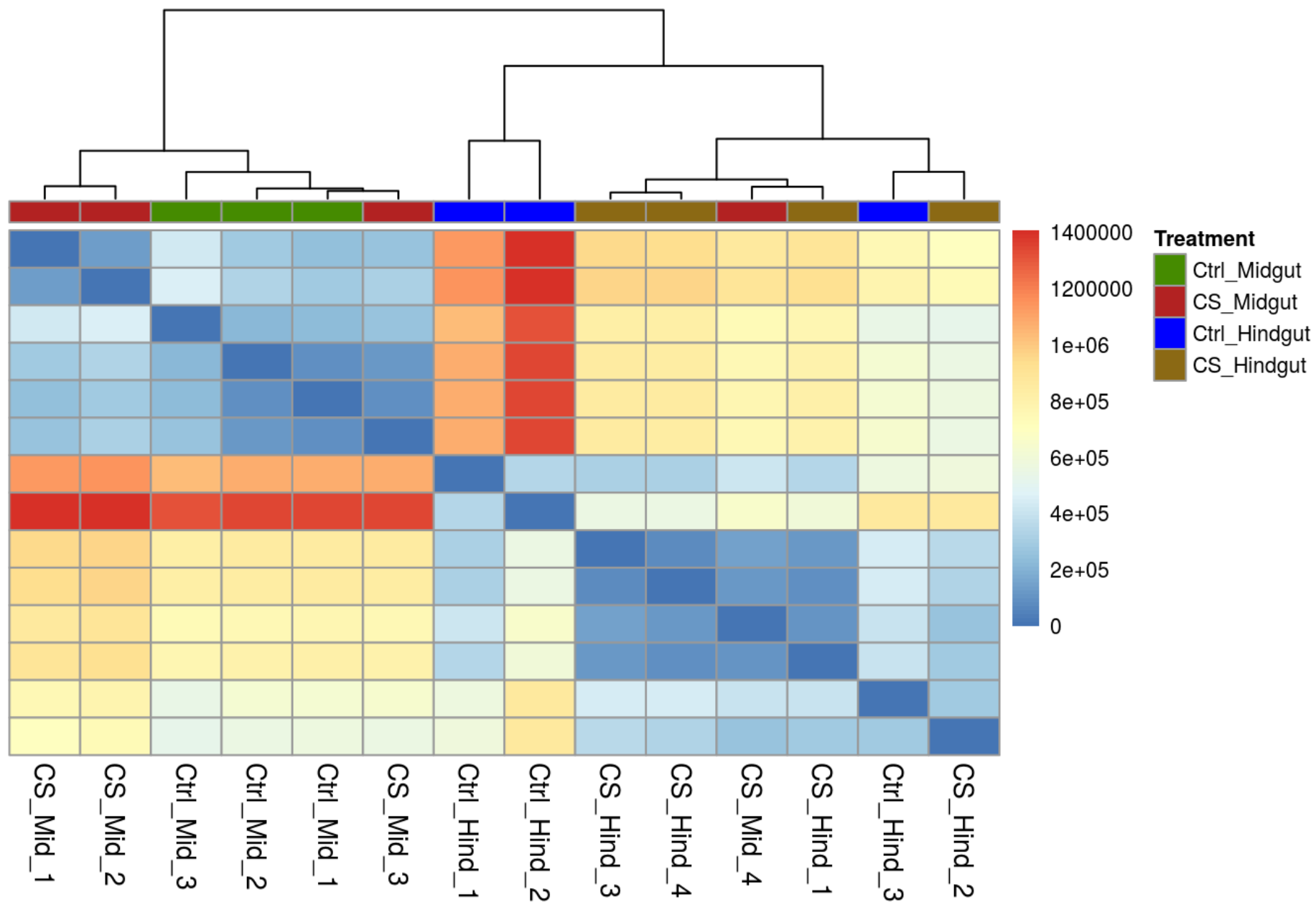
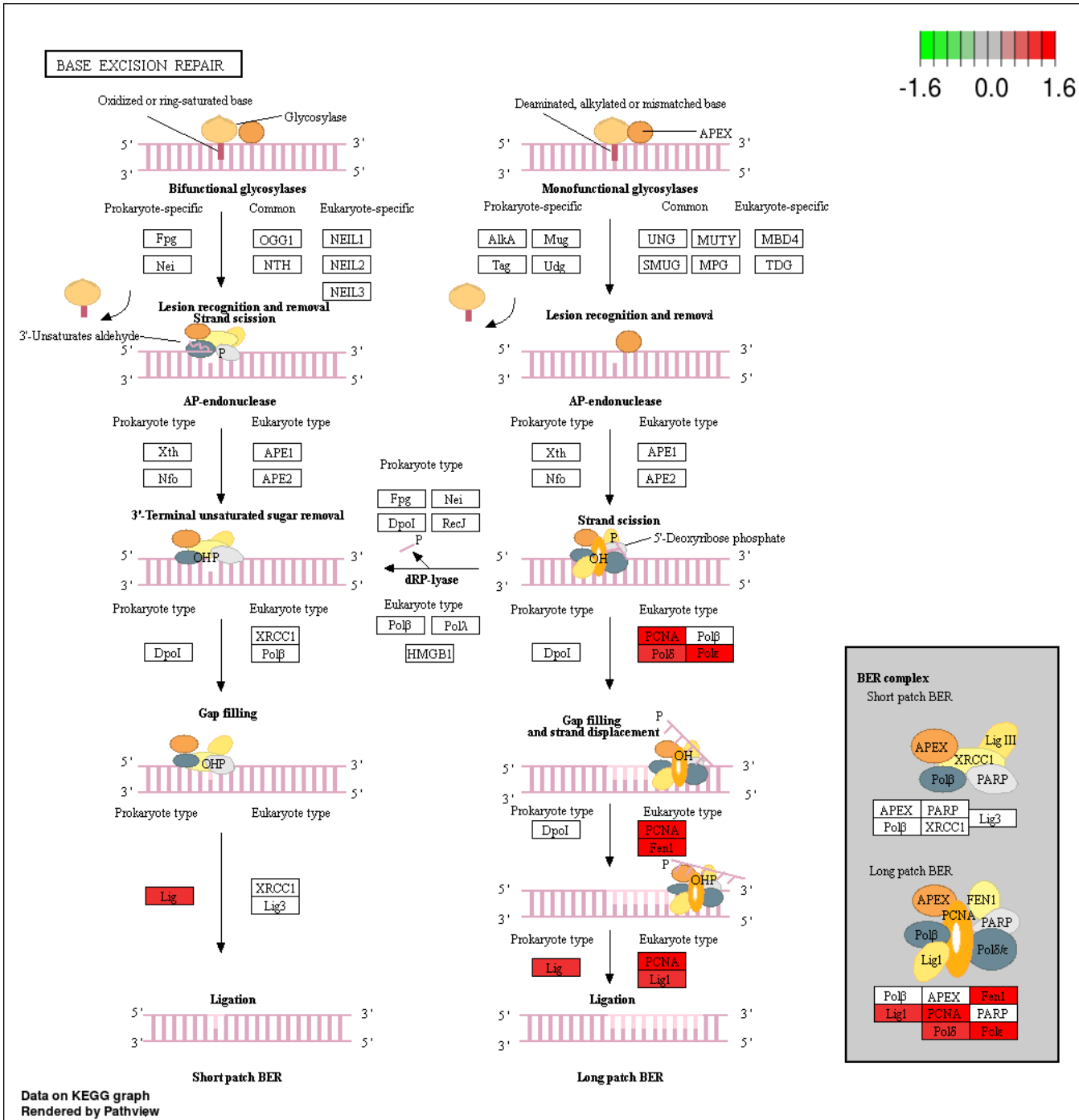
