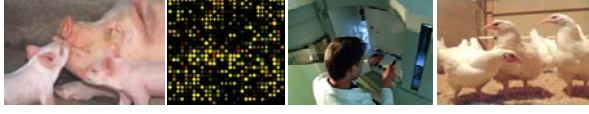


EADGENE **SABRE**
 CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

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Biological pathway analysis by ArrayUnlock and IPA

María Ramirez Boo, Cristina Arce Jiménez, Melania Collado Romero, Ángeles Jiménez Marín and Juan José Garrido Pavón
 University of Cordoba

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OVERVIEW

- Sub-project "Integration of the differentially expressed genes into biological pathways"(Group Leader-Jakob Hedegaard):
 - Data set 1: Chicken infection data
 - Summary Results

	MM8.PM8	MM8.MA8	MM8.MM24
-1	806	62	648
0	11428	13073	12358
1	924	23	152

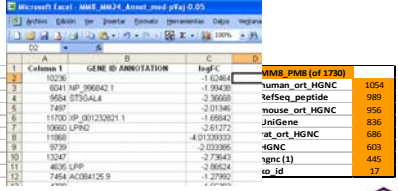
- Filter 0.05 cutoff values for adjusted p-values

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Working file

- The working file has one column with the higher number of genes ID annotation identified by softwares
 - ArrayUnlock
 - IPA



MM8_MAB (of 85)	RefSeq_peptide	human_ort_HGNC	mouse_ort_HGNC	UniGene	rat_ort_HGNC	HGNC	Hgnc (3)	bo_id
42	41	38	36	26	23	17	1	

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ArrayUnlock ArrayUnlock™ Rule your data, free the knowledge

OVERVIEW

- ArrayUnlock™ is an advanced data analysis tool, designed by Integromics to extract biological knowledge from gene expression data.
- ArrayUnlock™ allows the user to explore gene expression datasets or large gene lists in order to find the main biological processes associated to the experimental system.
- It incorporates advanced data mining techniques that provide a global understanding of the underlying biological processes, by integrating external biological information on genes and genes products.
- The significance of the analysis output is statistically supported.
- <http://www.integromics.com/ArrayUnlock.php>

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ArrayUnlock

BENEFITS

- Easy to use analysis frame
- Support for common input data files: Text files, Microsoft Excel
- Fast extraction of biological knowledge from gene expression data
- Advanced associations defined by the user
- Support for common commercial array platforms
- Fully integrated with Spotfire DecisionSite©

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ArrayUnlock

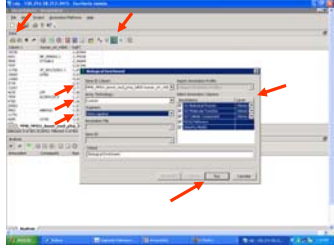
KEY FEATURES

- Gene Annotation from Gene Ontology(GO) or InterPro databases
- Large battery of analysis tools (Association among gene annotations and expression patterns, Associations among user defined items, Biological Enrichment, Gene Annotation concurrency discovery)
- Link to external databases (GO, NCBI or InterPro)
- Different visualization tools (Profile plot, Scatter plot and Heat map, Pie Chart and Hbar)
- Synchronization between associations, annotations, genes, data, external database and graphs
- Possibility to Export results

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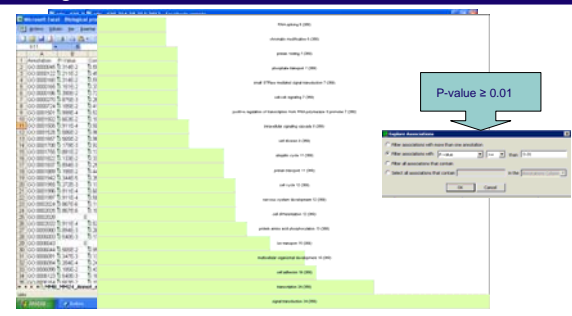
ArrayUnlock-pipeline

- Upload Excel file data set
- Biological enrichment
 - Select annotation columns
 - GO Biological Process
 - GO Molecular Function
 - GO Cellular component
 - KEGG pathways
 - INTERPRO motifs




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ArrayUnlock-RESULTS

Biological Process (Top 10)		
MMS_MAB	MMS_MM24	MMS_PMS
<ul style="list-style-type: none"> - Regulation of transcription, DNA-dependent (5) - Metabolic process - Cell adhesion (8) - Transcription (4) - Actin cytoskeleton organization and biogenesis (4) - Cytoskeleton organization and biogenesis (2) - Chromatin modification (2) - Small GTPase mediated signal transduction (2) - Integrin-mediated signalling pathway (2) - Cation transport (2) 	<ul style="list-style-type: none"> - Signal transduction (34) - Cell adhesion (19) - Multicellular organismal development (18) - Ion transport (15) - Protein amino acid phosphorylation (13) - Cell differentiation (12) - Nervous system development (12) - Cell cycle (12) - Protein transport (11) 	<ul style="list-style-type: none"> - Signal transduction (84) - Regulation of transcription, DNA-dependent (71) - Transcription (65) - Multicellular organismal development (44) - Cell cycle (34) - Protein transport (33) - Metabolic process (30) - Apoptosis (29) - Cell adhesion (28) - Protein amino acid phosphorylation (28)

Summary of pie and bar charts. In bold, altered functions in the three comparisons. In italics, functions altered in two of the three comparisons. In brackets, number of genes implicated.

