Table S1. *Outcome measures from experiments utilized for baseline behavioral analyses of DRD1-EGFP/Rpl10a DNE offspring and grandoffspring.* Within-subjects data are stacked in columns and reflect measured values for each outcome assessed in each mouse for F1 Veh (upper), F1 NIC (middle), and F2 NIC (lower) groups (n=20 for all groups). Data are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Experiment	Outcome Measure	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh
Daily Homecage (HC) Activity	Total HC Activity	2501.64	2368.65	2078.67	1167.00	2729.33	2681.68
	Active Phase	2099.66	2009.33	1657.34	971.00	2212.33	2183.66
	Inactive Phase	401.98	359.32	421.33	196.00	517.00	498.02
HC Activity Rhythmometry	MESOR	103.58	98.02	86.25	48.24	113.32	111.70
	Global Amplitude	133.31	126.01	96.75	77.28	154.40	134.85
	Orthophase	2.15	2.22	2.32	1.64	1.67	1.81
Open Field (OF) Behaviors	Total Distance	7657.80	10655.90	8617.81	6865.94	7647.48	9328.40
	Risk-taking	18.16	27.16	14.88	24.46	19.67	17.32
Four-Bottle Choice Test (FBCT)	Nicotine Intake (mg/kg)	4.58	5.27	3.18	6.55	1.09	1.98
	Preference (0µg/mL)	65.74	63.83	70.84	69.53	68.82	74.80
	Preference (25µg/mL)	16.57	15.63	17.91	13.21	24.51	12.31
	Preference (50µg/mL)	12.81	13.94	6.85	9.15	5.65	7.86
	Preference (100µg/mL)	4.88	6.60	4.40	8.11	1.03	5.04

Experiment	Outcome Measure	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC
Daily Homecage (HC) Activity	Total HC Activity	2632.99	3070.66	2641.01	3503.66	3879.02	3153.99
	Active Phase	2095.67	2267.33	2180.68	2721.00	3038.35	2745.66
	Inactive Phase	537.32	803.33	460.33	782.66	840.67	408.33
HC Activity Rhythmometry	MESOR	109.65	127.02	110.14	143.57	160.55	130.36
	Global Amplitude	128.09	140.15	126.62	187.61	179.84	178.65
	Orthophase	2.65	2.39	2.92	2.10	2.82	2.51
Open Field (OF) Behaviors	Total Distance	9423.02	9545.45	10383.51	6288.34	7715.75	8579.19
	Risk-taking	20.88	15.45	24.58	23.07	32.90	21.12
Four-Bottle Choice Test (FBCT)	Nicotine Intake (mg/kg)	3.46	7.11	4.64	3.98	4.98	8.40
	Preference (0µg/mL)	36.42	54.69	31.80	32.99	46.83	45.51
	Preference (25µg/mL)	25.43	23.70	25.02	28.43	27.66	18.62
	Preference (50µg/mL)	24.83	15.39	26.46	25.77	14.19	23.12
	Preference (100µg/mL)	13.32	6.22	16.72	12.80	11.32	12.74

Experiment	Outcome Measure	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC
Daily Homecage (HC) Activity	Total HC Activity	3078.35	2569.34	2821.64	3445.35	2772.00	4038.31
	Active Phase	2425.01	2131.66	2315.32	2645.01	2190.67	3292.99
	Inactive Phase	653.34	437.68	506.32	800.34	581.33	745.32
HC Activity Rhythmometry	MESOR	127.91	107.21	116.87	143.29	114.93	168.06
	Global Amplitude	152.78	149.73	167.15	166.62	129.45	218.87
	Orthophase	2.00	3.06	2.24	2.39	2.20	2.46
Open Field (OF) Behaviors	Total Distance	9628.91	8490.76	11904.32	11967.30	10737.22	10960.62
	Risk-taking	34.66	15.88	23.67	25.32	27.46	31.30
Four-Bottle Choice Test (FBCT)	Nicotine Intake (mg/kg)	7.68	4.26	6.73	8.96	5.16	6.52
	Preference (0µg/mL)	30.87	60.91	30.35	38.61	39.61	40.12
	Preference (25µg/mL)	43.43	18.25	43.06	27.49	41.53	36.06
	Preference (50µg/mL)	17.40	12.56	20.30	20.96	14.80	14.42
	Preference (100µg/mL)	8.30	8.28	6.28	12.93	4.06	9.41

Table S2. *Percent vs. control data derived from baseline behavioral analyses of DRD1-EGFP/Rpl10a DNE offspring and grandoffspring.* Within-subjects data are stacked in columns and reflect measured values for each outcome assessed in each mouse for F1 Veh (upper), F1 NIC (middle), and F2 NIC (lower) groups (n=20 for all groups). Data are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Experiment	Outcome Measure	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh
Daily Homecage (HC) Activity	Total HC Activity	122.5%	116%	101.8%	57.15%	133.7%	131.3%
	Active Phase	126.2%	120.8%	99.61%	58.36%	133%	131.3%
	Inactive Phase	106.3%	95.02%	111.4%	51.83%	136.7%	131.7%
HC Activity Rhythmometry	MESOR	122.5%	115.9%	102%	57.03%	134%	132.1%
	Global Amplitude	114.3%	108.1%	82.97%	66.27%	132.4%	115.6%
	Orthophase	121.8%	125.7%	131.4%	92.89%	94.59%	102.5%
Open Field (OF) Behaviors	Total Distance	108.1%	150.4%	121.6%	96.91%	108%	131.7%
	Risk-taking	109.5%	163.8%	89.73%	147.5%	118.6%	104.4%
Four-Bottle Choice Test (FBCT)	Nicotine Intake (mg/kg)	119.2%	137.1%	82.73%	170.4%	28.36%	51.51%
	Preference (0µg/mL)	102.6%	99.57%	110.5%	108.5%	107.4%	116.7%
	Preference (25µg/mL)	94.68%	89.31%	102.3%	75.48%	140.1%	70.34%
	Preference (50µg/mL)	108.1%	117.7%	57.82%	77.24%	47.69%	66.35%
	Preference (100µg/mL)	74.54%	100.8%	67.21%	123.9%	15.73%	76.98%

Experiment	Outcome Measure	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC
Daily Homecage (HC) Activity	Total HC Activity	129%	150.4%	129.3%	171.6%	190%	154.5%
	Active Phase	126%	136.3%	131.1%	163.5%	182.6%	165%
	Inactive Phase	142.1%	212.4%	121.7%	207%	222.3%	108%
HC Activity Rhythmometry	MESOR	129.6%	150.2%	130.2%	169.7%	189.8%	154.1%
	Global Amplitude	109.9%	120.2%	108.6%	160.9%	154.2%	153.2%
	Orthophase	150.1%	135.4%	165.4%	119%	159.7%	142.2%
Open Field (OF) Behaviors	Total Distance	133%	134.7%	146.6%	88.76%	108.9%	121.1%
	Risk-taking	125.9%	93.17%	148.2%	139.1%	198.4%	127.4%
Four-Bottle Choice Test (FBCT)	Nicotine Intake (mg/kg)	90.01%	185%	120.7%	103.5%	129.6%	218.5%
	Preference (0µg/mL)	56.81%	85.31%	49.6%	51.46%	73.05%	70.99%
	Preference (25µg/mL)	145.3%	135.4%	143%	162.5%	158.1%	106.4%
	Preference (50µg/mL)	209.6%	129.9%	223.4%	217.5%	119.8%	195.2%
	Preference (100µg/mL)	203.5%	95.01%	255.4%	195.5%	172.9%	194.6%

Experiment	Outcome Measure	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC
Daily Homecage (HC) Activity	Total HC Activity	150.8%	125.8%	138.2%	168.7%	135.8%	197.8%
	Active Phase	145.8%	128.1%	139.2%	159%	131.7%	197.9%
	Inactive Phase	172.8%	115.7%	133.9%	211.7%	153.7%	197.1%
HC Activity Rhythmometry	MESOR	151.2%	126.8%	138.2%	169.4%	135.9%	198.7%
	Global Amplitude	131%	128.4%	143.3%	142.9%	111%	187.7%
	Orthophase	113.3%	173.3%	126.9%	135.4%	124.6%	139.3%
Open Field (OF) Behaviors	Total Distance	135.9%	119.9%	168%	168.9%	151.6%	154.7%
	Risk-taking	209%	95.76%	142.7%	152.7%	165.6%	188.8%
Four-Bottle Choice Test (FBCT)	Nicotine Intake (mg/kg)	199.8%	110.8%	175.1%	233.1%	134.2%	169.6%
	Preference (0µg/mL)	48.15%	95.01%	47.34%	60.23%	61.79%	62.58%
	Preference (25µg/mL)	248.2%	104.3%	246.1%	157.1%	237.3%	206.1%
	Preference (50µg/mL)	146.9%	106%	171.4%	176.9%	124.9%	121.7%
	Preference (100µg/mL)	126.8%	126.5%	95.92%	197.5%	62.01%	143.7%

Table S3. *Raw hourly-binned home cage activity data for all DRD1-EGFP/Rpl10a DNE offspring and grandoffspring.* Within-subjects data are stacked in columns and reflect hourly-binned measurements of homecage activity across groups (n=20 for all groups). Data are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Hourly (ZT) HC Activity	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh	F1 Veh
ZT12 (Active Phase)	104.33	170.00	92.00	64.67	110.33	143.33	111.67	121.67	58.00
ZT13 (Active Phase)	188.33	188.33	119.67	133.00	301.67	260.33	221.00	257.33	189.67
ZT14 (Active Phase)	235.67	259.00	225.33	157.00	266.67	275.33	167.00	230.33	188.00
ZT15 (Active Phase)	271.00	242.00	170.67	99.00	198.00	245.33	169.00	175.67	162.33
ZT16 (Active Phase)	208.00	184.00	144.00	77.33	161.33	217.67	164.67	143.00	147.33
ZT17 (Active Phase)	173.00	106.33	128.67	53.67	172.67	162.00	136.33	100.33	81.00
ZT18 (Active Phase)	152.33	155.00	138.33	65.33	139.67	119.67	127.33	125.00	108.33
ZT19 (Active Phase)	153.33	135.67	99.00	37.33	142.33	93.00	72.33	103.00	79.33
ZT20 (Active Phase)	89.00	101.00	125.67	21.67	172.33	136.67	83.00	94.67	66.33
ZT21 (Active Phase)	74.67	103.00	109.00	49.33	153.00	159.33	96.67	123.33	89.67
ZT22 (Active Phase)	242.67	200.33	156.67	126.00	242.00	209.33	113.33	119.00	76.67
ZT23 (Active Phase)	207.33	164.67	148.33	86.67	152.33	161.67	124.67	113.00	83.00
ZT0 (Inactive Phase)	46.00	25.67	57.00	25.33	80.67	73.33	78.67	98.33	36.67
ZT1 (Inactive Phase)	44.33	37.33	36.67	3.00	7.00	75.67	42.00	69.33	5.33
ZT2 (Inactive Phase)	29.33	16.00	31.33	4.33	135.00	47.67	40.67	32.00	27.00
ZT3 (Inactive Phase)	41.33	67.00	58.67	30.00	77.00	90.67	55.67	62.33	23.67
ZT4 (Inactive Phase)	32.67	49.33	18.00	30.33	60.00	43.67	50.00	30.33	14.33
ZT5 (Inactive Phase)	23.67	19.33	19.67	17.00	0.00	29.67	20.33	15.00	22.00
ZT6 (Inactive Phase)	7.33	22.67	38.33	12.00	17.33	36.67	14.33	29.33	52.67
ZT7 (Inactive Phase)	19.33	18.33	40.67	34.67	13.67	28.00	17.33	25.00	26.00
ZT8 (Inactive Phase)	65.33	15.00	23.33	11.67	15.00	13.33	13.33	90.00	26.33
ZT9 (Inactive Phase)	21.33	37.33	43.33	4.00	21.00	11.67	8.00	36.67	0.00
ZT10 (Inactive Phase)	18.33	26.00	15.00	0.00	46.00	19.67	6.00	15.67	0.00
ZT11 (Inactive Phase)	53.00	25.33	39.33	23.67	44.33	28.00	27.00	42.00	14.33

Hourly (ZT) HC Activity	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC	F1 NIC
ZT12 (Active Phase)	101.33	88.33	118.67	108.00	139.00	164.00	136.33	86.33	79.00
ZT13 (Active Phase)	232.00	193.33	155.67	253.00	246.67	268.67	216.00	274.33	233.67
ZT14 (Active Phase)	230.00	310.33	202.00	392.67	323.67	339.33	281.67	352.33	342.33
ZT15 (Active Phase)	305.00	264.33	289.00	305.33	384.33	353.00	275.00	226.33	439.33
ZT16 (Active Phase)	219.67	199.00	222.33	268.33	334.33	321.33	240.33	206.00	286.67
ZT17 (Active Phase)	179.67	157.00	206.00	152.67	299.67	224.00	130.00	143.67	145.33
ZT18 (Active Phase)	142.00	185.67	141.00	261.67	215.00	213.67	247.67	98.67	225.00
ZT19 (Active Phase)	76.00	130.67	134.67	218.00	202.67	176.00	201.67	89.33	130.00
ZT20 (Active Phase)	96.33	95.33	136.67	116.00	194.67	162.33	102.33	70.33	121.67
ZT21 (Active Phase)	173.00	194.67	175.67	63.00	169.00	124.33	133.00	140.33	134.00
ZT22 (Active Phase)	198.00	238.00	188.00	312.00	237.67	167.00	255.33	303.00	170.67
ZT23 (Active Phase)	142.67	210.67	211.00	270.33	291.67	232.00	256.00	266.67	124.33
ZT0 (Inactive Phase)	63.33	129.33	83.67	243.67	223.33	80.33	118.33	56.67	42.00
ZT1 (Inactive Phase)	33.33	64.00	38.00	87.33	66.00	44.33	99.00	29.33	43.33
ZT2 (Inactive Phase)	59.33	52.33	68.00	86.33	75.00	17.67	111.67	30.33	57.33
ZT3 (Inactive Phase)	54.67	61.67	34.00	61.00	59.67	50.00	85.00	37.00	40.67
ZT4 (Inactive Phase)	28.33	86.00	34.00	67.00	25.33	26.33	47.33	32.00	71.67
ZT5 (Inactive Phase)	47.33	42.00	38.00	55.00	68.67	44.00	48.67	76.00	53.33
ZT6 (Inactive Phase)	22.67	87.67	38.33	14.33	77.33	6.00	18.00	24.33	88.33
ZT7 (Inactive Phase)	38.33	39.67	30.33	13.00	71.00	27.00	32.33	62.33	39.00
ZT8 (Inactive Phase)	25.67	34.33	25.00	57.33	17.00	17.67	58.00	49.33	65.67
ZT9 (Inactive Phase)	70.33	49.33	10.33	36.67	110.00	60.00	37.67	29.33	53.67
ZT10 (Inactive Phase)	52.67	94.67	31.00	28.33	37.67	5.67	29.67	38.33	94.33
ZT11 (Inactive Phase)	41.33	62.33	29.67	32.67	9.67	29.33	33.33	68.67	80.00

Hourly (ZT) HC Activity	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC	F2 NIC

Table S4. *Consensus D1-type striatal MSN translatome for DRD1-EGFP/Rpl10a mice.* The consensus translatome of DRD1-expressing striatal cells from DRD1-EGFP/Rpl10a mice is provided as a list of gene symbols and are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Whole Translatome of DRD1-EGFP/Rpl10a Mice						
AA414768	*Cep135*	*Fastkd3*	*Klhl23*	*Osgep*	*Rps15a-ps4*	*Tmco1*
AA986860	*Cep152*	*Fastkd5*	*Klhl24*	*Osgepl1*	*Rps15a-ps5*	*Tmco3*
Aaas	*Cep164*	*Fat1*	*Klhl25*	*Osgin2*	*Rps15a-ps6*	*Tmco4*
Aacs	*Cep170b*	*Fat3*	*Klhl26*	*Osmr*	*Rps16*	*Tmco6*
Aadac	*Cep19*	*Fat4*	*Klhl28*	*Ost4*	*Rps17*	*Tmed1*
Aadacl4fm1	*Cep192*	*Fate1*	*Klhl29*	*Ostc*	*Rps18*	*Tmed10*
Aak1	*Cep250*	*Fau*	*Klhl3*	*Ostf1*	*Rps19*	*Tmed2*
Aamdc	*Cep290*	*Faxc*	*Klhl32*	*Ostm1*	*Rps19-ps3*	*Tmed3*
Aar2	*Cep295*	*Fbf1*	*Klhl33*	*Ostn*	*Rps19bp1*	*Tmed4*
Aard	*Cep295nl*	*Fbh1*	*Klhl34*	*Otof*	*Rps2*	*Tmed5*
Aars	*Cep41*	*Fblim1*	*Klhl36*	*Otub1*	*Rps20*	*Tmed7*
Aars2	*Cep44*	*Fbll1*	*Klhl38*	*Otub2*	*Rps21*	*Tmed8*
Aasdhppt	*Cep57*	*Fbln1*	*Klhl4*	*Otud1*	*Rps23*	*Tmed9*
Aass	*Cep57l1*	*Fbln2*	*Klhl42*	*Otud3*	*Rps24*	*Tmeff2*
Aatf	*Cep63*	*Fbln5*	*Klhl5*	*Otud4*	*Rps25*	*Tmem100*
Aatk	*Cep68*	*Fbln7*	*Klhl6*	*Otud6a*	*Rps26*	*Tmem101*
Abat	*Cep70*	*Fbn1*	*Klhl7*	*Otud6b*	*Rps27*	*Tmem104*
Abca1	*Cep72*	*Fbn2*	*Klhl8*	*Otud7a*	*Rps27l*	*Tmem106a*
Abca17	*Cep76*	*Fbrsl1*	*Klhl9*	*Otud7b*	*Rps27rt*	*Tmem106b*
Abca2	*Cep78*	*Fbxl12*	*Klk1b22*	*Otulin*	*Rps28*	*Tmem106c*
Abca3	*Cep83*	*Fbxl14*	*Klk1b27*	*Otulinl*	*Rps3*	*Tmem107*
Abca4	*Cep85*	*Fbxl15*	*Klk1b3*	*Otx1*	*Rps3a1*	*Tmem108*
Abca5	*Cep85l*	*Fbxl16*	*Klk1b4*	*Otx2*	*Rps4l*	*Tmem109*
Abca6	*Cep89*	*Fbxl17*	*Klk1b5*	*Ovca2*	*Rps4x*	*Tmem11*
Abca8a	*Cep97*	*Fbxl18*	*Klk1b8*	*Ovgp1*	*Rps5*	*Tmem114*
Abca9	*Cept1*	*Fbxl19*	*Klk8*	*Oxa1l*	*Rps6*	*Tmem115*
Abcb10	*Cercam*	*Fbxl2*	*Klk9*	*Oxct1*	*Rps6ka1*	*Tmem116*
Abcb1a	*Cerk*	*Fbxl20*	*Kmt2a*	*Oxgr1*	*Rps6ka2*	*Tmem117*
Abcb1b	*Cerkl*	*Fbxl21*	*Kmt2b*	*Oxld1*	*Rps6ka3*	*Tmem119*
Abcb6	*Cers2*	*Fbxl22*	*Kmt2c*	*Oxnad1*	*Rps6ka4*	*Tmem120a*
Abcb7	*Cers4*	*Fbxl3*	*Kmt2d*	*Oxr1*	*Rps6ka5*	*Tmem120b*
Abcb9	*Cers5*	*Fbxl4*	*Kmt2e*	*Oxsm*	*Rps6ka6*	*Tmem121*
Abcc1	*Cers6*	*Fbxl5*	*Kmt5a*	*Oxsr1*	*Rps6kb1*	*Tmem121b*
Abcc10	*Ces1d*	*Fbxl6*	*Kmt5b*	*Oxtr*	*Rps6kb2*	*Tmem123*
Abcc4	*Cetn1*	*Fbxl8*	*Kmt5c*	*P2rx4*	*Rps6kc1*	*Tmem125*
Abcc5	*Cetn2*	*Fbxo11*	*Kndc1*	*P2rx7*	*Rps6kl1*	*Tmem126a*
Abcc6	*Cetn3*	*Fbxo2*	*Knl1*	*P2ry1*	*Rps7*	*Tmem126b*
Abcc8	*Cetn4*	*Fbxo21*	*Knop1*	*P2ry12*	*Rps8*	*Tmem127*
Abcc9	*Cfap100*	*Fbxo22*	*Knstrn*	*P2ry13*	*Rps9*	*Tmem128*
Abcd1	*Cfap126*	*Fbxo27*	*Kpna1*	*P2ry14*	*Rpsa*	*Tmem129*
Abcd2	*Cfap161*	*Fbxo28*	*Kpna2*	*P2ry6*	*Rptor*	*Tmem130*
Abcd3	*Cfap20*	*Fbxo3*	*Kpna3*	*P3h1*	*Rpusd1*	*Tmem131*
Abcd4	*Cfap298*	*Fbxo30*	*Kpna4*	*P3h2*	*Rpusd2*	*Tmem132b*
Abce1	*Cfap300*	*Fbxo31*	*Kpna6*	*P3h3*	*Rpusd3*	*Tmem132c*
Abcf1	*Cfap36*	*Fbxo32*	*Kpnb1*	*P3h4*	*Rpusd4*	*Tmem132d*
Abcf2	*Cfap410*	*Fbxo33*	*Kptn*	*P4ha3*	*Rrad*	*Tmem132e*
Abcf3	*Cfap43*	*Fbxo34*	*Kras*	*P4hb*	*Rraga*	*Tmem134*
Abcg1	*Cfap44*	*Fbxo36*	*Krba1*	*P4htm*	*Rragb*	*Tmem135*
Abcg2	*Cfap45*	*Fbxo38*	*Krcc1*	*Pa2g4*	*Rragc*	*Tmem136*
Abcg3	*Cfap46*	*Fbxo4*	*Kremen1*	*Pabpc1*	*Rragd*	*Tmem138*
Abcg4	*Cfap47*	*Fbxo41*	*Kremen2*	*Pabpc2*	*Rras*	*Tmem140*
Abhd1	*Cfap54*	*Fbxo42*	*Kri1*	*Pabpc4l*	*Rras2*	*Tmem141*
Abhd10	*Cfap61*	*Fbxo44*	*Krit1*	*Pabpc5*	*Rrbp1*	*Tmem144*
Abhd11	*Cfap65*	*Fbxo45*	*Krr1*	*Pabpc6*	*Rreb1*	*Tmem145*
Abhd12	*Cfap69*	*Fbxo46*	*Krt1*	*Pabpn1*	*Rrm1*	*Tmem147*

