

RIBOSOME

Large subunit (*Haloarcula marismortui*)

Small subunit (*Thermus aquaticus*)

Ribosomal RNAs

Bacteria / Archaea	23S	SS	16S
Eukaryotes	25S	5.8S	18S

Ribosomal proteins

EF-Tu

S10	L3	L4	L23	L2	S19	L22	S3	L16	L29
S20e	L3e	L4e	L23Ae	L8e	S15e	L17e	S3e		L35e

SecY

S17	L14	L24		L5	S14	S8	L6		L18	S5	L30	L15	
S11e	L23e	L26e	S4e	L11e	S29e	S15Ae	L9e	L32e	L19e	L5e	S2e	L7e	L27Ae

IF1

L36	S13	S11	S4	RpoA		L17	L13	S9
L34e	L14e	S18e	S14e	S9e		L18e	L13Ae	S16e

EF-Tu,G

S7	S12		L7A	RpoC,B		L7/L12	L12	L10	L1	L11
S5e	S23e	L30e	L7Ae			LP1,LP2	LP0	L10Ae	L12e	

EF-Ts

S2	IF2	IF3	RF1						
S Ae	S15 S13e	L35	L20	L34	L31	L32	L9	S18	S6

FtsY,FH

L28	L33	L21	L27		S1	S20	S21	L25				
L10e	L13e	L15e	L21e	L24e	L31e	L35Ae	L37e	L37Ae	L39e	L40e	L41e	L44e

S3Ae

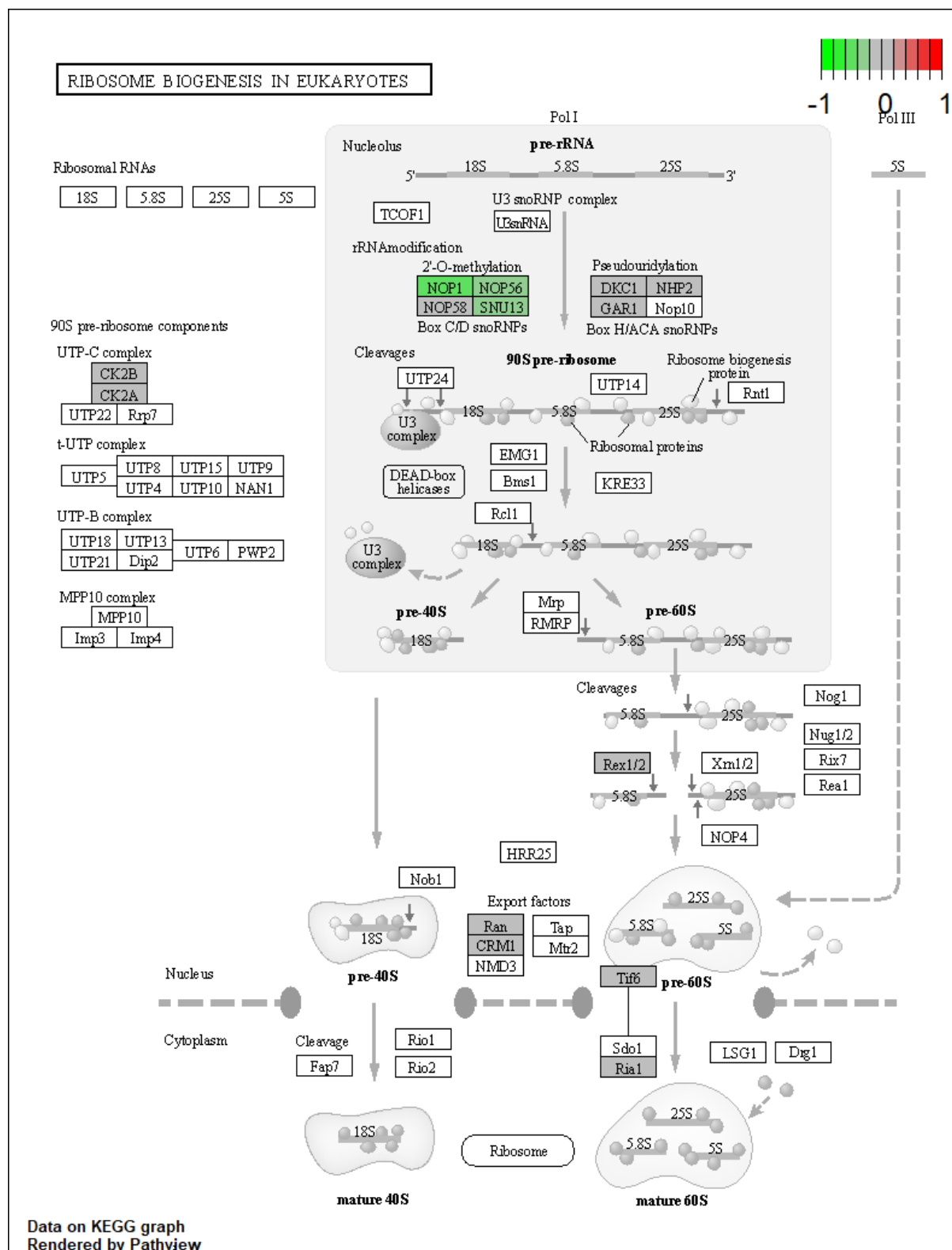
S6e	S8e	S17e	S19e	S24e	S25e	S26e	S27e	S27Ae	S28e	S30e	LX
L6e	L18Ae	L22e	L27e	L28e	L29e	L36e	L38e				

S7e

S10e	S12e	S21e

[illegible]

Figure S4. NMN treatment effects on the KEGG ribosome biogenesis pathway in mouse liver. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.



