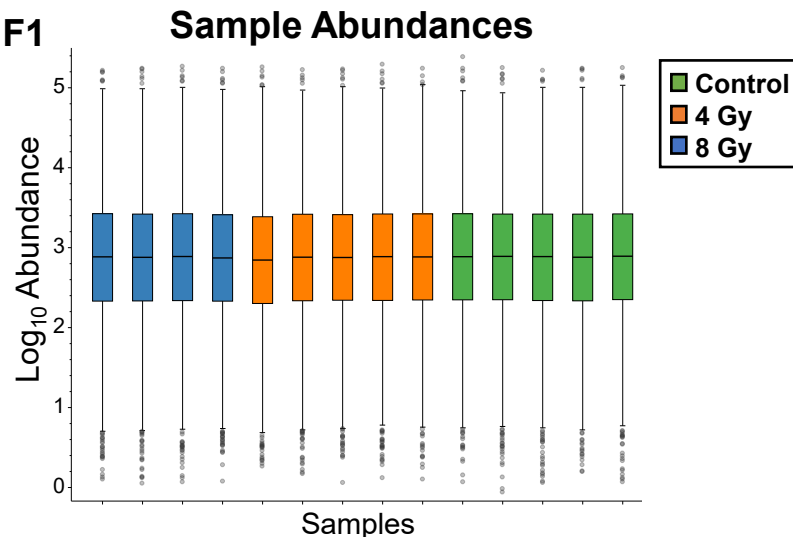


Supp Table T1: Summary of Animal Features and Experimental Timepoints

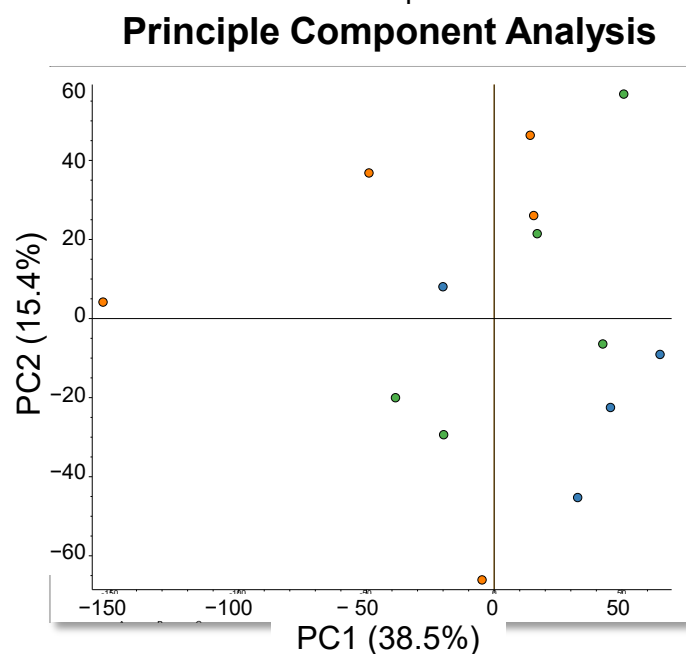
		Radiation	Irradiation	Years Since	Current Age		Time Under
WFU ID		Dose (Gy)	Age (years)	Irradiation	(years)	Death Date	Observation (yrs)
Control	1656	0			15.39	9/25/2019	11.6
	1730	0			15.73	1/23/2020	10.0
	1786	0			15.67	9/24/2020	8.2
	1987	0			11.51	9/1/2020	4.1
	1722	0			14.67	1/17/2019	9.0
	Range	11.51-15.73				2019-2020	4.1-11.6
	Average	14.60					8.6
4 Gy	1856	3.5	3.9	11.01	14.89	1/15/2020	6.5
	1857	3.5	3.9	10.75	14.62	10/9/2019	6.2
	2066	4	8.2	3.05	11.25	8/6/2020	2.8
	2015	4	5.9	1.36	7.22	8/3/2020	3.4
	2052	4	4.1	7.17	11.28	8/26/2019	1.8
	Range	3.5-4	3.9-8.2	1.4-11.0	7.22-14.89	2019-2020	1.8-6.5
	Average	3.8	5.2	6.67	11.85		4.1
8 Gy	1646	8.05	3.3	12.07	15.33	7/30/2019	11.6
	1651	8.05	3.3	13.69	16.99	3/11/2021	13.2
	1576	8.05	4.3	6.72	11.01	5/2/2013	6.4
	1905	8.5	3.9	5.14	9.00	6/8/2020	4.9
	Range	8.05-8.50	3.3-4.3	5.1-13.7	9.00-16.99	2013-2021	4.9-13.2
	Average	8.1625	3.7	9.40	13.08		9.0

Supp Figure F1

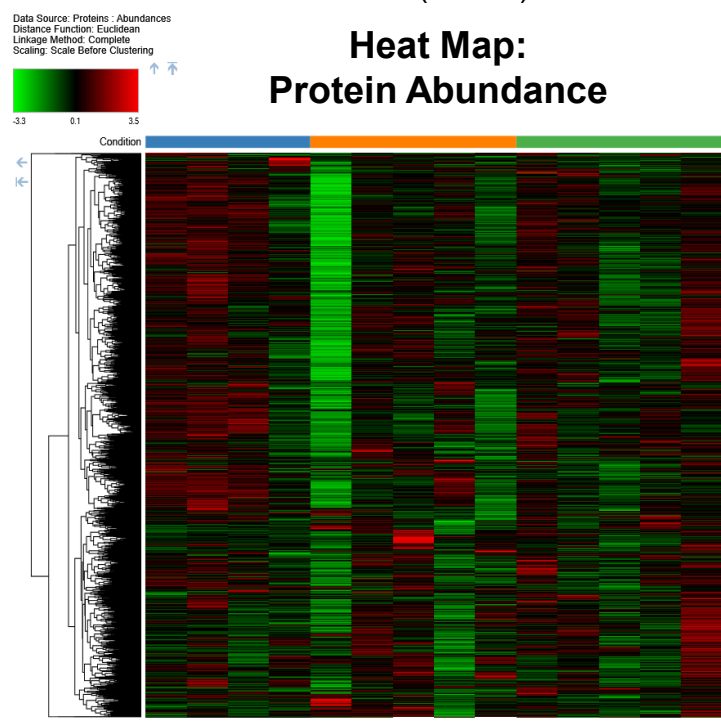
a.



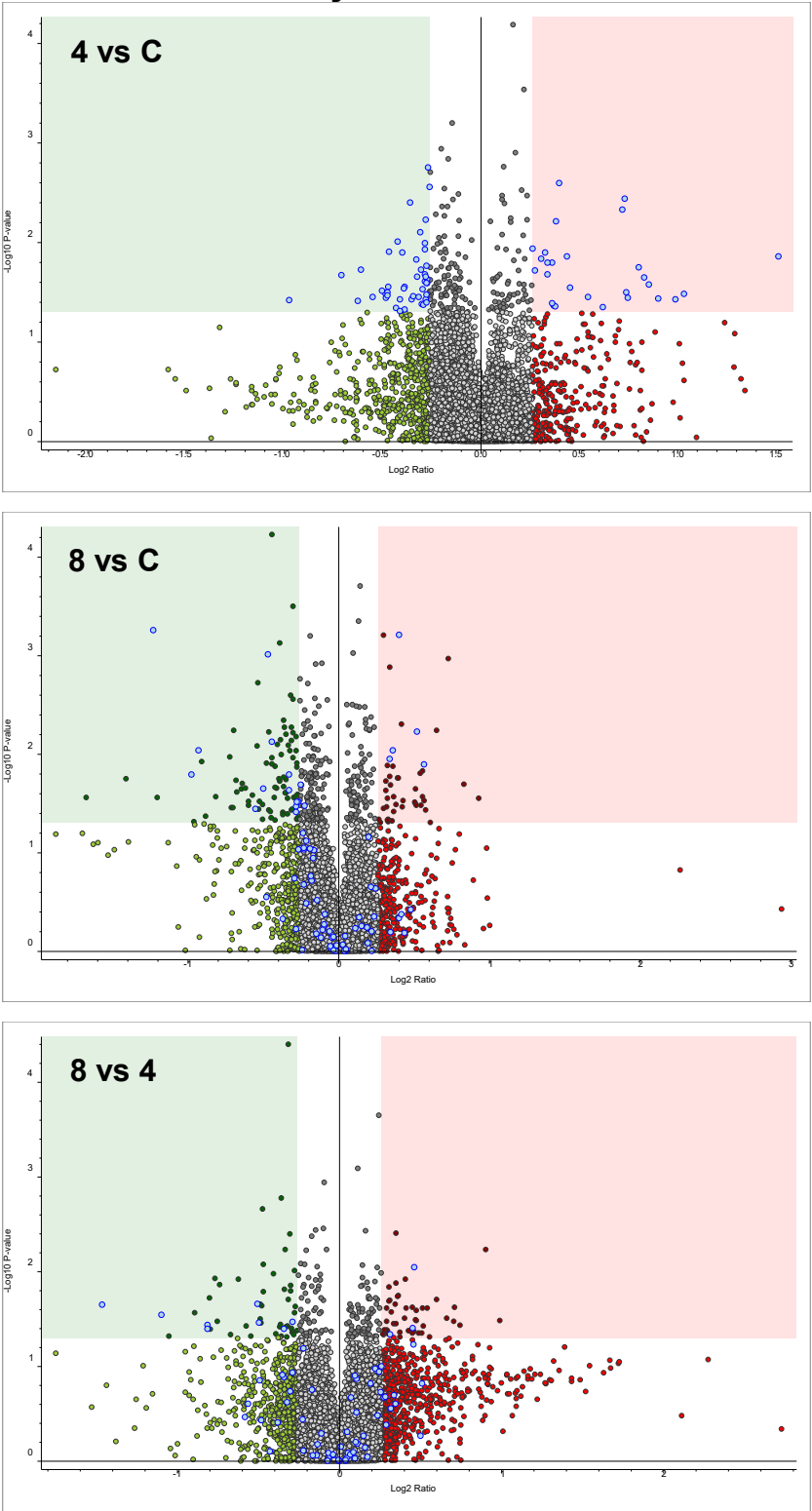
b.



