

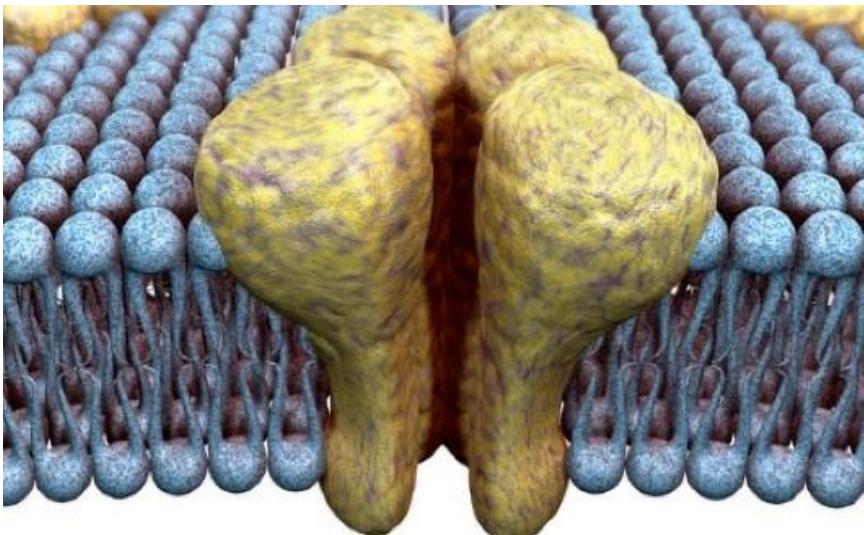
Up/down and left/right by the heart transcriptome

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Channelopathies: molecular and genetic mechanisms

www.nature.com/scientificreports/



Chapter 1: Drug discovery, tools and theory

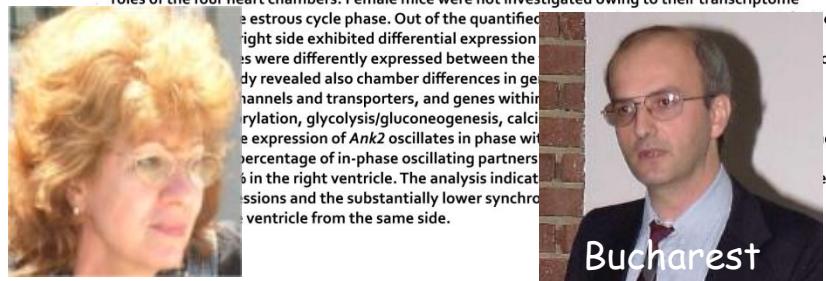
scientific reports

OPEN

Transcriptomic uniqueness and commonality of the ion channels and transporters in the four heart chambers

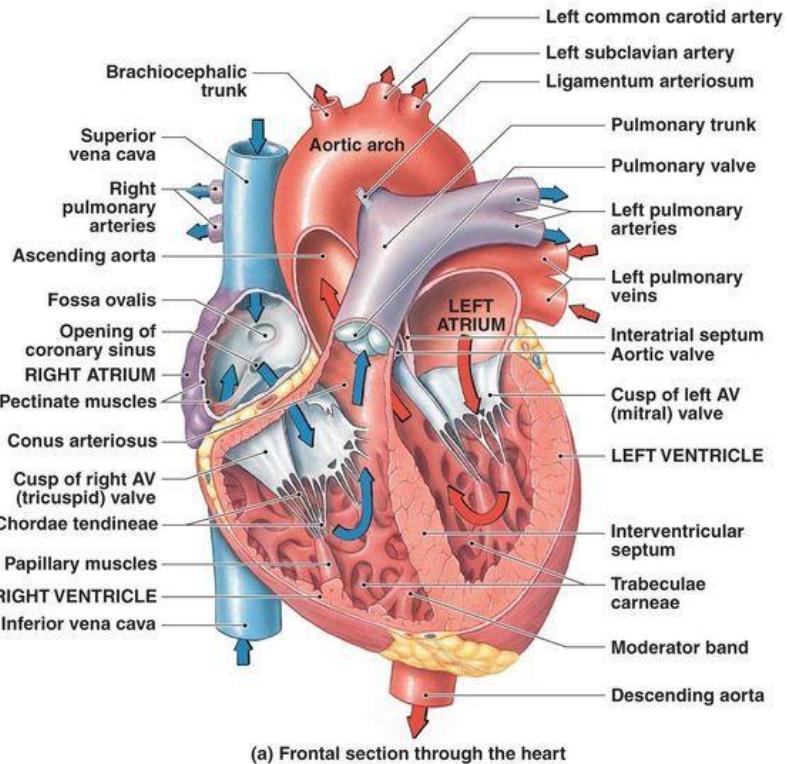
Sanda Iacobas¹, Bogdan Amuzescu² & Dumitru A. Iacobas^{3,4} 

Myocardium transcriptomes of left and right atria and ventricles from four adult male C57BL/6j mice were profiled with Agilent microarrays to identify the differences responsible for the distinct functional roles of the four heart chambers. Female mice were not investigated owing to their transcriptome

