

Table S1

List of upregulated proteins in presence of Mg was analysed through Gene Ontology (GO) knowledgebase, to describe them in terms of their associated biological processes (dark grey) and molecular functions (light grey). The processes and functions are classified *via* their *term identifier* (ID) and *term description*. *Observed gene count* represent the number of the asked proteins/genes (names can be found under *matching proteins in the network*) in the total number of protein (*background gene count*) contained in the network. *False discovery rate* (FDR) means the probability that a statistically significant result was a false positive. Selection of the term ID was performed when more than 3 proteins were matching with a FDR < 0.05.

	#Term ID	Term description	Observed gene count	Background gene count	False discovery rate	Matching proteins in the network
Biological process	GO:0009987	Cellular process	79	14652	6.10E-06	ACTC1,AHNAK,AKR1B1,AKR1C1,ALDH1L2,AMOT,ANKFY1,ANPEP,ARSB,ATP6V1B2,CNN3,COL1A1,COL6A1,COMT,CRTAP,DDX17,DDX5,DYNC1H1,ENO2,EPB41L2,FABP5,FERMT2,FLNA,FLNB,FN1,FUS,GBA,GCN1L1,HIST2H3A,HMGA1,HNRNPA0,HNRNPA3,HNRNPH2,HNRNPM,HNRNPUL1,LEPREL2,LGMN,MAP1A,MAP1B,MAP4,MMP2,MX2,MYH10,MYH14,MYH9,MYO1B,MYOF,NAMPT,NONO,NPC2,P4HA1,P4HA2,PALLD,PEPD,PLEC,PSAT1,PTGIS,RAB23,RBMX,RECQL,RPLP1,RPS9,SERPINE2,SERPINE2,SFPQ,SOD2,SPARC,SPTAN1,SPTBN1,SRDL,TAGLN,TGM2,THY1,TIMP1,TKT,TOLLIP,TRIM28,VDAC1,VDAC2
	GO:0071840	Cellular component organization or biogenesis	47	5342	6.10E-06	ACTC1,AHNAK,AKR1C1,AMOT,ANKFY1,ARSB,CNN3,COL1A1,COL6A1,DDX17,DYNC1H1,EPB41L2,FERMT2,FLNA,FLNB,FN1,GBA,HIST2H3A,HMGA1,LGMN,MAP1A,MAP1B,MAP4,MMP2,MX2,MYH10,MYH14,MYH9,MYO1B,MYOF,P4HA1,PALLD,PLEC,RAB23,RBMX,RECQL,RPS9,SERPINE2,SFPQ,SOD2,SPARC,SPTAN1,SPTBN1,TGM2,THY1,TIMP1,TRIM28
	GO:0000398	mRNA splicing, via spliceosome	11	284	1.77E-05	DDX17,DDX5,FUS,HNRNPA0,HNRNPA3,HNRNPH2,HNRNPM,HNRNPUL1,NONO,RBMX,SFPQ
	GO:0007010	Cytoskeleton organization	18	953	1.77E-05	ACTC1,AMOT,CNN3,DYNC1H1,EPB41L2,FLNA,FLNB,MAP1A,MAP1B,MAP4,MYH10,MYH14,MYH9,MYO1B,PALLD,SPTAN1,SPTBN1,THY1
	GO:0009888	Tissue development	23	1626	2.80E-05	ACTC1,AKR1C1,CNN3,COL1A1,COL6A1,DDX17,DDX5,FABP5,FLNA,FLNB,FN1,MMP2,MYH10,MYH14,PALLD,PTGIS,SERPINE2,TAGLN,TGM2,TIMP1,TOLLIP,TRIM28,VDAC1
	GO:0016071	mRNA metabolic process	14	667	1.50E-04	DDX17,DDX5,FLNA,FUS,HNRNPA0,HNRNPA3,HNRNPH2,HNRNPM,HNRNPUL1,NONO,RBMX,RPLP1,RPS9,SFPQ
	GO:0000380	Alternative mRNA splicing, via spliceosome	4	16	2.10E-04	DDX17,DDX5,HNRNPM,SFPQ
