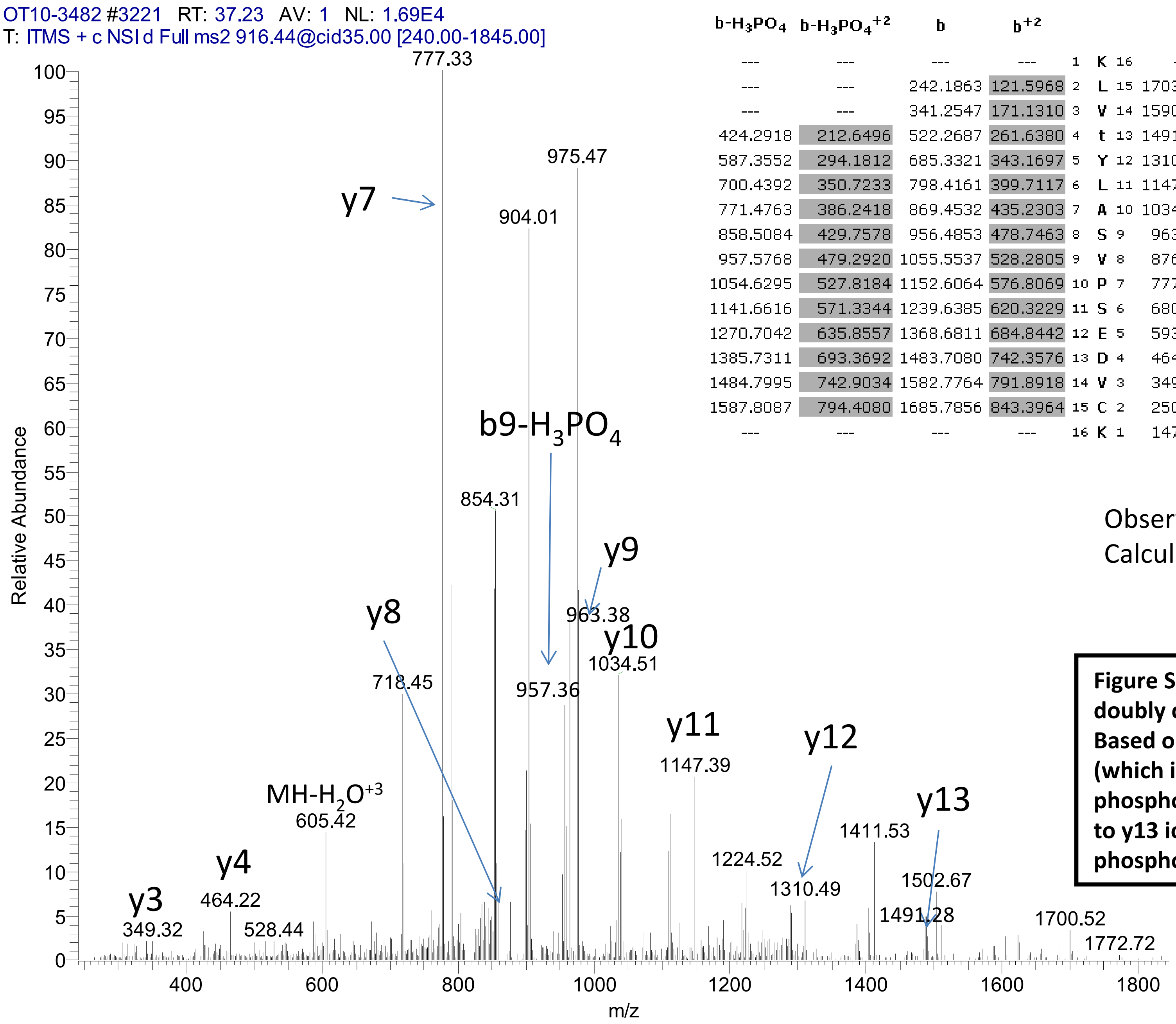
CamKII

MS/MS of peptide KLVpTYLASVPSEDVCK



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	K	16	---	---	---	---
---	---	242.1863	121.5968	2	L	15	1703.7962	852.4017	1605.8193	803.4133
---	---	341.2547	171.1310	3	V	14	1590.7121	795.8597	1492.7352	746.8712
424.2918	212.6496	522.2687	261.6380	4	t	13	1491.6437	746.3255	1393.6668	697.3370
587.3552	294.1812	685.3321	343.1697	5	Y	12	1310.6297	655.8185	---	---
700.4392	350.7233	798.4161	399.7117	6	L	11	1147.5664	574.2868	---	---
771.4763	386.2418	869.4532	435.2303	7	A	10	1034.4823	517.7448	---	---
858.5084	429.7578	956.4853	478.7463	8	S	9	963.4452	482.2262	---	---
957.5768	479.2920	1055.5537	528.2805	9	V	8	876.4131	438.7102	---	---
1054.6295	527.8184	1152.6064	576.8069	10	P	7	777.3447	389.1760	---	---
1141.6616	571.3344	1239.6385	620.3229	11	S	6	680.2920	340.6496	---	---
1270.7042	635.8557	1368.6811	684.8442	12	E	5	593.2599	297.1336	---	---
1385.7311	693.3692	1483.7080	742.3576	13	D	4	464.2173	232.6123	---	---
1484.7995	742.9034	1582.7764	791.8918	14	V	3	349.1904	175.0988	---	---
1587.8087	794.4080	1685.7856	843.3964	15	C	2	250.1220	125.5646	---	---
---	---	---	---	16	K	1	147.1128	74.0600	---	---

Observed M=1830.8685
Calculated M=1830.8838

Figure S1. MS/MS on the doubly charged 916.44 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y10 to y13 ions, residue 79 is a phosphothreonine.

CamKII

MS/MS of peptide LVTYLApSVPSEDVCKR

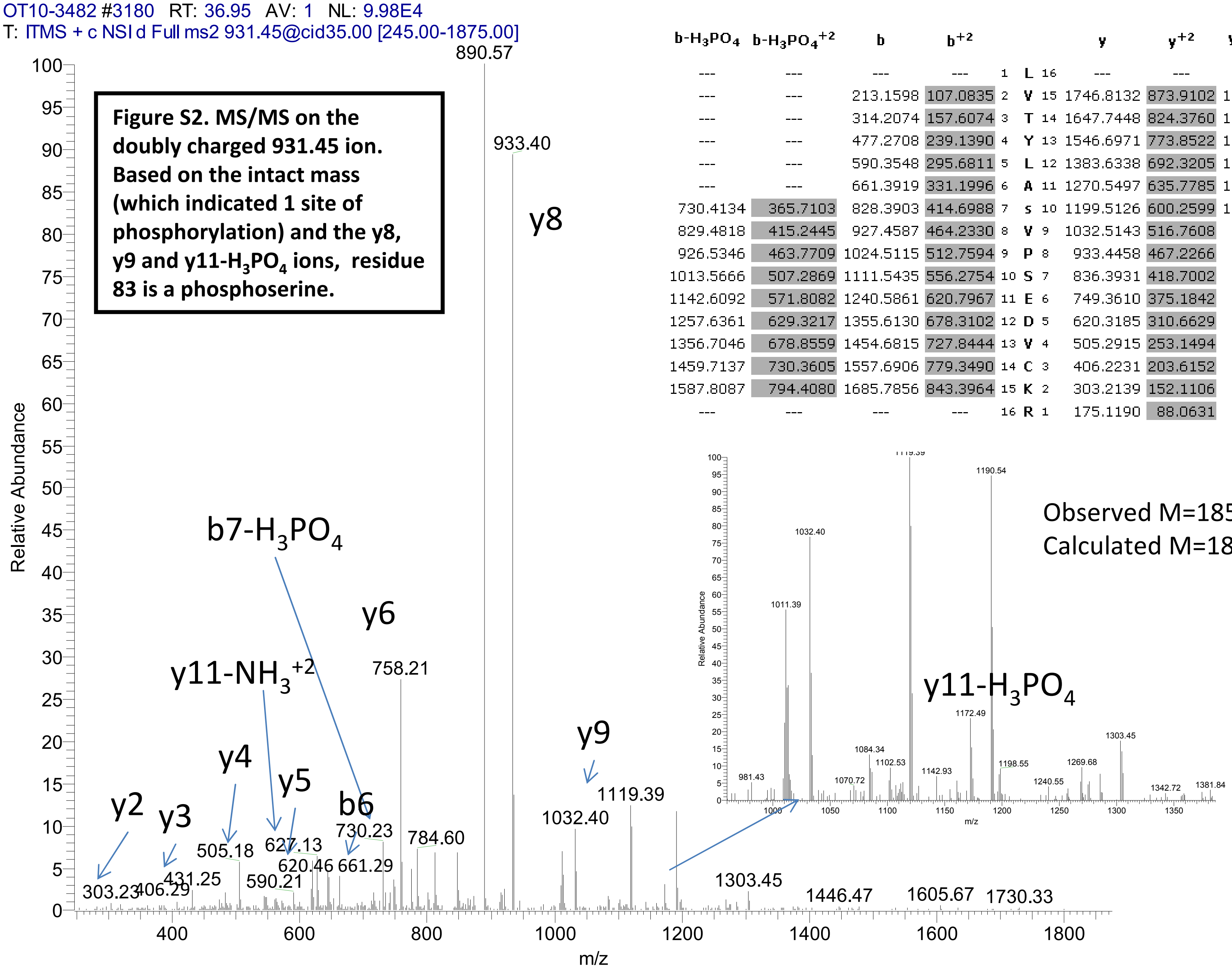


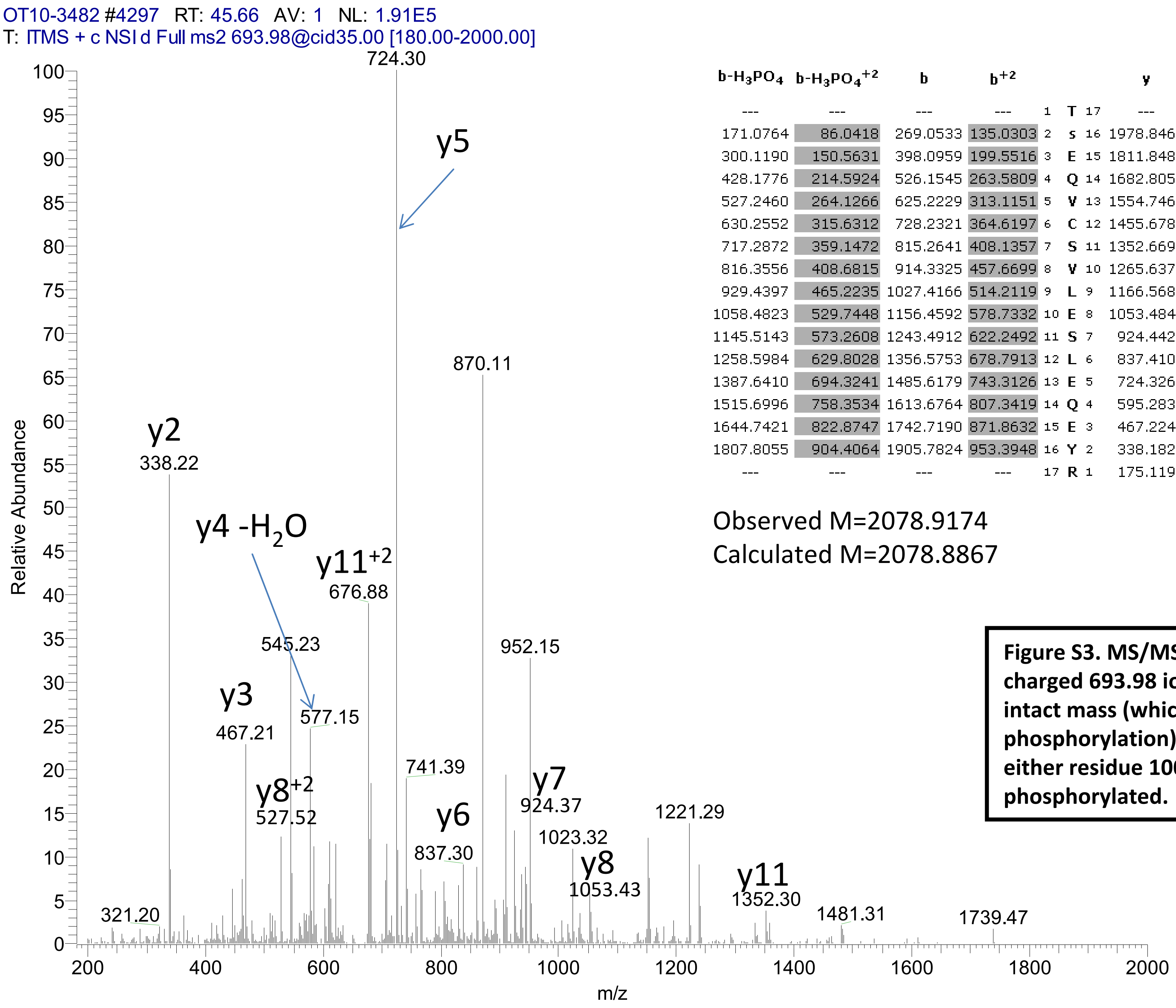
Figure S2. MS/MS on the doubly charged 931.45 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y8, y9 and y11-H_3PO_4 ions, residue 83 is a phosphoserine.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	16	---	---	---	---
---	---	213.1598	107.0835	2	V	15	1746.8132	873.9102	1648.8363	824.9218
---	---	314.2074	157.6074	3	T	14	1647.7448	824.3760	1549.7679	775.3876
---	---	477.2708	239.1390	4	Y	13	1546.6971	773.8522	1448.7202	724.8638
---	---	590.3548	295.6811	5	L	12	1383.6338	692.3205	1285.6569	643.3321
---	---	661.3919	331.1996	6	A	11	1270.5497	635.7785	1172.5728	586.7901
730.4134	365.7103	828.3903	414.6988	7	s	10	1199.5126	600.2599	1101.5357	551.2715
829.4818	415.2445	927.4587	464.2330	8	V	9	1032.5143	516.7608	---	---
926.5346	463.7709	1024.5115	512.7594	9	P	8	933.4458	467.2266	---	---
1013.5666	507.2869	1111.5435	556.2754	10	S	7	836.3931	418.7002	---	---
1142.6092	571.8082	1240.5861	620.7967	11	E	6	749.3610	375.1842	---	---
1257.6361	629.3217	1355.6130	678.3102	12	D	5	620.3185	310.6629	---	---
1356.7046	678.8559	1454.6815	727.8444	13	V	4	505.2915	253.1494	---	---
1459.7137	730.3605	1557.6906	779.3490	14	C	3	406.2231	203.6152	---	---
1587.8087	794.4080	1685.7856	843.3964	15	K	2	303.2139	152.1106	---	---
---	---	---	---	16	R	1	175.1190	88.0631	---	---

Observed M=1858.8736
Calculated M=1858.8900

CamKII

MS/MS of peptide pT/pSEQVCSVLESLEQEYR



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	T	17	---	---	---	---
171.0764	86.0418	269.0533	135.0303	2	s	16	1978.8464	989.9268	1880.8695	940.9384
300.1190	150.5631	398.0959	199.5516	3	E	15	1811.8480	906.4276	---	---
428.1776	214.5924	526.1545	263.5809	4	Q	14	1682.8054	841.9063	---	---
527.2460	264.1266	625.2229	313.1151	5	V	13	1554.7468	777.8771	---	---
630.2552	315.6312	728.2321	364.6197	6	C	12	1455.6784	728.3428	---	---
717.2872	359.1472	815.2641	408.1357	7	S	11	1352.6692	676.8383	---	---
816.3556	408.6815	914.3325	457.6699	8	V	10	1265.6372	633.3222	---	---
929.4397	465.2235	1027.4166	514.2119	9	L	9	1166.5688	583.7880	---	---
1058.4823	529.7448	1156.4592	578.7332	10	E	8	1053.4847	527.2460	---	---
1145.5143	573.2608	1243.4912	622.2492	11	S	7	924.4421	462.7247	---	---
1258.5984	629.8028	1356.5753	678.7913	12	L	6	837.4101	419.2087	---	---
1387.6410	694.3241	1485.6179	743.3126	13	E	5	724.3260	362.6667	---	---
1515.6996	758.3534	1613.6764	807.3419	14	Q	4	595.2835	298.1454	---	---
1644.7421	822.8747	1742.7190	871.8632	15	E	3	467.2249	234.1161	---	---
1807.8055	904.4064	1905.7824	953.3948	16	Y	2	338.1823	169.5948	---	---
---	---	---	---	17	R	1	175.1190	88.0631	---	---

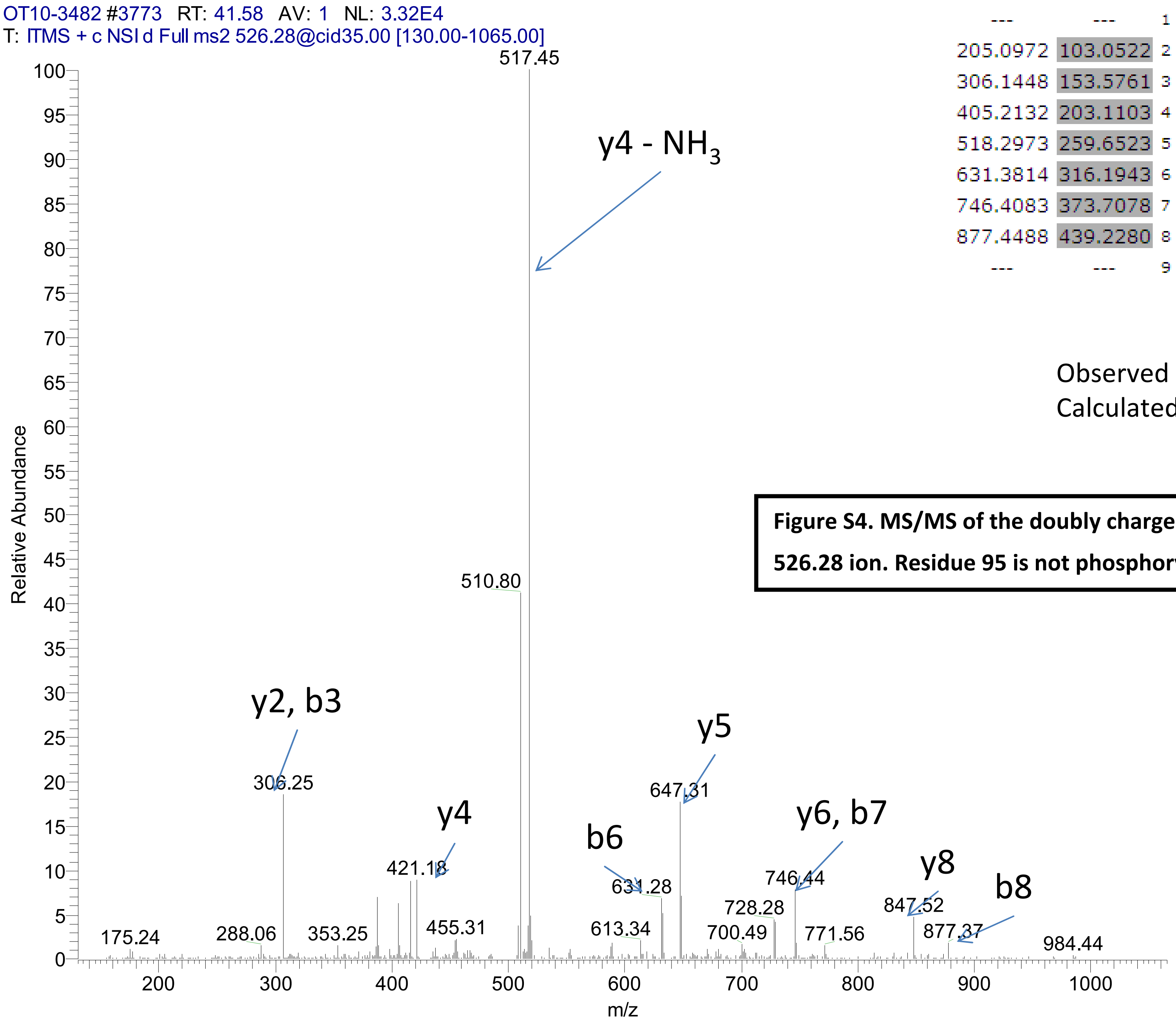
Observed M=2078.9174
Calculated M=2078.8867

Figure S3. MS/MS on the triply charged 693.98 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, either residue 1002 or 1003 is phosphorylated.

CamKII

MS/MS of peptide GFTVIIDMR

b	b^{+2}				y	y^{+2}
---	---	1	**G**	9	---	---
205.0972	103.0522	2	**F**	8	994.5390	497.7731
306.1448	153.5761	3	**T**	7	847.4706	424.2389
405.2132	203.1103	4	**V**	6	746.4229	373.7151
518.2973	259.6523	5	**I**	5	647.3545	324.1809
631.3814	316.1943	6	**I**	4	534.2704	267.6389
746.4083	373.7078	7	**D**	3	421.1864	211.0968
877.4488	439.2280	8	**M**	2	306.1594	153.5834
---	---	9	**R**	1	175.1190	88.0631

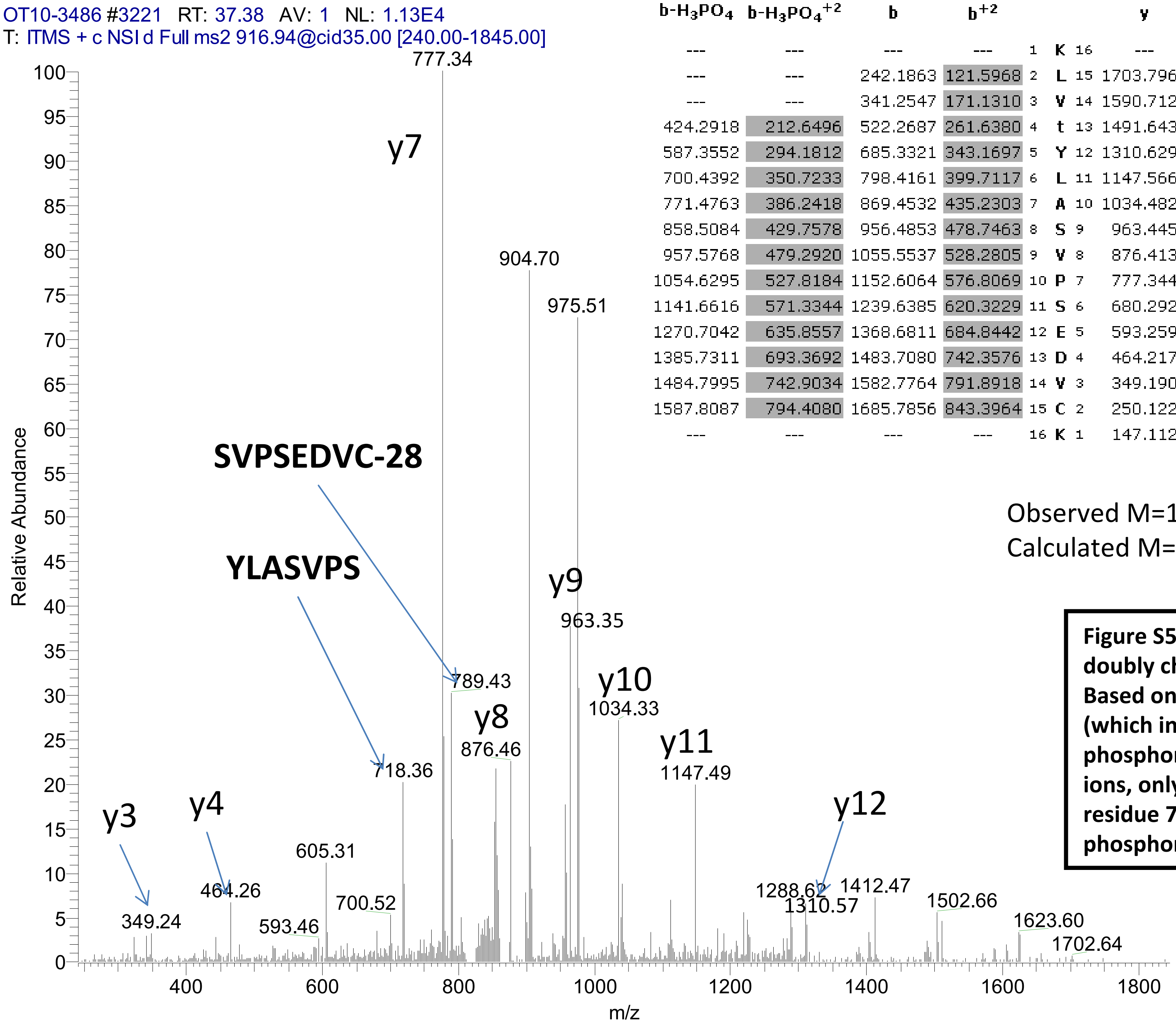


Observed M=1050.5511
Calculated M=1050.5532

Figure S4. MS/MS of the doubly charged 526.28 ion. Residue 95 is not phosphorylated.

PKA

MS/MS of peptide KLVpTYLASVPSEDVCK



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	K	16	---	---	---	---
---	---	242.1863	121.5968	2	L	15	1703.7962	852.4017	1605.8193	803.4133
---	---	341.2547	171.1310	3	V	14	1590.7121	795.8597	1492.7352	746.8712
424.2918	212.6496	522.2687	261.6380	4	t	13	1491.6437	746.3255	1393.6668	697.3370
587.3552	294.1812	685.3321	343.1697	5	Y	12	1310.6297	655.8185	---	---
700.4392	350.7233	798.4161	399.7117	6	L	11	1147.5664	574.2868	---	---
771.4763	386.2418	869.4532	435.2303	7	A	10	1034.4823	517.7448	---	---
858.5084	429.7578	956.4853	478.7463	8	S	9	963.4452	482.2262	---	---
957.5768	479.2920	1055.5537	528.2805	9	V	8	876.4131	438.7102	---	---
1054.6295	527.8184	1152.6064	576.8069	10	P	7	777.3447	389.1760	---	---
1141.6616	571.3344	1239.6385	620.3229	11	S	6	680.2920	340.6496	---	---
1270.7042	635.8557	1368.6811	684.8442	12	E	5	593.2599	297.1336	---	---
1385.7311	693.3692	1483.7080	742.3576	13	D	4	464.2173	232.6123	---	---
1484.7995	742.9034	1582.7764	791.8918	14	V	3	349.1904	175.0988	---	---
1587.8087	794.4080	1685.7856	843.3964	15	C	2	250.1220	125.5646	---	---
---	---	---	---	16	K	1	147.1128	74.0600	---	---

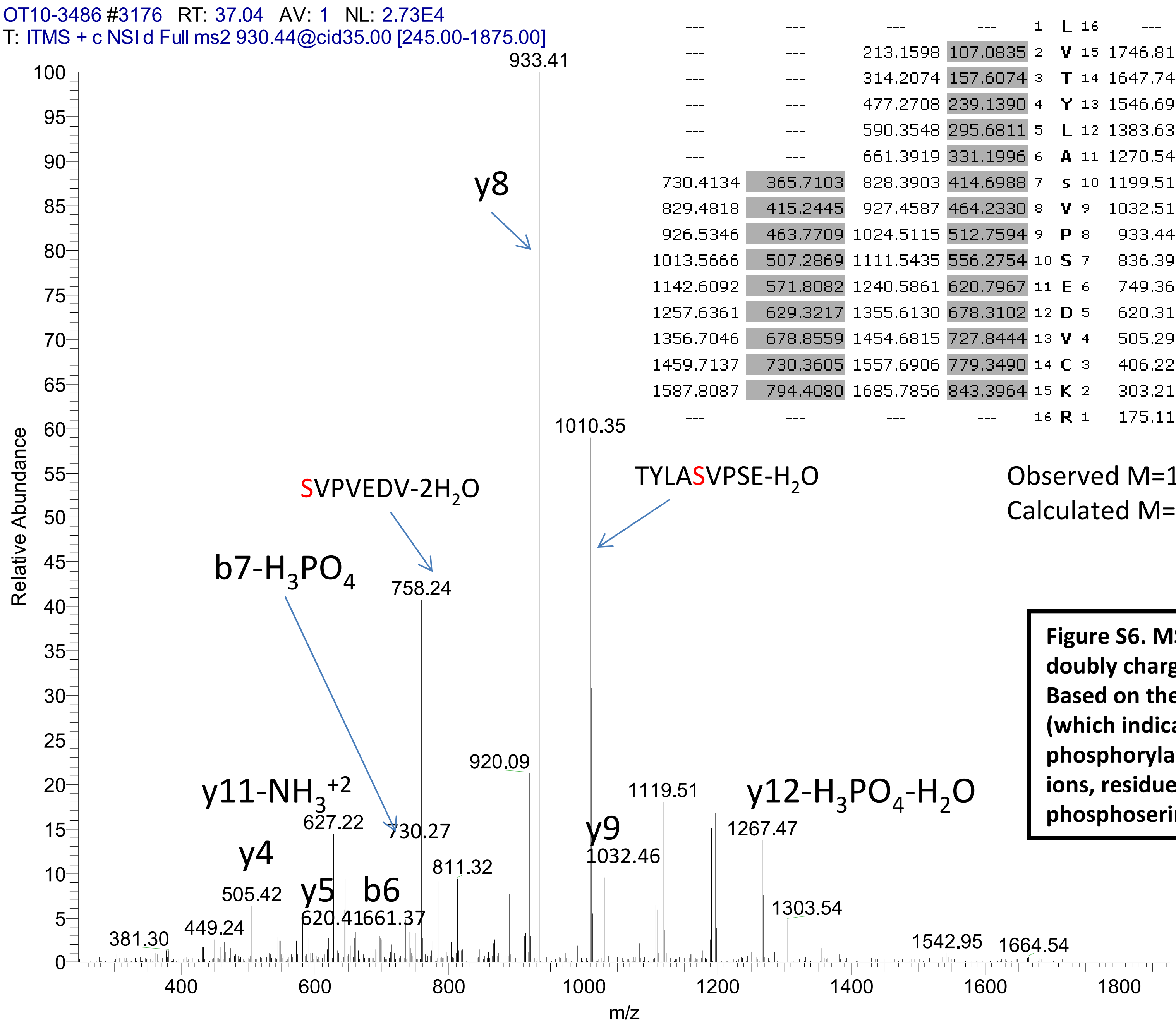
Observed M=1830.8690
Calculated M=1830.8838

Figure S5. MS/MS on the doubly charged 916.94 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, only the threonine at residue 79 can be phosphorylated.

PKA

MS/MS of peptide LVTYLApSVPSEDVCKR

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	L	16	---	---	---	---
---	---	213.1598	107.0835	2	V	15	1746.8132	873.9102	1648.8363	824.9218
---	---	314.2074	157.6074	3	T	14	1647.7448	824.3760	1549.7679	775.3876
---	---	477.2708	239.1390	4	Y	13	1546.6971	773.8522	1448.7202	724.8638
---	---	590.3548	295.6811	5	L	12	1383.6338	692.3205	1285.6569	643.3321
---	---	661.3919	331.1996	6	A	11	1270.5497	635.7785	1172.5728	586.7901
730.4134	365.7103	828.3903	414.6988	7	s	10	1199.5126	600.2599	1101.5357	551.2715
829.4818	415.2445	927.4587	464.2330	8	V	9	1032.5143	516.7608	---	---
926.5346	463.7709	1024.5115	512.7594	9	P	8	933.4458	467.2266	---	---
1013.5666	507.2869	1111.5435	556.2754	10	S	7	836.3931	418.7002	---	---
1142.6092	571.8082	1240.5861	620.7967	11	E	6	749.3610	375.1842	---	---
1257.6361	629.3217	1355.6130	678.3102	12	D	5	620.3185	310.6629	---	---
1356.7046	678.8559	1454.6815	727.8444	13	V	4	505.2915	253.1494	---	---
1459.7137	730.3605	1557.6906	779.3490	14	C	3	406.2231	203.6152	---	---
1587.8087	794.4080	1685.7856	843.3964	15	K	2	303.2139	152.1106	---	---
---	---	---	---	16	R	1	175.1190	88.0631	---	---



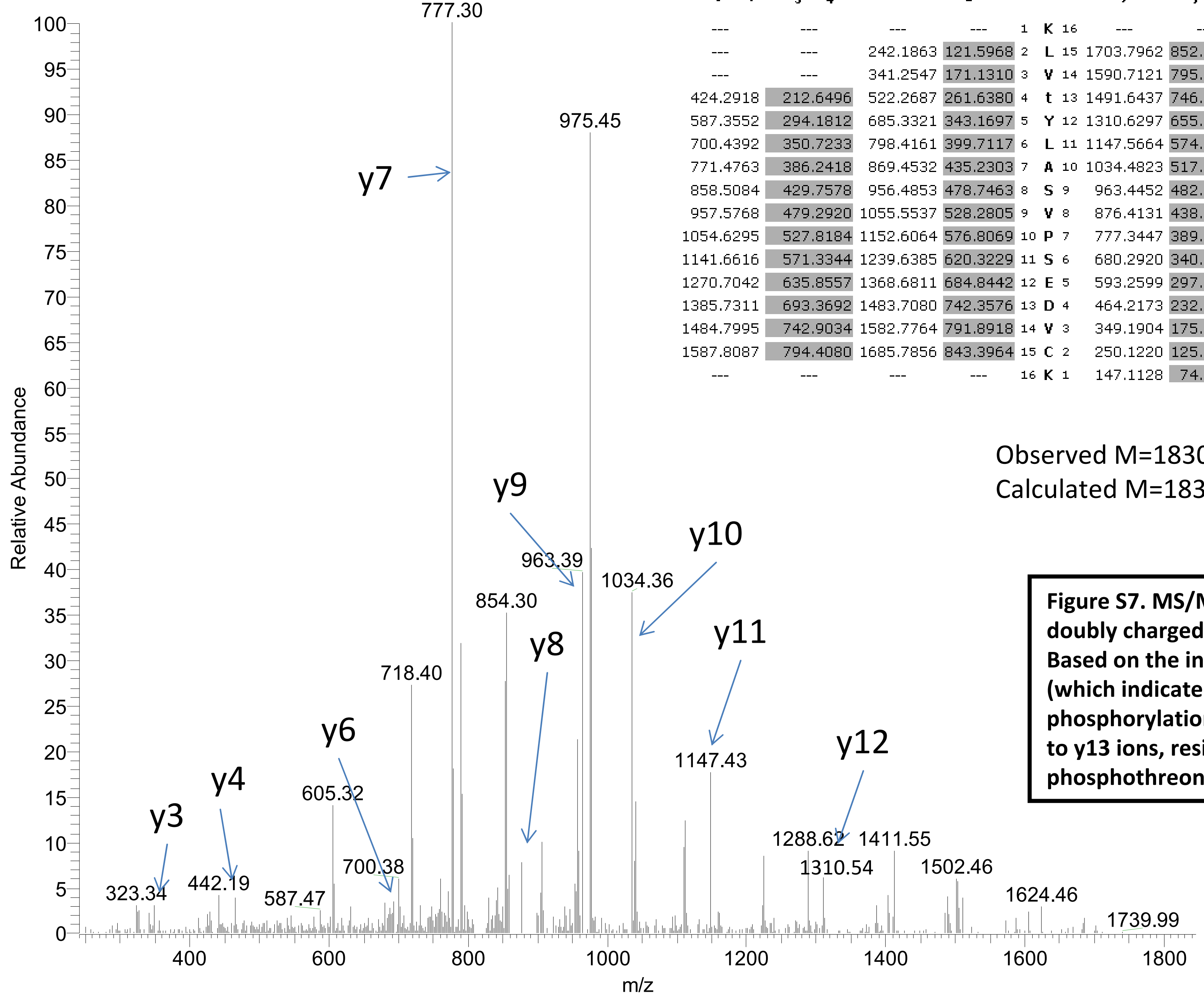
Observed M=1858.8751
Calculated M=1858.8900

Figure S6. MS/MS on the doubly charged 930.44 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, residue 83 is a phosphoserine.

PKC

MS/MS of peptide KLVpTYLASVPSEDVCK

OT10-3470 #3256 RT: 37.31 AV: 1 NL: 1.65E4
T: ITMS + c NSI d Full ms2 916.44@cid35.00 [240.00-1845.00]



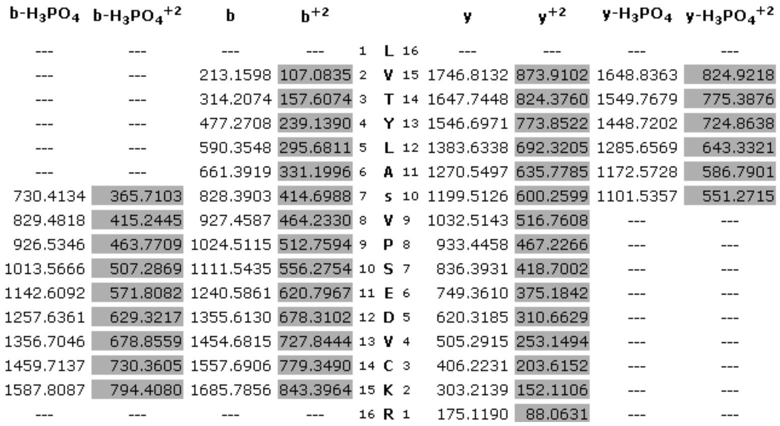
$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	K	16	---	---	---	---
---	---	242.1863	121.5968	2	L	15	1703.7962	852.4017	1605.8193	803.4133
---	---	341.2547	171.1310	3	V	14	1590.7121	795.8597	1492.7352	746.8712
424.2918	212.6496	522.2687	261.6380	4	t	13	1491.6437	746.3255	1393.6668	697.3370
587.3552	294.1812	685.3321	343.1697	5	Y	12	1310.6297	655.8185	---	---
700.4392	350.7233	798.4161	399.7117	6	L	11	1147.5664	574.2868	---	---
771.4763	386.2418	869.4532	435.2303	7	A	10	1034.4823	517.7448	---	---
858.5084	429.7578	956.4853	478.7463	8	S	9	963.4452	482.2262	---	---
957.5768	479.2920	1055.5537	528.2805	9	V	8	876.4131	438.7102	---	---
1054.6295	527.8184	1152.6064	576.8069	10	P	7	777.3447	389.1760	---	---
1141.6616	571.3344	1239.6385	620.3229	11	S	6	680.2920	340.6496	---	---
1270.7042	635.8557	1368.6811	684.8442	12	E	5	593.2599	297.1336	---	---
1385.7311	693.3692	1483.7080	742.3576	13	D	4	464.2173	232.6123	---	---
1484.7995	742.9034	1582.7764	791.8918	14	V	3	349.1904	175.0988	---	---
1587.8087	794.4080	1685.7856	843.3964	15	C	2	250.1220	125.5646	---	---
---	---	---	---	16	K	1	147.1128	74.0600	---	---

Observed M=1830.8675
Calculated M=1830.8838

Figure S7. MS/MS on the doubly charged 916.44 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y10 to y13 ions, residue 79 is a phosphothreonine.

PKC

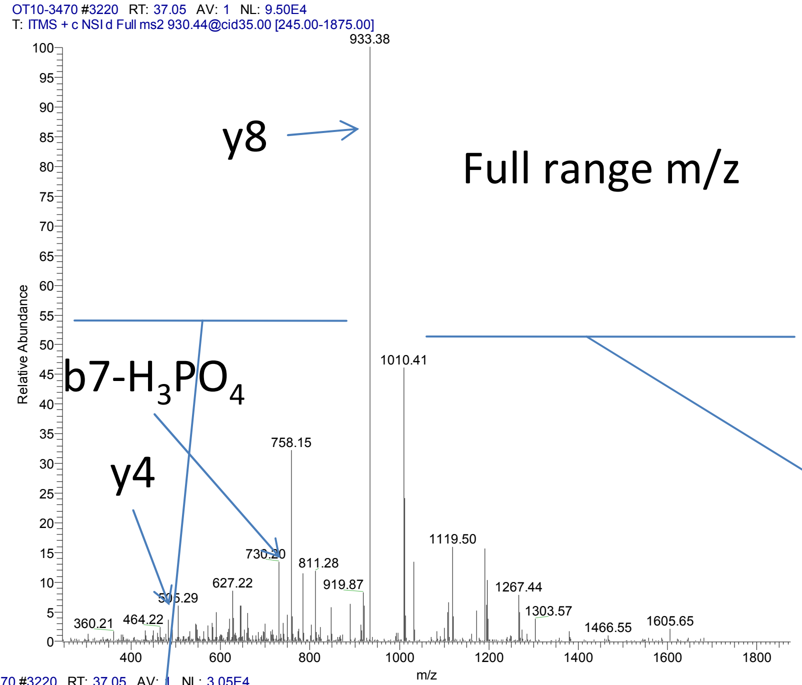
MS/MS of peptide LVTYLApSVPSEDVCKR



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	16	---	---	---	---
---	---	213.1598	107.0835	2	V	15	1746.8132	873.9102	1648.8363	824.9218
---	---	314.2074	157.6074	3	T	14	1647.7448	824.3760	1549.7679	775.3876
---	---	477.2708	239.1390	4	Y	13	1546.6971	773.8522	1448.7202	724.8638
---	---	590.3548	295.6811	5	L	12	1383.6338	692.3205	1285.6569	643.3321
---	---	661.3919	331.1996	6	A	11	1270.5497	635.7785	1172.5728	586.7901
730.4134	365.7103	828.3903	414.6988	7	s	10	1199.5126	600.2599	1101.5357	551.2715
829.4818	415.2445	927.4587	464.2330	8	V	9	1032.5143	516.7608	---	---
926.5346	463.7709	1024.5115	512.7594	9	P	8	933.4458	467.2266	---	---
1013.5666	507.2869	1111.5435	556.2754	10	S	7	836.3931	418.7002	---	---
1142.6092	571.8082	1240.5861	620.7967	11	E	6	749.3610	375.1842	---	---
1257.6361	629.3217	1355.6130	678.3102	12	D	5	620.3185	310.6629	---	---
1356.7046	678.8559	1454.6815	727.8444	13	V	4	505.2915	253.1494	---	---
1459.7137	730.3605	1557.6906	779.3490	14	C	3	406.2231	203.6152	---	---
1587.8087	794.4080	1685.7856	843.3964	15	K	2	303.2139	152.1106	---	---
---	---	---	---	16	R	1	175.1190	88.0631	---	---

Observed M=1858.8723

Calculated M=1858.8900

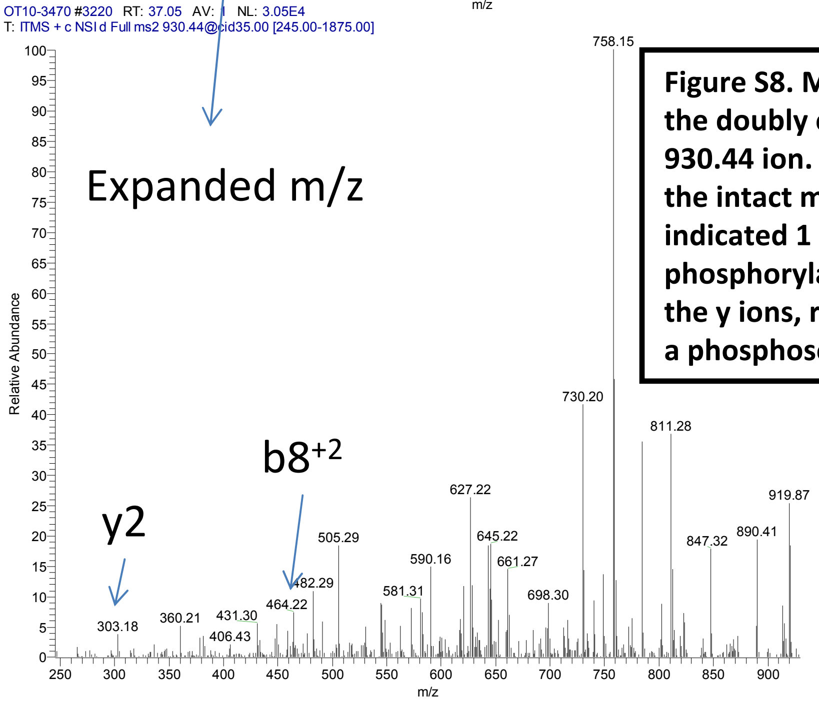


y8

Full range m/z

$b7-H_3PO_4$

y4

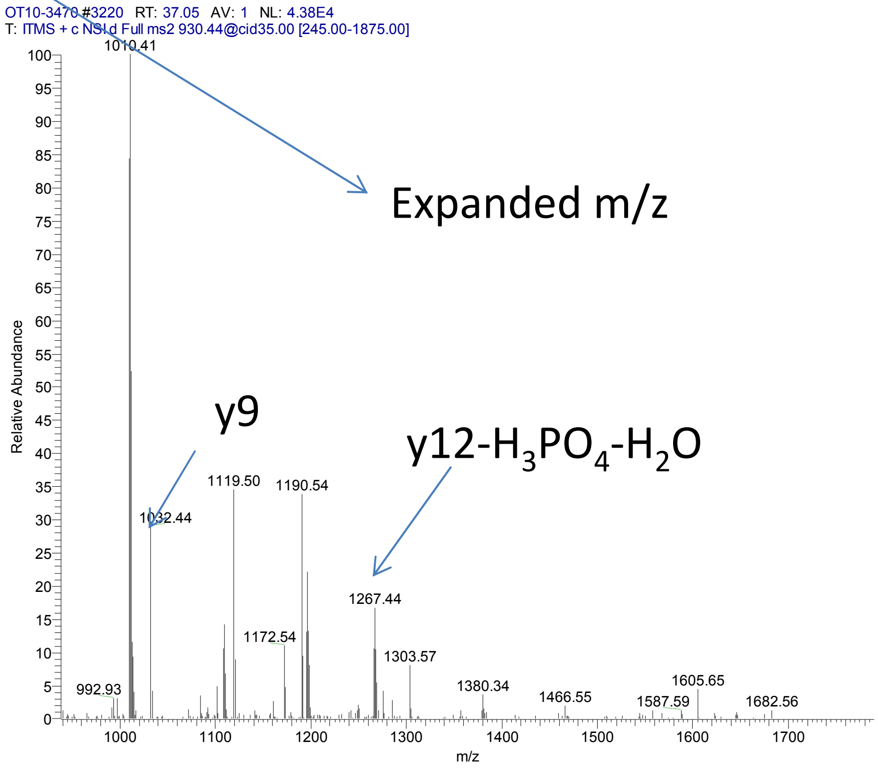


Expanded m/z

$b8^{+2}$

y2

Figure S8. MS/MS on the doubly charged 930.44 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, residue 83 is a phosphoserine.



