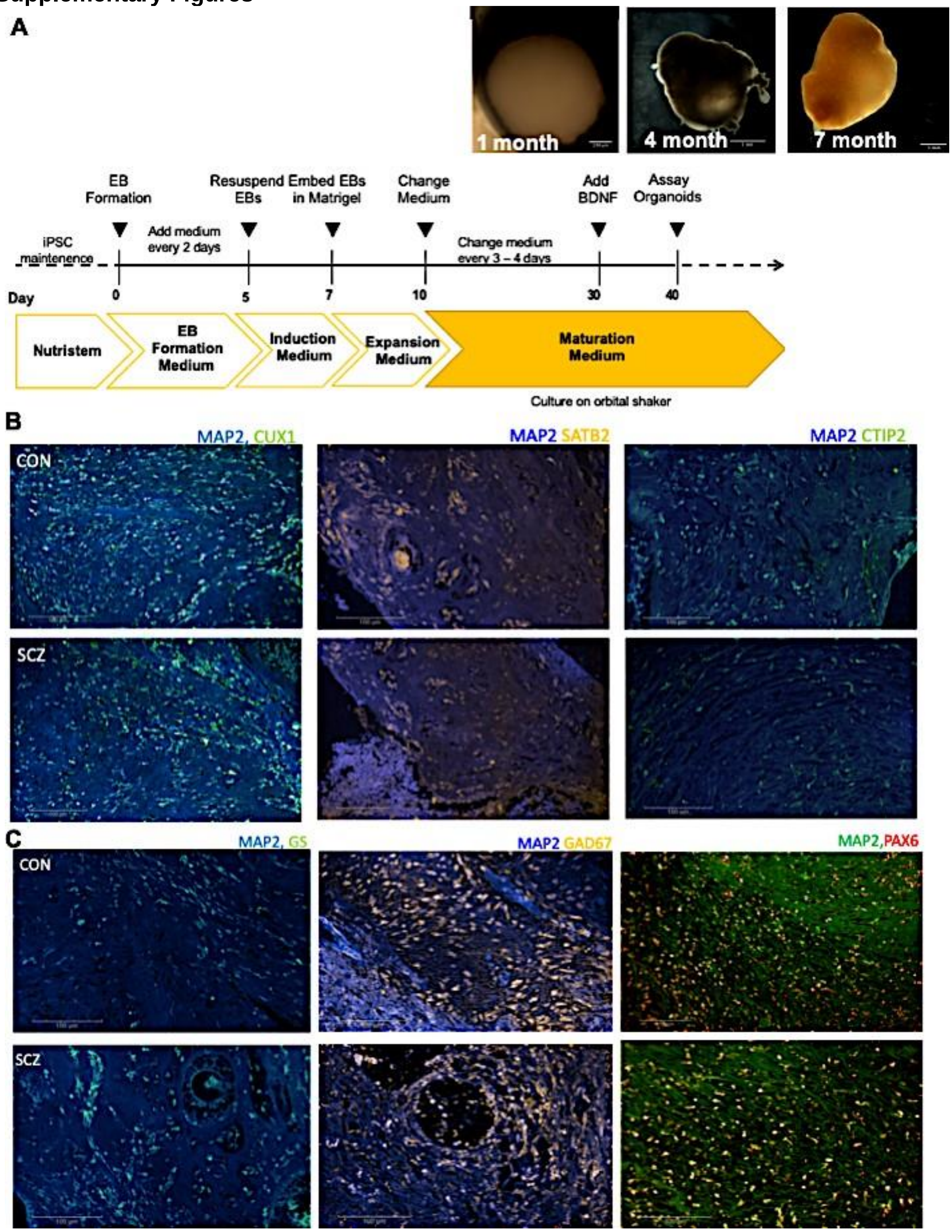
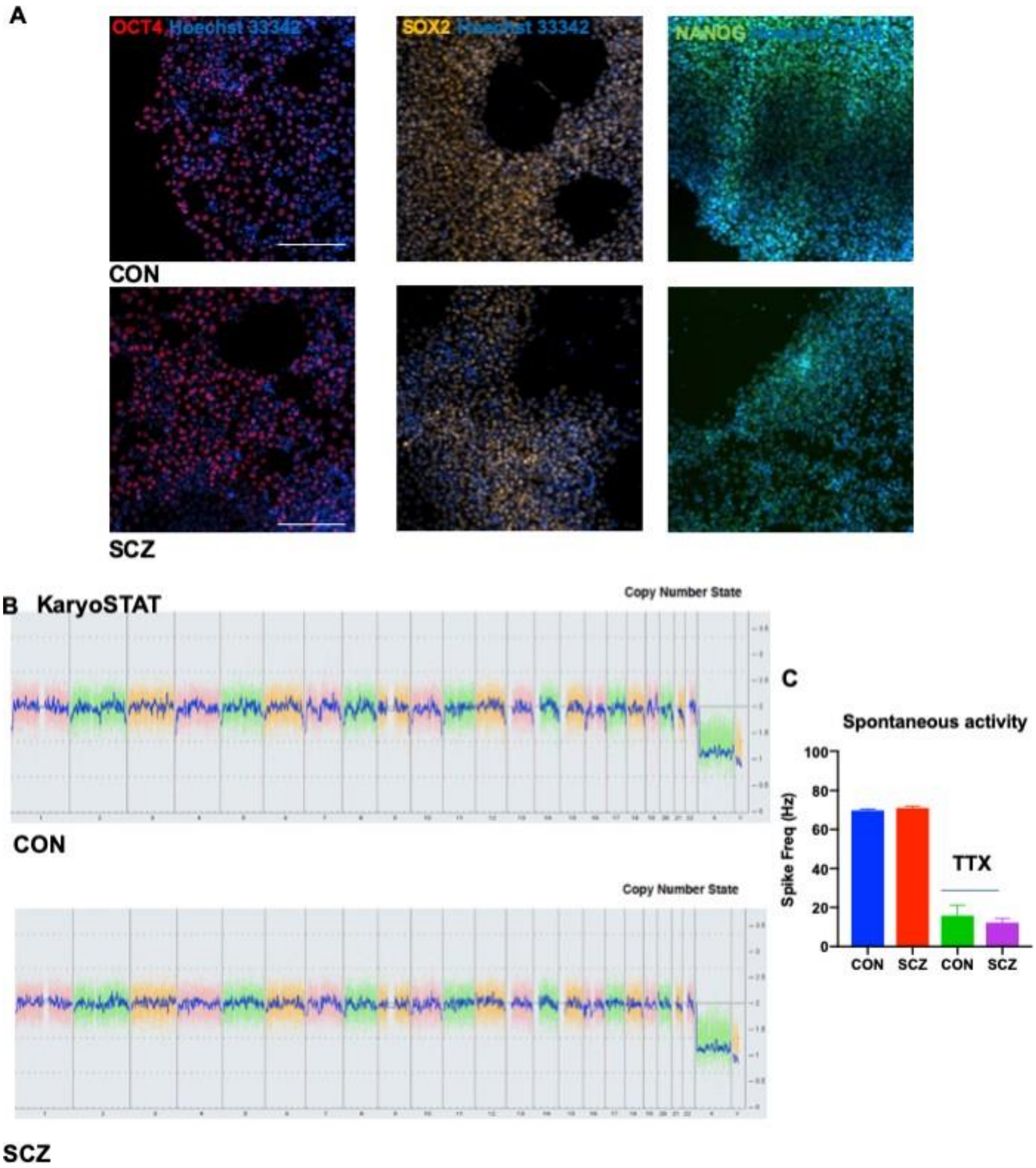
Supplementary Online Content

Kathuria A, Lopez-Lengowski K, Jagtap SS, et al. Transcriptomic landscape and functional characterization of induced pluripotent stem cells–derived cerebral organoids in schizophrenia. *JAMA Psychiatry*. Published online March 18, 2020. doi:10.1001/jamapsychiatry.2020.0196.

