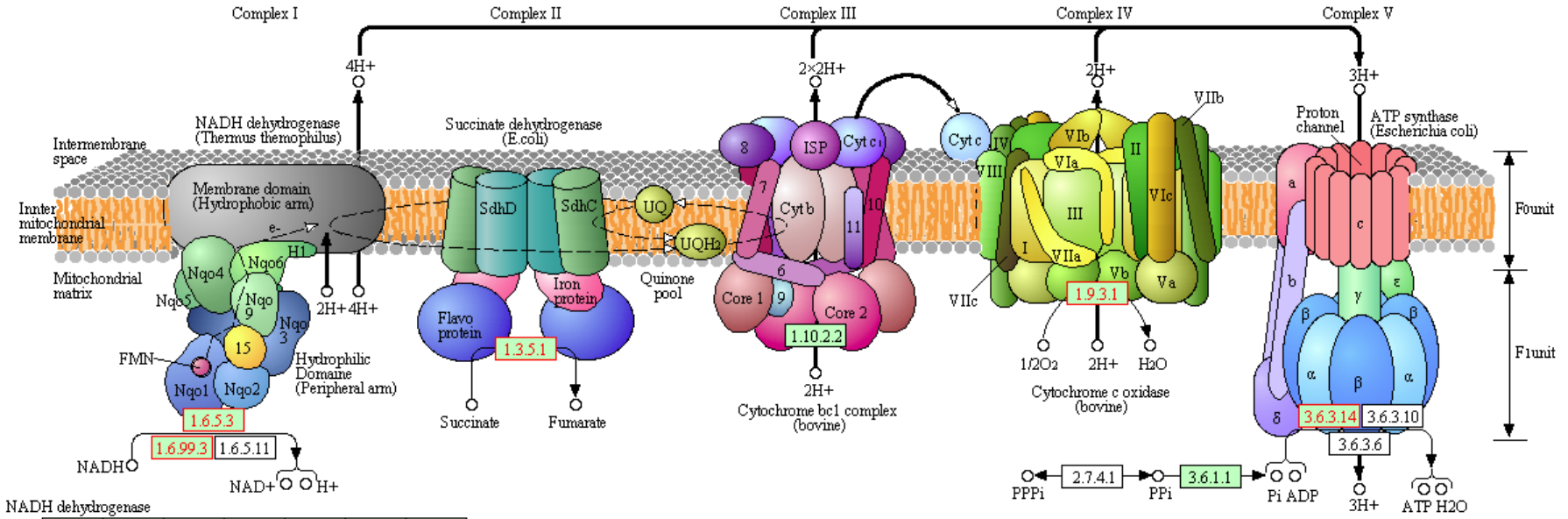
OXIDATIVE PHOSPHORYLATION



NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6
E	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3
B/A	NuoA	NuoB	NuoC	NuoD	NuoE	NuoF	NuoG	NuoH	NuoI	NuoJ	NuoK	NuoL	NuoM	NuoN
B/A	NdhC	NdhK	NdhJ	NdhH	NdhA	NdhI	NdhG	NdhE	NdhF	NdhD	NdhB	NdhL	NdhM	NdhN	HoxE	HoxF	HoxU
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7	Ndufa8	Ndufa9	Ndufa10	Ndufab1	Ndufa11	Ndufa12	Ndufa13
E	Ndufb1	Ndufb2	Ndufb3	Ndufb4	Ndufb5	Ndufb6	Ndufb7	Ndufb8	Ndufb9	Ndufb10	Ndufb11	Ndufc1	Ndufc2

Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB	
B/A	SdhC	SdhD	SdhA	SdhB	
			FrdA	FrdB	FrdC	FrdD

Cytochrome c reductase

E/B/A	ISP	Cyt b	Cyt 1							
E				COR1	QCR2	QCR6	QCR7	QCR8	QCR9	QCR10

Cytochrome c oxidase

E	COX10		COX3	COX1	COX2	COX4	COX5A	COX5B	COX6A	COX6B	COX6C	COX7A	COX7B	COX7C	COX8	E/B/A: COX11	COX15	COX17
B/A	CyoE	CyoD	CyoC	CyoB	CyoA													
		CoxD	CoxC	CoxA	CoxB													
		QoxD	QoxC	QoxB	QoxA													

Cytochrome c oxidase , cbb3-type

B	I	II	IV	III

Cytochrome bd complex

B/A	CydA	CydB

F-type ATPase (Bacteria)

alpha	beta	gamma	delta	epsilon
a	b	c		

F-type ATPase (Eukaryotes)

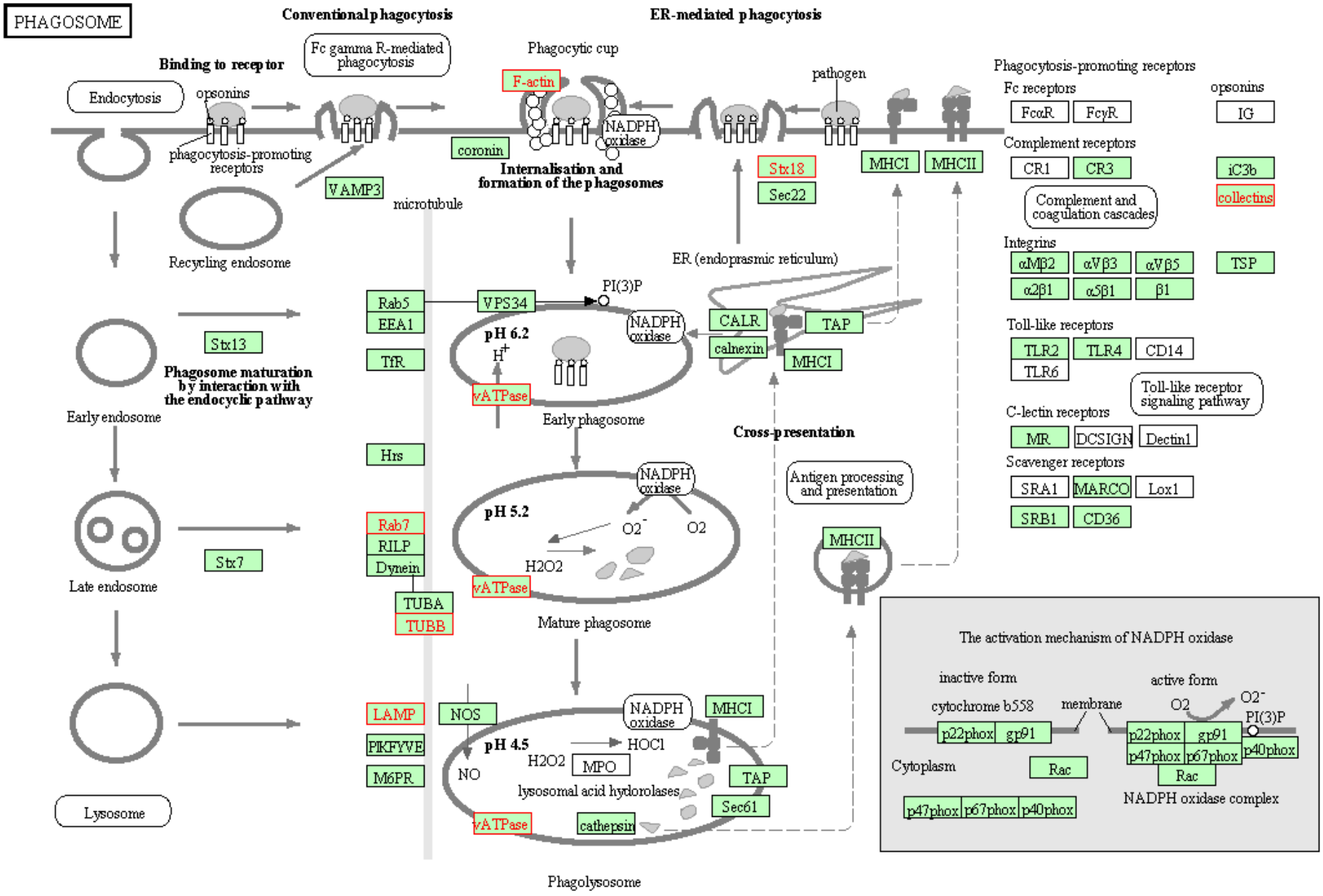
alpha	beta	gamma	delta	epsilon	
OSCP	a	b	c	d	e
f	g	f6/h	j	k	8

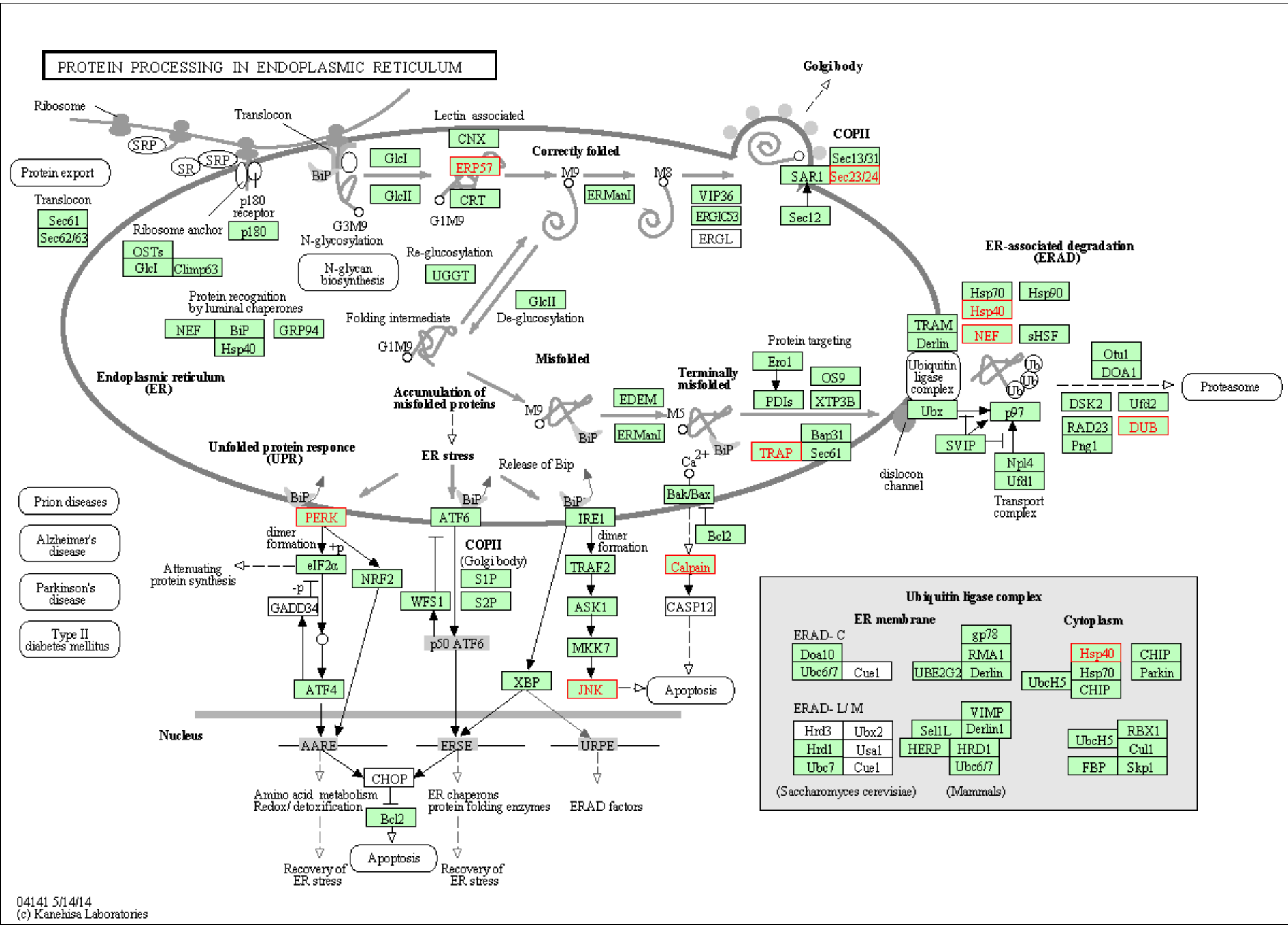
V/A-type ATPase (Bacteria, Archaeas)