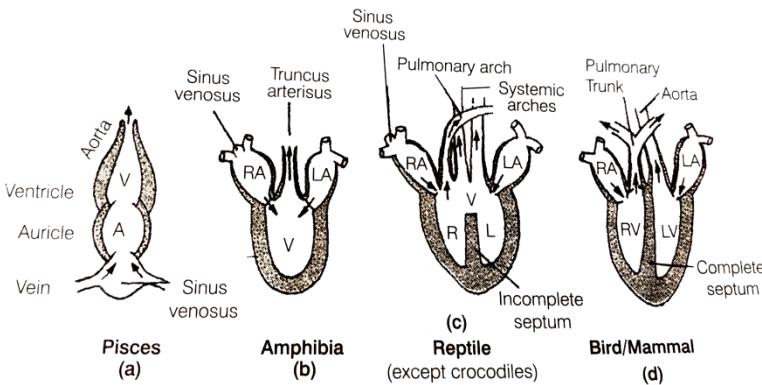


Bucharest

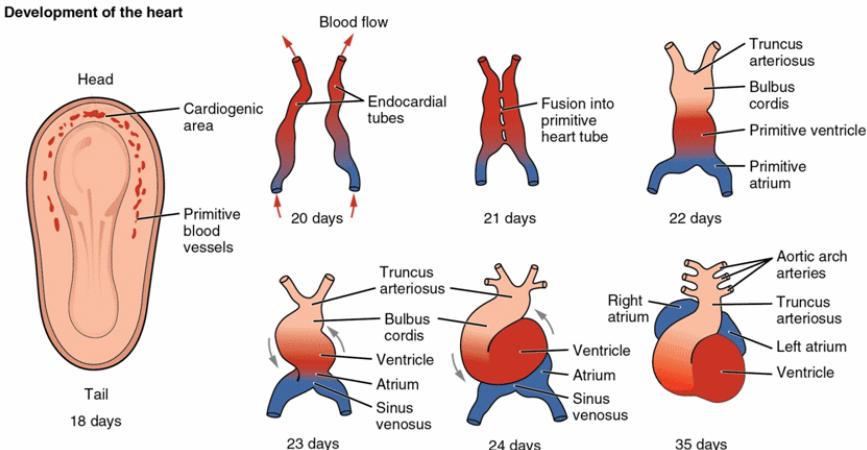
Heart



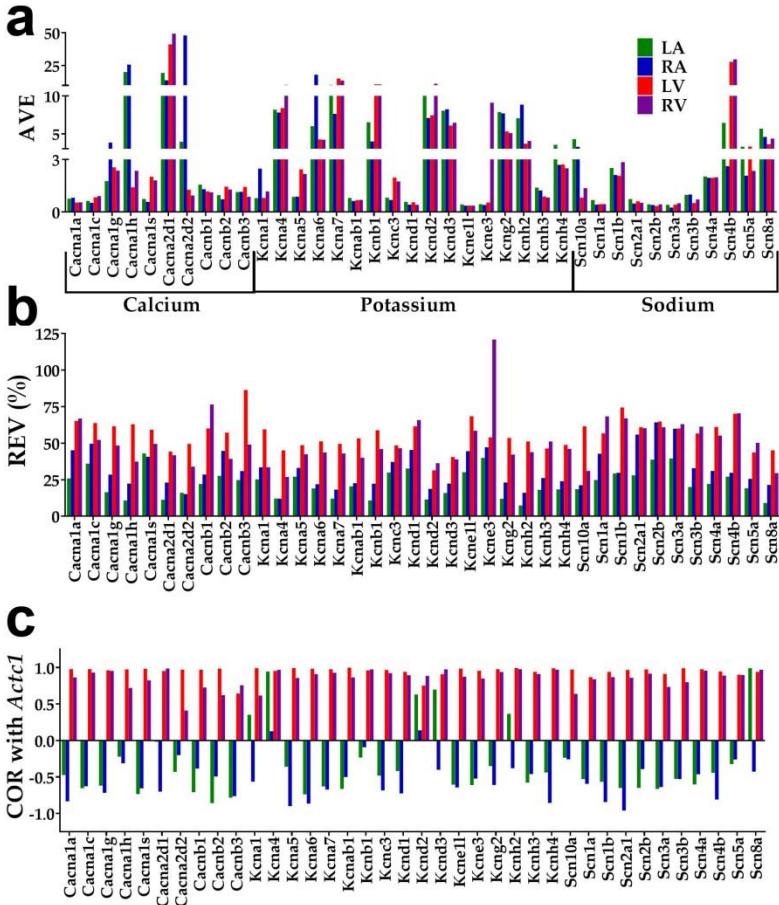
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Meckel-Serres Law "Ontogeny recapitulates phylogeny"



★Cardiogenic area begins right in the middle of head pole



Three independent variables.

Actc1 = actin, alpha, cardiac muscle 1

Transcriptomic topology

Genomic fabric : $F \equiv (\Gamma, \Pi, \Xi, \Theta)$

Γ = set of composing genes ($\{\Gamma\}$ = number of genes),

Π = transcriptomic profile (set of the 95% confidence intervals of the composing genes expression levels)

Ξ = control of transcript abundance

Θ = topology (series of many-gene expression correlation functions)

$$AVE_i^{(chamber)} = \frac{1}{R_i} \sum_{k=1}^{R_i} \mu_{i,k}^{(chamber)} = \frac{1}{R_i} \sum_{k=1}^{R_i} \left(\underbrace{\frac{1}{4} \sum_{j=1}^4 a_{i,k,j}^{(chamber)}}_{\mu_i^{(chamber)}} \right)$$

$$REV_i^{(chamber)} = \frac{1}{2} \left(\underbrace{\sqrt{\chi^2(r_i; 1 - \alpha/2)} + \sqrt{\chi^2(r_i; \alpha/2)}}_{\text{redundancy correction coefficient}} \right) \sqrt{\frac{1}{R_i} \sum_{k=1}^{R_i} \left(\frac{S_{ik}^{(chamber)}}{\mu_{ik}^{(chamber)}} \right)^2} \times 100\%$$

$$\Theta(\overrightarrow{g_1}, \overrightarrow{g_2}, \dots, \overrightarrow{g_n}) = \bigcup_{k=1}^n A_k \left[F_k \left(\overrightarrow{g_{i1}}, \dots, \overrightarrow{g_{ik}} \mid 1 \leq i_1 < \dots < i_k \leq n \right) \right]$$

$$\left[F_k \left(\overrightarrow{g_{i1}}, \overrightarrow{g_{i2}} \mid 1 \leq i_1 < i_2 \leq n \right) \right] = \left(\overrightarrow{g_{i1}} r \left(\overrightarrow{g_{i1}}, \overrightarrow{g_{i2}} \right) \overrightarrow{g_{i2}} - \overrightarrow{g_{i1}} \overrightarrow{g_{i2}} \times \hat{1} \right)_{1 \leq i_1 < i_2 \leq n} \quad \text{pair-wise topology}$$

$r(\overrightarrow{g_{i1}}, \overrightarrow{g_{i2}})$ = Pearson correlation coefficient between the sets of the expression levels of genes $i1$ and $i2$ within biological replicas

recurrence relation: $\left[F_k \left(\overrightarrow{g_{i1}}, \dots, \overrightarrow{g_{ik}} \mid 1 \leq i_1 < \dots < i_k \leq n \right) \right] = \left[\overrightarrow{g_{ik}} r \left(\overrightarrow{g_{ik}}, F_k \left(\overrightarrow{g_{i1}}, \dots, \overrightarrow{g_{ik-1}} \mid 1 \leq i_1 < \dots < i_{k-1} \leq n \right) \right) \right]$, multi dimensional correlations

$$A_1 \geq A_2 \geq A_3 \geq \dots \geq A_n \geq 0 \Rightarrow \Theta(\overrightarrow{g_1}, \overrightarrow{g_2}, \dots, \overrightarrow{g_n}) \approx \underbrace{A_1 \left(\overrightarrow{g_{i1}} \times \hat{1} \right)_{1 \leq i_1 \leq n}}_{\text{single-gene topology}} + A_2 \left(\overrightarrow{g_{i1}} r \left(\overrightarrow{g_{i1}}, \overrightarrow{g_{i2}} \right) \overrightarrow{g_{i2}} - \overrightarrow{g_{i1}} \overrightarrow{g_{i2}} \times \hat{1} \right)_{1 \leq i_1 < i_2 \leq n} \quad \text{pair-wise topology}$$

Differential expression

$$\forall A, B = RA, LA, RV, LV \quad , \quad A \neq B$$

$$x_i^{(A \rightarrow B)} = \begin{cases} \sum_{k=1}^{R_i} \mu_{ik}^{(B)} / \sum_{k=1}^{R_i} \mu_{ik}^{(A)} & \text{if } \sum_{k=1}^{R_i} \mu_{ik}^{(B)} \geq \sum_{k=1}^{R_i} \mu_{ik}^{(A)} \\ -\sum_{k=1}^{R_i} \mu_{ik}^{(A)} / \sum_{k=1}^{R_i} \mu_{ik}^{(B)} & \text{if } \sum_{k=1}^{R_i} \mu_{ik}^{(B)} < \sum_{k=1}^{R_i} \mu_{ik}^{(A)} \end{cases}, \quad \frac{1}{R_i} \sum_{k=1}^{R_i} \mu_{ik}^{(A)} = AVE_i^{(A)}$$

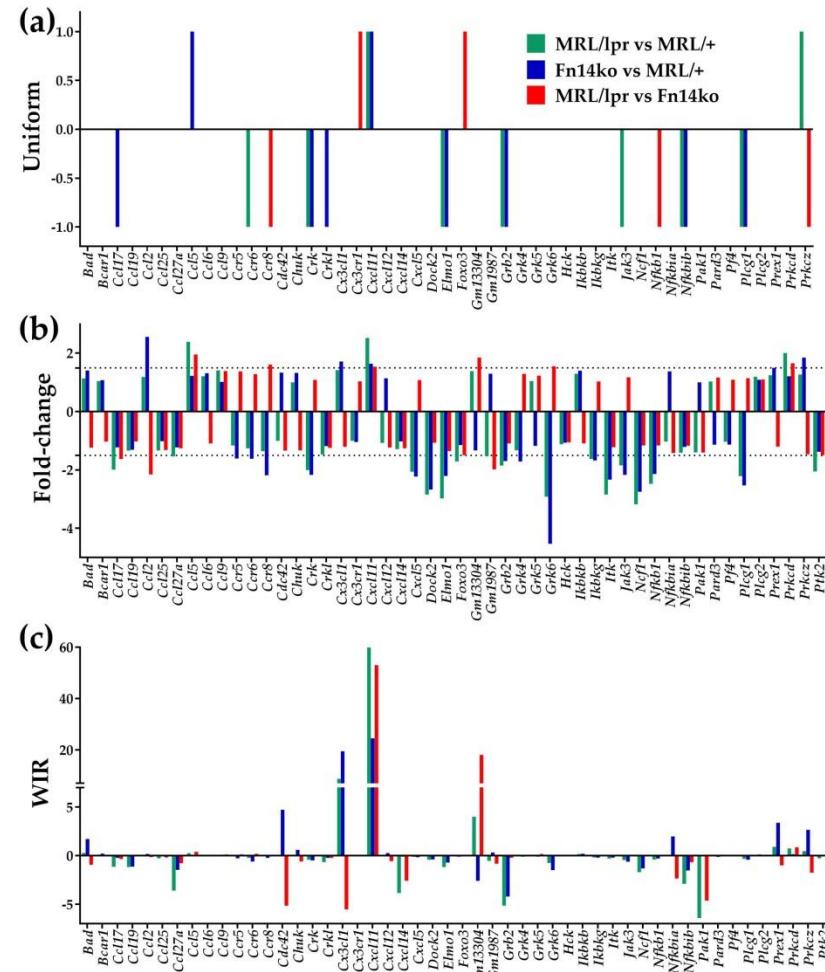
Statistically significant differential expression if:

$$\left| x_i^{(A \rightarrow B)} \right| > CUT_i^{(A \rightarrow B)} = 1 + \sqrt{2 \left(\left(REV_i^{(A)} \right)^2 + \left(REV_i^{(B)} \right)^2 \right)} \quad \wedge \quad p_i^{(A \rightarrow B)} < 0.05$$

