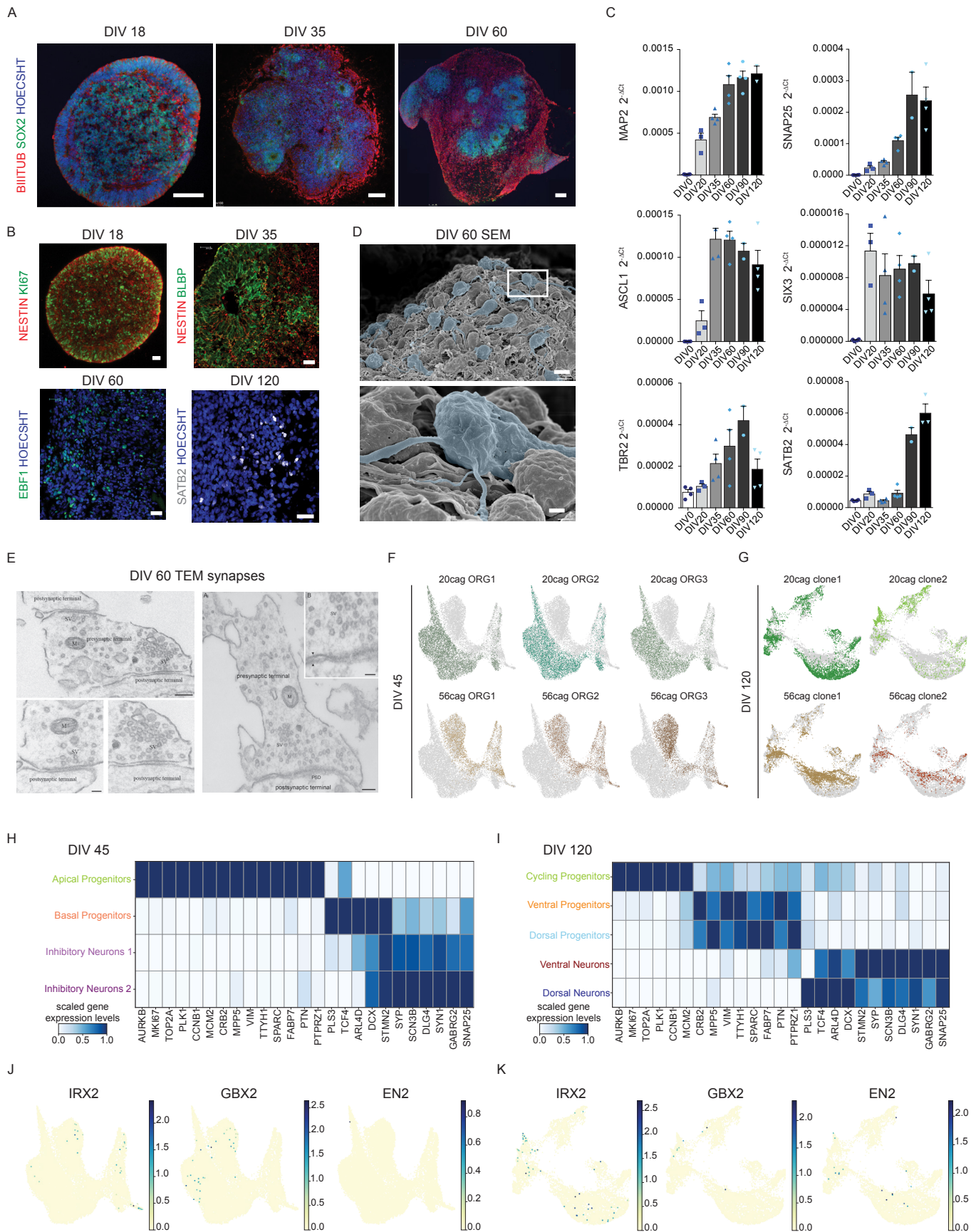


Supplementary Information for

**HUNTINGTON'S DISEASE CELLULAR PHENOTYPES ARE RESCUED NON-CELL
AUTONOMOUSLY BY HEALTHY CELLS IN MOSAIC TELENCEPHALIC
ORGANOIDS**

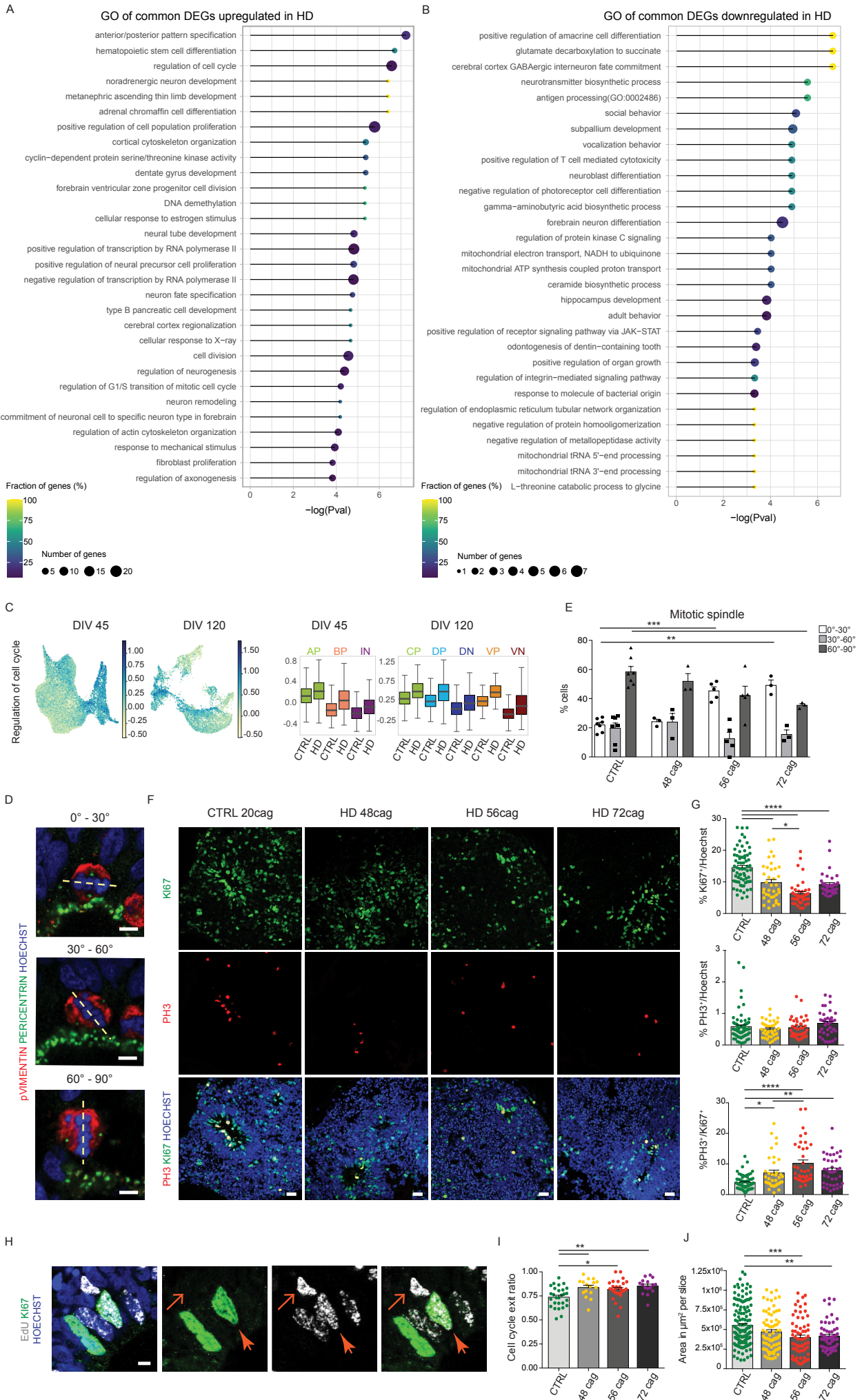
Maura Galimberti, Maria R Nucera, Vittoria D Bocchi, Paola Conforti, Elena Vezzoli, Matteo Cereda, Camilla Maffezzini, Raffaele Iennaco, Andrea Scolz, Andrea Falqui, Chiara Cordiglieri, Martina Cremona, Ira Espuny-Camacho, Andrea Faedo, Dan P Felsenfeld, Thomas F Vogt, Valeria Ranzani, Chiara Zuccato, Dario Besusso and Elena Cattaneo