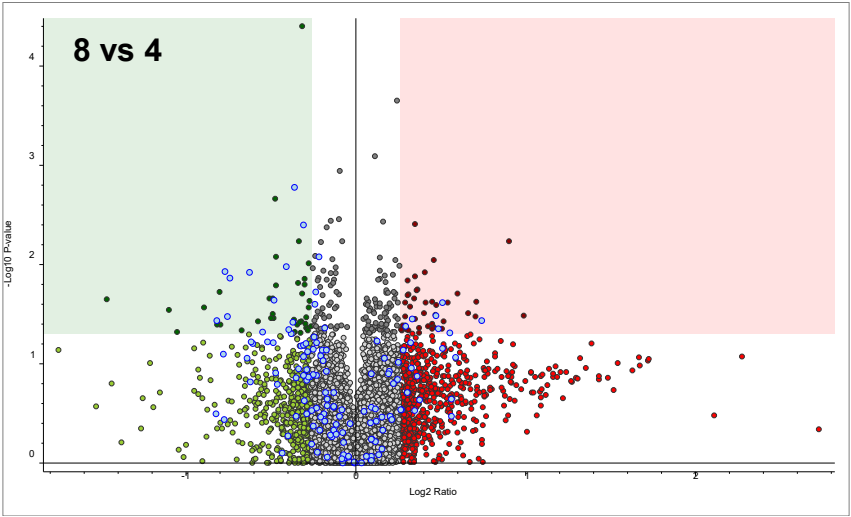
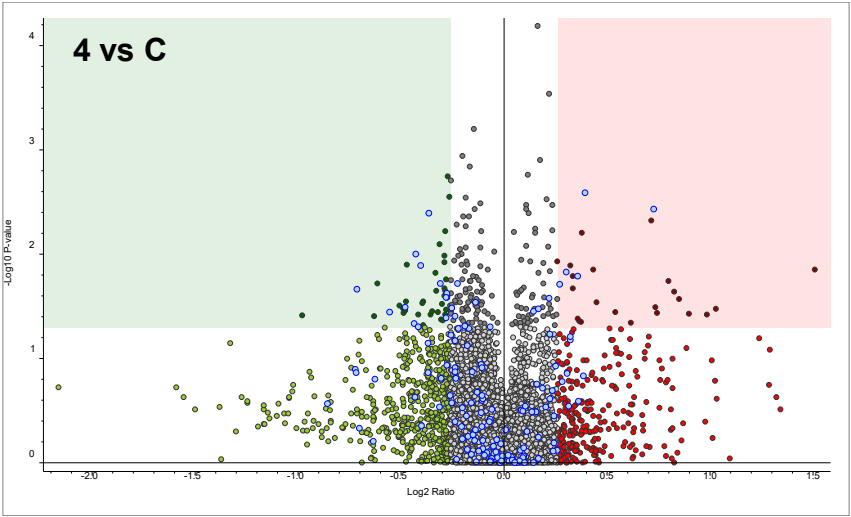
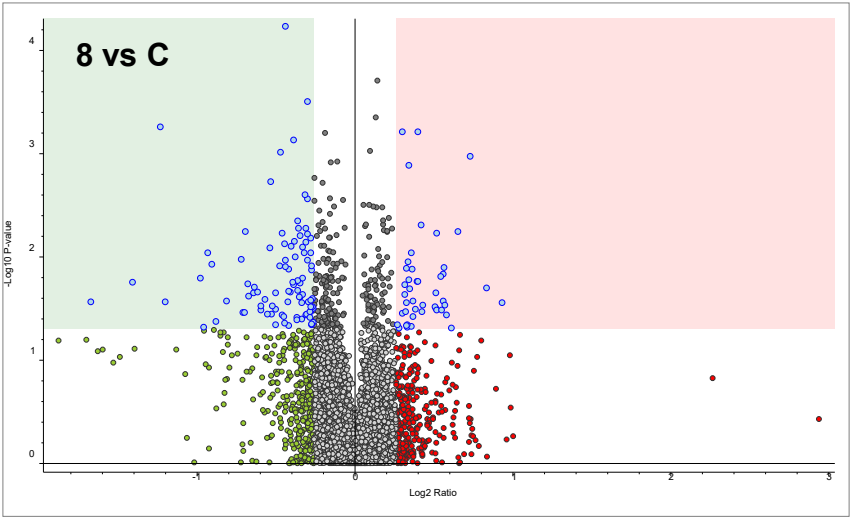
c.



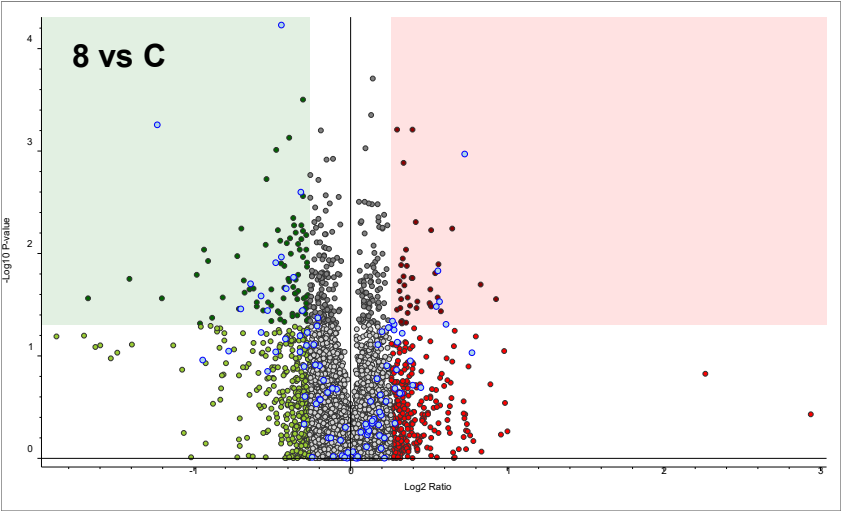
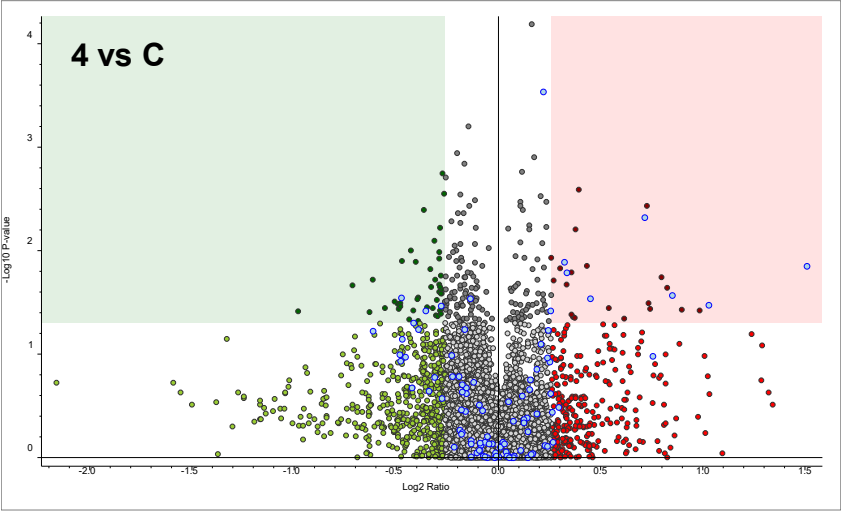
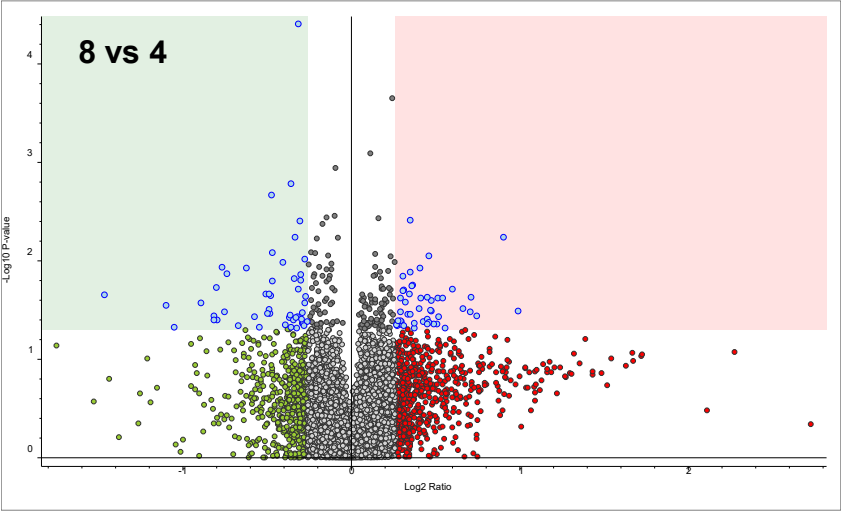
Significant Proteins:
4 Gy vs Control