	GO:0030036	Actin cytoskeleton organization	11	418	2.10E-04	ACTC1,AMOT,CNN3,EPB41L2,FLNA,FLNB,MYH10,MYH14,MYH9,MYO1B,PALLD
	GO:0048518	Positive regulation of biological process	41	5459	9.60E-04	ACTC1,AKR1B1,AMOT,ANKFY1,ARSB,COL1A1,COMT,DDX17,DDX5,DYNC1H1,EPB41L2,FABP5,FLNA,FN1,FUS,GBA,GCN1L1,HMGA1,HNRNPA0,LGMN,MAP1A,MAP1B,MMP2,MYH10,MYH9,NAMPT,NONO,PTGIS,RBMX,RPLP1,RPS9,SERPINE2,SFPQ,SOD2,SPARC,SPTBN1,TGM2,THY1,TIMP1,TOLLIP,TRIM28
	GO:0065008	Regulation of biological quality	31	3559	1.30E-03	AKR1B1,AKR1C1,AMOT,ANPEP,COL1A1,COMT,CRTAP,FABP5,FERMT2,FLNA,FLNB,FN1,GBA,HIST2H3A,HNRNPA0,LGMN,MAP1A,MAP1B,MYH10,MYH14,MYH9,NPC2,PTGIS,RPS9,SERPINE2,SERPINE2,SOD2,SPTAN1,SPTBN1,TGM2,THY1
	GO:0048519	Negative regulation of biological process	38	4953	1.50E-03	ACTC1,AKR1B1,AMOT,COL1A1,COMT,CRTAP,DDX17,DDX5,FABP5,FLNA,FN1,GBA,HIST2H3A,HMGA1,HNRNPA0,LEPREL2,LGMN,MAP1A,MAP1B,MAP4,MYH9,NONO,PTGIS,RAB23,RBMX,RPLP1,RPS9,SERPINE2,SERPINE2,SFPQ,SOD2,SPARC,SPTAN1,SPTBN1,THY1,TIMP1,TRIM28,VDAC2
	GO:0007018	Microtubule-based movement	8	276	1.60E-03	DYNC1H1,MAP1A,MAP1B,MAP4,MYH10,MYH14,MYH9,MYO1B
	GO:0042060	Wound healing	10	461	1.60E-03	COL1A1,FLNA,FN1,HIST2H3A,MYH10,MYOF,SERPINE2,SERPINE2,SPARC,TIMP1
GO:0044085	Cellular component	25	2556	1.60E-03	ACTC1,AHNAK,AKR1C1,AMOT,COL1A1,COL6A1,DDX17,DYNC1H1,FERMT2,FLNA,FN1,HIST2H3A,HMGA1,MX2,MYH10,MYO1B,PLEC,RAB23,RBMX,RPS9,SOD2,SPTBN1,TGM2,THY1,TRIM28	

		biogenesis				
GO:0007044	Cell-substrate junction assembly	4	40	2.10E-03	FERMT2, FN1, PLEC, THY1	
GO:0050789	Regulation of biological process	63	11116	2.10E-03	ACTC1, AHNAK, AKR1B1, AMOT, ANKFY1, ANPEP, ARSB, ATP6V1B2, COL1A1, COMT, CRTAP, DDX17, DDX5, DYNC1H1, EPB41L2, FABP5, FERMT2, FLNA, FLNB, FN1, FUS, GBA, GCN1L1, HIST2H3A, HMGA1, HNRNPA0, HNRNPM, HNRNPUL1, LEPREL2, LGMN, MAP1A, MAP1B, MAP4, MMP2, MX2, MYH10, MYH14, MYH9, MYL9, MYOF, NAMPT, NONO, NPC2, PTGIS, RAB23, RBMX, RPLP1, RPS9, SERPINB2, SERPINE2, SFPQ, SOD2, SPARC, SPTAN1, SPTBN1, TGM2, THY1, TIMP1, TKT, TOLLIP, TRIM28, VDAC1, VDAC2	
GO:0051128	Regulation of cellular component organization	23	2306	2.20E-03	AMOT, ANKFY1, ARSB, DYNC1H1, FERMT2, FLNA, FN1, GBA, HMGA1, MAP1B, MAP4, MYH10, MYH14, MYH9, SERPINE2, SFPQ, SPARC, SPTAN1, SPTBN1, THY1, TRIM28, VDAC1, VDAC2	
GO:0000904	Cell morphogenesis involved in differentiation	10	498	2.30E-03	FERMT2, FLNA, FLNB, FN1, MAP1B, MYH10, MYH9, PALLD, SPTAN1, SPTBN1	
GO:0032989	Cellular component morphogenesis	12	720	2.30E-03	ACTC1, FERMT2, FLNA, FLNB, FN1, MAP1B, MYH10, MYH14, MYH9, PALLD, SPTAN1, SPTBN1	
