

Supplementary Table S4: Significant overlapping proteins across all cohorts

Uniprot ID (XXX_MOUSE)	Accession Number	Name	Gene name	Cohort 1 PFC			Cohort 2 PFC			Cohort Combined PFC			Cohort 1 Hippocampus		
				PC	Ratio	adj. p	PC	Ratio	adj. p	PC	Ratio	adj. p	PC	Ratio	adj. p
Overlap across all cohorts															
MBP	P04370	Myelin basic protein	Mbp	36	1.14	3.5E-13	36	0.94	1.7E-06	38	1.07	9.1E-10	39	0.95	8.6E-03
ALBU	P07724	Serum albumin	Alb	57	1.05	3.1E-06	93	1.09	1.6E-13	50	1.06	1.6E-09	44	1.06	4.0E-04
SEPT5	Q9Z2Q6	Septin-5	Sept5	8	0.92	2.2E-03	14	0.82	<E-15	2	0.79	<E-15	2	0.74	1.2E-07
Overlap cohort 1 (FC), cohort 2(FC) and cohort combined INGEL (FC) - (overlap all frontal cortex studies)															
ODPA	P35486	Pyruvate dehydrogenase E1 component subunit alpha somatic form, mito.	Pdha1	4	1.17	6.5E-06	13	1.12	1.4E-03	6	0.87	4.5E-08	14	1.07	7.3E-01
H2B1B	Q64475	Histone H2B type 1-B (h2B-143)	Hist1h2bb	2	1.16	3.5E-03	4	1.11	7.3E-03	3	1.12	3.6E-03	NA	NA	NA
ENOG	P17183	Gamma-enolase	Eno2	46	1.03	1.0E-02	96	1.03	4.4E-03	31	0.96	1.3E-02	44	1.00	9.2E-01
PP2BC	P48455	Serine/threonine-protein phosphatase 2B catalytic subunit gamma isoform	Ppp3cc	3	1.16	1.2E-02	1	1.17	8.7E-04	1	1.06	4.6E-04	14	0.97	3.0E-01
BASP1	Q91XV3	Brain acid soluble protein 1	Basp1	39	0.95	2.8E-02	52	0.95	9.3E-05	13	1.20	<E-15	36	1.00	9.6E-01
Overlap cohort 2 (FC), cohort combined INGEL (FC) and cohort 1 (HC)															
CDC42	P60766	Cell division control protein 42 hon	Cdc42	2	0.94	1.3E-01	7	1.05	4.6E-02	2	1.10	2.0E-03	8	0.89	1.0E-02
MPCP	Q8VEM8	Phosphate carrier protein, mito.	Slc25a3	22	1.02	4.4E-01	25	0.94	5.1E-05	32	1.03	3.8E-02	23	0.97	4.6E-02
GSTM7	Q80W21	Glutathione S-transferase Mu 7	Gstm7	2	1.03	7.2E-01	2	0.93	5.7E-03	6	0.88	7.1E-03	7	0.90	2.5E-02
Overlap cohort 1 (FC), cohort combined INGEL (FC), cohort 1 (HC)															
H2B1P	Q8CGP2	Histone H2B type 1-P	Hist1h2bp	1	0.92	4.3E-05	5	0.98	6.3E-01	3	1.08	1.3E-02	3	0.90	3.4E-03
HBA	P01942	Hemoglobin subunit alpha	Hba	38	1.06	1.8E-03	36	1.00	9.4E-01	36	1.10	<E-15	33	1.06	3.5E-02
Overlap cohort 1 (FC) and cohort 2 (FC)															
GSTP1	P19157	Glutathione S-transferase P 1 (Gst I)	Gstp1	1	1.35	6.2E-11	1	0.64	<E-15	6	1.04	3.4E-01	3	0.93	1.1E-01
H2AX	P27661	Histone H2AX (H2a/x)	H2afx	1	1.16	4.7E-08	4	0.94	1.5E-02	3	1.06	1.4E-01	NA	NA	NA
NU4M	P03911	NADH-ubiquinone oxidoreductase	Mtnd4	1	1.15	3.1E-07	16	1.07	2.0E-02	NA	NA	NA	1	1.02	7.4E-01
AAK1	Q3UHJ0	AP2-associated protein kinase 1	Aak1	1	1.19	2.8E-05	2	1.51	9.1E-06	4	0.99	7.1E-01	NA	NA	NA
CLCA	O08585	Clathrin light chain A (Lca)	Cltc	1	1.03	2.6E-03	2	0.92	2.0E-03	1	0.94	1.4E-01	NA	NA	NA
RTN1	Q8K0T0	Reticulon-1	Rtn1	9	1.09	5.8E-03	6	1.21	9.8E-05	9	1.01	6.8E-01	17	0.95	2.4E-01
GDIA	P50396	Rab GDP dissociation inhibitor alpha	Gdi1	38	1.06	1.1E-02	49	1.04	9.3E-03	31	1.01	6.4E-01	38	0.97	2.4E-01
TPM3	P21107	Tropomyosin alpha-3 chain	Tpm3	1	1.07	1.1E-02	2	0.75	1.6E-09	NA	NA	NA	1	1.00	8.7E-01
QCR6	P99028	Cytochrome b-c1 complex subunit	Uqcrc	2	0.94	2.3E-02	1	0.92	5.0E-08	NA	NA	NA	1	1.00	9.4E-01
RAB37	Q9JKM7	Ras-related protein Rab-37	Rab37	23	1.05	3.3E-02	24	0.93	2.2E-03	13	1.00	9.0E-01	19	1.03	6.1E-01
CALL3	Q9D6P8	Calmodulin-like protein 3	Calml3	16	1.07	3.7E-02	16	1.12	1.3E-03	9	0.99	8.9E-01	9	1.07	4.8E-01
H2A1H	Q8CGP6	Histone H2A type 1-H	Hist1h2ah	1	1.11	3.7E-02	2	1.10	1.3E-04	NA	NA	NA	1	1.20	8.7E-02
DLG2	Q91XM9	Disks large homolog 2	Dlg2	2	1.11	4.1E-02	7	1.33	7.4E-04	NA	NA	NA	NA	NA	NA
H2B1H	Q64478	Histone H2B type 1-H	Hist1h2bh	1	1.07	4.1E-02	9	1.11	4.4E-02	4	1.02	6.4E-01	2	0.92	1.1E-01
NPTN	P97300	Neuroplastin	Nptn	1	1.02	4.1E-02	3	1.15	2.3E-02	2	1.00	9.7E-01	NA	NA	NA
AT1A3	Q6PIC6	Sodium/potassium-transporting ATPase subunit alpha-3	Atp1a3	108	1.02	4.7E-02	179	1.03	1.2E-05	114	1.01	3.4E-01	80	0.99	7.5E-01

