

Supplemental information

Unveiling differential gene

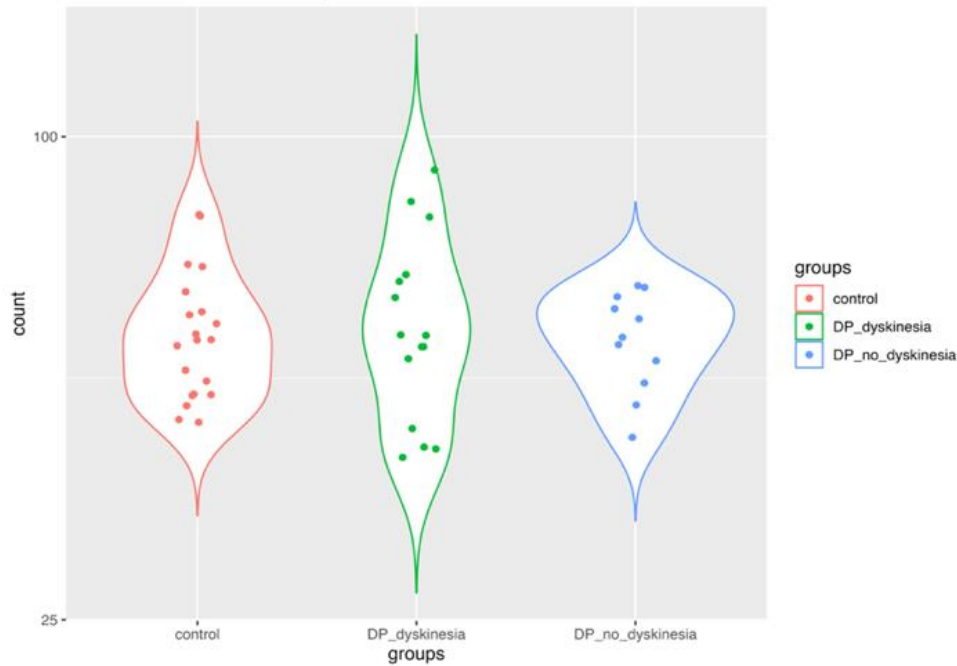
co-expression networks and its effects

on levodopa-induced dyskinesia

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FIGURE S1 – General RNA sequencing data, related to Figure 1.

A



B

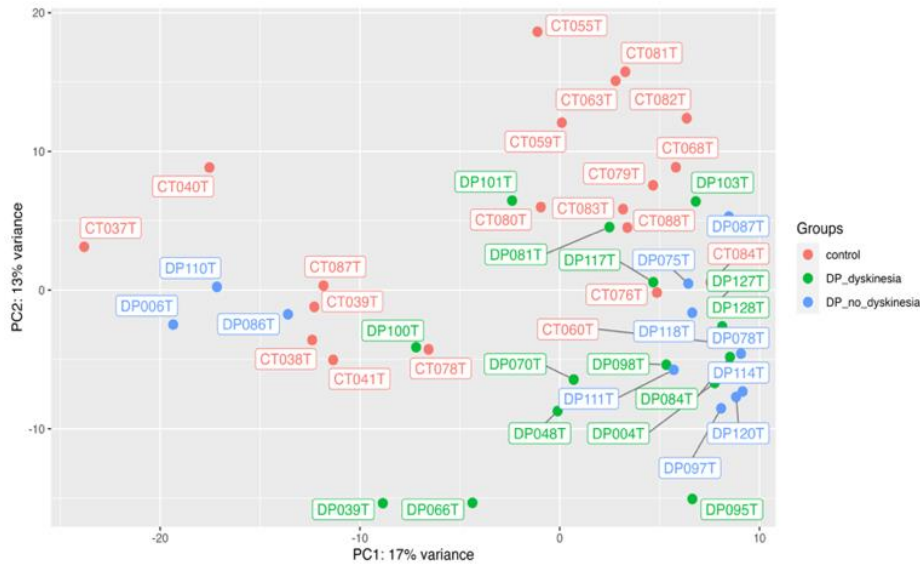
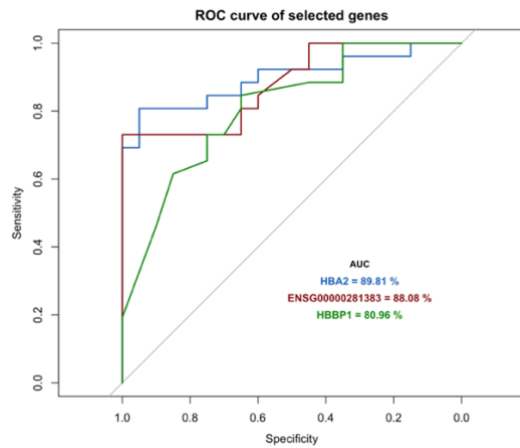


