

Supporting Information _Digging more missing proteins using an enrichment approach with ProteoMiner™

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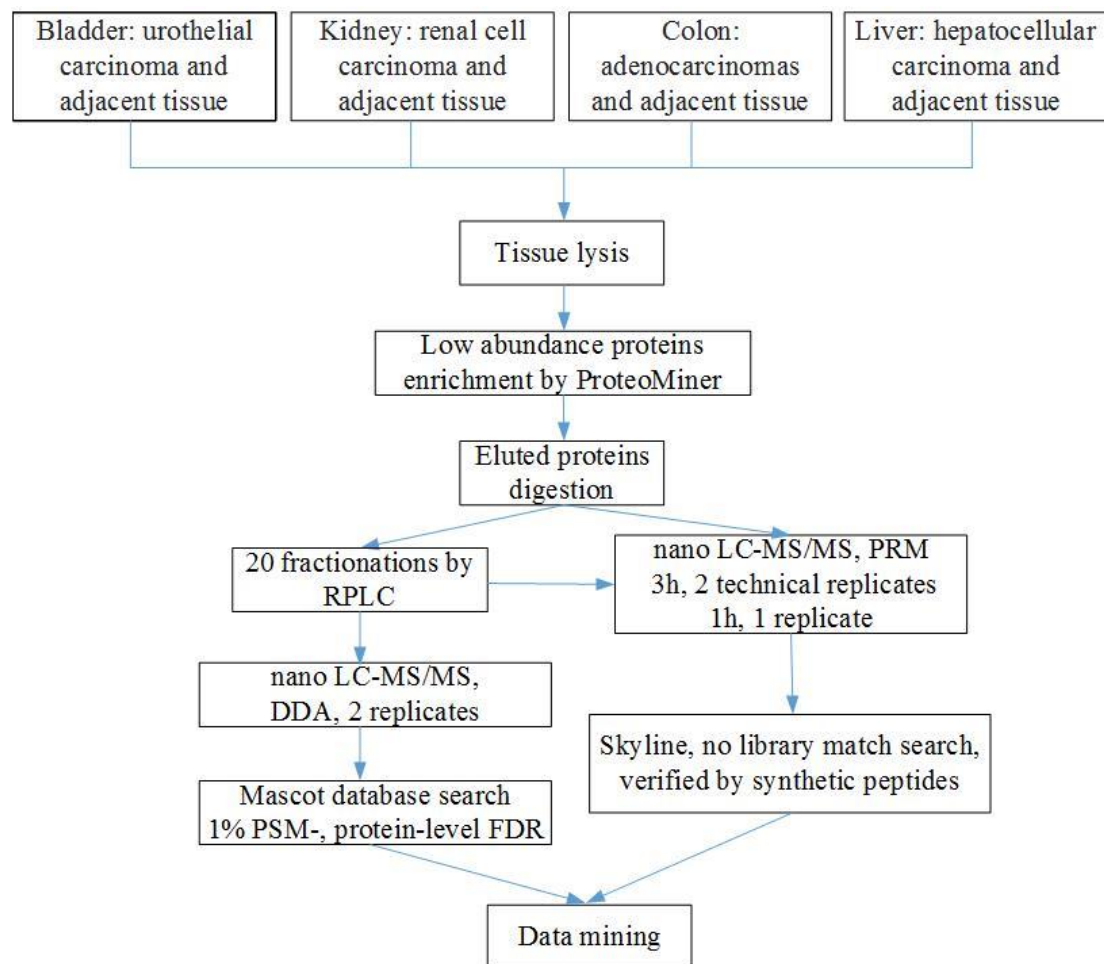
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Supplementary Figure 1: The scheme illustrating the tissue sample pathological information and experimental flowchart.

Supplementary Table 1: The list of target peptides with m/z and sequence obtained from Skyline analysis and used for the PRM assay

Mass [m/z]	CS [z]	Polarity	NCE	Comment
568.9724	3	Positive	26	AALSQGHGAPLALQQK (light)
569.2643	2	Positive	26	AC[+57.0]QMMLDIR (light)
351.1873	3	Positive	26	AFHLFGGFR (light)
402.218	3	Positive	26	AHILYMSLEK (light)
1004.522	2	Positive	26	AHTALSEYRPILSQEHR (light)
502.7644	4	Positive	26	AHTALSEYRPILSQEHR (light)
935.976	2	Positive	26	ALEGQLPLQENWYGR (light)
930.1289	3	Positive	26	ALGTSDSPVLFHC[+57.0]PGAAGTAQGLEYS (light)
1126.537	2	Positive	26	APAPSKPGESQESQGTPELPST (light)
685.8673	2	Positive	26	APETIESVAQGIR (light)
926.9974	2	Positive	26	APPALVVTANIGQAGGSSSR (light)
730.3912	2	Positive	26	ATVSEQLSQDLLR (light)
697.8529	2	Positive	26	C[+57.0]LTETPIEYLR (light)
718.3374	2	Positive	26	DMYFDIPLEHR (light)
756.3817	2	Positive	26	DSNQSSNLIIHQR (light)
982.5098	2	Positive	26	DVEPAVVGQLVDFVYTGR (light)
655.3423	3	Positive	26	DVEPAVVGQLVDFVYTGR (light)
825.7359	3	Positive	26	EEGARPGTLLGTFNAMDPDSQIR (light)
1011.79	3	Positive	26	EELVTILEEEEESSKEEEDQEPQR (light)
1111.527	2	Positive	26	EEPLEPDGGPDGELLEQR (light)
1059.182	3	Positive	26	EIFTKPLN[+1.0]FQ[+1.0]ETETDASKSDYELQALR (light)
785.4152	2	Positive	26	ESSQHVTQLVLSNK (light)
712.8908	2	Positive	26	EVSPVEIPGQTLR (light)
842.431	2	Positive	26	EYITSSLVQQVSSSR (light)
561.9565	3	Positive	26	EYITSSLVQQVSSSR (light)
633.8219	2	Positive	26	FIDDEPVYLR (light)
607.8281	2	Positive	26	FLLETMAYVK (light)
481.2382	3	Positive	26	FPM[+16.0]MGIGQ[+1.0]M[+16.0]LRK (light)
716.8534	2	Positive	26	FTEEVIEYFQK (light)
728.8825	2	Positive	26	GAPARPSLAMTQEK (light)
486.2574	3	Positive	26	GAPARPSLAMTQEK (light)
668.369	2	Positive	26	GNYLPLFIGDK (light)
444.5821	3	Positive	26	ILLTSDEAWKR (light)
1048.065	2	Positive	26	IQQLAFVYPELLAGEFTR (light)
638.6678	3	Positive	26	ISLEDLSPSVVLHM[+16.0]TEK (light)
645.8744	2	Positive	26	IVDTSLIFNIR (light)
430.9187	3	Positive	26	IVDTSLIFNIR (light)
465.2926	2	Positive	26	LLGTLAVSR (light)

597.6443	3	Positive	26	LLVQDRDSPFTSAWR (light)
661.9829	3	Positive	26	LNLSQLLEAWQDDMHR (light)
861.7452	3	Positive	26	LNTDLEAVKSDLQYQQWDSK (light)
1188.077	2	Positive	26	LSATLEEN[+1.0]DLLQ[+1.0]GTVEELQDR (light)
709.8779	2	Positive	26	LTATSTDQLEALR (light)
473.5877	3	Positive	26	LTATSTDQLEALR (light)
509.9642	3	Positive	26	LTLPTLYEIHKS (light)
794.3812	2	Positive	26	LWAAWGEEQENVR (light)
549.2558	2	Positive	26	LYMANAGDSR (light)
1080.13	3	Positive	26	M[+16.0]ETWLHEQEAQGQLLWDSSSSDSDEQ[+1.0]GK (light)
983.9678	2	Positive	26	MDMMSLN[+1.0]SQLLDIAQQK (light)
473.7569	4	Positive	26	METLVHLVLSQDHTIR (light)
817.087	3	Positive	26	MVDKEMN[+1.0]PLPTQLSTGAISFLR (light)
474.2525	3	Positive	26	NIKNYEEIIR (light)
492.8137	2	Positive	26	NILSVIAVR (light)
946.9748	2	Positive	26	NLTPYVAIEDKDMQQK (light)
612.9903	3	Positive	26	NSLQELQLDPDPGVRR (light)
708.3857	2	Positive	26	NWGQSVELLTLR (light)
1012.568	2	Positive	26	QLNQAGLVPPGLGPPPPQ[+1.0]ALR (light)
640.8252	4	Positive	26	QWAQEEENLNELTHIHQSLK (light)
531.2695	4	Positive	26	RDEIRPLSFEFTPETER (light)
752.7231	3	Positive	26	RWVITTELEEDPGPFPPK (light)
1237.262	3	Positive	26	SLQSSAATSTSLSEIEQSMEAELEQEREQLR (light)
888.4378	3	Positive	26	SYSEVAN[+1.0]HILDTAAISN[+1.0]WAFIPNK (light)
590.8015	2	Positive	26	TFNQSSDLLR (light)
886.4361	2	Positive	26	YELVHDPANWVSVDK (light)
969.9758	2	Positive	26	YIFQ[+1.0]LN[+1.0]EIEQEQLNR (light)

Note: Synthetic peptides are labeled in red.

Supplementary Table 2: The identification summary of equalized proteins by ProteoMiner™ from human four tissues.

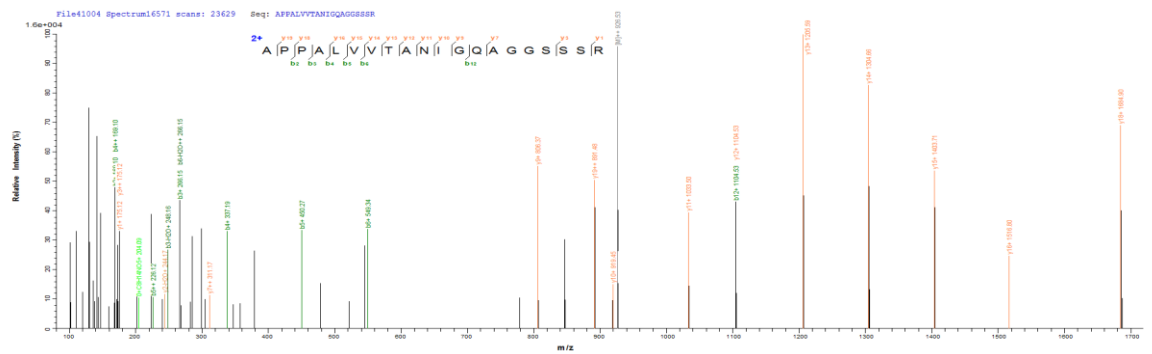
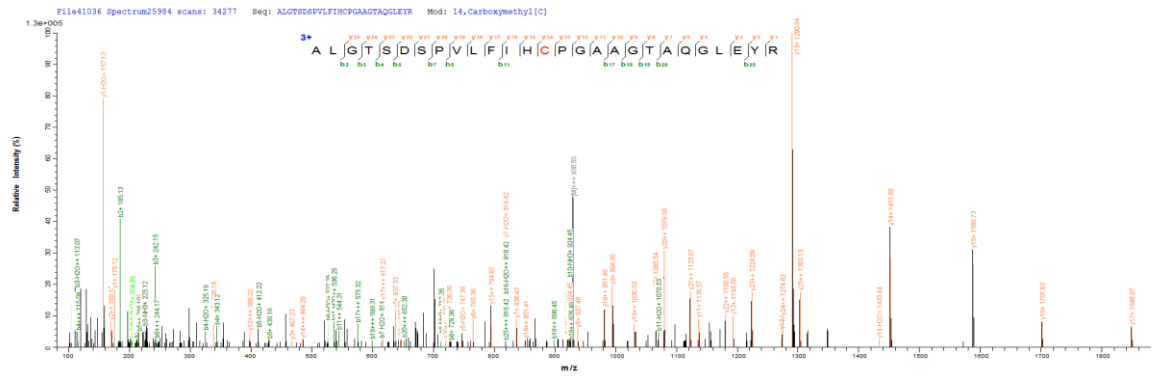
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Liver_NH4HCO3_1+2	1746051	407358	0.00999788	67091	6200	0.00983871	0
Liver_TX100_1	899765	223755	0.00999832	63955	6478	0.008644643	0
Liver_TX100_2	861691	212493	0.0099985	61129	6222	0.009964642	1
Liver_TX100_1+2	1761456	436318	0.00999888	76251	6778	0.009884922	1
Colon_TX100_1	784146	165282	0.00997675	54467	7464	0.009914255	0
Colon_TX100_2	775163	162020	0.0099964	54006	7509	0.009988014	0
Colon_TX100_1+2	1559309	327397	0.00999958	62454	7598	0.009739405	0
Kidney_TX100_1	857791	317359	0.00999762	92373	8790	0.009783845	7
Kidney_TX100_2	844666	310324	0.00999462	90806	8690	0.009781358	5
Kidney_TX100_1+2	1702457	627759	0.0099989	102964	8432	0.009724858	7
Bladder_TX100_1	816661	347449	0.00999819	93638	7724	0.009968928	7
Bladder_TX100_2	774339	326695	0.00999985	90453	8080	0.00990099	11
Bladder_TX100_1+2	1591000	674104	0.00999965	104390	7985	0.009643081	10

Supplementary Table 3: The list of proteins identified from the four human tissues in this study

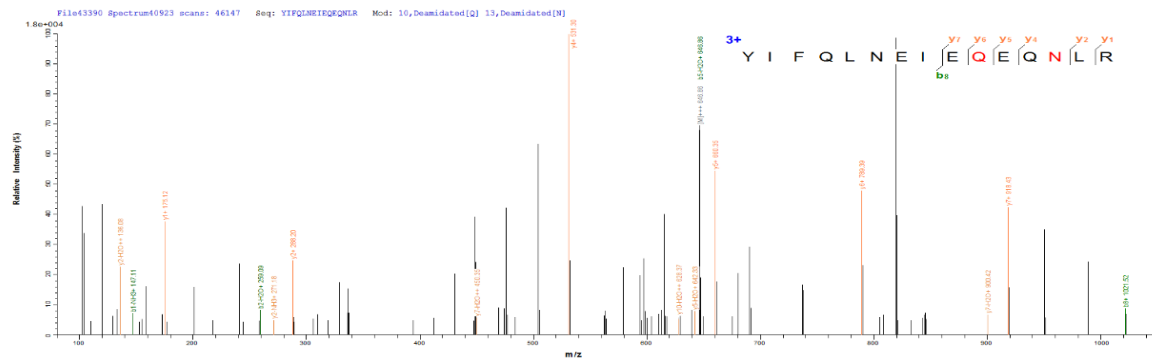
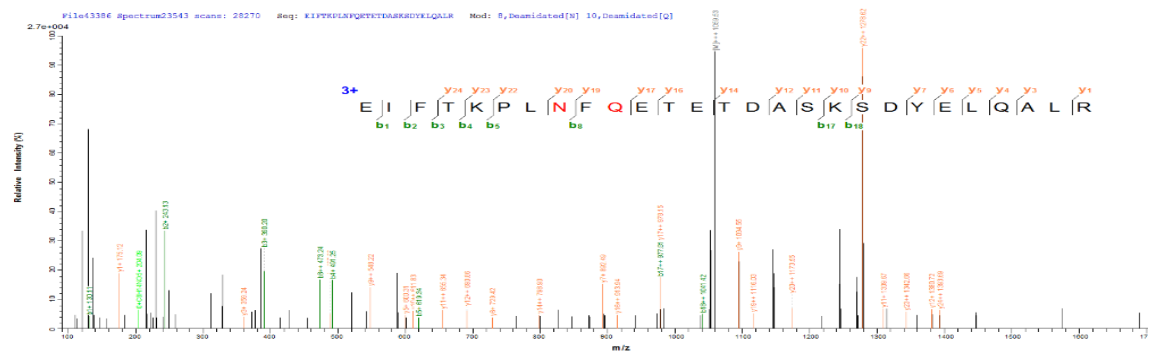
Protein_ID	Protein_Qscore	Protein_FDR	Protein_Mass	PeptideSeqs	PepIsUnique	Unique_Peptide_N um	Unique_Spectra_ Num	Coverage	Peptide_Query	Description
sp P30260 CDC2 7_HUMAN	94.99127656	0	91809.32731	AAAEGLMSLLR; AIQVDPNYAYA	1;1;1;1;1;1;1;1; 1;1;1;1;1;1	17	28	0.2828	114252;114255;737 044;9918;672503;3	Cell division cycle protein 27 homolog
sp P61201 CSN2 _HUMAN	133.7383126	0	51564.05432	AALSSFQK;AHT DFFEAFK;ALYE	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	24	119	0.5621	32494;32488;14691 3;146912;146911;1	COP9 signalosome complex subunit 2
sp Q5JRX3 PRE P_HUMAN	135.6039837	0	117338.079	ALIESGLGTDFSP DVGNGYTR;AV	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	25	40	0.3944	605836;31956;3715 09;249913;452123;	Presequence protease,
sp Q93100 KPB B_HUMAN	100.7892679	0	124805.3541	FNPILDMLAALK; FNPILDMLAALK	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1	18	43	0.2214	202927;260731;260 730;652330;459608	Phosphorylase b kinase regulatory
sp Q9NXR1 ND E1_HUMAN	67.71467451	0	38784.54041	AENTQEELREFQ EGSR;ATIMSLED	1;1;1;1;1;0;0;1;1; 1;1;1	11	20	0.4538	461965;461968;245 008;485349;285307	Nuclear distribution protein
sp Q96CW1 AP2 M1_HUMAN	95.10895226	0	49623.02468	ASENAIVWK;DII LPFR;EEQSQITS	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1	17	132	0.4483	76323;76317;38690 ;38694;38679;3868	AP-2 complex subunit mu
sp Q04446 GLG B_HUMAN	158.269938	0	80422.63274	AGLLFIFNFHPSK ;CADGGLYCK;EF	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	32	134	0.4886	268098;82692;8269 1;609595;609589;6	1,4-alpha-glucan- branching enzyme
sp Q86Y56 DAA F5_HUMAN	170.2087985	0	93462.06228	ACLQPSQDPQM R;AIQDAILEVLK;	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	30	76	0.476	240836;147187;179 804;179806;179805	Dynein assembly factor 5, axonemal
sp P43243 MAT R3_HUMAN	183.1175505	0	94564.79637	ALWFQGR;CRDD SFFGETSHNYHK;	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	34	231	0.5124	39744;39742;39734 ;39745;39737;3973	Matrin-3 OS=Homo sapiens
sp O43592 XPO T_HUMAN	173.3341405	0	109893.298	AAQVFALLFVTE YLTK;ALAYFEQ	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	30	90	0.4179	414963;414962;415 303;95290;95289;9	Exportin-T OS=Homo sapiens
sp Q99459 CDC 5L_HUMAN	126.5991424	0	92193.66072	AQDVLVQEMEV VK;DLPRPSEVNE	1;1;1;1;1;1;1;1; 1;1;1;1;1;1;1;1;	24	79	0.419	266588;266592;266 593;266591;733987	Cell division cycle 5-like protein

