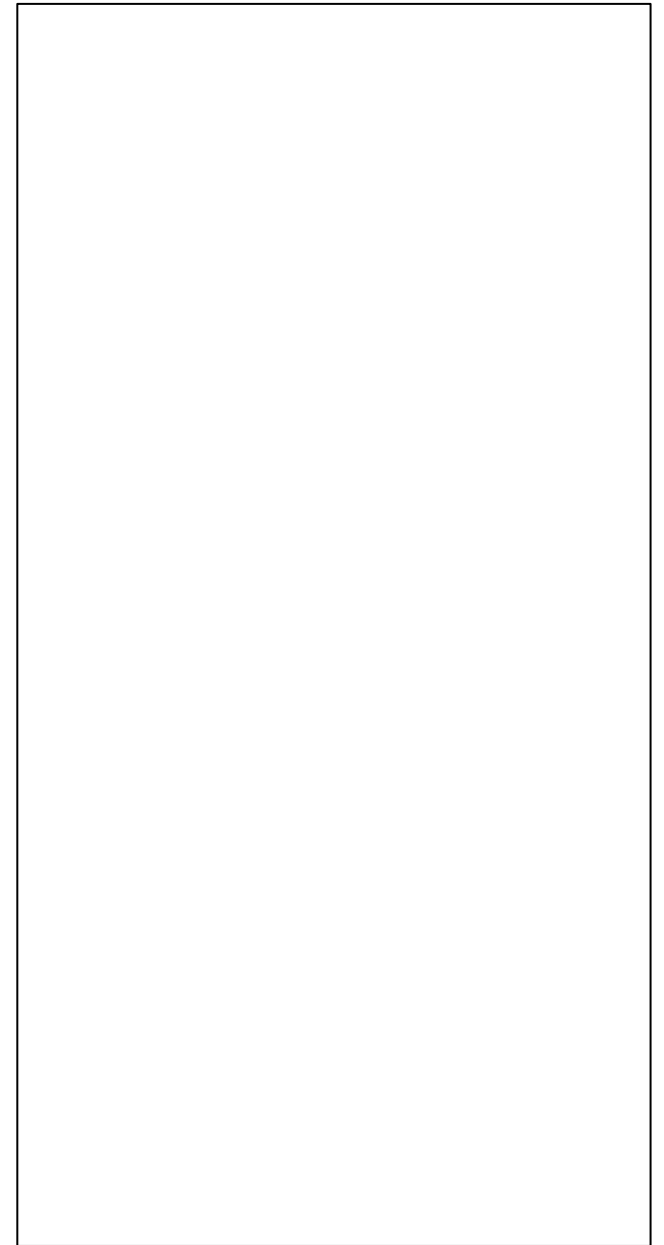
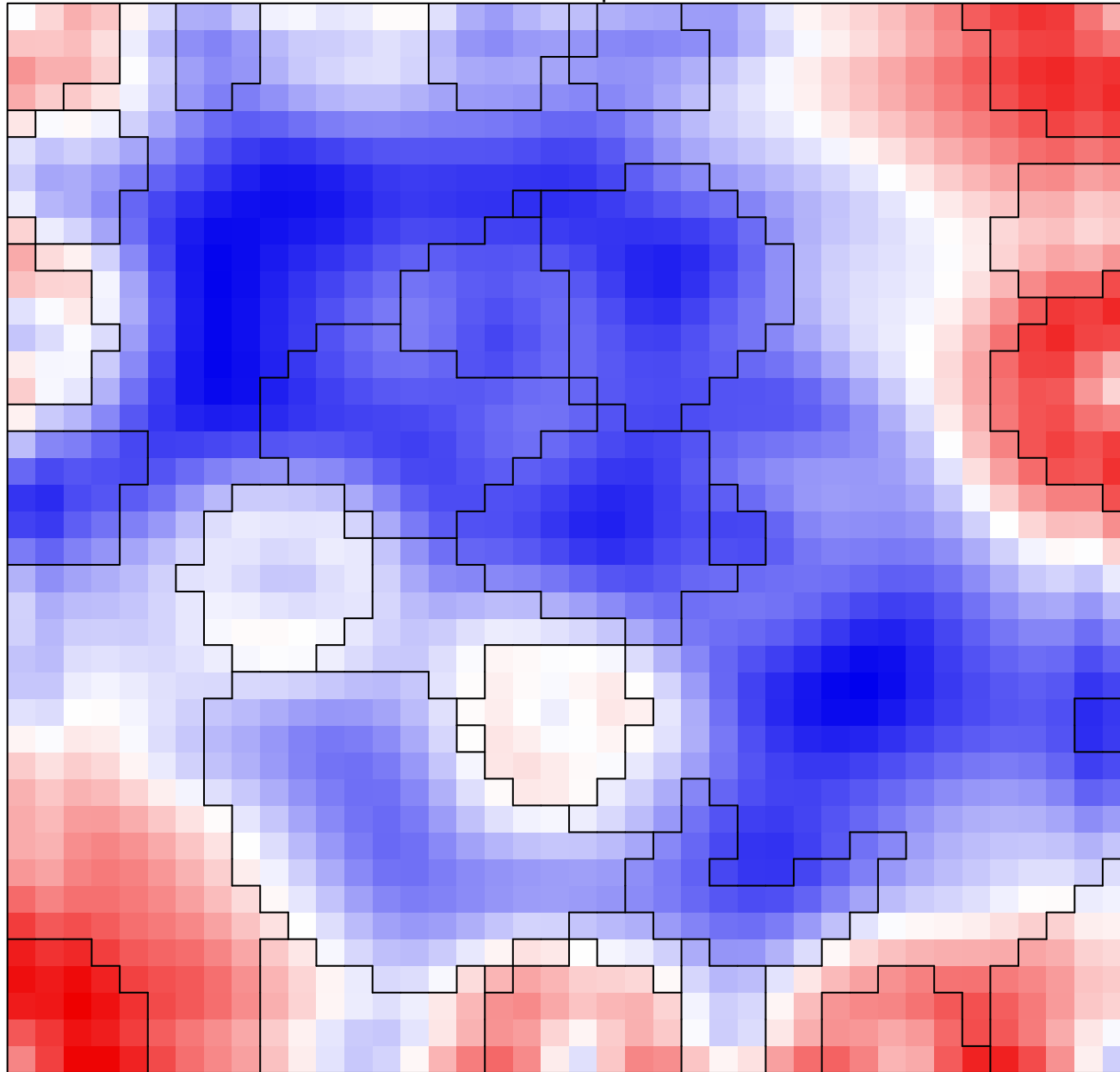


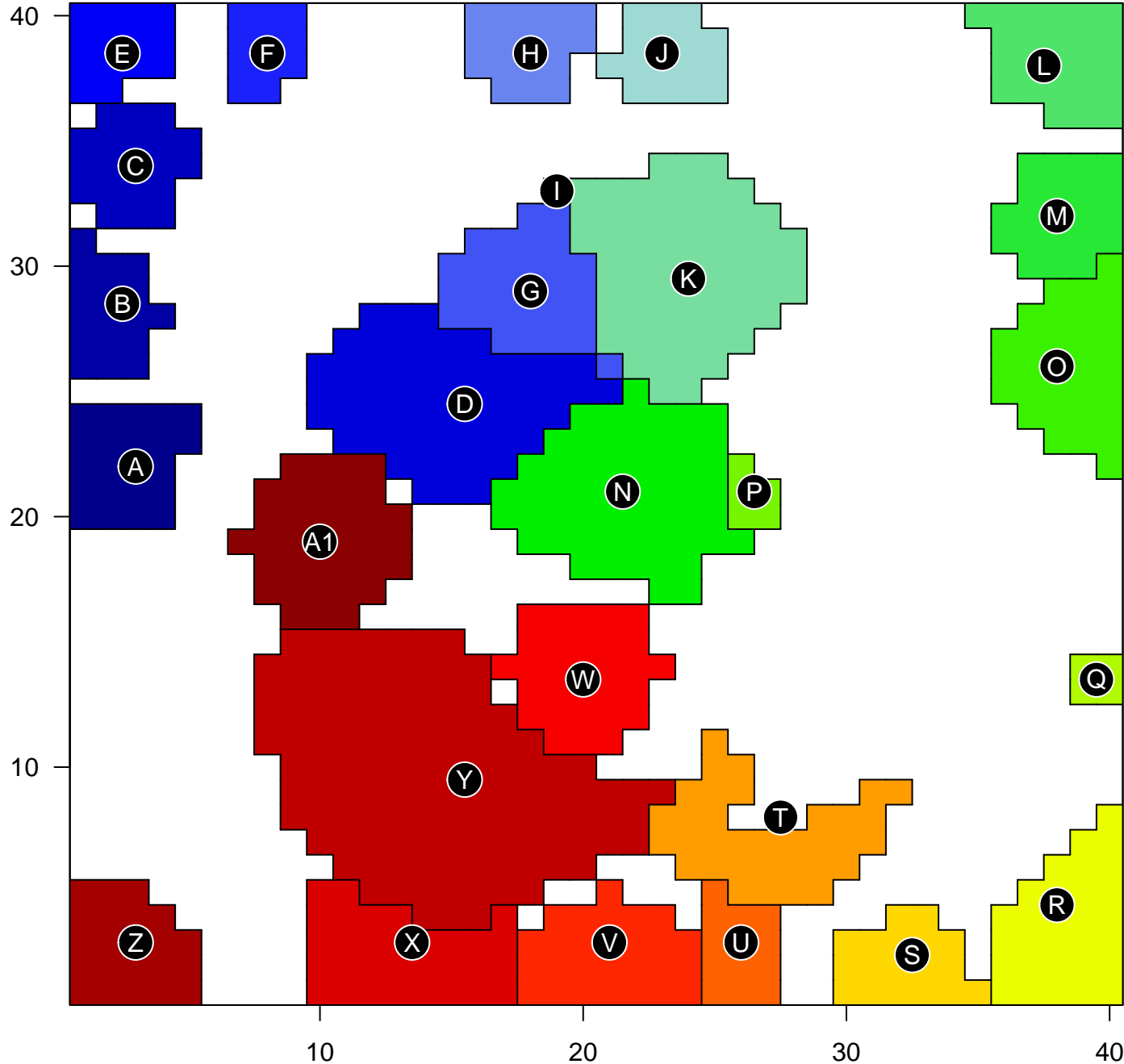
D-Cluster

landscape

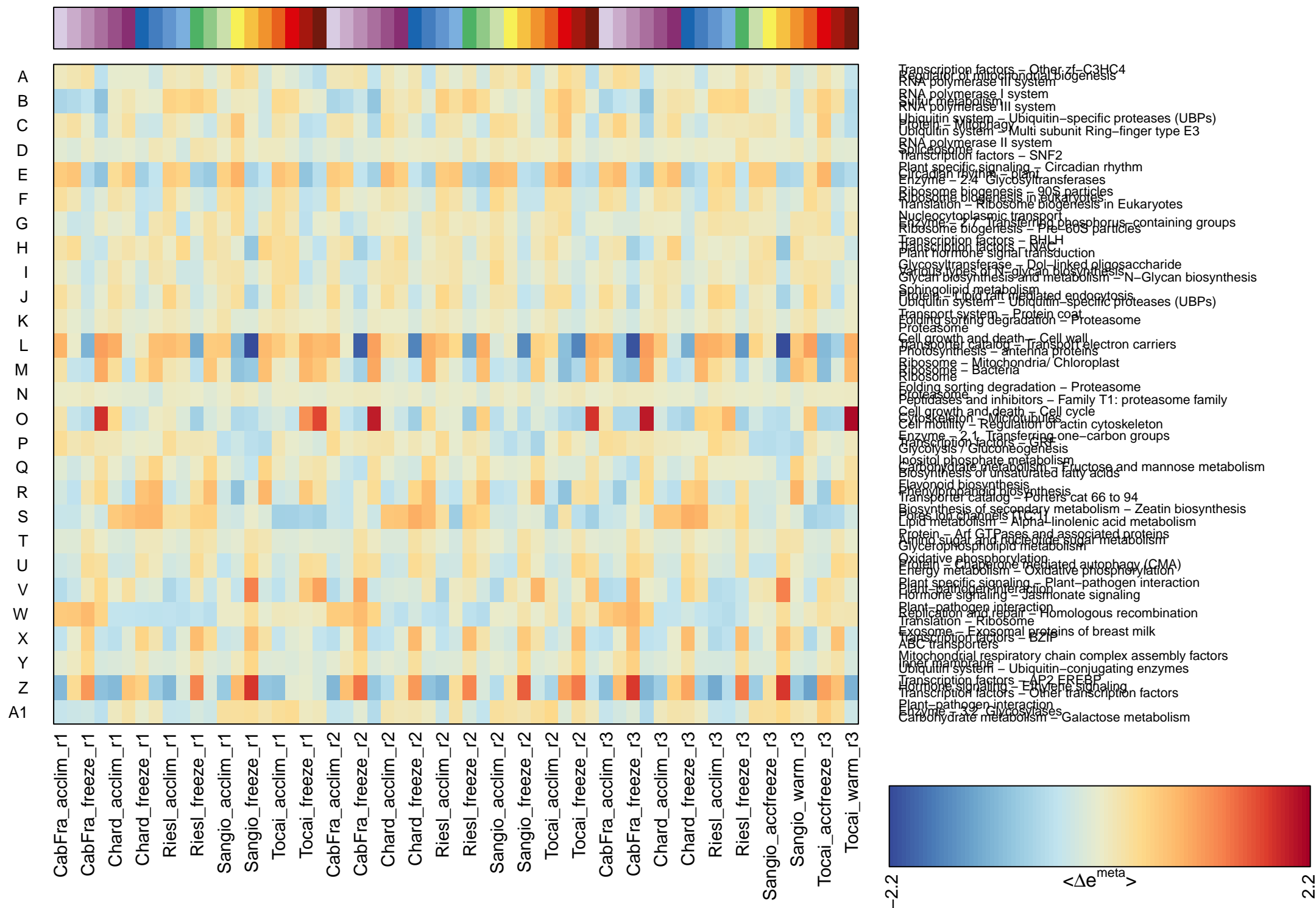


D-Cluster

annotation



- A ■ Transcription factors – Other zf-C3HC4
Regulator of mitochondrial biogenesis
- B ■ RNA polymerase I system
Sulfur metabolism
- C ■ Ubiquitin system – Ubiquitin-specific proteases (UBPs)
Protein – Mitophagy
- D ■ RNA polymerase II system
Spliceosome
- E ■ Plant specific signaling – Circadian rhythm
Circadian rhythm – plant
- F ■ Ribosome biogenesis – 90S particles
Ribosome biogenesis in eukaryotes
- G ■ Nucleocytoplasmic transport
Enzyme – 2.7 Transferring phosphorus-containing groups
- H ■ Transcription factors – BHLH
Transcription factors – NAC
- I ■ Glycosyltransferase – DoI-linked oligosaccharide
Various types of N-glycan biosynthesis
- J ■ Sphingolipid metabolism
Protein – Lipid raft mediated endocytosis
- K ■ Transport system – Protein coat
Folding sorting degradation – Proteasome
- L ■ Cell growth and death – Cell wall
Transporter catalog – Transport electron carriers
- M ■ Ribosome – Mitochondria/ Chloroplast
Ribosome – Bacteria
- N ■ Folding sorting degradation – Proteasome
Proteasome
- O ■ Cell growth and death – Cell cycle
Cytoskeleton – Microtubules
- P ■ Enzyme – 2.1 Transferring one-carbon groups
Transcription factors – GRF
- Q ■ Inositol phosphate metabolism
Carbohydrate metabolism – Fructose and mannose metabo
- R ■ Flavonoid biosynthesis
Phenylpropanoid biosynthesis
- S ■ Biosynthesis of secondary metabolism – Zeatin biosynthesi
Pores ion channels [TC:1]
- T ■ Protein – Arf GTPases and associated proteins
Amino sugar and nucleotide sugar metabolism
- U ■ Oxidative phosphorylation
Protein – Chaperone mediated autophagy (CMA)
- V ■ Plant specific signaling – Plant-pathogen interaction
Plant-pathogen interaction
- W ■ Plant-pathogen interaction
Replication and repair – Homologous recombination



D-Cluster

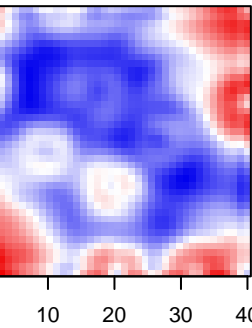
Spot Summary: A

metagenes = 22
genes = 333

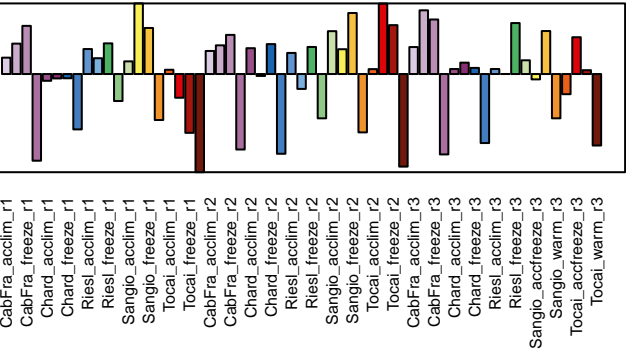
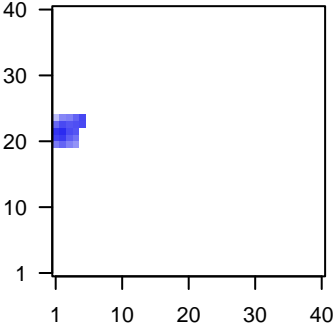
<r> metagenes = 0.97
<r> genes = 0.48
beta: r2= 3.51 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

