

Supplementary Information:

Deep learning and automated Cell Painting reveal Parkinson's disease-specific signatures in primary patient fibroblasts

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Cell line ID	Donor ID	Cross-val fold	Pair ID	Disease state	Sex	Age	European ancestry	UPDRS score	Biopsy collection year	Biopsy location	Thaw format	Thaw freeze date	Doubling time
01	50121	1	0	Healthy	F	54	99%		2012	unspecified	6w	6/17/2019	3.32
02	51255	1	0	LRRK2 PD	F	56	92%	71	2017	left upper thigh	6w	6/17/2019	2.68
03	51260	2	1	Healthy	F	64	96%		2017	left upper leg	12w→6w	8/9/2019	2.70
04	51253	2	1	Sporadic PD	F	63	99%	23	2017	left upper arm	6w	7/30/2019	3.41
05	50114	4	2	Healthy	M	67	94%		2012	unspecified	6w	7/31/2019	2.77
06	50463	4	2	Sporadic PD	M	69	92%	34	2013	unspecified	6w	8/15/2019	3.39
07	50752	4	3	Healthy	F	58	90%		2013	left upper arm	12w→6w	8/22/2019	5.36
08	50437	4	3	Sporadic PD	F	59	90%	45	2013	left upper leg	6w	7/11/2019	3.80
09	50665	1	4	Healthy	F	71	91%		2013	right lower leg	12w→6w	7/30/2019	3.24
10	50373	1	4	Sporadic PD	F	69	100%	61	2012	right thigh	6w	7/5/2019	4.37
11	51218	3	5	Healthy	F	60	100%		2016	left upper arm	6w	7/11/2019	2.47
12	51193	3	5	Sporadic PD	F	60	91%	53	2015	left thigh	6w	7/22/2019	2.49
13	50594	4	6	Healthy	M	81			2013	right lower cheek	6w	6/17/2019	3.11
14	51259	4	6	Sporadic PD	M	76	95%	29	2017	left arm	6w	9/3/2019	3.87
15	51005	4	7	Healthy	F	57	90%		2014	left upper arm	6w	7/5/2019	2.83
16	51149	4	7	Sporadic PD	F	57	97%	26	2015	left upper arm	6w	7/5/2019	2.50
17	50183	3	8	Healthy	M	62	98%		2012	chest	6w	7/18/2019	6.19
18	50951	3	8	Sporadic PD	M	62	98%	20	2014	left upper arm	12w→6w	7/30/2019	3.30
19	51107	0	9	Healthy	M	59	97%		2014	upper arm	6w	7/11/2019	2.53
20	51099	0	9	Sporadic PD	M	61	100%	19	2014	upper left arm	12w→6w	7/22/2019	4.06
21	51183	1	10	Healthy	M	66	89%		2015	left arm	6w	9/9/2019	2.12
22	50480	1	10	Sporadic PD	M	66	99%	56	2013	left upper arm	6w	7/31/2019	4.55
23	50764		11	Healthy	F	56	89%		2013	left upper arm	6w	6/7/2019	2.71
24	51266		11	GBA PD	F	54	96%	30	2017	unspecified	6w	6/7/2019	2.28
25	50167	0	12	Healthy	M	62	98%		2012	unspecified	12w→6w	7/22/2019	4.64
26	51156	0	12	Sporadic PD	M	68	100%	20	2015	left upper arm	6w	8/13/2019	2.41
27	50956		13	Healthy	M	47			2014	left upper arm	6w	6/11/2019	6.64
28	51249		13	GBA PD	M	46	92%	20	2016	right upper arm	6w	6/11/2019	2.44
29	50767	2	14	Healthy	F	71	88%		2013	left upper arm	6w	7/30/2019	2.71
30	50406	2	14	Sporadic PD	F	68	90%	24	2012	right upper arm	12w→6w	9/3/2019	5.24
31	51105	2	15	Healthy	M	59			2014	upper arm	6w	6/19/2019	2.28
32	51142	2	15	Sporadic PD	M	59	90%	36	2015	right arm	12w→6w	7/5/2019	3.07
33	51140	0	15	Healthy	M	55	96%		2015	left upper arm	6w	6/13/2019	3.53
34	51256	0	16	Sporadic PD	M	54	94%	31	2017	left inner arm	6w	6/13/2019	6.57
35	50939	1	17	Healthy	M	64	91%		2014	left upper arm	6w	7/22/2019	4.36
36	50449	1	17	Sporadic PD	M	64	98%	44	2013	left upper arm	12w→6w	7/30/2019	3.41
37	50128	3	18	Healthy	M	57	97%		2012	unspecified	6w	7/11/2019	2.72
38	50392	3	18	LRRK2 PD	M	59	93%	20	2012	right thigh	6w	7/11/2019	3.58
39	51239	0	19	Healthy	M	64	99%		2016	left upper inner arm	6w	7/31/2019	2.25
40	51037	0	19	Sporadic PD	M	68	93%	34	2014	left upper arm	12w→6w	8/29/2019	4.29
41	50199	1	20	Healthy	M	81	99%		2012	right arm	6w	6/7/2019	3.03
42	50590	1	20	Sporadic PD	M	76	92%	27	2013	left upper arm	6w	8/13/2019	3.30
43	50112	0	21	Healthy	F	77	92%		2012	unspecified	12w→6w	7/5/2019	4.28
44	51126	0	21	Sporadic PD	F	74	99%	35	2015	unspecified	6w	6/7/2019	3.42
45	50192	2	22	Healthy	M	77	97%		2012	nose	6w	6/25/2019	4.53
46	51261	2	22	LRRK2 PD	M	74	92%	29	2017	right upper arm	12w→6w	8/22/2019	2.78
47	51152		23	Healthy	F	74	100%		2015	left upper arm	12w→6w	6/19/2019	2.94
48*	10124*		23	GBA PD*	F	74	94%		2011	right arm	6w	6/13/2019	6.04
49	51030	2	24	Healthy	F	70	94%		2014	left arm	6w	7/18/2019	2.80
50	51220	2	24	Sporadic PD	F	69	98%	21	2016	left upper arm	6w	7/18/2019	3.22
51	51093	0	25	Healthy	F	73	99%		2015	left upper arm	12w→6w	7/11/2019	2.75
52	50864	0	25	Sporadic PD	F	78	98%	34	2013	left upper arm	6w	6/13/2019	3.48
53	51254		26	Healthy	M	68	92%		2017	unspecified	6w	7/5/2019	2.25
54	10198		26	GBA PD	M	66	98%	38	2012	right upper inner arm	6w	7/5/2019	2.40
55	51148	4	27	Healthy	M	61	90%		2015	left upper arm	6w	8/13/2019	2.68
56	50640	4	27	Sporadic PD	M	66	93%	21	2013	upper arm	6w	8/13/2019	2.90
57*	50634*	4	28	Healthy*	F	72	92%		2013	left upper arm	6w	7/5/2019	2.61
58	51243	4	28	Sporadic PD	F	72	90%	47	2016	right thigh	12w→6w	8/22/2019	2.66
59	51194	3	29	Healthy	M	80	99%		2015	left arm	6w	6/11/2019	3.75
60	51268	3	29	Sporadic PD	M	79	92%	44	2017	unspecified	6w	6/11/2019	2.70
61	51123	1	30	Healthy	F	54	92%		2015	left upper arm	6w	6/25/2019	3.21
62	50483	1	30	Sporadic PD	F	55	91%		2013	left upper leg	6w	6/25/2019	4.79
63	51004	3	31	Healthy	M	54	98%		2014	left upper arm	12w→6w	6/25/2019	3.09
64	50963	3	31	Sporadic PD	M	54	99%	42	2014	left upper arm	6w	6/7/2019	3.67
65	10130	4	32	Healthy	M	52			2011	left inner arm	6w	6/11/2019	2.52
66	50674	4	32	LRRK2 PD	M	51	91%	12	2013	right upper arm	6w	6/11/2019	4.23
67	50598	2	33	Healthy	M	58	91%		2013	left forearm	6w	7/30/2019	2.57
68	50610	2	33	Sporadic PD	M	59	97%	28	2013	left upper arm	6w	6/25/2019	2.88
69	51162	1	34	Healthy	M	47	98%		2015	left arm	6w	8/13/2019	2.01
70	50592	1	34	LRRK2 PD	M	45	91%		2013	left upper arm	12w→6w	8/22/2019	2.90
71	51235	0	35	Healthy	M	68	98%		2016	left arm	6w	9/9/2019	2.48
72	51212	0	35	Sporadic PD	M	70	98%	28	2013	left arm	6w	8/15/2019	3.08
73	50191		36	Healthy	M	61	92%		2012	right cheek	6w	7/22/2019	6.10
74	50660		36	GBA PD	M	65	91%		2013	left upper arm	12w→6w	7/30/2019	5.78
75	50105		37	Healthy	M	76	90%		2012	unspecified	12w→6w	7/22/2019	4.07
76	51221		37	GBA PD	M	74	93%	22	2016	left upper arm	6w	6/25/2019	2.63
77	51274		38	Healthy	M	64			2018	left upper arm	6w	8/13/2019	2.82
78	51021		38	GBA PD	M	65	93%		2014	left upper arm	6w	8/13/2019	2.86
79	50176		39	Healthy	M	58			2012	chin	6w	6/19/2019	3.16
80	50880		39	GBA PD	M	59	93%	18	2013	upper arm	6w	6/19/2019	3.50
81	50559	0	40	Healthy	F	64	91%		2013	left upper arm	6w	7/31/2019	2.58
82	51010	0	40	LRRK2 PD	F	63	94%	18	2013	left upper arm	12w→6w	8/28/2019	3.91
83	50617	4	41	Healthy	M	53			2013	right upper leg	6w	6/13/2019	2.79
84	51176	4	41	Sporadic PD	M	53	98%	31	2015	left arm	6w	6/13/2019	2.71
85	51139	3	42	Healthy	F	52	99%		2015	left upper arm	6w	8/15/2019	2.38
86	51187	3	42	Sporadic PD	F	66	98%	16	2015	left upper arm	6w	8/29/2019	2.52
87	50758	3	43	Healthy	F	78	91%		2013	left upper arm	6w	6/13/2019	4.02
88	51200	3	43	Sporadic PD	F	80	90%	79	2015	left arm	6w	6/11/2019	4.54
89	50174	2	44	Healthy	M	56	96%		2012	forehead	6w	6/17/2019	2.55
90	50421	2	44	Sporadic PD	M	55	99%	26	2012	left upper arm	6w	6/17/2019	4.98
91	50497			Sporadic PD	F	64	90%	45	2018	left upper arm	6w	7/11/2019	2.53
92	51239			Healthy	M	67	99%		2019	right arm	6w	7/31/2019	2.33
93	51083			Healthy	F	77	95%		2019	left arm	6w	6/19/2019	3.08
94	51148			Healthy	M	65	90%		2019	upper arm	6w	8/13/2019	2.21
95	50492			LRRK2 PD	M	51	91%		2019	left upper arm	6w	7/18/2019	3.55
96	50626			Sporadic PD	M	70	97%	43	2013	unspecified	6w	9/3/2019	2.60

