

<b>RNAseq data analysis</b>	<b>Page</b>
GO term and pathway analysis wildtype versus HSA-LT $\alpha/\beta$ at 6 months	1
GO term and pathway analysis wildtype versus HSA-LT $\alpha/\beta$ at 9 months	2
GO term and pathway analysis wildtype 6 months versus 9 months	3
GO term and pathway analysis HSA-LT $\alpha/\beta$ 6 months versus 9 months	4
Pathway visualization wildtype versus HSA-LT $\alpha/\beta$ at 6 months (Pathview)	
04060-Cytokine-cytokine receptor interaction	5
04062-Chemokine signaling pathway	6
04145-Phagosome	7
04640-Hematopoietic cell lineage	8
04650-Natural killer cell mediated cytotoxicity	9
04657-IL-17 signaling pathway	10
04658-Th1 and Th2 cell differentiation	11
04659-Th17 cell differentiation	12
04660-T cell receptor signaling pathway	13
04662-B cell receptor signaling pathway	14
04664-Fc epsilon RI signaling pathway	15
04666-Fc gamma R-mediated phagocytosis	16
04668-TNF signaling pathway	17
04140-Autophagy – animal	18
04137-Mitophagy – animal	19
04120-Ubiquitin mediated proteolysis	20
04150-mTOR signaling pathway	21
04151-PI3K-Akt signaling pathway	22
04141-Protein processing in endoplasmic reticulum	23
00190-Oxidative phosphorylation	24
Pathway visualization wildtype versus HSA-LT $\alpha/\beta$ at 9 months (Pathview)	
04060-Cytokine-cytokine receptor interaction	25
04062-Chemokine signaling pathway	26
04145-Phagosome	27
04640-Hematopoietic cell lineage	28
04650-Natural killer cell mediated cytotoxicity	29
04657-IL-17 signaling pathway	30
04658-Th1 and Th2 cell differentiation	31
04659-Th17 cell differentiation	32
04660-T cell receptor signaling pathway	33
04662-B cell receptor signaling pathway	34
04664-Fc epsilon RI signaling pathway	35
04666-Fc gamma R-mediated phagocytosis	36
04668-TNF signaling pathway	37
04140-Autophagy – animal	38
04137-Mitophagy – animal	39
04120-Ubiquitin mediated proteolysis	40
04150-mTOR signaling pathway	41
04151-PI3K-Akt signaling pathway	42
04141-Protein processing in endoplasmic reticulum	43
00190-Oxidative phosphorylation	44

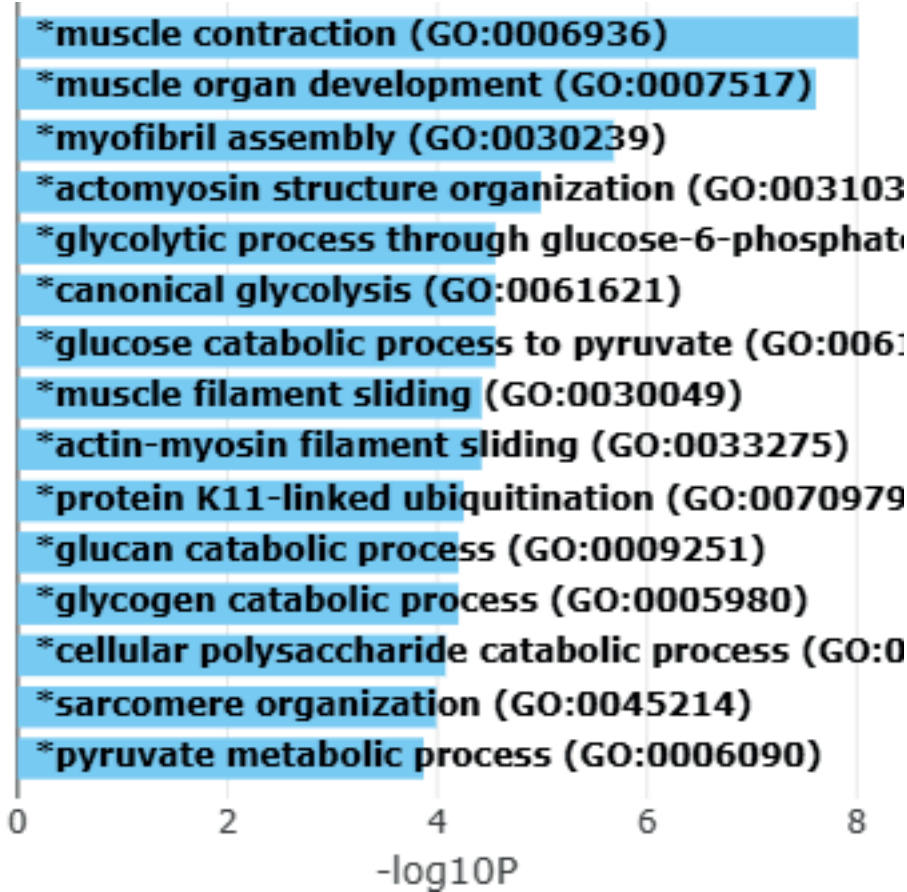
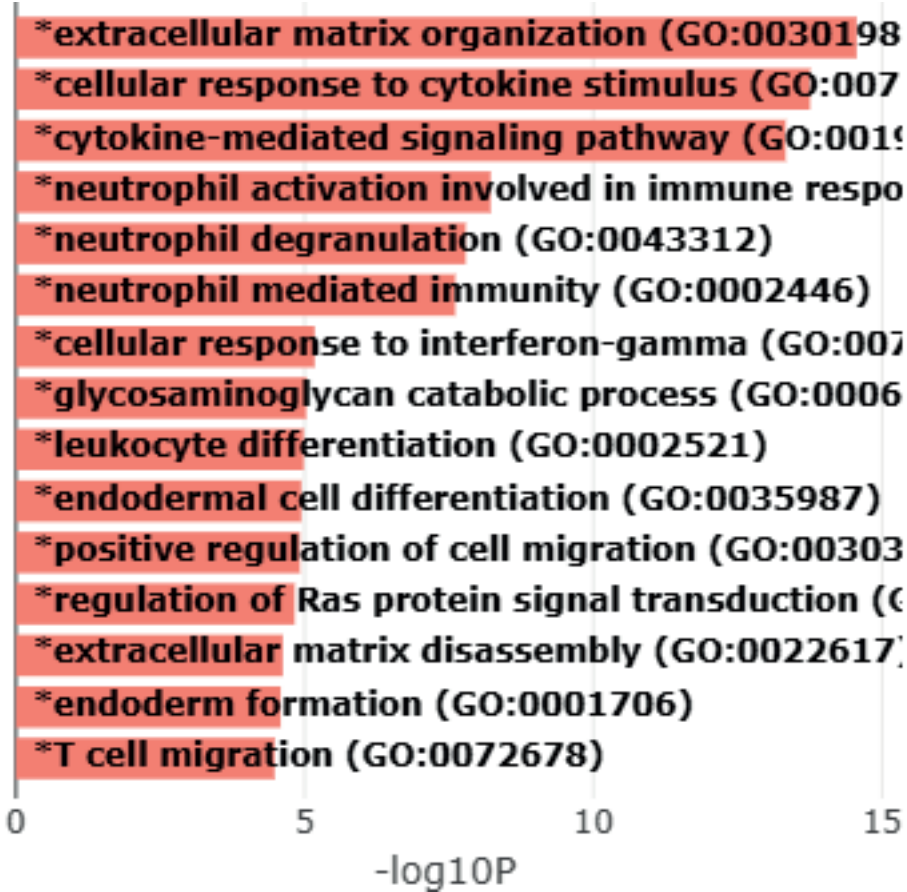


# wildtype versus HSA-LT $\alpha/\beta$ at 6 months

Gene Ontology Biological Process (2018 version)

up-regulated in HSA-LT $\alpha/\beta$

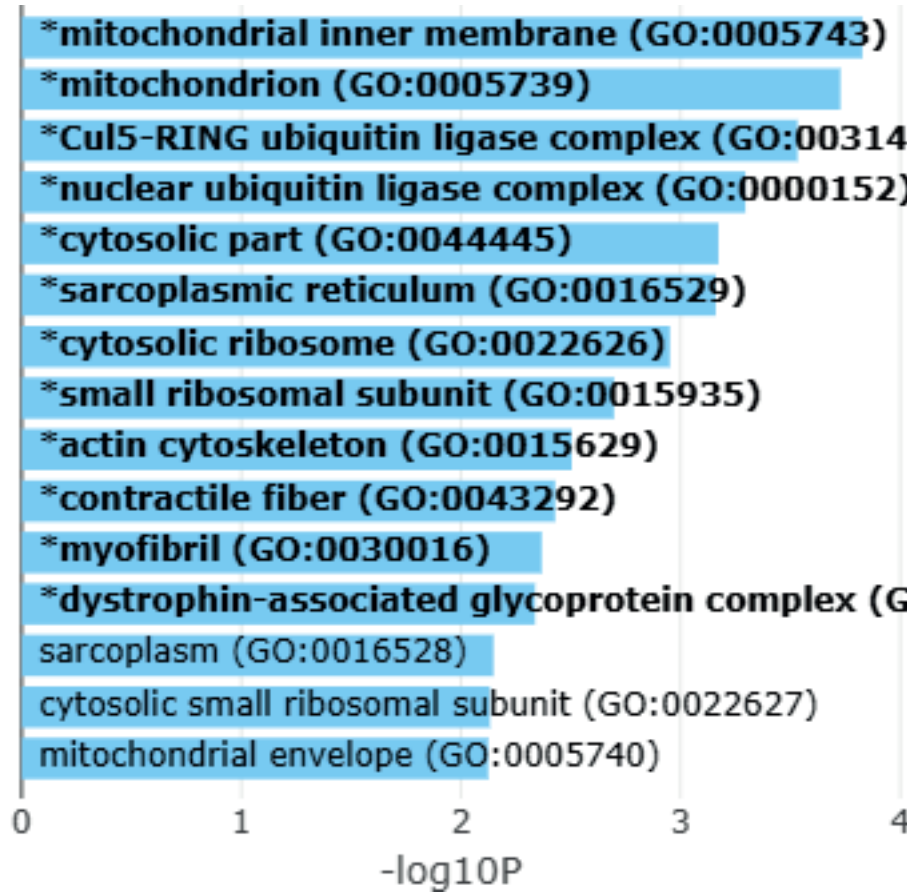
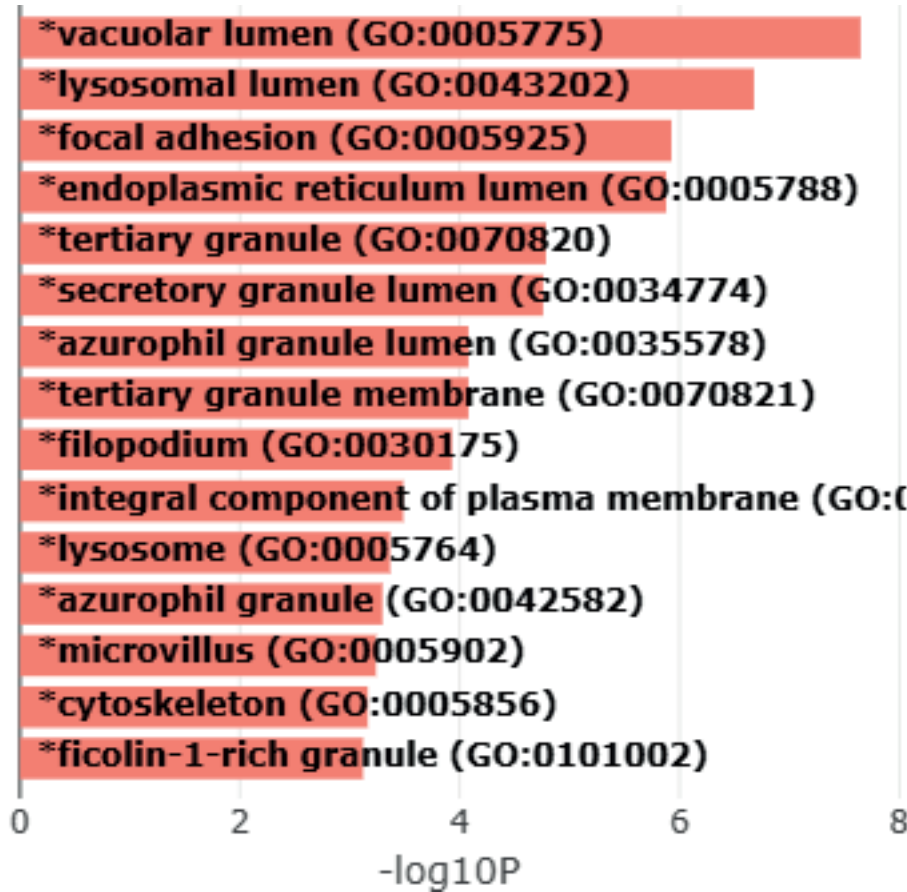
down-regulated in HSA-LT $\alpha/\beta$



Gene Ontology Cellular Component (2018 version)

up-regulated in HSA-LT $\alpha/\beta$

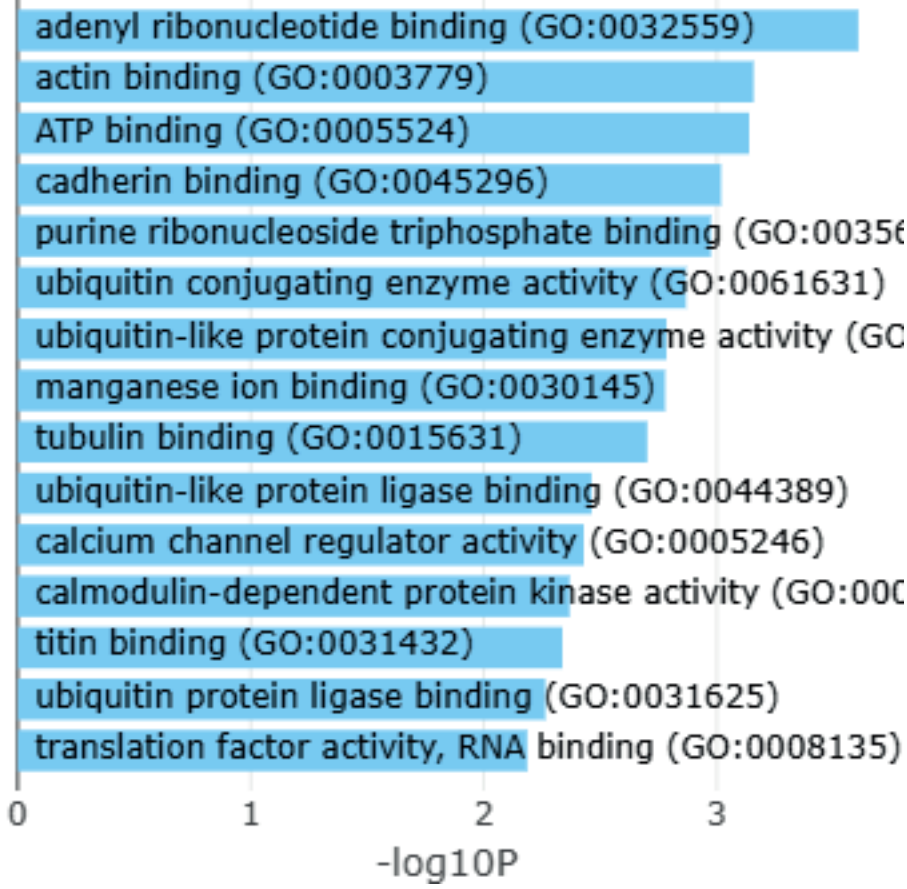
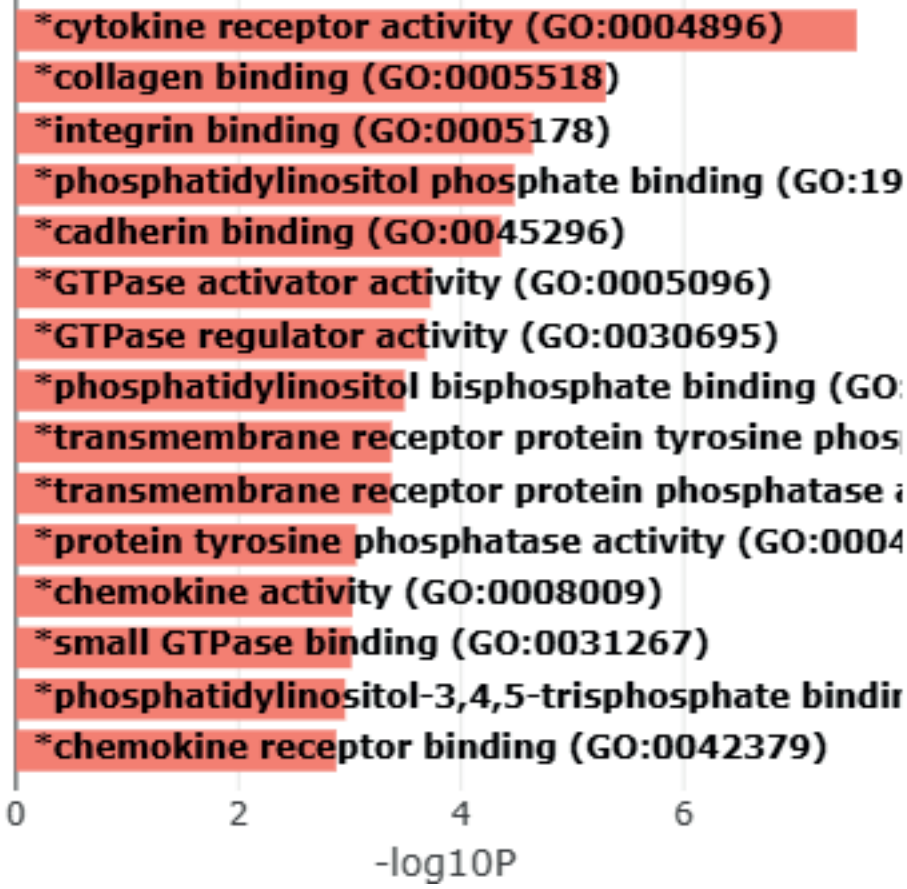
down-regulated in HSA-LT $\alpha/\beta$



