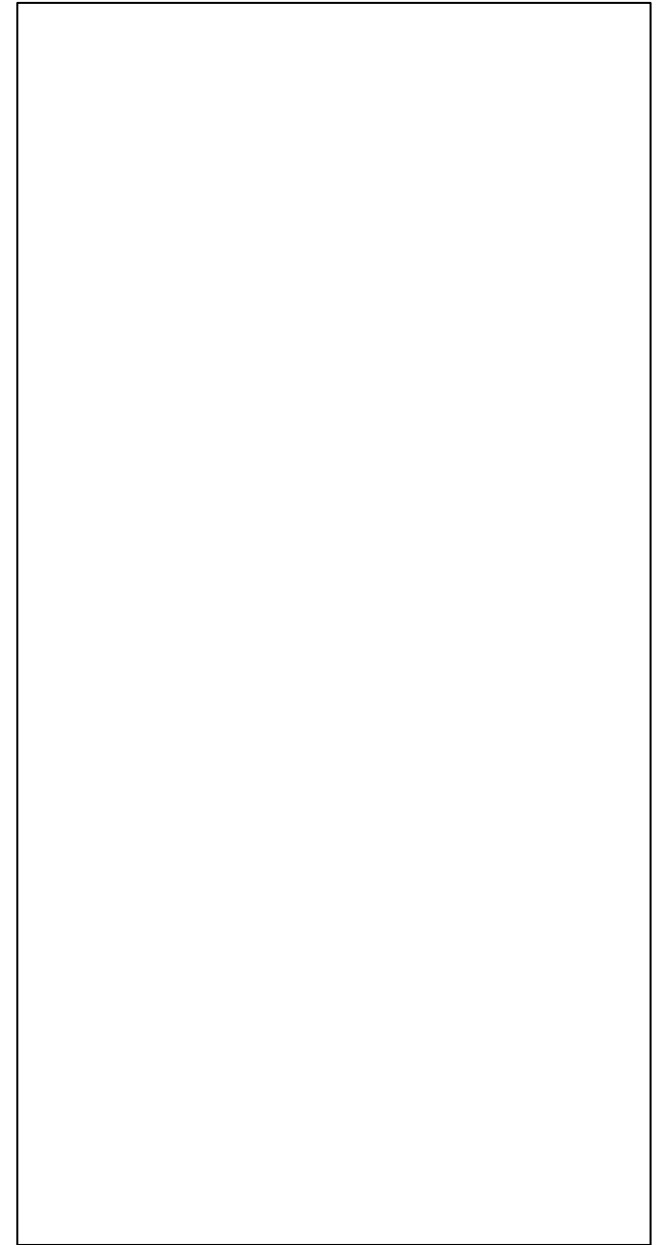
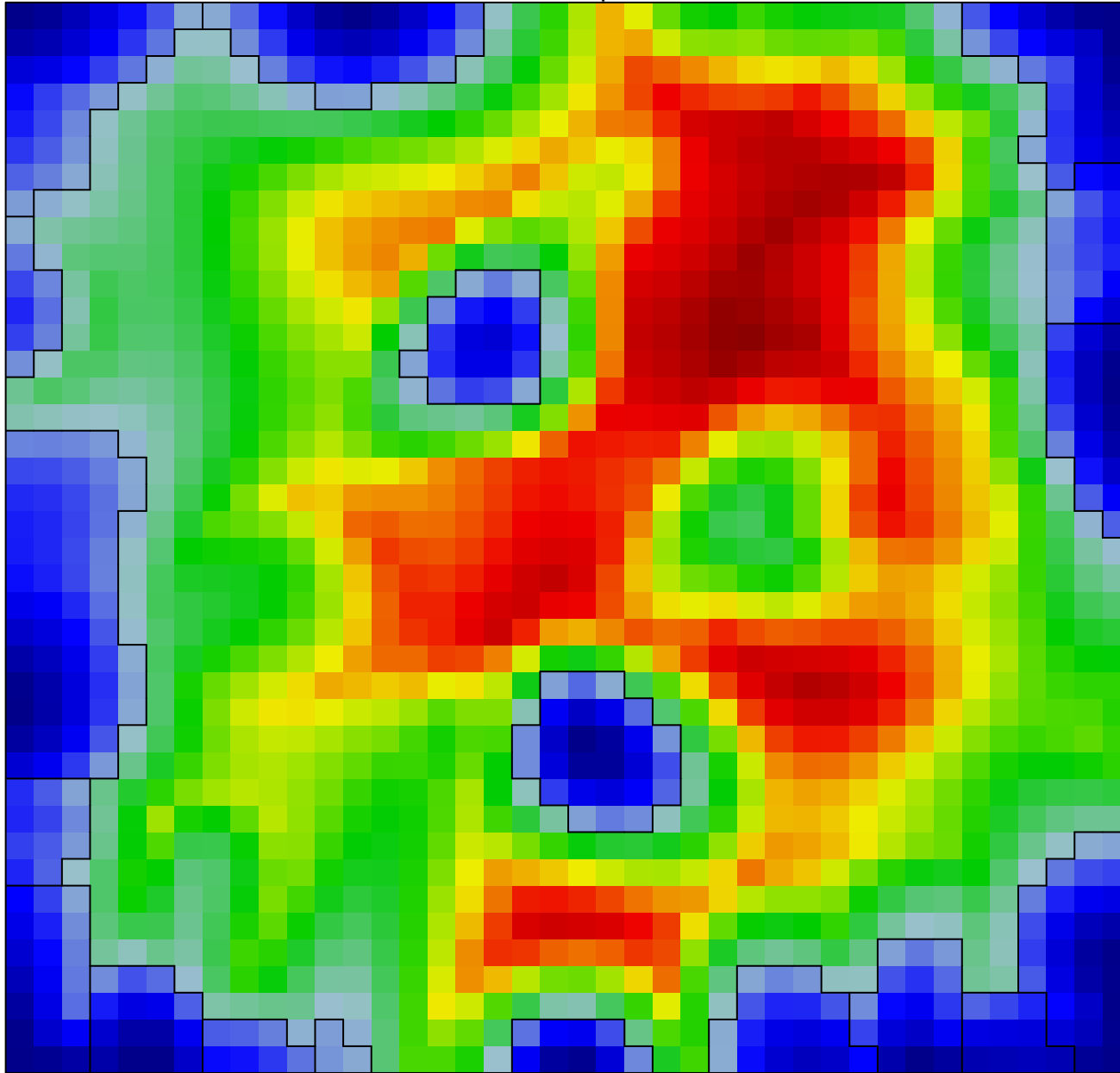
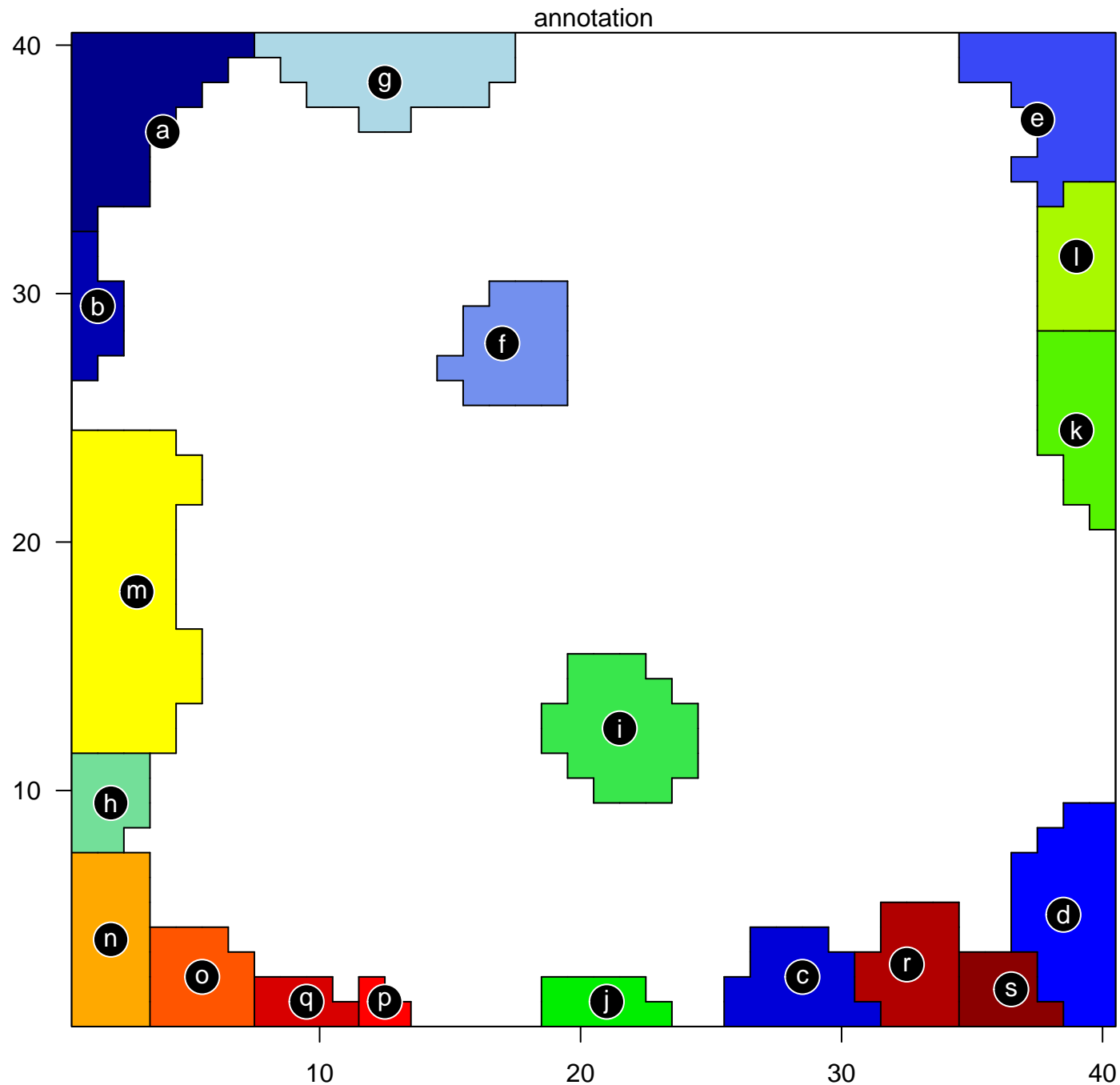


