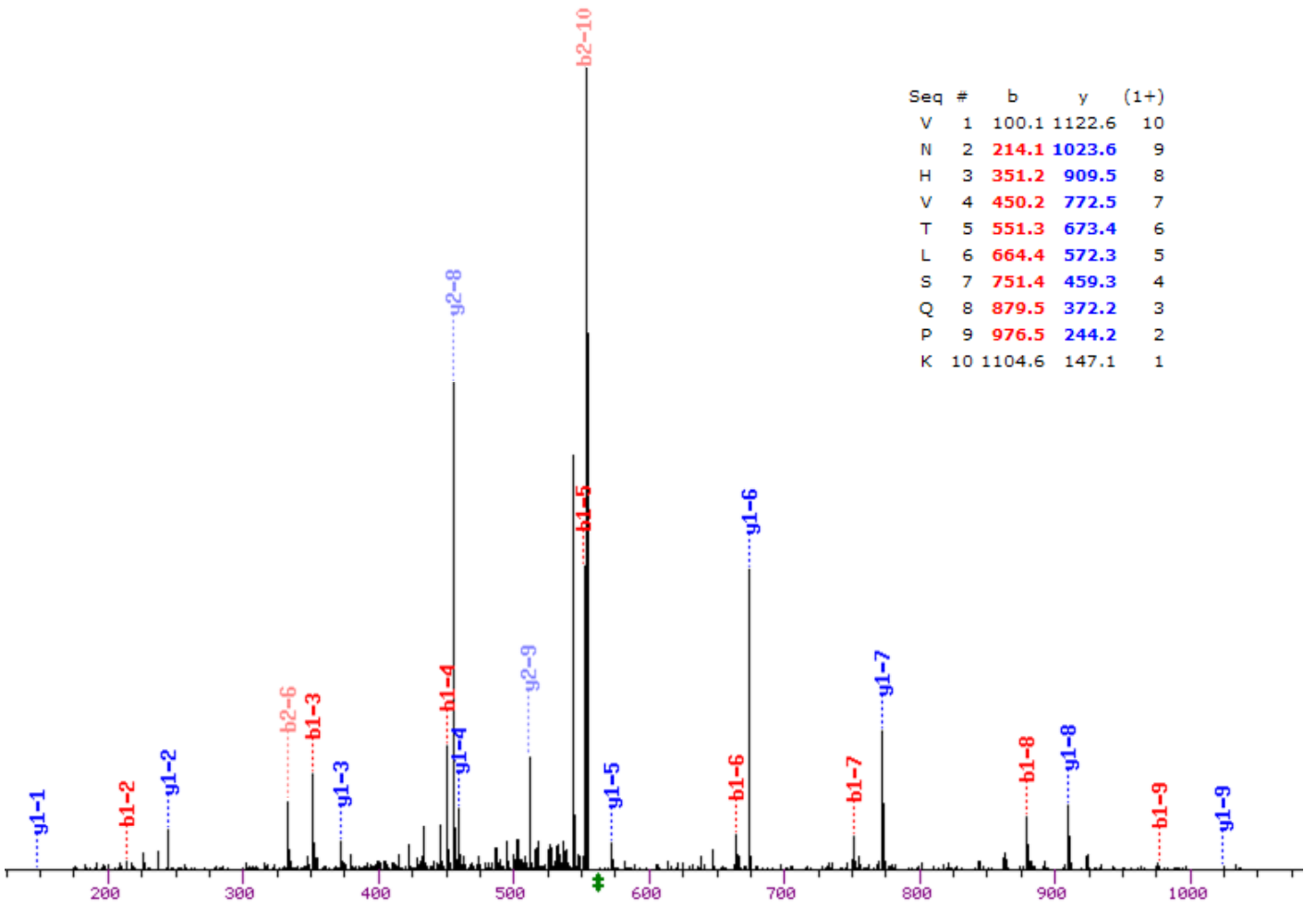