Supplementary Table 1 | Information about the 96 cell lines from 91 donors used in the study. Columns left to right: a 2-digit ID mapping to a cell line from a unique skin biopsy; the biopsy donor; the cross-validation fold for healthy vs. PD prediction; ID for PD individual and matched healthy control; PD status; donor sex; donor age; an ancestry score from genotyping; the Unified Parkinson Disease Rating Scale, a clinical measure of PD severity; skin biopsy collection year; location where biopsy was acquired; cell expansion in 6-well ("6w") or from 12-well to 6-well format ("12w→6w"); date expanded cells were frozen; and doubling time during cell expansion in days, respectively. *: unconfirmed cell line (see Methods).

			Cross-validation							
			set #1	set #2	set #3	set #4	set #5	set #6	set #7	set #8
Batch	Plate layout	Cell lines								
1	1	all 96	test	ignore	ignore	ignore	ignore	train	train	train
	2	all 96	ignore	train	train	train	test	ignore	ignore	ignore
2	1	all 96	ignore	test	ignore	ignore	train	ignore	train	train
	2	all 96	train	ignore	train	train	ignore	test	ignore	ignore
3	1	all 96	ignore	ignore	test	ignore	train	train	ignore	train
	2	all 96	train	train	ignore	train	ignore	ignore	test	ignore
4	1	all 96	ignore	ignore	ignore	test	train	train	train	ignore
	2	all 96	train	train	train	ignore	ignore	ignore	ignore	test

Supplementary Table 2 | Cross-validation strategy for 96-way cell line classification. For each of 8 cross-validation sets, both batch and plate layout were held out in the test set.

