

## SUPPLEMENTARY TABLES

**Supplementary Table 1. Information on number of samples, sex and age of samples in datasets.**

GEO Dataset		No. sample	Sex (male/female)	Mean Age ( $\pm$ SD)
GSE99039	PD	204	97/107	NA
	HC	230	150/80	NA
	All	434	247/187	NA
GSE63060 +	AD	245	166/79	76.5 ( $\pm$ 6.6)
GSE63061	MCI	142	79/66	74.9( $\pm$ 6.3)
	HC	182	110/72	73.6 ( $\pm$ 6.3)
	All	569	352/217	75.2 ( $\pm$ 6.5)

Please browse Full Text version to see the data of Supplementary Table 2.

**Supplementary Table 2. Excel table of differentially expressed genes found in the PD dataset.**

**Supplementary Table 3. Excel table of significant hubs found in non-preserved modules between PD and healthy controls.**

Module	Gene	Hub detection method	Score	P-value
<i>PD modules not preserved in HC</i>				
Darkseagreen4	GINS2	Betweenness	3826	0.005
	S1PR5	Kleinberg's centrality; PageRank; MM	0.30751; 0.02637; 0.90234	0.006; 0.006; 0.007
	AGBL2	Closeness	10.00256	0.007
	NKG7	PageRank	0.02512	0.007
Navajowhite2	SNRNP70	PageRank; Kleinberg's centrality	0.02359; 0.27933	0.003; 0.007
	POPDC2	Closeness	18.03573	0.008
	CHKB	Kleinberg's centrality	0.28034	0.009
	MIR142	MM	0.85297	0.009
Salmon	TYSND1	PageRank; MM; Kleinberg's centrality	0.00978; 0.84787; 0.17499	0.002; 0.002; 0.008
	C17orf97	Closeness	4.4882	0.002
	HDAC6	Kleinberg's centrality; MM; PageRank	0.17867; 0.83636; 0.00958	0.003; 0.006; 0.007
	FAM114A1	Betweenness	12901	0.004
	ZNF804A	Betweenness; Closeness	12956; 4.27567	0.005; 0.007
	ABCD1	PageRank; MM	0.00904; 0.83955	0.006; 0.006
HC modules not preserved in PD	ZNF526	PageRank	0.00908	0.006
	TMEM147-AS1	Betweenness	12566	0.008
	RENBP	PageRank	0.00823	0.009
Purple	FAM110C	Closeness; Betweenness	0.72585; 33683	0.000; 0.002

TXLNGY	Betweenness	40661	0
PAK4	Kleinberg's centrality; Pagerank; MM	0.12262; 0.00467; 0.83401	0.001; 0.002; 0.003
GIGYF1	Kleinberg's centrality; PageRank; MM	0.12332; 0.00473; 0.85428	0.002; 0.002; 0.002
WDTC1	Kleinberg's centrality; MM; PageRank	0.11337; 0.82836; 0.00441	0.002; 0.004; 0.008
NEB	Closeness; Betweenness	0.70015; 21395	0.003; 0.004
SH3BGR	Closeness; Betweenness	0.63727; 19636	0.004; 0.005
FCGBP	Betweenness	16988	0.005
INO80B	PageRank; Kleinberg's centrality; MM	0.00417; 0.10391; 0.82766	0.005; 0.007; 0.007
ZNF582-AS1	Closeness; Betweenness	0.59408; 0.06978	0.006; 0.008
PLA2G4C	Betweenness	20491	0.007
TBC1D25	PageRank; MM Kleinberg's	0.00401; 0.81547	0.007; 0.007
MFSD12	centrality; PageRank; MM	0.10808; 0.00411; 0.80996	0.007; 0.009; 0.009
MCM2	Closeness	0.57973	0.008
SPATA6	Closeness	0.65087	0.009
RPS6KA4	MM	0.80597	0.009
FIZ1	MM	0.81009	0.009

Please browse Full Text version to see the data of Supplementary Table 4.

