Table S1. Transcriptional changes 1 day after HD-GFP injection

Genes with the most significant changes in expression levels were sorted by SAM and ANOVA at 24 h postinjection in the right and left side in the frontal cortex, the striatum and the mesencephalon. RStr: right striatum; LStr: Left striatum; Ctrl: Control; FC: Fold change; RCx: right cortex; LCx:left cortex; RMes: right mesencephalon; LMes: left mesencephalon.

Striatum

Affymetrix Probesets	*Gene symbol*	Gene name	SAM q-value (FDR %)	ANOVA p-value	Mean Ctrl Str ± SD	Mean ± SD RStr	Mean ± SD LStr	FC RStr/Ctrl	FC LStr/Ctrl	FC RStr/LStr
206281_at	***ADCYAP1***	adenylate cyclase activating polypeptide 1 (pituitary)	52.94	0.05	406 ± 43	356 ± 74	306 ± 88	-1.14	-1.33	1.16
201196_s_at	***AMD1***	adenosylmethionine decarboxylase 1	52.94	0.05	396 ± 47	474 ± 95	378± 51	1.20	-1.05	1.25
232120_at	***EGFR***	Epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	52.94	0.005	19 ± 9	58 ± 23	57 ± 52	3.01	2.97	1.01
231930_at	***ELMOD1***	ELMO domain containing 1	42.86	0.003	1238 ± 199	1802 ± 186	1675 ±170	1.46	1.35	1.08
1555945_s_at	***FAM120A***	chromosome 9 open reading frame 10	0.00	0.009	1016 ±48	1262 ± 93	990 ± 141	1.24	-1.03	1.28
213552_at	***GLCE***	glucuronyl C5-epimerase	52.94	0.01	137 ± 28	201 ± 56	154 ± 60	1.47	1.12	1.31
206245_s_at	***IVNS1ABP***	influenza virus NS1A binding protein	0.00	0.05	1203 ± 433	1937 ± 153	1467 ± 505	1.61	1.22	1.32
227839_at	***MBD5***	methyl-CpG binding domain protein 5	52.94	0.05	237 ± 84	397 ± 85	283 ± 33	1.67	1.19	1.40

231867_at	***ODZ2***	odz, odd Oz/ten-m homolog 2 (Drosophila)	52.94	0.002	3612 ± 668	2885 ± 233	2658 ± 326	-1.25	-1.36	1.09
230563_at	***RASGEF1A***	RasGEF domain family, member 1A	52.94	0.05	217 ± 10	234 ± 64	250 ± 59	1.08	1.15	-1.07
201395_at	***RBM5***	RNA binding motif protein 5	52.94	0.05	663 ± 70	890 ± 272	738 ± 99	1.34	1.11	1.21
1553264_a_at	***SYN1***	synapsin I	42.86	0.003	515 ± 15	350 ± 63	402 ± 82	-1.47	-1.28	-1.15
1553037_a_at	***SYN2***	synapsin II	52.94	0.05	270 ± 26	188.5 ± 70	173 ± 36	-1.43	-1.56	1.09
224553_s_at	***TNFRSF18***	tumor necrosis factor receptor superfamily, member 18	42.86	0.0	29 ± 17	75 ± 16	46 ± 44	2.60	1.60	1.62
205883_at	***ZBTB16***	zinc finger and BTB domain containing 16	0.00	0.0	2022 ± 329	1062 ± 342	993 ± 461	-1.90	-2.04	1.07
222227_at	***ZNF236***	Zinc finger protein 236	52.94	0.0	40 ± 14	87 ± 33	19.8 ± 13	2.15	-2.046	4.39
212893_at	***ZZZ3***	zinc finger, ZZ domain containing 3	42.86	0.0	306 ± 49	393 ± 58	438 ± 112	1.28	1.42	-1.11

Frontal cortex

Affymetrix Probesets	***Gene symbol***	Gene name	SAM q-value (FDR %)	ANOVA p-value	Mean ± SD Ctrl	Mean ± SD RCx	Mean ± SD LCx	FC RCx/Ctrl	FC 24h LCx/Ctrl	FC RCx/LCx
202157_s_at	***CELF2***	CUG triplet repeat, RNA binding protein 2	18.65	0.005	6578 ± 433	7585 ± 655	7289 ± 1559	1.15	1.11	1.04
202570_s_at	***DLGAP4***	discs, large (Drosophila) homolog-associated protein 4	15.54	0.004	231 ± 42	326 ± 96	343 ± 39	1.41	1.48	-1.05
201637_s_at	***FXR1***	fragile X mental retardation, autosomal homolog 1	15.54	0.001	1330 ± 197	1749 ± 149	1762 ± 463	1.31	1.32	-1.01

206730_at	***GRIA3***	glutamate receptor, ionotrophic, AMPA 3	15.54	0.006	5565 ± 1020	8139 ± 627	6975 ± 1346	1.46	1.25	1.17
211969_at	***HSP90AA1***	heat shock 90kDa protein 1, alpha	14.72	0.001	30302 ± 3685	32969 ± 1029	29686 ± 2868	1.09	-1.02	1.11
208930_s_at	***ILF3***	interleukin enhancer binding factor 3, 90kDa	15.54	0.0	210 ± 40	347 ± 53	373 ± 36	1.65	1.78	-1.08
214577_at	***MAP1B***	microtubule-associated protein 1B	15.54	0.0	12826 ± 2776	11186 ± 2646	12482 ± 3907	-1.15	-1.03	-1.12
215354_s_at	***PELP1***	proline-, glutamic acid-, leucine-rich protein 1	18.65	0.0	75 ± 33	136 ± 23	178 ± 77	1.81	2.37	-1.31
202483_s_at	***RANBP1***	RAN binding protein 1	15.54	0.0	530 ± 70	409 ± 114	391 ± 48	-1.30	-1.35	1.047
225770_at	***RSPRY1***	KIAA1972 protein	15.54	0.002	171 ± 19	254 ± 56	272 ± 56	1.48	1.59	-1.07
210968_s_at	***RTN4***	reticulon 4	14.72	0.005	32973 ± 4245	36861 ± 2790	41704 ± 5655	1.12	1.26	-1.13
211073_x_at	***RPL3***	ribosomal protein L3	14.72	0.003	1057 ± 139	1030 ± 149	1073 ± 146	-1.03	1.02	-1.04
208939_at	***SEPHS1***	selenophosphate synthetase 1	15.54	0.0	376 ± 20	304 ± 52	336 ± 21	-1.24	-1.12	-1.11
1316_at	***THRA***	thyroid hormone receptor alpha	15.54	0.001	1373 ± 255	1662 ± 279	1862 ± 550	1.21	1.36	-1.12
208942_s_at	***SEC62***	translocation protein 1	18.65	0.004	5079 ± 662	4028 ± 300	4141 ± 1514	-1.26	-1.23	-1.03
228749_at	***ZDBF2***	KIAA1571 protein	15.54	0.001	691 ± 44	500 ± 119	490 ± 64	-1.38	-1.41	1.02
222227_at	***ZNF236***	Zinc finger protein 236	14.72	0.004	33 ± 20	79 ± 56	61 ± 21	2.35	1.83	1.28
213286_at	***ZFR***	zinc finger RNA binding protein	15.54	0.001	453 ± 193	632 ± 177	650 ± 157	1.39	1.43	-1.03
1559048_at	***---***	KIAA1447 protein	15.54	0.001	245 ± 12	239 ± 55	240 ± 32	-1.03	-1.02	-1.01

