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Figure S2. Detection of ERG-derived peptides in NCI-H660 vs. VCaP cell lines.















Figure S3. Detection of ERG-derived peptides in seven TMPRSS2-ERG fusion positive prostate tumor tissues

Figure S4

3_type_II_met1/1-462	1 HIQT VPDPAAHIKEALS VYSEDQSLFECAYGT PHLAKTENTASSSSDYGQT SKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1
2_type_V_met1/1-462	1 HIQTVPDPAAHIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNI	ITTNERRVI VPA	DPT
2_type_I_met1/1-462	1 HI QT VPDPAAHI KEALSV VSEDQSLFECAY GT PHLAKTENT ASSSSDY GQT SKHSPRVPQQDWL SQPPARVT I KHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA)PT
94449/1-462	1 HIQTYPDPAAHIKEALSYVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)PT
91243428/1-486	1 HI OT VPDPAAHI KEALS VYSED OSLFECAY GTPHLAKTENT ASSSS DY GOT SKIISPRVP OQDWL SOPPARVT I KNECNPSOVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA	ρPT
91136154/1-486	1 HIQTVPDPAAHIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA)P1
4_type_VIII_met1/1-423	1 NTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA)PT
4_type_VI_met2/1-423	1 HTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNI	ITTNERRVI VPA	ΟPT
3_type_II_met2/1-423	1 HTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA	ĴΡΊ
2_type_V_met2/1-423	1 HTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA	0P1
2_type_I_met2/1-423	1 HTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA)P1
4_type_III_met1/1-423	1 HTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA	ΟPT
4_type_III_met2/1-409	1 HISPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA)P1
4_type_VIII_met2/1-409	1 HSPRVPQQDWLSQPPARVTIKHECNPSQVNGSR <mark>N</mark>	SPDECSVAKGGK	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1
91136155/1-387	1		IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1
5_type_VII_met2/1-354	1		<mark>HNY G</mark> S	YNEEKHNPPPNN	ITTNERRVI VPA)P1
5_type_IV_met2/1-354	1		<mark>HNY G</mark> S	YNEEKHNPPPNN	ITTNERRVI VPA)P1
5_type_VII_met1/1-363	1		IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVIVPA)P1
5_type_IV_met1/1-363	1		IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1
91243429/1-363	1		IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVIVPA)P1
99090381877/1-455	1 · · · · · · <mark>HASTIK</mark> EALSVVSEDQSLFECAYGTPHLAKTEHTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVIVPA)P1
82918/1-479	1 · · · · · · <mark>HASTIK</mark> EALSVVSEDQSLFECAYGTPHLAKTEHTASSSSDYGQTSKHSPRVPQQDWLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1
4_type_VI_met1/1-454	1 · · · · · · · HALNSEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVIVPA)P1
99999381879/1-456	1 MASTIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1
99999381881/1-463	1 HIQTVPDPAAHIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA)P1
91243432/1-317	1 HIQTVPDPAAHIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA <mark>r</mark>	JP1
99090415659/1-172	1 MASTIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGK	IVGSPDTVGHNYGS	YHEEKHHPPPNH	ITTNERRVI VPA	
/ 1- 325	1 HIQTVPDPAAHIKEALSVVSEDQSLFECAYGTPHLAKTENTASSSSDYGQTSKNSPRVPQQDWLSQPPARVTIKNECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNI	ITTNERRVIVPA)P1
/ 1- 220	1HTASSSSDYGQTSKHSPRVPQQDwLSQPPARVTIKHECNPSQVNGSRN	SPDECSVAKGGKI	IVGSPDTVGHNYGS	YNEEKHNPPPNN	ITTNERRVI VPA)P1



ROWLEWAVKEYGLEDVITLLEONTDGKELCKNTKDDEORLTPSYNADTLLSHLH TPLPHLTSDDVDKALONSPRLMHARNTG PYOTI GPTSSRI ANPONTO EPPRRSAWT GHGHPT POSKIGT VI APHTI SENSOAVDD TPLPHLTSDDVDKALONSPRLHHARNTGGAAELEPNTSWPEATORITTREGTKTPLCDLFIERHPRCPAEIRALSHVIORELIPELKPVPDSLILPLLIWRLNPLKPFHSKTTLKELRA {VROWLEWAVKEYGLPDVNILLFONIDGKELCKMTKDDFORLTPSYNADILLSHLHYL HVROWLEWAVKEYGLPDVNILLEONIDGKELCKWTKDDFORLTPSYNADILLSHLHYI RETPL PHLT SDDVDKALONSPRLIHABNT GGAAFI FPNT SVY PEAT OR ITT RPVS