**Supplementary Table 4. Excel table of significant hubs found in non-preserved modules between AD, MCI and healthy controls.**

**Supplementary Table 5. Excel file containing the significant TFs (Pvalue < 0.01) associated with each non-preserved module between PD and healthy control networks found using Enrichr (ENCODE and ChEA Consensus TFs from CHIP-X).**

Module colour	Significant TFs	P-value	Gene overlap
<i>PD modules not preserved in HC</i>			
Darkseagreen4	FOXM1	4.004E-08	9/95
	E2F4	8.131E-08	21/710
Navajowhite2	RUNX1	0.008305	18/1294
Salmon	FOXM1	0.006578	6/95
<i>HC modules not preserved in PD</i>			
Purple	SIX5	0.0001626	55/1094
	ZBTB7A	0.0002814	94/2184
	SRF	0.0008434	20/299
	CREB1	0.001402	64/1444
	NFYB	0.004818	138/3715
	PBX3	0.007364	54/1269

**Supplementary Table 6. Excel file containing the significant TFs (Pvalue < 0.01) associated with each non-preserved module between AD, MCI and healthy control networks found using Enrichr (ENCODE and ChEA Consensus TFs from CHIP-X).**

Module colour	Significant TFs	P-value	Gene overlap	
<i>AD modules not preserved in HC and MCI</i>				
Blue	SUZ12	3.36E-10	150/1684	
	EZH2	0.0004579	26/237	
<i>MCI modules not preserved in AD and HC</i>				
Sienna3	SUZ12	8.24E-10	115/1684	
<i>HC modules not preserved in AD and MCI</i>				
Darkolivegreen	SUZ12	0.00392	68/1684	
	REST	0.009205	20/383	
	IRF3	0.000002884	24/663	
	SP2	0.000006359	30/994	
	NFYB	0.0000105	74/3715	
	GABPA	0.00001689	48/2082	
	BRCA1	0.0003388	61/3218	
	CTCF	0.0003775	39/1790	
	Darkorange2	NFYA	0.0004409	46/2250
		PBX3	0.0005193	30/1269
SIX5		0.00115	26/1094	
SMC3		0.003293	26/1181	
NR2C2		0.004466	11/350	
Skyblue	FOS	0.006121	16/637	
	CREB1	0.007005	29/1444	
	RCOR1	0.002542	15/702	
	BCLAF1	0.006338	16/851	
<i>HC modules not preserved in MCI</i>				
Red	SUZ12	1.21E-09	107/1684	
	EZH2	0.0001041	21/237	

**Supplementary Table 7. Excel file containing the SNPs associated with PD SNPs in bold are shared between PD and AD.**

Chromosome	SNPs	Associated PD related miRNAs	Modules with SNP associated gene	Genes
1	rs12140193	hsa-miR-495	PD darkseagreen4	METTL13
	rs1138729	hsa-miR-495	PD salmon	RRM2
	<b>rs12603</b>	hsa-miR-543	HC purple	EPB41L5
2	rs2058703	hsa-miR-1283	HC purple; PD salmon	BCL11A
	rs4852735	hsa-miR-4271	PD navajowhite2	TEX261
	<b>rs707718</b>	hsa-miR-543	HC purple	CYP26B1
	<b>rs1135750</b>	hsa-miR-147a	PD navajowhite2	IQCB1
3	<b>rs11551405</b>	hsa-miR-203	HC purple	DCP1A
4	rs3805317	hsa-miR-203	HC purple	CLGN
5	rs2561659	hsa-miR-543	HC purple	AHRR
	<b>rs12528857</b>	hsa-miR-203	HC purple; PD darkseagreen4; PD salmon; PD navajowhite2	TDRD6
6	<b>rs1966</b>	hsa-miR-543	HC purple; PD darkseagreen4	PSORS1C1
7	<b>rs1044718</b>	hsa-miR-147a	HC purple; PD darkseagreen4; PD salmon	PARP12
8	<b>rs2929969</b>	hsa-miR-133b; hsa-miR-203	PD darkseagreen4	WISP1
9	rs7047770	hsa-miR-133b	HC purple; PD navajowhite2	C9orf139
	rs818055	hsa-miR-147a	HC purple; PD navajowhite2	LAMC3
10	rs1042192	hsa-miR-376b	HC purple	CYP2C18
	<b>rs10832733</b>	hsa-miR-543	HC purple	PIK3C2A
	rs2512676	hsa-miR-147a	PD darkseagreen4; PD salmon	DLG2
11	rs7126647	hsa-miR-543	PD navajowhite2	MRGPRX2
	rs9444	hsa-miR-495	HC purple	RNF169
14	<b>rs1054195</b>	hsa-miR-543	PD navajowhite2	CLMN
16	rs1568391	hsa-miR-495	PD darkseagreen4	IRF8
17	<b>rs3744711</b>	hsa-miR-203	HC purple; PD salmon	DHX33
	rs1790974	hsa-miR-203	HC purple	DOK6
18	rs3745067	hsa-miR-4271	HC purple; PD darkseagreen4; PD salmon	ONECUT2
19	rs36621	hsa-miR-376b	PD navajowhite2	TSEN34
20	rs1060347	hsa-miR-134	HC purple	PCMTD2
22	rs712979	hsa-miR-203	HC purple	C22orf39

