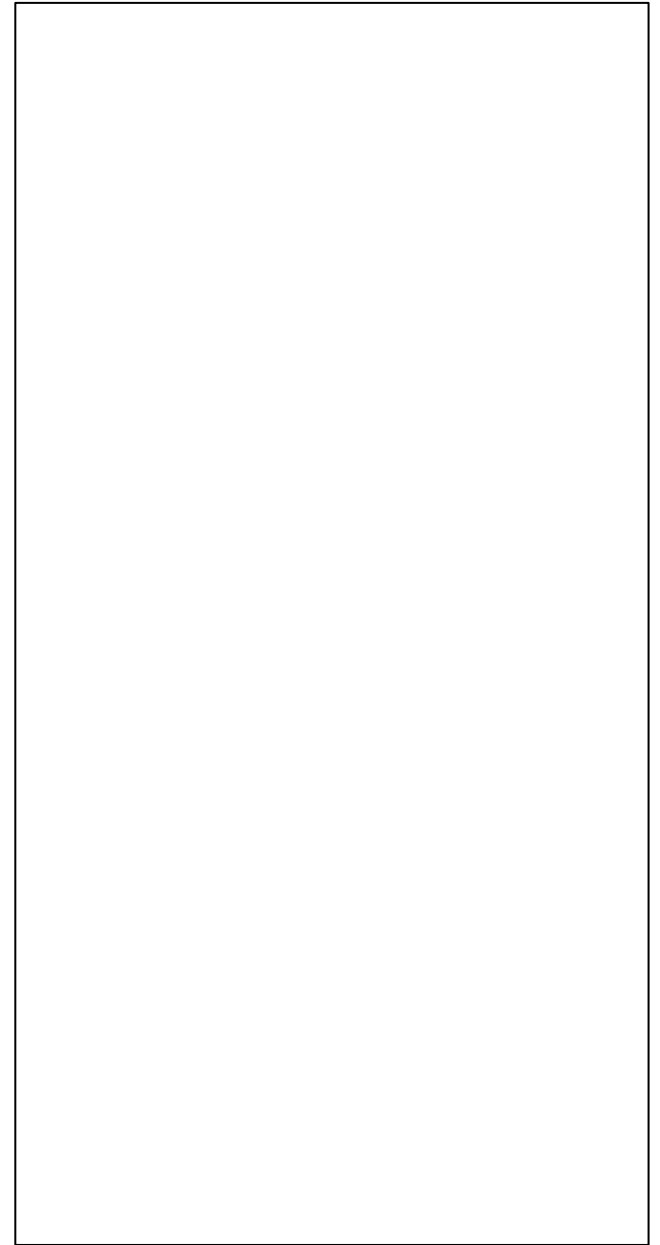
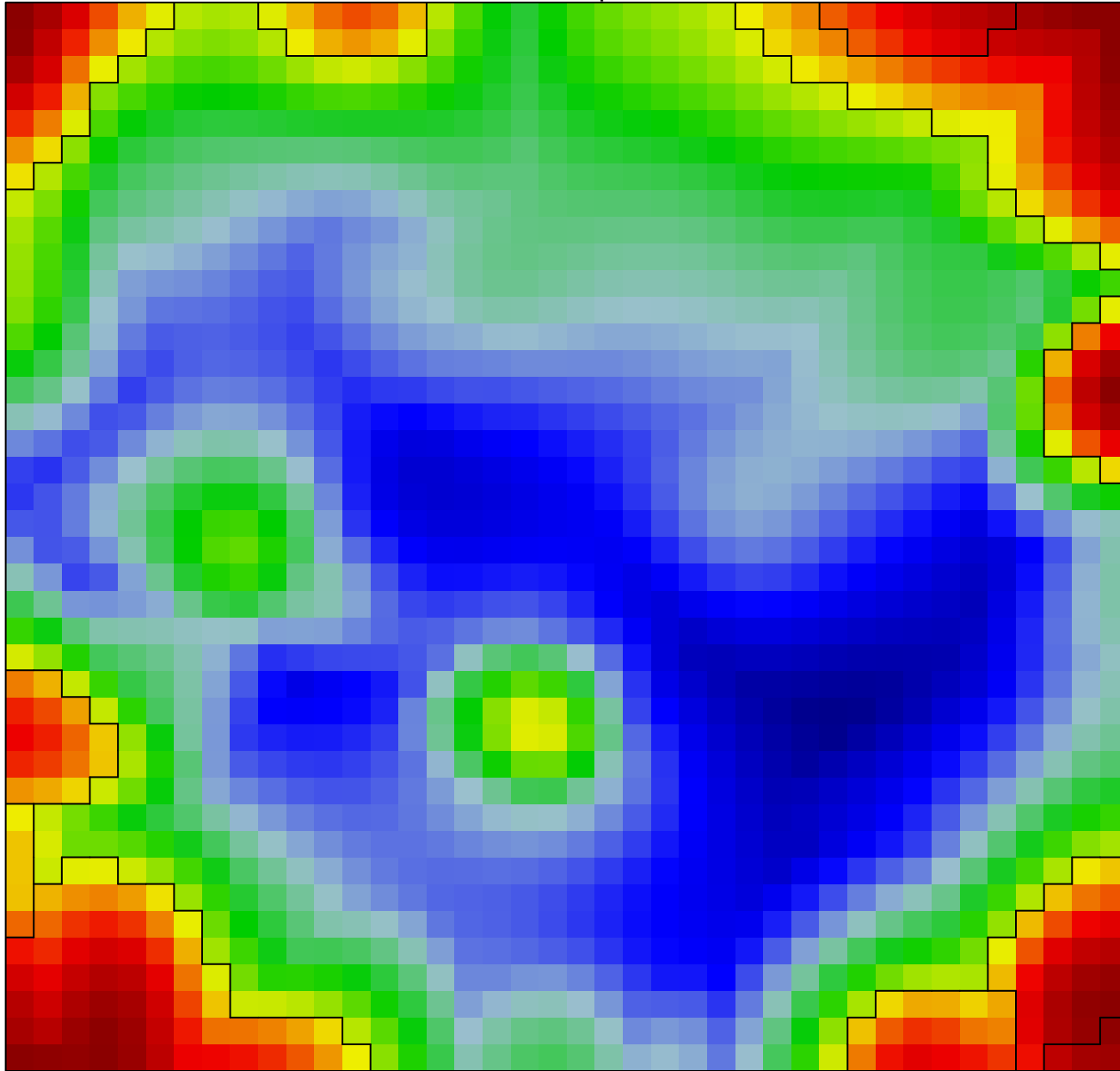