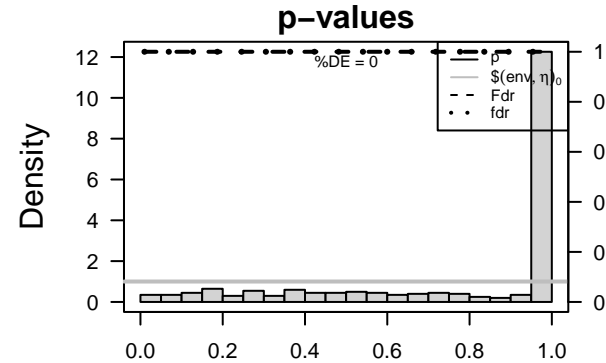


Spot Genelist

ID	Description
Vitvi19g00470	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi16g00681	
Vitvi05g00703	Binding to a metal ion.
Vitvi11g01300	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi16g01494	
Vitvi02g00060	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g00101	
Vitvi17g00019	Binding to a nucleic acid.
Vitvi06g01536	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.
Vitvi08g01011	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.
Vitvi17g01387	
Vitvi14g01437	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.
Vitvi12g00236	A semiautonomous, self replicating organelle that occurs in varying numbers, shapes, and sizes in the cytoplasm of virtually all eukaryotic cells. It is notably the site of tissue respiration.
Vitvi01g01558	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.
Vitvi13g02070	Binding to GTP, guanosine triphosphate.
Vitvi19g00678	A chlorophyll-containing plastid with thylakoids organized into grana and frets, or stroma thylakoids, and embedded in a stroma.
Vitvi00g01427	
Vitvi11g01452	
Vitvi07g03177	
Vitvi08g01805	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.01	8 / 170	Transcription factors – Other zf-C3HC4
2	0.01	3 / 27	Regulator of mitochondrial biogenesis
3	0.01	3 / 28	RNA polymerase III system
4	0.01	2 / 11	Transcription factors – SWIB
5	0.02	3 / 32	SNARE interactions in vesicular transport
6	0.03	10 / 290	Enzyme – 2.3 Acyltransferases
7	0.04	4 / 75	Translation – Ribosome biogenesis in Eukaryotes
8	0.06	2 / 24	Folate biosynthesis
9	0.06	2 / 24	Mitochondrial dynamics
10	0.07	5 / 126	Translation – RNA transport
11	0.07	5 / 128	Ubiquitin system – Single Ring-finger type E3
12	0.08	2 / 28	Transcription factors – SNF2
13	0.10	3 / 64	Ribosome biogenesis in eukaryotes
14	0.10	2 / 31	Autophagy – other
15	0.11	3 / 67	Amino acid metabolism – Tyrosine metabolism
16	0.12	2 / 34	Transcription factors – SET PCG
17	0.12	5 / 151	RNA polymerase II system
18	0.12	2 / 35	RNA polymerase
19	0.12	2 / 35	Mitophagy factors
20	0.12	3 / 71	Amino acid metabolism – Phenylalanine metabolism



D-Cluster

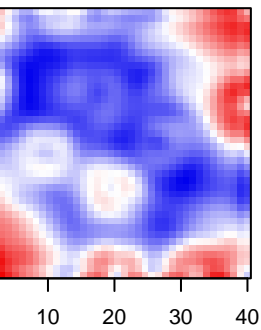
Spot Summary: B

metagenes = 17
genes = 220

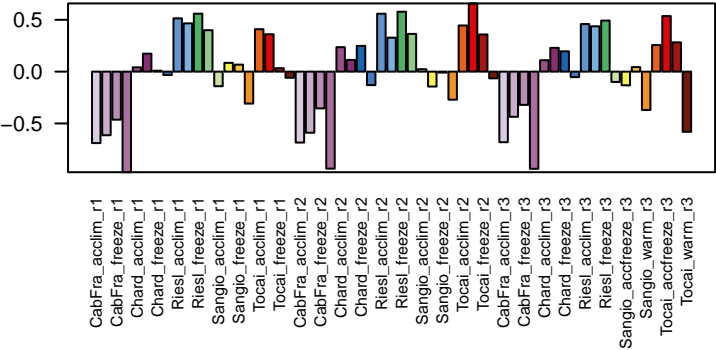
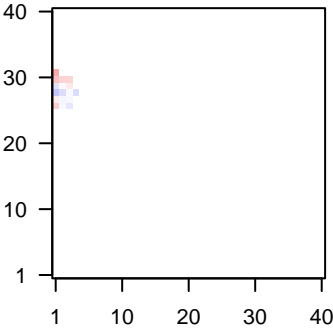
<r> metagenes = 0.97
<r> genes = 0.38
beta: r2= 5.33 / log p= -Inf

samples with spot = 8 (13.6 %)
Riesl_acclim : 2 (66.7 %)
Riesl_accfreeze : 1 (33.3 %)
Riesl_freeze : 3 (100 %)
Tocal_accfreeze : 2 (66.7 %)

Overview Map



Spot

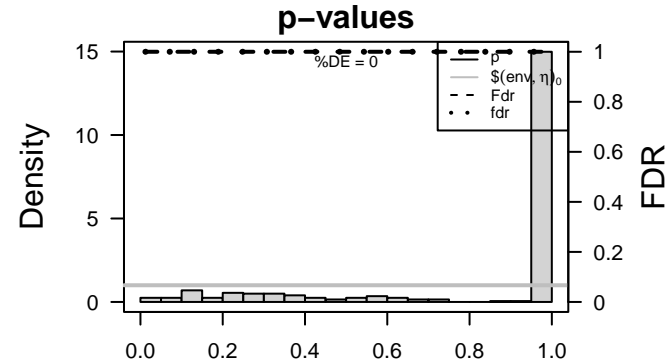


Spot Genelist

ID	Description
Vitvi14g01318	Catalysis of the hydrolysis of any ester bond.
Vitvi15g01643	
Vitvi12g00368	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.
Vitvi19g00283	Binding to a nucleotide, any compound consisting of a nucleoside that is esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the ribose or deoxyribose.
Vitvi14g02924	Any intracellular signal transduction in which the signal is passed on within the cell via calcium ions.
Vitvi12g02236	
Vitvi17g01380	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi13g00410	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 stimulus indicating an increase or decrease in the concentration of salt (particularly but not exclusively sodium and chloride ions) in the environment.
Vitvi15g01075	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.
Vitvi15g01073	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.
Vitvi18g03198	
Vitvi06g01100	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi00g02041	
Vitvi15g00172	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi05g00139	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi10g00973	Binding to a calcium ion (Ca2+).
Vitvi04g00467	
Vitvi18g03098	Binding to ADP, adenosine 5'-diphosphate.
Vitvi00g01146	
Vitvi18g02223	Binding to ADP, adenosine 5'-diphosphate.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.01	2 / 19	RNA polymerase I system
2	0.03	2 / 28	Sulfur metabolism
3	0.03	2 / 28	RNA polymerase III system
4	0.03	3 / 81	Translation – mRNA surveillance pathway
5	0.04	2 / 35	RNA polymerase
6	0.05	2 / 41	Transcription – RNA polymerase
7	0.06	4 / 162	Plant specific signaling – Plant-pathogen interaction
8	0.07	2 / 51	Other metabolism – Single reactions
9	0.09	3 / 119	Endocytosis
10	0.09	2 / 58	Other amino acids metabolism – Glutathione metabolism
11	0.10	1 / 12	Endoplasmic reticulum membrane and cytosol
12	0.10	2 / 62	Translation – Aminoacyl-tRNA biosynthesis
13	0.12	1 / 15	Chaperone – HSP70 / DNAK
14	0.13	2 / 71	Glutathione metabolism
15	0.13	2 / 71	Exosome – Proteins found in most exosomes
16	0.13	1 / 16	Transcription factors – HSF
17	0.14	1 / 17	Chaperone – Peptidyl prolyl isomerase
18	0.14	1 / 17	Proteasome – Assembling factors
19	0.14	1 / 17	Protein – Arf GTPases and associated proteins
20	0.15	1 / 18	Nicotinate and nicotinamide metabolism



D-Cluster

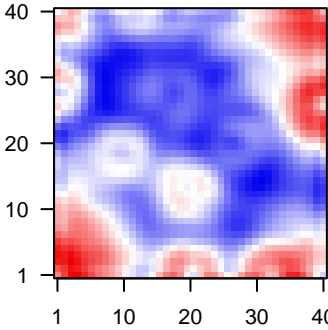
Spot Summary: C

metagenes = 20
genes = 322

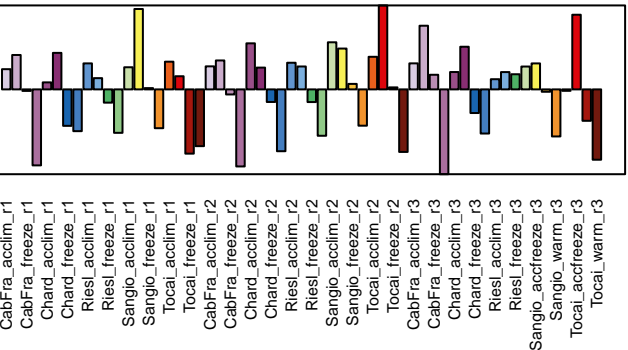
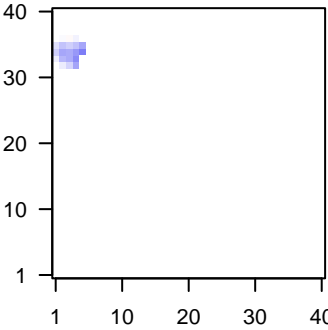
<r> metagenes = 0.98
<r> genes = 0.58
beta: r2= 5.95 / log p= -Inf

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

Overview Map



Spot

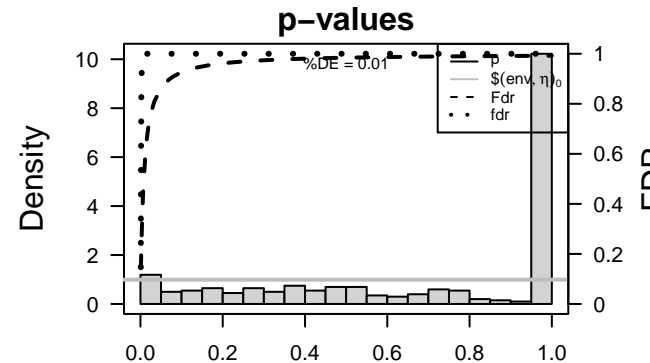


Spot Genelist

ID	Description
Vitvi06g01696	Binding to a metal ion.
Vitvi06g01629	
Vitvi08g02170	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.
Vitvi08g01412	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.
Vitvi09g00172	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.
Vitvi17g00470	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi10g00451	
Vitvi14g01683	The catalysis of certain rearrangements of a molecule to break or form a ring.
Vitvi05g00699	Binding to a metal ion.
Vitvi04g01160	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi01g01019	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi18g00228	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.
Vitvi12g00086	
Vitvi01g01265	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.
Vitvi10g00189	
Vitvi07g01637	Binding to a protein.
Vitvi05g00032	Catalysis of the transfer of an acyl group from one compound (donor) to another (acceptor).
Vitvi01g01808	Catalysis of the reaction: protein serine phosphate + H2O = protein serine + phosphate, and protein threonine phosphate + H2O = protein threonine + phosphate.
Vitvi08g02311	
Vitvi18g02740	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-04	5 / 39	Ubiquitin system – Ubiquitin-specific proteases (UBPs)
2	1e-03	3 / 11	Protein – Mitophagy
3	1e-03	8 / 110	Ubiquitin system – Multi subunit Ring-finger type E3
4	2e-03	6 / 72	Glycerophospholipid metabolism
5	4e-03	4 / 36	Fatty acid degradation
6	7e-03	5 / 64	Transcription factors – Other transcription factors
7	7e-03	4 / 41	Cofactors and vitamin metabolism – Riboflavin metabolism
8	1e-02	3 / 26	Protein – Small GTPases and associated proteins
9	2e-02	3 / 28	RNA polymerase III system
10	2e-02	2 / 11	Transcription factors – ABI3VP1
11	2e-02	2 / 11	Transcription factors – MADS
12	2e-02	5 / 80	Transport system – Tethering factors
13	2e-02	4 / 55	Glycerolipid metabolism
14	2e-02	3 / 31	GTP-binding proteins – Rab Family
15	2e-02	11 / 290	Enzyme – 2.3 Acyltransferases
16	2e-02	2 / 13	Glycosyltransferase – Dol-linked oligosaccharide
17	2e-02	6 / 119	Endocytosis
18	3e-02	5 / 90	Lipid metabolism – Glycerophospholipid metabolism
19	3e-02	5 / 95	Ubiquitin mediated proteolysis
20	3e-02	6 / 128	Ubiquitin system – Single Ring-finger type E3



D-Cluster

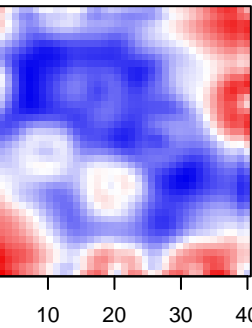
Spot Summary: D

metagenes = 58
genes = 581

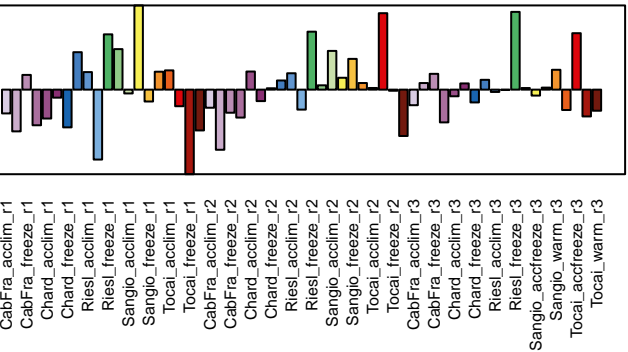
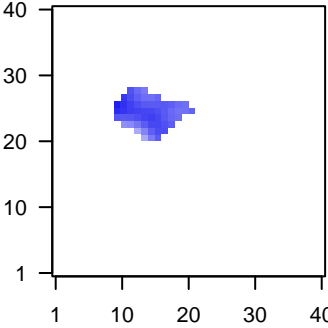
<r> metagenes = 0.76
<r> genes = 0.22
beta: r2= 0.93 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

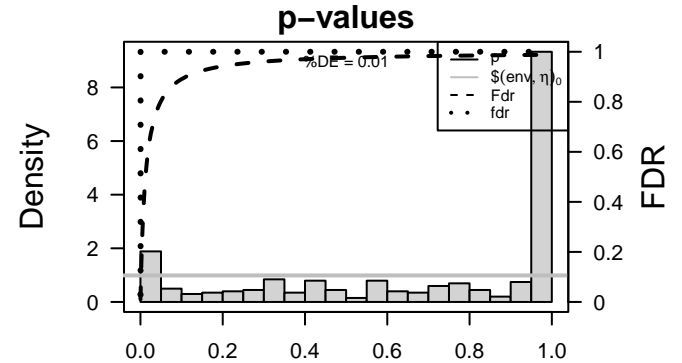


Spot Genelist

ID	Description
Vitvi09g00177	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi11g00678	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi09g01718	
Vitvi01g00216	
Vitvi17g01492	Binding to a metal ion.
Vitvi04g01525	
Vitvi00g01382	
Vitvi07g01669	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi18g01090	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.
Vitvi18g02403	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.
Vitvi04g00346	Binding to a nucleic acid.
Vitvi18g01299	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.
Vitvi12g00038	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.
Vitvi01g00313	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.
Vitvi07g02199	
Vitvi19g01697	Binding to ADP, adenosine 5'-diphosphate.
Vitvi19g01708	Organized structure of distinctive morphology and function, bounded by a single or double lipid bilayer membrane and occurring within the cell. Includes the nucleus, mitochondria, plastids, vacuoles, and vesicles. Excludes the plasma membrane.
Vitvi10g00425	Binding to a metal ion.
Vitvi19g01806	
Vitvi09g00047	A semiautonomous, self replicating organelle that occurs in varying numbers, shapes, and sizes in the cytoplasm of virtually all eukaryotic cells. It is notably the site of tissue respiration.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-05	16 / 151	RNA polymerase II system
2	2e-04	14 / 139	Spliceosome
3	2e-04	6 / 28	Transcription factors - SNF2
4	3e-04	15 / 165	Transcription - Spliceosome
5	3e-04	12 / 115	Enzyme - 3.6 Acting on acid anhydrides
6	3e-04	11 / 99	mRNA surveillance pathway
7	7e-04	5 / 23	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
8	7e-04	26 / 409	Enzyme - 2.7 Transferring phosphorus-containing groups
9	8e-04	7 / 48	Transport system - Nuclear pore complex
10	1e-03	9 / 81	Translation - mRNA surveillance pathway
11	2e-03	9 / 85	Nucleocytoplasmic transport
12	2e-03	7 / 57	Transcription factors - C3H
13	3e-03	3 / 10	Protein - Syntaxin (Qa)
14	4e-03	5 / 33	Glycan biosynthesis and metabolism - N-Glycan biosynthesis
15	5e-03	8 / 83	RNA degradation
16	7e-03	6 / 53	Protein - Forward pathways
17	7e-03	3 / 13	Glycosyltransferase - Dol-linked oligosaccharide
18	7e-03	3 / 13	Kinase - CDK family
19	8e-03	4 / 25	U4/U6.U5 tri-snRNP components
20	9e-03	5 / 40	N-Glycan biosynthesis