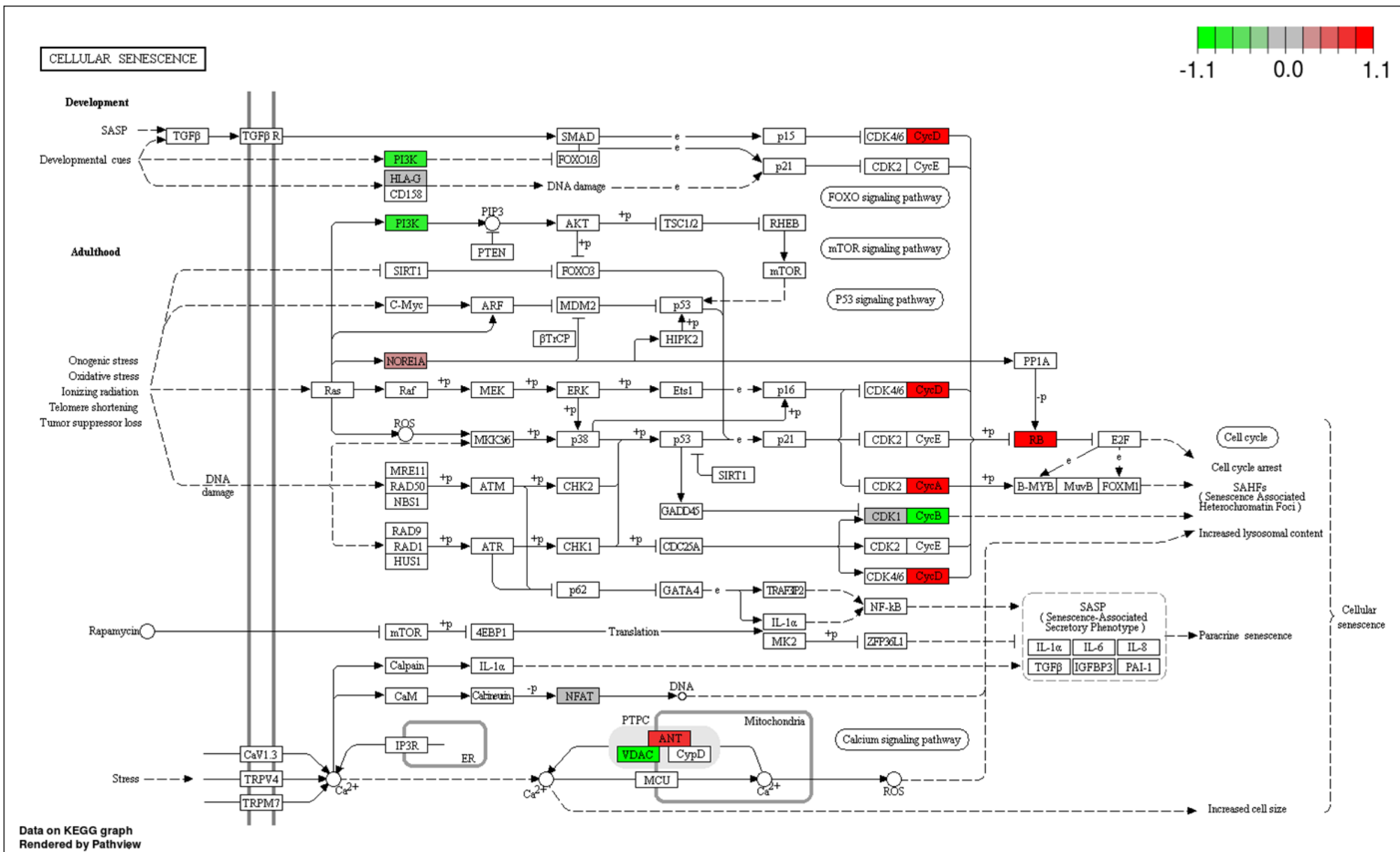


