

Network Biology and Evolution of Human Genetic Diseases



Sanguk Kim

POSTECH

Outline

• *Introduction of Network Biology and Medicine*

• *Network Distance & Localization -> Disease Comorbidity Nature Mol Sys Biol. 2011*

Human disease evolution Nature Scientific Reports 2012

Mitochondrial protein network Nature Scientific Reports

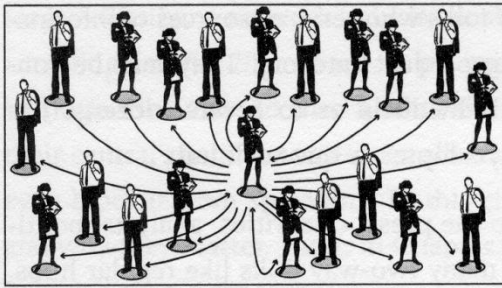
2013

• *Network Clustering -> Cancer PLoS Comp. Biol. 2011*

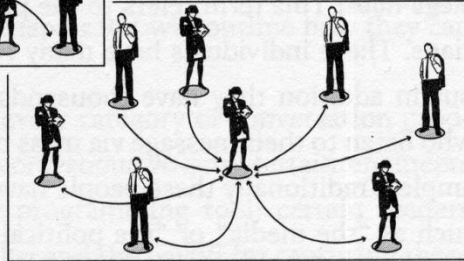
• *Network Rewiring and Evolution -> Gene essentiality changes Nature Scientific Reports 2012*

Neuronal Disease PLoS Genetics 2012

1. Spatial and functional organization of mitochondrial protein network. *Nature Scientific Reports 2013* 3:1403.
2. Network rewiring is an important mechanism of gene essentiality change. *Nature Scientific Reports 2012* 2:900.
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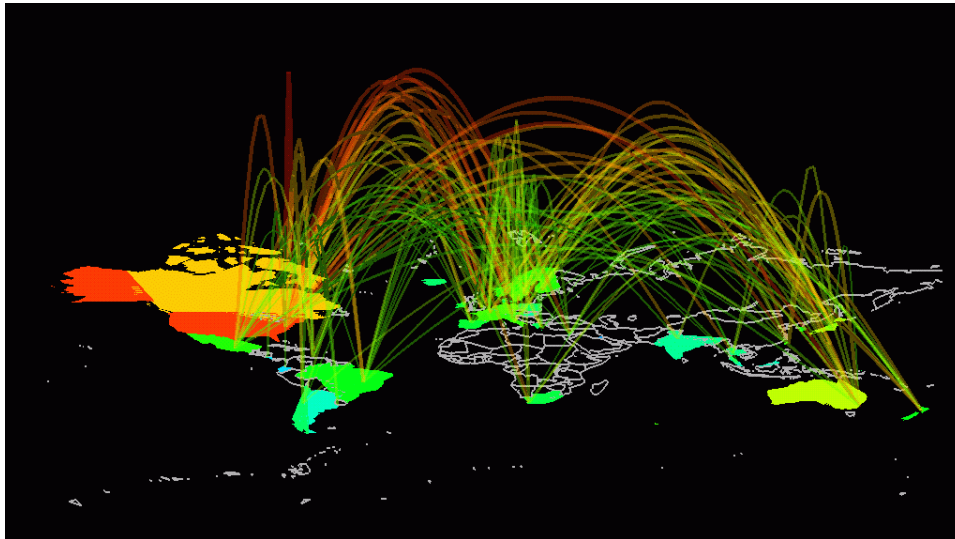
Mega-Hub. An MTV veejay spreads the word to thousands or millions of people through one-way links.



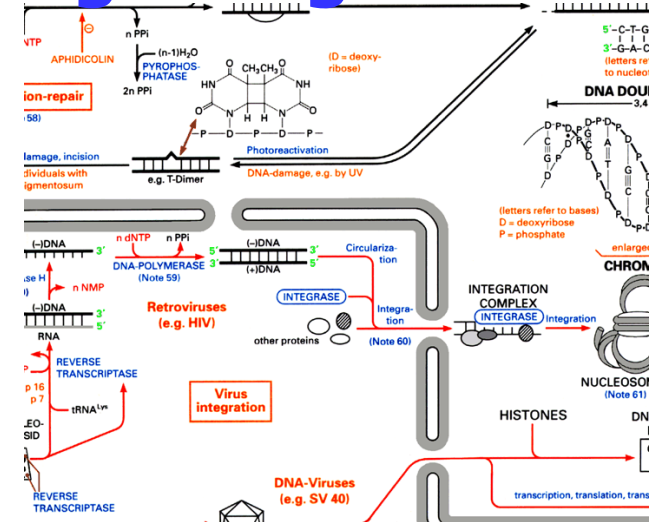
Hub. This undergraduate has spread the word to seven other people through two-way links.

Society

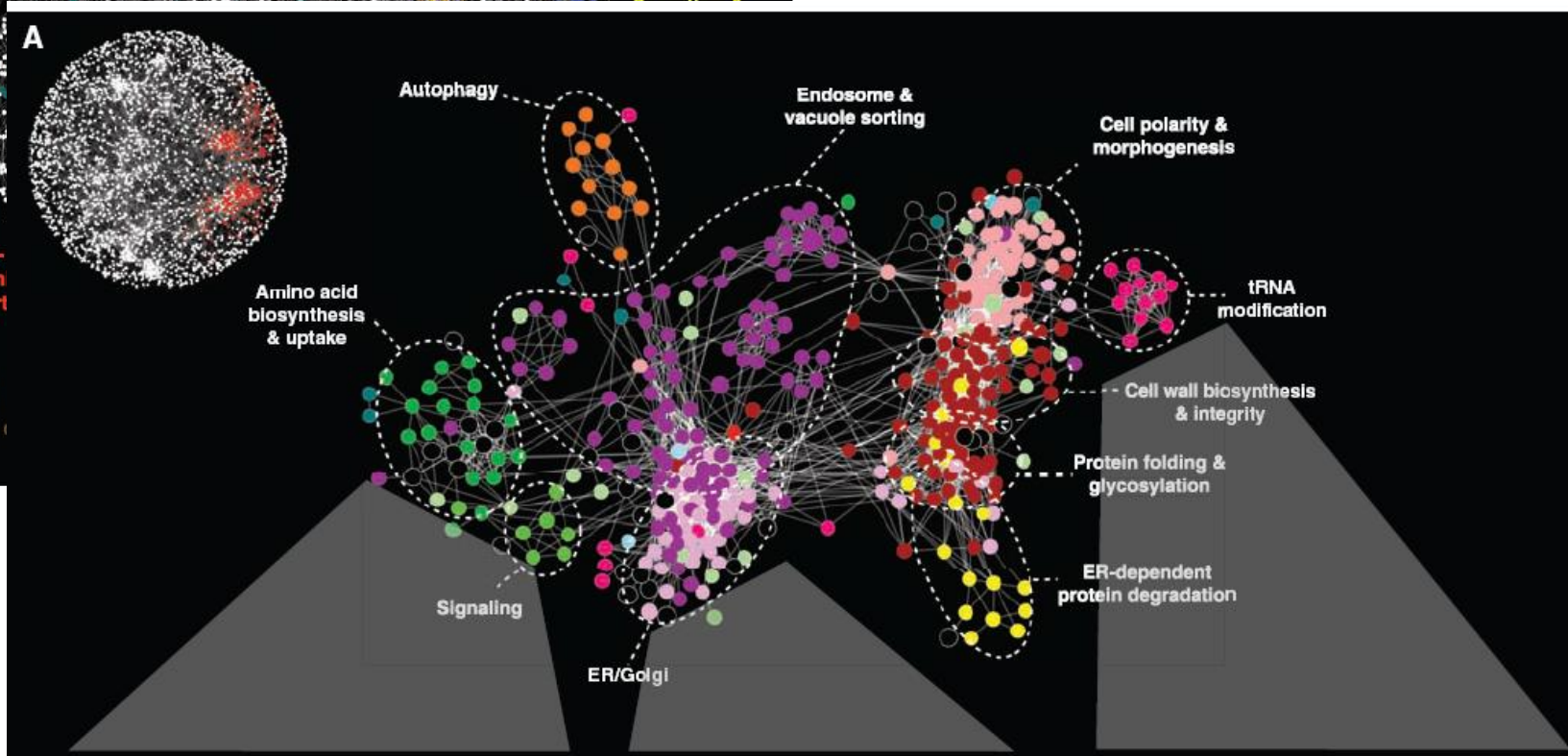
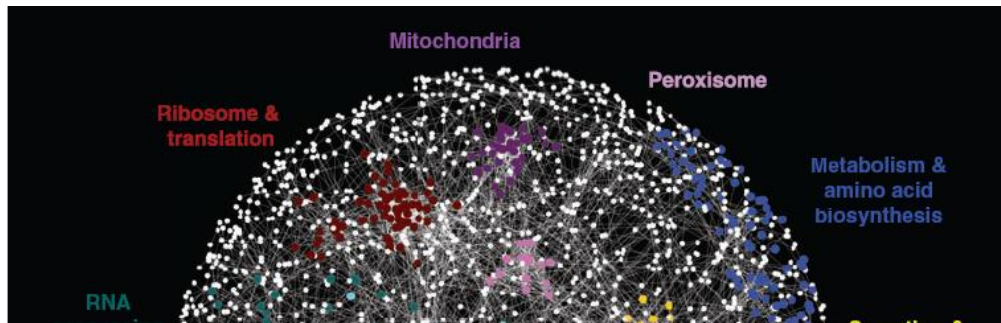
Internet



Biological signaling network



Biological Network



Disease pleiotropy and network modularity

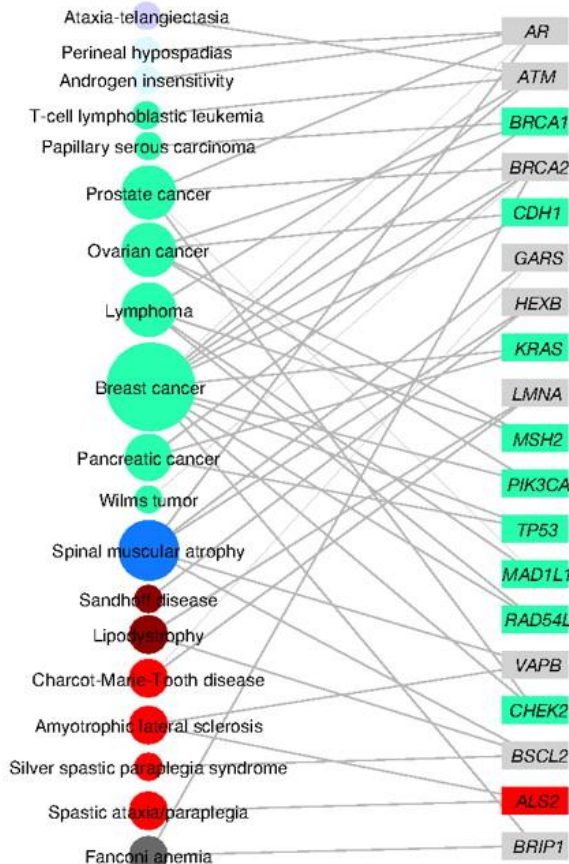
The human disease network

Construction of the diseasome bipartite network

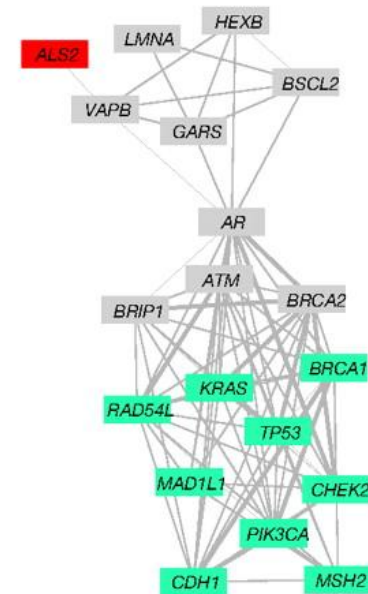
DISEASOME

disease phenotype

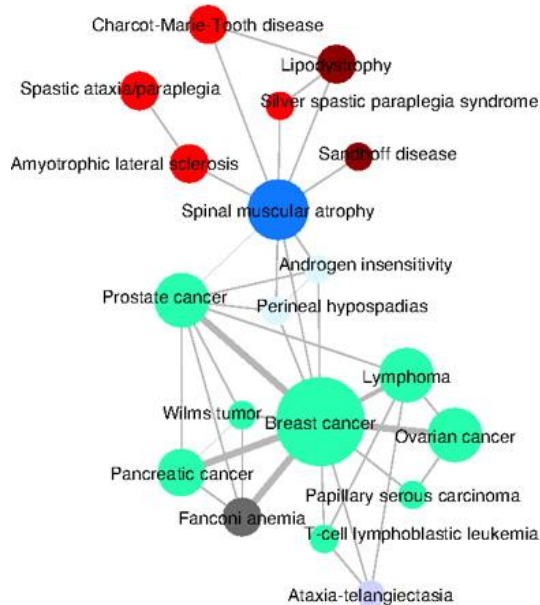
disease genome



Disease Gene Network (DGN)

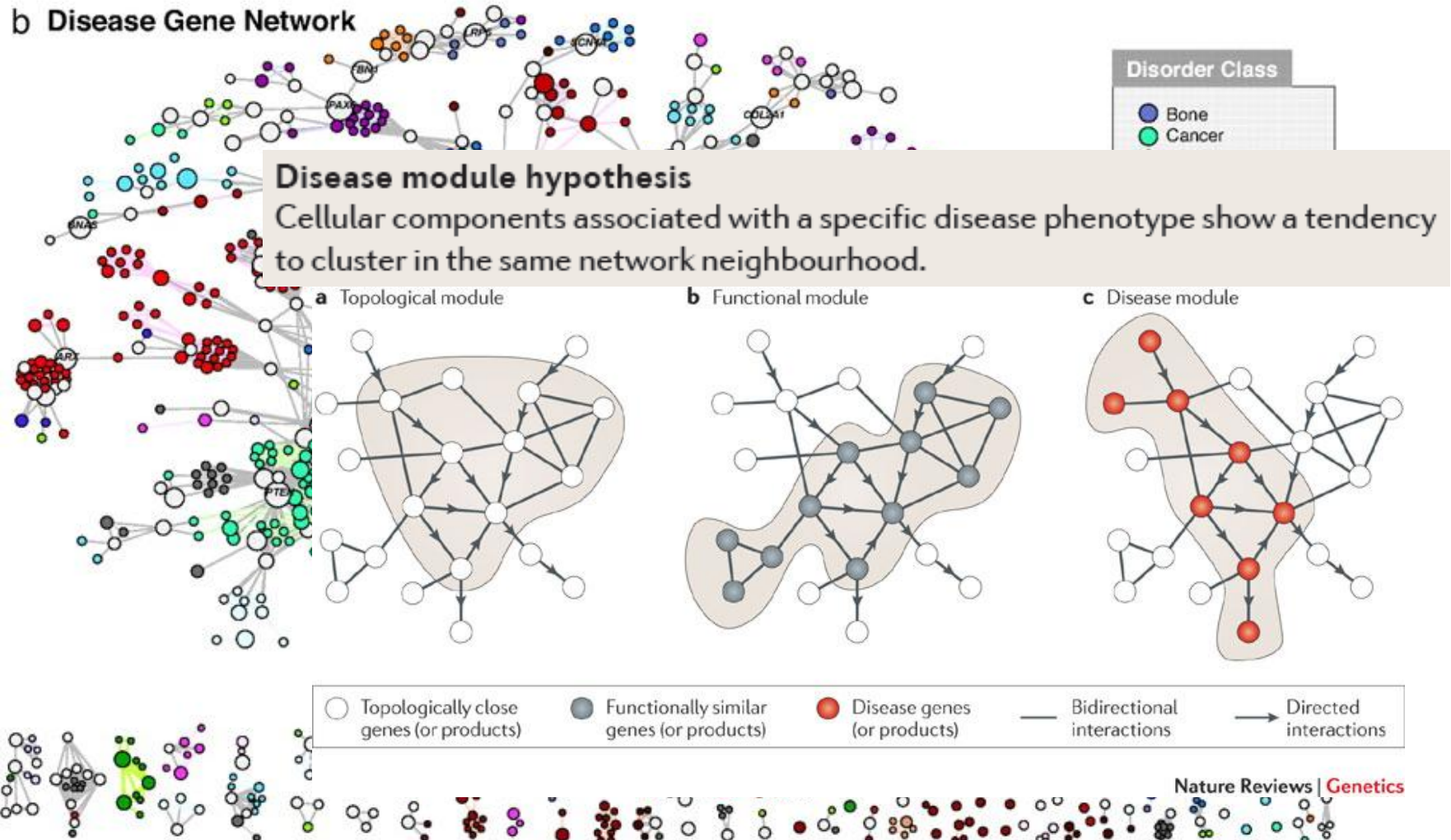


Human Disease Network (HDN)