GO:0030154	Cell differentiation	29	3457	0.0031	ACTC1, AKR1C1, AMOT, ANPEP, ARSB, CNN3, COL1A1, COL6A1, DDX17, DDX5, FERMT2, FLNA, FLNB, FN1, MAP1B, MAP4, MMP2, MYH10, MYH9, MYOF, PALLD, SERPINE2, SPTAN1, SPTBN1, TAGLN, THY1, TOLLIP, TRIM28, VDAC1	
GO:0050794	Regulation of cellular process	60	10484	0.0034	ACTC1, AHNAK, AKR1B1, AMOT, ANKFY1, ANPEP, ARSB, ATP6V1B2, COL1A1, COMT, CRTAP, DDX17, DDX5, DYNC1H1, FABP5, FERMT2, FLNA, FLNB, FN1, FUS, GBA, GCN1L1, HIST2H3A, HMGA1, HNRNPA0, HNRNPM, HNRNPUL1, LEPREL2, LGMN, MAP1A, MAP1B, MAP4, MMP2, MX2, MYH10, MYH14, MYH9, MYL9, MYOF, NAMPT, NONO, NPC2, PTGIS, RBMX, RPLP1, RPS9, SERPINB2, SERPINE2, SFPQ, SOD2, SPARC, SPTAN1, SPTBN1, TGM2, THY1, TIMP1, TOLLIP, TRIM28, VDAC1, VDAC2	
GO:0006887	Exocytosis	12	774	0.0036	ANPEP, ARSB, DYNC1H1, FABP5, FLNA, FN1, MYH10, NPC2, SPARC, SPTAN1, TIMP1, TOLLIP	
GO:0022604	Regulation of cell morphogenesis	9	442	0.0039	FERMT2, FLNA, FN1, MAP1B, MYH10, MYH14, MYH9, SPARC, THY1	
GO:0032963	Collagen metabolic process	4	54	0.0039	COL1A1, LEPREL2, MMP2, PEPD	
GO:0048522	Positive regulation of cellular process	36	4898	0.0039	AKR1B1, AMOT, ANKFY1, ARSB, COL1A1, COMT, DDX17, DDX5, DYNC1H1, FABP5, FLNA, FN1, FUS, GBA, GCN1L1, HMGA1, LGMN, MAP1B, MMP2, MYH10, MYH9, NAMPT, PTGIS, RAB23, RBMX, RPLP1, RPS9, SERPINE2, SFPQ, SOD2, SPARC, SPTBN1, TGM2, THY1, TIMP1, TOLLIP, TRIM28	
GO:0006396	RNA processing	12	825	0.0052	DDX17, DDX5, FUS, HNRNPA0, HNRNPA3, HNRNPH2, HNRNPM, HNRNPUL1, NONO, RBMX, RPS9, SFPQ	
GO:0030198	Extracellular matrix organization	7	296	0.008	COL1A1, COL6A1, FN1, MMP2, P4HA1, SPARC, TIMP1	
GO:0030334	Regulation of cell migration	11	753	0.0084	AMOT, ARSB, COL1A1, FLNA, FN1, LGMN, SERPINE2, SOD2, SPARC, THY1, TIMP1	
GO:0008360	Regulation of cell shape	5	143	0.0103	FERMT2, FN1, MYH10, MYH14, MYH9	
GO:0044237	Cellular metabolic process	51	8797	0.0148	AKR1B1, AKR1C1, ALDH1L2, ANPEP, ARSB, ATP6V1B2, COMT, CRTAP, DDX17, DDX5, ENO2, FABP5, FLNA, FN1, FUS, GBA, GCN1L1, HIST2H3A, HMGA1, HNRNPA0, HNRNPA3, HNRNPH2, HNRNPM, HNRNPUL1, LEPREL2, LGMN, MMP2, NAMPT, NONO, P4HA1, P4HA2, PEPD, PSAT1, PTGIS, RAB23, RBMX, RECQL, RPLP1, RPS9, SFPQ, SOD2, SPTAN1, SPTBN1, SQRDL, TGM2, THY1, TIMP1, TKT, TOLLIP, TRIM28, VDAC1	
GO:0008152	Metabolic process	54	9569	0.0154	AKR1B1, AKR1C1, ALDH1L2, ANPEP, ARSB, ATP6V1B2, COL1A1, COMT, CRTAP, DDX17, DDX5, ENO2, FABP5, FLNA, FN1, FUS, GBA, GCN1L1, HIST2H3A, HMGA1, HNRNPA0, HNRNPA3, HNRNPH2, HNRNPM, HNRNPUL1, LEPREL2, LGMN, MMP2, MYH9, NAMPT, NONO, NPC2, P4HA1, P4HA2, PEPD, PSAT1, PTGIS, RAB23, RBMX, RECQL, RPLP1, RPS9, SFPQ, SOD2, SPTAN1, SPTBN1, SQRDL, TGM2, THY1, TIMP1, TKT, TOLLIP, TRIM28, VDAC1	
