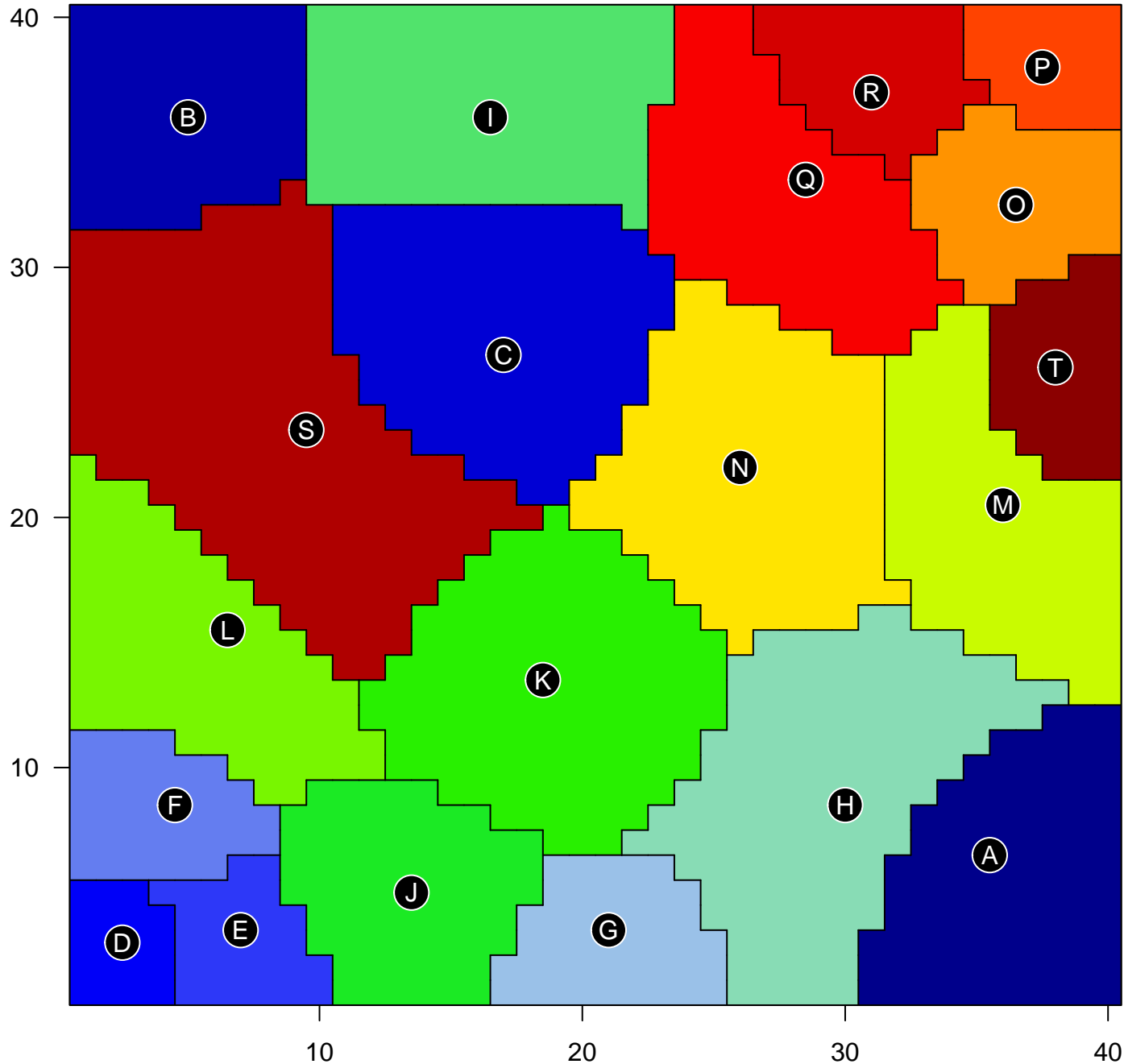
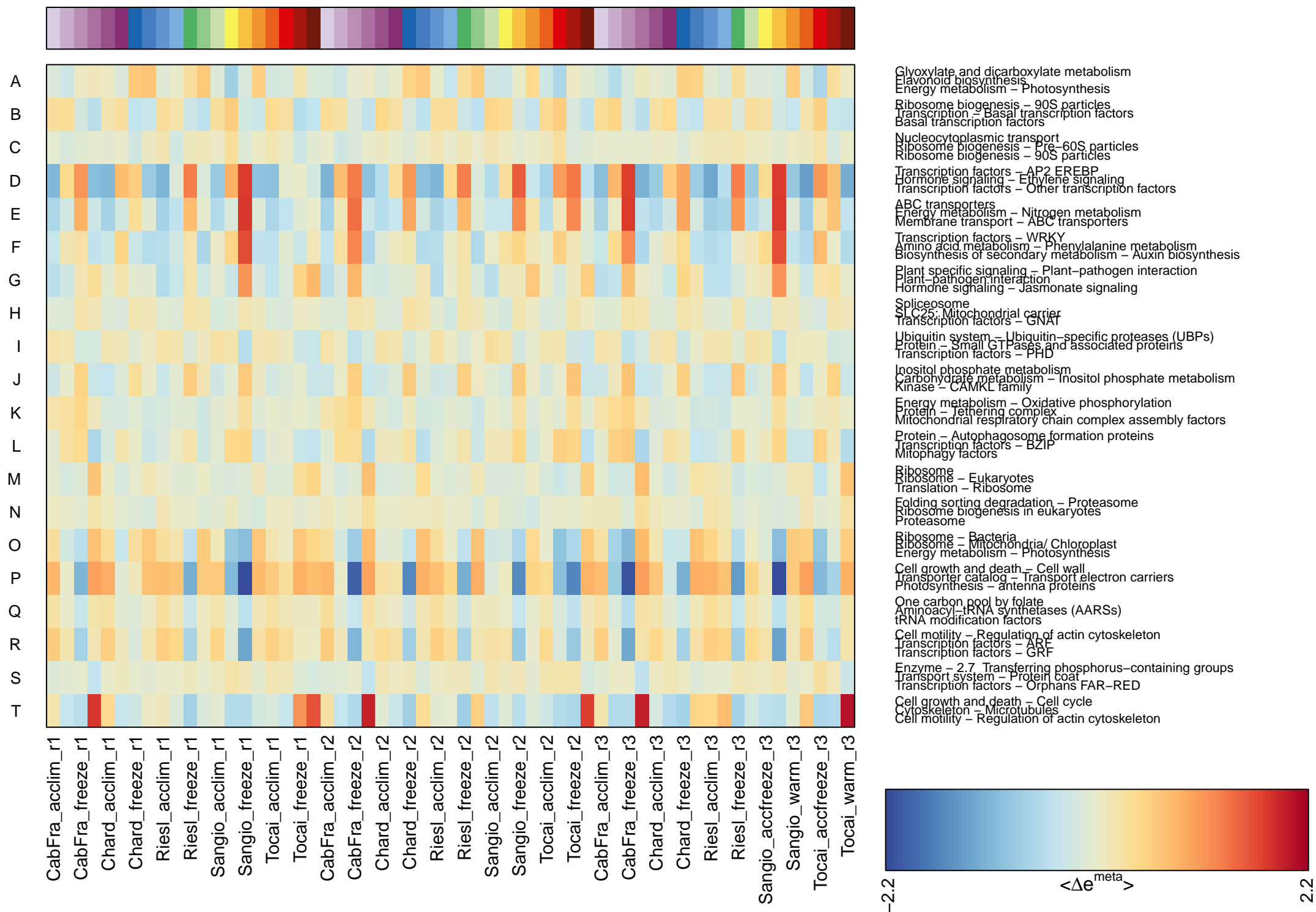


# K-Means Cluster

annotation



- A ■ Glyoxylate and dicarboxylate metabolism  
Flavonoid biosynthesis
- B ■ Ribosome biogenesis – 90S particles  
Transcription – Basal transcription factors
- C ■ Nucleocytoplasmic transport  
Ribosome biogenesis – Pre-60S particles
- D ■ Transcription factors – AP2 EREBP  
Hormone signaling – Ethylene signaling
- E ■ ABC transporters  
Energy metabolism – Nitrogen metabolism
- F ■ Transcription factors – WRKY  
Amino acid metabolism – Phenylalanine metabolism
- G ■ Plant specific signaling – Plant-pathogen interaction  
Plant-pathogen interaction
- H ■ Spliceosome  
SLC25: Mitochondrial carrier
- I ■ Ubiquitin system – Ubiquitin-specific proteases (UBPs)  
Protein – Small GTPases and associated proteins
- J ■ Inositol phosphate metabolism  
Carbohydrate metabolism – Inositol phosphate metabolism
- K ■ Energy metabolism – Oxidative phosphorylation  
Protein – Tethering complex
- L ■ Protein – Autophagosome formation proteins  
Transcription factors – BZIP
- M ■ Ribosome  
Ribosome – Eukaryotes
- N ■ Folding sorting degradation – Proteasome  
Ribosome biogenesis in eukaryotes
- O ■ Ribosome – Bacteria  
Ribosome – Mitochondria/ Chloroplast
- P ■ Cell growth and death – Cell wall  
Transporter catalog – Transport electron carriers
- Q ■ One carbon pool by folate  
Aminoacyl-tRNA synthetases (AARSs)
- R ■ Cell motility – Regulation of actin cytoskeleton  
Transcription factors – ARF
- S ■ Enzyme – 2.7 Transferring phosphorus-containing groups  
Transport system – Protein coat
- T ■ Cell growth and death – Cell cycle  
Cytoskeleton – Microtubules



K-Means Cluster

Spot Summary: A

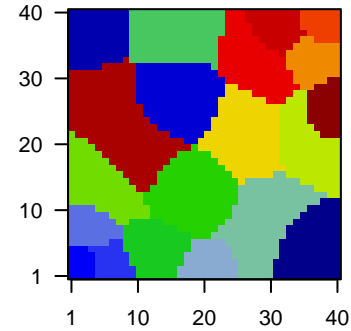
# metagenes = 94  
# genes = 1097

<r> metagenes = 0.78

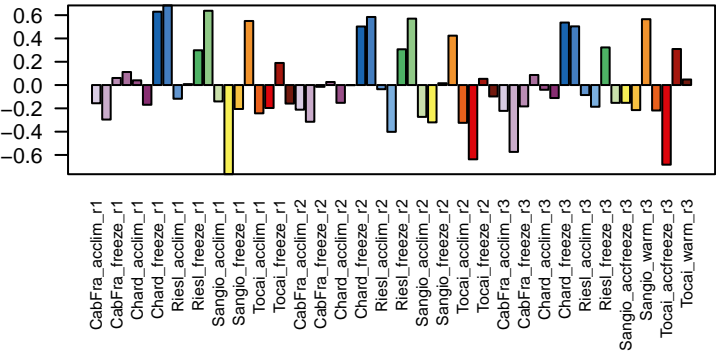
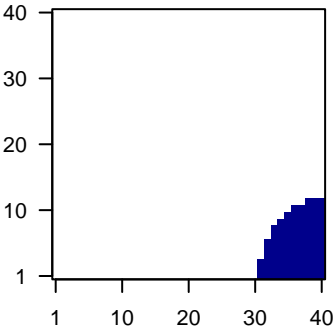
beta: r2= 8.14 / log p= -Inf

# samples with spot = 10 ( 16.9 %)  
Chard\_freeze : 3 ( 100 %)  
Chard\_warm : 3 ( 100 %)  
Riesl\_warm : 2 ( 100 %)  
Sangio\_warm : 2 ( 66.7 %)

Overview Map



Spot

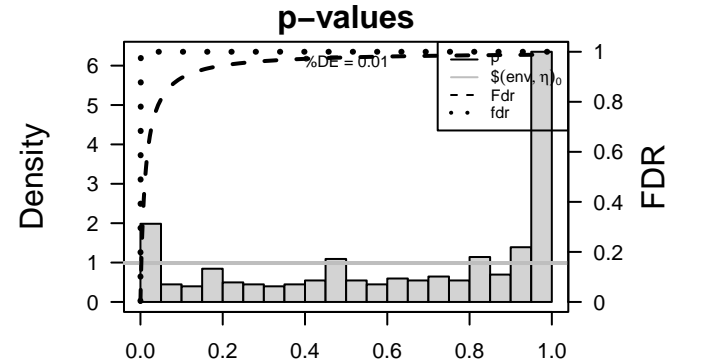


Spot Genelist

| ID            | Description   |
|---------------|---|
| Vitvi12g02565 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.  |
| Vitvi09g02008 | An intracellular non-membrane-bounded organelle comprising a matrix of coalesced lipids surrounded by a phospholipid monolayer. May include associated proteins.  |
| Vitvi04g01863 |   |
| Vitvi11g01446 | Any molecular entity that serves as an electron acceptor and electron donor in an electron transport chain. An electron transport chain is a process in which a series of electron carriers operate together to transfer electrons from donors to any of several different terminal electron acceptors to generate a transmembrane electrochemical gradient.                        |
| Vitvi11g01457 | Binding to a protein.   |
| Vitvi10g01863 |   |
| Vitvi03g00325 | A transcription regulator activity that modulates transcription of gene sets via selective and non-covalent binding to a specific double-stranded genomic DNA sequence (sometimes referred to as a motif) within a cis-regulatory region. Regulatory regions include promoters (proximal and distal) and enhancers. Genes are transcriptional units, and include bacterial operons. |
| Vitvi13g00369 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).  |
| Vitvi10g01433 |   |
| Vitvi17g00339 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.  |
| Vitvi13g02005 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).  |
| Vitvi00g00346 |   |
| Vitvi07g02904 |   |
| Vitvi08g01434 | The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.   |
| Vitvi10g00378 |   |
| 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.   |
| Vitvi19g01989 |   |
| Vitvi13g00870 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.   |
| Vitvi11g01421 |   |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 7e-07   | 15 / 57  | Glyoxylate and dicarboxylate metabolism                     |
| 2    | 1e-05   | 9 / 26   | Flavonoid biosynthesis                                      |
| 3    | 4e-05   | 15 / 78  | Energy metabolism – Photosynthesis                          |
| 4    | 2e-04   | 11 / 51  | Carbon fixation in photosynthetic organisms                 |
| 5    | 9e-04   | 15 / 102 | Membrane transport – ABC transporters                       |
| 6    | 1e-03   | 8 / 38   | Photosynthesis  |
| 7    | 2e-03   | 15 / 111 | Transporter catalog – Porters cat 66 to 94                  |
| 8    | 2e-03   | 12 / 79  | Transporter catalog – Porters cat 30 to 64                  |
| 9    | 2e-03   | 6 / 24   | Tropane piperidine and pyridine alkaloid biosynthesis       |
| 10   | 3e-03   | 6 / 25   | Nitrogen metabolism   |
| 11   | 3e-03   | 4 / 11   | Enzyme – 2.2 Transferring aldehyde or ketonic groups        |
| 12   | 3e-03   | 11 / 72  | Energy metabolism – Carbon fixation                         |
| 13   | 4e-03   | 5 / 19   | Cofactors and vitamin metabolism – Ubiquinone biosynthesis  |
| 14   | 5e-03   | 9 / 56   | Glycine serine and threonine metabolism                     |
| 15   | 6e-03   | 21 / 197 | Transporter catalog – Channels and pores                    |
| 16   | 8e-03   | 7 / 40   | SLC47: Multidrug and Toxin Extrusion (MATE) family          |
| 17   | 8e-03   | 7 / 40   | Transport system – Thylakoid targeting pathway              |
| 18   | 1e-02   | 9 / 63   | Phenylpropanoid biosynthesis                                |
| 19   | 1e-02   | 5 / 24   | Carbohydrate metabolism – Ascorbate and aldarate metabolism |
| 20   | 1e-02   | 4 / 16   | Enzyme – 1.4 Acting on the CH-NH2 group of donors           |



