

Supplementary Table S3. The MRM transitions of 119 ECM proteins

Gene name	Peptide sequence	Targetion	Light		Heavy		CE
			Q1 Mass (Da)	Q3 Mass (Da)	Q1 Mass (Da)	Q3 Mass (Da)	
COL11A2	GANEDELSPETSPYVK	+2y9	868.4	1007.5	872.4	1015.5	40.1
		+2y8	868.4	920.5	872.4	928.5	40.1
		+2b8	868.4	816.3	872.4	816.3	40.1
COL12A1	DLSFSEVTSYGFK	+2y7	740.4	801.4	744.4	809.4	35.5
		+2y6	740.4	702.3	744.4	710.4	35.5
		+2y5	740.4	601.3	744.4	609.3	35.5
COL14A1	IGILITDGK	+2y6	465.3	646.4	469.3	654.4	25.6
		+2y5	465.3	533.3	469.3	541.3	25.6
		+2y4	465.3	420.2	469.3	428.2	25.6
COL15A1	GGVLFAITDAFQK	+2y8	683.9	893.5	687.9	901.5	33.5
		+2y7	683.9	822.4	687.9	830.5	33.5
		+2y6	683.9	709.4	687.9	717.4	33.5
COL18A1	TEAPSATGQASSLLGGR	+2y11	801.9	1046.6	806.9	1056.6	37.7
		+2y10	801.9	945.5	806.9	955.5	37.7
		+2b2	801.9	231.1	806.9	231.1	37.7
COL1A1	GVQGPPGPAGPR	+2y9	545.3	805.4	550.3	815.4	28.5
		+2y8	545.3	748.4	550.3	758.4	28.5
		+2y7	545.3	651.4	550.3	661.4	28.5
COL1A2	GPAGPSGPAGK	+2y9	448.2	741.4	452.2	749.4	25
		+2y8	448.2	670.4	452.2	678.4	25
		+2y7	448.2	613.3	452.2	621.3	25
COL3A1	NGETGPQGPPGPTGPGGDK	+2y12	860.4	1036.5	864.4	1044.5	39.8
		+2y11	860.4	979.5	864.4	987.5	39.8
		+2y7	860.4	631.3	864.4	639.3	39.8
COL6A1	VFSVAITPDHLEPR	+2y9	790.9	1077.6	795.9	1087.6	37.3
		+2y8	790.9	964.5	795.9	974.5	37.3
		+2y7	790.9	863.4	795.9	873.4	37.3
COL6A2	YGGLHFSDQVEVFSPPGSDR	+2y8	1097.5	862.4	735.3	872.4	48.4
		+3b8	732.0	877.4	735.3	877.4	37.4
		+3b9	732.0	1005.4	735.3	1005.4	37.4
COL6A3	ALNLGYALDYAQR	+2y9	734.4	1056.5	739.4	1066.5	35.3
		+2y7	734.4	836.4	739.4	846.4	35.3
		+2y5	734.4	652.3	739.4	662.3	35.3
ABI3BP	FTEAIVDAEPK	+2y9	610.3	971.5	614.3	979.5	30.8
		+2y6	610.3	658.3	614.3	666.4	30.8
		+2y2	610.3	244.2	614.3	252.2	30.8
AEBP1	YLSPDATVSTEVR	+2y10	719.4	1074.5	724.4	1084.6	34.8
		+2y7	719.4	791.4	724.4	801.4	34.8

		+2y5	719.4	591.3	724.4	601.3	34.8
		+2y5	595.3	587.3	600.3	597.3	30.3
CILP	LFNLDVPESR	+2y4	595.3	488.2	600.3	498.3	30.3
		+2y2	595.3	262.2	600.3	272.2	30.3
		+2y8	652.3	816.4	657.3	826.4	32.3
CILP2	DLTSAASAPSDLR	+2y7	652.3	745.4	657.3	755.4	32.3
		+2y5	652.3	587.3	657.3	597.3	32.3
		+2y9	807.4	992.5	812.4	1002.5	37.9
COMP	NALWHTGDTESQVR	+2y8	807.4	891.4	812.4	901.4	37.9