			Cross-validation							
			set #1	set #2	set #3	set #4	set #5	set #6	set #7	set #8
Batch	Plate layout	Cell lines								
1	1	5 held-out biopsies	test	ignore	ignore	ignore	ignore	ignore	ignore	ignore
		remaining 91 lines	ignore	ignore	ignore	ignore	ignore	train	train	train
	2	5 held-out biopsies	ignore	ignore	ignore	ignore	test	ignore	ignore	ignore
		remaining 91 lines	ignore	train	train	train	ignore	ignore	ignore	ignore
2	1	5 held-out biopsies	ignore	test	ignore	ignore	ignore	ignore	ignore	ignore
		remaining 91 lines	ignore	ignore	ignore	ignore	train	ignore	train	train
	2	5 held-out biopsies	ignore	ignore	ignore	ignore	ignore	test	ignore	ignore
		remaining 91 lines	train	ignore	train	train	ignore	ignore	ignore	ignore
3	1	5 held-out biopsies	ignore	ignore	test	ignore	ignore	ignore	ignore	ignore
		remaining 91 lines	ignore	ignore	ignore	ignore	train	train	ignore	train
	2	5 held-out biopsies	ignore	ignore	ignore	ignore	ignore	ignore	test	ignore
		remaining 91 lines	train	train	ignore	train	ignore	ignore	ignore	ignore
4	1	5 held-out biopsies	ignore	ignore	ignore	test	ignore	ignore	ignore	ignore
		remaining 91 lines	ignore	ignore	ignore	ignore	train	train	train	ignore
	2	5 held-out biopsies	ignore	ignore	ignore	ignore	ignore	ignore	ignore	test
		remaining 91 lines	train	train	train	ignore	ignore	ignore	ignore	ignore

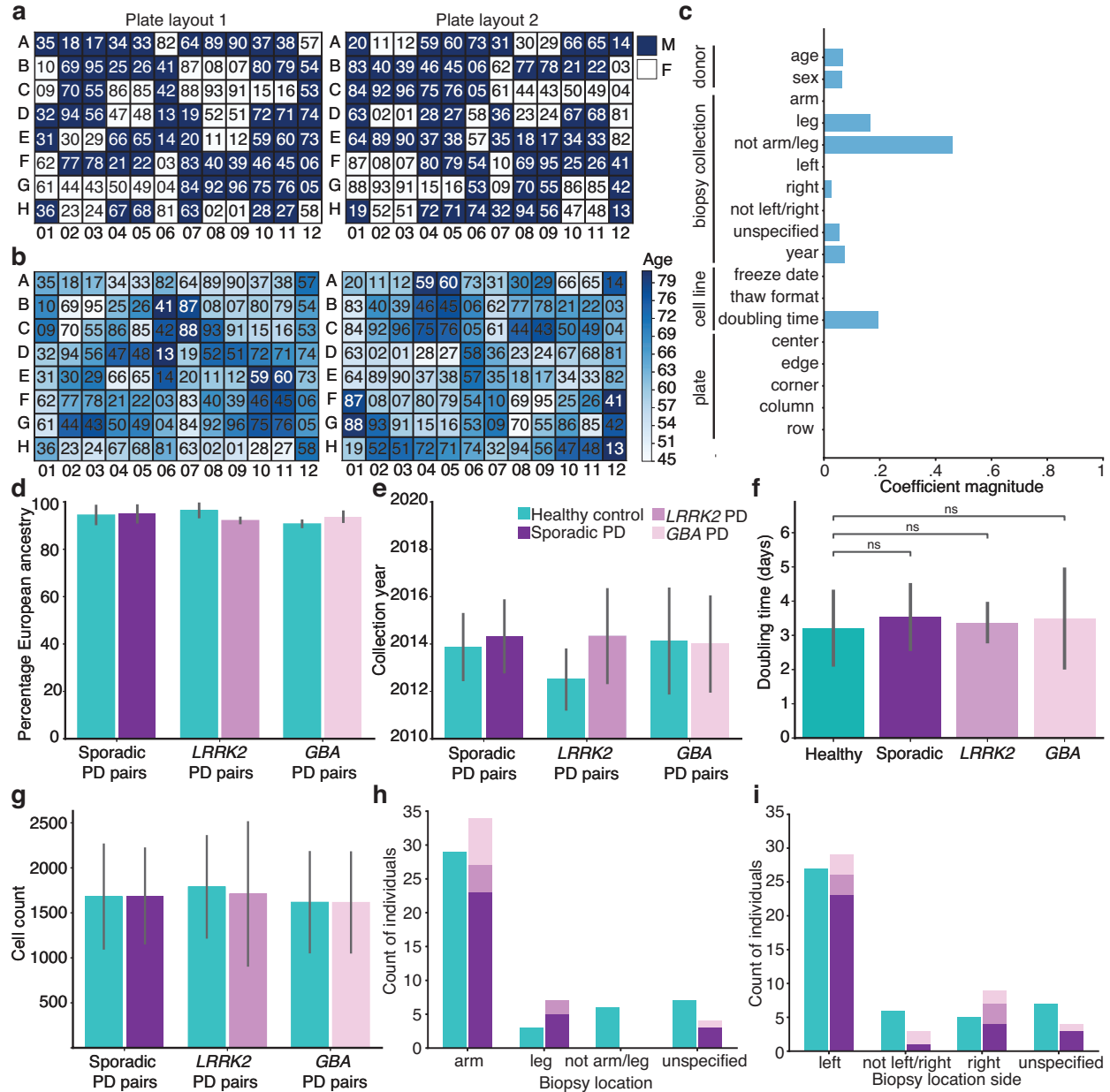
Supplementary Table 3 | Cross-validation strategy for 91-way biopsy donor classification. For each of 8 cross-validation sets, the test set consisted of cell lines from one of the two biopsies from the 5 individuals who donated two biopsies, while the train set consisted of cell lines from the complementary set of biopsies from these 5 individuals and the remaining 86 individuals who donated only a single biopsy. To avoid plate position biases as potential confounds, plate layout was also held out, and to assess model generalization to a test biopsy acquired in a new batch, batch was also held out. These 8 cross-validation sets were conducted twice, once holding out in the test sets the earlier set of skin biopsies from the 5 individuals who donated two biopsies (cell lines 08, 39, 51, 55, 70), and again holding out the later set (cell lines 91, 92, 93, 94, 95).