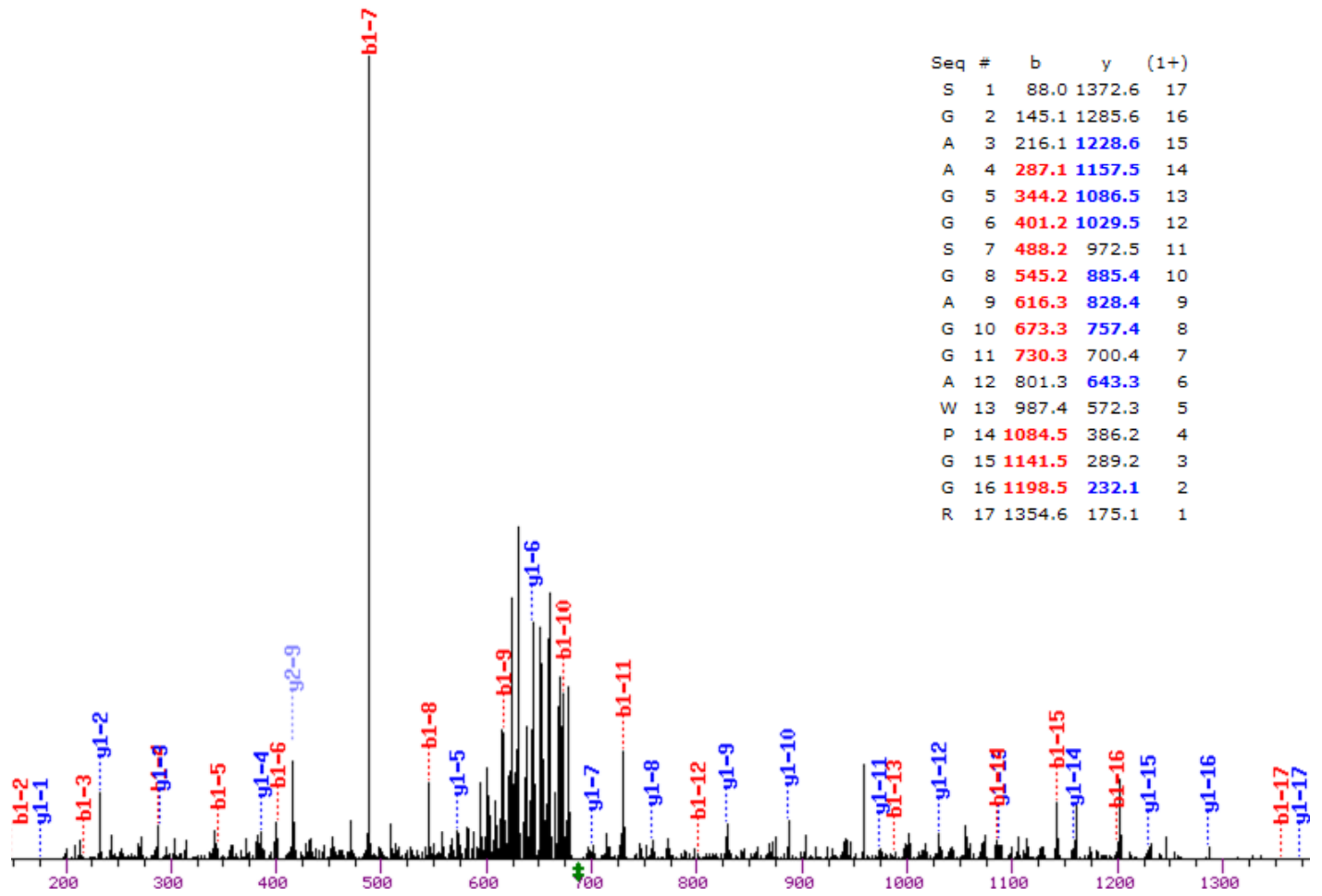


