Supplementary table 1 The significantly enriched GO terms by the DEGs between Parkinson’s disease and healthy control

Down regulated DEGs

Category	**Term**	**Count**	**P-value**
Biology Process	GO:0006357~regulation of transcription from RNA polymerase II promoter	16	0.006352
	GO:0010604~positive regulation of macromolecule metabolic process	16	0.025268
	GO:0031328~positive regulation of cellular biosynthetic process	15	0.008998
	GO:0009891~positive regulation of biosynthetic process	15	0.010142
	GO:0010605~negative regulation of macromolecule metabolic process	15	0.015735
	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	14	0.010089
	GO:0051173~positive regulation of nitrogen compound metabolic process	14	0.012878
	GO:0010557~positive regulation of macromolecule biosynthetic process	14	0.01448
	GO:0045941~positive regulation of transcription	13	0.011384
	GO:0010628~positive regulation of gene expression	13	0.014126
	GO:0046907~intracellular transport	13	0.032927
	GO:0006955~immune response	13	0.045116
	GO:0031327~negative regulation of cellular biosynthetic process	12	0.025931
	GO:0009890~negative regulation of biosynthetic process	12	0.02965
	GO:0006952~defense response	12	0.045693
Cellular Component	GO:0043232~intracellular non-membrane-bounded organelle	35	0.027486
	GO:0043228~non-membrane-bounded organelle	35	0.027486
	GO:0043233~organelle lumen	28	0.011802
	GO:0031974~membrane-enclosed lumen	28	0.015061
	GO:0070013~intracellular organelle lumen	27	0.016207
	GO:0005829~cytosol	20	0.047625

	GO:0005730~nucleolus	14	0.015726
	GO:0012505~endomembrane system	14	0.035623
Molecular Function	GO:0019899~enzyme binding	12	0.022542
	GO:0016564~transcription repressor activity	9	0.018834
	GO:0031406~carboxylic acid binding	7	0.0042
	GO:0005244~voltage-gated ion channel activity	7	0.017279
	GO:0022832~voltage-gated channel activity	7	0.017279
	GO:0003702~RNA polymerase II transcription factor activity	7	0.044643

Up regulated DEGs

Category	**Term**	**Count**	**P−value**
Biology Process	GO:0010604~positive regulation of macromolecule metabolic process	26	2.17E-05
	GO:0007242~intracellular signaling cascade	24	0.021454
	GO:0042127~regulation of cell proliferation	21	9.18E-04
	GO:0009611~response to wounding	18	1.66E-04
	GO:0031328~positive regulation of cellular biosynthetic process	18	0.002876
	GO:0009891~positive regulation of biosynthetic process	18	0.003334
	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	17	0.002772
	GO:0051173~positive regulation of nitrogen compound metabolic process	17	0.003774
	GO:0010557~positive regulation of macromolecule biosynthetic process	17	0.004378
	GO:0008283~cell proliferation	16	1.93E-04

	GO:0007267~cell-cell signaling	16	0.004731
	GO:0010033~response to organic substance	16	0.022649
Cellular Component	GO:0044459~plasma membrane part	43	3.04E-04
	GO:0005576~extracellular region	35	0.009396
	GO:0044421~extracellular region part	26	7.28E-05
	GO:0005887~integral to plasma membrane	25	0.00376
	GO:0031226~intrinsic to plasma membrane	25	0.004988
	GO:0005856~cytoskeleton	25	0.022075
	GO:0005615~extracellular space	20	2.68E-04
	GO:0044430~cytoskeletal part	19	0.022159
	GO:0030054~cell junction	13	0.014823
	GO:0015630~microtubule cytoskeleton	12	0.047853
	GO:0045202~synapse	10	0.019844
Molecular Function	GO:0030528~transcription regulator activity	27	0.016292
	GO:0003700~transcription factor activity	21	0.00589
	GO:0043565~sequence-specific DNA binding	16	0.003223
	GO:0046983~protein dimerization activity	14	0.007661
	GO:0019899~enzyme binding	13	0.014207
	GO:0016563~transcription activator activity	10	0.040439