Overlap cohort 1 (FC) and cohorts combined INGEL (FC)

HBB1	P02088	Hemoglobin subunit beta-1	Hbb-b1	47	1.10	1.7E-12	56	1.00	8.6E-01	42	1.07	2.4E-08	31	1.02	4.4E-01
HPRT	P00493	Hypoxanthine-guanine phosphoribosyltransferase	Hprt1	1	1.24	6.2E-11	NA	NA	NA	3	1.43	<E-15	NA	NA	NA
NFL	P08551	Neurofilament light polypeptide (N Nefl)		17	1.11	3.4E-05	NA	NA	NA	29	1.09	3.3E-12	11	0.98	6.3E-01
TPPP	Q7TQD2	Tubulin polymerization-promoting protein	Tppp	17	1.06	1.1E-04	9	0.97	2.1E-01	25	0.94	1.1E-02	12	0.97	6.1E-01
CPLX2	P84086	Complexin-2	Cplx2	9	1.10	5.4E-04	14	0.98	4.0E-01	1	1.11	1.1E-07	5	0.97	7.7E-01
AINX	P46660	Alpha-internexin	Ina	7	1.12	9.2E-04	NA	NA	NA	29	1.15	<E-15	16	0.96	6.2E-02
TBA4A	P68368	Tubulin alpha-4A chain	Tuba4a	45	1.05	1.7E-03	57	1.00	8.2E-01	38	1.02	3.4E-02	22	1.03	4.0E-01
COX2	P00405	Cytochrome c oxidase subunit 2	Mtco2	4	1.09	4.4E-03	11	0.97	8.7E-02	20	1.05	3.1E-04	12	0.97	3.7E-01
SNP23	O09044	Synaptosomal-associated protein 2	Snap23	1	0.88	6.2E-03	NA	NA	NA	2	1.24	4.7E-04	NA	NA	NA
ALDOA	P05064	Fructose-bisphosphate aldolase A	Aldoa	51	1.04	6.5E-03	106	0.98	6.0E-02	35	0.96	8.7E-03	55	0.97	1.8E-01
RS7	P62082	40S ribosomal protein S7	Rps7	2	1.08	8.3E-03	NA	NA	NA	1	0.97	2.8E-02	1	0.98	7.5E-02
QCR1	Q9CZ13	Cytochrome b-c1 complex subunit	Uqcrc1	23	1.05	8.8E-03	12	0.99	7.0E-01	3	0.93	1.0E-02	18	0.98	6.0E-01
DEST	Q9R0P5	Destrin	Dstn	2	1.11	3.7E-02	5	0.99	8.7E-01	1	0.86	1.2E-02	2	0.90	3.2E-01
CMC1	Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	Slc25a12	44	1.04	4.0E-02	70	1.02	1.9E-01	50	1.02	2.9E-02	27	1.01	7.8E-01