D-Cluster

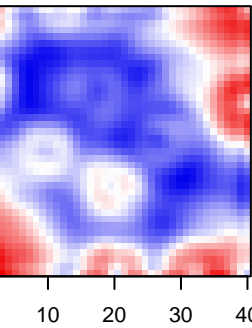
Spot Summary: E

metagenes = 14
genes = 270

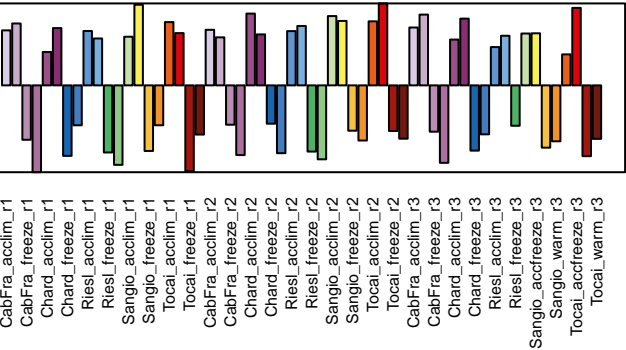
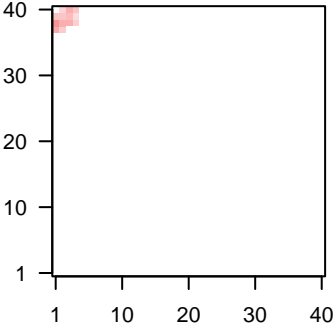
<r> metagenes = 0.99
<r> genes = 0.62
beta: r2= 16.16 / log p= -Inf

samples with spot = 27 (45.8 %)
CabFra_acclim : 3 (100 %)
CabFra_accfreeze : 3 (100 %)
Chard_acclim : 2 (66.7 %)
Chard_accfreeze : 3 (100 %)
Riesl_acclim : 2 (66.7 %)
Riesl_accfreeze : 3 (100 %)
Sangio_acclim : 3 (100 %)
Sangio_accfreeze : 3 (100 %)
Tocai_acclim : 2 (66.7 %)
Tocai_accfreeze : 3 (100 %)

Overview Map



Spot

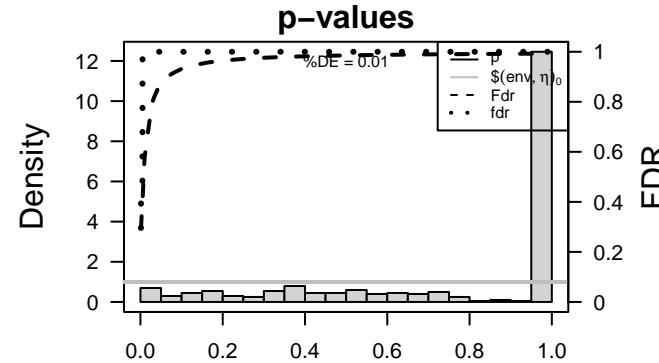


Spot Genelist

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.
Vitvi05g01758	
Vitvi17g00237	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi17g00914	
Vitvi16g01161	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g00985	Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a cold stimulus, a temperature stimulus below the optimal temperature for that organism.
Vitvi05g01453	Binding to a protein.
Vitvi04g01564	
Vitvi09g00046	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.
Vitvi17g00116	Modulates the activity of a protein kinase, an enzyme which phosphorylates a protein.
Vitvi11g01513	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g00164	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.001	5 / 51	Plant specific signaling – Circadian rhythm
2	0.001	4 / 32	Circadian rhythm – plant
3	0.004	10 / 238	Enzyme – 2.4 Glycosyltransferases
4	0.005	4 / 44	Hormone signaling – Cytokinin signaling
5	0.005	6 / 101	Starch and sucrose metabolism
6	0.010	4 / 54	Carbohydrate metabolism – Inositol phosphate metabolism
7	0.010	2 / 10	Transcription factors – C2C2-CO
8	0.027	4 / 73	Transcription factors – AP2 EREBP
9	0.029	5 / 110	Ubiquitin system – Multi subunit Ring-finger type E3
10	0.032	2 / 18	Chaperone – HSP20
11	0.034	7 / 195	Carbohydrate metabolism – Starch and sucrose metabolism
12	0.042	2 / 21	Thiamine metabolism
13	0.045	3 / 51	Signal transduction – Phosphatidylinositol signaling system
14	0.049	4 / 88	Electrochemical potential-driven transporters [TC:2]
15	0.058	2 / 25	Phenylalanine metabolism
16	0.058	4 / 93	Transcription factors – BHLH
17	0.066	2 / 27	Enzyme – 2.6 Transferring nitrogenous groups
18	0.071	4 / 100	Plant specific signaling – Flower development
19	0.078	3 / 64	Transcription factors – Other transcription factors
20	0.098	2 / 34	Tyrosine metabolism



D-Cluster

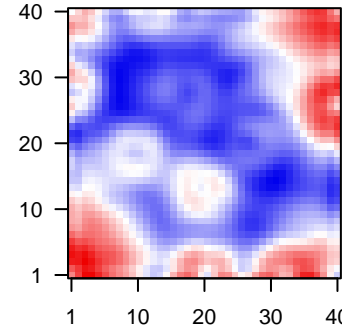
Spot Summary: F

metagenes = 11
genes = 200

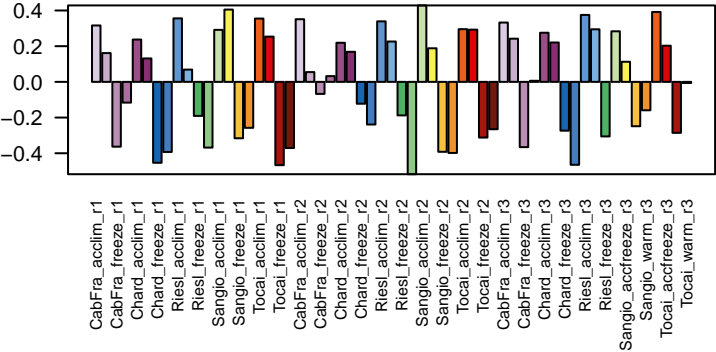
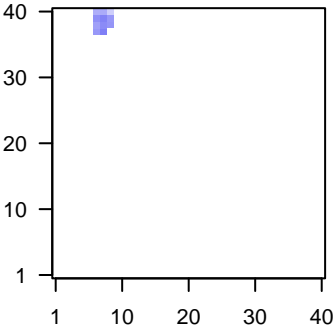
<r> metagenes = 0.99
<r> genes = 0.51
beta: r2= 5.01 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

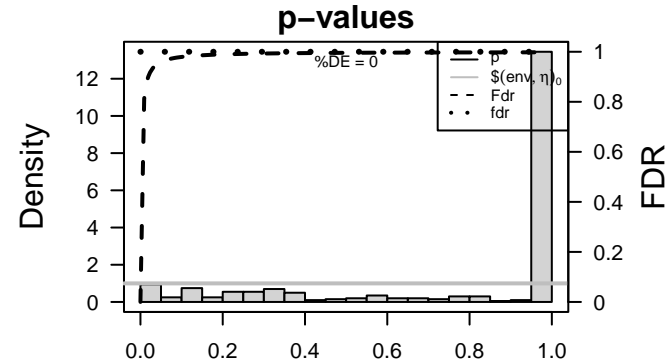


Spot Genelist

ID	Description
Vitvi05g00733	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.
Vitvi17g01576	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.
Vitvi07g01269	
Vitvi13g01973	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures. A transcription coregulator activity that represses or decreases the transcription of specific gene sets via binding to a DNA-bound DNA-binding transcription factor, either on its own or as part of a complex. Corepressors often act by altering chromatin structure and modifications. For example, one class of transcription corepressors modifies chromatin structure through covalent modification of histones. A second class remodels the conformation of chromatin in an ATP-dependent fashion. A third class modulates interactions of DNA-bound DNA-binding transcription factors with other transcription factors.
Vitvi18g00711	Protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi04g01312	
Vitvi07g00363	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi16g01753	Binding to ADP, adenosine 5'-diphosphate.
Vitvi00g01640	
Vitvi09g02101	
Vitvi10g01197	
Vitvi18g01137	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi12g01846	Binding to ADP, adenosine 5'-diphosphate.
Vitvi17g00880	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.
Vitvi10g01224	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi06g00106	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.
Vitvi15g00841	Binding to a zinc ion (Zn).
Vitvi11g00161	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.
Vitvi16g00291	Binding to a magnesium (Mg) ion.
Vitvi00g00292	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-08	9 / 62	Ribosome biogenesis – 90S particles
2	8e-06	7 / 64	Ribosome biogenesis in eukaryotes
3	2e-05	7 / 75	Translation – Ribosome biogenesis in Eukaryotes
4	9e-03	3 / 38	Protein – Other autophagy associated proteins
5	1e-02	5 / 116	Ribosome biogenesis – Pre-60S particles
6	1e-02	4 / 75	Mitochondrial transcription and translation factors
7	1e-02	3 / 41	Transcription – RNA polymerase
8	1e-02	7 / 217	Cell motility – Regulation of actin cytoskeleton
9	2e-02	2 / 17	Signal transduction – mTOR signaling pathway
10	2e-02	3 / 48	Amino acid metabolism – Lysine biosynthesis
11	2e-02	2 / 19	RNA polymerase I system
12	2e-02	3 / 54	Amino acid metabolism – Methionine metabolism
13	3e-02	2 / 24	Protein – Retrieval pathways
14	3e-02	3 / 62	Translation – Aminoacyl-tRNA biosynthesis
15	4e-02	2 / 27	Regulator of mitochondrial biogenesis
16	4e-02	2 / 28	Transcription factors – MTERF
17	4e-02	4 / 115	Enzyme – 3.6 Acting on acid anhydrides
18	5e-02	4 / 119	Endocytosis
19	5e-02	2 / 31	Autophagy – other
20	5e-02	2 / 33	Carbohydrate metabolism – Aminosugars metabolism



D-Cluster

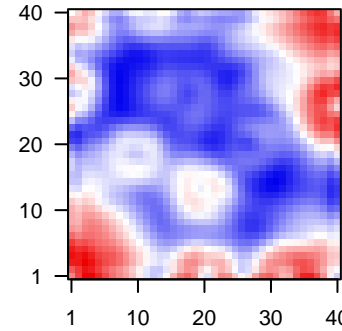
Spot Summary: G

metagenes = 29
genes = 337

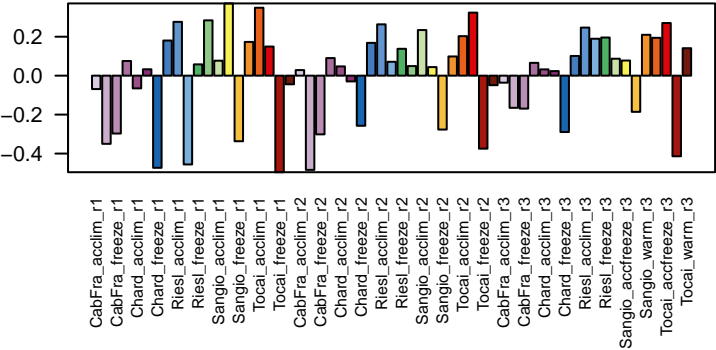
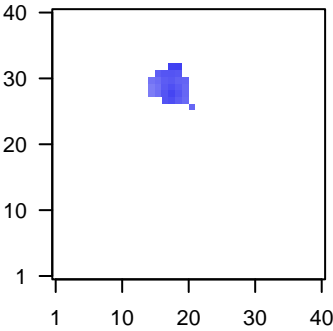
<r> metagenes = 0.93
<r> genes = 0.4
beta: r2= 1.85 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

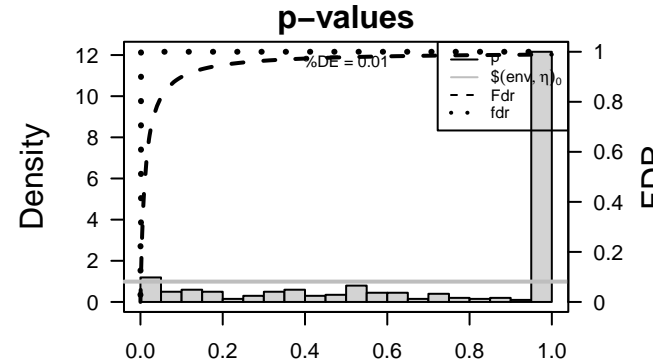


Spot Genelist

ID	Description
Vitvi18g02642	
Vitvi16g01326	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.
Vitvi09g00149	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g01773	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.
Vitvi10g00432	
Vitvi04g02107	
Vitvi05g01824	
Vitvi11g00514	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.
Vitvi13g01582	
Vitvi07g01075	Binding to a zinc ion (Zn).
Vitvi19g02185	Binding to ADP, adenosine 5'-diphosphate.
Vitvi17g00474	
Vitvi00g00997	
Vitvi10g00440	
Vitvi12g02736	Binding to a protein.
Vitvi13g01343	
Vitvi18g02996	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.
Vitvi01g00281	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi13g00219	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi13g01481	Binding to ADP, adenosine 5'-diphosphate.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-07	11 / 85	Nucleocytoplasmic transport
2	7e-05	19 / 409	Enzyme - 2.7 Transferring phosphorus-containing groups
3	2e-04	9 / 116	Ribosome biogenesis - Pre-60S particles
4	1e-03	5 / 48	Transport system - Nuclear pore complex
5	1e-03	8 / 126	Translation - RNA transport
6	3e-03	4 / 36	Ribosome biogenesis - Pre-40S particles
7	4e-03	8 / 151	RNA polymerase II system
8	6e-03	4 / 43	Aminoacyl-tRNA synthetases (AARSs)
9	6e-03	4 / 44	Enzyme - 6.1 Forming carbon-oxygen bonds
10	7e-03	6 / 100	Plant specific signaling - Flower development
11	9e-03	4 / 48	Aminoacyl-tRNA biosynthesis
12	2e-02	3 / 31	Autophagy - other
13	2e-02	4 / 62	Ribosome biogenesis - 90S particles
14	2e-02	4 / 62	Translation - Aminoacyl-tRNA biosynthesis
15	2e-02	7 / 165	Transcription - Spliceosome
16	2e-02	3 / 37	Homologous recombination
17	3e-02	3 / 38	Protein - Other autophagy associated proteins
18	3e-02	3 / 39	Ubiquitin system - Ubiquitin-specific proteases (UBPs)
19	3e-02	6 / 139	Spliceosome
20	3e-02	2 / 17	Signal transduction - mTOR signaling pathway



D-Cluster

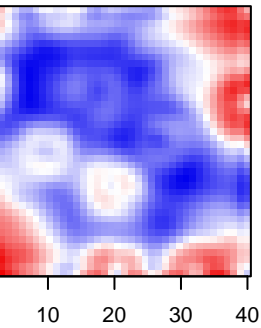
Spot Summary: H

metagenes = 17
genes = 243

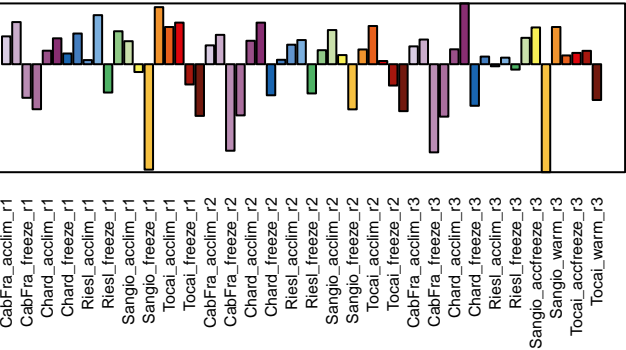
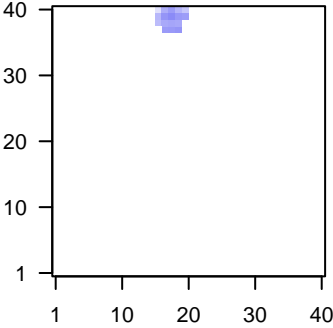
<r> metagenes = 0.97
<r> genes = 0.42
beta: r2= 4.89 / log p= -Inf

samples with spot = 2 (3.4 %)
Chard_accfreeze : 1 (33.3 %)
Sangio_warm : 1 (33.3 %)

Overview Map



Spot

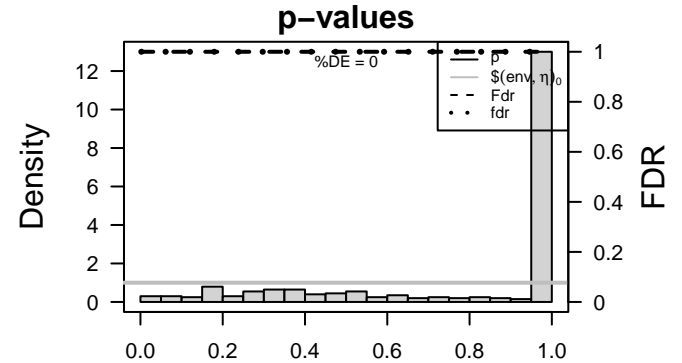


Spot Genelist

ID	Description
Vitvi10g00667	Catalysis of the hydrolysis of any ester bond.
Vitvi04g00012	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.
Vitvi12g02718	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.
Vitvi19g01784	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.
Vitvi04g01244	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.
Vitvi14g01651	
Vitvi14g02497	
Vitvi06g01357	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	
Vitvi19g01732	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi14g02498	
Vitvi12g02326	Binding to a protein.
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.
Vitvi08g01673	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi18g02638	The chemical reactions and pathways involving cytokinins, a class of adenine-derived compounds that can function in plants as growth regulators.
Vitvi18g02779	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a mechanism in which the sulfhydryl group of a cysteine residue at the active center acts as a nucleophile.
Vitvi18g00311	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.
Vitvi04g00060	Catalysis of the hydrolysis of phosphoric monoesters, releasing inorganic phosphate.
Vitvi15g01434	
Vitvi03g01300	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.002	6 / 93	Transcription factors – BHLH
2	0.005	4 / 49	Transcription factors – NAC
3	0.009	7 / 168	Plant hormone signal transduction
4	0.016	3 / 38	Hormone transport – Auxin transport
5	0.032	6 / 170	Transcription factors – Other zf–C3HC4
6	0.034	3 / 51	Carbon fixation in photosynthetic organisms
7	0.052	3 / 60	Enzyme – 4.1 Carbon-carbon lyases
8	0.058	2 / 28	Exosome – Exosomal proteins of breast milk
9	0.066	2 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
10	0.070	4 / 111	Hormone signaling – ABA signaling
11	0.080	3 / 72	Energy metabolism – Carbon fixation
12	0.099	2 / 38	Protein – Chaperone mediated autophagy (CMA)
13	0.126	2 / 44	Fructose and mannose metabolism
14	0.126	2 / 44	Pentose phosphate pathway
15	0.131	1 / 10	SLC39: Metal ion transporter
16	0.131	1 / 10	Transcription factors – ZIM
17	0.144	1 / 11	Zeatin biosynthesis
18	0.156	1 / 12	Enzyme – 1.17 Acting on CH or CH2 groups
19	0.156	1 / 12	Enzyme – Class I
20	0.156	1 / 12	SLC15: Proton oligopeptide cotransporter