Significant Proteins:
8 Gy vs Control



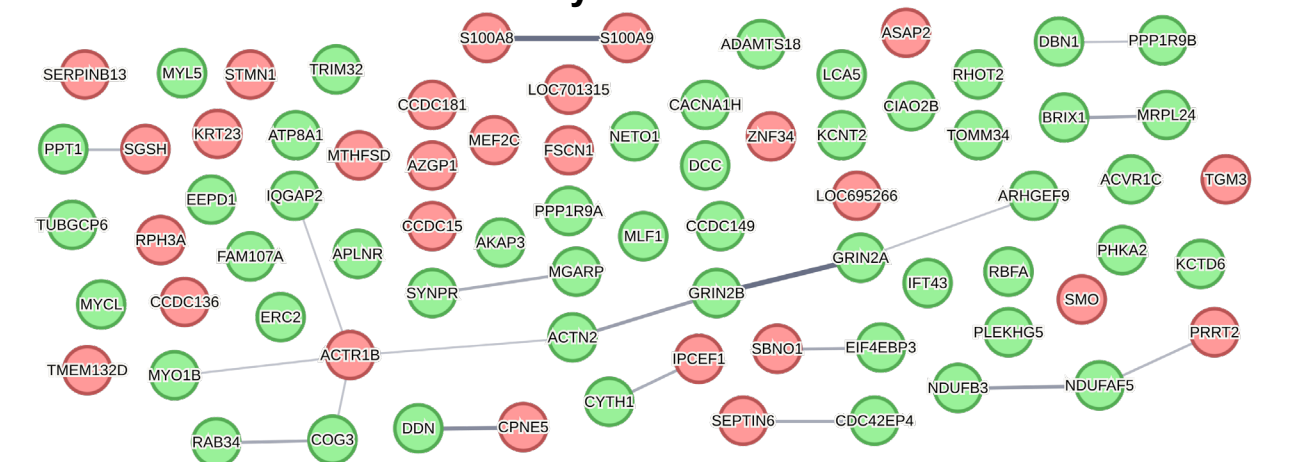
Significant Proteins:
8 Gy vs 4 Gy



Supp Figure F3

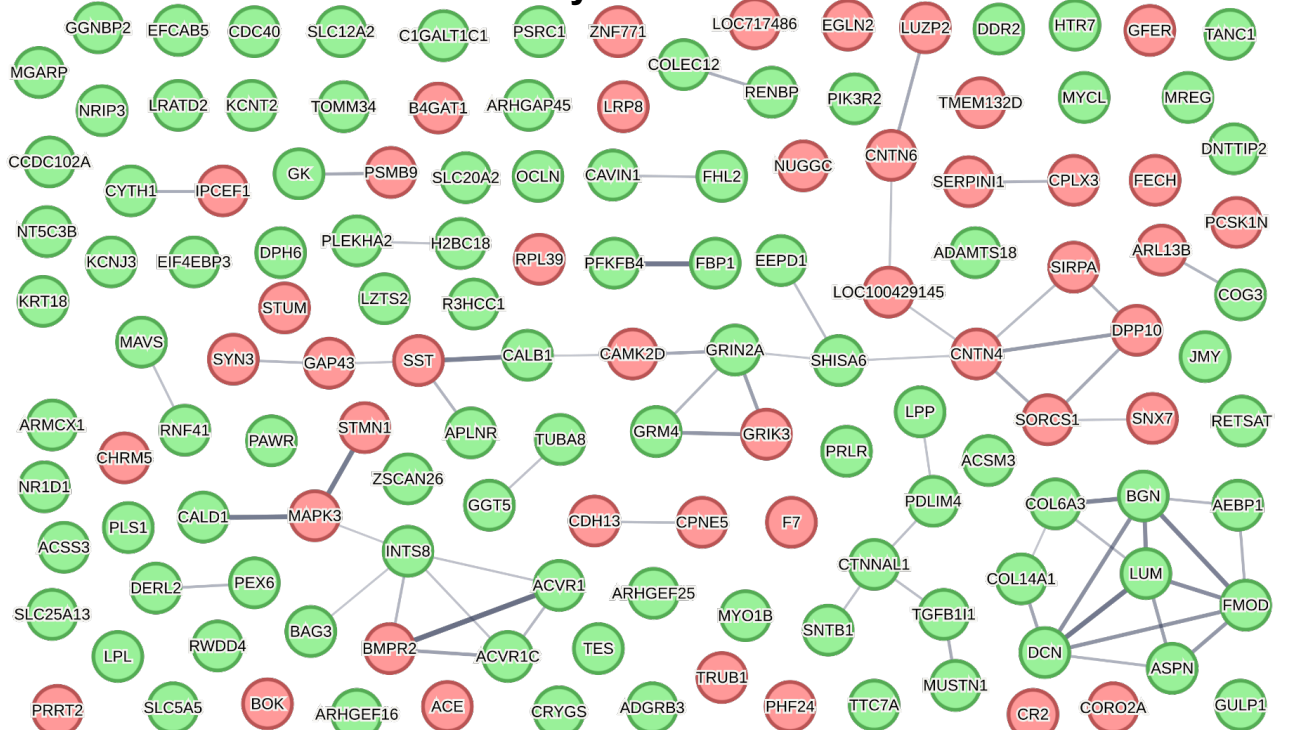
a.

4 Gy vs Control



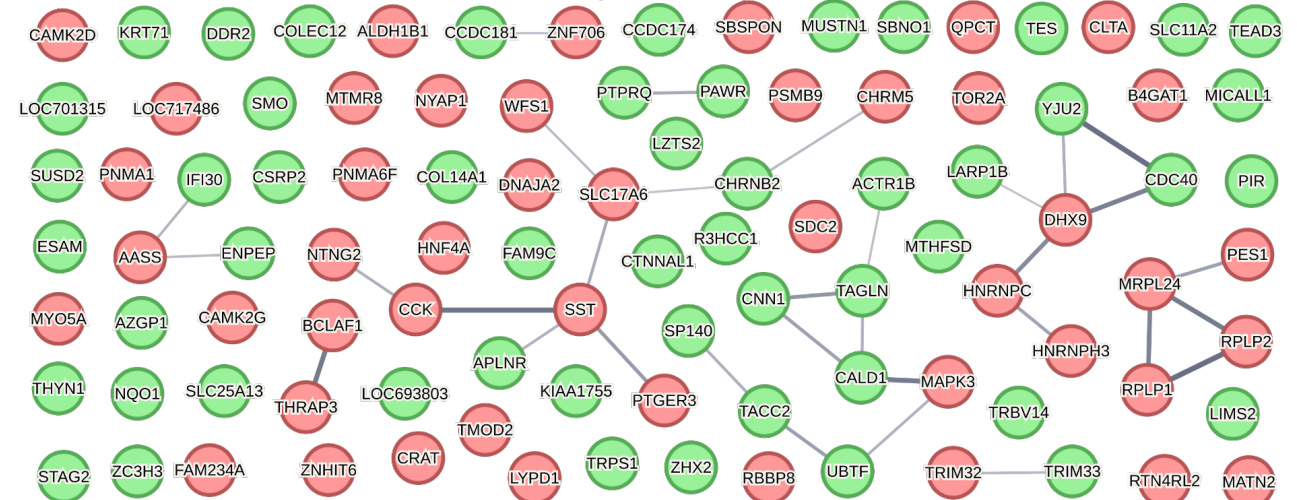
b.

8 Gy vs Control



c.

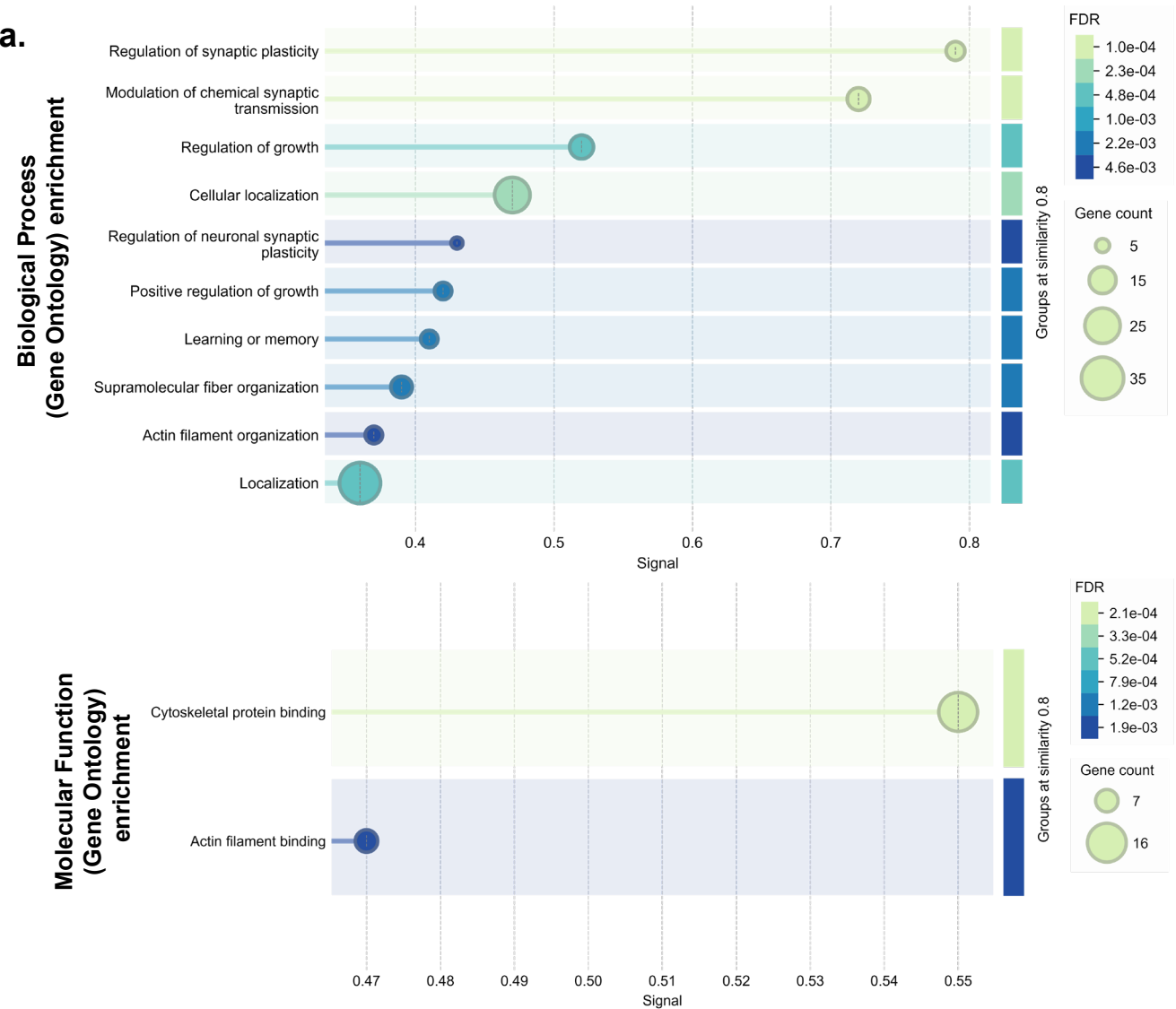
8 Gy vs 4 Gy



Supp Figure F4

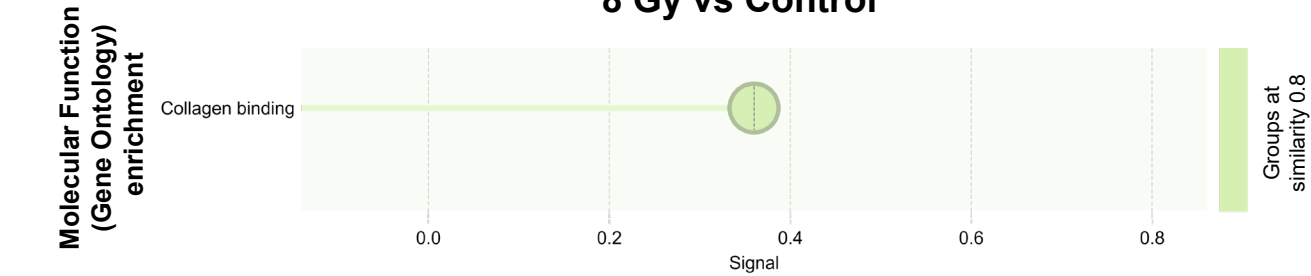
4 Gy vs Control

a.



