

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.

Cellular components (CC): Upregulated

Category	Term	Count	%	P-Value	FDR
GOTERM_CC_ALL	GO:0031012~extracellular matrix	49	6.834030683	8.52E-18	3.79E-15
GOTERM_CC_ALL	GO:0005788~endoplasmic reticulum lumen	31	4.323570432	3.97E-11	5.94E-09
GOTERM_CC_ALL	GO:0005578~proteinaceous extracellular matrix	37	5.160390516	4.00E-11	5.94E-09
GOTERM_CC_ALL	GO:0070062~extracellular exosome	159	22.17573222	9.48E-08	9.52E-06
GOTERM_CC_ALL	GO:0043231~intracellular membrane-bounded organelle	49	6.834030683	1.07E-07	9.52E-06
GOTERM_CC_ALL	GO:0016020~membrane	129	17.9916318	3.46E-07	2.57E-05
GOTERM_CC_ALL	GO:0009986~cell surface	44	6.136680614	4.15E-06	2.64E-04
GOTERM_CC_ALL	GO:0005604~basement membrane	14	1.952580195	7.74E-06	4.31E-04
GOTERM_CC_ALL	GO:0005783~endoplasmic reticulum	58	8.089260809	9.49E-06	4.69E-04
GOTERM_CC_ALL	GO:0005576~extracellular region	95	13.24965132	1.43E-05	6.36E-04
GOTERM_CC_ALL	GO:0043202~lysosomal lumen	14	1.952580195	1.76E-05	7.12E-04
GOTERM_CC_ALL	GO:0005789~endoplasmic reticulum membrane	58	8.089260809	3.06E-05	0.00113423
GOTERM_CC_ALL	GO:0005794~Golgi apparatus	56	7.810320781	1.14E-04	0.003892014
GOTERM_CC_ALL	GO:0005581~collagen trimer	13	1.813110181	1.79E-04	0.005681983
GOTERM_CC_ALL	GO:0001527~microfibril	5	0.69735007	3.56E-04	0.01057379
GOTERM_CC_ALL	GO:0005615~extracellular space	76	10.59972106	4.70E-04	0.013069175
GOTERM_CC_ALL	GO:0005764~lysosome	20	2.789400279	0.001011939	0.026488999
GOTERM_CC_ALL	GO:0044322~endoplasmic reticulum quality control compartment	5	0.69735007	0.001108059	0.027393686
GOTERM_CC_ALL	GO:0016607~nuclear speck	18	2.510460251	0.001706476	0.039967455
GOTERM_CC_ALL	GO:0005577~fibrinogen complex	4	0.557880056	0.003825532	0.084989294
GOTERM_CC_ALL	GO:0005765~lysosomal membrane	21	2.928870293	0.004010731	0.084989294
GOTERM_CC_ALL	GO:0071953~elastic fiber	3	0.418410042	0.008162977	0.165114759
GOTERM_CC_ALL	GO:0000786~nucleosome	10	1.394700139	0.009221211	0.178410392
GOTERM_CC_ALL	GO:0005911~cell-cell junction	14	1.952580195	0.013966119	0.253268809
GOTERM_CC_ALL	GO:0005925~focal adhesion	25	3.486750349	0.014228585	0.253268809
GOTERM_CC_ALL	GO:0009897~external side of plasma membrane	16	2.231520223	0.015832866	0.270454964
GOTERM_CC_ALL	GO:0016021~integral component of membrane	222	30.9623431	0.016409627	0.270454964
GOTERM_CC_ALL	GO:0005605~basal lamina	4	0.557880056	0.01749569	0.278056502
GOTERM_CC_ALL	GO:0010008~endosome membrane	14	1.952580195	0.02399065	0.36813238
GOTERM_CC_ALL	GO:0005681~spliceosomal complex	9	1.255230126	0.026070557	0.386713269
GOTERM_CC_ALL	GO:0005796~Golgi lumen	9	1.255230126	0.029110776	0.417880489
GOTERM_CC_ALL	GO:0005901~caveola	7	0.976290098	0.03606702	0.501557001
GOTERM_CC_ALL	GO:0005791~rough endoplasmic reticulum	6	0.836820084	0.043056693	0.555576664
GOTERM_CC_ALL	GO:0033179~proton-transporting V-type ATPase, V0 domain	3	0.418410042	0.043187999	0.555576664
GOTERM_CC_ALL	GO:0030176~integral component of endoplasmic reticulum membrane	9	1.255230126	0.043697041	0.555576664
GOTERM_CC_ALL	GO:0072546~ER membrane protein complex	3	0.418410042	0.052656925	0.650898102
GOTERM_CC_ALL	GO:0031093~platelet alpha granule lumen	6	0.836820084	0.056496713	0.661606246
GOTERM_CC_ALL	GO:0031594~neuromuscular junction	6	0.836820084	0.056496713	0.661606246
GOTERM_CC_ALL	GO:0005640~nuclear outer membrane	4	0.557880056	0.060623089	0.691724993
GOTERM_CC_ALL	GO:0043234~protein complex	23	3.207810321	0.067362354	0.74940619
GOTERM_CC_ALL	GO:0005584~collagen type I trimer	2	0.278940028	0.074292775	0.787149645
GOTERM_CC_ALL	GO:0034686~integrin alphav-beta8 complex	2	0.278940028	0.074292775	0.787149645
GOTERM_CC_ALL	GO:0005654~nucleoplasm	120	16.73640167	0.080652999	0.81616829
GOTERM_CC_ALL	GO:0008305~integrin complex	4	0.557880056	0.080699786	0.81616829
GOTERM_CC_ALL	GO:0000177~cytoplasmic exosome (RNase complex)	3	0.418410042	0.084743695	0.838020982
GOTERM_CC_ALL	GO:0042470~melanosome	8	1.115760112	0.088587609	0.846956736
GOTERM_CC_ALL	GO:0005770~late endosome	9	1.255230126	0.091977016	0.846956736
GOTERM_CC_ALL	GO:0045121~membrane raft	13	1.813110181	0.092668193	0.846956736
GOTERM_CC_ALL	GO:0031091~platelet alpha granule	3	0.418410042	0.096468506	0.846956736