Weighted Individual gene Regulation (WIR):

$$WIR_i^{(A \rightarrow B)} \equiv AVE_i^{(A)} \frac{\chi_i^{(A \rightarrow B)}}{\left| \chi_i^{(A \rightarrow B)} \right|} \underbrace{\left(\left| \chi_i^{(A \rightarrow B)} \right| - 1 \right)}_{\text{absolute net fold-change}} \underbrace{\left(1 - p_i^{(A \rightarrow B)} \right)}_{\text{confidence of the regulation}}$$

regulation sign



Transcriptomic chamber specificity

$$WPR_{\Gamma}^{(A \rightarrow B)} = \overline{\left(wpr_i^{(A \rightarrow B)} \right)_{i \in \Gamma}} \quad , \quad \text{where :}$$

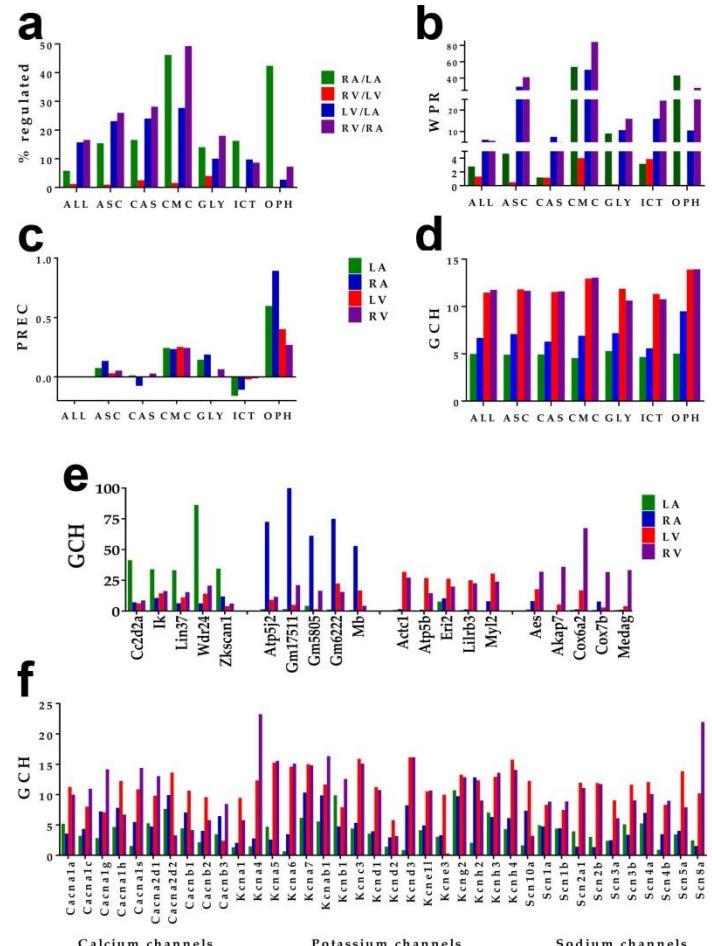
$$wpr_i^{(A \rightarrow B)} = \begin{cases} \mu_i^{(A)} \left(|x_i^{(A \rightarrow B)}| - CUT_i^{(A \rightarrow B)} \right) \left(1 - p_i^{(A \rightarrow B)} \right) & \text{if } |x_i^{(A \rightarrow B)}| > CUT_i^{(A \rightarrow B)} \\ 0 & \text{if } |x_i^{(A \rightarrow B)}| \leq CUT_i^{(A \rightarrow B)} \end{cases}$$

$p_i^{(A \rightarrow B)}$ = p-val of the heteroscedastic t-test of $\mu_i^{(B)} = \mu_i^{(A)}$

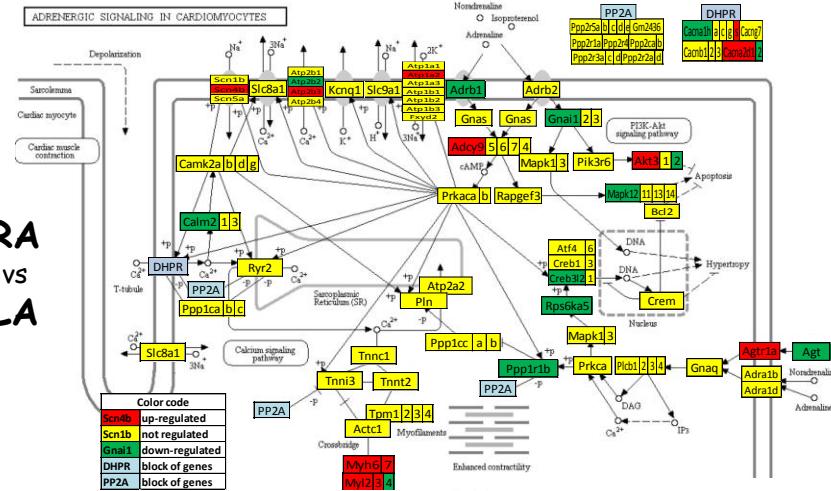
$$REC_i^{(chamber)} = \frac{\langle REV^{(chamber)} \rangle|_{ALL}}{REV_i^{(chamber)}} - 1 \quad , \quad PREC_{\Gamma}^{(chamber)} = \frac{\langle REV^{(chamber)} \rangle|_{ALL}}{\langle REV^{(chamber)} \rangle|_{\Gamma}} - 1$$

where : $\langle REV^{(chamber)} \rangle|_{\Gamma/ALL}$ ≡ median of REV over pathway Γ / entire transcriptome

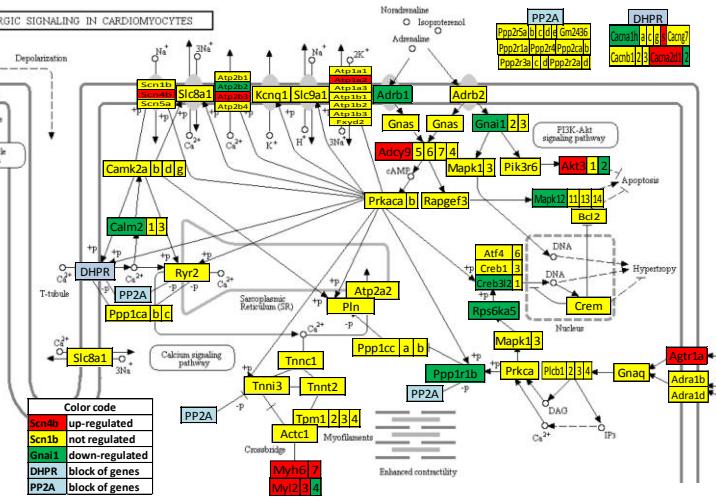
$$GCH_i^{(chamber)} = \left(REC_i^{(chamber)} + 1 \right) \times \exp \left(4 \overline{\rho_{ij}^2}^{(chamber)} \right)$$