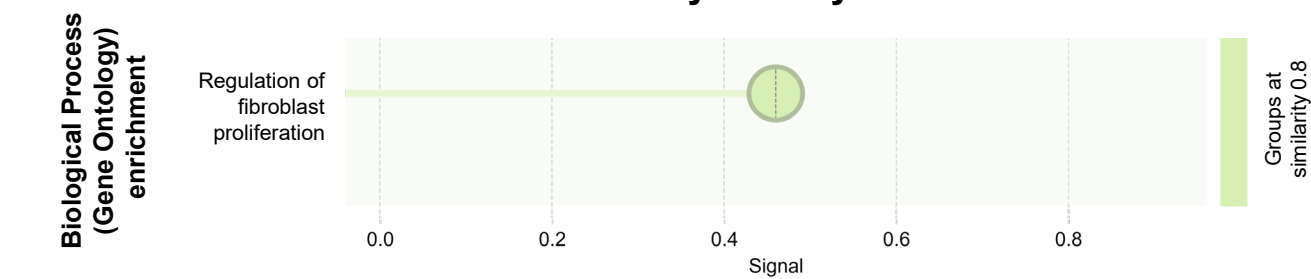
b.

8 Gy vs Control



c.

8 Gy vs 4 Gy

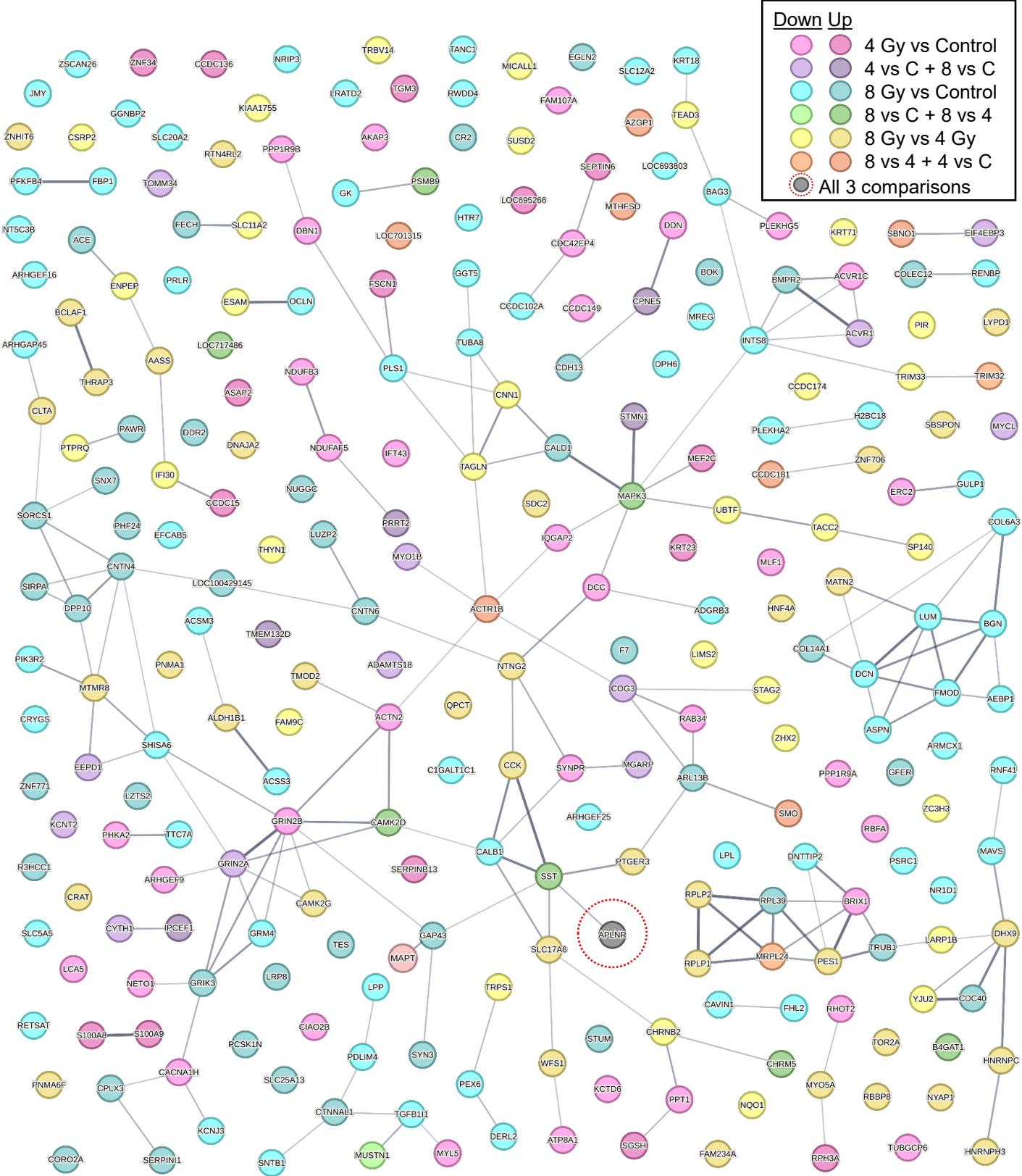


Combined Protein Network Interactions

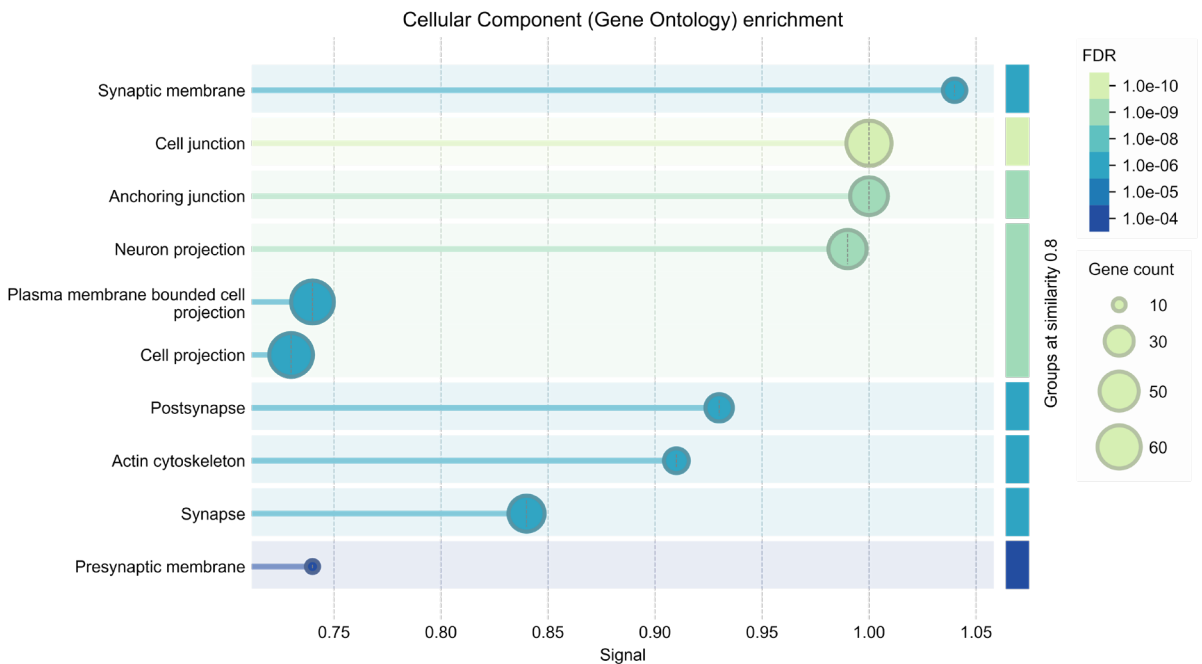
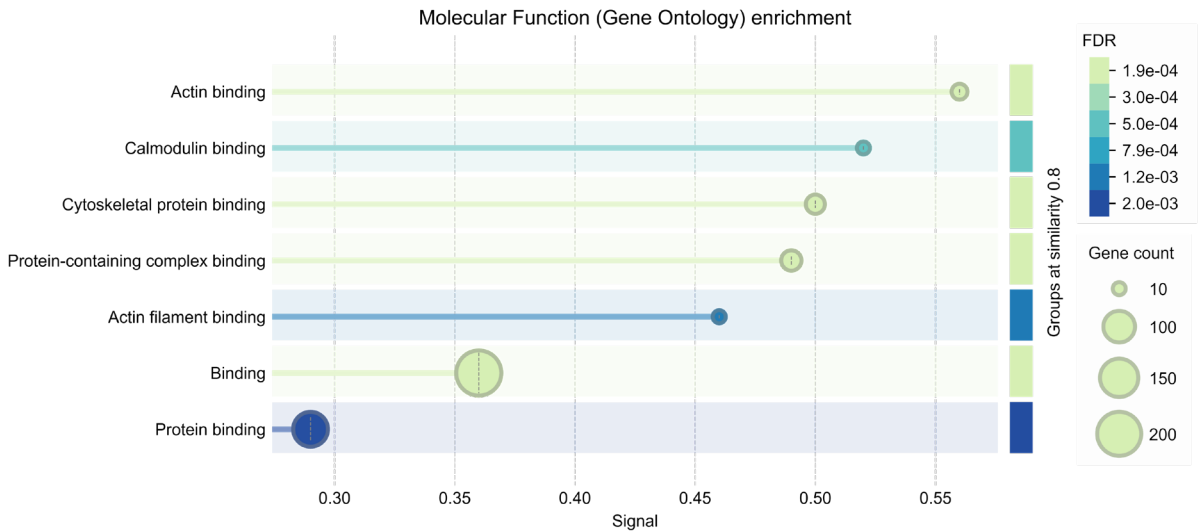
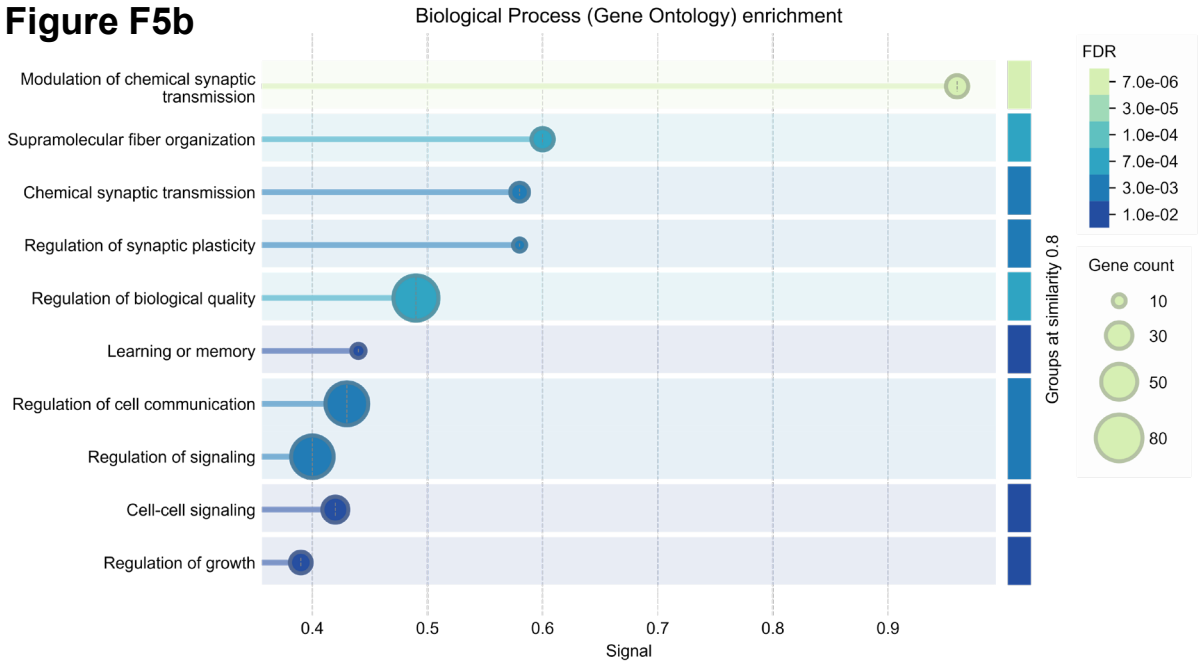
Protein Significance