Table S5. *Comprehensive lists of enriched and depleted DEGs unique to and shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Lists of gene symbols mapped to transcripts exhibiting statistically significant (q < 0.05) enrichment or depletion in F1 NIC and/or F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

F1 NIC Enriched DEGs	F1 NIC Depleted DEGs	F2 NIC Enriched DEGs	F2 NIC Depleted DEGs	Shared Enriched DEGs	Shared Depleted DEGs	F1 NIC Unique Enriched DEGs	F1 NIC Unique Depleted DEGs	F2 NIC Unique Enriched DEGs	F2 NIC Unique Depleted DEGs
Acad9	*Acot6*	*Acad9*	*Acot6*	*Acad9*	*Acot6*	*Rln3*	*Slc22a20*	*Lcn2*	*Nrk*
Acer2	*Alg1*	*Acer2*	*Alg1*	*Acer2*	*Alg1*	*Rnase6*	*Bpifa1*	*Usp18*	*Kcnab1*
Amd1	*Anxa5*	*Amd1*	*Anxa5*	*Amd1*	*Anxa5*	*Fau*	*Reg3g*	*Cxcl10*	*En2*
Amd2	*Aplnr*	*Amd2*	*Aplnr*	*Amd2*	*Aplnr*	*Dnah6*	*Aqp3*	*Ifi209*	*Ces1d*
Apopt1	*Cbln3*	*Apopt1*	*Cbln3*	*Apopt1*	*Cbln3*	*Plac9a*	*Cyp2a5*	*Ccl12*	*Car8*
Arl8a	*Ccl19*	*Arl8a*	*Ccl19*	*Arl8a*	*Ccl19*	*Gjc2*	*Cyp2g1*	*Ngp*	*Cnpy1*
Asb3	*Cdh7*	*Asb3*	*Cdh7*	*Asb3*	*Cdh7*	*Oxgr1*	*Vmo1*	*Ifit1*	*Gpr55*
Atp5j2	*Cercam*	*Atp5j2*	*Cercam*	*Atp5j2*	*Cercam*	*H2bc8*	*Gfy*	*Camp*	*Ppp1r17*
Avpi1	*Cetn4*	*Avpi1*	*Cetn4*	*Avpi1*	*Cetn4*	*Tcf23*	*Scgb1c1*	*Gbp10*	*Cbr2*
B2m	*Chac1*	*B2m*	*Chac1*	*B2m*	*Chac1*	*Selenbp2*	*Cyp2a4*	*Zbp1*	*Nvl*
B4galt5	*Clec16a*	*B4galt5*	*Clec16a*	*B4galt5*	*Clec16a*	*Praf2*	*Adamts12*	*H2-Q6*	*Olfr536*
BC024139	*Cstf2t*	*BC024139*	*Cstf2t*	*BC024139*	*Cstf2t*	*Fmo2*	*Pcdhb1*	*Gal3st2b*	*Orm2*
Ccl21a	*Cyhr1*	*Ccl21a*	*Cyhr1*	*Ccl21a*	*Cyhr1*	*Rpl34-ps1*	*Stoml3*	*S100a8*	*Ndufc2*
Ccl21b	*Dctn1*	*Ccl21b*	*Dctn1*	*Ccl21b*	*Dctn1*	*Cdh13*	*Ctdsp1*	*Wfdc21*	*Rbm42*
Ccl21c	*Ddhd2*	*Ccl21c*	*Ddhd2*	*Ccl21c*	*Ddhd2*	*Klhl1*	*Sult1d1*	*Mx1*	*H1f0*
Ccl21d	*Ddx17*	*Ccl21d*	*Ddx17*	*Ccl21d*	*Ddx17*	*Fam83d*	*Lrp6*	*Cxcl9*	*Rtp1*
Ccl5	*Dera*	*Ccl5*	*Dera*	*Ccl5*	*Dera*	*Mir100hg*	*Dlx4os*	*Oas1b*	*Tmem18*
Cd3eap	*Dhx36*	*Cd3eap*	*Dhx36*	*Cd3eap*	*Dhx36*	*H2bu1-ps*	*Brf1*	*Retnlg*	*Churc1*
Cd52	*Dmac2*	*Cd52*	*Dmac2*	*Cd52*	*Dmac2*	*Dbp*	*Cat*	*Phf11d*	*Leprot*
Cenps	*Dusp23*	*Cenps*	*Dusp23*	*Cenps*	*Dusp23*	*Tmem199*	*Firre*	*Zyg11b*	*Fam122a*
Chga	*Ecm2*	*Chga*	*Ecm2*	*Chga*	*Ecm2*	*Nop10*	*Pcdhgc3*	*Lgals3bp*	*AA414768*
Cog6	*Elof1*	*Cog6*	*Elof1*	*Cog6*	*Elof1*	*Sac3d1*	*Proz*	*H2-T24*	*Glod4*
Cplx1	*Eml5*	*Cplx1*	*Eml5*	*Cplx1*	*Eml5*	*Aldh3b2*	*Ccdc167*	*Mx2*	*Lyrm4*
Cpne8	*Emp2*	*Cpne8*	*Emp2*	*Cpne8*	*Emp2*	*Shb*	*Rell1*	*Ifi27l2a*	*Ramp1*
Ctse	*Exosc9*	*Ctse*	*Exosc9*	*Ctse*	*Exosc9*	*Dtnbp1*	*Gtf2h5*	*Rsad2*	*Lcmt2*
Ddx19a	*F11r*	*Ddx19a*	*F11r*	*Ddx19a*	*F11r*	*Syt4*	*Pcdhb11*	*Aadac*	*Khdrbs1*
Dnajb1	*Fabp7*	*Dnajb1*	*Fabp7*	*Dnajb1*	*Fabp7*	*Adsl*	*Ptn*	*Trim34b*	*Sox12*
Dpy19l1	*Gpatch1*	*Dpy19l1*	*Gpatch1*	*Dpy19l1*	*Gpatch1*	*Stard3nl*	*Seh1l*	*Zkscan16*	*Tmem123*
Eif3j1	*Gpr75*	*Eif3j1*	*Gpr75*	*Eif3j1*	*Gpr75*	*Trappc2l*	*Fgfbp3*	*Jchain*	*Wsb1*
Etaa1os	*H2-T10*	*Etaa1os*	*H2-T10*	*Etaa1os*	*H2-T10*	*Nrtn*	*Ewsr1*	*Ppbp*	*Polr3b*
Fam205a1	*H2af-ps2*	*Fam205a1*	*H2af-ps2*	*Fam205a1*	*H2af-ps2*	*Zfp622*	*Rb1*	*Bst2*	*Rbbp6*
Fam205a2	*H2bc21*	*Fam205a2*	*H2bc21*	*Fam205a2*	*H2bc21*	*Csmd3*	*Cyp4v3*	*Prg2*	*Zc3h6*
Fam205a4	*Hbq1a*	*Fam205a4*	*Hbq1a*	*Fam205a4*	*Hbq1a*	*Sp3os*	*Tor4a*	*Fam205a3*	*Zfp407*
Fkbp3	*Heatr3*	*Fkbp3*	*Heatr3*	*Fkbp3*	*Heatr3*	*Pcsk1n*	*Cyth1*	*Aadacl4fm1*	*Sprtn*
Fkbp5	*Hmgn3*	*Fkbp5*	*Hmgn3*	*Fkbp5*	*Hmgn3*	*Mchr1*	*Txnl4b*	*Arnt2*	*Dvl2*
Gabra2	*Hps1*	*Gabra2*	*Hps1*	*Gabra2*	*Hps1*	*Ndufb8*	*Zc3h7b*	*Gbp2*	*Npdc1*
Gins4	*Ica1*	*Gins4*	*Ica1*	*Gins4*	*Ica1*	*Prps1*	*Cep68*	*Ltf*	*Zbtb22*
Guk1	*Ints7*	*Guk1*	*Ints7*	*Guk1*	*Ints7*	*Rnf8*	*Prr7*	*Mmp8*	*Lrrc42*
H2-T23	*Keap1*	*H2-T23*	*Keap1*	*H2-T23*	*Keap1*	*Scrt2*	*Timm10*	*Cst7*	*Chmp5*
Habp4	*Klhdc9*	*Habp4*	*Klhdc9*	*Habp4*	*Klhdc9*	*Iscu*	*Nes*	*Ear2*	*Mrpl50*
Hars	*L3hypdh*	*Hars*	*L3hypdh*	*Hars*	*L3hypdh*	*Ndufa3*	*Pcdhgb7*	*Elane*	*Bex4*
Hba-a2	*Mars1*	*Hba-a2*	*Mars1*	*Hba-a2*	*Mars1*	*Cyp2j9*	*Erbb2*	*Chil3*	*Ndufaf5*
Hbb-bs	*Me3*	*Hbb-bs*	*Me3*	*Hbb-bs*	*Me3*	*Ccdc28a*	*Taz*	*H2-Q4*	*Zfp772*
Hbb-bt	*Med9*	*Hbb-bt*	*Med9*	*Hbb-bt*	*Med9*	*Nedd8*	*Col5a2*	*Mpo*	*Stk35os1*
Hcrt	*Mief2*	*Hcrt*	*Mief2*	*Hcrt*	*Mief2*	*Pmpcb*	*Ccr5*	*Adgre4*	*Magef1*

Table S6. *Excerpted differential expression analysis results for enriched and depleted DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice*. Tabular differential expression data for transcripts exhibiting statistically significant (q < 0.05) enrichment or depletion in both F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

			F1 NIC Shared Enriched				F2 NIC Shared Enriched				
REFSEQ ID	Gene Symbol	Log2 (BM)	Log2 (FC)	LFC SE	P_{adj}	π	Log2 (FC)	LFC SE	P_{adj}	π	ENTREZ Gene ID
NM_172678	***Acad9***	5.74	0.38	0.16	0.03372	+0.56	0.40	0.16	0.02722	+0.63	229211
NM_001290543	***Acer2***	4.73	1.27	0.36	0.00129	+3.66	1.04	0.37	0.00746	+2.22	230379
NM_009665	***Amd1***	11.58	0.15	0.05	0.04183	+0.21	0.19	0.05	0.00566	+0.43	11702
NM_007444	***Amd2***	10.53	0.18	0.05	0.00776	+0.38	0.21	0.05	0.00078	+0.65	100041585
NM_026511	***Apopt1***	7.80	0.57	0.13	7.4E-05	+2.34	0.42	0.13	0.00469	+0.98	68020
NM_026823	***Arl8a***	12.31	0.15	0.05	0.04803	+0.19	0.18	0.05	0.01161	+0.34	68724
XM_006514771	***Asb3***	3.46	1.71	0.40	0.00014	+6.60	1.78	0.40	4.8E-05	+7.69	65257
NM_020582	***Atp5j2***	11.77	0.35	0.09	0.0009	+1.06	0.27	0.09	0.01237	+0.52	57423
NM_027106	***Avpi1***	8.92	0.31	0.08	0.0009	+0.95	0.25	0.08	0.01017	+0.50	69534
NM_009735	***B2m***	11.19	0.46	0.16	0.0121	+0.88	1.05	0.15	1.2E-10	+10.37	12010
NM_019835	***B4galt5***	10.34	0.21	0.07	0.03356	+0.31	0.21	0.07	0.03847	+0.29	56336
NM_001142968	***BC024139***	4.70	0.61	0.24	0.02008	+1.04	0.55	0.25	0.03439	+0.81	271278
NM_011124	***Ccl21a***	4.82	2.28	0.48	1.5E-05	+10.99	2.99	0.47	2.9E-09	+25.50	18829
NM_011335	***Ccl21b***	4.13	3.86	0.69	6.1E-07	+23.99	4.58	0.68	9.6E-10	+41.27	100042493
NM_023052	***Ccl21c***	6.48	3.18	0.38	3.4E-15	+46.04	3.83	0.38	3.5E-22	+82.21	65956
NM_001270360	***Ccl21d***	3.00	3.74	0.77	2.7E-05	+17.10	3.62	0.77	4.3E-05	+15.78	100862177
NM_013653	***Ccl5***	4.78	1.94	0.60	0.00274	+4.97	3.60	0.55	1.2E-09	+32.05	20304
NM_145822	***Cd3eap***	9.11	0.19	0.07	0.04069	+0.27	0.25	0.07	0.00403	+0.60	70333
NM_013706	***Cd52***	5.74	0.87	0.28	0.00411	+2.09	1.76	0.26	1.1E-10	+17.56	23833
NM_027263	***Cenps***	6.56	0.65	0.21	0.00512	+1.48	0.85	0.20	9.6E-05	+3.42	69928
NM_007693	***Chga***	11.70	0.47	0.11	0.00031	+1.64	0.36	0.11	0.00664	+0.79	12652
NM_026225	***Cog6***	9.86	0.17	0.06	0.03293	+0.25	0.20	0.06	0.00589	+0.45	67542
NM_007756	***Cplx1***	14.00	0.20	0.06	0.01541	+0.37	0.26	0.06	0.00083	+0.79	12889
XM_006521285	***Cpne8***	2.74	5.61	1.53	6.1E-05	+23.64	2.36	0.67	0.00112	+6.97	66871
NM_007799	***Ctse***	3.86	3.69	0.66	9.7E-07	+22.20	4.84	0.65	1.4E-11	+52.66	13034
XM_006530650	***Ddx19a***	6.77	0.44	0.14	0.00619	+0.97	0.39	0.14	0.01577	+0.71	13680
NM_018808	***Dnajb1***	8.18	0.31	0.12	0.03509	+0.45	0.46	0.12	0.00089	+1.41	81489
NM_172920	***Dpy19l1***	8.19	0.36	0.13	0.02034	+0.60	0.44	0.13	0.00283	+1.12	244745
NM_144545	***Eif3j1***	10.00	0.20	0.07	0.03026	+0.30	0.20	0.07	0.02755	+0.32	78655
NR_131915	***Etaa1os***	2.26	6.86	2.41	2.1E-07	+45.86	6.44	2.37	1.5E-06	+37.44	102633673
XM_011250061	***Fam205a1***	5.05	2.72	0.40	4.5E-10	+25.46	3.09	0.40	3E-13	+38.74	433698
XM_017320323	***Fam205a2***	3.96	2.89	0.70	0.0003	+10.17	4.29	0.68	8.4E-09	+34.66	545611
XM_001481239	***Fam205a4***	2.39	0.11	0.21	0.04498	+0.15	2.35	0.75	0.00429	+5.56	100043920
NM_013902	***Fkbp3***	10.97	0.31	0.13	0.0462	+0.42	0.34	0.13	0.03159	+0.51	30795
NM_010220	***Fkbp5***	10.00	0.54	0.11	4.3E-06	+2.91	0.32	0.11	0.01243	+0.61	14229
XM_006503733	***Gabra2***	9.25	0.51	0.16	0.00542	+1.15	0.68	0.22	0.00422	+1.62	14395
NM_024240	***Gins4***	8.65	0.45	0.10	6.1E-05	+1.88	0.37	0.10	0.00108	+1.11	109145
NM_008193	***Guk1***	5.05	2.60	0.26	1.3E-20	+51.65	2.53	0.27	1.7E-19	+47.56	14923
NM_010398	***H2-T23***	8.59	0.96	0.42	0.02106	+1.61	1.75	0.37	1.3E-05	+8.54	15040
NM_019986	***Habp4***	12.33	0.19	0.07	0.03509	+0.28	0.19	0.07	0.04187	+0.26	56541
NM_008214	***Hars***	10.91	0.22	0.06	0.00129	+0.65	0.19	0.06	0.00919	+0.39	15115
NM_001083955	***Hba-a2***	12.00	1.03	0.25	0.00025	+3.70	0.97	0.26	0.00049	+3.23	110257
NM_001201391	***Hbb-bs***	12.47	0.97	0.26	0.00092	+2.96	1.11	0.26	7.9E-05	+4.57	100503605
NM_008220	***Hbb-bt***	11.79	1.02	0.27	0.00054	+3.33	1.15	0.26	5.2E-05	+4.95	101488143
NM_010410	***Hcrt***	8.08	5.47	1.25	4.1E-05	+23.97	3.96	1.34	0.00308	+9.95	15171
NR_037996	***Hmga2-ps1***	6.26	1.02	0.17	7.4E-08	+7.24	1.37	0.17	2.8E-14	+18.52	15365
NM_015818	***Hs6st1***	10.56	0.21	0.06	0.01023	+0.41	0.22	0.06	0.00579	+0.49	50785
XM_006503424	***Hspb11***	3.25	0.08	0.17	0.01564	+0.14	3.14	0.92	0.00141	+8.96	72938
NM_023831	***Ift46***	4.57	0.91	0.35	0.0149	+1.66	1.23	0.33	0.00066	+3.91	76568
NM_170599	***Igsf11***	6.18	0.38	0.17	0.04673	+0.50	0.54	0.17	0.0039	+1.29	207683