Supplementary Figure 2: The labeled spectra with MS identification information of all the identified unique peptides from 20 MPs

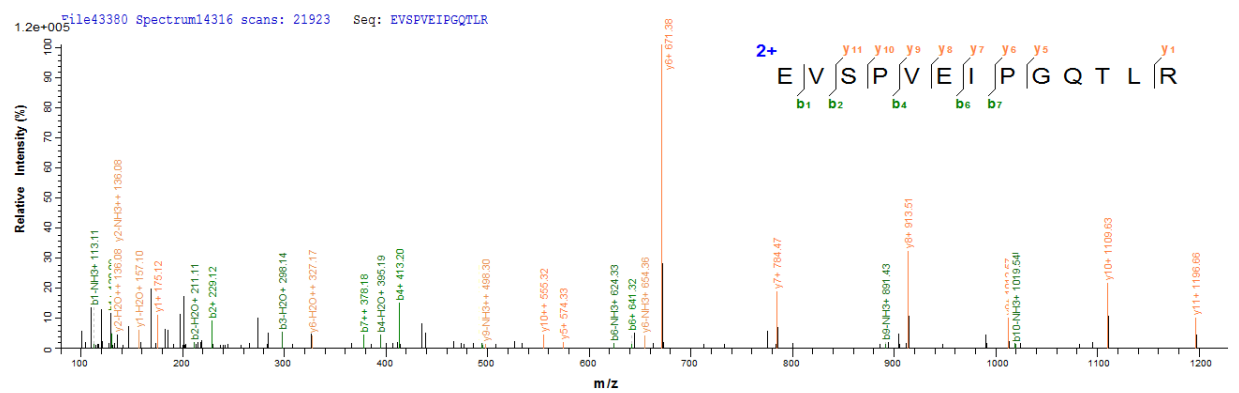
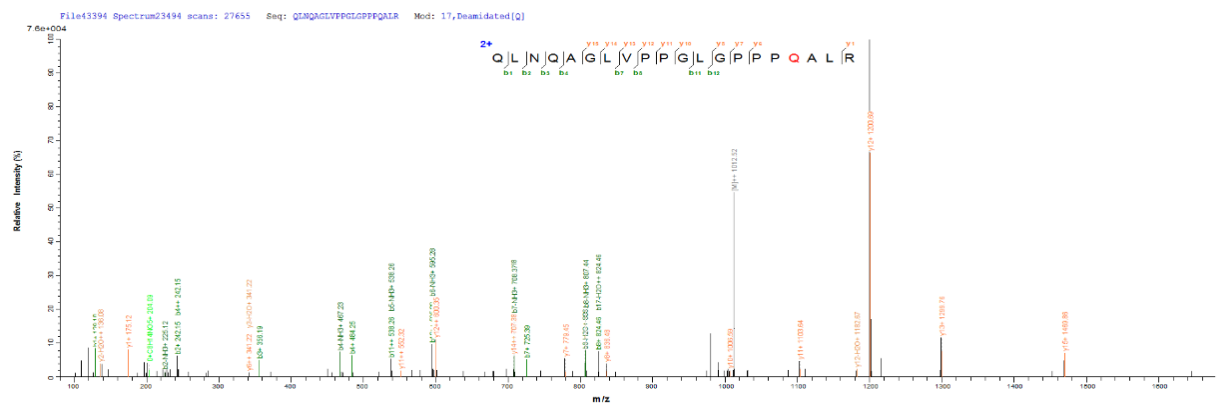
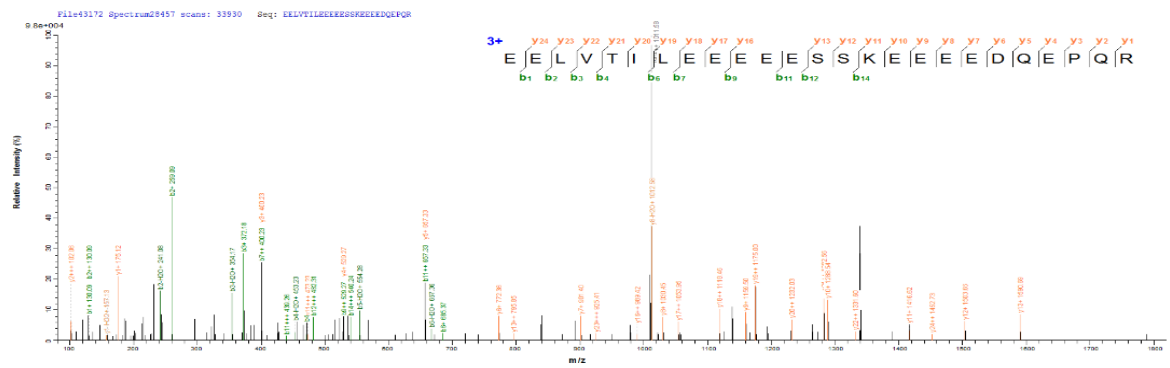
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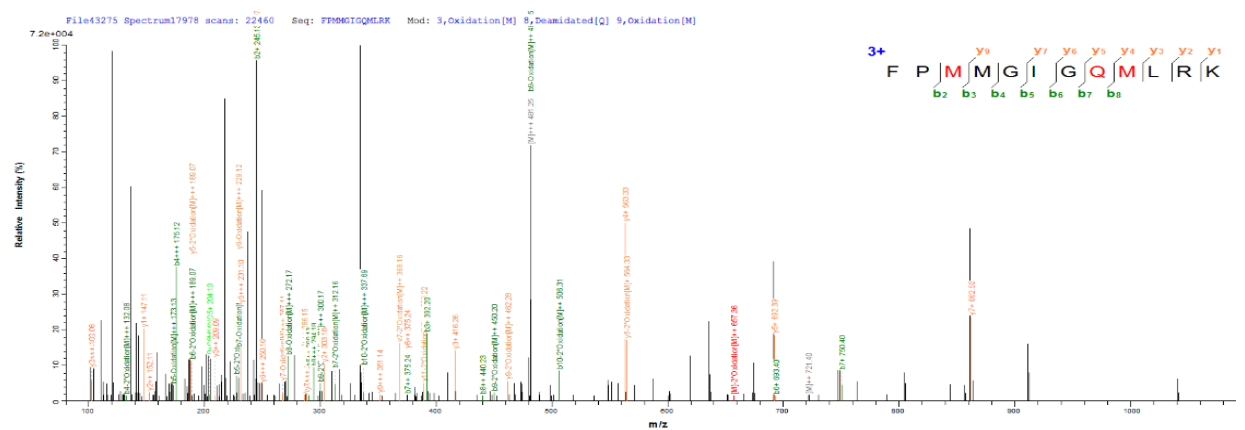
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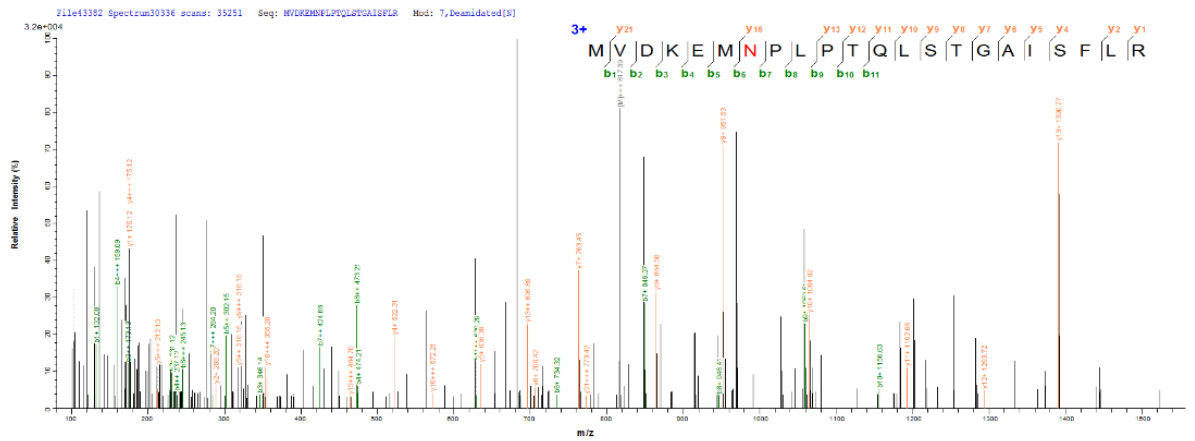
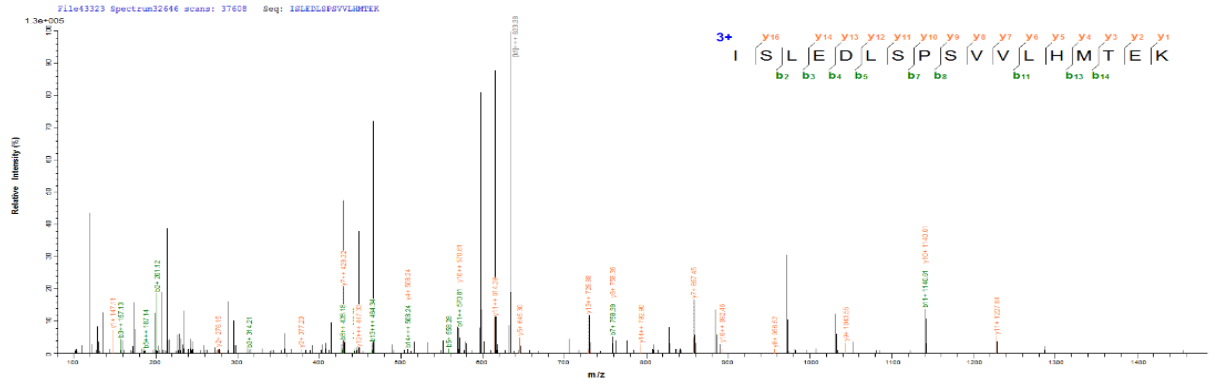


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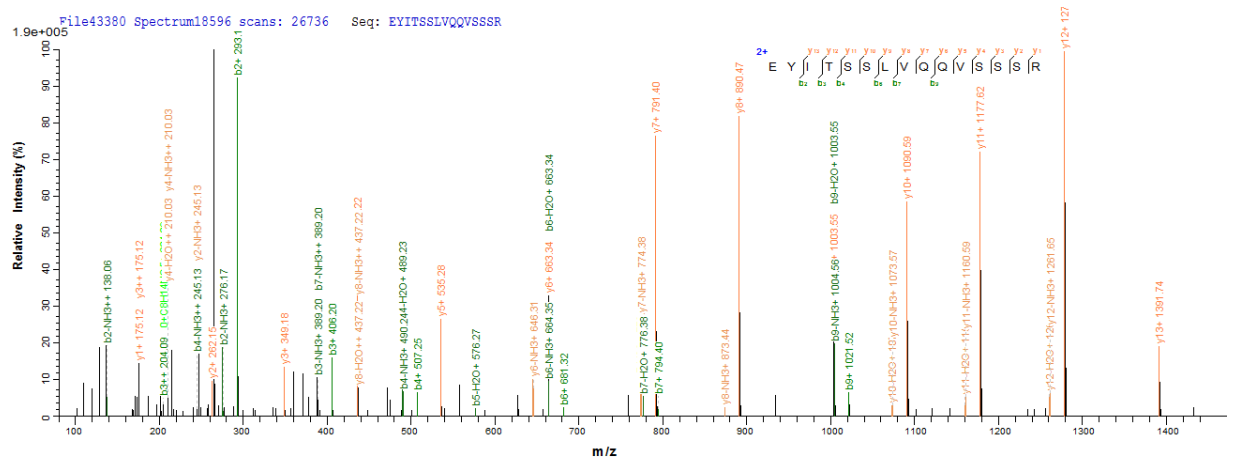
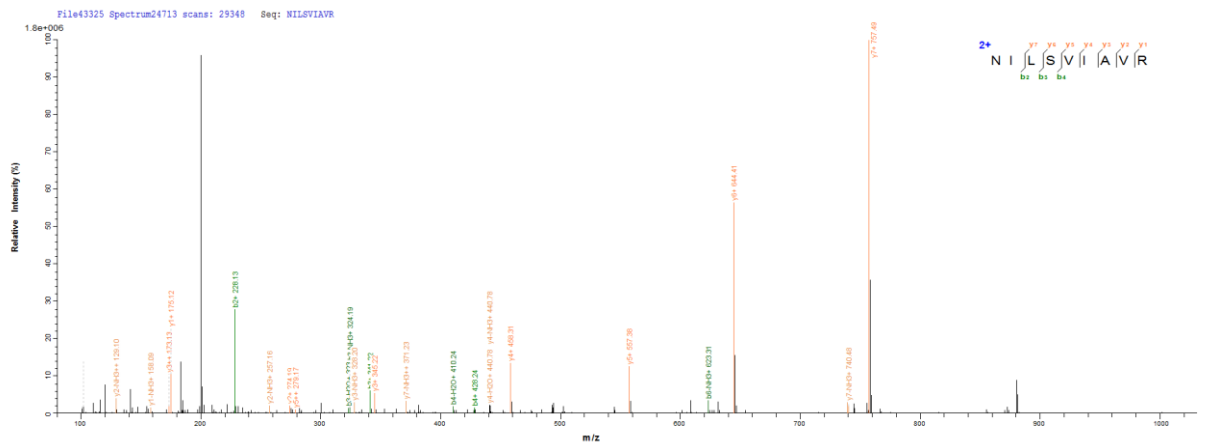


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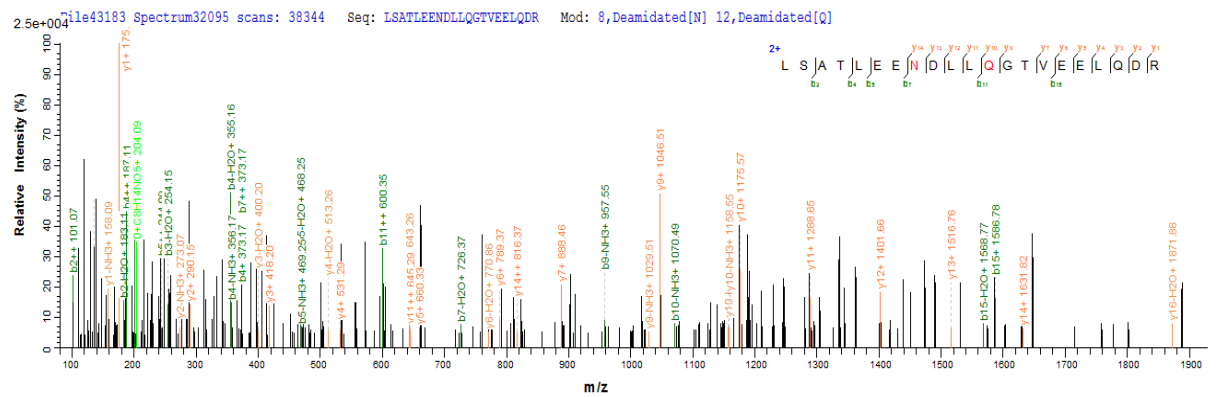
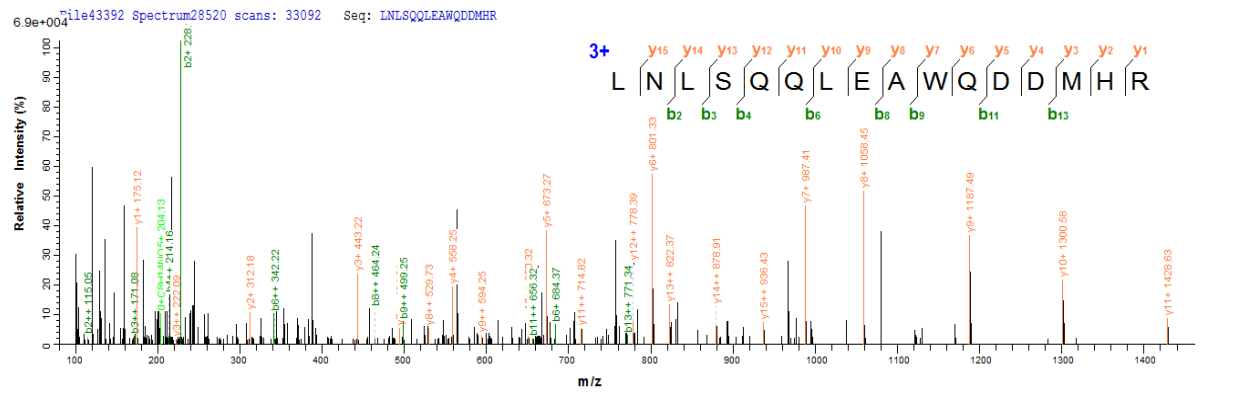