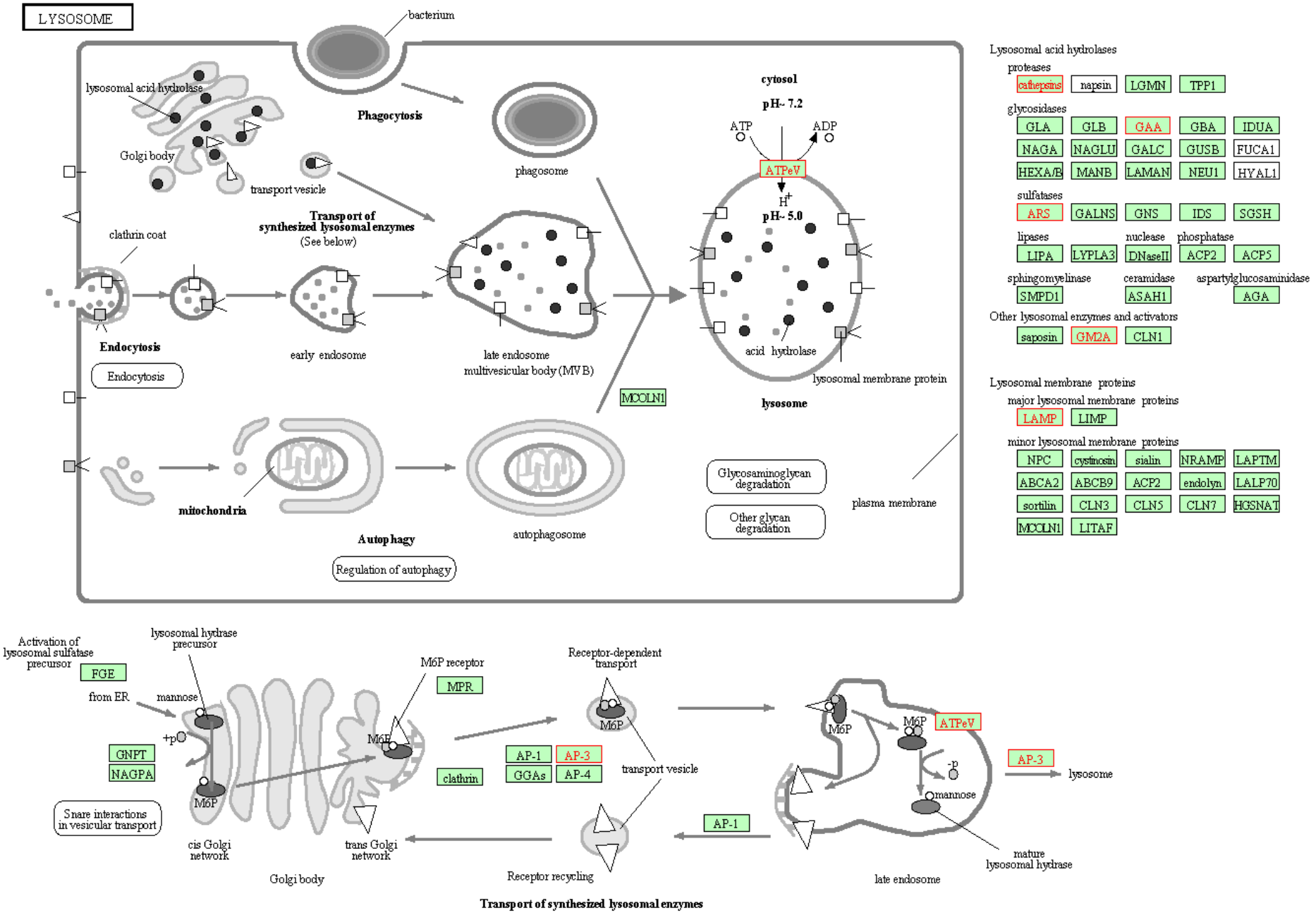
A	B	C	D	E	F	G/H
I	K					

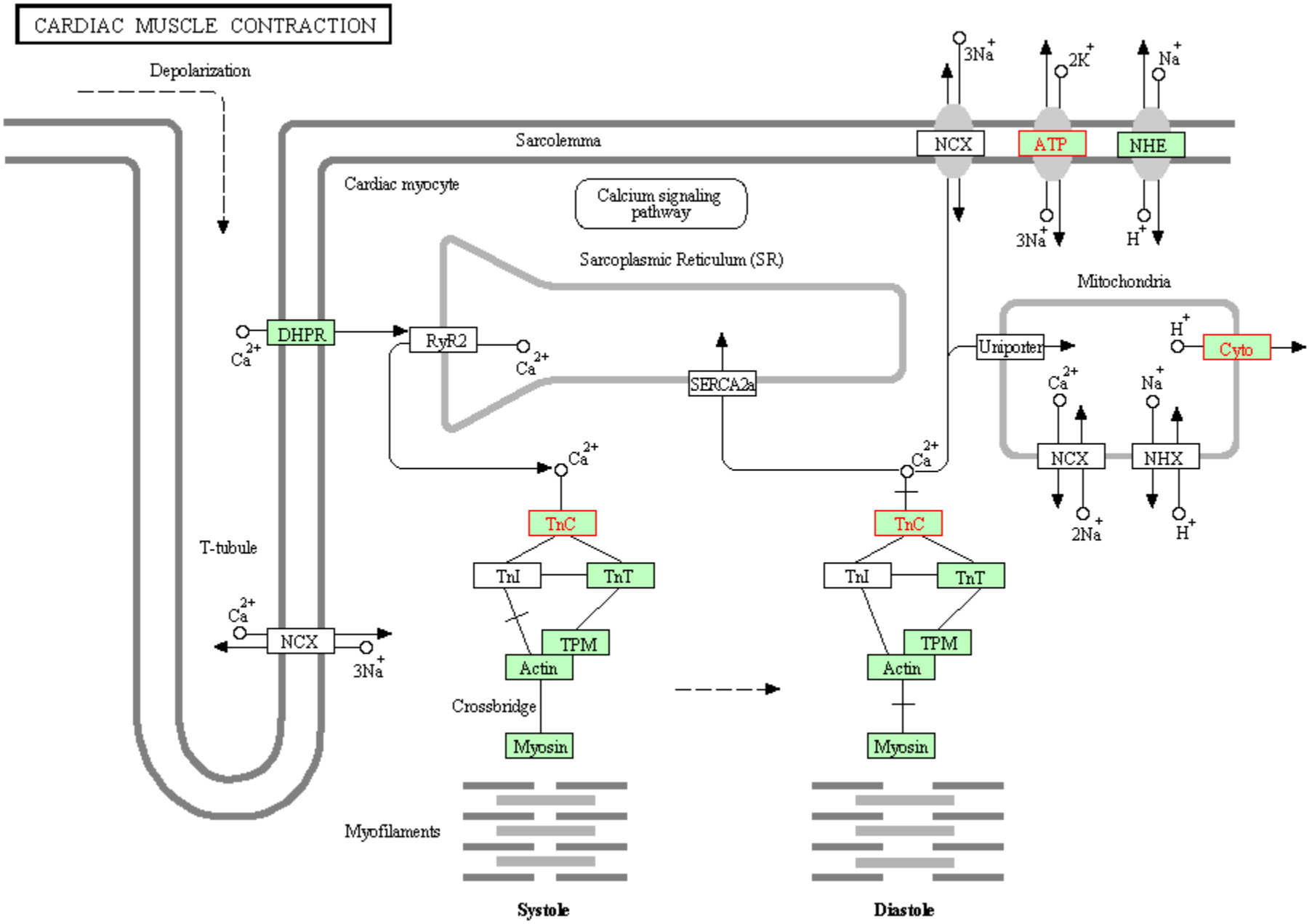
V-type ATPase (Eukaryotes)