Table S7. *Excerpted differential expression analysis results for enriched and depleted DEGs uniquely detected in DRD1-expressing striatal cells of F1 NIC but not F2 NIC mice.* Tabular differential expression data for transcripts exhibiting statistically significant (q < 0.05) enrichment or depletion in F1 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

F1 NIC Unique Enriched								
REFSEQ ID	Gene Symbol	Log2 (BM)	Log2. (FC)	LFC. SE	P_{adj}	π	ENTREZ Gene ID	ENSEMBL Gene ID
NM_173184	***Rln3***	3.06	2.83	0.87	0.00281	+7.23	212108	ENSMUSG00000045232
XM_006519698	***Rnase6***	1.99	2.59	1.01	0.0177	+4.53	78416	ENSMUSG00000021880
NM_001190436	***Fau***	6.72	1.69	0.61	0.00816	+3.53	14109	ENSMUSG00000038274
NM_001164669	***Dnah6***	3.66	1.24	0.42	0.00719	+2.65	330355	ENSMUSG00000052861
NM_207229	***Plac9a***	5.54	1.58	0.84	0.03189	+2.36	211623	ENSMUSG00000095304
XM_006532044	***Gjc2***	2.30	1.35	0.60	0.02621	+2.14	118454	ENSMUSG00000043448
NM_001001490	***Oxgr1***	2.69	1.26	0.53	0.0207	+2.12	239283	ENSMUSG00000044819
NM_178196	***H2bc8***	7.85	0.94	0.31	0.00542	+2.12	319181	ENSMUSG00000058385
NM_053085	***Tcf23***	1.94	1.38	0.66	0.03369	+2.03	69852	ENSMUSG00000006642
NM_019414	***Selenbp2***	5.55	0.75	0.24	0.00401	+1.80	20342	ENSMUSG00000068877
NM_138602	***Praf2***	10.58	0.31	0.06	2.3E-06	+1.73	54637	ENSMUSG00000031149
XM_006496949	***Fmo2***	4.36	1.02	0.44	0.02081	+1.72	55990	ENSMUSG00000040170
NM_001199350	***Rpl34-ps1***	9.75	0.72	0.25	0.00849	+1.49	619547	ENSMUSG00000068396
NM_019707	***Cdh13***	4.49	0.81	0.31	0.01566	+1.46	12554	ENSMUSG00000031841
NM_053105	***Klhl1***	7.28	0.80	0.31	0.01478	+1.46	93688	ENSMUSG00000022076
NM_027975	***Fam83d***	4.52	0.84	0.35	0.0207	+1.42	71878	ENSMUSG00000027654
NR_131930	***Mir100hg***	5.46	0.68	0.26	0.01582	+1.23	73144	ENSMUSG00000074415
NR_134309	***H2bu1-ps***	7.32	0.52	0.16	0.00537	+1.17	382522	ENSMUSG00000080712
NM_016974	***Dbp***	10.08	0.43	0.12	0.00236	+1.13	13170	ENSMUSG00000059824
NM_199199	***Tmem199***	9.45	0.29	0.06	0.00014	+1.11	195040	ENSMUSG00000051232
NM_025403	***Nop10***	9.45	0.50	0.16	0.00589	+1.11	66181	ENSMUSG00000027133
NM_133678	***Sac3d1***	8.74	0.34	0.08	0.00088	+1.03	66406	ENSMUSG00000024790
NM_001177438	***Aldh3b2***	5.71	0.67	0.31	0.03026	+1.02	621603	ENSMUSG00000075296
NM_001033306	***Shb***	9.05	0.53	0.19	0.01387	+0.99	230126	ENSMUSG00000044813
NM_025772	***Dtnbp1***	9.66	0.37	0.10	0.00232	+0.98	94245	ENSMUSG00000057531
NM_009308	***Syt4***	9.52	0.36	0.10	0.00233	+0.95	20983	ENSMUSG00000024261
NM_009634	***Adsl***	8.92	0.31	0.08	0.001	+0.93	11564	ENSMUSG00000022407
NM_024270	***Stard3nl***	8.19	0.33	0.09	0.0017	+0.90	76205	ENSMUSG00000003062
NM_021502	***Trappc2l***	9.44	0.31	0.08	0.00168	+0.85	59005	ENSMUSG00000015013
NM_008738	***Nrtn***	6.20	0.48	0.18	0.01873	+0.84	18188	ENSMUSG00000039481
NM_144523	***Zfp622***	10.16	0.28	0.07	0.00126	+0.82	52521	ENSMUSG00000052253
NM_001081391	***Csmd3***	4.59	0.53	0.23	0.02911	+0.81	239420	ENSMUSG00000022311
NR_045269	***Sp3os***	7.65	0.35	0.10	0.00499	+0.80	100503849	NA
NM_013892	***Pcsk1n***	14.77	0.34	0.10	0.00537	+0.78	30052	ENSMUSG00000039278
NM_145132	***Mchr1***	9.11	0.39	0.13	0.01103	+0.76	207911	ENSMUSG00000050164
NM_026061	***Ndufb8***	6.74	0.38	0.12	0.01068	+0.74	67264	ENSMUSG00000025204
NM_021463	***Prps1***	10.51	0.26	0.07	0.00175	+0.73	19139	ENSMUSG00000031432
NM_021419	***Rnf8***	6.90	0.37	0.12	0.01038	+0.73	58230	ENSMUSG00000090083
NM_001160410	***Scrt2***	9.30	0.40	0.14	0.01541	+0.72	545474	ENSMUSG00000060257
NM_025526	***Iscu***	10.97	0.34	0.10	0.00776	+0.71	66383	ENSMUSG00000025825
NM_025348	***Ndufa3***	10.11	0.33	0.10	0.00791	+0.70	66091	ENSMUSG00000035674
NM_028979	***Cyp2j9***	6.39	0.42	0.16	0.0242	+0.68	74519	ENSMUSG00000015224
NM_144820	***Ccdc28a***	8.73	0.29	0.09	0.00508	+0.67	215814	ENSMUSG00000059554
NM_008683	***Nedd8***	11.17	0.27	0.08	0.00386	+0.66	18002	ENSMUSG00000010376
NM_028431	***Pmpcb***	9.85	0.22	0.06	0.00109	+0.66	73078	ENSMUSG00000029017
NM_175511	***Fam78a***	6.40	0.45	0.20	0.03481	+0.66	241303	ENSMUSG00000050592
NM_029083	***Ddit4***	10.42	0.30	0.09	0.00679	+0.65	74747	ENSMUSG00000020108
NM_001160356	***Uqcc3***	8.81	0.29	0.09	0.00613	+0.64	107197	ENSMUSG00000071654
NM_026703	***Ndufa8***	11.11	0.28	0.08	0.00508	+0.63	68375	ENSMUSG00000026895
NM_153152	***Micos13***	10.24	0.36	0.13	0.01764	+0.63	224904	ENSMUSG00000049760

Table S8. *Excerpted differential expression analysis results for enriched and depleted DEGs uniquely detected in DRD1-expressing striatal cells of F2 NIC but not F1 NIC mice.* Tabular differential expression data for transcripts exhibiting statistically significant (q < 0.05) enrichment or depletion in F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

F2 NIC Unique Enriched								
REFSEQ ID	Gene Symbol	Log2 (BM)	Log2 (FC)	LFC SE	P_{adj}	π	ENTREZ Gene ID	ENSEMBL Gene ID
NM_008491	***Lcn2***	5.89	3.87	0.81	7.3E-06	+19.88	16819	ENSMUSG00000026822
NM_011909	***Usp18***	6.94	2.68	0.45	4E-08	+19.82	24110	ENSMUSG00000030107
NM_021274	***Cxcl10***	6.58	3.43	0.72	9.7E-06	+17.22	15945	ENSMUSG00000034855
NM_175026	***Ifi209***	3.80	2.62	0.49	9.6E-07	+15.77	236312	ENSMUSG00000043263
NM_011331	***Ccl12***	4.87	2.75	0.54	2.4E-06	+15.49	20293	ENSMUSG00000035352
NM_008694	***Ngp***	5.91	2.92	0.66	3.5E-05	+13.02	18054	ENSMUSG00000032484
NM_008331	***Ifit1***	7.71	2.11	0.40	9.2E-07	+12.71	15957	ENSMUSG00000034459
NM_009921	***Camp***	4.95	3.03	0.71	6.7E-05	+12.66	12796	ENSMUSG00000038357
NM_001039646	***Gbp10***	5.96	1.94	0.36	7E-07	+11.94	626578	ENSMUSG00000105096
NM_021394	***Zbp1***	2.84	3.26	0.84	0.00039	+11.12	58203	ENSMUSG00000027514
NM_207648	***H2-Q6***	5.07	1.83	0.34	9.2E-07	+11.03	110557	ENSMUSG00000073409
NM_001205249	***Gal3st2b***	1.76	3.60	1.10	0.00103	+10.76	100041596	ENSMUSG00000093805
NM_013650	***S100a8***	5.61	2.70	0.66	0.00014	+10.42	20201	ENSMUSG00000056054
NM_183249	***Wfdc21***	1.31	4.15	1.54	0.00319	+10.37	66107	ENSMUSG00000051748
NR_003520	***Mx1***	4.34	2.91	0.78	0.0005	+9.61	17857	ENSMUSG00000000386
NM_008599	***Cxcl9***	3.14	2.79	0.71	0.00036	+9.58	17329	ENSMUSG00000029417
NR_003507	***Oas1b***	3.93	1.92	0.41	1.3E-05	+9.41	23961	ENSMUSG00000029605
NM_181596	***Retnlg***	3.47	2.75	0.73	0.00043	+9.26	245195	ENSMUSG00000022651
NM_199015	***Phf11d***	4.55	1.98	0.47	8.3E-05	+8.10	219132	ENSMUSG00000068245
NM_001033634	***Zyg11b***	7.63	1.14	0.20	8.9E-08	+8.02	414872	ENSMUSG00000034636
NM_011150	***Lgals3bp***	9.10	1.32	0.25	9.2E-07	+7.97	19039	ENSMUSG00000033880
NM_008207	***H2-T24***	5.87	1.35	0.27	3.1E-06	+7.42	15042	ENSMUSG00000053835
NR_003508	***Mx2***	5.86	1.68	0.38	4.3E-05	+7.34	17858	ENSMUSG00000023341
NM_029803	***Ifi27l2a***	4.16	1.94	0.49	0.00022	+7.09	76933	ENSMUSG00000079017
NM_021384	***Rsad2***	6.41	1.57	0.36	4.3E-05	+6.85	58185	ENSMUSG00000020641
NM_023383	***Aadac***	1.31	3.03	1.07	0.00688	+6.55	67758	ENSMUSG00000027761
NM_001243916	***Trim34b***	2.88	1.84	0.46	0.00028	+6.54	434218	ENSMUSG00000090215
XM_006537508	***Zkscan16***	1.84	3.23	1.19	0.00956	+6.53	100041581	ENSMUSG00000038630
NM_152839	***Jchain***	3.48	2.22	0.66	0.00152	+6.25	16069	ENSMUSG00000067149
NM_023785	***Ppbp***	3.45	2.56	0.85	0.00377	+6.20	57349	ENSMUSG00000029372
NM_198095	***Bst2***	8.61	1.59	0.39	0.00016	+6.02	69550	ENSMUSG00000046718
NM_008920	***Prg2***	1.72	2.60	0.91	0.00828	+5.42	19074	ENSMUSG00000027073
XM_003688793	***Fam205a3***	2.71	2.12	0.65	0.00277	+5.42	100862261	ENSMUSG00000093996
NM_198662	***Aadacl4fm1***	2.58	2.35	0.81	0.00519	+5.36	381572	ENSMUSG00000028593
XM_006507238	***Arnt2***	3.55	2.76	1.13	0.01243	+5.26	11864	ENSMUSG00000015709
NM_010260	***Gbp2***	6.98	1.09	0.24	3E-05	+4.91	14469	ENSMUSG00000028270
NM_008522	***Ltf***	5.26	2.05	0.69	0.00423	+4.87	17002	ENSMUSG00000032496
NM_008611	***Mmp8***	2.77	2.47	1.00	0.01243	+4.70	17394	ENSMUSG00000005800
NM_009977	***Cst7***	2.49	2.40	0.92	0.01104	+4.69	13011	ENSMUSG00000068129
NM_007895	***Ear2***	1.38	2.52	0.95	0.01804	+4.40	13587	ENSMUSG00000072596
NM_015779	***Elane***	1.85	2.78	1.36	0.02896	+4.28	50701	ENSMUSG00000020125
NM_009892	***Chil3***	2.48	2.05	0.75	0.00943	+4.16	12655	ENSMUSG00000040809
NM_001143689	***H2-Q4***	8.08	1.11	0.27	0.00019	+4.12	15015	ENSMUSG00000035929
NM_010824	***Mpo***	3.23	1.95	0.74	0.01022	+3.89	17523	ENSMUSG00000009350
NM_139138	***Adgre4***	2.50	1.87	0.68	0.00852	+3.88	52614	ENSMUSG00000032915
NM_080464	***Ppp1r3a***	2.85	2.26	1.01	0.0206	+3.81	140491	ENSMUSG00000042717
NM_001005508	***Arhgap30***	6.85	0.72	0.14	5E-06	+3.81	226652	ENSMUSG00000048865
NM_053247	***Lyve1***	4.87	1.24	0.35	0.00114	+3.65	114332	ENSMUSG00000030787
NM_001143686	***Apol11b***	2.00	2.25	1.01	0.02594	+3.57	328563	ENSMUSG00000091694
NM_029084	***Slamf8***	1.29	2.31	1.02	0.03124	+3.48	74748	ENSMUSG00000053318

Table S9. *Reference index of gene attributes for all DEGs comprising the differential translatomes of F1 NIC and F2 NIC mice.* Attributes of DEGs including gene symbols, gene names, Ensembl Gene IDs, and Entrez Gene IDs are indexed by gene symbols and are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Gene Symbol	Gene Name	Entrez Gene ID	Ensembl Gene ID
AA414768	expressed sequence AA414768	245350	ENSMUSG00000083307
Aadac	arylacetamide deacetylase	67758	ENSMUSG00000027761
Aadacl4fm1	AADACL4 family member 1	381572	ENSMUSG00000028593
Aass	aminoadipate-semialdehyde synthase	30956	ENSMUSG00000029695
Abhd1	abhydrolase domain containing 1	57742	ENSMUSG00000006638
Acad9	acyl-Coenzyme A dehydrogenase family, member 9	229211	ENSMUSG00000027710
Acer2	alkaline ceramidase 2	230379	ENSMUSG00000038007
Acot4	acyl-CoA thioesterase 4	171282	ENSMUSG00000052392
Acot6	acyl-CoA thioesterase 6	217700	ENSMUSG00000043487
Adamts1	a disintegrin-like and metallopeptidase (reprolysin type)	11504	ENSMUSG00000022893
Adamts12	a disintegrin-like and metallopeptidase (reprolysin type)	239337	ENSMUSG00000047497
Adgre4	adhesion G protein-coupled receptor E4	52614	ENSMUSG00000032915
Adh1	alcohol dehydrogenase 1 (class I)	11522	ENSMUSG00000074207
Adrb1	adrenergic receptor, beta 1	11554	ENSMUSG00000035283
Adsl	adenylosuccinate lyase	11564	ENSMUSG00000022407
Ahctf1	AT hook containing transcription factor 1	226747	ENSMUSG00000026491
AI661453	expressed sequence AI661453	224833	ENSMUSG00000034382
Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	56847	ENSMUSG00000015134
Aldh3b2	aldehyde dehydrogenase 3 family, member B2	621603	ENSMUSG00000075296
Alg1	asparagine-linked glycosylation 1 (beta-1,4-mannosyltra	208211	ENSMUSG00000039427
Alox12b	arachidonate 12-lipoxygenase, 12R type	11686	ENSMUSG00000032807
Alox5	arachidonate 5-lipoxygenase	11689	ENSMUSG00000025701
Amd1	S-adenosylmethionine decarboxylase 1	11702	ENSMUSG00000075232
Amd2	S-adenosylmethionine decarboxylase 2	100041585	ENSMUSG00000063953
Ankdd1a	ankyrin repeat and death domain containing 1A	330963	ENSMUSG00000066510
Ankrd35	ankyrin repeat domain 35	213121	ENSMUSG00000038354
Anks1b	ankyrin repeat and sterile alpha motif domain containing	77531	ENSMUSG00000058589
Anxa5	annexin A5	11747	ENSMUSG00000027712
Aplnr	apelin receptor	23796	ENSMUSG00000044338
Apol11b	apolipoprotein L 11b	328563	ENSMUSG00000091694
Apold1	apolipoprotein L domain containing 1	381823	ENSMUSG00000090698
Apopt1	cytochrome c oxidase assembly factor 8	68020	ENSMUSG00000037787
Aqp3	aquaporin 3	11828	ENSMUSG00000028435
Arhgap30	Rho GTPase activating protein 30	226652	ENSMUSG00000048865
Arhgap33	Rho GTPase activating protein 33	233071	ENSMUSG00000036882
Arl2	ADP-ribosylation factor-like 2	56327	ENSMUSG00000024944
Arl8a	ADP-ribosylation factor-like 8A	68724	ENSMUSG00000026426
Arnt2	aryl hydrocarbon receptor nuclear translocator 2	11864	ENSMUSG00000015709
Asb3	ankyrin repeat and SOCS box-containing 3	65257	ENSMUSG00000020305
Aspdh	aspartate dehydrogenase domain containing	68352	ENSMUSG00000038704
Atcay	ataxia, cerebellar, Cayman type	16467	ENSMUSG00000034958
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 compl	57423	ENSMUSG00000038690
Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	11984	ENSMUSG00000024121
Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	73834	ENSMUSG00000021114
Atp8b2	ATPase, class I, type 8B, member 2	54667	ENSMUSG00000060671
AU022252	expressed sequence AU022252	230696	ENSMUSG00000078584
Avpi1	arginine vasopressin-induced 1	69534	ENSMUSG00000018821
AW046200	expressed sequence AW046200	100502619	ENSMUSG00000110419
AW557046	expressed sequence AW557046	102634078	
Axdnd1	axonemal dynein light chain domain containing 1	77352	ENSMUSG00000026601
B2m	beta-2 microglobulin	12010	ENSMUSG00000060802

