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#### Supplemental information

### Cell-type-specific profiling of human cellular

#### models of fragile X syndrome reveal PI3K-dependent

#### defects in translation and neurogenesis

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iPSCs

NPCs

Organoids



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## Figure S1. Characterization of induced pluripotent stem cell model of FXS. Related to STAR Methods.

(A) Immunofluorescence analysis for markers of pluripotency (OCT4, SOX2, NANOG, SSEA4, TRA1-60, and TRA1-81) and for FMRP in control and FXS iPSC lines used in this study. (B) Representative karyograms showing normal karyotypes control and FXS iPSC lines used in this study. (C) Representative images of one control and one FXS iPSC line at multiple stages of differentiation. iPSCs express stem cell markers (OCT4, SSEA4), NPCs express proliferative neural markers (Nestin, SOX2), neurons express mature neuronal markers (MAP2, vGlut1) and organoids express immature and mature neural markers (TUJ1, TBR1, SOX2) (D) *FMR1* mRNA expression measured by specific taqman assays in iPSCs, NPCs and neurons show loss of expression of *FMR1* in all patient lines (n=6 controls, 6 FXS) (E) Representative immunoblots for FMRP showing loss of FMRP protein across FXS patient iPSCs, NPCs and organoids.



Figure S2: FMRP deficiency results in elevated global protein synthesis. Related to Figure 1.

(A) BONCAT analysis in an isogenic control and FXS line shows increased incorporation of AHA in FMRP-deficient (ISO\_KO) NPCs, indicative of higher protein synthesis (Mann-Whitney test, \*P<0.05, n= 3 replicates normalized to isogenic control and FXS line shows increased incorporation of puromycin in FMRP-deficient (ISO\_KO) NPCs, indicative of higher protein synthesis (Mann-Whitney test, \*\*P<0.01, n= 3 replicates normalized to isogenic control for each replicate. Data are shown as mean  $\pm$  SEM). (C) Densitometry analysis of NPCs treated with FGF for 30'. FGF stimulation induced phosphorylation of S6K in control NPCs but not in FXS patient NPCs (Two-way ANOVA, Sidak's test, \* adj P=0.0416; n=4 CTR 4 FXS patient NPC lines from 2 CTR and 2 FXS iPSC lines) (D) Representative flow cytometry gating strategy to isolate single, live cells for analysis. (E) Representative histograms showing AHA incorporation is right-shifted in 3 FXS patient lines compared to 3 controls indicative of increased protein synthesis. Median Fluorescent Intensity (MFI) values are shown on the right. (F) Representative histograms showing puromycin incorporation is right-shifted in 3 FXS patient lines compared to 3 CTR lines indicative of increased protein synthesis in FXS. Median Fluorescent Intensity (MFI) values are shown on the right.





#### Figure S3: neurOMIP assay reveals cell-type-specific defects in translation. Related to Figure 2.

(A-D) Increased population of proliferative cells with higher protein synthesis in FXS differentiating cultures relative to controls (Mann-Whitney test, n=4 control, 6 FXS, \*\*P<0.01, \*P<0.05). Data are shown as Mean±SEM. (C-H) Decreased population of non-proliferating cells in FXS differentiating cultures relative to controls. No significant difference in puromycin incorporation between control and FXS cultures (Mann-Whitney test, n=4 control, 6 FXS, \*\*P<0.01, \*P<0.05). Data are shown as Mean±SEM. (I) Fluorescence-minus-one (FMO) controls setup for each neurOMIP experiment helps to establish gates for each marker. (J) Representative histograms of FMO controls showing positive and negative gating for each marker. Puro histogram shows FMO for puro (Red trace) and "no puro" control (Blue trace). "No puro" was used to set positive and negative gates for puromycin.



# Figure S4: Transcriptomic analysis reveals dysregulation of pathways related to neurogenesis, neural cell fate commitment and ERK1/ERK2/MAPK signaling and increased proliferation in FXS can be corrected with PI3K and S6K1 inhibitors. Related to Figure 3 and Figure 4.

(A) Representative contour plots image of single, live proliferating NPCs (Nestin-positive,TUJ1negative) in one control and one FXS patient line. (B) Increased active proliferation in FXS, evidenced by more Ki67+NESTIN+ positive cells in FXS patient NPCs (Mann-Whitney test, \*\*P<0.01, n= 3 CTR, 3 FXS lines) and isogenic engineered FXS line (unpaired t test, \*P<0.05, n= 3 replicates). (C) Volcano plot of differentially expressed genes in D28 FXS patient organoids versus control organoids. (D) Gene ontology (GO) analysis of DEGs in FXS. Downregulated genes in FXS are enriched for GO terms related to processes of neural cell fate commitment and neurogenesis, while upregulated genes in FXS are enriched for GO terms related to regulation of ERK/MAPK signaling and cell proliferation is up in FXS. (E) Acute treatment paradigm using TGX-221 followed by neurOMIP analysis (F,G) Acute TGX treatment reduces (F) Ki67 and (G) puromycin signals in proliferative populations. (H) Acute treatment paradigm does not correct increased NES+GFAP+ and NES+SOX2+ populations in FXS patient cultures. (I) Chronic treatment paradigm using TGX-221 followed by neurOMIP analysis (J) Chronic treatment reduces but does not significantly normalize increased NES+GFAP+ population in FXS patient cultures. (K) No significant effect of TGX-221 treatment on GFAP+MAP2- cells in FXS cultures. (L) Chronic TGX treatment normalizes Ki67 in NES+GFAP+ and NES+SOX2+ proliferative populations in FXS cultures. n= 4 CTR, 4 FXS NPCs; two-way ANOVA, Tukey's test, \*\*\* adj P<0.001, \*\* adj P<0.01, \* adj P<0.05. All data are shown as mean  $\pm$  SEM.