Supplementary figure 1. Hierarchical clustering of samples by read counts per gene. Heatmap and dendrogram. Heatmap legend and colours indicate between-sample Euclidean distance. Note that both axes of the heatmap represent the list of samples, but the sample labels on the x axis

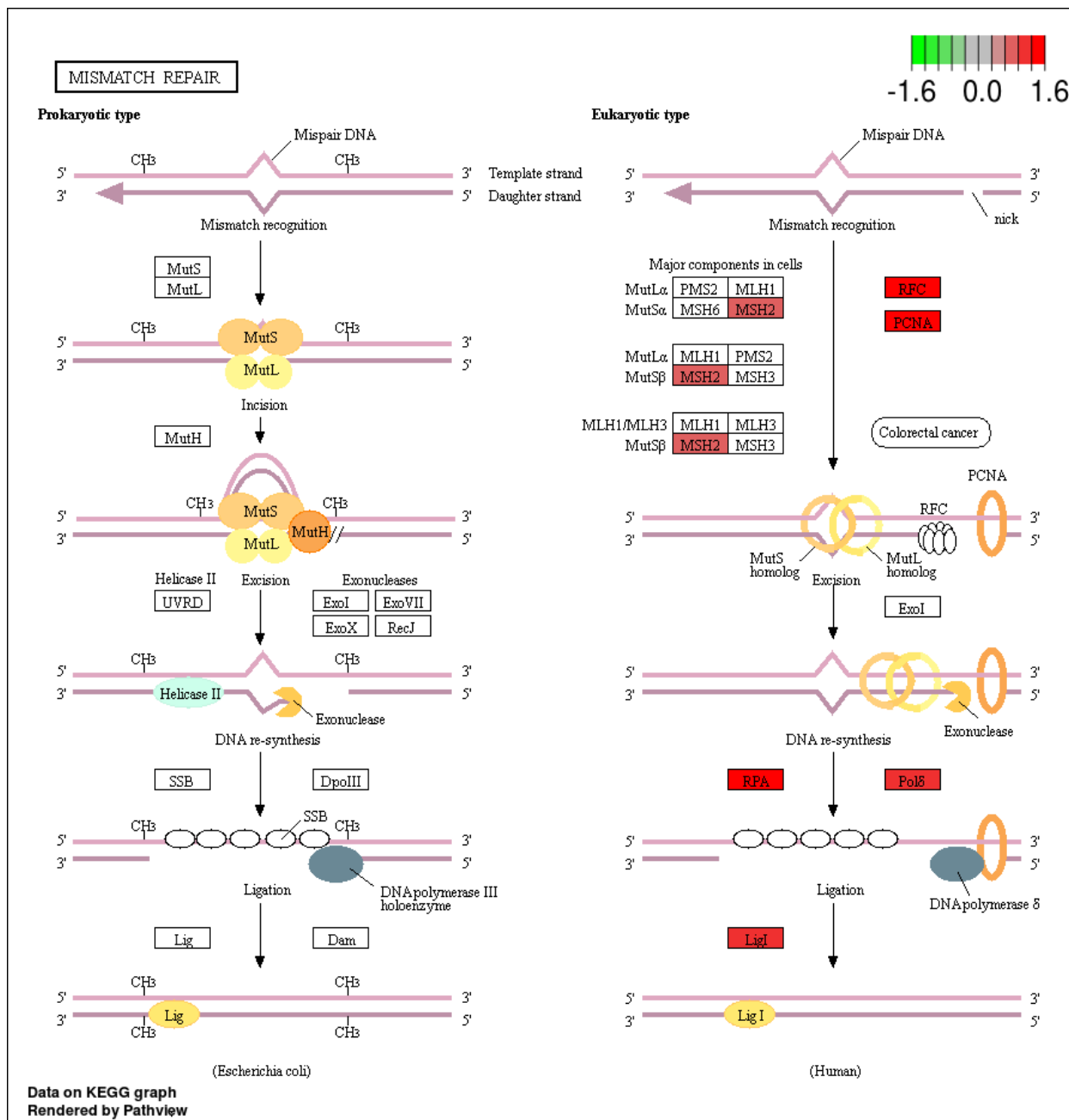


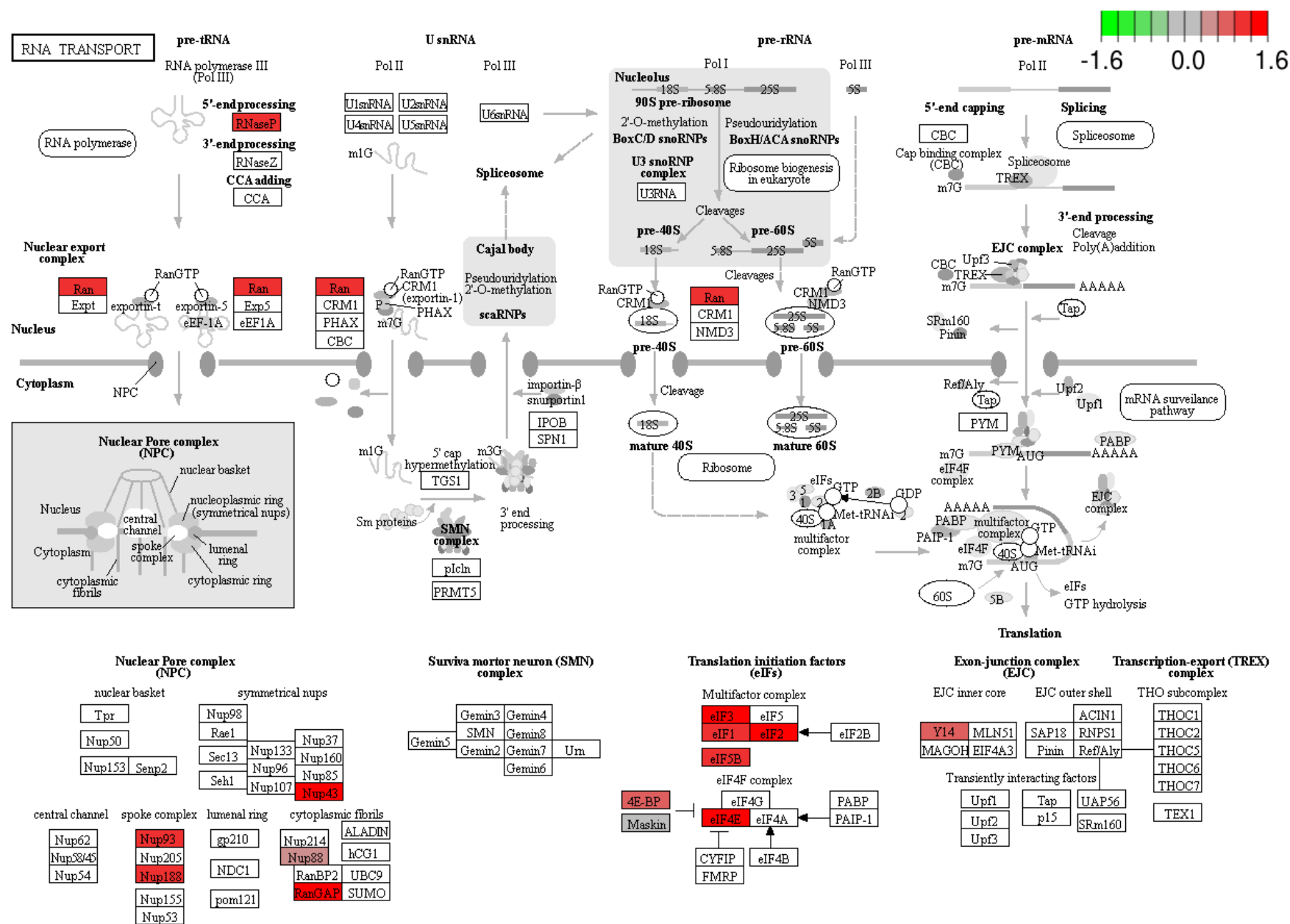


Supplementary figure 2. Metabolic pathway map showing differentially expressed genes within base excision repair for midgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated



