0.017	2 x 36 Binding to ATP, adenosine 5'-triphosphate, a universally impo
3	Vitv117g0124C	-1.55	2e-06	0.170	1 x 20
4	Vitv113g0184C	-1.04	1e-05	0.170	6 x 26 The component of a membrane consisting of the gene produc
5	Vitv111g0144E	-1.29	5e-05	0.170	12 x 19 The component of a membrane consisting of the gene produc
6	Vitv105g0067E	-2.39	8e-05	0.170	1 x 11 A lipid bilayer along with all the proteins and protein complex
7	Vitv105g01687	-1.7	1e-04	0.170	8 x 18 The part of the cytoplasm that does not contain organelles bu
8	Vitv103g0152A	-1.98	1e-04	0.174	12 x 40 The component of a membrane consisting of the gene produc
9	Vitv110g0075E	-1.34	2e-04	0.225	1 x 21 A membrane-bounded organelle of eukaryotic cells in which
10	Vitv113g0256E	-1.87	2e-04	0.225	3 x 28
11	Vitv104g01577	-0.9	4e-04	0.225	6 x 27 A lipid bilayer along with all the proteins and protein complex
12	Vitv104g0058E	-0.99	4e-04	0.225	20 x 30 Binding to a metal ion.
13	Vitv100g00897	-1.89	4e-04	0.225	34 x 4
14	Vitv109g0005E	-0.86	5e-04	0.225	15 x 37 A membrane-bounded organelle of eukaryotic cells in which
15	Vitv111g0072C	-2.34	5e-04	0.225	2 x 14 Catalysis of the transfer of an acyl group, other than amino-a
16	Vitv107g0016C	-0.73	5e-04	0.252	6 x 28 The part of the cytoplasm that does not contain organelles bu
17	Vitv105g0113E	-1.03	6e-04	0.252	6 x 21 The chemical reactions and pathways involving carbohydrates:
18	Vitv108g0103E	-0.77	6e-04	0.252	7 x 26 The membrane surrounding a cell that separates the cell from
19	Vitv101g0195A	-1.99	7e-04	0.252	3 x 36 The component of a membrane consisting of the gene produc
20	Vitv107g0149Z	-1.83	7e-04	0.252	3 x 17

p-values



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	13.13	0	211	Ribosome
2	13.01	0	247	Translation
3	12.98	0	219	Cell growth
4	12.48	0	144	Ribosome
5	12.38	0	80	Cytoskeleton
6	11.81	0	24	Replication
7	10.38	0	217	Cell motility
8	10.16	0	36	DNA replication
9	9.32	0	97	Ribosome
10	9.28	0	41	Replication
11	6.92	0	44	Replication
12	6.2	0	34	Peptidase
13	5.52	0	27	Mismatch repair
14	5.52	0	37	Homologous recombination
15	5.05	0	113	Exosome
16	5.03	0	66	Exosome
17	4.87	0	67	Ribosome
18	4.71	0	72	Ribosome
19	4.46	0	29	Base excision repair
20	4.13	0	25	Replication
Underexpressed				
1	-6.89	0e+00	49	Transcription
2	-6.61	0e+00	73	Transcription
3	-6.6	0e+00	140	Hormone signaling
4	-6.12	0e+00	48	Transcription
5	-4.83	0e+00	64	Transcription
6	-4.28	0e+00	92	Lipid metabolism
7	-3.89	8e-05	29	Carotenoid synthesis
8	-3.82	1e-04	162	Plant signaling
9	-3.74	1e-04	170	Transcription
10	-3.51	6e-04	153	Plant-pathogen interaction
11	-3.46	8e-04	55	Glycerolipid metabolism
12	-3.26	1e-03	86	Signal transduction
13	-3.19	2e-03	77	Carbohydrate metabolism
14	-3.03	2e-03	35	Mitochondrial factors
15	-2.88	5e-03	12	Transcription
16	-2.68	8e-03	31	Autophagy
17	-2.67	8e-03	45	Valine metabolism
18	-2.67	8e-03	11	Biosynthesis
19	-2.65	9e-03	74	Transcription
20	-2.65	9e-03	238	Enzyme

p-values