Gene Ontology Molecular Function (2018 version)

up-regulated in HSA-LT $\alpha/\beta$

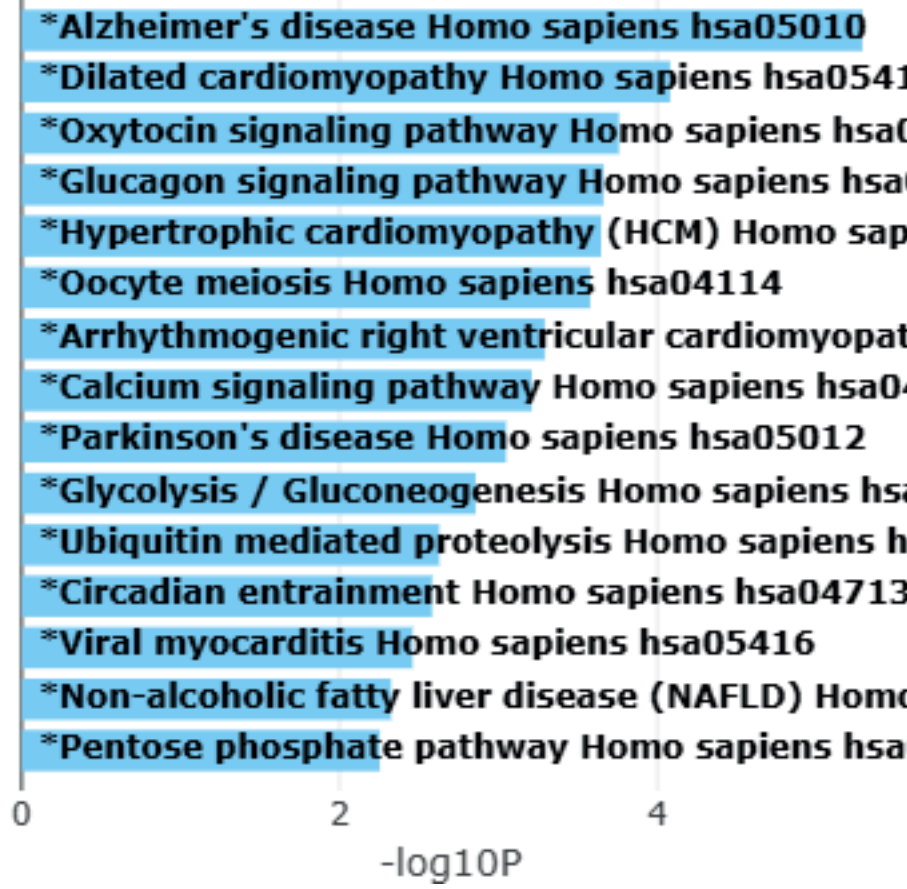
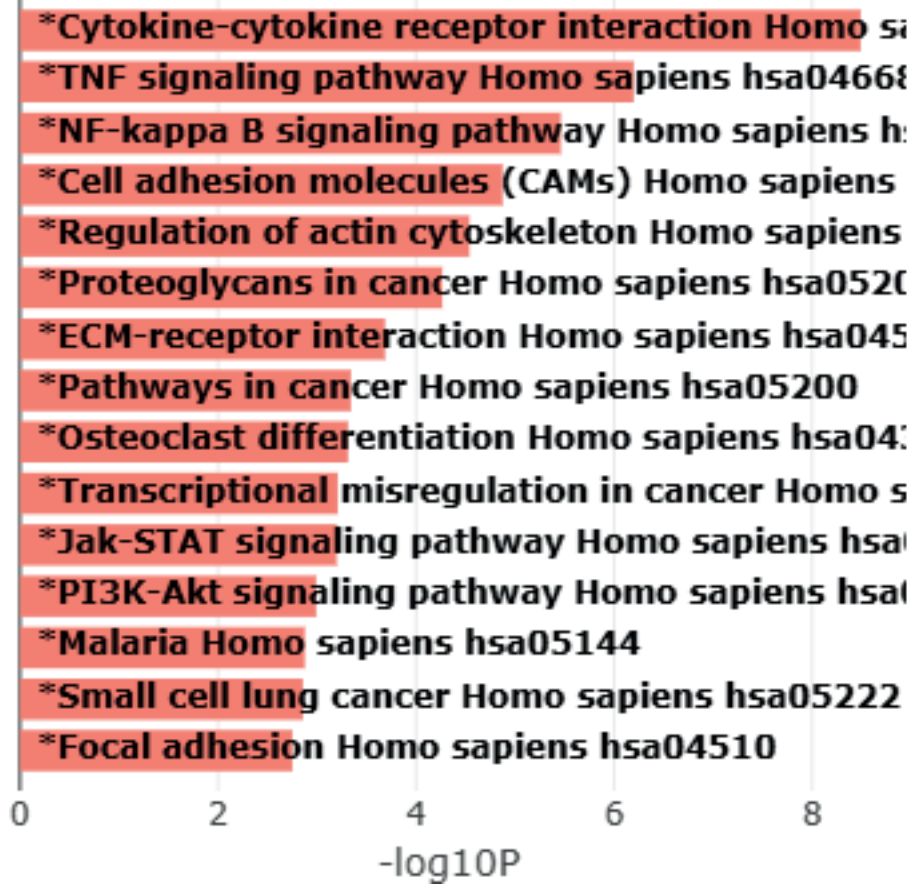
down-regulated in HSA-LT $\alpha/\beta$



KEGG pathway

up-regulated in HSA-LT $\alpha/\beta$

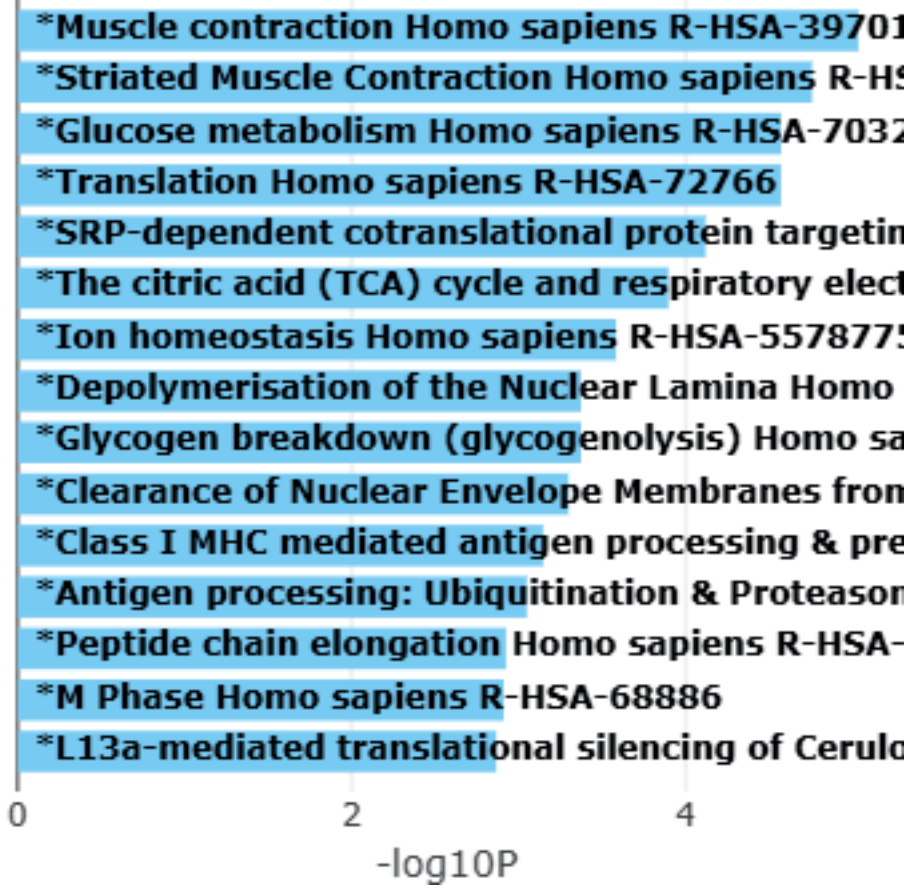
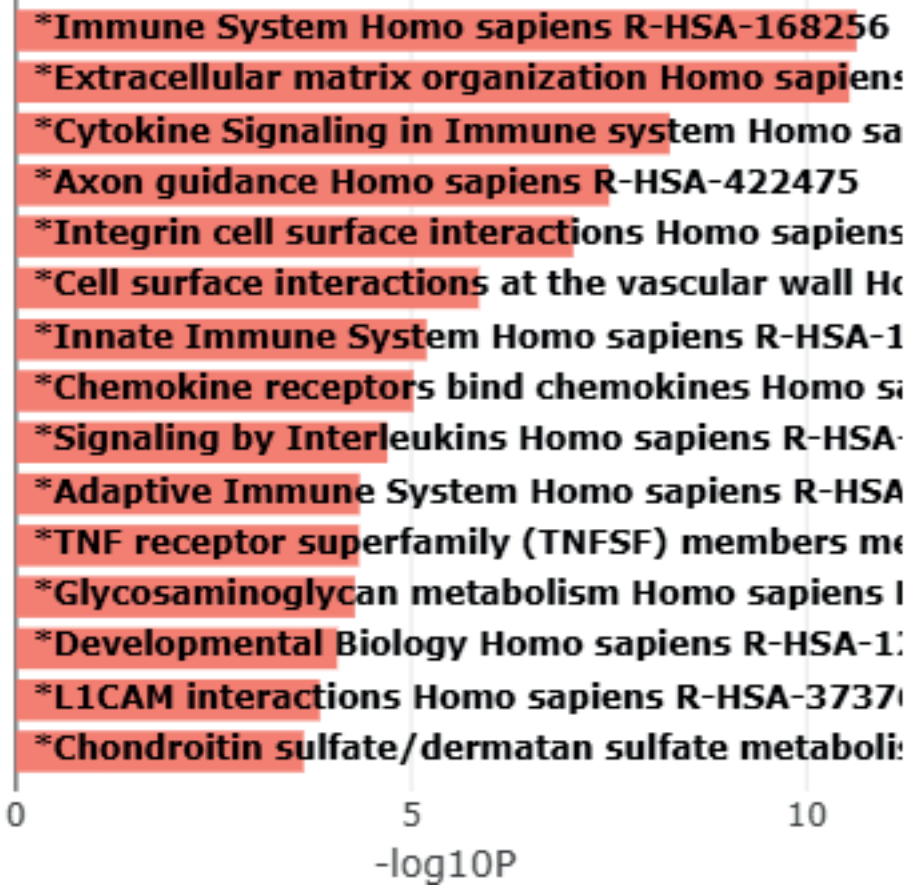
down-regulated in HSA-LT $\alpha/\beta$



Reactome Pathways

up-regulated in HSA-LT $\alpha/\beta$

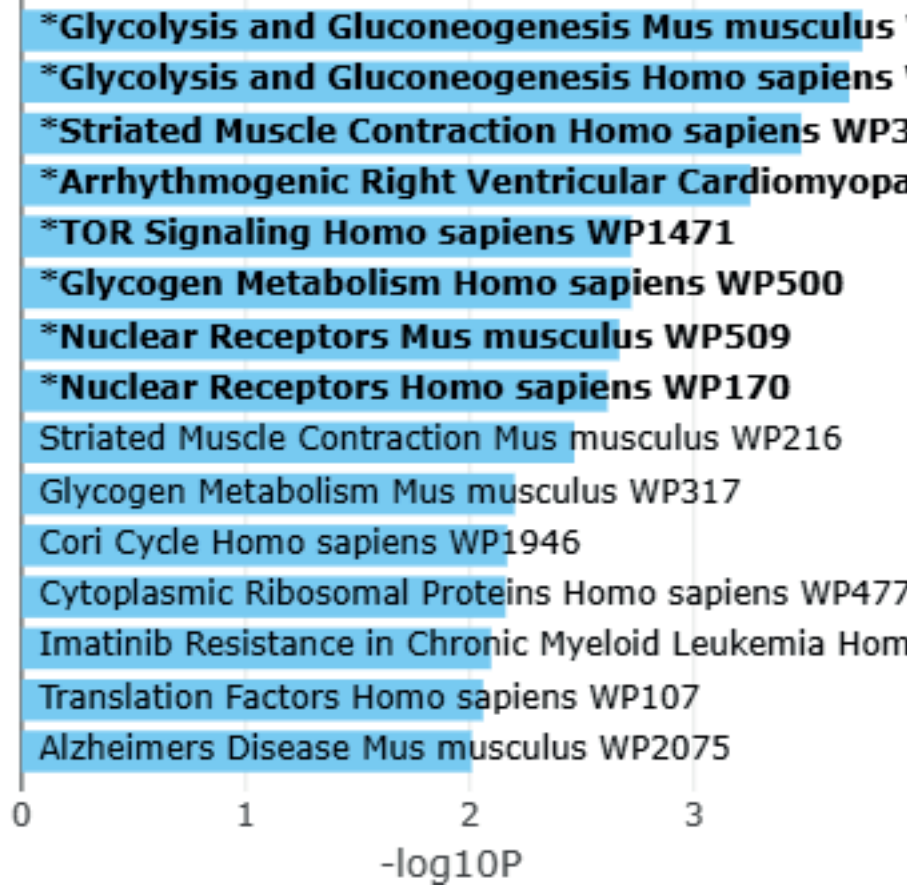
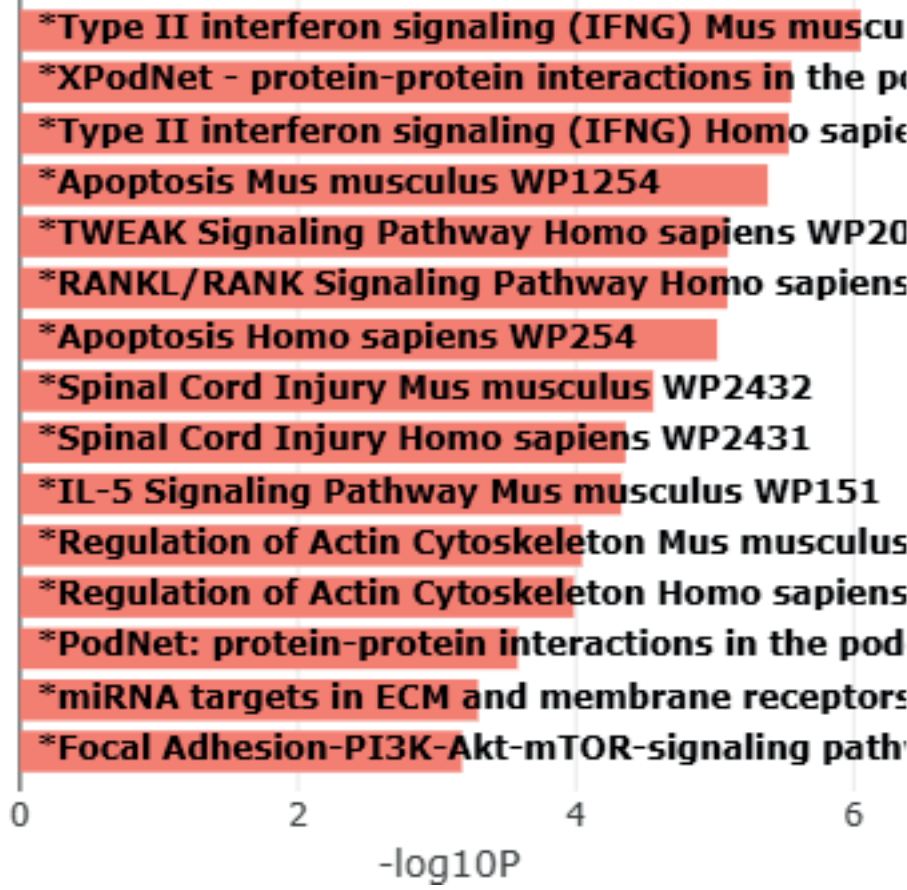
down-regulated in HSA-LT $\alpha/\beta$



