

A Split Biotin Ligase Approach to Revealing Proteins Associated with Oligomeric Alpha-Synuclein During Aggregation

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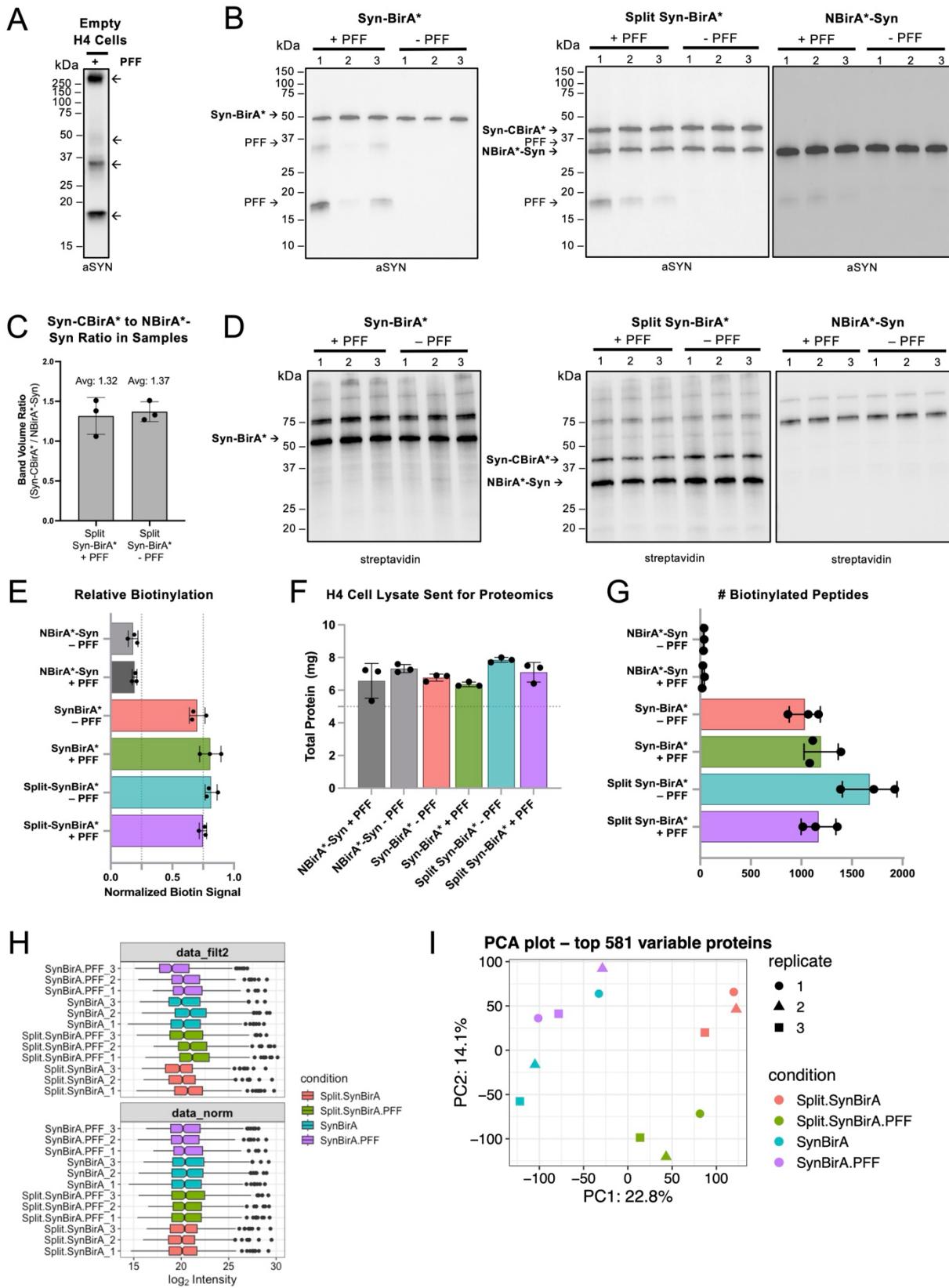
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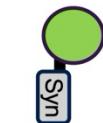
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Supplementary Fig. 1 Characterization of Samples Analyzed by Proteomics

