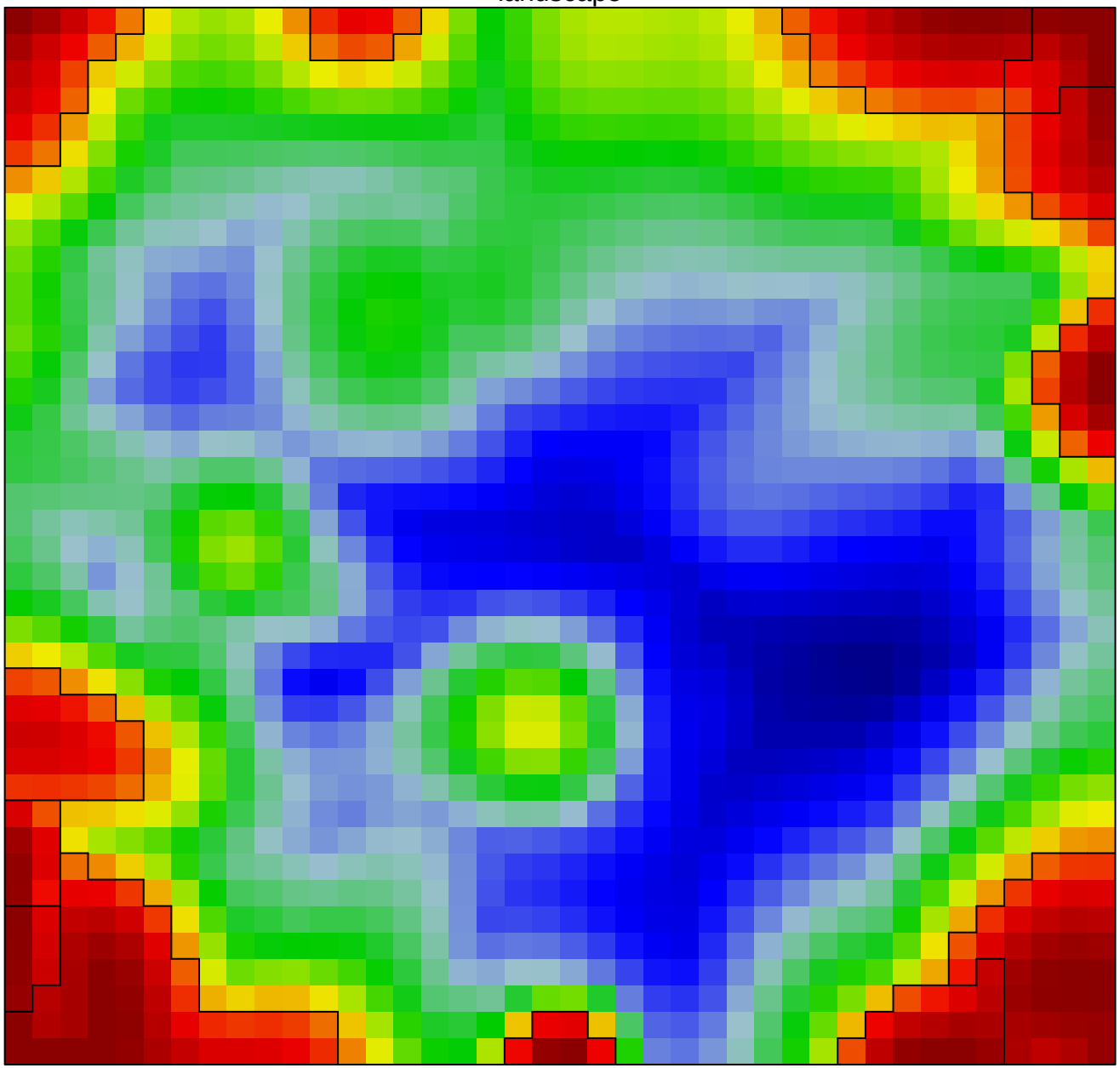
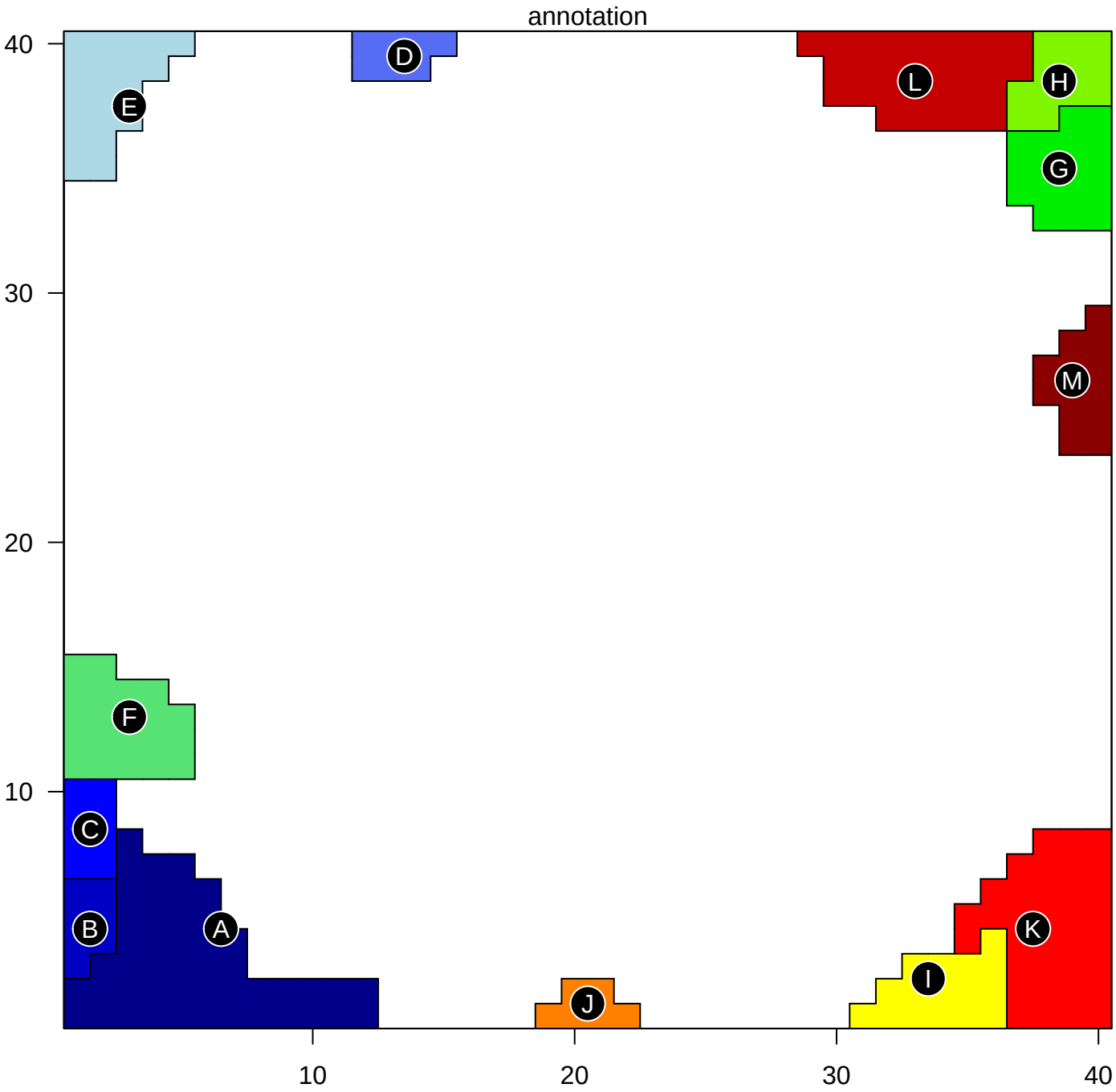
Overexpression Spots

