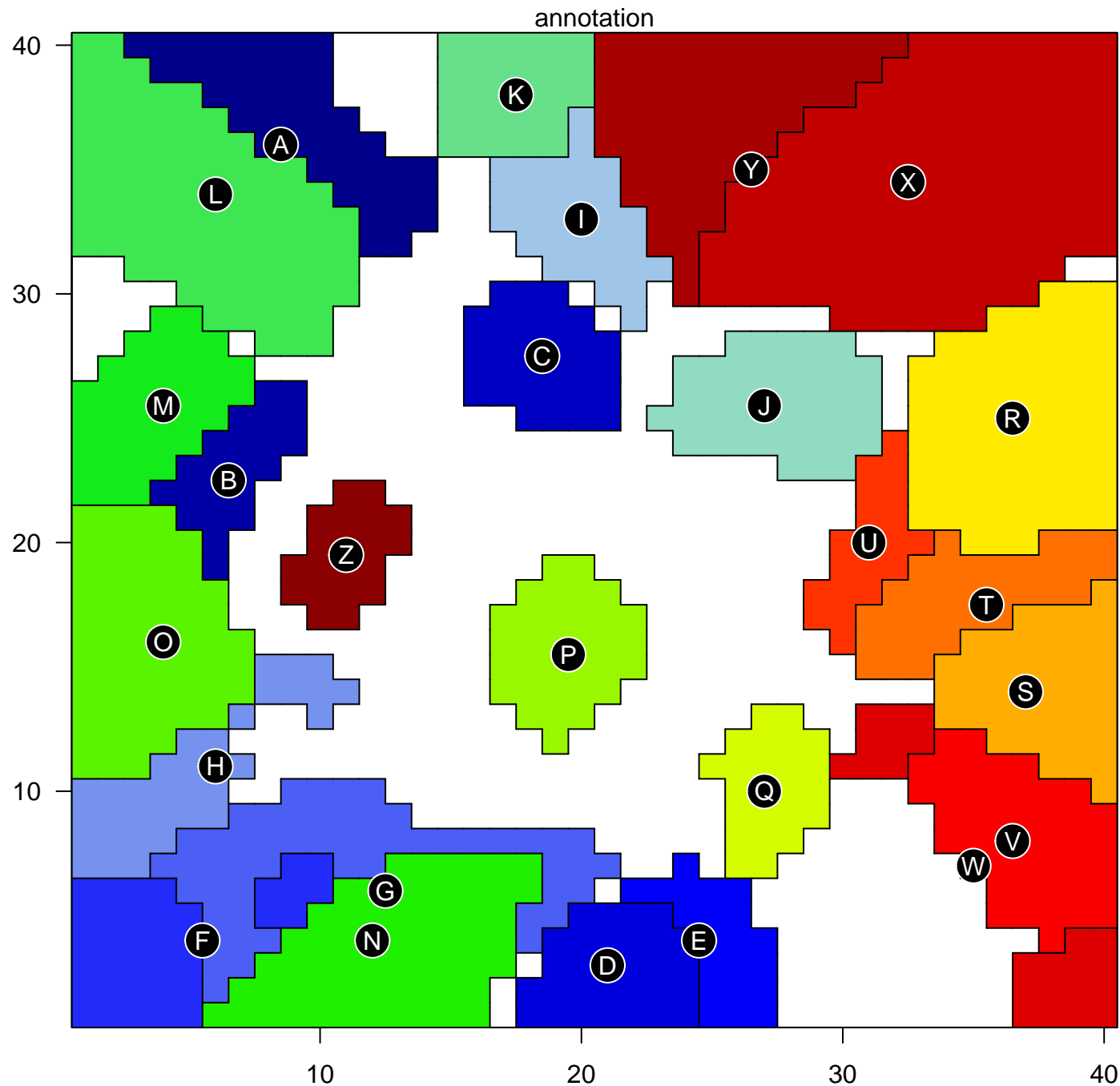
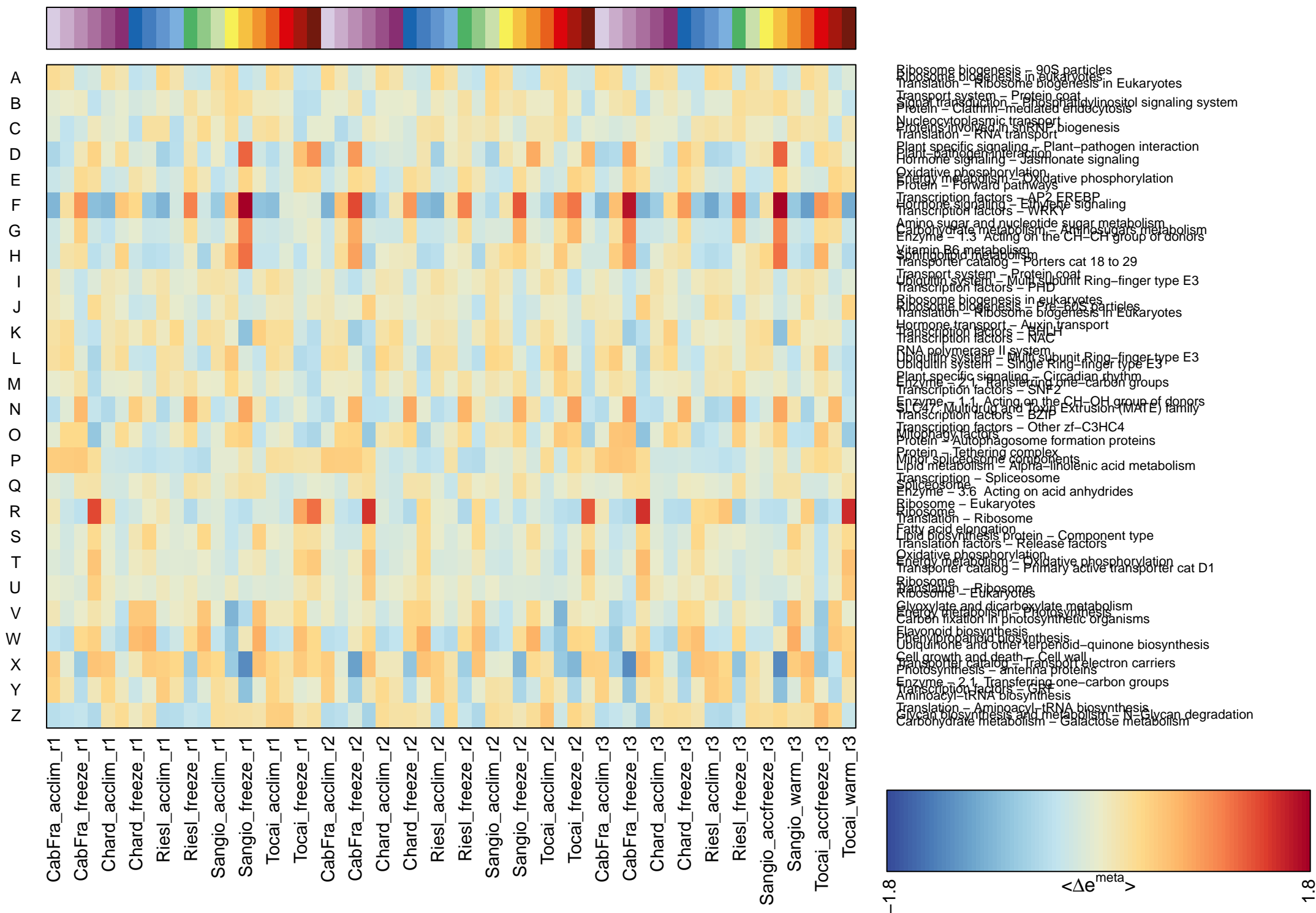


Correlation Cluster



- A ■ Ribosome biogenesis – 90S particles
Ribosome biogenesis in eukaryotes
- B ■ Transport system – Protein coat
Signal transduction – Phosphatidylinositol signaling system
- C ■ Nucleocytoplasmic transport
Proteins involved in snRNP biogenesis
- D ■ Plant specific signaling – Plant–pathogen interaction
Plant–pathogen interaction
- E ■ Oxidative phosphorylation
Energy metabolism – Oxidative phosphorylation
- F ■ Transcription factors – AP2 EREBP
Hormone signaling – Ethylene signaling
- G ■ Amino sugar and nucleotide sugar metabolism
Carbohydrate metabolism – Aminosugars metabolism
- H ■ Vitamin B6 metabolism
Sphingolipid metabolism
- I ■ Transport system – Protein coat
Ubiquitin system – Multi subunit Ring–finger type E3
- J ■ Ribosome biogenesis in eukaryotes
Ribosome biogenesis – Pre–60S particles
- K ■ Hormone transport – Auxin transport
Transcription factors – BHLH
- L ■ RNA polymerase II system
Ubiquitin system – Multi subunit Ring–finger type E3
- M ■ Plant specific signaling – Circadian rhythm
Enzyme – 2.1 Transferring one–carbon groups
- N ■ Enzyme – 1.1 Acting on the CH–OH group of donors
SLC47: Multidrug and Toxin Extrusion (MATE) family
- O ■ Transcription factors – Other zf–C3HC4
Mitophagy factors
- P ■ Protein – Tethering complex
Minor spliceosome components
- Q ■ Transcription – Spliceosome
Spliceosome
- R ■ Ribosome – Eukaryotes
Ribosome
- S ■ Fatty acid elongation
Lipid biosynthesis protein – Component type
- T ■ Oxidative phosphorylation
Energy metabolism – Oxidative phosphorylation
- U ■ Ribosome
Translation – Ribosome
- V ■ Glyoxylate and dicarboxylate metabolism
Energy metabolism – Photosynthesis
- W ■ Flavonoid biosynthesis
Phenylpropanoid biosynthesis



Correlation Cluster

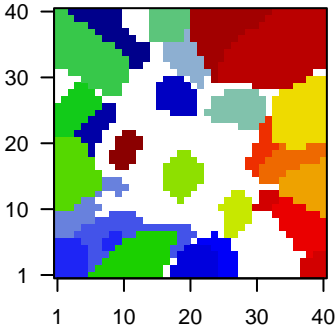
Spot Summary: A

metagenes = 44
genes = 618

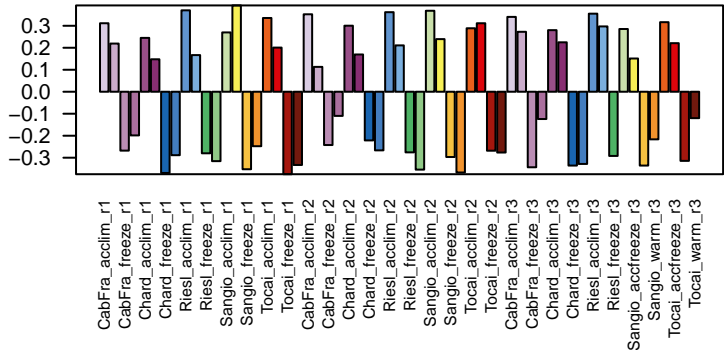
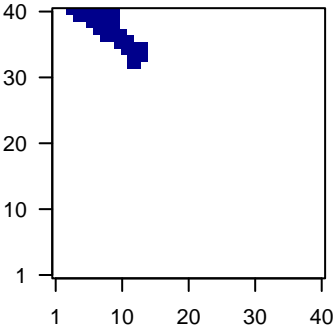
<r> metagenes = 0.95
<r> genes = 0.47
beta: r2= 4.81 / log p= -Inf

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

Overview Map



Spot

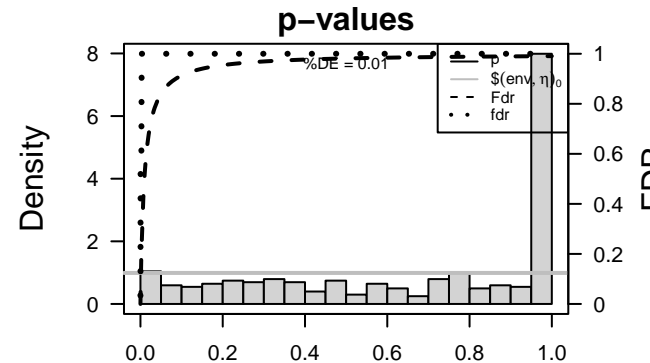


Spot Genelist

ID	Description
Vitvi12g00149	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.
Vitvi08g01995	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.
Vitvi05g00090	
Vitvi13g00409	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.
Vitvi10g01886	
Vitvi19g00174	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi10g00742	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.
Vitvi15g01705	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
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.
Vitvi10g00321	
Vitvi13g02017	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.
Vitvi09g00108	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi16g00623	
Vitvi17g00898	Binding to a copper (Cu) ion.
Vitvi13g01177	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.
Vitvi15g01161	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.
Vitvi14g01664	Catalysis of the hydrolysis of any ester bond.
Vitvi17g01386	Binding to ADP, adenosine 5'-diphosphate.
Vitvi05g01501	Binding to an RNA molecule or a portion thereof.
Vitvi14g00127	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-10	16 / 62	Ribosome biogenesis – 90S particles
2	8e-05	10 / 64	Ribosome biogenesis in eukaryotes
3	3e-04	10 / 75	Translation – Ribosome biogenesis in Eukaryotes
4	2e-03	17 / 217	Cell motility – Regulation of actin cytoskeleton
5	3e-03	11 / 116	Ribosome biogenesis – Pre-60S particles
6	7e-03	6 / 48	Transport system – Nuclear pore complex
7	8e-03	3 / 12	Ribosome biogenesis – Other ribosome biogenesis factors
8	9e-03	9 / 99	mRNA surveillance pathway
9	1e-02	3 / 13	Transcription factors – HMG
10	1e-02	5 / 38	Transcription – Basal transcription factors
11	1e-02	6 / 54	Amino acid metabolism – Methionine metabolism
12	2e-02	4 / 28	Transcription factors – SNF2
13	2e-02	11 / 151	RNA polymerase II system
14	2e-02	3 / 17	Kinase – IRAK family
15	3e-02	5 / 48	Amino acid metabolism – Lysine biosynthesis
16	3e-02	11 / 161	Enzyme – 2.1 Transferring one-carbon groups
17	3e-02	6 / 67	Replication and repair – RNA degradation
18	3e-02	6 / 68	Spliceosome associated proteins (SAPs)
19	4e-02	4 / 37	Basal transcription factors
20	4e-02	4 / 37	Homologous recombination



Correlation Cluster

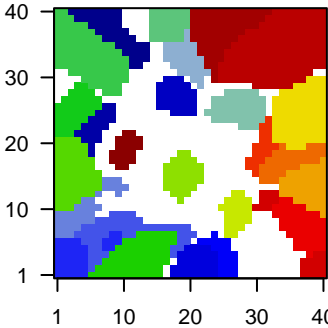
Spot Summary: B

metagenes = 22
genes = 212

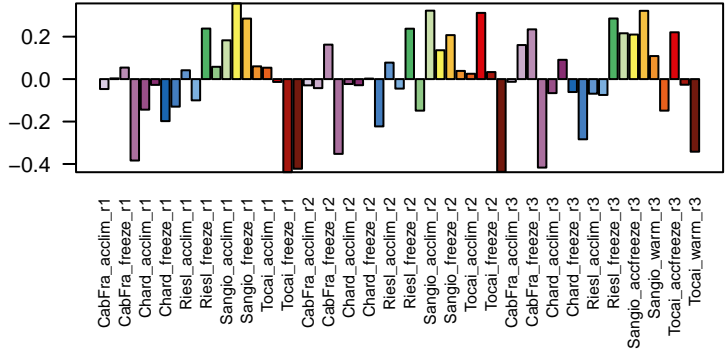
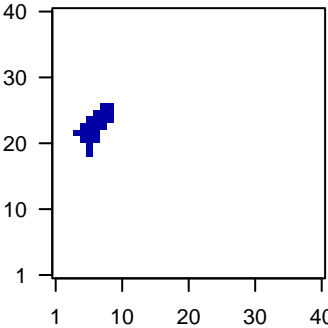
<r> metagenes = 0.95
<r> genes = 0.4
beta: r2= 2.1 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