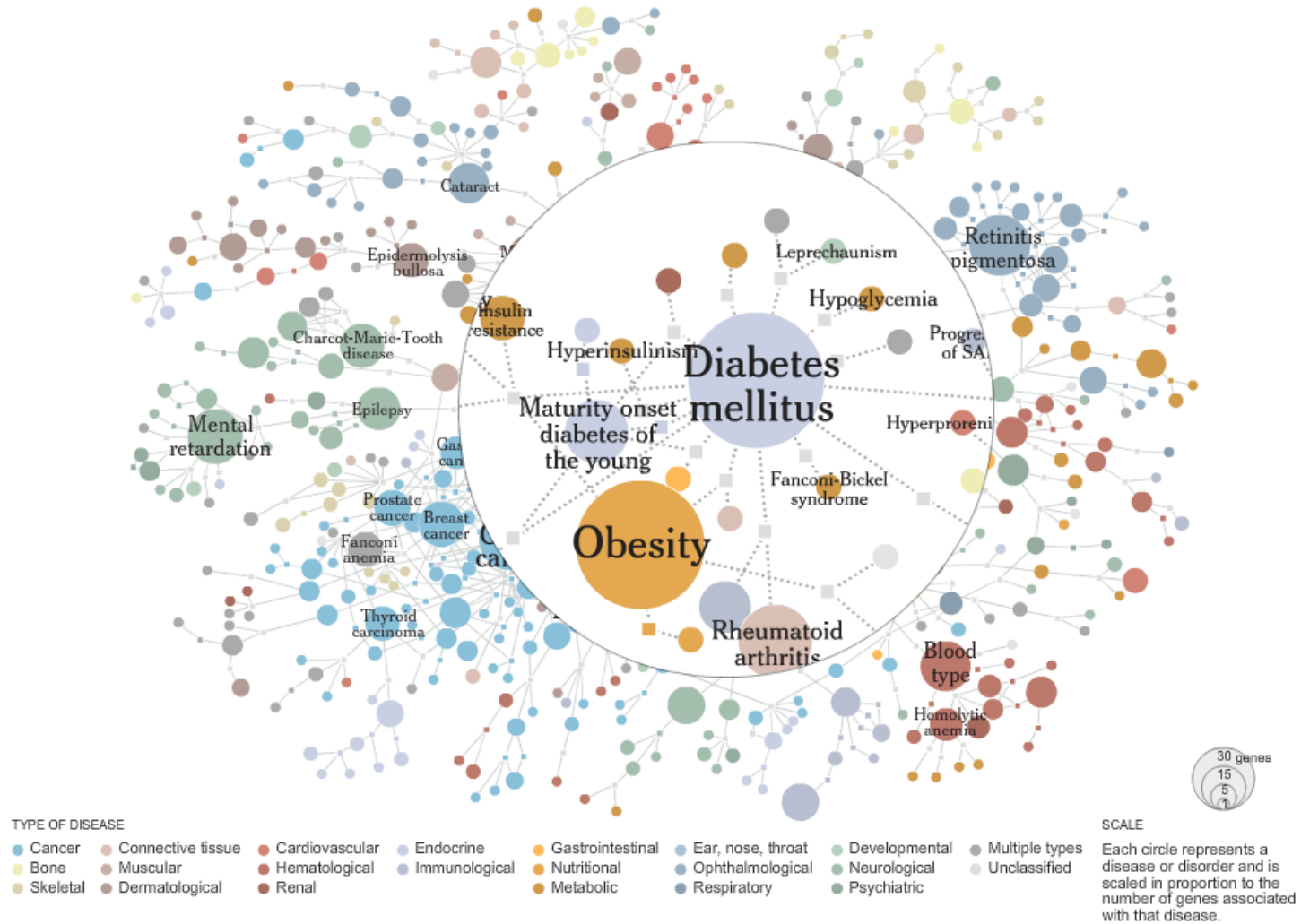


Disease Gene Network

b Disease Gene Network



Example: Diabetes in the Human disease network



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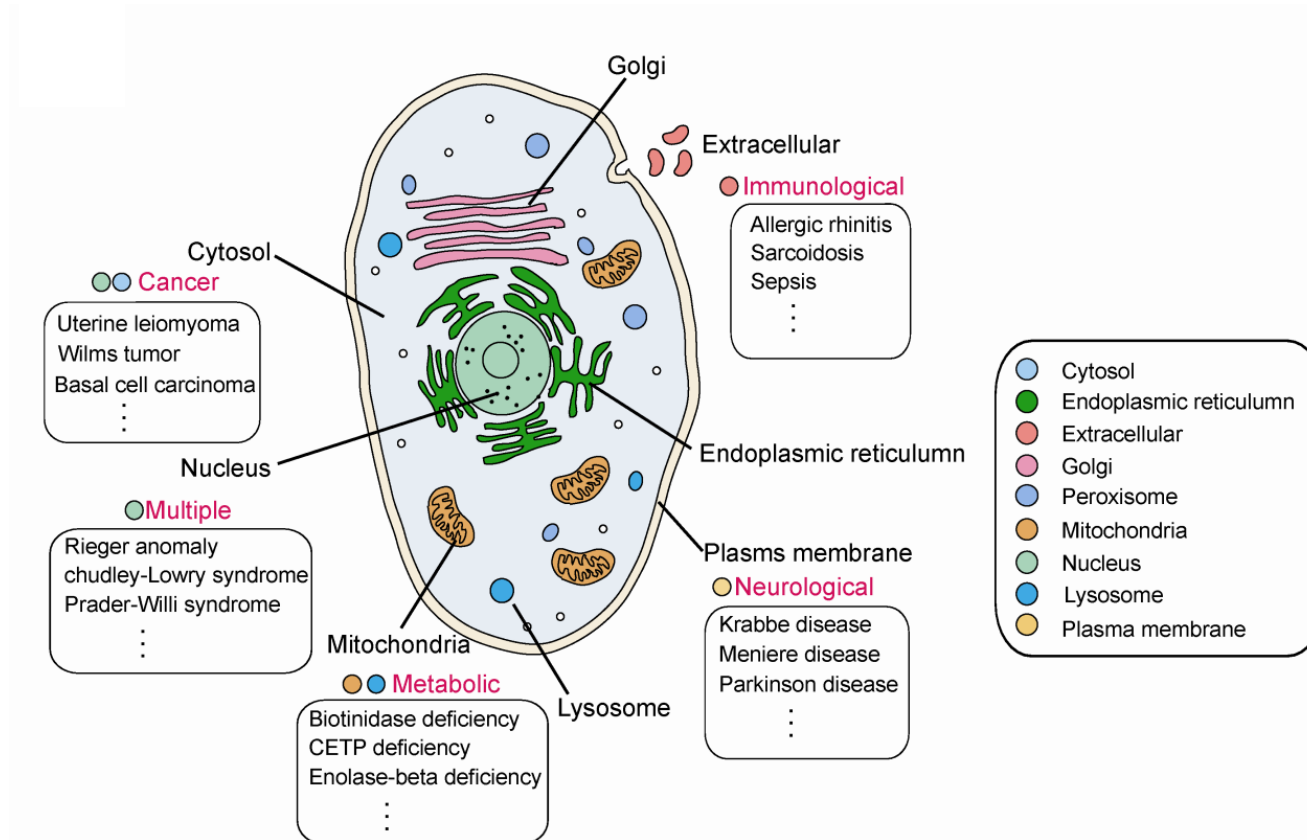
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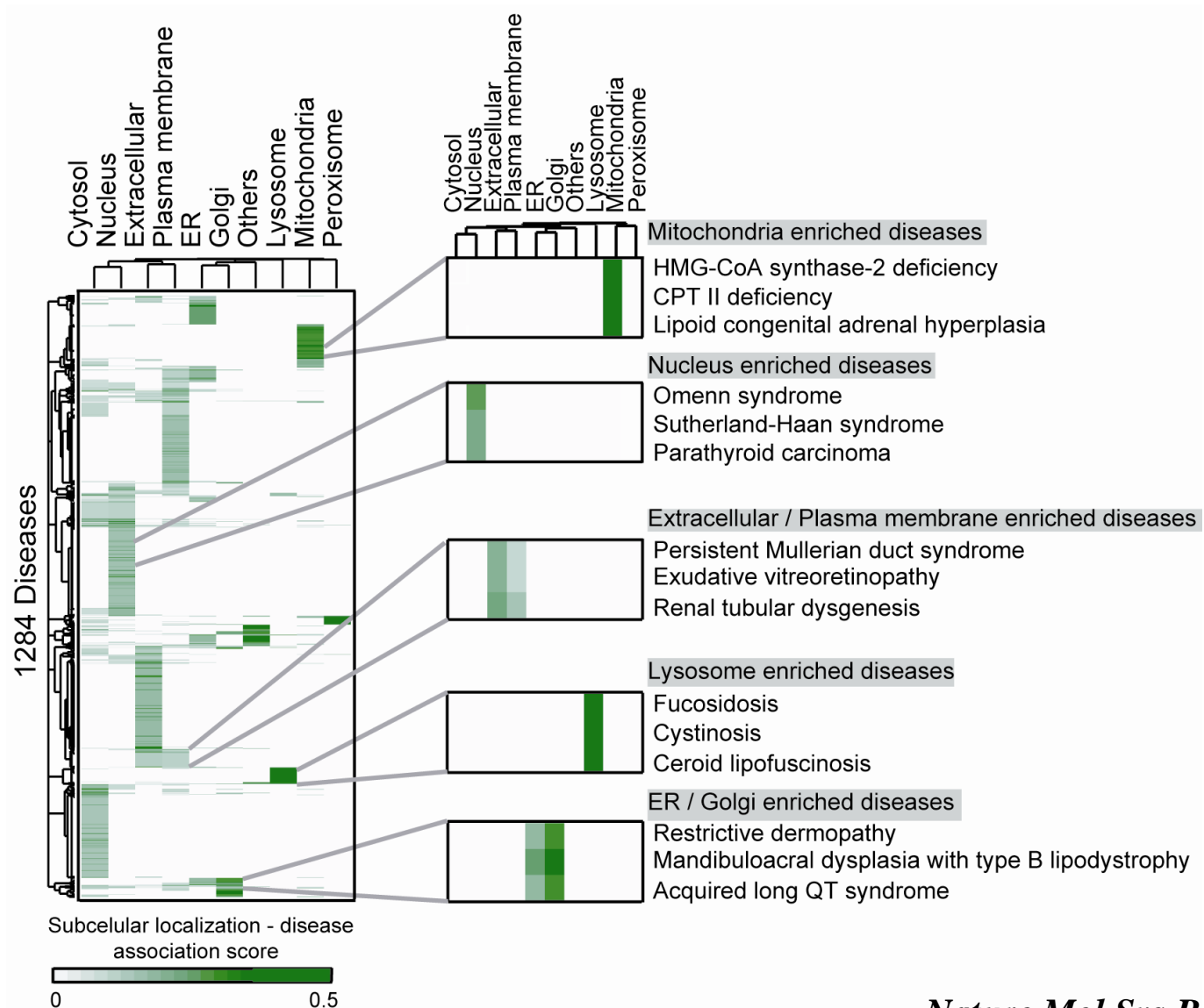
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Protein localization as a principal feature of the etiology and comorbidity of genetic diseases

Protein subcellular localization and Human diseases

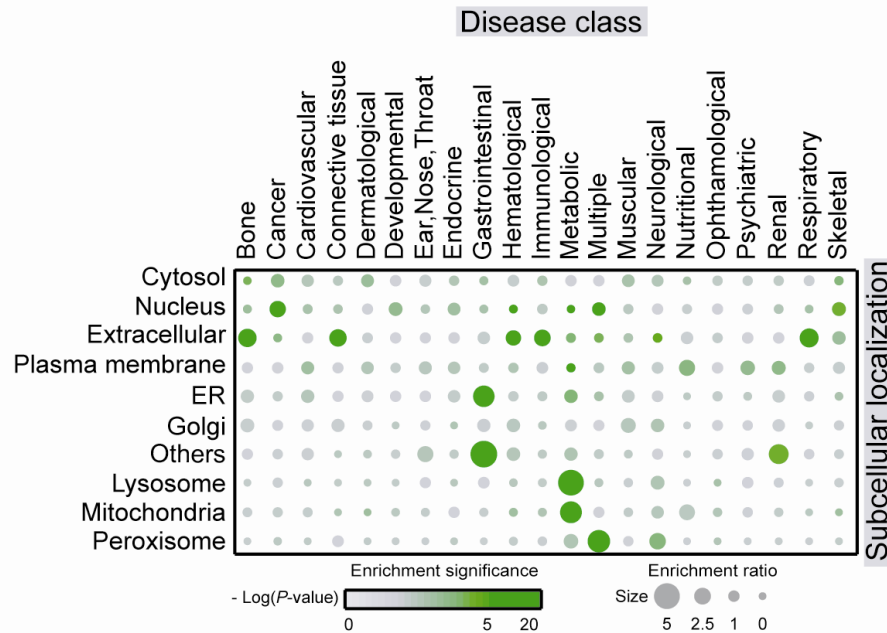


Relationships between disease-associated proteins and their subcellular localizations