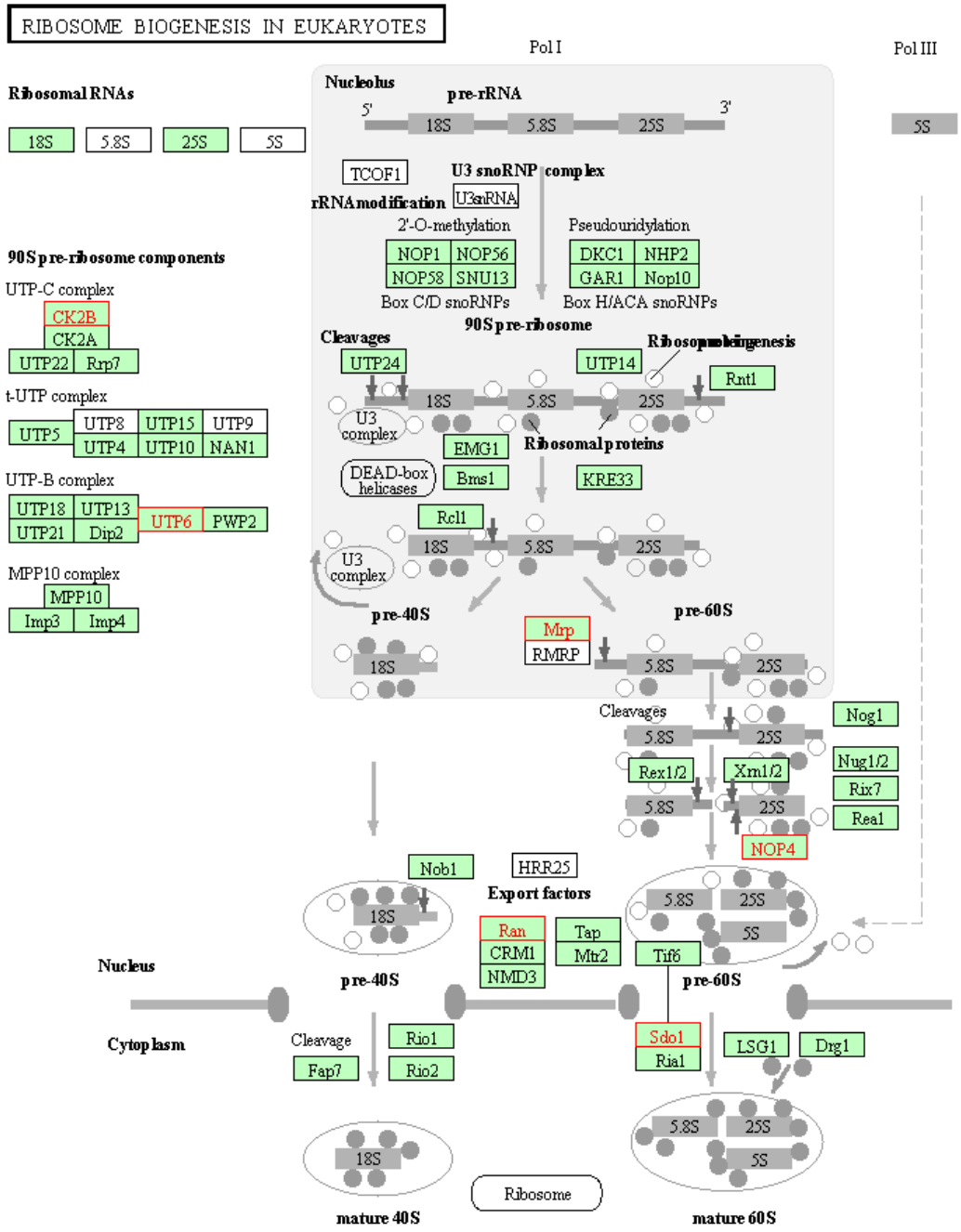
A	B	C	D	E	F	G	H
a	c	d	e	S1			

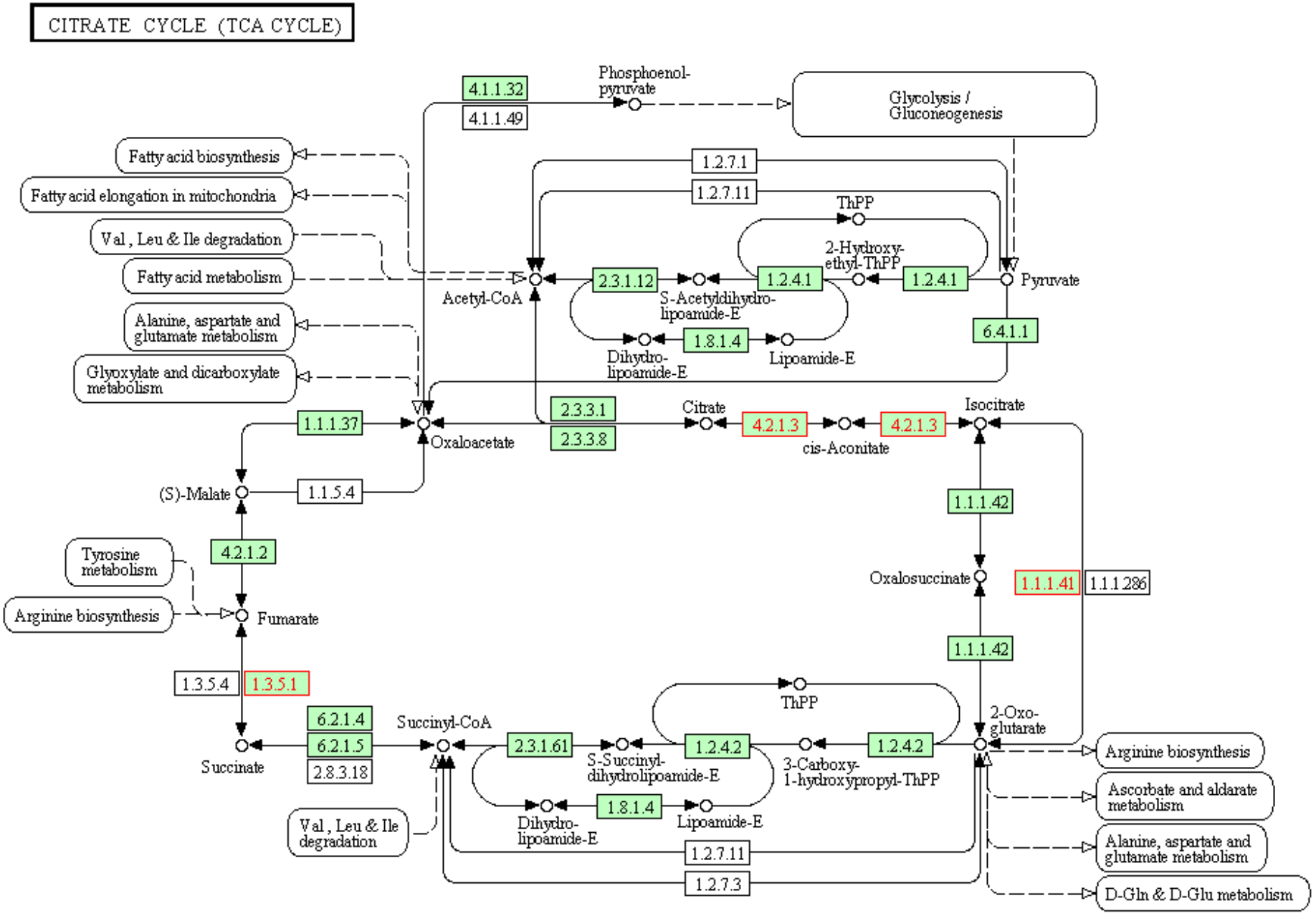


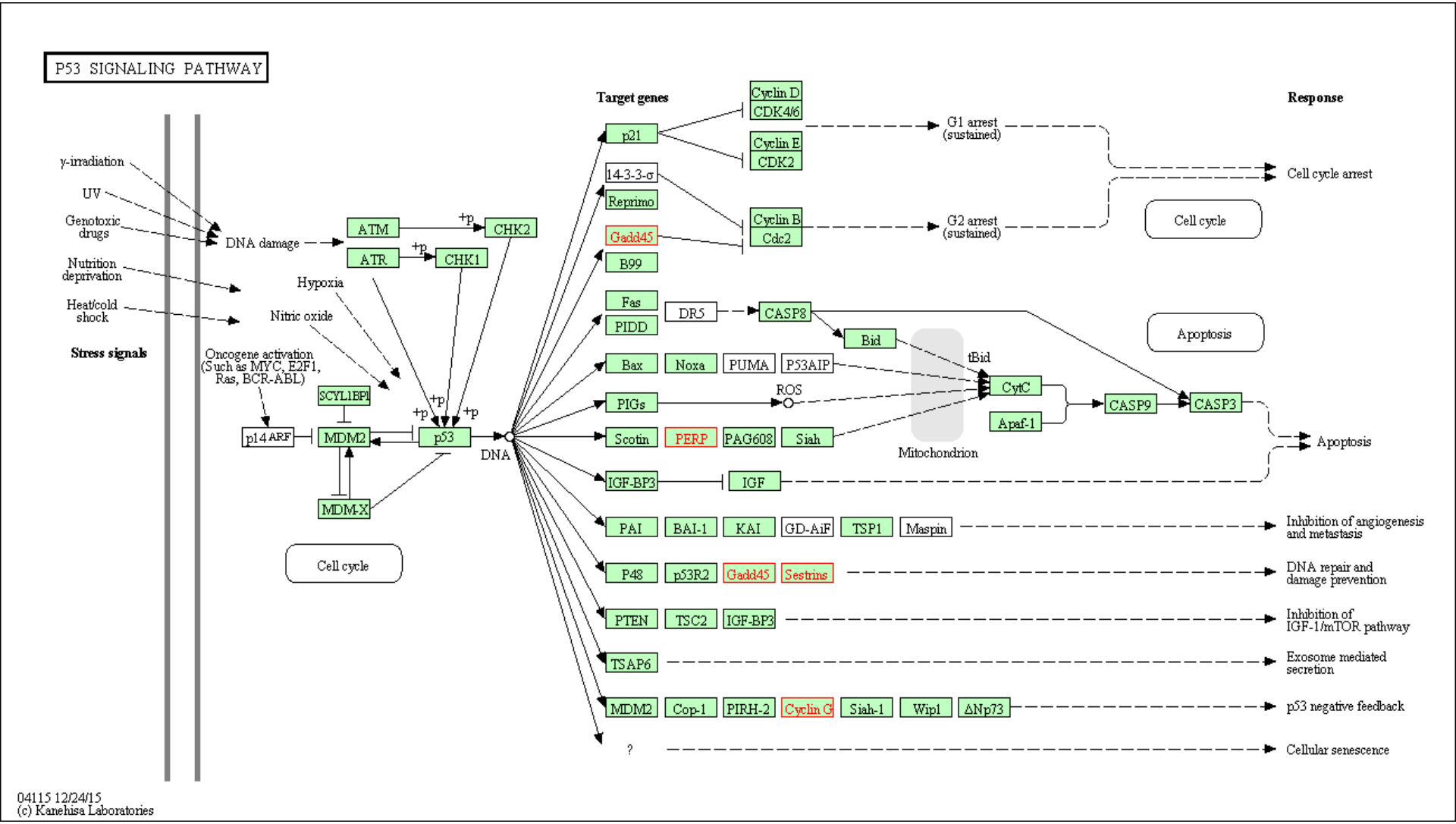


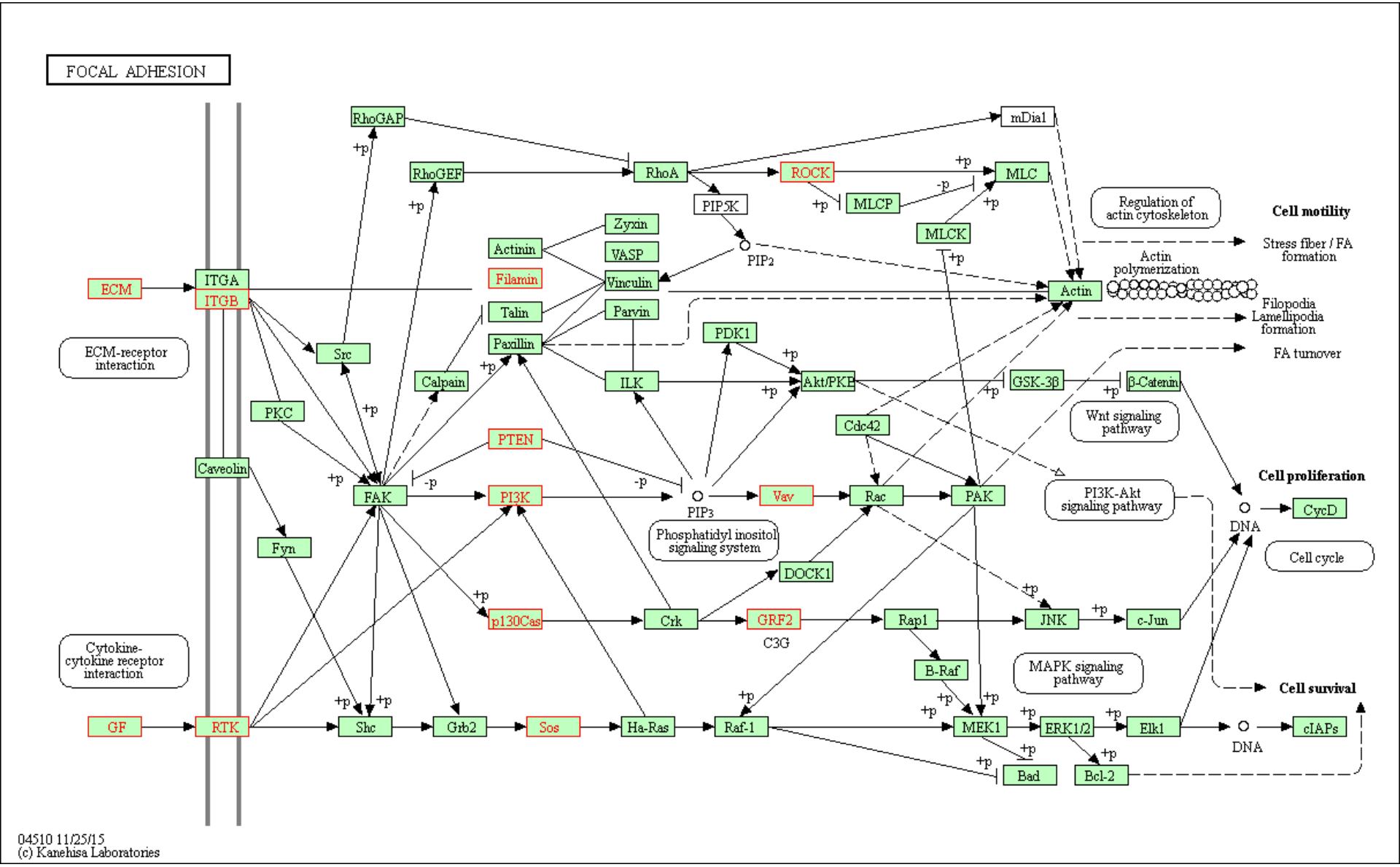


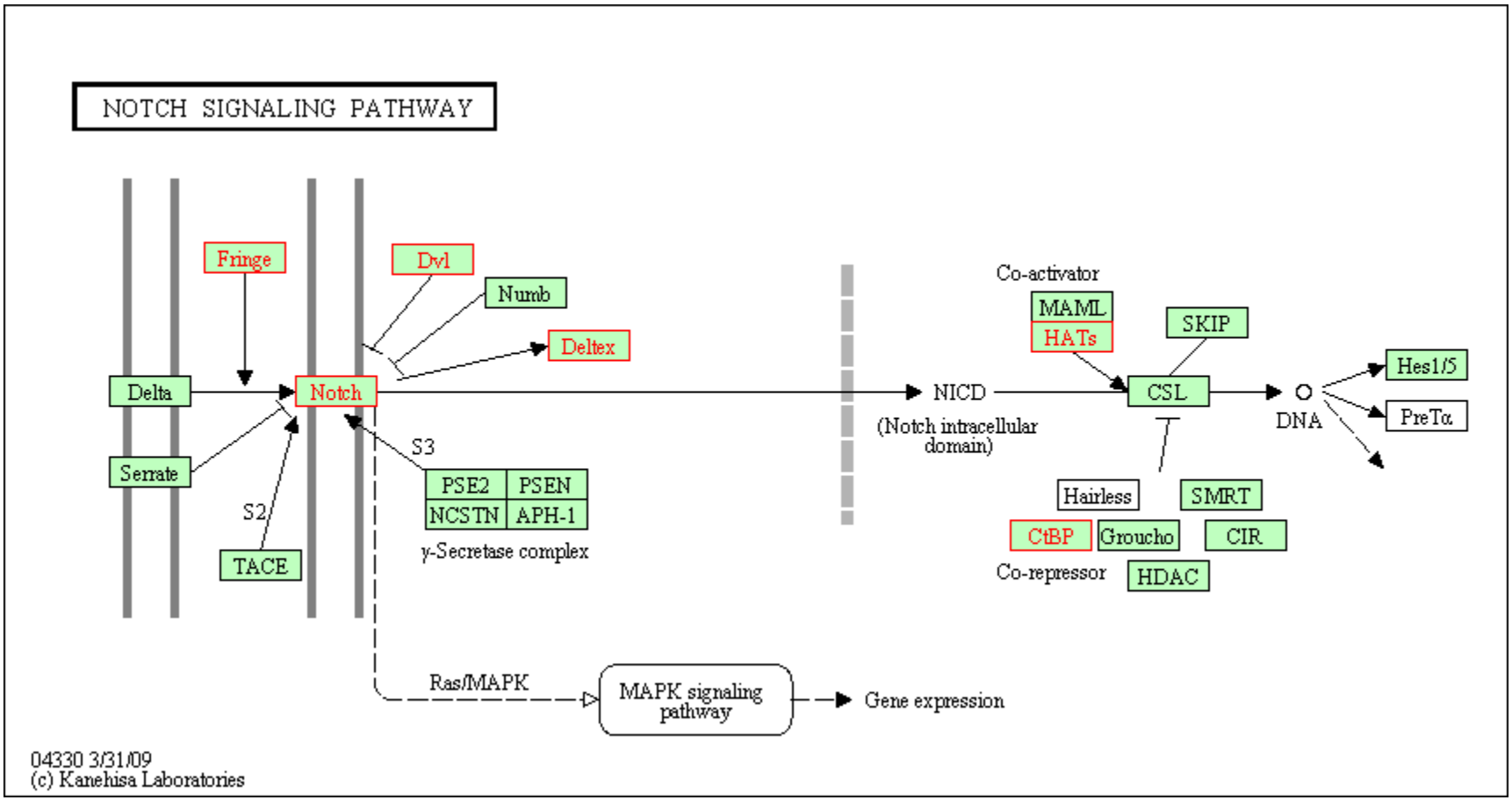


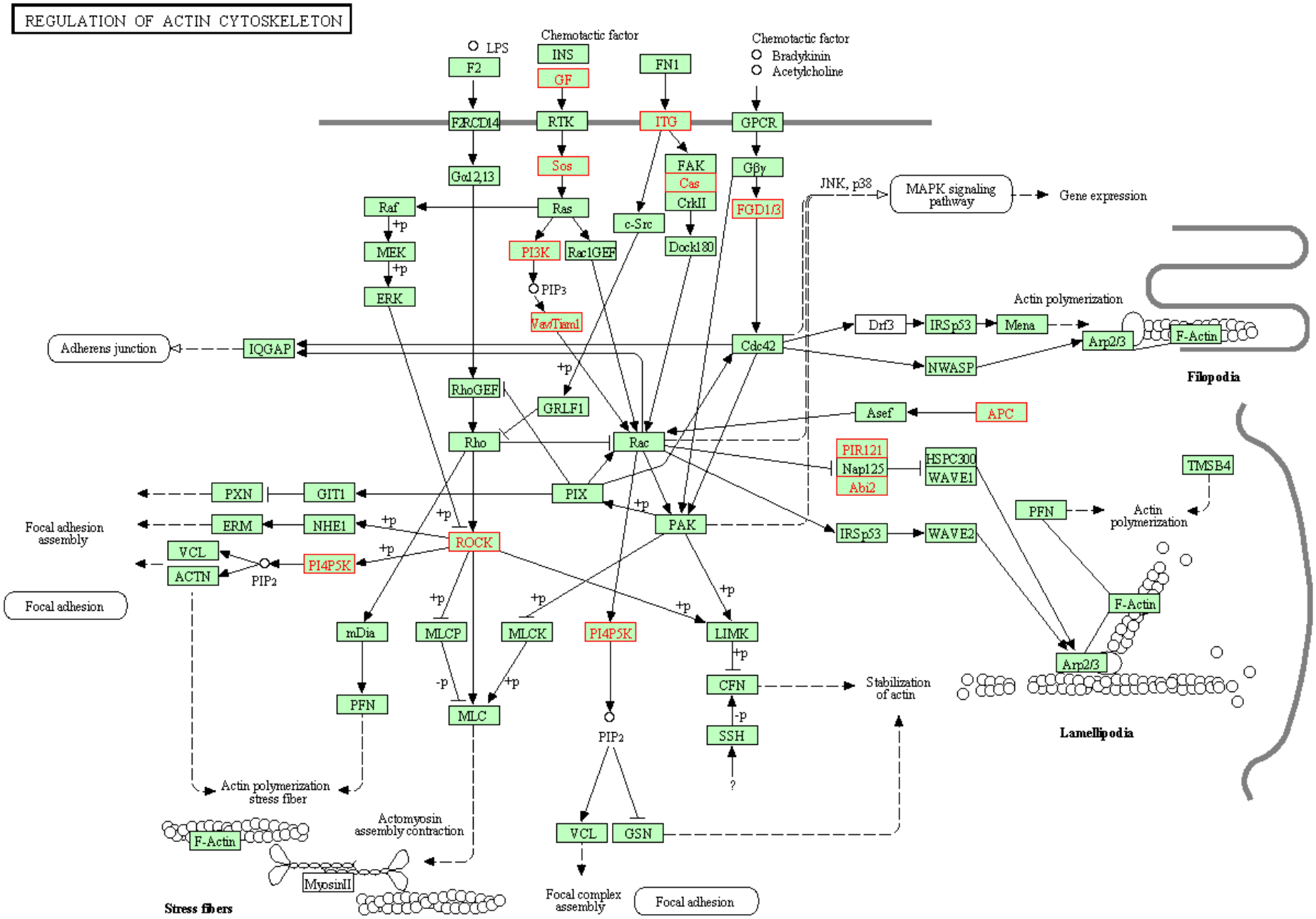


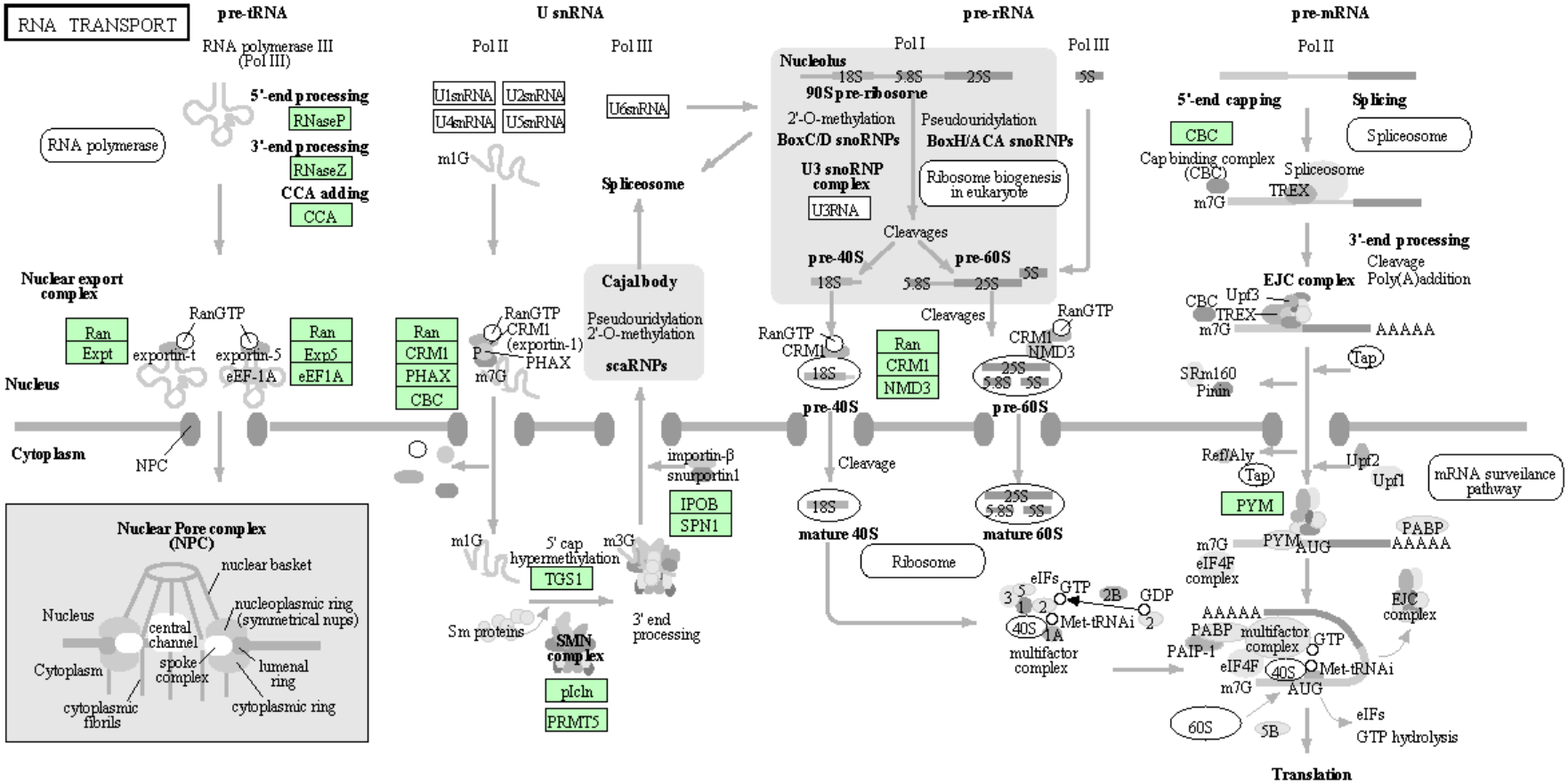

CITRATE CYCLE (TCA CYCLE)
4.1.1.32
4.1.1.49
Phosphoenol-pyruvate
Glycolysis / Gluconeogenesis
Fatty acid biosynthesis
Fatty acid elongation in mitochondria
Val , Leu & Ile degradation
Fatty acid metabolism
Alanine, aspartate and glutamate metabolism
Glyoxylate and dicarboxylate metabolism
