

Supplementary Table 2. Gene Ontology (GO) enrichment analysis based on 3 functional groups (biological processes (BP), cellular components (CC), and molecular functions (MF) in EVs isolated from RJ-treated ADSCs.

Molecular functions (MF): Upregulated

Category	Term	Count	%	P-Value	FDR
GOTERM_MF_ALL	GO:0005201~extracellular matrix structural constituent	21	2.928870293	3.00E-11	3.45E-08
GOTERM_MF_ALL	GO:0019838~growth factor binding	23	3.207810321	4.09E-09	1.76E-06
GOTERM_MF_ALL	GO:0005515~protein binding	489	68.20083682	4.58E-09	1.76E-06
GOTERM_MF_ALL	GO:0043394~proteoglycan binding	10	1.394700139	1.79E-06	5.15E-04
GOTERM_MF_ALL	GO:0005178~integrin binding	17	2.370990237	3.21E-06	7.38E-04
GOTERM_MF_ALL	GO:0005488~binding	598	83.40306834	3.86E-06	7.40E-04
GOTERM_MF_ALL	GO:0005539~glycosaminoglycan binding	24	3.347280335	6.49E-06	0.001066585
GOTERM_MF_ALL	GO:0050431~transforming growth factor beta binding	7	0.976290098	1.93E-05	0.002777237
GOTERM_MF_ALL	GO:0048407~platelet-derived growth factor binding	6	0.836820084	3.32E-05	0.004243064
GOTERM_MF_ALL	GO:0008201~heparin binding	19	2.649930265	5.12E-05	0.005893017
GOTERM_MF_ALL	GO:0005509~calcium ion binding	50	6.973500697	9.11E-05	0.00952967
GOTERM_MF_ALL	GO:0050839~cell adhesion molecule binding	36	5.020920502	1.29E-04	0.012384863
GOTERM_MF_ALL	GO:0044877~macromolecular complex binding	78	10.87866109	1.46E-04	0.012902646
GOTERM_MF_ALL	GO:0005518~collagen binding	11	1.534170153	1.67E-04	0.013704086
GOTERM_MF_ALL	GO:0046872~metal ion binding	202	28.17294282	2.40E-04	0.018423467
GOTERM_MF_ALL	GO:1901681~sulfur compound binding	22	3.068340307	3.10E-04	0.0222978
GOTERM_MF_ALL	GO:0016706~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	9	1.255230126	3.52E-04	0.023803772
GOTERM_MF_ALL	GO:0001968~fibronectin binding	7	0.976290098	3.98E-04	0.025453795
GOTERM_MF_ALL	GO:0043169~cation binding	202	28.17294282	4.52E-04	0.027400399
GOTERM_MF_ALL	GO:0019798~procollagen-proline dioxygenase activity	5	0.69735007	5.99E-04	0.03449016
GOTERM_MF_ALL	GO:0001948~glycoprotein binding	13	1.813110181	6.48E-04	0.035489562
GOTERM_MF_ALL	GO:0051213~dioxygenase activity	12	1.673640167	7.88E-04	0.041245965
GOTERM_MF_ALL	GO:0031418~L-ascorbic acid binding	6	0.836820084	0.001057444	0.05291819
GOTERM_MF_ALL	GO:0019955~cytokine binding	12	1.673640167	0.001131235	0.054252141
GOTERM_MF_ALL	GO:0032403~protein complex binding	48	6.694560669	0.001328557	0.061166771
GOTERM_MF_ALL	GO:0043167~ion binding	205	28.59135286	0.001568116	0.069419285
GOTERM_MF_ALL	GO:0046527~glucosyltransferase activity	5	0.69735007	0.00283047	0.116352529
GOTERM_MF_ALL	GO:0031543~peptidyl-proline dioxygenase activity	5	0.69735007	0.00283047	0.116352529
GOTERM_MF_ALL	GO:0015171~amino acid transmembrane transporter activity	10	1.394700139	0.003480864	0.134705433
GOTERM_MF_ALL	GO:0030246~carbohydrate binding	21	2.928870293	0.003511002	0.134705433
GOTERM_MF_ALL	GO:0005520~insulin-like growth factor binding	6	0.836820084	0.004080263	0.151460252
GOTERM_MF_ALL	GO:0050840~extracellular matrix binding	8	1.115760112	0.004225086	0.151460252
GOTERM_MF_ALL	GO:0043395~heparan sulfate proteoglycan binding	5	0.69735007	0.004474065	0.151460252
GOTERM_MF_ALL	GO:0070008~serine-type exopeptidase activity	5	0.69735007	0.004474065	0.151460252
GOTERM_MF_ALL	GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	15	2.092050209	0.005386834	0.177149884
GOTERM_MF_ALL	GO:0004656~procollagen-proline 4-dioxygenase activity	3	0.418410042	0.008586815	0.274429324
GOTERM_MF_ALL	GO:0019899~enzyme binding	90	12.55230126	0.008821794	0.274429324
GOTERM_MF_ALL	GO:0004540~ribonuclease activity	11	1.534170153	0.01053164	0.318328217
GOTERM_MF_ALL	GO:0016891~endoribonuclease activity, producing 5'-phosphomonoesters	6	0.836820084	0.010786099	0.318328217
GOTERM_MF_ALL	GO:0071813~lipoprotein particle binding	5	0.69735007	0.012924162	0.3628222
GOTERM_MF_ALL	GO:0071814~protein-lipid complex binding	5	0.69735007	0.012924162	0.3628222
GOTERM_MF_ALL	GO:0030023~extracellular matrix constituent conferring elasticity	3	0.418410042	0.013944108	0.364765194
GOTERM_MF_ALL	GO:0032296~double-stranded RNA-specific ribonuclease activity	3	0.418410042	0.013944108	0.364765194
GOTERM_MF_ALL	GO:0004525~ribonuclease III activity	3	0.418410042	0.013944108	0.364765194
GOTERM_MF_ALL	GO:0004185~serine-type carboxypeptidase activity	4	0.557880056	0.015433048	0.394646512
GOTERM_MF_ALL	GO:0046943~carboxylic acid transmembrane transporter activity	11	1.534170153	0.015772146	0.394646512
GOTERM_MF_ALL	GO:0046914~transition metal ion binding	72	10.041841	0.01695434	0.415200967
GOTERM_MF_ALL	GO:0005342~organic acid transmembrane transporter activity	11	1.534170153	0.01853036	0.4314852
GOTERM_MF_ALL	GO:0001618~virus receptor activity	8	1.115760112	0.018718596	0.4314852
GOTERM_MF_ALL	GO:0030169~low-density lipoprotein particle binding	4	0.557880056	0.018743927	0.4314852