WikiPathways

up-regulated in HSA-LT $\alpha/\beta$

down-regulated in HSA-LT $\alpha/\beta$



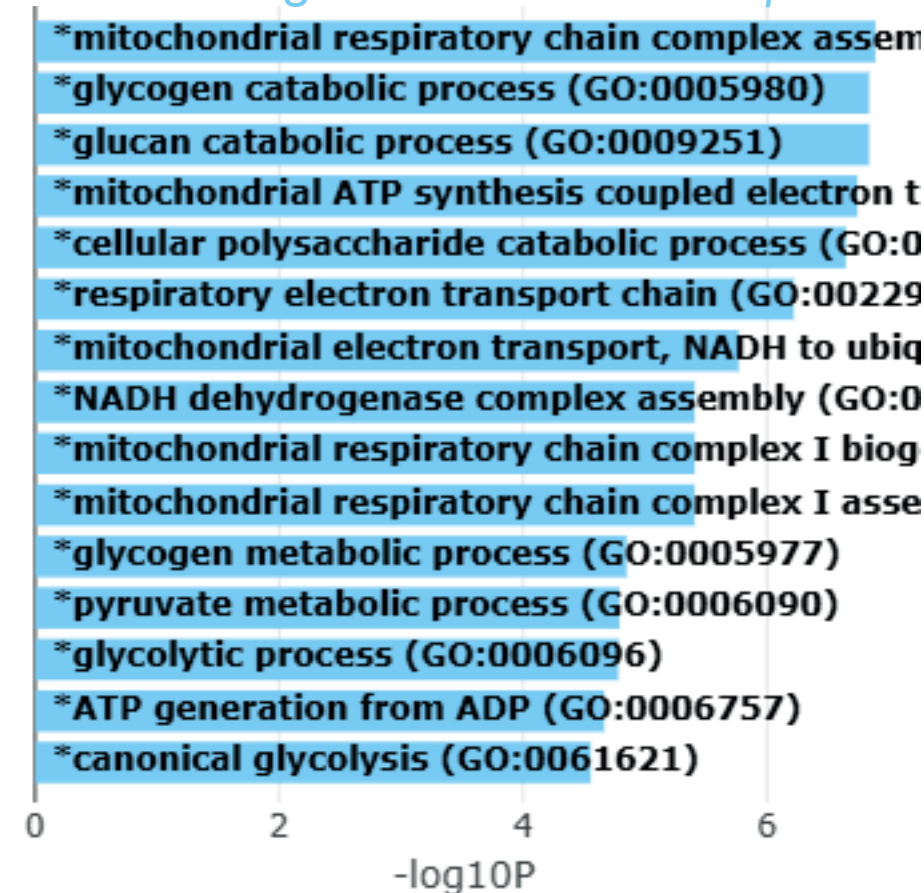
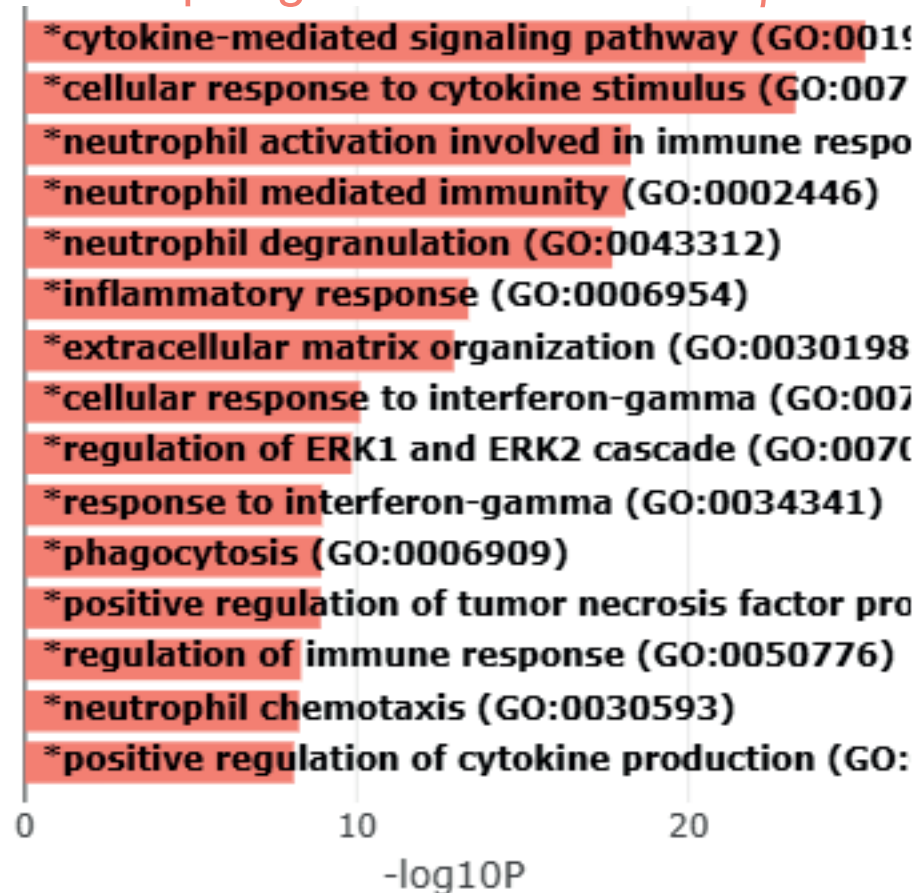


# wildtype versus HSA-LT $\alpha/\beta$ at 9 months

Gene Ontology Biological Process (2018 version)

up-regulated in HSA-LT $\alpha/\beta$

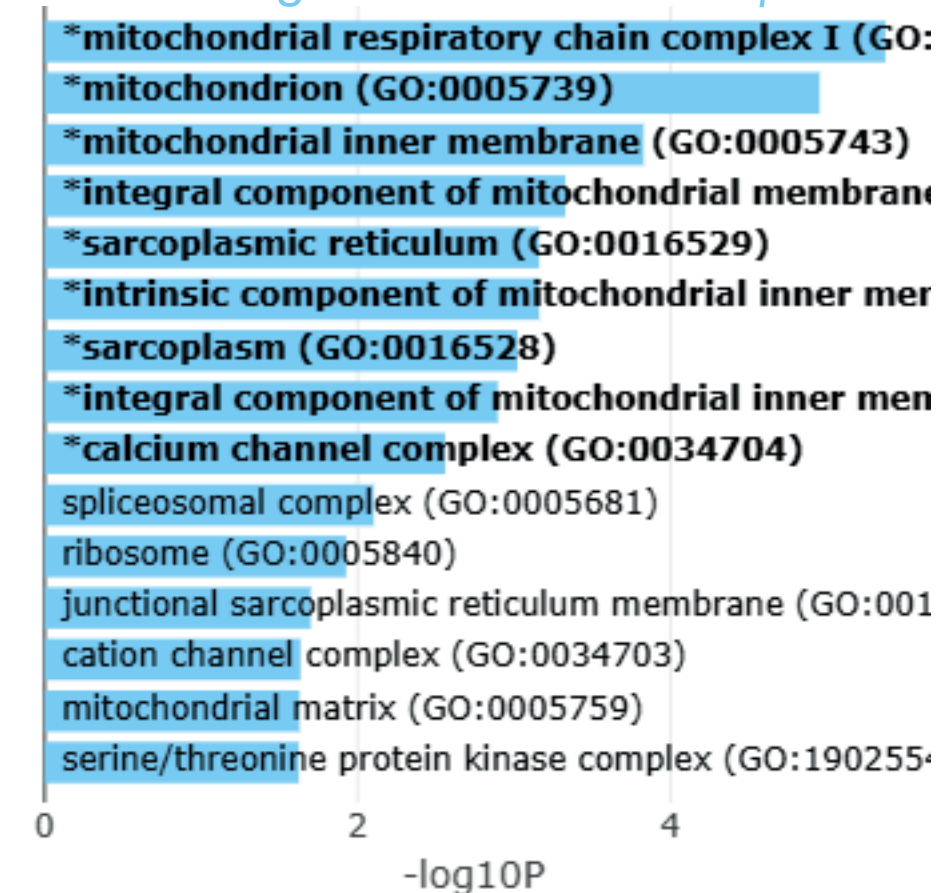
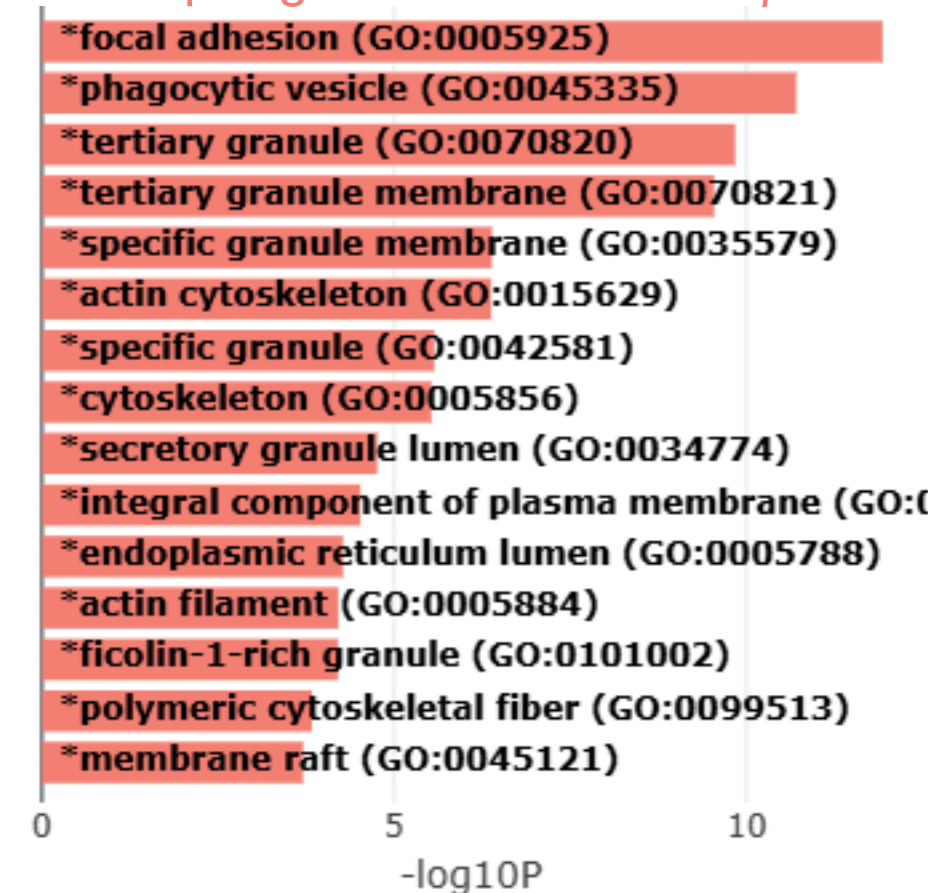
down-regulated in HSA-LT $\alpha/\beta$



Gene Ontology Cellular Component (2018 version)

up-regulated in HSA-LT $\alpha/\beta$

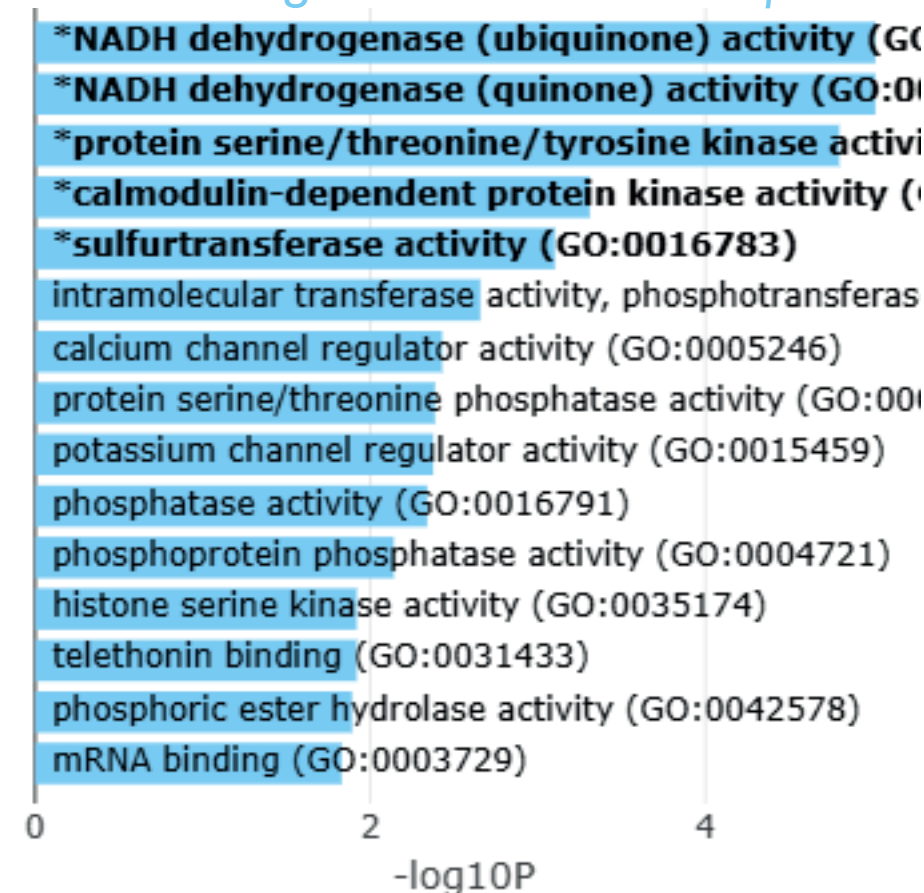
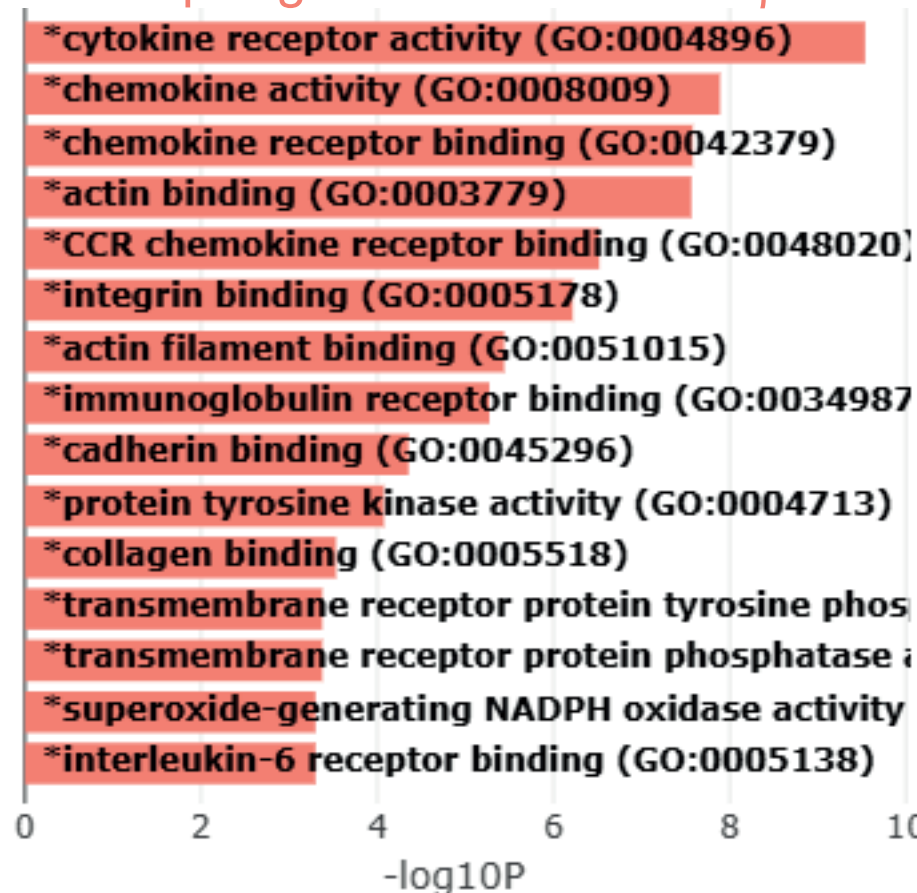
down-regulated in HSA-LT $\alpha/\beta$