This file includes Supplementary Figs. 1 to 10 and Tables 1-2

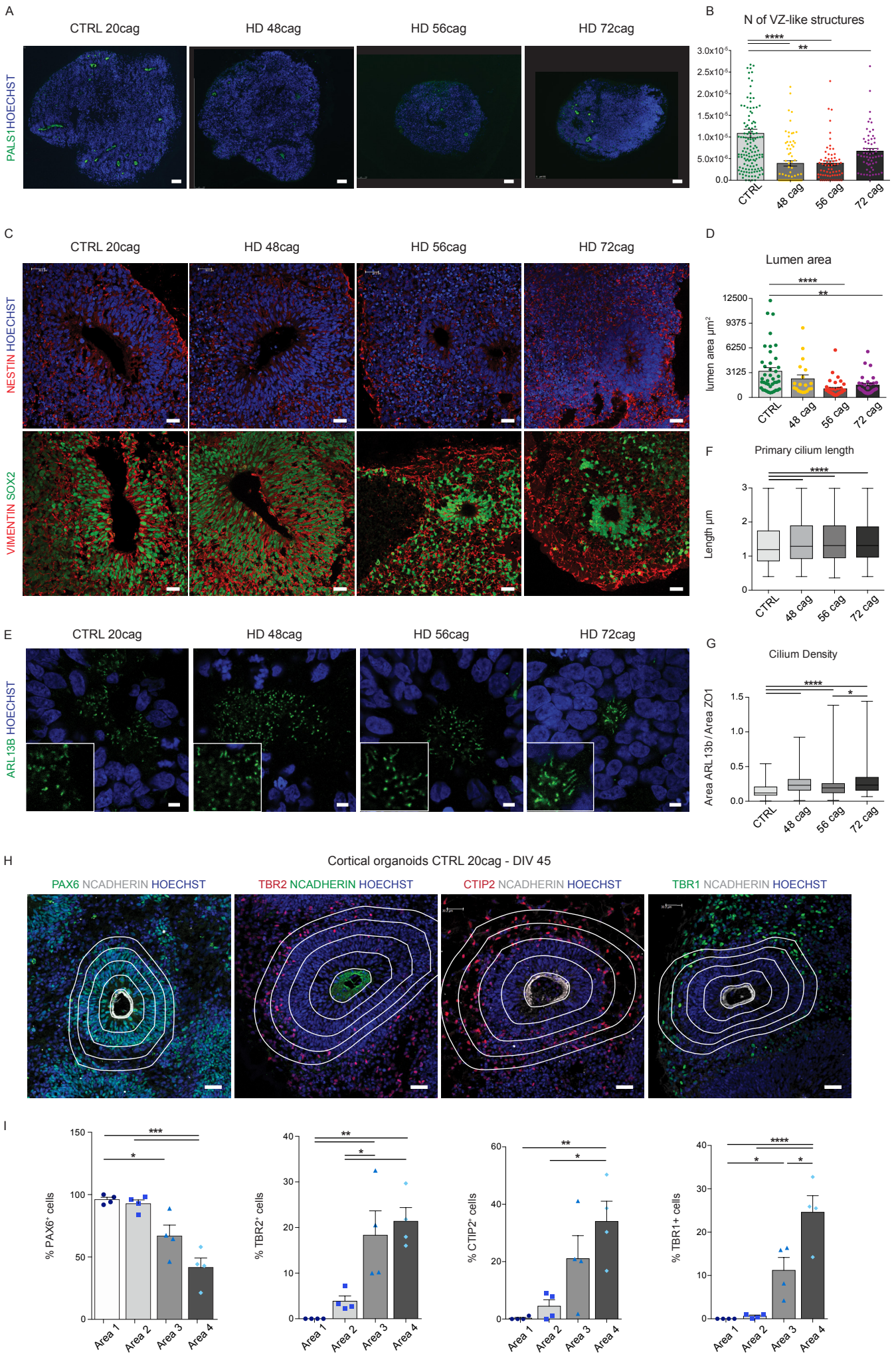


Supplementary Fig1 – Telencephalic organoids protocol and quality controls (A) Immunohistochemistry analyses of telencephalic organoids during differentiation. DIV 18, 35, and 60 for BIIIITUBULIN and SOX2. Scale bars =100 μm (B) Immunohistochemistry analyses of telencephalic organoids during differentiation. DIV 18 for NESTIN and KI67; DIV 35 for NESTIN and BLBP; DIV 60 for EBF1 and HOECHST; DIV 120 for SATB2 and HOECHST. Scale bars =100 μm (C) q-PCR for MAP2, SNAP25, ASCL1, SIX3, TBR2, and SATB2 on CTRL organoids at DIV 0, 20, 35, 60, 90, and 120 of differentiation. (N = 3/4 independent biological replicates; error bars represent \pm SEM) (D) Pseudo-colored scanning electron microscopy (SEM) images of internal part of CTRL (20CAG) organoids at DIV 60. Scale bars =5 μm in lower magnification on the top and =1 μm in higher magnification at the bottom (E) Transmission electron microscopy (TEM) images of synapses of CTRL (20CAG) organoids at DIV 60 with details of pre- and post- synaptic terminals and synaptic vesicles (SV). Scale bars =100nm in lower magnification and =50nm in higher magnification (F) UMAP plots of scRNAseq analyses on CTRL (20CAG) and HD (56CAG) organoids at DIV 45 with louvain algorithm of each individual organoid (3 per genotype) (G) UMAP plots of scRNAseq analyses on CTRL (20CAG) and HD (56CAG) organoids at DIV 120 with louvain algorithm of each individual sample (pool of 10 organoids for each cell line, 2 cell lines per genotype) (H-I) Heatmap of gene expression of neuronal progressive maturation genes in each subpopulation of organoids at DIV 45 and DIV 120 (J-K) UMAP plots for specific genes of caudal brain regions (IRX2, GBX2, and EN2) at DIV 45 and DIV 120.

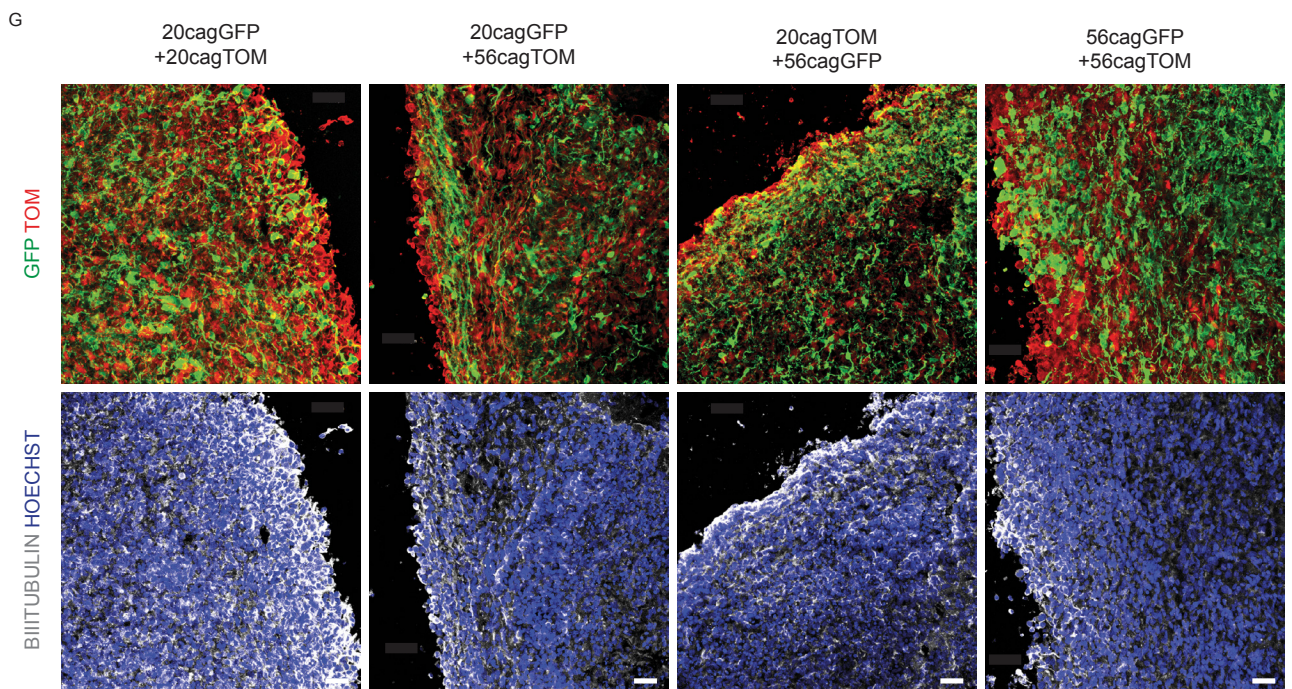
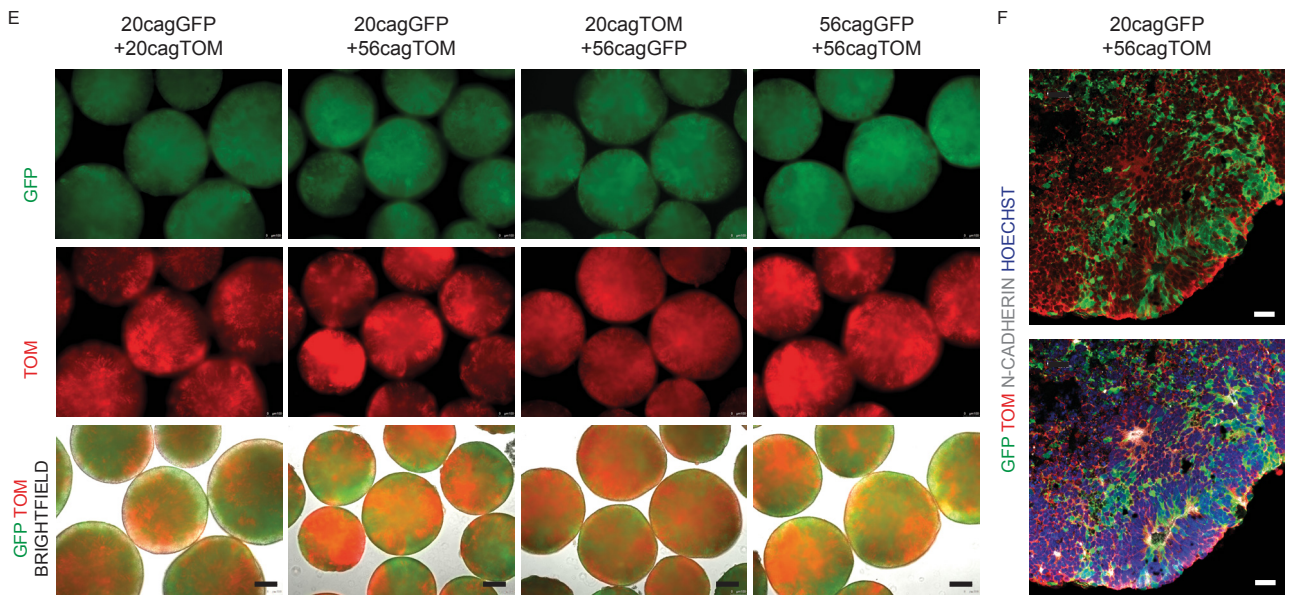
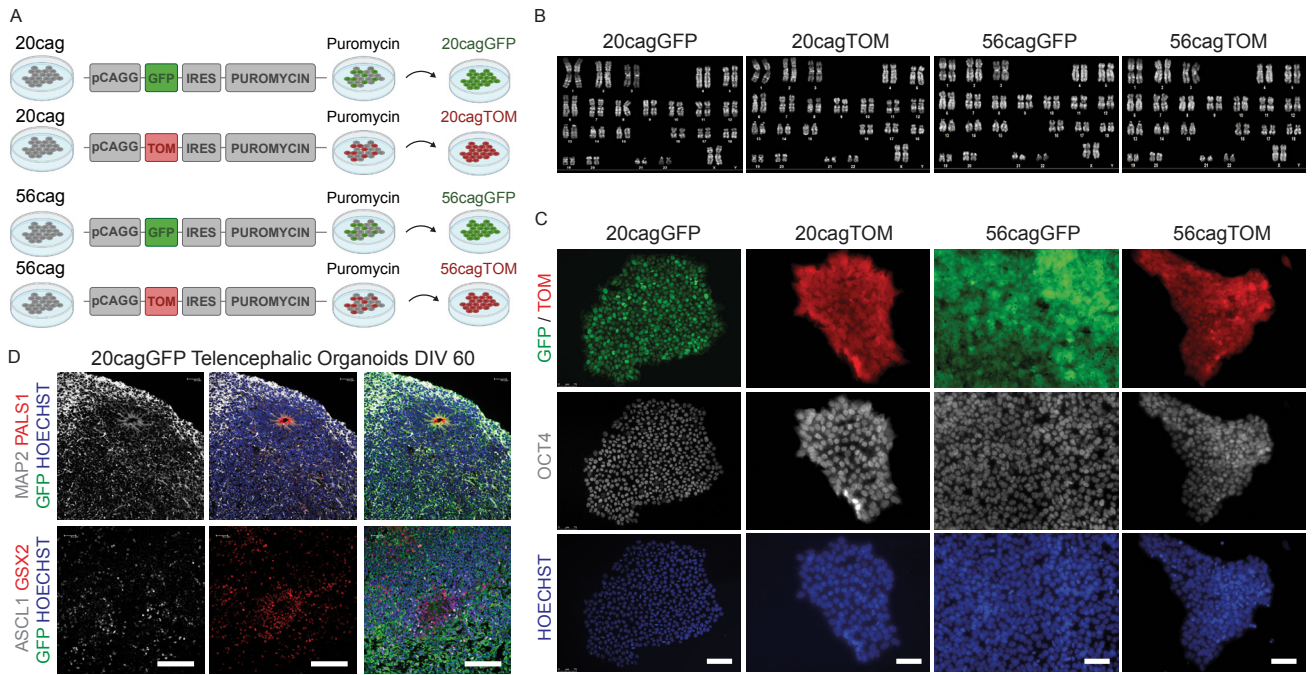
Supplementary Fig2 –Telencephalic organoids comparison with human fetal data, other organoids protocols, and HD postmortem data (A) Dotplot comparing our subpopulations from organoids at DIV 45 with human fetal cell types and tissues from Braun and colleagues.²⁹ **(B)** Dotplot comparing our subpopulations from organoids at DIV 120 with human fetal cell types and tissues from Braun et al.²⁹ **(C)** Heatmap comparing our subpopulations from both DIV 45 and DIV 120 organoids with published organoid protocols from the Human Neural Organoid Cell Atlas (HNOCA)³⁰ performed with the CellHint tool⁸⁵ **(D)** Venn diagram illustrating DEGs between CTRLs and HD organoids, indicating which are in common between DIV 45, DIV 120, and HD human postmortem brain tissues from Lee and colleagues.⁷