[illegible]

Data on KEGG graph
Rendered by Pathview

[illegible]

Data on KEGG graph
Rendered by Pathview

Figure S10. NMN treatment effects on the KEGG valine, leucine and isoleucine degradation pathway in mouse muscle. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

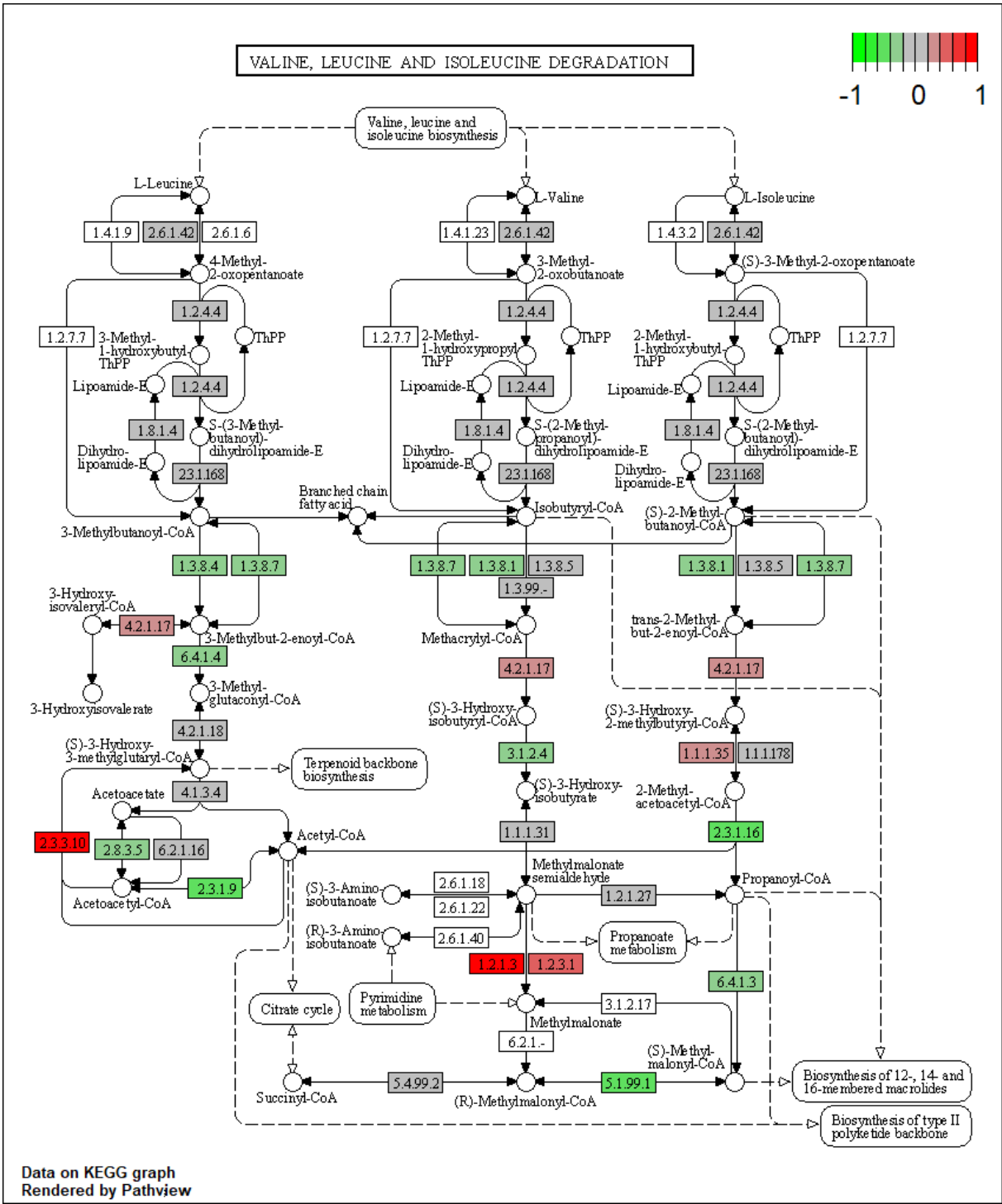


Figure S11. NMN treatment effects on the KEGG spliceosome pathway in mouse adipose tissue. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

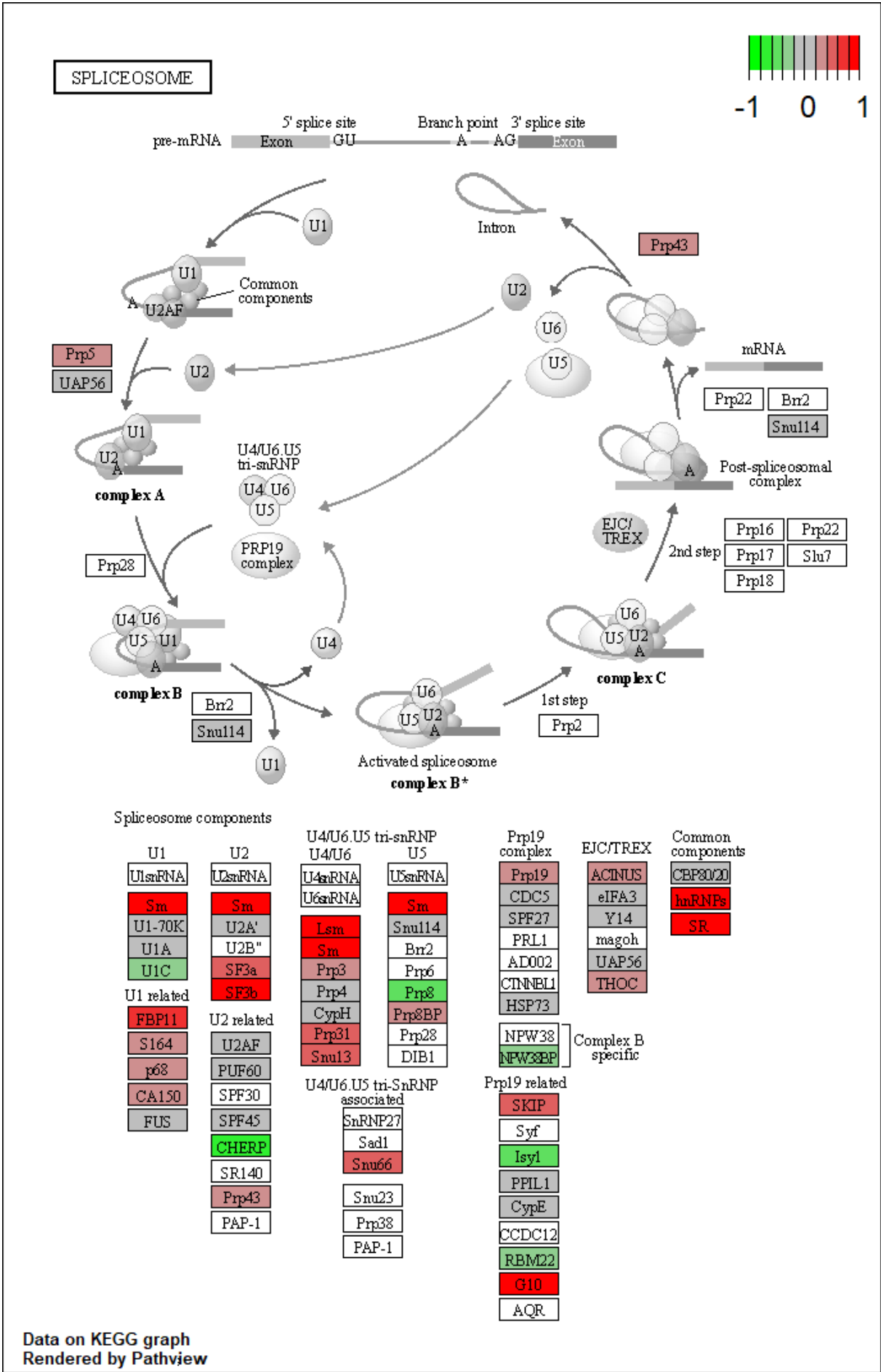


Figure S12. NMN treatment effects on the KEGG regulation of actin cytoskeleton pathway in mouse adipose tissue. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