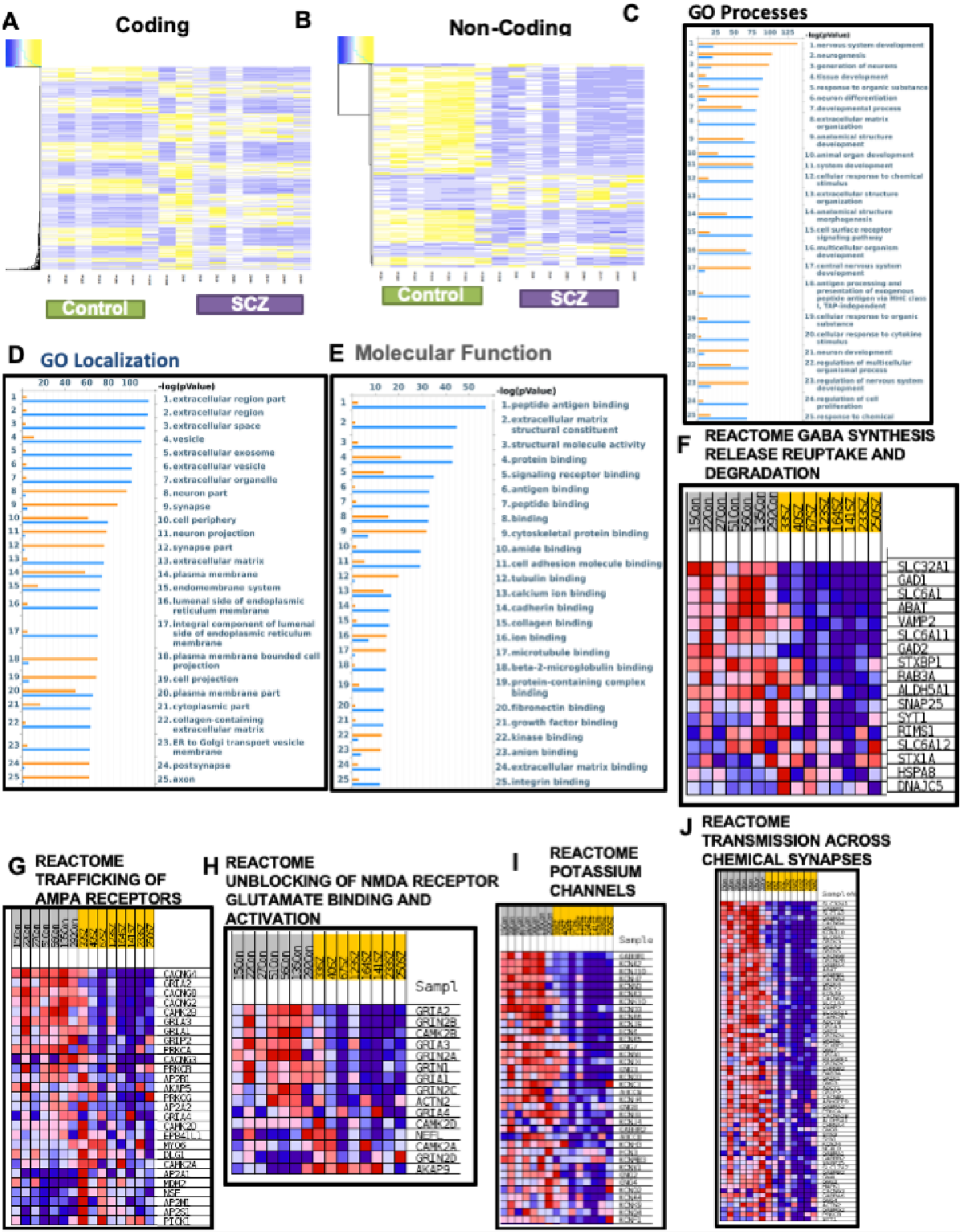
Supplementary Figures



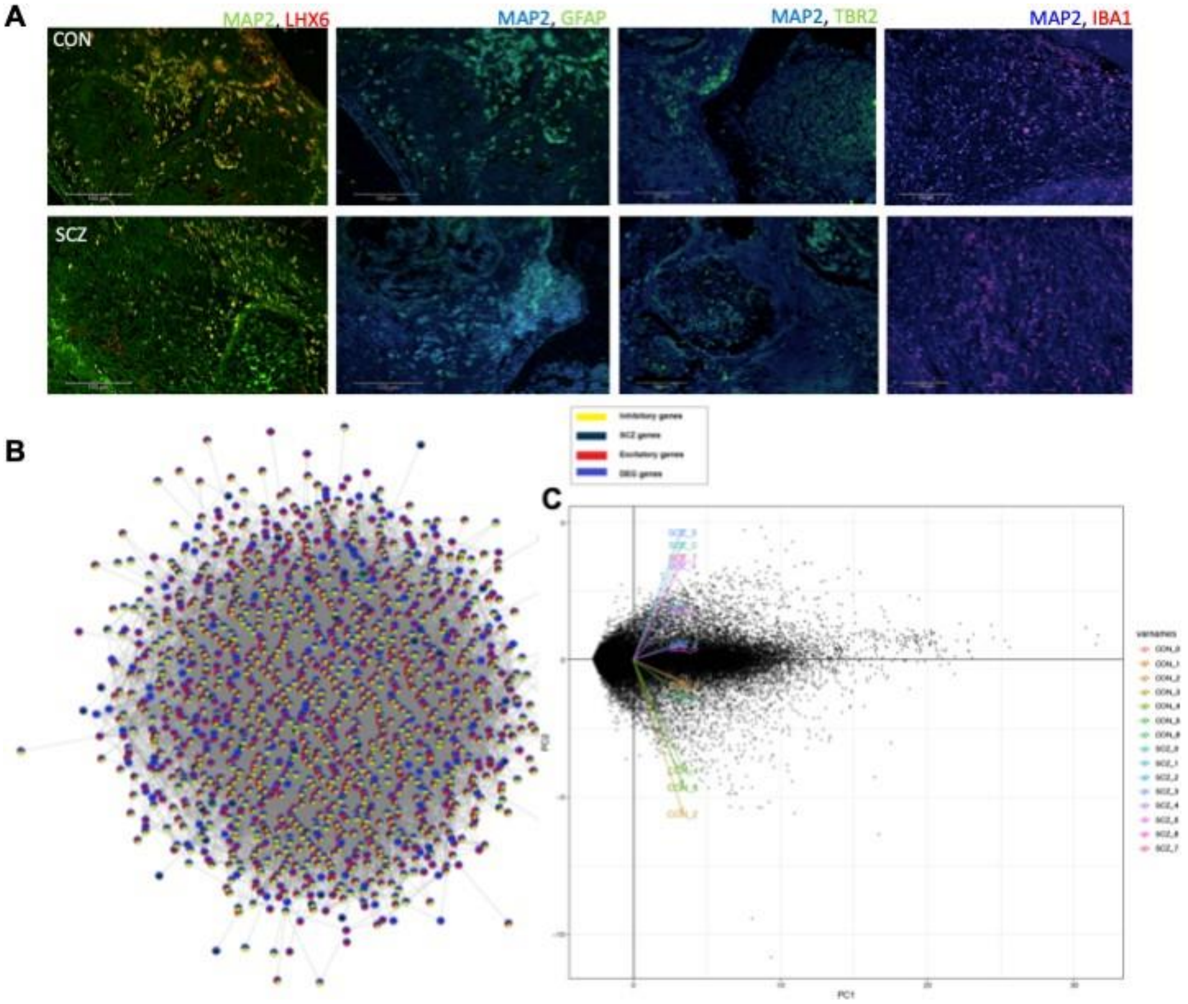
eFigure 1: Generation and characterization of cerebral organoids from human iPSCs. A) Protocol used for generation of cerebral organoids along with phase contrast images at different stages of development. Scale bar: 250 µm for image from 1 month and 1 mm for images from 4 months and 7 months. (B-F) Immunohistochemistry of cerebral organoid slices from schizophrenia and control iPSCs. Scale bar:100µm.



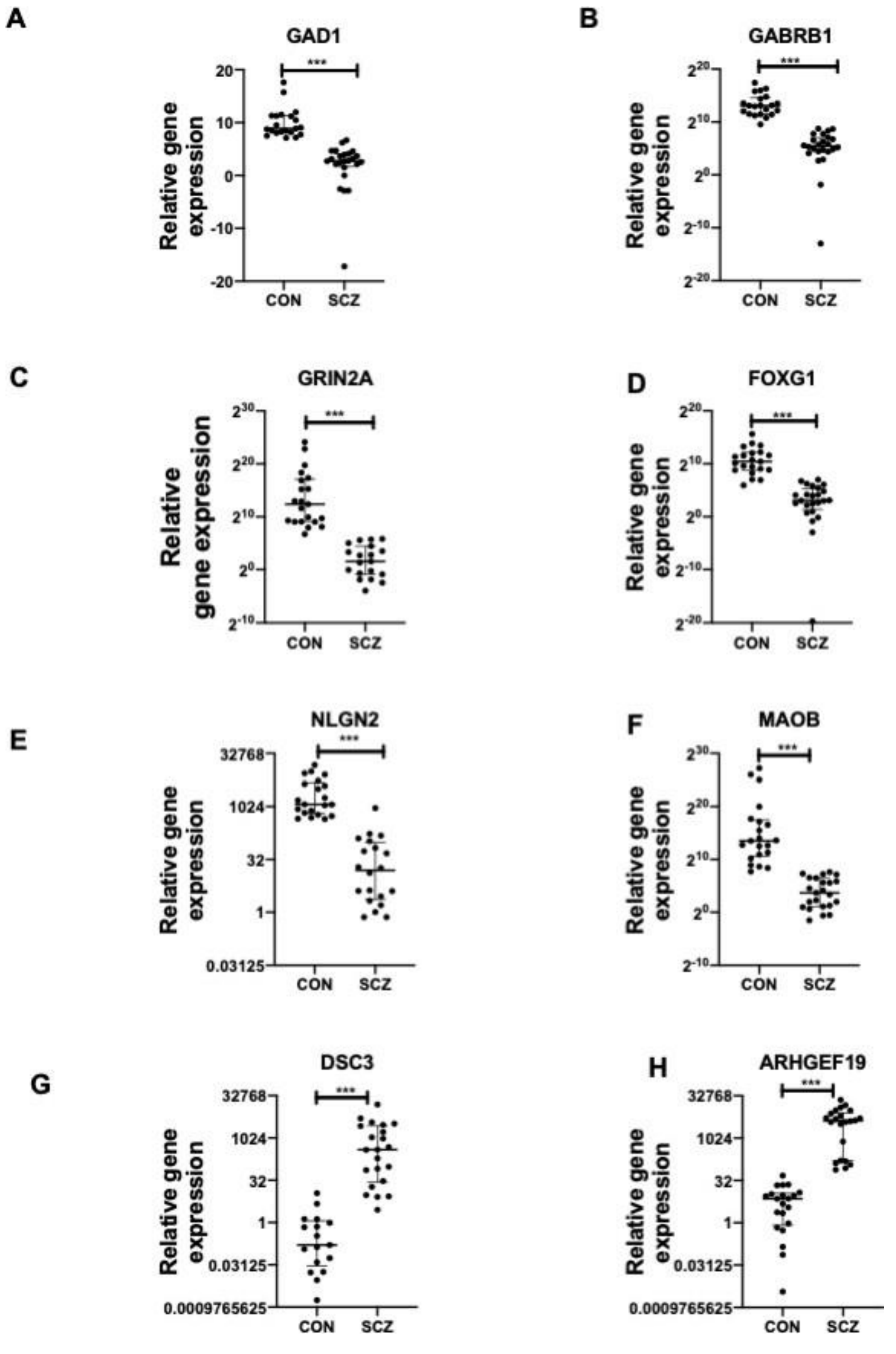
eFigure 2. iPSC characterization. (A) Representative images of immunocytochemistry of CON, SCZ iPSC lines which were positive for Nanog (green), Oct4 (red), SOX2 (yellow), and Hoechst (blue). Scale=50μm. This assay has been done for all 16 iPSC lines data will be available on request. (B) Representative images of the whole genome view of one CON line and one SCZ line. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any). (C) Spontaneous activity of CON and SCZ cerebral organoids with and without TTX 1mM.