					Cross-validation				
Cell line	Disease state	Pair ID	Batch	Plate layout	set #0	set #1	set #2	set #3	set #4
25	Healthy	12	all 4	both	test	train	train	train	train
26	Sporadic PD	12	all 4	both	test	train	train	train	train
33	Healthy	16	all 4	both	test	train	train	train	train
34	Sporadic PD	16	all 4	both	test	train	train	train	train
39	Healthy	19	all 4	both	test	train	train	train	train
40	Sporadic PD	19	all 4	both	test	train	train	train	train
43	Healthy	21	all 4	both	test	train	train	train	train
44	Sporadic PD	21	all 4	both	test	train	train	train	train
51	Healthy	25	all 4	both	test	train	train	train	train
52	Sporadic PD	25	all 4	both	test	train	train	train	train
71	Healthy	35	all 4	both	test	train	train	train	train
72	Sporadic PD	35	all 4	both	test	train	train	train	train
81	Healthy	40	all 4	both	test	train	train	train	train
82	LRRK2 PD	40	all 4	both	test	train	train	train	train
19	Healthy	9	all 4	both	test	train	train	train	train
20	Sporadic PD	9	all 4	both	test	train	train	train	train
1	Healthy	0	all 4	both	train	test	train	train	train
2	LRRK2 PD	0	all 4	both	train	test	train	train	train
21	Healthy	10	all 4	both	train	test	train	train	train
22	Sporadic PD	10	all 4	both	train	test	train	train	train
35	Healthy	17	all 4	both	train	test	train	train	train
36	Sporadic PD	17	all 4	both	train	test	train	train	train
41	Healthy	20	all 4	both	train	test	train	train	train
42	Sporadic PD	20	all 4	both	train	test	train	train	train
61	Healthy	30	all 4	both	train	test	train	train	train
62	Sporadic PD	30	all 4	both	train	test	train	train	train
69	Healthy	34	all 4	both	train	test	train	train	train
70	LRRK2 PD	34	all 4	both	train	test	train	train	train
9	Healthy	4	all 4	both	train	test	train	train	train
10	Sporadic PD	4	all 4	both	train	test	train	train	train
3	Healthy	1	all 4	both	train	train	test	train	train
4	Sporadic PD	1	all 4	both	train	train	test	train	train
29	Healthy	14	all 4	both	train	train	test	train	train
30	Sporadic PD	14	all 4	both	train	train	test	train	train
31	Healthy	15	all 4	both	train	train	test	train	train
32	Sporadic PD	15	all 4	both	train	train	test	train	train
45	Healthy	22	all 4	both	train	train	test	train	train
46	LRRK2 PD	22	all 4	both	train	train	test	train	train
49	Healthy	24	all 4	both	train	train	test	train	train
50	Sporadic PD	24	all 4	both	train	train	test	train	train
67	Healthy	33	all 4	both	train	train	test	train	train
68	Sporadic PD	33	all 4	both	train	train	test	train	train
89	Healthy	44	all 4	both	train	train	test	train	train
90	Sporadic PD	44	all 4	both	train	train	test	train	train
37	Healthy	18	all 4	both	train	train	train	test	train
38	LRRK2 PD	18	all 4	both	train	train	train	test	train
59	Healthy	29	all 4	both	train	train	train	test	train
60	Sporadic PD	29	all 4	both	train	train	train	test	train
63	Healthy	31	all 4	both	train	train	train	test	train
64	Sporadic PD	31	all 4	both	train	train	train	test	train
85	Healthy	42	all 4	both	train	train	train	test	train
86	Sporadic PD	42	all 4	both	train	train	train	test	train
87	Healthy	43	all 4	both	train	train	train	test	train
88	Sporadic PD	43	all 4	both	train	train	train	test	train
11	Healthy	5	all 4	both	train	train	train	test	train
12	Sporadic PD	5	all 4	both	train	train	train	test	train
17	Healthy	8	all 4	both	train	train	train	test	train
18	Sporadic PD	8	all 4	both	train	train	train	test	train
5	Healthy	2	all 4	both	train	train	train	train	test
6	Sporadic PD	2	all 4	both	train	train	train	train	test
55	Healthy	27	all 4	both	train	train	train	train	test
56	Sporadic PD	27	all 4	both	train	train	train	train	test
57*	Healthy*	28	all 4	both	train	train	train	train	test
58	Sporadic PD	28	all 4	both	train	train	train	train	test
7	Healthy	3	all 4	both	train	train	train	train	test
8	Sporadic PD	3	all 4	both	train	train	train	train	test
65	Healthy	32	all 4	both	train	train	train	train	test
66	LRRK2 PD	32	all 4	both	train	train	train	train	test
83	Healthy	41	all 4	both	train	train	train	train	test
84	Sporadic PD	41	all 4	both	train	train	train	train	test
13	Healthy	6	all 4	both	train	train	train	train	test
14	Sporadic PD	6	all 4	both	train	train	train	train	test
15	Healthy	7	all 4	both	train	train	train	train	test
16	Sporadic PD	7	all 4	both	train	train	train	train	test