Down Up

		4 Gy vs Control
		4 vs C + 8 vs C
		8 Gy vs Control
		8 vs C + 8 vs 4
		8 Gy vs 4 Gy
		8 vs 4 + 4 vs C
		All 3 comparisons



Supp Figure F5b



Supp Table T2a

DAVID Gene Ontology Analysis

		Term	Count	%	PValue	Genes
Molecular Function	4vsC	actin filament binding	6	8.108108	8.10E-04	MYO1B, FSCN1, IQGAP2, PPP1R9A, DBN1, PPP1R9B
		glutamate-gated calcium ion channel activity	2	2.702703	0.015798	GRIN2A, GRIN2B
		NMDA glutamate receptor activity	2	2.702703	0.022048	GRIN2A, GRIN2B
		small GTPase binding	4	5.405405	0.042568	RPH3A, RAB34, CDC42EP4, IQGAP2
	8vsC	cadherin binding	4	2.962963	2.03E-02	ACVR1, BMPR2, CDH13, CTNNA1
		oxygen sensor activity	2	1.481481	2.03E-02	EGLN2
		peptidyl-proline 4-dioxygenase activity	2	1.481481	0.026946	EGLN2
		adenylate cyclase inhibiting G protein-coupled glutamate receptor activity	2	1.481481	0.033569	GRM4, GRIK3
		activin receptor activity, type I	2	1.481481	0.033569	ACVR1, ACVR1C
		apolipoprotein binding	2	1.481481	0.046681	LPL, LRP8
	8vs4	RNA binding	9	9.278351	1.21E-02	MTHFS, DHX9, PES1, HNRNPH3, HNRNPC, MRPL24, TRIM32, LARP1B
		actin filament binding	5	5.154639	1.80E-02	CNN1, TAGLN, MICALL1, MYO5A, CTNNA1
		calmodulin binding	4	4.123711	0.018337	CNN1, CAMK2D, CALD1, CAMK2G
		RNA polymerase II-specific DNA-binding transcription factor binding	4	4.123711	0.020275	DHX9, HNF4A, RBBP8, TEAD3

Supp Table T2b

		Term	Count	%	PValue	Genes
Cellular Component	4vsC	filopodium	5	6.756757	4.67E-05	MYO1B, FSCN1, IQGAP2, PPP1R9A, PPP1R9B
		synaptic vesicle	5	6.756757	2.54E-04	SYNPR, GRIN2A, PRRT2, PPT1, SEPTIN6
		neuron projection	6	8.108108	2.41E-03	RPH3A, GRIN2A, CPNE5, STMN1, FAM107A, CACNA1H
		organelle membrane	3	4.054054	0.002416	GRIN2A, ATP8A1, GRIN2B
		actin cytoskeleton	5	6.756757	0.005265	MYO1B, CDC42EP4, FSCN1, PPP1R9A, PPP1R9B
		calprotectin complex	2	2.702703	0.006969	S100A9, S100A8
		dendrite	5	6.756757	0.011058	SMO, PPT1, PPP1R9A, DBN1, PPP1R9B
		lamellipodium	4	5.405405	0.01223	FSCN1, IQGAP2, DBN1, PPP1R9B
		postsynaptic membrane	4	5.405405	0.012961	RPH3A, GRIN2A, GRIN2B, DBN1
		cortical actin cytoskeleton	3	4.054054	0.013712	PPP1R9A, DBN1, PPP1R9B
		postsynaptic density	4	5.405405	0.013717	NETO1, PPP1R9A, DBN1, PPP1R9B
		microvillus	3	4.054054	0.016936	MYO1B, FSCN1, IQGAP2
		glutamatergic synapse	5	6.756757	0.019255	GRIN2A, PRRT2, NETO1, ERC2, DBN1
		postsynaptic density membrane	3	4.054054	0.02556	GRIN2A, NETO1, GRIN2B
		NMDA selective glutamate receptor complex	2	2.702703	0.02759	GRIN2A, GRIN2B
		cytoplasm	22	29.72973	0.038241	MEF2C, FAM107A, ASAP2, PPP1R9A, IQGAP2, AKAP3, MLF1, DCX
	8vsC	caveola	5	3.703704	4.84E-04	BMPR2, CAVIN1, CDH13, LRP8, MAPK3
		presynaptic membrane	5	3.703704	0.001521	GRIN2A, PRRT2, CNTN6, GRIK3, KCNJ3
		plasma membrane	38	28.14815	2.39E-03	DPP10, BMPR2, TES, CPNE5, ARHGEF25, CHRM5, GRIK3, LPL, LRP8
		postsynaptic density membrane	4	2.962963	0.009663	GRIN2A, ADGRB3, GRIK3, SHISA6
		glutamatergic synapse	7	5.185185	0.009726	TANC1, GRIN2A, CALB1, PRRT2, GRIK3, SYN3, MAPK3
		mitochondrial outer membrane	5	3.703704	0.014342	MAVS, GK, TOMM34, MGARP, BOK
		dendrite	6	4.444444	0.018916	TANC1, GAP43, BMPR2, CALB1, HTR7, CHRM5
		Z disc	4	2.962963	0.020469	BAG3, TGFB11, FHL2, PDLIM4
		neuronal cell body	5	3.703704	0.020783	SLC12A2, TANC1, CALB1, CPNE5, SERPINI1
		focal adhesion	5	3.703704	0.024575	TES, TGFB11, PIK3R2, LPP, MAPK3
		extracellular space	18	13.33333	0.024745	COLEC12, CR2, ACE, LUM, COL14A1, BGN, LPL, AEBP1, LRP8, DCX
		neuron projection	6	4.444444	0.025051	SLC12A2, CAMK2D, GRIN2A, CPNE5, STMN1, CDH13
	8vs4	receptor complex	5	3.703704	0.027321	CR2, BMPR2, PRLR, LRP8, DDR2
		activin receptor complex	2	1.481481	0.036467	ACVR1, ACVR1C
		collagen trimer	3	2.222222	0.039577	COLEC12, COL14A1, COL6A3
		actin cytoskeleton	8	8.247423	3.59E-05	CNN1, TAGLN, CALD1, DHX9, MICALL1, MYO5A, HNRNPC, DDR2
	8vs4	late endosome	4	4.123711	1.29E-02	SMO, MICALL1, MYO5A, MAPK3
		organelle	2	2.061856	3.59E-02	CAMK2D, CAMK2G
		focal adhesion	4	4.123711	0.047746	CNN1, TES, LIMS2, MAPK3