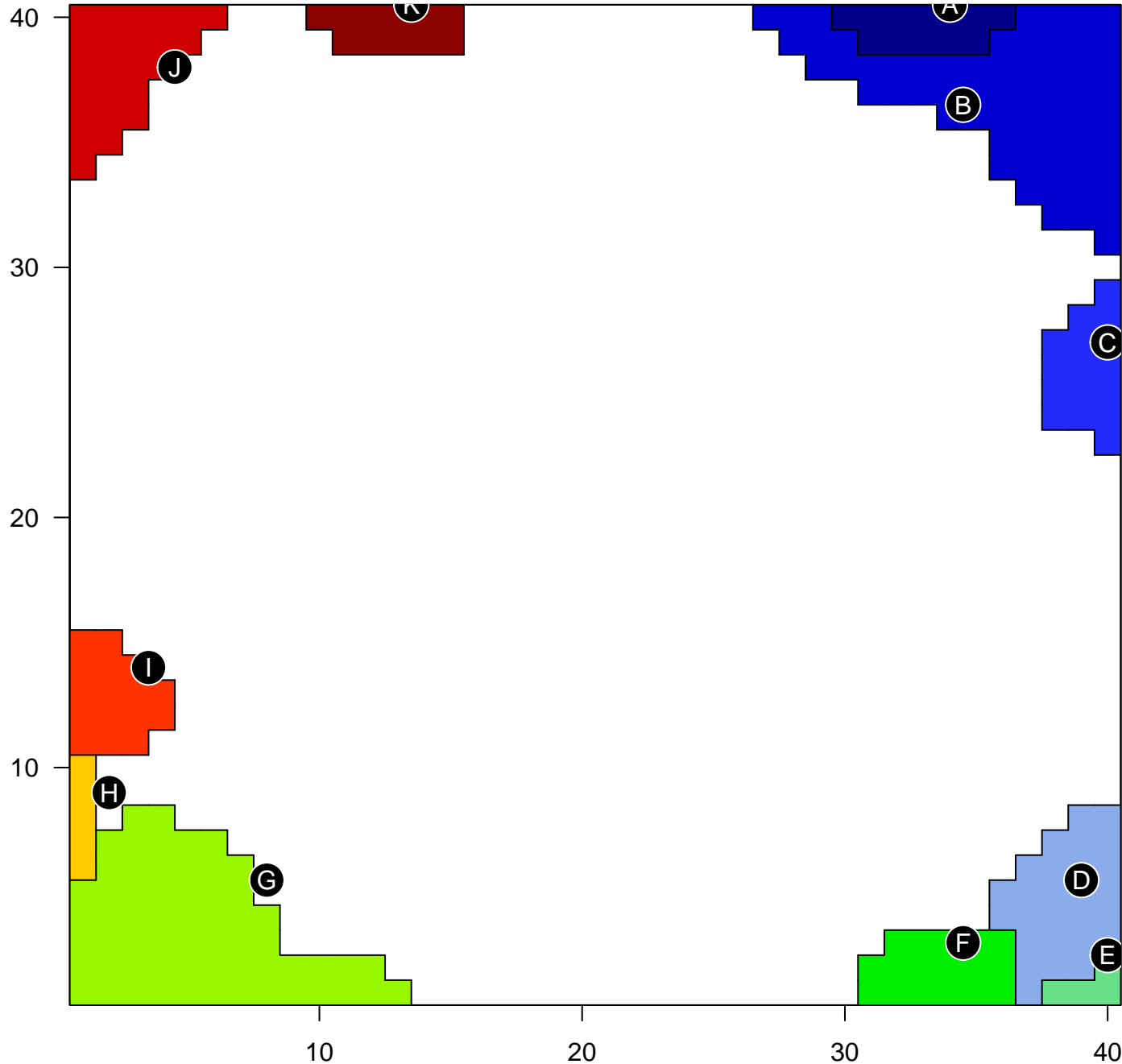
Group Overexpression Spots

landscape

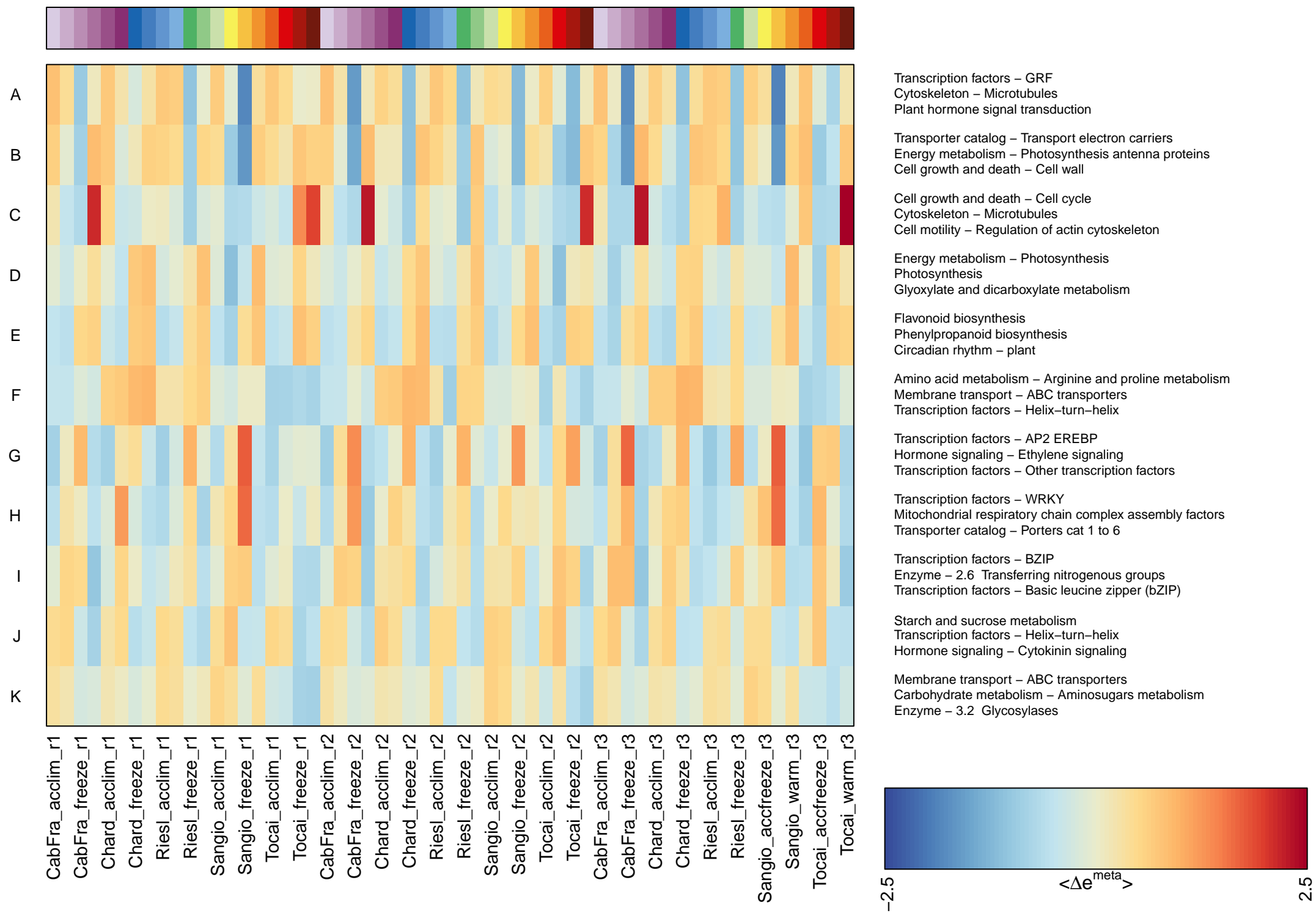


Group Overexpression Spots

annotation



- A ■ Transcription factors – GRF
Cytoskeleton – Microtubules
Plant hormone signal transduction
- B ■ Transporter catalog – Transport electron carriers
Energy metabolism – Photosynthesis antenna proteins
Cell growth and death – Cell wall
- C ■ Cell growth and death – Cell cycle
Cytoskeleton – Microtubules
Cell motility – Regulation of actin cytoskeleton
- D ■ Energy metabolism – Photosynthesis
Photosynthesis
Glyoxylate and dicarboxylate metabolism
- E ■ Flavonoid biosynthesis
Phenylpropanoid biosynthesis
Circadian rhythm – plant
- F ■ Amino acid metabolism – Arginine and proline metabolism
Membrane transport – ABC transporters
Transcription factors – Helix–turn–helix
- G ■ Transcription factors – AP2 EREBP
Hormone signaling – Ethylene signaling
Transcription factors – Other transcription factors
- H ■ Transcription factors – WRKY
Mitochondrial respiratory chain complex assembly factors
Transporter catalog – Porters cat 1 to 6
- I ■ Transcription factors – BZIP
Enzyme – 2.6 Transferring nitrogenous groups
Transcription factors – Basic leucine zipper (bZIP)
- J ■ Starch and sucrose metabolism
Transcription factors – Helix–turn–helix
Hormone signaling – Cytokinin signaling
- K ■ Membrane transport – ABC transporters
Carbohydrate metabolism – Aminosugars metabolism
Enzyme – 3.2 Glycosylases