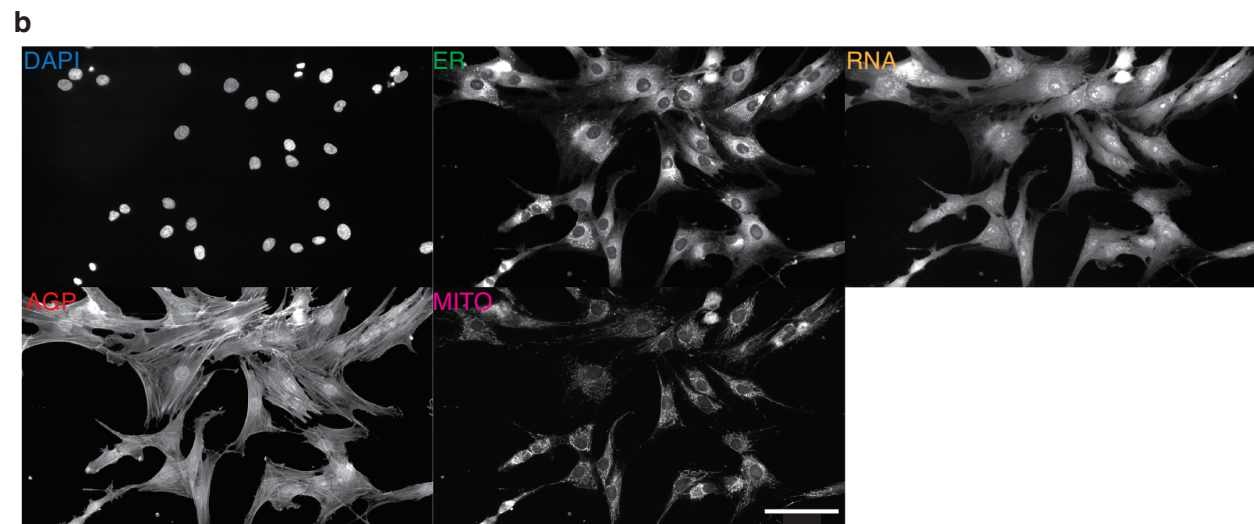
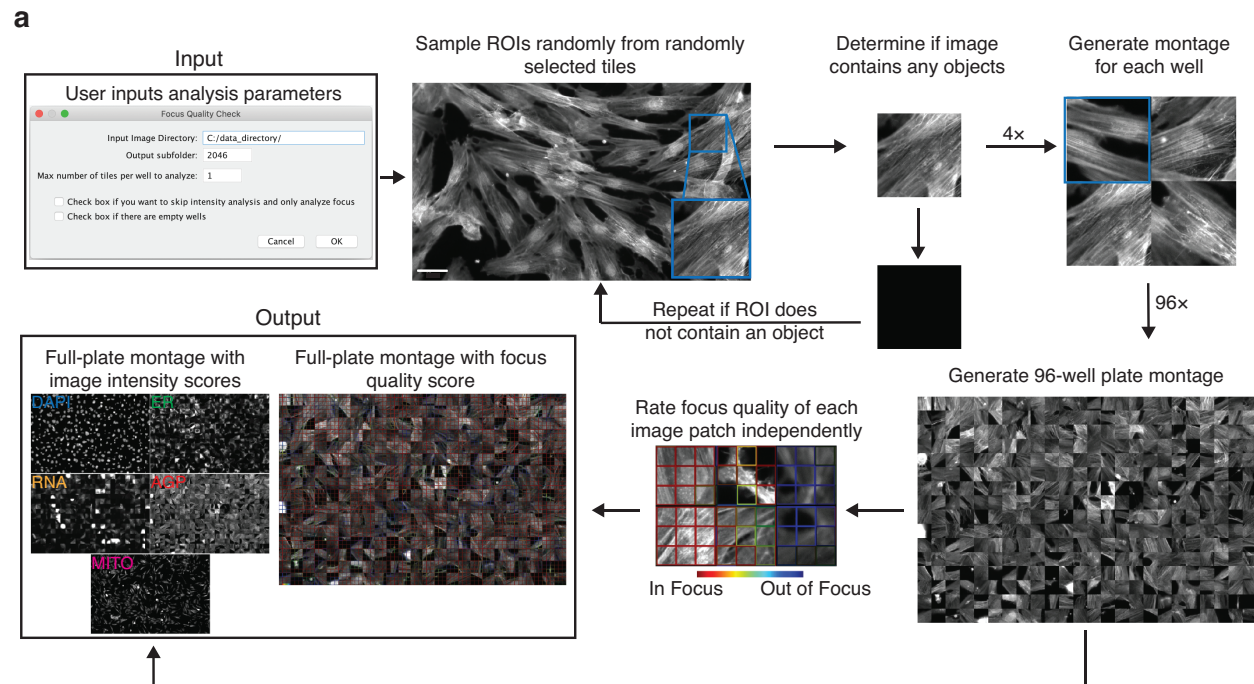
Supplementary Table 4 | 5-fold Cross-validation strategy for healthy vs. PD classification. A subset of 74 cell lines from 74 individuals (6 *LRRK2* PD and paired controls, and 31 sporadic PD and paired controls) was divided into 5 cross-validation folds. For each of 5 cross-validation sets, one fold of cell lines was held out in the test set. *: unconfirmed cell line (see Methods).