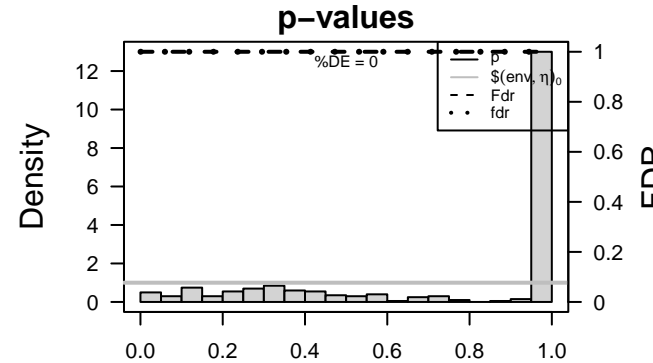


Spot Genelist

ID	Description
Vitvi04g00712	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi09g01692	
Vitvi18g01438	
Vitvi01g00083	Binding to ADP, adenosine 5'-diphosphate.
Vitvi00g01230	
Vitvi02g01833	
Vitvi19g00138	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.
Vitvi02g01187	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi11g01270	
Vitvi14g03137	
Vitvi00g01114	
Vitvi04g01261	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi04g01671	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi04g00118	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi19g00473	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.
Vitvi13g00042	Binding to ADP, adenosine 5'-diphosphate.
Vitvi02g00623	
Vitvi07g00526	
Vitvi12g02293	
Vitvi18g02524	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-04	8 / 142	Transport system - Protein coat
2	3e-03	4 / 51	Signal transduction - Phosphatidylinositol signaling system
3	9e-03	3 / 38	Protein - Clathrin-mediated endocytosis
4	2e-02	4 / 86	Signal transduction - Calcium signaling pathway
5	2e-02	3 / 54	Carbohydrate metabolism - Inositol phosphate metabolism
6	2e-02	2 / 21	Replication and repair - Mismatch repair
7	3e-02	5 / 151	RNA polymerase II system
8	3e-02	3 / 61	Peroxisome
9	3e-02	2 / 25	Protein - Calcium ion-dependent exocytosis
10	3e-02	2 / 26	Transcription factors - Orphans FAR-RED
11	5e-02	3 / 74	Transcription factors - C2H2
12	6e-02	2 / 35	RNA polymerase
13	7e-02	2 / 39	Carbohydrate metabolism - Citrate cycle
14	8e-02	2 / 41	Transcription - RNA polymerase
15	8e-02	3 / 89	MAPK signaling pathway - plant
16	9e-02	8 / 409	Enzyme - 2.7 Transferring phosphorus-containing groups
17	1e-01	2 / 48	Transcription factors - PHD
18	1e-01	1 / 10	Sulfur relay system
19	1e-01	1 / 10	Kinase - Wnk family
20	1e-01	2 / 50	Inositol phosphate metabolism



Correlation Cluster

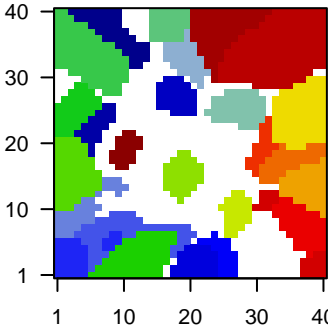
Spot Summary: C

metagenes = 30
genes = 337

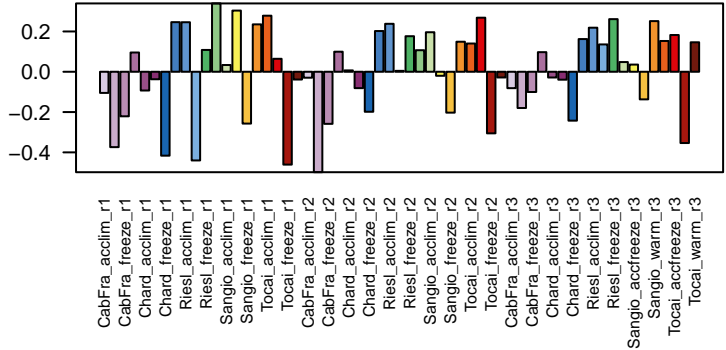
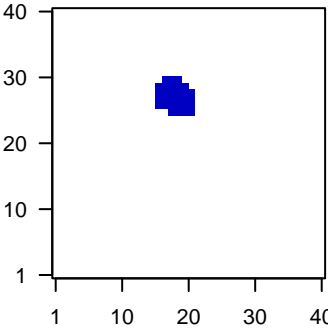
<r> metagenes = 0.93
<r> genes = 0.34
beta: r2= 1.54 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

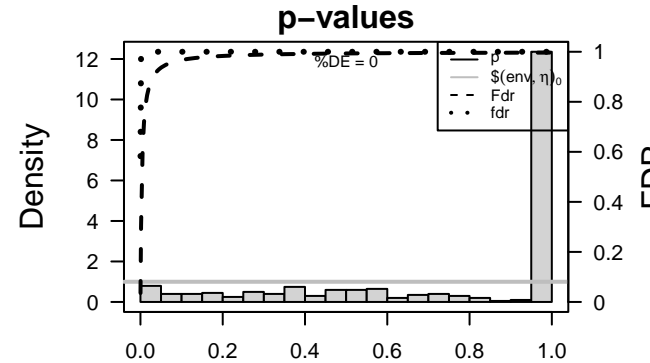


Spot Genelist

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.
Vitvi04g02107	
Vitvi09g01718	
Vitvi05g01824	
Vitvi04g00241	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.
Vitvi13g01582	
Vitvi07g01075	Binding to a zinc ion (Zn).
Vitvi19g02185	Binding to ADP, adenosine 5'-diphosphate.
Vitvi17g00474	
Vitvi00g00997	
Vitvi10g00440	
Vitvi12g02736	Binding to a protein.
Vitvi13g01343	
Vitvi07g02199	
Vitvi19g01697	Binding to ADP, adenosine 5'-diphosphate.
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.
Vitvi13g01481	Binding to ADP, adenosine 5'-diphosphate.
Vitvi18g02501	Binding to a zinc ion (Zn).

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-05	8 / 85	Nucleocytoplasmic transport
2	1e-03	3 / 14	Proteins involved in snRNP biogenesis
3	5e-03	7 / 126	Translation – RNA transport
4	8e-03	4 / 48	Transport system – Nuclear pore complex
5	9e-03	7 / 139	Spliceosome
6	9e-03	14 / 409	Enzyme – 2.7 Transferring phosphorus-containing groups
7	1e-02	6 / 115	Enzyme – 3.6 Acting on acid anhydrides
8	2e-02	3 / 32	Protein – Actin-binding proteins
9	2e-02	4 / 63	Messenger RNA Biogenesis – mRNA degradation factors
10	2e-02	7 / 165	Transcription – Spliceosome
11	3e-02	2 / 17	Signal transduction – mTOR signaling pathway
12	3e-02	3 / 42	Cytoskeleton – Actin filaments / Microfilaments
13	4e-02	2 / 19	Transcription factors – Jumoni
14	4e-02	6 / 151	RNA polymerase II system
15	5e-02	4 / 80	Other components
16	5e-02	3 / 48	Transcription factors – PHD
17	5e-02	4 / 83	RNA degradation
18	6e-02	2 / 24	Mitochondrial dynamics
19	7e-02	2 / 25	Lysine degradation
20	7e-02	2 / 25	Protein – Tethering complex



Correlation Cluster

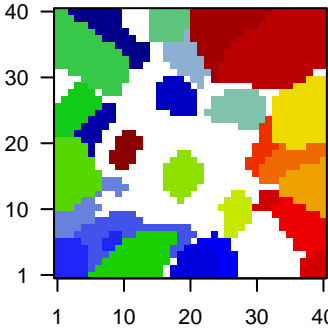
Spot Summary: D

metagenes = 30
genes = 429

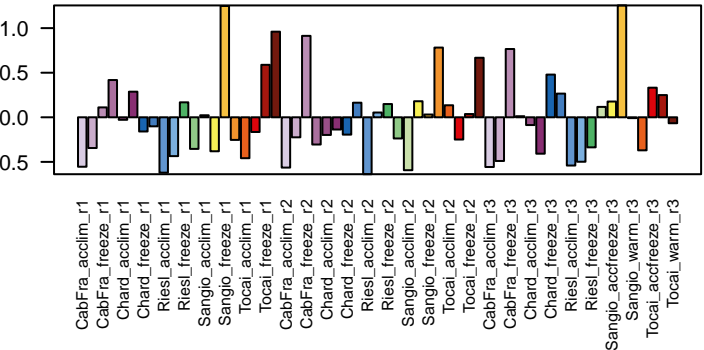
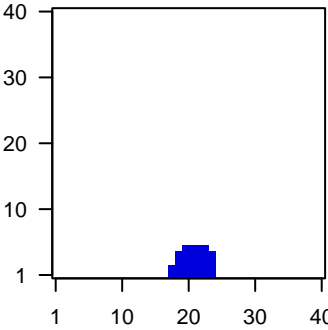
<r> metagenes = 0.96
<r> genes = 0.43
beta: r2= 8.29 / log p= -Inf

samples with spot = 10 (16.9 %)
CabFra_freeze : 2 (66.7 %)
CabFra_warm : 1 (33.3 %)
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

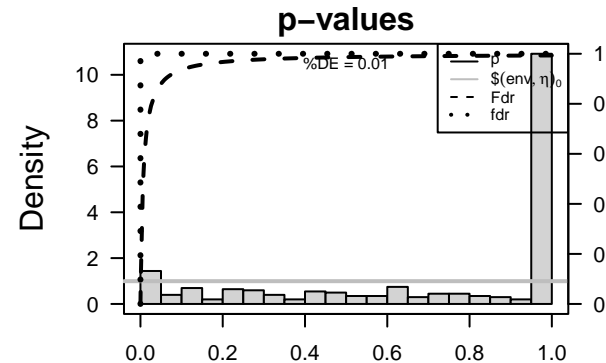


Spot Genelist

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	6e-10	20 / 162	Plant specific signaling – Plant-pathogen interaction
2	9e-09	18 / 153	Plant-pathogen interaction
3	3e-05	8 / 56	Hormone signaling – Jasmonate signaling
4	7e-04	6 / 48	Transcription factors – WRKY
5	6e-03	7 / 96	Transporter catalog – Porters cat 1 to 6
6	6e-03	3 / 17	Kinase – IRAK family
7	6e-03	4 / 33	Carbohydrate metabolism – Butanoate metabolism
8	7e-03	6 / 77	Pores ion channels [TC:1]
9	9e-03	9 / 157	Protein processing in endoplasmic reticulum
10	1e-02	4 / 38	Protein – Chaperone mediated autophagy (CMA)
11	1e-02	4 / 39	Carbohydrate metabolism – Citrate cycle
12	1e-02	3 / 21	Butanoate metabolism
13	1e-02	10 / 197	Transporter catalog – Channels and pores
14	1e-02	6 / 89	MAPK signaling pathway – plant
15	2e-02	4 / 45	Valine leucine and isoleucine degradation
16	2e-02	2 / 10	SLC39: Metal ion transporter
17	2e-02	2 / 10	Transcription factors – ZIM
18	2e-02	5 / 71	Exosome – Proteins found in most exosomes
19	3e-02	6 / 101	Glycolysis / Gluconeogenesis
20	4e-02	8 / 168	Plant hormone signal transduction



Correlation Cluster

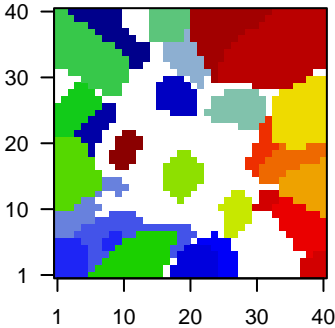
Spot Summary: E

metagenes = 21
genes = 295

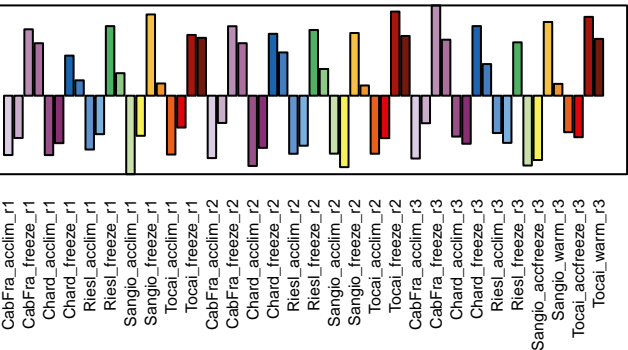
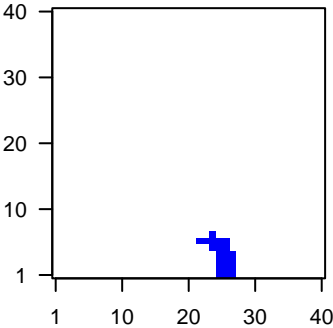
<r> metagenes = 0.95
<r> genes = 0.48
beta: r2= 3.46 / log p= -Inf

samples with spot = 4 (6.8 %)
CabFra_freeze : 1 (33.3 %)
Sangio_freeze : 1 (33.3 %)
Tocai_freeze : 2 (66.7 %)

Overview Map



Spot

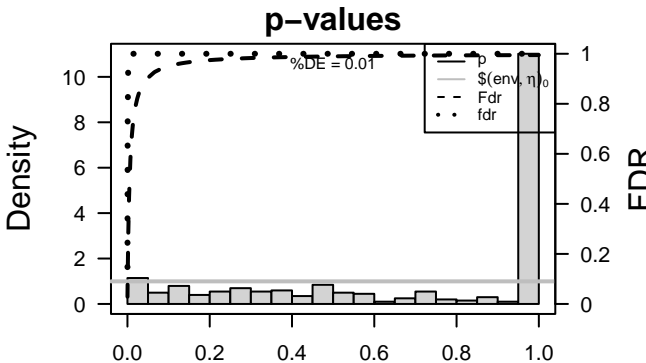


Spot Genelist

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	
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.
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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-05	8 / 81	Oxidative phosphorylation
2	4e-04	8 / 105	Energy metabolism – Oxidative phosphorylation
3	2e-03	5 / 53	Protein – Forward pathways
4	4e-03	4 / 38	Protein – Chaperone mediated autophagy (CMA)
5	7e-03	4 / 45	Galactose metabolism
6	1e-02	3 / 27	Common spliceosomal components
7	1e-02	3 / 28	Sulfur metabolism
8	1e-02	3 / 29	Energy metabolism – Sulfur metabolism
9	2e-02	8 / 195	Carbohydrate metabolism – Starch and sucrose metabolism
10	2e-02	2 / 13	Selenocompound metabolism
11	2e-02	4 / 64	Purine metabolism
12	3e-02	3 / 38	Lipid metabolism – Ether lipid metabolism
13	3e-02	3 / 40	N-Glycan biosynthesis
14	3e-02	3 / 40	Amino acid metabolism – Cysteine metabolism
15	3e-02	6 / 139	Spliceosome
16	3e-02	3 / 41	SLC25: Mitochondrial carrier
17	3e-02	4 / 71	Exosome – Proteins found in most exosomes
18	3e-02	2 / 17	Proteasome – Assembling factors
19	3e-02	2 / 17	Protein – Arf GTPases and associated proteins
20	4e-02	6 / 142	Transport system – Protein coat



Correlation Cluster

Spot Summary: F

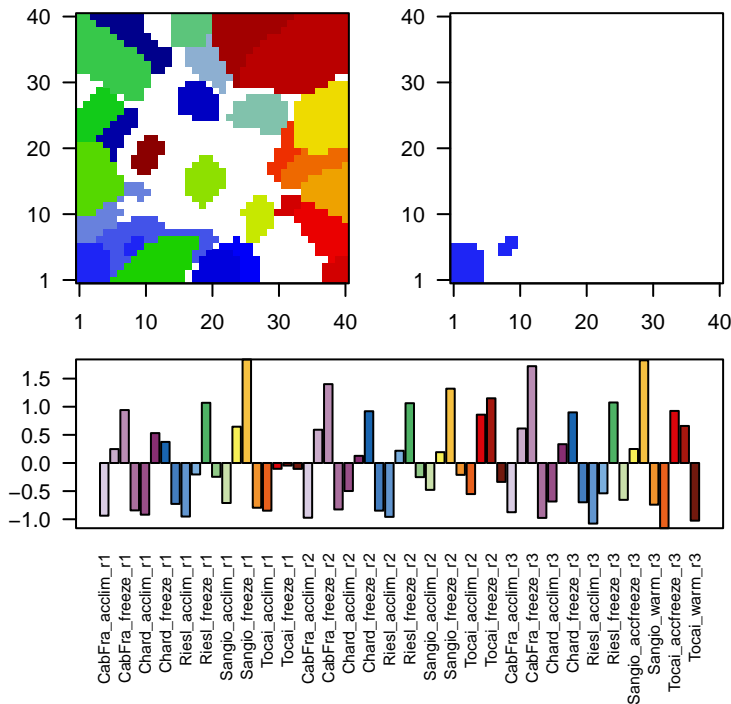
metagenes = 36
genes = 734

<r> metagenes = 0.96
<r> genes = 0.63
beta: r2= 36.61 / log p= -Inf

samples with spot = 19 (32.2 %)
CabFra_accfreeze : 2 (66.7 %)
CabFra_freeze : 3 (100 %)
Chard_accfreeze : 1 (33.3 %)
Chard_freeze : 2 (66.7 %)
Riesl_freeze : 3 (100 %)
Sangio_accfreeze : 1 (33.3 %)
Sangio_freeze : 3 (100 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 2 (66.7 %)

