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## SUPPLEMENTAL TABLES

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690 Table e-1. Top 20 differentially expressed genes by disease group.

A. PDD vs. PD Overexpressed			B. PDD vs. PD Underexpressed		
Gene	P-value	Fold Change	Gene	P-value	Fold Change
IGKV1-5	$1.49 \times 10^{-5}$	122.11	OR4N2	$4.32 \times 10^{-5}$	-25.85
CXCL9	$9.82 \times 10^{-34}$	77.64	UBD	$1.98 \times 10^{-6}$	-19.62
IGHG1	$3.69 \times 10^{-17}$	14.20	OTX2	$3.84 \times 10^{-6}$	-18.80
IGHG3	$8.08 \times 10^{-6}$	12.80	LMX1A	$4.51 \times 10^{-6}$	-17.45
IGHG2	$1.33 \times 10^{-9}$	10.25	CCL4	$1.65 \times 10^{-9}$	-12.48
IGHM	$4.43 \times 10^{-6}$	8.24	C6	$1.11 \times 10^{-11}$	-10.02
IGHG4	$7.30 \times 10^{-7}$	8.08	S100A14	$6.77 \times 10^{-9}$	-8.15
MTRNR2L8	$2.45 \times 10^{-9}$	7.71	LTF	$2.43 \times 10^{-16}$	-7.99
RAX2	$1.01 \times 10^{-6}$	7.40	HTR2B	$1.78 \times 10^{-5}$	-7.39
PSPN	$1.95 \times 10^{-5}$	7.07	FAM216B	$9.59 \times 10^{-12}$	-7.33
NPC1L1	$7.74 \times 10^{-12}$	6.35	IL1RN	$4.30 \times 10^{-7}$	-6.74
SELE	$1.07 \times 10^{-6}$	5.27	MYO1A	$8.57 \times 10^{-11}$	-6.51
NANOS2	$3.84 \times 10^{-6}$	5.18	ADGB	$1.01 \times 10^{-6}$	-6.30
CSF3	$1.01 \times 10^{-5}$	4.99	PZP	$2.72 \times 10^{-10}$	-6.17
IL8	$1.57 \times 10^{-6}$	4.69	NTS	$5.25 \times 10^{-8}$	-6.12
GRB7	$1.26 \times 10^{-6}$	3.96	FAM183A	$9.51 \times 10^{-5}$	-6.10
CNTD2	$4.51 \times 10^{-6}$	3.60	CDHR4	$2.57 \times 10^{-4}$	-5.79
HSPA6	$9.81 \times 10^{-7}$	3.58	CCL3	$9.73 \times 10^{-7}$	-5.68
HSD11B2	$1.01 \times 10^{-6}$	3.47	CCDC19	$6.73 \times 10^{-7}$	-4.95
HIST2H3C	$1.38 \times 10^{-5}$	3.15	NPY2R	$1.01 \times 10^{-6}$	-4.92

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692 PDD overexpressed genes, relative to PD (A) and PDD underexpressed genes, relative

693 to PD (B) ( $p \leq 0.001$ ,  $fc \geq |0.2|$ ).

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704 **Table e-2. Network functions from input of top 20 genes lists (disease vs. controls).**

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**A. PD Overexpressed**

<b>GO Function</b>	<b>FDR</b>	<b>Network Genes</b>	<b>Genome Genes</b>
cell chemotaxis	$5.22 \times 10^{-7}$	9	157
cytokine receptor binding	$5.60 \times 10^{-6}$	8	147
positive regulation of cAMP-mediated signaling	$2.74 \times 10^{-5}$	4	11
chemokine receptor binding	$2.74 \times 10^{-5}$	5	32
positive regulation of homeostatic process	$1.04 \times 10^{-4}$	5	46
regulation of cAMP-mediated signaling	$1.04 \times 10^{-4}$	4	17
positive regulation of release of sequestered calcium ion into cytosol	$1.04 \times 10^{-4}$	4	17
metal ion homeostasis	$2.72 \times 10^{-4}$	8	288
positive regulation of intracellular transport	$3.87 \times 10^{-4}$	6	122
positive regulation of calcium ion transport into cytosol	$4.40 \times 10^{-4}$	4	26

**B. PD Underexpressed**

<b>GO Function</b>	<b>FDR</b>	<b>Network Genes</b>	<b>Genome Genes</b>
neuropeptide hormone activity	$6.57 \times 10^{-2}$	3	15
hormone activity	$9.19 \times 10^{-1}$	3	44