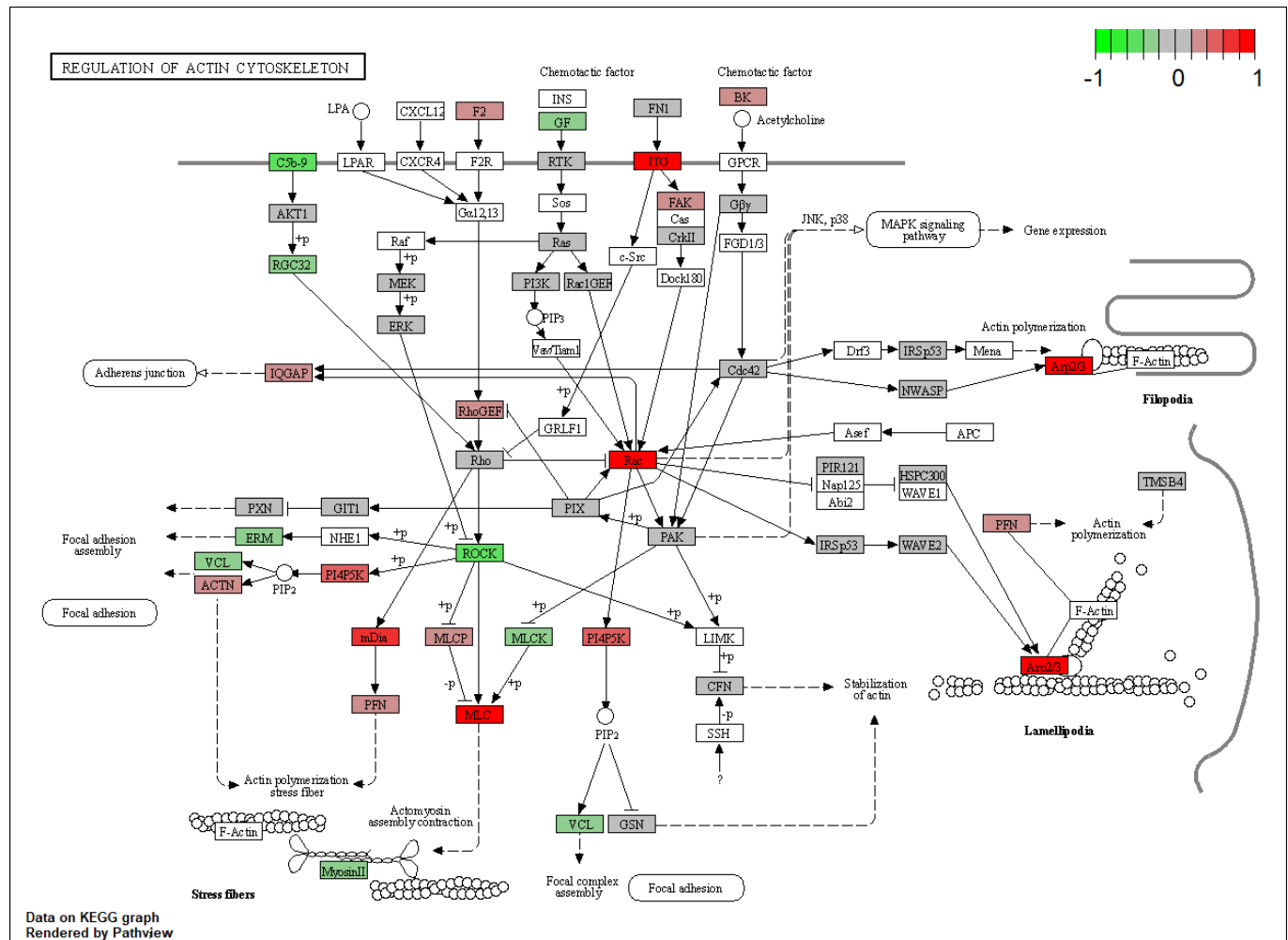


Figure S13. NMN treatment effects on the KEGG proteasome pathway in mouse adipose tissue. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