Supp Table T2c

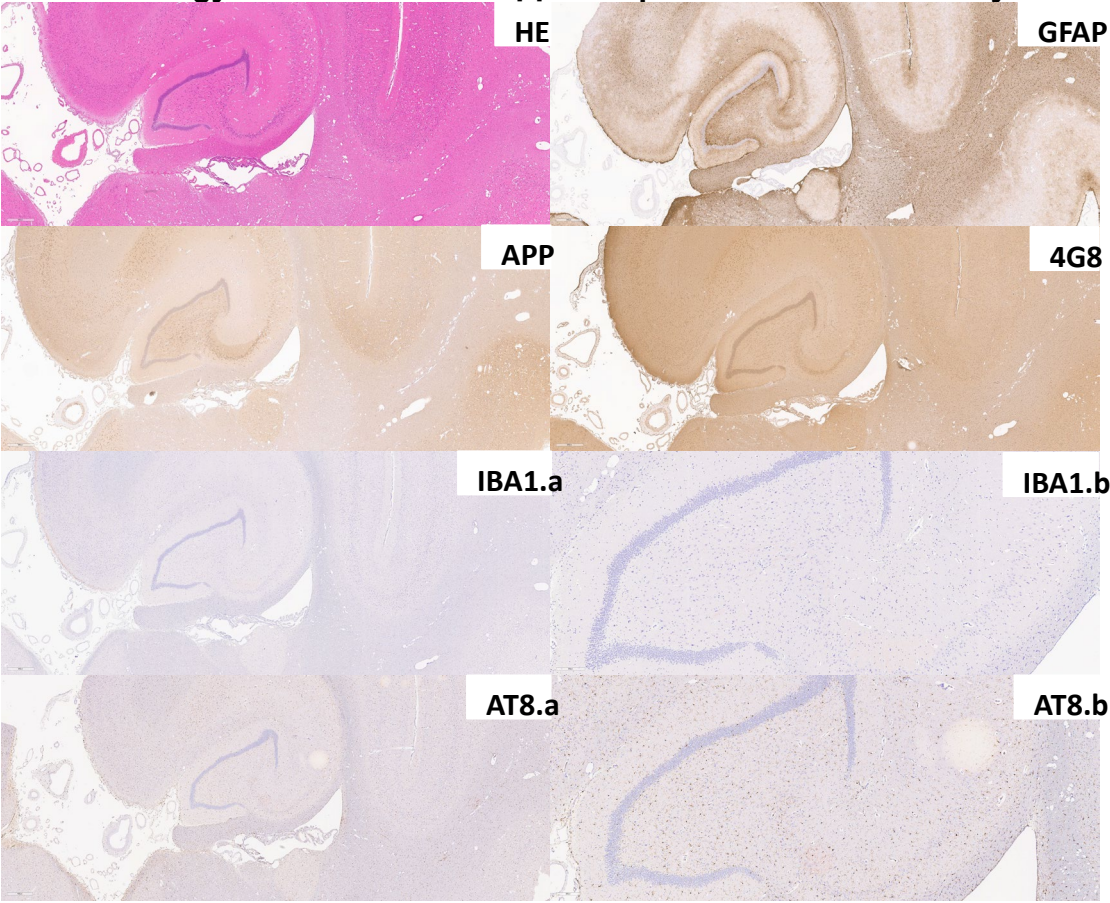
		Term	Count	%	PValue	Genes
Biological Process	4vsC	actin filament organization	5	6.756757	1.61E-03	MYO1B, RHOT2, PPP1R9A, DBN1, PPP1R9B
		regulation of calcium-dependent activation of synaptic vesicle fusion	2	2.702703	7.06E-03	PRRT2, ERC2
		neutrophil aggregation	2	2.702703	7.06E-03	S100A9, S100A8
		actin filament bundle assembly	3	4.054054	7.98E-03	MYO1B, FAM107A, FSCN1
		mitochondrial respiratory chain complex I assembly	3	4.054054	0.016785	NDUFB3, NDUFAF5, ND2
		calcium ion transmembrane import into cytosol	2	2.702703	0.017565	GRIN2A, GRIN2B
		regulation of actin cytoskeleton organization	3	4.054054	0.017935	FAM107A, FSCN1, IQGAP2
		autophagy	3	4.054054	0.023508	COG3, S100A9, S100A8
		calcium-mediated signaling	3	4.054054	0.024165	APLNR, PPP1R9A, PPP1R9B
		leukocyte migration involved in inflammatory response	2	2.702703	0.024506	S100A9, S100A8
		neuron projection development	3	4.054054	0.028978	STMN1, PPP1R9A, PPP1R9B
		astrocyte development	2	2.702703	0.034827	S100A9, S100A8
		response to ethanol	2	2.702703	0.034827	GRIN2A, GRIN2B
	8vsC	proteasomal protein catabolic process	3	2.222222	7.81E-03	DERL2, NR1D1, RNF41
		ventricular septum morphogenesis	3	2.222222	1.21E-02	ACVR1, BMPR2, APLNR
		low-density lipoprotein particle mediated signaling	2	1.481481	1.99E-02	CDH13, LPL
		cellular response to growth factor stimulus	3	2.222222	2.17E-02	ACVR1, BMPR2, ACVR1C
		positive regulation of bone mineralization	3	2.222222	0.021686	ACVR1, BMPR2, SLC20A2
		positive regulation of protein import into nucleus	3	2.222222	0.022901	MAVS, BAG3, PIK3R2
		venous blood vessel development	2	1.481481	0.026511	BMPR2, APLNR
		actin filament bundle assembly	3	2.222222	0.026709	MYO1B, CALD1, PLS1
		positive regulation of protein localization to plasma membrane	3	2.222222	0.033576	DPP10, ARHGEF16, PLS1
		positive regulation of positive chemotaxis	2	1.481481	0.039505	F7, CDH13
	8vs4	post-Golgi vesicle-mediated transport	2	1.481481	0.039505	MYO1B, SORCS1
		negative regulation of fibroblast proliferation	3	3.092784	4.80E-03	LZTS2, IFI30, TRIM32
		actin filament organization	4	4.123711	2.65E-02	CNN1, TAGLN, TMOD2, MYO5A

Supp Figure F6

Histology and IHC of NHP Hippocampus after Irradiation 0Gy

1656-19075
0 Gy

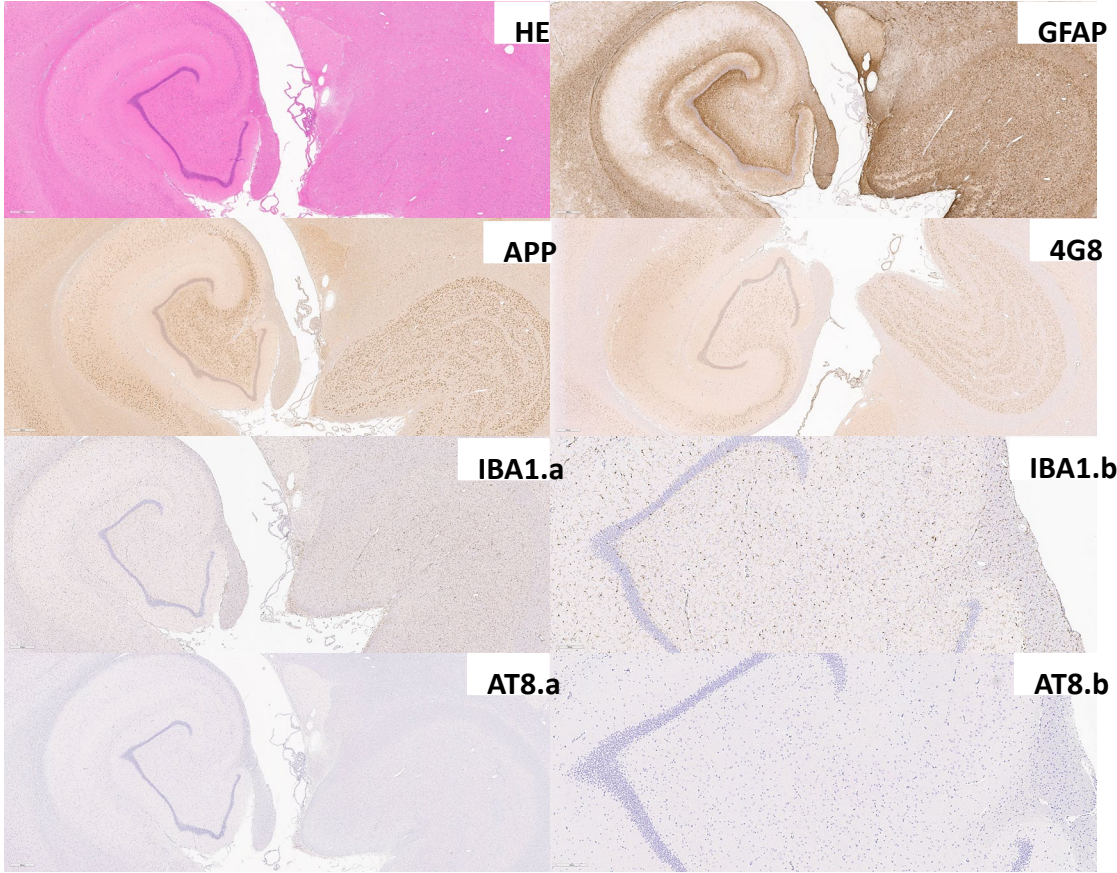
a.



b.