A. Western blot of cell lysate from construct-free H4 neuroglioma cells treated with human wildtype alpha-Synuclein (aSYN) recombinant pre-formed fibrils (PFF). Probed for aSYN (MJFR1). **B.** Construct expression remained equal across replicates sent for proteomics. Western blot of cell lysate from triplicates of the 6 groups sent for proteomics. Probed for aSYN (MJFR1). Left: seeded (+ PFF) and non-seeded (– PFF) Syn-BirA*. Center: seeded (+ PFF) and non-seeded (– PFF) Split Syn-BirA*. Right: seeded (+ PFF) and non-seeded (– PFF) NBirA*-Syn. All blots demonstrate self-biotinylation of the construct expressed: self-biotinylated Syn-BirA* at 51kDa (left), self-biotinylated Syn-CBirA* at 40kDa and NBirA*-Syn at 27kDa (center) or self-biotinylated NBirA*-Syn only at 27kDa (right). PFF-specific bands are visible in groups treated with PFFs on all blots. **C.** Quantification of bands from panel B demonstrates ratios of Syn-CBirA* and NBirA*-Syn were similar across Split Syn-BirA* samples. **D-E.** Syn-BirA* and Split Syn-BirA* cell lines expressing a functioning biotin ligase enzyme demonstrate more overall biotinylation than the negative control cell line, NBirA*-Syn, expressing an incomplete enzyme fragment. **(D)** Western blot of cell lysate from triplicates of the 6 groups sent for proteomics. Probed for biotin (neutravidin). All blots demonstrate self-biotinylation of the construct expressed. Bands present in NBirA*-Syn cell lysate correspond with sizes of known endogenously biotinylated proteins: pyruvate carboxylase (130kDa), 3-methylcrotonyl-CoA carboxylase (75kDa), and propionyl-CoA carboxylase (72kDa). **(E)** Quantification of biotinylation signal from each sample in panel D. **F.** For each replicate, a cell pellet containing > 5mg of total protein were sent for BioSITe and LC-MS/MS. **G.** The number of unique biotinylated peptides reported in the raw proteomic data, by group. **H.** Box plots of the proteomic data, by sample, before ('data_filt2') and after ('data_norm') normalization. Proteins present in negative control NBirA*-Syn groups or identified in < 2 of 3 replicates across all groups were excluded prior to normalization. **I.** Principal component analysis (PCA) plot demonstrating clustering among similar samples for the post-processed dataset of 581 proteins.

A


Gene Names of Identified Proteins in the Non-Seeded Syn-BirA* Interactome. Organized by Encoding Protein Class.

Calcium-Binding Protein				Cell Junction Protein											
ANXA2				EFHD2				S100A11							
S100A6				TJP1				TJP2							
Chaperone															
AHSA1				BAG2				BAG3							
CCT8				DNAJB1				FKBP3							
HSP90AA1				HSP90AB1				HSPA1B							
HSPA1B				HSPA8				HSPH1							
NPM1															
Chromatin/Chr.-Binding/Regulatory Protein															
BAZ2A				H2A21				H2B18							
H2B21				H2B26				H2B5							
H3-7				NAP1L4				SET							
SIN3B															
H3C1, H3C2, H3C3, H3C4, H3C6, H3C7, H3C8, H3C10, H3C11, H3C12 (Accession ID: P68431)															
H4C1, H4C2, H4C3, H4C4, H4C5, H4C6, H4C7, H4C8, H4C9, H4C10, H4C11, H4C12, H4C13, H4C14, H4C15, H4C16 (Accession ID: P62805)															
Cytoskeletal Protein															
ACTB				ACTC1				ANLN							
ARPC1B				CALD1				CAP1							
CAPG				CFL1				CKAP5							
CORO1B				CORO1C				CORO1C							
CSRP1															
EPB41				EPB41L2				EPB41L3							
EZR				GSN				JPT2							
LIMA1				LIMCH1				MAP4							
MSN				MYH13				MYH9							
MYO1B				NUDC				NUCD3							
NUMA1				PDLM1				PDLM4							
PDLM5				PDLM7				PFN1							
PLS3															
SYNP02L				TPM3				TPM4							
TPX2				TWF1				VIM							
ZYX															
Defense / Immunity Protein															
ANKRD17															
DNA Metabolism Protein															
BLCAF1				RPA1				SMARCA5							
THRAP3				TRIR				YLPM1							
Extracellular Matrix Protein															
MFAP1															
SART1															
Gene-Specific Transcriptional Regulator															
AFF4				GABPA				GATA2B							
HDGFL2				HMGA1				HMGB3							
IF16				LRRKIP1				MTA1							
RLF				SAP30BP				STAT1							
STAT3				TEAD1				TFE3							
THOC2				TOX4				ZBTB33							
ZC3H4				ZNF280C											
Intercellular Signal Molecule															
TMPO (Accession ID: P42166)															
Membrane Traffic Protein															
ARCN1				BET1				CHMP5							
CLINT1				COPG2				GAK							
REPS1				SEC61B				VAMP1							
VAPB															
Metabolite Interconversion Enzyme															
DPYSL4				G6PD				GAPDH							
HINT1				LBR				NAA10							
NME2				NUDT5				NUDT5							
PFKP				PGAM1				PRK2							
PLA2G4A				PRDX1				TXNRD1							
WWOX															
Protein Modifying Enzyme															
BAZ1B				CACYBP				CUL4B							
HERC4				PPME1				PSMD1							
PSMD8				PTPN1				PTPN1							
TRIM25				UBE2M				UBE2M							
USP15															
Protein-Binding Activity Modulator															
ARHGAP35				CAST				CCN1							
CNK				DOCK7				GAPVD1							
PPP1R37				NSFL1C				RAB11FIP5							
RABL3				RABL3				RABL3							
RANGAP1															
SIPA1L2															
RNA Metabolism Protein															
ATXN2				CSTF2T				DDX42							
HDX46				DHX9				GTF2F2							
HDLBP				HNRNPA1				HNRNPA1							
HNRNPA1				HNRNPA1				HNRNPA1							
KHSRP				KHSRP				LARP1							
LCL				LCL				LCL							
NONO				NONO				NONO							
NOP58				NOP58				NOP58							
PABPC1				PABPC1											

Supplementary Fig. 2 Proximal Proteome of Unseeded Monomeric and Multimeric aSYN

A. Gene names of the 342 identified proteins proximal to non-seeded Syn-BirA*, organized by encoding protein class. Proteins included were identified in ≥ 2 of 3 replicates. Protein classes were queried through PANTHER Database v19.