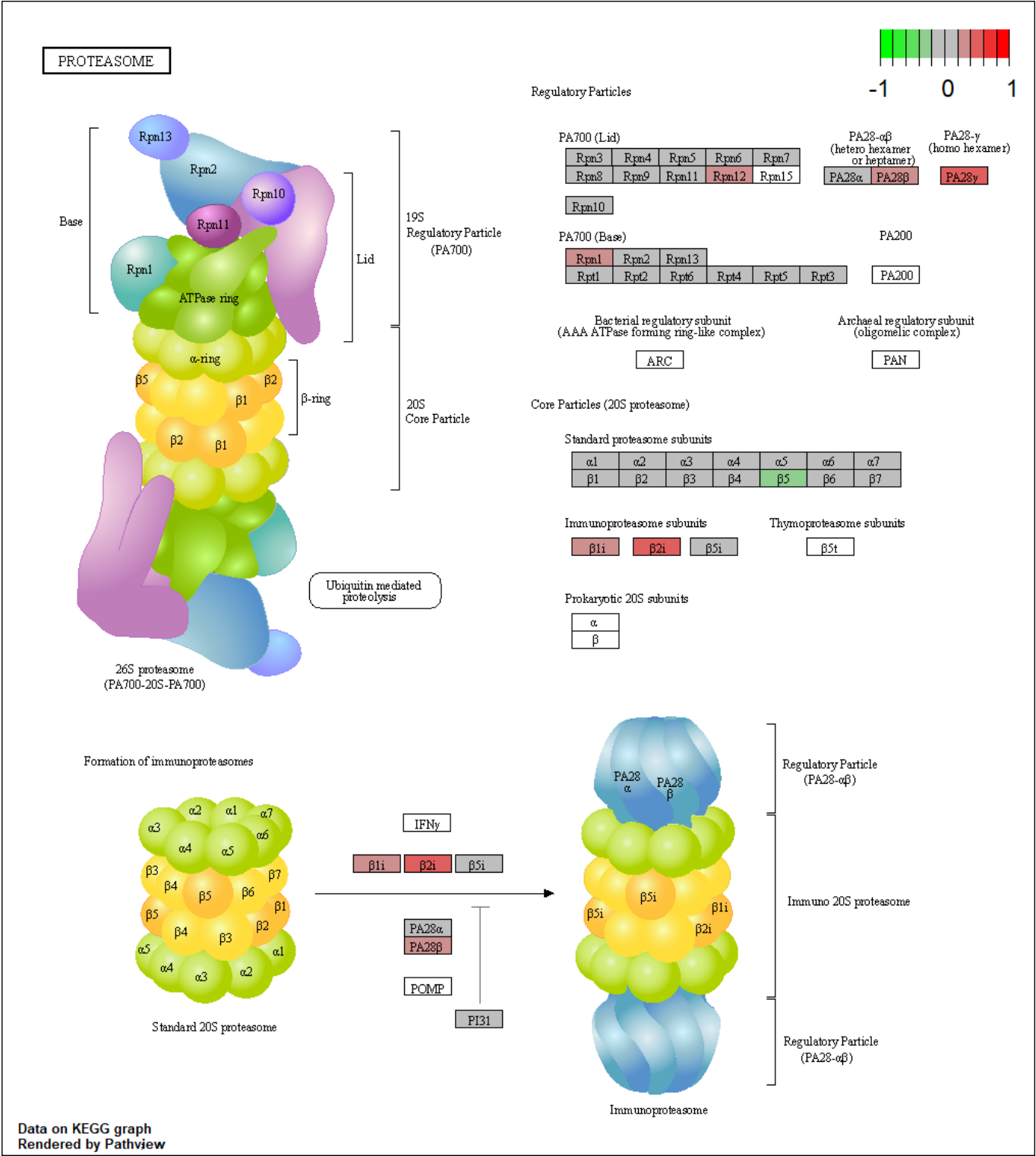


Figure S14. NMN treatment effects on the KEGG mTOR signaling pathway in mouse adipose tissue. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

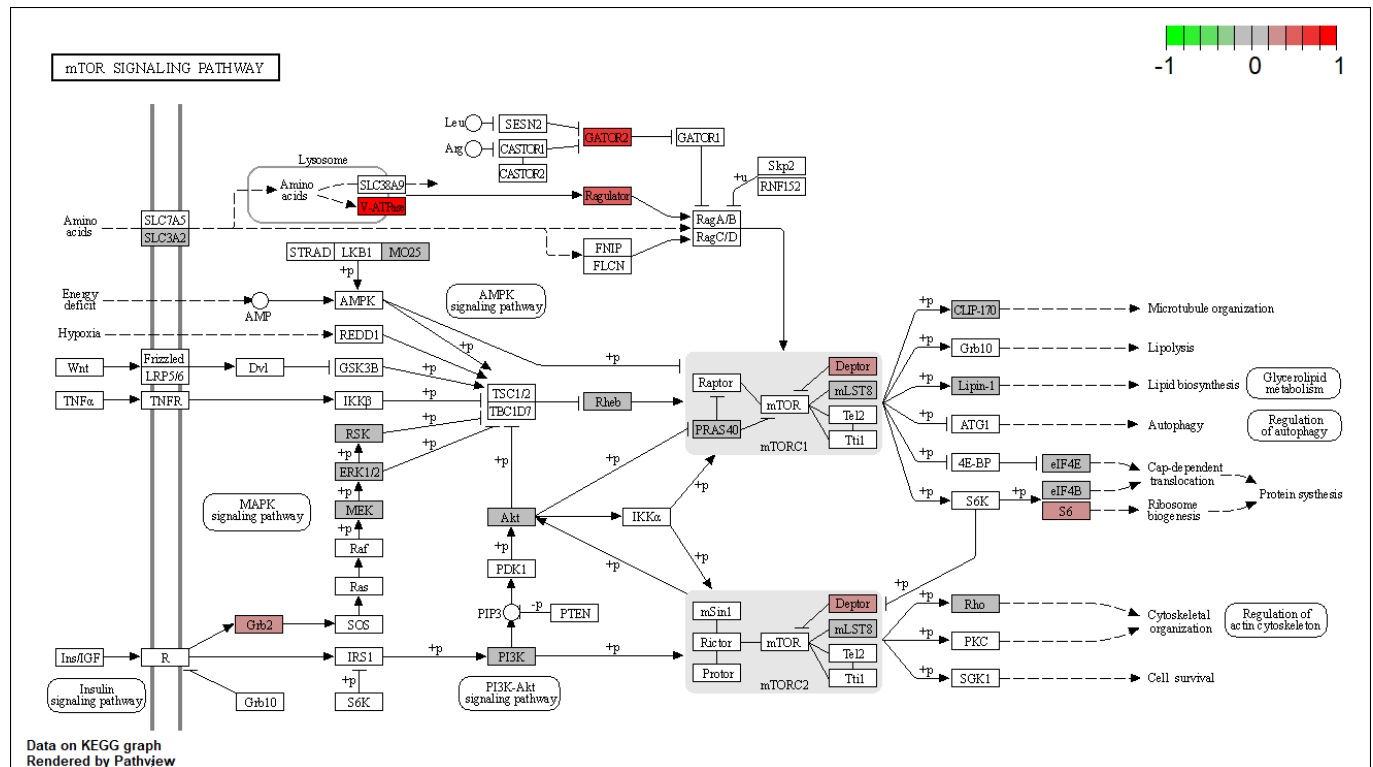


Figure S15. NMN treatment effects on the KEGG tight junction's pathway in mouse adipose tissue. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