Underexpression Spots

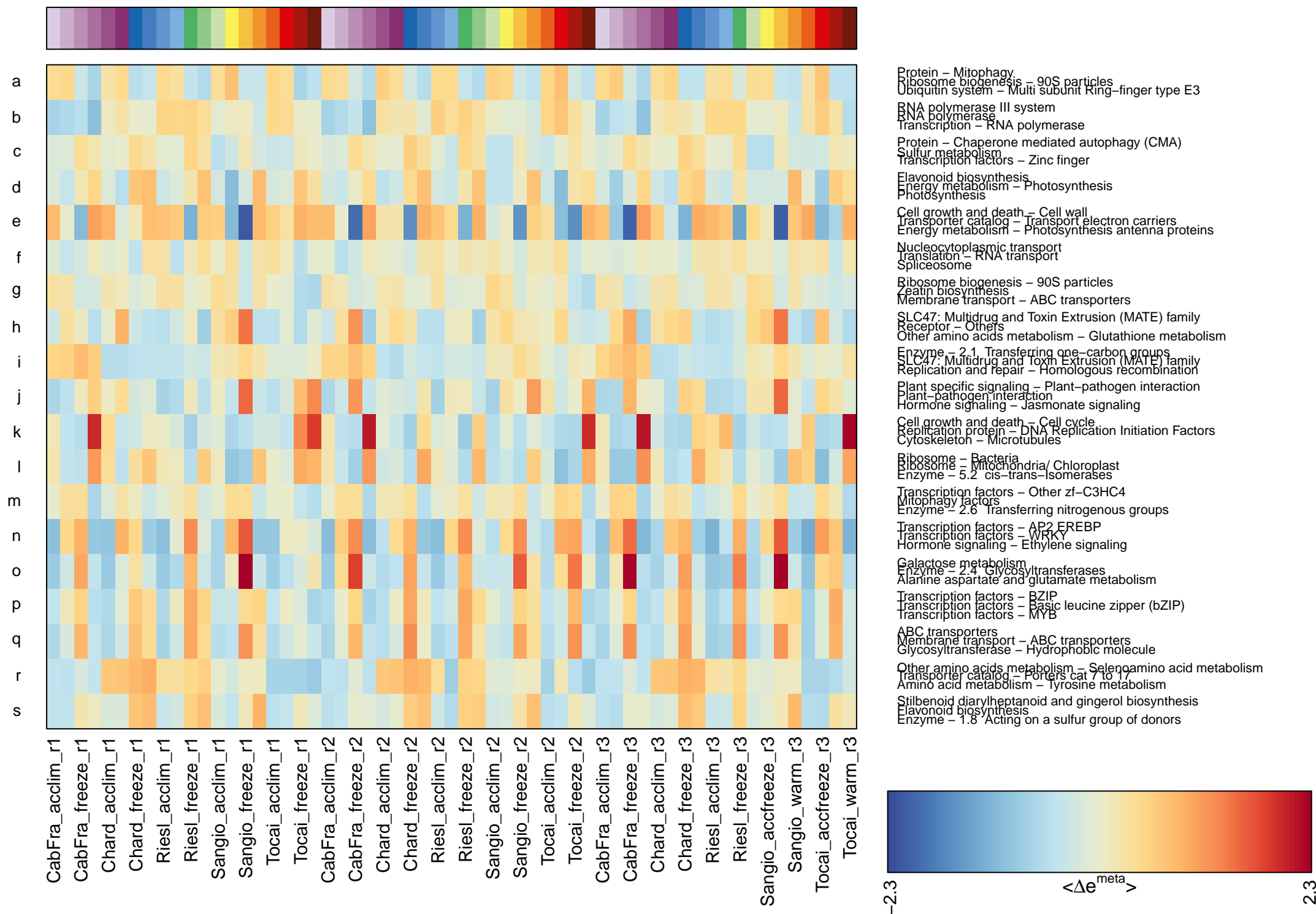
landscape



Underexpression Spots



- a Protein – Mitophagy
Ribosome biogenesis – 90S particles
- b RNA polymerase III system
RNA polymerase
- c Protein – Chaperone mediated autophagy (CMA)
Sulfur metabolism
- d Flavonoid biosynthesis
Energy metabolism – Photosynthesis
- e Cell growth and death – Cell wall
Transporter catalog – Transport electron carriers
- f Nucleocytoplasmic transport
Translation – RNA transport
- g Ribosome biogenesis – 90S particles
Zeatin biosynthesis
- h SLC47: Multidrug and Toxin Extrusion (MATE) family
Receptor – Others
- i Enzyme – 2.1 Transferring one-carbon groups
SLC47: Multidrug and Toxin Extrusion (MATE) family
- j Plant specific signaling – Plant-pathogen interaction
Plant-pathogen interaction
- k Cell growth and death – Cell cycle
Replication protein – DNA Replication Initiation Factors
- l Ribosome – Bacteria
Ribosome – Mitochondria/ Chloroplast
- m Transcription factors – Other zf-C3HC4
Mitophagy factors
- n Transcription factors – AP2 EREBP
Transcription factors – WRKY
- o Galactose metabolism
Enzyme – 2.4 Glycosyltransferases
- p Transcription factors – BZIP
Transcription factors – Basic leucine zipper (bZIP)
- q ABC transporters
Membrane transport – ABC transporters
- r Other amino acids metabolism – Selenoamino acid metabo
Transporter catalog – Porters cat 7 to 17
- s Stilbenoid diarylheptanoid and gingerol biosynthesis
Flavonoid biosynthesis



Underexpression Spots

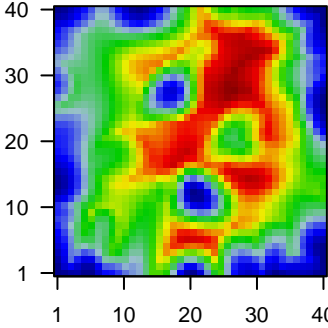
Spot Summary: a

metagenes = 32
genes = 659

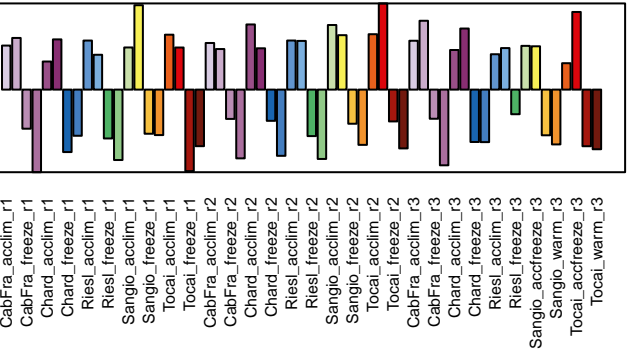
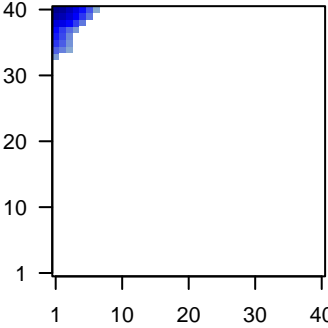
<r> metagenes = 0.95
<r> genes = 0.55
beta: r2= 10.99 / log p= -Inf

samples with spot = 6 (10.2 %)
CabFra_warm : 3 (100 %)
Riesl_warm : 2 (100 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

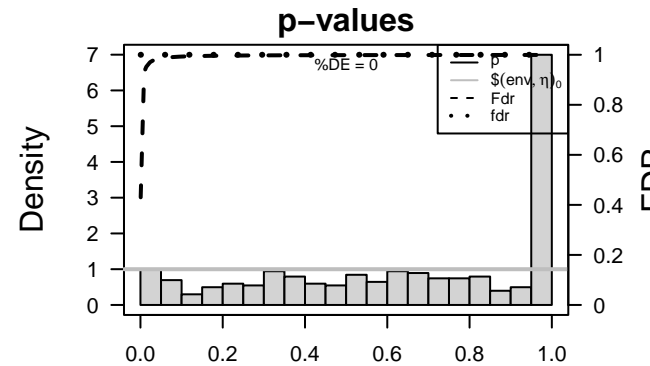


Spot Genelist

ID	Description
Vitvi12g02353	
Vitvi04g01564	
Vitvi04g01368	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi19g00581	
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.
Vitvi19g00255	
Vitvi17g00584	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.
Vitvi01g00499	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.
Vitvi05g01758	
Vitvi11g00657	
Vitvi11g01268	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi10g01384	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi05g01266	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi13g01900	
Vitvi09g00720	Binding to a metal ion.
Vitvi17g00237	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi16g01340	A conserved series of molecular signals found in prokaryotes and eukaryotes; involves autophosphorylation of a histidine kinase and the transfer of the phosphate group to an aspartate that then acts as a phospho-donor to response regulator proteins.
Vitvi11g00477	Binding to a protein.
Vitvi14g00119	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 cyclopentenone stimulus. Cyclopentenones are oxylipins derived from polyunsaturated fatty acids. They are structurally similar to jasmonic acid, but contain a reactive unsaturated carbonyl structure in the cyclo-ring. Cyclopentenones include phytosteranes and 12-oxo-phytodienoic acid.
Vitvi14g00291	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-04	4 / 11	Protein – Mitophagy
2	9e-03	7 / 62	Ribosome biogenesis – 90S particles
3	9e-03	10 / 110	Ubiquitin system – Multi subunit Ring-finger type E3
4	1e-02	5 / 36	Fatty acid degradation
5	1e-02	3 / 13	Transcription factors – HMG
6	1e-02	9 / 100	Plant specific signaling – Flower development
7	1e-02	10 / 118	Transcription factors – Helix–turn–helix
8	1e-02	7 / 68	Spliceosome associated proteins (SAPs)
9	1e-02	9 / 101	Starch and sucrose metabolism
10	2e-02	4 / 29	Other amino acids metabolism – Beta-alanine metabolism
11	2e-02	5 / 44	Hormone signaling – Cytokinin signaling
12	3e-02	3 / 18	Chaperone – HSP20
13	3e-02	9 / 115	Enzyme – 3.6 Acting on acid anhydrides
14	3e-02	4 / 32	Circadian rhythm – plant
15	3e-02	6 / 64	Transcription factors – Other transcription factors
16	4e-02	15 / 238	Enzyme – 2.4 Glycosyltransferases
17	4e-02	4 / 34	Tyrosine metabolism
18	4e-02	5 / 51	Lipid metabolism – Fatty acid metabolism
19	4e-02	5 / 51	Plant specific signaling – Circadian rhythm
20	4e-02	3 / 21	Thiamine metabolism



Underexpression Spots

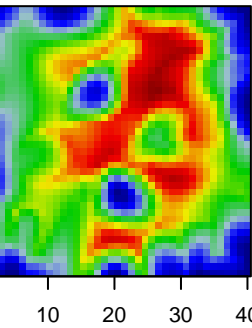
Spot Summary: b

metagenes = 9
genes = 188

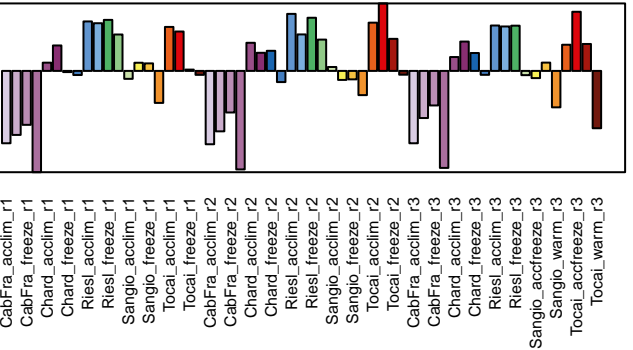
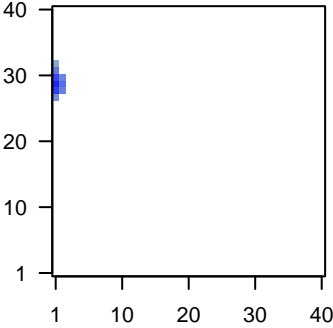
<r> metagenes = 0.95
<r> genes = 0.4
beta: r2= 5.85 / log p= -Inf

samples with spot = 8 (13.6 %)
CabFra_acclim : 3 (100 %)
CabFra_accfreeze : 2 (66.7 %)
CabFra_warm : 3 (100 %)

Overview Map



Spot

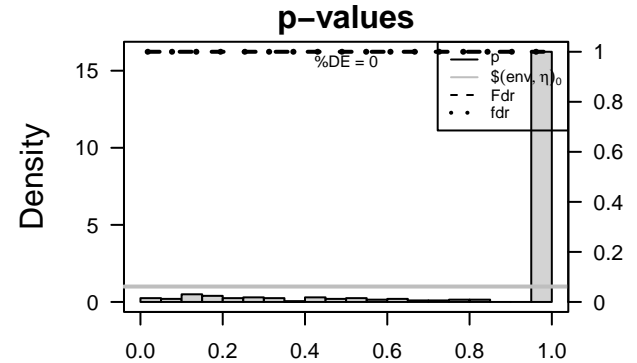


Spot Genelist

ID	Description
Vitvi12g00117	A membrane-bound cytoplasmic organelle of the endomembrane system that further processes the core oligosaccharides (N-glycans) added to proteins in the endoplasmic reticulum and packages them into membrane-bound vesicles. The Golgi apparatus operates at the intersection of the secretory, lysosomal, and endocytic pathways.
Vitvi14g01657	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi03g00919	
Vitvi16g00789	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi00g01146	
Vitvi00g00686	
Vitvi10g02298	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).
Vitvi13g00786	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi07g01651	
Vitvi19g02279	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.
Vitvi14g02924	Any intracellular signal transduction in which the signal is passed on within the cell via calcium ions.
Vitvi02g00620	Binding to a metal ion.
Vitvi10g00184	
Vitvi13g02475	Binding to ADP, adenosine 5'-diphosphate.
Vitvi19g00154	
Vitvi16g01449	
Vitvi10g00973	Binding to a calcium ion (Ca2+).
Vitvi19g02299	
Vitvi12g00890	
Vitvi00g01866	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.02	2 / 28	RNA polymerase III system
2	0.03	2 / 35	RNA polymerase
3	0.04	2 / 41	Transcription - RNA polymerase
4	0.04	2 / 44	Hormone signaling - Cytokinin signaling
5	0.05	2 / 47	ABC transporters
6	0.06	2 / 54	Amino acid metabolism - Methionine metabolism
7	0.07	2 / 58	Other amino acids metabolism - Glutathione metabolism
8	0.07	2 / 62	Translation - Aminoacyl-tRNA biosynthesis
9	0.09	2 / 71	Glutathione metabolism
10	0.10	3 / 153	Plant-pathogen interaction
11	0.11	2 / 77	Pores ion channels [TC:1]
12	0.11	1 / 16	Transcription factors - FHA
13	0.11	3 / 162	Plant specific signaling - Plant-pathogen interaction
14	0.12	1 / 17	Protein - Arf GTPases and associated proteins
15	0.12	2 / 81	Enzyme - 4.2 Carbon-oxygen lyases
16	0.12	1 / 18	Nicotinate and nicotinamide metabolism
17	0.12	1 / 18	Chaperone - HSP20
18	0.12	1 / 18	Transcription factors - Other zf-DHHC
19	0.13	1 / 19	RNA polymerase I system
20	0.16	1 / 24	Folate biosynthesis