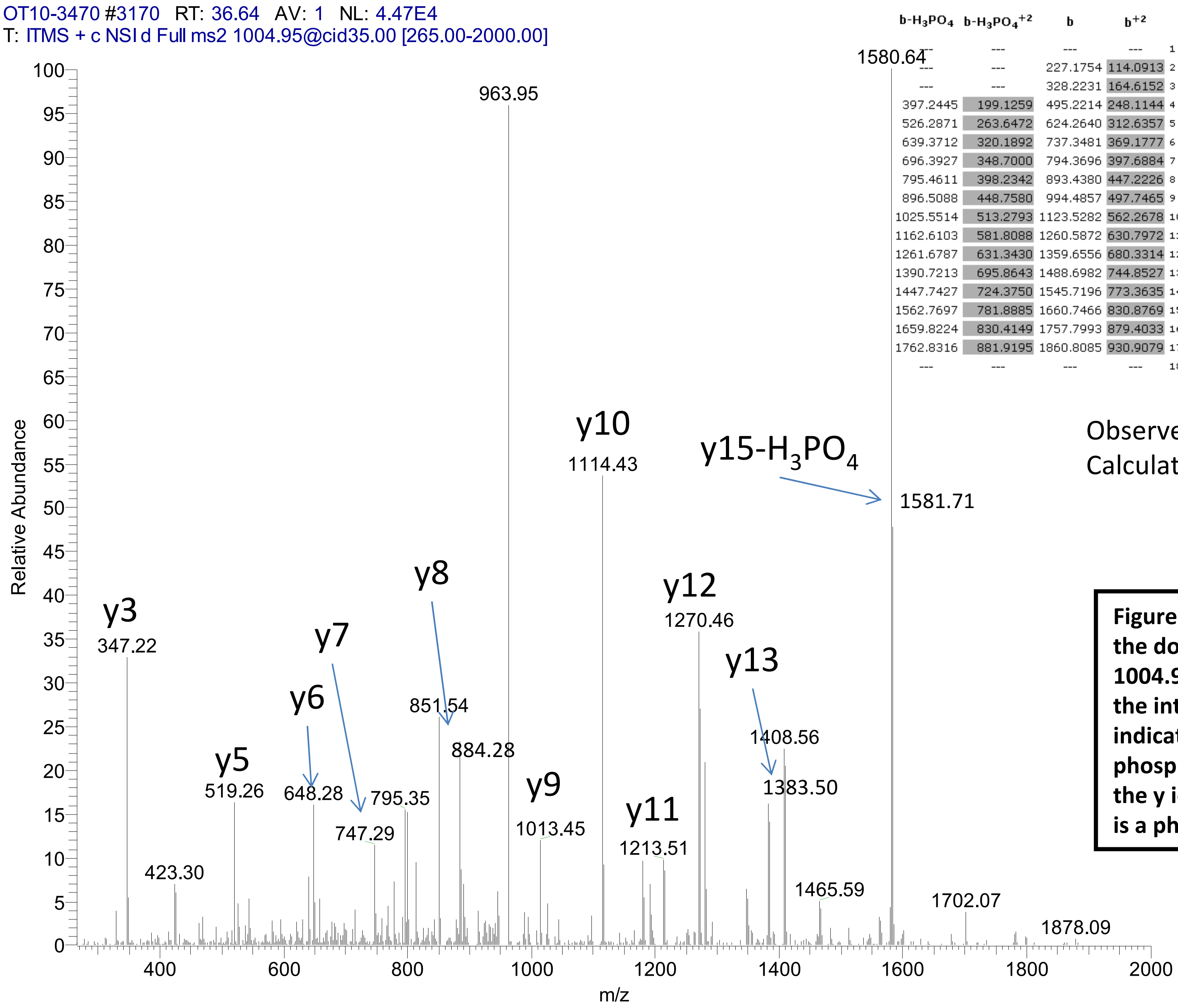
Expanded m/z

y9

$y12-H_3PO_4-H_2O$

PKC

MS/MS of peptide LLTpSELGVTEHVEGDPCK



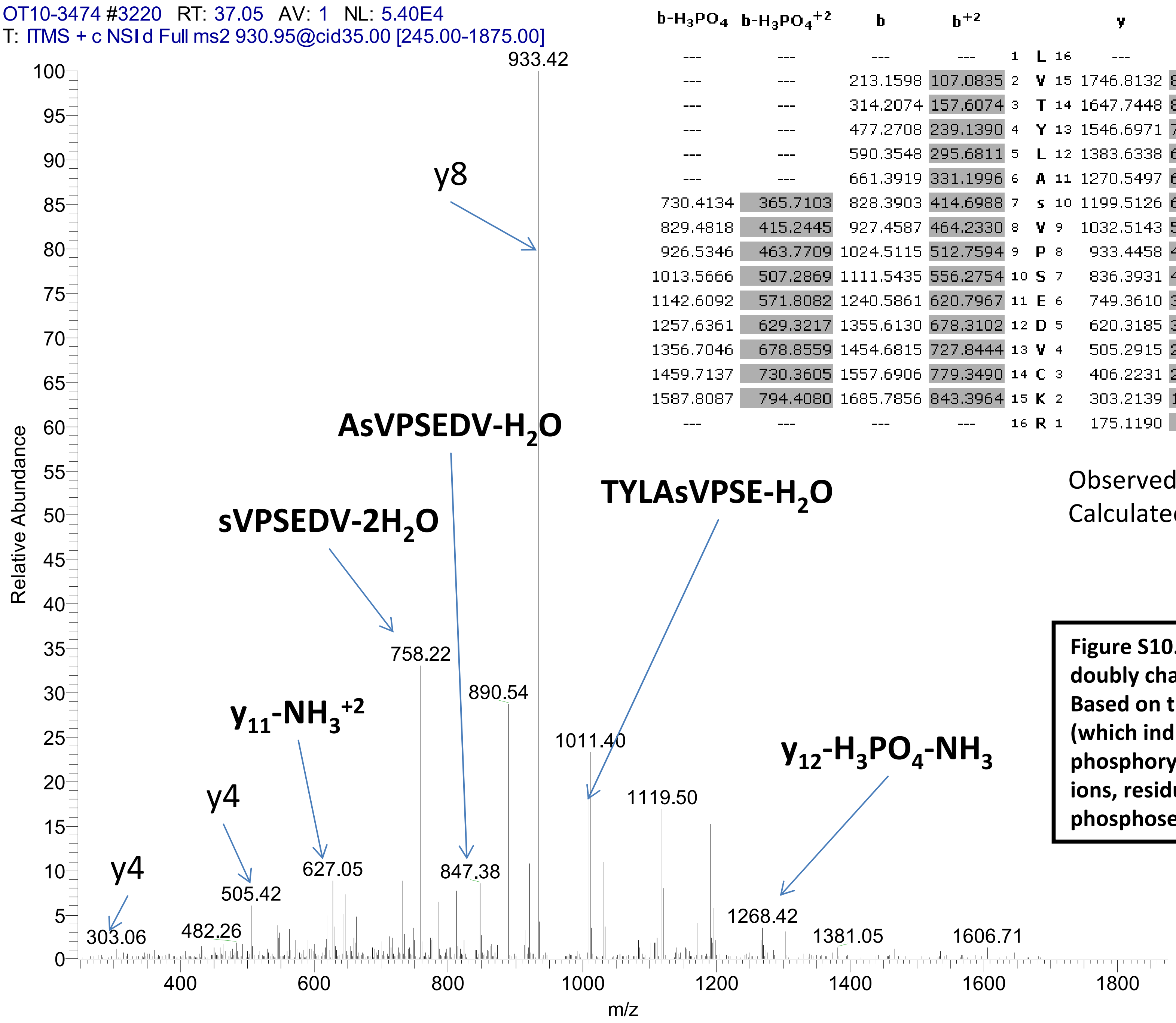
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	18	---	---	---	---
---	---	227.1754	114.0913	2	L	17	1893.8300	947.4186	1795.8531	898.4302
---	---	328.2231	164.6152	3	T	16	1780.7459	890.8766	1682.7690	841.8882
397.2445	199.1259	495.2214	248.1144	4	s	15	1679.6982	840.3528	1581.7213	791.3643
526.2871	263.6472	624.2640	312.6357	5	E	14	1512.6999	756.8536	---	---
639.3712	320.1892	737.3481	369.1777	6	L	13	1383.6573	692.3323	---	---
696.3927	348.7000	794.3696	397.6884	7	G	12	1270.5732	635.7903	---	---
795.4611	398.2342	893.4380	447.2226	8	V	11	1213.5518	607.2795	---	---
896.5088	448.7580	994.4857	497.7465	9	T	10	1114.4833	557.7453	---	---
1025.5514	513.2793	1123.5282	562.2678	10	E	9	1013.4357	507.2215	---	---
1162.6103	581.8088	1260.5872	630.7972	11	H	8	884.3931	442.7002	---	---
1261.6787	631.3430	1359.6556	680.3314	12	V	7	747.3342	374.1707	---	---
1390.7213	695.8643	1488.6982	744.8527	13	E	6	648.2658	324.6365	---	---
1447.7427	724.3750	1545.7196	773.3635	14	G	5	519.2232	260.1152	---	---
1562.7697	781.8885	1660.7466	830.8769	15	D	4	462.2017	231.6045	---	---
1659.8224	830.4149	1757.7993	879.4033	16	P	3	347.1748	174.0910	---	---
1762.8316	881.9195	1860.8085	930.9079	17	C	2	250.1220	125.5646	---	---
---	---	---	---	18	K	1	147.1128	74.0600	---	---

Observed M=2005.8886
Calculated M=2005.9068

Figure S9. MS/MS on the doubly charged 1004.95 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, residue 1520 is a phosphoserine.

CKII

MS/MS of peptide LVTYLApSVPSEDVCKR



$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	L	16	---	---	---	---
---	---	213.1598	107.0835	2	V	15	1746.8132	873.9102	1648.8363	824.9218
---	---	314.2074	157.6074	3	T	14	1647.7448	824.3760	1549.7679	775.3876
---	---	477.2708	239.1390	4	Y	13	1546.6971	773.8522	1448.7202	724.8638
---	---	590.3548	295.6811	5	L	12	1383.6338	692.3205	1285.6569	643.3321
---	---	661.3919	331.1996	6	A	11	1270.5497	635.7785	1172.5728	586.7901
730.4134	365.7103	828.3903	414.6988	7	s	10	1199.5126	600.2599	1101.5357	551.2715
829.4818	415.2445	927.4587	464.2330	8	V	9	1032.5143	516.7608	---	---
926.5346	463.7709	1024.5115	512.7594	9	P	8	933.4458	467.2266	---	---
1013.5666	507.2869	1111.5435	556.2754	10	S	7	836.3931	418.7002	---	---
1142.6092	571.8082	1240.5861	620.7967	11	E	6	749.3610	375.1842	---	---
1257.6361	629.3217	1355.6130	678.3102	12	D	5	620.3185	310.6629	---	---
1356.7046	678.8559	1454.6815	727.8444	13	V	4	505.2915	253.1494	---	---
1459.7137	730.3605	1557.6906	779.3490	14	C	3	406.2231	203.6152	---	---
1587.8087	794.4080	1685.7856	843.3964	15	K	2	303.2139	152.1106	---	---
---	---	---	---	16	R	1	175.1190	88.0631	---	---

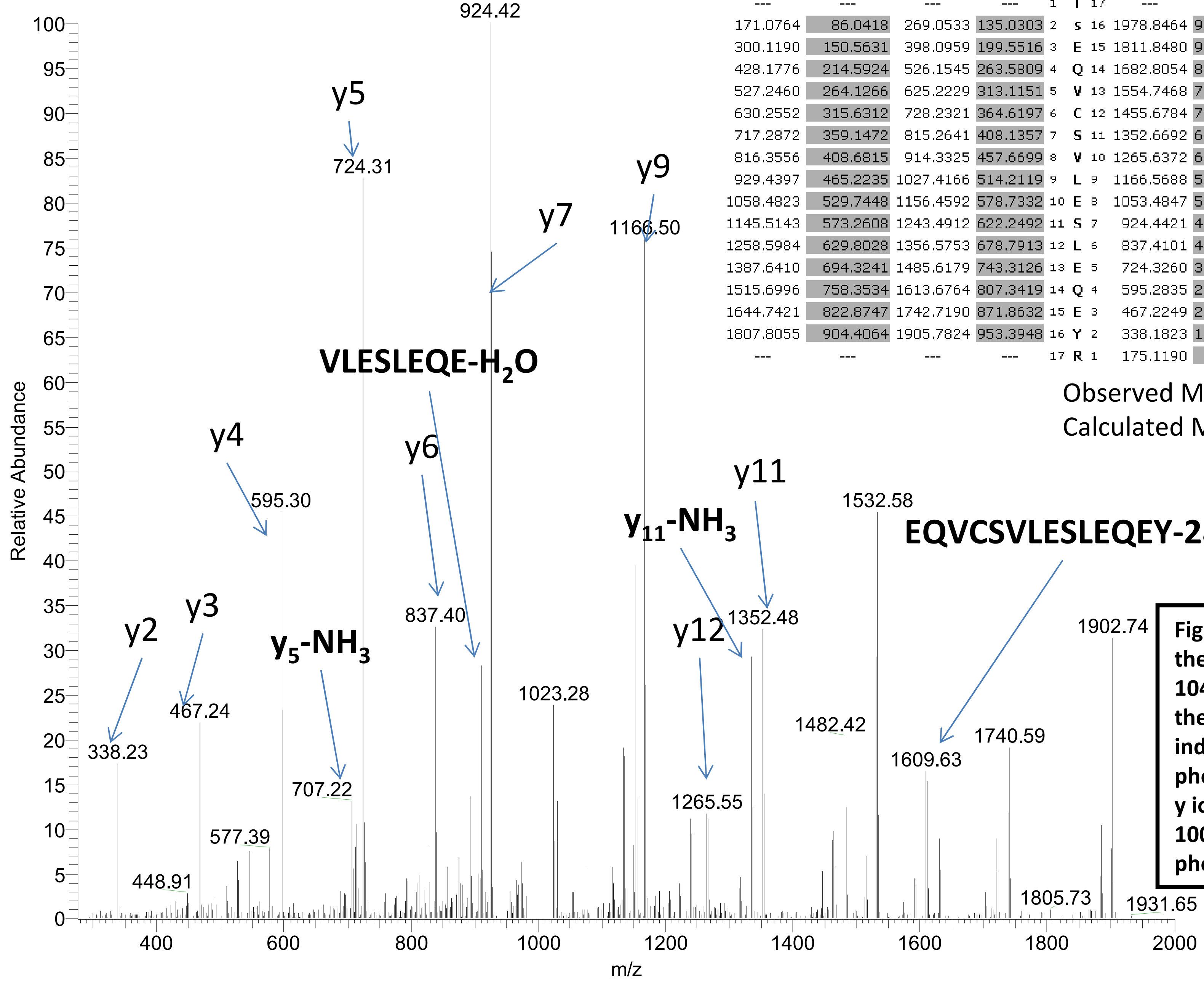
Observed M=1858.8710
Calculated M=1858.8900

Figure S10. MS/MS on the doubly charged 930.95 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, residue 83 is a phosphoserine.

CKII

MS/MS of peptide pTpSEQVCSVLESLEQEYR

OT10-3474 #4333 RT: 45.74 AV: 1 NL: 1.40E5
T: ITMS + c NSI d Full ms2 1040.47@cid35.00 [275.00-2000.00]

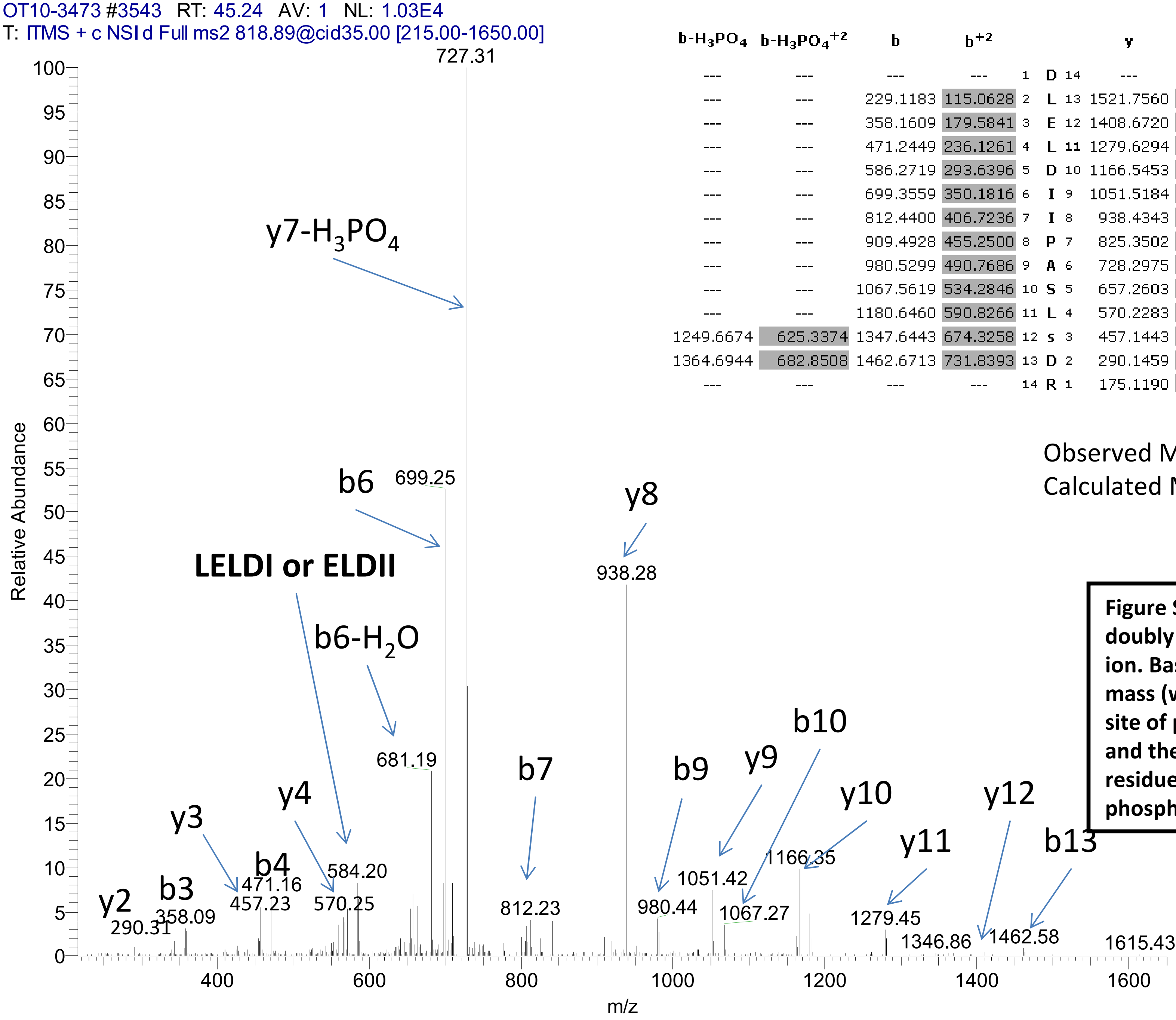


b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	T	17	---	---	---	---
171.0764	86.0418	269.0533	135.0303	2	s	16	1978.8464	989.9268	1880.8695	940.9384
300.1190	150.5631	398.0959	199.5516	3	E	15	1811.8480	906.4276	---	---
428.1776	214.5924	526.1545	263.5809	4	Q	14	1682.8054	841.9063	---	---
527.2460	264.1266	625.2229	313.1151	5	V	13	1554.7468	777.8771	---	---
630.2552	315.6312	728.2321	364.6197	6	C	12	1455.6784	728.3428	---	---
717.2872	359.1472	815.2641	408.1357	7	S	11	1352.6692	676.8383	---	---
816.3556	408.6815	914.3325	457.6699	8	V	10	1265.6372	633.3222	---	---
929.4397	465.2235	1027.4166	514.2119	9	L	9	1166.5688	583.7880	---	---
1058.4823	529.7448	1156.4592	578.7332	10	E	8	1053.4847	527.2460	---	---
1145.5143	573.2608	1243.4912	622.2492	11	S	7	924.4421	462.7247	---	---
1258.5984	629.8028	1356.5753	678.7913	12	L	6	837.4101	419.2087	---	---
1387.6410	694.3241	1485.6179	743.3126	13	E	5	724.3260	362.6667	---	---
1515.6996	758.3534	1613.6764	807.3419	14	Q	4	595.2835	298.1454	---	---
1644.7421	822.8747	1742.7190	871.8632	15	E	3	467.2249	234.1161	---	---
1807.8055	904.4064	1905.7824	953.3948	16	Y	2	338.1823	169.5948	---	---
---	---	---	---	17	R	1	175.1190	88.0631	---	---

Observed M=2078.9170
Calculated M=2078.8867

Figure S11. MS/MS on the doubly charged 1040.47 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, either residue 1002 or 1003 is phosphorylated.

CKII MS/MS of peptide DLELDIIPASLpSDR



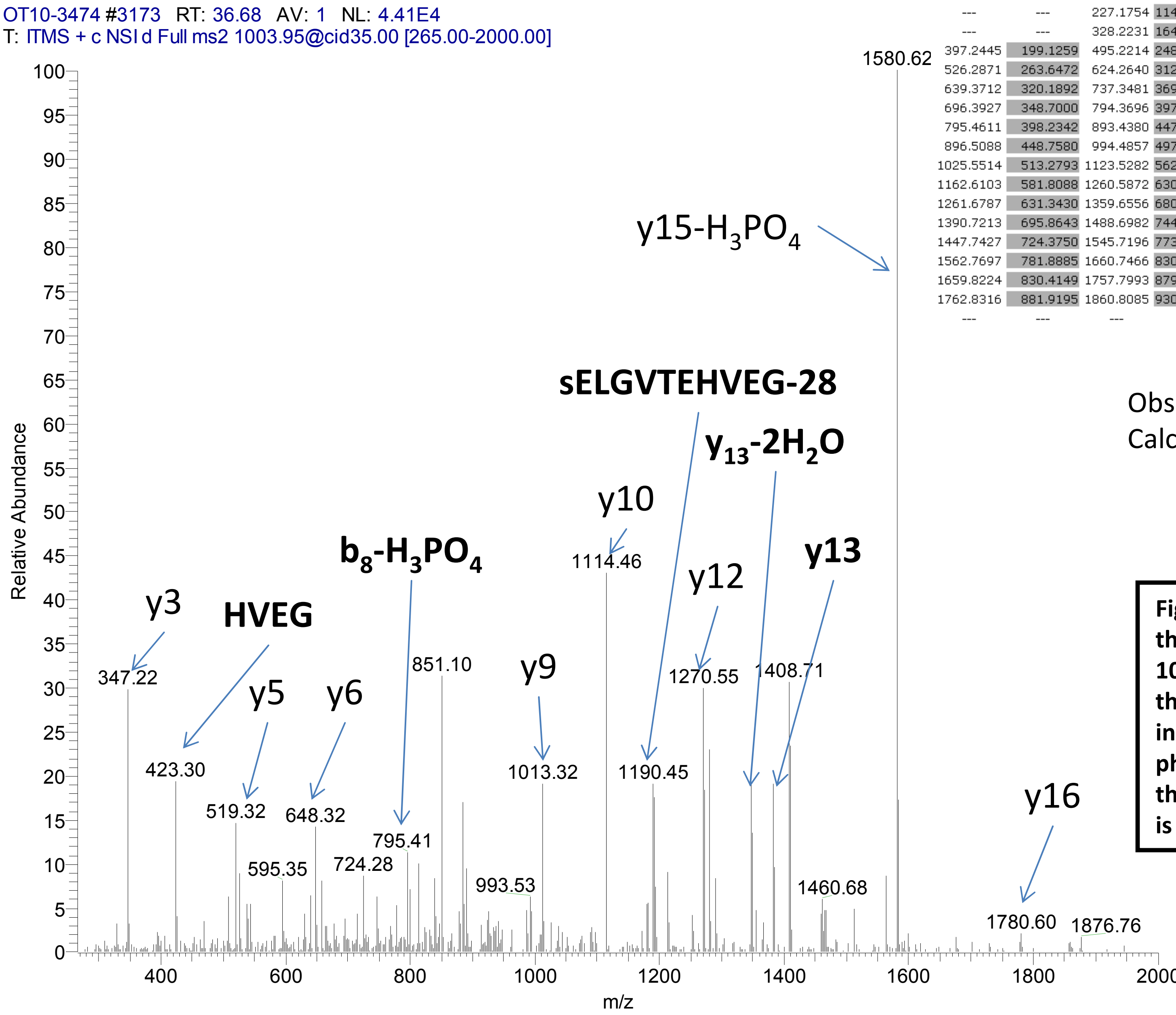
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	D	14	---	---	---	---
---	---	229.1183	115.0628	2	L	13	1521.7560	761.3816	1423.7791	712.3932
---	---	358.1609	179.5841	3	E	12	1408.6720	704.8396	1310.6951	655.8512
---	---	471.2449	236.1261	4	L	11	1279.6294	640.3183	1181.6525	591.3299
---	---	586.2719	293.6396	5	D	10	1166.5453	583.7763	1068.5684	534.7878
---	---	699.3559	350.1816	6	I	9	1051.5184	526.2628	953.5415	477.2744
---	---	812.4400	406.7236	7	I	8	938.4343	469.7208	840.4574	420.7323
---	---	909.4928	455.2500	8	P	7	825.3502	413.1788	727.3733	364.1903
---	---	980.5299	490.7686	9	A	6	728.2975	364.6524	630.3206	315.6639
---	---	1067.5619	534.2846	10	S	5	657.2603	329.1338	559.2835	280.1454
---	---	1180.6460	590.8266	11	L	4	570.2283	285.6178	472.2514	236.6293
1249.6674	625.3374	1347.6443	674.3258	12	s	3	457.1443	229.0758	359.1674	180.0873
1364.6944	682.8508	1462.6713	731.8393	13	D	2	290.1459	145.5766	---	---
---	---	---	---	14	R	1	175.1190	88.0631	---	---

Observed M=1635.7706
Calculated M=1635.7757

Figure S12. MS/MS on the doubly charged 818.89 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y2, y3 and y4 ions, residue 1249 is a phosphoserine.

CKII

MS/MS of peptide LLTpSELGVTEHVEGDPCK



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	18	---	---	---	---
---	---	227.1754	114.0913	2	L	17	1893.8300	947.4186	1795.8531	898.4302
---	---	328.2231	164.6152	3	T	16	1780.7459	890.8766	1682.7690	841.8882
397.2445	199.1259	495.2214	248.1144	4	s	15	1679.6982	840.3528	1581.7213	791.3643
526.2871	263.6472	624.2640	312.6357	5	E	14	1512.6999	756.8536	---	---
639.3712	320.1892	737.3481	369.1777	6	L	13	1383.6573	692.3323	---	---
696.3927	348.7000	794.3696	397.6884	7	G	12	1270.5732	635.7903	---	---
795.4611	398.2342	893.4380	447.2226	8	V	11	1213.5518	607.2795	---	---
896.5088	448.7580	994.4857	497.7465	9	T	10	1114.4833	557.7453	---	---
1025.5514	513.2793	1123.5282	562.2678	10	E	9	1013.4357	507.2215	---	---
1162.6103	581.8088	1260.5872	630.7972	11	H	8	884.3931	442.7002	---	---
1261.6787	631.3430	1359.6556	680.3314	12	V	7	747.3342	374.1707	---	---
1390.7213	695.8643	1488.6982	744.8527	13	E	6	648.2658	324.6365	---	---
1447.7427	724.3750	1545.7196	773.3635	14	G	5	519.2232	260.1152	---	---
1562.7697	781.8885	1660.7466	830.8769	15	D	4	462.2017	231.6045	---	---
1659.8224	830.4149	1757.7993	879.4033	16	P	3	347.1748	174.0910	---	---
1762.8316	881.9195	1860.8085	930.9079	17	C	2	250.1220	125.5646	---	---
---	---	---	---	18	K	1	147.1128	74.0600	---	---

Observed M=2005.8874
Calculated M=2005.9068

Figure S13. MS/MS on the doubly charged 1003.95 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions, residue 1520 is a phosphoserine.

CKII

MS/MS of peptide DGVEDGDpSQGDGSSQPDTISIASR

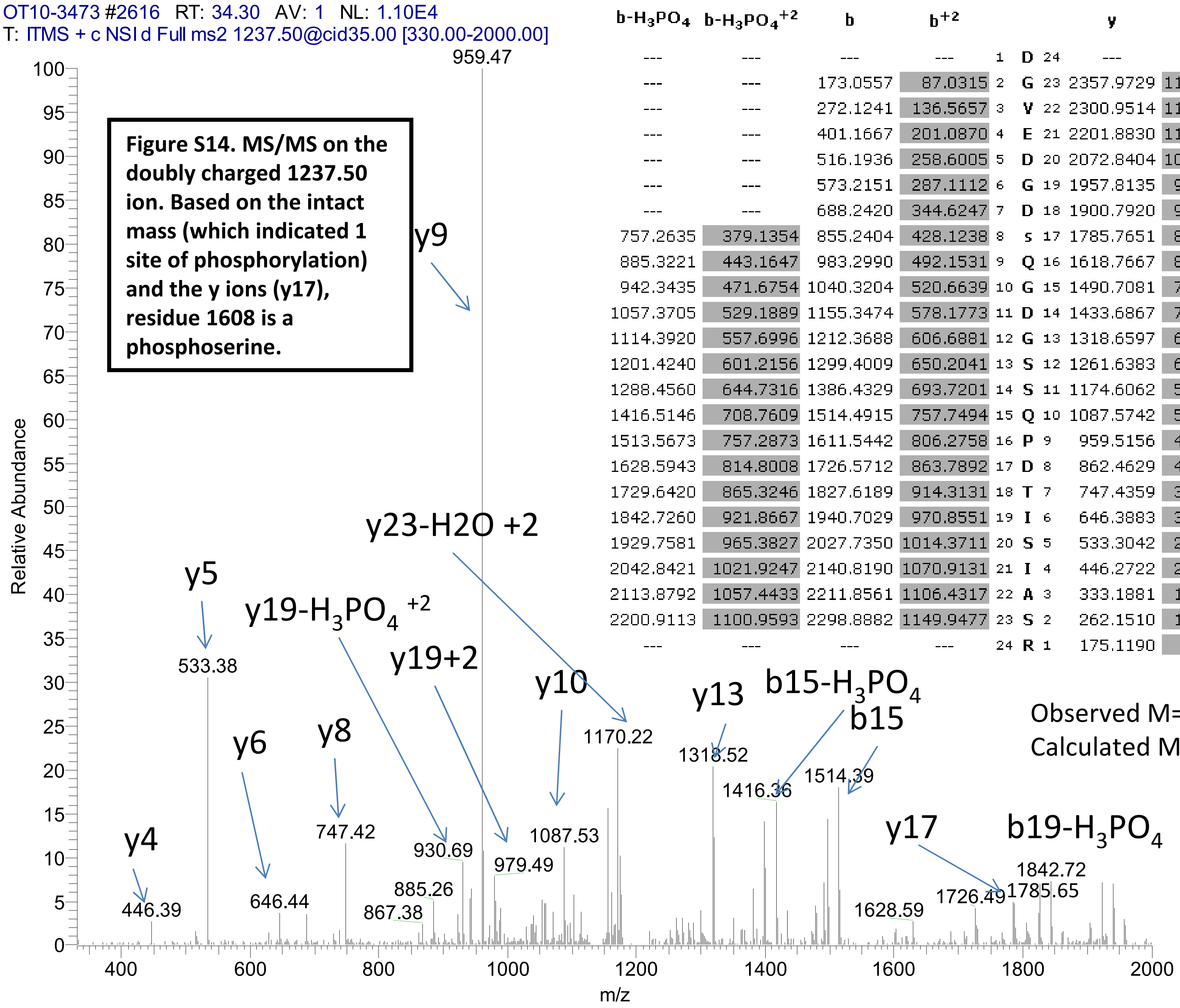


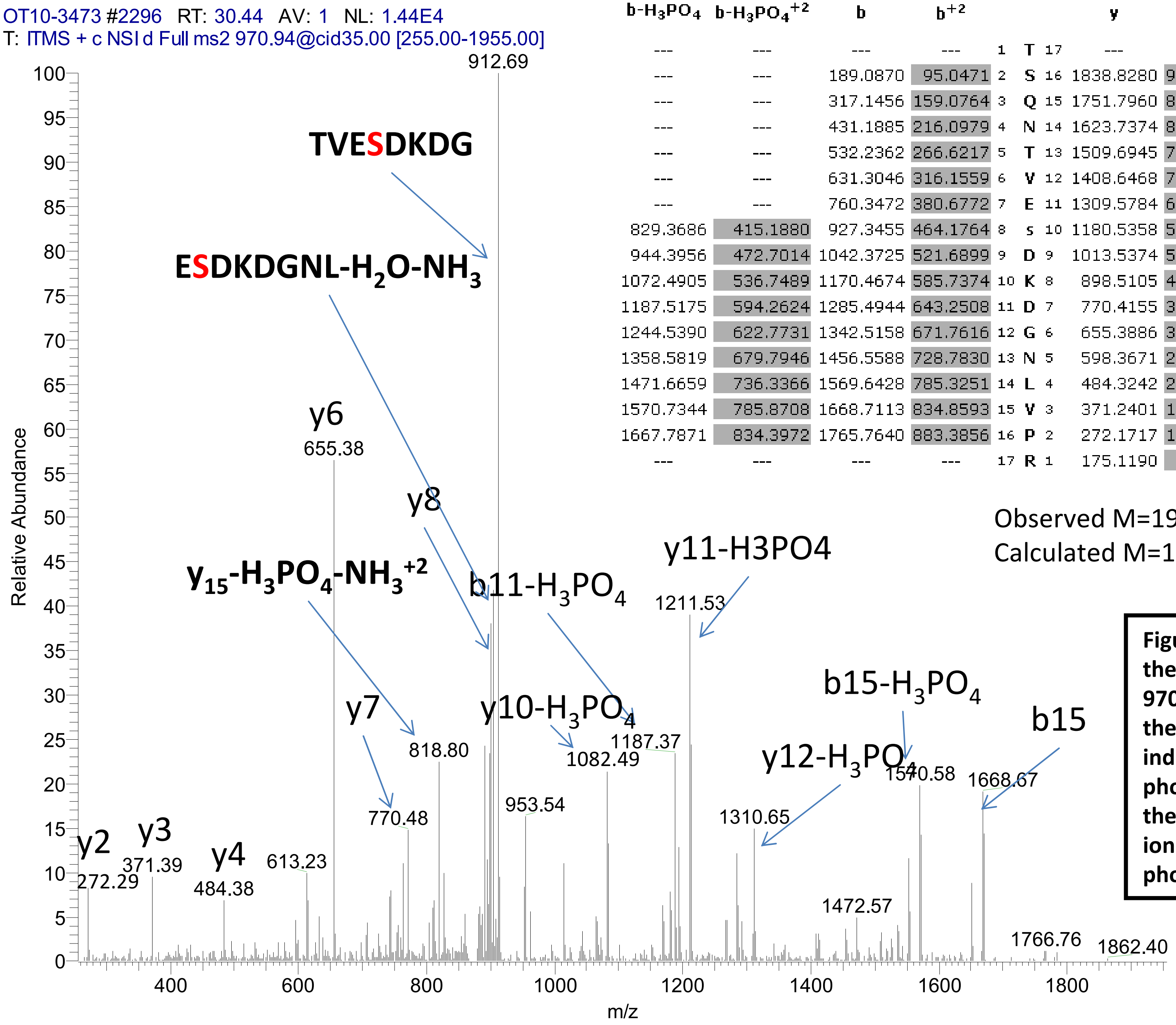
Figure S14. MS/MS on the doubly charged 1237.50 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ions (y17), residue 1608 is a phosphoserine.

$b\text{-}H_3PO_4$	$b\text{-}H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y\text{-}H_3PO_4$	$y\text{-}H_3PO_4^{+2}$
---	---	---	---	1	D	24	---	---	---	---
---	---	173.0557	87.0315	2	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	272.1241	136.5657	3	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	401.1667	201.0870	4	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	516.1936	258.6005	5	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	573.2151	287.1112	6	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	688.2420	344.6247	7	D	18	1900.7920	950.8996	1802.8151	901.9112
757.2635	379.1354	855.2404	428.1238	8	s	17	1785.7651	893.3862	1687.7882	844.3977
885.3221	443.1647	983.2990	492.1531	9	Q	16	1618.7667	809.8870	---	---
942.3435	471.6754	1040.3204	520.6639	10	G	15	1490.7081	745.8577	---	---
1057.3705	529.1889	1155.3474	578.1773	11	D	14	1433.6867	717.3470	---	---
1114.3920	557.6996	1212.3688	606.6881	12	G	13	1318.6597	659.8335	---	---
1201.4240	601.2156	1299.4009	650.2041	13	S	12	1261.6383	631.3228	---	---
1288.4560	644.7316	1386.4329	693.7201	14	S	11	1174.6062	587.8068	---	---
1416.5146	708.7609	1514.4915	757.7494	15	Q	10	1087.5742	544.2907	---	---
1513.5673	757.2873	1611.5442	806.2758	16	P	9	959.5156	480.2615	---	---
1628.5943	814.8008	1726.5712	863.7892	17	D	8	862.4629	431.7351	---	---
1729.6420	865.3246	1827.6189	914.3131	18	T	7	747.4359	374.2216	---	---
1842.7260	921.8667	1940.7029	970.8551	19	I	6	646.3883	323.6978	---	---
1929.7581	965.3827	2027.7350	1014.3711	20	S	5	533.3042	267.1557	---	---
2042.8421	1021.9247	2140.8190	1070.9131	21	I	4	446.2722	223.6397	---	---
2113.8792	1057.4433	2211.8561	1106.4317	22	A	3	333.1881	167.0977	---	---
2200.9113	1100.9593	2298.8882	1149.9477	23	S	2	262.1510	131.5791	---	---
---	---	---	---	24	R	1	175.1190	88.0631	---	---

Observed M=2471.9796
Calculated M=2471.9926

CKII

MS/MS of peptide TSQNTVEpSDKDGNLVPR



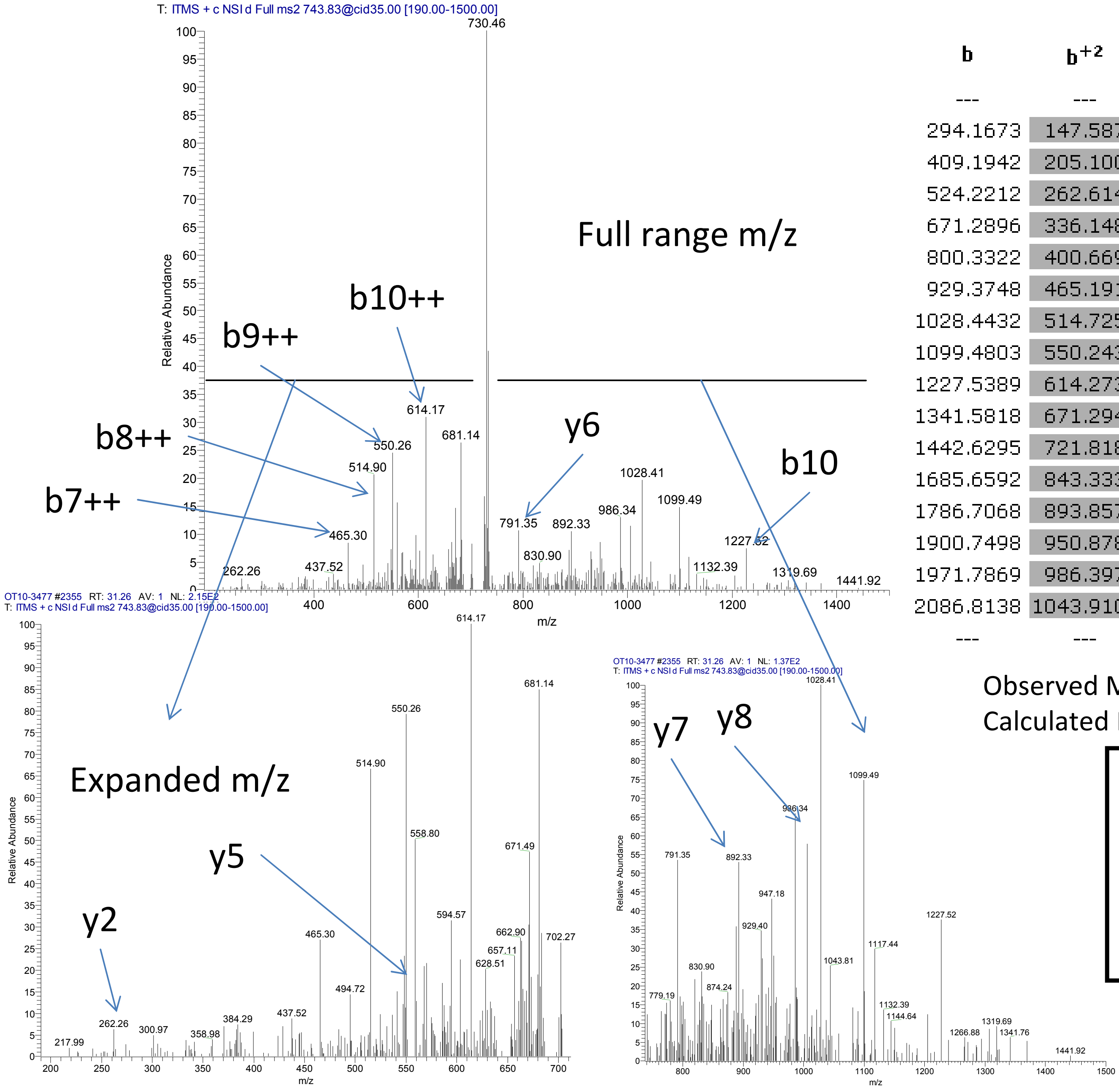
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	T	17	---	---	---	---
---	---	189.0870	95.0471	2	S	16	1838.8280	919.9176	1740.8511	870.9292
---	---	317.1456	159.0764	3	Q	15	1751.7960	876.4016	1653.8191	827.4132
---	---	431.1885	216.0979	4	N	14	1623.7374	812.3723	1525.7605	763.3839
---	---	532.2362	266.6217	5	T	13	1509.6945	755.3509	1411.7176	706.3624
---	---	631.3046	316.1559	6	V	12	1408.6468	704.8270	1310.6699	655.8386
---	---	760.3472	380.6772	7	E	11	1309.5784	655.2928	1211.6015	606.3044
829.3686	415.1880	927.3455	464.1764	8	s	10	1180.5358	590.7715	1082.5589	541.7831
944.3956	472.7014	1042.3725	521.6899	9	D	9	1013.5374	507.2724	---	---
1072.4905	536.7489	1170.4674	585.7374	10	K	8	898.5105	449.7589	---	---
1187.5175	594.2624	1285.4944	643.2508	11	D	7	770.4155	385.7114	---	---
1244.5390	622.7731	1342.5158	671.7616	12	G	6	655.3886	328.1979	---	---
1358.5819	679.7946	1456.5588	728.7830	13	N	5	598.3671	299.6872	---	---
1471.6659	736.3366	1569.6428	785.3251	14	L	4	484.3242	242.6657	---	---
1570.7344	785.8708	1668.7113	834.8593	15	V	3	371.2401	186.1237	---	---
1667.7871	834.3972	1765.7640	883.3856	16	P	2	272.1717	136.5895	---	---
---	---	---	---	17	R	1	175.1190	88.0631	---	---

Observed M=1938.8607
Calculated M=1938.8684

Figure S15. MS/MS on the doubly charged 970.94 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y2 to y10-H_3PO_4 ions, residue 1632 is a phosphoserine.