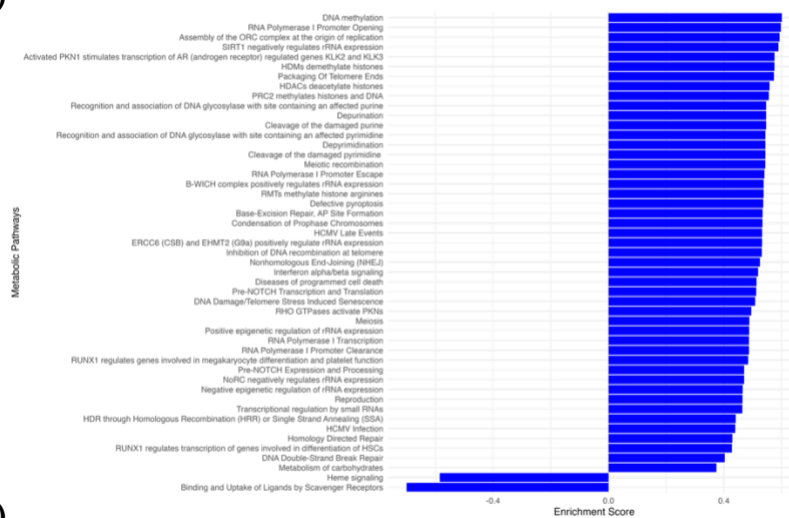
Figure S1. A) Distribution of counts of the samples by group, related to figure 1. Control group samples are represented in red, PD with dyskinesia group samples in green, and PD without dyskinesia group samples in blue. **B)** PCA of the sample distribution, related to figure 1. PCA plot showing sample distribution by group: control samples in red, PD with dyskinesia samples in green, and PD without dyskinesia samples in blue. Abbreviations: PD_dyskinesia, people with Parkinson's disease with levodopa-induced dyskinesia; PD_no_dyskinesia, people with Parkinson's disease without levodopa-induced dyskinesia.

FIGURE S2 - Results of differential expression analysis, related to Figure 2 and Table 2.

A



B)



C)



Figure S2. A) ROC curve of differentially expressed genes with areas under the curve (AUC) over 0.8, related to figure 2. HBA2 gene is represented in blue (AUC = 89.81), ENSG0000281383 in brown (AUC = 88.08), and HBBP1 in green (AUC = 80.96). **B)** Gene Set Enrichment Analysis of genes investigated in differential analysis expression for PD-ND group, related to figure 2A. Metabolic pathways enriched through GSEA, based on the ranking of gene expression levels (from highest to lowest) of the PD-ND group compared to the control group. The pathways are ordered from the highest enrichment scores to the lowest. **C)** Gene Set Enrichment Analysis of genes investigated in differential analysis expression for PD-D group, related to figure 2B. Metabolic pathways enriched through GSEA, based on the ranking of gene expression levels (from highest to lowest) of the PD-D group compared to the control group. The pathways are ordered from the highest enrichment scores to the lowest.

TABLE S1. Epidemiological data of patients with PD and healthy controls, related to Table 1.