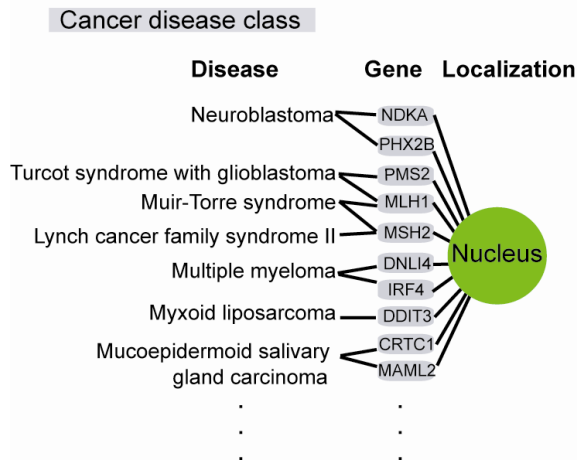


Correlation between disease classes and subcellular localizations

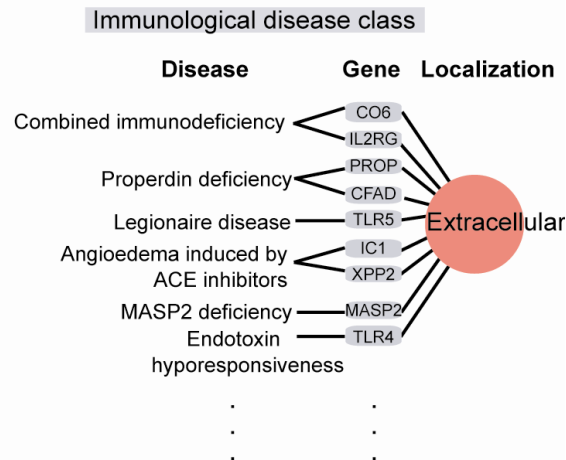
A



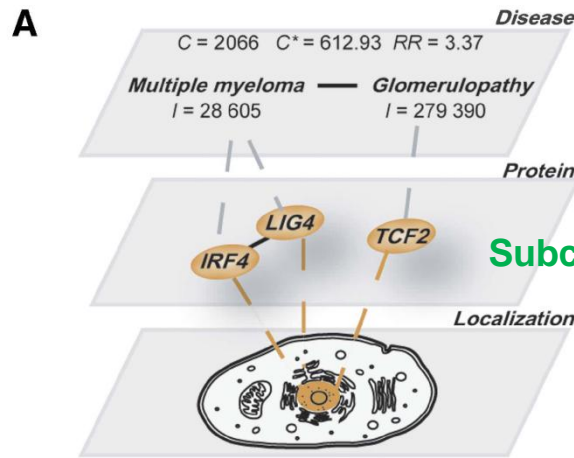
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C



The implication of subcellular localization for disease comorbidity



Subcellular localization similarity of human diseases

Subcellular localization similarity of comorbid disease pairs

Popultaion-level disease patterns

Patient

Diagnosis

Patient 1 $\left\{ \begin{array}{l} \text{Retinoblastoma} \\ \text{Stem-cell leukemia} \end{array} \right.$

Patient 2 $\left\{ \begin{array}{l} \text{Von Willebrand disease} \\ \text{Hemorrhagic diathesis} \end{array} \right.$

Disease comorbidity

Retinoblastoma

Nuc

Stem-cell leukemia

Nuc

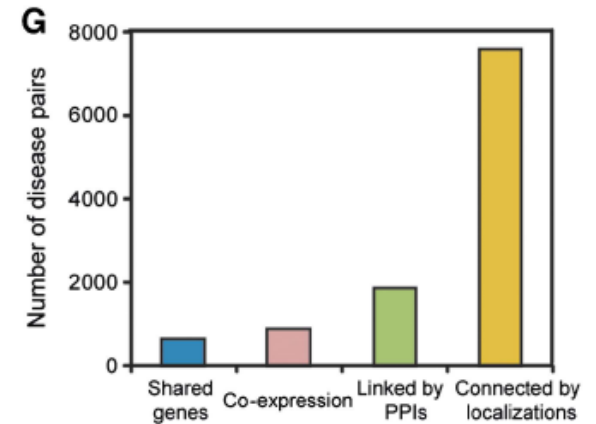
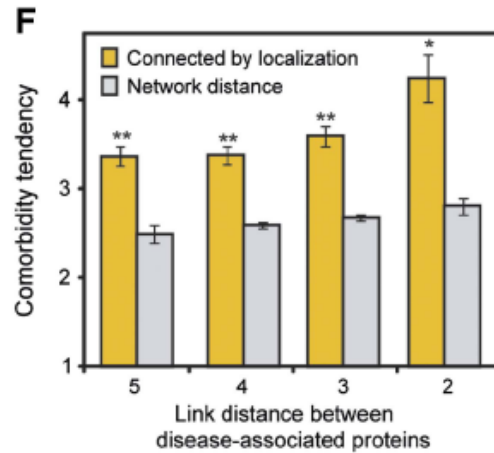
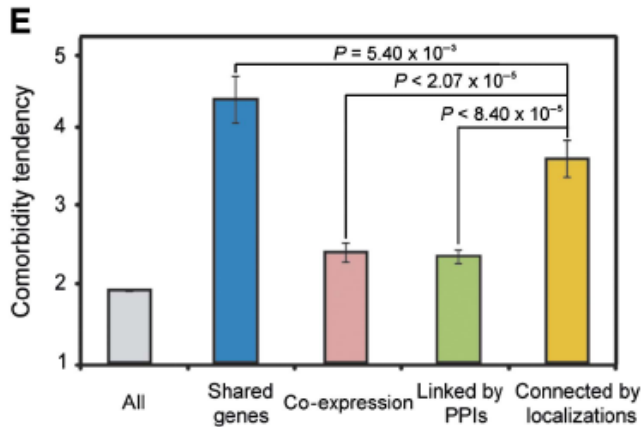
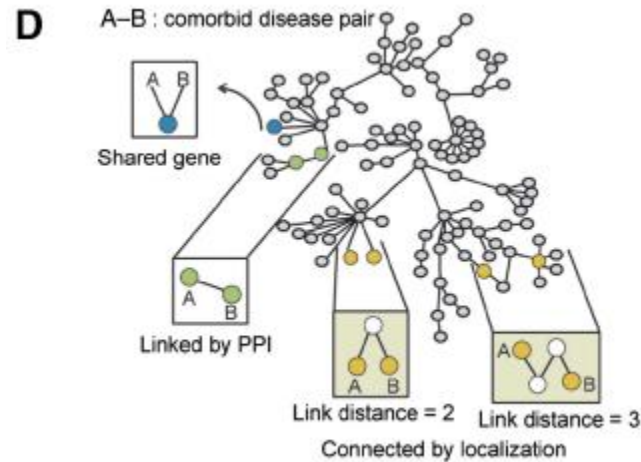
Von Willebrand disease

Ext

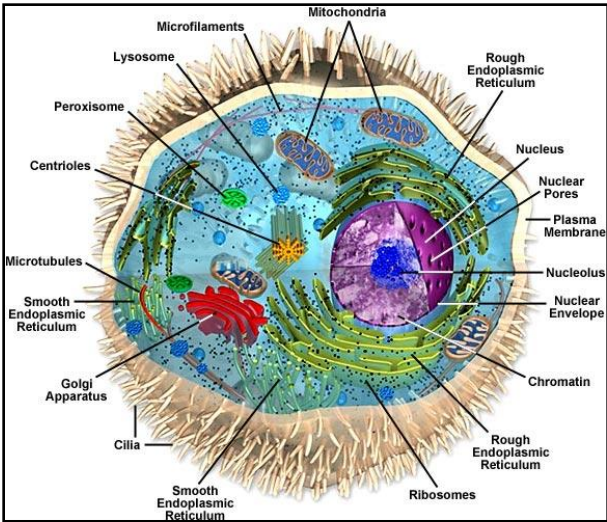
Hemorrhagic diathesis

Ext

The implication of subcellular localization for disease comorbidity



Disease gene finding through subcellular localization

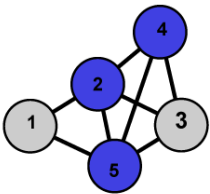


Construction of functional interaction networks through consensus localization predictions of the human proteome.

Park et al. J. Proteome Res., 2009, 8 (7), pp 3367–3376

A

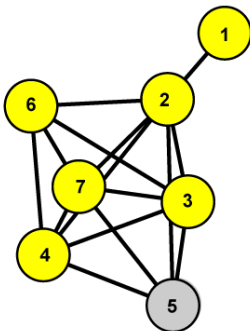
Localization: Plasma membrane
Disease: Basal cell carcinoma



- 1: GP107_Human
- 2: PTC1_Human
- 3: HHIP_Human
- 4: SMO_Human
- 5: PTC2_Human

B

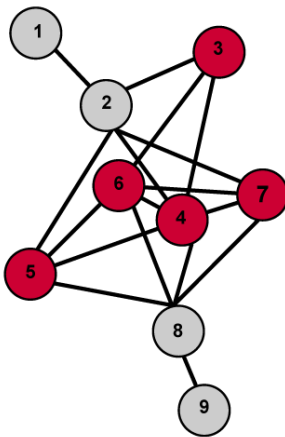
Localization: Cytosol
Disease: Deafness, autosomal dominant



- 1: MYO3A_Human (Con)
- 2: WHRN_Human
- 3: MYO15_Human
- 4: OMP_Human
- 5: MYO6_Human
- 6: MYO7A_Human
- 7: USH1C_Human (Con)

C

Localization: Nucleus
Disease: Mental retardation



- 1: VEX2_Human (Con)
- 2: ARX_Human
- 3: ZNF81_Human
- 4: JADIC_Human
- 5: AFF2_Human (Con)
- 6: OPHN1_Human
- 7: ZNF41_Human (Con)
- 8: ACSL4_Human
- 9: TMEM9_Human

> Protein **localization information** facilitates the identification of **disease** associated genes

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Human disease evolution *Nature Scientific Reports* 2012

Mitochondrial protein network *Nature Scientific Reports*

2013

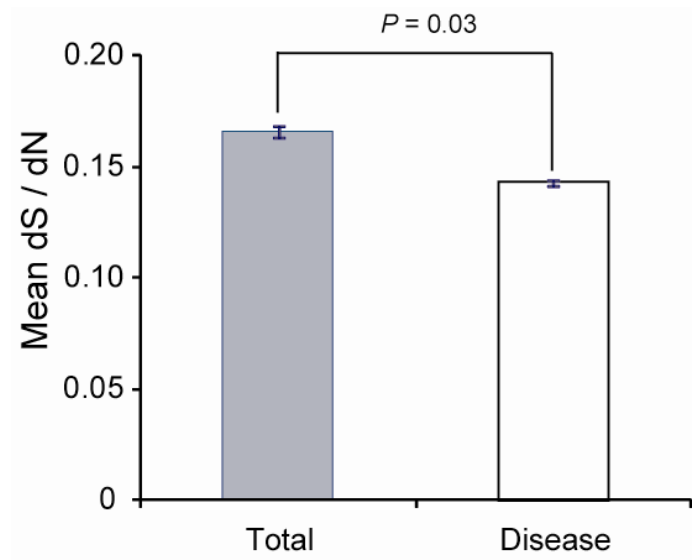
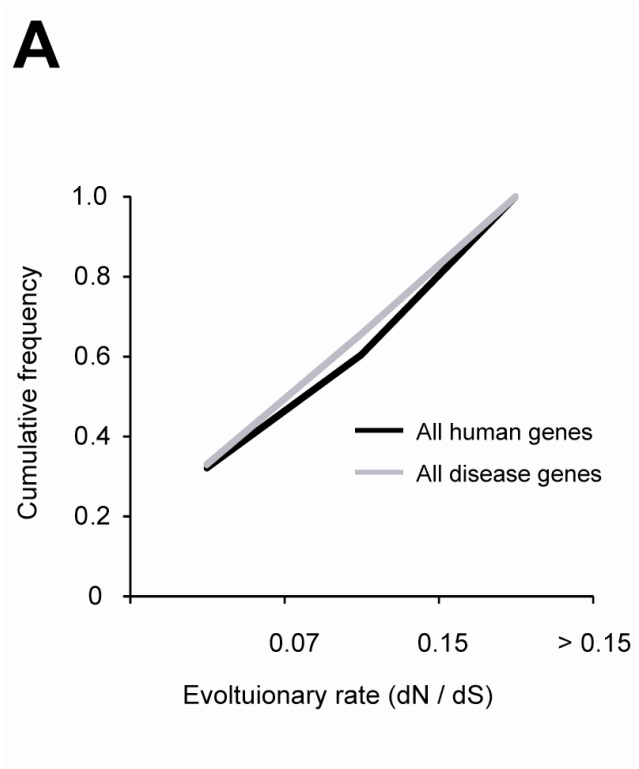
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Neuronal Disease *PLoS Genetics* 2012

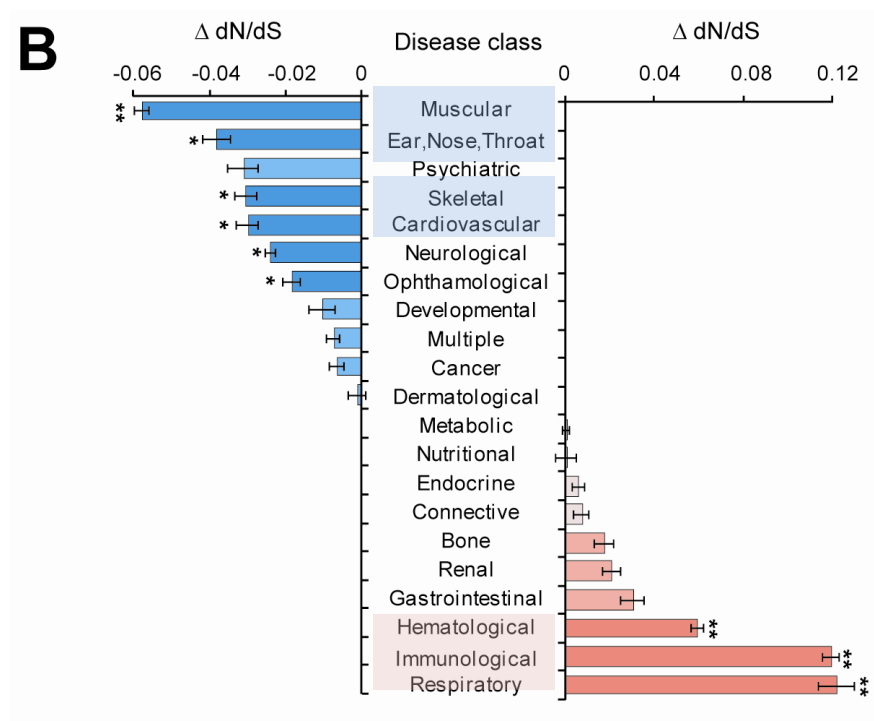
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Human disease genes; fast or slow evolving ?