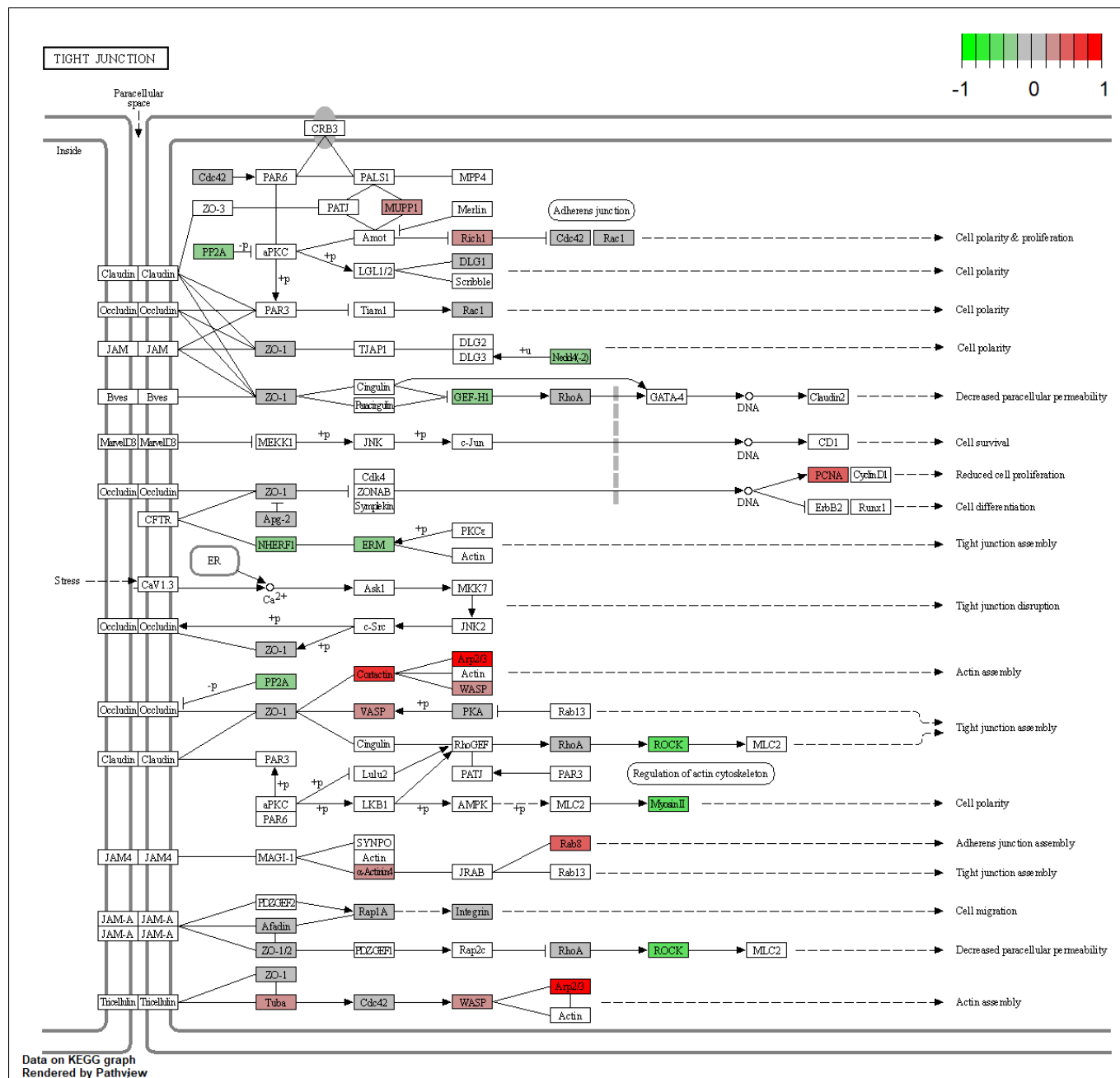


Figure S17. NMN treatment effects on the KEGG tight junctions' pathway in mouse brain. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

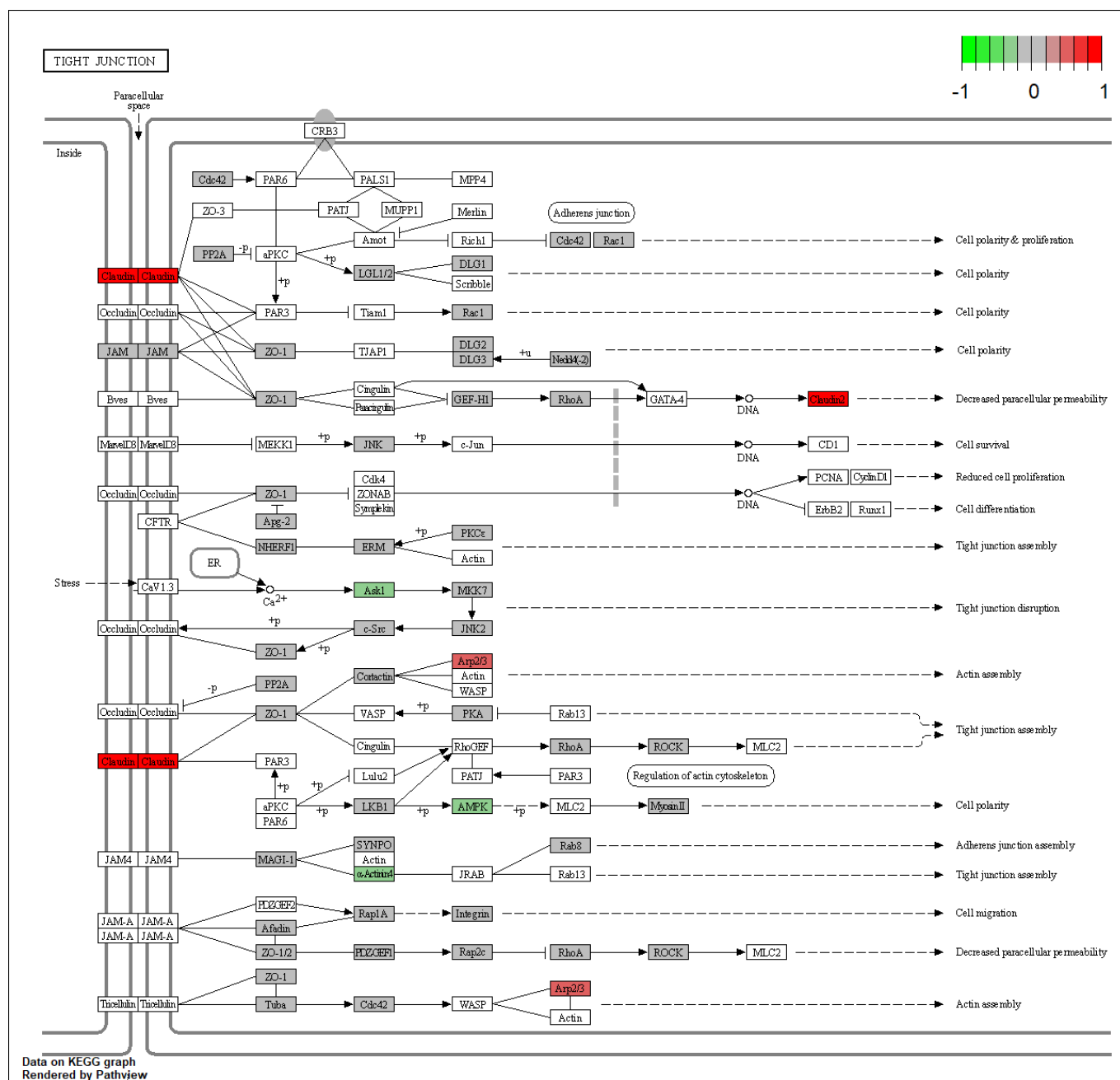


Figure S18. NMN treatment effects on the KEGG protein processing in endoplasmic reticulum pathway in mouse brain. The colour of the boxes represents the log2 fold change of the protein abundances, represented for HFD+NMN group versus HFD group comparison. Red: up-regulated; green: down-regulated; grey: no significant expression change.