Overview Map

Spot

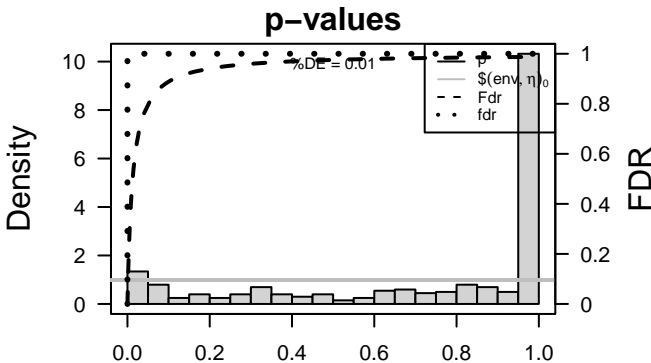


Spot Genelist

ID	Description
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	
Vitvi08g00957	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi02g01405	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi15g00770	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).
Vitvi06g00666	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi02g01408	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi04g01907	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi00g00932	
Vitvi02g01747	
Vitvi15g00960	Catalysis of the transfer of an acyl group to an oxygen atom on the acceptor molecule.
Vitvi05g00643	Catalysis of the hydrolysis of any ester bond.
Vitvi17g00819	Binding to a zinc ion (Zn).
Vitvi04g01685	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-16	24 / 73	Transcription factors - AP2 EREBP
2	8e-16	32 / 140	Hormone signaling - Ethylene signaling
3	3e-11	16 / 48	Transcription factors - WRKY
4	4e-10	17 / 64	Transcription factors - Other transcription factors
5	5e-09	14 / 49	Transcription factors - NAC
6	5e-05	18 / 153	Plant-pathogen interaction
7	8e-05	15 / 118	Transcription factors - Helix-turn-helix
8	3e-04	17 / 162	Plant specific signaling - Plant-pathogen interaction
9	4e-04	8 / 45	Galactose metabolism
10	1e-03	10 / 77	Carbohydrate metabolism - Galactose metabolism
11	2e-03	20 / 238	Enzyme - 2.4 Glycosyltransferases
12	2e-03	8 / 58	Other amino acids metabolism - Glutathione metabolism
13	3e-03	4 / 16	Transcription factors - HSF
14	4e-03	4 / 17	Isoquinoline alkaloid biosynthesis
15	6e-03	9 / 83	Transcription factors - MYB
16	7e-03	6 / 42	Tryptophan metabolism
17	8e-03	9 / 86	Signal transduction - Calcium signaling pathway
18	9e-03	3 / 11	Biosynthesis of secondary metabolism - ABA biosynthesis
19	1e-02	5 / 34	Tyrosine metabolism
20	1e-02	8 / 77	Pores ion channels [TC:1]



Correlation Cluster

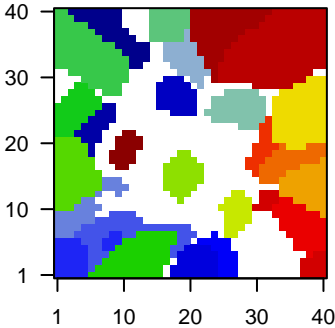
Spot Summary: G

metagenes = 53
genes = 522

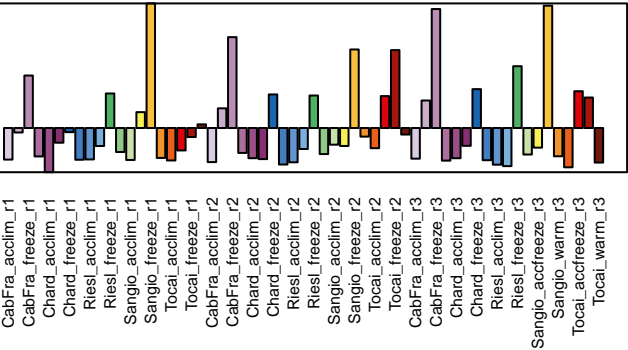
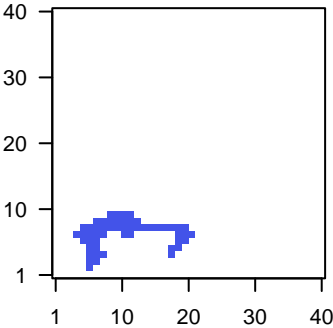
<r> metagenes = 0.91
<r> genes = 0.49
beta: r2= 8.88 / log p= -Inf

samples with spot = 8 (13.6 %)
CabFra_freeze : 3 (100 %)
Riesl_freeze : 1 (33.3 %)
Sangio_freeze : 3 (100 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

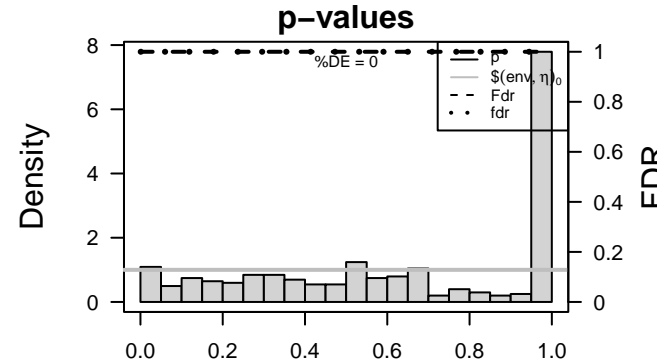


Spot Genelist

ID	Description
Vitvi18g00353	Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzyme possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic.
Vitvi16g01321	
Vitvi19g02038	
Vitvi11g00900	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.
Vitvi14g00485	
Vitvi04g02122	Binding to a metal ion.
Vitvi11g00486	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.
Vitvi08g01580	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi10g00877	
Vitvi17g01613	Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal peptide bonds in polypeptides.
Vitvi04g00798	
Vitvi17g01621	
Vitvi16g01025	
Vitvi02g00653	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.
Vitvi04g02210	Catalysis of the incorporation of one atom from molecular oxygen into a compound and the reduction of the other atom of oxygen to water.
Vitvi02g01273	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi17g01121	Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal peptide bonds in polypeptides.
Vitvi09g00383	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.
Vitvi05g01933	
Vitvi05g01910	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-04	10 / 102	Amino sugar and nucleotide sugar metabolism
2	2e-03	5 / 33	Carbohydrate metabolism – Aminosugars metabolism
3	2e-03	6 / 49	Enzyme – 1.3 Acting on the CH-CH group of donors
4	1e-02	5 / 51	Biosynthesis of secondary metabolism – Auxin biosynthesis
5	1e-02	15 / 290	Enzyme – 2.3 Acyltransferases
6	2e-02	8 / 119	Endocytosis
7	2e-02	8 / 121	Transporter catalog – Porters cat 18 to 29
8	2e-02	5 / 58	Other amino acids metabolism – Glutathione metabolism
9	2e-02	6 / 80	Transport system – Tethering factors
10	2e-02	15 / 309	Enzyme – 3.1 Acting on ester bonds
11	3e-02	8 / 128	Ubiquitin system – Single Ring-finger type E3
12	3e-02	3 / 24	Ubiquitin system – Ubiquitin-conjugating enzymes
13	3e-02	2 / 10	Linoleic acid metabolism
14	3e-02	2 / 10	Transcription factors – AS2
15	3e-02	9 / 157	Protein processing in endoplasmic reticulum
16	3e-02	3 / 25	Transcription factors – Other zf
17	4e-02	2 / 12	ABCB (MDR/TAP) subfamily
18	4e-02	3 / 29	Arginine biosynthesis
19	4e-02	3 / 29	Transcription factors – GRAS
20	5e-02	5 / 71	Glutathione metabolism



Correlation Cluster

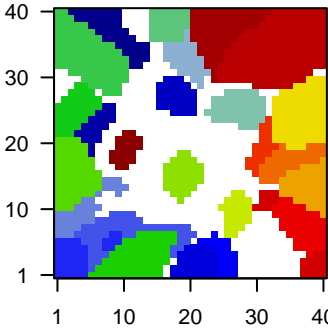
Spot Summary: H

metagenes = 34
genes = 443

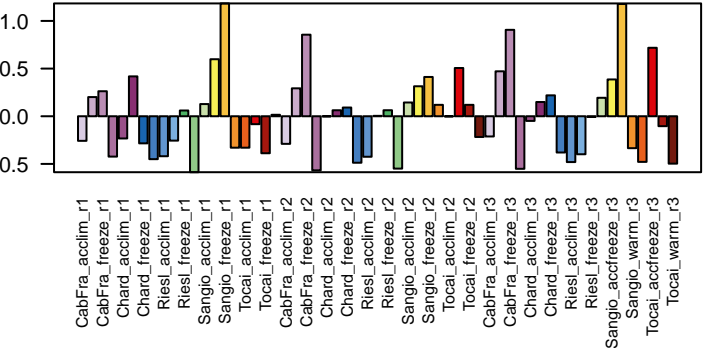
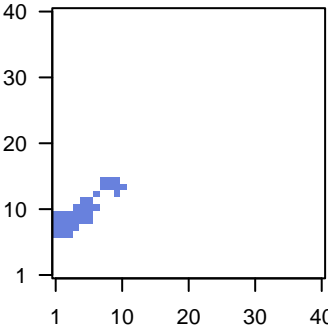
<r> metagenes = 0.94
<r> genes = 0.47
beta: r2= 10.93 / log p= -Inf

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

Overview Map



Spot

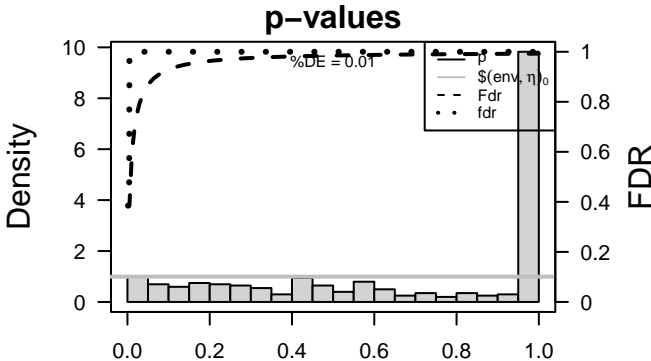


Spot Genelist

ID	Description
Vitvi18g02840	
Vitvi16g01469	
Vitvi07g01784	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.
Vitvi08g01744	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00111	
Vitvi19g01933	
Vitvi03g01517	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi16g01463	
Vitvi00g01438	
Vitvi07g03029	
Vitvi16g01986	
Vitvi05g01760	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi13g00680	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi08g01030	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi16g01461	
Vitvi19g00068	Binding to ATP; adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi05g00734	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi00g02300	
Vitvi01g00934	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi16g01475	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.001	3 / 11	Vitamin B6 metabolism
2	0.002	4 / 26	Sphingolipid metabolism
3	0.004	8 / 121	Transporter catalog – Porters cat 18 to 29
4	0.004	7 / 96	Transporter catalog – Porters cat 1 to 6
5	0.005	4 / 33	alpha-Linolenic acid metabolism
6	0.010	5 / 63	Phenylpropanoid biosynthesis
7	0.011	4 / 42	Tryptophan metabolism
8	0.013	3 / 24	Carbohydrate metabolism – Ascorbate and aldarate metabolism
9	0.014	13 / 309	Enzyme – 3.1 Acting on ester bonds
10	0.018	4 / 48	Transcription factors – WRKY
11	0.021	8 / 162	Plant specific signaling – Plant-pathogen interaction
12	0.021	2 / 11	Cofactors and vitamin metabolism – Vitamin B6 metabolism
13	0.022	3 / 29	Carotenoid biosynthesis
14	0.023	4 / 52	Transport and catabolism – Peroxisome
15	0.029	2 / 13	Biosynthesis of unsaturated fatty acids
16	0.029	2 / 13	Sugar transporters
17	0.039	3 / 36	Fatty acid degradation
18	0.044	5 / 92	Lipid metabolism – Glycerolipid metabolism
19	0.045	3 / 38	Amino acid metabolism – Arginine and proline metabolism
20	0.048	2 / 17	Kinase – IRAK family



Correlation Cluster

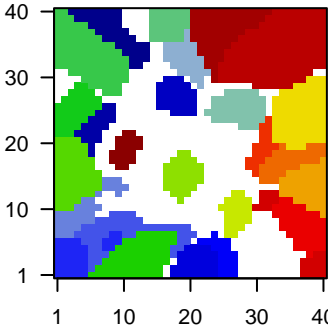
Spot Summary: I

metagenes = 31
genes = 196

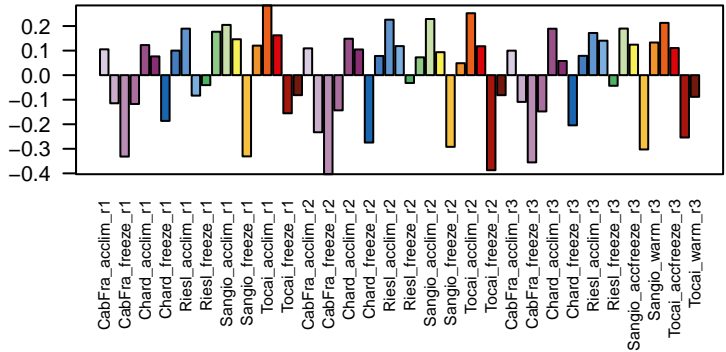
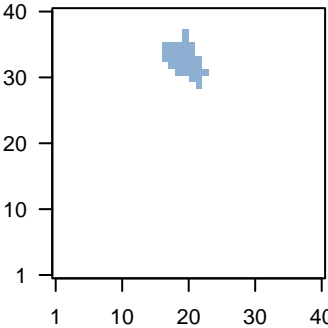
<r> metagenes = 0.93
<r> genes = 0.39
beta: r2= 1.88 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

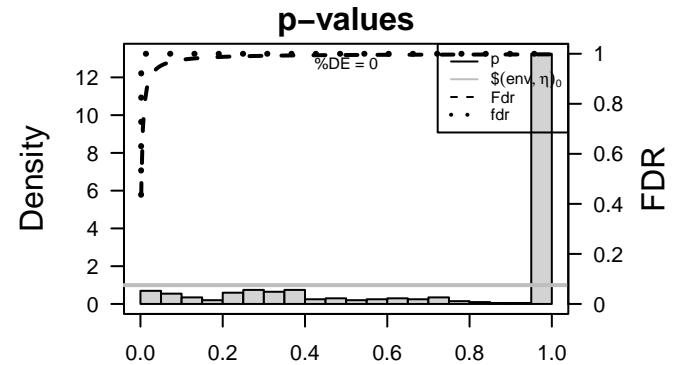


Spot Genelist

ID	Description
Vitvi16g01543	
Vitvi19g02300	Binding to ADP, adenosine 5'-diphosphate.
Vitvi01g00012	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi10g00639	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi06g00184	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi19g00484	Binding to ADP, adenosine 5'-diphosphate.
Vitvi16g01788	
Vitvi03g00413	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi02g01266	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.
Vitvi12g02168	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.
Vitvi12g02003	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi17g00640	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.
Vitvi18g02148	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.
Vitvi02g01696	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi00g00213	
Vitvi14g00640	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi09g00416	Binding to ADP, adenosine 5'-diphosphate.
Vitvi14g00314	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.
Vitvi11g00194	A protein complex composed of the Fanconi anaemia (FA) proteins including A, C, E, G and F (FANCA-F). Functions in the activation of the downstream protein FANCD2 by monoubiquitylation, and is essential for protection against chromosome breakage.
Vitvi01g00505	Binding to a nucleic acid.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.001	7 / 142	Transport system – Protein coat
2	0.002	6 / 110	Ubiquitin system – Multi subunit Ring-finger type E3
3	0.002	4 / 48	Transcription factors – PHD
4	0.006	2 / 10	Transcription factors – ZIM
5	0.010	4 / 71	Exosome – Proteins found in most exosomes
6	0.015	6 / 170	Transcription factors – Other zf-C3HC4
7	0.019	2 / 18	Transcription factors – ARF
8	0.030	2 / 23	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
9	0.038	3 / 63	Messenger RNA Biogenesis – mRNA degradation factors
10	0.043	2 / 28	Proteasome – Regulatory particles
11	0.045	3 / 67	Replication and repair – RNA degradation
12	0.046	2 / 29	Various types of N-glycan biosynthesis
13	0.046	3 / 68	Spliceosome associated proteins (SAPs)
14	0.047	4 / 115	Enzyme – 3.6 Acting on acid anhydrides
15	0.051	2 / 31	Chromosome and associated proteins – Gene silencing
16	0.052	4 / 119	Endocytosis
17	0.058	2 / 33	Enzyme – 5.4 Intramolecular transferases
18	0.058	2 / 33	Glycan biosynthesis and metabolism – N-Glycan biosynthesis
19	0.067	2 / 36	Ribosome biogenesis – Pre-40S particles
20	0.067	2 / 36	Transcription factors – Zinc finger