Underexpression Spots

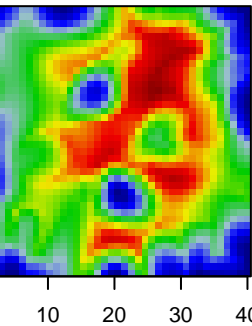
Spot Summary: c

metagenes = 18
genes = 283

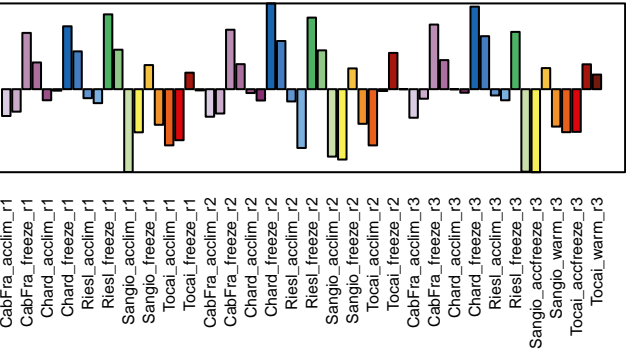
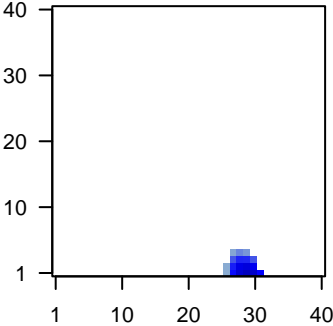
<r> metagenes = 0.88
<r> genes = 0.35
beta: r2= 4.54 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

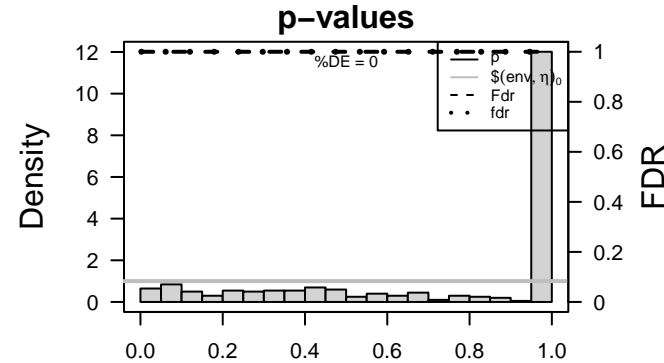


Spot Genelist

ID	Description
Vitvi18g01129	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.
Vitvi18g02715	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi14g00297	
Vitvi11g01457	Binding to a protein.
Vitvi04g02017	
Vitvi03g01392	
Vitvi18g00955	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi12g01982	
Vitvi02g01680	
Vitvi00g01074	
Vitvi11g00319	Stimulates the exchange of GDP to GTP on a signaling GTPase, changing its conformation to its active form. Guanine nucleotide exchange factors (GEFs) act by stimulating the release of guanosine diphosphate (GDP) to allow binding of guanosine triphosphate (GTP), which is more abundant in the cell under normal cellular physiological conditions.
Vitvi15g01669	Binding to ADP, adenosine 5'-diphosphate.
Vitvi02g01427	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.
Vitvi13g01713	Binding to a nucleic acid.
Vitvi09g01592	The inner, i.e. lumen-facing, lipid bilayer of the mitochondrial envelope. It is highly folded to form cristae.
Vitvi13g02449	Binding to ADP, adenosine 5'-diphosphate.
Vitvi14g00002	
Vitvi06g01418	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi13g00129	Binding to a protein.
Vitvi19g00994	Binding to a protein.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.002	4 / 38	Protein – Chaperone mediated autophagy (CMA)
2	0.007	3 / 28	Sulfur metabolism
3	0.014	3 / 36	Transcription factors – Zinc finger
4	0.019	3 / 40	Amino acid metabolism – Cysteine metabolism
5	0.023	2 / 17	Isoquinoline alkaloid biosynthesis
6	0.023	2 / 17	Proteasome – Assembling factors
7	0.024	4 / 77	Cysteine and methionine metabolism
8	0.026	3 / 45	Galactose metabolism
9	0.029	3 / 47	ABC transporters
10	0.030	3 / 48	Amino acid metabolism – Lysine biosynthesis
11	0.045	2 / 24	Tropane piperidine and pyridine alkaloid biosynthesis
12	0.048	2 / 25	Phenylalanine metabolism
13	0.048	2 / 25	Biosynthesis of secondary metabolism – Zeatin biosynthesis
14	0.055	2 / 27	ABCG (White) subfamily
15	0.056	4 / 102	Membrane transport – ABC transporters
16	0.059	2 / 28	Exosome – Exosomal proteins of breast milk
17	0.063	2 / 29	Energy metabolism – Sulfur metabolism
18	0.067	2 / 30	Lipid biosynthesis protein – Component type
19	0.069	3 / 67	Ribosome – Bacteria
20	0.072	5 / 157	Protein processing in endoplasmic reticulum



Underexpression Spots

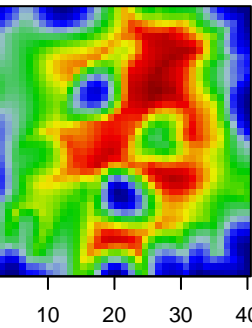
Spot Summary: d

metagenes = 29
genes = 430

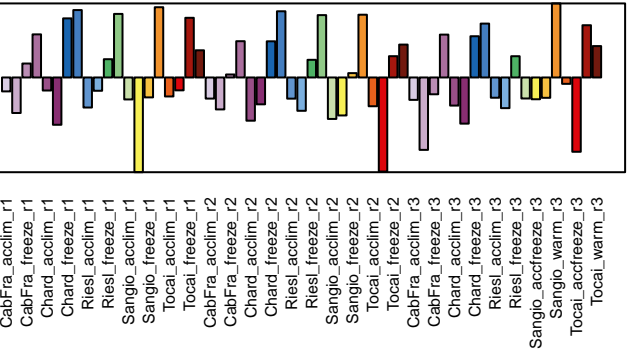
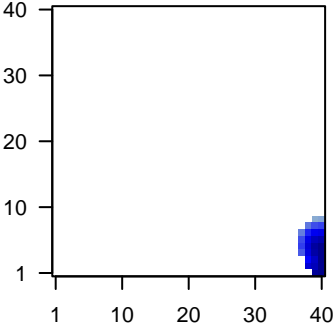
<r> metagenes = 0.94
<r> genes = 0.52
beta: r2= 11.42 / log p= -Inf

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

Overview Map



Spot

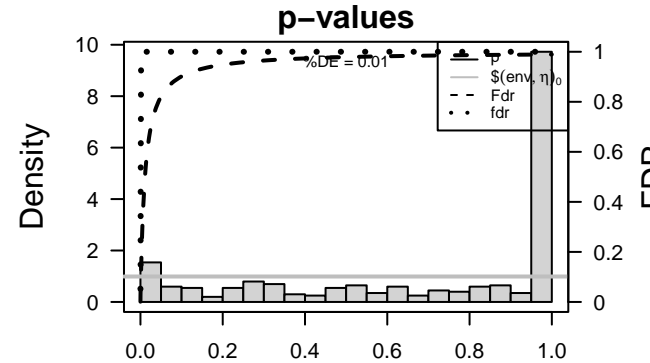


Spot Genelist

ID	Description
Vitvi19g02039	
Vitvi01g01982	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.
Vitvi14g01448	
Vitvi05g01044	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi13g02504	
Vitvi06g00158	Binding to a metal ion.
Vitvi00g00590	
Vitvi07g03060	
Vitvi07g02608	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. 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. 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.
Vitvi15g00938	
Vitvi11g01295	
Vitvi09g00206	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.
Vitvi04g00357	
Vitvi03g01833	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi14g01449	
Vitvi18g02574	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. 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	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.
Vitvi19g00007	
Vitvi08g01465	The series of molecular signals initiated upon sensing of blue light by photoreceptor molecule, at a wavelength between 400nm and 470nm.
Vitvi14g02493	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-06	7 / 26	Flavonoid biosynthesis
2	1e-04	9 / 78	Energy metabolism – Photosynthesis
3	3e-04	6 / 38	Photosynthesis
4	5e-04	7 / 57	Glyoxylate and dicarboxylate metabolism
5	2e-03	3 / 10	Linoleic acid metabolism
6	3e-03	5 / 40	Energy metabolism – Methane metabolism
7	5e-03	7 / 83	Transcription factors – MYB
8	5e-03	6 / 63	Phenylpropanoid biosynthesis
9	7e-03	8 / 111	Transporter catalog – Porters cat 66 to 94
10	1e-02	4 / 35	Lipid metabolism – Alpha-linolenic acid metabolism
11	1e-02	5 / 56	Glycine serine and threonine metabolism
12	1e-02	7 / 102	Membrane transport – ABC transporters
13	2e-02	4 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
14	2e-02	4 / 41	Cofactors and vitamin metabolism – Riboflavin metabolism
15	2e-02	3 / 24	Transporter catalog – Group translocators
16	2e-02	4 / 44	Energy metabolism – Nitrogen metabolism
17	2e-02	3 / 25	Nitrogen metabolism
18	2e-02	2 / 10	Photosynthesis protein – Photosynthetic electron transport
19	3e-02	10 / 197	Transporter catalog – Channels and pores
20	3e-02	7 / 118	Transcription factors – Helix-turn-helix



Underexpression Spots

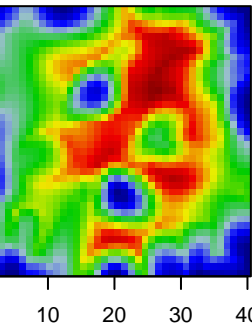
Spot Summary: e

metagenes = 27
genes = 537

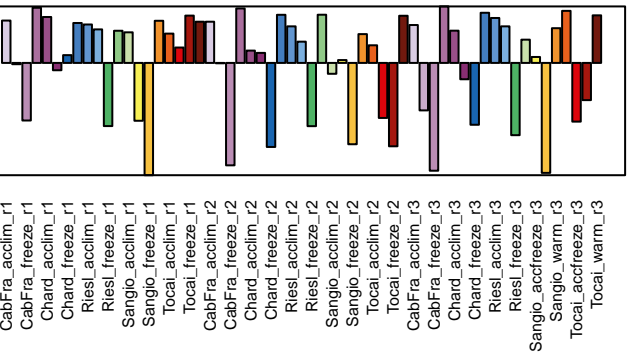
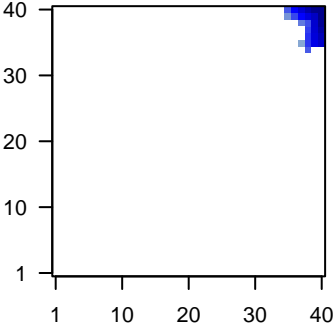
<r> metagenes = 0.97
<r> genes = 0.75
beta: r2= 47.63 / log p= -Inf

samples with spot = 17 (28.8 %)
CabFra_accfreeze : 1 (33.3 %)
CabFra_freeze : 3 (100 %)
Chard_freeze : 2 (66.7 %)
Riesl_freeze : 3 (100 %)
Sangio_accfreeze : 1 (33.3 %)
Sangio_freeze : 3 (100 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 2 (66.7 %)

Overview Map



Spot

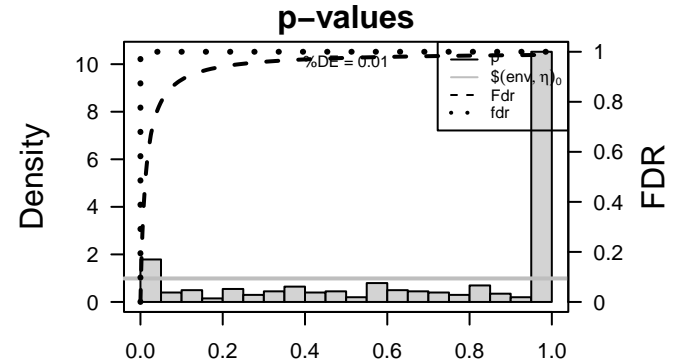


Spot Genelist

ID	Description
Vitvi19g00257	A chlorophyll-containing plastid with thylakoids organized into grana and frets, or stroma thylakoids, and embedded in a stroma.
Vitvi08g00853	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.
Vitvi07g02246	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi11g00518	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.
Vitvi07g02443	
Vitvi10g00740	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi15g00714	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.
Vitvi10g00100	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.
Vitvi12g02394	
Vitvi17g00234	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi04g00501	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.
Vitvi17g00480	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.
Vitvi19g00041	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.
Vitvi13g01855	
Vitvi08g00961	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi09g00264	Catalysis of the hydrolysis of any ester bond.
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.
Vitvi11g01450	
Vitvi12g00586	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-25	46 / 206	Cell growth and death – Cell wall
2	3e-15	18 / 47	Transporter catalog – Transport electron carriers
3	2e-14	12 / 18	Energy metabolism – Photosynthesis antenna proteins
4	1e-12	11 / 18	Photosynthesis – antenna proteins
5	4e-09	7 / 10	Photosynthesis protein – Photosystem I (P700 chlorophyll a)
6	1e-06	13 / 78	Energy metabolism – Photosynthesis
7	8e-06	5 / 10	Peptidases and inhibitors – Family A1: pepsin family
8	9e-06	21 / 217	Cell motility – Regulation of actin cytoskeleton
9	1e-05	12 / 80	Cytoskeleton – Microtubules
10	3e-05	8 / 38	Photosynthesis
11	3e-05	8 / 39	Pentose and glucuronate interconversions
12	4e-05	8 / 40	Transport system – Thylakoid targeting pathway
13	8e-05	14 / 129	Enzyme – 3.2 Glycosylases
14	3e-04	5 / 19	Aquaporins and small neutral solute transporters [TC:1.A.8]
15	1e-03	8 / 65	Phagosome
16	1e-03	12 / 134	Hormone signaling – Auxin signaling
17	3e-03	5 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
18	4e-03	7 / 63	Phenylpropanoid biosynthesis
19	5e-03	5 / 34	Peptidases and inhibitors – Family S10
20	5e-03	7 / 65	Transport and catabolism – Phagosome