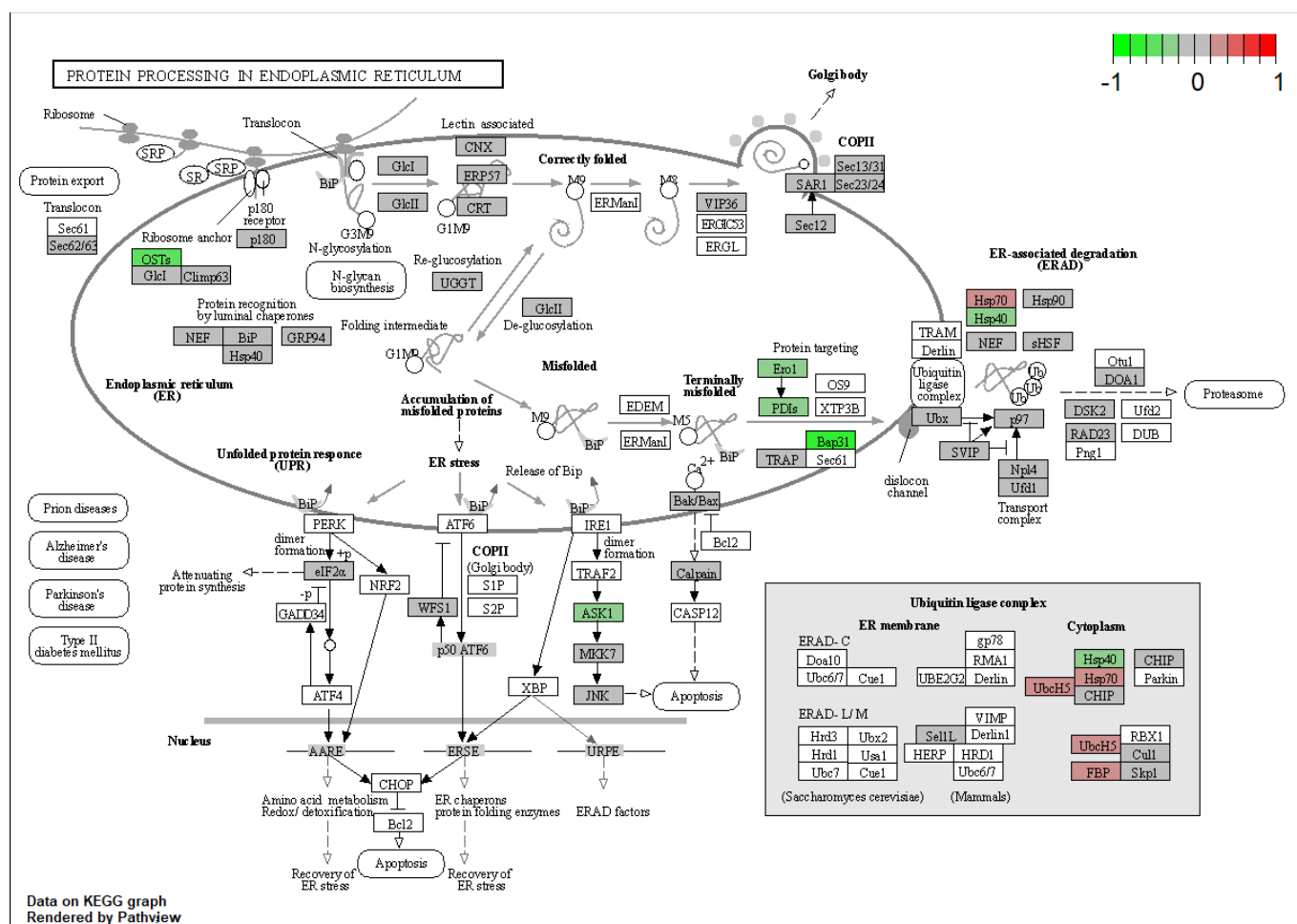
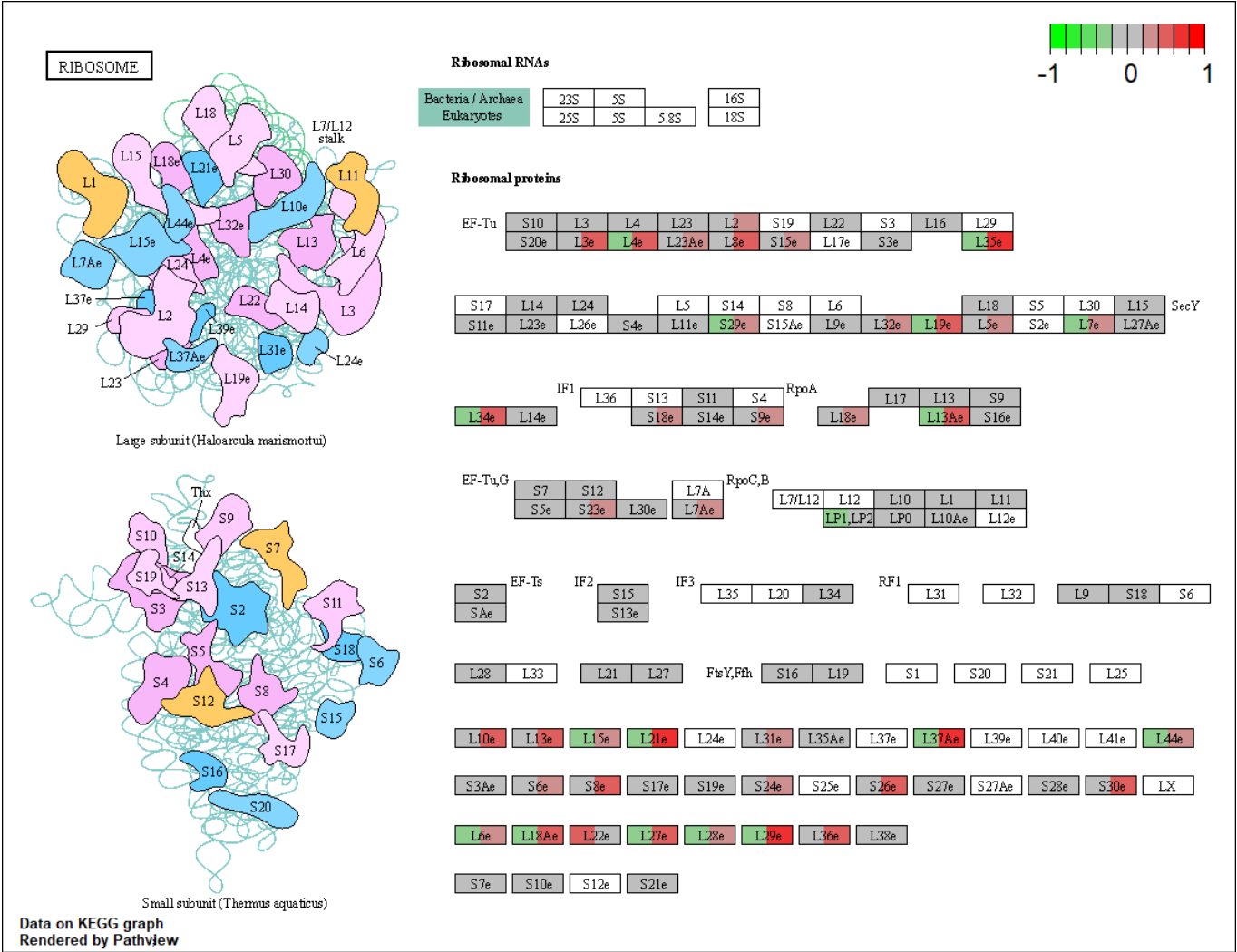


