Tocai_warm

Global Summary

%DE = NA

genes with fdr < 0.2 = 8199 (3700 + / 4499 −)

genes with fdr < 0.1 = 5570 (2635 + / 2935 −)

genes with fdr < 0.05 = 4263 (2045 + / 2218 −)

genes with fdr < 0.01 = 2483 (1206 + / 1277 −)

<FC> = 0

<p−value> = 0.02

<fdr> = 0.36

Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
Overexpressed						
1	Vitvi01g01085	2.35	1e−16	4e−14	40 x 27	
2	Vitvi00g00606	2.14	1e−16	4e−14	40 x 23	
3	Vitvi07g03049	2.13	1e−16	4e−14	40 x 23	A chlorophyll−containing plastid with thylakoids organized into
4	Vitvi01g00160	1.6	1e−16	4e−14	40 x 37	The space external to the outermost structure of a cell. For ce
5	Vitvi01g00576	0.52	1e−16	4e−14	37 x 18	
6	Vitvi02g00435	2.01	1e−16	4e−14	40 x 30	Catalysis of an oxidation−reduction (redox) reaction, a reversi
7	Vitvi02g01224	1.34	1e−16	4e−14	40 x 19	The component of a membrane consisting of the gene produc
8	Vitvi02g00553	2.74	1e−16	4e−14	40 x 26	Catalysis of the hydrolysis of a carboxylic ester bond.
9	Vitvi03g01255	1.02	1e−16	4e−14	40 x 31	Catalysis of the hydrolysis of a carboxylic ester bond.
10	Vitvi03g00569	2.15	1e−16	4e−14	40 x 36	Catalysis of the transfer of a glycosyl group from a UDP−suga
11	Vitvi03g00552	1.06	1e−16	4e−14	40 x 21	Catalysis of the hydrolysis of various bonds, e.g. C−O, C−N, (
12	Vitvi04g00536	1.1	1e−16	4e−14	37 x 22	The action of a molecule that contributes to the structural inte
13	Vitvi04g01454	1.65	1e−16	4e−14	40 x 32	Binding to a metal ion.
14	Vitvi05g00499	0.56	1e−16	4e−14	33 x 24	
15	Vitvi05g00033	0.48	1e−16	4e−14	32 x 24	The action of a molecule that contributes to the structural inte
16	Vitvi05g01692	1.07	1e−16	4e−14	40 x 21	The chemical reactions and pathways resulting in the formatio
17	Vitvi06g00280	1	1e−16	4e−14	38 x 21	The action of a molecule that contributes to the structural inte
18	Vitvi06g00656	2.13	1e−16	4e−14	40 x 27	The component of a membrane consisting of the gene produc
19	Vitvi06g00803	0.93	1e−16	4e−14	40 x 19	Binding to a heme, a compound composed of iron complexed
20	Vitvi06g01340	1.45	1e−16	4e−14	40 x 30	
Underexpressed						
1	Vitvi00g01651	−3.35	1e−16	4e−14	13 x 40	
2	Vitvi10g02090	−3.35	1e−16	4e−14	13 x 40	
3	Vitvi03g00294	−0.44	1e−16	4e−14	5 x 32	A lipid bilayer along with all the proteins and protein complexe
4	Vitvi04g02027	−0.56	1e−16	4e−14	16 x 38	The component of a membrane consisting of the gene produc
5	Vitvi06g00181	−0.55	1e−16	4e−14	5 x 19	The formation of a protein dimer, a macromolecular structure
6	Vitvi06g00354	−0.77	1e−16	4e−14	15 x 9	The component of a membrane consisting of the gene produc
7	Vitvi06g01261	−0.72	1e−16	4e−14	34 x 8	Catalysis of a biochemical reaction at physiological temperatu
8	Vitvi07g01840	−0.91	1e−16	4e−14	13 x 4	Binding to ATP, adenosine 5'−triphosphate, a universally impo
9	Vitvi07g01893	−0.88	1e−16	4e−14	15 x 40	The component of a membrane consisting of the gene produc
10	Vitvi08g01333	−1.34	1e−16	4e−14	14 x 40	The component of a membrane consisting of the gene produc
11	Vitvi08g01810	−0.47	1e−16	4e−14	13 x 12	The component of a membrane consisting of the gene produc
12	Vitvi08g02407	−0.81	1e−16	4e−14	5 x 13	
13	Vitvi09g01413	−1.65	1e−16	4e−14	33 x 1	
14	Vitvi09g02014	−1.41	1e−16	4e−14	1 x 16	
15	Vitvi10g01436	−1.12	1e−16	4e−14	16 x 13	
16	Vitvi11g00138	−0.44	1e−16	4e−14	7 x 24	A lipid bilayer along with all the proteins and protein complexe
17	Vitvi12g02153	−1.61	1e−16	4e−14	33 x 1	
18	Vitvi12g01627	−0.68	1e−16	4e−14	1 x 35	The directed movement of substances from endosomes to va
19	Vitvi13g00998	−0.64	1e−16	4e−14	15 x 36	The process whose specific outcome is the progression of the
20	Vitvi13g01028	−0.43	1e−16	4e−14	9 x 25	The contents of a cell excluding the plasma membrane and n