Mesencephalon

Affymetrix Probesets	Gene Symbol	Gene Name	SAM q-value (FDR %)	ANOVA p-value	Mean ± SD Ctrl	Mean ± SD RMes	Mean ± SD LMes	FC RMes/Ctrl	FC LMes/Ctrl	FC RMes/Lmes
243139_at	***ACTA2***	Actin, alpha 2, smooth muscle, aorta	62.17	0.05	516 ± 11	357 ± 83	375 ± 131	1.45	-1.38	-1.05
214783_s_at	***ANXA11***	annexin A11	62.17	0.05	189 ± 55	310 ± 92	263 ± 45	1.64	1.39	1.18
200982_s_at	***ANXA6***	annexin A6	63.69	0.05	277 ± 23	224 ± 87	223 ± 52	-1.24	-1.24	1.00
222700_at	***ATL2***	atlastin GTPase 2	63.69	0.0	1604 ± 614	3555 ± 489	4176 ± 600	2.22	2.60	-1.17
200837_at	***BCAP31***	B-cell receptor-associated protein 31	62.17	0.05	230 ± 23	250 ± 107	180 ± 74	1.09	-1.28	1.39
205298_s_at	***BTN2A2***	butyrophilin, subfamily 2, member A2	63.69	0.0	28 ± 14	94 ± 11	80 ± 32	3.31	2.83	1.17
204247_s_at	***CDK5***	cyclin-dependent kinase 5	62.17	0.003	376 ± 78	439 ± 47	461 ± 72	1.17	1.23	-1.05
216295_s_at	***CLTA***	clathrin, light chain A	63.69	0.05	2186 ± 176	1898 ± 223	2133 ± 242	-1.15	-1.02	-1.12
211070_x_at	***DBI***	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	63.69	0.05	271 ± 37	196 ± 61	157 ± 107	-1.39	-1.73	1.25
40612_at	***DOPEY1***	dopey family member 1	63.69	0.05	260 ± 41	156 ± 60	119 ± 65	-1.67	-2.18	1.31
214314_s_at	***EIF5B***	eukaryotic translation initiation factor 5B	63.69	0.005	1014 ± 261	657 ± 114	678 ± 59	-1.54	-1.49	-1.03
219325_s_at	***ELAC1***	elaC homolog 1 (E, coli)	63.69	0.0	43 ± 28	164 ± 18	103 ± 36	3.85	2.42	1.59
233924_s_at	***EXOC6***	exocyst complex component 6	63.69	0.05	61 ± 44	91 ± 62	107 ± 54	1.49	1.75	-1.17
223035_s_at	***FARSB***	phenylalanyl-tRNA synthetase, beta subunit	63.69	0.002	1119 ± 28	1291 ± 130	1486 ± 109	1.15	1.33	-1.15

1555471_a_at	***FMN2***	formin 2	63.69	0.05	184 ± 34	172 ± 76	125 ± 89	-1.07	-1.48	1.38
207389_at	***GP1BA***	glycoprotein Ib (platelet), alpha polypeptide	63.69	0.05	180 ± 3	219 ± 81	153 ± 20	1.21	-1.180	1.43
209631_s_at	***GPR37***	G protein-coupled receptor 37 (endothelin receptor type B-like)	63.69	0.05	1125 ± 105	791 ± 344	847 ± 145	-1.42	-1.33	-1.07
220642_x_at	***GPR89A | GPR89B | GPR89C***	G protein-coupled receptor 89A,B,C	63.69	0.009	596 ± 74	929 ± 167	719 ± 134	1.56	1.21	1.29
204738_s_at	***KRIT1***	KRIT1, ankyrin repeat containing…	63.69	0.05	211 ± 18	239 ± 85	235 ± 142	1.13	1.12	1.02
203203_s_at	***KRR1***	KRR1, small subunit (SSU) processome component, homolog (yeast)	63.69	0.006	1319 ± 245	849 ± 178	1180 ± 410	-1.55	-1.12	-1.39
200915_x_at	***KTN1***	kinectin 1 (kinesin receptor)	62.64	0.05	9681 ± 1047	10767 ± 849	9860 ± 896	1.11	1.02	1.09
224771_at	***NAV1***	neuron navigator 1	63.69	0.05	794 ± 125	613 ± 112	500 ± 92	-1.29	-1.59	1.23
217800_s_at	***NDFIP1***	Nedd4 family interacting protein 1	63.69	0.05	278 ± 26	133 ± 61	192 ± 54	-2.10	-1.45	-1.45
201227_s_at	***NDUFB8***	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	63.69	0.05	7974 ± 961	7176 ± 801	7512 ± 1679	-1.11	-1.06	-1.05
219293_s_at	***OLA1***	Obg-like ATPase 1	62.17	0.003	13429 ± 391	15238 ± 521	17995 ± 1334	1.13	1.34	-1.18
200768_s_at	***MAT2A***	methionine adenosyltransferase II, alpha	63.69	0.0	9692 ± 1110	7406 ± 567	7902 ± 1196	-1.31	-1.23	-1.07
226300_at	***MED19***	mediator complex subunit 19	63.69	0.0	520 ± 13	459 ± 82	580 ± 66	-1.13	1.11	-1.26
232676_x_at	***MYEF2***	myelin expression factor 2	62.17	0.05	395 ± 130	591 ± 131	502 ± 113	1.50	1.27	1.18

1554633_a_at	***MYT1L***	myelin transcription factor 1-like	63.69	0.0	272 ± 37	143 ± 40	146 ± 68	-1.90	-1.87	-1.02
219195_at	***PPARGC1A***	peroxisome proliferator-activated receptor gaPPa, coactivator 1 alpha	63.69	0.05	835 ± 73	956 ± 387	902 ± 178	1.15	1.08	1.06
203317_at	***PSD4***	pleckstrin and Sec7 domain containing 4	63.69	0.05	38 ± 20	90 ± 49	119 ± 90	2.36	3.12	-1.33
217492_s_at	***PTEN***	phosphatase and tensin homolog	63.69	0.05	182 ± 13	222 ± 42	204 ± 34	1.22	1.12	1.09
211542_x_at	***RPS10***	ribosomal protein S10	62.17	0.05	11058 ± 1491	9033 ± 3174	11127 ± 1880	-1.22	1.01	-1.23
201140_s_at	***RAB5C***	RAB5C, member RAS oncogene family	62.17	0.05	725 ± 93	610 ± 74	539 ± 100	-1.19	-1.34	1.13
202507_s_at	***SNAP25***	synaptosomal-associated protein, 25kDa	62.17	0.05	6696 ± 742	10575 ± 3219	13170 ± 2756	1.58	1.97	-1.25
227649_s_at	***SRGAP2***	SLIT-ROBO Rho GTPase activating protein 2	62.17	0.001	288 ± 54	313 ± 21	236 ± 29	1.09	-1.22	1.33
202688_at	***TNFSF10***	tumor necrosis factor (ligand) superfamily, member 10	62.17	0.001	5 ± 3	63 ± 17	59 ± 19	11.53	10.96	1.05
212284_x_at	***TPT1***	tumor protein, translationally-controlled 1	62.17	0.05	28931 ± 1996	24101.1 ± 2585	24650 ± 3776	-1.20	-1.17	-1.02
221506_s_at	***TNPO2***	transportin	62.17	0.05	88 ± 29	126 ± 41	71 ± 14	1.43	-1.24	1.78
201683_x_at	***TOX4***	TOX high mobility group box family member 4	63.69	0.01	940 ± 79	919 ± 170	892 ± 186	-1.02	-1.05	1.03
228988_at	***ZNF711***	zinc finger protein 711	62.17	0.0	2799 ± 221	1473 ± 332	2167 ± 767	-1.90	-1.29	-1.47