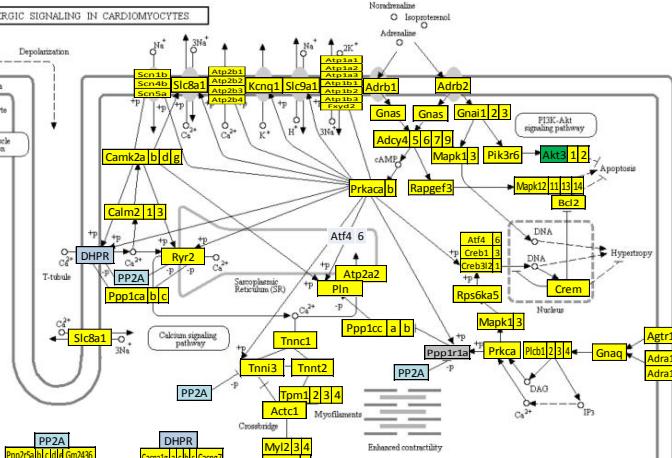
RA
vs
LA



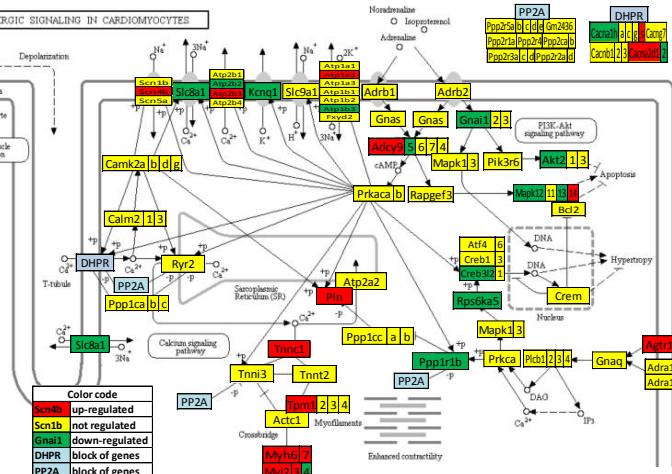
RV
vs
RA



RV
vs
LV

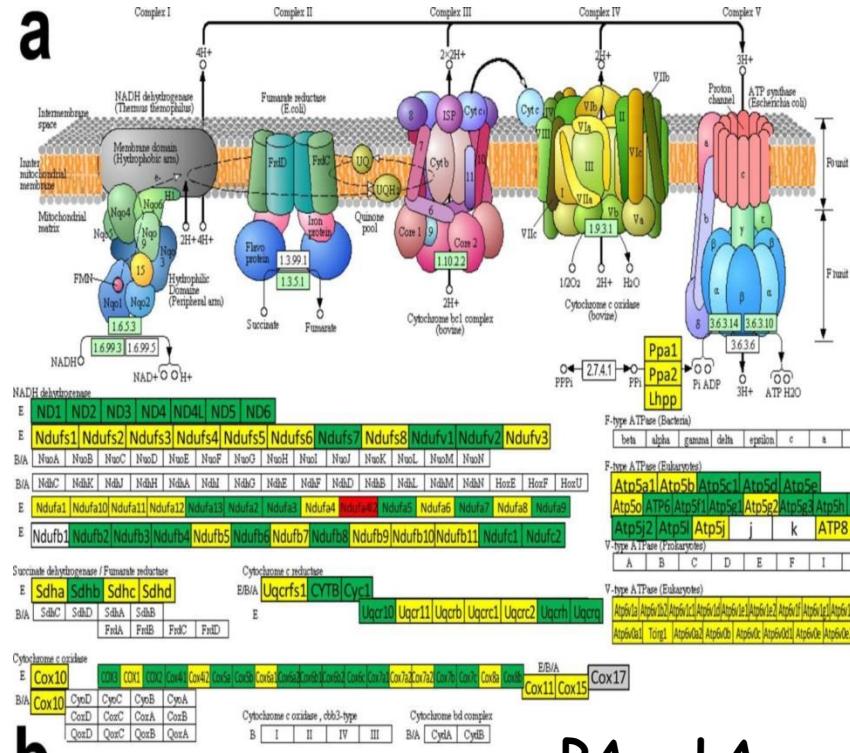


LV
vs
RA



Differential oxidative phosphorylation

a



RA vs LA

b

LV vs LA

C

RV vs RA

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6						
B/A	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3		
B/A	NadA	NadB	NadC	NadD	NadF	NadG	NadH	NadI	NadK	NadL	NadM	NadN	
B/A	NadC	NadK	NadJ	NadH	NadA	NadG	NadE	NadF	NadD	NadB	NadH	NadM	
E	Ndufa1	Ndufa10	Ndufa11	Ndufa12	Ndufa13	Ndufa2	Ndufa3	Ndufa4	Ndufa42	Ndufa5	Ndufa6	Ndufa8	Ndufa9
E	Ndufb10	Ndufb11	Ndufb12	Ndufb13	Ndufb4	Ndufb5	Ndufb6	Ndufb7	Ndufb8	Ndufc1	Ndufc2	Ndufc3	

Succinate dehydrogenase / Fumurate reductase

E	SdhA	SdhB	SdhC	SdhD
B/A	SdhB	SdhB	SdhA	SdhB
B/A	FmdA	FmdB	FmdC	FmdD

Cytochrome c reductase

E	Uqcrfts1	CYTB	Cyc1				
B/A	Uqcrfts1	CYTB	Cyc1				
E	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16
B/A	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16

Cytochrome c oxidase

E	Cox10	Cox11	Cox12	Cox42	Cox13	Cox5a	Cox6a	Cox6b	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	Cox10	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxA	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	CoxB	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17

Cytochrome c oxidase, cb3-type

B/A	I	II	IV	III
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Cytochrome bc complex

B/A	Cytb	CytcB
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RV vs RA

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6							
B/A	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3			
B/A	NadA	NadB	NadC	NadD	NadF	NadG	NadH	NadI	NadK	NadL	NadM	NadN		
B/A	NadC	NadK	NadJ	NadH	NadA	NadG	NadE	NadF	NadD	NadB	NadH	NadM		
E	Ndufa1	Ndufa10	Ndufa11	Ndufa12	Ndufa13	Ndufa2	Ndufa3	Ndufa4	Ndufa42	Ndufa5	Ndufa6	Ndufa7	Ndufa8	Ndufa9
E	Ndufb10	Ndufb11	Ndufb12	Ndufb13	Ndufb4	Ndufb5	Ndufb6	Ndufb7	Ndufb8	Ndufc1	Ndufc2	Ndufc3		

Succinate dehydrogenase / Fumurate reductase

E	SdhA	SdhB	SdhC	SdhD
B/A	SdhB	SdhB	SdhA	SdhB
B/A	FmdA	FmdB	FmdC	FmdD

Cytochrome c reductase

E	Uqcrfts1	CYTB	Cyc1				
B/A	Uqcrfts1	CYTB	Cyc1				
E	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16
B/A	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16

Cytochrome c oxidase

E	Cox10	Cox11	Cox12	Cox42	Cox13	Cox5a	Cox6a	Cox6b	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	Cox10	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxA	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	CoxB	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17

F-type ATPase (Bacteria)

beta	alpha	gamma	delta	epsilon	c	a	b
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F-type ATPase (Eukaryotes)

AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε			
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
j	k						

V-type ATPase (Prokaryotes)

A	B	C	D	E	F	I	K
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RV vs RA

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6							
B/A	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3			
B/A	NadA	NadB	NadC	NadD	NadF	NadG	NadH	NadI	NadK	NadL	NadM	NadN		
B/A	NadC	NadK	NadJ	NadH	NadA	NadG	NadE	NadF	NadD	NadB	NadH	NadM		
E	Ndufa1	Ndufa10	Ndufa11	Ndufa12	Ndufa13	Ndufa2	Ndufa3	Ndufa4	Ndufa42	Ndufa5	Ndufa6	Ndufa7	Ndufa8	Ndufa9
E	Ndufb10	Ndufb11	Ndufb12	Ndufb13	Ndufb4	Ndufb5	Ndufb6	Ndufb7	Ndufb8	Ndufc1	Ndufc2			

Succinate dehydrogenase / Fumurate reductase

E	SdhA	SdhB	SdhC	SdhD
B/A	SdhB	SdhB	SdhA	SdhB
B/A	FmdA	FmdB	FmdC	FmdD

Cytochrome c reductase

E	Uqcrfts1	CYTB	Cyc1				
B/A	Uqcrfts1	CYTB	Cyc1				
E	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16
B/A	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16