		+2y6	807.4	719.4	812.4	729.4	37.9
		+2y7	643.3	898.4	648.3	908.5	32
EFEMP1	SGNENGEFYLR	+2y6	643.3	784.4	648.3	794.4	32
		+2y4	643.3	598.3	648.3	608.3	32
		+2y7	589.8	857.4	594.8	867.4	30.1
FBLN1	TGYFDFGISR	+2y6	589.8	694.4	594.8	704.4	30.1
		+2y5	589.8	547.3	594.8	557.3	30.1
		+2y6	565.2	700.3	570.3	710.4	29.2
FBLN2	GNEEGYFGTR	+2y4	565.2	480.3	570.3	490.3	29.2
		+2y3	565.2	333.2	570.3	343.2	29.2
		+2y9	662.3	932.5	666.3	940.5	32.7
FBN1	DYLSGELGDNLK	+2y8	662.3	845.4	666.3	853.5	32.7
		+2b2	662.3	279.1	666.3	279.1	32.7
		+2y9	797.4	973.5	801.4	981.5	37.6
FGA	HPDEAAFFDTASTGK	+2y6	797.4	564.3	801.4	572.3	37.6
		+2b2	797.4	235.1	801.4	235.1	37.6
		+2y8	768.4	903.5	772.4	911.5	36.5
FGB	AHYGGFTVQNEANK	+2y6	768.4	703.3	772.4	711.4	36.5
		+2b3	768.4	372.2	772.4	372.2	36.5
		+2y8	746.4	928.5	751.4	938.5	35.7
FGG	YEASILTHDSSIR	+2y7	746.4	815.4	751.4	825.4	35.7
		+2y6	746.4	714.4	751.4	724.4	35.7
		+2y8	678.4	966.5	683.4	976.5	33.3
FN1	IYLYTLNDNAR	+2y7	678.4	803.4	683.4	813.4	33.3
		+2y5	678.4	589.3	683.4	599.3	33.3
		+2y10	927.4	974.5	932.4	984.5	42.2
FNDC1	TPHSGAAEEDSSASAPPSR	+2b10	927.4	995.4	932.4	995.4	42.2
		+2b11	927.4	1082.4	932.4	1082.4	42.2
		+2y8	657.8	868.5	662.8	878.5	32.5
IGFALS	DFALQNPSAVPR	+2y7	657.8	740.4	662.8	750.4	32.5
		+2y6	657.8	626.4	662.8	636.4	32.5
		+2y8	773.4	858.4	778.4	868.5	36.7
LAMC1	NTIEETGNLAEQAR	+2y5	773.4	574.3	778.4	584.3	36.7

		+2y4	773.4	503.3	778.4	513.3	36.7
		+2y8	495.3	819.4	500.3	829.5	26.7
LRG1	VAAGAFQGLR	+2y7	495.3	748.4	500.3	758.4	26.7
		+2y5	495.3	620.4	500.3	630.4	26.7
		+2y8	510.3	774.4	515.3	784.4	27.2
LTBP2	SSAAGEGTLAR	+2y7	510.3	703.4	515.3	713.4	27.2
		+2y3	510.3	359.2	515.3	369.2	27.2
		+2y8	582.8	895.5	586.8	903.5	29.8
MATN2	VGLLQYGSTVK	+2y7	582.8	782.4	586.8	790.4	29.8
		+2y6	582.8	654.3	586.8	662.4	29.8
		+2y9	1043.5	1062.6	1048.5	1072.6	46.4
MFGE8	NAVHVNLFETPVEAQYVR	+2y8	1043.5	961.5	1048.5	971.5	46.4
		+2b9	1043.5	1024.5	1048.5	1024.5	46.4
		+2y6	638.3	728.4	643.3	738.4	31.8
MGP	NANTFISPQQR	+2y5	638.3	615.3	643.3	625.3	31.8
		+2y4	638.3	528.3	643.3	538.3	31.8
		+2y7	547.8	908.5	551.8	916.5	28.6
MXRA5	WFLEWDAK	+2y6	547.8	761.4	551.8	769.4	28.6
		+2y5	547.8	648.3	551.8	656.3	28.6
		+2y10	829.4	967.5	834.4	977.5	38.7