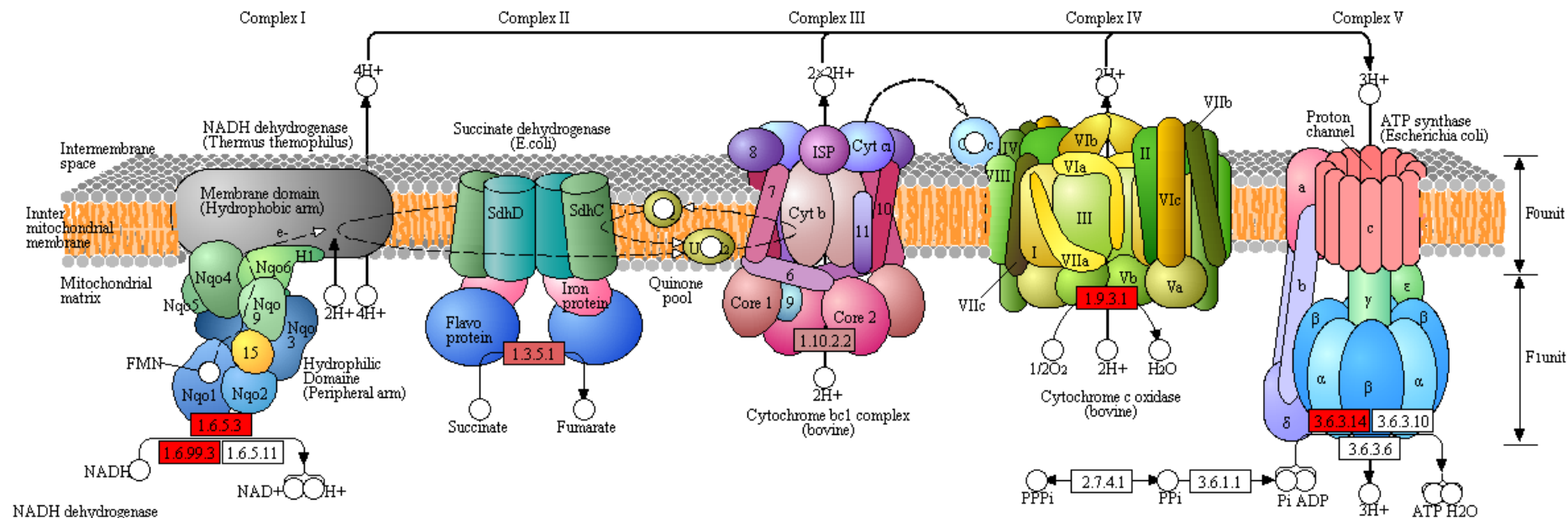
Supplementary figure 3. Metabolic pathway map showing differentially expressed genes within cellular senescence for hindgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated





Supplementary figure 6. Metabolic pathway map showing differentially expressed genes within RNA transport for midgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated

OXIDATIVE PHOSPHORYLATION

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6
---	-----	-----	-----	-----	------	-----	-----

F	Ndnfs1	Ndnfs2	Ndnfs3	Ndnfs4	Ndnfs5	Ndnfs6	Ndnfs7	Ndnfs8	Ndnfs9	Ndnfs10	Ndnfs11
---	--------	--------	--------	--------	--------	--------	--------	--------	--------	---------	---------

	NuoA1	NuoA2	NuoA3	NuoA4	NuoA5	NuoA6	NuoA7	NuoA8	NuoA9	NuoA10	NuoA11	NuoA12	NuoA13	NuoA14	NuoA15
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 oxidase

E COX10

COX3	COX1	COX2	COX4	COX5A	COX5B	COX6A	COX6B	COX6C	COX7A	COX7B	COX7C	COX8	E/B/A
------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	------	-------