{VROWLEWAVKEYGLPDVNILLFONIDGKELCKHTKDDFORLTPSYNADILLSHLHYL

HVROWLEWAVKEYGLPDVNILLFONIDGKELCKHTKDDFORLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALONSPRLHHARNT

HVROWLEWAVKEYGLPDVNILLFONIDGKELCKHTKDDFORLTPSYNADILLSHLHYLRETPLPHL<u>TSDDVDKALONSPRLHHARNT</u>G

HVROWLEWAVKEY GLPDVNILLFONIDGKELCKNTKDDFORLTPSYNADILLSHLHYLRETPLPHLTSDDVDKALONSPRLNHARNTG

TPLPHLTSDDVDKALONSPRLMHA

TEPNTSWYPEATORITTRPDLPYEPPRRSAWTGHGHPTPOSK



/OILGPTSSRLANPG<mark>S</mark>

(OTLIGPTSSRLANPG<mark>S</mark>

E13

I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNI NTKVHGKRYAYKFDFHGI AOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGI AOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL 0I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDE VARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL (OILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL 010LW0FLLELLSDSSNSSCITWEGTNGEFKHTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIA0AL0PHPPESSLYKYPSDLPYNGSYHAHP0KNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL 501 OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL 2YOILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKEDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL PYOILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL PYOILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL OILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL 501 OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL 501 OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL GOI OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGI AOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGI YPNTRLPTSHNPSHL YOILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL PYOILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL PYOILGPTSSRLANPGSGOIOLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKEDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL DI OLWOELLELLSDSSNSSCITWEGTNGEEKNTDPDEVARRWGERKSKPNINYDKLSRALRYYYDKNINTKVHGKRYAYKEDEHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKINNEVAPHPPALPYTSSSEEAAPNPYWNSPTGGIYPNTRLPTSHNPSHL OI OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAPNPYWNSPTGGIYPNTRLPTSHNPSHL I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDEVARRNGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGIAOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGIYPNTRLPTSHNPSHL I OLWOFLLELLSDSSNSSCITWEGTNGEFKNTDPDE VARRWGERKSKPNNNYDKLSRALRYYYDKNINTKVHGKRYAYKFDFHGI AOALOPHPPESSLYKYPSDLPYNGSYHAHPOKNNFVAPHPPALPVTSSSFFAAPNPYWNSPTGGI YPNTRLPTSHNPSHL OT LGPT SSRLANPGSGOT OLWOFL LELL SDSSNSSCT WEGT NGEFKNT OPDEVARR/ GERKSKPNINYDKL SRAL RYYYDKNT NT KVHGKRYAY KEDEHGT AOAL OPHPPESSLY KYPSDL PYNGSYHAHPOKNNEVAPHPPAL PYT SSSFFAAPNPYWNSPT GGT YPNT RL PT SHIPSHL

Figure S4. Mapping of the peptides that have been selected for SRM analysis to various potential TMPRSS2-ERG fusion protein products. Each peptide included in the final multiplexed PRISM-SRM assay (Table 1) is represented as a bar on top of the aligned sequences of various putative protein products of the reported TMPRSS2-ERG gene fusion events. Peptides with sequences that skipped at least one exon are shown in bars that are connected using a solid line. The bars representing peptides detected in prostate cancer cell lines or tumor tissues in this study are grey shadowed. The exons are color coded. Dotted lines indicate sequence gap. Take the two mutually exclusive peptides as an example, ITTRPDLPYEPPR has sequences from both exons 10 (red) and 11 (purple), while NTDLPYEPPR has sequences from both exons 9 (blue) and 11 (purple).



Figure S5. Calibration curves of six ERG-derived peptides.



Figure S6. Abundance of all 7 detected ERG peptides in TMPRSS2-ERG fusion positive cell lines and tissues. The abundance of these peptides was represented by $amol/\mu g$ of total protein. Each value represents the mean and SD of three replicate measurements.



Figure S7. ERG peptides detected in TMPRSS2-ERG fusion positive tissues. The abundance of these peptides was represented by amol/ μ g of total protein. Each value represents the mean and SD of three replicate measurements.

Sample ID in the				
manuscript	Original Sample Name	Disease State	Tumor location ²	ETS status ³
PT1	WA13	CRPC ¹	Lung	ERG^+
PT2	WA39	CRPC	Lymph node	ERG^+
PT3	WA40	CRPC	Liver	ERG^+
PT4	WA49	CRPC	Lower periaortic lymph node	ERG^+
PT5	WA53	CRPC	Liver	ERG^+
PT6	STID 10162 B55A	Localized PC	Prostate	ERG^+
PT7	STID 10060 B53A	Localized PC	Prostate	ERG^+
NT1	WA32	CRPC	Spleen	No ETS
NT2	WA33	CRPC	Periaortic lymph node	No ETS
NT3	WA35	CRPC	Mesentery	No ETS
NT4	WA42	CRPC	Left adrenal	No ETS
NT5	WA51	CRPC	Bone marrow	No ETS

Table S1: Prostate cancer tissue specimens used for PRISM-SRM analysis.

¹CRPC: Castrate resistant metastatic prostate cancer. ²Anatomic location of tissue. ³Rearrangement in ETS.

Table S2. Selected transitions and optimal collision energy of each transition for SRM analysis ofERG protein. Bold red amino acids represent isotopically labeled residues. Cysteines arecarbamidomethylated. CE, collision energy.