Suppl. Figure

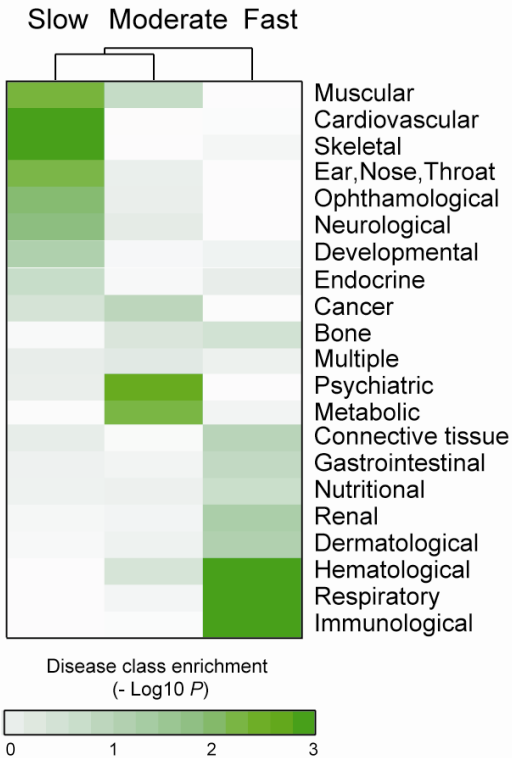
Human disease genes have diverse evolutionary rates



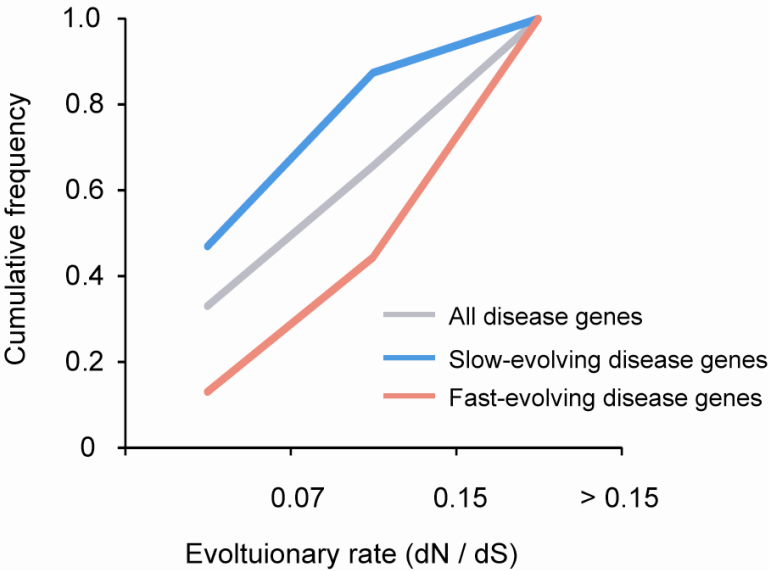
Phenotypically similar disease classes share similar evolutionary history

Human disease genes have diverse evolutionary rates

C

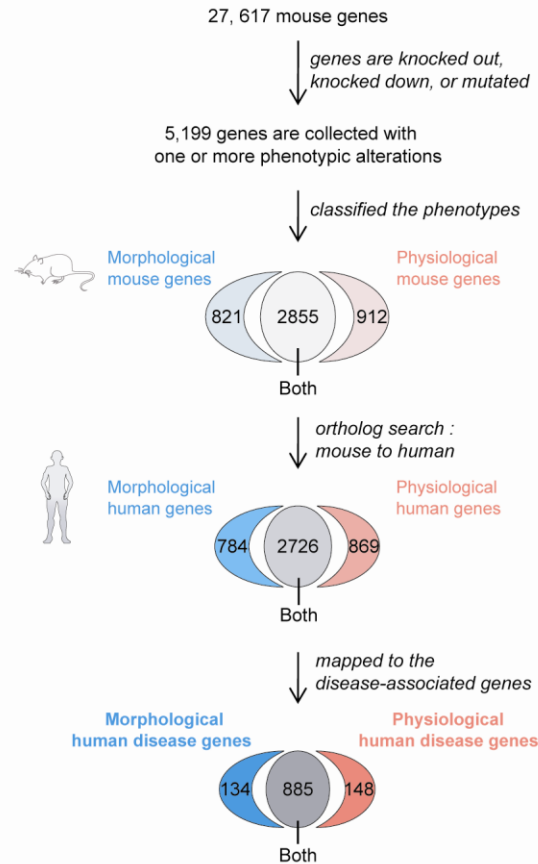


D

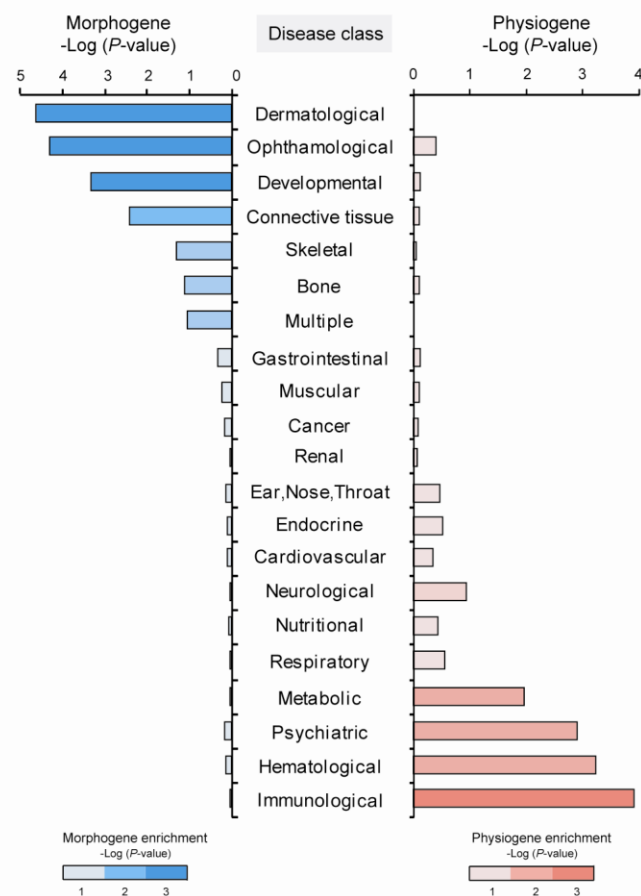


Morphogenes and physiogenes enriched differently In various disease classes

A



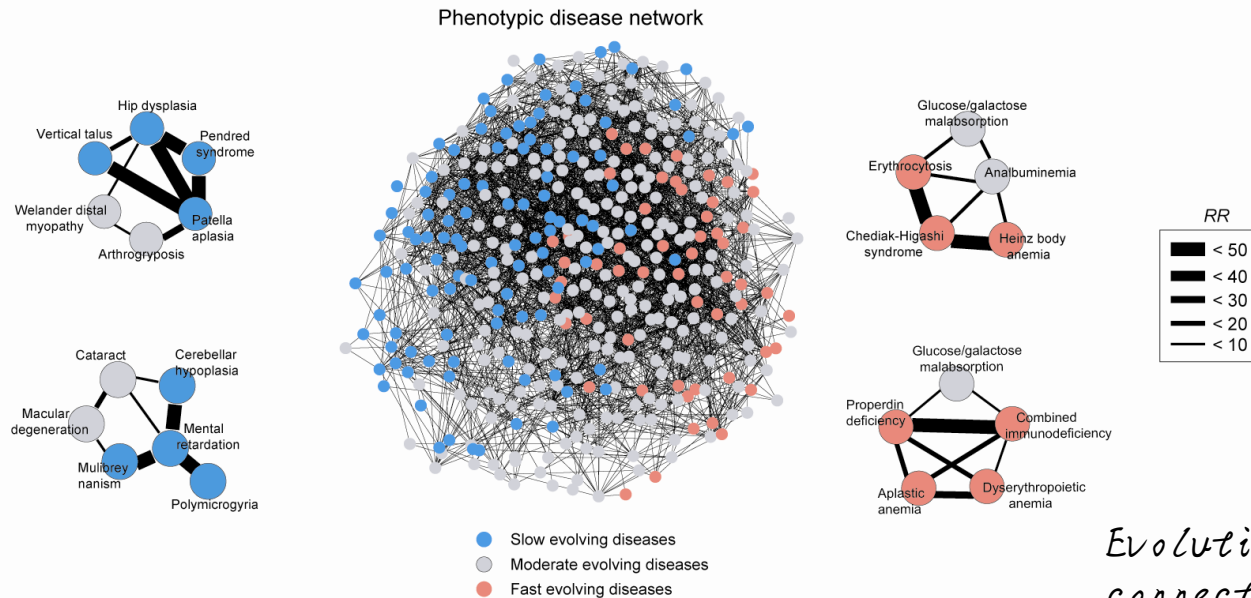
B



Evolution connect genotype to phenotype

Molecular connections in the comorbid disease pairs

A



Evolutionary connections



Molecular connections



*Phenotypic connections
: comorbidity*

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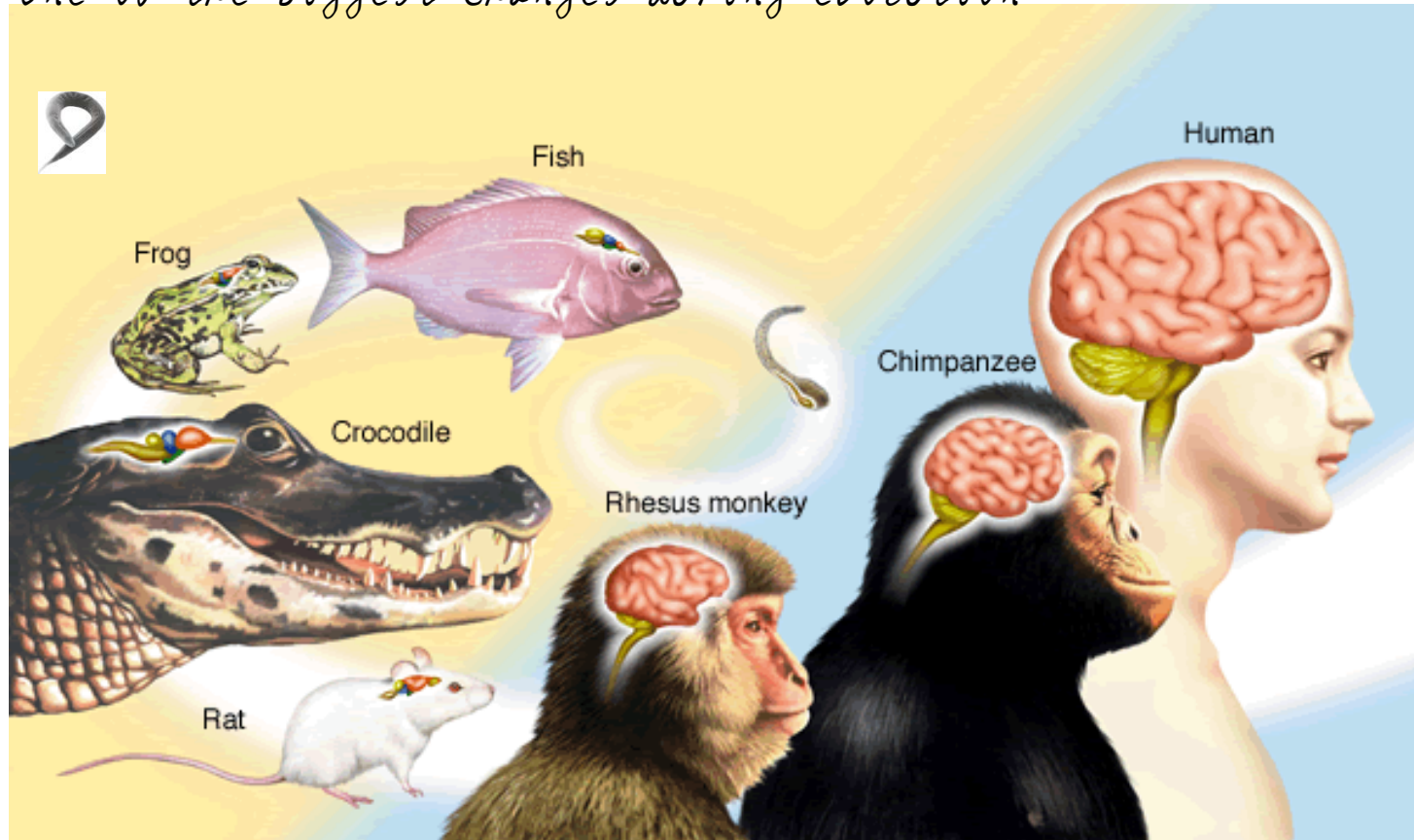
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Rewiring of PDZ domain-ligand interaction network contributed to eukaryotic evolution

Evolution of brain

One of the biggest changes during evolution

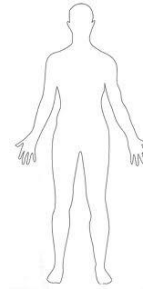
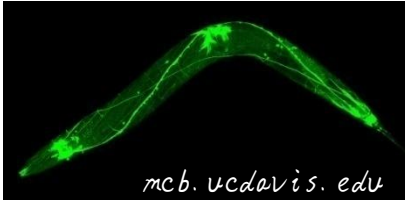
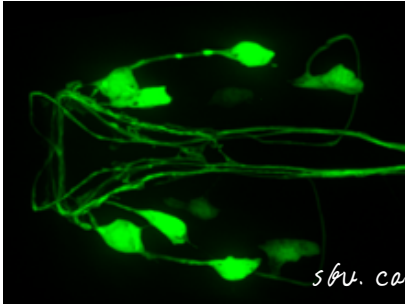


<http://www.brain.riken.jp>

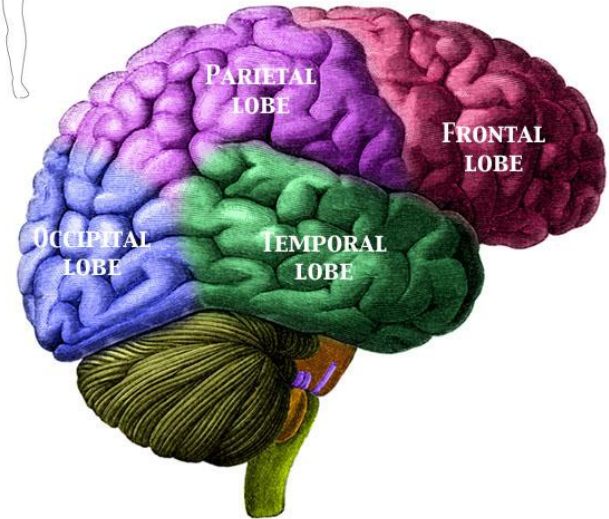
Increase of synaptic diversity (number of brain regions)



C. elegans brain



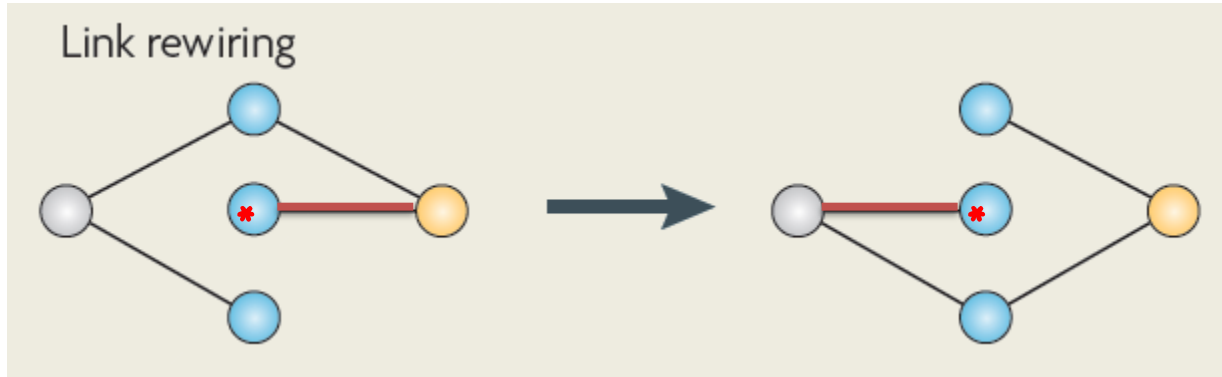
Human brain



lilachrysiou.wordpress.com

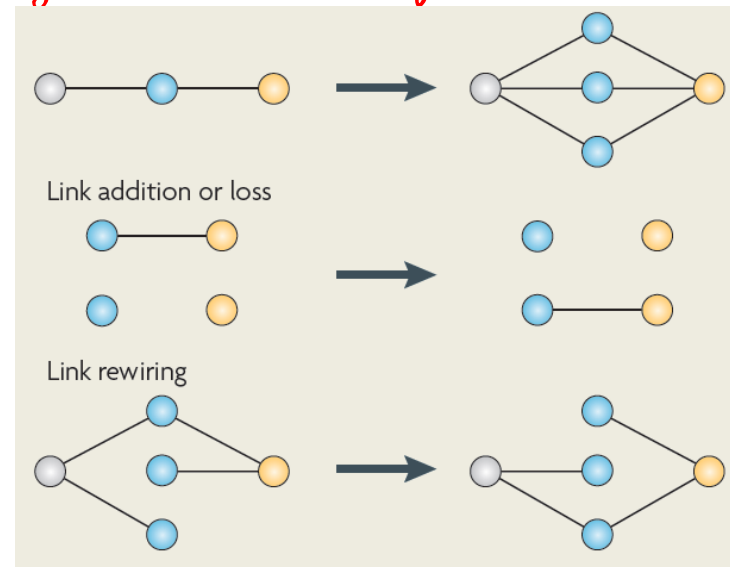
What is the molecular level explanation of neuronal development?