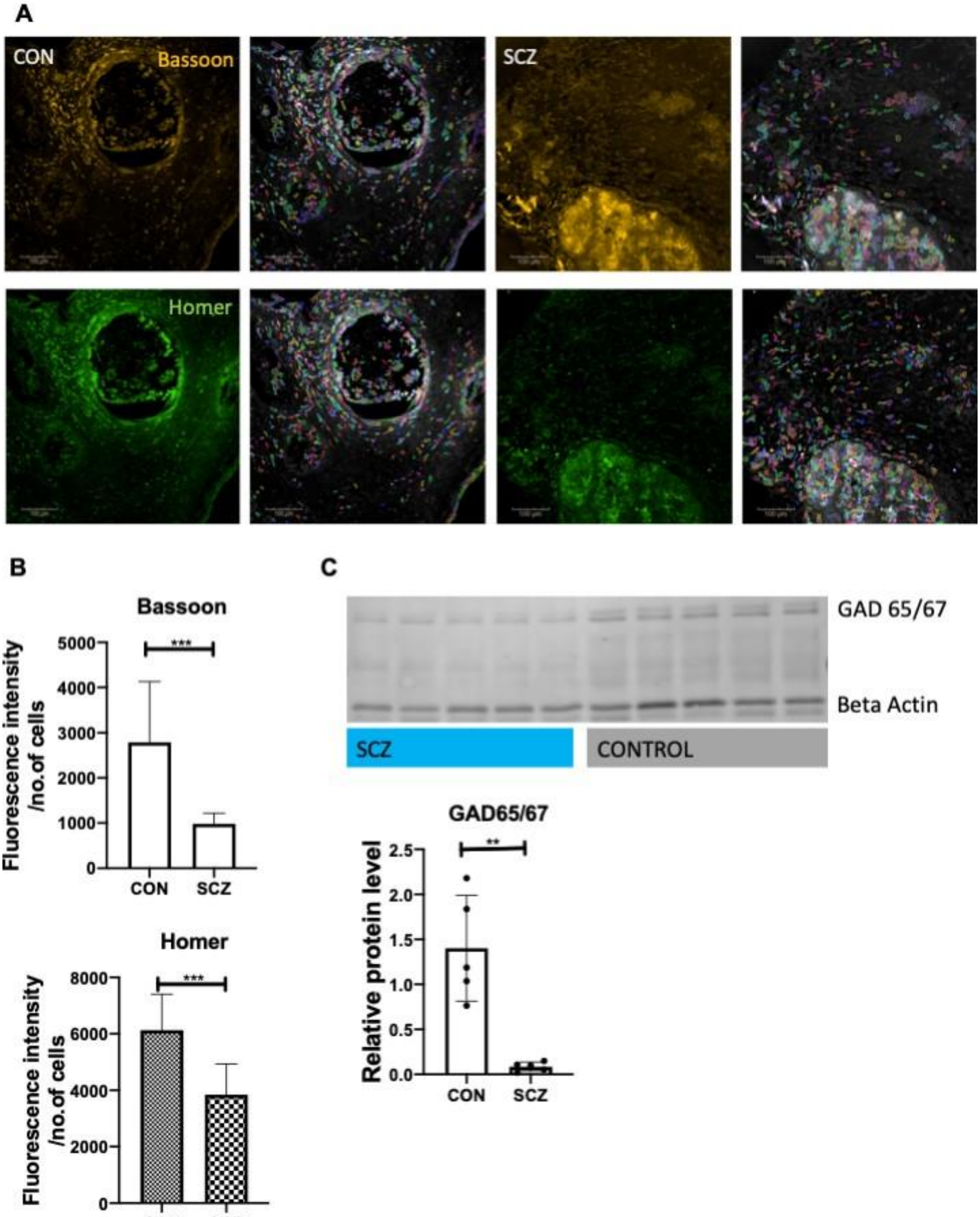
eFigure 3. Gene ontology (GO) analysis of differentially expressed genes (DEGs) in schizophrenia cerebral organoids. (A-B) Heat maps of DEGs for coding and non-coding genes in six-month-old cerebral organoids differentiated from schizophrenia and control iPSCs. (C-E) GO analysis for process, localization and molecular function for DEGs, rank-ordered according to significance (p value) and depicted as up-regulated (blue) or down-regulated (orange) genes. (F-J) Results of gene set enrichment analysis (GSEA) of DEGs depicted as heat maps, with red depicting high expression and blue depicting low to no expression.



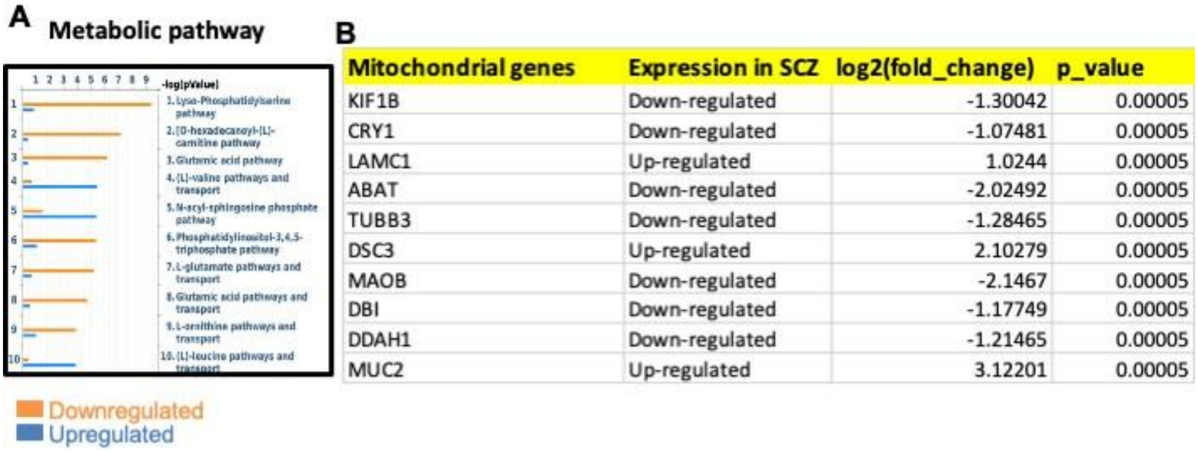
eFigure 4: Cerebral organoid characterization. (A) High-magnification images of IHC staining. Scale bar:100µm. (B) Visualization of gene co-expression of DEGs with genes expressed in excitatory and inhibitory neurons. (C) Principal component analysis (PCA) to show the distribution of CON and SCZ iPSC line generated organoid population.



eFigure 5: RT-PCR validation of DEGs. (A-H) Graphs showing relative gene expression in cerebral organoids compared to a control iPSC line assessed via quantitative PCR (qPCR). Values are median±IQR. Mann–Whitney U-test was performed. The significant differences between CON and SCZ groups are shown as ***p <0.001. The assay was performed in seven CON and eight SCZ lines, each with three replicates.

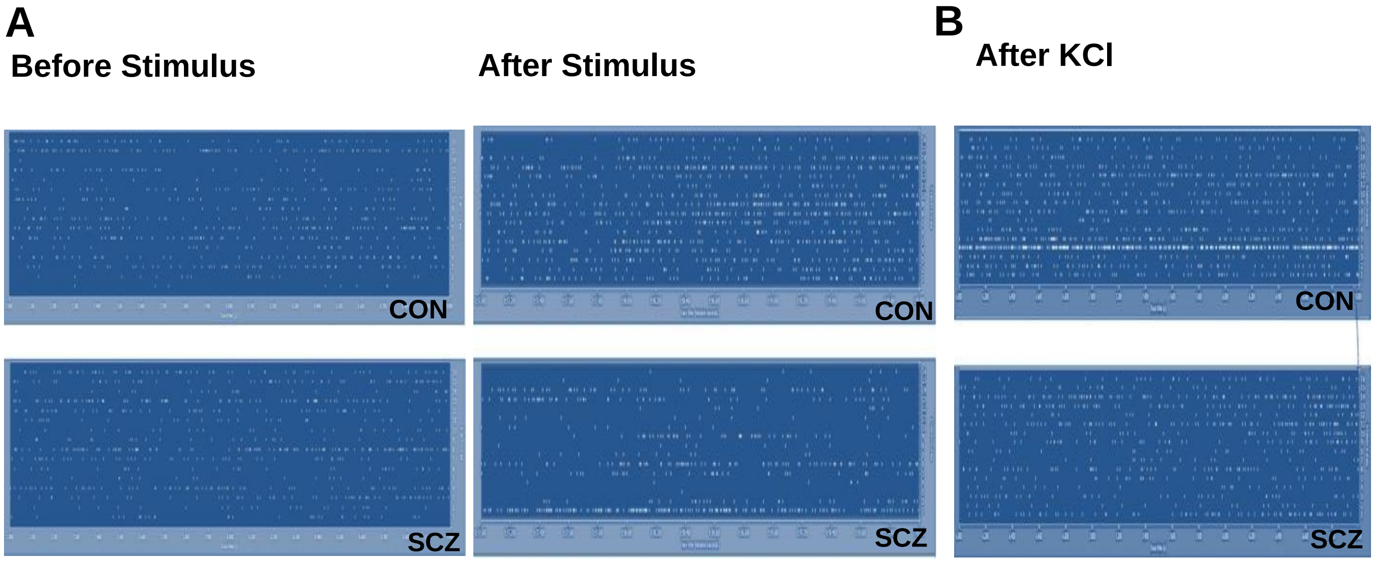


eFigure 6. Synaptic staining and western blots of cerebral organoids. (A) High-magnification images of IHC synaptic staining. Scale bar:100µm. (B) Quantification of synaptic staining in CON and SCZ, Values are median±IQR. Mann–Whitney U-test was performed. The significant differences between CON and SCZ groups is shown as ***p <0.001. Bassoon Basal -Two-tailed, Sum of ranks in column CON, SCZ- 4317264 , 145314, Mann-Whitney U- 5129 ***p=0.0001. Homer, Basal -Two- tailed, Sum of ranks in column CON, SCZ- 87908515 , 1222762, Mann-Whitney U- 1022101***p=0.0001 The assay was performed in three CON lines and three SCZ, each with three replicates. (C) GAD65/67 Western Blot and Quantification. Values are mean±SD. Student t-test was performed. R squared- 0.8598, CI 95 %- -2.043 to -0.5877, **p =0.0073. Each lane represents protein lysates from one organoid. 5 SCZ lines were compared to 5 CON lines.