Supplemental Figure 1. MS/MS spectra of single-peptide proteins listed in Table 1.

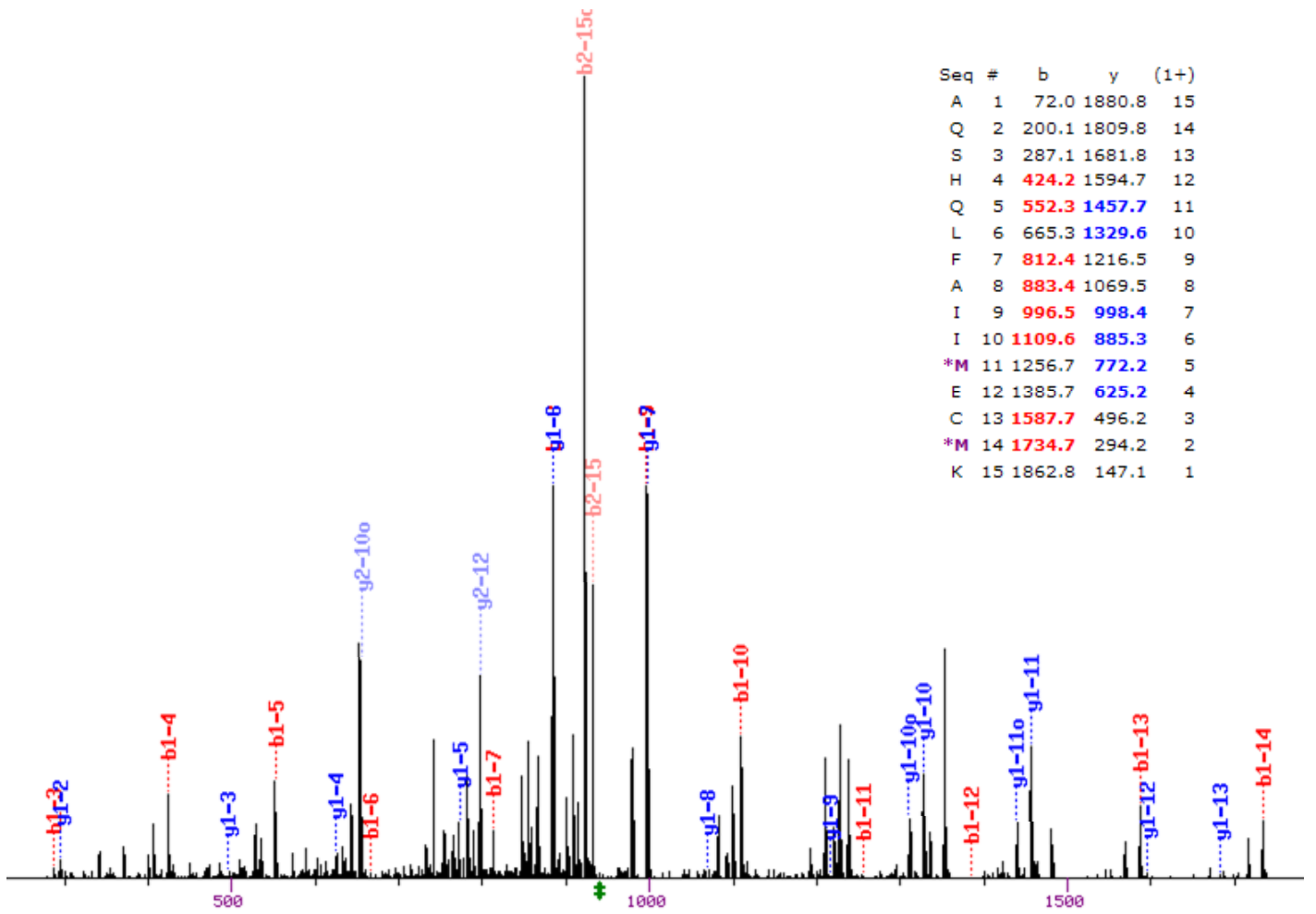
A. Beta-2-microglobulin (B2M)