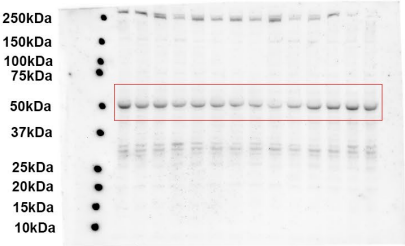
Histology and IHC of NHP Hippocampus after Irradiation 4Gy

2015-20068
4.0 Gy

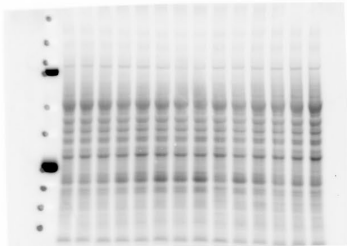


Supp Figure F7

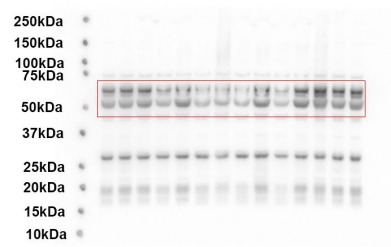
APLNR (50kDa)



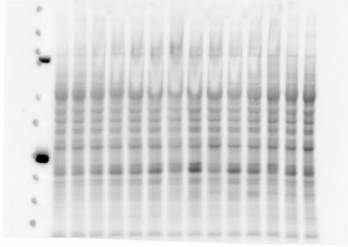
Total Protein for APLNR



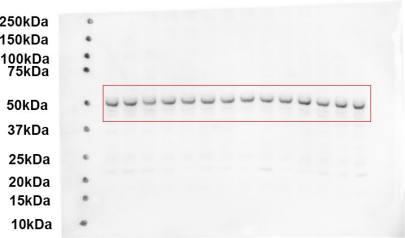
CAMK2D (50-59kDa)



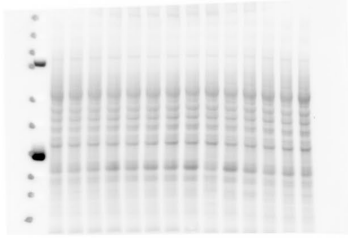
Total Protein for CAMK2D



CHRM5 (50kDa)



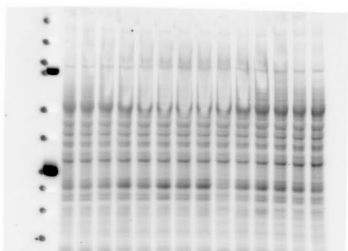
Total Protein for CHRM5



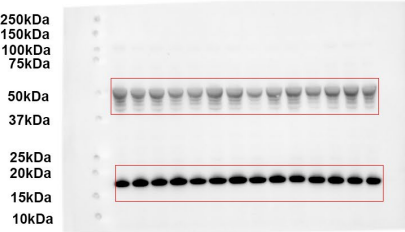
SST (15kDa)



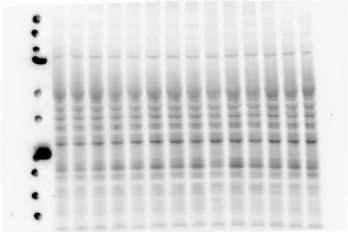
Total Protein for SST



GFAP (50kDa) and AIF1/IBA1 (17kDa)

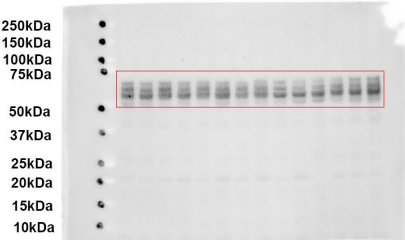


Total Protein for GFAP and AIF1/IBA1

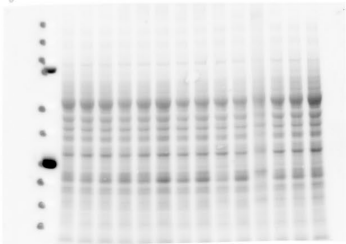


Supp Figure F8

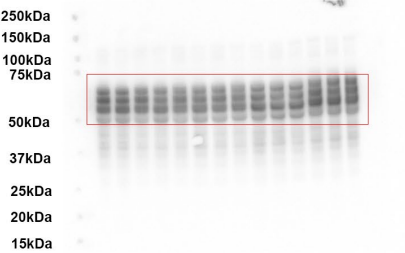
HT7 (50-75kDa)



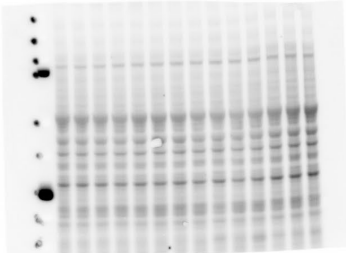
Total Protein for HT7



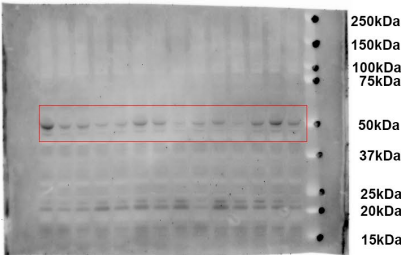
pTau S202 (50-75kDa)



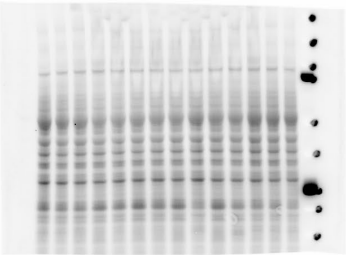
Total Protein for pTau S202



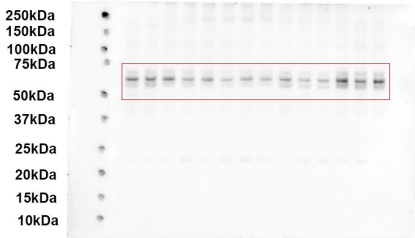
pTau S202/T205 (50-75kDa)



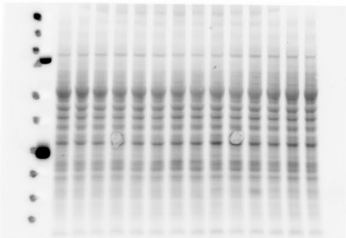
Total Protein for pTau S202/T205



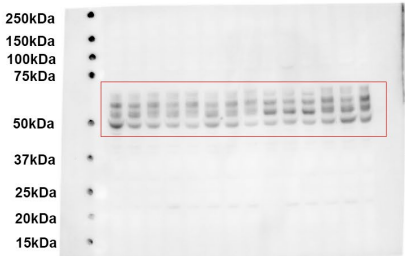
pTau T217 (50-75kDa)



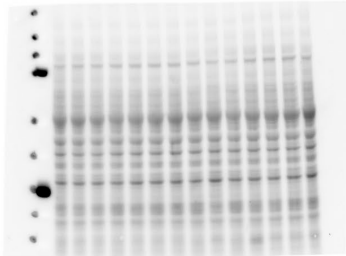
Total Protein for pTau T217



pTau T181

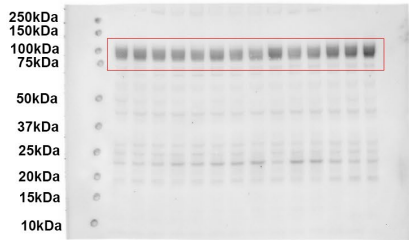


Total Protein for pTau T181

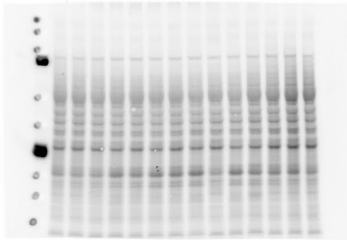


Supp Figure F9

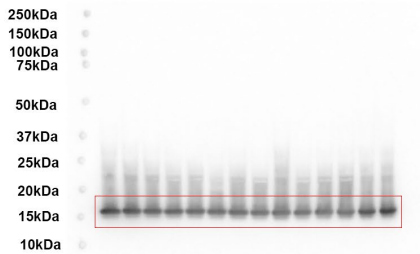
APP (87kDa)



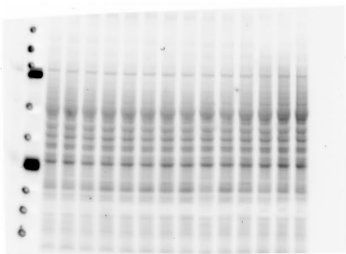
Total Protein for APP



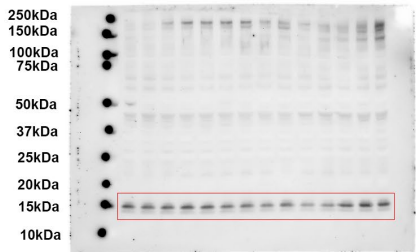
α -synuclein (15kDa)



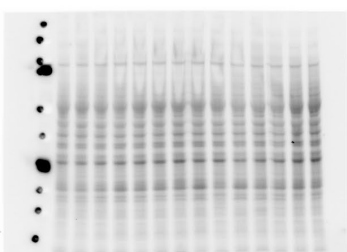
Total Protein for α -synuclein



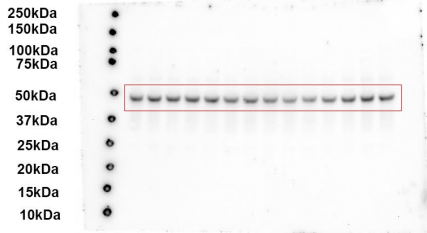
phos- α -synuclein (15kDa)



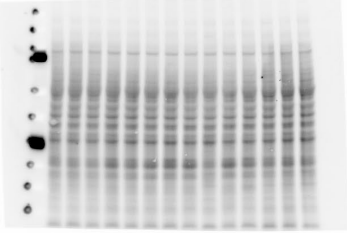
Total Protein for phos- α -synuclein



TDP43-C terminal (43kDa)



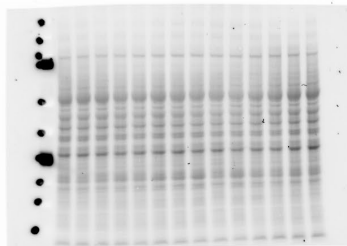
Total Protein for TDP43-C terminal



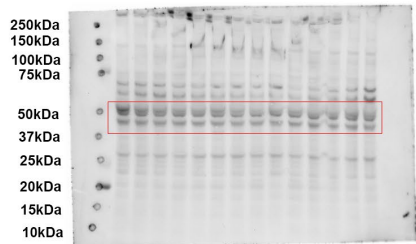
TDP43-N terminal (43kDa)



