Protein	Peptide Sequence	Q1 m/z	Q3 m/z	Ion Type	Peptide Peak Area (CPS)	Other Peak Area (CPS)	Total Peak Area (CPS)	% (Peptide Peak Area vs Total Peak Area)	Unique?
ACTB	SYELPDGQVITIGNER	895.9	1086.6	y10	57000	824	57824	98.57498616	Y
	SYELPDGQVITIGNER	895.9	706.4	y13, 2+	328000	5020	333020	98.49258303	Y
	SYELPDGQVITIGNER	895.9	1298.7	y12	170000	2370	172370	98.62505076	N
	SYELPDGQVITIGNER	895.9	475.2	y4	373000	2750	375750	99.26813041	N
	SYELPDGQVITIGNER	895.9	689.4	y6	358000	3650	361650	98.9907369	N
	HQGVMVGMGQK	586.3	249.1	b2-NH3	8730	13500	22230	39.27125506	Y
	HQGVMVGMGQK	586.3	422.2	b4	11900	4020	15920	74.74874372	Y
	HQGVMVGMGQK	586.3	906.5	y9	27900	1500	29400	94.89795918	N

HQGVMVGMGQK	586.3	266.1	b2-NH3	37600	1050	38650	97.28331177	N
HQGVMVGMGQK	586.3	520.3	y5	18600	3170	21770	85.43867708	N
AGFAGDDAPR	488.7	630.3	y6	1670000	19500	1689500	98.84581237	Y
AGFAGDDAPR	488.7	701.3	y7	1150000	0	1150000	100	Y
AGFAGDDAPR	488.7	343.2	y3	378000	0	378000	100	N
AGFAGDDAPR	488.7	424.7	y8	608000	0	608000	100	N
AGFAGDDAPR	488.7	276.1	b3	966000	0	966000	100	N
VAPEEHPVLLTEAPLNPK	977.5	1428.82	y13	629	0	629	100	Y
VAPEEHPVLLTEAPLNPK	977.5	1291.8	y12	5060	0	5060	100	N
VAPEEHPVLLTEAPLNPK	977.5	663.3	b6	43500	0	43500	100	N
VAPEEHPVLLTEAPLNPK	977.5	1386.73	b13	2290	0	2290	100	N

AVFPSIVGR	473.3	314.2	y3-NH3	1850000	0	1850000	100	Y
AVFPSIVGR	473.3	610.4	y6-H2O	71700	0	71700	100	Y
AVFPSIVGR	473.3	628.4	y6	3520000	0	3520000	100	N
AVFPSIVGR	473.3	531.3	y5	867000	0	867000	100	N
AVFPSIVGR	473.3	331.2	y3	356000	0	356000	100	N

GYSFTTTAER	566.8	437.2	b4-H2O	165000	0	165000	100	Y
GYSFTTTAER	566.8	308.1	b3	505000	2390	507390	99.52896194	Y
GYSFTTTAER	566.8	678.3	y6	806000	4600	810600	99.43251912	N
GYSFTTTAER	566.8	912.4	y8	436000	1670	437670	99.61843398	N
GYSFTTTAER	566.8	577.3	y5	406000	2150	408150	99.47323288	N

FPSIVGRPR	514.8	881.5	y8	1780	1570	3350	53.13432836	Y
FPSIVGRPR	514.8	697.4	y6	4720	1260	5980	78.92976589	Y
FPSIVGRPR	514.8	584.4	y5	3450	1260	4710	73.24840764	N
FPSIVGRPR	514.8	485.3	y4	2050	2080	4130	49.63680387	N
FPSIVGRPR	514.8	784.5	y7	5140	1250	6390	80.43818466	N