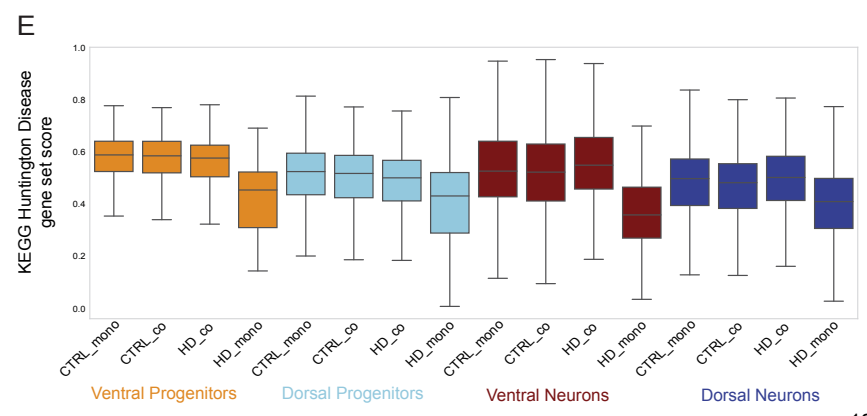
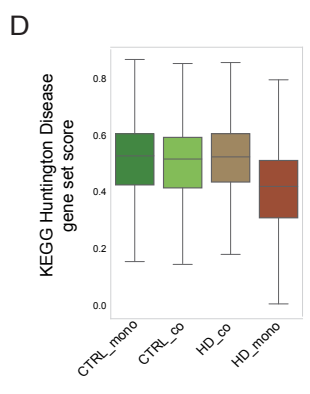
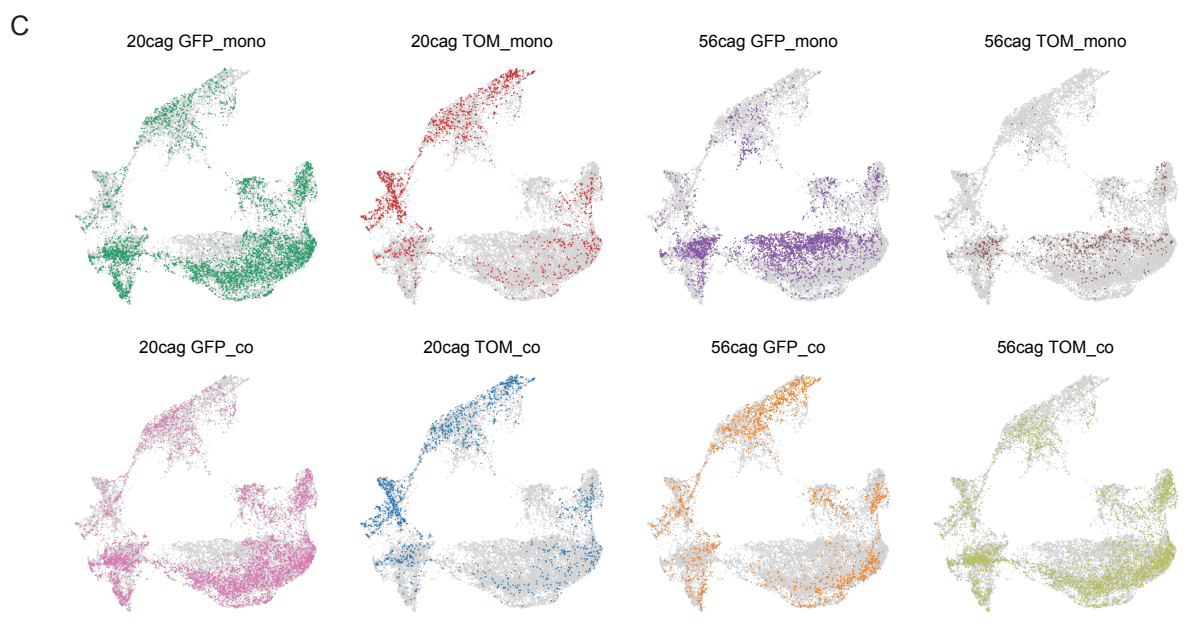
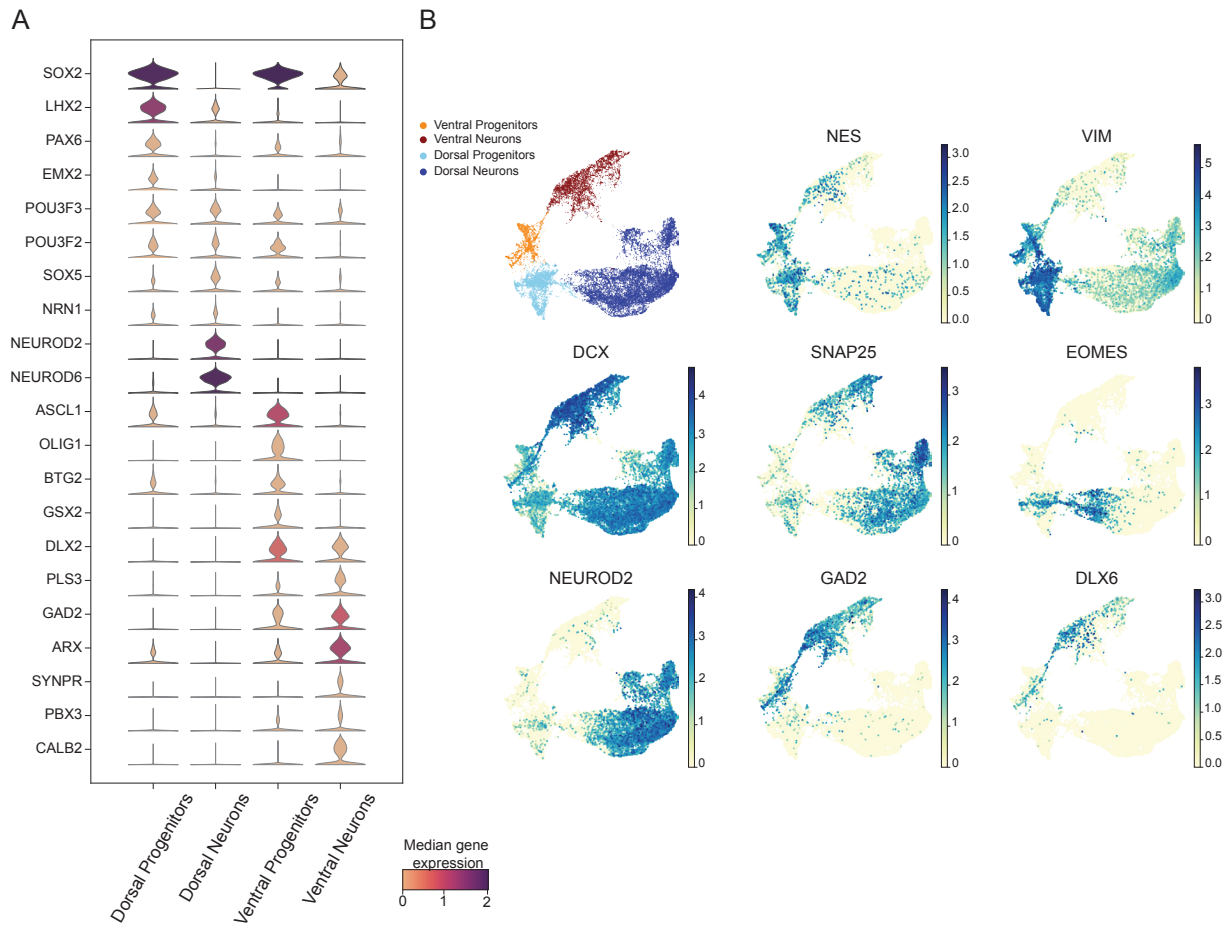
Supplementary Fig3– DEGs in HD organoids and cell cycle alterations (A-B) Top GO terms of the upregulated and downregulated genes in HD organoids, common between DIV 45 and 120 **(C)** UMAP and boxplot of module scores of DEGs belonging to “regulation of cell cycle” which is upregulated in HD organoids. Abbreviations: AP=Apical Progenitors; BP=Basal Progenitors; IN=Inhibitory Neurons; CP=Cycling Progenitors; DP=Dorsal Progenitors; DN=Dorsal Neurons; VP=Ventral Progenitors; VN=Ventral Neurons **(D)** Immunohistochemistry analyses and scheme of mitotic spindle in organoids at DIV 35 for pVIMENTIN and PERICENTRIN. Division are horizontal (angle between 0 and 30 degree), oblique (30-60) and vertical (60-90). Scale bar =5µm **(E)** Percentage of cells in each division (manual measurement with ImageJ. Unpaired t test, Welch’s correction, **p<0,01; ***p<0,001. N ≥ 100 cells from 10 organoids of 3/4 independent biological replicates) **(F)** Immunohistochemistry analyses of CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 for PH3 and KI67. Scale bar =30µm **(G)** Percentage of PH3+ and KI67+ cells (automatic counting with Cell Profiler. Anova One Way, Bonferroni post test, *p<0,05, ** p< 0,01, ****p<0,0001. N=12 organoids from 3 independent biological replicates) **(H)** Immunohistochemistry analyses of organoids at DIV 45 for EdU and KI67 after EdU treatment. Example of cells in active cell cycle (EdU+KI67+ orange arrowheads) and cells that have exited the cell cycle (EdU+KI67- orange arrows). Scale bar =5µm **(I)** Cell cycle exit ratio at DIV 45 (N cells EdU+KI67- / N cells EdU+) of CTRL (20CAG) and HD (48, 56, and 72 CAG) organoids (automatic quantification with Cell Profiler. Anova One Way, Bonferroni post test, *p<0,05, **p<0,01. N= 5/8 organoids of 1/2 independent biological replicates) **(J)** Quantification of the organoids area of CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 (manual measurement. Anova One Way, Bonferroni post test. **p<0,01; ***p<0,001. N= 10 organoids from 4 independent biological replicates).