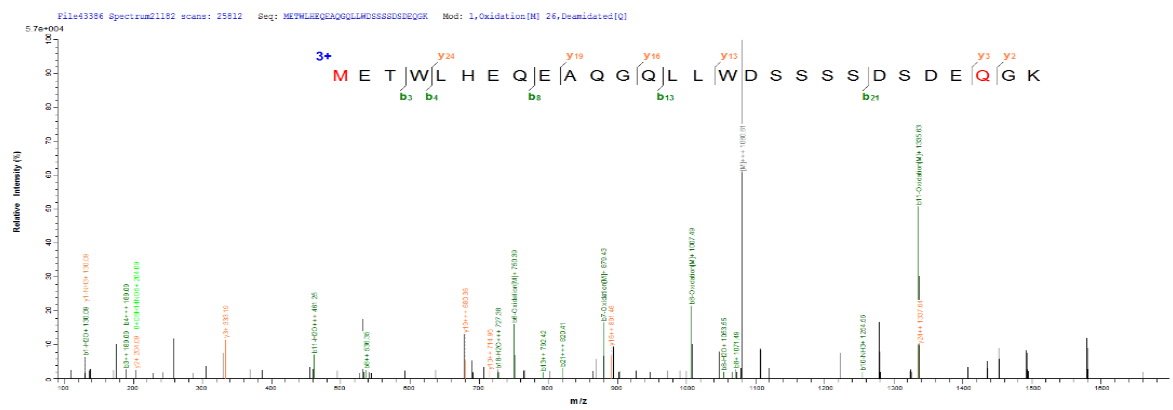
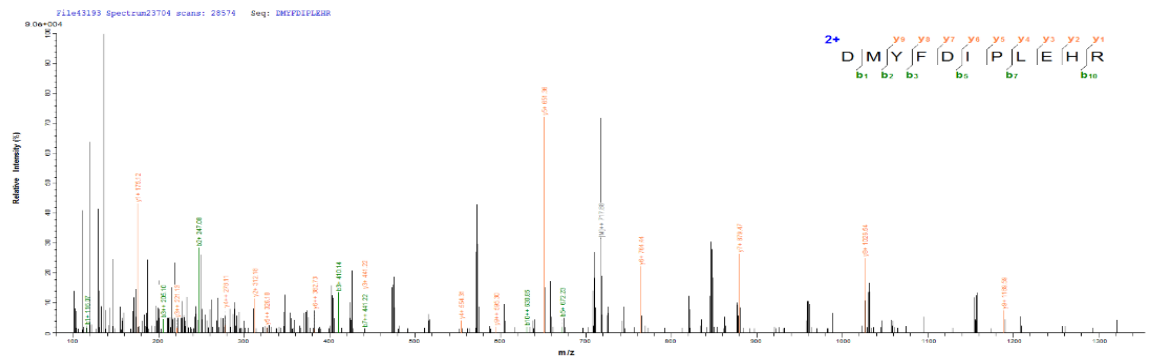
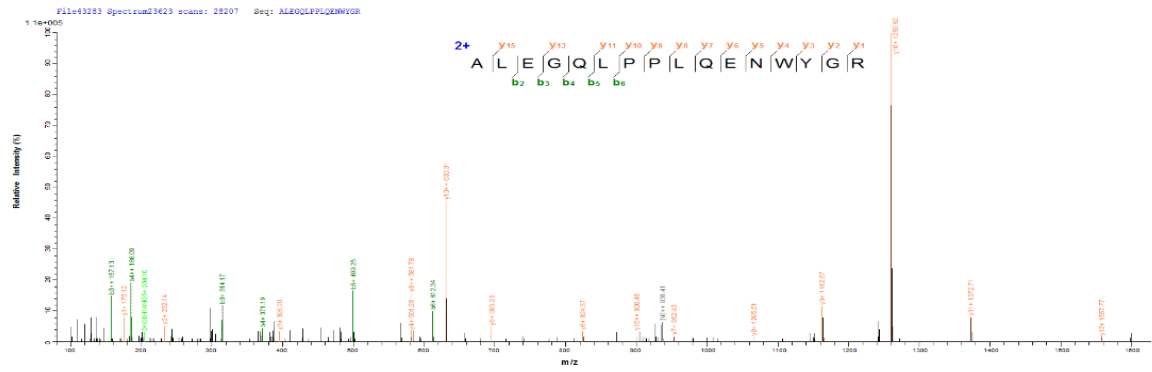
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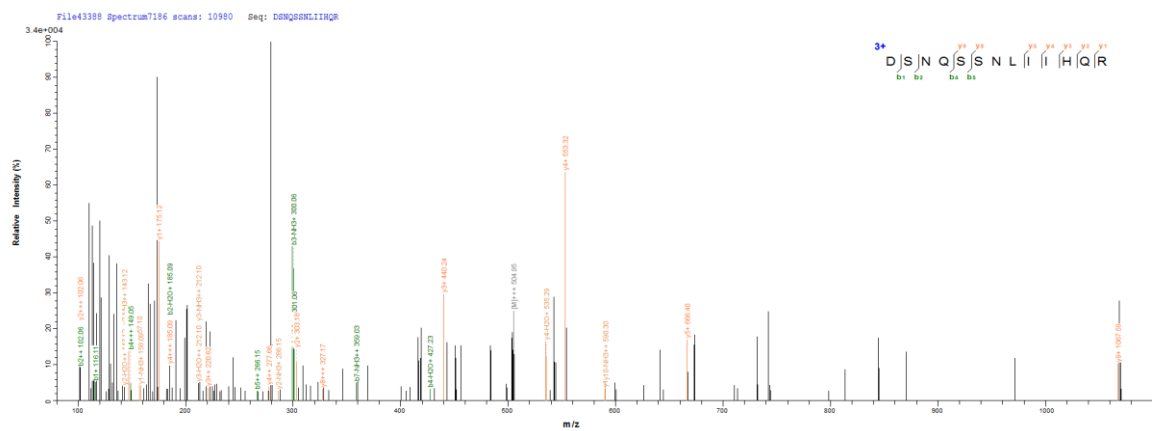
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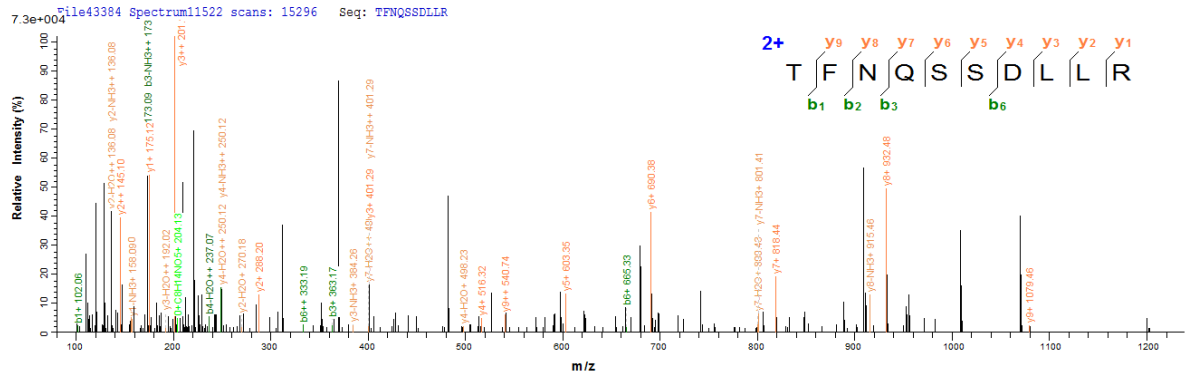


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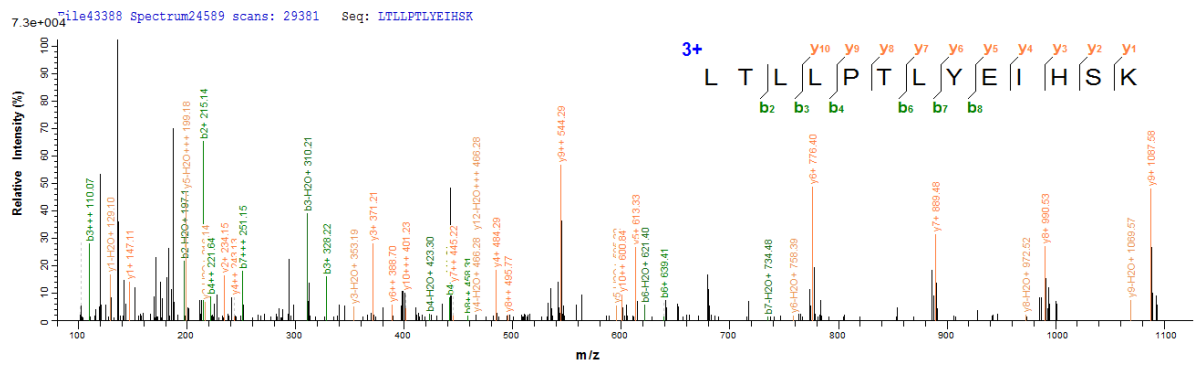
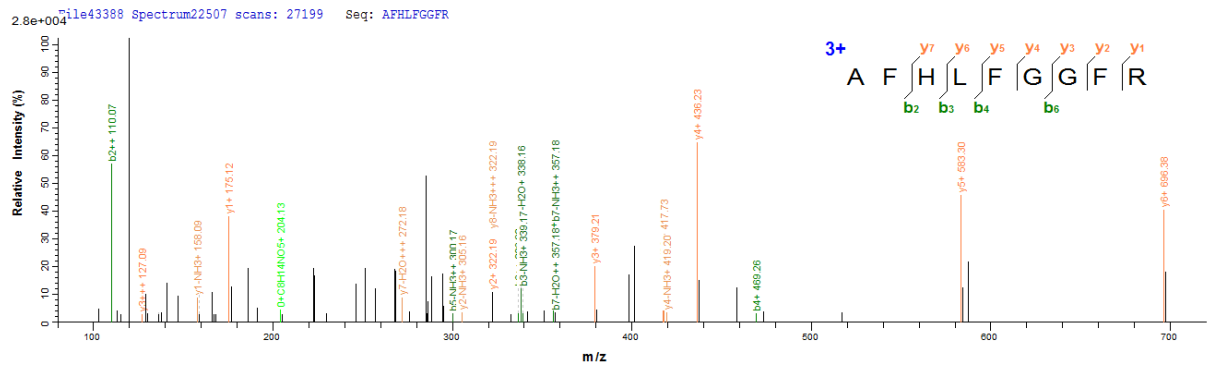


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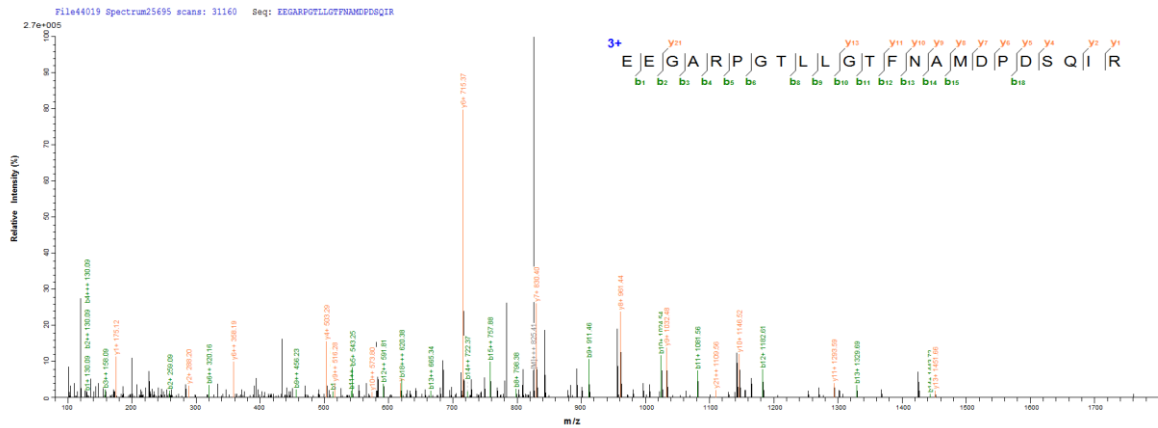


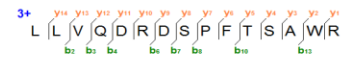
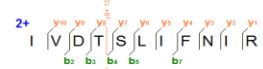
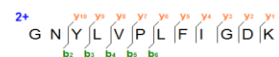


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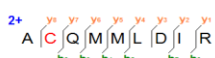
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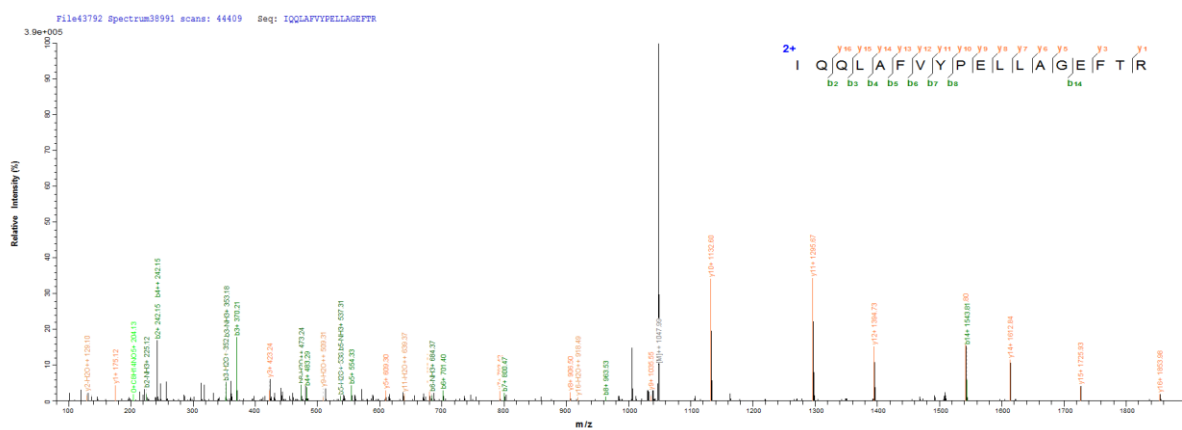
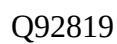