D-Cluster

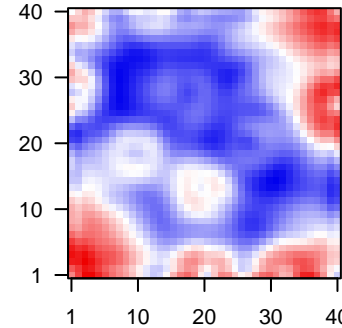
Spot Summary: I

metagenes = 1
genes = 5

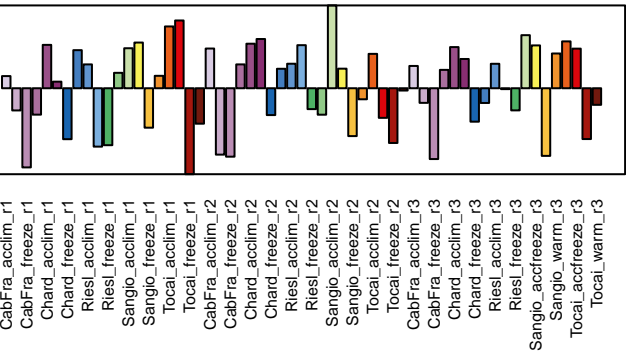
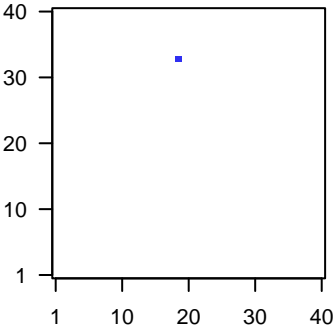
<r> metagenes = NA
<r> genes = 0.57
beta: r2= 1.89 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

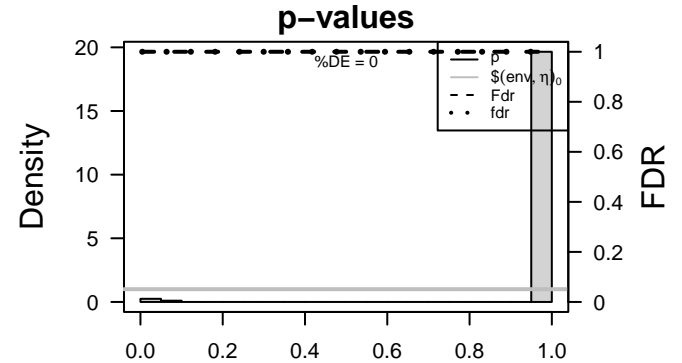


Spot Genelist

ID	Description
Vitvi13g01674	Binding to a protein.
Vitvi15g00540	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi15g00974	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi07g01205	An thiol-dependent isopeptidase activity that cleaves ubiquitin from a target protein to which it is conjugated.
Vitvi07g00481	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.004	1 / 13	Glycosyltransferase – Dol-linked oligosaccharide
2	0.009	1 / 29	Various types of N-glycan biosynthesis
3	0.011	1 / 33	Glycan biosynthesis and metabolism – N-Glycan biosynthesis
4	0.013	1 / 39	Ubiquitin system – Ubiquitin-specific proteases (UBPs)
5	0.013	1 / 40	N-Glycan biosynthesis
6	0.070	1 / 223	Enzyme – 3.4 Acting on peptide bonds (peptidases)
7	0.075	1 / 238	Enzyme – 2.4 Glycosyltransferases
8	1.000	0 / 47	ABC transporters
9	1.000	0 / 43	Alanine aspartate and glutamate metabolism
10	1.000	0 / 33	alpha-Linolenic acid metabolism
11	1.000	0 / 102	Amino sugar and nucleotide sugar metabolism
12	1.000	0 / 48	Aminoacyl-tRNA biosynthesis
13	1.000	0 / 41	Arginine and proline metabolism
14	1.000	0 / 29	Arginine biosynthesis
15	1.000	0 / 44	Ascorbate and aldarate metabolism
16	1.000	0 / 31	Autophagy – other
17	1.000	0 / 37	Basal transcription factors
18	1.000	0 / 29	Base excision repair
19	1.000	0 / 39	beta-Alanine metabolism
20	1.000	0 / 13	Biosynthesis of unsaturated fatty acids



D-Cluster

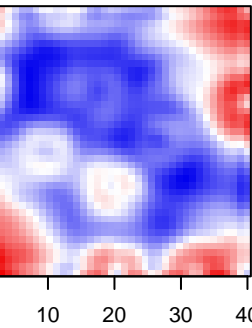
Spot Summary: J

metagenes = 16
genes = 188

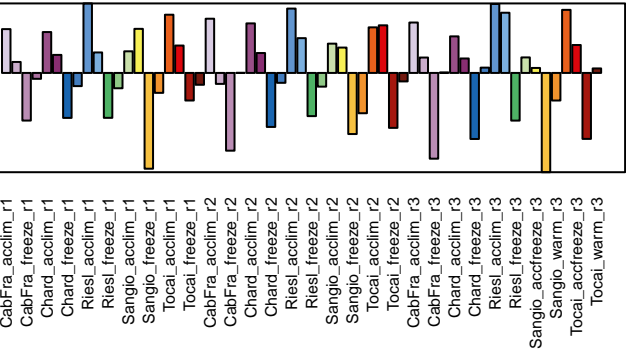
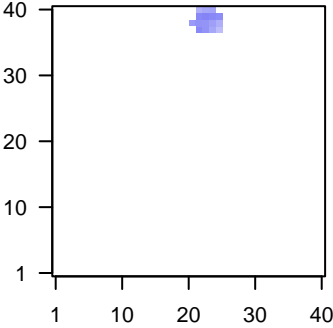
<r> metagenes = 0.98
<r> genes = 0.57
beta: r2= 5.51 / log p= -Inf

samples with spot = 3 (5.1 %)
Riesl_acclim : 3 (100 %)

Overview Map



Spot

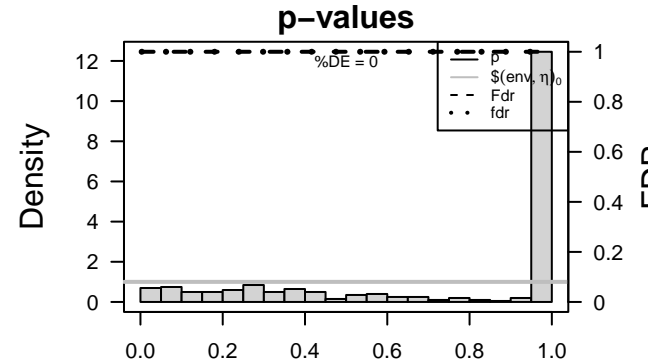


Spot Genelist

ID	Description
Vitvi09g01553	
Vitvi05g02157	Binding to a protein.
Vitvi18g01063	
Vitvi14g02049	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.
Vitvi19g00405	
Vitvi11g00460	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.
Vitvi12g00667	Binding to a metal ion.
Vitvi13g01379	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi10g01578	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi12g02469	
Vitvi10g01753	
Vitvi13g00242	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.
Vitvi16g00869	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi11g00245	
Vitvi15g00505	Binding to a protein.
Vitvi14g00432	Binding to an RNA molecule or a portion thereof.
Vitvi14g01960	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.
Vitvi11g00217	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi14g02987	The cell cycle process in which the sister chromatids of a replicated chromosome become tethered to each other.
Vitvi07g02617	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	3 / 26	Sphingolipid metabolism
2	0.009	2 / 13	Protein - Lipid raft mediated endocytosis
3	0.009	3 / 39	Ubiquitin system - Ubiquitin-specific proteases (UBPs)
4	0.010	2 / 14	Proteins involved in snRNP biogenesis
5	0.012	3 / 44	Replication protein - DNA Replication Termination Factors
6	0.013	2 / 16	Other glycan degradation
7	0.014	4 / 85	Nucleocytoplasmic transport
8	0.016	2 / 18	Protein - Macropinocytosis
9	0.020	2 / 20	tRNA modification factors
10	0.033	5 / 161	Enzyme - 2.1 Transferring one-carbon groups
11	0.033	2 / 26	Protein - Small GTPases and associated proteins
12	0.035	3 / 65	Phagosome
13	0.038	3 / 67	Replication and repair - RNA degradation
14	0.038	4 / 115	Enzyme - 3.6 Acting on acid anhydrides
15	0.051	4 / 126	Translation - RNA transport
16	0.053	3 / 77	Carbohydrate metabolism - Galactose metabolism
17	0.054	4 / 129	Enzyme - 3.2 Glycosylases
18	0.057	2 / 35	RNA polymerase
19	0.058	3 / 80	Transport system - Tethering factors
20	0.060	2 / 36	Enzyme - 6.3 Forming carbon-nitrogen bonds



D-Cluster

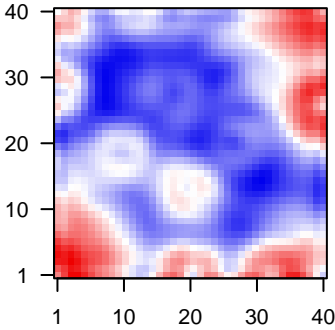
Spot Summary: K

metagenes = 62
genes = 500

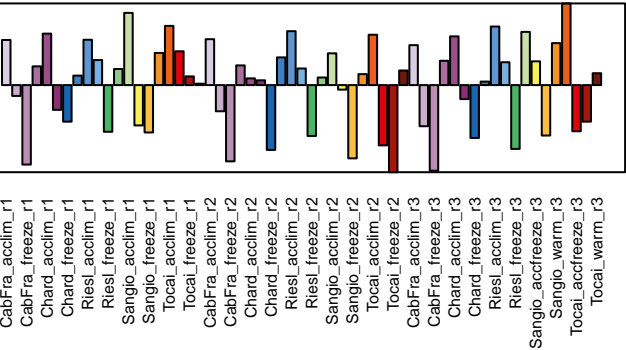
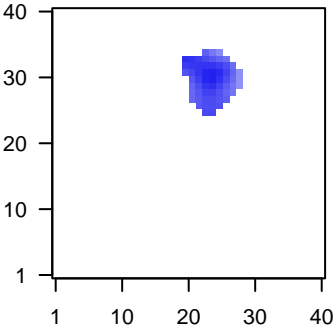
<r> metagenes = 0.85
<r> genes = 0.22
beta: r2= 1.34 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

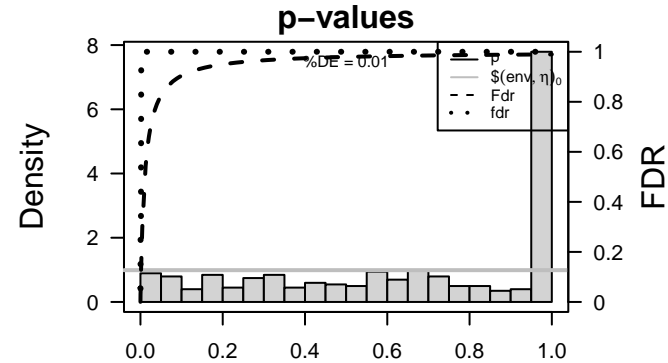


Spot Genelist

ID	Description
Vitvi07g02067	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.
Vitvi09g00246	
Vitvi14g02885	
Vitvi02g00242	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. 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 stimulus indicating an increase or decrease in the concentration of salt (particularly but not exclusively sodium and chloride ions) in the environment.
Vitvi10g02289	
Vitvi00g00895	
Vitvi16g01543	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.
Vitvi10g00227	
Vitvi14g00012	
Vitvi04g00365	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.
Vitvi06g00325	
Vitvi11g00053	
Vitvi19g00153	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.
Vitvi04g00241	
Vitvi06g01387	
Vitvi05g01400	Catalysis of the reaction: a very long chain fatty acyl-CoA + NADPH + H+ = a very long chain primary alcohol + NADP+ + CoA.
Vitvi04g00800	
Vitvi19g02032	
Vitvi19g01375	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.
Vitvi19g01375	
Vitvi19g01375	
Vitvi10g00639	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	9e-07	17 / 142	Transport system - Protein coat
2	2e-04	7 / 42	Folding sorting degradation - Proteasome
3	3e-04	7 / 44	Proteasome
4	1e-03	5 / 28	Proteasome - Regulatory particles
5	2e-03	9 / 95	Ubiquitin mediated proteolysis
6	4e-03	6 / 53	Protein - Forward pathways
7	1e-02	3 / 17	One carbon pool by folate
8	2e-02	3 / 19	Cofactors and vitamin metabolism - Ubiquinone biosynthesis
9	2e-02	20 / 409	Enzyme - 2.7 Transferring phosphorus-containing groups
10	2e-02	4 / 36	Enzyme - 6.3 Forming carbon-nitrogen bonds
11	2e-02	4 / 38	Protein - Clathrin-mediated endocytosis
12	3e-02	9 / 146	Transporter catalog - Porters cat 7 to 17
13	3e-02	3 / 23	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
14	3e-02	3 / 24	Protein - Retrieval pathways
15	3e-02	4 / 42	Phosphatidylinositol signaling system
16	4e-02	3 / 26	Transcription factors - Orphans FAR-RED
17	5e-02	2 / 12	Translation factors - Release factors
18	5e-02	6 / 90	Lipid metabolism - Glycerophospholipid metabolism
19	5e-02	7 / 115	Enzyme - 3.6 Acting on acid anhydrides
20	5e-02	2 / 13	Protein - Lipid raft mediated endocytosis



D-Cluster

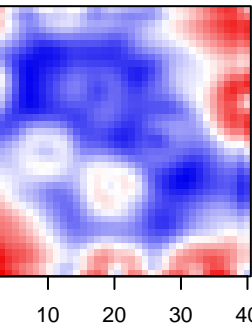
Spot Summary: L

metagenes = 24
genes = 520

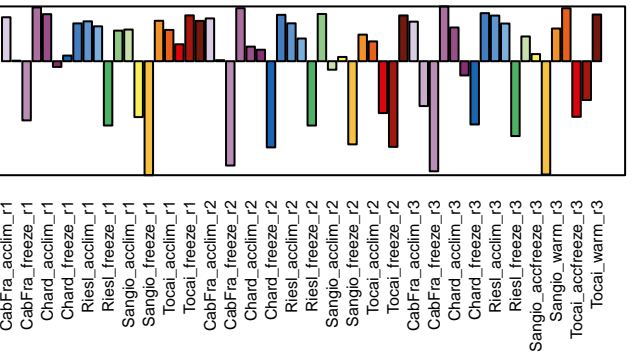
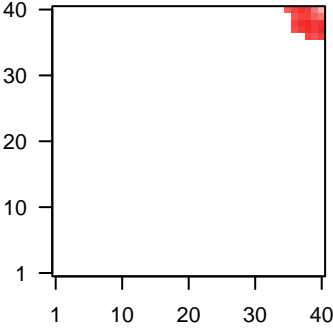
<r> metagenes = 0.98
<r> genes = 0.77
beta: r2= 48.51 / log p= -Inf

samples with spot = 29 (49.2 %)
CabFra_acclim : 3 (100 %)
CabFra_warm : 3 (100 %)
Chard_acclim : 2 (66.7 %)
Chard_warm : 3 (100 %)
Riesl_acclim : 3 (100 %)
Riesl_accfreeze : 2 (66.7 %)
Riesl_warm : 2 (100 %)
Sangio_acclim : 2 (66.7 %)
Sangio_warm : 3 (100 %)
Tocai_acclim : 2 (66.7 %)

Overview Map



Spot

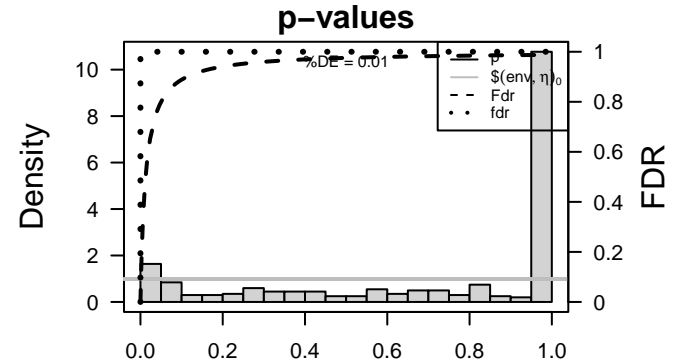


Spot Genelist

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.
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.
Vitvi12g02394	
Vitvi14g03084	
Vitvi01g01030	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi05g00067	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-21	41 / 206	Cell growth and death – Cell wall
2	1e-15	18 / 47	Transporter catalog – Transport electron carriers
3	7e-13	11 / 18	Photosynthesis – antenna proteins
4	7e-13	11 / 18	Energy metabolism – Photosynthesis antenna proteins
5	3e-09	7 / 10	Photosynthesis protein – Photosystem I (P700 chlorophyll a)
6	1e-07	14 / 78	Energy metabolism – Photosynthesis
7	2e-07	10 / 38	Photosynthesis
8	1e-06	13 / 80	Cytoskeleton – Microtubules
9	1e-06	22 / 217	Cell motility – Regulation of actin cytoskeleton
10	7e-06	5 / 10	Peptidases and inhibitors – Family A1: pepsin family
11	2e-05	8 / 39	Pentose and glucuronate interconversions
12	2e-04	7 / 40	Transport system – Thylakoid targeting pathway
13	8e-04	12 / 129	Enzyme – 3.2 Glycosylases
14	1e-03	12 / 134	Hormone signaling – Auxin signaling
15	1e-03	5 / 26	Steroid biosynthesis
16	2e-03	6 / 41	Porphyrin metabolism
17	2e-03	5 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
18	3e-03	4 / 19	Aquaporins and small neutral solute transporters [TC:1.A.8]
19	4e-03	7 / 63	Phenylpropanoid biosynthesis
20	6e-03	3 / 12	ABCB (MDR/TAP) subfamily