Figure S19. NMN treatment effects on the KEGG ribosome pathway in HepG2 cells. The colour of the boxes represents the log2 fold change of the protein abundances, represented simultaneously for HN and HH comparisons, H100N versus H0N left side, H100H versus H0H right side, in the corresponding box for each protein. Red: up-regulated; green: down-regulated; grey: no significant expression change.



OXIDATIVE PHOSPHORYLATION

Complex I: NADH dehydrogenase (Thermus thermophilus). Subunits: ND1, ND2, ND3, ND4, ND5, ND6. FMN, NADH, NAD⁺, H⁺.

Complex II: Succinate dehydrogenase (E. coli). Subunits: SdhA, SdhB, SdhC, SdhD. Succinate, Fumarate, Iron protein, Quinone pool.

Complex III: Cytochrome bc₁ complex (bovine). Subunits: Core 1, Core 2, Cyt b, Cyt c₁, ISP, Cyt c₂.

Complex IV: Cytochrome c oxidase (bovine). Subunits: VIa, VIb, VIc, VIIa, VIIb, VIIc. 1/2 O₂, 2H⁺, H₂O.

Complex V: ATP synthase (Escherichia coli). Subunits: a, b, c, d, e, f₁, f₀, f₁, f₀, f₁, f₀. Proton channel, ATP synthase.

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND5	ND6
E	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6
B/A	NuoA	NuoB	NuoC	NuoD	NuoE	NuoF
B/A	NdhC	NdhK	NdhJ	NdhH	NdhA	NdhI
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6
E	Ndufb1	Ndufb2	Ndufb3	Ndufb4	Ndufb5	Ndufb6

Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB
B/A	SdhC	SdhD	SdhA	SdhB
	Frda	Frdb	Frdc	Frdd

Cytochrome c reductase

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

Cytochrome c oxidase

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

Cytochrome c oxidase, cbb3-type

B	I	II	IV	III
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Cytochrome bd complex

B/A	CydA	CydB	CydX
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Cytochrome c

CYC

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
f	g	f6/h	j	k

V/A-type ATPase (Bacteria, Archaea)

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			

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Rendered by Pathview

Data on KEGG graph
Rendered by Pathvew

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Data on KEGG graph
Rendered by Pathview

Figure S22. NMN treatment effects on the KEGG DNA replication pathway in HepG2 cells. The colour of the boxes represents the log2 fold change of the protein abundances, represented simultaneously for HN and HH comparisons, H100N versus H0N left side, H100H versus H0H right side, in the corresponding box for each protein. Red: up-regulated; green: down-regulated; grey: no significant expression change.