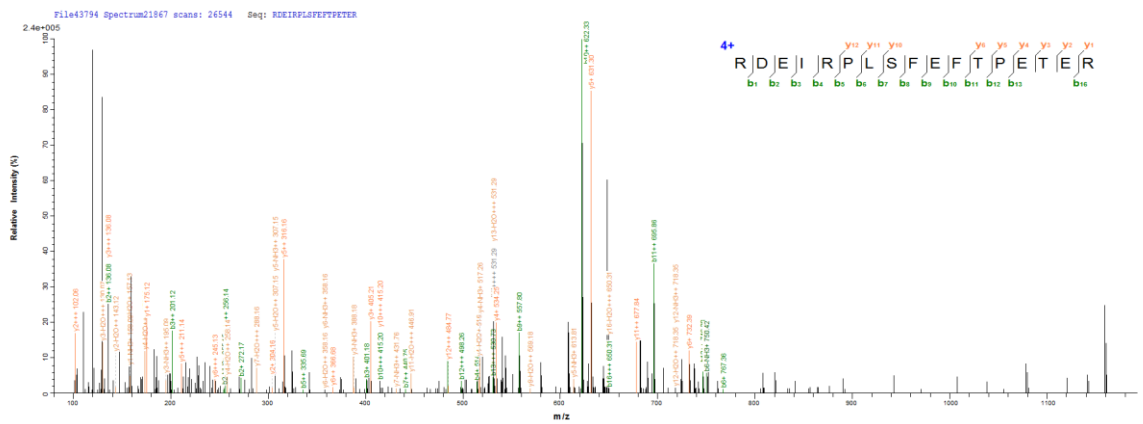
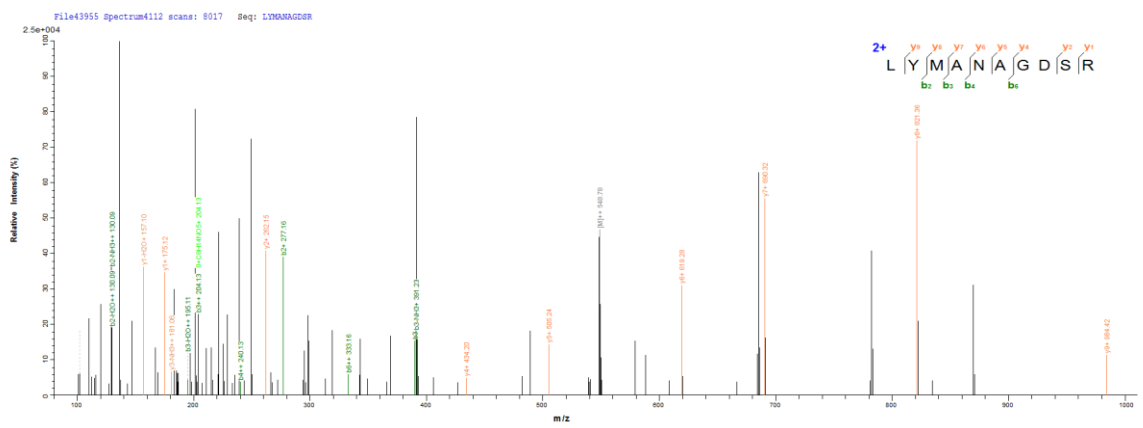
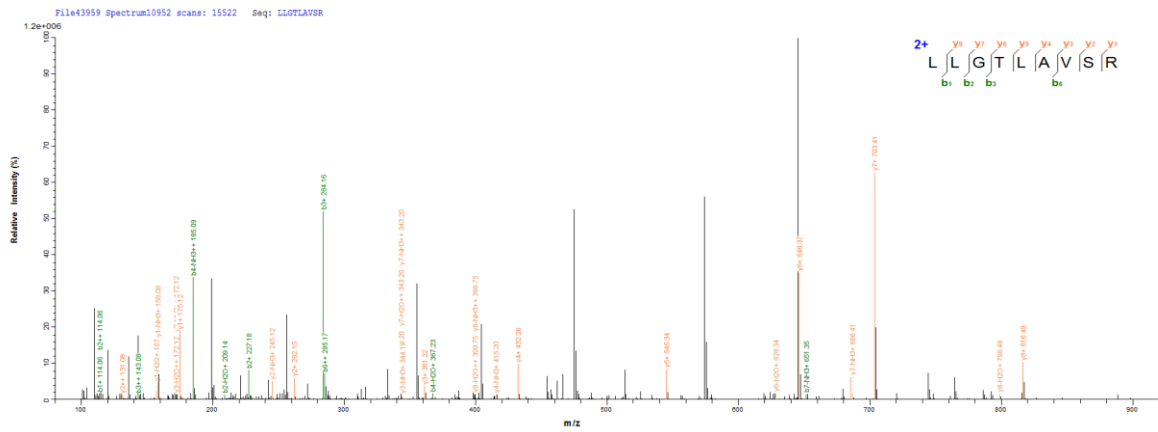




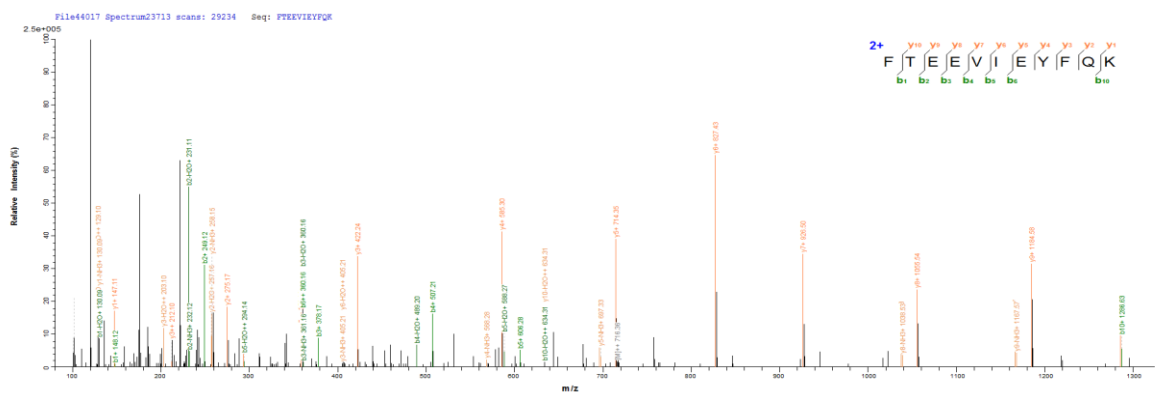
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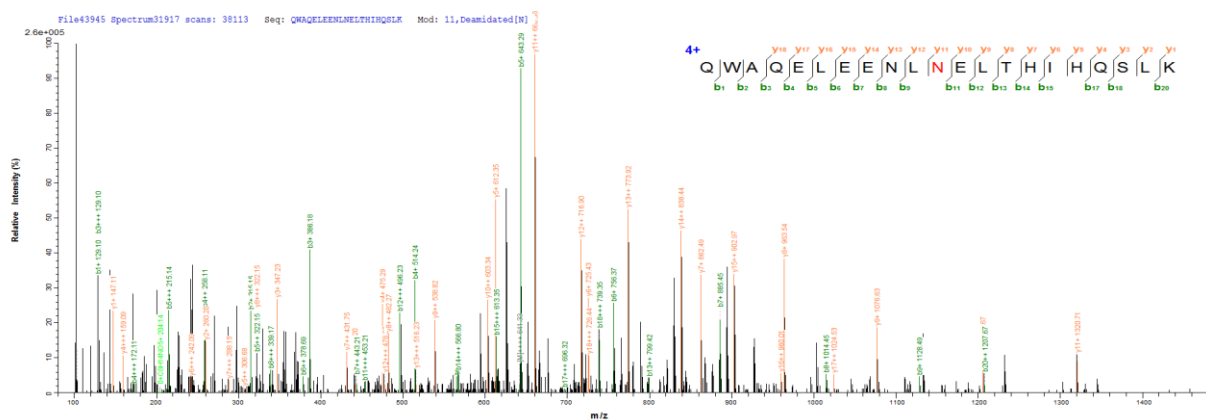
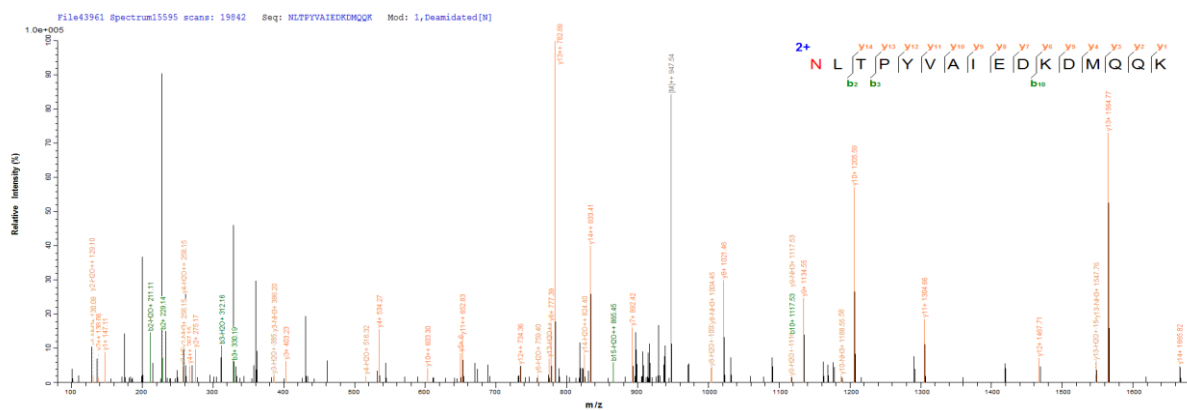
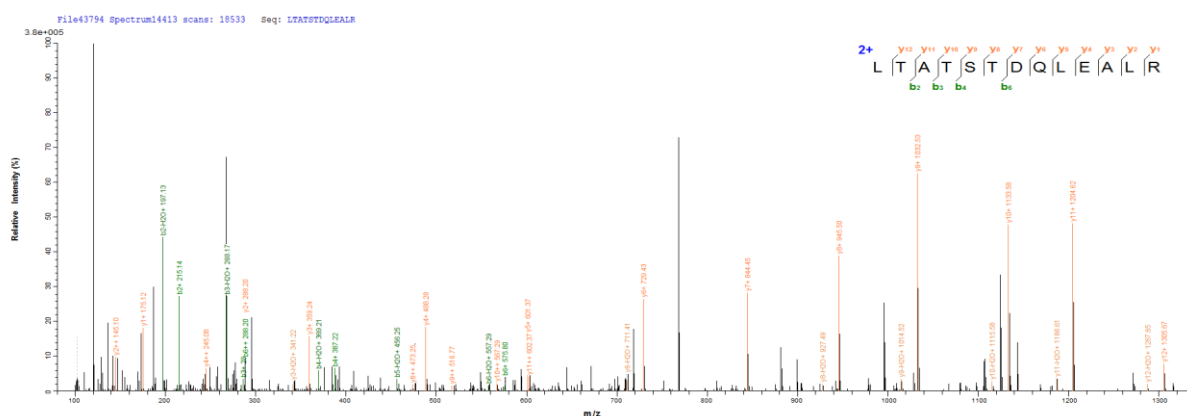
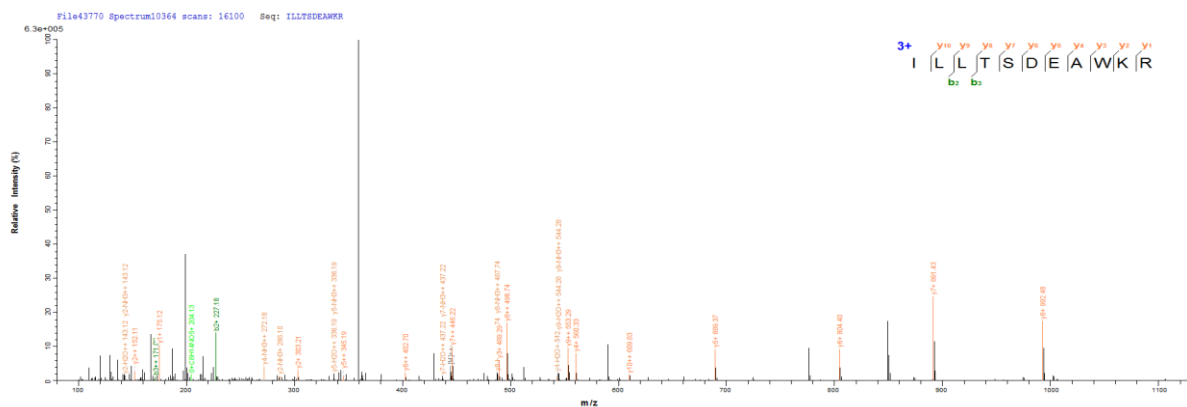




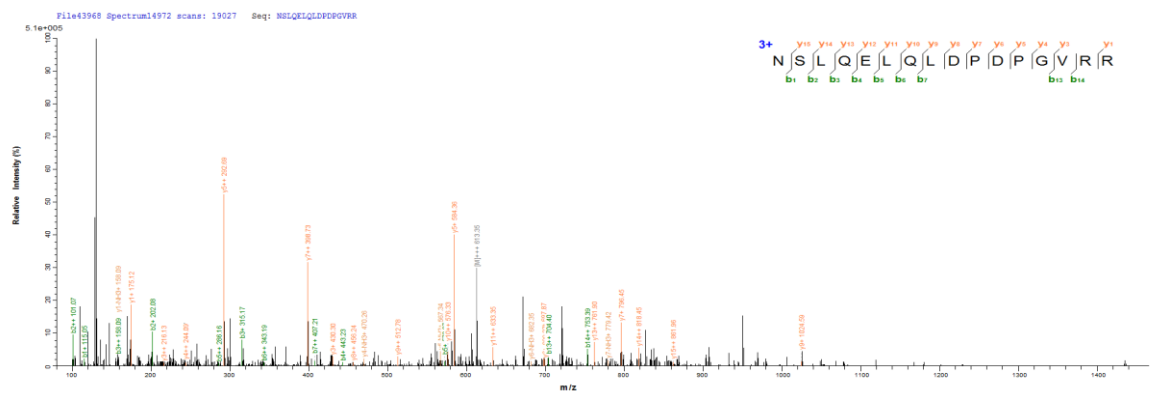
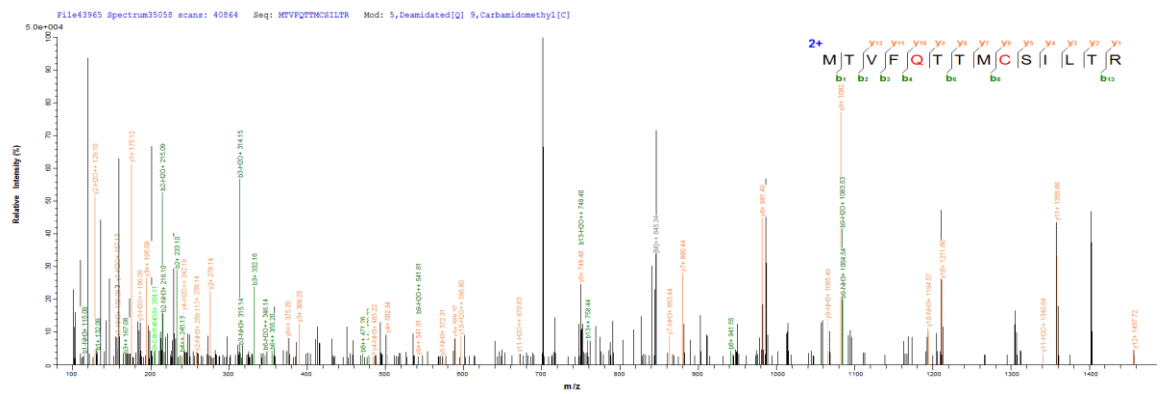
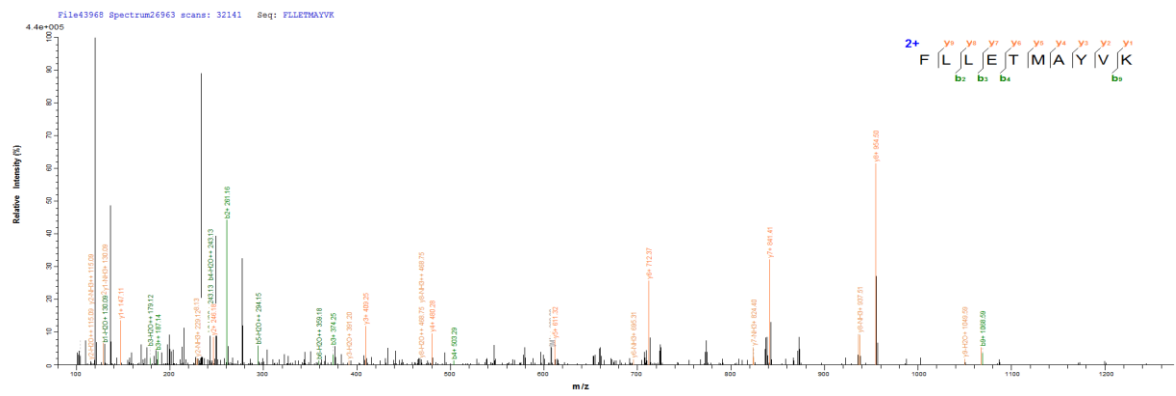