K–Means Cluster

Spot Summary: B

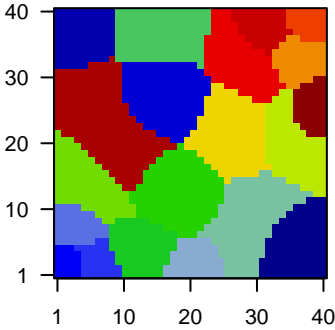
# metagenes = 76  
# genes = 1258

<r> metagenes = 0.93

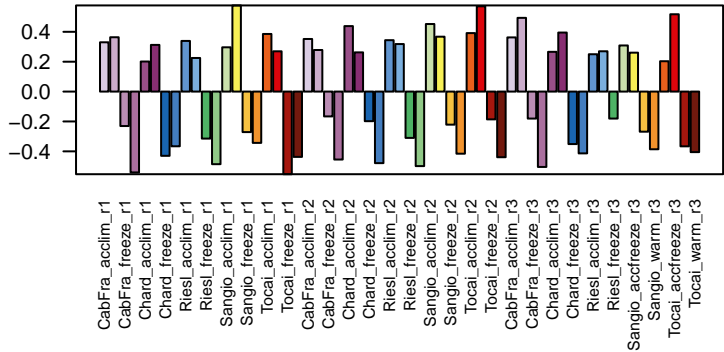
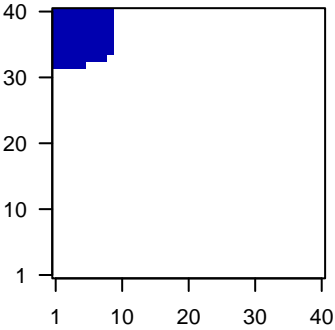
beta: r2= 7.4 / log p= -Inf

# samples with spot = 4 ( 6.8 %)  
CabFra\_accfreeze : 1 ( 33.3 %)  
Sangio\_accfreeze : 1 ( 33.3 %)  
Tocai\_accfreeze : 2 ( 66.7 %)

Overview Map



Spot

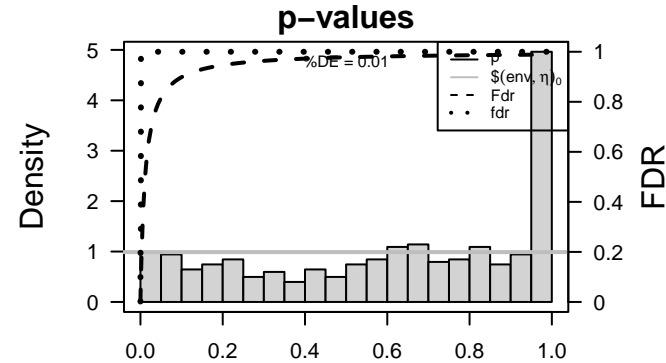


Spot Genelist

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

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 6e-06   | 16 / 62  | Ribosome biogenesis – 90S particles                  |
| 2    | 9e-06   | 12 / 38  | Transcription – Basal transcription factors          |
| 3    | 2e-04   | 10 / 37  | Basal transcription factors                          |
| 4    | 9e-04   | 11 / 51  | Plant specific signaling – Circadian rhythm          |
| 5    | 1e-03   | 22 / 151 | RNA polymerase II system                             |
| 6    | 2e-03   | 17 / 110 | Ubiquitin system – Multi subunit Ring-finger type E3 |
| 7    | 6e-03   | 4 / 11   | Protein – Mitophagy                                  |
| 8    | 7e-03   | 7 / 32   | Circadian rhythm – plant                             |
| 9    | 1e-02   | 4 / 13   | Transcription factors – HMG                          |
| 10   | 1e-02   | 6 / 28   | RNA polymerase III system                            |
| 11   | 2e-02   | 10 / 64  | Ribosome biogenesis in eukaryotes                    |
| 12   | 2e-02   | 7 / 38   | Protein – Other autophagy associated proteins        |
| 13   | 2e-02   | 15 / 116 | Ribosome biogenesis – Pre-60S particles              |
| 14   | 2e-02   | 8 / 48   | Transcription factors – PHD                          |
| 15   | 3e-02   | 13 / 100 | Plant specific signaling – Flower development        |
| 16   | 3e-02   | 4 / 17   | Kinase – IRAK family                                 |
| 17   | 3e-02   | 3 / 10   | Transcription factors – C2C2-CO                      |
| 18   | 4e-02   | 6 / 35   | RNA polymerase                                       |
| 19   | 4e-02   | 10 / 75  | Translation – Ribosome biogenesis in Eukaryotes      |
| 20   | 4e-02   | 15 / 128 | Ubiquitin system – Single Ring-finger type E3        |



K–Means Cluster

Spot Summary: C

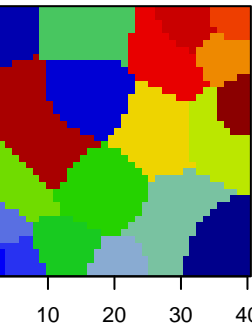
# metagenes = 120  
# genes = 1203

<r> metagenes = 0.64

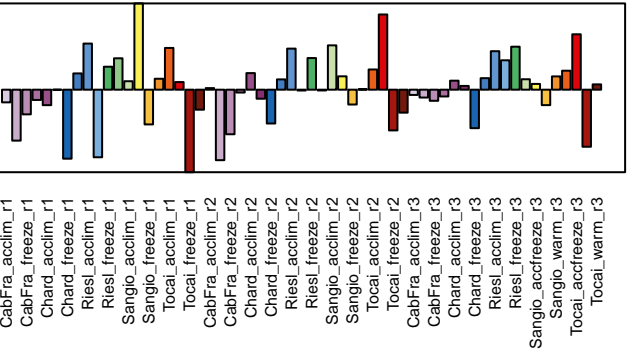
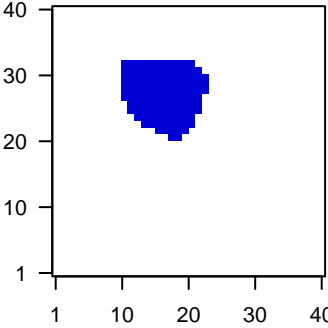
beta: r2= 1.26 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

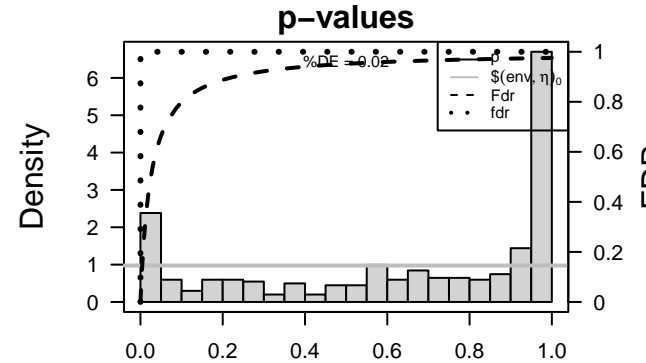


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi13g00646 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi14g01530 | 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.  |
| Vitvi09g00177 | The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.  |
| Vitvi07g00518 | Progression through the phases of the meiotic cell cycle, in which canonically a cell replicates to produce four offspring with half the chromosomal content of the progenitor cell via two nuclear divisions.   |
| Vitvi18g02642 |  |
| Vitvi02g01417 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi11g00678 | Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).  |
| Vitvi14g01532 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| 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 posses 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. |
| Vitvi16g01543 |  |
| Vitvi09g00149 | Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi07g01773 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi10g00432 |  |
| Vitvi04g02107 |  |
| Vitvi09g01718 |  |
| Vitvi05g01824 |  |
| Vitvi11g00514 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.   |
| Vitvi01g00216 |  |
| Vitvi17g01492 | Binding to a metal ion.  |
| Vitvi09g00007 | The chemical reactions and pathways involving lipids, compounds soluble in an organic solvent but not, or sparingly, in an aqueous solvent. Includes fatty acids; neutral fats, other fatty-acid esters, and soaps; long-chain (fatty) alcohols and waxes; sphingoids and other long-chain bases; glycolipids, phospholipids and sphingolipids; and carotenes, polyprenols, sterols, terpenes and other isoprenoids.                 |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 3e-09   | 23 / 85  | Nucleocytoplasmic transport                            |
| 2    | 4e-07   | 24 / 116 | Ribosome biogenesis – Pre-60S particles                |
| 3    | 2e-06   | 16 / 62  | Ribosome biogenesis – 90S particles                    |
| 4    | 9e-06   | 27 / 165 | Transcription – Spliceosome                            |
| 5    | 2e-05   | 21 / 115 | Enzyme – 3.6 Acting on acid anhydrides                 |
| 6    | 2e-05   | 16 / 75  | Translation – Ribosome biogenesis in Eukaryotes        |
| 7    | 5e-05   | 9 / 28   | Transcription factors – SNF2                           |
| 8    | 6e-05   | 21 / 126 | Translation – RNA transport                            |
| 9    | 7e-05   | 8 / 23   | Glycosylphosphatidylinositol (GPI)-anchor biosynthesis |
| 10   | 7e-05   | 10 / 36  | Ribosome biogenesis – Pre-40S particles                |
| 11   | 1e-04   | 23 / 151 | RNA polymerase II system                               |
| 12   | 1e-04   | 22 / 142 | Transport system – Protein coat                        |
| 13   | 2e-04   | 46 / 409 | Enzyme – 2.7 Transferring phosphorus-containing groups |
| 14   | 3e-04   | 21 / 139 | Spliceosome  |
| 15   | 6e-04   | 7 / 24   | Protein – Retrieval pathways                           |
| 16   | 8e-04   | 12 / 64  | Ribosome biogenesis in eukaryotes                      |
| 17   | 9e-04   | 10 / 48  | Transcription factors – PHD                            |
| 18   | 9e-04   | 10 / 48  | Transport system – Nuclear pore complex                |
| 19   | 3e-03   | 8 / 39   | Ubiquitin system – Ubiquitin-specific proteases (UBPs) |
| 20   | 4e-03   | 10 / 57  | Transcription factors – C3H                            |



K–Means Cluster

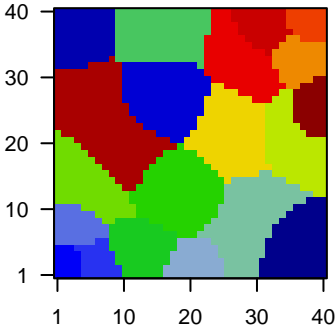
Spot Summary: D

# metagenes = 19  
# genes = 478

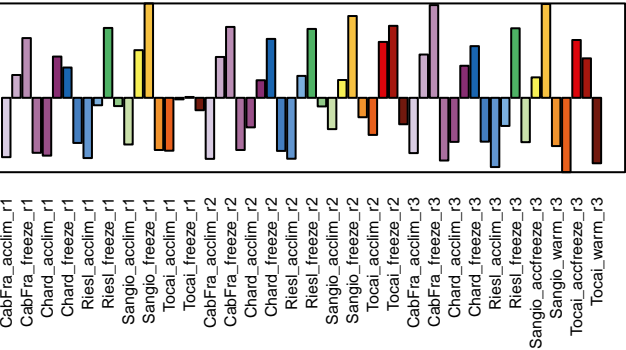
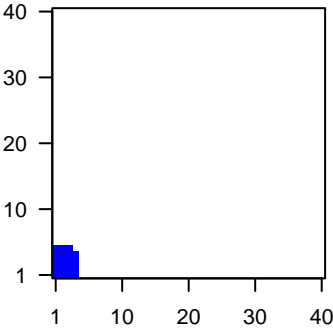
<r> metagenes = 0.98  
<r> genes = 0.68  
beta: r2= 46.38 / log p= -Inf

# samples with spot = 21 ( 35.6 %)  
CabFra\_accfreeze : 2 ( 66.7 %)  
CabFra\_freeze : 3 ( 100 %)  
Chard\_accfreeze : 2 ( 66.7 %)  
Chard\_freeze : 3 ( 100 %)  
Riesl\_freeze : 3 ( 100 %)  
Sangio\_accfreeze : 1 ( 33.3 %)  
Sangio\_freeze : 3 ( 100 %)  
Tocai\_accfreeze : 2 ( 66.7 %)  
Tocai\_freeze : 2 ( 66.7 %)

Overview Map



Spot

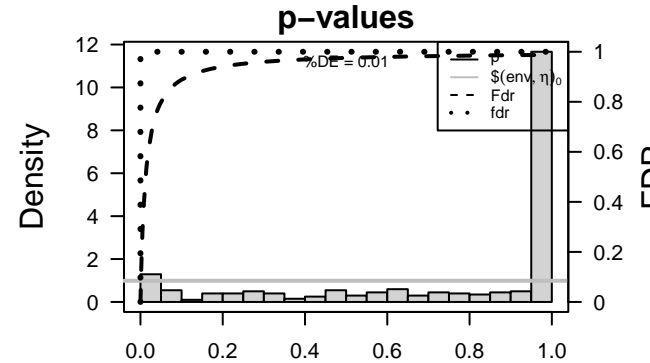


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi05g00204 | Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).   |
| Vitvi09g01554 |  |
| Vitvi05g00170 | Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor).   |
| Vitvi06g01917 | The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.  |
| Vitvi18g03065 |  |
| Vitvi06g01280 |  |
| Vitvi06g00666 | Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi02g01408 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite. |
| Vitvi00g00932 |  |
| Vitvi02g01747 |  |
| Vitvi15g00960 | Catalysis of the transfer of an acyl group to an oxygen atom on the acceptor molecule.   |
| Vitvi04g01685 |  |
| Vitvi06g01762 | Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.  |
| Vitvi16g01434 | Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).  |
| Vitvi18g03100 | Binds to and stops, prevents or reduces the activity of a cysteine-type endopeptidase, any enzyme that hydrolyzes peptide bonds in polypeptides by a mechanism in which the sulfhydryl group of a cysteine residue at the active center acts as a nucleophile.         |
| Vitvi14g00971 |  |
| Vitvi02g01288 | Binding to a metal ion.  |
| Vitvi13g02551 | 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.  |
| Vitvi12g02562 |  |
| Vitvi05g01583 | 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    | 2e-17   | 22 / 73  | Transcription factors – AP2 EREBP                       |
| 2    | 8e-17   | 28 / 140 | Hormone signaling – Ethylene signaling                  |
| 3    | 1e-11   | 16 / 64  | Transcription factors – Other transcription factors     |
| 4    | 3e-10   | 13 / 48  | Transcription factors – WRKY                            |
| 5    | 5e-09   | 12 / 49  | Transcription factors – NAC                             |
| 6    | 2e-05   | 15 / 153 | Plant-pathogen interaction                              |
| 7    | 3e-05   | 8 / 45   | Galactose metabolism                                    |
| 8    | 4e-05   | 10 / 77  | Carbohydrate metabolism – Galactose metabolism          |
| 9    | 9e-05   | 18 / 238 | Enzyme – 2.4 Glycosyltransferases                       |
| 10   | 1e-04   | 14 / 162 | Plant specific signaling – Plant-pathogen interaction   |
| 11   | 1e-03   | 10 / 118 | Transcription factors – Helix–turn–helix                |
| 12   | 2e-03   | 8 / 83   | Transcription factors – MYB                             |
| 13   | 3e-03   | 3 / 11   | Biosynthesis of secondary metabolism – ABA biosynthesis |
| 14   | 5e-03   | 6 / 58   | Other amino acids metabolism – Glutathione metabolism   |
| 15   | 5e-03   | 5 / 42   | Tryptophan metabolism                                   |
| 16   | 7e-03   | 4 / 29   | Transcription factors – GRAS                            |
| 17   | 1e-02   | 3 / 19   | Hormone signaling – Gibberellin signaling               |
| 18   | 2e-02   | 6 / 74   | Transcription factors – C2H2                            |
| 19   | 2e-02   | 5 / 57   | Transcription factors – HB                              |
| 20   | 3e-02   | 2 / 10   | Valine leucine and isoleucine biosynthesis              |