1.2.7.1
1.2.7.11
ThPP
2-Hydroxy-ethyl-ThPP
2.3.1.12
1.2.4.1
1.2.4.1
Pyruvate
Acetyl-CoA
S-Acetyldihydro-lipoamide-E
1.8.1.4
Dihydro-lipoamide-E
Lipoamide-E
6.4.1.1
1.1.1.37
Oxaloacetate
2.3.3.1
2.3.3.8
Citrate
4.2.1.3
4.2.1.3
cis-Aconitate
Isocitrate
(S)-Malate
1.1.5.4
1.1.1.42
Tyrosine metabolism
4.2.1.2
Oxalosuccinate
1.1.1.41
1.1.1.286
Arginine biosynthesis
Fumarate
1.1.1.42
1.3.5.4
1.3.5.1
ThPP
2-Oxo-glutarate
6.2.1.4
6.2.1.5
2.8.3.18
Succinyl-CoA
2.3.1.61
1.2.4.2
1.2.4.2
Succinate
S-Succinyl-dihydrolipoamide-E
3-Carboxy-1-hydroxypropyl-ThPP
Arginine biosynthesis
Ascorbate and aldarate metabolism
1.8.1.4
Dihydro-lipoamide-E
Lipoamide-E
Val , Leu & Ile degradation
Alanine, aspartate and glutamate metabolism
1.2.7.11
1.2.7.3
D-Gln & D-Glu metabolism
00020 11/26/15
(c) Kanehisa Laboratories



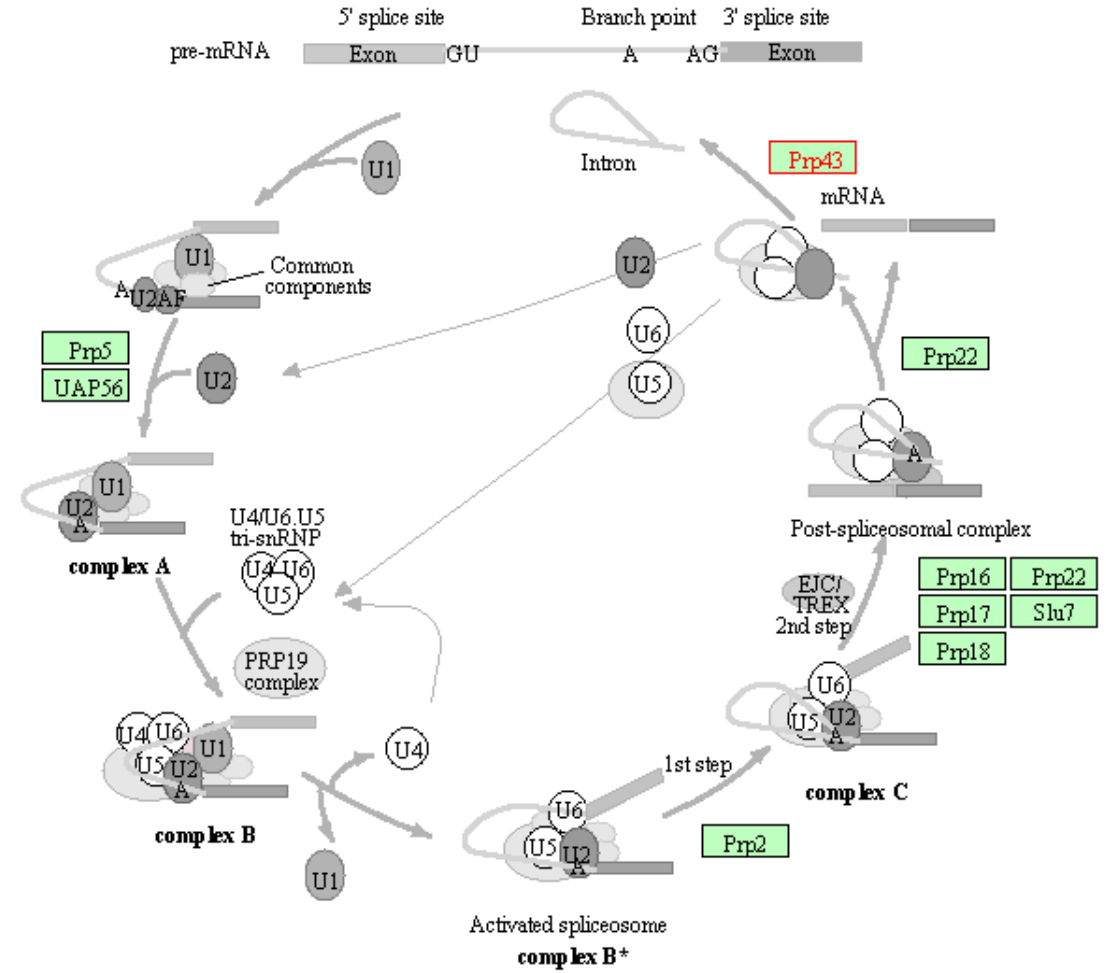


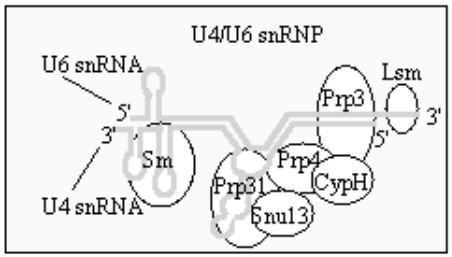

NOTCH SIGNALING PATHWAY
Fringe
Dvl
Numb
Deltex
Delta
Notch
Serrate
S2
TACE
S3
PSE2
PSEN
NCSTN
APH-1
γ-Secretase complex
NICD
(Notch intracellular domain)
Co-activator
MAML
HATs
SKIP
CSL
DNA
Hes1/5
PreTα
Hairless
SMRT
CtBP
Groucho
CIR
Co-repressor
HDAC
Ras/MAPK
MAPK signaling pathway
Gene expression
04330 3/31/09
(c) Kanehisa Laboratories