Gene Ontology Molecular Function (2018 version)

up-regulated in HSA-LT $\alpha/\beta$

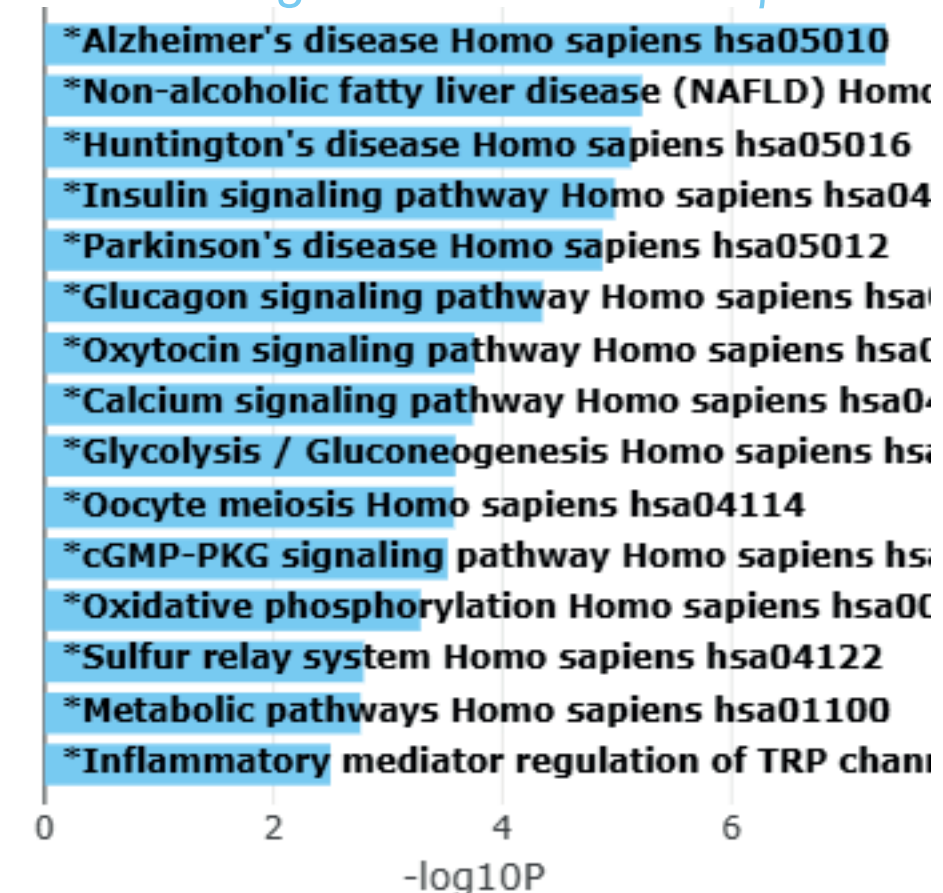
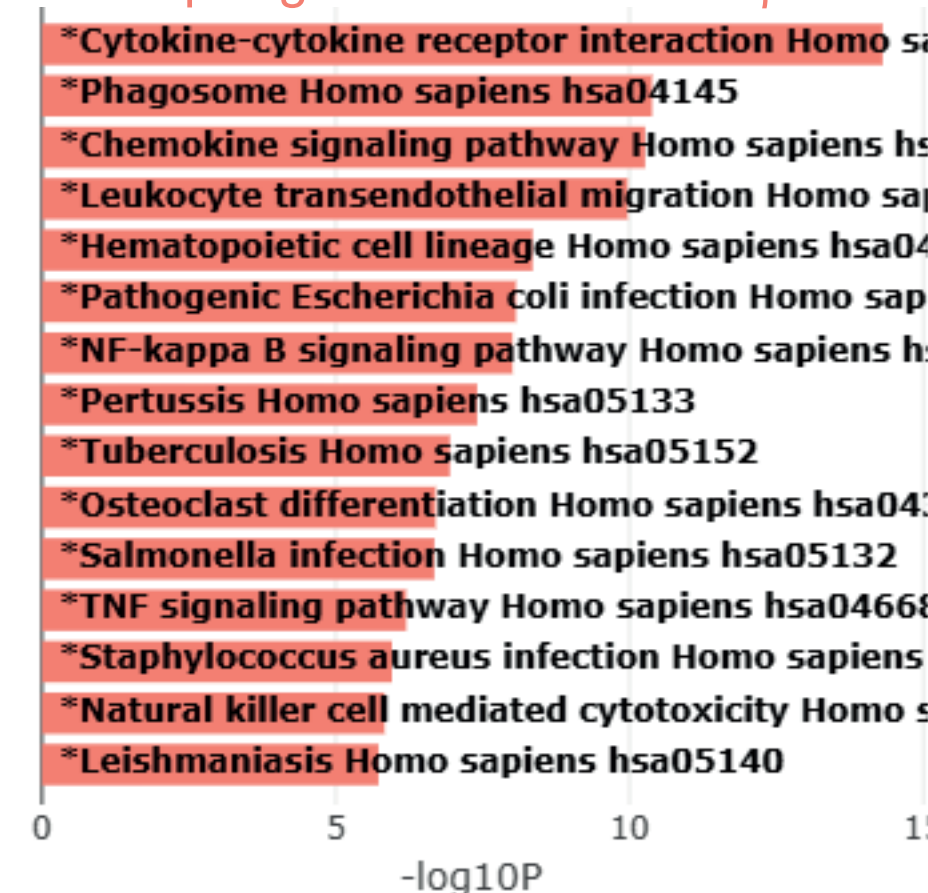
down-regulated in HSA-LT $\alpha/\beta$



KEGG pathway

up-regulated in HSA-LT $\alpha/\beta$

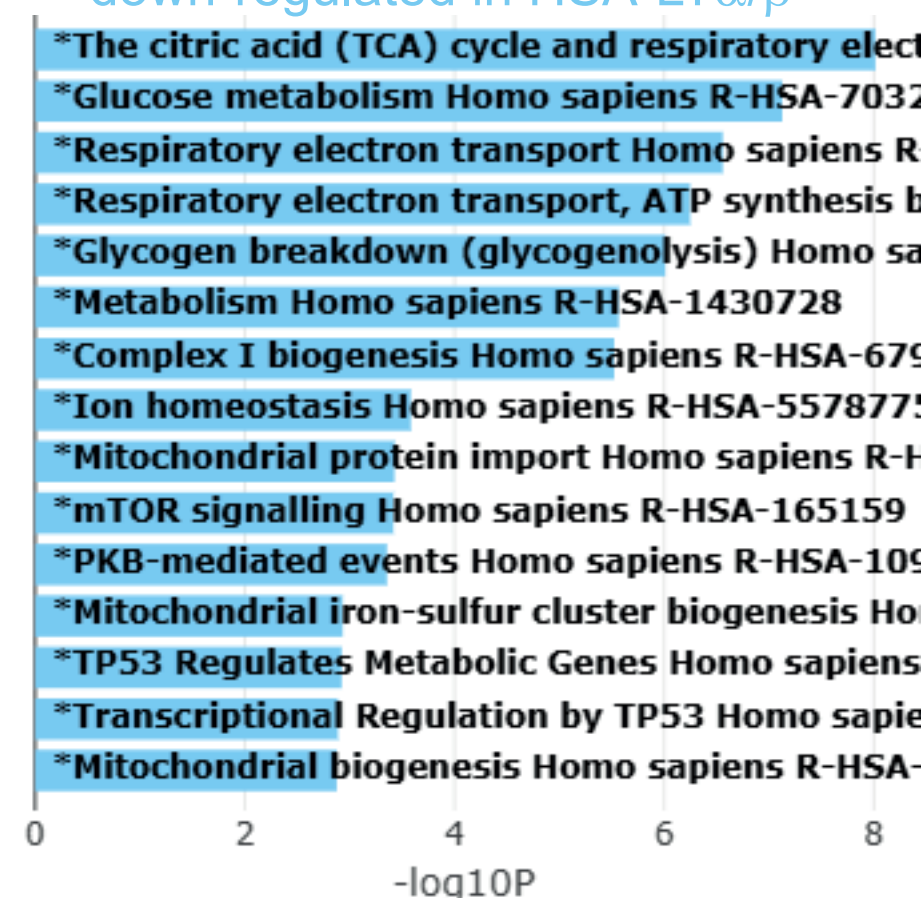
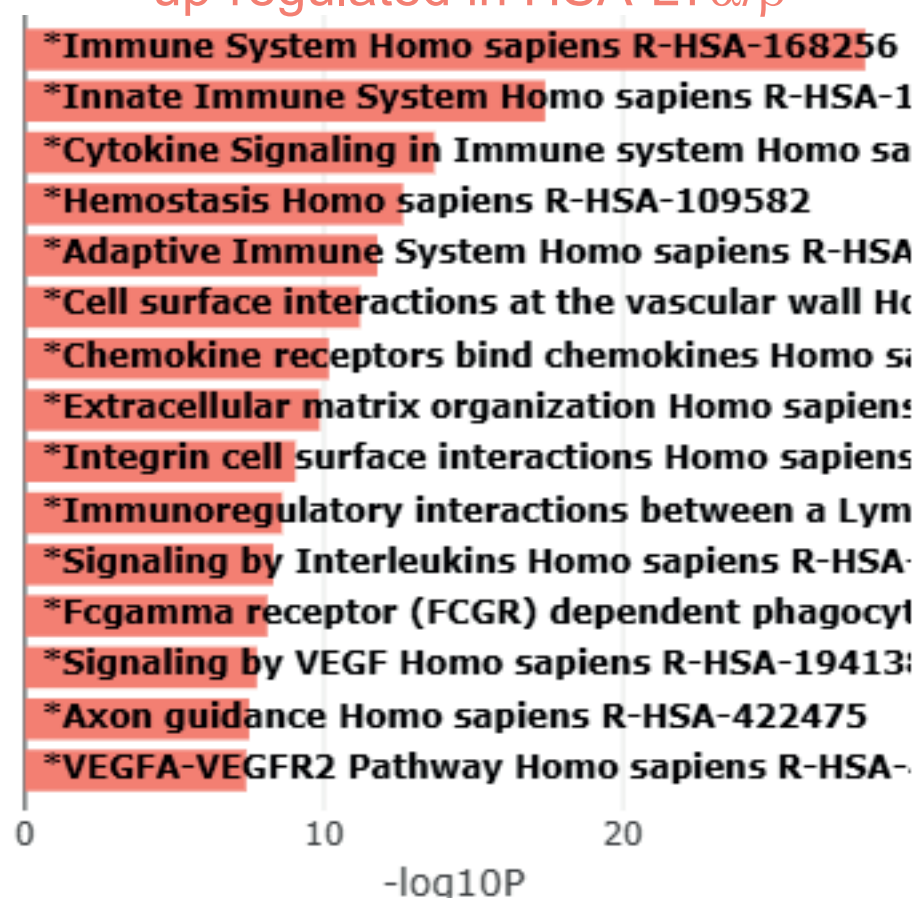
down-regulated in HSA-LT $\alpha/\beta$



Reactome Pathways

up-regulated in HSA-LT $\alpha/\beta$

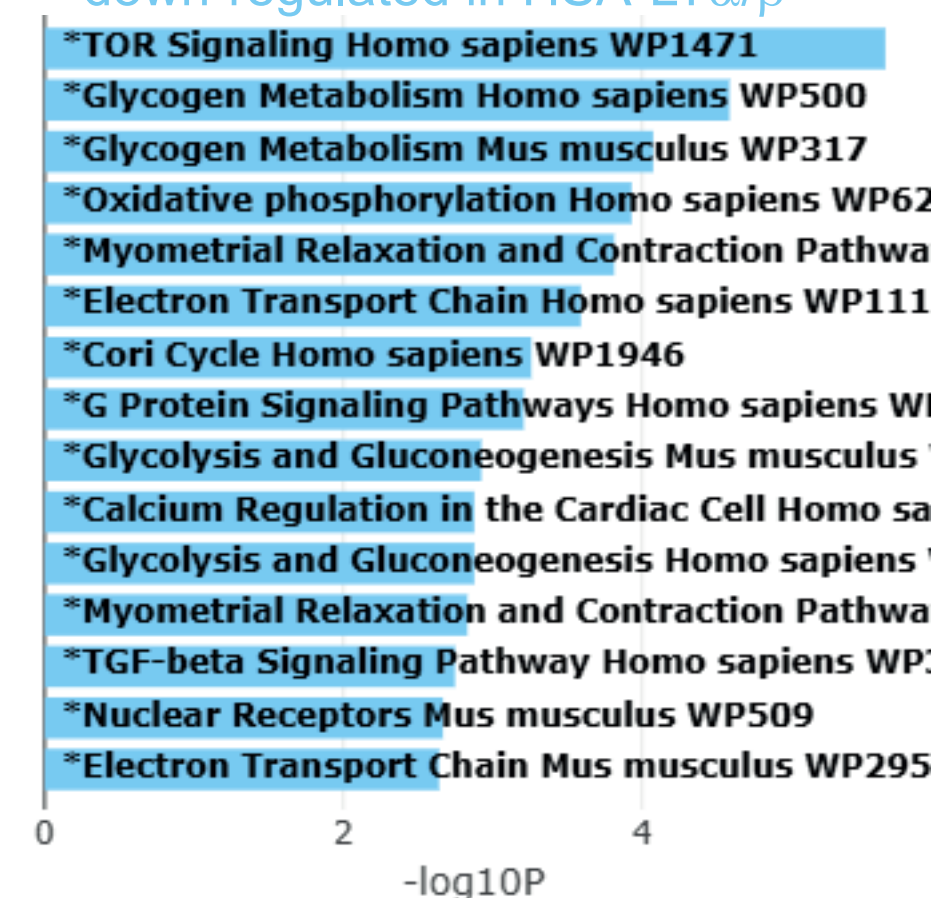
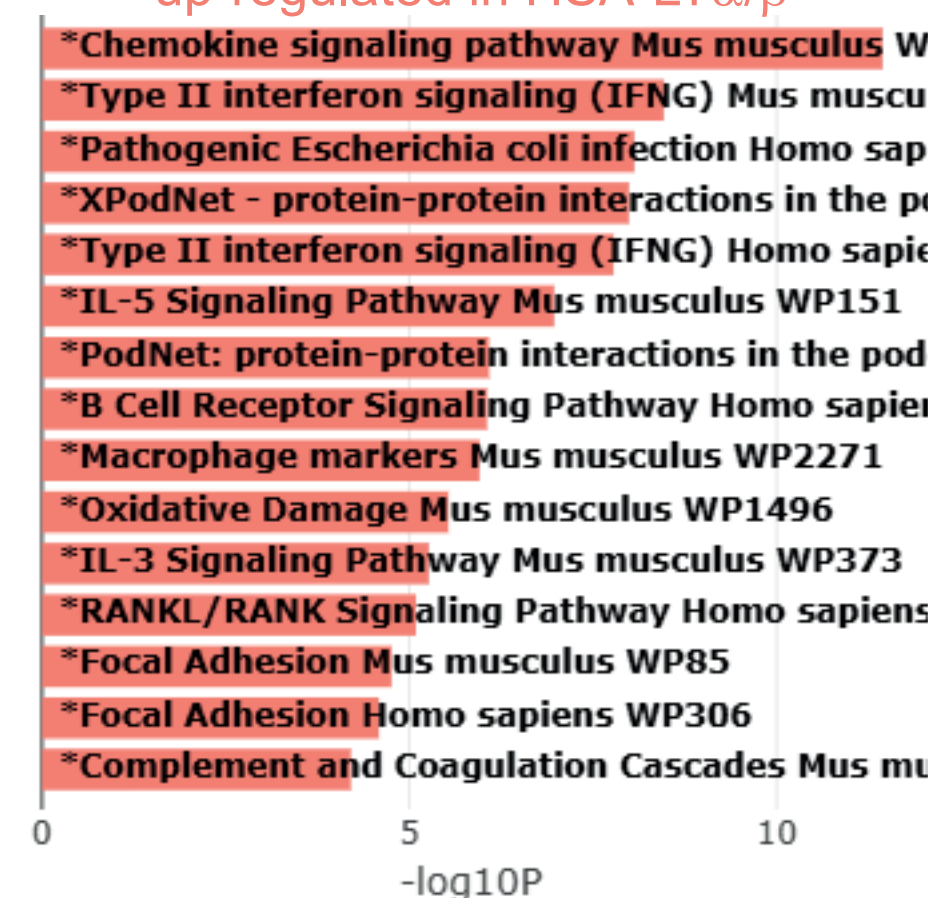
down-regulated in HSA-LT $\alpha/\beta$



WikiPathways

up-regulated in HSA-LT $\alpha/\beta$

down-regulated in HSA-LT $\alpha/\beta$

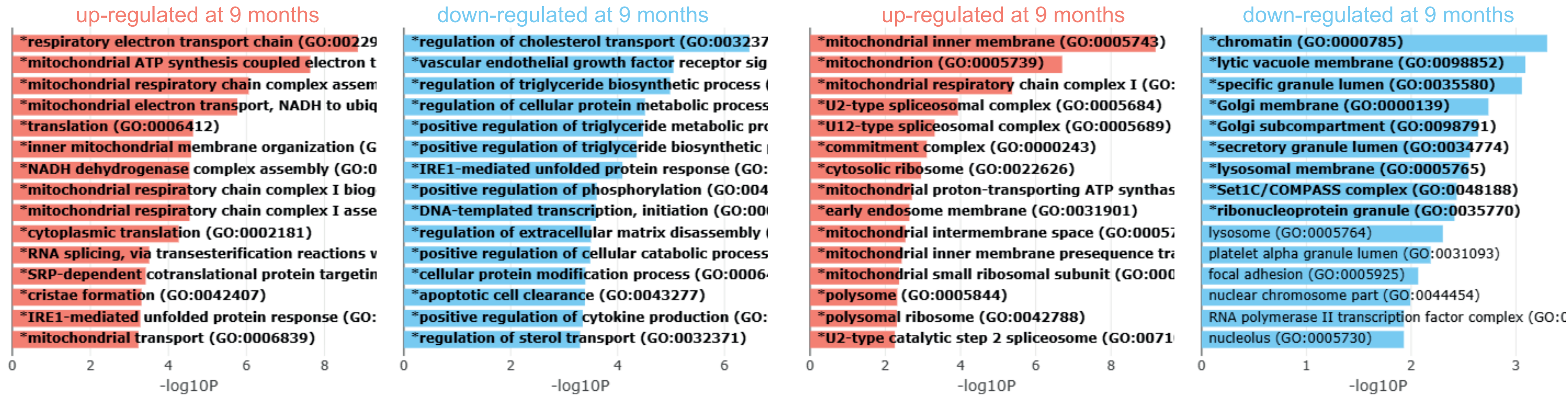




# wildtype 6 months versus 9 months

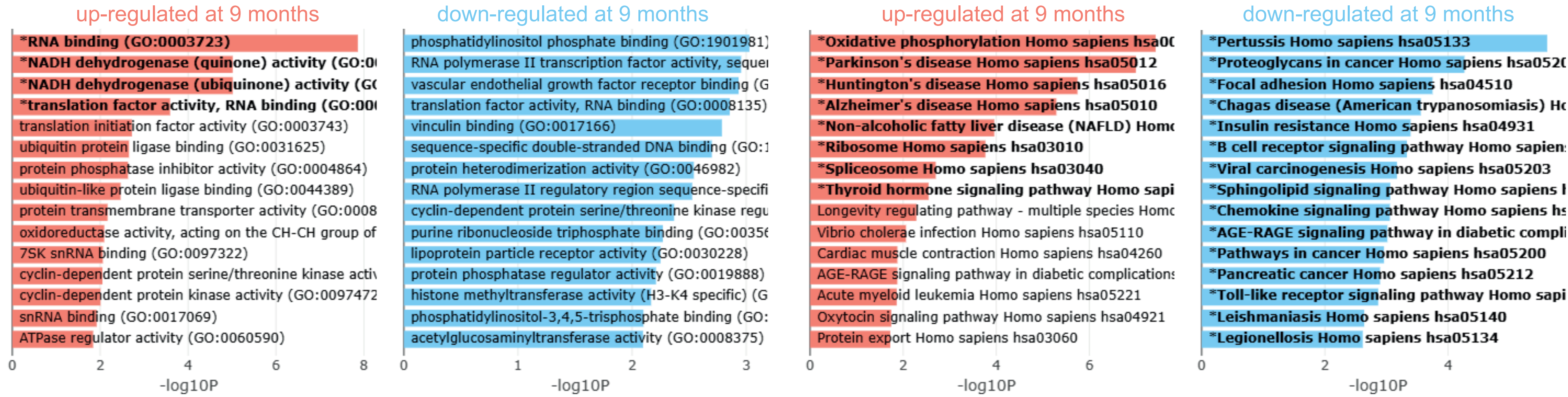
Gene Ontology Biological Process (2018 version)