Overlap cohort 2 (FC) and cohorts combined INGEL (FC)

SYN2	Q64332	Synapsin-2	Syn2	38	0.95	1.3E-01	70	1.04	1.1E-04	35	1.03	1.5E-02	52	1.00	9.9E-01
AT1B1	P14094	Sodium/potassium-transporting ATPase subunit beta-1	Atp1b1	27	1.03	1.3E-01	48	0.97	2.1E-02	22	1.05	8.4E-03	24	0.99	7.7E-01
PGAM1	Q9DBJ1	Phosphoglycerate mutase 1	Pgam1	30	1.04	1.6E-01	52	1.04	2.2E-02	28	0.95	3.8E-03	18	1.02	4.9E-01
EFHD2	Q9D8Y0	EF-hand domain-containing proteir	Efhd2	3	0.97	1.7E-01	7	0.88	1.2E-04	1	1.06	2.5E-02	NA	NA	NA
MAP6	Q7TJS2	Microtubule-associated protein 6 (Map6	46	1.03	1.8E-01	91	0.98	4.2E-02	76	1.03	7.2E-03	22	1.01	9.2E-01
TBA1A	P68369	Tubulin alpha-1A chain	Tuba1a	21	1.06	2.6E-01	36	1.05	3.3E-02	19	1.03	3.3E-02	5	1.06	8.8E-02
THIL	Q8QZT1	Acetyl-CoA acetyltransferase, mito	Acat1	14	1.03	2.7E-01	30	1.05	2.2E-03	1	0.91	3.8E-03	26	1.02	4.6E-01
GNAS2	P63094	Adenylate cyclase-stimulating G alpha protein	Gnas	8	0.97	3.3E-01	16	1.08	1.9E-03	3	1.14	3.0E-04	6	0.86	2.3E-01
ARF3	P61205	ADP-ribosylation factor 3	Arf3	6	1.04	3.8E-01	4	1.13	2.1E-02	9	1.04	4.6E-02	8	0.99	7.4E-01
1433E	P62259	14-3-3 protein epsilon	Ywhae	42	0.97	4.4E-01	53	1.03	3.6E-02	35	0.97	3.8E-02	38	1.00	8.9E-01
ENOA	P17182	Alpha-enolase	Eno1	69	1.01	4.9E-01	106	1.03	6.9E-04	40	0.97	8.1E-03	55	1.02	4.6E-01
HBAZ	P06467	Hemoglobin subunit zeta	Hbz	18	0.96	5.2E-01	19	1.09	1.4E-03	13	1.06	2.3E-02	11	0.93	1.1E-01
CTNB1	Q02248	Catenin beta-1	Ctnnb1	3	0.98	5.5E-01	2	1.42	1.8E-03	1	0.90	8.1E-04	NA	NA	NA
PURA	P42669	Transcriptional activator protein Pur-alpha	Pura	4	1.03	5.7E-01	7	0.89	1.9E-03	1	0.85	6.2E-08	2	0.93	4.9E-01
AATM	P05202	Aspartate aminotransferase, mito	Got2	62	1.02	5.8E-01	81	0.97	2.1E-04	36	0.97	3.5E-02	52	0.99	7.0E-01
VISL1	P62761	Visinin-like protein 1	Vsn1	31	1.02	6.5E-01	53	0.95	4.3E-06	10	1.05	3.1E-02	21	0.95	1.9E-01
PALM	Q9Z0P4	Paralemmin-1	Palm	5	1.01	7.5E-01	3	1.68	3.1E-08	1	1.15	1.3E-03	2	0.97	7.6E-01
2AAA	Q76MZ3	Ser/Thr-protein phosphatase 2A 65 kDa reg subunit A a isoform	Ppp2r1a	23	0.99	7.5E-01	69	1.04	2.1E-02	30	1.08	4.1E-09	23	0.98	6.1E-01
HSP7C	P63017	Heat shock cognate 71 kDa protein	Hspa8	77	1.01	7.8E-01	130	1.03	4.9E-04	111	1.02	2.8E-04	66	1.00	9.2E-01
STIP1	Q60864	Stress-induced-phosphoprotein 1	Stip1	4	1.03	8.4E-01	13	0.91	1.8E-04	1	0.85	1.2E-02	6	1.00	9.1E-01
PRDX6	O08709	Peroxiredoxin-6	Prdx6	26	0.98	8.6E-01	41	0.95	3.5E-03	32	0.97	2.4E-02	17	0.99	7.4E-01
NCAM1	P13595	Neural cell adhesion molecule 1	Ncam1	37	1.01	8.7E-01	19	1.08	4.9E-02	80	1.02	3.3E-02	19	1.03	6.3E-01
1433Z	P63101	14-3-3 protein zeta/delta	Ywhaz	33	1.00	9.8E-01	72	1.04	1.3E-04	33	0.93	6.0E-06	34	1.00	9.4E-01