Table S10. *Glossary of gene symbols, gene names, Entrez Gene summaries, and UniProt summaries for enriched and depleted DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Symbol	Gene Name	Δ	Entrez Gene Summary	UniProt Summary
Acad9	acyl-Coenzyme A dehydrogena	+	This gene encodes a member c	As part of the MCIA complex, p
Acer2	alkaline ceramidase 2	+	The sphingolipid metabolite sph	Golgi ceramidase that catalyzes
Acot6	acyl-CoA thioesterase 6	–	Acyl-CoA thioesterases are a group of enzymes that catalyze th	
Alg1	asparagine-linked glycosylation	–	Participates in the formation of t	The enzyme encoded by this ge
Amd1	S-adenosylmethionine decarbox	+	This gene encodes an importan	Essential for biosynthesis of the
Anxa5	annexin A5	–	This protein is an anticoagulant	The Annexin 5 gene spans 29 k
Aplnr	apelin receptor	–	(Microbial infection) Alternative	This gene encodes a member c
Apopt1	apoptogenic 1, mitochondrial	+	This gene encodes a protein tha	Required for cytochrome c com
Arl8a	ADP-ribosylation factor-like 8A	+		Plays a role in lysosome motility
Asb3	ankyrin repeat and SOCS box-	+	The protein encoded by this ger	Probable substrate-recognition
Atp5j2	ATP synthase, H+ transporting,	+	Mitochondrial ATP synthase ca	Mitochondrial membrane ATP s
Avpi1	arginine vasopressin-induced 1	+		May be involved in MAP kinase
B2m	beta-2 microglobulin	+	This gene encodes a serum pro	Component of the class I major
B4galt5	UDP-Gal:betaGlcNAc beta 1,4-	+	This gene is one of seven beta-	Catalyzes the synthesis of lacto
Cbln3	cerebellin 3 precursor protein	–	May be involved in synaptic fun	Members of the precerebellin fa
Ccl19	chemokine (C-C motif) ligand 19	–	May play a role not only in inflar	This antimicrobial gene is one o
Ccl21b	chemokine (C-C motif) ligand 21	+	This antimicrobial gene is one o	Inhibits hemopoiesis and stimula
Ccl5	chemokine (C-C motif) ligand 5	+	This gene is one of several che	Chemoattractant for blood mono
Cd3eap	CD3E antigen, epsilon polypept	+		DNA-dependent RNA polymera
Cd52	CD52 antigen	+		May play a role in carrying and
Cdh7	cadherin 7, type 2	–	Cadherins are calcium-depende	This gene encodes a type II cla
Cenps	centromere protein S	+	This gene was identified in the r	DNA-binding component of the
Cercam	cerebral endothelial cell adhesio	–	Probable cell adhesion protein involved in leukocyte transmigrat	
Cetn4	centrin 4	–	Centrins are members of the calcium-binding EF-hand protein s	
Chac1	ChaC, cation transport regulato	–	Catalyzes the cleavage of gluta	This gene encodes a member c
Chga	chromogranin A	+	The protein encoded by this ger	[Catestatin]: Inhibits catecholam
Clec16a	C-type lectin domain family 16,	–	Regulator of mitophagy through	This gene encodes a member c
Cog6	component of oligomeric golgi c	+	This gene encodes a subunit of	Required for normal Golgi functi
Cplx1	complexin 1	+	Proteins encoded by the comple	Positively regulates a late step i
Cpne8	copine VIII	+	Calcium-dependent membrane-	Probable calcium-dependent ph
Cstf2t	cleavage stimulation factor, 3' p	–	May play a significant role in AAUAAA-independent mRNA polya	
Ctse	cathepsin E	+	This gene encodes a member c	May have a role in immune func
Cyhr1	cysteine and histidine rich 1	–	Predicted to enable zinc ion bind	
Dctn1	dynactin 1	–	Plays a key role in dynein-medi	This gene encodes the largest s
Ddhd2	DDHD domain containing 2	–	Phospholipase that hydrolyzes	This gene encodes a phospholi
Ddx17	DEAD box helicase 17	–	As an RNA helicase, unwinds R	DEAD box proteins, characteriz
Ddx19a	DEAD box helicase 19a	+		ATP-dependent RNA helicase in
Dera	deoxyribose-phosphate aldolas	–	Catalyzes a reversible aldol reaction between acetaldehyde and	
Dhx36	DEAH (Asp-Glu-Ala-His) box p	–	Multifunctional ATP-dependent I	This gene is a member of the D
Dmac2	distal membrane arm assembly	–	Required for the assembly of the mitochondrial NADH:ubiquinon	
Dnajb1	DnaJ heat shock protein family	+	This gene encodes a member c	Interacts with HSP70 and can s
Dpy19l1	dpy-19-like 1 (C. elegans)	+		Probable C-mannosyltransferas
Dusp23	dual specificity phosphatase 23	–	Protein phosphatase that mediates dephosphorylation of protein	
Ecm2	extracellular matrix protein 2, fe	–	Promotes matrix assembly and	ECM2 encodes extracellular ma
Eif3j1	eukaryotic translation initiation f	+	This gene encodes a core subu	Component of the eukaryotic tra
Elof1	ELF1 homolog, elongation facto	–	Transcription elongation factor implicated in the maintenance of	
Eml5	echinoderm microtubule associ	–	May modify the assembly dynamics of microtubules, such that r	
Emp2	epithelial membrane protein 2	–	Functions as a key regulator of	This gene encodes a tetraspan
Exosc9	exosome component 9	–	Non-catalytic component of the	This gene encodes a componer
F11r	F11 receptor	–	(Microbial infection) Acts as a re	Tight junctions represent one m
Fabp7	fatty acid binding protein 7, brai	–	B-FABP could be involved in the	The gene encodes a small, high
Fkbp3	FK506 binding protein 3	+	The protein encoded by this ger	FK506- and rapamycin-binding
Fkbp5	FK506 binding protein 5	+	The protein encoded by this ger	Immunophilin protein with PPIas
Gabra2	gamma-aminobutyric acid (GAB	+	GABA is the major inhibitory neu	Ligand-gated chloride channel w

Table S11. *Index of DEG-encoded protein annotations used for word frequency analysis.* Data including gene symbols, STRING IDs, and STRING annotations for DEG-encoded proteins are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Symbol	STRING ID	DEG-Encoded Protein Annotation (STRING)
Aadac	10090.ENSMUSP00000029325	Arylacetamide deacetylase; Displays cellular triglyceride lipase
Aadacl4fm1	10090.ENSMUSP00000030328	Arylacetamide deacetylase-like 4; RIKEN cDNA 9430007A20 g
Aass	10090.ENSMUSP00000031707	Alpha-aminoadipic semialdehyde synthase, mitochondrial; Bifu
Acad9	10090.ENSMUSP00000011492	Acyl-CoA dehydrogenase family member 9, mitochondrial; Rec
Acer2	10090.ENSMUSP00000040048	Alkaline ceramidase 2; Hydrolyzes the sphingolipid ceramide ir
Acot4	10090.ENSMUSP00000021652	Acyl-coenzyme A thioesterase 4; Acyl-CoA thioesterases are
Acot6	10090.ENSMUSP00000056131	Acyl-coenzyme A thioesterase 6; Acyl-CoA thioesterase that c
Adamts1	10090.ENSMUSP00000023610	A disintegrin and metalloproteinase with thrombospondin motifs
Adamts12	10090.ENSMUSP00000057796	A disintegrin and metalloproteinase with thrombospondin motifs
Adgre4	10090.ENSMUSP00000025004	Adhesion G protein-coupled receptor E4; May mediate the cell
Adh1	10090.ENSMUSP00000004232	Alcohol dehydrogenase 1 (class I); Belongs to the zinc-contain
Adrb1	10090.ENSMUSP00000040847	Beta-1 adrenergic receptor; Beta-adrenergic receptors mediat
Adsl	10090.ENSMUSP00000023043	Adenylosuccinate lyase; Catalyzes two non-sequential steps ir
Ahctf1	10090.ENSMUSP00000027768	Protein ELYS; Required for the assembly of a functional nuclea
AI661453	10090.ENSMUSP00000120133	Uncharacterized protein C6orf132 homolog; Expressed seque
Aldh1a3	10090.ENSMUSP00000015278	Aldehyde dehydrogenase family 1 member A3; NAD-dependen
Aldh3b2	10090.ENSMUSP00000115356	Aldehyde dehydrogenase family 3 member B2; Oxidizes mediu
Alg1	10090.ENSMUSP00000097770	Chitobiosyldiphosphodolichol beta-mannosyltransferase; Partic
Alox12b	10090.ENSMUSP00000035250	Arachidonate 12-lipoxygenase, 12R-type; Non-heme iron-cont
Alox5	10090.ENSMUSP00000026795	Arachidonate 5-lipoxygenase; Catalyzes the first step in leukot
Amd1	10090.ENSMUSP00000097528	S-adenosylmethionine decarboxylase proenzyme 1; Essential
Amd2	10090.ENSMUSP00000079703	S-adenosylmethionine decarboxylase proenzyme 2; Essential
Ankdd1a	10090.ENSMUSP00000057040	Ankyrin repeat and death domain containing 1A
Ankrd35	10090.ENSMUSP00000047244	Ankyrin repeat domain 35
Anks1b	10090.ENSMUSP00000138539	Ankyrin repeat and sterile alpha motif domain-containing protei
Anxa5	10090.ENSMUSP00000029266	Annexin A5; This protein is an anticoagulant protein that acts a
Aplnr	10090.ENSMUSP00000053638	Apelin receptor; Receptor for apelin receptor early endogenous
Apol11b	10090.ENSMUSP00000129476	Apolipoprotein L 11b
Apold1	10090.ENSMUSP00000132366	Apolipoprotein L domain containing 1
Apopt1	10090.ENSMUSP00000038865	Apoptogenic protein 1, mitochondrial; Plays a role in the regula
Aqp3	10090.ENSMUSP00000055110	Aquaporin-3; Water channel required to promote glycerol perm
Arhgap30	10090.ENSMUSP00000059389	Rho GTPase activating protein 30; GTPase-activating protein
Arhgap33	10090.ENSMUSP00000038412	Rho GTPase-activating protein 33; May be involved in several
Arl2	10090.ENSMUSP00000025893	ADP-ribosylation factor-like protein 2; Small GTP-binding prote
Arl8a	10090.ENSMUSP00000027684	ADP-ribosylation factor-like protein 8A; May play a role in lysos
Arnt2	10090.ENSMUSP00000082154	Aryl hydrocarbon receptor nuclear translocator 2; Transcriptio
Asb3	10090.ENSMUSP00000020551	Ankyrin repeat and SOCS box protein 3; Probable substrate-re
Aspdh	10090.ENSMUSP00000039202	Putative L-aspartate dehydrogenase; Specifically catalyzes the
Atcay	10090.ENSMUSP00000036721	Caytaxin; Functions in the development of neural tissues, parti
Atp5j2	10090.ENSMUSP00000125504	ATP synthase subunit f, mitochondrial; Mitochondrial membran
Atp6v0c	10090.ENSMUSP00000024932	V-type proton ATPase 16 kDa proteolipid subunit; Proton-cond
Atp6v1d	10090.ENSMUSP00000021536	V-type proton ATPase subunit D; Subunit of the peripheral V1
Atp8b2	10090.ENSMUSP00000103019	Phospholipid-transporting ATPase ID; Catalytic component of a
AU022252	10090.ENSMUSP00000115729	Uncharacterized protein C1orf50 homolog; Expressed sequen
Avpi1	10090.ENSMUSP00000018965	Arginine vasopressin-induced protein 1; May be involved in MA
Axdnd1	10090.ENSMUSP00000137354	Axonemal dynein light chain domain containing 1
B2m	10090.ENSMUSP00000099534	Beta-2-microglobulin; Component of the class I major histocom
B4galt5	10090.ENSMUSP00000104844	Beta-1,4-galactosyltransferase 5; Responsible for the synthes
Baz2b	10090.ENSMUSP00000108169	Bromodomain adjacent to zinc finger domain, 2B
BC024139	10090.ENSMUSP00000053305	cDNA sequence BC024139
Bcat1	10090.ENSMUSP00000032402	Branched-chain-amino-acid aminotransferase, cytosolic; Cata
Bex1	10090.ENSMUSP00000060005	Protein BEX1; Signaling adapter molecule involved in p75NTR/

Table S12. *UniProt Keyword annotations mapped to depleted DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including UniProt Keyword IDs, UniProt Keyword annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	UniProt Keyword	FC	P	π
KW-0694	RNA-binding	–5.70	0.0000033	–13.76
KW-0543	Viral nucleoprotein	–28.20	0.0023	–12.71
KW-0617	Plasminogen activation	–77.70	0.013	–11.84
KW-0946	Virion	–23.00	0.0034	–11.17
KW-0269	Exonuclease	–12.90	0.01	–7.38
KW-0015	Albinism	–28.20	0.035	–7.01
KW-0306	Gastrulation	–28.20	0.035	–7.01
KW-0041	Annexin	–25.90	0.038	–6.67
KW-0662	Pyridine nucleotide biosynthesis	–25.90	0.038	–6.67
KW-0111	Calcium/phospholipid-binding	–23.90	0.041	–6.35
KW-0271	Exosome	–23.90	0.041	–6.35
KW-0704	Schiff base	–22.20	0.044	–6.07
KW-0507	mRNA processing	–5.10	0.0031	–5.90
KW-0420	Kringle	–20.70	0.047	–5.81
KW-0561	Oxygen transport	–19.40	0.05	–5.57
KW-0891	Chondrogenesis	–18.30	0.053	–5.35
KW-0177	Collagen degradation	–18.30	0.053	–5.35
KW-0880	Kelch repeat	–8.80	0.022	–5.20
KW-0546	Nucleotide metabolism	–13.50	0.072	–4.29
KW-0251	Elongation factor	–13.50	0.077	–4.18
KW-0011	Acute phase	–12.40	0.072	–4.15
KW-0243	Dynein	–10.00	0.095	–3.40
KW-0865	Zymogen	–4.40	0.031	–3.22
KW-0532	Neurotransmitter transport	–8.40	0.097	–3.11
KW-0333	Golgi apparatus	–2.90	0.011	–3.01
KW-0540	Nuclease	–5.00	0.061	–2.82
KW-0508	mRNA splicing	–3.90	0.042	–2.70
KW-0347	Helicase	–4.80	0.066	–2.67
KW-0378	Hydrolase	–2.30	0.006	–2.67
KW-0344	Guanine-nucleotide releasing factor	–4.70	0.069	–2.59
KW-0165	Cleavage on pair of basic residues	–3.80	0.046	–2.58
KW-0970	Cilium biogenesis/degradation	–4.40	0.075	–2.40
KW-0456	Lyase	–4.30	0.08	–2.31

Table S13. *UniProt Keyword annotations mapped to enriched DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including UniProt Keyword IDs, UniProt Keyword annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	UniProt Keyword	FC	P	π
KW-0745	Spermidine biosynthesis	+120.6	0.0001	+27.66
KW-0527	Neuropeptide	+35.70	0.000005	+27.58
KW-0670	Pyruvate	+51.70	0.000024	+26.30
KW-0561	Oxygen transport	+45.20	0.000037	+24.37
KW-0664	Pyridoxine biosynthesis	+241.3	0.0041	+18.89
KW-0620	Polyamine biosynthesis	+40.20	0.0011	+15.77
KW-0490	MHC I	+37.10	0.0013	+15.05
KW-0704	Schiff base	+34.50	0.0015	+14.43
KW-0027	Amidation	+17.70	0.00066	+13.19
KW-0068	Autocatalytic cleavage	+17.70	0.00066	+13.19
KW-0210	Decarboxylase	+23.00	0.0034	+11.17
KW-0145	Chemotaxis	+10.30	0.00063	+10.77
KW-0697	Rotamase	+13.80	0.0093	+7.69
KW-0202	Cytokine	+6.00	0.0015	+7.30
KW-0906	Nuclear pore complex	+11.80	0.013	+6.72
KW-0159	Chromosome partition	+11.00	0.014	+6.41
KW-0395	Inflammatory response	+6.00	0.0045	+6.07
KW-0064	Aspartyl protease	+21.90	0.045	+6.00
KW-0138	CF(0)	+20.10	0.049	+5.67
KW-0702	S-nitrosylation	+9.10	0.02	+5.41
KW-0066	ATP synthesis	+18.60	0.053	+5.38
KW-0143	Chaperone	+5.10	0.0082	+4.90
KW-0873	Pyrrolidone carboxylic acid	+8.20	0.025	+4.86
KW-0413	Isomerase	+5.90	0.014	+4.75
KW-0813	Transport	+2.40	0.00026	+4.53
KW-0891	Chondrogenesis	+14.20	0.068	+4.47
KW-0558	Oxidation	+14.20	0.068	+4.47
KW-0285	Flavoprotein	+5.60	0.017	+4.40
KW-0621	Polymorphism	+4.60	0.011	+4.31
KW-0301	Gamma-carboxyglutamic acid	+13.40	0.072	+4.28
KW-0288	FMN	+11.50	0.084	+3.79
KW-0346	Stress response	+6.40	0.039	+3.77
KW-0313	Glucose metabolism	+11.00	0.087	+3.67
KW-0543	Viral nucleoprotein	+11.00	0.087	+3.67
KW-0811	Translocation	+6.20	0.042	+3.62
KW-0165	Cleavage on pair of basic residues	+3.90	0.02	+3.34
KW-0509	mRNA transport	+5.60	0.05	+3.23
KW-0349	Heme	+4.20	0.034	+3.04
KW-0865	Zymogen	+3.40	0.059	+2.17
KW-0274	FAD	+4.10	0.086	+2.17
KW-0964	Secreted	+2.00	0.0094	+2.03
KW-0106	Calcium	+2.30	0.021	+2.02
KW-0328	Glycosyltransferase	+3.20	0.067	+1.97
KW-0130	Cell adhesion	+2.60	0.042	+1.90
KW-0498	Mitosis	+2.80	0.093	+1.53
KW-0391	Immunity	+2.40	0.085	+1.35
KW-0653	Protein transport	+2.10	0.092	+1.11