SPLICEOSOME

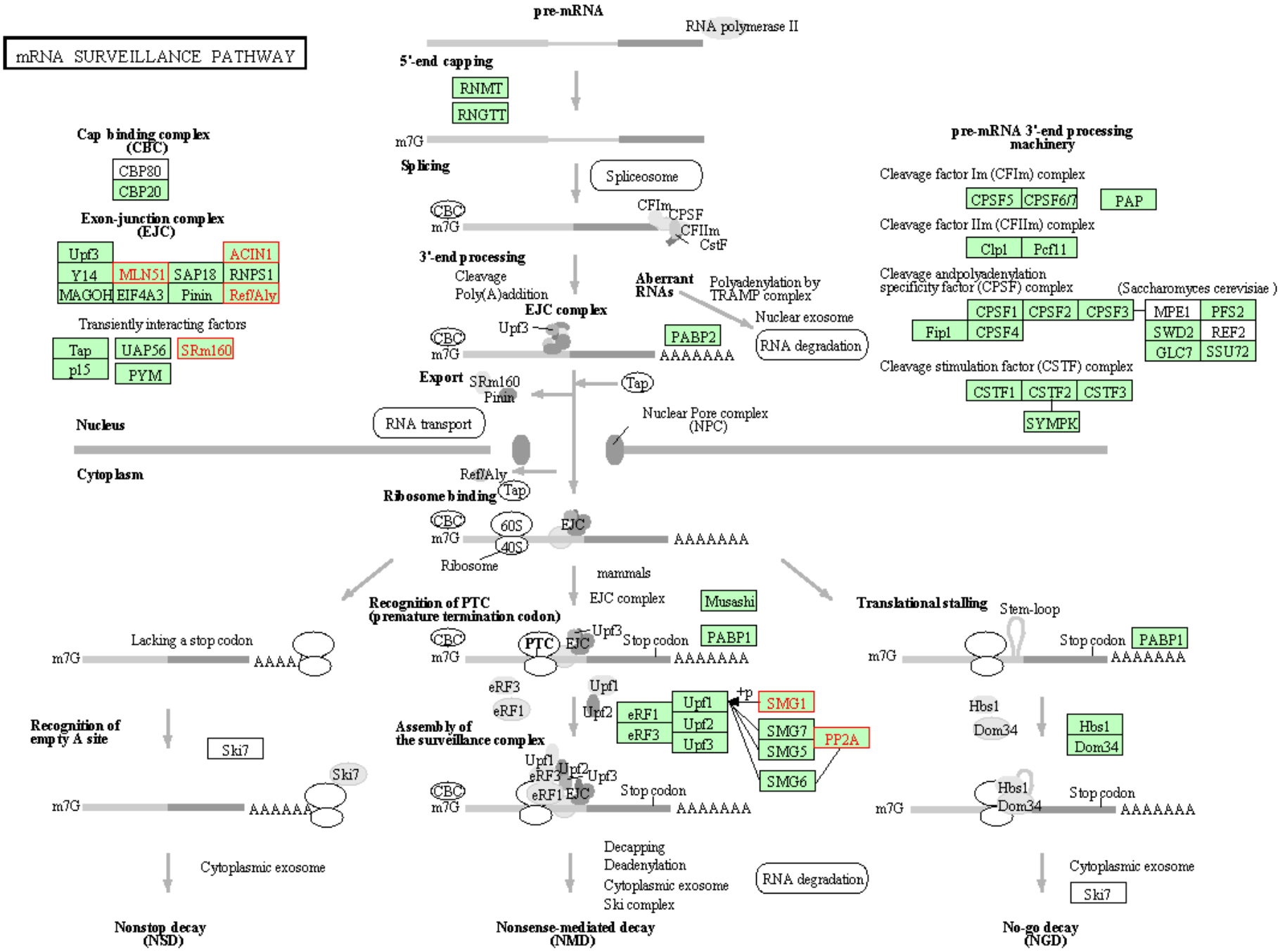




Spliceosome components

U1	U2	U4/U6	U5
U1snRNA	U2snRNA	U4snRNA	U5snRNA
Sm	Sm	U6snRNA	Sm
U1-70K	U2A'	Lsm	Snu114
U1A	U2B"	Sm	Brr2
U1C	SF3a	Prp3	Prp6
U1 related	SF3b	Prp4	Prp8
FBP11	U2 related	CypH	Prp8BP
S164	U2AF	Prp31	Prp28
p68	PUF60	Snu13	DIB1
CA150	SPF30	U4/U6.U5 tri-SnRNP associated	
	SPF45	SnRNP27	
	CHERP	Sad1	
	SR140	Snu66	
	Prp43	Snu23	
	PAP-1	Prp38	
		PAP-1	

Prp19 complex	Prp19 related	EJC/TREX	Common components
Prp19	SKIP	ACINUS	CBP80/20
CDC5	Syf	eIFA3	hnRNPs
SPF27	Isy1	Y14	SR
PRL1	PPIL1	magoh	
AD002	CypE	UAP56	
CTNNBL1	CCDC12	THOC	
HSP73	RBM22		
Complex B specific	G10		
NPW38	AQR		
NPW38BP			


mRNA SURVEILLANCE PATHWAY
pre-mRNA
RNA polymerase II
5'-end capping
RNMT
RNGTT
m7G
Cap binding complex (CBC)
CBP80
CBP20
Exon-junction complex (EJC)
Upf3
ACIN1
Y14
MLN51
SAP18
RNPS1
MAGOH
EIF4A3
Pinin
Ref/Aly
Transiently interacting factors
Tap
p15
UAP56
PYM
SRm160
Splicing
Spliceosome
CBC
CFIm
CPSF
CFIIm
CstF
3'-end processing
Cleavage
Poly(A)addition
Aberrant RNAs
Polyadenylation by TRAMP complex
Nuclear exosome
RNA degradation
EJC complex
Upf3
PABP2
AAAAAAA
Export
SRm160
Pinin
Tap
RNA transport
Nuclear Pore complex (NPC)
Nucleus
Cytoplasm
Ref/Aly
Tap
Ribosome binding
60S
40S
Ribosome
EJC
pre-mRNA 3'-end processing machinery
Cleavage factor Im (CFIm) complex
CPSF5
CPSF6/7
PAP
Cleavage factor IIm (CFIIm) complex
Clp1
Pcf11
Cleavage andpolyadenylation specificity factor (CPSF) complex
(Saccharomyces cerevisiae)
CPSF1
CPSF2
CPSF3
MPE1
PFS2
Fip1
CPSF4
SWD2
REF2
GLC7
SSU72
Cleavage stimulation factor (CSTF) complex
CSTF1
CSTF2
CSTF3
SYMPK
mammals
EJC complex
Musashi
Recognition of PTC (premature termination codon)
PTC
Stop codon
PABP1
eRF3
eRF1
Upf1
Upf2
Upf3
+p
SMG1
SMG7
SMG5
SMG6
PP2A
Assembly of the surveillance complex
Translational stalling
Stem-loop
Hbs1
Dom34
Lacking a stop codon
Recognition of empty A site
Ski7
Cytoplasmic exosome
Decapping
Deadenylation
Cytoplasmic exosome
Ski complex
Nonstop decay (NSD)
Nonsense-mediated decay (NMD)
No-go decay (NGD)
03015 5/14/14
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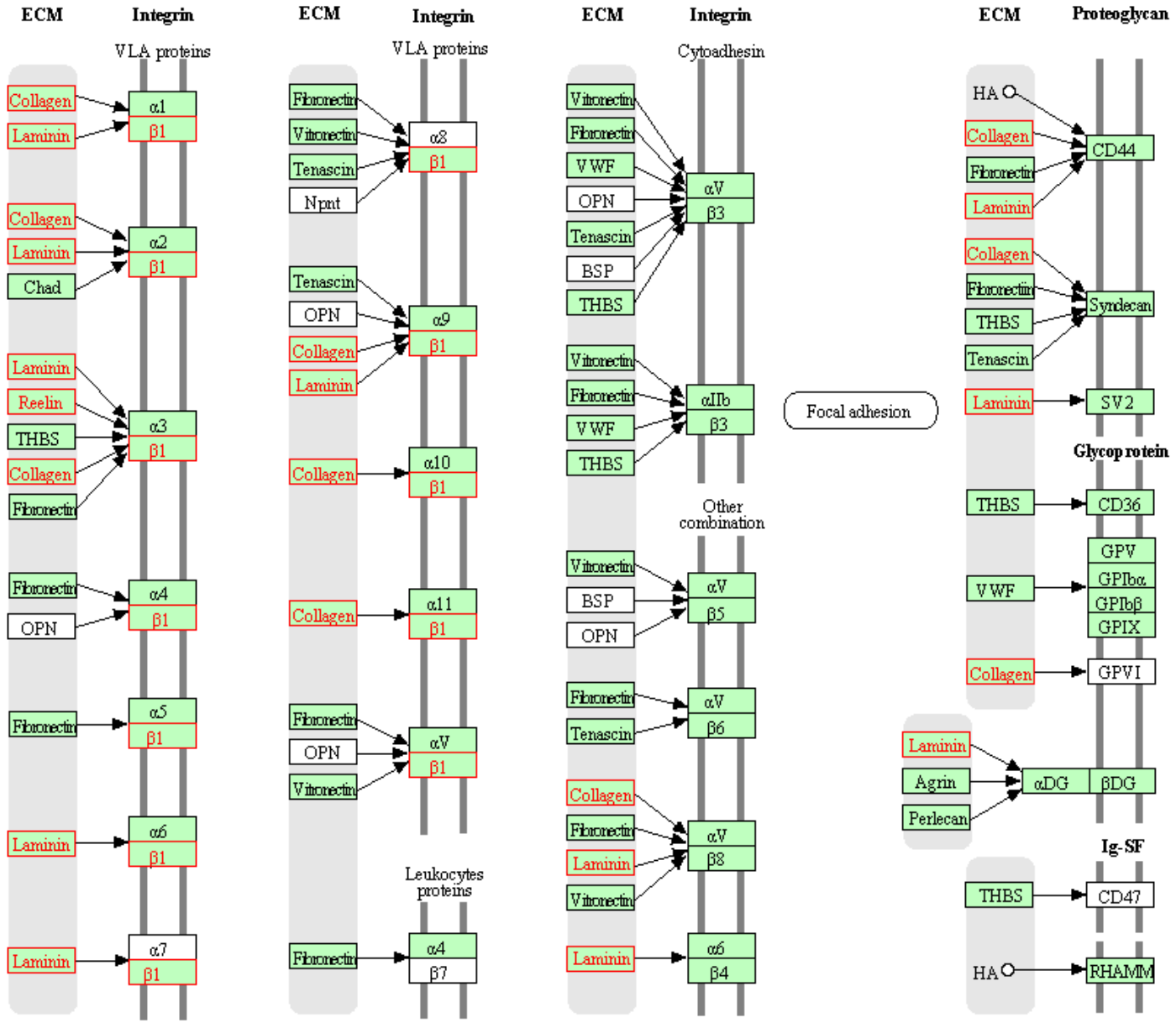
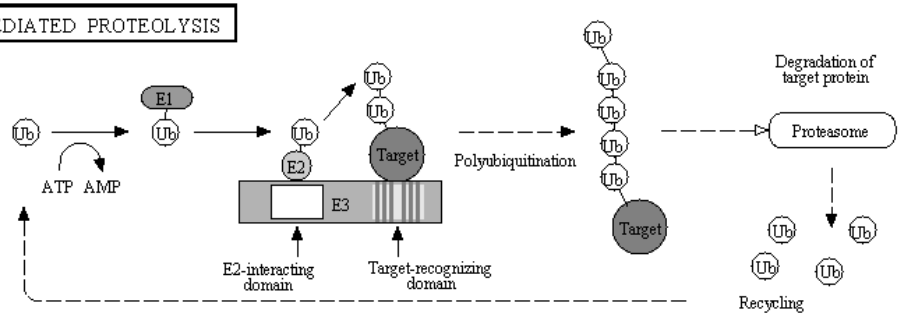
ECM-RECEPTOR INTERACTION