K–Means Cluster

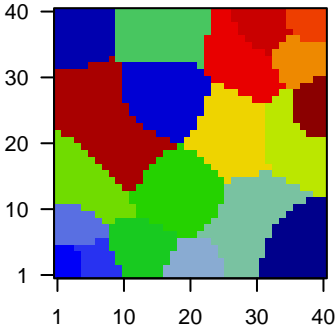
Spot Summary: E

# metagenes = 29  
# genes = 464

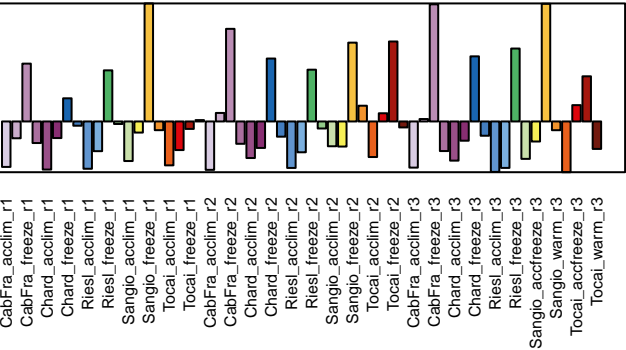
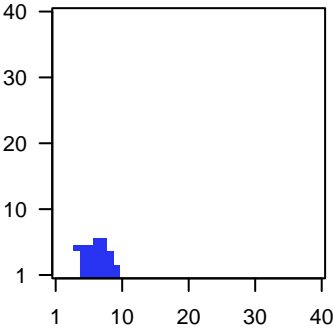
<r> metagenes = 0.97  
<r> genes = 0.62  
beta: r2= 24.41 / log p= -Inf

# samples with spot = 13 ( 22 %)  
CabFra\_freeze : 3 ( 100 %)  
Chard\_freeze : 2 ( 66.7 %)  
Riesl\_freeze : 3 ( 100 %)  
Sangio\_freeze : 3 ( 100 %)  
Tocai\_freeze : 2 ( 66.7 %)

Overview Map



Spot

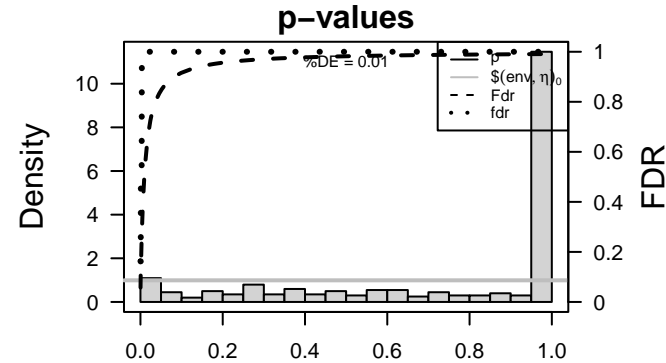


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi06g01713 |  |
| Vitvi15g00835 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| 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). |
| Vitvi04g01907 | Catalysis of the hydrolysis of various bonds, e.g. C–O, C–N, C–C, phosphoric anhydride bonds, etc.   |
| Vitvi16g01321 |  |
| Vitvi19g02038 |  |
| Vitvi05g00643 | Catalysis of the hydrolysis of any ester bond.   |
| Vitvi17g00819 | Binding to a zinc ion (Zn).  |
| Vitvi18g01263 |  |
| Vitvi18g00108 | 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.  |
| 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.  |
| Vitvi00g02226 |  |
| Vitvi08g01547 |  |
| Vitvi02g01406 | 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.   |
| Vitvi06g00709 | Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.  |
| Vitvi00g01827 |  |
| Vitvi16g02098 |  |
| Vitvi06g01423 |  |
| Vitvi11g00356 | 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.  |
| Vitvi16g01010 |  |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset  |
|------|---------|---------|--|
| 1    | 1e-04   | 7 / 47  | ABC transporters                                     |
| 2    | 7e-04   | 6 / 44  | Energy metabolism – Nitrogen metabolism              |
| 3    | 1e-03   | 9 / 102 | Membrane transport – ABC transporters                |
| 4    | 3e-03   | 5 / 40  | SLC47: Multidrug and Toxin Extrusion (MATE) family   |
| 5    | 3e-03   | 7 / 79  | Transporter catalog – Porters cat 30 to 64           |
| 6    | 4e-03   | 4 / 26  | Glycosyltransferase – Hydrophobic molecule           |
| 7    | 4e-03   | 5 / 43  | Alanine aspartate and glutamate metabolism           |
| 8    | 4e-03   | 4 / 27  | ABCG (White) subfamily                               |
| 9    | 5e-03   | 6 / 63  | Phenylpropanoid biosynthesis                         |
| 10   | 6e-03   | 4 / 30  | Cyanoamino acid metabolism                           |
| 11   | 6e-03   | 7 / 88  | Electrochemical potential-driven transporters [TC:2] |
| 12   | 1e-02   | 9 / 146 | Transporter catalog – Porters cat 7 to 17            |
| 13   | 2e-02   | 5 / 61  | Peroxisome   |
| 14   | 2e-02   | 2 / 10  | Transcription factors – AS2                          |
| 15   | 2e-02   | 4 / 45  | Galactose metabolism                                 |
| 16   | 3e-02   | 3 / 26  | Flavonoid biosynthesis                               |
| 17   | 3e-02   | 2 / 11  | Zeatin biosynthesis                                  |
| 18   | 3e-02   | 2 / 11  | Lipid metabolism – C21–Steroid hormone metabolism    |
| 19   | 3e-02   | 3 / 28  | Exosome – Exosomal proteins of breast milk           |
| 20   | 4e-02   | 6 / 101 | Glycolysis / Gluconeogenesis                         |



K–Means Cluster

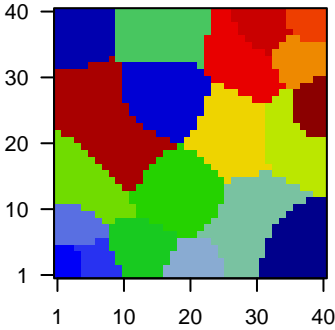
Spot Summary: F

# metagenes = 39  
# genes = 494

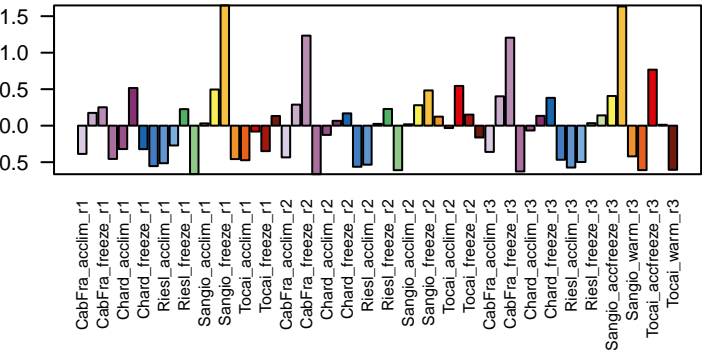
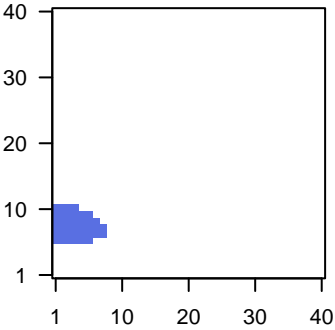
<r> metagenes = 0.95  
<r> genes = 0.51  
beta: r2= 16.64 / log p= -Inf

# samples with spot = 8 ( 13.6 %)  
CabFra\_freeze : 2 ( 66.7 %)  
Chard\_accfreeze : 1 ( 33.3 %)  
Sangio\_accfreeze : 1 ( 33.3 %)  
Sangio\_freeze : 2 ( 66.7 %)  
Tocai\_accfreeze : 2 ( 66.7 %)

Overview Map



Spot

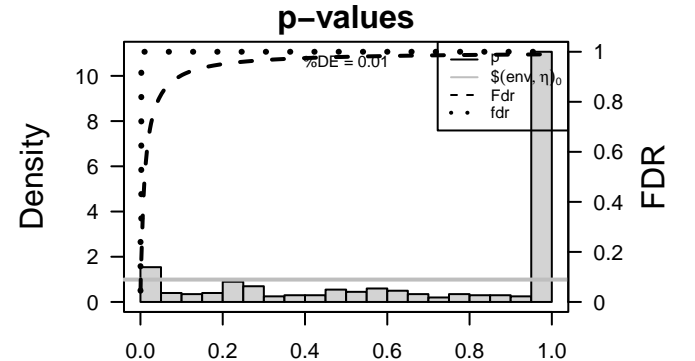


Spot Genelist

| 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. |
| 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.   |
| Vitvi05g00483 | Binding to a copper (Cu) ion.   |
| Vitvi09g00500 | 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 |   |
| Vitvi18g02840 |   |
| Vitvi07g02558 | Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.   |
| Vitvi04g01941 | 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.  |
| 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.  |
| 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.  |
| Vitvi18g02446 | Binding to a magnesium (Mg) ion.  |
| Vitvi04g00798 |   |
| Vitvi17g01621 |   |
| Vitvi16g01025 |   |
| 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.  |
| 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.  |
| Vitvi16g00054 |   |
| 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.   |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset   |
|------|---------|---------|---|
| 1    | 1e-04   | 7 / 48  | Transcription factors – WRKY                                |
| 2    | 2e-04   | 8 / 71  | Amino acid metabolism – Phenylalanine metabolism            |
| 3    | 1e-03   | 6 / 51  | Biosynthesis of secondary metabolism – Auxin biosynthesis   |
| 4    | 2e-03   | 9 / 121 | Transporter catalog – Porters cat 18 to 29                  |
| 5    | 2e-03   | 6 / 58  | Other amino acids metabolism – Glutathione metabolism       |
| 6    | 6e-03   | 3 / 17  | Isoquinoline alkaloid biosynthesis                          |
| 7    | 8e-03   | 3 / 18  | Receptor – Others   |
| 8    | 9e-03   | 7 / 102 | Amino sugar and nucleotide sugar metabolism                 |
| 9    | 1e-02   | 4 / 39  | beta-Alanine metabolism                                     |
| 10   | 1e-02   | 4 / 40  | SLC47: Multidrug and Toxin Extrusion (MATE) family          |
| 11   | 1e-02   | 5 / 63  | Phenylpropanoid biosynthesis                                |
| 12   | 2e-02   | 4 / 42  | Tryptophan metabolism                                       |
| 13   | 2e-02   | 3 / 24  | Tropane piperidine and pyridine alkaloid biosynthesis       |
| 14   | 2e-02   | 3 / 24  | Carbohydrate metabolism – Ascorbate and aldarate metabolism |
| 15   | 2e-02   | 5 / 67  | Amino acid metabolism – Tyrosine metabolism                 |
| 16   | 2e-02   | 3 / 25  | Phenylalanine metabolism                                    |
| 17   | 2e-02   | 3 / 26  | Pantothenate and CoA biosynthesis                           |
| 18   | 2e-02   | 3 / 26  | Enzyme – 5.1 Racemases and epimerases                       |
| 19   | 2e-02   | 4 / 47  | ABC transporters  |
| 20   | 2e-02   | 3 / 27  | ABCG (White) subfamily                                      |





K–Means Cluster

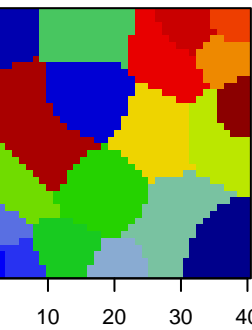
Spot Summary: G

# metagenes = 44  
# genes = 574

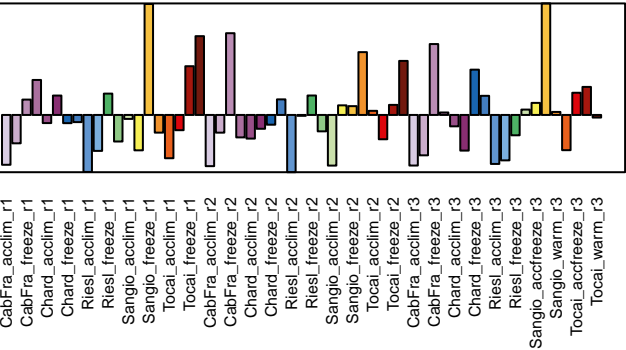
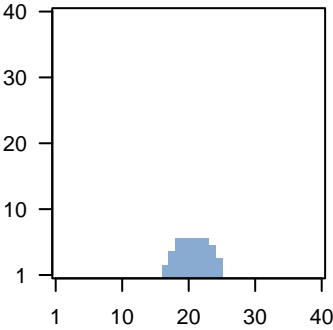
<r> metagenes = 0.93  
<r> genes = 0.41  
beta: r2= 7.23 / log p= -Inf

# samples with spot = 8 ( 13.6 %)  
CabFra\_freeze : 2 ( 66.7 %)  
Sangio\_freeze : 2 ( 66.7 %)  
Sangio\_warm : 1 ( 33.3 %)  
Tocai\_freeze : 1 ( 33.3 %)  
Tocai\_warm : 2 ( 66.7 %)