Table S14. *G.O. Biological Process annotations mapped to enriched DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including G.O. IDs, G.O. Biological Process annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	G.O. Biological Process	FC	P	π
GO:0035759	Mesangial cell-matrix adhesion	> +100	0.00000030	+43.38
GO:2000529	Positive regulation of myeloid dendritic cell chemotaxis	> +100	0.00000070	+40.90
GO:2000527	Regulation of myeloid dendritic cell chemotaxis	> +100	0.00000070	+40.90
GO:1903237	Negative regulation of leukocyte tethering or rolling	> +100	0.00000234	+37.41
GO:2000669	Negative regulation of dendritic cell apoptotic process	> +100	0.00000234	+37.41
GO:1904995	Negative regulation of leukocyte adhesion to vascular endoth	> +100	0.00000371	+36.08
GO:0048245	Eosinophil chemotaxis	+54.29	0.00000108	+34.38
GO:0072677	Eosinophil migration	+51.43	0.00000134	+33.38
GO:0006557	S-adenosylmethioninamine biosynthetic process	> +100	0.00002	+31.22
GO:2000668	Regulation of dendritic cell apoptotic process	+73.29	0.0000107	+30.80
GO:0001768	Establishment of T cell polarity	+73.29	0.0000107	+30.80
GO:0001767	Establishment of lymphocyte polarity	+73.29	0.0000107	+30.80
GO:0042823	Pyridoxal phosphate biosynthetic process	> +100	0.000033	+29.77
GO:0042819	Vitamin B6 biosynthetic process	> +100	0.000033	+29.77
GO:2000510	Positive regulation of dendritic cell chemotaxis	+66.63	0.0000142	+29.37
GO:0002692	Negative regulation of cellular extravasation	+66.63	0.0000142	+29.37
GO:0033630	Positive regulation of cell adhesion mediated by integrin	+40.72	0.00000336	+29.27
GO:0002407	Dendritic cell chemotaxis	+61.08	0.0000184	+28.09
GO:0006597	Spermine biosynthetic process	> +100	0.000074	+27.44
GO:0042822	Pyridoxal phosphate metabolic process	> +100	0.000074	+27.44
GO:0042816	Vitamin B6 metabolic process	> +100	0.000074	+27.44
GO:2000508	Regulation of dendritic cell chemotaxis	+56.38	0.0000234	+26.94
GO:0031274	Positive regulation of pseudopodium assembly	+56.38	0.0000234	+26.94
GO:0031272	Regulation of pseudopodium assembly	+56.38	0.0000234	+26.94
GO:0033628	Regulation of cell adhesion mediated by integrin	+24.93	0.00000206	+26.38
GO:0008295	Spermidine biosynthetic process	> +100	0.000131	+25.80
GO:0002548	Monocyte chemotaxis	+28.74	0.0000131	+23.66
GO:0036336	Dendritic cell migration	+38.58	0.0000717	+21.84
GO:1903236	Regulation of leukocyte tethering or rolling	+36.65	0.0000833	+21.20
GO:0034695	Response to prostaglandin E	+36.65	0.0000833	+21.20
GO:0042364	Water-soluble vitamin biosynthetic process	+69.80	0.000398	+20.83
GO:0008215	Spermine metabolic process	+69.80	0.000398	+20.83
GO:0048247	Lymphocyte chemotaxis	+23.27	0.0000298	+20.55
GO:0034694	Response to prostaglandin	+33.32	0.00011	+20.02
GO:0098869	Cellular oxidant detoxification	+31.50	0.00011	+19.70
GO:0008216	Spermidine metabolic process	+54.29	0.000655	+18.35
GO:0046184	Aldehyde biosynthetic process	+48.86	0.000807	+17.35
GO:0090023	Positive regulation of neutrophil chemotaxis	+25.27	0.000247	+16.81
GO:0031529	Ruffle organization	+25.27	0.000247	+16.81
GO:0070098	Chemokine-mediated signaling pathway	+17.45	0.0000903	+16.68
GO:0071622	Regulation of granulocyte chemotaxis	+16.85	0.000103	+16.25
GO:0071624	Positive regulation of granulocyte chemotaxis	+23.64	0.0003	+16.08
GO:0043552	Positive regulation of phosphatidylinositol 3-kinase activity	+23.64	0.0003	+16.08
GO:0098754	Detoxification	+14.78	0.0003	+13.69
GO:0072389	Flavin adenine dinucleotide catabolic process	> +100	0.00408	+15.87
GO:1903007	Positive regulation of Lys63-specific deubiquitinase activity	> +100	0.00408	+15.87
GO:2000548	Negative regulation of dendritic cell dendrite assembly	> +100	0.00408	+15.87
GO:0002014	Vasoconstriction of artery involved in ischemic response to lo	> +100	0.00408	+15.87
GO:0006185	Dgdp biosynthetic process	> +100	0.00408	+15.87
GO:1904803	Regulation of translation involved in cellular response to UV	> +100	0.00408	+15.87
GO:0009443	Pyridoxal 5'-phosphate salvage	> +100	0.00408	+15.87

Table S15. *G.O. Biological Process annotations mapped to depleted DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including G.O. IDs, G.O. Biological Process annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	G.O. Biological Process	FC	P	π
GO:0035928	rRNA import into mitochondrion	< –100	0.0000584	–28.13
GO:0071047	Polyadenylation-dependent mRNA catabolic process	< –100	0.000104	–26.46
GO:0071042	Nuclear polyadenylation-dependent mRNA catabolic process	< –100	0.000104	–26.46
GO:0035927	RNA import into mitochondrion	< –100	0.000161	–25.20
GO:0051029	rRNA transport	< –100	0.000161	–25.20
GO:0043633	Polyadenylation-dependent RNA catabolic process	–68.71	0.00041	–20.67
GO:0045604	Regulation of epidermal cell differentiation	–20.36	0.0000496	–18.71
GO:0045682	Regulation of epidermis development	–18.02	0.0000792	–17.11
GO:1902721	Negative regulation of prolactin secretion	< –100	0.00363	–16.21
GO:0019365	Pyridine nucleotide salvage	< –100	0.00363	–16.21
GO:2000549	Positive regulation of dendritic cell dendrite assembly	< –100	0.00363	–16.21
GO:0090616	Mitochondrial mRNA 3'-end processing	< –100	0.00363	–16.21
GO:1902064	Regulation of transcription from RNA polymerase II promoter	< –100	0.00363	–16.21
GO:2000119	Negative regulation of sodium-dependent phosphate transpor	< –100	0.00363	–16.21
GO:1904766	Negative regulation of macroautophagy by TORC1 signaling	< –100	0.00363	–16.21
GO:0015782	CMP-N-acetylneuraminate transmembrane transport	< –100	0.00363	–16.21
GO:0097222	Mitochondrial mRNA polyadenylation	< –100	0.00363	–16.21
GO:0034355	NAD salvage	< –100	0.00363	–16.21
GO:0002353	Plasma kallikrein-kinin cascade	< –100	0.00725	–14.22
GO:0090615	Mitochondrial mRNA processing	< –100	0.00725	–14.22
GO:0006431	Methionyl-tRNA aminoacylation	< –100	0.00725	–14.22
GO:0035683	Memory T cell extravasation	< –100	0.00725	–14.22
GO:1904325	Positive regulation of inhibitory G protein-coupled receptor ph	< –100	0.00725	–14.22
GO:1904323	Regulation of inhibitory G protein-coupled receptor phosphory	< –100	0.00725	–14.22
GO:0042357	Thiamine diphosphate metabolic process	< –100	0.00725	–14.22
GO:0003374	Dynamin family protein polymerization involved in mitochondri	< –100	0.00725	–14.22
GO:0003373	Dynamin family protein polymerization involved in membrane f	< –100	0.00725	–14.22
GO:0006772	Thiamine metabolic process	–91.62	0.0109	–12.79
GO:0060183	Apelin receptor signaling pathway	–91.62	0.0109	–12.79
GO:0002254	Kinin cascade	–91.62	0.0109	–12.79
GO:2000547	Regulation of dendritic cell dendrite assembly	–91.62	0.0109	–12.79
GO:1902174	Positive regulation of keratinocyte apoptotic process	–91.62	0.0109	–12.79
GO:0000962	Positive regulation of mitochondrial RNA catabolic process	–91.62	0.0109	–12.79
GO:0000958	Mitochondrial mRNA catabolic process	–91.62	0.0109	–12.79
GO:0000957	Mitochondrial RNA catabolic process	–91.62	0.0109	–12.79
GO:0070682	Proteasome regulatory particle assembly	–91.62	0.0109	–12.79
GO:0042723	Thiamine-containing compound metabolic process	–91.62	0.0109	–12.79
GO:1904582	Positive regulation of intracellular mRNA localization	–91.62	0.0109	–12.79
GO:0034476	U5 snRNA 3'-end processing	–91.62	0.0109	–12.79
GO:0034473	U1 snRNA 3'-end processing	–91.62	0.0109	–12.79
GO:0010482	Regulation of epidermal cell division	–91.62	0.0109	–12.79
GO:0031123	RNA 3'-end processing	–12.35	0.000332	–12.62
GO:0090141	Positive regulation of mitochondrial fission	–27.49	0.00249	–12.45
GO:0034472	snRNA 3'-end processing	–27.49	0.00249	–12.45
GO:0045606	Positive regulation of epidermal cell differentiation	–26.18	0.00274	–12.07
GO:0006397	mRNA processing	–5.95	0.0000214	–12.01
GO:0050684	Regulation of mRNA processing	–9.29	0.000218	–11.77
GO:0000380	Alternative mRNA splicing, via spliceosome	–24.99	0.003	–11.71
GO:0030856	Regulation of epithelial cell differentiation	–8.92	0.000262	–11.31
GO:0060279	Positive regulation of ovulation	–68.71	0.0144	–11.24
GO:2000627	Positive regulation of miRNA catabolic process	–68.71	0.0144	–11.24

Table S16. *Reactome Pathway annotations mapped to enriched DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including Reactome Pathway IDs, Reactome Pathway annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	Reactome Pathway	FC	P	π
R-MMU-964975	Vitamins B6 activation to pyridoxal phosphate	> +100	0.000074	+27.44
R-MMU-429593	Inositol transporters	+81.44	0.0122	+12.15
R-MMU-380108	Chemokine receptors bind chemokines	+14.96	0.00112	+11.52
R-MMU-375276	Peptide ligand-binding receptors	+7.80	0.000132	+11.50
R-MMU-176974	Unwinding of DNA	+61.08	0.0162	+10.62
R-MMU-389599	Alpha-oxidation of phytanate	+40.72	0.0243	+8.63
R-MMU-1236977	Endosomal/Vacuolar pathway	+15.76	0.00733	+8.49
R-MMU-389397	Orexin and neuropeptides FF and QRFP bind to their respect	+30.54	0.0322	+7.36
R-MMU-3371511	HSF1 activation	+30.54	0.0322	+7.36
R-MMU-110313	Translesion synthesis by Y family DNA polymerases bypasse	+12.53	0.0114	+7.09
R-MMU-1236974	ER-Phagosome pathway	+12.22	0.0119	+6.95
R-MMU-162658	Golgi Cisternae Pericentriolar Stack Reorganization	+24.43	0.0401	+6.44
R-MMU-1855167	Synthesis of pyrophosphates in the cytosol	+24.43	0.0401	+6.44
R-MMU-376172	DSCAM interactions	+24.43	0.0401	+6.44
R-MMU-6811440	Retrograde transport at the Trans-Golgi-Network	+10.86	0.0149	+6.29
R-MMU-373076	Class A/1 (Rhodopsin-like receptors)	+4.73	0.00178	+6.16
R-MMU-5689877	Josephin domain DUBs	+22.21	0.044	+6.07
R-MMU-983170	Antigen Presentation: Folding, assembly and peptide loading c	+10.40	0.0162	+6.05
R-MMU-73893	DNA Damage Bypass	+10.18	0.0168	+5.94
R-MMU-5620924	Intraflagellar transport	+9.22	0.0202	+5.43
R-MMU-3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR	+9.22	0.0202	+5.43
R-MMU-3371568	Attenuation phase	+17.45	0.0557	+5.17
R-MMU-2424491	DAP12 signaling	+8.73	0.0224	+5.16
R-MMU-6798695	Neutrophil degranulation	+3.57	0.00186	+5.01
R-MMU-975577	N-Glycan antennae elongation	+16.29	0.0596	+4.93
R-MMU-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	+16.29	0.0596	+4.93
R-MMU-114608	Platelet degranulation	+6.01	0.014	+4.80
R-MMU-204174	Regulation of pyruvate dehydrogenase (PDH) complex	+15.27	0.0634	+4.71
R-MMU-8949664	Processing of SMDT1	+15.27	0.0634	+4.71
R-MMU-76005	Response to elevated platelet cytosolic Ca2+	+5.77	0.0156	+4.57
R-MMU-8949215	Mitochondrial calcium ion transport	+14.37	0.0672	+4.51
R-MMU-264642	Acetylcholine Neurotransmitter Release Cycle	+14.37	0.0672	+4.51
R-MMU-8876725	Protein methylation	+14.37	0.0672	+4.51
R-MMU-2172127	DAP12 interactions	+7.52	0.0295	+4.45
R-MMU-181430	Norepinephrine Neurotransmitter Release Cycle	+13.57	0.0711	+4.32
R-MMU-181429	Serotonin Neurotransmitter Release Cycle	+13.57	0.0711	+4.32
R-MMU-163210	Formation of ATP by chemiosmotic coupling	+13.57	0.0711	+4.32
R-MMU-8949613	Cristae formation	+13.57	0.0711	+4.32
R-MMU-1428517	The citric acid (TCA) cycle and respiratory electron transport	+5.51	0.0176	+4.32
R-MMU-500792	GPCR ligand binding	+3.68	0.006	+4.18
R-MMU-888590	GABA synthesis, release, reuptake and degradation	+12.86	0.0749	+4.15
R-MMU-9603798	Class I peroxisomal membrane protein import	+12.86	0.0749	+4.15
R-MMU-110320	Translesion Synthesis by POLH	+12.86	0.0749	+4.15
R-MMU-212676	Dopamine Neurotransmitter Release Cycle	+10.62	0.0899	+3.57
R-MMU-163200	Respiratory electron transport, ATP synthesis by chemiosmo	+6.03	0.0439	+3.52
R-MMU-69190	DNA strand elongation	+10.18	0.0936	+3.44
R-MMU-210500	Glutamate Neurotransmitter Release Cycle	+10.18	0.0936	+3.44
R-MMU-3371571	HSF1-dependent transactivation	+10.18	0.0936	+3.44
R-MMU-975576	N-glycan antennae elongation in the medial/trans-Golgi	+9.77	0.0973	+3.33
R-MMU-373752	Netrin-1 signaling	+9.40	0.0954	+3.30
R-MMU-3371556	Cellular response to heat stress	+5.55	0.0509	+3.20

Table S17. *Reactome Pathway annotations mapped to depleted DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including Reactome Pathway IDs, Reactome Pathway annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	Reactome Pathway	FC	P	π
R-MMU-727802	Transport of nucleotide sugars	–61.08	0.000518	–19.49
R-MMU-196819	Vitamin B1 (thiamin) metabolism	–54.97	0.018	–10.09
R-MMU-174362	Transport and synthesis of PAPS	–45.81	0.0216	–9.19
R-MMU-420029	Tight junction interactions	–45.81	0.0216	–9.19
R-MMU-3134963	DEx/H-box helicases activate type I IFN and inflammatory cy	–39.26	0.0252	–8.46
R-MMU-6804114	TP53 Regulates Transcription of Genes Involved in G2 Cell C	–39.26	0.0252	–8.46
R-MMU-425397	Transport of vitamins, nucleosides, and related molecules	–13.41	0.00998	–7.49
R-MMU-421270	Cell-cell junction organization	–13.41	0.00998	–7.49
R-MMU-72203	Processing of Capped Intron-Containing Pre-mRNA	–5.75	0.00186	–6.89
R-MMU-163560	Triglyceride catabolism	–24.99	0.0392	–6.53
R-MMU-390247	Beta-oxidation of very long chain fatty acids	–24.99	0.0392	–6.53
R-MMU-9614399	Regulation of localization of FOXO transcription factors	–22.90	0.0427	–6.19
R-MMU-111447	Activation of BAD and translocation to mitochondria	–22.90	0.0427	–6.19
R-MMU-1614558	Degradation of cysteine and homocysteine	–22.90	0.0427	–6.19
R-MMU-75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 com	–22.90	0.0427	–6.19
R-MMU-174403	Glutathione synthesis and recycling	–22.90	0.0427	–6.19
R-MMU-72163	mRNA Splicing - Major Pathway	–6.07	0.00442	–6.13
R-MMU-75205	Dissolution of Fibrin Clot	–21.14	0.0462	–5.88
R-MMU-72172	mRNA Splicing	–5.85	0.00505	–5.85
R-MMU-72187	mRNA 3'-end processing	–9.64	0.0186	–5.66
R-MMU-5625740	RHO GTPases activate PKNs	–9.48	0.0192	–5.57
R-MMU-450604	KSRP (KHSRP) binds and destabilizes mRNA	–18.32	0.0531	–5.35
R-MMU-2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchym	–18.32	0.0531	–5.35
R-MMU-71336	Pentose phosphate pathway	–18.32	0.0531	–5.35
R-MMU-429958	mRNA decay by 3' to 5' exoribonuclease	–17.18	0.0566	–5.12
R-MMU-73856	RNA Polymerase II Transcription Termination	–8.33	0.0244	–4.93
R-MMU-450385	Butyrate Response Factor 1 (BRF1) binds and destabilizes m	–16.17	0.06	–4.91
R-MMU-450513	Tristetraprolin (TTP, ZFP36) binds and destabilizes mRNA	–16.17	0.06	–4.91
R-MMU-446728	Cell junction organization	–8.08	0.0258	–4.79
R-MMU-114452	Activation of BH3-only proteins	–15.27	0.0634	–4.71
R-MMU-77595	Processing of Intronless Pre-mRNAs	–14.47	0.0668	–4.53
R-MMU-197264	Nicotinamide salvaging	–14.47	0.0668	–4.53
R-MMU-446193	Biosynthesis of the N-glycan precursor and transfer to a nasc	–7.63	0.0286	–4.53
R-MMU-159236	Transport of Mature mRNA derived from an Intron-Containing	–7.53	0.0294	–4.46
R-MMU-69481	G2/M Checkpoints	–5.65	0.0165	–4.45
R-MMU-69473	G2/M DNA damage checkpoint	–7.43	0.0301	–4.40
R-MMU-156584	Cytosolic sulfonation of small molecules	–13.74	0.0702	–4.36
R-MMU-8953854	Metabolism of RNA	–3.41	0.00453	–4.15
R-MMU-380287	Centrosome maturation	–6.87	0.0347	–4.06
R-MMU-380270	Recruitment of mitotic centrosome proteins and complexes	–6.87	0.0347	–4.06
R-MMU-71403	Citric acid cycle (TCA cycle)	–12.49	0.077	–4.06
R-MMU-140837	Intrinsic Pathway of Fibrin Clot Formation	–12.49	0.077	–4.06
R-MMU-9614085	FOXO-mediated transcription	–12.49	0.077	–4.06
R-MMU-68886	M Phase	–3.89	0.00948	–3.96
R-MMU-72202	Transport of Mature Transcript to Cytoplasm	–6.70	0.0363	–3.95
R-MMU-8979227	Triglyceride metabolism	–11.95	0.0803	–3.92
R-MMU-1614635	Sulfur amino acid metabolism	–11.95	0.0803	–3.92
R-MMU-450531	Regulation of mRNA stability by proteins that bind AU-rich ele	–6.47	0.0387	–3.80
R-MMU-69620	Cell Cycle Checkpoints	–4.13	0.0164	–3.65
R-MMU-1500931	Cell-Cell communication	–6.11	0.0429	–3.57
R-MMU-380320	Recruitment of NuMA to mitotic centrosomes	–6.11	0.0429	–3.57