Group Overexpression Spots

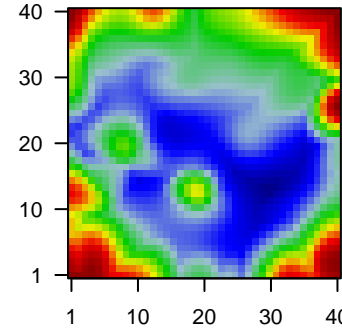
Spot Summary: A

metagenes = 12
genes = 287

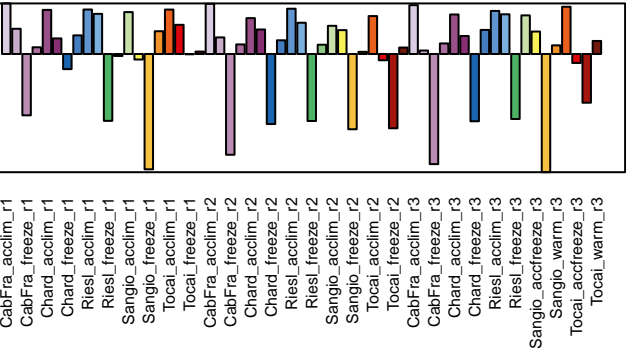
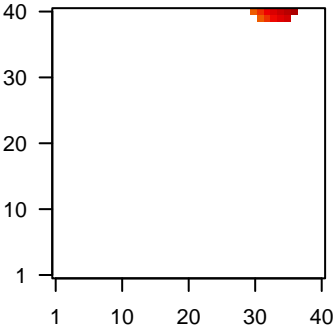
<r> metagenes = 0.99
<r> genes = 0.71
beta: r2= 25.52 / log p= -Inf

samples with spot = 11 (18.6 %)
CabFra_acclim : 3 (100 %)
Chard_acclim : 1 (33.3 %)
Riesl_acclim : 3 (100 %)
Riesl_accfreeze : 1 (33.3 %)
Sangio_acclim : 1 (33.3 %)
Tocai_acclim : 2 (66.7 %)

Overview Map



Spot

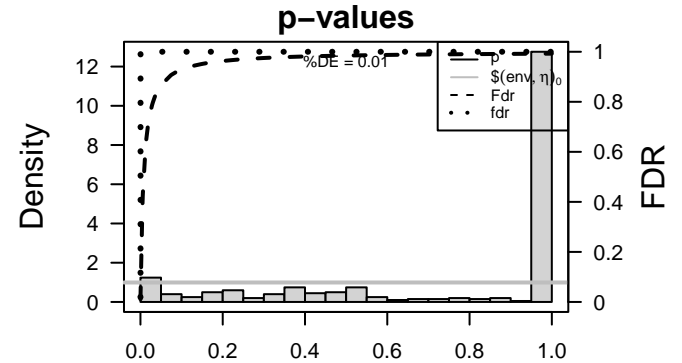


Spot Genelist

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.
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.
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.
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.
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.
Vitvi08g00827	The chemical reactions and pathways involving lipids, compounds soluble in an organic solvent but not, or sparingly, in an aqueous solvent. Includes fatty acids; neutral fats, other fatty-acid esters, and soaps; long-chain (fatty) alcohols and waxes; sphingoids and other long-chain bases; glycolipids, phospholipids and sphingolipids; and carotenes, polyprenols, sterols, terpenes and other isoprenoids.
Vitvi06g00626	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi10g00150	
Vitvi11g00712	That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.
Vitvi12g02681	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	3e-05	4 / 11	Transcription factors – GRF
2	8e-05	8 / 80	Cytoskeleton – Microtubules
3	2e-04	11 / 168	Plant hormone signal transduction
4	2e-04	4 / 18	Transcription factors – ARF
5	5e-03	10 / 217	Cell motility – Regulation of actin cytoskeleton
6	5e-03	5 / 65	Phagosome
7	5e-03	5 / 65	Transport and catabolism – Phagosome
8	6e-03	3 / 21	Thiamine metabolism
9	6e-03	5 / 66	Exosome – Exosomal proteins of bladder cancer cells
10	1e-02	2 / 10	Peptidases and inhibitors – Family A1: pepsin family
11	1e-02	6 / 111	Transporter catalog – Porters cat 66 to 94
12	1e-02	6 / 113	Exosome – Exosomal proteins of colorectal cancer cells
13	2e-02	2 / 12	Transcription factors – Basic helix–loop–helix (bHLH)
14	2e-02	5 / 89	MAPK signaling pathway – plant
15	2e-02	2 / 13	Cofactors and vitamin metabolism – Thiamine metabolism
16	2e-02	6 / 128	Ubiquitin system – Single Ring–finger type E3
17	3e-02	8 / 206	Cell growth and death – Cell wall
18	3e-02	3 / 38	Hormone transport – Auxin transport
19	3e-02	6 / 134	Hormone signaling – Auxin signaling
20	3e-02	3 / 39	Other amino acids metabolism – Selenoamino acid metabolism



Group Overexpression Spots

Spot Summary: B

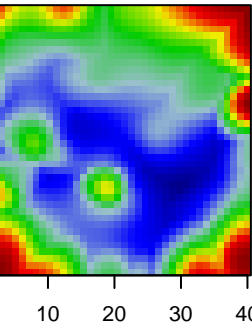
metagenes = 62
genes = 1039

<r> metagenes = 0.91

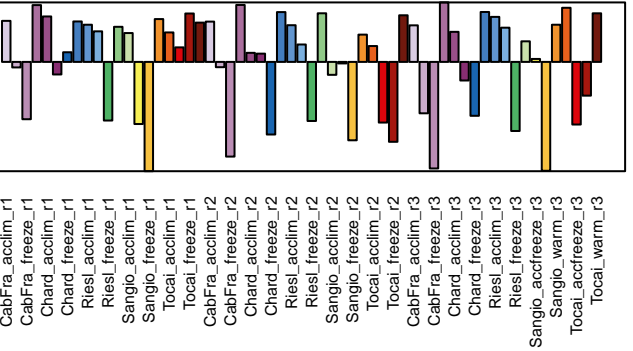
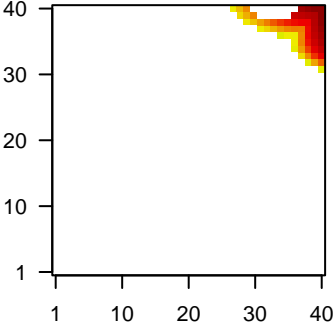
beta: r2= 31.79 / log p= -Inf

samples with spot = 13 (22 %)
CabFra_warm : 3 (100 %)
Chard_acclim : 1 (33.3 %)
Chard_warm : 2 (66.7 %)
Riesl_acclim : 1 (33.3 %)
Riesl_warm : 1 (50 %)
Sangio_warm : 1 (33.3 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 2 (66.7 %)