Rewiring of interactions



T. Yamada and P. Bork, Nat. Rev. Mol. Cell biol. 2009

Interaction rewiring can reconfigure molecular systems without a gain or loss of gene.

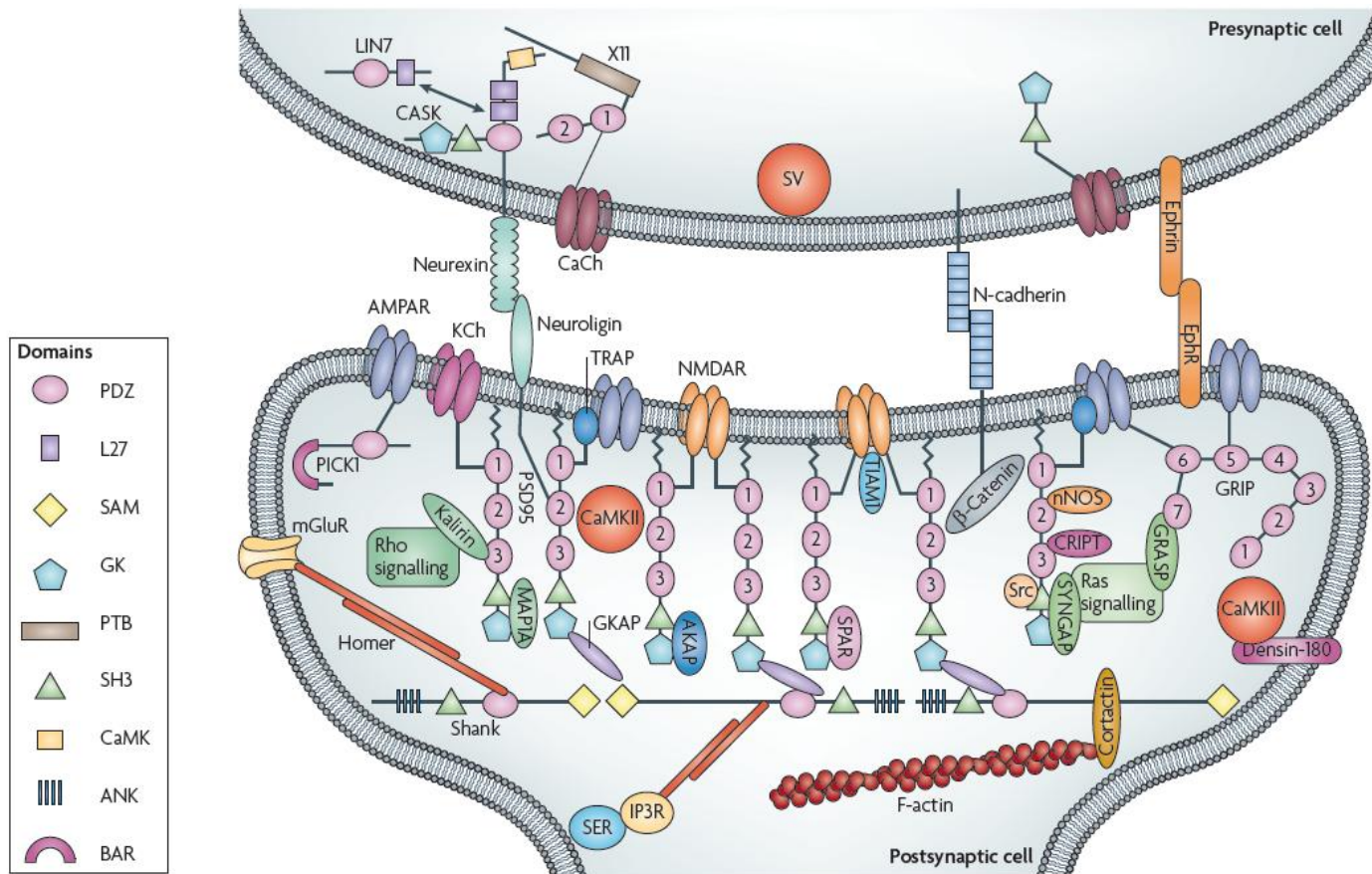


PDZ protein interactions play important roles in the postsynaptic density (PSD)

Organization and dynamics of PDZ-domain-related supramodules in the postsynaptic density

Wei Feng and Mingjie Zhang

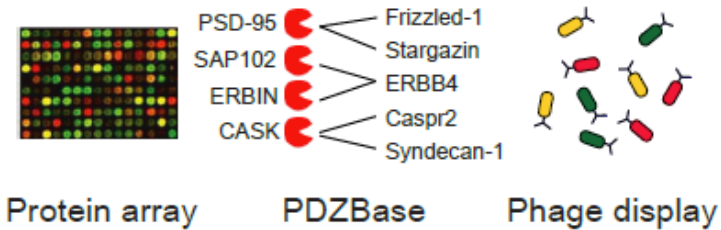
NATURE REVIEWS | **NEUROSCIENCE** | FEBRUARY 2009 |



Construction of human PDZ domain-ligand interaction network (PDZNet)

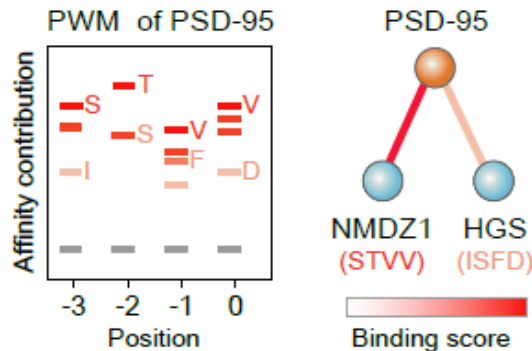
A

Experimental datasets of
PDZ domain-peptide interactions



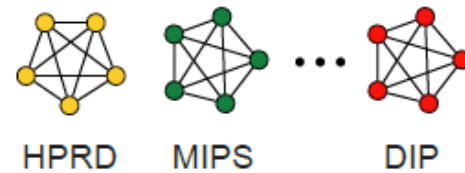
Build a quantitative model of
PDZ domain-peptide interactions

Generate Position Weight Matrices (PWMs)
and calculate binding scores of
PDZ protein-ligand interactions



B

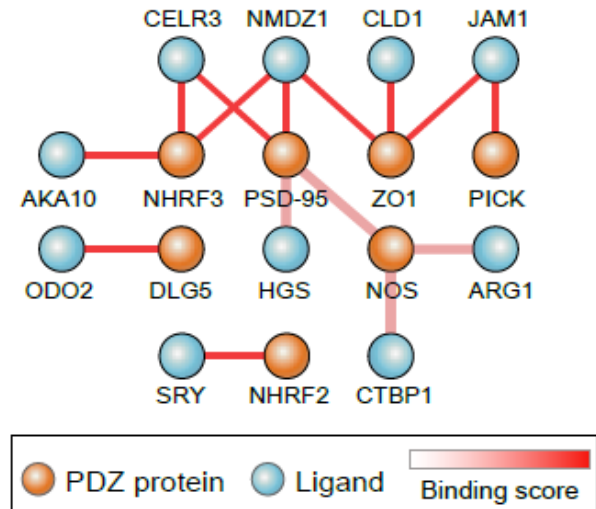
PPI databases



Select PDZ domain-
mediated interactions

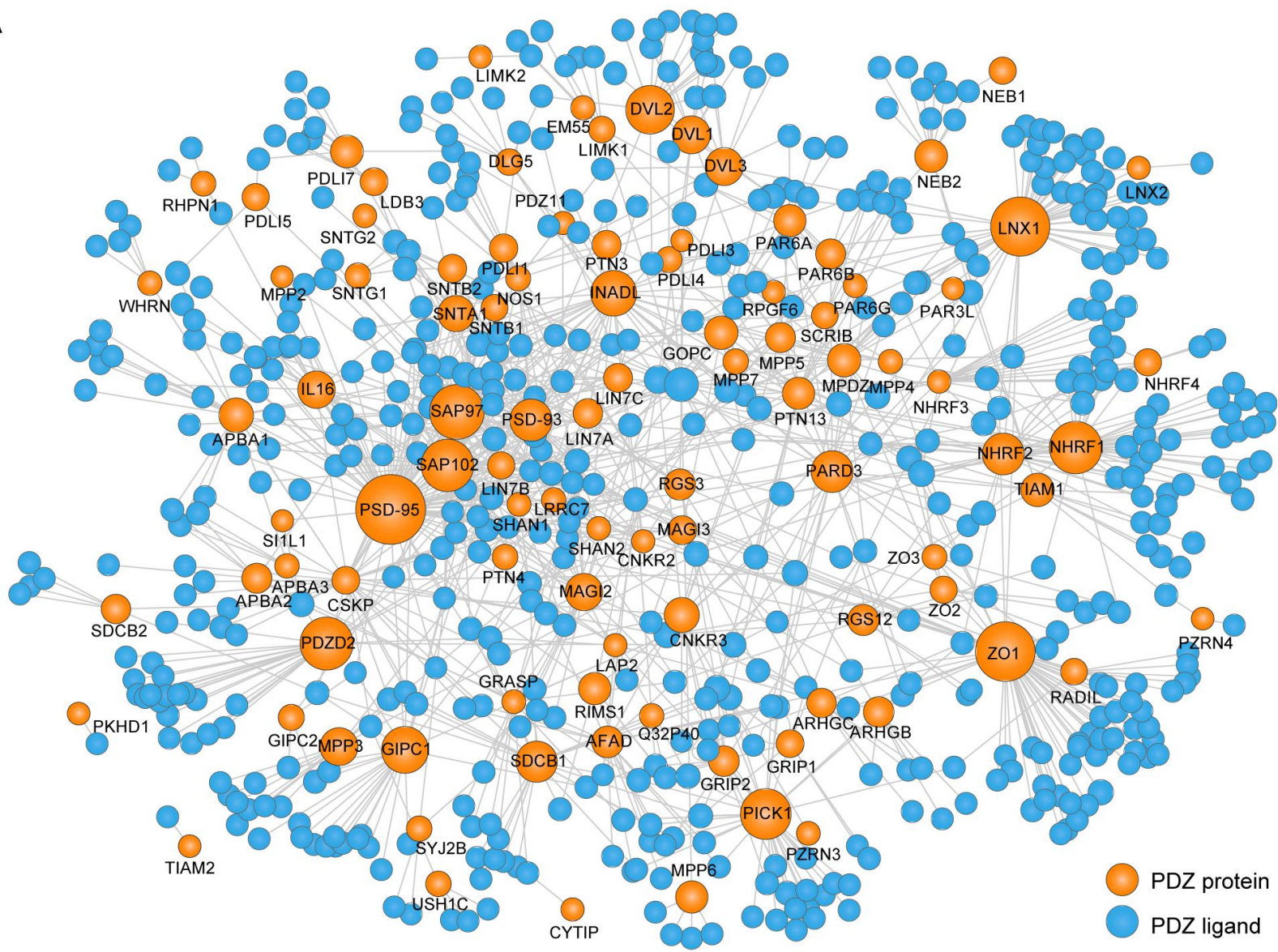
C

PDZNet

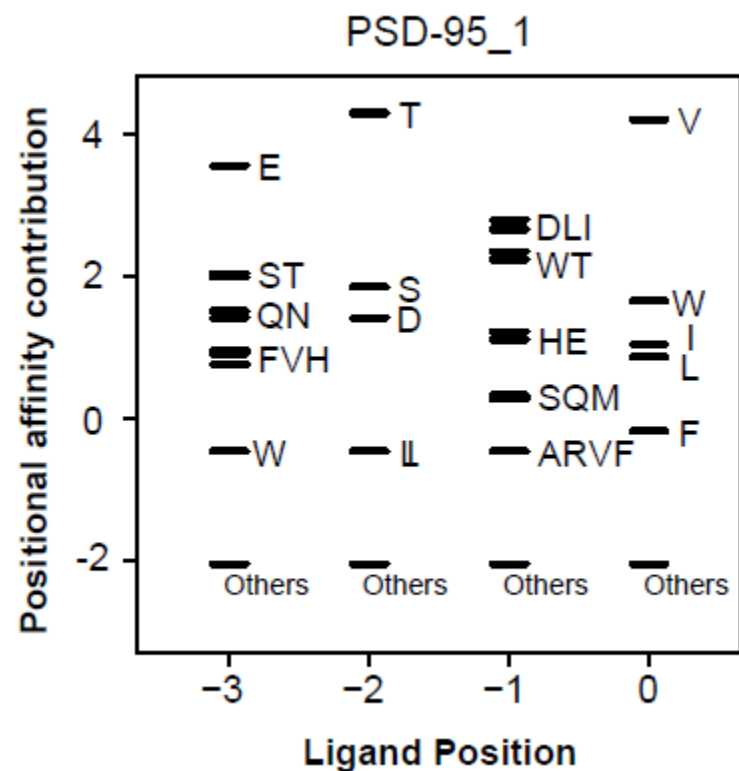


Human PDZNet

A



PWM can identify the known binders of PDZ domains

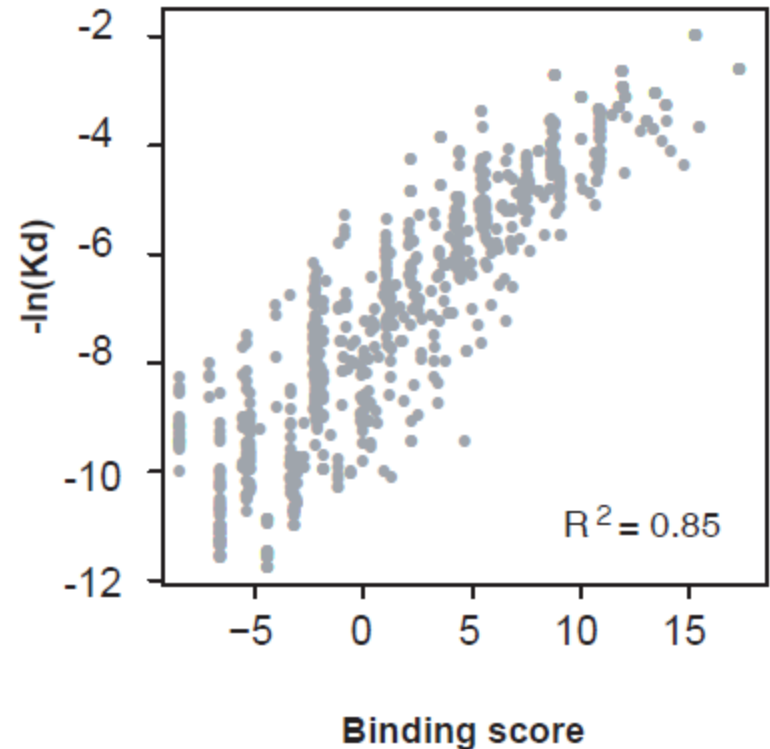
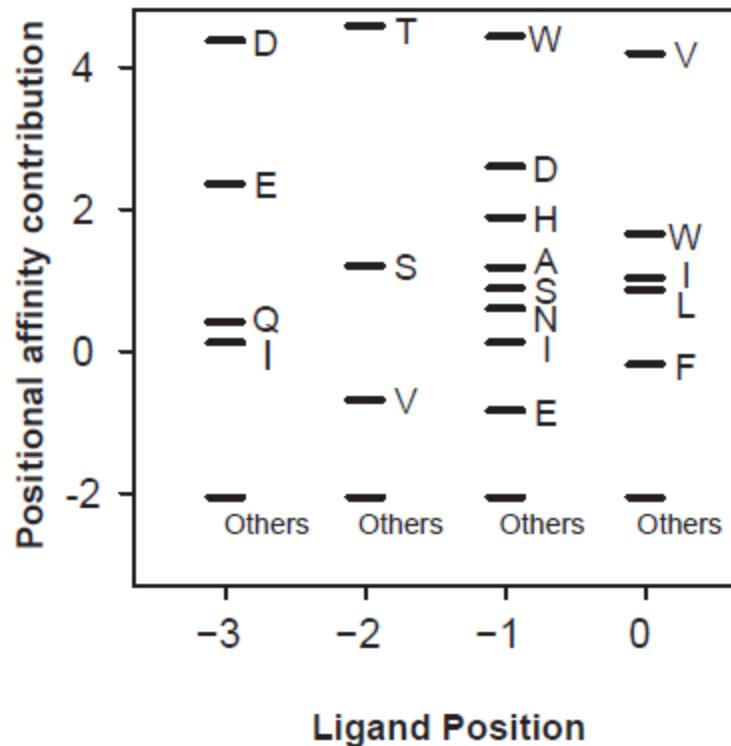