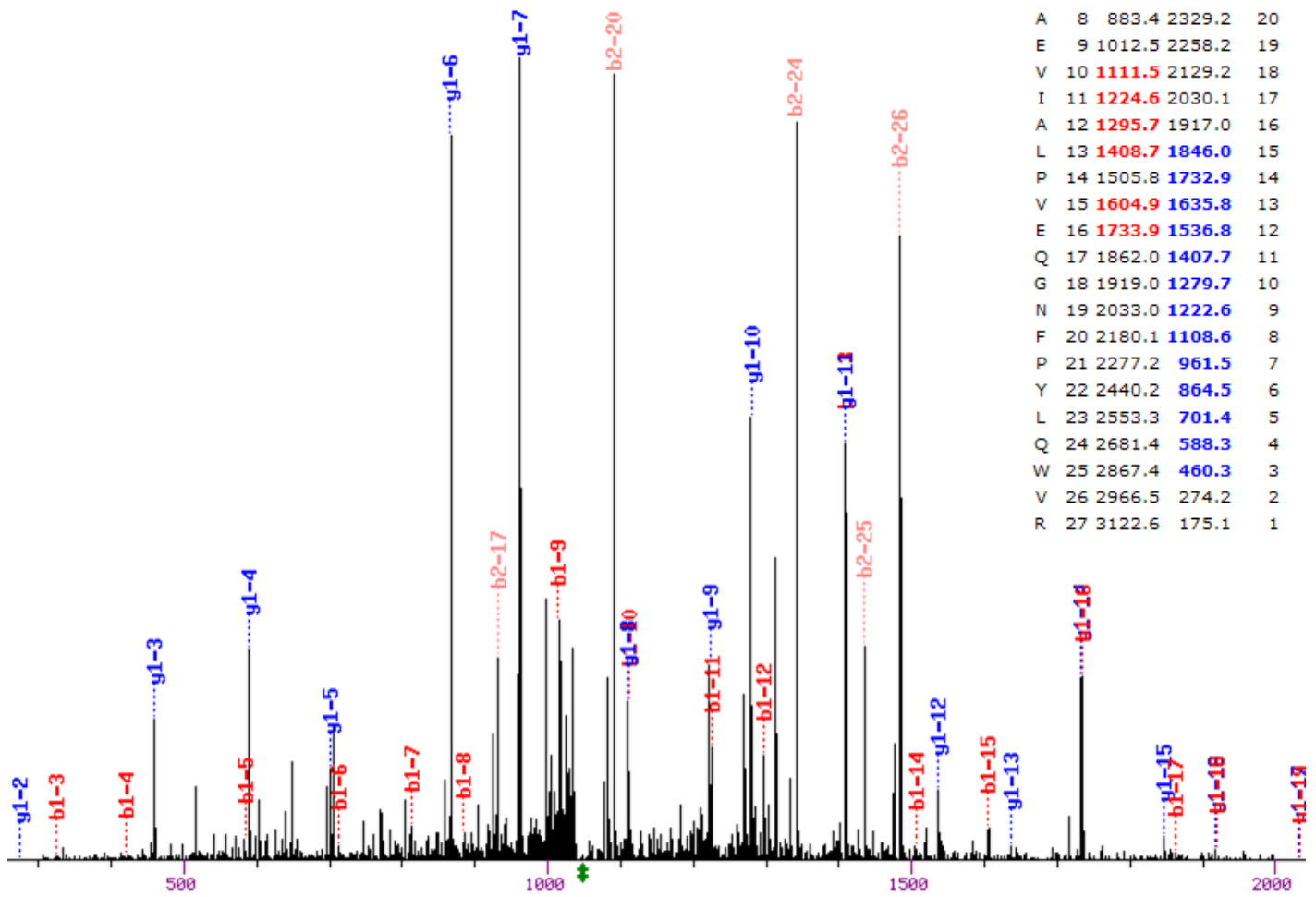
B. Homeobox protein HMX1