Overview Map



Spot

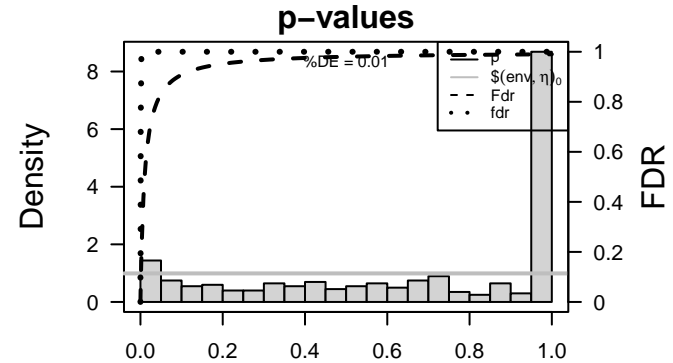


Spot Genelist

| 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. |
| Vitvi17g00450 | 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.   |
| Vitvi07g02243 | Binding to ATP, adenosine 5'–triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi09g00258 |  |
| Vitvi09g01557 |  |

Geneset Overrepresentation

| Rank | p–value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 5e–09   | 22 / 162 | Plant specific signaling – Plant–pathogen interaction      |
| 2    | 4e–08   | 20 / 153 | Plant–pathogen interaction                                 |
| 3    | 3e–04   | 8 / 56   | Hormone signaling – Jasmonate signaling                    |
| 4    | 6e–04   | 7 / 48   | Transcription factors – WRKY                               |
| 5    | 2e–03   | 8 / 77   | Pores ion channels [TC:1]                                  |
| 6    | 3e–03   | 5 / 33   | Carbohydrate metabolism – Butanoate metabolism             |
| 7    | 3e–03   | 5 / 33   | Glycan biosynthesis and metabolism – N–Glycan biosynthesis |
| 8    | 7e–03   | 5 / 40   | N–Glycan biosynthesis                                      |
| 9    | 9e–03   | 11 / 157 | Protein processing in endoplasmic reticulum                |
| 10   | 1e–02   | 3 / 15   | Stilbenoid diarylheptanoid and gingerol biosynthesis       |
| 11   | 1e–02   | 8 / 101  | Glycolysis / Gluconeogenesis                               |
| 12   | 1e–02   | 9 / 123  | Carbohydrate metabolism – Glycolysis                       |
| 13   | 1e–02   | 3 / 17   | Kinase – IRAK family                                       |
| 14   | 2e–02   | 4 / 33   | Enzyme – 5.4 Intramolecular transferases                   |
| 15   | 2e–02   | 6 / 71   | Glutathione metabolism                                     |
| 16   | 2e–02   | 5 / 53   | Protein – Forward pathways                                 |
| 17   | 3e–02   | 3 / 21   | Butanoate metabolism                                       |
| 18   | 3e–02   | 7 / 96   | Transporter catalog – Porters cat 1 to 6                   |
| 19   | 3e–02   | 4 / 38   | Protein – Chaperone mediated autophagy (CMA)               |
| 20   | 3e–02   | 4 / 39   | Enzyme – 1.2 Acting on the aldehyde or oxo group of donors |



K–Means Cluster

Spot Summary: H

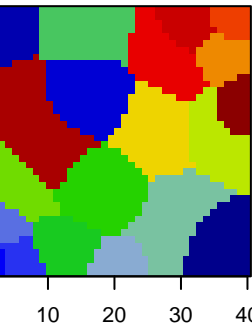
# metagenes = 135  
# genes = 1117

<r> metagenes = 0.66

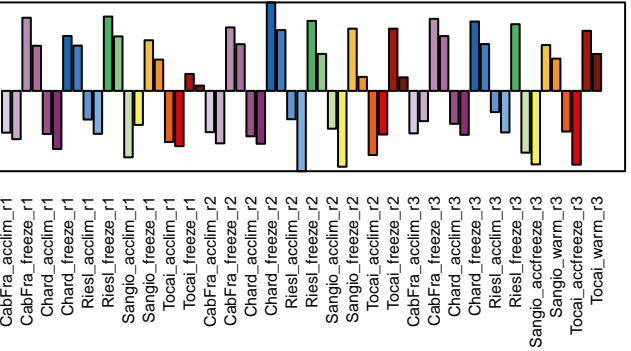
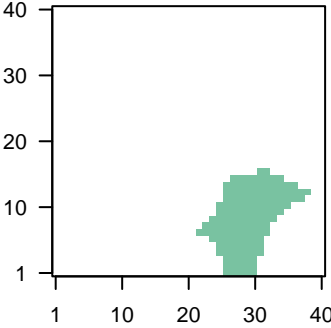
beta: r2= 1.99 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

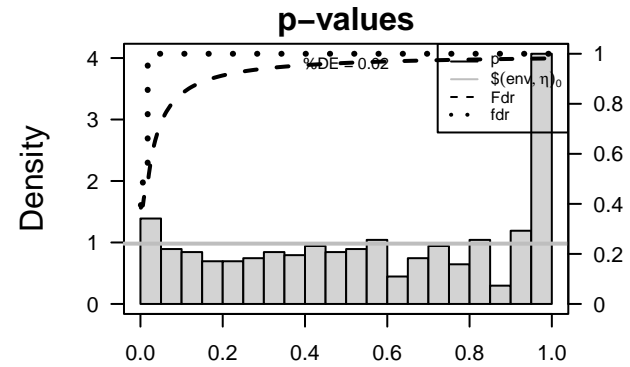


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi04g01940 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a mechanism in which a water molecule bound by the side chains of aspartic residues at the active center acts as a nucleophile.   |
| Vitvi02g01446 |  |
| Vitvi06g01329 | The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.  |
| Vitvi14g01840 | Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi16g01103 | Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi08g01380 |  |
| Vitvi15g00110 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| 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.  |
| Vitvi18g01129 | Catalysis of the transfer of a group, e.g. a methyl group, glycosyl group, acyl group, phosphorus-containing, or other groups, from one compound (generally regarded as the donor) to another compound (generally regarded as the acceptor). Transferase is the systematic name for any enzyme of EC class 2.  |
| Vitvi00g01736 |  |
| Vitvi16g02123 |  |
| Vitvi11g00319 | Stimulates the exchange of GDP to GTP on a signaling GTPase, changing its conformation to its active form. Guanine nucleotide exchange factors (GEFs) act by stimulating the release of guanosine diphosphate (GDP) to allow binding of guanosine triphosphate (GTP), which is more abundant in the cell under normal cellular physiological conditions. |
| 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.  |
| Vitvi17g01538 |  |
| Vitvi12g00696 |  |
| 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.  |
| 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.  |
| Vitvi18g01958 | Binding to ADP, adenosine 5'-diphosphate.  |
| Vitvi16g01509 | The process in which a methyl group is covalently attached to a molecule.  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 0.001   | 19 / 139 | Spliceosome  |
| 2    | 0.003   | 8 / 41   | SLC25: Mitochondrial carrier                           |
| 3    | 0.004   | 6 / 25   | Transcription factors - GNAT                           |
| 4    | 0.004   | 7 / 34   | Matrix   |
| 5    | 0.005   | 6 / 27   | Common spliceosomal components                         |
| 6    | 0.006   | 7 / 36   | Transcription factors - Zinc finger                    |
| 7    | 0.008   | 7 / 38   | Lipid metabolism - Ether lipid metabolism              |
| 8    | 0.009   | 6 / 30   | Ubiquinone and other terpenoid-quinone biosynthesis    |
| 9    | 0.010   | 5 / 22   | Transcription factors - CCAAT                          |
| 10   | 0.012   | 10 / 71  | Lipid metabolism - Biosynthesis of steroids            |
| 11   | 0.013   | 13 / 105 | Energy metabolism - Oxidative phosphorylation          |
| 12   | 0.015   | 6 / 33   | Propanoate metabolism                                  |
| 13   | 0.017   | 10 / 75  | Mitochondrial transcription and translation factors    |
| 14   | 0.017   | 29 / 309 | Enzyme - 3.1 Acting on ester bonds                     |
| 15   | 0.018   | 8 / 54   | Carbohydrate metabolism - Pentose phosphate            |
| 16   | 0.018   | 4 / 17   | Riboflavin metabolism                                  |
| 17   | 0.021   | 3 / 10   | Replication and repair - Sulfur relay system           |
| 18   | 0.025   | 6 / 37   | Enzyme - 5.3 Intramolecular oxidoreductases            |
| 19   | 0.027   | 4 / 19   | Cofactors and vitamin metabolism - Folate biosynthesis |
| 20   | 0.028   | 17 / 165 | Transcription - Spliceosome                            |



K–Means Cluster

Spot Summary: I

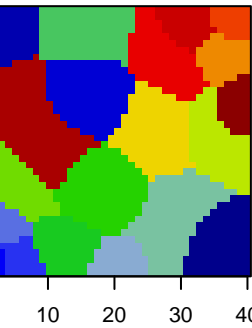
# metagenes = 109  
# genes = 1110

<r> metagenes = 0.83

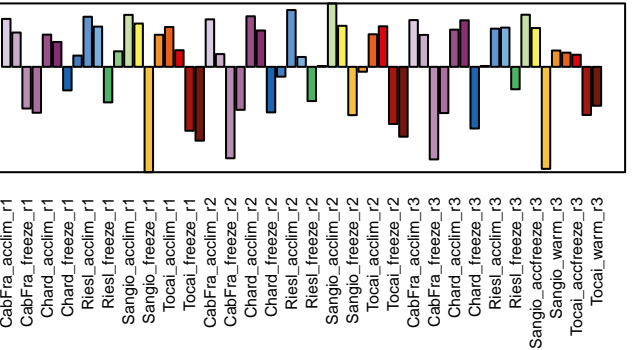
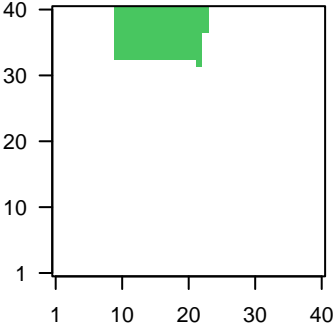
beta: r2= 3.39 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

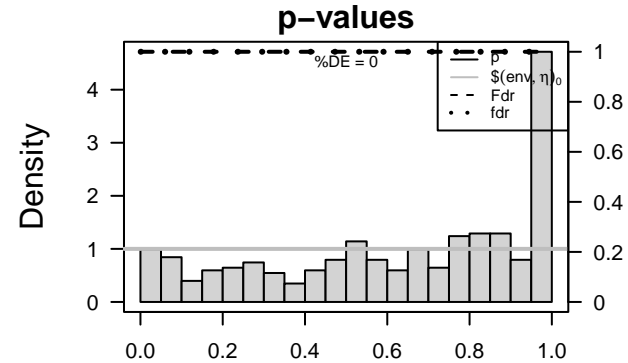


Spot Genelist

| ID            | Description   |
|---------------|---|
| Vitvi13g02110 | Binding to a protein.   |
| Vitvi00g01651 |   |
| Vitvi10g02090 |   |
| Vitvi10g00667 | Catalysis of the hydrolysis of any ester bond.  |
| Vitvi08g02122 |   |
| Vitvi05g00566 |   |
| Vitvi10g02094 |   |
| Vitvi00g01655 |   |
| Vitvi07g02092 | The initial step of transcription, consisting of the assembly of the RNA polymerase preinitiation complex (PIC) at a gene promoter, as well as the formation of the first few bonds of the RNA transcript. Transcription initiation includes abortive initiation events, which occur when the first few nucleotides are repeatedly synthesized and then released, and ends when promoter clearance takes place. |
| 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.  |
| 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.  |
| Vitvi11g01488 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.  |
| Vitvi04g01969 |   |
| 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.  |
| Vitvi15g01618 | Catalysis of the transfer of a nucleotidyl group to a reactant.   |
| Vitvi03g01162 | Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.   |
| 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.  |
| Vitvi04g00726 |   |
| Vitvi07g01734 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 6e-04   | 9 / 39   | Ubiquitin system – Ubiquitin-specific proteases (UBPs) |
| 2    | 5e-03   | 6 / 26   | Protein – Small GTPases and associated proteins        |
| 3    | 9e-03   | 8 / 48   | Transcription factors – PHD                            |
| 4    | 1e-02   | 5 / 23   | Glycosylphosphatidylinositol (GPI)-anchor biosynthesis |
| 5    | 1e-02   | 12 / 93  | Transcription factors – BHLH                           |
| 6    | 1e-02   | 15 / 128 | Ubiquitin system – Single Ring-finger type E3          |
| 7    | 2e-02   | 4 / 16   | Transcription factors – FHA                            |
| 8    | 2e-02   | 13 / 110 | Ubiquitin system – Multi subunit Ring-finger type E3   |
| 9    | 2e-02   | 18 / 170 | Transcription factors – Other zf-C3HC4                 |
| 10   | 2e-02   | 3 / 10   | Transcription factors – ZIM                            |
| 11   | 2e-02   | 12 / 100 | Plant specific signaling – Flower development          |
| 12   | 2e-02   | 5 / 27   | Common spliceosomal components                         |
| 13   | 3e-02   | 12 / 102 | Membrane transport – ABC transporters                  |
| 14   | 3e-02   | 3 / 11   | Zeatin biosynthesis                                    |
| 15   | 3e-02   | 5 / 28   | RNA polymerase III system                              |
| 16   | 3e-02   | 10 / 81  | Translation – mRNA surveillance pathway                |
| 17   | 3e-02   | 7 / 49   | Enzyme – 1.3 Acting on the CH-CH group of donors       |
| 18   | 4e-02   | 6 / 41   | Replication and repair – Nucleotide excision repair    |
| 19   | 4e-02   | 6 / 41   | Transcription – RNA polymerase                         |
| 20   | 4e-02   | 10 / 86  | Signal transduction – Calcium signaling pathway        |



K–Means Cluster

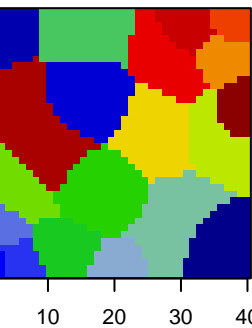
Spot Summary: J

# metagenes = 71  
# genes = 930

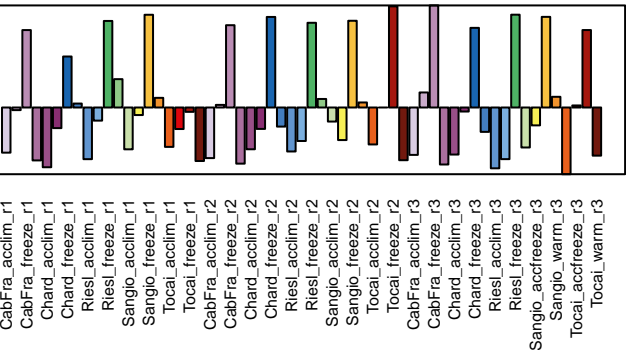
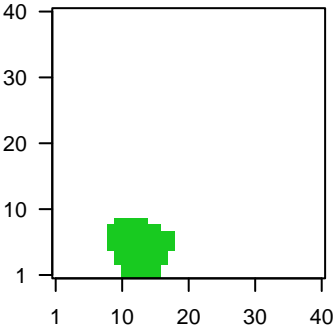
<r> metagenes = 0.93  
<r> genes = 0.49  
beta: r2= 7.42 / log p= -Inf