D-Cluster

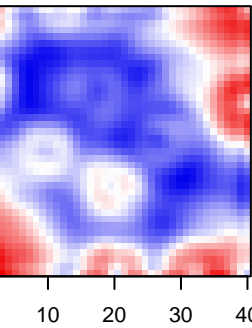
Spot Summary: M

metagenes = 21
genes = 274

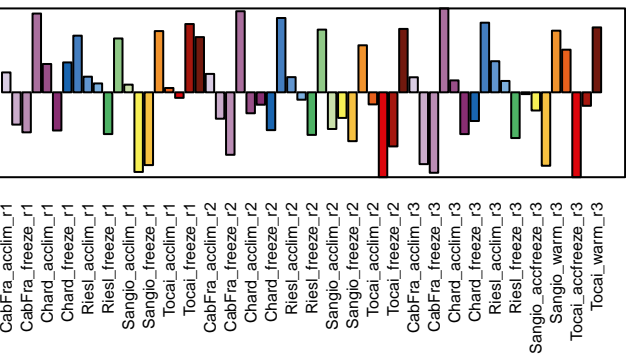
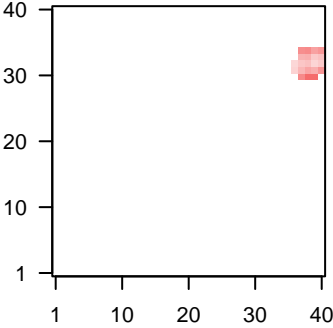
<r> metagenes = 0.98
<r> genes = 0.66
beta: r2= 19.11 / log p= -Inf

samples with spot = 16 (27.1 %)
CabFra_warm : 3 (100 %)
Chard_warm : 3 (100 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 3 (100 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 3 (100 %)

Overview Map



Spot

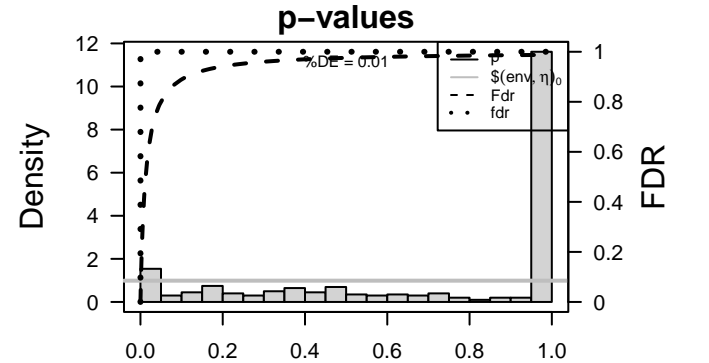


Spot Genelist

ID	Description
Vitvi19g02024	
Vitvi15g01693	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi01g00441	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi13g02009	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi06g01410	
Vitvi05g01577	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi03g01500	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi03g00221	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi15g01663	Binding to ADP, adenosine 5'-diphosphate.
Vitvi03g00134	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi15g00804	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi09g00040	Catalysis of the hydrolysis of any ester bond.
Vitvi03g01621	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi13g02416	Binding to a calcium ion (Ca2+).
Vitvi11g01437	
Vitvi03g01760	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.
Vitvi14g01350	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
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.
Vitvi14g01926	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi18g00260	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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-13	15 / 72	Ribosome - Mitochondria/ Chloroplast
2	3e-12	14 / 67	Ribosome - Bacteria
3	1e-05	14 / 211	Ribosome
4	2e-05	15 / 247	Translation - Ribosome
5	1e-04	6 / 48	Lipid metabolism - Fatty acid biosynthesis
6	3e-04	8 / 102	Amino sugar and nucleotide sugar metabolism
7	4e-04	4 / 22	Fatty acid elongation
8	6e-04	4 / 24	Carbohydrate metabolism - Ascorbate and aldarate metabolism
9	1e-03	7 / 97	Ribosome - Archaea
10	1e-03	4 / 30	Lipid biosynthesis protein - Component type
11	2e-03	4 / 31	Fatty acid biosynthesis
12	2e-03	4 / 32	Enzyme - 5.2 cis-trans-Isomerases
13	2e-03	4 / 33	Enzyme - 5.4 Intramolecular transferases
14	3e-03	3 / 17	Chaperone - Peptidyl prolyl isomerase
15	3e-03	4 / 38	Photosynthesis
16	4e-03	3 / 20	Lipid metabolism - Biosynthesis of unsaturated fatty acids
17	4e-03	4 / 41	Porphyrin metabolism
18	6e-03	4 / 44	Ascorbate and aldarate metabolism
19	9e-03	3 / 26	Flavonoid biosynthesis
20	9e-03	3 / 26	Steroid biosynthesis



D-Cluster

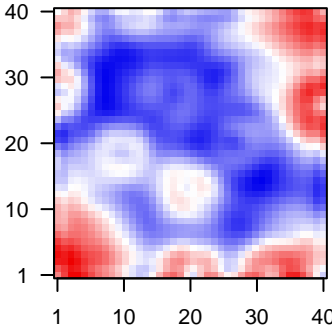
Spot Summary: N

metagenes = 56
genes = 528

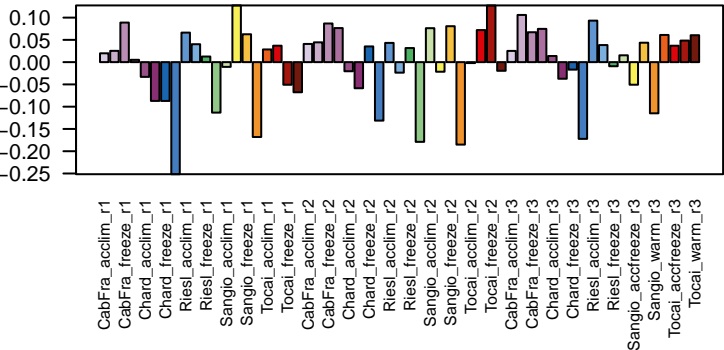
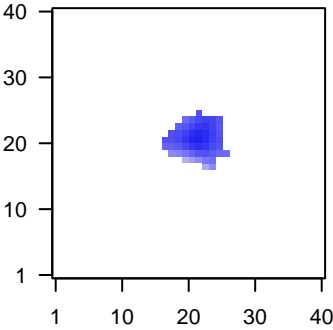
<r> metagenes = 0.57
<r> genes = 0.11
beta: r2= 0.52 / log p= -9.82

samples with spot = 0 (0 %)

Overview Map



Spot

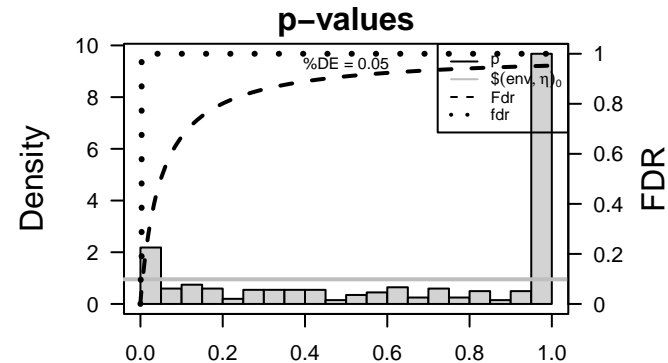


Spot Genelist

ID	Description
Vitvi11g00156	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.
Vitvi18g00766	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi05g00604	
Vitvi10g00209	Binds to and stops, prevents or reduces the activity of a cysteine-type endopeptidase, any enzyme that hydrolyzes peptide bonds in polypeptides by a mechanism in which the sulfhydryl group of a cysteine residue at the active center acts as a nucleophile.
Vitvi14g00233	Binding to a zinc ion (Zn).
Vitvi10g00937	Binds to and increases the activity of a GTPase, an enzyme that catalyzes the hydrolysis of GTP.
Vitvi06g00943	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.
Vitvi18g00401	The cell cycle process in which double strand breaks are formed and repaired through a single or double Holliday junction intermediate. This results in the equal exchange of genetic material between non-sister chromatids in a pair of homologous chromosomes. These reciprocal recombinant products ensure the proper segregation of homologous chrom during meiosis I and create genetic diversity.
Vitvi02g01545	
Vitvi18g01981	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.
Vitvi04g00295	A ubiquitin ligase complex in which a cullin from the Cul1 subfamily and a RING domain protein form the catalytic core; substrate specificity is conferred by a Skp1 adaptor and an F-box protein. SCF complexes are involved in targeting proteins for degradation by the proteasome. The best characterized complexes are those from yeast and mammals (with co subunits named Cdc53/Cul1, Rbx1/Hrt1/Roc1).
Vitvi18g02320	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.
Vitvi03g01484	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.
Vitvi13g02589	Binding to a calcium ion (Ca2+).
Vitvi00g01692	
Vitvi11g00303	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi05g00136	Catalysis of the hydrolysis of any ester bond.
Vitvi16g01001	The cell cycle process in which the sister chromatids of a replicated chromosome are joined along the entire length of the chromosome, from their formation in S phase through metaphase during a mitotic cell cycle. This cohesion cycle is critical for high fidelity chromosome transmission.
Vitvi06g00635	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.
Vitvi07g01244	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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-08	11 / 42	Folding sorting degradation – Proteasome
2	7e-08	11 / 44	Proteasome
3	5e-06	6 / 16	Peptidases and inhibitors – Family T1: proteasome family
4	5e-06	6 / 16	Proteasome – Core particles (20S proteasome)
5	2e-05	7 / 28	Transcription factors – MTERF
6	4e-05	11 / 80	Other components
7	2e-04	4 / 10	Replication and repair – Sulfur relay system
8	2e-04	10 / 81	Oxidative phosphorylation
9	2e-04	9 / 68	Spliceosome associated proteins (SAPs)
10	3e-04	10 / 85	Nucleocytoplasmic transport
11	4e-04	11 / 105	Energy metabolism – Oxidative phosphorylation
12	7e-04	14 / 165	Transcription – Spliceosome
13	7e-04	8 / 63	Messenger RNA Biogenesis – mRNA degradation factors
14	2e-03	5 / 28	Proteasome – Regulatory particles
15	2e-03	4 / 17	Chaperone – Peptidyl prolyl isomerase
16	2e-03	11 / 126	Translation – RNA transport
17	2e-03	8 / 75	Mitochondrial transcription and translation factors
18	2e-03	10 / 110	Ubiquitin system – Multi subunit Ring-finger type E3
19	3e-03	7 / 61	Messenger RNA Biogenesis – mRNA processing factors
20	3e-03	9 / 95	Ubiquitin mediated proteolysis



D-Cluster

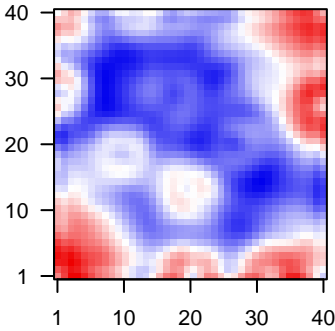
Spot Summary: O

metagenes = 31
genes = 460

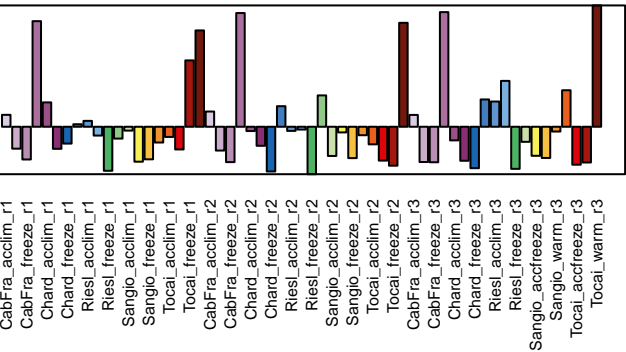
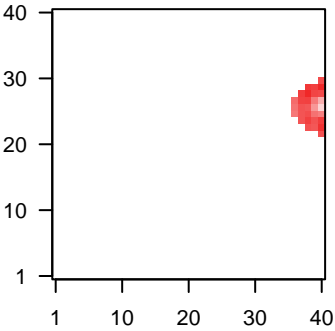
<r> metagenes = 0.98
<r> genes = 0.68
beta: r2= 26.26 / log p= -Inf

samples with spot = 11 (18.6 %)
CabFra_warm : 3 (100 %)
Chard_warm : 1 (33.3 %)
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

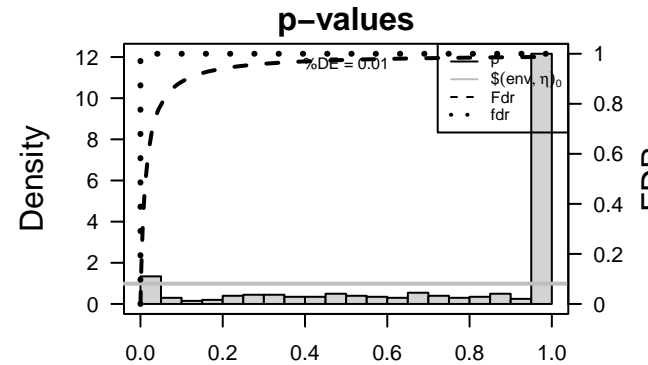


Spot Genelist

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	1e-27	45 / 219	Cell growth and death – Cell cycle
2	4e-18	23 / 80	Cytoskeleton – Microtubules
3	2e-16	33 / 217	Cell motility – Regulation of actin cytoskeleton
4	4e-15	13 / 24	Replication protein – DNA Replication Initiation Factors
5	3e-12	13 / 36	DNA replication
6	2e-11	13 / 41	Replication and repair – DNA replication
7	2e-05	8 / 44	Replication protein – DNA Replication Termination Factors
8	2e-03	6 / 51	Other metabolism – Single reactions
9	3e-03	5 / 37	Homologous recombination
10	4e-03	4 / 25	Replication and repair – Base excision repair
11	5e-03	4 / 27	Mismatch repair
12	5e-03	3 / 14	Cilium and associated proteins – Stereociliary proteins
13	6e-03	7 / 83	Transcription factors – MYB
14	7e-03	4 / 29	Base excision repair
15	8e-03	5 / 48	Pyrimidine metabolism
16	8e-03	12 / 206	Cell growth and death – Cell wall
17	1e-02	6 / 71	Glutathione metabolism
18	1e-02	4 / 34	Peptidases and inhibitors – Family S10
19	2e-02	4 / 39	Pentose and glucuronate interconversions
20	3e-02	2 / 10	Protein – Syntaxin (Qa)



D-Cluster

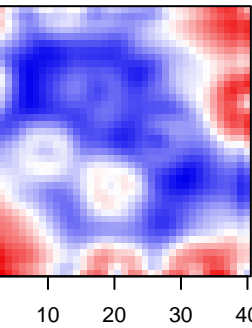
Spot Summary: P

metagenes = 5
genes = 77

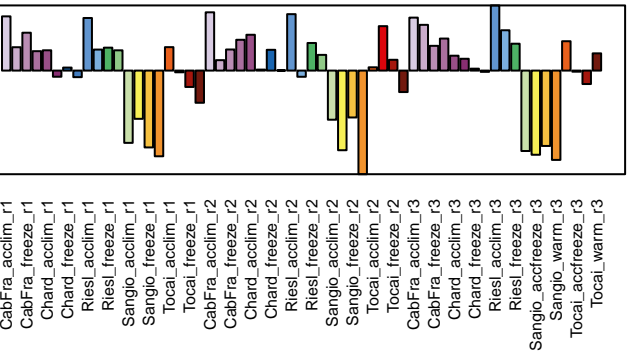
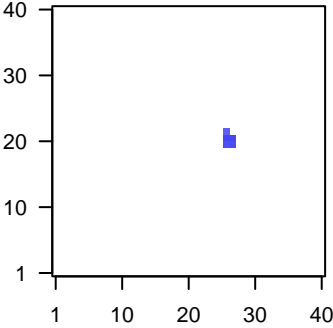
<r> metagenes = 0.98
<r> genes = 0.34
beta: r2= 1.27 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

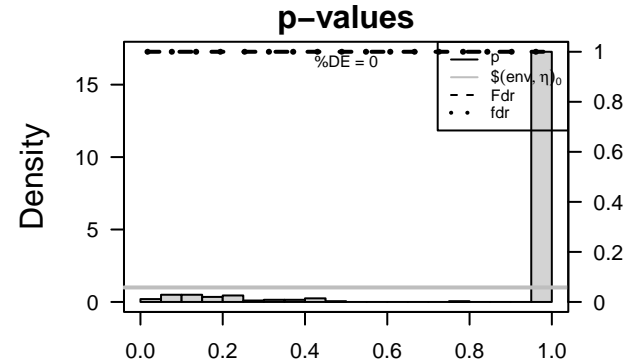


Spot Genelist

ID	Description
Vitvi09g00285	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.
Vitvi15g01503	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.
Vitvi17g00820	Binding to a zinc ion (Zn).
Vitvi11g00950	
Vitvi10g01613	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g01880	The action of a molecule that contributes to the structural integrity of the ribosome.
Vitvi12g02389	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi15g01710	
Vitvi18g00384	Catalysis of the reaction: trehalose 6-phosphate + H2O = trehalose + phosphate.
Vitvi12g02160	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.
Vitvi07g01525	
Vitvi14g02611	
Vitvi10g01523	
Vitvi04g01990	
Vitvi16g00072	
Vitvi16g01785	
Vitvi15g00815	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.
Vitvi16g00724	Binding to a zinc ion (Zn).
Vitvi05g01764	
Vitvi10g00361	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.02	3 / 161	Enzyme - 2.1 Transferring one-carbon groups
2	0.04	1 / 11	Transcription factors - GRF
3	0.05	2 / 101	Glycolysis / Gluconeogenesis
4	0.05	2 / 101	Starch and sucrose metabolism
5	0.05	3 / 247	Translation - Ribosome
6	0.06	1 / 18	Chaperone - HSP20
7	0.06	1 / 19	Cofactors and vitamin metabolism - Folate biosynthesis
8	0.06	2 / 123	Carbohydrate metabolism - Glycolysis
9	0.08	1 / 24	Folate biosynthesis
10	0.08	1 / 25	Nitrogen metabolism
11	0.08	1 / 26	Sphingolipid metabolism
12	0.08	1 / 26	Enzyme - 5.1 Racemases and epimerases
13	0.09	1 / 28	Transcription factors - MTERF
14	0.10	2 / 157	Protein processing in endoplasmic reticulum
15	0.11	1 / 34	Peptidases and inhibitors - Family S10
16	0.12	1 / 37	Enzyme - 5.3 Intramolecular oxidoreductases
17	0.12	1 / 38	Enzyme - 1.8 Acting on a sulfur group of donors
18	0.13	1 / 40	Amino acid metabolism - Cysteine metabolism
19	0.13	1 / 42	Tryptophan metabolism
20	0.14	1 / 44	Pentose phosphate pathway