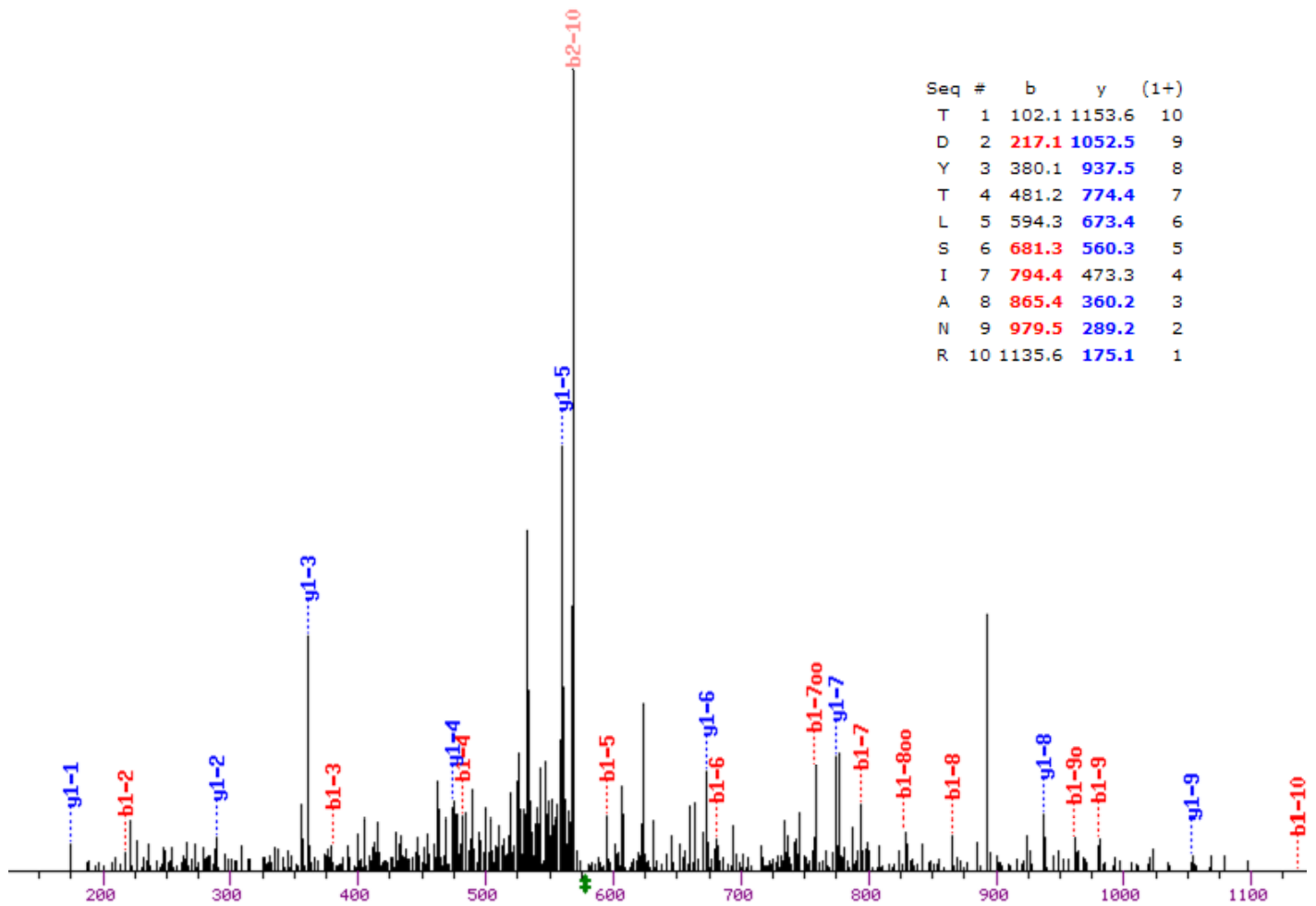
C. Melastatin 1 (TRPM1)