Overview Map



Spot

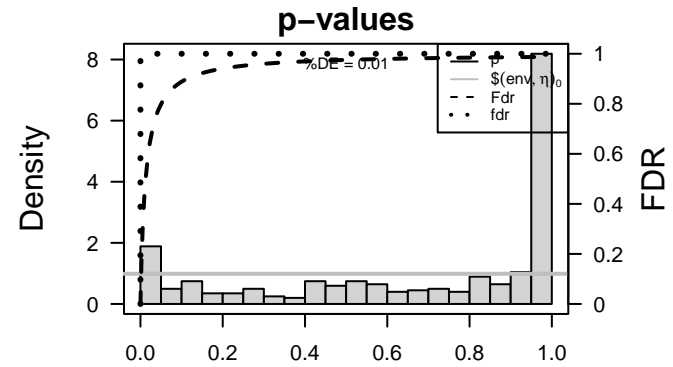


Spot Genelist

ID	Description
Vitvi14g01929	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi09g01282	Functions in the storage of nutritious substrates.
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.
Vitvi19g02024	
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	
Vitvi17g00977	Binding to a metal ion.
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.
Vitvi13g01788	
Vitvi01g00593	Binding to a metal ion.
Vitvi01g00441	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi12g02394	
Vitvi14g03084	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-19	26 / 47	Transporter catalog – Transport electron carriers
2	6e-18	16 / 18	Energy metabolism – Photosynthesis antenna proteins
3	4e-17	50 / 206	Cell growth and death – Cell wall
4	5e-16	15 / 18	Photosynthesis – antenna proteins
5	8e-15	28 / 78	Energy metabolism – Photosynthesis
6	1e-13	19 / 38	Photosynthesis
7	1e-10	9 / 10	Photosynthesis protein – Photosystem I (P700 chlorophyll a)
8	9e-08	14 / 41	Porphyrin metabolism
9	2e-07	35 / 217	Cell motility – Regulation of actin cytoskeleton
10	5e-07	13 / 40	Transport system – Thylakoid targeting pathway
11	3e-05	10 / 34	Peptidases and inhibitors – Family S10
12	3e-05	16 / 80	Cytoskeleton – Microtubules
13	1e-04	8 / 26	Steroid biosynthesis
14	2e-04	20 / 134	Hormone signaling – Auxin signaling
15	4e-04	19 / 129	Enzyme – 3.2 Glycosylases
16	8e-04	6 / 19	Transcription factors – AUXIAA
17	2e-03	11 / 63	Phenylpropanoid biosynthesis
18	2e-03	7 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
19	2e-03	4 / 10	Peptidases and inhibitors – Family A1: pepsin family
20	2e-03	4 / 10	Photosynthesis protein – Photosynthetic electron transport



Group Overexpression Spots

Spot Summary: C

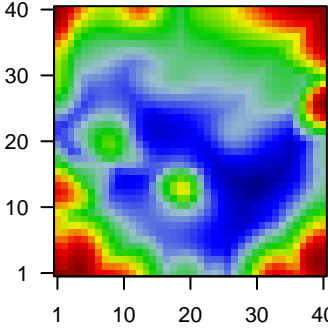
metagenes = 16
genes = 322

<r> metagenes = 0.99
<r> genes = 0.76
beta: r2= 31.05 / log p= -Inf

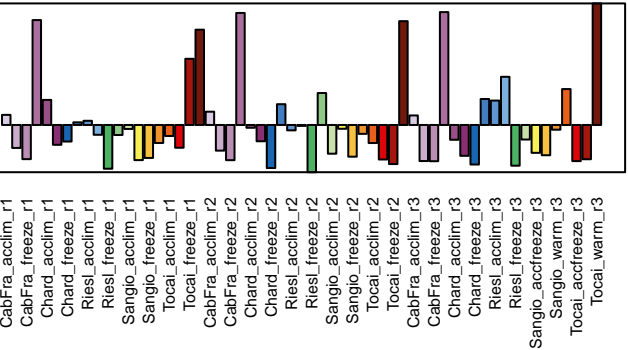
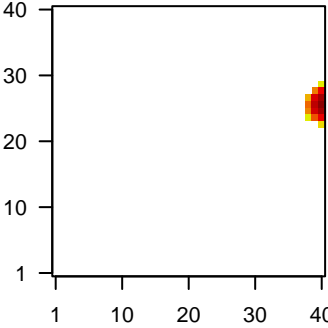
samples with spot = 10 (16.9 %)

CabFra_warm : 3 (100 %)
Riesl_accfreeze : 1 (33.3 %)
Riesl_warm : 1 (50 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 3 (100 %)

Overview Map



Spot

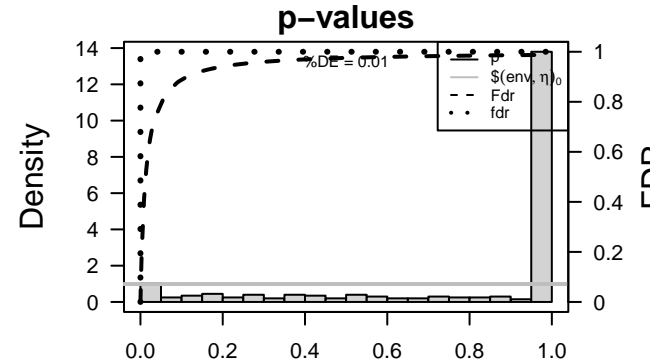


Spot Genelist

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.
Vitvi14g02893	
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	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-28	40 / 219	Cell growth and death – Cell cycle
2	3e-16	19 / 80	Cytoskeleton – Microtubules
3	5e-16	28 / 217	Cell motility – Regulation of actin cytoskeleton
4	3e-15	12 / 24	Replication protein – DNA Replication Initiation Factors
5	1e-12	12 / 36	DNA replication
6	1e-10	11 / 41	Replication and repair – DNA replication
7	1e-06	8 / 44	Replication protein – DNA Replication Termination Factors
8	6e-04	5 / 37	Homologous recombination
9	1e-03	4 / 25	Replication and repair – Base excision repair
10	1e-03	4 / 27	Mismatch repair
11	2e-03	4 / 29	Base excision repair
12	2e-03	5 / 51	Other metabolism – Single reactions
13	3e-03	4 / 34	Peptidases and inhibitors – Family S10
14	9e-03	4 / 44	Nucleotide excision repair
15	1e-02	2 / 10	Protein – Syntaxin (Qa)
16	2e-02	5 / 83	Transcription factors – MYB
17	2e-02	14 / 409	Enzyme – 2.7 Transferring phosphorus-containing groups
18	2e-02	2 / 13	Kinase – CDK family
19	2e-02	2 / 13	Transcription factors – HMG
20	3e-02	2 / 14	Cilium and associated proteins – Stereociliary proteins



Group Overexpression Spots

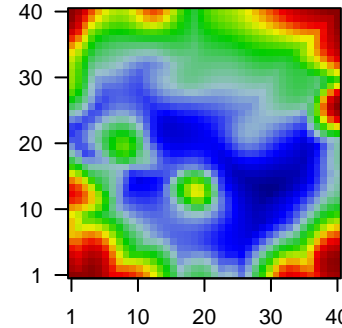
Spot Summary: D

metagenes = 27
genes = 327

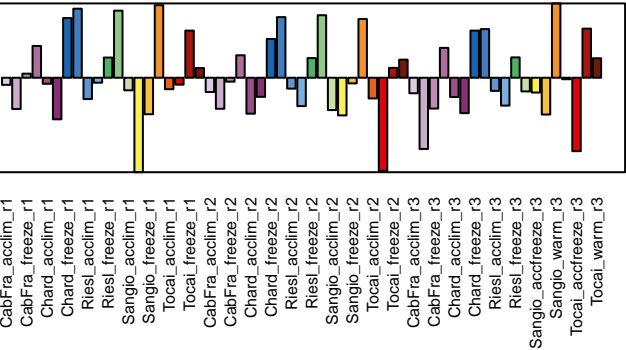
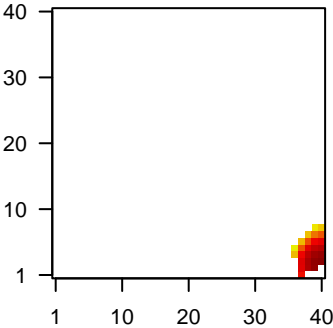
<r> metagenes = 0.95
<r> genes = 0.54
beta: r2= 10.34 / log p= -Inf

samples with spot = 8 (13.6 %)
Chard_freeze : 1 (33.3 %)
Chard_warm : 2 (66.7 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 3 (100 %)