cells_AreaShape_Compactness cells_AreaShape_Eccentricity cytoplasm_AreaShape_Compactness cytoplasm_AreaShape_Eccentricity	cytoplasm_AreaShape_Solidity cytoplasm_AreaShape_Extent cells_AreaShape_Solidity	nuclei_Granularity_11_ER nuclei_Granularity_8_ER nuclei_Granularity_7_ER
cells_AreaShape_Zernike_8_4	cytoplasm_AreaShape_Zernike_6_4 cytoplasm_AreaShape_Zernike_8_8 cells_AreaShape_Zernike_6_6 cytoplasm_AreaShape_Zernike_6_6	nuclei_Granularity_13_Mito
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cells_Correlation_Overlap_Mito_ER cytoplasm_Correlation_Overlap_Mito_ER	cytoplasm_Granularity_10_RNA	nuclei_Granularity_6_ER
cells_Correlation_RWC_RNA_Mito	cytoplasm_Granularity_1_AGP cells_Granularity_1_AGP	nuclei_Granularity_8_Mito
cells_Granularity_6_AGP cells_Granularity_7_AGP	cytoplasm_RadialDistribution_MeanFrac_AGP_1of4 cytoplasm_RadialDistribution_MeanFrac_AGP_3of4	nuclei_Intensity_IntegratedIntensityEdge_ER nuclei_Texture_Contrast_ER_10_02
cells_Intensity_IntegratedIntensity_Mito cytoplasm_Intensity_MassDisplacement_AGP cytoplasm_AreaShape_Area cytoplasm_Intensity_IntegratedIntensity_RNA cells_AreaShape_MeanRadius cells_AreaShape_MaximumRadius cytoplasm_Intensity_IntegratedIntensityEdge_Mito cells_Intensity_IntegratedIntensityEdge_Mito cytoplasm_Intensity_IntegratedIntensity_Mito cells_AreaShape_Area cytoplasm_Intensity_IntegratedIntensity_DNA cells_Intensity_IntegratedIntensity_RNA cytoplasm_Intensity_IntegratedIntensity_ER	cytoplasm_RadialDistribution_MeanFrac_RNA_3of4 cells_Granularity_15_RNA	nuclei_Intensity_IntegratedIntensity_RNA nuclei_Intensity_IntegratedIntensity_ER
cells_Intensity_MassDisplacement_DNA	cytoplasm_RadialDistribution_RadialCV_AGP_3of4 cytoplasm_RadialDistribution_RadialCV_RNA_2of4	nuclei_Neighbors_NumberOfNeighbors_1
cells_Neighbors_PercentTouching_5 cells_Neighbors_PercentTouching_Adjacent cells_Neighbors_NumberOfNeighbors_5 cells_Neighbors_NumberOfNeighbors_Adjacent	nuclei_AreaShape_Zernike_2_0	nuclei_Neighbors_SecondClosestDistance_1
cells_RadialDistribution_FracAtD_AGP_1of4	nuclei_AreaShape_Zernike_4_2	nuclei_RadialDistribution_FracAtD_RNA_3of4
cells_RadialDistribution_MeanFrac_ER_3of4	nuclei_AreaShape_Zernike_7_1	nuclei_RadialDistribution_MeanFrac_AGP_2of4
cells_RadialDistribution_MeanFrac_RNA_4of4	nuclei_Correlation_Correlation_DNA_RNA	nuclei_RadialDistribution_MeanFrac_Mito_3of4 nuclei_Correlation_Correlation_DNA_Mito
	nuclei_Correlation_Correlation_ER_AGP nuclei_Correlation_Correlation_Mito_AGP	nuclei_RadialDistribution_MeanFrac_Mito_4of4
	nuclei_Correlation_Manders_AGP_DNA nuclei_Correlation_Manders_RNA_DNA	nuclei_RadialDistribution_RadialCV_AGP_3of4
	nuclei_Correlation_Manders_Mito_ER nuclei_Correlation_Manders_RNA_ER	nuclei_RadialDistribution_RadialCV_ER_1of4
	nuclei_Correlation_Overlap_DNA_AGP	nuclei_RadialDistribution_RadialCV_ER_3of4 nuclei_RadialDistribution_RadialCV_ER_2of4
		nuclei_RadialDistribution_RadialCV_RNA_4of4 cells_RadialDistribution_RadialCV_RNA_3of4
		nuclei_Texture_Correlation_AGP_10_01 nuclei_Texture_InfoMeas2_AGP_10_01 nuclei_Texture_InfoMeas2_AGP_10_03

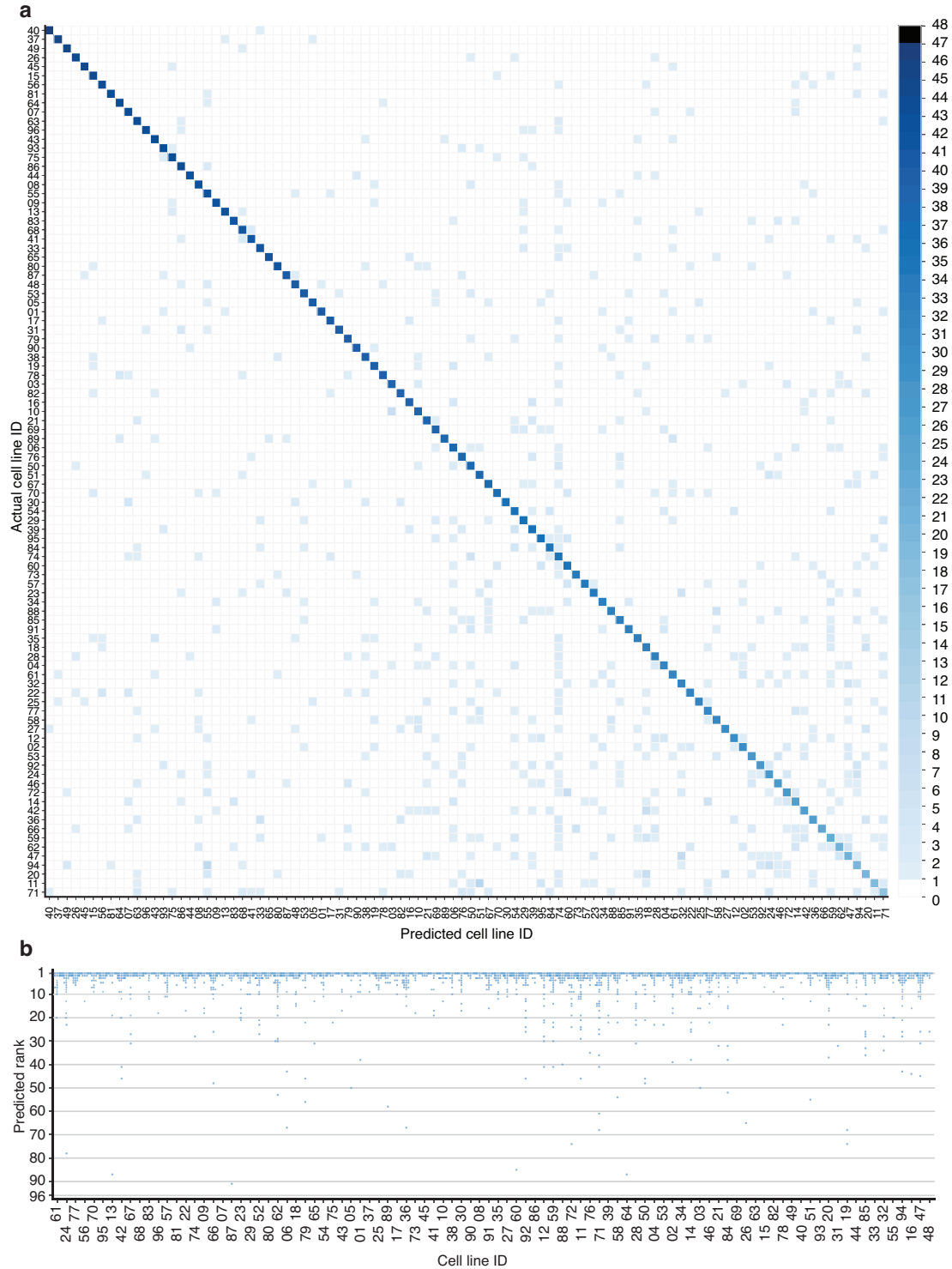
Supplementary Table 5 | Most common important CellProfiler features grouped based on correlation. The top 100 most important CellProfiler features from Fig. 6a, clustered into 55 groups based on Pearson correlation.