D. Protein CutA



E. SERPINB12 protein



Supplemental Table 1. Selected human proteins/peptides shed by ovarian TOV-112D tumors into SCID mouse blood

No.	Uniprot ID	Name	Description	Sequence	Spectrum	Sequence	MolWt	pI	ObsM+H+	ppm	z	XCorr	DeltCN	SpR	Sequence
				Count	Count	Coverage									
1	Q14624	ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4	10	2953	13.2	103358	7	877.444	-0.9	2	2.5315	0.0188	12	K.GSEMVVAGK.L
				1452.7358	2	2	5.0242	0.3996	1	K.NGDIYSLTVDSR.V					
				933.543	2.8	2	1.8485	0.0218	2	K.NVVFVIDK.S					
				1811.959	5.1	2	4.8543	0.2937	1	K.SPEQQETVLDGNLIIR.Y					
				1256.591	2.3	2	2.4519	0.2073	1	K.YIFHNFMER.L					
				1722.839	1.3	2	4.4757	0.3792	1	R.ANTVQEATFQM*ELPK.K					
				1017.5475	-0.1	2	3.0339	0.3329	2	R.FAHTVVTSR.V					
				1204.6698	1.1	3	3.3685	0.1134	2	R.FKPTLSQQQK.S					
				1144.623	1.9	2	3.7916	0.414	1	R.GPDVLTATVSGK.L					
				2415.1867	3.3	3	3.4237	0.2848	1	R.QGPNLLSDPEQGVEVTGQYER.E					
2	P02647	APOA1	Apolipoprotein A-I	10	3014	43.4	30778	5.8	1215.624	2	2	3.16	0.3214	1	K.ATEHLSTLSEK.A
				1235.69265	3.6	2	3.7731	0.3692	1	K.DLATVYVDVLK.D					
				1612.789	2.3	2	4.5011	0.4187	1	K.LLDNWDVSTVTFK.L					
				813.447	0.7	2	2.1938	0.0486	40	K.PALEDLR.Q					
				1252.62865	6.3	2	2.3686	0.2111	19	K.VQPYLDDFQK.K					
				1386.7208	4.1	2	4.8366	0.4728	1	K.VSFLSALEEYTK.K					
				1400.674	3.4	2	4.0743	0.4676	1	R.DYVSQFEGSALGK.Q					
				1932.939	2.7	2	4.4915	0.4571	1	R.EQLGPVTQEFWDNLEK.E					
				1230.7147	4.5	2	2.9204	0.203	1	R.QGLLPVLESFK.V					
				1301.651	2	2	3.1564	0.456	1	R.THLAPYSDELK.R					
3	P61769	B2M	Beta-2-microglobulin	1	9	8.4	13715	6.5	1122.6293	2.4	2	2.8905	0.1352	1	R.VNHVTLSPQK.I
4	P02766	TTR	Transthyretin	4	19	47.6	15887	5.7	1394.629	4.8	2	4.1445	0.4115	1	K.AADDTWEPFASGK.T
				2455.15565	1.9	3	6.6073	0.5253	1	K.TSESGELHGLTTEEFVEGIYK.V					
				1366.764	3.7	2	3.8033	0.3815	1	R.GSPAINVAVHVFR.K					
				2360.24865	4.4	2	5.1587	0.4571	1	R.YTIAALLSPYSYSTAVVTNPK.E					
5	P02787	TF	Transferrin	5	8	9.3	77050	7.1	2070.03365	2.2	2	5.0676	0.2878	1	K.EDLIWELLNQAQEHFGK.D
				1629.81865	1.7	2	3.2168	0.3047	1	K.EDPQTFYYAVAVVK.K					
				1273.648	-4.3	2	3.2423	0.365	1	K.HSTIFENLANK.A					
				1249.607	0.9	2	2.6172	0.191	6	K.SASDLTWDNLK.G					
				1581.757	-0.5	2	3.6935	0.2871	1	R.DQYELLCLDNTR.K					
6	P07195	LDHB	L-lactate dehydrogenase B chain	7	256	23.7	36507	6.1	957.6145	1.4	2	2.0985	0.0005	21	K.FIIPQIVK.Y
				913.58453	1.8	2	2.8624	0.2956	1	K.IVVVTAGVR.Q					
				1694.89365	-1.3	2	3.7462	0.2966	1	K.LIAPVAEEEEATVPNNK.I					
				1176.597	6.4	2	2.8992	0.1587	1	K.SADTLWDIQK.D					
				1629.869	6.7	2	5.0858	0.4016	1	K.SLADELALVDVLEDK.L					
				959.558	6.2	2	2.9135	0.1164	4	R.GLTSVINQK.L					
				1290.652	3.8	2	3.5928	0.4448	1	R.VIGSGCNLDSAR.F					
7	P23528	CFL1	Cofilin-1	8	70	51.5	18371	8.1	1223.6381	3.3	2	3.2213	0.3483	1	K.AVLFCLSEDK.K
				1351.737	5.9	2	2.5279	0.0574	6	K.AVLFCLSEDK.N					
				2166.11165	7	2	6.2231	0.5645	1	K.EILVGDVGGTQDDPYATFK.M					
				1561.73	-1	2	4.0859	0.0867	1	K.HELQANCYEEVK.D					
				1832.8549	-2.5	3	4.0433	0.2656	1	K.HELQANCYEEVKDR.C					
				1990.0759	3.8	3	4.2352	0.3407	1	K.KEDLVFVFWAPESAPLK.S					
				1130.647	4.8	2	3.9177	0.3099	1	K.LGGSAVISLEGK.P					
				1337.63465	6.5	2	3.8056	0.3303	1	R.YALYDATYETK.E					

Supplemental Table 1 (continued)