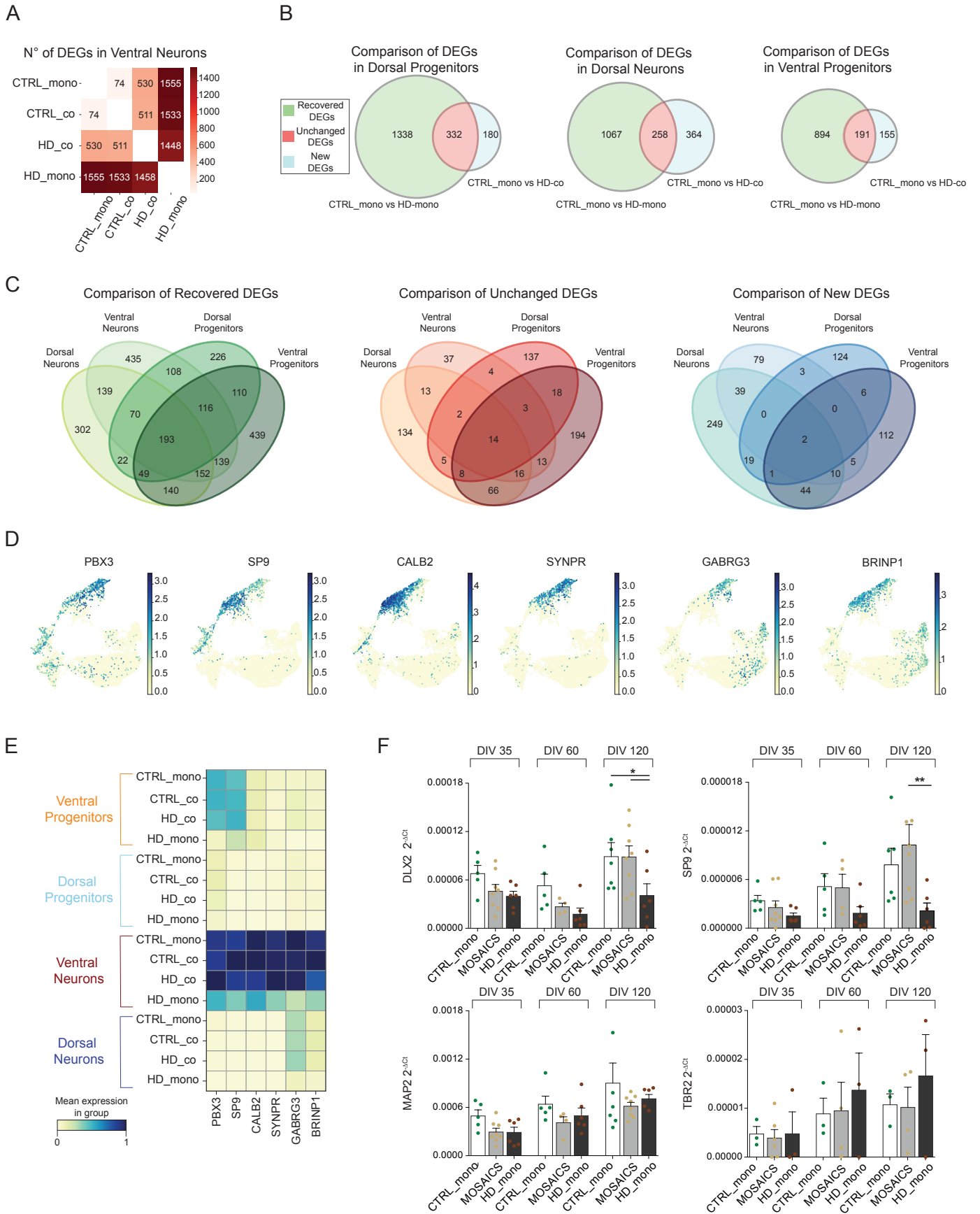
Supplementary Fig4 – Cytoarchitectural organization defects in HD organoids (A) Immunohistochemistry analyses of CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 for PALS1. Scale bar =100 μ m (B) Numbers of VZ-like structures per area of each organoids' slice at DIV 35 (Manual counting. Anova One Way, Bonferroni post test. **p<0,01; ****p< 0,0001. N \geq 30 slices for each cell line, from 10 organoids of 4 independent biological replicates) (C) Immunohistochemistry analyses of CTRL (20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 for NESTIN, VIMENTIN, and SOX2. Scale bar =30 μ m (D) Area of the VZ-like structures lumens in CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 of differentiation (Manual measurement. Anova One Way, Bonferroni post test, **p<0,01; ****p<0,0001. N \geq 30 structures, from 12 organoids of 2/3 independent biological replicates.) (E) Immunohistochemistry analyses of CTRL (20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 60 for ARL13B. Scale bar =10 μ m (F-G) Quantification of primary cilia length (F) and primary cilia density (G) calculated as cilia's area (ARL13b) over the area of the lumens (ZO1) in CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 60 (Automatic quantification with NIS software. Anova One Way, Bonferroni post test, *p<0,05; ****p<0,0001. N = 15-20 structures from 8/12 organoids of 2/3 independent biological replicates for each cell line) (H) Immunohistochemistry analyses of CTRL (20CAG) cortical organoids at DIV 45 for PAX6, TBR2, CTIP2, TBR1 and N-CADHERIN. Scale bar =30 μ m (I) Numbers of cells positive for each marker in each concentric area. (Manual measurement. Anova One Way, Bonferroni post test, * p< 0,05; ** p< 0,01; ***; p<0,001 ****; p<0,0001. N= 4 VZ structures from 4 organoids of 1 biological replicate).