PCOLCE	YDALEVFAAGSGTSGQR	+2y9	829.4	820.4	834.4	830.4	38.7
		+2y8	829.4	749.4	834.4	759.4	38.7
		+2y8	917.9	1022.5	921.9	1030.5	41.9
POSTN	FIEGGDGHLFEDEEIK	+2y7	917.9	909.4	921.9	917.4	41.9
		+2b8	917.9	813.4	921.9	813.4	41.9
		+2y8	772.4	968.5	777.4	978.5	36.7
SMOC1	FSEPDPSHTLEER	+2y2	772.4	304.2	777.4	314.2	36.7
		+2b5	772.4	576.2	777.4	576.2	36.7
		+2y8	755.4	968.5	760.4	978.5	36.1
SMOC2	LSEPDPSHTLEER	+2y2	755.4	304.2	760.4	314.2	36.1
		+2b5	755.4	542.2	760.4	542.2	36.1
		+2y8	648.4	843.4	653.4	853.4	32.2
SRPX2	LLHISAPDSPNR	+2y7	648.4	756.4	653.4	766.4	32.2
		+2y6	648.4	685.3	653.4	695.3	32.2
		+2y7	540.3	851.5	544.3	859.5	28.3
TGFBI	DLLNNHILK	+2y6	540.3	738.4	544.3	746.4	28.3
		+2b8	540.3	933.5	544.3	933.5	28.3
		+2y9	651.9	960.5	655.9	968.6	32.3
THBS1	AGTLDLSLTVQGK	+2y7	651.9	732.4	655.9	740.4	32.3
		+2y5	651.9	532.3	655.9	540.3	32.3
		+2y8	700.4	1012.6	705.4	1022.6	34.1
THBS2	GTTQIDPNWVIR	+2y7	700.4	899.5	705.4	909.5	34.1

		+2y6	700.4	784.4	705.4	794.5	34.1
		+2y7	623.8	893.5	627.8	901.5	31.3
THBS4	KPQDFLEELK	+2y4	623.8	518.3	627.8	526.3	31.3
		+2b8	623.8	987.5	627.8	987.5	31.3
		+2y7	967.5	860.5	971.5	868.5	43.7
TNC	DLQVSETAETSLTLLWK	+2y6	967.5	773.5	971.5	781.5	43.7
		+2y3	967.5	446.3	971.5	454.3	43.7
		+2y7	607.8	786.4	612.8	796.4	30.7
TNXB	EVTVQGLEPSR	+2y4	607.8	488.2	612.8	498.3	30.7
		+2y3	607.8	359.2	612.8	369.2	30.7
		+2y10	823.9	1076.5	828.9	1086.5	38.5
VTN	DVWGIEGPIDAAFTR	+2y9	823.9	947.5	828.9	957.5	38.5
		+2y8	823.9	890.5	828.9	900.5	38.5
		+2y8	584.8	926.5	589.8	936.5	29.9
ACAN	LEGEVFFATR	+2y6	584.8	740.4	589.8	750.4	29.9
		+2y5	584.8	641.3	589.8	651.3	29.9
		+2y9	990.1	1010.6	994.1	1018.6	44.5
ASPEN	LYLSHNQLSEIPLNLPK	+2y6	990.1	681.4	994.1	689.4	44.5
		+2b8	990.1	969.5	994.1	969.5	44.5
		+2y9	791.5	1033.6	795.5	1041.6	37.3
BGN	GLQHLYALVLVNNK	+2b5	791.5	549.3	795.5	549.3	37.3
		+2b9	791.5	995.6	795.5	995.6	37.3
		+2y10	683.4	1010.5	687.4	1018.5	33.5
CHAD	NQLSSYPSAALSK	+2y9	683.4	923.5	687.4	931.5	33.5
		+2y7	683.4	673.4	687.4	681.4	33.5
		+2y8	624.9	884.6	628.9	892.6	31.4
DCN	NLHALILVNNK	+2y7	624.9	813.5	628.9	821.5	31.4
		+2y6	624.9	700.4	628.9	708.4	31.4
		+2y7	629.8	869.4	634.8	879.4	31.5
FMOD	LYLDHNNLTR	+2y6	629.8	754.4	634.8	764.4	31.5
		+2y5	629.8	617.3	634.8	627.3	31.5