Fyn

MS/MS of peptide RHDDFEEVAQNTpYTNADK



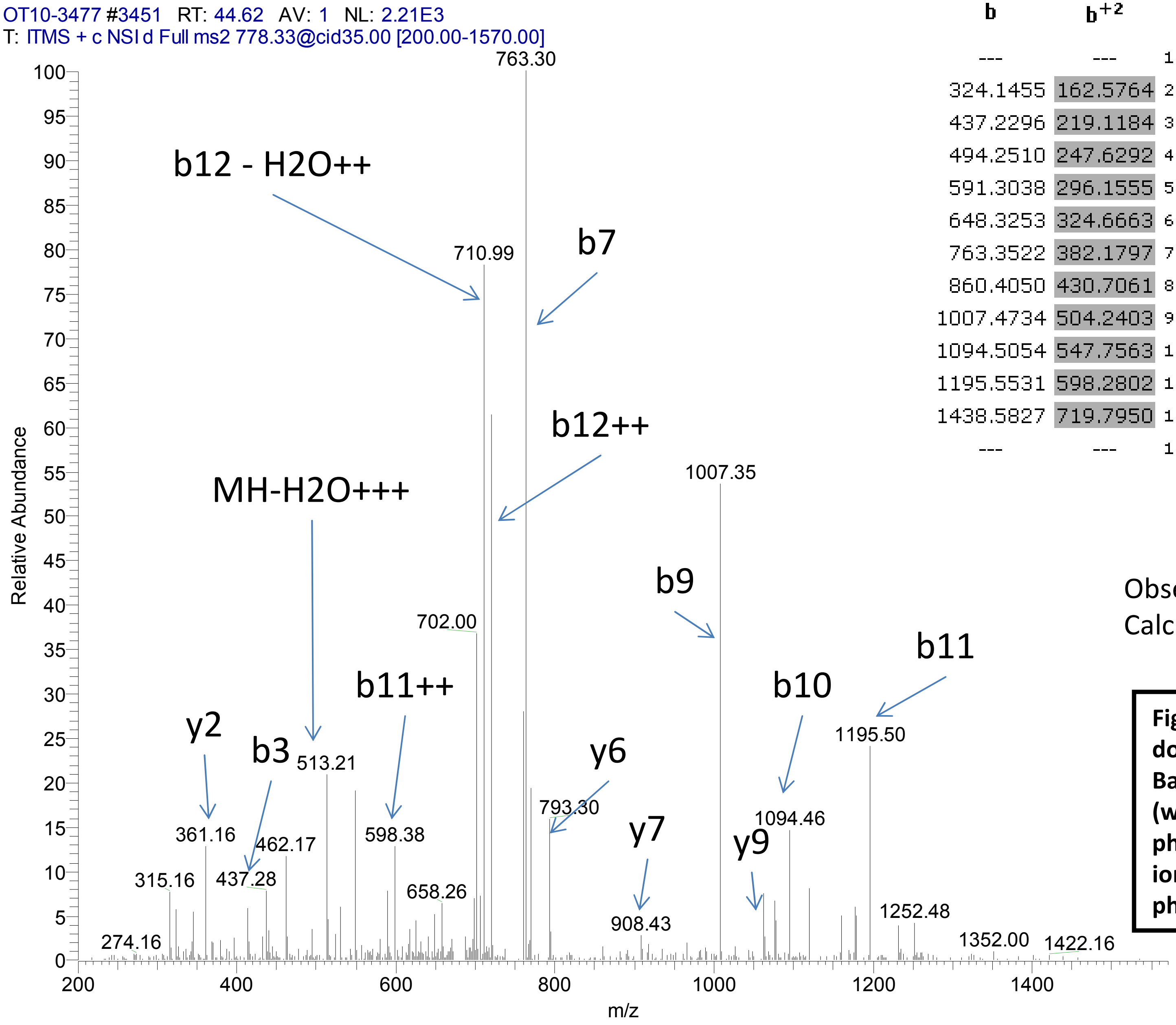
b	b+2				y	y+2
---	---	1	R	18	---	---
294.1673	147.5873	2	H	17	2076.8182	1038.9128
409.1942	205.1008	3	D	16	1939.7593	970.3833
524.2212	262.6142	4	D	15	1824.7324	912.8698
671.2896	336.1484	5	F	14	1709.7054	855.3564
800.3322	400.6697	6	E	13	1562.6370	781.8221
929.3748	465.1910	7	E	12	1433.5944	717.3009
1028.4432	514.7252	8	V	11	1304.5518	652.7796
1099.4803	550.2438	9	A	10	1205.4834	603.2453
1227.5389	614.2731	10	Q	9	1134.4463	567.7268
1341.5818	671.2945	11	N	8	1006.3877	503.6975
1442.6295	721.8184	12	T	7	892.3448	446.6760
1685.6592	843.3332	13	y	6	791.2971	396.1522
1786.7068	893.8571	14	T	5	548.2675	274.6374
1900.7498	950.8785	15	N	4	447.2198	224.1135
1971.7869	986.3971	16	A	3	333.1769	167.0921
2086.8138	1043.9105	17	D	2	262.1397	131.5735
---	---	18	K	1	147.1128	74.0600

Observed M=2231.9017
Calculated M=2231.9120

Figure S16. MS/MS on the triply charged 743.83 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y2 to y8 ions, residue 591 is a phosphotyrosine

Fyn

MS/MS of peptide WHLGPGDPFSTpYV

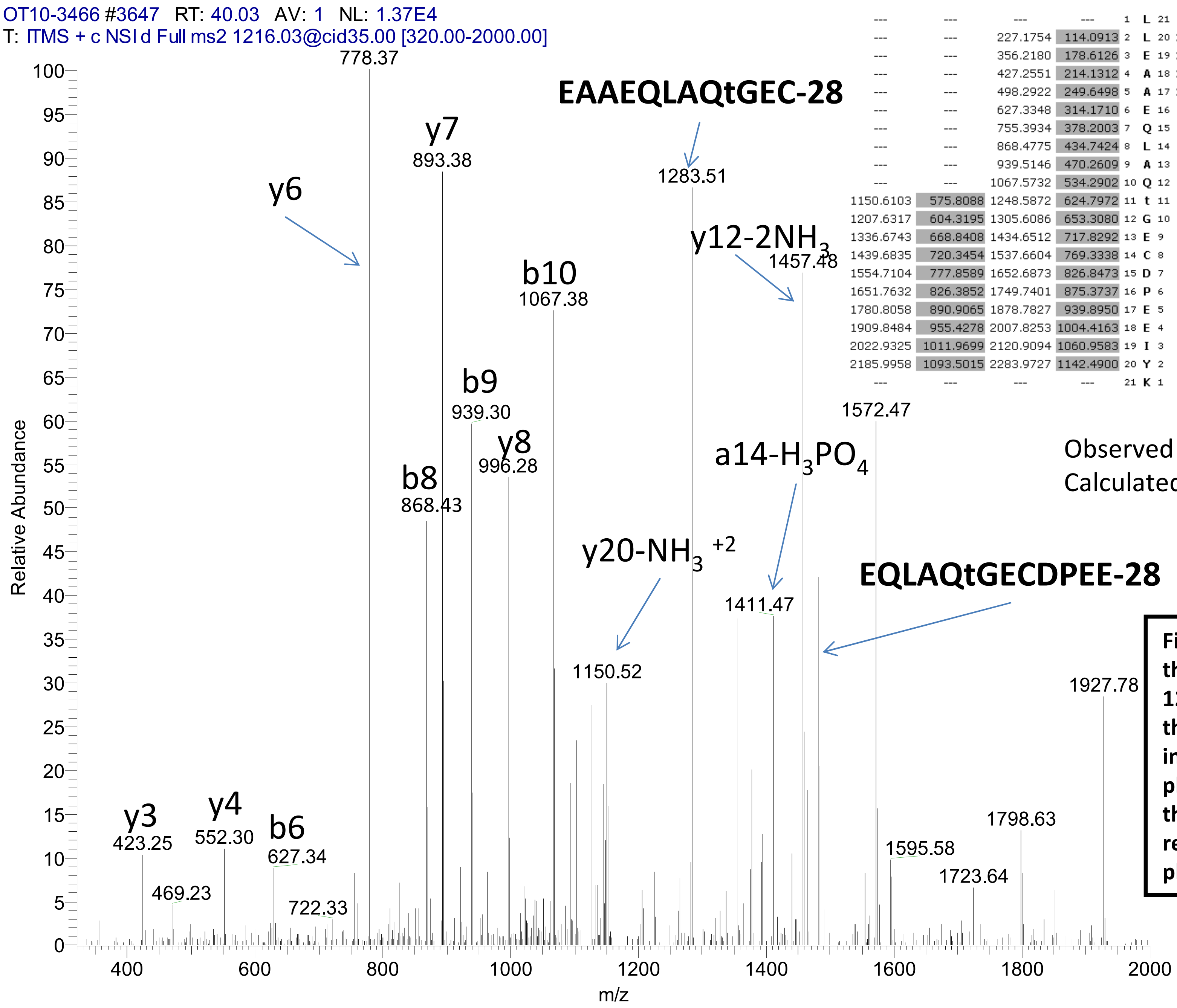


b	b^{+2}				y	y^{+2}
---	---	1	W	13	---	---
324.1455	162.5764	2	H	12	1369.5824	685.2948
437.2296	219.1184	3	L	11	1232.5235	616.7654
494.2510	247.6292	4	G	10	1119.4394	560.2234
591.3038	296.1555	5	P	9	1062.4180	531.7126
648.3253	324.6663	6	G	8	965.3652	483.1862
763.3522	382.1797	7	D	7	908.3437	454.6755
860.4050	430.7061	8	P	6	793.3168	397.1620
1007.4734	504.2403	9	F	5	696.2640	348.6357
1094.5054	547.7563	10	S	4	549.1956	275.1014
1195.5531	598.2802	11	T	3	462.1636	231.5854
1438.5827	719.7950	12	y	2	361.1159	181.0616
---	---	13	V	1	118.0863	59.5468

Observed M=1554.6487
Calculated M=1554.6545

Figure S17. MS/MS on the doubly charged 778.33 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y2 ion, residue 1653 is a phosphotyrosine.

Lambda MS/MS of peptide LLEAAEQLAQpTGECDPEEIYK

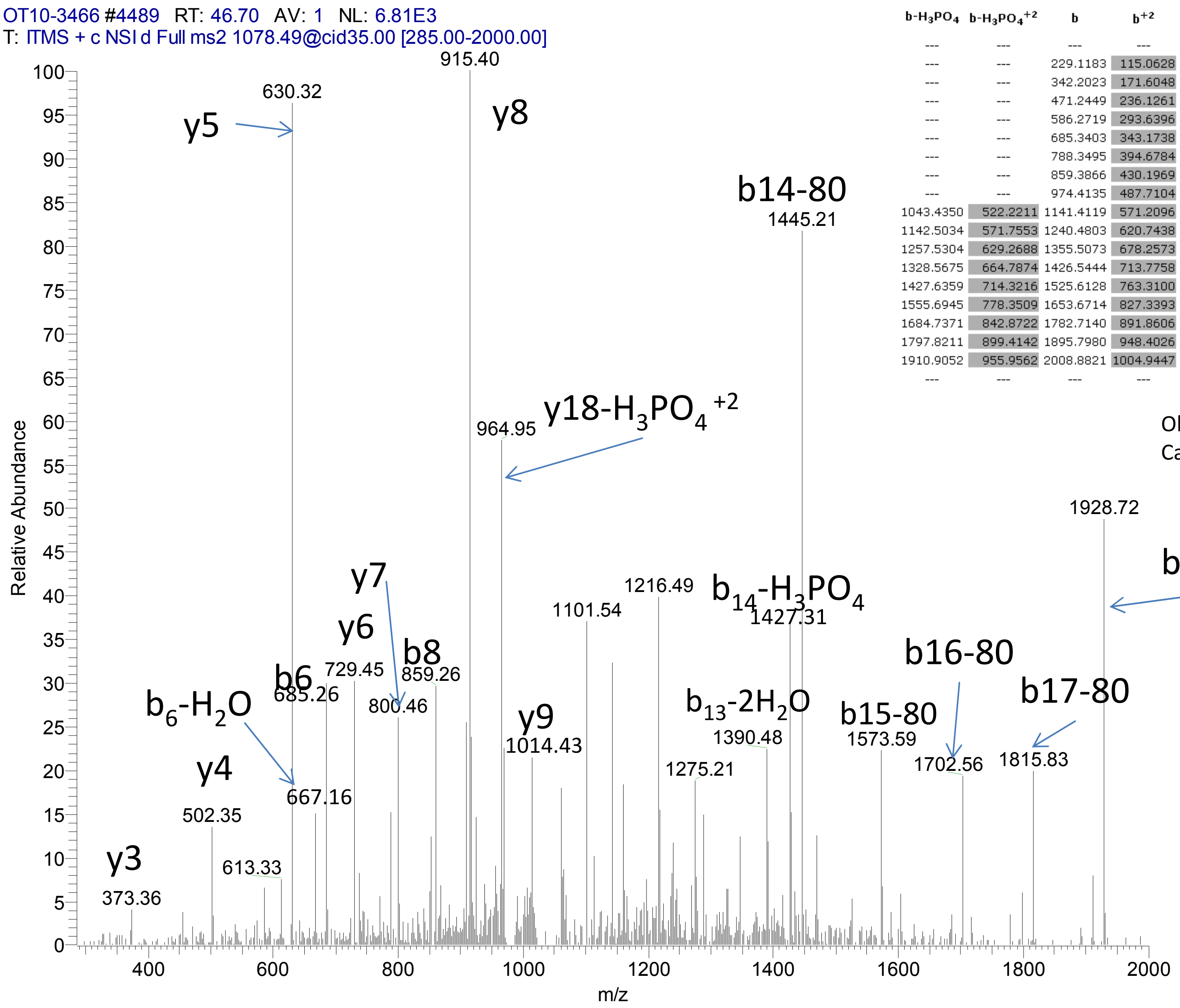


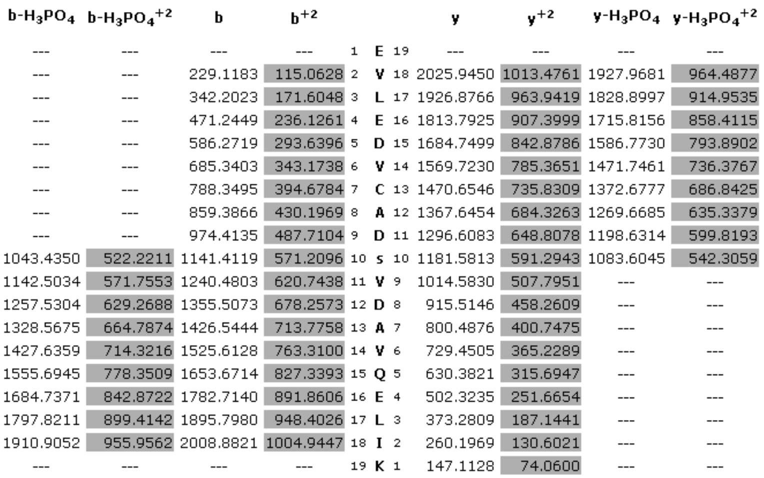
$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	L	21	---	---	---	---
---	---	227.1754	114.0913	2	L	20	2316.9942	1159.0007	2219.0173	1110.0123
---	---	356.2180	178.6126	3	E	19	2203.9101	1102.4587	2105.9332	1053.4702
---	---	427.2551	214.1312	4	A	18	2074.8675	1037.9374	1976.8906	988.9489
---	---	498.2922	249.6498	5	A	17	2003.8304	1002.4188	1905.8535	953.4304
---	---	627.3348	314.1710	6	E	16	1932.7933	966.9003	1834.8164	917.9118
---	---	755.3934	378.2003	7	Q	15	1803.7507	902.3790	1705.7738	853.3905
---	---	868.4775	434.7424	8	L	14	1675.6921	838.3497	1577.7152	789.3612
---	---	939.5146	470.2609	9	A	13	1562.6080	781.8077	1464.6311	732.8192
---	---	1067.5732	534.2902	10	Q	12	1491.5709	746.2891	1393.5940	697.3006
1150.6103	575.8088	1248.5872	624.7972	11	t	11	1363.5123	682.2598	1265.5354	633.2714
1207.6317	604.3195	1305.6086	653.3080	12	G	10	1182.4983	591.7528	---	---
1336.6743	668.8408	1434.6512	717.8292	13	E	9	1125.4769	563.2421	---	---
1439.6835	720.3454	1537.6604	769.3338	14	C	8	996.4343	498.7208	---	---
1554.7104	777.8589	1652.6873	826.8473	15	D	7	893.4251	447.2162	---	---
1651.7632	826.3852	1749.7401	875.3737	16	P	6	778.3981	389.7027	---	---
1780.8058	890.9065	1878.7827	939.8950	17	E	5	681.3454	341.1763	---	---
1909.8484	955.4278	2007.8253	1004.4163	18	E	4	552.3028	276.6550	---	---
2022.9325	1011.9699	2120.9094	1060.9583	19	I	3	423.2602	212.1337	---	---
2185.9958	1093.5015	2283.9727	1142.4900	20	Y	2	310.1761	155.5917	---	---
---	---	---	---	21	K	1	147.1128	74.0600	---	---

Observed M=2429.0478
Calculated M=2429.0709

Figure S18. MS/MS on the doubly charged 1216. 03 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the b10 and y ions, residue 607 is a phosphothreonine.

Lambda MS/MS of peptide EVLEDVCADpSVDAVQELIK





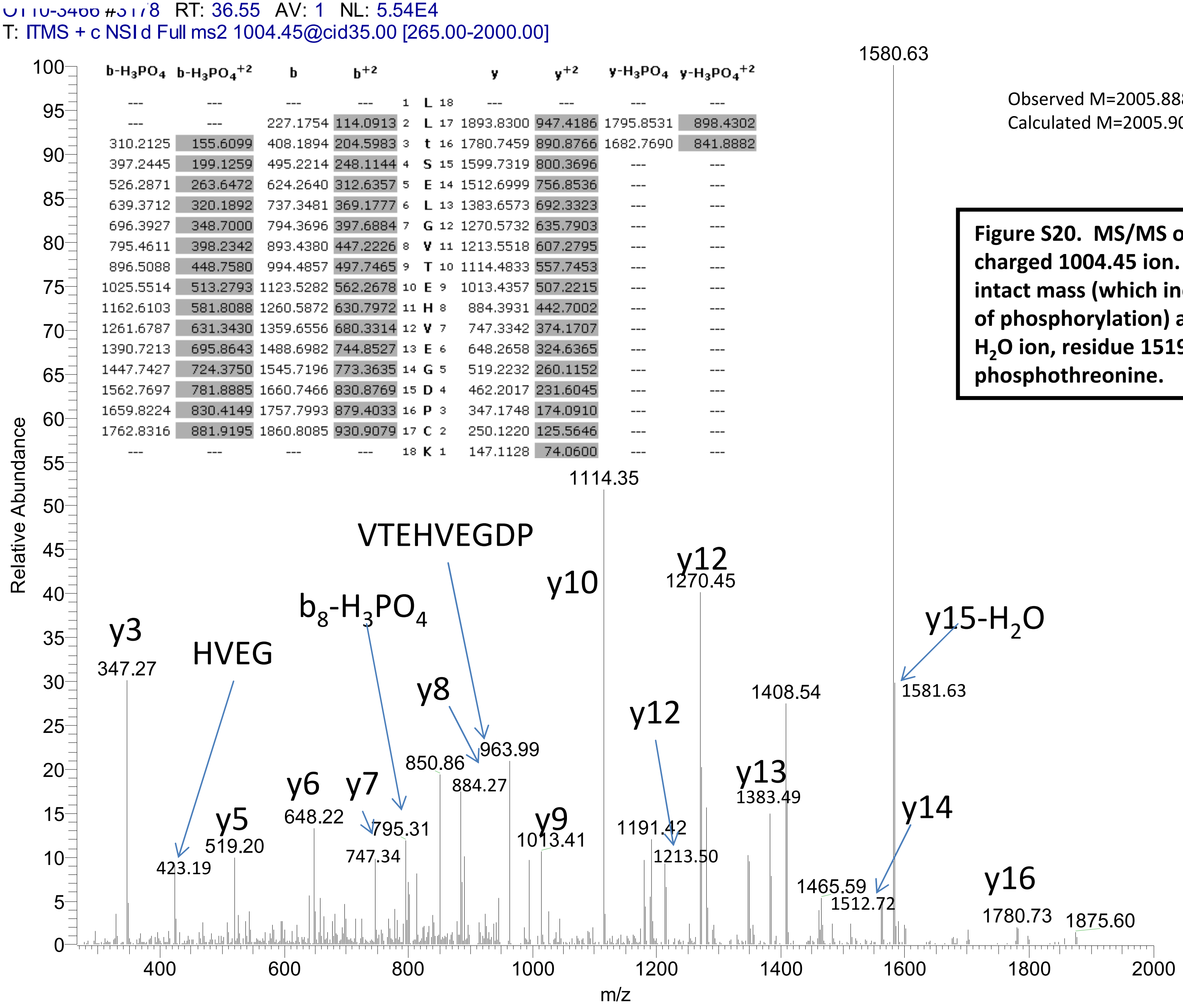
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	E	19	---	---	---	---
---	---	229.1183	115.0628	2	V	18	2025.9450	1013.4761	1927.9681	964.4877
---	---	342.2023	171.6048	3	L	17	1926.8766	963.9419	1828.8997	914.9535
---	---	471.2449	236.1261	4	E	16	1813.7925	907.3999	1715.8156	858.4115
---	---	586.2719	293.6396	5	D	15	1684.7499	842.8786	1586.7730	793.8902
---	---	685.3403	343.1738	6	V	14	1569.7230	785.3651	1471.7461	736.3767
---	---	788.3495	394.6784	7	C	13	1470.6546	735.8309	1372.6777	686.8425
---	---	859.3866	430.1969	8	A	12	1367.6454	684.3263	1269.6685	635.3379
---	---	974.4135	487.7104	9	D	11	1296.6083	648.8078	1198.6314	599.8193
1043.4350	522.2211	1141.4119	571.2096	10	s	10	1181.5813	591.2943	1083.6045	542.3059
1142.5034	571.7553	1240.4803	620.7438	11	V	9	1014.5830	507.7951	---	---
1257.5304	629.2688	1355.5073	678.2573	12	D	8	915.5146	458.2609	---	---
1328.5675	664.7874	1426.5444	713.7758	13	A	7	800.4876	400.7475	---	---
1427.6359	714.3216	1525.6128	763.3100	14	V	6	729.4505	365.2289	---	---
1555.6945	778.3509	1653.6714	827.3393	15	Q	5	630.3821	315.6947	---	---
1684.7371	842.8722	1782.7140	891.8606	16	E	4	502.3235	251.6654	---	---
1797.8211	899.4142	1895.7980	948.4026	17	L	3	373.2809	187.1441	---	---
1910.9052	955.9562	2008.8821	1004.9447	18	I	2	260.1969	130.6021	---	---
---	---	---	---	19	K	1	147.1128	74.0600	---	---

Observed M=2153.9606
Calculated M=2153.9803

b18-80

Figure S19. MS/MS on the doubly charged 1078.49 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the b14-H_3PO_4 and b-80 ions, residue 672 is a phosphoserine.

<u>Lambda</u> MS/MS of peptide LLpTSELGVTEHVEGDPCK


OT10-3466 #3178 RT: 36.55 AV: 1 NL: 5.54E4
T: ITMS + c NSI d Full ms2 1004.45@cid35.00 [265.00-2000.00]

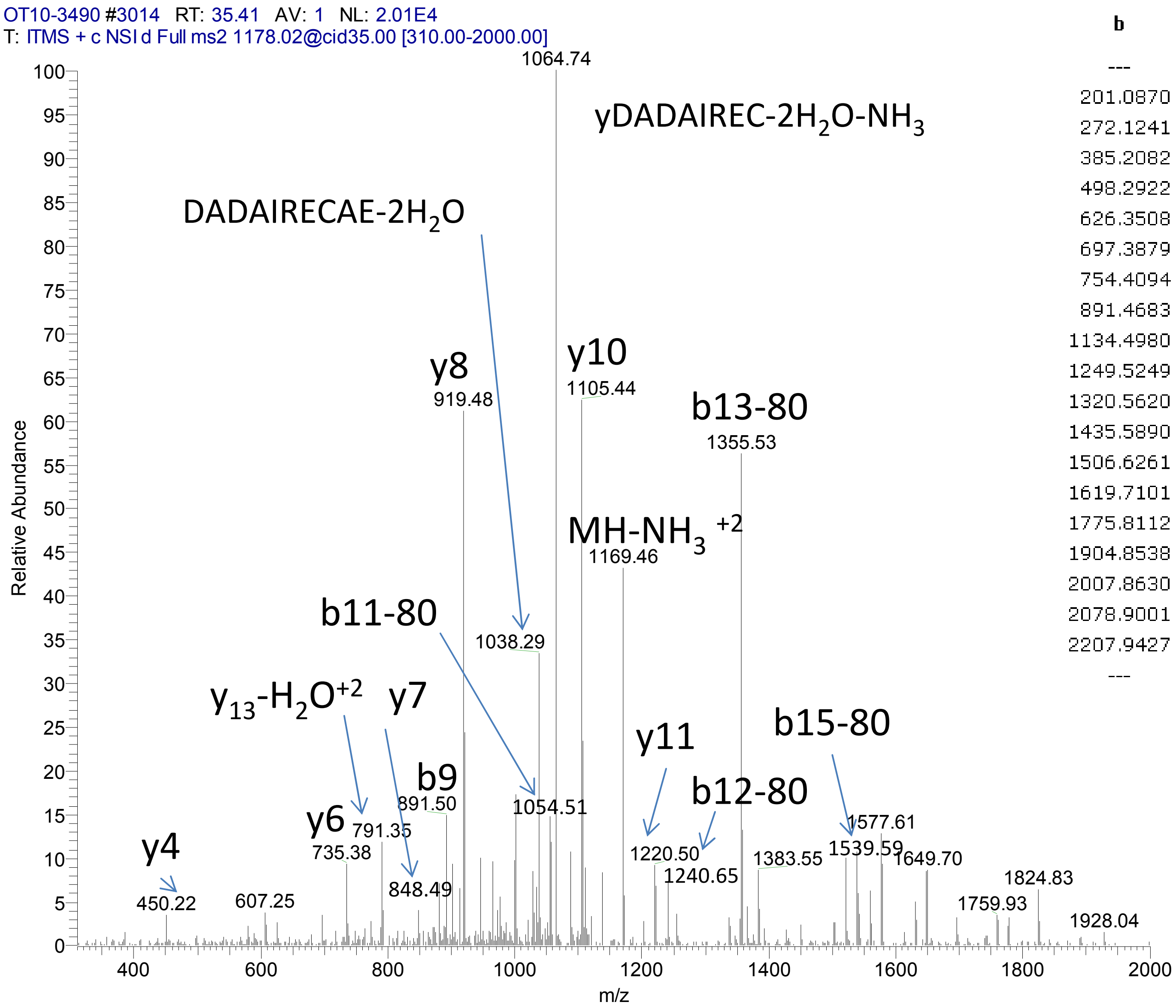
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	18	---	---	---	---
---	---	227.1754	114.0913	2	L	17	1893.8300	947.4186	1795.8531	898.4302
310.2125	155.6099	408.1894	204.5983	3	t	16	1780.7459	890.8766	1682.7690	841.8882
397.2445	199.1259	495.2214	248.1144	4	S	15	1599.7319	800.3696	---	---
526.2871	263.6472	624.2640	312.6357	5	E	14	1512.6999	756.8536	---	---
639.3712	320.1892	737.3481	369.1777	6	L	13	1383.6573	692.3323	---	---
696.3927	348.7000	794.3696	397.6884	7	G	12	1270.5732	635.7903	---	---
795.4611	398.2342	893.4380	447.2226	8	V	11	1213.5518	607.2795	---	---
896.5088	448.7580	994.4857	497.7465	9	T	10	1114.4833	557.7453	---	---
1025.5514	513.2793	1123.5282	562.2678	10	E	9	1013.4357	507.2215	---	---
1162.6103	581.8088	1260.5872	630.7972	11	H	8	884.3931	442.7002	---	---
1261.6787	631.3430	1359.6556	680.3314	12	V	7	747.3342	374.1707	---	---
1390.7213	695.8643	1488.6982	744.8527	13	E	6	648.2658	324.6365	---	---
1447.7427	724.3750	1545.7196	773.3635	14	G	5	519.2232	260.1152	---	---
1562.7697	781.8885	1660.7466	830.8769	15	D	4	462.2017	231.6045	---	---
1659.8224	830.4149	1757.7993	879.4033	16	P	3	347.1748	174.0910	---	---
1762.8316	881.9195	1860.8085	930.9079	17	C	2	250.1220	125.5646	---	---
---	---	---	---	18	K	1	147.1128	74.0600	---	---

Observed M=2005.8886
Calculated M=2005.9068

Figure S20. MS/MS on the doubly charged 1004.45 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y15-H_2O ion, residue 1519 is a phosphothreonine.

CIP

MS/MS of peptide AEALLQAGHYDADAIRECAEK



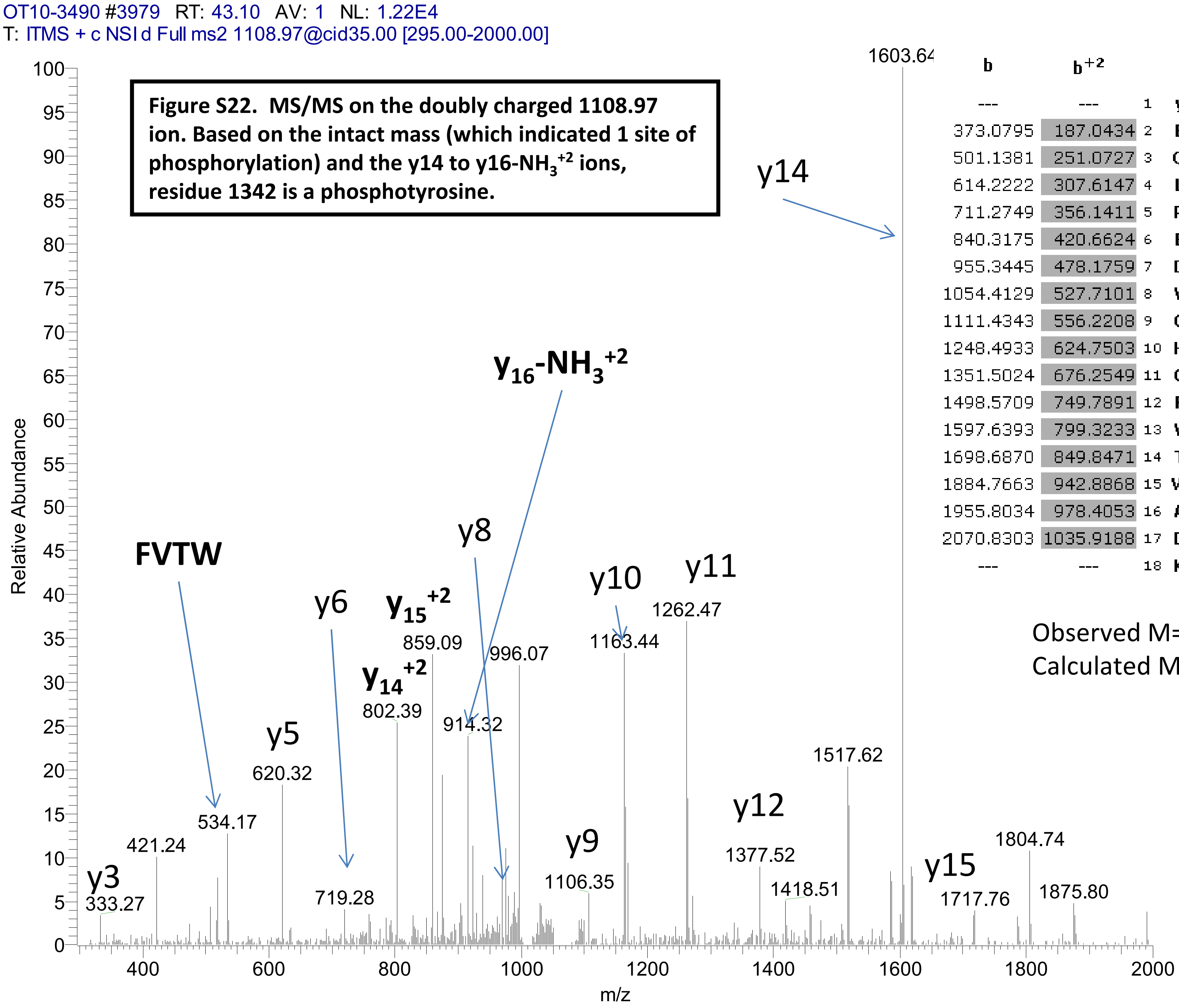
b	b^{+2}				y	y^{+2}
---	---	1	A	21	---	---
201.0870	101.0471	2	E	20	2283.0111	1142.0092
272.1241	136.5657	3	A	19	2153.9685	1077.4879
385.2082	193.1077	4	L	18	2082.9314	1041.9694
498.2922	249.6498	5	L	17	1969.8474	985.4273
626.3508	313.6790	6	Q	16	1856.7633	928.8853
697.3879	349.1976	7	A	15	1728.7047	864.8560
754.4094	377.7083	8	G	14	1657.6676	829.3374
891.4683	446.2378	9	H	13	1600.6461	800.8267
1134.4980	567.7526	10	y	12	1463.5872	732.2973
1249.5249	625.2661	11	D	11	1220.5576	610.7824
1320.5620	660.7846	12	A	10	1105.5306	553.2690
1435.5890	718.2981	13	D	9	1034.4935	517.7504
1506.6261	753.8167	14	A	8	919.4666	460.2369
1619.7101	810.3587	15	I	7	848.4295	424.7184
1775.8112	888.4093	16	R	6	735.3454	368.1763
1904.8538	952.9306	17	E	5	579.2443	290.1258
2007.8630	1004.4351	18	C	4	450.2017	225.6045
2078.9001	1039.9537	19	A	3	347.1925	174.0999
2207.9427	1104.4750	20	E	2	276.1554	138.5813
---	---	21	K	1	147.1128	74.0600

Observed M=2353.0228
Calculated M=2353.0409

Figure S21. MS/MS on the doubly charged 1178.02 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the b ions, residue 963 is a phosphotyrosine

CIP

MS/MS of peptide pYEQLPEDVGHCFVTWADK



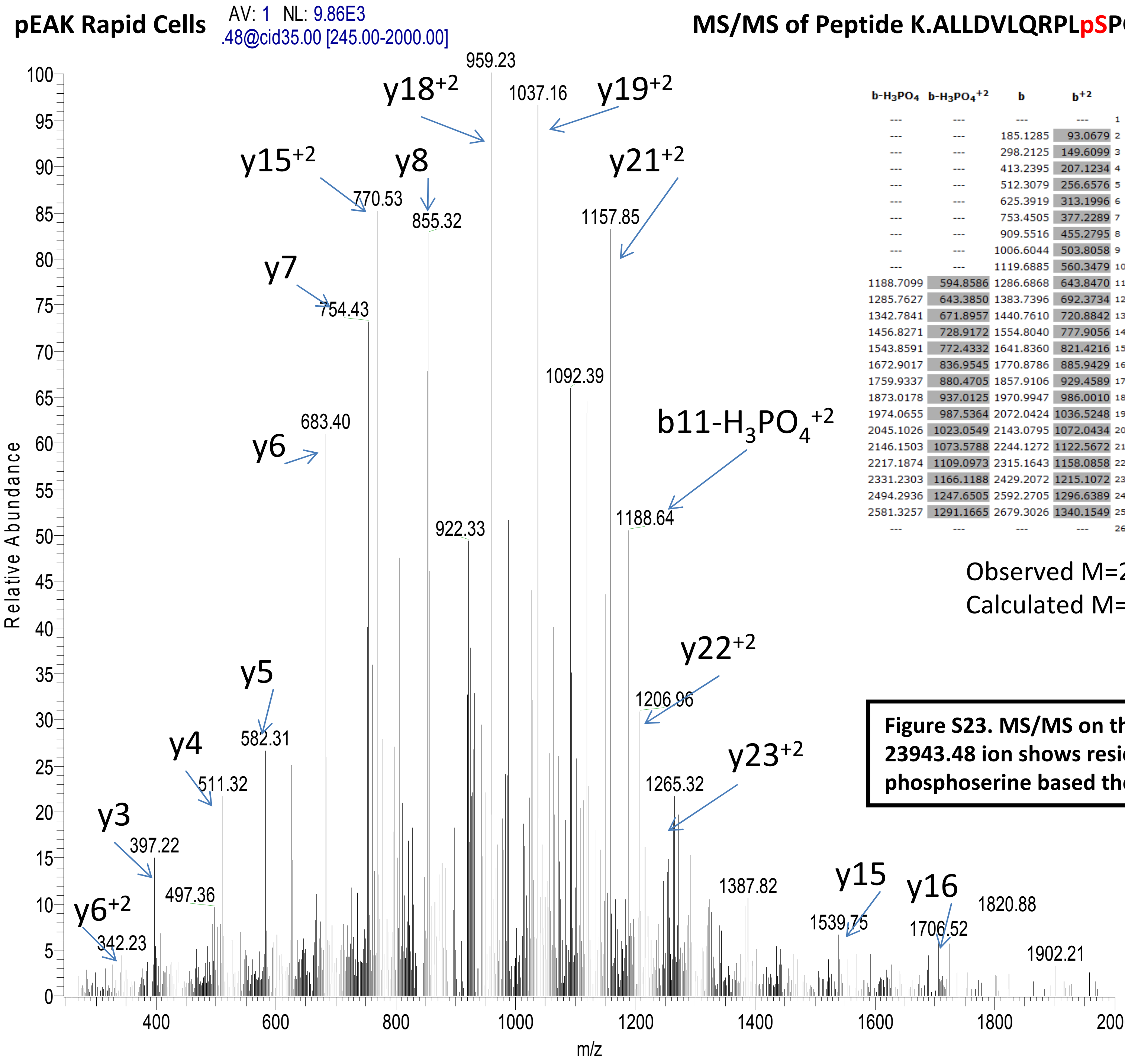
OT10-3490 #3979 RT: 43.10 AV: 1 NL: 1.22E4
T: ITMS + c NSI d Full ms2 1108.97@cid35.00 [295.00-2000.00]

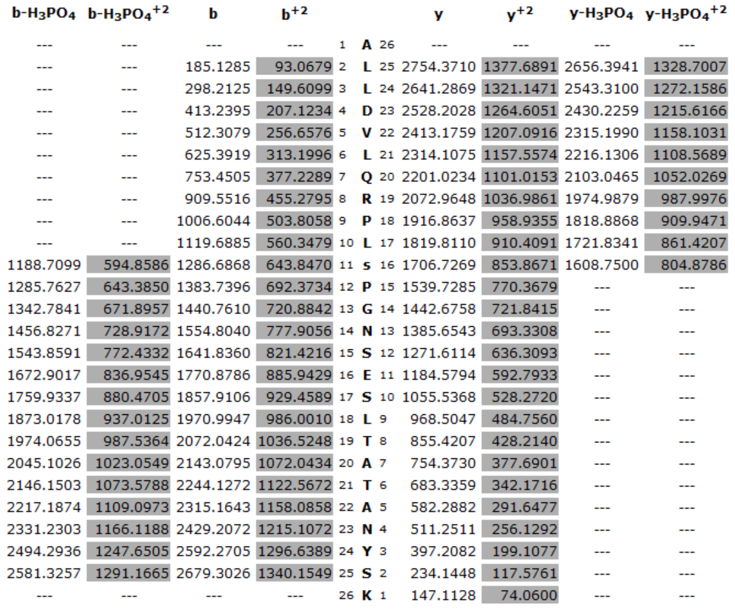
Figure S22. MS/MS on the doubly charged 1108.97 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y14 to y16-NH_3^{+2} ions, residue 1342 is a phosphotyrosine.

b	b^{+2}				y	y^{+2}
---	---	1	y	18	---	---
373.0795	187.0434	2	E	17	1973.9062	987.4567
501.1381	251.0727	3	Q	16	1844.8636	922.9354
614.2222	307.6147	4	L	15	1716.8050	858.9061
711.2749	356.1411	5	P	14	1603.7210	802.3641
840.3175	420.6624	6	E	13	1506.6682	753.8377
955.3445	478.1759	7	D	12	1377.6256	689.3164
1054.4129	527.7101	8	V	11	1262.5987	631.8030
1111.4343	556.2208	9	G	10	1163.5302	582.2688
1248.4933	624.7503	10	H	9	1106.5088	553.7580
1351.5024	676.2549	11	C	8	969.4499	485.2286
1498.5709	749.7891	12	F	7	866.4407	433.7240
1597.6393	799.3233	13	V	6	719.3723	360.1898
1698.6870	849.8471	14	T	5	620.3039	310.6556
1884.7663	942.8868	15	W	4	519.2562	260.1317
1955.8034	978.4053	16	A	3	333.1769	167.0921
2070.8303	1035.9188	17	D	2	262.1397	131.5735
---	---	18	K	1	147.1128	74.0600

Observed M=2215.9102
Calculated M=2215.9286

MS/MS of Peptide K.ALLDVLQRPLpSPGNSESLTATANYSK.A





b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	A	26	---	---	---	---
---	---	185.1285	93.0679	2	L	25	2754.3710	1377.6891	2656.3941	1328.7007
---	---	298.2125	149.6099	3	L	24	2641.2869	1321.1471	2543.3100	1272.1586
---	---	413.2395	207.1234	4	D	23	2528.2028	1264.6051	2430.2259	1215.6166
---	---	512.3079	256.6576	5	V	22	2413.1759	1207.0916	2315.1990	1158.1031
---	---	625.3919	313.1996	6	L	21	2314.1075	1157.5574	2216.1306	1108.5689
---	---	753.4505	377.2289	7	Q	20	2201.0234	1101.0153	2103.0465	1052.0269
---	---	909.5516	455.2795	8	R	19	2072.9648	1036.9861	1974.9879	987.9976
---	---	1006.6044	503.8058	9	P	18	1916.8637	958.9355	1818.8868	909.9471
---	---	1119.6885	560.3479	10	L	17	1819.8110	910.4091	1721.8341	861.4207
1188.7099	594.8586	1286.6868	643.8470	11	s	16	1706.7269	853.8671	1608.7500	804.8786
1285.7627	643.3850	1383.7396	692.3734	12	P	15	1539.7285	770.3679	---	---
1342.7841	671.8957	1440.7610	720.8842	13	G	14	1442.6758	721.8415	---	---
1456.8271	728.9172	1554.8040	777.9056	14	N	13	1385.6543	693.3308	---	---
1543.8591	772.4332	1641.8360	821.4216	15	S	12	1271.6114	636.3093	---	---
1672.9017	836.9545	1770.8786	885.9429	16	E	11	1184.5794	592.7933	---	---
1759.9337	880.4705	1857.9106	929.4589	17	S	10	1055.5368	528.2720	---	---
1873.0178	937.0125	1970.9947	986.0010	18	L	9	968.5047	484.7560	---	---
1974.0655	987.5364	2072.0424	1036.5248	19	T	8	855.4207	428.2140	---	---
2045.1026	1023.0549	2143.0795	1072.0434	20	A	7	754.3730	377.6901	---	---
2146.1503	1073.5788	2244.1272	1122.5672	21	T	6	683.3359	342.1716	---	---
2217.1874	1109.0973	2315.1643	1158.0858	22	A	5	582.2882	291.6477	---	---
2331.2303	1166.1188	2429.2072	1215.1072	23	N	4	511.2511	256.1292	---	---
2494.2936	1247.6505	2592.2705	1296.6389	24	Y	3	397.2082	199.1077	---	---
2581.3257	1291.1665	2679.3026	1340.1549	25	S	2	234.1448	117.5761	---	---
---	---	---	---	26	K	1	147.1128	74.0600	---	---

Observed M=2824.3990
Calculated M=2824.4008

Figure S23. MS/MS on the triply charged 23943.48 ion shows residue 487 is a phosphoserine based the $y15^{+2}$ ion.