Table S18. *Human orthologs mapped to all DEGs identified among DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* DEGs were aligned to GRCh37. Tabular data including mouse DEG gene symbols, human ortholog gene symbols, and Ensembl and Entrez Gene IDs for human orthologs of mouse DEGs are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Mouse DEG	Human Ortholog	Ensembl Gene ID	Entrez Gene ID
Aadac	*AADAC*	ENSG00000114771	13
Aass	*AASS*	ENSG00000008311	10157
Acad9	*ACAD9*	ENSG00000177646	28976
Acer2	*ACER2*	ENSG00000177076	340485
Acot4	*ACOT4*	ENSG00000177465	122970
Acot6	*ACOT6*	ENSG00000205669	641372
Adamts1	*ADAMTS1*	ENSG00000154734	9510
Adamts12	*ADAMTS12*	ENSG00000151388	81792
Adgre4	*ADGRE4P*	ENSG00000268758	326342
Adh1	*ADH1C*	ENSG00000248144	126
Adrb1	*ADRB1*	ENSG00000043591	153
Adsl	*ADSL*	ENSG00000239900	158
Ahctf1	*AHCTF1*	ENSG00000153207	25909
AI661453	*C6orf132*	ENSG00000188112	647024
Aldh1a3	*ALDH1A3*	ENSG00000184254	220
Aldh3b2	*ALDH3B2*	ENSG00000132746	222
Alg1	*ALG1*	ENSG00000033011	56052
Alox12b	*ALOX12B*	ENSG00000179477	242
Alox5	*ALOX5*	ENSG00000012779	240
Amd1	*AMD1*	ENSG00000123505	262
Amd2	*AMD1*	ENSG00000123505	262
Ankdd1a	*ANKDD1A*	ENSG00000166839	348094
Ankrd35	*ANKRD35*	ENSG00000198483	148741
Anks1b	*ANKS1B*	ENSG00000185046	56899
Anxa5	*ANXA5*	ENSG00000164111	308
Aplnr	*APLNR*	ENSG00000134817	187
Apold1	*APOLD1*	ENSG00000178878	81575
Apopt1	*COA8*	ENSG00000256053	84334
Aqp3	*AQP3*	ENSG00000165272	360
Arhgap30	*ARHGAP30*	ENSG00000186517	257106
Arhgap33	*ARHGAP33*	ENSG00000004777	115703
Arl2	*ARL2*	ENSG00000213465	402
Arl8a	*ARL8A*	ENSG00000143862	127829
Arnt2	*ARNT2*	ENSG00000172379	9915
Asb3	*ASB3*	ENSG00000115239	51130
Asb3	*GPR75-ASB3*	ENSG00000115239	100302652
Aspdh	*ASPDH*	ENSG00000204653	554235
Atcay	*ATCAY*	ENSG00000167654	85300
Atp5j2	*ATP5J2*	ENSG00000241468	9551
Atp6v0c	*ATP6V0C*	ENSG00000185883	527
Atp6v1d	*ATP6V1D*	ENSG00000100554	51382
Atp8b2	*ATP8B2*	ENSG00000143515	57198
AU022252	*C1orf50*	ENSG00000164008	79078
Avpi1	*AVPI1*	ENSG00000119986	60370
Axdnd1	*AXDND1*	ENSG00000162779	126859
B2m	*B2M*	ENSG00000166710	567
B4galt5	*B4GALT5*	ENSG00000158470	9334
Baz2b	*BAZ2B*	ENSG00000123636	29994
Bcat1	*BCAT1*	ENSG00000060982	586
Bex1	*BEX2*	ENSG00000133134	55859
Bex2	*BEX1*	ENSG00000133169	84707
Bex4	*BEX4*	ENSG00000102409	56271

Table S19. *Grouped human-mouse ortholog pairs for all DEGs detected in DRD1-expressing striatal cells of F1 NIC and F2 NIC mice and for all DEGs shared between F1 NIC and F2 NIC mice.* Tabular data including human orthologs of all DEGs detected in DRD1-expressing striatal cells of F1 NIC and F2 NIC mice as well as all DEGs shared between F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

F1 NIC DEGs	Human DEG Orthologs	F2 NIC DEGs	Human DEG Orthologs	Shared DEGs	Human DEG Orthologs
Acad9	*ACAD9*	*AI661453*	*C6orf132*	*Acad9*	*ACAD9*
Acer2	*ACER2*	*AU022252*	*C1orf50*	*Acer2*	*ACER2*
Acot4	*ACOT4*	*Aadac*	*AADAC*	*Acot6*	*ACOT6*
Acot6	*ACOT6*	*Aass*	*AASS*	*Alg1*	*ALG1*
Adamts1	*ADAMTS1*	*Acad9*	*ACAD9*	*Amd1*	*AMD1*
Adamts12	*ADAMTS12*	*Acer2*	*ACER2*	*Amd2*	*AMD1*
Adh1	*ADH1C*	*Acot6*	*ACOT6*	*Anxa5*	*ANXA5*
Adsl	*ADSL*	*Adgre4*	*ADGRE4P*	*Aplnr*	*APLNR*
Aldh1a3	*ALDH1A3*	*Adrb1*	*ADRB1*	*Apopt1*	*COA8*
Aldh3b2	*ALDH3B2*	*Ahctf1*	*AHCTF1*	*Arl8a*	*ARL8A*
Alg1	*ALG1*	*Alg1*	*ALG1*	*Asb3*	*ASB3*
Amd1	*AMD1*	*Alox12b*	*ALOX12B*	*Atp5j2*	*ATP5J2*
Amd2	*AMD1*	*Alox5*	*ALOX5*	*Avpi1*	*AVPI1*
Anxa5	*ANXA5*	*Amd1*	*AMD1*	*B2m*	*B2M*
Aplnr	*APLNR*	*Amd2*	*AMD1*	*B4galt5*	*B4GALT5*
Apopt1	*COA8*	*Ankdd1a*	*ANKDD1A*	*Cbln3*	*CBLN3*
Aqp3	*AQP3*	*Ankrd35*	*ANKRD35*	*Ccl19*	*CCL19*
Arhgap33	*ARHGAP33*	*Anks1b*	*ANKS1B*	*Ccl21b*	*CCL21*
Arl2	*ARL2*	*Anxa5*	*ANXA5*	*Ccl5*	*CCL5*
Arl8a	*ARL8A*	*Aplnr*	*APLNR*	*Cd3eap*	*CD3EAP*
Asb3	*ASB3*	*Apold1*	*APOLD1*	*Cd52*	*CD52*
Atp5j2	*ATP5J2*	*Apopt1*	*COA8*	*Cdh7*	*CDH7*
Atp6v0c	*ATP6V0C*	*Arhgap30*	*ARHGAP30*	*Cenps*	*APITD1*
Atp6v1d	*ATP6V1D*	*Arl8a*	*ARL8A*	*Cercam*	*CERCAM*
Avpi1	*AVPI1*	*Arnt2*	*ARNT2*	*Cetn4*	*CETN4P*
B2m	*B2M*	*Asb3*	*ASB3*	*Chac1*	*CHAC1*
B4galt5	*B4GALT5*	*Aspdh*	*ASPDH*	*Chga*	*CHGA*
Bcat1	*BCAT1*	*Atcay*	*ATCAY*	*Clec16a*	*CLEC16A*
Bloc1s5	*BLOC1S5*	*Atp5j2*	*ATP5J2*	*Cog6*	*COG6*
Bola2	*BOLA2*	*Atp8b2*	*ATP8B2*	*Cplx1*	*CPLX1*
Bpifa1	*BPIFA1*	*Avpi1*	*AVPI1*	*Cpne8*	*CPNE8*
Brf1	*BRF1*	*Axdnd1*	*AXDND1*	*Cstf2t*	*CSTF2T*
Cabin1	*CABIN1*	*B2m*	*B2M*	*Ctse*	*CTSE*
Cand2	*CAND2*	*B4galt5*	*B4GALT5*	*Cyhr1*	*CYHR1*
Cat	*CAT*	*Baz2b*	*BAZ2B*	*Dbp*	*DBP*
Cav2	*CAV2*	*Bex1*	*BEX2*	*Dctn1*	*DCTN1*
Cbln3	*CBLN3*	*Bex2*	*BEX1*	*Ddhd2*	*DDHD2*
Ccdc167	*CCDC167*	*Bex4*	*BEX4*	*Ddx17*	*DDX17*
Ccdc184	*C12orf68*	*Bspry*	*BSPRY*	*Ddx19a*	*DDX19A*
Ccdc28a	*CCDC28A*	*Bst2*	*BST2*	*Dera*	*DERA*
Ccl19	*CCL19*	*Btd*	*BTD*	*Dhx36*	*DHX36*
Ccl21b	*CCL21*	*C1qa*	*C1QA*	*Dmac2*	*ATP5SL*
Ccl5	*CCL5*	*C1qb*	*C1QB*	*Dnajb1*	*DNAJB1*
Ccnb1ip1	*CCNB1IP1*	*C3*	*C3*	*Dpy19l1*	*DPY19L1*
Ccr1	*CCR1*	*Calr*	*CALR*	*Dusp23*	*DUSP23*
Ccr5	*CCR5*	*Camp*	*CAMP*	*Ecm2*	*ECM2*
Cd209a	*CD209*	*Car8*	*CA8*	*Eif3j1*	*EIF3J*
Cd3eap	*CD3EAP*	*Castor2*	*GATSL2*	*Elof1*	*ELOF1*
Cd52	*CD52*	*Cbln3*	*CBLN3*	*Eml5*	*EML5*
Cdh13	*CDH13*	*Ccdc117*	*CCDC117*	*Emp2*	*EMP2*

Table S20. *Grouped trans-omic ortholog pairs for all DEGs detected in F1 NIC and F2 NIC mice and for all DEGs shared between F1 NIC and F2 NIC mice that overlap with human gene orthologs exhibiting differential methylation signatures in the PACE meta-analysis of cord blood DNA methylation profiles among maternal smokers.* Tabular data including gene symbols for PACE DMG human orthologs of all DEGs detected in DRD1-expressing striatal cells of F1 NIC and F2 NIC mice as well as all DEGs shared between F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

F1 NIC DEGs	F1 NIC PACE DMG Orthologs	F2 NIC DEGs	F2 NIC PACE DMG Orthologs	Shared DEGs	Shared PACE DMG Orthologs
Acad9	*ACAD9*	*Acad9*	*ACAD9*	*Acad9*	*ACAD9*
Adsl	*ADSL*	*Asb3*	*ASB3*	*Asb3*	*ASB3*
Aldh3b2	*ALDH3B2*	*B2m*	*B2M*	*B2m*	*B2M*
Aqp3	*AQP3*	*Baz2b*	*BAZ2B*	*Cbln3*	*CBLN3*
Asb3	*ASB3*	*Bst2*	*BST2*	*Ccl21b*	*CCL21*
B2m	*B2M*	*Camp*	*CAMP*	*Cd52*	*CD52*
Bcat1	*BCAT1*	*Cbln3*	*CBLN3*	*Cenps*	*APITD1*
Brf1	*BRF1*	*Ccl21b*	*CCL21*	*Clec16a*	*CLEC16A*
Cbln3	*CBLN3*	*Cd274*	*CD274*	*Ctse*	*CTSE*
Ccl21b	*CCL21*	*Cd52*	*CD52*	*Cyhr1*	*CYHR1*
Cd52	*CD52*	*Cdkn1b*	*CDKN1B*	*Dnajb1*	*DNAJB1*
Cenps	*APITD1*	*Cenps*	*APITD1*	*F11r*	*F11R*
Clec16a	*CLEC16A*	*Churc1*	*CHURC1*	*Fkbp5*	*FKBP5*
Clmp	*CLMP*	*Cirbp*	*CIRBP*	*H2-T23*	*HLA-E*
Cort	*CORT*	*Clec16a*	*CLEC16A*	*Heatr3*	*HEATR3*
Crhr1	*CRHR1*	*Cmpk2*	*CMPK2*	*Hmgn3*	*HMGN3*
Ctdsp1	*CTDSP1*	*Creb3l2*	*CREB3L2*	*Hs6st1*	*HS6ST1*
Ctse	*CTSE*	*Creld2*	*CRELD2*	*Ift46*	*IFT46*
Cyhr1	*CYHR1*	*Ctse*	*CTSE*	*Itpk1*	*ITPK1*
Ddit4	*DDIT4*	*Cxcl9*	*CXCL9*	*Mars1*	*MARS*
Dgke	*DGKE*	*Cyhr1*	*CYHR1*	*Mkrn3*	*MKRN3*
Dnajb1	*DNAJB1*	*Dnajb1*	*DNAJB1*	*Mmp14*	*MMP14*
Dtnbp1	*DTNBP1*	*Efcab14*	*EFCAB14*	*Nsmce2*	*NSMCE2*
Ets2	*ETS2*	*F11r*	*F11R*	*Pcdhga4*	*PCDHGA4*
Ewsr1	*EWSR1*	*Fkbp5*	*FKBP5*	*Pcdhga7*	*PCDHGA7*
F11r	*F11R*	*Gpr26*	*GPR26*	*Pcdhga8*	*PCDHGA8*
Fau	*FAU*	*H1f0*	*H1F0*	*Pcdhgb8*	*PCDHGB3*
Fbrsl1	*FBRSL1*	*H2-T23*	*HLA-E*	*Plac9b*	*PLAC9*
Fbxl5	*FBXL5*	*Heatr3*	*HEATR3*	*Prcp*	*PRCP*
Fkbp5	*FKBP5*	*Hmgcl*	*HMGCL*	*Snrnp70*	*SNRNP70*
Got2	*GOT2*	*Hmgn3*	*HMGN3*		
H2-T23	*HLA-E*	*Hs6st1*	*HS6ST1*		
H2bc11	*HIST1H2BL*	*Hspa1a*	*HSPA1A*		
Heatr3	*HEATR3*	*Hspb1*	*HSPB1*		
Hmgn3	*HMGN3*	*Ifi35*	*IFI35*		
Hs6st1	*HS6ST1*	*Ift46*	*IFT46*		
Ift46	*IFT46*	*Itpk1*	*ITPK1*		
Itpk1	*ITPK1*	*Jchain*	*IGJ*		
Kcnh3	*KCNH3*	*Kcnab1*	*KCNAB1*		
Lefty1	*LEFTY1*	*Kif5c*	*KIF5C*		
Mars1	*MARS*	*Klhl29*	*KLHL29*		
Mkrn3	*MKRN3*	*Lonrf1*	*LONRF1*		
Mmp14	*MMP14*	*Lrrc59*	*LRRC59*		
Nsmce2	*NSMCE2*	*Lrrk2*	*LRRK2*		
Pbx2	*PBX2*	*Ly86*	*LY86*		
Pcdhga4	*PCDHGA4*	*Man1a2*	*MAN1A2*		
Pcdhga7	*PCDHGA7*	*Mars1*	*MARS*		
Pcdhga8	*PCDHGA8*	*Mkrn3*	*MKRN3*		

Table S21. *G.O. Biological Process annotations mapped to DEGs from DRD1-expressing striatal cells of F1 NIC mice that are orthologs of DMGs in cord blood from newborns of maternal smokers reported by the PACE meta-analysis thereof.* Tabular data including G.O. IDs, G.O. Biological Process annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	G.O. Biological Process	FC	P	π
GO:0002477	Antigen processing and presentation of exogenous peptide ar	> 100	0.000048	28.69
GO:0002428	Antigen processing and presentation of peptide antigen via MI	86.53	0.000259	23.08
GO:0002481	Antigen processing and presentation of exogenous protein an	> 100	0.0033	16.49
GO:0001815	Positive regulation of antibody-dependent cellular cytotoxicity	> 100	0.0033	16.49
GO:0001712	Ectodermal cell fate commitment	> 100	0.0033	16.49
GO:2000548	Negative regulation of dendritic cell dendrite assembly	> 100	0.0033	16.49
GO:0032361	Pyridoxal phosphate catabolic process	> 100	0.0033	16.49
GO:0051458	Corticotropin secretion	> 100	0.0033	16.49
GO:1904766	Negative regulation of macroautophagy by TORC1 signaling	> 100	0.0033	16.49
GO:0042820	Vitamin B6 catabolic process	> 100	0.0033	16.49
GO:0010578	Regulation of adenylate cyclase activity involved in G protein-	> 100	0.0033	16.49
GO:0097026	Dendritic cell dendrite assembly	> 100	0.0033	16.49
GO:0002475	Antigen processing and presentation via MHC class Ib	43.27	0.00102	16.26
GO:0002478	Antigen processing and presentation of exogenous peptide ar	23.91	0.000288	16.21
GO:0051866	General adaptation syndrome	> 100	0.00608	14.72
GO:0019885	Antigen processing and presentation of endogenous peptide a	35.63	0.0015	14.56
GO:0052746	Inositol phosphorylation	> 100	0.00658	14.50
GO:0001813	Regulation of antibody-dependent cellular cytotoxicity	> 100	0.00658	14.50
GO:0001798	Positive regulation of type iia hypersensitivity	> 100	0.00658	14.50
GO:0001705	Ectoderm formation	> 100	0.00658	14.50
GO:2000529	Positive regulation of myeloid dendritic cell chemotaxis	> 100	0.00658	14.50
GO:2000527	Regulation of myeloid dendritic cell chemotaxis	> 100	0.00658	14.50
GO:0032759	Positive regulation of TRAIL production	> 100	0.00658	14.50
GO:0006431	Methionyl-tRNA aminoacylation	> 100	0.00658	14.50
GO:0032679	Regulation of TRAIL production	> 100	0.00658	14.50
GO:0071283	Cellular response to iron(III) ion	> 100	0.00658	14.50
GO:0036371	Protein localization to T-tubule	> 100	0.00658	14.50
GO:0035759	Mesangial cell-matrix adhesion	> 100	0.00658	14.50
GO:0035683	Memory T cell extravasation	> 100	0.00658	14.50
GO:0031247	Actin rod assembly	> 100	0.00658	14.50
GO:1904437	Positive regulation of transferrin receptor binding	> 100	0.00658	14.50
GO:1904435	Regulation of transferrin receptor binding	> 100	0.00658	14.50
GO:1904434	Positive regulation of ferrous iron binding	> 100	0.00658	14.50
GO:1904432	Regulation of ferrous iron binding	> 100	0.00658	14.50
GO:0009098	Leucine biosynthetic process	> 100	0.00658	14.50
GO:0042365	Water-soluble vitamin catabolic process	> 100	0.00658	14.50
GO:0002894	Positive regulation of type II hypersensitivity	> 100	0.00658	14.50
GO:0019551	Glutamate catabolic process to 2-oxoglutarate	> 100	0.00658	14.50
GO:0019550	Glutamate catabolic process to aspartate	> 100	0.00658	14.50
GO:0000712	Resolution of meiotic recombination intermediates	33.65	0.00167	14.09
GO:0019884	Antigen processing and presentation of exogenous antigen	19.33	0.000533	13.99
GO:0002483	Antigen processing and presentation of endogenous peptide a	31.88	0.00186	13.64
GO:2000978	Negative regulation of forebrain neuron differentiation	> 100	0.00986	13.33
GO:0002519	Natural killer cell tolerance induction	> 100	0.00986	13.33
GO:0002353	Plasma kallikrein-kinin cascade	> 100	0.00986	13.33
GO:0002254	Kinin cascade	> 100	0.00986	13.33
GO:0001796	Regulation of type IIa hypersensitivity	> 100	0.00986	13.33
GO:2000547	Regulation of dendritic cell dendrite assembly	> 100	0.00986	13.33
GO:0006532	Aspartate biosynthetic process	> 100	0.00986	13.33
GO:0006106	Fumarate metabolic process	> 100	0.00986	13.33