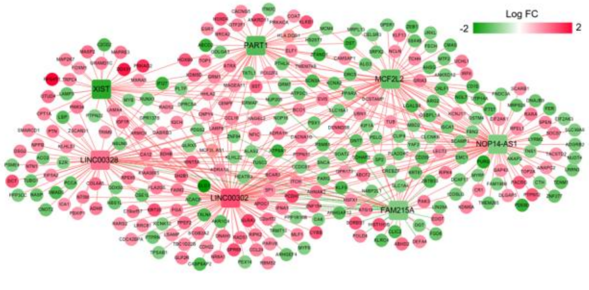

Log FC
-2
2
PART1
MCF2L2
XIST
LINC00328
NOP14-AS1
LINC00302
FAM215A

Fig S1

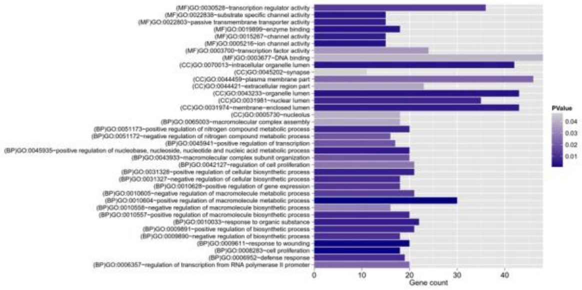
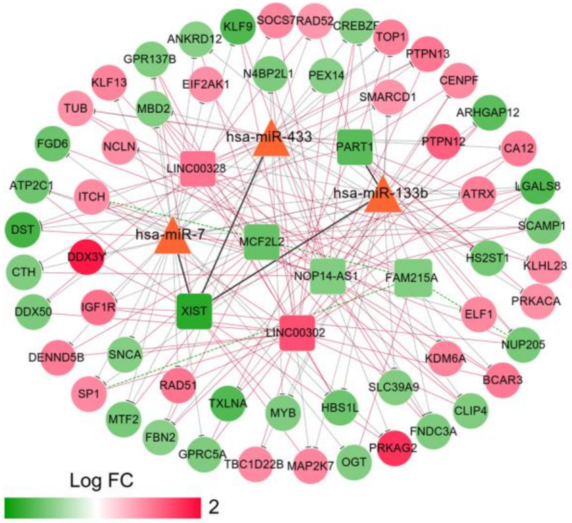

(MF)GO:0030528~transcription regulator activity
(MF)GO:0022838~substrate specific channel activity
(MF)GO:0022803~passive transmembrane transporter activity
(MF)GO:0019899~enzyme binding
(MF)GO:0015267~channel activity
(MF)GO:0005216~ion channel activity
(MF)GO:0003700~transcription factor activity
(MF)GO:0003677~DNA binding
(CC)GO:0070013~intracellular organelle lumen
(CC)GO:0045202~synapse
(CC)GO:0044459~plasma membrane part
(CC)GO:0044421~extracellular region part
(CC)GO:0043233~organelle lumen
(CC)GO:0031981~nuclear lumen
(CC)GO:0031974~membrane-enclosed lumen
(CC)GO:0005730~nucleolus
(BP)GO:0065003~macromolecular complex assembly
(BP)GO:0051173~positive regulation of nitrogen compound metabolic process
(BP)GO:0051172~negative regulation of nitrogen compound metabolic process
(BP)GO:0045941~positive regulation of transcription
(BP)GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
(BP)GO:0043933~macromolecular complex subunit organization
(BP)GO:0042127~regulation of cell proliferation
(BP)GO:0031328~positive regulation of cellular biosynthetic process
(BP)GO:0031327~negative regulation of cellular biosynthetic process
(BP)GO:0010628~positive regulation of gene expression
(BP)GO:0010605~negative regulation of macromolecule metabolic process
(BP)GO:0010604~positive regulation of macromolecule metabolic process
(BP)GO:0010558~negative regulation of macromolecule biosynthetic process
(BP)GO:0010557~positive regulation of macromolecule biosynthetic process
(BP)GO:0010033~response to organic substance
(BP)GO:0009891~positive regulation of biosynthetic process
(BP)GO:0009890~negative regulation of biosynthetic process
(BP)GO:0009611~response to wounding
(BP)GO:0008283~cell proliferation
(BP)GO:0006952~defense response
(BP)GO:0006357~regulation of transcription from RNA polymerase II promoter
0
10
20
30
40
Gene count
PValue
0.04
0.03
0.02
0.01

Fig S2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SOCS7
RAD52
CREBZF
ANKRD12
TOP1
PTPN13
GPR137B
KLF13
EIF2AK1
N4BP2L1
PEX14
CENPF
SMARCD1
TUB
MBD2
ARHGAP12
NCLN
hsa-miR-433
PART1
PTPN12
CA12
FGD6
LINC00328
hsa-miR-133b
ATP2C1
ITCH
ATRX
LGALS8
SCAMP1
DST
hsa-miR-7
MCF2L2
DDX3Y
HS2ST1
KLHL23
CTH
NOP14-AS1
FAM215A
PRKACA
IGF1R
XIST
ELF1
DDX50
LINC00302
NUP205
DENND5B
SNCA
KDM6A
BCAR3
SP1
RAD51
SLC39A9
TXLNA
MYB
HBS1L
CLIP4
MTF2
FNDC3A
FBN2
GPRC5A
TBC1D22B
MAP2K7
OGT
PRKAG2
Log FC
-2
2

Fig S3