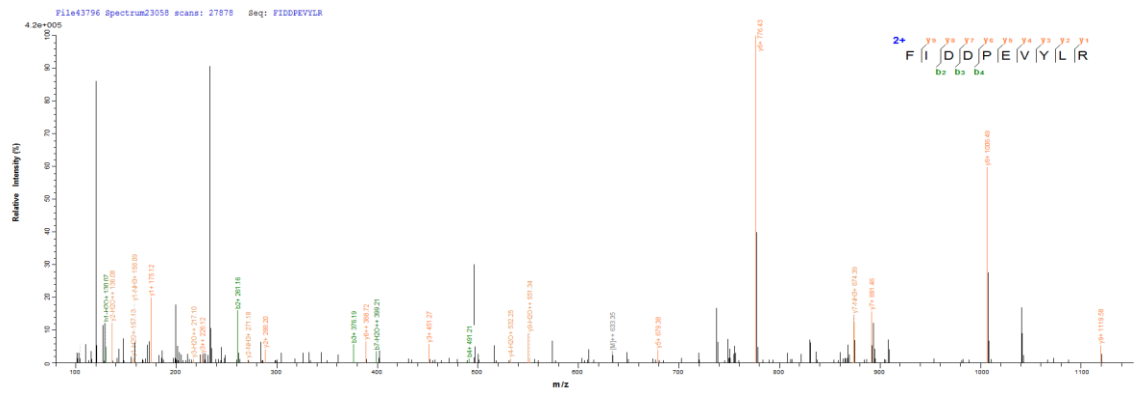
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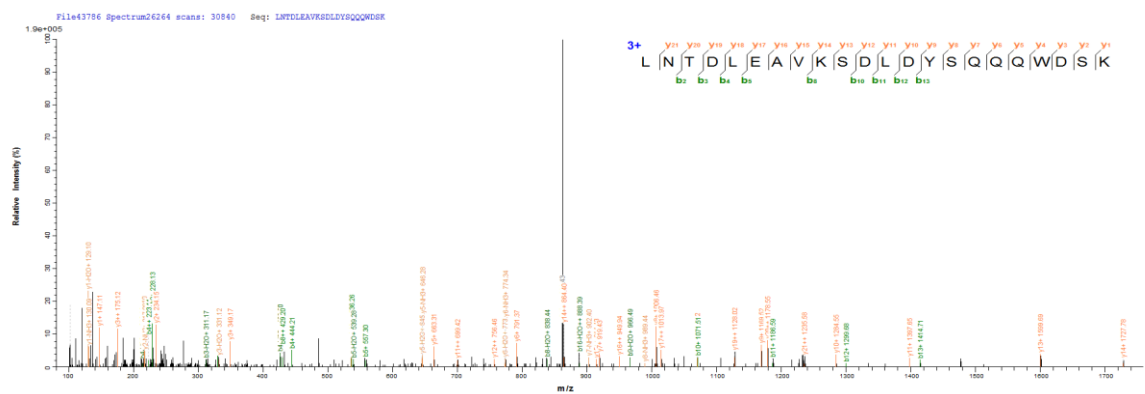
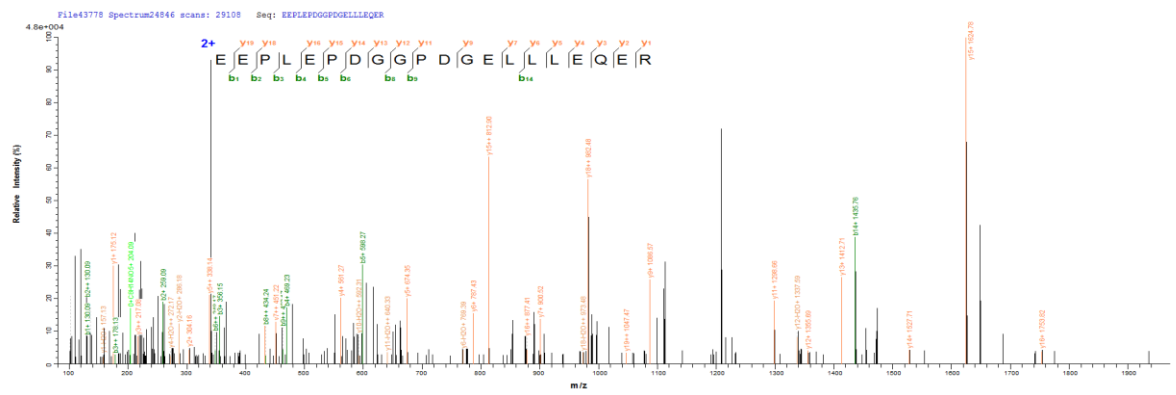
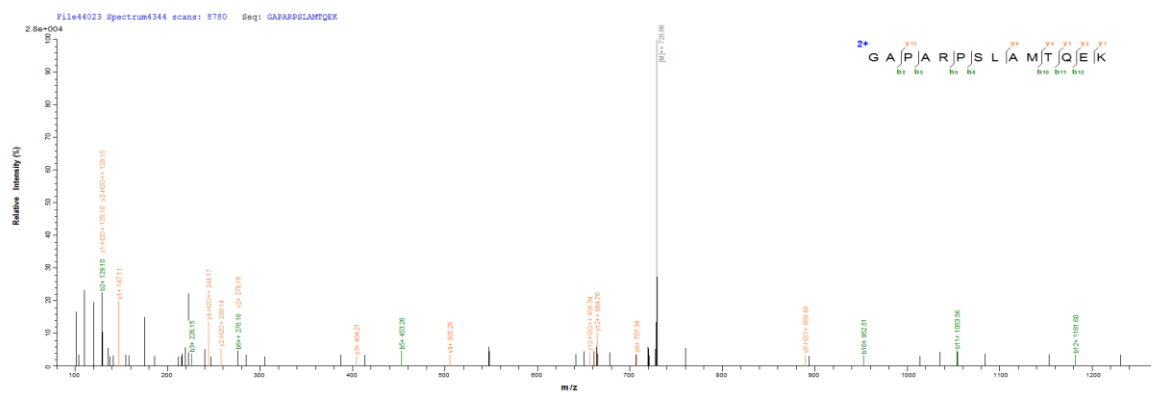


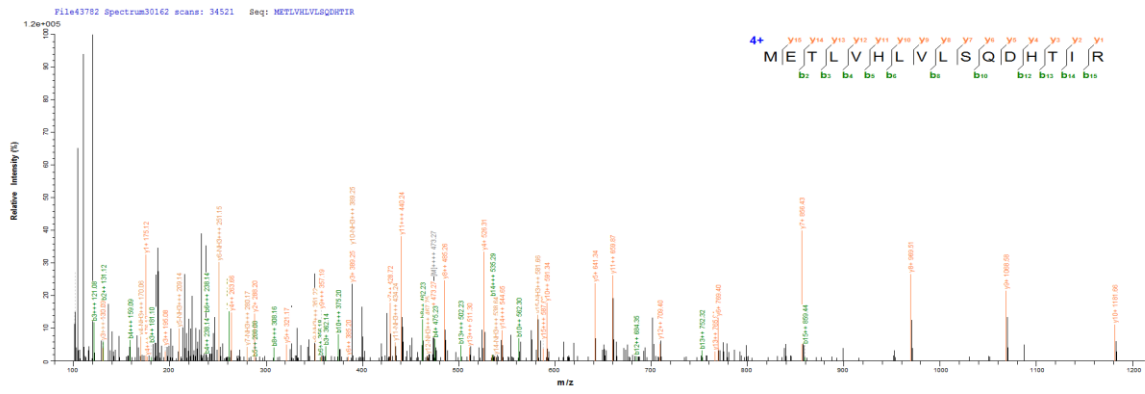
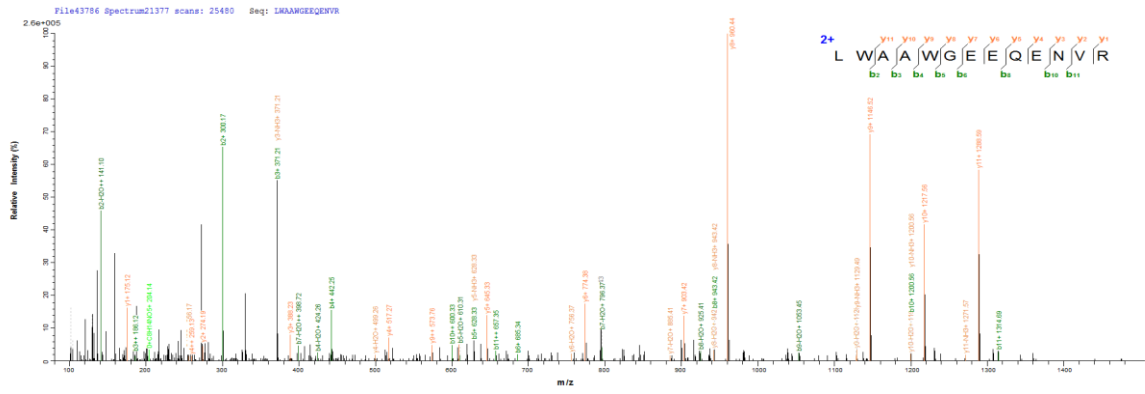
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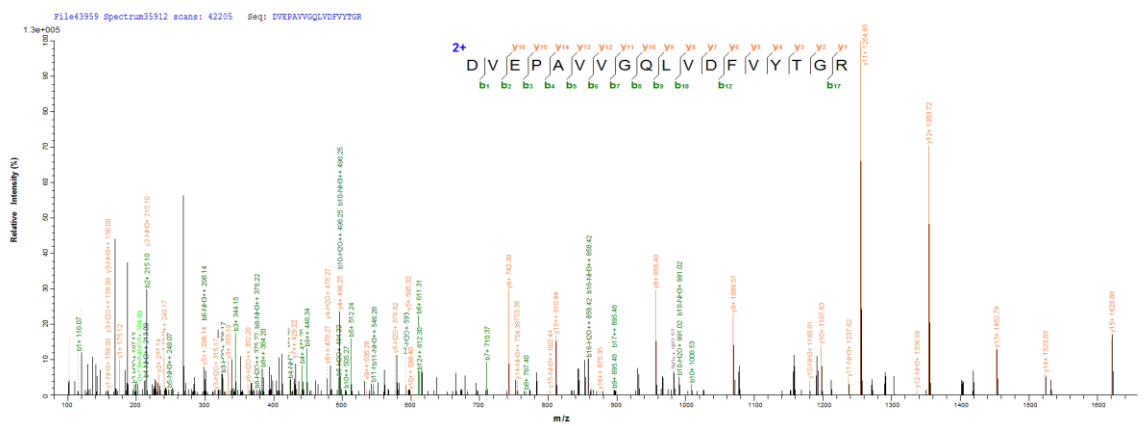
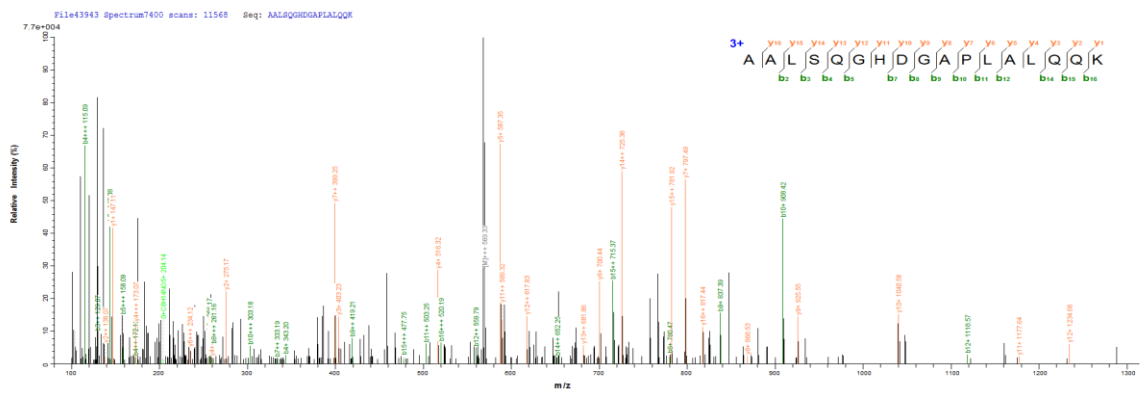


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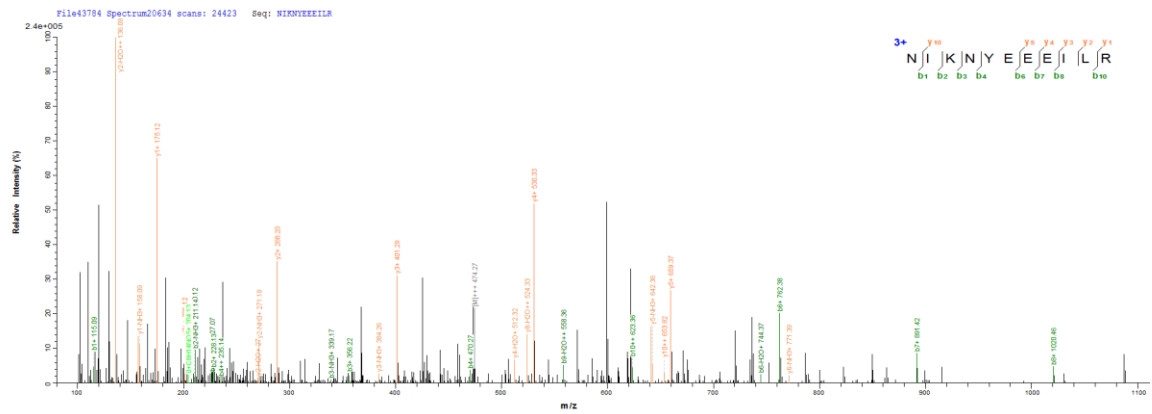
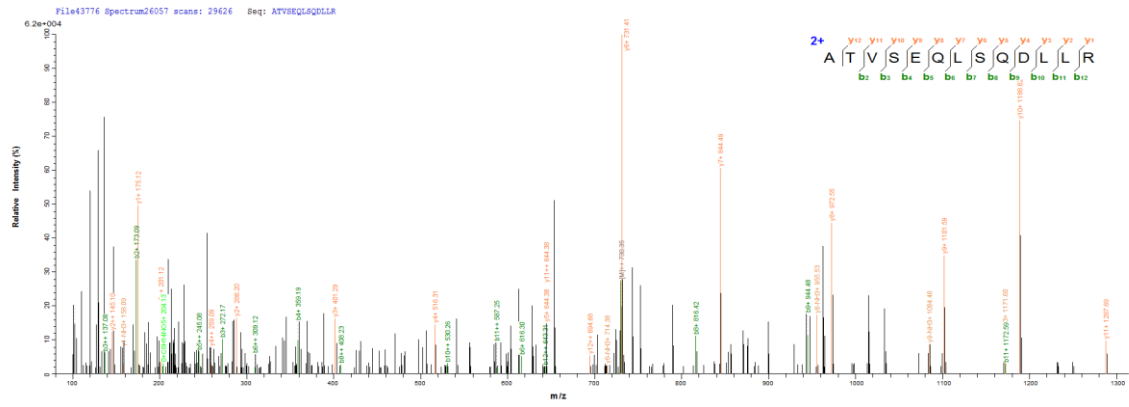




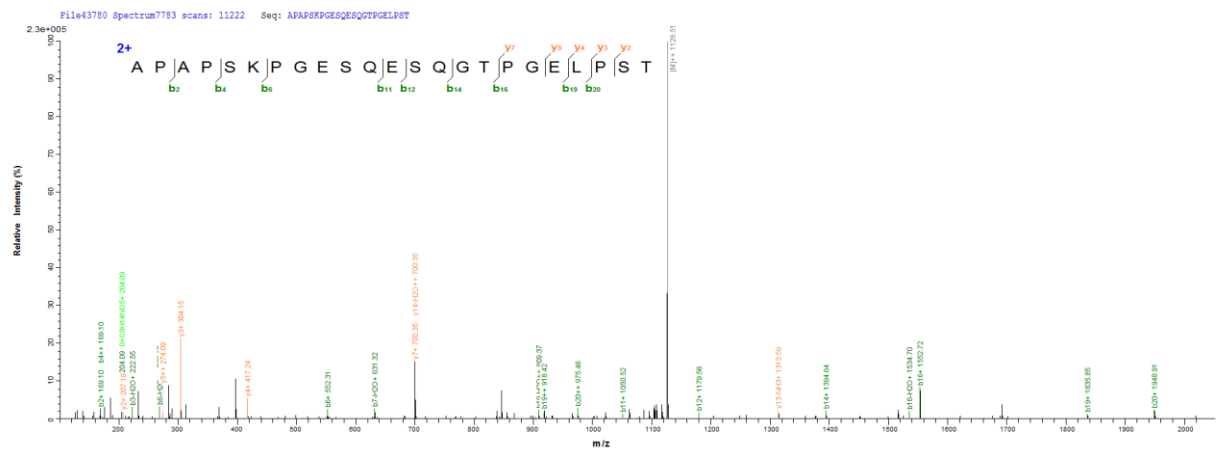
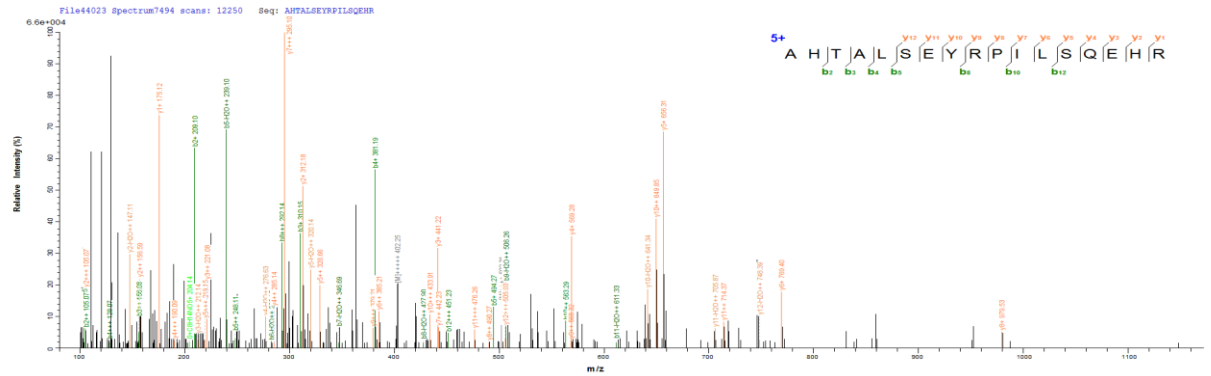
Q0D2K2



Q5XKL5



Q5UAW9



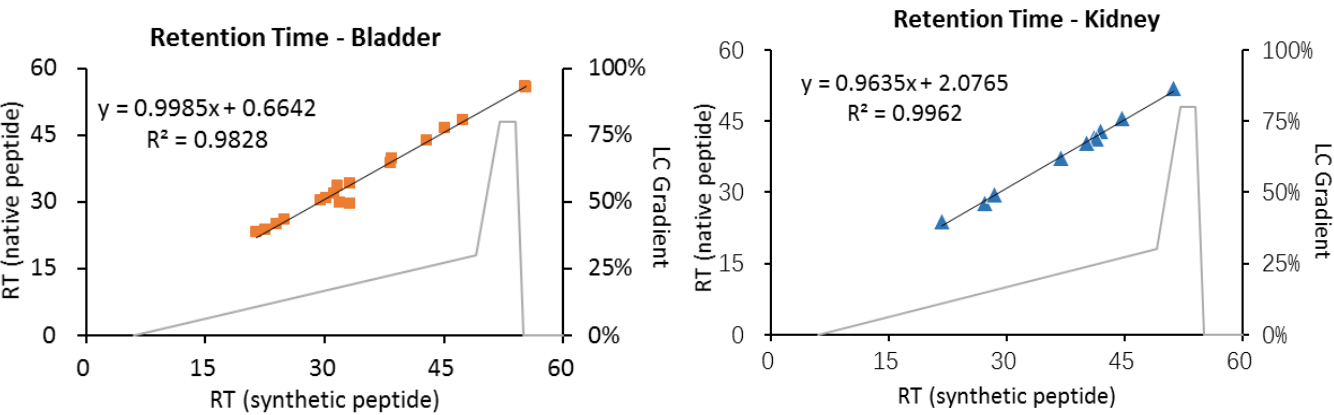
Supplementary Table 4: The precursor m/z, mass error, and E-value of all identified unique peptides from 20 MPs.