No.	Uniprot ID	Name	Description	Sequence Count	Spectrum Count	Sequence Coverage	MolWt	pI	ObsM+H+	ppm	z	XCorr	DeltCN	SpR	Sequence
8	P10909	CLU	Clusterin	7	34	16.7	52495	6.3	1873.99665	3.3	2	5.3043	0.4852	1	K.LFSDSDPTVTVPVEVSR.K
									1117.618	7.2	2	2.7757	0.1959	1	K.TLLSNLEEAK.K
									1245.713	6.5	2	3.1696	0.2532	1	K.TLLSNLEEAKK.K
									1393.7	3	2	4.0304	0.37	1	R.ASSIIDELFQDR.F
									1288.647	7.1	2	3.2366	0.2778	2	R.ELDESLOQVAER.L
									1245.70965	3.8	2	2.8017	0.1448	3	R.KTLLSNLEEAK.K
2314.18165	1.9	3	2.8497	0.116	15	R.VTTVASHTSDSQVPSGVTEVVVK.L									
9	P05090	APOD	Apolipoprotein D	3	9	20.1	21276	5.1	1699.822	6.6	2	3.8704	0.3679	1	K.CPNPPVQENFDVVK.Y
									1230.67	1	2	3.4477	0.2192	1	K.NILTSNNIDVK.K
									1423.7522	6.7	2	2.9596	0.2164	11	R.NPNLPPEVDSLK.N
10	P07339	CTSD	Cathepsin D	4	75	15.5	44552	6.5	2047.05365	-3.2	2	3.7367	0.352	1	K.AIGAVPLIQGEYM*IPCEK.V
									1239.62165	2.1	2	3.6871	0.3827	1	K.FDGILGMAYPR.I
									1803.81865	6.7	2	4.647	0.073	1	R.DPDAQPGGELM*LGGTDSK.Y
									1959.043	3.2	2	4.5561	0.4371	1	R.ISVNNVLPVFDNLMQK.L
11	O00299	CLIC1	Chloride intracellular channel protein 1	5	5	27.9	26792	5.2	1975.012	-4.3	2	5.106	0.0375	1	K.FLDGNETLADCNLLPK.L
									1281.667	-1.2	2	3.6909	0.3248	1	K.GVTFNVTTVDTK.R
									1844.98	2.6	2	4.3598	0.5206	1	K.LAALNPESNTAGLDIFAK.F
									1328.6461	1.5	2	2.811	0.2444	2	K.NSNPALNDNLEK.G
									1065.617	0.5	2	2.4933	0.0695	1	R.LFM*VLWLK.G
12	P15121	AKR1B1	Aldose reductase	4	13	21	35722	7	3262.67605	0.6	3	3.2635	0.3584	1	K.GIVVTAYSPGSDRPPWAKPEDPSLLEDPR.I
									1131.624	0.8	2	2.571	0.0728	5	K.M*PILGLTWK.S
									901.5472	0.7	2	2.6268	0.0717	9	K.TTAQVLIR.F
									2260.14765	2	2	5.4565	0.4768	1	K.YKPAVNQIECHPYLTQEK.L
13	Q9NP08	HMX1	Homeobox protein HMX1	1	1	4.6	39225	11.6	1372.62865	-4.8	2	3.0886	0.0265	3	R.SGAAGSGGAGAWPGGR.H
14	Q7Z4N2	TRPM1	Melastatin 1	1	1	1	174417	6.9	1880.9133	3.5	2	3.4248	0.0074	25	K.AQSHQLFAIM*ECM*K.K
15	O60888	CUTA	Protein CutA	1	1	15.1	19116	5.5	3140.62965	3	3	6.4221	0.4185	1	R.SVHPYEVAEIALPVEQGNFPYLQWVR.Q
16	Q3SYB4	SERPINB12	SERPINB12 protein	1	1	2.4	48446	5.4	1153.58365	-1	2	2.3854	0.213	10	K.TDYTLSIANR.L

Note: Human-specific peptides are indicated in red.

Supplemental Table 2. Normalized MRM peak area for peptides and proteins (average) in individual samples.