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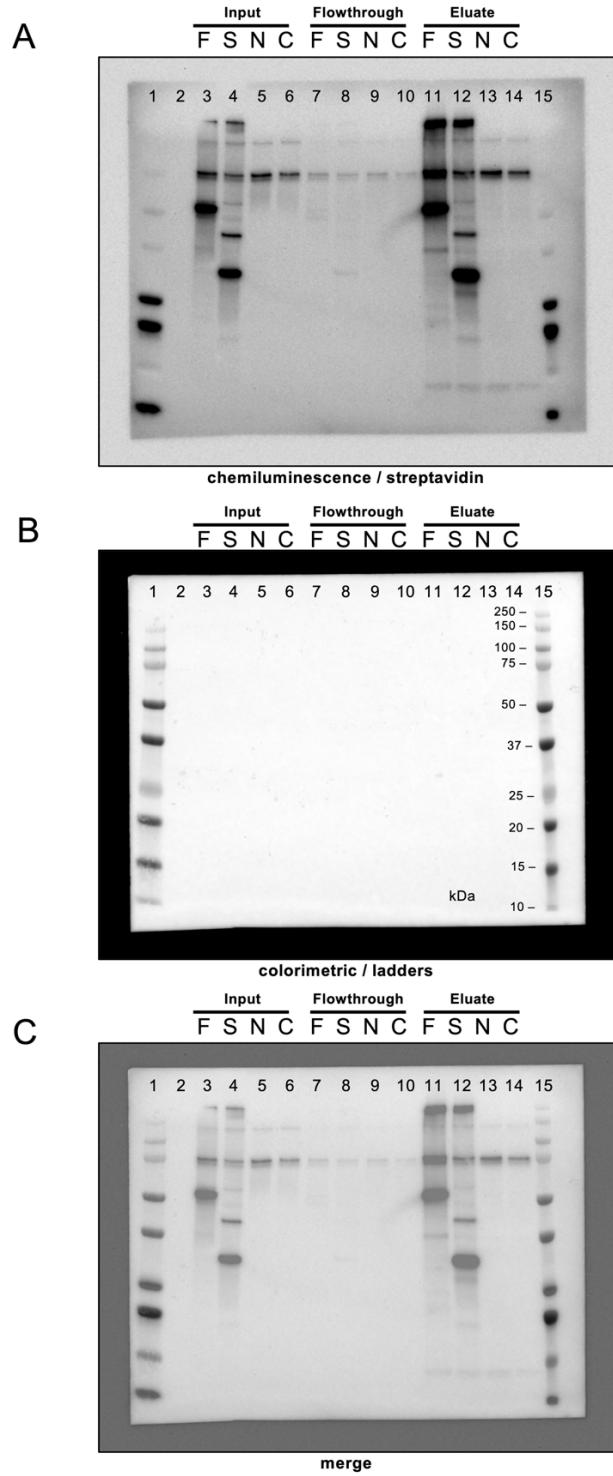
Split
Syn-BirA*