		+2y8	565.3	816.4	569.3	824.5	29.2
HAPLN1	DPTAFGSGIHK	+2y7	565.3	745.4	569.3	753.4	29.2
		+2y6	565.3	598.3	569.3	606.3	29.2
		+2y6	584.3	741.4	589.3	751.4	29.9
HSPG2	AFAHLQVPER	+2y5	584.3	628.3	589.3	638.4	29.9
		+2b7	584.3	767.4	589.3	767.4	29.9
		+2y7	649.3	853.5	653.3	861.5	32.2
LUM	SLEDLQLTHNK	+2y5	649.3	612.3	653.3	620.4	32.2
		+2y4	649.3	499.3	653.3	507.3	32.2
		+2y9	907.0	1015.6	911.0	1023.6	41.5
OGN	LSLLEELSLAENQLLK	+2y7	907.0	815.5	911.0	823.5	41.5

		+2y6	907.0	744.4	911.0	752.4	41.5
		+2y8	575.3	923.5	579.3	931.5	29.6
OMD	LLLGYNEISK	+2y7	575.3	810.4	579.3	818.4	29.6
		+2y6	575.3	753.4	579.3	761.4	29.6
		+2y9	830.9	1042.6	834.9	1050.6	38.8
PRELP	LSDGVFKPDTFHGLK	+2y8	830.9	914.5	834.9	922.5	38.8
		+2y6	830.9	702.4	834.9	710.4	38.8
		+2y6	826.0	699.4	831.0	709.4	38.6
PRG4	GLPNVVTSAISLPNIR	+2y5	826.0	612.4	831.0	622.4	38.6
		+2y4	826.0	499.3	831.0	509.3	38.6
		+2y8	657.9	930.5	662.9	940.5	32.5
VCAN	LATVGELQAAWR	+2y4	657.9	503.3	662.9	513.3	32.5
		+2y2	657.9	361.2	662.9	371.2	32.5
		+2y9	802.9	978.5	806.9	986.5	37.8
A2M	IAQWQSFQLEGGLK	+2y4	802.9	374.2	806.9	382.3	37.8
		+2b3	802.9	313.2	806.9	313.2	37.8
		+2y9	634.9	956.6	638.9	964.6	31.7
AGT	ALQDQLVLVAAK	+2y3	634.9	289.2	638.9	297.2	31.7
		+2b9	634.9	980.6	638.9	980.6	31.7
		+2y4	511.3	565.3	516.3	575.3	27.3
AMBP	ETLLQDFR	+2y3	511.3	437.2	516.3	447.2	27.3
		+2y2	511.3	322.2	516.3	332.2	27.3
		+2y6	927.5	708.4	932.5	718.4	42.2
CD109	SPVTLTAYIVTSSLGYR	+2b2	927.5	185.1	932.5	185.1	42.2
		+2b3	927.5	284.2	932.5	284.2	42.2
		+2y9	663.9	1012.5	667.9	1020.6	32.8
CSTB	SQVVAGTNYFIK	+2y8	663.9	913.5	667.9	921.5	32.8
		+2y7	663.9	842.4	667.9	850.5	32.8
		+2y8	521.8	856.6	525.8	864.6	27.6
CTSD	VSTLPAITLK	+2y6	521.8	642.4	525.8	650.4	27.6
		+2b2	521.8	187.1	525.8	187.1	27.6
		+2y7	609.3	830.4	614.3	840.4	30.8
CTSZ	NSWGEPWGER	+2y5	609.3	644.3	614.3	654.3	30.8
		+2b3	609.3	388.2	614.3	388.2	30.8
		+2y8	1015.0	1055.6	1020.0	1065.6	45.4
F12	NKPGVYTDVAYYLAWIR	+2y7	1015.0	984.5	1020.0	994.5	45.4
		+2b8	1015.0	875.4	1020.0	875.4	45.4
		+2y10	846.4	1083.5	850.4	1091.6	39.3
F13A1	DGTHVVENVDATHIGK	+2y6	846.4	626.4	850.4	634.4	39.3
		+2b5	846.4	510.2	850.4	510.2	39.3
		+2y8	781.4	1072.5	786.4	1082.5	37
F2	TATSEYQTFFNPR	+2y7	781.4	909.5	786.4	919.5	37