Table S2. Evolution of transcriptional changes from 1 day to 28 days postinjection by HD-GFP

Genes with the most significant changes in expression sorted by SAM and ANOVA at 1 and 28 days postinjection in the right striatum, in the right frontal cortex and in the right midbrain. RStr: right striatum; LStr: left striatum; Ctrl: control; FC: fold change; RCx: right cortex; LCx: left cortex; RMes: right midbrain; LMes: left midbrain.

Right striatum

Probesets	*Gene Symbol*	Gene Name	SAM q-value (FDR %)	ANOVA p-value	Mean ± SD Ctrl Str	Mean ± SD 24h RStr	Mean ± SD 28d RStr	FC 24h/Crtl	FC 28d/Ctrl
231045_x_at	***C11orf31***	chromosome 11 open reading frame 31	9.48	0.001	68 ± 13	786 ± 93	480 ± 81	1.15	-1.42
203166_at	***CFDP1***	craniofacial development protein 1	0.0	0.001	1858 ± 443	3689 ± 255	1538 ± 461	1.99	-1.21
201842_s_at	***EFEMP1***	EGF-containing fibulin-like extracellular matrix protein 1	0.0	0.004	1485 ± 295	3737 ± 852	1405 ± 470	2.52	-1.06
209356_x_at	***EFEMP2***	EGF-containing fibulin-like extracellular matrix protein 2	0.0	0.0	178 ± 9	280 ± 11	141 ± 26	1.57	-1.26
213502_x_at	***GUSBP11***	------	0.0	0.005	30 ± 15	310 ± 94	35 ± 28	10.37	1.18
212671_s_at	***HLA-DQA1 /// HLA-DQA2***	MHC, class II, DQ α 1 /// major histocompatibility complex, class II, DQ α 2	5.30	0.002	25 ± 20.11	230 ± 86	10 ± 5	9.35	-2.56
211654_x_at	***HLA-DQB1***	major histocompatibility complex, class II, DQ beta 1	0.0	0.005	464 ± 150	1071 ± 166	433 ± 110	2.30	-1.07
208306_x_at	***HLA-DRB1***	Major histocompatibility complex, class II, DR beta 1	0.0	0.0	523 ± 115	797 ± 21	346 ± 106	1.52	-1.51
211529_x_at	***HLA-G***	HLA-G histocompatibility antigen, class I, G	0.0	0.005	1200 ± 562	4555 ± 755	1431 ± 328	3.79	1.19
200943_at	***HMGN1***	high-mobility group nucleosome binding	9.01	0.003	532 ± 35	873 ± 87	660 ± 105	1.64	1.24

		domain 1							
211641_x_at	***IGHM***	Immunoglobulin heavy constant gamma 1	0.0	0.006	109 ± 53	318 ± 62	99 ± 24	2.92	-1.11
215946_x_at	***IGLL3P***	immunoglobulin lambda-like polypeptide 1	9.48	0.004	114 ± 70	344 ± 75	107 ± 27	3.01	-1.07
215379_x_at	***IGLV1-44***	-------	0.0	0.005	20 ± 21	957 ± 200	27 ± 30	48.99	1.37
223597_at	***ITLN1***	intelectin 1 (galactofuranose binding)	0.0	0.004	123 ± 18	325 ± 66	105 ± 48	2.65	-1.17
212082_s_at	***MYL6***	myosin, light polypeptide 6, smooth muscle and non-muscle	0.0	0.0	2833 ± 732	4664 ± 520	1591 ± 783	1.65	-1.78
219483_s_at	***PORCN***	porcupine homolog (Drosophila)	6.43	0.0	476 ± 25	414 ± 39	251 ± 65	-1.15	-1.90
205407_at	***RECK***	reversion-inducing-cysteine-rich protein with kazal motifs	0.0	0.0	22 ± 15	90 ± 18	132 ± 8	4.02	5.89
1553264_a_at	***SYN1***	synapsin I	5.30	0.003	515 ± 15	350 ± 63	334 ± 25	-1.47	-1.54
205883_at	***ZBTB16***	zinc finger and BTB domain containing 16	0.0	0.0	2022 ± 329	1062 ± 342	666 ± 188	-1.90	-3.03

Right frontal cortex

Probsets	***Gene Symbol***	**Gene Name**	**SAM q-value (FDR %)**	**ANOVA p-value**	**Mean ± SD Ctrl Cx**	**Mean ± SD 24h_RCx**	**Mean ± SD 28d_RCx**	**FC 24h/Crtl**	**FC 28d/Ctrl**
202157_s_at	***CELF2***	CUG triplet repeat, RNA binding protein 2	18.65	0.005	6578 ± 433	7585 ± 655	9527 ± 1447	1.15	1.45
202570_s_at	***DLGAP4***	discs, large (Drosophila) homolog-associated protein 4	15.54	0.004	231 ± 43	326 ± 96	509 ± 97	1.41	2.20
201693_s_at	***EGR1***	early growth response 1	15.54	0.0	602 ± 41	373 ± 52	351 ± 20	-1.61	-1.72
201637_s_at	***FXR1***	fragile X mental retardation, autosomal homolog 1	15.54	0.001	1330 ± 198	1749 ± 149	2056 ± 174	1.31	1.55
206730_at	***GRIA3***	glutamate receptor, ionotrophic, AMPA 3	15.54	0.006	5565 ± 1020	8139 ± 627	9483 ± 719	1.46	1.70