N = 487

Gene Names of Identified Proteins in the Non-Seeded Split Syn-BirA* Interactome. Organized by Encoding Protein Class.												
Calcium-Binding Protein					Cell Junction Protein					Cell Adhesion Molecule		
ANXA1 ANXA2 EFHD2 S100A11 S100A6					TJP1		TJP2	DSG2		ITGB1		
Chaperone					Chromatin/Chr.-Binding/Regulatory Protein							
AHSA1 BAG3 CCT8 CLIP1 DNAJB1					BAZ2A		CHD7	CHD8	H2A21	H2BC18	H2BC21	
DNAJC13 DNAJC8 FKBP3 HSP90AA1 HSP90AB1					H2BC26		H2BC5	H3-7	H4C1	JMD1C	KMT2B	
HSPA1B HSPA8 NASP NPM1 TBCB					NAP1L4		NCOR2	SAP130	SCML2	SIN3B		
H4C1, H4C2, H4C3, H4C4, H4C5, H4C6, H4C7, H4C8, H4C9, H4C10, H4C11, H4C12, H4C13, H4C14, H4C15, H4C16 (Accession ID: P62805)												
Cytoskeletal Protein					Defense / Immunity Protein					DNA Metabolism Protein		
ACTB ACTC1 ACTN4 ADD2 AFDN ANLN ARPC3 CALD1 CAP1 CAPG CFL1 CKAP5					ANKRD17		CORO1C CSRP1 CTNND1 EPB41	EPB41L2 EPB41L3 EVPL EZR GSN JPT1 JPT2				
CLASP1 CORO1C CSRP1 CTNND1 EPB41					KIF20B		KIF5B KRT18 LIMA1 LIMCH1 MACF1	MAPC1 MAP1A MAP1B MAP4 MAPRE2 MPRIP				
KIF15					MSN MYH9 MYL12B MYO1B NUDC		NUMA1 PARVA PDLIM1 PDLIM4 PDLIM5 PDLIM7 PFN1	PDLIM1 PDLIM4 PDLIM5 PDLIM7 PFN1				
PLS3 RDX SEPTIN2 SEPTIN9 SPTAN1					SPTBN1 STMN1 SYNP02L		TMSB10 TPM1 TPM3 TPM4					
TPX2 TWF1 VIM ZYX					Defense / Immunity Protein					DNA Metabolism Protein		
ANKRD17					BCLAF1 FEN1 MLH1 PRIM2 RPA1		SMARCA1 SMARCA5 THRAP3 TRIR			Extracellular Matrix Protein		
SMARCA1 SMARCA5 THRAP3 TRIR					Gene-Specific Transcriptional Regulator					MFAP1 SART1		
AFF4 AHR ATF7IP BTF3 EMSY GATAD2B HDGF HMGA1					HMGB3 HSF1 IIF16 LRRKIP1 MTA1 RLF SAP30BP STAT1					STAT3 TEAD1 TFE3 TOX4 ZBTB33 ZC3H15 ZNF148 ZNF451		
STAT3 TEAD1 TFE3 TOX4 ZBTB33 ZC3H15 ZNF148 ZNF451					Gene-Specific Transcriptional Regulator					Extracellular Matrix Protein		
ZNF93					Membrane Traffic Protein					IK		
ARCN1 ARFIP1 BCAP31 BET1 BET1L CHMP4B CHMPS CLINT1 CLTA COPG2 ERC1 ESYT1					ESYT2 GAK IGF2R REPS1 SDCBP SEC61B SNCB VAMP1 VAPA VAPB					TMPO (Accession ID: P42166)		
ESYT2 GAK IGF2R REPS1 SDCBP SEC61B SNCB VAMP1 VAPA VAPB					Membrane Traffic Protein					TMPO (Accession ID: P42166)		
Metabolite Interconversion Enzyme					Metabolite Interconversion Enzyme							
ADSL ALDH3A2 ALG13 DPYSL4 G6PD GAPDH GPT1 HINT1 HLC5 KYNU NME2 NMT1					NUDT5 PFKP PGAM1 PIP4K2C PKM PLA2G4A PPIP5K2 PRDX1 TXNRD1 WWOX							
NUDT5 PFKP PGAM1 PIP4K2C PKM PLA2G4A PPIP5K2 PRDX1 TXNRD1 WWOX					Phosphatase					Protein Modifying Enzyme		
INPP5F					ATG3 BAZ1B CACYBP CUL4B FER HERC4 MAP4K4 NEDD4L NRBP1 PA2G4		PAK2 PAK4 PPME1 PPP1CB PSMD1 PSMD12 PSMD2 PSMD8 PTPN1 PTPN11	RFPL4A RIPK2 SYVN1 TRIM25 TRIM56 UBE2M UBE2O USP7 UTRN VCP1P1				
ATG3 BAZ1B CACYBP CUL4B FER HERC4 MAP4K4 NEDD4L NRBP1 PA2G4					Protein Modifying Enzyme							
PAK2 PAK4 PPME1 PPP1CB PSMD1 PSMD12 PSMD2 PSMD8 PTPN1 PTPN11					Protein-Binding Activity Modulator							