Cytochrome c oxidase

E	Cox10	Cox11	Cox12	Cox42	Cox13	Cox5a	Cox6a	Cox6b	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	Cox10	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxA	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	CoxB	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17

F-type ATPase (Bacteria)

beta	alpha	gamma	delta	epsilon	c	a	b
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F-type ATPase (Eukaryotes)

AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε			
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
j	k						

V-type ATPase (Eukaryotes)

A	B	C	D	E	F	I	K
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RV vs RA

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6							
B/A	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3			
B/A	NadA	NadB	NadC	NadD	NadF	NadG	NadH	NadI	NadK	NadL	NadM	NadN		
B/A	NadC	NadK	NadJ	NadH	NadA	NadG	NadE	NadF	NadD	NadB	NadH	NadM		
E	Ndufa1	Ndufa10	Ndufa11	Ndufa12	Ndufa13	Ndufa2	Ndufa3	Ndufa4	Ndufa42	Ndufa5	Ndufa6	Ndufa7	Ndufa8	Ndufa9
E	Ndufb10	Ndufb11	Ndufb12	Ndufb13	Ndufb4	Ndufb5	Ndufb6	Ndufb7	Ndufb8	Ndufc1	Ndufc2			

Succinate dehydrogenase / Fumurate reductase

E	SdhA	SdhB	SdhC	SdhD
B/A	SdhB	SdhB	SdhA	SdhB
B/A	FmdA	FmdB	FmdC	FmdD

Cytochrome c reductase

E	Uqcrfts1	CYTB	Cyc1				
B/A	Uqcrfts1	CYTB	Cyc1				
E	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16
B/A	Uqcrr10	Uqcrr11	Uqcrr12	Uqcrr13	Uqcrr14	Uqcrr15	Uqcrr16

Cytochrome c oxidase

E	Cox10	Cox11	Cox12	Cox42	Cox13	Cox5a	Cox6a	Cox6b	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	Cox10	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxA	CoxB	CoxA	Cox42	CoxC	CoxA	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17
B/A	CoxD	CoxC	CoxB	CoxA	Cox42	CoxC	CoxA	CoxB	Cox7a	Cox7b	Cox7c	Cox7d	Cox7e	Cox17

F-type ATPase (Bacteria)

beta	alpha	gamma	delta	epsilon	c	a	b
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F-type ATPase (Eukaryotes)

AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε			
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
AtpS _α	AtpS _β	AtpS _γ	AtpS _δ	AtpS _ε	AtpS _γ	AtpS _δ	AtpS _ε
j	k						

V-type ATPase (Eukaryotes)

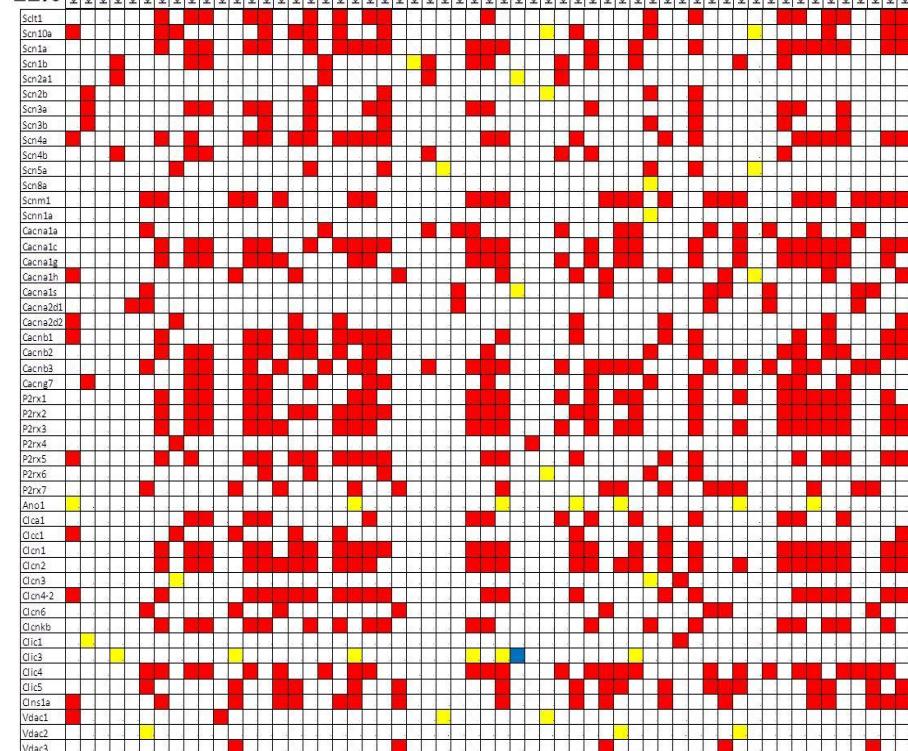
A	B	C	D	E	F	I	K
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LV vs LA