SYT1	P46096	Synaptotagmin-1	Syt1	28	1.00	1E+00	40	0.96	1.1E-02	40	1.08	2.2E-12	23	0.98	4.1E-01
NDUS8	Q8K3J1	NADH dehydrogenase iron-sulfur protein 8, mito.	Ndufs8	NA	NA	NA	1	0.92	1.6E-08	1	1.05	5.0E-03	NA	NA	NA
2ABA	Q6P1F6	Ser/Thr-protein phosphatase 2A 55 kDa reg. subunit B a isoform	Ppp2r2a	NA	NA	NA	5	1.48	7.8E-05	1	0.92	1.4E-02	NA	NA	NA
ARPC3	Q9JM76	Actin-related protein 2/3 complex subunit 3	Arpc3	NA	NA	NA	1	1.07	5.6E-03	1	1.05	1.1E-02	2	1.04	7.4E-01
NRDC	Q8BHG1	Nardilysin	Nrd1	NA	NA	NA	2	0.90	4.0E-02	1	0.90	4.3E-03	NA	NA	NA
RL31	P62900	60S ribosomal protein L31	Rpl31	NA	NA	NA	1	0.93	1.3E-04	1	1.07	6.1E-04	NA	NA	NA
VPS39	Q8R5L3	Vam6/Vps39-like protein	Vps39	NA	NA	NA	3	1.07	1.8E-02	1	0.83	2.0E-11	NA	NA	NA

Overlap cohort 1 (FC) and cohort 1 (HC)

G3P	P16858	Glyceraldehyde-3-phosphate dehydrogenase	Gapdh	53	1.06	7.3E-04	62	1.00	7.7E-01	72	0.98	6.3E-02	48	1.04	4.3E-02
IDHG1	P70404	Isocitrate dehydrogenase [NAD] subunit 3	Idh3g	4	1.14	3.1E-03	NA	NA	NA	NA	NA	NA	1	1.07	3.9E-03
CBR1	P48758	Carbonyl reductase [NADPH] 1	Cbr1	1	1.26	1.1E-02	NA	NA	NA	NA	NA	NA	1	1.17	4.8E-04
MYPR	P60202	Myelin proteolipid protein	Plp1	22	1.07	1.5E-02	28	0.98	3.7E-01	17	1.01	5.8E-01	32	0.94	3.2E-03
TBA3	P05214	Tubulin alpha-3 chain	Tuba3a	21	1.06	4.2E-02	34	1.01	8.3E-01	22	1.02	4.1E-01	21	1.05	2.0E-02

Overlap cohort 2 (FC) and cohort 1 (HC)