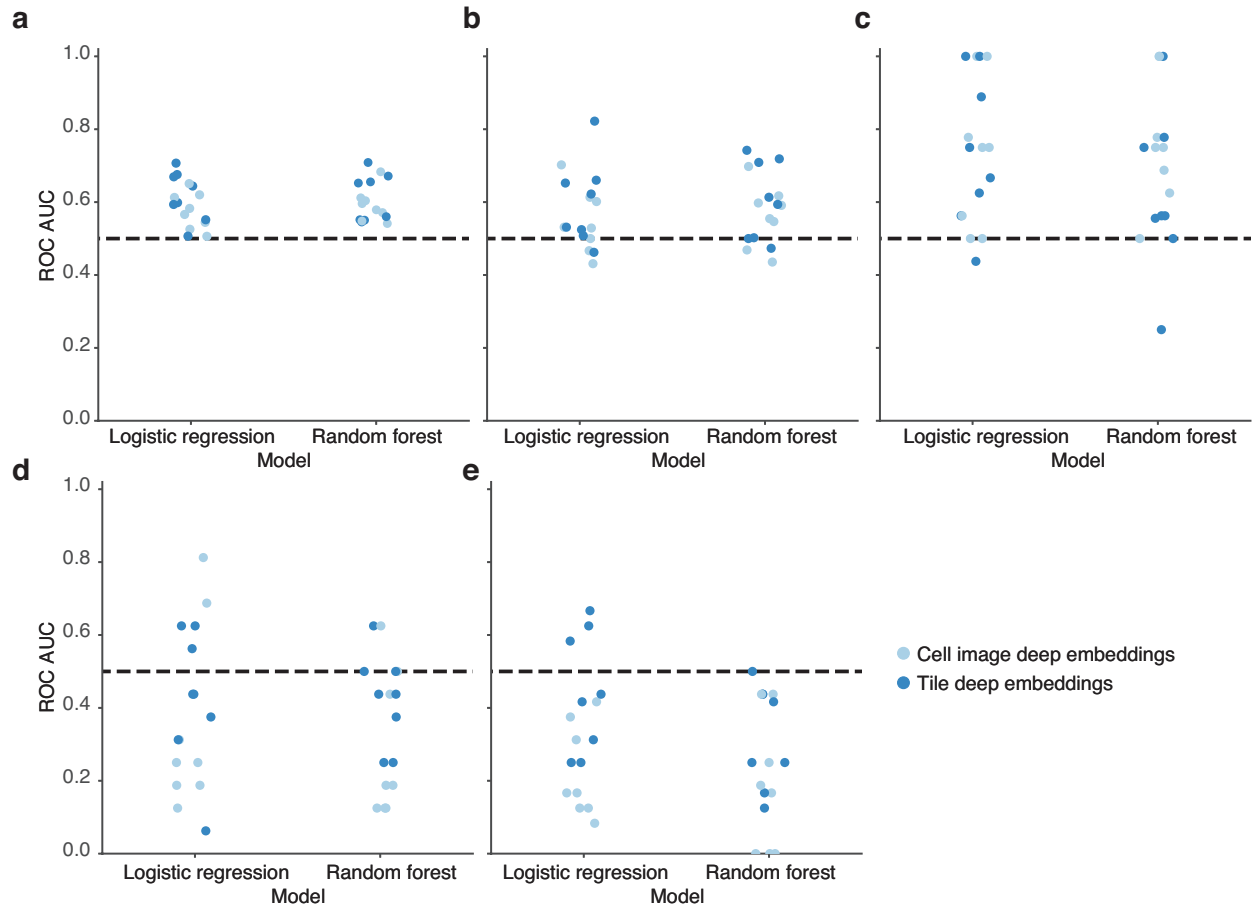
Supplementary Fig. 1 | Experiment design details for high-content screening. Various donor demographics including (a) sex (male (M), female (F)) and (b) age for the two 96-well plate layouts, where each well contains cells from the cell line denoted by the two-digit label. c, Lasso variable selection for healthy vs. PD on donor, biopsy, cell line, and plate covariates reveals no significant biases. Distributions of additional cell line covariates including (d) percentage European ancestry from genotyping analysis, (e) biopsy collection year, (f) cell doubling times (Mann–Whitney $U = 57.0, p = 1.0 \times 10^{-2}$ for sporadic, $U = 118.0, p = 6.4 \times 10^{-1}$ for *LRRK2 PD*, and $U = 193.5, p = 1.00$ for *GBA PD* vs. healthy, respectively, ns: $p > 5.0 \times 10^{-2}$), (g) well-level cell count, and biopsy location, (h) arm or leg and (i) left or right. Error bars denote standard deviation.



