

Table 1S: Gene Ontology (GO) for the differentially expressed miRNAs in exosomes derived from RDBP and NDBP subjects. GO analysis was used to assess (A) cellular components (CC), (B) biological processes (BP), and (C) molecular functions (MF).

(A) Cellular component			
Cellular component ID	Cellular component term	%	p- value
GO:0043226	Organelle	71.487	8.66E-30
GO:0044464	Cell part	85.189	3.99E-19
GO:0005623	Cell	85.306	4.74E-19
GO:0031974	Membrane-enclosed lumen	25.847	8.31E-13
GO:0044422	Organelle part	46.010	6.07E-12
GO:0030054	Cell junction	8.836	4.22E-10
GO:0045202	Synapse	4.866	3.09E-06
GO:0032991	Macromolecular complex	26.625	6.06E-06
GO:0044456	Synapse part	3.931	2.07E-05
(B) Biological process			
Biological process	Biological process term	%	p-value
GO:0032502	Developmental process	32.308	9.69E-12
GO:0065007	Biological regulation	62.398	9.82E-12
GO:0050789	Regulation of biological process	59.264	1.77E-11
GO:0071840	Cellular component organization or biogenesis	35.383	1.88E-10
GO:0008152	Metabolic process	59.031	1.19E-06
GO:0040007	Growth	5.995	1.66E-06
GO:0051179	Localization	32.036	6.75E-05
GO:0022610	Biological adhesion	10.023	7.38E-05
GO:0009987	Cellular process	80.498	1.07E-04
GO:0040011	Locomotion	8.914	4.55E-04
GO:0048511	Rhythmic process	2.083	0.001334
(C) Molecular function			
Molecular function ID	Molecular function term	%	p-value
GO:0005515	protein binding	59.848	1.36E-16
GO:0043167	ion binding	26.158	1.17E-13
GO:1901363	heterocyclic compound binding	34.566	2.02E-13
GO:0003700	transcription factor activity, sequence-specific DNA binding	8.447	9.27E-13
GO:0097159	organic cyclic compound binding	34.819	2.02E-12
GO:0000989	transcription factor activity, transcription factor binding	4.185	4.83E-07
GO:004487	macromolecular complex binding	8.097	3.35E-06
GO:0016740	transferase activity	14.247	2.09E-05

GO:0036094	small molecule binding	14.578	4.07E-04
GO:0097367	carbohydrate derivative binding	12.690	0.001197
GO:0005057	receptor signaling protein activity	1.090	0.002084
GO:0060090	binding, bridging	1.226	0.008638
GO:0016874	ligase activity	2.530	0.01051
GO:0030371	translation repressor activity	0.214	0.029598
GO:0032947	protein complex scaffold	0.506	0.032073
GO:0005487	nucleocytoplasmic transporter activity	0.272	0.032882
GO:0016247	channel regulator activity	0.895	0.043023