ATPD	Q9D3D9	ATP synthase subunit delta, mito.	Atp5d	5	1.10	2.4E-01	3	0.96	6.5E-03	3	0.97	5.8E-01	5	0.90	6.2E-04
UBA1	Q02053	Ubiquitin-like modifier-activating enzyme 1	Uba1	21	1.03	2.5E-01	32	1.05	4.2E-02	34	1.02	1.2E-01	25	0.93	1.1E-02
H32	P84228	Histone H3.2	Hist1h3b	11	1.03	4.4E-01	13	0.88	8.1E-05	7	1.04	2.0E-01	8	0.96	8.9E-03
H14	P43274	Histone H1.4	Hist1h1e	2	1.02	4.5E-01	3	0.91	2.5E-02	NA	NA	NA	10	0.86	2.9E-02
RSSA	P14206	40S ribosomal protein SA	Rpsa	5	0.99	7.2E-01	2	1.09	4.2E-03	3	0.98	5.8E-01	1	0.95	1.2E-02
VAMP2	P63044	Vesicle-associated membrane protein 2	Vamp2	10	1.01	8.9E-01	23	1.07	2.2E-03	14	1.02	2.7E-01	8	1.08	5.5E-03
H2B3A	Q9D2U9	Histone H2B type 3-A	Hist3h2ba	7	0.99	9.9E-01	4	0.74	6.5E-06	4	1.04	2.4E-01	3	0.94	4.6E-02
ARP2	P61161	Actin-related protein 2	Actr2	NA	NA	NA	1	0.95	5.0E-03	NA	NA	NA	3	1.11	3.3E-02
CSRP1	P97315	Cysteine and glycine-rich protein 1	Csrp1	NA	NA	NA	7	1.18	2.2E-02	NA	NA	NA	3	0.88	1.1E-02
EIF3H	Q91WK2	Eukaryotic translation initiation factor 3H	Eif3h	NA	NA	NA	1	0.88	9.1E-03	NA	NA	NA	1	0.91	6.4E-04
H2A1	P22752	Histone H2A type 1	Hist1h2ab	NA	NA	NA	2	1.31	4.6E-02	NA	NA	NA	1	0.83	5.8E-07
H2AJ	Q8R1M2	Histone H2A.J (H2a/j)	H2afj	NA	NA	NA	1	0.90	1.3E-06	4	0.92	2.4E-01	1	0.92	1.2E-03
NCOA5	Q91W39	Nuclear receptor coactivator 5	Ncoa5	NA	NA	NA	3	0.82	4.1E-02	NA	NA	NA	1	0.87	1.4E-02
NSG1	Q62092	Neuron-specific protein family member 1	Nsg1	NA	NA	NA	2	0.87	2.1E-02	NA	NA	NA	1	0.75	6.0E-03
SRC8	Q60598	Src substrate cortactin	Ctnn	NA	NA	NA	5	0.92	2.4E-02	4	1.00	9.3E-01	4	0.90	2.3E-02

Overlap cohorts combined INGEL (FC) and cohort 1 (HC)

HXX1	P17710	Hexokinase-1	Hk1	77	1.02	3.3E-01	153	0.99	3.3E-01	85	1.02	2.9E-02	87	0.95	4.7E-04
PDIA3	P27773	Protein disulfide-isomerase A3	Pdia3	4	0.99	8.8E-01	9	0.96	3.8E-01	7	1.10	2.1E-04	2	0.94	2.5E-02
DDX17	Q501J6	Probable ATP-dependent RNA helicase 17	Ddx17	NA	NA	NA	NA	NA	NA	2	1.07	2.3E-02	1	1.09	3.7E-04
HEXA	P29416	Beta-hexosaminidase subunit alpha 2	Hexa	NA	NA	NA	NA	NA	NA	1	1.13	1.4E-04	1	1.08	7.7E-03
K2C75	Q8BGZ7	Keratin, type II cytoskeletal 75	Krt75	NA	NA	NA	3	0.95	6.9E-01	30	1.03	3.5E-02	7	0.84	4.1E-02
OTUB1	Q7TQ13	Ubiquitin thioesterase OTUB1	Otub1	NA	NA	NA	2	0.92	2.3E-01	1	0.83	9.2E-07	1	0.80	5.9E-05
SPTB1	P15508	Spectrin beta chain, erythrocytic	Sptb	NA	NA	NA	NA	NA	NA	1	0.75	8.8E-09	1	0.90	2.7E-02