PEEHPVLLTEAPLNPK	892.5	1291.8	y12	3700	0	3700	100	Y
PEEHPVLLTEAPLNPK	892.5	639.4	y6	4440	870	5310	83.61581921	Y
PEEHPVLLTEAPLNPK	892.5	493.2	b4	20200	0	20200	100	N
PEEHPVLLTEAPLNPK	892.5	568.3	y5	6710	372	7082	94.74724654	N
PEEHPVLLTEAPLNPK	892.5	1216.6	b11	2500	0	2500	100	N
PDGQVITIGNER	649.8	398.2	b4	629	4180	4809	13.07964234	Y
PDGQVITIGNER	649.8	901.5	y8	2520	1300	3820	65.96858639	Y
PDGQVITIGNER	649.8	802.4	y7	1670	3350	5020	33.26693227	N
PDGQVITIGNER	649.8	689.4	y6	1290	1930	3220	40.0621118	N
PDGQVITIGNER	649.8	475.2	y4	234	1590	1824	12.82894737	N
TVLSGGTTMYPGIA	819.9	628.3	y6	122000	11400	133400	91.45427286	Y

	DR								
	TVLSGGTTMYPGIADR	819.9	1011.5	b10	11100	0	11100	100	Y
	TVLSGGTTMYPGIADR	819.9	791.4	y7	66400	0	66400	100	N
	TVLSGGTTMYPGIADR	819.9	201.1	b2	55300	0	55300	100	N
	TVLSGGTTMYPGIADR	819.9	1023.5	y9	16000	0	16000	100	N
	TTGIVMDSGDGVTH	695.3	918.4	y9	6940	0	6940	100	Y
	TTGIVMDSGDGVTH	695.3	355.2	b4-H2O	1210	3720	4930	24.54361055	Y
	TTGIVMDSGDGVTH	695.3	1017.4	y10	3400	0	3400	100	N
	TTGIVMDSGDGVTH	695.3	242.1	b3-H2O	3090	5300	8390	36.829559	N
	TTGIVMDSGDGVTH	695.3	787.3	y8	6180	3380	9560	64.64435146	N
THBS1	FVFGTTPEDILR	697.7	742.4	y6	572000	0	572000	100	Y
	FVFGTTPEDILR	697.7	574.8	y10, 2+	420000	5770	425770	98.64480823	Y
	FVFGTTPEDILR	697.7	219.1	a2	358000	13800	371800	96.28832706	N

FVFGTTPEDILR	697.7	688.9	y12-H2O, 2+	258000	187000	445000	57.97752809	N
FVFGTTPEDILR	697.7	565.8	y10-H2O, 2+	145000	8620	153620	94.38875146	N
GGVNDNFQGVLQNVR	808.9	1083.5	b11-H2O	525	0	525	100	Y
GGVNDNFQGVLQNVR	808.9	871.4	b9-H2O	4720	0	4720	100	Y
GGVNDNFQGVLQNVR	808.9	629.4	y5	154000	0	154000	100	N
GGVNDNFQGVLQNVR	808.9	913.5	y8	100000	0	100000	100	N
GGVNDNFQGVLQNVR	808.9	785.5	y7	180000	0	180000	100	N

IEDANLIPPVPDDKFQDLVDAVR	1290.2	906	y16, 2+	10400	0	10400	100	Y
IEDANLIPPVPDDKFQDLVDAVR	1290.2	672.4	y6	1270	0	1270	100	Y
IEDANLIPPVPDDKFQDLVDAVR	1290.2	752.4	b7-NH3	1800	0	1800	100	Y
IEDANLIPPVPDDKFQDLVDAVR	1290.2	769.4	y7-H2O	3070	0	3070	100	Y
IEDANLIPPVPDDKFQDLVDAVR	1290.2	1111.6	y20, 2+	110	0	110	100	N
IPESGGDNSVFDIFELTGAAR	1098	864.5	y8	1120	0	1120	100	Y
IPESGGDNSVFDIFELTGAAR	1098	1092.6	y10	3850	0	3850	100	Y
IPESGGDNSVFDIFELTGAAR	1098	1239.6	y11	3890	0	3890	100	N
IPESGGDNSVFDIFEL	1098	1041.5	y20, 2+	21700	414	22114	98.12788279	N

