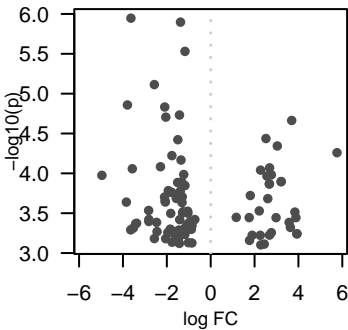
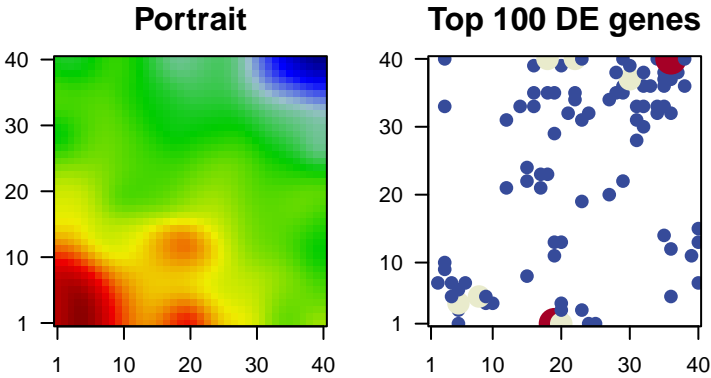


# CabFra\_freeze\_r2

## Global Summary

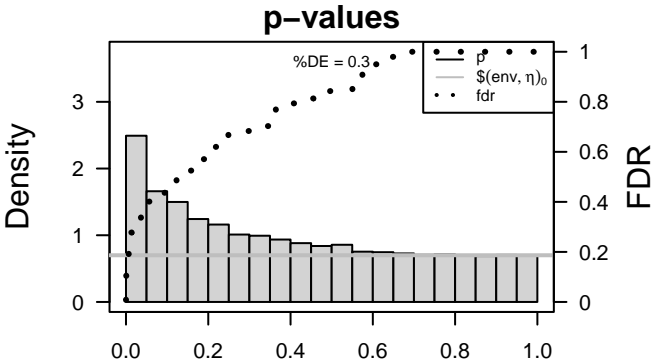
%DE = 0.3  
# genes with  $\text{fdr} < 0.2 = 524$  ( 197 + / 327 -)  
# genes with  $\text{fdr} < 0.1 = 43$  ( 14 + / 29 -)  
# genes with  $\text{fdr} < 0.05 = 8$  ( 0 + / 8 -)  
# genes with  $\text{fdr} < 0.01 = 1$  ( 0 + / 1 -)