Gene Ontology Cellular Component (2018 version)



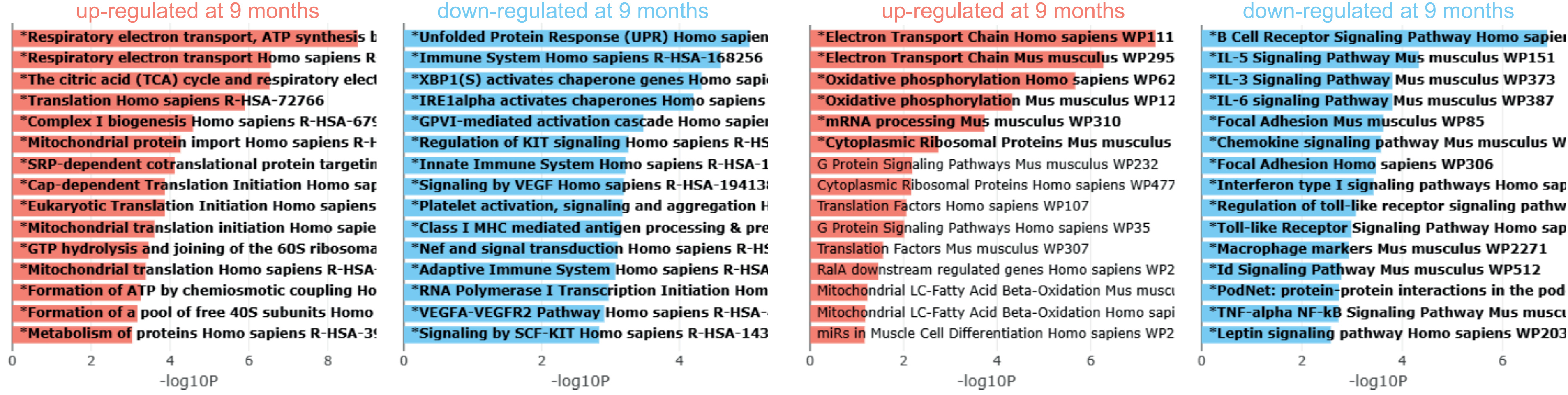
Gene Ontology Molecular Function (2018 version)

KEGG pathway



Reactome Pathways

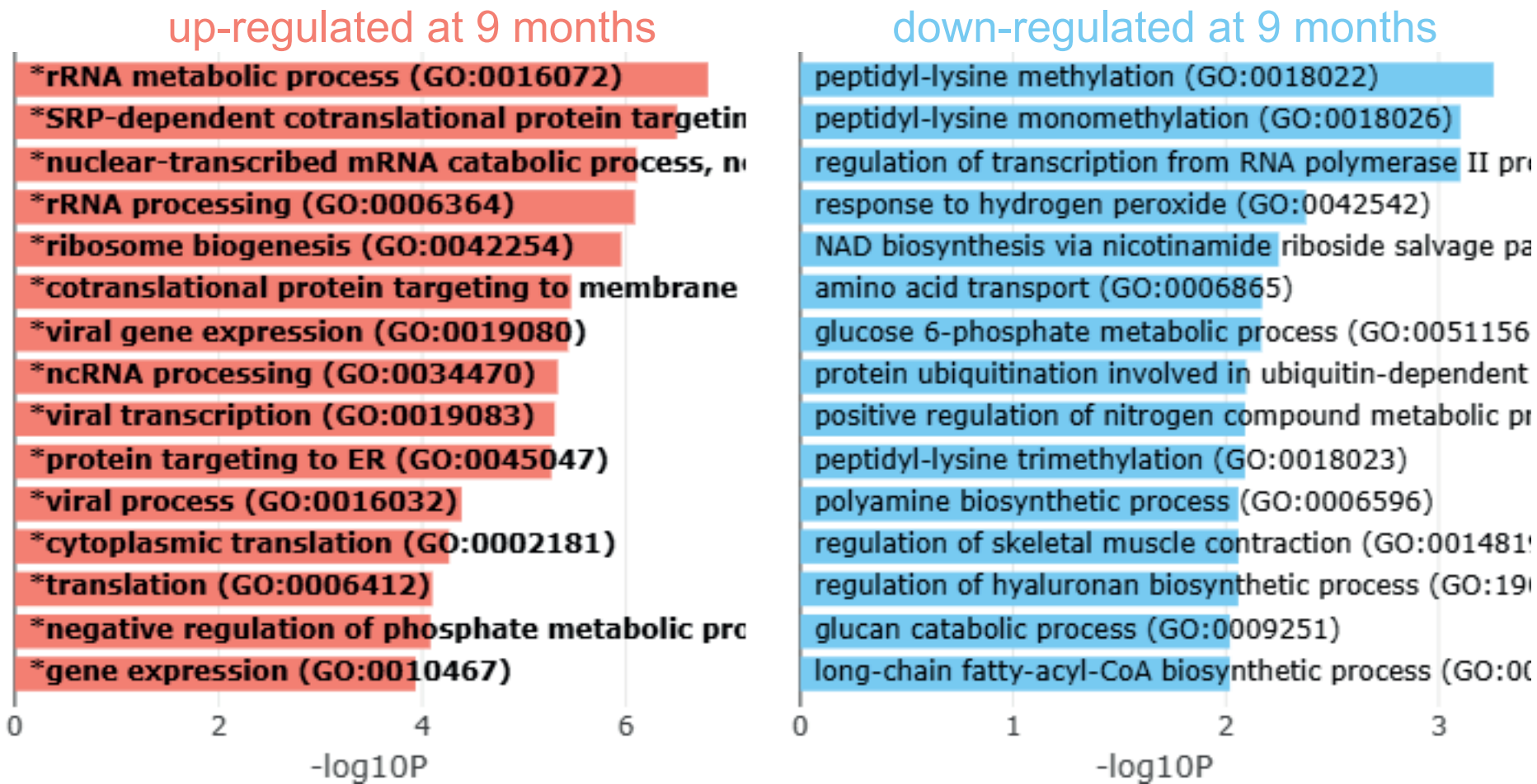
WikiPathways



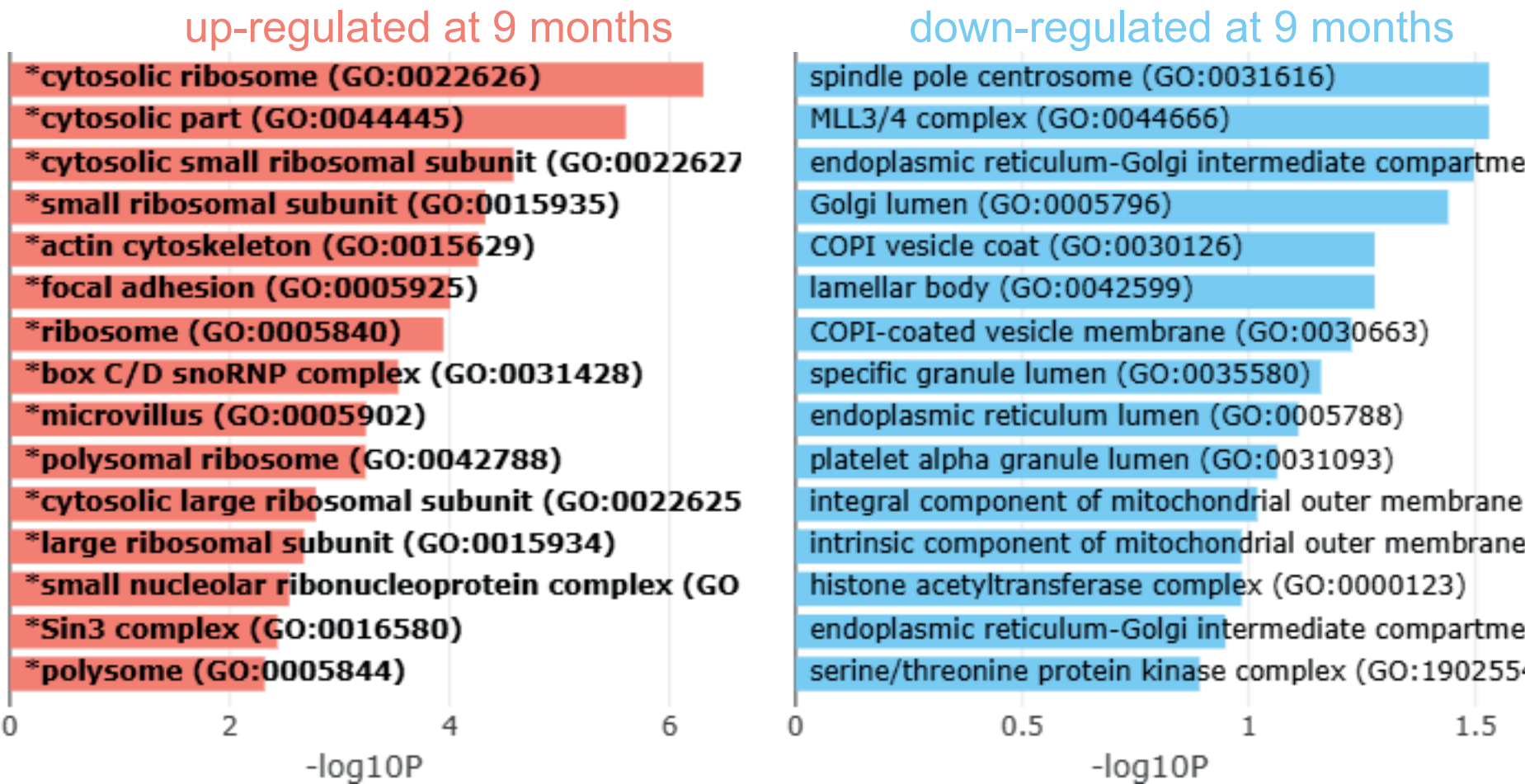


# HSA-LT $\alpha/\beta$ 6 months versus 9 months

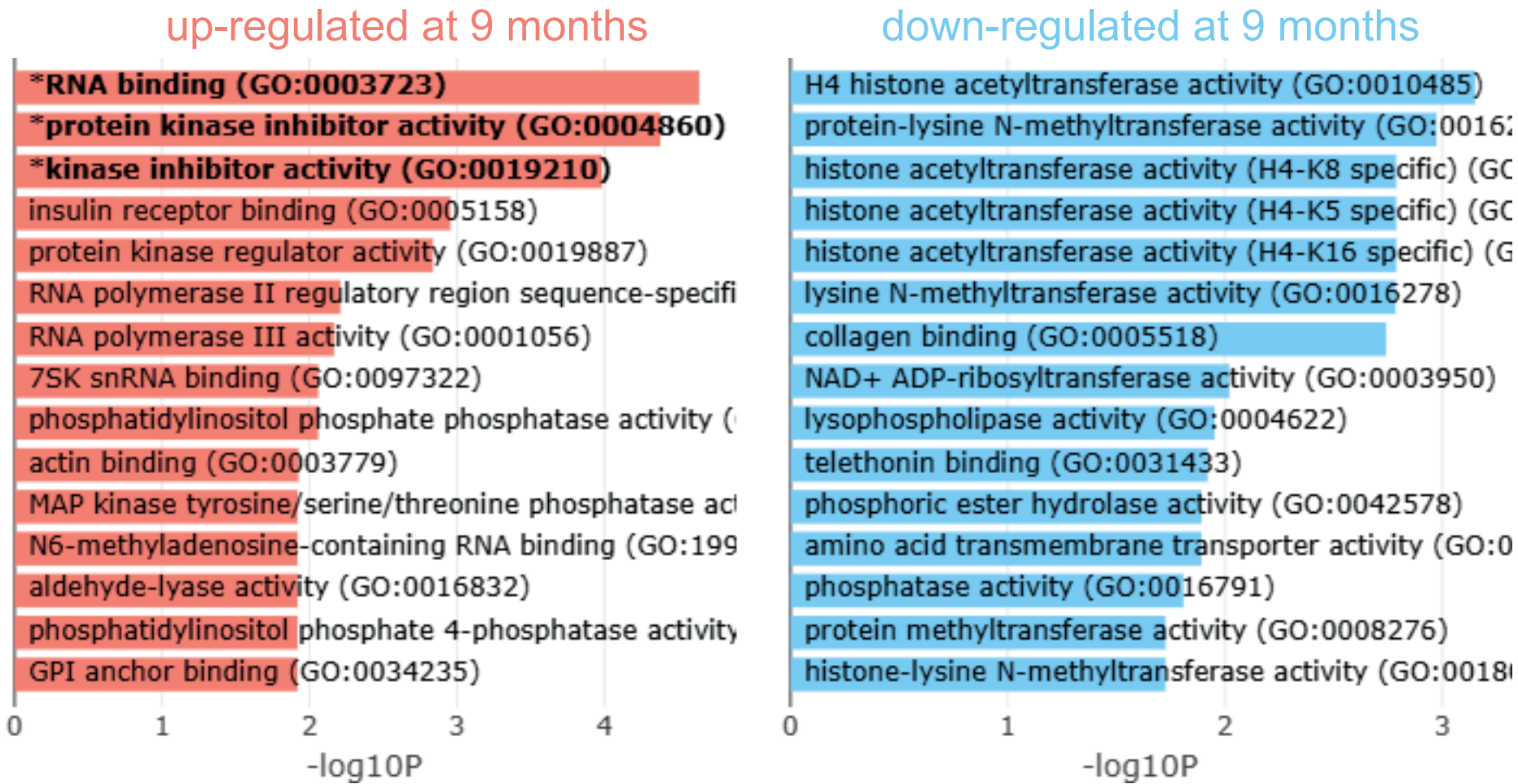
Gene Ontology Biological Process (2018 version)



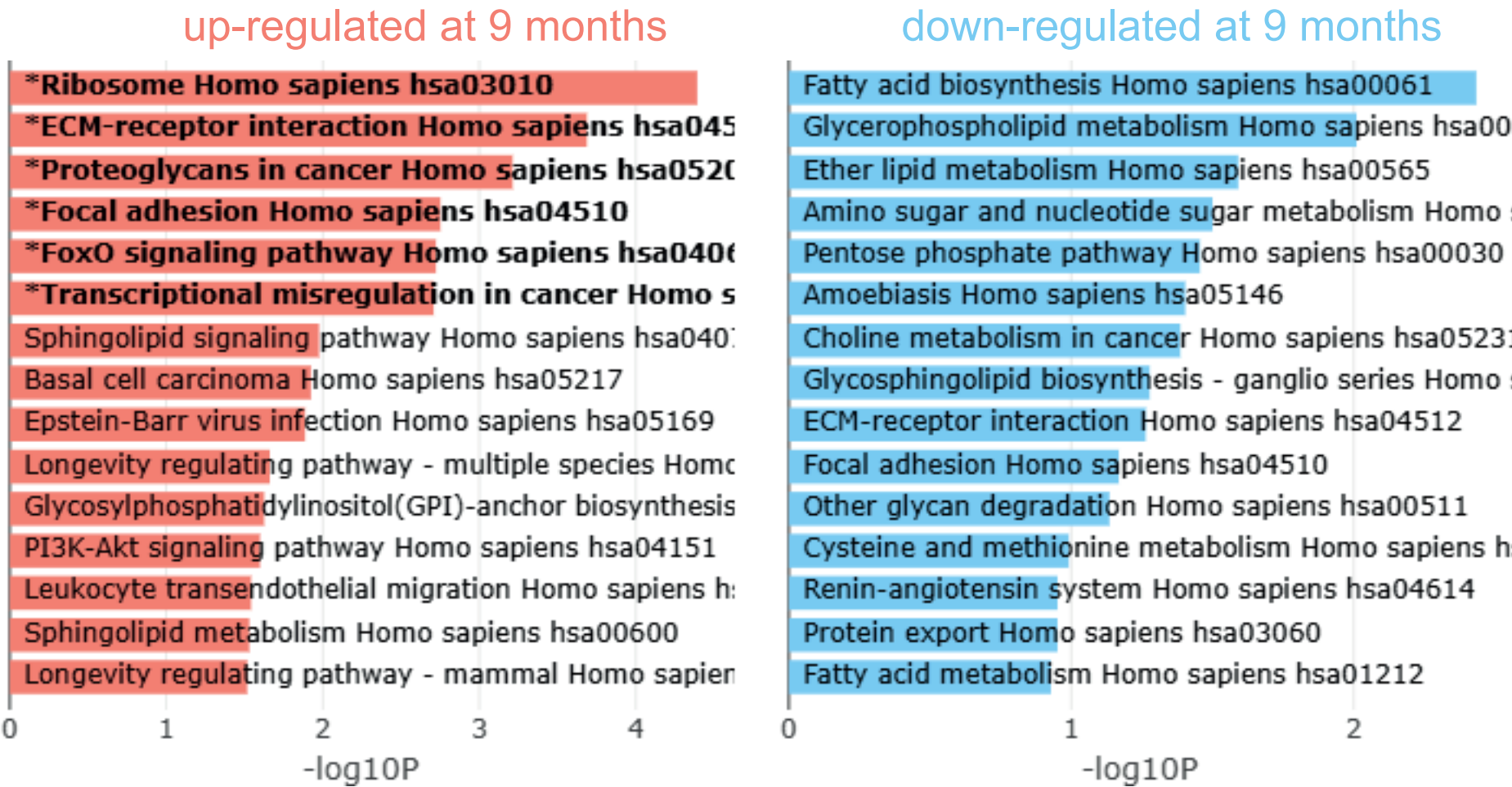
Gene Ontology Cellular Component (2018 version)