D-Cluster

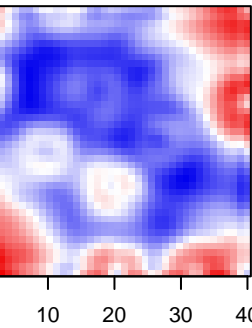
Spot Summary: Q

metagenes = 4
genes = 55

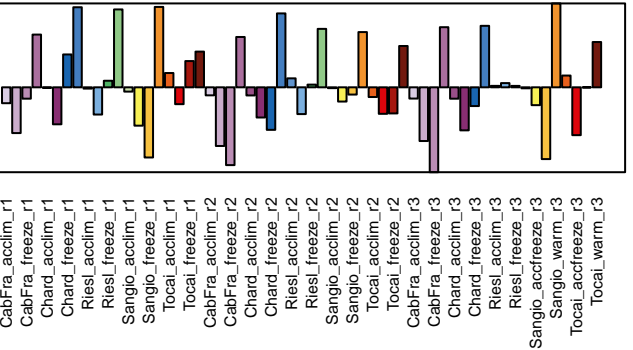
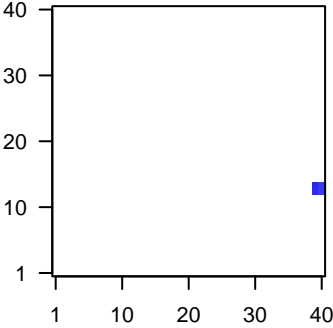
<r> metagenes = 1
<r> genes = 0.49
beta: r2= 2.99 / log p= -Inf

samples with spot = 4 (6.8 %)
Chard_warm : 1 (33.3 %)
Riesl_warm : 1 (33.3 %)
Sangio_warm : 2 (66.7 %)

Overview Map



Spot

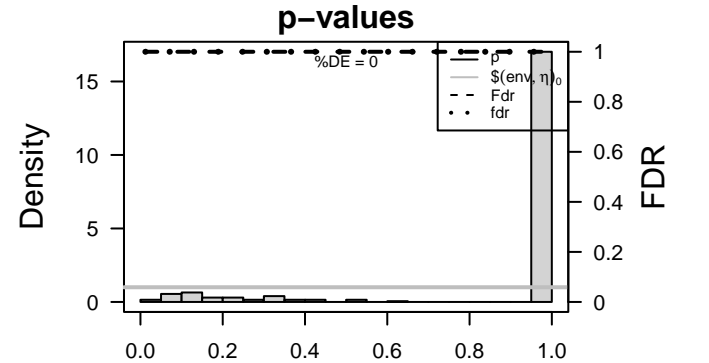


Spot Genelist

ID	Description
Vitvi17g00331	
Vitvi18g02031	
Vitvi18g00086	Binding to a protein.
Vitvi14g01524	Binding to a metal ion.
Vitvi18g02812	
Vitvi01g01793	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi11g00865	Binding to a protein.
Vitvi08g01839	The process in which an amino acid is transported across a membrane.
Vitvi11g00301	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.
Vitvi18g02766	
Vitvi07g00092	
Vitvi18g00322	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi10g00568	Catalysis of the reaction: 7,8-didemethyl-8-hydroxy-5-deazariboflavin + lactyl-2-diphospho-5'-guanosine = coenzyme F420-0 + GMP.
Vitvi04g00390	
Vitvi04g00230	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi18g00983	Organized structure of distinctive morphology and function, bounded by a single or double lipid bilayer membrane and occurring within the cell. Includes the nucleus, mitochondria, plastids, vacuoles, and vesicles. Excludes the plasma membrane.
Vitvi09g01588	Binding to ADP, adenosine 5'-diphosphate.
Vitvi12g02409	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.
Vitvi17g00188	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi01g01505	The process in which one or more ubiquitin groups are added to a protein.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.01	2 / 50	Inositol phosphate metabolism
2	0.02	2 / 58	Carbohydrate metabolism – Fructose and mannose metabolism
3	0.04	1 / 13	Biosynthesis of unsaturated fatty acids
4	0.05	1 / 17	Transcription factors – SBP
5	0.06	1 / 18	Receptor – Others
6	0.06	1 / 19	Cofactors and vitamin metabolism – Folate biosynthesis
7	0.06	1 / 19	Transcription factors – AUXIAA
8	0.06	1 / 20	Lipid metabolism – Biosynthesis of unsaturated fatty acids
9	0.07	1 / 22	Fatty acid elongation
10	0.08	1 / 24	Folate biosynthesis
11	0.08	1 / 25	Protein – Calcium ion-dependent exocytosis
12	0.08	2 / 142	Transport system – Protein coat
13	0.09	1 / 27	Enzyme – 1.6 Acting on NADH or NADPH
14	0.09	1 / 30	Lipid biosynthesis protein – Component type
15	0.10	1 / 32	Protein – Actin-binding proteins
16	0.11	1 / 36	Phenylalanine tyrosine and tryptophan biosynthesis
17	0.11	1 / 36	Enzyme – 6.3 Forming carbon–nitrogen bonds
18	0.12	1 / 37	Enzyme – 5.3 Intramolecular oxidoreductases
19	0.12	1 / 38	Protein – Chaperone mediated autophagy (CMA)
20	0.12	1 / 38	Protein – Clathrin-mediated endocytosis



D-Cluster

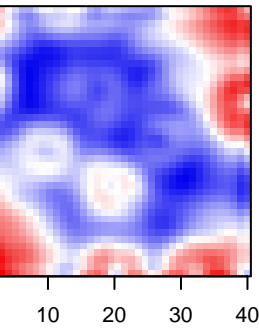
Spot Summary: R

metagenes = 30
genes = 468

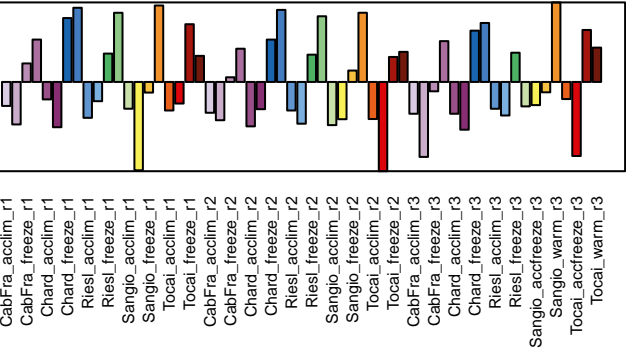
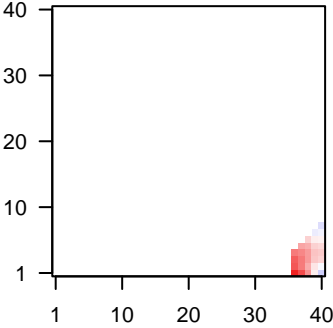
<r> metagenes = 0.93
<r> genes = 0.51
beta: r2= 12 / log p= -Inf

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

Overview Map



Spot

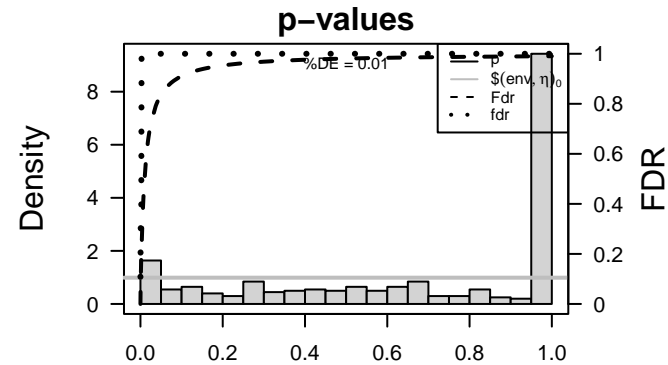


Spot Genelist

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.
Vitvi03g00325	A transcription regulator activity that modulates transcription of gene sets via selective and non-covalent binding to a specific double-stranded genomic DNA sequence (sometimes referred to as a motif) within a cis-regulatory region. Regulatory regions include promoters (proximal and distal) and enhancers. Genes are transcriptional units, and include bacterial operons.
Vitvi13g00369	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi13g02005	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi00g00346	
Vitvi07g02904	
Vitvi02g01118	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi01g01981	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi13g00870	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi11g01421	
Vitvi16g00731	
Vitvi02g00110	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi05g02017	
Vitvi15g01070	Catalysis of an oxidation-reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi01g01980	
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 siltlike cavities called cisternae. The ER takes two forms, rough (or granular), with ribosomes adhering to the outer surface, and smooth (with no ribosomes attached).
Vitvi12g02451	Catalysis of the transfer of a group, e.g. a methyl group, glycosyl group, acyl group, phosphorus-containing, or other groups, from one compound (generally regarded as the donor) to another compound (generally regarded as the acceptor). Transferase is the systematic name for any enzyme of EC class 2.
Vitvi05g01116	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi11g01303	Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzyme possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic.
Vitvi05g02019	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-08	9 / 26	Flavonoid biosynthesis
2	3e-04	8 / 63	Phenylpropanoid biosynthesis
3	8e-04	10 / 111	Transporter catalog - Porters cat 66 to 94
4	2e-03	3 / 10	Linoleic acid metabolism
5	3e-03	3 / 11	Enzyme - 2.2 Transferring aldehyde or ketonic groups
6	3e-03	5 / 38	Photosynthesis
7	3e-03	5 / 38	Enzyme - 1.8 Acting on a sulfur group of donors
8	4e-03	4 / 25	Nitrogen metabolism
9	5e-03	7 / 78	Energy metabolism - Photosynthesis
10	6e-03	5 / 44	Energy metabolism - Nitrogen metabolism
11	7e-03	3 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
12	7e-03	7 / 83	Transcription factors - MYB
13	8e-03	4 / 30	Ubiquinone and other terpenoid-quinone biosynthesis
14	1e-02	3 / 19	Cofactors and vitamin metabolism - Ubiquinone biosynthesis
15	1e-02	4 / 35	Lipid metabolism - Alpha-linolenic acid metabolism
16	1e-02	8 / 118	Transcription factors - Helix-turn-helix
17	2e-02	3 / 21	Butanoate metabolism
18	2e-02	5 / 57	Glyoxylate and dicarboxylate metabolism
19	2e-02	6 / 79	Transporter catalog - Porters cat 30 to 64
20	2e-02	4 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family



D-Cluster

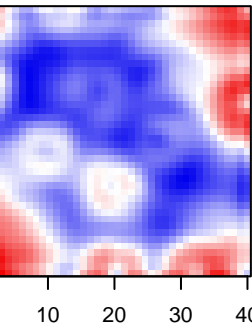
Spot Summary: S

metagenes = 18
genes = 238

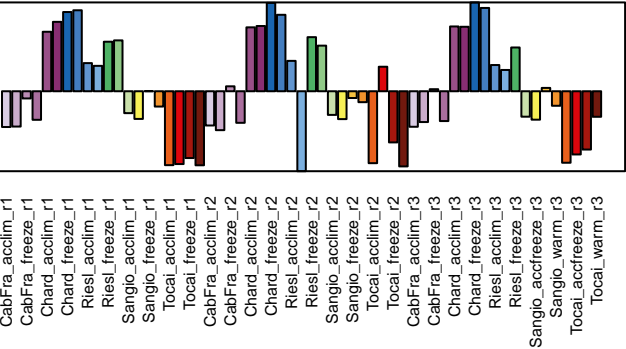
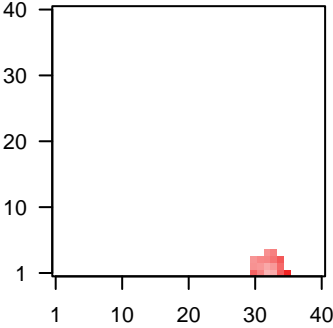
<r> metagenes = 0.95
<r> genes = 0.39
beta: r2= 9.16 / log p= -Inf

samples with spot = 16 (27.1 %)
Chard_acclim : 3 (100 %)
Chard_accfreeze : 3 (100 %)
Chard_freeze : 3 (100 %)
Chard_warm : 3 (100 %)
Riesl_freeze : 2 (66.7 %)
Riesl_warm : 2 (100 %)

Overview Map



Spot

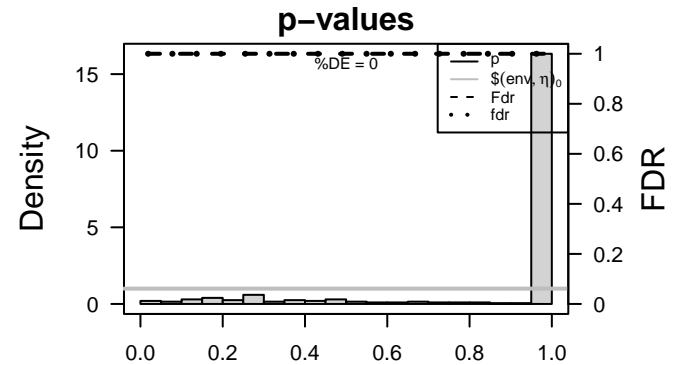


Spot Genelist

ID	Description
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.
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.
Vitvi04g01940	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.
Vitvi19g00427	
Vitvi15g00874	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.02	2 / 25	Biosynthesis of secondary metabolism – Zeatin biosynthesis
2	0.03	3 / 77	Pores ion channels [TC:1]
3	0.03	2 / 35	Lipid metabolism – Alpha-linolenic acid metabolism
4	0.04	2 / 39	Other amino acids metabolism – Selenoamino acid metabolism
5	0.05	3 / 102	Membrane transport – ABC transporters
6	0.08	2 / 58	Other amino acids metabolism – Glutathione metabolism
7	0.10	1 / 12	SLC15: Proton oligopeptide cotransporter
8	0.11	2 / 67	Amino acid metabolism – Tyrosine metabolism
9	0.12	2 / 71	Glutathione metabolism
10	0.12	3 / 146	Transporter catalog – Porters cat 7 to 17
11	0.13	2 / 75	Translation – Ribosome biogenesis in Eukaryotes
12	0.14	2 / 78	Energy metabolism – Photosynthesis
13	0.15	1 / 19	Cofactors and vitamin metabolism – Ubiquinone biosynthesis
14	0.15	3 / 161	Enzyme – 2.1 Transferring one-carbon groups
15	0.16	1 / 21	Replication and repair – Mismatch repair
16	0.17	1 / 22	Replication and repair – Homologous recombination
17	0.17	1 / 22	Transcription factors – CCAAT
18	0.18	1 / 24	Enzyme – 7.1 Catalysing the translocation of hydrons
19	0.20	1 / 26	Steroid biosynthesis
20	0.20	1 / 26	Glycosyltransferase – Hydrophobic molecule



D-Cluster

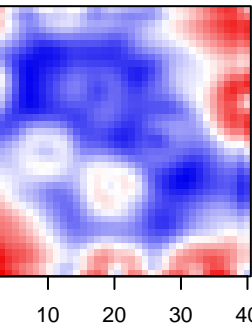
Spot Summary: T

metagenes = 34
genes = 271

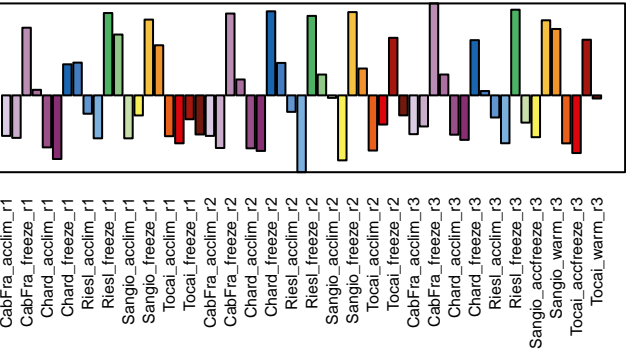
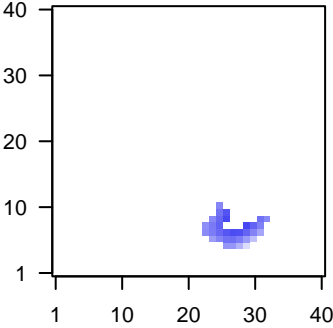
<r> metagenes = 0.82
<r> genes = 0.28
beta: r2= 1.77 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