Correlation Cluster

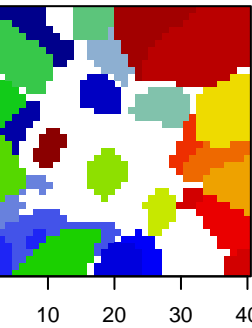
Spot Summary: J

metagenes = 41
genes = 412

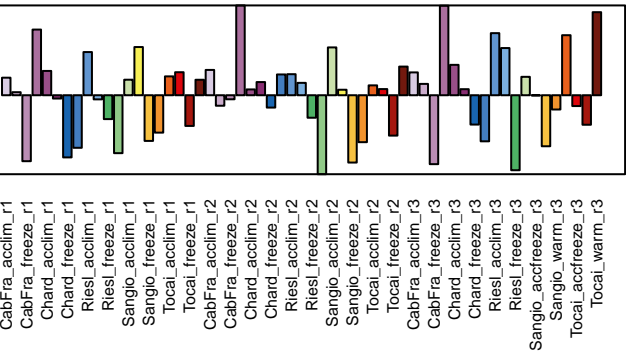
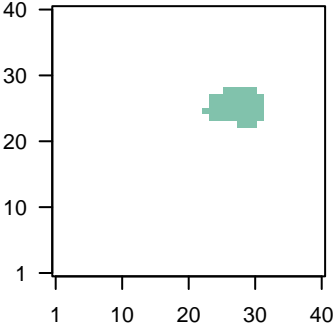
<r> metagenes = 0.92
<r> genes = 0.38
beta: r2= 1.94 / log p= -Inf

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

Overview Map



Spot

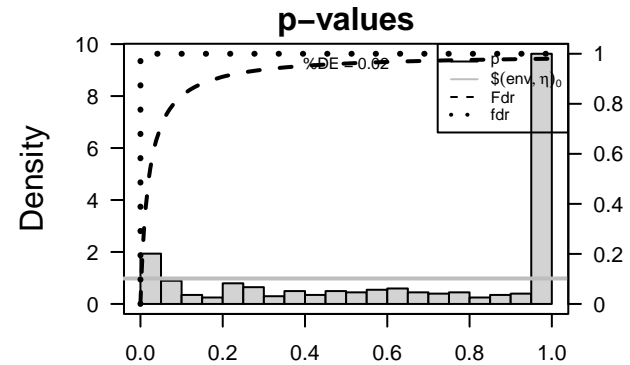


Spot Genelist

ID	Description
Vitvi07g03061	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.
Vitvi00g00589	
Vitvi06g00822	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi15g00419	Catalysis of the reaction: ATP + H2O = ADP + phosphate, to drive the unwinding of a DNA or RNA helix.
Vitvi11g00092	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.
Vitvi08g01813	A cellular process that results in the biosynthesis of constituent macromolecules, assembly, and arrangement of constituent parts of ribosome subunits; includes transport to the sites of protein synthesis.
Vitvi07g00542	
Vitvi09g00518	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, C-C, phosphoric anhydride bonds, etc.
Vitvi11g01347	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.
Vitvi01g00366	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.
Vitvi13g01558	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.
Vitvi18g02350	Binding to a zinc ion (Zn).
Vitvi11g00338	Catalysis of the reaction: N,N-dimethylaniline + NADPH + H+ + O2 = N,N-dimethylaniline N-oxide + NADP+ + H2O.
Vitvi04g01753	
Vitvi04g01645	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi09g00356	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi18g00421	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi08g00117	Binding to a metal ion.
Vitvi13g00354	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.
Vitvi15g00820	Catalysis of the dimethylation of two adjacent adenine residues in a rRNA, using S-adenosyl-L-methionine as a methyl donor.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-09	13 / 64	Ribosome biogenesis in eukaryotes
2	3e-08	16 / 116	Ribosome biogenesis – Pre-60S particles
3	3e-08	13 / 75	Translation – Ribosome biogenesis in Eukaryotes
4	2e-07	22 / 247	Translation – Ribosome
5	3e-07	6 / 13	Chaperone – HSP60 / Chaperonin
6	1e-06	7 / 24	Primary active transporters [TC:3]
7	1e-06	19 / 211	Ribosome
8	1e-05	14 / 144	Ribosome – Eukaryotes
9	2e-04	8 / 66	Exosome – Exosomal proteins of bladder cancer cells
10	3e-04	5 / 24	Inner mambrane
11	5e-04	10 / 113	Exosome – Exosomal proteins of colorectal cancer cells
12	5e-04	9 / 94	Nucleotide metabolism – Purine metabolism
13	5e-04	6 / 42	Folding sorting degradation – Proteasome
14	6e-04	6 / 43	Aminoacyl-tRNA synthetases (AARSs)
15	7e-04	6 / 44	Proteasome
16	7e-04	6 / 44	Enzyme – 6.1 Forming carbon-oxygen bonds
17	8e-04	7 / 62	Translation – Aminoacyl-tRNA biosynthesis
18	1e-03	6 / 48	Aminoacyl-tRNA biosynthesis
19	1e-03	6 / 48	Pyrimidine metabolism
20	2e-03	3 / 11	Ubiquitin system – UBL-specific proteases (ULPs)



Correlation Cluster

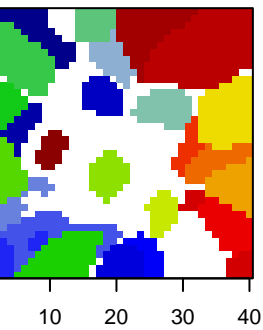
Spot Summary: K

metagenes = 28
genes = 326

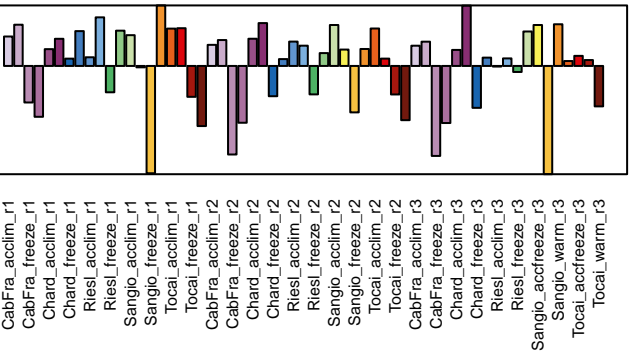
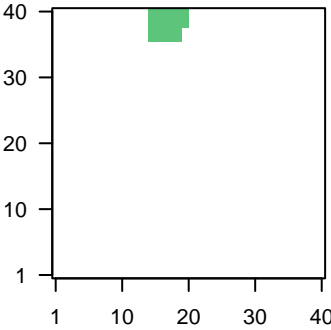
<r> metagenes = 0.95
<r> genes = 0.4
beta: r2= 4.44 / log p= -Inf

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

Overview Map



Spot

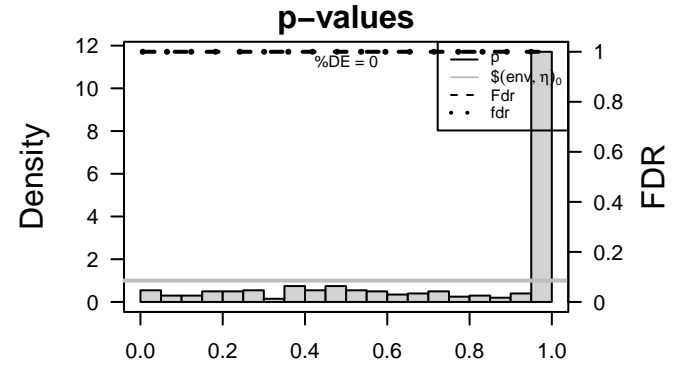


Spot Genelist

ID	Description
Vitvi13g02110	Binding to a protein.
Vitvi10g00667	Catalysis of the hydrolysis of any ester bond.
Vitvi05g00566	
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	
Vitvi10g01696	Binding to a calcium ion (Ca2+).
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.
Vitvi03g01185	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
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 sulphydryl group of a cysteine residue at the active center acts as a nucleophile.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.005	4 / 38	Hormone transport – Auxin transport
2	0.008	6 / 93	Transcription factors – BHLH
3	0.013	4 / 49	Transcription factors – NAC
4	0.013	8 / 168	Plant hormone signal transduction
5	0.015	3 / 28	Exosome – Exosomal proteins of breast milk
6	0.021	4 / 57	Transcription factors – HB
7	0.025	3 / 34	Transcription factors – SET PCG
8	0.033	3 / 38	Protein – Chaperone mediated autophagy (CMA)
9	0.039	2 / 17	Transcription factors – SBP
10	0.042	5 / 102	Membrane transport – ABC transporters
11	0.045	4 / 72	Energy metabolism – Carbon fixation
12	0.056	5 / 111	Hormone signaling – ABA signaling
13	0.069	3 / 51	Carbon fixation in photosynthetic organisms
14	0.078	2 / 25	Lysine degradation
15	0.080	5 / 123	Carbohydrate metabolism – Glycolysis
16	0.089	2 / 27	ABCG (White) subfamily
17	0.098	6 / 170	Transcription factors – Other zf-C3HC4
18	0.101	3 / 60	Enzyme – 4.1 Carbon-carbon lyases
19	0.107	2 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
20	0.119	2 / 32	Protein – Actin-binding proteins



Correlation Cluster

Spot Summary: L

metagenes = 88
genes = 1220

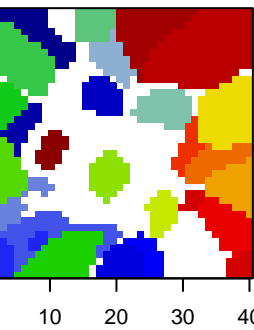
<r> metagenes = 0.93

beta: r2= 5.43 / log p= -Inf

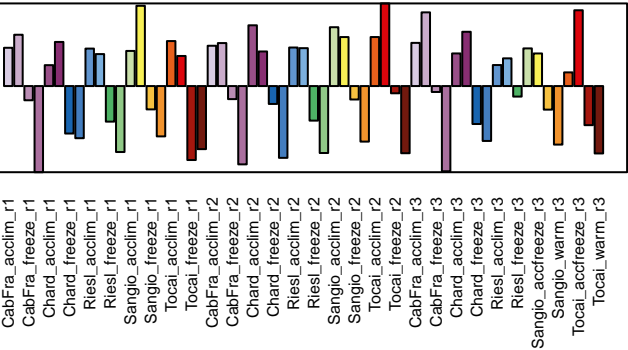
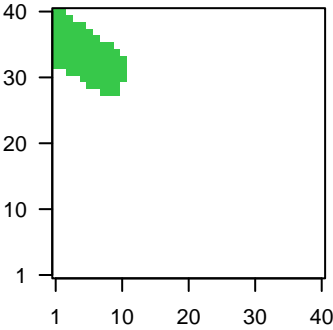
samples with spot = 6 (10.2 %)

- CabFra_accfreeze : 1 (33.3 %)
- Chard_acclim : 1 (33.3 %)
- Sangio_acclim : 1 (33.3 %)
- Sangio_accfreeze : 1 (33.3 %)
- Tocai_accfreeze : 2 (66.7 %)

Overview Map



Spot

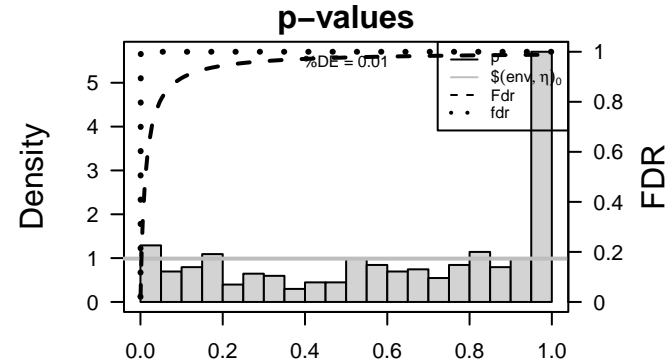


Spot Genelist

ID	Description
Vitvi04g01368	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
Vitvi18g00087	
Vitvi16g00733	Binds to and stops, prevents or reduces the activity of an enzyme.
Vitvi12g02353	
Vitvi19g00255	
Vitvi10g00647	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi14g01469	A chlorophyll-containing plastid with thylakoids organized into grana and frets, or stroma thylakoids, and embedded in a stroma.
Vitvi18g00122	The process whose specific outcome is the progression of the root over time, from its formation to the mature structure. The root is the water- and mineral-absorbing part of a plant which is usually underground, does not bear leaves, tends to grow downwards and is typically derived from the radicle of the embryo.
Vitvi05g00071	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi10g00649	
Vitvi18g00946	Any process that stops, prevents, or reduces the frequency, rate or extent of cellular DNA-templated transcription.
Vitvi05g01758	
Vitvi17g00237	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi06g01696	Binding to a metal ion.
Vitvi17g00914	
Vitvi06g01629	
Vitvi16g01161	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi16g00985	Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a cold stimulus, a temperature stimulus below the optimal temperature for that organism.
Vitvi05g01453	Binding to a protein.
Vitvi04g01564	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-04	24 / 151	RNA polymerase II system
2	2e-04	19 / 110	Ubiquitin system – Multi subunit Ring–finger type E3
3	2e-04	21 / 128	Ubiquitin system – Single Ring–finger type E3
4	2e-04	10 / 38	Transcription – Basal transcription factors
5	8e-04	9 / 37	Basal transcription factors
6	1e-03	9 / 38	Protein – Other autophagy associated proteins
7	1e-03	35 / 290	Enzyme – 2.3 Acyltransferases
8	2e-03	10 / 51	Plant specific signaling – Circadian rhythm
9	3e-03	7 / 28	RNA polymerase III system
10	3e-03	11 / 62	Ribosome biogenesis – 90S particles
11	4e-03	22 / 170	Transcription factors – Other zf–C3HC4
12	5e-03	4 / 11	Protein – Mitophagy
13	6e-03	7 / 32	Circadian rhythm – plant
14	6e-03	11 / 67	Replication and repair – RNA degradation
15	1e-02	10 / 63	Messenger RNA Biogenesis – mRNA degradation factors
16	2e-02	6 / 31	Autophagy – other
17	3e-02	3 / 10	Minor spliceosome components
18	3e-02	3 / 10	Transcription factors – C2C2–CO
19	3e-02	11 / 83	RNA degradation
20	3e-02	6 / 35	RNA polymerase



Correlation Cluster

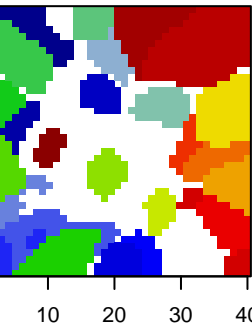
Spot Summary: M

metagenes = 37
genes = 361

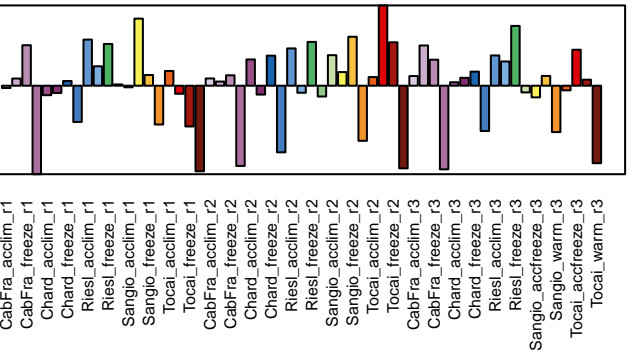
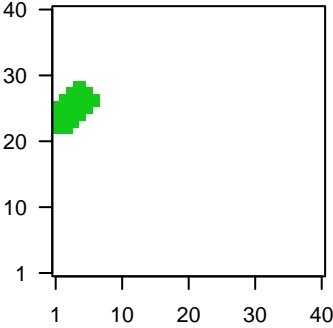
<r> metagenes = 0.92
<r> genes = 0.37
beta: r2= 2.84 / log p= -Inf

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

Overview Map



Spot

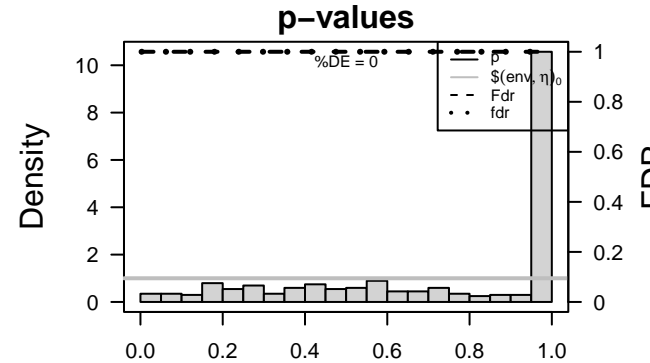


Spot Genelist

ID	Description
Vitvi07g00516	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi19g00470	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi16g00681	
Vitvi12g02393	
Vitvi05g00139	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi00g00794	
Vitvi05g00703	Binding to a metal ion.
Vitvi10g00224	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi09g00275	
Vitvi11g01300	The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.
Vitvi16g01494	
Vitvi11g00251	
Vitvi14g02597	Binding to a phospholipid, a class of lipids containing phosphoric acid as a mono- or diester, in the presence of calcium.
Vitvi07g01598	Binding to a metal ion.
Vitvi02g00060	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g00101	
Vitvi17g00019	Binding to a nucleic acid.
Vitvi10g01454	
Vitvi17g00319	
Vitvi17g01485	Binding to a zinc ion (Zn).