ARF3 ARFGAP1 ARHgap1 ARHGAP35 CAST CCNK CCNT1 DOCK7 GAPVD1 NSFL1C PDCD5 RAB11FIP5					RAB1A RAB3GAP1 RABL3 RAN RANGAP1 SIPA1L2 TRIO							
RAB1A RAB3GAP1 RABL3 RAN RANGAP1 SIPA1L2 TRIO					RNA Metabolism Protein							
ATXN2L CSTF2 CSTF2T DDX10 DDX3X DDX42 DDX46 DHX36 DHX9 DIDO1 EIF4A1 FUS					G3BP1 GTF2F1 GTF2F2 GTF2I GTF3CS HNRNPA1 IGF2BP3 KHSRP LARP1 LSM14A NCL NONO							
G3BP1 GTF2F1 GTF2F2 GTF2I GTF3CS HNRNPA1 IGF2BP3 KHSRP LARP1 LSM14A NCL NONO					NOP58 PCBP2 PES1 PRRC2A PRRC2C PSPC1 RBM26 SERBP1 SFPQ SNRPD2 SPEN SUB1							
NOP58 PCBP2 PES1 PRRC2A PRRC2C PSPC1 RBM26 SERBP1 SFPQ SNRPD2 SPEN SUB1					Scaffold/Adaptor Protein							
SH3D19 SH3GL1 SH3PXD2B SNRPA1 SNRPGP15 SNX1 SNX4 SON SUGP1 TANC1 XAB2 YWHAB					ZRANB2							
ZRANB2					Structural Protein					Transfer / Carrier Protein		
CRYBG1					OSBPL11 OSBPL8							
OSBPL11 OSBPL8					Translational Protein							
ABCF2 EEF1A1 EEF1A2 EEF1D EEF2 EIF3G EIF3H EIF4B EIF4E EIF4G1 EIF4G2					EIF4G3 EIF4H EIF5 EPRS1 GSPT2 RARS1 RPL19 RPL24 RPL6 RPS2 RPS20 RPS3A							
EIF4G3 EIF4H EIF5 EPRS1 GSPT2 RARS1 RPL19 RPL24 RPL6 RPS2 RPS20 RPS3A					Transmembrane Signal Receptor					Transporter		
GPRCSA PGRMC2 TMEM87A					ATP11B CCAR2 NUP214 NUP98 TPR VCP							
ATP11B CCAR2 NUP214 NUP98 TPR VCP					Unclassified							
AAK1 ACIN1 ADNP AGFG1 AHNAK AHNAK2 ALMS1 AP1AR ATIC BOD1L1 C1orf198 C2CD2					CBX3 CCDC124 CCDC50 CCZ1B CDV3 C1S2D CKAP4 CNN2 COMMD8 CSDE1 CWC15 DAP							
CBX3 CCDC124 CCDC50 CCZ1B CDV3 C1S2D CKAP4 CNN2 COMMD8 CSDE1 CWC15 DAP					DBN1 DNMBP EGLN1 EMD ENSA EFS1 FAM107B FASN FIP1L1 FLNB GEMIN5 GSDME							
DBN1 DNMBP EGLN1 EMD ENSA EFS1 FAM107B FASN FIP1L1 FLNB GEMIN5 GSDME					HCFC1 HGS HIVEP1 HNRNPU HNRNPU1 HNRNPU2 IWS1 KNL1 LASP1 LMO7 LSM12 LUZP1							
HCFC1 HGS HIVEP1 HNRNPU HNRNPU1 HNRNPU2 IWS1 KNL1 LASP1 LMO7 LSM12 LUZP1					MIA MTDH MTU51 NBR1 NCAPG NCAPH NEDD8 NELFE NHLCR2 NKAPD1 NOL11 NUCKS1							
MIA MTDH MTU51 NBR1 NCAPG NCAPH NEDD8 NELFE NHLCR2 NKAPD1 NOL11 NUCKS1					NUFIP2 PAICS PCNP PDAP1 PLEKHA1 PNISR PNN PPP1R10 PPP1R18 PTMA PTPN12 PUS7							
NUFIP2 PAICS PCNP PDAP1 PLEKHA1 PNISR PNN PPP1R10 PPP1R18 PTMA PTPN12 PUS7					RAI14 RBM10 RBM33 RCC2 RIC8A RP9 RUFY1 RUVBL1 SAFB SAMD9 SKA3 SLAIN2							
RAI14 RBM10 RBM33 RCC2 RIC8A RP9 RUFY1 RUVBL1 SAFB SAMD9 SKA3 SLAIN2					SLTM SMAP SMC4 SND1 SP100 SQSTM1 SRP72 SRRM2 STBD1 STEEP1 STIP1 SYMPK							
SLTM SMAP SMC4 SND1 SP100 SQSTM1 SRP72 SRRM2 STBD1 STEEP1 STIP1 SYMPK					SYNM TACC3 TAGLN2 THOC7 TLN1 TMA7 TNKS1BP1 UBA2L1 UFD1 UNC45A VCL VMA12							
SYNM TACC3 TAGLN2 THOC7 TLN1 TMA7 TNKS1BP1 UBA2L1 UFD1 UNC45A VCL VMA12					WBP11 WDR36 YKT6 ZC3H18 ZC3H1C ZDBF2 ZMYND8 ZNF318							
WBP11 WDR36 YKT6 ZC3H18 ZC3H1C ZDBF2 ZMYND8 ZNF318					Not Found							
Not Found					PALM2AKAP2 TMPO (Accession ID: P42167)							