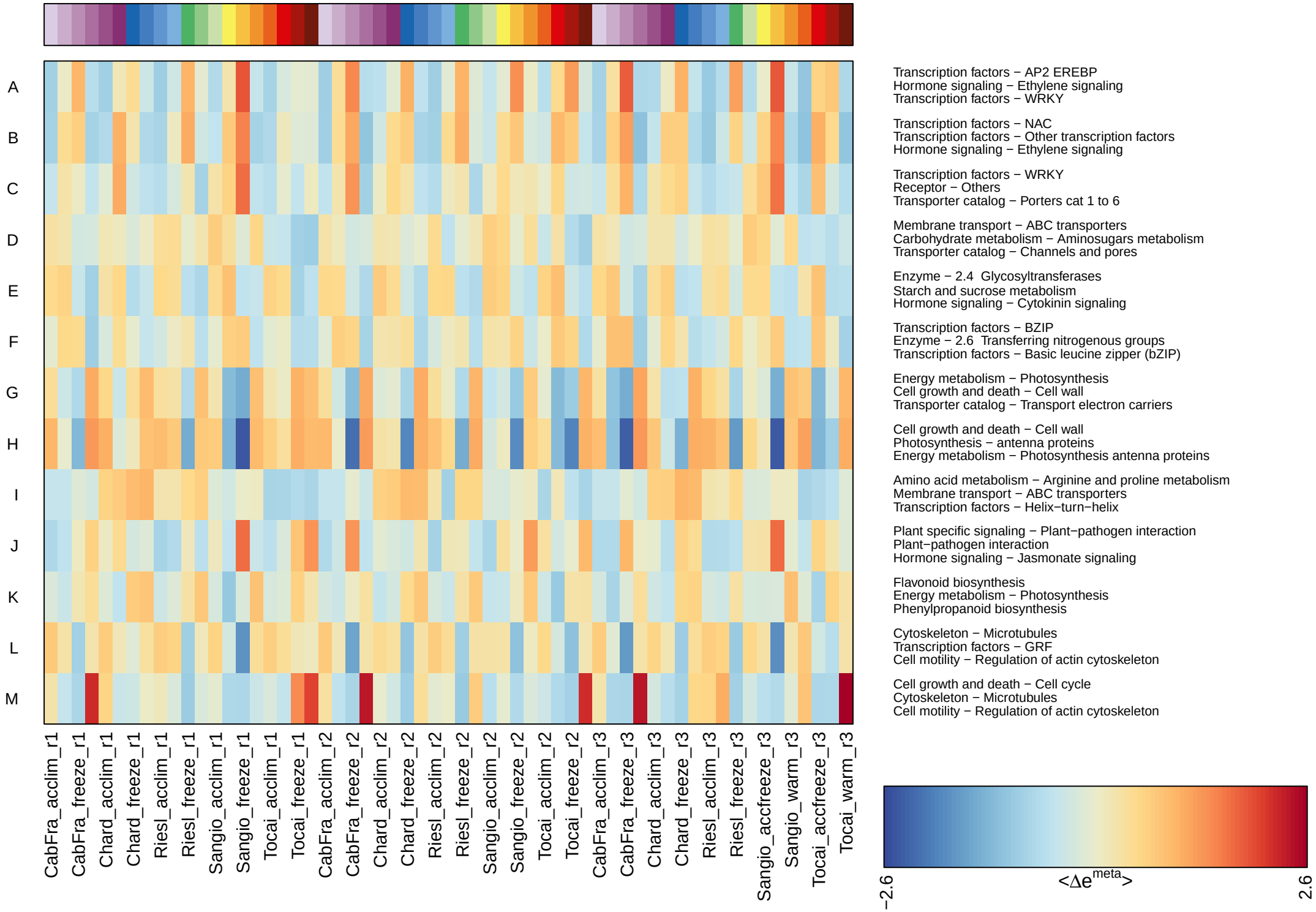
landscape



Overexpression Spots



A Transcription factors − AP2 EREBP
Hormone signaling − Ethylene signaling
Transcription factors − WRKY
B Transcription factors − NAC
Transcription factors − Other transcription factors
Hormone signaling − Ethylene signaling
C Transcription factors − WRKY
Receptor − Others
Transporter catalog − Porters cat 1 to 6
D Membrane transport − ABC transporters
Carbohydrate metabolism − Aminosugars metabolism
Transporter catalog − Channels and pores
E Enzyme − 2.4 Glycosyltransferases
Starch and sucrose metabolism
Hormone signaling − Cytokinin signaling
F Transcription factors − BZIP
Enzyme − 2.6 Transferring nitrogenous groups
Transcription factors − Basic leucine zipper (bZIP)
G Energy metabolism − Photosynthesis
Cell growth and death − Cell wall
Transporter catalog − Transport electron carriers
H Cell growth and death − Cell wall
Photosynthesis − antenna proteins
Energy metabolism − Photosynthesis antenna proteins
I Amino acid metabolism − Arginine and proline metabolism
Membrane transport − ABC transporters
Transcription factors − Helix−turn−helix
J Plant specific signaling − Plant−pathogen interaction
Plant−pathogen interaction
Hormone signaling − Jasmonate signaling
K Flavonoid biosynthesis
Energy metabolism − Photosynthesis
Phenylpropanoid biosynthesis
L Cytoskeleton − Microtubules
Transcription factors − GRF
Cell motility − Regulation of actin cytoskeleton
M Cell growth and death − Cell cycle
Cytoskeleton − Microtubules
Cell motility − Regulation of actin cytoskeleton


A
B
C
D
E
F
G
H
I
J
K
L
M
CabFra_acclim_r1
CabFra_freeze_r1
Chard_acclim_r1
Chard_freeze_r1
RiesI_acclim_r1
RiesI_freeze_r1
Sangio_acclim_r1
Sangio_freeze_r1
Tocai_acclim_r1
Tocai_freeze_r1
CabFra_acclim_r2
CabFra_freeze_r2
Chard_acclim_r2
Chard_freeze_r2
RiesI_acclim_r2
RiesI_freeze_r2
Sangio_acclim_r2
Sangio_freeze_r2
Tocai_acclim_r2
Tocai_freeze_r2
CabFra_acclim_r3
CabFra_freeze_r3
Chard_acclim_r3
Chard_freeze_r3
RiesI_acclim_r3
RiesI_freeze_r3
Sangio_accfreeze_r3
Sangio_warm_r3
Tocai_accfreeze_r3
Tocai_warm_r3
Transcription factors − AP2 EREBP
Hormone signaling − Ethylene signaling
Transcription factors − WRKY
Transcription factors − NAC
Transcription factors − Other transcription factors
Hormone signaling − Ethylene signaling
Transcription factors − WRKY
Receptor − Others
Transporter catalog − Porters cat 1 to 6
Membrane transport − ABC transporters
Carbohydrate metabolism − Aminosugars metabolism
Transporter catalog − Channels and pores
Enzyme − 2.4 Glycosyltransferases
Starch and sucrose metabolism
Hormone signaling − Cytokinin signaling
Transcription factors − BZIP
Enzyme − 2.6 Transferring nitrogenous groups
Transcription factors − Basic leucine zipper (bZIP)
Energy metabolism − Photosynthesis
Cell growth and death − Cell wall
Transporter catalog − Transport electron carriers
Cell growth and death − Cell wall
Photosynthesis − antenna proteins
Energy metabolism − Photosynthesis antenna proteins
Amino acid metabolism − Arginine and proline metabolism
Membrane transport − ABC transporters
Transcription factors − Helix−turn−helix
Plant specific signaling − Plant−pathogen interaction
Plant−pathogen interaction
Hormone signaling − Jasmonate signaling
Flavonoid biosynthesis
Energy metabolism − Photosynthesis
Phenylpropanoid biosynthesis
Cytoskeleton − Microtubules
Transcription factors − GRF
Cell motility − Regulation of actin cytoskeleton
Cell growth and death − Cell cycle
Cytoskeleton − Microtubules
Cell motility − Regulation of actin cytoskeleton
−2.6
<Δe^meta>
2.6

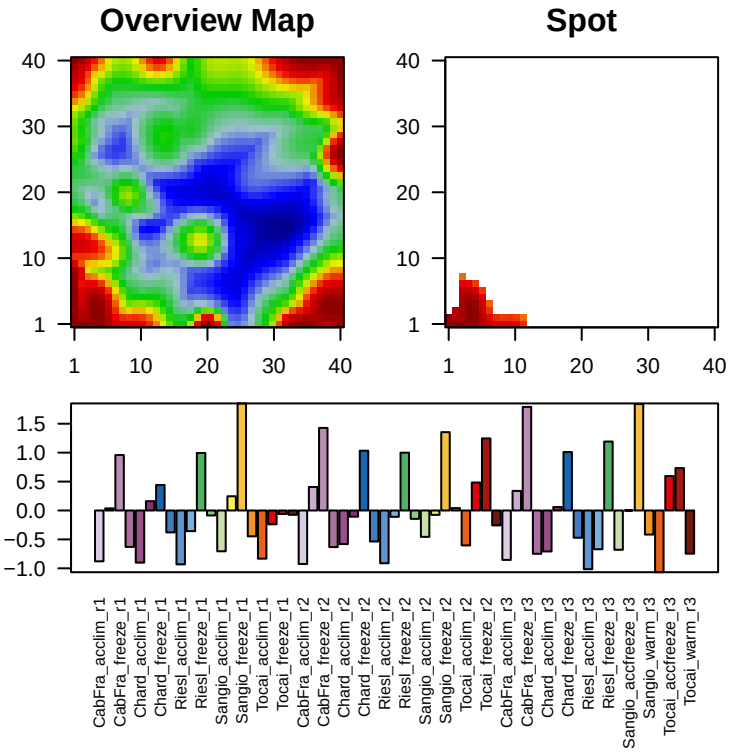
Overexpression Spots

Spot Summary: A

metagenes = 47
genes = 885

<r> metagenes = 0.92
<r> genes = 0.58
beta: r2= 32.64 / log p= −Inf

samples with spot = 13 (22 %)
CabFra_freeze : 3 (100 %)
Chard_freeze : 2 (66.7 %)
Riesl_freeze : 3 (100 %)
Sangio_freeze : 3 (100 %)
Tocai_freeze : 2 (66.7 %)

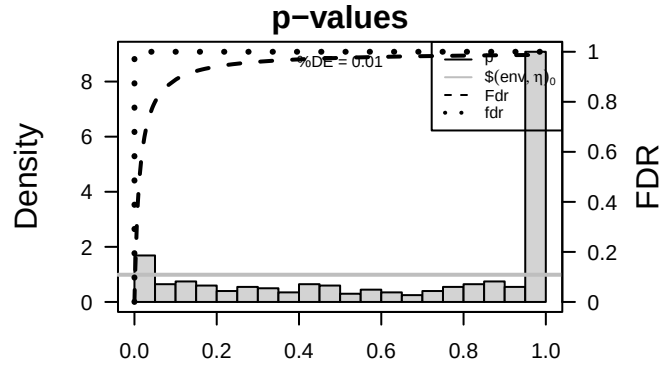


Spot Genelist

ID	Description
Vitvi06g01713	
Vitvi05g00204	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi15g00835	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi09g01554	
Vitvi05g00170	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi18g00353	Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzyme possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic.
Vitvi06g01917	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi18g03065	
Vitvi06g01280	
Vitvi02g01405	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi15g00770	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi06g00666	Binding to ATP, adenosine 5'−triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi02g01408	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi04g01907	Catalysis of the hydrolysis of various bonds, e.g. C−O, C−N, C−C, phosphoric anhydride bonds, etc.
Vitvi00g00932	
Vitvi02g01747	
Vitvi16g01321	
Vitvi15g00960	Catalysis of the transfer of an acyl group to an oxygen atom on the acceptor molecule.
Vitvi19g02038	
Vitvi05g00643	Catalysis of the hydrolysis of any ester bond.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	1e−14	24 / 73	Transcription factors − AP2 EREBP
2	2e−12	30 / 140	Hormone signaling − Ethylene signaling
3	2e−08	14 / 48	Transcription factors − WRKY
4	1e−06	14 / 64	Transcription factors − Other transcription factors
5	4e−05	10 / 45	Galactose metabolism
6	8e−05	10 / 49	Transcription factors − NAC
7	3e−04	9 / 47	ABC transporters
8	5e−04	12 / 83	Transcription factors − MYB
9	6e−04	9 / 51	Biosynthesis of secondary metabolism − Auxin biosynthesis
10	7e−04	12 / 86	Signal transduction − Calcium signaling pathway
11	8e−04	12 / 88	Electrochemical potential−driven transporters [TC:2]
12	9e−04	23 / 238	Enzyme − 2.4 Glycosyltransferases
13	1e−03	14 / 118	Transcription factors − Helix−turn−helix
14	1e−03	6 / 27	ABCG (White) subfamily
15	7e−03	5 / 26	Glycosyltransferase − Hydrophobic molecule
16	8e−03	11 / 102	Membrane transport − ABC transporters
17	1e−02	5 / 29	Carotenoid biosynthesis
18	1e−02	10 / 92	Lipid metabolism − Glycerolipid metabolism
19	1e−02	9 / 79	Transporter catalog − Porters cat 30 to 64
20	1e−02	3 / 11	Zeatin biosynthesis