Species	Ligand	C-terminal	Percentile rank (%)	Binding score
Human	PMCA4b	ETSV	99.86	13.05
	PMCA2b	ETSL	99.26	9.49
Mouse	Frizzled-4	ETVV	99.96	13.80
	Frizzled-1	ETTV	99.93	13.49
	Frizzled-2	ETTV	99.93	13.49
	Frizzled-7	ETAV	99.87	13.19
	Sema4c	ESSV	99.59	10.61
	BAI1	QTEV	99.56	10.52
	Stargazin	TTPV	99.36	9.77
Rat	Kv1.4	ETDV	99.98	14.72
	ERBB4	NTVV	99.76	12.67
	NMDAR2A	ESDV	99.72	12.28
	NMDAR2B	ESDV	99.72	12.28
	SynGAP	QTRV	99.19	9.79
	PKC-A	QSAV	98.64	8.99
	Sec8	ITTV	98.12	7.93
	GluR6	ETMA	96.19	6.00

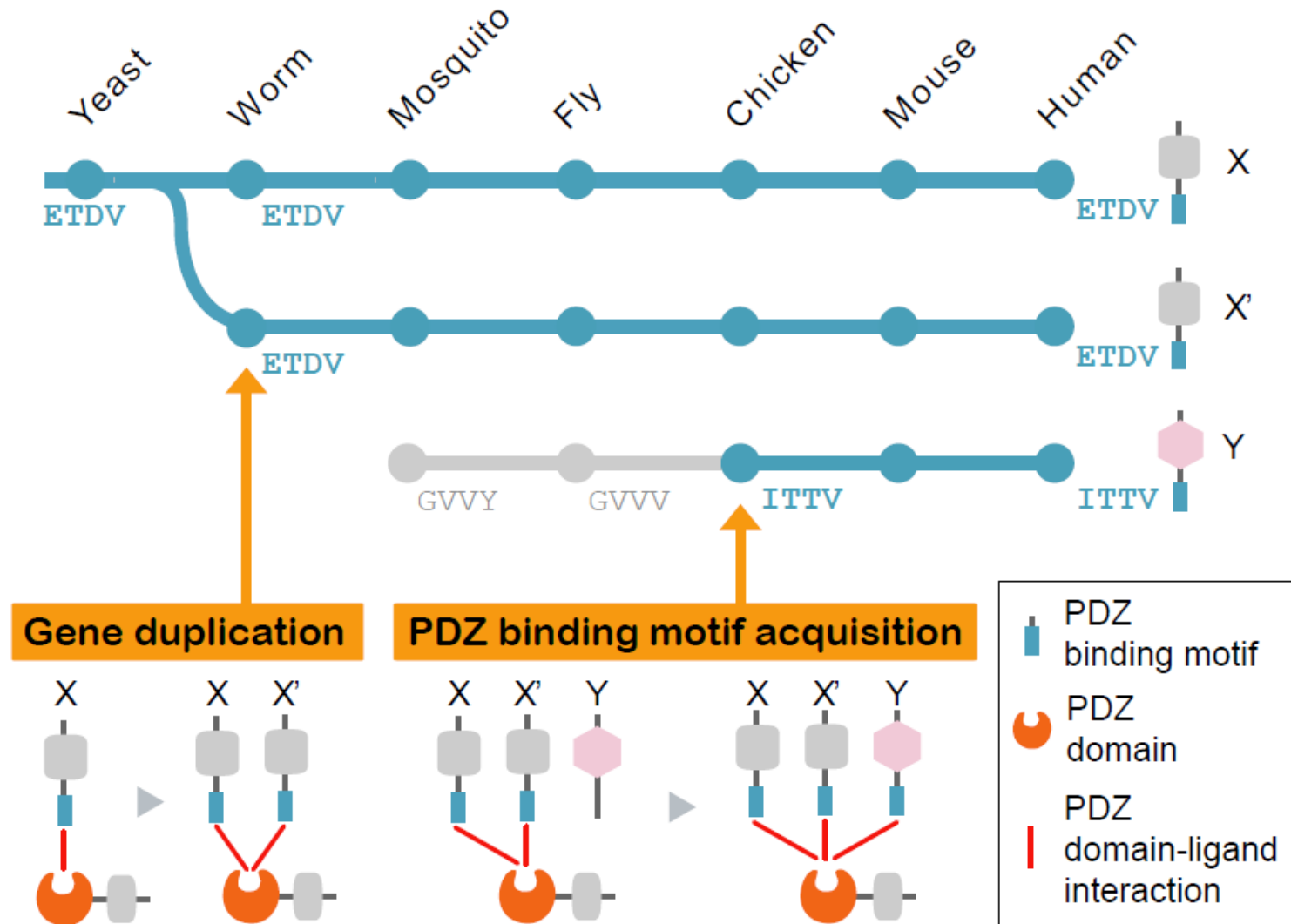
Binding scores correlate well with experimental affinities

ERBIN human

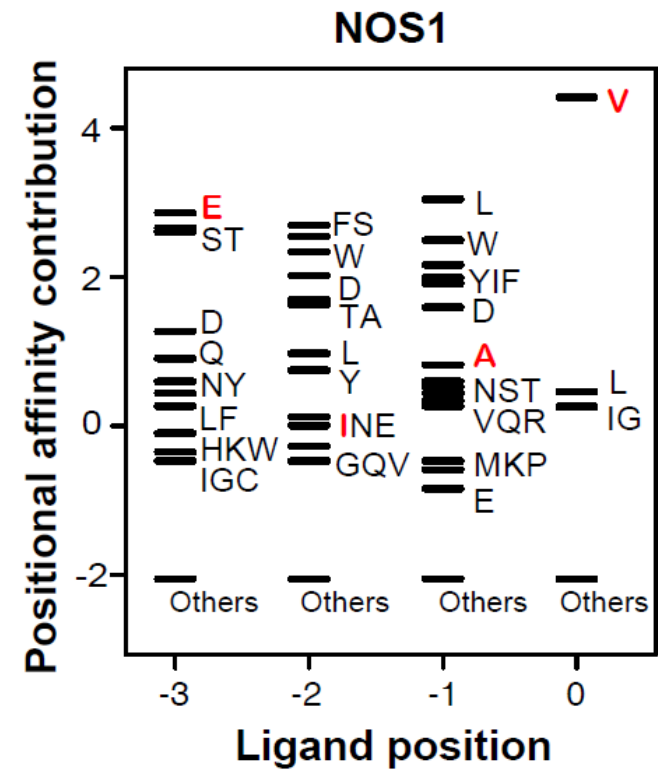
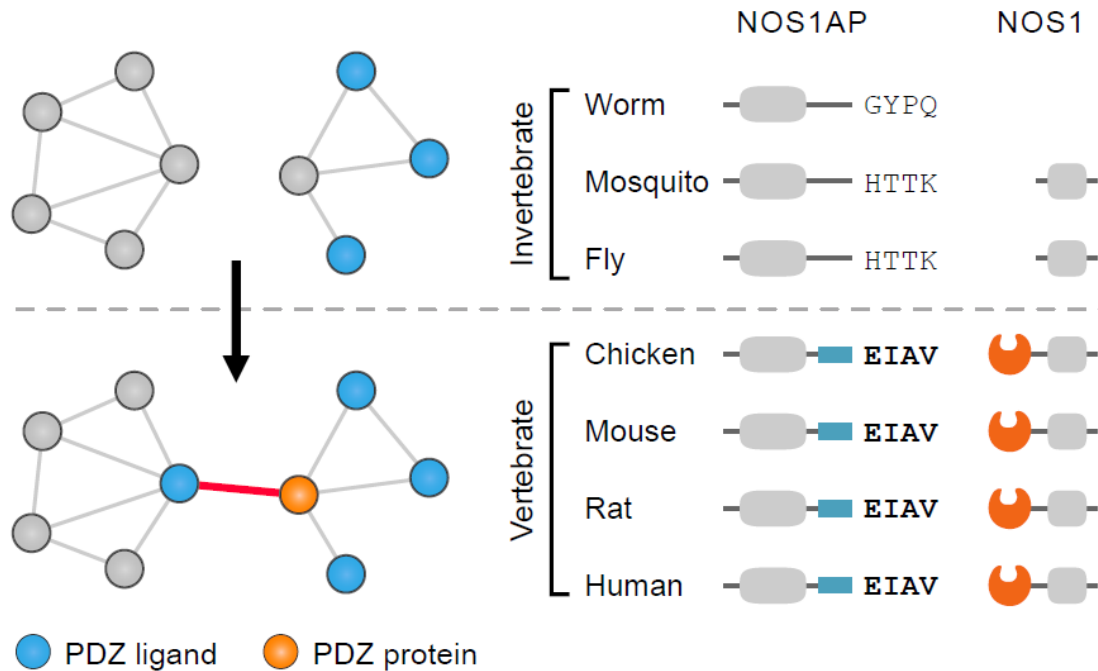
D



Two evolutionary models describe the expansion of PDZ domain-ligand interactions

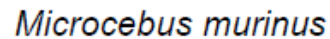


Examples of a PDZ domain-ligand interaction created by sequence mutations





Macaca mulatta  ETDV



Macaca mulatta

P S A A R I V E A L E I D V Q
CCTTCTGCTGCACGTATCGTTGAAGCTTTGGAAATAGATGTCCAG
| | | | | . | . | . | | | . | | | | . | | | | . |
CCTTCTGCTGCCACATTGTTGGAGCTCTGGAAA CAGATGTC TAG
P S A A H I V G A L E T D V Stop

Point mutations

A DNA segment insertion generated a PDZ-binding motif in the C-terminal amino acids of the *Oryzias latipes* EXOC4 protein.



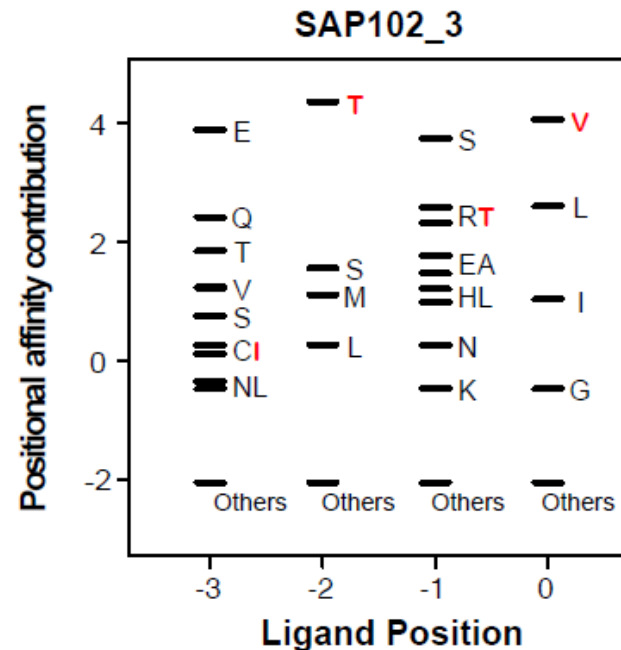
Anopheles gambiae

EXOC4

GVTV

Oryzias latipes

ITTV



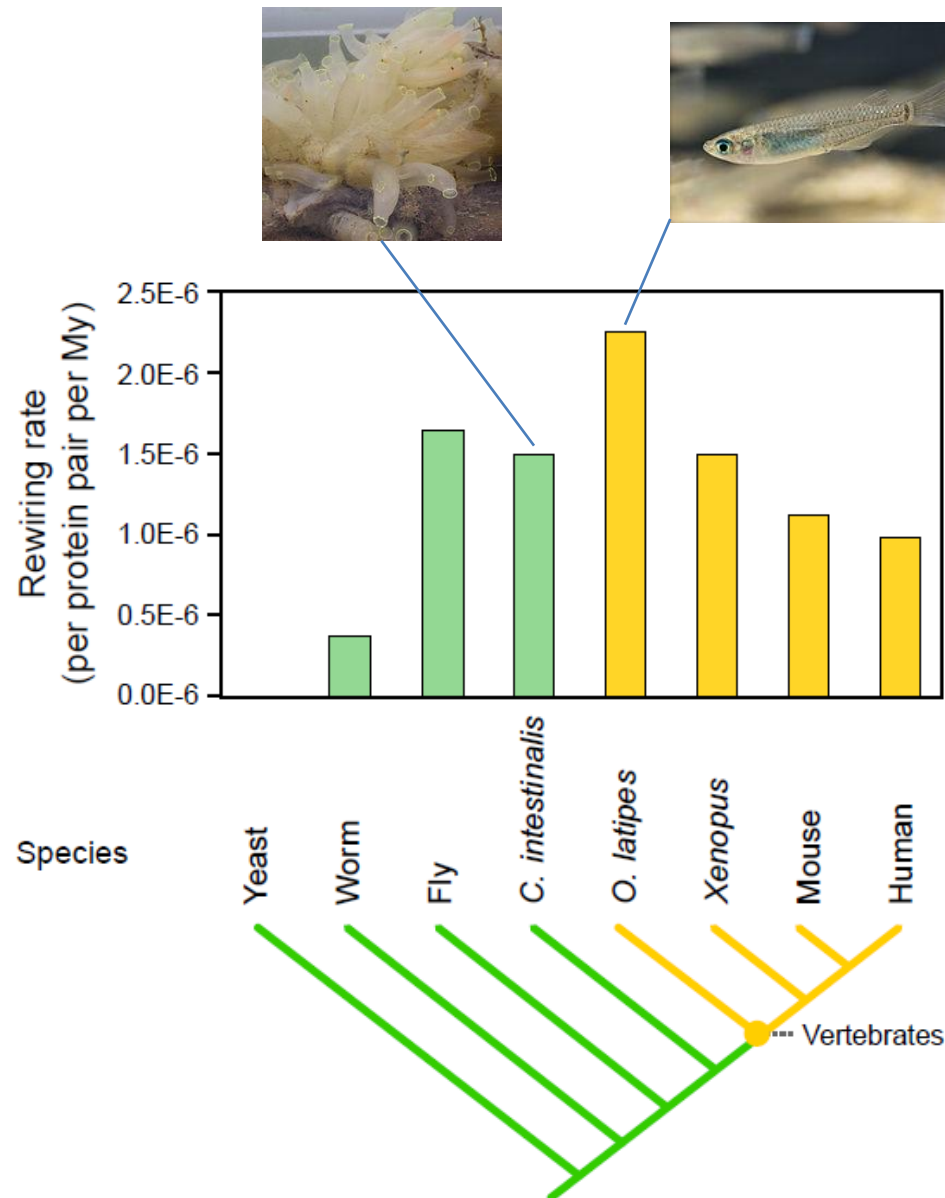
Anopheles gambiae

Oryzias latipes

G	T	K	P	A				L	G	V	T	V	Stop
-CGGCA-CAA--AGCCCGC-----CCTCGGTGTGACCGGTGTGA													
.													
-CGCCATCAAACAGGCCACCAAGGATAAGAAGATCACCCACGGTGTAA													
A I K Q A T K D K K I T T V Stop													

Frame shift
by DNA insertion

Rewiring of PDZ domain-ligand interactions plays an important role in the evolution of nervous systems in vertebrates.