Overview Map



Spot

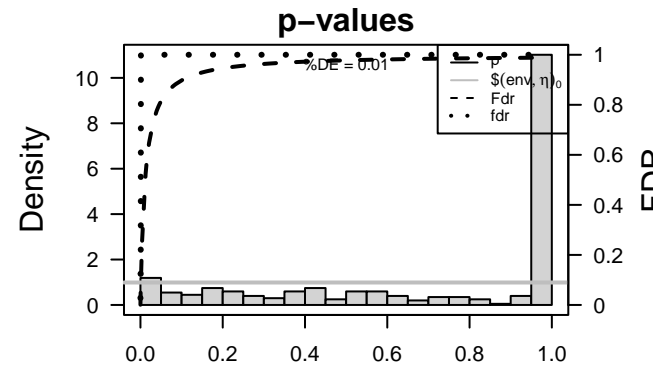


Spot Genelist

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).
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.
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	
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).
Vitvi14g01336	
Vitvi19g00302	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi16g01984	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.
Vitvi00g00915	
Vitvi10g02309	Binding to a metal ion.
Vitvi11g01295	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.
Vitvi08g02222	Any cellular process that depends upon or alters the microtubule cytoskeleton, that part of the cytoskeleton comprising microtubules and their associated proteins.
Vitvi01g00822	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi03g01495	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.
Vitvi09g01562	Functions in the storage of nutritious substrates.
Vitvi08g01699	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi03g00666	Binding to a metal ion.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-06	10 / 78	Energy metabolism – Photosynthesis
2	7e-05	6 / 38	Photosynthesis
3	7e-04	6 / 57	Glyoxylate and dicarboxylate metabolism
4	7e-04	5 / 38	Enzyme – 1.8 Acting on a sulfur group of donors
5	1e-03	4 / 25	Nitrogen metabolism
6	1e-03	5 / 44	Energy metabolism – Nitrogen metabolism
7	4e-03	6 / 79	Transporter catalog – Porters cat 30 to 64
8	1e-02	3 / 26	Flavonoid biosynthesis
9	1e-02	2 / 10	Linoleic acid metabolism
10	1e-02	2 / 10	Photosynthesis protein – Photosynthetic electron transport
11	2e-02	4 / 51	Carbon fixation in photosynthetic organisms
12	2e-02	2 / 11	Enzyme – 2.2 Transferring aldehyde or ketonic groups
13	2e-02	5 / 81	Enzyme – 4.2 Carbon-oxygen lyases
14	2e-02	3 / 30	Ubiquinone and other terpenoid-quinone biosynthesis
15	2e-02	6 / 111	Transporter catalog – Porters cat 66 to 94
16	2e-02	4 / 56	Glycine serine and threonine metabolism
17	3e-02	4 / 63	Phenylpropanoid biosynthesis
18	3e-02	2 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
19	4e-02	3 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
20	4e-02	3 / 40	Transport system – Thylakoid targeting pathway



Group Overexpression Spots

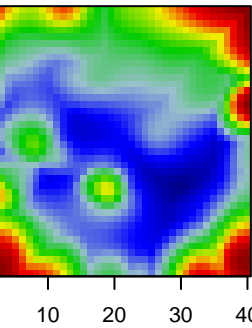
Spot Summary: E

metagenes = 4
genes = 154

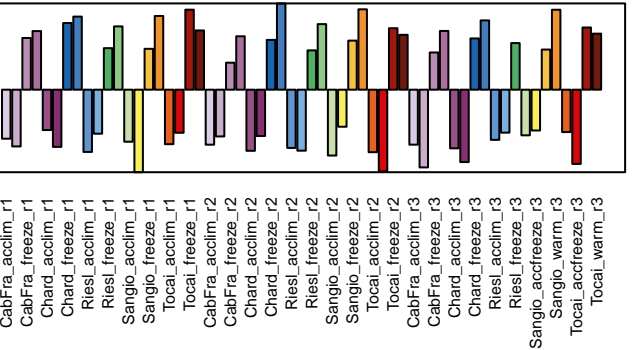
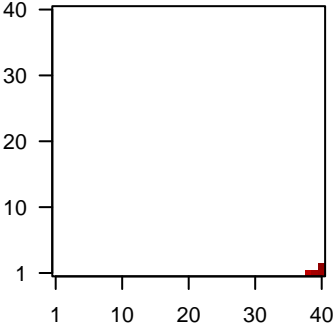
<r> metagenes = 0.99
<r> genes = 0.6
beta: r2= 15.03 / log p= -Inf

samples with spot = 9 (15.3 %)
Chard_freeze : 1 (33.3 %)
Chard_warm : 3 (100 %)
Riesl_warm : 1 (50 %)
Sangio_warm : 3 (100 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

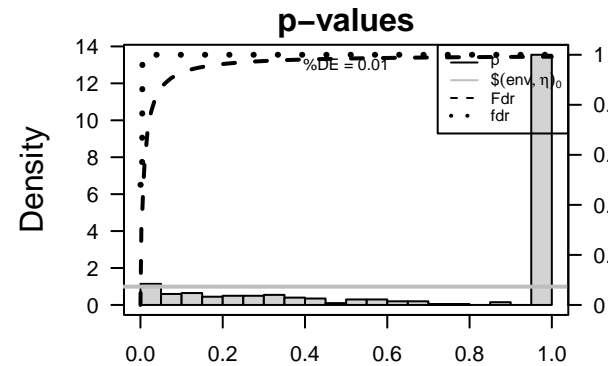


Spot Genelist

ID	Description
Vitvi00g00346	
Vitvi07g02904	
Vitvi02g01118	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
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	
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	
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	
Vitvi02g01121	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.
Vitvi03g01833	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi08g02355	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.
Vitvi09g01537	
Vitvi08g01904	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.
Vitvi11g00805	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi07g01779	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.
Vitvi08g02334	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-08	6 / 26	Flavonoid biosynthesis
2	2e-03	4 / 63	Phenylpropanoid biosynthesis
3	3e-03	3 / 32	Circadian rhythm – plant
4	4e-03	5 / 118	Transcription factors – Helix–turn–helix
5	5e-03	2 / 12	Endoplasmic reticulum membrane and cytosol
6	5e-03	3 / 40	Energy metabolism – Methane metabolism
7	6e-03	4 / 83	Transcription factors – MYB
8	8e-03	2 / 15	Chaperone – HSP70 / DNAK
9	1e-02	2 / 17	Proteasome – Assembling factors
10	2e-02	4 / 111	Transporter catalog – Porters cat 66 to 94
11	2e-02	2 / 24	Tropane piperidine and pyridine alkaloid biosynthesis
12	2e-02	2 / 24	Transporter catalog – Group translocators
13	3e-02	2 / 28	Enzyme – 6.2 Forming carbon–sulfur bonds
14	3e-02	2 / 29	Transcription factors – Trihelix
15	3e-02	2 / 33	alpha–Linolenic acid metabolism
16	3e-02	3 / 81	Translation – mRNA surveillance pathway
17	4e-02	2 / 35	Lipid metabolism – Alpha–linolenic acid metabolism
18	4e-02	3 / 88	Electrochemical potential–driven transporters [TC:2]
19	4e-02	2 / 38	Protein – Chaperone mediated autophagy (CMA)
20	4e-02	2 / 38	Protein – Clathrin–mediated endocytosis