		+2y4	781.4	533.3	786.4	543.3	37
		+2y9	912.9	1001.5	917.0	1009.5	41.7
HRG	ADLFYDVEALDLESPK	+2y6	912.9	688.4	917.0	696.4	41.7
		+2y3	912.9	331.2	917.0	339.2	41.7
		+2y8	599.3	920.5	603.3	928.5	30.4
HTRA1	YNFIADVVEK	+2y6	599.3	660.4	603.3	668.4	30.4
		+2b2	599.3	278.1	603.3	278.1	30.4
		+2y9	1003.5	973.5	1008.5	983.5	45
ITIH1	FAHYVVTSQVVNTANEAR	+2y8	1003.5	874.4	1008.5	884.4	45
		+2y7	1003.5	775.4	1008.5	785.4	45
		+2y8	902.9	1019.5	907.9	1029.5	41.4
ITIH2	AEDHFSVIDFNQIR	+2y6	902.9	791.4	907.9	801.4	41.4
		+2b7	902.9	786.3	907.9	786.3	41.4
		+2y5	937.9	697.4	942.9	707.4	42.6
KNG1	YNSQNSNNQFVLYR	+2y4	937.9	550.3	942.9	560.3	42.6
		+2y3	937.9	451.3	942.9	461.3	42.6
		+2y8	687.9	919.5	692.9	929.5	33.6
MMP2	QDIVFDGIAQIR	+2y6	687.9	657.4	692.9	667.4	33.6
		+2y4	687.9	487.3	692.9	497.3	33.6
		+2y8	597.8	966.5	602.8	976.5	30.4
MMP3	LDSDTLEVM[Oxi]R	+2y5	597.8	663.3	602.8	673.4	30.4
		+2y4	597.8	550.3	602.8	560.3	30.4
		+2y8	678.3	1045.5	683.3	1055.5	33.3
P4HA2	YFEQLLEER	+2y4	678.3	562.2	683.3	572.3	33.3
		+2y3	678.3	433.2	683.3	443.2	33.3
		+2y9	649.8	1074.6	654.8	1084.6	32.3
PLG	HSIFTPETNPR	+2y8	649.8	961.5	654.8	971.5	32.3
		+2y6	649.8	713.4	654.8	723.4	32.3
		+2y9	1029.5	1010.4	1033.5	1018.5	45.9
SERPINA1	LYHSEAF TVNFGDTEAK	+2y5	1029.5	577.3	1033.5	585.3	45.9
		+2b7	1029.5	848.4	1033.5	848.4	45.9
		+2y11	954.5	1005.5	958.5	1013.5	43.2
SERPINA3	AVLDVFEEGTEASAATAVK	+2y8	954.5	718.4	958.5	726.4	43.2
		+2b8	954.5	903.4	958.5	903.4	43.2
		+2y9	596.8	1008.5	601.8	1018.5	30.3
SERPINA4	IAPANADFAFR	+2y8	596.8	911.4	601.8	921.4	30.3
		+2y7	596.8	840.4	601.8	850.4	30.3
		+2y8	581.3	892.4	586.3	902.4	29.8
SERPINA5	AVVEVDESGTR	+2y7	581.3	763.4	586.3	773.4	29.8
		+2y6	581.3	664.3	586.3	674.3	29.8
		+2y7	638.4	748.4	642.4	756.4	31.8
SERPINE2	DIVTVANAVFVK	+2y3	638.4	393.3	642.4	401.3	31.8

		+2b9	638.4	883.5	642.4	883.5	31.8
		+2y5	607.8	544.3	611.8	552.3	30.7
SERPINF1	ELLDTVTAPQK	+2y4	607.8	443.3	611.8	451.3	30.7
		+2y3	607.8	372.2	611.8	380.2	30.7
		+2y8	977.0	870.6	981.0	878.6	44
SERPINF2	QLTSGPNQEQVSPLTLLK	+2y7	977.0	771.5	981.0	779.5	44
		+2y6	977.0	684.5	981.0	692.5	44
		+2y9	914.0	1055.6	919.0	1065.6	41.8
SERPING1	GVTSVSQIFHSPDLAIR	+2y7	914.0	771.4	919.0	781.4	41.8
		+2y4	914.0	472.3	919.0	482.3	41.8