MS/MS of Peptide K.ALLDVLQRPLSPGNpSESLTATANYSK.A

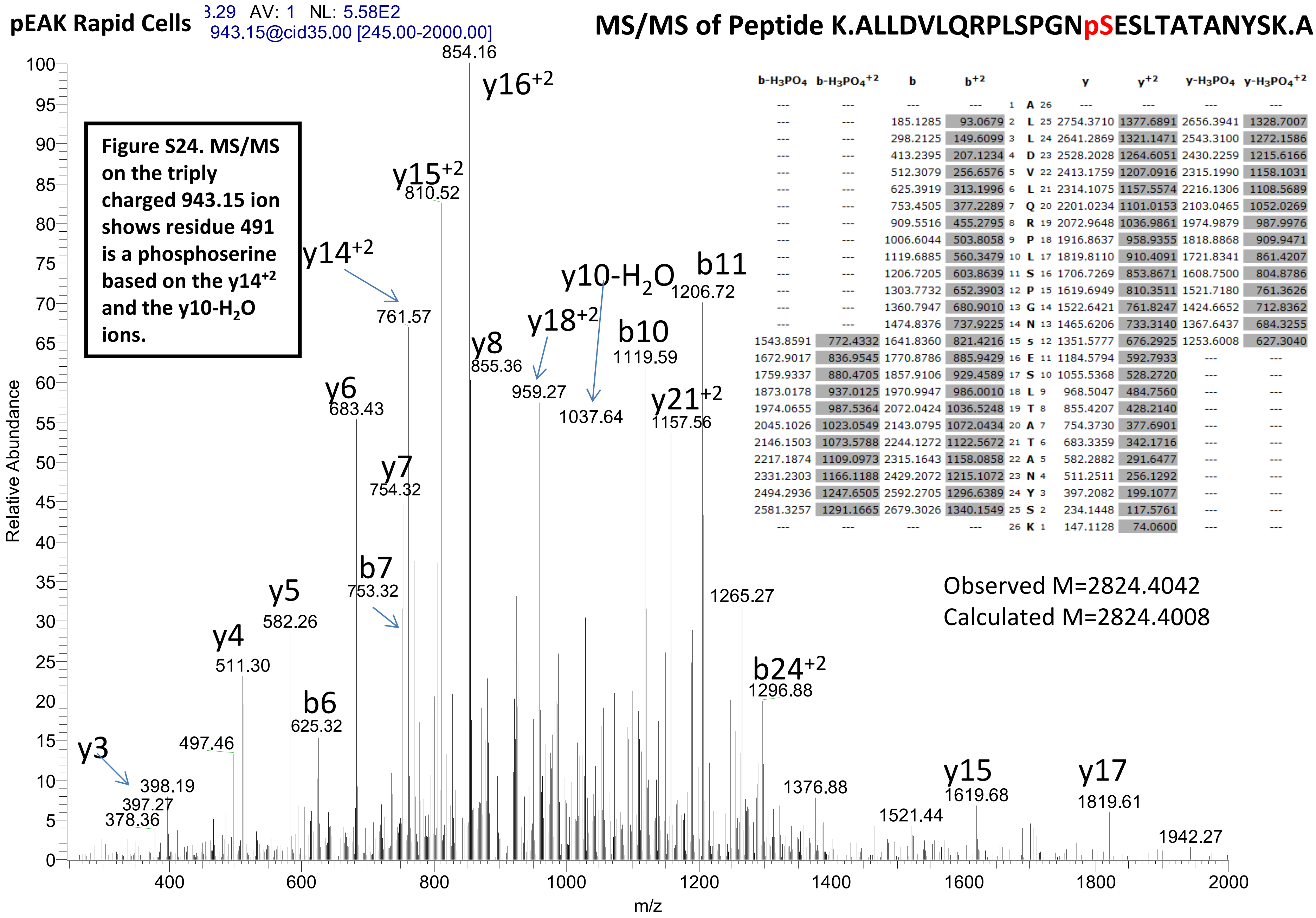


Figure S24. MS/MS on the triply charged 943.15 ion shows residue 491 is a phosphoserine based on the $y14^{+2}$ and the $y10\text{-}H_2O$ ions.

$b\text{-}H_3PO_4$	$b\text{-}H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y\text{-}H_3PO_4$	$y\text{-}H_3PO_4^{+2}$
---	---	---	---	1	A	26	---	---	---	---
---	---	185.1285	93.0679	2	L	25	2754.3710	1377.6891	2656.3941	1328.7007
---	---	298.2125	149.6099	3	L	24	2641.2869	1321.1471	2543.3100	1272.1586
---	---	413.2395	207.1234	4	D	23	2528.2028	1264.6051	2430.2259	1215.6166
---	---	512.3079	256.6576	5	V	22	2413.1759	1207.0916	2315.1990	1158.1031
---	---	625.3919	313.1996	6	L	21	2314.1075	1157.5574	2216.1306	1108.5689
---	---	753.4505	377.2289	7	Q	20	2201.0234	1101.0153	2103.0465	1052.0269
---	---	909.5516	455.2795	8	R	19	2072.9648	1036.9861	1974.9879	987.9976
---	---	1006.6044	503.8058	9	P	18	1916.8637	958.9355	1818.8868	909.9471
---	---	1119.6885	560.3479	10	L	17	1819.8110	910.4091	1721.8341	861.4207
---	---	1206.7205	603.8639	11	S	16	1706.7269	853.8671	1608.7500	804.8786
---	---	1303.7732	652.3903	12	P	15	1619.6949	810.3511	1521.7180	761.3626
---	---	1360.7947	680.9010	13	G	14	1522.6421	761.8247	1424.6652	712.8362
---	---	1474.8376	737.9225	14	N	13	1465.6206	733.3140	1367.6437	684.3255
1543.8591	772.4332	1641.8360	821.4216	15	s	12	1351.5777	676.2925	1253.6008	627.3040
1672.9017	836.9545	1770.8786	885.9429	16	E	11	1184.5794	592.7933	---	---
1759.9337	880.4705	1857.9106	929.4589	17	S	10	1055.5368	528.2720	---	---
1873.0178	937.0125	1970.9947	986.0010	18	L	9	968.5047	484.7560	---	---
1974.0655	987.5364	2072.0424	1036.5248	19	T	8	855.4207	428.2140	---	---
2045.1026	1023.0549	2143.0795	1072.0434	20	A	7	754.3730	377.6901	---	---
2146.1503	1073.5788	2244.1272	1122.5672	21	T	6	683.3359	342.1716	---	---
2217.1874	1109.0973	2315.1643	1158.0858	22	A	5	582.2882	291.6477	---	---
2331.2303	1166.1188	2429.2072	1215.1072	23	N	4	511.2511	256.1292	---	---
2494.2936	1247.6505	2592.2705	1296.6389	24	Y	3	397.2082	199.1077	---	---
2581.3257	1291.1665	2679.3026	1340.1549	25	S	2	234.1448	117.5761	---	---
---	---	---	---	26	K	1	147.1128	74.0600	---	---

Observed M=2824.4042
Calculated M=2824.4008

pEAK Rapid Cells

MS/MS of Peptide K.ALLDVLQRPLSPGNpSEpSLTATANYSK.A

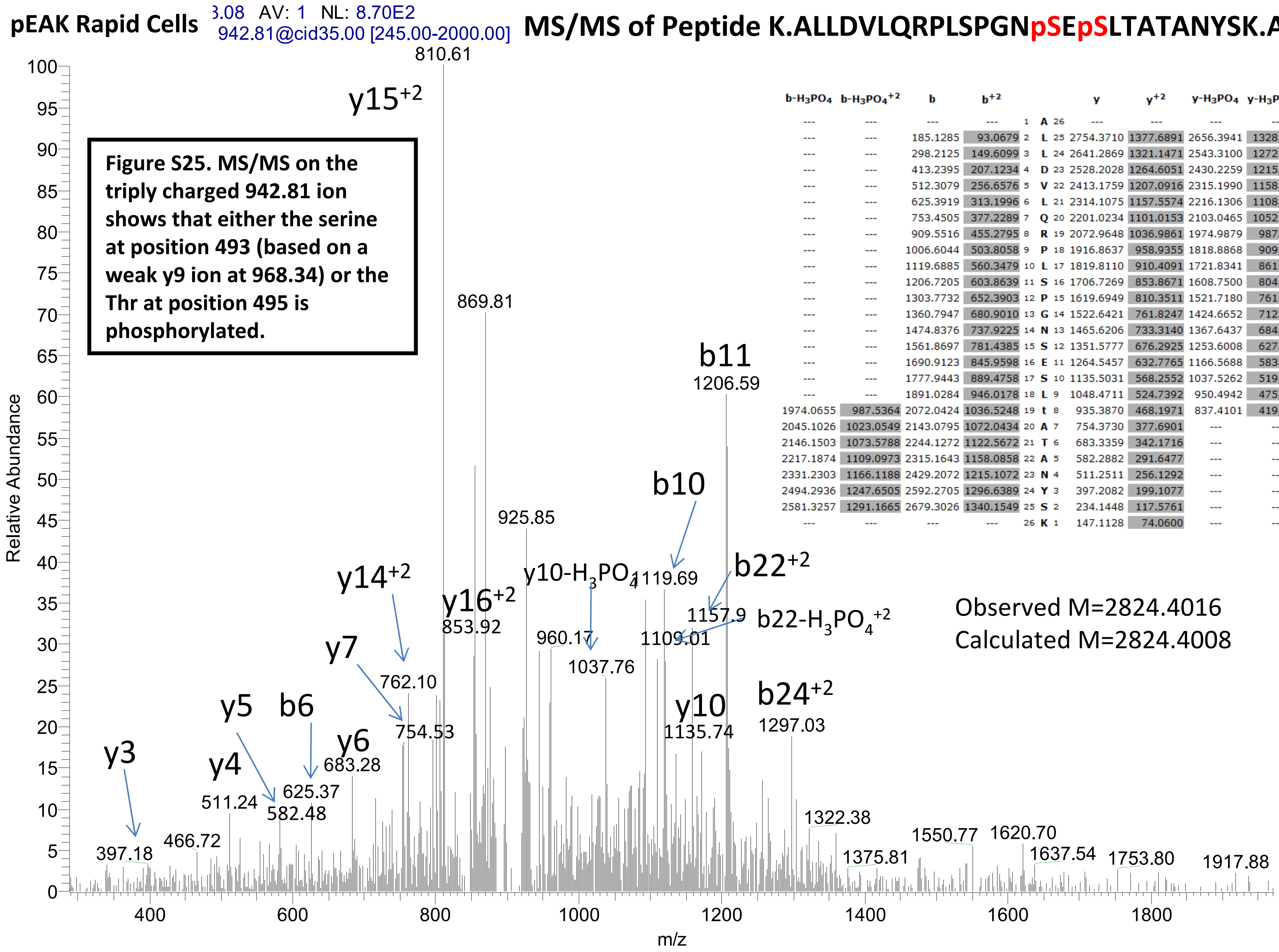


Figure S25. MS/MS on the triply charged 942.81 ion shows that either the serine at position 493 (based on a weak y9 ion at 968.34) or the Thr at position 495 is phosphorylated.

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	**A**	26	---	---	---	---
---	---	185.1285	93.0679	2	**L**	25	2754.3710	1377.6891	2656.3941	1328.7007
---	---	298.2125	149.6099	3	**L**	24	2641.2869	1321.1471	2543.3100	1272.1586
---	---	413.2395	207.1234	4	**D**	23	2528.2028	1264.6051	2430.2259	1215.6166
---	---	512.3079	256.6576	5	**V**	22	2413.1759	1207.0916	2315.1990	1158.1031
---	---	625.3919	313.1996	6	**L**	21	2314.1075	1157.5574	2216.1306	1108.5689
---	---	753.4505	377.2289	7	**Q**	20	2201.0234	1101.0153	2103.0465	1052.0269
---	---	909.5516	455.2795	8	**R**	19	2072.9648	1036.9861	1974.9879	987.9976
---	---	1006.6044	503.8058	9	**P**	18	1916.8637	958.9355	1818.8868	909.9471
---	---	1119.6885	560.3479	10	**L**	17	1819.8110	910.4091	1721.8341	861.4207
---	---	1206.7205	603.8639	11	**S**	16	1706.7269	853.8671	1608.7500	804.8786
---	---	1303.7732	652.3903	12	**P**	15	1619.6949	810.3511	1521.7180	761.3626
---	---	1360.7947	680.9010	13	**G**	14	1522.6421	761.8247	1424.6652	712.8362
---	---	1474.8376	737.9225	14	**N**	13	1465.6206	733.3140	1367.6437	684.3255
---	---	1561.8697	781.4385	15	**S**	12	1351.5777	676.2925	1253.6008	627.3040
---	---	1690.9123	845.9598	16	**E**	11	1264.5457	632.7765	1166.5688	583.7880
---	---	1777.9443	889.4758	17	**S**	10	1135.5031	568.2552	1037.5262	519.2667
---	---	1891.0284	946.0178	18	**L**	9	1048.4711	524.7392	950.4942	475.7507
1974.0655	987.5364	2072.0424	1036.5248	19	**t**	8	935.3870	468.1971	837.4101	419.2087
2045.1026	1023.0549	2143.0795	1072.0434	20	**A**	7	754.3730	377.6901	---	---
2146.1503	1073.5788	2244.1272	1122.5672	21	**T**	6	683.3359	342.1716	---	---
2217.1874	1109.0973	2315.1643	1158.0858	22	**A**	5	582.2882	291.6477	---	---
2331.2303	1166.1188	2429.2072	1215.1072	23	**N**	4	511.2511	256.1292	---	---
2494.2936	1247.6505	2592.2705	1296.6389	24	**Y**	3	397.2082	199.1077	---	---
2581.3257	1291.1665	2679.3026	1340.1549	25	**S**	2	234.1448	117.5761	---	---
---	---	---	---	26	**K**	1	147.1128	74.0600	---	---

Observed M=2824.4016
Calculated M=2824.4008

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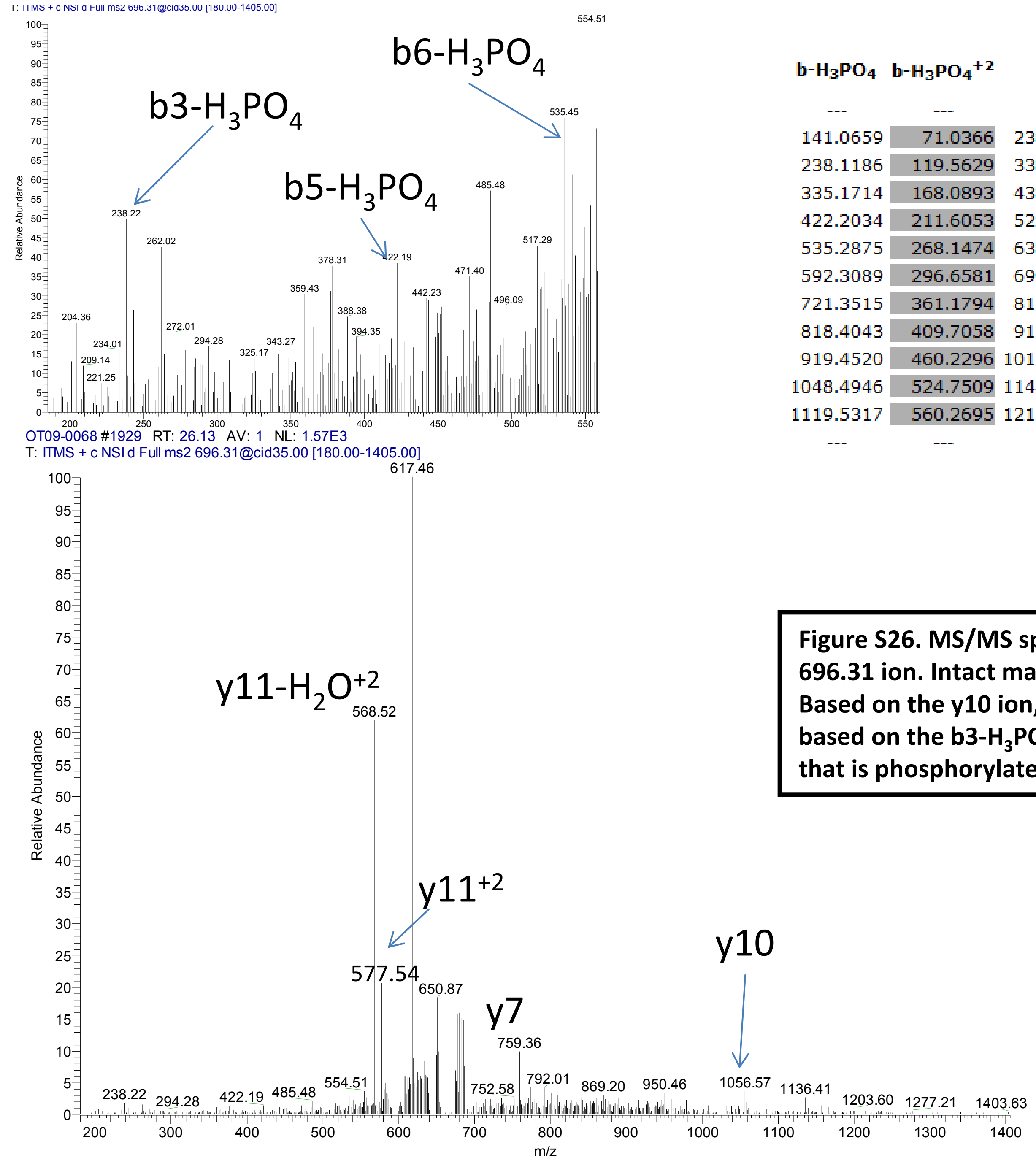

MS/MS of Peptide R.pSAPPSLGEPTEAR.D

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}
---	---	---	---	1	S	13	---	---
141.0659	71.0366	239.0427	120.0250	2	A	12	1224.6219	612.8146
238.1186	119.5629	336.0955	168.5514	3	P	11	1153.5848	577.2960
335.1714	168.0893	433.1483	217.0778	4	P	10	1056.5320	528.7696
422.2034	211.6053	520.1803	260.5938	5	S	9	959.4793	480.2433
535.2875	268.1474	633.2644	317.1358	6	L	8	872.4472	436.7272
592.3089	296.6581	690.2858	345.6466	7	G	7	759.3632	380.1852
721.3515	361.1794	819.3284	410.1679	8	E	6	702.3417	351.6745
818.4043	409.7058	916.3812	458.6942	9	P	5	573.2991	287.1532
919.4520	460.2296	1017.4289	509.2181	10	T	4	476.2463	238.6268
1048.4946	524.7509	1146.4715	573.7394	11	E	3	375.1987	188.1030
1119.5317	560.2695	1217.5086	609.2579	12	A	2	246.1561	123.5817
---	---	---	---	13	R	1	175.1190	88.0631

Observed M=1390.6141
Calculated M=1390.6129

Figure S26. MS/MS spectra of doubly charged 696.31 ion. Intact mass indicates one site of phosphorylation. Based on the y10 ion, the threonine is not phosphorylated; based on the b3-H_3PO_4 ion, it is the first serine at residue 710 that is phosphorylated.

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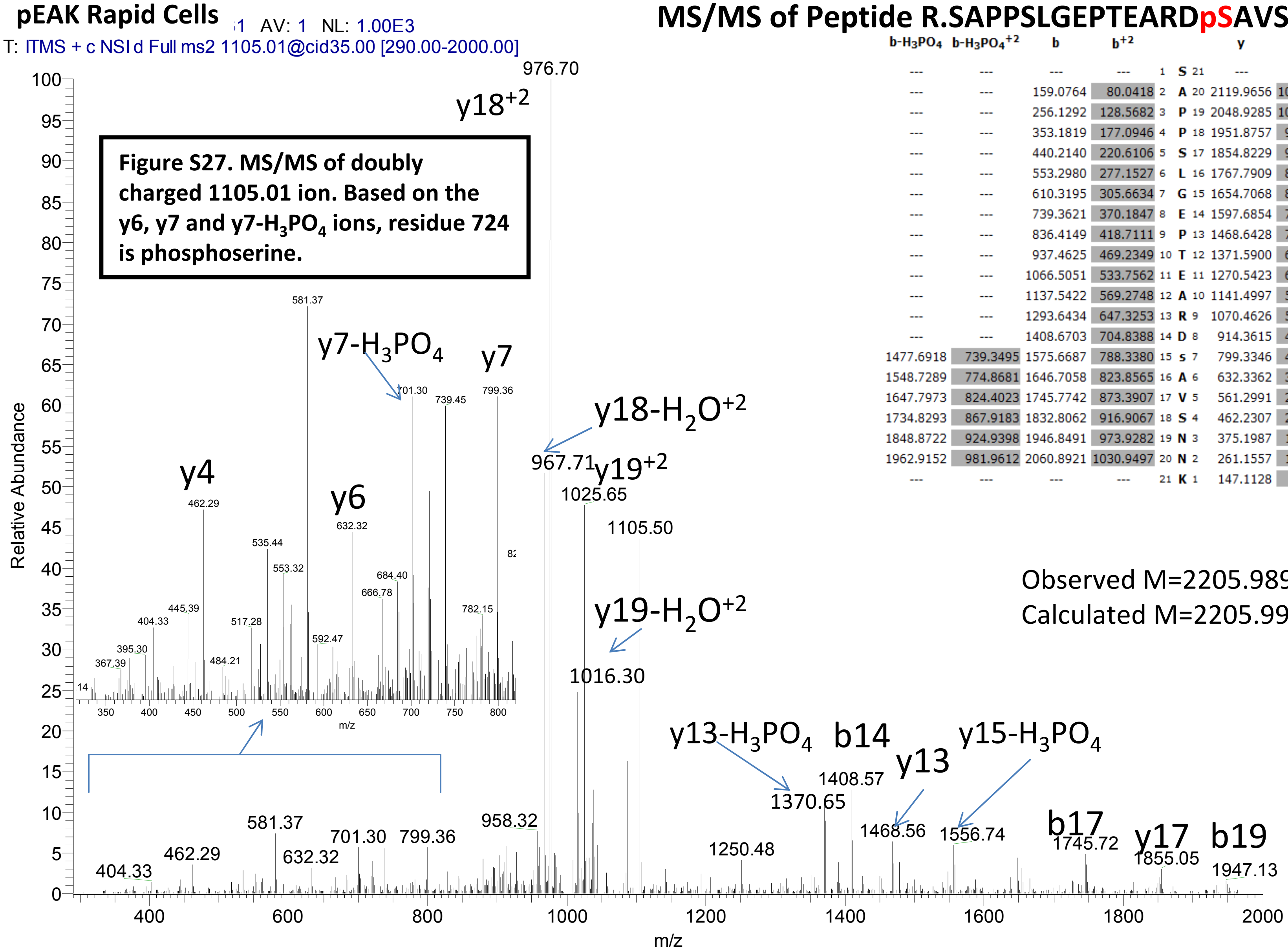

Figure S27. MS/MS of doubly charged 1105.01 ion. Based on the y6, y7 and y7-H_3PO_4 ions, residue 724 is phosphoserine.

MS/MS of Peptide R.SAPPSLGEPTEARDpSAVSNNK.T

$b\text{-}H_3PO_4$	$b\text{-}H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y\text{-}H_3PO_4$	$y\text{-}H_3PO_4^{+2}$
---	---	---	---	1	**S**	21	---	---	---	---
---	---	159.0764	80.0418	2	**A**	20	2119.9656	1060.4864	2021.9887	1011.4980
---	---	256.1292	128.5682	3	**P**	19	2048.9285	1024.9679	1950.9516	975.9794
---	---	353.1819	177.0946	4	**P**	18	1951.8757	976.4415	1853.8988	927.4530
---	---	440.2140	220.6106	5	**S**	17	1854.8229	927.9151	1756.8460	878.9267
---	---	553.2980	277.1527	6	**L**	16	1767.7909	884.3991	1669.8140	835.4106
---	---	610.3195	305.6634	7	**G**	15	1654.7068	827.8571	1556.7299	778.8686
---	---	739.3621	370.1847	8	**E**	14	1597.6854	799.3463	1499.7085	750.3579
---	---	836.4149	418.7111	9	**P**	13	1468.6428	734.8250	1370.6659	685.8366
---	---	937.4625	469.2349	10	**T**	12	1371.5900	686.2986	1273.6131	637.3102
---	---	1066.5051	533.7562	11	**E**	11	1270.5423	635.7748	1172.5654	586.7864
---	---	1137.5422	569.2748	12	**A**	10	1141.4997	571.2535	1043.5228	522.2651
---	---	1293.6434	647.3253	13	**R**	9	1070.4626	535.7350	972.4857	486.7465
---	---	1408.6703	704.8388	14	**D**	8	914.3615	457.6844	816.3846	408.6959
1477.6918	739.3495	1575.6687	788.3380	15	**s**	7	799.3346	400.1709	701.3577	351.1825
1548.7289	774.8681	1646.7058	823.8565	16	**A**	6	632.3362	316.6717	---	---
1647.7973	824.4023	1745.7742	873.3907	17	**V**	5	561.2991	281.1532	---	---
1734.8293	867.9183	1832.8062	916.9067	18	**S**	4	462.2307	231.6190	---	---
1848.8722	924.9398	1946.8491	973.9282	19	**N**	3	375.1987	188.1030	---	---
1962.9152	981.9612	2060.8921	1030.9497	20	**N**	2	261.1557	131.0815	---	---
---	---	---	---	21	**K**	1	147.1128	74.0600	---	---

Observed M=2205.9892
Calculated M=2205.9903

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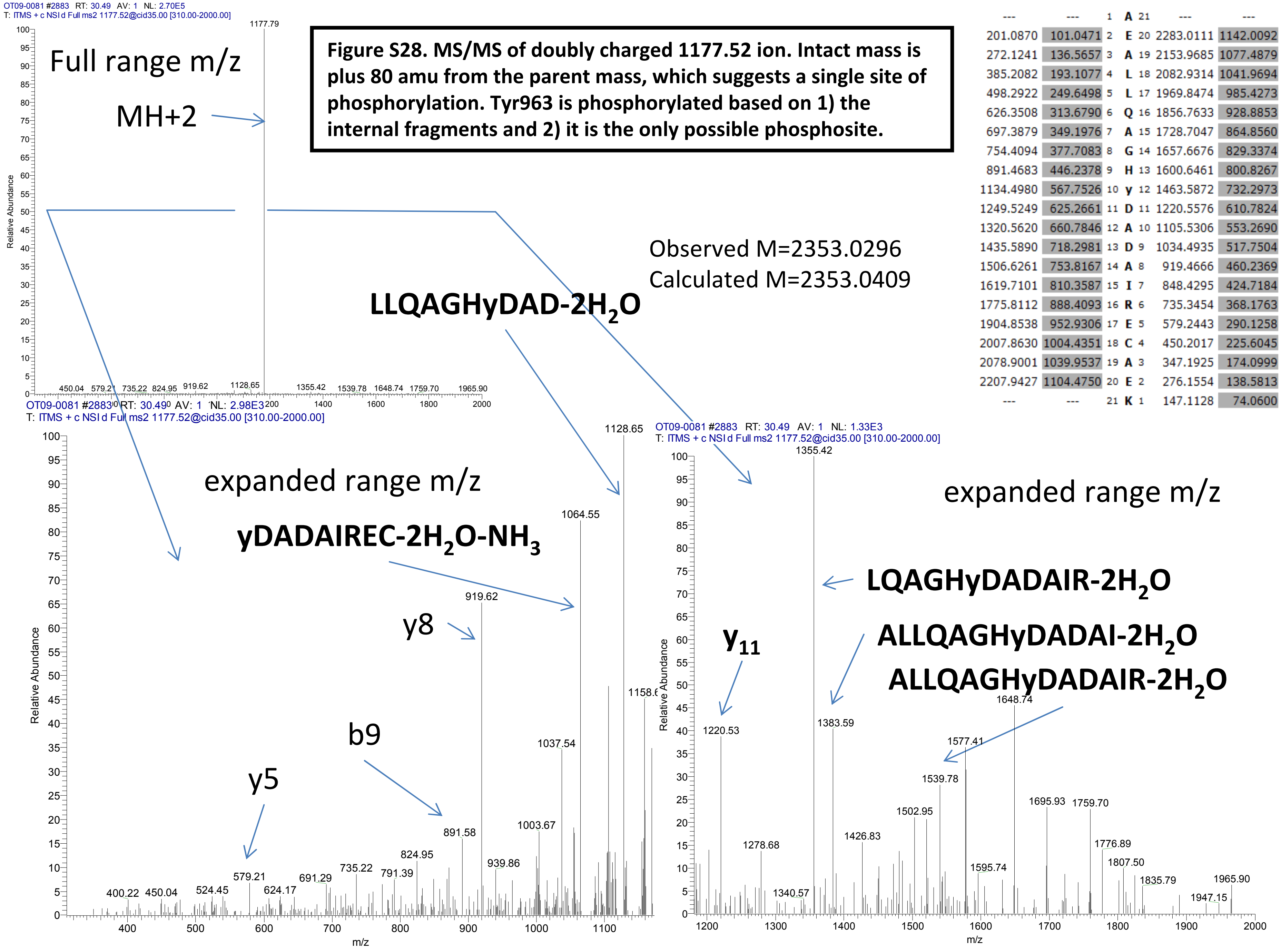
MS/MS of Peptide K.AEALLQAGHpYDADAIRECAEK.V

b	b^{+2}				y	y^{+2}
---	---	1	**A**	21	---	---
201.0870	101.0471	2	**E**	20	2283.0111	1142.0092
272.1241	136.5657	3	**A**	19	2153.9685	1077.4879
385.2082	193.1077	4	**L**	18	2082.9314	1041.9694
498.2922	249.6498	5	**L**	17	1969.8474	985.4273
626.3508	313.6790	6	**Q**	16	1856.7633	928.8853
697.3879	349.1976	7	**A**	15	1728.7047	864.8560
754.4094	377.7083	8	**G**	14	1657.6676	829.3374
891.4683	446.2378	9	**H**	13	1600.6461	800.8267
1134.4980	567.7526	10	**y**	12	1463.5872	732.2973
1249.5249	625.2661	11	**D**	11	1220.5576	610.7824
1320.5620	660.7846	12	**A**	10	1105.5306	553.2690
1435.5890	718.2981	13	**D**	9	1034.4935	517.7504
1506.6261	753.8167	14	**A**	8	919.4666	460.2369
1619.7101	810.3587	15	**I**	7	848.4295	424.7184
1775.8112	888.4093	16	**R**	6	735.3454	368.1763
1904.8538	952.9306	17	**E**	5	579.2443	290.1258
2007.8630	1004.4351	18	**C**	4	450.2017	225.6045
2078.9001	1039.9537	19	**A**	3	347.1925	174.0999
2207.9427	1104.4750	20	**E**	2	276.1554	138.5813
---	---	21	**K**	1	147.1128	74.0600

Figure S28. MS/MS of doubly charged 1177.52 ion. Intact mass is plus 80 amu from the parent mass, which suggests a single site of phosphorylation. Tyr963 is phosphorylated based on 1) the internal fragments and 2) it is the only possible phosphosite.

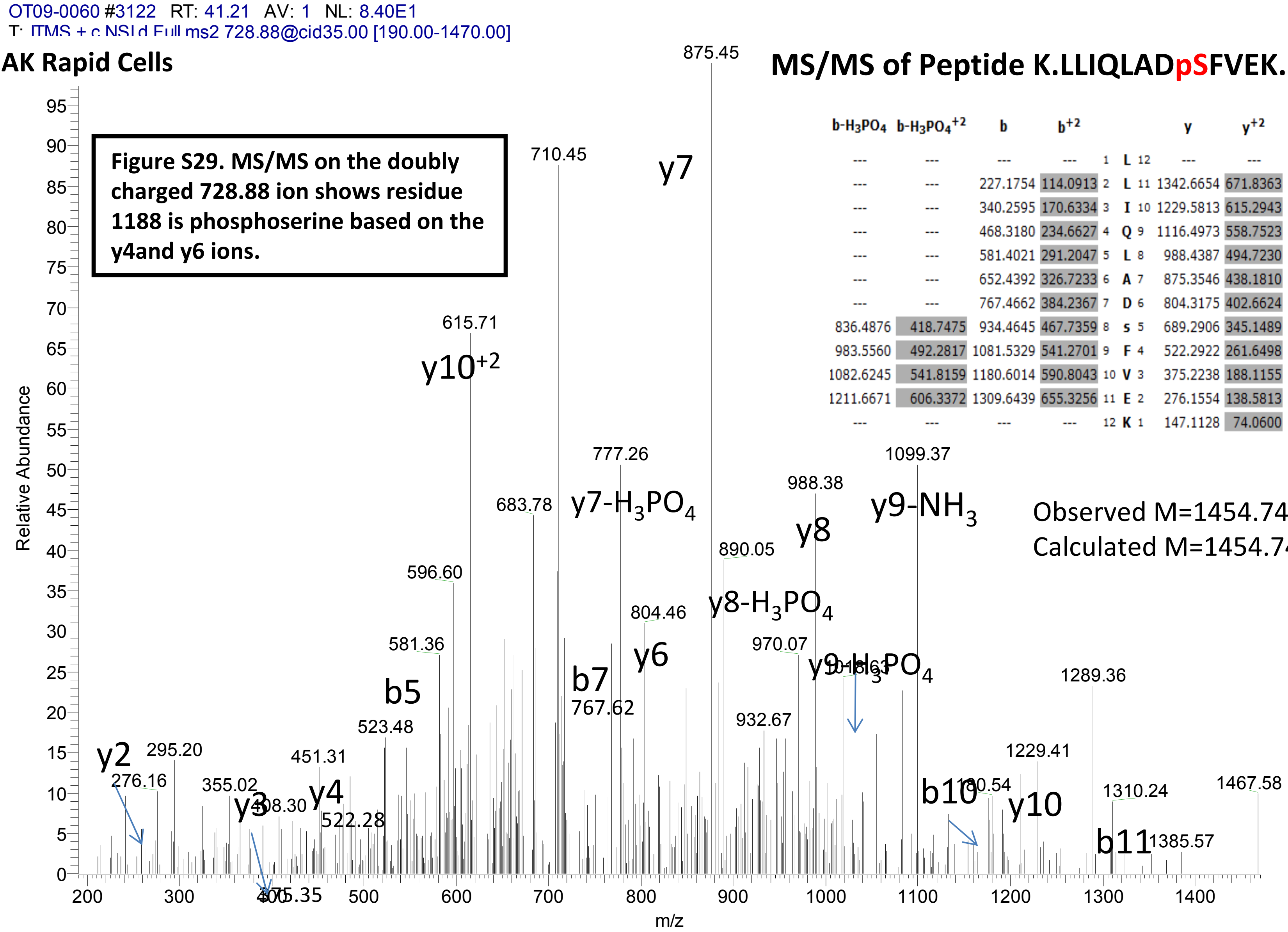
Observed M=2353.0296
Calculated M=2353.0409



pEAK Rapid Cells

MS/MS of Peptide K.LLIQLADpSFVEK.G

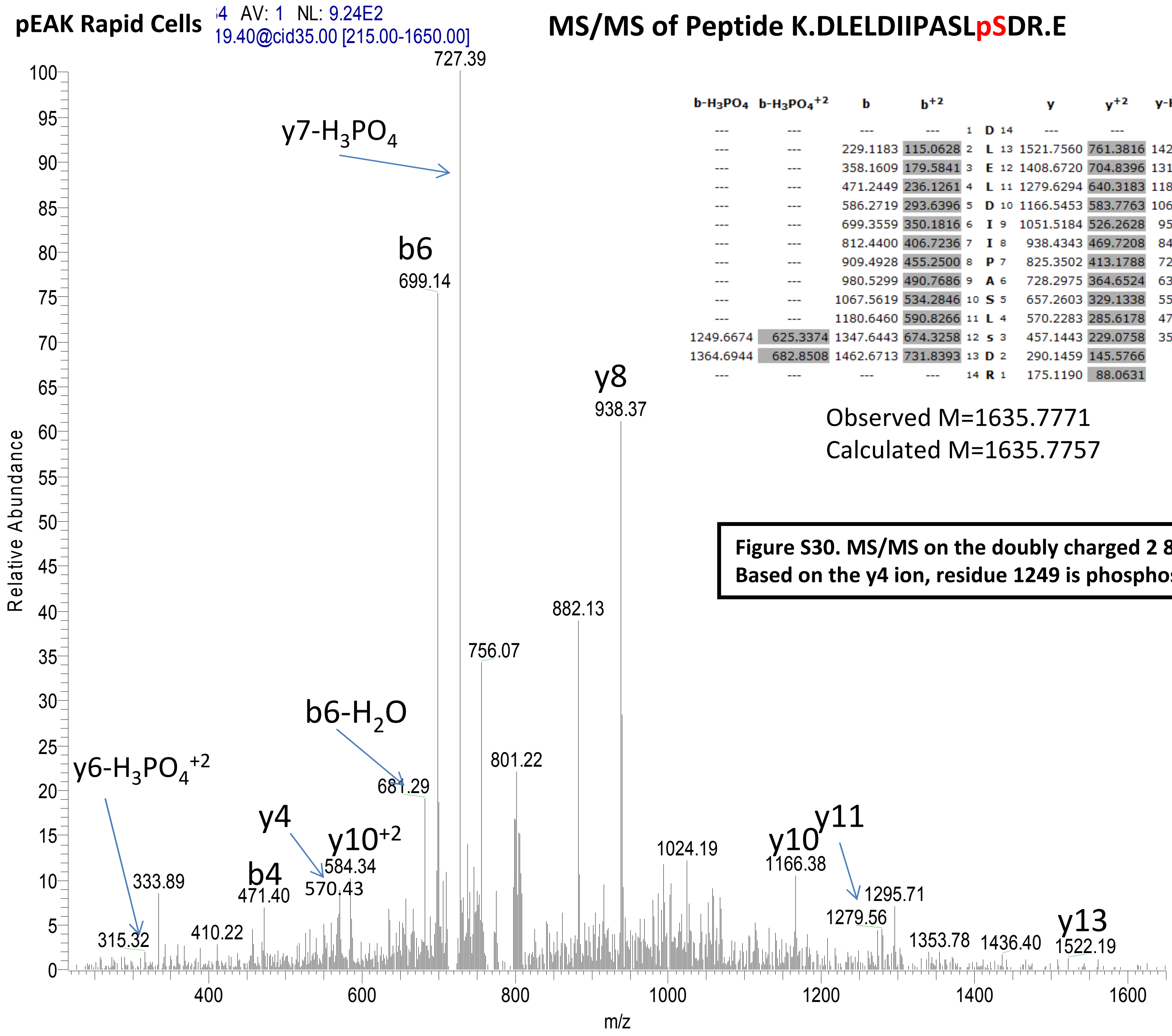
Figure S29. MS/MS on the doubly charged 728.88 ion shows residue 1188 is phosphoserine based on the y4and y6 ions.



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	12	---	---	---	---
---	---	227.1754	114.0913	2	L	11	1342.6654	671.8363	1244.6885	622.8479
---	---	340.2595	170.6334	3	I	10	1229.5813	615.2943	1131.6045	566.3059
---	---	468.3180	234.6627	4	Q	9	1116.4973	558.7523	1018.5204	509.7638
---	---	581.4021	291.2047	5	L	8	988.4387	494.7230	890.4618	445.7345
---	---	652.4392	326.7233	6	A	7	875.3546	438.1810	777.3777	389.1925
---	---	767.4662	384.2367	7	D	6	804.3175	402.6624	706.3406	353.6740
836.4876	418.7475	934.4645	467.7359	8	s	5	689.2906	345.1489	591.3137	296.1605
983.5560	492.2817	1081.5329	541.2701	9	F	4	522.2922	261.6498	---	---
1082.6245	541.8159	1180.6014	590.8043	10	V	3	375.2238	188.1155	---	---
1211.6671	606.3372	1309.6439	655.3256	11	E	2	276.1554	138.5813	---	---
---	---	---	---	12	K	1	147.1128	74.0600	---	---

Observed M=1454.7472
Calculated M=1454.7422

MS/MS of Peptide K.DLELDIIPASLpSDR.E



b-H3PO4	b-H3PO4+2	b	b+2				y	y+2	y-H3PO4	y-H3PO4+2
---	---	---	---	1	**D**	14	---	---	---	---
---	---	229.1183	115.0628	2	**L**	13	1521.7560	761.3816	1423.7791	712.3932
---	---	358.1609	179.5841	3	**E**	12	1408.6720	704.8396	1310.6951	655.8512
---	---	471.2449	236.1261	4	**L**	11	1279.6294	640.3183	1181.6525	591.3299
---	---	586.2719	293.6396	5	**D**	10	1166.5453	583.7763	1068.5684	534.7878
---	---	699.3559	350.1816	6	**I**	9	1051.5184	526.2628	953.5415	477.2744
---	---	812.4400	406.7236	7	**I**	8	938.4343	469.7208	840.4574	420.7323
---	---	909.4928	455.2500	8	**P**	7	825.3502	413.1788	727.3733	364.1903
---	---	980.5299	490.7686	9	**A**	6	728.2975	364.6524	630.3206	315.6639
---	---	1067.5619	534.2846	10	**S**	5	657.2603	329.1338	559.2835	280.1454
---	---	1180.6460	590.8266	11	**L**	4	570.2283	285.6178	472.2514	236.6293
1249.6674	625.3374	1347.6443	674.3258	12	**s**	3	457.1443	229.0758	359.1674	180.0873
1364.6944	682.8508	1462.6713	731.8393	13	**D**	2	290.1459	145.5766	---	---
---	---	---	---	14	**R**	1	175.1190	88.0631	---	---

Observed M=1635.7771

Calculated M=1635.7757

Figure S30. MS/MS on the doubly charged 2 819.4 ion. Based on the y4 ion, residue 1249 is phosphoserine.