Underexpression Spots

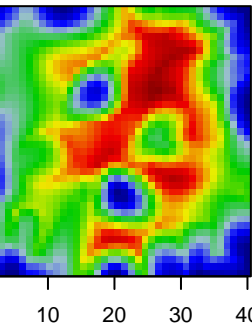
Spot Summary: f

metagenes = 20
genes = 256

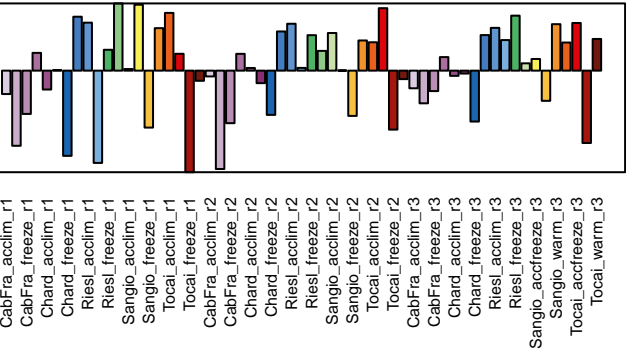
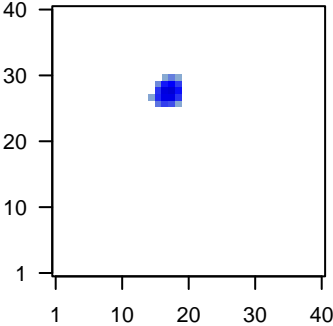
<r> metagenes = 0.95
<r> genes = 0.41
beta: r2= 1.88 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

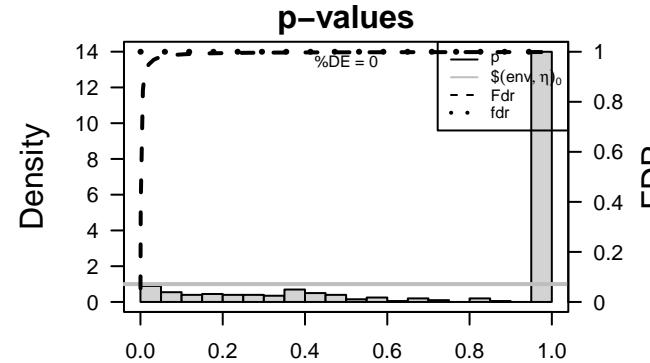


Spot Genelist

ID	Description
Vitvi04g02107	
Vitvi18g02642	
Vitvi13g01364	
Vitvi06g00368	A conserved series of molecular signals found in prokaryotes and eukaryotes; involves autophosphorylation of a histidine kinase and the transfer of the phosphate group to an aspartate that then acts as a phospho-donor to response regulator proteins.
Vitvi05g01824	
Vitvi06g01250	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi13g01620	Binding to ADP, adenosine 5'-diphosphate.
Vitvi17g00474	
Vitvi13g02309	Binding to ADP, adenosine 5'-diphosphate. A small, dense body one or more of which are present in the nucleus of eukaryotic cells. It is rich in RNA and protein, is not bounded by a limiting membrane, and is not seen during mitosis. Its prime function is the transcription of the nucleolar DNA into 45S ribosomal-precursor RNA, the processing of this RNA into 5.8S, 18S, and 28S components of ribosomal RNA, and the association of these components with 5S RNA and proteins synthesized outside the nucleolus. This association results in the formation of ribonucleoprotein precursors; these pass into the cytoplasm and mature into the 40S and 60S subunits 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.
Vitvi11g01102	
Vitvi14g01462	
Vitvi16g00437	A cellular process that results in the biosynthesis of constituent macromolecules, assembly, and arrangement of constituent parts of ribosome subunits, includes transport to the sites of protein synthesis.
Vitvi18g00908	Binding to a protein.
Vitvi13g02473	
Vitvi13g01420	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi13g01473	
Vitvi16g00148	The space enclosed by the double membrane of a chloroplast but excluding the thylakoid space. It contains DNA, ribosome, and some temporary products of photosynthesis.
Vitvi14g01710	
Vitvi15g00307	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi09g01718	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-05	7 / 85	Nucleocytoplasmic transport
2	7e-04	7 / 126	Translation - RNA transport
3	6e-03	6 / 139	Spliceosome
4	9e-03	11 / 409	Enzyme - 2.7 Transferring phosphorus-containing groups
5	1e-02	2 / 14	Proteins involved in snRNP biogenesis
6	1e-02	5 / 115	Enzyme - 3.6 Acting on acid anhydrides
7	1e-02	4 / 75	Translation - Ribosome biogenesis in Eukaryotes
8	2e-02	3 / 48	Transport system - Nuclear pore complex
9	2e-02	2 / 19	Transcription factors - Jumonji
10	3e-02	2 / 24	Mitochondrial dynamics
11	3e-02	5 / 151	RNA polymerase II system
12	3e-02	2 / 25	Lysine degradation
13	3e-02	2 / 25	Protein - Tethering complex
14	4e-02	3 / 62	Ribosome biogenesis - 90S particles
15	4e-02	3 / 63	Messenger RNA Biogenesis - mRNA degradation factors
16	4e-02	2 / 27	Common spliceosomal components
17	4e-02	2 / 28	RNA polymerase III system
18	5e-02	4 / 116	Ribosome biogenesis - Pre-60S particles
19	5e-02	2 / 32	Protein - Actin-binding proteins
20	6e-02	2 / 34	Transcription factors - SET PCG



Underexpression Spots

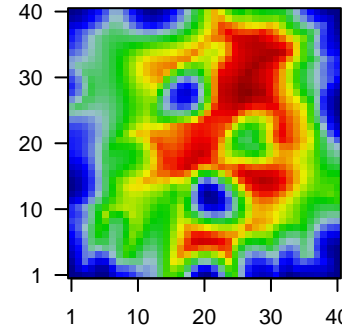
Spot Summary: g

metagenes = 28
genes = 387

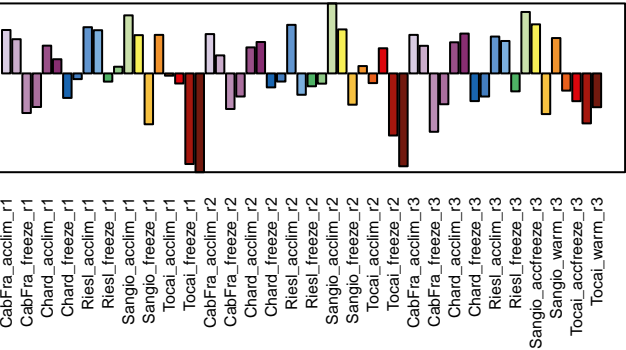
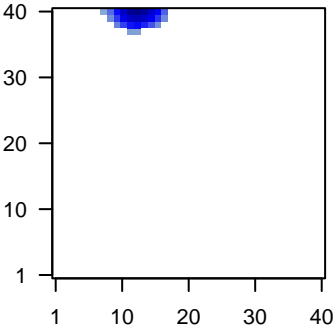
<r> metagenes = 0.88
<r> genes = 0.29
beta: r2= 4.39 / log p= -Inf

samples with spot = 3 (5.1 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 2 (66.7 %)

Overview Map



Spot

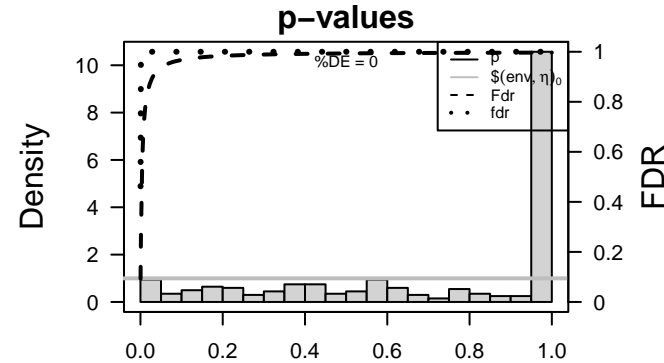


Spot Genelist

ID	Description
Vitvi00g01651	
Vitvi10g02090	
Vitvi12g02726	
Vitvi07g01407	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.
Vitvi18g00150	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
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.
Vitvi12g02680	
Vitvi03g01162	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi04g00104	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.
Vitvi08g02224	
Vitvi16g01407	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi10g00241	Any process that modulates the frequency, rate or extent of defense response to fungus.
Vitvi11g01693	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi04g00161	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.
Vitvi09g01933	
Vitvi04g01300	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi03g01524	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.
Vitvi14g00017	
Vitvi10g00570	
Vitvi19g00618	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-04	7 / 62	Ribosome biogenesis – 90S particles
2	1e-03	3 / 11	Zeatin biosynthesis
3	4e-03	7 / 102	Membrane transport – ABC transporters
4	7e-03	5 / 60	Enzyme – 4.1 Carbon-carbon lyases
5	9e-03	5 / 64	Ribosome biogenesis in eukaryotes
6	1e-02	4 / 44	Pentose phosphate pathway
7	1e-02	7 / 123	Carbohydrate metabolism – Glycolysis
8	1e-02	3 / 25	Biosynthesis of secondary metabolism – Zeatin biosynthesis
9	1e-02	5 / 72	Energy metabolism – Carbon fixation
10	2e-02	5 / 75	Translation – Ribosome biogenesis in Eukaryotes
11	2e-02	4 / 51	Carbon fixation in photosynthetic organisms
12	2e-02	4 / 54	Carbohydrate metabolism – Pentose phosphate
13	2e-02	2 / 12	Enzyme – Class I
14	2e-02	2 / 12	SLC15: Proton oligopeptide cotransporter
15	3e-02	7 / 146	Transporter catalog – Porters cat 7 to 17
16	3e-02	3 / 33	Carbohydrate metabolism – Aminosugars metabolism
17	3e-02	2 / 14	Enzyme – 1.5 Acting on the CH-NH group of donors
18	4e-02	4 / 64	Purine metabolism
19	4e-02	3 / 38	Protein – Chaperone mediated autophagy (CMA)
20	5e-02	5 / 101	Glycolysis / Gluconeogenesis



Underexpression Spots

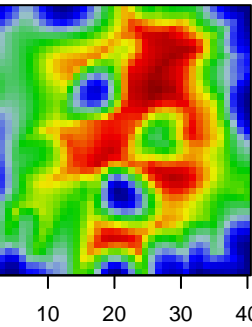
Spot Summary: h

metagenes = 11
genes = 173

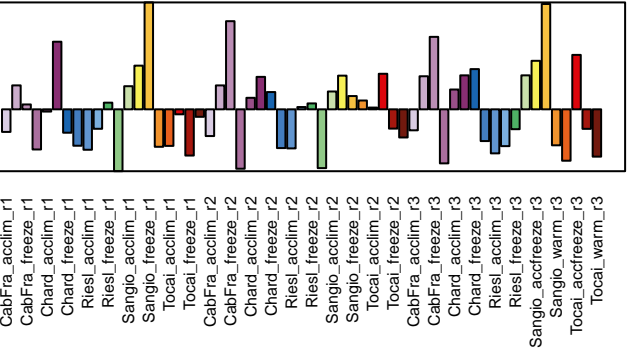
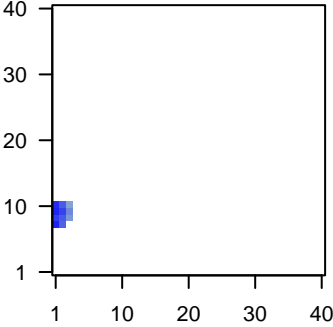
<r> metagenes = 0.98
<r> genes = 0.54
beta: r2= 16.35 / log p= -Inf

samples with spot = 8 (13.6 %)
CabFra_warm : 2 (66.7 %)
Riesl_acclim : 1 (33.3 %)
Riesl_warm : 2 (100 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 1 (33.3 %)