Tissue	Protein_Accession	Peptide	Experiment_Mass	Theory_Mass	Delta_ppm	Qvalue
liver	F8WCM5	APPALVVTANIGQAGGSSSR	1851.98	1851.98027	0.29	0
liver	F8WCM5	ALGTSDSPVLFIHCPGAAGTAQGLEYSR	2787.37	2787.365021	1.66	0
kidney	A6NGH7	YIFQLNEIEQEQLNR	1937.92	1937.937012	-11.23	5.00E-05
kidney	A6NGH7	EIFTKPLNFQETETDASKSDYELQALR	3174.56	3174.524414	10.2	0.000122199
kidney	A6NGS2	EELVTILEEEEESSKEEEEDQEPQR	3032.34	3032.346878	-3.04	0
kidney	A6NGS2	EVSPVEIPGQTLR	1423.77	1423.76709	4.27	4.31E-05
kidney	A6NGS2	QLNQAGLVPPGLGPPQALR	2023.14	2023.121445	10.19	0.000593322
kidney	P57058	ISLEDLSPSVVLHMTK	1896.99	1896.986649	-0.54	8.02E-06
kidney	P57058	MVDKEMNPLPTQLSTGAISFLR	2448.26	2448.239243	8.77	1.47E-05
kidney	P57058	FPMMGIGQMLRK	1440.71	1440.692734	13.6	0.00629672
kidney	Q14916	EYITSSLVQQVSSSR	1682.85	1682.847519	0.58	0
kidney	Q14916	NILSVIAVR	983.613	983.612747	0.02	1.80E-05
kidney	Q6ZP65	SLQSSAATSTSLSEIEQSMEAELEQEREQLR	3708.75	3708.763519	-2.91	0
kidney	Q6ZP65	MDMMSLNSQLLDALQK	1965.94	1965.920929	11.71	0
kidney	Q6ZP65	LNLSQQLQLEAWQDDMR	1982.93	1982.926834	0.03	0
kidney	Q6ZP65	LSATLEENDLLQGTVEELQDR	2374.14	2374.138702	-1.1	0.000976926
kidney	Q86T96	LTLLPTLYEIHAK	1526.87	1526.870804	0.59	0
kidney	Q86T96	AFHLFGGFR	1050.54	1050.539948	0.77	2.27E-05
kidney	Q96JF6	TFNQSSDLLR	1179.59	1179.588394	0.89	2.31E-05
kidney	Q96JF6	DSNQSSNLIHQK	1510.76	1510.748795	8.36	0.00198887
kidney	Q9NVL8	ALEGQLPPLQENWYGR	1869.93	1869.937317	-1.48	0
kidney	Q9NVL8	DMYFDIPLEHR	1434.66	1434.660172	-0.96	2.27E-05
kidney	Q9NVL8	METWLHEQEAQGQLLWDSSSDSDEQK	3237.42	3237.368027	17.36	0.0065958

bladder	A6NK89	METLVHLVLSQDHTIR	1891	1890.998566	-0.63	0
bladder	A6NK89	LWAAWGEEQENVR	1586.75	1586.747726	1.8	0
bladder	A6NK89	LNTDLEAVKSDLDYSQQQWDSK	2582.22	2582.213623	2.09	0
bladder	A6NES4	FLLETMAYVK	1213.64	1213.641663	0.73	1.15E-05
bladder	A6NK89	EEPLEPDGGPDGELLLEQER	2221.03	2221.038605	-4.47	1.96E-05
bladder	A6NK89	GAPARPSLAMTQEK	1455.75	1455.750366	-0.78	5.12E-05
bladder	A6NES4	MTVFQTTMCSILTR	1688.81	1688.793594	9.73	0.000147887
bladder	A6NES4	NSLQELQLDPDPGVRR	1835.95	1835.948959	-0.25	0.000329084
bladder	Q0D2K2	DVEPAVVGQLVDFVYTGR	1963	1963.005127	-2.81	0
bladder	Q0D2K2	AALSQGHGAPLALQKQK	1703.9	1703.895462	-0.25	0
bladder	Q5UAW9	AHTALSEYRPILSQEHR	2007.03	2007.02858	-0.52	1.05E-05
bladder	Q5UAW9	APAPSKPGESQESQGTPGELPST	2251.06	2251.060425	0.64	0.000338371
bladder	Q5XKL5	ATVSEQLSQDLLR	1458.77	1458.767807	0.25	2.94E-05
bladder	Q5XKL5	NIKNYEEEEILR	1419.74	1419.735733	-0.3	0.00186086
bladder	Q8IXH8	LLVQDRDSPFTSAWR	1789.91	1789.911133	0.65	0
bladder	Q8IXH8	IVDTSLIFNIR	1289.73	1289.734329	0.11	0
bladder	Q8IXH8	GNYLVPPLFIGDK	1334.72	1334.723434	-0.05	2.49E-06
bladder	Q8IXH8	RWVITTTLEEEEDPGPFPK	2255.15	2255.147385	-0.96	2.49E-06
bladder	Q8IXH8	YELVHDPANWVSVDK	1770.85	1770.857697	-5.34	4.47E-06
bladder	Q8IXH8	EEGARPGTLLGTFNAMDPDSQIR	2474.18	2474.185974	-0.85	4.47E-06
bladder	Q8IXH8	NWGQSVELLTLR	1414.76	1414.756851	0.58	4.61E-06
bladder	Q8IZF3	APETIESVAQGIR	1369.72	1369.720123	1.2	0
bladder	Q8IZF3	ACQMMLDIR	1136.51	1136.514038	-1.1	0.000138693
bladder	Q8IZF3	SYSEVANHILDTAAISNWAFIPNK	2662.32	2662.291443	11.47	0.00907733
bladder	Q92819	CLTETPIEYLR	1393.69	1393.691132	-1.75	2.49E-06
bladder	Q92819	ESSQHVTQLVLSNK	1568.82	1568.815826	2.22	6.91E-05

bladder	Q96MI6	IQQLAFVYPELLAGEFTR	2094.12	2094.11496	1.81	0
bladder	Q96MI6	LYMANAGDSR	1096.5	1096.497116	2.27	3.56E-05
bladder	Q96MI6	LLGTLAVSR	928.57	928.570557	-0.16	8.46E-05
bladder	Q96MI6	RDEIRPLSFETPETER	2121.05	2121.049057	0.32	0.000141211
bladder	Q9BPW4	NLTPYVAIEDKDMQQK	1891.94	1891.934937	0.96	0
bladder	Q9BPW4	LTATSTDQLEALR	1417.74	1417.741257	0.12	0
bladder	Q9BPW4	FTEEVIEYFQK	1431.69	1431.692184	0.03	0
bladder	Q9BPW4	QWAQEELENLNELTHIHQSLK	2559.26	2559.271713	-3.93	0
bladder	Q9BPW4	ILLTSDEAWKR	1330.73	1330.724472	0.88	2.65E-06
bladder	Q9NUC0	FIDDPEVYLR	1265.63	1265.629196	0.52	2.49E-06
bladder	Q9NUC0	AHILYMSLEK	1203.63	1203.632141	0	0.00127503

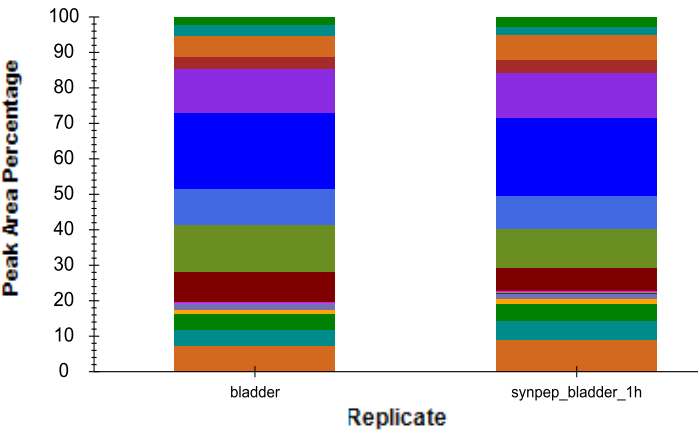
Supplementary Figure 3: The comparison of RT and fragment abundance pattern for the native peptides in human tissues and synthetic peptides from 16 MPs identified in PRM assay



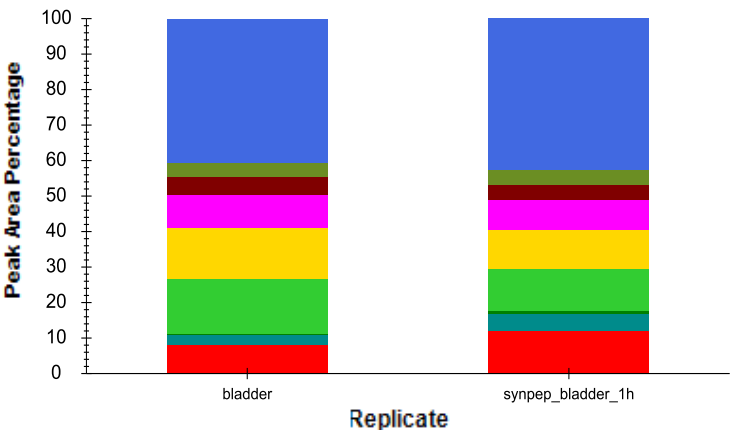
The correlation of RT for synthetic peptides and native peptides identified from bladder and kidney tissue MPs