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MS/MS of Peptide K.GALKEPIQLPKpTPAK.L

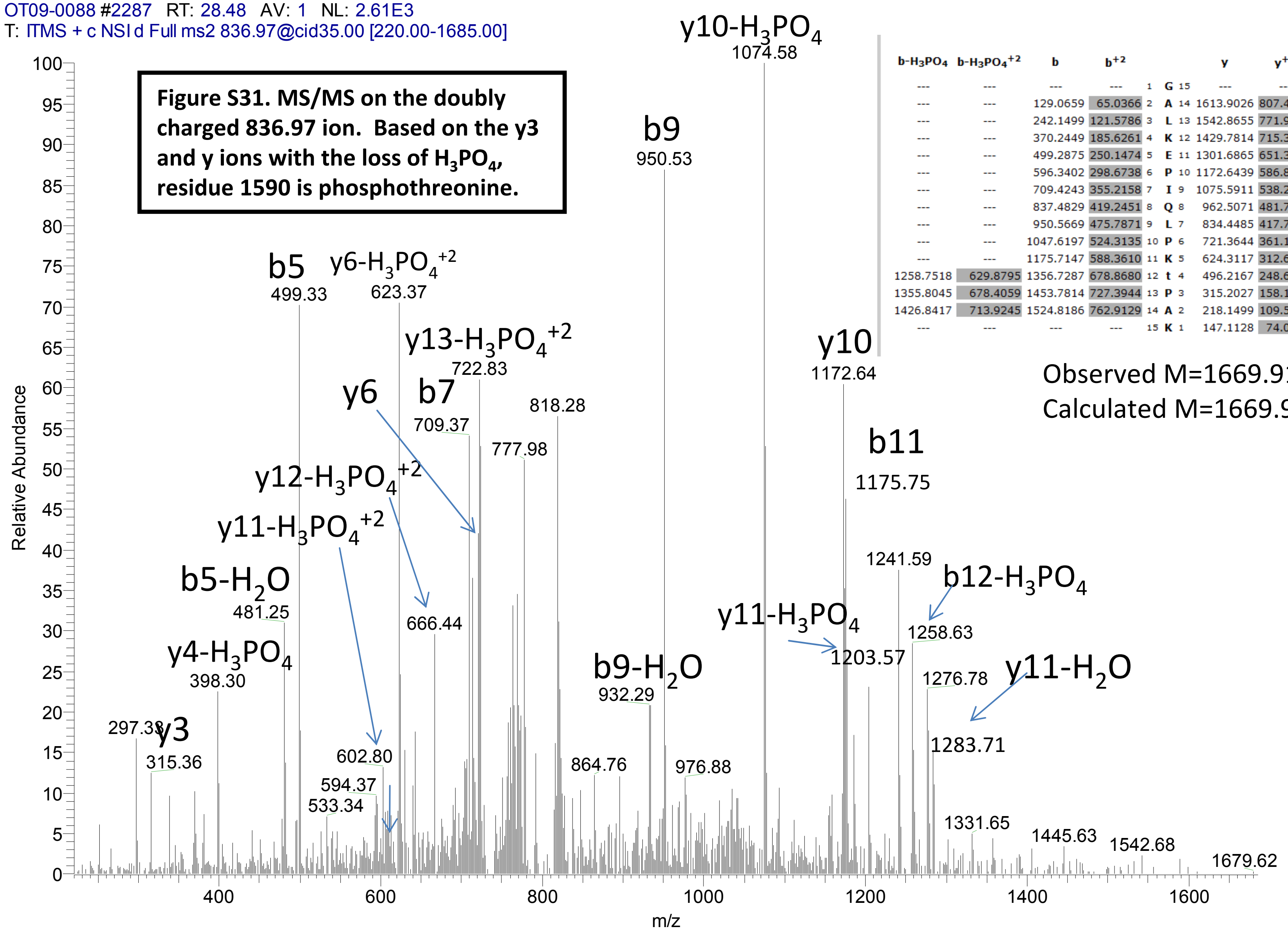

Figure S31. MS/MS on the doubly charged 836.97 ion. Based on the y3 and y ions with the loss of H_3PO_4, residue 1590 is phosphothreonine.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	**G**	15	---	---	---	---
---	---	129.0659	65.0366	2	**A**	14	1613.9026	807.4549	1515.9257	758.4665
---	---	242.1499	121.5786	3	**L**	13	1542.8655	771.9364	1444.8886	722.9479
---	---	370.2449	185.6261	4	**K**	12	1429.7814	715.3944	1331.8045	666.4059
---	---	499.2875	250.1474	5	**E**	11	1301.6865	651.3469	1203.7096	602.3584
---	---	596.3402	298.6738	6	**P**	10	1172.6439	586.8256	1074.6670	537.8371
---	---	709.4243	355.2158	7	**I**	9	1075.5911	538.2992	977.6142	489.3108
---	---	837.4829	419.2451	8	**Q**	8	962.5071	481.7572	864.5302	432.7687
---	---	950.5669	475.7871	9	**L**	7	834.4485	417.7279	736.4716	368.7394
---	---	1047.6197	524.3135	10	**P**	6	721.3644	361.1858	623.3875	312.1974
---	---	1175.7147	588.3610	11	**K**	5	624.3117	312.6595	526.3348	263.6710
1258.7518	629.8795	1356.7287	678.8680	12	**t**	4	496.2167	248.6120	398.2398	199.6235
1355.8045	678.4059	1453.7814	727.3944	13	**P**	3	315.2027	158.1050	---	---
1426.8417	713.9245	1524.8186	762.9129	14	**A**	2	218.1499	109.5786	---	---
---	---	---	---	15	**K**	1	147.1128	74.0600	---	---

Observed M=1669.9193

Calculated M=1669.9168

pEAK Rapid Cells

MS/MS of Peptide R.NNpSKRDGVEDGDSQGDGSSQPDTISIASR.T

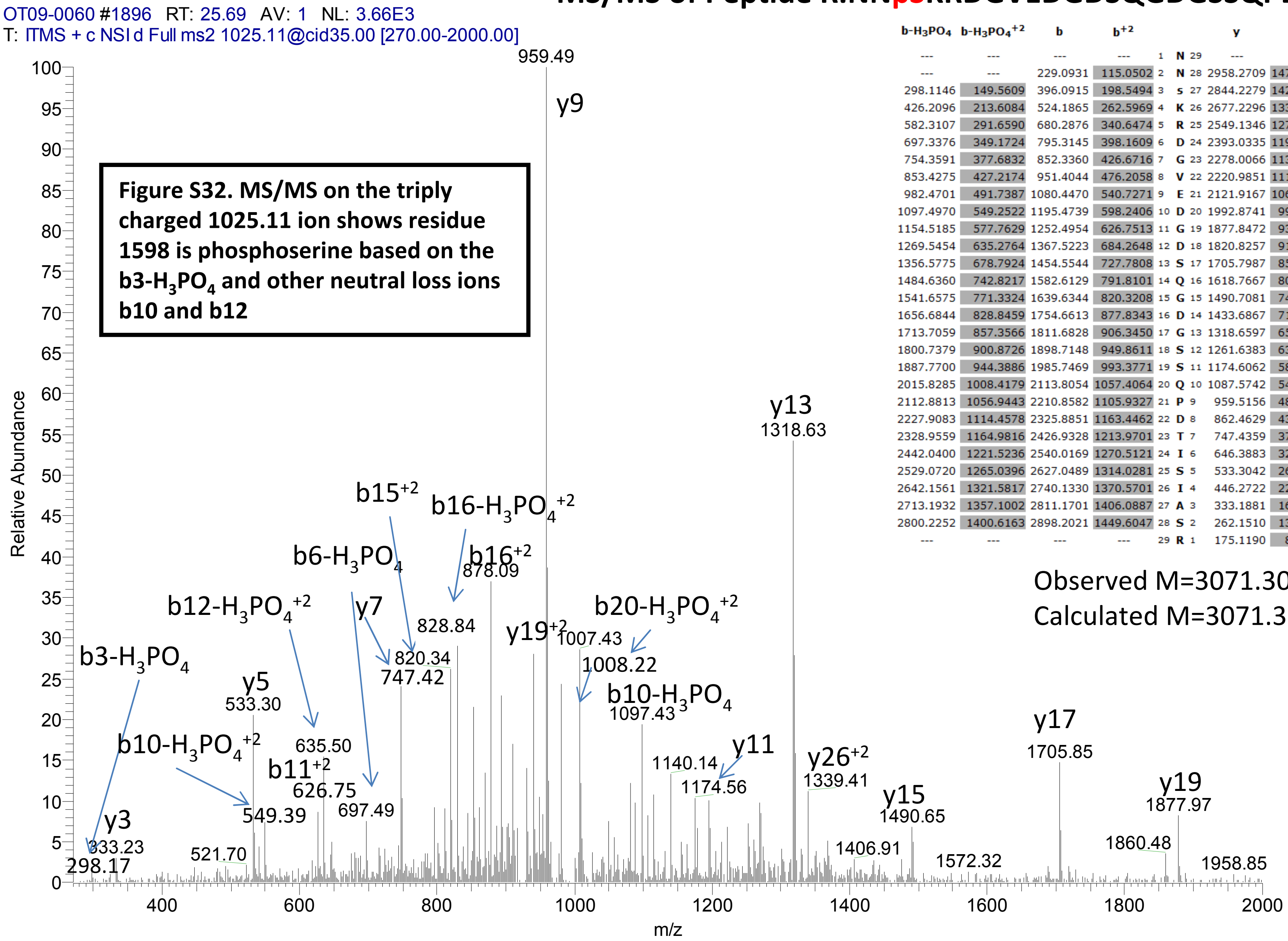

Figure S32. MS/MS on the triply charged 1025.11 ion shows residue 1598 is phosphoserine based on the b3-H_3PO_4 and other neutral loss ions b10 and b12

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	N	29	---	---	---	---
---	---	229.0931	115.0502	2	N	28	2958.2709	1479.6391	2860.2940	1430.6506
298.1146	149.5609	396.0915	198.5494	3	s	27	2844.2279	1422.6176	2746.2510	1373.6292
426.2096	213.6084	524.1865	262.5969	4	K	26	2677.2296	1339.1184	---	---
582.3107	291.6590	680.2876	340.6474	5	R	25	2549.1346	1275.0709	---	---
697.3376	349.1724	795.3145	398.1609	6	D	24	2393.0335	1197.0204	---	---
754.3591	377.6832	852.3360	426.6716	7	G	23	2278.0066	1139.5069	---	---
853.4275	427.2174	951.4044	476.2058	8	V	22	2220.9851	1110.9962	---	---
982.4701	491.7387	1080.4470	540.7271	9	E	21	2121.9167	1061.4620	---	---
1097.4970	549.2522	1195.4739	598.2406	10	D	20	1992.8741	996.9407	---	---
1154.5185	577.7629	1252.4954	626.7513	11	G	19	1877.8472	939.4272	---	---
1269.5454	635.2764	1367.5223	684.2648	12	D	18	1820.8257	910.9165	---	---
1356.5775	678.7924	1454.5544	727.7808	13	S	17	1705.7987	853.4030	---	---
1484.6360	742.8217	1582.6129	791.8101	14	Q	16	1618.7667	809.8870	---	---
1541.6575	771.3324	1639.6344	820.3208	15	G	15	1490.7081	745.8577	---	---
1656.6844	828.8459	1754.6613	877.8343	16	D	14	1433.6867	717.3470	---	---
1713.7059	857.3566	1811.6828	906.3450	17	G	13	1318.6597	659.8335	---	---
1800.7379	900.8726	1898.7148	949.8611	18	S	12	1261.6383	631.3228	---	---
1887.7700	944.3886	1985.7469	993.3771	19	S	11	1174.6062	587.8068	---	---
2015.8285	1008.4179	2113.8054	1057.4064	20	Q	10	1087.5742	544.2907	---	---
2112.8813	1056.9443	2210.8582	1105.9327	21	P	9	959.5156	480.2615	---	---
2227.9083	1114.4578	2325.8851	1163.4462	22	D	8	862.4629	431.7351	---	---
2328.9559	1164.9816	2426.9328	1213.9701	23	T	7	747.4359	374.2216	---	---
2442.0400	1221.5236	2540.0169	1270.5121	24	I	6	646.3883	323.6978	---	---
2529.0720	1265.0396	2627.0489	1314.0281	25	S	5	533.3042	267.1557	---	---
2642.1561	1321.5817	2740.1330	1370.5701	26	I	4	446.2722	223.6397	---	---
2713.1932	1357.1002	2811.1701	1406.0887	27	A	3	333.1881	167.0977	---	---
2800.2252	1400.6163	2898.2021	1449.6047	28	S	2	262.1510	131.5791	---	---
---	---	---	---	29	R	1	175.1190	88.0631	---	---

Observed M=3071.3071
Calculated M=3071.3065

pEAK Rapid Cells

MS/MS of Peptide K.RDGVEDGDpSQGDGSSQPDTISIASR.T

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	**R**	25	---	---	---	---
---	---	272.1353	136.5713	2	**D**	24	2472.9998	1237.0036	2375.0229	1188.0151
---	---	329.1568	165.0820	3	**G**	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	428.2252	214.6162	4	**V**	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	557.2678	279.1375	5	**E**	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	672.2947	336.6510	6	**D**	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	729.3162	365.1617	7	**G**	19	1957.8135	979.4104	1859.8366	930.4219
---	---	844.3432	422.6752	8	**D**	18	1900.7920	950.8996	1802.8151	901.9112
913.3646	457.1859	1011.3415	506.1744	9	**s**	17	1785.7651	893.3862	1687.7882	844.3977
1041.4232	521.2152	1139.4001	570.2037	10	**Q**	16	1618.7667	809.8870	---	---
1098.4447	549.7260	1196.4216	598.7144	11	**G**	15	1490.7081	745.8577	---	---
1213.4716	607.2394	1311.4485	656.2279	12	**D**	14	1433.6867	717.3470	---	---
1270.4931	635.7502	1368.4700	684.7386	13	**G**	13	1318.6597	659.8335	---	---
1357.5251	679.2662	1455.5020	728.2546	14	**S**	12	1261.6383	631.3228	---	---
1444.5571	722.7822	1542.5340	771.7706	15	**S**	11	1174.6062	587.8068	---	---
1572.6157	786.8115	1670.5926	835.7999	16	**Q**	10	1087.5742	544.2907	---	---
1669.6685	835.3379	1767.6454	884.3263	17	**P**	9	959.5156	480.2615	---	---
1784.6954	892.8513	1882.6723	941.8398	18	**D**	8	862.4629	431.7351	---	---
1885.7431	943.3752	1983.7200	992.3636	19	**T**	7	747.4359	374.2216	---	---
1998.8271	999.9172	2096.8040	1048.9057	20	**I**	6	646.3883	323.6978	---	---
2085.8592	1043.4332	2183.8361	1092.4217	21	**S**	5	533.3042	267.1557	---	---
2198.9432	1099.9753	2296.9201	1148.9637	22	**I**	4	446.2722	223.6397	---	---
2269.9804	1135.4938	2367.9572	1184.4823	23	**A**	3	333.1881	167.0977	---	---
2357.0124	1179.0098	2454.9893	1227.9983	24	**S**	2	262.1510	131.5791	---	---
---	---	---	---	25	**R**	1	175.1190	88.0631	---	---

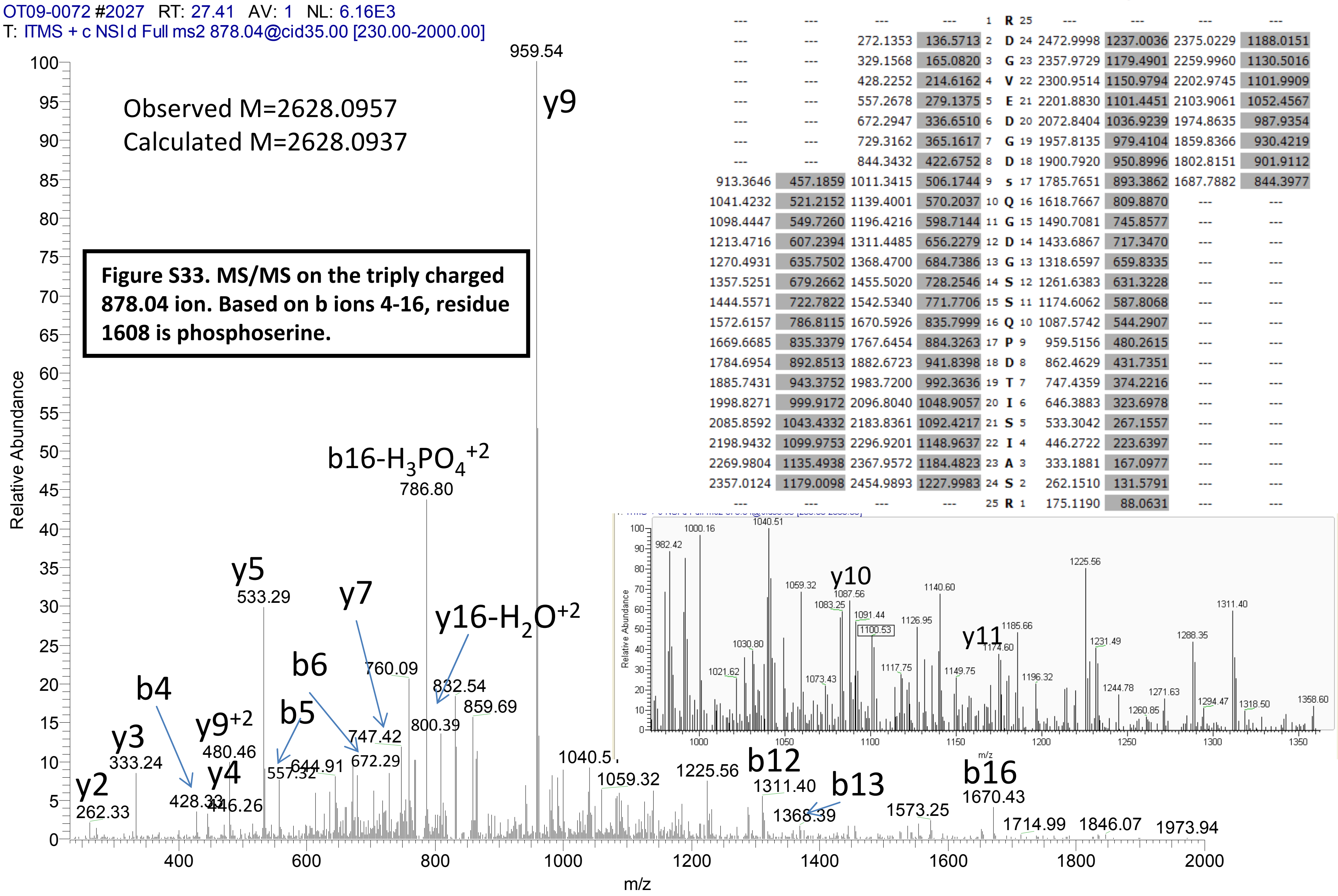

Figure S33. MS/MS on the triply charged 878.04 ion. Based on b ions 4-16, residue 1608 is phosphoserine.

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MS/MS of Peptide K.RDGVEDGDSQGDGpSSQPDTISIASR.T

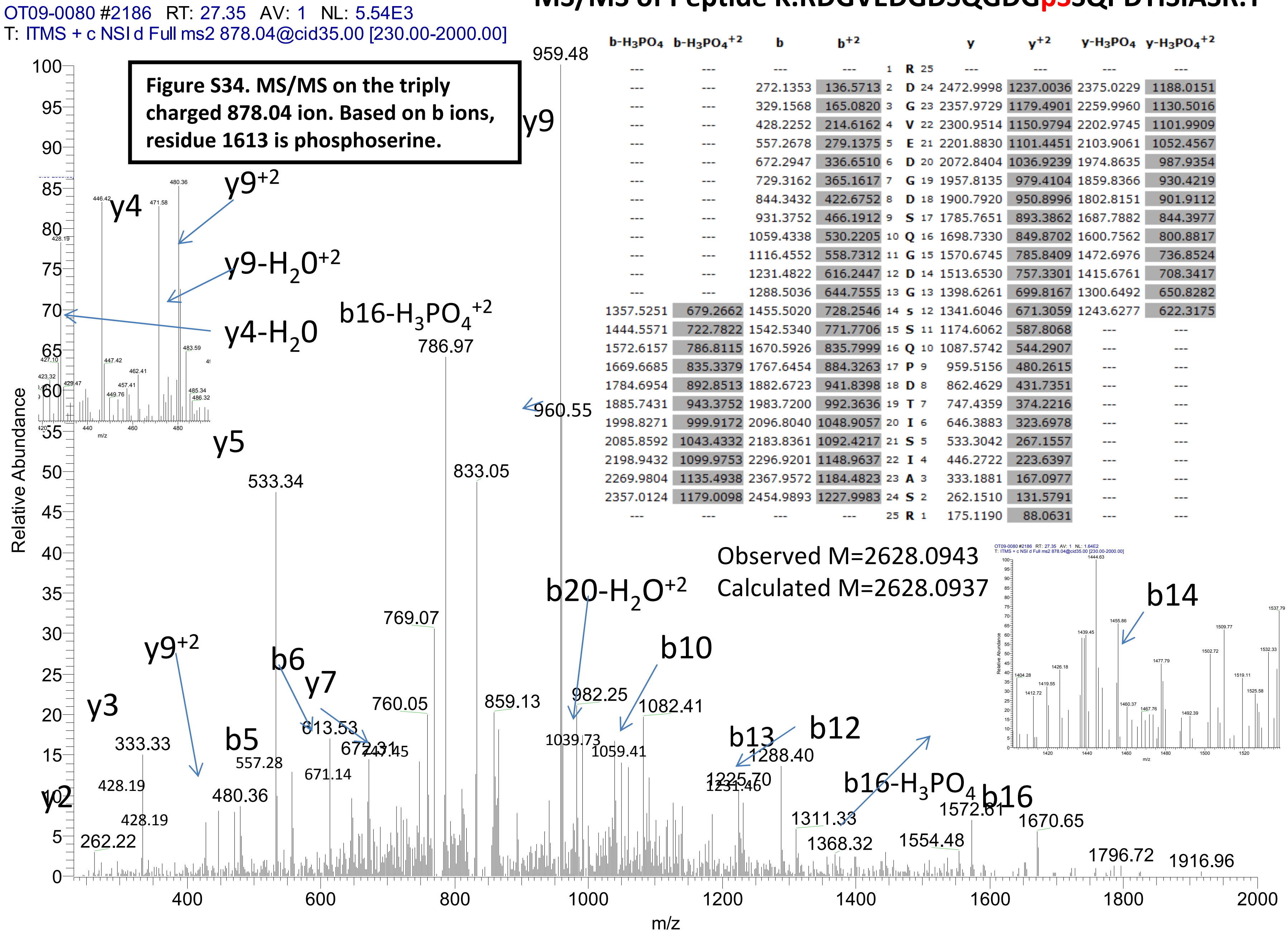
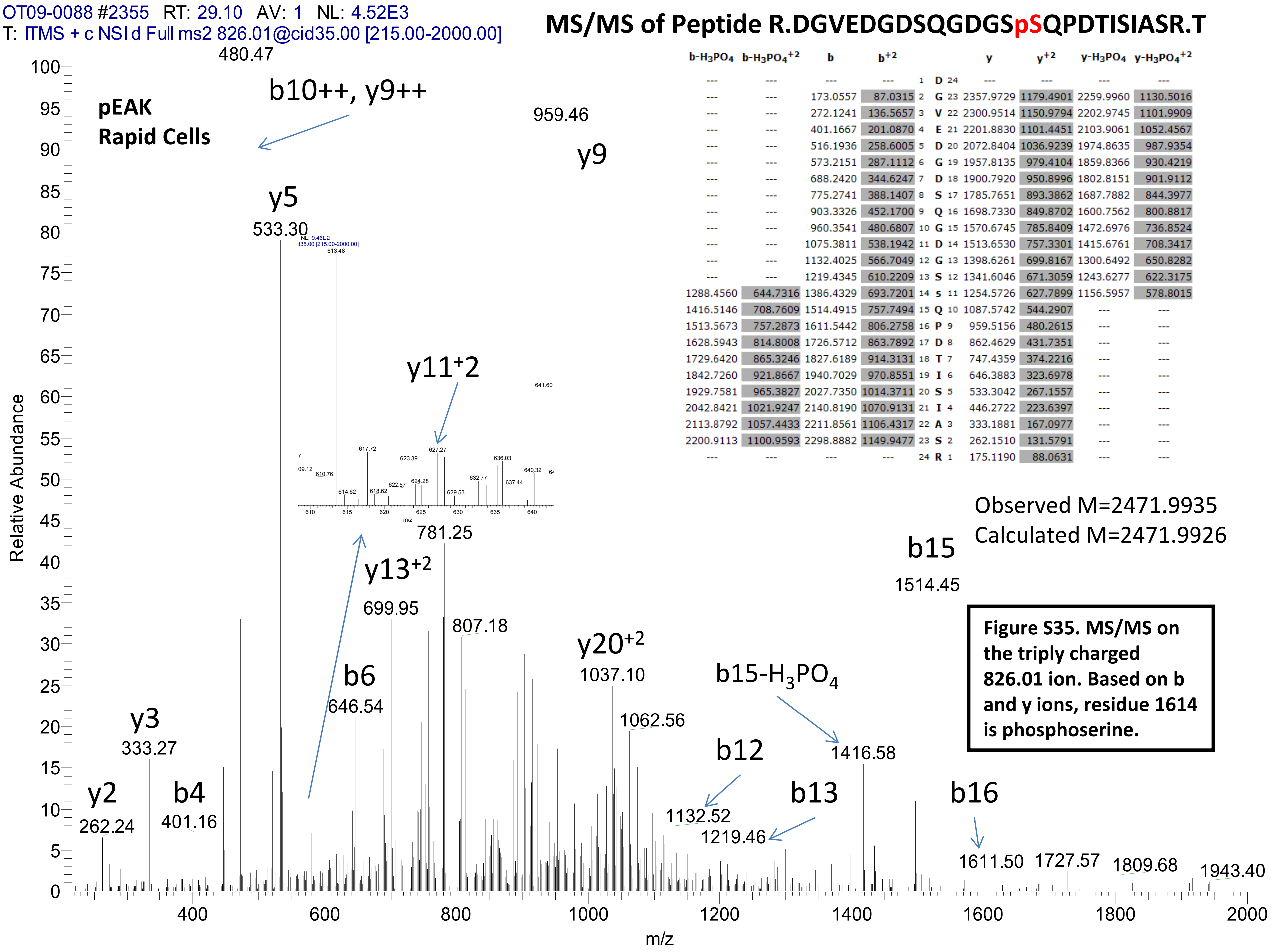


Figure S34. MS/MS on the triply charged 878.04 ion. Based on b ions, residue 1613 is phosphoserine.

$b\text{-}H_3PO_4$	$b\text{-}H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y\text{-}H_3PO_4$	$y\text{-}H_3PO_4^{+2}$
---	---	---	---	1	R	25	---	---	---	---
---	---	272.1353	136.5713	2	D	24	2472.9998	1237.0036	2375.0229	1188.0151
---	---	329.1568	165.0820	3	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	428.2252	214.6162	4	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	557.2678	279.1375	5	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	672.2947	336.6510	6	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	729.3162	365.1617	7	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	844.3432	422.6752	8	D	18	1900.7920	950.8996	1802.8151	901.9112
---	---	931.3752	466.1912	9	S	17	1785.7651	893.3862	1687.7882	844.3977
---	---	1059.4338	530.2205	10	Q	16	1698.7330	849.8702	1600.7562	800.8817
---	---	1116.4552	558.7312	11	G	15	1570.6745	785.8409	1472.6976	736.8524
---	---	1231.4822	616.2447	12	D	14	1513.6530	757.3301	1415.6761	708.3417
---	---	1288.5036	644.7555	13	G	13	1398.6261	699.8167	1300.6492	650.8282
1357.5251	679.2662	1455.5020	728.2546	14	s	12	1341.6046	671.3059	1243.6277	622.3175
1444.5571	722.7822	1542.5340	771.7706	15	S	11	1174.6062	587.8068	---	---
1572.6157	786.8115	1670.5926	835.7999	16	Q	10	1087.5742	544.2907	---	---
1669.6685	835.3379	1767.6454	884.3263	17	P	9	959.5156	480.2615	---	---
1784.6954	892.8513	1882.6723	941.8398	18	D	8	862.4629	431.7351	---	---
1885.7431	943.3752	1983.7200	992.3636	19	T	7	747.4359	374.2216	---	---
1998.8271	999.9172	2096.8040	1048.9057	20	I	6	646.3883	323.6978	---	---
2085.8592	1043.4332	2183.8361	1092.4217	21	S	5	533.3042	267.1557	---	---
2198.9432	1099.9753	2296.9201	1148.9637	22	I	4	446.2722	223.6397	---	---
2269.9804	1135.4938	2367.9572	1184.4823	23	A	3	333.1881	167.0977	---	---
2357.0124	1179.0098	2454.9893	1227.9983	24	S	2	262.1510	131.5791	---	---
---	---	---	---	25	R	1	175.1190	88.0631	---	---

Observed M=2628.0943
Calculated M=2628.0937

MS/MS of Peptide R.DGVEDGDSQGDGSpSQPDTISIASR.T



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	D	24	---	---	---	---
---	---	173.0557	87.0315	2	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	272.1241	136.5657	3	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	401.1667	201.0870	4	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	516.1936	258.6005	5	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	573.2151	287.1112	6	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	688.2420	344.6247	7	D	18	1900.7920	950.8996	1802.8151	901.9112
---	---	775.2741	388.1407	8	S	17	1785.7651	893.3862	1687.7882	844.3977
---	---	903.3326	452.1700	9	Q	16	1698.7330	849.8702	1600.7562	800.8817
---	---	960.3541	480.6807	10	G	15	1570.6745	785.8409	1472.6976	736.8524
---	---	1075.3811	538.1942	11	D	14	1513.6530	757.3301	1415.6761	708.3417
---	---	1132.4025	566.7049	12	G	13	1398.6261	699.8167	1300.6492	650.8282
---	---	1219.4345	610.2209	13	S	12	1341.6046	671.3059	1243.6277	622.3175
1288.4560	644.7316	1386.4329	693.7201	14	s	11	1254.5726	627.7899	1156.5957	578.8015
1416.5146	708.7609	1514.4915	757.7494	15	Q	10	1087.5742	544.2907	---	---
1513.5673	757.2873	1611.5442	806.2758	16	P	9	959.5156	480.2615	---	---
1628.5943	814.8008	1726.5712	863.7892	17	D	8	862.4629	431.7351	---	---
1729.6420	865.3246	1827.6189	914.3131	18	T	7	747.4359	374.2216	---	---
1842.7260	921.8667	1940.7029	970.8551	19	I	6	646.3883	323.6978	---	---
1929.7581	965.3827	2027.7350	1014.3711	20	S	5	533.3042	267.1557	---	---
2042.8421	1021.9247	2140.8190	1070.9131	21	I	4	446.2722	223.6397	---	---
2113.8792	1057.4433	2211.8561	1106.4317	22	A	3	333.1881	167.0977	---	---
2200.9113	1100.9593	2298.8882	1149.9477	23	S	2	262.1510	131.5791	---	---
---	---	---	---	24	R	1	175.1190	88.0631	---	---

Observed M=2471.9935
Calculated M=2471.9926

Figure S35. MS/MS on the triply charged 826.01 ion. Based on b and y ions, residue 1614 is phosphoserine.

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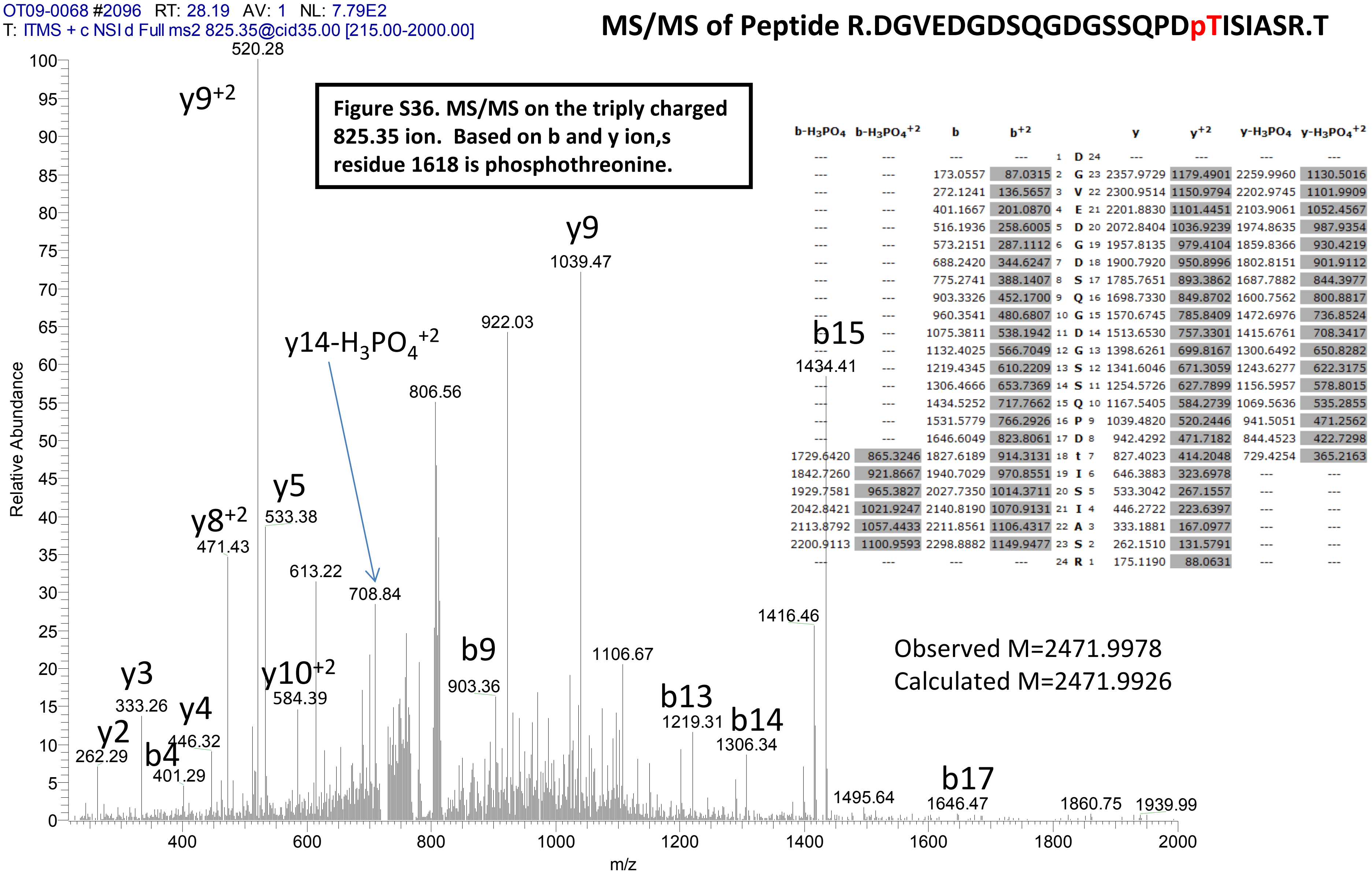
MS/MS of Peptide R.DGVEDGDSQGDGSSQPDpTISIASR.T

Figure S36. MS/MS on the triply charged 825.35 ion. Based on b and y ion,s residue 1618 is phosphothreonine.



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	**D**	24	---	---	---	---
---	---	173.0557	87.0315	2	**G**	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	272.1241	136.5657	3	**V**	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	401.1667	201.0870	4	**E**	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	516.1936	258.6005	5	**D**	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	573.2151	287.1112	6	**G**	19	1957.8135	979.4104	1859.8366	930.4219
---	---	688.2420	344.6247	7	**D**	18	1900.7920	950.8996	1802.8151	901.9112
---	---	775.2741	388.1407	8	**S**	17	1785.7651	893.3862	1687.7882	844.3977
---	---	903.3326	452.1700	9	**Q**	16	1698.7330	849.8702	1600.7562	800.8817
---	---	960.3541	480.6807	10	**G**	15	1570.6745	785.8409	1472.6976	736.8524
---	---	1075.3811	538.1942	11	**D**	14	1513.6530	757.3301	1415.6761	708.3417
---	---	1132.4025	566.7049	12	**G**	13	1398.6261	699.8167	1300.6492	650.8282
---	---	1219.4345	610.2209	13	**S**	12	1341.6046	671.3059	1243.6277	622.3175
---	---	1306.4666	653.7369	14	**S**	11	1254.5726	627.7899	1156.5957	578.8015
---	---	1434.5252	717.7662	15	**Q**	10	1167.5405	584.2739	1069.5636	535.2855
---	---	1531.5779	766.2926	16	**P**	9	1039.4820	520.2446	941.5051	471.2562
---	---	1646.6049	823.8061	17	**D**	8	942.4292	471.7182	844.4523	422.7298
1729.6420	865.3246	1827.6189	914.3131	18	**t**	7	827.4023	414.2048	729.4254	365.2163
1842.7260	921.8667	1940.7029	970.8551	19	**I**	6	646.3883	323.6978	---	---
1929.7581	965.3827	2027.7350	1014.3711	20	**S**	5	533.3042	267.1557	---	---
2042.8421	1021.9247	2140.8190	1070.9131	21	**I**	4	446.2722	223.6397	---	---
2113.8792	1057.4433	2211.8561	1106.4317	22	**A**	3	333.1881	167.0977	---	---
2200.9113	1100.9593	2298.8882	1149.9477	23	**S**	2	262.1510	131.5791	---	---
---	---	---	---	24	**R**	1	175.1190	88.0631	---	---

Observed M=2471.9978
Calculated M=2471.9926

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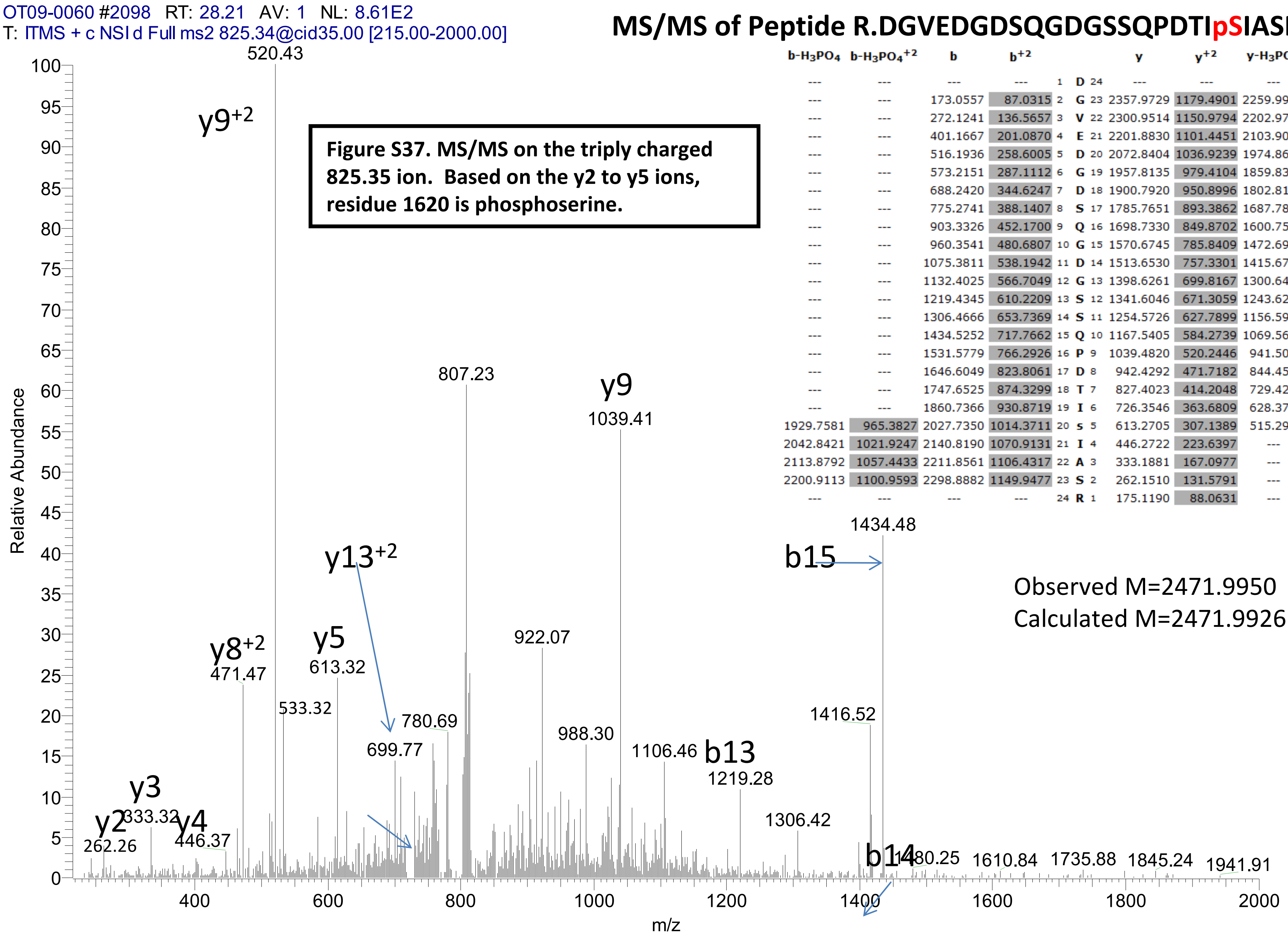

MS/MS of Peptide R.DGVEDGDSQGDGSSQPDTIpSIASR.T

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	D	24	---	---	---	---
---	---	173.0557	87.0315	2	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	272.1241	136.5657	3	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	401.1667	201.0870	4	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	516.1936	258.6005	5	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	573.2151	287.1112	6	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	688.2420	344.6247	7	D	18	1900.7920	950.8996	1802.8151	901.9112
---	---	775.2741	388.1407	8	S	17	1785.7651	893.3862	1687.7882	844.3977
---	---	903.3326	452.1700	9	Q	16	1698.7330	849.8702	1600.7562	800.8817
---	---	960.3541	480.6807	10	G	15	1570.6745	785.8409	1472.6976	736.8524
---	---	1075.3811	538.1942	11	D	14	1513.6530	757.3301	1415.6761	708.3417
---	---	1132.4025	566.7049	12	G	13	1398.6261	699.8167	1300.6492	650.8282
---	---	1219.4345	610.2209	13	S	12	1341.6046	671.3059	1243.6277	622.3175
---	---	1306.4666	653.7369	14	S	11	1254.5726	627.7899	1156.5957	578.8015
---	---	1434.5252	717.7662	15	Q	10	1167.5405	584.2739	1069.5636	535.2855
---	---	1531.5779	766.2926	16	P	9	1039.4820	520.2446	941.5051	471.2562
---	---	1646.6049	823.8061	17	D	8	942.4292	471.7182	844.4523	422.7298
---	---	1747.6525	874.3299	18	T	7	827.4023	414.2048	729.4254	365.2163
---	---	1860.7366	930.8719	19	I	6	726.3546	363.6809	628.3777	314.6925
1929.7581	965.3827	2027.7350	1014.3711	20	s	5	613.2705	307.1389	515.2936	258.1504
2042.8421	1021.9247	2140.8190	1070.9131	21	I	4	446.2722	223.6397	---	---
2113.8792	1057.4433	2211.8561	1106.4317	22	A	3	333.1881	167.0977	---	---
2200.9113	1100.9593	2298.8882	1149.9477	23	S	2	262.1510	131.5791	---	---
---	---	---	---	24	R	1	175.1190	88.0631	---	---

Figure S37. MS/MS on the triply charged 825.35 ion. Based on the y2 to y5 ions, residue 1620 is phosphoserine.