Overview Map



Spot

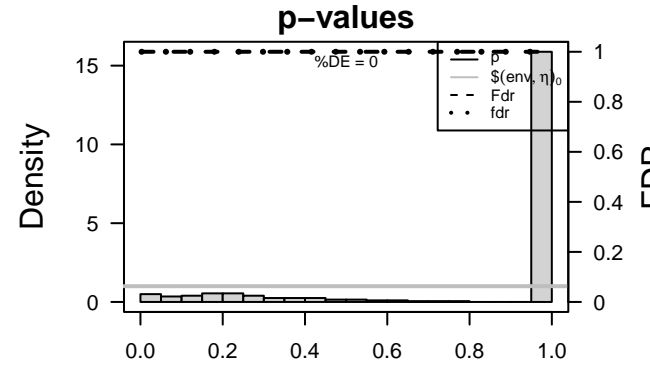


Spot Genelist

ID	Description
Vitvi19g01824	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi18g02837	
Vitvi16g01999	
Vitvi19g00566	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.
Vitvi00g01747	
Vitvi16g02104	
Vitvi13g00351	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.
Vitvi05g00675	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi00g00710	
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.
Vitvi00g01746	
Vitvi16g02105	
Vitvi10g02249	
Vitvi00g00328	
Vitvi06g00784	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.
Vitvi17g01451	Binding to a manganese ion (Mn).
Vitvi19g00700	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.
Vitvi00g01732	
Vitvi16g02119	
Vitvi09g01664	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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	3 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
2	0.007	2 / 18	Receptor - Others
3	0.007	3 / 58	Other amino acids metabolism - Glutathione metabolism
4	0.014	2 / 26	Sphingolipid metabolism
5	0.029	2 / 39	beta-Alanine metabolism
6	0.032	2 / 41	Cofactors and vitamin metabolism - Riboflavin metabolism
7	0.035	2 / 43	Mitochondrial respiratory chain complex assembly factors
8	0.041	3 / 111	Transporter catalog - Porters cat 66 to 94
9	0.043	2 / 48	Transcription factors - WRKY
10	0.045	2 / 49	Transcription factors - NAC
11	0.054	4 / 206	Cell growth and death - Cell wall
12	0.067	1 / 10	Kinase - Wnk family
13	0.086	2 / 71	Glutathione metabolism
14	0.086	2 / 71	Amino acid metabolism - Phenylalanine metabolism
15	0.086	1 / 13	Biosynthesis of unsaturated fatty acids
16	0.098	2 / 77	Pores ion channels [TC:1]
17	0.098	1 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
18	0.101	3 / 162	Plant specific signaling - Plant-pathogen interaction
19	0.104	1 / 16	Other glycan degradation
20	0.104	1 / 16	Enzyme - 1.4 Acting on the CH-NH2 group of donors



Underexpression Spots

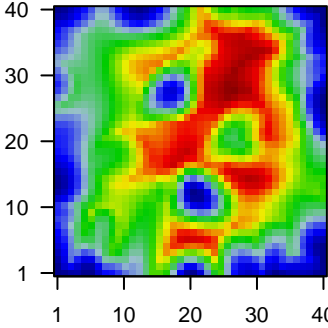
Spot Summary: i

metagenes = 27
genes = 214

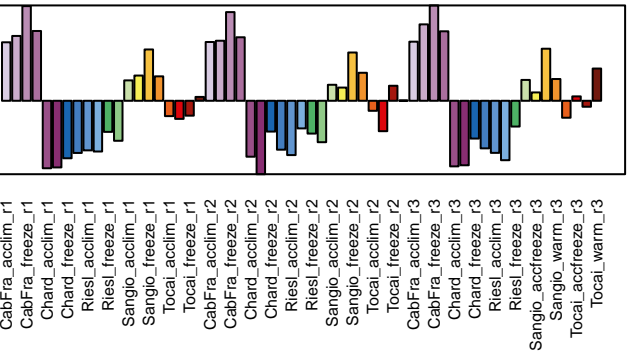
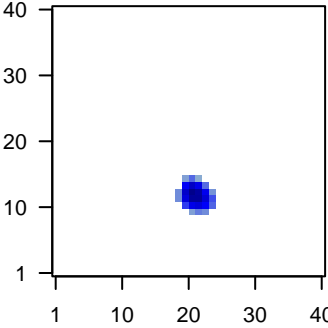
<r> metagenes = 0.92
<r> genes = 0.37
beta: r2= 4.23 / log p= -Inf

samples with spot = 1 (1.7 %)
Chard_accfreeze : 1 (33.3 %)

Overview Map



Spot

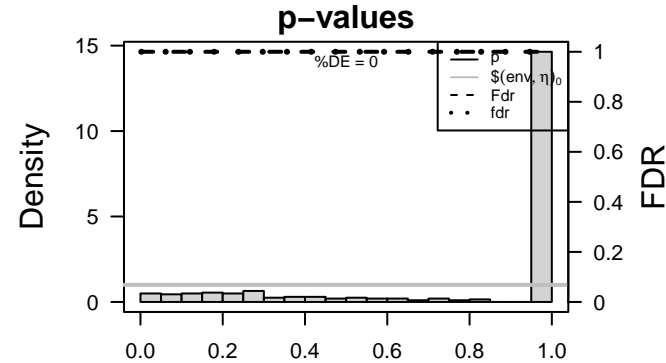


Spot Genelist

ID	Description
Vitvi11g01692	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi04g01103	Binding to a protein.
Vitvi00g01805	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.
Vitvi15g01711	
Vitvi07g02478	
Vitvi12g02011	Binding to ADP, adenosine 5'-diphosphate.
Vitvi12g02725	
Vitvi18g01016	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.
Vitvi09g01698	Binding to ADP, adenosine 5'-diphosphate.
Vitvi05g01751	
Vitvi04g00432	
Vitvi01g01859	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.
Vitvi12g02066	Binding to ADP, adenosine 5'-diphosphate.
Vitvi19g00256	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi05g01816	
Vitvi15g01706	
Vitvi19g02147	
Vitvi14g03015	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.
Vitvi02g01339	
Vitvi14g01791	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.002	6 / 161	Enzyme - 2.1 Transferring one-carbon groups
2	0.004	3 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
3	0.013	2 / 22	Replication and repair - Homologous recombination
4	0.020	2 / 27	Mismatch repair
5	0.032	2 / 35	Lipid metabolism - Alpha-linolenic acid metabolism
6	0.034	2 / 36	DNA replication
7	0.035	4 / 153	Plant-pathogen interaction
8	0.036	2 / 37	Homologous recombination
9	0.049	2 / 44	Nucleotide excision repair
10	0.049	5 / 247	Translation - Ribosome
11	0.053	3 / 105	Energy metabolism - Oxidative phosphorylation
12	0.060	3 / 111	Transporter catalog - Porters cat 66 to 94
13	0.089	2 / 62	Translation - Aminoacyl-tRNA biosynthesis
14	0.091	2 / 63	Phenylpropanoid biosynthesis
15	0.092	1 / 12	Enzyme - Class I
16	0.096	2 / 65	Phagosome
17	0.096	2 / 65	Transport and catabolism - Phagosome
18	0.100	1 / 13	Biosynthesis of unsaturated fatty acids
19	0.100	1 / 13	Kinase - CAMKL family
20	0.101	2 / 67	Amino acid metabolism - Tyrosine metabolism



Underexpression Spots

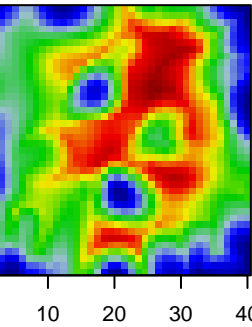
Spot Summary: j

metagenes = 9
genes = 244

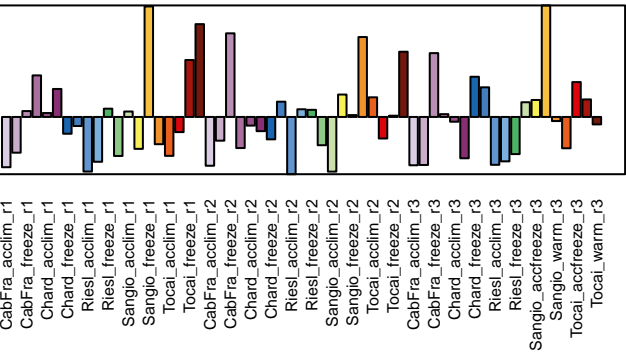
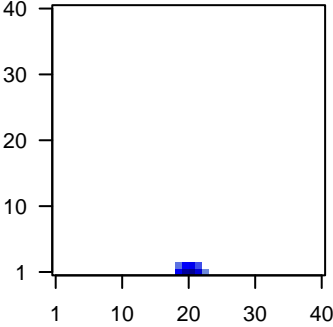
<r> metagenes = 0.99
<r> genes = 0.49
beta: r2= 10.96 / log p= -Inf

samples with spot = 10 (16.9 %)
CabFra_acclim : 3 (100 %)
CabFra_accfreeze : 1 (33.3 %)
Riesl_acclim : 3 (100 %)
Riesl_accfreeze : 2 (66.7 %)
Sangio_acclim : 1 (33.3 %)

Overview Map



Spot

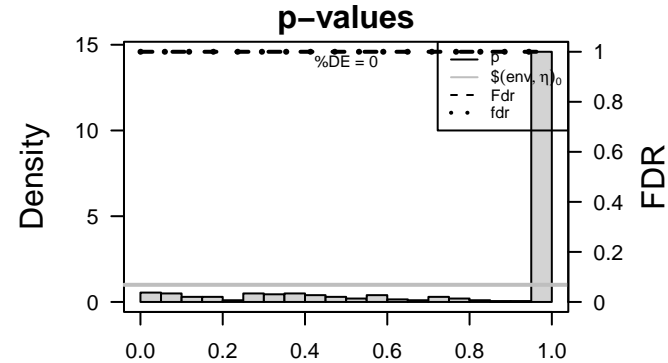


Spot Genelist

ID	Description
Vitvi04g00031	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi01g02058	Catalysis of the reaction: NADP(+) + thioredoxin = H(+) + NADPH + thioredoxin disulfide.
Vitvi14g01967	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi16g01336	Binding to a metal ion.
Vitvi14g03031	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.
Vitvi08g01702	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi09g01555	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi04g01937	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.
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.
Vitvi02g00391	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.
Vitvi10g00214	Transfer of ubiquitin to a substrate protein via the reaction X-ubiquitin + S -> X + S-ubiquitin, where X is either an E2 or E3 enzyme, the X-ubiquitin linkage is a thioester bond, and the S-ubiquitin linkage is an amide bond: an isopeptide bond between the C-terminal glycine of ubiquitin and the epsilon-amino group of lysine residues in the substrate or, in the linear extension of ubiquitin chains, a peptide bond between the C-terminal glycine and N-terminal glycine of ubiquitin residues.
Vitvi11g00097	Nuclear envelope 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.
Vitvi19g01957	
Vitvi07g01847	Any process that modulates the frequency, rate or extent of cellular DNA-templated transcription.
Vitvi15g01035	
Vitvi04g00021	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi18g02534	
Vitvi04g01888	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi04g00029	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi06g00153	Binding to a metal ion.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-10	16 / 162	Plant specific signaling – Plant-pathogen interaction
2	5e-07	12 / 153	Plant-pathogen interaction
3	6e-06	7 / 56	Hormone signaling – Jasmonate signaling
4	3e-04	5 / 48	Transcription factors – WRKY
5	1e-02	2 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
6	2e-02	4 / 83	Transcription factors – MYB
7	3e-02	4 / 89	MAPK signaling pathway – plant
8	3e-02	2 / 21	Butanoate metabolism
9	3e-02	4 / 96	Transporter catalog – Porters cat 1 to 6
10	4e-02	6 / 197	Transporter catalog – Channels and pores
11	5e-02	5 / 157	Protein processing in endoplasmic reticulum
12	6e-02	5 / 168	Plant hormone signal transduction
13	6e-02	4 / 118	Transcription factors – Helix-turn-helix
14	6e-02	2 / 33	alpha-Linolenic acid metabolism
15	6e-02	2 / 33	Carbohydrate metabolism – Aminosugars metabolism
16	6e-02	2 / 33	Carbohydrate metabolism – Butanoate metabolism
17	7e-02	2 / 35	Lipid metabolism – Alpha-linolenic acid metabolism
18	7e-02	3 / 77	Pores ion channels [TC:1]
19	8e-02	4 / 129	Enzyme – 3.2 Glycosylases
20	9e-02	2 / 40	Amino acid metabolism – Cysteine metabolism