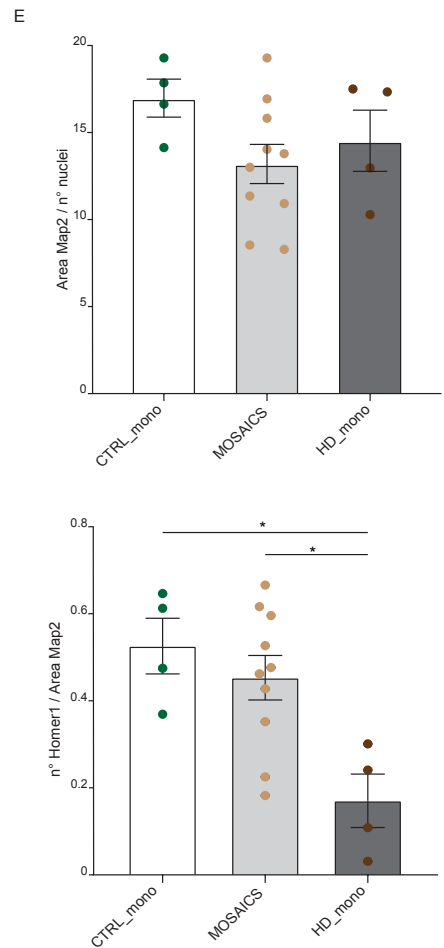
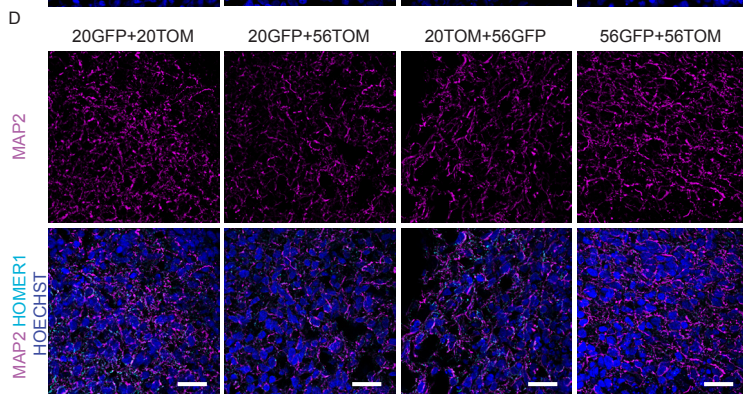
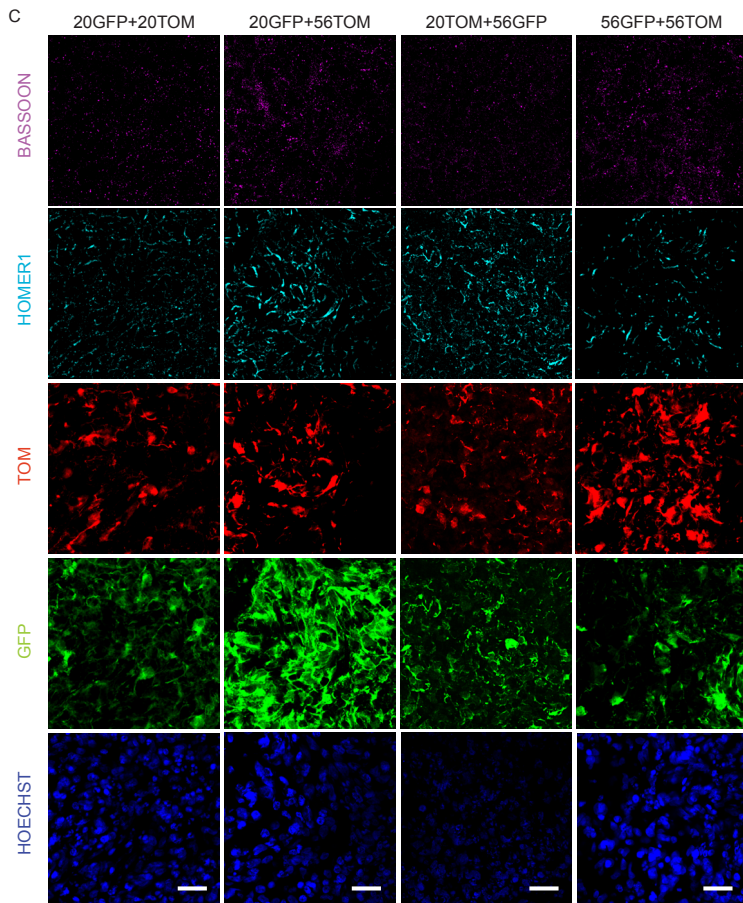
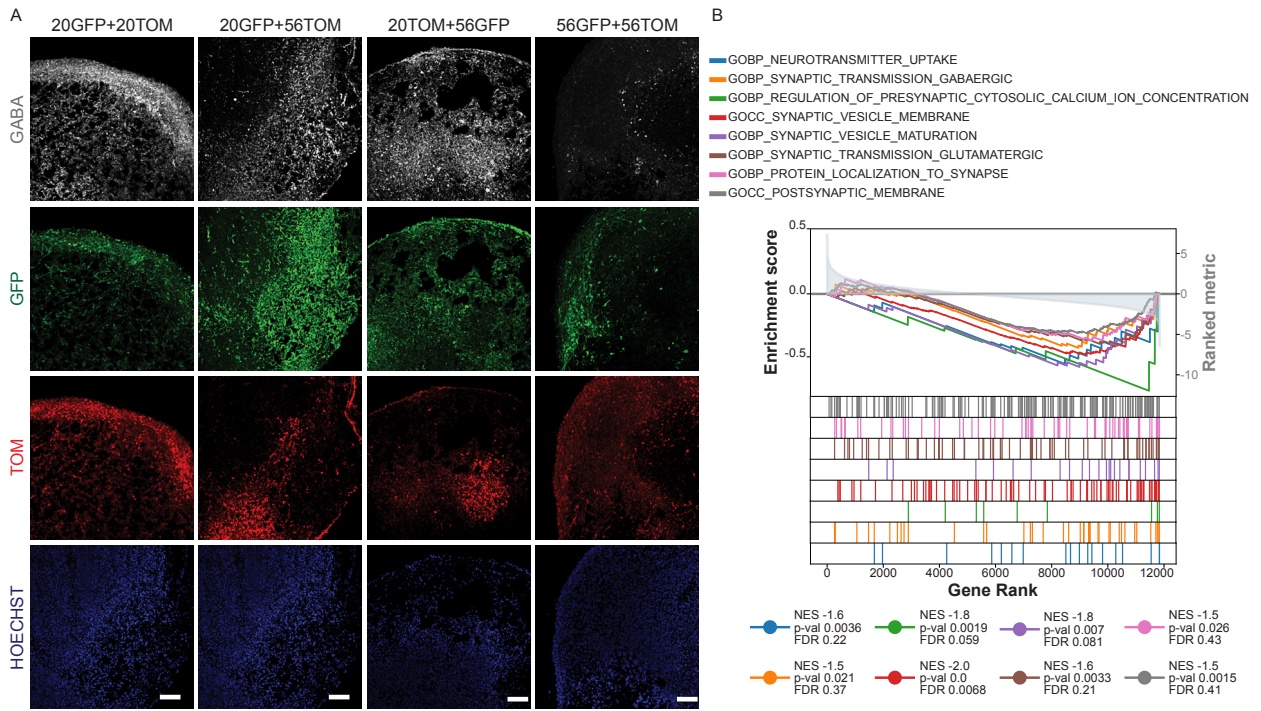
Supplementary Fig5 – Quality controls of mosaic organoids (A) Experimental scheme for the generation of GFP and TOM clones of both CTRL 20CAG and HD 56CAG cell lines. Created with BioRender.com, released under a Creative Commons Attribution-NonCommercial-NoDerivs 4.0 International license (B) Q-banding karyotype analyses of GFP and TOM clones of both CTRL 20CAG and HD 56CAG cell lines in metaphase (C) Immunohistochemistry analyses of GFP and TOM clones of both CTRL 20CAG and HD 56CAG cell lines in pluripotency for GFP, TOM, OCT4, and HOECHST. Scale bar =100µm (D) Immunohistochemistry analyses of organoids from 20CAG-GFP line at DIV 60 for MAP2, PALS1, GSX2, ASCL1, GFP, and HOECHST. Scale bar =100µm (E) Live imaging pictures of mosaic organoids at DIV 18 to check for maintenance of GFP or TOM fluorescence. Scale bar =150µm (F) Immunohistochemistry analyses of mosaic organoids composed of 20CAG-GFP and 56CAG-TOM at DIV 60 for GFP, TOM and N-CADHERIN showing mosaicism of cell lines in the VZ-like structures. Scale bar =30µm (G) Immunohistochemistry analyses of all mosaic organoids at DIV 120 for GFP, TOM and BIITUBULIN to check differentiation. Scale bar =30µm.



Supplementary Fig6 – scRNAseq characterization of mosaic organoids (A) Violin plot of gene expression of selective markers per cell subpopulation at DIV 120 (B) UMAP plots of scRNAseq analyses on mosaic organoids at DIV 120 with louvain algorithm for specific markers of progenitors (NES, VIM), neurons (DCX, SNAP25), dorsal identity (EOMES, NEUROD2), and ventral identity (GAD2, DLX6) (C) UMAP plots of scRNAseq analyses on mosaic organoids at DIV 120 of each cell line clone: 20CAG-GFP_mono, 20CAG-GFP_co, 20CAG-TOM_mono, 20CAG-TOM_co, 56CAG-GFP_mono, 56CAG-GFP_co, 56CAG-TOM_mono, 56CAG-TOM_co (pool of 10 organoids per culture samples) (D) Boxplot showing the gene set score for genes belonging to the KEGG pathway in mosaic organoids at bulk level (E) Boxplot illustrating the gene set score for genes belonging to the KEGG pathway in mosaic organoids at single cell level



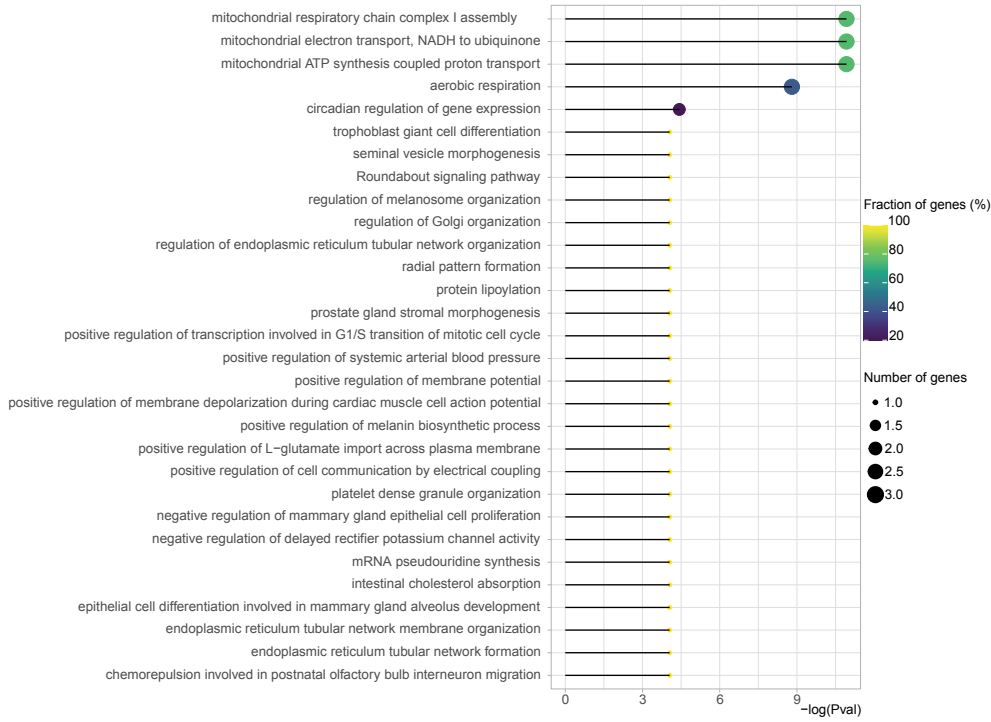
Supplementary Fig3– DEGs in HD organoids and cell cycle alterations (A-B) Top GO terms of the upregulated and downregulated genes in HD organoids, common between DIV 45 and 120 **(C)** UMAP and boxplot of module scores of DEGs belonging to “regulation of cell cycle” which is upregulated in HD organoids. Abbreviations: AP=Apical Progenitors; BP=Basal Progenitors; IN=Inhibitory Neurons; CP=Cycling Progenitors; DP=Dorsal Progenitors; DN=Dorsal Neurons; VP=Ventral Progenitors; VN=Ventral Neurons **(D)** Immunohistochemistry analyses and scheme of mitotic spindle in organoids at DIV 35 for pVIMENTIN and PERICENTRIN. Division are horizontal (angle between 0 and 30 degree), oblique (30-60) and vertical (60-90). Scale bar =5µm **(E)** Percentage of cells in each division (manual measurement with ImageJ. Unpaired t test, Welch’s correction, **p<0,01; ***p<0,001. N ≥ 100 cells from 10 organoids of 3/4 independent biological replicates) **(F)** Immunohistochemistry analyses of CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 for PH3 and KI67. Scale bar =30µm **(G)** Percentage of PH3+ and KI67+ cells (automatic counting with Cell Profiler. Anova One Way, Bonferroni post test, *p<0,05, ** p< 0,01, ****p<0,0001. N=12 organoids from 3 independent biological replicates) **(H)** Immunohistochemistry analyses of organoids at DIV 45 for EdU and KI67 after EdU treatment. Example of cells in active cell cycle (EdU+KI67+ orange arrowheads) and cells that have exited the cell cycle (EdU+KI67- orange arrows). Scale bar =5µm **(I)** Cell cycle exit ratio at DIV 45 (N cells EdU+KI67- / N cells EdU+) of CTRL (20CAG) and HD (48, 56, and 72 CAG) organoids (automatic quantification with Cell Profiler. Anova One Way, Bonferroni post test, *p<0,05, **p<0,01. N= 5/8 organoids of 1/2 independent biological replicates) **(J)** Quantification of the organoids area of CTRL (parental and 20CAG) and HD (48, 56 and 72 CAG) organoids at DIV 35 (manual measurement. Anova One Way, Bonferroni post test. **p<0,01; ***p<0,001. N= 10 organoids from 4 independent biological replicates).