Observed M=2471.9950
Calculated M=2471.9926

MS/MS of Peptide R.pTpSQNTVESDKDGNLVPR.W

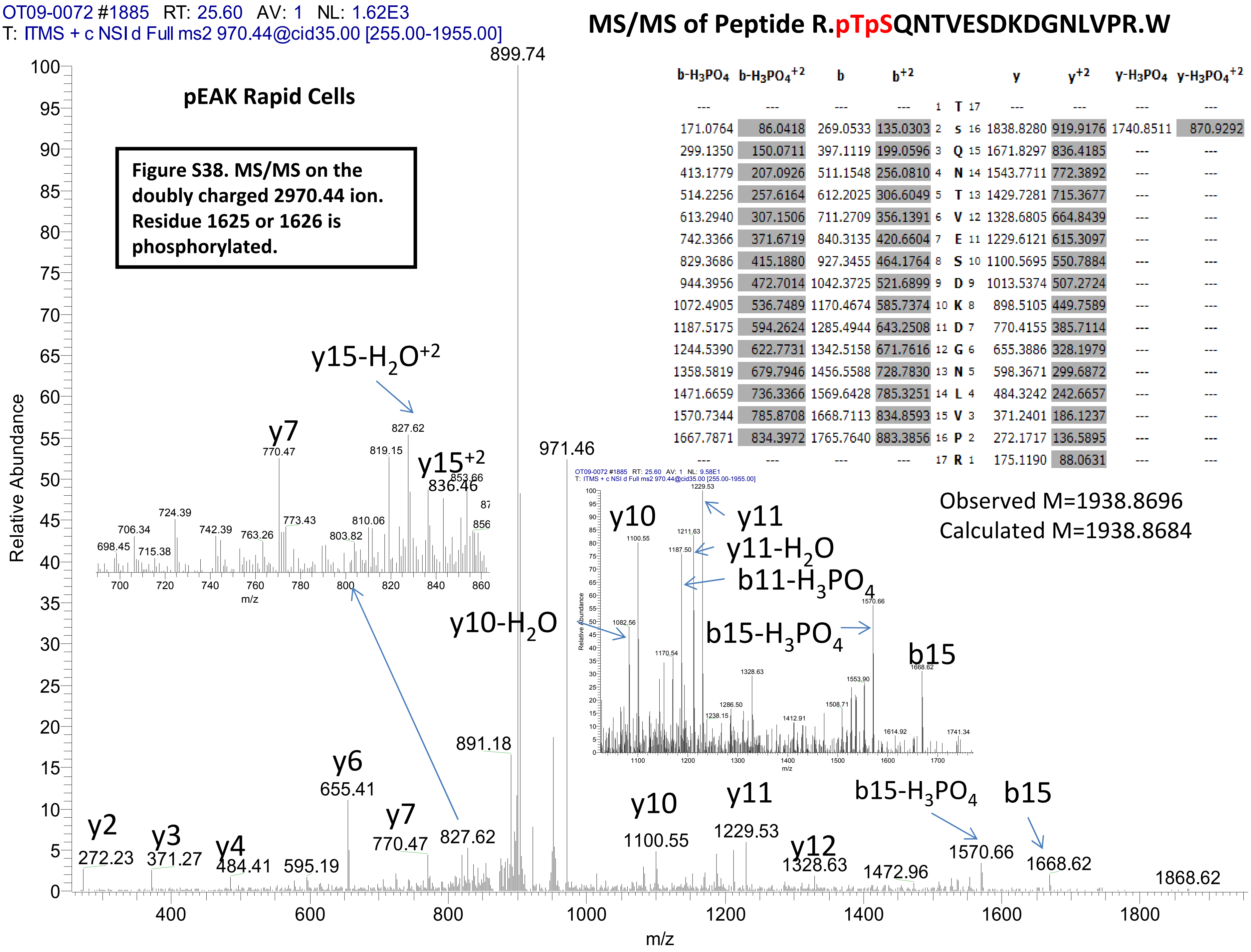

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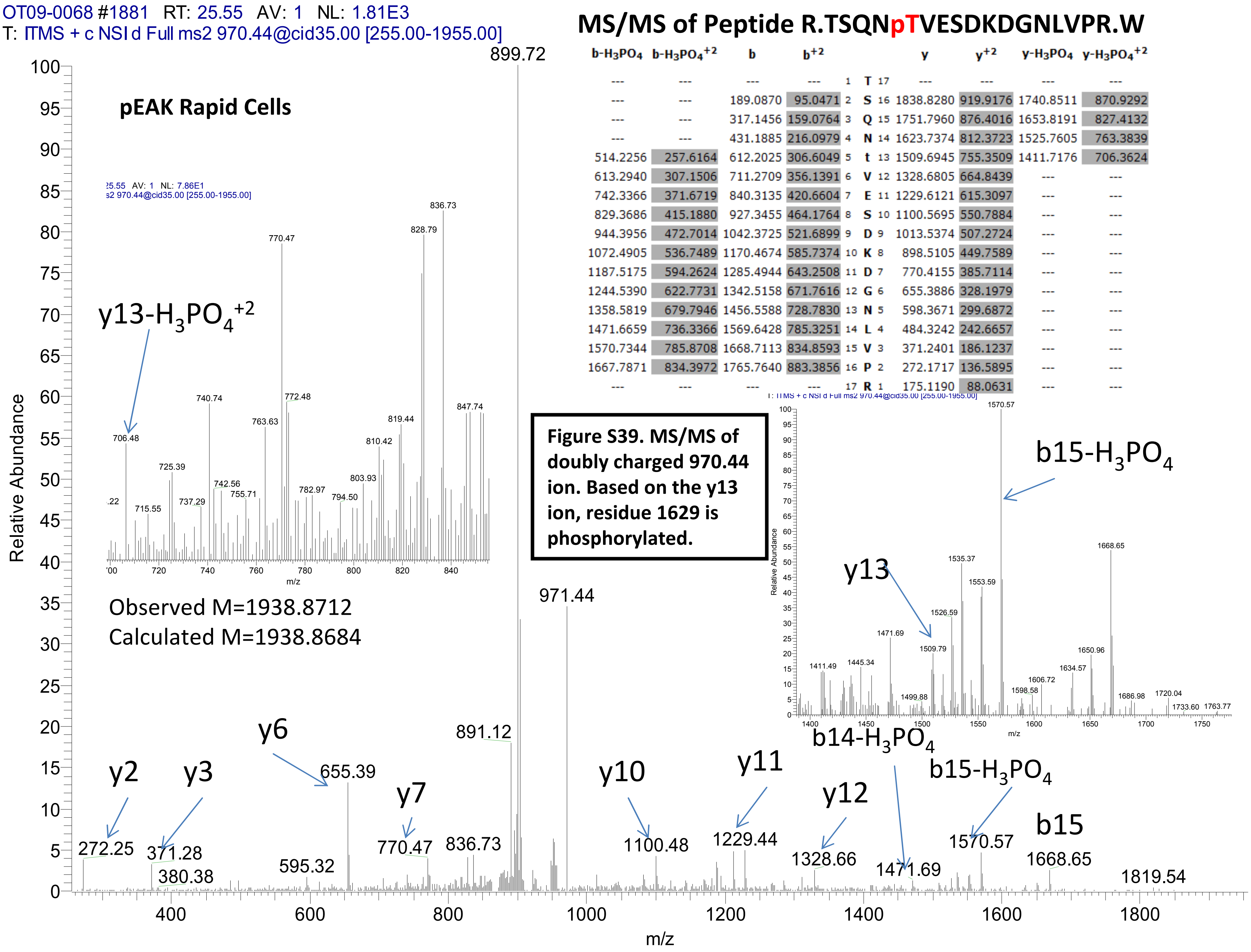
Figure S38. MS/MS on the doubly charged 2970.44 ion. Residue 1625 or 1626 is phosphorylated.

b-H$_3$PO$_4$	b-H$_3$PO$_4$$^{+2}$	b	b^{+2}				y	y^{+2}	y-H$_3$PO$_4$	y-H$_3$PO$_4$$^{+2}$
---	---	---	---	1	**T**	17	---	---	---	---
171.0764	86.0418	269.0533	135.0303	2	**s**	16	1838.8280	919.9176	1740.8511	870.9292
299.1350	150.0711	397.1119	199.0596	3	**Q**	15	1671.8297	836.4185	---	---
413.1779	207.0926	511.1548	256.0810	4	**N**	14	1543.7711	772.3892	---	---
514.2256	257.6164	612.2025	306.6049	5	**T**	13	1429.7281	715.3677	---	---
613.2940	307.1506	711.2709	356.1391	6	**V**	12	1328.6805	664.8439	---	---
742.3366	371.6719	840.3135	420.6604	7	**E**	11	1229.6121	615.3097	---	---
829.3686	415.1880	927.3455	464.1764	8	**S**	10	1100.5695	550.7884	---	---
944.3956	472.7014	1042.3725	521.6899	9	**D**	9	1013.5374	507.2724	---	---
1072.4905	536.7489	1170.4674	585.7374	10	**K**	8	898.5105	449.7589	---	---
1187.5175	594.2624	1285.4944	643.2508	11	**D**	7	770.4155	385.7114	---	---
1244.5390	622.7731	1342.5158	671.7616	12	**G**	6	655.3886	328.1979	---	---
1358.5819	679.7946	1456.5588	728.7830	13	**N**	5	598.3671	299.6872	---	---
1471.6659	736.3366	1569.6428	785.3251	14	**L**	4	484.3242	242.6657	---	---
1570.7344	785.8708	1668.7113	834.8593	15	**V**	3	371.2401	186.1237	---	---
1667.7871	834.3972	1765.7640	883.3856	16	**P**	2	272.1717	136.5895	---	---
---	---	---	---	17	**R**	1	175.1190	88.0631	---	---

Observed M=1938.8696
Calculated M=1938.8684

MS/MS of Peptide R.TSQNpTVESDKDGNLVPR.W

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	**T**	17	---	---	---	---
---	---	189.0870	95.0471	2	**S**	16	1838.8280	919.9176	1740.8511	870.9292
---	---	317.1456	159.0764	3	**Q**	15	1751.7960	876.4016	1653.8191	827.4132
---	---	431.1885	216.0979	4	**N**	14	1623.7374	812.3723	1525.7605	763.3839
514.2256	257.6164	612.2025	306.6049	5	**t**	13	1509.6945	755.3509	1411.7176	706.3624
613.2940	307.1506	711.2709	356.1391	6	**V**	12	1328.6805	664.8439	---	---
742.3366	371.6719	840.3135	420.6604	7	**E**	11	1229.6121	615.3097	---	---
829.3686	415.1880	927.3455	464.1764	8	**S**	10	1100.5695	550.7884	---	---
944.3956	472.7014	1042.3725	521.6899	9	**D**	9	1013.5374	507.2724	---	---
1072.4905	536.7489	1170.4674	585.7374	10	**K**	8	898.5105	449.7589	---	---
1187.5175	594.2624	1285.4944	643.2508	11	**D**	7	770.4155	385.7114	---	---
1244.5390	622.7731	1342.5158	671.7616	12	**G**	6	655.3886	328.1979	---	---
1358.5819	679.7946	1456.5588	728.7830	13	**N**	5	598.3671	299.6872	---	---
1471.6659	736.3366	1569.6428	785.3251	14	**L**	4	484.3242	242.6657	---	---
1570.7344	785.8708	1668.7113	834.8593	15	**V**	3	371.2401	186.1237	---	---
1667.7871	834.3972	1765.7640	883.3856	16	**P**	2	272.1717	136.5895	---	---
---	---	---	---	17	**R**	1	175.1190	88.0631	---	---



pEAK Rapid Cells

Observed M=1938.8712
Calculated M=1938.8684

Figure S39. MS/MS of doubly charged 970.44 ion. Based on the y13 ion, residue 1629 is phosphorylated.

pEAK Rapid Cells

MS/MS of Peptide R.TSQNTVEpSDKDGNLVPR.W

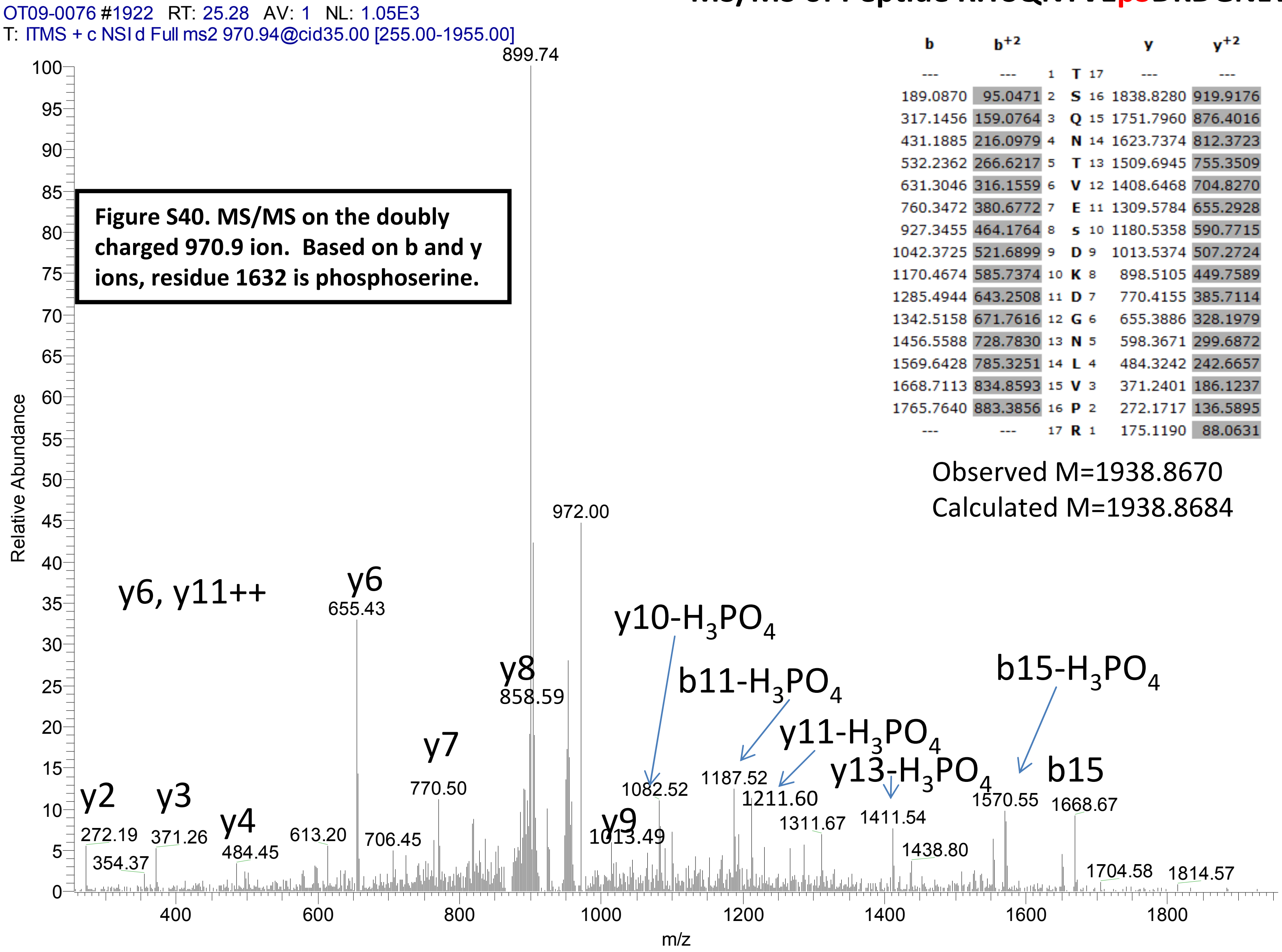


Figure S40. MS/MS on the doubly charged 970.9 ion. Based on b and y ions, residue 1632 is phosphoserine.

b	b^{+2}				y	y^{+2}
---	---	1	T	17	---	---
189.0870	95.0471	2	S	16	1838.8280	919.9176
317.1456	159.0764	3	Q	15	1751.7960	876.4016
431.1885	216.0979	4	N	14	1623.7374	812.3723
532.2362	266.6217	5	T	13	1509.6945	755.3509
631.3046	316.1559	6	V	12	1408.6468	704.8270
760.3472	380.6772	7	E	11	1309.5784	655.2928
927.3455	464.1764	8	s	10	1180.5358	590.7715
1042.3725	521.6899	9	D	9	1013.5374	507.2724
1170.4674	585.7374	10	K	8	898.5105	449.7589
1285.4944	643.2508	11	D	7	770.4155	385.7114
1342.5158	671.7616	12	G	6	655.3886	328.1979
1456.5588	728.7830	13	N	5	598.3671	299.6872
1569.6428	785.3251	14	L	4	484.3242	242.6657
1668.7113	834.8593	15	V	3	371.2401	186.1237
1765.7640	883.3856	16	P	2	272.1717	136.5895
---	---	17	R	1	175.1190	88.0631

Observed M=1938.8670
Calculated M=1938.8684

pEAK Rapid Cells

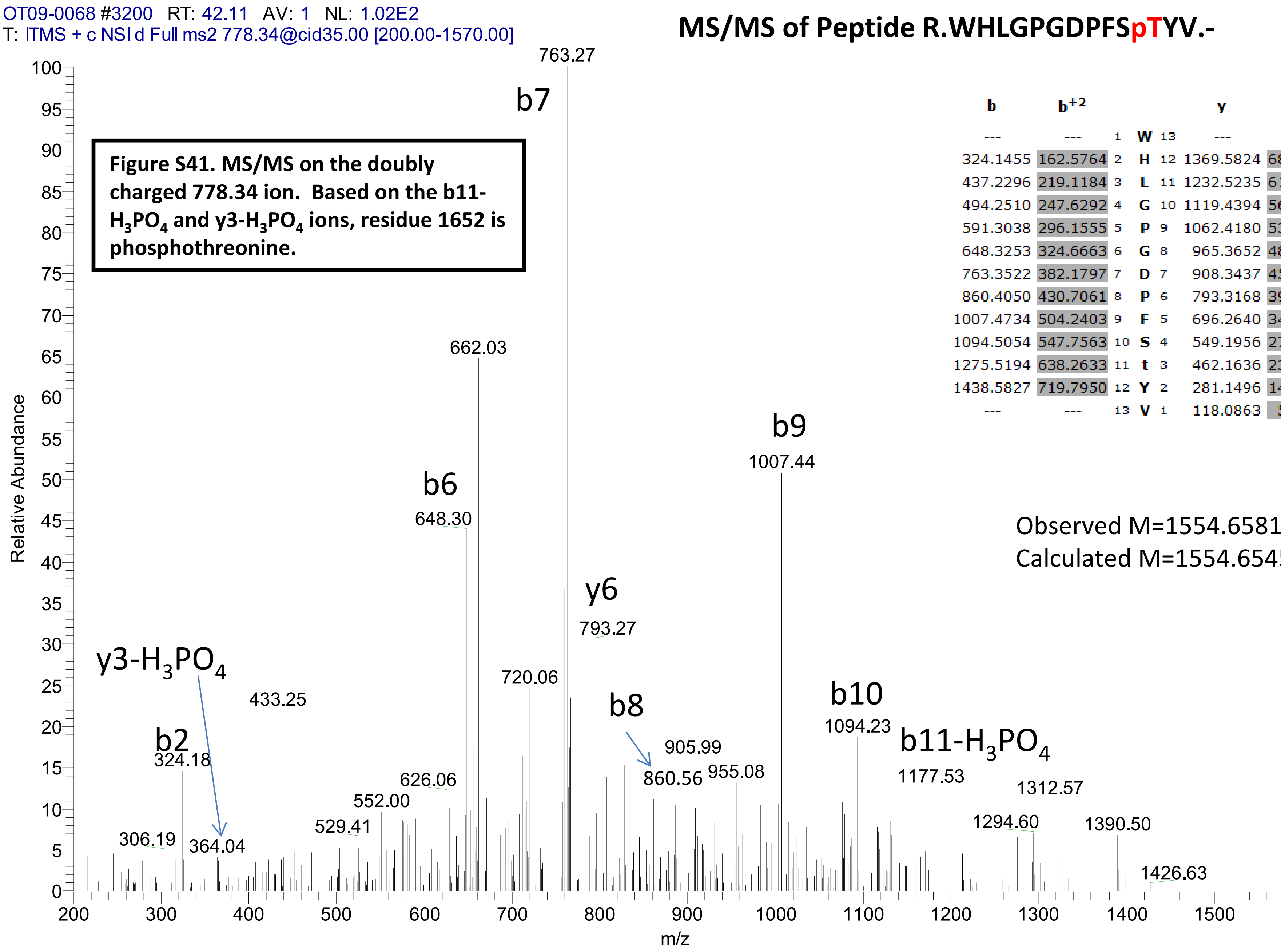
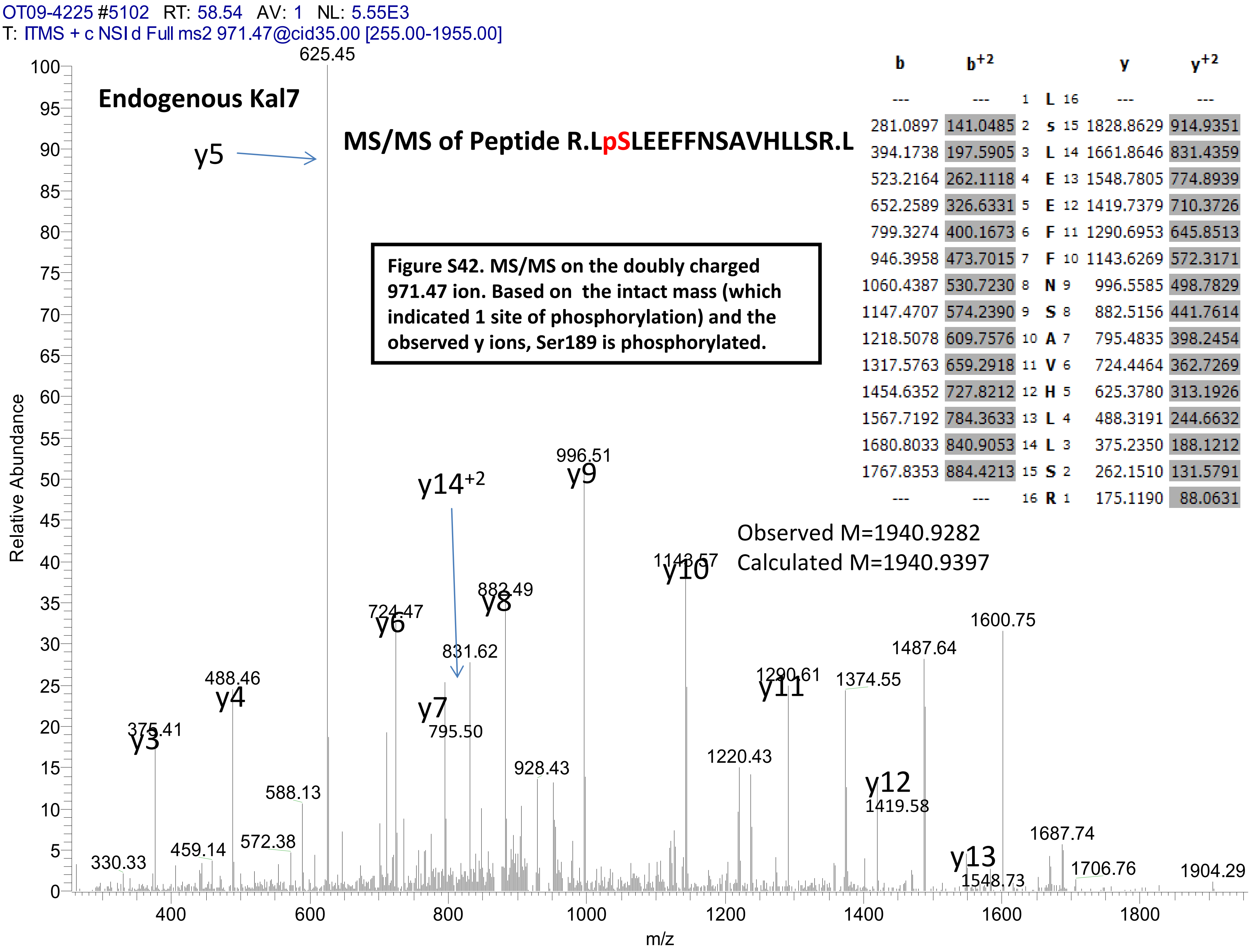


Figure S41. MS/MS on the doubly charged 778.34 ion. Based on the b11-H_3PO_4 and y3-H_3PO_4 ions, residue 1652 is phosphothreonine.

MS/MS of Peptide R.WHLGPGDPFSpTYV.-

b	b^{+2}				y	y^{+2}
---	---	1	W	13	---	---
324.1455	162.5764	2	H	12	1369.5824	685.2948
437.2296	219.1184	3	L	11	1232.5235	616.7654
494.2510	247.6292	4	G	10	1119.4394	560.2234
591.3038	296.1555	5	P	9	1062.4180	531.7126
648.3253	324.6663	6	G	8	965.3652	483.1862
763.3522	382.1797	7	D	7	908.3437	454.6755
860.4050	430.7061	8	P	6	793.3168	397.1620
1007.4734	504.2403	9	F	5	696.2640	348.6357
1094.5054	547.7563	10	S	4	549.1956	275.1014
1275.5194	638.2633	11	t	3	462.1636	231.5854
1438.5827	719.7950	12	Y	2	281.1496	141.0784
---	---	13	V	1	118.0863	59.5468

Observed M=1554.6581
Calculated M=1554.6545



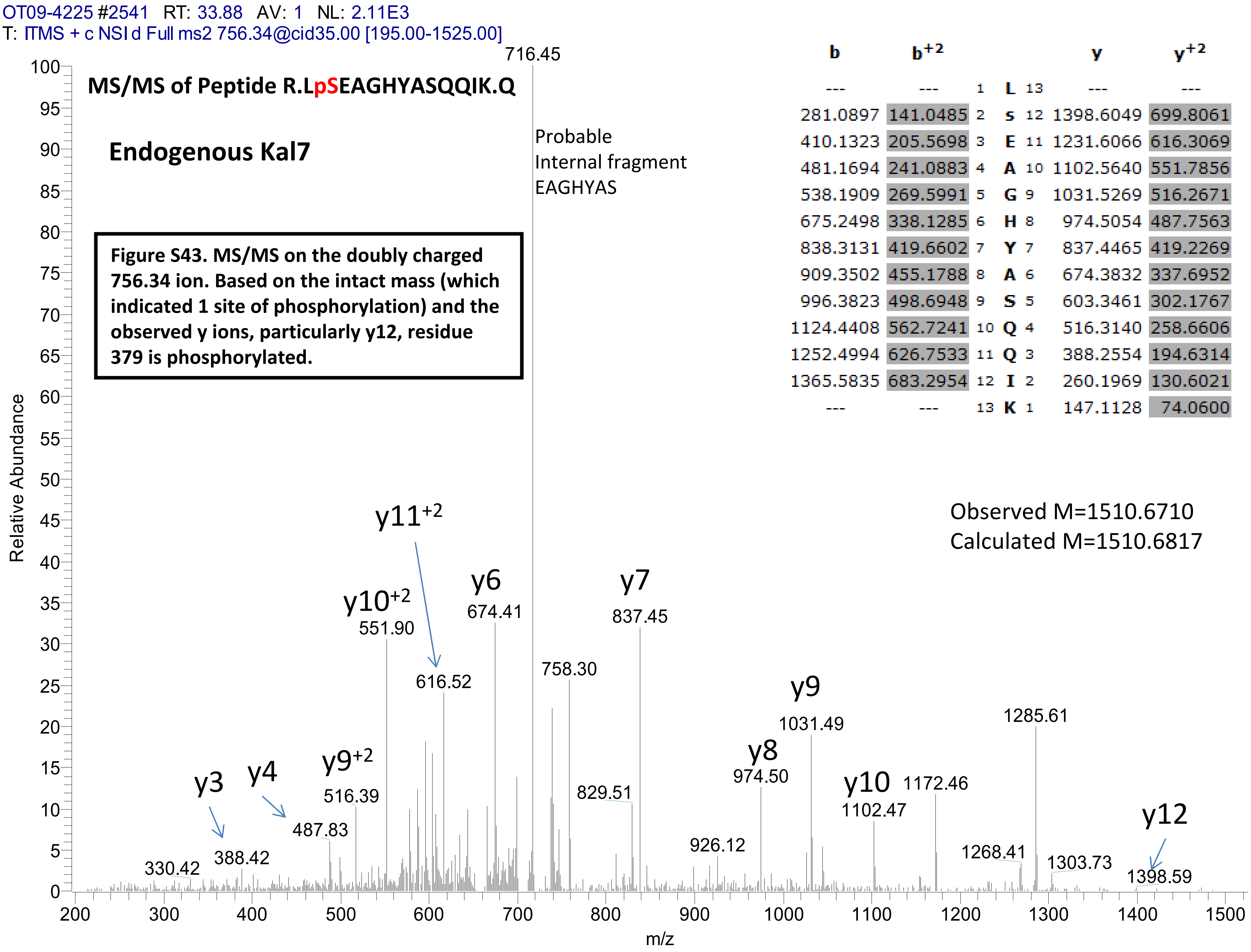
Endogenous Kal7

MS/MS of Peptide R.LpSLEEFFNSAVHLLSR.L

b	b+2				y	y+2
---	---	1	**L**	16	---	---
281.0897	141.0485	2	**s**	15	1828.8629	914.9351
394.1738	197.5905	3	**L**	14	1661.8646	831.4359
523.2164	262.1118	4	**E**	13	1548.7805	774.8939
652.2589	326.6331	5	**E**	12	1419.7379	710.3726
799.3274	400.1673	6	**F**	11	1290.6953	645.8513
946.3958	473.7015	7	**F**	10	1143.6269	572.3171
1060.4387	530.7230	8	**N**	9	996.5585	498.7829
1147.4707	574.2390	9	**S**	8	882.5156	441.7614
1218.5078	609.7576	10	**A**	7	795.4835	398.2454
1317.5763	659.2918	11	**V**	6	724.4464	362.7269
1454.6352	727.8212	12	**H**	5	625.3780	313.1926
1567.7192	784.3633	13	**L**	4	488.3191	244.6632
1680.8033	840.9053	14	**L**	3	375.2350	188.1212
1767.8353	884.4213	15	**S**	2	262.1510	131.5791
---	---	16	**R**	1	175.1190	88.0631

Figure S42. MS/MS on the doubly charged 971.47 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the observed y ions, Ser189 is phosphorylated.

Observed M=1940.9282
Calculated M=1940.9397



MS/MS of Peptide R.LpSEAGHYASQQIK.Q

Endogenous Kal7

Figure S43. MS/MS on the doubly charged 756.34 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the observed y ions, particularly y12, residue 379 is phosphorylated.

b	b^{+2}				y	y^{+2}
---	---	1	L	13	---	---
281.0897	141.0485	2	s	12	1398.6049	699.8061
410.1323	205.5698	3	E	11	1231.6066	616.3069
481.1694	241.0883	4	A	10	1102.5640	551.7856
538.1909	269.5991	5	G	9	1031.5269	516.2671
675.2498	338.1285	6	H	8	974.5054	487.7563
838.3131	419.6602	7	Y	7	837.4465	419.2269
909.3502	455.1788	8	A	6	674.3832	337.6952
996.3823	498.6948	9	S	5	603.3461	302.1767
1124.4408	562.7241	10	Q	4	516.3140	258.6606
1252.4994	626.7533	11	Q	3	388.2554	194.6314
1365.5835	683.2954	12	I	2	260.1969	130.6021
---	---	13	K	1	147.1128	74.0600

Observed M=1510.6710
Calculated M=1510.6817

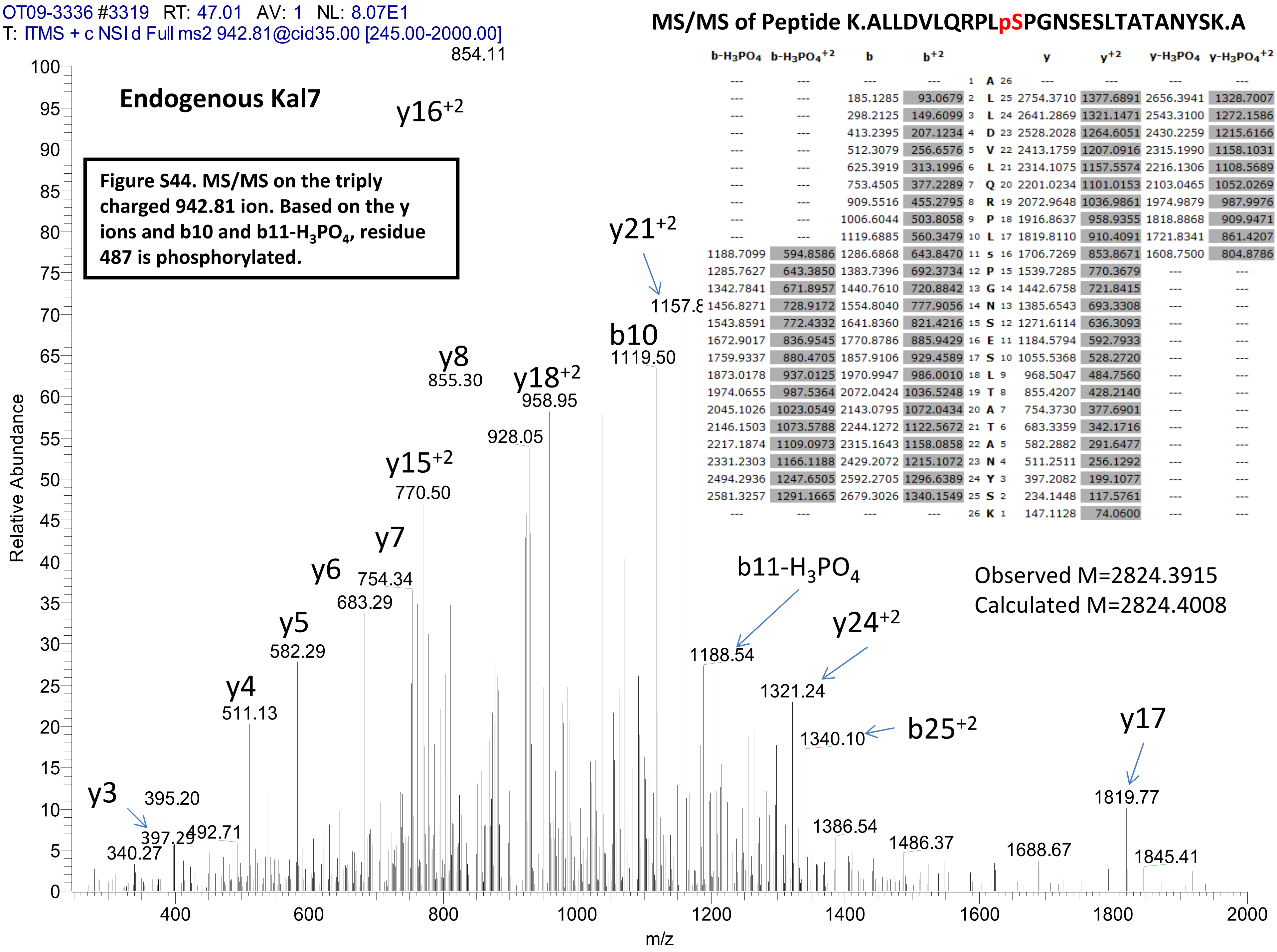


Figure S44. MS/MS on the triply charged 942.81 ion. Based on the y ions and b10 and b11-H_3PO_4, residue 487 is phosphorylated.

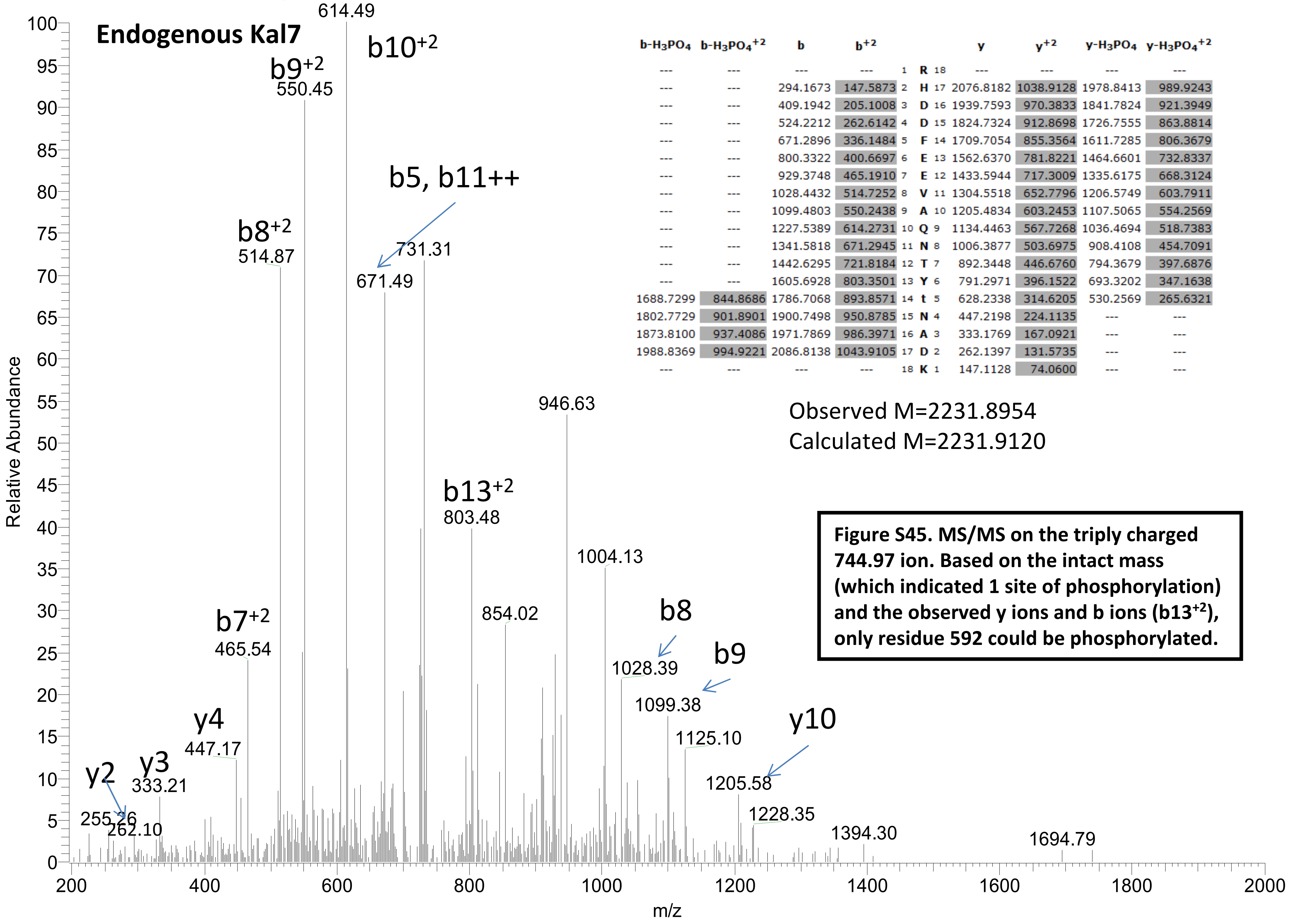
MS/MS of Peptide K.ALLDVLQRPLpSPGNSESLTATANYSK.A

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	A	26	---	---	---	---
---	---	185.1285	93.0679	2	L	25	2754.3710	1377.6891	2656.3941	1328.7007
---	---	298.2125	149.6099	3	L	24	2641.2869	1321.1471	2543.3100	1272.1586
---	---	413.2395	207.1234	4	D	23	2528.2028	1264.6051	2430.2259	1215.6166
---	---	512.3079	256.6576	5	V	22	2413.1759	1207.0916	2315.1990	1158.1031
---	---	625.3919	313.1996	6	L	21	2314.1075	1157.5574	2216.1306	1108.5689
---	---	753.4505	377.2289	7	Q	20	2201.0234	1101.0153	2103.0465	1052.0269
---	---	909.5516	455.2795	8	R	19	2072.9648	1036.9861	1974.9879	987.9976
---	---	1006.6044	503.8058	9	P	18	1916.8637	958.9355	1818.8868	909.9471
---	---	1119.6885	560.3479	10	L	17	1819.8110	910.4091	1721.8341	861.4207
1188.7099	594.8586	1286.6868	643.8470	11	s	16	1706.7269	853.8671	1608.7500	804.8786
1285.7627	643.3850	1383.7396	692.3734	12	P	15	1539.7285	770.3679	---	---
1342.7841	671.8957	1440.7610	720.8842	13	G	14	1442.6758	721.8415	---	---
1456.8271	728.9172	1554.8040	777.9056	14	N	13	1385.6543	693.3308	---	---
1543.8591	772.4332	1641.8360	821.4216	15	S	12	1271.6114	636.3093	---	---
1672.9017	836.9545	1770.8786	885.9429	16	E	11	1184.5794	592.7933	---	---
1759.9337	880.4705	1857.9106	929.4589	17	S	10	1055.5368	528.2720	---	---
1873.0178	937.0125	1970.9947	986.0010	18	L	9	968.5047	484.7560	---	---
1974.0655	987.5364	2072.0424	1036.5248	19	T	8	855.4207	428.2140	---	---
2045.1026	1023.0549	2143.0795	1072.0434	20	A	7	754.3730	377.6901	---	---
2146.1503	1073.5788	2244.1272	1122.5672	21	T	6	683.3359	342.1716	---	---
2217.1874	1109.0973	2315.1643	1158.0858	22	A	5	582.2882	291.6477	---	---
2331.2303	1166.1188	2429.2072	1215.1072	23	N	4	511.2511	256.1292	---	---
2494.2936	1247.6505	2592.2705	1296.6389	24	Y	3	397.2082	199.1077	---	---
2581.3257	1291.1665	2679.3026	1340.1549	25	S	2	234.1448	117.5761	---	---
---	---	---	---	26	K	1	147.1128	74.0600	---	---

Observed M=2824.3915
Calculated M=2824.4008

MS/MS of Peptide K.RHDDFEEVAQNTYpTNADK.L

OT09-3336 #2575 RT: 37.05 AV: 1 NL: 1.34E2
T: ITMS + c NSI d Full ms2 744.97@cid35.00 [195.00-2000.00]



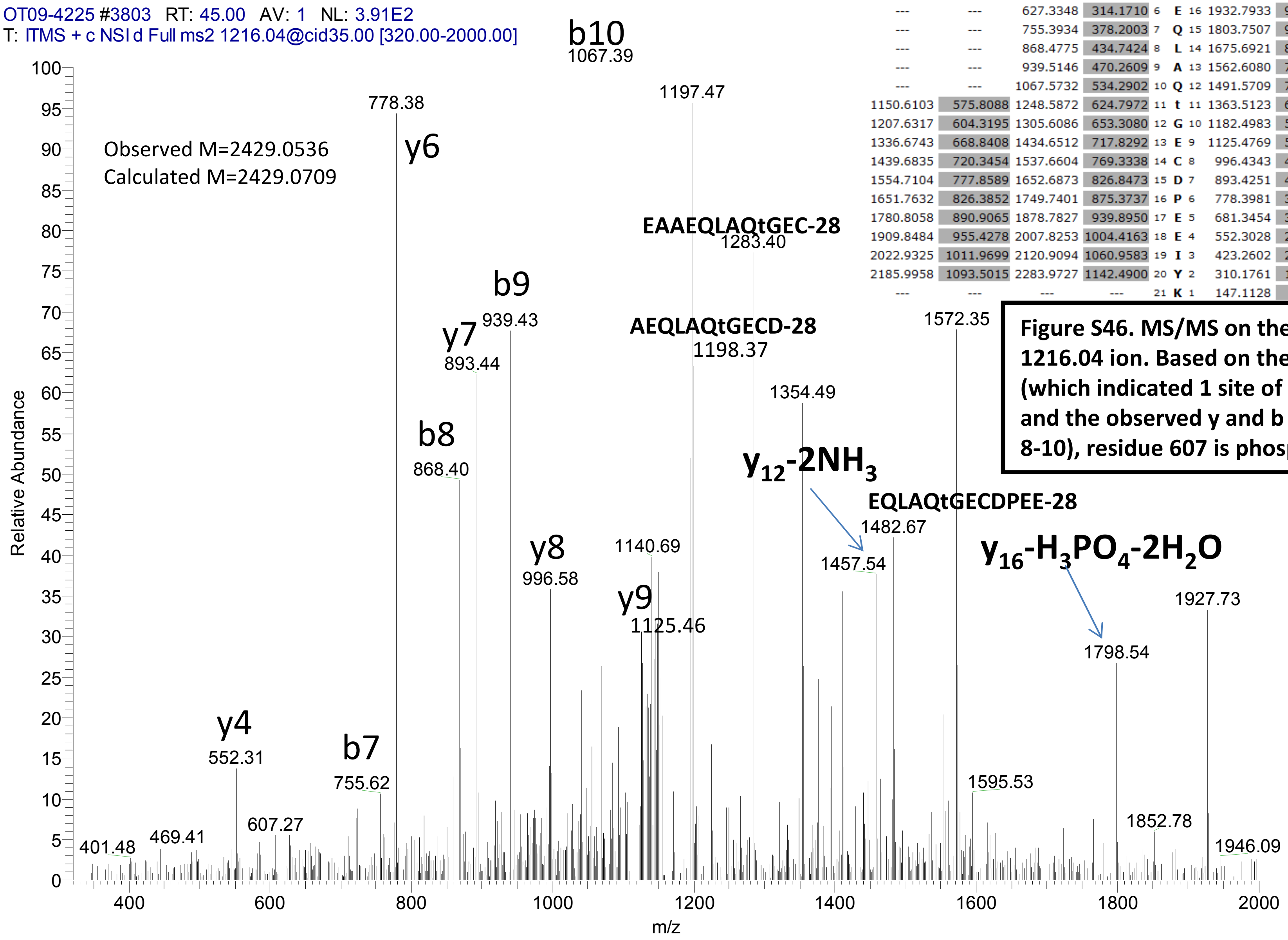
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	**R**	18	---	---	---	---
---	---	294.1673	147.5873	2	**H**	17	2076.8182	1038.9128	1978.8413	989.9243
---	---	409.1942	205.1008	3	**D**	16	1939.7593	970.3833	1841.7824	921.3949
---	---	524.2212	262.6142	4	**D**	15	1824.7324	912.8698	1726.7555	863.8814
---	---	671.2896	336.1484	5	**F**	14	1709.7054	855.3564	1611.7285	806.3679
---	---	800.3322	400.6697	6	**E**	13	1562.6370	781.8221	1464.6601	732.8337
---	---	929.3748	465.1910	7	**E**	12	1433.5944	717.3009	1335.6175	668.3124
---	---	1028.4432	514.7252	8	**V**	11	1304.5518	652.7796	1206.5749	603.7911
---	---	1099.4803	550.2438	9	**A**	10	1205.4834	603.2453	1107.5065	554.2569
---	---	1227.5389	614.2731	10	**Q**	9	1134.4463	567.7268	1036.4694	518.7383
---	---	1341.5818	671.2945	11	**N**	8	1006.3877	503.6975	908.4108	454.7091
---	---	1442.6295	721.8184	12	**T**	7	892.3448	446.6760	794.3679	397.6876
---	---	1605.6928	803.3501	13	**Y**	6	791.2971	396.1522	693.3202	347.1638
1688.7299	844.8686	1786.7068	893.8571	14	**t**	5	628.2338	314.6205	530.2569	265.6321
1802.7729	901.8901	1900.7498	950.8785	15	**N**	4	447.2198	224.1135	---	---
1873.8100	937.4086	1971.7869	986.3971	16	**A**	3	333.1769	167.0921	---	---
1988.8369	994.9221	2086.8138	1043.9105	17	**D**	2	262.1397	131.5735	---	---
---	---	---	---	18	**K**	1	147.1128	74.0600	---	---

Observed M=2231.8954
Calculated M=2231.9120

Figure S45. MS/MS on the triply charged 744.97 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the observed y ions and b ions ($b13^{+2}$), only residue 592 could be phosphorylated.

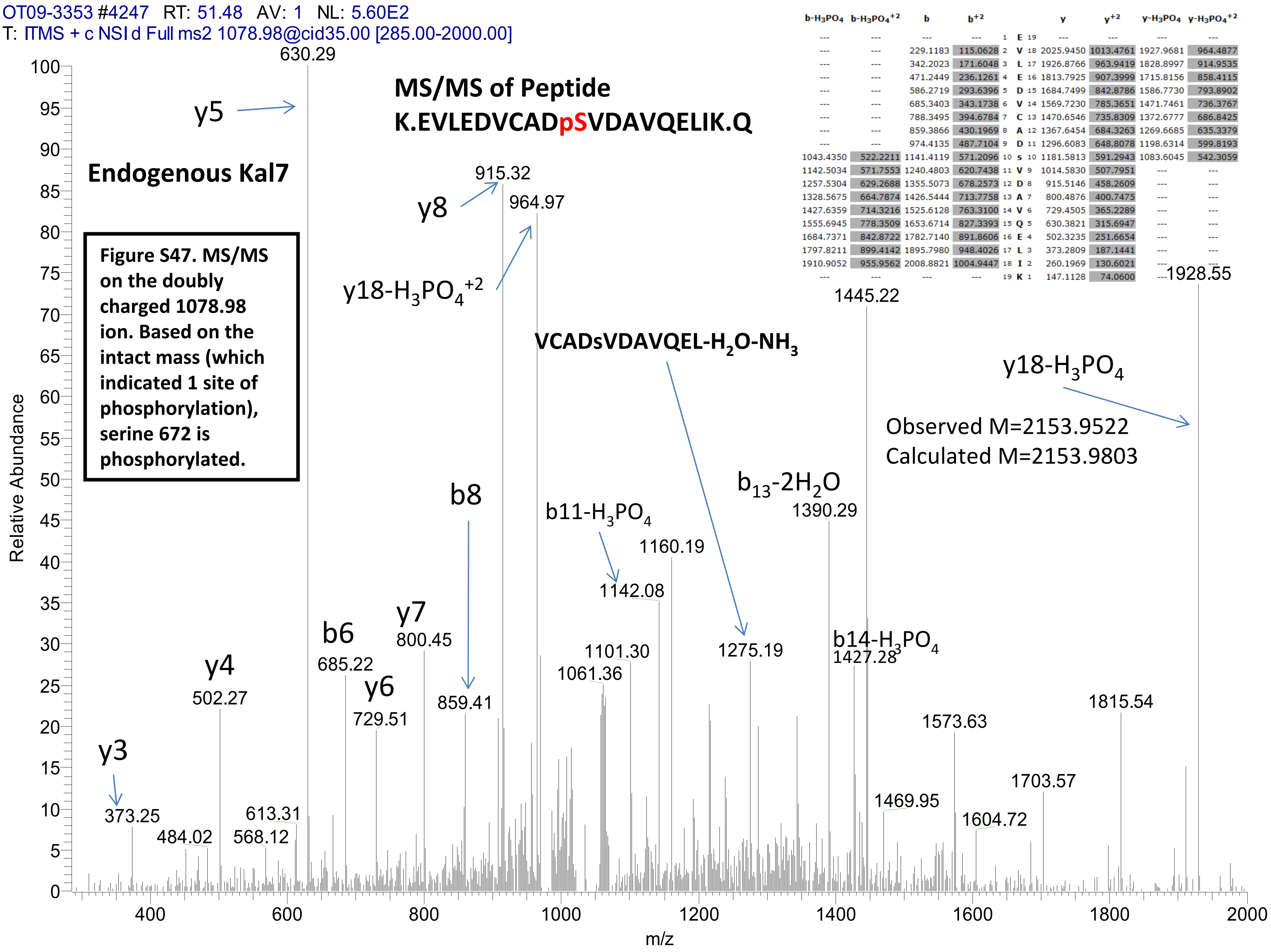
Endogenous Kal7

MS/MS of Peptide K.LLEAAEQLAQpTGECDPEEIYK.A



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	21	---	---	---	---
---	---	227.1754	114.0913	2	L	20	2316.9942	1159.0007	2219.0173	1110.0123
---	---	356.2180	178.6126	3	E	19	2203.9101	1102.4587	2105.9332	1053.4702
---	---	427.2551	214.1312	4	A	18	2074.8675	1037.9374	1976.8906	988.9489
---	---	498.2922	249.6498	5	A	17	2003.8304	1002.4188	1905.8535	953.4304
---	---	627.3348	314.1710	6	E	16	1932.7933	966.9003	1834.8164	917.9118
---	---	755.3934	378.2003	7	Q	15	1803.7507	902.3790	1705.7738	853.3905
---	---	868.4775	434.7424	8	L	14	1675.6921	838.3497	1577.7152	789.3612
---	---	939.5146	470.2609	9	A	13	1562.6080	781.8077	1464.6311	732.8192
---	---	1067.5732	534.2902	10	Q	12	1491.5709	746.2891	1393.5940	697.3006
1150.6103	575.8088	1248.5872	624.7972	11	t	11	1363.5123	682.2598	1265.5354	633.2714
1207.6317	604.3195	1305.6086	653.3080	12	G	10	1182.4983	591.7528	---	---
1336.6743	668.8408	1434.6512	717.8292	13	E	9	1125.4769	563.2421	---	---
1439.6835	720.3454	1537.6604	769.3338	14	C	8	996.4343	498.7208	---	---
1554.7104	777.8589	1652.6873	826.8473	15	D	7	893.4251	447.2162	---	---
1651.7632	826.3852	1749.7401	875.3737	16	P	6	778.3981	389.7027	---	---
1780.8058	890.9065	1878.7827	939.8950	17	E	5	681.3454	341.1763	---	---
1909.8484	955.4278	2007.8253	1004.4163	18	E	4	552.3028	276.6550	---	---
2022.9325	1011.9699	2120.9094	1060.9583	19	I	3	423.2602	212.1337	---	---
2185.9958	1093.5015	2283.9727	1142.4900	20	Y	2	310.1761	155.5917	---	---
---	---	---	---	21	K	1	147.1128	74.0600	---	---

Figure S46. MS/MS on the doubly charged 1216.04 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the observed y and b ions, (y4-9 and b 8-10), residue 607 is phosphorylated.