UBIQUITIN MEDIATED PROTEOLYSIS



E1
(Ubiquitin-activating enzyme)

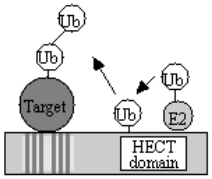
UBE1	UBLE1A	UBLE1B	UBE1C

E2
(Ubiquitin-conjugating enzyme)

UBE2A	UBE2B	UBE2C	UBE2D_E	UBE2F	UBE2G1	UBE2G2	UBE2H
UBE2I	UBE2J1	UBE2J2	UBE2L3	UBE2L6	UBE2M	UBE2N	UBE2O
UBE2Q	UBE2R	UBE2S	UBE2U	UBE2W	UBE2Z	HIP2	AFC1.CN

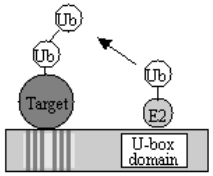
E3
(Ubiquitin ligase)

HECT type E3



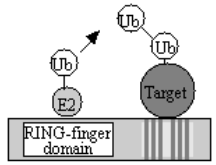
E6AP	UBE3B	UBE3C	Smurf	Itch
WWP1	WWP2	TRIP12	NEDD4	ARF-BP1
EDD1	HERC1	HERC2	HERC3	HERC4

U-box type E3



UBE4A	UBE4B	CHIP
CYC4	PRP19	UIP5

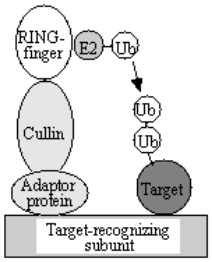
single RING-finger type E3



Mdm2	CBL	Parkin	SIAH-1	PML	TRAF6	MEKK1
COP1	PIRH2	cIAPs	PIAS	SYVN	NHLRC1	AIRE
MGRN1	BRCA1	FANCL	MID1	Trim32	Trim37	

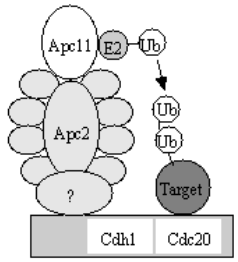
multi subunit RING-finger type E3

Cullin-Rbx E3

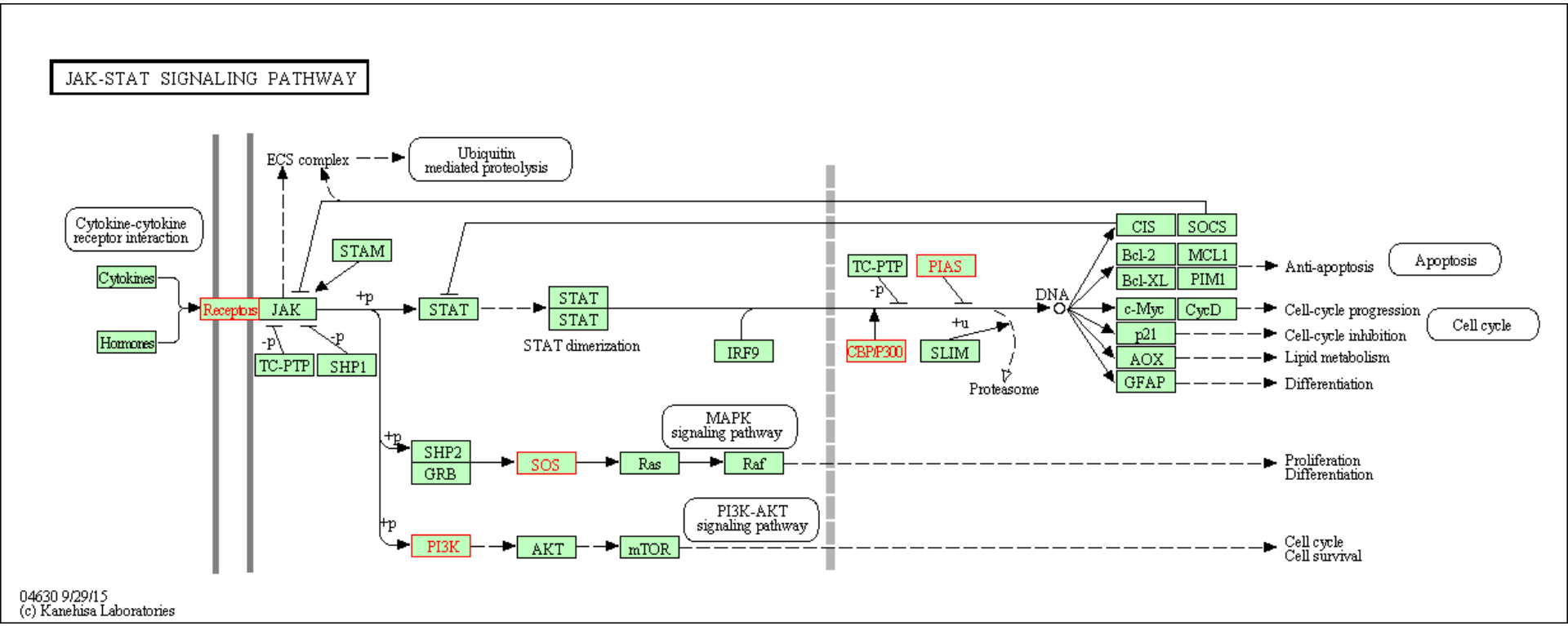


	RING finger	Cullin	Adaptor protein	Target recognizing subunit
SCF complex	RBX1	Cul1	Skp1	F-box
ECV complex	RBX1	Cul2	EloB	VHLbox
			EloC	
Cul3 complex	RBX1	Cul3		BTB
Cul4 complex	RBX1	Cul4	DDB1	DCAF
ECS complex	RBX2	Cul5	EloB	SOCSbox
			EloC	
Cul7 complex	RBX1	Cul7	Skp1	Fbxw8

APC/C



RING finger	Cullin	Adaptor protein	Target recognizing subunit	Other subunits	
Apc11	Apc2	?	Cdc20	Apc1	Apc3
			Cdh1	Apc4	Apc5
				Apc6	Apc7
				Apc8	Apc9
				Apc10	Apc12
					Apc13



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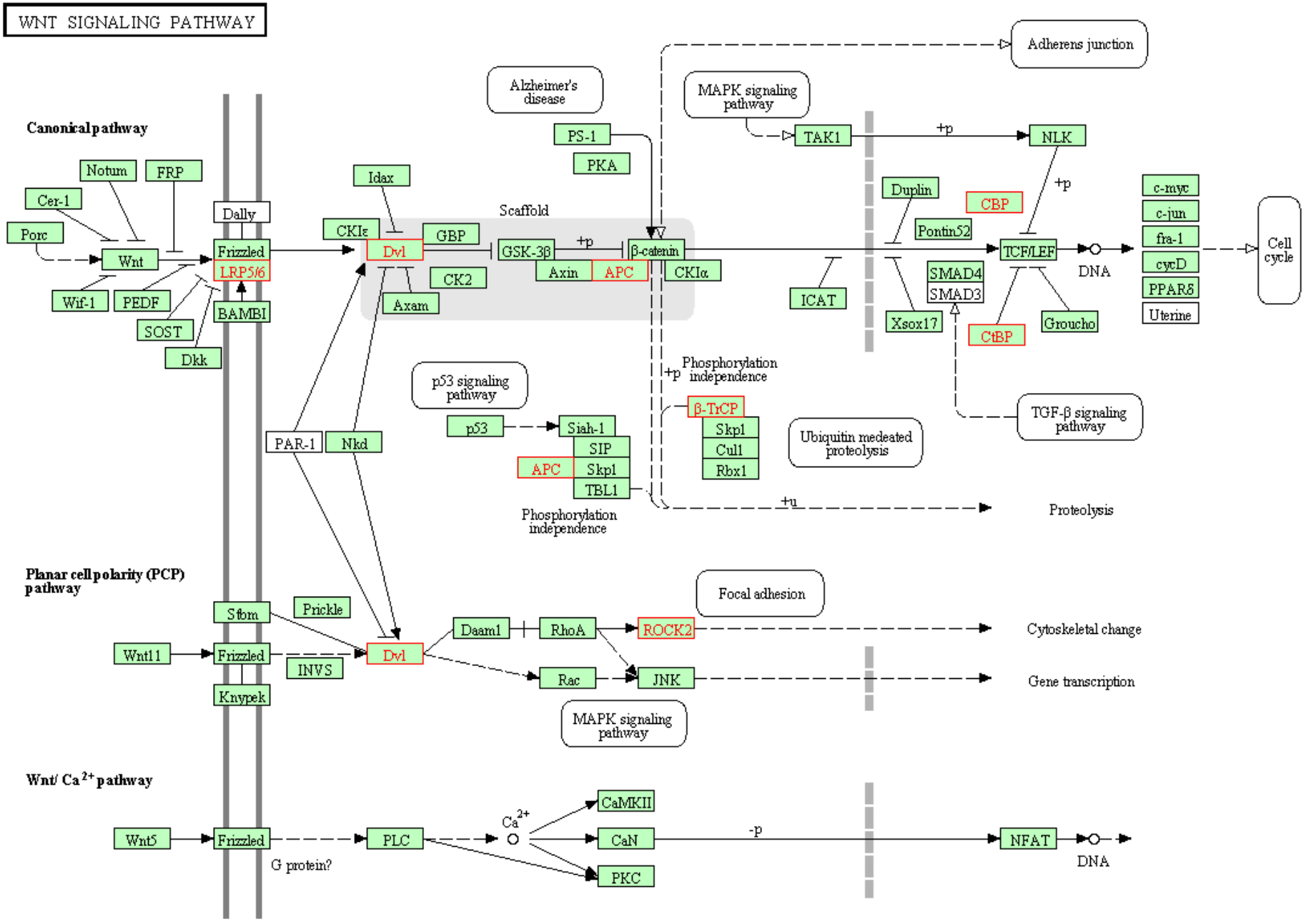