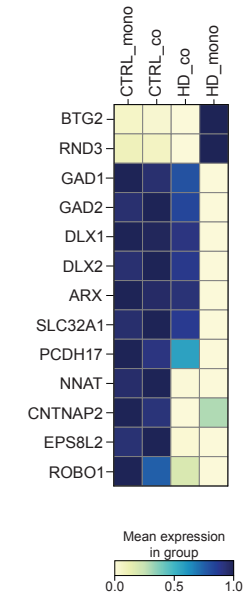
Supplementary Fig8 – GABAergic neurons and synapse density recovery in HD_co grown with CTRL cells (A) Immunohistochemistry analyses of mosaic organoids at DIV 120 for GABA, GFP, TOM and HOECHST. Scale bar =100µm. (B) GSEA for terms linked to synapses in ventral neurons of HD_mono compared to CTRL_mono. (C) Immunohistochemistry analyses of mosaic organoids at DIV 120 for HOMER1, BASSOON, GFP, TOM and HOECHST. Scale bar =25µm (D) Immunohistochemistry analyses of mosaic organoids at DIV 120 for HOMER1, MAP2 and HOECHST. Scale bar =25µm (E) Automatic quantification of Map2 positive area (on top) and for Homer1 amount over Map2 area (on the bottom) (N=4 organoids from 1 independent biological replicates. error bars represent ± SEM. Anova One Way, Bonferroni post test. *p<0.05).

A

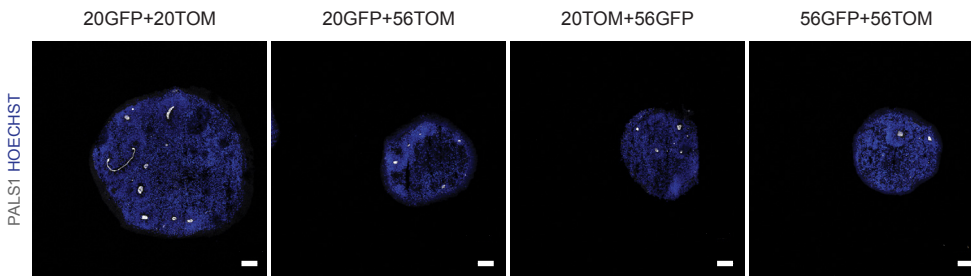
GO of Unchanged DEGs in Ventral Neurons



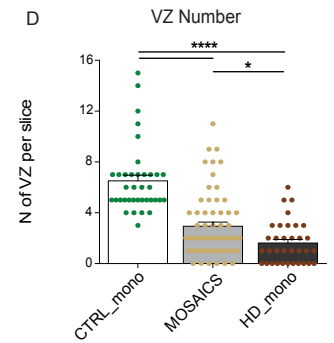
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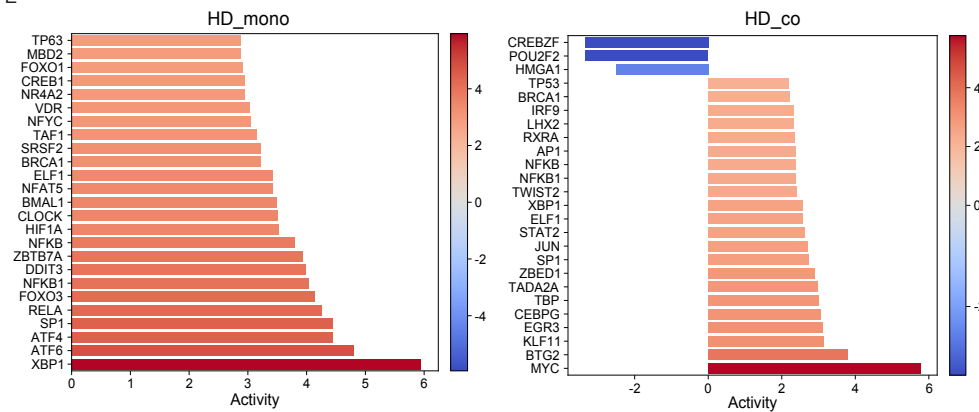
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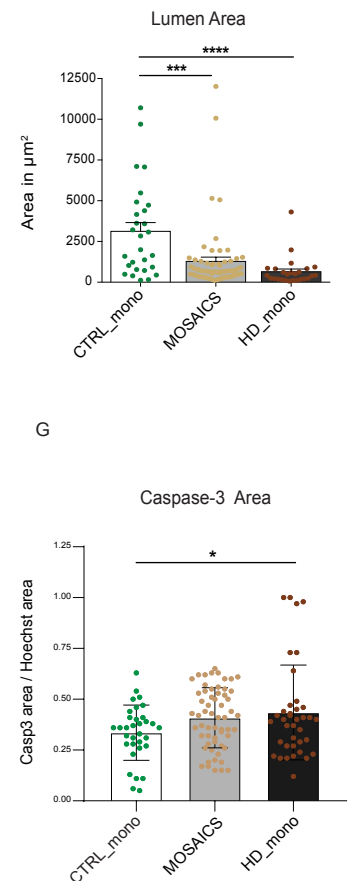
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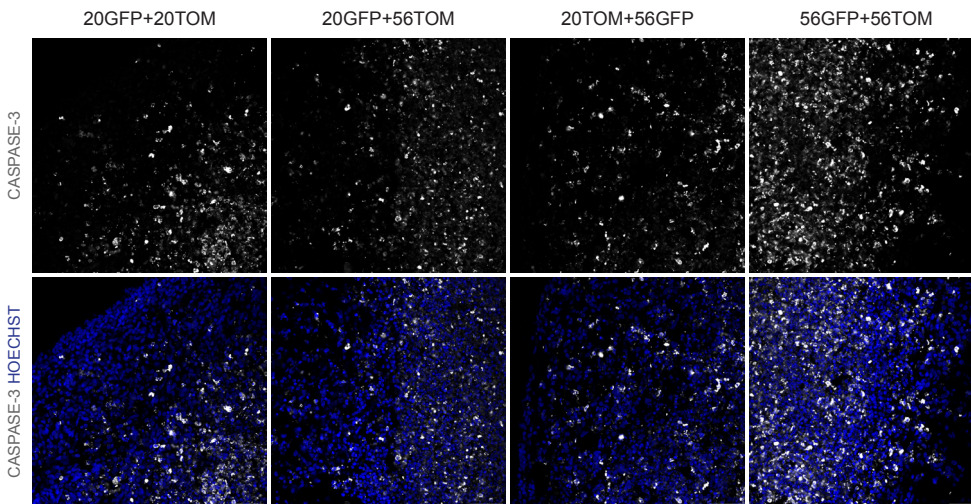
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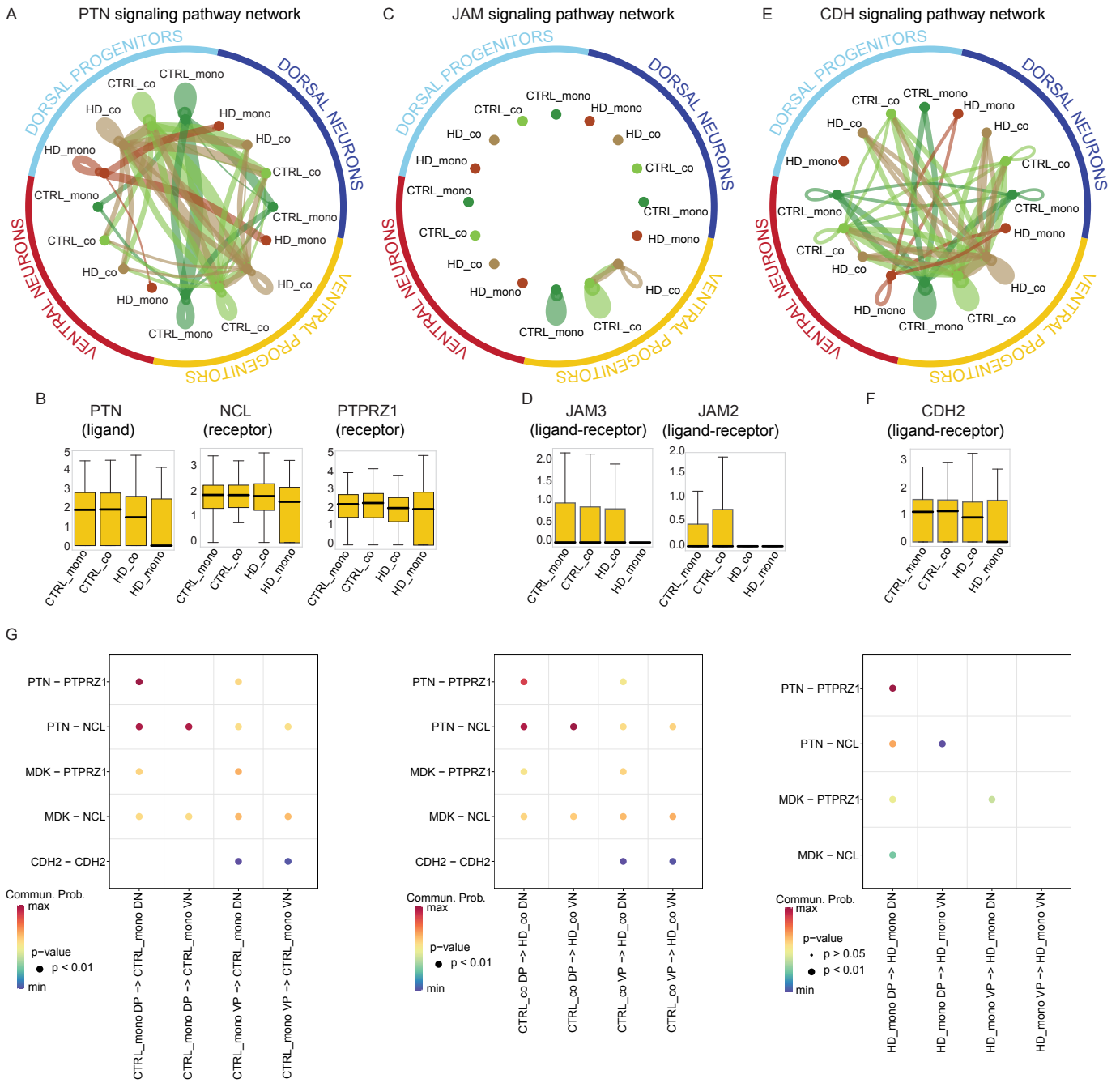
G