Differential gene networking

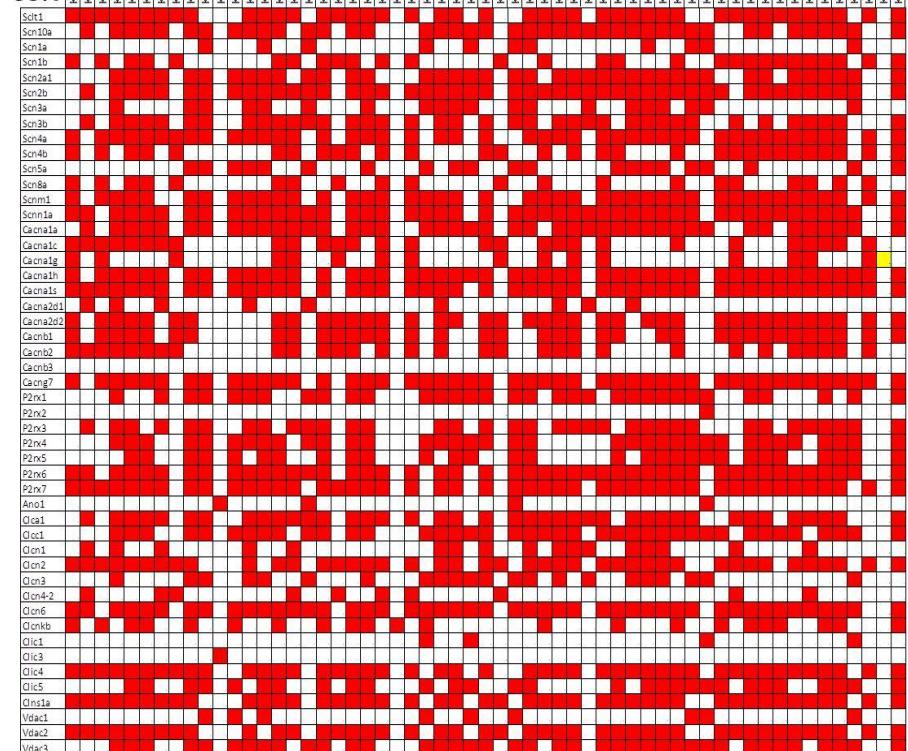
MAR

22%

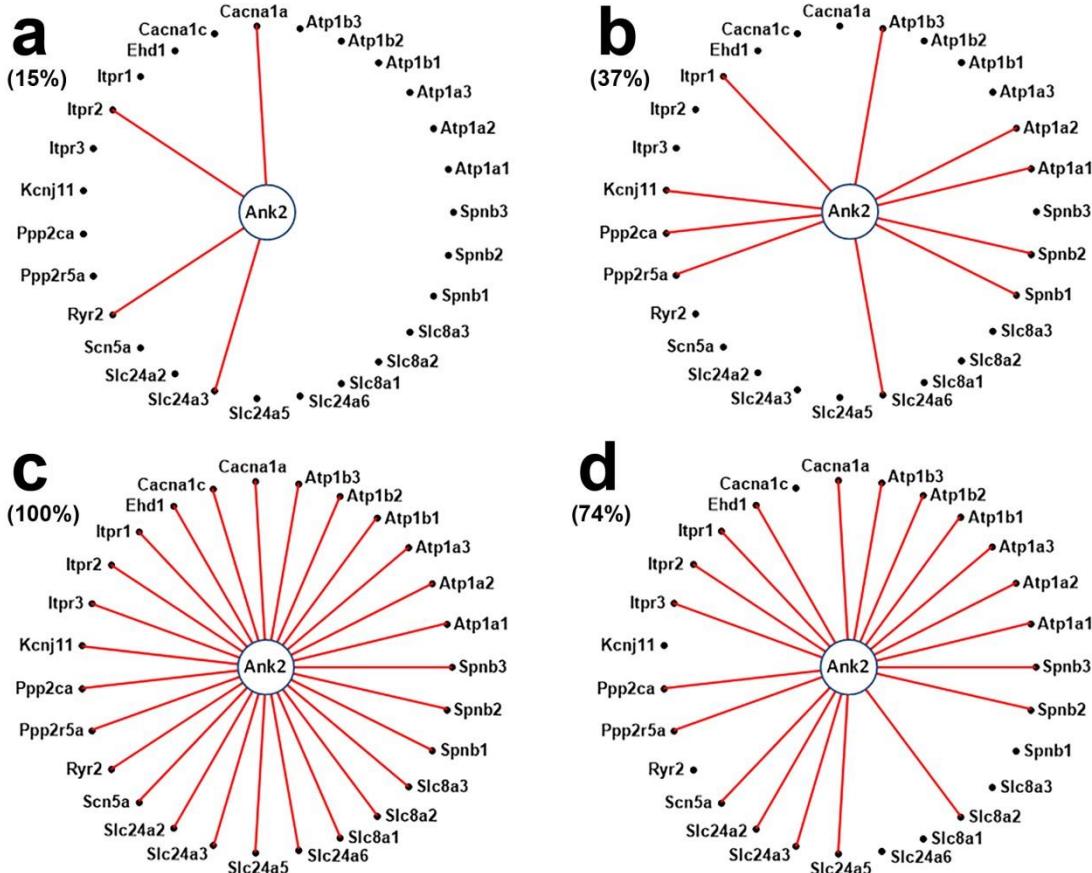


MVL

53%

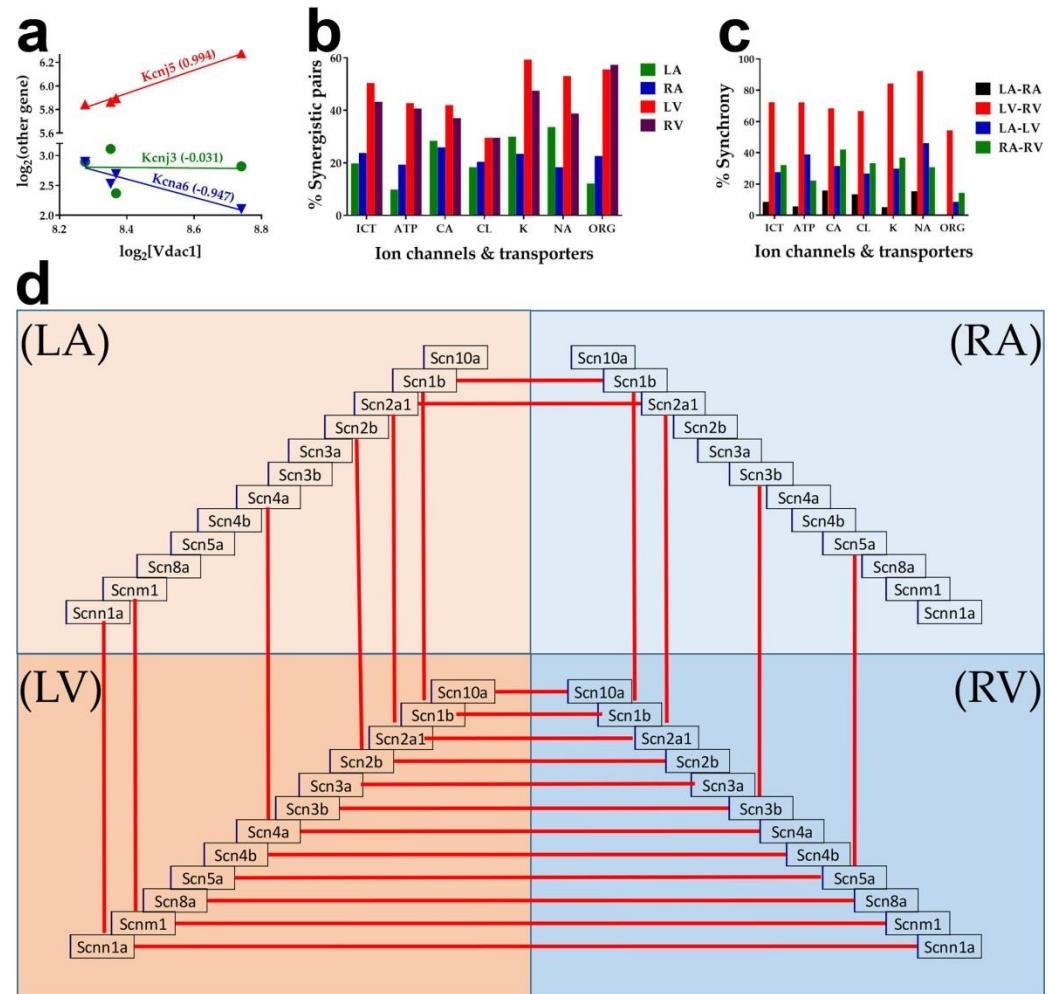


Differential gene networking



Expression coordination of *Ank2* (a major player in cardiac physiology and a hub-bottleneck gene in atrial fibrillation) with its known binding partners in: **a.** left atrium, **b.** right atrium, **c.** left ventricle, **d.** right ventricle.

Expression synchrony of ionic channels and transporters



Sexual dichotomy

Sex-dependent gene regulatory networks of the heart rhythm

D. A. Iacobas · S. Iacobas · N. Thomas · I.

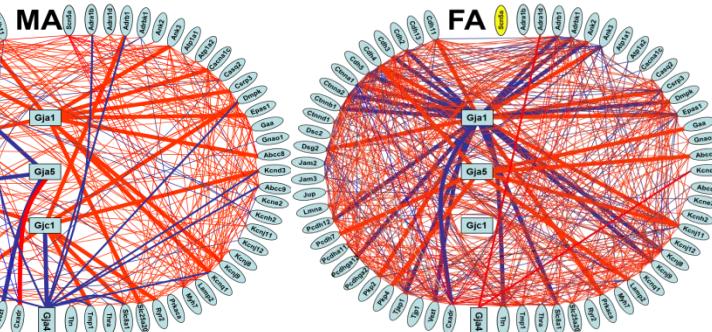


UFRJ, Brazil

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Abstract Expression level, control, and intercoordination of 66 selected heart rhythm determinant (HRD) genes were compared in atria and ventricles of four male and four female adult mice. We found that genes encoding various adrenergic receptors, ankyrins, ion channels and transporters, connexins, cadherins, plakophilins, and other components of the

higher expression in atria than ventricles for males and higher expression in ventricles than atria for females. We have ranked the selected genes according to their prominence (new concept) within the HRD gene web defined as extent of expression coordination with the other web genes and stability of expression. Interestingly, the prominence

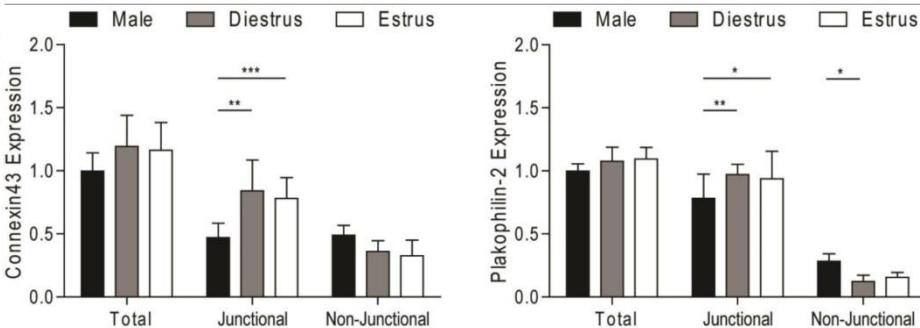


Sex differences in expression and subcellular localization of heart rhythm determinant proteins

N.M. Thomas ^{a,*}, J.F. Jasmin ^b, M.P. Lisanti ^b, D.A. Iacobas ^a

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^bThomas Jefferson University, Department of Stem Cell Biology and Regenerative Medicine, Bluhm Building, 233 South 10th St., Philadelphia, PA 19107, USA



Gja1 (*Cx43*), Gja5 (*Cx40*), Gjc1 (*Cx45*)

Heart connexins

Physiol Genomics 20: 211–223, 2005.