Bladder

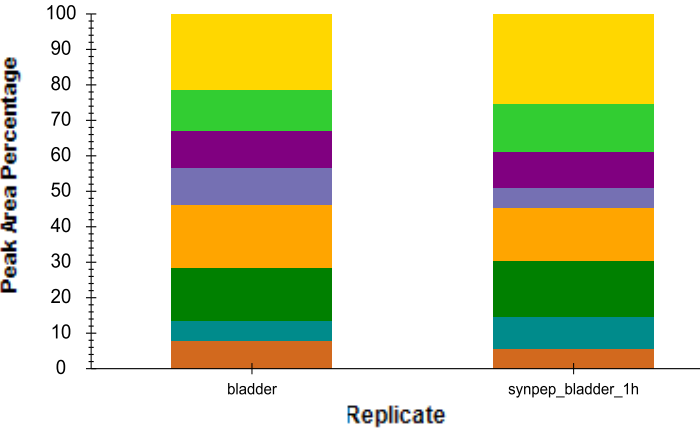
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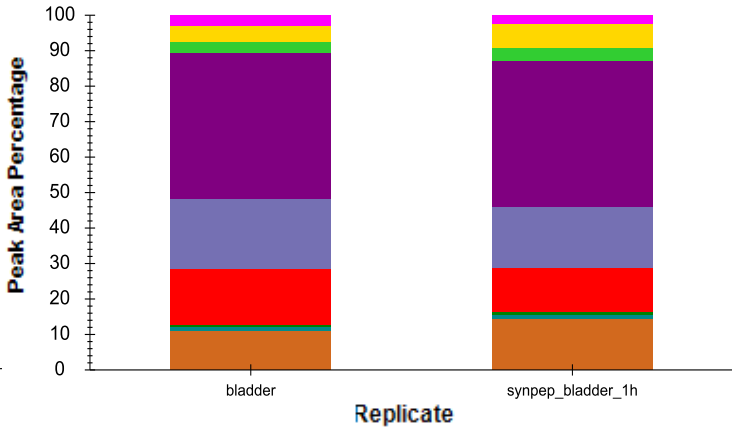
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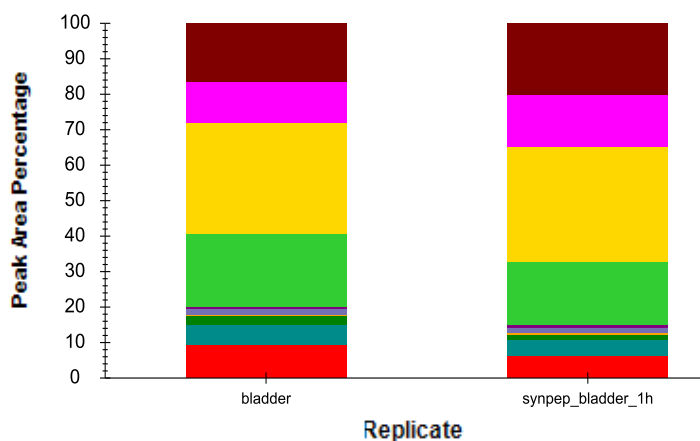
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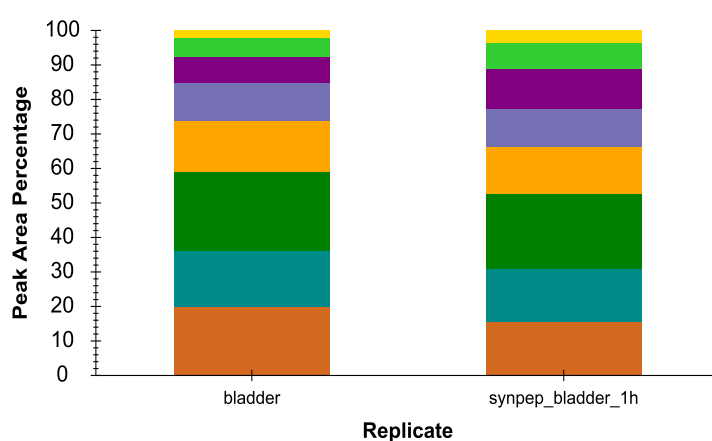
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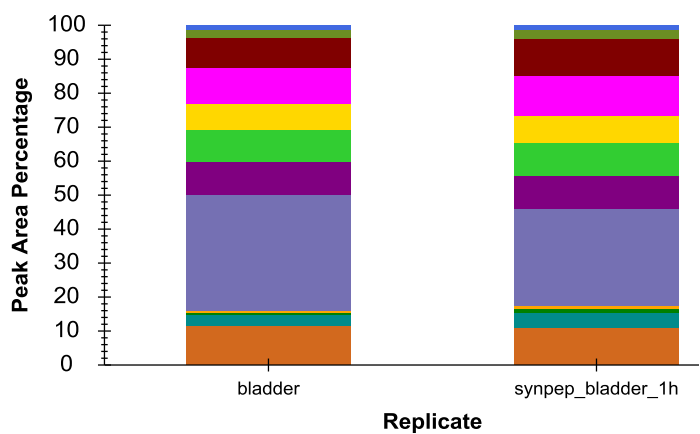
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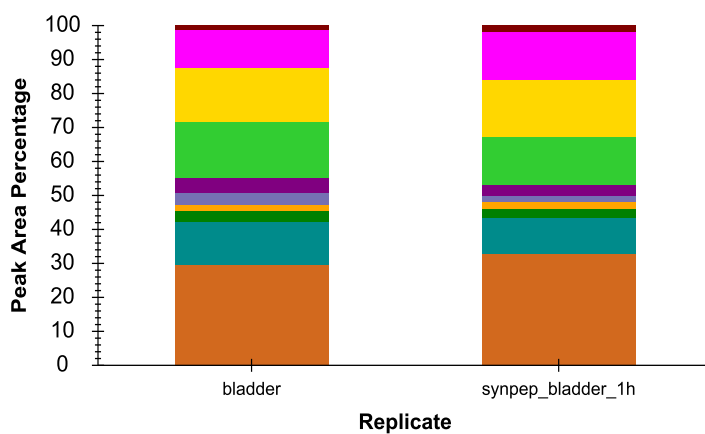
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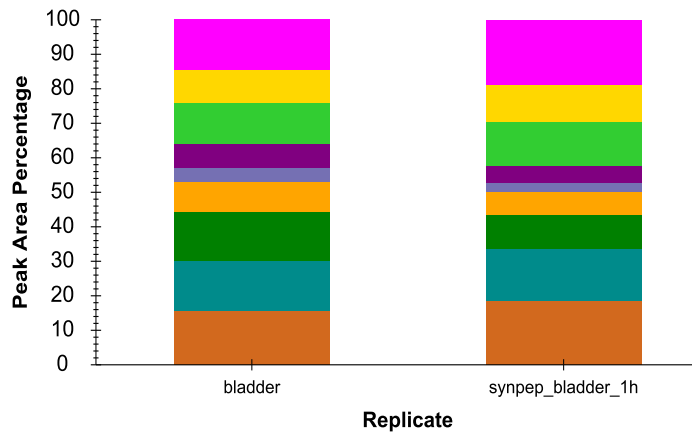
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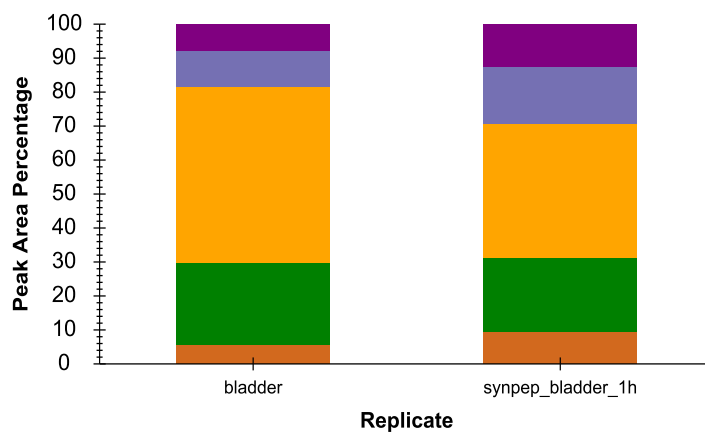
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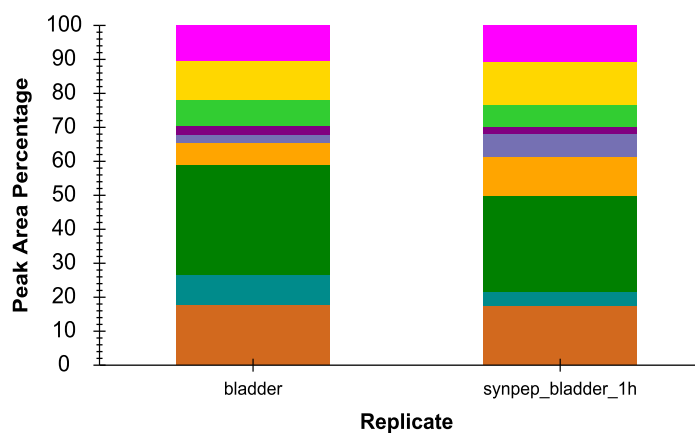
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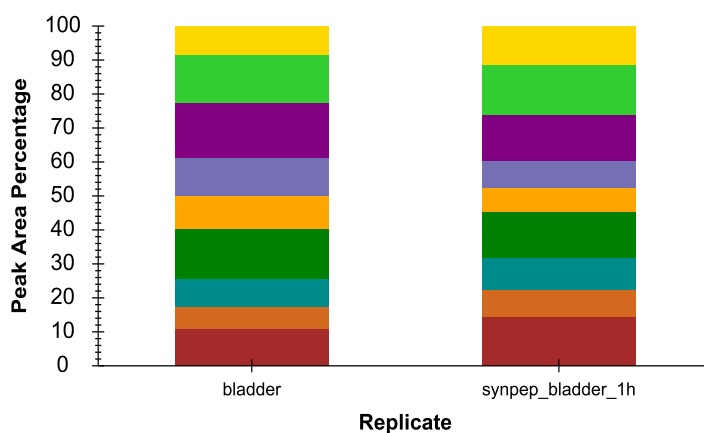
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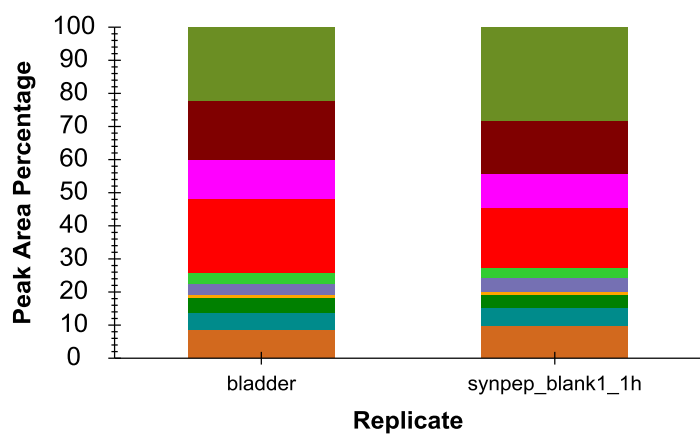
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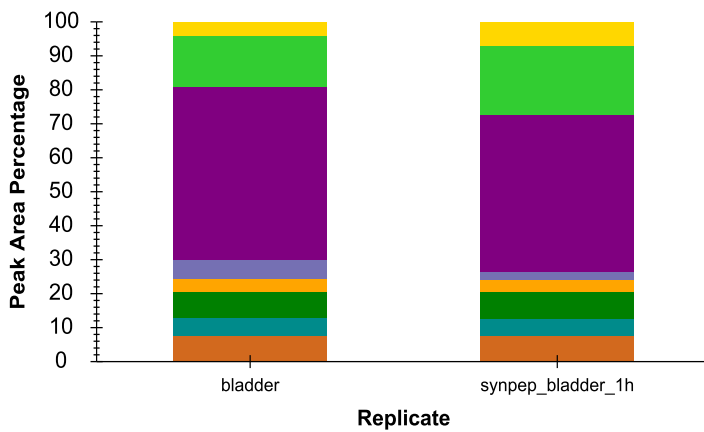
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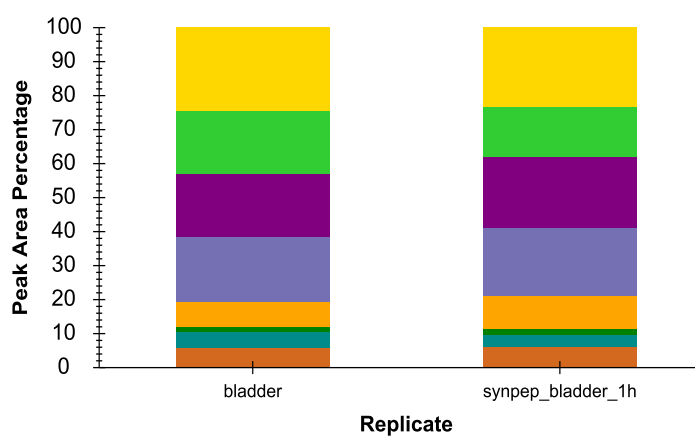
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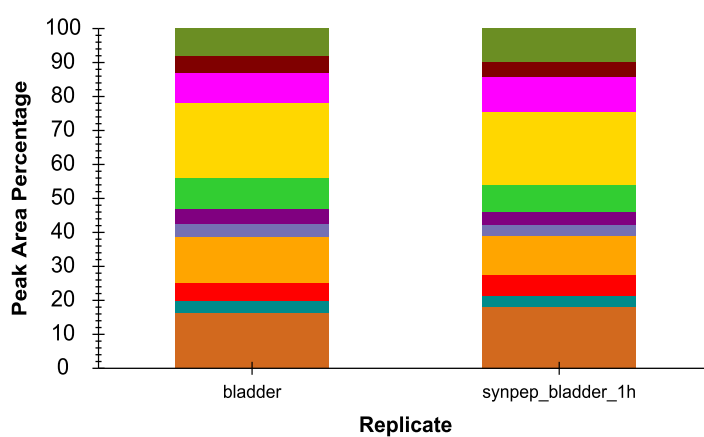
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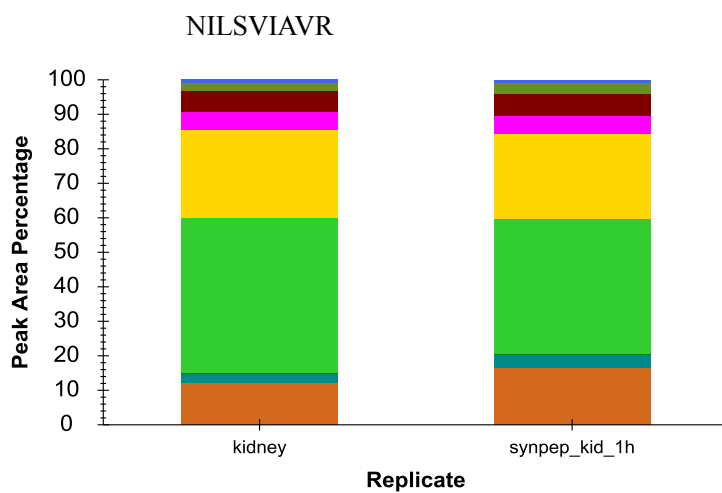
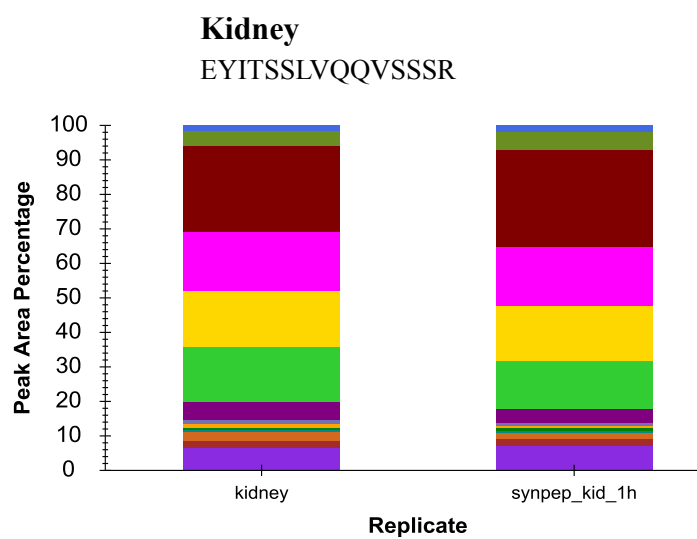
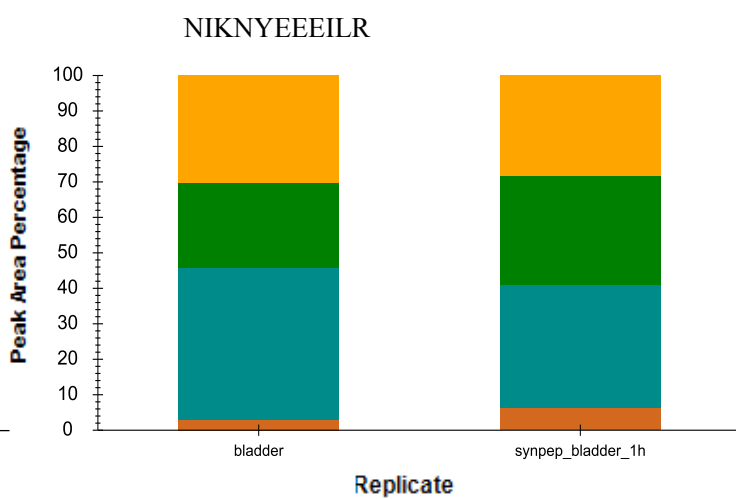
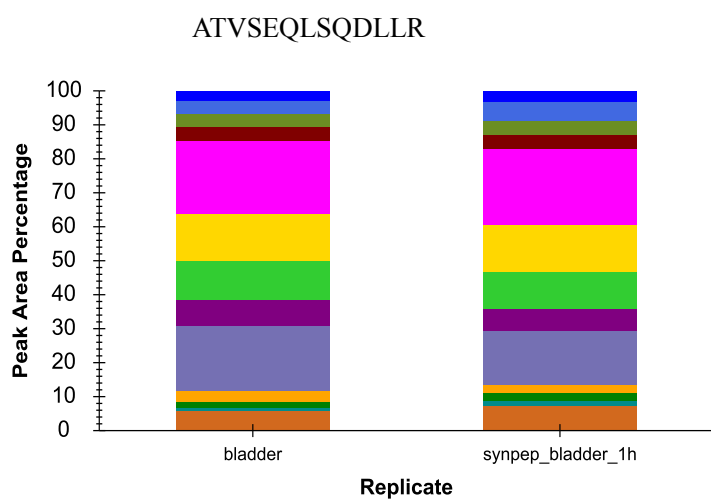
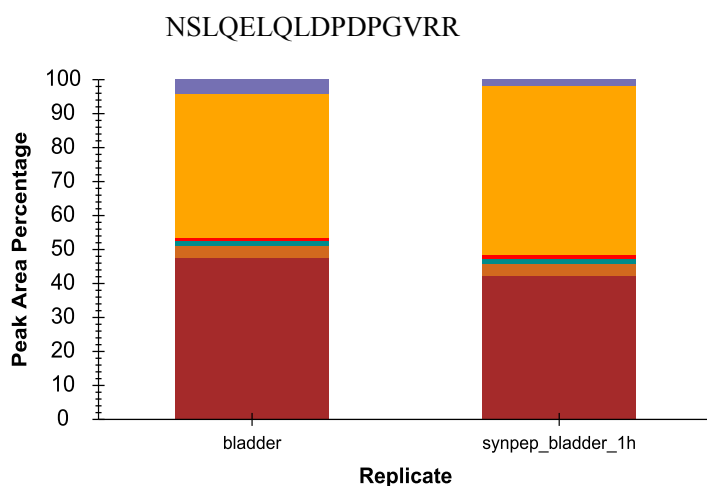
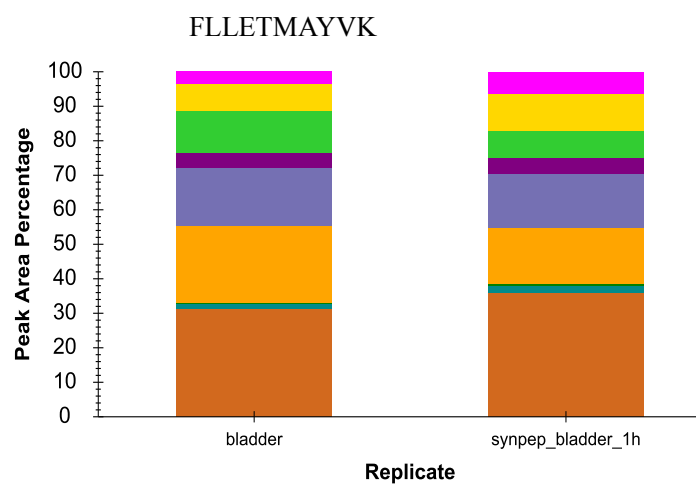


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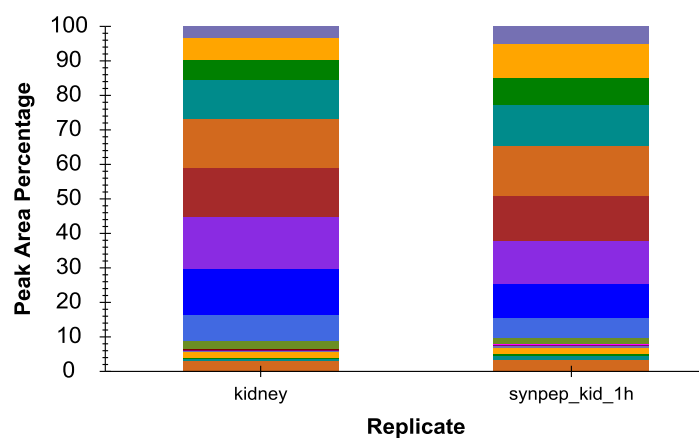