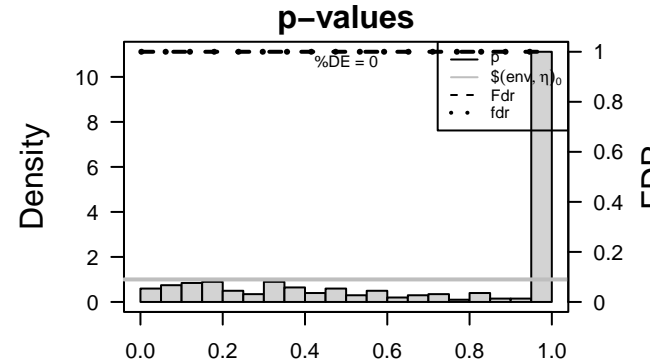


Spot Genelist

ID	Description
Vitvi01g00331	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.
Vitvi14g01984	A chlorophyll-containing plastid with thylakoids organized into grana and frets, or stroma thylakoids, and embedded in a stroma.
Vitvi19g01326	
Vitvi04g00005	
Vitvi07g00934	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi05g00018	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.
Vitvi16g00137	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.
Vitvi06g01551	
Vitvi12g01792	Binding to ADP, adenosine 5'-diphosphate.
Vitvi18g01038	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.
Vitvi19g00532	
Vitvi18g00679	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.
Vitvi08g01043	Binding to a zinc ion (Zn).
Vitvi07g00413	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.
Vitvi07g01567	
Vitvi13g00191	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.
Vitvi17g00387	
Vitvi03g01085	Binding to a metal ion.
Vitvi18g01254	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.
Vitvi13g02471	Binding to ADP, adenosine 5'-diphosphate.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.002	3 / 17	Protein - Arf GTPases and associated proteins
2	0.005	6 / 102	Amino sugar and nucleotide sugar metabolism
3	0.005	5 / 72	Glycerophospholipid metabolism
4	0.007	5 / 78	Glycosyltransferase - Structural polysaccharide
5	0.015	3 / 34	Carbohydrate metabolism - Nucleotide sugars metabolism
6	0.017	4 / 65	Phagosome
7	0.018	2 / 14	GTP-binding proteins - Arf/Sar Family
8	0.023	4 / 71	Lipid metabolism - Biosynthesis of steroids
9	0.027	2 / 17	Riboflavin metabolism
10	0.029	3 / 44	Energy metabolism - Nitrogen metabolism
11	0.040	3 / 50	Transcription factors - MYBrelated
12	0.046	9 / 309	Enzyme - 3.1 Acting on ester bonds
13	0.051	3 / 55	Glycerolipid metabolism
14	0.051	2 / 24	Folate biosynthesis
15	0.055	2 / 25	Transcription factors - GNAT
16	0.055	2 / 25	Transcription factors - Other zf
17	0.061	5 / 139	Spliceosome
18	0.064	4 / 99	mRNA surveillance pathway
19	0.069	4 / 102	Membrane transport - ABC transporters
20	0.071	7 / 238	Enzyme - 2.4 Glycosyltransferases



D-Cluster

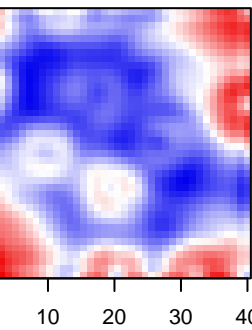
Spot Summary: U

metagenes = 13
genes = 230

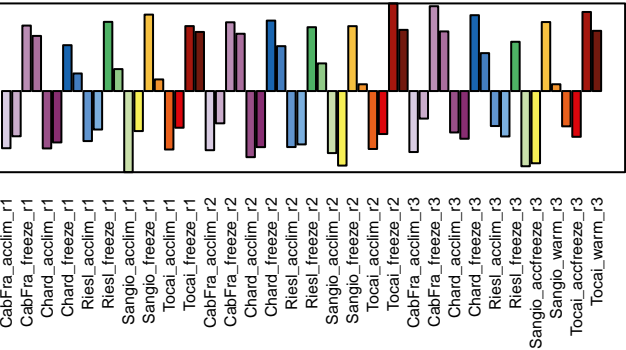
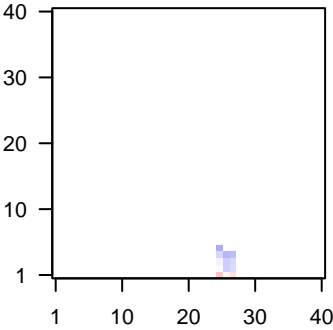
<r> metagenes = 0.97
<r> genes = 0.52
beta: r2= 3.88 / log p= -Inf

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

Overview Map



Spot

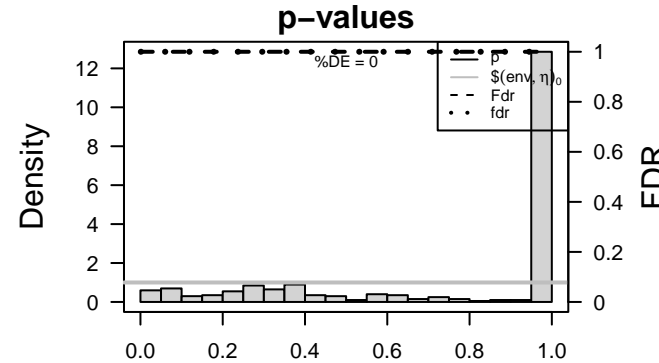


Spot Genelist

ID	Description
Vitvi03g01558	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi16g01103	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi08g01380	
Vitvi08g02383	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.
Vitvi12g02125	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi05g00527	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.
Vitvi12g00409	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.
Vitvi13g00221	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.
Vitvi08g01337	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi02g00085	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.
Vitvi15g01764	
Vitvi00g02025	
Vitvi13g00620	
Vitvi04g01792	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 stimulus indicating an increase or decrease in the concentration of salt (particularly but not exclusively sodium and chloride ions) in the environment.
Vitvi07g00237	
Vitvi08g00998	A complex composed of TATA binding protein (TBP) and TBP associated factors (TAFs); the total mass is typically about 800 kDa. Most of the TAFs are conserved across species. In TATA-containing promoters for RNA polymerase II (Pol II), TFIID is believed to recognize at least two distinct elements, the TATA element and a downstream promoter element. TFIID is also involved in recognition of TATA-less Pol II promoters. Binding of TFIID to DNA is necessary but not sufficient for transcription initiation from most RNA polymerase II promoters.
Vitvi11g00670	
Vitvi11g00565	Binding to a metal ion.
Vitvi03g00737	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi09g00837	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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-04	6 / 81	Oxidative phosphorylation
2	2e-03	4 / 38	Protein - Chaperone mediated autophagy (CMA)
3	3e-03	6 / 105	Energy metabolism - Oxidative phosphorylation
4	3e-03	4 / 45	Galactose metabolism
5	1e-02	3 / 38	Lipid metabolism - Ether lipid metabolism
6	2e-02	3 / 41	SLC25: Mitochondrial carrier
7	2e-02	3 / 44	Pentose phosphate pathway
8	2e-02	2 / 17	Proteasome - Assembling factors
9	2e-02	3 / 47	ABC transporters
10	3e-02	3 / 54	Carbohydrate metabolism - Pentose phosphate
11	5e-02	6 / 195	Carbohydrate metabolism - Starch and sucrose metabolism
12	5e-02	2 / 27	Common spliceosomal components
13	5e-02	3 / 64	Purine metabolism
14	5e-02	8 / 309	Enzyme - 3.1 Acting on ester bonds
15	6e-02	2 / 29	Arginine biosynthesis
16	6e-02	2 / 29	Transcription factors - Trihelix
17	6e-02	2 / 30	Lipid biosynthesis protein - Component type
18	7e-02	3 / 71	Exosome - Proteins found in most exosomes
19	7e-02	2 / 33	Carbohydrate metabolism - Aminosugars metabolism
20	8e-02	2 / 35	Mitophagy factors



D-Cluster

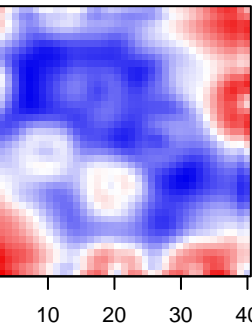
Spot Summary: V

metagenes = 27
genes = 390

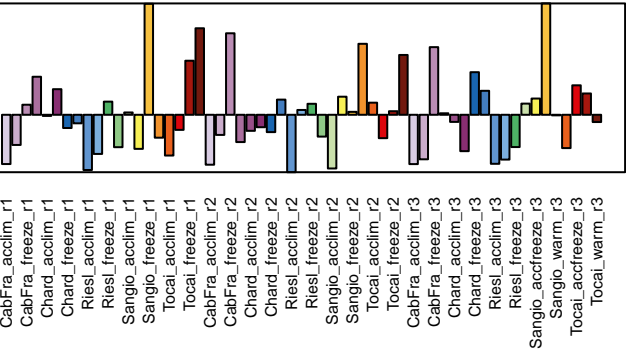
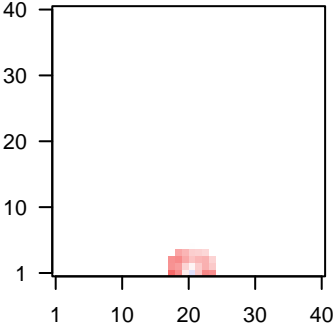
<r> metagenes = 0.96
<r> genes = 0.43
beta: r2= 8.93 / log p= -Inf

samples with spot = 9 (15.3 %)
CabFra_freeze : 2 (66.7 %)
Chard_freeze : 1 (33.3 %)
Sangio_freeze : 2 (66.7 %)
Sangio_warm : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 2 (66.7 %)

Overview Map



Spot

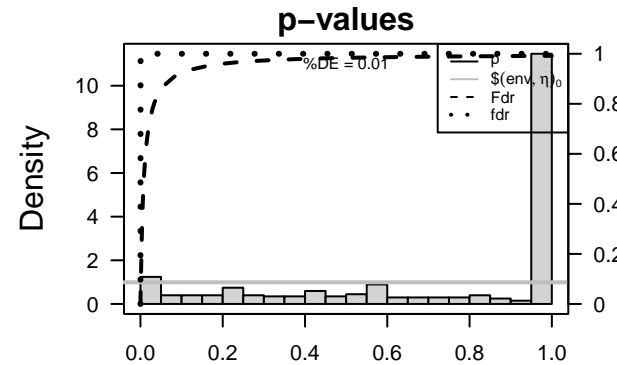


Spot Genelist

ID	Description
Vitvi18g02709	Any molecular entity that serves as an electron acceptor and electron donor in an electron transport chain. An electron transport chain is a process in which a series of electron carriers operate together to transfer electrons from donors to any of several different terminal electron acceptors to generate a transmembrane electrochemical gradient.
Vitvi02g00393	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi16g01336	Binding to a metal ion.
Vitvi18g03250	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g00253	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.
Vitvi15g00871	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi12g02245	Binding to a metal ion.
Vitvi02g00270	Binding to a metal ion.
Vitvi15g01035	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.
Vitvi06g01559	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.
Vitvi03g01651	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi08g01702	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.
Vitvi07g02676	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi12g02241	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi00g01989	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.
Vitvi07g03053	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.
Vitvi17g00450	
Vitvi07g02243	
Vitvi09g01557	
Vitvi02g01403	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-10	19 / 162	Plant specific signaling – Plant-pathogen interaction
2	8e-08	16 / 153	Plant-pathogen interaction
3	2e-05	8 / 56	Hormone signaling – Jasmonate signaling
4	4e-04	6 / 48	Transcription factors – WRKY
5	4e-03	4 / 33	Carbohydrate metabolism – Butanoate metabolism
6	5e-03	3 / 17	Kinase – IRAK family
7	5e-03	6 / 77	Pores ion channels [TC:1]
8	7e-03	10 / 197	Transporter catalog – Channels and pores
9	8e-03	3 / 21	Butanoate metabolism
10	9e-03	6 / 89	MAPK signaling pathway – plant
11	1e-02	4 / 45	Valine leucine and isoleucine degradation
12	1e-02	6 / 96	Transporter catalog – Porters cat 1 to 6
13	1e-02	8 / 157	Protein processing in endoplasmic reticulum
14	2e-02	7 / 129	Enzyme – 3.2 Glycosylases
15	2e-02	2 / 10	SLC39: Metal ion transporter
16	2e-02	2 / 10	Transcription factors – ZIM
17	2e-02	8 / 168	Plant hormone signal transduction
18	3e-02	3 / 33	alpha-Linolenic acid metabolism
19	3e-02	3 / 33	Enzyme – 5.4 Intramolecular transferases
20	3e-02	3 / 33	Carbohydrate metabolism – Aminosugars metabolism



D-Cluster

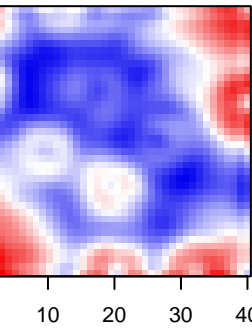
Spot Summary: W

metagenes = 30
genes = 240

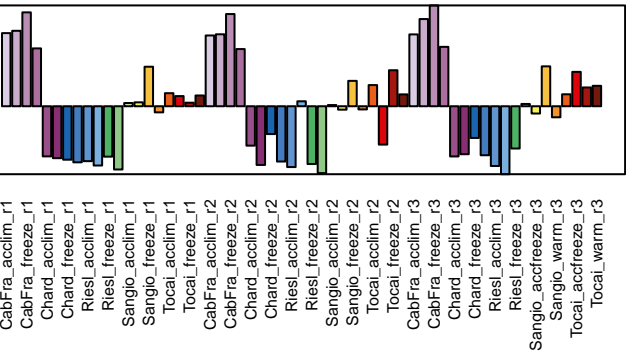
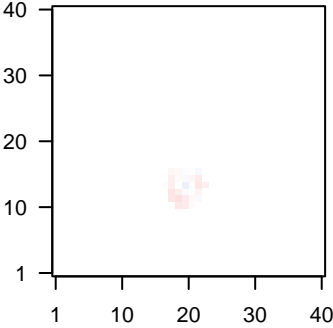
<r> metagenes = 0.92
<r> genes = 0.36
beta: r2= 4.43 / log p= -Inf

samples with spot = 12 (20.3 %)
CabFra_acclim : 3 (100 %)
CabFra_accfreeze : 3 (100 %)
CabFra_freeze : 3 (100 %)
CabFra_warm : 3 (100 %)

Overview Map



Spot

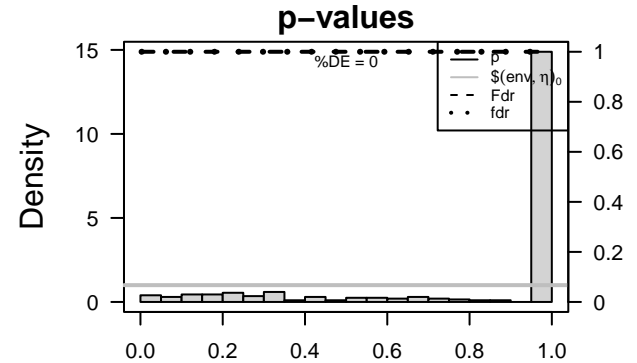


Spot Genelist

ID	Description
Vitvi06g01714	
Vitvi01g02000	
Vitvi01g02070	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi04g00345	
Vitvi01g01998	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi18g01669	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi16g01259	
Vitvi07g02587	
Vitvi07g00329	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi14g00149	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.
Vitvi07g02578	
Vitvi18g00878	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
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.
Vitvi12g02574	
Vitvi19g01935	
Vitvi02g00524	
Vitvi12g02554	The action of a molecule that contributes to the structural integrity of the ribosome.
Vitvi12g00883	
Vitvi05g02074	Binding to a protein.
Vitvi05g01819	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	6 / 153	Plant-pathogen interaction
2	0.017	2 / 22	Replication and repair – Homologous recombination
3	0.024	6 / 247	Translation – Ribosome
4	0.024	2 / 27	Mismatch repair
5	0.037	2 / 34	Peptidases and inhibitors – Family S10
6	0.039	2 / 35	Lipid metabolism – Alpha-linolenic acid metabolism
7	0.042	2 / 36	DNA replication
8	0.044	2 / 37	Homologous recombination
9	0.060	2 / 44	Nucleotide excision repair
10	0.069	3 / 105	Energy metabolism – Oxidative phosphorylation
11	0.079	3 / 111	Transporter catalog – Porters cat 66 to 94
12	0.082	2 / 53	Protein – Forward pathways
13	0.087	1 / 10	Minor spliceosome components
14	0.096	2 / 58	Other amino acids metabolism – Glutathione metabolism
15	0.107	2 / 62	Translation – Aminoacyl-tRNA biosynthesis
16	0.111	1 / 13	Kinase – CAMKL family
17	0.119	1 / 14	Kinase – CDPK family
18	0.122	2 / 67	Ribosome – Bacteria
19	0.134	2 / 71	Glutathione metabolism
20	0.135	1 / 16	Biotin metabolism



D-Cluster

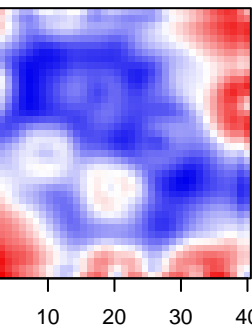
Spot Summary: X

metagenes = 31
genes = 463

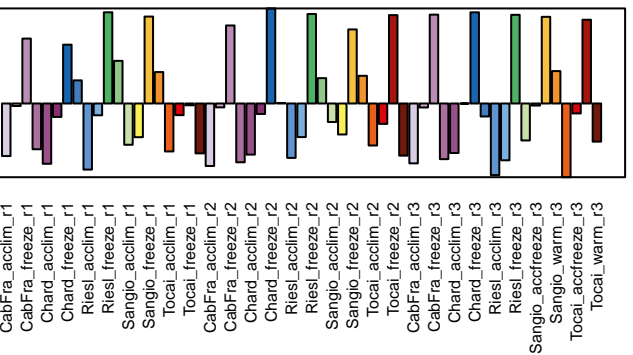
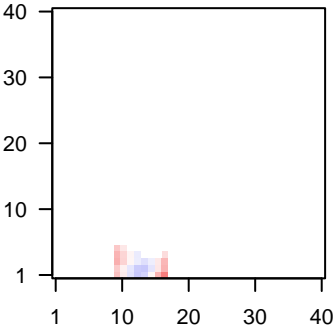
<r> metagenes = 0.96
<r> genes = 0.54
beta: r2= 10.96 / log p= -Inf

samples with spot = 14 (23.7 %)
CabFra_freeze : 3 (100 %)
Chard_freeze : 3 (100 %)
Riesl_freeze : 3 (100 %)
Sangio_freeze : 3 (100 %)
Tocai_freeze : 2 (66.7 %)