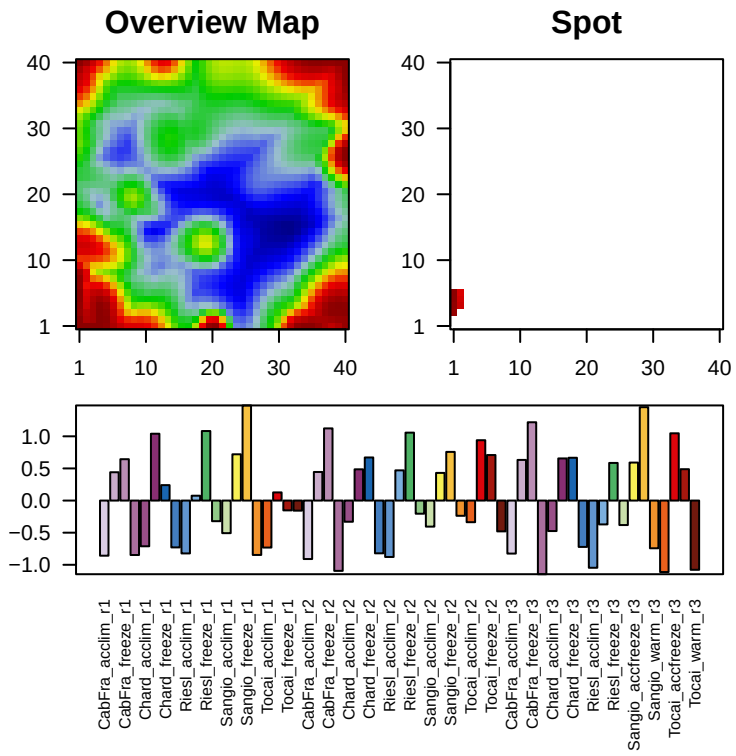
Overexpression Spots

Spot Summary: B

metagenes = 7
genes = 183

<r> metagenes = 0.99
<r> genes = 0.69
beta: r2= 35.58 / log p= −Inf

samples with spot = 11 (18.6 %)
CabFra_freeze : 2 (66.7 %)
Chard_accfreeze : 1 (33.3 %)
Riesl_freeze : 2 (66.7 %)
Sangio_accfreeze : 1 (33.3 %)
Sangio_freeze : 3 (100 %)
Tocai_accfreeze : 2 (66.7 %)

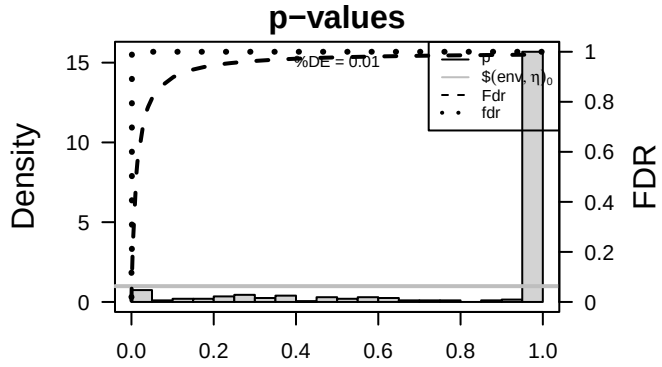


Spot Genelist

ID	Description
Vitvi08g00957	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi07g02558	Catalysis of the transfer of a glycosyl group from a UDP−sugar to a small hydrophobic molecule.
Vitvi08g00761	Binding to a ferric iron ion, Fe(III).
Vitvi05g01733	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi10g01778	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi18g02512	Binding to ATP, adenosine 5'−triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi13g00766	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g01213	Any process that modulates the frequency, rate or extent of cellular DNA−templated transcription.
Vitvi08g00764	
Vitvi16g01472	
Vitvi05g00761	Binding to ATP, adenosine 5'−triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi08g01264	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi02g01182	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi18g02513	Binding to a calcium ion (Ca2+).
Vitvi17g00395	Binding to ATP, adenosine 5'−triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi08g00763	
Vitvi17g00787	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi01g00188	
Vitvi12g02758	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi05g00482	Binding to ATP, adenosine 5'−triphosphate, a universally important coenzyme and enzyme regulator.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	1e−05	6 / 49	Transcription factors − NAC
2	6e−05	6 / 64	Transcription factors − Other transcription factors
3	8e−04	7 / 140	Hormone signaling − Ethylene signaling
4	1e−03	4 / 42	Tryptophan metabolism
5	1e−03	5 / 73	Transcription factors − AP2 EREBP
6	1e−03	7 / 153	Plant−pathogen interaction
7	2e−03	6 / 118	Transcription factors − Helix−turn−helix
8	3e−03	4 / 58	Other amino acids metabolism − Glutathione metabolism
9	1e−02	2 / 16	Transcription factors − HSF
10	1e−02	3 / 48	Transcription factors − WRKY
11	3e−02	5 / 162	Plant specific signaling − Plant−pathogen interaction
12	4e−02	2 / 29	Transcription factors − GRAS
13	4e−02	3 / 71	Glutathione metabolism
14	4e−02	4 / 121	Transporter catalog − Porters cat 18 to 29
15	5e−02	3 / 77	Pores ion channels [TC:1]
16	6e−02	3 / 83	Transcription factors − MYB
17	7e−02	3 / 89	MAPK signaling pathway − plant
18	1e−01	1 / 10	Peptidases and inhibitors − Family A1: pepsin family
19	1e−01	1 / 13	Sugar transporters
20	1e−01	1 / 14	Enzyme − 1.5 Acting on the CH−NH group of donors



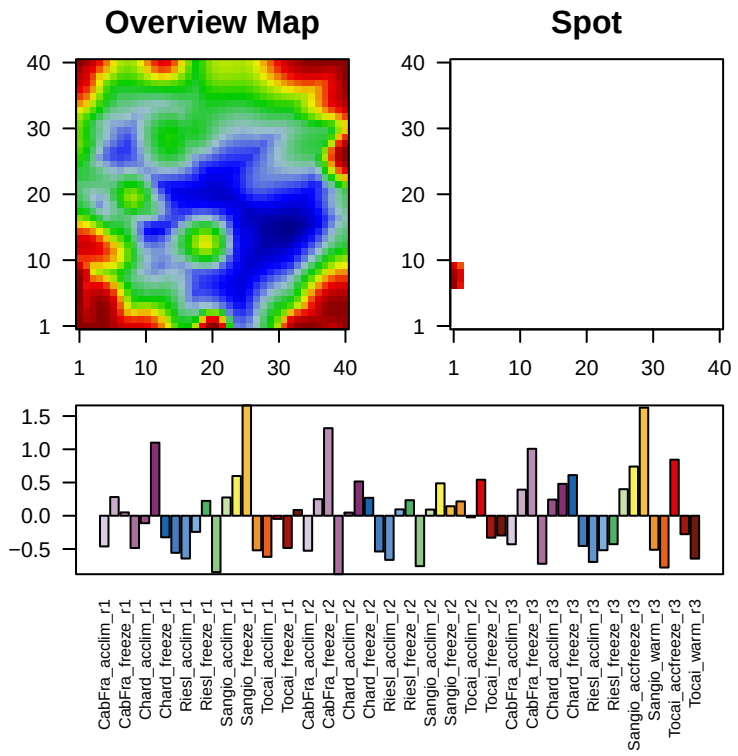
Overexpression Spots

Spot Summary: C

metagenes = 8
genes = 148

<r> metagenes = 0.99
<r> genes = 0.55
beta: r2= 18.51 / log p= −Inf

samples with spot = 7 (11.9 %)
CabFra_freeze : 2 (66.7 %)
Chard_accfreeze : 1 (33.3 %)
Sangio_accfreeze : 1 (33.3 %)
Sangio_freeze : 2 (66.7 %)
Tocai_accfreeze : 1 (33.3 %)

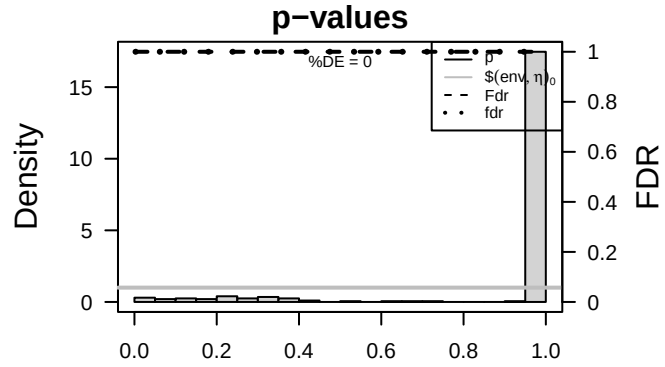


Spot Genelist

ID	Description
Vitvi16g01469	
Vitvi08g01744	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g01463	
Vitvi16g01986	
Vitvi05g01760	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi13g00680	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi16g01461	
Vitvi05g00734	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi00g02300	
Vitvi16g01475	
Vitvi16g02105	
Vitvi00g01746	
Vitvi08g02220	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi07g01791	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi06g01599	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi18g00882	Binding to a protein.
Vitvi18g01608	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi04g00760	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi01g01990	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi10g01392	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	0.002	3 / 48	Transcription factors − WRKY
2	0.005	2 / 18	Receptor − Others
3	0.017	3 / 96	Transporter catalog − Porters cat 1 to 6
4	0.021	2 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
5	0.024	2 / 43	Mitochondrial respiratory chain complex assembly factors
6	0.025	3 / 111	Transporter catalog − Porters cat 66 to 94
7	0.064	3 / 162	Plant specific signaling − Plant−pathogen interaction
8	0.075	2 / 80	Transport system − Tethering factors
9	0.081	1 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
10	0.097	2 / 93	Transcription factors − BHLH
11	0.127	1 / 24	Ubiquitin system − Ubiquitin−conjugating enzymes
12	0.127	1 / 24	Carbohydrate metabolism − Ascorbate and aldarate metabolism
13	0.132	1 / 25	Transcription factors − GNAT
14	0.137	1 / 26	Sphingolipid metabolism
15	0.146	1 / 28	Transcription factors − Basic leucine zipper (bZIP)
16	0.151	1 / 29	Carotenoid biosynthesis
17	0.180	1 / 35	Lipid metabolism − Sphingolipid metabolism
18	0.189	1 / 37	Repair protein − Check point factors
19	0.198	1 / 39	Enzyme − 1.2 Acting on the aldehyde or oxo group of donors
20	0.203	1 / 40	Energy metabolism − Methane metabolism