Group Overexpression Spots

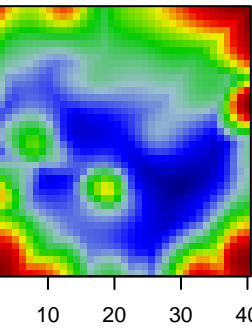
Spot Summary: F

metagenes = 17
genes = 215

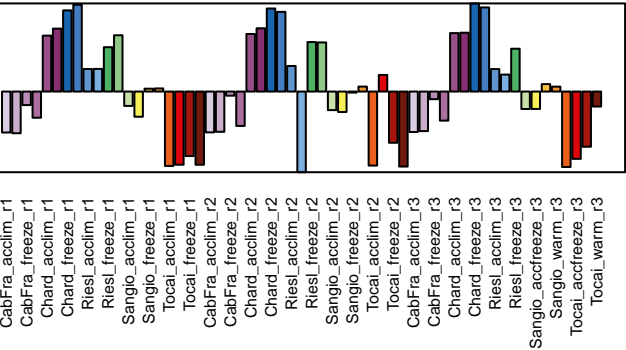
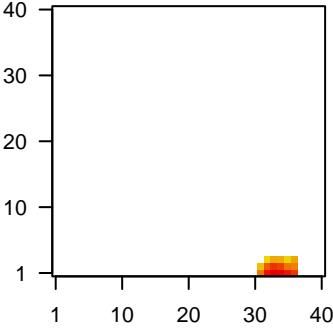
<r> metagenes = 0.92
<r> genes = 0.39
beta: r2= 10.03 / log p= -Inf

samples with spot = 10 (16.9 %)
Chard_acclim : 1 (33.3 %)
Chard_accfreeze : 3 (100 %)
Chard_freeze : 3 (100 %)
Chard_warm : 3 (100 %)

Overview Map



Spot

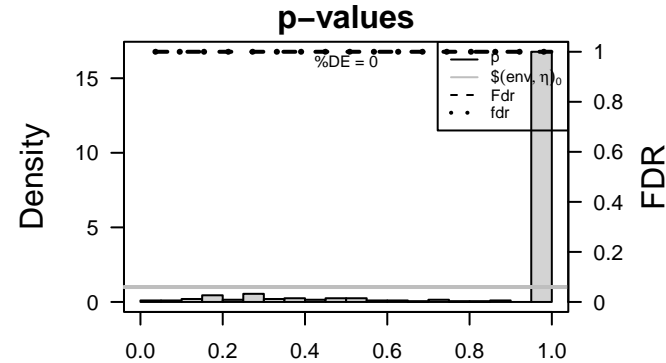


Spot Genelist

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-bound 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	0.15	1 / 21	Replication and repair – Mismatch repair
10	0.16	1 / 22	Replication and repair – Homologous recombination
11	0.17	1 / 24	Enzyme – 7.1 Catalysing the translocation of hydrons
12	0.19	1 / 26	Steroid biosynthesis
13	0.19	1 / 26	Glycosyltransferase – Hydrophobic molecule
14	0.19	1 / 26	Transcription factors – Orphans FAR–RED
15	0.19	2 / 101	Starch and sucrose metabolism
16	0.19	1 / 27	ABCG (White) subfamily
17	0.20	1 / 28	Exosome – Exosomal proteins of breast milk
18	0.23	1 / 33	Enzyme – 5.4 Intramolecular transferases
19	0.24	1 / 35	Lipid metabolism – Alpha–linolenic acid metabolism
20	0.25	2 / 121	Transporter catalog – Porters cat 18 to 29



Group Overexpression Spots

Spot Summary: G

metagenes = 61
genes = 1125

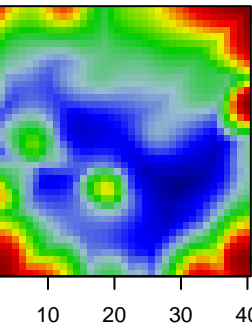
<r> metagenes = 0.92

beta: r2= 31.78 / log p= -Inf

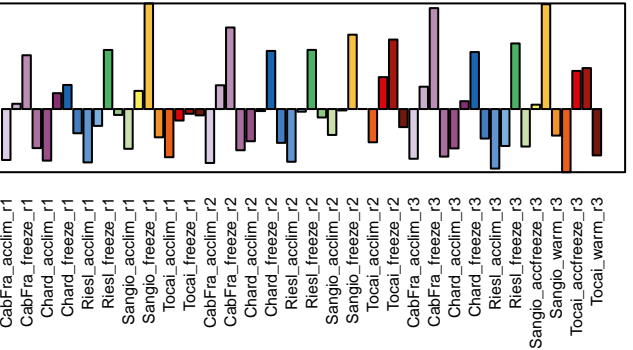
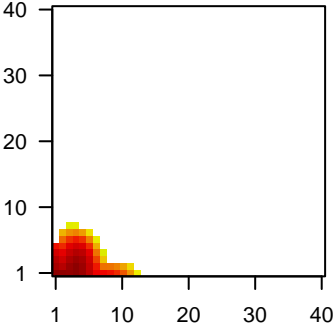
samples with spot = 13 (22 %)

- CabFra_freeze : 3 (100 %)
- Chard_freeze : 2 (66.7 %)
- Riesl_freeze : 3 (100 %)
- Sangio_freeze : 3 (100 %)
- Tocai_freeze : 2 (66.7 %)

Overview Map



Spot

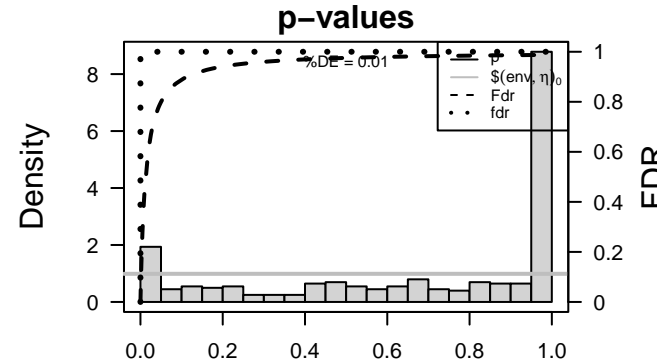


Spot Genelist

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 possesses 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	5e-16	28 / 73	Transcription factors - AP2 EREBP
2	7e-14	36 / 140	Hormone signaling - Ethylene signaling
3	4e-09	19 / 64	Transcription factors - Other transcription factors
4	1e-08	16 / 48	Transcription factors - WRKY
5	1e-07	15 / 49	Transcription factors - NAC
6	1e-05	12 / 45	Galactose metabolism
7	3e-05	16 / 83	Transcription factors - MYB
8	9e-05	19 / 118	Transcription factors - Helix-turn-helix
9	8e-04	9 / 42	Tryptophan metabolism
10	8e-04	10 / 51	Biosynthesis of secondary metabolism - Auxin biosynthesis
11	1e-03	27 / 238	Enzyme - 2.4 Glycosyltransferases
12	2e-03	9 / 47	ABC transporters
13	2e-03	20 / 162	Plant specific signaling - Plant-pathogen interaction
14	2e-03	13 / 86	Signal transduction - Calcium signaling pathway
15	2e-03	19 / 153	Plant-pathogen interaction
16	4e-03	5 / 18	Receptor - Others
17	4e-03	6 / 26	Glycosyltransferase - Hydrophobic molecule
18	4e-03	8 / 44	Energy metabolism - Nitrogen metabolism
19	5e-03	6 / 27	ABCG (White) subfamily
20	7e-03	11 / 77	Carbohydrate metabolism - Galactose metabolism