F



Supplementary Fig9 – The unchanged DEGs in HD_unravel cell-autonomous pathways (A) Results of GO analysis performed with R package topGO for the Unchanged DEGs (not rescued) in ventral neurons (B) Heatmap of selected genes from top DEGs which show non-cell-autonomous rescue (BTG2, RND3, GAD1, GAD2, DLX1, DLX2, ARX, SLC32A1) or not rescued (PCH17, NNAT, CNTNAP2, EPS8L2, ROBO1) in HD_co (C) Immunohistochemistry analyses of CTRL, HD and co-culture mosaic organoids at DIV 35 for PALS1 and HOECHST to visualize VZ-like structures. Scale bar =100µm (D) Quantification of VZ-like structures number per slice, and area of VZ-like structures lumens (Manual measurement. N ≥ 30 slices for each condition, from 10 organoids of 3 independent biological replicates, error bars represent ± SEM. Anova One Way, Bonferroni post test. *p<0,05; **p<0,001; ***p<0,0001) (E) Transcription Factor activity inference analysis performed in pseudo-bulk with Decoupler for the most active TFs in HD_mono compared to CTRL_mono and HD_co compared to CTRL_mono (F) Immunohistochemistry analyses of mosaic organoids at DIV 120 for CASPASE-3 and HOECHST. Scale bar = 30µm (G) Quantification of CASPASE3 positive area (from slices for immunohistochemistry) in CTRL, HD and co-culture mosaic organoids (Automatic quantification. N ≥ 30 slices for each condition, from 5 organoids of 1 independent biological replicate, error bars represent ± SEM. Anova One Way, Tukey post test. *p<0,05).



Supplementary Fig10 – Progenitors communications pathways rescued in mosaic organoids (A) CellChat circle plot showing PTN signalling network of communications between all subpopulations and conditions (B) Box plots of gene expression for PTN ligand and his receptors NCL and PTPRZ1. (C) CellChat circle plot showing JAM signalling network of communications between all subpopulations and conditions (D) Box plots of gene expression for JAM3 and JAM2 transmembrane ligand-receptor (E) CellChat circle plot showing CDH2 signalling network of communications between all subpopulations and condition (F) Box plot of gene expression for CDH2 transmembrane ligand-receptor (G) CellChat bubble plots of gene expression for couples of ligands and receptors looking at communication only between CTRL_co progenitors and HD_co neurons (at the center) compared to similar communications between CTRL_mono progenitors and CTRL_mono neurons (on the left) and between HD_mono progenitors and HD_mono neurons (on the right). Abbreviations: DP=Dorsal Progenitors; DN=Dorsal Neurons; VP=Ventral Progenitors; VN=Ventral Neurons

A)

CELL	CTRL/HD	NAME OF THE LINE	CAG	ID
hESC-Rues2	CTRL	parental	22-20 cag	CHDI-90001539
hESC-Rues2	CTRL	20cag cl30	22-20 cag	CHDI-90001585
hESC-Rues2	HD	48cag cl20.4	48-20 cag	CHDI-90001587
hESC-Rues2	HD	56cag cl21.1	56-20 cag	CHDI-90001589
hESC-Rues2	HD	72cag cl12	72-20 cag	CHDI-90002877-1

B)

NAME	FW SEQUENCE (5'-3')	REV SEQUENCE (5'-3')
ASCL1	GTCCTGTCGCCCACCATCTC	CCCTCCAACGCCACTGAC
DLX2	ACGCTCCCTATGGAACCAGTT	TCCGAATTCAGGCTCAAGGT
DLX6	TACCTCCAGTCTACCACAAC	AATAAATGGTCCGAGGCTTCCG
GAD1	GAGGGAAGTACGAGAACGA	ACCAGGTATCGTACGTTGTGG
MAP2	CAAATGTGGCTCTCTGAAGAACA	GGGCCTTTCTTTGAAATCTAGTTT
SATB2	CCTCCTCCGACTGAAGACAG	TGGTCTGGGTACAGGCCTAC
SIX3	AGGTCAGTCCATGGTATTCC	CAGAAGTATGGAGCGGTGGT
SNAP25	TACACAGAATCGCCAGATCG	ACCACTTCCCAGCATCTTTG
SP9	CCTGCTATGGCCACGTCTAT	GAGAGACTGGAGCCGAGGTT
TBR2	CAGCGCCACCAAAGTGTAGAT	CGAACACATTGTAGTGGGCAG

Supplementary Table 1 – Tables relative to materials used in the study (A) table listing used cell lines (B) table listing used primers.

A) Exact p-values (FIG 4E)

HD_mono	HD_co	ventral progenitors				dorsal progenitors				ventral neurons				dorsal neurons			
		CTRL_mono	CTRL_co	HD_co	HD_mono	CTRL_mono	CTRL_co	HD_co	HD_mono	CTRL_mono	CTRL_co	HD_co	HD_mono	CTRL_mono	CTRL_co	HD_co	HD_mono
neurons	0.000894722	0.00386106	1	1.47644e-11	6.1772e-212	3.3013e-213	8.353e-222	0	3.3095e-179	6.9307e-193	2.9265e-187	0.023039947	1	1	0.00671859	0	
progenitors	3.668e-49	3.65162e-54	2.5425e-40	1	1	1	0.004660588	3.1995e-1279	9.9668e-230	1.2732e-234	2.9275e-235	1.00162e-39	1.4528e-198	3.3013e-213	6.8803e-216	7.0656e-62	
neurons	2.43153e-69	1.8171e-67	6.34561e-44	1.83149e-34	6.4628e-235	1.2732e-234	1.1822e-232	5.9555e-256	1	1	0.027016704	4.55538e-22	9.0748e-198	6.9307e-193	3.7344e-167	0	
progenitors	1	1	1	0.00208209	4.15162e-51	3.65162e-54	9.41229e-68	4.4481e-157	2.89923e-64	1.8171e-67	2.88478e-59	0.15713588	0.076726602	0.00386106	3.40455e-05	7.1909e-137	
neurons	0.0225647570	0.076726602	1	1.60753e-10	9.7389e-197	1.4528e-198	1.8115e-208	4.5684e-308	3.3544e-184	9.0748e-198	1.8568e-192	0.005782145	1	1	4.08459e-05	0	
progenitors	2.54356e-46	4.15162e-51	2.37982e-38	1	1	1	7.16432e-10	4.5208e-130	4.3359e-230	6.4628e-235	1.1288e-235	7.39054e-39	9.7389e-197	6.1772e-212	1.514e-214	2.53257e-67	
neurons	2.77958e-66	2.89923e-64	9.56211e-42	2.11275e-33	4.3359e-230	8.9668e-230	5.5859e-229	3.5477e-255	1	1	0.232508801	1.5022e-20	3.3544e-184	3.3095e-179	0.0242e-155	0	
progenitors	1	1	1	0.00072207	2.54356e-46	3.668e-49	5.37372e-63	3.189e-148	2.77958e-66	2.43153e-69	4.03716e-61	0.05741131	0.0225647570	0.00894722	5.54621e-06	7.3038e-132	
neurons	5.54621e-06	3.40455e-05	1	5.15036e-13	1.514e-214	5.8803e-216	1.5142e-224	0	6.0242e-155	7.3444e-167	4.7208e-155	0.9626256624	0.04859e-05	0.00671859	1	0	
progenitors	5.37372e-63	4.11229e-64	6.07896e-50	0.024994759	7.16432e-05	0.004660588	1	1.43546e-93	5.859e-229	1.1822e-232	1.1749e-233	2.64326e-45	1.8115e-208	8.353e-222	1.5142e-224	4.87237e-32	
neurons	4.03716e-61	2.88478e-59	4.24661e-36	1.54352e-33	1.1288e-235	2.9275e-235	1.1749e-233	1.837e-255	0.232508801	0.027016704	1	4.0364e-16	1.8568e-192	2.9265e-187	4.7208e-155	0	
progenitors	1	1	1	5.66554e-05	2.37982e-38	2.5425e-40	6.07896e-50	2.9193e-112	9.56211e-42	6.34561e-44	4.24661e-36	1	1	1	1	1.82528e-94	
neurons	7.3038e-132	7.1909e-137	1.82528e-94	5.34122e-09	2.53257e-67	2.70656e-62	4.87237e-32	1.11983e-47	1	1	0.107249e-69	0	0	0	0	1	
progenitors	1.3189e-148	4.4481e-157	2.9193e-112	9.0293e-22	4.5208e-130	2.3195e-127	1.43546e-93	1	3.5477e-255	5.9555e-256	1.837e-255	1.91189e-80	4.5684e-308	0	0	1.11963e-47	
neurons	0.05741131	0.15713588	1	6.82113e-08	7.39054e-39	1.00162e-39	2.64326e-45	1.91189e-80	1.5022e-20	4.55538e-22	4.0364e-16	1	0.005782145	0.023039947	9.626256621	0.7249e-69	
progenitors	0.00072207	0.00208209	5.66554e-05	1	1	1	0.024994759	9.0293e-22	2.11275e-33	1.83149e-34	1.54352e-33	6.82113e-08	1.60753e-10	1.47644e-11	5.15036e-13	5.34122e-09	