211969_at	***HSP90AA1***	heat shock 90kDa protein 1, alpha	14.72	0.001	30302 ± 3685	32969 ± 1029	36779 ± 941	1.09	1.21
208930_s_at	***ILF3***	interleukin enhancer binding factor 3, 90kDa	15.54	0.0	210 ± 40	347 ± 53	755 ± 196	1.65	3.60
1559048_at	**---**	KIAA1447 protein	15.54	0.001	245 ± 12	238 ± 55	167 ± 23	-1.03	-1.47
214577_at	***MAP1B***	microtubule-associated protein 1B	15.54	0.0	12826 ± 2776	11186 ± 2646	8624 ± 2552	-1.15	-1.49
218330_s_at	***NAV2***	neuron navigator 2	15.54	0.0	1682 ± 89	2671 ± 457	1798 ± 178	1,59	1,07
215354_s_at	***PELP1***	proline-, glutamic acid-, leucine-rich protein 1	18.65	0.0	75 ± 33	136 ± 23	138 ± 39	1.81	1.83
202483_s_at	***RANBP1***	RAN binding protein 1	15.54	0.0	529 ± 70	409 ± 114	329 ± 54	-1.30	-1.61
225770_at	***RSPRY1***	KIAA1972 protein	15.54	0.002	171 ± 19	254 ± 56	289 ± 31	1.48	1.69
210968_s_at	***RTN4***	reticulon 4	14.72	0.005	32973 ± 4245	36861 ± 2791	45440 ± 4544	1.12	1.38
211073_x_at	***RPL3***	ribosomal protein L3	14.72	0.003	1057 ± 140	1030 ± 149	656 ± 104	-1.03	-1.61
208939_at	***SEPHS1***	selenophosphate synthetase 1	15.54	0.0	376 ± 20	304 ± 52	300 ± 17	-1.24	-1.25
1316_at	***THRA***	thyroid hormone receptor, alpha	15.54	0.001	1373 ± 255	1662 ± 279	1579 ± 51	1.21	1.15
208942_s_at	***SEC62***	translocation protein 1	18.65	0.004	5079 ± 663	4028 ± 300	3179.13 ± 555.55	-1.26	-1.60
202818_s_at	***TCEB3***	transcription elongation factor B (SIII)	12.82	0.01	526 ± 93	690 ± 64	986 ± 150	1.31	1.88
228749_at	***ZDBF2***	KIAA1571 protein	15.54	0.001	691 ± 44	500 ± 119	492 ± 52	-1.38	-1.40
222227_at	***ZNF236***	Zinc finger protein 236	14.72	0.004	33 ± 20	79 ± 56	201 ± 69	2.35	6.00
213286_at	***ZFR***	zinc finger RNA binding protein	15.54	0.001	453 ± 193	632 ± 177	1100 ± 213	1.39	2.43

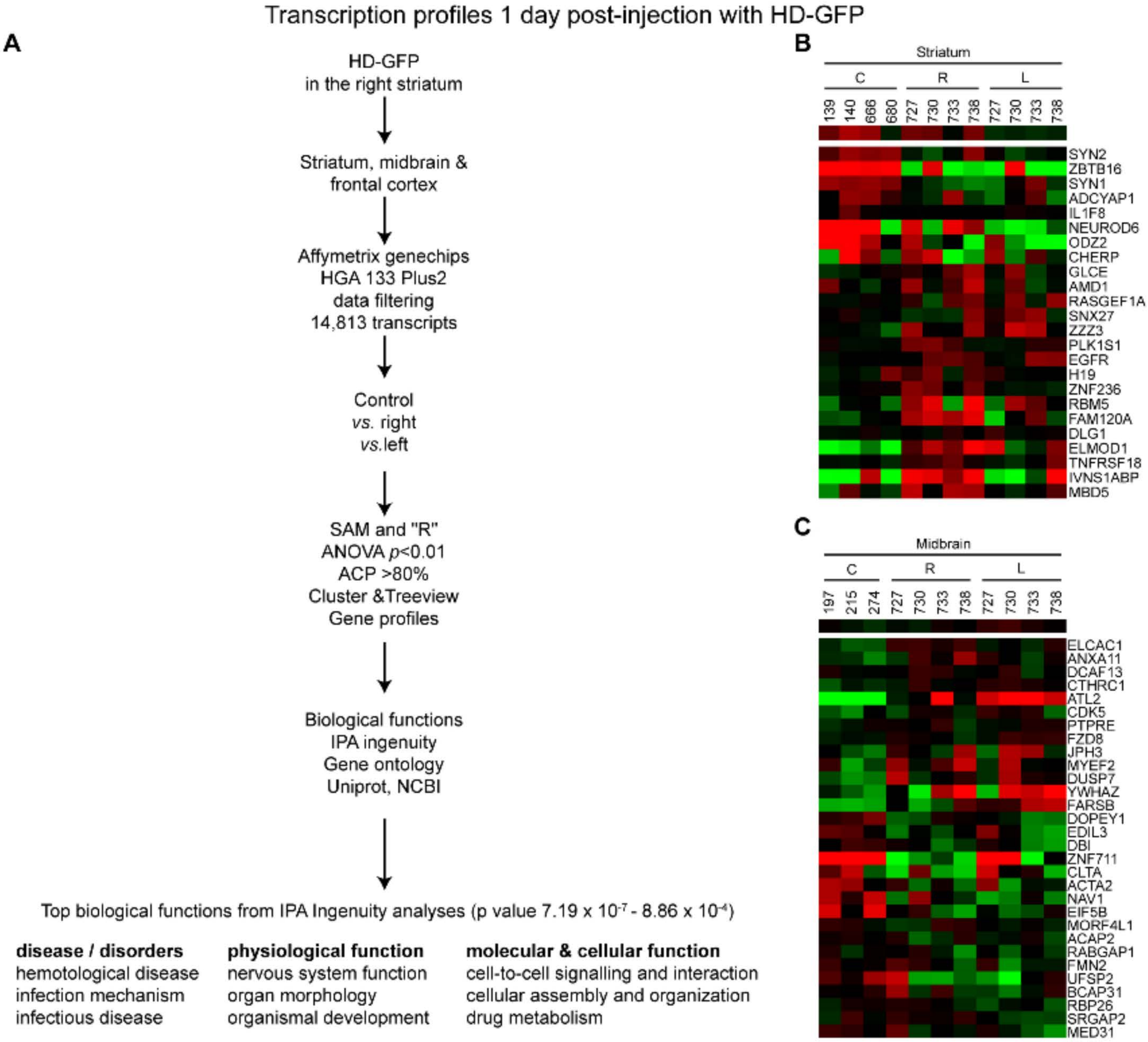
Right mesencephalon

Probesets	***Gene Symbol***	**Gene Name**	**SAM q-value (FDR %)**	**ANOVA p-value**	**Mean ± SD Ctrl_RMes**	**Mean ± SD 24h_RMes**	**Mean ± SD 28d_RMes**	**FC 24h/Ctrl_RMes**	**FC 28d/Ctrl_RMes**
243139_at	***ACTA2***	Actin, alpha 2, smooth muscle, aorta	62.17	0.05	516 ± 111	356 ± 83	289 ± 39	-1.45	-1.38
214783_s_at	***ANXA11***	annexin A11	62.17	0.05	189 ± 55	310 ± 92	252 ± 19	1.64	1.39
200982_s_at	***ANXA6***	annexin A6	63.69	0.05	277 ± 23	224 ± 88	200 ± 50	-1.24	-1.24