Supplementary Fig. 3 Proximal Proteome of Unseeded Multimeric Only aSYN

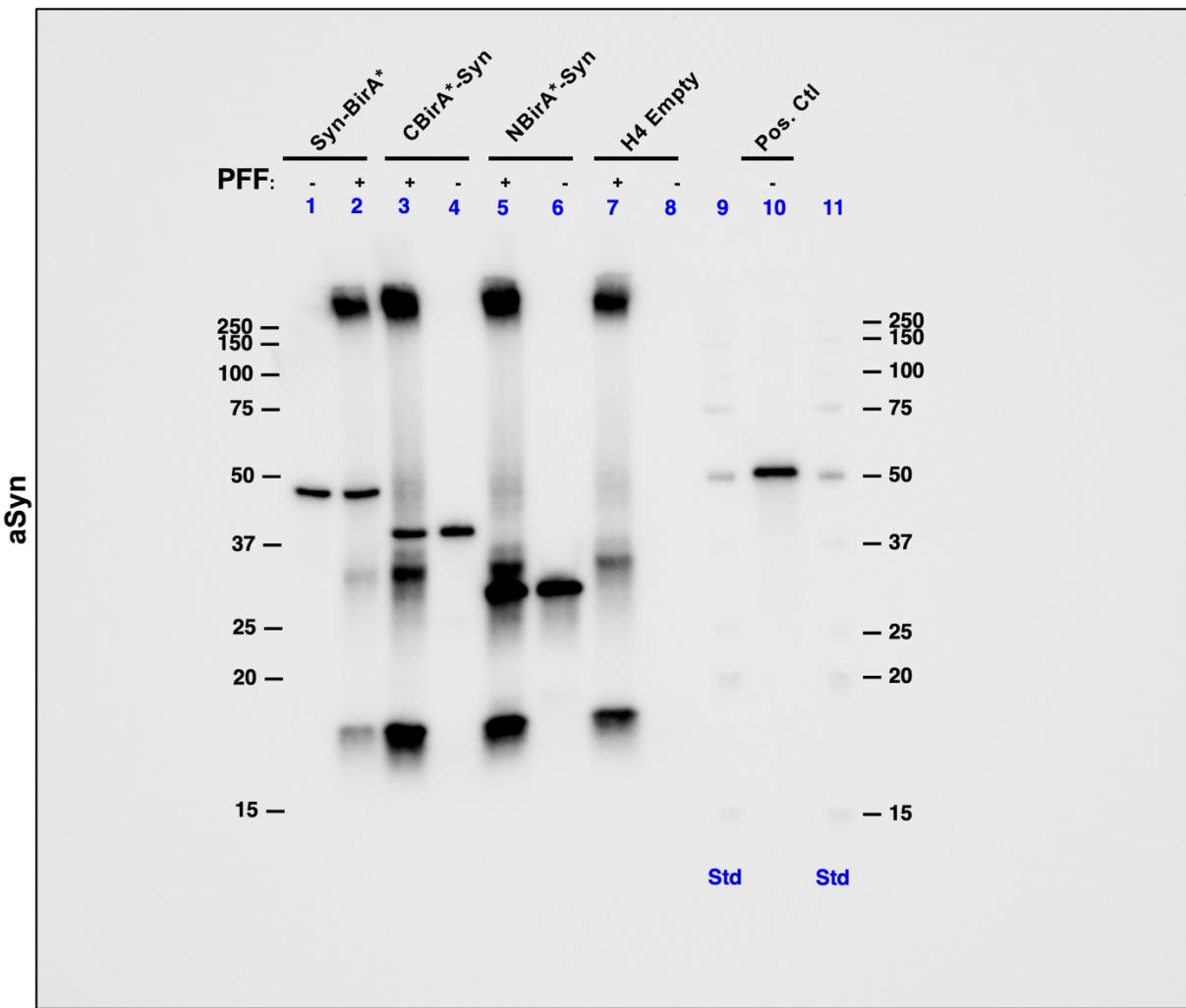
A. Gene names of the 487 identified proteins proximal to non-seeded Split Syn-BirA*, organized by encoding protein class. Proteins included were identified in ≥ 2 of 3 replicates. Protein classes were queried through PANTHER Database v19. These proteins represent potential interactors of physiologically healthy multimeric aSYN.



Supplementary Fig. 4 Uncropped Blot from Figure 1D Demonstrating Enrichment of Biotinylated Proteins