Differentially expressed gene sets

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	12.95	0	211	Ribosome Ribosome
2	12.57	0	80	Cytoskeleton Cytoskeleton − Microtubules
3	12.31	0	247	Translation Translation − Ribosome
4	12.16	0	219	Cell growth and death Cell growth and death − Cell cycle
5	11.73	0	144	Ribosome Ribosome − Eukaryotes
6	11.26	0	24	Replication protein Replication protein − DNA Replication Initiation Factors
7	9.39	0	217	Cell motility Cell motility − Regulation of actin cytoskeleton
8	9.27	0	36	DNA replication DNA replication
9	9.01	0	97	Ribosome Ribosome − Archaea
10	7.95	0	41	Replication and repair Replication and repair − DNA replication
11	7.51	0	34	Peptidases and inhibitors Peptidases and inhibitors − Family S10
12	5.8	0	67	Ribosome Ribosome − Bacteria
13	5.69	0	113	Exosome Exosome − Exosomal proteins of colorectal cancer cells
14	5.56	0	44	Replication protein Replication protein − DNA Replication Termination Factors
15	5.3	0	72	Ribosome Ribosome − Mitochondria/Chloroplast
16	4.95	0	66	Exosome Exosome − Exosomal proteins of bladder cancer cells
17	4.9	0	31	Biosynthesis of various plant secondary metabolites
18	4.65	0	19	Aquaporins and small neutral solute transporters [TC:1.A.8]
19	4.48	0	81	Enzyme − 4.2 Carbon−oxygen lyases
20	4.33	0	51	Other metabolism − Single reactions
Underexpressed				
1	−5.94	0e+00	73	Transcription factors − AP2 EREBP
2	−5.46	0e+00	140	Hormone signaling − Ethylene signaling
3	−4.04	0e+00	49	Transcription factors − NAC
4	−3.94	0e+00	64	Transcription factors − Other transcription factors
5	−3.9	0e+00	170	Transcription factors − Other zf−C3HC4
6	−3.88	0e+00	12	Transcription factors − Orphans zf−b box
7	−3.83	0e+00	35	Mitophagy factors
8	−3.69	2e−04	29	Carotenoid biosynthesis
9	−3.46	7e−04	26	Transcription factors − G2−like
10	−3.18	2e−03	27	Regulation of mitochondrial biogenesis
11	−3.12	3e−03	146	Transporter catalog − Porters cat 7 to 17
12	−3.09	3e−03	51	Signal transduction − Phosphatidylinositol signaling system
13	−3.02	4e−03	111	Hormone signaling − ABA signaling
14	−2.95	4e−03	92	Lipid metabolism − Glycerolipid metabolism
15	−2.92	4e−03	18	Chaperone − HSP20
16	−2.81	6e−03	151	RNA polymerase II system
17	−2.73	8e−03	31	Autophagy − other
18	−2.7	8e−03	11	Biosynthesis of secondary metabolism − ABA biosynthesis
19	−2.69	8e−03	74	Transcription factors − C2H2
20	−2.6	1e−02	20	Protein − Autophagosome formation proteins