Group Overexpression Spots

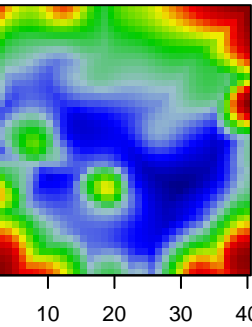
Spot Summary: H

metagenes = 5
genes = 151

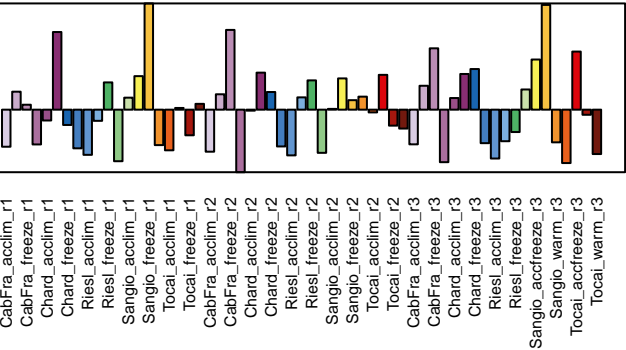
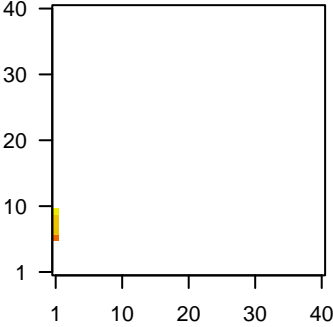
<r> metagenes = 0.98
<r> genes = 0.56
beta: r2= 20.21 / log p= -Inf

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 %)

Overview Map



Spot

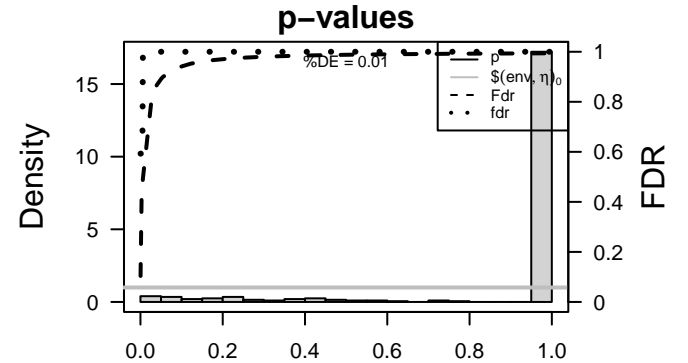


Spot Genelist

ID	Description
Vitvi08g00957	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
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.
Vitvi16g01213	Any process that modulates the frequency, rate or extent of cellular DNA-templated transcription.
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.
Vitvi16g01461	
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.
Vitvi17g00395	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
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	
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.
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	3e-04	4 / 48	Transcription factors – WRKY
2	3e-03	3 / 43	Mitochondrial respiratory chain complex assembly factors
3	3e-03	4 / 96	Transporter catalog – Porters cat 1 to 6
4	5e-03	2 / 16	Transcription factors – HSF
5	6e-03	2 / 18	Receptor – Others
6	3e-02	2 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
7	4e-02	3 / 111	Transporter catalog – Porters cat 66 to 94
8	4e-02	2 / 49	Transcription factors – NAC
9	5e-02	2 / 56	Hormone signaling – Jasmonate signaling
10	5e-02	2 / 58	Other amino acids metabolism – Glutathione metabolism
11	8e-02	2 / 71	Glutathione metabolism
12	8e-02	1 / 13	Sugar transporters
13	8e-02	2 / 73	Transcription factors – AP2 EREBP
14	9e-02	3 / 162	Plant specific signaling – Plant-pathogen interaction
15	9e-02	2 / 77	Pores ion channels [TC:1]
16	1e-01	2 / 93	Transcription factors – BHLH
17	1e-01	1 / 24	Enzyme – 7.1 Catalysing the translocation of hydrons
18	1e-01	1 / 24	Ubiquitin system – Ubiquitin-conjugating enzymes
19	1e-01	1 / 24	Carbohydrate metabolism – Ascorbate and aldarate metabolism
20	2e-01	1 / 25	Transcription factors – GNAT



Group Overexpression Spots

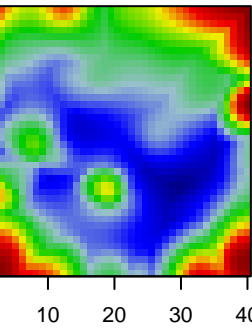
Spot Summary: I

metagenes = 16
genes = 281

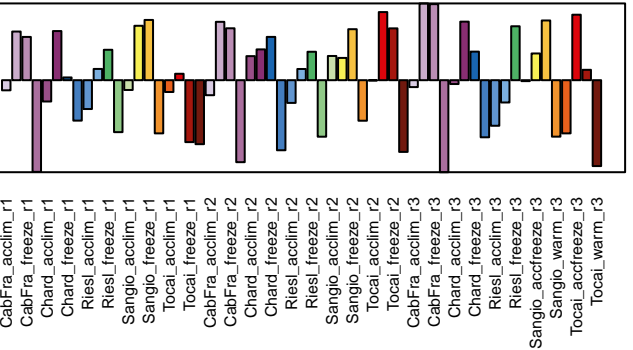
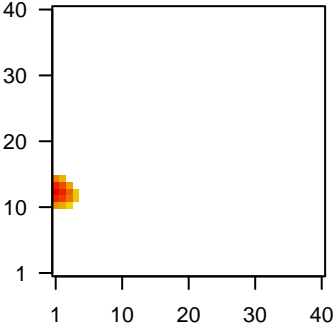
<r> metagenes = 0.98
<r> genes = 0.59
beta: r2= 12.35 / log p= -Inf

samples with spot = 8 (13.6 %)
CabFra_accfreeze : 2 (66.7 %)
CabFra_freeze : 1 (33.3 %)
Chard_accfreeze : 1 (33.3 %)
Sangio_freeze : 2 (66.7 %)
Tocai_accfreeze : 2 (66.7 %)

Overview Map



Spot

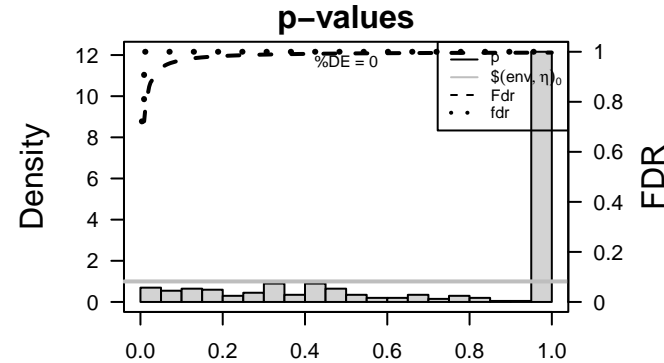


Spot Genelist

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.
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.
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.
Vitvi05g00108	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.
Vitvi05g00857	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.
Vitvi11g00613	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	4 / 43	Transcription factors – BZIP
2	0.007	3 / 27	Enzyme – 2.6 Transferring nitrogenous groups
3	0.007	3 / 28	Transcription factors – Basic leucine zipper (bZIP)
4	0.009	2 / 10	Kinase – Wnk family
5	0.009	5 / 88	Electrochemical potential–driven transporters [TC:2]
6	0.012	2 / 12	Transcription factors – Orphans zf–b box
7	0.013	3 / 34	Tyrosine metabolism
8	0.021	3 / 41	Arginine and proline metabolism
9	0.022	5 / 111	Hormone signaling – ABA signaling
10	0.022	5 / 111	Transporter catalog – Porters cat 66 to 94
11	0.025	2 / 17	Isoquinoline alkaloid biosynthesis
12	0.045	3 / 55	Glycerolipid metabolism
13	0.047	2 / 24	Tropane piperidine and pyridine alkaloid biosynthesis
14	0.049	3 / 57	Glyoxylate and dicarboxylate metabolism
15	0.050	2 / 25	Phenylalanine metabolism
16	0.050	2 / 25	Biosynthesis of secondary metabolism – Zeatin biosynthesis
17	0.054	2 / 26	Flavonoid biosynthesis
18	0.054	2 / 26	Enzyme – 5.1 Racemases and epimerases
19	0.061	5 / 146	Transporter catalog – Porters cat 7 to 17
20	0.065	2 / 29	Arginine biosynthesis