I.D.	Source material	Genotype	Source
SC173	Fibroblast	CTR	P. H. Schwartz (CHOC)
SC176	Fibroblast	CTR	P. H. Schwartz (CHOC)
v36	Fibroblast	CTR	E.M. Berry-Kravis (Rush University)
v44	Fibroblast	CTR	E.M. Berry-Kravis (Rush University)
v48	Fibroblast	CTR	E.M. Berry-Kravis (Rush University)
SC128	Fibroblast	FXS	P.H. Schwartz (CHOC)
CH095	Fibroblast	FXS	C.M. Hales (Emory University)
SO02	Fibroblast	FXS	E.M. Berry-Kravis (Rush University)
SO03	Fibroblast	FXS	E.M. Berry-Kravis (Rush University)
SO04	Fibroblast	FXS	E.M. Berry-Kravis (Rush University)
SO05	Fibroblast	FXS	E.M. Berry-Kravis (Rush University)
SO10	Fibroblast	FXS	E.M. Berry-Kravis (Rush University)
FXSB2	iPSC	FXS	S.T. Warren (Emory University)
C1-2	iPSC (Isogenic 1)	CTR (engineered)	S.T. Warren (Emory University)
FXS	iPSC (Isogenic 1)	FXS	S.T. Warren (Emory University)
F33F7	ESC (Isogenic 2)	CTR	L. Chen, M. Wernig (Stanford)
F33cKO	ESC (Isogenic 2)	FXS (engineered)	L. Chen, M. Wernig (Stanford)
UCD-17-02	Frontal Cortex	Control	V. Martinez-Cerdeño (UC Davis)
UCD-17-07	Frontal Cortex	Control	V. Martinez-Cerdeño (UC Davis)
UCD-18-04	Frontal Cortex	Control	V. Martinez-Cerdeño (UC Davis)
1031-08-GP	Frontal Cortex	Full Mutation	V. Martinez-Cerdeño (UC Davis)
1018-10-RH	Frontal Cortex	Full Mutation	V. Martinez-Cerdeño (UC Davis)
1031-09-LZ	Frontal Cortex	Full Mutation	V. Martinez-Cerdeño (UC Davis)

Table S1: Control and Subject patient material used in this study. Related to STARMethods.

ID	Cells generated			Experiments <sup>a</sup>					
1.D.	iPS	NPC	Organoid	BON	SUn	OMIP	EdU	WB	IF
SC173	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$			-		-
SC176	$\checkmark$	$\checkmark$	-	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$		$\checkmark$
v36	$\checkmark$	-	$\checkmark$	-	-	-	-	-	-
v44	$\checkmark$	$\checkmark$	-	-		$\checkmark$	-		$\checkmark$
v48	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$
SC128			-	$\checkmark$		$\checkmark$		$\checkmark$	
CH095			-	$\checkmark$		$\checkmark$		$\checkmark$	
SO02	$\checkmark$		-	$\checkmark$	$\checkmark$	$\checkmark$	-	$\checkmark$	-
SO03			$\checkmark$	-		$\checkmark$	-	-	-
SO04			$\checkmark$	-	$\checkmark$	$\checkmark$	-	-	-
SO05				$\checkmark$	$\checkmark$	$\checkmark$	-	$\checkmark$	$\checkmark$
SO10	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$			$\checkmark$
FXSB2	-	-	$\checkmark$	-	-	-	-	-	-
C1-2	-		$\checkmark$	$\checkmark$		-		$\checkmark$	-
FXS	-		$\checkmark$	$\checkmark$		-			-
F33F7	_		-	$\checkmark$		$\checkmark$			-
F33cKO	-	$\checkmark$	-	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$		-
UCD-17-02									
UCD-17-07								$\checkmark$	
UCD-18-04									
1031-08-GP									
1018-10-RH									
1031-09-LZ									

Table S2: Summary of cell lines/patient tissue used in experiments. Related to STAR Methods.

<sup>a</sup> BON= BONCAT western blots; SUn= SUnSET western blots; EdU= EdU immunofluorescence; OMIP= neurOMIP flow cytometry assay; WB= western blotting, IF= immunofluorescence

Antibody	uL/test	Fluorophore	Company	Purpose
Ki67	0.25	PE-Cy7	<b>BD</b> Biosciences	Proliferation quantification
Puromycin	0.5	Alexa 488	Millipore	Protein synthesis quantification
Nestin	1	V450	BD Biosciences	Neural Stem Cell/Progenitor
SOX2	1	PerCP-Cy5.5	<b>BD</b> Biosciences	Neural Stem Cell
DCX	1	PE	<b>BD</b> Biosciences	Neuroblast/Immature Neuron
MAP2	1	Alexa 647	<b>BD</b> Biosciences	Mature Neuron
GFAP	0.5	Alexa 700	<b>BD</b> Biosciences	Glial Cell

 Table S3: neurOMIP antibody panel. Related to Figure 2 and Figure S3.