First published December 7, 2004; doi:10.1152/physiolgenomics.00229.2003.



Available online at www.sciencedirect.com



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ophysiology and Molecular Biology 94 (2007) 245–264

www.cls

Review

The role of connexins in controlling cell growth and gene expression

Elissavet Kardami^{a,*}, Xitong Dang^a, Dumitru A. Iacobas^b, Barbara E. Nick^b, Madhumathy Jeyaraman^a, Wattamon Srisakuldee^a, Janna Makazan^a, Stephane Tanguy^a, David C. Spray^b

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Available online 16 March



Toronto, CAN

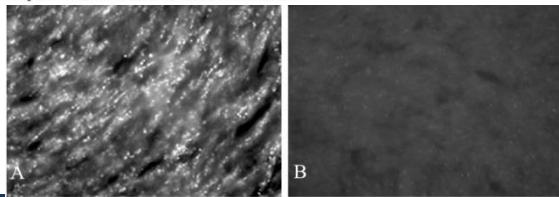


Gap Junctions and Chagas Disease

Daniel Adesse,^{*†} Regina Coeli Goldenberg,^{Einstein, NY} Fabio S. Fortes,[‡] Jasmin,^{*§} Dumitru A. Iacobas,[§] Sanda Iacobas,[§] Antonio Carlos Campos de Carvalho,^{*§} Maria de Narareth Meirelles,[†] Huan Huang,[†] Milena B. Soares,^{||} Herbert B. Tanowitz,[†] Luciana Ribeiro Garzoni,[†] and David C. Spray[§]

Genes controlling multiple functional pathways are transcriptionally regulated in connexin43 null mouse heart

Dumitru A. Iacobas,¹ Sanda Iacobas,¹ W. E. I. Li,¹ Georg Zoidl,³ Rolf Dermietzel,³ and Accepted in final form 30 November 2004



Bochum,
GER

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Neurochemistry International 45 (2004) 243–250

NEUROCHEMISTRY
International

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Gene expression alterations in connexin null mice extend beyond the gap junction

Dumitru A. Iacobas, Eliana Scemes, David C. Spray*

Valhalla, NY

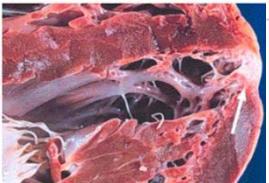


Chagas cardiomyopathy

Parasitol Res (2003) 91: 187–196
DOI 10.1007/s00436-003-0937-z

ORIGINAL PAPER

Hipertrofia



Bronx, NY

Shankar Mukherjee · Thomas J. David C. Spray · Dumitru A. Iacobas · Richard N. Kitsis · Murray Witman · Philip E. Scherer · Aihao Ding

Microarray analysis of changes in gene expression in a mouse model of chronic chagasic cardiomyopathy

Gene Expression Changes Associated with Myocarditis and Fibrosis in Hearts of Mice with Chronic Chagasic Cardiomyopathy

Milena Botelho Pereira Soares,^{1,2} Ricardo Santana de Lima,¹ Leonardo Lima Rocha,¹ Juliana Fraga Vasconcelos,¹ Sílvia Regina Rogatto,^{3,4} Ricardo Ribeiro dos Santos,^{1,2} Sandra Iacobas,⁵ Regina Coeli Goldenberg,⁵ Dumitru Andrei Iacobas,⁶ Herbert Bernard Tanowitz,^{6,8} Antonio Carlos Campos de Carvalho,^{5,6} and David Conover Spray^{7,8}



Chagas I, Brazil

Reversion of gene expression alterations in hearts of mice with chronic chagasic cardiomyopathy after transplantation of bone marrow cells

Milena B.P. Soares,^{1,2,*} Ricardo S. Lima,³ Bruno S.F. Souza,^{1,2} Juliana F. Vasconcelos,^{1,2} Leonardo L. Rocha,¹ Ricardo Ribeiro dos Santos,^{1,2} Sandra Iacobas,⁴ Regina C. Goldenberg,⁵ Michael P. Lisanti,⁶ Dumitru A. Iacobas,⁴ Herbert B. Tanowitz,^{6,7,*} David C. Spray^{4,6} and Antonio C. Campos de Carvalho^{4,5,8}



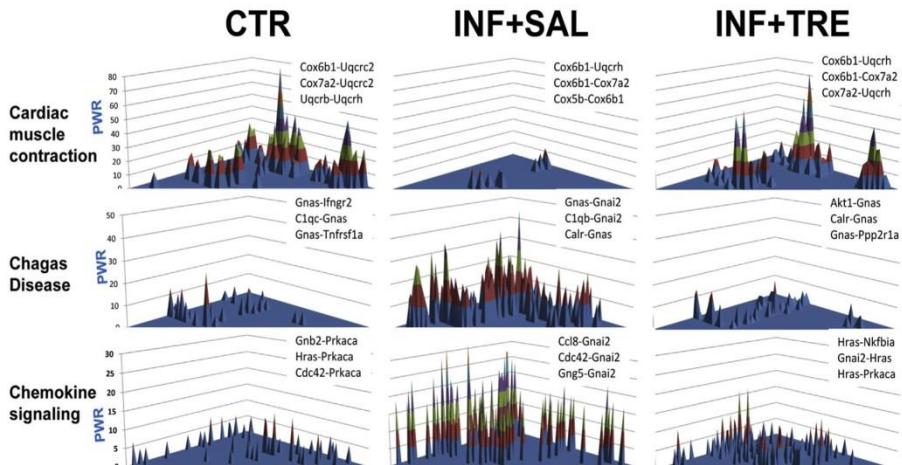
Institut Pasteur

Microbes and Infection xx (2017) 1–11

Original article

Functional genomic fabrics are remodeled in a mouse model of Chagasic cardiomyopathy and restored following cell therapy

Dumitru A. Iacobas^{a,b,*}, Sandra Iacobas^a, Herbert B. Tanowitz^{c,d}, Antonio Campos de Carvalho^{b,e}, David C. Spray^{b,c}



Chagas I, Brazil



 INSTITUT PASTEUR

Microbes and Infection 11 (2009) 1140–1149

www.elsevier.com/locate/micinf

Original article

Transcriptomic alterations in *Trypanosoma cruzi*-infected cardiac myocytes

Regina Coeli dos Santos Goldenberg ^{a,b,c}, Dumitru A. Iacobas ^b, Sandra Leonardo Lima Rocha ^{a,1}, Fabio da Silva de Azevedo Fortes ^{a,b,c}, Leandro Fnu Nagayoshi ^a, Antonio Carlos Campos de Carvalho ^{b,c}, Herbert B. T. David C. Spray ^{b,*}



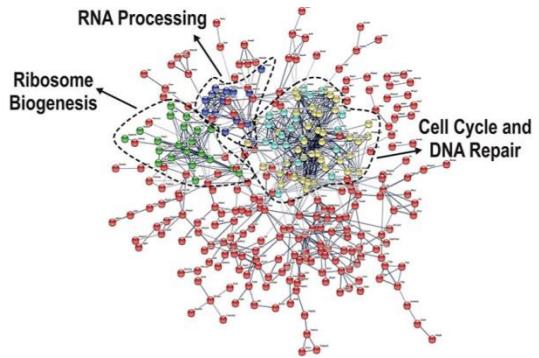
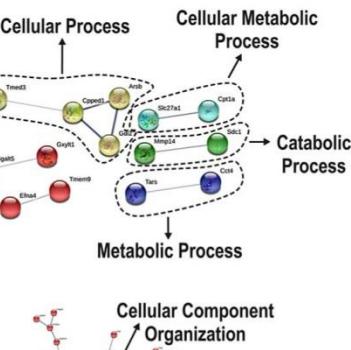
UFRJ Brazil