Overexpression Spots

Spot Summary: D

metagenes = 7
genes = 125

<r> metagenes = 0.97
<r> genes = 0.37
beta: r2= 4.52 / log p= −Inf

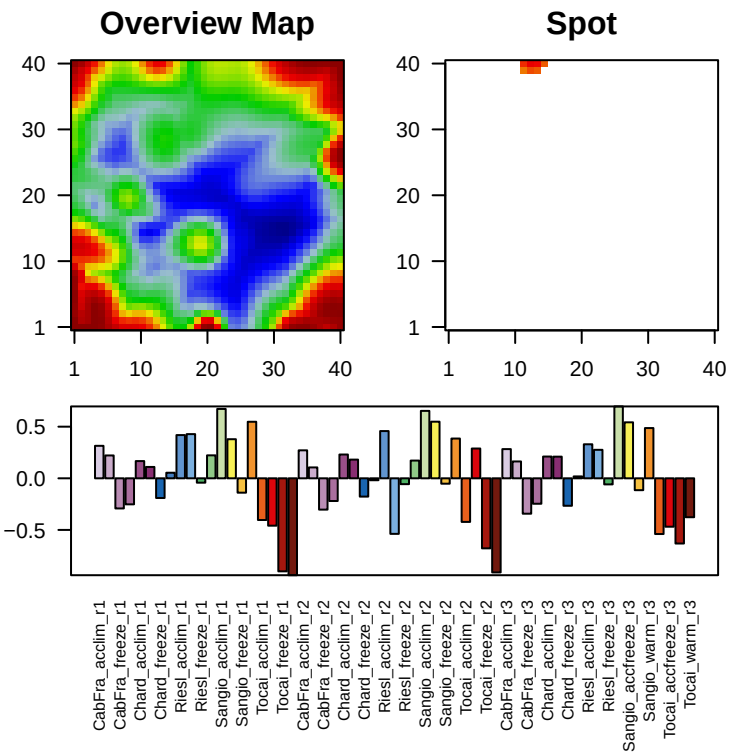
samples with spot = 0 (0 %)

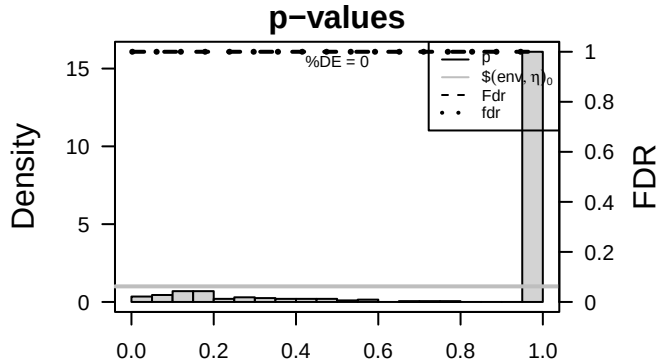
Spot Genelist

ID	Description
Vitvi13g02110	Binding to a protein.
Vitvi00g01651	
Vitvi10g02090	
Vitvi08g02122	
Vitvi05g00566	
Vitvi10g02094	
Vitvi00g01655	
Vitvi07g02092	The initial step of transcription, consisting of the assembly of the RNA polymerase preinitiation complex (PIC) at a gene promoter, as well as the formation of the first few bonds of the RNA transcript. Transcription initiation includes abortive initiation events, which occur when the first few nucleotides are repeatedly synthesized and then released, and ends when promoter clearance takes place.
Vitvi11g01488	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi04g01969	
Vitvi15g01618	Catalysis of the transfer of a nucleotidyl group to a reactant.
Vitvi03g01162	Catalysis of the transfer of a glycosyl group from a UDP−sugar to a small hydrophobic molecule.
Vitvi04g00726	
Vitvi07g01734	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi10g01696	Binding to a calcium ion (Ca2+).
Vitvi18g01643	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi16g01541	
Vitvi06g00547	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi01g00088	Binding to ADP, adenosine 5'−diphosphate.
Vitvi03g01185	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	0.002	4 / 102	Membrane transport − ABC transporters
2	0.012	2 / 33	Carbohydrate metabolism − Aminosugars metabolism
3	0.018	4 / 197	Transporter catalog − Channels and pores
4	0.019	3 / 111	Transporter catalog − Porters cat 66 to 94
5	0.021	2 / 44	Enzyme − 1.11 Acting on a peroxide as acceptor
6	0.045	2 / 67	Amino acid metabolism − Tyrosine metabolism
7	0.049	1 / 10	Protein − Syntaxin (Qa)
8	0.050	2 / 71	Amino acid metabolism − Phenylalanine metabolism
9	0.054	1 / 11	Zeatin biosynthesis
10	0.059	1 / 12	Channel − Cyclic nucleotide−gated channel (CNG)
11	0.059	1 / 12	Enzyme − Class I
12	0.059	1 / 12	SLC15: Proton oligopeptide cotransporter
13	0.063	2 / 81	Translation − mRNA surveillance pathway
14	0.068	1 / 14	Proteins involved in snRNP biogenesis
15	0.083	1 / 17	Isoquinoline alkaloid biosynthesis
16	0.092	2 / 101	Starch and sucrose metabolism
17	0.101	1 / 21	Thiamine metabolism
18	0.115	1 / 24	Tropane piperidine and pyridine alkaloid biosynthesis
19	0.115	1 / 24	Enzyme − 7.1 Catalysing the translocation of hydrons
20	0.119	1 / 25	Nitrogen metabolism





Overexpression Spots

Spot Summary: E

metagenes = 19
genes = 406

<r> metagenes = 0.97
<r> genes = 0.59
beta: r2= 13.79 / log p= −Inf

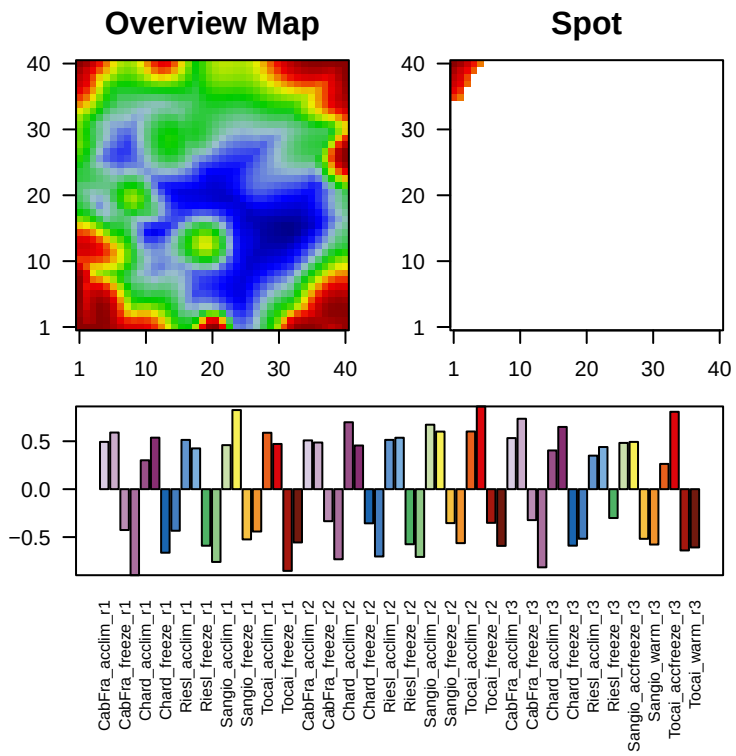
samples with spot = 4 (6.8 %)
CabFra_accfreeze : 1 (33.3 %)
Sangio_accfreeze : 1 (33.3 %)
Tocai_accfreeze : 2 (66.7 %)

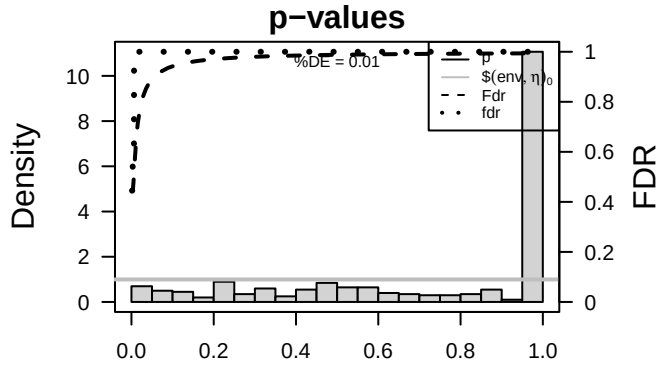
Spot Genelist

ID	Description
Vitvi04g01368	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi18g00087	
Vitvi16g00733	Binds to and stops, prevents or reduces the activity of an enzyme.
Vitvi12g02353	
Vitvi19g00255	
Vitvi10g00647	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi14g01469	A chlorophyll−containing plastid with thylakoids organized into grana and frets, or stroma thylakoids, and embedded in a stroma.
Vitvi18g00122	The process whose specific outcome is the progression of the root over time, from its formation to the mature structure. The root is the water− and mineral−absorbing part of a plant which is usually underground, does not bear leaves, tends to grow downwards and is typically derived from the radicle of the embryo.
Vitvi05g00071	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi10g00649	
Vitvi18g00946	Any process that stops, prevents, or reduces the frequency, rate or extent of cellular DNA−templated transcription.
Vitvi05g01758	
Vitvi17g00237	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi06g01696	Binding to a metal ion.
Vitvi17g00914	
Vitvi16g01161	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g00985	Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a cold stimulus, a temperature stimulus below the optimal temperature for that organism.
Vitvi05g01453	Binding to a protein.
Vitvi04g01564	
Vitvi17g00116	Modulates the activity of a protein kinase, an enzyme which phosphorylates a protein.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	0.001	14 / 238	Enzyme − 2.4 Glycosyltransferases
2	0.002	8 / 101	Starch and sucrose metabolism
3	0.003	5 / 44	Hormone signaling − Cytokinin signaling
4	0.006	4 / 32	Circadian rhythm − plant
5	0.006	5 / 51	Plant specific signaling − Circadian rhythm
6	0.008	4 / 34	Tyrosine metabolism
7	0.012	3 / 21	Thiamine metabolism
8	0.015	10 / 195	Carbohydrate metabolism − Starch and sucrose metabolism
9	0.021	2 / 10	Transcription factors − C2C2−CO
10	0.026	2 / 11	Zeatin biosynthesis
11	0.029	6 / 100	Plant specific signaling − Flower development
12	0.035	2 / 13	Transcription factors − HMG
13	0.036	4 / 54	Carbohydrate metabolism − Inositol phosphate metabolism
14	0.042	6 / 110	Ubiquitin system − Multi subunit Ring−finger type E3
15	0.053	5 / 88	Electrochemical potential−driven transporters [TC:2]
16	0.053	3 / 37	Basal transcription factors
17	0.056	6 / 118	Transcription factors − Helix−turn−helix
18	0.057	3 / 38	Transcription − Basal transcription factors
19	0.058	2 / 17	Kinase − IRAK family
20	0.061	4 / 64	Transcription factors − Other transcription factors