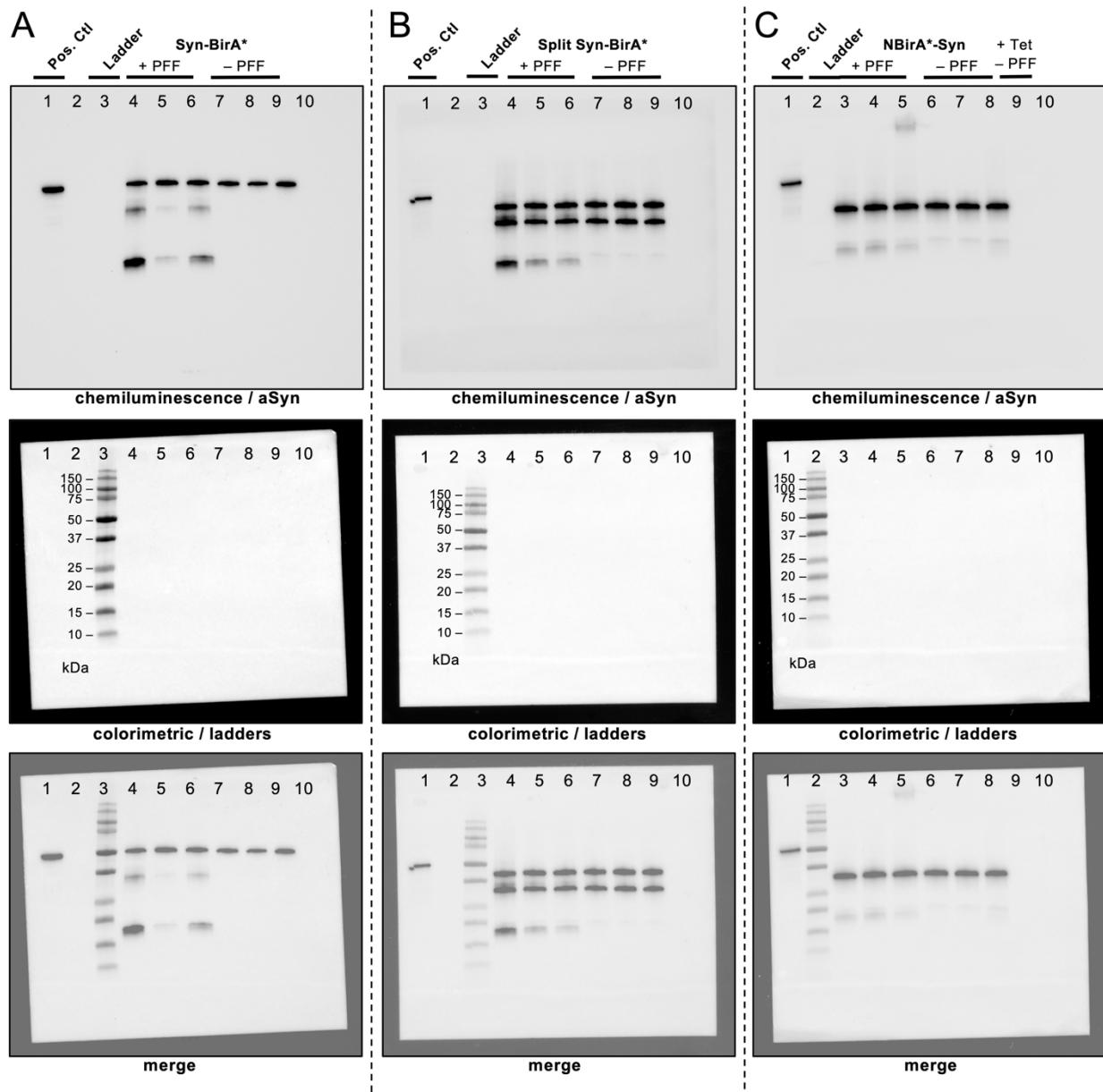
Lanes 11-14 were shown in the main text to highlight the biotinylated proteins found in lysates after streptavidin enrichment. Lanes 1 & 15 are ladders. Lane 2 is blank (no sample). Lanes 3-6 represent starting H4 stable cell lysate for pulldown (aka “input”) for Syn-BirA* (“F”), Split Syn-BirA* (“S”), NBirA*-Syn (“N”) and Syn-CBirA* (“C”).

Lanes 7-10 represent the flowthrough from the streptavidin pulldown; these samples are expected to show reduced levels of biotinylated proteins. Lanes 11-14 represent final enriched biotinylated proteins (aka “eluate). **A.** Chemiluminescence only imaging showing anti-streptavidin HRP signal. **B.** Colormetric only imaging to visualize the ladder. **C.** Merge of blots from (A) and (B). Blot was not moved between colorimetric and chemiluminescent imaging.