Table S22. *G.O. Biological Process annotations mapped to DEGs from DRD1-expressing striatal cells of F2 NIC mice that are orthologs of DMGs in cord blood from newborns of maternal smokers reported by the PACE meta-analysis thereof.* Tabular data including G.O. IDs, G.O. Biological Process annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	G.O. Biological Process	FC	P	π
GO:0002477	Antigen processing and presentation of exogenous peptide ar	> 100	0.0000769	27.33
GO:0097201	Negative regulation of transcription from RNA polymerase II p	55.26	0.0000247	26.67
GO:0002155	Regulation of thyroid hormone mediated signaling pathway	> 100	0.000136	25.69
GO:0002428	Antigen processing and presentation of peptide antigen via MI	68.42	0.000414	20.62
GO:0099641	Anterograde axonal protein transport	59.87	0.00054	19.29
GO:0099640	Axo-dendritic protein transport	59.87	0.00054	19.29
GO:1905383	Protein localization to presynapse	59.87	0.00054	19.29
GO:1900122	Positive regulation of receptor binding	53.22	0.000681	18.16
GO:0090647	Modulation of age-related behavioral decline	47.9	0.000839	17.17
GO:0019731	Antibacterial humoral response	17.11	0.0000972	16.44
GO:0090084	Negative regulation of inclusion body assembly	43.54	0.00101	16.31
GO:1903125	Negative regulation of thioredoxin peroxidase activity by pepti	> 100	0.00417	15.81
GO:0002481	Antigen processing and presentation of exogenous protein an	> 100	0.00417	15.81
GO:0002364	NK T cell lineage commitment	> 100	0.00417	15.81
GO:0001815	Positive regulation of antibody-dependent cellular cytotoxicity	> 100	0.00417	15.81
GO:2000548	Negative regulation of dendritic cell dendrite assembly	> 100	0.00417	15.81
GO:1902380	Positive regulation of endoribonuclease activity	> 100	0.00417	15.81
GO:0002149	Hypochlorous acid biosynthetic process	> 100	0.00417	15.81
GO:0002148	Hypochlorous acid metabolic process	> 100	0.00417	15.81
GO:2000469	Negative regulation of peroxidase activity	> 100	0.00417	15.81
GO:1990268	Response to gold nanoparticle	> 100	0.00417	15.81
GO:0000435	Positive regulation of transcription from RNA polymerase II pr	> 100	0.00417	15.81
GO:0000431	Regulation of transcription from RNA polymerase II promoter	> 100	0.00417	15.81
GO:0000411	Positive regulation of transcription by galactose	> 100	0.00417	15.81
GO:0000409	Regulation of transcription by galactose	> 100	0.00417	15.81
GO:1905404	Positive regulation of activated CD8-positive, alpha-beta T cel	> 100	0.00417	15.81
GO:1904887	Wnt signalosome assembly	> 100	0.00417	15.81
GO:1904766	Negative regulation of macroautophagy by TORC1 signaling	> 100	0.00417	15.81
GO:0002845	Positive regulation of tolerance induction to tumor cell	> 100	0.00417	15.81
GO:0002843	Regulation of tolerance induction to tumor cell	> 100	0.00417	15.81
GO:0097026	Dendritic cell dendrite assembly	> 100	0.00417	15.81
GO:0002737	Negative regulation of plasmacytoid dendritic cell cytokine pro	> 100	0.00417	15.81
GO:0002736	Regulation of plasmacytoid dendritic cell cytokine production	> 100	0.00417	15.81
GO:0036037	CD8-positive, alpha-beta T cell activation	39.91	0.0012	15.53
GO:0019730	Antimicrobial humoral response	10.19	0.0000303	15.13
GO:0001878	Response to yeast	36.84	0.00141	14.83
GO:0098840	Protein transport along microtubule	36.84	0.00141	14.83
GO:0099118	Microtubule-based protein transport	36.84	0.00141	14.83
GO:0061077	Chaperone-mediated protein folding	14.3	0.000192	14.26
GO:0002475	Antigen processing and presentation via MHC class Ib	34.21	0.00163	14.21
GO:0033120	Positive regulation of RNA splicing	19.42	0.000531	14.01
GO:0002660	Positive regulation of peripheral tolerance induction	> 100	0.00832	13.82
GO:0002658	Regulation of peripheral tolerance induction	> 100	0.00832	13.82
GO:0002654	Positive regulation of tolerance induction dependent upon imm	> 100	0.00832	13.82
GO:1903217	Negative regulation of protein processing involved in protein ta	> 100	0.00832	13.82
GO:1903216	Regulation of protein processing involved in protein targeting t	> 100	0.00832	13.82
GO:0052746	Inositol phosphorylation	> 100	0.00832	13.82
GO:0046077	dUDP metabolic process	> 100	0.00832	13.82
GO:0046072	dTDP metabolic process	> 100	0.00832	13.82
GO:2001038	Regulation of cellular response to drug	> 100	0.00832	13.82

Table S23. *G.O. Biological Process annotations mapped to DEGs shared between DRD1-expressing striatal cells of F1 NIC and F2 NIC mice that are orthologs of DMGs in cord blood from newborns of maternal smokers reported by the PACE meta-analysis thereof.* Tabular data including G.O. IDs, G.O. Biological Process annotations, fold change values, FDR-adjusted p-values, and π-values are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. FC, fold change (sign*fold enrichment). P, FDR-adjusted p-value. π, π-value (Log2FC*Log10P).

ID	G.O. Biological Process	FC	P	π
GO:0002477	Antigen processing and presentation of exogenous peptide ar	> 100	0.0000098	33.28
GO:0002428	Antigen processing and presentation of peptide antigen via MI	> 100	0.0000534	28.39
GO:0002478	Antigen processing and presentation of exogenous peptide ar	52.45	0.0000272	26.08
GO:0002475	Antigen processing and presentation via MHC class Ib	94.91	0.000212	24.13
GO:0019884	Antigen processing and presentation of exogenous antigen	42.41	0.0000509	23.21
GO:0019885	Antigen processing and presentation of endogenous peptide a	78.16	0.000312	22.05
GO:0002483	Antigen processing and presentation of endogenous peptide a	69.93	0.000389	20.90
GO:0048002	Antigen processing and presentation of peptide antigen	33.22	0.000105	20.11
GO:0002481	Antigen processing and presentation of exogenous protein an	> 100	0.0015	18.76
GO:0001815	Positive regulation of antibody-dependent cellular cytotoxicity	> 100	0.0015	18.76
GO:2000548	Negative regulation of dendritic cell dendrite assembly	> 100	0.0015	18.76
GO:1904766	Negative regulation of macroautophagy by TORC1 signaling	> 100	0.0015	18.76
GO:0097026	Dendritic cell dendrite assembly	> 100	0.0015	18.76
GO:0019883	Antigen processing and presentation of endogenous antigen	51.10	0.000723	17.83
GO:0002474	Antigen processing and presentation of peptide antigen via MI	47.45	0.000837	17.14
GO:0001916	Positive regulation of T cell mediated cytotoxicity	45.82	0.000897	16.81
GO:0052746	Inositol phosphorylation	> 100	0.00301	16.75
GO:0001813	Regulation of antibody-dependent cellular cytotoxicity	> 100	0.00301	16.75
GO:0001798	Positive regulation of type IIa hypersensitivity	> 100	0.00301	16.75
GO:2000529	Positive regulation of myeloid dendritic cell chemotaxis	> 100	0.00301	16.75
GO:2000527	Regulation of myeloid dendritic cell chemotaxis	> 100	0.00301	16.75
GO:0032759	Positive regulation of TRAIL production	> 100	0.00301	16.75
GO:0006431	Methionyl-tRNA aminoacylation	> 100	0.00301	16.75
GO:0032679	Regulation of TRAIL production	> 100	0.00301	16.75
GO:0071283	Cellular response to iron(III) ion	> 100	0.00301	16.75
GO:0036371	Protein localization to T-tubule	> 100	0.00301	16.75
GO:0035759	Mesangial cell-matrix adhesion	> 100	0.00301	16.75
GO:0035683	Memory T cell extravasation	> 100	0.00301	16.75
GO:1904437	Positive regulation of transferrin receptor binding	> 100	0.00301	16.75
GO:1904435	Regulation of transferrin receptor binding	> 100	0.00301	16.75
GO:1904434	Positive regulation of ferrous iron binding	> 100	0.00301	16.75
GO:1904432	Regulation of ferrous iron binding	> 100	0.00301	16.75
GO:0002894	Positive regulation of type II hypersensitivity	> 100	0.00301	16.75
GO:0019886	Antigen processing and presentation of exogenous peptide ar	44.29	0.000959	16.51
GO:0002495	Antigen processing and presentation of peptide antigen via MI	41.52	0.00109	15.93
GO:0007156	Homophilic cell adhesion via plasma membrane adhesion mol	15.91	0.000114	15.74
GO:2000978	Negative regulation of forebrain neuron differentiation	> 100	0.00451	15.59
GO:0002519	Natural killer cell tolerance induction	> 100	0.00451	15.59
GO:0002353	Plasma kallikrein-kinin cascade	> 100	0.00451	15.59
GO:0002254	Kinin cascade	> 100	0.00451	15.59
GO:0001796	Regulation of type IIa hypersensitivity	> 100	0.00451	15.59
GO:2000547	Regulation of dendritic cell dendrite assembly	> 100	0.00451	15.59
GO:1904715	Negative regulation of chaperone-mediated autophagy	> 100	0.00451	15.59
GO:0002892	Regulation of type II hypersensitivity	> 100	0.00451	15.59
GO:0002504	Antigen processing and presentation of peptide or polysaccha	39.08	0.00123	15.39
GO:0019882	Antigen processing and presentation	21.20	0.000388	15.03
GO:1903237	Negative regulation of leukocyte tethering or rolling	> 100	0.006	14.76
GO:2000566	Positive regulation of CD8-positive, alpha-beta T cell proliferat	> 100	0.006	14.76
GO:0038116	Chemokine (C-C motif) ligand 21 signaling pathway	> 100	0.006	14.76
GO:0002155	Regulation of thyroid hormone mediated signaling pathway	> 100	0.006	14.76

Table S24. *Perturbagen analysis input lists of human orthologs mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including human orthologs of all DEGs uniquely detected in DRD1-expressing striatal cells of either F1 NIC or F2 NIC mice as well as all DEGs shared between F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu.

Shared Up Orthologs	Shared Down Orthologs	F1 NIC Unique Up Orthologs	F1 NIC Unique Down Orthologs	F2 NIC Unique Up Orthologs	F2 NIC Unique Down Orthologs
ACAD9	ACOT6	ADSL	ACOT4	C6orf132	ALOX5
ACER2	ALG1	ALDH3B2	ADAMTS1	C1orf50	ANKDD1A
AMD1	ANXA5	ARL2	ADAMTS12	AADAC	ANKRD35
AMD1	APLNR	ATP6V0C	ADH1C	AASS	APOLD1
COA8	CBLN3	ATP6V1D	ALDH1A3	ADGRE4P	ASPDH
ARL8A	CCL19	BLOC1S5	AQP3	ADRB1	BAZ2B
ASB3	CDH7	BOLA2	ARHGAP33	AHCTF1	BEX2
ATP5J2	CERCAM	C12orf68	BCAT1	ALOX12B	BEX1
AVPI1	CETN4P	CCDC28A	BPIFA1	ANKS1B	BEX4
B2M	CHAC1	CDH13	BRF1	ARHGAP30	BSPRY
B4GALT5	CLEC16A	CHCHD2	CABIN1	ARNT2	BTD
CCL21	CSTF2T	CHMP4B	CAND2	ATCAY	CA8
CCL5	CYHR1	COPS6	CAT	ATP8B2	CCDC142
CD3EAP	DCTN1	COX15	CAV2	AXDND1	CDKN1B
CD52	DDHD2	CSMD3	CCDC167	BST2	CEP89
APITD1	DDX17	DBP	CCNB1IP1	C1QA	CES1
CHGA	DERA	DDIT4	CCR1	C1QB	CHMP5
COG6	DHX36	DDT	CCR5	C3	CHST6
CPLX1	ATP5SL	DDX47	CD209	CALR	CHURC1
CPNE8	DUSP23	DEXI	CEP68	CAMP	CIRBP
CTSE	ECM2	DGKE	CLDN3	GATSL2	CISD2
DDX19A	ELOF1	DNAH6	CLMP	CCDC117	CNPY1
DNAJB1	EML5	DTNBP1	COL5A2	CCL13	DBP
DPY19L1	EMP2	DUSP28	CORT	CD274	DCTN3
EIF3J	EXOSC9	EID2	CPNE6	CD300LD	DDX46
FAM205A	F11R	EMC4	CRHR1	CH25H	DVL2
FAM205A	FABP7	ETS2	CTDSP1	CMPK2	ECHDC3
FAM205A	GPATCH1	FAM78A	CTSC	COPG1	EFCAB7
FKBP3	GPR75	FAM83D	CXCL12	CREB3L2	EN2
FKBP5	HIST1H2BJ	FAU	CYP2A7	CRELD2	FAM122A
GABRA2	HEATR3	FBXL14	CYP2G1P	CST7	FAM214A
GINS4	HMGN3	FBXL5	CYP4V2	CXCL10	C1orf233
GUK1	HPS1	FBXO28	CYTH1	CXCL9	FOXRED2
HLA-E	ICA1	FMO2	DCN	DDX58	FRAT1
HABP4	INTS7	GJC2	DPF3	DNAJC3	GDF10
HARS	KEAP1	GLRX5	DTX4	DPT	GEM
HBA1	KLHDC9	GOT2	EPCAM	DTX3L	GGCT
HBB	L3HYPDH	GPX1	ERBB2	EFCAB14	GLOD4
HBB	MARS	GRPEL1	EWSR1	EIF2AK2	GPR55
HCRT	ME3	H2AFX	FAM205A	ELANE	GTPBP4
HS6ST1	MED9	HIST1H2BG	FBRSL1	FASN	H1F0
HSPB11	MIEF2	HIST3H2BB	FGFBP3	FCGR3B	HDHD3
IFT46	MKRN3	IFT27	FYN	FGD6	HECTD3
IGSF11	MMP14	IGIP	GFY	GAL3ST2	HIPK4
IRGM	MOB3B	PRR24	GOLT1A	GBP6	HNRNPA0
ITPK1	NAPRT1	ISCU	GSTM1	GBP2	HNRNPDL
LRRC3	NME7	KCNK1	GTF2H5	GBP5	KAT5
LYRM7	NSRP1	KLHL1	HIST1H2BL	GIMAP6	KCNAB1
MANF	NXF1	LMAN1	HIST1H4E	GPR26	KHDRBS1
MGP	PLAT	LRRC8A	KCNH3	HLA-A	KRT20

Table S25. *Pharmacologic perturbagen classes mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including connectivity scores assigned to all pharmacologic perturbagen classes mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. Connectivity scores >90 or <-90 are highlighted in green or red, respectively

Pharmacologic Perturbagen Class	Connectivity Score		
	Shared	F1 NIC Unique	F2 NIC Unique
Adenosine receptor agonist	5.5	-13.18	1.91
Androgen receptor modulator	3.23	-1.37	0.59
Angiotensin receptor antagonist	1.39	-3.51	10.03
Aromatase inhibitor	0.06	10.14	4.96
ATP synthase inhibitor	15.79	5.55	33.55
ATPase inhibitor	-0.13	-6.56	11.61
Aurora kinase inhibitor	0.1	2.11	1.72
Bacterial 30S ribosomal subunit inhibitor	-2.65	33.25	-28.05
Bacterial cell wall synthesis inhibitor	-0.24	-35.1	0.80
Bacterial DNA gyrase inhibitor	-0.69	-30.34	2.14
BCL inhibitor	0.09	-0.41	3.52
Benzodiazepine receptor agonist	7.26	-5.61	-18.79
Beta-adrenergic receptor agonist	0.2	1.3	-0.10
Bile acid	33.31	16.07	42.08
Bromodomain Inhibitor	13	30	-0.67
Calcium channel blocker	1.13	-37.33	0.63
Calmodulin antagonist	1.51	-1.62	0.57
Cannabinoid receptor agonist	8.14	0.1	-0.20
CCK receptor antagonist	61.33	-0.63	1.73
CDK inhibitor	16.04	-15.65	14.78
Cyclooxygenase inhibitor	2.97	-3.51	2.38
Dihydrofolate reductase inhibitor	9.31	2.72	-0.91
DNA dependent protein kinase inhibitor	-0.7	-34.1	-3.03
DNA polymerase inhibitor	1.01	-12.44	7.81
DNA synthesis inhibitor	0.4	2.89	0.16
Dopamine receptor antagonist	0.01	-2.1	1.25
EGFR inhibitor	-15.85	-8.19	-6.74
Estrogen receptor agonist	0.1	-0.31	0.45
Estrogen receptor antagonist	0.05	0.78	-0.01
FGFR inhibitor	-46.15	5.24	-0.70
FLT3 inhibitor	-20.06	-26.53	3.82
FXR antagonist	2.71	6.52	51.91
GABA receptor antagonist	-0.1	-12.19	0.74
Gamma secretase inhibitor	-3.9	-26.21	14.80
Glucocorticoid receptor agonist	7.99	21.1	2.23
Glycogen synthase kinase inhibitor	14.34	9.6	1.62
HDAC inhibitor	98.66	52.93	26.87
HIF activator	-3.41	-49.04	-40.49
HIV protease inhibitor	20.44	-17.38	2.01
HMGCR inhibitor	0.18	-13.24	8.36
HRH1 antagonist	2.31	-9.56	1.27
HSP inhibitor	29.37	0.28	98.77
IGF-1 inhibitor	-22.47	-53.89	-6.46
IKK inhibitor	-0.77	-14	5.93
Imidazoline ligand	0.95	-14.62	6.76
IMPDH inhibitor	0.57	2.76	15.56
JAK inhibitor	-6.65	-12.3	-6.43
KCNJ11 modulator	-2.3	-17.15	0.60
Leucine rich repeat kinase inhibitor	74.71	68.47	-2.25
MDM inhibitor	2.93	25.49	-5.49

Table S26. *Individual pharmacologic perturbagens mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including perturbagen ID, individual pharmacologic perturbagen, perturbagen class, perturbagen target, and connectivity scores for all individual pharmacologic perturbagens mapped to DEGs shared between and unique to F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open'. Connectivity scores >90 or <-90 are highlighted in green or red, respectively.