		+2y7	612.8	840.5	616.8	848.5	30.9
SERPINH1	GVVEVTHDLQK	+2y6	612.8	741.4	616.8	749.4	30.9
		+2b10	612.8	1078.6	616.8	1078.6	30.9
		+2y9	617.3	901.5	622.3	911.5	31.1
TIMP1	GFQALGDAADIR	+2y8	617.3	830.4	622.3	840.4	31.1
		+2y7	617.3	717.4	622.3	727.4	31.1
		+2y9	803.5	1013.6	807.5	1021.6	37.8
ANXA1	ALTGHLEEVVLALLK	+2b6	803.5	593.3	807.5	593.3	37.8
		+2b10	803.5	1049.6	807.5	1049.6	37.8
		+2y9	843.4	957.4	848.4	967.4	39.2
ANXA11	SLYHDISGDTSGDYR	+2y6	843.4	698.3	848.4	708.3	39.2
		+2y2	843.4	338.2	848.4	348.2	39.2
		+2y6	556.3	755.4	561.3	765.4	28.9
ANXA2	QDIAFAYQR	+2y5	556.3	684.3	561.3	694.4	28.9
		+2y3	556.3	466.2	561.3	476.2	28.9
		+2y9	833.9	971.6	837.9	979.6	38.9
ANXA4	SETSGSFEDALLAIVK	+2y5	833.9	543.4	837.9	551.4	38.9
		+2y4	833.9	430.3	837.9	438.3	38.9
		+2y9	853.0	1003.6	858.0	1013.6	39.6
ANXA5	GLGTDEESILTLTSTR	+2y7	853.0	803.5	858.0	813.5	39.6
		+2y6	853.0	690.4	858.0	700.4	39.6
		+2y7	588.8	744.5	592.8	752.5	30.1
ANXA6	DAFVAIVQSVK	+2y5	588.8	560.3	592.8	568.4	30.1
		+2b4	588.8	433.2	592.8	433.2	30.1
		+2y9	845.9	956.6	850.9	966.6	39.3
ANXA7	GFGTDEQAIVDVVANR	+2y7	845.9	772.4	850.9	782.4	39.3
		+2y6	845.9	673.4	850.9	683.4	39.3
		+2b2	964.5	262.1	968.5	262.1	43.6
C1QC	FNAVLTNPQG DYDTSTGK	+2b3	964.5	333.2	968.5	333.2	43.6
		+2b4	964.5	432.2	968.5	432.2	43.6
		+2y6	643.3	688.3	648.3	698.3	32
CLEC11A	DAVQALQEAQGR	+2b9	643.3	926.5	648.3	926.5	32

		+2b10	643.3	1054.5	648.3	1054.5	32
		+2y8	933.5	1050.5	938.5	1060.5	42.5
CLEC3A	FVDVNGIAISFLNWDR	+2y5	933.5	703.4	938.5	713.4	42.5
		+2y4	933.5	590.3	938.5	600.3	42.5
		+2y8	657.4	871.5	661.4	879.5	32.5
CLEC3B	LDTLAQEVALLK	+2y7	657.4	800.5	661.4	808.5	32.5
		+2b3	657.4	330.2	661.4	330.2	32.5
		+2y7	965.5	742.4	970.5	752.4	43.6
CSPG4	ALLHVVAGGPWPQGATLR	+2b5	965.5	534.3	970.5	534.3	43.6
		+2b7	965.5	791.5	970.5	791.5	43.6
		+2y7	571.8	820.5	575.8	828.5	29.4
HPX	QGHNSVFLIK	+2y6	571.8	706.5	575.8	714.5	29.4
		+2y2	571.8	260.2	575.8	268.2	29.4
		+2y6	538.7	776.4	543.7	786.4	28.3
LGALS1	DGGAWGTEQR	+2y5	538.7	590.3	543.7	600.3	28.3
		+2b5	538.7	487.2	543.7	487.2	28.3
		+2y6	486.8	744.4	491.8	754.4	26.4
LMAN1	DIDNLVQR	+2y3	486.8	402.2	491.8	412.3	26.4
		+2b5	486.8	571.3	491.8	571.3	26.4
		+2y9	1092.6	903.5	1096.6	911.5	48.2