Supplementary Fig. 5 Uncropped Blot Demonstrating PFF-associated Bands

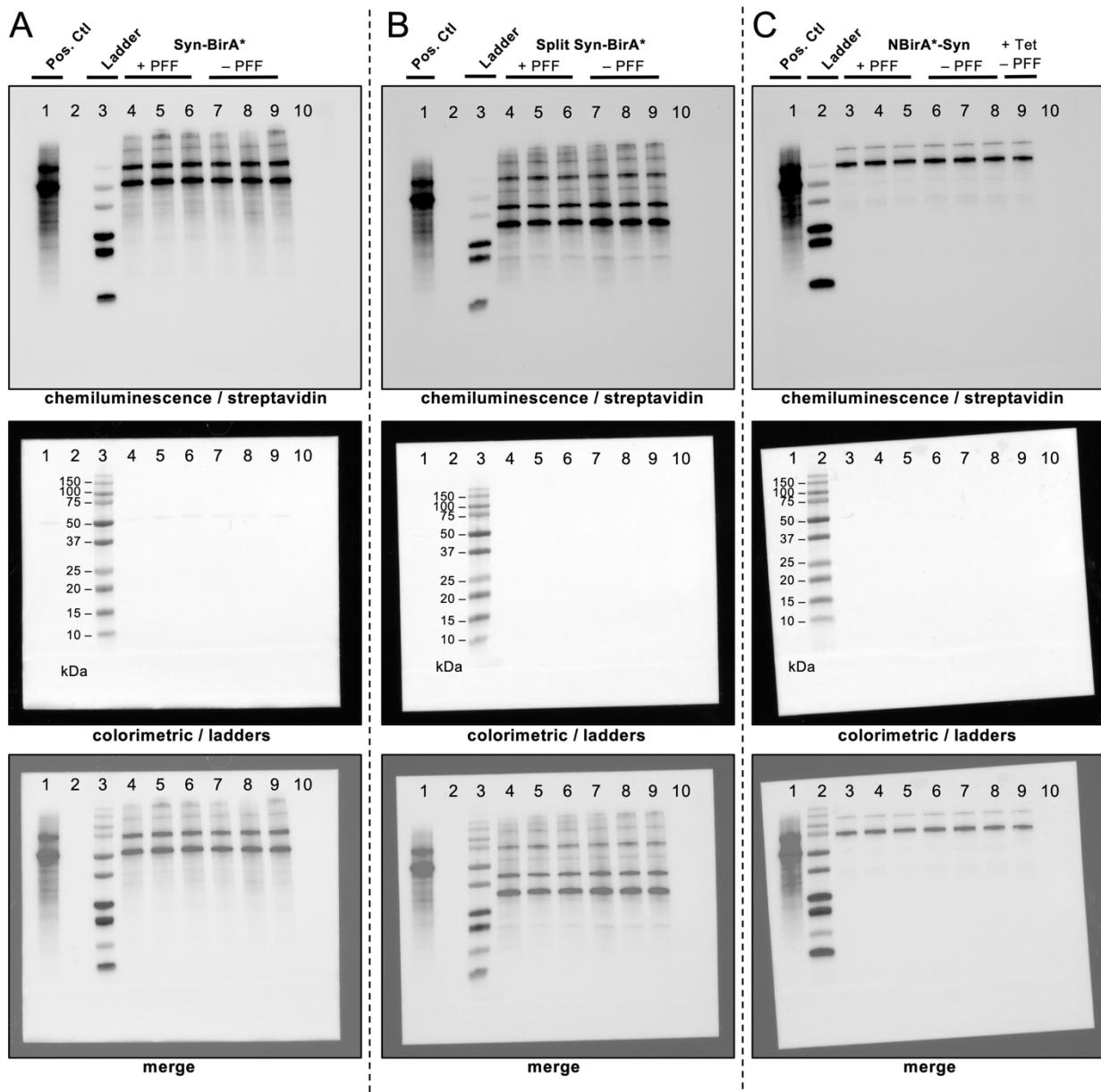
Uncropped blots used for Supp. Figure 1A. Lane 7 was chosen for Supplementary Figure 1A to demonstrate bands associated with the addition of pre-formed fibrils (PFFs) in H4 cells lacking the expression of a BirA* construct. Lanes 9 & 11 are ladders. Lanes 1, 4, 6 and 8 represent H4 cell lysates no fibrils added. Lanes 2, 3, 5 and 7 represent H4 cell lysates with the addition of PFFs. H4 Empty Cells had no construct integration or expression. Lane 10 represents a western blot positive control using Syn-BirA* cell lysate generated during a prior experiment. This control ensured the western blot procedure worked as expected and was not relevant to subsequent analysis of the blot. Chemiluminescence imaging was used.



Supplementary Fig. 6 Uncropped anti-aSyn Blots of Samples Analyzed by Proteomics

Uncropped blots used for Supp. Figure 1B. Three blots (panels A-C) were visualized via chemiluminescent imaging for the probe of interest (top), colorimetric imaging to visualize ladders (middle), and the merged images were used for analysis (bottom). In all blots, Lane 1 represents a western blot positive control using cell lysate generated during a prior experiment. This control ensured the western blot procedure worked as expected and was not relevant to subsequent analysis of the blot. Lane 10 was blank in all blots. Lysate from Syn-BirA* (A), Split Syn-BirA* (B) and NBirA*-Syn (C) samples analyzed by proteomics were run on western blot and probed for aSyn via

chemiluminescent imaging. Blots were not moved between colorimetric and chemiluminescent imaging. **C.** An additional cell lysate – H4 NBirA*-Syn cells + tetracycline was run on western blot (Panel C, Lane 9) demonstrating that no construct was expressed in the presence of tetracycline.



Supplementary Fig. 7 Uncropped Biotinylated Protein Blots of Samples Analyzed by Proteomics

Uncropped blots used for Supp. Figure 1D. Three blots (panels A-C) were visualized via chemiluminescent imaging for the probe of interest (top), colorimetric imaging to visualize ladders (middle), and the merged images were used for analysis (bottom). In all blots, Lane 1 represents a western blot positive control using cell lysate generated during a prior experiment. This control ensured the western blot procedure worked as expected and was not relevant to subsequent analysis of the blot. Lane 10 was blank in all blots. Lysate from Syn-BirA* (A), Split Syn-BirA* (B) and NBirA*-Syn (C) samples analyzed by proteomics were run on western blot and probed for biotinylated proteins via

chemiluminescent imaging using streptavidin-HRP. Blots were not moved between colorimetric and chemiluminescent imaging. **C.** An additional cell lysate – H4 NBirA*-Syn cells + tetracycline was run on western blot (Panel C, Lane 9) demonstrating that endogenous biotinylation detected was not noticeably different with or without NBirA*-Syn expression.