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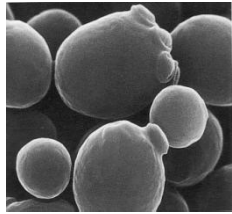
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Increase of network complexity has a major impact on gene essentiality changes.



Mechanism of gene essentiality

Complex relationship between genotype and phenotype

Gene essentiality often changes during evolution

Map2k1 (nonessential in yeast but essential in mouse)

- "Map2k1^{-/-} embryos die at mid-gestation from abnormal development and hypovascularization of the placenta." (Vikram Bissonauth, et al. Development 2006)
- "In the mouse, loss of Map2k1 function causes embryonic lethality." (Valérie Nadeau, et al. Development 2009)

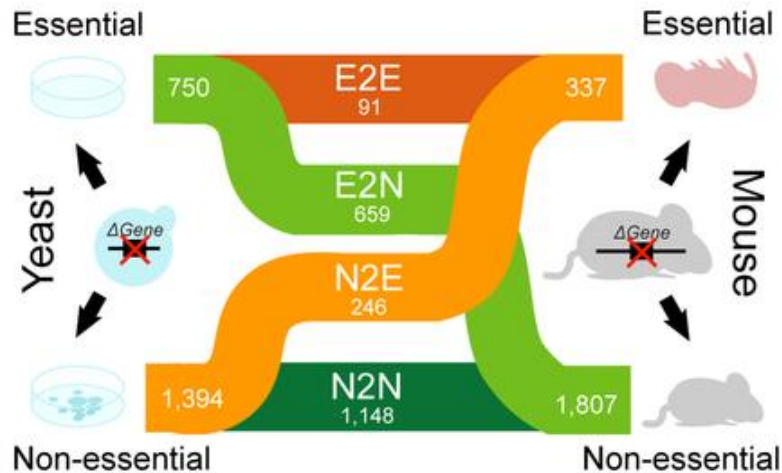
Ada (nonessential in yeast but essential in mouse)

- "Adenosine deaminase deficient (*Ada*) mice die perinatally." (Alexandra A. J. Migchielsen, et al. Nat. Genetics 1995)

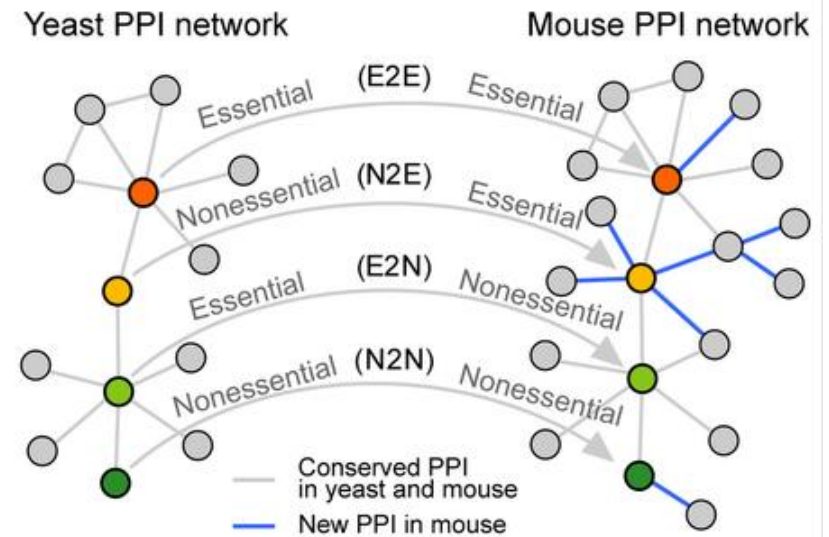
It is unclear how nonessential genes become essential in more complex organisms

Increase in network connections and gene essentiality changes between yeast and mouse

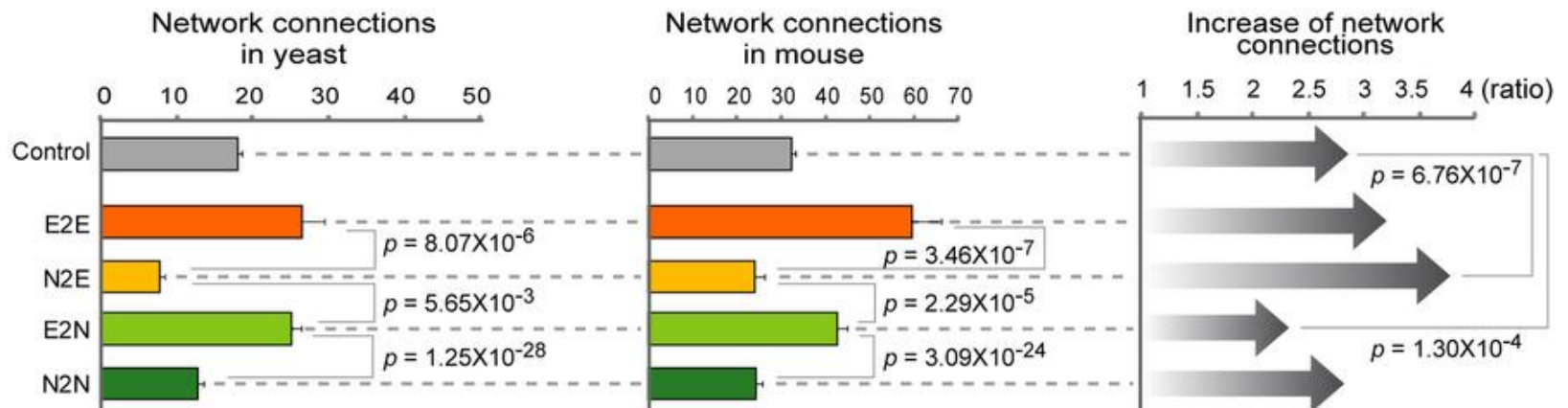
a



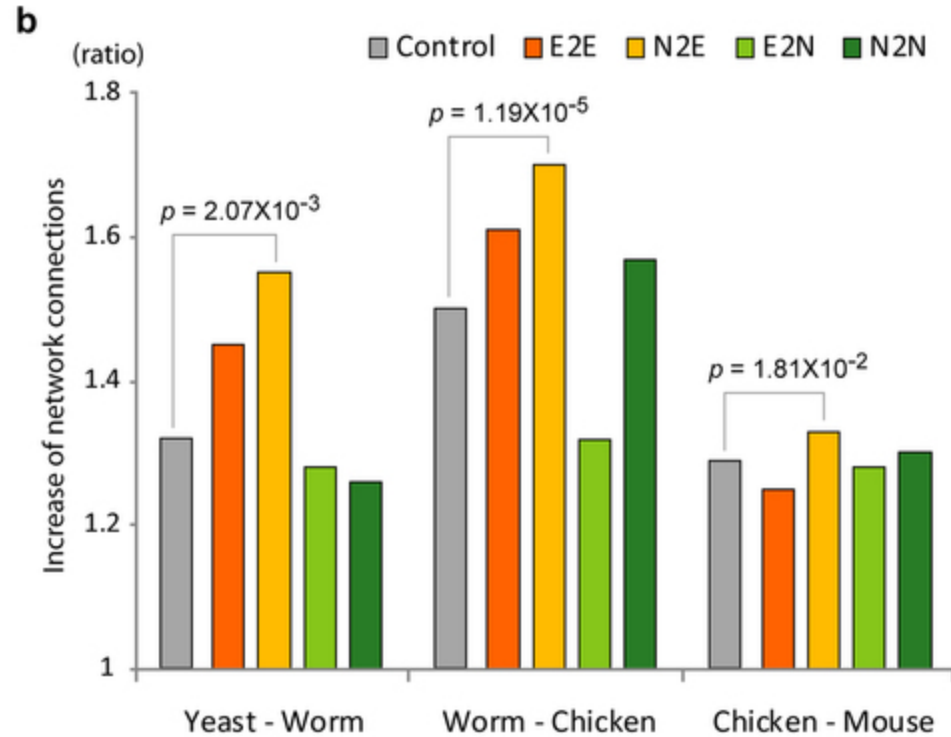
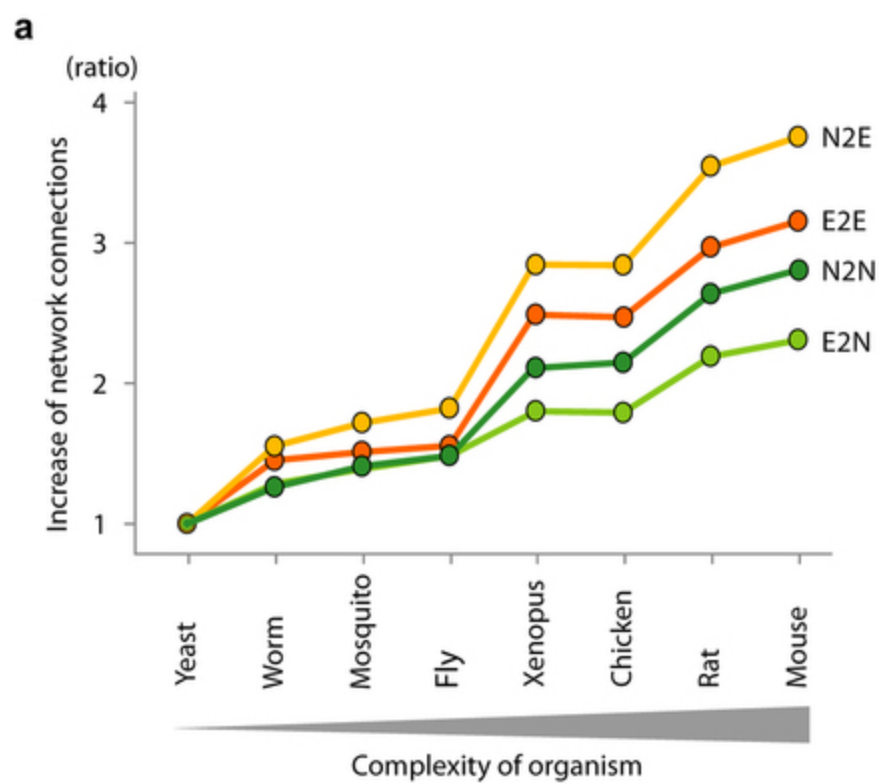
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c