Mitochondrial genes	Expression in SCZ	log2(fold_change)	p_value
KIF1B	Down-regulated	-1.30042	0.00005
CRY1	Down-regulated	-1.07481	0.00005
LAMC1	Up-regulated	1.0244	0.00005
ABAT	Down-regulated	-2.02492	0.00005
TUBB3	Down-regulated	-1.28465	0.00005
DSC3	Up-regulated	2.10279	0.00005
MAOB	Down-regulated	-2.1467	0.00005
DBI	Down-regulated	-1.17749	0.00005
DDAH1	Down-regulated	-1.21465	0.00005
MUC2	Up-regulated	3.12201	0.00005

eFigure 7: Mitochondrial DEGs in SCZ organoids. (A) Metabolic pathways that were most differentially regulated in schizophrenia cerebral organoids, listed according to significance (p value). (B) The top ten significant mitochondrial genes that were represented in the DEGs, listed according to significance (p value).



eFigure 8: Raster plots from MEAs. (A) Representative raster plot recording before and after electrical stimulation in control (CON) and schizophrenia (SCZ) organoids. (B) Raster plot recording after depolarization with 30 mM KCl.

eTable 1. Demographic and treatment information on subjects

Sample ID	Diagnosis	Gender	Age	Race	Age of onset	Antipsychotic history	Medical comorbidities
ML-15	Control	Male	37	Caucasian	-		
ML-22	Control	Male	24	Caucasian	-		
ML-27	Control	Male	24	Caucasian	-		
ML-33	SCZ	Male	32	Caucasian	22	clozapine, risperidal, ziprasidone, haloperidol	None
ML-40	SCZ	Female	46	Caucasian	13	clozapine, haloperidol	hypertension, hypothyroidism
ML-51	Control	Male	31	Caucasian	-		
ML-56	Control	Female	52	Caucasian	-		
ML-67	SCZ	Male	50	Caucasian	17	clozapine	
ML-123	SCZ	Male	32	Caucasian	-		
ML-135	Control	Male	49	Caucasian	-		
ML-141	SCZ	Male	40	Caucasian	24	aripiprazole	None
ML-164	SCZ	Female	67	Caucasian	unknown	perphenazine	unknown
ML-233	SCZ	Female	39	Caucasian	unknown	haloperidol	hypothyroidism
ML-250	SCZ	Male	23	Caucasian	unknown	aripiprazole	unknown
ML-292	Control	Male	43	Caucasian	-		
ML-300	Control	Female	32	Caucasian	-		

eTable 2. GO analysis of DEGs that are associated specifically with SCZ, BPD or ASD.

GO (DEGs CON vs SCZ) and SCZ	**76 genes**	**p value**
Localization	synapse	6.03E-09
Process	nervous system development	3.12E-13
Molecular Function	phosphatase regulator activity	2.56E-05
GO (DEGs CON vs SCZ) and ASD	**217 genes**	
Localization	lumenal side of endoplasmic reticulum membrane	6.35E-99
Process	interferon-gamma-mediated signaling pathway	6.34E-95
Molecular Function	peptide antigen binding	5.68E-93
GO (DEGs CON vs SCZ) and BPI	**18 genes**	
Localization	integral component of presynaptic membrane	3.01E-03
Process	regulation of presynaptic membrane potential	2.26E-07
Molecular Function	pyruvate carboxylase activity	7.77E-04

eTable 3. Excitatory and inhibitory genes: Up-regulated DEGs. List of top ten significantly up-regulated genes that are primarily expressed in excitatory and inhibitory neurons, listed according to significance (*p* value).

Up-regulated Excitatory genes	log2(fold-change)	p_value
MUC12	5.22054	5.00E-05
MUC5B	4.59009	5.00E-05
ASB4	3.85217	5.00E-05
NKX3-2	3.69844	0.00025
DSG4	3.54697	0.0029
MUC2	3.52932	5.00E-05
CD34	3.3625	0.00035
AFP	3.25741	5.00E-05
GCNT3	3.25196	5.00E-05
B3GNT6	3.23074	0.0001
Up-regulated Inhibitory genes	**log2(fold-change)**	**p_value**
ALDH1A2	3.01225	5.00E-05
TFF1	3.00824	0.00115
ABCB5	2.83042	0.0029
GJB6	2.65629	0.00015
KRT4	2.58442	5.00E-05
PKHD1	2.49082	5.00E-05
ALDH1A3	2.48333	0.00075
WFDC1	2.39754	0.0001
OGN	2.20641	0.00165
RERG	2.11802	5.00E-05

eTable 4. Excitatory and inhibitory genes: Down-regulated DEGs. List of top ten significantly down-regulated genes that are primarily expressed in excitatory and inhibitory neurons, listed according to significance (*p* value)

Down-regulated Excitatory genes	**log2(fold-change)**	**p_value**
GLRA3	-4.57526	0.00055
SMOC1	-3.88093	0.00015
ST8SIA5	-3.27257	0.00135
BAIAP3	-3.08113	0.0036
SLCO1C1	-3.01626	5.00E-05
MGAT4C	-2.97603	5.00E-05
CA3	-2.93028	0.00095
AQP4	-2.89686	0.00045
GPR17	-2.8276	0.0057
MLC1	-2.77549	5.00E-05
Down-regulated Inhibitory genes	**log2(fold-change)**	**p_value**
PSD2	-3.52559	5.00E-05
SNTG2	-3.10909	5.00E-05
FOXG1	-3.1037	5.00E-05
SEMA5B	-3.08829	5.00E-05
MYT1L	-2.97149	0.0002
MDGA2	-2.81431	5.00E-05
ASTN1	-2.72078	5.00E-05
POU3F3	-2.71539	5.00E-05
DPF1	-2.63659	5.00E-05
TTBK1	-2.6163	0.0002

eTable 5. Primary antibodies used

Primary antibody	Type	Dilution	Source
Iba-1	Goat polyclonal	1/500	Abcam
GAD 67	Mouse monoclonal	1/1000	Abcam
Glutamate Synthase	Rabbit polyclonal	1/10000	Novus
LHX6 (A-9)	Mouse monoclonal	1/100	Santa Cruz Biotechnolog
MAP2	Guinea pig polyclonal antiserum	1/1000	Synaptic Systems
Myelin Basic Protein	Mouse monoclonal	1/200	Abcam
Oligodendrocyte Specific Protein	Rabbit polyclonal	1/200	Abcam
Somatostatin (Clone YC7)	Rat monoclonal	1/100	EMD Millipore Corp.
TBR2	Rabbit polyclonal	1/200	Abcam

eTable 6. KaryoSTAT code for each line.

Control Lines		
KaryoSTAT Labels	**Line**	**Sex**
CUB12899-8	ML22	M
CUB12899-9	ML15	M
CUB12899-10	ML51	M
CUB12899-11	ML135	M
CUB12899-12	ML292	M
CUB12899-18	ML27	M
CUB12899-21	ML300	F
CUB12899-22	ML56	F
Schizoprenia lines		
KaryoSTAT Labels	**Line**	**Sex**
CUB12899-1	ML123	M
CUB12899-2	ML67	M
CUB12899-3	ML233	F
CUB12899-17	ML141	M
CUB12899-20	ML250	M
CUB12899-23	ML40	F
CUB12899r-2	ML164	F
CUB12899-14	ML37	F

KaryoStat™ Results: CUB12899-12

1. KaryoStat™ analysis of CUB12899-12 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 21)

Copy Number State

Figure 21: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

Disclaimer: This assay was conducted solely for the listed investigator/institution. The results of this assay are for research use only.