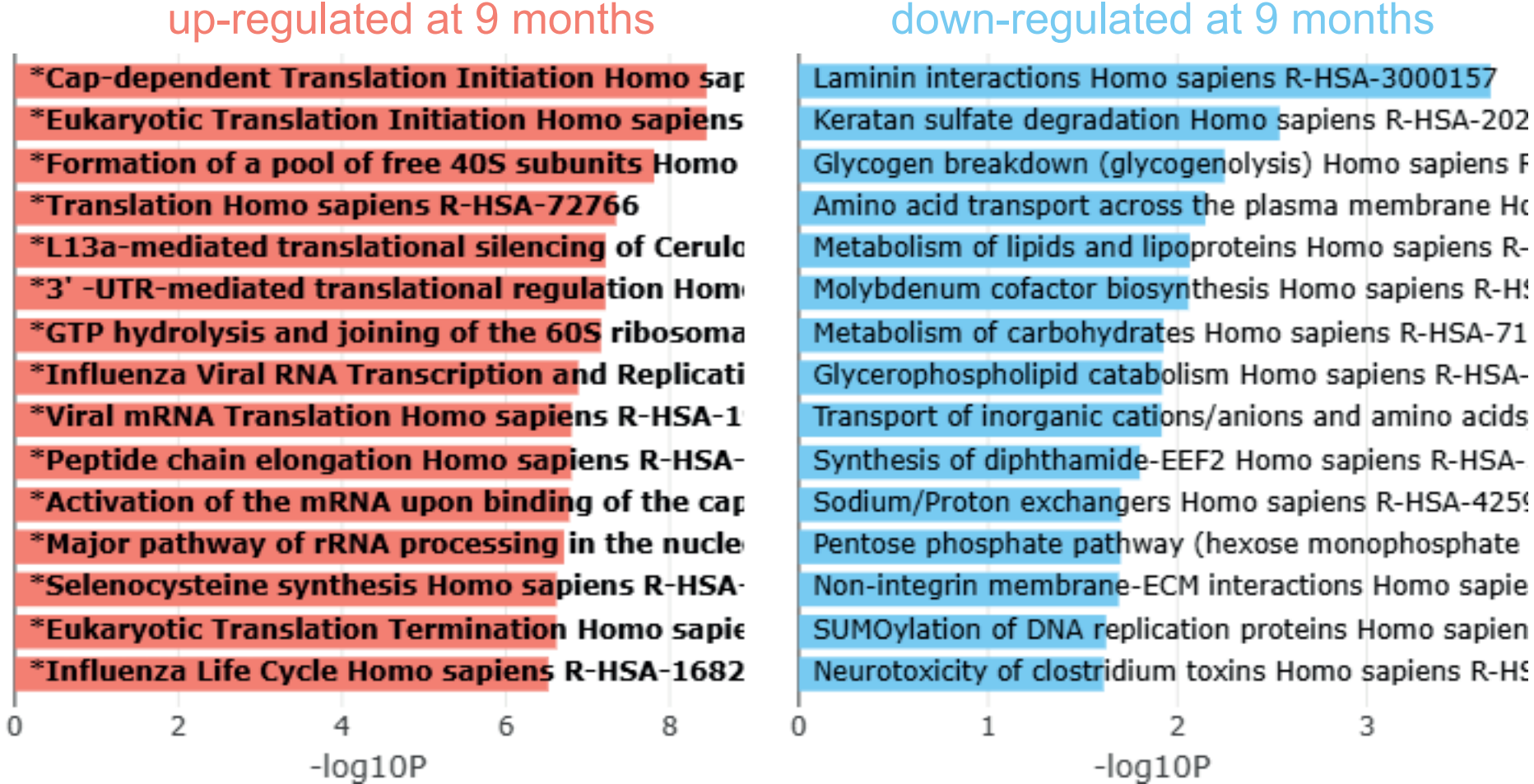
Gene Ontology Molecular Function (2018 version)



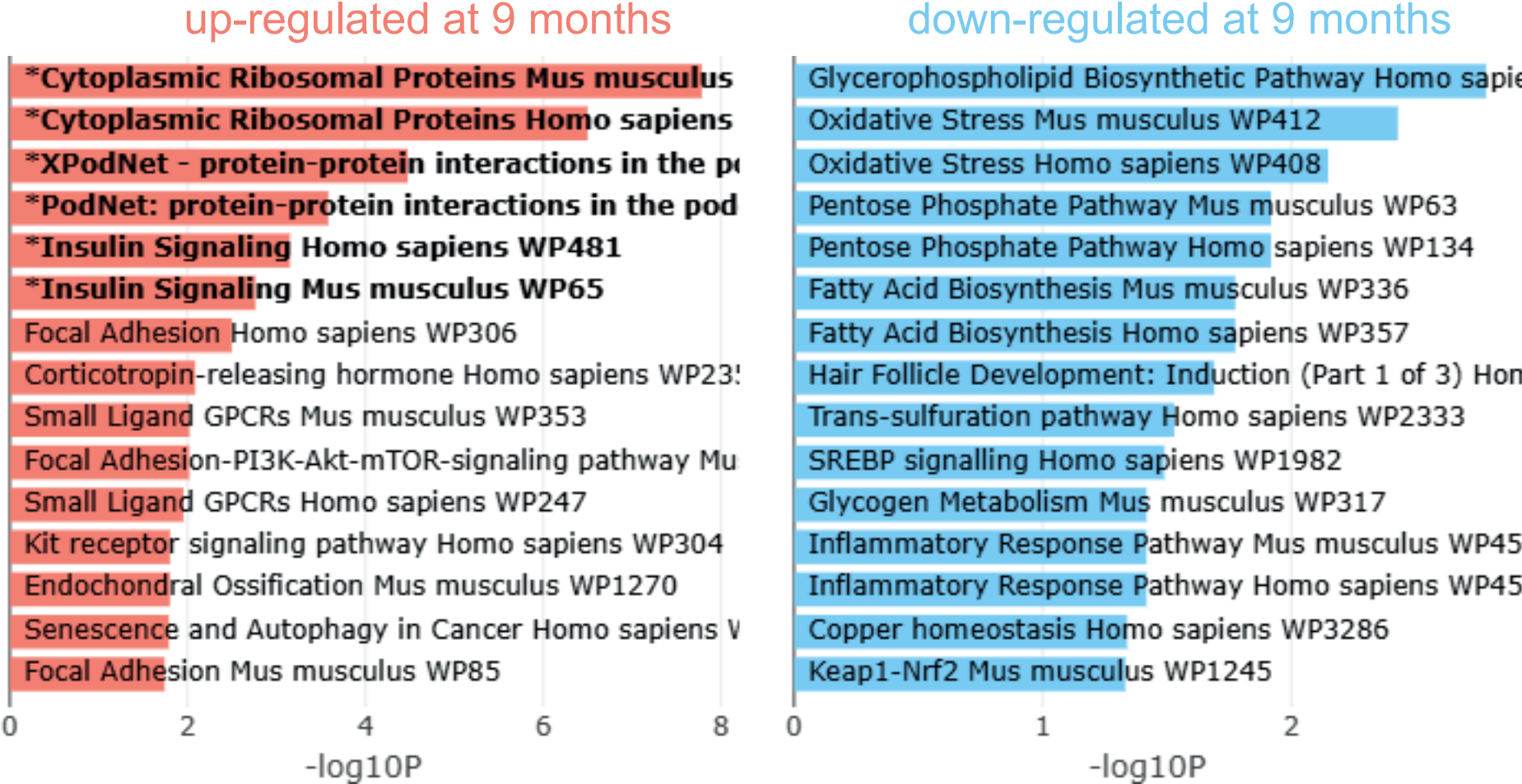
KEGG pathway



Reactome Pathways



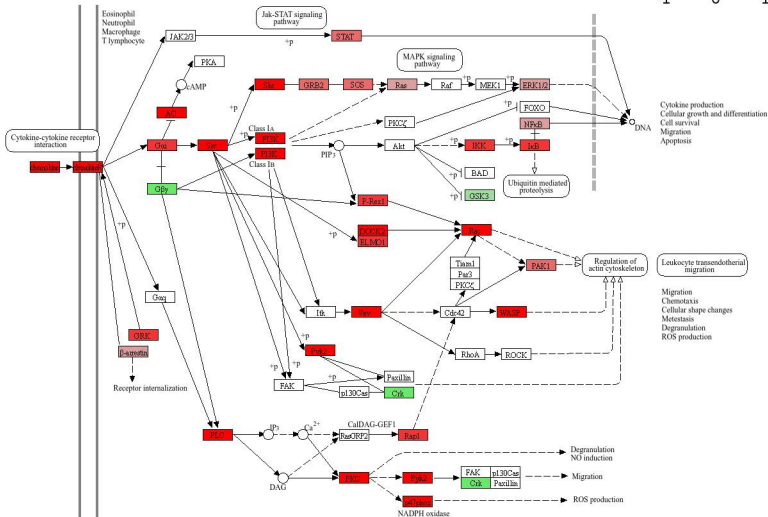
WikiPathways









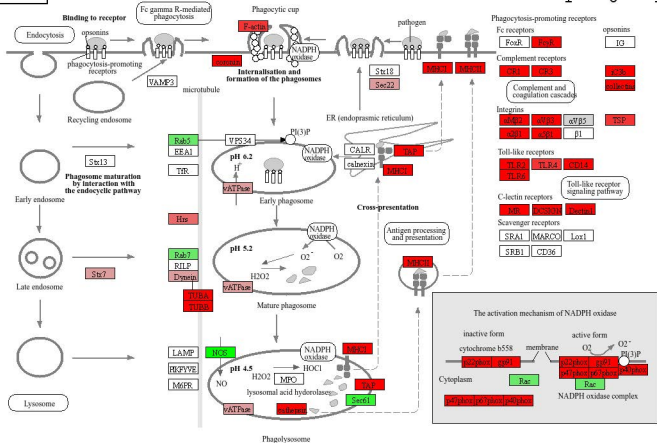
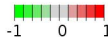




# PHAGOSOME

## Conventional phagocytosis

## ER-mediated phagocytosis

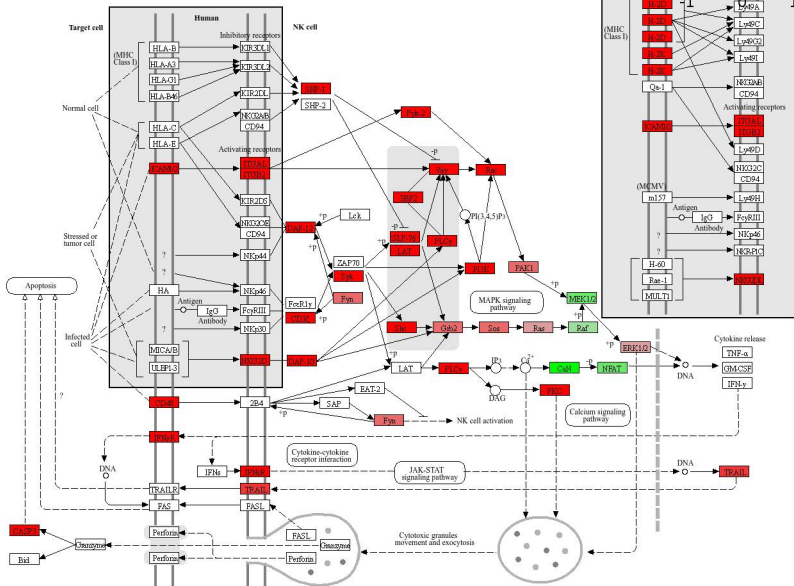








## NATURAL KILLER CELL MEDIATED CYTOTOXICITY

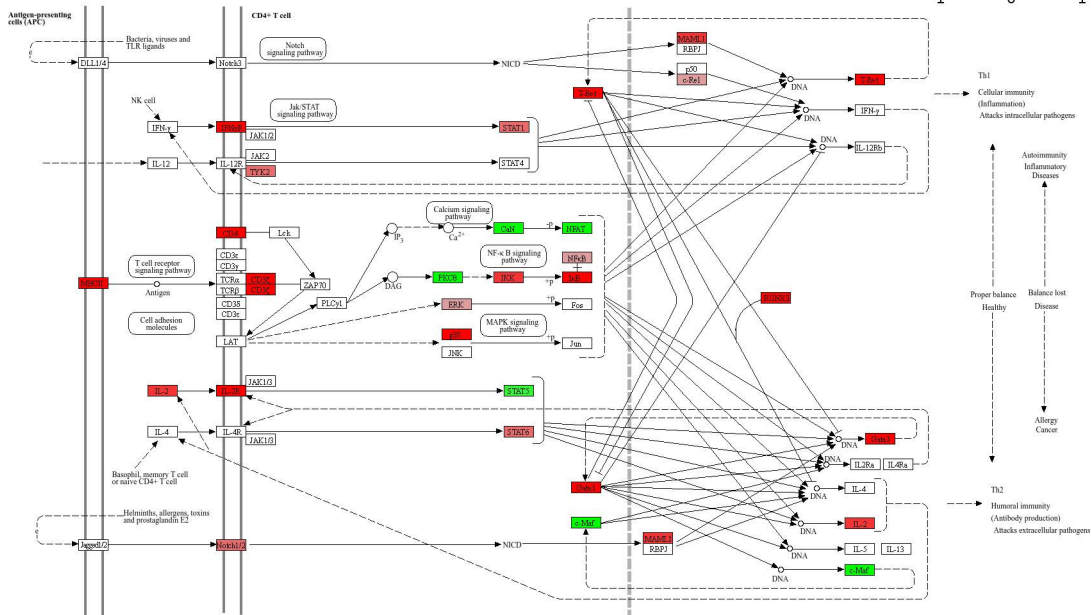








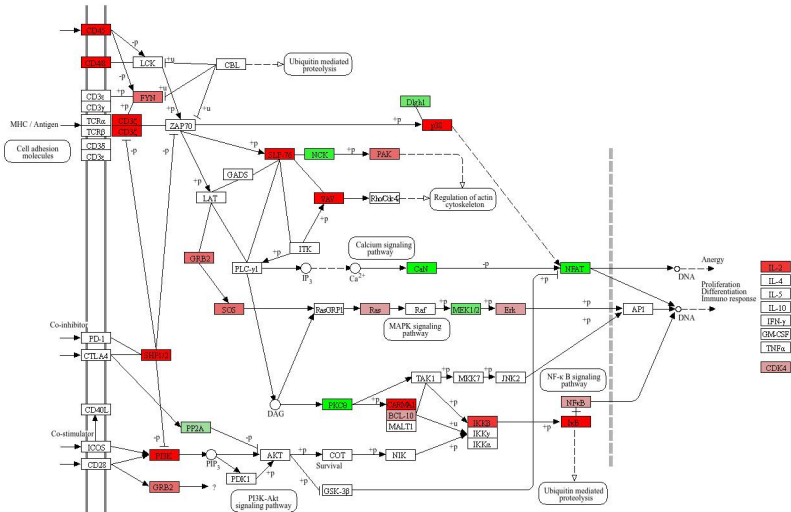
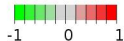
# Th1 AND Th2 CELL DIFFERENTIATION







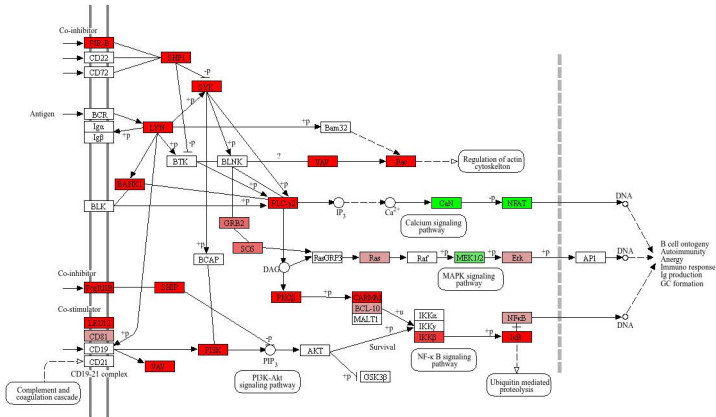
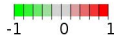
# T CELL RECEPTOR SIGNALING PATHWAY