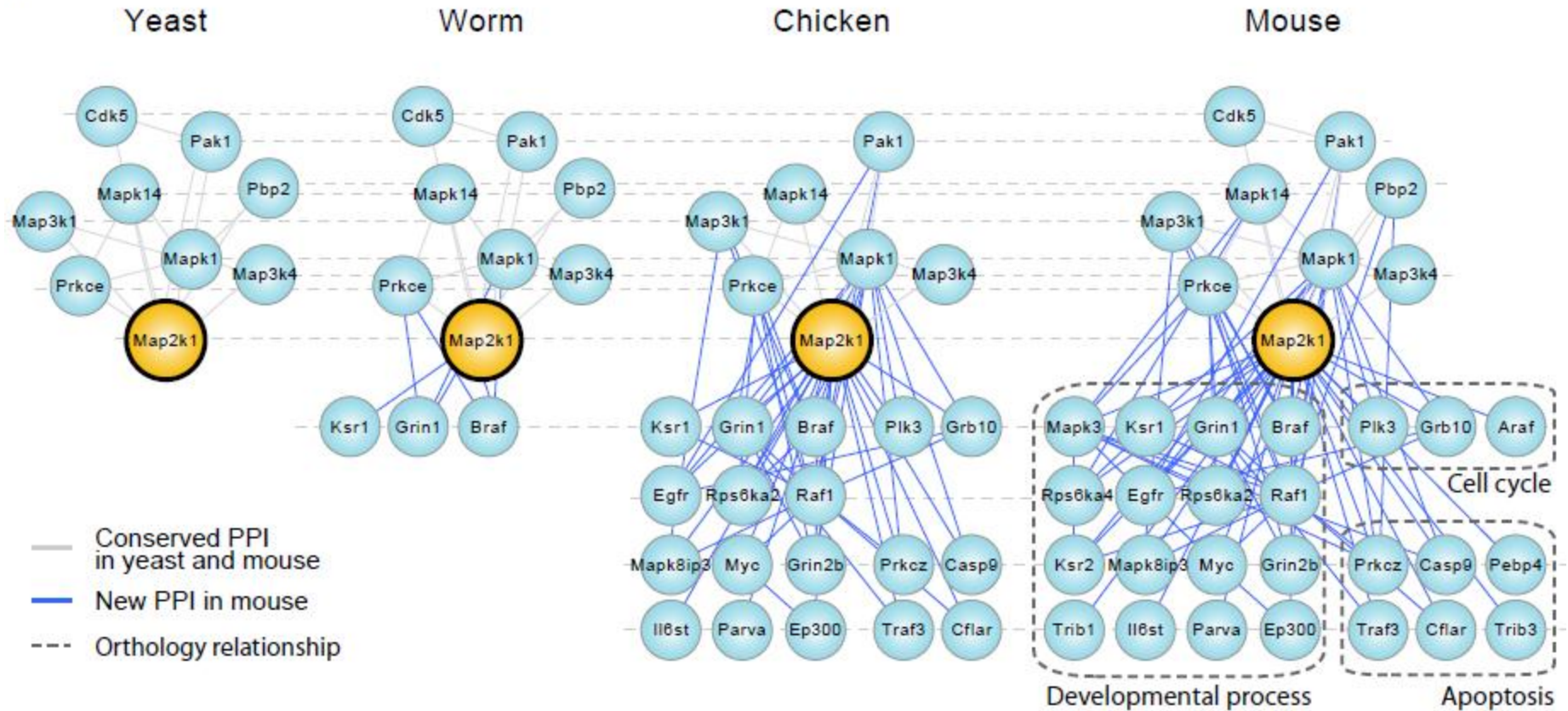


Comparison of network connections in various species



Network connections of Map2k1 in yeast, worm, chicken, and mouse

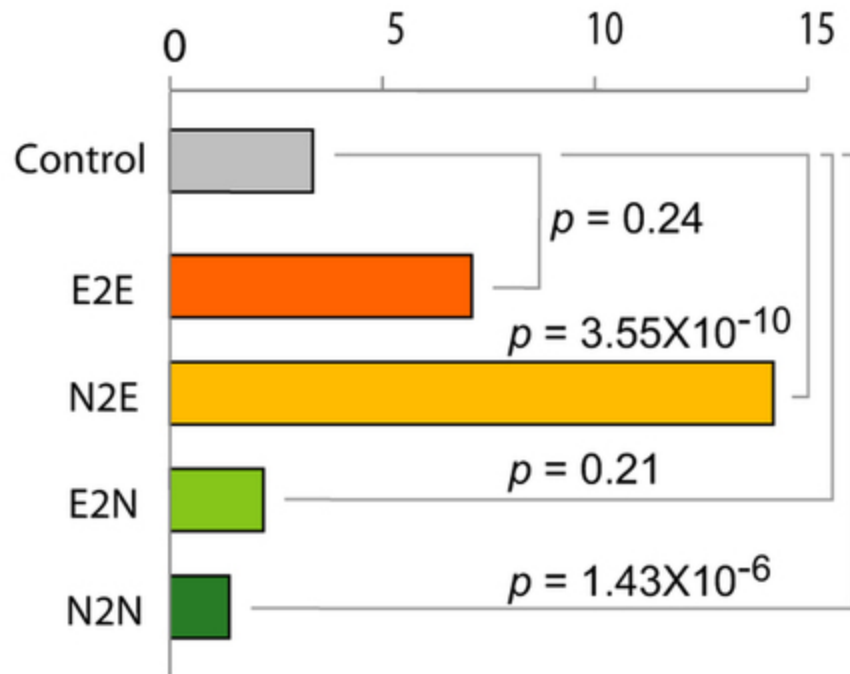
c



Protein complex membership and evolution of gene essentiality changes

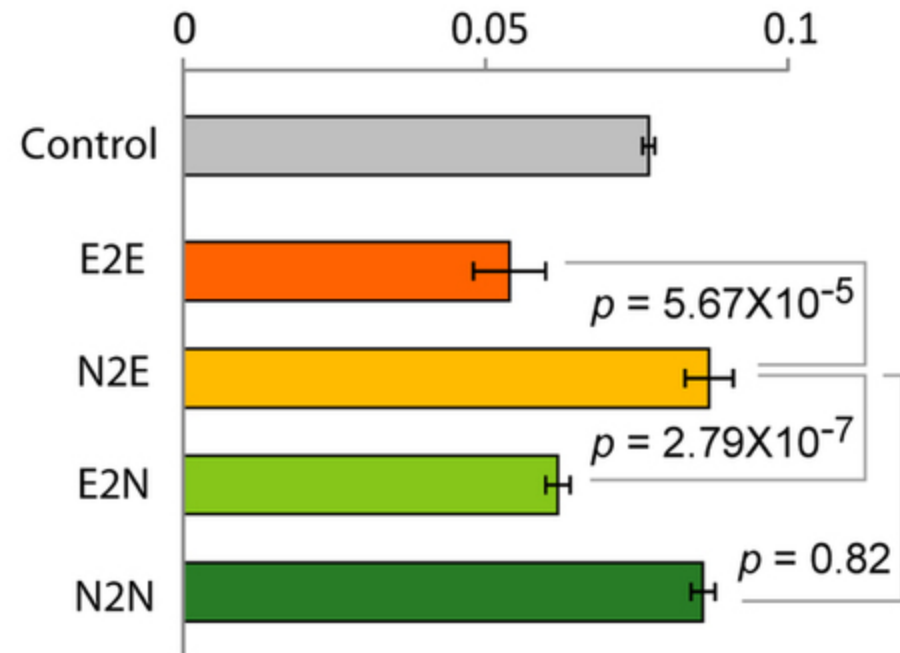
a

Fraction of genes newly involved in complexes (%)

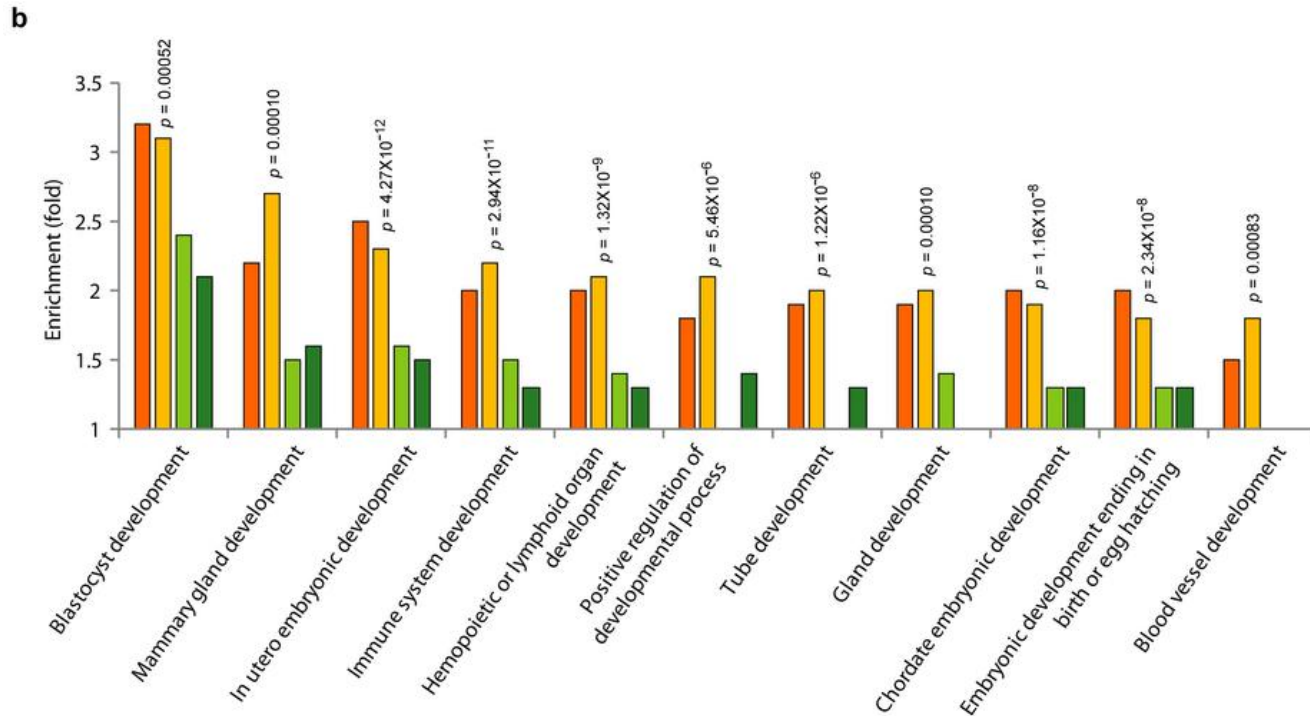
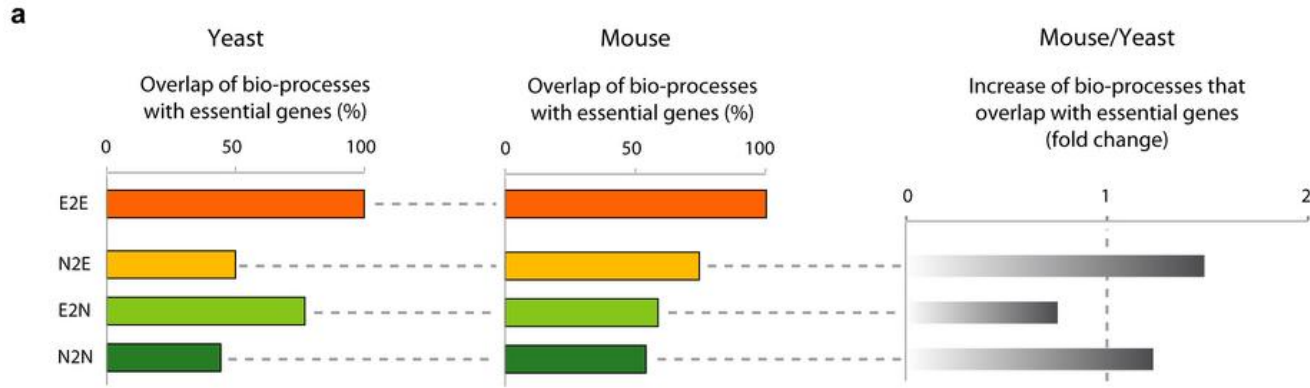


b

Evolutionary rate (dN/dS)

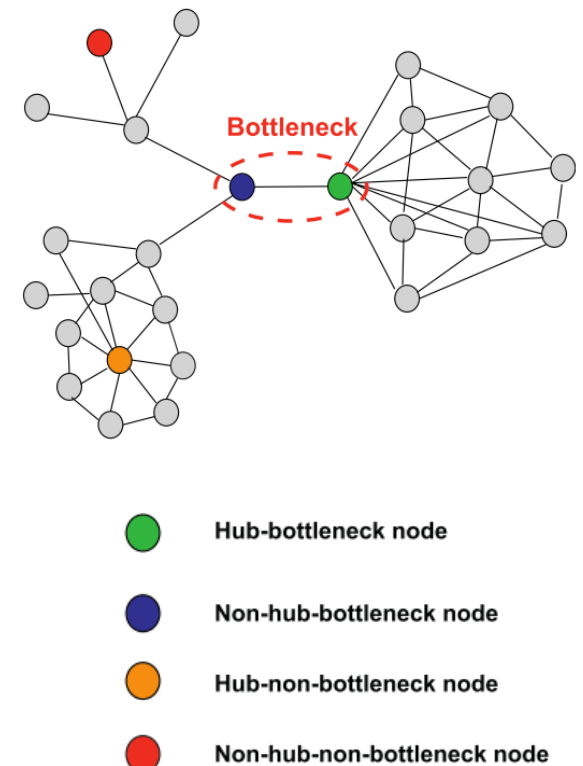
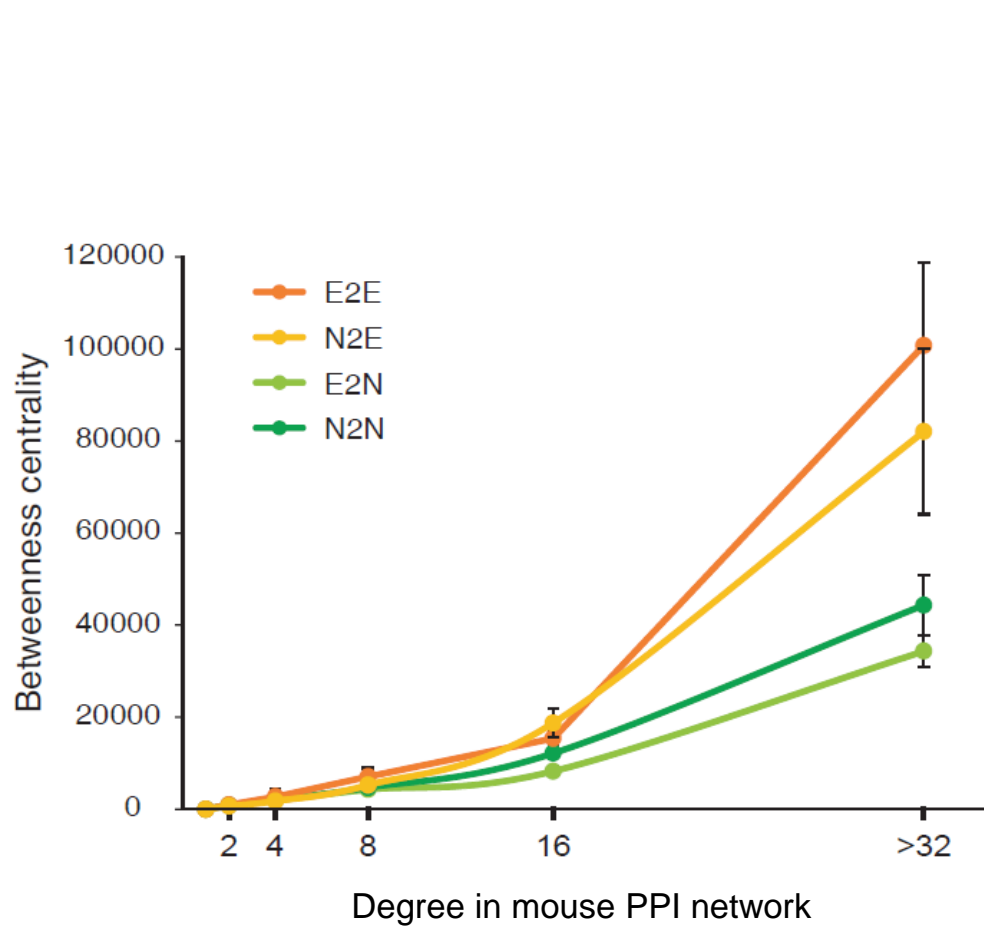


N2E genes integrated into vital pathways via interaction rewiring



Old genes became essential by participating into vital pathways.

N2E genes often bridge functional modules and control information flow in the PPI network.



Haiguan Yu, Mark Gerstein, Plos CB 2007

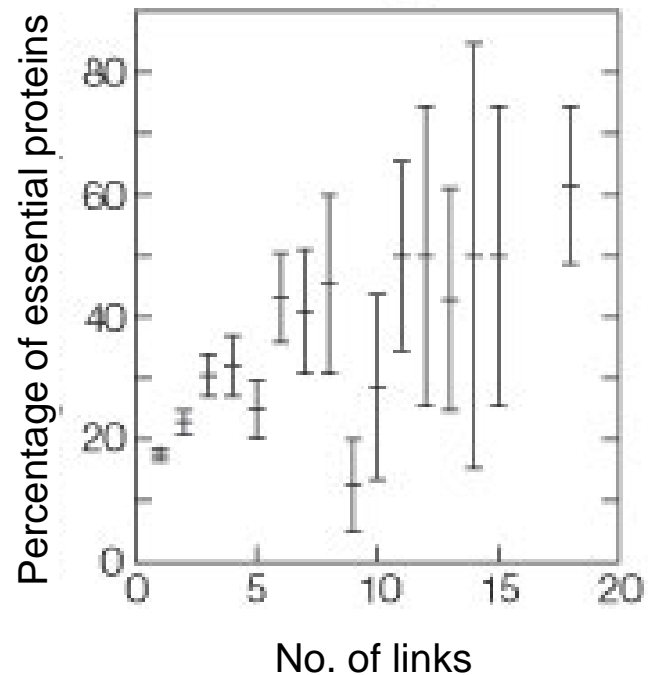
controversy over the centrality-lethality rule

Centrality-lethality rule

- The most highly connected proteins in the cell are the most important for its survival.
- But the weak correlation has been a problem.



red, lethal; green, non-lethal;
orange, slow growth; yellow, unknown



H. Jeong, S. P. Mason, A.-L. Barabási and Z. N. Oltvai
Nature 2001

The C-L rule dramatically improved for the genes keeping their essentiality both in yeast and mouse