# samples with spot = 13 ( 22 %)  
CabFra\_freeze : 3 ( 100 %)  
Chard\_freeze : 2 ( 66.7 %)  
Riesl\_freeze : 3 ( 100 %)  
Sangio\_freeze : 3 ( 100 %)  
Tocai\_freeze : 2 ( 66.7 %)

Overview Map



Spot

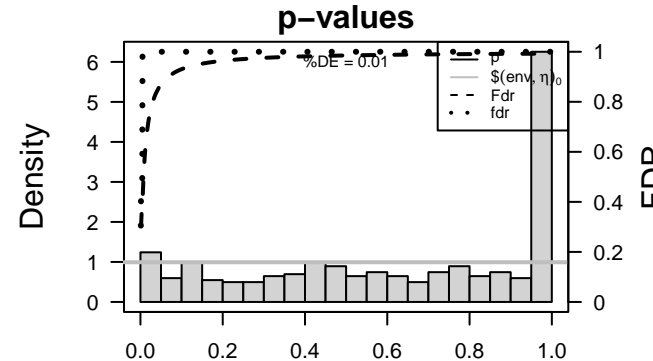


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi05g00640 | The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.  |
| Vitvi18g00993 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi06g01454 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi11g00285 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent. |
| Vitvi16g00370 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent. |
| Vitvi09g00028 | Binding to a nucleic acid.   |
| Vitvi18g02685 | Binding to a calcium ion (Ca2+).   |
| Vitvi18g02684 | Binding to a calcium ion (Ca2+).   |
| Vitvi06g00526 |  |
| Vitvi18g02683 | Binding to a calcium ion (Ca2+).   |
| Vitvi19g02040 |  |
| Vitvi02g00673 | Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).  |
| Vitvi03g00379 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| Vitvi05g00475 |  |
| Vitvi10g01879 |  |
| Vitvi11g01072 | The process in which a solute is transported across a lipid bilayer, from one side of a membrane to the other.   |
| Vitvi03g01432 |  |
| Vitvi10g01455 | Binding to ADP, adenosine 5'-diphosphate.  |
| Vitvi18g02686 |  |
| Vitvi06g00903 |  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 9e-04   | 9 / 50   | Inositol phosphate metabolism                           |
| 2    | 2e-03   | 9 / 54   | Carbohydrate metabolism – Inositol phosphate metabolism |
| 3    | 3e-03   | 4 / 13   | Kinase – CAMKL family                                   |
| 4    | 4e-03   | 13 / 111 | Hormone signaling – ABA signaling                       |
| 5    | 5e-03   | 7 / 42   | Phosphatidylinositol signaling system                   |
| 6    | 6e-03   | 7 / 43   | Transcription factors – BZIP                            |
| 7    | 7e-03   | 6 / 34   | Chaperone – HSP40 / DNAJ                                |
| 8    | 9e-03   | 5 / 26   | Transcription factors – G2-like                         |
| 9    | 1e-02   | 5 / 27   | Regulator of mitochondrial biogenesis                   |
| 10   | 1e-02   | 4 / 18   | Chaperone – HSP20                                       |
| 11   | 1e-02   | 5 / 28   | Transcription factors – Basic leucine zipper (bZIP)     |
| 12   | 2e-02   | 3 / 11   | Biosynthesis of secondary metabolism – ABA biosynthesis |
| 13   | 2e-02   | 6 / 42   | Protein export  |
| 14   | 2e-02   | 4 / 21   | Secretion system – Eukaryotic Sec-SRP protein           |
| 15   | 3e-02   | 3 / 13   | Cutin suberine and wax biosynthesis                     |
| 16   | 3e-02   | 5 / 35   | Mitophagy factors                                       |
| 17   | 3e-02   | 4 / 24   | Folate biosynthesis                                     |
| 18   | 4e-02   | 12 / 131 | Enzyme – 1.1 Acting on the CH-OH group of donors        |
| 19   | 4e-02   | 9 / 89   | MAPK signaling pathway – plant                          |
| 20   | 4e-02   | 3 / 15   | Chaperone – HSP70 / DNAK                                |



K–Means Cluster

Spot Summary: K

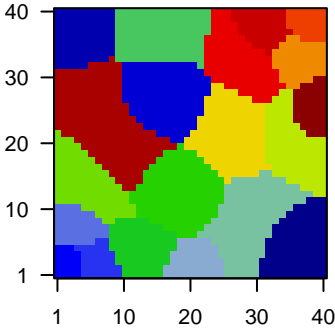
# metagenes = 128  
# genes = 1121

<r> metagenes = 0.72

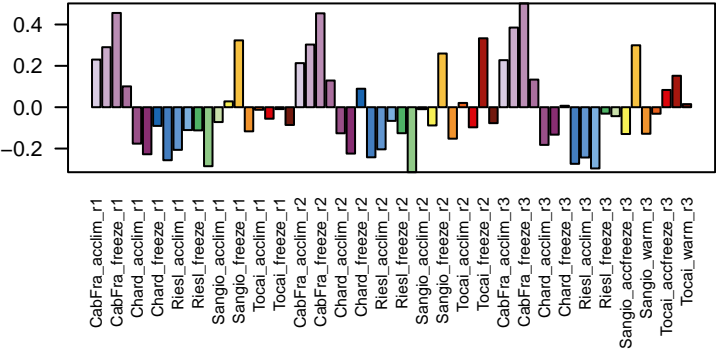
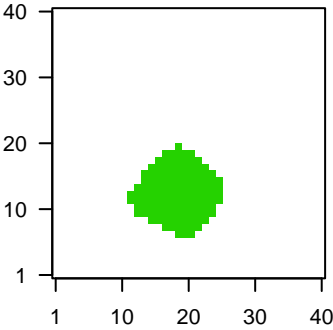
beta: r2= 2.64 / log p= -Inf

# samples with spot = 1 ( 1.7 %)  
CabFra\_freeze : 1 ( 33.3 %)

Overview Map



Spot

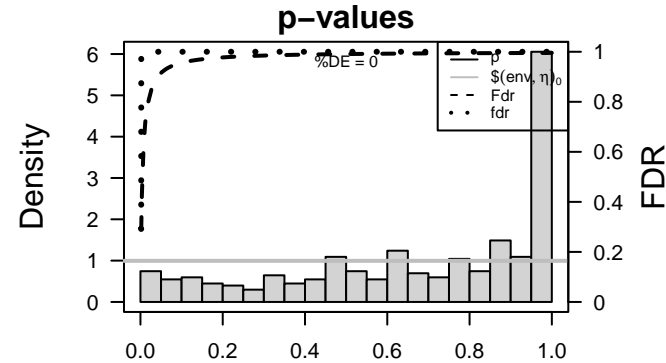


Spot Genelist

| ID            | Description   |
|---------------|---|
| Vitvi06g01714 |   |
| Vitvi01g02000 |   |
| Vitvi13g00517 | Catalysis of the transfer of an acyl group, other than amino–acyl, from one compound (donor) to another (acceptor).   |
| Vitvi01g02070 | The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.   |
| Vitvi04g00345 |   |
| Vitvi01g01998 | Catalysis of the transfer of a methyl group to an acceptor molecule.  |
| Vitvi18g01669 | Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.   |
| Vitvi16g01259 |   |
| Vitvi07g02587 |   |
| Vitvi07g00329 | Binding to ATP, adenosine 5'–triphosphate, a universally important coenzyme and enzyme regulator.   |
| Vitvi14g00149 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane. |
| Vitvi07g02578 |   |
| Vitvi18g00878 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.  |
| Vitvi00g01805 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane. |
| Vitvi12g02574 |   |
| Vitvi12g00354 |   |
| Vitvi19g01935 |   |
| Vitvi02g00524 |   |
| Vitvi12g02554 | The action of a molecule that contributes to the structural integrity of the ribosome.  |
| Vitvi12g00883 |   |

Geneset Overrepresentation

| Rank | p–value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 0.002   | 14 / 105 | Energy metabolism – Oxidative phosphorylation            |
| 2    | 0.002   | 6 / 25   | Protein – Tethering complex                              |
| 3    | 0.002   | 8 / 43   | Mitochondrial respiratory chain complex assembly factors |
| 4    | 0.003   | 16 / 139 | Spliceosome  |
| 5    | 0.008   | 6 / 33   | Carbohydrate metabolism – Butanoate metabolism           |
| 6    | 0.012   | 10 / 81  | Oxidative phosphorylation                                |
| 7    | 0.014   | 3 / 10   | Minor spliceosome components                             |
| 8    | 0.017   | 16 / 165 | Transcription – Spliceosome                              |
| 9    | 0.028   | 9 / 80   | Other components   |
| 10   | 0.030   | 6 / 44   | Proteasome   |
| 11   | 0.038   | 4 / 24   | Inner mambrane   |
| 12   | 0.043   | 4 / 25   | U4/U6.U5 tri–snRNP components                            |
| 13   | 0.043   | 4 / 25   | Transcription factors – Other zf                         |
| 14   | 0.044   | 13 / 142 | Transport system – Protein coat                          |
| 15   | 0.046   | 7 / 61   | Peroxisome   |
| 16   | 0.052   | 3 / 16   | Peptidases and inhibitors – Family T1: proteasome family |
| 17   | 0.052   | 3 / 16   | Proteasome – Core particles (20S proteasome)             |
| 18   | 0.061   | 7 / 65   | Phagosome  |
| 19   | 0.061   | 7 / 65   | Transport and catabolism – Phagosome                     |
| 20   | 0.065   | 6 / 53   | Protein – Forward pathways                               |



K–Means Cluster

Spot Summary: L

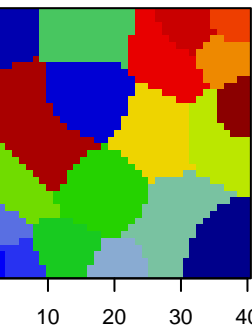
# metagenes = 91  
# genes = 1158

<r> metagenes = 0.91

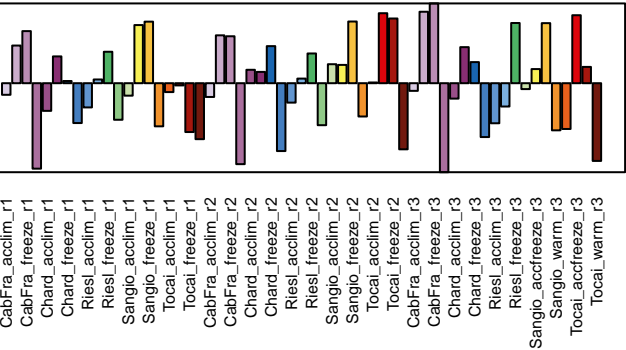
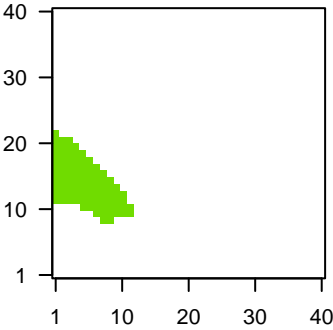
beta: r2= 6.52 / log p= -Inf

# samples with spot = 4 ( 6.8 %)  
CabFra\_accfreeze : 1 ( 33.3 %)  
CabFra\_freeze : 1 ( 33.3 %)  
Tocai\_accfreeze : 2 ( 66.7 %)

Overview Map



Spot

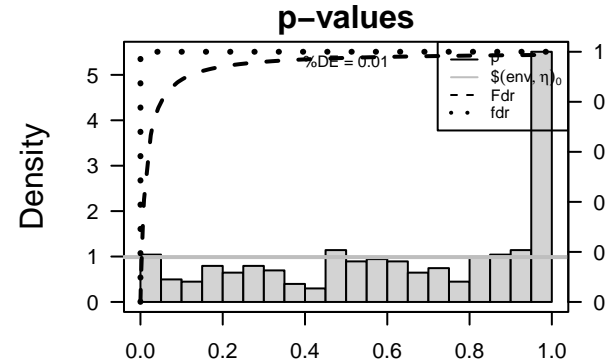


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi16g01022 | Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an abscisic acid stimulus.   |
| 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.   |
| Vitvi17g01613 | Binds to and stops, prevents or reduces the activity of an endopeptidase, any enzyme that hydrolyzes nonterminal peptide bonds in polypeptides.  |
| 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.   |
| 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.  |
| Vitvi19g00111 |  |
| Vitvi03g01517 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| Vitvi05g02238 |  |
| 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. |
| Vitvi01g00934 | Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).  |
| Vitvi13g01904 |  |
| Vitvi14g02476 |  |
| Vitvi19g00470 | Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi18g00802 | Binding to a calcium ion (Ca2+).   |
| Vitvi14g01525 |  |
| 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. |
| Vitvi13g01623 | Binding to ADP, adenosine 5'-diphosphate.  |
| Vitvi11g01683 |  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 1e-06   | 9 / 20   | Protein – Autophagosome formation proteins          |
| 2    | 2e-06   | 13 / 43  | Transcription factors – BZIP                        |
| 3    | 6e-06   | 11 / 35  | Mitophagy factors                                   |
| 4    | 1e-05   | 10 / 31  | Autophagy – other                                   |
| 5    | 2e-05   | 8 / 20   | Transport and catabolism – Regulation of autophagy  |
| 6    | 4e-05   | 9 / 28   | Transcription factors – Basic leucine zipper (bZIP) |
| 7    | 5e-04   | 14 / 80  | Transport system – Tethering factors                |
| 8    | 5e-04   | 23 / 170 | Transcription factors – Other zf–C3HC4              |
| 9    | 7e-04   | 7 / 25   | Transcription factors – Other zf                    |
| 10   | 1e-03   | 22 / 168 | Plant hormone signal transduction                   |
| 11   | 1e-03   | 18 / 128 | Ubiquitin system – Single Ring–finger type E3       |
| 12   | 7e-03   | 8 / 45   | Valine leucine and isoleucine degradation           |
| 13   | 9e-03   | 6 / 29   | Transcription factors – GRAS                        |
| 14   | 3e-02   | 11 / 89  | MAPK signaling pathway – plant                      |
| 15   | 3e-02   | 5 / 27   | Enzyme – 2.6 Transferring nitrogenous groups        |
| 16   | 3e-02   | 5 / 27   | Hormone signaling – Brassinosteroids signaling      |
| 17   | 3e-02   | 3 / 11   | Protein – SNAP–25[C] (Qc)                           |
| 18   | 3e-02   | 27 / 290 | Enzyme – 2.3 Acyltransferases                       |
| 19   | 3e-02   | 15 / 140 | Hormone signaling – Ethylene signaling              |
| 20   | 4e-02   | 3 / 12   | Channel – Cyclic nucleotide–gated channel (CNG)     |