TGAAR								
IPESGGDNSVFDIFELTGAAR	1098	977.5	y9	5560	2060	7620	72.96587927	N
IMADSGPIYDK	613.3	425.2	y3	1870	12200	14070	13.29068941	Y
IMADSGPIYDK	613.3	180.2	y4, 3+	2420	726	3146	76.92307692	Y
IMADSGPIYDK	613.3	965.5	y9	10100	662	10762	93.848727	N
IMADSGPIYDK	613.3	779.4	y7	8700	13600	22300	39.01345291	N
IMADSGPIYDK	613.3	894.4	y8	761	4580	5341	14.24826811	N
QVTQSYWDTNPTR	789.9	889.4	y7	5900	1050	6950	84.89208633	Y
QVTQSYWDTNPTR	789.9	876.4	b7	1520	2310	3830	39.68668407	Y
QVTQSYWDTNPTR	789.9	373.2	y3	7870	5850	13720	57.36151603	N
QVTQSYWDTNPTR	789.9	703.3	y6	4920	7600	12520	39.2971246	N
QVTQSYWDTNPTR	789.9	672.3	b6-H2O	2580	7030	9610	26.84703434	N
LCNNPTPQFGGK	666.8	485.2	b4-NH3	16600	14850	31450	52.78219396	Y
LCNNPTPQFGGK	666.8	683.3	b6-NH3	9510	7900	17410	54.62377944	Y

LCNNPTPQFGGK	666.8	831.4	y8	98000	24540	122540	79.97388608	N
LCNNPTPQFGGK	666.8	633.3	y6	91000	7020	98020	92.83819629	N
LCNNPTPQFGGK	666.8	1059.5	y10	14400	4943	19343	74.44553585	N
SITLFVQEDR	604.3	504.3	y8, 2+	37000	14460	51460	71.90050525	Y
SITLFVQEDR	604.3	397.2	y6, 2+	44200	11100	55300	79.92766727	Y
SITLFVQEDR	604.3	595.3	y18-H2O, 2+	21600	193300	214900	10.0511866	N
SITLFVQEDR	604.3	793.4	y6	117000	3384	120384	97.18899522	N
SITLFVQEDR	604.3	646.3	y5	64900	6140	71040	91.35698198	N
DCVGDVTENQICNK	826.3	776.4	y6	7480	11600	19080	39.2033543	Y
DCVGDVTENQICNK	826.3	421.2	y3	22400	1680	24080	93.02325581	Y
DCVGDVTENQICNK	826.3	1006.5	y8	9550	469	10019	95.3188941	N
DCVGDVTENQICNK	826.3	1277.6	y11	2940	0	2940	100	N
DCVGDVTENQICNK	826.3	646.3	b6	10600	3560	14160	74.85875706	

GFLLLASLR	495.3	672.4	y6	73000	0	73000	100	Y
GFLLLASLR	495.3	318.2	b3	134000	0	134000	100	Y
GFLLLASLR	495.3	446.3	y4	89300	13000	102300	87.29227761	N
GFLLLASLR	495.3	559.4	y5	106000	0	106000	100	N
GFLLLASLR	495.3	544.3	b5	20200	4630	24830	81.35320177	N
AQLYIDCEK	570.3	827.4	y6	37900	6020	43920	86.29326047	Y
AQLYIDCEK	570.3	555	?	476	16700	17176	2.771308803	Y
AQLYIDCEK	570.3	940.4	y7	31700	0	31700	100	N
AQLYIDCEK	570.3	200.1	b2	93600	0	93600	100	N
AQLYIDCEK	570.3	664.3	y5	27100	0	27100	100	N

Supplemental Table 1: The utility of choosing peptides listed as unique in the GPM database when designing MRM transitions. Table 2 lists GPM-predicted MRM transitions for several peptides from β-Actin (ACTB, Swissprot accession number P60709) and Thrombospondin-1 (THBS1, Swissprot accession number P07996) and their experimentally determined peak areas. For most peptides, the two most intense unique transitions and the three most intense non-unique transitions were monitored. The peptide peak area as a percentage of total peak area seen in the MRM tracing is calculated as an indication of the specificity of the each MRM transition. Whether the peptide is listed as unique in the GPM database is listed in the final column. Overall, the GPM-archived relative fragment ion intensity appears to be a good indicator of the quality of the transition, while the uniqueness of the peptide does not appear to play a major role in contributing to the specificity of the MRM transition.