GOTERM_MF_ALL	GO:0030228~lipoprotein particle receptor activity	4	0.557880056	0.022416263	0.505904295
GOTERM_MF_ALL	GO:0016893~endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	6	0.836820084	0.027168231	0.601358346
GOTERM_MF_ALL	GO:0097493~structural molecule activity conferring elasticity	3	0.418410042	0.027806361	0.603870213
GOTERM_MF_ALL	GO:0097367~carbohydrate derivative binding	105	14.64435146	0.029135019	0.611074053
GOTERM_MF_ALL	GO:0008233~peptidase activity	40	5.578800558	0.02919989	0.611074053
GOTERM_MF_ALL	GO:0005506~iron ion binding	13	1.813110181	0.032436005	0.666675737
GOTERM_MF_ALL	GO:0031545~peptidyl-proline 4-dioxygenase activity	3	0.418410042	0.036133292	0.717058944
GOTERM_MF_ALL	GO:0008035~high-density lipoprotein particle binding	3	0.418410042	0.036133292	0.717058944
GOTERM_MF_ALL	GO:0002020~protease binding	10	1.394700139	0.038652618	0.754053613
GOTERM_MF_ALL	GO:0019199~transmembrane receptor protein kinase activity	8	1.115760112	0.040085763	0.768978555
GOTERM_MF_ALL	GO:0032947~protein complex scaffold	7	0.976290098	0.045473504	0.858032844
GOTERM_MF_ALL	GO:0030165~PDZ domain binding	8	1.115760112	0.049748983	0.923565805
GOTERM_MF_ALL	GO:0003756~protein disulfide isomerase activity	4	0.557880056	0.05195553	0.934387743
GOTERM_MF_ALL	GO:0016864~intramolecular oxidoreductase activity, transposing S-S bonds	4	0.557880056	0.05195553	0.934387743
GOTERM_MF_ALL	GO:0001786~phosphatidylserine binding	5	0.69735007	0.054223898	0.960180101
GOTERM_MF_ALL	GO:0008140~cAMP response element binding protein binding	3	0.418410042	0.055173102	0.962185454
GOTERM_MF_ALL	GO:0003682~chromatin binding	28	3.905160391	0.057925445	0.982081911
GOTERM_MF_ALL	GO:0016758~transferase activity, transferring hexosyl groups	14	1.952580195	0.060932707	0.982081911
GOTERM_MF_ALL	GO:0005035~death receptor activity	4	0.557880056	0.064534487	0.982081911
GOTERM_MF_ALL	GO:0005031~tumor necrosis factor-activated receptor activity	4	0.557880056	0.064534487	0.982081911
GOTERM_MF_ALL	GO:0005198~structural molecule activity	40	5.578800558	0.065014126	0.982081911
GOTERM_MF_ALL	GO:0008238~exopeptidase activity	9	1.255230126	0.067452106	0.982081911
GOTERM_MF_ALL	GO:0008237~metallopeptidase activity	13	1.813110181	0.067539302	0.982081911
GOTERM_MF_ALL	GO:0005102~receptor binding	69	9.623430962	0.0675451	0.982081911
GOTERM_MF_ALL	GO:0004222~metalloendopeptidase activity	9	1.255230126	0.073224736	0.982081911
GOTERM_MF_ALL	GO:0003980~UDP-glucose:glycoprotein glucosyltransferase activity	2	0.278940028	0.076212607	0.982081911
GOTERM_MF_ALL	GO:0004923~leukemia inhibitory factor receptor activity	2	0.278940028	0.076212607	0.982081911
GOTERM_MF_ALL	GO:0048185~activin binding	3	0.418410042	0.076909551	0.982081911
GOTERM_MF_ALL	GO:0016538~cyclin-dependent protein serine/threonine kinase regulator activity	4	0.557880056	0.085729101	0.982081911
GOTERM_MF_ALL	GO:0070011~peptidase activity, acting on L-amino acid peptides	36	5.020920502	0.085966332	0.982081911
GOTERM_MF_ALL	GO:0016787~hydrolase activity	115	16.0390516	0.087352355	0.982081911
GOTERM_MF_ALL	GO:0004521~endoribonuclease activity	6	0.836820084	0.08783706	0.982081911
GOTERM_MF_ALL	GO:0005165~neurotrophin receptor binding	3	0.418410042	0.088623859	0.982081911
GOTERM_MF_ALL	GO:0005041~low-density lipoprotein receptor activity	3	0.418410042	0.088623859	0.982081911
GOTERM_MF_ALL	GO:0019842~vitamin binding	7	0.976290098	0.094950453	0.982081911