K–Means Cluster

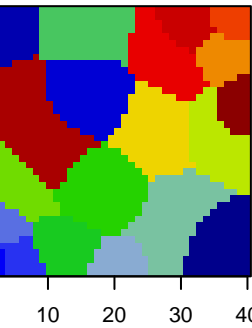
Spot Summary: M

# metagenes = 92  
# genes = 930

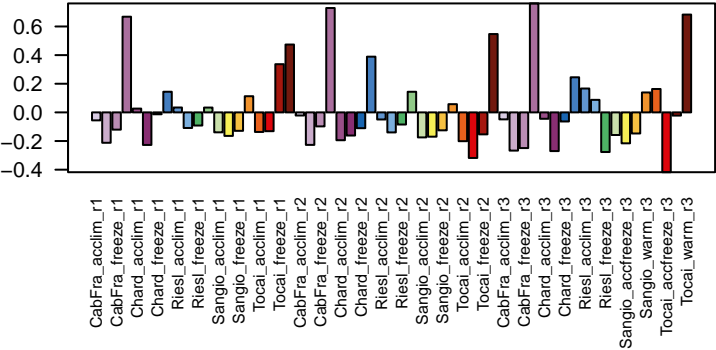
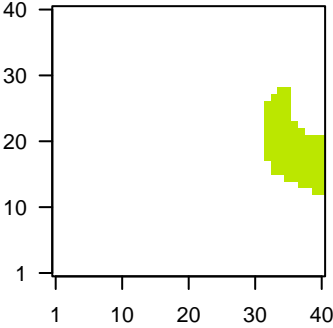
<r> metagenes = 0.86  
<r> genes = 0.41  
beta: r2= 4.68 / log p= -Inf

# samples with spot = 5 ( 8.5 %)  
CabFra\_warm : 3 ( 100 %)  
Tocai\_warm : 2 ( 66.7 %)

Overview Map



Spot

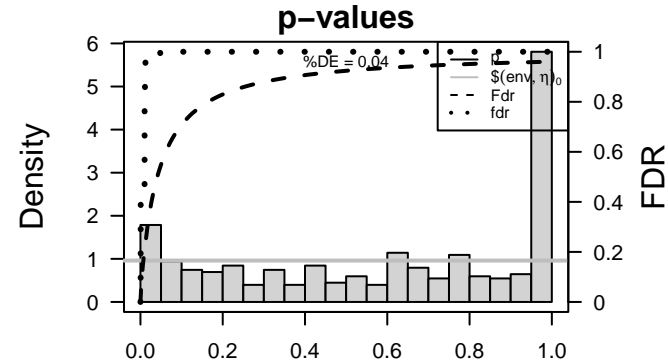


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi04g02117 | Binding to a metal ion.  |
| Vitvi04g00533 | Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).  |
| 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.   |
| Vitvi08g02147 | The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.  |
| Vitvi03g00432 |  |
| 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.   |
| Vitvi15g01582 | Catalysis of the transfer of an acyl group to an oxygen atom on the acceptor molecule.   |
| Vitvi19g00505 |  |
| Vitvi08g00175 | Binding to a calcium ion (Ca2+).   |
| 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 compo of potential pathogens.  |
| Vitvi06g00679 | Catalysis of the transfer of an acetyl group to a nitrogen atom on the acceptor molecule.  |
| 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.  |
| Vitvi03g00442 |  |
| Vitvi01g00424 | Binding to a metal ion.  |
| Vitvi17g00331 |  |
| Vitvi13g02541 | The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.  |
| Vitvi17g00231 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.   |

Geneset Overrepresentation

| Rank | p-value | #in/all   | Geneset   |
|------|---------|-----------|---|
| 1    | 1e-99   | 121 / 211 | Ribosome  |
| 2    | 1e-99   | 113 / 144 | Ribosome – Eukaryotes                                   |
| 3    | 2e-97   | 127 / 247 | Translation – Ribosome                                  |
| 4    | 4e-48   | 57 / 97   | Ribosome – Archaea                                      |
| 5    | 7e-07   | 17 / 81   | Oxidative phosphorylation                               |
| 6    | 2e-06   | 19 / 105  | Energy metabolism – Oxidative phosphorylation           |
| 7    | 6e-06   | 10 / 34   | Matrix  |
| 8    | 4e-05   | 10 / 41   | Transporter catalog – Primary active transporter cat D1 |
| 9    | 3e-04   | 14 / 94   | Nucleotide metabolism – Purine metabolism               |
| 10   | 4e-04   | 11 / 64   | Purine metabolism                                       |
| 11   | 6e-04   | 12 / 77   | Cysteine and methionine metabolism                      |
| 12   | 2e-03   | 9 / 54    | Amino acid metabolism – Methionine metabolism           |
| 13   | 3e-03   | 15 / 131  | Enzyme – 1.1 Acting on the CH-OH group of donors        |
| 14   | 6e-03   | 13 / 113  | Exosome – Exosomal proteins of colorectal cancer cells  |
| 15   | 7e-03   | 9 / 66    | Exosome – Exosomal proteins of bladder cancer cells     |
| 16   | 8e-03   | 9 / 67    | Ribosome – Bacteria                                     |
| 17   | 1e-02   | 6 / 36    | Phenylalanine tyrosine and tryptophan biosynthesis      |
| 18   | 1e-02   | 6 / 36    | Enzyme – 6.3 Forming carbon-nitrogen bonds              |
| 19   | 1e-02   | 4 / 17    | Riboflavin metabolism                                   |
| 20   | 1e-02   | 9 / 72    | Energy metabolism – Carbon fixation                     |



K–Means Cluster

Spot Summary: N

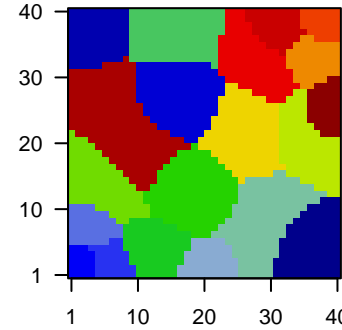
# metagenes = 121  
# genes = 1114

<r> metagenes = 0.63

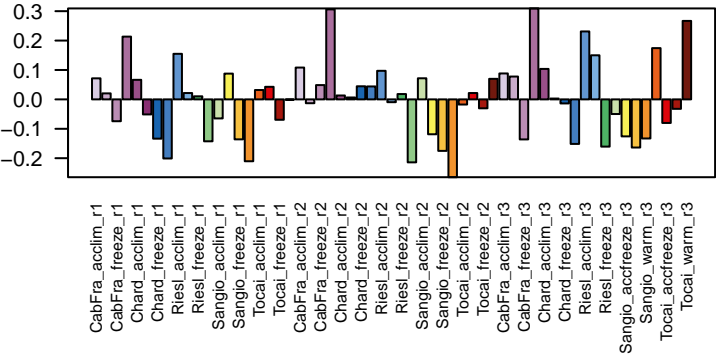
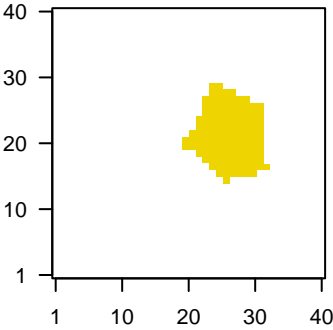
beta: r2= 1.27 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

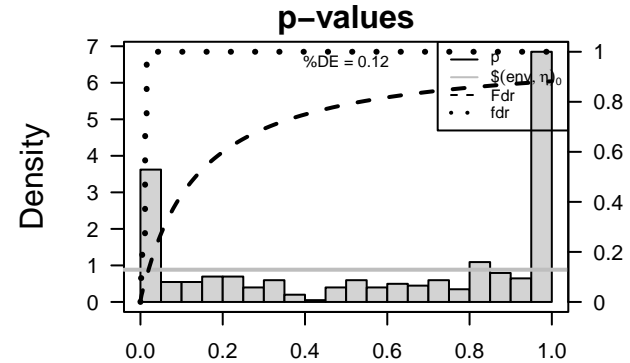


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi09g00285 | Catalysis of an oxidation–reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.  |
| Vitvi15g01503 | Catalysis of an oxidation–reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.  |
| Vitvi17g00820 | Binding to a zinc ion (Zn).  |
| Vitvi11g00950 |  |
| Vitvi06g01650 |  |
| Vitvi17g01556 |  |
| Vitvi10g01613 | Binding to ATP;adenosine 5′–triphosphate, a universally important coenzyme and enzyme regulator.   |
| 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.  |
| Vitvi07g01880 | The action of a molecule that contributes to the structural integrity of the ribosome.   |
| Vitvi00g00589 |  |
| Vitvi12g02375 |  |
| Vitvi08g02357 | 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. |
| Vitvi12g02389 | Catalysis of the transfer of a methyl group to the oxygen atom of an acceptor molecule.  |
| Vitvi11g00156 | A membrane–bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell’s chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.   |
| 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.   |
| Vitvi14g00012 |  |
| Vitvi03g00392 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| 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.  |

Geneset Overrepresentation

| Rank | p–value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 3e–11   | 18 / 42  | Folding sorting degradation – Proteasome                  |
| 2    | 3e–11   | 22 / 64  | Ribosome biogenesis in eukaryotes                         |
| 3    | 7e–11   | 18 / 44  | Proteasome  |
| 4    | 8e–10   | 28 / 116 | Ribosome biogenesis – Pre–60S particles                   |
| 5    | 1e–09   | 22 / 75  | Translation – Ribosome biogenesis in Eukaryotes           |
| 6    | 7e–09   | 10 / 16  | Peptidases and inhibitors – Family T1: proteasome family  |
| 7    | 7e–09   | 10 / 16  | Proteasome – Core particles (20S proteasome)              |
| 8    | 6e–08   | 31 / 165 | Transcription – Spliceosome                               |
| 9    | 5e–07   | 38 / 247 | Translation – Ribosome                                    |
| 10   | 8e–07   | 26 / 139 | Spliceosome   |
| 11   | 6e–06   | 7 / 13   | Chaperone – HSP60 / Chaperonin                            |
| 12   | 1e–05   | 31 / 211 | Ribosome  |
| 13   | 2e–05   | 12 / 44  | Replication protein – DNA Replication Termination Factors |
| 14   | 2e–05   | 15 / 66  | Exosome – Exosomal proteins of bladder cancer cells       |
| 15   | 2e–05   | 17 / 83  | RNA degradation   |
| 16   | 5e–05   | 15 / 72  | Ribosome – Mitochondria/ Chloroplast                      |
| 17   | 5e–05   | 21 / 126 | Translation – RNA transport                               |
| 18   | 8e–05   | 14 / 67  | Replication and repair – RNA degradation                  |
| 19   | 9e–05   | 8 / 24   | Primary active transporters [TC:3]                        |
| 20   | 1e–04   | 19 / 113 | Exosome – Exosomal proteins of colorectal cancer cells    |





K–Means Cluster

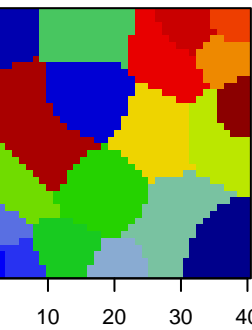
Spot Summary: O

# metagenes = 47  
# genes = 653

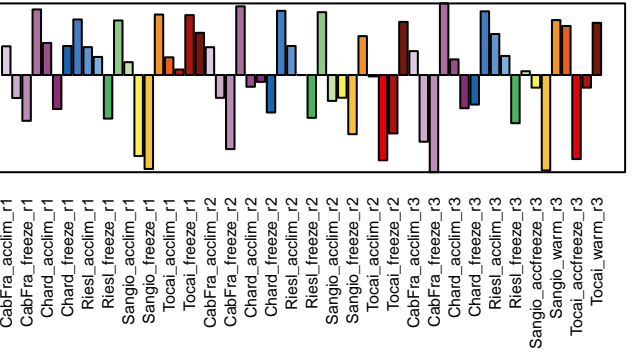
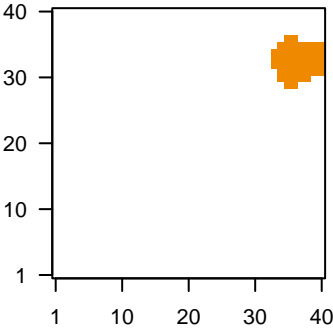
<r> metagenes = 0.96  
<r> genes = 0.62  
beta: r2= 16.67 / log p= -Inf

# samples with spot = 14 ( 23.7 %)  
CabFra\_warm : 3 ( 100 %)  
Chard\_warm : 3 ( 100 %)  
Riesl\_warm : 2 ( 100 %)  
Sangio\_warm : 2 ( 66.7 %)  
Tocai\_acclim : 1 ( 33.3 %)  
Tocai\_freeze : 1 ( 33.3 %)  
Tocai\_warm : 2 ( 66.7 %)

Overview Map



Spot

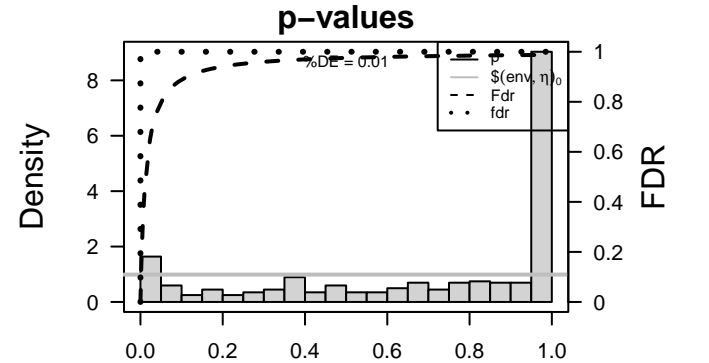


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi19g02024 |  |
| Vitvi15g01693 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi01g00441 | Catalysis of the transfer of a methyl group to an acceptor molecule.   |
| Vitvi13g02009 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).                               |
| Vitvi13g02008 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a catalytic mechanism that involves a catalytic triad consisting of a serine nucleophile that is activated by a proton relay involving an acidic residue (e.g. aspartate or glutamate) and a basic residue (usually histidine).                               |
| Vitvi06g01410 |  |
| Vitvi05g01577 | The chemical reactions and pathways involving carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.  |
| Vitvi03g01503 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi03g01500 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi03g00227 | A membrane-bound 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. |
| Vitvi03g00221 | Binding to ATP, adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi15g01663 | Binding to ADP, adenosine 5'-diphosphate.  |
| Vitvi03g00134 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi15g00804 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| Vitvi05g01478 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi02g00125 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.   |
| Vitvi09g00040 | Catalysis of the hydrolysis of any ester bond.   |
| Vitvi03g01621 | Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).  |
| Vitvi13g02416 | Binding to a calcium ion (Ca2+).   |
| Vitvi11g01437 |  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 3e-16   | 23 / 67  | Ribosome – Bacteria   |
| 2    | 2e-15   | 23 / 72  | Ribosome – Mitochondria/ Chloroplast                        |
| 3    | 5e-08   | 16 / 78  | Energy metabolism – Photosynthesis                          |
| 4    | 1e-07   | 11 / 38  | Photosynthesis  |
| 5    | 1e-06   | 11 / 47  | Transporter catalog – Transport electron carriers           |
| 6    | 3e-06   | 10 / 41  | Porphyrin metabolism  |
| 7    | 3e-05   | 22 / 211 | Ribosome  |
| 8    | 4e-05   | 6 / 18   | Energy metabolism – Photosynthesis antenna proteins         |
| 9    | 1e-04   | 13 / 97  | Ribosome – Archaea  |
| 10   | 1e-04   | 23 / 247 | Translation – Ribosome                                      |
| 11   | 5e-04   | 8 / 48   | Lipid metabolism – Fatty acid biosynthesis                  |
| 12   | 5e-04   | 5 / 18   | Photosynthesis – antenna proteins                           |
| 13   | 9e-04   | 5 / 20   | Lipid metabolism – Biosynthesis of unsaturated fatty acids  |
| 14   | 1e-03   | 6 / 31   | Fatty acid biosynthesis                                     |
| 15   | 2e-03   | 5 / 24   | Carbohydrate metabolism – Ascorbate and aldarate metabolism |
| 16   | 3e-03   | 5 / 26   | Steroid biosynthesis  |
| 17   | 3e-03   | 9 / 78   | Glycosyltransferase – Structural polysaccharide             |
| 18   | 6e-03   | 4 / 19   | Transcription factors – AUXIAA                              |
| 19   | 6e-03   | 5 / 30   | Lipid biosynthesis protein – Component type                 |
| 20   | 6e-03   | 3 / 10   | Photosynthesis protein – Photosystem I (P700 chlorophyll a) |