Underexpression Spots

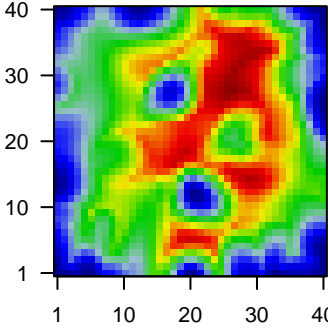
Spot Summary: k

metagenes = 20
genes = 368

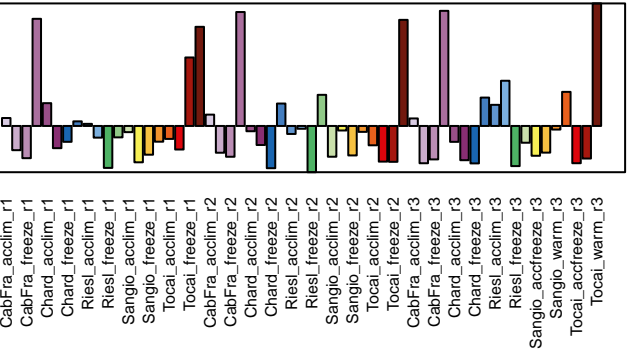
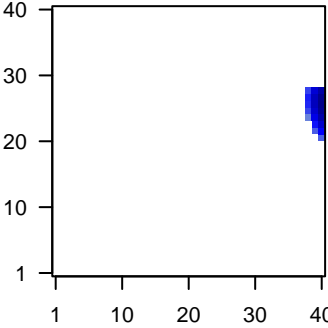
<r> metagenes = 0.98
<r> genes = 0.71
beta: r2= 28.15 / log p= -Inf

samples with spot = 14 (23.7 %)
CabFra_accfreeze : 1 (33.3 %)
CabFra_freeze : 2 (66.7 %)
Chard_accfreeze : 1 (33.3 %)
Chard_freeze : 2 (66.7 %)
Riesl_freeze : 3 (100 %)
Sangio_accfreeze : 1 (33.3 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 2 (66.7 %)

Overview Map



Spot

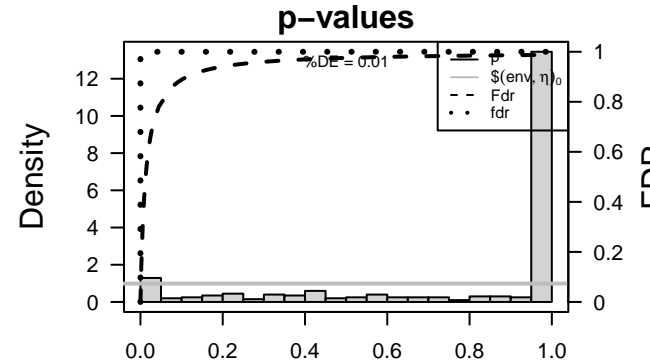


Spot Genelist

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.
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.
Vitvi18g02991	
Vitvi18g00687	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.
Vitvi06g00569	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi10g00669	Catalysis of the hydrolysis of any ester bond.
Vitvi12g01813	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.
Vitvi10g00442	
Vitvi14g00821	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi18g00040	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.
Vitvi13g01699	Binding to a metal ion.
Vitvi06g00656	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.
Vitvi14g00189	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.
Vitvi03g00542	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.
Vitvi07g02188	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi04g00602	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.
Vitvi08g01436	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi16g01310	Any process carried out at the cellular level that reduces or removes the toxicity superoxide radicals or hydrogen peroxide.
Vitvi19g00090	
Vitvi00g00723	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-26	40 / 219	Cell growth and death – Cell cycle
2	1e-14	12 / 24	Replication protein – DNA Replication Initiation Factors
3	4e-14	18 / 80	Cytoskeleton – Microtubules
4	1e-13	27 / 217	Cell motility – Regulation of actin cytoskeleton
5	5e-12	12 / 36	DNA replication
6	5e-10	11 / 41	Replication and repair – DNA replication
7	3e-06	8 / 44	Replication protein – DNA Replication Termination Factors
8	9e-05	7 / 51	Other metabolism – Single reactions
9	1e-03	5 / 37	Homologous recombination
10	2e-03	7 / 83	Transcription factors – MYB
11	2e-03	3 / 13	Transcription factors – HMG
12	2e-03	4 / 27	Mismatch repair
13	5e-03	4 / 34	Peptidases and inhibitors – Family S10
14	9e-03	4 / 39	Pentose and glucuronate interconversions
15	1e-02	10 / 206	Cell growth and death – Cell wall
16	1e-02	4 / 44	Nucleotide excision repair
17	1e-02	3 / 25	Replication and repair – Base excision repair
18	2e-02	5 / 71	Glutathione metabolism
19	2e-02	2 / 10	Protein – Syntaxin (Qa)
20	2e-02	3 / 29	Base excision repair



Underexpression Spots

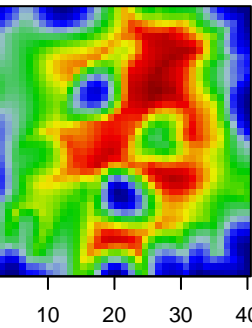
Spot Summary: I

metagenes = 17
genes = 214

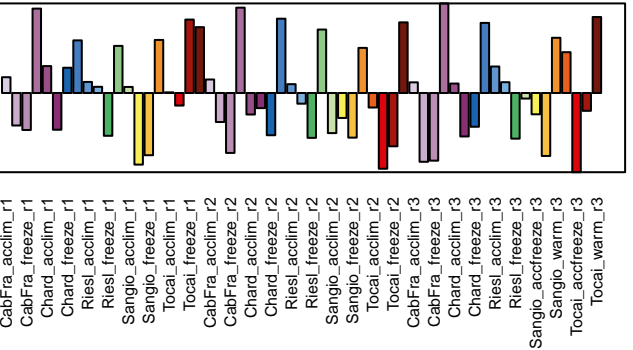
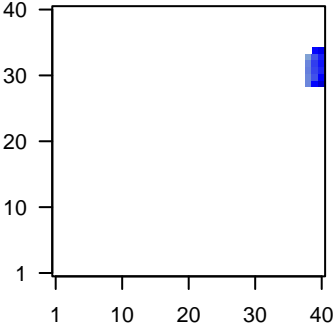
<r> metagenes = 0.97
<r> genes = 0.66
beta: r2= 21.81 / log p= -Inf

samples with spot = 12 (20.3 %)
CabFra_accfreeze : 1 (33.3 %)
CabFra_freeze : 2 (66.7 %)
Riesl_freeze : 2 (66.7 %)
Sangio_accfreeze : 1 (33.3 %)
Sangio_freeze : 3 (100 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

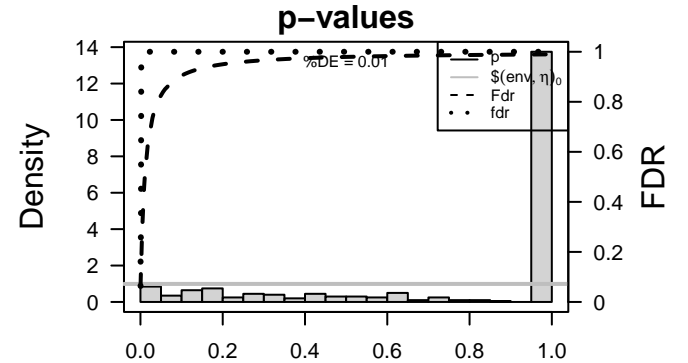


Spot Genelist

ID	Description
Vitvi14g01763	Binding to a zinc ion (Zn).
Vitvi03g00708	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi02g01404	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.
Vitvi06g00761	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.
Vitvi03g01621	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi02g00435	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.
Vitvi13g00230	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi17g00283	The directed movement of lipids into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore. Lipids are compounds soluble in an organic solvent but not, or sparingly, in an aqueous solvent.
Vitvi10g01476	Binding to a metal ion.
Vitvi14g02869	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.
Vitvi12g00202	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi08g01556	Catalysis of the reaction: peptidyl-proline (omega=180) = peptidyl-proline (omega=0).
Vitvi00g00530	
Vitvi10g02185	Catalysis of an oxidation-reduction (redox) reaction in which a CH-OH group acts as a hydrogen or electron donor and reduces NAD+ or NADP.
Vitvi15g01028	Catalysis of the hydrolysis of any ester bond.
Vitvi06g00182	Binding to a protein.
Vitvi04g01454	Binding to a metal ion.
Vitvi11g00730	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi03g01543	
Vitvi12g00631	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-04	6 / 67	Ribosome - Bacteria
2	3e-04	6 / 72	Ribosome - Mitochondria/ Chloroplast
3	7e-04	4 / 32	Enzyme - 5.2 cis-trans-Isomerases
4	1e-03	3 / 17	Chaperone - Peptidyl prolyl isomerase
5	2e-03	6 / 102	Amino sugar and nucleotide sugar metabolism
6	3e-03	4 / 48	Lipid metabolism - Fatty acid biosynthesis
7	4e-03	3 / 26	Flavonoid biosynthesis
8	9e-03	3 / 33	Enzyme - 5.4 Intramolecular transferases
9	9e-03	3 / 34	Peptidases and inhibitors - Family S10
10	1e-02	4 / 67	Amino acid metabolism - Tyrosine metabolism
11	2e-02	4 / 78	Glycosyltransferase - Structural polysaccharide
12	3e-02	5 / 134	Hormone signaling - Auxin signaling
13	3e-02	2 / 22	Fatty acid elongation
14	4e-02	2 / 24	Carbohydrate metabolism - Ascorbate and aldarate metabolism
15	4e-02	7 / 247	Translation - Ribosome
16	4e-02	2 / 25	Phenylalanine metabolism
17	5e-02	3 / 63	Phenylpropanoid biosynthesis
18	5e-02	6 / 211	Ribosome
19	6e-02	2 / 31	Fatty acid biosynthesis
20	6e-02	2 / 31	GTP-binding proteins - Rab Family



Underexpression Spots

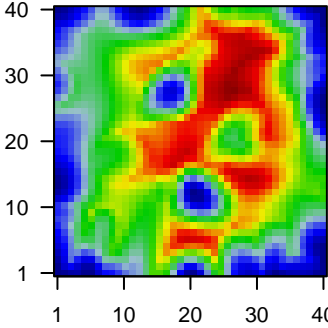
Spot Summary: m

metagenes = 57
genes = 854

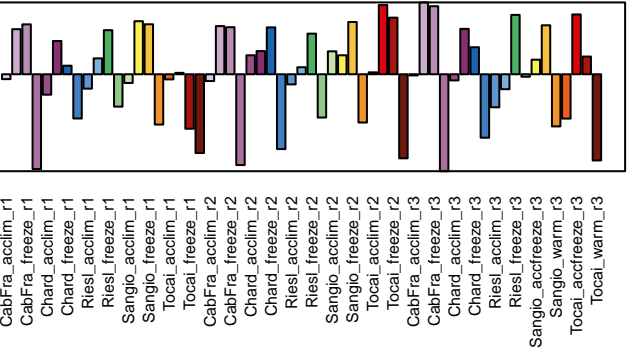
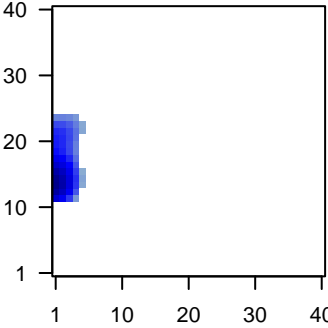
<r> metagenes = 0.94
<r> genes = 0.5
beta: r2= 6.73 / log p= -Inf

samples with spot = 5 (8.5 %)
CabFra_warm : 3 (100 %)
Tocai_warm : 2 (66.7 %)