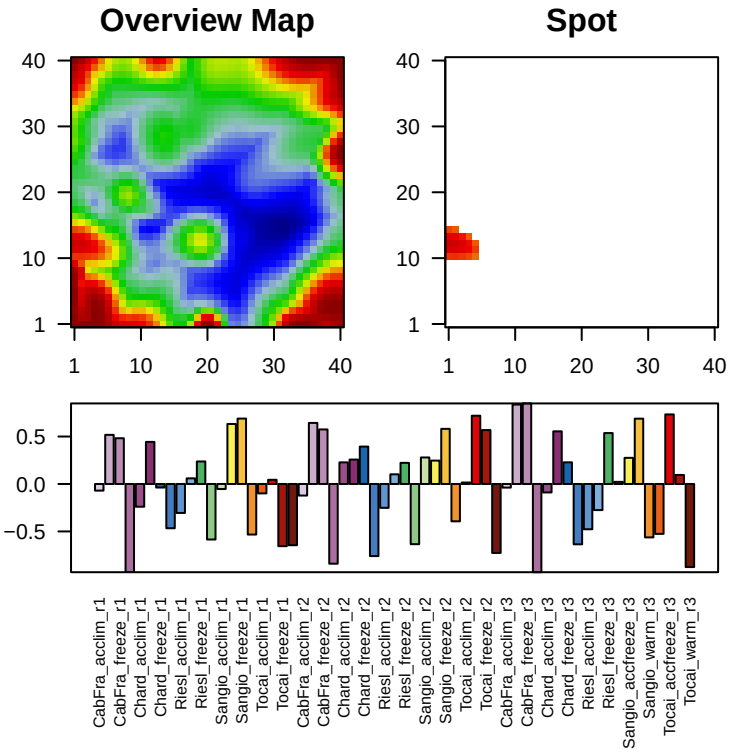
Overexpression Spots

Spot Summary: F

metagenes = 21
genes = 354

<r> metagenes = 0.97
<r> genes = 0.57
beta: r2= 11.72 / log p= −Inf

samples with spot = 4 (6.8 %)
CabFra_accfreeze : 1 (33.3 %)
CabFra_freeze : 1 (33.3 %)
Tocai_accfreeze : 2 (66.7 %)

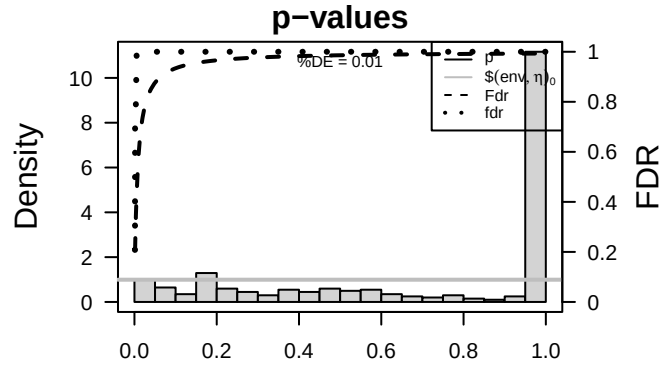


Spot Genelist

ID	Description
Vitvi16g01022	Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an abscisic acid stimulus.
Vitvi14g01808	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi08g01587	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi05g01833	Binding to a metal ion.
Vitvi18g00480	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi13g01904	
Vitvi14g02476	
Vitvi18g02398	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi06g01601	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi13g01623	Binding to ADP, adenosine 5'−diphosphate.
Vitvi05g00342	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi06g01462	The directed movement of malate into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore.
Vitvi16g01642	
Vitvi02g00719	Binding to a protein.
Vitvi17g00175	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00271	Any molecular function by which a gene product interacts selectively and non−covalently with DNA (deoxyribonucleic acid).
Vitvi08g00107	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi03g01703	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi19g00565	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi04g02075	Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an auxin stimulus.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	0.001	5 / 43	Transcription factors − BZIP
2	0.001	4 / 27	Enzyme − 2.6 Transferring nitrogenous groups
3	0.002	4 / 28	Transcription factors − Basic leucine zipper (bZIP)
4	0.003	5 / 56	Glycine serine and threonine metabolism
5	0.005	6 / 88	Electrochemical potential−driven transporters [TC:2]
6	0.009	4 / 45	Valine leucine and isoleucine degradation
7	0.010	3 / 25	Lysine degradation
8	0.010	3 / 25	Biosynthesis of secondary metabolism − Zeatin biosynthesis
9	0.013	2 / 10	Kinase − Wnk family
10	0.016	6 / 111	Hormone signaling − ABA signaling
11	0.016	6 / 111	Transporter catalog − Porters cat 66 to 94
12	0.018	7 / 146	Transporter catalog − Porters cat 7 to 17
13	0.018	4 / 55	Glycerolipid metabolism
14	0.019	2 / 12	Transcription factors − Orphans zf−b box
15	0.020	4 / 57	Glyoxylate and dicarboxylate metabolism
16	0.024	3 / 34	Tyrosine metabolism
17	0.038	2 / 17	Isoquinoline alkaloid biosynthesis
18	0.038	3 / 41	Arginine and proline metabolism
19	0.041	3 / 42	Tryptophan metabolism
20	0.048	3 / 45	Galactose metabolism



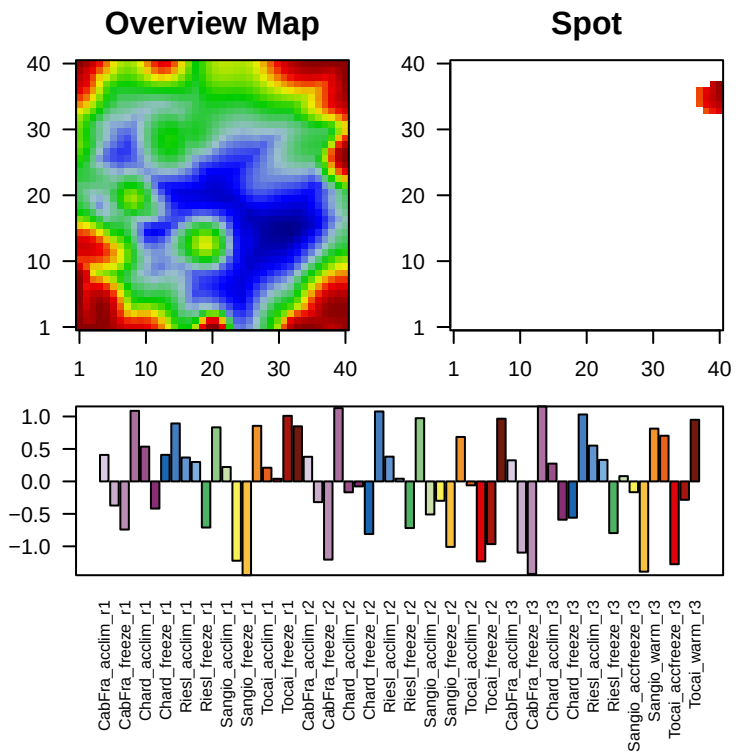
Overexpression Spots

Spot Summary: G

metagenes = 17
genes = 252

<r> metagenes = 0.99
<r> genes = 0.72
beta: r2= 30.63 / log p= −Inf

samples with spot = 14 (23.7 %)
CabFra_warm : 3 (100 %)
Chard_warm : 3 (100 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 2 (66.7 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 3 (100 %)

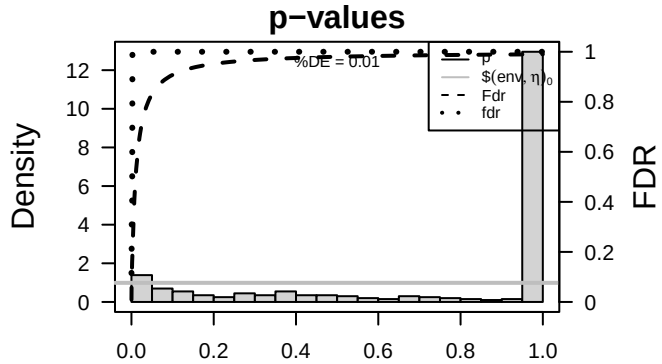


Spot Genelist

ID	Description
Vitvi09g01282	Functions in the storage of nutritious substrates.
Vitvi19g02024	
Vitvi17g00977	Binding to a metal ion.
Vitvi13g01788	
Vitvi01g00441	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi02g00236	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi13g02008	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi06g01410	
Vitvi03g01503	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi03g01500	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi01g00747	
Vitvi03g00227	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi03g00134	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi03g00124	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite. The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non−living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.
Vitvi13g01555	
Vitvi15g00804	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi02g00125	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi03g01621	Catalysis of the transfer of an acyl group, other than amino−acyl, from one compound (donor) to another (acceptor).
Vitvi13g02416	Binding to a calcium ion (Ca2+).
Vitvi11g01437	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	2e−05	8 / 78	Energy metabolism − Photosynthesis
2	3e−04	11 / 206	Cell growth and death − Cell wall
3	7e−04	5 / 47	Transporter catalog − Transport electron carriers
4	2e−03	4 / 34	Peptidases and inhibitors − Family S10
5	2e−03	3 / 18	Energy metabolism − Photosynthesis antenna proteins
6	3e−03	4 / 38	Photosynthesis
7	3e−03	5 / 63	Phenylpropanoid biosynthesis
8	3e−03	4 / 40	Transport system − Thylakoid targeting pathway
9	7e−03	3 / 26	Flavonoid biosynthesis
10	7e−03	5 / 80	Cytoskeleton − Microtubules
11	1e−02	2 / 10	Photosynthesis protein − Photosystem I (P700 chlorophyll a)
12	1e−02	3 / 30	Glycan biosynthesis and metabolism − N−Glycan degradation
13	1e−02	2 / 11	Enzyme − 4.3 Carbon−nitrogen lyases
14	1e−02	4 / 58	Carbohydrate metabolism − Fructose and mannose metabolism
15	2e−02	8 / 217	Cell motility − Regulation of actin cytoskeleton
16	2e−02	5 / 102	Amino sugar and nucleotide sugar metabolism
17	2e−02	2 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
18	2e−02	3 / 41	Porphyrin metabolism
19	3e−02	3 / 44	Fructose and mannose metabolism
20	3e−02	3 / 44	Energy metabolism − Nitrogen metabolism