K–Means Cluster

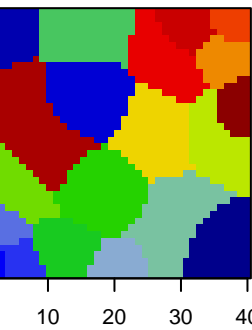
Spot Summary: P

# metagenes = 27  
# genes = 564

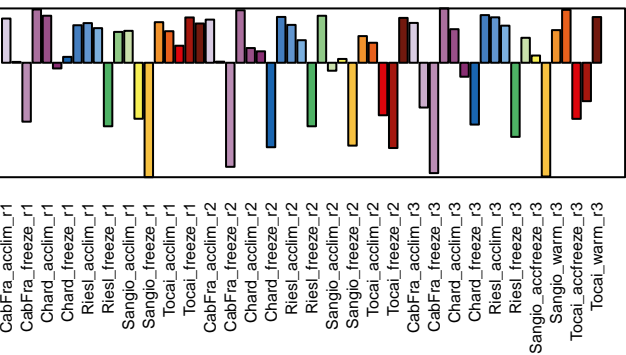
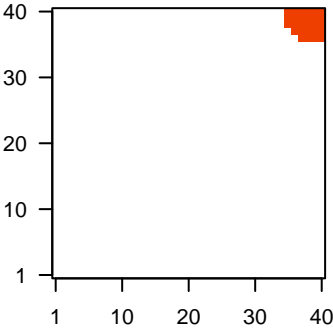
<r> metagenes = 0.98  
<r> genes = 0.76  
beta: r2= 46.75 / log p= -Inf

# samples with spot = 28 ( 47.5 %)  
CabFra\_acclim : 3 ( 100 %)  
CabFra\_warm : 3 ( 100 %)  
Chard\_acclim : 2 ( 66.7 %)  
Chard\_warm : 3 ( 100 %)  
Riesl\_acclim : 3 ( 100 %)  
Riesl\_accfreeze : 2 ( 66.7 %)  
Riesl\_warm : 2 ( 100 %)  
Sangio\_acclim : 1 ( 33.3 %)  
Sangio\_warm : 3 ( 100 %)  
Tocai\_acclim : 2 ( 66.7 %)

Overview Map



Spot

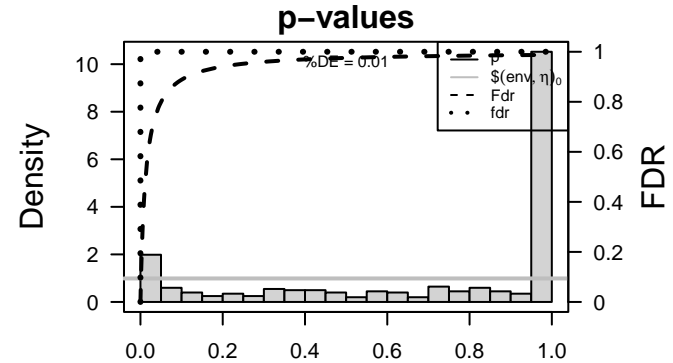


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi14g01929 | The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.  |
| Vitvi09g01282 | Functions in the storage of nutritious substrates.   |
| Vitvi13g00172 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite. |
| Vitvi17g01251 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite. |
| Vitvi13g01337 | Catalysis of the hydrolysis of internal, alpha-peptide bonds in a polypeptide chain by a mechanism in which a water molecule bound by the side chains of aspartic residues at the active center acts as a nucleophile.   |
| Vitvi06g01346 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi19g00680 | Binding to a metal ion.  |
| Vitvi10g01636 |  |
| Vitvi17g00601 |  |
| Vitvi00g02243 |  |
| Vitvi17g00977 | Binding to a metal ion.  |
| Vitvi01g00816 | Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.                                      |
| Vitvi07g01844 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi19g00008 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi13g01788 |  |
| Vitvi01g00593 | Binding to a metal ion.  |
| Vitvi12g02394 |  |
| Vitvi14g03084 |  |
| Vitvi01g01030 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite. |
| Vitvi05g00067 | Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.                                      |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 4e-22   | 43 / 206 | Cell growth and death – Cell wall                           |
| 2    | 5e-15   | 18 / 47  | Transporter catalog – Transport electron carriers           |
| 3    | 2e-12   | 11 / 18  | Photosynthesis – antenna proteins                           |
| 4    | 2e-12   | 11 / 18  | Energy metabolism – Photosynthesis antenna proteins         |
| 5    | 3e-09   | 12 / 38  | Photosynthesis  |
| 6    | 6e-09   | 7 / 10   | Photosynthesis protein – Photosystem I (P700 chlorophyll a) |
| 7    | 6e-09   | 16 / 78  | Energy metabolism – Photosynthesis                          |
| 8    | 3e-06   | 13 / 80  | Cytoskeleton – Microtubules                                 |
| 9    | 5e-06   | 22 / 217 | Cell motility – Regulation of actin cytoskeleton            |
| 10   | 1e-05   | 5 / 10   | Peptidases and inhibitors – Family A1: pepsin family        |
| 11   | 3e-05   | 15 / 129 | Enzyme – 3.2 Glycosylases                                   |
| 12   | 4e-05   | 8 / 39   | Pentose and glucuronate interconversions                    |
| 13   | 5e-05   | 8 / 40   | Transport system – Thylakoid targeting pathway              |
| 14   | 4e-04   | 7 / 41   | Porphyrin metabolism  |
| 15   | 4e-04   | 6 / 30   | Glycan biosynthesis and metabolism – N-Glycan degradation   |
| 16   | 7e-04   | 13 / 134 | Hormone signaling – Auxin signaling                         |
| 17   | 2e-03   | 5 / 26   | Steroid biosynthesis  |
| 18   | 3e-03   | 4 / 19   | Aquaporins and small neutral solute transporters [TC:1.A.8] |
| 19   | 5e-03   | 7 / 63   | Phenylpropanoid biosynthesis                                |
| 20   | 5e-03   | 5 / 34   | Peptidases and inhibitors – Family S10                      |



K–Means Cluster

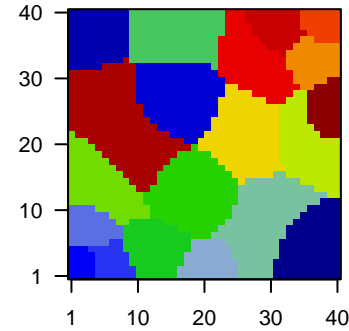
Spot Summary: Q

# metagenes = 95  
# genes = 885

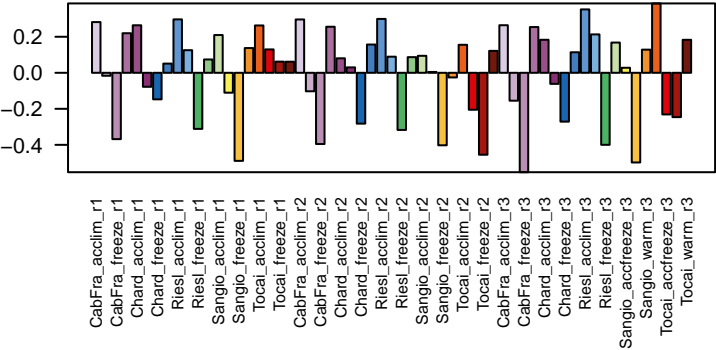
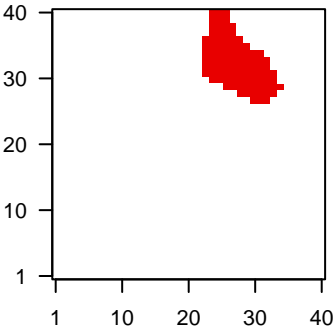
<r> metagenes = 0.89  
<r> genes = 0.37  
beta: r2= 4.35 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

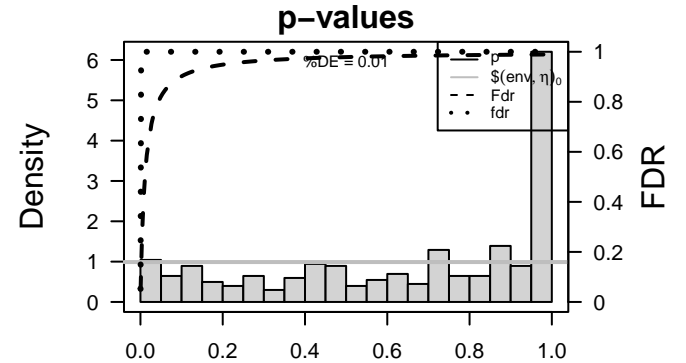


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi09g01553 |  |
| 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. |
| Vitvi07g02067 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent. |
| Vitvi19g00109 |  |
| Vitvi05g01450 | Binding to a protein.  |
| 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.   |
| Vitvi19g01854 | Catalysis of the transfer of a glycosyl group from a UDP-sugar to a small hydrophobic molecule.  |
| 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.  |
| 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.  |
| Vitvi09g00448 | Binding to a metal ion.  |
| Vitvi09g00246 |  |
| Vitvi18g01063 |  |
| Vitvi14g02049 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent. |
| Vitvi17g00427 | Catalysis of the reaction: H2O + L-arginyl- + NH4+, resulting in citrullination of the target protein. This reaction is calcium-dependent.   |
| Vitvi08g01656 | The chemical reactions and pathways resulting in the formation of substances; typically the energy-requiring part of metabolism in which simpler substances are transformed into more complex ones.  |
| Vitvi14g02885 |  |
| Vitvi18g01605 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi14g02888 | 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.   |
| Vitvi04g02062 | Growth of pollen via tip extension of the intine wall.   |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset   |
|------|---------|---------|---|
| 1    | 1e-04   | 6 / 17  | One carbon pool by folate                                 |
| 2    | 3e-04   | 9 / 43  | Aminoacyl-tRNA synthetases (AARs)                         |
| 3    | 4e-04   | 6 / 20  | tRNA modification factors                                 |
| 4    | 7e-04   | 9 / 48  | Aminoacyl-tRNA biosynthesis                               |
| 5    | 2e-03   | 8 / 44  | Enzyme - 6.1 Forming carbon-oxygen bonds                  |
| 6    | 3e-03   | 6 / 28  | Transcription factors - MTERF                             |
| 7    | 4e-03   | 9 / 62  | Translation - Aminoacyl-tRNA biosynthesis                 |
| 8    | 8e-03   | 4 / 16  | Repair protein - SSBR (single strand breaks repair)       |
| 9    | 1e-02   | 3 / 10  | Kinase - Wnk family                                       |
| 10   | 1e-02   | 3 / 10  | Transcription factors - C2C2-CO                           |
| 11   | 2e-02   | 5 / 29  | Base excision repair                                      |
| 12   | 3e-02   | 3 / 13  | Selenocompound metabolism                                 |
| 13   | 3e-02   | 3 / 13  | Protein - Lipid raft mediated endocytosis                 |
| 14   | 3e-02   | 5 / 34  | Carbohydrate metabolism - Nucleotide sugars metabolism    |
| 15   | 3e-02   | 5 / 34  | Transcription factors - SET PCG                           |
| 16   | 3e-02   | 7 / 58  | Carbohydrate metabolism - Fructose and mannose metabolism |
| 17   | 3e-02   | 3 / 14  | GTP-binding proteins - Arf/Sar Family                     |
| 18   | 4e-02   | 4 / 25  | Protein - Calcium ion-dependent exocytosis                |
| 19   | 4e-02   | 8 / 75  | Mitochondrial transcription and translation factors       |
| 20   | 5e-02   | 8 / 78  | Glycosyltransferase - Structural polysaccharide           |



K–Means Cluster

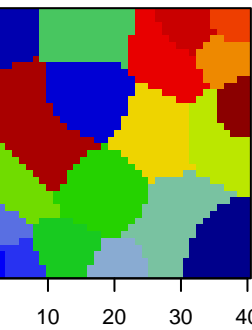
Spot Summary: R

# metagenes = 42  
# genes = 629

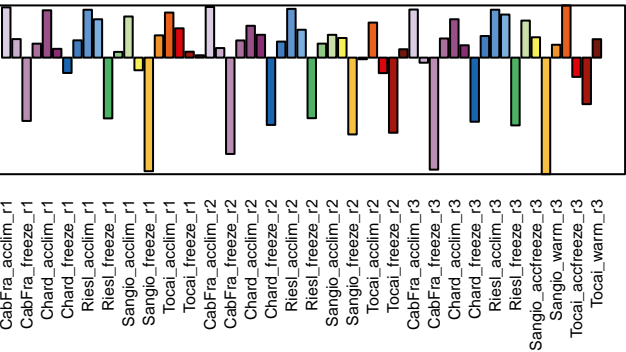
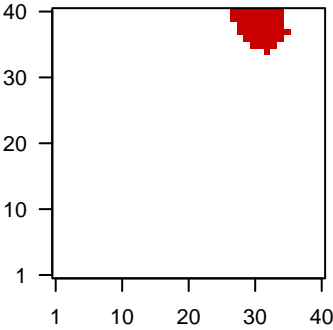
<r> metagenes = 0.96  
<r> genes = 0.61  
beta: r2= 15.59 / log p= -Inf