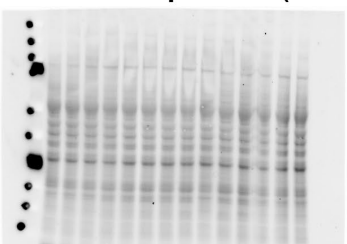
Total Protein for TDP43-N terminal



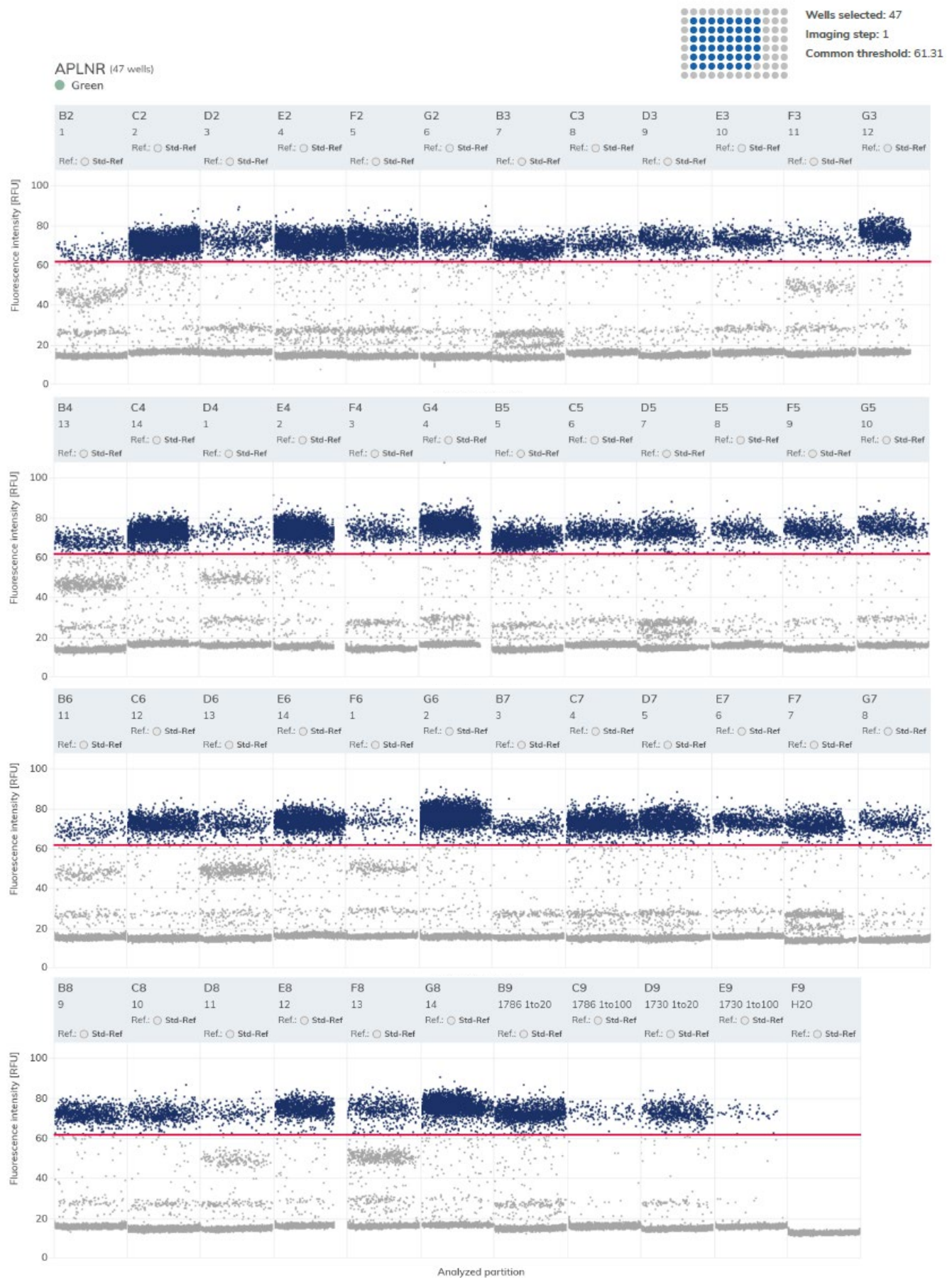
pTDP43 (S403/404) (43-50kDa)



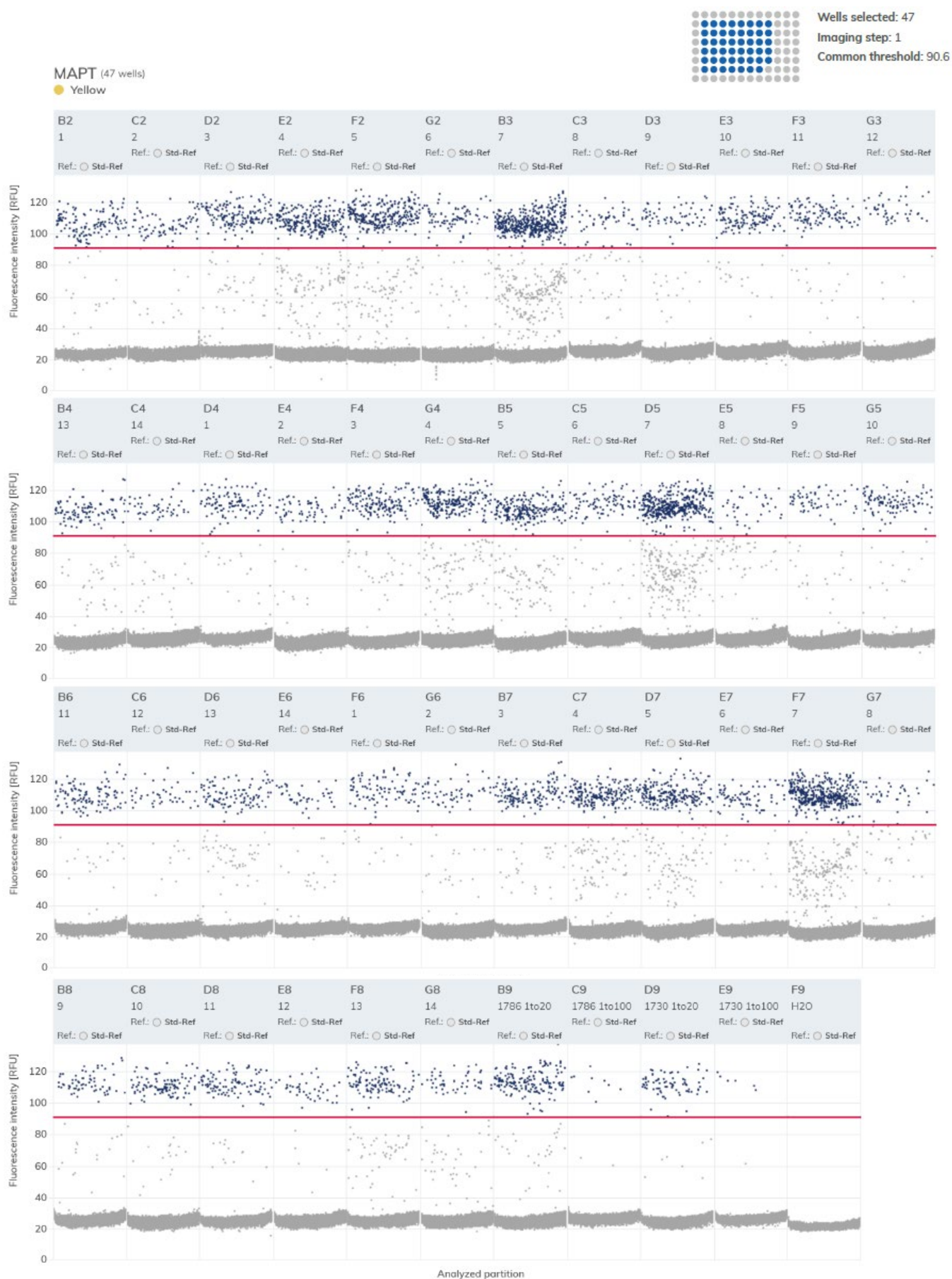
Total Protein for pTDP43 (S403/404)



Supp Figure F10a



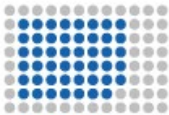
Supp Figure F10b



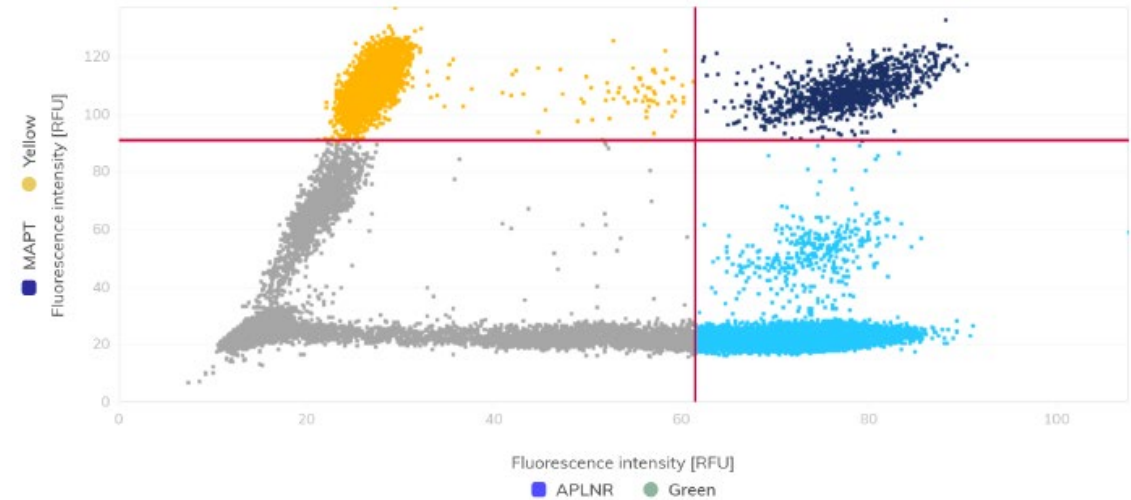
Supp Figure F10c

2D Scatterplot (47 wells)

X-axis: APLNR (Green)
Y-axis: MAPT (Yellow)



Wells selected: 47
Imaging step: 1
X-axis common threshold: 61.31
Y-axis common threshold: 90.6



	X	Y	Results
	-	-	304 897
	-	+	4 659
	+	-	54 623
	+	+	1 002
Invalid on X			34 785
Invalid on Y			11 866