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	5 / 51	Plant specific signaling – Circadian rhythm
2	0.011	8 / 161	Enzyme – 2.1 Transferring one-carbon groups
3	0.015	3 / 28	Transcription factors – SNF2
4	0.021	2 / 12	Enzyme – Class I
5	0.022	3 / 32	SNARE interactions in vesicular transport
6	0.022	11 / 290	Enzyme – 2.3 Acyltransferases
7	0.049	2 / 19	Transcription factors – Jumonji
8	0.051	4 / 74	Transcription factors – C2H2
9	0.062	3 / 48	Amino acid metabolism – Lysine biosynthesis
10	0.068	3 / 50	Transcription factors – MYBrelated
11	0.071	3 / 51	Lipid metabolism – Fatty acid metabolism
12	0.075	3 / 52	Transport and catabolism – Peroxisome
13	0.086	2 / 26	Transcription factors – G2-like
14	0.091	2 / 27	Regulator of mitochondrial biogenesis
15	0.103	2 / 29	Other amino acids metabolism – Beta-alanine metabolism
16	0.122	2 / 32	Circadian rhythm – plant
17	0.122	2 / 32	Carbohydrate metabolism – Propanoate metabolism
18	0.124	3 / 65	Transport and catabolism – Phagosome
19	0.134	2 / 34	Transcription factors – SET PCG
20	0.150	3 / 71	Amino acid metabolism – Phenylalanine metabolism



Correlation Cluster

Spot Summary: N

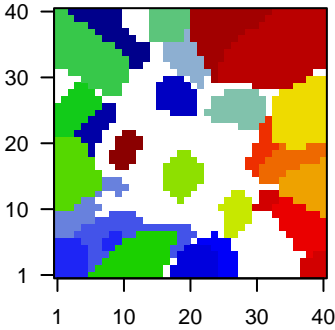
metagenes = 62
genes = 943

<r> metagenes = 0.96
<r> genes = 0.54
beta: r2= 11.26 / log p= -Inf

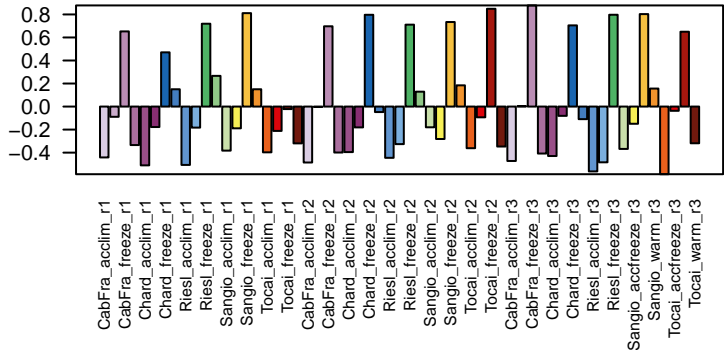
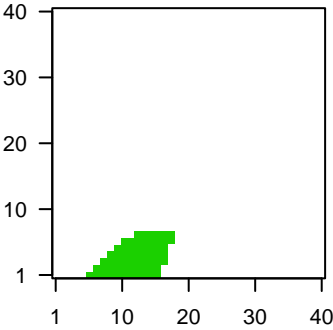
samples with spot = 14 (23.7 %)

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

Overview Map



Spot

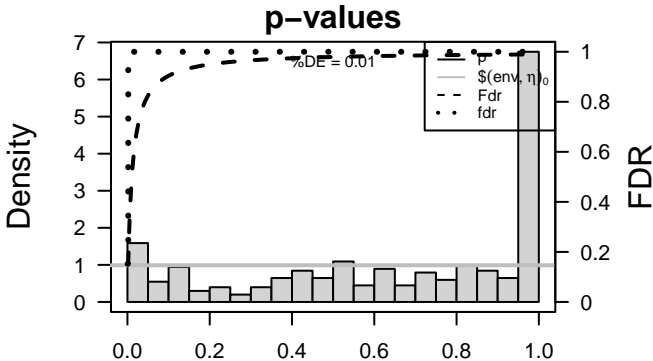


Spot Genelist

ID	Description
Vitvi08g01547	
Vitvi10g02181	
Vitvi00g01459	
Vitvi07g01990	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.
Vitvi08g01058	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.
Vitvi07g00259	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi14g00973	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi10g00286	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.
Vitvi19g01028	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi19g01014	
Vitvi05g00640	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi13g00784	
Vitvi18g03161	
Vitvi14g00063	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi01g00300	Binding to a metal ion.
Vitvi00g01460	
Vitvi10g02194	
Vitvi04g01233	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi14g01128	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.
Vitvi02g01264	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	5e-04	17 / 131	Enzyme - 1.1 Acting on the CH-OH group of donors
2	1e-03	8 / 40	SLC47: Multidrug and Toxin Extrusion (MATE) family
3	2e-03	8 / 43	Transcription factors - BZIP
4	2e-03	5 / 18	Chaperone - HSP20
5	2e-03	6 / 26	Transcription factors - G2-like
6	3e-03	8 / 47	ABC transporters
7	3e-03	6 / 28	Exosome - Exosomal proteins of breast milk
8	3e-03	6 / 28	Transcription factors - Basic leucine zipper (bZIP)
9	3e-03	7 / 38	Enzyme - 1.8 Acting on a sulfur group of donors
10	4e-03	4 / 13	Cutin suberine and wax biosynthesis
11	4e-03	13 / 108	Carbohydrate metabolism - Pyruvate metabolism
12	5e-03	13 / 111	Transporter catalog - Porters cat 66 to 94
13	7e-03	8 / 54	Carbohydrate metabolism - Inositol phosphate metabolism
14	1e-02	5 / 26	Glycosyltransferase - Hydrophobic molecule
15	1e-02	5 / 27	ABCG (White) subfamily
16	1e-02	5 / 27	Regulator of mitochondrial biogenesis
17	1e-02	12 / 111	Hormone signaling - ABA signaling
18	1e-02	7 / 50	Inositol phosphate metabolism
19	2e-02	8 / 63	Phenylpropanoid biosynthesis
20	2e-02	3 / 11	Biosynthesis of secondary metabolism - ABA biosynthesis



Correlation Cluster

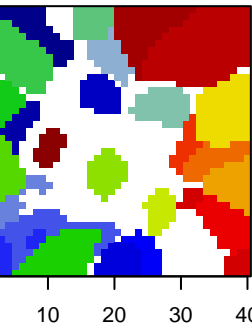
Spot Summary: O

metagenes = 60
genes = 831

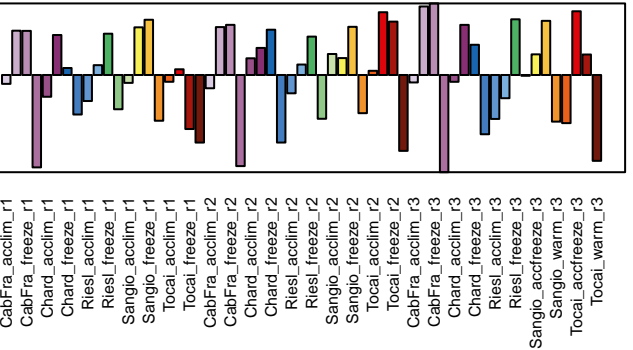
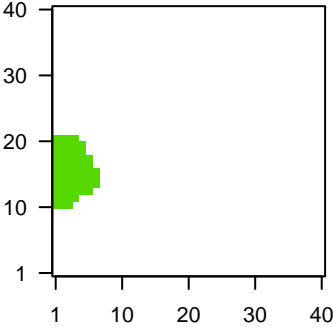
<r> metagenes = 0.95
<r> genes = 0.53
beta: r2= 7.63 / log p= -Inf

samples with spot = 13 (22 %)
CabFra_accfreeze : 2 (66.7 %)
CabFra_freeze : 2 (66.7 %)
Chard_accfreeze : 1 (33.3 %)
Riesl_freeze : 1 (33.3 %)
Sangio_accfreeze : 1 (33.3 %)
Sangio_freeze : 3 (100 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

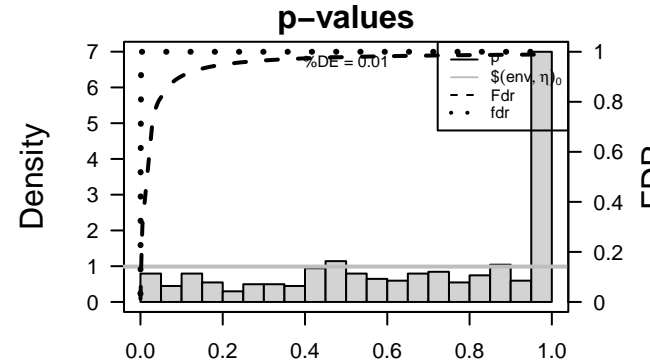


Spot Genelist

ID	Description
Vitvi16g01022	Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an abscisic acid stimulus.
Vitvi05g01353	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.
Vitvi16g00363	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.
Vitvi14g01808	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi08g01587	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi05g01833	Binding to a metal ion.
Vitvi18g00480	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi05g02238	
Vitvi14g02476	
Vitvi18g02398	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi06g01601	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi13g01623	Binding to ADP, adenosine 5'-diphosphate.
Vitvi11g01683	
Vitvi05g00342	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi06g01462	The directed movement of malate into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore.
Vitvi17g00175	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00271	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi08g00107	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi03g01703	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi19g00565	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-05	21 / 170	Transcription factors – Other zf-C3HC4
2	1e-04	8 / 35	Mitophagy factors
3	2e-04	6 / 20	Protein – Autophagosome formation proteins
4	4e-04	7 / 31	Autophagy – other
5	2e-03	5 / 20	Transport and catabolism – Regulation of autophagy
6	3e-03	7 / 43	Transcription factors – BZIP
7	3e-03	10 / 80	Transport system – Tethering factors
8	5e-03	5 / 25	Transcription factors – Other zf
9	3e-02	10 / 111	Hormone signaling – ABA signaling
10	3e-02	11 / 128	Ubiquitin system – Single Ring-finger type E3
11	3e-02	4 / 27	Enzyme – 2.6 Transferring nitrogenous groups
12	4e-02	4 / 28	Transcription factors – Basic leucine zipper (bZIP)
13	4e-02	5 / 41	Arginine and proline metabolism
14	4e-02	3 / 17	Riboflavin metabolism
15	4e-02	4 / 29	Transcription factors – GRAS
16	4e-02	13 / 168	Plant hormone signal transduction
17	7e-02	9 / 111	Transporter catalog – Porters cat 66 to 94
18	7e-02	2 / 10	Kinase – Wnk family
19	8e-02	16 / 238	Enzyme – 2.4 Glycosyltransferases
20	8e-02	25 / 409	Enzyme – 2.7 Transferring phosphorus-containing groups



Correlation Cluster

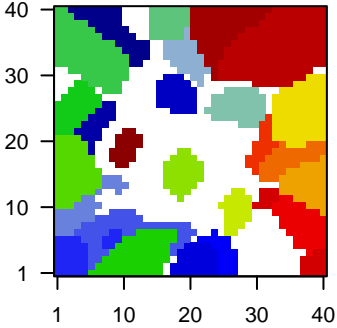
Spot Summary: P

metagenes = 33
genes = 285

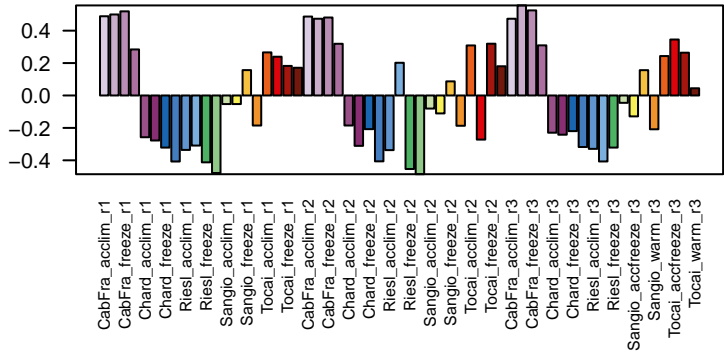
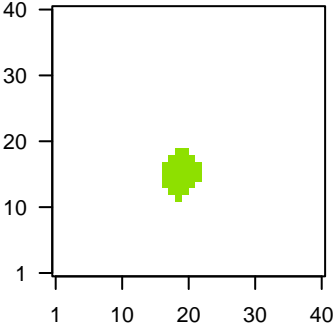
<r> metagenes = 0.92
<r> genes = 0.31
beta: r2= 2.88 / log p= -Inf

samples with spot = 9 (15.3 %)
CabFra_acclim : 3 (100 %)
CabFra_accfreeze : 3 (100 %)
CabFra_freeze : 3 (100 %)

Overview Map



Spot

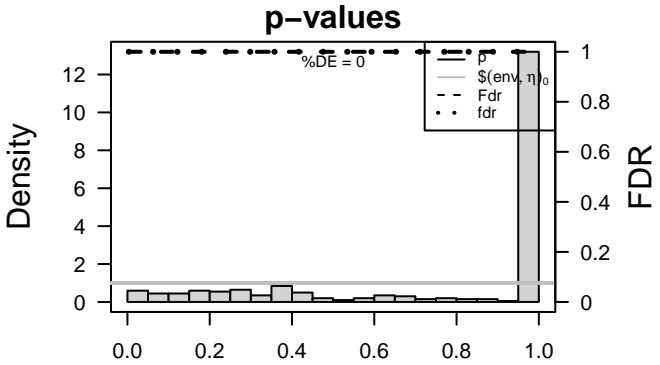


Spot Genelist

ID	Description
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.
Vitvi16g01259	
Vitvi07g02587	
Vitvi07g00329	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g02578	
Vitvi18g00878	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi12g02574	
Vitvi12g00354	
Vitvi19g01935	
Vitvi02g00524	
Vitvi12g02554	The action of a molecule that contributes to the structural integrity of the ribosome.
Vitvi05g02074	Binding to a protein.
Vitvi05g01819	
Vitvi17g00609	Catalysis of the hydrolysis of any ester bond.
Vitvi12g02596	
Vitvi13g01937	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi15g01711	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.003	3 / 25	Protein – Tethering complex
2	0.006	2 / 10	Minor spliceosome components
3	0.008	3 / 35	Lipid metabolism – Alpha-linolenic acid metabolism
4	0.014	3 / 42	Folding sorting degradation – Proteasome
5	0.015	3 / 44	Proteasome
6	0.017	2 / 17	Chaperone – Peptidyl prolyl isomerase
7	0.025	3 / 53	Protein – Forward pathways
8	0.036	5 / 153	Plant-pathogen interaction
9	0.037	4 / 105	Energy metabolism – Oxidative phosphorylation
10	0.044	2 / 28	Proteasome – Regulatory particles
11	0.044	4 / 111	Transporter catalog – Porters cat 66 to 94
12	0.049	2 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
13	0.056	2 / 32	Enzyme – 5.2 cis-trans-Isomerases
14	0.059	2 / 33	alpha-Linolenic acid metabolism
15	0.059	2 / 33	Carbohydrate metabolism – Butanoate metabolism
16	0.060	3 / 75	Mitochondrial transcription and translation factors
17	0.062	2 / 34	Peptidases and inhibitors – Family S10
18	0.072	3 / 81	Oxidative phosphorylation
19	0.086	2 / 41	Transporter catalog – Primary active transporter cat D1
20	0.090	4 / 142	Transport system – Protein coat