222700_at	***ATL2***	atlastin GTPase 2	63.69	0.0	1604 ± 614	3555 ± 489	4353 ± 590	2.22	2.60
200837_at	***BCAP31***	B-cell receptor-associated protein 31	62.17	0.05	230 ± 23	250 ± 107	241 ± 44	1.09	-1.28
205298_s_at	***BTN2A2***	butyrophilin, subfamily 2, member A2	63.69	0.0	28 ± 14	94 ± 11	112 ± 21	3.31	2.83
202769_at	***CCNG2***	cyclin G2	63.69	0.0	32 ± 20	135 ± 9	102 ± 25	4.19	3.19
204247_s_at	***CDK5***	cyclin-dependent kinase 5	62.17	0.003	376 ± 78	439 ± 47	591 ± 60	1.17	1.23
216295_s_at	***CLTA***	clathrin, light chain A	63.69	0.05	2186 ± 176	1898 ± 223	2028 ± 72	-1.15	-1.02
211070_x_at	***DBI***	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	63.69	0.05	271 ± 37	196 ± 61	172 ± 47	-1.39	-1.73
40612_at	***DOPEY1***	dopey family member 1	63.69	0.05	260 ± 41	156 ± 60	194 ± 38	-1.67	-2.18
214314_s_at	***EIF5B***	eukaryotic translation initiation factor 5B	63.69	0.005	1014 ± 261	657 ± 114	563 ± 67	-1.54	-1.49
219325_s_at	***ELAC1***	elaC homolog 1 (E, coli)	63.69	0.0	43 ± 28	164 ± 18	160 ± 23	3.85	3.76
233924_s_at	***EXOC6***	exocyst complex component 6	63.69	0.05	61 ± 44	91 ± 62	157 ± 19	1.49	1.75
223035_s_at	***FARSB***	phenylalanyl-tRNA synthetase, beta subunit	63.69	0.002	1119 ± 28	1291 ± 130	1525 ± 94	1.15	1.33
1555471_a_at	***FMN2***	formin 2	63.69	0.05	184 ± 34	172 ± 76	128 ± 17	-1.08	-1.48
207389_at	***GP1BA***	glycoprotein Ib (platelet), alpha polypeptide	63.69	0.05	180 ± 3	219 ± 81	182 ± 35	1.21	-1.18
209631_s_at	***GPR37***	G protein-coupled receptor 37 (endothelin receptor type B-like)	63.69	0.05	1125 ± 105	791 ± 344	839 ± 102	-1.42	-1.33
220642_x_at	***GPR89A | GPR89B | GPR89C***	G protein-coupled receptor 89A,B,C	63.69	0.009	596 ± 74	929 ± 167	1021 ± 133	1.56	1.21
231875_at	***KIF21A***	kinesin family member 21A	63.69	0.0	109 ± 25	188 ± 10	139 ± 13	1.72	1.27
204738_s_at	***KRIT1***	KRIT1, ankyrin repeat containing…	63.69	0.05	211 ± 18	239 ± 85	251 ± 20	1.13	1.12
203203_s_at	***KRR1***	KRR1, small subunit (SSU) processoPe coPponent, hoPolog	63.69	0.006	1319 ± 245	849 ± 178	746 ± 102	-1.55	-1.12

		(yeast)							
200915_x_at	***KTN1***	kinectin 1 (kinesin receptor)	62.64	0.05	9681 ± 1047	10767 ± 849	10927 ± 701	1.11	1.02
219760_at	***LIN7B***	lin-7 homolog B (C, elegans)	63.69	0.05	55 ± 42	115 ± 76	175 ± 25	2.10	2.82
220044_x_at	***LUC7L3***	LUC7-like 3 (S, cerevisiae)	63.69	0.05	797 ± 105	1051 ± 135	860 ± 34	1.32	1.27
224561_s_at	***MORF4L1***	Mortality factor 4 like 1	63.69	0.05	125 ± 34	103 ± 58	95 ± 20	-1.22	-1.43
224771_at	***NAV1***	neuron navigator 1	63.69	0.05	794 ± 125	613 ± 112	664 ± 107	-1.29	-1.59
217800_s_at	***NDFIP1***	Nedd4 family interacting protein 1	63.69	0.05	278 ± 26	133 ± 61	131 ± 59	-2.10	-1.45
201227_s_at	***NDUFB8***	NADH dehydrogenase (ubiquinone) 1 beta subcoPplex, 8, 19kDa	63.69	0.05	7974 ± 961	7176 ± 801	6665 ± 260	-1.11	-1.06
219293_s_at	***OLA1***	Obg-like ATPase 1	62.17	0.003	13429 ± 392	15238 ± 521	15003 ± 534	1.13	1.34
200768_s_at	***MAT2A***	methionine adenosyltransferase II, alpha	63.69	0.0	9692 ± 1110	7406 ± 567	6538 ± 660	-1.31	-1.23
226300_at	***MED19***	mediator coPplex subunit 19	63.69	0.0	520 ± 13	459 ± 82	666 ± 42	-1.13	1.11
232676_x_at	***MYEF2***	myelin expression factor 2	62.17	0.05	395 ± 130	591 ± 131	722 ± 101	1.50	1.27
1554633_a_at	***MYT1L***	myelin transcription factor 1-like	63.69	0.0	272 ± 37	143 ± 40	114 ± 27	-1.90	-1.87
211302_s_at	***PDE4B***	phosphodiesterase 4B	63.69	0.0	52.88 ± 68	195 ± 17	203 ± 36	3.69	3.85
219195_at	***PPARGC1A***	peroxisome proliferator-activated receptor gaPPa, coactivator 1 alpha	63.69	0.05	834.74 ± 73.47	956 ± 386	846 ± 62	1.15	1.08
203317_at	***PSD4***	pleckstrin and Sec7 domain containing 4	63.69	0.05	38 ± 20	90 ± 49	125 ± 21	2.36	3.12
217492_s_at	***PTEN***	phosphatase and tensin homolog	63.69	0.05	182 ± 13	222 ± 42	205 ± 16	1.22	1.12
211542_x_at	***RPS10***	ribosomal protein S10	62.17	0.05	11058 ± 1491	9033 ± 3174	12541 ± 1968	-1.22	1.01

1564377_at	***SHANK2***	SH3 and Pultiple ankyrin repeat doPains 2	62.17	0.0	57 ± 6	41 ± 28	10 ± 12	-1.41	-5.88
202507_s_at	***SNAP25***	synaptosomal-associated protein, 25kDa	62.17	0.05	6696 ± 742	10575 ± 3218	12809 ± 2447	1.58	1.97
227649_s_at	***SRGAP2***	SLIT-ROBO Rho GTPase activating protein 2	62.17	0.001	288 ± 54	313 ± 21	419 ± 22	1.09	-1.22
221506_s_at	***TNPO2***	transportin	63.7	0.05	88 ± 29	126 ± 41	119 ± 8	1.43	-1.24
201683_x_at	***TOX4***	TOX high mobility group box family member 4	63.69	0.01	940 ± 80	919 ± 170	1513 ± 256	-1.02	-1.05
228988_at	***ZNF711***	zinc finger protein 711	62.17	0.0	2799 ± 221	1473 ± 333	1611 ± 372	-1.90	-1.30



disease / disorders	**physiological function**	**molecular & cellular function**
hemotological disease	nervous system function	cell-to-cell signalling and interaction
infection mechanism	organ morphology	cellular assembly and organization
infectious disease	organismal development	drug metabolism

Figure S1. Transcriptional changes following HD-GFP injection in the *M. murinus* brain at day 1

A. Schematic representation of the different steps of the analyses. The microarray data of each brain sample were filtered to detect the present transcripts. Then, the transcriptional changes were sorted by SAM, ANOVA and principal component analysis (PCA) analyses. The main biological functions involved in these transcriptional changes in relation with the HD-GFP injection in the brain. **B.** Transcriptional profiles in the right striatum (R) compared to the left contralateral side (L) and to the control obtained by hierarchical. **C.** Transcriptional profiles in the midbrain. Red: up-regulated genes; green: down-regulated genes; black: no change in the gene expression; each line corresponding to a gene and each column to an animal.