GO:0007051	Spindle organization	4	123	0.028	DYNC1H1, FLNA, MAP4, MYH9	
GO:0042127	Regulation of cell population proliferation	15	1594	0.0289	AKR1B1, COMT, FLNA, FN1, HMGA1, LEPREL2, LGMN, MMP2, NAMPT, RPS9, SERPINE2, SOD2, SPARC, TGM2, TIMP1	

	GO:0048762	Mesenchymal cell differentiation	4	130	0.0317	DDX17,DDX5,FN1,TRIM28
	GO:0044238	Primary metabolic process	49	8808	0.0367	AKR1B1,AKR1C1,ANPEP,ARSB,ATP6V1B2,COMT,CRTAP,DDX17,DDX5,ENO2,FABP5,FLNA,FN1,FUS,GBA,GCN1L1,HIST2H3A,HMGA1,HNRNPA0,HNRNPA3,HNRNPH2,HNRNPM,HNRNPUL1,LEPREL2,LGMN,MMP2,MYH9,NAMPT,NONO,NPC2,P4HA1,P4HA2,PEPD,PSAT1,PTGIS,RAB23,RBMX,RECQL,RPLP1,RPS9,SFPQ,SPTAN1,SPTBN1,TGM2,THY1,TIMP1,TKT,TOLLIP,TRIM28
Molecular function	GO:0003779	Actin binding	15	413	6.94E-08	CNN3,EPB41L2,FERMT2,FLNA,FLNB,MAP1A,MYH10,MYH14,MYH9,MYO1B,PALLD,PLEC,SPTAN1,SPTBN1,TAGLN
	GO:0008092	Cytoskeletal protein binding	20	882	7.49E-08	ACTC1,CNN3,EPB41L2,FERMT2,FLNA,FLNB,FUS,MAP1A,MAP1B,MAP4,MX2,MYH10,MYH14,MYH9,MYO1B,PALLD,PLEC,SPTAN1,SPTBN1,TAGLN
	GO:0005515	Protein binding	51	6605	4.58E-06	ACTC1,AHNAK,AMOT,ANKFY1,CNN3,COL1A1,COL6A1,DDX5,DYNC1H1,EPB41L2,FABP5,FERMT2,FLNA,FLNB,FN1,FUS,GBA,GCN1L1,HIST2H3A,HMGA1,HNRNPA0,HNRNPM,HNRNPUL1,MAP1A,MAP1B,MAP4,MX2,MYH10,MYH14,MYH9,MYO1B,NAMPT,NONO,NPC2,P4HA1,P4HA2,RAB23,RECQL,RBMX,SERPINE2,SFPQ,SOD2,SPTAN1,SPTBN1,TAGLN,TGM2,THY1,TIMP1,TKT,TOLLIP,TRIM28,VDAC1
	GO:0008017	Microtubule binding	9	253	9.71E-05	CNN3,MAP1A,MAP1B,MAP4,MX2,MYH10,MYH14,MYH9,MYO1B
	GO:0005516	Calmodulin binding	8	194	1.10E-04	CNN3,DDX5,MYH10,MYH14,MYH9,MYO1B,SPTAN1,SPTBN1
	GO:0016887	ATPase activity	10	392	2.90E-04	ACTC1,ATP6V1B2,DDX17,DDX5,DYNC1H1,MYH10,MYH14,MYH9,MYO1B,RECQL
	GO:0051015	Actin filament binding	7	158	2.90E-04	FERMT2,FLNA,MYH10,MYH14,MYH9,MYO1B,TAGLN
	GO:0043168	Anion binding	25	2696	0.0014	ACTC1,AKR1C1,ANKFY1,ATP6V1B2,DDX17,DDX5,DYNC1H1,FABP5,FERMT2,FN1,LEPREL2,MX2,MYH10,MYH14,MYH9,MYO1B,MYOF,P4HA1,P4HA2,RAB23,RECQL,SERPINE2,SPTBN1,TGM2,THY1
	GO:0017111	Nucleoside-triphosphatase activity	12	778	0.0022	ACTC1,ATP6V1B2,DDX17,DDX5,DYNC1H1,MX2,MYH10,MYH14,MYH9,MYO1B,RAB23,RECQL
	GO:0043167	Ion binding	41	6066	0.0027	ACTC1,AKR1C1,ANKFY1,ANPEP,ARSB,ATP6V1B2,COL1A1,COMT,DDX17,DDX5,DYNC1H1,ENO2,FABP5,FERMT2,FN1,FUS,LEPREL2,MMP2,MX2,MYH10,MYH14,MYH9,MYL9,MYO1B,MYOF,P4HA1,P4HA2,PEPD,PTGIS,RAB23,RECQL,SERPINE2,SOD2,SPARC,SPTAN1,SPTBN1,TGM2,THY1,TIMP1,TKT,TRIM28
	GO:0005543	Phospholipid binding	6	382	0.0421	ANKFY1,FERMT2,MYO1B,MYOF,SPTBN1,THY1