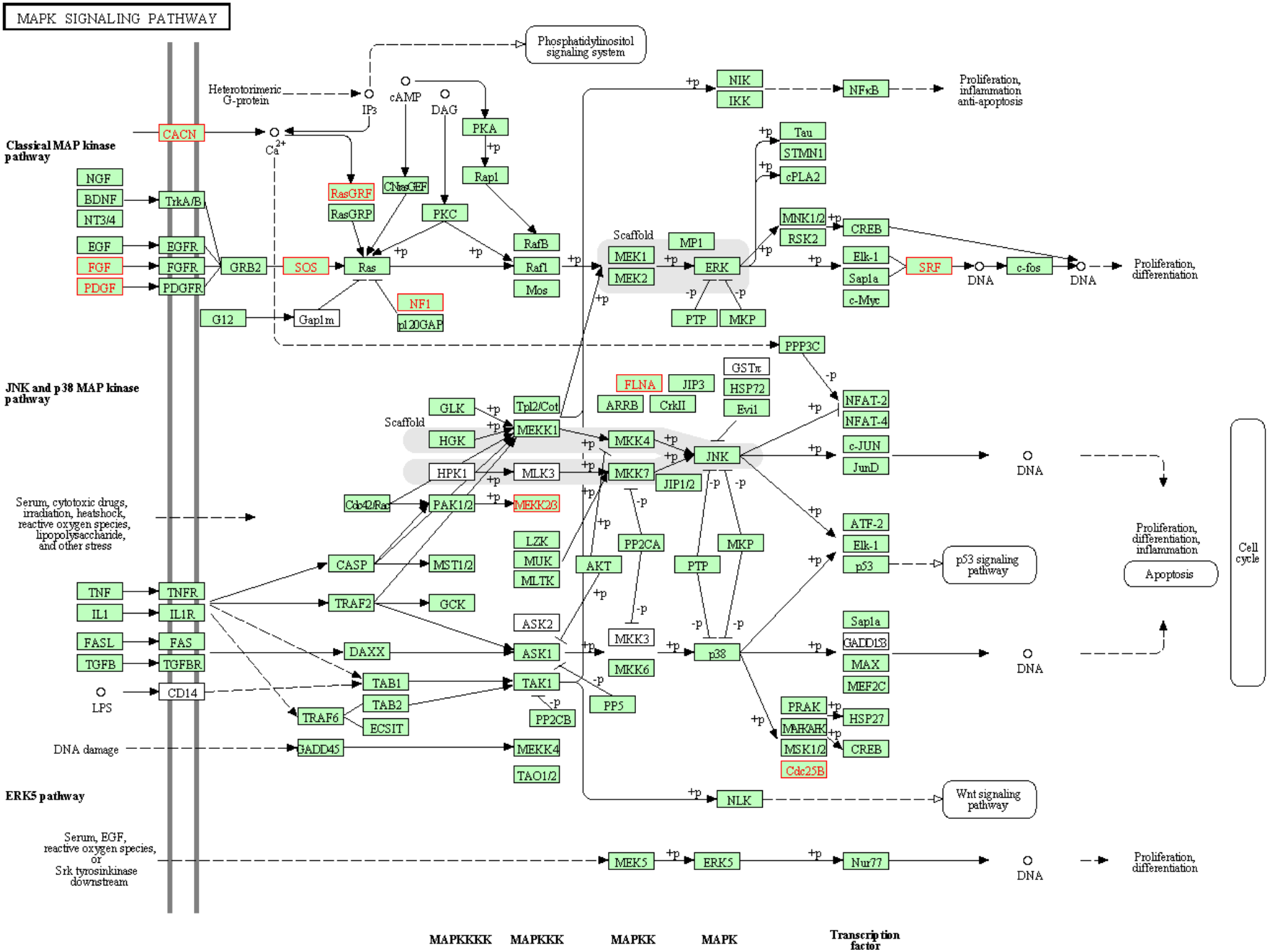

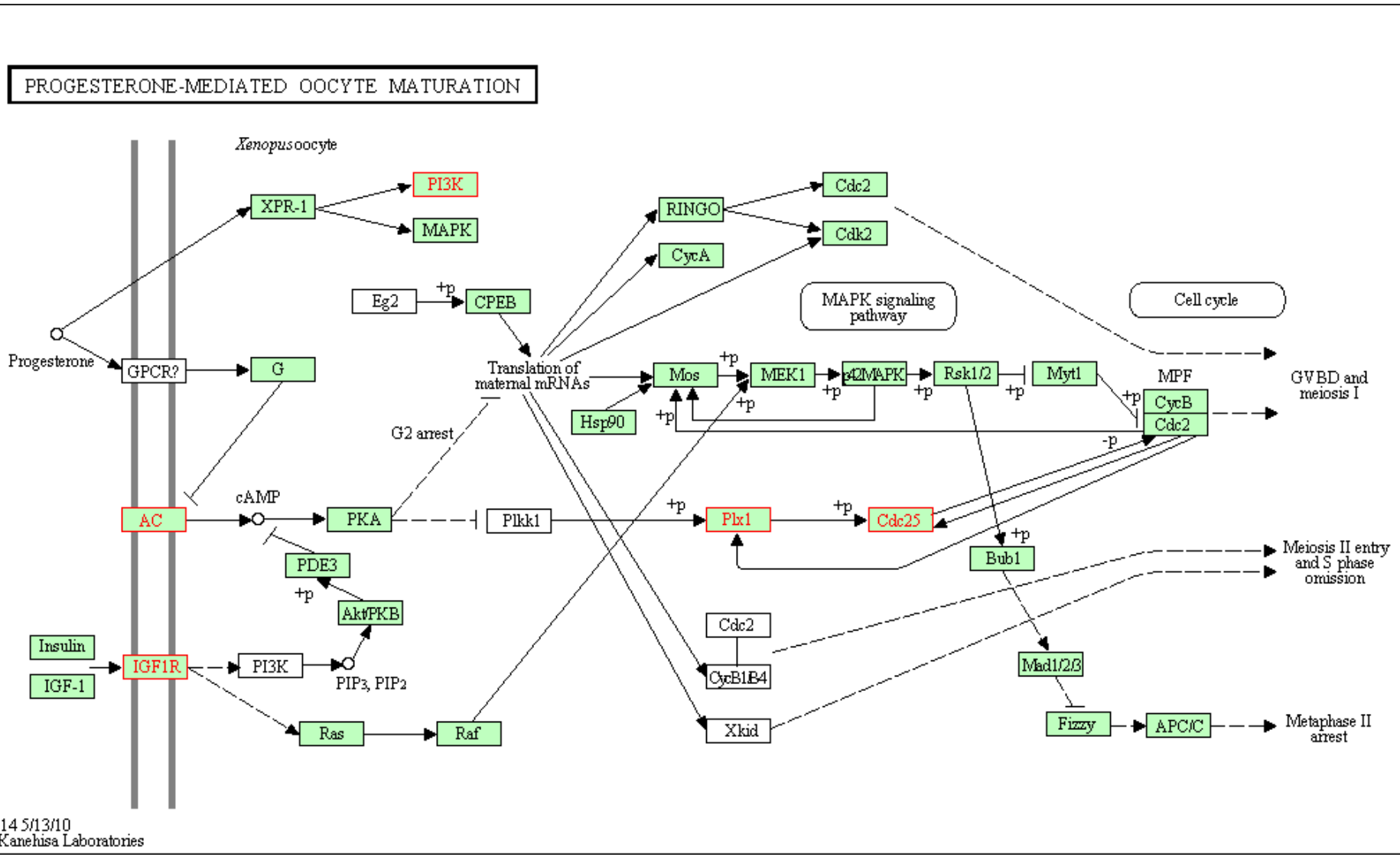
PROGESTERONE-MEDIATED OOCYTE MATURATION
Xenopus oocyte
XPR-1
PI3K
MAPK
Progesterone
GPCR?
G
Eg2
+p
CPEB
Translation of maternal mRNAs
RINGO
CycA
Cdc2
Cdk2
MAPK signaling pathway
Cell cycle
Mos
MEK1
p42MAPK
Rsk1/2
Myt1
MPF
CycB
Cdc2
GVBD and meiosis I
Hsp90
G2 arrest
cAMP
AC
PKA
Plkk1
Plx1
Cdc25
Bub1
PDE3
Akt/PKB
Meiosis II entry and S phase omission
Insulin
IGF-1
IGF1R
PI3K
PIP3, PIP2
Ras
Raf
Cdc2
CycB1B4
Xkid
Mad1/2/3
Fizzy
APC/C
Metaphase II arrest
04914 5/13/10
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CELL ADHESION MOLECULES