# 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

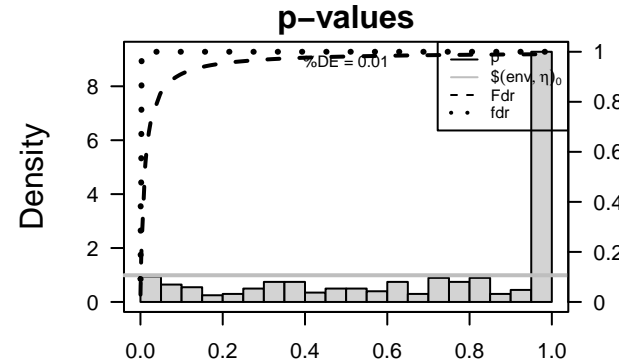


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi02g00532 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.   |
| Vitvi02g01239 |  |
| Vitvi15g01388 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi16g01176 |  |
| Vitvi14g03036 | Binding to a zinc ion (Zn).  |
| Vitvi04g01221 | A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it.  |
| Vitvi18g03009 |  |
| Vitvi10g01138 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| Vitvi10g02114 |  |
| Vitvi00g01861 |  |
| Vitvi18g00473 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.   |
| Vitvi14g01641 | The formation of the principal food-conducting tissue of a vascular plant.   |
| Vitvi18g01848 |  |
| Vitvi17g00750 |  |
| Vitvi05g01940 |  |
| 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.   |
| Vitvi14g02469 |  |
| Vitvi08g00827 | The chemical reactions and pathways involving lipids, compounds soluble in an organic solvent but not, or sparingly, in an aqueous solvent. Includes fatty acids; neutral fats, other fatty-acid esters, and soaps; long-chain (fatty) alcohols and waxes; sphingoids and other long-chain bases; glycolipids, phospholipids and sphingolipids; and carotenes, polyprenols, sterols, terpenes and other isoprenoids. |
| Vitvi06g00626 | Binding to ATP; adenosine 5'-triphosphate, a universally important coenzyme and enzyme regulator.  |
| Vitvi17g00046 | The formation of a protein dimer, a macromolecular structure consists of two noncovalently associated identical or nonidentical subunits.  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 7e-05   | 21 / 217 | Cell motility – Regulation of actin cytoskeleton     |
| 2    | 4e-04   | 5 / 18   | Transcription factors – ARF                          |
| 3    | 5e-04   | 4 / 11   | Transcription factors – GRF                          |
| 4    | 2e-03   | 15 / 168 | Plant hormone signal transduction                    |
| 5    | 3e-03   | 9 / 79   | Transporter catalog – Porters cat 30 to 64           |
| 6    | 3e-03   | 9 / 80   | Cytoskeleton – Microtubules                          |
| 7    | 1e-02   | 3 / 13   | Transcription factors – TCP                          |
| 8    | 1e-02   | 4 / 24   | Enzyme – 7.1 Catalysing the translocation of hydrons |
| 9    | 1e-02   | 7 / 66   | Exosome – Exosomal proteins of bladder cancer cells  |
| 10   | 1e-02   | 11 / 134 | Hormone signaling – Auxin signaling                  |
| 11   | 2e-02   | 6 / 54   | Carbohydrate metabolism – Pentose phosphate          |
| 12   | 2e-02   | 3 / 15   | Transcription factors – C2C2–GATA                    |
| 13   | 2e-02   | 3 / 16   | Biotin metabolism                                    |
| 14   | 2e-02   | 9 / 111  | Transporter catalog – Porters cat 66 to 94           |
| 15   | 2e-02   | 3 / 17   | Kinase – IRAK family                                 |
| 16   | 3e-02   | 7 / 78   | Glycosyltransferase – Structural polysaccharide      |
| 17   | 5e-02   | 3 / 22   | Fatty acid elongation                                |
| 18   | 5e-02   | 3 / 22   | Transcription factors – C2C2–DOF                     |
| 19   | 5e-02   | 10 / 146 | Transporter catalog – Porters cat 7 to 17            |
| 20   | 5e-02   | 4 / 38   | Hormone transport – Auxin transport                  |



K–Means Cluster

Spot Summary: S

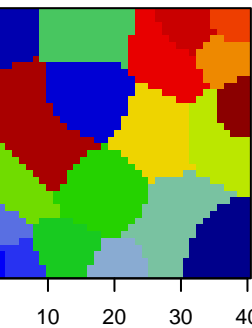
# metagenes = 183  
# genes = 1854

<r> metagenes = 0.66

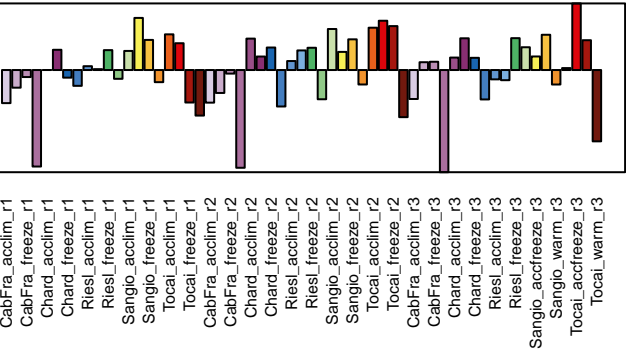
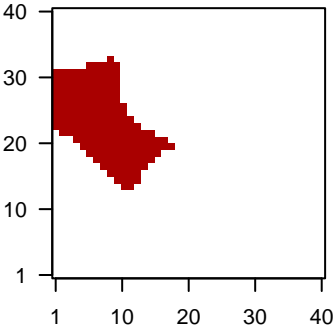
beta: r2= 2.27 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

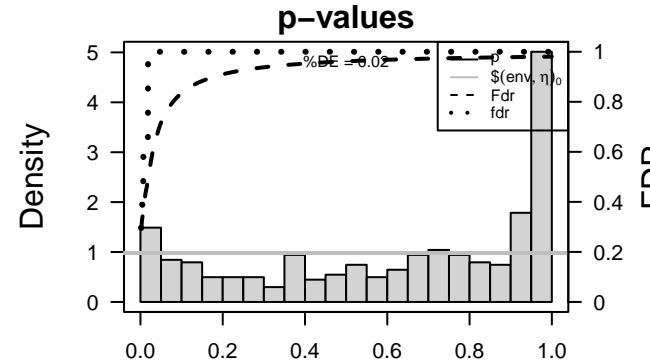


Spot Genelist

| ID            | Description  |
|---------------|--|
| Vitvi14g01318 | Catalysis of the hydrolysis of any ester bond.   |
| Vitvi14g02722 | Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid).  |
| Vitvi15g01643 |  |
| Vitvi12g00368 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi07g00516 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| Vitvi13g00807 | Binding to a protein.  |
| Vitvi19g00283 | Binding to a nucleotide, any compound consisting of a nucleoside that is esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the ribose or deoxyribose.   |
| Vitvi14g02924 | Any intracellular signal transduction in which the signal is passed on within the cell via calcium ions.   |
| Vitvi04g01352 | Binding to a heme, a compound composed of iron complexed in a porphyrin (tetrapyrrole) ring.   |
| Vitvi04g00352 |  |
| Vitvi10g00365 | Binding to a protein.  |
| Vitvi12g02236 |  |
| Vitvi03g01481 | The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.   |
| Vitvi17g01380 | The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures.  |
| Vitvi13g00410 | Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus indicating an increase or decrease in the concentration of salt (particularly but not exclusively sodium and chloride ions) in the environment. |
| Vitvi04g00282 | The membrane surrounding a cell that separates the cell from its external environment. It consists of a phospholipid bilayer and associated proteins.  |
| Vitvi15g01075 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| Vitvi15g01073 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.  |
| 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.  |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset  |
|------|---------|----------|--|
| 1    | 0.002   | 58 / 409 | Enzyme – 2.7 Transferring phosphorus-containing groups |
| 2    | 0.002   | 25 / 142 | Transport system – Protein coat                        |
| 3    | 0.002   | 8 / 26   | Transcription factors – Orphans FAR-RED                |
| 4    | 0.004   | 8 / 28   | Viral life cycle – HIV-1                               |
| 5    | 0.005   | 25 / 151 | RNA polymerase II system                               |
| 6    | 0.005   | 13 / 62  | Ribosome biogenesis – 90S particles                    |
| 7    | 0.007   | 11 / 50  | Transcription factors – MYBrelated                     |
| 8    | 0.007   | 41 / 290 | Enzyme – 2.3 Acyltransferases                          |
| 9    | 0.009   | 15 / 81  | Translation – mRNA surveillance pathway                |
| 10   | 0.011   | 4 / 10   | Kinase – Wnk family                                    |
| 11   | 0.012   | 17 / 99  | mRNA surveillance pathway                              |
| 12   | 0.017   | 7 / 29   | Various types of N-glycan biosynthesis                 |
| 13   | 0.018   | 19 / 119 | Endocytosis  |
| 14   | 0.019   | 5 / 17   | Protein – Arf GTPases and associated proteins          |
| 15   | 0.019   | 5 / 17   | Protein – SNARE associated proteins                    |
| 16   | 0.019   | 5 / 17   | Signal transduction – mTOR signaling pathway           |
| 17   | 0.019   | 20 / 128 | Ubiquitin system – Single Ring-finger type E3          |
| 18   | 0.024   | 10 / 52  | Transport and catabolism – Peroxisome                  |
| 19   | 0.025   | 7 / 31   | Autophagy – other                                      |
| 20   | 0.025   | 8 / 38   | Protein – Clathrin-mediated endocytosis                |



K–Means Cluster

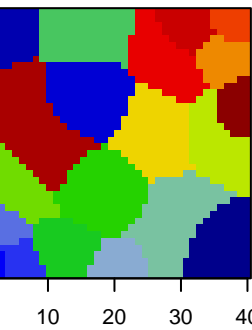
Spot Summary: T

# metagenes = 38  
# genes = 514

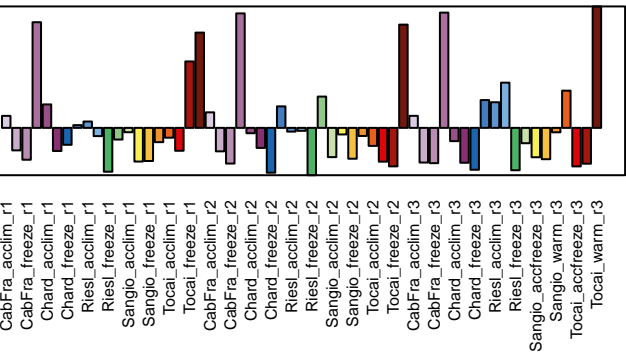
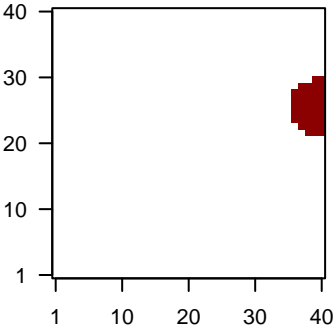
<r> metagenes = 0.97  
<r> genes = 0.66  
beta: r2= 24.64 / log p= -Inf

# samples with spot = 10 ( 16.9 %)  
CabFra\_warm : 3 ( 100 %)  
Riesl\_accfreeze : 1 ( 33.3 %)  
Riesl\_warm : 1 ( 50 %)  
Tocai\_acclim : 1 ( 33.3 %)  
Tocai\_freeze : 1 ( 33.3 %)  
Tocai\_warm : 3 ( 100 %)

Overview Map



Spot



Spot Genelist

| ID            | Description   |
|---------------|---|
| Vitvi03g00752 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.  |
| Vitvi18g02927 | The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non-living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.                            |
| Vitvi11g01227 | Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).   |
| Vitvi11g01222 | Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).   |
| Vitvi07g02007 | Reactions, triggered in response to the presence of a foreign body or the occurrence of an injury, which result in restriction of damage to the organism attacked or prevention/recovery from the infection caused by the attack.   |
| Vitvi01g00742 | Catalysis of an oxidation-reduction (redox) reaction, a reversible chemical reaction in which the oxidation state of an atom or atoms within a molecule is altered. One substrate acts as a hydrogen or electron donor and becomes oxidized, while the other acts as hydrogen or electron acceptor and becomes reduced.   |
| Vitvi07g02362 | The space external to the outermost structure of a cell. For cells without external protective or external encapsulating structures this refers to space outside of the plasma membrane. This term covers the host cell environment outside an intracellular parasite.  |
| Vitvi18g01488 | The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non-living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.                            |
| Vitvi11g01224 | Catalysis of the transfer of an acyl group, other than amino-acyl, from one compound (donor) to another (acceptor).   |
| Vitvi04g00312 | Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzyme possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic. |
| Vitvi13g01768 |   |
| Vitvi18g02991 |   |
| Vitvi04g02223 |   |
| Vitvi12g00025 | The component of a membrane consisting of the gene products and protein complexes having at least some part of their peptide sequence embedded in the hydrophobic region of the membrane.   |
| Vitvi07g02097 | A membrane-bounded organelle of eukaryotic cells in which chromosomes are housed and replicated. In most cells, the nucleus contains all of the cell's chromosomes except the organellar chromosomes, and is the site of RNA synthesis and processing. In some species, or in specialized cell types, RNA metabolism or DNA replication may be absent.  |
| Vitvi18g02928 | The cell membranes and intracellular regions in a plant are connected through plasmodesmata, and plants may be describe as having two major compartments: the living symplast and the non-living apoplast. The apoplast is external to the plasma membrane and includes cell walls, intercellular spaces and the lumen of dead structures such as xylem vessels. Water and solutes pass freely through it.                            |
| Vitvi14g02893 |   |
| Vitvi12g00722 | Binding to nicotinamide-adenine dinucleotide phosphate, a coenzyme involved in many redox and biosynthetic reactions; binding may be to either the oxidized form, NADP+, or the reduced form, NADPH.  |
| Vitvi06g00433 |   |
| Vitvi03g00593 |   |

Geneset Overrepresentation

| Rank | p-value | #in/all  | Geneset   |
|------|---------|----------|---|
| 1    | 2e-25   | 45 / 219 | Cell growth and death – Cell cycle                        |
| 2    | 5e-17   | 23 / 80  | Cytoskeleton – Microtubules                               |
| 3    | 1e-16   | 35 / 217 | Cell motility – Regulation of actin cytoskeleton          |
| 4    | 2e-14   | 13 / 24  | Replication protein – DNA Replication Initiation Factors  |
| 5    | 1e-11   | 13 / 36  | DNA replication   |
| 6    | 8e-11   | 13 / 41  | Replication and repair – DNA replication                  |
| 7    | 4e-05   | 8 / 44   | Replication protein – DNA Replication Termination Factors |
| 8    | 6e-04   | 4 / 14   | Cilium and associated proteins – Stereociliary proteins   |
| 9    | 7e-04   | 7 / 51   | Other metabolism – Single reactions                       |
| 10   | 3e-03   | 8 / 83   | Transcription factors – MYB                               |
| 11   | 4e-03   | 5 / 37   | Homologous recombination                                  |
| 12   | 6e-03   | 4 / 25   | Replication and repair – Base excision repair             |
| 13   | 6e-03   | 3 / 13   | Transcription factors – HMG                               |
| 14   | 7e-03   | 4 / 27   | Mismatch repair   |
| 15   | 1e-02   | 4 / 29   | Base excision repair                                      |
| 16   | 1e-02   | 5 / 48   | Pyrimidine metabolism                                     |
| 17   | 2e-02   | 4 / 34   | Peptidases and inhibitors – Family S10                    |
| 18   | 2e-02   | 6 / 71   | Glutathione metabolism                                    |
| 19   | 2e-02   | 12 / 206 | Cell growth and death – Cell wall                         |
| 20   | 2e-02   | 4 / 37   | Chaperone – Protein disulfide isomerase                   |