Sample Classification	Histotype ¹	Sample Code	Type_Model	CLIC1				PRDX6				CTSD-30 kDa		
				GVTFNVTVDTK (641.3/877.5)	NSNPALNDNLEK (664.8/1013.5)	LAALNPESNTAGLDIFAK (923.0/1136.6)	Average	VVVFVFGPK (504.3/809.4)	LSILYPATTGR (596.3/765.4)	LFPPIIDDR (543.3/728.4)	Average	QVFGKATK (440.2/652.2)	VGFAEAAAR (410.7/721.4)	Average
Stage 3	MC	T_455	Cancer	0.779	0.760	0.701	0.747	0.466	0.841	0.769	0.692	1.998	2.135	2.066
Stage 4	SP	T_474	Cancer	1.839	1.638	1.864	1.780	0.645	1.281	1.147	1.024	2.631	2.541	2.586
Stage 3	EN	T_475	Cancer	0.877	0.753	0.799	0.810	0.361	0.738	0.622	0.574	0.409	0.447	0.428
Stage 3	MU	T_476	Cancer	1.420	1.195	0.955	1.190	0.596	0.856	0.904	0.785	0.673	0.700	0.686
Stage 3	SP	T_478	Cancer	0.605	0.348	0.561	0.505	0.915	0.410	0.523	0.616	1.044	0.799	0.921
Stage 4	SP	T_482	Cancer	2.597	2.206	2.158	2.320	0.797	1.248	1.228	1.091	1.618	1.469	1.544
Stage 3	SP	T_536	Cancer	1.612	1.751	1.438	1.600	7.542	3.226	3.955	4.908	0.954	0.694	0.824
Stage 3	SP	T_539	Cancer	0.998	0.960	0.982	0.980	0.719	0.393	0.441	0.518	1.251	1.493	1.372
Stage 3	SP	T_541	Cancer	0.062	0.066	0.060	0.063	0.056	0.352	0.061	0.156	0.506	0.641	0.573
Stage 3	SP	T_543	Cancer	0.430	0.210	0.368	0.336	0.221	0.507	0.362	0.364	0.194	0.303	0.249
Stage 3	SP	T_553	Cancer	1.558	1.610	2.081	1.749	2.256	2.540	3.352	2.716	1.218	1.420	1.319
Stage 3	SP	T_556	Cancer	1.762	3.158	1.920	2.280	1.696	2.254	2.366	2.105	1.429	1.246	1.338
Stage 4	UN	T_557	Cancer	1.540	1.542	1.612	1.565	0.403	0.728	0.653	0.594	1.831	1.817	1.824
Stage 3	UN	T_577	Cancer	0.288	0.394	0.528	0.404	0.381	0.956	0.422	0.586	0.672	0.631	0.651
Stage 3	AD	T_600	Cancer	0.770	0.775	1.090	0.878	0.325	0.512	0.369	0.402	0.720	0.594	0.657
Stage 3	UN	T_602	Cancer	0.215	0.234	0.141	0.197	0.147	0.410	0.243	0.267	0.079	0.219	0.149
Stage 3	MU	T_603	Cancer	0.455	0.305	0.448	0.403	0.301	0.501	0.383	0.395	0.444	0.410	0.427
Stage 3	SP	T_604	Cancer	0.192	0.094	0.294	0.193	0.174	0.246	0.200	0.207	0.330	0.442	0.386
Benign		T_B-23	Normal	0.234	0.263	0.127	0.208	0.227	0.331	0.213	0.257	0.355	0.351	0.353
Benign		T_B-25	Normal	0.168	0.150	0.147	0.155	0.133	0.419	0.303	0.285	0.371	0.493	0.432
Benign		T_B-70	Normal	0.476	0.068	0.341	0.295	0.406	0.521	0.623	0.517	0.163	0.081	0.122
Benign		T_B-77	Normal	0.685	0.164	0.609	0.486	0.359	0.850	0.586	0.598	0.110	0.131	0.120
Benign		T_B-79	Normal	0.417	0.213	0.435	0.355	0.203	0.429	0.262	0.298	0.234	0.344	0.289
Benign		T_B-80	Normal	1.218	0.204	1.091	0.837	0.328	0.378	0.498	0.401	0.335	0.362	0.349
Benign		T_B-81	Normal	0.188	0.126	0.154	0.156	0.117	0.121	0.106	0.114	0.305	0.248	0.276
Benign		T_B-82	Normal	0.635	0.832	1.579	1.015	1.416	2.048	2.160	1.875	0.143	0.207	0.175
Benign		T_B-83	Normal	0.400	0.380	0.475	0.418	0.593	0.945	1.021	0.853	0.129	0.297	0.213
Normal		WCS-02	Normal	0.057	0.043	0.161	0.087	0.120	0.436	0.142	0.233	0.679	0.600	0.639
Normal		WCS-04	Normal	0.297	0.110	0.341	0.250	0.070	0.265	0.055	0.130	0.382	0.359	0.370
Normal		WCS-12	Normal	0.082	0.076	0.053	0.070	0.050	0.185	0.055	0.097	0.849	0.645	0.747
Normal		WCS-13	Normal	0.062	0.034	0.060	0.052	0.021	0.236	0.044	0.101	0.402	0.337	0.369
Normal		WCS-14	Normal	0.203	0.090	0.174	0.156	0.262	0.720	0.557	0.513	0.234	0.175	0.204
Normal		WCS-15	Normal	0.113	0.162	0.261	0.179	0.165	0.321	0.184	0.223	0.708	0.744	0.726

¹ MC, Mucinous; SP, Serous papillary; EN, Endometrioid; MU, Mullerian; UN, Undifferentiated; AD, Serous papillary adenocarcinoma

Supplemental Table 3. Sensitivity, Specificity, and Positive and Negative Predicted Values for Tumor vs. Normal and Benign^a

Biomarker	Cut-point^b	Sensitivity	Specificity	Positive Predictive Value	Negative Predictive Value
CTSD-30 kDa	0.378	88.9	73.3	80.0	84.6
CLIC1	0.495	66.7	86.7	85.7	68.4
PRDX6	0.517	66.7	80.0	80.0	66.7

^aCases are 18 tumor samples and 15 normal/benign samples.

^bOptimal cut-points expressed as normalized relative abundance and defined by maximizing sensitivity and specificity.