**Supplementary Table 8. Excel file containing the SNPs associated with AD SNPs in bold are shared between AD and PD.**

Chromosome	SNPs	Associated PD related miRNAs	Modules with SNP associated gene	Genes
1	rs6660019	hsa-miR-433	AD blue; HC darkolivegreen; MCI sienna3	SASS6
	<b>rs12603</b>	hsa-miR-543	HC darkorange2	EPB41L5
2	<b>rs707718</b>	hsa-miR-543	AD blue; HC darkolivegreen; HC red; MCI sienna3	CYP26B1
	<b>rs1135750</b>	hsa-miR-147a	HC skyblue	IQCB1
	<b>rs11551405</b>	hsa-miR-203	AD blue; HC darkorange2; HC red	DCP1A
3	rs340833	hsa-miR-433	HC skyblue	IL5RA
	rs6792607	hsa-miR-153	HC skyblue	EIF5A2
	<b>rs3805317</b>	hsa-miR-203	AD blue; HC red; MCI sienna3	CLGN
4	rs8336	hsa-miR-203	AD blue	SMARCAD1
	rs10864	hsa-miR-433	AD blue; HC red; MCI sienna3	BCKDHB
	<b>rs12528857</b>	hsa-miR-203	AD blue; HC darkorange2; HC red; MCI sienna3	TDRD6
6	<b>rs1966</b>	hsa-miR-543	AD blue; HC red; MCI sienna3	PSORS1C1
	rs4709266	hsa-miR-433	AD blue; HC red; MCI sienna3	TAGAP
7	<b>rs1044718</b>	hsa-miR-147a	HC red	PARP12
	rs1042992	hsa-miR-495	HC darkorange2	BNIP3L
8	<b>rs2929969</b>	hsa-miR-133b; hsa-miR-203	AD blue	WISP1
	rs732338	hsa-miR-134	AD blue; HC red; MCI sienna3	LZTS1
10	rs7071789	hsa-miR-495	HC darkolivegreen	TRUB1
11	<b>rs10832733</b>	hsa-miR-543	HC darkorange2	PIK3C2A
14	<b>rs1054195</b>	hsa-miR-543	AD blue; MCI sienna3	CLMN
16	rs7294	hsa-miR-147a	HC darkolivegreen	VKORC1
17	<b>rs3744711</b>	hsa-miR-203	HC darkorange2; HC skyblue	DHX33
	rs1046699	hsa-miR-433	AD blue; HC red; MCI sienna3	C18orf54
18	rs608823	hsa-miR-433	AD blue; HC red; MCI sienna3	ONECUT2
21	rs243609	hsa-miR-543	AD blue; HC red; MCI sienna3	C21orf91
22	rs137124	hsa-miR-134	AD blue	CYB5R3
	rs17032	hsa-miR-495	HC darkolivegreen	SUN2