<FC> = 0  
<p-value> = 0.23  
<fdr> = 0.7



## Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
Overexpressed						
1	Vitv06g01714	3.69	2e-05	0.07	19 x 11	
2	Vitv03g0155E	2.52	4e-05	0.07	25 x 1	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-S bonds.
3	Vitv09g0002E	3.04	5e-05	0.07	10 x 4	Binding to a nucleic acid.
4	Vitv06g01713	5.76	6e-05	0.07	5 x 1	
5	Vitv13g0125C	2.68	9e-05	0.07	20 x 1	Binding to a metal ion.
6	Vitv16g0202E	2.27	9e-05	0.07	20 x 3	
7	Vitv05g0194E	2.77	1e-04	0.07	6 x 7	
8	Vitv03g0156C	2.56	1e-04	0.07	24 x 1	
9	Vitv00g0198E	3.21	1e-04	0.07	19 x 1	
10	Vitv07g0305C	3.21	1e-04	0.07	19 x 1	
11	Vitv00g01844	2.68	1e-04	0.07	8 x 5	
12	Vitv10g0222C	2.68	1e-04	0.08	8 x 5	
13	Vitv04g0035E	1.81	2e-04	0.08	15 x 8	Any process involved in the conversion of a primary mRNA transcript into a mature mRNA.
14	Vitv08g0063C	2.6	2e-04	0.08	20 x 1	Catalysis of the transfer of ubiquitin from one protein to another.
15	Vitv16g0081E	2.21	3e-04	0.10	23 x 3	
16	Vitv04g0035E	3.84	3e-04	0.10	5 x 3	The component of a membrane consisting of the gene product of this gene.
17	Vitv06g0094C	1.17	4e-04	0.10	23 x 19	The component of a membrane consisting of the gene product of this gene.
18	Vitv02g0136E	1.76	4e-04	0.10	20 x 4	The component of a membrane consisting of the gene product of this gene.
19	Vitv16g0101C	3.89	4e-04	0.10	4 x 5	
20	Vitv13g0068C	2.98	4e-04	0.10	2 x 7	A lipid bilayer along with all the proteins and protein complexes.
Underexpressed						
1	Vitv14g01294	-3.64	1e-06	0.008	35 x 37	Binding to ATP, adenosine 5'-triphosphate, a universally important energy source.
2	Vitv02g0093E	-1.38	1e-06	0.021	21 x 32	A lipid bilayer along with all the proteins and protein complexes.
3	Vitv03g0076C	-1.17	3e-06	0.040	22 x 34	The component of a membrane consisting of the gene product of this gene.
4	Vitv12g0048C	-2.57	8e-06	0.040	30 x 39	The component of a membrane consisting of the gene product of this gene.
5	Vitv19g00581	-3.8	1e-05	0.040	3 x 40	
6	Vitv11g00287	-2.09	1e-05	0.040	30 x 37	Catalysis of the transfer of a glycosyl group from one compound to another.
7	Vitv02g00437	-1.42	2e-05	0.040	20 x 39	Binding to nicotinamide adenine dinucleotide, a coenzyme involved in energy metabolism.
8	Vitv12g00032	-2.05	2e-05	0.040	32 x 36	Binding to ATP, adenosine 5'-triphosphate, a universally important energy source.
9	Vitv19g00491	-1.5	4e-05	0.073	22 x 35	The process of restoring DNA after damage. Genomes are susceptible to damage.
10	Vitv19g0229C	-1.77	6e-05	0.073	31 x 33	
11	Vitv13g0091E	-1.35	7e-05	0.073	17 x 23	Any molecular entity that serves as an electron acceptor and is involved in energy metabolism.
12	Vitv01g0010E	-2.29	8e-05	0.073	33 x 36	Catalysis of a biochemical reaction at physiological temperature.
13	Vitv08g0116E	-3.57	9e-05	0.073	36 x 40	Catalysis of an oxidation-reduction (redox) reaction, a reversible reaction.
14	Vitv17g00361	-1.23	1e-04	0.073	29 x 22	
15	Vitv10g0010C	-4.96	1e-04	0.073	38 x 40	The space external to the outermost structure of a cell. For example, the space outside a cell.
16	Vitv08g0120E	-1.32	1e-04	0.073	18 x 23	The component of a membrane consisting of the gene product of this gene.
17	Vitv15g0070E	-1.51	1e-04	0.073	40 x 15	The component of a membrane consisting of the gene product of this gene.
18	Vitv05g0055E	-1.17	1e-04	0.082	23 x 31	A membrane-bounded organelle of eukaryotic cells in which biochemical reactions take place.
19	Vitv08g0151E	-1.93	2e-04	0.082	34 x 33	Catalysis of a biochemical reaction at physiological temperature.
20	Vitv09g0057E	-1.39	2e-04	0.082	16 x 33	Binding to a protein.



## Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	7.5	0e+00	48	Transcription factor binding site (TFBS) - WRKY
2	4.75	0e+00	162	Plant species-specific signaling pathway
3	4.43	0e+00	58	Other amino acid metabolism
4	4.4	0e+00	49	Transcription factor binding site (TFBS) - NAC
5	3.94	4e-05	77	Pore ion channels (TC:1)
6	3.73	1e-04	24	Tropane alkaloid biosynthesis
7	3.57	4e-04	51	Biosynthesis of secondary metabolites
8	3.56	5e-04	42	Tryptophan metabolism
9	3.51	6e-04	45	Galactose metabolism
10	3.37	9e-04	71	Glutathione metabolism
11	3.18	2e-03	26	Flavonoid biosynthesis
12	3.17	2e-03	26	Glycosyltransferase activity
13	3.08	2e-03	96	Transporter activity
14	2.8	6e-03	17	Isoquinoline alkaloid biosynthesis
15	2.8	6e-03	10	Linoleic acid metabolism
16	2.75	7e-03	24	Inner mitochondrial membrane
17	2.71	8e-03	57	Glyoxylate cycle
18	2.62	1e-02	80	Transporter activity
19	2.55	1e-02	10	SLC39: Metal ion transporter
20	2.5	1e-02	29	Carotenoid biosynthesis
Underexpressed				
1	-9.47	0e+00	206	Cell growth
2	-8.89	0e+00	80	Cytoskeleton
3	-8.59	0e+00	217	Cell motility
4	-6.49	0e+00	18	Photosynthesis
5	-6.1	0e+00	18	Energy metabolism
6	-5.69	0e+00	11	Transcription factor binding site (TFBS) - GRF
7	-5.41	0e+00	219	Cell growth
8	-5.38	0e+00	134	Hormone signaling
9	-5.31	0e+00	10	Peptidase activity
10	-5.07	0e+00	78	Glycosyltransferase activity
11	-4.56	0e+00	30	Glycan biosynthesis
12	-4.43	0e+00	47	Transporter activity
13	-4.36	0e+00	19	Transcription factor binding site (TFBS) - AUXIAA
14	-4.12	0e+00	65	Phagosome
15	-3.97	4e-05	39	Pentose phosphate cycle
16	-3.96	4e-05	18	Transcription factor binding site (TFBS) - ARF
17	-3.91	4e-05	113	Exosome
18	-3.81	1e-04	78	Energy metabolism
19	-3.72	1e-04	66	Exosome
20	-3.71	1e-04	19	Aquaporin