MS/MS of Peptide
K.EVLEDVCADpSVDAVQELIK.Q

Figure S47. MS/MS on the doubly charged 1078.98 ion. Based on the intact mass (which indicated 1 site of phosphorylation), serine 672 is phosphorylated.

Observed M=2153.9522
Calculated M=2153.9803

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	**E**	19	---	---	---	---
---	---	229.1183	115.0628	2	**V**	18	2025.9450	1013.4761	1927.9681	964.4877
---	---	342.2023	171.6048	3	**L**	17	1926.8766	963.9419	1828.8997	914.9535
---	---	471.2449	236.1261	4	**E**	16	1813.7925	907.3999	1715.8156	858.4115
---	---	586.2719	293.6396	5	**D**	15	1684.7499	842.8786	1586.7730	793.8902
---	---	685.3403	343.1738	6	**V**	14	1569.7230	785.3651	1471.7461	736.3767
---	---	788.3495	394.6784	7	**C**	13	1470.6546	735.8309	1372.6777	686.8425
---	---	859.3866	430.1969	8	**A**	12	1367.6454	684.3263	1269.6685	635.3379
---	---	974.4135	487.7104	9	**D**	11	1296.6083	648.8078	1198.6314	599.8193
1043.4350	522.2211	1141.4119	571.2096	10	**s**	10	1181.5813	591.2943	1083.6045	542.3059
1142.5034	571.7553	1240.4803	620.7438	11	**V**	9	1014.5830	507.7951	---	---
1257.5304	629.2688	1355.5073	678.2573	12	**D**	8	915.5146	458.2609	---	---
1328.5675	664.7874	1426.5444	713.7758	13	**A**	7	800.4876	400.7475	---	---
1427.6359	714.3216	1525.6128	763.3100	14	**V**	6	729.4505	365.2289	---	---
1555.6945	778.3509	1653.6714	827.3393	15	**Q**	5	630.3821	315.6947	---	---
1684.7371	842.8722	1782.7140	891.8606	16	**E**	4	502.3235	251.6654	---	---
1797.8211	899.4142	1895.7980	948.4026	17	**L**	3	373.2809	187.1441	---	---
1910.9052	955.9562	2008.8821	1004.9447	18	**I**	2	260.1969	130.6021	---	---
---	---	---	---	19	**K**	1	147.1128	74.0600	---	---

MS/MS of Peptide R.SAPPpSLGEPTEAR.D

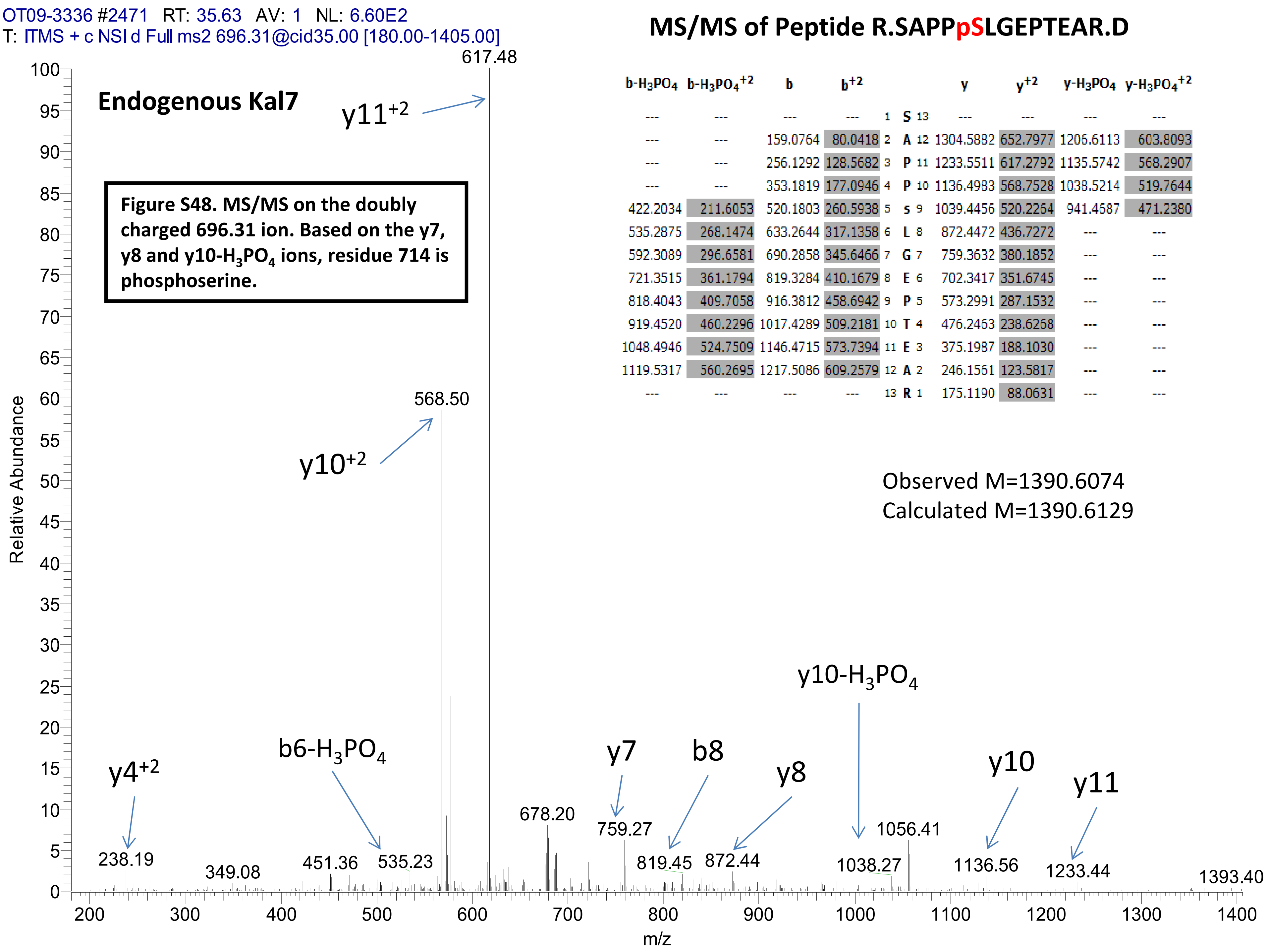


Figure S48. MS/MS on the doubly charged 696.31 ion. Based on the y7, y8 and y10-H_3PO_4 ions, residue 714 is phosphoserine.

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	S	13	---	---	---	---
---	---	159.0764	80.0418	2	A	12	1304.5882	652.7977	1206.6113	603.8093
---	---	256.1292	128.5682	3	P	11	1233.5511	617.2792	1135.5742	568.2907
---	---	353.1819	177.0946	4	P	10	1136.4983	568.7528	1038.5214	519.7644
422.2034	211.6053	520.1803	260.5938	5	s	9	1039.4456	520.2264	941.4687	471.2380
535.2875	268.1474	633.2644	317.1358	6	L	8	872.4472	436.7272	---	---
592.3089	296.6581	690.2858	345.6466	7	G	7	759.3632	380.1852	---	---
721.3515	361.1794	819.3284	410.1679	8	E	6	702.3417	351.6745	---	---
818.4043	409.7058	916.3812	458.6942	9	P	5	573.2991	287.1532	---	---
919.4520	460.2296	1017.4289	509.2181	10	T	4	476.2463	238.6268	---	---
1048.4946	524.7509	1146.4715	573.7394	11	E	3	375.1987	188.1030	---	---
1119.5317	560.2695	1217.5086	609.2579	12	A	2	246.1561	123.5817	---	---
---	---	---	---	13	R	1	175.1190	88.0631	---	---

Observed M=1390.6074
Calculated M=1390.6129

MS/MS of Peptide K.pTHQSALQVQQK.A

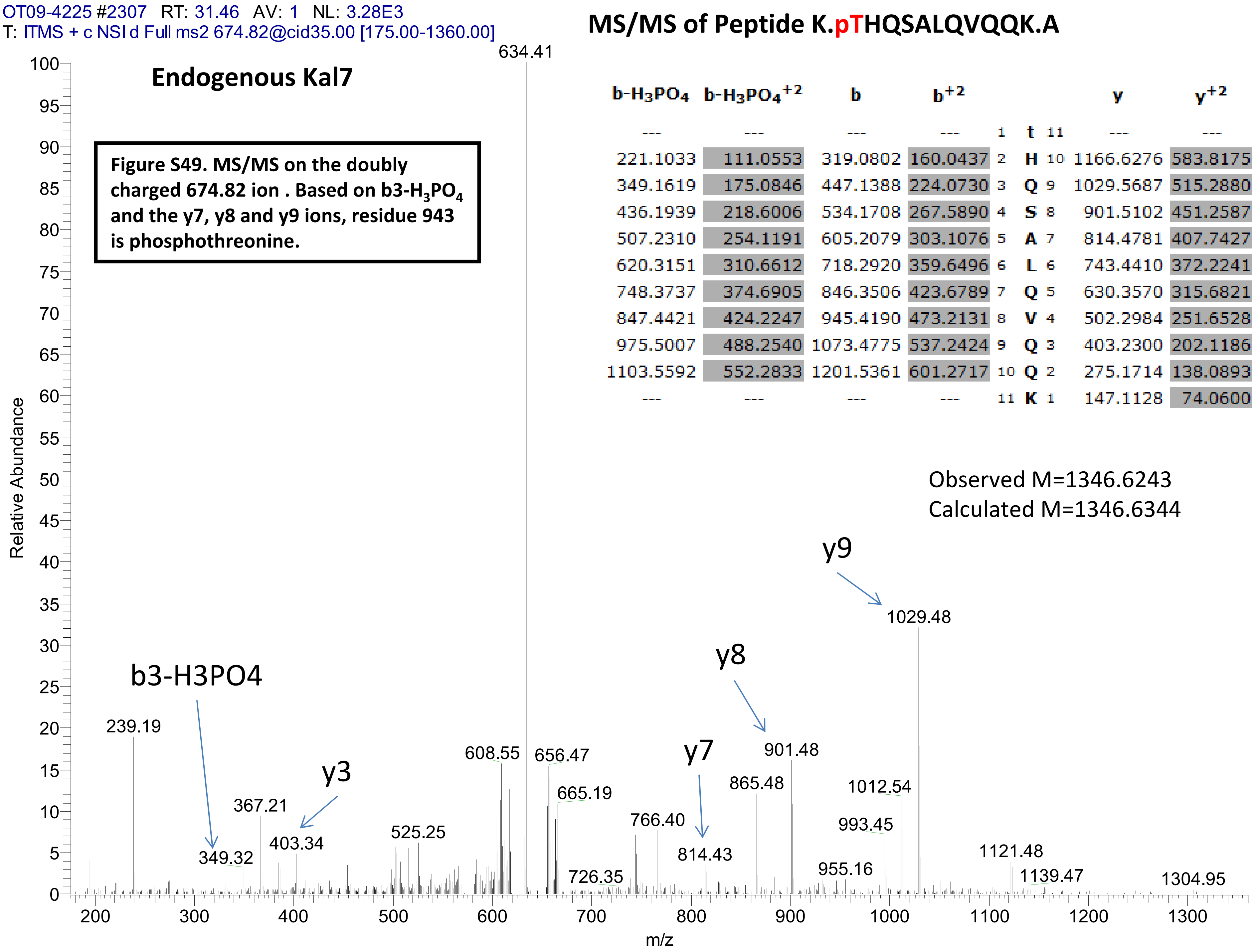


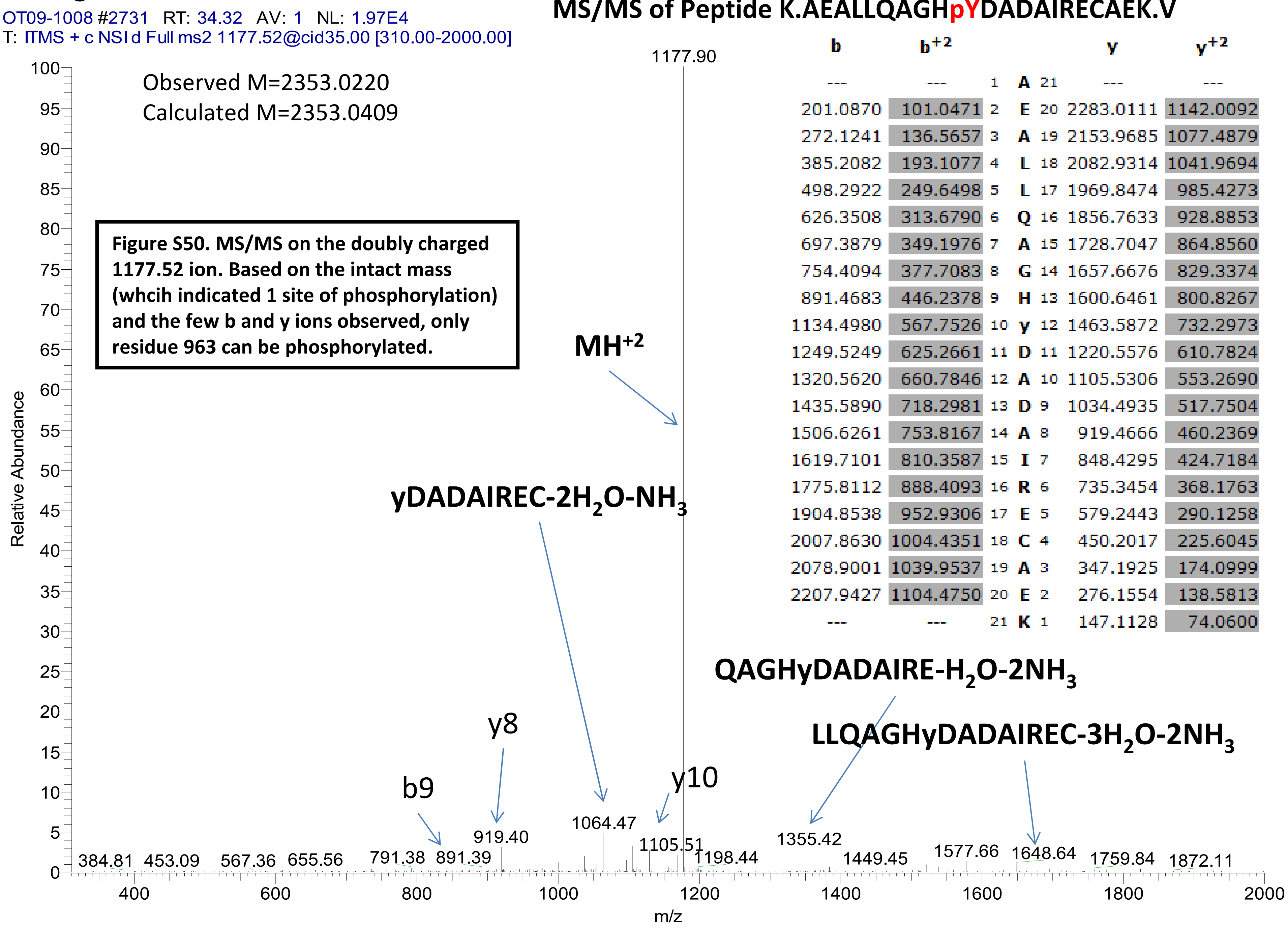
Figure S49. MS/MS on the doubly charged 674.82 ion . Based on b3-H_3PO_4 and the y7, y8 and y9 ions, residue 943 is phosphothreonine.

$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}
---	---	---	---	1	**t**	11	---	---
221.1033	111.0553	319.0802	160.0437	2	**H**	10	1166.6276	583.8175
349.1619	175.0846	447.1388	224.0730	3	**Q**	9	1029.5687	515.2880
436.1939	218.6006	534.1708	267.5890	4	**S**	8	901.5102	451.2587
507.2310	254.1191	605.2079	303.1076	5	**A**	7	814.4781	407.7427
620.3151	310.6612	718.2920	359.6496	6	**L**	6	743.4410	372.2241
748.3737	374.6905	846.3506	423.6789	7	**Q**	5	630.3570	315.6821
847.4421	424.2247	945.4190	473.2131	8	**V**	4	502.2984	251.6528
975.5007	488.2540	1073.4775	537.2424	9	**Q**	3	403.2300	202.1186
1103.5592	552.2833	1201.5361	601.2717	10	**Q**	2	275.1714	138.0893
---	---	---	---	11	**K**	1	147.1128	74.0600

Observed M=1346.6243
Calculated M=1346.6344

Endogenous Kal7

MS/MS of Peptide K.AEALLQAGHpYDADAIRECAEK.V



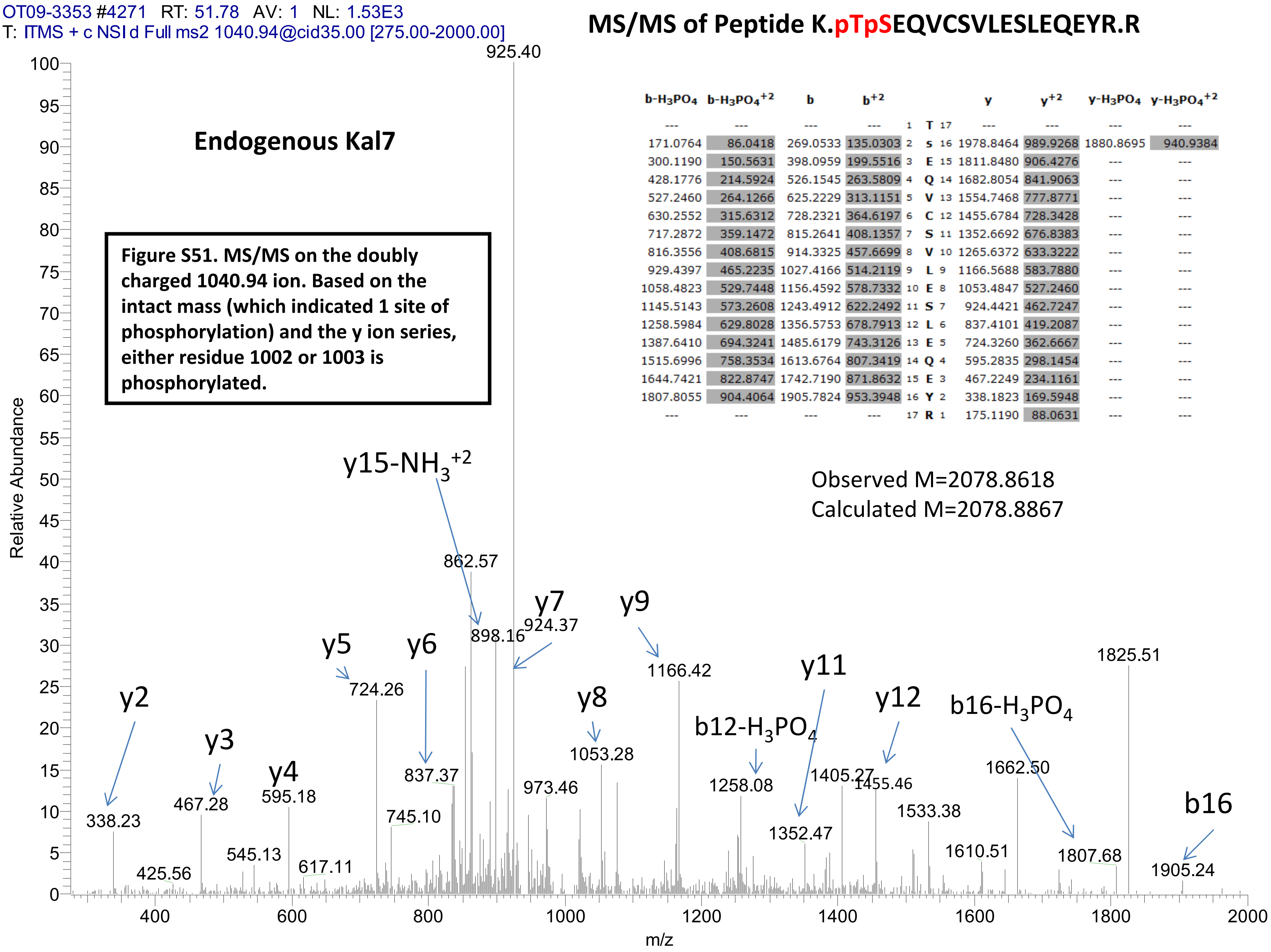
Observed M=2353.0220
Calculated M=2353.0409

Figure S50. MS/MS on the doubly charged 1177.52 ion. Based on the intact mass (whcih indicated 1 site of phosphorylation) and the few b and y ions observed, only residue 963 can be phosphorylated.

b	b^{+2}				y	y^{+2}
---	---	1	A	21	---	---
201.0870	101.0471	2	E	20	2283.0111	1142.0092
272.1241	136.5657	3	A	19	2153.9685	1077.4879
385.2082	193.1077	4	L	18	2082.9314	1041.9694
498.2922	249.6498	5	L	17	1969.8474	985.4273
626.3508	313.6790	6	Q	16	1856.7633	928.8853
697.3879	349.1976	7	A	15	1728.7047	864.8560
754.4094	377.7083	8	G	14	1657.6676	829.3374
891.4683	446.2378	9	H	13	1600.6461	800.8267
1134.4980	567.7526	10	y	12	1463.5872	732.2973
1249.5249	625.2661	11	D	11	1220.5576	610.7824
1320.5620	660.7846	12	A	10	1105.5306	553.2690
1435.5890	718.2981	13	D	9	1034.4935	517.7504
1506.6261	753.8167	14	A	8	919.4666	460.2369
1619.7101	810.3587	15	I	7	848.4295	424.7184
1775.8112	888.4093	16	R	6	735.3454	368.1763
1904.8538	952.9306	17	E	5	579.2443	290.1258
2007.8630	1004.4351	18	C	4	450.2017	225.6045
2078.9001	1039.9537	19	A	3	347.1925	174.0999
2207.9427	1104.4750	20	E	2	276.1554	138.5813
---	---	21	K	1	147.1128	74.0600

MS/MS of Peptide K.pTpSEQVCSVLESLEQEYR.R

Figure S51. MS/MS on the doubly charged 1040.94 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ion series, either residue 1002 or 1003 is phosphorylated.



Endogenous Kal7

b-H$_3$PO$_4$	b-H$_3$PO$_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H$_3$PO$_4$	y-H$_3$PO$_4^{+2}$
---	---	---	---	1	**T**	17	---	---	---	---
171.0764	86.0418	269.0533	135.0303	2	**s**	16	1978.8464	989.9268	1880.8695	940.9384
300.1190	150.5631	398.0959	199.5516	3	**E**	15	1811.8480	906.4276	---	---
428.1776	214.5924	526.1545	263.5809	4	**Q**	14	1682.8054	841.9063	---	---
527.2460	264.1266	625.2229	313.1151	5	**V**	13	1554.7468	777.8771	---	---
630.2552	315.6312	728.2321	364.6197	6	**C**	12	1455.6784	728.3428	---	---
717.2872	359.1472	815.2641	408.1357	7	**S**	11	1352.6692	676.8383	---	---
816.3556	408.6815	914.3325	457.6699	8	**V**	10	1265.6372	633.3222	---	---
929.4397	465.2235	1027.4166	514.2119	9	**L**	9	1166.5688	583.7880	---	---
1058.4823	529.7448	1156.4592	578.7332	10	**E**	8	1053.4847	527.2460	---	---
1145.5143	573.2608	1243.4912	622.2492	11	**S**	7	924.4421	462.7247	---	---
1258.5984	629.8028	1356.5753	678.7913	12	**L**	6	837.4101	419.2087	---	---
1387.6410	694.3241	1485.6179	743.3126	13	**E**	5	724.3260	362.6667	---	---
1515.6996	758.3534	1613.6764	807.3419	14	**Q**	4	595.2835	298.1454	---	---
1644.7421	822.8747	1742.7190	871.8632	15	**E**	3	467.2249	234.1161	---	---
1807.8055	904.4064	1905.7824	953.3948	16	**Y**	2	338.1823	169.5948	---	---
---	---	---	---	17	**R**	1	175.1190	88.0631	---	---

Observed M=2078.8618
Calculated M=2078.8867

MS/MS of Peptide R.NNVpSoxMPSVASHTR.G

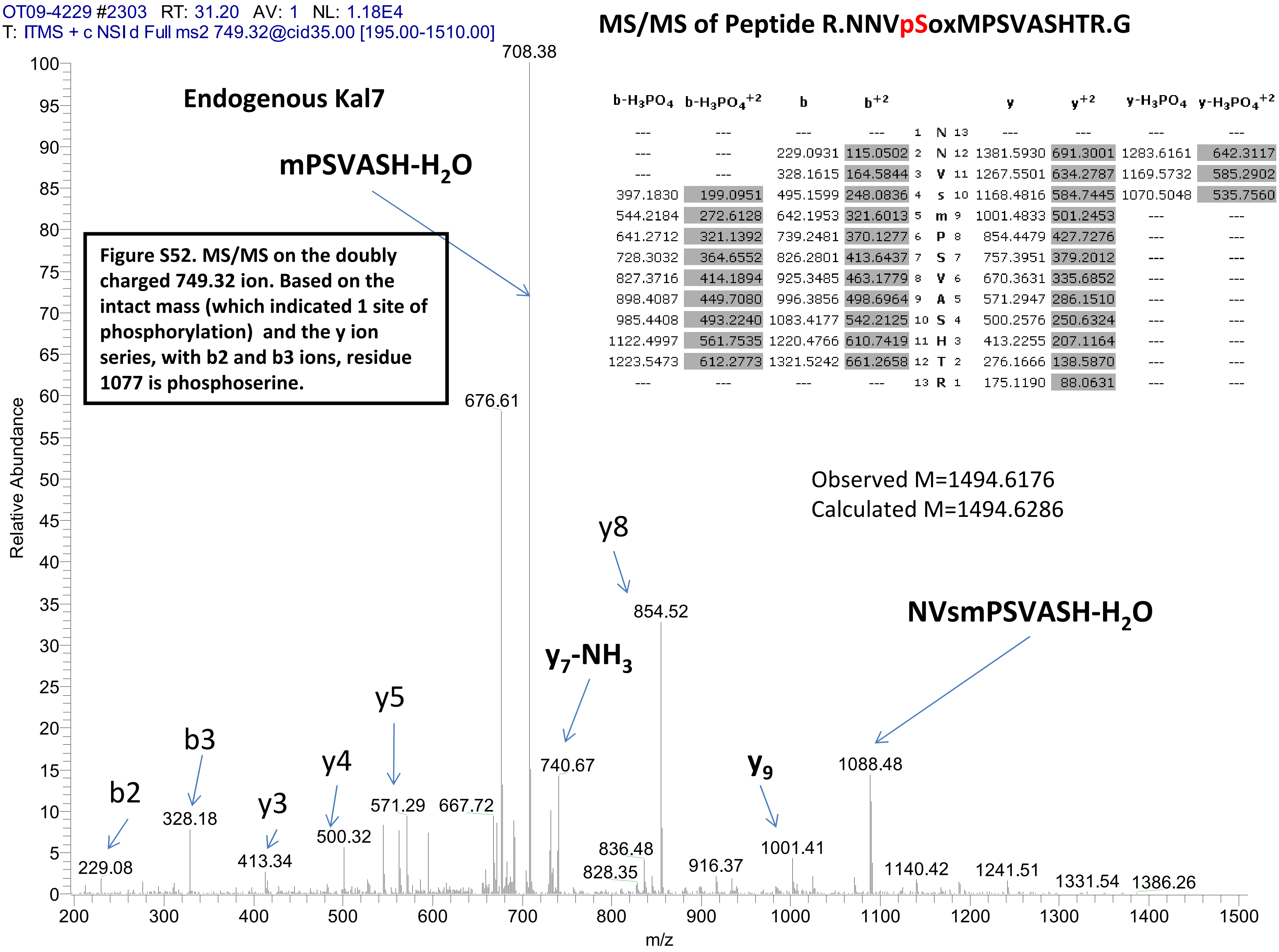


Figure S52. MS/MS on the doubly charged 749.32 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ion series, with b2 and b3 ions, residue 1077 is phosphoserine.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	N	13	---	---	---	---
---	---	229.0931	115.0502	2	N	12	1381.5930	691.3001	1283.6161	642.3117
---	---	328.1615	164.5844	3	V	11	1267.5501	634.2787	1169.5732	585.2902
397.1830	199.0951	495.1599	248.0836	4	s	10	1168.4816	584.7445	1070.5048	535.7560
544.2184	272.6128	642.1953	321.6013	5	m	9	1001.4833	501.2453	---	---
641.2712	321.1392	739.2481	370.1277	6	P	8	854.4479	427.7276	---	---
728.3032	364.6552	826.2801	413.6437	7	S	7	757.3951	379.2012	---	---
827.3716	414.1894	925.3485	463.1779	8	V	6	670.3631	335.6852	---	---
898.4087	449.7080	996.3856	498.6964	9	A	5	571.2947	286.1510	---	---
985.4408	493.2240	1083.4177	542.2125	10	S	4	500.2576	250.6324	---	---
1122.4997	561.7535	1220.4766	610.7419	11	H	3	413.2255	207.1164	---	---
1223.5473	612.2773	1321.5242	661.2658	12	T	2	276.1666	138.5870	---	---
---	---	---	---	13	R	1	175.1190	88.0631	---	---

Observed M=1494.6176
Calculated M=1494.6286

MS/MS of Peptide R.NNVSoxMPSVASHpTR.G

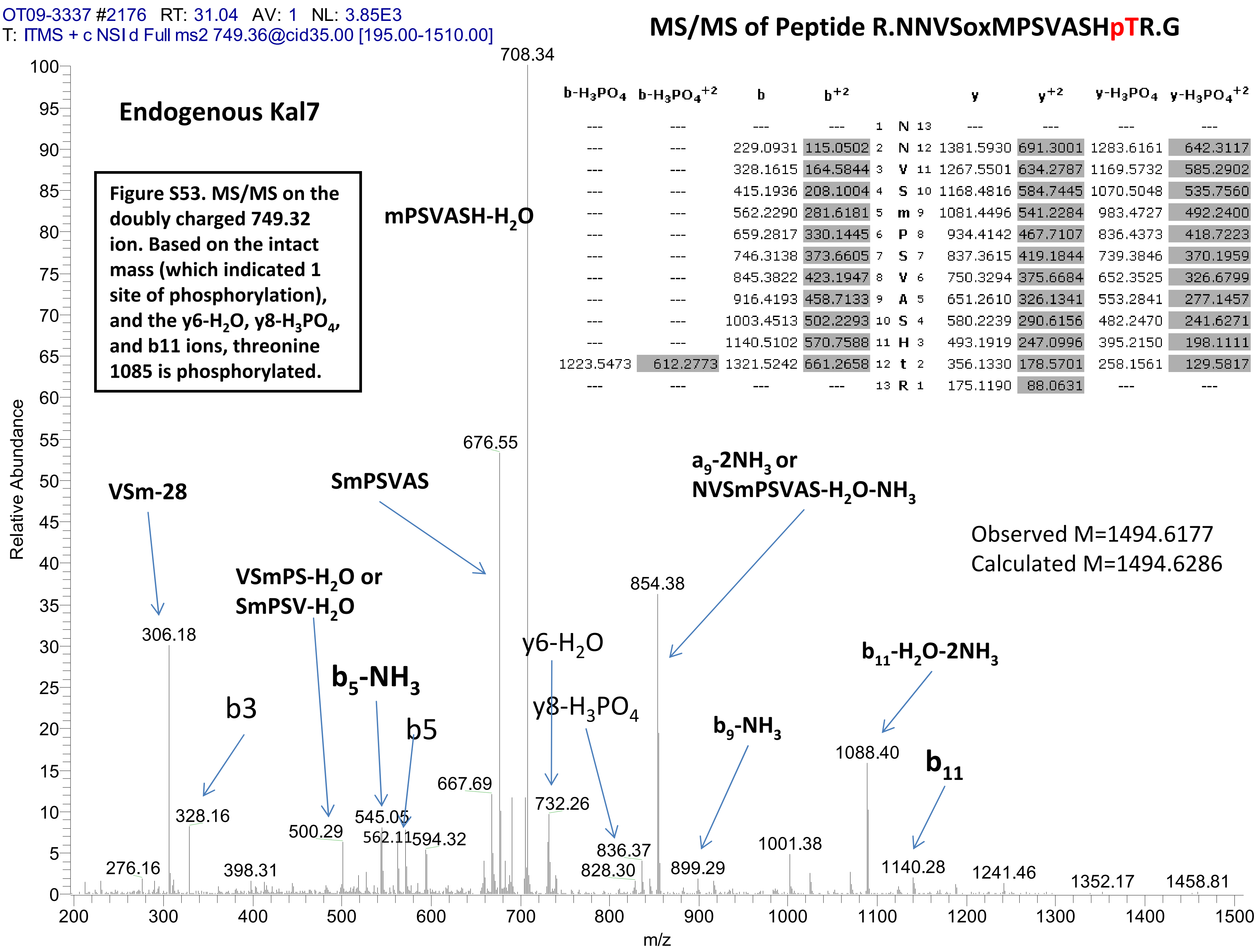
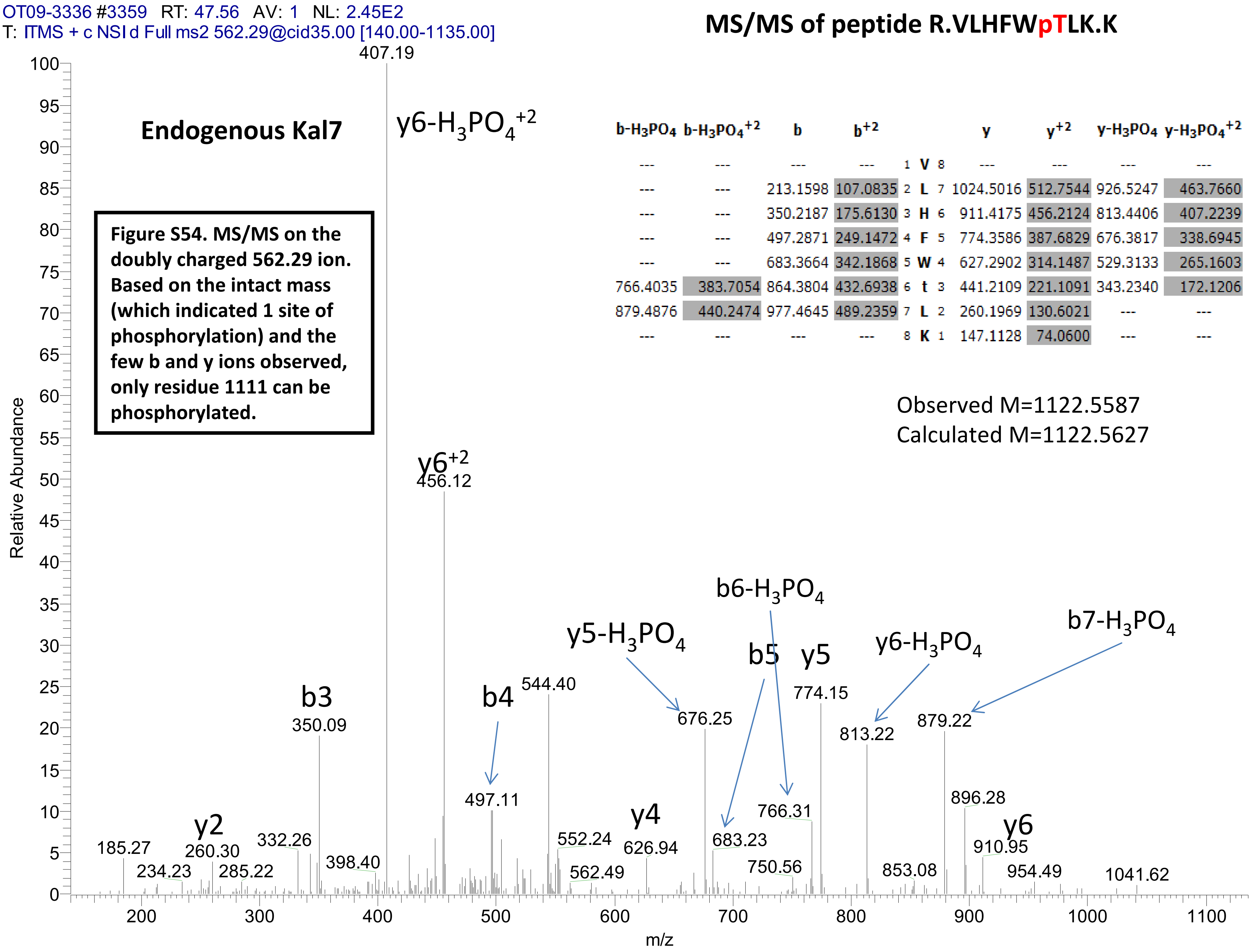


Figure S53. MS/MS on the doubly charged 749.32 ion. Based on the intact mass (which indicated 1 site of phosphorylation), and the y6-H_2O, y8-H_3PO_4, and b11 ions, threonine 1085 is phosphorylated.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	N	13	---	---	---	---
---	---	229.0931	115.0502	2	N	12	1381.5930	691.3001	1283.6161	642.3117
---	---	328.1615	164.5844	3	V	11	1267.5501	634.2787	1169.5732	585.2902
---	---	415.1936	208.1004	4	S	10	1168.4816	584.7445	1070.5048	535.7560
---	---	562.2290	281.6181	5	m	9	1081.4496	541.2284	983.4727	492.2400
---	---	659.2817	330.1445	6	P	8	934.4142	467.7107	836.4373	418.7223
---	---	746.3138	373.6605	7	S	7	837.3615	419.1844	739.3846	370.1959
---	---	845.3822	423.1947	8	V	6	750.3294	375.6684	652.3525	326.6799
---	---	916.4193	458.7133	9	A	5	651.2610	326.1341	553.2841	277.1457
---	---	1003.4513	502.2293	10	S	4	580.2239	290.6156	482.2470	241.6271
---	---	1140.5102	570.7588	11	H	3	493.1919	247.0996	395.2150	198.1111
1223.5473	612.2773	1321.5242	661.2658	12	t	2	356.1330	178.5701	258.1561	129.5817
---	---	---	---	13	R	1	175.1190	88.0631	---	---

Observed M=1494.6177
Calculated M=1494.6286

MS/MS of peptide R.VLHFWpTLK.K



$b-H_3PO_4$	$b-H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y-H_3PO_4$	$y-H_3PO_4^{+2}$
---	---	---	---	1	V	8	---	---	---	---
---	---	213.1598	107.0835	2	L	7	1024.5016	512.7544	926.5247	463.7660
---	---	350.2187	175.6130	3	H	6	911.4175	456.2124	813.4406	407.2239
---	---	497.2871	249.1472	4	F	5	774.3586	387.6829	676.3817	338.6945
---	---	683.3664	342.1868	5	W	4	627.2902	314.1487	529.3133	265.1603
766.4035	383.7054	864.3804	432.6938	6	t	3	441.2109	221.1091	343.2340	172.1206
879.4876	440.2474	977.4645	489.2359	7	L	2	260.1969	130.6021	---	---
---	---	---	---	8	K	1	147.1128	74.0600	---	---

Observed M=1122.5587
Calculated M=1122.5627

Figure S54. MS/MS on the doubly charged 562.29 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the few b and y ions observed, only residue 1111 can be phosphorylated.