B/A	CyoE	CyoD	CyoC	CyoB	CyoA
-----	------	------	------	------	------

	CoxD	CoxC	CoxA	CoxB
--	------	------	------	------

Cytochrome c oxidase , cbb3-type

B	I	II	IV	III
---	---	----	----	-----

Cytochrome bd complex

B/A	CydA	CydB	CydX
-----	------	------	------

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	f5/h	i	k	8

V/A-type ATPase (Bacteria, Archaeas)

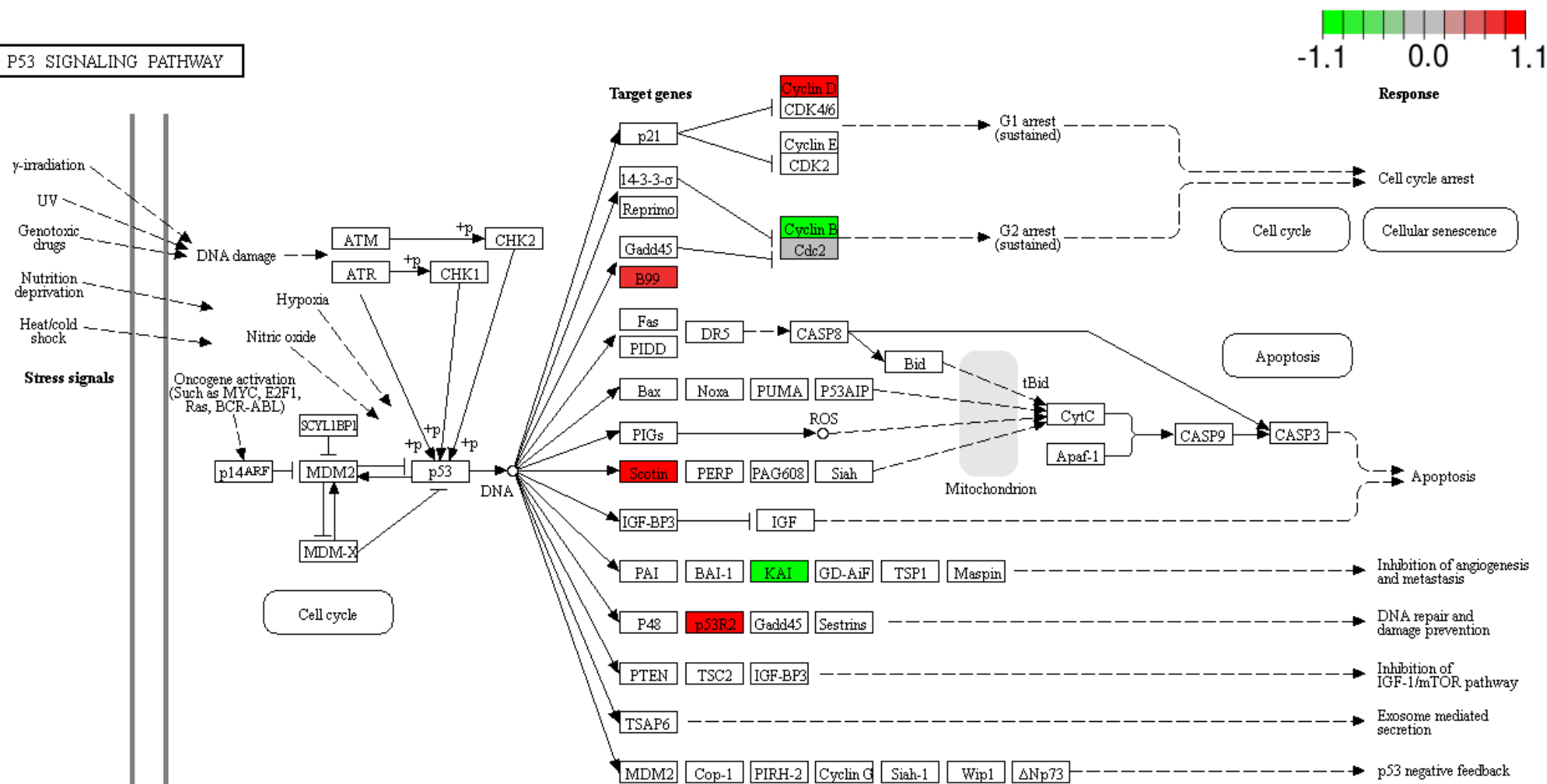
A	B	C	D	E	F	G/H
I	K					

V-type ATPase (Eukaryotes)