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ArrayUnlock-RESULTS

Molecular Functions (Top 10)		
MMS_MAB	MMS_MM24	MMS_PMS
<ul style="list-style-type: none"> - Protein binding (12) - Metal ion binding (7) - Zinc ion binding (6) - Transferase activity (4) - Calcium ion binding (4) - Actin binding (4) - Transcription factor activity (4) - Nucleotide binding (4) - Sequence-specific DNA binding (2) - Transferase activity, transferring glycosyl groups (2) 	<ul style="list-style-type: none"> - Protein binding (98) - Zinc ion binding (40) - Metal ion binding (42) - Nucleotide binding (39) - ATP binding (31) - Transferase activity (29) - Calcium ion binding (24) - Receptor activity (24) - Transcription factor activity (23) - Hydrolase activity (18) 	<ul style="list-style-type: none"> - Protein binding (262) - Zinc ion binding (88) - Nucleotide binding (86) - Metal ion binding (84) - ATP binding (64) - Transferase activity (61) - Hydrolase activity (57) - Receptor activity (54) - Calcium ion binding (47) - DNA binding (47)

Summary of pie and bar charts. In bold, altered functions in the three comparisons. In italics, functions altered in two of the three comparisons. In brackets, number of genes implicated.

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ArrayUnlock-RESULTS

2nd vs 1st immune response

KEGG (Top 10)		
MMS_MAB	MMS_MM24	MMS_PMS
<ul style="list-style-type: none"> - G1RH signalling (1) - Regulation of actin cytoskeleton (1) - Long-term potentiation (1) - Leukocyte transendothelial migration (1) - Focal adhesion (1) - Ubiquitin mediated proteolysis (1) - MAPK signalling pathway (1) - Glycan structures-degradation (1) - Glycan structures-biosynthesis 2 (1) - Glycan structures-biosynthesis 1 (1) 	<ul style="list-style-type: none"> - MAPK signalling pathway (13) - Neuroactive ligand-receptor interaction (10) - Regulation of actin cytoskeleton (8) - Focal adhesion (8) - G1RH signalling pathway (6) - Axon guidance (6) - Calcium signalling pathway (6) - Pancreatic cancer (4) - Long-term potentiation (4) - Leukocyte transendothelial migration (4) 	<ul style="list-style-type: none"> - Focal adhesion (22) - MAPK signalling pathway (21) - Jak-STAT signalling pathway (16) - Cytokine-cytokine receptor interaction (16) - Cell cycle (14) - Tc epsilon R1 signalling pathway (11) - Natural killer cell mediated cytotoxicity (11) - Insulin signalling pathway (10) - Apoptosis (10) - T cell receptor signalling pathway (9)

Summary of pie and bar charts. In bold, altered functions in the three comparisons. In italics, functions altered in two of the three comparisons. In brackets, number of genes implicated.

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Ingenuity Pathways Analysis (IPA)

OVERVIEW

- Ingenuity Pathways Analysis (IPA) is an all-in-one software application that enables researchers to model, analyze, and understand the complex biological and chemical systems at the core of life science research.
- IPA has been broadly adopted by the life sciences research community and cited in hundreds of peer-reviewed journal articles.

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Ingenuity Pathways Analysis (IPA)

HIGHLIGHTS

- Easily search the scientific literature** for insights relevant to your experiment
- Build dynamic pathway models** to extend your understanding of your research
- Quickly analyze your experimental data** to identify key insights
- Share your research and collaborate** with your colleagues with the easy-to-use IPA interface
- Join your peers** in using the most highly-referenced pathway solution

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IPA: pipeline

BIOLOGICAL FUNCTIONS

PATHWAYS

NETWORKS

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IPA: pipeline

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IPA: pipeline

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IPA- SUMMARY SCREEN

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Biological pathway analysis by ArrayUnlock and IPA

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University of Cordoba, Spain

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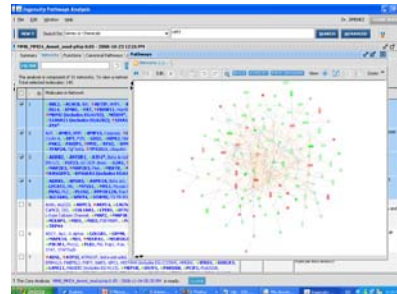
IPA- NETWORKS



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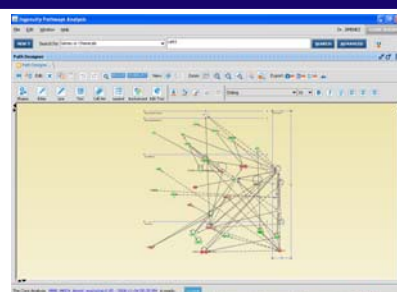
IPA- NETWORKS



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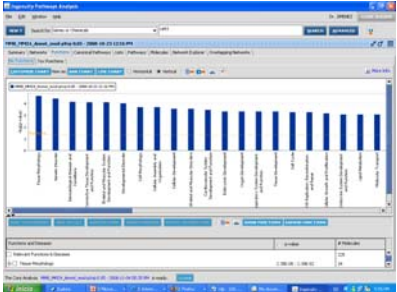
IPA- NETWORKS



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IPA- BIOFUNCTIONS

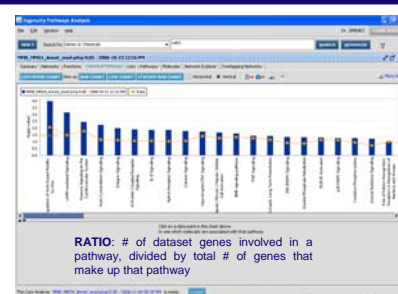


- DISEASE AND DISORDERS
- MOLECULAR AND CELLULAR FUNCTION
- PHYSIOLOGICAL SYSTEM DEVELOPMENT AND FUNCTION

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IPA- CANONICAL PATHWAYS




RATIO: # of dataset genes involved in a pathway, divided by total # of genes that make up that pathway

- METABOLIC PATHWAY
- SIGNALING PATHWAY

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IPA- CANONICAL PATHWAYS



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