Correlation Cluster

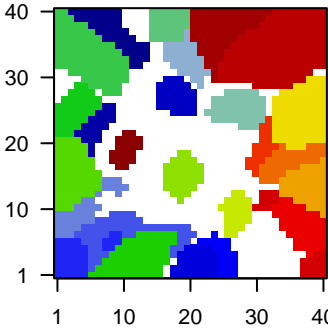
Spot Summary: Q

metagenes = 24
genes = 148

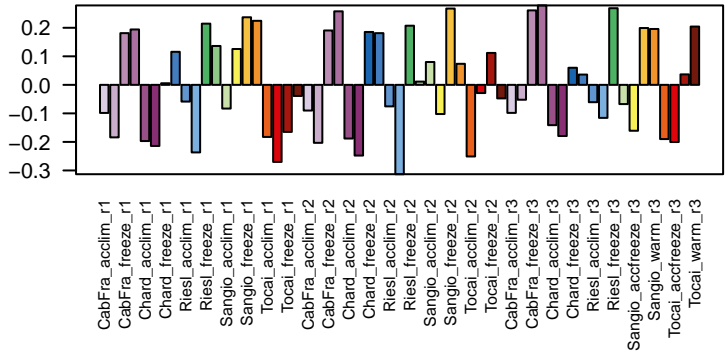
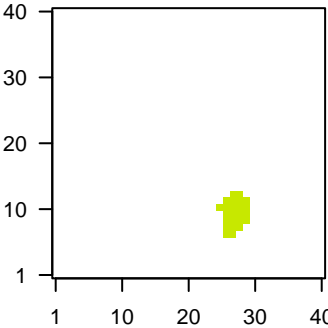
<r> metagenes = 0.92
<r> genes = 0.33
beta: r2= 1.31 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

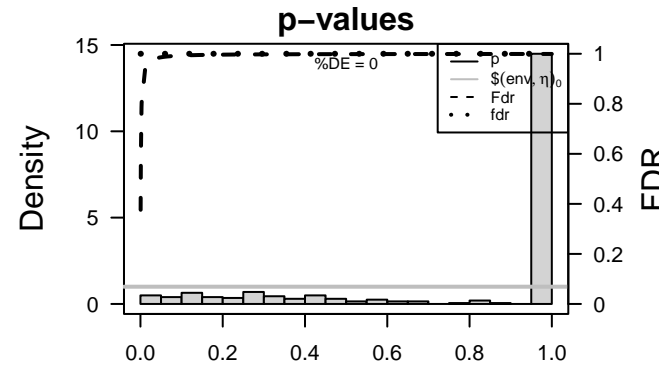


Spot Genelist

ID	Description
Vitvi14g01984	A chlorophyll-containing plastid with thylakoids organized into grana and frets, or stroma thylakoids, and embedded in a stroma.
Vitvi14g02500	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi15g00495	
Vitvi15g00528	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.
Vitvi13g01992	Any process that stops, prevents or reduces the rate or extent of cell proliferation.
Vitvi19g02086	
Vitvi18g00081	Binding to a protein.
Vitvi14g01806	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.
Vitvi04g02131	
Vitvi17g00167	Binding to a protein.
Vitvi00g00766	
Vitvi10g02268	The process of restoring DNA after damage. Genomes are subject to damage by chemical and physical agents in the environment (e.g. UV and ionizing radiations, chemical mutagens, fungal and bacterial toxins, etc.) and by free radicals or alkylating agents endogenously generated in metabolism. DNA is also damaged because of errors during its replication. A variety of different DNA repair pathways have been reported that include direct reversal, base excision repair, nucleotide excision repair, photoreactivation, bypass, double-strand break repair pathway, and mismatch repair pathway.
Vitvi00g01285	
Vitvi09g00049	
Vitvi17g00197	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi09g00297	
Vitvi00g01980	
Vitvi02g01750	
Vitvi17g00149	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.
Vitvi12g01856	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-04	7 / 165	Transcription - Spliceosome
2	1e-03	6 / 139	Spliceosome
3	3e-03	5 / 115	Enzyme - 3.6 Acting on acid anhydrides
4	3e-03	4 / 72	Ribosome - Mitochondria/ Chloroplast
5	1e-02	2 / 20	tRNA modification factors
6	2e-02	4 / 121	Transporter catalog - Porters cat 18 to 29
7	2e-02	3 / 67	Ribosome - Bacteria
8	2e-02	3 / 75	Mitochondrial transcription and translation factors
9	4e-02	2 / 41	SLC25: Mitochondrial carrier
10	5e-02	3 / 99	mRNA surveillance pathway
11	5e-02	2 / 46	Amino acid metabolism - Glutamate metabolism
12	6e-02	2 / 48	Aminoacyl-tRNA biosynthesis
13	6e-02	2 / 48	Lipid metabolism - Fatty acid biosynthesis
14	7e-02	2 / 51	Biosynthesis of secondary metabolism - Auxin biosynthesis
15	9e-02	1 / 11	Ubiquitin system - UBL-specific proteases (ULPs)
16	9e-02	2 / 62	Ribosome biogenesis - 90S particles
17	9e-02	1 / 12	Enzyme - 4.4 Carbon-sulfur lyases
18	1e-01	2 / 64	Ribosome biogenesis in eukaryotes
19	1e-01	1 / 13	Cofactors and vitamin metabolism - Thiamine metabolism
20	1e-01	2 / 68	Amino acid metabolism - Alanine and aspartate metabolism



Correlation Cluster

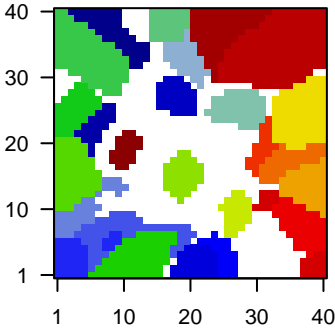
Spot Summary: R

metagenes = 74
genes = 897

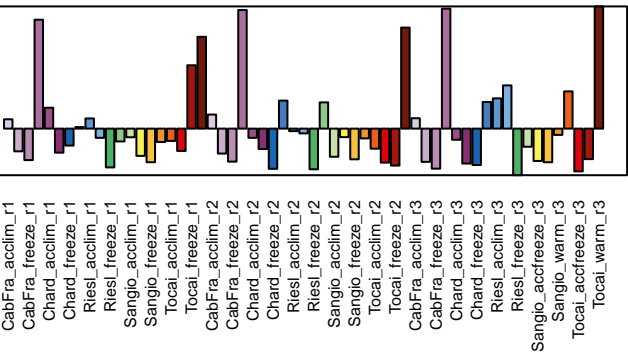
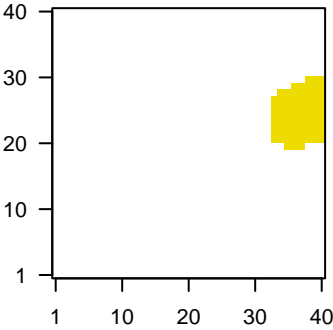
<r> metagenes = 0.94
<r> genes = 0.58
beta: r2= 15.94 / log p= -Inf

samples with spot = 10 (16.9 %)
CabFra_warm : 3 (100 %)
Riesl_acclim : 1 (33.3 %)
Riesl_accfreeze : 1 (33.3 %)
Tocai_acclim : 1 (33.3 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 3 (100 %)

Overview Map



Spot

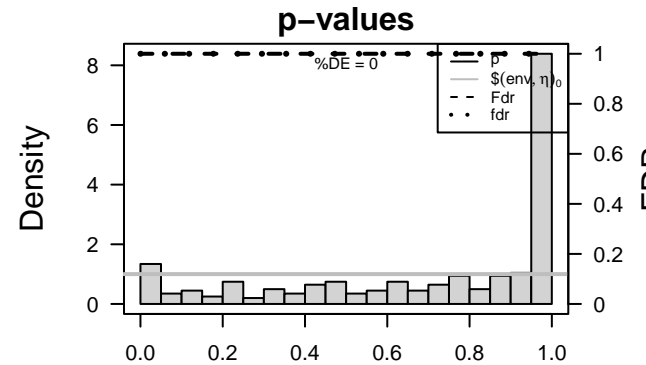


Spot Genelist

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	7e-76	87 / 144	Ribosome – Eukaryotes
2	1e-59	89 / 211	Ribosome
3	5e-58	94 / 247	Translation – Ribosome
4	5e-29	42 / 97	Ribosome – Archaea
5	3e-22	53 / 219	Cell growth and death – Cell cycle
6	2e-17	17 / 24	Replication protein – DNA Replication Initiation Factors
7	8e-13	40 / 217	Cell motility – Regulation of actin cytoskeleton
8	5e-12	23 / 80	Cytoskeleton – Microtubules
9	6e-11	15 / 36	DNA replication
10	6e-10	15 / 41	Replication and repair – DNA replication
11	2e-04	10 / 51	Other metabolism – Single reactions
12	3e-04	9 / 44	Replication protein – DNA Replication Termination Factors
13	3e-04	7 / 27	Mismatch repair
14	4e-04	5 / 14	Cilium and associated proteins – Stereociliary proteins
15	2e-03	14 / 113	Exosome – Exosomal proteins of colorectal cancer cells
16	7e-03	4 / 16	Biotin metabolism
17	7e-03	5 / 25	Replication and repair – Base excision repair
18	1e-02	7 / 48	Pyrimidine metabolism
19	1e-02	6 / 37	Homologous recombination
20	1e-02	6 / 37	Chaperone – Protein disulfide isomerase



Correlation Cluster

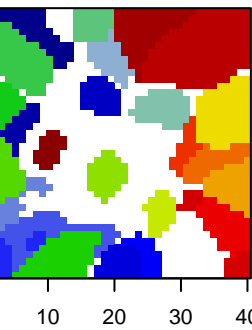
Spot Summary: S

metagenes = 41
genes = 413

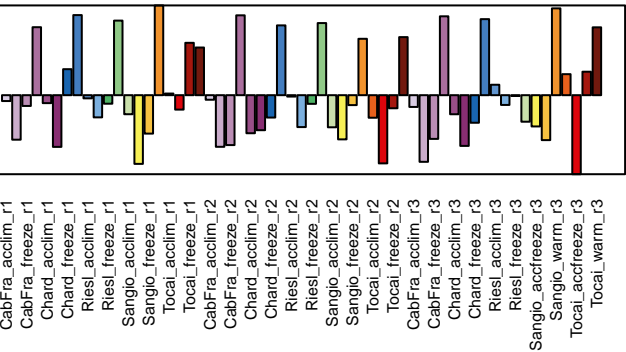
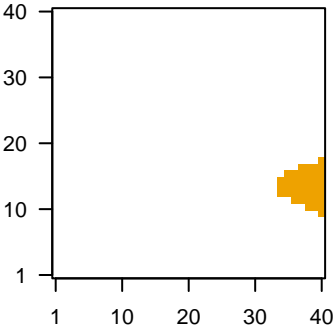
<r> metagenes = 0.93
<r> genes = 0.36
beta: r2= 3.04 / log p= -Inf

samples with spot = 5 (8.5 %)
CabFra_warm : 2 (66.7 %)
Chard_warm : 1 (33.3 %)
Sangio_warm : 2 (66.7 %)

Overview Map



Spot

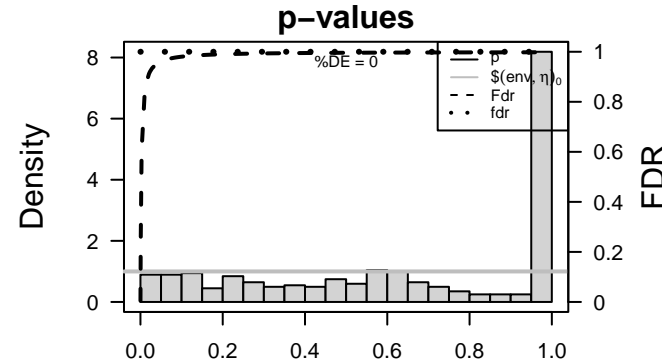


Spot Genelist

ID	Description
Vitvi04g00641	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.
Vitvi18g02763	Binding to a metal ion.
Vitvi12g02450	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.
Vitvi19g00505	
Vitvi05g00546	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.
Vitvi17g00331	
Vitvi14g01645	
Vitvi17g01015	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.
Vitvi05g00520	
Vitvi10g01814	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).
Vitvi03g00318	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.
Vitvi18g02551	
Vitvi07g00454	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.
Vitvi16g01285	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.
Vitvi04g00831	Catalysis of the reaction: UDP-glucose + D-fructose = UDP + sucrose.
Vitvi07g00445	The irregular network of unit membranes, visible only by electron microscopy, that occurs in the cytoplasm of many eukaryotic cells. The membranes form a complex meshwork of tubular channels, which are often expanded into slitlike cavities called cisternae. The ER takes two forms, rough (or granular), with ribosomes adhering to the outer surface, and smooth (with no ribosomes attached).
Vitvi19g01432	Binding to a metal ion.
Vitvi02g01279	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.
Vitvi07g00381	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi09g00045	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.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-05	6 / 22	Fatty acid elongation
2	7e-04	5 / 30	Lipid biosynthesis protein – Component type
3	3e-03	3 / 12	Translation factors – Release factors
4	3e-03	3 / 13	Biosynthesis of unsaturated fatty acids
5	1e-02	4 / 36	Phenylalanine tyrosine and tryptophan biosynthesis
6	1e-02	5 / 60	Enzyme – 4.1 Carbon-carbon lyases
7	2e-02	6 / 90	Lipid metabolism – Glycerophospholipid metabolism
8	2e-02	5 / 68	Amino acid metabolism – Alanine and aspartate metabolism
9	3e-02	4 / 48	Lipid metabolism – Fatty acid biosynthesis
10	3e-02	3 / 28	Exosome – Exosomal proteins of breast milk
11	3e-02	5 / 72	Glycerophospholipid metabolism
12	3e-02	5 / 72	Energy metabolism – Carbon fixation
13	4e-02	7 / 131	Enzyme – 1.1 Acting on the CH-OH group of donors
14	4e-02	4 / 54	Amino acid metabolism – Methionine metabolism
15	4e-02	3 / 32	Protein – Actin-binding proteins
16	4e-02	5 / 79	Pyruvate metabolism
17	4e-02	4 / 56	Hormone signaling – Jasmonate signaling
18	4e-02	6 / 108	Carbohydrate metabolism – Pyruvate metabolism
19	6e-02	2 / 17	One carbon pool by folate
20	7e-02	2 / 18	Nicotinate and nicotinamide metabolism



Correlation Cluster

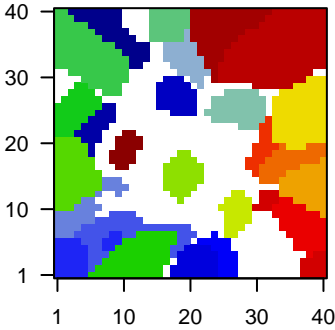
Spot Summary: T

metagenes = 33
genes = 293

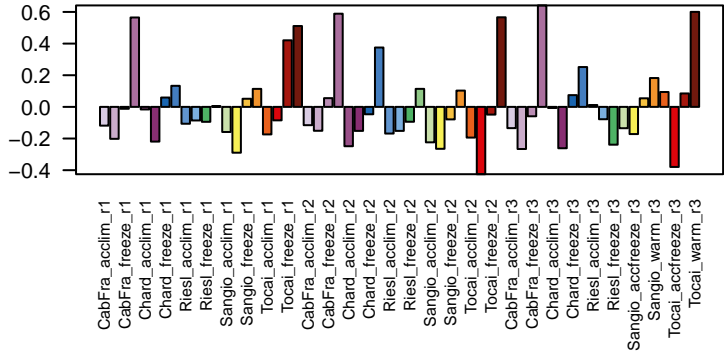
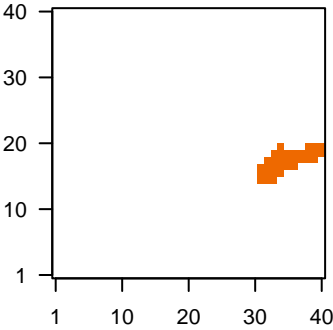
<r> metagenes = 0.97
<r> genes = 0.44
beta: r2= 3.5 / log p= -Inf

samples with spot = 7 (11.9 %)
CabFra_warm : 3 (100 %)
Tocai_freeze : 1 (33.3 %)
Tocai_warm : 3 (100 %)