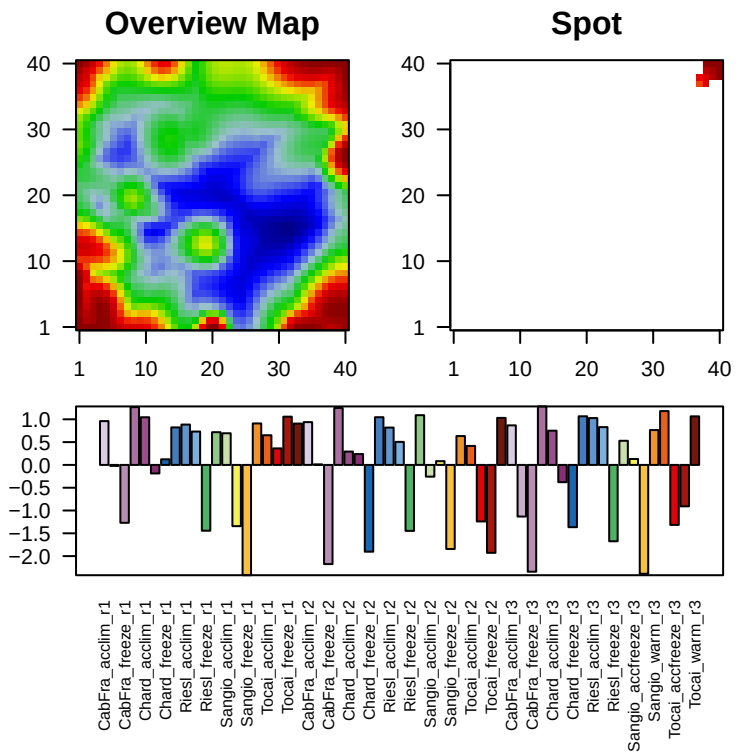
Overexpression Spots

Spot Summary: H

metagenes = 12
genes = 284

<r> metagenes = 1
<r> genes = 0.81
beta: r2= 57.14 / log p= −Inf

samples with spot = 25 (42.4 %)
CabFra_acclim : 3 (100 %)
CabFra_warm : 3 (100 %)
Chard_acclim : 2 (66.7 %)
Chard_warm : 3 (100 %)
Riesl_acclim : 3 (100 %)
Riesl_accfreeze : 2 (66.7 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 2 (66.7 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)

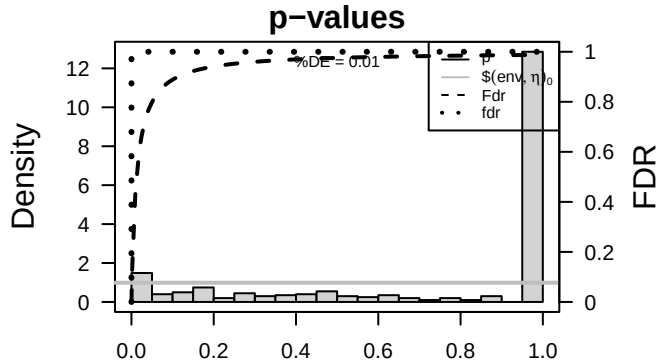


Spot Genelist

ID	Description
Vitvi14g01929	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi13g00172	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi17g01251	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi13g01337	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a mechanism in which a water molecule bound by the side chains of aspartic residues at the active center acts as a nucleophile.
Vitvi06g01346	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00680	Binding to a metal ion.
Vitvi10g01636	
Vitvi17g00601	
Vitvi00g02243	
Vitvi01g00816	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi07g01844	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00008	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi01g00593	Binding to a metal ion.
Vitvi12g02394	
Vitvi14g03084	
Vitvi01g01030	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi05g00067	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi10g01035	Binding to a lipid.
Vitvi12g00342	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi18g00510	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a mechanism in which a water molecule bound by the side chains of aspartic residues at the active center acts as a nucleophile.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	2e−14	25 / 206	Cell growth and death − Cell wall
2	6e−12	9 / 18	Photosynthesis − antenna proteins
3	6e−12	9 / 18	Energy metabolism − Photosynthesis antenna proteins
4	2e−11	12 / 47	Transporter catalog − Transport electron carriers
5	2e−05	4 / 10	Photosynthesis protein − Photosystem I (P700 chlorophyll a)
6	5e−05	6 / 38	Photosynthesis
7	5e−05	6 / 39	Pentose and glucuronate interconversions
8	9e−05	10 / 129	Enzyme − 3.2 Glycosylases
9	3e−04	4 / 19	Aquaporins and small neutral solute transporters [TC:1.A.8]
10	4e−04	7 / 78	Energy metabolism − Photosynthesis
11	6e−04	3 / 10	Peptidases and inhibitors − Family A1: pepsin family
12	6e−04	9 / 134	Hormone signaling − Auxin signaling
13	6e−04	5 / 40	Transport system − Thylakoid targeting pathway
14	7e−04	5 / 41	Porphyrin metabolism
15	1e−03	3 / 13	Cutin suberine and wax biosynthesis
16	2e−03	4 / 30	Glycan biosynthesis and metabolism − N−Glycan degradation
17	2e−03	6 / 77	Carbohydrate metabolism − Galactose metabolism
18	9e−03	4 / 47	ABC transporters
19	1e−02	3 / 26	Steroid biosynthesis
20	1e−02	4 / 49	Enzyme − 1.3 Acting on the CH−CH group of donors



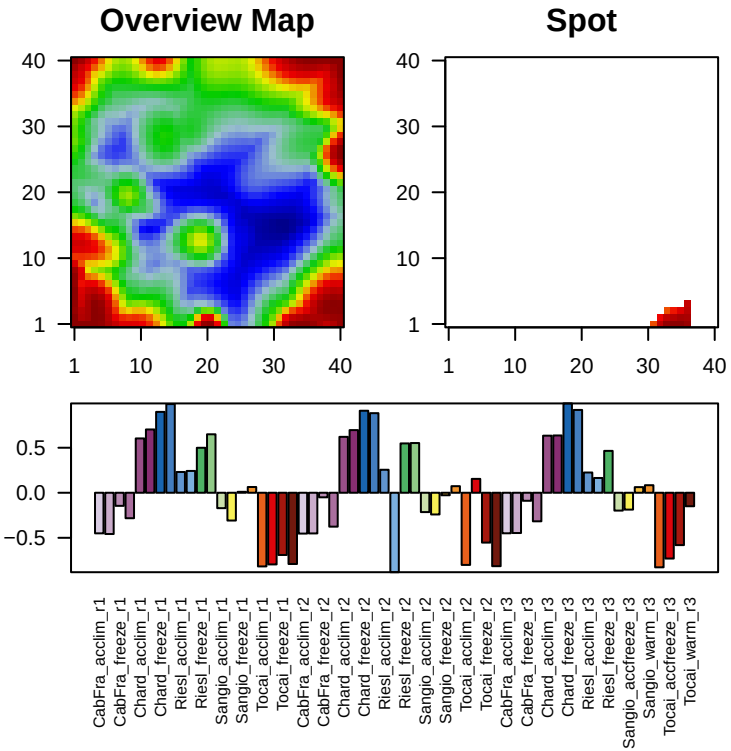
Overexpression Spots

Spot Summary: I

metagenes = 16
genes = 215

<r> metagenes = 0.91
<r> genes = 0.38
beta: r2= 9.96 / log p= −Inf

samples with spot = 6 (10.2 %)
Chard_freeze : 3 (100 %)
Chard_warm : 3 (100 %)

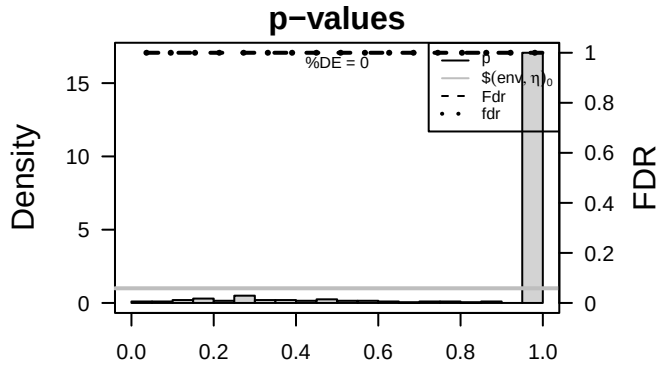


Spot Genelist

ID	Description
Vitvi12g02565	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi09g02008	An intracellular non−membrane−bounded organelle comprising a matrix of coalesced lipids surrounded by a phospholipid monolayer. May include associated proteins.
Vitvi04g01863	
Vitvi11g01446	Any molecular entity that serves as an electron acceptor and electron donor in an electron transport chain. An electron transport chain is a process in which a series of electron carriers operate together to transfer electrons from donors to any of several different terminal electron acceptors to generate a transmembrane electrochemical gradient.
Vitvi11g01457	Binding to a protein.
Vitvi10g01863	
Vitvi10g01433	
Vitvi17g00339	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi08g01434	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi10g00378	
Vitvi19g01989	
Vitvi19g01990	
Vitvi01g00319	Catalysis of an oxidation−reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi07g01624	The irregular network of unit membranes, visible only by electron microscopy, that occurs in the cytoplasm of many eukaryotic cells. The membranes form a complex meshwork of tubular channels, which are often expanded into slitlike cavities called cisternae. The ER takes two forms, rough (or granular), with ribosomes adhering to the outer surface, and smooth (with no ribosomes attached).
Vitvi19g01988	
Vitvi12g02324	Binding to a protein.
Vitvi18g02715	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi12g00462	
Vitvi19g01058	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi02g01110	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	0.04	2 / 38	Amino acid metabolism − Arginine and proline metabolism
2	0.05	3 / 102	Membrane transport − ABC transporters
3	0.07	3 / 118	Transcription factors − Helix−turn−helix
4	0.10	2 / 67	Amino acid metabolism − Tyrosine metabolism
5	0.12	2 / 75	Translation − Ribosome biogenesis in Eukaryotes
6	0.12	1 / 16	Transcription factors − HSF
7	0.13	2 / 78	Energy metabolism − Photosynthesis
8	0.14	1 / 19	Cofactors and vitamin metabolism − Ubiquinone biosynthesis
9	0.17	1 / 24	Enzyme − 7.1 Catalysing the translocation of hydrons
10	0.19	1 / 26	Steroid biosynthesis
11	0.19	1 / 26	Glycosyltransferase − Hydrophobic molecule
12	0.19	1 / 26	Transcription factors − Orphans FAR−RED
13	0.19	1 / 27	ABCG (White) subfamily
14	0.20	1 / 28	Exosome − Exosomal proteins of breast milk
15	0.23	1 / 33	Enzyme − 5.4 Intramolecular transferases
16	0.24	1 / 35	Lipid metabolism − Alpha−linolenic acid metabolism
17	0.25	2 / 121	Transporter catalog − Porters cat 18 to 29
18	0.25	3 / 219	Cell growth and death − Cell cycle
19	0.26	1 / 38	Photosynthesis
20	0.27	1 / 39	Other amino acids metabolism − Selenoamino acid metabolism