MS/MS of peptide K.GHIHApTEIR.K

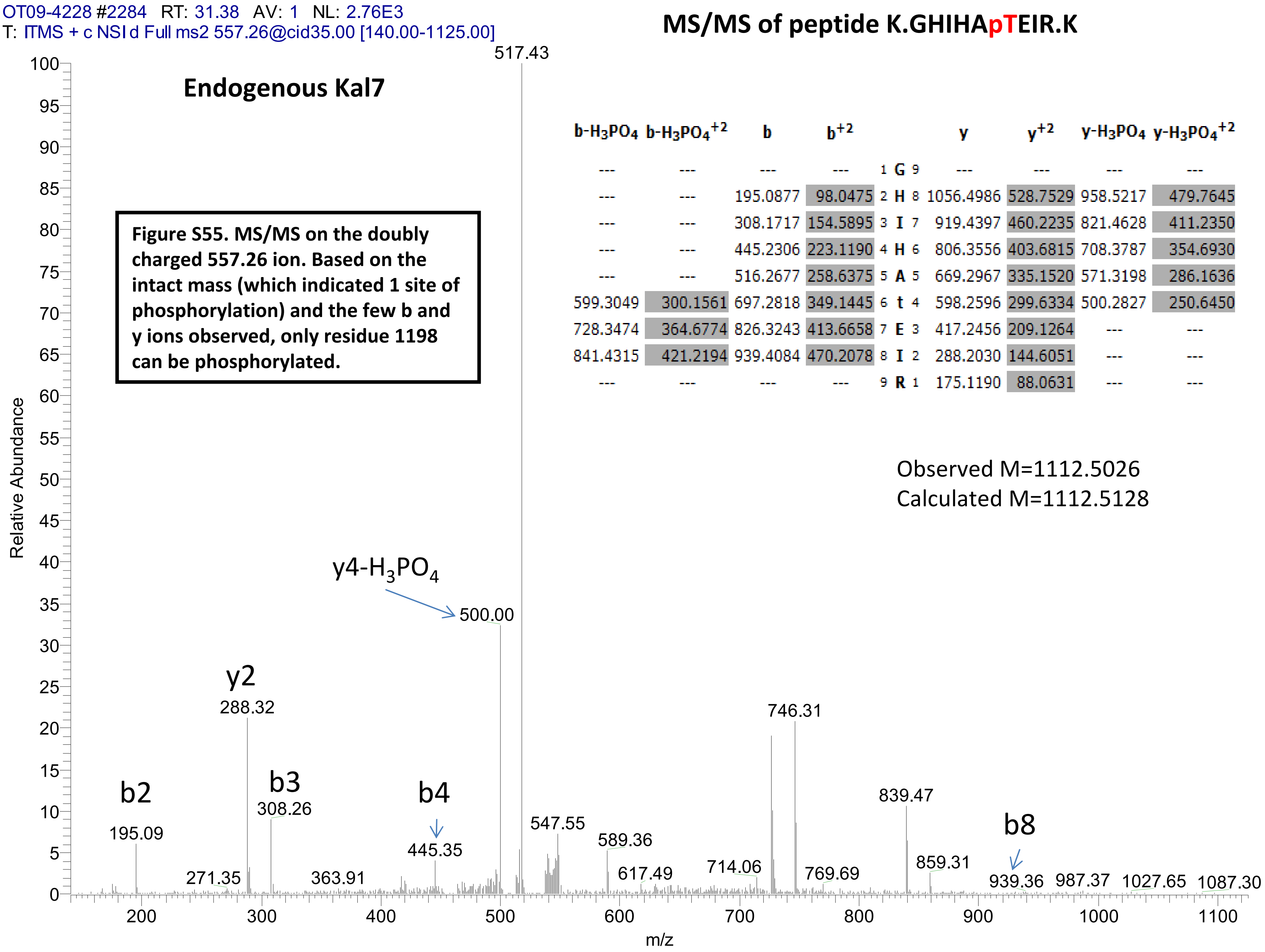


Figure S55. MS/MS on the doubly charged 557.26 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the few b and y ions observed, only residue 1198 can be phosphorylated.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	G	9	---	---	---	---
---	---	195.0877	98.0475	2	H	8	1056.4986	528.7529	958.5217	479.7645
---	---	308.1717	154.5895	3	I	7	919.4397	460.2235	821.4628	411.2350
---	---	445.2306	223.1190	4	H	6	806.3556	403.6815	708.3787	354.6930
---	---	516.2677	258.6375	5	A	5	669.2967	335.1520	571.3198	286.1636
599.3049	300.1561	697.2818	349.1445	6	t	4	598.2596	299.6334	500.2827	250.6450
728.3474	364.6774	826.3243	413.6658	7	E	3	417.2456	209.1264	---	---
841.4315	421.2194	939.4084	470.2078	8	I	2	288.2030	144.6051	---	---
---	---	---	---	9	R	1	175.1190	88.0631	---	---

Observed M=1112.5026
Calculated M=1112.5128

MS/MS of peptide R.DFpSLR.M

Endogenous Kal7

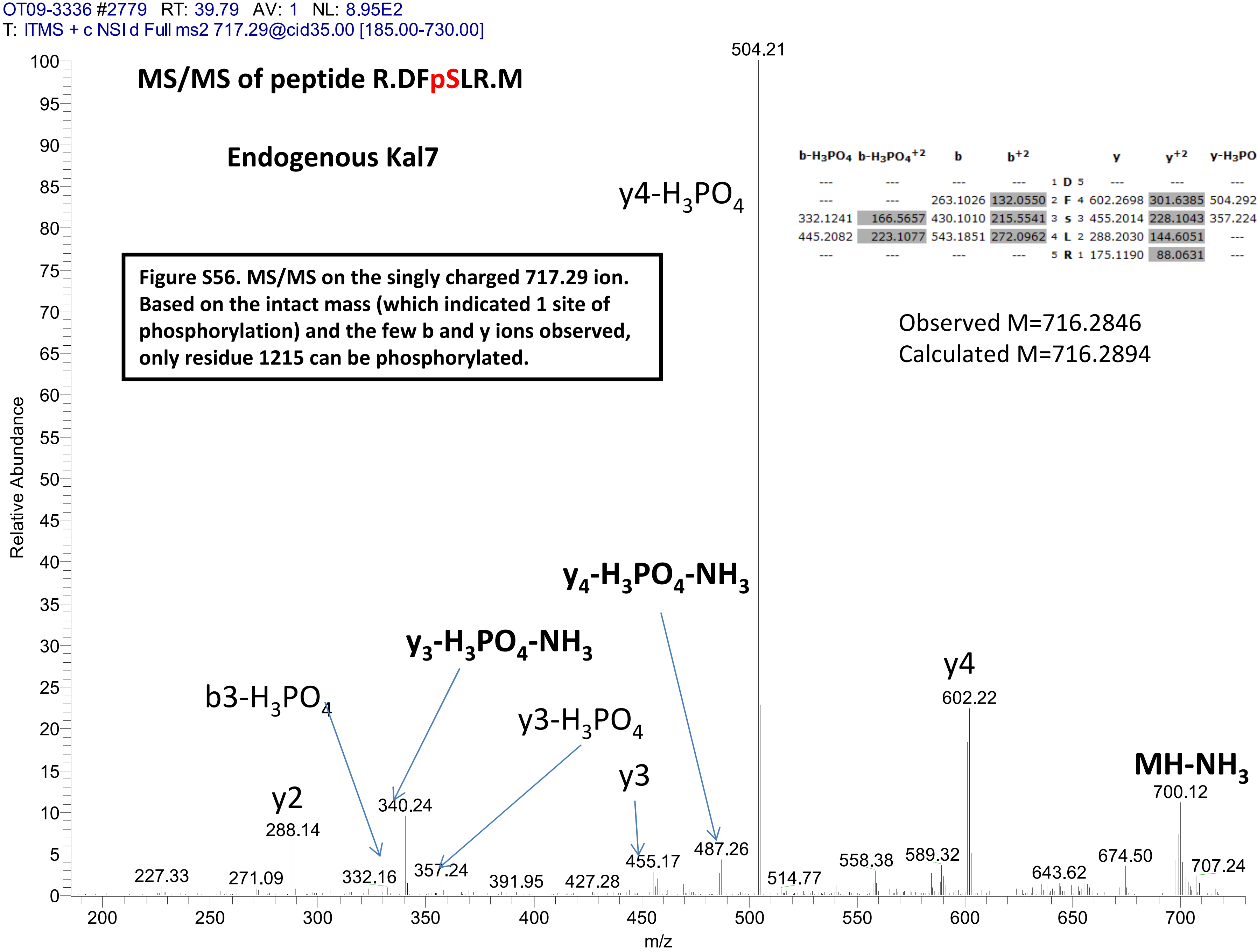


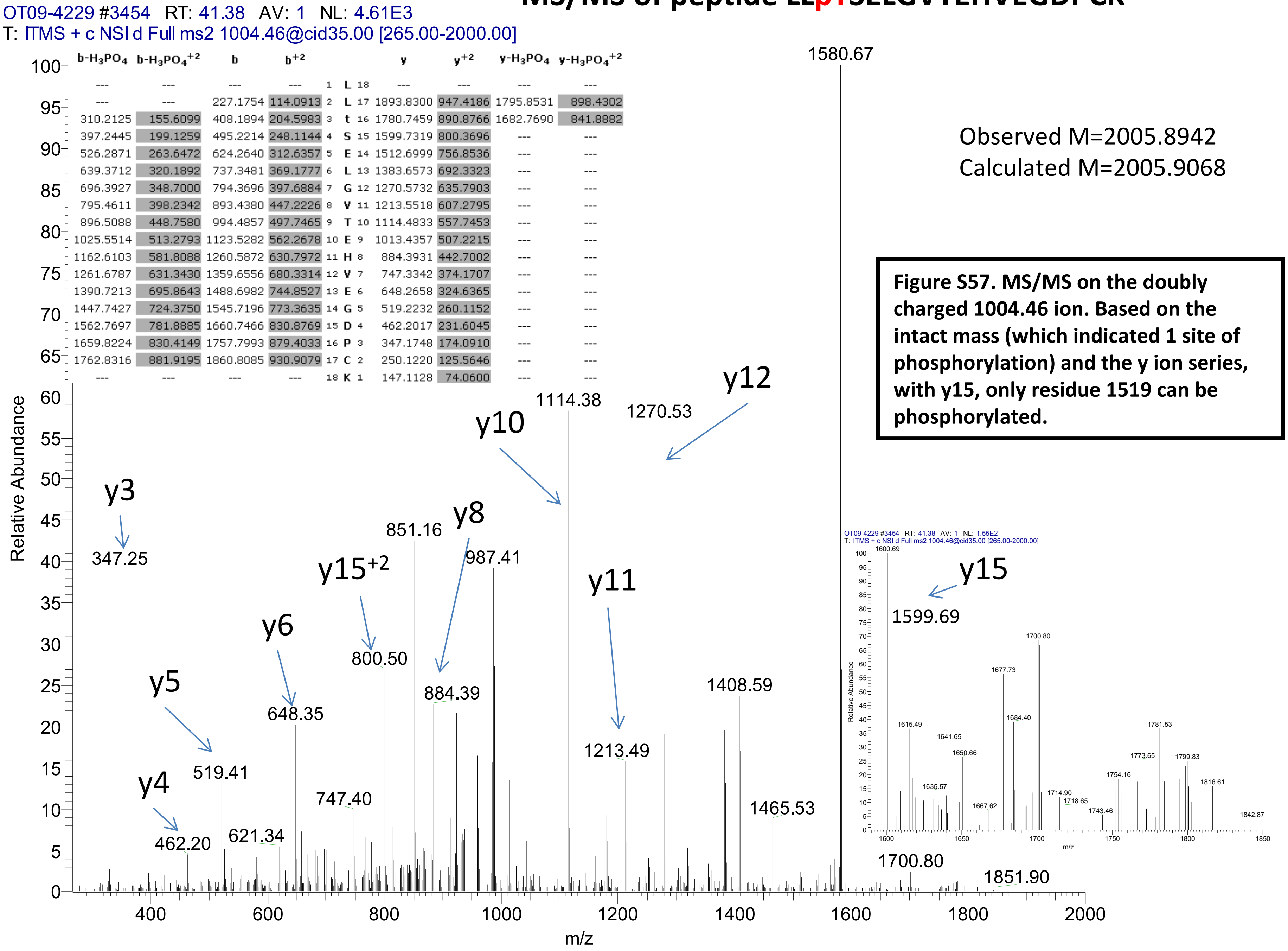
Figure S56. MS/MS on the singly charged 717.29 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the few b and y ions observed, only residue 1215 can be phosphorylated.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	D	5	---	---	---	---
---	---	263.1026	132.0550	2	F	4	602.2698	301.6385	504.2929	252.6501
332.1241	166.5657	430.1010	215.5541	3	s	3	455.2014	228.1043	357.2245	179.1159
445.2082	223.1077	543.1851	272.0962	4	L	2	288.2030	144.6051	---	---
---	---	---	---	5	R	1	175.1190	88.0631	---	---

Observed M=716.2846
Calculated M=716.2894

Endogenous Kal7

MS/MS of peptide LLpTSELGVTEHVEGDPCK



b-H$_3$PO$_4$	b-H$_3$PO$_4$$^{+2}$	b	b^{+2}				y	y^{+2}	y-H$_3$PO$_4$	y-H$_3$PO$_4$$^{+2}$
---	---	---	---	1	L	18	---	---	---	---
---	---	227.1754	114.0913	2	L	17	1893.8300	947.4186	1795.8531	898.4302
310.2125	155.6099	408.1894	204.5983	3	t	16	1780.7459	890.8766	1682.7690	841.8882
397.2445	199.1259	495.2214	248.1144	4	S	15	1599.7319	800.3696	---	---
526.2871	263.6472	624.2640	312.6357	5	E	14	1512.6999	756.8536	---	---
639.3712	320.1892	737.3481	369.1777	6	L	13	1383.6573	692.3323	---	---
696.3927	348.7000	794.3696	397.6884	7	G	12	1270.5732	635.7903	---	---
795.4611	398.2342	893.4380	447.2226	8	V	11	1213.5518	607.2795	---	---
896.5088	448.7580	994.4857	497.7465	9	T	10	1114.4833	557.7453	---	---
1025.5514	513.2793	1123.5282	562.2678	10	E	9	1013.4357	507.2215	---	---
1162.6103	581.8088	1260.5872	630.7972	11	H	8	884.3931	442.7002	---	---
1261.6787	631.3430	1359.6556	680.3314	12	V	7	747.3342	374.1707	---	---
1390.7213	695.8643	1488.6982	744.8527	13	E	6	648.2658	324.6365	---	---
1447.7427	724.3750	1545.7196	773.3635	14	G	5	519.2232	260.1152	---	---
1562.7697	781.8885	1660.7466	830.8769	15	D	4	462.2017	231.6045	---	---
1659.8224	830.4149	1757.7993	879.4033	16	P	3	347.1748	174.0910	---	---
1762.8316	881.9195	1860.8085	930.9079	17	C	2	250.1220	125.5646	---	---
---	---	---	---	18	K	1	147.1128	74.0600	---	---

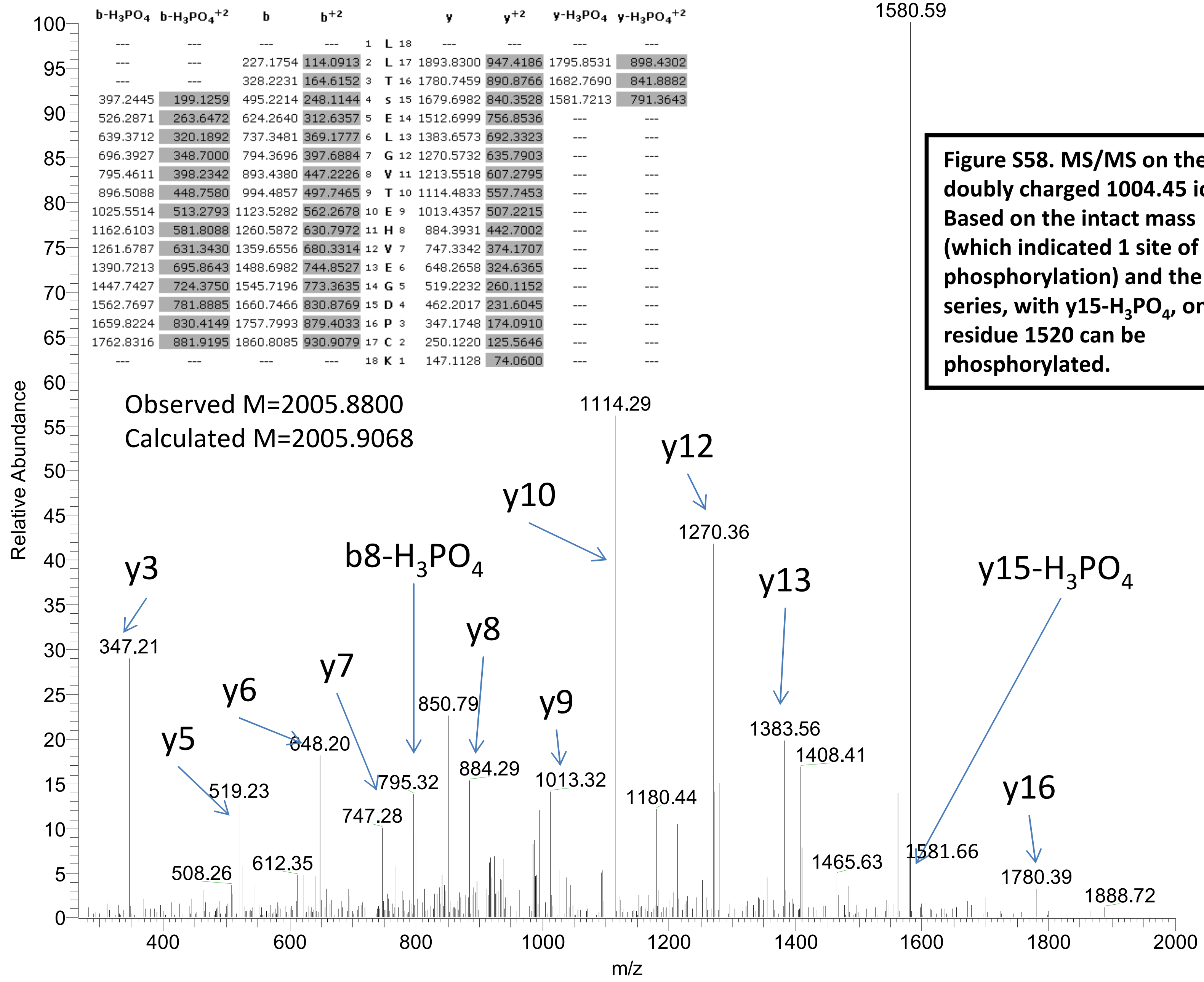
Observed M=2005.8942
Calculated M=2005.9068

Figure S57. MS/MS on the doubly charged 1004.46 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ion series, with y15, only residue 1519 can be phosphorylated.

Endogenous Kal7

MS/MS of peptide LLTpSELGVTEHVEGDPCK

OT09-3352 #2895 RT: 41.33 AV: 1 NL: 2.11E2
T: ITMS + c NSI d Full ms2 1004.45@cid35.00 [265.00-2000.00]



b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	L	18	---	---	---	---
---	---	227.1754	114.0913	2	L	17	1893.8300	947.4186	1795.8531	898.4302
---	---	328.2231	164.6152	3	T	16	1780.7459	890.8766	1682.7690	841.8882
397.2445	199.1259	495.2214	248.1144	4	s	15	1679.6982	840.3528	1581.7213	791.3643
526.2871	263.6472	624.2640	312.6357	5	E	14	1512.6999	756.8536	---	---
639.3712	320.1892	737.3481	369.1777	6	L	13	1383.6573	692.3323	---	---
696.3927	348.7000	794.3696	397.6884	7	G	12	1270.5732	635.7903	---	---
795.4611	398.2342	893.4380	447.2226	8	V	11	1213.5518	607.2795	---	---
896.5088	448.7580	994.4857	497.7465	9	T	10	1114.4833	557.7453	---	---
1025.5514	513.2793	1123.5282	562.2678	10	E	9	1013.4357	507.2215	---	---
1162.6103	581.8088	1260.5872	630.7972	11	H	8	884.3931	442.7002	---	---
1261.6787	631.3430	1359.6556	680.3314	12	V	7	747.3342	374.1707	---	---
1390.7213	695.8643	1488.6982	744.8527	13	E	6	648.2658	324.6365	---	---
1447.7427	724.3750	1545.7196	773.3635	14	G	5	519.2232	260.1152	---	---
1562.7697	781.8885	1660.7466	830.8769	15	D	4	462.2017	231.6045	---	---
1659.8224	830.4149	1757.7993	879.4033	16	P	3	347.1748	174.0910	---	---
1762.8316	881.9195	1860.8085	930.9079	17	C	2	250.1220	125.5646	---	---
---	---	---	---	18	K	1	147.1128	74.0600	---	---

Observed M=2005.8800
Calculated M=2005.9068

Figure S58. MS/MS on the doubly charged 1004.45 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y ion series, with y15-H_3PO_4, only residue 1520 can be phosphorylated.

Endogenous Kal7

MS/MS of peptide RDGVEDGDpSQGDGSSQPDTISIASR

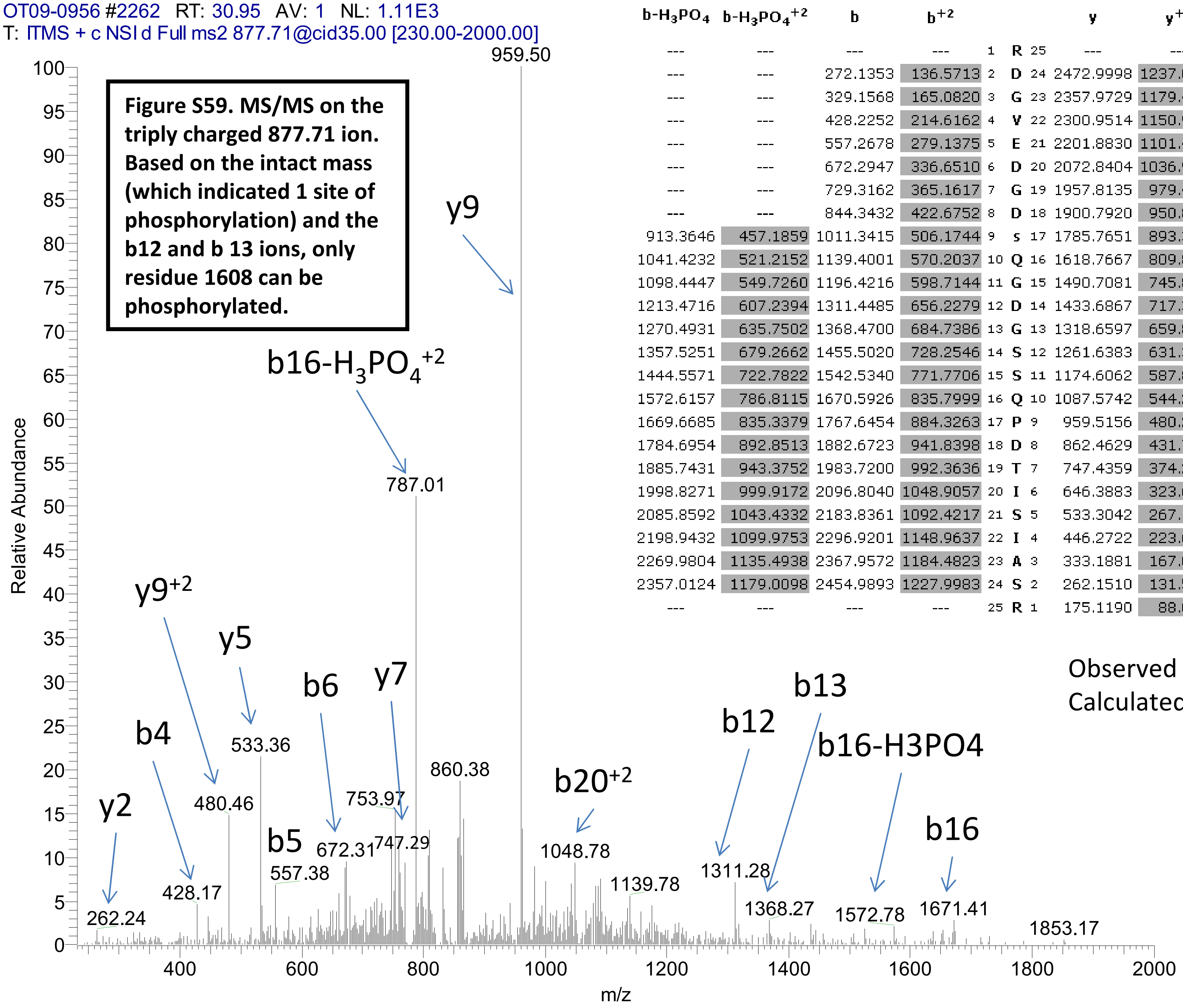


Figure S59. MS/MS on the triply charged 877.71 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the b12 and b 13 ions, only residue 1608 can be phosphorylated.

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	R	25	---	---	---	---
---	---	272.1353	136.5713	2	D	24	2472.9998	1237.0036	2375.0229	1188.0151
---	---	329.1568	165.0820	3	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	428.2252	214.6162	4	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	557.2678	279.1375	5	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	672.2947	336.6510	6	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	729.3162	365.1617	7	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	844.3432	422.6752	8	D	18	1900.7920	950.8996	1802.8151	901.9112
913.3646	457.1859	1011.3415	506.1744	9	s	17	1785.7651	893.3862	1687.7882	844.3977
1041.4232	521.2152	1139.4001	570.2037	10	Q	16	1618.7667	809.8870	---	---
1098.4447	549.7260	1196.4216	598.7144	11	G	15	1490.7081	745.8577	---	---
1213.4716	607.2394	1311.4485	656.2279	12	D	14	1433.6867	717.3470	---	---
1270.4931	635.7502	1368.4700	684.7386	13	G	13	1318.6597	659.8335	---	---
1357.5251	679.2662	1455.5020	728.2546	14	S	12	1261.6383	631.3228	---	---
1444.5571	722.7822	1542.5340	771.7706	15	S	11	1174.6062	587.8068	---	---
1572.6157	786.8115	1670.5926	835.7999	16	Q	10	1087.5742	544.2907	---	---
1669.6685	835.3379	1767.6454	884.3263	17	P	9	959.5156	480.2615	---	---
1784.6954	892.8513	1882.6723	941.8398	18	D	8	862.4629	431.7351	---	---
1885.7431	943.3752	1983.7200	992.3636	19	T	7	747.4359	374.2216	---	---
1998.8271	999.9172	2096.8040	1048.9057	20	I	6	646.3883	323.6978	---	---
2085.8592	1043.4332	2183.8361	1092.4217	21	S	5	533.3042	267.1557	---	---
2198.9432	1099.9753	2296.9201	1148.9637	22	I	4	446.2722	223.6397	---	---
2269.9804	1135.4938	2367.9572	1184.4823	23	A	3	333.1881	167.0977	---	---
2357.0124	1179.0098	2454.9893	1227.9983	24	S	2	262.1510	131.5791	---	---
---	---	---	---	25	R	1	175.1190	88.0631	---	---

Observed M=2628.0927
Calculated M=2628.0937

Endogenous Kal7

MS/MS of peptide DGVEDGDSQGDGpSSQPDTISIASR

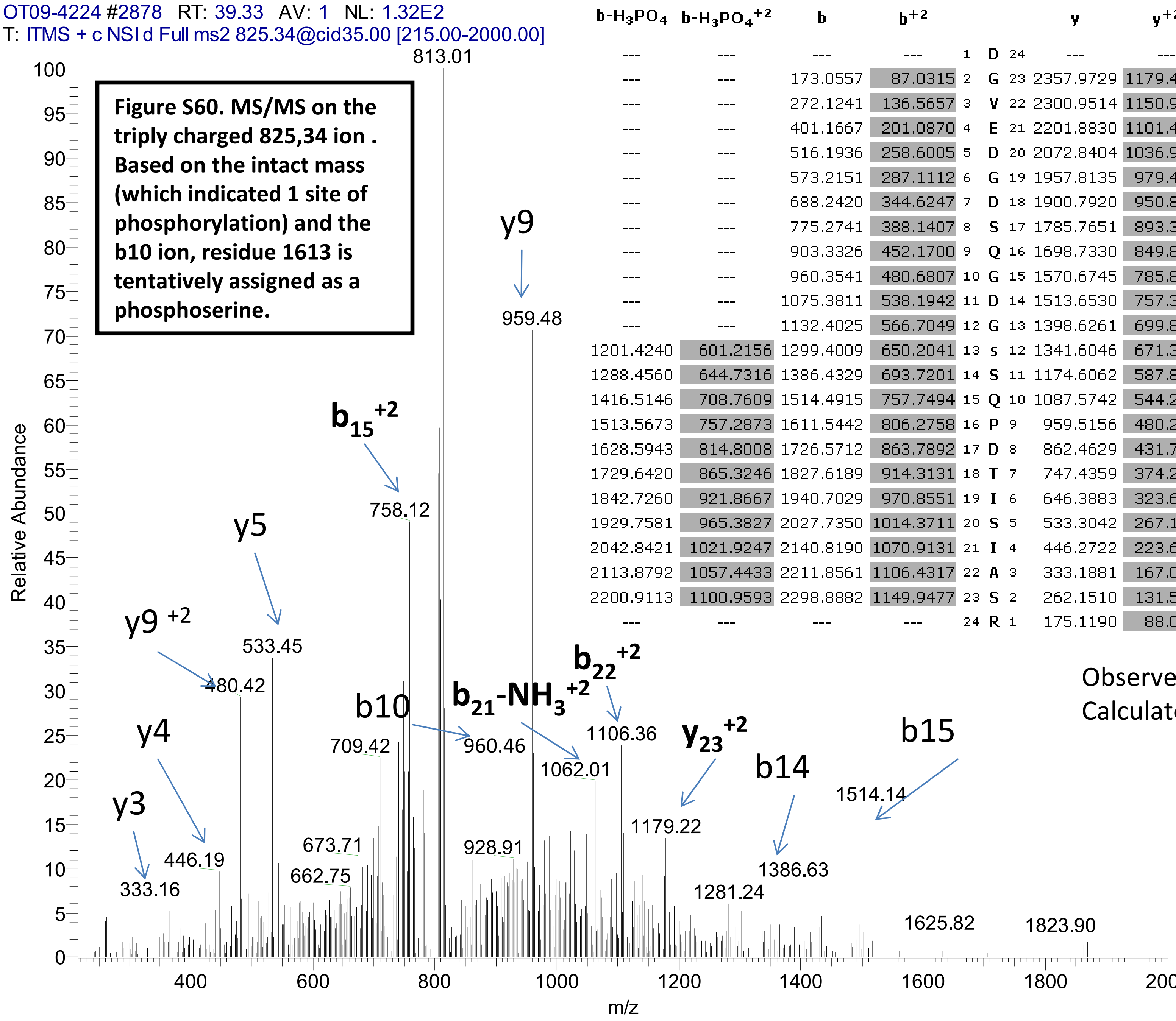


Figure S60. MS/MS on the triply charged 825,34 ion . Based on the intact mass (which indicated 1 site of phosphorylation) and the b10 ion, residue 1613 is tentatively assigned as a phosphoserine.

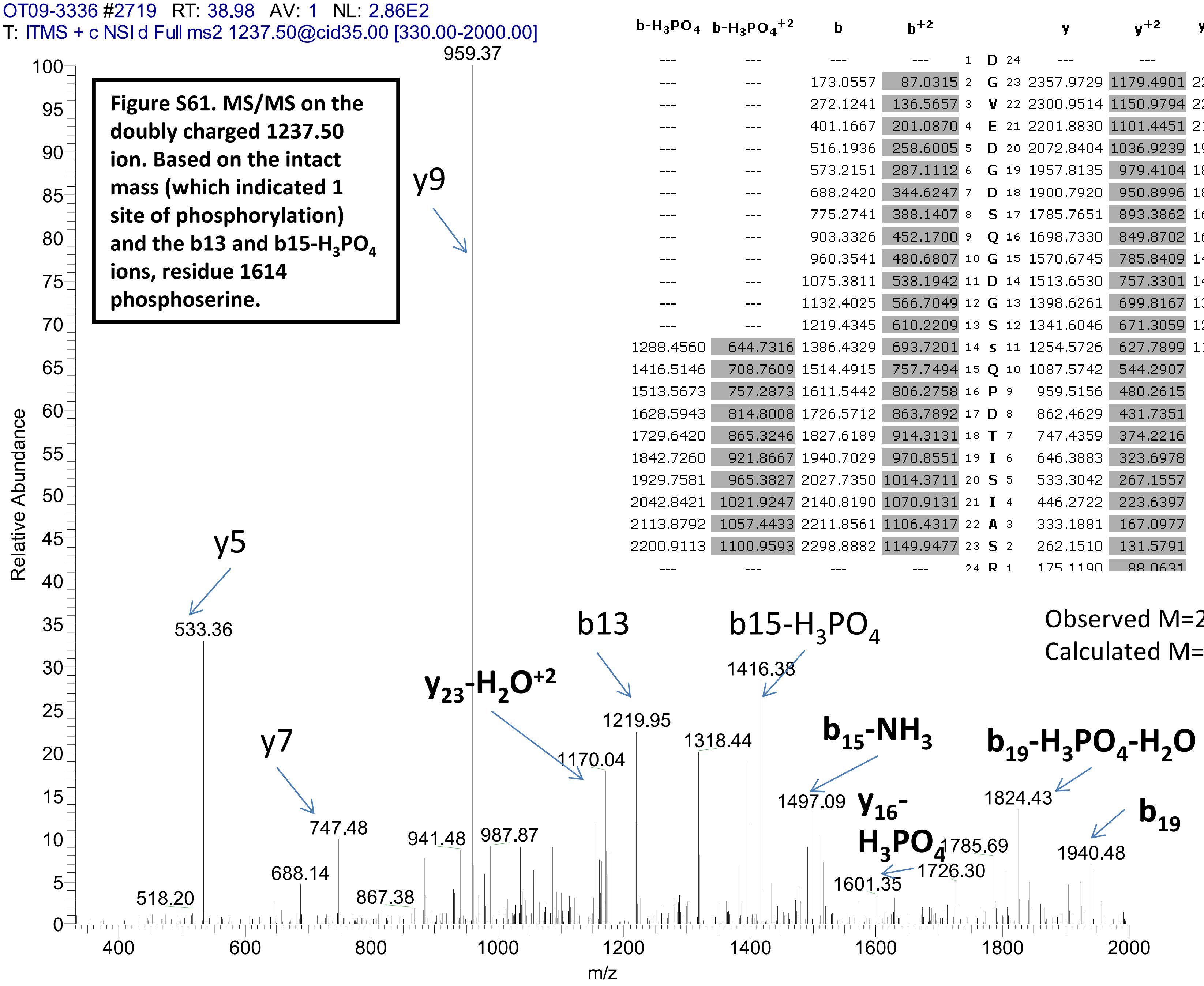
$b\text{-}H_3PO_4$	$b\text{-}H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	$y\text{-}H_3PO_4$	$y\text{-}H_3PO_4^{+2}$
---	---	---	---	1	D	24	---	---	---	---
---	---	173.0557	87.0315	2	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	272.1241	136.5657	3	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	401.1667	201.0870	4	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	516.1936	258.6005	5	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	573.2151	287.1112	6	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	688.2420	344.6247	7	D	18	1900.7920	950.8996	1802.8151	901.9112
---	---	775.2741	388.1407	8	S	17	1785.7651	893.3862	1687.7882	844.3977
---	---	903.3326	452.1700	9	Q	16	1698.7330	849.8702	1600.7562	800.8817
---	---	960.3541	480.6807	10	G	15	1570.6745	785.8409	1472.6976	736.8524
---	---	1075.3811	538.1942	11	D	14	1513.6530	757.3301	1415.6761	708.3417
---	---	1132.4025	566.7049	12	G	13	1398.6261	699.8167	1300.6492	650.8282
1201.4240	601.2156	1299.4009	650.2041	13	s	12	1341.6046	671.3059	1243.6277	622.3175
1288.4560	644.7316	1386.4329	693.7201	14	S	11	1174.6062	587.8068	---	---
1416.5146	708.7609	1514.4915	757.7494	15	Q	10	1087.5742	544.2907	---	---
1513.5673	757.2873	1611.5442	806.2758	16	P	9	959.5156	480.2615	---	---
1628.5943	814.8008	1726.5712	863.7892	17	D	8	862.4629	431.7351	---	---
1729.6420	865.3246	1827.6189	914.3131	18	T	7	747.4359	374.2216	---	---
1842.7260	921.8667	1940.7029	970.8551	19	I	6	646.3883	323.6978	---	---
1929.7581	965.3827	2027.7350	1014.3711	20	S	5	533.3042	267.1557	---	---
2042.8421	1021.9247	2140.8190	1070.9131	21	I	4	446.2722	223.6397	---	---
2113.8792	1057.4433	2211.8561	1106.4317	22	A	3	333.1881	167.0977	---	---
2200.9113	1100.9593	2298.8882	1149.9477	23	S	2	262.1510	131.5791	---	---
---	---	---	---	24	R	1	175.1190	88.0631	---	---

Observed M=2471.9883
Calculated M=2471.9926

Endogenous Kal7

MS/MS of peptide DGVEDGDSQGDGSpSQPDTISIASR

Figure S61. MS/MS on the doubly charged 1237.50 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the b13 and b15-H_3PO_4 ions, residue 1614 phosphoserine.



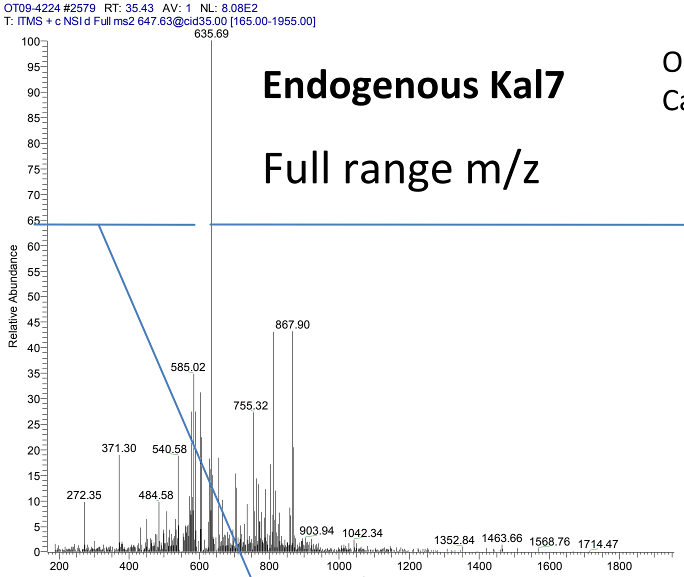
b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	D	24	---	---	---	---
---	---	173.0557	87.0315	2	G	23	2357.9729	1179.4901	2259.9960	1130.5016
---	---	272.1241	136.5657	3	V	22	2300.9514	1150.9794	2202.9745	1101.9909
---	---	401.1667	201.0870	4	E	21	2201.8830	1101.4451	2103.9061	1052.4567
---	---	516.1936	258.6005	5	D	20	2072.8404	1036.9239	1974.8635	987.9354
---	---	573.2151	287.1112	6	G	19	1957.8135	979.4104	1859.8366	930.4219
---	---	688.2420	344.6247	7	D	18	1900.7920	950.8996	1802.8151	901.9112
---	---	775.2741	388.1407	8	S	17	1785.7651	893.3862	1687.7882	844.3977
---	---	903.3326	452.1700	9	Q	16	1698.7330	849.8702	1600.7562	800.8817
---	---	960.3541	480.6807	10	G	15	1570.6745	785.8409	1472.6976	736.8524
---	---	1075.3811	538.1942	11	D	14	1513.6530	757.3301	1415.6761	708.3417
---	---	1132.4025	566.7049	12	G	13	1398.6261	699.8167	1300.6492	650.8282
---	---	1219.4345	610.2209	13	S	12	1341.6046	671.3059	1243.6277	622.3175
1288.4560	644.7316	1386.4329	693.7201	14	s	11	1254.5726	627.7899	1156.5957	578.8015
1416.5146	708.7609	1514.4915	757.7494	15	Q	10	1087.5742	544.2907	---	---
1513.5673	757.2873	1611.5442	806.2758	16	P	9	959.5156	480.2615	---	---
1628.5943	814.8008	1726.5712	863.7892	17	D	8	862.4629	431.7351	---	---
1729.6420	865.3246	1827.6189	914.3131	18	T	7	747.4359	374.2216	---	---
1842.7260	921.8667	1940.7029	970.8551	19	I	6	646.3883	323.6978	---	---
1929.7581	965.3827	2027.7350	1014.3711	20	S	5	533.3042	267.1557	---	---
2042.8421	1021.9247	2140.8190	1070.9131	21	I	4	446.2722	223.6397	---	---
2113.8792	1057.4433	2211.8561	1106.4317	22	A	3	333.1881	167.0977	---	---
2200.9113	1100.9593	2298.8882	1149.9477	23	S	2	262.1510	131.5791	---	---
---	---	---	---	24	R	1	175.1190	88.0631	---	---

Observed M=2471.9766
Calculated M=2471.9926

MS/MS of peptide TSQNTVEpSDKDGNLVPR

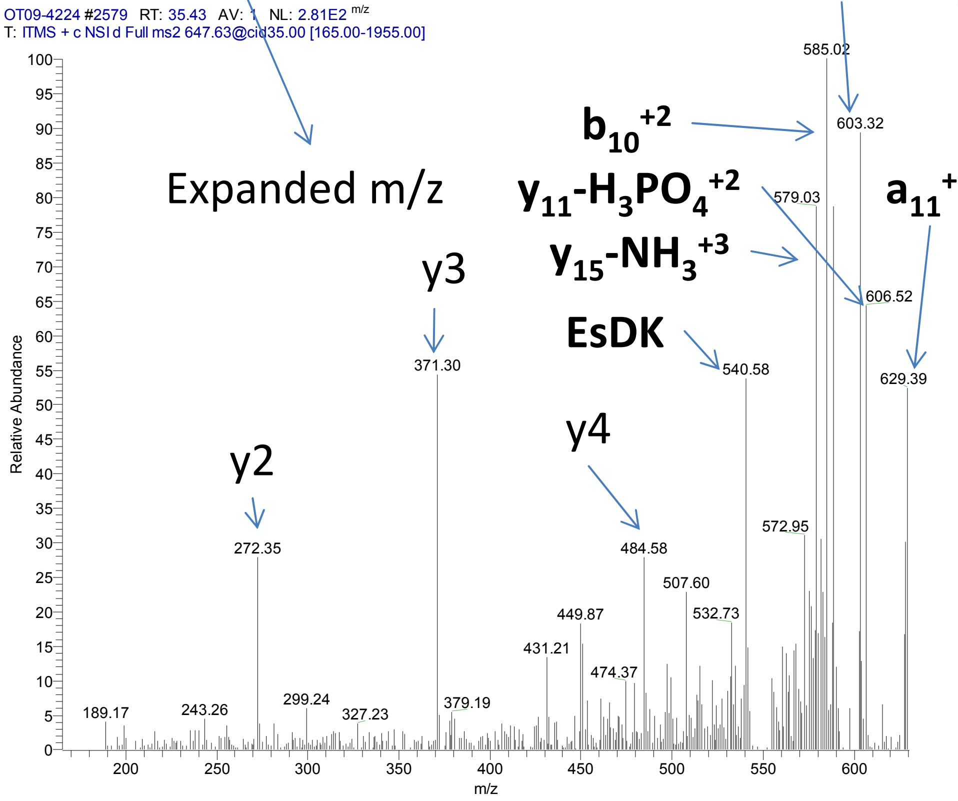
Endogenous Kal7

Full range m/z



Observed M=1938.8669
Calculated M=1938.8684

b-H_3PO_4	b-$H_3PO_4^{+2}$	b	b^{+2}				y	y^{+2}	y-H_3PO_4	y-$H_3PO_4^{+2}$
---	---	---	---	1	T	17	---	---	---	---
---	---	189.0870	95.0471	2	S	16	1838.8280	919.9176	1740.8511	870.9292
---	---	317.1456	159.0764	3	Q	15	1751.7960	876.4016	1653.8191	827.4132
---	---	431.1885	216.0979	4	N	14	1623.7374	812.3723	1525.7605	763.3839
---	---	532.2362	266.6217	5	T	13	1509.6945	755.3509	1411.7176	706.3624
---	---	631.3046	316.1559	6	V	12	1408.6468	704.8270	1310.6699	655.8386
---	---	760.3472	380.6772	7	E	11	1309.5784	655.2928	1211.6015	606.3044
829.3686	415.1880	927.3455	464.1764	8	s	10	1180.5358	590.7715	1082.5589	541.7831
944.3956	472.7014	1042.3725	521.6899	9	D	9	1013.5374	507.2724	---	---
1072.4905	536.7489	1170.4674	585.7374	10	K	8	898.5105	449.7589	---	---
1187.5175	594.2624	1285.4944	643.2508	11	D	7	770.4155	385.7114	---	---
1244.5390	622.7731	1342.5158	671.7616	12	G	6	655.3886	328.1979	---	---
1358.5819	679.7946	1456.5588	728.7830	13	N	5	598.3671	299.6872	---	---
1471.6659	736.3366	1569.6428	785.3251	14	L	4	484.3242	242.6657	---	---
1570.7344	785.8708	1668.7113	834.8593	15	V	3	371.2401	186.1237	---	---
1667.7871	834.3972	1765.7640	883.3856	16	P	2	272.1717	136.5895	---	---
---	---	---	---	17	R	1	175.1190	88.0631	---	---



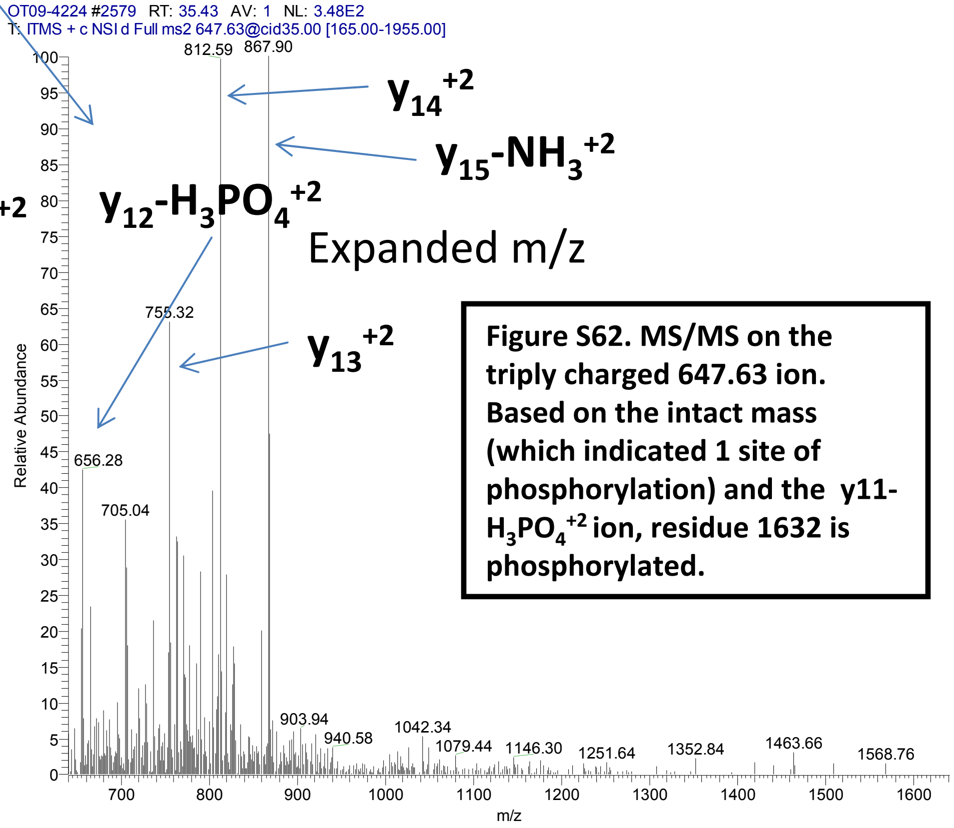


Figure S62. MS/MS on the triply charged 647.63 ion. Based on the intact mass (which indicated 1 site of phosphorylation) and the y11-$H_3PO_4^{+2}$ ion, residue 1632 is phosphorylated.