Overview Map



Spot

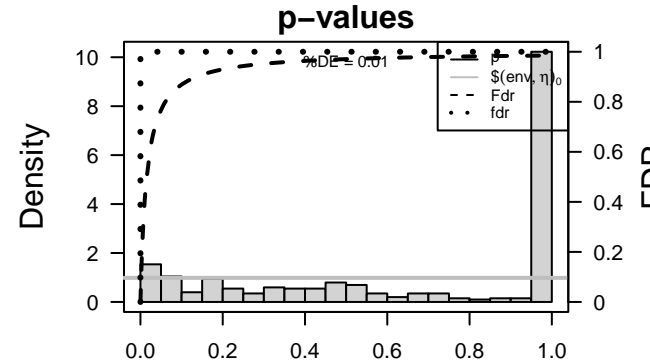


Spot Genelist

ID	Description
Vitvi04g00533	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi11g00033	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.
Vitvi03g00692	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi01g02263	Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.
Vitvi02g01324	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.
Vitvi18g01433	Innate immune responses are defense responses mediated by germline encoded components that directly recognize compx of potential pathogens.
Vitvi07g01565	
Vitvi19g02192	
Vitvi15g01579	
Vitvi01g01907	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi08g01637	
Vitvi08g02107	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.
Vitvi05g01285	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.
Vitvi14g01141	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi13g00322	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.
Vitvi05g01330	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).
Vitvi07g03045	
Vitvi00g00602	
Vitvi10g00345	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.
Vitvi01g00260	Any process that modulates the frequency, rate or extent of cellular DNA-templated transcription.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-13	16 / 81	Oxidative phosphorylation
2	1e-12	17 / 105	Energy metabolism – Oxidative phosphorylation
3	2e-08	9 / 41	Transporter catalog – Primary active transporter cat D1
4	5e-07	8 / 44	Proteasome
5	4e-06	5 / 16	Peptidases and inhibitors – Family T1: proteasome family
6	4e-06	5 / 16	Proteasome – Core particles (20S proteasome)
7	5e-06	7 / 42	Folding sorting degradation – Proteasome
8	2e-05	9 / 94	Nucleotide metabolism – Purine metabolism
9	8e-05	7 / 64	Purine metabolism
10	7e-04	11 / 211	Ribosome
11	8e-04	4 / 26	Flavonoid biosynthesis
12	2e-03	6 / 77	Cysteine and methionine metabolism
13	2e-03	3 / 17	Riboflavin metabolism
14	3e-03	8 / 144	Ribosome – Eukaryotes
15	3e-03	11 / 247	Translation – Ribosome
16	4e-03	4 / 39	Carbohydrate metabolism – Citrate cycle
17	4e-03	4 / 40	Citrate cycle (TCA cycle)
18	4e-03	4 / 41	Cofactors and vitamin metabolism – Riboflavin metabolism
19	6e-03	3 / 23	Energy metabolism – Reductive carboxylate cycle
20	1e-02	3 / 27	Enzyme – 1.6 Acting on NADH or NADPH



Correlation Cluster

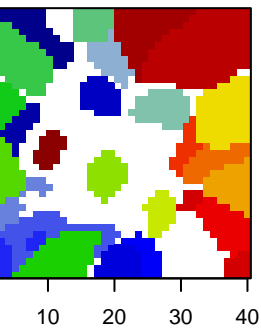
Spot Summary: U

metagenes = 20
genes = 123

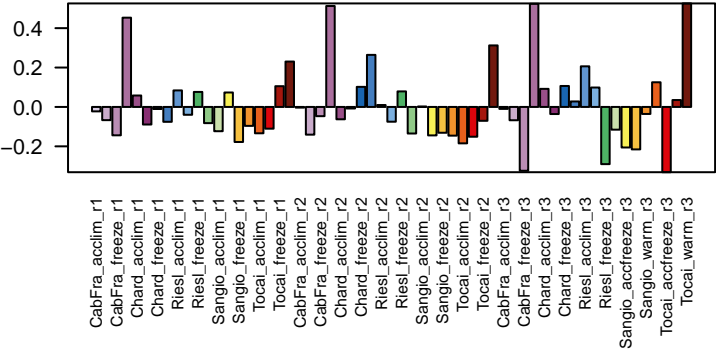
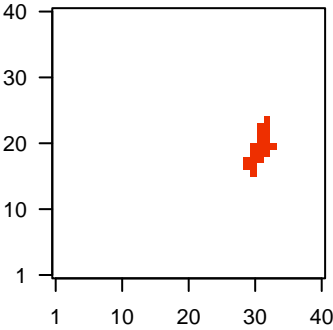
<r> metagenes = 0.94
<r> genes = 0.4
beta: r2= 2.01 / log p= -Inf

samples with spot = 4 (6.8 %)
CabFra_warm : 3 (100 %)
Tocai_warm : 1 (33.3 %)

Overview Map



Spot

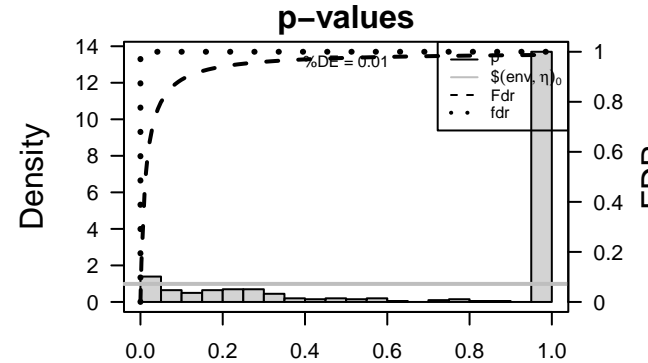


Spot Genelist

ID	Description
Vitvi12g02375	
Vitvi01g01378	In base excision repair, an altered base is removed by a DNA glycosylase enzyme, followed by excision of the resulting sugar phosphate. The small gap left in the DNA helix is filled in by the sequential action of DNA polymerase and DNA ligase.
Vitvi07g00277	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.
Vitvi08g01737	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi17g01181	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.
Vitvi13g00106	The action of a molecule that contributes to the structural integrity of the ribosome.
Vitvi18g02392	Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).
Vitvi12g01922	The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.
Vitvi11g00220	
Vitvi05g01254	The action of a molecule that contributes to the structural integrity of the ribosome.
Vitvi04g01176	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.
Vitvi16g00745	Binding to a protein.
Vitvi16g01488	The joining together of exons from one or more primary transcripts of messenger RNA (mRNA) and the excision of intron sequences, via a spliceosomal mechanism, so that mRNA consisting only of the joined exons is produced.
Vitvi01g01013	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.
Vitvi17g00433	Binding to a zinc ion (Zn).
Vitvi08g01630	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.
Vitvi17g01229	Binding to a nucleic acid.
Vitvi08g01147	The action of a molecule that contributes to the structural integrity of the ribosome.
Vitvi02g00383	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.
Vitvi06g00329	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	4e-18	21 / 211	Ribosome
2	7e-18	22 / 247	Translation – Ribosome
3	2e-17	18 / 144	Ribosome – Eukaryotes
4	7e-12	12 / 97	Ribosome – Archaea
5	9e-06	8 / 139	Spliceosome
6	2e-05	4 / 23	U2 snRNP components
7	2e-04	7 / 165	Transcription – Spliceosome
8	3e-04	4 / 44	Replication protein – DNA Replication Termination Factors
9	4e-04	3 / 19	U1 snRNP components
10	8e-04	3 / 25	U4/U6.U5 tri-snRNP components
11	2e-03	2 / 10	Valine leucine and isoleucine biosynthesis
12	1e-02	2 / 21	Replication and repair – Mismatch repair
13	1e-02	3 / 61	Messenger RNA Biogenesis – mRNA processing factors
14	1e-02	3 / 64	Ribosome biogenesis in eukaryotes
15	1e-02	3 / 67	Ribosome – Bacteria
16	2e-02	3 / 72	Ribosome – Mitochondria/ Chloroplast
17	2e-02	2 / 27	Mismatch repair
18	2e-02	2 / 29	Base excision repair
19	2e-02	2 / 31	GTP-binding proteins – Rab Family
20	3e-02	2 / 36	DNA replication



Correlation Cluster

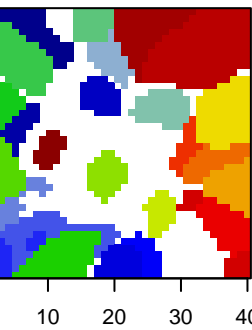
Spot Summary: V

metagenes = 45
genes = 440

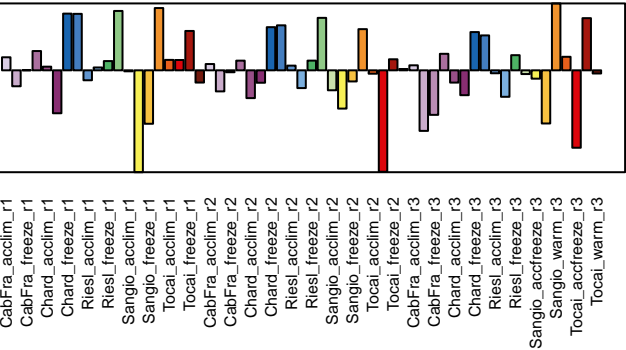
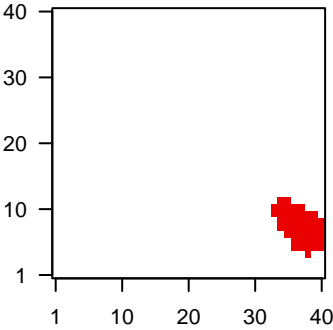
<r> metagenes = 0.95
<r> genes = 0.45
beta: r2= 5.79 / log p= -Inf

samples with spot = 10 (16.9 %)
Chard_freeze : 2 (66.7 %)
Chard_warm : 2 (66.7 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 3 (100 %)
Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

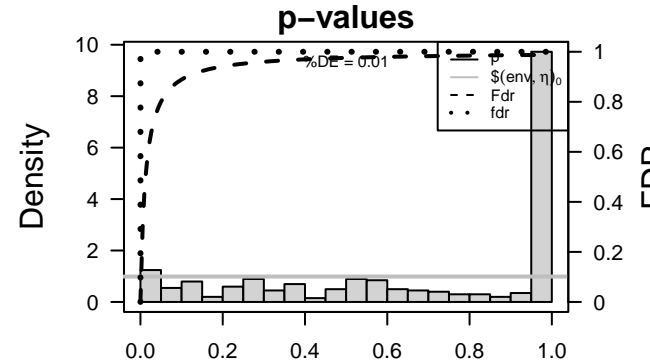


Spot Genelist

ID	Description
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).
Vitvi10g00020	Catalysis of an oxidation-reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi05g01116	Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).
Vitvi19g00302	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi08g02222	Any cellular process that depends upon or alters the microtubule cytoskeleton, that part of the cytoskeleton comprising microtubules and their associated proteins.
Vitvi03g01495	A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.
Vitvi09g01562	Functions in the storage of nutritious substrates.
Vitvi15g01389	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.
Vitvi06g00149	Binding to a metal ion.
Vitvi15g00406	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.
Vitvi08g01621	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi04g00357	
Vitvi13g00155	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.
Vitvi17g00695	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi12g02162	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi07g01625	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.
Vitvi02g01507	
Vitvi13g00385	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).
Vitvi09g01493	
Vitvi01g00815	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	2e-07	11 / 57	Glyoxylate and dicarboxylate metabolism
2	7e-07	12 / 78	Energy metabolism - Photosynthesis
3	6e-06	9 / 51	Carbon fixation in photosynthetic organisms
4	5e-05	7 / 38	Photosynthesis
5	9e-05	8 / 56	Glycine serine and threonine metabolism
6	1e-04	9 / 72	Energy metabolism - Carbon fixation
7	4e-04	11 / 123	Carbohydrate metabolism - Glycolysis
8	5e-03	5 / 44	Pentose phosphate pathway
9	9e-03	3 / 17	One carbon pool by folate
10	1e-02	7 / 92	Lipid metabolism - Glycerolipid metabolism
11	1e-02	5 / 54	Carbohydrate metabolism - Pentose phosphate
12	1e-02	6 / 75	Mitochondrial transcription and translation factors
13	2e-02	4 / 38	Enzyme - 1.8 Acting on a sulfur group of donors
14	2e-02	7 / 102	Membrane transport - ABC transporters
15	2e-02	5 / 60	Enzyme - 4.1 Carbon-carbon lyases
16	2e-02	4 / 41	Transporter catalog - Primary active transporter cat D1
17	2e-02	4 / 42	Tryptophan metabolism
18	3e-02	2 / 10	Linoleic acid metabolism
19	3e-02	2 / 10	Photosynthesis protein - Photosynthetic electron transport
20	3e-02	2 / 11	Enzyme - 2.2 Transferring aldehyde or ketonic groups



Correlation Cluster

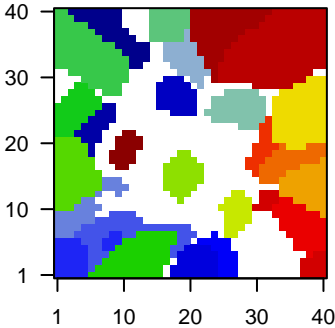
Spot Summary: W

metagenes = 23
genes = 331

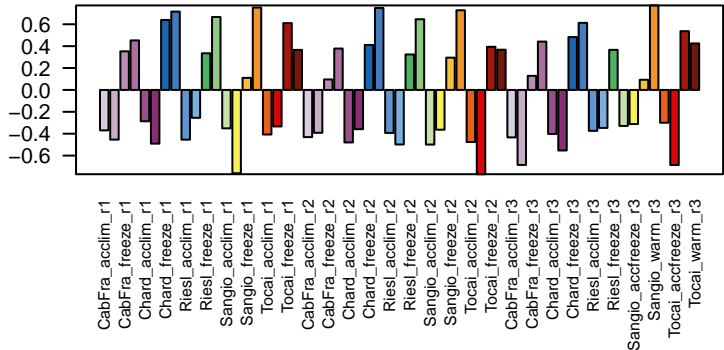
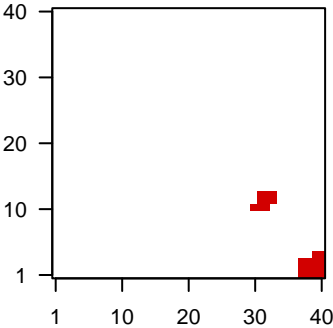
<r> metagenes = 0.94
<r> genes = 0.49
beta: r2= 10.78 / log p= -Inf

samples with spot = 17 (28.8 %)
CabFra_warm : 2 (66.7 %)
Chard_freeze : 3 (100 %)
Chard_warm : 3 (100 %)
Riesl_warm : 2 (100 %)
Sangio_warm : 3 (100 %)
Tocai_freeze : 3 (100 %)
Tocai_warm : 1 (33.3 %)