Perturbagen ID	Individual Pharmacologic Perturbagen	Perturbagen Class	Perturbagen Target	Connectivity Score		
				Shared	F1 NIC Unique	F2 NIC Unique
BRD-K32795028	1-benzylimidazole	Thromboxane synthas	CYP11B1, QP(	4.09	-45.67	-36.07
BRD-A80928489	1-monopalmitin	P-glycoprotein inhibito	ABCB1	-23.33	-10.44	0.00
BRD-K31491153	1-phenylbiguanide	Serotonin receptor ag	HTR3A, HTR3	-76.1	26.87	46.17
BRD-K74430258	1,2-dichlorobenzel	Hepatotoxicant		-27.13	61.34	3.57
BRD-K94919853	10H-phenothiazin-	Butyrylcholinesterase	BCHE	29.42	-47.12	47.08
BRD-K05396879	15-delta-prostagla	PPAR receptor agonis	PPARG, NR1H	-7.32	0.63	1.16
BRD-K92301463	16,16-dimethylpro	Prostanoid receptor a	HPGD	56.59	10.56	55.01
BRD-K66766661	17-beta-estradiol	Estrogen receptor ago	ESR1	14.78	20.95	-48.59
BRD-A29731977	17-hydroxyproges	progesterone recepto	CYP1A2, CYP2	79.05	66.98	-6.32
BRD-K48115423	2-(4-methoxybenz	Matrix metalloprotease	MMP13	-30.93	-82.32	3.28
BRD-A71657825	2-(biphenyl-4-ylsu	Matrix metalloprotease	MMP13, MMP8	39.33	-27.66	3.21
BRD-K35128472	2-aminopurine	Serine/threonine kinase inhibitor		0	-9.95	-26.08
BRD-A20131130	2',5'-dideoxyadeno	Adenylyl cyclase inhibitor		-0.88	5.46	4.34
BRD-K08703257	3-amino-benzamid	PARP inhibitor	PARP1	9.82	-1.09	-24.95
BRD-A87125127	3-matida	Glutamate receptor ar	GRM1	16.82	-12.51	-8.17
BRD-A62890442	3-methyl-GABA	GABA aminotransferase activator		0	77.14	-24.35
BRD-K37846922	3,3'-diindolylmetha	CHK inhibitor	AHR, AR, CYP	-35.27	55.79	-20.26
BRD-K14643723	4-(2-Amino-ethyl)-	carbonic anhydrase ir	CA2, CA1, CA9	0	22.34	28.70
BRD-A15914070	4-hydroxy-2-none	Cytotoxic lipid peroxid	IKBKB	-62.64	-59.47	-6.46
BRD-A96799240	4-hydroxyretinoic-	Retinoid receptor binder		0	-48.59	30.71
BRD-K13087974	4,5-dianilinophthali	EGFR inhibitor	EGFR	-53.21	-10.32	3.71
BRD-K97118047	4,5,6,7-tetrabromo	Casein kinase inhibito	CSNK2A1, AK	16.9	-21.24	-0.95
BRD-A18497530	5-iodotubercidin	Adenosine kinase inhi	MAPK3, ADK,	6.59	-59.28	26.61
BRD-K30197592	5-methoxytryptam	Serotonin receptor ag	HTR2A, HTR6	22.36	11.53	6.67
BRD-K08219523	5-nonyloxytryptam	Serotonin receptor ag	HTR1B, HTR1	-11.05	0	-5.46
BRD-A33084410	5'-guanidinonaltrin	Opioid receptor antagonist		-1.72	10.38	5.15
BRD-K00656370	6-aminochrysene	Transferase inhibitor		5.39	-39.89	3.17
BRD-K62929068	6-benzylaminopuri	Purinergic receptor activator		-1.76	-5	-10.68
BRD-K04430056	7-nitroindazole	nitric oxide synthase i	NOS1, NOS2,	-0.46	-21.17	10.50
BRD-K50384076	7,4'-dihydroxyflavo	Opioid receptor antag	CYP19A1	-80.29	18.79	63.57
BRD-A01317026	7,8-dihydro-L-biop	Dihydroneopterin aldo	NOS2, TPH1	-3.81	-91.6	-26.58
BRD-K61829047	7b-cis	Exportin antagonist	XPO1	-3.81	-0.92	39.88
BRD-K14696368	9-methyl-5H-6-thia	NFkB pathway inhibito	RELA	40.73	-24.28	18.72
BRD-K38615104	A-443644	AKT inhibitor	AKT1, AKT2, A	-25.26	-74.55	40.44
BRD-K55301415	abiraterone	17,20 lyase inhibitor	CYP17A1, CYP	0	5.64	10.43
BRD-K56301217	ABT-737	BCL inhibitor	BCL2, BCL2L1	60.18	-3.38	90.61
BRD-K91623615	ABT-751	Tubulin inhibitor	TUBB	32.65	-1.37	14.75
BRD-K93176058	AC-55649	Retinoid receptor agor	RARB, RARA	11.83	43.91	-50.90
BRD-A95696820	acadesine	AMPK activator		20.63	-30.69	4.57
BRD-M41783010	acamprosate	Glutamate receptor ar	GABRA1, GAE	4.45	-3.25	25.35
BRD-A16444946	acarbose	Glucosidase inhibitor	GAA, MGAM, A	69.35	1.94	-22.81
BRD-A29260609	acebutolol	Adrenergic receptor a	ADRB1, ADRB	22.52	-7.79	-58.44
BRD-K37814297	acepromazine	Dopamine receptor ar	ADRA1A, ADR	1.41	-1.2	-2.01
BRD-K74112339	acetohydroxamic-	Urease inhibitor		11.8	-28.22	39.65
BRD-K79437791	acetyl-farnesyl-cy	Inhibitor of methylation	PPARG	5.25	71.87	7.75
BRD-K75181824	acetyl-geranygera	Inhibitor of methyl esterification of ger		20.16	23.74	-3.59
BRD-U01690642	acetyl-geranyl-cys	Isoprenylated protein methylation inhi		-2.08	43.9	-3.14
BRD-K82381502	acetylcholine	Acetylcholine receptor	ACHE, CHRM1	8.45	-42.81	11.80
BRD-K62012036	acitretin	Retinoid receptor agor	RARA, RARB,	37.65	-34.39	0.00

Table S27. *Individual pharmacologic perturbagens contributing to pharmacologic perturbagen classes with connectivity scores >90 or <-90 mapped to DEGs shared between and unique to F1 NIC and F2 NIC mice.* Tabular data including perturbagen class, perturbagen ID, individual perturbagen, perturbagen target, and connectivity scores assigned to all individual pharmacologic perturbagens belonging to pharmacologic perturbagen classes with connectivity scores >90 or <-90 are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. Connectivity scores >90 or <-90 are highlighted in green or red, respectively.

Perturbagen Class	Perturbagen ID	Individual Perturbagen	Perturbagen Target	Connectivity Score		
				Shared	F1 NIC Unique	F2 NIC Unique
HDAC Inhibitor	BRD-K11558771	droxinostat	HDAC6, HDA	99.15	86.26	11.93
	BRD-K11663430	pyroxamide	HDAC1	98.94	80.15	43.08
	BRD-K69840642	ISOX	HDAC6	98.52	80.66	49.14
	BRD-K74761218	WT-171	HDAC6	98.48	90.33	9.78
	BRD-K13810148	givinostat	HDAC2, HDA	97.68	-50.62	72.05
	BRD-K64606589	apicidin	HDAC1, HDA	97.67	82.41	59.81
	BRD-K81418486	vorinostat	HDAC1, HDA	97.64	87.36	45.08
	BRD-K22503835	scriptaid	HDAC1, HDA	97.6	50.78	1.06
	BRD-K56957086	dacinostat	HDAC1, HDA	97.25	59.45	33.10
	BRD-K68202742	trichostatin-a	HDAC7, HDA	96.77	27.11	62.52
	BRD-K17743125	belinostat	HDAC1, HDA	96.37	79.24	73.14
	BRD-K12867552	THM-I-94	HDAC1, HDA	96.1	63.98	55.98
	BRD-A39646320	HC-toxin	HDAC1	95.84	65.71	46.77
	BRD-K74733595	APHA-compoun	HDAC8	95	2.18	82.61
	BRD-K02130563	panobinostat	HDAC1, HDA	94.5	2.29	42.95
	BRD-K52313696	tacedinaline	HDAC1	91.62	-55.54	9.52
	BRD-K52522949	NCH-51	HDAC1, HDA	88.88	12.58	29.53
	BRD-K77908580	entinostat	HDAC1, HDA	85.53	-65	65.25
	BRD-K04466929	Merck60	HDAC1, HDA	80.7	-20.81	49.63
	BRD-K98426715	tubacin	HDAC6	49.22	63.55	-49.81
	BRD-K83837640	JNJ-26854165	HDAC1, HDA	48.15	14.1	-2.82
	BRD-K07888107	depudecin	HDAC1, HDA	25.18	-3.93	0.00
	BRD-K00627859	tubastatin-a	HDAC6	23.92	0.14	46.74
	BRD-K41260949	valproic-acid	ABAT, HDAC1	22.32	18.47	-47.82
	BRD-K88742110	BRD-K8874211	HDAC8, IL1B	17.66	43.68	-1.80
	BRD-K29313308	HDAC3-selectiv	HDAC3	3.52	-61.4	35.74
	BRD-K16485616	mocetinostat	HDAC1, HDA	1.85	-71.4	1.23
	BRD-K67102207	phenylbutyrate	CYP3A5, HDA	0	-56.94	-6.85
	BRD-K76698671	HNHA	HDAC1	-1.9	44.45	59.55
	BRD-K85133207	HDAC1-selective		-11.84	2.49	9.04
	BRD-K37206356	rhamnetin	ALOX5, MAPK	-12.01	-19.1	25.98
	BRD-K13169950	NSC-3852	HDAC1	-13.55	-18.38	34.89
HSP Inhibitor	BRD-K41859756	NVP-AUY922	HSP90AA1, H	95.1	-5.06	99.01
	BRD-K83988098	alvespimycin	HSP90AA1	55.37	22.5	92.02
	BRD-A47144777	dihydro-7-desac	HSP90AA1	53.87	-19.42	7.78
	BRD-A19500257	geldanamycin	HSP90AA1, H	50.93	0	97.08
	BRD-K36529613	PU-H71	HSP90AA1	45.31	4.76	69.54
	BRD-K33551950	radicicol	ACLY, DLAT,	43.38	-2.94	85.76
	BRD-K51967704	BIIB021	AOX1, HSP90	34.23	13.29	98.63
	BRD-A17819071	gedunin	HSP90AA1	6.2	5.28	-23.21
	BRD-A52326238	isogedunin		3.62	7.64	-12.68
	BRD-K96799727	pifithrin-mu	HSPA1A, TP5	-0.11	-0.25	1.20
	BRD-K32330832	VER-155008	HSPA1A	-11.25	-16.61	52.72
	BRD-K65503129	HSP90-inhibitor	HSP90AA1, H	-13.72	-24.51	91.76
	BRD-A09161221	nomilin		-26.68	-32.14	-19.58
Proteasome Inhibitor	BRD-K78659596	MLN-2238	PSMB1	44.35	28.11	91.89
	BRD-K15935639	z-leu3-VS		14.41	-0.54	91.00
	BRD-K17140735	SCH-79797	F2R	8	-30.23	74.34
	BRD-K60230970	MG-132	PSMB1	6.62	30.38	79.49

Table S28. *Genetic perturbagen classes mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including connectivity scores assigned to all genetic perturbagen classes mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. Connectivity scores >90 or <-90 are highlighted in green or red, respectively.

Genetic Perturbagen Class	Connectivity Score		
	Shared	F1 NIC Unique	F2 NIC Unique
AHSP Pathway LOF	-0.58	-9.18	1.52
Akt Signaling GOF	-3.24	9.3	-12.89
Akt Signaling LOF	-8.55	-27.09	0.01
Aldehyde dehydrogenases LOF	-78.14	-60.5	4.36
Aminoacyl tRNA synthetases class II LOF	-0.01	-23.35	-9.50
Apolipoproteins LOF	81.72	0.23	-1.65
Baculoviral IAP repeat domain containing LOF	0.06	3.04	13.52
BMP Signaling LOF	4.03	-30.61	62.03
C2 domain containing LOF	83.04	-12.24	2.25
C2 domain containing protein kinases LOF	-1.05	38.16	-3.11
Canonical high mobility group proteins LOF	-31.99	-52.83	2.37
Cell Cycle Inhibition GOF	0.36	11.29	65.30
Cyclin dependent kinases LOF	3.27	13.61	6.08
Cyclins LOF	-0.01	-59.29	-0.57
DNA Replication LOF	1.3	-10.1	37.55
EIF Proteins LOF	-95.35	1.76	-6.19
EMSY complex LOF	6.47	-1.03	-39.79
FOS transcription factor family GOF	74.86	-0.36	19.59
G2 M Checkpoint LOF	8.96	-0.19	-0.02
GATA Zinc finger domain containing LOF	11.86	-4.56	6.80
General transcription factors group 1 LOF	-0.64	3.68	-1.24
General transcription factors group 2 LOF	3.35	-2.59	0.31
GPCR Subset GOF	54.17	17.25	0.00
Heat shock 70kDa proteins LOF	-34.29	-45.92	49.80
Histone deacetylases LOF	53.02	0.03	17.05
Homeobox Gene GOF	40.62	6.13	28.25
HOXL subclass homeoboxes LOF	-0.94	-1.84	1.23
IL4 Pathway LOF	-2.95	-24.04	-0.13
Integrin subunits alpha LOF	-27.23	-63.96	-0.30
Integrin subunits beta LOF	13.23	46.27	-72.51
Interleukin receptors LOF	-31.77	-27.18	-1.77
Interleukins GOF	24.94	-0.38	0.31
Kinase anchoring proteins LOF	-14.64	-60.84	45.49
Kruppel like transcription factors LOF	59.35	10.7	15.10
LIM class homeoboxes GOF	63.03	8.13	9.82
Lipocalins GOF	6.83	-0.33	2.53
Lysine acetyltransferases LOF	1.59	-11.89	73.81
MCM family LOF	3.95	-21.88	3.55
Mediator complex LOF	19.51	-1.98	0.39
Minor histocompatibility antigens LOF	58.54	-60.11	-33.52
Mitochondrial complex IV LOF	4.78	-26.63	2.23
Mitogen activated protein kinases LOF	17.63	9.58	-4.79
NADH ubiquinone oxidoreductase core subunits GOF	-24.91	-19.18	-0.42
NADH ubiquinone oxidoreductase supernumerary subunits LOF	40.92	9.94	-61.26
NFKB Activation GOF	41.31	-35.17	91.77
NKL subclass homeoboxes and pseudogenes LOF	-4.4	-1.55	1.75
Non Homologous End Joining LOF	-7.34	15.82	-5.50
Nucleoporin LOF	0.76	-45.45	14.64
Phospholipases GOF	0.07	-10.5	-0.02
Phospholipases LOF	25.42	41.62	-3.90

Table S29. *Individual genetic perturbagens mapped to DEGs shared between and unique to DRD1-expressing striatal cells of F1 NIC and F2 NIC mice.* Tabular data including perturbagen ID, genetic perturbation, target gene symbol, target gene description, and connectivity scores for all individual genetic perturbagens mapped to DEGs shared between and unique to F1 NIC and F2 NIC mice are embedded in an Excel workbook accessible by right-clicking the below preview and selecting 'open' from the drop-down menu. Connectivity scores >90 or <-90 are highlighted in green or red, respectively.

Perturbagen ID	Genetic Perturbation	Target Gene Symbol	Target Gene Description	Connectivity Score		
				Shared	F1 NIC Unique	F2 NIC Unique
CGS001-2	KD	A2M	-	0	54.92	-46.97
ccsbBroad304_05749	OE	A2M	-	1.25	-12.81	-65.31
CGS001-16	KD	AARS	Aminoacyl tRNA synth	21.28	17.21	41.92
CGS001-26574	KD	AATF	-	-25.47	-83.61	37.60
CGS001-18	KD	ABAT	GABA turnover	1.26	-55.66	15.32
ccsbBroad304_00003	OE	ABAT	GABA turnover	-59.69	0	19.31
CGS001-19	KD	ABCA1	ATP binding cassette	-19.61	-62.11	85.69
CGS001-21	KD	ABCA3	ATP binding cassette	-92.86	42.6	-3.92
CGS001-23461	KD	ABCA5	ATP binding cassette	-4.98	-2.8	-98.16
CGS001-5243	KD	ABCB1	ATP binding cassette	0	-35.49	2.34
CGS001-5244	KD	ABCB4	ATP binding cassette	8.88	-27.14	20.86
CGS001-340273	KD	ABCB5	ATP binding cassette	0	89.85	17.15
ccsbBroad304_05471	OE	ABCB5	ATP binding cassette	0	-12.95	-54.95
CGS001-10058	KD	ABCB6	ATP binding cassette	75.95	11.57	-81.09
CGS001-22	KD	ABCB7	ATP binding cassette	93.34	-51.19	53.53
CGS001-4363	KD	ABCC1	ATP binding cassette	97.48	-15.74	0.00
CGS001-89845	KD	ABCC10	ATP binding cassette	-51.64	-9.32	8.37
CGS001-1244	KD	ABCC2	ATP binding cassette	22.3	-3.5	0.00
CGS001-8714	KD	ABCC3	ATP binding cassette	80.08	3.61	-15.05
ccsbBroad304_01998	OE	ABCC3	ATP binding cassette	1.36	-2.2	1.67
CGS001-10257	KD	ABCC4	ATP binding cassette	75.58	72.9	-64.69
CGS001-10057	KD	ABCC5	ATP binding cassette	14.9	7.29	-5.16
CGS001-5825	KD	ABCD3	ATP binding cassette	72.23	-89.42	44.42
CGS001-23	KD	ABCF1	ATP binding cassette	-2.13	71.41	-40.74
CGS001-10061	KD	ABCF2	ATP binding cassette	19.37	0	0.00
ccsbBroad304_07542	OE	ABCF2	ATP binding cassette	26.36	-50.58	28.99
CGS001-55324	KD	ABCF3	ATP binding cassette	5.58	60.84	-4.88
ccsbBroad304_03580	OE	ABCF3	ATP binding cassette	21.37	35.93	-21.81
CGS001-9429	KD	ABCG2	ATP binding cassette	22.66	-62.43	0.00
CGS001-64240	KD	ABCG5	ATP binding cassette	0	95.84	-59.34
CGS001-64241	KD	ABCG8	ATP binding cassette	75.03	-43.89	36.70
ccsbBroad304_08849	OE	ABCG8	ATP binding cassette	6.25	-5.32	0.00
CGS001-11057	KD	ABHD2	Abhydrolase domain c	85.35	64.86	5.95
ccsbBroad304_07738	OE	ABHD2	Abhydrolase domain c	31.88	-10.83	20.67
CGS001-63874	KD	ABHD4	Abhydrolase domain c	66.44	81.11	72.69
ccsbBroad304_03903	OE	ABHD4	Abhydrolase domain c	9.44	0	0.00
CGS001-57406	KD	ABHD6	Abhydrolase domain c	-81.65	-2.68	0.00
CGS001-25	KD	ABL1	Abl family	0.32	-22.12	0.00
CGS001-27	KD	ABL2	Abl family	-6.17	-47.79	58.41
CGS001-30	KD	ACAA1	-	56.7	40.25	-18.41
ccsbBroad304_05756	OE	ACAA1	-	21.02	-2.36	0.00
CGS001-31	KD	ACACA	Carboxylases	-11.82	-35.84	0.00
CGS001-32	KD	ACACB	Carboxylases	4.47	40.28	3.55
CGS001-27034	KD	ACAD8	-	0	-56.97	0.00
CGS001-34	KD	ACADM	-	11.07	81.18	69.98
ccsbBroad304_00006	OE	ACADM	-	-1.24	-50.75	0.00
CGS001-35	KD	ACADS	-	6.95	-79.9	0.00
ccsbBroad304_05757	OE	ACADS	-	0	-44.41	4.81
CGS001-36	KD	ACADSB	-	90.46	49.43	0.00