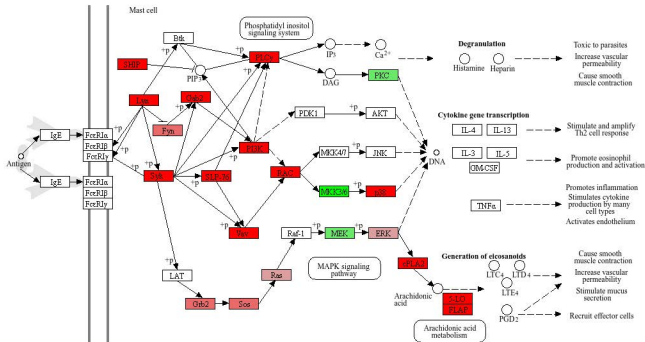
- IL-2
- IL-4
- IL-5
- IL-10
- IFN-γ
- GM-CSF
- TNFα
- CDK4



# B CELL RECEPTOR SIGNALING PATHWAY



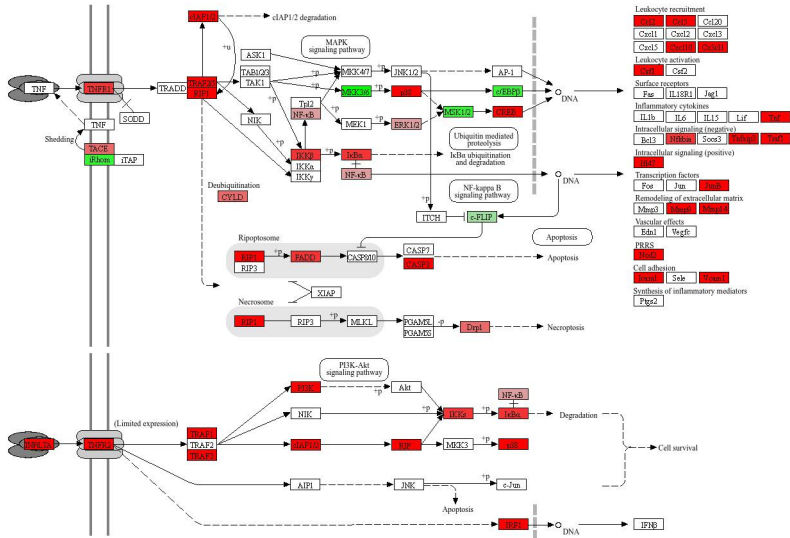
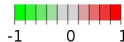
# FcεRI SIGNALING PATHWAY



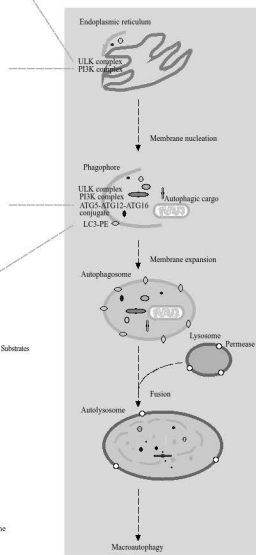


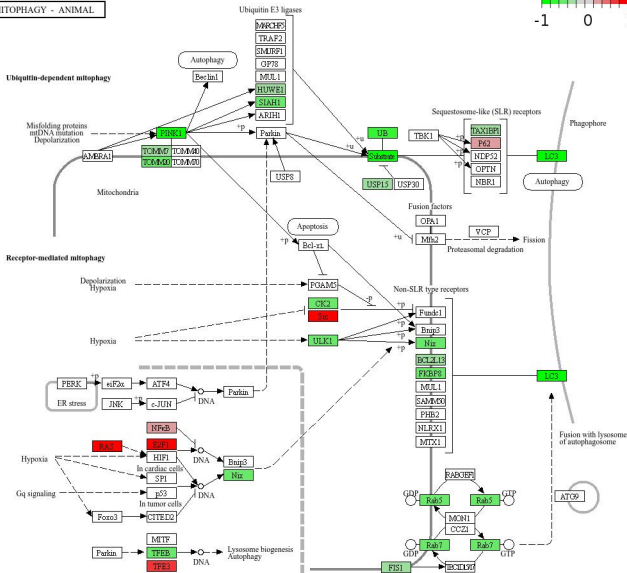


# TNF SIGNALING PATHWAY



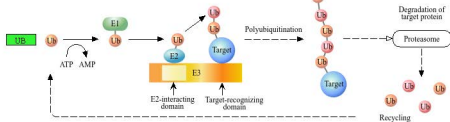








# UBIQUITIN MEDIATED PROTEOLYSIS



E1 (Ubiquitin-activating enzyme)

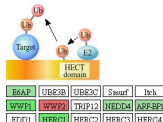
UBE1A UBE1B UBE1C

E2 (Ubiquitin-conjugating enzyme)

UBE2A UBE2B UBE2C UBE2D UBE2E UBE2F UBE2G UBE2H UBE2I UBE2J UBE2K UBE2L UBE2M UBE2N UBE2O UBE2P UBE2Q UBE2R UBE2S UBE2T UBE2U UBE2V UBE2W UBE2X UBE2Y UBE2Z

E3 (Ubiquitin ligase)

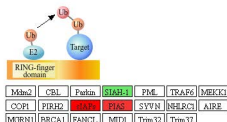
HECT type E3



U-box type E3



single RING-finger type E3

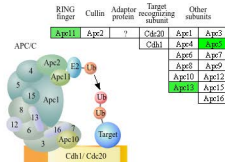


multi subunit RING-finger type E3

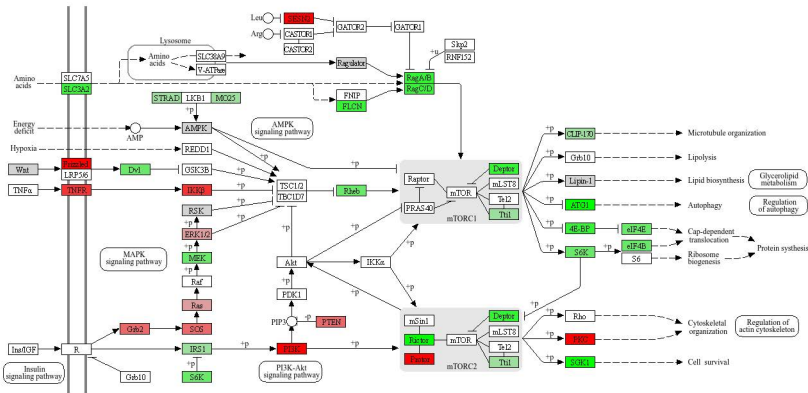
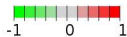
Cullin-Rbx E3



	RING finger	Cullin	Adaptor protein	Target recognizing subunit
SCF complex	RBX1	Cul1	Skp1	F-box
ECV complex	RBX1	Cul2	ElcB	VHLbox
			FloC	
Cul3 complex	RBX1	Cul3		BTR
Cul4 complex	RBX1	Cul4	DDB1	DCAF
ECS complex	RBX2	Cul5	ElcB	SCSbox
			FloC	
Cul7 complex	RBX1	Cul7	Skp1	Phoxb

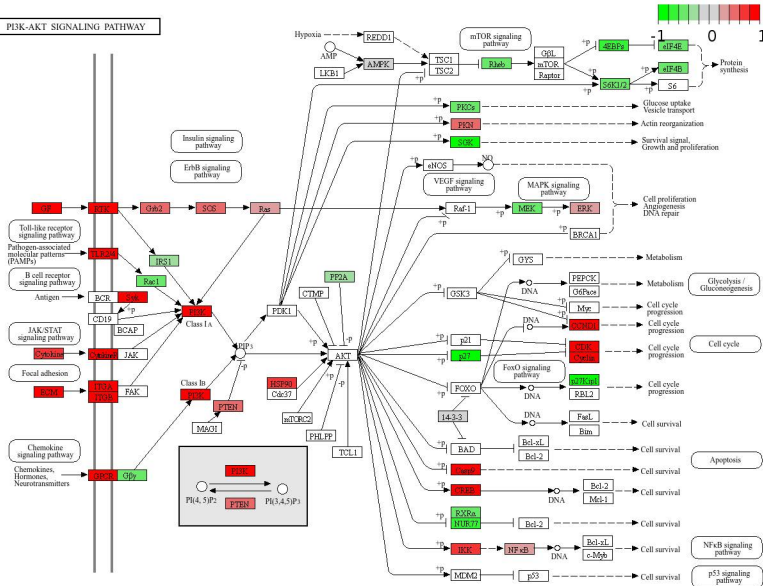


# mTOR SIGNALING PATHWAY

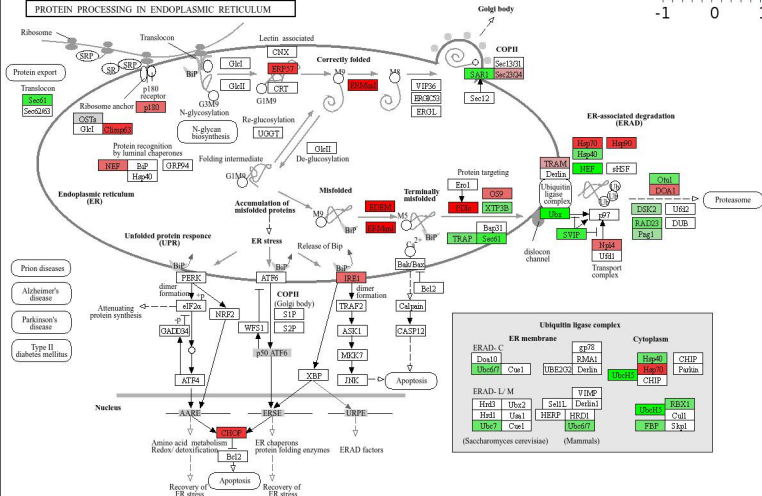
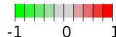




# PI3K-AKT SIGNALING PATHWAY

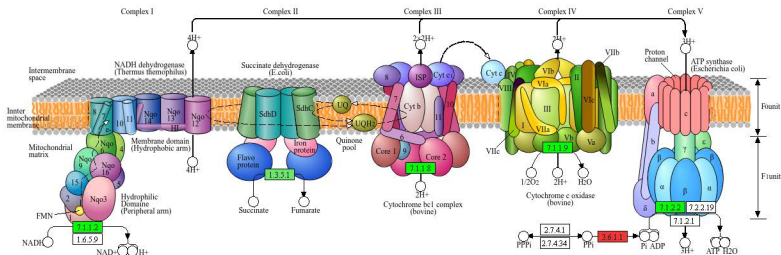
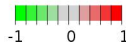


# PROTEIN PROCESSING IN ENDOPLASMIC RETICULUM





# OXIDATIVE PHOSPHORYLATION



## NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6
B/A	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7
E/B	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7

## Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB
B/A	SdhC	SdhD	SdhA	SdhB
E	SdhC	SdhD	SdhA	SdhB

## Cytochrome c reductase

E/B/A	ISP	Cyt b	Cyt c1
E	COX1	QCR2	QCR6
E	COX1	QCR2	QCR6

## Cytochrome c oxidase

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

## Cytochrome c oxidase, cbb3-type

B	I	II	IV	III
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## Cytochrome bd complex

B/A	CydA	CydB	CydeX
-----	------	------	-------

## Cytochrome c

CYC
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## F-type ATPase (Bacteria)

alpha	beta	gamma	delta	epsilon
a	b	c		

## F-type ATPase (Eukaryotes)

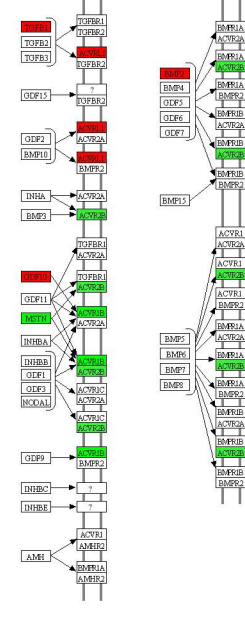
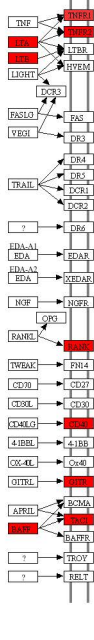
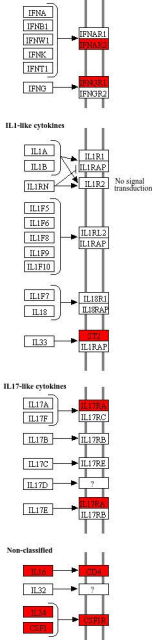
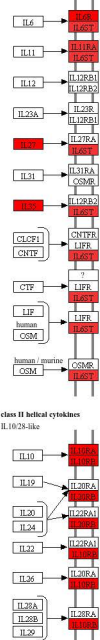
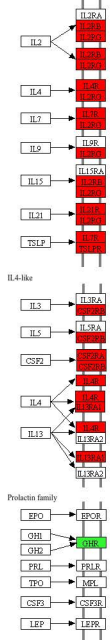
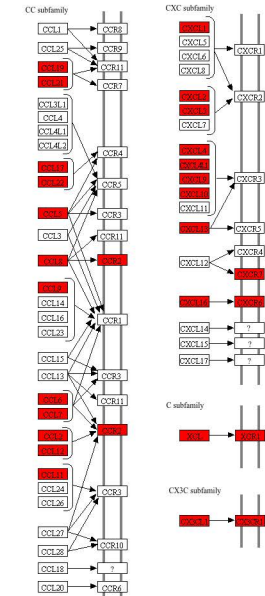
alpha	beta	gamma	delta	epsilon
OSCP	a	b	d	e
f	g	h	j	k

## V/A-type ATPase (Bacteria, Archaea)

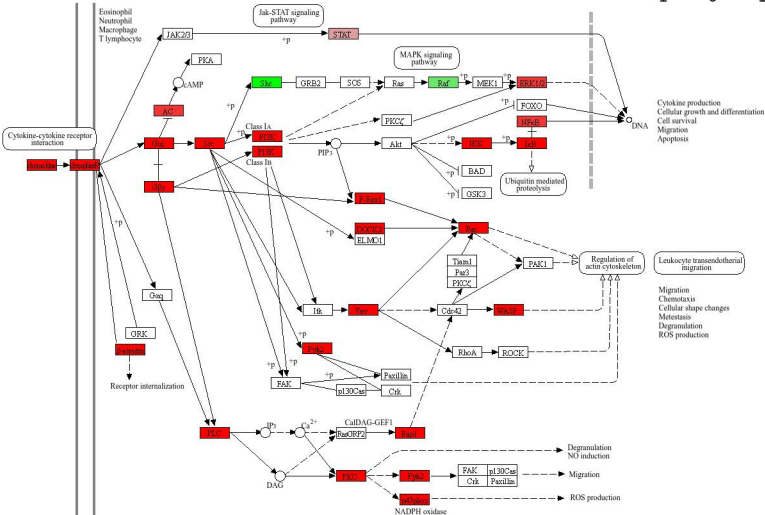
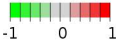
A	B	C	D	E	F	G/H
I	K					

## V-type ATPase (Eukaryotes)

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



## CHEMOKINE SIGNALING PATHWAY

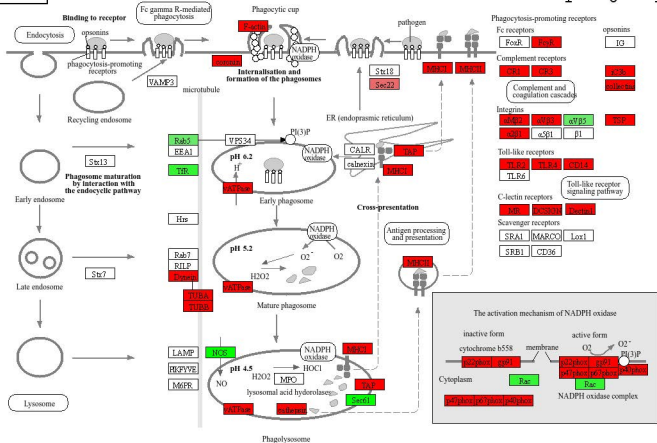
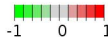