Dontido Comunica	Devention	Transition	1	Transition	2	Transition 3		
Peptide Sequence	Parent Ion	Product ion 1	CE1	Product ion 2	CE2	Product ion 3	CE3	
MIQTVPDPAAHIK	474.26+++	424.73++	14	636.38+	17	848.46+	15	
MIQTVPDPAAHI <mark>K</mark>	476.93+++	428.74++	14	644.40+	17	856.48+	15	
MASTIK	325.68++	237.63++	21	448.28+	9	519.31+	15	
MASTIK	329.69++	241.64++	21	456.29+	9	527.33+	15	
TEMTASSSSDYGQTSK	840.36++	1059.46+	23	1146.49+	28	1217.53+	28	
TEMTASSSSDYGQTS K	844.36++	1067.47+	23	1154.51+	28	1225.54+	28	
MTASSSSDYGQTSK	725.31++	972.43+	26	1146.49+	27	1217.53+	27	
MTASSSSDYGQTS <mark>K</mark>	729.32++	980.44+	26	1154.51+	27	1225.54+	27	
ME <u>C</u> NPSQVNGSR	689.80++	532.28+	25	844.43+	22	958.47+	25	
ME <u>C</u> NPSQVNGS <mark>R</mark>	694.80++	542.29+	25	854.44+	22	968.48+	25	
MVGSPDTVGMNYGSYMEEK	1047.94++	375.17+	33	1120.46+	30	1308.52+	33	
MVGSPDTVGMNYGSYMEE <mark>K</mark>	1051.95++	375.17+	33	1128.48+	30	1316.54+	33	
MNYGSYMEEK	626.25++	843.36+	21	1006.42+	21	1120.46+	21	
MNYGSYMEE <mark>K</mark>	630.26++	851.37+	21	1014.43+	21	1128.48+	21	
HMPPPNMTTNER	712.82++	530.25++	29	578.77+	23	1156.54+	23	
HMPPPNMTTNE <mark>R</mark>	717.83++	535.25++	29	583.78+	23	1166.55+	23	
VIVPADPTLWSTDHVR	602.66+++	531.94+++	15	747.87++	15	797.40++	15	
VIVPADPTLWSTDHV <mark>R</mark>	605.99+++	535.27+++	15	752.88++	15	802.41++	15	
VIVPADLPYEPPR	733.41++	577.80++	21	758.38+	29	1154.58+	23	
VIVPADLPYEPP <mark>R</mark>	738.41++	582.80++	21	768.39+	29	1164.59+	23	
ITTRPDLPYEPPR	518.95++	379.70++	14	670.85++	16	684.37+	20	
ITTRPDLPYEPP <mark>R</mark>	522.28+++	384.70++	14	675.86++	16	684.37+	20	
ITTRPAAQPSPSTVPK	550.98+++	406.73++	15	812.45+	15	839.47+	17	
ITTRPAAQPSPSTVP <mark>K</mark>	553.65+++	410.74++	15	820.47+	15	839.47+	17	
NTDLPYEPPR	601.30++	369.22+	21	758.38+	16	986.49+	16	
NTDLPYEPP <mark>R</mark>	606.30++	379.23+	21	768.39+	16	996.50+	16	
ITTRPGTK	437.26++	380.72++	17	659.38+	20	760.43+	19	
ITTRPGT <mark>K</mark>	441.27++	384.73++	17	667.40+	20	768.45+	19	
ITTRPVSYR	364.88+++	439.75++	12	490.27++	13	621.34+	18	
ITTRPVSY <mark>R</mark>	368.21+++	444.75++	12	495.27++	13	631.34+	18	
ALSHVIQR	308.52+++	326.70++	12	370.21++	10	515.33+	14	
ALSHVIQR	311.85+++	331.70++	13	375.22++	10	525.34+	14	

Table S3. Summary of peak area ratios and CV values for the detected peptides in this study. Ratio represents light peptide to heavy peptide peak area ratio.

CV, or coefficient of variation, is calculated by dividing the standard deviation by the mean.

Peptide	VCaP		NCI-H660		PT1		PT2		PT3		PT4		PT5		PT6		PT7	
	Ratio	CV	Ratio	CV	Ratio	CV	Ratio	cv	Ratio	CV	Ratio	CV	Ratio	CV	Ratio	cv	Ratio	CV
TEMTASSSSDYGQTSK																	0.0601	8.3%
MECNPSQVNGSR	0.0376	9.6%																
MVGSPDTVGMNYGSYMEEK	0.131	9.5%			0.0752	1.5%	0.0159	22.7%			0.0233	14.4%	0.0838	10.8%	0.0307	9.3%	0.116	12.8%
HMPPPNMTTNER	0.260	6.1%	0.0294	12.3%	0.255	7.7%	0.0464	13.3%	0.0162	8.2%	0.0281	12.9%	0.165	12.5%	0.121	9.7%	0.165	11.0%
VIVPADPTLWSTDHVR	0.145	2.3%	0.0197	3.9%	0.0098	2.7%	0.00027	11.2%			0.0038	39.8%	0.0062	9.1%	0.0150	9.3%	0.0071	4.1%
ITTRPDLPYEPPR	0.0147	3.5%			0.0062	10.4%	0.0011	13.6%										
NTDLPYEPPR	0.0035	10.2%			0.0052	8.5%	0.0014	3.3%			0.00049	5.7%						