Overview Map



Spot

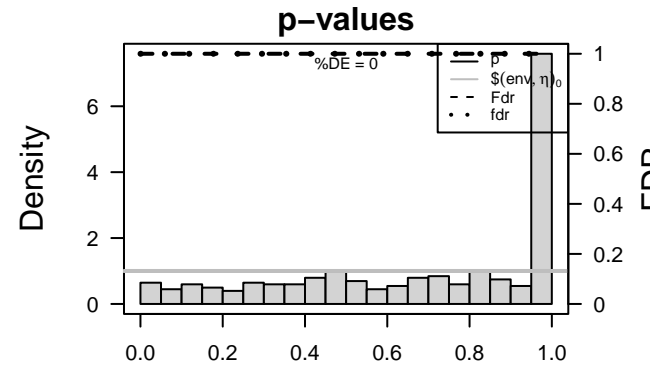


Spot Genelist

ID	Description
Vitvi05g01756	
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.
Vitvi18g00482	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.
Vitvi05g02238	
Vitvi18g01174	Mitochondrial complex that possesses alpha-ketoglutarate dehydrogenase activity.
Vitvi13g00116	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi05g01833	Binding to a metal ion.
Vitvi01g01165	The component of the plasma membrane consisting of the gene products that are tethered to the membrane only by a covalently attached anchor, such as a lipid group, that is embedded in the membrane. Gene products with peptide sequences that are embedded in the membrane are excluded from this grouping.
Vitvi00g01022	
Vitvi02g00529	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi02g00507	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.
Vitvi07g01347	
Vitvi17g00936	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.
Vitvi18g00604	
Vitvi12g00429	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi18g00879	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi13g01556	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.
Vitvi02g00250	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi11g00720	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi18g02643	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-05	20 / 170	Transcription factors - Other zf-C3HC4
2	4e-03	6 / 35	Mitophagy factors
3	7e-03	5 / 27	Enzyme - 2.6 Transferring nitrogenous groups
4	1e-02	11 / 111	Hormone signaling - ABA signaling
5	2e-02	4 / 24	Folate biosynthesis
6	2e-02	4 / 25	Transcription factors - Other zf
7	3e-02	4 / 27	Regulator of mitochondrial biogenesis
8	3e-02	5 / 40	N-Glycan biosynthesis
9	4e-02	5 / 41	Arginine and proline metabolism
10	4e-02	4 / 29	Transcription factors - GRAS
11	4e-02	5 / 43	Transcription factors - BZIP
12	5e-02	3 / 18	Nicotinate and nicotinamide metabolism
13	5e-02	4 / 31	Autophagy - other
14	5e-02	4 / 32	SNARE interactions in vesicular transport
15	6e-02	3 / 20	Protein - Autophagosome formation proteins
16	6e-02	9 / 111	Transporter catalog - Porters cat 66 to 94
17	7e-02	10 / 128	Ubiquitin system - Single Ring-finger type E3
18	8e-02	6 / 67	Amino acid metabolism - Tyrosine metabolism
19	9e-02	2 / 11	Protein - SNAP-25[C] (Qc)
20	9e-02	2 / 11	Biosynthesis of secondary metabolism - ABA biosynthesis



Underexpression Spots

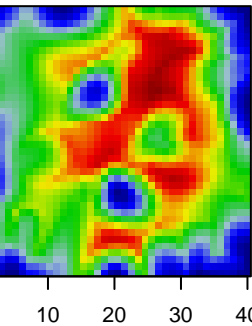
Spot Summary: n

metagenes = 21
genes = 490

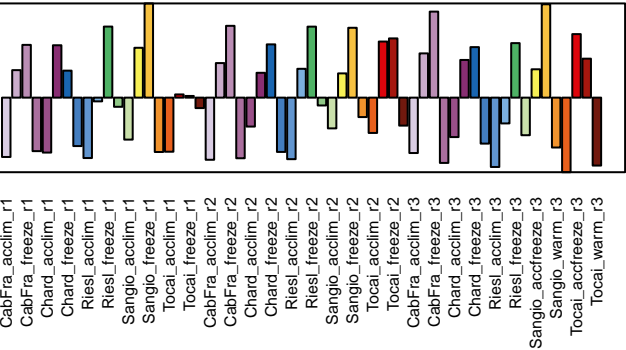
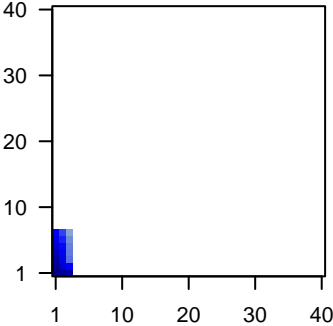
<r> metagenes = 0.97
<r> genes = 0.66
beta: r2= 42.36 / log p= -Inf

samples with spot = 22 (37.3 %)
CabFra_acclim : 3 (100 %)
CabFra_warm : 3 (100 %)
Chard_acclim : 2 (66.7 %)
Chard_warm : 3 (100 %)
Riesl_acclim : 3 (100 %)
Sangio_acclim : 2 (66.7 %)
Sangio_warm : 2 (66.7 %)
Tocai_acclim : 3 (100 %)
Tocai_warm : 1 (33.3 %)

Overview Map



Spot

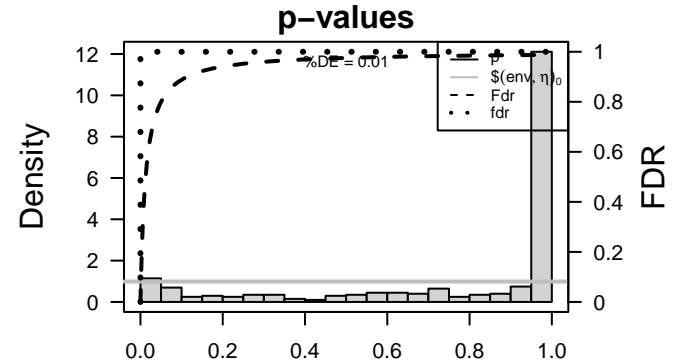


Spot Genelist

ID	Description
Vitvi02g00605	Catalysis of the reaction: n H2O + an exposed unphosphorylated, unbranched malto--oligosaccharide tail on amylopectin <= amylopectin + maltose.
Vitvi01g00714	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi01g01038	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi19g01356	Binding to a metal ion.
Vitvi19g00270	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi19g02230	Binding to a metal ion.
Vitvi08g01377	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.
Vitvi13g01972	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi02g00114	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.
Vitvi11g00140	Binding to a metal ion.
Vitvi18g02584	That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.
Vitvi15g01084	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi02g01288	Binding to a metal ion.
Vitvi03g00630	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 operators.
Vitvi04g00511	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.
Vitvi12g00594	Binding to a calcium ion (Ca2+).
Vitvi16g01036	Catalysis of the joining of two molecules, or two groups within a single molecule, using the energy from the hydrolysis of ATP, a similar triphosphate, or a pH gradient.
Vitvi06g00666	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi17g00173	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.
Vitvi18g00432	That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-17	22 / 73	Transcription factors - AP2 EREBP
2	1e-13	16 / 48	Transcription factors - WRKY
3	1e-13	25 / 140	Hormone signaling - Ethylene signaling
4	1e-12	17 / 64	Transcription factors - Other transcription factors
5	4e-11	14 / 49	Transcription factors - NAC
6	3e-05	15 / 153	Plant-pathogen interaction
7	2e-04	14 / 162	Plant specific signaling - Plant-pathogen interaction
8	5e-04	11 / 118	Transcription factors - Helix-turn-helix
9	3e-03	3 / 11	Biosynthesis of secondary metabolism - ABA biosynthesis
10	6e-03	5 / 42	Tryptophan metabolism
11	8e-03	4 / 29	Carotenoid biosynthesis
12	8e-03	4 / 29	Transcription factors - GRAS
13	9e-03	7 / 83	Transcription factors - MYB
14	1e-02	7 / 86	Signal transduction - Calcium signaling pathway
15	2e-02	3 / 19	Hormone signaling - Gibberellin signaling
16	2e-02	5 / 57	Transcription factors - HB
17	2e-02	5 / 58	Other amino acids metabolism - Glutathione metabolism
18	3e-02	3 / 24	Carbohydrate metabolism - Ascorbate and aldarate metabolism
19	3e-02	2 / 10	Valine leucine and isoleucine biosynthesis
20	4e-02	12 / 238	Enzyme - 2.4 Glycosyltransferases



Underexpression Spots

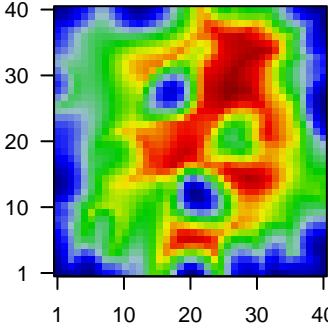
Spot Summary: o

metagenes = 15
genes = 275

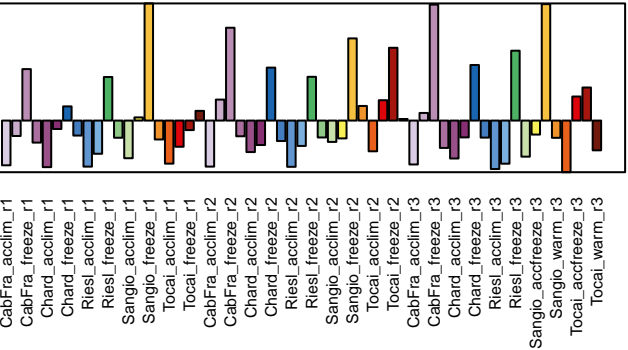
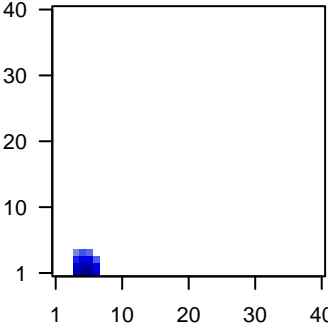
<r> metagenes = 0.99
<r> genes = 0.67
beta: r2= 34.66 / log p= -Inf

samples with spot = 16 (27.1 %)
CabFra_acclim : 3 (100 %)
Chard_acclim : 3 (100 %)
Riesl_acclim : 3 (100 %)
Riesl_accfreeze : 2 (66.7 %)
Sangio_acclim : 2 (66.7 %)
Tocai_acclim : 3 (100 %)

Overview Map



Spot

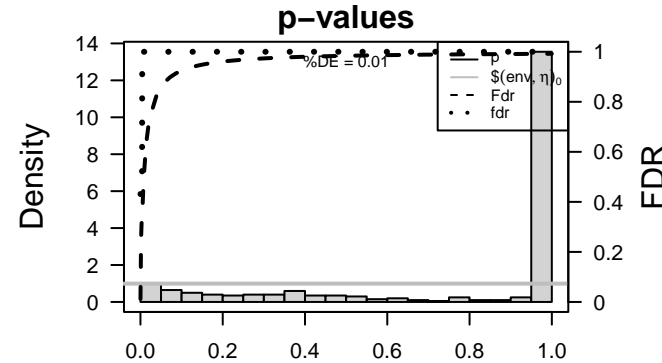


Spot Genelist

ID	Description
Vitvi02g01341	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.
Vitvi05g01930	Binding to a metal ion.
Vitvi01g00556	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.
Vitvi19g01938	
Vitvi18g00635	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.
Vitvi18g00408	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi13g01389	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi18g02548	Binding to a calcium ion (Ca2+).
Vitvi11g01153	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi11g01329	The chemical reactions and pathways resulting in the formation of substances; typically the energy-requiring part of metabolism in which simpler substances are transformed into more complex ones.
Vitvi19g01937	
Vitvi06g01917	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi05g00548	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.
Vitvi13g01395	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.
Vitvi07g01610	Any process that modulates the frequency, rate or extent of gene expression. Gene expression is the process in which a gene's coding sequence is converted into a mature gene product (protein or RNA).
Vitvi07g00736	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi02g00101	Binding to monomeric or multimeric forms of actin, including actin filaments.
Vitvi07g01325	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi12g01724	
Vitvi02g00702	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-05	6 / 45	Galactose metabolism
2	2e-03	10 / 238	Enzyme - 2.4 Glycosyltransferases
3	3e-03	4 / 43	Alanine aspartate and glutamate metabolism
4	4e-03	5 / 77	Carbohydrate metabolism - Galactose metabolism
5	4e-03	5 / 79	Transporter catalog - Porters cat 30 to 64
6	5e-03	3 / 25	Lysine degradation
7	8e-03	3 / 30	Cyanoamino acid metabolism
8	8e-03	4 / 58	Other amino acids metabolism - Glutathione metabolism
9	8e-03	5 / 92	Lipid metabolism - Glycerolipid metabolism
10	8e-03	3 / 31	Biosynthesis of various plant secondary metabolites
11	1e-02	4 / 68	Amino acid metabolism - Alanine and aspartate metabolism
12	1e-02	2 / 14	Enzyme - 1.5 Acting on the CH-NH group of donors
13	2e-02	2 / 16	Histidine metabolism
14	2e-02	3 / 44	Ascorbate and aldarate metabolism
15	2e-02	3 / 44	Energy metabolism - Nitrogen metabolism
16	2e-02	3 / 45	Valine leucine and isoleucine degradation
17	4e-02	3 / 56	Glycine serine and threonine metabolism
18	4e-02	5 / 140	Hormone signaling - Ethylene signaling
19	5e-02	2 / 26	Pantothenate and CoA biosynthesis
20	5e-02	3 / 61	Peroxisome