# PHAGOSOME

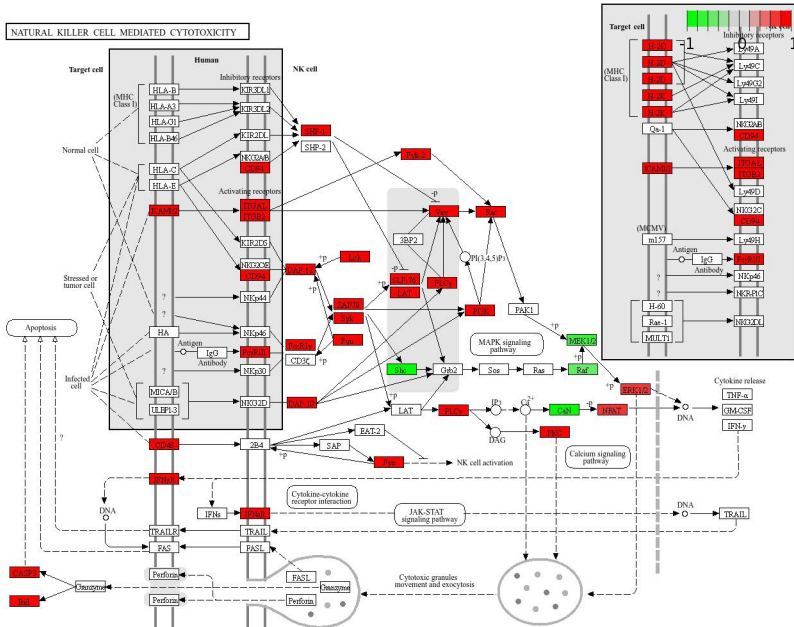
## Conventional phagocytosis

## ER-mediated phagocytosis



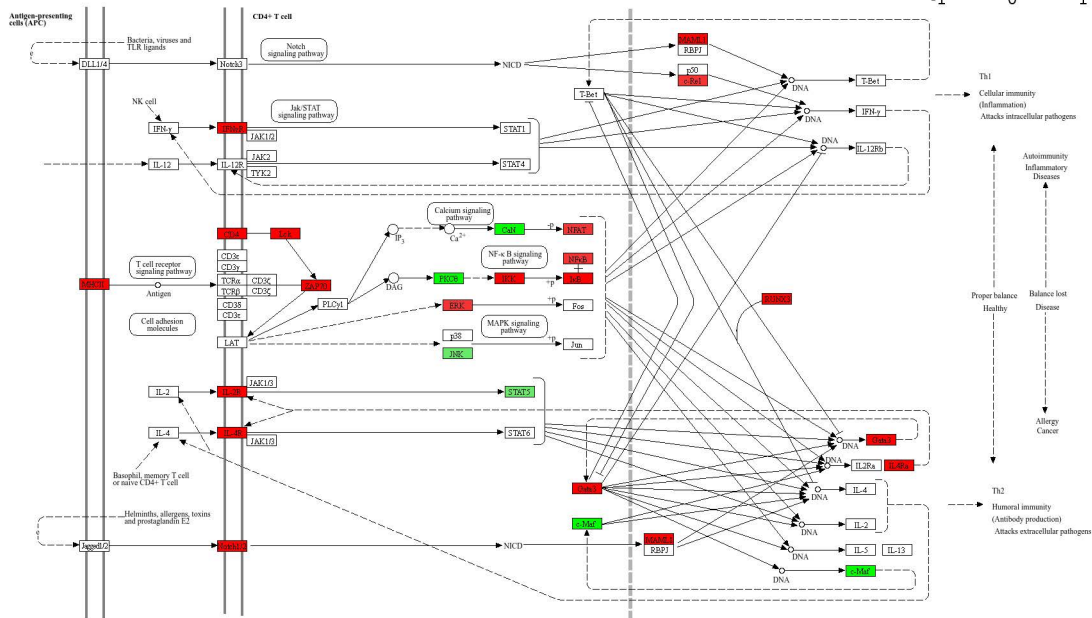


# NATURAL KILLER CELL MEDIATED CYTOTOXICITY





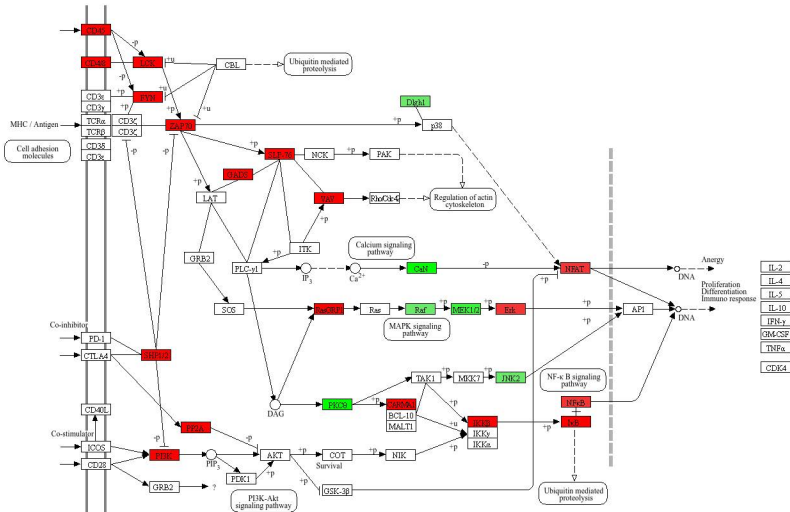




Data on KEGG graph  
Rendered by Pathview

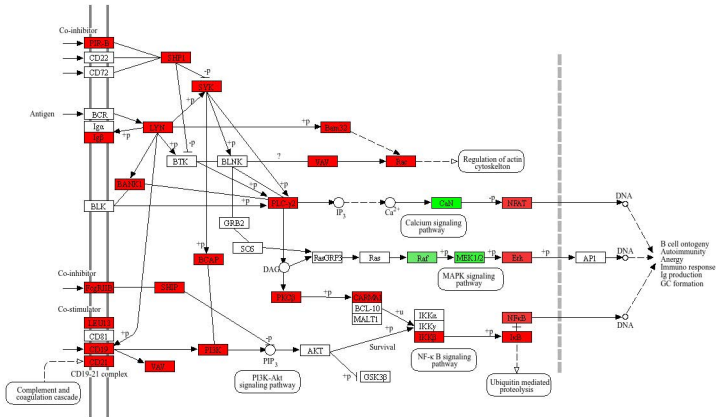
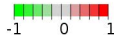






Data on KEGG graph  
Rendered by Pathview

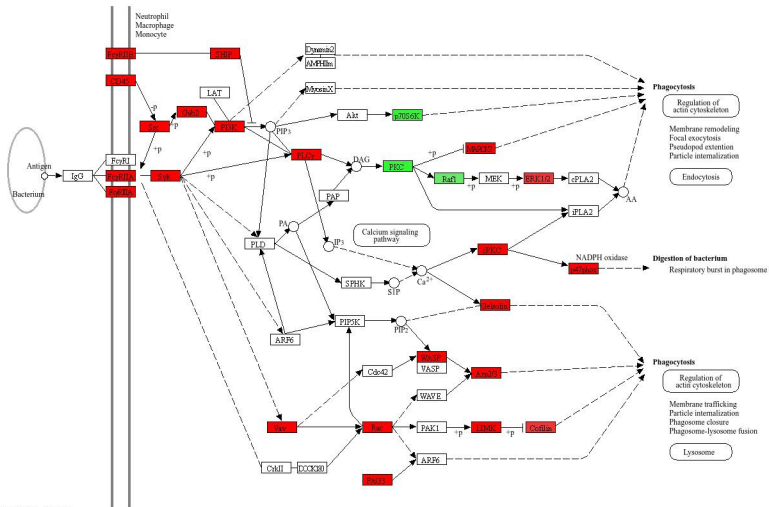
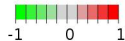
# B CELL RECEPTOR SIGNALING PATHWAY



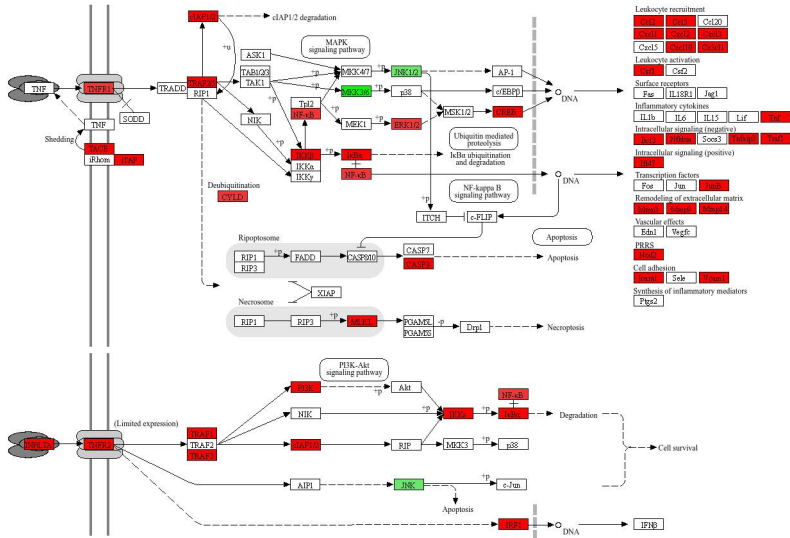
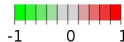


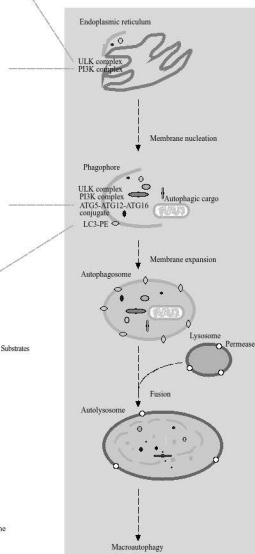
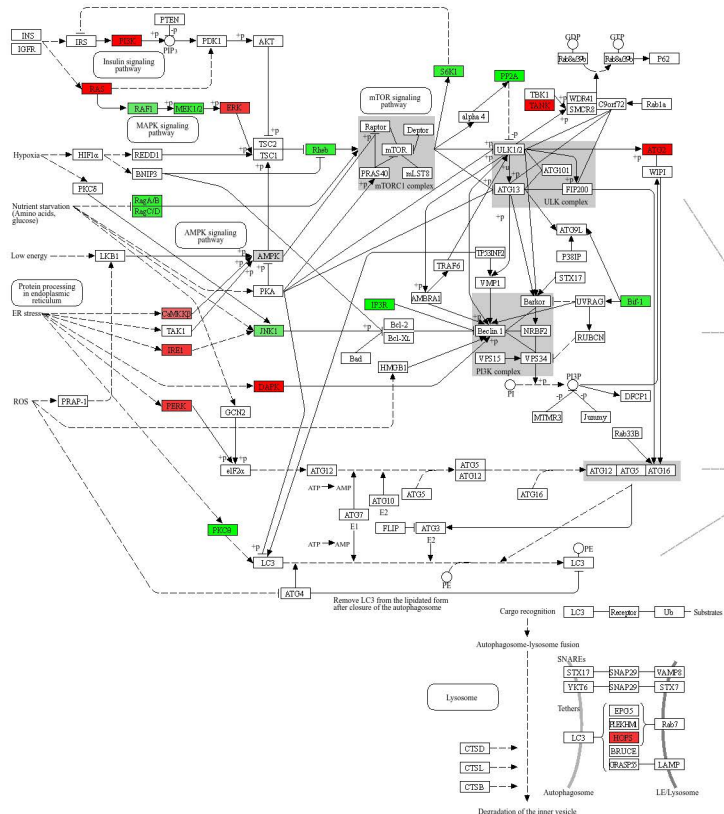


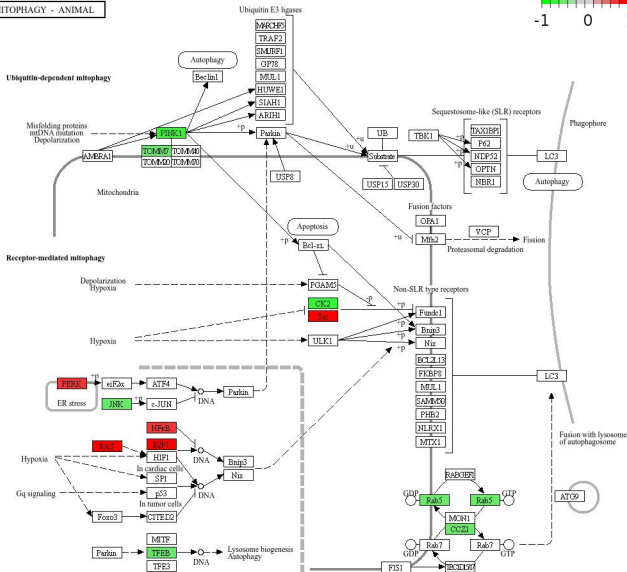
## FcγR-MEDIATED PHAGOCYTOSIS



# TNF SIGNALING PATHWAY

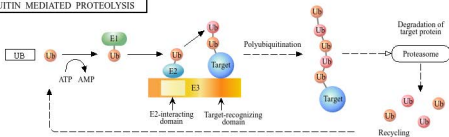








# UBIQUITIN-MEDIATED PROTEOLYSIS



E1 (Ubiquitin-activating enzyme)

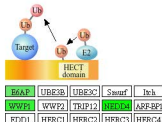
UBE1A	UBE1B	UBE1C
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E2 (Ubiquitin-conjugating enzyme)

UBE2A	UBE2B	UBE2C	UBE2D	UBE2E	UBE2F	UBE2G	UBE2H	UBE2I	UBE2J	UBE2K	UBE2L	UBE2M	UBE2N	UBE2O
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

E3 (Ubiquitin ligase)

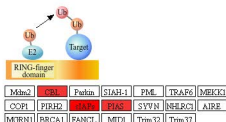
HECT type E3



U-box type E3



single RING-finger type E3



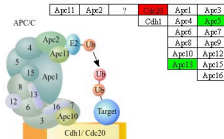
multi subunit RING-finger type E3

Cullin-Rbx E3



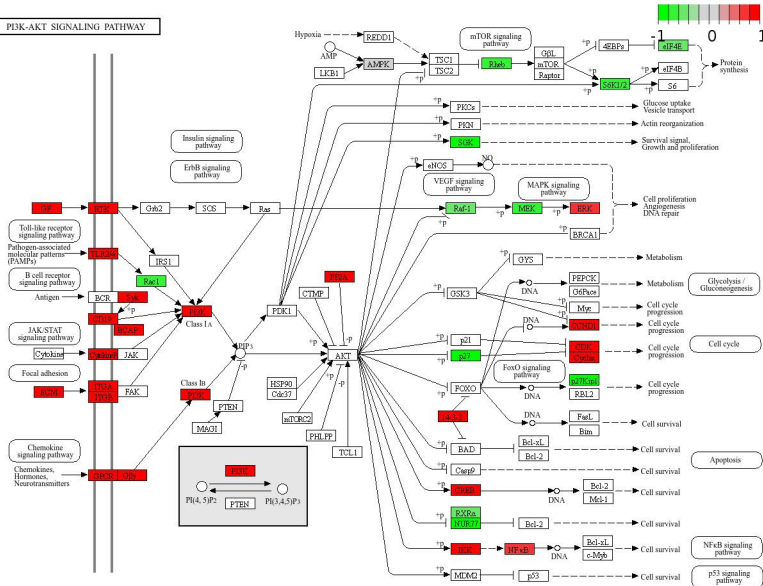
	RING finger	Cullin	Adaptor protein	Target recognizing subunit
SCF complex	RBX1	Cul1	Skp1	F-box
ECV complex	RBX1	Cul2	EloB	VHLbox EloC
Cul3 complex	RBX1	Cul3		STB
Cul4 complex	RBX1	Cul4	DD1	DCAF
ECS complex	RBX2	Cul5	EloB	SCSbox EloC
Cul7 complex	RBX1	Cul7	Skp1	Phoxb

APC/C



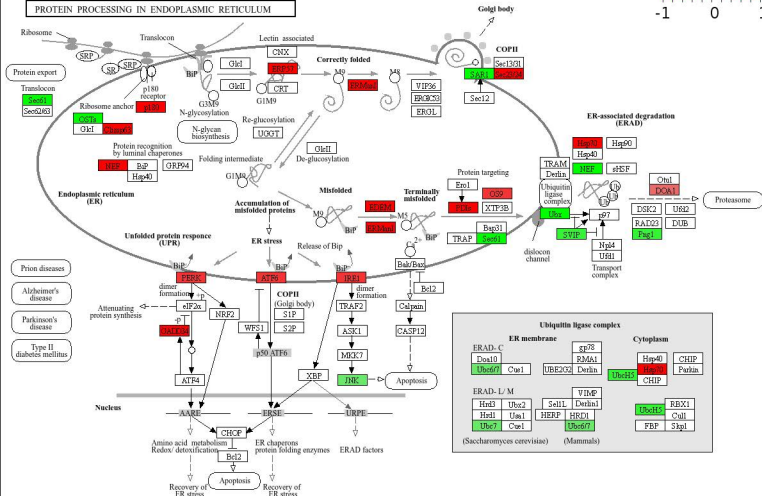


## PI3K-AKT SIGNALING PATHWAY

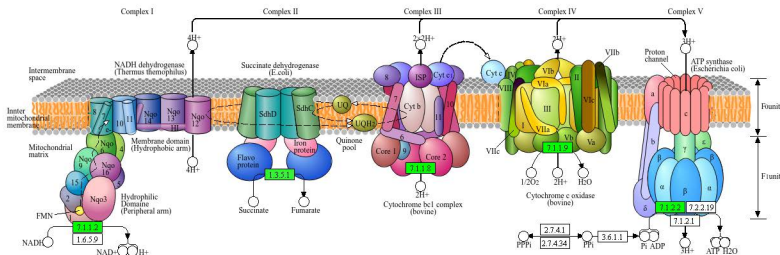
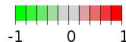


Data on KEGG graph  
Rendered by Pathview

# PROTEIN PROCESSING IN ENDOPLASMIC RETICULUM



# OXIDATIVE PHOSPHORYLATION



## NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6
B/A	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7
E/B	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7

## Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB
B/A	SdhC	SdhD	SdhA	SdhB
E	SdhC	SdhD	SdhA	SdhB
E	SdhC	SdhD	SdhA	SdhB

## Cytochrome c reductase

E/B/A	ISP	Cyt b	Cyt c1
E	ISP	Cyt b	Cyt c1
E	ISP	Cyt b	Cyt c1
E	ISP	Cyt b	Cyt c1

## Cytochrome c oxidase

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

## Cytochrome c oxidase, cbb3-type

B	I	II	IV	III
B	I	II	IV	III

## Cytochrome bd complex

B/A	CydA	CydB	CydeX
B/A	CydA	CydB	CydeX

## Cytochrome c

E	Cyt c
E	Cyt c

## F-type ATPase (Bacteria)

alpha	beta	gamma	delta	epsilon
a	a	b	c	

## F-type ATPase (Eukaryotes)

alpha	beta	gamma	delta	epsilon
OSCP	a	b	c	d
f	g	h	i	j

## 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	f	g	h	i