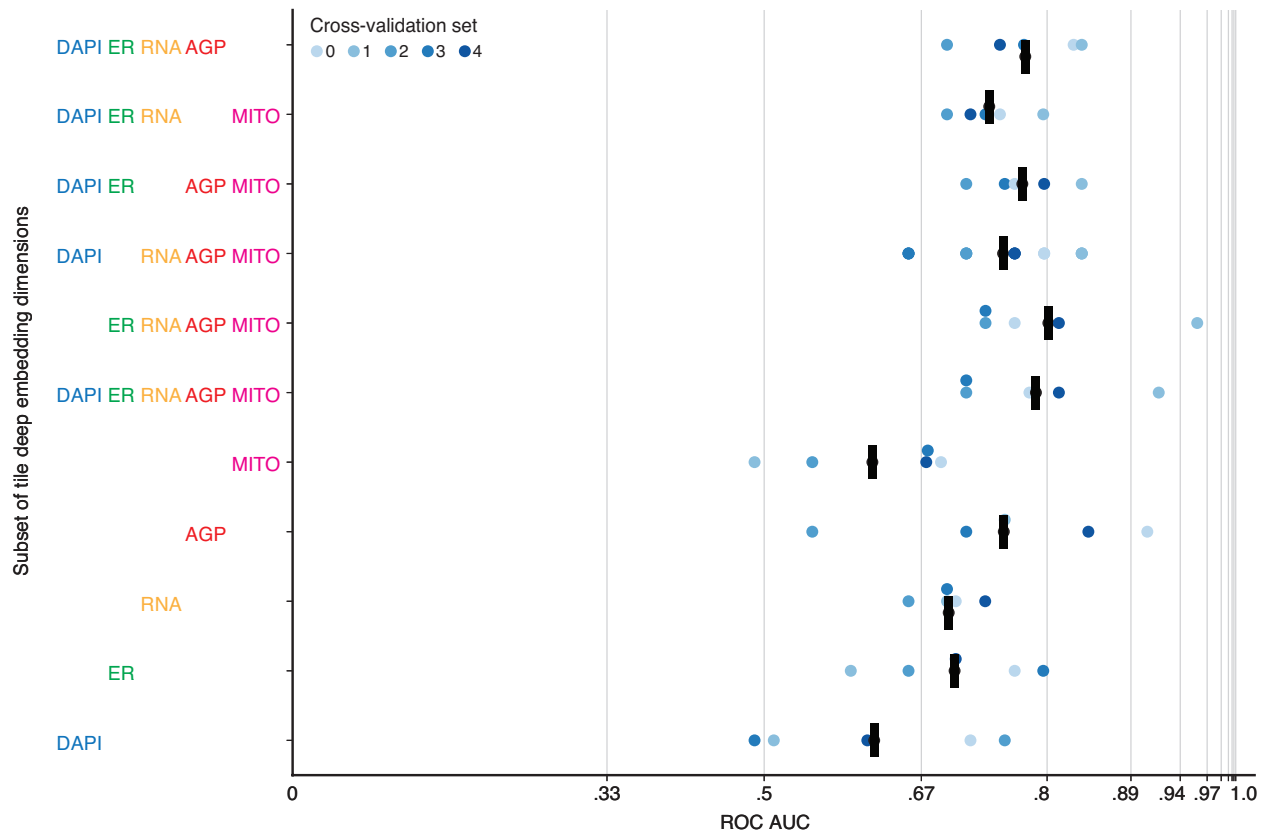
Supplementary Fig. 2 | Overview of near real-time image quality analysis and sample Cell Painting images of primary human fibroblasts. A Fiji (an ImageJ distribution) macro assesses the quality and consistency of the images sampled from a full 96-well plate. **a**, Four random regions of interest (ROI) are cropped from images in each channel and in each well, and 96-well montages are constructed for viewing. A measurement of mean image intensity across the plate is reported for each plate montage. Next, the montage corresponding to the user-designated focus channel is inputted to a microscope image focus classifier which calculates a focus quality score for each image patch. For visualization, a color-coded overlay on top of the montage highlights regions that are in focus (red) or out of focus (blue). Scale bar: 50 μm . **b**, Sample images of one tile from the 5 Cell Painting channels. Scale bar: 100 μm .



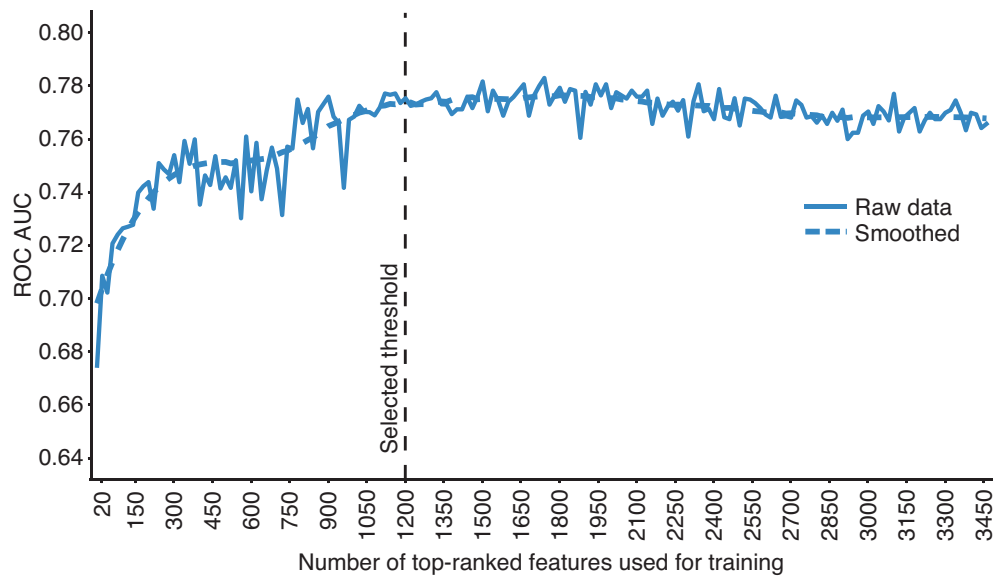
Supplementary Fig. 3 | Identification of individual cell lines in held-out batches and plate layouts at the well-level. a, Confusion matrix, sorted by the diagonal, showing the test set well-level predicted and actual cell lines for each of 6 wells in each of 8 held-out batch and held-out plate layouts for the model in **Fig. 3c**. **b**, Test set well-level predicted rank, among 96 of the 6 wells in each of 8 held-out batch and held-out plate layouts for the model in **Fig. 3c**.



Supplementary Fig. 4 | Preliminary evaluation of PD classification performance. Test set cell line–level PD classification for (a) all PD ($n = 45$ participants) and matched controls ($n = 45$ participants), (b) sporadic PD ($n = 31$) and matched controls ($n = 31$ participants), (c) *LRRK2* PD ($n = 6$ participants) and matched controls ($n = 6$ participants), (d) *GBA* PD ($n = 8$ participants) and matched controls ($n = 8$ participants), and (e) *GBA* PD ($n = 7$ participants) and matched controls ($n = 8$ participants), excluding the unconfirmed *GBA* line (see Methods). In each case, for cross-validation, matched cell line pairs were randomly divided into a train half and a test half 8 times. Dashed line denotes chance performance.



Supplementary Fig. 5 | Impact of individual Cell Painting channels on PD classification. The same logistic regression model with tile deep embeddings from **Fig. 5b** evaluated with a subset of the deep embedding dimensions corresponding to a subset of the 5 channels. Black bars denote the mean across all cross-validation sets. Grid line spacing denotes a doubling of the odds of correctly ranking a random healthy control and PD cell line. Dashed line denotes chance performance.



Supplementary Fig. 6 | Estimating threshold for number of top-ranked CellProfiler features required for PD classification. Performance of the random forest classifier as a function of number of top-ranked features used for training, evaluated in increments of 20 features. The dashed line represents the threshold selected for subsequent analyses.