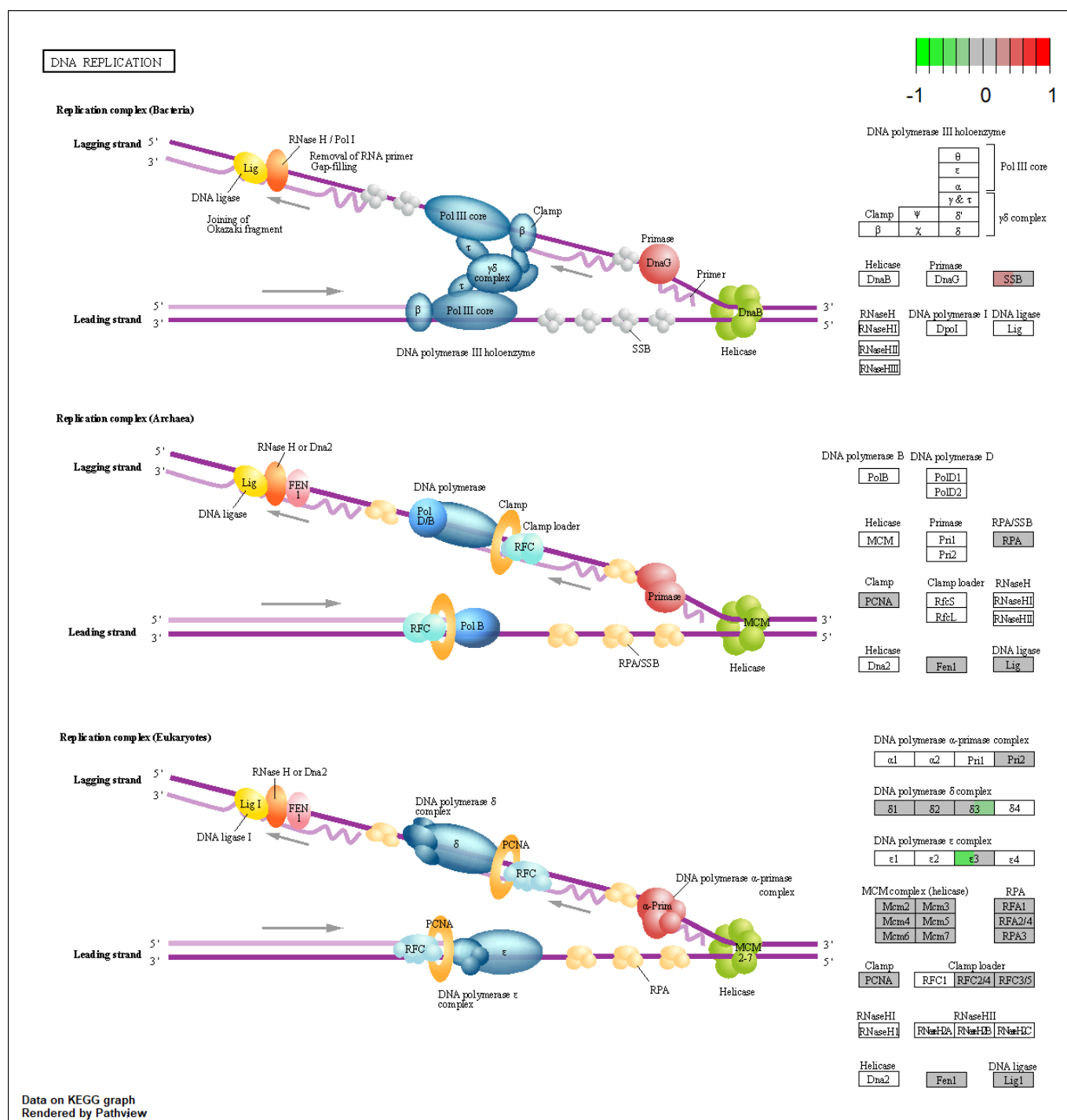


Figure S26. NMN treatment effects on the KEGG proteasome pathway in C2C12 derived myotubes. The colour of the boxes represents the log2 fold change of the protein abundances, represented simultaneously for HN and HH comparisons, H100N versus H0N left side, H100H versus H0H right side, in the corresponding box for each protein. Red: up-regulated; green: down-regulated; grey: no significant expression change.

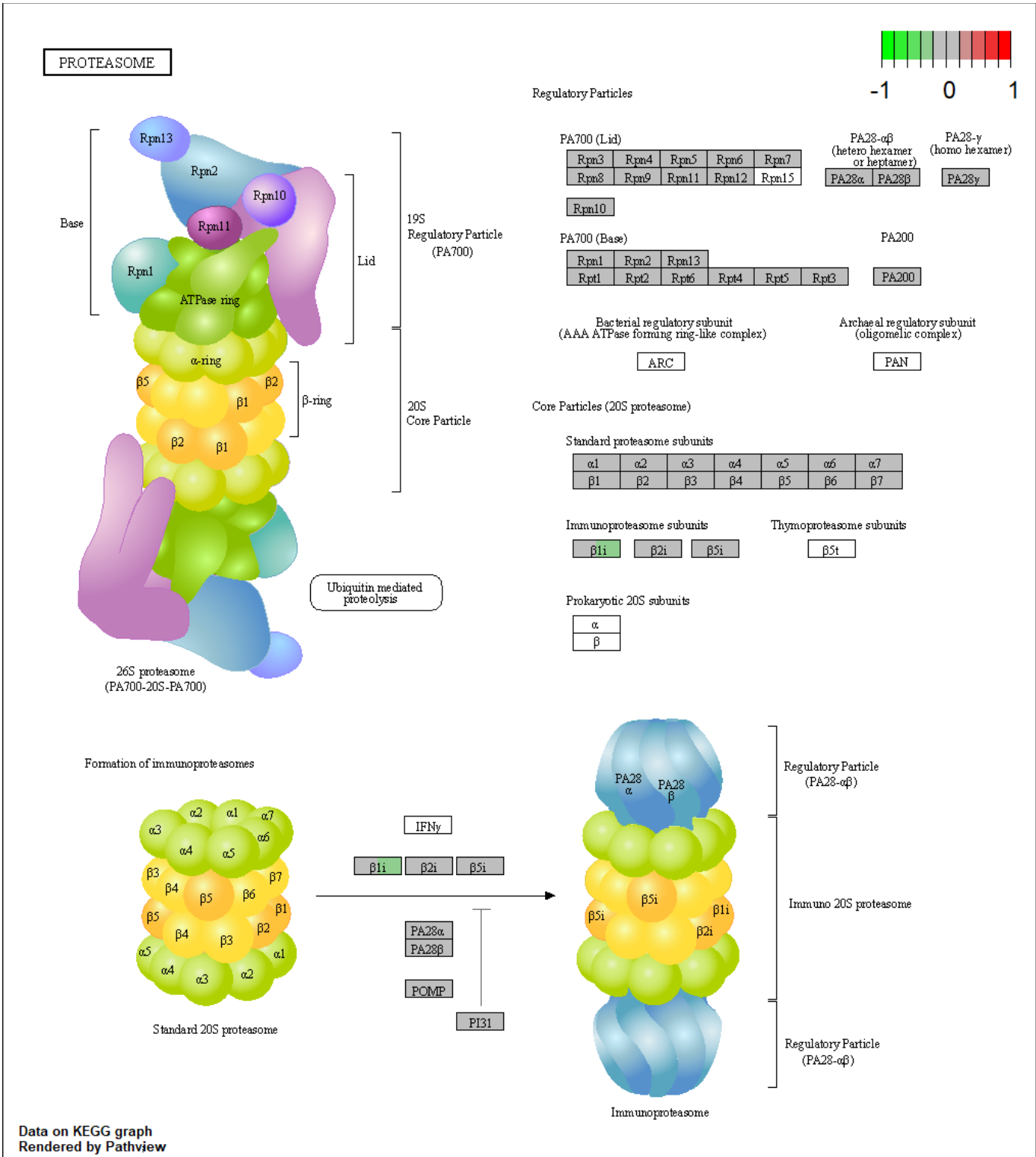


Figure S27. NMN treatment effects on the KEGG spliceosome pathway in C2C12 derived myotubes. The colour of the boxes represents the log2 fold change of the protein abundances, represented simultaneously for HN and HH comparisons, H100N versus H0N left side, H100H versus H0H right side, in the corresponding box for each protein. Red: up-regulated; green: down-regulated; grey: no significant expression change.