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

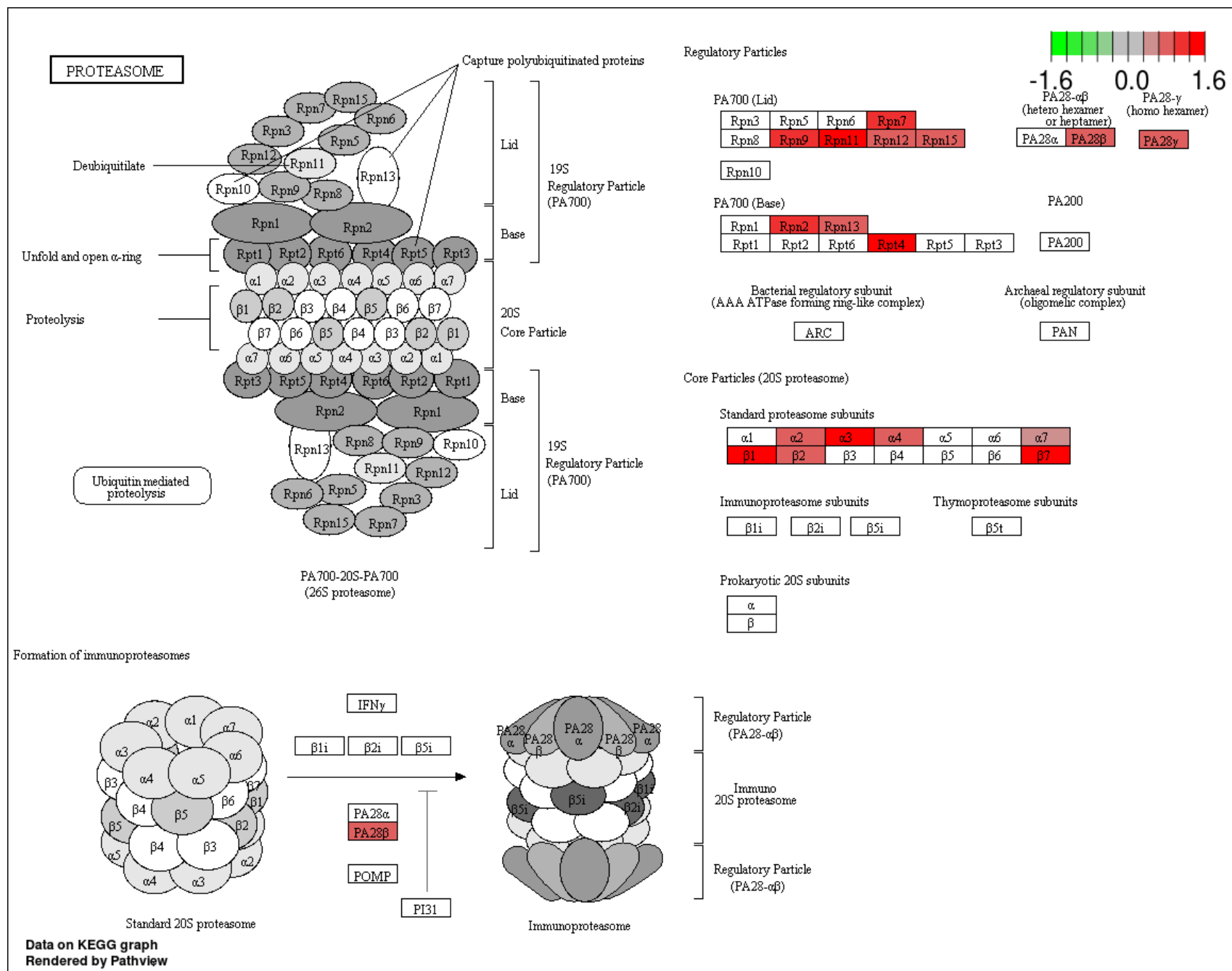
Supplementary figure 7.
Metabolic pathway map showing differentially expressed genes within oxidative phosphorylation for midgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated

P53 SIGNALING PATHWAY

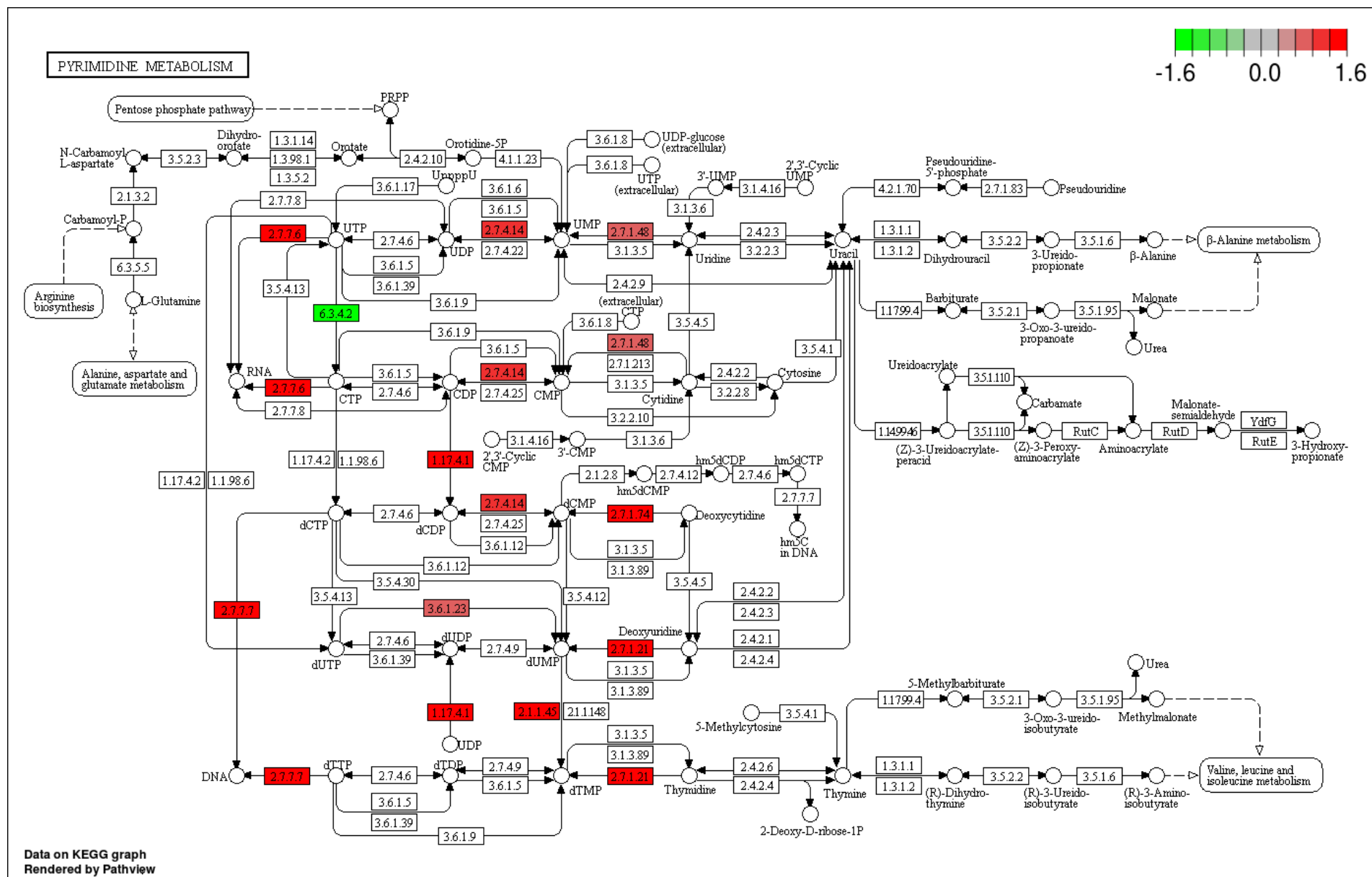


Data on KEGG graph
Rendered by Pathview

Supplementary figure 8. Metabolic pathway map showing differentially expressed genes within P53 signalling pathway for hindgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated



Supplementary figure 9. Metabolic pathway map showing differentially expressed genes within the proteasome complex for midgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated



Supplementary figure 10. Metabolic pathway map showing differentially expressed genes within pyrimidine metabolism for midgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated

Large subunit (*Haloarcula marismortui*)

Small subunit (*Thermus aquaticus*)

Data on KEGG graph
Rendered by Pathview

Ribosomal RNAs

Bacteria / Archaea	23S	5S		16S
Eukaryotes	25S	5S	5.8S	18S

Ribosomal proteins

EF-Tu

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

L7/L12 stalk

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

SecY

IF1

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

RpoA

L34e	L14e
------	------

EF-TuG

S7	S12		L7A		L7/L12	L12	L10	L1	L11
S5e	S23e	L30e	L7Ae			L11e	L10e	L12e	

RpoC,B

S2 EF-Ts IF2 IF3 RF1

S2	S15	L35	L20	L34	L31	L32	L9	S18	S6
S4e	S13e								

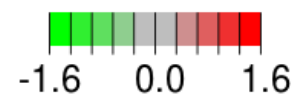
L28	L33	L21	L27	FtsY,Ffh	S16	L19	S1	S20	S21	L25
-----	-----	-----	-----	----------	-----	-----	----	-----	-----	-----

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
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S7e	S10e	S12e	S21e
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Supplementary figure 12. Metabolic pathway map showing differentially expressed genes within ribosome complex for midgut control vs UCS. Red colored genes are upregulated and green colored genes are downregulated