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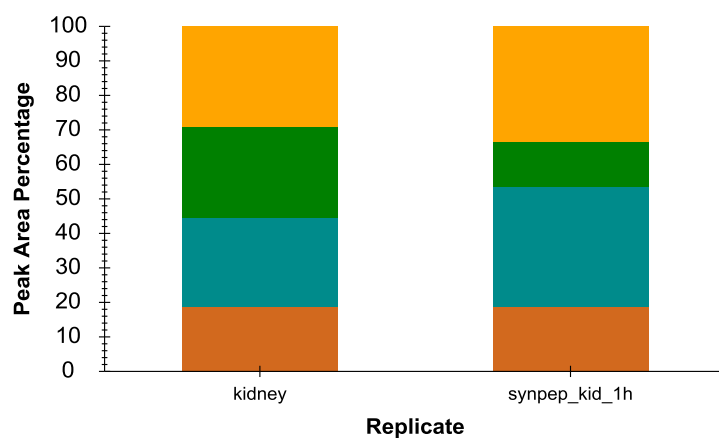




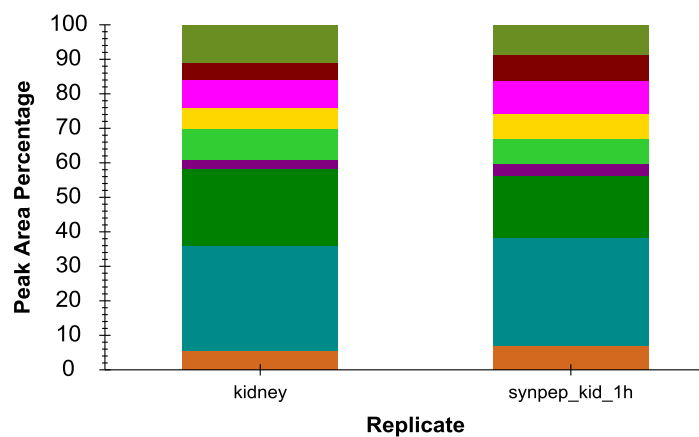
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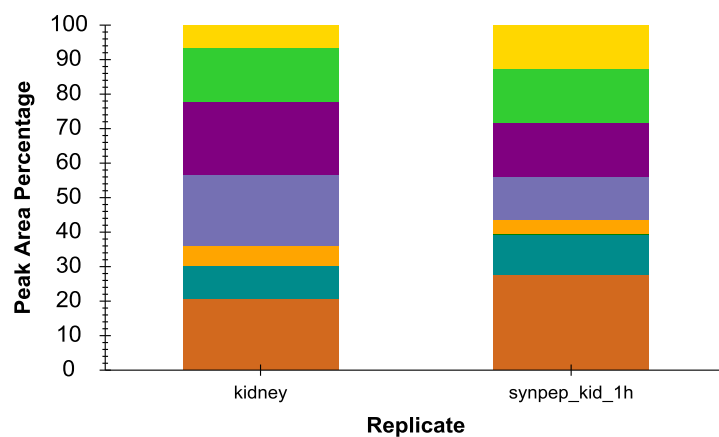
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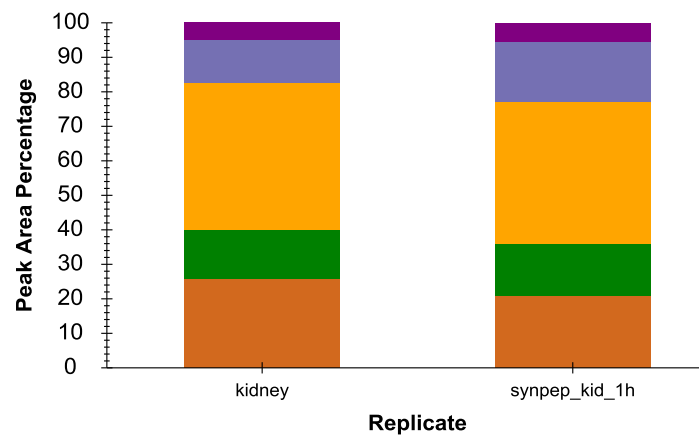
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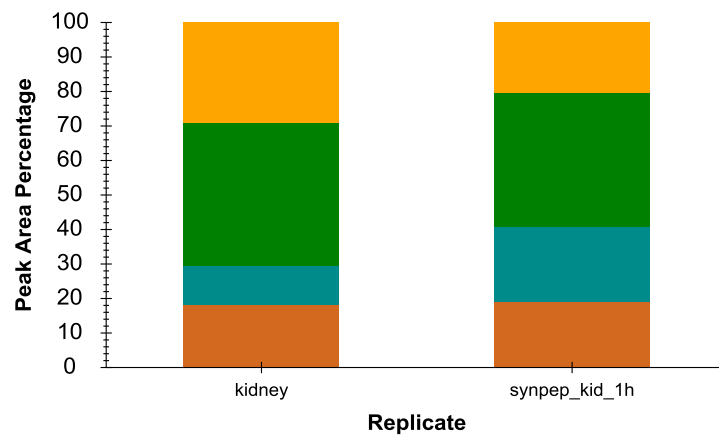
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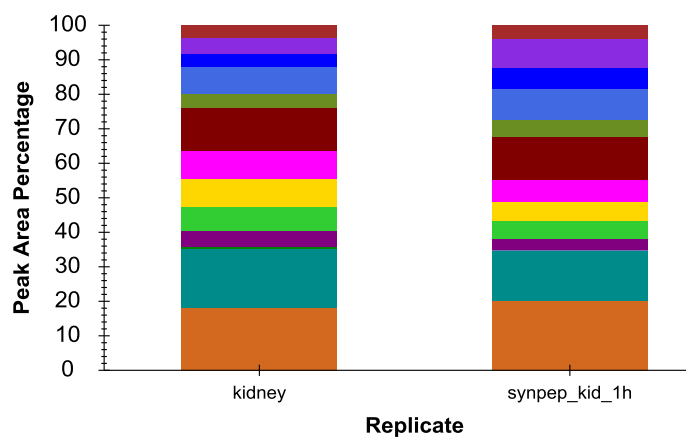
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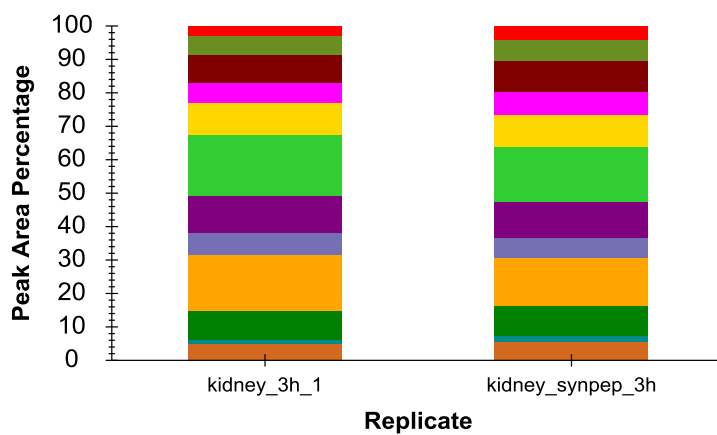
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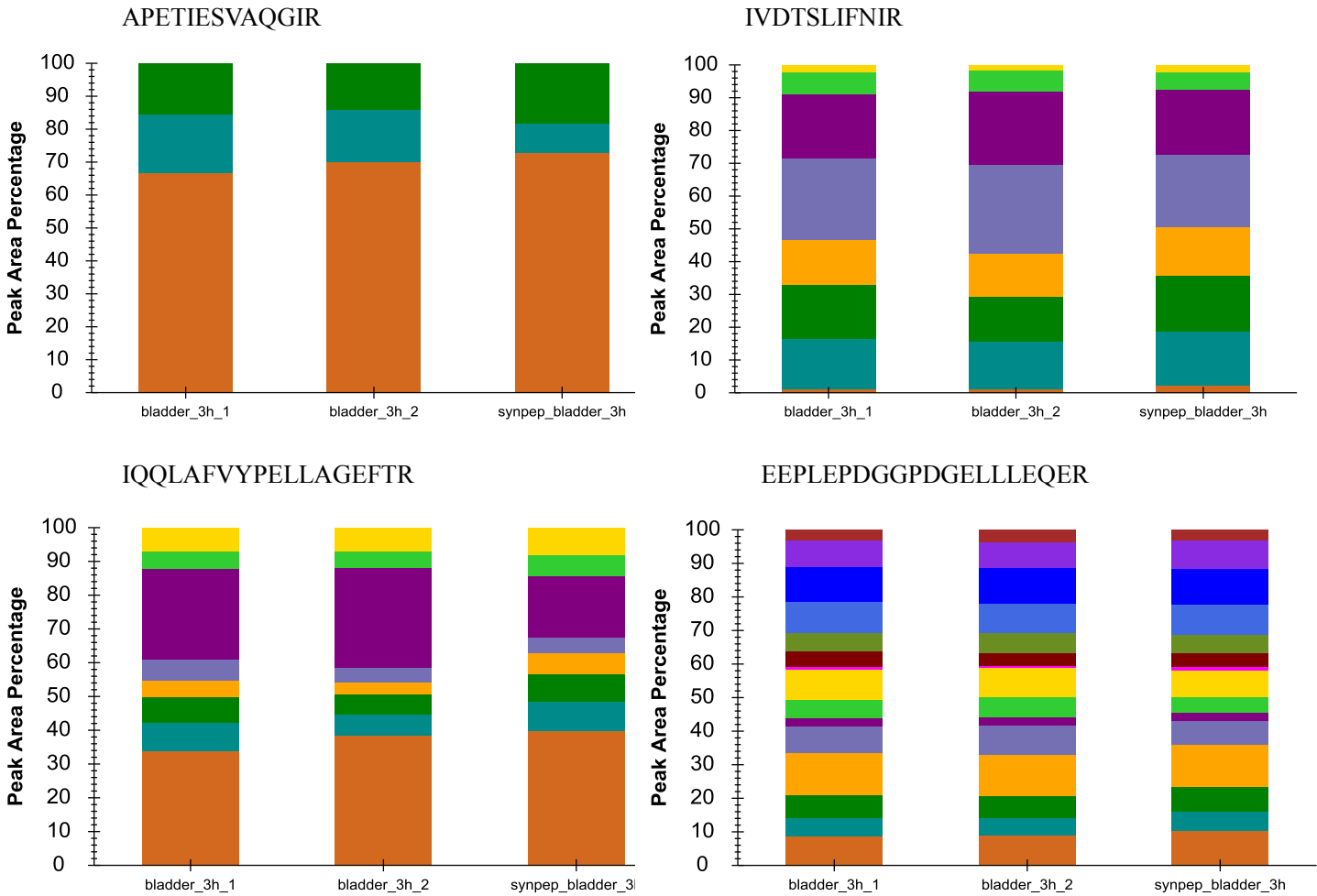


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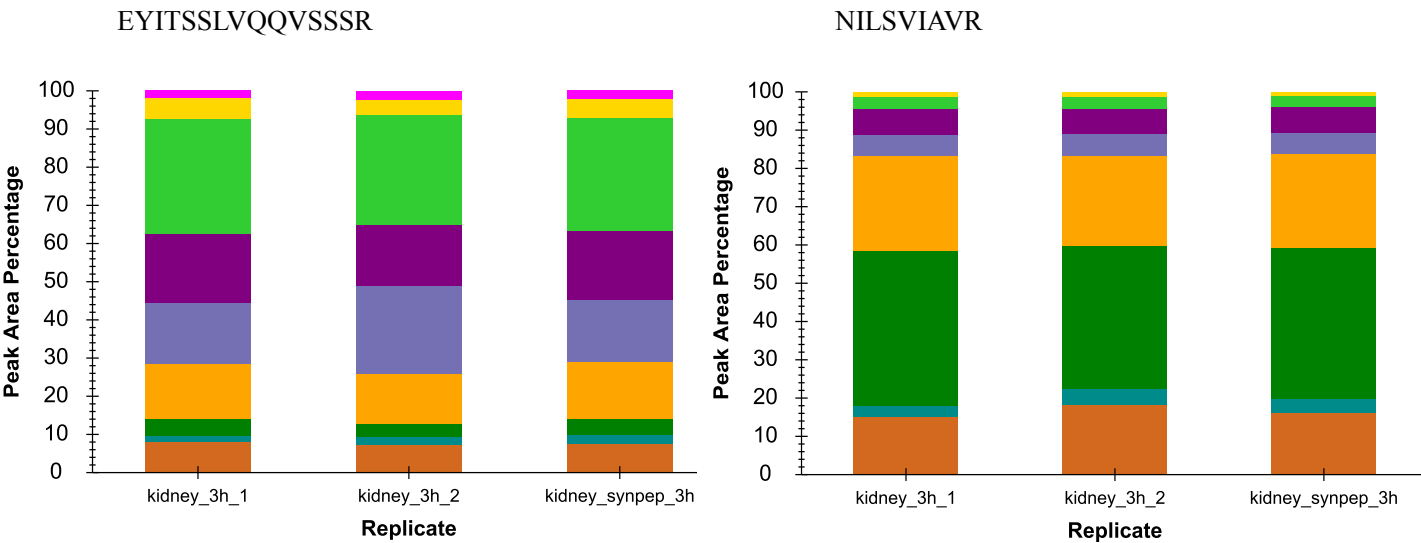


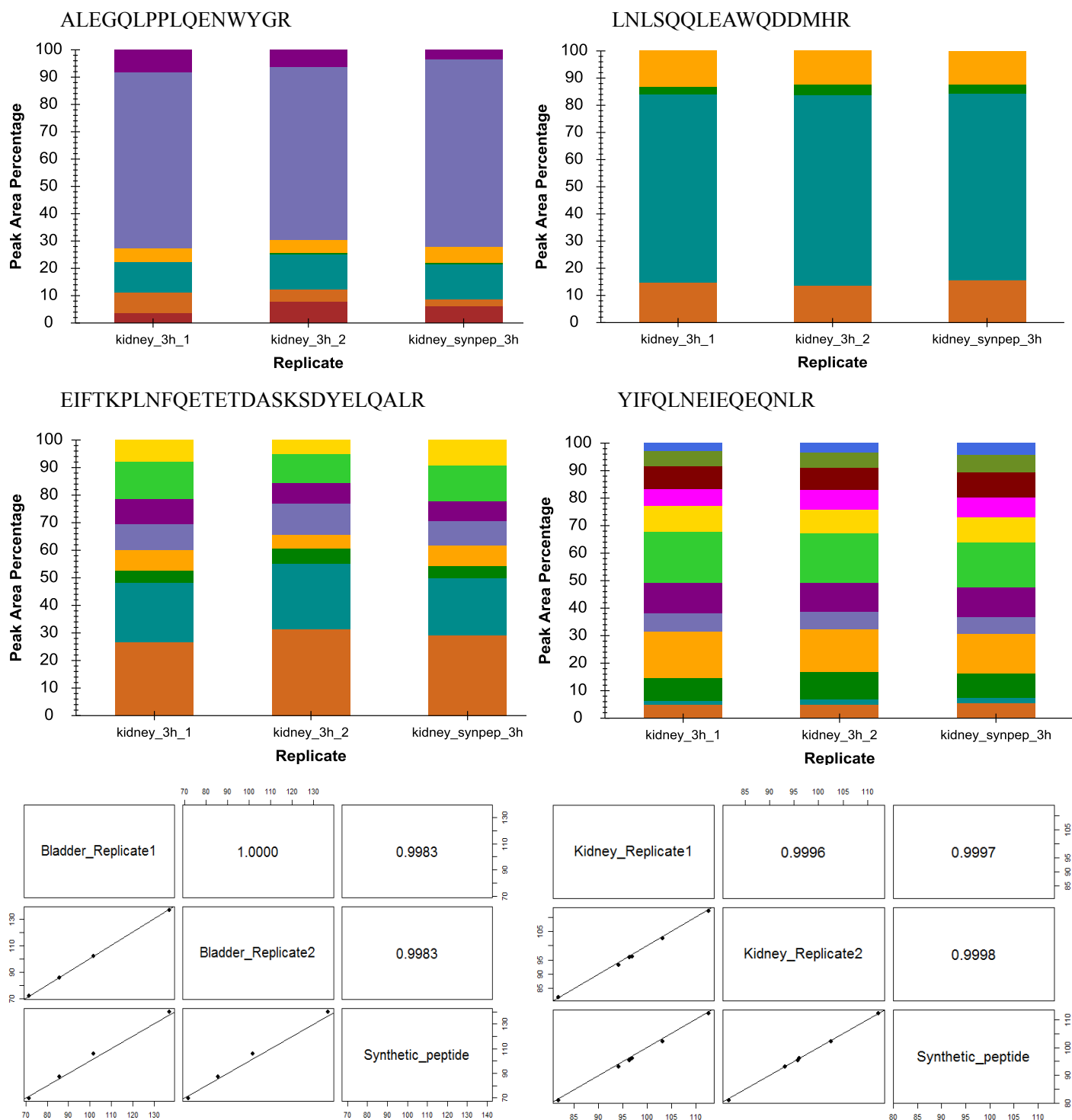
Supplementary Figure 4: The evaluation for the reproducibility of ProteoMiner depletion treatment by PRM assay

Bladder



Kidney





The correlation of RT for synthetic peptides and native peptides identified in duplicate depletion treatment to bladder and kidney tissue MPs