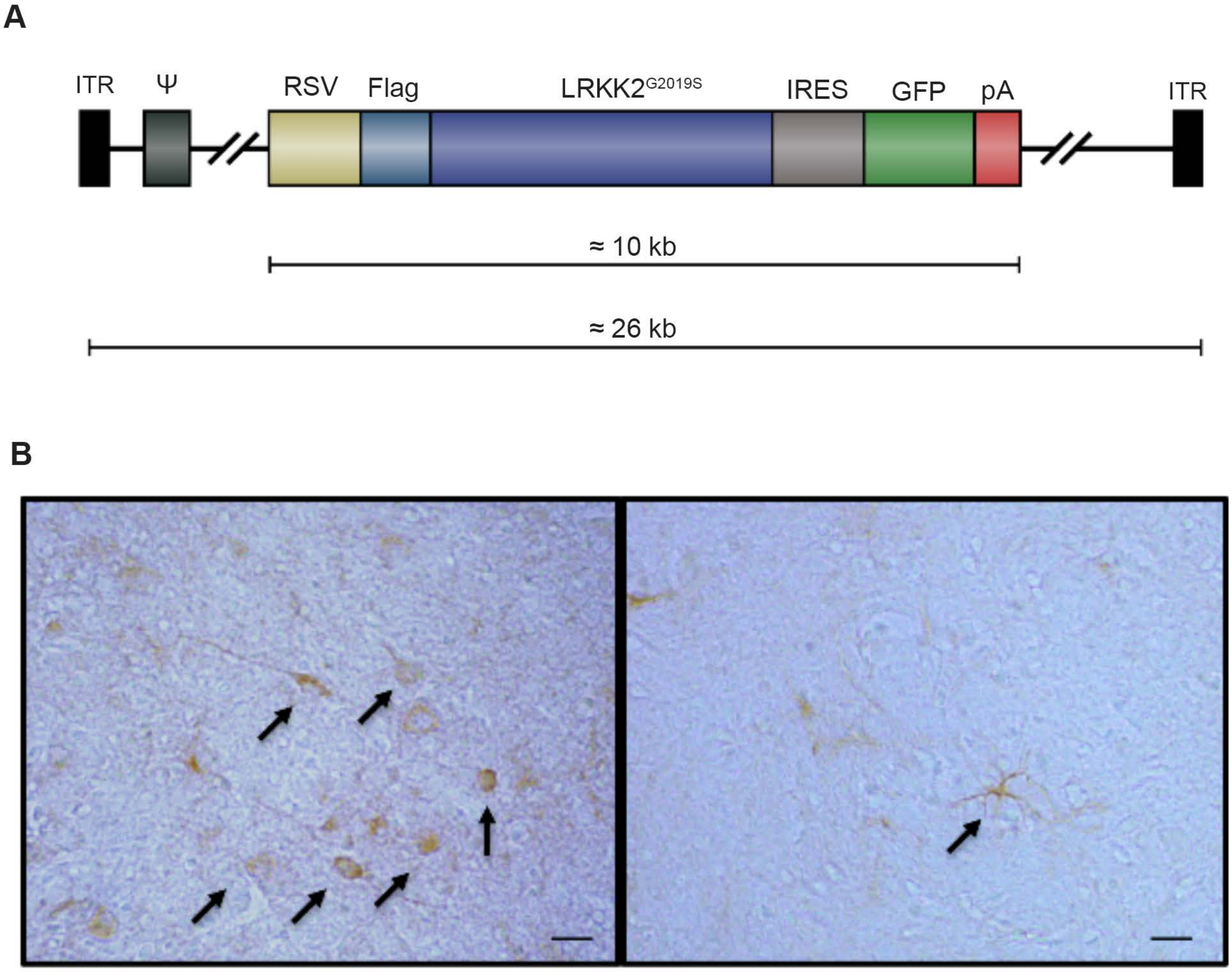


Figure S2. Vector schema and controls for injections

A. Schematic representation of the genome of the ~26 kbp HD-LRRK2^{G2019S} vector
ITR= ~200 bp inverted terminal repeats; Ψ = ~150 bp CAV-2 packaging domain; RSV = ~700 bp Rous sarcoma virus early promoter; Flag = ~100 bp Flag Tag; LRRK2G2019S = ~7.8 kbp codon-optimized cDNA; IRES = ~500 bp internal ribosome entry site; GFP – 700 bp green fluorescent protein ORF; polyA = ~100 bp SV40 polyA signal.
B. LRRK2 expression in the putamen at 15 days post-injection
Black arrows indicate LRRK2-immunoreactive neurons in the injected hemisphere (left) and LRRK2 immunoreactive astrocytes in the contralateral hemisphere (right) (n = 2 animals with 3 sections per animal). Scale bar = 30 µm.