KaryoStat™ Results: CUB12899-18

1. KaryoStat™ analysis of CUB12899-18 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 10)

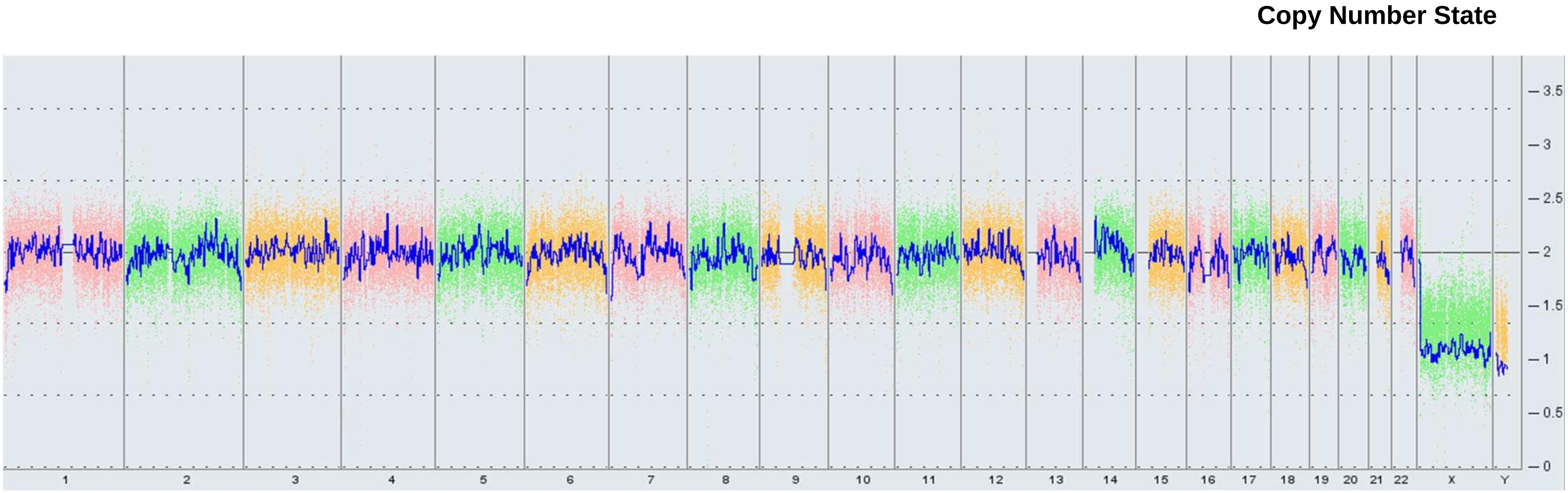


Figure 10: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899-9

1. KaryoStat™ analysis of CUB12899-9 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 4)

Copy Number State

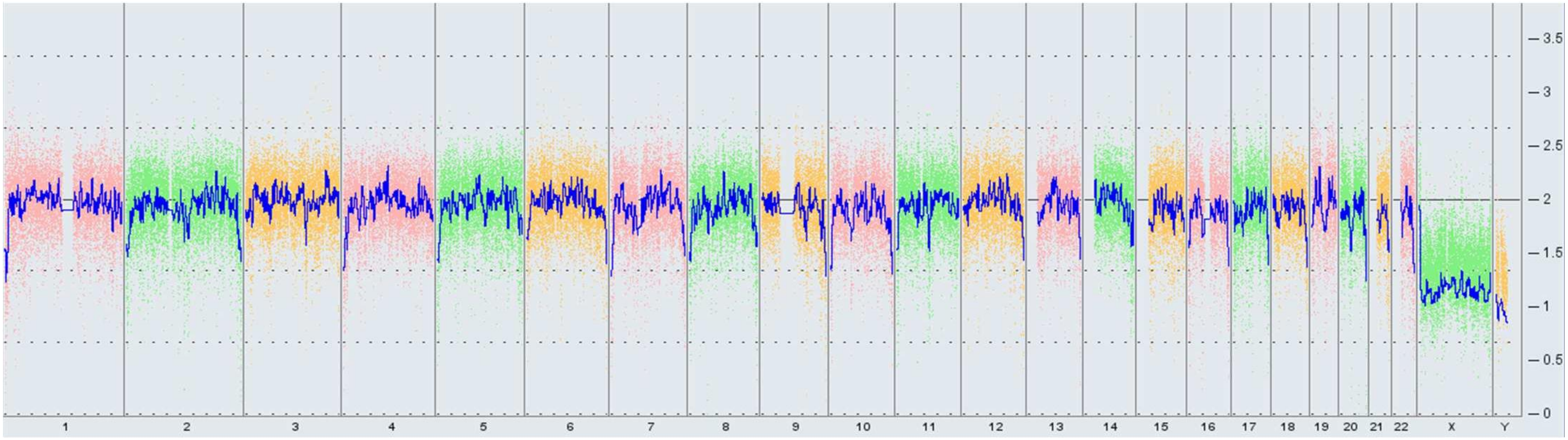

Figure 4: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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ThermoFisher SCIENTIFIC

KaryoStat™ Results: CUB12899-10

1. KaryoStat™ analysis of CUB12899-10 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 5)

Copy Number State

Figure 5: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

KaryoStat™ Results: CUB12899-11

1. KaryoStat™ analysis of CUB12899-11 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 6)

Copy Number State

Figure 6: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

KaryoStat™ Results: CUB12899-8

1. KaryoStat™ analysis of CUB12899-8 revealed the sample originated from a male individual
2. Chromosomal aberrations were observed when comparing to the reference set (Table 3, Figure 3)
3. A supplemental document with detailed information on the aberration will be provided to the Client

Chromosome	Type	Cytoband Start	CN State	Size (kbp)
2	Gain	q33.2	3	2,618

Table 3: KaryoStat™ analysis. Chromosomal aberrations are indicated in the table shown**.** See supplemental data for more details.

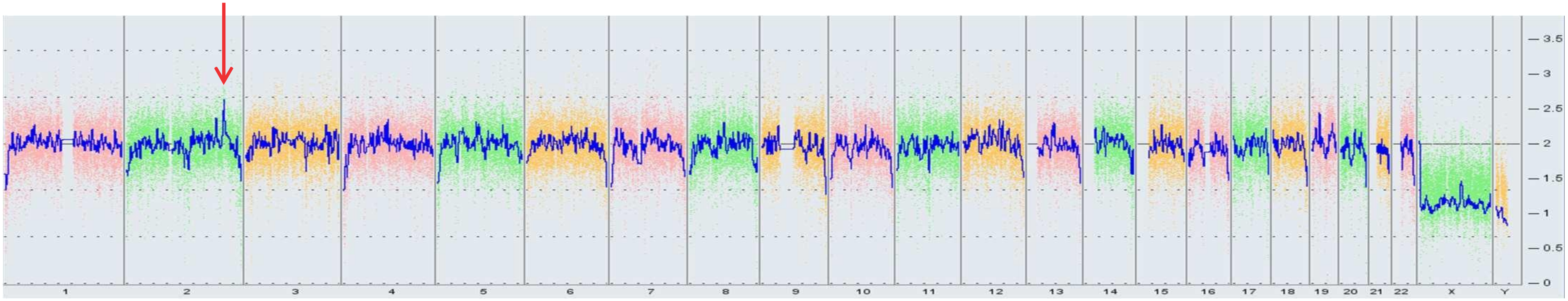

Figure 3: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any). The whole genome view analysis revealed chromosomal aberrations indicated by the red arrow.

KaryoStat™ Results: CUB12899-21

1. KaryoStat™ analysis of CUB12899-21 revealed the sample originated from a female individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 22)

Copy Number State

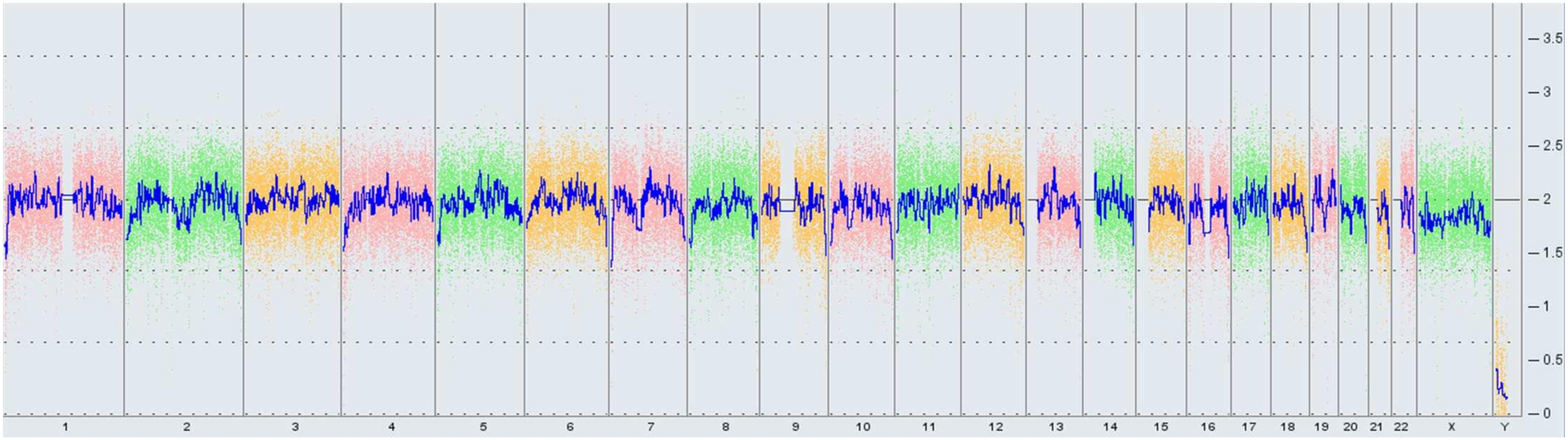

Figure 22: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

KaryoStat™ Results: CUB12899-22

1. KaryoStat™ analysis of CUB12899-22 revealed the sample originated from a female individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 23)

Copy Number State

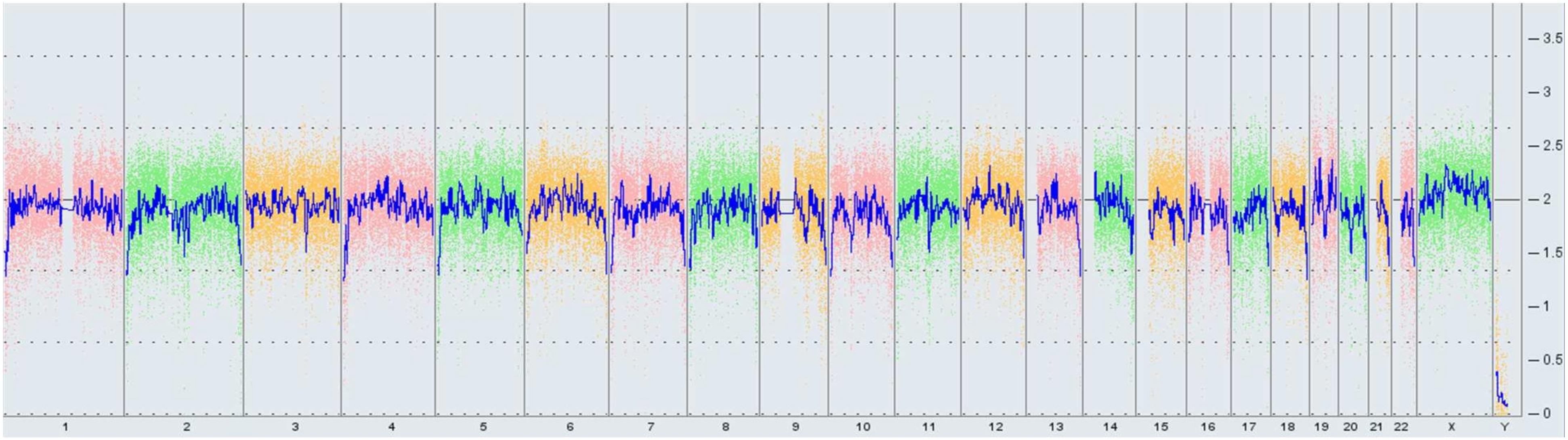

Figure 23: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899-1

1. KaryoStat™ analysis of CUB12899-1 revealed the sample originated from a male individual
2. Chromosomal aberrations were observed when comparing to the reference set (Table 5, Figure 18)
3. A supplemental document with detailed information on the aberration will be provided to the Client

Chromosome	Type	Cytoband Start	CN State	Size (kbp)
12	Gain	p13.33	3	6,947

Table 5: KaryoStat™ analysis. Chromosomal aberrations are indicated in the table shown**.** See supplemental data for more details.