**C. PD-D Overexpressed**

<b>GO Function</b>	<b>FDR</b>	<b>Network Genes</b>	<b>Genome Genes</b>
response to unfolded protein	$3.66 \times 10^{-18}$	14	106
response to topologically incorrect protein	$4.71 \times 10^{-18}$	14	113
protein folding	$3.81 \times 10^{-5}$	7	124
cell chemotaxis	$2.57 \times 10^{-3}$	6	157
COP9 signalosome	$2.57 \times 10^{-3}$	4	34
cytokine receptor binding	$2.57 \times 10^{-3}$	6	147
leukocyte chemotaxis	$6.76 \times 10^{-3}$	5	106
blood microparticle	$6.76 \times 10^{-3}$	5	108
unfolded protein binding	$8.52 \times 10^{-3}$	4	52
defense response to Gram-negative bacterium	$8.73 \times 10^{-3}$	3	16

**D. PD-D Underexpressed**

<b>GO Function</b>	<b>FDR</b>	<b>Network Genes</b>	<b>Genome Genes</b>
neuropeptide hormone activity	$3.04 \times 10^{-2}$	3	15
hormone activity	$3.04 \times 10^{-2}$	4	44
calcium-mediated signaling	$7.66 \times 10^{-2}$	4	72
bicarbonate transport	$1.20 \times 10^{-1}$	3	29
regulation of system process	$1.78 \times 10^{-1}$	5	203
blood microparticle	$1.90 \times 10^{-1}$	4	108
second-messenger-mediated signaling	$2.78 \times 10^{-1}$	4	124
gas transport	$4.05 \times 10^{-1}$	2	10
hydrogen peroxide catabolic process	$4.08 \times 10^{-1}$	2	14
cellular ion homeostasis	$4.08 \times 10^{-1}$	5	292

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707 GeneMANIA measures significance by false discovery rate (FDR). Numbers of genes  
708 involved in a particular cellular function are shown, both within the resulting network and from  
709 the entire genome. The first 10 functions (of 87) are listed from overexpressed PD genes, and  
710 the first 10 (of 56) from overexpressed PD-D genes (A,C). All functions from underexpressed  
711 genes are shown (B,D).

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738 **Table e-3. SpliceSeq-predicted Event Statistics for Genes to be Validated by qRT-PCR**

<b>PD-D</b>						
<b>Gene (exon #)</b>	<b>P-Value</b>	<b>dPSI</b>	<b>Magnitude</b>	<b>% Observed</b>	<b>RPKM<sub>CON</sub></b>	<b>RPKM<sub>PD-D</sub></b>
ATXN2 (21)	$7.81 \times 10^{-3}$	-0.231	1.000	100%	15.9	14.0
DST (104)	$3.21 \times 10^{-3}$	-0.255	1.000	100%	81.4	85.6
HSPH1 (13)	$9.50 \times 10^{-3}$	-0.231	0.962	100%	48.8	99.6
RELA (10.2)	$5.09 \times 10^{-4}$	0.286	0.978	100%	16.1	24.9
SRRM1 (16)	$4.95 \times 10^{-3}$	-0.250	0.994	100%	34.2	25.6
<b>PD</b>						
<b>Gene (exon #)</b>	<b>P-Value</b>	<b>dPSI</b>	<b>Magnitude</b>	<b>% Observed</b>	<b>RPKM<sub>CON</sub></b>	<b>RPKM<sub>PD</sub></b>
LRRFIP1 (18-19)	$8.76 \times 10^{-3}$	-0.257	1.000	100%	12.5	8.7
TRIM9 (8-10)	$1.83 \times 10^{-3}$	-0.264	0.932	100%	22.9	22.6

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740 Top alternatively spliced genes obtained by filtering for  $p < 0.01$ ,  $dPSI > |0.2|$ , magnitude and741 % observed  $> |0.8|$  ( $1.0 = 100\%$ ). The resulting lists contained 40 PD-D genes and 10 PD

742 genes. Finally, genes with the highest RPKM values were chosen for validation by qRT-PCR.

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762 **Table e-4. qRT-PCR fold change values**

<b>PD-D</b>		
<b>Gene</b>	<b>FC<sub>as</sub></b>	<b>FC<sub>ns</sub></b>
ATXN2	0.674	2.201
DST	1.160	1.171
HSPH1	0.952	1.924
RELA	3.467	1.323
SRRM1	0.598	0.780

<b>PD</b>		
<b>Gene</b>	<b>FC<sub>as</sub></b>	<b>FC<sub>ns</sub></b>
LRRFIP1	0.821	1.352
TRIM9	0.930	1.431

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764 Fold change values ( $2^{-\Delta\Delta C_t}$ ) for predicted alternative splice sites (FC<sub>as</sub>) and adjacent sites765 lacking any predicted splicing activity, "no-splice" (FC<sub>ns</sub>).

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