Group Overexpression Spots

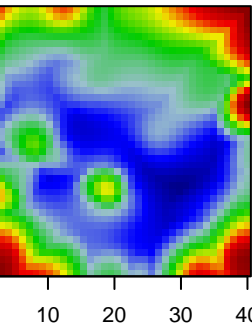
Spot Summary: J

metagenes = 24
genes = 518

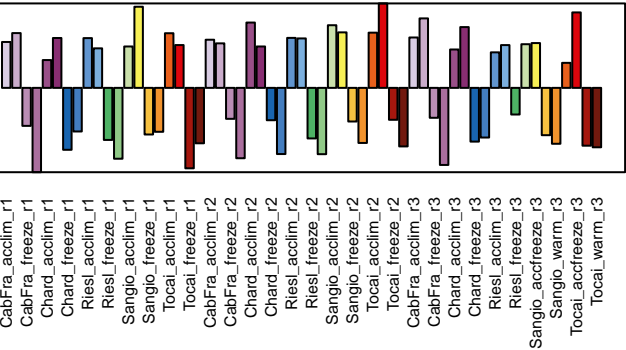
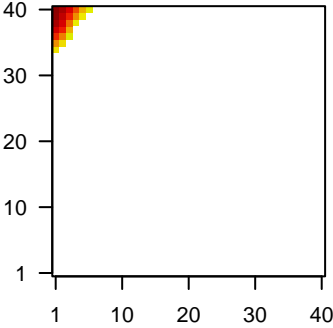
<r> metagenes = 0.96
<r> genes = 0.57
beta: r2= 12.38 / log p= -Inf

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

Overview Map



Spot

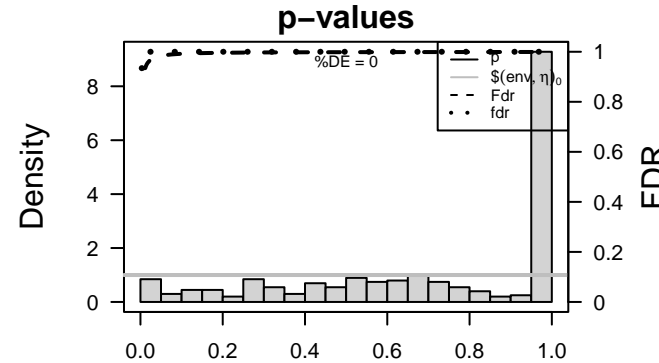


Spot Genelist

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	
Vitvi06g01629	
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	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	9 / 101	Starch and sucrose metabolism
2	0.008	9 / 118	Transcription factors – Helix–turn–helix
3	0.009	5 / 44	Hormone signaling – Cytokinin signaling
4	0.010	8 / 100	Plant specific signaling – Flower development
5	0.012	14 / 238	Enzyme – 2.4 Glycosyltransferases
6	0.013	12 / 195	Carbohydrate metabolism – Starch and sucrose metabolism
7	0.014	4 / 32	Circadian rhythm – plant
8	0.015	3 / 18	Chaperone – HSP20
9	0.017	5 / 51	Plant specific signaling – Circadian rhythm
10	0.017	4 / 34	Tyrosine metabolism
11	0.023	3 / 21	Thiamine metabolism
12	0.034	2 / 10	Transcription factors – C2C2–CO
13	0.036	6 / 83	Transcription factors – MYB
14	0.040	2 / 11	Zeatin biosynthesis
15	0.040	3 / 26	Protein – Small GTPases and associated proteins
16	0.041	5 / 64	Transcription factors – Other transcription factors
17	0.048	5 / 67	Replication and repair – RNA degradation
18	0.053	3 / 29	Other amino acids metabolism – Beta–alanine metabolism
19	0.055	2 / 13	Transcription factors – HMG
20	0.075	4 / 54	Carbohydrate metabolism – Inositol phosphate metabolism



Group Overexpression Spots

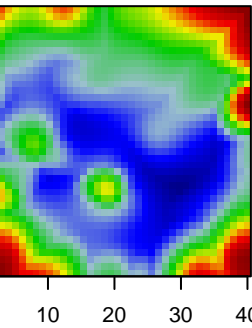
Spot Summary: K

metagenes = 11
genes = 170

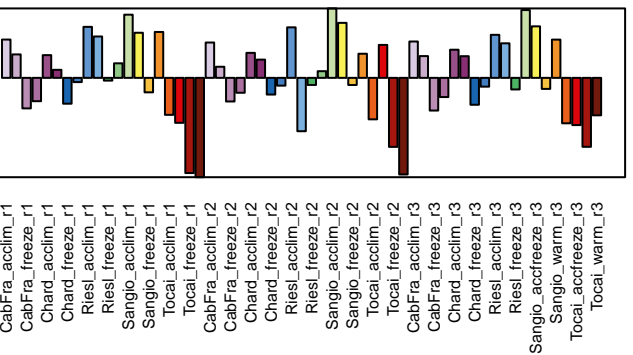
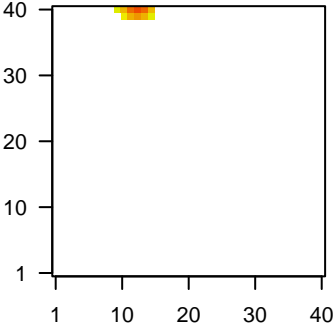
<r> metagenes = 0.93
<r> genes = 0.35
beta: r2= 4.4 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot



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. 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.
Vitvi11g01488	
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	
Vitvi06g01069	The pigmented membrane of a chloroplast thylakoid. An example of this component is found in Arabidopsis thaliana.
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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-04	6 / 102	Membrane transport – ABC transporters
2	2e-03	3 / 33	Carbohydrate metabolism – Aminosugars metabolism
3	3e-03	5 / 129	Enzyme – 3.2 Glycosylases
4	3e-03	2 / 11	Zeatin biosynthesis
5	1e-02	3 / 64	Purine metabolism
6	1e-02	2 / 25	Biosynthesis of secondary metabolism – Zeatin biosynthesis
7	4e-02	3 / 101	Starch and sucrose metabolism
8	4e-02	2 / 44	Enzyme – 1.11 Acting on a peroxide as acceptor
9	5e-02	2 / 47	ABC transporters
10	5e-02	3 / 111	Transporter catalog – Porters cat 66 to 94
11	6e-02	4 / 197	Transporter catalog – Channels and pores
12	7e-02	1 / 10	Protein – Syntxin (Qa)
13	9e-02	1 / 12	Channel – Cyclic nucleotide-gated channel (CNG)
14	9e-02	1 / 12	Enzyme – Class I
15	9e-02	1 / 12	SLC15: Proton oligopeptide cotransporter
16	9e-02	2 / 67	Amino acid metabolism – Tyrosine metabolism
17	1e-01	2 / 71	Amino acid metabolism – Phenylalanine metabolism
18	1e-01	1 / 14	Enzyme – 1.5 Acting on the CH-NH group of donors
19	1e-01	1 / 14	Proteins involved in snRNP biogenesis
20	1e-01	4 / 238	Enzyme – 2.4 Glycosyltransferases