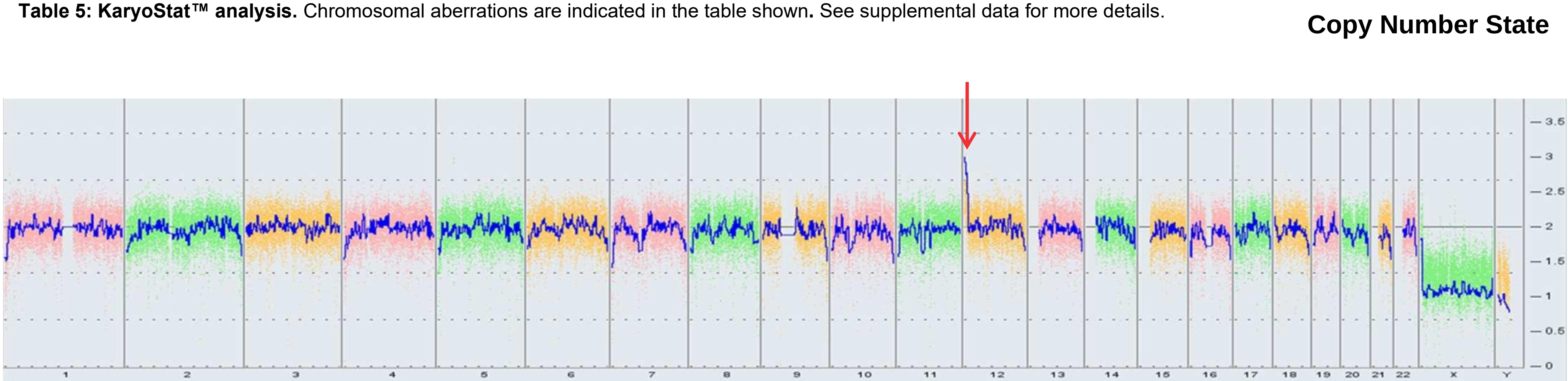

Figure 18: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any). The whole genome view analysis revealed chromosomal aberrations indicated by the red arrow.

KaryoStat™ Results: CUB12899-2

1. KaryoStat™ analysis of CUB12899-2 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 19)

Copy Number State

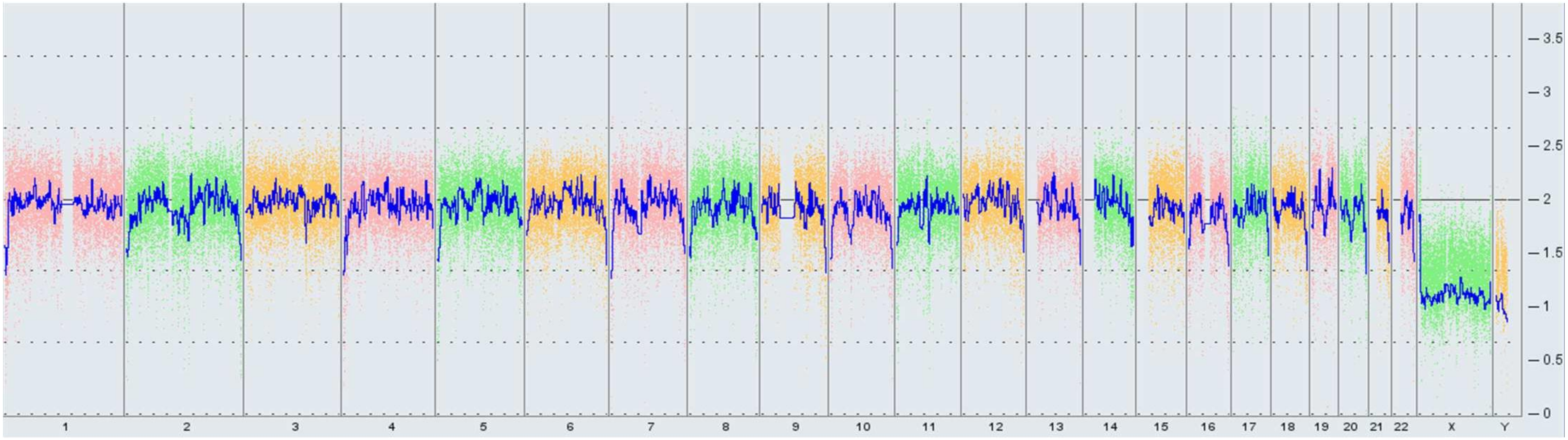

Figure 19: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899-3

1. KaryoStat™ analysis of CUB12899-3 revealed the sample originated from a female individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 20)

Copy Number State

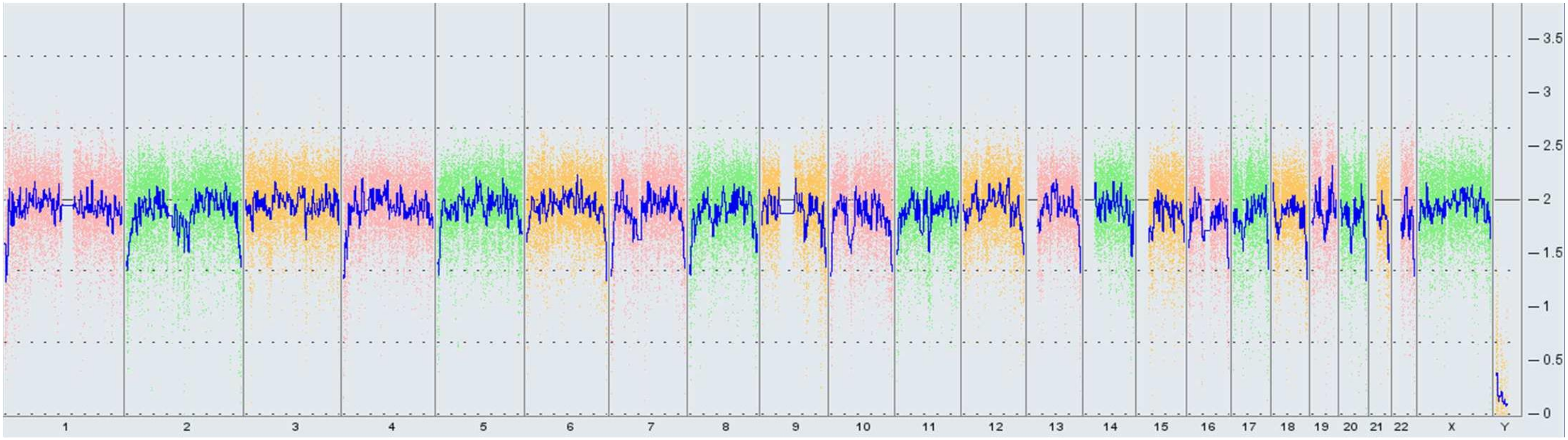

Figure 20: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899-14

1. KaryoStat™ analysis of CUB12899-14 revealed the sample originated from a female individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 7)

Figure 7: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899-17

1. KaryoStat™ analysis of CUB12899-17 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 9)

Copy Number State

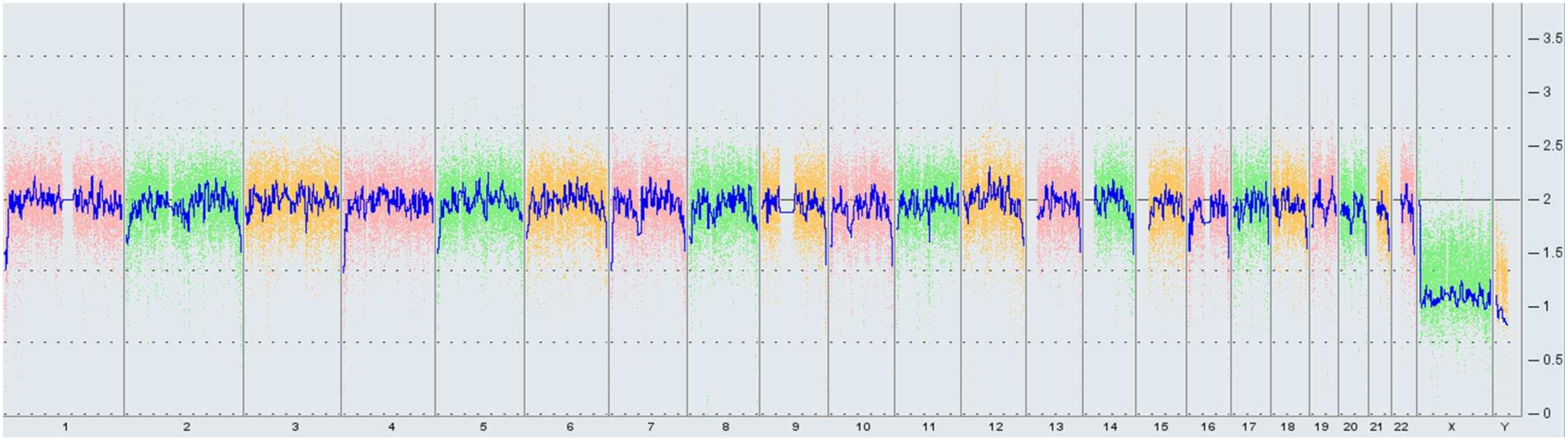

Figure 9: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899-20

1. KaryoStat™ analysis of CUB12899-20 revealed the sample originated from a male individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 12)

Copy Number State

Figure 12: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

Disclaimer: This assay was conducted solely for the listed investigator/institution. The results of this assay are for research use only.