Am. J. Trop. Med. Hyg., 82(5), 2010, pp. 846–854
doi:10.4269/ajtmh.2010.09-0399

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Transcriptomic Signatures of Alterations in a Myoblast Cell Line Infected with Four Distinct Strains of *Trypanosoma cruzi*

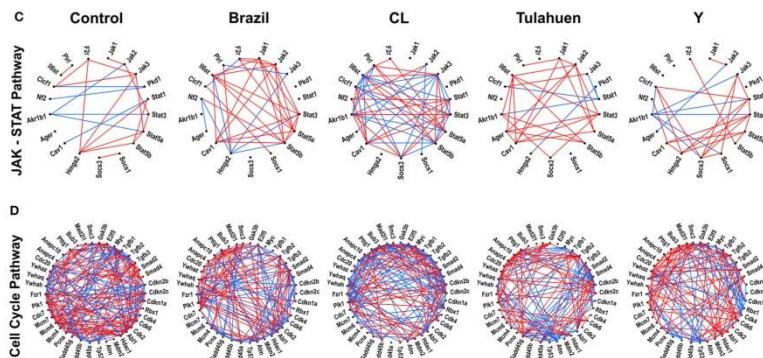
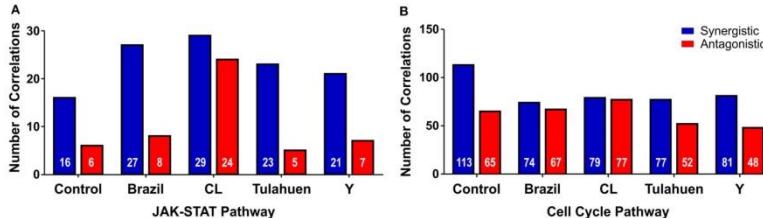
Daniel Adesse,* Dumitru A. Iacobas, Sanda Iacobas, Luciana R. Garzoni, Maria de Nazareth Meirelles, Herbert B. Tanowitz, and David C. Spray



Oswaldo Cruz, BRA

***Trypanosoma cruzi* Promotes Transcriptomic Remodeling of the JAK/STAT Signaling and Cell Cycle Pathways in Myoblasts**

Lindice M. Nisimura¹, Laura L. Coelho², Tatiana G. de Melo³, Paloma de Carvalho Vieira⁴, Pedro H. Victorino⁵, Luciana R. Garzoni², David C. Spray⁶, Dumitru A. Iacobas⁷, Sandra Iacobas⁸, Herbert B. Tanowitz^{9†} and Daniel Adesse^{4*}



Cardiac ischemia



Fluminense, Brazil

Stem Cell Rev and Rep (2012) 8:251–261
DOI 10.1007/s12015-011-9282-2



Functional and Transcriptomic Recovery of Infarcted Mouse Myocardium Treated with Bone Marrow Mononuclear Cells

Stephan Lachtermacher · Bruno L. B. Esporcatte · Fábio da Silva de Azevedo Fortes · Nazareth Novaes Rocha · Fabrício Montalvão · Patricia C. Costa · Luciano Belem · Arnaldo Rabischoffsky · Hugo C. C. Faria Neto · Rita Vasconcellos · Dumitru A. Iacobas · Sandra Iacobas · David C. Spray · Neil M. Thomas · Regina C. S. Goldenberg · Antonio C. Campos de Carvalho

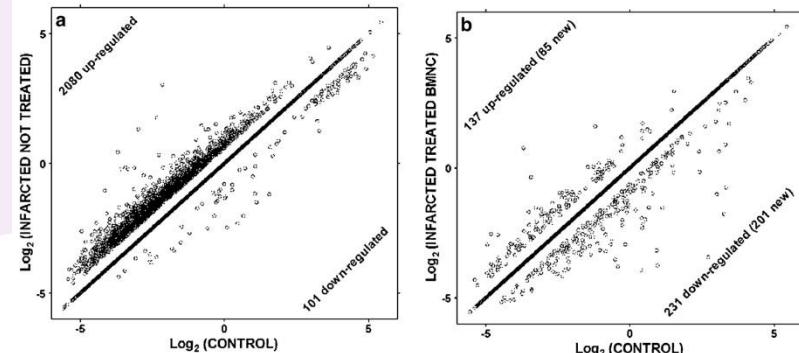
Permanent myocardial infarcts produced by ligation of the descending branch of the left coronary artery BMNC was directly injected using a 10 µl syringe into 3 different regions (30 µl total) at the borders of cardiac scar tissue 10 days after experimental infarction.

Braz J Med Biol Res, March 2010, Volume 43(4) 377-389

Cardiac gene expression and systemic cytokine profile are complementary in a murine model of post-ischemic heart failure

S. Lachtermacher, B.L.B. Esporcatte, F. Montalvão, P.C. Costa, D.C. Rodrigues, L. Belem, A. Rabischoffsky, H.C.C. Faria Neto, R. Vasconcellos, S. Iacobas, D.A. Iacobas, H.F.R. Dohmann, D.C. Spray, R.C.S. Goldenberg and A.C. Campos-de-Carvalho

Stem Cell Rev and Rep (2012) 8:251–261



Constant and Intermittent Hipoxia

Physiol Genomics 22: 292–307, 2005.
First published May 31, 2005; 10.1152/physiolgenomics.00217.2004.

Gene expression and phenotypic characterization of mouse heart after chronic constant or intermittent hypoxia



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Biochemical and Biophysical Research Communications

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Pocatello, ID

Integrated transcriptomic response to cardiac chronic hypoxia: translation regulators and response to stress in cell survival



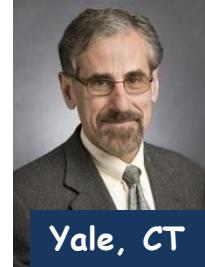
San Diego, CA

Dumitru A. Iacobas • Chenhao Fan • Sandra Iacobas •
Gabriel G. Haddad

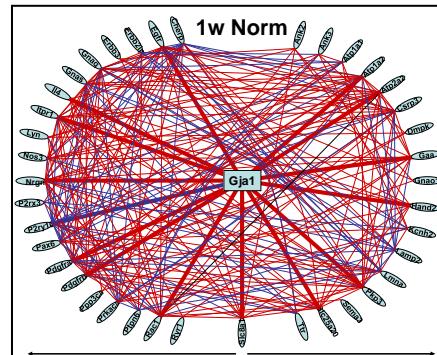
Heart rhythm genomic fabric in hypoxia

Dumitru A. Iacobas ^{a,*}, Sandra Iacobas ^a, Gabriel G. Haddad ^b

Effects of Chronic Intermittent Hypoxia on Cardiac Rhythm Transcriptomic Networks

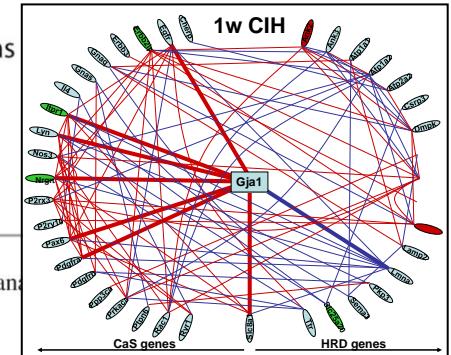


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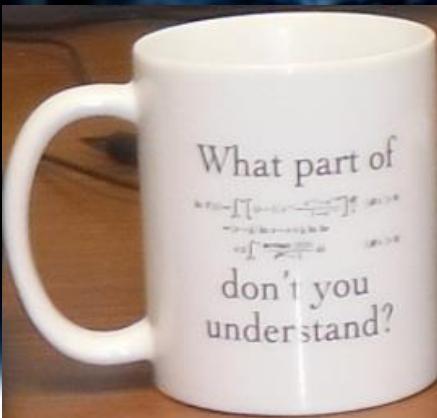
Iacobas

studies and



Transcriptomic differences

- LA vs LV > RA vs RV > LA vs RA > LV vs RV in gene expression level, control and coordination
- Male vs female (changes during the estrogen cycle)
- Young vs adult
- Normoxic vs hypoxic (constant or intermittent) or ischemia
- Healthy vs Chagasic cardiomyopathy
- Wildtype vs connexin null/knockdown



Thank you!

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