B) Exact p-values (FIG 4F)

HD_mono	HD_co	ventral progenitors				dorsal progenitors				ventral neurons				dorsal neurons			
		CTRL_mono	CTRL_co	HD_co	HD_mono	CTRL_mono	CTRL_co	HD_co	HD_mono	CTRL_mono	CTRL_co	HD_co	HD_mono	CTRL_mono	CTRL_co	HD_co	HD_mono
neurons	3.34807e-35	5.6811e-39	5.67606e-09	8.38451e-21	1	1	1.41463e-17	2.4007e-158	7.92062e-49	3.25837e-51	5.94173e-54	9.52045e-21	1	1	1	1.356e-270	
progenitors	9.93366e-27	1.20921e-29	7.63606e-08	1.22675e-16	1	1	3.05231e-09	1.6055e-92	2.13191e-33	3.85925e-35	1.0082e-35	5.42281e-15	1	1	1	4.1595e-115	
neurons	1	1	0.024371982	3.65801e-24	8.70069e-33	3.85925e-35	4.23583e-61	4.5201e-133	1	1	1	5.25692e-34	1.46577e-50	3.25837e-51	3.97826e-44	2.2499e-184	
progenitors	1	1	0.054388654	5.98605e-33	3.20996e-27	1.20921e-29	1.83921e-57	7.3939e-143	1	1	1	1.90618e-40	6.91554e-38	5.6811e-39	1.7744e-34	2.1183e-174	
neurons	3.54237e-34	6.91554e-38	1.07496e-08	6.92192e-20	1	1	2.44183e-17	2.8352e-152	2.77752e-48	1.46577e-50	1.54625e-52	5.26632e-20	1	1	1	3.7601e-261	
progenitors	3.79002e-24	3.20996e-27	9.92007e-07	7.2565e-17	1	1	1.65907e-10	7.6854e-94	2.08624e-31	8.70069e-33	1.55742e-32	1.94142e-15	1	1	1	8.254e-117	
neurons	1	1	0.045216054	1.5577e-24	2.08624e-31	1.23191e-33	2.20913e-59	7.184e-132	1	1	1	1.03659e-33	2.77752e-48	7.92062e-49	9.0327e-42	3.481e-184	
progenitors	1	1	0.237469082	4.1161e-31	3.79002e-24	9.93366e-27	2.08773e-53	7.671e-135	1	1	1	7.8197e-38	3.54237e-34	3.34807e-35	7.35433e-31	1.9305e-164	
neurons	7.35433e-31	1.77443e-34	1.13287e-07	4.48239e-21	1	1	4.79605e-19	5.4736e-158	3.90327e-42	3.97826e-44	2.41197e-46	2.05577e-21	1	1	1	5.1095e-269	
progenitors	2.08773e-53	1.83921e-57	6.64922e-24	3.67846e-08	1.65907e-10	3.05231e-09	1.99316e-43	2.20913e-59	4.23583e-61	1.80926e-68	1.80926e-68	2.44183e-17	1.41463e-17	7.92062e-49	5.25116e-47		
neurons	1	1	0.142173385	1.92916e-29	1.5742e-32	1.0082e-35	1.80926e-68	7.528e-164	1	1	1	3.84017e-39	1.54625e-52	5.94173e-54	2.41197e-46	6.0942e-228	
progenitors	0.237469082	0.054388654	1	1.33294e-23	9.92007e-07	7.63606e-08	6.64922e-24	6.0226e-84	0.045216054	0.024371982	1.42173385	2.47247e-24	1.07496e-08	6.7606e-09	1.13287e-07	1.31242e-91	
neurons	1.9305e-164	2.1183e-174	1.31242e-91	1	2.8254e-117	4.1595e-115	2.5116e-47	0.247404235	4.3481e-184	2.2499e-184	6.0942e-228	1	3.7601e-261	1.356e-270	5.1095e-269	1	
progenitors	1.7671e-135	3.7393e-143	3.60226e-84	1	7.6854e-93	7.16055e-92	1.99316e-43	1	1.7184e-132	4.5201e-133	3.7528e-164	0.297542532	2.8352e-152	2.4007e-158	5.4736e-158	0.247404235	
neurons	7.8197e-38	1.90618e-40	2.47247e-24	1	1.94142e-15	5.42281e-15	0.00018897	0.297542532	0.03659e-33	5.25692e-34	3.84017e-39	1	5.26632e-20	9.52045e-21	2.05577e-21	1	
progenitors	4.4116e-31	5.98605e-33	1.33294e-23	1	7.2565e-17	1.22675e-16	3.67846e-08	1	3.15577e-24	3.65801e-24	1.92916e-29	1	6.92192e-20	8.38451e-21	4.48239e-21	1	

D) Exact p-values (FIG 4H)

HD_mono	HD_co	CTRL_mono		ventral		dorsal		ventral		dorsal		ventral		dorsal		ventral	
		neurons	progenitors	neurons	progenitors	neurons	progenitors	neurons	progenitors	neurons	progenitors	neurons	progenitors	neurons	progenitors	neurons	progenitors
neurons	1	1.63602e-88	9.141e-108	7.9395e-165	1	2.2775e-97	3.0703e-102	5.976e-161	0.003286574	4.5928e-41	2.42524e-93	1.9319e-91	1	2.96169e-67	0.013789842	4.3426e-05	
progenitors	1.63602e-88	1	0.007752188	9.0464e-27	5.30892e-83	1	0.027366517	6.9011e-25	2.35543e-63	0.000459166	0.629832969	1.28378e-08	1.04541e-79	1	9.62466e-07	0.29907337	
neurons	9.141e-108	0.007752188	1	3.67513e-08	1.3825e-102	0.022821389	1	4.99186e-07	1.81735e-82	2.55215e-13	1	1	1.9437e-99	2.76115e-05	9.50612e-11	0.001769234	
progenitors	9.9395e-165	9.0464e-27	3.67513e-08	1	8.9414e-160	1.77195e-27	1.06906e-08	1	4.0332e-138	2.40911e-44	9.60449e-110	0.152639626	4.2672e-157	1.69207e-31	2.0952e-29	7.8288e-16	
neurons	1	5.30892e-83	1.3825e-102	8.9414e-160	1	2.7195e-91	6.37336e-97	3.2764e-156	0.421733484	9.9096e-37	4.45943e-88	4.42393e-88	1	3.7082e-62	0.099174573	0.000155363	
progenitors	2.2775e-97	1	0.022821389	1.71915e-27	2.7775e-91	1	0.064114638	8.3104e-26	1.5033e-70	0.0764e-05	1	6.88963e-09	6.91285e-88	1	1.05733e-07	0.13474369	
neurons	3.0703e-102	0.027366517	1	1.06906e-08	6.37336e-97	0.064114638	1	1.70704e-07	4.97531e-78	2.2888e-134	1.50579e-25	5.73308e-70	1.54211e-73	1	3.81722e-46	1	
progenitors	5.976e-161	6.9011e-25	4.99186e-07	1	3.2764e-156	8.3104e-26	1.70704e-07	1	2.2888e-134	3.86352e-42	2.53478e-09	0.60788628	1.3237e-153	1.59481e-29	3.84086e-28	4.75121e-15	
neurons	0.003286574	2.35543e-63	1.81735e-82	4.0332e-138	0.421733484	1.5033e-70	4.97531e-78	2.2888e-134	1	1	1	1	1	1	1	1	
progenitors	4.45928e-41	0.000459166	2.55215e-13	2.40911e-44	8.99096e-37	7.07641e-05	8.87894e-12	3.86352e-42	5.90579e-25	1	2.20682e-09	1.14873e-19	9.11443e-35	0.306968318	0.338280464	1	
neurons	2.42524e-93	0.629832969	1	9.60449e-110	1.45943e-88	1	2.53478e-09	6.73308e-70	2.20682e-09	1	0.126075115	1.79942e-85	0.007475323	2.0529e-08	0.01907081		
progenitors	1.09319e-91	1.28378e-08	1	0.152639626	4.42393e-88	6.88963e-09	8.65286437	0.60788628	1.54211e-73	1.14873e-19	0.126075115	1	2.6062e-86	1.13768e-11	3.96777e-17	6.8229e-09	
neurons	1	1.04541e-79	1.9437e-99	4.2672e-157	1	6.91285e-88	4.09103e-94	3.237e-153	1	9.11443e-35	1.79942e-85	2.6062e-86	1	7.71732e-60	0.09442248	0.000226238	
progenitors	2.96169e-67	1	2.76115e-05	1.69207e-31	3.7082e-62	1	0.000138736	1.59481e-29	8.1722e-46	0.306968318	0.007475323	1.13768e-11	1.71732e-60	1	0.00022096	1	
neurons	0.013178984	9.62466e-07	9.50612e-11	2.0952e-29	0.099174573	1.05733e-07	3.44687e-10										