Underexpression Spots

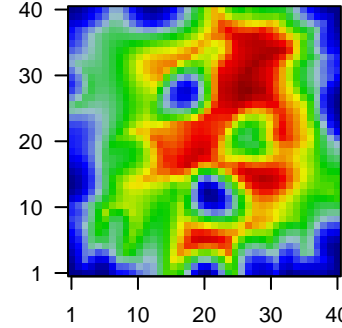
Spot Summary: p

metagenes = 3
genes = 61

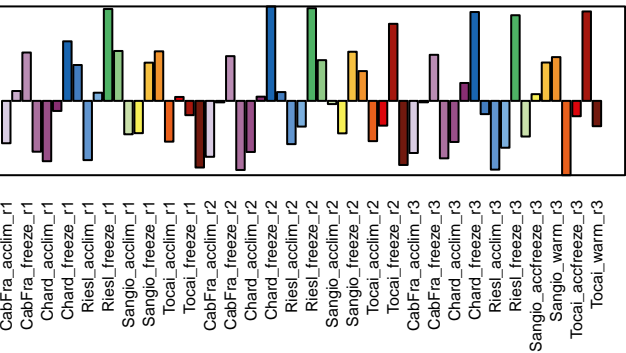
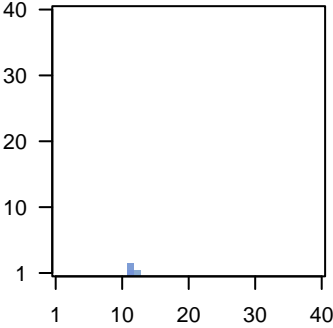
<r> metagenes = 1
<r> genes = 0.61
beta: r2= 12.51 / log p= -Inf

samples with spot = 9 (15.3 %)
CabFra_acclim : 1 (33.3 %)
CabFra_warm : 2 (66.7 %)
Chard_acclim : 1 (33.3 %)
Riesl_acclim : 2 (66.7 %)
Tocai_acclim : 1 (33.3 %)
Tocai_warm : 2 (66.7 %)

Overview Map



Spot

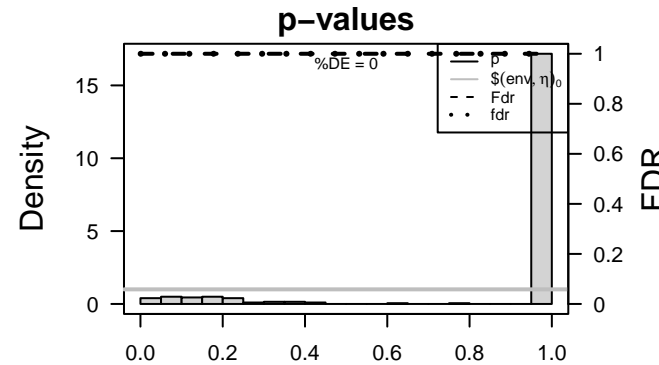


Spot Genelist

ID	Description
Vitvi13g00161	
Vitvi18g02683	Binding to a calcium ion (Ca2+).
Vitvi18g00770	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).
Vitvi02g00160	Catalysis of the reaction: a protein with reduced sulfide groups = a protein with oxidized disulfide bonds.
Vitvi01g00214	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi17g00945	
Vitvi12g00763	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.
Vitvi13g01609	Any process that modulates the frequency, rate or extent of cellular DNA-templated transcription.
Vitvi17g01570	
Vitvi02g00112	Catalysis of an oxidation-reduction (redox) reaction in which a CH-OH group acts as a hydrogen or electron donor and reduces NAD+ or NADP.
Vitvi18g02230	
Vitvi12g01906	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi18g02817	Catalysis of the hydrolysis of any ester bond.
Vitvi08g00069	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.
Vitvi16g00370	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.
Vitvi18g00020	
Vitvi02g00025	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi12g00053	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.
Vitvi02g01261	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi19g01897	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-04	3 / 43	Transcription factors - BZIP
2	4e-03	2 / 28	Transcription factors - Basic leucine zipper (bZIP)
3	3e-02	2 / 83	Transcription factors - MYB
4	3e-02	2 / 86	Signal transduction - Calcium signaling pathway
5	4e-02	1 / 11	Vitamin B6 metabolism
6	4e-02	1 / 11	Enzyme - 4.3 Carbon-nitrogen lyases
7	4e-02	1 / 11	Cofactors and vitamin metabolism - Vitamin B6 metabolism
8	5e-02	1 / 14	Cilium and associated proteins - Stereociliary proteins
9	6e-02	1 / 17	Proteasome - Assembling factors
10	6e-02	1 / 18	Chaperone - HSP20
11	6e-02	1 / 18	Receptor - Others
12	6e-02	2 / 118	Transcription factors - Helix-turn-helix
13	7e-02	1 / 23	Energy metabolism - Reductive carboxylate cycle
14	8e-02	1 / 25	Nitrogen metabolism
15	8e-02	1 / 26	Enzyme - 5.1 Racemases and epimerases
16	8e-02	1 / 26	Protein - Small GTPases and associated proteins
17	9e-02	2 / 153	Plant-pathogen interaction
18	1e-01	2 / 157	Protein processing in endoplasmic reticulum
19	1e-01	1 / 35	Mitophagy factors
20	1e-01	1 / 37	Chaperone - Protein disulfide isomerase



Underexpression Spots

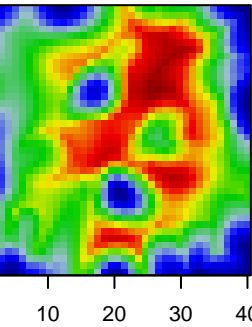
Spot Summary: q

metagenes = 7
genes = 167

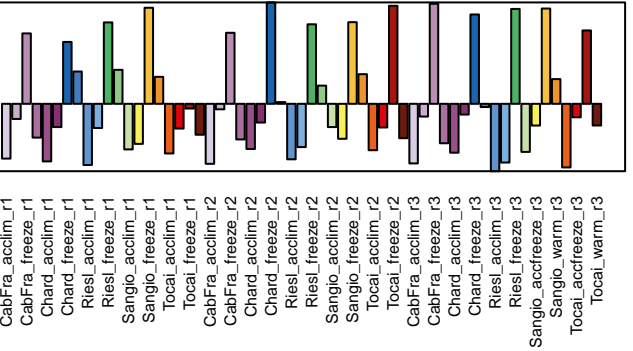
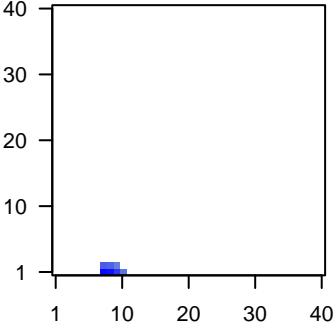
<r> metagenes = 0.99
<r> genes = 0.65
beta: r2= 19.97 / log p= -Inf

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

Overview Map



Spot

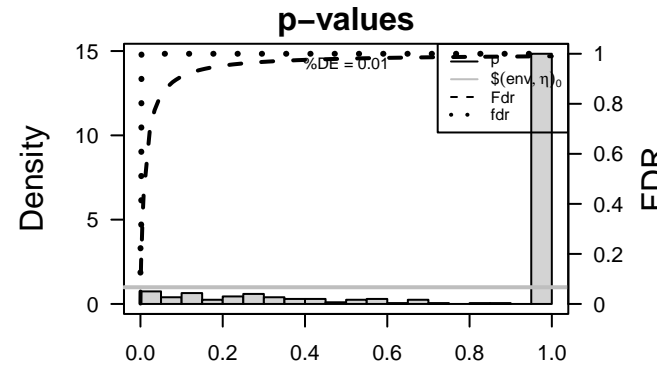


Spot Genelist

ID	Description
Vitvi03g00359	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.
Vitvi18g02684	Binding to a calcium ion (Ca2+).
Vitvi14g00488	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.
Vitvi17g00011	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi05g01193	Catalysis of the reaction: UDP-glucose + D-fructose = UDP + sucrose.
Vitvi07g01777	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi03g00170	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.
Vitvi12g01684	
Vitvi13g00779	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi08g01056	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.
Vitvi08g02249	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.
Vitvi18g02685	Binding to a calcium ion (Ca2+).
Vitvi15g00507	
Vitvi16g01210	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.
Vitvi19g02058	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.
Vitvi17g01571	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.
Vitvi18g02686	
Vitvi08g01611	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi15g00795	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi11g00304	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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-06	6 / 47	ABC transporters
2	3e-04	6 / 102	Membrane transport – ABC transporters
3	2e-03	3 / 26	Glycosyltransferase – Hydrophobic molecule
4	2e-03	3 / 27	ABCG (White) subfamily
5	2e-03	4 / 63	Phenylpropanoid biosynthesis
6	4e-03	2 / 11	Lipid metabolism – C21–Steroid hormone metabolism
7	5e-03	3 / 38	Enzyme – 1.8 Acting on a sulfur group of donors
8	6e-03	3 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
9	7e-03	5 / 131	Enzyme – 1.1 Acting on the CH–OH group of donors
10	8e-03	2 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
11	2e-02	2 / 26	Flavonoid biosynthesis
12	2e-02	2 / 26	Transcription factors – G2-like
13	3e-02	2 / 28	Exosome – Exosomal proteins of breast milk
14	3e-02	3 / 79	Transporter catalog – Porters cat 30 to 64
15	5e-02	3 / 88	Electrochemical potential–driven transporters [TC:2]
16	5e-02	2 / 40	Energy metabolism – Methane metabolism
17	6e-02	2 / 44	Hormone signaling – Cytokinin signaling
18	7e-02	4 / 168	Plant hormone signal transduction
19	8e-02	2 / 51	Biosynthesis of secondary metabolism – Auxin biosynthesis
20	8e-02	2 / 51	Plant specific signaling – Circadian rhythm



Underexpression Spots

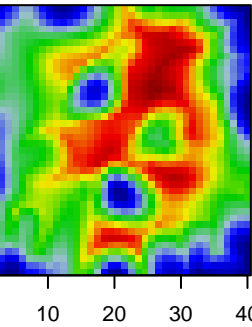
Spot Summary: r

metagenes = 17
genes = 180

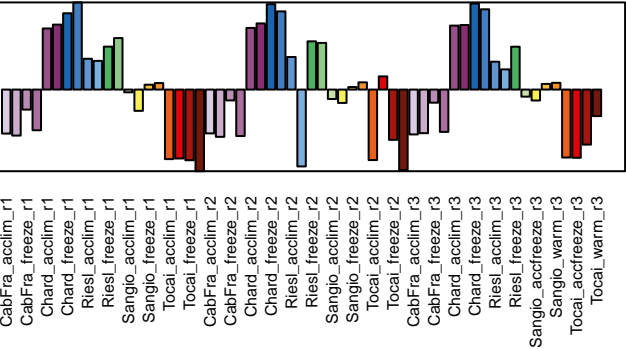
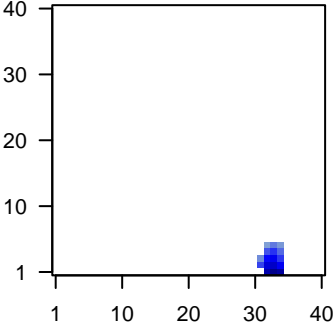
<r> metagenes = 0.94
<r> genes = 0.42
beta: r2= 9.26 / log p= -Inf

samples with spot = 10 (16.9 %)
Riesl_accfreeze : 1 (33.3 %)
Tocai_acclim : 3 (100 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 2 (66.7 %)
Tocai_warm : 2 (66.7 %)

Overview Map



Spot



Spot Genelist

ID	Description
Vitvi03g01127	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.
Vitvi16g01158	
Vitvi13g02129	
Vitvi07g01586	
Vitvi12g00598	
Vitvi07g02606	
Vitvi16g01526	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.
Vitvi07g02631	
Vitvi16g01949	
Vitvi13g02109	Binding to a protein.
Vitvi16g00811	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi12g00424	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.
Vitvi07g01395	
Vitvi02g00586	
Vitvi10g01433	
Vitvi13g02560	
Vitvi18g02221	Binding to ADP, adenosine 5'-diphosphate.
Vitvi13g00026	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi18g01877	
Vitvi09g01413	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.02	2 / 39	Other amino acids metabolism – Selenoamino acid metabolism
2	0.06	3 / 146	Transporter catalog – Porters cat 7 to 17
3	0.06	2 / 67	Amino acid metabolism – Tyrosine metabolism
4	0.07	1 / 12	SLC15: Proton oligopeptide cotransporter
5	0.07	2 / 72	Energy metabolism – Carbon fixation
6	0.08	3 / 161	Enzyme – 2.1 Transferring one-carbon groups
7	0.08	2 / 78	Energy metabolism – Photosynthesis
8	0.10	1 / 17	One carbon pool by folate
9	0.12	1 / 21	Replication and repair – Mismatch repair
10	0.13	1 / 22	Replication and repair – Homologous recombination
11	0.13	1 / 22	Transcription factors – CCAAT
12	0.13	2 / 101	Starch and sucrose metabolism
13	0.13	2 / 102	Membrane transport – ABC transporters
14	0.14	1 / 24	Enzyme – 7.1 Catalysing the translocation of hydrons
15	0.15	1 / 26	Steroid biosynthesis
16	0.15	1 / 26	Glycosyltransferase – Hydrophobic molecule
17	0.15	3 / 219	Cell growth and death – Cell cycle
18	0.15	1 / 27	SLC35: Nucleoside-sugar transporter
19	0.16	2 / 118	Transcription factors – Helix-turn-helix
20	0.17	1 / 30	Cyanoamino acid metabolism