Overview Map



Spot

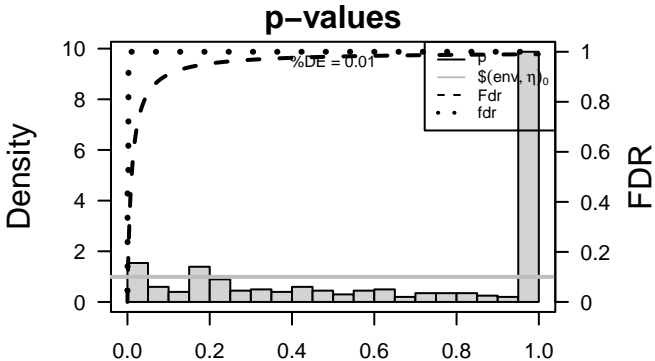


Spot Genelist

ID	Description
Vitvi03g00325	A transcription regulator activity that modulates transcription of gene sets via selective and non-covalent binding to a specific double-stranded genomic DNA sequence (sometimes referred to as a motif) within a cis-regulatory region. Regulatory regions include promoters (proximal and distal) and enhancers. Genes are transcriptional units, and include bacterial operons. 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).
Vitvi13g00369	
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	
Vitvi11g01421	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.
Vitvi16g00731	Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.
Vitvi02g00110	
Vitvi05g02017	
Vitvi15g01070	Catalysis of an oxidation-reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.
Vitvi01g01980	
Vitvi12g02451	Catalysis of the transfer of a group, e.g. a methyl group, glycosyl group, acyl group, phosphorus-containing, or other groups, from one compound (generally regarded as the donor) to another compound (generally regarded as the acceptor). Transferase is the systematic name for any enzyme of EC class 2. 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.
Vitvi11g01303	
Vitvi05g02019	
Vitvi14g00930	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.
Vitvi02g01121	
Vitvi03g01833	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi14g01336	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-10	9 / 26	Flavonoid biosynthesis
2	2e-04	7 / 63	Phenylpropanoid biosynthesis
3	2e-04	5 / 30	Ubiquinone and other terpenoid-quinone biosynthesis
4	2e-03	4 / 29	Transcription factors - Trihelix
5	3e-03	3 / 15	Stilbenoid diarylheptanoid and gingerol biosynthesis
6	5e-03	7 / 111	Transporter catalog - Porters cat 66 to 94
7	7e-03	7 / 118	Transcription factors - Helix-turn-helix
8	1e-02	3 / 24	Tropane piperidine and pyridine alkaloid biosynthesis
9	1e-02	3 / 24	Transporter catalog - Group translocators
10	1e-02	9 / 197	Transporter catalog - Channels and pores
11	1e-02	3 / 27	Common spliceosomal components
12	2e-02	3 / 28	Enzyme - 6.2 Forming carbon-sulfur bonds
13	2e-02	4 / 51	Other metabolism - Single reactions
14	2e-02	2 / 11	Enzyme - 2.2 Transferring aldehyde or ketonic groups
15	2e-02	5 / 81	Translation - mRNA surveillance pathway
16	2e-02	5 / 83	Transcription factors - MYB
17	2e-02	2 / 12	Endoplasmic reticulum membrane and cytosol
18	2e-02	2 / 12	Enzyme - 1.17 Acting on CH or CH2 groups
19	2e-02	3 / 32	Circadian rhythm - plant
20	3e-02	2 / 15	Chaperone - HSP70 / DNAK



Correlation Cluster

Spot Summary: X

metagenes = 145
genes = 1979

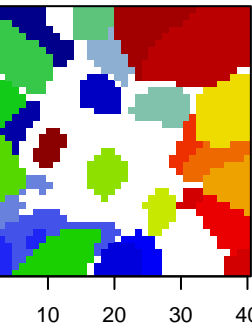
<r> metagenes = 0.93

beta: r2= 19.85 / log p= -Inf

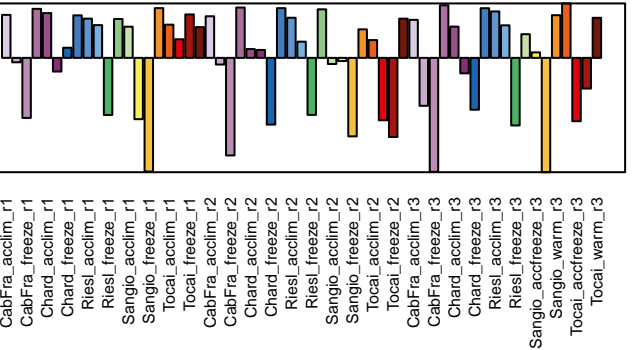
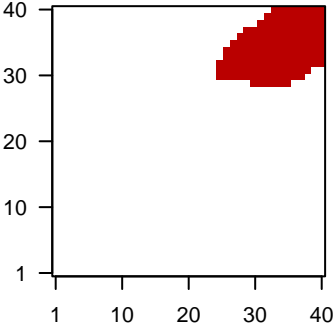
samples with spot = 24 (40.7 %)

- CabFra_acclim : 3 (100 %)
- CabFra_warm : 3 (100 %)
- Chard_acclim : 1 (33.3 %)
- Chard_warm : 3 (100 %)
- Riesl_acclim : 3 (100 %)
- Riesl_accfreeze : 2 (66.7 %)
- Riesl_warm : 2 (100 %)
- Sangio_warm : 2 (66.7 %)
- Tocai_acclim : 2 (66.7 %)
- Tocai_freeze : 1 (33.3 %)

Overview Map



Spot

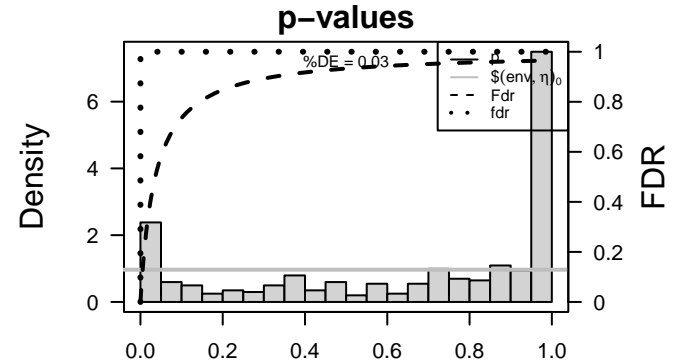


Spot Genelist

ID	Description
Vitvi14g01929	The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.
Vitvi09g01282	Functions in the storage of nutritious substrates.
Vitvi13g00172	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi19g02024	
Vitvi17g01251	The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.
Vitvi13g01337	Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a mechanism in which a water molecule bound by the side chains of aspartic residues at the active center acts as a nucleophile.
Vitvi06g01346	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00680	Binding to a metal ion.
Vitvi10g01636	
Vitvi17g00601	
Vitvi00g02243	
Vitvi17g00977	Binding to a metal ion.
Vitvi01g00816	Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.
Vitvi07g01844	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi19g00008	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi13g01788	
Vitvi01g00593	Binding to a metal ion.
Vitvi01g00441	Catalysis of the transfer of a methyl group to an acceptor molecule.
Vitvi12g02394	
Vitvi14g03084	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-18	72 / 206	Cell growth and death – Cell wall
2	5e-16	29 / 47	Transporter catalog – Transport electron carriers
3	2e-15	17 / 18	Photosynthesis – antenna proteins
4	2e-15	17 / 18	Energy metabolism – Photosynthesis antenna proteins
5	6e-15	25 / 38	Photosynthesis
6	3e-13	35 / 78	Energy metabolism – Photosynthesis
7	5e-10	10 / 10	Photosynthesis protein – Photosystem I (P700 chlorophyll a)
8	6e-09	20 / 41	Porphyrin metabolism
9	5e-07	26 / 78	Glycosyltransferase – Structural polysaccharide
10	1e-06	23 / 67	Ribosome – Bacteria
11	1e-06	36 / 134	Hormone signaling – Auxin signaling
12	5e-06	23 / 72	Ribosome – Mitochondria/ Chloroplast
13	5e-06	49 / 217	Cell motility – Regulation of actin cytoskeleton
14	1e-05	24 / 80	Cytoskeleton – Microtubules
15	1e-05	12 / 26	Steroid biosynthesis
16	7e-05	13 / 34	Peptidases and inhibitors – Family S10
17	1e-04	14 / 40	Transport system – Thylakoid targeting pathway
18	4e-04	6 / 10	Peptidases and inhibitors – Family A1: pepsin family
19	8e-04	16 / 58	Carbohydrate metabolism – Fructose and mannose metabolism
20	8e-04	8 / 19	Transcription factors – AUXIAA



Correlation Cluster

Spot Summary: Y

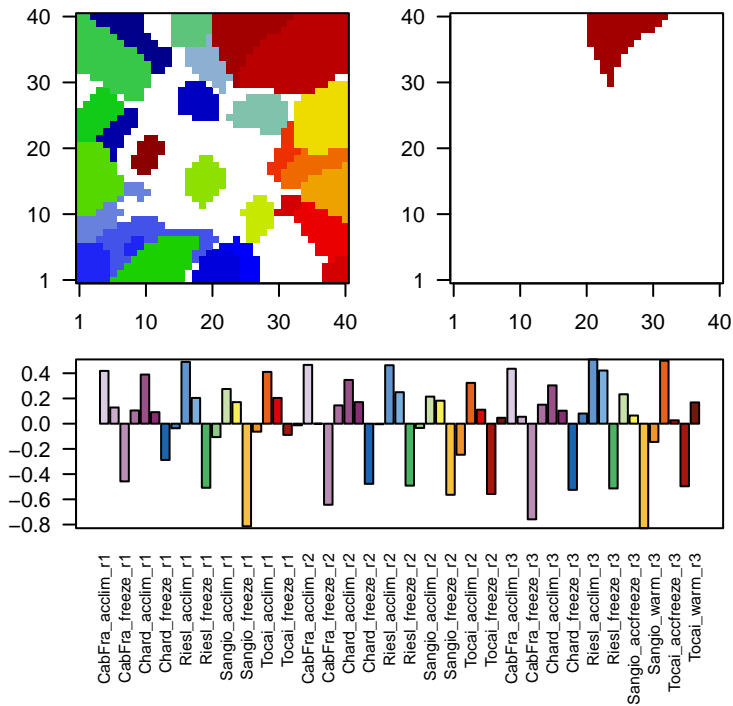
metagenes = 64
genes = 769

<r> metagenes = 0.94
<r> genes = 0.49
beta: r2= 7.47 / log p= -Inf

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

Overview Map

Spot

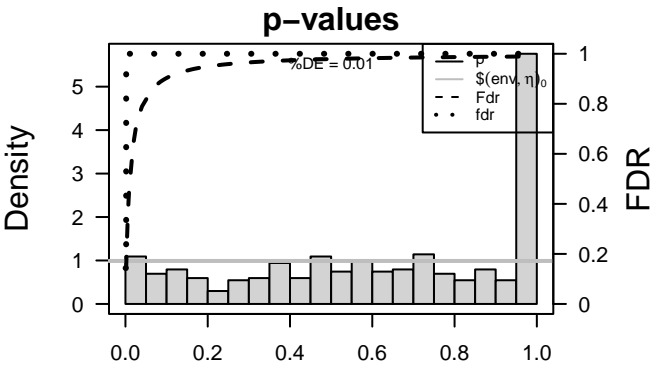


Spot Genelist

ID	Description
Vitvi09g01553	
Vitvi02g01440	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.
Vitvi18g00967	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.
Vitvi04g01221	A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.
Vitvi18g03009	
Vitvi10g02114	
Vitvi00g01861	
Vitvi19g00109	
Vitvi18g01848	
Vitvi19g01896	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.
Vitvi08g00768	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.
Vitvi06g00626	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi07g00251	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.
Vitvi17g00046	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi18g00431	That part of a multicellular organism outside the cells proper, usually taken to be outside the plasma membranes, and occupied by fluid.
Vitvi05g02157	Binding to a protein.
Vitvi12g02681	The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.
Vitvi05g00444	Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.
Vitvi09g00246	
Vitvi16g01549	Binding to a protein.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-04	18 / 161	Enzyme - 2.1 Transferring one-carbon groups
2	1e-03	4 / 11	Transcription factors - GRF
3	1e-03	8 / 48	Aminoacyl-tRNA biosynthesis
4	2e-03	5 / 20	tRNA modification factors
5	2e-03	9 / 62	Translation - Aminoacyl-tRNA biosynthesis
6	3e-03	9 / 66	Exosome - Exosomal proteins of bladder cancer cells
7	3e-03	7 / 43	Aminoacyl-tRNA synthetases (AARSs)
8	3e-03	7 / 44	Enzyme - 6.1 Forming carbon-oxygen bonds
9	3e-03	7 / 44	Replication protein - DNA Replication Termination Factors
10	5e-03	6 / 36	Enzyme - 6.3 Forming carbon-nitrogen bonds
11	6e-03	4 / 17	One carbon pool by folate
12	7e-03	10 / 89	MAPK signaling pathway - plant
13	8e-03	5 / 28	Transcription factors - MTERF
14	9e-03	9 / 79	Transporter catalog - Porters cat 30 to 64
15	2e-02	3 / 13	Chaperone - HSP60 / Chaperonin
16	2e-02	9 / 93	Transcription factors - BHLH
17	3e-02	8 / 80	Cytoskeleton - Microtubules
18	3e-02	4 / 26	Sphingolipid metabolism
19	3e-02	10 / 113	Exosome - Exosomal proteins of colorectal cancer cells
20	3e-02	3 / 16	Biotin metabolism



Correlation Cluster

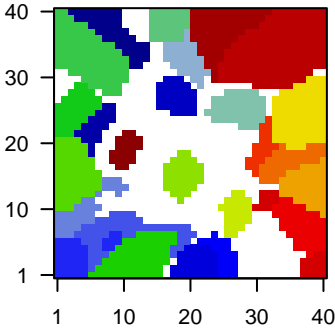
Spot Summary: Z

metagenes = 20
genes = 206

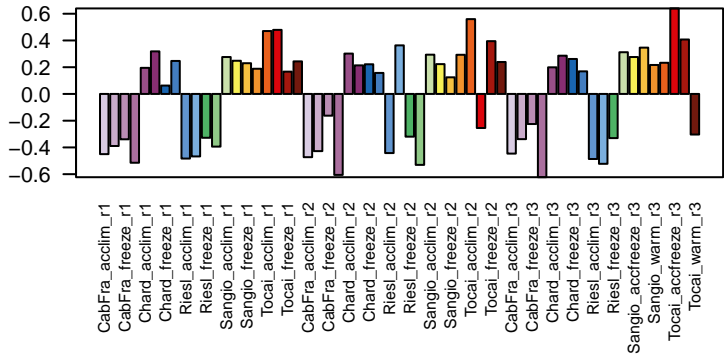
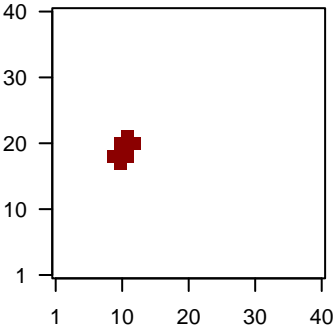
<r> metagenes = 0.95
<r> genes = 0.34
beta: r2= 2.82 / log p= -Inf

samples with spot = 6 (10.2 %)
Tocai_acclim : 2 (66.7 %)
Tocai_accfreeze : 2 (66.7 %)
Tocai_freeze : 2 (66.7 %)

Overview Map



Spot



Spot Genelist

ID	Description
Vitvi13g00807	Binding to a protein.
Vitvi04g01352	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi04g00352	
Vitvi03g01481	The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.
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	
Vitvi17g00343	Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.
Vitvi14g02706	Binding to ADP, adenosine 5'-diphosphate.
Vitvi14g00593	Binding to ADP, adenosine 5'-diphosphate.
Vitvi10g00243	
Vitvi12g02307	The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.
Vitvi18g02150	
Vitvi14g02707	Binding to ADP, adenosine 5'-diphosphate.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.01	3 / 62	Translation – Aminoacyl-tRNA biosynthesis
2	0.02	2 / 30	Glycan biosynthesis and metabolism – N-Glycan degradation
3	0.03	3 / 77	Carbohydrate metabolism – Galactose metabolism
4	0.03	2 / 33	Enzyme – 5.4 Intramolecular transferases
5	0.04	4 / 153	Plant-pathogen interaction
6	0.04	4 / 162	Plant specific signaling – Plant-pathogen interaction
7	0.04	2 / 41	Cofactors and vitamin metabolism – Riboflavin metabolism
8	0.05	2 / 43	Aminoacyl-tRNA synthetases (AARSs)
9	0.05	2 / 44	Enzyme – 6.1 Forming carbon-oxygen bonds
10	0.06	2 / 48	Aminoacyl-tRNA biosynthesis
11	0.06	2 / 49	Transcription factors – NAC
12	0.07	2 / 53	Protein – Forward pathways
13	0.08	2 / 58	Carbohydrate metabolism – Fructose and mannose metabolism
14	0.08	3 / 126	Translation – RNA transport
15	0.09	1 / 11	Enzyme – Class II (C/G)
16	0.09	3 / 129	Enzyme – 3.2 Glycosylases
17	0.10	1 / 13	Kinase – CDK family
18	0.11	1 / 14	Lipid metabolism – Fatty acid elongation in mitochondria
19	0.11	2 / 71	Lipid metabolism – Biosynthesis of steroids
20	0.12	1 / 16	Repair protein – SSBR (single strand breaks repair)