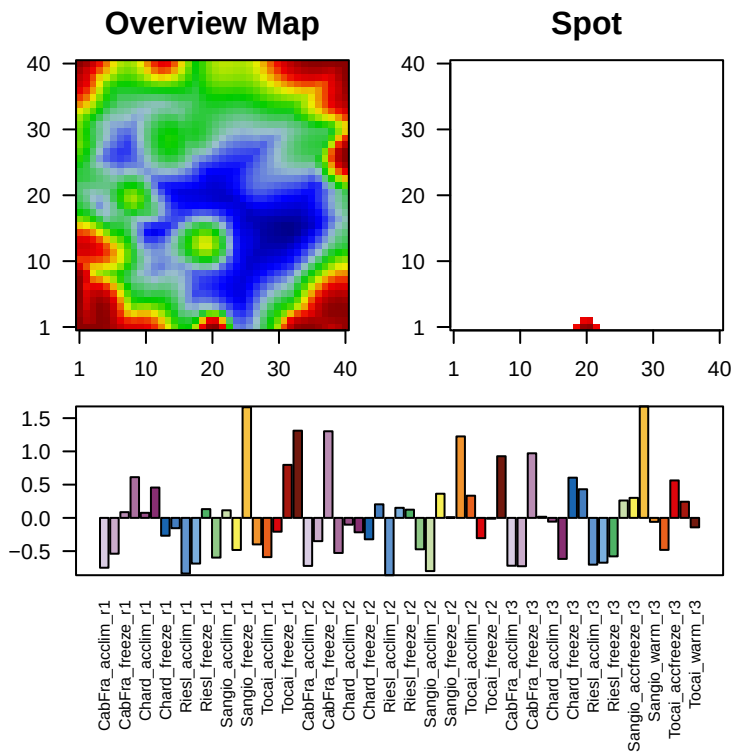
Overexpression Spots

Spot Summary: J

metagenes = 6
genes = 207

<r> metagenes = 0.99
<r> genes = 0.51
beta: r2= 11.45 / log p= −Inf

samples with spot = 8 (13.6 %)
CabFra_freeze : 2 (66.7 %)
Sangio_freeze : 2 (66.7 %)
Sangio_warm : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 2 (66.7 %)

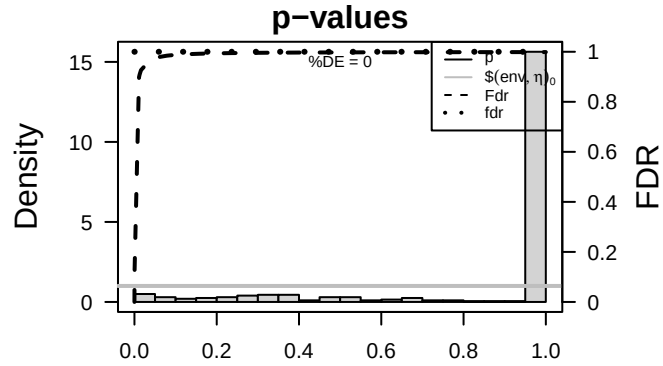


Spot Genelist

ID	Description
Vitvi18g02709	Any molecular entity that serves as an electron acceptor and electron donor in an electron transport chain. An electron transport chain is a process in which a series of electron carriers operate together to transfer electrons from donors to any of several different terminal electron acceptors to generate a transmembrane electrochemical gradient.
Vitvi02g00393	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi16g01336	Binding to a metal ion.
Vitvi18g03250	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g00253	
Vitvi15g00871	Catalysis of an oxidation−reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi12g02245	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi02g00270	Binding to a metal ion.
Vitvi15g01035	
Vitvi06g01559	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi03g01651	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi08g01702	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi07g02676	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi12g02241	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi00g01989	
Vitvi07g03053	
Vitvi17g00450	The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non−living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.
Vitvi07g02243	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi09g01557	
Vitvi02g01403	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	2e−09	14 / 162	Plant specific signaling − Plant−pathogen interaction
2	6e−06	10 / 153	Plant−pathogen interaction
3	3e−05	6 / 56	Hormone signaling − Jasmonate signaling
4	2e−04	5 / 48	Transcription factors − WRKY
5	1e−02	2 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
6	1e−02	4 / 83	Transcription factors − MYB
7	2e−02	4 / 89	MAPK signaling pathway − plant
8	4e−02	4 / 118	Transcription factors − Helix−turn−helix
9	5e−02	2 / 33	alpha−Linolenic acid metabolism
10	5e−02	2 / 33	Carbohydrate metabolism − Aminosugars metabolism
11	5e−02	3 / 77	Pores ion channels [TC:1]
12	5e−02	4 / 129	Enzyme − 3.2 Glycosylases
13	5e−02	2 / 35	Lipid metabolism − Alpha−linolenic acid metabolism
14	8e−02	2 / 43	Alanine aspartate and glutamate metabolism
15	9e−02	3 / 96	Transporter catalog − Porters cat 1 to 6
16	9e−02	2 / 46	Amino acid metabolism − Glutamate metabolism
17	1e−01	1 / 10	Linoleic acid metabolism
18	1e−01	1 / 10	SLC39: Metal ion transporter
19	1e−01	4 / 168	Plant hormone signal transduction
20	1e−01	1 / 13	Sugar transporters



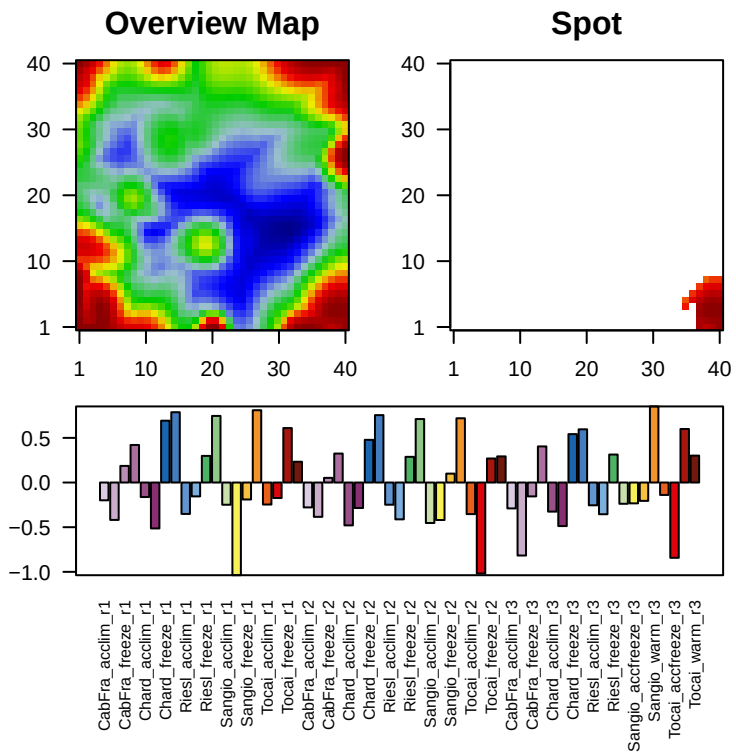
Overexpression Spots

Spot Summary: K

metagenes = 35
genes = 505

<r> metagenes = 0.92
<r> genes = 0.5
beta: r2= 11.37 / log p= −Inf

samples with spot = 7 (11.9 %)
Chard_warm : 2 (66.7 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 3 (100 %)

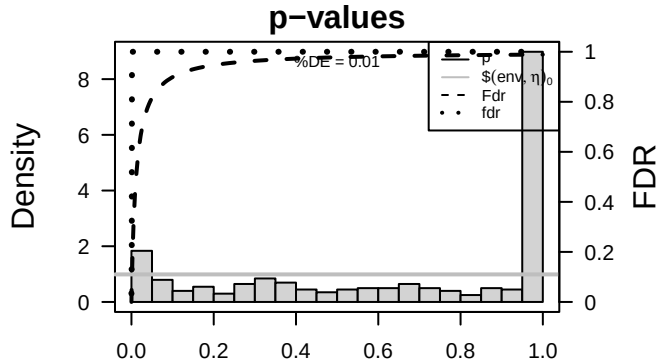


Spot Genelist

ID	Description
Vitvi03g00325	A transcription regulator activity that modulates transcription of gene sets via selective and non−covalent binding to a specific double−stranded genomic DNA sequence (sometimes referred to as a motif) within a cis−regulatory region. Regulatory regions include promoters (proximal and distal) and enhancers. Genes are transcriptional units, and include bacterial operons.
Vitvi13g00369	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi13g02005	Catalysis of the hydrolysis of internal, alpha−peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi00g00346	
Vitvi07g02904	
Vitvi02g01118	Catalysis of the transfer of an acyl group, other than amino−acyl, from one compound (donor) to another (acceptor).
Vitvi01g01981	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi13g00870	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi11g01421	
Vitvi10g00020	Catalysis of an oxidation−reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi16g00731	
Vitvi02g00110	Catalysis of the transfer of a glycosyl group from a UDP−sugar to a small hydrophobic molecule.
Vitvi05g02017	
Vitvi15g01070	Catalysis of an oxidation−reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi01g01980	
Vitvi12g02451	Catalysis of the transfer of a group, e.g. a methyl group, glycosyl group, acyl group, phosphorus−containing, or other groups, from one compound (generally regarded as the donor) to another compound (generally regarded as the acceptor). Transferase is the systematic name for any enzyme of EC class 2.
Vitvi05g01116	Catalysis of the transfer of an acyl group, other than amino−acyl, from one compound (donor) to another (acceptor).
Vitvi11g01303	Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzyme possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic.
Vitvi05g02019	
Vitvi14g00930	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	3e−08	9 / 26	Flavonoid biosynthesis
2	8e−05	10 / 78	Energy metabolism − Photosynthesis
3	5e−04	8 / 63	Phenylpropanoid biosynthesis
4	7e−04	6 / 38	Photosynthesis
5	1e−03	7 / 57	Glyoxylate and dicarboxylate metabolism
6	1e−03	10 / 111	Transporter catalog − Porters cat 66 to 94
7	3e−03	3 / 10	Linoleic acid metabolism
8	3e−03	3 / 11	Enzyme − 2.2 Transferring aldehyde or ketonic groups
9	3e−03	6 / 51	Carbon fixation in photosynthetic organisms
10	5e−03	5 / 38	Enzyme − 1.8 Acting on a sulfur group of donors
11	5e−03	4 / 24	Tropane piperidine and pyridine alkaloid biosynthesis
12	6e−03	4 / 25	Nitrogen metabolism
13	6e−03	5 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
14	6e−03	5 / 40	Energy metabolism − Methane metabolism
15	9e−03	3 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
16	9e−03	5 / 44	Energy metabolism − Nitrogen metabolism
17	1e−02	8 / 102	Membrane transport − ABC transporters
18	1e−02	7 / 83	Transcription factors − MYB
19	1e−02	4 / 30	Ubiquinone and other terpenoid−quinone biosynthesis
20	1e−02	5 / 47	ABC transporters