KaryoStat™ Results: CUB12899-23

1. KaryoStat™ analysis of CUB12899-23 revealed the sample originated from a female individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 13)

Copy Number State

Figure 13: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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KaryoStat™ Results: CUB12899r-2

1. KaryoStat™ analysis of CUB12899r-2 revealed the sample originated from a female individual
2. No chromosomal aberrations were found when comparing against the reference dataset (Figure 2)

Copy Number State

Figure 2: Whole genome view. The whole genome view displays all somatic and sex chromosomes in one frame with high level copy number. The smooth signal plot (right y-axis) is the smoothing of the log2 ratios which depict the signal intensities of probes on the microarray. A value of 2 represents a normal copy number state (CN = 2). A value of 3 represents chromosomal gain (CN = 3). A value of 1 represents a chromosomal loss (CN = 1). The pink, green and yellow colors indicate the raw signal for each individual chromosome probe, while the blue signal represents the normalized probe signal which is used to identify copy number and aberrations (if any).

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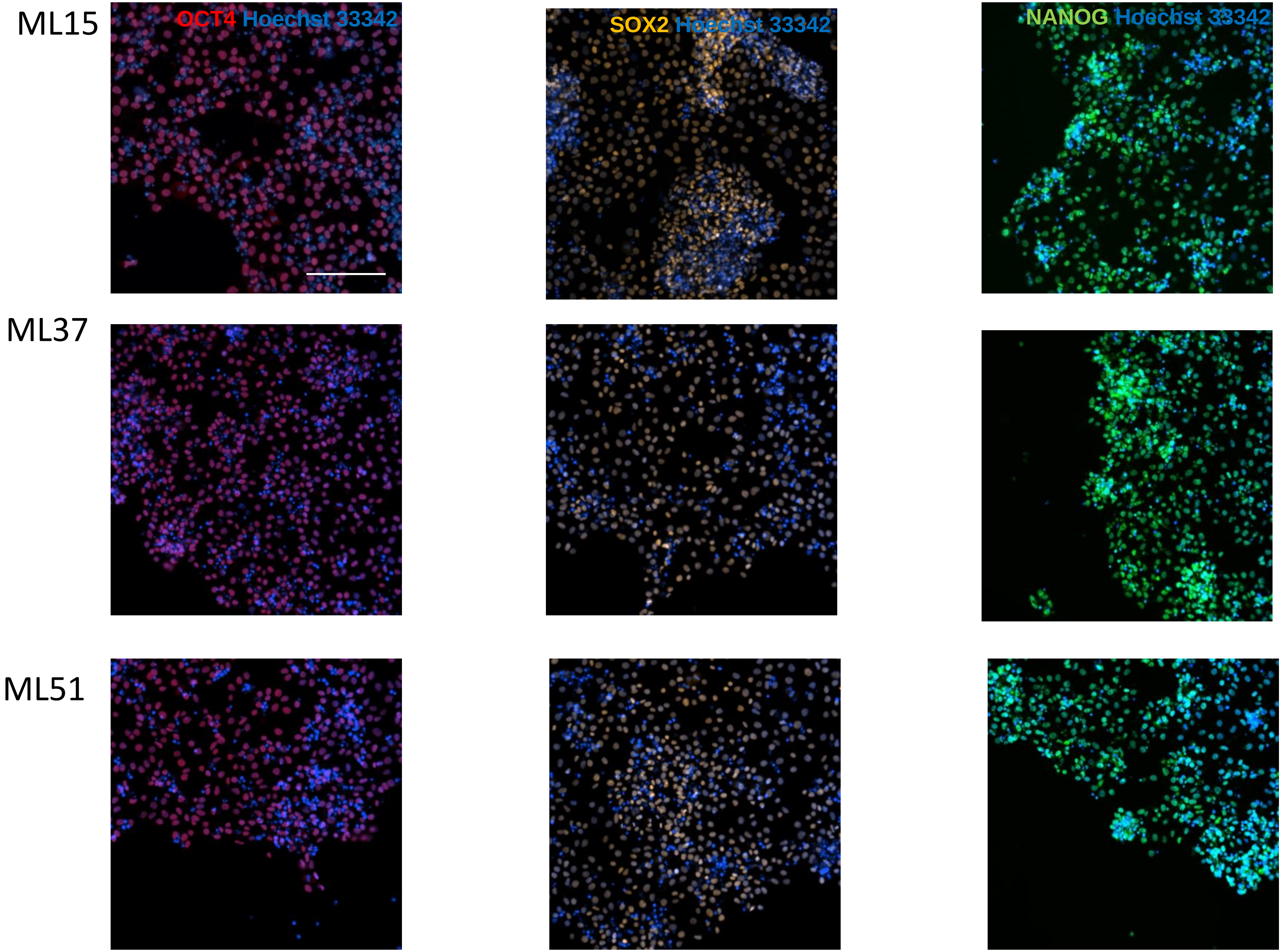
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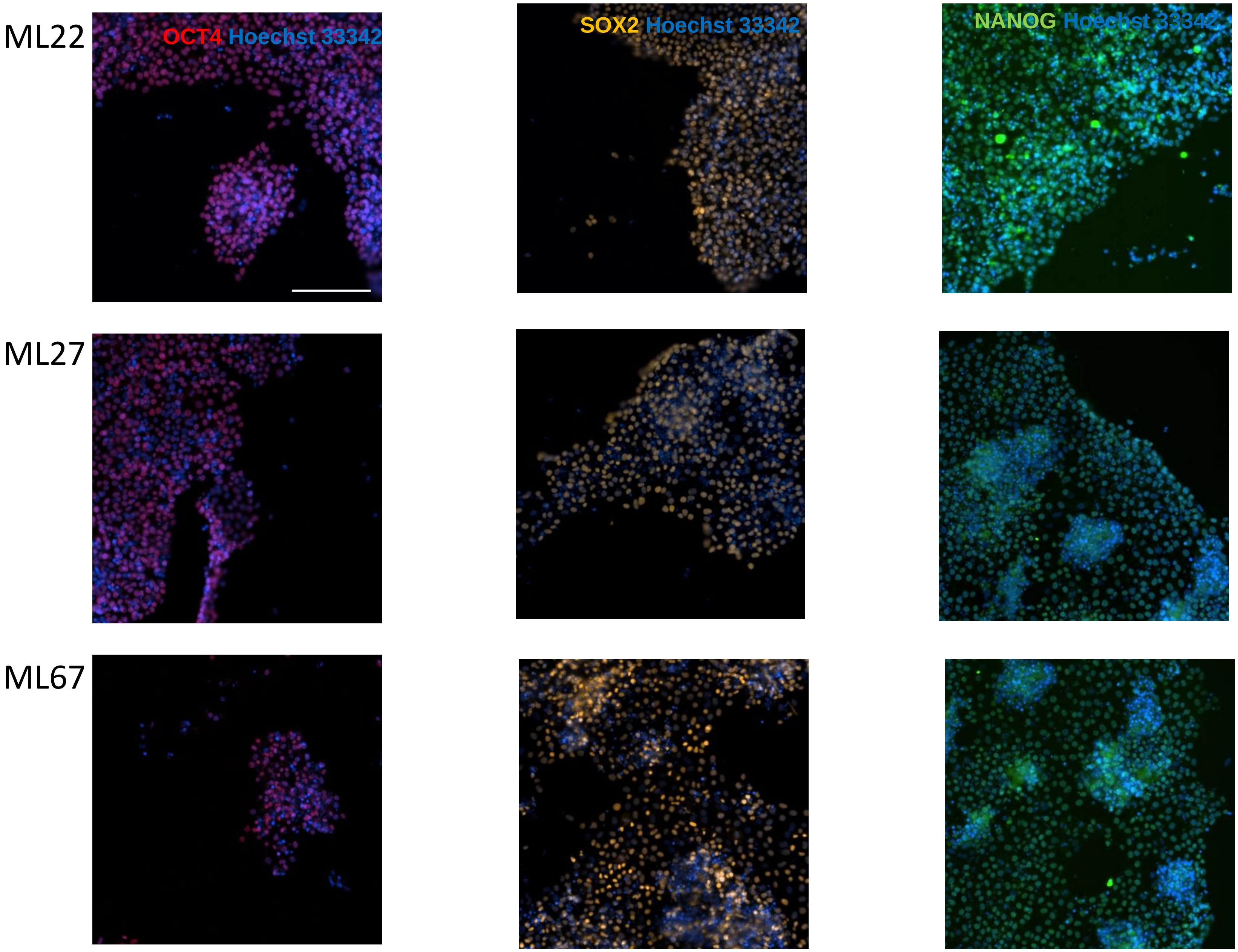
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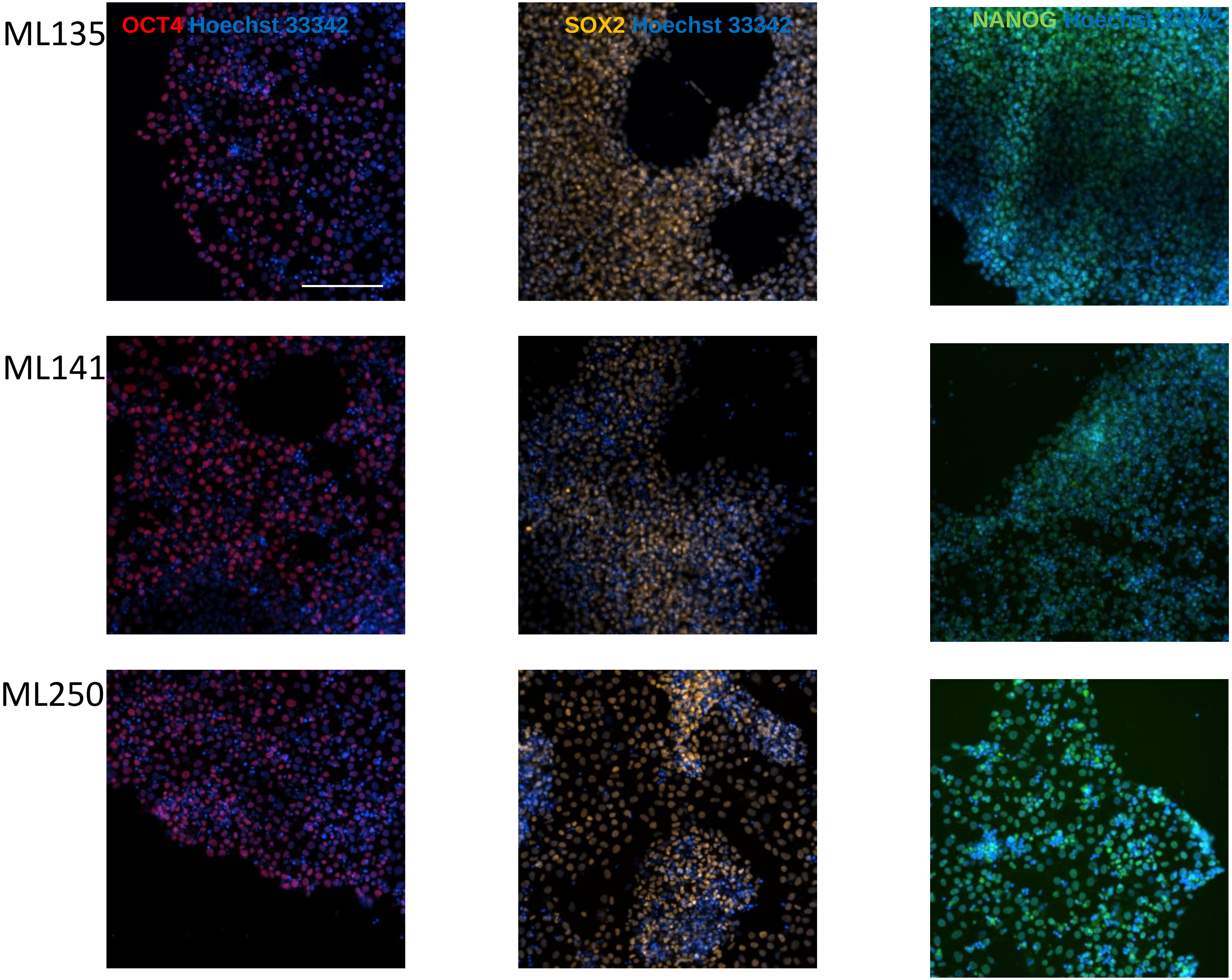
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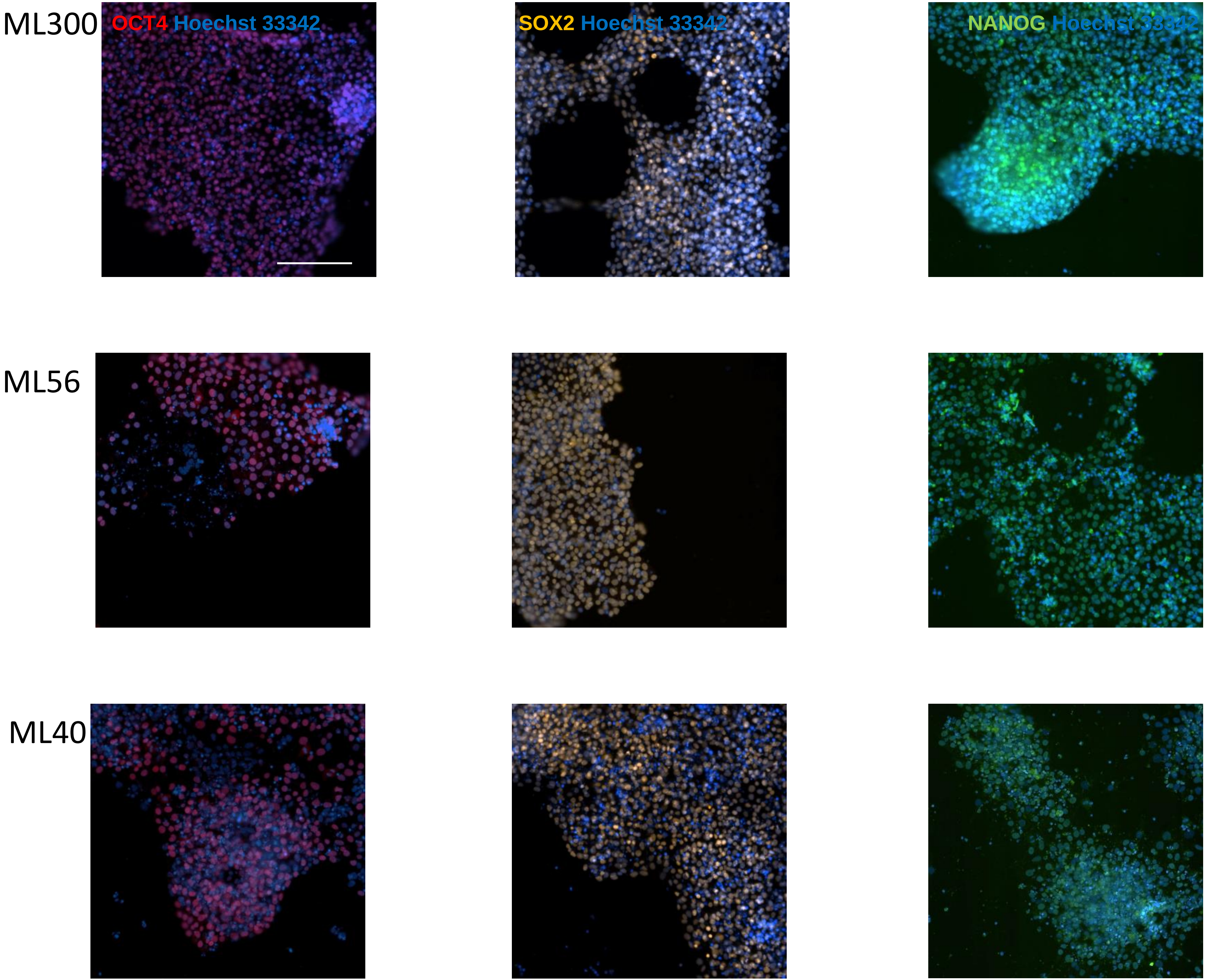
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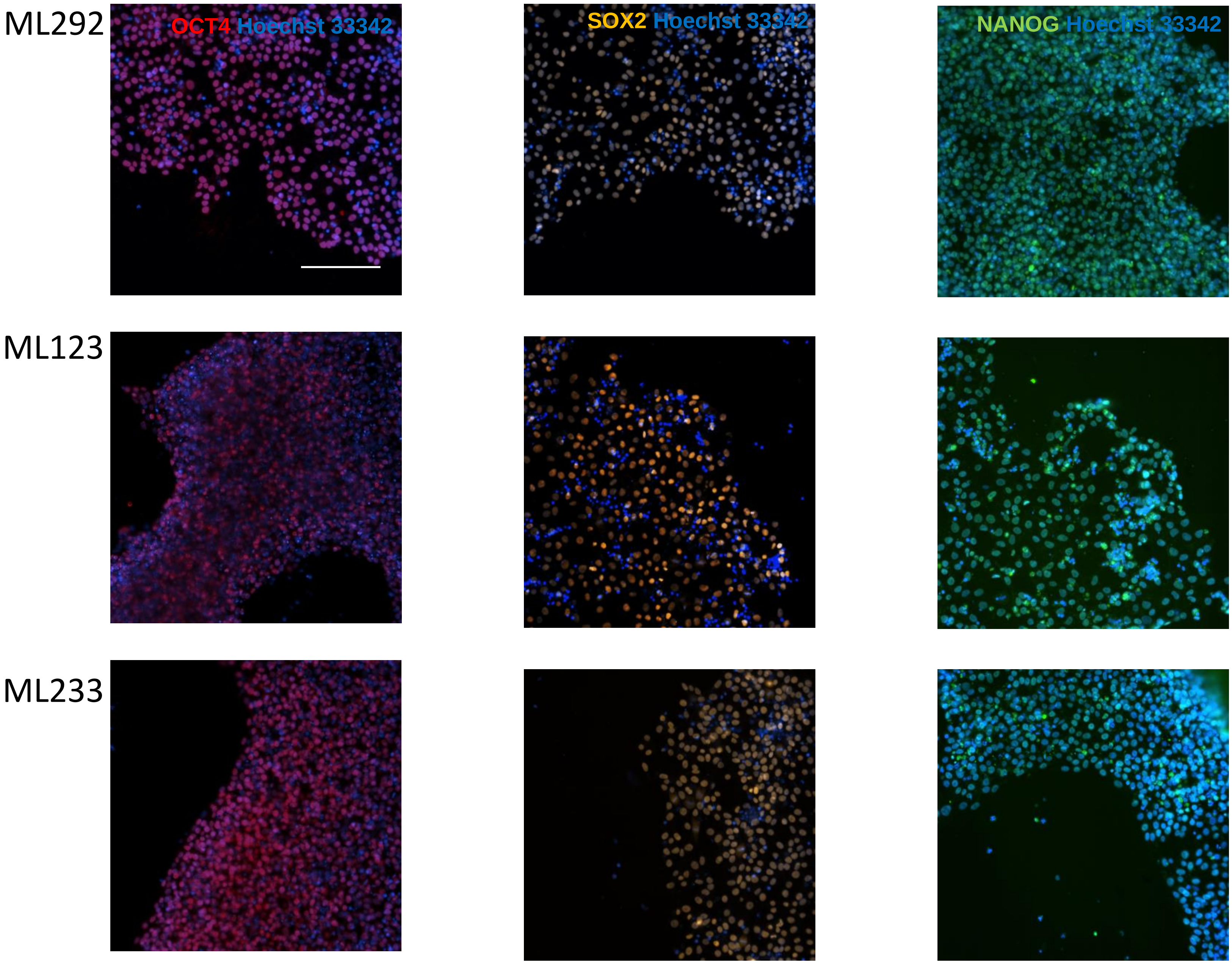
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