Overview Map



Spot

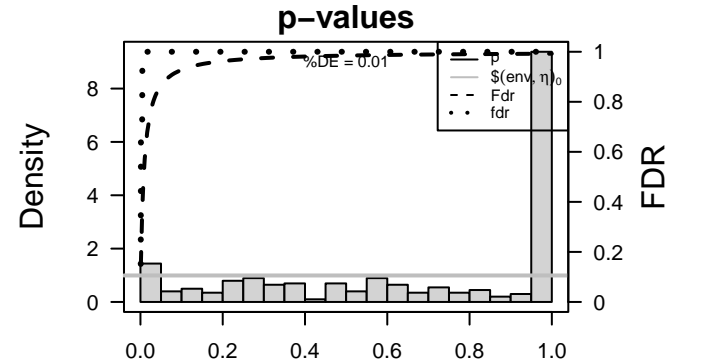


Spot Genelist

ID	Description
Vitvi05g00640	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi09g00258	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi18g00993	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.
Vitvi11g00285	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.
Vitvi09g00028	Binding to a nucleic acid.
Vitvi18g02685	Binding to a calcium ion (Ca2+).
Vitvi18g02684	Binding to a calcium ion (Ca2+).
Vitvi06g00526	
Vitvi17g00973	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a mechanism in which the sulfhydryl group of a cysteine residue at the active center acts as a nucleophile.
Vitvi02g01167	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi18g02683	Binding to a calcium ion (Ca2+).
Vitvi05g01193	Catalysis of the reaction: UDP-glucose + D-fructose = UDP + sucrose.
Vitvi02g00673	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi10g01879	
Vitvi11g01072	The process in which a solute is transported across a lipid bilayer, from one side of a membrane to the other.
Vitvi03g01432	
Vitvi10g01455	Binding to ADP, adenosine 5'-diphosphate.
Vitvi02g00066	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.
Vitvi18g02686	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-04	5 / 28	Exosome - Exosomal proteins of breast milk
2	8e-04	6 / 43	Transcription factors - BZIP
3	1e-03	6 / 47	ABC transporters
4	4e-03	4 / 26	Transcription factors - G2-like
5	5e-03	4 / 27	ABCG (White) subfamily
6	5e-03	4 / 28	Transcription factors - Basic leucine zipper (bZIP)
7	7e-03	8 / 108	Carbohydrate metabolism - Pyruvate metabolism
8	7e-03	9 / 131	Enzyme - 1.1 Acting on the CH-OH group of donors
9	8e-03	7 / 89	MAPK signaling pathway - plant
10	1e-02	3 / 18	Receptor - Others
11	2e-02	7 / 102	Membrane transport - ABC transporters
12	2e-02	5 / 58	Carbohydrate metabolism - Fructose and mannose metabolism
13	2e-02	7 / 111	Hormone signaling - ABA signaling
14	3e-02	3 / 25	Nitrogen metabolism
15	3e-02	4 / 44	Fructose and mannose metabolism
16	3e-02	4 / 44	Enzyme - 1.11 Acting on a peroxide as acceptor
17	3e-02	8 / 140	Hormone signaling - Ethylene signaling
18	3e-02	3 / 26	Glycosyltransferase - Hydrophobic molecule
19	3e-02	2 / 11	Cofactors and vitamin metabolism - Vitamin B6 metabolism
20	3e-02	2 / 11	Lipid metabolism - C21-Steroid hormone metabolism



D-Cluster

Spot Summary: Y

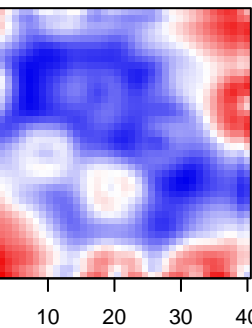
metagenes = 120
genes = 1271

<r> metagenes = 0.82

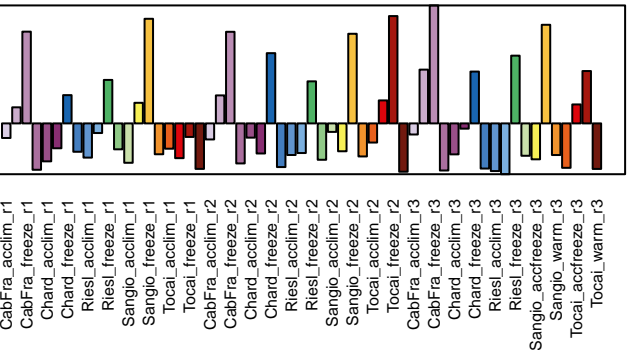
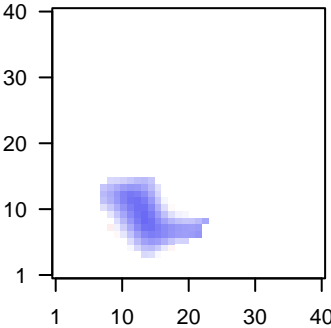
beta: r2= 3.61 / log p= -Inf

samples with spot = 3 (5.1 %)
CabFra_freeze : 1 (33.3 %)
Sangio_freeze : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

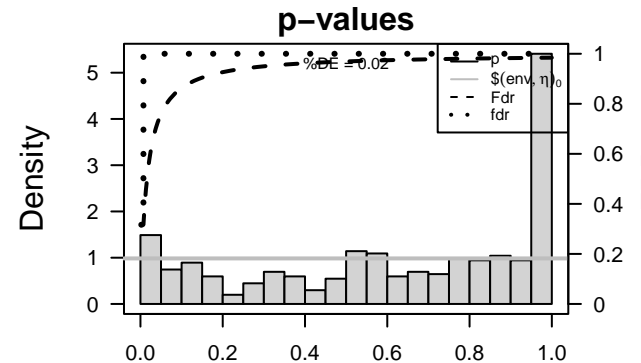


Spot Genelist

ID	Description
Vitvi14g01525	
Vitvi19g02040	
Vitvi03g00379	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi11g01506	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi08g01826	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.
Vitvi02g00096	
Vitvi08g02393	Any process that modulates the frequency, rate or extent of DNA endoreduplication.
Vitvi12g00298	
Vitvi18g01510	The process of assisting in the covalent and noncovalent assembly of single chain polypeptides or multisubunit complexes into the correct tertiary structure.
Vitvi17g00747	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.
Vitvi13g01724	Catalysis of an oxidation-reduction (redox) reaction in which hydrogen or electrons are transferred from one donor, and two oxygen atoms is incorporated into a donor.
Vitvi09g00281	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.
Vitvi04g01904	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi14g00423	
Vitvi13g02024	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 stimulus indicating an increase or decrease in the concentration of salt (particularly but not exclusively sodium and chloride ions) in the environment.
Vitvi08g01156	Any process involved in the conversion of a primary mRNA transcript into one or more mature mRNA(s) prior to translation into polypeptide.
Vitvi19g00143	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.
Vitvi11g00178	A closed structure, found only in eukaryotic cells, that is completely surrounded by unit membrane and contains liquid material. Cells contain one or several vacuoles, that may have different functions from each other. Vacuoles have a diverse array of functions. They can act as a storage organelle for nutrients or waste products, as a degradative compartment, as a cost-effective way of increasing cell size, and as a homeostatic regulator controlling both turgor pressure and pH of the cytosol.
Vitvi13g00490	The process of assisting in the covalent and noncovalent assembly of single chain polypeptides or multisubunit complexes into the correct tertiary structure.
Vitvi17g00685	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.002	9 / 43	Mitochondrial respiratory chain complex assembly factors
2	0.004	6 / 24	Inner mambrane
3	0.004	6 / 24	Ubiquitin system – Ubiquitin–conjugating enzymes
4	0.006	17 / 128	Ubiquitin system – Single Ring–finger type E3
5	0.006	7 / 33	Carbohydrate metabolism – Butanoate metabolism
6	0.006	9 / 50	Inositol phosphate metabolism
7	0.007	7 / 34	Chaperone – HSP40 / DNAJ
8	0.007	12 / 80	Other components
9	0.007	12 / 80	Transport system – Tethering factors
10	0.007	5 / 19	Cofactors and vitamin metabolism – Folate biosynthesis
11	0.008	6 / 27	Regulator of mitochondrial biogenesis
12	0.011	5 / 21	Secretion system – Eukaryotic Sec–SRP protein
13	0.012	6 / 29	Transcription factors – Trihelix
14	0.013	30 / 290	Enzyme – 2.3 Acyltransferases
15	0.020	8 / 51	Lipid metabolism – Fatty acid metabolism
16	0.020	5 / 24	Folate biosynthesis
17	0.020	5 / 24	Primary active transporters [TC:3]
18	0.021	7 / 42	Protein export
19	0.024	5 / 25	Transcription factors – Other zf
20	0.030	4 / 18	Chaperone – HSP20



D-Cluster

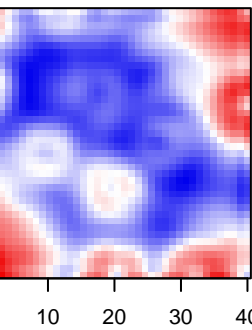
Spot Summary: Z

metagenes = 22
genes = 521

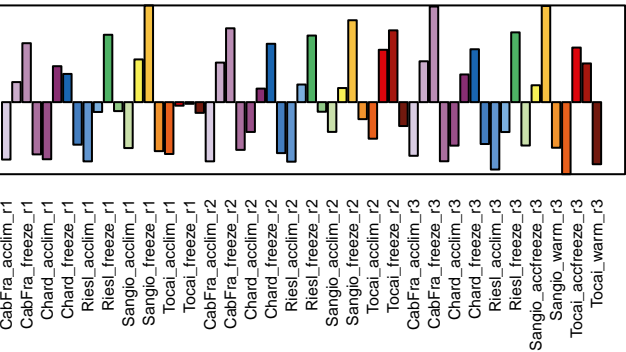
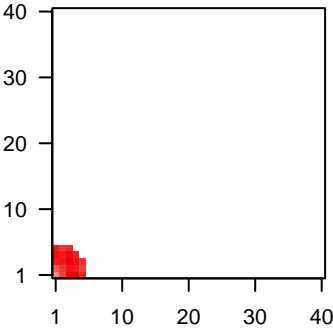
<r> metagenes = 0.98
<r> genes = 0.67
beta: r2= 45.67 / log p= -Inf

samples with spot = 21 (35.6 %)
CabFra_accfreeze : 2 (66.7 %)
CabFra_freeze : 3 (100 %)
Chard_accfreeze : 2 (66.7 %)
Chard_freeze : 3 (100 %)
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

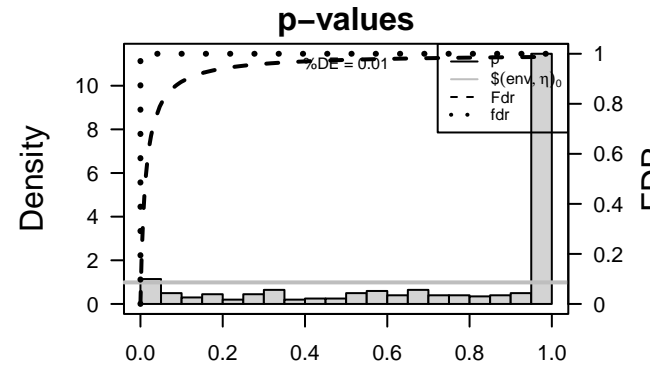


Spot Genelist

ID	Description
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).
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	
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	
Vitvi15g00960	Catalysis of the transfer of an acyl group to an oxygen atom on the acceptor molecule.
Vitvi17g00819	Binding to a zinc ion (Zn).
Vitvi04g01685	
Vitvi06g01762	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi16g01434	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi18g03100	Binds to and stops, prevents or reduces the activity of a cysteine-type endopeptidase, any enzyme that hydrolyzes peptide bonds in polypeptides by a mechanism in which the sulphydryl group of a cysteine residue at the active center acts as a nucleophile.
Vitvi14g00971	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-17	22 / 73	Transcription factors - AP2 EREBP
2	6e-16	28 / 140	Hormone signaling - Ethylene signaling
3	3e-11	16 / 64	Transcription factors - Other transcription factors
4	8e-10	13 / 48	Transcription factors - WRKY
5	1e-09	13 / 49	Transcription factors - NAC
6	1e-05	16 / 153	Plant-pathogen interaction
7	4e-05	8 / 45	Galactose metabolism
8	8e-05	10 / 77	Carbohydrate metabolism - Galactose metabolism
9	9e-05	15 / 162	Plant specific signaling - Plant-pathogen interaction
10	2e-04	18 / 238	Enzyme - 2.4 Glycosyltransferases
11	3e-03	10 / 118	Transcription factors - Helix-turn-helix
12	3e-03	8 / 83	Transcription factors - MYB
13	3e-03	3 / 11	Biosynthesis of secondary metabolism - ABA biosynthesis
14	7e-03	6 / 58	Other amino acids metabolism - Glutathione metabolism
15	7e-03	5 / 42	Tryptophan metabolism
16	1e-02	4 / 29	Transcription factors - GRAS
17	1e-02	7 / 86	Signal transduction - Calcium signaling pathway
18	2e-02	3 / 19	Hormone signaling - Gibberellin signaling
19	2e-02	6 / 74	Transcription factors - C2H2
20	3e-02	5 / 57	Transcription factors - HB



D-Cluster

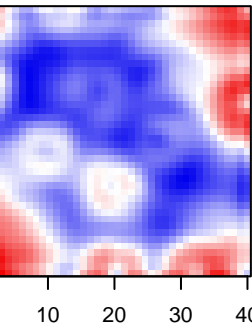
Spot Summary: A1

metagenes = 36
genes = 306

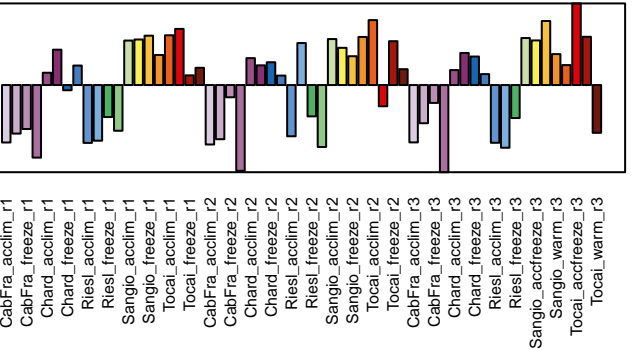
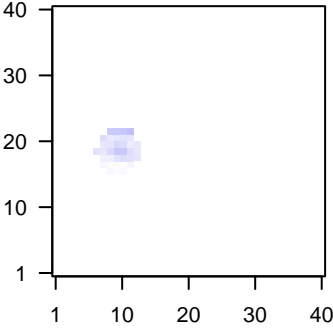
<r> metagenes = 0.9
<r> genes = 0.29
beta: r2= 2.83 / log p= -Inf

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

Overview Map



Spot



Spot Genelist

ID	Description
Vitvi14g02722	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi13g00807	Binding to a protein.
Vitvi04g01352	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi04g00352	
Vitvi10g00365	Binding to a protein.
Vitvi03g01481	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi04g00282	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi13g01298	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.
Vitvi14g02663	Catalysis of the reaction: a D-threo--aldose + NAD+ = a D-threo--aldono--1,5--lactone + NADH.
Vitvi07g02123	Catalysis of the hydrolysis of a carboxylic ester bond.
Vitvi18g03382	
Vitvi00g00239	
Vitvi19g01984	Binding to ADP, adenosine 5'-diphosphate.
Vitvi10g00984	Binding to a calcium ion (Ca2+).
Vitvi19g01961	
Vitvi16g00162	
Vitvi14g02720	Binding to ADP, adenosine 5'-diphosphate.
Vitvi17g00343	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi14g02706	Binding to ADP, adenosine 5'-diphosphate.
Vitvi13g02224	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.004	7 / 153	Plant-pathogen interaction
2	0.007	6 / 129	Enzyme - 3.2 Glycosylases
3	0.018	4 / 77	Carbohydrate metabolism - Galactose metabolism
4	0.020	6 / 162	Plant specific signaling - Plant-pathogen interaction
5	0.022	4 / 81	Enzyme - 4.2 Carbon-oxygen lyases
6	0.023	2 / 18	Nicotinate and nicotinamide metabolism
7	0.025	2 / 19	Cofactors and vitamin metabolism - Folate biosynthesis
8	0.033	4 / 92	Lipid metabolism - Glycerolipid metabolism
9	0.037	4 / 96	Transporter catalog - Porters cat 1 to 6
10	0.039	2 / 24	Folate biosynthesis
11	0.045	6 / 197	Transporter catalog - Channels and pores
12	0.048	3 / 62	Translation - Aminoacyl-tRNA biosynthesis
13	0.058	2 / 30	Glycan biosynthesis and metabolism - N-Glycan degradation
14	0.066	3 / 71	Lipid metabolism - Biosynthesis of steroids
15	0.069	2 / 33	Carbohydrate metabolism - Aminosugars metabolism
16	0.100	2 / 41	Cofactors and vitamin metabolism - Riboflavin metabolism
17	0.109	2 / 43	Terpenoid backbone biosynthesis
18	0.109	2 / 43	Aminoacyl-tRNA synthetases (AARSs)
19	0.113	2 / 44	Enzyme - 1.11 Acting on a peroxide as acceptor
20	0.113	2 / 44	Enzyme - 6.1 Forming carbon-oxygen bonds