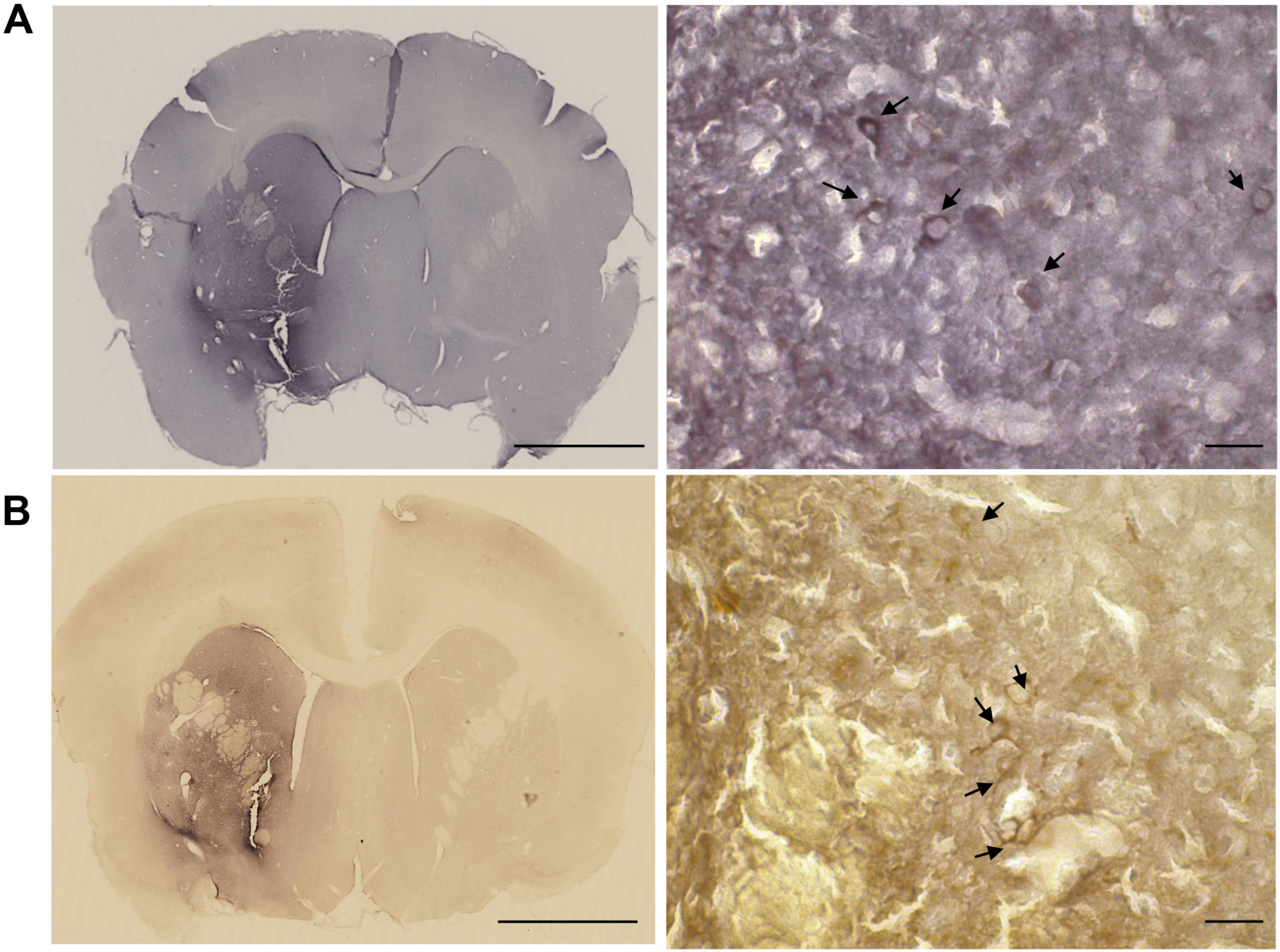


Figure S3. Microglial activation into the striatum of the HD-LRRK2^{G2019S}-injected mouse lemur (15 days post injection)

As demonstrated by **A.** Iba1 (ionized calcium binding adaptor molecule 1, DAB with nickel enhancement, black) and **B.** BRCA1 (breast cancer type 1 susceptibility protein, DAB, brown) immunoreactivity (n = 2 animals with 3 sections per animal). Arrows: cells with microglia morphology. Scale bars = 3 mm top panels, 20 µm bottom panels.

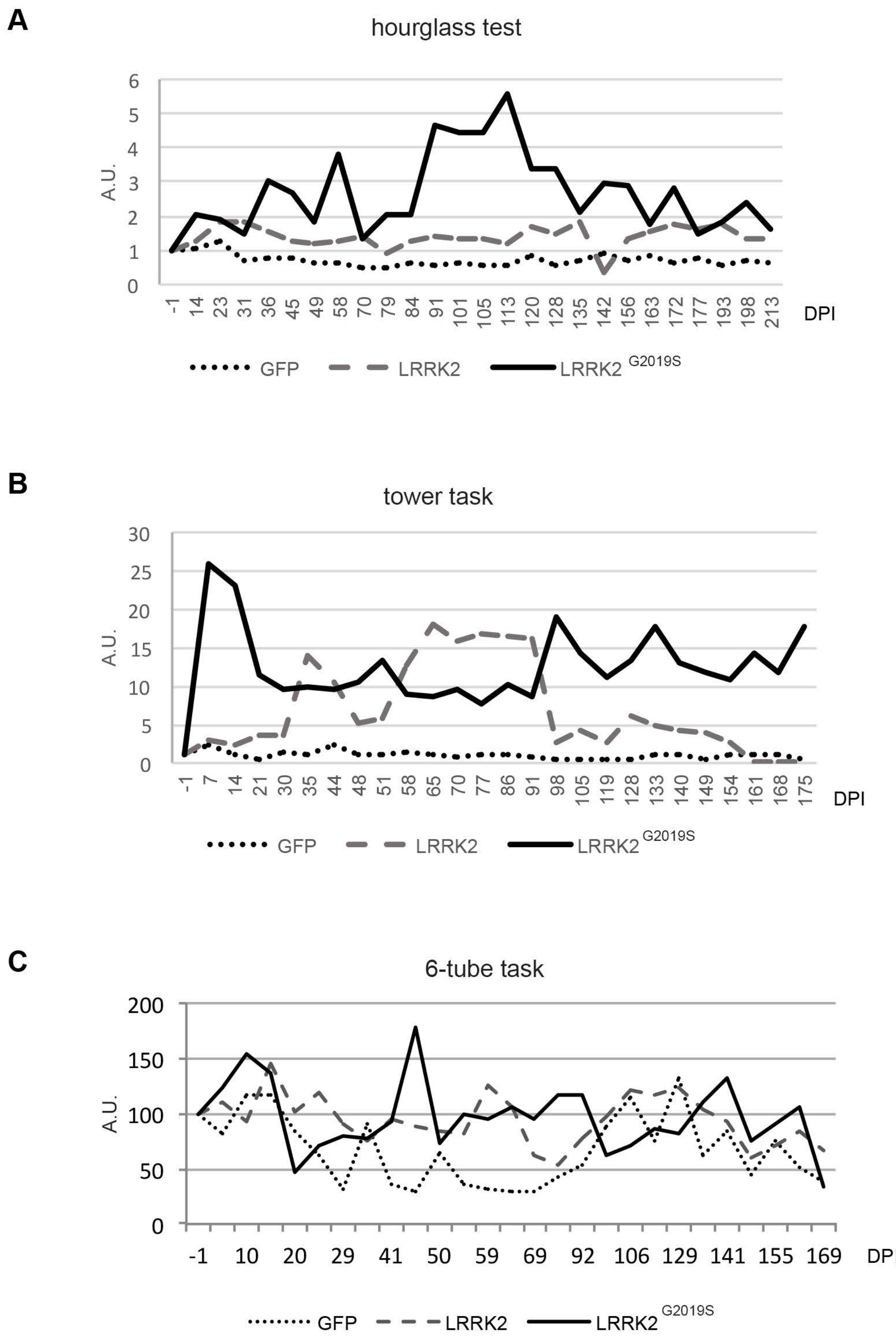


Figure S4. Behavioral assays following GFP, LRRK2 and LRRK2^{G2019S} expression

A. Hourglass test (4 GFP, 4 LRRK2, and 8 LRRK2^{G2019S} animals); **B.** Tower task (6 GFP, 4 LRRK2 and 8 LRRK2^{G2019S} animals); and **C.** Six-tube task (2 GFP, 4 LRRK2 and 8 LRRK2^{G2019S} animals).