ID	GROUP	AAO	AAE	SEX
CT001	CT	-	67	Female
CT002	CT	-	53	Female
CT003	CT	-	67	Female
CT004	CT	-	45	Female
CT005	CT	-	68	Female
CT006	CT	-	64	Male
CT007	CT	-	63	Male
CT008	CT	-	60	Male
CT009	CT	-	62	Male
CT010	CT	-	52	Male
CT011	CT	-	55	Male
CT012	CT	-	60	Female
CT013	CT	-	53	Male
CT014	CT	-	74	Male
CT015	CT	-	64	Male
CT016	CT	-	59	Male
CT017	CT	-	53	Male
CT018	CT	-	50	Male
CT019	CT	-	55	Female
CT020	CT	-	49	Male
DP001	PD-D	39	51	Male
DP002	PD-ND	44	49	Female
DP003	PD-D	37	48	Female
DP004	PD-D	39	49	Female
DP005	PD-D	42	54	Female
DP006	PD-D	38	52	Male
DP007	PD-ND	56	61	Male
DP008	PD-ND	47	51	Male
DP009	PD-D	49	52	Male
DP010	PD-D	49	60	Male
DP011	PD-ND	54	60	Female
DP012	PD-ND	63	64	Male
DP013	PD-D	49	61	Male
DP014	PD-ND	62	67	Male
DP015	PD-D	58	64	Male
DP016	PD-D	52	60	Female
DP017	PD-D	41	53	Male
DP018	PD-D	34	46	Male
DP019	PD-ND	50	54	Female
DP020	PD-ND	50	60	Male
DP021	PD-ND	48	50	Male
DP022	PD-D	36	46	Male
DP023	PD-ND	45	47	Male
DP024	PD-ND	40	46	Male
DP025	PD-D	61	66	Male
DP026	PD-D	41	59	Male

Abbreviations: AAE, age at evaluation; AAO, age at disease onset; CT, control group; -, not applied; PD-D, Patients with PD with LID; PD-ND, Patients with PD without LID.

TABLE S3. Over Representation Analysis - Exclusive enriched pathways in PD-D, related to Figure 3F.

Module	Description	BgRatio	pvalue	p.adjust	qvalue
M4	Signaling by ROBO receptors	71/967	1,92E-35	2,27E-33	1,94E-33
M4	Metabolism of amino acids and derivatives	69/967	1,14E-33	1,25E-32	1,06E-32
M4	Axon guidance	108/967	1,45E-20	1,53E-19	1,30E-19
M4	Nervous system development	109/967	2,68E-20	2,72E-19	2,32E-19
M4	Cellular responses to stimuli	147/967	8,30E-16	7,61E-15	6,48E-15
M4	Cellular responses to stress	147/967	8,30E-16	7,61E-15	6,48E-15
M4	Infectious disease	164/967	3,29E-15	2,92E-14	2,49E-15
M4	SARS-CoV-1 modulates host translation machinery	29/967	3,16E-07	2,64E-06	2,25E-06
M4	Metabolism	197/967	4,21E-07	3,42E-06	2,91E-07
M4	SARS-CoV-2 modulates host translation machinery	28/967	3,93E-06	3,10E-05	2,64E-05
M4	Formation of the ternary complex, and subsequently, the 43S complex	30/967	5,38E-05	4,13E-04	3,52E-04
M4	SARS-CoV-2 Infection	68/967	5,90E+03	3,64E+04	3,10E+04
M4	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	32/967	5,23E-04	3,62E-03	3,09E-04
M4	Developmental Biology	146/967	2,18E-12	1,87E-11	1,60E-11
M4	SARS-CoV-1-host interactions	40/967	1,42E-03	9,62E-03	8,20E-03
M4	Ribosomal scanning and start codon recognition	33/967	1,47E-03	9,73E-04	8,29E-03
M4	SARS-CoV-1 Infection	46/967	1,23E-01	7,95E-01	6,78E-01
M4	Downstream TCR signaling	20/967	0.00456532186563808	0.0270114877050253	0.02302684274335
M4	SARS-CoV-2-host interactions	56/967	3,64E+01	2,30E+02	1,96E+02
M4	Translation initiation complex formation	32/967	5,23E-04	3,62E-03	3,09E-04
M4	Disease	245/967	1,12E-04	8,16E-04	6,96E-04
M6	L1CAM interactions	13/967	6,59E+09	0.0208332995039624	0.0169331281777709
M6	Extracellular matrix organization	21/967	0.000181301676642804	0.028645664909563	0.023282952158339
M4	SARS-CoV Infections	85/967	3,15E+04	1,90E+05	1,62E+05