Overexpression Spots

Spot Summary: L

metagenes = 29
genes = 521

<r> metagenes = 0.98
<r> genes = 0.69
beta: r2= 25.26 / log p= −Inf

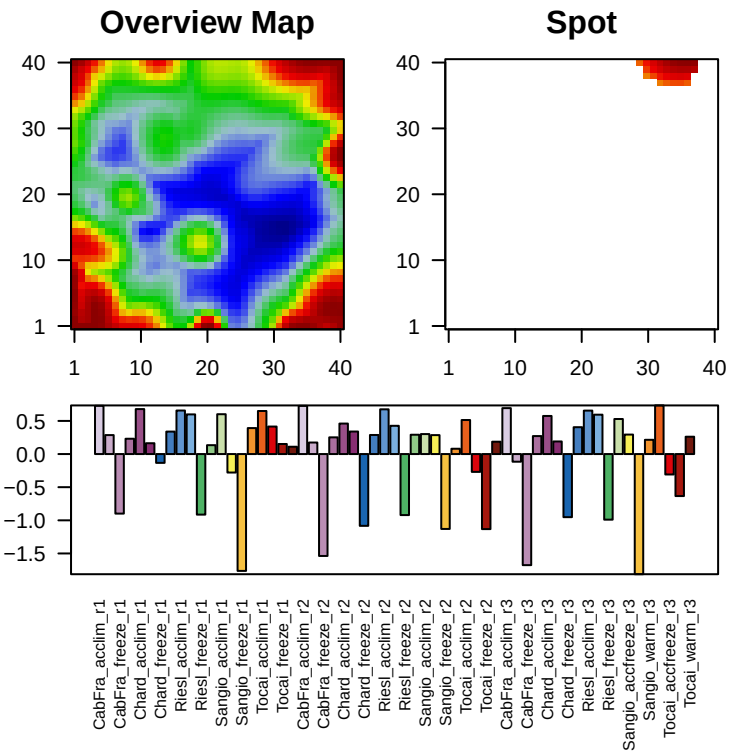
samples with spot = 3 (5.1 %)
CabFra_acclim : 2 (66.7 %)
Tocai_acclim : 1 (33.3 %)

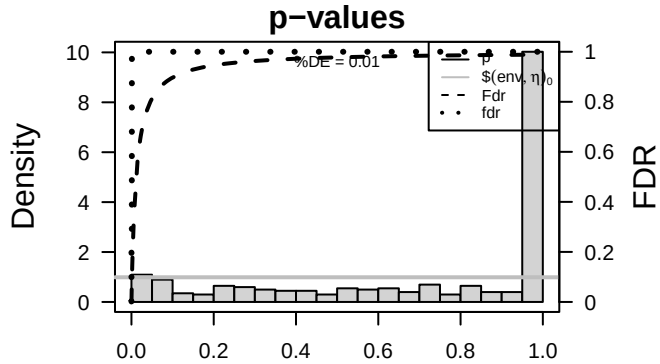
Spot Genelist

ID	Description
Vitvi02g00532	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi02g01239	
Vitvi02g01355	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi04g01873	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi15g01388	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g01176	
Vitvi18g02045	
Vitvi14g03036	Binding to a zinc ion (Zn).
Vitvi09g00593	Any molecular function by which a gene product interacts selectively and non−covalently with DNA (deoxyribonucleic acid).
Vitvi18g03009	
Vitvi10g00027	The chemical reactions and pathways resulting in the formation of thiamine (vitamin B1), a water soluble vitamin present in fresh vegetables and meats, especially liver.
Vitvi10g01138	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi18g00473	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi03g00860	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi05g01934	
Vitvi14g01641	The formation of the principal food−conducting tissue of a vascular plant.
Vitvi17g00750	
Vitvi11g00016	Binds to and stops, prevents or reduces the activity of an enzyme.
Vitvi18g00995	Binding to a metal ion.
Vitvi05g02122	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	6e−06	12 / 80	Cytoskeleton − Microtubules
2	1e−05	5 / 11	Transcription factors − GRF
3	2e−05	20 / 217	Cell motility − Regulation of actin cytoskeleton
4	8e−04	14 / 168	Plant hormone signal transduction
5	1e−03	6 / 38	Photosynthesis
6	2e−03	4 / 18	Transcription factors − ARF
7	2e−03	15 / 206	Cell growth and death − Cell wall
8	2e−03	4 / 19	Transcription factors − AUXIAA
9	3e−03	8 / 78	Energy metabolism − Photosynthesis
10	3e−03	3 / 10	Peptidases and inhibitors − Family A1: pepsin family
11	3e−03	3 / 10	Photosynthesis protein − Photosynthetic electron transport
12	3e−03	3 / 10	Photosynthesis protein − Photosystem I (P700 chlorophyll a)
13	6e−03	5 / 38	Hormone transport − Auxin transport
14	1e−02	3 / 17	Kinase − IRAK family
15	2e−02	5 / 47	Transporter catalog − Transport electron carriers
16	2e−02	7 / 89	MAPK signaling pathway − plant
17	2e−02	8 / 111	Transporter catalog − Porters cat 66 to 94
18	3e−02	3 / 21	Thiamine metabolism
19	3e−02	3 / 22	Transcription factors − C2C2−DOF
20	4e−02	6 / 79	Transporter catalog − Porters cat 30 to 64





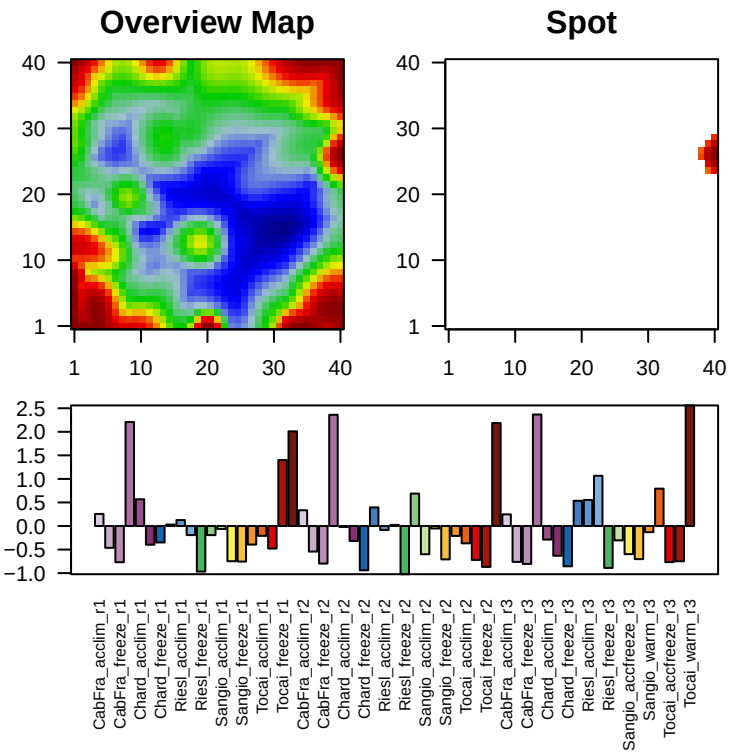
Overexpression Spots

Spot Summary: M

metagenes = 13
genes = 282

<r> metagenes = 0.99
<r> genes = 0.78
beta: r2= 32.59 / log p= −Inf

samples with spot = 9 (15.3 %)
CabFra_warm : 3 (100 %)
Riesl_accfreeze : 1 (33.3 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 3 (100 %)



Spot Genelist

ID	Description
Vitvi03g00752	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi18g02927	The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non−living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.
Vitvi11g01227	Catalysis of the transfer of an acyl group, other than amino−acyl, from one compound (donor) to another (acceptor).
Vitvi11g01222	Catalysis of the transfer of an acyl group, other than amino−acyl, from one compound (donor) to another (acceptor).
Vitvi07g02007	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi01g00742	Catalysis of an oxidation−reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi07g02362	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi18g01488	The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non−living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.
Vitvi11g01224	Catalysis of the transfer of an acyl group, other than amino−acyl, from one compound (donor) to another (acceptor).
Vitvi04g00312	Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzyme possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic.
Vitvi13g01768	
Vitvi18g02991	
Vitvi04g02223	
Vitvi12g00025	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi07g02097	A membrane−bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi18g02928	The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non−living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.
Vitvi12g00722	Binding to nicotinamide−adenine dinucleotide phosphate, a coenzyme involved in many redox and biosynthetic reactions; binding may be to either the oxidized form, NADP+, or the reduced form, NADPH.
Vitvi06g00433	
Vitvi03g00593	
Vitvi01g02265	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	1e−25	36 / 219	Cell growth and death − Cell cycle
2	3e−17	19 / 80	Cytoskeleton − Microtubules
3	3e−16	27 / 217	Cell motility − Regulation of actin cytoskeleton
4	7e−16	12 / 24	Replication protein − DNA Replication Initiation Factors
5	8e−12	11 / 36	DNA replication
6	9e−10	10 / 41	Replication and repair − DNA replication
7	7e−06	7 / 44	Replication protein − DNA Replication Termination Factors
8	9e−04	4 / 27	Mismatch repair
9	1e−03	5 / 51	Other metabolism − Single reactions
10	2e−03	4 / 34	Peptidases and inhibitors − Family S10
11	3e−03	4 / 37	Homologous recombination
12	6e−03	4 / 44	Nucleotide excision repair
13	8e−03	3 / 25	Replication and repair − Base excision repair
14	1e−02	3 / 29	Base excision repair
15	2e−02	13 / 409	Enzyme − 2.7 Transferring phosphorus−containing groups
16	2e−02	2 / 13	Kinase − CDK family
17	2e−02	2 / 13	Transcription factors − HMG
18	2e−02	2 / 14	Cilium and associated proteins − Stereociliary proteins
19	2e−02	4 / 66	Exosome − Exosomal proteins of bladder cancer cells
20	4e−02	5 / 113	Exosome − Exosomal proteins of colorectal cancer cells