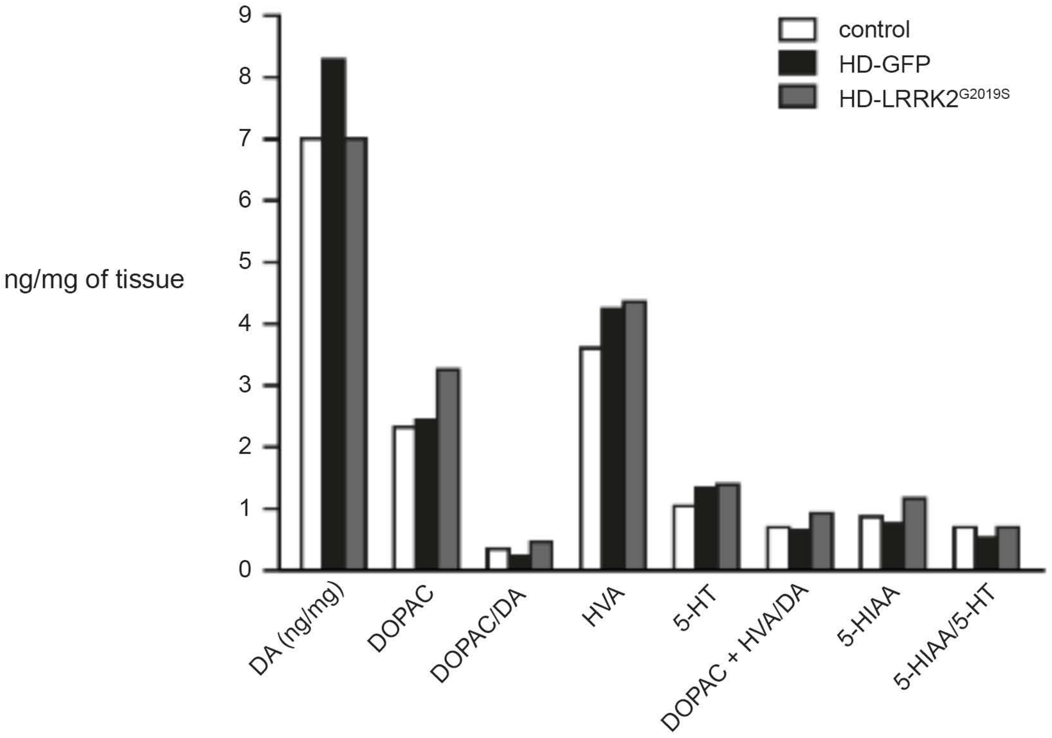


Figure S5. Quantification of biogenic amines by HPLC

HPLC with electrochemical detection was used to measure the concentration of the biogenic amines, dopamine (DA), 3,4- dihydroxyphenylacetic acid (DOPAC), homovanillic acid (HVA), 5-hydroxytryptamine (5-HT), and 5-hydroxyindoleacetic acid (5-HIAA). Samples were prepared from striatum of 4 naive animals, 4 HD-GFP and 4 HD-LRRK2G2019S. Tissue dosages of monoamines (DA, 5-HT) and their metabolites (DOPAC, HVA, 5-HIAA) were performed by an HPLC-ECD system* with minor modification. The tissues were homogenized in 400 µl of 0.1 N HClO4 and centrifuged at 13,000 rpm for 30 min at 4 °C Samples were injected using an S.I.L. 20AC autosampler (Schimadzu, Marne-la-Vallée, France) and injected into the HPLC column (Hypersil C18, 150 X 4.6 mm, 5 µm; Cluzeau Info Labo, Sainte-Foy-La-Grande, France) protected by a Brownlee–NewGuard pre-column (RP-8, 15 x 3.2 mm, 7 µm; Cluzeau Info Labo). The mobile phase, delivered at 1.2 ml/min flow rate using a HPLC pump (Gold 116, Beckman, France) was as follows (in mM): 60 NaH2PO4, 0.1 M disodium EDTA, and 2 octane sulfonic acid plus 7% methanol, adjusted to pH 3.9 with orthophosphoric acid and filtered through a 0.22 mm Millipore filter. Detection of monoamines and their metabolites was performed with a coulometric detector (ESA Coulochem II) coupled to a dual-electrode analytic cell (model 5011). The potential of the electrodes was set at +350 and -270 mV. Output signals were analyzed using Jasco software (ChromNav, Lisses, France). Results are expressed as ng/mg of tissue.

* Villaescusa JC et al. A PBX1 transcriptional network controls dopaminergic neuron development and is impaired in Parkinson's disease. EMBO J. 2016;1–16doi:10.15252/embj.201593725.

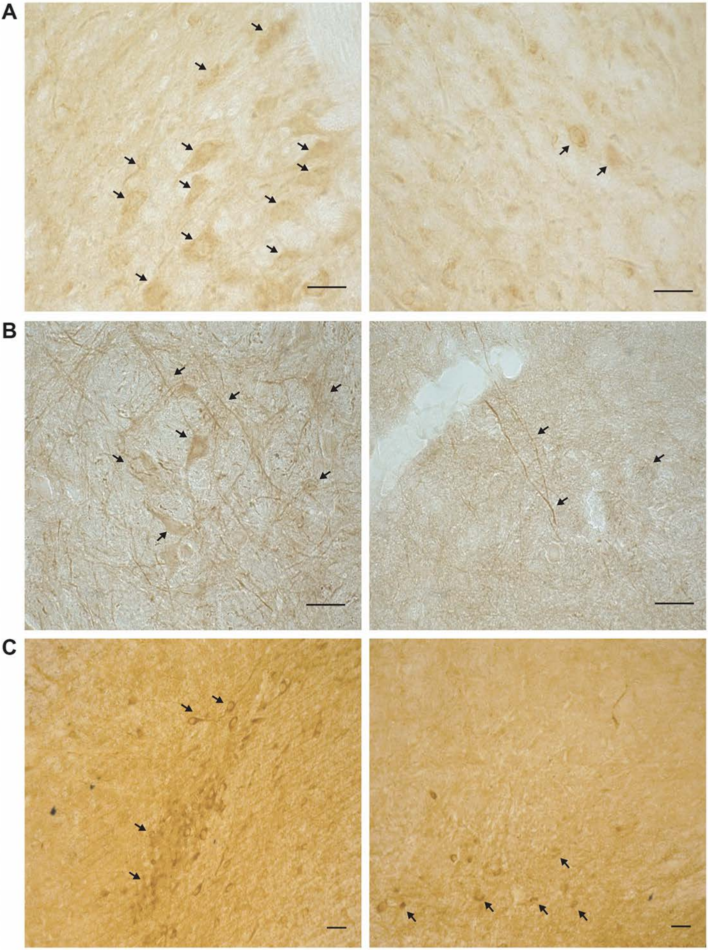


Figure S6. LRRK2^{G2019S} expression leads to increased α-synuclein and phospho-tau immunoreactivity into the substantia nigra

A. LRRK2 (leucine-rich repeat kinase 2) immunoreactivity (arrows) in nigral neurons; **B.** α-synuclein^{pS129} immunoreactivity (arrows); and **C.** phospho-tau^{Ser396} immunoreactivity (arrows) from LRRK2^{G2019S}-expressing animals. The left-hand column is the injected hemisphere and the right-hand column the contralateral hemisphere from animals killed 6 months post-injection (n = 3 animals and ≥ 3 sections/animal). Scale bar = 40 μm.