ANGPTL2	QIETLQQLVEVDGGIVSEVK	+2y8	1092.6	788.5	1096.6	796.5	48.2
		+2b9	1092.6	1053.6	1096.6	1053.6	48.2
		+2y5	464.7	671.4	469.8	681.4	25.6
ANGPTL7	SGLVSFYR	+2y4	464.7	572.3	469.8	582.3	25.6
		+2y3	464.7	485.3	469.8	495.3	25.6
		+2y9	819.4	1078.5	824.4	1088.5	38.4
FGFBP2	QGSTGEEFHFQTGGR	+2y8	819.4	949.5	824.4	959.5	38.4
		+2b9	819.4	973.4	824.4	973.4	38.4
		+2y9	586.4	945.5	590.4	953.5	30
FRZB	LLLVEGSIAEK	+2y8	586.4	832.4	590.4	840.5	30
		+2y7	586.4	733.4	590.4	741.4	30
		+2y6	926.9	674.4	931.0	682.4	42.2
MST1	WDLQHPHQHPFEPGK	+2y3	926.9	301.2	931.0	309.2	42.2
		+2b5	926.9	680.3	931.0	680.3	42.2
		+2y9	846.4	978.5	850.5	986.5	39.3
S100A1	ELLQTELSGFLDAQK	+2y8	846.4	865.4	850.5	873.5	39.3
		+2b2	846.4	243.1	850.5	243.1	39.3
		+2y8	604.8	932.5	608.8	940.5	30.6
S100A10	EFPGFLENQK	+2y5	604.8	631.3	608.8	639.4	30.6
		+2y4	604.8	518.3	608.8	526.3	30.6
		+2y6	530.8	725.4	534.8	733.4	28
S100A11	DGYNYTL SK	+2y5	530.8	611.3	534.8	619.4	28

		+2y4	530.8	448.3	534.8	456.3	28
		+2y9	624.3	1047.5	628.3	1055.5	31.3
S100A13	SLDVNQDSELK	+2y7	624.3	833.4	628.3	841.4	31.3
		+2b3	624.3	316.2	628.3	316.2	31.3
		+2y6	455.2	693.4	459.2	701.4	25.2
S100A4	TDEAAFQK	+2y5	455.2	564.3	459.2	572.3	25.2
		+2b2	455.2	217.1	459.2	217.1	25.2
		+2y6	458.2	674.3	463.3	684.4	25.4
S100A6	LQDAEIAR	+2y5	458.2	559.3	463.3	569.3	25.4
		+2b2	458.2	242.2	463.3	242.2	25.4
		+2y5	482.2	645.3	487.2	655.4	26.2
S100A8	GNFHAVYR	+2y4	482.2	508.3	487.2	518.3	26.2
		+2y3	482.2	437.3	487.2	447.3	26.2
		+2y7	459.7	755.4	464.7	765.4	25.4
SCUBE1	YALHSDGR	+2y6	459.7	684.3	464.7	694.4	25.4
		+2y5	459.7	571.3	464.7	581.3	25.4
		+2y8	587.3	958.6	591.3	966.6	30
SFRP1	SQYLLTAIHK	+2y7	587.3	795.5	591.3	803.5	30
		+2y6	587.3	682.4	591.3	690.4	30
		+2y9	706.3	839.4	711.3	849.4	34.3
ADIPOQ	GDIGETGVPGAEGPR	+2y7	706.3	683.3	711.3	693.4	34.3
		+2b8	706.3	729.3	711.3	729.3	34.3
		+2y7	570.3	809.4	575.3	819.4	29.4
DPT	GATTTFAVER	+2y6	570.3	708.4	575.3	718.4	29.4
		+2y5	570.3	561.3	575.3	571.3	29.4

NOTE: Endogenous peptides (light) and isotope-labeled peptides (heavy) were chosen to measure the target proteins of interest. C-terminal peptides (arginine [R] or lysine [K]) were labeled with the ¹³C¹⁵N heavy isotope. Quantitative ion is marked in bold font.